

Table S2. Age estimates for mutations c.306+5G>A and c.1865T>A. Quantities used in the age estimation and the haplotype frequencies in controls are also shown.

Mutation	Disease haplotype map length (cM)	Haplotype frequency in controls	Recombination count in diseased families	Number of families n	Multiplier c	Age estimate (generations)	95% confidence interval (generations)	Age estimate (years)
c.306+5G>A (Ebro)	0.9796	0.069	3	17	0.2324	75	[53-122]	1,879
c.1865T>A (Jaén)	2.2578	0.048	1	12	0.2569	15	[12- 22]	384