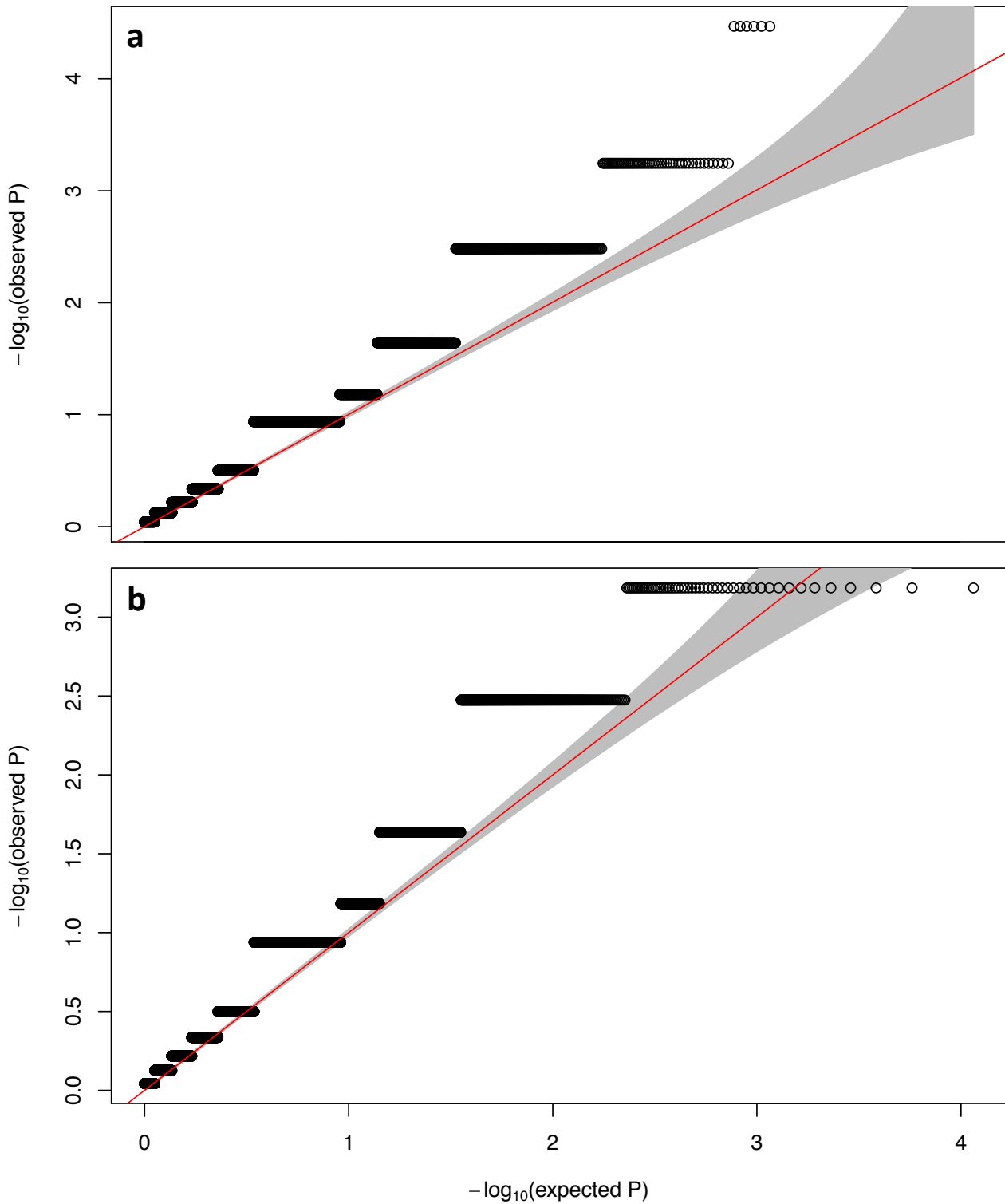**Supplementary Figure 1:** Quantile-quantile (QQ) plot of observed versus expected p-values from the treeWAS "terminal" tests a) including all values, b) with values in the Pcl7 gene region removed. QQ plots excluding causal polymorphisms are expected to fall approximately along the y=x line.

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.

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Multiple sequence alignment (nucleotide with translated amino acid "Frame 1" tracks). Ruler positions: 850, 860, 870, 880, 890, 900, 910, 920, 930, 940.

Identity

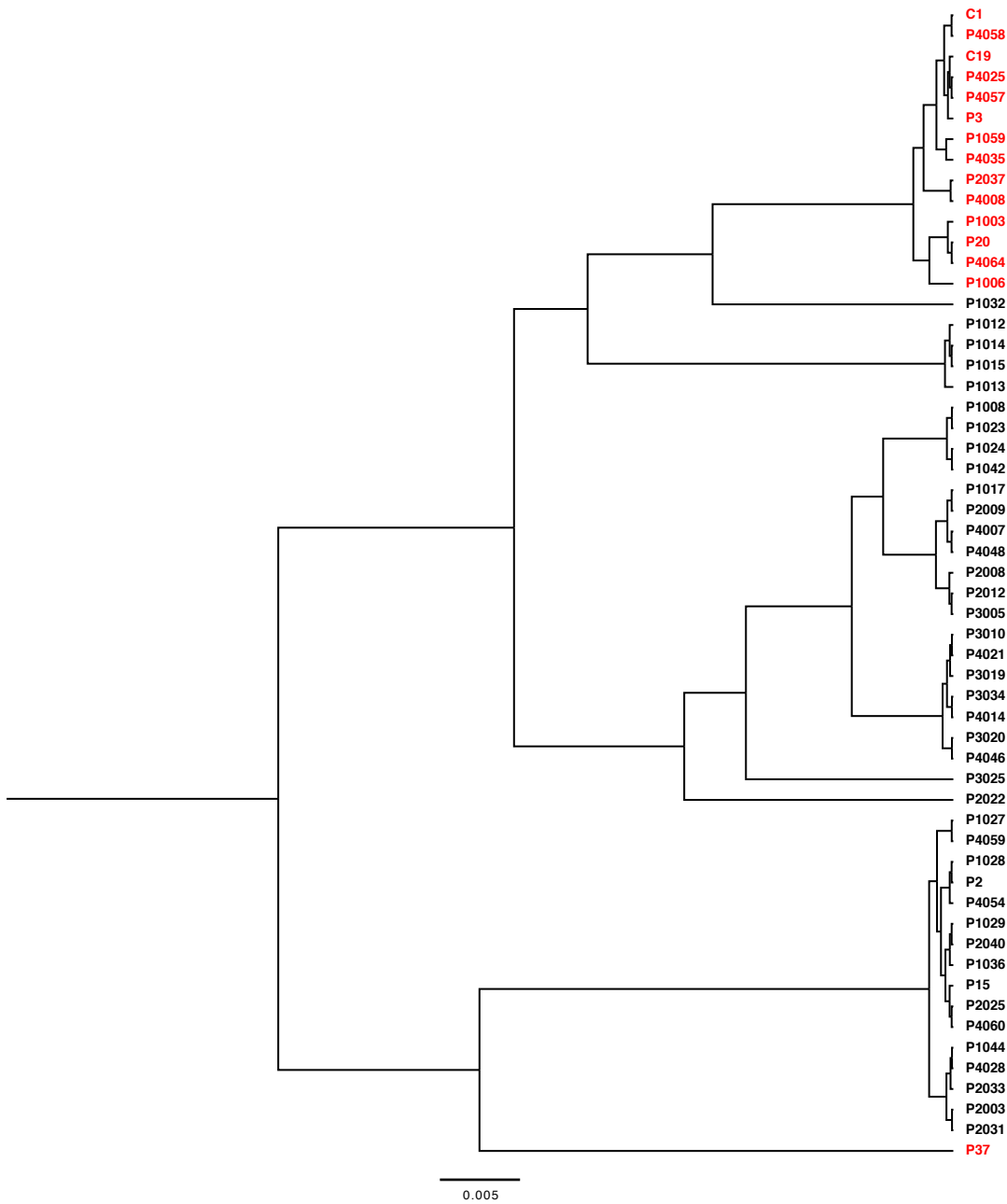| Sequence	
C1(+)	Frame 1
C19(+)	Frame 1
P3(+)	Frame 1
P20(+)	Frame 1
P1003(+)	Frame 1
P1006(+)	Frame 1
P1059(+)	Frame 1
P4025(+)	Frame 1
P4035(+)	Frame 1
P4056(+)	Frame 1
P4058(+)	Frame 1
P2037(+)	Frame 1
P4008(+)	Frame 1
P37(+)	Frame 1
P1008(-)	Frame 1
P1023(-)	Frame 1
P1024(-)	Frame 1
P1042(-)	Frame 1
P1017(-)	Frame 1
P2008(-)	Frame 1
P2009(-)	Frame 1
P2012(-)	Frame 1
P3022(-)	Frame 1
P4007(-)	Frame 1
P2022(-)	Frame 1
P3010(-)	Frame 1
P3019(-)	Frame 1
P3020(-)	Frame 1
P3034(-)	Frame 1
P4014(-)	Frame 1
P4021(-)	Frame 1
P4046(-)	Frame 1
P1032(-)	Frame 1
P3025(-)	Frame 1
P1012(-)	Frame 1
P1013(-)	Frame 1
P1014(-)	Frame 1
P1015(-)	Frame 1
P2(-)	Frame 1
P15(-)	Frame 1
P1044(-)	Frame 1
P2003(-)	Frame 1
P2033(-)	Frame 1
P4028(-)	Frame 1
P1027(-)	Frame 1
P1028(-)	Frame 1
P1029(-)	Frame 1
P1036(-)	Frame 1
P2025(-)	Frame 1
P2040(-)	Frame 1
P4054(-)	Frame 1
P4059(-)	Frame 1
P4060(-)	Frame 1

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Supplementary Figure 3: Nucleotide alignment and ORF translation of partial Pcl7 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.
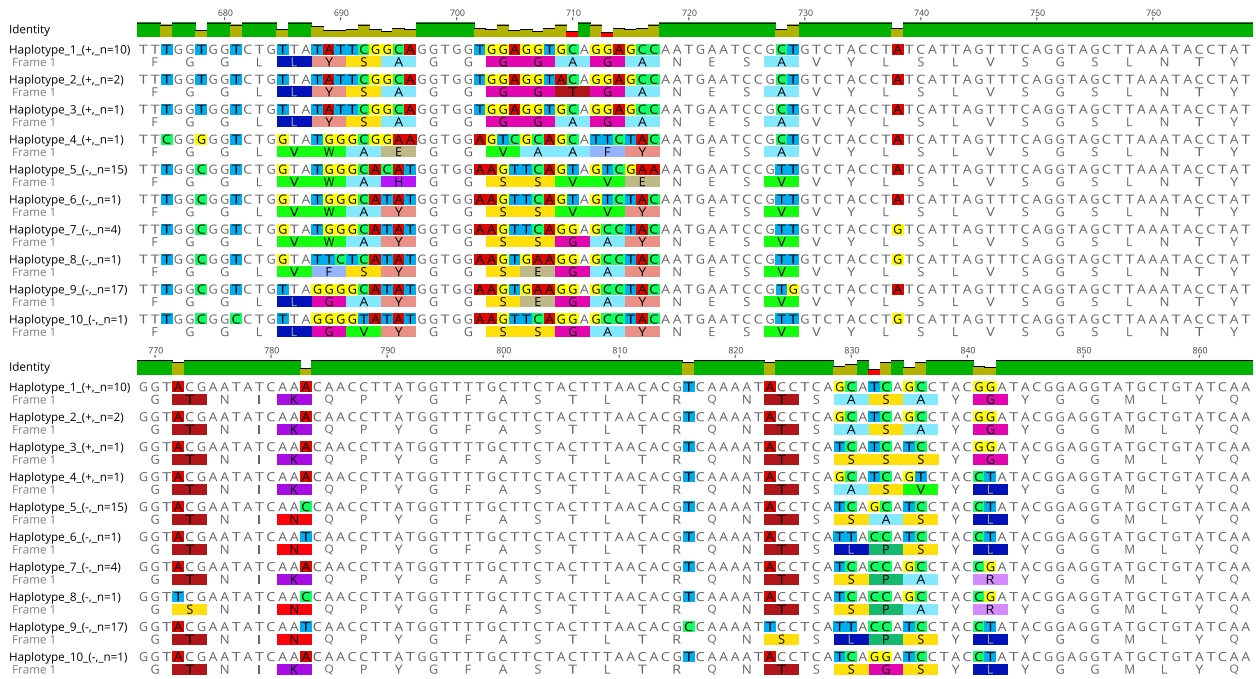
Supplementary Figure 3: a) Structural model and corresponding quality scores of C-terminal globular domain of Pcl7 homotrimer, based on alignment with BclA. Colors correspond to the QMEAN score, with purple indicating a high-quality local alignment and orange indicating a low-quality local alignment. **b)** Predicted local similarity of Pcl7 query sequence to BclA target sequence. **c)** Alignment of Pcl7 translated sequence to BclA target sequence, with same alignment-quality color scheme as Panel a.
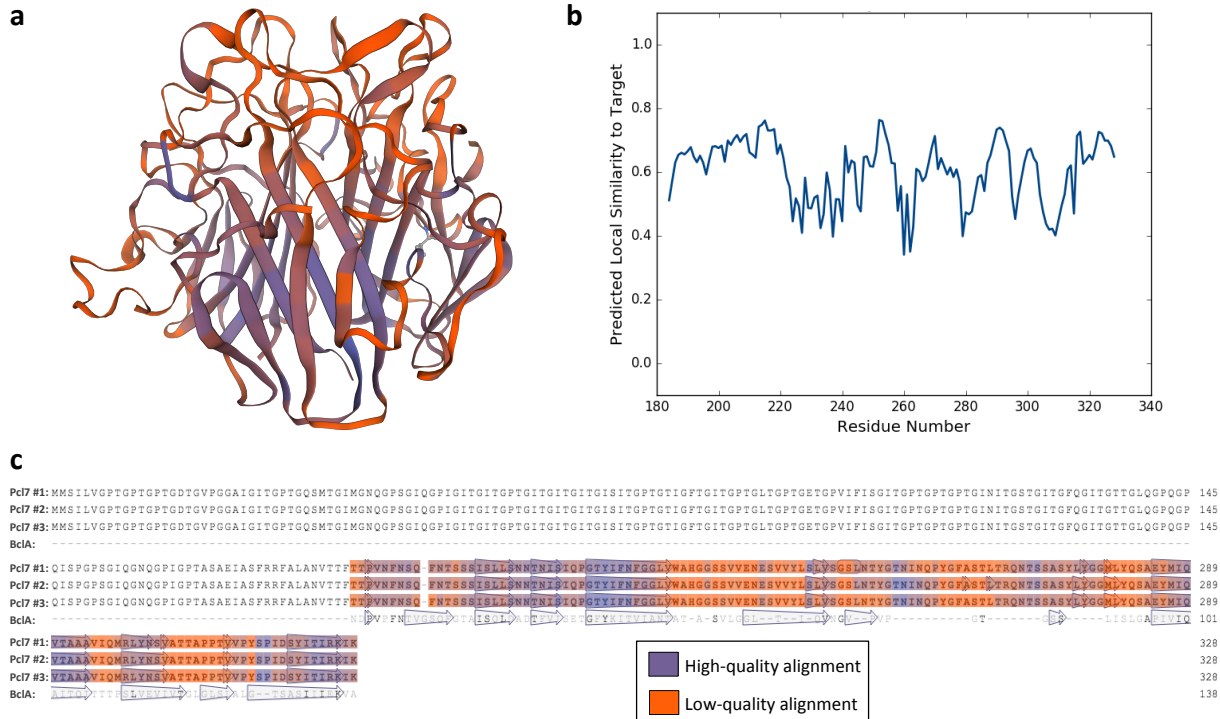
Supplementary Figure 4: Phylogenies of all 56 clones in the *P. ramosa* diversity panel (24 genome-sequenced clones plus 32 additional clones), based on the full coding sequence of the Pcl7 gene. Red branch tips indicate clones that were infectious to host phenotype HU-HO-2/CH-H-67, and black branch 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