



Quality Tracking #:	<input type="text" value="2023-051"/>	Classification:	<input type="text" value="Incident"/>
Risk Level:	<input type="text" value="Low"/>	Section:	<input type="text" value="Biology/DNA"/>
Date of Discovery:	<input type="text" value="07/05/22"/>	Date of Incident:	<input type="text" value="07/05/22"/>

Forensic Case Number(s), if applicable:	Agency Case Number(s), if applicable:
See appendix A.	See appendix A.

**Description of Nonconformance:**

As part of a retroactive audit that was conducted on all cases reported using STRmix™ related to Quality Report 2023-029, 212 additional cases were identified as containing a wide HPD interval that were not assessed as high risk. These additional cases were assessed as moderate risk when there was no change in proposition support but there was a change in verbal qualifier and/or low risk when there was no change in proposition support and no change in verbal qualifier. Some cases may contain both moderate and low risk samples.

**Additional Information:**

The Forensic Biology section recognized an inherent subtlety present in the probabilistic genotyping software that affected the reported likelihood ratios for five cases. The five cases were defined as high risk since the two primary likelihood ratios generated support for two different scenarios (inclusionary vs. exclusionary), refer to Quality Report 2023-029 for more information. In addition to these five high risk cases, 212 additional cases were identified during this audit that were classified as moderate and low risk.

The Forensic Biology section utilizes STRmix™ version 2.6.1, a probabilistic genotyping software system that is based on biological models, statistical theory and computer algorithms to assist DNA analysts in the interpretation of DNA typing results.

STRmix™ calculates a statistical result in the form of a likelihood ratio (LR). The LR is a statistical measure that considers the probability of obtaining the evidence under two different competing propositions, Hypothesis 1 (H1: prosecution hypothesis), the person of interest is the source or a contributor of DNA to a sample, and Hypothesis 2 (H2: defense hypothesis) the person of interest is not the source, nor a contributor of DNA to a sample.

The Forensic Biology section at HFSC has adopted the scale of verbal qualifiers recommended by the Scientific Working Group on DNA Analysis Methods that categorizes the weight of LR values as uninformative, limited, moderate, strong, and very strong support for one proposition relative to an alternate proposition.



The Forensic Biology section first became aware in January 2022 that in rare instances the STRmix™ version 2.6.1 may calculate lower bound highest posterior density (HPD) LR and point estimate (sub-source) LR values that largely support different propositions. This was discovered by a DNA analyst which noted that the difference in LR values in her case supported different propositions and brought this to the attention of the Technical Leader. At the time, the Forensic Biology section was reporting the lower bound highest posterior density (HPD) which is a conservative estimate of the likelihood ratio (LR), as required per the DNA Interpretation Standard Operating Procedure (SOP).

While investigating the difference between these two LR values, the section discovered that the manufacturer of STRmix™ published an article titled “Why do my LR and HPD values differ?” in February 2020. This article discussed the rare instances where the sub-source LR and the HPD LR values can vary significantly and referred to this as a “wide HPD interval”. According to the manufacturer’s article, these “wide HPD intervals” may be caused by an allele that is rare or unseen within the allele frequency database, particularly if it is being modeled within Hypothesis 1 as drop-in and/or very low weight assigned to the genotype set aligning with the person of interest. The manufacturer of STRmix™ recommended three options for reporting the LR in these scenarios: 1. report the point estimate (sub-source LR), 2. report the lower bound interval, 3. report both point estimate and the lower bound interval. The manufacturer cautioned that it would be misleading to only report the relatively strong LR in favor of exclusion when the point estimate strongly supports inclusion. Conversely, they also stated that it would also be misleading to solely report the point estimate without indicating that a significant portion of the LR distribution supports exclusion. The manufacturer also stated that all these options are acceptable if analysts can explain them appropriately during testimony and it is the laboratories responsibility to determine the manner in which LR values should be reported.

To identify additional instances of “wide HPD intervals” that occurred in casework, the aforementioned retroactive audit was conducted on all data generated by STRmix™ since the software was first implemented in December 2019 (timeframe audited: December 2019 through May 1, 2023) resulting in a total of 8,359 calculations from 1,153 cases.

From the audit the Technical Leader and Assistant Technical Leader identified the following three types of scenarios of “wide HPD interval” and their risk was assessed:

**High Risk:** change in proposition support. For example, one likelihood ratio may state “limited support [NAME] is not a contributor to the DNA profile.” While the other likelihood ratio states “limited support [NAME] is a contributor to the DNA profile.”. See quality report 2023-029 for further information.

**Moderate Risk:** no change in proposition support; however, the weight of the verbal qualifier changes. For example, one likelihood ratio may state “moderate support [NAME] is not a contributor to the DNA profile.” While the other likelihood ratio states “very strong support [NAME] is not a contributor to the DNA profile.”.

**Low Risk:** no change in proposition support and no change in the weight of the verbal qualifier. For example, both likelihood ratios would state “very strong support [NAME] is not a contributor to the DNA profile.”.



The DNA analysts were informed of the “wide HPD interval” at the DNA analyst meeting on July 5, 2022, and instructed to contact the Technical Leader if they came across a “wide HPD interval” instance in casework to assess how to proceed.

The Technical Leader consulted several STRmix™ reporting laboratories and there was no clear consensus on the best reporting practices for these instances.

The DNA Interpretation SOP was revised on September 6, 2023, to implement the reporting of the sub-source LR to mitigate future instances of reporting the lower bound HPD LR.

The report template was also revised on September 6, 2023, to modify note #13 in the “Notes” section from “The LR is a statistic that considers the probability of obtaining the evidence given two competing explanations, Hypothesis 1 and Hypothesis 2. The LR reported is a lower bound highest posterior density (HPD) which is a conservative estimate of the LR. The LR reported is the lowest LR for African American, Asian, Caucasian, or Hispanic populations, using allele frequencies taken from the revised “U.S. population data for 29 autosomal STR loci.” Forensic Sci. Int. Genet. 7: e82-e83 and Forensic Sci. Int. Genet. 31: e36-e40.” to “The LR is a statistic that considers the probability of obtaining the evidence given two competing explanations, Hypothesis 1 and Hypothesis 2. The LR reported is the lowest LR for the African American, Asian, Caucasian, or Hispanic populations, using allele frequencies taken from the revised “U.S. population data for 29 autosomal STR loci.” Forensic Sci. Int. Genet. 7: e82-e83 and Forensic Sci. Int. Genet. 31: e36-e40.”

HFSC acknowledges that once future versions of STRmix™ are validated reporting of the lower bound HPD LR may be feasible.

#### Summary of Root Cause Analysis:

The cause of this issue is outside the control of the Houston Forensic Science Center as this subtlety is inherent to the STRmix™ version 2.6.1 software. This quality report is being used to document the retroactive audit and additional actions taken on “moderate risk” and “low risk” scenarios by the Forensic Biology section.



**Actions Taken:**

As a result of the thorough investigation into the "wide HPD interval" scenarios, the Technical Leader determined that for "high risk" cases, it was not appropriate to report only the HPD LR, see Quality Report 2023-029 for further information on "high risk" cases.

A further review was carried out on the other types of cases that were identified as having a "wide HPD interval" and were classified as either "moderate risk" or "low risk" cases. A total of 34 "moderate risk" cases and 145 "low risk" cases were identified (a total of 212). Within these 212 cases, 33 cases include both "moderate risk" and "low risk" scenarios.

As a result of this audit and in an abundance of caution, the cases identified as "moderate risk" and "low risk" were evaluated by the Technical Leader and Assistant Technical Leader. Based on the evaluation of each risk level the following was determined:

For "moderate risk" samples HFSC will issue a supplemental report with the sub-source likelihood ratio statistic, at the request of the associated stakeholder.

For "low risk" samples HFSC will not report any additional likelihood ratio calculations for those cases because the verbal qualifier will not change. Refer to Appendix A for a list of cases identified as moderate and/or low risk cases.

Section Manager: Courtney Head \_\_\_\_\_

Date: 05/08/24 \_\_\_\_\_

Division Director: Amy Castillo \_\_\_\_\_

Date: 06/05/24 \_\_\_\_\_

Technical Leader: Cheron Maxwell \_\_\_\_\_

Date: 05/08/2024 \_\_\_\_\_

CODIS Administrator: Jennifer Clay \_\_\_\_\_

Date: 05/08/2024 \_\_\_\_\_

Quality Director: Jackeline Moral \_\_\_\_\_

Date Closed: 06/10/24 \_\_\_\_\_



Appendix A

Low Risk Cases				
155676896	2018-08048	2019-20155	2020-17054	2021-27780
2010-01197	2018-09518	2019-20418	2021-18002	2021-28666
2010-25942	2018-19611	2020-00274	2021-18375	2021-29402
2011-14276	2018-19629	2020-00357	2021-18444	2021-29659
2012-17494	2018-19630	2020-00558	2021-19647	2021-31046
2013-31530	2019-00818	2020-00630	2021-19706	2021-31471
2014-10441	2019-05111	2020-00802	2021-19999	2021-31929
2014-23668	2019-07212	2020-01074	2021-20028	2021-32395
2014-23889	2019-08601	2020-01212	2021-20677	2021-32601
2015-00480	2019-09343	2020-01848	2021-20940	2021-32902
2015-03830	2019-09471	2020-01859	2021-21182	2021-33016
2015-09939	2019-10950	2020-02022	2021-21592	2021-33363
2015-14845	2019-12381	2020-02461	2021-21853	2021-33602
2016-04094	2019-13402	2020-03870	2021-22744	2021-34544
2016-10505	2019-13587	2020-04131	2021-24011	2021-34821
2016-13015	2019-14020	2020-04771	2021-24060	2021-35594
2016-18382	2019-14186	2020-05492	2021-24081	2022-00162
2016-20625	2019-14968	2020-06617	2021-24206	2022-00560
2016-21356	2019-15347	2020-06710	2021-24465	2022-00663
2016-24255	2019-16100	2020-07379	2021-24499	2022-00868
2017-00604	2019-16349	2020-07665	2021-25213	2022-01507
2017-13448	2019-16809	2020-09351	2021-25216	2022-02160
2017-16386	2019-16896	2020-09856	2021-25221	2022-02314
2017-16390	2019-16910	2020-11310	2021-25346	2022-02698
2017-17946	2019-17232	2020-11503	2021-25671	2022-03658
2017-19781	2019-17380	2020-12253	2021-25993	2022-09094
2017-23051	2019-18399	2020-13750	2021-26102	2022-12548
2018-00768	2019-18683	2020-13752	2021-27340	2022-12550
2018-03168	2019-19993	2020-15510	2021-27380	2023-03571



<b>Moderate Risk Cases</b>				
28940801	2019-05795	2020-08662	2021-19229	2021-33488
2016-14834	2019-14089	2020-09214	2021-26321	2021-34088
2016-24256	2019-17077	2020-11898	2021-26322	2022-00072
2018-05238	2019-18502	2020-12028	2021-28487	2022-00240
2018-06532	2019-20156	2020-13608	2021-29982	2022-00372
2018-12278	2019-20568	2020-14665	2021-31538	2022-02248
2018-17479	2020-01602	2020-15382	2021-31548	

<b>Moderate and Low Risk Cases</b>				
2016-01837	2018-09939	2019-17948	2020-11428	2021-26089
2016-05777	2018-17619	2019-18309	2020-11549	2021-27360
2016-08673	2019-04438	2019-20428	2020-15959	2021-27401
2017-02425	2019-08600	2020-02567	2020-16268	2021-33145
2017-08093	2019-09245	2020-06129	2021-20764	2022-14834
2017-11764	2019-12150	2020-07960	2021-21780	
2017-19627	2019-17168	2020-11157	2021-22722	