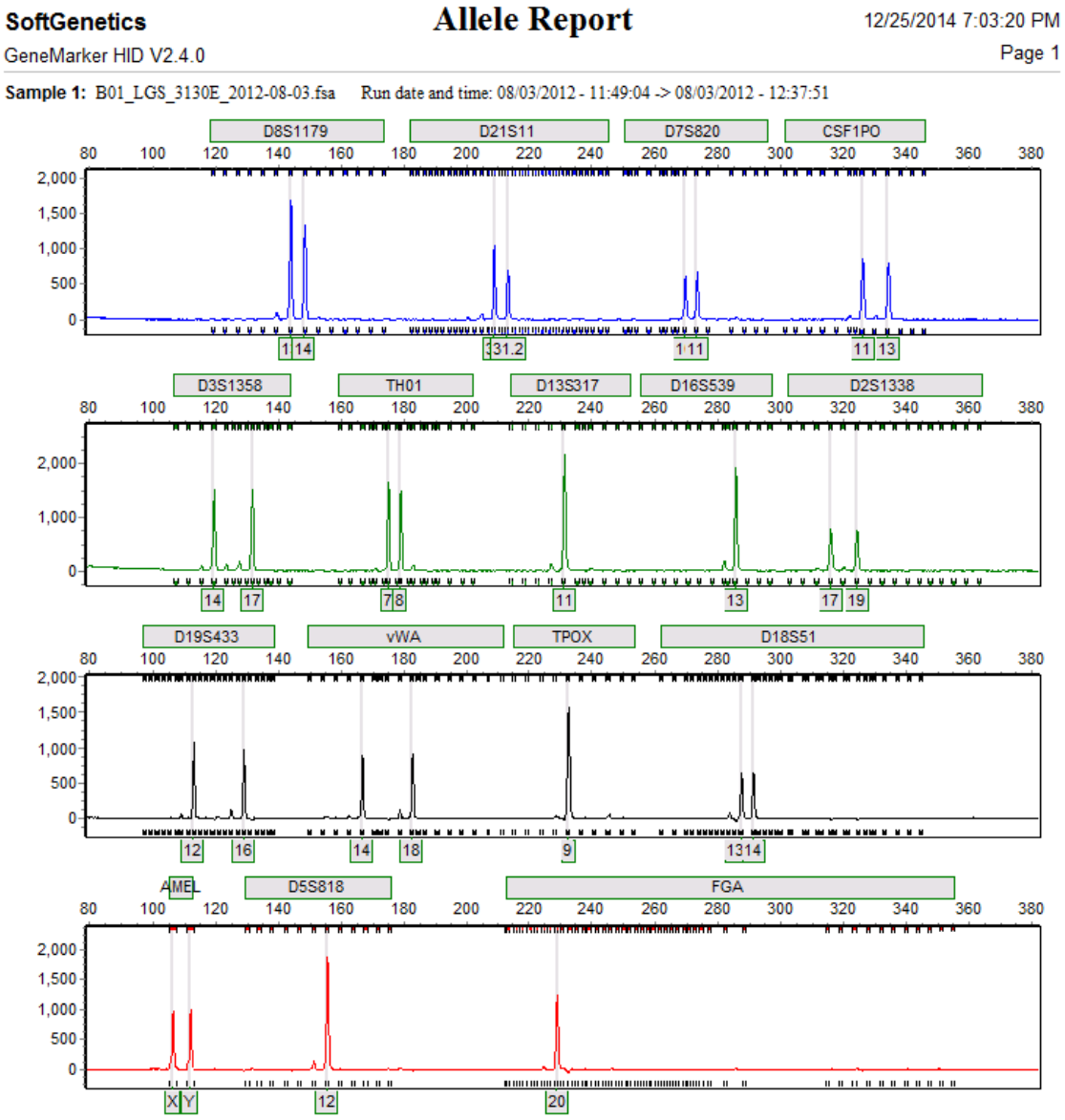
8 Questions to Ask About Forensic DNA

1. Was any human DNA detected in the sample? Forensic detection methods differ; some methods have human-specific DNA probes that monitor only human DNA in the sample, not bacterial or mold species.

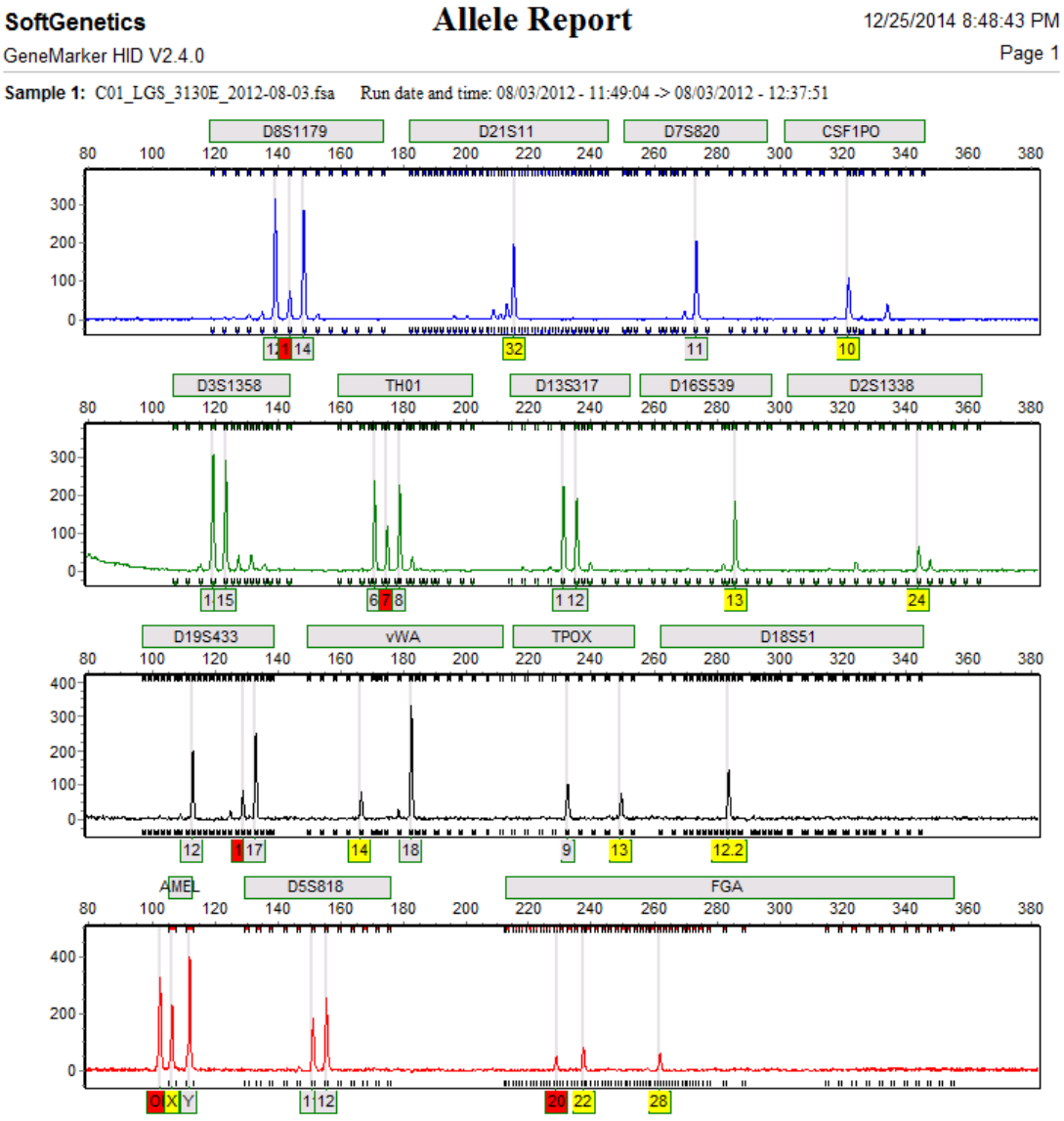
2. How much DNA was detected? Target amount for human genotyping is 1 nanogram and partial DNA profiles can be generated with the 28 cycle Identifiler method to 125 picograms. Less than 100 picograms of DNA uses high sensitivity test/low copy number methods.

3. Was a DNA profile identified from the sample? A single source or 1 person DNA sample will have no more than 2 peaks (alleles) present at any given chromosome (locus) position in the test. This is based on genetics of inheritance where one allele at any given locus is inherited from one parent (mother) and the other allele at any given locus is inherited from the other parent (father). A DNA mixture may have at least 2 sources or individuals and is defined as having 3 or more peaks (alleles) present at any given chromosome (locus) position. The minimum number of individuals should be stated in the report but in actuality more individuals may have contributed to the mixture.

Typical single source or one person sample:



Typical DNA mixture (two or more people) sample:



4. Was the DNA profile degraded? This can be visualized by the size of DNA fragment on the molecular ruler used in human identification tests that spans 0 - 500 nucleotide bases (x-axis in figures). A degraded DNA sample is typically where the larger peaks on the right are shorter or absent and the peak heights are less intense in the larger fragments.

5. Has allele drop-out occurred? This occurs in degraded DNA samples or with samples that have low amounts of DNA and essentially means alleles or information has "dropped out" of the DNA profile and no information or incomplete information was detected at a chromosome position.

6. Has allele drop-in occurred? This represents a contamination event where an allele is found in a control sample or evidentiary sample and does not represent the sample. Contamination events are most easily identified in negative control samples that should have no DNA present or if the DNA in the evidence matches to another laboratory person on file. A log of contamination events is kept by the Quality Assurance Manager and can be requested for a case or for the laboratory. From this log, one can calculate estimated frequency of events (contamination rate) and likely sources and potential causative reasons for contamination.

7. Are there other explanations for how the DNA came to be at the scene or on the object or person? Other explanations include deposition at an earlier time, accidental transfer from inadvertent contact between evidentiary items or personnel, and false inclusions resulting from coincidental matching of alleles.

8. Was the most appropriate statistical database and statistical calculation used to come to the most scientifically accurate conclusion for the DNA samples in the case? Most forensic laboratories use a random match probability (RMP) estimate which allows for report statements such as included, excluded or inconclusive. Some laboratories are using probabilistic genotypic software programs and likelihood ratios (LR) which allow for only two options in reporting such as exclude or include and use a numeric rating scale to demonstrate strength of the association of an individual to the DNA from the evidence.