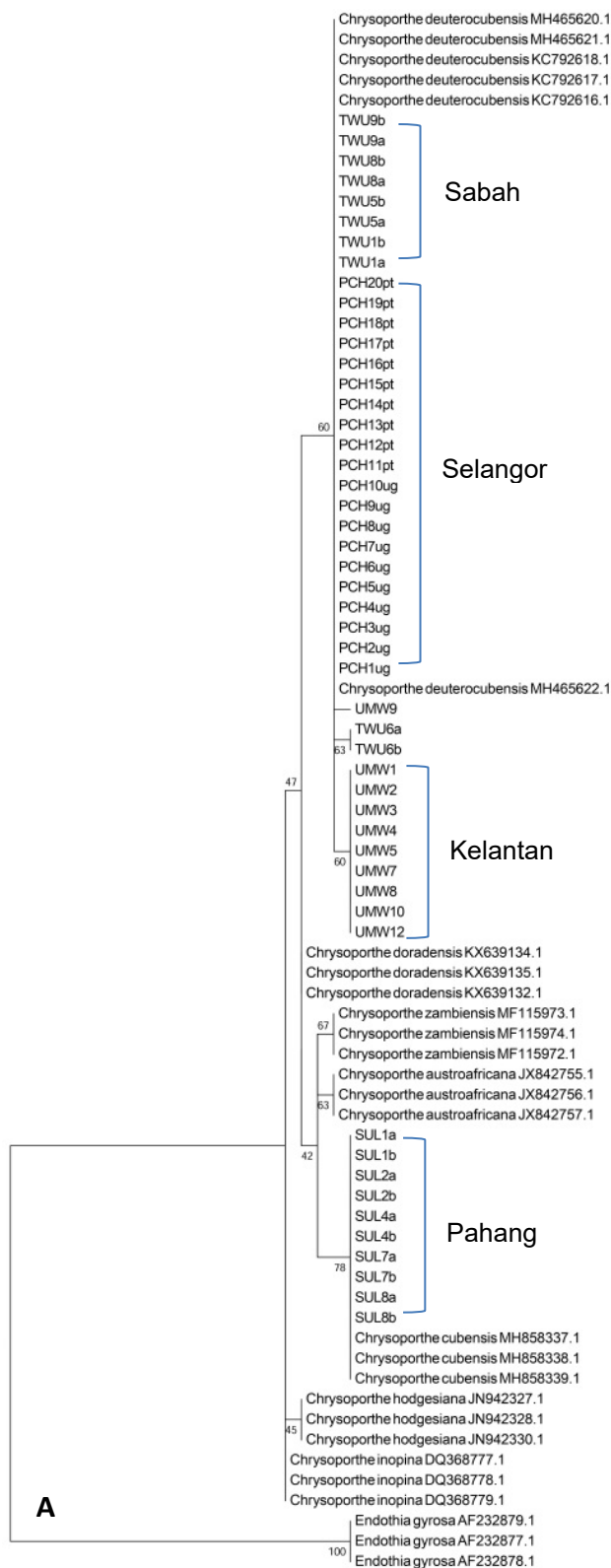
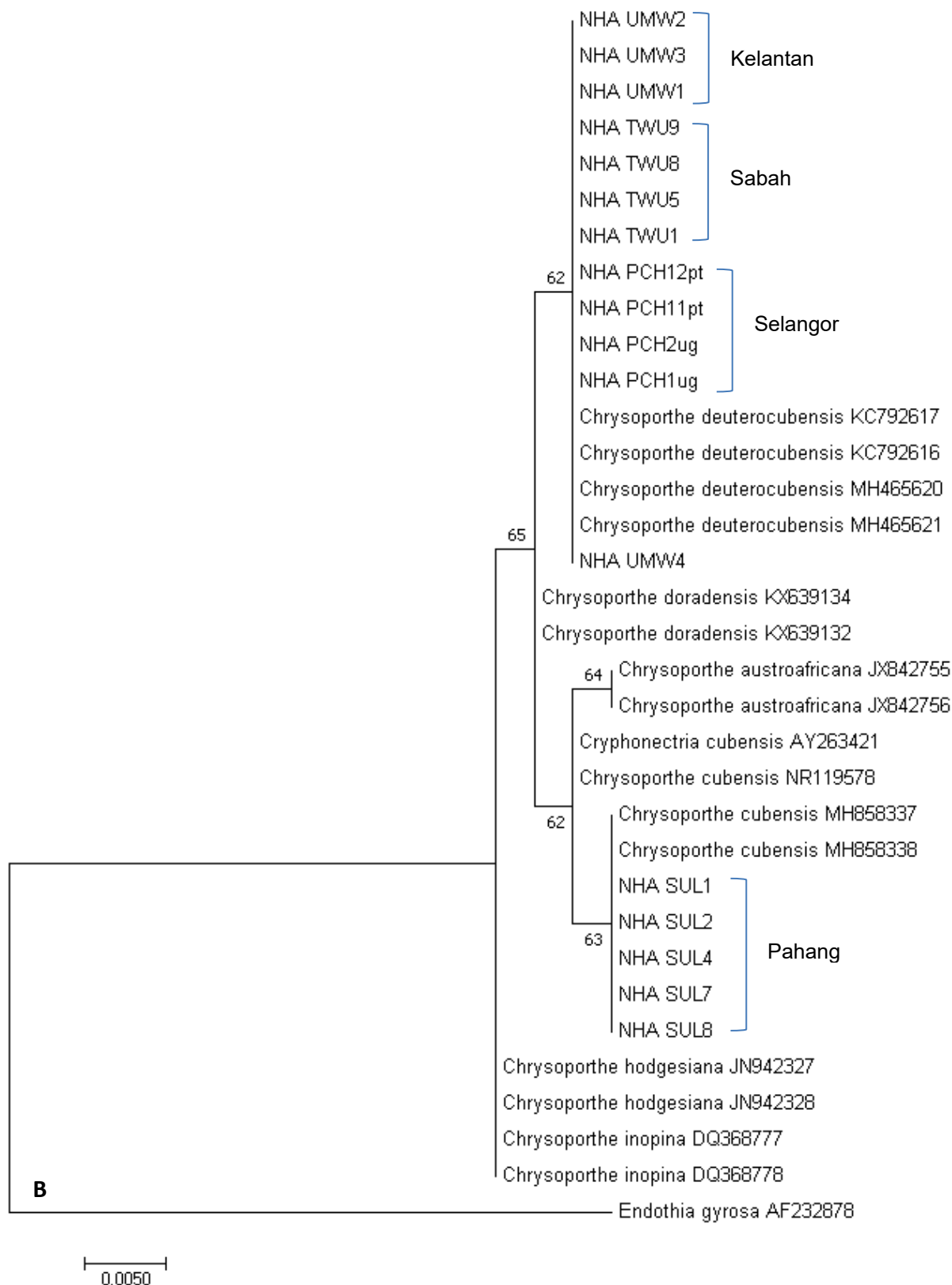


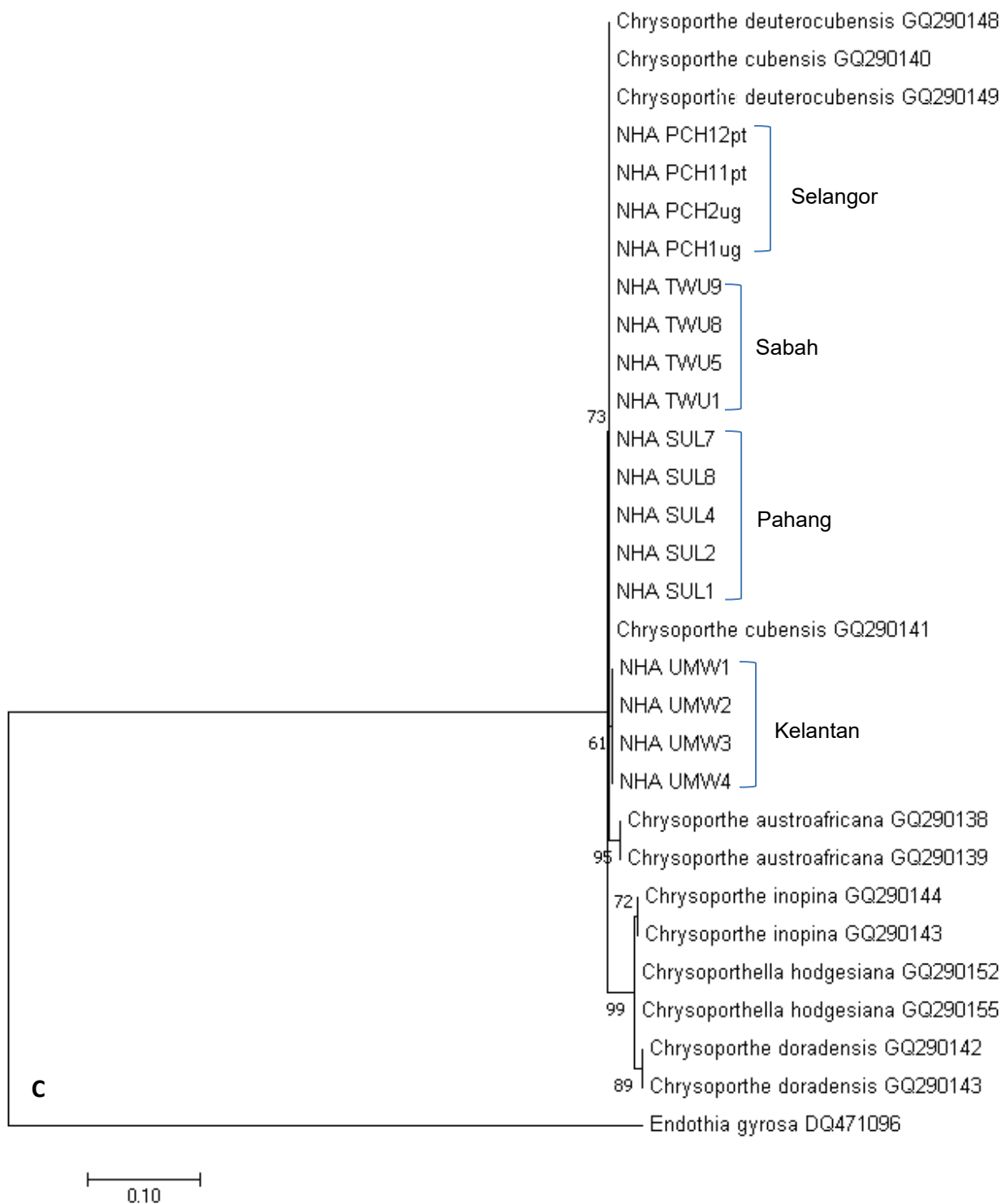
Supplementary Figure S1: Alignment of a region of partial ITS sequence showed single polymorphism between *Chrysoporthe cubensis* and *Chrysoporthe deuterocubensis* with the reference sequences of *Chrysoporthe cubensis* MH858337 and *Chrysoporthe deuterocubensis* MH465621 respectively. Red arrow indicated polymorphism site.



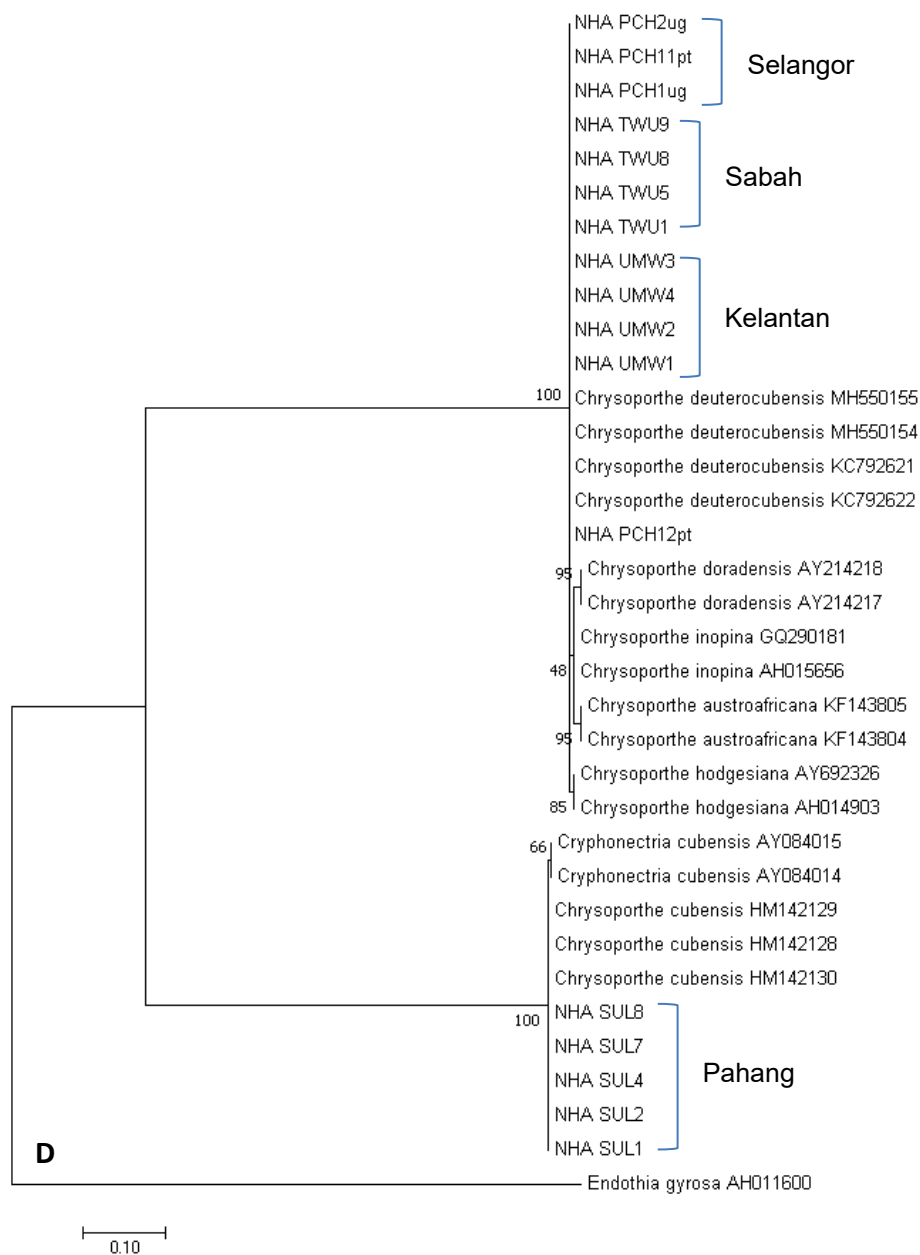
Supplementary Figure S2 (A): Phylogram from a maximum likelihood of six *Chrysoporthe* spp. and *Endothia gyrosa* as outgroup based on the combined ITS, β -tubulin 2 gene and TEF-1 α , UltraFast Bootstrap values and genealogical concordance factors are indicated on branch nodes. The isolates identified in this study as *Chrysoporthe cubensis* and *Chrysoporthe deuterocubensis* from Malaysia



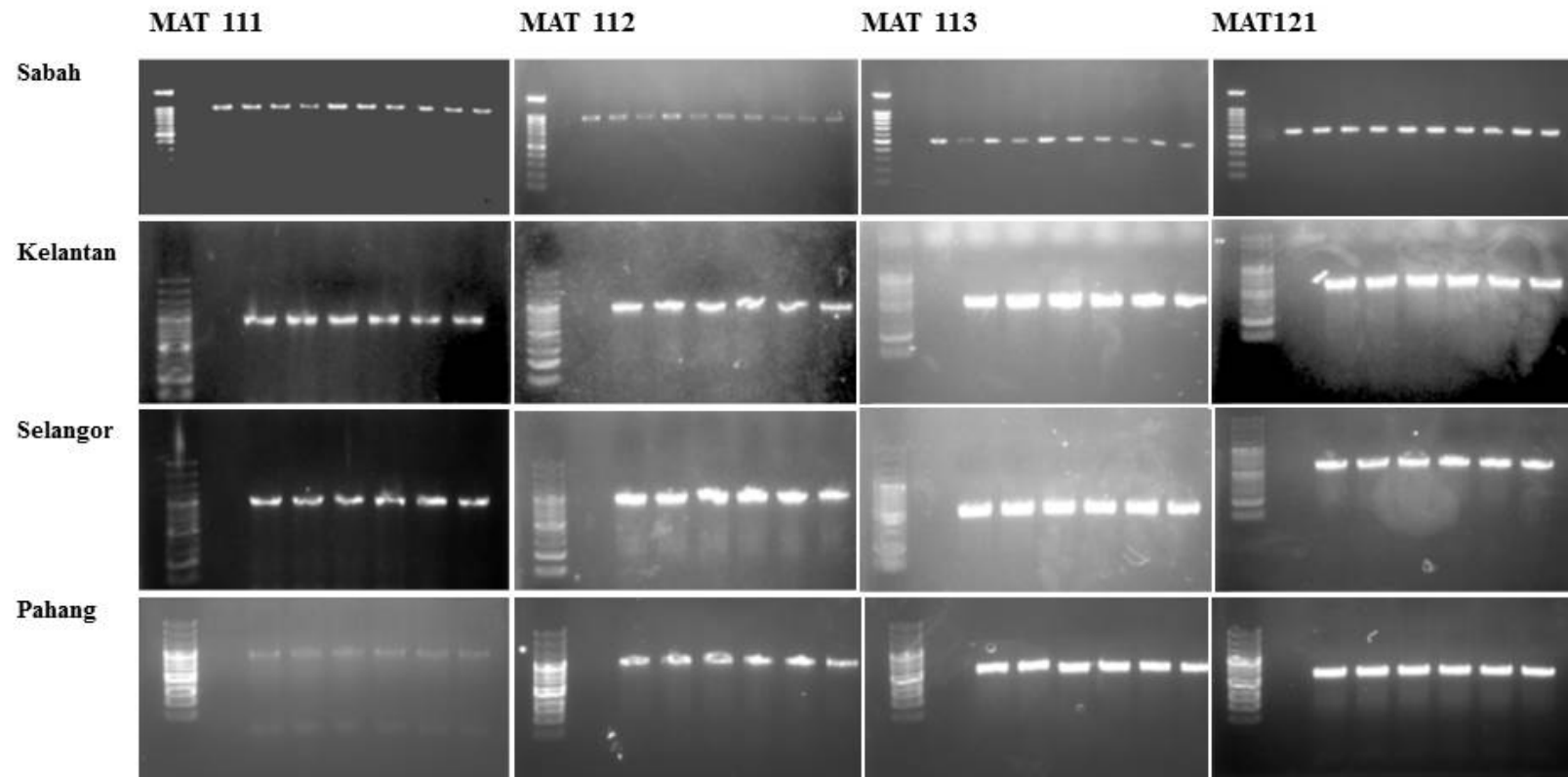
Supplementary Figure S2 (B): Phylogram from a maximum likelihood of six *Chrysoporthe* spp. and *Endothia gyrosa* as outgroup based on the ITS regions. UltraFast Bootstrap values and genealogical concordance factors are indicated on branch nodes. The isolates identified in this study as *Chrysoporthe deuterocubensis* fall within the reference *Chrysoporthe deuterocubensis* MH465621 clade and *Chrysoporthe cubensis* fall within the reference *Chrysoporthe cubensis* MH858337 clade



Supplementary Figure S2 (C): Phylogram from a maximum likelihood search of six *Chrysoporthe* spp. and *Endothia gyrosa* as outgroup based on the β -tubulin 2 region. UltraFast Bootstrap values and genealogical concordance factors are indicated on branch nodes. The isolates identified in this study as *Chrysoporthe deuterocubensis* fall within the reference *Chrysoporthe deuterocubensis* CQ290149 clade and *Chrysoporthe cubensis* fall within the reference *Chrysoporthe cubensis* CQ290141



Supplementary Figure S2 (D): Phylogram from a maximum likelihood of six *Chrysoporthe* spp. and *Endothia gyrosa* as outgroup based on the TEF-1 α . UltraFast Bootstrap values and genealogical concordance factors are indicated on branch nodes. The isolates identified in this study as *Chrysoporthe deuterocubensis* fall within the reference *Chrysoporthe deuterocubensis* MH550155 clade and *Chrysoporthe cubensis* fall within the reference *Chrysoporthe cubensis* HM142130 clade



Supplementary Figure S3: Amplicon of *MAT1-1* locus genes and *MAT1-2* locus gene. a. *MAT1-1-1* 842bp, b. *MAT1-1-2* 912bp, c. *MAT1-1-3* 467bp and d. *MAT1-2-1* 536bp