# Data S1
## Worked ConTAMPR Examples

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Sample: B11
Locus: mtCO1 marker

Hypothesis: DNA from Species A was contaminated with DNA from Species E
Arrows indicate base calls shared by Hap6 [A] and Hap31 [E]

Numbered arrows show peaks matching Hap31 [E] but not Hap6 [C], with relative height ranks

Sample B11 mtCO1 minority peak ranks

Species E Hap31 (as seen in Individual 81)
Sample: B14
Locus: 28S rDNA (first fragment)

Hypothesis: DNA from Species A was contaminated with DNA from Species E
Species A Hap1 shown at top

Arrows indicate base calls shared by Hap1 [A] and Hap 16 [E]

Numbered arrows indicate peaks matching Hap 16[E] but not Hap1 [A], with relative height ranks

Sample B14 28S minority peak ranks

Species E Hap16 (as seen in Individual 70)
Note that the pattern of ‘1bp-slipped’ versus ‘in-phase’ double peaks flips in opposite directions for the forward and reverse traces precisely at this 1bp indel between Species A and Species E.
Here, the small adenine peaks expected for Hap16[E] coincide with 1bp phase-shifted majority peaks. All first-ranked “minority” peaks were excluded from analysis.
Sample: D14
Locus: EPIC25 marker

Hypothesis: congruent DNA from Species A is present as expected; incongruent DNA from Species C is contamination
Species A Hap4 [A], as seen in Individual 12

Species C Hap10 shown at top

Arrows indicate base calls shared by Hap10 [C] and Hap4 [A]

Numbered arrows indicate peaks matching Hap 4 [A] but not Hap10 [C], with relative height ranks

Sample D14 EPIC25 minority peak ranks (first PCR)

NB: The EPIC25 reference haplotypes appear to have been uploaded to GenBank in the 3’ to 5’ direction, so the sequence from the forward primer (EPIC25F) is shown in reverse complement here.

Species A Hap4 [A], as seen in Individual 12

NB: Owing to alignment difficulties caused by indels such as this one, the minority and majority peaks are almost never superimposed, but shifted by different amounts in different sections.
Here, we can determine how many variable copy GAA tandem repeats the native Species A haplotype had. The answer is GAA$_5$, not GAA$_4$, which indicates EPIC25 Hap4 [A], not Hap1 [A]. Species C Hap10 does not have any GAA tandem repeats here at all. NB: these correspond to TTC repeats on the coding strand, as discussed by Debortoli et al. [S1].
Sample D14, EPIC25F chromatogram
“ND_25_D14-25SPEF_C05_043.scf”
Hap4 [A], not Hap3 [A]
End of readable sequence from forward chromatogram. The last indel between Hap 10 (C) and Hap 4 (A) creates so much noise that bases can no longer be reliably read after this point.
This is the end of Hap10 [C], but Hap4 [A] can be read along the chromatogram a little further, since Individual 12 was one of the samples where Debortoli et al. [S1] sequenced additional flanking regions.
Comparison of chromatograms from two replicate PCRs using Sample D14

The files from the first amplification (labelled ‘C05’) show strong peaks in both directions corresponding precisely to EPIC25 Hap4 [A], as shown previously. However, a second PCR from the same tube of template (‘B02’ files, below) showed almost no evidence of Hap4 [A]. If the ‘B02’ chromatograms had been examined alone, contamination might have been missed, and it would have been less easy to reject the hypothesis that Hap10 [C] had replaced Hap4 [A].