

Table 1

Samples in the Study Population

HA LOG O DEFINITION	NO. OF SAMPLES	
	a	b
H: -7025AluI, -10394DdeI	188	31
: -		

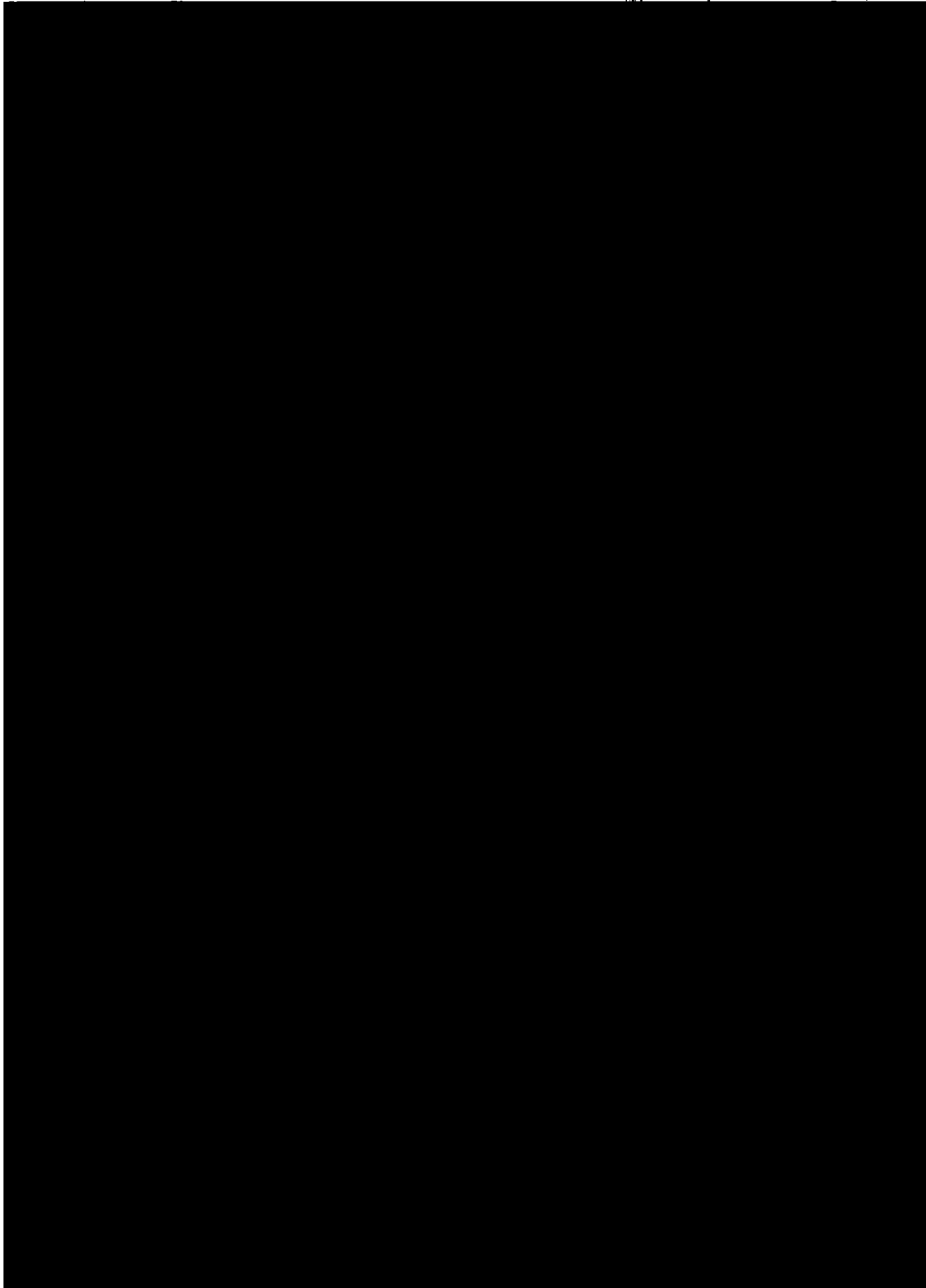


Figure 1

The figure shows a comparison of DNA sequences from two sources: the *Arabidopsis thaliana* genome (GenBank accession number AF346980) and a library of 192 *Arabidopsis thaliana* DNA fragments (GenBank accession number AF123456). The sequences are aligned, and the differences are indicated by arrows. The mutations are: 3423G→T, 4985G→A, 9559G→C, 11335G→C, 13702G→C, 14199G→T, 14272G→C, 14365G→C, 14368G→C, 23106C→T. The symbols used are: # = insertion, * = deletion, @ = match, and ; = mismatch.

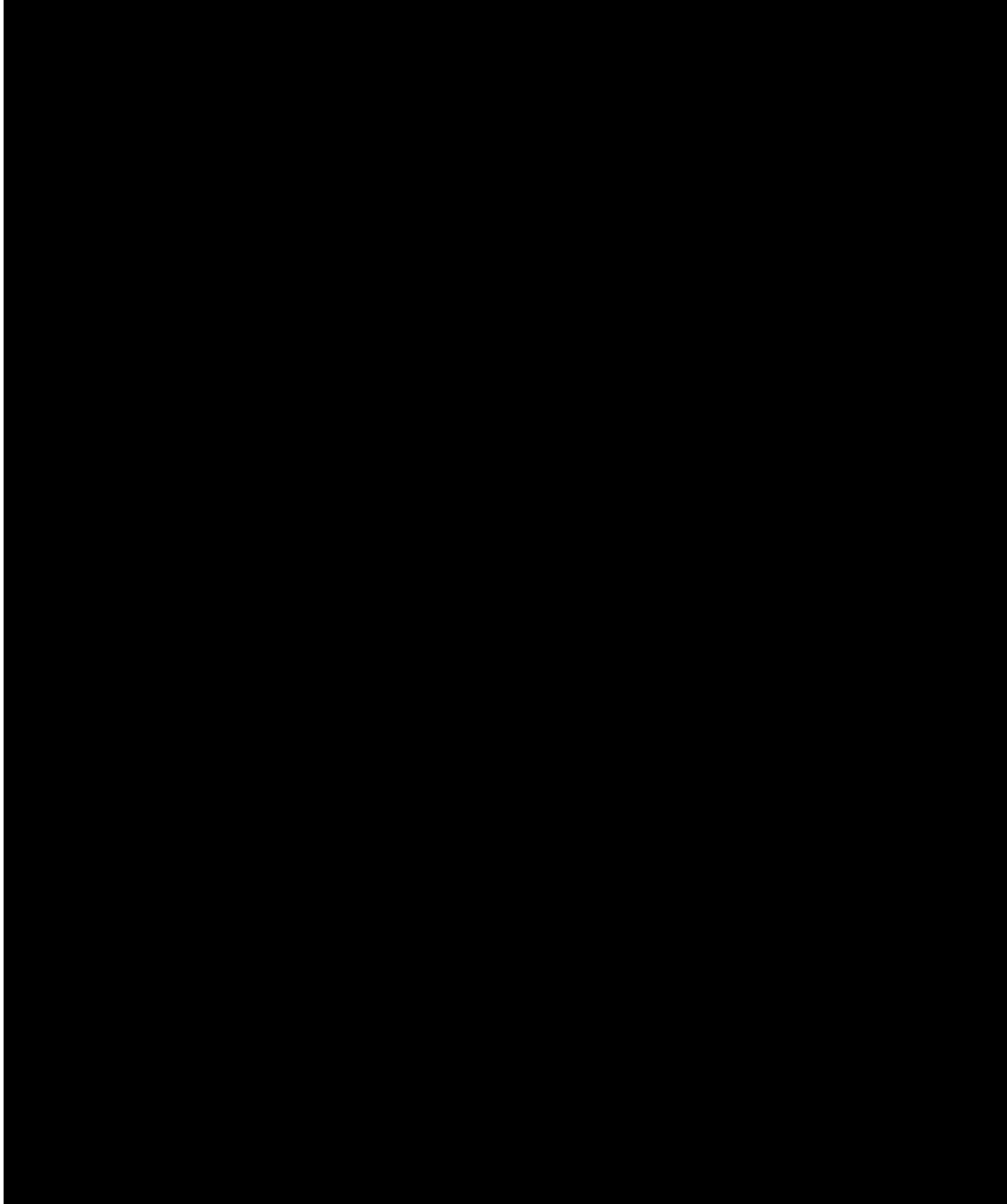
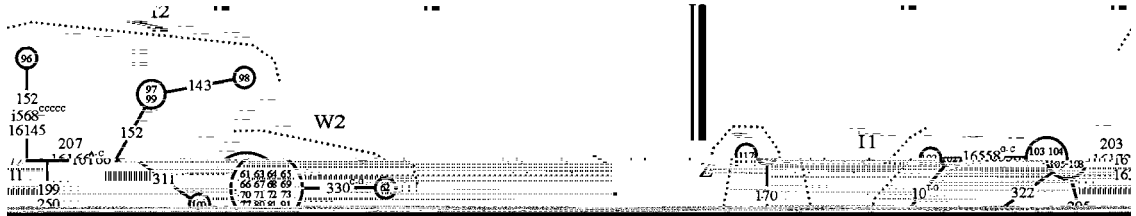


Figure 2. Schematic diagram of DNA sequence alignment. The sequence is shown with various annotations including node numbers (90, 152, 1568, 16145, 207, 152, 97, 99, 143, 98, 311, 61, 63, 65, 66, 67, 68, 69, 70, 71, 72, 73, 330, 170, 10, 322, 16558, 103, 104, 203, 16) and labels (W2, II). The sequence is aligned with a reference sequence (AF346980). The alignment is shown with a vertical double line and a barcode-like pattern below the sequence line.

Table 3

Parallel Mutations Detected in the Coding Region of mtDNA in 192 Finnish Samples

POSITION	GENE	AMINO ACID POSITION	HAPLOGROUP					
			H	K	J	I	Z	

Table 4

Parallel Mutations Detected in the D Loop of mtDNA in 192 Finnish Samples

POSITION	Nucleotide Change	Haplotype									
		H	K	T	J	I	#	Z			
16051	A→G	-	-	2	-	-	-	-	-	-	-
16093	T→C	-	-	+	+	-	-	-	-	-	-
16129	G→A	-	-	+	-	-	-	-	+	-	+
16145	G→A	-	-	-	-	-	+	-	+	-	-
16146	A→G	-	-	+	-	+	-	-	-	-	-
16172	T→C	-	-	-	-	+	+	-	+	-	-
16182	A→C	-	-	-	-	2	-	-	-	-	-
16183	A→C	-	-	+	-	2	-	-	-	+	-
16186	C→T	-	-	-	-	+	2	-	-	-	-
16189	T→C	-	-	4	-	2	+	-	-	+	-
16192	C→T	-	-	3	-	-	+	-	-	-	-
16223 ^b	C→T	-	-	+	-	+	-	+	+	+	+
16224	T→C	-	-	-	+	-	-	-	-	-	+
16256	C→T	-	-	+	-	+	-	-	-	-	-
16261	C→T	+	-	-	-	-	+	-	-	-	-
16274	G→A	+	-	-	-	-	+	-	-	-	-
16278	C→T	-	-	-	-	-	+	-	-	+	-
16292	C→T	-	-	-	-	+	-	+	-	-	-
16294	C→T	-	-	2	-	+	-	-	-	-	-
16298	T→C	-	+	-	-	+	-	-	-	-	+
16304	T→C	+	-	-	-	2	-	-	-	-	-
16311	T→C	-	-	+	+	-	+	-	+	-	-
16362	T→C	-	-	2	-	-	-	-	-	-	-
16558	G→A	-	2	-	-	-	-	-	+	+	-
73 ^c	A→G	+	-	+	+	+	+	+	+	+	+
93	A→G	-	3	-	-	-	-	-	-	-	-
143	G→A	-	-	-	-	-	-	+	+	-	-
146	T→C	+	-	+	+	-	-	-	-	-	-
150	C→T	-	-	+	-	-	2	-	-	-	-
152	T→C	+	-	+	+	+	+	-	+	-	+
185	G→A	-	-	-	-	-	2	-	-	-	-
188	A→G	-	-	-	-	-	3	-	-	-	-
189	A→G	-	+	-	-	-	+	+	-	-	-
195	T→C	-	+	+	2	2	2	2	-	+	-
199	T→C	-	-	-	-	+	-	-	+	-	-
207	G→A	-	+	-	-	-	-	+	+	-	-
217	T→C	-	-	2	-	-	-	-	-	-	-
227	A→G	-	2	-	-	-	-	+	-	+	-
228	G→A	-	-	-	-	-	+	-	-	-	-
248	A→G	-	-	+	-	-	-	-	-	-	+
295	C→T	-	-	-	-	-	+	-	+	-	-
311	C→T	2	+	-	-	+	+	-	+	-	-
322	G→A	-	-	-	-	-	-	+	+	-	-
462	C→T	-	+	-	-	-	+	-	-	-	-
489	T→C	-	-	-	-	-	+	-	-	-	+
497	C→T	-	-	-	+	-	-	-	-	-	-
498	C→T	-	-	-	+	-	-	-	-	-	-
514	T→C	2	-	2	2	+	+	-	-	-	-
568	T→C	-	+	+	-	-	-	-	-	-	-

Note. The first column shows the position of the mutation in the D-loop region of mtDNA. The second column shows the nucleotide change. The third to twelfth columns show the number of samples in which the mutation was detected in the H, K, T, J, I, #, and Z haplotypes, respectively. The # haplotype is defined as the haplotype with the 16166A→G mutation. The H, K, T, J, I, #, and Z haplotypes are defined as the haplotypes with the 16166A→G, 16166A→G, 16166A→G, 16166A→G, 16166A→G, 16166A→G, and 16166A→G mutations, respectively. The # haplotype is defined as the haplotype with the 16166A→G mutation. The H, K, T, J, I, #, and Z haplotypes are defined as the haplotypes with the 16166A→G, 16166A→G, 16166A→G, 16166A→G, 16166A→G, 16166A→G, and 16166A→G mutations, respectively.

^a Nucleotide change. ^b Haplotype. ^c Haplotype. The # haplotype is defined as the haplotype with the 16166A→G mutation. The H, K, T, J, I, #, and Z haplotypes are defined as the haplotypes with the 16166A→G, 16166A→G, 16166A→G, 16166A→G, 16166A→G, 16166A→G, and 16166A→G mutations, respectively.

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 317, 321

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 c s i - i i f G a e a i i A f i a . A J
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 1174, 1183