DECLARATION OF MARK W. PERLIN

I, Mark W. Perlin, declare I have personal knowledge of the following, and if called upon to do so, could and would testify competently to the matters contained herein:

1.   I hold the following academic degrees: a B.A. in Chemistry from SUNY/ Binghamton, a Ph.D. in Mathematics from CUNY/Graduate School, an M.D. from the University of Chicago Pritzker School of Medicine, and a Ph.D. in Computer Science from Carnegie Mellon University. I have been issued thirteen patents. Prior to founding my own technology company, I was a senior research faculty member of Carnegie Mellon University's School of Computer Science. I have been qualified to testify as an expert in thirty-five jurisdictions. I am currently a scholar-in-residence faculty member in the Forensic Science and Law program at Duquesne University.

2.   I reside at 5885 Marlborough Avenue, Pittsburgh, PA 15217.

3.   Cybergenetics is a Pennsylvania corporation located at 160 North Craig Street, Suite 210, Pittsburgh, PA 15213. Cybergenetics is the owner of the TrueAllele software, as well as its proprietary source code.

The Role of TrueAllele in DNA Analysis

4.   TrueAllele is a probabilistic genotyping computer system that interprets DNA evidence using a statistical model.

5.   TrueAllele is used to analyze DNA evidence, particularly in cases where human review might be less reliable or not possible.

6.   A definite genotype can be readily determined when abundant DNA from one person produces unambiguous genetic data.

7.   However, when data signals are less definitive, or when two or more people contribute to the evidence, uncertainty arises.

8.   This uncertainty is expressed in the derived contributor genotype, which may describe different genetic identity possibilities.

9.   Such genotype uncertainty may translate into reduced identification information when a comparison is made with a suspect.

10.   The DNA identification task can thus be understood as a two-step process:

(1.) objectively inferring genotypes from evidence data, accounting for allele pair uncertainty using probability, and

(2.) subsequently matching genotypes, comparing evidence with a suspect relative to a population, to express the strength of association using probability.

11. The match strength is reported as a single number, the likelihood ratio (LR), which quantifies the change in identification information produced by having examined the DNA evidence.

12. The TrueAllele® Casework system is Cybergenetics' computer implementation of this two-step DNA identification inference approach.

13. Cybergenetics began developing TrueAllele 25 years ago, adding a mixture module 20 years ago.

14. The casework system underwent many rounds of testing and model refinement over 10 years before it was used in criminal casework, with the current version 25 released in 2009.

15. The TrueAllele computer objectively infers genotypes from DNA data through statistical modeling, without reference to a known comparison genotype.

16. To preserve the identification information present in the data, the system represents genotype uncertainty using probability.

17. These probabilistic genotypes are stored on a relational database.

18. Subsequent comparison with suspects or other individuals provides identification information that can be used as evidence.

TrueAllele's Widespread Acceptance

19. TrueAllele has been used by Cybergenetics in over 1,000 criminal cases, with expert witness testimony given in over 100 trials. TrueAllele results have been reported in 45 of the 50 states.

20. Courts accepting TrueAllele evidence include California, Florida, Georgia, Idaho, Indiana, Louisiana, Maryland, Massachusetts, Michigan, Nebraska, New Hampshire, New York, Ohio, Pennsylvania, South Carolina, Tennessee, Texas, Virginia, Washington, West Virginia, Wyoming, United States (Northern District of Georgia, Middle and Eastern Districts of Louisiana, Eastern District of Virginia), United States Marine Corps, Northern Ireland, and Australia.

21.   Over 12 crime laboratories have purchased the TrueAllele system for their own in-house use, and 10 labs are on-line with their validated systems.

22.   TrueAllele was used to identify human remains in the World Trade Center disaster, comparing 18,000 victim remains with 2,700 missing people.

23.   Both prosecutors and defenders use TrueAllele for determining DNA match statistics. TrueAllele is also used by innocence projects and for post-conviction relief (*Connecticut v. Ralph Birch, Connecticut v. Shawn Henning, Georgia v. Johnny Lee Gates, Georgia v. Jimmy Meders, Georgia v. Kerry Robinson, Idaho v. Christopher Tapp, Indiana v. Roosevelt Glenn, Indiana v. Darryl Pinkins, Maryland v. William Jamison, Montana v. Paul Jenkins, Montana v. Freddie Lawrence, New Mexico v. Gregory Hobbs, Texas v. Lydell Grant, Washington v. Raymond Ben*).

24.   TrueAllele's reliability has been affirmed in appellate precedent in Florida, Nebraska, New York, Pennsylvania, and Tennessee. *See: State of Florida v. Lajayvian Daniels,* 312 So. 3d 926 (Fla. Dist. Ct. App. 2021)*; State of Nebraska v. Charles Simmer,* 302 Neb. 369 (2019); *People of New York v. John Wakefield*, N.Y. App. Div. LEXIS 6153, A-812-29 (2019); *Commonwealth of Pennsylvania v. Kevin Foley*, 47 A.3d 882 (Pa. Super. 2012); and *State of Tennessee v. Demontez Watkins*, No. M2020-00035-CCA-R3-CD (2021).

25.   The TrueAllele calculation is entirely objective: when it determines the genotypes for the contributors to the mixture evidence, the computer has no knowledge of the comparison genotypes. Genotype comparison and match statistic determination are only done *after* genotypes have been computed. Moreover, the computer uses all the data, without user intervention. In this way, TrueAllele computing avoids human examination bias, and provides a fair match statistic.

26.   I agree with the conclusions that were reached in the *Foley* case, which found that (i) scientists can validate the reliability of a computerized process even if the source code is not available to the public; (ii) it would not be possible to market TrueAllele if it were available for free; (iii) TrueAllele has been tested and validated.

TrueAllele is Considered to be Reliable

27.   There is no genuine controversy as to the validity and reliability of the TrueAllele method. To the contrary, computer analysis of uncertain data using probability modeling is the

scientific norm. Forensic science researchers see this as the best approach.

28. Cybergenetics thoroughly tests its software before it is released.

29. Over forty validation studies have been conducted by Cybergenetics and other groups to establish the reliability of the TrueAllele method and software. Eight of these studies have been published in peer-reviewed scientific journals, for both laboratory-generated and casework DNA samples. Source code was not needed or used in any of these studies.

30. In the "peer-review" process, scientists describe their research methods, results and conclusions in a scientific paper, which they submit to a journal for publication. An editor at the journal has (at least) two independent and anonymous scientists in the field read the paper, assess its merits, and advise on the suitability of the manuscript for publication. The paper is then accepted, rejected, or sent back to the authors for revision and another round of review.

31. A "laboratory-generated" validation study uses data that has been synthesized in a DNA laboratory, and is of known genotype composition. Five published TrueAllele papers of this type are: Perlin MW, Sinelnikov A. An information gap in DNA evidence interpretation. *PLoS ONE*. 2009;4(12):e8327; Ballantyne J, Hanson EK, Perlin MW. DNA mixture genotyping by probabilistic computer interpretation of binomially-sampled laser captured cell populations: combining quantitative data for greater identification information. *Science & Justice*. 2013;52(2):103-14; Perlin MW, 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; Greenspoon SA, Schiermeier-Wood L, and Jenkins BC. Establishing the limits of TrueAllele® Casework: a validation study. *Journal of Forensic Sciences*. 2015;60(5):1263-1276; Bauer DW, Butt N, Hornyak JM, Perlin MW. Validating TrueAllele® interpretation of DNA mixtures containing up to ten unknown contributors. *Journal of Forensic Sciences*. 65(2):380-398, 2020.

32. A "casework" validation study uses DNA data exhibiting real-world issues developed by a crime laboratory in the course of their usual casework activity. Three published TrueAllele papers of this type are: Perlin MW, Legler MM, Spencer CE, Smith JL, Allan WP, Belrose JL, Duceman BW. Validating TrueAllele® DNA mixture interpretation. *Journal of Forensic Sciences*. 2011;56(6):1430-1447; Perlin MW, Belrose JL, Duceman BW. New York State TrueAllele®

Casework validation study. *Journal of Forensic Sciences*. 2013;58(6):1458-66; Perlin MW, Dormer K, Hornyak J, Schiermeier-Wood L, and Greenspoon S, TrueAllele® Casework on Virginia DNA mixture evidence: computer and manual interpretation in 72 reported criminal cases. *PLoS ONE*. 2014:9(3):e92837.

33. Conducting such validations is consistent with the FBI's 2010 Scientific Working Group on DNA Analysis Methods (SWGDAM) interpretation guidelines. TrueAllele complies with the 2015 SWGDAM validation guidelines for probabilistic genotyping systems. Regulatory bodies in New York and Virginia have had independent scientists review validation studies before they granted approval for their state crime laboratories to use TrueAllele for casework.

34. TrueAllele has been admitted into evidence after opposition challenge in thirty-five courts, located in California, Florida, Georgia, Indiana, Louisiana, Maryland, Massachusetts, Nebraska, New York, Ohio, Pennsylvania, South Carolina, Tennessee, Virginia, Washington, United States, Northern Ireland and Australia.

35. Thirty-three admissibility decisions in the United States are: People of California v. Dupree Langston, Kern County (Kelly-Frye), BF139247B, January 10, 2013; State of Florida v. Lajayvian Daniels, Palm Beach County (Frye), 2015CF009320AMB, October 31, 2018; State of Georgia v. Adedoja Bah, Douglas Judicial Circuit (Harper), 17CR00938, October 16, 2019; State of Georgia v. Alexander Battle, Ben Hill County (Harper), 16-CR-082, May 22, 2019; State of Georgia v. Monte Baugh and Thaddeus Howell, Coweta County (Harper), 2017 R 618, March 11, 2019; State of Georgia v. Rahul Joseph Das, Western Judicial Circuit (Harper), 2020-CR-125-S, August 16, 2021; State of Georgia v. Nathaniel Day, Tifton Judicial Circuit (Harper), 2018CR141, October 23, 2019; State of Georgia v. Zarren Garner, Western Judicial Circuit (Harper), SU-19-CR-0586-S, April 26, 2021; State of Georgia v. Thaddus Nundra, South Georgia Circuit (Harper), 18-CR-134, January 21, 2019; State of Georgia v. Lashumbia Session, Cobb County (Harper), Indictment 18-9-4511-58, December 30, 2021; State of Georgia v. Guy Sewell, Floyd County (Harper), 17-CR-1675 JFL004, August 7, 2019; State of Indiana v. Randal Coalter, Perry County (Daubert), 62C01-1703-MR-192, August 2, 2017; State of Indiana v. Dugniqio Forest, Vanderburgh County (Daubert), 82D03-1501-F2-566, June 3, 2016; State of Indiana v. Vaylen Glazebrook, Monroe County (Daubert), 53C02-

1411-F1-1066, February 16, 2018; State of Indiana v. Malcolm Wade, Monroe County (Daubert), 53C02-1411-F3-1042, August 3, 2016; State of Louisiana v. Chattley Chesterfield and Samuel Nicolas, East Baton Rouge Parish (Daubert), 01-13-0316 (II), November 6, 2014; State of Louisiana v. Harold Houston, Jefferson Parish (Daubert), 16-3682, May 19, 2017; State of Louisiana v. Kyle Russ, East Baton Rouge Parish (Daubert), 01-14-0566, April 30, 2019; State of Maryland v. Tyrone Harvin, Baltimore City (Daubert), 118261014, October, 2021; Commonwealth of Massachusetts v. Heidi Bartlett, Plymouth County (Daubert), PLCR2012-00157, May 25, 2016; State of Nebraska v. Charles Simmer, Douglas County (Daubert), CR16-1634, February 2, 2018; People of New York v. John Wakefield, Schenectady County (Frye), A-812-29, February 11, 2015; People of New York v. Casey Wilson, Chemung County (Frye), 2013-331, May 1, 2019; State of Ohio v. David Mathis, Cuyahoga County (Daubert), CR-16-611539-A, April 13, 2018; State of Ohio v. Maurice Shaw, Cuyahoga County (Daubert), CR-13-575691, October 10, 2014; Commonwealth of Pennsylvania v. Kevin Foley, Indiana County (Frye); State of South Carolina v. Jaquard Aiken, Beaufort County (Jones), 20121212-683, October 27, 2015; State of Tennessee v. Abdullah Powell, Stewart County (Daubert), 2017-CR-155, January 15, 2021; State of Tennessee v. Demontez Watkins, Davidson County (Daubert), 2017-C-1811, December 17, 2018; Commonwealth of Virginia v. Matthew Brady, Colonial Heights County (Spencer-Frye), CR11000494, July 26, 2013; State of Washington v. Emanuel Fair, King County (Frye), 10-1-09274-5 SEA, January 12, 2017; United States v. Lenard Gibbs, Northern District of Georgia (Daubert), 1:17-CR-207, May 30, 2019; United States v. Curtis Johnson, Eastern District of Louisiana (Daubert), 17-201, July 14, 2021.

36.   The Pennsylvania Superior Court affirmed the Foley decision on February 15, 2012, 2012 PA Super 31, No. 2039 WDA 2009. The New York State Supreme Court affirmed the Wilson decision on August 15, 2019, 175 A.D.3d 158 (3d Dep't 2019). The Nebraska Supreme Court affirmed the Simmer decision on November 1, 2019, 302 Neb. 369. The Florida Court of Appeal affirmed the Daniels decision on February 24, 2021, 312 So. 3d 926 (Fla. Dist. Ct. App. 2021). The Tennessee Court of Criminal Appeals affirmed the Watkins decision on December 16, 2021, No. M2020-00035-CCA-R3-CD.

37.   Cybergenetics has a strong financial incentive to ensure the reliability of its widely

used TrueAllele system.

38. Cybergenetics continually tests its software and conducts scientific validation studies to ensure TrueAllele's reliability. Source code is not used in validation studies.

39. Cybergenetics improved the speed, accuracy and generality of the user interface LR match statistic calculation in February of 2014. The previous LR estimate could understate the match statistic by around a factor of ten. Genotype computation was not affected. This change is described in Cybergenetics application note "TrueAllele® VUIer™ Likelihood Ratio Calculation."

Background on Software Source Code

40. People write a computer program in a human-readable programming language using "source code", which is text that is used for developing and editing software.

41. This source code is later translated into computer-readable "executable" software, which is an application program used for testing and running the software on a computer.

42. The source code details step-by-step human-readable instructions that describe to the computer and programmers how the program operates.

43. TrueAllele is written in MATLAB (for MATrix LABoratory), a high-level mathematical language for programming and visualizing numerical algorithms made by the MathWorks (Natick, MA).

44. Here is an example of MATLAB source code, simplified from a few lines of the MathWorks built-in "mhsample" function that performs Metropolis-Hastings statistical sampling:

```
U = log(rand(nchain,nsamples+burnin));
for i = 1-burnin:nsamples
    y = proprnd(x0);
    q1 = logproppdf(x0,y);
    q2 = logproppdf(y,x0);
    rho = (q1+logpdf(y))-(q2+logpdf(x0));
    Ui = U(:,i+burnin);
    acc = Ui<= min(rho,0);
    x0(acc,:) = y(acc,:);
```

```
    accept = accept+(acc);
end
```

45.   Thus, source code is written in language that humans are capable of understanding, but only if they are fluent in reading, writing and interpreting the particular language that the program is written in.

46.   TrueAllele has about 170,000 lines of computer source code, written by multiple programmers over two decades. The computer code is dense mathematical text. It can take hours for a person to read through even a few dozen lines of MATLAB to decipher what it does. Reading at ten lines per hour would entail eight and a half person-years to review all the source code.

47.   In my opinion, it is wholly unrealistic to expect that reading through TrueAllele source code would yield meaningful information.

Why TrueAllele is a Trade Secret

48.   People can easily copy a computer program if they have its source code.

49.   Source code contains the software design, engineering know-how, and algorithmic implementation of the entire computer program.

50.   Cybergenetics has invested millions of dollars over two decades to develop its TrueAllele system, the company's flagship product. Although the technology is patented, the source code itself is not disclosed by any patent and cannot be derived from any publicly disclosed source. Patent protection is not automatic, and litigation can cost tens of millions of dollars.

51.   Cybergenetics considers the TrueAllele source code to be a trade secret. Cybergenetics does not disclose the source code to anyone outside the company. The source code is not distributed to most employees of Cybergenetics, and copies are not provided to individuals, businesses or government agencies that use or license the software.

52.   The fact that the source code is kept secret provides Cybergenetics with a significant advantage over others who do not have access to the source code and do not have the programming know-how or are not willing to make the investment necessary to develop comparable software.

53.   Cybergenetics operates in a highly competitive commercial environment.

54.   In recent years, at least ten other groups have developed similar software.

55.   There is keen interest from competitors to find out how to replicate TrueAllele. The TrueAllele software represents a technological breakthrough that has not been successfully replicated by any other company as of this date.

56.   Disclosure of the TrueAllele source code trade secret would cause irreparable harm to the company, enabling competitors to easily copy the company's proprietary products and services.

57.   Ownership of the TrueAllele program and source code provides Cybergenetics with an advantage over its competitors who do not know the proprietary code and could not legally duplicate it.

58.   Cybergenetics takes reasonable measures to protect the secrecy of the source code. For example, all information relating to the source code is housed on secure computers.

59.   TrueAllele's source code derives value from remaining secret, and it has never been disclosed to the public.

60.   In contrast to so-called "open source" programs, for-profit companies generally do not make their source code available to the public. The relatively few companies that have an open source business model tend to operate in a very large market, utilize free programmer coding, conduct little innovation, and earn their main revenue by providing software services.

61.   Commercial software programs are extensively validated while in development and before release and commercialization. By their nature, open source programs typically are not validated prior to release, because the process of perfecting software is costly. Open source forensic DNA analysis software programs tend to be relatively short programs consisting of several hundreds of lines of code that realistically can be reviewed by a human being.

62.   Open source software suffers from a lack of version control and quality assurance, since any unrelated party can make code changes and release untested products. This chaotic development approach is in marked contrast to the more controlled reliability and versioning requirements of forensic software that is used in criminal proceedings.

Irremediable Risks of Source Code Disclosure

63.   Third party review of source code can divulge proprietary trade secrets wholly unrelated to reliability, but valuable to competitors. Once a review results in a release of hard-earned

engineering know-how, that disclosure cannot be reversed. The source code reviewer's knowledge can be written into other software systems, shared with interested parties, or sold for profit. There are no adequate remedies for redress once this proprietary information has been released.

64.   The credibility and trustworthiness of retained witnesses who testify about the alleged need for forensic source code has been undermined in cross-examination (*New York v. Jaquan Collins*, *Pennsylvania v. Michael Robinson*). Permitting such individuals to see proprietary information that is immaterial to a case is not reasonable, nor is it in the interest of justice.

65.   Protective orders for source code are sometimes used in expensive civil litigation for patent infringement, which is not germane to criminal proceedings. Protective orders may fail to protect valuable trade secrets, leading to unwanted disclosure of proprietary designs, methods, and know-how (*Superspeed LLC v. Google*, United States District Court for the Southern District of Texas; *Bradford Technologies, Inc. v. NCV Software.com*, United States District Court for the Northern District of California; *Apple v. Samsung*, United States District Court for the Northern District of California; *Eli Lilly & Co. v. Gottstein*, United States Court of Appeals for the Second Circuit; *Smith & Fuller, PA v. Cooper Tire & Rubber Co.*, United States Court of Appeals for the Fifth Circuit).

66.   There is no real effective remedy once a protective order is violated. Courts typically merely reimburse the fees that were incurred by the party whose secrets were revealed. In a case involving source code that is a trade secret, however, once the source code has been revealed in breach of a protective order, it generally loses its status as a trade secret. The genie can't be put back in the bottle, and reimbursement of legal fees does nothing to compensate for the loss of commercial value.

67.   Cybergenetics uniquely provides accurate, objective, and neutral DNA identification information for criminal justice. TrueAllele DNA match results are used by both prosecution and defense for an unbiased statistical assessment of biological evidence. Crime laboratories rely on their validated TrueAllele systems for effective interpretation of complex DNA data. Jeopardizing the existence of Cybergenetics through a disclosure of its source code is unreasonable, and does not serve the interests of justice.

Why TrueAllele Source Code is Not Needed

68.   Cybergenetics offers the TrueAllele software for license by crime labs and to other interested parties. The company currently charges a base license fee of $40,000. Source code is not provided to the labs, only the executable software.

69.   Cybergenetics makes the software available to defendants without charge, so that they can conduct their own testing. Source code is not needed for this access or testing.

70.   Individuals and companies can also submit samples to Cybergenetics for testing and analysis for a fee. Source code is not needed for this service.

71.   Cybergenetics provides opposing experts the opportunity to review the TrueAllele process, examine results, and ask questions. This review can be done in Cybergenetics's Pittsburgh office, or through an Internet Skype-like meeting. Cybergenetics regularly explains the system, and the results obtained in a case, to both prosecution and defense. This introduction to the TrueAllele method, the case data, and the application of the method to the data, is a logical first step in understanding how the system works. Source code is not necessary for this review.

72.   The TrueAllele method is inherently objective, since the computer determines evidence genotypes without any knowledge of the comparison reference genotypes or user manipulation of DNA data. Hence there is no possibility of examination bias when determining genotypes from the DNA data. Match statistics, whether inclusionary or exclusionary, are calculated only afterwards by comparing evidence genotypes with reference genotypes. Source code is not needed to understand that the TrueAllele process is objective.

73.   TrueAllele's reliability was established on the evidence in this case. The report and its supporting case packet described the system's sensitivity, specificity and reproducibility on the DNA evidence. The case packet gives the data and parameter inputs used in running the program in the case. The packet also includes a case-specific mini-validation study of reported TrueAllele match statistics, measuring match specificity by comparison with non-contributor genotypes. Source code is not needed to understand or interpret these materials.

74.   Additional discovery material for this case was provided on an optical disc. The DVD contains documents related to TrueAllele's reliability, such as background reading, over thirty

validation studies and publications, regulatory approvals, general acceptance, and admissibility rulings. There are tutorial videos that describe TrueAllele methods and explain how the system works, as well as continuing legal education talks. The VUIer™ software for reviewing TrueAllele results is provided (with both Windows and Macintosh installers), along with instructions and user manuals. Case-specific files (data, reports, PowerPoint, case packet, VUIer input) are disclosed, enabling a thorough expert review. Source code is not needed to access these materials, read the files, use the executable VUIer software, or examine the computer results.

75.   Cybergenetics offers commercial services for validating DNA mixture interpretation methods. Any party can provide DNA validation data and obtain these services to assess TrueAllele reliability. Since TrueAllele is an objective process, and produces unbiased DNA identification results that do not "know" comparison genotypes during analysis, it is easy for Cybergenetics to perform these studies. Source code is not needed for obtaining these services.

76.   TrueAllele processing is available on-line through Cloud computing. Therefore, the system's capability can be operated as an Internet service, without purchasing a product. Any party can operate TrueAllele on the Cloud, and process their own DNA case or validation data. Moreover, Cybergenetics makes this TrueAllele Cloud capability available to opposing parties at no charge so that they can conduct their own testing. Source code is not needed or useful for assessing TrueAllele reliability, which is done by empirically testing the executable program on actual data.

77.   Although the source code for TrueAllele is a secret, the methodology it employs and implements has been disclosed. Cybergenetics has published the core mathematics of TrueAllele's underlying mathematical model for over 20 years. These publications include scientific papers (1995, 2001, 2009, and 2011) and patent specifications (2000 and 2001). Cybergenetics provides a compilation of these mathematical methods in a single summary document. This information discloses TrueAllele's genotype modeling mechanism, and enables others to understand or replicate the basic method. Indeed, at least ten other groups have developed their own software that uses TrueAllele's linear mixture analysis approach. The source code is not necessary or helpful to understand or test the methodology or reliability of the analysis.

78.   To my knowledge, source code is not generally made available for most other commercial software that is regularly used and relied upon in the area of forensic DNA identification. Such software includes Life Technology's "Genemapper ID" for generating and analyzing DNA data signals, the Federal Bureau of Investigation's "PopStats" for producing DNA match statistics or "CODIS" for maintaining a DNA database, and Microsoft "Excel" for conducting additional DNA data analysis. Source code is not needed to assess the reliability of these essential software programs, since they have all been tested and empirically validated.

79. Access to source code does not help identify problems in commercial probabilistic genotyping software. In a peer-reviewed scientific paper, the developers of the commercial STRmix™ probabilistic genotyping software wrote that "any miscode found that has been identified in STRmix™ development or use, was identified by examination of the program's output and not the source code. It would be nearly impossible to identify subtle errors in code by viewing the code. The identification has always been a result of comparison of the results produced by a program to some known control. The results of these comparisons then trigger the examination of a specific section of the code in order to discover the source of the discrepancy."

Courts Have Ruled that TrueAllele Source Code is Not Needed

80.   Courts in virtually all states that have considered the matter have ruled that defendants do not need TrueAllele source code to assess the software's reliability.

81.   When TrueAllele source code discovery has been requested by an opposing party, courts have rarely required its disclosure, and then only under a suitably restrictive protective order. The requesting parties have been unable to show why source code would be material, reasonable, and in the interest of justice. Courts have denied such discovery requests in California, Georgia, Maryland, Nebraska, New York, Ohio, Pennsylvania, Tennessee, Virginia, and Washington, often providing written rulings (*California v. Martell Chubbs*, *Nebraska v. Charles Simmer, New York v. John Wakefield*, *Ohio v. Maurice Shaw*, *Pennsylvania v. Chelsea Arganda and Chester White*, *Pennsylvania v. Kevin Foley, Pennsylvania v. Michael Robinson, Washington v. Emanuel Fair*).

82.   The Commonwealth of Pennsylvania Superior Court decided the TrueAllele source code trade secret issue in their 2012 appellate admissibility ruling in *Commonwealth v. Kevin Foley*.

Their opinion stated, '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.' 38 A.3d 882, 2012 Pa. Super. 31 (Pa. Super. Ct 2012)

83. The Pennsylvania Superior Court opinion continued, '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, the computer was four and a half orders of magnitude more efficacious than human review." Both of these papers were published in peer-reviewed journals; thus, their contents were reviewed by other scholars in the field.'

84. In his 2013 *Spencer* decision on TrueAllele reliability, Chief Judge W. Allan Sharrett of the Sixth Judicial Circuit of Virginia denied a defendant's request for source code in *Commonwealth of Virginia v. Matthew Brady*. He wrote, "The first [Daubert factor] is whether the science could and had been tested. *Id.* at 593. Here, much is made of the inability to thoroughly test the TrueAllele protocol, because its source code is unknown. However, the Court places great emphasis on the observation in *Commonwealth* v. *Foley*, 38 A.3d 882, 2012 Pa. Super. 31 (Pa. Super. Ct 2012) that validation studies are the best tests of the reliability of source codes. In this case, validation studies have been performed with positive results. They have not shown that the TrueAllele system is junk science; they have shown, in fact, that it is reliable."

85.   In a 2015 unpublished Decision for a Writ of Mandate, the California Court of Appeals ruled on why TrueAllele source code was not needed in *People v. Martell Chubbs*. Judge Willhite wrote "Chubbs has received extensive information regarding TrueAllele's methodology and underlying assumptions, but he has not demonstrated how TrueAllele's source code is necessary to his ability to test the reliability of its results. We therefore conclude that Chubbs has not made a prima facie showing of the particularized need for TrueAllele's source code."

86.   In a 2015 Decision and Order, Chief Administrative Judge (Outside New York City) Michael Coccoma ruled on why TrueAllele source code was not needed in *People of New York v. John Wakefield*. Judge Coccoma wrote, 'Simply put, the Defendant's <u>Crawford</u> argument is misplaced. The source code is <u>not</u> a witness, it is <u>not</u> testimonial in nature, and it is <u>not</u> "a surrogate for accusatory in-court testimony."' The state Supreme Court *affirmed*, N.Y. App. Div. LEXIS 6153, August 15, 2019.

87.   In a 2016 Memorandum Order, Allegheny County Judge Jill Rangos ruled on why TrueAllele source code was not needed in *Commonwealth of Pennsylvania v. Michael Robinson*. Judge Rangos wrote, "As the defense has argued that *Foley* is not controlling on the question of materiality of the source code, this Court held a two-day hearing and considered expert testimony and argument. After considering the testimony, this Court determined that the source code is not material to the defendant's ability to pursue a defense."

88.   Judge Rangos continued, "An order requiring Cybergenetics to produce the source code would be unreasonable, as release would have the potential to cause great harm to Cybergenetics. Rather than comply, Dr. Perlin could decline to act as a Commonwealth expert, thereby seriously handicapping the Commonwealth's case."

89.   In a 2017 Findings of Fact and Conclusions of Law on Defense Motion to Compel Cybergenetics' TrueAllele Casework Source Code, King County Judge Mariane Spearman ruled on why TrueAllele source code was not needed in *State of Washington v. Emanuel Fair*. In her ten-page

Order, Judge Spearman wrote, "The Defense has not articulated with particularity what material information, if any, could be found by reviewing the source code. As several experts who work in the field of forensic DNA testing have testified, an examination of the source code is not necessary in order to determine the reliability of TrueAllele and validate it for casework."

90. Judge Spearman continued, "The Defense has failed to meet its burden to show that disclosure of the source code is material and reasonable. Based upon the factual findings set forth above, this Court is not persuaded that a review of the source code is necessary in order to determine whether TrueAllele is reliable. The defense demand for the source code is not material or reasonable because the testimony in this case from both state and defense experts establishes that scientists can confirm the reliability of TrueAllele without access to the source code. This testimony is consistent with the holding of other courts that have addressed this same issue."

91. Judge Spearman concluded, "Further, the usefulness of disclosing the source code is outweighed by a substantial risk of financial harm to Cybergenetics. Scientists can confirm the reliability of Trueallele without access to the source code. Dr. Perlin and Cybergenetics have a legitimate interest in keeping the source code, a trade secret, confidential."

92. Another published case is from the Nebraska Supreme Court in *State of Nebraska v. Charles Simmer*, 935 N.W.2d 167, 172 (Neb. 2019). Regarding source code, The Nebraska Supreme Court affirmed the trial court's decision to not compel production of the source code. The court in *Simmer* determined that it was not "required to find that TrueAllele had been validated 'from a software engineering perspective' to find it reliable." Id. at 180. Rather, the court relied on the State's presentation of "significant evidence that TrueAllele is reliable." Id. at 181. The evidence included "Perlin's testimony and copious documentary evidence describing TrueAllele's methodology," the fact that "SWGDAM has approved the use of validated and documented probabilistic genotyping software and provided guidelines for its validation," which "TrueAllele has complied with" and finally that "TrueAllele's methodology has been repeatedly tested and validated in peer-reviewed studies."

93.   In the following fourteen decisions, after holding a hearing with expert testimony, the court denied TrueAllele source code access. Commonwealth of Pennsylvania v. Kevin Foley, 2012 PA Super 31, No. 2039 WDA 2009, February 15, 2012; Commonwealth of Virginia v. Matthew Brady, Circuit Court for the City of Colonial Heights, CR11000494, July 26, 2013; State of Ohio v. Maurice Shaw, Court of Common Pleas Cuyahoga County, 13-CR-575691, October 9, 2014; People of New York v. John Wakefield, Schenectady County Court, A-812-29, February 9, 2015; Commonwealth of Pennsylvania v. Michael Robinson, Superior Court of Pennsylvania Pittsburgh District, CC 20130007777, December 7, 2015; State of Washington v. Emanuel Fair, Superior Court Of Washington For King County, 10-1-09274-5 SEA, January 2017; State of Missouri v. Reginald Clemons, St. Louis City Circuit, 22911-01758B-01, November 27, 2017; State of Nebraska v. Charles Simmer, District Court of Douglas County, CR16-1634, February 2, 2018; State of Tennessee v. Demontez Watkins, Criminal Court of Davidson County, 2017-C-1811, December 17, 2018; State of Georgia v. Thaddus Nundra, Superior Court of Decatur County, 18-CR-134, January 21, 2019; Georgia v. Monte Baugh and Thaddeus Howell, Superior Court of Coweta County, 2017-CR-618, March 11, 2019; State of Georgia v. Alexander Battle, Superior Court of Ben Hill County, 16-CR-082, May 22, 2019; State of Georgia v. Adedoja Bah, Superior Court of Douglas County, 17CR00938, October 22, 2019; Commonwealth of Pennsylvania v. Anthony Spudis, Court of Common Pleas of Luzerne County, 1305 OF 2018, October 20, 2021.

94.   In the following seven decisions, without holding a hearing or expert testimony, the court denied TrueAllele source code access. State of Maryland v. Adan Espinoza Canela, Baltimore City Circuit, 104176021, March 11, 2013; Commonwealth of Virginia v. Darwin Bowman, Loudoun County, 22005, May 24, 2013; People of California v. Martell Chubbs, Los Angeles County Superior Court, NA093179, 2015; Commonwealth of Pennsylvania v. Allen Wade, Court of Common Pleas of Allegheny County, CC201404799, January 14, 2016; Commonwealth of Pennsylvania v. Jake Knight, Superior Court of Pennsylvania, 9 WDM 2016, May 5, 2016; Commonwealth of Pennsylvania v. Chelsea Arganda and Chester White, Superior Court of Pennsylvania Pittsburgh District, CC 201317748 and 201317753, June 8, 2016; People of California v. Billy Ray Johnson, California Fifth Appellate District Court, F071640, July 11, 2019.

Cybergenetics is Makes its TrueAllele Technology Available to Defendants

95.   For transparency, the TrueAllele algorithms have been published. Moreover, Cybergenetics has collated descriptions of its algorithms, and provided them to the defense.

96.   Empirical testing of interpretation software on actual DNA data is the scientific and legal standard for assessing reliability. Cybergenetics provides free access to the TrueAllele application software, so that the defense can test the system on its own at no charge.

I declare the above is true and correct under penalty of perjury under the law of the Commonwealth of Pennsylvania, executed this __ day of January 2022 in Pittsburgh, Pennsylvania.

By: _____