

**Table S1**

Oligonucleotide primers used in this study.

Contig	Primer	Sequence (5' – 3')	PCR product
<u><i>Erysiphe</i>-specific ITS primer</u>			
	EryF	TACAGAGTGCAGGCTCAGTCG	
	EryR	GGTCAACCTGTGATC CATGTGACTGG	
<u>RT-PCR</u>			
Contig 1	RPaTV1b_65-6F2	TAGGTTGACAACATTCTTAAA	536 bp
	RPaTV1_65-6/114R	CCGACGCGTCGGAGTCGGT	
Contig 2	RPaTV1a_65-114F	TAGACTGACCACGTTTTTGA	517 bp
	RPaTV1_65-6/114R	CCGACGCGTCGGAGTCGGT	
Contig 3	RPaTV2_75-52F	GTGCAGTAGATGAGGCATTATTG	596 bp
	RPaTV2_75-52R	TTACGGCTAAGTCGCTTCGTATC	
Contig 4	RPaTV3_75-77F	GATGAATAGACGGGCGCAGAGA	380 bp
	RPaTV3_75-77R	CGACTGCTGCATACATGTCTTG	
Contig 5	RPaTV4_6052F	GCACGGGACCTGGTGGAAAGTA	344 bp
	RPaTV4_6052R	CTAACCCCTACTGACCAGCAATT	
Contig 6	RPaTV5_75-14F	CTCTGTGGACCTACACTGTTTC	532 bp
	RPaTV5_75-14R	CTCCTCACGTTAACCTCGTTCG	
Contig 7	RPaTV6_75-22F	ACACGAACAGAGGGCTGCATTTCG	488 bp
	RPaTV6_75-22R	CCACATCTGCGCCACGTTCTTTG	
Contig 8	RPaTV7_75-7F	TGAGAGTCAGGGCGGAAGAGGC	444 bp
	RPaTV7_75-7R	CTTTGCGCTTATGTGCGGCAAGT	
Contig 9	RPaTV8_85-65F	CTCTGAAGCGCAACGCACATGCA	464 bp
	RPaTV8_85-65R	ATCTCCCTTGTCCGAGCCCGTC	
Contig 10	RPaTV9_85-21F	GAGCACGTTGGTGGAAAGAATA	492 bp
	RPaTV9_85-21R	CTCGTCCAATGTGTCCCTTGACC	
<u>3'RLM-RACE</u>			
Contig 1	TV1a_65-114_5R341	TATTTAGGTTACCCTCGGGTGTGTCAGAC	
	TV1a_65-114_3F4286	AACGGATCTTCGAAGACGAAGATGGTA	
Contig 3	TV2_75-52_5R66	GACGTAACATTATCTACACAGGTGTGCG	
	TV2_75-52_3F3772	CTGGACAGCATGGCTTATGAACTGGCC	
Contig 4	TV3_75-77_5R328	ACCGTCGTAGTCAGCTGATGCTGTCGC	
	TV3_75-77_3F4408	GTGGCGAAGGTGTTGCCGATAGAAAGC	
Contig 5	TV4_6052_5R209	AGGCTGCATGGCTTGTCTACCATGCTT	
	TV4_6052_3F4365	AATCCTAATGTTTCAGGCGTCTAAGCAC	
Contig 6	TV5_75-14_5R319	GTTGACCGTAGAGTGTTGACTACTCCA	
	TV5_75-14_3F4706	GGTAAGGTAGAGCACGCAGTGAGTCGA	
Contig 7	TV6_75-22_5R297	CCTCCGCAAGGGTGTGGTAGGCGCAC	
	TV6_75-22_3F4687	AGCACTCGACGCATCGGTGACGAAGAC	
Contig 8	TV7_75-7_5R252	TGACAGGACGGCAGTTTCACGTCTGGC	
	TV7_75-7_3F4638	AGCGCTATAGGTAGAGCAGCCATAGAA	
Contig 9	TV8_85-65_5R295	GGTGAGGCTCTCCGCGTGCAACACTTC	
	TV8_85-65_3F4580	ATAGAGAGTGTGTAGTGTCTAGAGAGG	
Contig 10	TV9_85-21_5R300	GACCAAGTTGGCTGACTGTGCTGAAC	
	TV9_85-21_3F5442	GGCGGTATATTCACAGCTAGGCAACAA	
	PC3-T7 loop (anchor primer, cDNA synthesis)	GGATCCCGGAATTCGGTAATACGACT- CACTATATTTTTATAGTGAGTCGTATTA	
	PC2 (RACE PCR)	CCGAATTCCCGGGATCC	
	3RACE-adaptor (anchor primer)	CAATACCTTCTGACCATGCAGTGACAG TCAGCATG	
	3RACE-1st (cDNA synthesis)	CATGCTGACTGTCAGTGCAT	
	3RACE-2nd (RACE PCR)	TGCATGGTCAGAAGGTATTG	

**Table S2**  
Top matches for global and BLAST-based alignments.

Virus/contig name	Best-matched virus <sup>a</sup>	Identity <sup>a</sup>
<u>global alignments</u>		
RPaTV1-a/ 65-114	Saccharomyces cerevisiae virus L-A-lus	56%
RPaTV1-b/ 65-6	Saccharomyces cerevisiae virus L-A-lus	56%
RPaTV2 / 75-52	Saccharomyces cerevisiae virus L-BC (La)	52%
RPaTV3 / 75-77	Xanthophyllomyces dendrorhous virus L1A	56%
RPaTV4 / 6052	Xanthophyllomyces dendrorhous virus L1A	57%
RPaTV5 / 75-14	black raspberry virus F	54%
RPaTV6 / 75-22	black raspberry virus F	53%
RPaTV7 / 75-7	black raspberry virus F	53%
RPaTV8 / 85-65	Saccharomyces cerevisiae virus L-BC (La)	50%
RPaTV9 / 85-21	Camponotus yamaokai virus <sup>b</sup>	52%
<u>BLAST-based alignments</u>		
RPaTV1-a/ 65-114	black raspberry virus F	42%
RPaTV1-b/ 65-6	black raspberry virus F	42%
RPaTV2 / 75-52	Saccharomyces cerevisiae virus L-BC (La)	32%
RPaTV3 / 75-77	Xanthophyllomyces dendrorhous virus L1A	44%
RPaTV4 / 6052	Xanthophyllomyces dendrorhous virus L1A	49%
RPaTV5 / 75-14	Saccharomyces cerevisiae virus L-A-lus	27%
RPaTV6 / 75-22	Saccharomyces cerevisiae virus L-A-lus	29%
RPaTV7 / 75-7	Xanthophyllomyces dendrorhous virus L1A	25%
RPaTV8 / 85-65	Xanthophyllomyces dendrorhous virus L1A	21%
RPaTV9 / 85-21	Helicobasidium mompa totivirus 1-17 <sup>c</sup>	15%

<sup>a</sup> Based on analysis using pairwise global or BLAST alignment with the PASC (Pairwise Sequence Comparison) site at NCBI.

<sup>b</sup> unclassified totivirus.

<sup>c</sup> unclassified victorivirus.