

## Supplementary Information

### **Single tooth reveals multiple forensic insights for human identification**

**—applicability to remains with advanced postmortem changes—**

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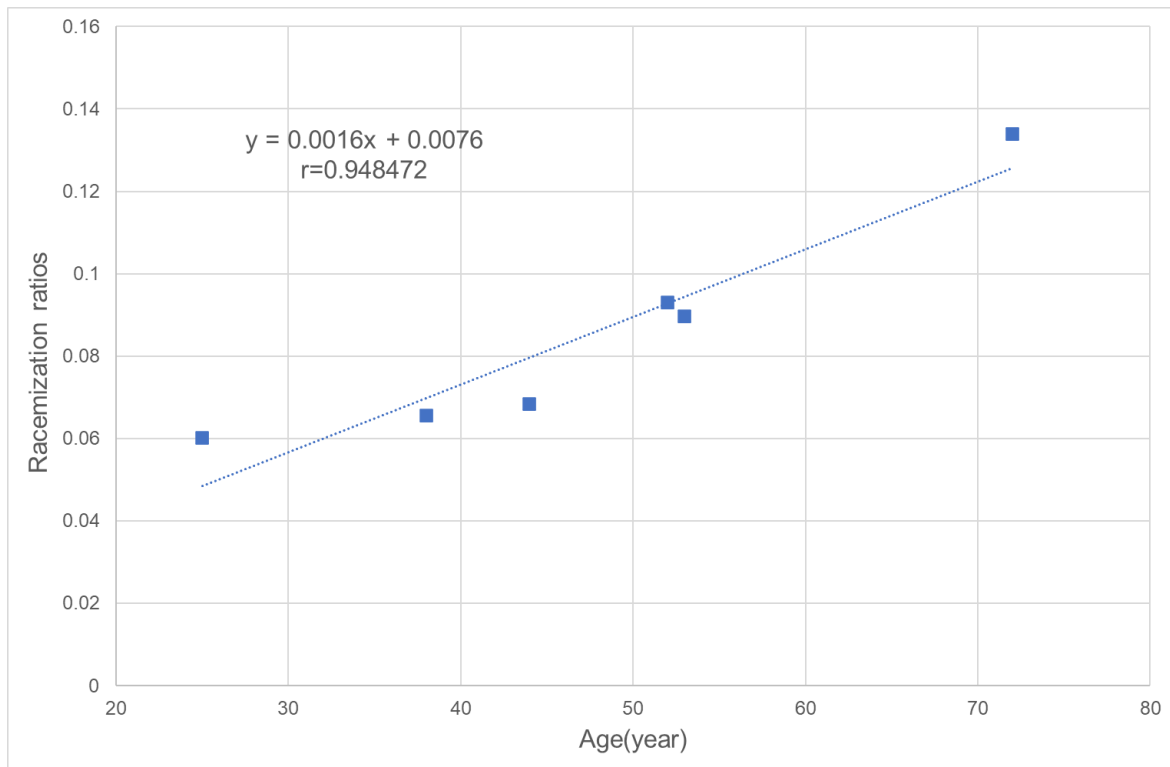
Supplementary Figs. S1–S3

Supplementary Tables S1–S3

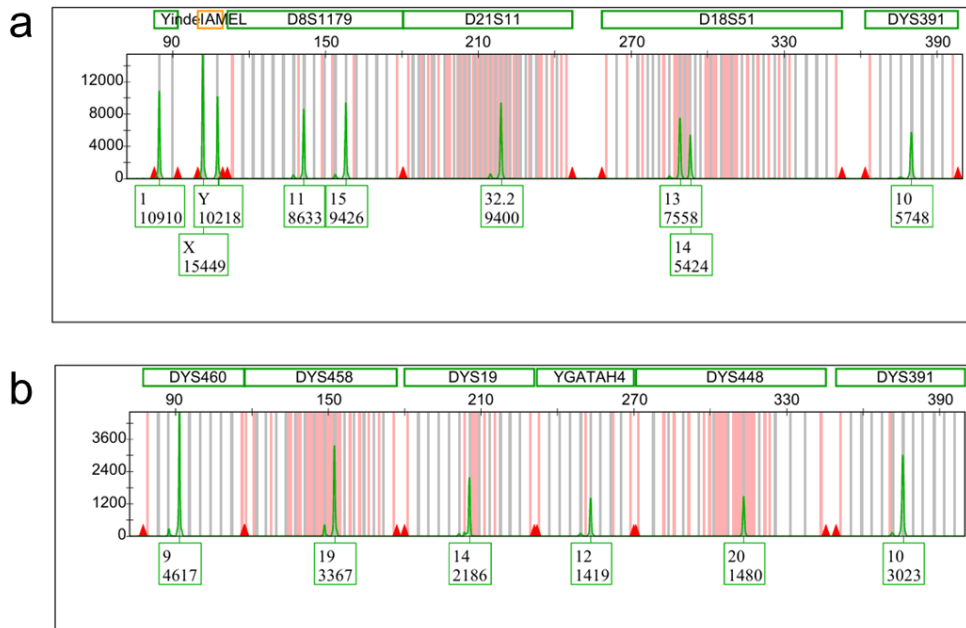
Supplementary Fig. S1 Serial longitudinal sections approximately 1 mm thick were prepared according to the size of each tooth. Enamel was removed from each section.



Supplementary Fig S2 Calibration curve used for amino acid racemization analysis. We measured the rate of racemization in the mandibular first premolars of individuals aged 25 to 72. Age and racemization rate showed a strong positive correlation ( $r = 0.95$ ).



Supplementary Fig. S3 Example of STR typing and Y-STR results. Partial analysis results for sample no. 5 are shown below. a: STR typing. b: Y-STR typing.



Supplementary Table S1 Comparison of Final estimated year of birth (YOB) and Actual YOB with absolute error.

<b>Case no.</b>	<b>Final estimated YOB</b>	<b>Actual YOB</b>	<b>Absolute error</b>
1	1955.33	1957.74	2.41
2	1963.57	1959.45	4.12
3	1950.42	1952.67	2.25
4	1966.48	1960.80	5.68
5	1954.74	1956.57	1.83
6	1953.47	1954.20	0.73
7	1971.06	1966.95	4.11
8	ND	1952.32	ND
9	2000.00	1990.70	9.30
10	1975.64	1971.04	4.60
11	1991.83	1986.51	5.32
12	1934.66	1948.59	13.93
13	1957.18	1967.12	9.94
14	1945.89	1944.00	1.89
15	1976.07	1972	4.04

The estimated YOB derived from  $^{14}\text{C}$  analysis and AAR analysis is presented as the final estimated YOB , and the difference between the final estimated YOB and the actual YOB is presented as the margin of error.

For no. 15, because the date of birth of the leading candidate for the identity was unknown, actual YOB was calculated by assuming 1972 based on their age at the time (41 years old).

Supplementary Table S2 Results of mtDNA HV1 region analysis.

<b>Case no.</b>	<b>Range</b>	<b>Haplotype</b>
1	16,086–16,195	16111T 16189C
2	16,086–16,228	16189C 16194G 16195C 16223T 16223T 16227G
3	16,086–16,254	16223T
4	Not performed	Not performed
5	Not detected	Not detected
6	16,086–16,255	16209C 16223T
7	16,086–16,255	16129A 16223T
8	16,086–16,254	16129A 16189Y 16223T
9	16,086–16,255	16223T
10	16,086–16,254	16187T 16223T
11	16,086–16,255	16209C 16223T
12	16,086–16,201	16111T 16189C
13	16,086–16,193	16111T 16189C
14	16,086–16,254	16209C 16223T
15	16,086–16,193	16182C 16183C 16189C

Base pair ranges and haplotypes of the mtDNA HV1 region are shown for each sample.

Supplementary Table S3 Results of mtDNA HV2 region analysis.

<b>Case no.</b>	<b>Range</b>	<b>Haplotype</b>
1	Not detected	Not detected
2	97–340	263G 315.1C
3	109–367	263G 315.1C
4	Not performed	Not performed
5	96–315	103A 152C 199C 203A 204C 263G 309.1C
6	Not detected	Not detected
7	96–360	152C 263G 315.1C
8	97–318	263G 309.1C 315.1C
9	97–320	263G 315.1C
10	Not detected	Not detected
11	295–380	315.1C
12	293–370	315.1C
13	287–340	315.1C
14	Not detected	Not detected
15	111–315	150T 263G 309.2C

Sequence ranges and haplotypes of the mtDNA HV2 region are shown for each sample.