

Table S1. Ancient sequences nucleotide misincorporation calculations and nucleotide misincorporation rate within each mitochondrial fragment.

| Mitochondrial fragment | Number of clones | Length of fragment | Number of nucleotide misincorporations | m | AT/GC Ratio | Nucleotide misincorporation | | | | | | | | | | | | Complementary Groups | | | | | | |
|------------------------|------------------|--------------------|--|----------|-------------|-----------------------------|-------|-------|------|------|------|-------|------|------|------|--------|-------|----------------------|-------|------|------|-------|------|-------|
| | | | | | | A→C | T→C | A→G | T→G | A→T | T→A | C→A | G→T | C→G | G→C | C→T | G→A | Total | A→G | A→T | A→C | C→T | C→G | C→A |
| | | | | | | T→C | T→A | T→G | G→A | T→G | G→A | T→C | T→A | T→G | G→A | T→C | T→A | T→G | G→A | T→C | T→A | T→G | G→A | T→C |
| L16518/H47 | 270 | 97 | 222 | 0.008477 | 1.16 | 0 | 6 | 22 | 0 | 0 | 0 | 0 | 1.16 | 0 | 0 | 198.76 | 24.27 | 252.19 | 28 | 0 | 0 | 223 | 0 | 1.16 |
| L39/H118 | 108 | 78 | 86 | 0.010209 | 0.77 | 0 | 5.16 | 0 | 0 | 1.29 | 2.58 | 0 | 2 | 0 | 0 | 50 | 27 | 88.1 | 5.16 | 3.87 | 0 | 77 | 0 | 2 |
| L207/H343 | 41 | 135 | 43 | 0.007769 | 1.45 | 1 | 1 | 0 | 0 | 0 | 1 | 1.45 | 0 | 0 | 0 | 56.73 | 0 | 61.18 | 1 | 1 | 1 | 56.73 | 0 | 1.45 |
| L707/H809 | 220 | 101 | 181 | 0.008146 | 0.91 | 0 | 8.8 | 24.2 | 0 | 1.1 | 0 | 2 | 0 | 1 | 0 | 107 | 40 | 184.22 | 33 | 1.1 | 0 | 147 | 1 | 2 |
| L1135/H1202 | 481 | 66 | 225 | 0.007088 | 0.94 | 3.18 | 13.78 | 13.78 | 2.12 | 0 | 1.06 | 11 | 4 | 0 | 0 | 102 | 76 | 227 | 27.56 | 1.06 | 5.3 | 178 | 0 | 15 |
| L1170/H1211 | 134 | 40 | 48 | 0.008955 | 0.75 | 8.1 | 5.4 | 0 | 0 | 0 | 0 | 9 | 0 | 0 | 0 | 27 | 2 | 51.33 | 5.4 | 0 | 8.1 | 29 | 0 | 9 |
| L1177/H1238 | 112 | 61 | 45 | 0.006587 | 0.97 | 1.03 | 1.03 | 5.15 | 0 | 0 | 1.03 | 2 | 0 | 0 | 0 | 30 | 5 | 45.26 | 6.18 | 1.03 | 1.03 | 35 | 0 | 2 |
| L1361/H1493 | 19 | 131 | 10 | 0.004018 | 1.08 | 0 | 2 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1.08 | 6.48 | 10.56 | 3 | 0 | 0 | 7.56 | 0 | 0 |
| L1720/H1833 | 62 | 112 | 36 | 0.005184 | 1.8 | 0 | 2 | 2 | 0 | 1 | 0 | 5.4 | 3.6 | 0 | 0 | 27 | 19.8 | 60.8 | 4 | 1 | 0 | 46.8 | 0 | 9 |
| L2643/H2746 | 76 | 112 | 52 | 0.006109 | 1.24 | 0 | 6 | 2 | 0 | 0 | 0 | 0 | 1.24 | 0 | 0 | 34.72 | 18.6 | 62.56 | 8 | 0 | 0 | 53.32 | 0 | 1.24 |
| L3380/H3497 | 89 | 116 | 66 | 0.006393 | 1 | 0 | 0 | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 48 | 16 | 66 | 2 | 0 | 0 | 64 | 0 | 0 |
| L3477/H3530 | 165 | 52 | 47 | 0.005478 | 0.79 | 0 | 0 | 2.52 | 0 | 0 | 0 | 6 | 0 | 0 | 0 | 38 | 1 | 47.52 | 2.52 | 0 | 0 | 39 | 0 | 6 |
| L4687/H4776 | 93 | 88 | 41 | 0.005010 | 2.14 | 0 | 1 | 6 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 70.71 | 2.14 | 79.85 | 7 | 0 | 0 | 72.85 | 0 | 0 |
| L4730/H4849 | 131 | 119 | 153 | 0.009815 | 1.38 | 0 | 18 | 12 | 2 | 1 | 0 | 4.14 | 2.76 | 0 | 0 | 155.94 | 2.76 | 198.6 | 30 | 1 | 2 | 158.7 | 0 | 6.9 |
| L6951/H7074 | 155 | 122 | 120 | 0.006346 | 1.3 | 5 | 9 | 16 | 0 | 2 | 1 | 0 | 1.3 | 0 | 0 | 89.83 | 22.13 | 146.26 | 25 | 3 | 5 | 112 | 0 | 1.3 |
| L6999/H7107 | 93 | 107 | 106 | 0.010652 | 1.33 | 1 | 6 | 3 | 0 | 0 | 0 | 0 | 0 | 1.33 | 0 | 70.28 | 55.7 | 137.31 | 9 | 0 | 1 | 126 | 1.33 | 0 |
| L8081/H8165 | 142 | 83 | 77 | 0.006533 | 1.13 | 0 | 4 | 4 | 0 | 0 | 0 | 0 | 5.64 | 0 | 2.26 | 40.62 | 29.33 | 85.85 | 8 | 0 | 0 | 69.95 | 2.26 | 5.64 |
| L8776/H8872 | 21 | 95 | 9 | 0.004511 | 0.98 | 0 | 0 | 2.04 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 4 | 3 | 9.04 | 2.04 | 0 | 0 | 7 | 0 | 0 |
| L8840/H8932 | 59 | 91 | 54 | 0.010058 | 1.07 | 1 | 3 | 1 | 13 | 0 | 0 | 0 | 0 | 0 | 0 | 36.32 | 2.14 | 56.46 | 4 | 0 | 14 | 38.46 | 0 | 0 |
| L9027/H9105 | 245 | 77 | 133 | 0.007050 | 1.33 | 0 | 15 | 5 | 0 | 0 | 0 | 1.33 | 0 | 0 | 0 | 144 | 5.33 | 170.66 | 20 | 0 | 0 | 149.3 | 0 | 1.33 |
| L9612/H9715 | 100 | 102 | 49 | 0.004804 | 1.68 | 0 | 4 | 3 | 0 | 0 | 7 | 0 | 0 | 0 | 0 | 30.32 | 28.63 | 72.95 | 7 | 7 | 0 | 58.95 | 0 | 0 |
| L9678/H9740 | 247 | 61 | 91 | 0.006040 | 1.77 | 0 | 5 | 8 | 0 | 0 | 0 | 0 | 1.77 | 0 | 0 | 108.14 | 28.36 | 151.27 | 13 | 0 | 0 | 136.5 | 0 | 1.77 |
| L9696/H9785 | 151 | 88 | 85 | 0.006397 | 1.26 | 0 | 6 | 2 | 4 | 0 | 1 | 1.26 | 0 | 0 | 0 | 76.64 | 12.56 | 103.46 | 8 | 1 | 4 | 89.2 | 0 | 1.26 |
| L10377/H10500 | 37 | 122 | 15 | 0.003323 | 2.7 | 0 | 1 | 5 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 16.18 | 8.09 | 30.27 | 6 | 0 | 0 | 24.27 | 0 | 0 |
| L10476/H10599 | 57 | 122 | 42 | 0.006040 | 1.9 | 0 | 5 | 0 | 0 | 1 | 1 | 1.9 | 0 | 0 | 0 | 60.95 | 3.81 | 73.66 | 5 | 2 | 0 | 64.76 | 0 | 1.9 |
| L10545/H10646 | 142 | 100 | 104 | 0.007324 | 1.62 | 0 | 3 | 10 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 129.52 | 16.19 | 159.71 | 13 | 1 | 0 | 145.7 | 0 | 0 |
| L11261/H11325 | 293 | 63 | 213 | 0.011539 | 1.25 | 0 | 3 | 8 | 0 | 0 | 1 | 1.25 | 0 | 0 | 0 | 243.75 | 6.25 | 263.25 | 11 | 1 | 0 | 250 | 0 | 1.25 |
| L11274/H11381 | 172 | 106 | 148 | 0.008118 | 1.72 | 0 | 14 | 9 | 0 | 0 | 4 | 0 | 0 | 1.72 | 0 | 175.23 | 30.92 | 234.87 | 23 | 4 | 0 | 206.2 | 1.72 | 0 |
| L11408/H11536 | 60 | 108 | 42 | 0.006481 | 1.04 | 1 | 5 | 2 | 0 | 0 | 1 | 0 | 1.04 | 0 | 0 | 29.06 | 4.15 | 43.25 | 7 | 1 | 1 | 33.21 | 0 | 1.04 |
| L11456/H11536 | 72 | 79 | 31 | 0.005450 | 1.19 | 0 | 0 | 2 | 0 | 0 | 1 | 0 | 2.39 | 0 | 0 | 27.47 | 3.58 | 36.44 | 2 | 1 | 0 | 31.05 | 0 | 2.39 |
| L11620/H11742 | 72 | 122 | 42 | 0.004781 | 1.1 | 0 | 1 | 6 | 0 | 0 | 1 | 1.1 | 2.21 | 0 | 0 | 32 | 2.21 | 45.52 | 7 | 1 | 0 | 34.21 | 0 | 3.31 |
| L11711/H11778 | 169 | 67 | 80 | 0.007065 | 1.09 | 1 | 1 | 12 | 0 | 0 | 0 | 1.09 | 0 | 0 | 0 | 62.34 | 8.75 | 86.18 | 13 | 0 | 1 | 71.09 | 0 | 1.09 |
| L12233/H12315 | 79 | 81 | 31 | 0.004845 | 1.45 | 0 | 1 | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 34.91 | 5.82 | 43.73 | 3 | 0 | 0 | 40.73 | 0 | 0 |
| L12283/H12398 | 42 | 95 | 33 | 0.008271 | 1.44 | 1 | 5 | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 34.46 | 1.44 | 43.9 | 7 | 0 | 1 | 35.9 | 0 | 0 |
| L12370/H12449 | 111 | 78 | 78 | 0.009009 | 1.52 | 1 | 7 | 8 | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 89.45 | 1.52 | 108.97 | 15 | 0 | 3 | 90.97 | 0 | 0 |
| L14097/H14204 | 1030 | 106 | 853 | 0.007813 | 1.65 | 6 | 66 | 60 | 2 | 1 | 4 | 34.65 | 3.3 | 1.65 | 0 | 1112.1 | 26.4 | 1317.1 | 126 | 5 | 8 | 1139 | 1.65 | 37.95 |
| L14697/H14799 | 97 | 102 | 74 | 0.007479 | 1.91 | 1 | 7 | 12 | 0 | 0 | 0 | 0 | 1.91 | 0 | 0 | 95.71 | 5.74 | 123.36 | 19 | 0 | 1 | 101.5 | 0 | 1.91 |
| L14752/H14869 | 118 | 116 | 91 | 0.006648 | 1.07 | 1 | 5 | 2 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 79.29 | 8.57 | 96.86 | 7 | 1 | 1 | 87.86 | 0 | 0 |
| L15292/H15384 | 352 | 91 | 401 | 0.012519 | 1.02 | 2 | 12 | 25 | 0 | 0 | 2 | 0 | 3.07 | 0 | 1.02 | 349.6 | 14.31 | 409 | 37 | 2 | 2 | 363.9 | 1.02 | 3.07 |
| L15320/H15418 | 103 | 97 | 118 | 0.011811 | 1.06 | 3 | 12 | 4 | 0 | 1 | 0 | 2.13 | 0 | 0 | 0 | 101.06 | 1.06 | 124.25 | 16 | 1 | 3 | 102.1 | 0 | 2.13 |
| L16209/H16331 | 41 | 121 | 44 | 0.008869 | 1.16 | 0 | 1 | 5 | 0 | 0 | 0 | 1.16 | 0 | 0 | 0 | 42.95 | 0 | 50.11 | 6 | 0 | 0 | 42.95 | 0 | 1.16 |
| L16303/H16407 | 161 | 103 | 132 | 0.007960 | 1.02 | 4 | 7 | 12 | 0 | 1 | 0 | 3.06 | 1.02 | 0 | 2.04 | 100.94 | 3.06 | 134.12 | 19 | 1 | 4 | 104 | 2.04 | 4.08 |
| L16347/H16473 | 174 | 125 | 162 | 0.007448 | 0.67 | 0 | 9 | 6 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 128 | 22 | 167 | 15 | 0 | 0 | 150 | 0 | 2 |
| L16429/H16537 | 123 | 107 | 69 | 0.005243 | 0.95 | 0 | 5.29 | 13.75 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 30 | 19 | 70.04 | 19.04 | 0 | 0 | 49 | 0 | 2 |

NOTE. — Mitochondrial fragments are numbered with reference to the Cambridge reference sequence (rCRS)[28].