SUPERIOR COURT OF WASHINGTON FOR KING COUNTY

STATE OF WASHINGTON, Plaintiff, vs. EMANUEL FAIR, Defendant.	)	No. 10-1-09274-5 SEA FINDINGS OF FACT AND CONCLUSIONS OF LAW RE: ADMISSIBILITY OF TRUEALLELE CASEWORK

From September 19, 2016 through November 28, 2016, the Court held a hearing on the defense motion to exclude DNA evidence pursuant to Frye[1] and ER 702 and the defense motion to compel the TrueAllele Casework source code. The Court heard testimony from two State experts: Mr. Jay Caponera, and Dr. Mark Perlin. The Court also heard testimony from five defense experts: Mr. Nathaniel Adams, Dr. Dan Krane, Dr. Kirk Lohmueller, Dr. David Balding and Mr. Brian Ferguson. The Court, having heard the testimony of witnesses and arguments of counsel, reviewed the 88 pretrial exhibits, as well as the pleadings and appendices thereto, now makes and enters the following findings of fact and conclusions of law:

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

King County Superior Court
516 3rd Avenue, Room C203
Seattle, Washington 98104
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I. FINDINGS OF FACT

Frye

1. The human body is made up of trillions of cells. Each cell has a nuclei where the DNA is stored. Forensic scientists have identified certain polymorphic loci or markers along DNA strands that vary from person to person. At each locus, an individual has a pair of alleles, one from each parent. The two alleles at a given locus may be the same (homozygote) or different (heterozygote). The overall combination of alleles at these various loci is so different from person to person that no two people except identical twins have the same DNA profile. The FBI has identified 13 standardized markers or loci that are widely used for forensic analysis.
2. When a human analyst examines a sample of evidence containing DNA, the analyst extracts the DNA from the sample, then amplifies the DNA using a process called PCR (Polymerase chain reaction) which copies the DNA segments millions of times so that the analyst can determine which alleles are present. The alleles are separated by size and dye markers are added during the amplification process which causes the alleles to fluoresce differently as they are illuminated. The Washington State Patrol Crime Lab (WSPCL) uses a computer software program called GeneMapper which plots the results on a graph called an electropherogram and assigns peak heights so that the analyst can visually examine and compare the alleles. Each allele that is detected at a particular locus is plotted as a peak along the electropherogram's x-axis. The intensity of fluorescence of the allele is reflected as the allele's peak height along the electropherogram's y-axis. The intensity of the fluorescence is measured in relative fluorescent units (RFUs).

3. The Scientific Working Group on DNA Analysis Methods (SWGDAM) is a group of approximately 50 scientists representing federal, state and local forensic DNA laboratories in the United States and Canada. They meet twice a year and issue documents to provide direction and guidance for the scientific community. On June 15, 2015, SWGDAM issued *Guidelines for the Validation of Probabilistic Genotyping Systems.* SWGDAM described probabilistic genotyping as 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. Ex 48 at 2.
4. Probabilistic genotyping as a scientific theory is generally accepted by the relevant scientific community. This fact was not disputed by the parties. In fact two of the Defense experts have developed their own probabilistic genotyping (PG) software: Dr. Balding created LikeLTD and Dr. Loehmueller created Lab Retriever.
5. The issue in this case is whether the technique that TrueAllele uses to analyze DNA samples is generally accepted in the relevant scientific community.
6. TrueAllele was developed by Dr. Mark Perlin at Cybergenetics, a Pennsylvania corporation. Dr. Mark Perlin has a Ph.D. in computer science from Carnegie Mellon University, a Ph.D. in mathematics from the City University of New York, and an M.D. from the University of Chicago. He began developing TrueAllele over 22 years ago and first began using it in criminal cases in 2009.
7. TrueAllele Casework ("TrueAllele") is a fully continuous probabilistic genotyping computer system that interprets DNA evidence using a statistical model[2]. TrueAllele

[2] Fully continuous systems examine allele peak heights. Semi-continuous models do not use peak heights.

uses hierarchical Bayesian probability modeling to represent genotypes and data in a DNA mixture problem. Bayes theorem, first published in 1762, is a theorem of probability. It is a way of updating beliefs or guesses based on observation. From observations of the data, one can obtain hypotheses. The probability equations in TrueAllele are based on Bayesian modeling and the solutions to these equations are based on Markov Chain Monte Carlo (MCMC) statistical sampling.

8. Mr. Jay Caponera, a forensic scientist with the New York State Police, explained that MCMC sampling is similar to walking blindly around in a room looking for an area in the room where the answers to the problem are most concentrated. MCMC sampling solves one variable at a time. Then stitches all the answers to each variable together. There will not be just one answer, rather there will be multiple answers but the cloud will be concentrated around the "best" answer that fits the data.

9. Dr. Perlin testified that, in a typical case, TrueAllele will consider 10,000 genotype solutions. Some will explain the data better and those explanations will be assigned a higher probability. Answers that don't explain the data as well will be assigned lower probabilities. The computer then determines the probability of a random person having the particular genotype. It compares the random probability to the highest probability genotype generated by the computer to obtain a match statistic or likelihood ratio (LR).

10. Dr. David Balding, a professor at the University of Melbourne in Australia who has a Ph.D. in Mathematics, created a probabilistic genotyping system called LikeLTD. He testified that the view of the general scientific community is that probabilistic genotyping (PG) systems are the best way forward for the evaluation of DNA profile evidence.

11. Dr. Balding also testified that after reviewing the mathematical and statistical models that underlie TrueAllele, he had concerns about the absence of thresholds, how TrueAllele accounts for drop out and drop in and how it handles stutter. He believed that TrueAllele relies on modeling assumptions that are not fully understood by anyone outside of Cybergenetics. However, he ultimately concluded that TrueAllele generally appears to perform well in computing likelihood ratios for complex DNA mixtures. Ex. 15.
12. Dr. Kirk Lohmueller, an Assistant Professor at the UCLA with a Ph.D. in Genetics, has (along with Keith Inman and Nora Rudin) developed a PG system called Lab Retriever. He testified that he had concerns about whether the TrueAllele model handles allelic drop out appropriately. TrueAllele does not have any drop out parameters. Instead, it uses a minimum logLR of -2. That is, TrueAllele assumes that uninformative data will arise at least once in every 100 experiments. Dr. Loehmueller testified that the -2 minimum value was too harsh and could result in false exclusions of true contributors.
13. Dr. Daniel Krane is a Professor of Biological Sciences at Wright State University with a PhD. in Biochemistry. He is the President and CEO of BioInformatics, a consulting company for DNA Profiling. Dr. Krane testified that the determination of the number of contributors to a mixture is made by human analysts at Cybergenetics and not by the TrueAllele software. He believed that this approach is likely to underestimate the number of contributors due to allelic drop out and masking. If a 3-person mixture is erroneously evaluated as a 2-person mixture, the likelihood ratio will be artificially higher, providing more weight to the prosecution's hypothesis. Cybergenetics has no guidelines or standard operating procedures (SOPs) for how analysts are to identify the number of contributors to a DNA mixture.

14. Mr. Caponera testified that he conducted two separate validation studies of TrueAllele in 2013. In the first study, he examined low template single source data in two and three person DNA mixtures of known composition. He found that TrueAllele was accurate in evaluating samples containing at least 15 pcg of DNA and that sensitivity increased up to 125 pcg then increased DNA had no effect. In the second study, Mr. Caponera found that TrueAllele could reliably separate out donors from non-donors in 4-person mixtures. Overall he found that the TrueAllele software was more sensitive, used more available genetic information and provided evidentiary weight to profiles currently deemed inconclusive by the threshold-based systems. Ex 1.

15. Mr. Caponera also testified about a 2014 study in which the National Institute of Standards and Technology (NIST) sent out five different DNA mixtures to 100 different forensic laboratories. Each mixture was slightly different in terms of number of contributors and complexity. NIST provided the labs with three different known reference profiles, however, one of the reference profiles (suspect C) was not actually in any mixture. 76 labs identified suspect C in the mixture (76% error rate), 25 labs were inconclusive and 7 labs (one lab was using TrueAllele) correctly excluded suspect C.

16. Since 2009, 34 validation studies have been conducted by Cybergenetics and other forensic scientists to establish the reliability of TrueAllele. These studies have used TrueAllele on both laboratory-generated and casework DNA samples. The laboratory studies have tested TrueAllele to determine how it handles mixtures of varying composition and weights. Seven of these studies have been published in peer-reviewed scientific journals. Ex. 44.

17. The "peer-review" process entails the scientist describing their research methods, results and conclusions in a scientific paper which is submitted to a journal for publication. An editor of the journal has at least two independent and anonymous scientists in the relevant field read the paper, assess its merits and advise on the suitability of the paper for publication. The paper is then either accepted, rejected or sent back to the author for edits and another round of review.

18. One of the earliest published peer-reviewed article authored by Dr. Perlin and Dr. Alexander Sinelnikov in 2009 compared the DNA information extracted using the newer quantitative computer-based methods with the current qualitative manual methods. They found that qualitative methods are limited to mixtures with DNA quantities above 100 pg while the quantitative methods were able to analyze DNA information down to 10 pg. The paper discusses the "information gap" between the match sensitivities of the older qualitative methods in comparison to the newer quantitative methods which utilize more DNA information. Perlin M., Sinelnikov, A. *An Information Gap in DNA Evidence Interpretation.* Plos One Journal. 2009:4(12):1-12. Ex 44(4).

19. A published peer-reviewed paper co-authored by Dr. Perlin and others was presented at the 62nd Annual Meeting of the American Academy for Forensic Sciences, February 22-27, 2010, in Seattle, WA. This study concluded that the use of genetic calculators such as TrueAllele can improve DNA mixture interpretation in several ways. A computer can process information faster than any human analyst thereby reducing DNA case backlogs. Genetic calculators can extract more DNA information from low template samples. And the use of computers increases the objectivity of the analysis since there is sometimes a concern that prematurely exposing a human analyst to a suspect's profile can introduce

observer bias. Perlin, M, Legler, M., Spencer, C., Smith, J., Allan, W., Belrose, J., Duceman, B., *Validating TrueAllele DNA Mixture Interpretation.* Journal of Forensic Sciences, 2011:56(6):1430-1447. Ex 44(13).

20. A peer-reviewed article published in The Science and Justice Journal described the challenges of interpreting 2-person DNA mixtures containing non-distinguishable cell types particularly where the DNA contribution is approximately equal. The study found physically isolating multiple samplings of groups of cells (binomial sampling) would create separate cell sub-populations with differing weight ratios that could then be analyzed with a computer-based statistical modeling system such as TrueAllele to produce more precise DNA information about the data. Ballantyne, J., Hanson, E., Perlin, M., *DNA Mixture Genotyping by Probabilistic Computer Interpretation of Binomially-Sampled Lase Captured Cell Populations: Combining Quantitative Data for Greater Identification Information,* Science and Justice Journal, 2013:53:103-114. Ex 44(14).
21. In a validation study published in 2013, TrueAllele and a human analyst reviewed 368 evidence items from 41 test cases. The study compared the computer results with the human review and found whenever there was a human result, the computer's genotype was concordant. Further, in interpreting mixtures, TrueAllele produced a match statistic on 81 mixture items compared to 25 items using human review. This is due to the computer's ability to examine DNA mixtures more thoroughly through statistical sampling as compared to a manual review by human analyst. This study was submitted to the DNA Subcommittee of the New York State Commission on Forensic Science. The DNA Subcommittee recommended that TrueAllele be approved for casework in 2011. This recommendation was ratified by the Commission on June 27, 2011. Perlin, M.,

Belrose, J., Duceman, B., *New York State TrueAllele Casework Validation Study,* Journal of Forensic Sciences, 2013, 58(6):1458-1466. Ex 44(17).

22. In a peer reviewed study published in Plos One, three different mixture interpretation methods were used to analyze 92 evidence samples in 72 criminal cases. The study found that the results from TrueAllele were more sensitive, specific, precise and accurate than the manual interpretation methods (CPI and mCPI). Further, manual interpretation requires the use of thresholds which result in a loss of DNA evidence. Perlin, M., Dormer, K., Hornyak, J., Schiermeier-Wood, L., Greenspoon, S., *TrueAllele Casework on Virginia DNA Mixture Evidence: Computer and Manual Interpretation in 72 Reported Criminal Cases,* Plos One, 2014:9(3):1-15. Ex 44(19).

23. In a published peer-reviewed paper, co-authored by Dr. Kevin Miller and Dr. Perlin, a validation study was done using TrueAllele on known mixtures having 2, 3, 4, and 5 contributors, with both high and low DNA amounts. Randomly generated mixtures were used to simulate actual casework. The study concluded that TrueAllele was reliable for the interpretation of DNA mixture evidence over a broad range of forensic casework conditions. Perlin M., Hornyak J, Sugimoto G, Miller K*., TrueAllele genotype identification on DNA mixtures containing up to five unknown contributors.* Journal of Forensic Sciences. 2015;60(4):857-868. Ex 44(27).

24. Another peer-reviewed paper published in 2015, explored the limits of TrueAllele in examining single-source as well as 2, 3 and 4 person mixtures. Some of the samples exhibited dropout and other stochastic effects. The study focused on the sensitivity (ability to detect donors) and specificity (ability to exclude non-donors). The study found that even with the more challenging 4-person mixtures, TrueAllele was capable of

performing an accurate analysis and demonstrated its ability to include true donors and exclude or find no statistical support for non-donors. Based on the results of this study, the Virginia Department of Forensic Science implemented the use of TrueAllele in 2014 in selected cases. Greenspoon, S., Schiermeier-Wood, L., Jenkins, B., *Establishing the Limits of TrueAllele Casework: A Validation Study, Journal of Forensic Sciences,* 2015:60(5):1263-1276. Ex 44(29).

25. This Court has reviewed declarations from forensic scientists throughout the United States who have experience working with TrueAllele. These included declarations from Dr. Kevin Miller (formerly with the Kern Regional County Laboratory), Dr. Susan Greenspoon (forensic scientist with the Virginia Department of Forensic Science), John Donahue (forensic scientist with Beaufort County Forensic Services Laboratory), Thomas Hebert (DNA technical leader for the Baltimore Police Department), Jay Caponera (forensic scientist with the New York State Police), and Joanne Sgueglia (formerly a forensic scientist with the Massachusetts State Police Crime Laboratory). All attested to TrueAllele's reliability and validity.

26. None of the defense experts who testified at the hearing have ever actually used TrueAllele. Cybergenetics provides defense experts with a license to use TrueAllele. They can use the TrueAllele Cloud to test their own mixtures using their own data at no charge.

27. Over ten crime laboratories have purchased the TrueAllele system for their own in-house use, and 7 labs are on-line with their validated systems

28. Since 2009, there have been at least 10 Frye admissibility hearings conducted in the United States concerning TrueAllele. To date, every court (California, Indiana,

Louisiana, Maryland, Massachusetts, New York, Ohio, Pennsylvania, South Carolina and Virginia) has admitted TrueAllele. Ex. 50.

29. There are two published decisions both finding TrueAllele admissible under Frye. State v. Wakefield, 47 Misc. 3d 850, 851, 9 N.Y.S.3d 540, 541 (N.Y. Sup. Ct. 2015) and Commonwealth v. Foley, 38 A.3d 882 (2012).

30. Court decisions admitting STRMix under Frye have cited to the similarities between the two systems and relied upon prior decisions admitting TrueAllele. John Buckleton, one of STRMix's creators, has testified that STRMix is based on the same principles as TrueAllele and he isn't aware of any significant differences between the two programs. People v. Muhummad, Case No. 14-65263-FC, p. 4 fn3 (Mich. Cir. Ct. 2015). Ex. 80. The court in People v. Bullard-Daniel, 2016 WL 5724204, at *1 (N.Y. Co. Ct. 2016) noted that there was a "plethora of evidence" in favor of TrueAllele and "no significant evidence to the contrary." Ex. 79.

31. In a recent published article, two renowned scientists specializing in DNA statistics, Dr. Bruce Weir and Dr. James Curran, discussed the evolution of DNA interpretation from manual calculation to probabilistic genotyping systems such as TrueAllele and STRMix. They acknowledge that by eliminating the steps that go into the manual calculation and replacing it with a reliance on a computer to do the calculations, there is a natural fear about the "black box" nature of these modern methods. However, they point out that many other scientific procedures require the user to rely on equipment without an understanding of their inner working. Scientists trust instruments because they have been subjected to many studies that have been published in peer-reviewed scientific literature. We use them because they are the best methods we have. The same is true for advanced

statistical methods for the interpretation of DNA. Curran, J., Weir, B., *Modern Methods of DNA Interpretation*, Chance, 2016:29(1):17-26. Ex. 49.

32. In September 2016, the President's Council of Advisors on Science and Technology ("PCAST") issued a "REPORT TO THE PRESIDENT Forensic Science in Criminal Courts: Ensuring Scientific Validity of Feature-Comparison Methods." PCAST is an advisory group of the nation's leading scientists and engineers appointed by the president to augment the science and technology advice available to him.

33. The PCAST report noted that probabilistic genotyping software programs clearly represent a major improvement over purely subjective interpretation. As of March 2014, at least 8 different probabilistic genotyping software programs had been developed. The report further noted that the two most widely used methods (STRMix and TrueAllele) appear to be reliable within a certain range, based on the available evidence and the inherent difficulty of the problem. Specifically, the report concluded that STR Mix and TrueAllele appear to be reliable for three person mixtures in which the minor contributor constitutes at least 20% of the intact DNA in the mixture and in two person mixtures where the minor contributor constitutes at least 10% of the mixture. Ex 7 at 80.

34. According to the TrueAllele results, the DNA mixtures from the Robe-4, Robe-6 and Tape-end samples were from 2 or more, or 2 or 3 contributors. The genotype attributed to Mr. Fair was 7.3% (Robe-4), 4.79% (Robe-6) and 15.6% (Tape-end) of the total mixture. Ex. 25.

35. The court heard testimony from several experts who expressed criticisms of the PCAST report. Dr. Perlin testified that there was no scientific support for the PCAST report's mixture percentage limitation for the minor contributor.

36. Defense expert Dr. David Balding agreed that this percentage limitation was irrational because if a suspect contributes a good amount of DNA, it doesn't matter if there are other contributors with lower percentage contributions. He testified that this limitation was added hurriedly at the last minute to the final draft of the PCAST report without any scientific justification.

37. John Buckleton, creator of STRMix, commented that insufficient research was undertaken by the PCAST committee, their conclusions are incorrect and need to be revisited. Ex. 76.

38. The FBI also disagreed with many of the scientific assertions and conclusions of the PCAST report. Ex. 47.

39. The PCAST report does not cite to any study that supports the mixture percentage limitations it recommends for TrueAllele and STRMix.

40. A study of TrueAllele conducted by the New South Wales Forensic & Analytical Science Service (New South Wales) identified issues with stutter modeling and functioning in samples were the minor contributors are at low levels. However, they ultimately concluded that TrueAllele was a powerful interpretation tool, particularly for complex mixtures, increasing the information recovered from the DNA data and moving towards standardization of DNA interpretation nationally. To advance their understanding of the system, NSW purchased a small system so that they could continue with validation and evaluation. Ex 11 p. 69.

41. In 2014 the California Department of Justice Bureau of Forensic Services (CalDOJ) completed an internal study comparing STRMix and TrueAllele. The purpose of the study was to compare the two systems to determine which one to purchase. The study

compared the sensitivity and reproducibility of STR mix and TrueAllele on complex 2 and 3-person mixtures. They found that in 2-person mixtures, TrueAllele excluded true contributors 18% of the time compared to 0% for STR mix. In 3-person mixtures, TrueAllele had no errors and STR mix excluded true contributors 3.7% of the time. The results for TrueAllele were even more skewed when overriding the minimum locus LR threshold of 0.01. Ex. 24.

42. The CalDOJ study was never published nor were the results reported to the forensic science community. A copy of the study was obtained through a Freedom of Information Act request. Dr. Perlin testified that CalDOJ personnel never completed the TrueAllele training, never communicated or consulted with him during the study, and changed significant TrueAllele parameters when conducting the study.

43. The CalDOJ study did report differences between STRMix and TrueAllele results. However, STRMix's creator, John Buckleton, testified in a Frye hearing in July 2016 that STR mix and TrueAllele reach the same result 99 percent of the time. Ex 78.

44. In light of the foregoing facts, the Court finds that TrueAllele has been empirically tested and found to be reliable and accurate. Moreover, TrueAllele has been subjected to favorable peer review and extensive publication.

ER 702

45. The defense seeks to exclude the TrueAllele statistical results on the following evidence: robe-4, robe-6, tape-end, tape-side and the oil bottle.

46. The defense challenged certain particulars of how TrueAllele operates. Among other things, defense experts questioned how TrueAllele handles stutter, dropout and the modelling of peak heights.

47. None of the defense experts examined or discussed in any depth the TrueAllele results on the data in this case. None of the experts testified that they believed that TrueAllele erroneously included the defendant as a likely contributor to the DNA mixtures on the relevant evidence items.

48. There are other statistical analyses of the relevant DNA mixtures in this case, and they are consistent with the TrueAllele results. The Washington State Patrol's LR calculations also provide evidentiary support for the proposition that the defendant's DNA is on robe-4, robe-6 and the tape-end. Dr. Perlin ran the relevant data through Dr. Balding's PG system, LikeLTD, and the results are consistent with the TrueAllele results and support the proposition that the defendant's DNA is on the evidence. Exh. 41.

49. The defense's own DNA trial expert, Keith Inman, also analyzed the DNA data in this case using Lab Retriever, his probabilistic genotyping software. Inman's reported likelihood ratios indicate that the defendant is a likely contributor to the mixed DNA profiles on the relevant evidence items. Those results also provide incriminating statistical evidence supporting the proposition that the defendant's DNA is on the evidence.

50. The defense has not shown that TrueAllele calculations in this case are so unreliable as to be excluded.

II. CONCLUSIONS OF LAW

Frye

1. The State as the proponent of the novel scientific evidence bears the burden of demonstrating its admissibility under Frye v. United States, 293 F. 1013 (D.C. Cir. 1923) and ER 702.

2. Under the Frye test, the court considers (1) whether the scientific theory upon which the evidence is based is generally accepted in the relevant scientific community, and (2) whether the technique used to implement that theory is also generally accepted by that scientific community. State v. Gentry, 125 Wn.2d 570, 585, 888 P.2d 1105 (1995).
3. The court does not determine if the scientific theory underlying the proposed testimony is correct. Judges do not have the expertise to make these types of decisions and must defer this judgment to scientists. The court looks to see whether the theory has achieved general acceptance in the appropriate scientific community. State v. Riker, 123 Wn.2d 351, 359–60, 869 P.2d 43 (1994). The "appropriate scientific community" is the community of scientists familiar with the challenged theory, and the "ideal community" would be scientists with direct empirical experience with the procedure in question. State v. Russell, 125 Wn.2d 24, 41, 882 P.2d 747, 761 (1994).
4. In determining whether a particular theory or technique is generally accepted, the court may consider expert opinions as well as evidence not in the record such as scientific and law review articles, and decisions from other jurisdictions. State v Cauthron, 120 Wn.2d 879, 888 (1993).
5. If there is a significant dispute between qualified experts as to the validity of scientific evidence, it may not be admitted. Cauthron, 120 Wash.2d at 887. However, unanimity is not required. State v. Copeland, 130 Wn.2d 244, 270 (1996).
6. Frye is not concerned with the acceptance of the results of a particular study or of the particular testing procedures followed in the case before the court. These concerns are addressed under the ER 702 inquiry of whether the expert testimony would be helpful to the trier of fact. Russell, 125 Wn.2d at 51.

7. The particular issues about TrueAllele raised by defense, such as those about dropout, stutter, and peak heights, are matters of weight that can be explored at trial. People v. Debraux, 21 N.Y.S.3d 535 (2015). These topics can be addressed on cross-examination and through the use of defense expert testimony.
8. Similarly issues regarding whether or not the analyst correctly estimated the number of contributors to the DNA mixture is an issue that goes to the weight of the evidence, not its admissibility. State v Gregory, 158 Wn.2d 759, 830 (2006).
9. Based upon the factual findings set forth above, the Court concludes that TrueAllele casework satisfies the Frye standard. The scientific theory upon which TrueAllele is based is generally accepted by the scientific community familiar with TrueAllele and probabilistic genotyping. Similarly, the technique used by TrueAllele is also generally accepted by that scientific community.

ER 702

10. Under ER 702, expert opinion evidence is admissible if (1) the witness qualifies as an expert and (2) the expert testimony would be helpful to the trier of fact. If the testing procedure is so flawed as to be unreliable, the results may be inadmissible because they are not helpful to the trier of fact. Russell, 125 Wn.2d at 51.
11. There is no dispute Dr. Mark Perlin is an expert. Defense expert David Balding referred to Dr. Perlin as one of the most foremost experts in the field of probabilistic genotyping.
12. Dr. Perlin's testimony about the TrueAllele results on the evidence would be helpful to the trier of fact. Based upon the factual findings set forth above, this Court concludes

that the defense has not shown that the TrueAllele results are so flawed as to be unreliable.

ORDER

For the reasons stated above, the defense motion to exclude the TrueAllele statistical results on the basis of *Frye* and ER 702 is DENIED.

Signed this _____ day of January, 2017.

_____e-filed_____
JUDGE MARIANE SPEARMAN

King County Superior Court
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King County Superior Court
Judicial Electronic Signature Page

Case Number:	10-1-09274-5
Case Title:	STATE OF WASHINGTON VS FAIR, EMANUEL DEMELVIN AKA
Document Title:	ORDER

Signed by:	Mariane Spearman
Date:	1/12/2017 2:06:07 PM

Judge/Commissioner: Mariane Spearman

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