AMERICAN SOCIETY OF
CRIME LABORATORY DIRECTORS®, INC.

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ASCLD Comments to Draft of DNA Mixture Interpretation: A NIST Scientific Foundation Review (NISTIR 8351-DRAFT)

The currently proposed Draft of *DNA Mixture Interpretation: A NIST Scientific Foundation Review* (NISTIR 8351-DRAFT) includes a tremendous amount of information about forensic DNA analysis and specifically, interpretation of DNA mixtures. ASCLD thanks the authors and the DNA Mixture Resource Group for their work on this review.

The following are specific comments on the draft NIST report, our issues, and explanations along with recommended changes, where applicable, to help provide a consensus document:

1. Comment: "KEY TAKEAWAY #4.3: Currently, there is not enough publicly available data to enable an external and independent assessment of the degree of reliability of DNA mixture interpretation practices, including the use of probabilistic genotyping software (PGS) systems. To allow for external and independent assessments of reliability going forward, we encourage forensic laboratories to make their underlying PGS validation data publicly available and to regularly participate in interlaboratory studies."

Issue: The proposed NIST draft implies that because there is not enough publicly available data, the use of PGS is unreliable.

Suggested Change: ASCLD respectfully requests the authors note publicly available data is available in both the Bright article (Bright, 2018) and the FBI article (Moretti, 2017) for over 3000 samples for DNA Mixture interpretation. These 3000 plus samples were analyzed using the STRmix™ program to determine that the DNA mixture interpretation, as employed by forensic laboratories, is reliable. Prior to implementing any technology, including PGS, an accredited forensic laboratory performs validation studies that encompass the types of samples routinely tested in laboratories. These validation studies also determine the limitations of the technology.

It is not uncommon for laboratories to use DNA samples from casework and laboratory staff, friends, and family. ASCLD requests the authors acknowledge in this report that due to legal and privacy issues surrounding

the sources of these samples, laboratories may not be able to freely share the data observed. It is unclear to the reader what "reasonably accessible" means. While true that data generated by laboratories may not be found via an internet search, laboratories may be able to share such data with those interested in researching and reviewing the data such as academic institutions, assessors, customers, and organizations such as NIST.
ASCLD also requests the authors note that accredited and CODIS participating laboratories are rigorously assessed including an evaluation of validation studies and the underlying data. Policies and procedures developed and used by a laboratory are evaluated against results obtained during validation studies to ensure they are within the scope of the validation.

2. Comment: "KEY TAKEAWAY #4.4: Additional PGS validation studies have been published since the 2016 PCAST Report. However, publicly available information continues to lack sufficient details needed to independently assess reliability of specific LR values produced in PGS systems for complex DNA mixture interpretation. Even when a comparable reliability can be assessed (results for a two-person mixed sample are generally expected to be more reliable than those for a four-person mixed sample, for example), there is no threshold or criteria established to determine what is an acceptable level of reliability."

Issue: The proposed NIST draft implies that the forensic laboratories' studies need to be held to a higher standard than any other science by publishing the underlying data as well.

Suggested Change: ASCLD respectfully requests that Key Takeaway #4.4 be removed. Data is available for review at forensic laboratories and is reviewed by independent auditors through the accreditation process. Validation studies are conducted following FBI Quality Assurance Standards and typically the SWGDAM guidelines. Laboratories determine a threshold or criteria for acceptable reliability dependent upon the various factors unique to each laboratory from their validation studies.

3. Comment: "KEY TAKEAWAY #4.5: Current proficiency tests are focused on single-source samples and simple two-person mixtures with large quantities of DNA. To appropriately assess the ability of analysts to interpret complex DNA mixtures, proficiency tests should evolve to address mixtures with low-template components or more than two contributors – samples of the type often seen in modern casework."

Issue: The use of lower-level complex DNA mixture proficiency tests is not a practical nor a feasible recommendation. Currently, accreditation bodies require proficiency tests to be scored in a binary manner (i.e., pass or fail). Due to the inherent variability of stochastic effects of PCR products of low-level input DNA, it would be impossible to score proficiency tests as pass/fail because the test results variability may not correlate to the proficiency and competency of the test taker.

Suggested Change: ASCLD respectfully requests that Key Takeaway #4.5 be removed or modified to change the key takeaway from "proficiency test" to "challenge test," which are not graded in the same manner.

4. Comment: 4.4 Discussion, line 3201-3204: "Based on an examination of publicly available information reviewed during the time frame of this study, there is not enough information for the authors of this report to independently assess the degree of reliability of DNA mixture interpretation at any one point in the factor space."

Issue: The DNA mixture factor space, as defined by the NIST draft, contains 26 variables (Table 4.1, page 69-70) and as such is exceedingly large and complex. Utilizing the factor space and user defined acceptability, with a potential 10 increments for each variable to cover the factor space, with 26 variables, this would require 403 septillion samples. Accreditation standards dictate that the determination of a method to be "fit for purpose" to meet the needs of the customer is the responsibility of the accredited forensic laboratory.

Suggested change: ASCLD requests that lines 3201-3204 be removed. Validation and determination of a method to be "fit for purpose" is the responsibility of forensic laboratories.

References:

Bright JA, et al., Internal validation of STRmix™ - A multi laboratory response to PCAST, *Forensic Science International: Genetics*, 6-1-2018, DOI: https://doi.org/10.1016/j.fsigen.2018.01.003

Moretti TR, Just RS, Kehl SC, Willis LE, Buckleton JS, Bright JA, Taylor DA, Onorato AJ (2017) Internal validation of STRmix for the interpretation of single source and mixed DNA profiles. *Forensic Science International: Genetics* 29:126-144.