**S1 Table.** PCR primers used in this study

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| Primer pair | Primer position, sequence | Amplicon (bp) |
| 1 | 15259F, 5’-CCTCGGAGACCCAGATAACT-3’15362R, 5’-TTGATCGTAAGATTGCGTATG-3’ | 104 |
| 2 | 10052F, 5’-GAGCCTCACAAACAACAAACTT-3’10175R, 5’-GTACCATATTCGGTTCATTCTAGTC-3’ | 124 |
| 3 | 14711F, 5’-ACCCATATCTGCCGAGAC-3’14812R, 5’-TCGTCCTACGTGCATATATAA-3’ | 102 |
| 4 | 14768F, 5’-GGAGCTTCAATGTTTTTTATCTG-3’14867R, 5’-GGATTACTCCAATATTTCATGTTT-3’ | 100 |
| 5 | 14818F, 5’-ATATTACGGGTCTTACACTTTTC-3’14919R, 5’-CCTCATGGTAGGACGTATCC-3’ | 102 |
| 6 | 14936F, 5’-GGAGCAACAGTCATCACCAA-3’15053R, 5’-AAGCGAAGAATCGGGTAAGG-3’ | 118 |
| 7 | 15357F, 5’-GATCAATCCCCAACAAAC-3’15438R, 5’-GTGTGTAGTAGGGGAATTAGA-3’ | 82 |
| 8 | 15883F, 5’-AACCAAATATTACAAACACCACTA-3’16012R, 5’-GGGGCATATAATTTAATGTACT-3’ | 130 |
| 9 | 16010F, 5’-CCCATGCATATAAGCAAGT-3’16148R, 5’-TGGTAATTAAGCTCGTGATCTA-3’ | 139 |
| 10 | 16162F, 5’-CAGCAACCCGCTAGGCA-3’16266R, 5’-GCCCTGAAGAAAGAACCAGATGT-3’ | 105 |
| 11 | 156F, 5’-CATAATGGTAGGCATGCACA-3’254R, 5’-AGTGGTAAATATTTAAGGGGGAA-3’ | 99 |
| 12 | 156F, 5’-CATAATGGTAGGCATGCACA-3’270R, 5’-AAAATCTGTTAAAAGCAGTGGT-3’ | 115 |
| 13 | 304F, 5’-CAATACTCAAATTAGCACTCCA-3’399R, 5’-ATTTTCAGTGCCTTGCTTT-3’ | 96 |
| 14 | 1394F, 5’-AGCTTAAACAAAGCATCCAGT-3’1483R, 5’-AGTTAAGAGGGTATTTTGGGCTA-3’ | 90 |
| 15 | 1457F, 5’-AATCTAGCCCAAAATACCCTC-3’1559R, 5’-CGCCATATTCTAGATTTCTATCTCC-3’ | 103 |
| 16 | 1900F, 5’-GGTACAGCCTTTTAGAAACGGAT-3’1998L, 5’-TTAACGCTTTCTCAATTGGTGG-3’ | 99 |
| 17 | 2013F, 5’-AATTAAACAGATCCCAATAACA-3’2132R, 5’-CTTATGCAAGGAGAAAGTT-3’ | 120 |
| 18 | 3060F, 5’-AACTTTTATACCCAGAGATTCA-3’3177R, 5’-TTTTCGTTCTACTAATGTGAGG-3’ | 118 |
| 19 | 4024F, 5’-ATCCTTACATCAGGCATCCCA-3’4134R, 5’-CCTATAGTTCTAGAAATAAGAGGGTT-3’ | 111 |
| 20 | 4037F, 5’-GCATCCCACCACAAACAT-3’4156R, 5’-ATTCTTAGGAGTAGGTTCAATTC-3’ | 120 |
| 21 | 4251F, 5’-CCCTTCCCGTACTAATAAATCCAA-3’4359R, 5’-CCGATTCAGACAAGTAGTCAGT-3’ | 109 |
| 22 | 4439F, 5’-TATTTTCTAACCCAATCAACAGC-3’4539R, 5’-GGGTTAAATAATTTTATTACGGTTCA-3’ | 101 |
| 23 | 5179F, 5’-CCCCTCTACAAACAACAT-3’5258R, 5’-ATACGGCTATTGTTGGTAGG-3’ | 80 |
| 24 | 5493F, 5’-ACCCCAATTAATCAGGCTTC-3’5605R, 5’-AGTTTACACGTTGAATTGCAAA-3’ | 113 |
| 25 | 6431F, 5’-CCTGGATTTGGAATAATCTCCC-3’6513R, 5’-GCTCAGACTATTCCTATATATCCG-3’ | 83 |
| 26 | 7264F, 5’-TTCAAGCCAACATCATAACCTC-3’7357R, 5’-TTTCACTTGTAACTTAACTTTGACA-3’ | 94 |
| 27 | 8219F, 5’-CACAACTTTCACTACAATCCAG-3’8301R, 5’-ATTTTCGTTCATTTTGTTTCTCA-3’ | 83 |
| 28 | 8290F, 5’-ATGAACGAAAATTTATTTGCCTCT-3’8403R, 5’-CACTAATCGATTTGATGTTGGGA-3’ | 114 |
| 29 | 11068F, 5’-ATACTGAGTACAACCTGTGCAT-3’11173R, 5’-TCAAAGGTGGAGGCCGTAT-3’ | 106 |
| 30 | 11838F, 5’-TATCGCTGCACATCTTACCT-3’11939R, 5’-CACAATCTAATGTTTTTGTTAAACT-3’ | 102 |
| 31 | 11851F, 5’-CTTACCTTTACTACTCTTATCCCT-3’11960R, 5’-ATGAGTTTCTATTGTTAGATTCAC-3’ | 110 |
| 32 | 12077F, 5’-CGAAAAATTGGTGCAACTCC-3’12178R, 5’-AGGCTTGTTATTATAATGGGTAC-3’ | 102 |
| 33 | 12320F, 5’-CCAAACCCTTAAACTATCCCTC-3’12393R, 5’-CGAATAGTGCTACTGGGACA-3’ | 74 |
| 34 | 12876F, 5’-ATCTTCCTATTAATCCGCTTT-3’12977R, 5’-TATCGCTGTAAATAACGTGGT-3’ | 102 |
| 35 | 14087F, 5’-TCAAACACAATCTCTACCTCC-3’14173R, 5’-TTTAGGGGCATTTATTACTGG-3’ | 87 |
| 36 | 14353F, 5’-CCCATAAATAGGTGAAGGC-3’14457R, 5’-AGATTCCATGTAAGAATAATGA-3’ | 105 |
| 37 | 15547F, 5’-CCCATATATCATCATCGGACA-3’15639R, 5’-AGTTTGTTTTCAATTGTGCC-3’ | 93 |
| 38 | 15922F, 5’-CCCCAAAATGCATTACCCAA-3’16016R, 5’-GCATGGGGCATATAATTTAATGT-3’ | 95 |

Primer pair 1 was used to analyze all four bone samples for *Bos* and *Bison* mitochondrial DNA. Primer pairs 2-10 were used to characterize further the SGE2 sample before initiating Illumina sequencing. Primer pairs 11-38 were used to fill in the gaps in the genome reconstructed by shotgun DNA sequencing and check the sequence of the genome regions where a single Illumina read was obtained. The position of each forward (F) and reverse (R) primer is numbered according to the SGE2seq sequence.