Table S1. Information on population, sample name and haplogroup for the individuals used to generate the mixtures in this study (from Strobl et. al.2019).

| Population | Sample Name | Haplogroup |
|---|---|---|
| Brazilian Native American | NaBr02 | B2e |
| Brazilian Native American | NaBr04 | A2+(64) |
| Brazilian Native American | NaBr05 | B2e |
| Brazilian Native American | NaBr06 | D1 |
| Brazilian Native American | NaBr07 | B2e |
| Brazilian Native American | NaBr08 | B+C17:C572 |
| Brazilian Native American | NaBr09 | A2ac |
| Brazilian Native American | NaBr10 | K1a4a1 |
| Brazilian Native American | NaBr11 | C1b |
| Brazilian Native American | NaBr12 | A2+(64)+16129 |

Table S2. Hamming distances within and between haplotypes used in this study.

| | |
|---|---|
| Minimum pairwise distance | 1.0 |
| Maximum pairwise distance | 56.0 |
| Average pairwise distance | 38.6 |
| Smallest minimum distance from the panel | 1.0 |
| Largest minimum distance from the panel | 39.0 |
| Average minimum distance from the panel | 9.7 |

Table S3. List of assumptions involved in the deconvolution of mtDNA mixtures using the proposed method and ramifications when these assumptions are violated. He = one copy of the alternative (i.e. non reference) allele and one of the reference; HoR = two copies of the reference nucleotide

| Assumption | Result of violation |
|---|---|
| No allelic drop-outs | The algorithm lacks information to assign dropped sites to phased haplotypes |
| No point heteroplasmies | The algorithm duplicates the heteroplasmic position in the phased haplotype |
| All He sites called | The algorithm falsely calls the position a HoR site |
| Relative proportions of allele approximately constant across all sites (i.e. low variance) | The algorithm lacks information to assign sites that deviate from other sits in relative proportion |