



June Newsletter

Better Justice Through Better Science™

Cybergenetics response to Thompson is highest-ranked SSRN forensics paper

Cybergenetics responded to over a hundred statements made in a highly flawed Case Report published by Bill Thompson (University of California). Our [response](#) is now the most downloaded Forensic Science preprint paper on Elsevier's Social Science Research Network (SSRN) repository.

For example, analyzing a DNA mixture of two people can require at least 4 peaks per locus. Thompson preferred foreign STR mixture software averaged just 1.7 locus peaks – clearly insufficient for a meaningful answer. Working as an opposition consultant, his partisan report ignored TrueAllele's use of all the DNA data to find accurate match statistics.

Learn how to properly analyze DNA mixtures and write accurate case reports. Read Cybergenetics top-ranked [response](#).

Thompson Response

TrueAllele helps deliver justice in college footballer shooting

A Cybergenetics expert recently testified in a Massachusetts [shooting case](#). On October 14, 2017, 20-year-old Franklin Pierce University football player Kevin Raymond was shot in a Somerville parking lot. He was rushed to a hospital and pronounced dead. Police collected a firearm and cartridge casings found near the crime. They swabbed a rental car steering wheel for DNA. The complex DNA evidence contained 4 (firearm) or 5 (rental car) contributors, too hard for less effective software to solve. The Middlesex County District Attorney's Office sent their case to Cybergenetics for informative TrueAllele processing.

TrueAllele resolved the mixtures, associating the firearm and rental car with [suspect](#) Tony Harris. The computer connected the firearm to Harris with a 277 million match statistic. And connected Harris to the rental car at 3.08 million. On May 25, 2023, Cybergenetics analyst Jennifer Bracamontes testified at the Woburn trial about these DNA match results. On June 6, the jury found Tony Harris guilty of second-degree murder. Sentencing is pending.



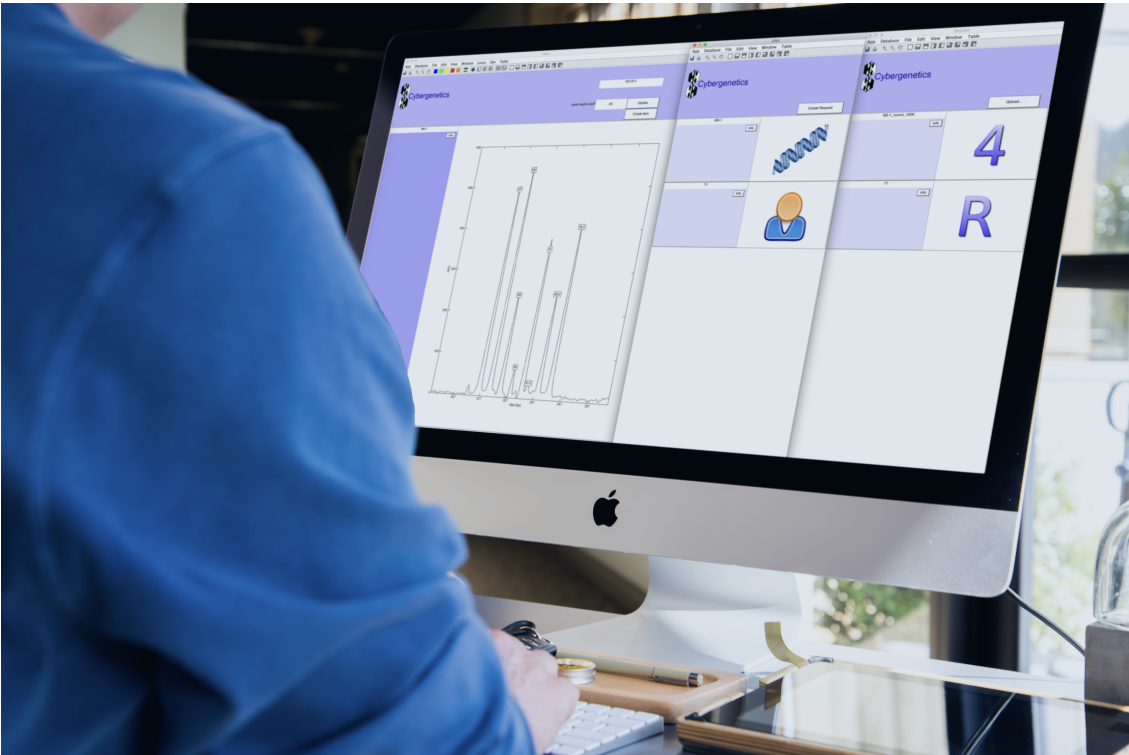
Kern County presents its NGS findings at 2023 AAFS conference

Kern County was the [first American crime lab](#) to deploy TrueAllele. The lab presented its next-generation sequencing (NGS) experiences at the 2023 American Academy of Forensic Sciences (AAFS) conference. NGS, an advanced DNA sequencing technology for forensic science identification, may well be the future of forensic DNA analysis. Kern County DNA tech lead and TrueAllele user Mandi Van Buren gave two [AAFS talks](#) on her lab's NGS system decision, validation, and implementation. Here are some presentation highlights:

- *Internal validation of Verogen ForenSeq DNA Signature Prep Kit Primer Set B using the Hamilton Nimbus HD and MiSeq FGX*
 - The Kern Regional Crime Laboratory performed an internal validation of the Verogen ForenSeq DNA Signature Prep Kit Primer Set B using the Hamilton Nimbus HD and MiSeq FGX. Precision and accuracy studies, sensitivity and stochastic studies, mixture studies, mock evidence sample studies and a contamination assessment study were performed during the validation.
- *One laboratory's experience with next-generation sequencing: the decision, the validation, and the implementation.*
 - The decision for the laboratory to make the leap from CE to NGS for all casework samples involved many considerations and support from various stakeholders. This presentation will take a further look into why the laboratory made the decision to move towards NGS as the standard for casework, what was considered, what challenges we faced throughout the validation process, and recommendations for other laboratories considering NGS. Additionally, this presentation will fast forward to where the laboratory is today: discussing implementation, training, case acceptance and triage, integration with our existing probabilistic genotyping and local databasing system, and testimony preparation.

Cybergenetics TrueAllele software can [input and process NGS](#) data. This powerful pathway brings Verogen MiSeq FGx autosomal STR data into the TrueAllele Casework process. Once NGS data has been imported, downstream TrueAllele processing integrates seamlessly into the lab's existing workflow. TrueAllele on NGS data interprets and matches DNA

mixtures, using it like any other STR data source. TrueAllele automation makes the DNA analyst's job fast and easy.



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