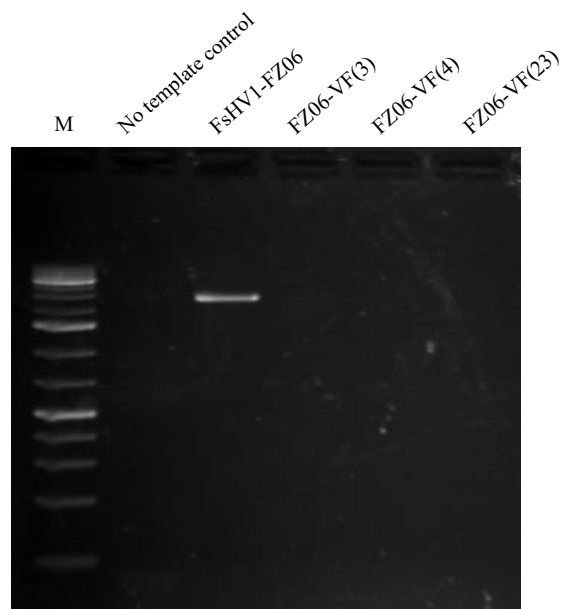
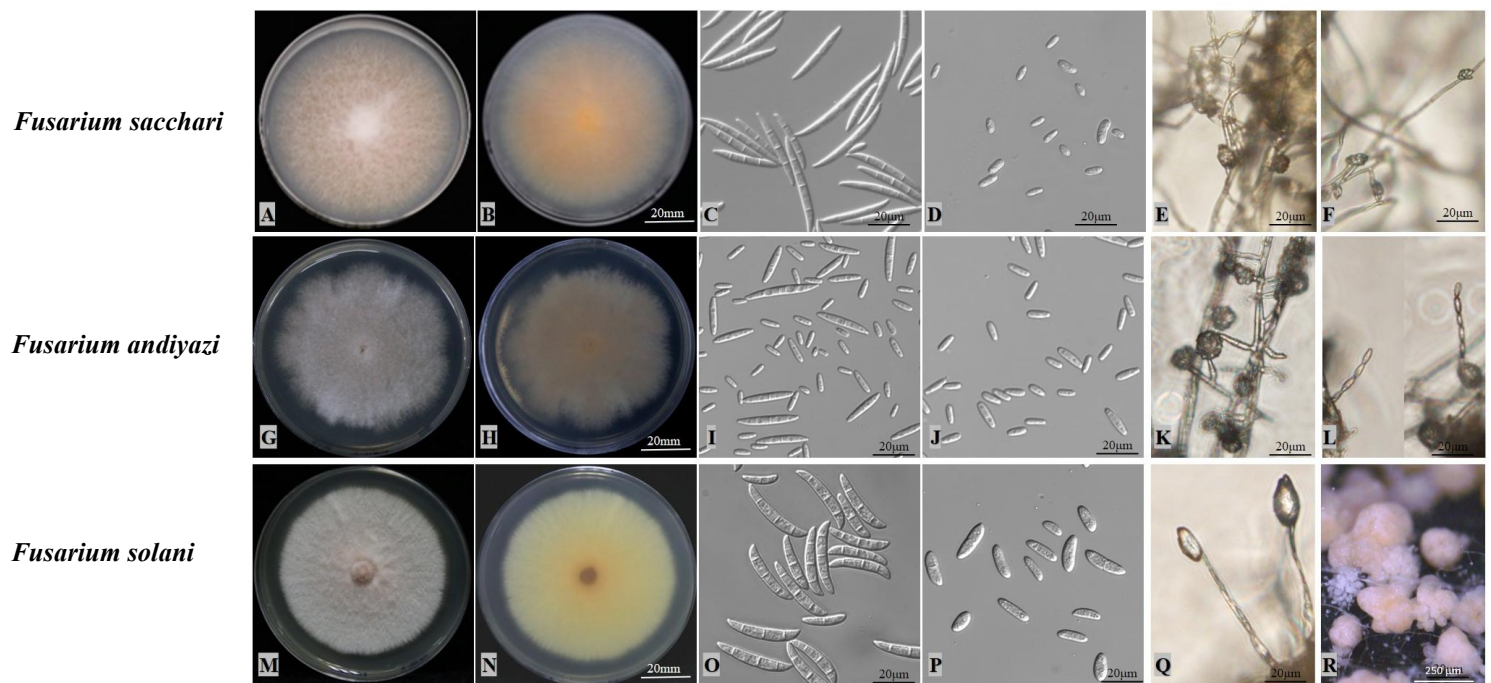


## Supplementary Figure S1.



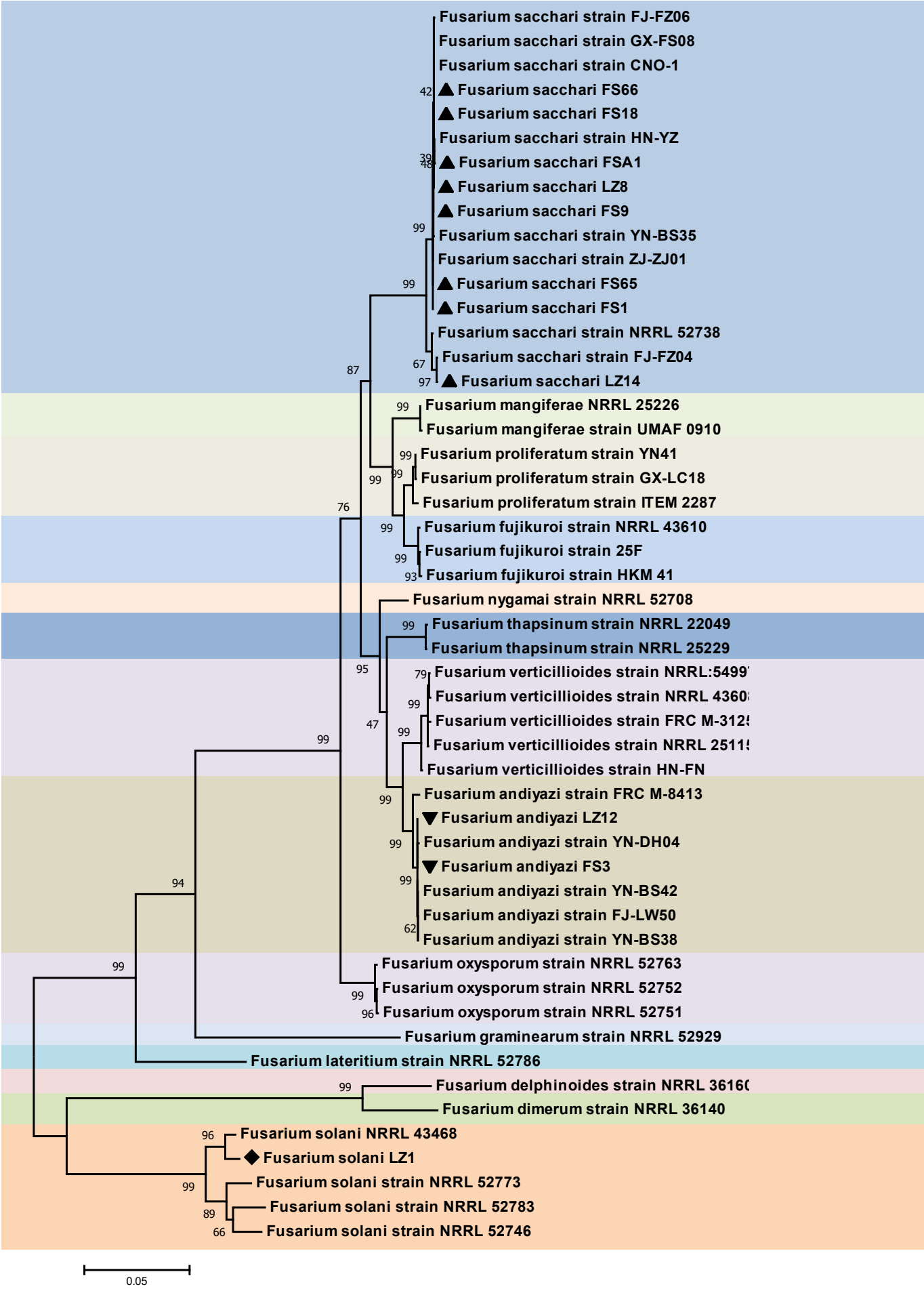
**Supplementary Figure S1.** Detection of detoxified strain FZ06-VF. RT-PCR detection of virus-free strains FZ06-VF by specific primer pairs FshV1-DefectF/R. Lane M, GeneRuler 1 kb Plus DNA adder; FshV1-FZ06 as a positive control.

## Supplementary Figure S2.



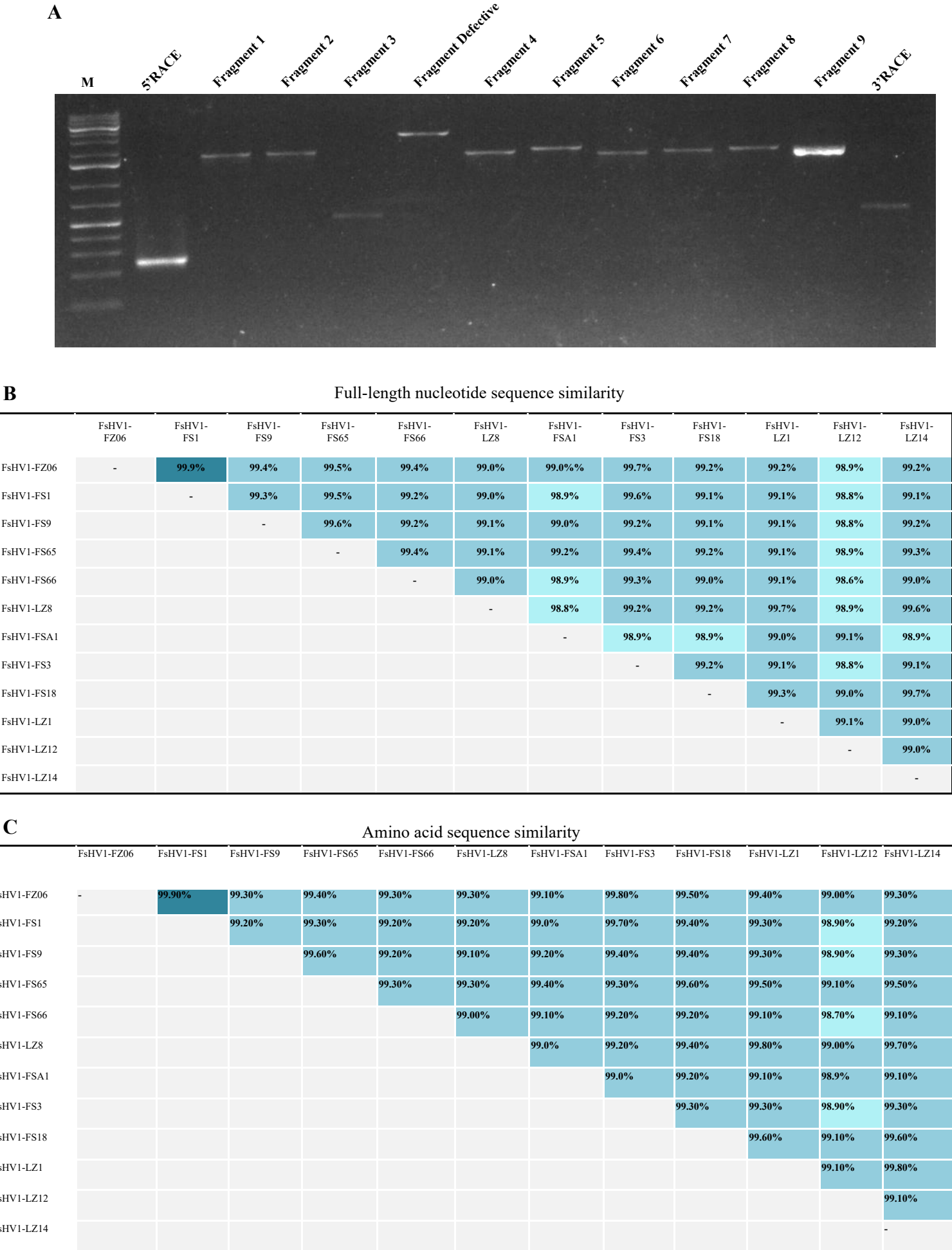
Supplementary Figure S2. Morphological characterization of *Fusarium sacchari*, *Fusarium andiyazi* and *Fusarium solani*. (A-F): Morphological characterization of *Fusarium sacchari*. (A and B) Fungal colony growing on the PDA. (C) Macroconidia. (D) Microconidia. (E-F) Microconidia formed on short aerial conidiophores arising from hyphae on CLA. (G-L) Morphological characterization of *Fusarium andiyazi*. (G and H) Fungal colony growing on the PDA. (I) Macroconidia. (J) Microconidia. (K) Microconidia in situ on CLA. (L) Microconidial chains. (M-R) Morphological characterization of *Fusarium solani*. (M and N) Fungal colony growing on the PDA. (O) Macroconidia. (P) Microconidia. (Q and R) Microconidia in situ on CLA. A, B, G, H, M, N, scale bar = 25mm. C-F, I-L, O-R, scale bar = 25µm.

Supplementary Figure S3.



**Supplementary Figure S3.** Phylogenetic analysis of *Fusarium*. Phylogenetic tree inferred by Maximum Likelihood using TEF-1 $\alpha$ +RPB1+RPB2 gene sequence with the reference sequences from other *Fusarium* species, including *F. sacchari*, *F. mangiferae*, *F. proliferatum*, *F. fujikuroi*, *F. nygamai*, *F. thapsinum*, *F. verticillioides*, *F. andiyazi*, *F. oxysporum*, *F. graminearum*, *F. lateritium*, *F. delphinoides*, *F. dimerum*, *F. solani*. Phylogenetic reconstruction was performed by bootstrap test (1000 replicates) showing the relationship between the 12 *Fusarium* spp. isolates identified in this study.

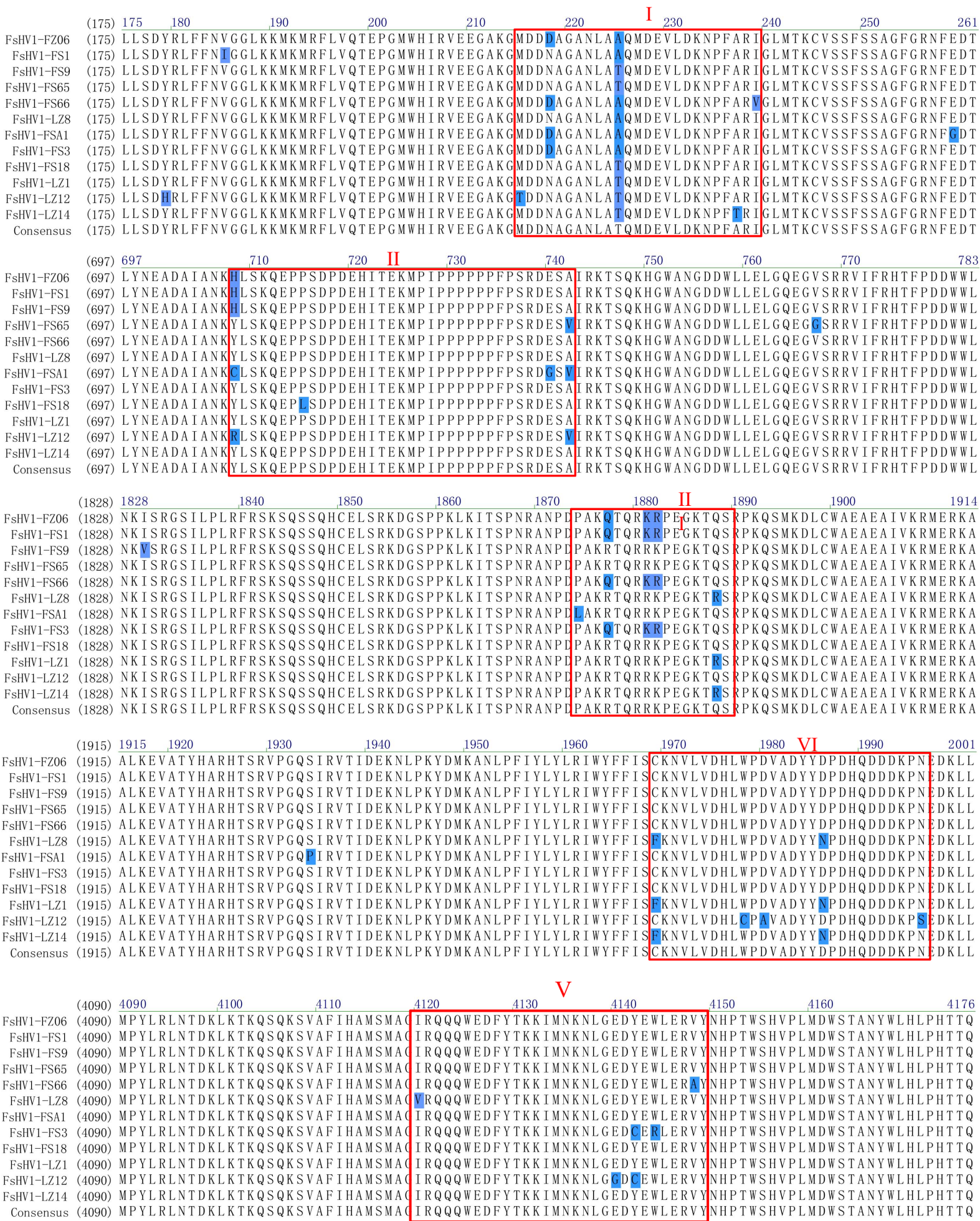
Supplementary Figure S4.



**Supplementary Figure S4.**Full-length amplification and sequence homology of 12 FsHV1 isolates. (A) Full-length amplification of FsHV1, including 12 fragments. Lane M, GeneRuler 1 kb Plus DNA Ladder. (B)The percent identity analysis between 12 FsHV1 full-length nucleotide sequence.(C)The percent identity analysis between 12 FsHV1 full-length nucleotide sequence.



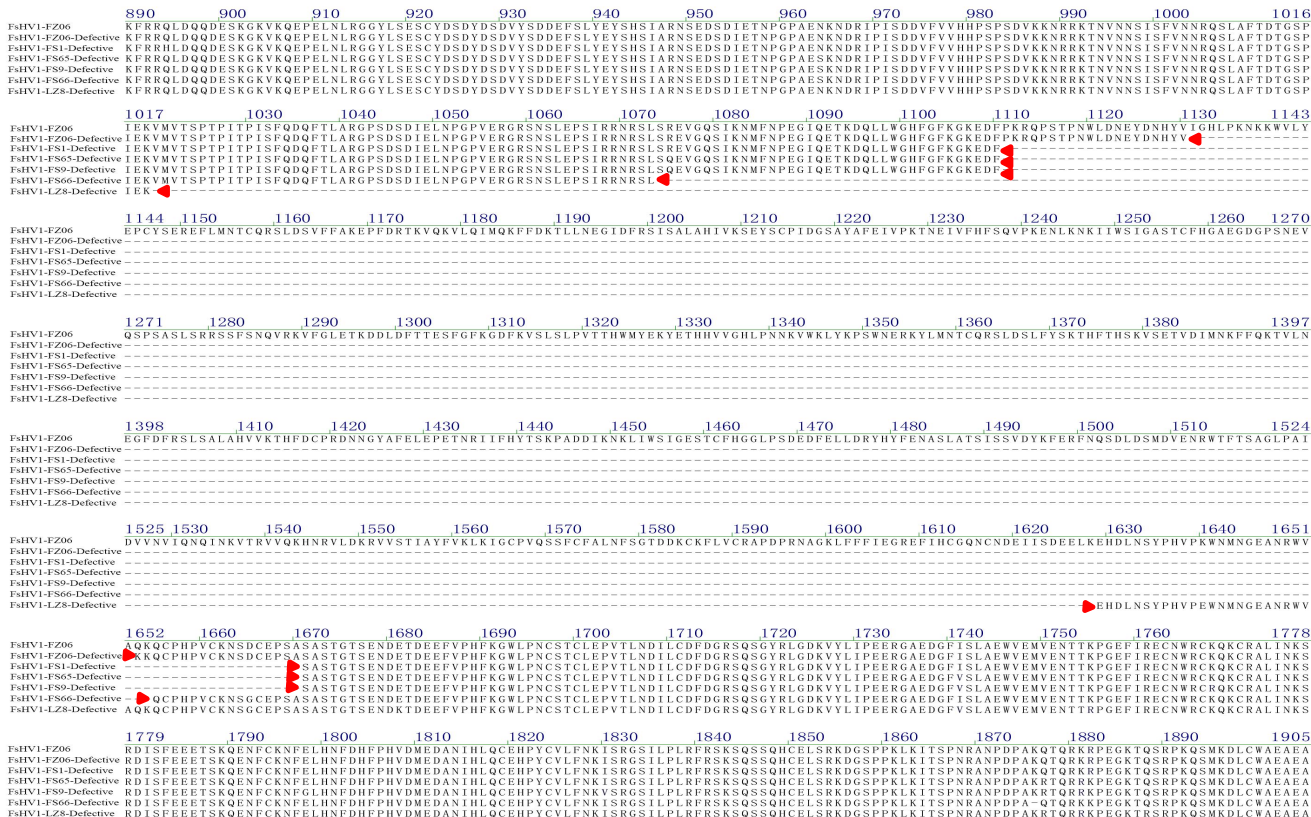
**Supplementary Figure S5.** Amino acid sequence alignment of 12 FsHV1 isolates. The red boxed regions I~V with more differences in amino acids.



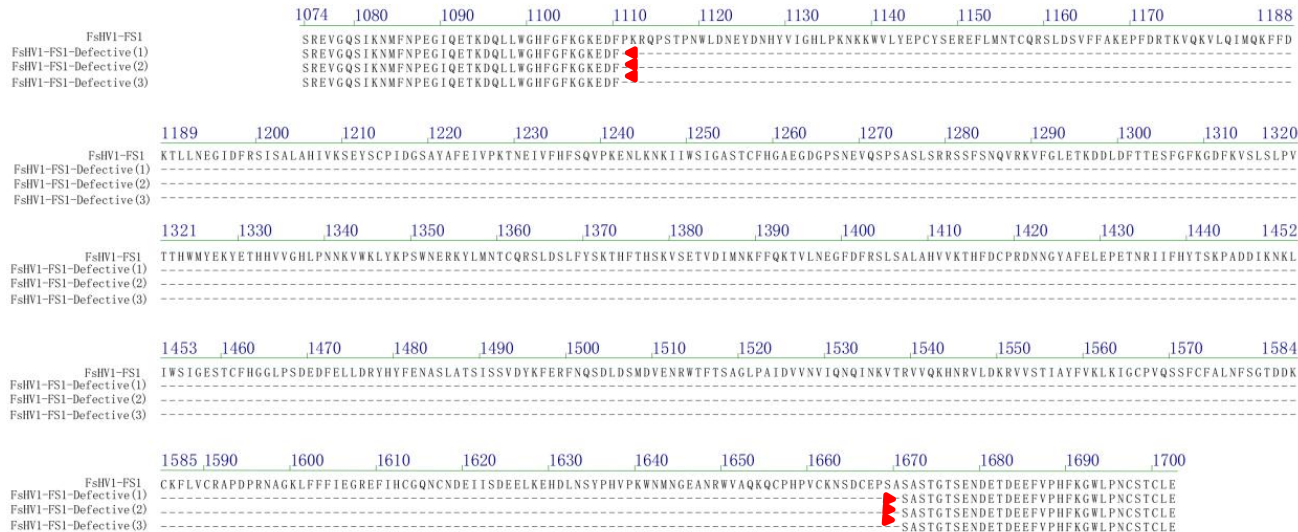


### Supplementary Figure S6.

A

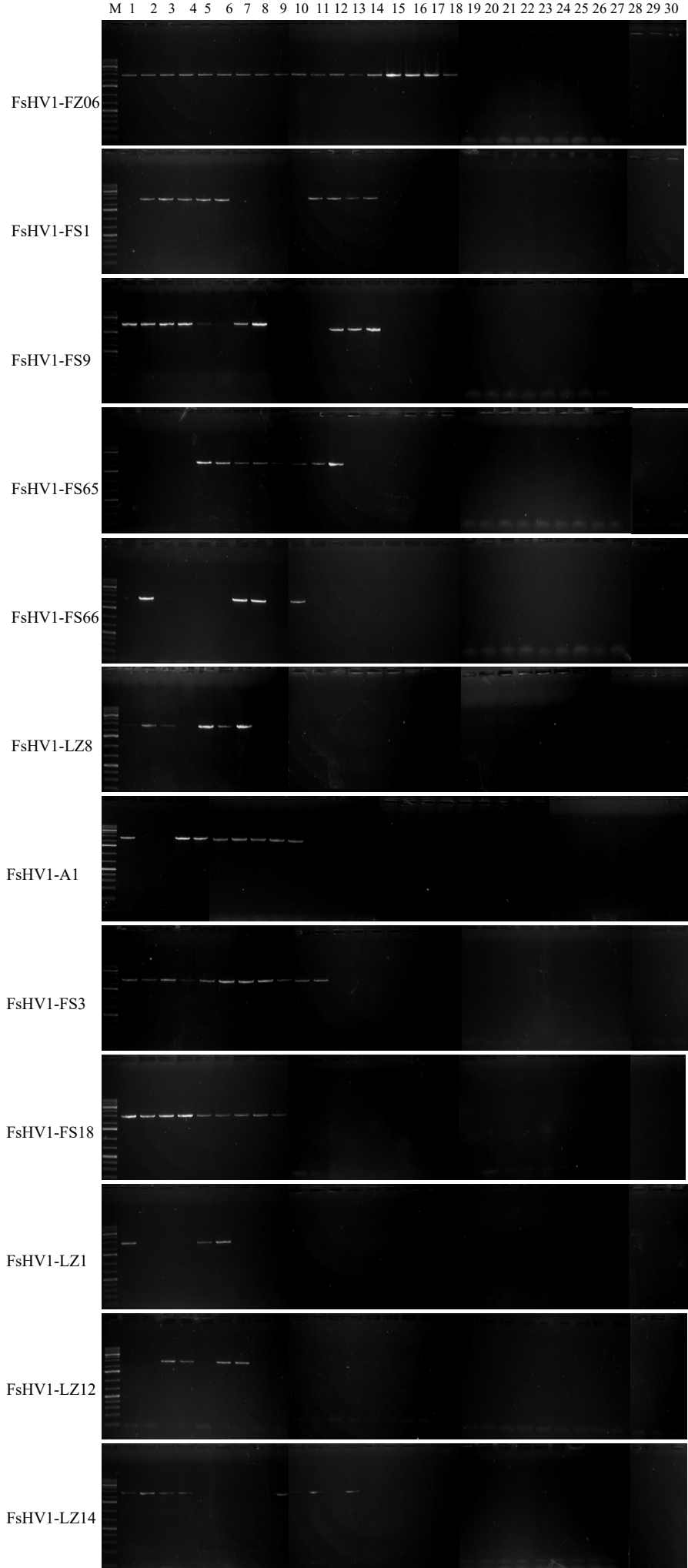


# B



**Supplementary Figure S6.** The positional of amino acid sequences of FsHV1-Defective RNA. **(A)** Amino acid sequence alignment of the region corresponding between FsHV1-FZ06 and 6 FsHV1-Defective RNA. -----, regions that are absent in 6 FsHV1 RNA. **(B)** Amino acid sequence alignment of the region corresponding between the same strain.

Supplementary Figure S7.



**Supplementary Figure S7.** Detection of FsHV1 after mycelial fusion. The target size of intact virus are 2500bp or the target size of defective virus about 800bp. Lane M, GeneRuler 1 kb Plus DNA Ladder .1~30, each of the 12 FsHV1 isolates horizontal transmission to the FZ06-VF strain.