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512 **Table 1. Primers used for the PCR and qPCR studies and for sequencing the pPCP1**513 **plasmids (supplementary material)**

Gene	Primers 5' → 3'	Reference	Amplicon size (bp)
yp0120ms01 F	CTAAGCACAAATTGTTATGCTGAACC	Pourcel et al 2004	
yp0120ms01 R	TACTGAATCTGCTTCATTGTTCAAA		
yp1290ms04 F	CGCTGTGAAGTTTTAGTGTAAGAA	Pourcel et al 2004	
yp1290ms04 R	AAATGTAACCTGCCAAACGTG		
yp2769ms06 F	AATTTTGCTCCCAAATAGCAT	Pourcel et al 2004	
yp2769ms06 R	TTTTCCCATTAGCGAAATAAGTA		
yp2916ms07 F	ATACCGCTACGATCAGCCTCTAT	Pourcel et al 2004	
yp2916ms07 R	ATTTAATATTGATTTTGGGACTTGC		
yp1335ms46 F	CAGGTTTTACGTTATTTCTGAAGG	Pourcel et al 2004	
yp1335ms46 R	CAGCATGAAGTATGACGGGTATATTA		
yp4280ms62 F	TTTAGTCTTGATTAAGCTGCGTTTT	Pourcel et al 2004	
yp4280ms62 R	ACGGAAGACAACCTTATTATTGATG		
yp1580ms70 F	AAACCAACGGTTCATATTGAATAAA	Pourcel et al 2004	
yp1580ms70 R	CTTCTCCGCTATTTTCCTACAGA		
Pla F1	AAG TTC TAT TGT GGC AAC C	This study	470
Pla R1	CGTGTTCCTGATATCCTGCT		
Pst F	GGTGTCCGGCTTTTCTCTT	This study	201
Pst R	TTCCTGGCGGATCTTATTTG		
Pim F	CATGGCATCTATGGGAAACA	This study	197
Pim R	GCTACATATGTTGGCGGTCCT		
glnAF	AAGCGGTTACTTCCCTGTT	This study	156
glnAR	CGGGTAGCCACTTCGTTTT		
PlaF2	TGTGAAAGGCTGGTACTCC	This study	145
PlaR2	CCTATTACCCGCACTCCTTT		
pcp1F	CGGTGCAATAGTGATCCACA	This study	660
pcp1R	CACGTTGCAGAACCACAGTT		
pcp2F	GGAGACCTGCCATCGTAATG	This study	673
pcp2R	GAAGCAGATGCTCCAGGAAG		
pcp3F	GTTGCAACTGGAAAGCCTTA	This study	663
pcp3R	TGAACGACATGTGAGTGGTG		
pcp4F	GGTATGCAGCACTGACCT	This study	654
pcp4R	TCTGACGACATGAAACGAAAA		
pcp5F	GTAACGCGATTTCCGTACC	This study	670
pcp5R	GCATCCAGAGCATCCAGTTT		
pcp6F	ATGGCGGATTTATCAGAAG	This study	659
pcp6R	TTAAGTCCTGTCGGGTTTCG		

pcp7F	CCTGACGAGCATCACAAAAA	This study	650
pcp7R	GTGTTACCGCAGCAATACCC		
pcp8F	CCGATCAGTTCAGCAGAAGA	This study	650
pcp8R	TGAGGGGCTTGCTATTAATGAT		
pcp9F	AAAGAAATCTATCCCTGGTTGC	This study	649
pcp9F	GTTGACCACGATATTTCTCCA		
pcp10F	CGGATTAACCCTTCAAAACC	This study	655
pcp10F	CAGAGAAAATAAAGCGGCGTA		
pcp11F	CCATTGTATCTGACATAAAAAATCC	This study	689
pcp11F	CGTTTTCTCGTCGTCTGACA		
pcp12F	CCTGGATATTTCCACCGTTT	This study	670
pcp12F	GAACCACCTGTAGCTGTCCAA		
pcp13F	GGCTGGTTACTCCAGGATGA	This study	686
pcp13F	TGGAGAATGTCAAGGCAAAA		
pcp14F	TGACCAACCTTCAGATGTGTG	This study	698
pcp14F	CAGGAAAAGGTTTTGGCTGA		
pcp15F	GCATATGGCCTGGGTAACTC	This study	696
pcp15F	GGGAGCGTTTTAAGCAGGTT		
pcp16F	CATGCGTATCCAGGATGAGT	This study	770
pcp16F	GCAGATTACCCCTGGATCT		

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**Table 2. Tandem repeat numbers for 7 loci used in this study (supplementary material)**

Strains	ms01	ms04	ms06	ms07	ms46	ms62	ms70
1390G	7.1	4.8	7.6	8.3	6.0	11.3	2.7
1391G	7.1	4.8	7.6	8.3	6.0	11.3	2.6
1392G	7.1	4.8	7.6	8.3	6.0	11.3	2.7
1393G	7.1	4.8	7.6	8.3	6.0	11.3	2.7
1412G	7.6	4.8	7.4	8.3	6.0	11.3	2.1
1413G	7.3	4.8	7.6	8.3	6.0	11.3	2.6
1670G	7.3	4.8	7.6	8.3	6.0	11.3	2.6
1851G	7.1	4.8	7.6	8.3	6.0	11.3	2.7
1852G	7.1	4.8	7.5	8.2	6.0	11.3	2.6
1853G	7.3	4.8	7.6	8.3	6.0	11.3	3.5
1952G	7.1	4.8	6.7	8.3	6.0	11.3	2.6
1953G	7.1	4.8	7.6	8.3	6.0	11.3	2.7
1954G	7.1	4.8	7.3	8.3	6.0	11.3	2.7
2095G	7.1	4.8	7.6	8.3	6.0	11.3	2.7
3064G	7.1	4.8	7.6	8.3	6.0	11.3	2.7
3065G	7.1	4.8	7.3	8.3	6.0	11.3	2.7
3066G	7.1	4.8	7.6	8.3	6.0	11.3	2.6
3067G	7.1	4.8	7.6	8.3	6.0	11.3	2.1
3072G	7.3	4.8	7.6	8.3	6.0	11.3	2.6
3073G	7.1	4.8	7.6	8.3	6.0	11.3	2.7
3082G	7.1	4.8	7.6	8.3	6.0	11.3	2.7
3083G	7.1	4.8	7.6	8.3	6.0	11.3	2.6
3757G	7.1	4.8	7.6	8.2	6.0	9.3	2.7
3758G	7.1	4.8	7.3	8.3	6.0	11.3	2.1
3768G	7.1	4.8	7.6	8.3	6.0	11.3	2.7
3769G	7.1	4.8	7.6	8.3	6.0	11.3	2.6
3770G	7.1	4.8	7.6	8.3	6.0	11.3	2.3
8786G	7.1	4.8	7.6	6.4	6.0	11.3	2.6
8787G	7.1	4.8	7.6	7.4	6.0	11.3	2.7
8788G	7.1	4.8	7.6	8.3	6.0	11.3	3.0
8789G	7.3	4.8	7.6	7.4	6.0	11.3	2.7
8790G	7.1	4.8	7.6	8.3	6.0	11.3	2.7
8791G	7.1	4.8	7.6	8.3	6.0	11.3	2.7
8792G	7.1	4.8	7.6	8.3	6.0	11.3	2.1
8793G	7.2	4.8	7.6	8.3	6.0	11.3	2.6
8794G	7.1	4.8	7.5	8.3	6.0	11.3	2.7
8906G	7.1	4.8	7.6	8.3	6.0	11.3	2.6
8907G	7.3	4.8	6.6	8.3	6.0	11.3	2.6
8908G	7.1	4.8	7.6	8.3	6.0	11.3	2.7
C1045	7.1	5.5	3.5	7.4	0.0	13.3	4.7
C14735	7.3	4.8	7.5	9.4	6.0	10.3	2.7
C1522	7.3	4.8	7.5	9.4	6.0	10.3	7.6
C2614	7.1	5.8	3.5	8.3	0.0	17.3	7.7
C2944	7.1	5.8	3.5	8.3	0.0	17.3	6.6
C771	7.1	5.8	3.5	8.2	3.4	13.3	6.7
C790	6.1	6.8	7.5	7.4	0.0	7.3	2.1
CO92	8.3	7.8	8.5	9.3	7.0	6.3	5.7
KIM	6.1	5.8	3.5	6.4	0.0	10.3	5.7