Table S2. Diversity statistics for mtDNA per population. Nucleotide (π) and haplotype (*h*) diversities, and neutrality statistics (Fu's F_s and Fu and Li's D^*) are shown. Though neither neutrality statistic was significant at $\alpha = 0.05$, only samples TAR and SCA show an increase in new mutations with negative D^* values.

Sample	n, mtDNA	*π*	*h*	F_s	D^*
LAP	17	0.0008	0.4412	5.435	0.677
MAZ	22	0.0008	0.4156	5.709	0.064
TAR	20	0.0013	0.6158	4.087	-1.193
SCA	22	0.0013	0.5974	2.869	-1.729
CEB	18	0.0012	0.5686	4.196	-0.552
GPA	7	0.0010	0.5714	4.276	0.953
MAN	20	0.0010	0.5263	6.643	0.650