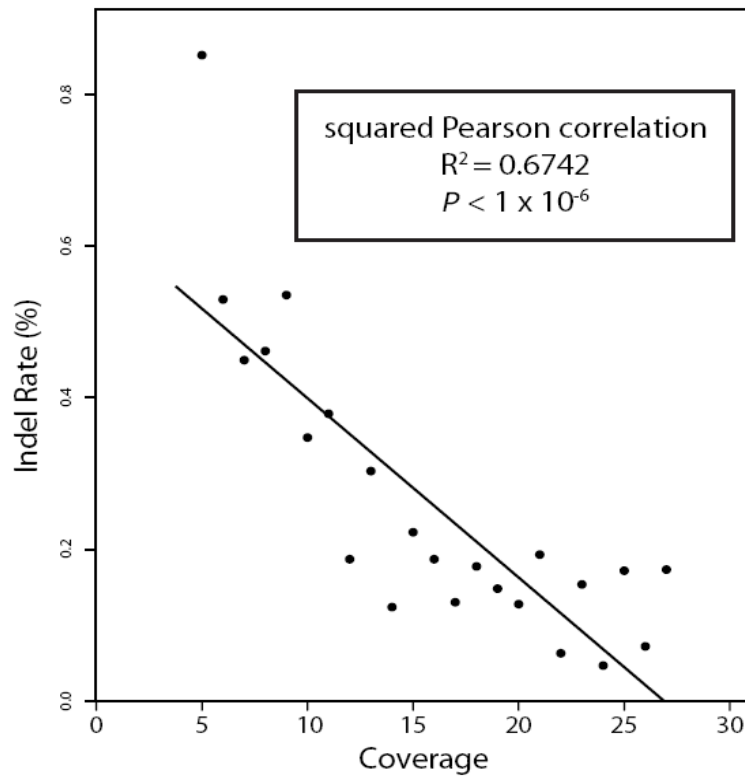


Supplementary Figure 1.

Coverage plots for all sequenced human mitochondrial genomes.



Supplementary Figure 2.

Indel rate as a function of coverage. For each fold coverage, the indel rate is calculated as the proportion of positions that were affected by an indel. Only positions that had been sequenced at least 1000 times were included and this reduced the analysis to coverages between 5 and 27. Indel rates outside of this range were considered unreliable.