IN THE UNITED STATES DISTRICT COURT
FOR THE NORTHERN DISTRICT OF OHIO

CYBERGENETICS CORP.,

Plaintiff,

v.

INSTITUTE OF ENVIRONMENTAL SCIENCE AND RESEARCH and NICHEVISION INC.,

Defendants.

Case No. 5:19-CV-1197

JURY TRIAL DEMANDED

AMENDED COMPLAINT FOR PATENT INFRINGEMENT

Plaintiff Cybergenetics Corp. ("Cybergenetics") hereby asserts a claim for patent infringement against Defendants the Institute of Environmental Science and Research ("ESR") and NicheVision Inc. ("NicheVision") (collectively, "Defendants"), and in support thereof alleges, based on actual knowledge as to Cybergenetics' own activities and on information and belief as to the activities of others, as follows:

Nature of the Action

1. This is an action for patent infringement arising under the patent laws of the United States, 35 U.S.C. § 1 *et seq.*, specifically including 35 U.S.C. § 271.

2. As set forth in detail below, ESR and NicheVision have infringed U.S. Patent No. 8,898,021 ("the '021 Patent") and U.S. Patent No. 9,708,642 ("the '642 Patent) (collectively, "the Patents-in-Suit"), both individually and through their combined actions, in connection with supplying the STRmix™ probabilistic genotyping software product and related services to customers in the United States.

The Parties

3. Cybergenetics Corp. is a corporation organized under the laws of the Commonwealth of Pennsylvania, with its principal place of business at 160 N Craig Street, Suite 210, Pittsburgh, Pennsylvania 15213.

4. On information and belief, the Institute of Environmental Science and Research is a corporation organized and existing under the laws of New Zealand, with a principal place of business at 34 Kenepuru Drive, Kenepuru, Porirua 5022, New Zealand. ESR is a Crown Research Institute of the New Zealand Government.

5. On information and belief, NicheVision Inc. is a corporation organized and existing under the laws of the State of Ohio, with a principal of business at 526 South Main Street, Suite 714G, Akron, Ohio 44311.

Jurisdiction and Venue

6. This Court has subject matter jurisdiction over this patent infringement action pursuant to 28 U.S.C. §§ 1331 and 1338(a).

7. This Court has personal jurisdiction over ESR pursuant to the Ohio Long-arm Statute, Ohio Revised Code § 2307.382, at least because ESR: (i) has transacted business in Ohio, (ii) has contracted to supply services or goods in Ohio, and (iii) has caused tortious injury by an act in Ohio. More particularly, on information and belief, ESR has entered into an agreement with NicheVision pursuant to which NicheVision acts as the exclusive sales representative and distributor of the STRmix™ probabilistic genotyping software product and related services for the entire United States, including Ohio. Through its contractual relationship with NicheVision, ESR has purposefully directed its activities towards Ohio, and thus this Court's exercise of personal jurisdiction over ESR is reasonable and consistent with the requirements of the Due Process Clause of the United States Constitution.

8. This Court has personal jurisdiction over NicheVision by virtue of NicheVision being incorporated in the State of Ohio, maintaining its principal place of business in the State of Ohio, and doing business in the State of Ohio.

9. Venue may lie in this judicial district as to Cybergenetics' claims against ESR pursuant to 28 U.S.C. §§ 1391(c) and/or 1400(b) at least because ESR, as an entity not resident in the United States, may be sued in any judicial district.

10. Venue may lie in this judicial district as to Cybergenetics' claims against NicheVision pursuant to 28 U.S.C. §§ 1391(b)-(d) and/or 1400(b) at least because NicheVision resides in this judicial district, and because a substantial part of the events giving rise to this infringement claim occurred in this judicial district.

11. Joinder of Cybergenetics' claims against ESR and NicheVision is permissible under 35 U.S.C. § 299 because (a) Cybergenetics is seeking to hold Defendants jointly and severally liable for infringement of the Patents-in-Suit, and the claims against each Defendant arise out of the same transaction, occurrence, or series of transactions or occurrences relating to the making, using, importing, offering for sale, or selling of the same accused product, and (b) questions of fact common to all Defendants will arise in this action. More particularly, on information and belief, ESR makes the accused STRmix™ probabilistic genotyping software product in New Zealand, ESR and/or NicheVision import the product into the United States, and ESR and/or NicheVision offer to sell and sell the product to customers in the United States.

The Patents-in-Suit

12. The '021 Patent, titled "Method and System for DNA Mixture Analysis," was duly and legally issued by the United States Patent and Trademark Office on November 25, 2014. The '021 Patent issued from U.S. Patent Application No. 09/776,096 filed February 2,

2001 ("the '096 Application"). The '021 Patent will expire on February 2, 2021. A true and correct copy of the '021 Patent is attached hereto as Exhibit A.

13. The '642 Patent, titled "Method and System for DNA Mixture Analysis," was duly and legally issued by the United States Patent and Trademark Office on July 18, 2017. The '642 Patent issued from U.S. Patent Application No. 14/548,972 filed November 20, 2014 ("the '972 Application"). The '972 Application is a continuation of the '096 Application. The '642 Patent will expire on February 2, 2021. A true and correct copy of the '642 Patent is attached hereto as Exhibit B.

14. The Patents-in-Suit are generally directed to computer-based systems and methods for analyzing a DNA sample comprising a mixture of DNA from multiple sources in order to determine a likelihood that a particular person's DNA is, or is not, contained within the mixture. The patented DNA mixture analysis inventions have particular applicability in the field of forensic science, being useful for helping to find and convict criminals, as well as to exonerate innocent suspects, from a sample comprising a mixture of DNA from multiple individuals.

15. In accordance with a particular embodiment, the method may comprise the steps of (i) obtaining a mixed DNA sample, (ii) amplifying the DNA sample to produce a product, (iii) detecting the product to produce a signal, and (iv) analyzing the signal to determine information about the composition of the mixed DNA sample. A system implementing the inventions can provide high-quality estimates, and can be used to determine genotypes, mixture weights, and likelihood ratios. Such a system provides confidence measures in the results it computes, and can be used to generate reports and intuitive visualizations. Accordingly, the patented inventions can be applied to assist in the identification of a suspect from a mixture of DNA from multiple individuals, thereby greatly improving the effectiveness of DNA crime analysis compared to

previously known methods for analyzing DNA mixtures. The patented inventions are described in more detail below.

16. Cybergenetics is the owner by assignment of the Patents-in-Suit, having received the entire right, title and interest in and to the inventions covered by the Patents-in-Suit.

Scientific Background

Forensic Identification of Individuals Using "STR" DNA Sequences

17. Deoxyribonucleic acid (DNA) is an informational molecule present in every cell in the human body that contains the instructions for reproduction, development, and life. DNA information can also be used to identify people, apprehend suspects, convict the guilty, and exonerate the innocent.[1]

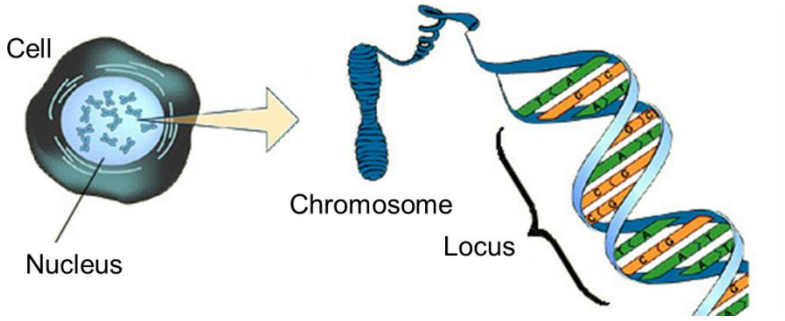
18. A cell's genetic material is contained in its nucleus. The DNA text is packaged into 23 chromosomes. Chromosomes come in pairs, with an individual inheriting one maternal copy from their mother, and one paternal copy from their father.

19. The genetic book of life is written in a four-letter DNA alphabet—A (for the nucleotide base adenine), C (cytosine), G (guanine) and T (thymine). Long DNA sentences of A, C, G and T record human genes, typically 100 to 10,000 letters long. A gene usually "codes" for some biological function. Because a change in the sequences of these coding genes often results in a lack of that biological function, such coding genes are "conserved" over evolutionary time. This leads to little variation in coding sequences between individuals. Other portions of DNA are considered "non-coding" because they are not associated with a biological function.

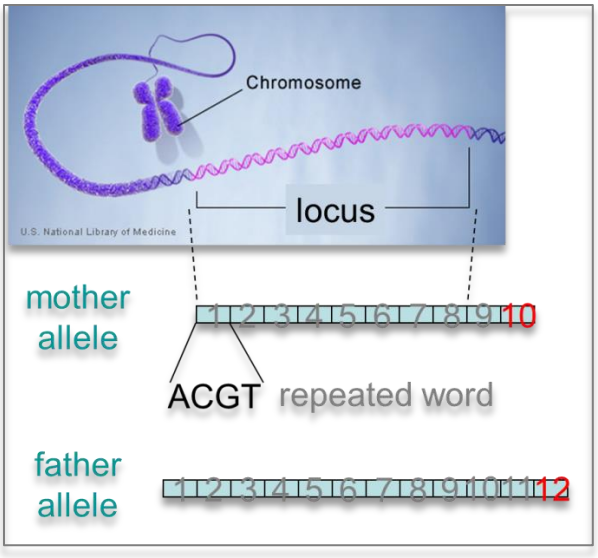
[1] Paragraphs 17-35 are summarized from Mark W. Perlin, *DNA Identification Science: An Introduction for Lawyers*, *in* Forensic Sciences (Cyril H. Wecht, ed. 2017), unless otherwise noted.

Each possible variation in a specific genetic sequence, whether coding or non-coding, is called an "allele".

20. Forensic DNA-based identification relies on relatively unique features that can distinguish between different people. Because conserved genes do not serve this purpose, forensic scientists use non-coding DNA locations (or "loci"), to develop highly polymorphic (i.e., genetically varied) markers that have many different alleles.



21. Currently, and at the time of the inventions described and claimed in the Patents-in-Suit, forensic identification uses markers referred to as short tandem repeats, or STRs. Short tandem repeat markers are genetic loci that have many allele variants, are abundant throughout the genome, and are easy to measure in the laboratory. A forensic STR allele is a short DNA word, typically four or five letters long, that tandemly repeats a fixed number of times (e.g., 10 to 20). More repeat units in an allele results in greater DNA sentence length. For example, the D5S818 STR locus has the four letter repeat unit "AGAT":



22. A locus allele containing ten of these repeat units would have a repeat section 40 DNA letters long (10 units times 4 letters per unit), and is designated "10". An "11" D5 allele has a repeat section 44 letters long. These different allele lengths serve no known biological purpose, and do not affect health or disease, but they can be used as distinguishing markers for human identification.

23. At each genetic locus, an individual has a genotype (or, "genetic type") comprised of two alleles, each inherited from one parent. Ten different allele variants occurring would provide 55 possible allele pairs (10 + 9 + ... + 1), while twenty alleles can form 210 different allele pairs. So one STR locus typically yields around a hundred population genotype possibilities. Any given person has just one of these allele pair possibilities, so chances are that any two particular people will have different genotypes.

24. To better differentiate between individual genotypes, more STR loci are used in the forensic analysis. Standard STR panels contain ten to twenty-five different loci. These loci are chosen to be genetically independent. The total number of multi-locus genotype possibilities is the product of multiplying together the individual locus possibilities. With even just 10

different allele pair choices at a locus, 15 loci produce a quadrillion (10^{15}, or a "1" followed by 15 zeros) possible genotypes. The STR loci thereby provide tremendous DNA identification power, with far more possible genotypes than there are (or ever were) people in the world.

25. In order to perform DNA-based identification analysis, a forensic laboratory first transforms biological evidence into DNA data. The biological evidence contains genotypes from one or more individuals, and the task is to determine those genotypes (with the ultimate goal of assessing whether a particular person's DNA is or is not contained in the biological evidence). Through a series of successive separations, the lab transforms the DNA molecules in the evidence into electronic signals. Following data generation, these DNA signals can be interpreted to infer genotypes.

Polymerase Chain Reaction

26. The advent of short tandem repeat (STR) polymerase chain reaction (PCR)-based amplification processes in the early 1990s revolutionized forensic science, enabling minute amounts of DNA extracted from just dozens of human cells found at a crime scene to be used as identifying evidence.

27. PCR amplification is a man-made laboratory technique extensively used in molecular biology to manufacture large numbers of synthetic (i.e., non-naturally occurring) copies of a specific DNA segment, making subsequent detection and analysis processing far more practical. "The PCR reaction has been likened to a molecular photocopier. It enables the exponential amplification of very small amounts of DNA." Buckleton at 3. "Beginning with a single molecule of the genetic material DNA, the PCR can generate 100 billion similar molecules in an afternoon." Kary B. Mullis, *The Unusual Origin of the Polymerase Chain Reaction*, Scientific American, Apr. 1990, at 56, 56. Kary Mullis was awarded the Nobel Prize

in Chemistry in 1993 (along with Michael Smith) for his work in developing PCR ten years earlier. With PCR amplification, forensic scientists have the power to easily and reliably develop STR genotype data from very small biological samples.

28. PCR amplification of an STR locus is done in a tube that contains the extracted template DNA (e.g., from an evidence sample), the polymerase copying enzyme, other chemicals, and an abundance of fluorescently labeled, man-made DNA primers. These primers (about 20 DNA letters long) lie outside the STR repeat region that is being measured for the genetic analysis, and, through the specificity of DNA double helix pairing, isolate the locus region within the genome. Twenty eight (or so) rounds of copying then ensue, heating to separate DNA strands and cooling to initiate copying. Each cycle doubles the number of fluorescently labeled DNA molecules:

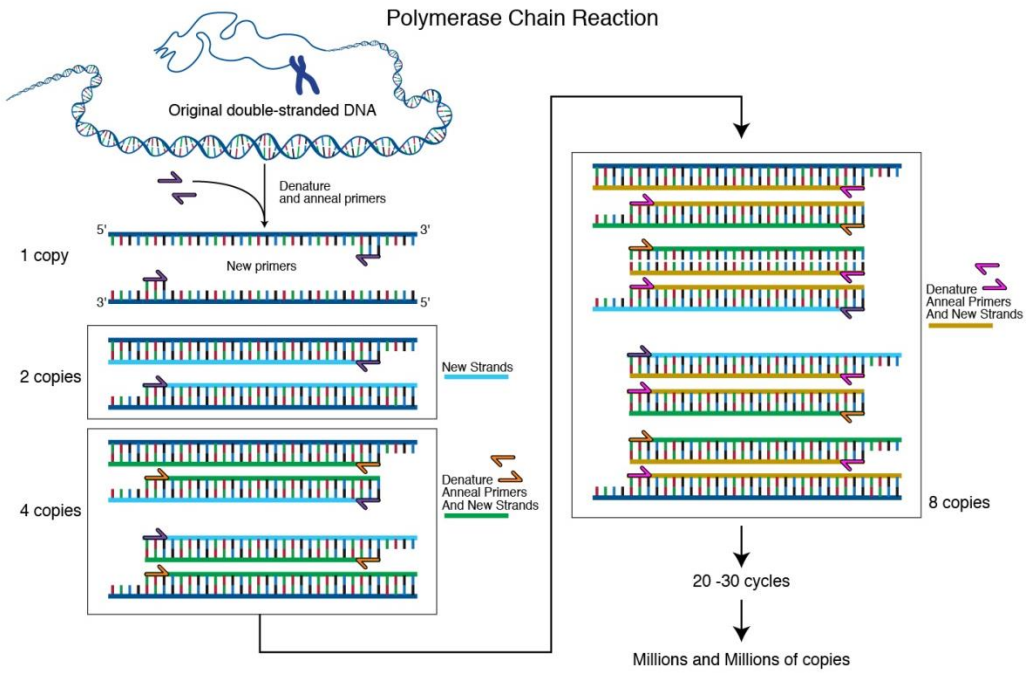
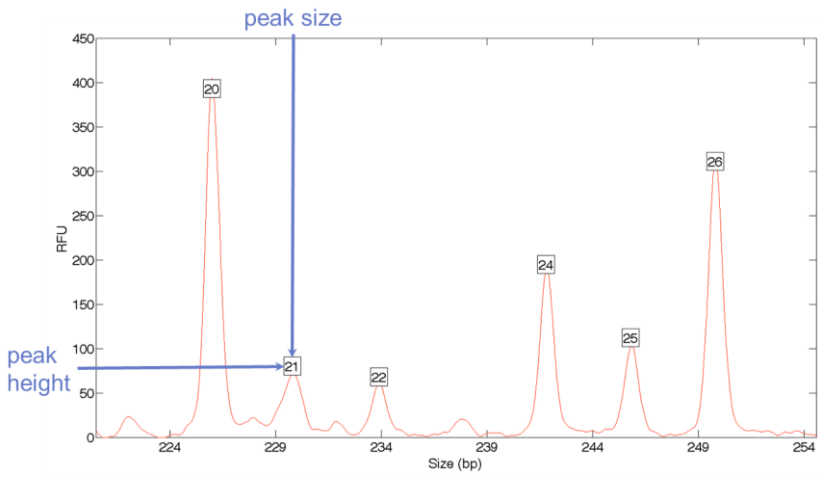


Figure: NIH, National Human Genome Research Institute, Talking Glossary of Genetic Terms, *Polymerase Chain Reaction*, https://www.genome.gov/genetics-glossary/Polymerase-Chain-Reaction, last visited October 16, 2019.

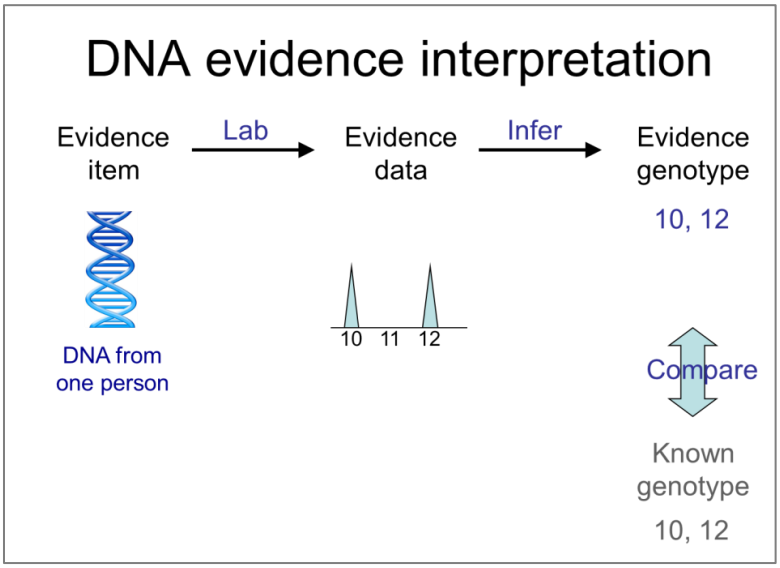
29. The DNA copies of each locus region are not identical to the DNA that would be found in a cell: they are molecularly attached to a fluorescent label for purposes of analysis and they may contain differences from the original, naturally occurring DNA fragments resulting from the PCR process. For efficiency, 10 to 25 different STR loci, each assigned their own fluorescent dye and size range, are amplified together in a single multiplex reaction tube.

30. The artificially amplified DNA is then injected into an automated DNA sequencer to measure genetic sequence length and amount. Another man-made laboratory technique, called capillary electrophoresis, is then applied to separate the DNA molecules according to their length, while a laser excites DNA-linked fluorescent labels whose light is detected by a CCD camera. The resulting electropherogram (EPG) signal contains data peaks:



31. A peak has a DNA length that corresponds to an allele—more repeats in the allele make for a longer molecule that appears farther to the right on a length scale (the horizontal axis in the graph above). A peak's height reflects the quantity of DNA—more DNA in the sample input to the PCR amplification process results in more fluorescently labeled synthetic copies, which produce a stronger fluorescence signal for a taller peak (the vertical axis in the graph above).

32. The image below very generally summarizes the steps of DNA evidence interpretation for a biological sample containing DNA from one person:



DNA Data Complexity

33. DNA mixtures arise when more than one person contributes their DNA to biological evidence. Mixtures are found in rape (victim plus assailant), homicide, touch (handgun, clothing, surfaces) and other DNA evidence. In many crime labs, mixed samples form the majority of processed DNA items.

34. Simple DNA yields simple STR EPG signals. A hundred cells from one individual are amplified into a signal having one or two tall peaks at any given locus. When the person's genotype is a homozygote (the same allele inherited from both parents) there will be one peak (Fig. A, below), and with a heterozygote (two different inherited alleles) there will be two peaks (Fig. B, below). A single source reference sample from one individual usually has such simple data that only one possible genotype can be inferred, that is, only one possible genotype would account for the data observed.

Fig. A

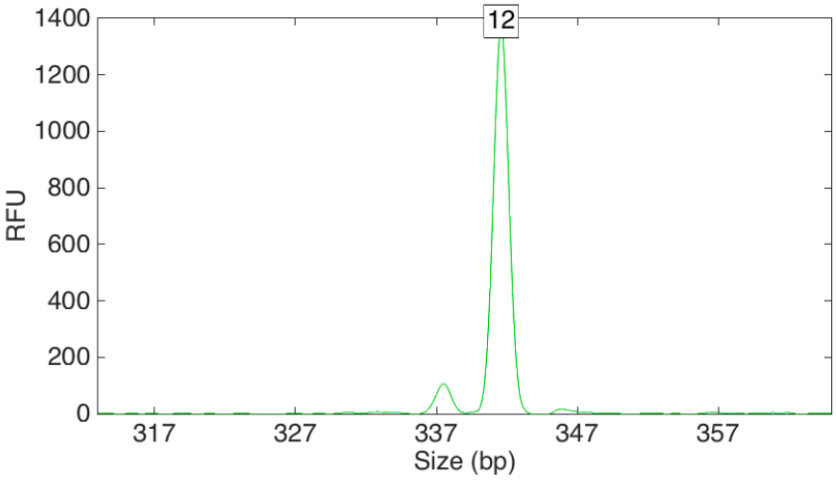
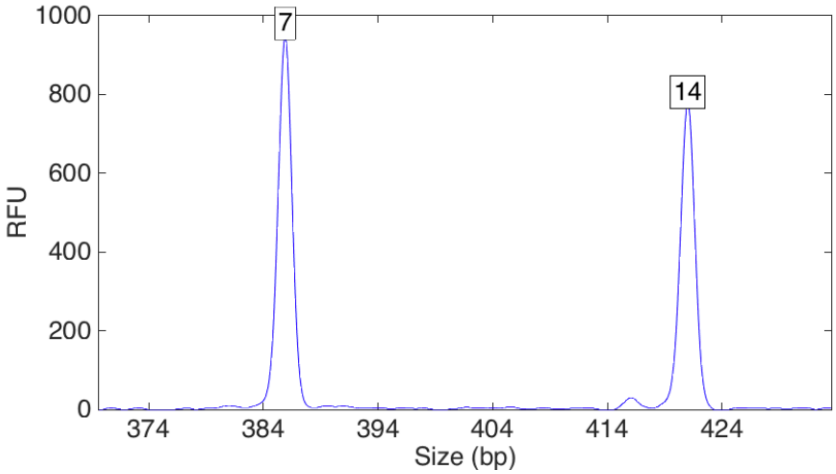
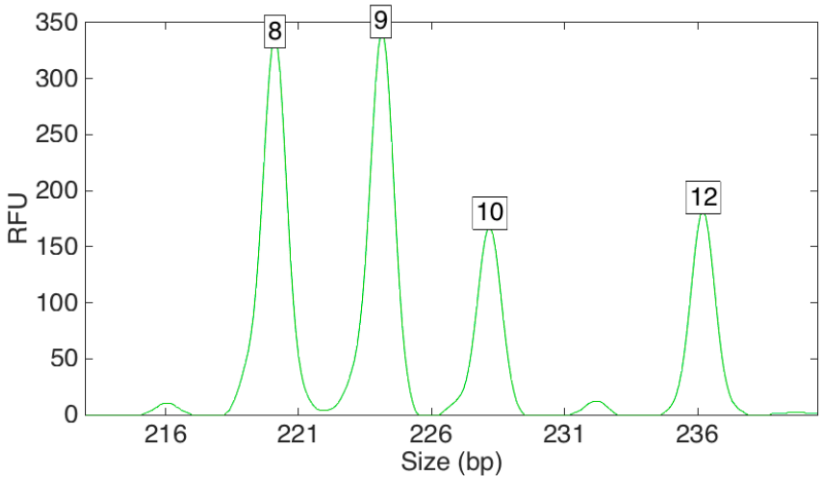


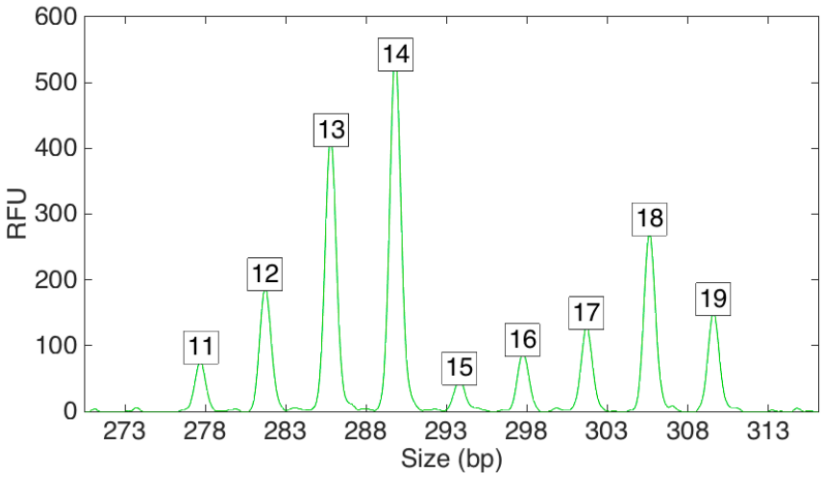
Fig. B



35. DNA evidence that is mixed (two or more contributors), low-level (far fewer than 100 cells) or degraded (larger molecules broken down) produces more complex EPG peak patterns. As just one simple example, the mixture shown below comes from two contributors in different amounts, producing two lower peaks from one person and two higher peaks from someone else, at just one locus:



36. But mixtures (and other complex DNA samples) can have multiple genotype explanations that account for the data. Therefore, unlike with a simple single source DNA sample, it is no longer possible to just "look" at the data and draw a reliable genotype conclusion. Instead, some statistical inference method is needed to properly interpret the mixture data, or separate the data into contributor genotypes. For example, the image below shows data resulting from analysis of a mixture containing DNA from at least 5 people, at just one locus:



The State of the Art at the Time of the Invention

37. Prior to the inventions described and claimed in the Patents-in-Suit, there was no practical, accurate, and reliable method for separating mixture data into genotypes—or

determining the likelihood that a mixture contains the DNA of a particular person—for mixed DNA samples, whether manually or using computers.

38. As recently summarized by the court in *People v. Wakefield*, Case No. 107724, Aug. 15, 2019 N.Y. A.D. 3d., there are—and were at the time of the invention—"two basic methodologies used in forensic DNA analysis. The first is a traditional approach and is undertaken through a process known as combined probability [of] inclusion (CPI), which involves, in relevant part, an analyst choosing which loci to report on and the application of thresholds to the data. These thresholds, which are often set by a manufacturer or laboratory, are intended to simplify the DNA for visual human review by eliminating consideration of possible artifacts and low template DNA so as to increase reporting confidence. The other method of DNA testing at issue is known as a probabilistic method, which can be either semi- or fully-continuous. According to [the inventor of the Patents-in-Suit], semi-continuous probabilistic systems still derive information from the alleles actually present and still apply certain thresholds, but these systems seek to make more use of the data available than that utilized in CPI." NY Slip Op 06143 at 9-10. These two methods, CPI and semi-continuous represent the methods that were available prior to the inventions claimed in the Patents-in-Suit. "In contrast, fully-continuous probabilistic systems, such as TrueAllele, do not employ initial human analyst decision-making and, instead, consider all available data to look at more patterns." *Id.* at 10.

39. The methods available at the time of the patented inventions were inferior to the claimed methods: "manual qualitative peak analysis of mixed DNA samples [was] slow, tedious, and expensive," generating "considerable delay in the casework analysis of forensic DNA mixtures." '021 Patent, col. 1, ln. 34-37 (Exhibit A). This was evident from the then-current "USA backlog comprised of over 100,000 unanalyzed rape kits." *Id.* at col. 1, ln. 37-38. Even

when manual qualitative peak analysis of mixed DNA samples was tediously performed, the results were often inconclusive. At the time the original application that led to the Patents-in-Suit was filed, methods for quantitatively analyzing STR peak data were also limited "in that they typically analyze[d] each STR locus separately," and potentially required "human intervention when combining the locus results into a complete nonoptimized solution." *Id.* at col. 1, ln. 44-46. Specifically, the methods at the time the Patents-in-Suit were filed had "a limited single-locus view of the data, which restrict[ed] the amount of derivable useful information; there [was] no known way to combine the separate single locus partial solutions into one global optimum." *Id.* at col. 8, ln. 52-56. These methods were therefore also inferior because they made less use of the available data in the analysis.

40. Additionally, some prior methods were impractical because they could entail "vast combinatorial searches of discrete genotype possibilities that [were] intractable on even the most powerful computers." *Id.* at col. 9, ln. 66-col. 10, ln. 1. These methods were therefore also inferior because DNA mixtures could not be efficiently resolved, if at all.

41. As described in the patent specification:

> When using mixed DNA evidence in court, the goal is to obtain a conviction or exoneration, depending on the evidence. The [then-current] art produces imprecise, qualitative results that are ill-suited to this purpose. Current assessments often vastly understate the true weight of the evidence. The value added [by the invention] is the capability of the technology to convict the guilty (and keep them off the street) and to exonerate the innocent (and return them to Society).

'021 Patent, col. 46, ln. 30-37.

The Inventions of the Patents-in-Suit

42. PCR amplification, described *supra* Paragraphs 26-31, is a random process that generates a different chain reaction each time DNA copes are synthesized, even if the input to

the process is identical. Therefore, repeated amplification of the same STR loci from the same DNA template—the original sequence obtained from a biological sample—will produce different peak heights and patterns compared to the original, naturally occurring DNA fragment. For example, greater quantities of DNA will statistically yield more reproducible peak patterns; smaller DNA amounts typically exhibit "stochastic effects" with more pronounced peak variation. Because the random process of PCR amplification generates a slightly different result each time copies are made, each PCR amplification produces a data peak pattern that is a variant of the underlying "naturally occurring" allele distribution of the cellular DNA contained in the reaction tube—in other words, the output of the process describes something that does not exist in nature, but instead was manufactured in a laboratory. This variability of the man-made laboratory PCR experiment is entirely different from naturally-occurring variation of genotypes seen in the population.

43. The inventions described in the Patents-in-Suit make use of the fact that these variations in the data generated by the PCR amplification process can be accounted for through computer modeling of the amplification process. In essence, by appropriately accounting for the variability arising from the PCR amplification process, the patented invention makes it possible to draw reliable conclusions about the naturally occurring DNA in the original mixed sample through analysis of the data generated from the synthesized copies of the DNA fragments produced by the PCR amplification process. This use of the observable variation present in the data generated from PCR process to mathematically resolve genotype profiles of DNA samples containing DNA from two or more individuals represented a significant advance in forensic science. Such use was not well-understood, routine, or conventional at the time of the invention.

44. More particularly, in accordance with embodiments of the inventions described and claimed in the Patents-in-Suit, the analytical method includes the step of calculating a statistical variance of the PCR amplification process from data generated from the synthetic copies of DNA fragments produced by that process, not from the naturally occurring DNA. In essence, this variance is a measure of how close observed data patterns detected from the synthetically generated copies are to the expected data patterns of naturally occurring DNA fragments that were input to the PCR amplification process. The inventions numerically describe the variability of the PCR amplification, as observed in the EPG data. The calculated variance is then taken into account when calculating the likelihood of a genotype from the STR data generated from the synthetic copies produced by the PCR amplification process. This provides far more reliable genotype likelihoods and probabilities than would have been possible with prior art approaches that ignored the variability injected into the data as a result of the PCR amplification process. *See, e.g.*, '021 Patent, col. 19, ln. 40. The resulting likelihood ratio match statistics enable accurate human identification based on previously unresolvable DNA mixture evidence.

45. The prior art DNA analysis methods over which the patented inventions improved did not account for the variance of the PCR amplification process, and thus could not accurately calculate genotype likelihoods or likelihood ratio match statistics. Such likelihoods or match statistics can help determine, among other things, a defendant's guilt or innocence in a criminal case.

46. The inventions described and claimed in the Patents-in-Suit are embodied in the TrueAllele software product manufactured, licensed and sold in the United States by Cybergenetics. Courts across the country have recognized the innovative nature of the

TrueAllele software product (and, by extension, the inventions it embodies) and the substantial improvements it provides over prior forensic DNA mixture analysis methods in the context of extensive admissibility hearings conducted during criminal proceedings:

> Cybergenetics TrueAllele Casework is a fully continuous probabilistic approach that analyzes the electropherograms (EPG) (computerized DNA data that a local laboratory extracted and amplified) and considers the genotypes (pair 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 [likelihood ratio].
>
> …
>
> Cybergenetics TrueAllele Casework has undergone 20 unpublished validating studies and 6 published validation studies . . . to confirm that the laboratory is producing the same type of reliable results or determining the extent of reliability for the method or technology that's already been developmentally validated. Four of these were independent validation studies . . . . Without exception, each of these validation studies found Cybergenetics TrueAllele Casework to be sensitive (the extent to which interpretation identifies the correct person) and specific (the extent to which the interpretation does not misidentify the wrong person). And Cybergenetics TrueAllele Casework was shown to have provided objectivity, achieved greater genotype accuracy, and proved reproducible (the extent to which the interpretation gives the same answer to the same question).
>
> …
>
> The evidence shows that computerized probabilistic approaches and likelihood ratio principles used by Cybergenetics TrueAllele Casework are superior to current methods.

Decision and Order at 4-7, 12, *New York v. Wakefield*, Feb. 9, 2015; affirmed NY Slip Op 06143 at 9-10. The New York appellate court affirmed, noting "TrueAllele 'automates the interpretation of the data signals that have already been generated by a laboratory.'" *Id.* at 3 (citing testimony of Dr. Mark W. Perlin, inventor of the Patents-in-Suit).

47. Additionally:

> TrueAllele® is a probabilistic genotyping computer system that interprets DNA evidence using a statistical model. TrueAllele is used to analyze DNA evidence, particularly in cases where human review might be less reliable or not possible. A definite genotype can be readily determined when abundant DNA from one person produces unambiguous genetic data.
>
> However, when data signals are less definitive, or when two or more people contribute to the evidence, uncertainty arises. This uncertainty is expressed in the derived contributor genotype, which may describe different genetic identity possibilities.
>
> Such genotype uncertainty may translate into reduced identification information when a comparison is made with a suspect. 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.
>
> 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. The TrueAllele Casework system [based on the invention in the Patents-in-Suit] is Cybergenetics computer implementation of this two-step DNA identification inference approach. Cybergenetics began developing TrueAllele 22 years ago, adding a mixture module 17 years ago. 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. The TrueAllele computer objectively infers genotypes from DNA data through statistical modeling, without reference to a known comparison genotype. To preserve the identification

> information present in the data, the system represents genotype uncertainty using probability. These probabilistic genotypes are stored on a relational database. Subsequent comparison with suspects or other individuals provides identification information that can be used as evidence.
>
> …
>
> 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. In this way, [the invention] avoids human examination bias, and provides a fair match statistic.

Order at 1-2, *Georgia v. Nundra*, Case No. 18-CR-134, Jan. 21, 2019 (Ga. Sup. Ct.); *see also id.* at 5-6 (listing 18 admissibility decisions in the United States involving use of the patented technology); *Commonwealth of Pennsylvania v. Foley*, 2012 Pa. Super. 31 (2012).

48. The claimed inventions of the Patents-in-Suit thus provided an innovative solution to a technological problem specific to the field of forensic DNA analysis in at least the following specific areas:

a) Solving the previously unsolved problem in which a DNA mixture contained evidence of two unknown contributors:

> This can happen, for example, in a sexual assault when there are (a) multiple assailants, or (b) a consensual partner and an assailant. If the unknown genotypes b1 and b2 were determined, they could be used to match specific suspects, or for searching a DNA database of likely suspects (e.g., convicted offenders) for a matching profile. Such (relatively) unique b1 and b2 would greatly improve upon the current art, in which a large set of candidate suspect genotypes is generated.
>
> This problem (more than one unknown contributor) is quite hard, and not feasibly solved in the prior art. Within the vast K-dimensional search space of quantitative allele measurements, two genotype profiles are to be ascertained. With J=2 individuals, and K=100, how can the genotypes possibly be separated and uniquely identified? For with three feasible allelic values, each person can have one of 10^{50} possibilities, and in combination, the number of

possibilities is the square of that figure: 10^{100}, or a "google" of possible genotype solutions. Brute force computation is clearly not a viable approach.

However, with a novel combination of mathematics, computation, and information, the described invention can usefully solve this problem. In a nonobvious way, the invention combines the method detailed above [calculating a variance from the PCR-generated data] for deriving one unknown (and its confidence) from a mixed DNA profile, together with DNA database information. '021 Patent col. 15, ln. 25 – col. 16, ln. 4.

b) Increasing precision and accuracy of quantitative analysis of DNA mixtures, thereby increasing certainty of identification:

DNA mixtures are currently analyzed by human inspection of qualitative data (e.g., electrophoretic bands are present, absent, or something in between). Moreover, they are recorded on databases and reported in court in a similarly qualitative way, using descriptors such as "major" or "minor" band, and "the suspect cannot be excluded" from the mixture. Such statements are not optimally compelling in court, and lead to crude database searches generating multiple hits. Linear mixture analysis of quantitative data changes this situation. Precise and accurate quantitative analysis of the mixture data can reveal unique identities in many cases. Moreover, these mixture analyses can be backed up by statistical certainties that are useful in convincing presentation of evidence. The increased certainty of identification is reflected in the increased likelihood ratios, as well as other probabilities and statistics, as described above. '021 Patent col. 35, ln. 60 – col. 36, ln. 8.

c) Reducing the overall cost to society by increasing the likelihood that criminals are apprehended:

The ultimate cost of degenerate DNA matches is losing the ability to use DNA technology to find criminals at all. Too many leads amount to no useful leads, since large numbers of low information leads cannot be practically acted upon due to finite law enforcement resources. Then society pays the highest cost: the criminal is not found, not brought to justice, and continues to commit further crimes. This has a high financial, societal, economic, and human cost, which can be quantified. For example, with sexual assault crimes the estimated dollar cost to the victim and society (when the victim's quality of life is quantified) is $87,000 per case (Victim Costs and Consequences: A New Look,

> National Institute of Justice Research Report, January 1996, http://www.ncjrs.org/txtfiles/victcost.txt) . . . .
>
> The mixture deconvolution invention can reduce this ultimate cost by cleaning up the DNA mixture samples prior to using the data with a database. This clean up reduces the degeneracy of the DNA matches, increases the information resulting from a database match, and increases the likelihood of catching criminals using DNA technology. '021 Patent col. 38, ln. 18-36.

d) Providing objective resolution of DNA mixtures and thereby avoiding human examination bias. *See* Order at 1-2, *Georgia v. Nundra,* Case No. 18-CR-134, Jan. 21, 2019 (Ga. Sup. Ct.).

49. Importantly, the patented inventions have had a profound, real-world impact on the criminal justice system. Guilty suspects have been convicted, rather than acquitted; innocent suspects have been acquitted or released, rather than being kept in prison. As just one example, in 2016 and 2017, the patented invention was used to exonerate two men convicted of rape in 1991 and 1993 by providing a more complete analysis of decades-old DNA evidence than was possible in the prior art at the time of the invention. *See* Mark W. Perlin, *Hidden DNA Evidence: Exonerating the Innocent,* Mar. 30, 2018, https://www.forensicmag.com/article/2018/03/hidden-dna-evidence-exonerating-innocent?cmpid=horizontalcontent.

50. The patented inventions also have applicability outside the field of forensic science. Most notably, Cybergenetics' TrueAllele system was used after the World Trade Center disaster to analyze the data from over 18,000 pieces of victim remains evidence and compare the genotypes to approximately 2,700 missing people, in an effort to provide closure to the loved ones of thousands of people killed in the tragedy.

51. These noted improvements over the prior art represent meaningful limitations and/or inventive concepts based on the state of the art over 18 years ago. The innovations reflected in the claims of the Patents-in-Suit were not in existence or even considered in the field previously. Thus, the asserted claims of the Patents-in-Suit, when viewed as a whole, including

as an ordered combination, are not merely the recitation of well-understood, routine, conventional, typical, or well-known technologies or components. The claimed inventions were not well-known, routine, or conventional at the time of the invention, over 19 years ago, and represent specific and profound improvements over previously existing DNA analysis methods.

52. The claimed inventions are necessarily rooted in computer technology because they rely on complex statistical and mathematical modeling and analysis unresolvable by a human in order to overcome the problems, including those noted above, specifically arising in the realm of probabilistic genotyping. This probabilistic analysis includes consideration of DNA's known biological and PCR properties, in combination with the prevalence of DNA variation in the population. The claimed solutions amount to an inventive concept for resolving the particular problems and inefficiencies described above, including in connection with accurately determining whether a particular person's DNA is in a biological sample that contains a mixture of DNA from at least two people.

COUNT I

Infringement of U.S. Patent No. 8,898,021

53. Cybergenetics incorporates by reference the allegations in Paragraphs 1 through 52 above.

54. Defendants are indirectly infringing the '021 Patent in connection with their licensing, sale and/or distribution of the STRmix™ probabilistic genotyping software to customers in the United States who then use the software to practice methods covered by one or more claims of the patent, in violation of 35 U.S.C. §§ 271(b)-(c). Defendants are also directly infringing the '021 Patent in connection with their own use of the STRmix™ probabilistic genotyping software to practice methods covered by one or more claims of the patent on behalf of customers and/or potential customers in the United States, in violation of 35 U.S.C. §§ 271(a).

55. An example of how use of the STRmix™ probabilistic genotyping software infringes the ’021 Patent follows, based on information currently available to Cybergenetics. This example is not intended to limit the scope of Cybergenetics’ infringement claim in any way, and is intended to be without prejudice to Cybergenetics’ ability to assert different or additional claims of the ’021 Patent against Defendants and/or to apply such claims to the accused product differently in view of additional information that Cybergenetics may acquire during the course of the litigation.

56. Claim 1 of the ’021 Patent recites as follows:

> 1. A method of analyzing a DNA mixture comprised of the steps:
>
> (a) obtaining a DNA mixture that contains genetic material from at least two contributing individuals;
>
> (b) amplifying the DNA mixture in a DNA amplification process to produce an amplification product comprising DNA fragments;
>
> (c) producing from the amplification product a signal comprising signal peaks from the DNA fragments;
>
> (d) detecting signal peak amounts in the signal, and quantifying the amounts to produce DNA lengths and concentrations from the mixture to form quantitative genotyping data;
>
> (e) assuming a genotype value of alleles for a contributor to the quantitative genotyping data at a genetic locus;
>
> (f) setting a mixture weight value for a relative proportion of the contributors to the quantitative genotyping data;
>
> (g) forming a linear combination of the genotype values based on the mixture weight value;
>
> (h) deriving with a computer a data variance of the amplification process from a model that includes both the quantitative genotyping data and the linear combination;

> (i) determining with the computer a probability of the quantitative genotyping data corresponding to a set of suspects from the DNA mixture at the locus using both the linear combination and the data variance value;
>
> (j) computing a probability of a genotype for one of the contributing individuals using the determined probability of the quantitative genotyping data; and
>
> (k) comparing the genotype probability with a set of suspect genotypes to identify a likely suspect.

'021 Patent at col. 46, ln. 61 – col. 47, ln. 25 (Ex. A). On information and belief, use of the STRmix™ probabilistic genotyping software satisfies each and every limitation of claim 1.

57. With reference to the preamble of claim 1 of the '021 Patent, the STRmix™ probabilistic genotyping software is configured to perform a "method of analyzing a DNA mixture." *See, e.g.*, STRmix™ Website, https://www.strmix.com/#what (last accessed 5/23/19) (Ex. C hereto) (hereinafter, "STRmix™ Website"); D. Taylor *et al.*, "The Interpretation of Single Source and Mixed DNA Profiles," *Forensic Sci. Int. Genet.*, Vol. 7, Issue 5, Sept. 2013, 517 (Ex. D hereto) (hereinafter, "Taylor").

58. With reference to element (a) of claim 1, use of STRmix™ requires, as a necessary precondition, performing the step of "obtaining a DNA mixture that contains genetic material from at least two contributing individuals." *See, e.g.*, STRmix™ Website; Taylor at 524; STRmix™ Probabilistic Genotyping Software Operating Instructions, ¶¶ 1.1.1-1.1.2 (June 25, 2018) (Ex. E hereto) (hereinafter, "STRmix™ Operating Instructions").

59. With reference to element (b) of claim 1, use of STRmix™ requires, as a necessary precondition, performing the step of "amplifying the DNA mixture in a DNA amplification process to produce an amplification product comprising DNA fragments." *See, e.g.*, STRmix™ Operating Instructions at ¶ 1.1.3; Taylor at 524; J. Buckleton *et al.*, Forensic

DNA Evidence Interpretation, 3-5 (2nd ed. 2016) (excerpts at Ex. F hereto) (hereinafter, "Buckleton").

60. With reference to element (c) of claim 1, use of STRmix™ requires, as a necessary precondition, performing the step of "producing from the amplification product a signal comprising signal peaks from the DNA fragments." *See, e.g.*, STRmix™ Operating Instructions at ¶¶ 1.1.3, 1.1.5; Buckleton at 3-5; Taylor at 524.

61. With reference to element (d) of claim 1, use of STRmix™ requires, as a necessary precondition, performing the step of "detecting signal peak amounts in the signal, and quantifying the amounts to produce DNA lengths and concentrations from the mixture to form quantitative genotyping data." *See, e.g.*, STRmix™ Operating Instructions at ¶¶ 1.1.3, 1.1.5; Buckleton at 281-86; Taylor at 516-28.

62. With reference to element (e) of claim 1, STRmix™ is used to perform a method that includes the step of "assuming a genotype value of alleles for a contributor to the quantitative genotyping data at a genetic locus." *See, e.g.*, Buckleton at 295, Fig. 9.10; Taylor at 517-8, 520.

63. With reference to element (f) of claim 1, STRmix™ is used to perform a method that includes the step of "setting a mixture weight value for a relative proportion of the contributors to the quantitative genotyping data." *See, e.g.*, Buckleton at 281; Taylor at 518, 520; STRmix™ Operating Instructions at ¶ 6.8.2.

64. With reference to element (g) of claim 1, STRmix™ is used to perform a method that includes the step of "forming a linear combination of the genotype values based on the mixture weight value." *See, e.g.*, Buckleton at Fig. 9.10; Taylor at 518, 520.

65. With reference to element (h) of claim 1, STRmix™ is used to perform a method that includes the step of "deriving with a computer a data variance of the amplification process from a model that includes both the quantitative genotyping data and the linear combination." *See, e.g.*, Buckleton at 293; Taylor at 518-19, 521.

66. With reference to element (i) of claim 1, STRmix™ is used to perform a method that includes the step of "determining with the computer a probability of the quantitative genotyping data corresponding to a set of suspects from the DNA mixture at the locus using both the linear combination and the data variance value." *See, e.g.*, STRmix™ Operating Instructions at ¶¶ 6.6-6.7; Buckleton at 293; Taylor at 519.

67. With reference to element (j) of claim 1, STRmix™ is used to perform a method that includes the step of "computing a probability of a genotype for one of the contributing individuals using the determined probability of the quantitative genotyping data." *See, e.g.*, STRmix™ Operating Instructions at ¶¶ 2.9-2.10; Buckleton at Fig. 9.11; Taylor at 517, 519-20, 524.

68. With reference to element (k) of claim 1, STRmix™ is used to perform a method that includes the step of "comparing the genotype probability with a set of suspect genotypes to identify a likely suspect." *See, e.g.*, STRmix™ Website; STRmix™ Operating Instructions at ¶¶ 3-4; Buckleton at 293-94; Taylor at 523; S. Cooper et al., "STRmix: The Application of a Continuous Statistical Model Expert System to Forensic Casework in New Zealand (and Australia)," *Promega ISHI Conference*, 2017, ¶¶ 3, 5 (Ex. G hereto) (hereinafter, "Cooper").

69. The foregoing element-by-element comparison demonstrates that use of the accused STRmix™ probabilistic genotyping software product on suitable biological input data literally satisfies each and every element of at least claim 1 of the '021 Patent, thus literally

infringing the patent. To the extent any element of claim 1 is deemed not to be literally satisfied, use of STRmix™ would nevertheless still infringe under the doctrine of equivalents because any differences between the claimed invention and the method performed by the accused software product are insubstantial.

70. On information and belief, based on the publicly available information of which Cybergenetics is presently aware, use of the STRmix™ probabilistic genotyping software also infringes claims 4-6, 9, 12-17, 22, 25, 26, 31-33, 37, 38, 51, 53, 55, 57, 58, 60, 61, 63, and 66-69 of the '021 Patent, as detailed in Cybergenetics' Initial Infringement Contentions served on Defendants on October 10, 2019.

71. On information and belief, ESR and NicheVision (as ESR's exclusive sales representative) sell and offer to sell the STRmix™ probabilistic genotyping software product to customers in this judicial district and elsewhere in the United States, including numerous state and local law enforcement agencies and forensics laboratories.

72. The STRmix™ probabilistic genotyping software product constitutes a material part of the invention recited in claim 1 of the '021 Patent, being programmed to cause a material and substantial portion of the recited method steps to be performed, and it is not a staple article or commodity of commerce suitable for substantial non-infringing use. Moreover, on information and belief, Defendants are aware of the '021 Patent at least as a result of communications and interactions between Dr. Mark Perlin, the named inventor on the Patents-in-Suit and a co-founder of Cybergenetics, and Dr. John Buckleton, one of the developers of STRmix™ and a Principal Scientist at ESR. Consequently, Defendants know that the STRmix™ probabilistic genotyping software product is especially made or especially adapted for use in a manner that infringes the '021 Patent. Accordingly, Defendants' sale of the STRmix™

probabilistic genotyping software product contributes to infringement of the ’021 Patent by their customers in violation of 35 U.S.C. § 271(c).

73. On information and belief, both by configuring the STRmix™ probabilistic genotyping software product to operate in a manner that Defendants know infringes the ’021 Patent, and by encouraging customers to use the STRmix™ probabilistic genotyping software product in a manner that Defendants know infringes the ’021 Patent through training, product literature and customer support, Defendants are inducing infringement of the ’021 Patent by their customers in violation of 35 U.S.C. § 271(b).

74. Defendants’ infringement of the ’021 Patent has caused Cybergenetics to suffer substantial monetary harm, including lost profits and price erosion relating to Cybergenetics’ sale of competing and related products and services in the same markets served by Defendants.

75. The ’021 Patent includes only method claims, and therefore the notice requirements of 35 U.S.C. § 287(a) are inapplicable. Cybergenetics is thus entitled to collect damages for any infringement of the ’021 Patent by Defendants occurring up to six (6) years prior to the filing of this complaint in accordance with 35 U.S.C. § 286.

76. Defendants’ infringement of the ’021 Patent has caused and will continue to cause irreparable harm to Cybergenetics for which there is no adequate remedy at law, including but not limited to lost market share and lost goodwill that Cybergenetics would otherwise garner as the recognized innovator and sole authorized source of supply for probabilistic genotyping software configured to practice the methods covered by the ’021 Patent.

77. On information and belief, Defendants’ infringement of the ’021 Patent has been willful, done deliberately and with full knowledge that the sale, offer to sell and use of the STRmix™ probabilistic genotyping software product infringes the ’021 Patent, and without any

reasonable, good-faith belief that the '021 Patent is invalid and/or not infringed, thereby justifying an increase in the damages to be awarded to Cybergenetics by up to three times the amount found or assessed, in accordance with 35 U.S.C. § 284.

78. Defendants' willful infringement of the '021 Patent renders this an exceptional case within the meaning of 35 U.S.C. § 285, justifying an award to Cybergenetics of its reasonable attorney fees incurred in connection with this litigation.

COUNT II

Infringement of U.S. Patent No. 9,708,642

79. Cybergenetics incorporates by reference the allegations in Paragraphs 1 through 78 above.

80. Defendants are indirectly infringing the '642 Patent in connection with their licensing, sale and/or distribution of the STRmix™ probabilistic genotyping software to customers in the United States who then use the software to practice methods covered by one or more claims of the patent, in violation of 35 U.S.C. §§ 271(b)-(c). Defendants are also directly infringing the '642 Patent in connection with their own use of the STRmix™ probabilistic genotyping software to practice methods covered by one or more claims of the patent on behalf of customers and/or potential customers in the United States, in violation of 35 U.S.C. §§ 271(a).

81. An example of how use of the STRmix™ probabilistic genotyping software infringes the '642 Patent follows, based on the information currently available to Cybergenetics. This example is not intended to limit the scope of Cybergenetics' infringement claim in any way, and is intended to be without prejudice to Cybergenetics' ability to assert different or additional claims of the '642 Patent against Defendants and/or to apply such claims to the accused product differently in view of additional information that Cybergenetics may acquire during the course of the litigation.

82. Claim 1 of the ’642 Patent recites as follows:

> 1. A method of analyzing a biological sample comprised of the steps:
>
> (a) obtaining a biological sample that contains DNA;
>
> (b) amplifying the DNA to produce a product;
>
> (c) detecting the product to generate data, where the data can be explained by more than one genotype value;
>
> (d) assuming a genotype value which is stored in a nontransient memory;
>
> (e) deriving with a computer a variance of the amplification; and
>
> (f) determining a likelihood using a computer in communication with the memory, where the likelihood is defined as a probability of observing the generated data, and said probability depends on the genotype value and the variance.

’642 Patent at col. 48, ln. 37-51. On information and belief, use of the STRmix™ probabilistic genotyping software product satisfies each and every limitation of claim 1.

83. With reference to the preamble of claim 1 of the ’642 Patent, the STRmix™ probabilistic genotyping software is configured to perform a “method of analyzing a biological sample.” *See, e.g.*, STRmix™ Website; Buckleton at 1-35, 281.

84. With reference to element (a) of claim 1, use of STRmix™ requires, as a necessary precondition, performing the step of “obtaining a biological sample that contains DNA.” *See, e.g.*, STRmix™ Website; STRmix™ Operating Instructions at ¶¶ 1.1.1-1.1.2; Buckleton at 1-3.

85. With reference to element (b) of claim 1, use of STRmix™ requires, as a necessary precondition, performing the step of “amplifying the DNA to produce a product.” *See, e.g.*, STRmix™ Operating Instructions at ¶ 1.1.3; Buckleton at 3-5.

86. With reference to element (c) of claim 1, use of STRmix™ requires, as a necessary precondition, performing the step of "detecting the product to generate data, where the data can be explained by more than one genotype value." *See, e.g.*, STRmix™ Operating Instructions at ¶¶ 1.1.3, 1.1.5; Buckleton at 4, 281-86; Taylor at 517.

87. With reference to element (d) of claim 1, STRmix™ is used to perform a method that includes the step of "assuming a genotype value which is stored in a nontransient memory." *See, e.g.*, Buckleton at Fig. 9.10; Taylor at 518.

88. With reference to element (e) of claim 1, STRmix™ is used to perform a method that includes the step of "deriving with a computer a variance of the amplification." *See, e.g.*, Buckleton at 293; Taylor at 519.

89. With reference to element (f) of claim 1, STRmix™ is used to perform a method that includes the step of "determining a likelihood using a computer in communication with the memory, where the likelihood is defined as a probability of observing the generated data, and said probability depends on the genotype value and the variance." *See, e.g.*, STRmix™ Operating Instructions at ¶¶ 3-4, 6.6-6.7; Buckleton at Fig. 9.11; Taylor at 517, 519.

90. The foregoing element-by-element comparison demonstrates that use of the accused STRmix™ probabilistic genotyping software product on suitable biological input data literally satisfies each and every element of at least claim 1 of the '642 Patent, thus literally infringing the patent. To the extent any element of claim 1 is deemed not to be literally satisfied, use of STRmix™ would nevertheless still infringe under the doctrine of equivalents because any differences between the claimed invention and the method performed by the accused product are insubstantial.

91. On information and belief, based on the publicly available information of which Cybergenetics is presently aware, use of the STRmix™ probabilistic genotyping software also infringes claims 3, 4, 6, 7, 10, and 14 of the '642 Patent, as detailed in Cybergenetics' Initial Infringement Contentions served on Defendants on October 10, 2019.

92. On information and belief, ESR and NicheVision (as ESR's exclusive sales representative) sell and offer to sell the STRmix™ probabilistic genotyping software product to customers in this judicial district and elsewhere in the United States, including numerous state and local law enforcement agencies and forensics laboratories.

93. The STRmix™ probabilistic genotyping software product constitutes a material part of the invention recited in claim 1 of the '642 Patent, being programmed to cause a material and substantial portion of the recited method steps to be performed, and it is not a staple article or commodity of commerce suitable for substantial non-infringing use. Moreover, on information and belief, Defendants are aware of the '642 Patent at least as a result of communications and interactions between Dr. Mark Perlin, the named inventor on the Patents-in-Suit and a co-founder of Cybergenetics, and Dr. John Buckleton, one of the developers of STRmix™ and a Principal Scientist at ESR. Consequently, Defendants know that the STRmix™ probabilistic genotyping software product is especially made or especially adapted for use in a manner that infringes the '642 Patent. Accordingly, Defendants' sale of the STRmix™ probabilistic genotyping software product contributes to infringement of the '642 Patent by their customers in violation of 35 U.S.C. § 271(c).

94. On information and belief, both by configuring the STRmix™ probabilistic genotyping software product to operate in a manner that Defendants know infringes the '642 Patent and by encouraging customers to use the STRmix™ probabilistic genotyping software

product in a manner that Defendants know infringes the '642 Patent through training, product literature and customer support, Defendants are inducing infringement of the '642 Patent by their customers in violation of 35 U.S.C. § 271(b).

95. Defendants' infringement of the '642 Patent has caused Cybergenetics to suffer substantial monetary harm, including lost profits and price erosion relating to Cybergenetics' sale of competing products and services in the same markets served by Defendants.

96. The '642 Patent includes only method claims, and therefore the notice requirements of 35 U.S.C. § 287(a) are inapplicable. Cybergenetics is thus entitled to collect damages for any infringement of the '642 Patent by Defendants occurring up to six (6) years prior to the filing of this complaint in accordance with 35 U.S.C. § 286.

97. Defendants' infringement of the '642 Patent has caused and will continue to cause irreparable harm to Cybergenetics for which there is no adequate remedy at law, including but not limited to lost market share and lost goodwill that Cybergenetics would otherwise garner as the recognized innovator and sole authorized source of supply for probabilistic genotyping software configured to practice the methods covered by the '642 Patent.

98. On information and belief, Defendants' infringement of the '642 Patent has been willful, done deliberately and with full knowledge that the sale, offer to sell and use of the STRmix™ probabilistic genotyping software product infringes the '642 Patent, and without any reasonable, good-faith belief that the '642 Patent is invalid and/or not infringed, thereby justifying an increase in the damages to be awarded Cybergenetics by up to three times the amount found or assessed, in accordance with 35 U.S.C. § 284.

99. Defendants' willful infringement of the '642 Patent renders this an exceptional case within the meaning of 35 U.S.C. § 285, justifying an award to Cybergenetics of its reasonable attorney fees incurred in connection with this litigation.

PRAYER FOR RELIEF

WHEREFORE, Cybergenetics prays for a judgment in its favor granting the following relief:

A. A finding that ESR and NicheVision have infringed the '021 and '642 Patents, holding them jointly and severally liable for such infringement;

B. A permanent injunction barring ESR and NicheVision, and all persons acting in concert with them, from infringing the '021 and '642 Patents;

C. An award of monetary damages pursuant to 35 U.S.C. § 284 in an amount adequate to compensate Cybergenetics for ESR's and NicheVision's infringement of the '021 and '642 Patents;

D. An order requiring ESR and NicheVision to pay Cybergenetics supplemental damages for any continuing post-verdict infringement up until entry of the final judgment, with an accounting, as needed;

E. A finding that ESR's and NicheVision's infringement of the '021 and '642 Patents has been willful;

F. An increase in the damages awarded to Cybergenetics up to three times the amount found by the jury or assessed by the Court, pursuant to 35 U.S.C. § 284;

G. A finding that this is an exceptional case within the meaning of 35 U.S.C. § 285, and a corresponding award of Cybergenetics' reasonable attorney fees incurred in connection with this litigation;

H. An award of pre-judgment interest, post-judgment interest and costs, in amounts to be fixed by the Court; and

I. Any additional and further relief the Court deems just and proper.

JURY DEMAND

Pursuant to Federal Rule of Civil Procedure 38(b), Cybergenetics hereby demands a trial by jury on all issues so triable.

Dated: October 16, 2019

/s/ Mark Supko

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CERTIFICATE OF SERVICE

I hereby certify that on October 16, 2019, a copy of the foregoing **AMENDED COMPLAINT FOR PATENT INFRINGEMENT** was filed electronically. Notice of this filing will be sent by operation of the Court's electronic filing system to all parties indicated on the electronic filing receipt. Parties may access this filing through the Court's system.

Dated: October 16, 2019

/s/ Mark Supko

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