SUPPLEMENTARY FIGURE LEGENDS

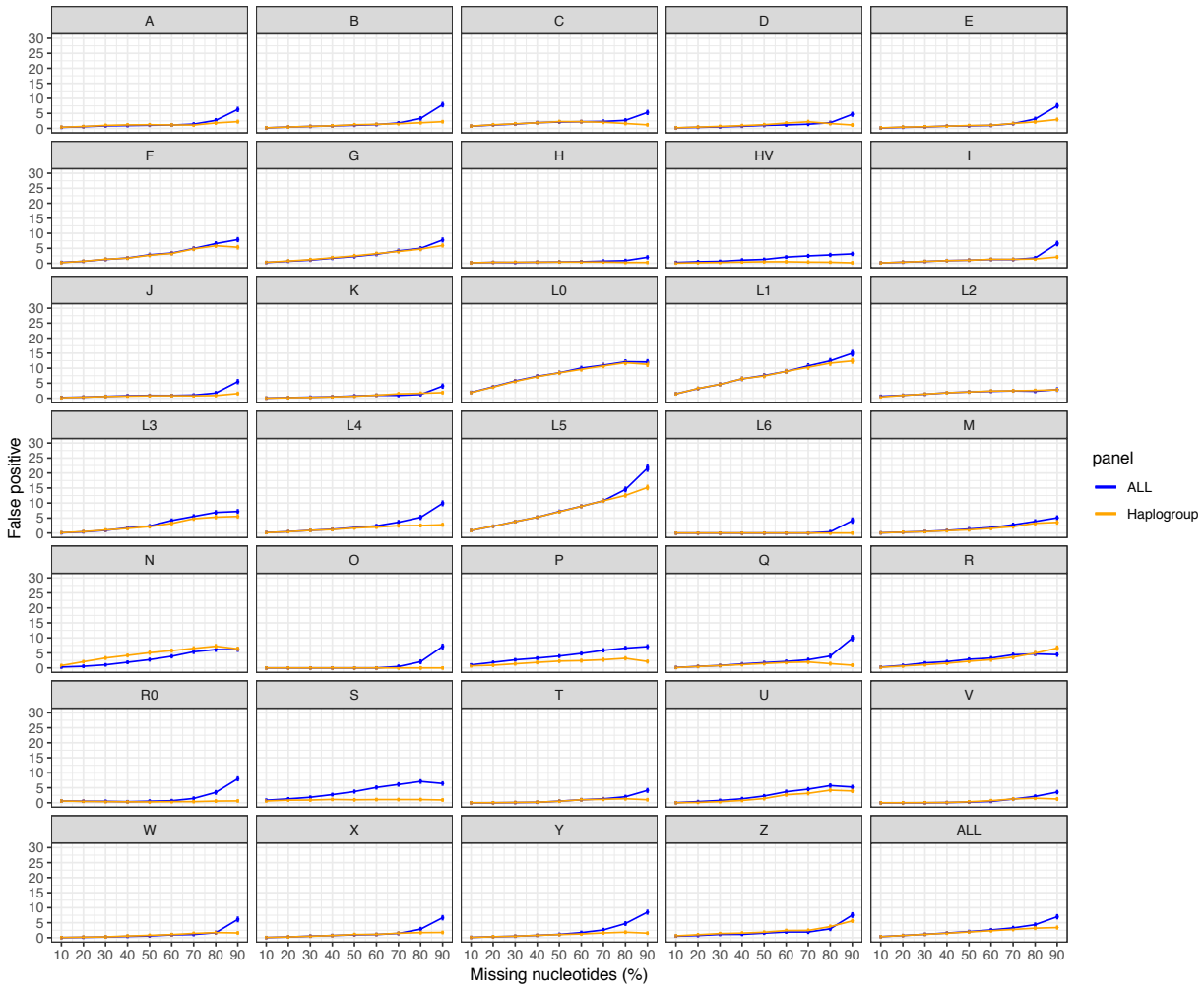

Figure S1. The impact of the loss of genome coverage on false positives.

The vertical axis shows the false positive rate, which is the number of erroneously inferred nucleotides. The horizontal axis indicates the percentage of missing nucleotides (10%–90%) in the partial mitochondrial genome sequences. Error bars indicate the standard error of the mean (SEM). The results in the case of the "ALL" panel including all macro-haplogroup lineages are indicated by the blue line, and those of the "Haplogroup" panel consisting of the same macro-haplogroup lineages are indicated by the orange line.

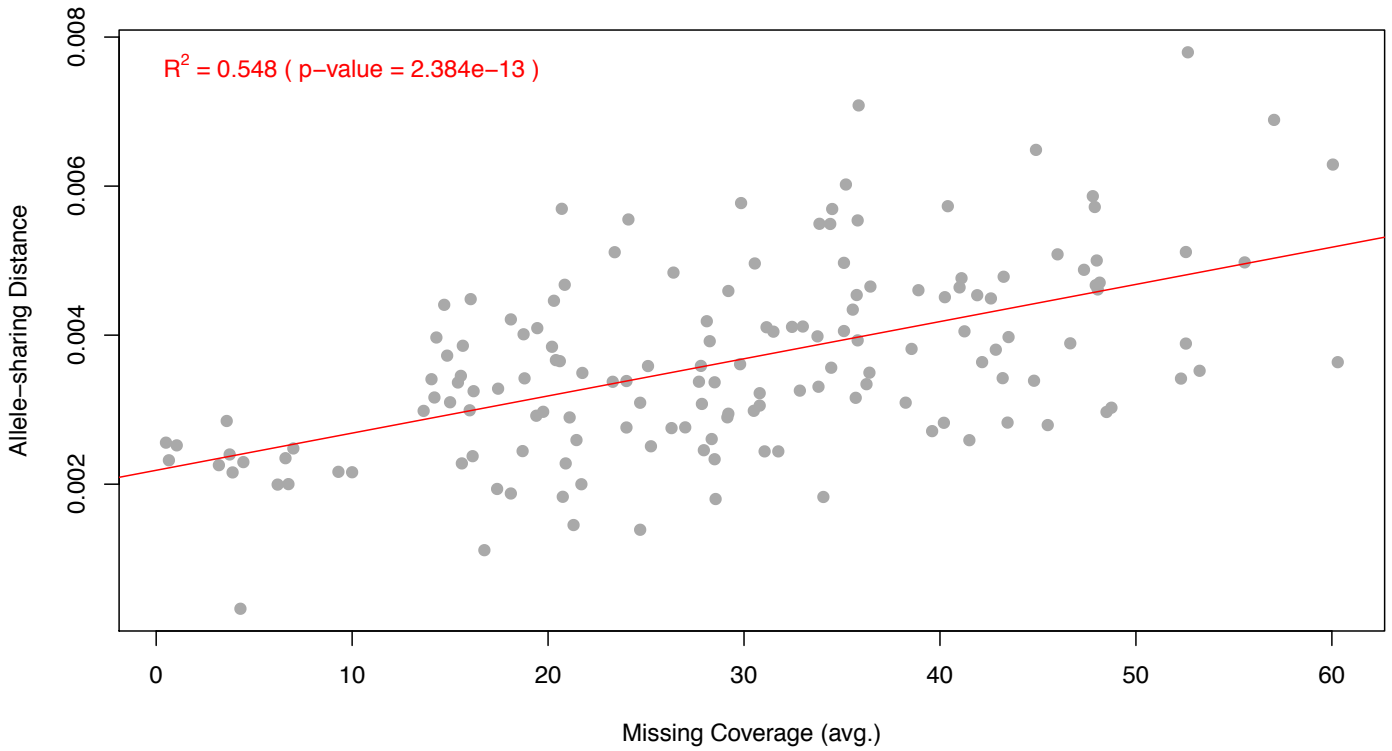

Figure S2. Scatter plot between the pairwise allele-sharing distance and the missing mitochondrial genome coverage.

This figure shows the correlation between the pairwise allele-sharing distances and the loss of mitochondrial genome coverage for the partial human mitochondrial genome sequences from Lipson et al. (2018). Pearson's correlation test was performed in R ($R^2 = 0.548$, p-value = 2.384e-13).