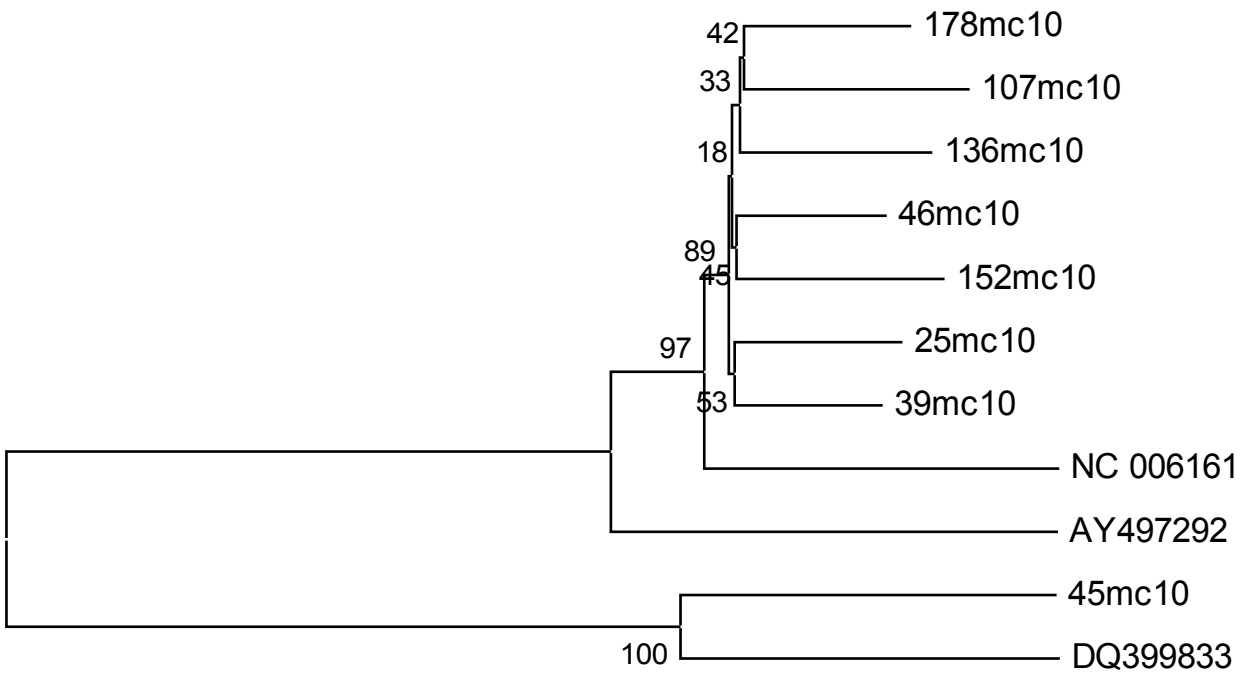
Supplementary phylogenetic analyses of the unresolved part of the tree presented in Figure 5

The analysis involved 11 nucleotide sequences and was conducted in MEGA6 (Tamura et al. 2013). To increase the phylogenetic resolution, the alignement was created containing the continuous section of the genomes in question, beginning at the start of the first *trn* gene (*trnY*) and ending within the *lrn*, immediately before the identified F-M breakpoint. The alignment was checked for potential missed recombination signatures but none was found, therefore this section of the genomes was considered valid for phylogenetic analysis using classic, substitution based models of evolution. The alignment was also straightforward as there were only minor (5 bp in total) length differences, all constituting single nucleotide deletions within the reference NC_006161 genome (most likely sequencing errors, but these columns were excluded from the analyses anyway since all positions containing gaps and missing data were eliminated). There were a total of 15160 positions in the final dataset, 3202 bp more than in the alignment used to obtain the tree presented in Figure 5. In addion to all protein coding genes, this alignment contained also all *trn* genes, *srn* gene, the portion of *lrn* not involved in recombination and all intergenic sequences. The only excluded part was the control region and the part of *lrn* involved in recombination.

Conclusion: No increase in the resolution was observed in any analysis (Supplementary Figures S1-S3), as compared to the tree presented in Figure 5.

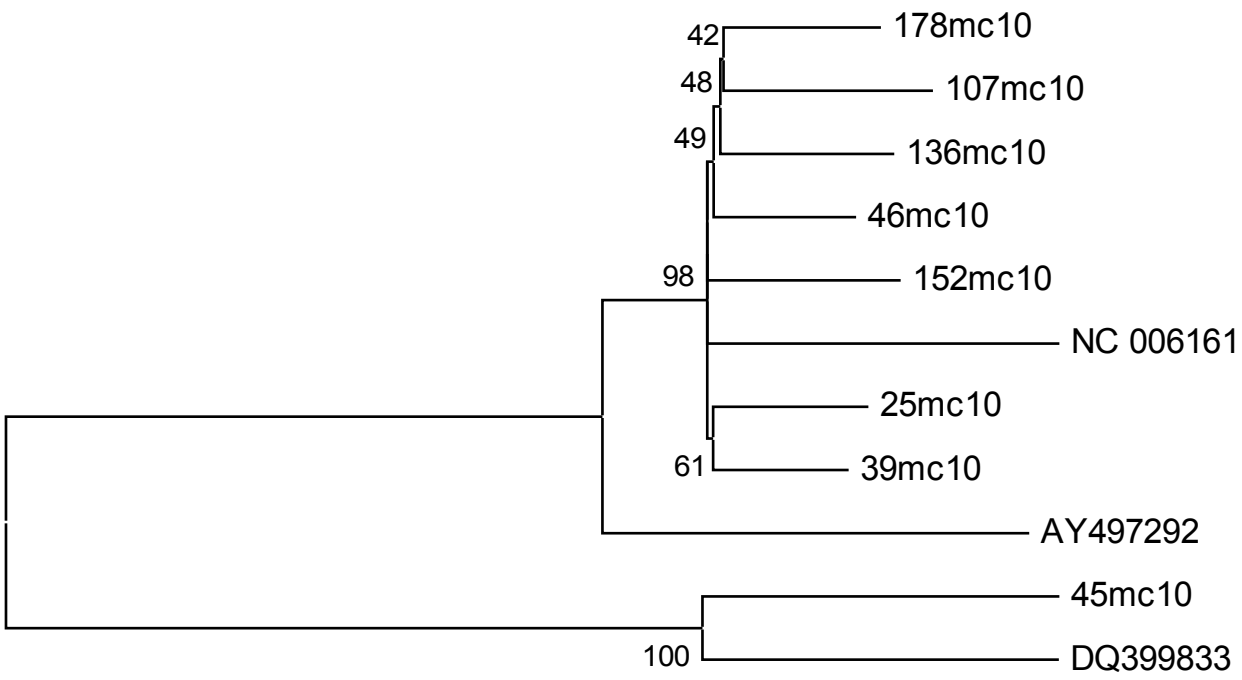


Supplementary Figure S1. Evolutionary relationships of taxa inferred using the Neighbor-Joining method (Saitou and Nei 1987).
The optimal tree with the sum of branch length = 0.03998550 is shown. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (100 replicates) are shown next to the branches (Felsenstein 1985). The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Maximum Composite Likelihood method (Tamura et al. 2004) and are in the units of the number of base substitutions per site.

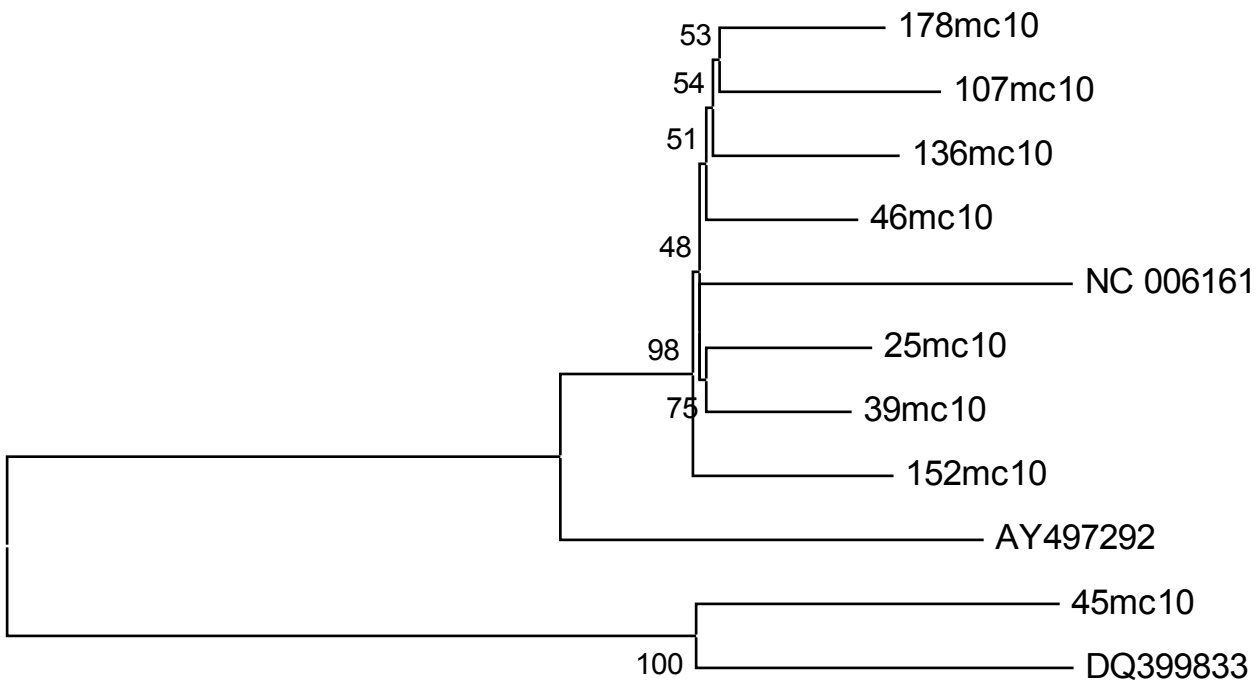
Supplementary Table S3. Model selection for ML (Maximum Likelihood) analysis: fits of 24 different nucleotide substitution models.

Model	BIC	AICc	*lnL*	*R*	*f(A)*	*f(T)*	*f(C)*	*f(G)*	*r(AT)*	*r(AC)*	*r(AG)*	*r(TA)*	*r(TC)*	*r(TG)*	*r(CA)*	*r(CT)*	*r(CG)*	*r(GA)*	*r(GT)*	*r(GC)*
TN93+G	49268.052	49017.452	-24483.722	5.65	0.272	0.348	0.143	0.236	0.023	0.009	0.082	0.018	0.202	0.015	0.018	0.491	0.015	0.094	0.023	0.009
GTR+G	49277.348	48996.677	-24470.334	4.58	0.272	0.348	0.143	0.236	0.019	0.010	0.082	0.015	0.191	0.017	0.019	0.465	0.039	0.094	0.025	0.024
TN93+G+I	49280.077	49019.453	-24483.722	5.65	0.272	0.348	0.143	0.236	0.023	0.009	0.082	0.018	0.202	0.016	0.018	0.491	0.016	0.094	0.023	0.009
GTR+G+I	49289.373	48998.678	-24470.334	4.58	0.272	0.348	0.143	0.236	0.019	0.010	0.082	0.015	0.191	0.017	0.019	0.465	0.039	0.094	0.025	0.024
TN93	49315.694	49075.117	-24513.555	5.45	0.272	0.348	0.143	0.236	0.024	0.010	0.084	0.018	0.200	0.016	0.018	0.485	0.016	0.096	0.024	0.010
GTR	49316.985	49046.338	-24496.164	4.73	0.272	0.348	0.143	0.236	0.015	0.010	0.083	0.012	0.192	0.018	0.020	0.466	0.040	0.095	0.026	0.024
TN93+I	49327.680	49077.080	-24513.536	5.45	0.272	0.348	0.143	0.236	0.024	0.010	0.084	0.018	0.200	0.016	0.018	0.485	0.016	0.096	0.024	0.010
GTR+I	49328.564	49047.893	-24495.942	4.73	0.272	0.348	0.143	0.236	0.015	0.010	0.083	0.012	0.192	0.018	0.020	0.466	0.040	0.095	0.026	0.024
HKY+G	49449.617	49209.041	-24580.517	5.64	0.272	0.348	0.143	0.236	0.024	0.010	0.203	0.019	0.123	0.016	0.019	0.300	0.016	0.234	0.024	0.010
HKY+G+I	49461.621	49211.021	-24580.507	5.65	0.272	0.348	0.143	0.236	0.024	0.010	0.203	0.019	0.123	0.016	0.019	0.300	0.016	0.234	0.024	0.010
HKY	49515.039	49284.487	-24619.240	5.43	0.272	0.348	0.143	0.236	0.025	0.010	0.202	0.020	0.123	0.017	0.020	0.298	0.017	0.233	0.025	0.010
HKY+I	49526.897	49286.321	-24619.157	5.43	0.272	0.348	0.143	0.236	0.025	0.010	0.202	0.020	0.123	0.017	0.020	0.298	0.017	0.233	0.025	0.010
T92+G	49901.495	49680.966	-24818.480	5.62	0.310	0.310	0.190	0.190	0.022	0.014	0.163	0.022	0.163	0.014	0.022	0.266	0.014	0.266	0.022	0.014
T92+G+I	49913.512	49682.959	-24818.476	5.62	0.310	0.310	0.190	0.190	0.022	0.014	0.163	0.022	0.163	0.014	0.022	0.266	0.014	0.266	0.022	0.014
T92	49966.324	49755.819	-24856.907	5.43	0.310	0.310	0.190	0.190	0.023	0.014	0.162	0.023	0.162	0.014	0.023	0.264	0.014	0.264	0.023	0.014
T92+I	49978.043	49757.514	-24856.754	5.43	0.310	0.310	0.190	0.190	0.023	0.014	0.162	0.023	0.162	0.014	0.023	0.264	0.014	0.264	0.023	0.014
K2+G	50791.026	50580.521	-25269.258	5.61	0.250	0.250	0.250	0.250	0.019	0.019	0.212	0.019	0.212	0.019	0.019	0.212	0.019	0.212	0.019	0.019
K2+G+I	50802.746	50582.217	-25269.106	5.63	0.250	0.250	0.250	0.250	0.019	0.019	0.212	0.019	0.212	0.019	0.019	0.212	0.019	0.212	0.019	0.019
K2	50859.838	50659.357	-25309.676	5.42	0.250	0.250	0.250	0.250	0.019	0.019	0.211	0.019	0.211	0.019	0.019	0.211	0.019	0.211	0.019	0.019
K2+I	50871.811	50661.306	-25309.650	5.42	0.250	0.250	0.250	0.250	0.019	0.019	0.211	0.019	0.211	0.019	0.019	0.211	0.019	0.211	0.019	0.019
JC+G	51462.485	51262.003	-25610.999	0.50	0.250	0.250	0.250	0.250	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083
JC+G+I	51474.509	51264.004	-25610.999	0.50	0.250	0.250	0.250	0.250	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083
JC	51522.906	51332.449	-25647.222	0.50	0.250	0.250	0.250	0.250	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083
JC+I	51534.889	51334.408	-25647.201	0.50	0.250	0.250	0.250	0.250	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083

NOTE.-- Models with the lowest BIC scores (Bayesian Information Criterion) are considered to describe the substitution pattern the best. For each model, AICc value (Akaike Information Criterion, corrected), Maximum Likelihood value (lnL), and the number of parameters (including branch lengths) are also presented (Nei and Kumar 2000). Non-uniformity of evolutionary rates among sites may be modeled by using a discrete Gamma distribution (+G) with 4 rate categories and by assuming that a certain fraction of sites are evolutionarily invariable (+I). Assumed or estimated values of transition/transversion bias (R) are shown for each model. They are followed by nucleotide frequencies (f) and rates of base substitutions (r) for each nucleotide pair. Relative values of instantaneous r should be considered when evaluating them. For simplicity, sum of r values is made equal to 1 for each model. For estimating ML values, a tree topology was automatically computed.
Abbreviations: GTR: General Time Reversible; HKY: Hasegawa-Kishino-Yano; TN93: Tamura-Nei; T92: Tamura 3-parameter; K2: Kimura 2-parameter; JC: Jukes-Cantor.



Supplementary Figure S2. Molecular Phylogenetic analysis by Maximum Likelihood (ML) method.
The evolutionary history was inferred by using the Maximum Likelihood method based on the Tamura-Nei model (Tamura and Nei 1993), selected based on Bayesian Information Criterion (Supplementary Table S3). The tree with the highest log likelihood (-24480.3394) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial trees for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using the Maximum Composite Likelihood (MCL) approach, and then selecting the topology with superior log likelihood value. A discrete Gamma distribution was used to model evolutionary rate differences among sites (4 categories (+G, alpha parameter = 0.0905)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site.



Supplementary Figure S3. Maximum Parsimony (MP) analysis of taxa
The evolutionary history was inferred using the Maximum Parsimony method. Tree #1 out of 3 most parsimonious trees (length = 605) is shown. The consistency index is (0.865613), the retention index is (0.869231), and the composite index is 0.820381 (0.752417) for all sites and parsimony-informative sites (in parentheses). The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches (Felsenstein 1985). The MP tree was obtained using the Tree-Bisection-Regrafting (TBR) algorithm (Nei and Kumar 2000, pg. 126) with search level 5 in which the initial trees were obtained by the random addition of sequences (30 replicates). The tree is drawn to scale , with branch lengths calculated using the average pathway method (Nei and Kumar 2000, pg. 132) and are in the units of the number of changes over the whole sequence.

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