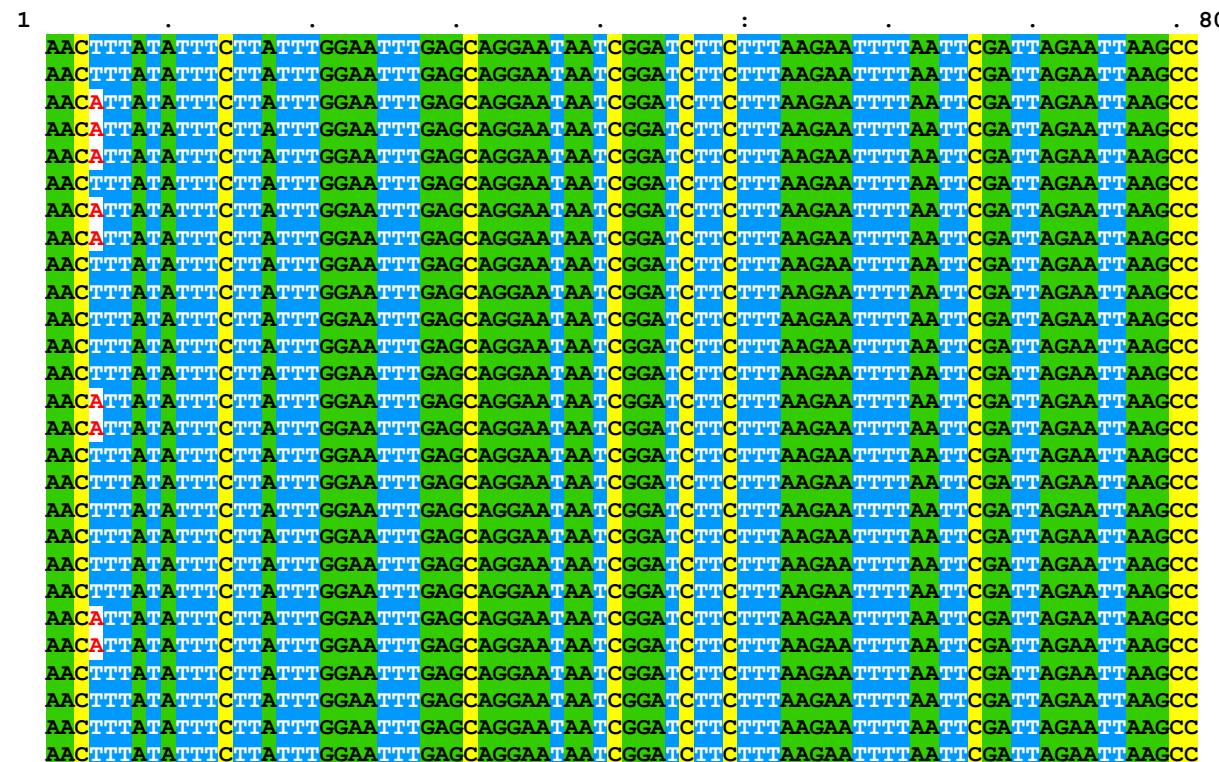
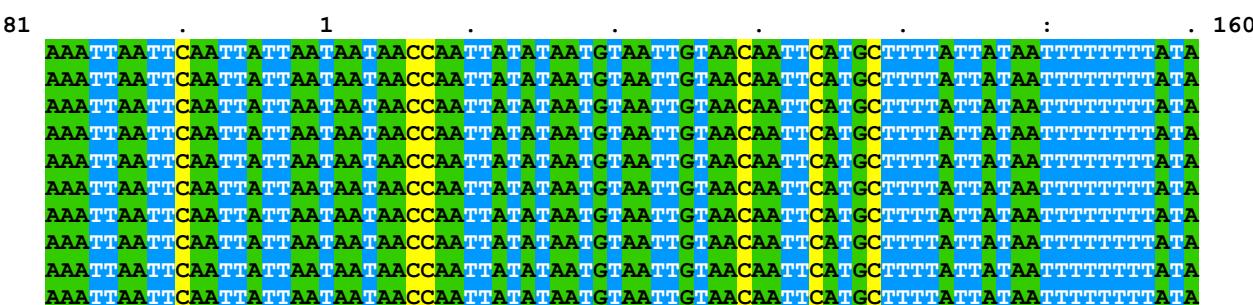


Supplementary file 2. *P. juglandis* COI sequence alignment performed with CLUSTAL and edited with Mview (nucleotide coloured by identity). cov: sequence coverage. pid: percentage of identity

	cov	pid
1 PANJUG.G1.sample1_COI	100.0%	100.0%
2 PANJUG.G1.sample2_COI	100.0%	100.0%
3 PANJUG.G2.sample1_COI	100.0%	99.7%
4 PANJUG.G2.sample2_COI	100.0%	99.7%
5 PANJUG.G2.sample3_COI	100.0%	99.7%
6 PANJUG.G3.sample10_COI	100.0%	100.0%
7 PANJUG.G3.sample11_COI	100.0%	99.7%
8 PANJUG.G3.sample12_COI	100.0%	99.7%
9 PANJUG.G3.sample13_COI	100.0%	99.8%
10 PANJUG.G3.sample14_COI	100.0%	100.0%
11 PANJUG.G3.sample15_COI	100.0%	100.0%
12 PANJUG.G3.sample16_COI	100.0%	100.0%
13 PANJUG.G3.sample17_COI	100.0%	100.0%
14 PANJUG.G3.sample18_COI	100.0%	99.7%
15 PANJUG.G3.sample19_COI	100.0%	99.7%
16 PANJUG.G3.sample1_COI	100.0%	100.0%
17 PANJUG.G3.sample20_COI	100.0%	99.8%
18 PANJUG.G3.sample21_COI	100.0%	100.0%
19 PANJUG.G3.sample22_COI	100.0%	100.0%
20 PANJUG.G3.sample2_COI	100.0%	100.0%
21 PANJUG.G3.sample3_COI	100.0%	100.0%
22 PANJUG.G3.sample4_COI	100.0%	99.7%
23 PANJUG.G3.sample5_COI	100.0%	99.7%
24 PANJUG.G3.sample6_COI	100.0%	99.8%
25 PANJUG.G3.sample7_COI	100.0%	100.0%
26 PANJUG.G3.sample8_COI	100.0%	100.0%
27 PANJUG.G3.sample9_COI	100.0%	100.0%



	cov	pid
1 PANJUG.G1.sample1_COI	100.0%	100.0%
2 PANJUG.G1.sample2_COI	100.0%	100.0%
3 PANJUG.G2.sample1_COI	100.0%	99.7%
4 PANJUG.G2.sample2_COI	100.0%	99.7%
5 PANJUG.G2.sample3_COI	100.0%	99.7%
6 PANJUG.G3.sample10_COI	100.0%	100.0%
7 PANJUG.G3.sample11_COI	100.0%	99.7%
8 PANJUG.G3.sample12_COI	100.0%	99.7%
9 PANJUG.G3.sample13_COI	100.0%	99.8%
10 PANJUG.G3.sample14_COI	100.0%	100.0%



11	PANJUG.G3.sample15_COI	100.0%	100.0%
12	PANJUG.G3.sample16_COI	100.0%	100.0%
13	PANJUG.G3.sample17_COI	100.0%	100.0%
14	PANJUG.G3.sample18_COI	100.0%	99.7%
15	PANJUG.G3.sample19_COI	100.0%	99.7%
16	PANJUG.G3.sample1_COI	100.0%	100.0%
17	PANJUG.G3.sample20_COI	100.0%	99.8%
18	PANJUG.G3.sample21_COI	100.0%	100.0%
19	PANJUG.G3.sample22_COI	100.0%	100.0%
20	PANJUG.G3.sample2_COI	100.0%	100.0%
21	PANJUG.G3.sample3_COI	100.0%	100.0%
22	PANJUG.G3.sample4_COI	100.0%	99.7%
23	PANJUG.G3.sample5_COI	100.0%	99.7%
24	PANJUG.G3.sample6_COI	100.0%	99.8%
25	PANJUG.G3.sample7_COI	100.0%	100.0%
26	PANJUG.G3.sample8_COI	100.0%	100.0%
27	PANJUG.G3.sample9_COI	100.0%	100.0%

A sequence alignment of 27 samples (labeled 11 to 27) against a reference sequence. The alignment shows high conservation, with most positions matching the reference (A, T, C, G). A few variations are highlighted in yellow, green, and blue, indicating polymorphisms or sequencing artifacts.

		cov	pid
1	PANJUG.G1.sample1_COI	100.0%	100.0%
2	PANJUG.G1.sample2_COI	100.0%	100.0%
3	PANJUG.G2.sample1_COI	100.0%	99.7%
4	PANJUG.G2.sample2_COI	100.0%	99.7%
5	PANJUG.G2.sample3_COI	100.0%	99.7%
6	PANJUG.G3.sample10_COI	100.0%	100.0%
7	PANJUG.G3.sample11_COI	100.0%	99.7%
8	PANJUG.G3.sample12_COI	100.0%	99.7%
9	PANJUG.G3.sample13_COI	100.0%	99.8%
10	PANJUG.G3.sample14_COI	100.0%	100.0%
11	PANJUG.G3.sample15_COI	100.0%	100.0%
12	PANJUG.G3.sample16_COI	100.0%	100.0%
13	PANJUG.G3.sample17_COI	100.0%	100.0%
14	PANJUG.G3.sample18_COI	100.0%	99.7%
15	PANJUG.G3.sample19_COI	100.0%	99.7%
16	PANJUG.G3.sample1_COI	100.0%	100.0%
17	PANJUG.G3.sample20_COI	100.0%	99.8%
18	PANJUG.G3.sample21_COI	100.0%	100.0%
19	PANJUG.G3.sample22_COI	100.0%	100.0%
20	PANJUG.G3.sample2_COI	100.0%	100.0%
21	PANJUG.G3.sample3_COI	100.0%	100.0%
22	PANJUG.G3.sample4_COI	100.0%	99.7%
23	PANJUG.G3.sample5_COI	100.0%	99.7%
24	PANJUG.G3.sample6_COI	100.0%	99.8%
25	PANJUG.G3.sample7_COI	100.0%	100.0%
26	PANJUG.G3.sample8_COI	100.0%	100.0%

A sequence alignment of 26 samples (labeled 1 to 26) against a reference sequence. The alignment shows high conservation, with most positions matching the reference (A, T, C, G). A few variations are highlighted in yellow, green, and blue, indicating polymorphisms or sequencing artifacts. The alignment starts at position 161 and ends at position 240.

27 PANJUG.G3.sample9_COI 100.0% 100.0%

ACTAATACCTATTGTAAATTGGAGGGTTGGAAATTGATTAACTTAAATAGGATGTCAGATATCATTCCACG

cov pid 241

1 PANJUG.G1.sample1_COI 100.0% 100.0%
2 PANJUG.G1.sample2_COI 100.0% 100.0%
3 PANJUG.G2.sample1_COI 100.0% 99.7%
4 PANJUG.G2.sample2_COI 100.0% 99.7%
5 PANJUG.G2.sample3_COI 100.0% 99.7%
6 PANJUG.G3.sample10_COI 100.0% 100.0%
7 PANJUG.G3.sample11_COI 100.0% 99.7%
8 PANJUG.G3.sample12_COI 100.0% 99.7%
9 PANJUG.G3.sample13_COI 100.0% 99.8%
10 PANJUG.G3.sample14_COI 100.0% 100.0%
11 PANJUG.G3.sample15_COI 100.0% 100.0%
12 PANJUG.G3.sample16_COI 100.0% 100.0%
13 PANJUG.G3.sample17_COI 100.0% 100.0%
14 PANJUG.G3.sample18_COI 100.0% 99.7%
15 PANJUG.G3.sample19_COI 100.0% 99.7%
16 PANJUG.G3.sample1_COI 100.0% 100.0%
17 PANJUG.G3.sample20_COI 100.0% 99.8%
18 PANJUG.G3.sample21_COI 100.0% 100.0%
19 PANJUG.G3.sample22_COI 100.0% 100.0%
20 PANJUG.G3.sample2_COI 100.0% 100.0%
21 PANJUG.G3.sample3_COI 100.0% 100.0%
22 PANJUG.G3.sample4_COI 100.0% 99.7%
23 PANJUG.G3.sample5_COI 100.0% 99.7%
24 PANJUG.G3.sample6_COI 100.0% 99.8%
25 PANJUG.G3.sample7_COI 100.0% 100.0%
26 PANJUG.G3.sample8_COI 100.0% 100.0%
27 PANJUG.G3.sample9_COI 100.0% 100.0%

3 320

cov pid 321

1 PANJUG.G1.sample1_COI 100.0% 100.0%
2 PANJUG.G1.sample2_COI 100.0% 100.0%
3 PANJUG.G2.sample1_COI 100.0% 99.7%
4 PANJUG.G2.sample2_COI 100.0% 99.7%
5 PANJUG.G2.sample3_COI 100.0% 99.7%
6 PANJUG.G3.sample10_COI 100.0% 100.0%
7 PANJUG.G3.sample11_COI 100.0% 99.7%
8 PANJUG.G3.sample12_COI 100.0% 99.7%
9 PANJUG.G3.sample13_COI 100.0% 99.8%
10 PANJUG.G3.sample14_COI 100.0% 100.0%
11 PANJUG.G3.sample15_COI 100.0% 100.0%
12 PANJUG.G3.sample16_COI 100.0% 100.0%

4 400

13	PANJUG.G3.sample17_COI	100.0%	100.0%
14	PANJUG.G3.sample18_COI	100.0%	99.7%
15	PANJUG.G3.sample19_COI	100.0%	99.7%
16	PANJUG.G3.sample1_COI	100.0%	100.0%
17	PANJUG.G3.sample20_COI	100.0%	99.8%
18	PANJUG.G3.sample21_COI	100.0%	100.0%
19	PANJUG.G3.sample22_COI	100.0%	100.0%
20	PANJUG.G3.sample2_COI	100.0%	100.0%
21	PANJUG.G3.sample3_COI	100.0%	100.0%
22	PANJUG.G3.sample4_COI	100.0%	99.7%
23	PANJUG.G3.sample5_COI	100.0%	99.7%
24	PANJUG.G3.sample6_COI	100.0%	99.8%
25	PANJUG.G3.sample7_COI	100.0%	100.0%
26	PANJUG.G3.sample8_COI	100.0%	100.0%
27	PANJUG.G3.sample9_COI	100.0%	100.0%

Sequence alignment of 27 samples showing high similarity. The sequence is: GAACAGGTTGAACAACTTATCCACCCTCTCAAAATAACATTGCACATAATTAATTTCAGTTGATTTAACAA.

		cov	pid	401			480
1	PANJUG.G1.sample1_COI	100.0%	100.0%				
2	PANJUG.G1.sample2_COI	100.0%	100.0%				
3	PANJUG.G2.sample1_COI	100.0%	99.7%				
4	PANJUG.G2.sample2_COI	100.0%	99.7%				
5	PANJUG.G2.sample3_COI	100.0%	99.7%				
6	PANJUG.G3.sample10_COI	100.0%	100.0%				
7	PANJUG.G3.sample11_COI	100.0%	99.7%				
8	PANJUG.G3.sample12_COI	100.0%	99.7%				
9	PANJUG.G3.sample13_COI	100.0%	99.8%				
10	PANJUG.G3.sample14_COI	100.0%	100.0%				
11	PANJUG.G3.sample15_COI	100.0%	100.0%				
12	PANJUG.G3.sample16_COI	100.0%	100.0%				
13	PANJUG.G3.sample17_COI	100.0%	100.0%				
14	PANJUG.G3.sample18_COI	100.0%	99.7%				
15	PANJUG.G3.sample19_COI	100.0%	99.7%				
16	PANJUG.G3.sample1_COI	100.0%	100.0%				
17	PANJUG.G3.sample20_COI	100.0%	99.8%				
18	PANJUG.G3.sample21_COI	100.0%	100.0%				
19	PANJUG.G3.sample22_COI	100.0%	100.0%				
20	PANJUG.G3.sample2_COI	100.0%	100.0%				
21	PANJUG.G3.sample3_COI	100.0%	100.0%				
22	PANJUG.G3.sample4_COI	100.0%	99.7%				
23	PANJUG.G3.sample5_COI	100.0%	99.7%				
24	PANJUG.G3.sample6_COI	100.0%	99.8%				
25	PANJUG.G3.sample7_COI	100.0%	100.0%				
26	PANJUG.G3.sample8_COI	100.0%	100.0%				
27	PANJUG.G3.sample9_COI	100.0%	100.0%				

Sequence alignment of 27 samples showing high similarity. The sequence is: TTACACTTAGCAGGAACTCATCAAATTTAGGAGCTATTAAATTTTATTTGTACAATTCTTAATATAATACCAAAATAAATTT.

		cov	pid	481	5	:	560
1	PANJUG.G1.sample1_COI	100.0%	100.0%				
2	PANJUG.G1.sample2_COI	100.0%	100.0%				
3	PANJUG.G2.sample1_COI	100.0%	99.7%				
4	PANJUG.G2.sample2_COI	100.0%	99.7%				
5	PANJUG.G2.sample3_COI	100.0%	99.7%				
6	PANJUG.G3.sample10_COI	100.0%	100.0%				
7	PANJUG.G3.sample11_COI	100.0%	99.7%				
8	PANJUG.G3.sample12_COI	100.0%	99.7%				
9	PANJUG.G3.sample13_COI	100.0%	99.8%				
10	PANJUG.G3.sample14_COI	100.0%	100.0%				
11	PANJUG.G3.sample15_COI	100.0%	100.0%				
12	PANJUG.G3.sample16_COI	100.0%	100.0%				
13	PANJUG.G3.sample17_COI	100.0%	100.0%				
14	PANJUG.G3.sample18_COI	100.0%	99.7%				
15	PANJUG.G3.sample19_COI	100.0%	99.7%				
16	PANJUG.G3.sample1_COI	100.0%	100.0%				
17	PANJUG.G3.sample20_COI	100.0%	99.8%				
18	PANJUG.G3.sample21_COI	100.0%	100.0%				
19	PANJUG.G3.sample22_COI	100.0%	100.0%				
20	PANJUG.G3.sample2_COI	100.0%	100.0%				
21	PANJUG.G3.sample3_COI	100.0%	100.0%				
22	PANJUG.G3.sample4_COI	100.0%	99.7%				
23	PANJUG.G3.sample5_COI	100.0%	99.7%				
24	PANJUG.G3.sample6_COI	100.0%	99.8%				
25	PANJUG.G3.sample7_COI	100.0%	100.0%				
26	PANJUG.G3.sample8_COI	100.0%	100.0%				
27	PANJUG.G3.sample9_COI	100.0%	100.0%				

		cov	pid	561	6	:	640
1	PANJUG.G1.sample1_COI	100.0%	100.0%				
2	PANJUG.G1.sample2_COI	100.0%	100.0%				
3	PANJUG.G2.sample1_COI	100.0%	99.7%				
4	PANJUG.G2.sample2_COI	100.0%	99.7%				
5	PANJUG.G2.sample3_COI	100.0%	99.7%				
6	PANJUG.G3.sample10_COI	100.0%	100.0%				
7	PANJUG.G3.sample11_COI	100.0%	99.7%				
8	PANJUG.G3.sample12_COI	100.0%	99.7%				
9	PANJUG.G3.sample13_COI	100.0%	99.8%				
10	PANJUG.G3.sample14_COI	100.0%	100.0%				
11	PANJUG.G3.sample15_COI	100.0%	100.0%				
12	PANJUG.G3.sample16_COI	100.0%	100.0%				
13	PANJUG.G3.sample17_COI	100.0%	100.0%				

14	PANJUG.G3.sample18_COI	100.0%	99.7%
15	PANJUG.G3.sample19_COI	100.0%	99.7%
16	PANJUG.G3.sample1_COI	100.0%	100.0%
17	PANJUG.G3.sample20_COI	100.0%	99.8%
18	PANJUG.G3.sample21_COI	100.0%	100.0%
19	PANJUG.G3.sample22_COI	100.0%	100.0%
20	PANJUG.G3.sample2_COI	100.0%	100.0%
21	PANJUG.G3.sample3_COI	100.0%	100.0%
22	PANJUG.G3.sample4_COI	100.0%	99.7%
23	PANJUG.G3.sample5_COI	100.0%	99.7%
24	PANJUG.G3.sample6_COI	100.0%	99.8%
25	PANJUG.G3.sample7_COI	100.0%	100.0%
26	PANJUG.G3.sample8_COI	100.0%	100.0%
27	PANJUG.G3.sample9_COI	100.0%	100.0%

The sequence alignment shows a highly conserved COI gene region across 27 samples. The sequence is: CTGGTGCCATTACAAATACTTAACTGACC... The samples are color-coded by group: blue (samples 1-10), green (samples 11-15), yellow (samples 16-20), red (samples 21-25), and purple (sample 26). The alignment highlights a single polymorphism at position 658, where sample 26 (red) has a T, while all other samples have C.

		cov	pid
1	PANJUG.G1.sample1_COI	100.0%	100.0%
2	PANJUG.G1.sample2_COI	100.0%	100.0%
3	PANJUG.G2.sample1_COI	100.0%	99.7%
4	PANJUG.G2.sample2_COI	100.0%	99.7%
5	PANJUG.G2.sample3_COI	100.0%	99.7%
6	PANJUG.G3.sample10_COI	100.0%	100.0%
7	PANJUG.G3.sample11_COI	100.0%	99.7%
8	PANJUG.G3.sample12_COI	100.0%	99.7%
9	PANJUG.G3.sample13_COI	100.0%	99.8%
10	PANJUG.G3.sample14_COI	100.0%	100.0%
11	PANJUG.G3.sample15_COI	100.0%	100.0%
12	PANJUG.G3.sample16_COI	100.0%	100.0%
13	PANJUG.G3.sample17_COI	100.0%	100.0%
14	PANJUG.G3.sample18_COI	100.0%	99.7%
15	PANJUG.G3.sample19_COI	100.0%	99.7%
16	PANJUG.G3.sample1_COI	100.0%	100.0%
17	PANJUG.G3.sample20_COI	100.0%	99.8%
18	PANJUG.G3.sample21_COI	100.0%	100.0%
19	PANJUG.G3.sample22_COI	100.0%	100.0%
20	PANJUG.G3.sample2_COI	100.0%	100.0%
21	PANJUG.G3.sample3_COI	100.0%	100.0%
22	PANJUG.G3.sample4_COI	100.0%	99.7%
23	PANJUG.G3.sample5_COI	100.0%	99.7%
24	PANJUG.G3.sample6_COI	100.0%	99.8%
25	PANJUG.G3.sample7_COI	100.0%	100.0%
26	PANJUG.G3.sample8_COI	100.0%	100.0%
27	PANJUG.G3.sample9_COI	100.0%	100.0%

The sequence alignment shows a highly conserved COI gene region across 27 samples. The sequence is: TTATATCAACATTTATTTC... The samples are color-coded by group: blue (samples 1-10), green (samples 11-15), yellow (samples 16-20), red (samples 21-25), and purple (sample 26). The alignment highlights a single polymorphism at position 641, where sample 26 (red) has a T, while all other samples have C.