




	..... .....	..... .....	..... .....	..... .....	..... .....	..... .....	..... .....	..... .....	..... .....	..... .....	..... .....
	5	15	25	35	45	55	65	75	85	95	
LN7_f	*****AGC	T**CT*AA*C	**GTTTACG*	*TG*G*AAGT	AATT*AGAAA	GAAT*ACAGA	AATCT*CAGC	GCAGTGGG*A	CGA**C***C	TAT*G**T**	
N329_f	*****GTT	A**TT*AG*C	**ATTTTCC*	*CT*A*AAAG	TAAT*CAGAT	GCTT*ACAGC	ATTCA*CAAC	TCCTTGGG*A	AGA**T***C	TAT*A**G**	
N329_ns	*****GTT	A**TT*AG*C	**ATTTTCC*	*CT*A*AAAG	TAAT*CAGAT	GCTT*ACAGC	ATTCA*CAAC	TCCTTGGG*A	AGA**T***C	TAT*A**G**	
N329_t	*****GTT	A**TT*AG*C	**ATTTTCC*	*CT*A*AAAG	TAAT*CAGAT	GCTT*ACAGC	ATTCA*CAAC	TCCTTGGG*A	AGA**T***C	TAT*A**G**	
N360_s	*****GTT	A**TT*AG*C	**ATTTTCC*	*CT*A*AAAG	TAAT*CAGAT	GCTT*ACAGC	ATTCA*CAAC	TCCTTGGG*A	AGA**T***C	TAT*A**G**	
N340_s	*****GTT	A**TT*AG*C	**ATTTTCC*	*CT*A*AAAG	TAAT*CAGAT	GCTT*ACAGC	ATTCA*CAAC	TCCTTGGG*A	AGA**T***T	TAT*G**G**	
N332_ns	*****GTT	A**TT*AG*C	**ATTTTCC*	*CT*A*AAAG	TAAT*CAGAT	GCTC*CCAGC	ATTCG*CTAC	TCCTTGGG*T	CGT**T***C	TAT*G**G**	
N346_s	*****TAT	T**CT*AG*T	**GTTTACC*	*CT*G*AAGT	GATC*AGGAT	GCTC*TGTTT	CTTCA*AAGC	TAAGTGGG*A	AGA**T***C	TAT*A**G**	
LV15_f	*****AGT	A**CT*AA*A	**ATTTTCC*	*CG*G*AAAT	CGTC*AGGAG	TCGC*TCAAC	ACTCG*CAAG	TAGAGAAG*G	ACT**C***C	TAT*A**G**	
V85_s	*****AGT	A**CT*AA*A	**ATTTTCC*	*CG*G*AAAT	CGTC*AGGAG	TCGC*TCAAC	ACTCG*CAAG	TAGAGAAG*G	ACT**C***C	TAT*A**G**	
N320_f	*****AGT	A**CT*AA*A	**ATTTTCC*	*CG*G*AAAT	CGTC*AGGAG	TCGC*TCAAC	ACTCG*CAAG	TAGAGAAG*G	ACT**C***T	TAT*A**G**	
N327_f	*****AGT	A**CT*AA*A	**ATTTTCC*	*CG*G*AAAT	CGTC*AGGAG	TCGC*TCAAC	ACTCG*CAAG	TAGAGAAG*G	ACT**C***T	TAT*A**G**	
N325_f	*****AGT	A**CT*AA*A	**ATTTTCC*	*CG*G*AAAT	CGTC*AGGAG	TCGC*TCAAC	ACTCG*CAAG	TAGAGAAG*G	ACT**C***T	TAT*A**G**	
N331_f	*****AGT	A**CT*AA*A	**ATTTTCC*	*CG*G*AAAT	CGTC*AGGAG	TCGC*TCAAC	ACTCG*CAAG	TAGAGAAG*G	ACT**C***T	TAT*A**G**	
N331_n	*****AGT	A**CT*AA*A	**ATTTTCC*	*CG*G*AAAT	CGTC*AGGAG	TCGC*TCAAC	ACTCG*CAAG	TAGAGAAG*G	ACT**C***T	TAT*A**G**	
N331_t	*****AGT	A**CT*AA*A	**ATTTTCC*	*CG*G*AAAT	CGTC*AGGAG	TCGC*TCAAC	ACTCG*CAAG	TAGAGAAG*G	ACT**C***T	TAT*A**G**	
N349_f	*****AGT	A**CT*AA*A	**ATTTTCC*	*CG*G*AAAT	CGTC*AGGAG	TCGC*TCAAC	ACTCG*CAAG	TAGAGAAG*G	ACT**C***T	TAT*A**G**	
LV2_f	*****GAC	A**CC*GG*A	**AGCTGGC*	*TG*C*TTG	AATC*AGAGT	TGGA*CACAC	ATTCG*CACT	TCAGTGGG*A	AGA**C***T	GCA*T**G**	
LV7_f	*****GAC	A**CC*GG*A	**AGCTGGC*	*TG*C*TTG	AATT*AGAAT	TGTG*CGCTC	AGTCC*CGCT	TGAGTGGG*T	AGA**C***T	GCA*G**A**	
LV10_f	*****GAC	A**CC*GG*A	**AGCTGGC*	*TG*C*TTG	AATT*AGAAT	TGTG*CGCTC	AGTCC*CGCT	TGAGTGGG*T	AGA**C***T	GCA*G**A**	
LV12_f	*****GAC	A**CC*GG*A	**AGCTGGC*	*TG*C*TTG	AATT*AGAAT	TGTG*CGCTC	AGTCC*CGCT	TGAGTGGG*T	AGA**C***T	GCA*G**A**	
V92_f	*****GAC	A**CC*GG*A	**AGCTGGC*	*TG*C*TTG	AATT*AGAAT	TGTG*CGCTC	AGTCC*CACT	TGAGTGGG*T	AGA**C***T	GCA*G**A**	
N325_ns	*****GAC	A**CC*AA*A	**AGCCGGT*	*CG*C*TTA	AATC*AGGAT	TGTA*TGCTC	ATAGC*CACT	CGAGTGGG*T	CGA**C***T	GCA*G**A**	
	CGATGTC	AA T T GA	T T C C		C	T	C	T	GA TAC	C CC TG	
	..... .....	..... .....	..... .....	..... .....	..... .....	..... .....	..... .....	..... .....	..... .....	...	
	105	115	125	135	145	155	165	175	185		

LN7_f	*CTT**A*TT	**GGAC**T*	*GCTTACCC*	C**CAAG***	***  AGTG	GCGAACCAA*	C*AT*****	*****	*G*****	***
N329_f	*CAA**C*TT	**ATTC**A*	*AGAAACAC*	G**TAAG***	***  CAAG	GCCAGCATA*	T*AT*****	*****	*A*****	***
N329_ns	*CAA**C*TT	**ATTC**A*	*AGAAACAC*	G**TAAG***	***  CAAG	GCCAGCATA*	T*AT*****	*****	*A*****	***
N329_t	*CAA**C*TT	**ATTC**A*	*AGAAACAC*	G**TAAG***	***  CAAG	GCCAGCATA*	T*AT*****	*****	*A*****	***
N360_s	*CAA**C*TT	**ATTC**A*	*AGAAACAC*	G**TAAG***	***  CGAG	GCCAGCATA*	T*AT*****	*****	*A*****	***
N340_s	*CAA**C*TT	**ATTC**A*	*AGAAACAC*	G**TAAG***	***  AAAG	GCCAGCATA*	T*AT*****	*****	*A*****	***
N332_ns	*TTG**C*TT	**ATTC**A*	*AGAAACGC*	G**CAAG***	***  AAAG	GCCAACATA*	T*TA*****	*****	*A*****	***
N346_s	*CAA**C*AT	**AGAT**T*	*GAGGACTT*	A**TCTT***	***  ACGG	GCCAAAACG*	A*AT*****	*****	*G*****	***
LV15_f	GGAG**G*AT	**GGTC**T*	*GCGTACTC*	A**CTCT***	***CCTAACG	GCTCACAGG*	T*TT*****	*****	*G*****	***
V85_s	GGAG**G*AT	**GGTC**T*	*GCGTACTC*	A**CTCT***	***CCTAACG	GCTCACAGG*	T*TT*****	*****	*G*****	***
N320_f	GGAG**G*AT	**GGTC**T*	*GCGTACTC*	A**CTCT***	***CCTAACG	GCTCACAGG*	T*TT*****	*****	*G*****	***
N327_f	GGAG**G*AT	**GGTC**T*	*GCGTACTC*	A**CTCT***	***CCTAACG	GCTCACAGG*	T*TT*****	*****	*G*****	***
N325_f	GGAG**G*AT	**GGTC**T*	*GCGTACTC*	A**CTCT***	***CCCAACG	GCTCACAGG*	T*TT*****	*****	*G*****	***
N331_f	GGAG**G*AT	**GGTC**T*	*GCGTACTC*	A**CTCT***	***CCCAACG	GCTCACAGG*	T*TT*****	*****	*G*****	***
N331_n	GGAG**G*AT	**GGTC**T*	*GCGTACTC*	A**CTCT***	***CCCAACG	GCTCACAGG*	T*TT*****	*****	*G*****	***
N331_t	GGAG**G*AT	**GGTC**T*	*GCGTACTC*	A**CTCT***	***CCCAACG	GCTCACAGG*	T*TT*****	*****	*G*****	***
N349_f	GGAG**G*AT	**GGTC**T*	*GCGCACTC*	A**CTCT***	***CCTAACG	GCTCACAGG*	T*TT*****	*****	*G*****	***
LV2_f	*CTT**T*TT	**GCAC**A*	*AGGTGTGC*	T**GAAG***	***CCGATGA	ACGCTGTGA*	C*CT*****	*****	*G*****	***
LV7_f	*CTC**A*TC	**GCAT**T*	*AAGTGTGC*	A**AAAG***	***CCCGACA	AAGCAGCGA*	A*TA*****	*****	*G*****	***
LV10_f	*CTC**A*TC	**GCAT**T*	*AAGTGTGC*	A**AAAG***	***CCCGACA	AAGCAGCGA*	A*TA*****	*****	*G*****	***
LV12_f	*CTC**A*TC	**GCAT**T*	*AAGTGTGC*	A**AAAG***	***CCCGACA	AAGCAGCGA*	A*TA*****	*****	*G*****	***
V92_f	*CTC**A*TC	**GCAT**C*	*AAGTGTGC*	G**AAAG***	***CCCGACA	AAGCAGCGA*	C*TT*****	*****	*G*****	***
N325_ns	*TTG**T*TT	**CCAT**G*	*GAGTGTGC*	G**AAAG***	***CCTCATG	AAGCAGCAA*	A*TT*****	*****	*G*****	***
	G GG T	GA GT A A	T AC	CAG TGG		T G GGTGA	GACACCTA	A ATGGATGC	ACA	

**Figure S1.** Alignment of the partial RNA-dependent RNA polymerase (RdRp) gene sequences of PBVs GII discovered in the present study. A ‘\*’ denotes an identical nucleotide residue, whilst ‘-’ indicates absence of nucleotide residue. Numbers to the top indicate the positions of the nucleotide for respective PBV strains. Gap positions are highlighted in green.