Figure S1  Consensus motifs identified by MEME software in 41 neighboring bases centered around the four main editing types: C to U (A), A to G (B), G to A (C), and U to C (D). The position of each base in this motif is shown on the horizontal ordinate. Vertical ordinate shows the probability of each base occurring at the specific position.
Figure S2  Nucleotide composition of flanking regions (20 bp both upstream and downstream) of the four main RNA editing types: C to U (A), U to C (B), A to G (C), and G to A (D).
Figure S3  Domain organization of seven PPR proteins. PPR domains in red were identified from the Pfam database by using Pfamscan.
Figure S4  Validation of RNA editing sites for different editing degrees. Four main types of RNA editing were listed at different editing degrees, including A) low (0% to 5%), B) medium (30% to 60%), and C) high (80% to 100%) editing degrees.
Figure S5 Gene ontology (GO) classification of genes affected by RNA editing. GO terms were obtained according to InterPro ID. These genes were classified into cellular component, molecular function, and biological process, as well as their subclasses by using GO databases.
Figure S6  RNA editing of genes involved in the mevalonate pathway. Each asterisk represents one editing locus on this gene. A total of 135 loci were subjected to RNA editing in CYPs.
Tables S1-S14

Table S1 List of data stored in GenBank and used in this paper.

Table S2 List of RNA editing sites from fruiting bodies identified in this study. Sequencing depth was generated from RNASeq-Illumina datasets.

Table S3 Target prediction of seven PPR proteins using TargetP v1.0.

Table S4 Target prediction of seven PPR proteins using Predotar v1.03.

Table S5 PCR validation of predicted RNA editing sites based on Sanger sequencing. Validated results were shown as three types in this table: 'TRUE' indicates a true discovery, 'FALSE' indicates a false prediction, 'Not predicted' indicates that a true locus was not predicted.

Table S6 PCR primers used for validation of inferred RNA editing sites.

Table S7 KEGG enrichment results of genes containing RNA editing sites.

Table S8 List of RNA editing genes identified as CAZy.

Table S9 List of editing sites identified in genes involved in lignin degradation.

Table S10 List of editing sites identified in genes involved in transcriptional regulation.

Table S11 List of editing sites identified in genes involved in MVA pathway.

Table S12 List of editing sites identified in CYP genes.

Table S13 List of editing sites identified in genes involved in polysaccharide biosynthesis.

Table S14 Changes for start codons and generation for stop codons.