

Fig. S1



Fig. S1. Sample collection by us and other people from various regions in China. **A.** S.L. Han collecting rice spikelet rot samples at Jiangsu Province, Yangzhou city. **B.** Y.J. Li collecting diseased maize samples at Shanxi Province, Yangquan city. **C.** M.Y. Wang collecting wheat crown rot samples at Shandong Province, Taian city. **D.** S.Q. Wang collecting diseased maize samples at Guangdong Province, Qingyuan city. **E.** X.Y. Liu collecting diseased maize samples at Shandong Province, Jinan city. **F.** Y.M. Wu collecting maize ear rot samples at Guangdong Province, Meizhou city. **G.** M.L. Feng collecting rice spikelet rot samples at Sichuan Province, Mianyang city. **H.** G.J. Han collecting maize ear rot samples at Shandong Province, Rizhao city. **I–N.** Local collectors showing photos of diseased cereals to us to confirm the occurrence of cereal diseases. **O–S.** We received the diseased samples and information from local collectors.

Fig. S1 (Continued).



Fig. S2. (Continued).

Fig. S2

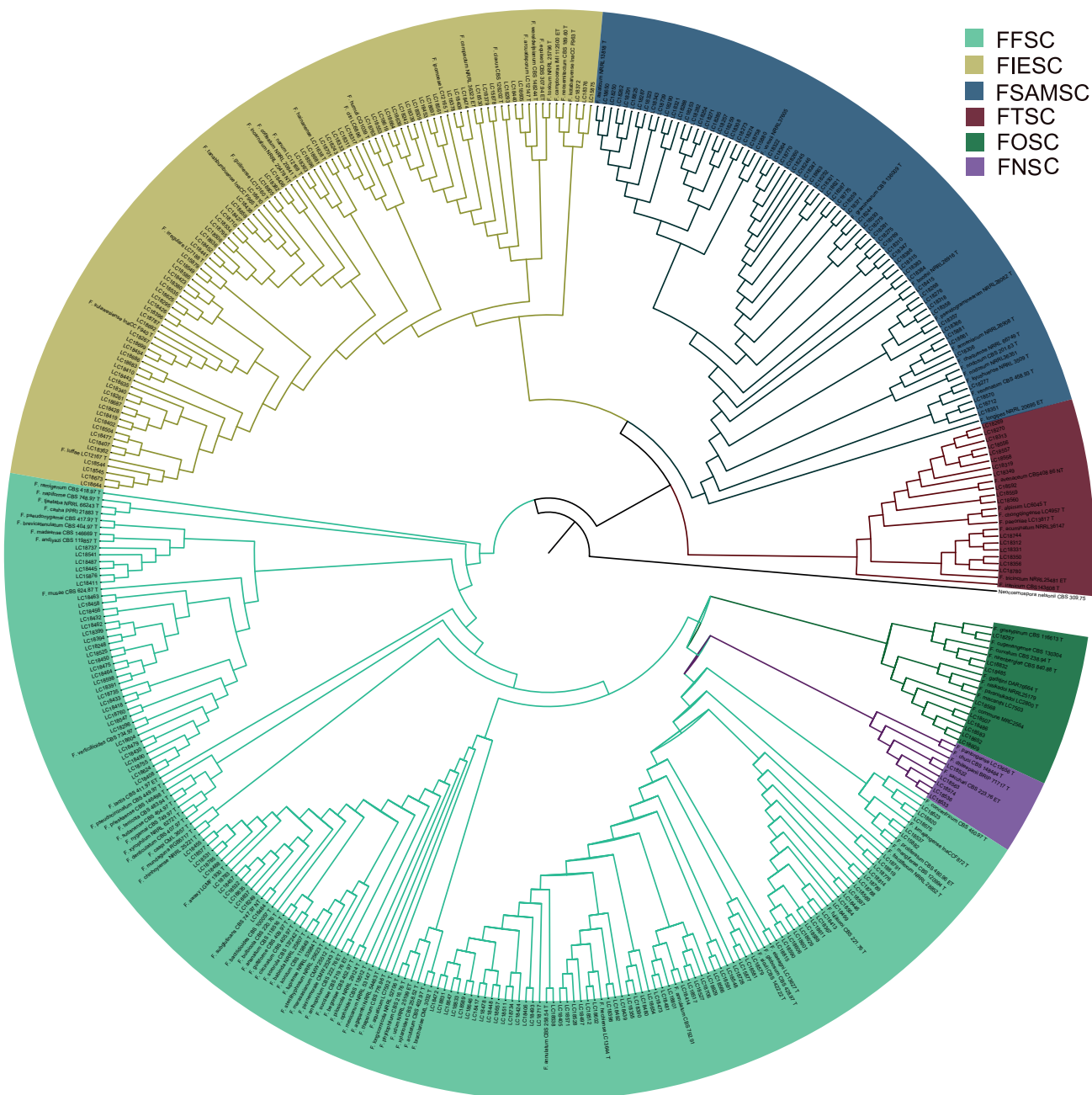


Fig. S2. Phylogeny inferred based on the combined *rpb2-tef1* gene regions of 608 representative *Fusarium* strains. *Neocosmospora nelsonii* (CBS 309.75) was used as an outgroup. Ex-type, ex-epitype and ex-neotype strains were indicated with T, ET, and NT, respectively. Subdivision of the *Fusarium* clade represent the recognised species complexes, including *F. fujikuroi* SC (FFSC), *F. incarnatum-equiseti* SC (FIESC), *F. nisikadoi* SC (FNESC), *F. oxysporum* SC (FOSC), *F. sambucinum* SC (FSAMSC), and *F. tricinctum* SC (FTSC), which were shown in different colours.

Fig. S3

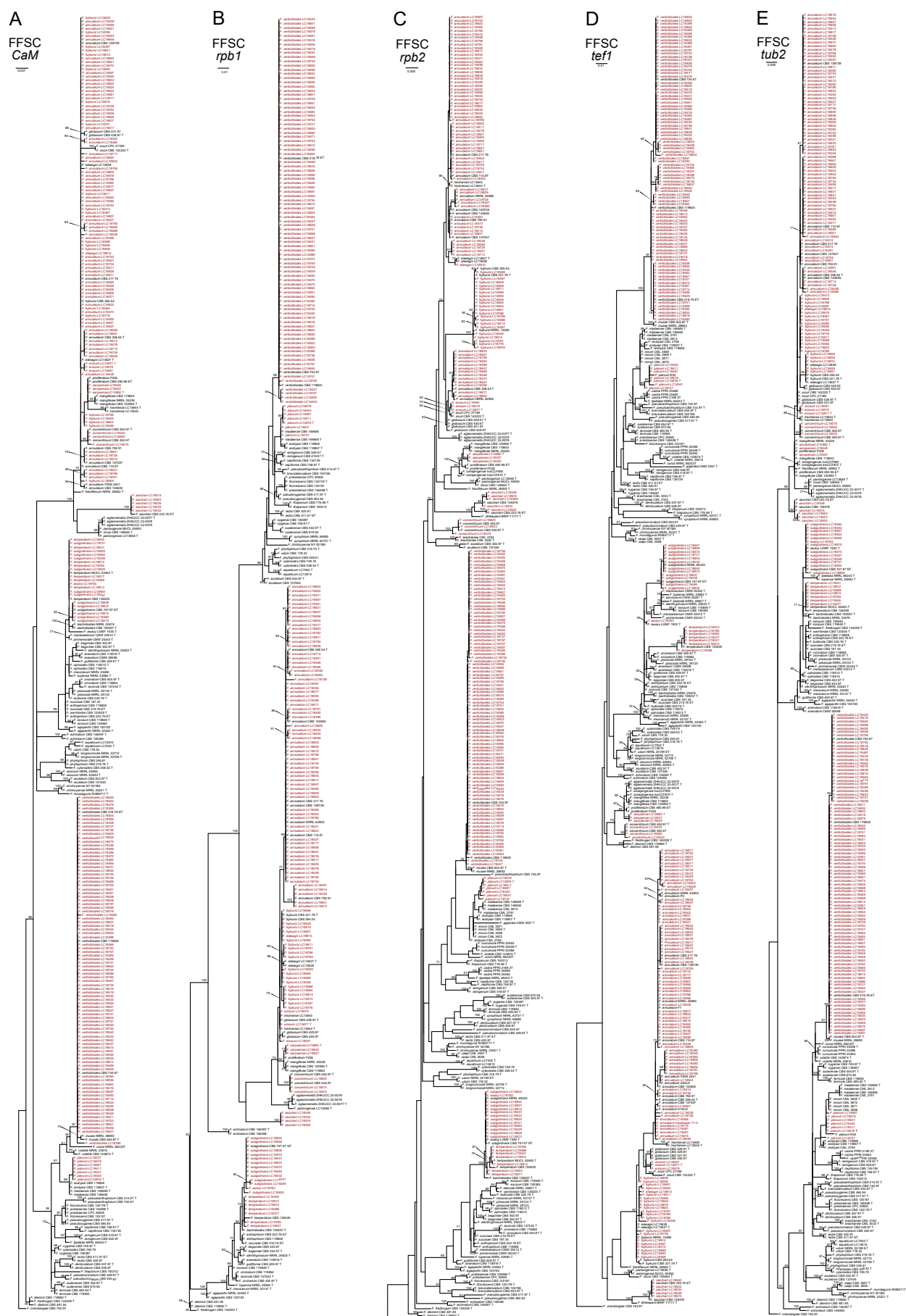


Fig. S3. Phylogeny of the *Fusarium fujikuroi* species complex (FFSC) inferred based on the *CaM* (A), *rpb1* (B), *rpb2* (C), *tef1* (D), and *tub2* (E) loci, respectively. *Fusarium nirenbergiae* (CBS 744.97) was used as an outgroup. Strains sequenced in this study were indicated in red. The RAXML Bootstrap support values (ML-BS > 70 %) were displayed at the nodes. Ex-type, ex-epitype and ex-neotype strains were indicated with T, ET, and NT, respectively.

Fig. S4



Fig. S4. Phylogeny of the *Fusarium incarnatum-equiseti* species complex (FIESC) inferred based on the *CaM* (A), *rbp2* (B), and *tef1* (C) loci, respectively. *Fusarium concolor* (NRRL 13459) was used as an outgroup. Strains sequenced in this study were indicated in red. The RAxML Bootstrap support values (ML-BS > 70 %) were displayed at the nodes. Ex-type, ex-epitype and ex-neotype strains were indicated with T, ET, and NT, respectively.

Fig. S5

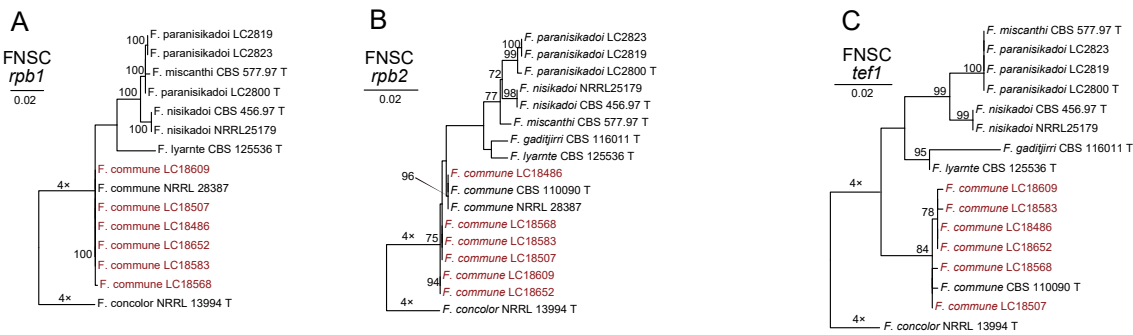


Fig. S5. Phylogeny of the *Fusarium nisikadoi* species complex (FNSC) inferred based on the *rpb1* (A), *rpb2* (B), and *tef1* (C) loci, respectively. *Fusarium concolor* (NRRL 13994) was used as an outgroup. Strains sequenced in this study were indicated in red. The RAxML Bootstrap support values (ML-BS > 70 %) were displayed at the nodes. Ex-type strains were indicated with T.

Fig. S6

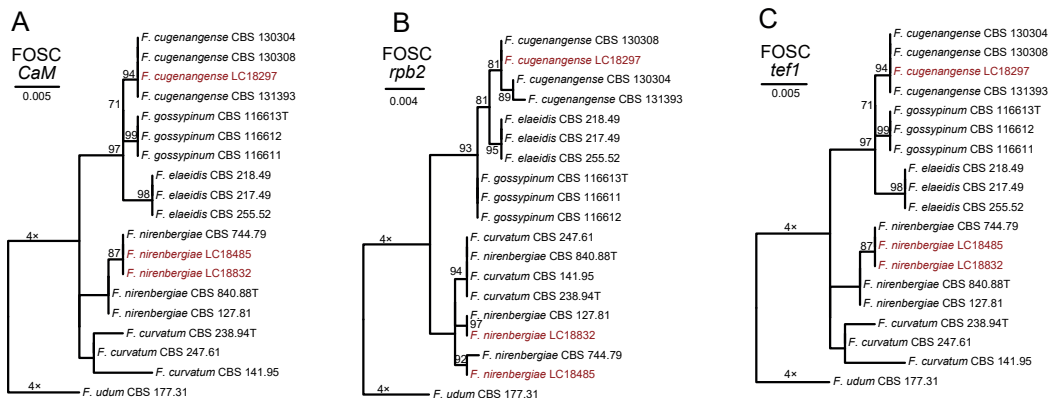


Fig. S6. Phylogeny of the *Fusarium oxysporum* species complex (FOSC) inferred based on the *CaM* (A), *rpb2* (B), and *tef1* (C) loci, respectively. *Fusarium udum* (CBS 177.31) was used as an outgroup. Strains sequenced in this study were indicated in red. The RAxML Bootstrap support values (ML-BS > 70 %) were displayed at the nodes. Ex-type strains were indicated with T.

Fig. S7

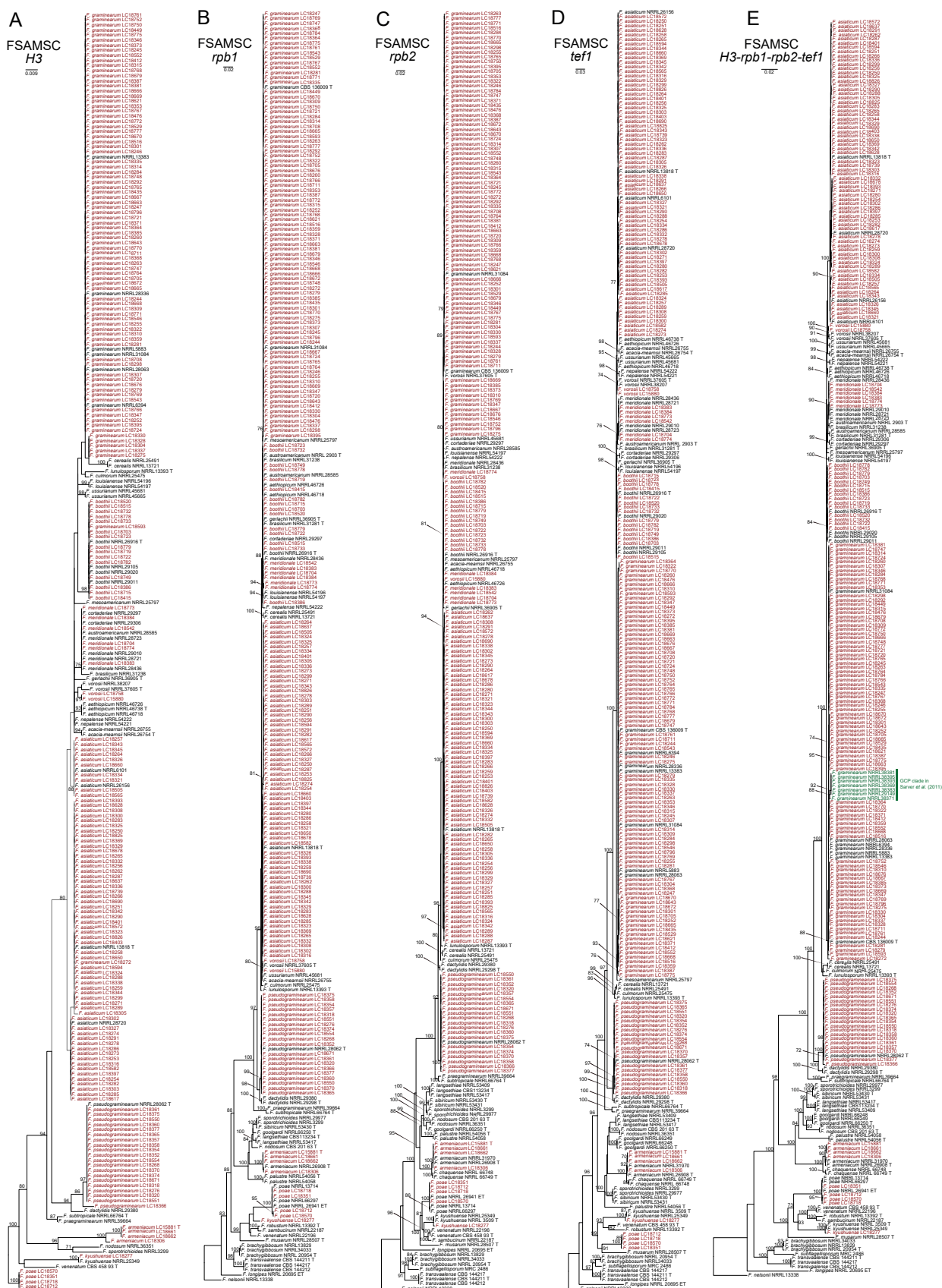


Fig. S7. Phylogeny of the *Fusarium sambucinum* species complex (FSAMSC) inferred based on the *H3* (A), *rpb1* (B), *rpb2* (C), *tef1* (D), and *H3-rpb1-rpb2-tef1* loci (E), respectively. *Fusarium nelsonii* (NRRL 13338) was used as an outgroup. GCP clade in Sarver *et al.* (2011) were indicated in green. Strains sequenced in this study were indicated in red. The RAxML Bootstrap support values (ML-BS > 70 %) were displayed at the nodes. Ex-type, ex-epitype and ex-neotype strains were indicated with T, ET, and NT, respectively.

Fig. S8

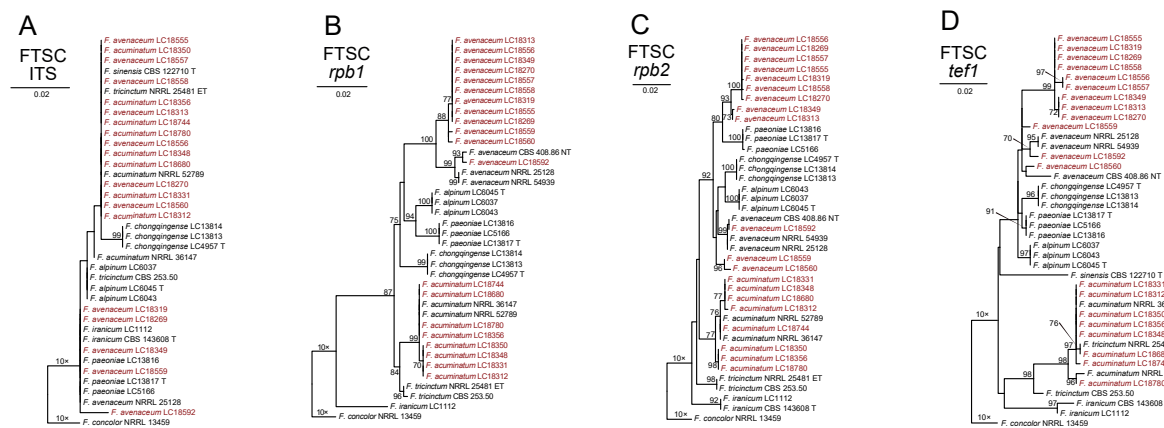


Fig. S8. Phylogeny of the *Fusarium tricinctorum* species complex (FTSC) inferred based on the ITS (A), *rpb1* (B), *rpb2* (C), and *tef1* (D) loci, respectively. *Fusarium udum* (CBS 177.31) was used as an outgroup. Strains sequenced in this study were indicated in red. The RAxML Bootstrap support values (ML-BS > 70 %) were displayed at the nodes. Ex-type, ex-epitype, and ex-neotype strains were indicated with T, ET, and NT, respectively.

Fig. S9

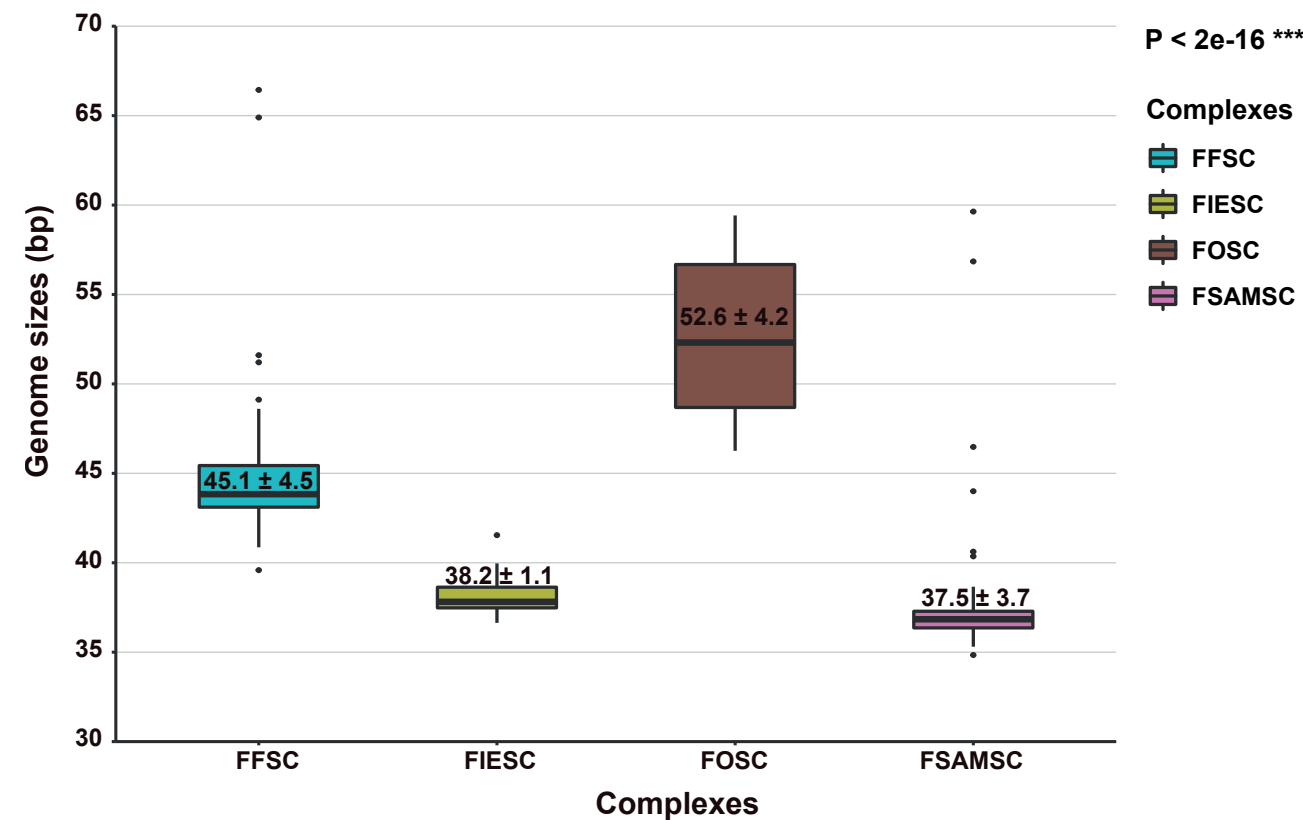


Fig. S9. Genome sizes of the four cereal-associated species-rich complexes (*i.e.*, FFSC, FIESC, FOSC and FSAMSC) differs significantly ($P < 2e-16$), average and standard deviation (av. ± SD) were annotated on the corresponding boxplots.

Fig. S10

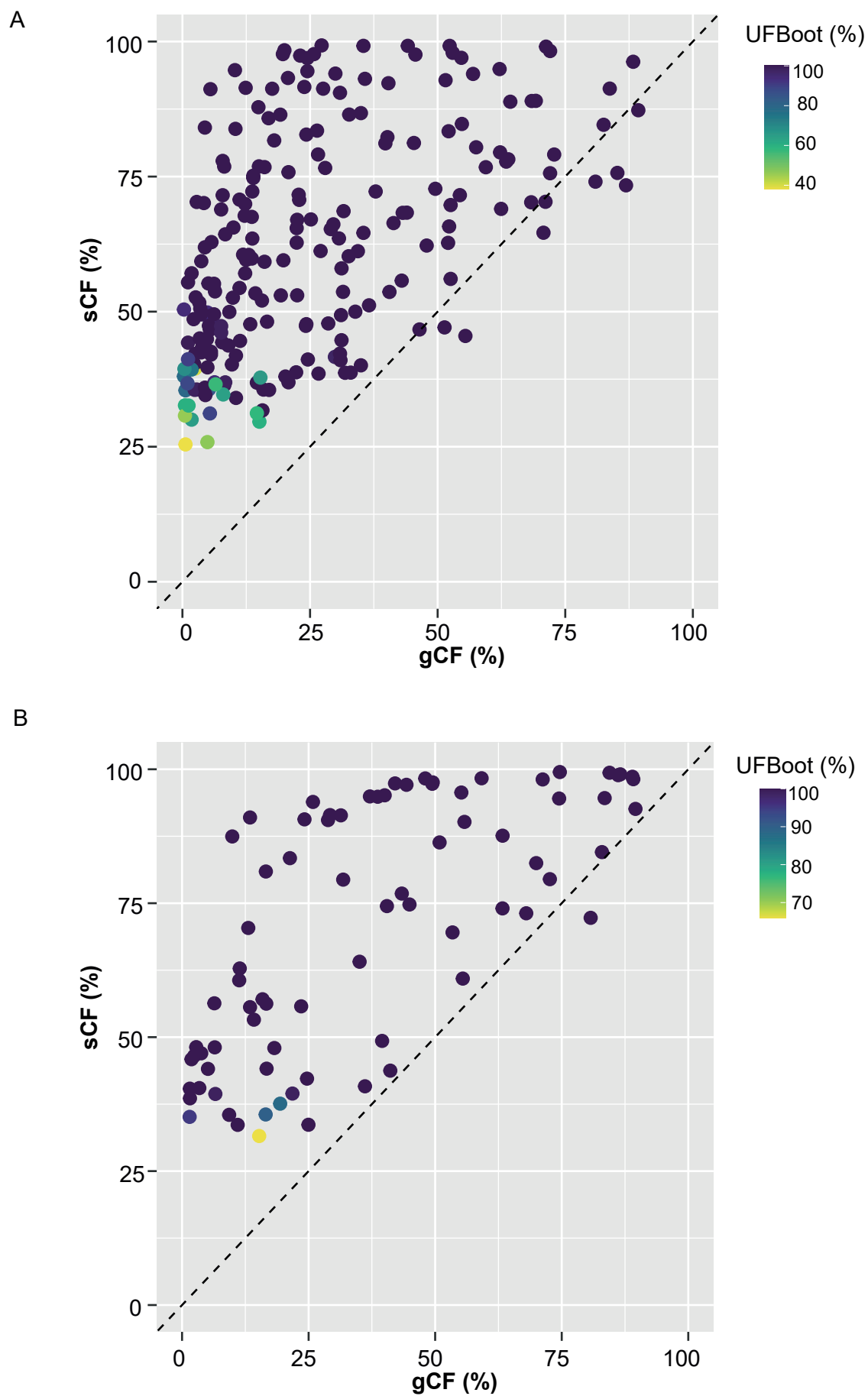


Fig. S10. The scatter plot of gCF values against sCF values for all branches of the phylogenetic tree of Fig. 14 (**A**) and Fig. 15 (**B**) is shown. The shade of colour (bright to dark) indicated the support values of UFBoot (0–100).

Fig. S11

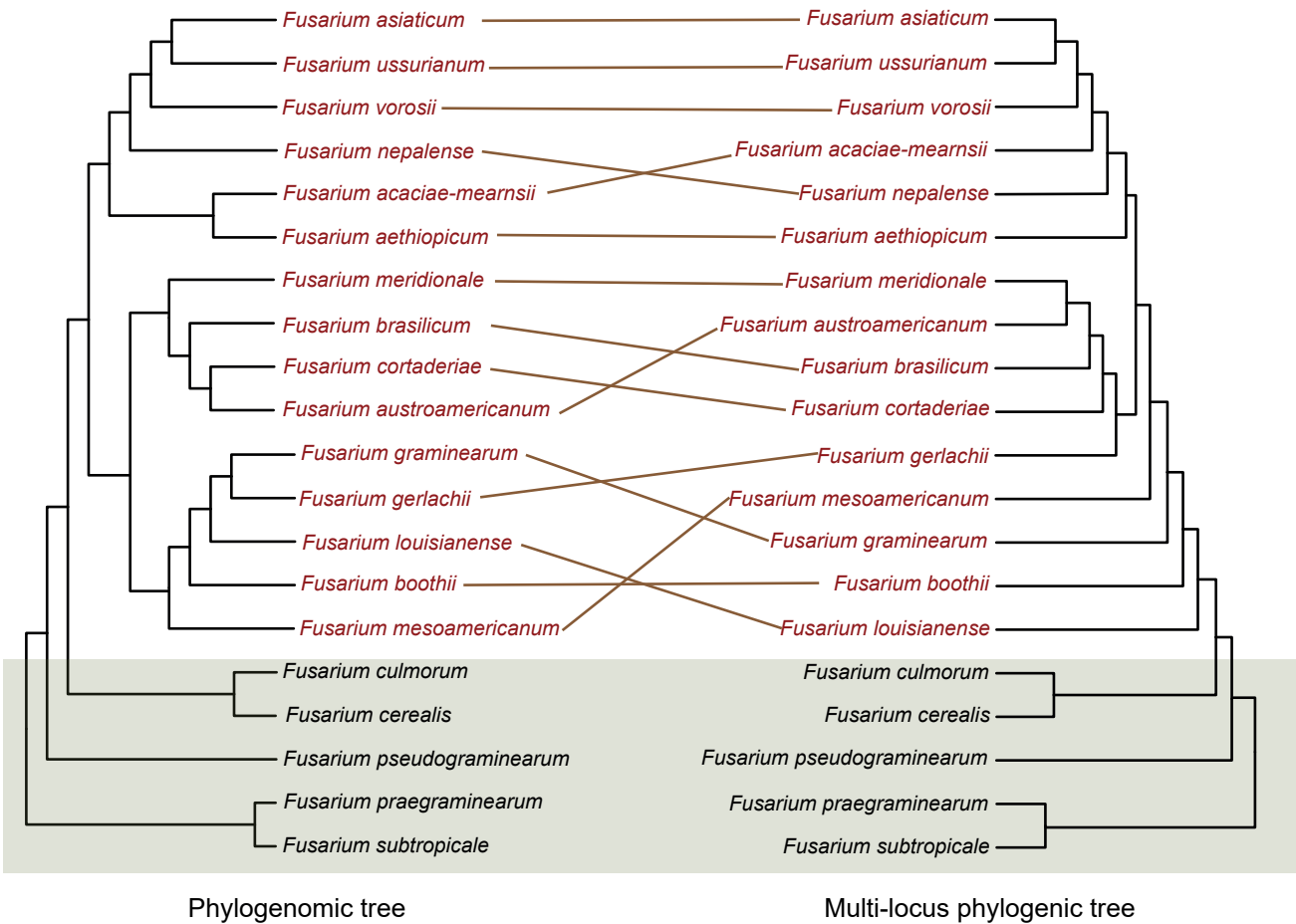


Fig. S11. The topology conflicts within the *Fg* clade, between the phylogenomic tree and the multi-locus phylogenetic tree.

Fig. S12

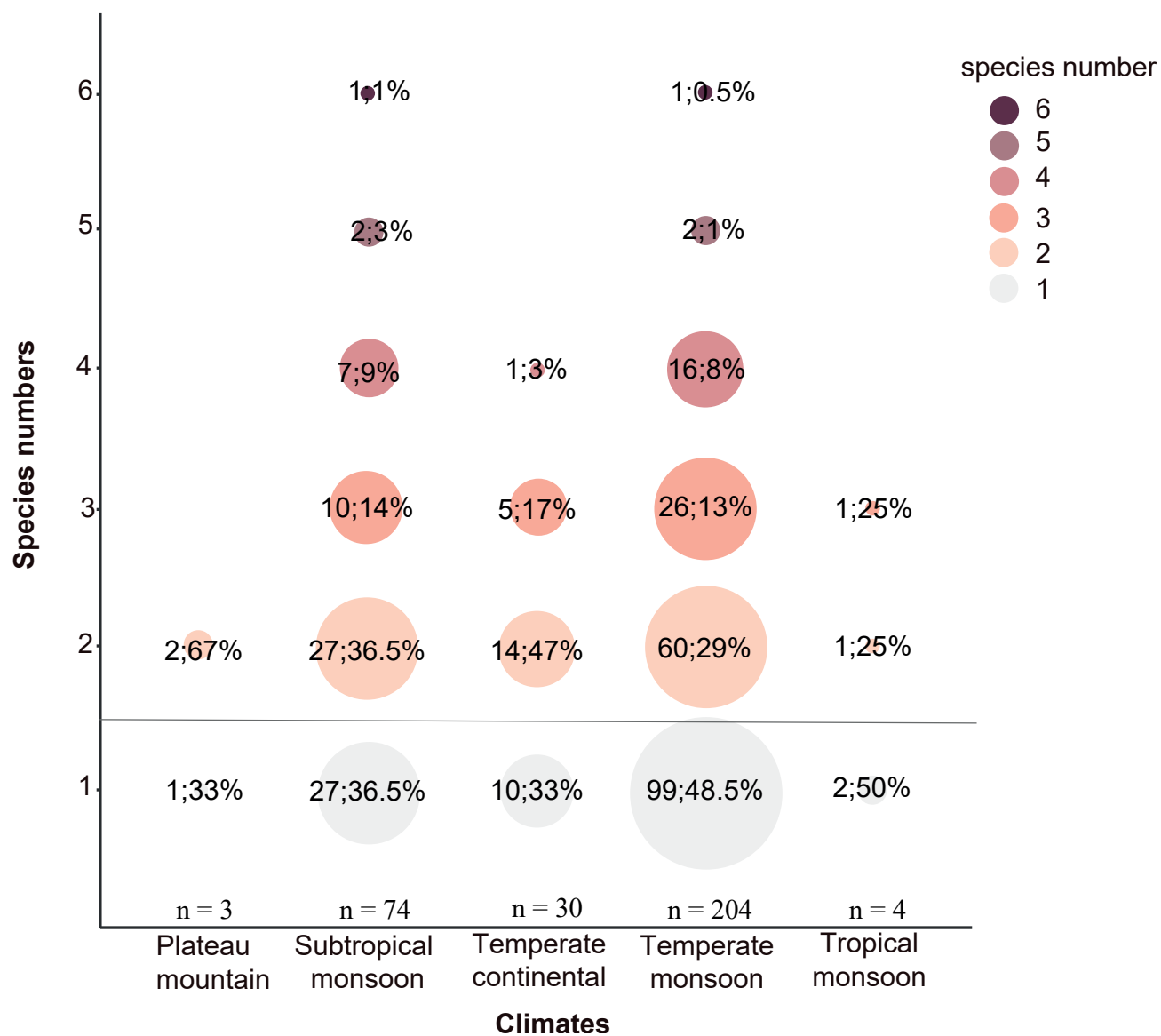


Fig. S12. The total number of species discovered in samples collected from various climate zones. The number on the diagram indicates the species number detected from different climate zone, and the percentage indicates the proportion of samples collected. The number of species co-occurrence on one sample was represented by different colour.