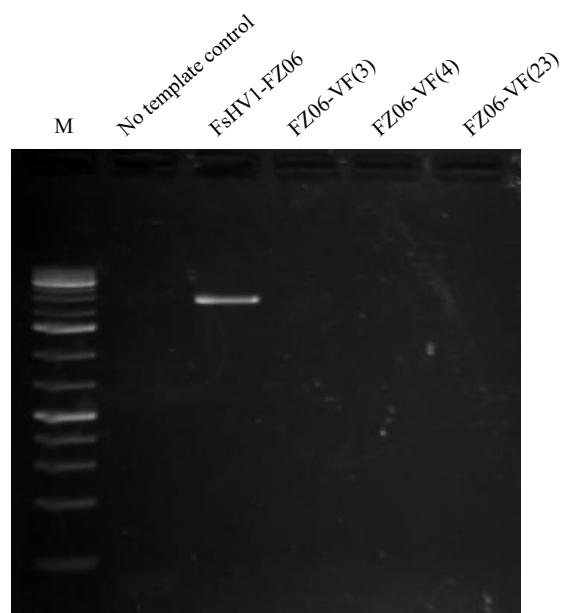
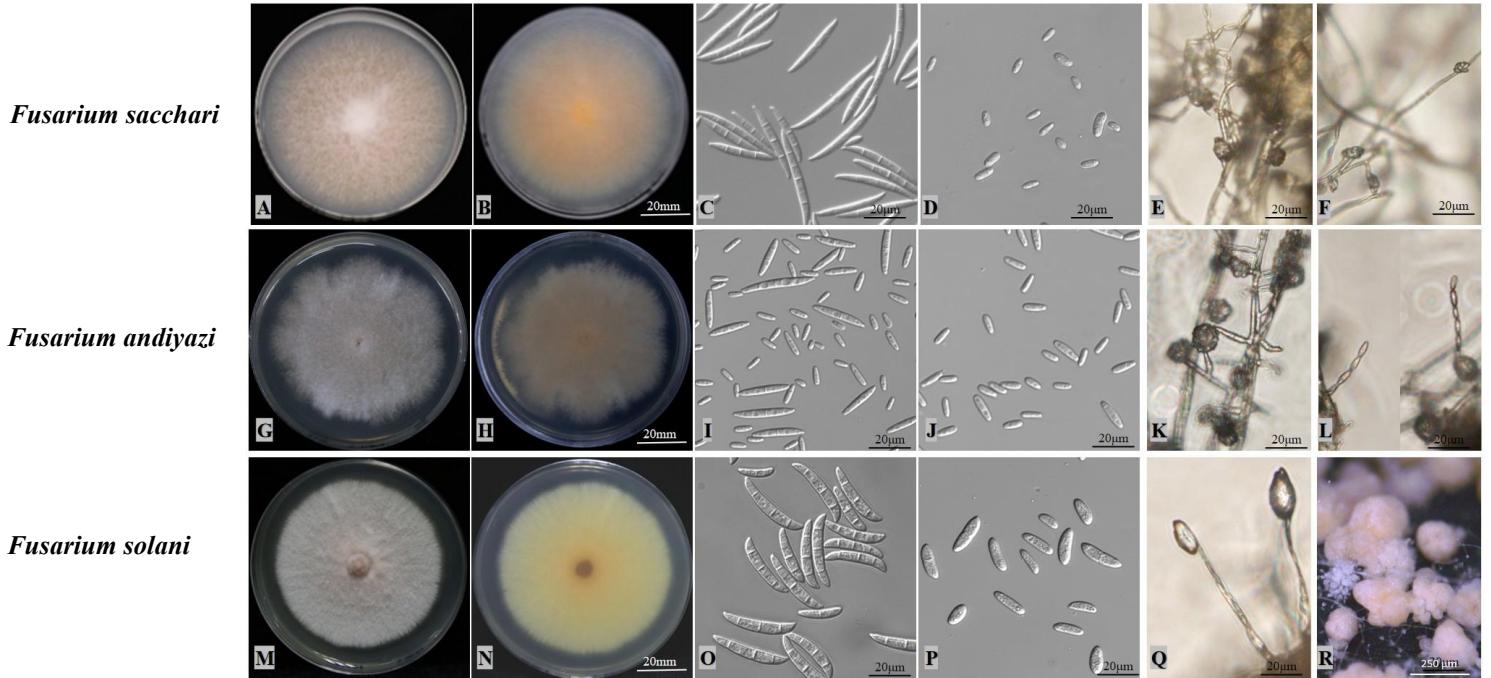


## Supplementary Figure S1.



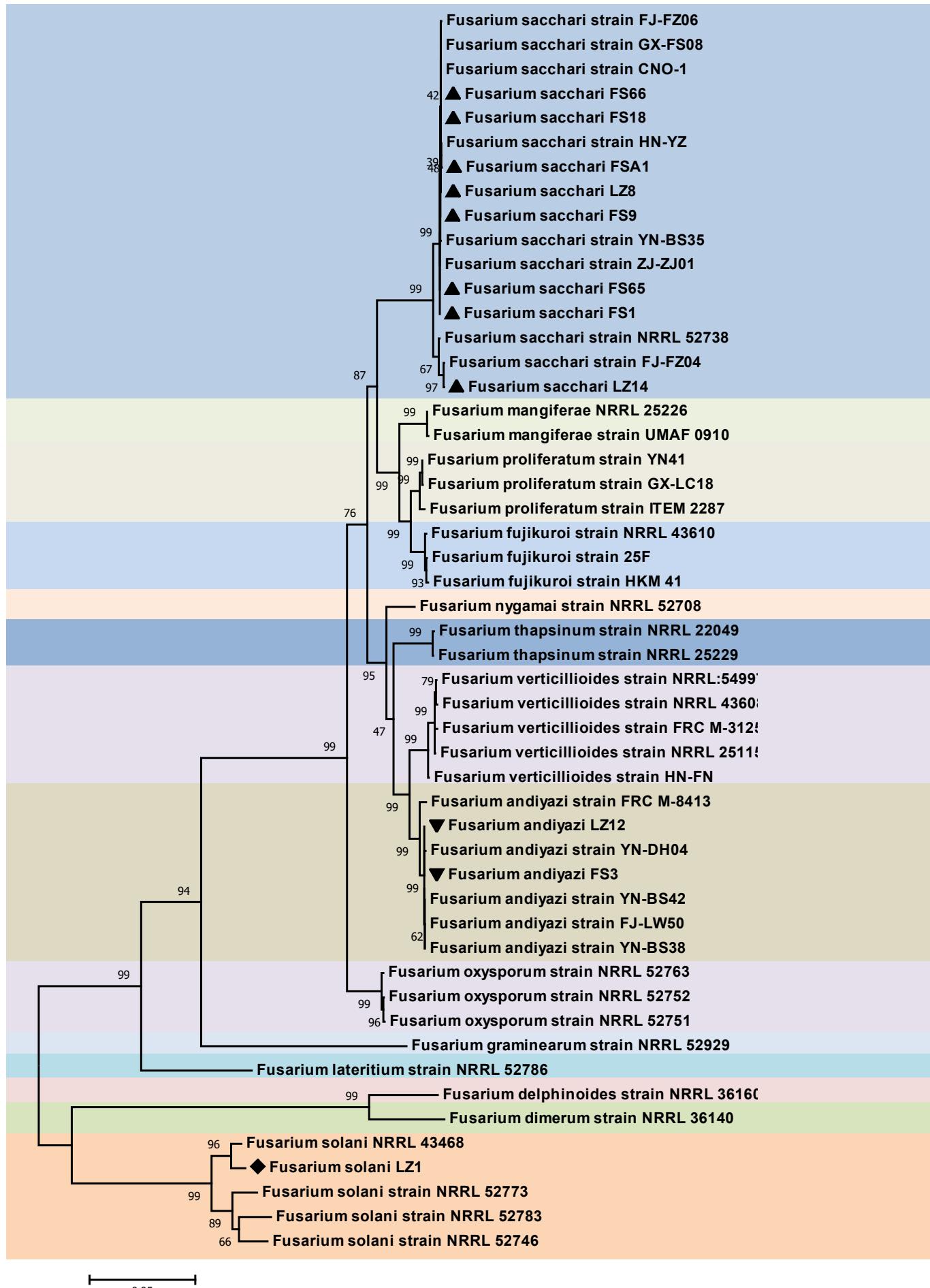
**Supplementary Figure S1.** Detection of detoxified strain FZ06-VF. RT-PCR detection of virus-free strains FZ06-VF by specific primer pairs FsHV1-DefectF/R. Lane M, GeneRuler 1 kb Plus DNA adder; FsHV1-FZ06 as a positive control.

## 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 andiyazi*. (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 = 25 $\mu$ m.

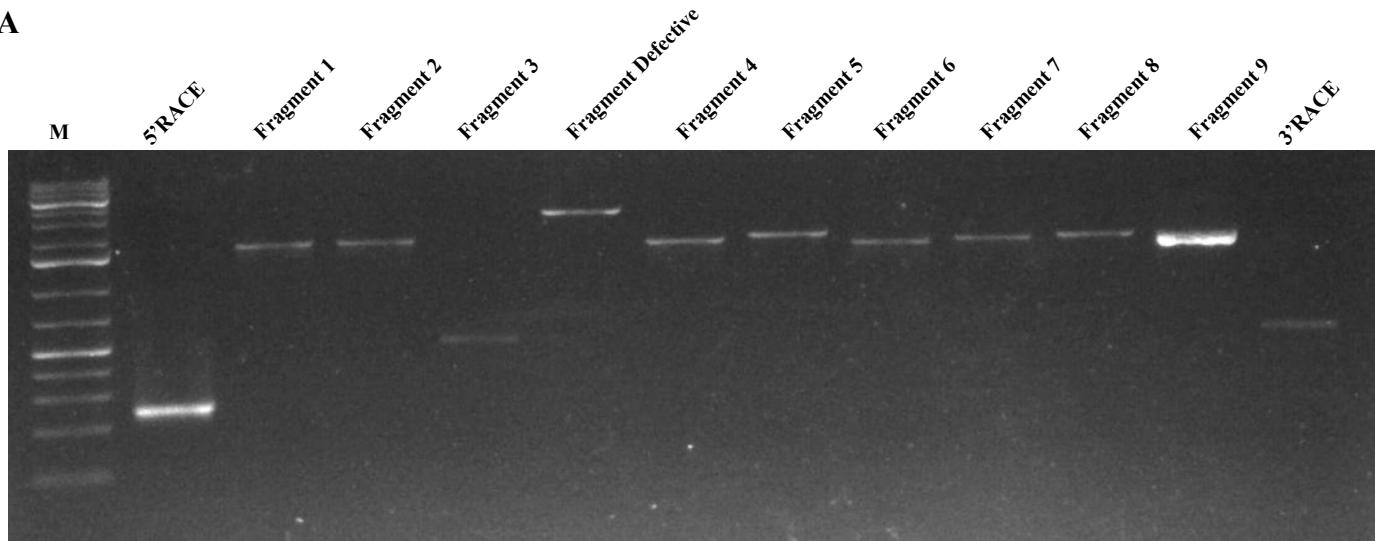
### Supplementary Figure S3.



**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.oxyphorum*, *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.

**A**



**B**

Full-length nucleotide sequence similarity

	FsHV1-FZ06	FsHV1-FS1	FsHV1-FS9	FsHV1-FS65	FsHV1-FS66	FsHV1-LZ8	FsHV1-FSA1	FsHV1-FS3	FsHV1-FS18	FsHV1-LZ1	FsHV1-LZ12	FsHV1-LZ14
FsHV1-FZ06	-	99.9%	99.4%	99.5%	99.4%	99.0%	99.0%	99.7%	99.2%	99.2%	98.9%	99.2%
FsHV1-FS1		-	99.3%	99.5%	99.2%	99.0%	98.9%	99.6%	99.1%	99.1%	98.8%	99.1%
FsHV1-FS9			-	99.6%	99.2%	99.1%	99.0%	99.2%	99.1%	99.1%	98.8%	99.2%
FsHV1-FS65				-	99.4%	99.1%	99.2%	99.4%	99.2%	99.1%	98.9%	99.3%
FsHV1-FS66					-	99.0%	98.9%	99.3%	99.0%	99.1%	98.6%	99.0%
FsHV1-LZ8						-	98.8%	99.2%	99.2%	99.7%	98.9%	99.6%
FsHV1-FSA1							-	98.9%	98.9%	99.0%	99.1%	98.9%
FsHV1-FS3								-	99.2%	99.1%	98.8%	99.1%
FsHV1-FS18									-	99.3%	99.0%	99.7%
FsHV1-LZ1										-	99.1%	99.0%
FsHV1-LZ12											-	99.0%
FsHV1-LZ14												-

**C**

Amino acid sequence similarity

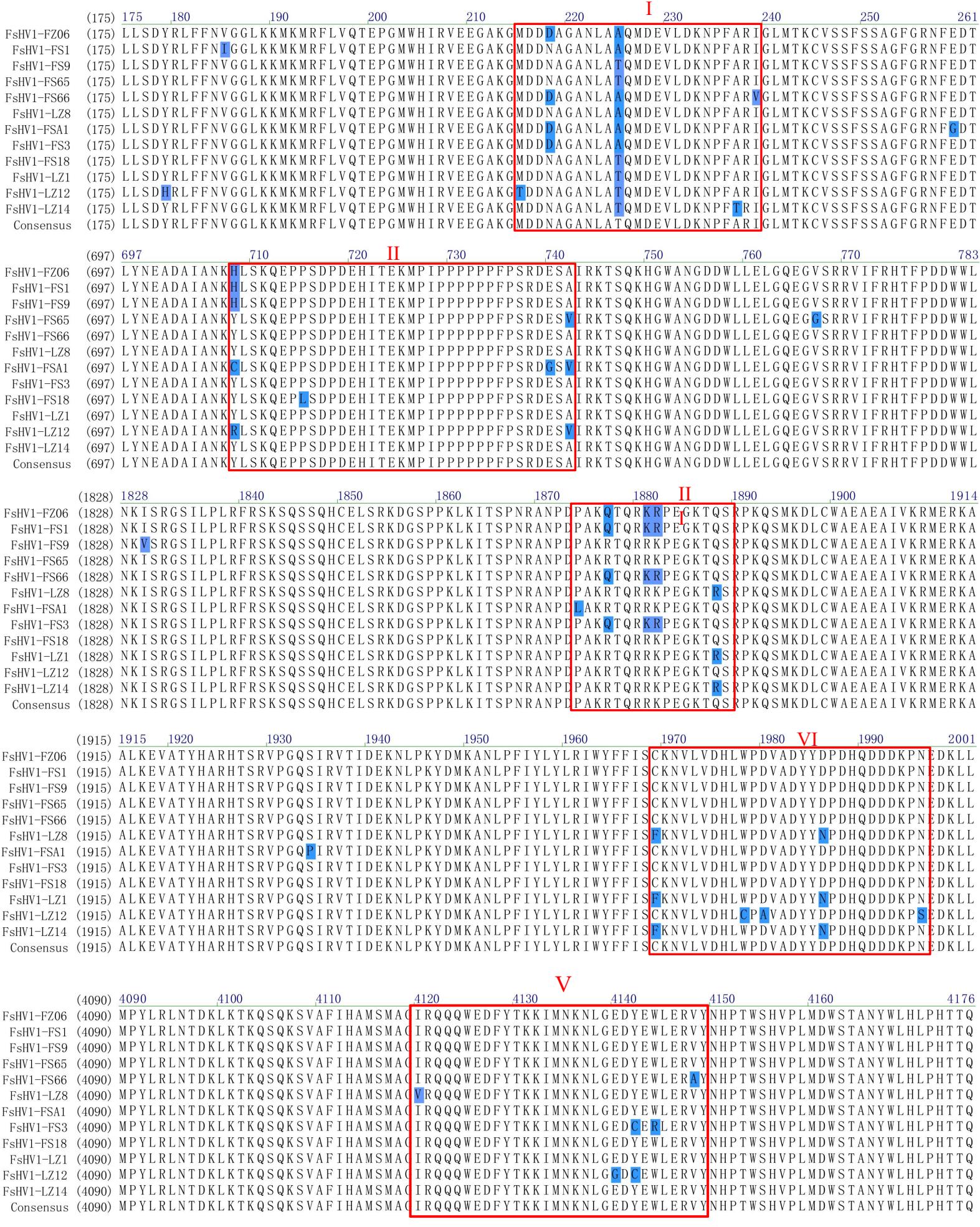
	FsHV1-FZ06	FsHV1-FS1	FsHV1-FS9	FsHV1-FS65	FsHV1-FS66	FsHV1-LZ8	FsHV1-FSA1	FsHV1-FS3	FsHV1-FS18	FsHV1-LZ1	FsHV1-LZ12	FsHV1-LZ14
FsHV1-FZ06	-	99.90%	99.30%	99.40%	99.30%	99.30%	99.10%	99.80%	99.50%	99.40%	99.00%	99.30%
FsHV1-FS1			99.20%	99.30%	99.20%	99.20%	99.0%	99.70%	99.40%	99.30%	98.90%	99.20%
FsHV1-FS9				99.60%	99.20%	99.10%	99.20%	99.40%	99.40%	99.30%	98.90%	99.30%
FsHV1-FS65					99.30%	99.30%	99.40%	99.30%	99.60%	99.50%	99.10%	99.50%
FsHV1-FS66						99.00%	99.10%	99.20%	99.20%	99.10%	98.70%	99.10%
FsHV1-LZ8							99.0%	99.20%	99.40%	99.80%	99.00%	99.70%
FsHV1-FSA1								99.0%	99.20%	99.10%	98.9%	99.10%
FsHV1-FS3									99.30%	99.30%	98.90%	99.30%
FsHV1-FS18										99.60%	99.10%	99.60%
FsHV1-LZ1											99.10%	99.80%
FsHV1-LZ12												99.10%
FsHV1-LZ14												-

**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.



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

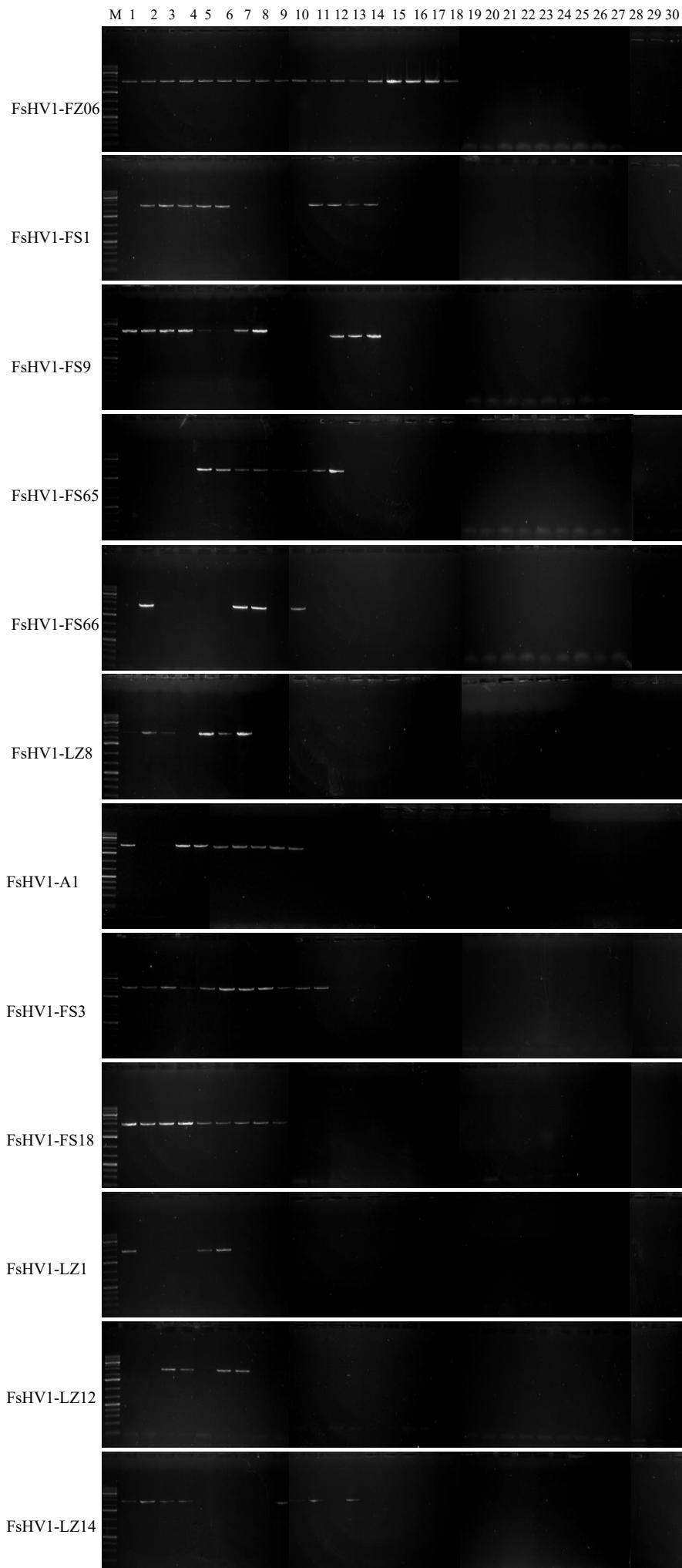
## Supplementary Figure S6.

A



**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 DNAAdder .1~30, each of the 12 *FsHV1* isolates horizontal transmission to the FZ06-VF strain.