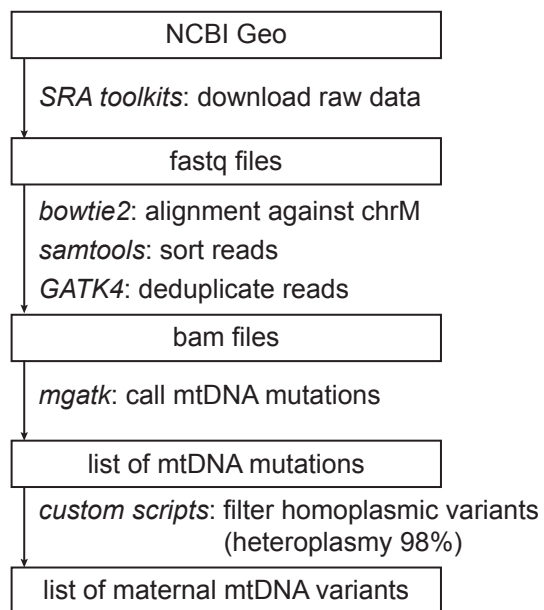
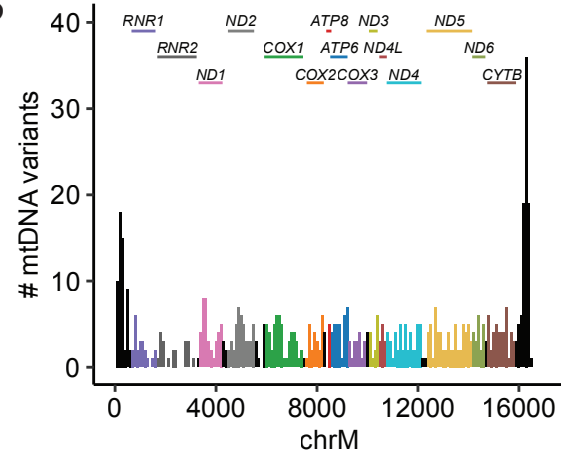
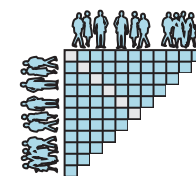
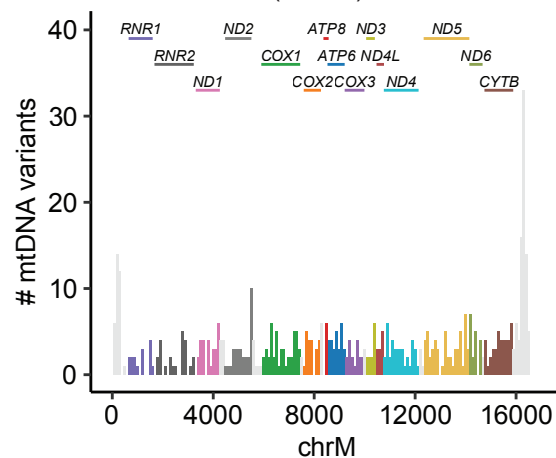
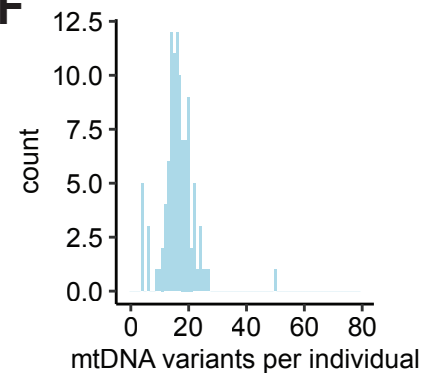
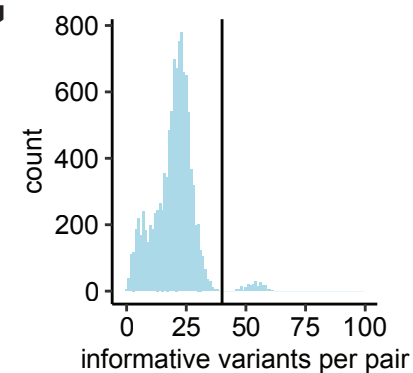
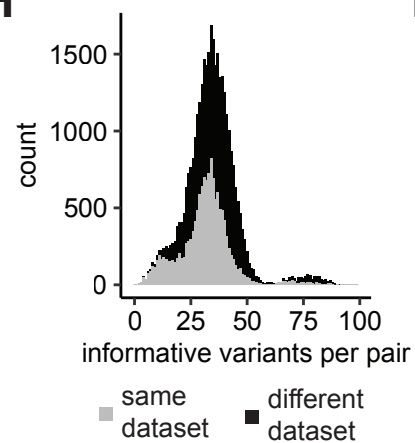
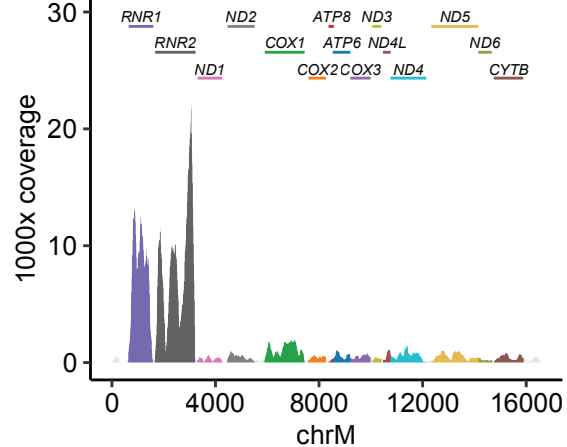
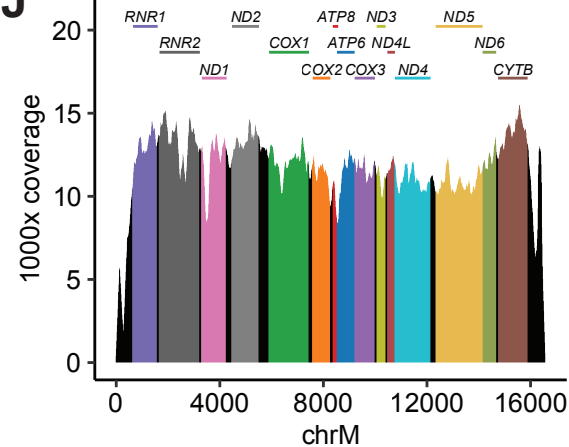


**A****B**

Hu 2022 (n=108)

RNA  
sequencing393 individual-specific  
expressed mtDNA variantsdonor - recipient  
paring simulation**E****F****G****H****I****J**

Suppl. Fig. 10. Applicability of expressed mitochondrial DNA (mtDNA) mutations to distinguish unrelated individuals. A Workflow for extraction of maternal mtDNA variants from public sequencing data (1,2). B Position of 624 homoplasmic mitochondrial DNA mutations representing maternal DNA variants that allow to identify individuals across the mitochondrial genome chrM (hg38) C A median of 30 homoplasmic mtDNA mutations (heteroplasmy >98%) per individual (range 7 – 78) were detectable in bulk mtDNA-seq datasets. D Distribution of the number of mtDNA mutations that distinguish unrelated individuals from the same mtDNA haplotype (orange) or from different mtDNA haplotypes (grey). E Distribution of expressed mtDNA mutations across the mitochondrial chromosome (hg38) identified in 108 bulk RNA-seq profiles. (2) Grey – non-expressed variants. F Number of mtDNA mutations expressed per individual. G Number of expressed mtDNA mutations that distinguish any simulated pair of two individuals. Outlier pairs with >40 mtDNA mutations are indicated by the vertical line. H Distribution of the number of mtDNA mutations that distinguish unrelated individuals from the same dataset (grey) or from different published datasets (black), indicating that the number of mtDNA mutations are not related to the underlying data source. I Coverage of transcripts across the mitochondrial chromosome obtained from bulk RNA-seq profiles. J Coverage of DNA fragments across the mitochondrial chromosome obtained from bulk mtDNA-seq profiles.