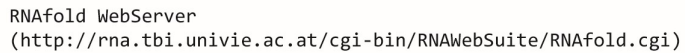
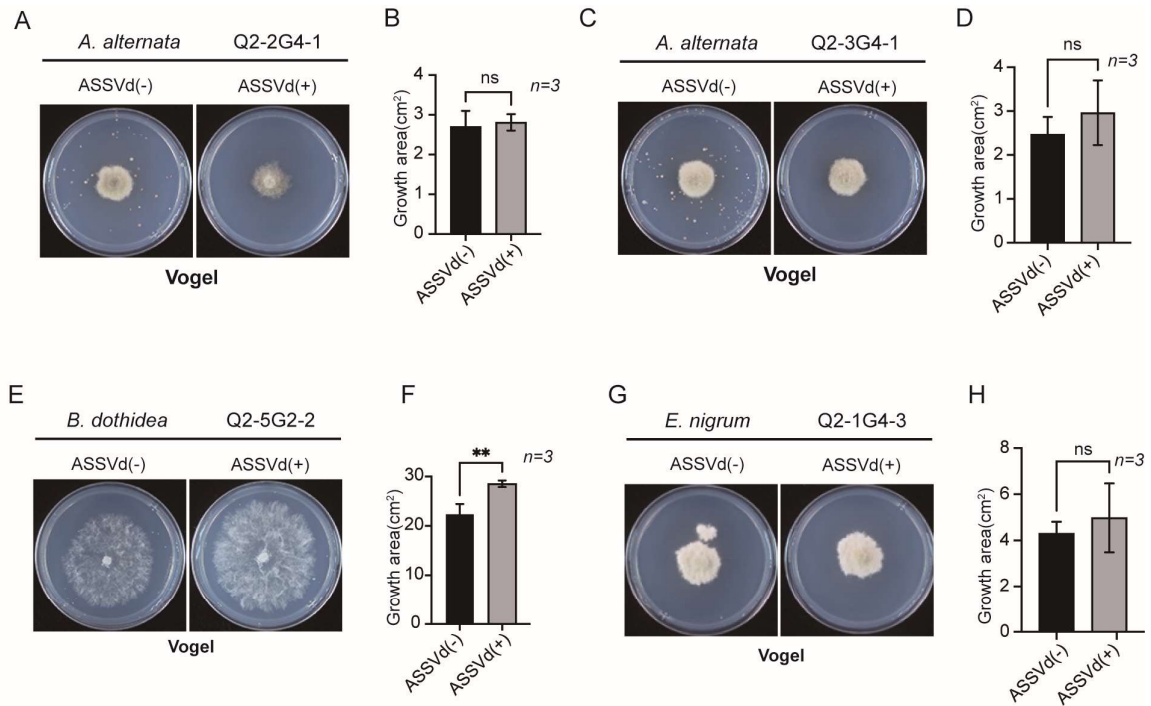


Supplementary Figure S1. Detection of ASSVd in fungal isolates by RT-PCR. A DNA ladder (Marker) was used as the size standard. ASSVd (-) and ASSVd (+) indicate the negative and positive control for the RT-PCR reaction, respectively, using RNA templates extracted from ASSVd-free and ASSVd-containing samples. RT-PCR primer sets are specific for ASSVd (Supplementary Table S1).

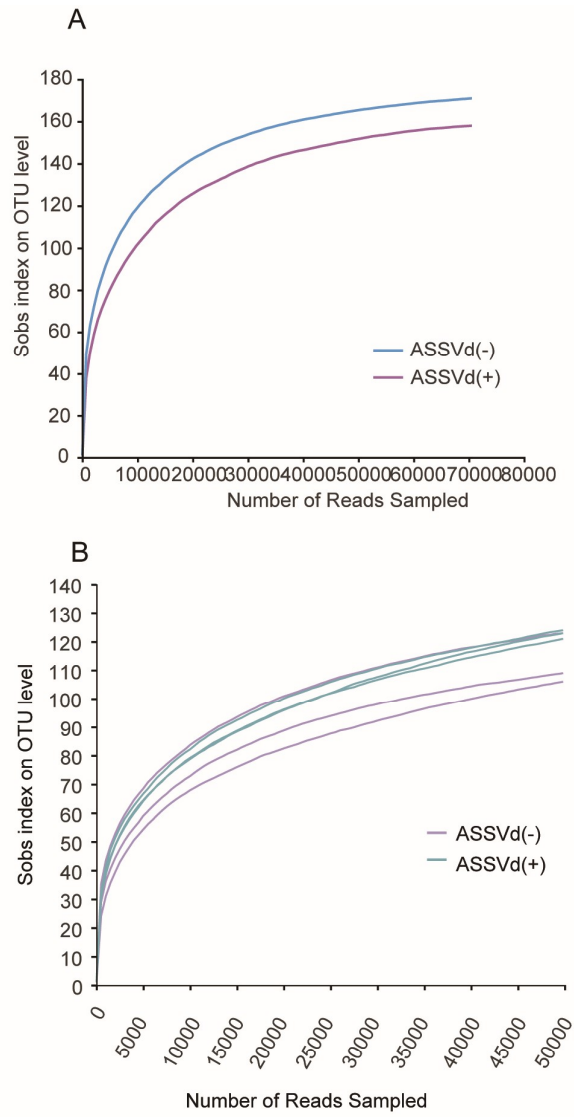
[illegible]

2



Supplementary Figure S3. The effects of ASSVd infection on fungal isolates grown on Vogel's minimal medium.

A, C, E, and G. Phenotypic growth of ASSVd-carrying and ASSVd-free fungal isolates. All isolates were grown on Vogel's minimal medium (6-cm plate) for 5–6 days and photographed. ASSVd (+) and ASSVd (–) indicate carrying and free isolates respectively. **B, D, F, and H.** The lesion area measured on inoculated apple leaves described in the data are presented as mean \pm SD ($n = 3$). ** indicates a significant difference at $p < 0.01$ (Student's t -test).



Supplementary Figure S4. The dilution curves based on the Sobs index at the OTU level.

A. ASSVd-infected (+) and ASSVd-free (-) samples collected in the autumn of 2019.

B. ASSVd-infected (+) and ASSVd-free (-) samples collected in the spring of 2020.

Supplementary Table S1. List of primers used in this study.

Primer Name	Oligonucleotide sequence (5'-3')	Size of PCR product
F-MdEF-1 α	ATTCAAGTATGCCTGGGTGC	174 bp
R-MdEF-1 α	CAGTCAGCCTGTGATGTTCC	
ASSVd-1F	CCGGCCTTCGTCGACGACGA	330 bp
ASSVd-330R	TGAGAAAGGAGCTGCCAGCAC	
ASSVd-173R	TGTTCTCTCACGCTCTTTTCTTT	150 bp
ASSVd-24F	GTGAGTTCCTTCTTCTCCTCGTTTT	
ITS4R	TCCTCCGCTTATTGATATGC	608 bp
ITS1F	CTTGGTCATTTAGAGGAAGTAA	282 bp
ITS2R	GCTGCGTTCCTTCATCGATGC	

Supplementary Table S2. List of software and databases used for the data analysis in this study.

Analysis software / Database	Version number	Function	Link
Flash	1.2.11	Splicing paired-end sequences	https://ccb.jhu.edu/software/FLASH/index.shtml
Qiime	1.9.1	Generating tables of abundances at each taxonomic level; calculating the distances of beta diversity	http://qiime.org/install/index.html
Uparse	7.0.1090	OTU clustering	http://www.drive5.com/uparse/
RDP Classifier	2.11	For sequence classification annotation	https://sourceforge.net/projects/rdp-classifier/
Usearch	7	OTU statistics	http://www.drive5.com/usearch/
Mothur	1.30.2	Alpha diversity analysis	https://www.mothur.org/wiki/Download_mothur
UNITE	8	ITS database of fungal	https://unite.ut.ee/
FunGene	9.6	Functional gene databases	http://www.fungene-db.fr/
Funguild	1	Annotation databases of fungal functional	http://www.funguild.org/
MAFFT	7.2	Multiple sequence alignment	https://mafft.cbrc.jp/alignment/software/
Fastp	0.19.6	Quality control	https://github.com/OpenGene/fastp

Information of the analysis software / database for each analysis in this paper.

Supplementary Table S3. Summary of fungal amplicon sequencing data.

Collecting time	Places / plant number	Name	Raw reads	Trimmed Sequence reads	OTUs	Genus
Harvesting stage (2019)	Site 1-3 /9	ASSVd(-)	146892	73446	171	75
	Site 1-3/9	ASSVd(+)	143268	71634	158	74
Flowering stage (2020)	Site 1/3	ASSVd(-)	126006	63003	123	56
	Site 1/3	ASSVd(+)	100488	50244	125	54
	Site 2/3	ASSVd(-)	142772	71386	106	47
	Site 2/3	ASSVd(+)	123812	61906	123	48
	Site 3/3	ASSVd(-)	122600	61300	109	49
	Site 3/3	ASSVd(+)	141552	70776	121	51

Supplementary Table S4. Relative abundance of the 10 most abundant fungal groups (genera) present in ASSVd-infected and ASSVd-free apple stem samples collected in the autumn of 2019.

Fungal Genus	ASSVd(-) %	ASSVd(+) %
<i>Genera in Phaeosphaeriaceae</i>	32.69	8.26
<i>Cladosporium</i>	15.43	22.62
<i>Setomelanomma</i>	7.84	17.80
<i>Pyrenochaeta</i>	1.01	22.64
<i>Alternaria</i>	6.30	16.53
<i>Erythrobasidium</i>	10.18	1.03
<i>Leotiomycetes</i>	6.97	0.37
<i>Didymellaceae</i>	1.66	2.39
<i>Neosetophoma</i>	3.34	0.43
<i>Filobasidium</i>	0.82	1.93
Others	13.76	6.00

Supplementary Table S5. Relative abundance of the 10 most abundant fungal groups (genera) present in ASSVd-infected and ASSVd-free apple stem samples collected in the spring of 2020.

Fungal Genus	Site 1		Site 2		Site 3	
	ASSVd(-) %	ASSVd(+) %	ASSVd(-) %	ASSVd(+) %	ASSVd(-) %	ASSVd(+) %
<i>Genera in Phaeosphaeriaceae</i>	17.39	44.68	64.76	61.59	49.39	50.7
<i>Alternaria</i>	12.85	22.67	3.02	11.65	6.67	11.88
<i>Genera in Pleosporales</i>	24.64	9.42	12.23	2.3	0.31	6.73
<i>Cladosporium</i>	13.56	7.95	1.52	10.58	3.14	4.538
<i>Genera in Didymellaceae</i>	4.13	5.55	11.16	0.61	8.87	10.76
<i>Setophoma</i>	1.64	0.62	0.04	2.34	12.36	1.04
<i>Erythrobasidium</i>	4.03	2.53	2.68	1.98	1.92	1.03
<i>Chaetosphaeronema</i>	5.31	0.41	0.39	0.21	5.80	0.06
<i>Vishniacozyma</i>	0.52	0.46	0.25	1.05	7.06	0.95
<i>Pyrenochaeta</i>	0.18	0.49	0.24	0.02	0.04	6.67
Others	15.75	5.22	3.71	7.67	4.44	5.642