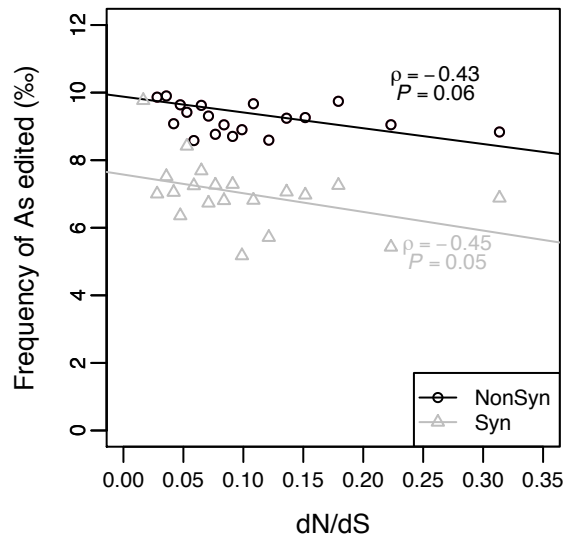
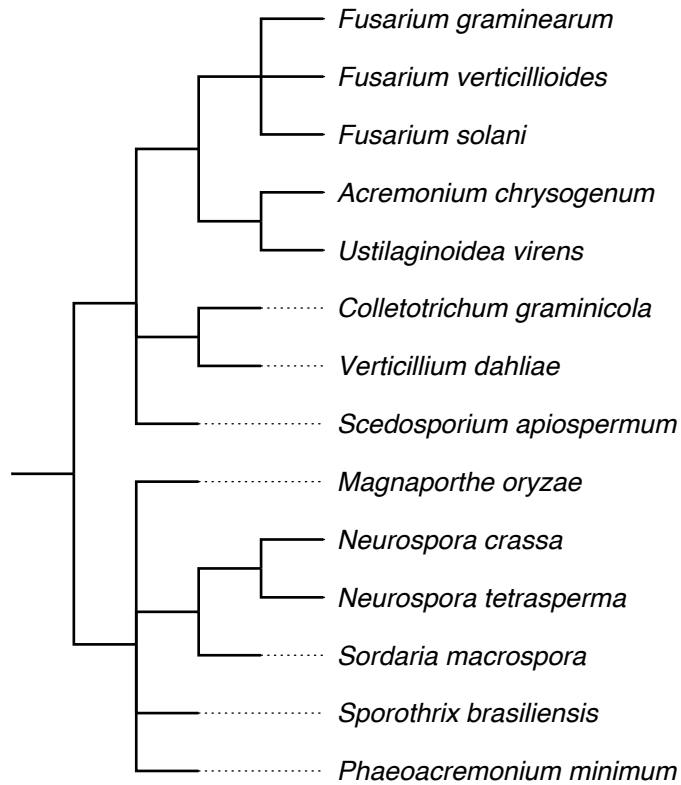


## SUPPLEMENTARY MATERIALS



**Supplementary Figure S1. Correlation between the frequencies of nonsynonymous or synonymous random editable sites and the medians of dN/dS ratios for each group.** The random editable sites are generated by randomly selecting 21,095 editable A sites with U at the -1 position from the coding regions of the 5,043 edited genes. Each point represents a group with 5% of edited genes. Rho and  $P$ -value are from statistical analyses with two-tailed Spearman's rank correlation test.



**Supplementary Figure S2. The tree of 14 Sordariomycete fungi used in the conservation analysis.** The tree was retrieved from NCBI taxonomy database. All the proteins and coding regions sequences were obtained from Ensembl except those of *Magnaporthe oryzae*, *Neurospora crassa*, and *Neurospora tetrasperma* which were downloaded from Broad Institute.