

Supporting Information

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SI Methods

Amino Acid Racemization Analysis. Because it has been reported that archeological samples containing authentic ancient DNA display a specific pattern of amino acid racemization (1), we measured the D/L ratio for aspartic acid and alanine. Amino acids were derivatized as described in ref. 2, resolved by high-pressure liquid chromatography (HPLC), using a HyPURITY C18 column (Thermo Electron), and measured through fluorescence detection. The HPLC elution gradient consisted of a mixture of 50 mM sodium acetate and methanol (gradient, 0–10 min: 0% methanol; 10–11 min: 0–30% methanol; 11–30 min: 30% methanol). The extent of racemization caused by the experimental procedure was measured using commercial BSA, and yielded D/L ratios of 0.02 and <0.01 for aspartic acid and alanine, respectively. For the Chauvet cave bear *Us18* sample, we obtained D/L ratios of 0.06 (aspartic acid) and 0.01 (alanine). This pattern is consistent with that described for a series of

archeological samples from which ancient DNA could be recovered (1).

Radiocarbon Dating by Accelerator Mass Spectrometry (AMS). The samples underwent standard chemical pretreatment for removal of contaminants (3), and collagen was extracted using the method of Longin (4). The collagen was combusted into CO₂. CO₂ was cryogenically trapped using an automatic device (5), transformed into graphite, and analyzed for ¹⁴C by the Groningen AMS facility (6). The ¹⁴C activities in the graphite were measured, relative to a standard radioactivity, corrected for isotopic fractionation using the stable isotope ratio ¹³C/¹²C to $\delta^{13}\text{C} = -25\text{‰}$, and calculated using the conventional half-life (7). They are reported in years before present (B.P.). The errors quoted are all 1-sigma. For samples relatively old on the ¹⁴C time scale, the exponential decay law of radioactivity conveys asymmetric errors for the reported ages (8).

1. Poinar HN, Höss M, Bada JL, Pääbo S (1996) Amino acid racemization and the preservation of ancient DNA. *Science* 272:864–866.
2. Nimura N, Kinoshita T (1986) o-phthalaldehyde-N-acetyl-L-cysteine as a chiral derivatization reagent for liquid chromatographic optical resolution of amino acid enantiomers and its application to conventional amino acid analysis. *J Chromatogr* 352:169–177.
3. Mook WG, Streurman HJ (1983) Physical and chemical aspects of radiocarbon dating. *PACT* 8:31–55.
4. Longin, R (1971) *Nature* 230:241–242.
5. Aerts-Bijma AT, van der Plicht J, Meijer HAJ (2001) Automatic AMS sample combustion and CO₂ collection. *Radiocarbon* 43:293–298.
6. van der Plicht J, Wijma S, Aerts AT, Pertuisot MH, Meijer HAJ (2000) Status report: The Groningen AMS facility. *Nuclear Instr Methods Phys Res B* 172:58–65.
7. Mook WG, van der Plicht J (1999) Reporting ¹⁴C activities and concentrations. *Radiocarbon* 41:227–239.
8. Olsson IU (1989) The ¹⁴C method - its possibilities and some pitfalls. *PACT* 24:161–177.

For Figs. S1 and S2, please see page 14 of the Supporting Information.

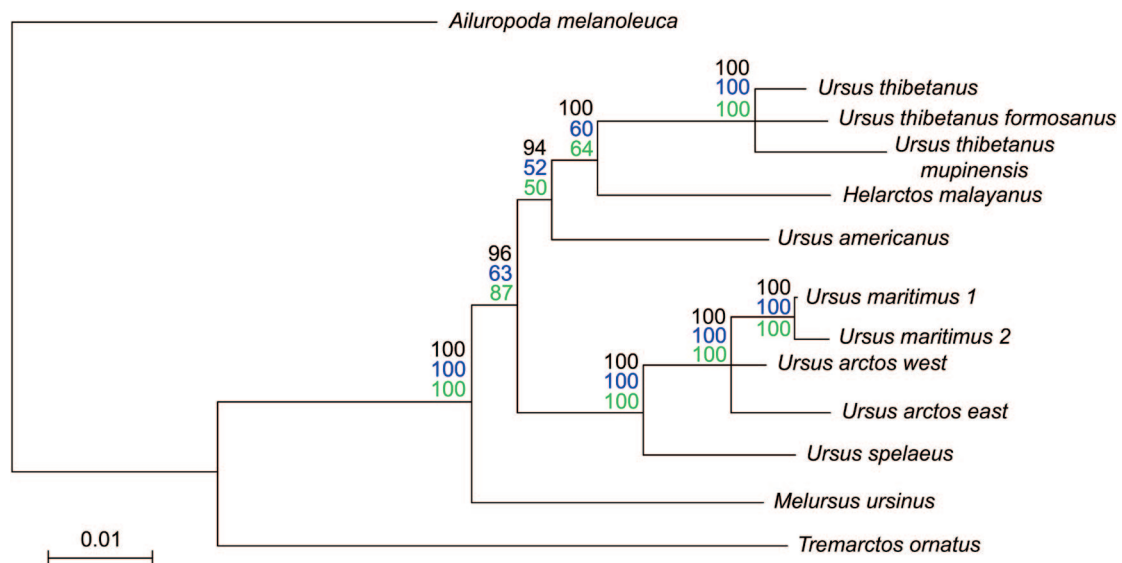


Fig. S3. Phylogeny based on the amino acid sequence of all 13 proteins encoded by the mitochondrial genome. Tree construction was performed using the giant panda (*Ailuropoda melanoleuca*) as an outgroup. The topology is supported by MrBayes, PhyML, and neighbor joining analysis; the corresponding support values for each node are indicated in black, blue, and green characters, respectively. The scale bar depicts the genetic distance relevant for MrBayes analysis. The *Ursus spelaeus* and *Ursus arctos* western lineage (west) sequences are from this study. GenBank accession numbers for the other sequences are indicated in Fig. 4.

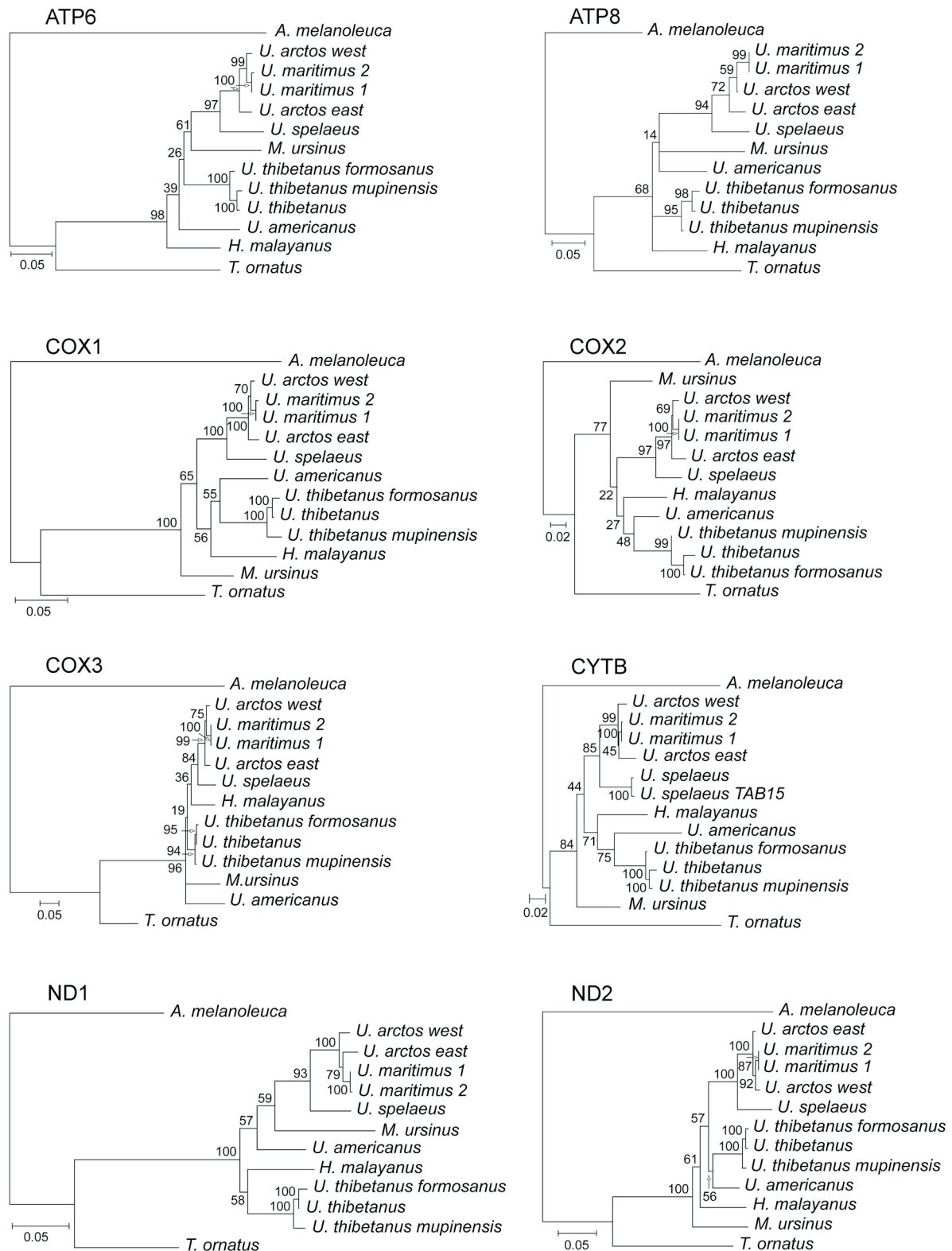


Fig. S4. Phylogeny based on individual mitochondrial coding genes. The nucleotide sequence of each protein coding gene was used to infer phylogenetic relationships by PhyML analysis, with the giant panda (*Ailuropoda melanoleuca*) serving as an outgroup. Bootstrap values for each node and the scale for the genetic distance are indicated. The *Ursus spelaeus* and *Ursus arctos* western lineage (west) sequences are from this study. GenBank accession numbers for the other sequences are indicated in Fig. 4.

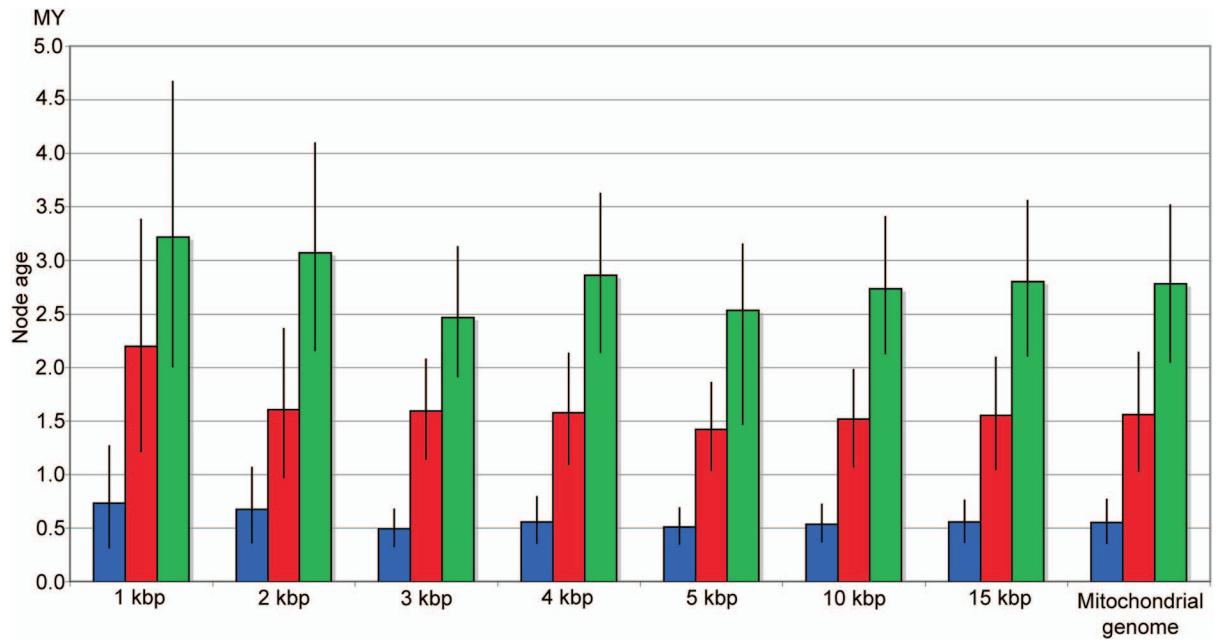


Fig. S6. Comparison of the divergence dates obtained for dataset of various lengths. Only node 3 (blue), 6 (red) and 7 (green), as defined in Fig. 5, are shown. Black bars represent posterior densities (95% credibility interval) of nodal age estimates.

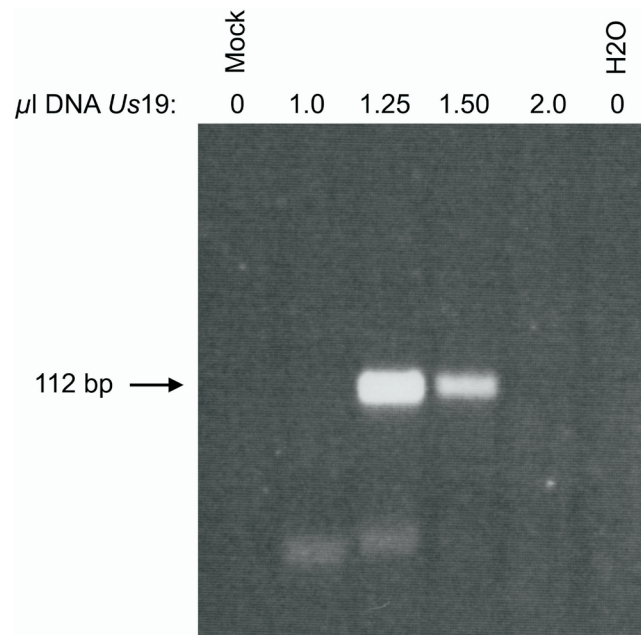


Fig. S7. Amplification of a fragment of the cave bear 16S ribosomal RNA gene. Variable amounts of the Chauvet-Pont d’Arc *Us19* DNA extract were amplified using primer pair 46, yielding a 112-bp DNA fragment. The total reaction volume was electrophoresed through an acrylamide gel stained with SYBR Green I. Negative controls included reactions carried out on a mock extract (Mock) or in the absence of any extract (H₂O). Sequencing analysis of the cloned PCR products confirmed that they correspond to cave bear DNA.

Table S1. Oligonucleotide primers used for PCR amplification of cave bear mitochondrial genome fragments

Primer pair	Primer position	Forward primer	Reverse primer	Amplicon, bp
1	83F 206R	AAAGGTCTCGTCGAGTCA	GCGTCGTTGTTGCGATTTA	142
2	83F 207R	AAAGGTCTCGTCGAGTCAA	TGCGTCGTTGTTGCGATTT	143
3	170F 267R	TCAATGGTCGCGAGCATATAGTA	TGCGTACACGTGCGTACAC	106–256
4	201F 267R	GCCACTAAATCGAACGAACA	TGCGTACACGTGCGTACAC	205–265
5	546F 592R	CGTGTACGCACGTGTACG	GGGGGTTTGATTAAGCTAAGTT	148–228
6	546F 644R	CGTGTACGCACGTGTACG	GGCAAGACAACCATAAATGTG	119–239
7	546F 657R	CGTGTACGCACGTGTACG	TTTGGGGTTTGGCAAAGAC	119
8	572F 705R	CGCACGCGTTTTTAGATA	GTGGGATTTGGATATGATAGC	155
9	599F 730R	CTTAATCAAAACCCCTTACC	TATTTGGCTGGGAATTTTAGCTTAT	156
10	658F 829R	TCTTGCCAAACCCCAAAAA	GATAATAACGGAAAAATCAATAGGA	196
11	758F 890R	ACTGTAATCATAGGCATGAGACTTT	GTTGGATTTGGGGATTTGTA	152
12	862F 1021R	GGCCACGAGCTTTACTAGAT	CGGAGACTTGATGTGTAAT	179
13	862F 1024R	GGCCACGAGCTTTACTAGAT	GCGGAGACTTGATGTGTT	180
14	997F 1163R	GCCTTCCCATTAGCTACTAACAA	CTTTCGTTTCATGGCTTAATTTTT	189
15	1060F 1163R	TTTGGATCTTAAAGCGATTTGA	CTTTCGTTTCATGGCTTAATTTTT	126
16	1143F 1273R	CCACGGGATACAGCAGTG	TTTTCTTTCACACGCTTTACG	151
17	1238F 1358R	GGTTATACGATTGACCCGAGTT	GAGAGCATTAAAGTCACTTTCGTAGC	146
18	1317F 1467R	TTTAATCCAGCTGTAAAAGCTATC	GCTAGTAGTTCTCTGGCAATAA	173
19	1422F 1599R	CCCCACTATGCTTAGCCTTAAA	TTGCTGAAGATGGCGGTATA	197
20	1429F 1576R	ATGCTTAGCCTTAAACATAAATAAT	AGACTGAATTAGCAAGAGGTGG	169
21	1554F 1663R	CGATAAACCCGATAGACC	ATGGGTTACACCTTGACCTAACTT	133
22	1637F 1743R	AGTAAGCACAATCATCTCGCATA	AATCCACCTTTAGTTTTAGTTTCAT	132
23	1699F 1799R	AATGGGCTACATTTTCTATTCAAG	CATGCTTCATTGCCTTATTCA	121
24	1767F 1899R	TTTAGTAGTAAATCAAGAATAGAGAG	ATGCTTACCTGTTACGACTT	153
25	1768F 1903R	TTAGTAGTAAATCAAGAATAGAGAGC	CAGTATGCTTACCTGTTACG	156
26	1877F 2001R	CAAATAAAACGCAAGAGGAGAC	CTAGCTCTGGGTTCAAAGTGG	145
27	1882F 2033R	AAAACGCAAGAGGAGACAAG	AATTGGTTTATGGTAGTTGGTTAGT	177
28	1971F 2094R	GCTTACCCAGAGGATTTCA	AGCTCCGATTAAGAAGAATTTCTATCT	149
29	2009F 2168R	AACCCAGAGCTAGCCCAGATAA	AGGAGGGGTAATCTTGTCTGTT	181
30	2009F 2168R	AACCCAGAGCTAGCCCAGATAA	AGGTAGAAGGGATAATCTTGTCTGTT	185
31	2022F 2166R	CCCAGATAACAATAACCAAATA	GAAGGGATAATCTTGTCTGTTA	167
32	2134F 2275R	GCAAGGGAAATGATGAAAGATTAC	GAGTTTACCCAGTGGATTGT	162
33	2182F 2300R	TCCCTTCACTTTTGCATAAT	TCTTCTCACTATTTGCGACAT	140
34	2250F 2398R	CCGAAACCCAGAGCTACC	AATTTTTAAGTTTTGTGGCAAGTT	173
35	2271F 2360R	ATGAACAATCCACTGGGGTAAA	CTATTCTGGGCAACCAGCTA	109
36	2365F 2521R	GGTTGCCAGAATAGAATTTT	TTAATTGATGGCTGCTTCTAGG	178
37	2467F 2635R	GAATCAAGGATACAGCCTTACTT	TTACTCATATTAGCATTGTTGCTTCT	194
38	2470F 2627R	TCAAGGATACAACCTTACTTAGAGAG	TTAGCATTGTTGCTTCTATATTTAA	182
39	2600F 2721R	CCTAATAATAAAGTGGGCTAATCT	TGTTGGATTATTTCTACGTTGTTG	145
40	2693F 2856R	ACAGCAACGGATAACCACTGA	GGGAATGCTGGAGGTGATG	182
41	2818F 2973R	GAACCTCGCAACACAAAC	CGTGTGGCCTTTTCATAACA	174
42	2835F 2964R	ACCCCGCTGTTTACCAA	GTGGCCTTTCATAACAAGTCTTATT	154
43	2935F 3061R	GCAAAGGTAGCATAATCATTTGTCT	GCTCCATAGGGTCTTCTCGTCTTA	150
44	3037F 3210R	CGTGAAGAGGCGGGAATA	GTGAGCATTTTGACTGGTACGCTA	198
45	3038F 3155R	GTGAAGAGGCGGGAATAAAAT	TCGCCCAACCTAAATTTG	135
46	3129F 3215R	AACAACATATTCCTCCATGAGC	AAGTAAGTGAGCATTTTGACTGGTAC	112
47	3183F 3330R	CAAAATAACCTCCGAGTGATATTA	ATCCAACATCGAGGTCGTAA	167
48	3303F 3420R	TTTAAGAGTCCATATCGACAATAGGG	CTGGATTGCTCCGGTCTGAACT	139
49	3392F 3542R	TTCAACGATTAAGTCTACGTGAT	TGGGGGTAGACTTACTAGGTTTAG	174
50	3515F 3609R	CGCCTAAGACCAATAGATG	AAAGGTTAAGTTTTATGCAATCAC	119
51	3575F 3692R	AAGAGACAGGGCCTTGTTAG	CGAGGAGAATGGGTACGACTA	138
52	3576F 3736R	AGAGACAGGGCCTTGTTAG	AGCCCACTACTTTTGGCTT	179
53	3586F 3746R	CTTTGTTAGGGTGGCAGAG	ACGAAGTTGTATATAGCCAGTA	183
54	3606F 3735R	CCGGTGATTGCATAAAACTT	ATAGCCAGTACTTTTCTGTTCT	151
55	3711F 3840R	CGCCGTAGCCTTCTTAACA	AGTGGGCGCAAGGGTCT	147
56	3712F 3840R	GCCGTAGCCTTCTTAACA	AGTGGGCGTAAGGGTCT	146
57	3735F 3822R	AGAACGAAAAGTACTGGGCTATA	GGGTTCTTTGGTAAAAAGTTTTATA	112
58	3807F 3981R	ACCTATCGCAGATGCTACAAA	TACAGCTAAGCTTGATATTGCTAAT	199
59	3815F 3974R	CAGATGCTATAAAACTTTTTACCA	TAAGCTTGATATTGCTAATAAACA	185
60	3926F 4051R	TTCCTCTACCAATGCCATA	GCTCGTAGAGCTCCAAATTAG	145
61	3950F 4136R	TTGTCAACATAAACCTTGGAGTA	GTAGAAAAGTGTGAATGAGCCAT	208
62	4025F 4175R	GATGGGCTTCAAACCTAAAATAC	GGGAAAATTAGTCAGAGGTGCT	172
63	4104F 4272R	AGCCATTATCTCTATCAGTCCTAC	AACCTGAGACTAATTCTGACTCCT	194
64	4114F 4244R	CTCCTATCAGTCTACTAATGAATG	CAAAAGGGGCTCGGTTAG	148

Primer pair	Primer position	Forward primer	Reverse primer	Amplicon, bp
65	4218F 4397R	ATGATTTATCTCCACTCTAGCAGAA	GGGGCTGTGAAATGCTC	196
66	4364F 4492R	TAATAAATGCCTCACGACTATCC	TCGGAATCGGGGTATGA	146
67	4459F 4593R	CTCCTAACAGCTTCTTCTATGA	AGGAGGAATGCTGTGTGATA	156
68	4541F 4695R	ATTTCTACCCCTCACACTG	TTAAGATTAGTTTCGATTCTATAA	179
69	4668F 4812R	GAGGTTAAAATCCTCTATTCTAG	GTACGGGAAGGGGATGAA	162
70	4791F 4910R	CCCATACCCGAAAATGTT	TTCAAAGCCAATTACAGATTATGAG	143
71	4886F 5007R	ATCGTTCTATTACGCTCCCACTG	CGGTGGCTTGTGTGAGGAAAT	142
72	4977F 5123R	ATCCACGGGCCATAGAAG	TGCTAGGGCAATGGTGAT	164
73	5102F 5254R	AATCCAATGCATCACTGT	TGGATGGTAAAATTTGATATAGG	175
74	5228F 5317R	TGACAAAAAATCGCACCTCTAT	GTCTCCTCAGCTCCTACTAAT	112
75	5228F 5337R	TGACAAAAAATCGCACCTCTAT	TCGGAGTTGAGTTTGGTTTAGTC	132
76	5313F 5467R	CCGTATTAGTAGGAGGCTGAG	ACATGAATAGTATAAATGTCCCTAGA	180
77	5345F 5455R	CAAACCTCAACTCCGAAAAATC	AAATGTCCCTAAAGTTATTATGATG	135
78	5439F 5575R	TCAACCTCACAATCTACATCATAATA	GAGGCCCGCTAGTGATAGT	155
79	5541F 5691R	TACCACTAATTGCCTCACTAATC	CGCATGTAGAAAATAAGGTTTAATA	175
80	5541F 5699R	TACCACTAATTGCCTCACTAATC	TAGGCGCATGTAGAAAATAAG	179
81	5666F 5813R	CCCATATTATAGCCATCACAGC	GTATGTTGATGCTACGATTAGAGG	172
82	5720F 5881R	GCATACGCTACAGCACTAACAAT	GCCCTTGGTCTATTTTAGCCTA	183
83	5796F 5892R	AAATAATCTTCTACCCCTCTAA	CTTTGAAGGCCCTTGGTC	114
84	5824F 5980R	AGCATCAACCATACTTCTCCACTAA	AGCGGTTGTTTTGCGTTCA	175
85	5949F 6085R	TAAGGACTGCAAGGACATATCTCA	GCGGCGGGAGAAGTAGATT	155
86	6059F 6204R	GCTAAAAACCCAAAACAAC	TGTAATCTAAGAATAGAGGTCAAGT	171
87	6059F 6224R	GCTAAAAACCCAAAACAAC	GGCTGATAAAAAGTATTAGCATGAAA	191
88	6179F 6318R	CACCACAGAGCTTGCCAAAAA	GGCTCATGCACCGAACAGA	158
89	6237F 6420R	GCTTTTATCAGCCATTTTACCT	ATGGGCAGTTACGATTACATTG	205
90	6296F 6398R	AAGACATTGGCACCCCTTACC	ATCTGATCATCCCCAACCA	121
91	6394F 6529R	GCCCTGTTGGGGGATGAT	ATTTATTCGAGGGAAACGCTATGTC	159
92	6498F 6630R	CTGATTAGTGCCTTAATGATCG	GGGGGTAGACAGTTTCACTCA	152
93	6592F 6766R	CTTCTGGCTCCTCTATGGTA	TTGCAGGGGGTTTCATGTT	193
94	6610F 6722R	GTAGAAGCAGGTGCAGGAA	AATAGCTCCCAGAATAGAAGAGA	135
95	6649F 6762R	CCTCTAGCGGGTAATCTG	GGGGGCTTCATGTTAATA	131
96	6732F 6883R	TCTGGGAGCTATAATTTTCATCA	GTGTTAAGGTTTCGATCTGTAAGTAG	177
97	6857F 6995R	CAGTCTTAGCAGCTGGGATTACTAT	CCGAACCCAGGAAGGATTA	157
98	6857F 7007R	CAGTCTTAGCAGCTGGGATTACTAT	TGTGAGAGATCATTCCGAACC	171
99	6969F 7124R	CTTCGGACATCCTGAGGTTTACA	ACCTACGGTAAACATGTGGTGAG	178
100	6969F 7145R	CTTCGGACATCCTGAGGTTTACA	AAGCTCGTGTGCAACGTCTATAC	200
101	7095F 7254R	CATTGGATTCTTAGGATTTATCG	TCATAGCGGGAGATCATTTA	179
102	7234F 7387R	ACTCTGCACGGAGGGAATA	TCCATTGATAACACATAGTGAAA	177
103	7360F 7508R	CATGACACGTAATGTGGTAGC	GAATGTCATGTTAACTCCAATGAATA	174
104	7468F 7616R	ACACTTAACAACACATGAGCAAAAAT	TGAAATGAATGAGCCTACAGAAGATA	174
105	7552F 7657R	GGCCTGTCCAGGAATACCTC	TCCCAATCATGAAAATTATCAG	128
106	7624F 7775R	ATAGGCTCATTTTACTAACAG	TTAGTGTGACGTAGGCGAGTTCTT	175
107	7624F 7775R	ATAGGCTCATTTTACTAACAG	TATAACGTAGGCGGGTTCTT	171
108	7751F 7887R	GCCCTCCTCATATCATACTT	AACCTGACAAAAGTTATGTAATTTT	162
109	7832F 7991R	TGGTTTCAAGCCAATATCATAAC	CATGAAAATGCAGAAGTTCCTCTAT	184
110	7965F 8101R	GCCTTCAAGACGCAACTTCTC	CTTCTGTGCGTCCATTGTACTT	159
111	8071F 8211R	AACTATACTAACCAAAATTAACA	TTTACAGTTAGTGAGGGATTATTGA	165
112	8107F 8211R	AATGGACGCAACAAGAAGTAGAG	TTTACAGTTAGTGAGGGATTATTGA	129
113	8175F 8323R	TCCATCACTACGGATCCTCTAT	CGCAATTCTCCAGGCTTTAGT	169
114	8191F 8334R	CCTCTACATGATGGATGAAGTCAATA	TCTACTTCTAATAGCCGAGTTCTC	168
115	8296F 8393R	TGACTCTTATATGATCCGACACAA	TCTTCTGACGAGATCAGCATACG	120
116	8298F 8394R	ACTCTTATATGATCCGACACAA	ATCTTCTGACGAGATCAGCATAAC	119
117	8298F 8452R	ACTCTTATATGATCCGACACAA	CCTGGGATTGCATCAGTTTTT	175
118	8363F 8513R	CGAGTAGTGCTGCCCATAGAAA	TGAGCATTGGCCGTAATATAG	171
119	8492F 8641R	CTTATAGCCATGCGACCAG	AACTTAAAAGGTTAACGCTATGTTA	174
120	8601F 8763R	AAGAATGATCCGCTTCAACTACT	TTTGAGACTTTTAACTGGAGAATAAT	188
121	8611F 8757R	CGCCTCAATACTATAGAATCATT	GACTTTTAACTGGAGAATAATAAATAA	173
122	8687F 8842R	CTCCTTAATGAAGATGCCACAACCTA	TCATTTTTCTTCTCAAGGCACAA	178
123	8731F 8876R	TTACAATTCTATCCATAGCTCTAACA	TGGGGTGATAAAAAGAGGTTAAA	166
124	8847F 8994R	CCTTGAGAAGAAAATGAACGAAAA	AGCCGAACCTAGTCACTGTTGAA	169
125	8953F 9080R	TCCTTCTCCGATCGATTGA	TTGAGCCAATAAATAGGATTAGTGA	152
126	9053F 9202R	GGACAAACCTGGGCACTAATA	GGTCTGTATCGGAATCCAGTA	171
127	9125F 9276R	CCGCACCTATTACACCTAC	TGTTTCGATAATTACGAGCATTG	174
128	9180F 9337R	CCTTGTGGGCAGGTACAGTC	GCCTGCAAGTAAATTTAGCGGTTAGT	182
129	9232F 9335R	CCTGGCTCACTTCTACCTCAA	GCAGTAATATTAGCGGTTAGTCG	126

Primer pair	Primer position	Forward primer	Reverse primer	Amplicon, bp
130	9300F 9404R	TTAGCCTATTTATCCAACCTATG	AGGCTGTAATAGTGCTAATACTTGT	129
131	9325F 9492R	CTTGGCCGTGCGACTAAC	CTTACTAGCAGGGTAAAGACGTAGG	192
132	9379F 9492R	AATTGGGGGAGCTACCTTG	CTTACTAGCAGGGTAAAGACGTAGG	138
133	9379F 9533R	AATTGGGGGAGCTACCTTG	ATGTGTTTGGTGAGTCATTAAGTGTT	180
134	9468F 9591R	AGTTCGCTGTAGCCCTCATT	GCTGAGAGGGCTCCTGTTAGT	144
135	9468F 9595R	AGTTCGCTGTAGCCCTCATT	GGCTGAAAGGGCTCCTGT	145
136	9572F 9721R	TCAATCCAAGCCCATGAC	CCTTCAAATGTACTCTCTCGAATAAT	175
137	9573F 9703R	CAATCCAAGCCCATGACC	GTCCCGCCACCATTGATA	148
138	9573F 9717R	CAATCCAAGCCCATGACC	GAAATGTAATCTCTCGAATAATGTCC	170
139	9685F 9839R	ACCAATATACTTACCATGTATCAATG	GCTAGGCTTGAGTGATAAAAAAG	176
140	9720F 9845R	CATTATTCGAGAGAGTACCTTTCAG	GTAGGTGCTAGGCTTGAGTGAT	147
141	9815F 9943R	TCTTCTTTCAGGATTCTTCTG	CCGGATGCAAGAAGTACTGA	148
142	9889F 10019R	CCGCCACAGGTATTACTC	GAGATAGTAATGAATAGGGCTGAA	155
143	9910F 10040R	CTGAATCCGCTAGAAGTGC	AGTGTGAAGTATACGCCTAGAGAGA	155
144	10000F 10108R	GGAAGCCGCAAGCACATA	AAAGTTGAGCCATAGACTCCATC	131
145	10082F 10228R	ACTATGAGGCATCCTTCACTATT	CAAAGCCGAAATGGTGACT	165
146	10165F 10263R	ATCATTGGCTCAACTTTTCTCAC	GTCATACGACATCTACGAAGTGTC	124
147	10170F 10313R	TGGCTCAACTTTTCTCACAGT	TAAAGAAGCAGGACCCTCATC	164
148	10242F 10396R	CTTTGAAGCAGCAGCATGAT	GGTGAATAGTGCTAGGATTAAGTTG	179
149	10248F 10377R	AGCAGCAGCATGATATTGACACTTC	AAGTTGATTGCTTCTTCTGGACTG	154
150	10374F 10528R	GCGCAGTCCAGAAAGAAGCAA	GAAAAAGGGAGGCGTGCCGAT	175
151	10494F 10645R	CAAGCCCTTGAATGCGGGTTT	ACGCTATGGTGAGTATCGTTATT	174
152	10605F 10755R	TACTCTCCCTCTTCCCTGAGCA	AGTCGAAATCACTTGTGTTGGTT	173
153	10725F 10871R	TAGAATGGGCCGAATATGATA	GGATATTAGATGGGATCGATAAA	169
154	10834F 10937R	TTCTTAGCATTATTGTATCCCTAAT	ATTGTTTAAAAGTGTACTGTTAGCA	129
155	10907F 11041R	TAGAGGGTATAGTGCTATCCTTATT	CCGTAAGTGTGGAGACTATTACTAG	160
156	10907F 11046R	TAGAGGGTATAGTGCTATCCTTATT	GTTCCGTAAGTGTGGAGACTATT	163
157	11017F 11092R	GAGGCAGCACTAGGACTGTC	AAGATGATTTTTAGCATTGTAAGAG	100
158	11017F 11092R	GAAGCAGCACTAGGACTGTC	AAGATGATTTTTAGCATTGTAAGAG	100
159	11065F 11196R	GGAAGTACTATGTACAAAACCTC	TACGTCAAAGTATGAGACTAATAAG	157
160	11156F 11290R	GCCCAATATAATTTGGATCAATA	CATGTTGTGAGGGCTAATAGAG	156
161	11156F 11294R	GCCCAATATAATTTGGATCAATA	GTAGTCATGTTGTGAGGGCTAAT	161
162	11157F 11290R	CCCAATATAATTTGGATCAATACA	CATGTTGTGAGGGCTAATAGAG	155
163	11263F 11394R	TATTTCTTACCCTCCCTATCAG	TCAGGAGTAATTGTAGGAGATTAG	156
164	11355F 11516R	AAGGAAACTCTGACCCGAAAG	CCGCGTTTGTGCTGTTGTT	181
165	11481F 11594R	CCCCTCTGGTTATTATCACTCG	AGCCTAGATTATTTGGGTGTGT	136
166	11569R 11693R	CTTTGCCATTACTAATTGCACTAC	TTTTACCATAAATGCCATTATACAC	149
167	11657F 11818R	GCCAACTCCTGATCCAGTATCT	TGTAATTCGTATCATGCCGTAGC	184
168	11665F 11818R	CCTGATCCAGTATCTTCTATGACT	ATTCGTATCATGCCGTAGC	172
169	11793F 11918R	GCTGCCGTACTCCTAAAATA	TTGGCGTAGGCAGATAGAA	144
170	11878F 11993R	CCTTCATAACTCTCGCTATGG	GGGGTTGGATTAATCTGCTACA	139
171	11970F 12101R	GTCAGTCACATGGCCCTAGT	CGGCTATGGATTCCGTTCA	149
172	12075F 12211R	CTATTCTGTCTTGCAAACTCCAAT	TTCTCCGATAAGGTTGATGGTAG	159
173	12181F 12305R	TAGCAAGTCTACTAACCTAGCAC	GTAGAGGGAGTAGAGGGCAGTA	146
174	12274F 12358R	CCATCACTCTAATAGGAACCAACAT	GGTTTAATACTTTTGACGTGGTCTG	109
175	12318F 12438R	TCCCTCTACATACTAATCACCACACA	GAATTATTTGGGGTTAAGGGATAG	145
176	12392F 12538R	ACGAGAAAACGCCCTGATAG	CTTGCGTACTTTTTCGGTAATAA	170
177	12392F 12542R	ACGAGAAAACGCCCTGATAG	GTTCTTGCGTACTTTTTCGGTA	173
178	12511F 12622R	AATCTAATAATAAAAAGCCCAAGTC	GGTTCCTAAGACCAATGGATTACT	135
179	12590F 12754R	AATCATGGCTTTTTCACTTTTA	TGTGGGTAGGATTTATTTTTGTG	187
180	12705F 12874R	AACTTTGCTCATATTAACGATACC	TTAGGGTTTGAATAGTTATCAATG	194
181	12830F 12962R	TGATATTCCTTACTCAGGGCAAGA	GAAAATTCATGATTGATCATGTGA	157
182	12942F 13095R	CATGCCAGTAGCCCTGTTT	TCCTTCTCAGCCGATGAAT	172
183	12946F 13082R	CCAGTAGCCCTATTGCTACA	CAGCCGATGAATAGTTGAAATAGAT	161
184	13066F 13192R	CTAGTGACCCGAAATAATCT	TCTCCGATGCGATTGTATAG	146
185	13154F 13277R	GACGAATAGACGCCAACACAG	GGTTTTCATGTTCAATTGCAAAGA	147
186	13169F 13351R	ATACAGCCGCTCTACAAG	TGGATGAAGGCCGAATTG	200
187	13249F 13351R	AATACAATGCATGAGACTCCAACA	TGGGTGAAGGCCGAATTG	120
188	13326F 13482R	CCTAGCAGCCACTGGAAAAAT	GGCTGTTTGGATAGTCTTGTG	178
189	13330F 13482R	GCAGCCACTGGAAAAATCA	GGCTGTTTGGATAGTCTTGTG	174
190	13441F 13627R	GGGGTATTTCTTCTAATCCGATTTT	TGCTAGGTGAGGCTGATTAATTCC	210
191	13459F 13618R	CGATTTTACCCTTGATAGAAC	GGCTGGTTAATTCCAATTGTTAC	182
192	13594F 13760R	TCAAGCCAGCTAGGACTAATAATCG	GGTAAGTGGCAGGGCTTTGAATA	189
193	13598F 13760R	GCCAGCTAGGACTAATAATTGTAACA	GGTAAGTGGCAGGGCTTTGAATA	185
194	13732F 13832R	GAACAAGACATCCGAAAAATAG	TTAGGTCTTTAGAGTAGAATCCTGTTA	127

Table S3. Summary of statistics obtained for the various datasets used in this study

Dataset	PhyML	MrBayes
Whole-genome (16,542 nt)		
ln(Likelihood)	-57567	-57568
α parameter	0.20	1.60
Proportion of invariant transition vs transversion	0 22.5	0.57 22.7
Protein Coding genes (amino acid) (3 797 aa)		
ln(Likelihood)	-16851	-16872
α parameter	0.59	0.23
Proportion of invariant	0.39	
Protein coding genes (nucleotide) (11,385 nt)		
ln(Likelihood)	-42107	-42110
α parameter	0.23	1.21
Proportion of invariant	0	0.29
Transition vs. transversion	28.3	28.0
tRNA (1,525 nt)		
ln(Likelihood)	-3942	
α parameter	0.27	
Proportion of invariant	0.31	
Transition vs. transversion	20.3	
16S (1,590 nt)		
ln(Likelihood)	-4325	
α parameter	0.26	
Proportion of invariant	0.32	
Transition vs. transversion	14.2	
12S (987 nt)		
ln(Likelihood)	-2718	
α parameter	0.16	
Proportion of invariant	0	
Transition vs. transversion	14.3	
ATP6 gene (678 nt)		
ln(Likelihood)	-2759	
α parameter	4.51	
Proportion of invariant	0.48	
Transition vs. transversion	24.9	
ATP8 (201 nt)		
ln(Likelihood)	-851	
α parameter	0.99	
Proportion of invariant	0.23	
Transition vs. transversion	13.8	
Cox1 (1,542 nt)		
ln(Likelihood)	-5471	
α parameter	0.67	
Proportion of invariant	0.44	
Transition vs. transversion	23.9	
Cox2 (681 nt)		
ln(Likelihood)	-2406	
α parameter	14.2	
Proportion of invariant	0.62	
Transition vs. transversion	12.8	
Cox3 (783 nt)		
ln(Likelihood)	-2789	
α parameter	6.00	
Proportion of invariant	0.64	
Transition vs. transversion	36.1	
Cytb (1,140 nt)		
ln(Likelihood)	-4104	
α parameter	0.25	
Proportion of invariant	0	
Transition vs. transversion	16.1	
ND1 (954 nt)		
ln(Likelihood)	-3357	
α parameter	0.27	
Proportion of invariant	0.08	
Transition vs. transversion	11.0	

Dataset	PhyML	MrBayes
ND2 (1,041 nt)		
ln(Likelihood)	-3521	
α parameter	0.31	
Proportion of invariant	0.14	
Transition vs. transversion	26.2	
ND3 (345 nt)		
ln(Likelihood)	-1324	
α shape parameter	0.54	
Proportion of invariant	0.33	
Transition vs. transversion	23.9	
ND4 (1,377 nt)		
ln(Likelihood)	-5064	
α parameter	2.98	
Proportion of invariant	0.56	
Transition vs. transversion	34.5	
ND4L (294 nt)		
ln(Likelihood)	-1150	
α parameter	0.44	
Proportion of invariant	0.19	
Transition vs. transversion	4.48	
ND5 (1,827 nt)		
ln(Likelihood)	-7024	
α parameter	0.27	
Proportion of invariant	0	
Transition vs. transversion	22.8	
ND6 (525 nt)		
ln(Likelihood)	-1980	
α parameter	3.62	
Proportion of invariant	0.52	
Transition vs transversion	2.04	

The table displays statistical results obtained from analyses with PhyML and MrBayes. Gene by gene analyses were only conducted with PhyML. The size of each dataset in nucleotides (nt) or amino acids (aa) is indicated.

Other Supporting Information Files

[Fig. S1.](#)

[Fig. S2.](#)