

## DNA: Steps for Profile Interpretation- Step 1

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**Step one**      *Identify the profile as being from a single contributor or being from multiple contributors.*

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### **Single contributor profiles**

A profile may be considered to be from a single contributor when the observed number of alleles at each locus and the peak height ratios of alleles at a locus are consistent with a profile from a single contributor. All loci should be evaluated in making this determination.

Partial profiles may also be observed. Partial profiles contain alleles from fewer loci than tested and can arise from degradation, inhibition or a limited quantity of DNA.

For the single-contributor profile, identify genotypes for all loci with a typeable signal. A locus with two distinct peaks results in a heterozygote genotype (10, 12 for example). A locus with one peak, in which the height of the peak is greater than the stochastic threshold results in a homozygote genotype (8, 8 for example). If the height of a single peak is less than the stochastic threshold, the resulting interpretation should include the obligate allele paired with any other allele (9+, for example).

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### **Multiple contributor profiles**

A profile may be considered to be a mixture of DNA from multiple contributors when:

- at least three detected alleles are present at one or more loci
- peak height ratio imbalances are observed
- peaks in stutter positions exceed the maximum stutter threshold. Refer to *DNA: Profile Quality* for information on stutter
- peaks below the detection threshold are not consistent with artifact peaks.

The entire profile must be taken into consideration when making the determination if the profile is a mixture. The presence of more than two peaks, imbalanced peak height ratios, or peaks below the detection threshold do not, by themselves, necessitate the profile being designated as a mixture. High stutter peaks, peak height ratio imbalances, noisy baselines, and tri-allelic patterns have been observed in single-source profiles.

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