Supporting Information

Knapp et al. 10.1073/pnas.1209896109

SI Text

All DNA extraction and 454 sequencing library preparation before PCR amplification were conducted in the purpose-built University of Otago aDNA facility. The facility is located in a building with no other molecular laboratories. It is fitted with a positive pressure system and HEPA air filters. The facility is UVC-irradiated (λ = 254 nm) when not in use, and all surfaces are regularly bleached. It is fitted with separate, UVC-irradiated, enclosed workspaces for sample manipulation, DNA extraction and manipulation, and PCR setup. Consumables are delivered directly to the facility and, where possible, UVC treated before entering the core (clean room) of the facility. No laboratory equipment has ever been used in a post-PCR laboratory. Access is limited to trained staff who enter the facility only first thing in the morning, before having entered any building containing post-PCR laboratories (1).

1. Knapp M, Clarke AC, Horsburgh KA, Matisoo-Smith EA (2011) Setting the stage: Building and working in an ancient DNA laboratory. *Ann Anat* 194(1):3–6.

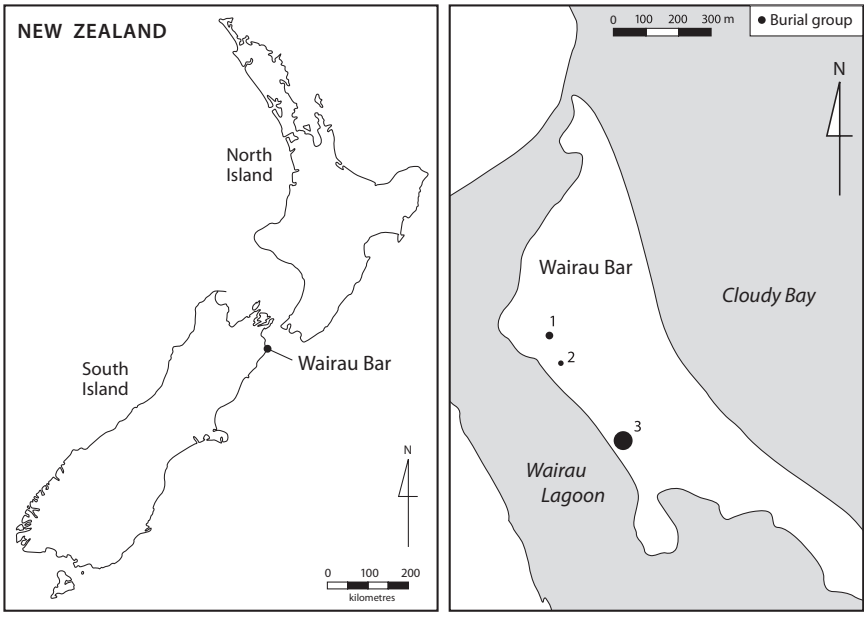

Fig. S1. Location of the Wairau Bar archaeological site (*Left*) and a site map identifying the general location of the three burial groups at Wairau Bar (*Right*).

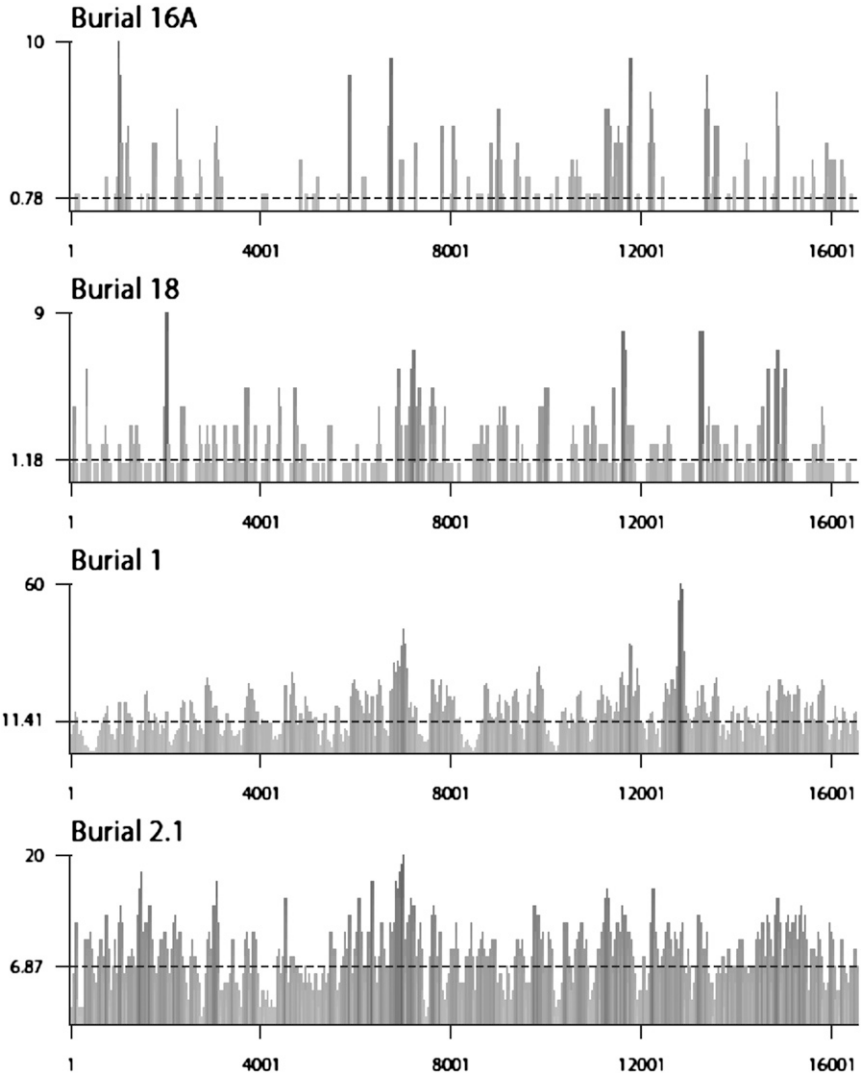

Fig. S2. Coverage plots. The *x* axis represents the length of the human mitochondrial genome in base pairs. The *y* axis is the number of unique reads covering each site of the mitochondrial genome. Dashed line indicates mean coverage.

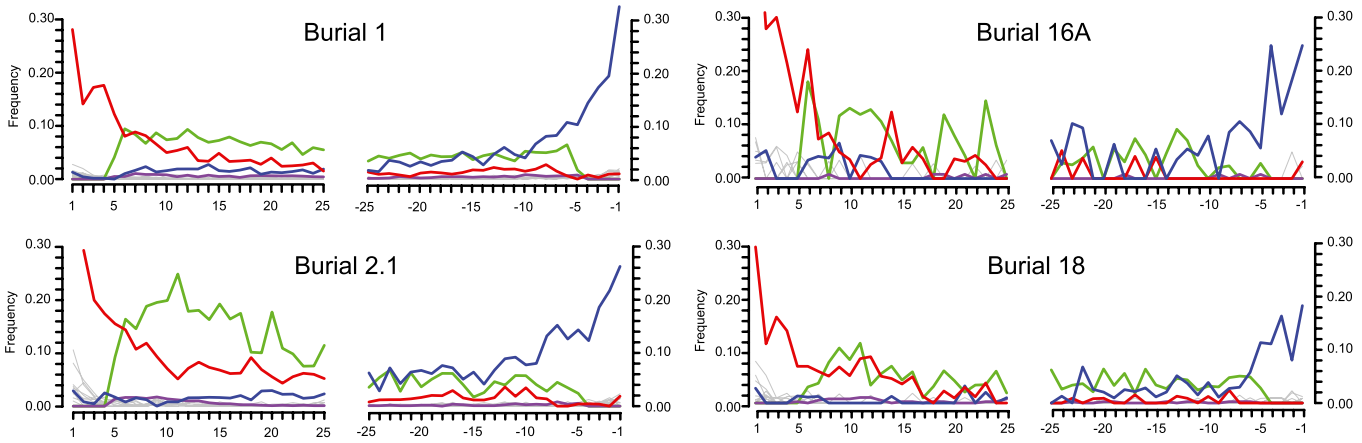

Fig. S3. C to T nucleotide misincorporations at the first and last 25 bases of endogeneous mtDNA fragments from burials 1, 2.1, 16A, and 18. Red, T; green, C; blue, A; purple, G. Note the increased frequency of T at the 5′ end and A at the 3′ end (G to A misincorporation on the opposite strand of C to T misincorporation), which is a typical pattern for aDNA damage (1–3).

1. Briggs AW, et al. (2007) Patterns of damage in genomic DNA sequences from a Neandertal. *Proc Natl Acad Sci USA* 104(37):14616–14621.
2. Krause J, et al. (2010) A complete mtDNA genome of an early modern human from Kostenki, Russia. *Curr Biol* 20(3):231–236.
3. Sawyer S, Krause J, Guschanski K, Savolainen V, Pääbo S (2012) Temporal patterns of nucleotide misincorporations and DNA fragmentation in ancient DNA. *PLoS ONE* 7(3):e34131.

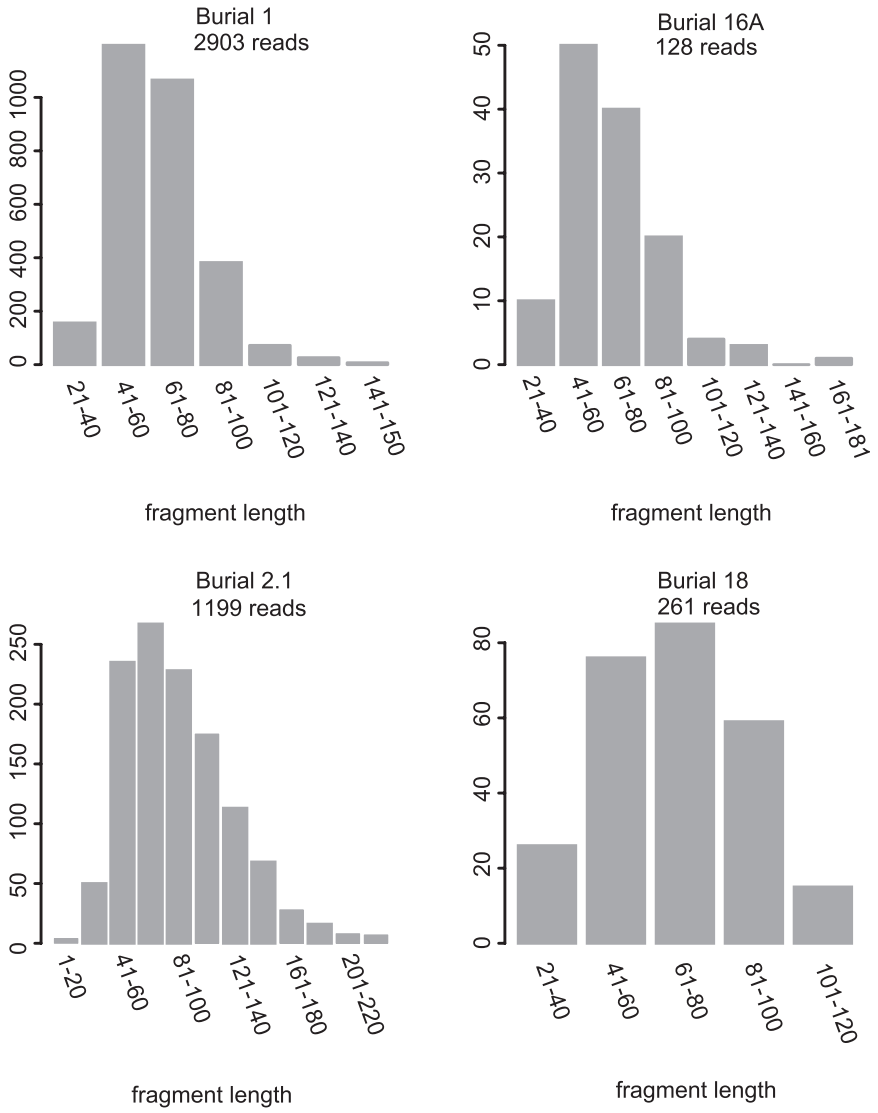

Fig. S4. Size distribution of endogenous mtDNA fragments from burials 1, 2.1, 16A, and 18. Number of reads and fragment length are provided.

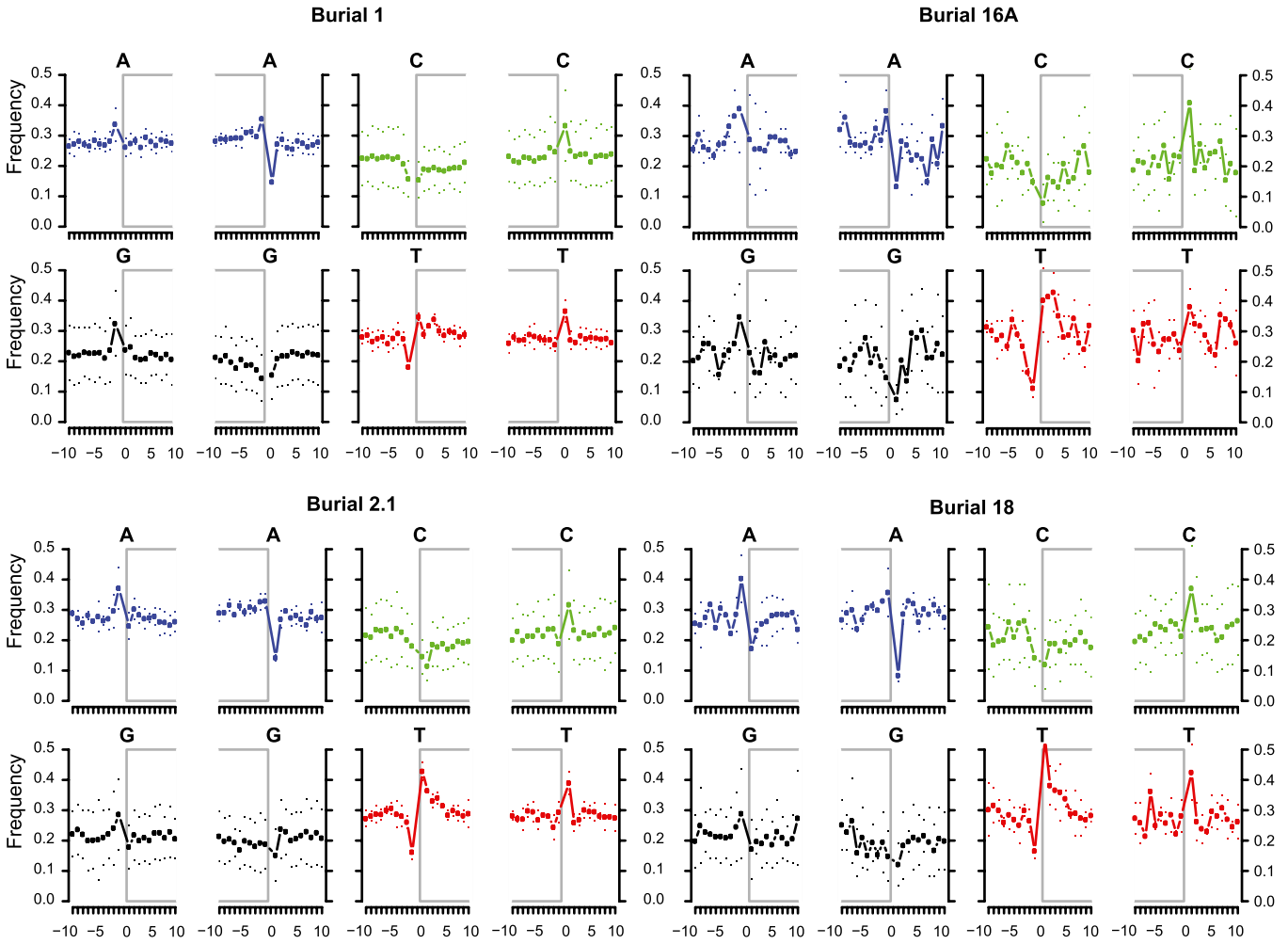

Fig. S5. Base frequency 5′ and 3′ of strand breaks. The gray brackets indicate start and end of molecules (strand breaks). Frequencies are shown for A, G, C, and T for the 10 bases 5′ and 3′ of the breaking site. Purines (A and G) show an elevated frequency before strand breaks (1).

1. Sawyer S, Krause J, Guschanski K, Savolainen V, Pääbo S (2012) Temporal patterns of nucleotide misincorporations and DNA fragmentation in ancient DNA. *PLoS ONE* 7(3):e34131.

Table S1. Number of reads supporting/conflicting with haplotype defining SNPs

Expected SNP	73 G	146 C	263 G	750 G	1185 T	1438 G	2706 G	4769 G	5465 C	6719 C	7028 T	8860 G	9123 A	10238 C	11719 A	12239 T	14022 G	14766 T	15326 G	15746 G	16189 C	16217 C	16247 G	16261 T
Burial 1																								
A				1				na					10		17				3	2				
T					13			na		1	34					12		3						12
C		7						na	2	12				1							3	6		
G	6		3	6		8	7	na				7					11		15	16			15	
Burial 2.1																								
A			1	2	na			2					2		3						na		2	
T					na						6					14		4			na			6
C		2x			na				11	8				3							na			
G	4		1	8	na	13	4	5				8					2		12	10	na	10	8	
Burial 16A																								
A	—			1																				
T					4											4								2
C		1								8				2								3		
G				1			1					4											3	
Burial 18																								
A													4		2									
T																1								
C					1				3															
G	2		1	1		1	1	2									1							

Red, ambiguity; green, conflicting reads present at this site. na, not applicable.

Table S2. Private mutations

Private mutations	4917G	8790A	12174T
Burial 2.1	5/0	5/0	
Burial 16A			4/0

Number of reads covering SNP/number of reads conflicting with consensus.

Table S3. Number of reads supporting bait (T2b) mutations

T2b mutations	709A	930A	1888A	4216C	4917G	5147A	8697A	10463C	11251G	11812G	13368A	14233G	14905A	15452A	15607G	15928A	16126C	16294T	16304C
Burial 1	5/0	3/0	5/0	11/0	12/0	8/0	13/0	6/0	13/0	25/0	12/0	13/0	23/0	11/0	10/0	6/0	8/0	4/0	7/0
Burial 2.1	5/0	10/0	7/0	2/0	5/5	5/0	9/0	11/0	13/0	8/0	9/0	6/0	9/1	10/0	8/0	5/0	3/0	2/0	4/0
Burial 16A	0/0	0/0	0/0	0/0	0/0	1/0	0/0	0/0	5/0	0/0	6/0	3/0	0/0	0/0	3/0	3/0	0/0	0/0	0/0
Burial 18	2/0	0/0	1/1	0/0	2/0	1/0	1/0	0/0	2/0	3/0	0/0	1/0	1/0	0/0	2/0	1/0	0/0	0/0	1/0

Number of reads covering informative SNP/number of those reads supporting bait. Red, reads supporting bait are present.

Table S4. GenBank accession numbers of complete mitochondrial genome sequences used for statistical parsimony network reconstruction

GenBank accession no.	Origin
AF347007	Samoa
AJ842744	Taiwan
AJ842745	Taiwan
AJ842746	Taiwan
AJ842747	Taiwan
AJ842748	Taiwan
AJ842749	Taiwan
AY289068	Cook Islands
AY289069	Cook Islands
AY289076	PNG
AY289077	PNG
AY289080	PNG
AY289083	PNG
AY289093	Samoa
AY289094	Samoa
AY289102	Tonga
AY963574	Bougainville
DQ372871	Trobriand Islands
DQ372873	Trobriand Islands
DQ372874	Kapingamarangi
DQ372875	Kapingamarangi
DQ372877	Marshall Islands
DQ372878	Vanuatu
DQ372881	Vanuatu
DQ372886	Tonga
FJ767910	Madagascar
FJ767910	Madagascar
FJ767911	Madagascar