IN THE CRIMINAL COURT OF DAVIDSON COUNTY, TENNESSEE
DIVISION III

STATE OF TENNESSEE	)	
	)	
	)	
v.	)	Case No. 2017-C-1811
	)	
	)	
DEMONTEZ D. WATKINS	)	

ORDER

I. Introduction

This matter comes before the Court on the Defendant's motion to exclude expert testimony concerning the probabilistic genotyping conducted on the DNA evidence collected in this case. At the request of the Defendant, the Court held a Daubert hearing where the State presented the testimony of proposed trial witness Dr. Mark Perlin, Chief Scientific Officer at Cybergenetics, the company that developed the TrueAllele computer program. The defense presented the testimony of Nathanial Adams, Systems Engineer at Forensic Biometric Services, Inc., who was proffered as an expert in the field of forensic science with respect to DNA. Due to the admissibility of TrueAllele analysis being an issue of first impression in Tennessee, the parties supplied voluminous materials. Having reviewed the testimony, exhibits[1], and briefing, the Court finds the Defendant's motion to exclude shall be denied for the reasons set forth herein.

[1] Exhibits summarized in Part IV.B..

II. Factual & Procedural Background

The Defendant, Demontez Watkins, and three co-defendants—his brother Troyvonte Watkins, Rolandus Denzmore, and Davonte Sherrill—were charged with multiple offenses arising from the August 6, 2015 shooting of Reginald E. Ford, Sr. Specifically, the Grand Jury indicated all of four co-defendants on two counts of first degree murder (Count 1 charging first degree premeditated murder and Count 2 charging felony murder), two counts of attempted first degree murder (Counts 3 and 4), two counts of employment of a firearm during the commission or attempted commission of a dangerous felony (Counts 5 and 6), and one count of attempted especially robbery (Count 7).[2]

Since the Defendant, Mr. Sherrill, and Mr. Denzmore gave incriminating statements to the police, which implicated their co-defendants, their cases were severed for trial, and the State has elected to try the Defendant first.[3]

The State's theory is the Defendant shot and killed Mr. Ford and then rifled through the Mr. Ford's pants pockets. A DNA sample was obtained from inside the victim's pocket ("touch DNA"). During the Defendant's police interview (addressed in a separate order), the Defendant consented to a DNA sample. The DNA sample from the victim's pocket and the DNA swab from the Defendant were submitted for testing.

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[2] The Davidson County Grand Jury returned the seven-count indictment on August 18, 2017; said indictment superseded case number 2016-B-772 (indicted on May 20, 2016), which superseded case number 2016-A-370 (filed by direct presentment on March 22, 2016).

[3] Co-Defendant Troyvante Watkins also was severed for trial; however, since the Defendant's brother did not make any statements about himself or his other co-defendants, the State advised at the May 30, 2018 hearing on the speedy trial motion filed by Troyvonte Watkins that he could be jointly tried with any co-defendant, and the State was willing to proceed with a joint trial of Devonte and Troyvonte Watkins. Ultimately, the Defendant will be tried first.

The Metro Crime Lab performed its typical procedures for DNA extraction, amplification, and processing, and in its report dated December 1, 2015, the lab concluded, "The mixed DNA profile demonstrates the presence of at least four contributors. Due to the complexity of the mixture, no determinations will be made regarding the contributors to the mixed DNA profile."

The State sent the data generated by the Metro Crime Lab to the private company Cybergenetics where probabilistic genotyping was conducted using TrueAllele software.[4] The most succinct explanation of this program is as follows:

> Cybergenetics TrueAllele Casework is a fully continuous probabilistic approach that analyzes the electropherograms (computerized DNA data that a local laboratory extracted and amplified) and considers the genotypes (pairs of alleles) at every locus (pair of DNA sentences) of each contributor, taking into consideration the mixture weights of the contributors, the DNA template mass, polymerase chain reaction (PCR) stutter, relative amplification, DNA degradation, and the uncertainties of all these variables. Its genetic calculator uses Markov chain Monte Carlo (MCMC) to give the probabilities of all the different possibilities, not just a maximum possibility, and by using Bayes theorem, it decomposes that calculation into a prior probability and a likelihood function that compares genotypes relative to a population and computes a match LR [Likelihood Ratio].

State v. Wakefield, 47 Misc. 3d 850, 853, 9 N.Y.S.3d 540 (N.Y. Sup. Ct. 2015) (end-notes omitted).

The Defendant filed his "Motion for Daubert Hearing to Exclude DNA Evidence" on August 15, 2018, and requested this Court to determine admissibility of evidence proffered by the Nashville Crime Lab analysis and Dr. Mark Perlin of behalf of

[4] The State provided evidence related to the DNA testing and the TrueAllele Analysis in the "State's Response to Request for Discovery" filed on July 11, 2016, and the "State's Supplemental Response[s] to Request for Discovery," filed on January 9, February 14, and May 18, 2018. The Cybergenetics reports also are available on the disc admitted as Ex. 3.

Cybergenetics. The Court granted the request, and due to the expert witnesses' schedules, the Court held a bifurcated Daubert hearing on September 12 and October 30, 2018. The State's witness, Dr. Mark Perlin, and the defense witness, Nathanial Adams, appeared at both hearings via videoconference. Voluminous materials, summarized in Part IV.B., were introduced into evidence during the evidentiary hearings. The defense filed a comprehensive post-hearing memorandum on November 13, 2018, styled "Motion in Limine to Exclude Expert Testimony Regarding Likelihood Ratio."

III. Overview of DNA Analysis and Probabilistic Genotyping

DNA analysis, in general, has been deemed a reliable methodology in the field of forensic science, and Tennessee courts have routinely found DNA evidence admissible.[5] At issue, is the admissibility of TrueAllele probability genotyping conducted on the "touch DNA," the term used when small quantities of DNA are left by multiple

[5] The Tennessee Supreme Court summarizes the underlying science for forensic DNA applications in State v. Begley, 956 S.W.2d 471, 473-74 (Tenn. 1997). See also State v. Harris, 866 S.W.2d 583, 586–87 (Tenn. Crim. App. 1992) (discussion of DNA molecules and DNA typing as well as the Tennessee legislature's adoption of Tenn. Pub. Acts ch. 480, § 5 concerning DNA evidence admissibility); TENN. CODE ANN. § 24-7-118. The Tennessee statute provides:

> (b)(1) In any civil or criminal trial, hearing or proceeding, the results of DNA analysis, as defined in subsection (a), are admissible in evidence without antecedent expert testimony that DNA analysis provides a trustworthy and reliable method of identifying characteristics in an individual's genetic material upon a showing that the offered testimony meets the standards of admissibility set forth in the Tennessee Rules of Evidence.

TENN. CODE ANN. § 24-7-118(b)(1) (formerly 24-7-117).

contributors on a surface.[6] In its 2016 report (admitted as Ex. 22), the President's Council of Advisors on Science and Technology explained:

> Such samples result in a DNA profile that superimposes multiple individual DNA profiles. Interpreting a mixed profile is different for multiple reasons: each individual may contribute two, one or zero alleles at each locus; the alleles may overlap with one another; the peak heights may differ considerably, owing to differences in the amount and state of preservation of the DNA from each source; and the "stutter peaks" that surround alleles (common artifacts of the DNA amplification process) can obscure alleles that are present or suggest alleles that are not present. It is often impossible to tell with certainty which alleles are present in the mixture or how many separate individuals contributed to the mixture, let alone accurately to infer the DNA profile of each individual.[7]

The Council further noted, "The fundamental difference between DNA analysis of complex-mixture samples [defined as mixtures with two or more contributors] and DNA analysis of single source and simple mixtures lies not in the laboratory processing, but in the interpretation of the resulting DNA profile."[8]

Analyses of multi-contributor samples have evolved over the last decade. "Initial approaches to the interpretation of complex mixtures relied on subjective judgment by examiners, together with the use of simplified statistical methods such as the 'Combined Probability of Inclusion' (CPI)."[9] Subjective analysis of complex DNA mixtures proved systemically problematic, as revealed in 2015.[10] In attempt to remedy this issue,

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[6] See EXEC. OFFICE OF THE PRESIDENT, PRESIDENT'S COUNSEL OF ADVISORS ON SCI. & TECH., REPORT TO THE PRESIDENT: FORENSIC SCIENCE IN CRIMINAL COURTS: ENSURING SCIENTIFIC VALIDITY OF FEATURE-COMPARISON METHODS 75 (Sept. 2016) [hereinafter "2016 PCAST Report"], *available at* https://obamawhitehouse.archives.gov/sites/default/files/microsites/ostp/PCAST/pcast_forensic_science_report_final.pdf (also admitted as Ex. 22)

[7] Id. at 21.

[8] 2016 PSCAT Report, at 75.

[9] 2016 PCAST Report, at 76.

[10] 2016 PCAST Report, at 77-78 (discussing investigation led by the Texas Forensic Science Commission statewide DNA Mixture Notification Subcommittee that revealed problems in relation to CPI

scientists developed computer programs that apply algorithms to interpret multi-contributor samples, or "probabilistic genotyping."[11]

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statistic calculations—particularly in regard to how laboratories "dealt with phenomena such as 'allelic dropout' at Particular DNA loci"—and the subsequent international panel clarifying proper CPI usage).

[11] Id. at 78. The Scientific Working Group on DNA Analysis Methods (SWGDAM)—a group of approximately 50 scientists representing federal, state, and local forensic DNA laboratories in the United States and Canada—provided the following explanation of "probabilistic genotyping" in its publication that was admitted as part of Exhibit 12:

> Probabilistic genotyping refers to the use of biological modeling, statistical theory, computer algorithms, and probability distributions to calculate likelihood ratios (LRs) and/or infer genotypes for the DNA typing results of forensic samples ("forensic DNA typing results"). Human interpretation and review is required for the interpretation of forensic DNA typing results in accordance with the FBI Director's Quality Assurance Standards for Forensic DNA Testing Laboratories. Probabilistic genotyping is a tool to assist the DNA analyst in the interpretation of forensic DNA typing results. Probabilistic genotyping is not intended to replace the human evaluation of the forensic DNA typing results or the human review of the output prior to reporting.
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> A probabilistic genotyping system is comprised of software, or software and hardware, with analytical and statistical functions that entail complex formulae and algorithms. Particularly useful for low-level DNA samples (i.e., those in which the quantity of DNA for individuals is such that stochastic effects may be observed) and complex mixtures (i.e., multi-contributor samples, particularly those exhibiting allele sharing and/or stochastic effects), probabilistic genotyping approaches can reduce subjectivity in the analysis of DNA typing results. Historical methods of mixture interpretation consider all interpreted genotype combinations to be equally probable, whereas probabilistic approaches provide a statistical weighting to the different genotype combinations. Probabilistic genotyping does not utilize a stochastic threshold. Instead, it incorporates a probability of alleles dropping out or in. In making use of more genotyping information when performing statistical calculations and evaluating potential DNA contributors, probabilistic genotyping enhances the ability to distinguish true contributors and non-contributors. A higher LR is typically obtained when evaluating a person of interest (POI) who is a true contributor to the evidence profile, and a lower LR is typically obtained when the POI is not a true contributor. While the absence of an allele or the presence of additional allele(s) relative to a reference sample may support an exclusion, probabilistic genotyping approaches allow inclusion and exclusion hypotheses to be considered by calculating a LR in which allele drop-out and drop-in may be incorporated.

Scientific Working Group on DNA Analysis Methods, SWGDAM Guidelines for the Validation of Probabilistic Genotyping Systems [hereinafter "SWGDAM Probabilistic Genotyping Guidelines"], at 2 (2015), *available at*: https://docs.wixstatic.com/ugd/4344b0_22776006b67c4a32a5ffc04fe3b56515.pdf (also available in Ex. 13 binder titled "Method Reports"; Ex. 3).

The Guidelines note "Guidance is provided herein for the validation of probabilistic genotyping software used for the analysis of autosomal short tandem repeat (STR) typing results. These guidelines are not intended to be applied retroactively. It is anticipated that they will evolve with future developments in probabilistic genotyping systems." Id. at 1-2.

Probabilistic genotypes have been recognized by regulatory bodies such as the Scientific Working Group on DNA Analysis Methods (SWGDAM) and the American National Standards Institute (ANSI). SWGDAM referenced probabilistic genotypes in its 2010 "Interpretation guidelines for autosomal STR typing by forensic DNA testing laboratories" and in 2015 SWGDAM issued guidelines for validation of probabilistic genotyping systems like TrueAllele.[12]

More than a dozen probabilistic genotyping systems currently are in use and the number is increasing. For example, PSCAT noted at least eight probabilistic genotyping software programs had been developed as of March 2014, some being open source and some commercial products.[13] According to a forthcoming article in the January 2019 publication of *Forensic Science International: Genetics*, a minimum of fifteen genotyping programs exist as of October 2018.[14]

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[12] SWGDAM Probabilistic Genotyping Guideline's, supra note 12.

[13] Id. at 78 (identifying the software programs LRmix, Lab Retriever, Like LTD, Armed Xpert, TrueAllele, STRmix, and DNA View Mixture Solution).

[14] Michael D. Coble & Jo-Anne Bright, *Probabilistic genotyping software: An overview*, 38 FORENSIC SCI. INT'L: GENETICS 219, Appendix A, Table S1 (Jan. 2019), *available at* https://www.fsigenetics.com/article/S1872-4973(18)30552-0/fulltext (posted online Nov. 11, 2018). Table S1 provides a "non-exhaustive list" of probabilistic genotyping software programs with notations about each type. Software identified and categorized as follows:

Semi-continuous software solutions
- Lab Retriever (open source)
- LRmix/LRmix Studio (open source)
- FST (Forensic Statistical Tool, created by the New York Office of the Chief Medical Examiner and used only by that office until replaced with STRmix)

Fully-continuous software solutions
- Like LTD (open source)
- TrueAllele (commercial)
- GenoProof Mixture (commercial)
- EuroForMix (open source)
- STRmix (commercial)
- Konogoh (open source)
- MaSTR (commercial)
- DNA-View Mixture Solution (commercial)

The two most widely used probabilistic genotyping programs, and thus most often addressed in the limited case law, are: (1) STRmix, which has been used by the Federal Bureau of Investigation (FBI) Laboratory since December 2015[15] and (2) TrueAllele by Cybergenetics, which is the program the State used in this case.

It is important to note that probabilistic genotyping software like TrueAllele does not retest any samples. All laboratory procedures for this case were performed by the Metro Crime Lab. The State then provided the DNA data files to Cybergenetics, which used its proprietary algorithm to provide likelihood ratios (LRs) of sample matches through its TrueAllele program.

IV. Analysis

Here, the Defendant challenges the reliability of the probabilistic genotyping analysis and moves "to exclude the expert testimony regarding the Cybergenetics computer program 'TrueAllele.'" (Motion in Limine to Exclude Expert Testimony Regarding Likelihood Ration, filed Nov. 13, 2018).[16]

- DNAmixtures (open source but requires commercial software program HUGIN to operate)
- CeesIT (freely available)
- LiRa HT (initially semi-continuous and now incorporates peak height model)
- eDNA (freely available web-based software with two programs, Bullet (semi-continuous) and BulletProof (fully-continuous) available by subscription).

Id. at Appendix A, Table S1. Additionally, this article, in Table S2, supplies a "non-exhaustive list of admissibility hearings for probabilistic software programs from Australia and the United States." Specifically, courts in Australia have addressed STRmix and TrueAllele; a court in Northern Ireland addressed TrueAllele, and courts in the United States have addressed STRmix, TrueAllele, FST, and Lab Retriever.

[15] Id. at 79, 80. At the time the PSCAT report was published (Sept. 2016), the FBI was "still in the process of publishing its own internal developmental validation." Id.

[16] Dr. Mark Perlin stated he or TrueAllele Analyst Jennifer Hornyak would testify at trial should the probabilistic genotyping evidence be determined admissible.

A. Legal Standard for Scientific Evidence

The admission of expert testimony regarding scientific and technical evidence is governed by Rules 702 and 703 of the Tennessee Rules of Evidence. McDaniel v. CSX Transportation, Inc., 955 S.W.2d 257 (Tenn. 1997). In McDaniel, the Tennessee Supreme Court promulgated the principles the trial court should consider when determining whether to admit scientific or technical evidence.

First, the evidence must be relevant to a fact at issue in the case. TENN. R. EVID. 401, 402. Second, the expert must be qualified by specialized knowledge, skill, experience, training, or education in the field of expertise, and the testimony in question must substantially assist the trier of fact to understand the evidence or determine a fact in issue. TENN. R. EVID. 702; McDaniel, 955 S.W.2d at 264; see also Otis v. Cambridge Mutual Fire Ins. Co., 850 S.W.2d 439, 443 (Tenn.1992). Lastly, when the expert witness offers an opinion or states an inference, the underlying facts or data upon which the expert relied must be trustworthy. TENN. R. EVID. 703; McDaniel, 955 S.W.2d at 264.

The trial court's role is to act gatekeeper for the admissibility of expert testimony to assure the expert's testimony is based on the same intellectual rigor that is expected of persons engaged in the relevant field of endeavor, (Kumho Tire Co. v. Carmichael, 526 U.S. 137, 152(1999); Brown v. Crown Equip. Corp., 181 S.W.3d 268, 275 (Tenn. 2005)), and that the expert's testimony will *substantially* assist the trier of fact. McDaniel v. CSX Transp., Inc., 955 S.W.2d at 264; Boles v. Nat'l Dev. Co., 175 S.W.3d 226, 235 (Tenn.Ct.App.2005); TENN. R. EVID. 702 & 703. In other words, evidence and expert

testimony regarding scientific theory must be both relevant and reliable before it may be admitted. McDaniel, 955 S.W.2d at 265.

The reliability of scientific evidence is determined by considering the following nonexclusive list of factors:

1) Whether the scientific evidence has been tested and the methodology with which it has been tested;

2) Whether the evidence has been subjected to peer review or publication;

3) Whether a potential rate of error is known;

4) Whether, as formerly required by Frye[17] the evidence is generally accepted in the scientific community; and

5) Whether the expert's research in the field has been conducted independent of litigation.

McDaniel, 955 S.W.2d at 265. Trial courts may also consider other non-definitive factors in assessing the reliability of an expert's methodology, such as the expert's qualifications for testifying on the subject at issue and the connection between the expert's knowledge and the basis for the expert's opinion. Brown, 181 S.W.3d at 274–75 (citations omitted).

Here, the Court finds the TrueAllele analysis relevant under Rule 401 because it tends to identify the Defendant as a participant in the aggravated robbery. The State's proposed expert, Dr. Mark Perlin, was shown to be extensively qualified, by education and experience, in the fields of DNA interpretation and computer science. His testimony would substantially assist the jury to understand the complex genotyping evidence.

[17] Frye v. United States, 293 F.1013 (D.C. Cir. 1923).

Accordingly, the Court now turns to its analysis of whether the TrueAllele probabilistic genotyping program satisfies the requirements for scientific reliability.

B. Materials Reviewed by the Court

Since the admissibility of TrueAllele probability genotyping is an issue of first impression in Tennessee, the parties supplied this Court with substantial materials. In addition to the testimony of the State's proposed witness, Dr. Perlin, and defense expert Mr. Adams, the parties admitted into evidence 22 exhibits, as summarized below.

Exhibit 1	**Curriculum Vitae of Dr. Mark Perlin,** CEO and Chief Scientific Officer, Cybergenetics
Exhibit 2	**TrueAllele Cases** (as of Aug. 2018)
Exhibit 3	**Disc** The DVD contains all evidence introduced as hard copies (including contents of binders marked Exhibits 5-16), the slide presentations used during the hearing testimony of Dr. Perlin (PowerPoint file titled "Demonstrative Aid"), and additional materials referenced by Dr. Perlin during his testimony.[18] The PDF titled "Read Me" provides a list of files in each folder.
Exhibit 4	**Cybergenetics Report** (Dec. 13, 2017)
Exhibit 5	**Binder titled "Background Reading"** containing a glossary and 17 publications
Exhibit 6	**Binder titled "Validation Paper"** containing 6 publications/studies
Exhibit 7A	**Binder titled "Validation Study (1)" with disc** Disc contains 34 "TrueAllele Validation Reports and Papers" and the binder contains hardcopies of 7 reports and papers
Exhibit 7B	**Binder titled "Validation Study (2)"** containing hardcopies of 9 reports and papers

[18] Cybergenetics makes much of this information available on their website, www.cybgen.com.

Exhibit 8	**Binder titled "Scientific Development"** containing 5 articles and studies
Exhibit 9	**Binder titled "Other Papers"** containing 5 publications
Exhibit 10	**Binder titled "General Acceptance"** containing 5 publications
Exhibit 11	**Binder titled "Forensic Application"** containing 9 publications
Exhibit 12	**Binder titled "Regulatory Approval"** containing 5 publications
Exhibit 13	**Binder titled "Method Reports"** containing 3 reports published by Cybergenetics/TrueAllele
Exhibit 14	**Binder titled "Related Systems"** containing 7publications
Exhibit 15	**Binder titled "Legal Commentary"** containing 6 articles from law journals and legal publications
Exhibit 16	**Binder titled "Admissibility Rulings"** containing orders, opinions, and decisions from other jurisdictions (published and unpublished) concerning the admissibility of testimony about TrueAllele analysis as well as other legal documents (transcript excerpts, motions, etc.)
Exhibit 17	**Document:** **"Access to TrueAllele Source Code by Defense Experts"**
Exhibit 18	**Lyrics to song titled "Threshold" written by Dr. Perlin** (copyrighted 2011), printed from https://soundcloud.com/markperlin/threshold
Exhibit 19	**Article:** ***NIST launches wasteful study that undermines science and justice*, Back to Newsroom** (Oct. 5, 2017) (authored by Dr. Perlin)
Exhibit 20	**Curriculum Vitae of Nathaniel D. Adams,** Systems Engineer, Forensic Bioinformatic Services, Inc.
Exhibit 21	**Declaration of Nathaniel Adams with Appendices**
Exhibit 22	**PSCAT Report**: Executive Office of the President, President's Counsel of Advisors on Science and Technology, Report to the President: Forensic Science in Criminal Courts: Ensuring Scientific Validity of Feature-Comparison Methods (Sept. 2016)

Additionally, to gain an understanding and history of probabilistic genotyping programs, the Court found useful a law journal article on black box algorithms[19] as well as open-source articles published in *Forensic Science International: Genetics.*[20]

C. Daubert Analysis Genotyping Program TrueAllele

Although an issue of first impression in Tennessee, the reliability of probabilistic genotyping has been addressed in other jurisdictions, and TrueAllele has been the subject of much of that litigation. See, e.g., Ex. 16 (binder containing 13 decisions from other jurisdictions[21]) & Ex. 3. The first case addressing the admissibility of TrueAllele

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[19] Katherine Kwong, Note, *The Algorithm Says You Did It: The Use of Black Box Algorithms to Analyze Complex DNA Evidence*, 31 HARVARD J. LAW & TECH. 275 (Fall 2017), *available at* https://jolt.law.harvard.edu/assets/articlePDFs/v31/31HarvJLTech275.pdf (article focuses on lack of transparency for source code but also provides a history for probabilistic genotyping programs).

[20] FSI GENETICS, https://www.fsigenetics.com/. See, e.g., Coble & Jo-Anne Bright, supra note 14.

[21] Exhibit 16 contains four written orders from U.S. courts as well as bench ruling transcripts and other legal documents (listed in order provided in binder):

1. Order, State v. Charles Simmer, CR16-1634 (Douglas Co., Neb., Dist. Ct. Feb. 2, 2018) (applying Daubert standard);
2. Commonwealth v. Foley, 38 A.3d 882 (Pa. Super. Ct., Feb. 15, 2012) (applying Frye standard);
3. Transcript excerpt of bench ruling, State v. Dugniqio Dishay Forest, Cause No. 82-D02-1501-F2-00566 (Vanderburgh Co., Ind., Sup. Ct. June 3, 2016) (applying Daubert standard);
4. Opinion and Order, Commonwealth. Kevin. J. Foley, No. 1170 CRIM 2007 (Indiana Co. , Neb., Ct. of Common Pleas Mar. 2, 2009) (applying Frye standard);
5. People v. John Wakefield, 47 Misc.3d 850, 9 N.Y.S.3d 540, N.Y. slip. op. 25037 (N.Y. Sup. Ct. Feb. 9, 2015) (applying Frye standard);
6. Order, State v. Maurice Shaw, Case No. CR-13-575691 (Cayhua Co., Ohio, Ct. of Common Pleas Oct. 10, 2014) (applying Daubert standard);
7. Order, Commonwealth v. Matthew Franklin Brady, Case Nos. CR11-465-01and CR11-494 (Colonial Heights, Va., Circuit Ct. Dec. 17, 2013) (applying Daubert standard);

analysis appears to be a 2009 murder case in Pennsylvania, which applied the Frye test and was affirmed on appeal. Commonwealth v. Foley, 38 A.3d 882 (Pa. Super. Ct. 2012).

Since 2011, a number of U.S. courts, have addressed the admissibility of TrueAllele, and all have found the TrueAllele evidence admissible under either the Frye or Daubert standards.[22] During Dr. Perlin's qualification as an expert in this case, he

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8. Transcript of bench ruling, Regina v. Mel Broughton, OCC Ref: T20107052 (Oxford, Eng. June 29, 2010) (finding TrueAllele results admissible);

9. Findings of Fact and Conclusions of Law, State v. Emanuel Fair, No. 10-1-09274-5 SEA (King County, Wash., Sup. Ct. Jan. 12, 2017) (applying Frye standard);

10. Transcript excerpt of bench ruling, State v. Heidi Bartlett, Case No. 1283CR0157 (Plymouth Co., Mass., Sup Ct. May 25, 2016) (finding TrueAllele results admissible) (applying Daubert standard);

11. People's Motion in Limine to Admit DNA Analysis, People v. Charles Lewis Lawton et al., No. BF 139247 ABC (Kern County, Ca., Sup. Ct. Oct. 2, 2012), with docket entry showing motion granted on Jan. 10, 2013 (applying Frye standard);

12. Defense Motion for Daubert hearing, State v. Samuel Nicholas, No. 01-13-0316 (II) (19th Jud. Dist., Baton Rouge, La. June 12, 2014), with docket entry showing motion denied Nov. 6, 2014

13. Transcript of oral ruling, Regina v. Colin F. Duffy & Brian P. Shivers, ICOS No. 09/143857 (Northern Ireland, Dec.1, 2011);

14. Transcript of bench ruling, State v. Malcom Bryan Wade, Cause No. 53C02-1411-F3-001042 (Monroe Co., Ind. Circuit Ct., Aug. 3, 2016) (applying Daubert standard); and

15. Director of Public Prosecutions v. Lian Bin "Robert" Xie, Case number 2011/00147183 (New South Wales, Australia Apr. 30, 2014).

TrueAllele evidence was also admitted in State v. Baylan Glazebrook, Case number 53C02-1411-F1-1066 (Monroe Co., Ind. Circuit Ct. Feb. 16, 2018); State v. Harold Houston, Case number 16-3682 (Jefferson Parrish, La. May 19, 2017); State v. Mathis, Case number CR-16-611539-A (Cleveland Co., Ohio Apr. 13, 2018); and State v. Jaquard Aiken, Case number 20121212-683 (Beaufort Co., S. Car. Oct. 27, 2015). Copies of court documents are also available on Cybergenetics website at https://www.cybgen.com/information/admissibility/page.shtml.

[22] Dr. Perlin provided a list of cases where he has testified, along with a list of cases where a ruling issued on a TrueAllele admissibility challenge. (Ex. 2, dated Aug. 2018; Ex. 3 "TrueAllele_cases" in "General Acceptance" folder under "1-reliability"). In this document, Dr. Perlin states, "TrueAllele Casework DNA match results have been reported in over five hundred criminal cases, in over two thirds of the states. Most are prosecution case, with many for the defense. TrueAllele trial testimony is often not needed, due to plea agreement or stipulation." Id. All of the courts in the 16 cases from the United States admitted the

testified he has been called to court as a witness more than fifty times in fifteen state courts as well as military and federal courts. (Tr. Sept. 12, 2018 Hrg., at 66). Dr. Perlin reviewed his credentials, summarized in his curriculum vitae admitted as Exhibit 1, and the Court declared him "an expert in DNA evidence interpretation and likelihood ratio (LR) as well as in the field of computer science." (Tr. Sept. 12, 2018 Hrg., at 14).

Dr. Perlin first walked the court through the science of DNA analysis and the processes TrueAllele uses to calculate LRs, using a slide shows, which is included on the disc admitted as Exhibit 3. (Tr. Sept. 12, 2018 Hrg., at 8-41; see also Ex. 3 (PowerPoint file in folder titled "5-Demonstrative aid" under "5-case files"). Dr. Perlin then testified about how TrueAllele had been tested and used a second slide presentation as he described the validation process and explained the sensitivity, specificity, and reproducibility of TrueAllele. (Tr. Sept. 12, 2018 Hrg., at 43-157; see also Ex. 3, PowerPoint file titled "validate," located in "Presentations" folder under "2-reliability").

Although probabilistic genotyping software programs have been recognized as an improvement from prior methods such as CPI, the 2016 PSCAT report advises:

> [These programs] still require careful scrutiny to determine (1) whether the methods are scientifically valid, including defining the limitations on their reliability (that is, the circumstances in which they may yield unreliable

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TrueAllele evidence as did the courts in Australia, England, and Northern Ireland.

Additionally, the probabilistic genotyping software overview to be published in the January 2019 issue of *Forensic Science International: Genetics* provides a non-exhaustive list all admissibility hearings known by the authors for any probabilistic software program from the United States, Australia, and Ireland. Coble & Bright, supra note 14, at Table S2. The decisions concern namely TrueAllele, STRmix, FST, and Lab Retriever. For cases concerning the admissibility of TrueAllele, the authors listed all the cases provided by the State in Ex. 16 or listed in Ex. 2, indicating there have been no additional known rulings since the article's October 2018 acceptance date.

results) and (2) whether the software correctly implements the methods. This is particularly important because the programs employ different mathematical algorithms and can yield different results for the same mixture profile.211

Appropriate evaluation of the proposed methods should consist of studies by multiple groups, *not associated with the software developers*, that investigate the performance and define the limitations of programs by testing them on a wide range of mixtures with different properties. In particular, it is important to address the following issues:

(1) How well does the method perform as a function of the number of contributors to the mixture? How well does it perform when the number of contributors to the mixture is *unknown*?

(2) How does the method perform as a function of the number of alleles shared among individuals in the mixture? Relatedly, how does it perform when the mixtures include related individuals?

(3) How well does the method perform—and how does accuracy degrade—as a function of the absolute and relative amounts of DNA from the various contributors? For example, it can be difficult to determine whether a small peak in the mixture profile represents a true allele from a minor contributor or a stutter peak from a nearby allele from a different contributor. (parenthetical omitted)

(4) Under what circumstances—and why—does the method produce results (random inclusion probabilities) that differ substantially from those produced by other methods?

(2016 PSCAT Report, at 79-80) (footnotes omitted). The Court shall now apply the Daubert factors to Dr. Perlin's testimony and TrueAllele, taking into consideration the guidelines in the 2016 PSCAT Report and the SWGDAM Guidelines on probabilistic genotyping.

1. Testing and Testing Methodology

Dr. Perlin testified thirty-six validation studies have been conducted on TrueAllele either by Cybergenetics, independent crime labs, or collaboration of both; of those

studies, twenty-three are internal validation studies. (Tr. Sept. 12, 2018 Hrg., 53, 138; see also Exs. 7A & 7B (containing 34 validations studies); Ex. 3, folder labeled "validation" contains 39 files).

Seven of thirty-six studies have been published in peer-reviewed journals—the first published in 2009. Six of the seven published studies were authored or co-authored by Dr. Perlin. The 2016 PSCAT Report states, "it is completely appropriate for method developers to evaluate their own methods", while noting that "establishing scientific validity also requires scientific evaluation by other scientific groups that did not develop the method." (2016 PSCAT Report, at 80). Here, although the majority of the publications have been by Cybergenetics, other entities have also reviewed TrueAllele's method. See S. Greenspoon, L. Schiermeir-Wood & B. Jenkins, *Establishing the Limits of TrueAllele Casework: A Validation Study*, 60 J. FORENSIC SCI. 1263 (2015) (included in Ex. 3, file named "JFS2015VS" in "Validation Paper" folder under "2-reliability").

Dr. Perlin further testified TrueAllele abides by quality assurance standards established by the FBI, as well as guidelines issued by the SWGDAM, noting in 2015, the SWGDAM issued guidelines specifically for validation of probabilistic genotyping systems like TrueAllele. (Tr. Sept. 12, 2018 Hrg., 74-75, 83; see also Ex. 13 binder titled "Method Reports"; Ex. 3).[23]

Dr. Perlin explained TrueAllele is based on Bayesian[24] modeling, a statistical standard that goes back to 1763. (Tr. Sept. 12, 2018 Hrg., 77; see also Ex. 9 binder

[23] Dr. Perlin also testified about this issue at the October 30, 2018 hearing, which had not been transcribed at the time this order issued.

[24] The Bayesian Method briefly explained:

titled "Other Papers"). Dr. Perlin testified sophisticated computer programs solve problems with a hundred dimensions, and TrueAllele uses Markov chain Monte Carlo (MCMC)[25] computing, one of the oldest and well-adopted methods, dating back to the 1950s. Id. at 60, 78.[26] Dr. Perlin testified the MCMC algorithm is considered one of the ten most widely used in computer science. Id. TrueAllele's Visual User Interface (VUIer) tool uses MATLAB[27] programming language, which Dr. Perlin described as "a standard, high level programming language for visualization, finding numerical solutions and problems." Id.

> Bayesian Statistics are a technique that assigns "degrees of belief," or Bayesian probabilities, to traditional statistical modeling. In this interpretation of statistics, probability is calculated as the reasonable expectation of an event occurring based upon currently known triggers. Or in other words, that probability is a subjective process that can change as new information is gathered, rather than a fixed value based upon frequency or propensity.

BAYESIAN STATISTICS, DEEPAI, https://deepai.org/machine-learning-glossary-and-terms/bayesian-statistics (last accessed Dec. 16, 2018). For additional information on Bayesian Methods, see Dale J. Poirier, *The Growth of Bayesian Methods in Statistics and Economics Since 1970*, BAYESIAN ANALYSIS (2006), which is included in the binder admitted into evidence as Exhibit 9 and on the disc marked Exhibit 3 (located in "Foundation" folder filed within the "Other papers" file under "1-reliability").

[25] Markov chain Monte Carlo (MCMC) methods comprise a class of algorithms for sampling from a probability distribution. For additional information on MCMC, see Matthew Richey, *The Evolution of Markov Chain Monte Carlo Methods*, MATH. ASSOC. OF AM. (May 2010), which is included in the binder admitted into evidence as Exhibit 9 and on the disc marked Exhibit 3 (located in "Foundation" folder filed within the "Other papers" file under "1-reliability").

[26] Both "STRmix and TrueAllele perform Markov chain Monte Carlo simulation to estimate the distributions of peak heights by incorporating many biological parameters." See, e.g., Sho Manab, et al., *Development and validation of open-source software for DNA mixture interpretation based on a quantitative continuous model*, PLos One (Nov. 2017), www.ncbi.nlm.nih.gov/pmc/articles/PMC5693437/.

[27] MathWorks provides the following definition of MATLAB:

> MATLAB®, the language of technical computing, is a programming environment for algorithm development, data analysis, visualization, and numeric computation

MATHWORKS, mathworks.com (printout included in the binder admitted into evidence as Exhibit 9 and on the disc marked Exhibit 3).

When asked whether he would characterize Cybergenetics and TrueAllele as an outlier in genotyping software, Dr. Perlin replied although TrueAllele was the first of its type, and in his view, "more advanced" and "more powerful than other systems," he believes probabilistic genotyping programs are "quite mainstream" given the current state of forensic science. He noted at least ten programs are available on the market, citing the primarily programs as TrueAllele and the software used by the FBI, STRmix. (Tr. Sept. 12, 2018 Hrg., 84; see also Ex. 14 binder titled "Related Systems" containing eight documents, most of which are peer-reviewed papers describing other scientists' implementation of systems like TrueAllele).

One of the main challenges raised by the defense and addressed by Nathanial Adams at the October hearing was lack of transparency as to True Allele's proprietary source code. This issue has been raised before other courts and has been the subject of legal articles criticizing TrueAllele.[28] (Tr. Sept. 12, 2018 Hrg., at 115-21).

Dr. Perlin explained the TrueAllele source code is a trade secret, and defined source code as "the text that a programmer writes in, in order to instruct a computer about how to execute a certain set of instructions, or statistical methods." (Tr. Sept. 12, 2018 Hrg., 114-15). In other words, source code is "a description of the program that a computer, then, turns into a running program." (Tr. Sept. 12, 2018 Hrg., at 69)

Dr. Perlin explained initially he had concerns about disclosing the TrueAllele source code, particularly in 2014; however, since the source code has been a

[28] See, e.g. Katherine Kwong, Note, *The Algorithm Says You Did It: The Use of Black Box Algorithms to Analyze Complex DNA Evidence*, 31 HARVARD J. LAW & TECH. 275, 285-288 (Fall 2017). The defense also provided the Court a collection of articles on this issue (from publications such as the *ABA Journal*, *Wired*, and *The Atlantic*) as part of its motion for funds pursuant to Rule 13 of the Tennessee Supreme Court Rules. (*Ex Parte* Motion for Funds for DNA Expert, filed under seal Apr. 13, 2018, at Exs. 2, 3 & 4).

continually litigated issue, Cybergenetics made a decision around 2017, to disclose its source code under specific conditions. (Tr. Sept. 12, 2018 Hrg., 68, 115-122). He noted in this case, the defense received an invitation to view the source code as part of the discovery. Id. at 123; see also Ex. 17. Dr. Perlin testified the defense did not accept the offer nor has anyone else; however, he noted attorneys became upset in general once Cybergenetics decided to release the code since it rendered moot litigation of the issue.

Dr. Perlin noted, however, that he did not think access to the source code is useful since it would take about ten *years* to review the entire source code, adding he believed would be "a waste of time" because it would take only one to two hours to validate the source code through testing. (Tr. Sept. 12, 2018 Hrg., 125; see also id. at 127-28). Dr. Perlin stated source code is something lawyers like to dispute, but it is less of an issue to scientists who simply test the system. Regardless, Cybergenetics has made the source code available although this Court agrees with the finding that validation studies are generally the best test of reliability codes. See Pennsylvania v. Foley, 38 A.3d 882, 889–90 (Pa. Sup. Ct. 2012)[29]; Virginia v. Matthew Franklin Brady, Case No. CR11-465 (Va. Circuit Ct., Dec. 17, 2013) (included in Ex. 16).

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[29] In Foley, the Court provided the following reasoning:

> Foley's third reason for exclusion is misleading because scientists can validate the reliability of a computerized process even if the "source code" underlying that process is not available to the public. TrueAllele is proprietary software; it would not be possible to market TrueAllele if it were available for free. See N.T., Hearing, February 18, 2009, at 54. Nevertheless, TrueAllele has been tested and validated in peer-reviewed studies. One study used laboratory-generated DNA samples and found that quantitative analysis performed by TrueAllele was much more sensitive than qualitative analysis such as that performed by the FBI. See Perlin & Sinelnikov, An Information Gap in DNA Evidence Interpretation, 4 PLoS ONE e8327, at 10 (2009), available at http://dx.doi.org/10. 1371/journal. pone.0008327. A recent paper entitled "Validating TrueAllele® DNA Mixture Interpretation" used DNA samples from actual cases and reached similar results. See Perlin et al., Validating TrueAllele® DNA Mixture Interpretation, 56 Journal of Forensic Sciences 1430 (2011). The study "validated the TrueAllele genetic calculator for DNA mixture interpretation" and found that "[w]hen a victim reference was available,

Since the sample at issue here included four contributors, Dr. Perlin was asked about the 2016 PSCAT report's conclusion evidence supports the foundational validity of analysis, with some programs, of specific DNA mixtures not exceeding three contributors:

> These methods [STRmix and TrueAllele] appear to be reliable for three-person mixtures in which the minor contributor constitutes at least 20 percent of the intact DNA in the mixture and in which the DNA amount exceeds the minimum level required for the method.

(2016 PSCAT Report, at 80) (citation omitted).

Dr. Perlin agreed PSCAT was comprised of many distinguished scientists across disciplines, but he noted the Council did not include statistical forensic scientists. He further noted although the Report quoted Dr. John Butler as in support of PSCAT's conclusion probabilistic genotyping had not been validated below 20% or beyond a three-person mixture, the Report (1) misidentified Dr. Butler as a forensic scientist when he is an analytical chemist and (2) the studies cited by Report "flatly contradicted" its own conclusion. (Tr. Sept. 12, 2018 Hrg., at 151; see also id at 150-52).

Dr. Perlin testified TrueAllele is now designed for use where sample contributors range from one to ten individuals. He noted at the time TrueAllele began analyzing samples with five unknown contributors, other programs had limited their analysis to two- or three-person mixtures; however, those programs now offer analysis of five-

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> the computer was four and a half orders of magnitude more efficacious than human review." Id., at 1444. Both of these papers were published in peer-reviewed journals; thus, their contents were reviewed by other scholars in the field.

Com. v. Foley, 2012 PA Super 31, 38 A.3d 882, 889–90 (2012) (endnotes omitted).

person mixtures. (Tr. Sept. 12, 2018 Hrg., at 100-101). Further, the FBI has validated its probabilistic genotyping system for use on up to five-person mixtures. [30]

Dr. Perlin testified validation studies considering seven contributors have been conducted. Although the study had not been published by the date of the Daubert hearing, Dr. Perlin anticipated publication would occur soon since the study had been discussed recently at the American Academy for Forensic Science, with preliminary copies distributed to the contributors; Dr. Perlin provided a draft in his materials. (Tr. Sept. 12, 2018 Hrg., at 139; Ex. 3).[31]

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[30] See, e.g., Michael Coble, *Current Issues in Forensic DNA Testing*, Eighth Annual Prescriptions for Criminal Justice Forensics (June 2, 2017), https://www.americanbar.org/content/dam/aba/events/criminal_justice/2017/Current_Issues_Forensic_DNA_Testing.pdf (citing Tammy Wait, *FBI Validates STRmix for Use on Up to Five-Persona Mixtures*, American Security Today (May 17, 2017), https://americansecuritytoday.com/fbi-validates-strmix-use-five-person-mixtures-video).

The creator of STRmix, John Buckleton, has testified at court hearings; in July 2016, he testified STRmix and TrueAelle reach the same result 99% of the time. See, e.g., Findings of Fact and Conclusions of Law, Washington v. Emanuel Fair, No. 10-1-09274-5 SEA (King County Sup. Ct., Jan. 12, 2017) (included in Ex. 16 & Ex. 3).

[31] During cross-examination, Dr. Perlin briefly touched on the National Institute of Standards and Technology (NIST) study, which concluded the majority of the participating labs erred in their conclusion. (Tr. Sept. 12, 2018 Hrg., at 146-47; see also Ex. 10, PowerPoint by Michael Coble, titled "MIX13: Overview and Lessons Learned"). Dr. Perlin testified none of those labs used TrueAllele and Cybergenetics was one of the few labs that correctly interpreted the data. Id. The Court has reviewed this study and finds it supports TrueAllele's validity:

> Seven laboratories (6%) correctly excluded 5C, but for a variety of reasons. Four of the laboratories mentioned the missing allele 15 at Penta E with PP16HS data. One laboratory (using Identifiler Plus data) assumed major and minor contributors and noted that the suspects did not fit the needed combination to produce the mixture data reported. Another laboratory (using Identifiler Plus data) turned in results with detailed manual genotype assessments and noted that 5C would not fit and therefore should be excluded. The single use of a probabilistic genotyping program in this study (True Allele) resulted in a negative log likelihood ratio and therefore correctly reported that evidence did not support 5C being in the MIX13 Case 5 mixture profile under an assumption of three or four contributors. Developers of the TrueAllele probabilistic genotyping software program submitted results that correctly excluded 5C, but they were not included in the 108-laboratory tally as they were not considered a forensic "laboratory" for the purposes of this study. Developers of the Lab Retriever program also submitted results for MIX13 cases 1-4, but not case 5 because their software at the time was limited to a maximum of three contributors. Following completion of the study, analysis with other continuous probabilistic genotyping software programs (e.g., STRmix and DNA-View Mixture Solution) obtained similar results with "excluding" 5C (personal communication).

2. Peer-Review and Publications

As previously referenced, seven of the thirty-six validation studies have been published in peer-reviewed journals; Dr. Perlin acknowledged on cross-examination that six of the seven published studies were authored or co-authored by him. (Tr. Sept. 12, 2018 Hrg., 53, 69-70; see also Ex. 7A & 7B; Ex. 3).[32] Dr. Perlin testified at length about these studies, and particularly the Virginia TrueAllele Validation study. (Tr. Sept. 12, 2018 Hrg., at 44-48, 91,141-44).

3. Potential Error Rate

Dr. Perlin testified the mathematics underlying TrueAllele comply with the SWGDAM guidelines and recommendations. He provided a document that described the TrueAllele methods with both statistical equations and plain English. (Ex. 9, binder titled "Other Reports"). Dr. Perlin further testified TrueAllele has a known error rate

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John M. Butler, Margaret C. Kline & Michael D. Coble, *NIST interlaboratory studies involving DNA mixtures (MIX05 and MIX13): Variation observed and lessons learned* 37 FORENSIC SCI. INT'L: GENETICS 81, 90 (2018), *available at* https://www.fsigenetics.com/article/S1872-4973(18)30248-5/fulltext (emphasis added).

[32] The seven published studies , and included on Ex. 3, are:

(1) M.W. Perlin & A. Sinelnikov, *An information gap in DNA evidence interpretation,* PLoS ONE (2009);
(2) J. Ballantyne, E.K. Hanson & M.W. Perlin, *DNA mixture genotyping by probabilistic computer interpretation of binomially-sampled laser captured cell populations: Combining quantitative data for greater identification information.* 53 SCI. & JUSTICE. 103 (2013);
(3) M.W. Perlin, J. Hornyak, G. Sugimoto & K. Miller, *TrueAllele® genotype identification on DNA mixtures containing up to five unknown contributors,* 60 J.FORENSIC SCI. 857 (2015);
(4) S. Greenspoon, L. Schiermeir-Wood & B. Jenkins, *Establishing the Limits of TrueAllele Casework: A Validation Study,* 60 J. FORENSIC SCI. 1263 (2015);
(5) M.W. Perlin, M.M. Legler, C.E. Spencer, J.L. Smith, W.P. Allan, J.L. Belrose & B.W. Duceman, *Validating TrueAllele® DNA mixture interpretation.* 56 J. FORENSIC SCI.1430 (2011);
(6) M.W. Perlin, J.L. Belrose & B.W. Duceman, *New York State TrueAllele® Casework validation study.* 58 J. FORENSIC SCI. 1458 (2013); and
(7) M.W. Perlin, K. Dormer, J. Hornyak, L. Schiermeier-Wood & S. Greenspoon, *TrueAllele® Casework on Virginia DNA mixture evidence: computer and manual interpretation in 72 reported criminal cases.* PLoS ON (2014).

under a fraction of 1%, and the calculation for a false positive in this case was included on the Cybergenetics Report.

He explained false-positive error rates are stratified by the strength of the match statistic; he demonstrated with data on the slides, that when a match statistic, or LR, is up to a hundred, the error rate is one in a million, but by the time TrueAllele gets a match statistic of a thousand, no false positives were seen in the study. (Tr. Sept. 12, 2018 Hrg., at 58-60; see also id. at 129-30).

When asked about the California Department of Justice (CDOJ) study that revealed an 18% error rate with True Allele, Dr. Perlin referred to it as a "secret study" that he had learned about last year through a FOIA request; the study was not published nor were the results reported to the forensic community. Dr. Perlin testified once he reviewed the study, it was clear CDOJ had changed, or modified, some key features of TrueAllele and did not use the VUIer program to calculate statistics; thus, the study demonstrated error rate when the program is not run correctly rather than the accuracy of the program. (Tr. Sept. 12, 2018 Hrg., at 144-45).

During cross-examination, Dr. Perlin also was asked about the case People v. Hillary. Since that case did not concern the admissibility of TrueAllele (but the admissibility of STRmix results), Dr. Perlin noted he did not supply the Hillary decision materials; Cybergenetics, however, had participated in a pro bono capacity prior to indictment. (Tr. Sept. 12, 2018 Hrg., at 148-150). The Hillary case came up in the context of how human operators had manipulated threshold for different outcomes; that

is, STRmix could include or exclude the defendant based on which threshold was selected by the human operator.[33]

As reflected in the Hillary decision, the New York State Police crime lab had contacted Cybergenetics in 2013 to run data obtained from fingernail scrapings, and the TrueAllele report was inconclusive. New York v. Oral Nicholas Hillary, Ind. #: 2015-15, at 3 (Aug. 26, 2016), *available at* http://www.kccba.org/wp-content/uploads/2017/09/STRMix-People-v-Hillary-decision.pdf. The defendant was indicted in 2014, and at the request of the prosecution, the data was submitted to the Institute of Environmental Science and Research for a second interpretation. Using STRmix, that lab determined a match. Id. The Hillary Court excluded the probabilistic genotyping data as applied in that case due to testimony the lab conducted no internal validation. In making its ruling, however, the Court held "STRmix has been developmentally validated and is generally accepted as reliable within the scientific community." Id. at 7.

The defense also raised concern about "bugs" in the TrueAllele system, and Mr. Adams provided testimony as to this issue; however, he admitted he has conducted no testing of the TrueAllele system. On cross-examination, Dr. Perlin addressed these concerns and the possibility of human errors in coding as well as the steps TrueAllele has taken to prevent errors. He explained most bugs in the system, which were documented in an internal wiki record, occurred as the database was expanded. He testified the bugs did not affect the calculation statistically but related to how the user

[33] Dr. Perlin has written on this issue. See, e.g., Mark Perlin, PhD, MD, *Suspect-centric Bias in DNA Mixture Interpretation*, FORENSIC MAG. (Sept. 2018), www.forensicmag.com/article/2018/09/suspect-centric-bias-dna-mixture-interpretation.

phrased questions; thus, they were user interface issues, not statistical issues. (Tr. Sept. 12, 2018 Hrg., 93-97, 101-09).

4. General Acceptance in Scientific Community

The literature demonstrates probabilistic genotyping programs are generally accepted in scientific communities—with at least fourteen such programs, open source and commercial, available at October 2018.[34] See Exs. 3; 8, 10, 11, 12 & 14.

Dr. Perlin testified these different programs use different types of methods, and directed the Court to the Department of Justice ""Landscape Study of DNA Mixture Interpretation Software" and the citation index listing more than 400 scientific articles referring to the work of TrueAllele. (Tr. Sept. 12, 2018 Hrg., 80; Ex. 10, both the 2015 study and citation index are contained inside the binder titled "General Acceptance").

5. Research Independent of Litigation.

Dr. Perlin testified how TrueAllele has been used outside of litigation for casualties and mass disasters, citing its forensic application used for World Trade Center 9/11 victim identification. He also testified a number of labs in the United States and United Kingdom use the TrueAllele program. (Tr. Sept. 12, 2018 Hrg., 81-82; see also Ex. 11, binder titled "Forensic Application"; Ex. 3). Dr Perlin notes numerous laboratories in the United States are using TrueAllele, including eight crime labs.[35] Id. at

[34] Coble & Jo-Anne Bright, supra note 14, at Table S1.

[35] Dr. Perlin acknowledged the cost of the TrueAllele system ranges $40K-$120K to implement, and the Metro Crime Lab—who had employees at the hearing—intended to purchase the system. (Tr. Sept. 12, 2018 Hrg., at 90). To Dr. Perlin's knowledge, no validation studies have been conducted in Tennessee.

90-92. Dr. Perlin explained when some state crime labs incorporate new equipment or software, the lab must receive permission from the state's forensic science commission. TrueAllele went through the vetting process in Virginia and New York. (Tr. Sept. 12, 2018 Hrg., 82; see also id. at 53-4; Ex. 12, binder titled "Regulatory Approval").

Cybergenetics also has used TrueAllele in exoneration cases as detailed in Dr. Perlin's case list. (Exs. 2 & 3; see also Ex. 11).

6. Conclusion

The Court finds the probabilistic genotyping program TrueAllele satisfies the Daubert standard. Substantial evidence has been presented to the Court, which supports the admission of TrueAllele analysis, and no significant evidence has been presented to the contrary. As noted by another court addressing this issue, "TrueAllele Casework has been around since 1999, a time frame that would certainly allow for a thorough critical review to be put forth if it was warranted." State v. Wakefield, 47 Misc. 3d 850, 858–59, 9 N.Y.S.3d 540, 546–47 (N.Y. Sup. Ct. 2015) (included in Exs. 3 & 16).

The Court now turns to the challenges raised by the defense about the application of TrueAllele in this case.

V. Probabilistic Genotyping as Applied to this Case

Dr. Perlin testified about the application of TrueAllele to the instant case, (Tr. Sept. 12, 2018 Hrg., at 98), and the report generated by Cybergenetics. (ex. 3). Specifically, Cybergenetics reported a match between the khaki pants and the Defendant is:

- 470 thousand times more probable than a coincidental match to an unrelated African-American person
- 7.64 million times more probable than a coincidental match to an unrelated Caucasian person
- 5.12 million times more probable than a coincidental match to an unrelated Hispanic person

(Cybergenetics Report dated Dec. 13, 2017; Demonstrative Aid, slide 18 (both contained on Ex. 3 under "5-case files")). The report provided information about known false positive error rate:

> A false positive would occur if a non-contributor (someone who didn't contribute their DNA) to the khaki pants had a match statistic of 470 thousand or more. The chance of a false positive for this comparison is one in 6.1 million for an African-American person. The calculation is shown in the "Non-contributor Analysis" section.

Id. Dr. Perlin explained the tables provided with the report show all contributors in the sample were minor contributors, meaning all contributed less than 51%. The defense cross-examined Dr. Perlin about his specific findings in this case at the October 30, 2018 hearing.

Based on all the evidence presented, this Court finds the TrueAllele analysis reliable as applied in this case, and the testimony of either Dr. Perlin or Jennifer Hornyak would substantially assist the trier of fact in understanding the evidence. The criticisms raised by the defense go towards the weight of the evidence, not admissibility.

VI. Conclusion

For the reasons set forth above, the Court finds the TrueAllele analysis reliable, and the testimony concerning probabilistic genotyping is admissible at trial. The Defendant's "Motion in Limine to Exclude Expert Testimony Regarding Likelihood Ratio" is hereby DENIED. This matter remains scheduled for trial on January 14, 2019.

IT IS SO ORDERED.

ENTERED this the 17 day of December, 2018.

Cheryl Blackburn

Cheryl Blackburn,
Judge

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