

# **DNA ISSUE**

**COURT OF CRIMINAL APPEALS  
APPELLANT'S SUPPLEMENTAL BRIEF**

**JUNE 18, 2018**

No. AP-77,046

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**IN THE COURT OF CRIMINAL APPEALS OF TEXAS  
AT AUSTIN**

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**HENRY W. SKINNER,**  
*Appellant*

v.

**THE STATE OF TEXAS,**  
*Appellee*

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On Appeal from the Finding Under Tex. Code Crim. Proc. Art 64.04  
by the 31st District Court of Gray County

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**APPELLANT'S SUPPLEMENTAL BRIEF**

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Dated: June 18, 2018

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## **Introduction**

Mr. Skinner's prior briefing addressed whether, if the jury at his 1995 trial had heard the results of certain DNA tests from 2012-13, there is a reasonable probability the outcome would have been different. Appellant's Opening Brief ("AOB") at 24-43; Appellant's Reply Brief ("RB") at 21-26. Those post-conviction DNA test results would have given trial counsel the tools to construct a powerful case for reasonable doubt, particularly in light of the other evidence favorable to Mr. Skinner that was already before the jury. *See* AOB at 6-13.

After briefing was complete, the Texas Department of Public Safety laboratory in Lubbock ("DPS") reanalyzed those DNA test results from 2012-13, using different standards for determining the presence of mixtures and a computer program called "STRmix"<sup>1</sup> to calculate match probabilities. *See infra*. This supplemental brief addresses whether this 2016-17 reanalysis changed the original test results in any way that is material to this appeal. As shown below, nothing about the reanalysis changes the conclusion that, had the post-conviction DNA test results been before the trial jury in 1995, it is reasonably probable that the jury would not have unanimously found Mr. Skinner guilty beyond a reasonable doubt.

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<sup>1</sup> STRmix is pronounced "star-mix."

## Statement of the Case

Mr. Skinner was convicted of capital murder and sentenced to death in 1995. This Court affirmed, *Skinner v. State*, 956 S.W.2d 532 (Tex. Crim. App. 1997), and a series of post-conviction challenges followed.<sup>2</sup> Simultaneously, Mr. Skinner filed a series of motions with the convicting court requesting post-conviction DNA testing under Tex. Code Crim. Proc., Ch. 64. After the convicting court denied his third such motion,<sup>3</sup> and while Mr. Skinner's appeal was pending in this Court, the parties agreed that the DNA testing Mr. Skinner had long sought, as well as additional testing proposed by the State, should be performed. Accordingly, the appeal was dismissed as moot. *Skinner v. State*, No. AP-76,675 (Tex. Crim. App., June 20, 2012) (*per curiam*) (not designated for publication).

DPS conducted two rounds of STR testing and issued reports describing the results in October 2012 and February 2013. The convicting court then permitted mitochondrial DNA ("mtDNA") testing by an outside laboratory on a limited number of items for which no STR results had been obtained; a report of those results was issued in August 2013. In February 2014, the convicting court held an

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<sup>2</sup> See *Skinner v. Quarterman*, 2007 WL 582808 (N.D. Tex., Feb. 22, 2007); *Skinner v. Quarterman*, 528 F.3d 336 (5th Cir. 2008); *Skinner v. Quarterman*, 576 F.3d 214 (5th Cir. 2009).

<sup>3</sup> The district court's denial of his first two motions were both affirmed by this Court. See *Skinner v. State*, 122 S.W.3d 808, 811 (Tex. Crim. App. 2003) (initial motion); *Skinner v. State*, 293 S.W.3d 196 (Tex. Crim. App. 2009) (second motion).

evidentiary hearing concerning the DNA testing results from 2012-13. In July 2014, it adopted *in toto* the State's proposed findings. Mr. Skinner appealed. The case was briefed and the Court heard argument in April 2015.

Between June and September 2015, DPS began to notify convicted persons that it had learned of errors in the FBI-developed population database used by DPS for calculating DNA match statistics and offered to recalculate match probabilities using a corrected database. In response to these concerns, the Court abated Mr. Skinner's appeal, remanding to the convicting court with instructions to monitor the recalculation of the relevant DNA test results and "make any further findings and conclusions necessary upon receiving [those] results ...." *Skinner v. State*, 484 S.W.3d 434, 439 (Tex. Crim. App. 2016).

By the time DPS got around to reanalyzing the original test results in this case, however, it had moved beyond just recalculating match probabilities using the corrected FBI database. Instead, it had adopted new standards for when to call a sample a mixture, and it had acquired and begun using the commercially marketed proprietary software "STRmix" to calculate probabilities. Both were employed to reanalyze the original DNA test results in this case. DPS reported the new results in June 2016 and May 2017.

On January 9, 2018, the convicting court heard evidence concerning the 2016-17 reanalysis. The parties thereafter submitted proposed findings. *See Supplemental*



Clerk's Record (filed with this Court on May 11, 2018) (hereinafter "2018 CR") at 28-86, 88-118. The convicting court again adopted the State's proposed findings *in toto*. 2018 CR at 124-150. The record was returned to this Court for the reinstatement of Mr. Skinner's appeal, and the parties moved the Court for a briefing schedule. The Court granted that motion, directing Mr. Skinner to file this supplemental brief no later than June 20.

### **Request for Oral Argument**

Oral argument is requested. Since the Court originally heard argument on April 15, 2015, the factual record has expanded and the Court's membership has changed. Moreover, DPS's new mixture guidelines and its adoption of STRmix are major developments in Texas criminal justice, and this case is one of the first to reach the Court with a comprehensive record regarding some of the benefits and limitations of those developments. Oral argument will help the Court gain a better understanding of the case and promote a more fully developed decision. Perhaps most important, of course, this is a capital case in which Mr. Skinner's life is at stake.

### **Statement of Facts**

In late 2014 and early 2015, DPS made *two* principal changes in the operating procedures for its DNA laboratory that shaped its subsequent reanalysis of the 2012-

13 DNA test results. RR 186-87 (Hester).<sup>4</sup> The first was to adjust downward the analytical threshold (“AT”) it would use in determining whether peaks appearing on electropherograms produced in the testing process represented true alleles, as opposed to “noise” that is simply an artifact of DNA amplification. *See id.* at 185-86; *see also* RR 141-42 (Budowle). This change led DPS, when it reanalyzed the 2012-13 test results here, to reinterpret as DNA *mixtures* certain samples that it had previously deemed to come from a single source, and also to change the number of presumed contributors to samples it had previously identified as mixtures. *See, e.g.,* RR 206-207 (Hester) (lowering the AT meant that more peaks would be “called” as true alleles, such as one that led a DPS analyst to interpret a particular sample “as a three-person mixture instead of a two-person mixture”); *see also infra*.

The second change, occurring at about the same time but reflecting a separate decision, RR 186-87 (Hester), was to begin employing the computer program STRmix to calculate the likelihood that a particular person contributed DNA to a given evidentiary sample. STRmix is one of a number of commercially available software programs designed to assist laboratories in DNA analysis. On what is

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<sup>4</sup> The Reporter’s Record of the January 9, 2018 hearing spans 3 volumes, but Volume 2 contains all the testimony (Volume 1 is the Master Index). Accordingly, we cite testimony from the 2018 hearing simply as “RR,” followed by the page number, with the understanding that all such citations refer to Volume 2. The witness’s name will also be indicated if it is not otherwise apparent from the context. Volume 3 contains all exhibits admitted at the 2018 hearing; we cite them as “DX” or “SX.” Exhibits admitted at the January 2018 hearing were numbered to be consecutive with those admitted at the February 2014 hearing.

sometimes called the “wet” side of the DNA testing process, *see* RR 83 (Hornyak), the DNA from an evidentiary sample is collected and amplified, after which the extracted material is run through an electrophoresis machine (sometimes called a genetic analyzer), which creates an electronic picture of the DNA known as an electropherogram.<sup>5</sup> STRmix then analyzes the electropherograms, assigning statistical probabilities to the likelihood that persons for whom the lab has reference samples (*i.e.*, complete DNA profiles) contributed their DNA to the evidentiary sample. *See* RR 12-13 (Adams); 127-29, 132 (Budowle).

The end product of the STRmix analysis is a “likelihood ratio,” or “LR.” The LR, while expressed as a decimal, represents a fraction. The numerator of that fraction is what STRmix calculates as the likelihood that the known individual contributed to the sample (the “inclusion,” or “contributor,” hypothesis); the denominator of that fraction is the calculated likelihood that that individual was not a contributor (the “exclusion,” or “non-contributor,” hypothesis). If STRmix considers the inclusion hypothesis to be better supported by the data than the exclusion hypothesis (*i.e.*, if the numerator is greater than the denominator), the LR will be greater than 1. If the exclusion hypothesis is better supported, the LR will be between 1 and zero. *See generally* RR 22-23 (Adams); RR 133-34 (Budowle).

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<sup>5</sup> *See, e.g.*, DX 48 at 7-9 (electropherograms related to blanket from boys’ bedroom, Stain 3 (CO#25a, laboratory item number I.24.3)).

Put slightly differently, the LR is above 1 when STRmix considers it more likely that the known individual contributed to the sample than that a random unknown and unrelated person did so, and when the LR is below 1, the reverse is true. RR 26 (Adams).

As the LR increases above 1 towards infinity, support for the inclusionary hypothesis grows stronger. As it shrinks below 1 toward zero, the exclusionary hypothesis does likewise. RR 22-23 (Adams); 177 (Hester) (“1 is the dividing line” between favoring one hypothesis or the other). At some point, the LR grows large enough that the result may confidently be characterized as an “inclusion,”<sup>6</sup> or small enough to warrant being labeled an “exclusion.” But there remains an intermediate zone that extends both above and below 1, where the result is described as “inconclusive.” RR 26 (Adams).

A laboratory using STRmix first conducts validation studies to determine the reliability of the program under a variety of circumstances; based on the results of those studies, it chooses where to set the boundaries of the “inclusion,” “exclusion,”

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<sup>6</sup> In its reports, DPS prefers to say that a given individual “cannot be excluded” as a contributor, rather than that the individual has been “included.” RR 194 (Hester). However, both sides’ experts at the 2018 hearing often treated the two terms as functionally equivalent. *See, e.g.*, RR 67 (Adams); RR 129, 144, 173 (Budowle). “Included” avoids the need to write sentences using potentially cumbersome multiple negatives, and Mr. Hester himself granted that it is often easier to say “included,” and that he sometimes does so himself. RR 194. Thus, this brief will use “included” as synonymous with “not excluded.”

and “inconclusive” ranges. RR 23-24 (Adams). For STRmix results based on STR DNA testing using the Identifiler Plus kit, DPS has set the boundary between “included” and “inconclusive” at 1,000 (*i.e.*, a person whose LR is 1,000 or above will be reported as included), and has set the boundary between “inconclusive” and “excluded” at 0.01. DX 56 at 29; *see also* RR 24 (Adams).<sup>7</sup> For STRmix results based on Minifiler kit results, the LR threshold above which an individual is considered included is 10,000 instead of 1,000, but the boundary between inconclusive and excluded remains the same at 0.01. DX 57 at 24; *see also* RR 24 (Adams).

In reporting results, DPS will provide the LRs for those persons who are considered included (or who, as DPS prefers to say, are “not excluded”) in an evidentiary sample.<sup>8</sup> DPS does not, however, report LRs for those persons whose LRs fall in the “inconclusive” or “excluded” categories. As a result of this

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<sup>7</sup> These settings apply with respect to DPS’s use of the particular version of STRmix employed for the reanalysis of the results in this case, version 2.3.07. RR 17-18 (Adams). All the features of STRmix discussed in this brief pertain to version 2.3.07, and may not pertain to later versions of STRmix. *Id.*

<sup>8</sup> Thus, for example, when STRmix in 2016 produced an LR of 10.7 million for Randy Busby for stain 1 from a bedsheet on the upper bunk, DPS reported that result as follows:

Obtaining this profile is 10.7 million times more likely if the DNA came from R. Busby than if the DNA came from an unrelated, unknown individual. Based on the likelihood ratio results, R. Busby cannot be excluded as the possible contributor to this profile.

SX 40 at 8.

convention, in reporting STRmix results DPS would describe a person whose LR is 999 (*i.e.*, someone who is 999 times *more* likely than an unrelated, unknown person to have contributed to a mixture) exactly the same way it would describe a person whose LR is 0.01 (*i.e.*, one who is 100 times *less* likely to have contributed to the mixture than an unrelated, unknown person). Both are reported simply as “inconclusive.” *See* RR 73-76, 78-79 (Adams). One would have to search through the lab’s case files to find the LRs that support these findings.

When calculating LRs, STRmix performs thousands of calculations of possible allelic combinations at each locus employing Markov chain Monte Carlo (“MCMC”) mathematical algorithms.<sup>9</sup> Because MCMC uses randomly generated numbers to begin each successive set of calculations, and because by definition those numbers, being random, will be different with each run, the LR produced by STRmix for a particular sample with respect to a particular known individual is also different each time the program is run, *even though the input data is exactly the same*. The differences between these successively calculated LRs can be as great as an order of magnitude. RR 21 (Adams).

This variability characteristic of STRmix is immaterial when LRs are well within the included or excluded ranges. For example, if STRmix assigns an

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<sup>9</sup> *See* [https://en.wikipedia.org/wiki/Markov\\_chain\\_Monte\\_Carlo](https://en.wikipedia.org/wiki/Markov_chain_Monte_Carlo) (last visited June 3, 2018).

individual a LR of 10 million on one run of the software and 100 million on the next, the difference, while large in absolute terms, is not material because both numbers are well within the inclusion range (*i.e.*, far above 1,000 or 10,000). *See* RR 143, 164 (Budowle). But the variability can be critical if one tries to attach significance to LRs in the inconclusive range, and especially for LRs close to 1. For example, an LR of exactly 1 on the first run could be as much as 10 (*i.e.*, ten times more likely) on a second run, and as low as 0.1 (ten times *less* likely) on a third. *Id.*; *see also* RR 143-45 (Budowle).

DPS ran STRmix on each sample in this case only once. *See* RR 30 (Adams). No one disputes that running the samples again would necessarily produce different LRs. *See supra*; *see also, e.g.*, RR 19 (Adams) (if STRmix is run a second time using identical data inputs, it “will produce different likelihood ratios”), 30 (same). And, where the LRs generated by STRmix are within an order of magnitude in either direction of 1 (*i.e.*, between 0.01 and 10), it is possible that on subsequent runs, LRs that DPS had previously reported as greater than 1 would drop below 1, and vice versa. RR 20-21 (Adams). Thus, while the LRs produced by STRmix are expressed with what appears to be great precision, those LRs will *always* change if STRmix is run again. For this reason, among others, LRs in the inconclusive range cannot be

relied upon. *See* RR 197 (Hester) (“[the] fact that it varies slightly from run to run . . . partly leads to DPS’s decision to have that inconclusive range”).<sup>10</sup>

Another key fact about the operation of STRmix is that while STRmix results may characterize a particular evidentiary sample as containing a mixture of DNA (and assign LRs to any number of potential contributors to that purported mixture), that conclusion – that the sample *is*, in fact, a mixture – is not attributable to STRmix. STRmix cannot examine an electropherogram and determine whether the sample it depicts is a mixture. Instead, a human DNA analyst must read the electropherogram, decide whether the data indicates a mixture and, if so, how many individuals likely contributed to it, and then set the parameters of STRmix accordingly. *See* RR 19 (Adams) (before running STRmix, the human analyst must tell the program, *inter alia*, “the overall number of contributors assumed to be present in the sample”); *id.* at 217 (Hester) (same). STRmix then analyzes the data based on the assumptions provided by the human analyst in order to derive LRs for potential contributors. *See* RR 18-19 (Adams).

Finally, and importantly, respecting generally the samples that are the focus of Mr. Skinner’s arguments in his opening brief, some of the samples that DPS “called” as mixtures in 2016 (and to which STRmix then dutifully assigned LRs for

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<sup>10</sup> We will return to the significance of this feature of STRmix *infra*, in discussing the convicting court’s conclusions with respect to particular items of evidence.



potential contributors) contained very little actual DNA material from the presumed minor contributor(s). *See, e.g.*, RR 37-45 (Adams) (describing the process for quantifying the amount of DNA originating from the minor contributor in samples analyzed as mixtures, and the tiny size of that contribution in some of the relevant samples); RR 197 (Hester) (the samples here contained “very low level DNA information”), 198 (same), 243 (same), 244 (same).<sup>11</sup> No witness at the 2018 hearing disputed that great caution was required in drawing inferences from LRs based on such low-level DNA information. RR 46 (Adams) (“any signal produced by [such small quantities of DNA] is going to be very small,” leading to “greater uncertainty about the origin of that DNA in terms of genotype, in terms of contributor quantity [in a mixture]”; the less DNA from the minor contributor is present in a presumed mixture, the more STRmix’s LRs for the presumed minor contributor “tend to trend towards 1”); RR 240 (Hester) (it is especially difficult to

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<sup>11</sup> In some cases the amount of DNA attributable to the minor contributor was only a few picograms, which is equivalent to *one trillionth* of a typical single-serving pack of sugar. RR 43 (Adams). The presence of such small amounts of DNA is unsurprising, given that most of the items of evidence from which DNA was recovered in 2012-2013 were collected in 1994. In the ensuing 18 years, those items were not stored or maintained in a manner designed to preserve and protect biological evidence. *See* RR 48 (Adams) (DNA “degrade[s] over time,” a process “accelerated by ... environmental factors” such as exposure to “heat,” “increased moisture,” or “UV light”); *see also* DX 18 at 2 (a 2012 memo by Mr. Hester commenting that after the verdict in this case in 1995, “the evidence was stored in a non-temperature controlled storage room,” and that by 2012 many of the bags in which evidence had been stored “showed damage from rodents or insects, indicating that the evidence was exposed to the outside environment;” Mr. Hester attributed the difficulty in obtaining results in part to “[t]he age [of the evidence] combined with the lack of proper long term storage,” which “likely led to ... degraded DNA”).

identify whether a sample contains a mixture of DNA from two contributors where, as here, “the possible second contributor is low level”); RR 138 (Budowle) (“as the amount of DNA [present in a given sample] gets less and less, ... the amount of information you have is less,” and accordingly “the strength of the evidence is going to be less”).

### **Issue Presented for Supplemental Briefing**

Did the 2016-17 STRmix reanalysis change in any material way the results from 2012-13 on which the parties relied in their original round of briefing in this case?

### **Summary of Argument**

As Mr. Skinner showed during the first round of briefing on this appeal, several of the DNA test results originally obtained in 2012-13 significantly undermine the State’s case for guilt – *e.g.*, the absence of the victims’ DNA from places Mr. Skinner is known to have touched (and where one would expect to find their DNA mixed together if he were guilty) and a combination of DNA and other evidence suggesting that hairs recovered from Twila Busby’s hand belonged to alternative suspect Robert Donnell. *See generally* AOB at 24-43.

Although the 2012-13 results were reanalyzed in 2016 using different standards for determining the presence of mixtures and the probabilistic genotyping

software STRmix, nothing about that reanalysis undermines in any way the exculpatory value of the original DNA test results. Accordingly, there remains a reasonable probability that, when added to the substantial exculpatory evidence already before the jury, those DNA test results would have left the jury in 1995 with reasonable doubt about Mr. Skinner's guilt, leading to a different outcome. This Court should reverse the convicting court's finding to the contrary, which reflects that the court below fundamentally misapplied the relevant statutory standard and either ignored or misunderstood key testimony from the 2018 evidentiary hearing.

### **Argument**

- A. The relevant original DNA results, which Mr. Skinner has shown would probably have resulted in a different outcome at trial by dramatically strengthening the case for reasonable doubt, are unaffected by the 2016-17 reanalysis.**

In Mr. Skinner's opening and reply briefs, he made the following arguments, briefly summarized here, as to why the 2012-13 DNA test results, when added to the substantial exonerating evidence that the jury did have before it,<sup>12</sup> would have given

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<sup>12</sup> That evidence included testimony by a toxicology expert that Mr. Skinner was too impaired by alcohol and codeine to have committed the murders, testimony from an eyewitness corroborating that Mr. Skinner was in a near comatose state from excessive alcohol and drug consumption shortly before the murders occurred, physical evidence that Mr. Skinner was literally falling down drunk shortly after the murders occurred, testimony from an occupational therapist that Mr. Skinner would have had difficulty grasping the murder weapons due to a previous injury to his right hand, and testimony that Robert Donnell had both motive and opportunity to have committed the murders. *See* AOB at 4-14.

his defense attorneys powerful arguments to convince the jury that there was reasonable doubt as to his guilt:

- A DPS analyst determined that the hairs found clutched in Twila Busby's hands were visually dissimilar to her own hair and that of her sons Randy Busby and Elwin Caler. Yet the mitochondrial DNA in these hairs matched that of the three victims. If those hairs didn't come from the victims, then they had to have come from a maternal relative. Alternate suspect Robert Donnell, who had both motive and opportunity to commit the murders, was the brother of Twila's mother, and thus was such a maternal relative. *See* AOB at 24-29.
- Blood stains taken from a back door and two sets of back doorknobs contained only the DNA of Mr. Skinner and not that of any of the victims. These results would have been highly unlikely if Mr. Skinner were the killer, as the true killer would almost certainly have had the blood of one or more of the victims on his hands. *See* AOB at 30-33.
- There was no DNA from Mr. Skinner on the dishtowel found in the plastic trash bag in the living room. That dishtowel did, however, contain both Twila Busby's blood and the DNA of at least one other unknown person, raising the possibility that the real killer used the towel to wipe blood from his hands before throwing it in the trash bag. *See* AOB at 36-40.
- The DNA of both Elwin Caler and Randy Busby was found mixed in blood stains on the carpet in the boys' bedroom. That stain would likely also have contained the blood of Mr. Skinner if he was the killer and had cut his hand with the knife when stabbing Randy, as the State insisted at trial. Yet Mr. Skinner's DNA was not found in those stains. *See* AOB at 33.
- There was no DNA from Mr. Skinner on the blanket that covered Randy Busby and through which he was fatally stabbed, making it highly improbable that Mr. Skinner sustained his own hand injury while stabbing Randy. *See* AOB at 34-36.
- Mr. Skinner bled from a cut on his right hand and therefore left his blood at several locations inside the house, not just on the back doors. Yet in every one of those instances where the testing showed the presence of Mr.

Skinner's DNA, it was not mixed with that of any of the victims, a highly improbable result if he were the killer. *See* AOB at 32-33; RB at 23-24.

As noted, the question to be addressed here is whether the 2016-17 reanalysis in any way changed the original results for these items of evidence such that Mr. Skinner's arguments have been undermined. The answer is no.

We discuss each item in turn.

**1. The 2016-17 reanalysis changed nothing about the results concerning the hairs in Twila Busby's hands.**

Two of the hairs recovered from Twila Busby's hands were subjected to STR testing in 2012-13, but no results were obtained; a third hair lacked the biological material necessary for STR DNA analysis. The reanalysis in 2016 also did not produce any STR results from these hairs. *See* 2018 CR at 71 (Defendant's Proposed Findings of Fact, Appendix A, at 2<sup>13</sup>). The mtDNA results from these hairs were not a subject of the 2016-17 reanalysis. Thus, nothing about the STRmix analysis affects Mr. Skinner's argument about the potential exculpatory relevance of these hairs.

**2. The 2016-17 reanalysis changed nothing about the results concerning the bloodstains on the back doors.**

Bloodstains were recovered from two doors at the rear of the home. *See* DX 26 (admitted at 2014 hearing). At trial, evidence was introduced that the palm prints

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<sup>13</sup> These hairs were assigned laboratory item numbers I.6e3, I.7c, and I.9c2.

on the door knobs were Mr. Skinner's, indicating that he exited the house through those doors. Original DNA testing of these bloodstains in 2012 showed them to have originated from a single source – Mr. Skinner. Twila Busby, Elwin Caler, and Randy Busby were all excluded as contributors to these stains. The 2016-17 reanalysis confirmed these results. RR 212-213; *see also* 2018 CR at 74.<sup>14</sup> Thus, nothing about the reanalysis affects Mr. Skinner's argument about the potential exculpatory relevance of these bloodstains.

**3. The only changes in the results concerning the dishtowel were not material.**

**a. Two of the three results relating to the dishtowel did not change.**

The dishtowel found in a trash bag at the crime scene was processed via “mini-taping.” *See* AOB at 36-37. Possible DNA was lifted separately from each side, producing two “stains”; each was DNA-tested. *Id.* In addition, a single area on one side tested presumptively positive for blood, and that visible stain was separately collected and then DNA-tested as stain 3. *Id.*

In 2012, DPS found that stain 3 tested positive for blood, contained DNA solely from Twila Busby, and excluded all other individuals for whom the lab had

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<sup>14</sup> These stains were assigned laboratory item numbers III.13, III.14, and III.17. *See* DX 10 (admitted at 2014 hearing) at 6-7.

reference samples, including Mr. Skinner, Randy Busby, and Elwin Caler. In 2016, DPS reached the same result. RR 211 (Hester); 2018 CR at 73.

With respect to “side 2,” the original test results from 2012 (*i.e.*, the number of contributors and their identity) also did not change when reanalyzed in 2016. RR 211 (Hester); *see also* 2018 CR at 73 (comparing results for “Dishtowel from plastic bag in living room, side 2”).

**b. There was no material change in the third result from the dishtowel.**

The “side 1” stain was the only one of the three for which the results changed at all, and the change was immaterial. In 2012, DPS determined that the stain was a mixture of at least two, that Mr. Porton (the court reporter) was a contributor and that all of the other persons for whom DPS had reference samples, including Mr. Skinner and the three victims, were excluded (meaning, therefore, that the second contributor was unknown). *See* 2018 CR at 73. In 2016, the DPS analyst added a third contributor to the mixture and STRmix placed Mr. Skinner, Mr. White (a police officer who helped collect the evidence) and Mr. Miller (a defense consultant who was present when DPS processed the evidence) into the “inconclusive” category. While that addition makes the STRmix results for this sample different, it does not make them *materially* so. An “inconclusive” finding by STRmix, as explained *supra*, represents an LR that falls within the zone where it provides no meaningful support for either inclusion or exclusion. DPS has set those boundaries at 0.01 on

the lower end, and 1,000 (for Identifiler Plus results) or 10,000 (for Minifiler results) on the top end. STRmix calculated the LR for Mr. Skinner for this item at 0.0355, barely above the boundary DPS established between inconclusive and excluded.<sup>15</sup>

Consistent with the core science behind STRmix explained *supra*, every expert at the 2018 hearing agreed that an “inconclusive” STRmix result with respect to whether a particular individual contributed DNA to an evidentiary sample *lacks any evidentiary value whatsoever*. See, e.g., RR 38 (defense expert Mr. Adams) (such a result “wouldn’t inform a decision” about whether a particular person had contributed DNA to an evidentiary sample); RR 140 (State’s expert Dr. Budowle) (such LRs are “just not informative”); *see also* RR 178 (Budowle) (agreeing that for the purposes at issue in this case, an LR around 1 is “uninformative”); *id.* (agreeing that one should “be careful about attaching any significance” to an LR between 0.1 and 10). Mr. Hester emphasized that LRs in the inconclusive range are “just not reliable,” RR 197, and entitled to “no weight.” See RR 209, 213, 223, 224, 229, 220 (inconclusive results are consistent with not having enough DNA to render an opinion), 246 (an LR around 1 is “uninformative to a [trier] of fact at a trial”). Therefore, the experts’ unanimous view forecloses treating the STRmix result for “side 1” of the dishtowel as materially different from the result reported in 2012-13.

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<sup>15</sup> An LR of .0355, if read literally even though it is in the “inconclusive” zone, means that Mr. Skinner is over 28 times ( $1 \div .0355$ ) *less* likely than a unknown, unrelated person to have contributed to the mixture.



**4. Nothing material changed about the results concerning the stains from the carpet in the sons' bedroom.**

Three stains were cut from the carpet in the bedroom shared by Elwin Caler and Randy Busby. In 2012-13, stain 1 was tested using only the Identifiler Plus kit, while stains 2 and 3 were tested using both Identifiler Plus and Minifiler.

The relevant aspects of the results for stain 1 did not change when it was subjected to reanalysis. RR 223 (Hester) (respecting this stain, “the number of contributors and the conclusions did not change”).

The original results for stain 2 (both using Identifiler Plus and Minifiler) showed a mixture of at least three contributors, with Elwin Caler and Randy Busby included and all other persons for whom DPS had reference samples (including Mr. Skinner) excluded. 2018 CR at 81 (Identifiler Plus), 85 (Minifiler). The reanalysis of the Identifiler Plus results for stain 2, reflecting the lowered analytical threshold, changed to the extent of postulating a possible fourth contributor, but did not change regarding inclusions (Caler and Randy Busby) or exclusions (all other reference samples). *See* RR 223-224 (Hester). The reanalysis of the Minifiler results for stain 2 found a mixture of four contributors, with the same inclusions (Caler and Randy Busby), but “inconclusive” results as to Mr. Skinner (with an LR of 0.282), Twila Busby, Mr. Porton, and Ms. Hayes (a lawyer for the State). Mr. Hester agreed that these inconclusive results with respect to stain 2 (even that for Twila Busby, who

had an LR of 2,490) possessed “no evidentiary weight.” RR 229; *see also supra* (inconclusive results have zero weight).

For carpet stain 3, the STR DNA result in 2012 using Identifiler Plus was “[n]o interpretable DNA results.” In 2013, the Minifiler result was a mixture of at least three, with Caler included and everyone else for whom DPS had a reference sample excluded. DPS’s 2016 reanalysis of the Identifiler Plus non-results found a mixture of two contributors, with Elwin Caler included, Twila and Randy Busby both “inconclusive,” and all other reference samples excluded. *See* 2018 CR at 81 (comparing results for “Stain on carpet cut from boys’ bedroom floor, stain 3”); *see also* RR 224 (Hester) (summarizing the difference between the two sets of results as going from “no interpretable results” in 2012-13 to “Mr. Caler could not be excluded” in 2016). The reanalysis of the Minifiler results for stain 3 indicated a mixture of three contributors; Elwin Caler and Randy Busby were included, the results were “inconclusive” as to Mr. Skinner (with an LR of 0.0352), Twila Busby, Mr. Porton, and Mr. Robinson (one of Mr. Skinner’s lawyers). *See* 2018 CR at 85.

Because “inconclusive” results as a scientific matter possess zero weight, *see supra*, from an evidentiary standpoint the reanalysis in 2016 did not materially change the significance of the DNA test results obtained for all three stains on item (4) in 2012-13.

**5. Nothing material changed about the results concerning the blanket on Randy Busby's bed – if there was a change at all.**

Three stains, all of which tested positive for blood, were found on the blanket that covered Randy Busby's body and through which he was stabbed. In 2012, all three stains were tested using only the Identifiler Plus kit. All were found to come from a single source, Randy Busby, and all of the other persons for whom DPS had reference samples, including Mr. Skinner, were excluded.

**a. Two of the three results relating to the blanket showed no change, and the change regarding the third was immaterial.**

The relevant aspects of the results for stains 1 and 2 did not change when they were reanalyzed in 2016. *See* 2018 CR 78; RR 219 (Hester) (respecting this stain, the 2012 and 2016 results are “consistent”). With respect to stain 3, in 2016 DPS declared it to be a mixture of two, with Randy Busby included, Mr. Skinner “inconclusive” (with an LR of 8.75), and everyone else excluded. Therefore, even with respect to stain 3, because Mr. Skinner's LR fell well within the inconclusive range,<sup>16</sup> there was no material change between the 2012 and 2016 results, for the

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<sup>16</sup> To be sure, in this instance Mr. Skinner's LR was greater than 1, but barely so. At 8.75, it was only 1/114<sup>th</sup> (less than eight-tenths of one percent) of what it would need to be to put it in the “included” range, and, as discussed *supra*, it is close enough to 1 that in subsequent runs STRmix could easily assign it an LR of less than 1. In any event, as discussed in the text, all the experts agreed that all LRs anywhere in the inconclusive range have no evidentiary weight.

reason that, as all experts agreed and as discussed in greater detail *supra*, results in the inconclusive range possess no evidentiary value.

Even this “inconclusive” STRmix result on blanket stain 3 is called into question by an analysis of the same stain performed by another widely accepted probabilistic genotyping software program, True Allele. *See generally* RR 81-115 (Hornyak). TrueAllele, currently used by seven U.S. crime labs and undergoing validation studies for use by five more, is STRmix’s principal domestic competitor. RR 86, 106 (Hornyak). Like STRmix, TrueAllele employs an MCMC algorithm and therefore reaches somewhat different results for each run on a given sample. RR 102-03 (Hornyak). Like DPS with STRmix, True Allele was asked to assume that blanket stain 3 was a mixture of two. Unlike DPS with STRmix, however, TrueAllele was run multiple times on the blanket stain to confirm that the LR it reported was representative of the full range of results obtained. RR 103-04 (Hornyak). TrueAllele calculated that, if blanket stain 3 is a mixture, Mr. Skinner was at least 249 times *less* likely than an unrelated, unknown person to have contributed to it. Accordingly, it *excluded* Mr. Skinner as a contributor.

**b. DPS was likely wrong in calling blanket stain 3 a mixture at all.**

An even more fundamental problem exists, however, regarding DPS’s 2016 reported results on blanket stain 3: the DPS analyst was almost certainly wrong in calling, and then telling STRmix to assume, the sample was a mixture. As explained

above, it is the human analyst, not STRmix, who initially determines whether a given sample is a mixture. RR 50 (Adams) (whether a sample is a mixture is “something STRmix is told [by the analyst], not something it figures out”); RR 179 (Budowle) (agreeing that “[a]t the beginning of the process, before you put data into STRmix,” it is a matter of “human judgment as to whether or not the sample that you’re putting into STRmix is a mixture”); RR 233 (Hester) (agreeing that the analyst, not STRmix, makes this determination). And, as also discussed above, sometime after the original DNA testing was performed in 2012-13, DPS decided to lower its analytical threshold, or AT, to treat lower peaks on an electropherogram as alleles rather than “noise” for purposes of deciding whether an evidentiary sample is a mixture. It was entirely because of DPS’s decision to lower the analytic threshold that the analyst, Mr. Hester, called stain 3 on the blanket a mixture of two, even though in 2012 he had just as confidently deemed it to have originated from a single source.

To decide whether an evidentiary sample is a mixture, the analyst examines the peaks displayed on that sample’s electropherogram. The analyst disregards as “noise” those peaks whose relative fluorescence unit (“rfu”) values fall below a predetermined AT, as well as those above the AT that are better explained not as true alleles, but as products of defects inherent in the amplification process. *See* RR 55-56 (Adams). The most common such defect is “stutter,” the presence of a small

peak immediately before or after a large peak.<sup>17</sup> *Id.* Another possible explanation for a peak barely above the AT is the phenomenon called “drop-in,” where a “stray piece of genetic material ... somehow g[ets] into the sample,” usually appearing at just one locus. RR 56-57 (Adams); RR 147-48 (Budowle) (drop-in is a trace allele that is “almost a euphemism ... for a peak that [the analyst doesn’t] know how to explain ... on all the other evidence.”). After eliminating peaks that likely represent artifacts like stutter and drop-in, the analyst counts the remaining (presumably true allelic) peaks. Because a person generally has only two alleles at each locus, an evidentiary sample that has more than two alleles at any locus is likely a mixture. A sample with three or four alleles at a locus is interpreted as a mixture of two, a sample with five or six alleles at a locus as a mixture of three, and so on.

When Mr. Hester analyzed the electropherogram for stain 3 on the blanket in 2012, he applied DPS’s then-AT of 100 rfus and found two peaks – and only two peaks – at each locus. All the peaks he did find matched Randy Busby’s profile perfectly. This allowed him to state in his 2012 report, with “a reasonable degree of

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<sup>17</sup> Stutter comes in two types. “Negative” (also called “minus” or “backward”) stutter is typically represented on an electropherogram as a short peak one position lower than a taller peak and having an rfu value of no more than 10-15% (depending on the locus) of the taller peak’s. RR 56 (Adams); *see also* RR 146 (Budowle). “Positive” (also called “plus” or “forward”) stutter is represented on an electropherogram as a small peak one position higher than a taller peak and having an rfu value of no more than 1-3% (depending on the locus) of the taller peak’s. RR 56 (Adams); *see also* RR 146 (Budowle).

scientific certainty,” that Randy Busby was the sole source of the DNA in stain 3. See DX 48 at 2.

Applying the new 50-rfu AT to the very same electropherogram in 2016, Mr. Hester had to account for two additional peaks. Both barely met the new threshold. Specifically, at locus D3, there was a peak at the 17 allelic position having an rfu value of *exactly* 50, and at locus vWA there was a peak at the 18 position, also having an rfu value of *exactly* 50. Despite this scant evidence, contemporaneous DPS guidelines gave Mr. Hester no choice but to call this stain a mixture. Those guidelines allowed DPS analysts to deviate from the strict 50-rfu threshold to take into account *negative* stutter, but neither positive stutter nor drop-in. Concerning blanket stain 3, these restrictions were the difference in making the mixture call, as the 18 peak at vWA could just as readily have been explained as drop-in, and the 17 peak at D3 could just as readily have been explained as either positive stutter or drop-in, if these restrictions had not been in place. RR 62 (Adams); DX 60 at 2.<sup>18</sup>

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<sup>18</sup> The version of STRmix DPS used to reanalyze the evidence in this case was not programmed to take into account positive stutter (although a later version, now used by DPS, has that capability). RR 57 (Adams); RR 235 (Hester). Consequently, STRmix may not only have been told, incorrectly, to assume that the sample was a mixture, but it may also have overstated the value of the peak in the positive stutter position at locus D3 when calculating Mr. Skinner’s likelihood ratio.

State's expert Dr. Budowle agreed with defense expert Mr. Adams on this issue. He repeatedly opined – contrary to Mr. Hester's interpretation in the 2016 report – that stain 3 on the blanket should be interpreted not as a mixture but as a “*single source profile* with 1 trace allele.” RR 148 (emphasis added), 153, 170-71; *see also* RR 153 (Bowdle) (acknowledging that all small peaks but the 18 at vWA on the blanket were in “traditional stutter position . . . below stutter thresholds”). Thus, the independent experts for both Mr. Skinner and the State agreed that DPS erred in interpreting stain 3 on the blanket as a mixture.

Even Mr. Hester, the analyst who made the call on the blanket, stain 3, acknowledged that he could very well have been wrong. He admitted that when he prepared the 2016 report, DPS's then-applicable operating procedures did not allow him to consider forward stutter. *See, e.g.*, RR 234 (Hester) (“Even if I personally as an analyst thought it was forward stutter . . . I couldn't issue a report that stated that. . . . [I]f I'm not allowed to report on that, then it's kind of an avenue that's closed off to us.”); *see also* DX 60 at 2 (17 peak at D3 for the blanket “may be foreward [sic] stutter but *could not assign it at the time per SOP* [standard operating procedure]”) (emphasis added). Nor was Mr. Hester allowed to take account of possible drop-in. *E.g.*, RR 211-12 (if one extra allele is “not in a stutter position, . . . I'm very limited on what I can do. . . . I have no choice but to interpret that [peak] as a minor contributor or a second person if you will.”); *id.* at 234.



The conclusion that blanket stain 3 is not a mixture is unaffected by the fact that STRmix produced a likelihood ratio for Mr. Skinner with respect to that stain. As noted many times above, the lab analyst, not STRmix, determines whether an evidentiary sample is a mixture. Even if the analyst is mistaken, STRmix still tries to produce results consistent with that mistaken characterization. When DPS in its internal validation study took laboratory-created samples it knew had originated with a single source and deliberately told STRmix to analyze them as two-person mixtures, STRmix always generated LRs for the fictional second person and *almost a quarter of the time* even produced false inclusions for that person (*i.e.*, LRs greater than 1.0). DX 56 at 19; *see* RR 64-67 (Adams); RR 256 (Hester). Thus, while STRmix assigned Mr. Skinner an LR respecting the blanket that is above 1 (however slightly), that result in no way indicates that a second person in fact contributed DNA to the sample.

**6. There was no material change in the results from the many blood stains Mr. Skinner left throughout the house resulting from his bleeding right hand.**

Numerous blood stains (in addition to those on the back doors, already discussed above) were found throughout the house, and especially in the boys' bedroom. In several instances those stains were shown by the testing to have emanated from Mr. Skinner, no doubt due to his bleeding right hand. Yet in none of

these instances did the 2012-13 testing show that his DNA was mixed with that of any of the victims.

The same results held true for most of these stains after the 2016-17 reanalysis. Particularly notable is the handprint stain 18 inches above the floor on a door jam in the boys' bedroom – a stain likely left when Mr. Skinner reached out to break his fall when he fell down drunk. In 2012, this stain was found to have originated from Mr. Skinner alone. The same result was obtained when it was reanalyzed in 2016. *See* 2018 CR at 80 (item I.41)

The only stains for which the 2016 results differed were two blood droplets on a tennis shoe in the boys' bedroom and a single droplet on a cassette tape found in that same room. In 2012, DPS determined all three stains were from single source, Mr. Skinner. All the victims were excluded. In the 2016 reanalysis, DPS, applying its revised AT standard, determined all three of these stains to be mixtures, and STR deemed one or more of the victims “inconclusive” as to whether they contributed to these “mixtures.” *See* 2018 CR at 75 (item I.13 (tennis shoe)), 81 (item I.43 (cassette)).

Because the STRmix results as to the victims were inconclusive, these changes were not material, for the same reasons discussed above as to why inconclusive results on the dishtowel, the carpet and blanket stain 3 were not material – *i.e.*, inconclusive results carry no weight. Furthermore, like blanket stain 3, it is

highly doubtful that the stains on the tennis shoe and the cassette tape are mixtures at all. *See, e.g.*, RR 214 (Hester) (on the tennis shoe, he had “no choice,” due to DPS policy, but to interpret as “a second person” the “one extra allele at D5”); DX 60 at 3 (Hester notes on cassette tape) (“1 additional allele called due to lower [analytical] threshold, enough to change number of contributors.”). Finally, even if these stains were mixtures, the tennis shoe belonged to one of the boys (probably Randy), and the cassette tape was frequently handled by both boys, so it would not be surprising that trace amounts of their DNA would be found mixed with the blood that dripped from Mr. Skinner’s hand onto these objects.

For all these reasons, the STRmix reanalysis does not undercut in any respect the arguments advanced in Mr. Skinner’s opening and reply briefs that, in conjunction with the substantial defensive evidence already before the jury, *see* AOB at 8-14, a powerful case for reasonable doubt could have been fashioned by trial counsel from the post-conviction DNA test results.

**B. The findings by the convicting court on remand reflect a misapplication of the relevant legal standard and either misunderstand, or are indifferent to, the specifics of the evidence presented at the 2018 hearing.**

This Court’s purpose in remanding this case was to determine whether the 2012-13 results would change in any material respect if they were reanalyzed. Originally, the Court expected that reanalysis to take the form of a recalculation of the original results using a database free of the errors that had infected the FBI

database previously in use. The fact that in the interim DPS instead moved to change the way it identified mixtures and adopt STRmix (making the anticipated recalculations unnecessary) does not change the expectation that the focus on remand would be on whether and how the new analysis (whatever its nature) changed the import of the original results. The findings entered below – written *in toto* by the State and adopted by the convicting court without any change whatsoever – shed no light on that question. By contrast, the proposed findings Mr. Skinner offered to the convicting court did address that issue directly and in detail. Those are the findings that should have been adopted. Fortunately, they are included in the clerk’s supplemental record and can be reviewed by this Court to better understand the record developed on remand. *See* 2018 CR at 31-86.

There are two things of particular note about the 2018 findings the convicting court did sign. First, the original findings in 2014 – which were likewise authored by the State and adopted verbatim by the convicting court – misstated the governing legal standard under art. 64.04. *See* AOB at 18-21 (discussing this error and its significance); RB at 6-21 (same). While the 2018 findings try to correct that clear error by reciting the language of the statute, the substance of the convicting court’s analysis shows that it still does not understand the inquiry required by art. 64.04.

For one thing, the convicting court plainly failed to consider the collective impact of the DNA test results. *See, e.g.*, 2018 CR at 137 (“The Court has reviewed

whether *any of the reported DNA testing results* would have made it reasonably probable that [Mr.] Skinner would not have been convicted, and the answer is ‘No.’”) (emphasis added). Art. 64.04 does not contemplate such piece-by-piece parsing.

For another, the convicting court nowhere considers the fact that a favorable finding under art. 64.04 can rest solely on the tendency of evidence to raise a reasonable doubt, as that is the only interpretation of “would not have been convicted” that makes sense within the framework of a criminal trial. Nor does the convicting court ever address the significance of the fact that there was already substantial exculpatory evidence before the jury, such that the impact of the DNA test results would have been to reinforce and strengthen that evidence, not to be considered in isolation from it. Notwithstanding that it correctly quotes the language of art. 64.04, the convicting court continues to misunderstand the statute as placing on Mr. Skinner the burden of presenting affirmative proof of innocence via the presence of another person at the crime scene. *See, e.g.*, 2018 CR at 106 (stating that Mr. Skinner’s showing under art. 64.04 falls short because he has “identified only 2 areas of evidence in support of an affirmative showing,” and citing (1) the extraneous alleles on the dishtowel and (2) the evidence supporting the inference that the hairs recovered from Twila Busby’s hands belonged to alternative suspect Robert Donnell).

Finding that the post-conviction DNA test results deserve no exculpatory weight despite their significant potential to strengthen the argument for reasonable doubt – as the convicting court did here, on the view that some of the results do not conclusively show Mr. Skinner’s actual innocence by implicating someone else in the murders – violates due process. Consider *Brady v. Maryland*, 373 U.S. 83 (1963) and its progeny, which forbid State suppression of exculpatory or impeaching information. A *Brady* violation requires relief where it is reasonably likely that the disclosure of the suppressed information would have led to a different outcome. *See, e.g., Kyles v. Whitley*, 514 U.S. 419 (1995). This is, of course, the very same standard incorporated in art. 64.04. New, even strong, exculpatory evidence often does not prove innocence outright and thus may not definitively forecast an acquittal. Likewise, new impeaching evidence often only adds more doubt, as by undermining the credibility of a key prosecution witness but leaving other inculpatory evidence untouched. Yet courts regularly sustain *Brady* claims in such circumstances, without suggesting that the evidence is immaterial because it does not “affirmatively” (to use the convicting court’s word) prove the defendant’s innocence. *See, e.g., Kyles*, 514 U.S. at 434 (“a showing of [*Brady*] materiality does not require demonstration by a preponderance that disclosure of the suppressed evidence would have resulted ultimately in the defendant’s acquittal (whether based on the presence of reasonable doubt or acceptance of an explanation for the crime that does not inculcate the

defendant)"); *id.* at 453-54 (granting relief under *Brady* despite acknowledging that even if the suppressed evidence had been disclosed, the remaining evidence from the State was legally sufficient to convict).

The inescapable conclusion is that in the art. 64.04 context, just as in the *Brady* context, a reviewing court's focus must be on the capacity of the evidence to leave jurors with reasonable doubt about the defendant's guilt, rather than its capacity to persuade them conclusively of his innocence. For that reason, this Court cannot uphold the convicting court's findings on the theory that the post-conviction DNA test results in this case merely "muddy the waters" as to Mr. Skinner's possible guilt. To do so is fundamentally unfair and contrary to the central place the burden of proof beyond a reasonable doubt occupies in our legal tradition. *See Sullivan v. Louisiana*, 508 U.S. 275, 281 (1993) (requiring jury to find that a criminal charge has been proven beyond a reasonable doubt "reflects ... a profound judgment about the way in which law should be enforced and justice administered.") (internal quotation marks omitted); *cf. Do Muddy Waters Shift Burdens?*, 76 Md. L. Rev. 629 (2017) (arguing that the dominance of the "muddying the waters" metaphor in Texas decisions applying Ch. 64 has had destructive consequences, effectively frustrating the Legislature's attempt to lighten the burden on defendants seeking post-conviction DNA testing). Indeed, "muddied waters" are the very definition of reasonable doubt.

The other grave problem with the convicting court’s findings is that they reflect either misunderstanding of, or indifference to, the undisputed scientific evidence at the 2018 hearing. This is most evident with respect to the convicting court’s statements attaching evidentiary weight or significance to STRmix results that assign “inconclusive” LR’s to particular contributors. For example, the convicting court asserts that Mr. Skinner’s DNA may be present on the dishtowel notwithstanding the fact that the original DNA testing excluded him as a possible contributor to any of the DNA profiles from either side of the dishtowel, citing Mr. Hester’s testimony from the first hearing that “an exclusion does not mean that Skinner is ruled out as a possible contributor to an allele at a given locus.” 2018 CR at 139 (¶ 73.C). But then the convicting court contends that this “explanation” is “reinforced by the fact that, after reanalysis [with STRmix], [Mr.] Skinner is not excluded, but rather is inconclusive as to whether he contributed his DNA to side one of the dishtowel.” *Id.*<sup>19</sup>

But that claim – that an “inconclusive” STRmix result equates to a finding that the person cannot be excluded – was resoundingly rejected not only by Mr. Skinner’s expert, but *by the State’s own experts*. *See supra*. Indeed, the convicting

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<sup>19</sup> Nor was this the only instance where the convicting court alluded to the potentially confirmatory weight of an “inconclusive” STRmix result. *See, e.g.*, 2018 CR at 147 (¶ 104) (“This [non-exculpatory inference] is especially true given that the re-analysis did not exclude [Mr.] Skinner, but rather determined it was inconclusive as to whether he was a possible contributor”).



court appears not to have recalled the testimony of Mr. Hester, which was explicit on this point. Under cross examination, Mr. Hester agreed that an inclusion under STRmix meant that the individual in question “[could not] be excluded as a contributor of this sample.” RR 244. He then was asked specifically whether it was not equally true that a person to whom STRmix had returned an “inconclusive” result on the same sample “also cannot be excluded as a contributor to this profile.” *Id.* Mr. Hester’s rejoinder was emphatic: Such a characterization would be “incorrect,” he said, because there is “a very big difference” between “cannot be excluded” and “inconclusive.” *Id.* at 245. His and the other experts’ unanimous refusal to attach any evidentiary significance to “inconclusive” STRmix results was not a matter of opinion but was dictated by the scientific principles that underlie STRmix itself and are explained *supra*. For this reason, too, the convicting court’s findings are insupportable.

In similar fashion, several times the convicting court asserts that the presence of alleles from an unknown person (as, for example, on the dishtowel and the carpet stain) was irrelevant because Mr. Skinner had not shown that they were deposited at the time of the crime. *See, e.g.*, 2018 CR at 147 (¶ 104) (“As the Court previously found, no evidence was presented at the hearings to show that any extraneous allele was deposited at the time of the crime”); *id.* at 139 (¶ 73.B) (same, regarding the

extraneous alleles on the dishtowel).<sup>20</sup> For two reasons, the convicting court erred in relying on that inference.

First, strictly speaking, this would be true of any piece of DNA evidence, as it is never possible to tell from a DNA profile “when” the sample containing it was deposited; thus, the convicting court’s reasoning would effectively render all DNA evidence irrelevant. Second, and more important, the convicting court’s demand for affirmative evidence from Mr. Skinner (here, evidence that a particular unknown profile was deposited at a particular time) reflects once again the court’s insistence that Mr. Skinner prove his innocence and its refusal to review the evidence or consider its significance in terms of *whether there is a reasonable probability it would have swayed at least one juror to harbor reasonable doubt*, which is the art. 64.04 standard. A juror reviewing the entire evidentiary picture regarding, for example, the dishtowel (including Mr. Skinner’s severe incapacitation, the evidence pointing to Robert Donnell, the presence of Twila Busby’s blood on the dishtowel, and the manner in which it was placed in a trash bag) could readily have credited the possibility that the extraneous alleles on the dishtowel were deposited on the night of the crime and thus concluded that the State’s case did not exclude every

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<sup>20</sup> The same failure to engage with the evidentiary picture as a whole is illustrated by the convicting court’s statement that “without more,” the presence of the extraneous alleles does not carry Mr. Skinner’s burden under art. 64.04. 2018 CR at 139 (¶ 73.D).

reasonable doubt about Mr. Skinner's guilt. That is how art. 64.04 must be applied, and is why Mr. Skinner is entitled to a favorable finding.

### **Conclusion**

Mr. Skinner showed in his opening and reply briefs that the original round of DNA testing in 2012-13 would have provided his trial counsel with more than enough evidence, when coupled with the substantial exonerating evidence they already had, to convince the jury to return a verdict of not guilty based on reasonable doubt. The issue now is whether any of the arguments made in the initial round of briefing is affected by the STRmix results. The answer is no. To the contrary, the STRmix results only confirm the 2012-13 results in every material respect. Thus, for all the reasons stated in Mr. Skinner's opening and reply briefs, he respectfully requests that the Court reverse the convicting court and find that, had all the DNA test results been available at the time of trial, there is a reasonable probability that he would not have been convicted.

Respectfully submitted,

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