Supplementary Figure 1: Quantile-quantile (QQ) plot of observed versus expected p-values from the treeWAS "terminal" tests a) including all values, b) with values in the PcI7 gene region removed. QQ plots excluding causal polymorphisms are expected to fall approximately along the y=x line.



 $-\log_{10}(expected P)$

Supplementary Figure 2: Nucleotide alignment and ORF translation of 56 Pcl7 sequences. Symbols, "+" and "-", in sample name signify the polymorphism-associated infectotype. Colors in sequences highlight nucleotide and amino acid polymorphisms. Running bar graph at header depicts degree of sequence identity across samples, with green indicating the same base across all sequences, yellow indicating less than complete identity, and red indicating very low identity for the given position.

Identity	1 10	20	30	40	50	60	70	80	90 100
C1(+)	ATGATGAGTATATI	AGTAGGACCCAC	AGGCCCGAC	AGGACCTACA	GGTGATACCGGT	GT <mark>G</mark> CCCGGA	GGAGCCATAGO	TATTACAGGCC	CAACAGGTCAAAGTATG
Frame 1	M M S I L	AGTAGGACCCAC	G P T	G P T	G D T G	V P G	G A I G	I T G	P T G Q S M
Frame 1	M M S I L	V G P T	G P T	G P T	G D T G	V P G	G A I G	I T G	P T G Q S M
Frame 1	M M S I L	V G P T	G P T	G P T	G D T G	V P G	G A I G		P T G Q S M
P20(+) Frame 1	M M S I L	AGTAGGACCCAC V G P T	AGGCCCGAC	G P T	GGTGATACCGGT G D T G	V P G	GGAGCCATAGO G A I G	TATMACAGGCC	CAACAGGTCAAAGTATG P T G Q S M
P1003(+) Frame 1	ATGATGAGTATATI M M S I L	AGTAGGACCCAC V G P T	AGGCCCGAC	AGGACCTACA G P T	GGTGATACCGGT G D T G	GT <mark>G</mark> CCCGGA	GGAGCCATAGO G A I G	TATAACAGGCC	CAACAGGTCAAAGTATG P T G Q S M
P1006(+) Frame 1	ATGATGAGTATATT	AGTAGGACCCAC	AGGCCCGAC	AGGACCTACA G P T	GGTGATACCGGT	GT <mark>G</mark> CCCGGA	GGAGCCATAGO	TATTACAGGCC	CAACAGGTCAAAGTATG
P1059(+)	ATGATGAGTATATT	AGTAGGACCCAC	AGGCCCGAC	AGGACCTACA	GETGATACCGET	GTGCCCGGA	GGAGCCATAG	TATTACAGGCC	CAACAGGTCAAAGTATG
P4025(+)	ATGATGAGTATAT	AGTAGGACCCAC	AGGCCCGAC	AGGACCTACA	GGTGATACCGGT	GTGCCCGGA	GGAGCCATAG	TATTACAGGCC	CAACAGGTCAAAGTATG
Frame 1 P4035(+)	M M S I L	. V G P T AGTAGGACCCAC	G P T AGGCCCGAC	G P T AGGACCTACA	G D T G GGTGATACCGGT	GT <mark>G</mark> CCCGGA	G A I G GGAGCCATAGG	TAT ACAGGCC	P T G Q S M CAACAGGTCAAAGTATG
Frame 1 P4056(+)	M M S I L	V G P T	G P T		G D T G	V P G	G A I G	I T G	P T G Q S M
Frame 1	M M S I L	V G P T	G P T	G P T	G D T G	V P G	G A I G	TAT ACACCCC	P T G Q S M
Frame 1	M M S I L	V G P T	G P T	G P T	G D T G	V P G	G A I G	TAT ACAGGCC	P T G Q S M
P2037(+) Frame 1	M M S I L	V G P T	G P T	G P T	G D T G	V P G	G A I G		P T G Q S M
P4008(+) Frame 1	ATGATGAGTATATI M M S I L	AGTAGGACCCAC V G P T	AGGCCCGAC	AGGACCTACA G P T	GGTGATACCGGT G D T G	GTGCCCGGA	GGAGCCATAGO G A I G	TATMACAGGCC	CAACAGGTCAAAGTATG P T G Q S M
P37(+) Frame 1	ATGATGAGTATATI M M S I L	AGTAGGACCCAC V G P T	AGGCCCGAC	AGGACCTACA G P T	GGTGATACCGGT G D T G	GT <mark>G</mark> CCCGGA	GGAGCCATAGO G A I G	TATMACAGGCC	CAACAGGTCAAAGTATG P T G Q S M
P1008(-)	ATGATGAGTATATT	AGTAGGACCCAC	AGGCCCGAC	AGGACCTACA	GGTGATACCGGT	GT <mark>G</mark> CCCGGA	GAGCCATAG	TATMACAGGCC	CAACAGGTCAAAGTATG
P1023(-)	ATGATGAGTATATT	AGTAGGACCCAC	AGGCCCGAC	AGGACCTACA	GGTGATACCGGT	GTGCCCGGA	GGAGCCATAG	TATMACAGGCC	CAACAGGTCAAAGTATG
P1024(-)	ATGATGAGTATATI	AGTAGGACCCAC	AGGCCCGAC	AGGACCTACA	GGTGATACCGGT	GTGCCCGGA	GGAGCCATAG	TATMACAGGCC	CAACAGGTCAAAGTATG
P1042(-)	ATGATGAGTATATI	AGTAGGACCCAC	AGGCCCGAC	AGGACCTACA	GGTGATACCGGT	GTGCCCGGA	GGAGCCATAGG	TATMACAGGCC	CAACAGGTCAAAGTATG
Frame 1 P1017(-)	M M S I L	. V G P T AGTAGGACCCAC	G P T	G P T AGGACCTACA	G D T G GGTGATACCGGT	V P G GT <mark>G</mark> CCCGGA	G A I G GGAGCCATAGO	I T G TATMACAGGCC	P T G Q S M CAACAGGTCAAAGTATG
Frame 1	M M S I L	V G P T	G P T	G P T	G D T G	V P G	G A I G	I T G	P T G Q S M
Frame 1			G P T	G P T	G D T G	V P G	G A I G		P T G Q S M
Frame 1	M M S I L	V G P T	G P T	G P T	G D T G	V P G	G A I G		P T G Q S M
P2012(-) Frame 1	M M S I L	AGTAGGACCCAC V G P T	AGGCCCGAC	AGGACCTACA G P T	GGTGATACCGGT G D T G	V P G	GGAGCCATAGO G A I G	TATAACAGGCC	CAACAGGTCAAAGTATG P T G Q S M
P3022(-) Frame 1	ATGATGAGTATATI M M S I L	AGTAGGACCCAC V G P T	AGGCCCGAC	AGGACCTACA G P T	GGTGATACCGGT G D T G	GTGCCCGGA	GGAGCCATAGO G A I G	TATMACAGGCC	CAACAGGTCAAAGTATG P T G Q S M
P4007(-) Frame 1	ATGATGAGTATATT M M S I L	AGTAGGACCCAC V G P T	AGGCCCGAC	AGGACCTACA G P T	GGTGATACCGGT G D T G	GT <mark>G</mark> CCCGGA	GGAGCCATAGO G A I G	TATMACAGGCC	CAACAGGTCAAAGTATG P T G Q S M
P2022(-) Frame 1	ATGATGAGTATATI M M S I I	AGTAGGACCCAC	AGGCCCGAC	AGGACCTACA G P T	GGTGATACCGGT G D T G	GT <mark>G</mark> CCCGGA	GGAGCCATAGO G A I G	TATMACAGGCC	CAACAGGTCAAAGTATG P T G Q S M
P3010(-)	ATGATGAGTATATT	AGTAGGACCCAC	AGGCCCGAC	AGGACCTACA	GGTGATACCGGT	GTGCCCGGA	GGAGCCATAG	TATMACAGGCC	CAACAGGTCAAAGTATG
P3019(-)	ATGATGAGTATATT	AGTAGGACCCAC	AGGCCCGAC	AGGACCTACA	GGTGATACCGGT	GTGCCCGGA	GGAGCCATAG	TATMACAGGCC	CAACAGGTCAAAGTATG
P3020(-)	ATGATGAGTATATT	AGTAGGACCCAC	AGGCCCGAC	AGGACCTACA	GGTGATACCGGT	GTGCCCGGA	GEAGCCATAGE	TATMACAGOCC	CAACAGGTCAAAGTATG
P3034(-)	ATGATGAGTATATI	AGTAGGACCCAC	AGGCCCGAC	AGGACCTACA	GGTGATACCGGT	GTGCCCGGA	GGAGCCATAG	TATMACAGGCC	CAACAGGTCAAAGTATG
P4014(-)	ATGATGAGTATATT	AGTAGGACCCAC	AGGCCCGAC	AGGACCTACA	GGTGATACCGGT	GT <mark>G</mark> CCCGGA	GGAGCCATAGO	TATMACAGGCC	CAACAGGTCAAAGTATG
Frame 1 P4021(-)	M M S I L	. V G P T AGTAGGACCCAC	G P T AGGCCCGAC	G P T AGGACCTACA	G D T G GGTGATACCGGT	V P G GT <mark>G</mark> CCCGGA	G A I G GGAGCCATAGG	I T G TATAACAGGCC	P T G Q S M CAACAGGTCAAAGTATG
Frame 1 P4046(-)	M M S I L	. V G P T	G P T	G P T	G D T G	V P G	G A I G	I T G	P T G Q S M
Frame 1 P1032(-)	M M S I L	V G P T	G P T	G P T	G D T G	V P G	G A I G	I T G	P T G Q S M
Frame 1	M M S I L			G P T			G A I G		P T G Q S M
Frame 1			G P T	G P T	G D T G	V P G	G A I G		P T G Q S M
Frame 1	M M S I L	V G P T	G P T	G P T	G D T G	V P G	G A I G		P T G Q S M
P1013(-) Frame 1	M M S I L	AGTAGGACCCAC V G P T	AGGCCCGAC	G P T	GGTGATACCGGT G D T G	V P G	GGAGCCATAGO G A I G	TATAACAGGCC	CAACAGGTCAAAGTATG P T G Q S M
P1014(-) Frame 1	M M S I L	AGTAGGACCCAC V G P T	AGGCCCGAC	AGGACCTACA G P T	GGTGATACCGGT G D T G	GT <mark>G</mark> CCCGGA V P G	GGAGCCATAGO G A I G	TATAACAGGCC	CAACAGGTCAAAGTATG P T G Q S M
P1015(-) Frame 1	ATGATGAGTATATI M M S I L	AGTAGGACCCAC V G P T	AGGCCCGAC	AGGACCTACA G P T	GGTGATACCGGT G D T G	GT <mark>G</mark> CCCGGA V P G	GGAGCCATAGO G A I G	TATMACAGGCC	CAACAGGTCAAAGTATG P T G Q S M
P2(-) Frame 1	ATGATGAGTATATT M M S I L	AGTAGGACCCAC V G P T	AGGCCCGAC	AGGACCTACA G P T	GGTGATACCGGT G D T G	GT <mark>G</mark> CCCGGA	GGAGCCATAGO G A I G	TATTACAGGCC	CAACAGGTCAAAGTATG P T G Q S M
P15(-) Frame 1	ATGATGAGTATATT	AGTAGGACCCAC V G P T	AGGCCCGAC	AGGACCTACA G P T	GGTGATACCGGT G D T G	GT <mark>G</mark> CCCGGA	GGAGCCATAGO	TAT ACAGGCC	CAACAGGTCAAAGTATG
P1044(-)	ATGATGAGTATATT	AGTAGGACCCAC	AGGCCCGAC	AGGACCTACA	GGTGATACCGGT	GTECCCGGA	GGAGCCATAG	TATTACAGGCC	CAACAGGTCAAAGTATG
P2003(-)	ATGATGAGTATATT	AGTAGGACCCAC	AGGCCCGAC	AGGACCTACA	GGTGATACCGGT	GTECCOGA	GGAGCCATAG	TATTACAGGCC	CAACAGGTCAAAGTATG
P2033(-)	ATGATGAGTATAT	AGTAGGACCCAC	AGGCCCGAC	AGGACCTACA	GGTGATACCGGT	GTTCCCGGA	GGAGCCATAG	TATTACAGGCC	CAACAGGTCAAAGTATG
P4028(-)	ATGATGAGTATATT	AGTAGGACCCAC	AGGCCCGAC	AGGACCTACA	GGTGATACCGGT	GTTCCCGGA	GGAGCCATAGO	TATTACAGGCC	CAACAGGTCAAAGTATG
Frame 1 P1027(-)	ATGATGAGTATATI	AGTAGGACCCAC	AGGCCCGAC	G P I AGGACCTACA	G D I G GGTGATACCGGT	GT <mark>G</mark> CCCGGA	G A I G	TAT ACAGGCC	P I G Q S M CAACAGGTCAAAGTATG
Frame 1 P1028(-)	M M S I L	. V G P T Agtaggacccac	G P T	G P T AGGACCTACA	G D T G GGTGATACCGGT	V P G GT <mark>G</mark> CCCGGA	G A I G GGAGCCATAGO	I T G TATTACAGGCC	P T G Q S M CAACAGGTCAAAGTATG
Frame 1 P1029(-)	M M S I L	V G P T	G P T	G P T	G D T G	V P G	G A I G	I T G	P T G Q S M
Frame 1 P1036(-)	M M S I L	V G P T	G P T	G P T	G D T G	V P G	G A I G	I T G	P T G Q S M
Frame 1	M M S I L	V G P T	G P T	G P T	G D T G	V P G	G A I G		P T G Q S M
Frame 1	M M S I L	V G P T	G P T	G P T	G D T G	V P G	G A I G		P T G Q S M
P2040(-) Frame 1	M M S I L	V G P T	AGGCCCGAC	G P T	G D T G	V P G	G A I G		P T G Q S M
P4054(-) Frame 1	M M S I L	AGTAGGACCCAC V G P T	AGGCCCGAC	G P T	G D T G	GT <mark>G</mark> CCCGGA V P G	GGAGCCATAGO G A I G	TAT ACAGGCC	CAACAGGTCAAAGTATG P T G Q S M
P4059(-) Frame 1	ATGATGAGTATATI M M S I L	AGTAGGACCCAC V G P T	AGGCCCGAC	AGGACCTACA G P T	GGTGATACCGGT G D T G	GT <mark>G</mark> CCCGGA V P G	GGAGCCATAGO G A I G	TAT ACAGGCC	CAACAGGTCAAAGTATG P T G Q S M
P4060(-) Frame 1	ATGATGAGTATATI M M S I L	AGTAGGACCCAC V G P T	AGGCCCGAC	AGGACCTACA G P T	GGTGATACCGGT G D T G	GT <mark>G</mark> CCCGGA V P G	GGAGCCATAGO G A I G	TATTACAGGCC I T G	CAACAGGTCAAAGTATG P T G Q S M

Identity	110	120	130	140	150	160	170	180	190	200 210
C1(+)	ACTGGTATAAT	GGGTAATCAAG	GT CCA A	GTGGTATACAAGG				GGTATAACAGGCA	TAACAGGCC	CAACAGGTATAACAGGT
Frame 1 C19(+)	ACTGGTATAAT	GGGTAATCAAGO	TCCAA	GTGGTATACAAGG				G I I G GGTATAACAGGCA	TAACAGGCC	CAACAGGTATAACAGGT
Frame 1 P3(+)	T G I N ACTGGTATAAT	1 G N Q 0 GGGTAATCAAG0	G TCCAA	S G I Q G GTGGTATACAAGG				G I T G GGTATAACAGGCA	I T G I	P T G I T G
Frame 1 P20(+)	T G I N			S G I Q G				G I T G		T G I T G
Frame 1							P	G I T G		
Frame 1				S G I Q G				G I T G		
Frame 1	T G I N	I G N Q C	SICCAA	S G I Q G				G I T G		T G I T G
P1059(+) Frame 1	ACTGGTATAAT T G I M	GGGTAATCAAGO	GTCCAA G	GTGGTATACAAGG S G I Q G			P	G I T G	TAACAGGCCC	CAACAGGTATAACAGGT
P4025(+) Frame 1	ACTGGTATAAT T G I N	GGGTAATCAAGO	GTCCAA F	GTGGTATACAAGG S G I Q G			CCAACA	G I T G	TAACAGGCCC	CAACAGGTATAACAGGT P T G I T G
P4035(+) Frame 1	ACTGGTATAAT T G I M	GGGTAATCAAGC		GTGGTATACAAGG S G I Q G	•			GGTATAACAGGCA G I T G	TAACAGGCC I T G I	CAACAGGTATAACAGGT T G I T G
P4056(+) Frame 1	ACTGGTATAAT T G I M	GGGTAATCAAGG		GTGGTATACAAGG S G I Q G	•			GGTATAACAGGCA G I T G	TAACAGGCCC	CAACAGGTATAACAGGT
P4058(+) Frame 1	ACTGGTATAAT T G I N	GGGTAATCAAGO		GTGGTATACAAGG				GGTATAACAGGCA G I T G		CAACAGGTATAACAGGT
P2037(+)	ACTGGTATAAT	GGGTAATCAAG		GTGGTATACAAGG				GTATAACAGGCA	TAACAGGCC	CAACAGGTATAACAGGT
P4008(+)	ACTEGTATAAT	GGGTAATCAAG		GTGGTATACAAGG			CCAACA	GGTATAACAGGCA	TAACAGGCC	CAACAGGTATAACAGGT
P37(+)	ACTEGTATAAT	GGGTAATCAAG	TCCAA	GTGGTATACAAGG			CCAACA	GGTATAAÇAGGCA	TAACAGGCC	CAACAGGTATAACAGGT
P1008(-)	ACTGGTATAAT	GGGTAATCAAG		GTGGTATACAAGG			CCAACA	GTATAACAGGCA	TAACAGGAC	CAACAGGTATAACAGGT
P1023(-)	ACTGGTATAAT	GGGTAATCAAGO		GTGGTATACAAGG			CCAACA	G I I G GGTATAACAGGCA	TAACAGG <mark>M</mark> C	CAACAGGTATAACAGGT
Frame 1 P1024(-)	T G I N ACTGGTATAAT	I G N Q C GGGTAATCAAGC	GTCTAA	S G I Q G				G I T G GGTATAACAGGCA	TAACAGGAC	P T G I T G CAACAGGTATAACAGGT
Frame 1 P1042(-)	T G I N ACTGGTATAAT	1 G N Q G GGGTAATCAAGG	STC T AA	S G I Q G GTGGTATACAAGG				G I T G GGTATAACAGGCA		P T G I T G CAACAGGTATAACAGGT
Frame 1 P1017(-)	T G I M	1 G N Q 0 GGGTAATCAAG0	GTCCAA	S G I Q G GTGGTATACAAGG				G I T G GGTATAACAGGCA	I T G I	P T G I T G
Frame 1 P2008(-)	T G I N	I G N Q O		S G I Q G				G I T G		P T G I T G
Frame 1 P2009(-)	T G I N	G N Q C		S G I Q G				G I T G	I T G I	T G I T G
Frame 1	T G I N			S G I Q G				G I T G	I T G I	
Frame 1							P			
Frame 1										
Frame 1	T G I N	I G N Q C		S G I Q G			P	G I T G		P T G I T G
Frame 1	T G I N	I G N Q C		S G I Q G			P	G I T G		T G I T G
P3010(-) Frame 1	T G I N	I G N Q O		S G I Q G			P	G I T G	TAACAGGCCC	T G I T G
P3019(-) Frame 1	ACTGGTATAAT T G I M	GGGTAATCAAGO I G N Q O	БТССАА	GTGGTATACAAGG S G I Q G			P	G I T G	TAACAGGCCC	CAACAGGTATAACAGGT T G I T G
P3020(-) Frame 1	ACTGGTATAAT T G I M	GGGTAATCAAGO	GTCCAA P	GTGGTATACAAGG S G I Q G			P	G I T G	TAACAGGCCC	CAACAGGTATAACAGGT
P3034(-) Frame 1	ACTGGTATAAT T G I M	GGGTAATCAAGO		GTGGTATACAAGG S G I Q G			P	G I T G	TAACAGGCCC	CAACAGGTATAACAGGT
P4014(-) Frame 1	ACTGGTATAAT T G I M	GGGTAATCAAGO	STCCAA P	GTGGTATACAAGG S G I Q G				GGTATAACAGGCA G I T G	TAACAGGCCC	CAACAGGTATAACAGGT T G I T G
P4021(-) Frame 1	ACTGGTATAAT T G I M	GGGTAATCAAGO		GTGGTATACAAGG S G I Q G			CCAACA	GGTATAACAGGCA G I T G	TAACAGGCCC	CAACAGGTATAACAGGT T G I T G
P4046(-) Frame 1	ACTGGTATAAT T G I M	GGGTAATCAAGG	TCCAA	GTGGTATACAAGG S G I Q G	•			GGTATAACAGGCA G I T G	TAACAGGCCC	CAACAGGTATAACAGGT T G I T G
P1032(-) Frame 1	ACTGGTATAAT T G I M	GGGTAATCAAGC	GTCCAA	GTGGTATACAAGG S G I Q G	•		CCAACA	GGTATAACAGGCA G I T G	TAACAGGCCC	CAACAGGTATAACAGGT
P3025(-) Frame 1	ACTGGTATAAT T G I M	GGGTAATCAAGG		GTGGTATACAAGG S G I Q G				GGTATAACAGGCA G I T G	TAACAGGCCC	CAACAGGTATAACAGGT
P1012(-) Frame 1	ACTGGTATAAT T G I M	GGGTAATCAAGG		GTGGTATACAAGG S G I Q G	•			GGTATAACAGGCA G I T G		CAACAGGTATAACAGGT
P1013(-) Frame 1	ACTGGTATAAT T G I N	GGGTAATCAAGG		GTGGTATACAAGG S G I Q G				GGTATAACAGGCA G I T G		CAACAGGTATAACAGGT T G I T G
P1014(-)	ACTGGTATAAT	GGGTAATCAAG		GTGGTATACAAGG				GGTATAACAGGCA		CAACAGGTATAACAGGT
P1015(-)	ACTGGTATAAT	GGGTAATCAAG		GTGGTATACAAGG				G TATAACAGGCA		CAACAGGTATAACAGGT
P2(-)	ACTGGTATAAT	GGGTAATCAAG		GTGGTATACAAGG				GGTATAACAGGCA	TAACAGGCC	CAACAGGTATAACAGGT
P15(-)	ACTOGTATAAT	GGGTAATCAAG		GTGGTATACAAGG				GETATAACAGECA	TAACAGGCC	CAAÇAGGTATAAÇAGGT
P1044(-)	ACTEGTATAAT	GGGTAATCAAG		GTGGTATACAAGG			CCAATA	GGTATAAÇAGGCA	TAACAGGCC	CAAÇAGGTATAAÇAGGT
P2003(-)	ACTGGTATAAT	GGGTAATCAAG		GTGGTATACAAGG			CCAATA	GGTATAACAGGCA	TAACAGGCC	CAACAGGTATAACAGGT
P2033(-)	ACTGGTATAAT	GGGTAATCAAG		GTGGTATACAAGG			CCAATA	GTATAACAGGCA	TAACAGGCC	CAACAGGTATAACAGGT
Frame 1 P4028(-)	ACTGGTATAAT	GGGTAATCAAGO	TCCAA	GTGGTATACAAGG				G I I G GGTATAACAGGCA	TAACAGGCC	CAACAGGTATAACAGGT
Frame 1 P1027(-)	T G I N ACTGGTATAAT	1 G N Q G GGGTAATCAAGG	GTCCAA	S G I Q G				G I T G GGTATAACAGGCA	TAACAGGCC	P T G I T G CAACAGGTATAACAGGT
Frame 1 P1028(-)	T G I N ACTGGTATAAT	1 G N Q G GGGTAATCAAGG	5 P 5 T C C A A	S G I Q G GTGGTATACAAGG				G I T G GGTATAACAGGCA	I T G I	P T G I T G CAACAGGTATAACAGGT
Frame 1 P1029(-)	T G I M ACTGGTATAAT	I G N Q C GGGTAATCAAGC	GTCCAA	S G I Q G GTGGTATACAAGG				G I T G GGTATAACAGGCA		P T G I T G CAACAGGTATAACAGGT
Frame 1 P1036(-)	T G I N ACTGGTATAAT	GGGTAATCAAGO		S G I Q G				G I T G		P T G I T G
Frame 1 P2025(-)	T G I N	GGGTAATCAAGO		S G I Q G				G I T G	I T G I	T G I T G
Frame 1 P2040(-)				S G I Q G				G I T G	I T G I	T G I T G
Frame 1 P4054/-)				S G I Q G				G I T G		
Frame 1				S G I Q G			P	G I T G	TAACAGC	
Frame 1		G N Q C		S G I Q G			P	G I T G		
F4000(-)	TGILAN	G N O		GIGGIAIACAAGG			CLAARA	GIA AACAGGCA	T	T G A A CAGGI

	330	330	240	100	270	20		200	310
Identity	220	250	240	250 2	270			500	510
C1(+) Frame 1	ATAACAGGAATC I T G I	CGGGCATATCTAT G I S I	AACAGGCCCAACA T G P T	GGTACAACAG G T T	GTTTTACAGGAA G F T G	TAACAGG I T G	CCACGGGA <mark>G</mark> T P T G V	AACAGGCCCAA T G P	CAGGAGAAACAGG TGETG
C19(+) Frame 1	ATAACAGGAATC	CGGGGCATATCTAT G I S I	AACAGGCCCAACA T G P T	G TACAACAG G T	GTTTTACAGGAA G F T G	TAACAGG C	CCACGGGAGT P T G V	AACAGGCCCAA T G P	CAGGAGAAACAGG T G E T G
P3(+) Frame 1	ATAACAGGAATC	CGGGCATATCTAT G I S I	AACAGGCCCAACA T G P T	G T T	GTTTTACAGGAA G F T G	TAACAGG I T G	CCACGGGA <mark>G</mark> T P T G V	AACAGGCCCAA T G P	CAGGAGAAACAGG T G E T G
P20(+) Frame 1	ATAACAGGAATC I T G I	CGGGCATATCTAT G I S I	AACAGGCCCAACA T G P T	GGTACAACAG G T	GTTTTACAGGAA G F T G	TAACAGG I T G	CCACGGGA <mark>G</mark> T P T G V	AACAGGCCCAA T G P	CAGGAGAAACAGG <mark>G</mark> T G E T G
P1003(+) Frame 1	ATAACAGGAATC I T G I	CGGGCATATCTAT G I S I	AACAGGCCCAACA T G P T	G G T A C A A C A G G T T	GTTTTACAGGAA G F T G	TAACAGG I T G	CCACGGGA <mark>G</mark> T P T G V	AACAGGCCCAA T G P	CAGGAGAAACAGG <mark>G</mark> T G E T G
P1006(+) Frame 1	ATAACAGGAATC I T G I	CGGGGCATATCTAT G I S I	AACAGGCCCAACA T G P T	G TACAACAG G T	GTTTTACAGGAA G F T G	TAACAGG T C I T G	CCACGGGA <mark>G</mark> T P T G V	AACAGGCCCAA T G P	CAGGAGAAACAGG T G E T G
P1059(+) Frame 1	ATAACAGGAATC	CGGGGCATATCTAT G I S I	AACAGGCCCAACA T G P T	G T T	GTTTTACAGGAA G F T G	TAACAGG C	CCACGGGAGT P T G V	AACAGGCCCAA T G P	CAGGAGAAACAGG T G E T G
P4025(+) Frame 1	ATAACAGGAATC I T G I	CGGGGCATATCTAT G I S I	AACAGGCCCAACA T G P T	G T A C A A C A G G T T	GTTTTACAGGAA G F T G	TAACAGGTC I T G	CCACGGGA <mark>G</mark> T P T G V	AACAGGCCCAA T G P	CAGGAGAAACAGG T G E T G
P4035(+) Frame 1	ATAACAGGAATC	CGGGGCATATCTAT G I S I	AACAGGCCCAACA T G P T	G T T	GTTTTACAGGAA G F T G		CCACGGGAGT P T G V	AACAGGCCCAA T G P	CAGGAGAAACAGG TGETG
P4056(+) Frame 1	ATAACAGGAATC	CGGGCATATCTAT G I S I	AACAGGCCCAACA T G P T		GTTTTACAGGAA G F T G		CCACGGGAGT P T G V	AACAGGCCCAA T G P	CAGGAGAAACAGG TGETG
P4058(+) Frame 1	ATAACAGGAATC	CGGGCATATCTAT G I S I	AACAGGCCCAACA T G P T	G T T G T G T	GTTTTACAGGAA G F T G	TAACAGG I T G	CCACGGGAGT P T G	AACAGGCCCAA T G P	CAGGAGAAACAGG TGETG
P2037(+) Frame 1	ATAACAGGAATC	CGGGCATATCTAT G I S I	AACAGGCCCAACA T G P T		GTTTTACAGGAA G F T G		CCACGGGAGT P T G	AACAGGCCCAA T G P	CAGGAGAAACAGG T G E T G
P4008(+) Frame 1	ATAACAGGAATC	CGGGCATATCTAT G I S I	AACAGGCCCAACA T G P T		GTTTTACAGGAA G F T G		CCACGGGAGT P T G V	AACAGGCCCAA T G P	CAGGAGAAACAGG TGETG
P37(+) Frame 1	ATAACAGGAATC	CGGGCATATCTAT G I S I	AACAGGCCCAACA T G P T		GTTTTACAGGAA G F T G		CCACGGGAGT P T G V	AACAGGCCCAA T G P	CAGGAGAAACAGG TGETG
P1008(-) Frame 1	ATAACAGGAATC	GCGGGCATATCTAT A G I S I	AACAGGCCCAACA T G P T		GTTTTACAGGAA G F T G		CCACGGGAGT P T G V	AACAGGCCCAA T G P	CAGGAGAAACAGG T G E T G
P1023(-) Frame 1	ATAACAGGAATC	GCGGGCATATCTAT A G I S I	AACAGGCCCAACA T G P T		GTTTTACAGGAA G F T G	TAACAGGCC	CCACGGGAGT P T G V	AACAGGCCCAA T G P	CAGGAGAAACAGG T G E T G
P1024(-) Frame 1	ATAACAGGAATC	GCGGGCATATCTAT A G I S I	AACAGGCCCAACA T G P T		GTTTTACAGGAA G F T G		CCACGGGAGT P T G V	AACAGGCCCAA T G P	CAGGAGAAACAGG T G E T G
P1042(-) Frame 1	ATAACAGGAATC	GCGGGCATATCTAT A G I S I	AACAGGCCCAACA T G P T		GTTTTACAGGAA G F T G		CCACGGGAGT P T G V	AACAGGCCCAA T G P	CAGGAGAAACAGG T G E T G
P1017(-) Frame 1	ATAACAGGAATC	GCGGGCATATCTAT A G I S I	AACAGGCCCAACA T G P T		GTTTTACAGGAA G F T G		CCACGGGAGT P T G	AACAGGCCCAA T G P	CAGGAGAAACAGG T G E T G
P2008(-) Frame 1	ATAACAGGAATC	GCGGGCATATCTAT	AACAGGCCCAACA T G P T		GTTTTACAGGAA G F T G		CCACGGGAGT P T G	AACAGGCCCAA	
P2009(-) Frame 1	ATAACAGGAATC	GCGGGCATATCTAT A G I S I	AACAGGCCCAACA T G P T		GTTTTACAGGAA G F T G		CCACGGGAGT P T G	AACAGGCCCAA T G P	CAGGAGAAACAGG T G E T G
P2012(-) Frame 1	ATAACAGGAATC	GCGGGCATATCTAT	AACAGGCCCAACA T G P T		GTTTTACAGGAA G F T G		CCACGGGAGT P T G	AACAGGCCCAA	
P3022(-) Frame 1	ATAACAGGAATC	GCGGGCATATCTAT A G I S I	AACAGGCCCAACA T G P T		GTTTTACAGGAA G F T G		CCACGGGAGT P T G	AACAGGCCCAA T G P	CAGGAGAAACAGG T G E T G
P4007(-) Frame 1	ATAACAGGAATC	GCGGGCATATCTAT A G I S I	AACAGGCCCAACA T G P T		GTTTTACAGGAA G F T G		CCACGGGAGT P T G V	AACAGGCCCAA	
P2022(-) Frame 1	ATAACAGGAATC	CGGGCATATCTAT	AACAGGCCCAACA T G P T		GTTTTACAGGAA G F T G		CCACGGGAGT P T G V	AACAGGCCCAA T G P	CAGGAGAAACAGG T G E T G
P3010(-) Frame 1	ATAACAGGAATC	CGGGCATATCTAT	AACAGGCCCAACA T G P T		GTTTTACAGGAA G F T G		CCACGGGAGT P T G V	AACAGGCCCAA T G P	CAGGAGAAACAGG TGETG
P3019(-) Frame 1	ATAACAGGAATC	CGGGCATATCTAT	AACAGGCCCAACA T G P T		GTTTTACAGGAA G F T G		CCACGGGAGT P T G	AACAGGCCCAA	
P3020(-) Frame 1	ATAACAGGAATC	CGGGCATATCTAT	AACAGGCCCAACA T G P T		GTTTTACAGGAA G F T G		CCACGGGAGT P T G	AACAGGCCCAA T G P	CAGGAGAAACAGG T G E T G
P3034(-) Frame 1	ATAACAGGAATC	CGGGCATATCTAT	AACAGGCCCAACA T G P T		GTTTTACAGGAA G F T G	TAACAGGCC	CCACGGGAGT P T G V	AACAGGCCCAA	
P4014(-) Frame 1	ATAACAGGAATC	CGGGCATATCTAT G I S I	AACAGGCCCAACA T G P T		GTTTTACAGGAA G F T G		CCACGGGAGT P T G V	AACAGGCCCAA T G P	CAGGAGAAACAGG T G E T G
P4021(-) Frame 1	ATAACAGGAATC	CGGGCATATCTAT G I S I	AACAGGCCCAACA T G P T		GTTTTACAGGAA G F T G		CCACGGGAGT P T G V	AACAGGCCCAA T G P	CAGGAGAAACAGG T G E T G
P4046(-) Frame 1	ATAACAGGAATC	CGGGCATATCTAT G I S I	AACAGGCCCAACA T G P T		GTTTTACAGGAA G F T G		CCACGGGAGT P T G V	AACAGGCCCAA T G P	CAGGAGAAACAGG TGETG
P1032(-) Frame 1	ATAACAGGAATC	CGGGCATATCTAT G I S I	AACAGGCCCAACA T G P T		GTTTTACAGGAA G F T G		CCACGGGAGT P T G	AACAGGCCCAA T G P	CAGGAGAAACAGG T G E T G
P3025(-) Frame 1	ATAACAGGAATC	CGGGCATATCTAT G I S I	AACAGGCCCAACA T G P T		GTTTTACAGGAA G F T G		CCACGGGATT P T G	AACAGGCCCAA T G P	CAGGAGAAACAGG TGETG
P1012(-) Frame 1	ATAACAGGAATC	CGGGCATATCTAT G I S I	AACAGGCCCAACA T G P T		GTTTTACAGGAA G F T G		CCACGGGA <mark>G</mark> T P T G V	AACAGGCCCAA T G P	CAGGAGAAACAGG <mark>G</mark> T G E T G
P1013(-) Frame 1	ATAACAGGAATC	CGGGCATATCTAT G I S I	AACAGGCCCAACA T G P T		GTTTTACAGGAA G F T G		CCACGGGAGT P T G V	AACAGGCCCAA T G P	CAGGAGAAACAGG <mark>G</mark> T G E T G
P1014(-) Frame 1	ATAACAGGAATC	CGGGCATATCTAT G I S I	AACAGGCCCAACA T G P T		GTTTTACAGGAA G F T G		CCACGGGA <mark>G</mark> T P T G V	AACAGGCCCAA T G P	CAGGAGAAACAGG <mark>G</mark> T G E T G
P1015(-) Frame 1	ATAACAGGAATC I T G I	CGGGCATATCTAT G I S I	AACAGGCCCAACA T G P T		GTTTTACAGGAA G F T G		CCACGGGAGT P T G V	AACAGGCCCAA T G P	CAGGAGAAACAGG <mark>G</mark> T G E T G
P2(-) Frame 1	ATAACAGGAATC	CGGGGCATATCTAT G I S I	AACAGGCCCAACA T G P T	G TACAATAG	GTTTTACAGGAA G F T G		CCACGGGATT P T G	AACAGGCCCAA T G P	CAGGAGAAACAGG T G E T G
P15(-) Frame 1	ATAACAGGAATC I T G I	CGGGGCATATCTAT G I S I	AACAGGCCCAACA T G P T	G T ACAATAG	GTTTTACAGGAA G F T G	TAACAGGTC I T G	CCACGGGATT P T G	AACAGGCCCAA T G P	CAGGAGAAACAGG TGETG
P1044(-) Frame 1	ATAACAGGAATC I T G I	CGGGGCATATCTAT G I S I	AACAGGCCCAACA T G P T	G G T A C A A A G	GTTTTACAGGAA G F T G		CCACGGGATT P T G L	AACAGGCCCAA T G P	CAGGAGAAACAGG T G E T G
P2003(-) Frame 1	ATAACAGGAATC I T G I	CGGGGCATATCTAT G I S I	AACAGGCCCAACA T G P T	G T ACAATAG	GTTTTACAGGAA G F T G	TAACAGG ^{II} C I T G	CCACGGGATT P T G L	AACAGGCCCAA T G P	CAGGAGAAACAGG T G E T G
P2033(-) Frame 1	ATAACAGGAATC I T G I	ACGGGGCATATCTAT G I S I	AACAGGCCCAACA T G P T	G G T A C A A A G	GTTTTACAGGAA G F T G		CCACGGGATT P T G	AACAGGCCCAA T G P	CAGGAGAAACAGG T G E T G
P4028(-) Frame 1	ATAACAGGAATC	ACGGGGCATATCTAT G I S I	AACAGGCCCAACA T G P T	G TACAATAG	GTTTTACAGGAA G F T G	TAACAGG C	CCACGGGATT P T G	AACAGGCCCAA T G P	CAGGAGAAACAGG T G E T G
P1027(-) Frame 1	ATAACAGGAATC I T G I	CGGGGCATATCTAT G I S I	AACAGGCCCAACA T G P T	G TACAATAG	GTTTTACAGGAA G F T G	TAACAGG C	CCACGGGATT P T G	AACAGGCCCAA T G P	CAGGAGAAACAGG TGETG
P1028(-) Frame 1	ATAACAGGAATC I T G I	CGGGGCATATCTAT G I S I	AACAGGCCCAACA T G P T	G G T A C A A T A G G T T	GTTTTACAGGAA G F T G	TAACAGGTC I T G	CCACGGGATT P T G	AACAGGCCCAA T G P	CAGGAGAAACAGG T G E T G
P1029(-) Frame 1	ATAACAGGAATC I T G I	CGGGCATATCTAT G I S I	AACAGGCCCAACA T G P T	G T A C A A T A G	GTTTTACAGGAA G F T G	TAACAGGTC I T G	CCACGGGATT P T G	AACAGGCCCAA T G P	CAGGAGAAACAGG T G E T G
P1036(-) Frame 1	ATAACAGGAATC I T G I	CGGGGCATATCTAT G I S I	AACAGGCCCAACA T G P T	G T A C A A T A G	GTTTTACAGGAA G F T G	TAACAGGTC I T G		AACAGGCCCAA T G P	CAGGAGAAACAGG T G E T G
P2025(-) Frame 1	ATAACAGGAATC I T G I	CGGGGCATATCTAT G I S I	AACAGGCCCAACA T G P T	G T A C A A T A G	GTTTTACAGGAA G F T G	TAACAGGTC I T G	CCACGGGATT P T G	AACAGGCCCAA T G P	CAGGAGAAACAGG T G E T G
P2040(-) Frame 1	ATAACAGGAATC I T G I	CGGGGCATATCTAT G I S I	AACAGGCCCAACA T G P T	G T A C A A T A G	GTTTTACAGGAA G F T G	TAACAGGTC I T G	CCACGGGATT P T G	AACAGGCCCAA T G P	CAGGAGAAACAGG T G E T G
P4054(-) Frame 1	ATAACAGGAATC I T G I	CGGGCATATCTAT G I S I	AACAGGCCCAACA T G P T	G T ACAATAG	GTTTTACAGGAA G F T G	TAACAGGTC I T G	CCACGGGATT P T G	AACAGGCCCAA T G P	CAGGAGAAACAGG T G E T G
P4059(-) Frame 1	ATAACAGGAATC I T G I	CGGGCATATCTAT G I S I	AACAGGCCCAACA T G P T	G G T A C A A A A G G T A C A A A G	GTTTTACAGGAA G F T G	TAACAGGTC I T G	CCACGGGATT P T G	AACAGGCCCAA T G P	CAGGAGAAACAGG T G E T G
P4060(-)	ATAACAGGAATC	ACGGGCATATCTAT	AACAGGCCCAACA	GGTACAATAG	GTTTTACAGGAA	TAACAGG	CCACGGGATT	AACAGGCCCAA	

Identity	320	330	340	350	360	370	380	390	4	00	410	420
C1(+)	CCAGTTATATT	ATATCTGGTA	TAACAGGC	CCTACAGGGC	CAACAGGTCC	TACAGGTG	TAAATATA		ACAGGTATT			TAACA
Frame 1 C19(+)	CCAGTTATATT	ATATCTGGTA	TAACAGGC	CCTACAGGGC	P I G P CAACAGGTCC	TACAGGTG	TAAATATA	ACGGGTTCG	I G I ACAGGTATTA		CAAGG <mark>T</mark> A	TAACA
Frame 1 P3(+)	P V I F	I S G	I T G	P T G I	P T G P		V N I Тааатата.	T G S	T G I	T G S	Q G	I T
Frame 1			I T G			T G		T G S	T G I	T G S	QG	I T
Frame 1	P V I F	I S G	I T G	P T G I	P T G P	T G	V N I	T G S	T G I	T G S	Q G	
P1003(+) Frame 1	CCAGTTATATTT P V I F	ATATCTGGTA I S G	TAACAGGC	CCTACAGGGCC P T G	CAACAGGTCC P T G P	TACAGGTG T G	V N I	ACGGGTTCG. T G S	T G I	ACAGGATC T G S	Q G	TAACA I T
P1006(+) Frame 1	CCAGTTATATTT PVIF	ATATCTGGTA I S G	TAACAGGC	CCTACAGGGC	CAACAGGTCC P T G P	TACAGGTG T G	TAAATATA. V N I	ACGGGTTCG	ACAGGTATT. T G I	ACAGGAT <mark>C</mark> O T G <mark>S</mark>	CAAGG <mark>T</mark> A Q G	TAACA I T
P1059(+) Frame 1	CCAGTTATATTT PVIF	ATATCTGGTA	TAACAGGC	CCTACAGGGC	CAACAGGTCC P T G P	TACAGGT	TAAATATA	ACGGGTTCG. T G S	ACAGGTATT			TAACA
P4025(+)	CCAGTTATATTT	ATATCTGGTA	TAACAGGC	CCTACAGGGC	CAACAGGTCC	TACAGGT			CAGGTATT			TAACA
P4035(+)	CCAGTTATATT	ATATCTGGTA	TAACAGGC	CCTACAGGGC	CAACAGGTCC	TACAGGTG	TAAATATA		CAGGTATT		CAAGG	TAACA
P4056(+)	CCAGTTATATT	ATATCTGGTA	TAACAGGC	CCTACAGGGC	CAACAGGTCC	TACAGGTG	TAAATATA	ACGGGTTCG	ACAGGTATT.		CAAGGTA	TAACA
P4058(+)	CCAGTTATATT	ATATCTGGTA	TAACAGGC	CCTACAGGGC	CAACAGGTCC	TACAGGT	TAAATATA	ACGGGTTCG	ACAGGTATT.	ACAGGATC	CAAGGTA	TAACA
Frame 1 P2037(+)	P V I F CCAGTTATATTT	I S G ATATCTGGTA	TAACAGGC	P T G I	Р Т G Р СААСАББТСС	T G TACAGGTG	V N I	T G S ACGGGTT	T G I ACAGGTATT	T G S ACAGGAT	Q G CAAGG <mark>T</mark> A	TAACA
Frame 1 P4008(+)	P V I F	I S G	I T G		P T G P		V N I Тааатата.	T G S ACGGGTT	T G I	T G S ACAGGAT	Q G	I T
Frame 1	P V I F	I S G	I T G	P T G I	P T G P	T G	V Ν Ι ΤΑΑΑΤΑΤΑ	T G S	T G I	T G S	Q G	I T
Frame 1			T T G			T G	V N I		T G I		QG	T
Frame 1	P V I F	I S G	I T G	P T G I	P T G P	T G	N I	T G S	T G I	T G S	Q G	
P1023(-) Frame 1	CCAGTTATATTT PVIF	ATATCTGGTA I S G	TAACAGGC	P T G	CAACAGGTCC P T G P	TACAGGTA T G	N I	ACGGGTTCG. T G S	T G I	ACAGGATC T G S	Q G	TAACA I T
P1024(-) Frame 1	CCAGTTATATTT PVIF	ATATCTGGTA I S G	TAACAGGC	CCTACAGGGC	CAACAGGTCC P T G P	TACAGGTA T G	TAAATATA N I	ACGGGTTCG. T G S	ACAGGTATT. T G I		CAAGGCA Q G	TAACA I T
P1042(-) Frame 1	CCAGTTATATTT PVIF	ATATCTGGTA I S G	TAACAGGC	CCTACAGGGCC P T G	CAACAGGTCC P T G P	TACAGGTA T G	TAAATATA N I	ACGGGTTCG T G S	ACAGGTATT. T G I	ACAGGAT <mark>C</mark> O T G <mark>S</mark>	CAAGGCA Q G	TAACA I T
P1017(-) Frame 1	CCAGTTATATTT PVIF	ATATCTGGTA I S G	TAACAGGC	CCTACAGGGC	CAACAGGTCC P T G P	TACAGGTA T G	TAAATATA N I	ACGGGTTTG. T G L	ACAGGTATT. T G I	ACAGGATC T G S		TAACA
P2008(-)	CCAGTTATATTT P V I F	ATATCTGGTA	TAACAGGC	CCTACAGGGC		TACAGGT			ACAGGTATT.			TAACA
P2009(-)	CCAGTTATATT	ATATCTGGTA	TAACAGGC	CCTACAGGGC	CAACAGGTCC	TACAGGT			ACAGGTATT			TAACA
P2012(-)	CCAGTTATATT	ATATCTGGTA	TAACAGGC	CCTACAGGGC	CAACAGGTCC	TACAGGT	TAAATATA	ACGGGTTTG	ACAGGTATT.		CAAGGTA	TAACA
P3022(-)	CCAGTTATATT	ATATCTGGTA	TAACAGGC	CCTACAGGGC	CAACAGGTCC	TACAGGT	TAAATATA		ACAGGTATT.	ACAGGATC	CAAGG	TAACA
Frame 1 P4007(-)	P V I F CCAGTTATATTT	ATATCTGGTA	TAACAGGC	CCTACAGGGC	P T G P CAACAGGTCC	T G TACAGGT	TAAATATA.	T G L ACGGGTT	T G I ACAGGTATTA	T G S ACAGGAT	Q G CAAGG <mark>T</mark> A	TAACA
Frame 1 P2022(-)	P V I F	I S G ATATCTGGTA	I T G	P T G I	P T G P CAACAGGTCC	T G	Ν Ι	T G L	T G I	T G S ACAGGAT	Q G	I T TAACA
Frame 1 P3010(-)	P V I F	I S G	I T G	P T G I	P T G P	T G	Ν Ι	T G S	T G I	T G S	Q G	Ι Τ
Frame 1			T T G			T G	ΝΙ		T G I	T G S	Q G	ΤΑΑΓΑ
Frame 1			I T G	P T G I	P T G P	TG	N I		T G I	T G S	QG	I T
Frame 1	P V I F	I S G	I T G	P T G	P T G P	T G	N I		T G I	T G S	Q G	I T
P3034(-) Frame 1	CCAGTTATATTT PVIF	ATATCTGGTA I S G	TAACAGGC	P T G	CAACAGGTCC P T G P	TACAGGTA T G	N I	ACGGGTT G	T G I	ACAGGATC T G S	Q G	TAACA I T
P4014(-) Frame 1	CCAGTTATATTT P V I F	ATATCTGGTA I S G	TAACAGGC	CCTACAGGGCC P T G	CAACAGGTCC P T G P	TACAGGTA T G	TAAATATA N I	ACGGGTT G	T G I		CAAGG <mark>T</mark> A Q G	TAACA I T
P4021(-) Frame 1	CCAGTTATATTT PVIF	ATATCTGGTA I S G	TAACAGGC	CCTACAGGGC	CAACAGGTCC P T G P	TACAGGTA T G	TAAATATA N I		ACAGGTATT. T G I	ACAGGAT <mark>C</mark> O T G S	CAAGG A Q G	TAACA I T
P4046(-) Frame 1	CCAGTTATATTT PVIF	ATATCTGGTA I S G	TAACAGGC	CCTACAGGGC	CAACAGGTCC P T G P	TACAGGTA T G		ACGGGTTIG	ACAGGTATT. T G I			TAACA
P1032(-)	CCAGTTATATTT P V I F	ATATCTGGTA	TAACAGGC	CCTACAGGGC	CAACAGGTCC	TACAGGTG			ACAGGTATT.			TAACA
P3025(-)	CCAGTTATATT	ATATCTGGTA	TAACAGGC	CCTACAGGGC	CAACAGGTCC	TACAGGT	TAAATATA		ACAGGTATT			TAACA
P1012(-)	CCAGTTATATT	ATATETGETA	TAACAGGC	CCTACAGGGC	CAACAGGTCC	TACAGGTA	TAAATATA		ACAGGTATT.		CAAGGCA	TAACA
P1013(-)	CCAGTTATATT	ATATCTGGTA	TAACAGGC	CCTACAGGGC	CAACAGGTCC	TACAGGT	TAAATATA	ACGGGTTCG	ACAGGTATT.		CAAGGCA	TAACA
P1014(-)	CCAGTTATATT	ATATCTGGTA	TAACAGGC	CCTACAGGGC	CAACAGGTCC	TACAGGT	TAAATATA	ACGGGTTCG	ACAGGTATT		CAAGGCA	TAACA
P1015(-)	CCAGTTATATT	ATATCTGGTA	TAACAGGC	CCTACAGGGC	CAACAGGTCC	TACAGGT	TAAATATA.	ACGGGTTCG	ACAGGTATT	ACAGGAT	CAAGGCA	TAACA
Frame 1 P2(-)	P V I F CCAGTTATATTT	I S G ATATCTGGTA	I T G	P T G I	Р Т G Р СААСАББТСС	T G TACAGGT	N I Тааатата	T G <mark>S</mark> Acgggtt g	T G I ACAGGTATT	T G S ACAGGAT	Q G CAAGG <mark>T</mark> A	I T TAACA
Frame 1	P V I F	I S G	I T G	P T G I	P T G P	T G	Ν Ι		T G I			I T
Frame 1			I T G			T G			T G I	T G F	QG	TAACA
Frame 1			T T G	PTGI	P T G P	T G	N I	T G S	T G I	T G F	QG	TAACA
P2003(-) Frame 1	P V I F	ATAICIGGIA I S G	TAACAGGC	P T G I	P T G P	T G	N I	T G S	T G I	T G F	Q G	I AACA
P2033(-) Frame 1	CCAGTTATATTT PVIF	ATATCTGGTA I S G	TAACAGGC	CCTACAGGGCC	CAACAGGTCC P T G P	TACAGGTA T G	TAAATATA N I	ACGGGTTCG T G S	ACAGGTATT. T G I		CAAGGAA Q G	TAACA I T
P4028(-) Frame 1	CCAGTTATATTT PVIF	ATATCTGGTA I S G	TAACAGGC	CCTACAGGGC	CAACAGGTCC P T G P	TACAGGTA T G	TAAATATA N I	ACGGGTTCG. T G S	ACAGGTATT. T G I		CAAGG T A Q G	TAACA I T
P1027(-) Frame 1	CCAGTTATATTT PVIF	ATATCTGGTA I S G	TAACAGGC I T G	CCTACAGGGC	CAACAGGTCC P T G P	TACAGGTA T G	TAAATATA N I	ACGGGTTCG	ACAGGTATT. T G I		CAAGG T A Q G	TAACA I T
P1028(-) Frame 1	CCAGTTATATTT PVIF	ATATCTGGTA	TAACAGGC	CCTACAGGGC	CAACAGGTCC P T G P	TACAGGT			ACAGGTATT			TAACA
P1029(-)	CCAGTTATATT	ATATCTGGTA	TAACAGGC	CCTACAGGGC	CAACAGGTCC	TACAGGT	TAAATATA		ACAGGTATT		CAAGGTA	TAACA
P1036(-)	CCAGTTATATT	ATATCTGGTA	TAACAGGC	CCTACAGGGC	CAACAGGTCC	TACAGGT	TAAATATA	ACGGGTTCG	ACAGGTATT.		CAAGGTA	TAACA
P2025(-)	CCAGTTATATT	ATATCTGGTA	TAACAGGC	CCTACAGGGC	CAACAGGTCC	TACAGGT	TAAATATA	ACGGGTTCG	ACAGGTATT.		CAAGGTA	TAACA
Prame 1 P2040(-)	P V I F CCAGTTATATTT	ATATCTGGTA	TAACAGGC	CCTACAGGGC	CAACAGGTCC	TACAGGT	TAAATATA	ACGGGTTCG	ACAGGTATT.	I G F ACAGGAT	CAAGG	TAACA
Frame 1 P4054(-)	P V I F CCAGTTATATTT	I S G ATATCTGGTA	I T G	P T G I	P T G P CAACAGGTCC	T G TACAGGT	Ν Ι	T G <mark>S</mark> ACGGGTT C G.	T G I ACAGGTATT.	T G F ACAGGAT	Q G CAAGG T A	I T TAACA
Frame 1 P4059(-)	P V I F CCAGTTATATTT	I S G ATATCTGGTA	I T G	P T G I	P T G P	T G	Ν Ι	T G S ACGGGTT	T G I	T G F	Q G	I T TAACA
Frame 1	P V I F	I S G	I T G	P T G I	P T G P	T G	ΝΙ		T G I		Q G	I T
Frame 1	PVIF	I S G	TG	PTGI	PTGP	TG	N	T G S	TGI	TGF	O G	T

Identity		430	440	450	_	460	470		480	490		500		510	520
C1(+)	GGTAM	TACAGGGTTA	CAAGGCCCA	CAAGGTCC	CAAAT	CTCA	CCAGGACCA	TCGGGAA	TACAA	GGAAATC	AGGGGC	CGATAGG	GCCTA		GCTGAAATT
C19(+)	GGTAA	TACAGGGTTA	CAAGGCCCA	CAAGGTCC	CAAAT	CTCA	CCAGGACCA	TCGGGAA	TACAA	GGAAATC	AGGGGC	CGATAGG	GCCTA		GCTGAAATT
Frame 1 P3(+)	GGTAA	T G L	Q G P	Q G P		S	P G P	S G	I Q TACAA	G N GGAAATC	Q G	P I G			A E I
Frame 1	GN	T G L	Q G P	Q G P	Q I	S	P G P	S G	I Q	G N	Q G	P I G	P		A E I
Frame 1	G	T G L	Q G P	Q G P	Q	S	P G P	S G	I Q	GN	Q G	P I G	P	A S	A E I
P1003(+) Frame 1	G G T A A	TACAGGGTTA T G L	Q G P	Q G P	Q I	S	P G P	S G	I Q	GGAAATC G N	AGGG <mark>G</mark> C Q G	P I G	P	CAGCCAGIC A S	A E I
P1006(+) Frame 1	GGTAA	TACAGGGTTA T G L	CAAGGCCCA Q G P	CAAGGTCC Q G P	Q I	CTCA	CCAGGACCA P G P	TCGGGAA S G	TACAA I Q	GGAAATC G N	AGGG <mark>G</mark> C Q G	CGATAGG P I G	P	CAG <mark>CCAGT</mark> O	A E I
P1059(+)	GGTAA	TACAGGGTTA	CAAGGCCCA	CAAGGTCC	CAAAT	CTCA		TCGGGAA	TACAA	GGAAATC	AGGGCC	CGATAGG	GCCTA		GCTGAAATT
P4025(+)	GGTAM	TAÇAGGGTTA	CAAGGCCCA	CAAGGTCC	CAAAT	CTCA	CCAGGACCA	TEGGGAA	TACAA	GGAAATC	AGGGGC	CGATAGO	GCCTA		SCTGAAATT
P4035(+)	GGTAA	TACAGGGTTA	CAAGGCCCA	CAAGGTCC	CAAAT	CTCA	CCAGGACCA	TCGGGAA	TACAA	GGAAATC	AGGGGC	CGATAGG	GCCTA		GCTGAAATT
Frame 1 P4056(+)	GGTAM	T G L	Q G P	Q G P	Q I CAAAT	S CTCA	P G P CCAGGACCA	S G	I Q TACAA	G N GGAAATC	Q G AGGG <mark>G</mark> C	P I G	P GCCTA	CAGCAAGT	A E I SCTGAAATT
Frame 1	GETAN	T G L	Q G P	Q G P	Q I	S	P G P	S G	I Q	G N	Q G	P I G	P		A E I
Frame 1	GN		Q G P	Q G P	Q	S	P G P	SG	Q	GN	Q G	P I G	P	A S	A E I
Frame 1	GGTAA	T G L	Q G P	Q G P	Q I	S	P G P	S G	I Q	GGAAAIC G N	Q G	P I G	P		A E I
P4008(+) Frame 1	G G T A A	TACAGGGTTA T G L	CAAGGCCCA Q G P	CAAGGTCC Q G P	Q I	CTCA	CCAGGACCA P G P	S G	TACAA I Q	GGAAATC G N	AGGG <mark>G</mark> C Q G	P I G	GCCTA P		A E I
P37(+) Frame 1	GGTAA	TACAGGGTTA T G L	CAAGGCCCA Q G P	CAAGGTCC		CTCA	CCAGGACCA P G P	TCGGGAA	TACAA	GGAAATC G N	AGGGCC	CGATAGG	GCCTA		GCTGAAATT A E I
P1008(-)	GGTAA	TACAGGGTTA	CAAGGCCCA	CAAGGTCC	CAAAT	TCA	CCAGGACCA	TCGGGAA	TACAA	GGAAATC	AGGGGC	CGATAGG	GCCTA	CAGCAAGG	GCTGAAATT
P1023(-)	GGTA	TAÇAGGGTTA	CAAGGCCCA	CAAGGTCC	CAAAT	TCA	CCAGGACCA	TEGGGAA	TACAA	GGAAATC	AGGGGC	CGATAG	GCCTA		SCTGAAATT
P1024(-)	GGTAA	TACAGGGTTA	CAAGGCCCA	CAAGGTCC	CAAAT	TCA	CCAGGACCA	TCGGGAA	TACAA	GGAAATC	AGGGGC	CGATAGG	GCCTA	CAGCAAGG	GCTGAAATT
Frame 1 P1042(-)	GGTAA	T G L	Q G P CAAGGCCCA	Q G P	Q I CAAAT	S TCA	P G P CCAGGACCA	S G	I Q TACAA	G N GGAAATC	Q G AGGG <mark>G</mark> C	P I G	P GCCTA	CAG <mark>CAAGG</mark>	A E I GCTGAAATT
Frame 1	GGTAN	T G L	Q G P	Q G P		S	P G P	S G	I Q	G N	Q G	P I G			
Frame 1	GN		Q G P	Q G P	QI	S	P G P	SG	I Q	GN	Q G	P I G	P	AR	A E I
Frame 1	G	T G L	Q G P	Q G P	Q	S	P G P	S G	I Q	GNAATC	Q G	P I G	P		A E I
P2009(-) Frame 1	GGTAA G	TACAGGGTTA T G L	CAAGGCCCA Q G P	Q G P	Q I	S	P G P	S G	TACAA I Q	GGAAATC G N	AGGG <mark>G</mark> C Q G	P I G	P	CAG <mark>CAAGG</mark> O	A E I
P2012(-) Frame 1	GGTAA	TACAGGGTTA T G L	CAAGGCCCA Q G P	CAAGGTCC Q G P	Q I	CTCA	CCAGGACCA P G P	TCGGGAA S G	TACAA I Q	GGAAATC G N	AGGGGC Q G	P I G	GCCTA P	CAG <mark>CAAGG</mark> O	A E I
P3022(-) Frame 1	GGTAN	TACAGGGTTA T G L	CAAGGCCCA Q G P	CAAGGTCC	Q I	CTCA	CCAGGACCA P G P	TCGGGAA S G	TACAA I Q	GGAAATC G N	AGGG <mark>G</mark> C Q G	CGATAGG	GCCTA	CAG <mark>CAAGG</mark> O	GCTGAAATT A E I
P4007(-)	GGTAM	TACAGGGTTA	CAAGGCCCA			CTCA		TCGGGAA		GGAAATC	AGGGGC		GCCTA		GCTGAAATT
P2022(-)	GGTAM	TACAGGGTTA	CAAGGCCCA	CAAGGTCC	CAAAT	CTCA	CCAGGACCA	TCGGGAA	TACAA	GGAAATC	AGGGGC	CGATAG	GCCTA		GCTGAAATT
P3010(-)	GGTAM	TACAGGGTTA	CAAGGCCCA	CAAGGTCC	CAAAT	CTCA	CCAGGACCA	TCGGGAA	TACAA	GGAAATC	AGGGGC	CGATAGG	GCCTA		GCTGAAATT
P3019(-)	GGTAM	TAÇAGGGTTA	CAAGGCCCA	CAAGGTCC	CAAAT	CTCA	CCAGGACCA	TEGGGAA	TACAA	GGAAATC	AGGGGC	CGATAG	GCCTA		GCTGAAATT
P3020(-)	GGTAA	TACAGGGTTA	CAAGGCCCA	CAAGGTCC	CAAAT	CTCA	CCAGGACCA	TCGGGAA	TACAA	GGAAATC	AGGGGC	CGATAGG	GCCTA	CAGCAAGG	GCTGAAATT
P3034(-)	GGTAA	TACAGGGTTA	CAAGGCCCA	CAAGGTCC	CAAAT	CTCA	P G P CCAGGACCA	TCGGGAA	TACAA	G N GGAAATC	AGGGGC	CGATAGG	GCCTA	CAG <mark>CAAGG</mark>	A E I GCTGAAATT
Frame 1 P4014(-)	GGTAM	T G L	Q G P CAAGGCCCA	Q G P		S	P G P CCAGGACCA	S G	I Q TACAA	G N GGAAATC	Q G AGGG <mark>G</mark> C	P I G	P GCCTA	CAGCAAGG	A E I GCTGAAATT
Frame 1 P4021(-)	GGTAA	T G L	Q G P	Q G P	Q I	S	P G P	S G	I Q	G N	Q G	P I G			A E I
Frame 1	GN	T G L	Q G P	Q G P	QI	S	P G P	S G	I Q	G N	Q G	P I G	P	AR	A E I
Frame 1	G		Q G P	Q G P	QI	S	P G P	S G	I Q	GN	Q G	P I G	P	AR	A E I
Frame 1	GGTAM		Q G P	Q G P	Q I	S	P G P	S G	I Q	G N	Q G	P I G	P		A E I
P3025(-) Frame 1	G G T A C	TACAGGGTTA T G L	CAAGGCCCA Q G P	Q G P	Q I	S	P G P	S G	TACAA I Q	GGAAATC G N	AGGG <mark>G</mark> C Q G	P I G	P		A E I
P1012(-) Frame 1	GGTAM G	TACAGGGTTA T G L	CAAGGCCCA Q G P	CAAGGTCC Q G P	Q I	CTCA	CCAGGACCA P G P	TCGGGAA S G	TACAA I Q	GGAAATC G N	AGGG <mark>G</mark> C Q G	CGATAGG P I G	P	C A G TT (A V	GCTGAAATT A E I
P1013(-) Frame 1	GGTAN	TACAGGGTTA T G L	CAAGGCCCA Q G P	CAAGGTCC	CAAAT Q I	CTCA	CCAGGACCA P G P	TCGGGAA	TACAA I Q	GGAAATC G N	AGGG <mark>G</mark> C	CGATAGG P I G	P CCTG P		GCTGAAATT A E I
P1014(-) Frame 1	GGTAM	TACAGGGTTA T G L	CAAGGCCCA Q G P	CAAGGTCC	CAAAT	CTCA	CCAGGACCA P G P	TCGGGAA	TACAA	GGAAATC G N	AGGGGC	CGATAGG P I G	CCTG P		GCTGAAATT A E I
P1015(-)	GGTAM	TACAGGGTTA	CAAGGCCCA	CAAGGTCC	CAAAT	CTCA		TCGGGAA	TACAA	GGAAATC	AGGGGC	CGATAGG	CCTG		GCTGAAATT
P2(-)	GGTAC	TAÇAGGGTTA	CAAGGCCCA	CAAGGTCC	CAAAT	CTCA	CCAGGACCA	TEGGEAA	TACAA	GGAAATC	AGGGC	CGATAGG	CCTA		GCTGAAATT
P15(-)	GGTAC	TACAGGGTTA	CAAGGCCCA	CAAGGTCC	CAAAT	CTCA	CCAGGACCA	TCGGGAA	TACAA	GGAAATC	AGGGCC	CGATAGG	CCTA		GCTGAAATT
P1044(-)	GGTAC	TACAGGGTTA	CAAGGCCCA	CAAGGTCC	Q I CAAAT	CTCA	P G P CCAGGACCA	TCGGGAA	TACAA	G N GGAAATC		CGATAGG	CCTA	CAG <mark>CAAGT</mark> O	A E I GCTGAAATT
Frame 1 P2003(-)	G G T A C	T G L	Q G P CAAGGCCCA	Q G P	Q I CAAAT	S CTCA	P G P CCAGGACCA	S G	I Q TACAA	G N GGAAATC		P I G	P	CAGCAAGT	A E I GCTGAAATT
Frame 1 P2033(-)	GGTAC	T G L	Q G P	Q G P		S	P G P	S G	I Q	G N	Q G	P I G	P		A E I
Frame 1 P4028(-)	GGTAC	T G L	Q G P	Q G P		S	P G P	S G	I Q	G N	Q G	P I G	P		
Frame 1	G		Q G P	Q G P	QI	S	P G P	SG	I Q	GN	QG	P I G	P	A S	A E I
Frame 1	G	T G L	Q G P	Q G P	QI	S	P G P	S G	I Q	G N	Q G	P I G	P		A E I
Frame 1	G G T A C	T G L	Q G P	Q G P	Q I	S	P G P	S G	I Q	G N	Q G	P I G	P		A E I
P1029(-) Frame 1	G G T A C	TACAGGGTTA T G L	CAAGGCCCA Q G P	CAAGGTCC	Q I	CTCA S	P G P	S G	TACAA I Q	GGAAATC G N	AGGGCC QG	P I G	P	CAG <mark>CAAGT</mark> O	A E I
P1036(-) Frame 1	GGTAC	TACAGGGTTA T G L	CAAGGCCCA Q G P	CAAGGTCC Q G P	Q I	CTCA	CCAGGACCA P G P	TCGGGAA	TACAA I Q	GGAAATC G N		CGATAGG P I G	P	CAGCAAGT (GCTGAAATT A E I
P2025(-) Frame 1	G G T A C	TACAGGGTTA T G L	CAAGGCCCA Q G P	CAAGGTCC	Q I	CTCA	CCAGGACCA P G P	TCGGGAA	TACAA I Q	GGAAATC G N	AGGGCC	CGATAGG P I G	P	CAG <mark>CAAGT</mark> O TAAS	GCTGAAATT A E I
P2040(-) Frame 1	GGTAC	TACAGGGTTA T G I	CAAGGCCCA Q G P		CAAAT	CTCA	CCAGGACCA P G P	TCGGGAA	TACAA	GGAAATC G N	AGGGCC	CGATAGG	CCTA		GCTGAAATT A E I
P4054(-)	GGTAC	TACAGGGTTA	CAAGGCCCA	CAAGGTCC	CAAAT	CTCA		TCGGGAA	TACAA	GGAAATC	AGGGC	CGATAGG	CCTA		GCTGAAATT A E I
P4059(-)	GGTAC	TACAGGGTTA	CAAGGCCCA	CAAGGTCC	CAAAT	CTCA		TCGGGAA	TACAA	GGAAATC	AGGGC	CGATAGG	CCTA		GCTGAAATT
P4060(-)	GGTAC	TACAGGGTTA	CAAGGCCCA	CAAGGTCC	CAAAT	CTCA	CCAGGACCA	TCGGGAA	TACAA	GGAAATC	AGGGCC	GATAG	CCTA		GCTGAAATT

Identity	530 540	550	560	570	580	590	600	610	620	630
C1(+)	GCTTCTTTCAGAAGATT	CATTAGCA	ATGTAACTACAT	TTACAACACC	AGTCAATTTC	AATAGTCAGTT			TATCATTGTTAA	GTAAT
Frame 1		L A	N V T T I	F Τ Τ Ρ ΤΤΑΓΑΑΓΑΓΟ	V N F			S S S	I S L L	S N GTAAT
Frame 1	A S F R R F			F T T P	V N F	N S Q F	NL	S S S	S L L	S N
Frame 1	A S F R R F	LA	N V T T I	F T T P	V N F	N S Q F	NL	S S S	S L L	S N
P20(+) Frame 1	A S F R R F	CATTAGCAA	N V T T	F T T P	AGTCAATTTC V N F		NL	S S S	FATCATTGTTAA SLL	GTAAT S N
P1003(+) Frame 1	GCTTCTTTCAGAAGATT	CATTAGCAA L A	ATGTAACTACAT	TTACAACACC/	AGTCAATTTC V N F		AATCTI		TATCATTGTTAA S L L	GTAAT S N
P1006(+)	GCTTCTTTCAGAAGATT	CATTAGCA	ATGTAACTACAT	TTACAACACC	AGTCAATTTC	AATAGTCAGTT		AGTAGTAGCA	TATCATTGTTAA	GTAAT
P1059(+)	GCTTCTTTCAGAAGATT	CATTAGCA	ATGTAACTACAT	TTACAACACC	AGTCAATTTC	AATAGICAGIT	AATCT	AGTAGTAGCA	TATCATTGTTAA	GTAAT
Frame 1 P4025(+)	A S F R R F	CATTAGCA	N V T T I	F Τ Τ Ρ ΤΤΑCΑACACC/	V N F	N S Q F AATAGTCAGTT	AATCT	S S S FAGTAG T AG C A ⁻	I S L L FATCATTGTTAA	S N GTAAT
Frame 1 P4035(+)			N V T T I					S S S	I S L L	S N
Frame 1	A S F R R F			F T T P	V N F	N S Q F	NL	S S S		S N
Frame 1	A S F R R F		N V T T I	F T T P	V N F	N S Q F	NL	S S S	I S L L	S N
P4058(+) Frame 1	A S F R R F	CATTAGCAA	ATGTAACTACAT	TTACAACACC/ F T T P	AGTCAATTTC V N F	AATAGTCAGTT N S Q F	AATCTI N L	FAGTAGTAGCA SSSS	FATCATTGTTAA SLL	GTAAT S N
P2037(+) Frame 1	GCTTCTTTCAGAAGATT	CATTAGCAA L A	ATGTAACTACAT	TTACAACACC/	AGTCAATTTC V N F		AATCTI	AGTAGTAGCA S S S	TATCATTGTTAA	GTAAT S N
P4008(+)	GCTTCTTTCAGAAGATT		ATGTAACTACAT	TTACAACACC	AGTCAATTTC			AGTAGTAGCA	TATCATTGTTAA	GTAAT
P37(+)	GCTTCTTTCAGAAGATTCG	CATTAGCA	GTGTAACTACAT	TTACAACACC	AGTCAATTTC	AATAGTCAGTT	AATCC	AGTAGCAG	TATCATTGTTAA	GTAAT
Frame 1 P1008(-)	A S F R R F GCTTCTTTCAGAAGATT ∎G	A L A CATTAGCA	G V I I I ATGTAACTACAT	Ε Ι Ι Ρ ΤΤΑCΑACACC/	AGTCAATTTC	AATAGCAGTT		S S S FAGTAG T AG C A	I S L L FATCATTGTTAA	S N GTAAT
Frame 1 P1023(-)	A S F R R F	A L A	N V T T I	F Τ Τ Ρ	V N F			S S S	I S L L	S N GTAAT
Frame 1		A L A		F T T P	V N F	N S Q F	NL	S S S	S L L	S N
Frame 1	A S F R R F	A L A	N V T T I	F T T P	V N F	N S Q F	N L	S S S	S L L	S N
P1042(-) Frame 1	A S F R R F	A L A	N V T T I	F T T P	V N F	N S Q F	NL	S S S	I S L L	S N
P1017(-) Frame 1	GCTTCTTTCAGAAGATT TG A S F R R F	CATTAGCA A L A	ATGTAACTACAT	TTACAACACC/ F T T P	AGTCAATTTC V N F	AATAGCAGTT NSQF	AATCII N L	AGTAG AGCA	FATCATTGTTAA SLL	GTAAT S N
P2008(-)	GCTTCTTTCAGAAGATT	CATTAGCA A L A	ATGTAACTACAT	TTACAACACC/	AGTCAATTTC V N F		AATCTT		TATCATTGTTAA	GTAAT S N
P2009(-)	GCTTCTTTCAGAAGATT		ATGTAACTACAT	TTACAACACC	AGTCAATTTC	AATAGCCAGTT		AGTAGAGCA	TATCATTGTTAA	GTAAT
P2012(-)	GCTTCTTTCAGAAGATT	CATTAGCA	ATGTAACTACAT	TTACAACACC	AGTCAATTTC	AATAGCAGT		AGTAGTAGCA	TATCATTGTTAA	GTAAT
P3022(-)	a 5 F R R F GCTTCTTTCAGAAGATT ∎G	CATTAGCA	ATGTAACTACAT	F I I P TTACAACACC/	AGTCAATTTC	AATAGCAGTT	AATCT	AGTAGTAGCA	TATCATTGTTAA	GTAAT
Frame 1 P4007(-)	A S F R R F	A L A	N V T T I	F Τ Τ Ρ ΤΤΑCΑACACC/	V N F	N S Q F	AATCT	S S S FAGTAG T AG C A ⁻	I S L L FATCATTGTTAA	S N GTAAT
Frame 1		A L A			V N F			S S S	I S L L	S N
Frame 1		A L A		F T T P	V N F		N	S S S		SN
Frame 1		A L A		F T T P	V N F	N S Q F	N L	s s s		SN
Frame 1	A S F R R F	A L A	V T T I	F T T P	V N F	N S Q F	N L	S S S	I S L L	S N
P3020(-) Frame 1	GCTTCTTTCAGAAGATT TG A S F R R F	A L A	N V T T I	F T T P	AGTCAATTTC V N F		NL	S S S	FATCATTGTTAA SLL	GTAAT S N
P3034(-) Frame 1	GCTTCTTTCAGAAGATT TG A S F R R F	CATTAGCA A L A	ATGTAACTACAT	TTACAACACC/ F T T P	AGTCAATTTC V N F	AATAGCAGTT NSQF	AATCII N L	AGTAG AGCA	FATCATTGTTAA I S L L	GTAAT S N
P4014(-)	GCTTCTTTCAGAAGATT	CATTAGCA	ATGTAACTACAT	TTACAACACC/	AGTCAATTTC V N F		AATCTT		TATCATTGTTAA	GTAAT S N
P4021(-)	GCTTCTTTCAGAAGATT		ATGTAACTACAT	TTACAACACC	AGTCAATTTC			AGTAGTAGCA	TATCATTGTTAA	GTAAT
P4046(-)	GCTTCTTTCAGAAGATT	CATTAGCA	ATGTAACTACAT	TTACAACACC	AGTCAATTTC	AATAGCAGTT		AGTAGTAGCA	TATCATTGTTAA	GTAAT
P1032(-)	GCTTCTTTCAGAAGATT	A L A CATTAGCA	ATGTAACTACAT	F I I P TTACAACACC/	AGTCAATTTC	AATAG T CAG T T	AATCT	AGTAGTAGCA	TATCATTGTTAA	GTAAT
Frame 1 P3025(-)	A S F R R F	CATTAGCA	N V T T I	F Τ Τ Ρ ΤΤΑCΑACACC/	V N F	N S Q F		S S S FAGTAG T AG C A ⁻	I S L L FATCATTGTTAA	S N GTAAT
Frame 1			N V T T I	F Τ Τ Ρ				S S S	I S L L	S N
Frame 1	A S F R R F			F T T P	V N F	N S Q F	NP	S S S	S L L	S N
Frame 1	A S F R R F	LA	N V T T I	F T T P	V N F	N S Q F	N P	S S S	S L L	S N
P1014(-) Frame 1	A S F R R F		N V T T I	F T T P	V N F	N S Q F	N P	S S S	I S L L	GIAAI S N
P1015(-) Frame 1	A S F R R F	CATTAGCA	N V T T	F T T P	AGTMAATTTC V N F		AATCCI N P	S S S	FATCATTGTTAA SLL	GTAAT S N
P2(-) Frame 1	GCTTCTTTCAGAAGATT IG A S F R R F	CATTAGCA A L A	ATGTAACTACAT	TTACAACACC/ F T T P	AGTAATTTC V N F	AATAGTCAGTT N S Q F	AATACI N	AGTAGCAGAA S S S	TATCATTGTTAA SLL	GTAAT S N
P15(-) Frame 1	GCTTCTTTCAGAAGATT		ATGTAACTACAT	TTACAACACC	AGTMAATTTC			AGTAGCAGTA	TATCATTGTTAA	GTAAT
P1044(-)	GCTTCTTTCAGAAGATT	CATTAGCA	ATGTAACTACAT	TTACAACACC	AGTMAATTTC	AATAGTCAGTT	AATAC	AGTAGCAGTA	TATCATTGTTAA	GTAAT
P2003(-)	GCTTCTTTCAGAAGATT	CATTAGCA	ATGTAACTACAT	TTACAACACC	AGTMAATTTC	AATAG T CAG T T		AGTAGCAGAA	TATCATTGTTAA	GTAAT
Frame 1 P2033(-)	A S F R R F	A L A	N V T T I	F Τ Τ Ρ ΤΤΑCΑACACC	V N F	N S Q F		S S S FAGTAGCAGTA	I S L L FATCATTGTTAA	S N GTAAT
Frame 1 P4028(-)		A L A	N V T T I	F Τ Τ Ρ	V N F			S S S	I S L L	S N GTAAT
Frame 1	A S F R R F	A L A		F T T P	V N F	N S Q F	N	S S S		S N
Frame 1	A S F R R F	A L A	N V T T I	F T T P	V N F	N S Q F	N	S S S		SN
Frame 1	A S F R R F	A L A	N V T T I	F T T P	V N F	N S Q F	N T	S S S	I S L L	S N
P1029(-) Frame 1	GCTTCTTTCAGAAGATT TG A S F R R F	A L A	N V T T	F T T P	AGTAATTTC V N F	AATAG CAGTT N S Q F		AGTAGCAGTA' S S S	ATCATTGTTAA	GTAAT S N
P1036(-) Frame 1	GCTTCTTTCAGAAGATT IG A S F R R F	CATTAGCA A L A	ATGTAACTACAT	TTACAACACC/ F T T P	AGTAATTTC V N F	AATAGICAGITT N S Q F	AATACI	AGTAGCAGMA S S S	TATCATTGTTAA SLL	GTAAT S N
P2025(-) Frame 1	GCTTCTTTCAGAAGATT TG A S F R R F	CATTAGCA A L A	ATGTAACTACAT	TTACAACACC/ F T T P	AGTAATTTC V N F	AATAGTCAGTT N S Q F		AGTAGCAGAA S S S	TATCATTGTTAA SLL	GTAAT S N
P2040(-) Frame 1	GCTTCTTTCAGAAGATT		ATGTAACTACAT							GTAAT S N
P4054(-)	GCTTCTTTCAGAAGATT TG	CATTAGCA	ATGTAACTACAT	TTACAACACC	AGTAATTTC			AGTAGCAGTA	TATCATTGTTAA	GTAAT
P4059(-)	GCTTCTTTCAGAAGATTTG	CATTAGCA	ATGTAACTACAT	TACAACACC	AGTAATTTC	AATAGICAG		AGTAGCAGTA	TATCATTGTTAA	GTAAT
P4060(-)	GCTTCTTTCAGAAGATT	CATTAGCA	ATGTAACTACAT	TACAACACC	AGTAATTTC	AATAGICAG	AATAC	TAGTAGCAGTA	TATCATTGTTAA	GTAAT

Identity	640	650	660	670	680	690	700	710	720	730
C1(+)	AATACTGATA	TCAGTATACAA	CMGGTACCTATAT	ATTTAATTT	бе∎ее∎сте	TATATTCGGCA	бетбе <mark>∎бе</mark>	GGTGCAGGAGCC	AATGAATCCG	сп атстас
C19(+)	AATACTGATA	TCAGTATACAA	CMGGTACCTATAT	ATTTAATTT		TTATATTCGGCA	GGTGGTGGA	GGTGCAGGAGCC	AATGAATCCG	CT GTCTAC
Frame 1 P3(+)	AATACT <mark>GAT</mark> A	TCAGTATACAA	C G I Y I	F N F		TATATTCGGCA	G G G G G G G G G G G G G G G G G G G	G A G A GGTGCAGGAGCC	AATGAATCCG	A V Y
Frame 1 P20(+)	N T D AATACTGATA	I S I Q T C AGTATACAA	CMGGTACCTATAT	F N F	G G L GGTGGTCTO	TATATTCGGCA	G G G G G G G G G G G G G G G G G G G	G A G A A	N E S AATGAATCCG	A V Y
Frame 1 P1003(+)	N T D	I S I Q T C AGTATACAA	CAGTACCTATAT	F N F	G G L		G G G G G T G G T G G A		N E S	A V Y
Frame 1 P1006(+)	N T D		P G T Y I	F N F	G G L	Y S A	G G G		N E S	A V Y
Frame 1				F N F	G G L	Y S A				A V Y
Frame 1				F N F		Y S A			N E S	A V Y
Frame 1	N T D				G G L	Y S A				A V Y
P4035(+) Frame 1	N T D	I S I Q	P G T Y I	F N F	G G L	Y S A	G G G			A V Y
P4056(+) Frame 1	N T D	I S I Q	P G T Y I	F N F	G G G C I G G G L		GGTGG <mark>TGG</mark> A		N E S	A V Y
P4058(+) Frame 1	AATACTGATA N T D	TCAGTATACAAC	CAGGTACCTATAT P G T Y I	ATTTAATTT F N F	G G G G C T G G G L	TTATATTCGGCA	GGTGG <mark>TGGA</mark> G G <mark>G</mark>	G A G A A	AATGAATCCG N E S	GTCTAC A V Y
P2037(+) Frame 1	AATACTGATA	TCAGTATACAAC	CMGGTACCTATAT P G T Y I	ATTTAATTT F N F	G G G C T G		GGTGG <mark>TGGA</mark> G G G	G G T A G G A G C C	AATGAATCCG N E S	GTCTAC A V Y
P4008(+) Frame 1	AATACTGATA N T D	TCAGTATACAAC	G T Y I	ATTTAATTT F N F	G G G G G C T G G G L		GGTGG <mark>TGGA</mark> G G G	G G T A G G A G C C A G C C A G C C A G C C A G C C A G C C A G C C A G C C A G C C C A G C C C C	AATGAATCCG N E S	GTCTAC A V Y
P37(+) Frame 1	AATACTGATA N T D	TCAGTATACAAC	CCGGTACCTATAT G T Y I	ATTTAATTTC F N F	G G G G G C T C G G L	GTATGGGCGGAA V W A E	G G T G G G G T C	GCAGCATTCTAC A A F Y	AATGAATCCG N E S	GTCTAC A V Y
P1008(-) Frame 1	AATACTGATA N T D	TCAGTATACAAC	CEGGTACCTATAT P G T Y I	ATTTAATTT F N F	G G G G G C T G	TTAGGGGCATAT	GGTGG <mark>AA</mark> GT G G <mark>S</mark>	GAAGGAGCCTAC E G A Y	AATGAATCCG N E S	■GGTCTAC
P1023(-) Frame 1	AATACTGATA		G T Y I	ATTTAATTT F N F	G G G G G C T G		GGTGGAAG		AATGAATCCG N E S	GTCTAC
P1024(-)	AATACTGATA	CAGTATACAA	C G G T A C T A T A T	ATTTAATTT	GGGGGGCTC		GGTGGAAG		AATGAATCCG	GTCTAC
P1042(-)	AATACTGATA	TCAGTATACAA	CMGGTACCTATAT	ATTTAATTT		TAGGGGCATAT	GGTGGAAG	GAAGGAGCCTAC	AATGAATCCG	GTCTAC
P1017(-)	AATACTGATA	TCAGTATACAA	CAGGTACCTATAT	ATTTAATTT	GGCGGTCTC	TAGGGGCATAT	GGTGGAAG	GAAGGAGCCTAC	AATGAATCCG	TG GTCTAC
P2008(-)	AATACTGATA	TCAGTATACAA	CEGTACCTATAT	ATTTAATTT	Geegercie	TAGGGGCATAT	GETGE	GAAGGAGCCTAC	AATGAATCCG	TG GTCTAC
P2009(-)	AATACTGATA	TCAGTATACAA	C G G TACCTATAT	ATTTAATTT	GGCGGTCTG	TAGGGGCATAT	GGTGGAAG	GAAGGAGCCTAC	AATGAATCCG	TG GTCTAC
P2012(-)	AATACTGATA	TCAGTATACAA	CMGGTACCTATAT	ATTTAATTT	GGCGGTCTC	TAGGGGCATAT	GGTGGAAG	GAAGGAGCCTAC	AATGAATCCG	I GGTCTAC
P3022(-)	AATACT <mark>GAT</mark> A	TCAGTATACAA	C G T Y I	ATTTAATTT	GGCGGTCTC	TAGGGGCATAT	G G G S GGTGGAAGT	GAAGGAGCCTAC	AATGAATCCG	V V Y ■GTCTAC
P4007(-)	AATACT <mark>GAT</mark> A	I S I Q T C AGTATACAA	CMGGTACCTATAT	F N F	G G L G G C G G T C T G	TAGGGGCATAT	G G G S GGTGG <mark>AAG</mark>	GAAGGAGCCTAC	AATGAATCCG	V V Y ■GTCTAC
Frame 1 P2022(-)	N T D AATACT <mark>G</mark> ATA	I S I Q T C AGTATACAA	P G T Y I Cmggtacctatat	F N F	G G L GGCGGCCTO	TAGGGGTATAT	G G <mark>S</mark> GGTGG <mark>AAG</mark>	E G A Y	N E S AATGAATCCG	V V Y
Frame 1 P3010(-)	N T D AATACTGATA	I S I Q T C AGTATACAA	P G T Y I C G G T A C C T A T A T	F N F	G G L GGCGGTCTO	TAGGGGCATAT	G G S GGTGG <mark>AAG</mark>	S G A Y	N E S AATGAATCCG	V V Y TGGTCTAC
Frame 1 P3019(-)	N T D AATACTGATA	Ι S Ι Q Τ ΄ Α G ΤΑ ΤΑ C Α A	G T Y I	F N F	G G L GGCGGCCTG	TAGGGGCATAT	G G S GGTGGAAG	E G A Y	N E S AATGAATCCG	V V Y TGGTCTAC
Frame 1 P3020(-)	N T D AATACTGATA	I S I Q T C AGTATACAA	CAGGTACCTATAT	F N F	G G L GGCGGTCTO	TAGGGGCATAT	G G S GGTGGAAGT	E G A Y	N E S AATGAATCCG	V V Y TGGTCTAC
Frame 1 P3034(-)	N T D	I S I Q	CAGTACCTATAT	F N F	G G L		G G S GGTGGAAG		N E S AATGAATCCG	V V Y
Frame 1 P4014(-)	N T D	I S I Q	P G T Y I	F N F			G G S		N E S	V V Y
Frame 1 P4021(-)	N T D	I S I Q	P G T Y I	F N F	G G L		G G S		N E S	V V Y
Frame 1 P4046(-)	N T D	I S I Q	P G T Y I	F N F	G G L		G G S		N E S	V V Y
Frame 1 P1032(-)	N T D	I S I Q	P G T Y I	F N F	G G L		G G S		N E S	V V Y
Frame 1 P3025(-)			P G T Y I	F N F			G G S			V V Y
Frame 1					G G L		G G S			V V Y
Frame 1					G G L					V V Y
Frame 1					G G L					V V Y
Frame 1					G G L					VVY
Frame 1					G G L		G G S	S G A Y		V V Y
Frame 1		I S I Q		F N F	G G L		G G S	S V V E		V V Y
P15(-) Frame 1	N T N	I S I Q	P G T Y I	F N F	G G L	V W A H	G G G S	S V V E		V V Y
P1044(-) Frame 1	N T N	I S I Q	P G T Y I	F N F	G G L		G G G S	S V V E	N E S	V V Y
P2003(-) Frame 1	N T N	I S I Q	P G T Y I	F N F	GGCGGCTG G G L	V W A H	GGTGG <mark>AAG</mark> G G <mark>S</mark>	S V V E		V V Y
P2033(-) Frame 1	N T N	I S I Q	P G T Y I	F N F	GGCGGCCTG G G L	GTATGGGCACAT	GGTGGAAG G G S	S V V E	AATGAATCCG N E S	V V Y
P4028(-) Frame 1	AATACTAATA N T	TAGTATACAA	CAGGTACCTATAT P G T Y I	ATTTAATTT F N F	G G G G C T G G G L	GTATGGGCACAT	GGTGGAAG G G S		AATGAATCCG N E S	GTCTAC V V Y
P1027(-) Frame 1	AATACTAATA N T	TAGTATACAA I S I Q	G T Y I	ATTTAATTT F N F	G G G G C T G G G L	GTA GGGCACAT	GGTGG <mark>AAG</mark> G G S	S V V E	AATGAATCCG N E S	GTCTAC
P1028(-) Frame 1	AATACTAATA N T N	TAGTATACAA I S I Q	G T Y I	ATTTAATTT F N F	G G G G C T G G G L		GGTGG <mark>AAG</mark> G G S	S V V E	AATGAATCCG N E S	V V Y
P1029(-) Frame 1	AATACTMATA N T	TAGTATACAA I S I Q	G T Y I	ATTTAATTT F N F	G G G G C T G G G L	GTA GGGCACAT	GGTGG <mark>AAG</mark> G G S	S V V E	AATGAATCCG N E S	GTCTAC V V Y
P1036(-) Frame 1	AATACTMATA N T N	TAGTATACAA I S I Q	G T Y I	ATTTAATTT F N F	G G G G G C T G G G L	GTATGGGCACAT V W A H	GGTGG <mark>AAG</mark> GG S	S V V E	AATGAATCCG N E S	GTCTAC
P2025(-) Frame 1	AATACTMATA N T	TTAGTATACAAC	CMGGTACCTATAT P G T Y I	ATTTAATTT F N F	G G G G G C T G G G L	GTATGGGCACAT	GGTGG <mark>AAG</mark> G G S	S CAGTAGTCGAA	AATGAATCCG N E S	GTCTAC
P2040(-) Frame 1	AATACTMATA N T N	TTAGTATACAA	CEGGTACCTATAT P G T Y I	ATTTAATTT F N F	G G G G G C T G G G L	GTATGGGCACAT	GGTGG <mark>AAG</mark> G G S	S V V E	AATGAATCCG N E S	T GTCTAC
P4054(-) Frame 1	AATACTAATA	TAGTATACAA	C G G T A C C T A T A T P G T Y I	ATTTAATTT F N F	G G G G C T G		GGTGGAAG G G S		AATGAATCCG N E S	TTGTCTAC V V Y
P4059(-) Frame 1	AATACTAATA		G T Y I	ATTTAATTT F N F	G G G G C T G		GGTGGAAGT G G S		AATGAATCCG N E S	GTCTAC
P4060(-) Frame 1	AATACTMATA N T		C G G T A C C T A T A T P G T Y I	ATTTAATTT F N F	G G G G C T G		GGTGGAAG G G S		AATGAATCCG N E S	TTGTCTAC V V Y

Information -	740	750	760	770	780	790	800	810	820	830 840
Identity C1(+)	CTMTCATTAGT	TTTCAGGTAG	ICTTAAATACCI			CAACCTTATGG	TTTTGCTTC	ТАСТТТААСАС	GTCAAAATOCC	TCAGCATCAGCCTAC
Frame 1 C19(+)	L S L V	/ S G S	L N T	Y G T ATGGTACO	AATATCAA	Q P Y G	F A S	T L T	GICAAAATACC	S A S A Y TCA <mark>GCATCAGC</mark> CTAC
Frame 1 P3(+)	L S L V	/ S G S	L N T	Y G T ATGGTACO	AATATCAA	Q P Y G	F A S	T L T TACTTTAACAC	R Q N T	TCAGCATCAGCCTAC
P20(+)	CTMTCATTAGT	TTCAGGTAG	ICTTAAATACCI	TATGGTAC	AATATCAA	CAACCTTATG	TTTTGCTTC	TACTTTAACAC	GICAAAATACC	TCAGCATCAGCCTAC
P1003(+)	CTATCATTAGT	TTCAGGTAG	ICTTAAATACCI	TATGGTAC	AATATCAA	CAACCTTATG	TTTTGCTTC	TAÇTTTAAÇAC	GICAAAATACC	TCA <mark>GCATCAGC</mark> CTAC
P1006(+)	CTATCATTAG	TTCAGGTAG	CTTAAATACCI	TATGGTAC		CAACCTTATG	TTTTGCTTC	TAÇTTTAAÇAC	GICAAAATACC	TCATCATCATCCTAC
P1059(+)	CTATCATTAGT	TTCAGGTAG	CTTAAATACCI	ATGGTAC		CAACCTTATG	TTTTGCTTC	TACTTTAACAC	GICAAAATACC	TÇA <mark>GÇATÇ</mark> AG Ç CTAC
P4025(+)	CTATCATTAGT	TTCAGGTAG	CTTAAATACCI	ATGGTAC		CAACCTTATGG	TTTTGCTTC	TACTTTAACAC	GICAAAATACC	TCAGCATCAGCCTAC
P4035(+)	CTATCATTAGT	TTCAGGTAG	CTTAAATACCI	ATGGTACO		CAACCTTATGG	TTTTGCTTC	TACTTTAACAC	GICAAAATACC	
P4056(+)	CTATCATTAGT	TTCAGGTAG	CTTAAATACCI			CAACCTTATGG	TTTTGCTTC	TACTTTAACAC	GICAAAATACC	TCAGCATCAGCCTAC
P4058(+)	CTETCATTAGT	TTCAGGTAG	CTTAAATACCI			CAACCTTATGG	TTTTGCTTC	TACTTTAACAC	GICAAAATACC	
P2037(+)	CTATCATTAGT	TTCAGGTAG	CTTAAATACCI			CAACCTTATGG	TTTTGCTTC	TACTTTAACAC	GICAAAATACC	
P4008(+) Frame 1	CTATCATTAGT	TTCAGGTAG	CTTAAATACCI			CAACCTTATGG	TTTTGCTTC F A S	TACTTTAACAC		TCAGCATCAGCCTAC
P37(+) Frame 1	CTATCATTAGT	TTCAGGTAG				CAACCTTATGG	TTTTGCTTC	TACTTTAACAC		
P1008(-) Frame 1	CTNTCATTAGT	TTCAGGTAG	CTTAAATACCI			CAACCTTATGG	TTTTGCTTC F A S	TACTTTAACAC		
P1023(-) Frame 1	CTNTCATTAGT	TTCAGGTAG	CTTAAATACCI L N T		AATATCAA	CAACCTTATGG Q P Y G	TTTTGCTTC F A S	TACTTTAACAC T L T		TCATTACCATCCTAC S L P S Y
P1024(-) Frame 1	CTNTCATTAGT	TTCAGGTAG	CTTAAATACCI L N T		AATATCAA	CAACCTTATGG Q P Y G	TTTTGCTTC F A S	TACTTTAACAC		TCATTACCATCCTAC S L P S Y
P1042(-) Frame 1	CTNTCATTAGT L S L V	TTTCAGGTAG	CTTAAATACCI L N T		AATATCAA N I N	CAACCTTATGG Q P Y G	TTTTGCTTC F A S	TACTTTAACAC T L T	GCCAAAATTCC R Q N S	S L P S Y
P1017(-) Frame 1	CTNTCATTAGT L S L V	TTTCAGGTAG / S G S	CTTAAATACCI L N T		AATATCAA N I N	CAACCTTATGG Q P Y G	TTTTGCTTC F A S	TACTTTAACAC T L T	GCCAAAATTCC R Q N S	TCATTACCATCCTAC S L P S Y
P2008(-) Frame 1	CTATCATTAGT L S L V	TTCAGGTAG / S G S	CTTAAATACCI L N T		AATATCAA	CAACCTTATGG Q P Y G	TTTTGCTTC F A S	TACTTTAACAC T L T	GCAAAATICC R Q N S	TCATTACCATCCTAC S L P S Y
P2009(-) Frame 1	CTATCATTAGT L S L V	TTTCAGGTAG / S G S	CTTAAATACCI L N T	Y G	AATATCAA	CAACCTTATGG Q P Y G	TTTTGCTTC F A S	TACTTTAACAC T L T	GCAAAATICC R Q N S	TCATTACCATCCTAC S L P S Y
P2012(-) Frame 1	CTATCATTAGT L S L V	TTTCAGGTAG / S G S	CTTAAATACCI L N T		N I N	CAACCTTATGG Q P Y G	F A S	TACTTTAACAC T L T	GCAAAATICC R Q N S	TCATTACCATCCTAC S L P S Y
P3022(-) Frame 1	CTATCATTAGT L S L V	TTTCAGGTAG / S G S	CTTAAATACCI L N T		N I N	CAACCTTATGG Q P Y G	F A S	TACTTTAACAC T L T	GCCAAAATICC R Q N S	S CATTACCATCCTAC
P4007(-) Frame 1	CTNTCATTAGT L S L V	TTTCAGGTAG / S G S	CTTAAATACCI L N T	Y G	N I N	CAACCTTATGG Q P Y G	F A S	TACTTTAACAC T L T	GCAAAATICC R Q N S	TCATTACCATCCTAC S L P S Y
P2022(-) Frame 1	CTGTCATTAGT L S L V	TTTCAGGTAG / S G S	L N T	Y G T	N I K	CAACCTTATGG Q P Y G	F A S	TACTTTAACAC T L T	R Q N	TCATCAGGATCCTAC
P3010(-) Frame 1	CTATCATTAGT L S L V	FTTCAGGTAG / S G S	L N T	Y G	N I N	CAACCTTATGG Q P Y G	F A S	TACTTTAACAC T L T	R Q N S	S P S Y
P3019(-) Frame 1	CTATCATTAGT L S L V	FTTCAGGTAG / S G S	L N T	Y G	N I N	CAACCTTATGG Q P Y G	F A S	TACTTTAACAC T L T	R Q N S	S L P S Y
P3020(-) Frame 1	CTATCATTAGT L S L V	FTTCAGGTAG / S G S	CTTAAATACCI L N T	Y G	N I N	CAACCTTATGG Q P Y G	F A S		R Q N S	S L P S Y
P3034(-) Frame 1		/ S G S		Y G			F A S			
Frame 1		/ S G S		Y G			F A S			
Frame 1		S G S		Y G			F A S			
Frame 1		S G S					F A S			
Frame 1 P3025(-)		S G S					F A S			
Frame 1		/ S G S		Y G			F A S			
Frame 1 P1013(-)	L S L V CTGTCATTAGT	/ S G S	L Ν Τ	Y G T	AATATCAA	Q P Y G	F A S	Τ Ι Τ ΤΑΟΤΤΤΑΑΟΑΟ		S S P A Y
Frame 1 P1014(-)	L S L V CT <mark>G</mark> TCATTAGT	/ S G S TTTCAGGTAG	L Ν Τ	Y G T ATGGTACO	AATATCAA	Q P Y G	F A S	T L T TACTTTAACAC	R Q N	S S P A Y TCA TC ACCAGCCTAC
Frame 1 P1015(-)	L S L V CT <mark>G</mark> TCATTAGT	/ S G S TTTCAGGTAG	L N T	Y G TATGGTACO	AATATCAA	Q P Y G	F A S	T L T TACTTTAACAC	R Q N TACC	S S P A Y TCA TC A CC A GC CTAC
Frame 1 P2(-)	L S L V CTMTCATTAGT	/ S G S FTTCAGGTAG	L N T	Y G TATGGTACC	AATATCAAC	Q P Y G CAACCTTATGG	F A S	T L T TACTTTAACAC	R Q N T G CAAAAT ACC	S S P A Y TCATCAGCATCCTAC
Frame 1 P15(-)	L S L V CTNTCATTAGT	/ S G S	L N T	Y G TATGGTACC	AATATCAA	Q P Y G	F A S	T L T TACTTTAACAC		S S A S Y TCA TC AGCA TC CTAC
Frame 1 P1044(-)	L S L V	/ S G S TTTCAGGTAG	L N T	Y G T ATGGTACO	AATATCAAC	Q P Y G	F A S	T L T	GTCAAAATACC	S S A S Y TCA TC AGCA TC CTAC
Frame 1 P2003(-)	CTMTCATTAGT	/ S G S	L N T	Y G TATGGTACO	AATATCAAC	CAACCTTATGG	F A S	T L T		S S A S Y TCA TC AGCA TC CTAC
P2033(-)	CTATCATTAGT	TTCAGGTAG	ICTTAAATACCI	TATGGTAC	AATATCAAC	CAACCTTATGG	TTTTGCTTC	TACTTTAACAC	GICAAAATACC	TCATCAGCATCCTAC
P4028(-)	CTMTCATTAGT	TTCAGGTAG	ICTTAAATACCI	TATGGTAC		CAACCTTATG	TTTTGCTTC	TAÇTTTAAÇAC	GICAAAATACC	TCATCAGCATCCTAC
P1027(-)	CTATCATTAGT	TTCAGGTAG	CTTAAATACCI	TATGGTAC		CAACCTTATG	TTTTGCTTC	TACTTTAACAC	GICAAAATACC	TCATCAGCATCCTAC
P1028(-)	CTATCATTAGT	TTCAGGTAG	CTTAAATACCI	ATGGTAC		CAACCTTATG	TTTTGCTTC	TACTTTAACAC	GICAAAATACC	
P1029(-)	CTATCATTAGT	TTCAGGTAG					TTTTGCTTC	TACTTTAACAC		
P1036(-)	CTMTCATTAGT	TTCAGGTAG	CTTAAATACCI			CAACCTTATGG	TTTTGCTTC	TACTTTAACAC	GTCAAAATACC	
P2025(-) Frame 1	CTATCATTAGT	TTTCAGGTAG	CTTAAATACCI			CAACCTTATGG	TTTTGCTTC	TACTTTAACAC		TCATCAGCATCCTAC
P2040(-) Frame 1	CT TCATTAGT	TTCAGGTAG	CTTAAATACCI			CAACCTTATGG Q P Y G	TTTTGCTTC	TACTTTAACAC		TCATCAGCATCCTAC S S A S Y
P4054(-) Frame 1	CT TCATTAGT	TTCAGGTAG	CTTAAATACCI			CAACCTTATGG Q P Y G	TTTTGCTTC F A S	TACTTTAACAC T L T		
P4059(-) Frame 1	CTNTCATTAGT	TTCAGGTAG	CTTAAATACCI L N T		AATATCAAC	CAACCTTATGG Q P Y G	TTTTGCTTC F A S	TACTTTAACAC T L T	GTCAAAATACC R Q N	TCATCAGCATCCTAC S S A S Y
P4060(-)	CTATCATTAGT	TTCAGGTAG	CTTAAATACCI			CAACCTTATGG	TTTTGCTTC	TACTTTAACAC		

	850	860	870	880	890	900	910	920	930	940
C1(+)	GGATACGGAGGTA	ATGCTGTATCAAG	GCAGAGTA	TATGAT	TTACTGCC	GCAGCTGTTATI		TGTTCAATGC		
Frame 1 C19(+)	G Y G G GGATACGGAGGTA	M L Y Q	V A E Y	M I Q TATGAT T CAAG	V T A	A A V I GCAGCTGTTATI	R M L	L F A A		YUTACC
Frame 1 P3(+)	G Y G G GGATACGGAGGTA	M L Y Q ATGCTGTATCAAG	V A E Y	M I Q TATGAT T CAAG	V T A	A A V I GCAGCTGTTATI	R M L	L F A A		Y TATACO
Frame 1 P20(+)	G Y G G	M L Y Q	V A E Y	M I Q		A A V I GCAGCTGTTATI				
Frame 1 P1003(+)	G Y G G		V A E Y		V T A	A A V I			<u>S</u> S	
Frame 1 P1006(+)	G Y G G				V T A	A A V I			<u>S</u> <u>S</u>	
Frame 1	G Y G G		V A E Y		V T A				<u>s</u> s	Y T
Frame 1			V A E Y		V T A				<u>S</u> S	Y
Frame 1			V A E Y		V T A				<u>s</u> s	Y
Frame 1	GGATACGGAGGTA		V A E Y		V T A	A A V I			S F	
P4056(+) Frame 1	GGATACGGAGGTA	M L Y Q	A E Y	M I Q	V T A	A A V I	R M		S S	
P4058(+) Frame 1	GGATACGGAGGTA	M L Y Q	A E Y	M I Q	V T A	A A V I				
P2037(+) Frame 1	GGATACGGAGGTA G Y G G	M L Y Q	A E Y	M I Q	T AC GCC V T A	GCAGCTGTTATI	R M L	L F N A	S F	
P4008(+) Frame 1	GGATACGGAGGTA G Y G G	M L Y Q	GCAGAGTA V A E Y	TATGAT CAAG M I Q	TAC GCC V T A	GCAGCTGTTATI A A V I	R M L	L F N A	S F	
P37(+) Frame 1	CTATACGGAGGTA L Y G G	ATGCTGTATCAA <mark>G</mark> M L Y Q	GCAGAGTA V A E Y	TATGAT∎CAAG M I Q	T AC GCC V T A	GCAGCTGTTATI A A V I		L Y N S		
P1008(-) Frame 1	CTATACGGAGGTA Y G G	M L Y Q	GCAGAGTA V A E Y	TATGAT CAAG M I Q	T AC GCC V T A	GCAGCTGTTATI A A V I	R M	TGTTCGAATC		TATA G (Y S
P1023(-) Frame 1	CTATACGGAGGTA Y G G	ATGCTGTATCAAG M L Y Q	GCAGAGTA V A E Y	TATGAT CAAG M I Q	T∎AC∎GCC V T A	GCAGCTGTTATT A A V I	R M	TGT <mark>TCGAMTC</mark> L F E S		
P1024(-) Frame 1		ATGCTGTATCAAG M L Y 0	GCAGAGTA V A E Y	TATGAT CAAG		GCAGCTGTTATI		TGTTCGAMTC		
P1042(-) Frame 1		ATGCTGTATCAAG M L Y O		TATGAT CAAG	T AC GCC	GCAGCTGTTATI				
P1017(-)	CTATACGGAGGT	TGCTGTATCAA	GCAGAGTA	TATGATCAAG		GCAGCTGTTATT		TGTTCAATTC		
P2008(-)	CTATACGGAGGT	TGCTGTATCAA	GCAGAGTA	TATGATCAAG	TACEGCC	GCAGCTGTTATT		TGTTCAATTC		
P2009(-)	CTATACGGAGGTA	TGCTGTATCAA	GCAGAGTA	TATGATCAAG	TTACTGCC	GCAGCTGTTATI		TGTTCAATTC		
P2012(-)	CTATACGGAGGT/	TGCTGTATCAAG	GCAGAGTA	TATGATCAAG	TTACTGCC	GÇAGÇTGTTATI		TGTTCAATTC		
P3022(-)	CTATACGGAGGT/	ATGCTGTATCAA	GCAGAGTA	TATGATCAAG	TTACTGCC	GÇAGÇTGTTATI	R M L			TATA G
P4007(-)	CTATACGGAGGT	M L Y Q	GCAGAGTA	TATGATCAAG	TTACTGCC	GCAGCTGTTATI		TGT TCA A TTC		<mark>TATA</mark> GC
Frame 1 P2022(-)	CTATACGGAGGT	M L Y Q	GCAGAGTA	M I Q TATGATCAAG	V T A	GCAGCTGTTATI	R M L	L F N S		YS
Frame 1 P3010(-)	CTATACGGAGGT	M L Y Q ATGCTGTATCAAG	V A E Y	M I Q TATGAT C CAAG	V T A	A A V I GCAGCTGTTATI	R M L FC <mark>G</mark> AATG <mark>CTC</mark> T	L F N S		Y S G ATACC
Frame 1 P3019(-)	TATACGGAGGT	M L Y Q	V A E Y	M I Q TATGAT C CAAG	V T A	A A V I GCAGCTGTTATI	R M L	L F A A		<mark>GATACO</mark>
Frame 1 P3020(-)	TATACGGAGGT	M L Y Q	V A E Y	M I Q TATGAT C CAAG	V T A	A A V I GCAGCTGTTATI				
Frame 1 P3034(-)	TATACGGAGGT	M L Y Q	V A E Y	M I Q		A A V I				
Frame 1 P4014(-)	Y G G		V A E Y		V T A	A A V I			S S	
Frame 1	Y G G		V A E Y		V T A	A A V I			<u>S</u> <u>S</u>	
Frame 1			V A E Y		V T A				<u>S</u> S	D
Frame 1					V T A				<u>s</u> s	D
Frame 1			A A E Y		V T A				A S S	P Y S
Frame 1	Y G G	M L Y Q	V A E Y		V T A				V S	Y S
Frame 1	R Y G G	M L Y Q	A A E Y		V T A	A A V I				
Frame 1	R Y G G	M L Y Q	A A E Y		V T A	A A V I				
P1014(-) Frame 1	R Y G G	M L Y Q	A A E Y	M I Q	V T A	A A V I				
P1015(-) Frame 1	R Y G G	M L Y Q	A A E Y	M I Q	V T A	A A V I				
P2(-) Frame 1	CTATACGGAGGTA	M L Y Q	CGGCAGAGTA S A E Y	M I Q	TCACAGCC V T A	GCAGCTGTTATI A A V I		L Y N S		<mark>GC1</mark> A
P15(-) Frame 1	CTATACGGAGGTA L Y G G	M L Y Q	CGGCAGAGTA S A E Y	TATGATCCAAG M I Q	TCACAGCC V T A	GCAGCTGTTATI A A V I		L Y N S		<mark>GC</mark>
P1044(-) Frame 1	CTATACGGAGGTA Y G G	M L Y Q	CGGCAGAGTA S A E Y	TATGATCAAG M I Q	TCACAGCC V T A	GCAGCTGTTATI A A V I		L Y N S		<mark>GC</mark>
P2003(-) Frame 1	TATACGGAGGTA Y G G	ATGCTGTATCAA M L Y Q	CGGCAGAGTA S A E Y	TATGATCAAG M I Q	TCACMGCC V T A	GCAGCTGTTATI A A V I		L Y N S		<mark>GC1</mark> A
P2033(-) Frame 1	CTATACGGAGGT/	M L Y Q	CGGCAGAGTA S A E Y	TATGATCAAG M I Q	TCACMGCC V T A	GCAGCTGTTATI A A V I		L Y N S		<mark>GC</mark>
P4028(-) Frame 1	CTATACGGAGGTA Y G G	ATGCTGTATCAA M L Y Q	CGGCAGAGTA S A E Y	TATGATCAAG MIQ	TCACAGCC V T A	GCAGCTGTTATT A A V I		L Y N S		<mark>GC</mark>
P1027(-) Frame 1	CTATACGGAGGTA Y G G	ATGCTGTATCAA M L Y 0	CGGCAGAGTA S A E Y	TATGATCAAG M I O	TCACMGCC V T A	GCAGCTGTTATI				<mark>GC1</mark>
P1028(-) Frame 1				TATGATCAAG M I O	TCACMGCC V T A	GCAGCTGTTATT				
P1029(-) Frame 1	CTATACGGAGGT	TGCTGTATCAA		TATGATCAAG	TCACAGCC	GCAGCTGTTATT				
P1036(-)	CTATACGGAGGTA	TGCTGTATCAA	CGGCAGAGTA	TATGATCAAG	TCACAGCC	GCAGCTGTTATT				<mark>GC</mark>
P2025(-)	CTATACGGAGGTA	TGCTGTATCAA	CGGCAGAGTA	TATGATCAAG	TCACMGCC	GCAGCTGTTATI				
P2040(-)	CTATACGGAGGT	TGCTGTATCAA		TATGATCAAG	TCACMGCC	GCAGCTGTTATI		TGTATAACTC		
P4054(-)	CTATACGGAGGT	TGCTGTATCAA		TATGATCAAG	TCACMGCC	GCAGCTGTTATI		TGTATAACTC		<mark>GC</mark>
P4059(-)	CTATACGGAGGTA	ATGCTGTATCAA		TATGATCAAG	TCACEGCC	GCAGCTGTTATI		TGTATAACTC		<mark>GC</mark>
P4060(-)	CTATACGGAGGT	ATGCTGTATCAA	CGGCAGAGTA	TATGATCAAG	TCACEGCC	GCAGCTGTTATI				<mark>GC</mark>
Frame 1	Y G G	MLYQ	SAEY	MIQ	V I A	A A V I	MR	L Y N S	V	A

I de contra a	950	960	970	980	990	1,000	1,010 1,017
C1(+)	ATGACTCCTGC		GCTACCATATAG	CCTATTGAT.	AGTTATATTA		ΑΤΑΑΑΑΤΑΑ
Frame 1 C19(+)				P I D	S Y I	Γ Ι R Κ ΤΑΤΤΑGΑΑΑ	Ι Κ *
Frame 1 P3(+)				P I D	S Y I		Ι Κ *
Frame 1					S Y I	F I R K	
Frame 1					S Y I		
Frame 1	M T P A			P I D	S Y I		
P1006(+) Frame 1	M T P A		P Y S	P I D	S Y I	TATTAGAAA TIRK	ATAAAATAA T K *
P1059(+) Frame 1	M T P A			P I D	S Y I	F I R K	ATAAAATAA T K *
P4025(+) Frame 1	M T P A			P I D	S Y I		ATAAAATAA I K *
P4035(+) Frame 1	M T P A			P I D	S Y I		A I A A A A I A A I K *
P4056(+) Frame 1				P I D	S Y I	TATTAGAAAA FIRK	АТААААТАА K *
P4058(+) Frame 1	ATGACTCCTGC M T P A		CTACCATATAG	P I D	AGTTATATTAC S Y I	TATTAGAAAA F I R K	ΑΤΑΑΑΑΤΑΑ Ι Κ *
P2037(+) Frame 1	A GACTCCTGC M T P A		CTACCATATAG	CCTATTGAT P I D	AGTTATATTAC S Y I	TATTAGAAAA FIRK	ΑΤΑΑΑΑΤΑΑ Ι Κ *
P4008(+) Frame 1	A GACTCCTGC M T P A		CTECCATATAG	P I D	AGTTATATTA S Y I	TATTAGAAA FIR K	ΑΤΑΑΑΑΤΑΑ Ι Κ *
P37(+) Frame 1		GCCGATAGT	F P Y S	CCTATTGAT P I D	AGTTATATTA S Y I	TATTAGAAA	ΑΤΑΑΑΑΤΑΑ Ι Κ *
P1008(-) Frame 1			CTRCCATATAG	CCTATTGAT P I D	AGTTATATTAC S Y I	TATTAGAAA	ΑΤΑΑΑΑΤΑΑ Ι Κ *
P1023(-) Frame 1	ACGGCTGTTT AV		CTCCATATAG PYS	CCTATTGAT P I D	AGTTATATTA S Y I	CTATTAGAAA FIRK	ΑΤΑΑΑΑΤΑΑ Ι Κ *
P1024(-) Frame 1	ACGGCTGTTTT AV F		CTACCATATAG	CCTATTGAT P I D	AGTTATATTAC S Y I	TATTAGAAAA FIRK	ΑΤΑΑΑΑΤΑΑ Ι Κ *
P1042(-) Frame 1	ACGGCTGTTT AV		CTACCATATAG	CCTATTGAT P I D	AGTTATATTA S Y I	TATTAGAAA F I R K	ΑΤΑΑΑΑΤΑΑ Ι Κ *
P1017(-) Frame 1			CTRCCATATAG	CCTATTGAT P I D	AGTTATATTA S Y I	TATTAGAAA FIRK	ΑΤΑΑΑΑΤΑΑ Ι Κ *
P2008(-) Frame 1				CCTATTGAT P I D	AGTTATATTA S Y I	TATTAGAAA FIRK	ΑΤΑΑΑΑΤΑΑ Ι Κ *
P2009(-) Frame 1				CCTATTGAT. P I D	AGTTATATTA S Y I	TATTAGAAA FIRK	ΑΤΑΑΑΑΤΑΑ Ι Κ *
P2012(-) Frame 1				CCTATTGAT P I D	AGTTATATTA	TATTAGAAA	ΑΤΑΑΑΑΤΑΑ Ι Κ *
P3022(-) Frame 1				CCTATTGAT P I D	AGTTATATTA S Y I	TATTAGAAA	ΑΤΑΑΑΑΤΑΑ Ι Κ *
P4007(-) Frame 1				CCTATTGAT P I D	AGTTATATTA S Y I	TATTAGAAA	ΑΤΑΑΑΑΤΑΑ
P2022(-)			CTACCATATAG	CCTATTGAT	AGTTATATTA	TATTAGAAA	
P3010(-)			CTACCATATAG	CCTATTGAT	AGTTATATTA		
P3019(-)				CCTATTGAT	AGTTATATTA		
P3020(-)				CCTATTGAT	AGTTATATTA		ΑΤΑΑΑΑΤΑΑ
P3034(-)				CCTATTGAT	AGTTATATTA		
P4014(-)				CCTATTGAT	AGTTATATTA		
P4021(-)			CTACCATATAG	CCTATTGAT	AGTTATATTA		
P4046(-)				CCTATTGAT	AGTTATATTA		
P1032(-)			CTACCATATAG	CCTATTGAT.	AGTTATATTA		ΑΤΑΑΑΑΤΑΑ
P3025(-)			GCTACCATATAG	CCTATTGAT	AGTTATATTA		
P1012(-)	AATGTGCCTCT		CTACCATATAG	CCTATTGAT	AGTTATATTA	TATTAGAAAG	
P1013(-)	AATGTGCCTCT		CT CCATATAG	CCTATTGAT	AGTTATATTA	TATTAGAAAG	
P1014(-)	AATGTGCCTCT		CTACCATATAG	CCTATTGAT	AGTTATATTA	TATTAGAAAG	
P1015(-)	AATGTGCCTCT		CTACCATATAG	CCTATTGAT	AGTTATATTA	TATTAGAAAG	
P2(-)	ACAACTGCTCC		GT CCATATAG	CCTATTGAT	AGTTATATTA	TATTAGAAA	
P15(-)	ACAACTGCTCC	GCCGACAGT	GTTCCATATAG	CCTATTGAT	AGTTATATTA	TATTAGAAA	АТААААТАА
P1044(-)	ACAACTGCTCC	GCCGACAGT	GTTCCATATAG	CCTATTGAT	AGTTATATTA	TATTAGAAA	АТААААТАА
P2003(-)		GCCGACAGT	IGT CCATATAG	CCTATTGAT	AGTTATATTA	TATTAGAAA	АТААААТАА
P2033(-)		GCCGACAGT	IGT CCATATAG	CCTATTGAT	AGTTATATTA	TATTAGAAA	АТААААТАА
P4028(-)		GCCGACAGT	IGT CCATATAG	CCTATTGAT	AGTTATATTA	TATTAGAAA	ATAAAATAA
P1027(-)		GCCGACAGT	IGT CCATATAG	CCTATTGAT	AGTTATATTA	TATTAGAAA	АТААААТАА
P1028(-)		GCICGACAGT	IGT CCATATAG	CCTATTGAT	AGTTATATTA	TATTAGAAA	ATAAAATAA
P1029(-)		GCCGACAGT	IGTICCATATAG	CCTATTGAT.	AGTTATATTA	TATTAGAAA	ATAAAATAA
Prame 1 P1036(-)		GCCGACAGT	GTTCCATATAG	CCTATTGAT	AGTTATATTA	TATTAGAAA	ATAAAATAA
P2025(-)		GCCGACAGT	GTTCCATATAG	CCTATTGAT.	AGTTATATTA	TATTAGAAA	ATAAAATAA
P2040(-)		GCCGACAGT	GTTCCATATAG	CCTATTGAT	AGTTATATTA	TATTAGAAA	ΑΤΑΑΑΑΤΑΑ
Frame 1 P4054(-)		GCCGACAGT	GTTCCATATAG	CCTATTGAT	AGTTATATTA	TATTAGAAA	ΑΤΑΑΑΑΤΑΑ
P4059(-)		GCCGACAGT	GTTCCATATAG	CCTATTGAT	AGTTATATTA	I I R K	ΑΤΑΑΑΑΤΑΑ
P4060(-)		GCCGACAGT	GTTCCATATAG	CCTATTGAT	AGTTATATTA	TATTAGAAA	ATAAAATAA
crame 1			P Y Y	P 1 1)	a r l		1 15 *

Supplementary Figure 3: Nucleotide alignment and ORF translation of partial PcI7 sequence containing infectotype-associated polymorphisms. Designated haplotypes are based on polymorphisms in this region of sequence only. Notations after haplotype name signify the polymorphism-associated infectotype (+ or -) and the number of *P. ramosa* clones with that haplotype. Nucleotide coordinates correspond to the full gene alignment positions detailed in Table 1 and Supplementary Figure 1. Colors in sequences highlight nucleotide and amino acid polymorphisms. Running bar graph at header depicts degree of sequence identity across samples, with green indicating the same base across all sequences, yellow indicating less than complete identity, and red indicating very low identity for the given position.

	680	690	700	710	720	730	740	750 7	50
Identity									
Haplotype_1_(+,_n=10) Frame 1	TTTGGGTGGTCTC F G G L	TATATTCGGCA	GGTGG <mark>TGGA</mark> G G G <mark>G</mark>	G A G A A	CAATGAATCCG N E S	GTCTACCTA A V Y L	TCATTAGTTTC S L V S	CAGGTAGCTTA/ G S L	N T Y
Haplotype_2_(+,_n=2) Frame 1	TTTGGTGGTCTC F G G L	TATATTCGGCA	GGTGG <mark>TGGA</mark> G G G <mark>G</mark>	G T A C A G G A G C G T G A	CAATGAATCCG N E S	GTCTACCTA A V Y L	TCATTAGTTTC S L V S	CAGGTAGCTTA/ G S L	ATACCTAT N T Y
Haplotype_3_(+,_n=1) Frame 1	TTTGGGTGGTCTC F G G L	TTA TATTC GGCA	GGTGG <mark>TGGA</mark> G G G <mark>G</mark>	G G C A G G A G C A	CAATGAATCCG N E S	CTGTCTACCTA A V Y L	TCATTAGTTTC S L V S	CAGGTAGCTTA/ G S L	ATACCTAT N T Y
Haplotype_4_(+,_n=1) Frame 1	TT <mark>⊂</mark> GG <mark>G</mark> GG∎CTO F G G L	GTA <mark>TGGGCGGAA</mark> V W A E	GGTGG <mark>AGTC</mark> G G G V	CAGCATTCTA A A F Y	CAATGAATCCG N E S	CTGTCTACCTA A V Y L	TCATTAGTTTC S L V S	CAGGTAGCTTA/ G S L	ATACCTAT N T Y
Haplotype_5_(-,_n=15) Frame 1	TTTGGGGGGTCTC F G G L	GTATGGGCACAT	GGTGG <mark>AAGTT</mark> G G S		AATGAATCCG N E S	TTGTCTACCTA V V Y L	TCATTAGTTTC S L V	AGGTAGCTTA/	ATACCTAT N T Y
Haplotype_6_(-,_n=1) Frame 1	TTTGGCGGTCTC F G G L	GTATGGGCATAT V W A Y	GGTGG <mark>AAGTT</mark> G G S	CAGTAGTCTA S V V Y	CAATGAATCCG N E S	TTGTCTACCTA V V Y L	TCATTAGTTTC S L V	AGGTAGCTTA/	ATACCTAT N T Y
Haplotype_7_(-,_n=4) Frame 1	TTTGGCGGTCTC F G G L	GTATGGGCATAT V W A Y	GGTGG <mark>AAGTT</mark> G G S	CAGGAGCCTA S G A Y	CAATGAATCCG N E S	TTGTCTACCTG V V Y L	TCATTAGTTTC S L V	AGGTAGCTTA/	ATACCTAT N T Y
Haplotype_8_(-,_n=1) Frame 1	TTTGGCGGTCTC F G G L		GGTGG <mark>AAGTG</mark> G G S	AAGGAGCCTA E G A Y	CAATGAATCCG N E S	TTGTCTACCTG V V Y L	TCATTAGTTTC S L V	AGGTAGCTTA/	ATACCTAT N T Y
Haplotype_9_(-,_n=17) Frame 1	TTTGGCGGTCTC F G G L		GGTGG <mark>AAGTG</mark> G G S	AAGGAGCCTA E G A Y	CAATGAATCCG N E S	TGGTCTACCTA V V Y L	TCATTAGTTTC S L V	AGGTAGCTTA/	ATACCTAT N T Y
Haplotype_10_(-,_n=1) Frame 1	TTTGGCGGCTC F G G L		GGTGG <mark>AAGTT</mark> G G S		CAATGAATCCG N F S	TTGTCTACCTG	TCATTAGTTTC S L V S	AGGTAGCTTA/	ATACCTAT N T Y
	770 78	30 790	800	810	820	830	840	850	860
Identity	770 78	30 790	800	810	820	830	840	850	860
ldentity Haplotype_1_(+,_n=10) Frame 1	770 74 GGTACGAATATO GTAN	NO 790	BDD GGTTTTGCTT G F A	BIO CTACTTTAAC S T L T	B20 ACG T CAAAAT R Q N	B30 CCTCAGCATCA T S A S	840 GCCTACGGATA A Y G	850 ACGGAGGTATGO AGG M	860 TGTATCAA L Y Q
Identity Haplotype_1_(+,_n=10) Frame 1 Haplotype_2_(+,_n=2) Frame 1	GGTACGAATATC GGTACGAATATC GGTACGAATATC GGTACGAATATC GTAN	30 790 САА <mark>М</mark> СААССТТАТ К Q Р Ү САА <mark>М</mark> СААССТТАТ К Q Р Ү	BOD GGTTTTGCTT GGTTTTGCTT G F A	BIO CTACTTTAAC S T L T CTACTTTAAC S T L T	ACGTCAAAATA RQN ACGTCAAAATA ACGTCAAAATA RQN		840 GCCTACGGATA AYGG GCCTACGGATA AYGG	850 ACGGAGGTATGO ACGGAGGTATGO ACGGAGGTATGO ACGGAGGTATGO	B60 TGTATCAA L Y Q TGTATCAA
Identity Haplotype_1_(+,_n=10) Frame 1 Haplotype_2_(+,_n=2) Frame 1 Haplotype_3_(+,_n=1) Frame 1	GGTACGAATATC GGTACGAATATC GGTACGAATATC GGTACGAATATC GGTACGAATATC GTACGAATATC		BộO G G T T T G C T T G F A G G T T T G C T T G G T T T G C T T G G T T T G C T T	810 CTACTTTAAC S T L T CTACTTTAAC S T L T CTACTTAAC S T L T	820 A C G T C A A A A T A R Q N A C G C A A A A T A R Q N A C G C A A A A T A R Q N	REAL AND A CONTRACT OF A CONTR	840 GCCTACGGAT/ A Y G GCCTACGGAT/ A Y G TCCTACGGAT/ S Y G	850 ACGGAGGTATG ACGGAGGTATG ACGGAGGTATG CGGAGGTATG CGGAGGTATG CGGAGGTATG	860 TGTATCAA TGTATCAA L Y Q TGTATCAA L Y Q
Identity Haplotype_1_(+,_n=10) Frame 1 Haplotype_2_(+,_n=2) Frame 1 Haplotype_3_(+,_n=1) Frame 1 Haplotype_4_(+,_n=1) Frame 1	70 74 GGTNCGAATATC N GGTNCGAATATC N GGTCGAATATC N GGTCGAATATC G GGTCGAATATC N GGTCGAATATC N	50 730 САА СААССТТАТ К Q Р У САА ССАССТТАТ К Q Р У АА СААССТТАТ С АА ССАССТТАТ К Q Р У А К Q Р Р У	GGTTTTGCTT G F A GGTTTTGCTT G F A GGTTTTGCTT G F A GGTTTTGCTT G F A	BID CTACTTTAAC S T L T CTACTTTAAC S T L T CTACTTTAAC C C T L A C T C T C T C T C T C T C T C T C T C T	ACGTCAAAATA RQN ACGTCAAAATA RQN ACGTCAAAATA RQN ACGTCAAAATA ACGTCAAAATA	CCTCA GCATCA CCTCA GCATCA CCTCA GCATCA CCTCA GCATCA CCTCA CATCA S CCTCA GCATCA S CCTCA GCATCA	B40 GCCTACGGATA A Y G GCCTACGGATA A Y G TCCTACGGATA GCCTACGGATA GCCTACGGATA GCCTACGGATA	B50 CGGAGGTATGC CGGAGGTATGC CGGAGGTATGC CGGAGGTATGC CGGAGGTATGC CGGAGGTATGC	860 CTGTATCAA L Y Q CTGTATCAA L Y Q CTGTATCAA L Y Q CTGTATCAA L Y Q
Identity Haplotype_1_(+,_n=10) Frame 1 Haplotype_2_(+,_n=2) Frame 1 Haplotype_3_(+,_n=1) Frame 1 Haplotype_4_(+,_n=1) Frame 1 Haplotype_5_(-,_n=15) Frame 1	770 74 GGT CGAATATC GGT CGAATATC GT CGAATATC GT CGAATATC GT CGAATATC GT CGAATATC GT CGAATATC G N I GGT CGAATATC	ы 770 ААТССААССТТАТ КОСАССТТАТ КАТССААССТТАТ КОСАССТТАТ КОСАССТТАТ КОСАССТТАТ КОСАССТТАТ САССААССТТАТ	BO GGTTTTGCTT G F A GGTTTTGCTT G F A GGTTTTGCTT G F A GGTTTTGCTT G F A GGTTTTGCTT G F A	В10 СТАСТТТААС S T L T СТАСТТТААС S T L T СТАСТТТААС S T L T СТАСТТТААС S T L T СТАСТТТААС S T L T				SPO CGGAGGTATGC G G M CGGAGGTATGC CGGAGGTATGC G G M CGGAGGTATGC G G M CGGAGGTATGC G G M	TGTATCAA L Y Q TGTATCAA L Y Q TGTATCAA L Y Q TGTATCAA L Y Q TGTATCAA L Y Q TGTATCAA
Identity Haplotype_1_(+,_n=10) Frame 1 Haplotype_2_(+,_n=2) Frame 1 Haplotype_3_(+,_n=1) Frame 1 Haplotype_4_(+,_n=1) Frame 1 Haplotype_5_(-,_n=15) Frame 1 Haplotype_6_(-,_n=1) Frame 1	70 71 G G T & C G A A T A T G G G G T & C G A A T A T G G G G T & C G A A T A T G G G G T & C G A A T A T G N G G T & C G A A T A T G N G G T & C G A A T A T G N G G T & C G A A T A T G N G G T & C G A A T A T G N G G T & C G A A T A T G N G G T & C G A A T A T G N G G T & C G A A T A T G N G G T & C G A A T A T G N G G T & C G A A T A T G N G G T & C G A A T A T G N G G T & C G A A T A T G N G G T & C G A A T A T G N G G T & C G A A T A T G N	p 790 A A M C A A C C T T A T Y A A M C A A C C T T A T Y A A M C A A C C T T A T Y A A M C A A C C T T A T Y A A M C A A C C T T A T Y A A C C A C C T T A T Y A A C C A C C T T A T Y A A C C A C C T T A T Y A A C C A A C C T T A T Y A A C C A A C C T T A T Y A A C C A A C C T T A T Y A A C C A A C C T T A T Y A A C C A A C C T T A T Y A A C C A A C C T T A T Y A A M C C A A C C T T A T Y A A M C C A A C C T T A T Y A A M C C A A C C T T A T Y A A M C A A C C A A C C T T A T Y	BO GGTTTTGCTT G F A GGTTTTGCTT G F A GGTTTTGCTT G F A GGTTTTGCTT G F A GGTTTTGCTT G F A GGTTTTGCTT G F A	BIO CTACTTTAAC S T CTACTTTAAC S CTACTTTAAC S CTACTTTAAC S CTACTTAAC S CTACTTTAAC S CTACTTAAC S CTACTTAAC S CTACTTAAC S CTACTTAAC S CTACTTTAAC S CTACTTTAAC S CTACTTTAAC S CTACTTTAAC S CTACTTTAAC S CTACTTTAC S CTACTTAC S CTACTTAC S CTACTTACTTAC S CTACTTACTTAC S CTACTTAC S CTACTTACTTAC S CTACTTACTAC S CTACTTACTAC <th>ερο A C GI C AAAA TA R A C GI C AAAA TA A C GI C AAAA TA A C GI C AAAA TA R R A C GI C AAAA TA R A C GI C AAAA TA R R A C GI C AAAA TA R A C GI C AAAA TA R</th> <th></th> <th></th> <th>BO CGGGAGGTATG CGGAGGTATG CGGAGGTATG CGGAGGTATG CGG CGG CGG CGG CGG CGG CGG CGG CGG C</th> <th>TGTATCAA L Y Q TGTATCAA L Y Q TGTATCAA L Y Q TGTATCAA L Y Q TGTATCAA L Y Q TGTATCAA</th>	ερο A C GI C AAAA TA R A C GI C AAAA TA A C GI C AAAA TA A C GI C AAAA TA R R A C GI C AAAA TA R A C GI C AAAA TA R R A C GI C AAAA TA R A C GI C AAAA TA R			BO CGGGAGGTATG CGGAGGTATG CGGAGGTATG CGGAGGTATG CGG CGG CGG CGG CGG CGG CGG CGG CGG C	TGTATCAA L Y Q TGTATCAA L Y Q TGTATCAA L Y Q TGTATCAA L Y Q TGTATCAA L Y Q TGTATCAA
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Supplementary Figure 3: a) Structural model and corresponding quality scores of C-terminal globular domain of PcI7 homotrimer, based on alignment with BcIA. Colors correspond to the QMEAN score, with purple indicating a high-quality local alignment and orange indicating a low-quality local alignment. b) Predicted local similarity of PcI7 query sequence to BcIA target sequence. c) Alignment of PcI7 translated sequence to BcIA target sequence, with same alignment-quality color scheme as Panel a.



Supplementary Figure 4: Phylogenies of all 56 clones in the *P. ramosa* diversity panel (24 genome-sequenced clones plus 32 additional clones), based on the full coding sequence of the PcI7 gene. Red branch tips indicate clones that were infectious to host phenotype HU-HO-2/CH-H-67, and black branch tips indicate non-infectious clones.



Supplementary Table 1: Details of the 56 *P. ramosa* clones included in this study, including name, locality of origin, GPS coordinates, and infection phenotypes.

Clone	Locality	Country/Region	Lat, Long	Sequencing	HU-HO-2/CH-H-67	FI-XINB3	FI-KELA-39-9
C1	RU-M2	Russia	55.728, 37.556	Whole Genome	1	0	1
C19	DE-G1	Germany	54.282, 10.966	Whole Genome	1	1	0
P20	CH-H	Switzerland	47.558, 8.863	Whole Genome	1	0	0
P4035	DE-R1	Germany	54.207, 10.406	Whole Genome	1	0	0
P4057	FI-VIW5	Finland	59.83, 23.201	Whole Genome	1	0	1
P4064	CH-H	Switzerland	47.558, 8.863	Whole Genome	1	0	1
P1013	PL-1	Poland	52.212, 21.001	Whole Genome	0	0	1
P1029	BE-KN	Belgium	51.357, 3.343	Whole Genome	0	0	0
P1036	FI-SEG1	Finland	59.764, 23.374	Whole Genome	0	0	0
P1042	DE-L1	Germany	54.222, 10.429	Whole Genome	0	0	1
P1044	DE-KN1	Germany	54.169, 10.773	Whole Genome	0	0	0
P15	BE-OM2	Belgium	50.863, 4.721	Whole Genome	0	1	0
P2009	RU-SYR1	Russia	53.212, 48.488	Whole Genome	0	0	0
P2022	FI-SEG1	Finland	59.764, 23.374	Whole Genome	0	1	0
P2031	DE-KN1	Germany	54.169, 10.773	Whole Genome	0	0	0
P2040	GB-S8	England	51.621, -1.376	Whole Genome	0	0	0
P3005	RU-SYR1	Russia	53.212, 48.488	Whole Genome	0	0	0
P3010	CZ-1	Czech Republic	50.125, 14.869	Whole Genome	0	0	1
P3019	DE-KN1	Germany	54.169, 10.773	Whole Genome	0	0	0
P3020	BE-WH2	Belgium	51.335, 3.348	Whole Genome	0	0	0
P3034	CH-H	Switzerland	47.558, 8.863	Whole Genome	0	0	0
P4048	RU-M1	Russia	55.763, 37.582	Whole Genome	0	0	0
P4054	RU-RT1	Russia	45.222, 36.808	Whole Genome	0	0	0
P4059	GB-S8	England	51.621, -1.376	Whole Genome	0	1	0
P1003	CH-H	Switzerland	47.558, 8.863	Pcl7	1	NA	NA
P1006	RU-BN	Russia	50.248, 43.65	Pcl7	1	NA	NA
P1059	RU-M1	Russia	55.763, 37.582	Pcl7	1	NA	NA
P2037	GB-K1	England	55.703, -2.341	Pcl7	1	NA	NA
P3	FI-VIW2	Finland	59.83, 23.201	Pcl7	1	NA	NA
P37	IL-NS	Israel	31.724, 34.626	Pcl7	1	NA	NA
P4008	GB-A1	England	51.878, -1.116	Pcl7	1	NA	NA
P4025	FI-SEG2	Finland	59.764, 23.375	Pcl7	1	NA	NA
P4058	FI-VIW5	Finland	59.83, 23.201	Pcl7	1	NA	NA
P1008	GB-A1	England	51.878, -1.116	Pcl7	0	NA	NA
P1012	PL-1	Poland	52.212, 21.001	Pcl7	0	NA	NA
P1014	PL-1	Poland	52.212, 21.001	Pcl7	0	NA	NA
P1015	PL-1	Poland	52.212, 21.001	Pcl7	0	NA	NA
P1017	RU-SYR1	Russia	53.212, 48.488	Pcl7	0	NA	NA
P1023	GB-A1	England	51.878, -1.116	Pcl7	0	NA	NA
P1024	GB-A1	England	51.878, -1.116	Pcl7	0	NA	NA
P1027	GB-S17	England	51.622, -1.367	Pcl7	0	NA	NA
P1028	GB-S17	England	51.622, -1.367	Pcl7	0	NA	NA
P1032	GB-C1	England	51.734, -1.336	Pcl7	0	NA	NA
P2	GB-K1	England	55.703, -2.341	Pcl7	0	NA	NA
P2003	CH-H	Switzerland	47.558, 8.863	Pcl7	0	NA	NA
P2008	RU-BN	Russia	50.248, 43.65	Pcl7	0	NA	NA
P2012	RU-SYR1	Russia	53.212, 48.488	Pcl7	0	NA	NA
P2025	FI-SEG2	Finland	59.764, 23.375	Pcl7	0	NA	NA
P2033	DE-N1	Germany	54.309, 10.625	Pcl7	0	NA	NA
P3025	RU-RT1	Russia	45.222, 36.808	Pcl7	0	NA	NA
P4007	RU-BN	Russia	50.248, 43.65	Pcl7	0	NA	NA
P4014	CZ-1	Czech Republic	50.125, 14.869	Pcl7	0	NA	NA
P4021	BE-KN2	Belgium	51.356, 3.335	Pcl7	0	NA	NA
P4028	DE-L1	Germany	54.222, 10.429	Pcl7	0	NA	NA
P4046	BE-WH2	Belgium	51.335, 3.348	Pcl7	0	NA	NA
P4060	GB-S8	England	51.621, -1.376	Pcl7	0	NA	NA

Supplementary Table 2: *D. magna* test clones for infection phenotyping, including their geographic origin and their resistance phenotype to two common lab clones of *P. ramosa* (C1 & C19).

D. magna Clone Name	Resistotype (C1/C19)	Geographic Origin
FI-KELA-39-9	SR	Tvärminne, Finland
FI-XINB3	RS	Tvärminne, Finland
DE-K1-IINB1	RR	Munich, Germany
HU-HO-2	SS	Bogarzo-to, Hungary
CH-H-67	SS	Hohliberg, Switzerland
CH-H-159	RR	Hohliberg, Switzerland

Supplementary Table 3: Nucleotide diversity (π) of annotated genome regions (100-b.p. windows) in the top 99th diversity percentile across the 24 genome-sequenced *P. ramosa* clones.

Chromosome Starting Position	Annotation	Nucleotide Diversity (π)
8901	PCL7	0.0463768
9001	PCL7	0.0469252
9101	PCL7	0.0399608
9201	PCL7	0.0655902
10301	PCL8	0.0515715
10401	PCL8	0.0423551
10501	PCL8	0.044058
63301	PCL3	0.0438768
88101	PCL22	0.0724267
88201	PCL22	0.0582949
88401	PCL22	0.0425635
88601	PCL22	0.0379515
89001	PCL21	0.054453
89401	PCL21	0.0457622
89801	PCL21	0.0500546
89901	PCL21	0.0438685
316801	PCL27	0.0527608
318701	PCL28	0.0389855
318901	PCL28	0.0387965
319001	PCL28	0.0404348
323501	hypothetical protein	0.0517993
697501	hypothetical protein	0.0379495
1033001	hypothetical protein	0.0398386
1200101	PCL16	0.0400858
1201201	PCL16	0.0393478
1202401	PCL16	0.0436594
1518101	PCL24	0.0404978
1518201	PCL24	0.052136
1518501	PCL24	0.0384699
1518601	PCL24	0.0660113
1518701	PCL24	0.0540388
1518801	PCL24	0.0432896
1519001	PCL25	0.0506445
1519401	PCL25	0.0387319
1519501	PCL25	0.0670124
1519601	PCL25	0.0393056
1519701	PCL25	0.0390438
1519801	PCL25	0.0446108
1519901	PCL25	0.0670554
1520601	PCL26	0.0440213
1520801	PCL26	0.0826377
1571101	hypothetical protein	0.0422779
1571201	PCL9	0.0580719
1577901	PCL12	0.0495656
1578201	PCL12	0.0919916
1578301	PCL12	0.0437067
1578401	PCL12	0.0463719
1580801	PCL14	0.0435965
1581001	PCL14	0.0410002
1588301	PCL37	0.0480666
1589301	PCL36	0.0425605
1589401	PCL36	0.0380611
1600301	xylanase/chitin deacetylase	0.0457971