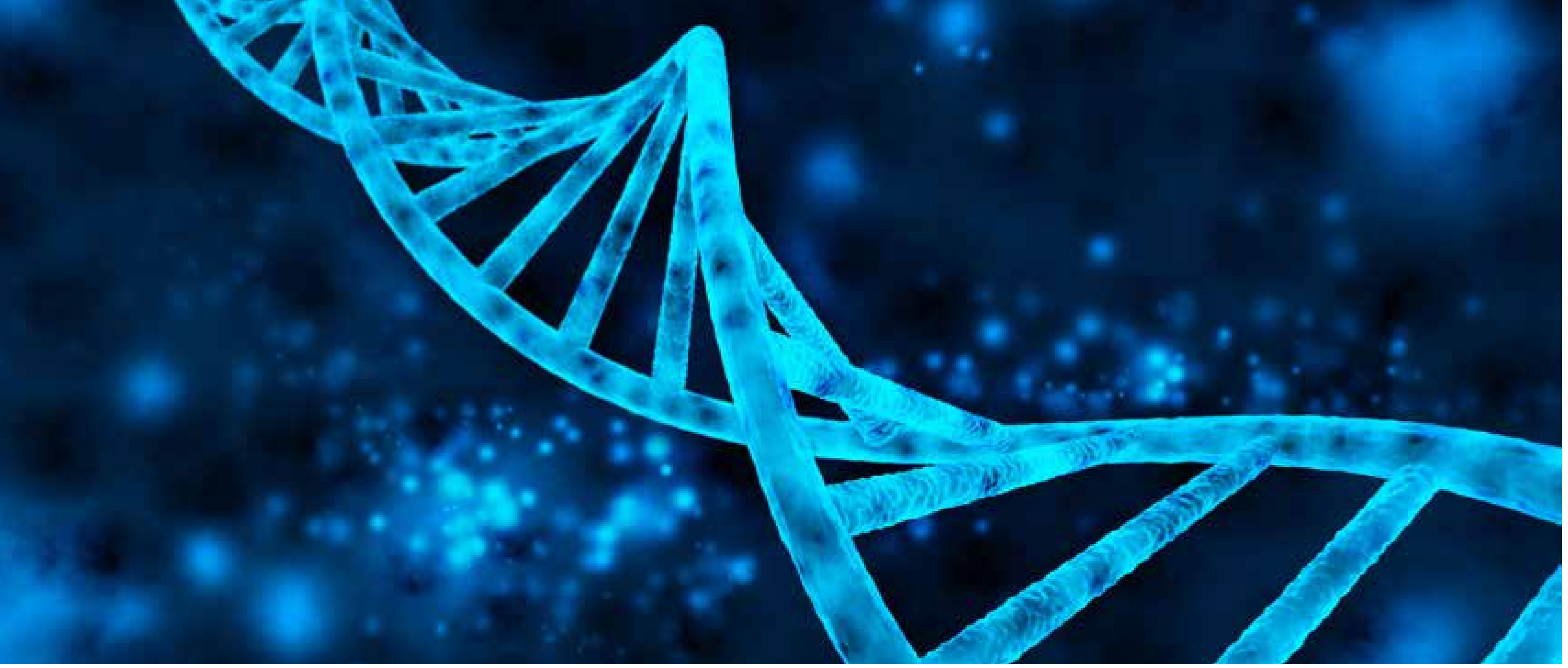
Probabilistic genotyping

Implementation support from our Human
Identification Professional Services (HPS) team



Probabilistic genotyping refers to the use of biological modeling, statistical theory, computer algorithms, and probability distributions to calculate likelihood ratios and infer genotypes of a DNA profile.* Probabilistic genotyping is an advanced approach to the statistical analysis of DNA mixtures developed in response to the increased complexity of DNA samples submitted to DNA laboratories.

Streamline your probabilistic genotyping with HPS

The validation of probabilistic genotyping software requires generating hundreds of DNA profiles using the laboratory's amplification and capillary electrophoresis parameters. The number and variety of single-source and mixture samples required are typically beyond the scope of what was assessed during the internal validation of a laboratory's STR amplification kit. Laboratories implementing probabilistic genotyping must spend a significant amount of time and resources to identify, prepare, and genotype the necessary samples for validation.

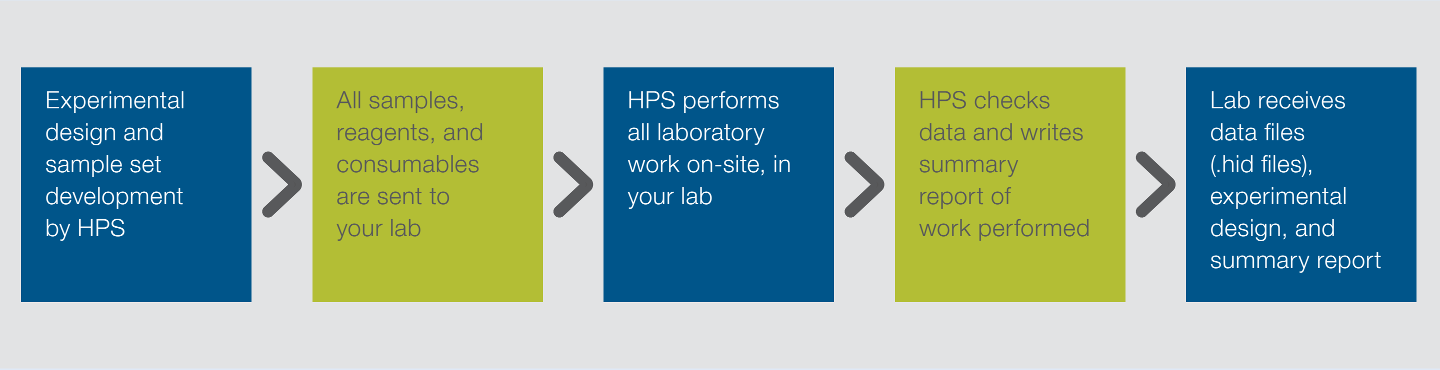
The probabilistic genotyping implementation support package from HPS includes provision of the experimental design, all applicable sample sets, on-site laboratory work, and summary report. Our validation application specialists will prepare, quantify, amplify, and run the samples needed for the validation of your probabilistic genotyping software, saving you months of hands-on laboratory work (Figure 1).

Samples for software parameter settings

- The sample set provides data to determine the initial software parameter settings needed before your laboratory can perform the validation of the probabilistic genotyping software (Figure 2)
- The sample set includes single-source, casework-type samples with corresponding reference samples for use with software parameter settings

Samples for internal validation

- The sample set aligns with the SWGDAM guidelines for the validation of probabilistic genotyping systems (Table 1)
- The sample set provides representative data for single-source and mixture samples (Figure 2); the data can be used by your laboratory to validate the probabilistic genotyping software



Experimental design and sample set development by HPS

All samples, reagents, and consumables are sent to your lab

HPS performs all laboratory work on-site, in your lab

HPS checks data and writes summary report of work performed

Lab receives data files (.hid files), experimental design, and summary report

Figure 1. The probabilistic genotyping implementation solution from HPS.

Sensitivity samples

132 single-source profiles of varying quantity derived from 8 different donors

- Saturated samples
- Partial profiles

Casework and reference samples

Degraded, inhibited, and low-template samples

- 90 evidence-type samples
- 90 corresponding reference samples

Mixtures

Total of 136 samples from 2-, 3-, and 4-person mixture samples

- Variable number of contributors
- Variable concentrations
- Variable contributor ratios
- Degraded contributors

Figure 2. The probabilistic genotyping implementation sample package from HPS.

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* Scientific Working Group on DNA Analysis Methods (SWGDAM) Guidelines for Validation of Probabilistic Genotyping Systems, 2015

Table 1. SWGDAM-recommended considerations that a probabilistic genotyping internal validation should address.

Sample type and parameter assessed	Samples provided in HPS implementation support
Samples with known contributors, and case-type samples	•
Saturated samples	•
Single-source samples	•
Allele drop-in	•
Forward and reverse stutter	•
Intra- and inter-locus peak variance	•
Degraded and inhibited samples	•
Mixed samples	•
Variable contributor ratios	•
Variable DNA template quantities	•
Variable number of contributors	•
Partial profiles	•

Contact your local HPS representative for more information
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