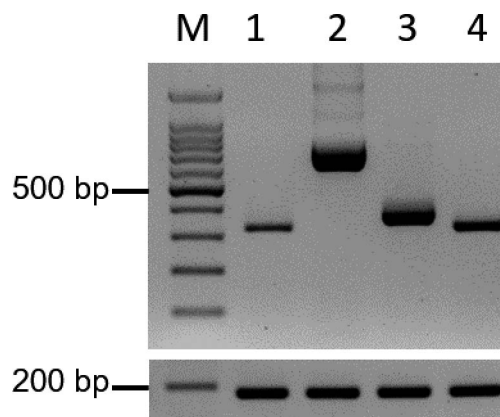


Supplementary Table 1. Summary of *de novo* assembled transcriptomes using gsAssembler program

Index	Niikata (SG)
SRA no.	SRR8466619
Sequencing method	Paired end
Total data size	6.7 Gb
Total no. of reads	78,624,272
GC (%)	45.98
Contig N50	1,126
Average contig	1,041
Largest contig size	21,154
Total assembled bases	60,059,198

Supplementary Table 2. Summary of identified virus-associated contigs

Library	SRA no.	Virus	No. of contigs	Minimum contig length (bp)	Maximum contig length (bp)
SG	SRR8466619	AGCaV	6	236	2,331
SG	SRR8466619	ASGV	101	201	3,237
SG	SRR8466619	ASPV	384	200	9,156
SG	SRR8466619	CMV	10	212	388



Supplementary Fig. 1. Confirmation of virus identity by RT-PCR using virus-specific primers. *nad5* was used as a positive control. M, marker; 1, apple green crinkle associated virus; 2, apple stem grooving virus; 3, apple stem pitting virus; 4, cucumber mosaic virus.