

Figure S1. Graphical description of the average read depths observed in the SweGen dataset. The scatterplot (a) shows the correlation between the number of reads mapped to the mitochondrial DNA (mtDNA) reference genome and average read depth for all 934 SweGen samples. The R-squared (R^2) value for the linear regression is shown on the plot. The box-and-whisker plot (b) presents the distribution of average read depths for each coverage classification group. Haplotypes are separated based on mitochondrial genome coverage at 100X with complete, nearly complete (four or less positions below 100X), and incomplete (more than four positions below 100X) classifications.

