Supporting Information

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Table S1. Primers used for the amplification of mtDNA sequences on Botocudo DNA samples

Target region	Primer	Sequences (5′–3′)	Ta*	Source
HVSI	L15989	5′- CCCAAAGCTAAGATTCTAAT -3′	60	1
	H16251	5′- GGAGTTGCAGTTGATGTGTGAT - 3′	60	1
HVSI	L16190	5′- CCCCATGCTTACAAGCAAGT -3′	60	1
	H16410	5′- GAGGATGGTGGTCAAGGGAC -3′	60	1
HVSII	L00034	5′- GGGAGCTCTCCATGCATTTGGTATT -3′	60	1
	H00160	5′- CCTGTAATATTGAACGTAGGTGCGAT -3′	60	1
14022	L13981	5′- GCCCCTACTCCTCCTAGACC -3′	60	—
	H14118	5′- GGGAAGAAGAAAGAGAGGAAGT -3′	60	—
6719	L6618	5′- CGGTCACCCTGAAGTTTATATTCTT -3′	60	—
	H6829	5′- TAGCGGAGGTGAAATATGCTC -3′	60	—
12239	L12192	5′- CGACCCCTTATTTACCGAGA -3′	60	—
	H12310	5′- TTTTGGGGCCTAAGACCAAT- 3′	60	—
15746	L15700	5′- GCCCACTAAGCCAATCACTT- 3′	59	—
	H15813	5′- CGGATGCTACTTGTCCAATG- 3′	59	—
6905	L6809	5′- GAGCATATTTCACCTCCGCTAC- 3′	60	—
	H6952	5′- CGGTGAAAAGAAAGATGAATCC- 3′	60	—
Copenhagen Replication study primers				
HVSI	L16181	5′- CATAAAAACCCAATCCACATCAA -3′	46	—
	H16204	5′- GAGGGTTGATTGCTGTACTTGC -3′	46	—
HVSI	L16208	5′- CCCCCCATGCTTACAAGCAAG -3′	46	—
	H16221	5′- GTTGATGTGTGATAGTTGAGGG -3′	46	—
HVSI	L16218	5′- CAACCCTCAACTATCACACATC -3′	46	—
	H16267	5′- AGGTTTGTTGGTATCCTAGTGG -3′	46	—
HVSI	L16171	5′- GACCACCTGTAGTACATAAAAACCCAA -3′	55	—
	H16225	5′- GTTGCAGTTGATGTGTGATAGTTG -3′	55	—
HVSII	L00034	5′- GGGAGCTCTCCATGCATTTGGTATT -3′	60	—
	H00160	5′- CCTGTAATATTGAACGTAGGTGCGAT -3′	60	—
9bp-deletion	LB	5′- AGGGCCCGTATTTACCCTAT -3′	60	—
	HB	5′- CTAAGTTAGCTTTACAGTGGGCTC -3′	60	—
14022	L13981	5′- GCCCCTACTCCTCCTAGACC -3′	60	—
	H14118	5′- GGGAAGAAGAAAGAGAGGAAGt -3′	60	—
Cloning	M13F	5′- GTAAAACGACGGCCAG -3′	55	—
	M13R	5′- CAGGAAAACAGCATGAC -3′	55	—

HVSI-HVSII, first and second hypervariable segments.
*Annealing temperature (°C).

1. Gonçalves VF, et al. (2010) Recovering mitochondrial DNA lineages of extinct Amerindian nations in extant homopatric Brazilian populations. *Investig Genet* 1(1):13.

Table S2. Restriction fragment-length polymorphism primers with respective annealing temperatures

Target region	Primer	Primer sequences (5′–3′)*	Enzyme\defining marker	Ta (°C)
Hg A	L607	5′- CACTGAAAAATGTTTAGACGGG -3′	HaeIII 663 (+)	60
	H707	5′- GGGATGCTTGCATGTGTAATC -3′		
Hg B	L8209	5′- CATCGTCCTAGAATTAATTCC -3′	9-bp deletion†	60
	H8304	5′- CTTTACAGTGGGCTCTAGAGG -3′		
Hg C	L13209	5′- CGCCCTTACACAAAATGACATCAA -3′	*Alu*I 13262 (+)	60
	H13301	5′- GGTTGGTTGATGCCGATTGTA -3′		
Hg D	L5150	5′- CCTACTACTATCTCGCACCTG -3′	*Alu*I 5176 (–)	60
	H5217	5′- AGAGGAGGGTGGATGGAATTA -3′		

*All primers sequences were obtained from the literature (1).
†Between *COII* and *tRNA* (Lys) genes in the coding region of the mtDNA.

1. Alves-Silva J, et al. (2000) The ancestry of Brazilian mtDNA lineages. *Am J Hum Genet* 67(2):444–461.