

DNA profiling of Hungarian King Béla III and other skeletal remains originating from the Royal Basilica of Székesfehérvár

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ESM 10 Detailed sequencing results for the mitochondrial control regions of King Béla III, Anna of Antioch and person II/52

1. Béla III

16009 **TTAAACTATTCTCTGTTCTTTCATGGGGAAGCAGATTTGGGTACCACCAAGTATTGACTCACCATCAACAACCGCTATGTATTTTCGTACATTACTGCCAGCCACCATGAATATTGTACG** 16129¹
TTAAACTATTCTCTGTTCTTTCATGGGGAAGCAGATTTGGGTACCACCAAGTATTGACTCACCATCAACAACCGCTATGTATTTTCGTACATTACTGCCAGCCACCATGAATATTGTACG BT2
TTAAACTATTCTCTGTTCTTTCATGGGGAAGCAGATTTGGGTACCACCAAGTATTGACTCACCATCAACAACCGCTATGTATTTTCGTACATTACTGCCAGCCACCATGAATATTGTACG BT3*

Cons. TTAAACTATTCTCTGTTCTTTCATGGGGAAGCAGATTTGGGTACCACCAAGTATTGACTCACCATCAACAACCGCTATGTATTTTCGTACATTACTGCCAGCCACCATGAATATTGTACG

16113 **AGCCACCATGAATATTGTACGGTACCATAAATACTTGACCACCTGTAGTACATAAAAAACCAATCCACATCAAAACCCCCCCCCATGCTTACAAGCAAGTACAGCAATCAACCCCTCAA** 16227
AGCCACCATGAATATTGTACGGTACCATAAATACTTGACCACCTGTAGTACATAAAAAACCAATCCACATCAAAACCCCCCCCCATGCTTACAAGCAAGTACAGCAATCAACCCCTCAA BT1
AGCCACCATGAATATTGTACGGTACCATAAATACTTGACCACCTGTAGTACATAAAAAACCAATCCACATCAAAACCCCCCCCCATGCTTACAAGCAAGTACAGCAATCAACCCCTCAA BT3*
AGCCACCATGAATATTGTACGGTACCATAAATACTTGACCACCTGTAGTACATAAAAAACCAATCCACATCAAAACCCCCCCCCATGCTTACAAGCAAGTACAGCAATCAACCCCTCAA BT3*

Cons. AGCCACCATGAATATTGTACGGTACCATAAATACTTGACCACCTGTAGTACATAAAAAACCAATCCACATCAAAACCCCCCCCCATGCTTACAAGCAAGTACAGCAATCAACCCCTCAA

16222 **CCTCAACTATCACACATCAACTGCAACTCCAAAGCCACCCCTCACCCACTAGGATACCAACAAACCTACCACCCCTTAACAGTACATAGTACATAAAGCCATTTACCGTACATAGCACATTACAGTCAAATCCCTTCTCGTCCCATGGATGACCCCCCTCAGATAGGGGTCCCTTGACCACCATCCCTC** 16411
CCTCAACTATCACACATCAACTGCAACTCCAAAGCCACCCCTCACCCACTAGGATACCAACAAACCTACCACCCCTTAACAGTACATAGTACATAAAGCCATTTACCGTACATAGCACATTACAGTCAAATCCCTTCTCGTCCCATGGATGACCCCCCTCAGATAGGGGTCCCTTGACCACCATCCCTC BT1
CCTCAACTATCACACATCAACTGCAACTCCAAAGCCACCCCTCACCCACTAGGATACCAACAAACCTACCACCCCTTAACAGTACATAGTACATAAAGCCATTTACCGTACATAGCACATTACAGTCAAATCCCTTCTCGTCCCATGGATGACCCCCCTCAGATAGGGGTCCCTTGACCACCATCCCTC BT3*
CCTCAACTATCACACATCAACTGCAACTCCAAAGCCACCCCTCACCCACTAGGATACCAACAAACCTACCACCCCTTAACAGTACATAGTACATAAAGCCATTTACCGTACATAGCACATTACAGTCAAATCCCTTCTCGTCCCATGGATGACCCCCCTCAGATAGGGGTCCCTTGACCACCATCCCTC BT3*

Cons. CCTCAACTATCACACATCAACTGCAACTCCAAAGCCACCCCTCACCCACTAGGATACCAACAAACCTACCACCCCTTAACAGTACATAGTACATAAAGCCATTTACCGTACATAGCACATTACAGTCAAATCCCTTCTCGTCCCATGGATGACCCCCCTCAGATAGGGGTCCCTTGACCACCATCCCTC

16381 **TCAGATAGGGGTCCCTTGACCACCATCCCTCCGTGAAATCAATATCCCGCACAAAGTGTACTCTCCTCGTCCGGGCCATAAACACTTGGGGGTAGCTAAAGTGAAC** 16489
TCAGATAGGGGTCCCTTGACCACCATCCCTCCGTGAAATCAATATCCCGCACAAAGTGTACTCTCCTCGTCCGGGCCATAAACACTTGGGGGTAGCTAAAGTGAAC BT1
TCAGATAGGGGTCCCTTGACCACCATCCCTCCGTGAAATCAATATCCCGCACAAAGTGTACTCTCCTCGTCCGGGCCATAAACACTTGGGGGTAGCTAAAGTGAAC BT2
TCAGATAGGGGTCCCTTGACCACCATCCCTCCGTGAAATCAATATCCCGCACAAAGTGTACTCTCCTCGTCCGGGCCATAAACACTTGGGGGTAGCTAAAGTGAAC BT3*

Cons. TCAGATAGGGGTCCCTTGACCACCATCCCTCCGTGAAATCAATATCCCGCACAAAGTGTACTCTCCTCGTCCGGGCCATAAACACTTGGGGGTAGCTAAAGTGAAC

16471 **GGGTAGCTAAAGTGAACGTATCCGACATCTGGTTCCTACTTCAGGGTCATAAAGCCATAAATAGCCACACGTTCCCTTAAATAAGACATCAGATGGATCACAGGTCATCACCCCTATTAACCACTCAC** 33
GGGTAGCTAAAGTGAACGTATCCGACATCTGGTTCCTACTTCAGGGTCATAAAGCCATAAATAGCCACACGTTCCCTTAAATAAGACATCAGATGGATCACAGGTCATCACCCCTATTAACCACTCAC BT1
GGGTAGCTAAAGTGAACGTATCCGACATCTGGTTCCTACTTCAGGGTCATAAAGCCATAAATAGCCACACGTTCCCTTAAATAAGACATCAGATGGATCACAGGTCATCACCCCTATTAACCACTCAC BT2
GGGTAGCTAAAGTGAACGTATCCGACATCTGGTTCCTACTTCAGGGTCATAAAGCCATAAATAGCCACACGTTCCCTTAAATAAGACATCAGATGGATCACAGGTCATCACCCCTATTAACCACTCAC BT3*

Cons. GGGTAGCTAAAGTGAACGTATCCGACATCTGGTTCCTACTTCAGGGTCATAAAGCCATAAATAGCCACACGTTCCCTTAAATAAGACATCAGATGGATCACAGGTCATCACCCCTATTAACCACTCAC

16552 **AAATAAGACATCAGCATGGATCAGAGTCTATCACCCCTATTAACCACTCACGGGAGCTCTCCATGCATTTGGTATTTTCGCTGGGGGGTATGCACGGATAGCATTGCGAGACGCTGGAGCCGGAGCACCCCTATGTCGAGTATCTGTCTTTGATTCCTGCCTCATCTTAT** 155
AAATAAMACATCAGCATGGATCAGAGTCTATCACCCCTATTAACCACTCACGGGAGCTCTCCATGCATTTGGTATTTTCGCTGGGGGGTATGCACGGATAGCATTGCGAGACGCTGGAGCCGGAGCACCCCTATGTCGAGTATCTGTCTTTGATTCCTGCCTCATCTTAT BT2
AAATAAGACATCAGCATGGATCAGAGTCTATCACCCCTATTAACCACTCACGGGAGCTCTCCATGCATTTGGTATTTTCGCTGGGGGGTATGCACGGATAGCATTGCGAGACGCTGGAGCCGGAGCACCCCTATGTCGAGTATCTGTCTTTGATTCCTGCCTCATCTTAT BT3*
AAATAAGACATCAGCATGGATCAGAGTCTATCACCCCTATTAACCACTCACGGGAGCTCTCCATGCATTTGGTATTTTCGCTGGGGGGTATGCACGGATAGCATTGCGAGACGCTGGAGCCGGAGTACCCTATGTCGAGTATCTGTCTTTGATTCCTGCCTCATCTTAT BT3*

Cons. AAATAAGACATCAGCATGGATCAGAGTCTATCACCCCTATTAACCACTCACGGGAGCTCTCCATGCATTTGGTATTTTCGCTGGGGGGTATGCACGGATAGCATTGCGAGACGCTGGAGCCGGAGTACCCTATGTCGAGTATCTGTCTTTGATTCCTGCCTCATCTTAT

133 **TTTGATTCCTGCCTCATCTTATTTATTCGACACCTACGTTCAATATTACAGGCGAACATACTACTAAAGTGTGTTAAATTAATGCTTTAGGACATAATAAACAATTTGAATGTCTGCACAGCCACTTT** 267
TTTGATTCCTGCCTCATCTTATTTATTCGACACCTACGTTCAATATTACAGGCGAACATACTACTAAAGTGTGTTAAATTAATGCTTTAGGACATAATAAACAATTTGAATGTCTGCACAGCCACTTT BT1
TTTGATTCCTGCCTCATCTTATTTATTCGACACCTACGTTCAATATTACAGGCGAACATACTACTAAAGTGTGTTAAATTAATGCTTTAGGACATAATAAACAATTTGAATGTCTGCACAGCCACTTT BT3*
TTTGATTCCTGCCTCATCTTATTTATTCGACACCTACGTTCAATATTACAGGCGAACATACTACTAAAGTGTGTTAAATTAATGCTTTAGGACATAATAAACAATTTGAATGTCTGCACAGCCACTTT BT3*

Cons. TTTGATTCCTGCCTCATCTTATTTATTCGACACCTACGTTCAATATTACAGGCGAACATACTACTAAAGTGTGTTAAATTAATGCTTTAGGACATAATAAACAATTTGAATGTCTGCACAGCCACTTT

241 **ACAATTTGAATGTCTGCACAGCCACTTTCCACACAGACATCATAACAAAAAATTTCCACCAAAACCCCCCTCCCCCGCTTCTGGCCACAGCACTTAAACACATCTCTGCCAAACCCCAAAAACAAGA** 367
ACAATTTGAATGTCTGCACAGCCACTTTCCACACAGACATCATAACAAAAAATTTCCACCAAAACCCCCCTCCCCCGCTTCTGGCCACAGCACTTAAACACATCTCTGCCAAACCCCAAAAACAAGA BT2
ACAATTTGAATGTCTGCACAGCCACTTTCCACACAGACATCATAACAAAAAATTTCCACCAAAACCCCCCTCCCCCGCTTCTGGCCACAGCACTTAAACACATCTCTGCCAAACCCCAAAAACAAGA BT3*
ACAATTTGAATGTCTGCACAGCCACTTTCCACACAGACATCATAACAAAAAATTTCCACCAAAACCCCCCTCCCCCGCTTCTGGCCACAGCACTTAAACACATCTCTGCCAAACCCCAAAAACAAGA BT3*

Cons. ACAATTTGAATGTCTGCACAGCCACTTTCCACACAGACATCATAACAAAAAATTTCCACCAAAACCCCCCTCCCCCGCTTCTGGCCACAGCACTTAAACACATCTCTGCCAAACCCCAAAAACAAGA

339 **ACATCTCTGCCAAACCCCAAAAACAAGAACCCTAACACCAGCCTAACAGATTTCAAATTTTATCTTTTGGCGGTATGCACTTTTAACAGTACACCCCA** 439
ACATCTCTGCCAAACCCCAAAAACAAGAACCCTAACACCAGCCTAACAGATTTCAAATTTTATCTTTTGGCGGTATGCACTTTTAACAGTACACCCCA BT2
ACATCTCTGCCAAACCCCAAAAACAAGAACCCTAACACCAGCCTAACAGATTTCAAATTTTATCTTTTGGCGGTATGCACTTTTAACAGTACACCCCA BT3*

Cons. ACATCTCTGCCAAACCCCAAAAACAAGAACCCTAACACCAGCCTAACAGATTTCAAATTTTATCTTTTGGCGGTATGCACTTTTAACAGTACACCCCA

426 **ACAGTACACCCCAACTAACACATTTATTTCCCTCCCACTCCCATACTACTAATCTCATCAATACAACCCCGCCCATCTTACCCAGCACACACACACCGCTGCTAACCCCATACCCCGAACCAACCAACCCCAAGACACCCCCACAGTTTATGTAGCTTACCTC** 594
ACAGTACACCCCAACTAACACATTTATTTCCCTCCCACTCCCATACTACTAATCTCATCAATACAACCCCGCCCATCTTACCCAGCACACACACACCGCTGCTAACCCCATACCCCGAACCAACCAACCCCAAGACACCCCCACAGTTTATGTAGCTTACCTC BT1
ACAGTACACCCCAACTAACACATTTATTTCCCTCCCACTCCCATACTACTAATCTCATCAATACAACCCCGCCCATCTTACCCAGCACACACACACCGCTGCTAACCCCATACCCCGAACCAACCAACCCCAAGACACCCCCACAGTTTATGTAGCTTACCTC BT3*
ACAGTACACCCCAACTAACACATTTATTTCCCTCCCACTCCCATACTACTAATCTCATCAATACAACCCCGCCCATCTTACCCAGCACACACACACCGCTGCTAACCCCATACCCCGAACCAACCAACCCCAAGACACCCCCACAGTTTATGTAGCTTACCTC BT3*

Cons. ACAGTACACCCCAACTAACACATTTATTTCCCTCCCACTCCCATACTACTAATCTCATCAATACAACCCCGCCCATCTTACCCAGCACACACACACCGCTGCTAACCCCATACCCCGAACCAACCAACCCCAAGACACCCCCACAGTTTATGTAGCTTACCTC

¹The first lines in bold indicate the Cambridge Reference Sequence (NCBI Reference Sequence: NC_012920.1)

*Before DNA extraction, the bone powder was treated with additional 0.5% NaOCl for 7 minutes to remove the residual mitochondrial DNA contamination.

Y = C or T; M = A or C;

Cons.: Consensus sequence

2. Anna of Antioch

16009 **TTAAACTATTCTCTGTTCTTTCATGGGGAAGCAGATTGGGTACCACCAAGTATTGACTCACCCATCAACAACCGCTATGTATTTTCGTACATTACTGCCAGCCACCATGAATATTGTACG** 16129¹
TTAAACTATTCTCTGTTCTTTCATGGGGAAGCAGATTGGGTACCACCAAGTATTGACTCACCCATCAACAACCGCTATGTATTTTCGTACATTACTGCCAGCCACCATGAATATTGTACG AAC2
TTAAACTATTCTCTGTTCTTTCATGGGGAAGCAGATTGGGTACCACCAAGTATTGACTCACCCATCAACAACCGCTATGTATTTTCGTACATTACTGCCAGCCACCATGAATATTGTACG AAC3
Cons. TTAAACTATTCTCTGTTCTTTCATGGGGAAGCAGATTGGGTACCACCAAGTATTGACTCACCCATCAACAACCGCTATGTATTTTCGTACATTACTGCCAGCCACCATGAATATTGTACG

16113 **AGCCACCATGAATATTGTACGGTACCATAAATACTTGACCACCTGTAGTACATAAAAAACCAATCCACATCAAAACCCCTCCCATGCTTACAAGCAAGTACAGCAATCAACCCCTCAA** 16227
AGCCACCATGAATATTGTACGGTACCATAAATACTTGACCACCTGTAGTACATAAAAAACCAATCCACATCAAAACCCCTCCCATGCTTACAAGCAAGTACAGCAATCAACCCCTCAA AAC1
AGCCACCATGAATATTGTACGGTACCATAAATACTTGACCACCTGTAGTACATAAAAAACCAATCCACATCAAAACCCCTCCCATGCTTACAAGCAAGTACAGCAATCAACCCCTCAA AAC2
Cons. AGCCACCATGAATATTGTACGGTACCATAAATACTTGACCACCTGTAGTACATAAAAAACCAATCCACATCAAAACCCCTCCCATGCTTACAAGCAAGTACAGCAATCAACCCCTCAA

16222 **CCTCAACTATCACACATCAACTGCAACTCCAAAGCCACCCCTCACCCACTAGGATACCAACAACCTACCACCCCTTAACAGTACATAGTACATAAAGCCATTACCGTACATAGCACATTACAGTCAAATCCCTTCTCGTCCCATGGATGACCCCTCAGATAGGGGTCCCTTGACCACCATCCTCC** 16411
CCTCAACTATCACACATCAACTGCAACTCCAAAGCCACCCCTCACCCACTAGGATACCAACAACCTACCACCCCTTAACAGTACATAGTACATAAAGCCATTACCGTACATAGCACATTACAGTCAAATCCCTTCTCGTCCCATGGATGACCCCTCAGATAGGGGTCCCTTGACCACCATCCTCC AAC1
CCTCAACTATCACACATCAACTGCAACTCCAAAGCCACCCCTCACCCACTAGGATACCAACAACCTACCACCCCTTAACAGTACATAGTACATAAAGCCATTACCGTACATAGCACATTACAGTCAAATCCCTTCTCGTCCCATGGATGACCCCTCAGATAGGGGTCCCTTGACCACCATCCTCC AAC2
Cons. CCTCAACTATCACACATCAACTGCAACTCCAAAGCCACCCCTCACCCACTAGGATACCAACAACCTACCACCCCTTAACAGTACATAGTACATAAAGCCATTACCGTACATAGCACATTACAGTCAAATCCCTTCTCGTCCCATGGATGACCCCTCAGATAGGGGTCCCTTGACCACCATCCTCC AAC2

16381 **TCAGATAGGGTCCCTTGACCACCATCCTCCGTGAATCAATATCCCGCACAGAGTGCTACTCTCCTCGTCCGGGCCATAACACTTGGGGGTAGCTAAAGTGAAC** 16489
TCAGATAGGGTCCCTTGACCACCATCCTCCGTGAATCAATATCCCGCACAGAGTGCTACTCTCCTCGTCCGGGCCATAACACTTGGGGGTAGCTAAAGTGAAC AAC1
TCAGATAGGGTCCCTTGACCACCATCCTCCGTGAATCAATATCCCGCACAGAGTGCTACTCTCCTCGTCCGGGCCATAACACTTGGGGGTAGCTAAAGTGAAC AAC2
Cons. TCAGATAGGGTCCCTTGACCACCATCCTCCGTGAATCAATATCCCGCACAGAGTGCTACTCTCCTCGTCCGGGCCATAACACTTGGGGGTAGCTAAAGTGAAC

16471 **GGGTAGCTAAAGTGAACGTATCCGACATCTGGTTCCTACTTTCAGGGTCAATAAGCCATAAAGCCACACGTTCCCTTAAATAAGACATCAGATGGATCACAGTCTATCACCCATTAAACCCTCAC** 33
GGGTAGCTAAAGTGAACGTATCCGACATCTGGTTCCTACTTTCAGGGTCAATAAGCCATAAAGCCACACGTTCCCTTAAATAAGACATCAGATGGATCACAGTCTATCACCCATTAAACCCTCAC AAC1
GGGTAGCTAAAGTGAACGTATCCGACATCTGGTTCCTACTTTCAGGGTCAATAAGCCATAAAGCCACACGTTCCCTTAAATAAGACATCAGATGGATCACAGTCTATCACCCATTAAACCCTCAC AAC3
Cons. GGGTAGCTAAAGTGAACGTATCCGACATCTGGTTCCTACTTTCAGGGTCAATAAGCCATAAAGCCACACGTTCCCTTAAATAAGACATCAGATGGATCACAGTCTATCACCCATTAAACCCTCAC

16552 **AAATAAGACATCAGATGGATCAGAGTCTATCACCCATTAAACCCTCACGGGAGCTCTCCATGCATTTGGTATTTTCGCTGGGGGGTATGCACGGATAGCATTGCGAGACGCTGGAGCCGGAGCACCCCTATGCGCAGTATCTGTCTTTGATTCTGCCTCATCTTATT** 155
AAATAAGACATCAGATGGATCAGAGTCTATCACCCATTAAACCCTCACGGGAGCTCTCCATGCATTTGGTATTTTCGCTGGGGGGTATGCACGGATAGCATTGCGAGACGCTGGAGCCGGAGCACCCCTATGCGCAGTATCTGTCTTTGATTCTGCCTCATCTTATT AAC1
AAATAAGACATCAGATGGATCAGAGTCTATCACCCATTAAACCCTCACGGGAGCTCTCCATGCATTTGGTATTTTCGCTGGGGGGTATGCACGGATAGCATTGCGAGACGCTGGAGCCGGAGCACCCCTATGCGCAGTATCTGTCTTTGATTCTGCCTCATCTTATT AAC2
AAATAAGACATCAGATGGATCAGAGTCTATCACCCATTAAACCCTCACGGGAGCTCTCCATGCATTTGGTATTTTCGCTGGGGGGTATGCACGGATAGCATTGCGAGACGCTGGAG AAC3
Cons. AAATAAGACATCAGATGGATCAGAGTCTATCACCCATTAAACCCTCACGGGAGCTCTCCATGCATTTGGTATTTTCGCTGGGGGGTATGCACGGATAGCATTGCGAGACGCTGGAGCCGGAGCACCCCTATGCGCAGTATCTGTCTTTGATTCTGCCTCATCTTATT

133 **TTTGATTCCTGCCTCATCTTATTATTCGCACTACGTTCAATATTACAGGCGAACATACTACTAAAGTGTGTTAATTAATTAATGCTTGTAGGACATAATAAACAATTGAATGTCTGCACAGCCGCTTT** 267
TTTGATTCCTGCCTCATCTTATTATTCGCACTACGTTCAATATTACAGGCGAACATACTACTAAAGTGTGTTAATTAATTAATGCTTGTAGGACATAATAAACAATTGAATGTCTGCACAGCCGCTTT AAC1
TTTGATTCCTGCCTCATCTTATTATTCGCACTACGTTCAATATTACAGGCGAACATACTACTAAAGTGTGTTAATTAATTAATGCTTGTAGGACATAATAAACAATTGAATGTCTGCACAGCCGCTTT AAC3
Cons. TTTGATTCCTGCCTCATCTTATTATTCGCACTACGTTCAATATTACAGGCGAACATACTACTAAAGTGTGTTAATTAATTAATGCTTGTAGGACATAATAAACAATTGAATGTCTGCACAGCCGCTTT

241 **ACAATTGAATGTCTGCACAGCCACTTCCACACAGACATCATAACAAAAAATTTCCACCAAAACCCCTCCCGCTTCTGGCCACAGCACTTAAACACATCTCTGCCAAACCCCAAAAAACAAGA** 367
ACAATTGAATGTCTGCACAGCCACTTCCACACAGACATCATAACAAAAAATTTCCACCAAAACCCCTCCCGCTTCTGGCCACAGCACTTAAACACATCTCTGCCAAACCCCAAAAAACAAGA AAC2
ACAATTGAATGTCTGCACAGCCACTTCCACACAGACATCATAACAAAAAATTTCCACCAAAACCCCTCCCGCTTCTGGCCACAGCACTTAAACACATCTCTGCCAAACCCCAAAAAACAAGA AAC3
Cons. ACAATTGAATGTCTGCACAGCCACTTCCACACAGACATCATAACAAAAAATTTCCACCAAAACCCCTCCCGCTTCTGGCCACAGCACTTAAACACATCTCTGCCAAACCCCAAAAAACAAGA

339 **ACATCTCTGCCAAACCCCAAAAAACAAGAACCCTAACACCAGCCTAACAGATTTCAAATTTTATCTTTTGGCGGTATGCACTTTAAACAGTACACCCCA** 439
ACATCTCTGCCAAACCCCAAAAAACAAGAACCCTAACACCAGCCTAACAGATTTCAAATTTTATCTTTTGGCGGTATGCACTTTAAACAGTACACCCCA AAC2
ACATCTCTGCCAAACCCCAAAAAACAAGAACCCTAACACCAGCCTAACAGATTTCAAATTTTATCTTTTGGCGGTATGCACTTTAAACAGTACACCCCA AAC3
Cons. ACATCTCTGCCAAACCCCAAAAAACAAGAACCCTAACACCAGCCTAACAGATTTCAAATTTTATCTTTTGGCGGTATGCACTTTAAACAGTACACCCCA

426 **ACAGTACACCCCAACTAACACATTTATTTCCCTCCCACTCCCATACTACTAATCTCATCAATAACCCCGCCATCTACCCAGCACACACACACCGCTGTAAACCCATACCCCGAACCAACCCCAAGACACCCCCACAGTTTATGTAGCTTACCTC** 594
ACAGTACACCCCAACTAACACATTTATTTCCCTCCCACTCCCATACTACTAATCTCATCAATAACCCCGCCATCTACCCAGCACACACACACCGCTGTAAACCCATACCCCGAACCAACCCCAAGACACCCCCACAGTTTATGTAGCTTACCTC AAC1
ACAGTACACCCCAACTAACACATTTATTTCCCTCCCACTCCCATACTACTAATCTCATCAATAACCCCGCCATCTACCCAGCACACACACACCGCTGTAAACCCATACCCCGAACCAACCCCAAGACACCCCCACAGTTTATGTAGCTTACCTC AAC3
Cons. ACAGTACACCCCAACTAACACATTTATTTCCCTCCCACTCCCATACTACTAATCTCATCAATAACCCCGCCATCTACCCAGCACACACACACCGCTGTAAACCCATACCCCGAACCAACCCCAAGACACCCCCACAGTTTATGTAGCTTACCTC

¹The first lines in bold indicate the Cambridge Reference Sequence (NCBI Reference Sequence: NC_012920.1)

Cons.: Consensus sequence

3. II/52

16009 TTAACATATTCTCTGTTCTTTCATGGGGAAGCAGATTTGGGTACCACCAAGTATTGACTCACCATCAACAACCGCTATGTATTTTCGTACATTACTGCCAGCCACCATGAATATTGTACG 16129
TTAAACTATTCTCTGTTCTTTCATGGGGAAGCAGATTTGGGTACCACCAAGTATTGACTCACCATCAACAACCGCTATGTATTTTCGTACATTACTGCCAGCCACCATGAATATTGCAGG II 52T3
TTAAACTATTCTCTGTTCTTTCATGGGGAAGCAGATTTGGGTACCACCAAGTATTGACTCACCATCAACAACCGCTATGTATTTTCGTACATTACTGCCAGCCACCATGAATATTGCAGG II 52T6*
Cons. TTAACATATTCTCTGTTCTTTCATGGGGAAGCAGATTTGGGTACCACCAAGTATTGACTCACCATCAACAACCGCTATGTATTTTCGTACATTACTGCCAGCCACCATGAATATTGCAGG

16113 AGCCACCATGAATATTGTCACGGTACCATAAATACTTGACCACCTGTAGTACATAAAAAACCAATCCACATCAAAAACCCCTCCCATGCTTACAAGCAAGTACAGCAATCAACCCCTCAA 16227
AGCCACCATGAATATTGTCACGGTACCATAAATACTTGACCACCTGTAGTACATAAAAAACCAATCCACATCAAAAACCCCTCCCATGCTTACAAGCAAGTACAGCAATCAACCCCTCAA II 52T2
AGCCACCATGAATATTGTCACGGTACCATAAATACTTGACCACCTGTAGTACATAAAAAACCAATCCACATCAAAAACCCCTCCCATGCTTACAAGCAAGTACAGCAATCAACCCCTCAA II 52T6*
AGCCACCATGAATATTGTCACGGTACCATAAATACTTGACCACCTGTAGTACATAAAAAACCAATCCACATCAAAAACCCCTCCCATGCTTACAAGCAAGTACAGCAATCAACCCCTCAA II 52T6*
AGCCACCATGAATATTGTCACGGTACCATAAATACTTGACCACCTGTAGTACATAAAAAACCAATCCACATCAAAAACCCCTCCCATGCTTACAAGCAAGTACAGCAATCAACCCCTCAA II 52F2**
Cons. AGCCACCATGAATATTGTCACGGTACCATAAATACTTGACCACCTGTAGTACATAAAAAACCAATCCACATCAAAAACCCCTCCCATGCTTACAAGCAAGTACAGCAATCAACCCCTCAA

16222 CCTCAACTATCACACATCAACTGCAACTCCAAAGCCACCCCTCACCACCTAGGATACCAACAACCTACCACCCCTAACAGTACATAGTACATAAAGCCATTACCGTACATAGCACCATTACAGTCAAATCCCTTCTCGTCCCATGGATGACCCCCCTCAGATAGGGGTCCCTTGACCACCATCCCTCC 16411
CCTCAACTATCACACATCAACTGCAACTCCAAAGCCACCCCTCACCACCTAGGATACCAACAACCTACCACCCCTAACAGTACATAGTACATAAAGCCATTACCGTACATAGCACCATTACAGTCAAATCCCTTCTCGTCCCATGGATGACCCCCCTCAGATAGGGGTCCCTTGACCACCATCCCTCC II 52T2
CCTCAACTATCACACATCAACTGCAACTCCAAAGCCACCCCTCACCACCTAGGATACCAACAACCTACCACCCCTAACAGTACATAGTACATAAAGCCATTACCGTACATAGCACCATTACAGTCAAATCCCTTCTCGTCCCATGGATGACCCCCCTCAGATAGGGGTCCCTTGACCACCATCCCTCC II 52T6*
CCTCAACTATCACACATCAACTGCAACTCCAAAGCCACCCCTCACCACCTAGGATACCAACAACCTACCACCCCTAACAGTACATAGTACATAAAGCCATTACCGTACATAGCACCATTACAGTCAAATCCCTTCTCGTCCCATGGATGACCCCCCTCAGATAGGGGTCCCTTGACCACCATCCCTCC II 52T6*
Cons. CCTCAACTATCACACATCAACTGCAACTCCAAAGCCACCCCTCACCACCTAGGATACCAACAACCTACCACCCCTAACAGTACATAGTACATAAAGCCATTACCGTACATAGCACCATTACAGTCAAATCCCTTCTCGTCCCATGGATGACCCCCCTCAGATAGGGGTCCCTTGACCACCATCCCTCC

16381 TCAGATAGGGGTCCCTTGACCACCATCCCTCGTGAAATCAATATCCCGCACAAGAGTGTACTCTCTCCGCTCCGGGCCATAAACACTTGGGGGTAGCTAAAGTGAAC 16489
TCAGATAGGGGTCCCTTGACCACCATCCCTCGTGAAATCAATATCCCGCACAAGAGTGTACTCTCTCCGCTCCGGGCCATAAACACTTGGGGGTAGCTAAAGTGAAC II 52T2
TCAGATAGGGGTCCCTTGACCACCATCCCTCGTGAAATCAATATCCCGCACAAGAGTGTACTCTCTCCGCTCCGGGCCATAAACACTTGGGGGTAGCTAAAGTGAAC II 52T6*
TCAGATAGGGGTCCCTTGACCACCATCCCTCGTGAAATCAATATCCCGCACAAGAGTGTACTCTCTCCGCTCCGGGCCATAAACACTTGGGGGTAGCTAAAGTGAAC II 52F2**
Cons. TCAGATAGGGGTCCCTTGACCACCATCCCTCGTGAAATCAATATCCCGCACAAGAGTGTACTCTCTCCGCTCCGGGCCATAAACACTTGGGGGTAGCTAAAGTGAAC

16471 GGGGTAGCTAAAGTGAACGTGTATCCGACATCTGGTTCCTACTTCAGGGTCATAAAGCCATAAAGTACCCACAGCTTCCCTTAAATAAGACATCAGATGGATCACAGGTTCTATCACCCCTATTAACCACTCAC 33
GGGTAGCTAAAGTGAACGTGTATCCGACATCTGGTTCCTACTTCAGGGTCATAAAGCCATAAAGTACCCACAGCTTCCCTTAAATAAGACATCAGATGGATCACAGGTTCTATCACCCCTATTAACCACTCAC II 52T3
GGGTAGCTAAAGTGAACGTGTATCCGACATCTGGTTCCTACTTCAGGGTCATAAAGCCATAAAGTACCCACAGCTTCCCTTAAATAAGACATCAGATGGATCACAGGTTCTATCACCCCTATTAACCACTCAC II 52T6*
GGGTAGCTAAAGTGAACGTGTATCCGACATCTGGTTCCTACTTCAGGGTCATAAAGCCATAAAGTACCCACAGCTTCCCTTAAATAAGACATCAGATGGATCACAGGTTCTATCACCCCTATTAACCACTCAC II 52F2**
Cons. GGGGTAGCTAAAGTGAACGTGTATCCGACATCTGGTTCCTACTTCAGGGTCATAAAGCCATAAAGTACCCACAGCTTCCCTTAAATAAGACATCAGATGGATCACAGGTTCTATCACCCCTATTAACCACTCAC

16552 AAATAAGACATCAGATGGATCAGAGGTCATACCCCTATTAACCACTCAGCGGAGCTCTCCATGCATTTGGTATTTTCGCTGGGGGGTATGCACGGATAGCATTGCGAGACGCTGGAGCCGGAGCACCCTATGTCGCAGTATCTGTCTTTGATTCTGCCTCATCTTATT 155
AAATAAGACATCAGATGGATCAGAGGTCATACCCCTATTAACCACTCAGCGGAGCTCTCCATGCATTTGGTATTTTCGCTGGGGGGTATGCACGGATAGCATTGCGAGACGCTGGAGCCGGAGCACCCTATGTCGCAGTATCTGTCTTTGATTCTGCCTCATCTTATT II 52T3
AAATAAGACATCAGATGGATCAGAGGTCATACCCCTATTAACCACTCAGCGGAGCTCTCCATGCATTTGGTATTTTCGCTGGGGGGTATGCACGGATAGCATTGCGAGACGCTGGAGCCGGAGCACCCTATGTCGCAGTATCTGTCTTTGATTCTGCCTCATCTTATT II 52T6*
AAATAAGACATCAGATGGATCAGAGGTCATACCCCTATTAACCACTCAGCGGAGCTCTCCATGCATTTGGTATTTTCGCTGGGGGGTATGCACGGATAGCATTGCGAGACGCTGGAGCCGGAGCACCCTATGTCGCAGTATCTGTCTTTGATTCTGCCTCATCTTATT II 52F2**
Cons. AAATAAGACATCAGATGGATCAGAGGTCATACCCCTATTAACCACTCAGCGGAGCTCTCCATGCATTTGGTATTTTCGCTGGGGGGTATGCACGGATAGCATTGCGAGACGCTGGAGCCGGAGCACCCTATGTCGCAGTATCTGTCTTTGATTCTGCCTCATCTTATT

133 TTTGATTCTGCCTCATCTCTATTATTTATCGCACCTACGTTCAATATTACAGGCGAACAATACTTAAAGTGTGTTAAATTAATTAATGCTTTGAGGACATAATAAACAATTGAATGCTGCACAGCCGCTTT 267
TTTGATTCTGCCTCATCTCTATTATTTATCGCACCTACGTTCAATATTACAGGCGAACAATACTTAAAGTGTGTTAAATTAATTAATGCTTTGAGGACATAATAAACAATTGAATGCTGCACAGCCGCTTT II 52T4
TTTGATTCTGCCTCATCTCTATTATTTATCGCACCTACGTTCAATATTACAGGCGAACAATACTTAAAGTGTGTTAAATTAATTAATGCTTTGAGGACATAATAAACAATTGAATGCTGCACAGCCGCTTT II 52T6*
TTTGATTCTGCCTCATCTCTATTATTTATCGCACCTACGTTCAATATTACAGGCGAACAATACTTAAAGTGTGTTAAATTAATTAATGCTTTGAGGACATAATAAACAATTGAATGCTGCACAGCCGCTTT II 52T6*
TTTGATTCTGCCTCATCTCTATTATTTATCGCACCTACGTTCAATATTACAGGCGAACAATACTTAAATTAATTAATGCTTTGAGGACATAATAAACAATTGAATGCTGCACAGCCGCTTT II 52F2**
Cons. TTTGATTCTGCCTCATCTCTATTATTTATCGCACCTACGTTCAATATTACAGGCGAACAATACTTAAAGTGTGTTAAATTAATTAATGCTTTGAGGACATAATAAACAATTGAATGCTGCACAGCCGCTTT

241 ACAATTGAATGCTGCACAGCCACTTCCACACAGACATCATAAACAATAAATTTCCACCAAAACCCCCCTCCCGCTTCTGGCCACAGCACTTAAACACATCTCTGCCAAACCCCAAAAACAAGA 367
ACAATTGAATGCTGCACAGCCACTTCCACACAGACATCATAAACAATAAATTTCCACCAAAACCCCCCTCCCGCTTCTGGCCACAGCACTTAAACACATCTCTGCCAAACCCCAAAAACAAGA II 52T4
ACAATTGAATGCTGCACAGCCACTTCCACACAGACATCATAAACAATAAATTTCCACCAAAACCCCCCTCCCGCTTCTGGCCACAGCACTTAAACACATCTCTGCCAAACCCCAAAAACAAGA II 52T6*
Cons. ACAATTGAATGCTGCACAGCCACTTCCACACAGACATCATAAACAATAAATTTCCACCAAAACCCCCCTCCCGCTTCTGGCCACAGCACTTAAACACATCTCTGCCAAACCCCAAAAACAAGA

339 ACATCTCTGCCAAACCCCAAAAACAAGAACCCTAACACCAGCCTAACAGATTTCAAATTTTATCTTTTGGCGGTATGCACCTTTTAAACAGTACACCCCA 439
ACATCTCTGCCAAACCCCAAAAACAAGAACCCTAACACCAGCCTAACAGATTTCAAATTTTATCTTTTGGCGGTATGCACCTTTTAAACAGTACACCCCA II 52T4
ACATCTCTGCCAAACCCCAAAAACAAGAACCCTAACACCAGCCTAACAGATTTCAAATTTTATCTTTTGGCGGTATGCACCTTTTAAACAGTACACCCCA II 52T6*
ACATCTCTGCCAAACCCCAAAAACAAGAACCCTAACACCAGCCTAACAGATTTCAAATTTTATCTTTTGGCGGTATGCACCTTTTAAACAGTACACCCCA II 52F2**
Cons. ACATCTCTGCCAAACCCCAAAAACAAGAACCCTAACACCAGCCTAACAGATTTCAAATTTTATCTTTTGGCGGTATGCACCTTTTAAACAGTACACCCCA

426 ACAGTACACCCCAACTAACACATTTATTTCCCTCCCACTCCCATACTACTAATCTCATCAATAACAACCCCGCCCATCTACCCAGCACACACACAGCGTGTAAACCCATACCCCGAACCAACCAACCCCAAAAGACACCCCCACAGTTTATGTAGCTTACCTC 594
ACAGTACACCCCAACTAACACATTTATTTCCCTCCCACTCCCATACTACTAATCTCATCAATAACAACCCCGCCCATCTACCCAGCACACACACAGCGTGTAAACCCATACCCCGAACCAACCAACCCCAAAAGACACCCCCACAGTTTATGTAGCTTACCTC II 52T2
ACAGTACACCCCAACTAACACATTTATTTCCCTCCCACTCCCATACTACTAATCTCATCAATAACAACCCCGCCCATCTACCCAGCACACACACAGCGTGTAAACCCATACCCCGAACCAACCAACCCCAAAAGACACCCCCACAGTTTATGTAGCTTACCTC II 52T6*
ACAGTACACCCCAACTAACACATTTATTTCCCTCCCACTCCCATACTACTAATCTCATCAATAACAACCCCGCCCATCTACCCAGCACACACACAGCGTGTAAACCCATACCCCGAACCAACCAACCCCAAAAGACACCCCCACAGTTTATGTAGCTTACCTC II 52T6*
ACAGTACACCCCAACTAACACATTTATTTCCCTCCCACTCCCATACTACTAATCTCATCAATAACAACCCCGCCCATCTACCCAGCACACACACAGCGTGTAAACCCATACCCCGAACCAACCAACCCCAAAAGACACCCCCACAGTTTATGTAGCTTACCTC II 52F2**
Cons. ACAGTACACCCCAACTAACACATTTATTTCCCTCCCACTCCCATACTACTAATCTCATCAATAACAACCCCGCCCATCTACCCAGCACACACACAGCGTGTAAACCCATACCCCGAACCAACCAACCCCAAAAGACACCCCCACAGTTTATGTAGCTTACCTC

¹The first lines in bold indicate the Cambridge Reference Sequence (NCBI Reference Sequence: NC_012920.1)
*Before DNA extraction, the bone powder was treated with additional 0.5% NaOCl for 7 minutes to remove the residual mitochondrial DNA contamination.
** Before DNA extraction, the bone powder was treated with additional 0.8% NaOCl for 7 minutes to remove the residual mitochondrial DNA contamination.
Y = C or T; M = A or C; R = A or G
Cons.: Consensus sequence