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Quantification of the forensic genetics proof: Evaluating the impact of different statistical approaches

Camila Ferreira da Costa

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Genética Forense
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Orientador
Nádia Maria Gonçalves, Instituto de Investigação e Inovação em Saúde (i3s),
Instituto de Patologia e Imunologia Molecular da Universidade do Porto (IPATIMUP),
Centro de Matemática da Universidade do Porto (CMUP)

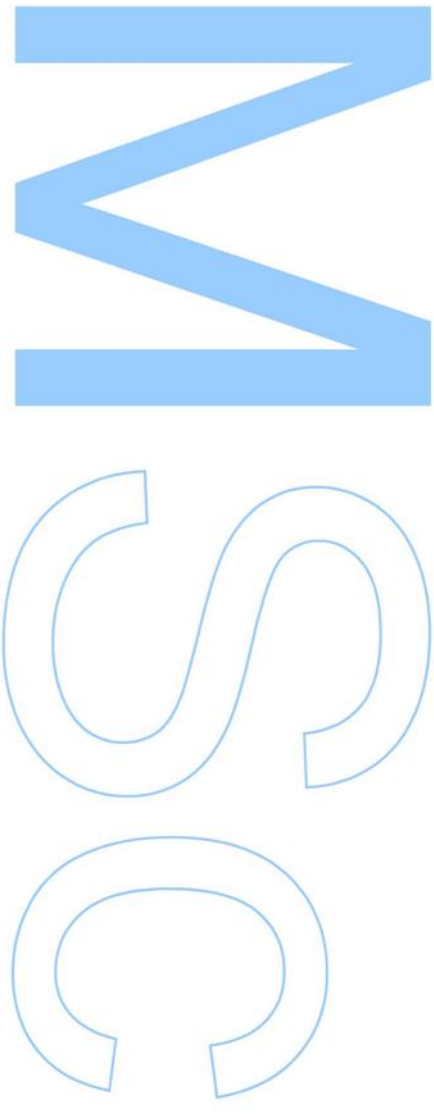
Orientador Externo
Paulo Miguel Ferreira, Especialista Superior,
Laboratório de Polícia Científica da Polícia Judiciária (LPC-PJ)



Todas as correções determinadas pelo júri, e só essas, foram efetuadas.

O Presidente do Júri,

Porto, _____/_____/_____



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Resumo

Atualmente, sempre que material biológico é encontrado numa de cena de crime, uma análise de ADN é realizada para auxiliar a investigação em curso. O peso atribuído a esse tipo de prova aumentou a necessidade de gerar perfis de ADN e obtê-los através de cada vez menos ADN inicial. No entanto, as amostras recolhidas no contexto de uma investigação criminal têm vários fatores associados que as tornam mais complexas e consequentemente, mais difíceis de interpretar e analisar. Esse tipo de amostras geralmente resulta da contribuição de mais de um dador e, portanto, são designadas de amostras de mistura de ADN sendo que, o verdadeiro número de contribuidores é desconhecido e a sua estimativa constitui um dos grandes desafios. Adicionalmente, outras limitações associadas a estes perfis dificultam a sua interpretação, tais como, contaminação, degradação, baixa quantidade e/ou qualidade da amostra que potencializa a ocorrência de efeitos estocásticos (*drop-in*, *drop-out* e/ou desequilíbrio heterozigótico), e ainda, a presença de artefactos no eletroferograma, nomeadamente, *stutters*, picos *pull-up*, *spikes* e *dye-blobs*.

Para superar a complexidade multifatorial intrínseca à análise e interpretação das amostras de mistura de ADN, foram desenvolvidos e implementados *software* baseados em métodos de genotipagem probabilística, que têm em conta informações qualitativas ou quantitativas do eletroferograma. Os modelos qualitativos consideram apenas as informações qualitativas (alelos observados), enquanto que os quantitativos têm em consideração também as informações quantitativas associadas (altura dos picos dos alelos). Por esse motivo, os modelos quantitativos são considerados mais eficientes, tornando-se, portanto, a abordagem preferencial para a análise deste tipo de perfis e o foco deste trabalho. Em ambos os modelos, o peso da prova é quantificado através do cálculo do *Likelihood ratio* (LR), que consiste na razão entre as probabilidades dos perfis de ADN observados assumindo duas hipóteses alternativas mutuamente exclusivas: “O indivíduo é contribuidor da amostra da mistura.” e “O indivíduo não é contribuidor da mistura, nem é geneticamente aparentado com nenhum contribuidor.”, sendo o indivíduo o dador da amostra de referência.

O objetivo principal desta dissertação é comparar os resultados obtidos através de duas ferramentas informáticas quantitativas distintas, nomeadamente, o STRmix™ v.2.7 e o EuroForMix v.1.9.3. Para tal, foram utilizados perfis de amostras de misturas reais recuperadas de cenas de crime e perfis de referência associados, de casos antigos do Laboratório de Polícia Científica da Polícia Judiciária. Um total de 158 pares

mistura/referência com dois (79) ou três (79) contribuidores estimados foram analisados para 21 marcadores autossomais *short tandem repeats*.

Primeiramente, foi realizada uma comparação entre os valores LR globais calculados em ambos os *software* para cada par mistura/referência, considerando a presença de *stutters* e valores de parâmetros previamente estabelecidos [1], nomeadamente, a estimativa do número de contribuidores, limite de deteção, *drop-in* (frequência e distribuição) e coeficiente de co-ancestralidade. Esta comparação espelhou as divergências existentes entre as ferramentas informáticas sob análise, sendo observados maiores valores de LR no STRmix™ do que no EuroForMix. A acumulação de pequenas discrepâncias obtidas no LR de cada marcador refletiu-se nas diferenças encontradas no valor LR global, atingindo diferenças superiores a pelo menos seis unidades (escala $\log_{10}$) em 13% e 17% dos casos com misturas com dois e três contribuidores estimados, respectivamente. Porém, estas proporções poderiam ter sido mais substanciais, porque, para o mesmo caso, havia marcadores em que o LR computado no STRmix™ era maior do que o calculado no EuroForMix e nos restantes marcadores a situação inversa ocorria, suavizando assim, as diferenças no LR global.

Posteriormente, foi testado o impacto que os parâmetros supracitados podem ter nos valores LR globais, bem como a consequência de considerar ou não *stutters* nas amostras problema. Para tal, os valores/condições desses parâmetros foram variados, e os valores LR globais comparados numa análise intra-software.

Ainda que, tenha sido observada uma tendência para aumentar ou diminuir o valor LR global quando as condições de alguns parâmetros foram variadas, o maior impacto foi verificado aquando da sub- e sobrestimação do número de contribuidores. Dependendo do *software* e do número de contribuidores estimados, a proporção de casos que mostram diferenças maiores que quatro unidades (escala $\log_{10}$) quando o número de contribuidores foi sobrestimado variou entre 11% e 0%. Quando este foi subestimado (análise de misturas com três contribuidores estimados assumindo apenas dois), essas proporções aumentaram para 16% e 10%. Já, na variação dos restantes parâmetros essa proporção não ultrapassou os 5%.

Considerando as diferenças encontradas na análise intra-software, o STRmix™ parece ter uma maior sensibilidade à variação de parâmetros comparativamente ao EuroForMix.

Isto enfatiza que, soluções informáticas baseadas em métodos de genotipagem probabilística devem ser vistas apenas como uma ferramenta para auxiliar o perito na interpretação de perfis. A estimativa dos valores de alguns parâmetros do *software* e a

avaliação dos eletroferogramas dos perfis das amostras problemas realizados pelo perito, podem ter uma grande influência no valor LR computado e como tal, a experiência e formação dos peritos é fulcral e não deve ser descurada. Este trabalho também permitiu demostrar a importância da validação de *software* para aplicação forense.

Palavras-chave: Forense, Interpretação de amostras de misturas de ADN, Peso da prova genética, *Likelihood ratio*, Genotipagem probabilística, *EuroForMix*, *STRmix*^{TM}.

Abstract

Currently, whenever biological material is found in a crime scene investigation, a DNA analysis is performed to assist the ongoing investigation. The weight attributed to this type of evidence increased the need to generate DNA profiles, through less and less initial DNA. However, samples collected in the context of the criminal investigation have associated several conditions that make it more complex and difficult to interpret and analyze. Firstly, these types of samples usually result from the contribution of more than one donor and are therefore called DNA mixture samples. The true number of contributors is unknown, and its estimation constitutes one of the great challenges. Additionally, several other constraints are associated with these samples and their consequent interpretation, such as, contamination, degradation, low quantity and/or quality that potentiates the occurrence of stochastic effects (drop-in, drop-out and/or heterozygotic imbalance), and even, the presence of artifacts in its electropherogram (epg) like stutter peaks, pull-up peaks, spikes and dye-blobs.

To overcome the multifactorial complexity intrinsic to the analysis and interpretation of the DNA mixture samples, probabilistic genotyping methods were developed and implemented as software, based on the qualitative or quantitative information of the epg. Qualitative models consider the epg qualitative information (observed alleles), while the quantitative ones take also into account the quantitative information associated (height of allele peaks). For this reason, quantitative models are considered more efficient and accurate, becoming therefore the preferred approach for this type of analysis and the focus of this work. In one and another case the weight of the evidence is quantified via the computation of likelihood ratio (LR), comparing the probabilities of the evidence given two mutually exclusive hypotheses: “The individual is contributor of the mixture sample.”, and “The individual is neither a contributor of the mixture, nor genetically related to any contributor.”, where the individual is the donor of the reference sample.

The main goal of this dissertation is to compare the results obtained through two different quantitative informatic tools, specifically, STRmix™ v.2.7 and EuroForMix v.1.9.3 software. To develop this study, real casework mixture samples profiles recovered from crime scenes and reference profiles associated, from former *Laboratório de Polícia Cientifica da Polícia Judiciária* cases, were used. A total of 158 mixture/reference pairs with two (79) or three (79) estimated contributors were analyzed for 21 autosomal short tandem repeat markers.

A comparison between LR values computed in both software for each mixture/reference pair was performed, considering the presence of stutters and previously established parameter values [1], namely, the estimation of the number of contributors, threshold detection, drop-in (frequency and distribution) and co-ancestry coefficient. This analysis reflected the divergences between the two different inference approaches, with a trend to STRmix™ values to be higher than those computed by EuroForMix. These differences were due to small discrepancies obtained in the LR of each marker, which resulted in LR values differing in at least six units (log_{10} scale) in 13% and 17% for cases with mixtures with two and three estimated contributors, respectively. However, the proportion of these cases was not greater since, for the same case, there were markers where the LR was greater when computed with STRmix™ than when EuroForMix was used, occurring the opposite situation for others, smoothing global LR differences.

The impact that the above-mentioned software parameters may have on the global LR values, was tested, as well as the consequence of considering or not stutters, in the mixture sample files. For that, these parameter values/conditions were varied, and the LR values were compared in an intra-software analysis.

Even though, in some parameters when considered varied conditions, a trend was showed to increase or decrease the global LR value, the major impact was verified when the number of contributors was under- and overestimated. Depending on the software and number of estimated contributors of the mixtures, the proportion of cases showing LR differences greater than four units (log_{10} scale) when the number of contributors was overestimated varied between 11% and 0%. When the number of estimators was underestimated and mixtures with three estimated contributors were analyzed as having two, these proportions increased to 16% and 10%. The variation of all the other parameters led to a difference of more than four units (log_{10} scale) in less than 5% of the cases.

The STRmix™ software seems to have a greater sensitivity to parameter variation compared to EuroForMix.

This emphasize that software based in probabilistic genotyping methods should be seen only as a tool to assist the expert in interpreting profiles. The estimation of software parameter values and the evaluation of the problem profile epg performed by the expert may greatly influence the computed LR value. As such, his/her experience and training are central and cannot be neglected. This work also shows the importance of validating software for forensic application.

Keywords: Forensic DNA, Mixture samples interpretation, Weight-of-evidence, Likelihood ratio, Probabilistic genotyping, EuroForMix, STRmix™.

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Figure 18: Values of LR (log_{10} scale) computed for the same mixture/reference pairs, with two (left plots) and three estimated contributors (right plots) in STRmix™ v.2.7 (in green – uppers plots) under the conditions ɣ=(0.1,0.1) (default) and Uniform (varied); and in EuroForMix v.1.9.3 [1] (in blue – lowers plots) under the conditions of λ=0.01 (default value) and λ=0.05 (varied value). The mixture/reference pairs that are highlighted with a continuous, dashed, or double continuous line circle correspond to the cases where less than 21 markers were analyzed. The outliers, where the discrepancy between values is greater than four units in a log_{10} scale, are highlighted with a X. 57
Figure 19: Values of LR (log_{10} scale) computed for the same mixture/reference sample pairs, with two (left plots) and three estimated contributors (right plots) in STRmix™ v.2.7 (uppers plots) and in EuroForMix v.1.9.3 [1] (lowers plots) for the F_{ST} default value (0.010) and all F_{ST} varied values considered (0.000, 0.015 and 0.030). Each group of four vertically placed dots concerns the analysis of the same mixture/reference sample pair. The mixture/reference pairs that are highlighted with a continuous, dashed, or double continuous line circle correspond to the cases where less than 21 markers were analyzed. 60
Figure 20: Values of LR (log_{10} scale) computed in EuroForMix v.1.9.3 without (x axis) and with stutters [1] (y axis), for the same mixture /reference samples pair, with two (left plot) and three estimated contributors (right plot). The outliers (Out.) are highlighted with an X representing the biggest discrepancy between analyzes (greater than four units in a log_{10} scale). 62

Figure 21: Comparison between the number of markers that presented modifications between the analysis with and without stutters (x axis) and the differences found for LRs values (in a $\log_{10}$ scale) computed in EuroForMix with and without stutters (y axis), for the same mixture sample/reference sample pair, with two (upper plot) and three estimated contributors (lower plot).The outliers (Out.) highlighted in figure 20 are also highlighted in this figure with an X..... 65

Abbreviations

ALS	Alternate Light Sources
Bp	Base pair
CE	Capillary Electrophoresis
CT	Cycle Threshold
DNA	Deoxyribonucleic Acid
dNTP's	Deoxynucleotide Triphosphates
DTT	Dithiothreitol
Epg	Electropherogram
et al.	et alli/et aliae
ESR	Institute of Environmental Science and Research
F_{ST}	Co-ancestry Coefficient
FSSA	Forensic Science South Australia
HWE	Hardy-Weinberg equilibrium
IBD	Identical by Descent
INDELs	Insertions and Deletions
IPC	Internal Positive Control
ISFG	International Society for Forensic Genetics
KM	Kastle-Meyer
LPC-PJ	Laboratório de Polícia Científica da Polícia Judiciária
LIF	Laser-induced Fluorescence
LSAE	Locus Specific Amplification Efficiency
LCN	Low Copy Number
LT-DNA	Low-template-DNA
MCMC	Markov Chain Monte Carlo

MPS	Massively Parallel Sequencing
MAC	Maximum Allele Count
MLE	Maximum Likelihood Estimation
NIST	National Institute of Standards and Technology
NGS	Next Generation Sequencing
NTC	No-Template Control
POI	Person of Interest
PCR	Polymerase Chain Reaction
PG	Probabilistic Genotyping
qPCR	Real-time PCR
RFLP	Restriction Fragment Length Polymorphism
STRs	Short Tandem Repeats
SNPs	Single Nucleotide Polymorphisms
SDS	Sodium Dodecyl Sulfate
VNTRs	Variable Number Tandem Repeats

1. Introduction

1.1. A Brief History of Forensic Genetics

Forensic Genetics is defined by *Forensic Science International: Genetics* Journal – one of the leading journals in forensic genetics – as "The application of genetics to human and non-human material (in the sense of a science with the purpose of studying inherited characteristics for the analysis of inter- and intra-specific variations in populations) for the resolution of legal conflicts." [2].

Over the years, different techniques have been developed to resolve legal conflicts or criminal cases. It started in the early year of the 20th century, with Karl Landsteiner describing the ABO blood grouping system, where individuals could be considered into different categories based on their blood type (A, B, AB, and O) [3-5]. This discovery resulted in the emergence of a branch known as Forensic Hemogenetics, in which the absorption–inhibition ABO typing technique was developed and became standard in forensic laboratories [6].

However, this technique presented limitations in the resolution of many forensic cases due to the high amount of biological material needed, the degradation of the proteins, and the low discriminating power [7]. With new discoveries and the appearance of new techniques, including restriction enzymes, Sanger sequencing [8], or Southern blotting [9], the DNA sequences examination became possible. This resulted in the replacement of blood typing for DNA profiling and the Forensic Hemogenetics gave rise to Forensic Genetics.

1.1.1. Discovering DNA structure: Impact on Forensic Genetics

In 1953, James Watson and Francis Crick described the structure of deoxyribonucleic acid (DNA) molecule as a double stranded molecule in helical arrangement. They showed that each chain is composed by nucleotides units, which contains (from the outside to the inside of the chain) a triphosphate group, a deoxyribose sugar and a nitrogenous base. Both chains follow right-handed helices, but the sequences of the atoms in the phosphate-sugar structure of each runs in opposite directions. The two polynucleotide chains are held together by hydrogen bonds formed between the specific complementary base pairing of nucleotides – adenine with thymine, and guanine with cytosine [10, 11].

Going deeper into the DNA molecule and considering the structure and function of their different regions, it can be divided into two major categories: 'coding' and 'non-coding' regions. The coding regions, where information on the coding and regulation of protein synthesis is contained, are known as genes. The non-coding regions are either extragenic regions or introns (within the genes) and include several elements that are involved in the regulation of genes but do not encode protein synthesis [7, 12].

Around 99.7% of DNA information are shared among individuals, with the remaining fraction showing variations between individuals as a result of segmental duplications, inversions, insertions, deletions and length polymorphisms [7]. These variations, usually within non-coding regions, are responsible for some of the individuals' distinct phenotype (physical characteristics) [13] as well as their unique DNA pattern or profile. For that reason, they became the main focus of forensic genetics, inciting the development of methods to locate and characterize these specific polymorphic sites – commonly referred to as loci (singular: locus) – in the human genome [12, 14].

The DNA pattern of one individual results from the combination of genotypes – pair of alleles present in a locus – obtained in a multiple loci examination. The more loci are considered, the more unlikely is two individuals sharing the same DNA profile, enabling the use of DNA information for human identity testing purposes [12].

1.1.2. Genetic polymorphisms: Evolution of DNA profiling

DNA sequences repeated several times next to each other are known as tandem repeats. According to their period size, the repeats can be classified as satellite DNA (period size greater than 100 base pairs – bp), minisatellites or Variable Number Tandem Repeats (VNTRs) (less than 100 bp and greater than ten bp) and microsatellites or Short Tandem Repeats (STRs) (less than ten bp) [15]. A variation in the number of tandem repeats of a DNA sequence results in alleles with different lengths. Throughout human genome, several loci present these length polymorphisms, and given their hypervariability within the population – due to a high mutation rate (order of magnitude estimated between 10^{-3} and 10^{-4}) [16, 17] – have been used as human DNA markers in individuals DNA typing through the years [18-20].

Alec Jeffreys in 1985 realized the potential forensic application of highly polymorphic locus, five years after their discovery [19], developing a method called "DNA fingerprint" [16, 21]. This became a milestone in Forensic Genetics and consisted in determining the size variations of VNTRs using the Restriction Fragment Length Polymorphism (RFLP) technique [22]. After the restriction enzymes cut the DNA

molecule at specific nucleotide sequence (namely, in the DNA regions surrounding the VNTRs) and the variable lengths fragments being separated by size in an agarose gel electrophoresis, the fragments are transferred to a nitrocellulose filter, which later hybridize with unique DNA labelled probes complementary to the VNTRs. Afterwards, the filter is exposed to an x-ray film and the labeled probes turn into a black band creating an autoradiogram with a single pattern for each individual [21, 23].This method was firstly applied in an immigration case [24], and shortly thereafter to solve a double homicide case [25], making VNTRs the first polymorphic DNA markers used to solve a criminal casework.

Nevertheless, the RFLP technique revealed some limitations such as being a time-consuming process and requiring a high DNA quantity. Since most of the samples collected from crime scenes present low DNA quantity, this technique was often unable to return reliable results, being replaced by a new technique that overcome those restrictions, entitled Polymerase Chain Reaction (PCR) [12, 26].

Developed in 1983 by Kary Mullis, PCR is an automated cyclic process, which consists in an enzymatic amplification of a specific nucleotide sequence. In each cycle, the strands in each targeted DNA are separated by heating and then cooled to allow the oligonucleotide primers to bind by complementarily at the begging of the DNA sequence. Afterwards, the strands are heated again, to DNA polymerase enzyme extend the primers by adding the appropriate complementary deoxynucleotide triphosphates (dNTP's) to the three-prime end of the primer, duplicating the original DNA-strand (figure 1) [27-29].

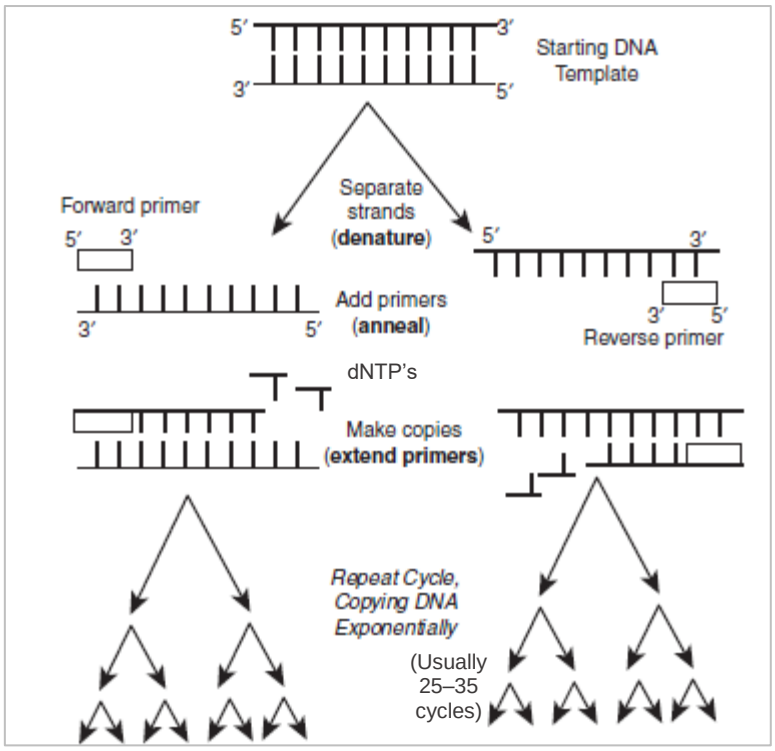


Figure 1:Diagram of the DNA amplification process through a PCR (Adapted from J.M. Butler [12]).

Although the VNTR analysis was a very powerful tool and used for several years, the difficulty in interpreting the profiles and the need for large amounts of non-degraded DNA (hardly achieved in forensic samples) were the motto for the VNTRs to be replaced by STRs in the 1990s [12]. The smaller size of the repeated sequence (two to six bp) associated with the possibility of multiplexing, i.e. several different loci can be analyzed at the same time (saving time and material resources) turned STRs the DNA markers of choice for the analysis of biological samples recovered from crime scenes, until nowadays [6, 30, 31].

The number of loci considered in the multiplex PCR reaction increased and the commercial multiplex STRs typing kits are now composed by more than 20 STRs [32-34], presenting a higher discriminatory power comparing to the 13 STRs considered in the first ones [35].

Single Nucleotide Polymorphisms (SNPs) are sequence polymorphisms and the most common genetic variation in human genome [36]. SNPs are constituted from a single nucleotide substitution at a specific DNA sequence position and only two different alleles are normally found at the specific locus [7]. Despite of the low level of polymorphism, SNPs can be a useful resource in cases where the DNA is found extremely degraded since its typing can be performed on small DNA sequences (40 to 50 bp) [37-39]. Additionally, its low mutation rate (order of magnitude estimated 10^{-8})

[40], comparing to others genetic polymorphisms [16, 17], allow its application in several situations, such as, population structure inference and population histories reconstruction [41-43]. The drawback of such a low mutation rate (and level of polymorphism) is that their use can be problematic in some kinship analyses [44].

The second most abundant type of variation in humans is the insertion or deletion of one or more nucleotides in genome, which result in INDEL polymorphisms [45]. These length polymorphisms, just like SNPs, have a low mutation rate (order of magnitude estimated 10^{-8}) [46] and can be typed in small size amplicons, which also makes them useful for population studies [47, 48] and cases with highly degraded DNA [49].

In recent years, the use of INDEL markers in forensic studies has increased. Even though INDELs and SNPs shared the above-mentioned characteristics, the first showed to be simpler to analyze and less time consuming [50].

Over the last few years, with the development of next generation sequencing (NGS) techniques that employ massively parallel sequencing (MPS) became possible to sequence whole genomes in a single run. Thinking about the possibility of getting more information from a problem sample from a single run, there are commercial companies developing kits that combine all types of DNA markers currently in use in forensics (STRs and SNPs autosomal, X-STRs and Y-STRs) into one single multiplex. However, to date, NGS platforms and theoretical framework still not met the forensic standards [51-53].

1.2. Forensic Samples: From Crime Scene to Profile Interpretation

The collection of biological evidence of a criminal case can be carried out either at the crime scene itself – requiring proper identification, packaging, and preservation (low temperature and humidity) – or at the forensic laboratory, from items collected at the crime scene. In both cases, it is vital to take extreme care in collecting and handling biological material to avoid contamination, and also carefully document all the steps to preserve/maintain the chain of custody so that the evidence can have value in court [54].

Even though some biological stains are more easily detected (blood stain) than others (semen or saliva), all identified stains must be tested to ensure that, in fact, they are biological traces and, as such, must be collected for further DNA analyses. Alternate Light Sources (ALS) are a helpful method to detect and/or identify body fluids, since

through emission of light in different wavelengths the diverse types of fluids (semen, saliva and blood) fluoresce [55, 56]. Rapid presumptive tests, like Kastle-Meyer (KM) [57] or acid phosphatase test [58], can be also applied to identify blood or semen stains, respectively.

In order to identify the origin of the DNA profiles obtained from the collected samples, reference samples should be collected, whenever possible, from victim(s), suspect(s) and/or other possible contributors.

The next step is the DNA extraction and isolation from the biological samples, which consists in the cell lysis – bursting of the cell membrane, denaturalization of proteins – e.g. histones in which the DNA is wrapped, and consequent release of the DNA molecule [7].

There are several methods for DNA extraction: i) Phenol/chloroform-based extraction, that has been widely used in molecular biology but due to the high toxicity of phenol fell into disuse from the mid-1990s [59]; ii) Chelex® 100 resin, a quick and low-cost technique, was one of the first adopted by forensic community [60]; iii) FTA® paper, developed to collect and store samples (particularly blood and buccal swabs) through cell lysis and DNA binding to paper, was also applied to DNA extraction and purification [61]; and iv) Solid-phase extraction – where the DNA binds to a solid substrate (silica, glass or magnetic beads), which is a more mechanized process, and therefore, more appealing to forensic laboratories. Nowadays, there are several commercial kits based on the latter type of extraction [62, 63] like, Qiagen® QIAsymphony® DNA Investigator®. The process starts with placing the collected evidence into a filter column within a spin tube, where the lysis buffer (ATL buffer), Proteinase K and dithiothreitol (DTT) are added. Depending on the type of samples under analysis, the proportion of these reagents can be different. Then, the tubes are placed in a thermal shaker and centrifuged, causing the passage of the lysed samples containing the biological material to the spin tube (figure 2A) [64]. The remaining DNA extraction and purification are performed automatically in an equipment where are inserted the cartridges included in the kit. These cartridges have different compartments with the necessary reagents (including the magnetic microspheres, which DNA binds to) (figure 2B) [65].

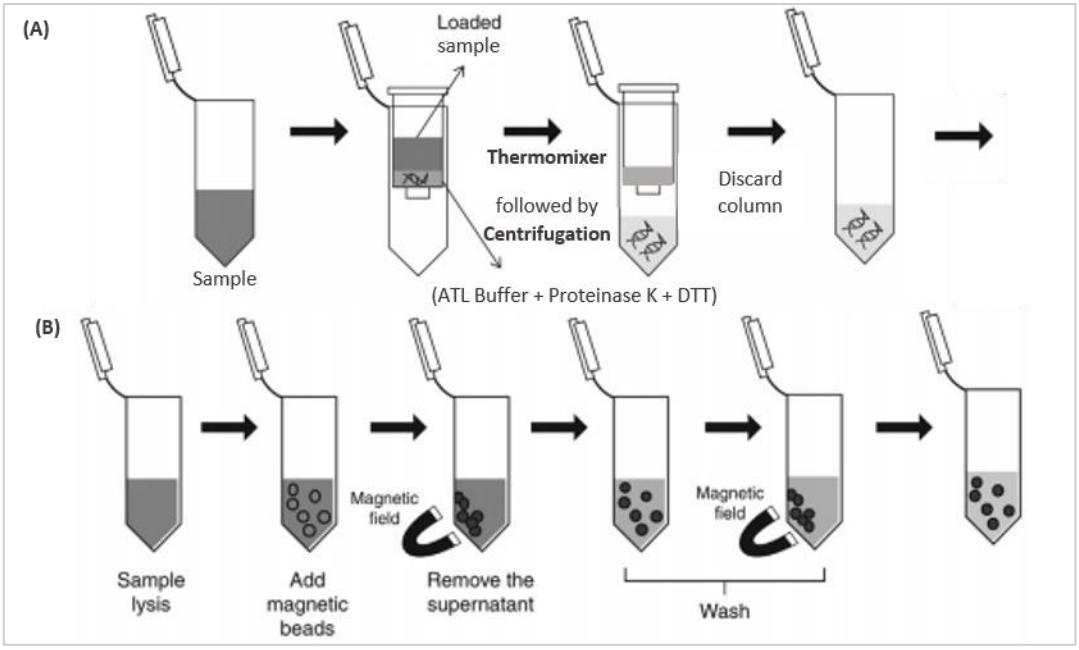


Figure 2: DNA extraction and purification steps with magnetic beads (Adapted from C. Barbosa et al. [66]).

Nowadays, several forensic laboratories perform a differential extraction on mixture DNA samples collected usually in sexual assault cases. This method, described in 1985, consists in separate female epithelial cells from male sperm cells [67]. This type of extraction is only possible because the nucleus of the sperm cells is surrounded by a capsule called acrosome that is only dissolved in the presence of DTT. For this reason, the process is divided into two phases: i) Incubation of the sample in a mixture with sodium dodecyl sulfate (SDS) and proteinase K that only break the membrane of the female cells allowing the extraction of the female portion of the mixture; ii) Addition of DTT for lysing the acrosome and thus proceed with the extraction of the male fraction of the mixture (figure 3).

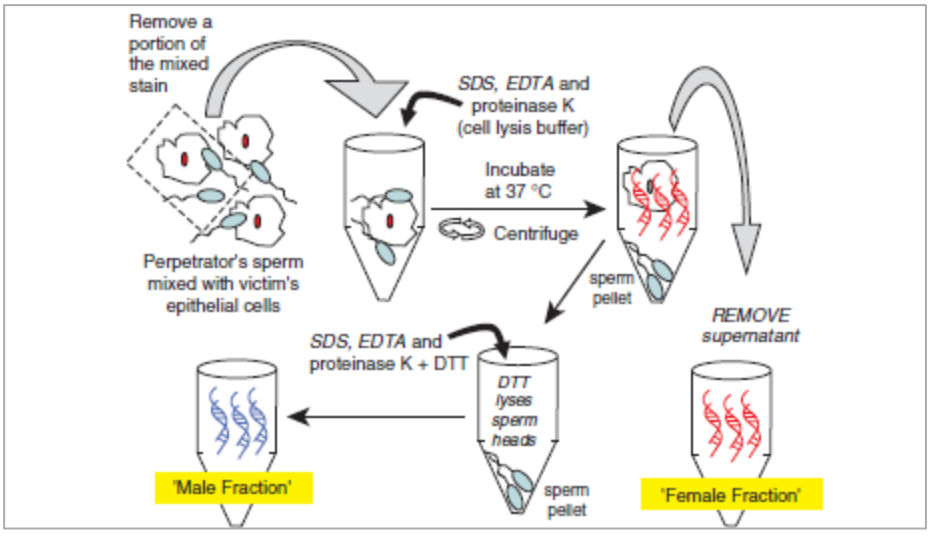


Figure 3: Representation of the differential extraction process (From J.M. Butler [12]).

Different kits, such as SwabSolution^{TM} kit, are used for rapid processing for reference samples. Since they are usually optimal samples and, as such, there is no need of previous DNA purification or quantification, these kits generate a DNA extract prior to their direct amplification [68]. This type of samples must be analyzed at different times than the samples collected at the crime scene, in order to reduce the possibility of contamination of the problem samples.

After extracting the DNA from the problem samples, it is necessary to proceed with their quantification. At this stage, a DNA dilution or concentration should be performed to guarantee the correct amount to carry out the next step (DNA amplification) and produce a high quality epg. For this, real-time PCR, also known as quantitative PCR (qPCR), can be used, which is a highly sensitive, specific human and not labor-intensive method. These characteristics overcome the limitations found in other methods, such as the subjectivity and low sensibility associated with the gel-based analysis [69] and the dot blot with human-specific probe hybridization method (which is also a labor intensive process) [70]. It also overcomes the limitation of not being human specific associated to the fluorescent [71] and ultraviolet spectrophotometry techniques. This last one also hardly quantifies small amounts of DNA [72].

The method of qPCR consists in monitor the process of amplification in real time by using fluorescence techniques, in which the fluorescence emission is proportional to the quantity of amplified DNA. Depending on the number of cycles, this process can be divided into four phases regarding fluorescence (figure 4). The first phase can be called Baseline, corresponding to the initial cycles of PCR, when does not yet exist or there is little DNA produced to be emitted a signal. Following this phase, the Exponential phase begins, with all reagents available in good quantities an efficiency amplification occurs, duplicating the PCR product at each cycle. It is in this stage that the DNA is quantified, by calculating the number of cycles (cycle threshold (C_T)) that were necessary for the fluorescence to reach a threshold set by the software. Afterwards, the Linear phase initiates, consisting with the stage in which the reaction components are being consumed, the reaction is slowing, and the PCR products are starting to degrade. Finally, when the reaction is over, the Plateau phase is reached [73-76].

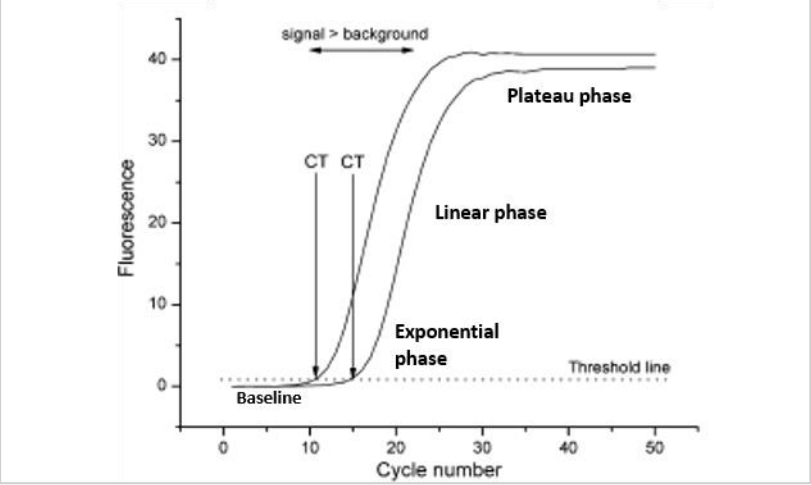


Figure 4: Illustration of the real-time PCR phases (Adapted from M. Kubista et al. [75]).

The qPCR kits include controls like a No-template control (NTC) – a negative control, containing all reagents except the template, used to identify set-up contamination and primer-dimer product amplification – and an internal PCR control (IPC) that contains a synthetic DNA template and provides a positive confirmation that all components are functioning as expected. The kits also offer information regarding to the quantity of three genomic targets (Large Autosomal, Small Autosomal and Y-chromosome) that allows the expert to draw some conclusions. Comparing the autosomal quantity with the one of Y-chromosome, it is possible to know the male to female ratio in mixture samples, which may be helpful in its interpretation. Through the ratio between small and large autosomal quantity, it is possible to analyze how degraded is the sample. Since the large autosomal is more difficult to keep intact in a degraded sample and, therefore, be amplified in the same proportion as small one, the more closer to one the ratio between the two proportions, the less degraded the sample is [77].

DNA amplification is accomplished by a PCR reaction of STR targeted sequences (already described in section 1.1.2). The possibility of multiplex PCR reaction, that is, amplifying several DNA target sequences simultaneously in the same reaction, and the advantages associated to this technique, several commercial kits were developed and applied to different areas, such as forensic genetics [78, 79]. Each pair of primers present in these kits have a fluorescent dye bound to one of its ends, which during the amplification of the STR targeted sequences will be associated to the amplified fragments. This allow to detect the PCR products and to distinguish alleles from different loci overlapping in size, during the STRs detection. Nowadays, the use of STR multiplex kits is a common practice in forensic laboratories [32-34], in which is fundamental to exist a physical separation between pre- and post-PCR areas in order to minimize the possibility of contamination.

Before STR genotyping, it is necessary to separate (by length) and detect the different STR markers that combined will constitute the STR profile. Currently, this is achieved by capillary electrophoresis (CE) [80] and the STRs are detected by fluorescent. The DNA fragments' separation is carried out by a polymer solution inside a capillary tube, where an electric voltage is applied ensuring that DNA enters the tube and migrates along it. Near the end of the tube, a laser-induced fluorescence (LIF) detects the fluorochromes attached to the DNA molecules as they pass by, with smaller fragments migrating faster. Indeed, there is a direct correlation between the fragment size and the time occurred between it was injected into the tube and it was detected (figure 5A). On a CE system such as 3500 Genetic Analyzer [81], an allelic ladder (all alleles of the loci previously sequenced) is co-electrophoresed with an internal size standard composed by DNA fragments of known size labeled with a different dye color. Subsequently, the sample alleles are run in injections into the capillary sequentially with the same internal size standard. This information (fragment size and fluorochrome dye color) is then received in the integrated software, that collects and generates .hid files, which will be used to perform the STR genotyping in software like GeneMapper® HID [82].

Through comparison with the alleles' size of the allelic ladder, the software program GeneMapper® HID determines the sample alleles' size, assigning them a number compatible with the number of repeats (figure 5B). Then, all detected alleles are arranged by marker (ordered by dye color) and represented in a peak form in an epg [83], which illustrates the entire STR profile. The amount of DNA detected is positively correlated with the alleles' peak height, measured in relative fluorescent units (RFUs) (figure 5C).

After the GeneMapper® HID automatically determines the STR profile, a human revision must be performed, since there may be artifacts wrongly assigned as peaks that should be identified and edited by the expert.

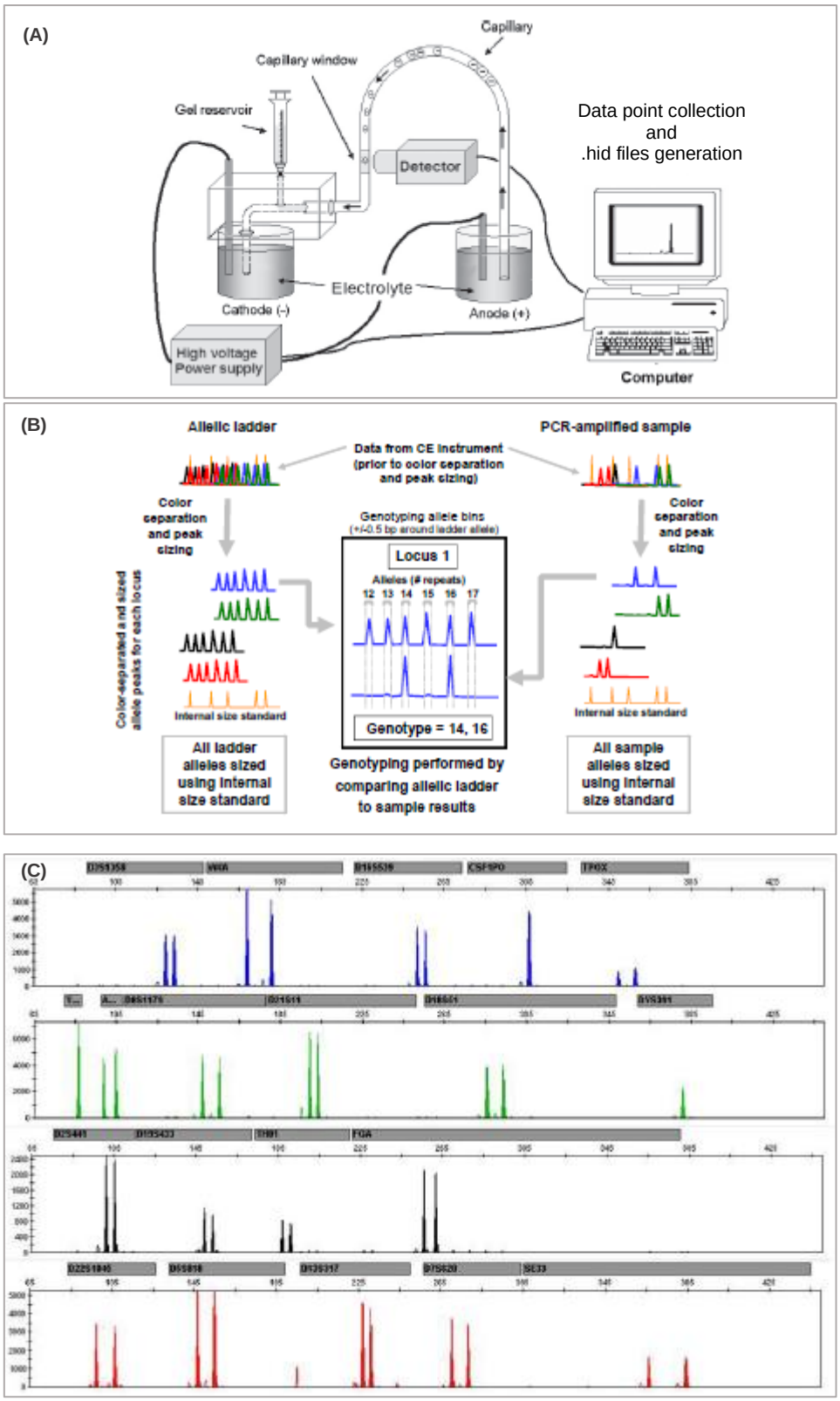


Figure 5: (A) Scheme of the process of STR markers separation and detection by CE (Adapted from (A) B. Sanchez-Vega [84]); (B) STR genotyping performed in GeneMapper® software (From J.M. Butler [85]); (C) Electropherogram of a STR profile (Adapted from D. Taylor and D. Powers [86]).

1.2.1. Profile Interpretation of Forensic Samples

The processes involved in the processing of DNA traces are increasingly evolved, like, magnetic bead-based DNA extraction or highly sensitive kits for STR amplification, which enable the production of a DNA profile from less and less DNA. However, there are still many limitations associated with the interpretation of these profiles, and experience and proper training are crucial for the expert to overcome the difficulties.

A type of sample typically encountered in forensic laboratories are mixture DNA sample profiles, i.e., samples containing biological material from more than one contributor. These samples have associated several characteristics which difficult its interpretation, such as, stochastic effects (heterozygotic imbalance, drop-in and drop-out), contributors in different proportions, possible degradation, or stutters which may be confounded with alleles of a minor contributor (or otherwise) - see 1.2.1.1. to 1.2.1.3 for more details. In 2006, to facilitate and standardize the experts' interpretation of this type of sample profiles, the DNA commission of the International Society for Forensic Genetics (ISFG) outlined some guidelines [87].

First of all, we must make sure that we are looking at a DNA mixture sample and not to a single profile. For that, a careful analysis of the loci with more than two alleles should be carried out in order to perceive and identify if the extra alleles belong to an extra contributor or if they are artifacts and/or stochastic effects. Focusing on the loci with more alleles and the relative height of the allelic peaks, an estimation of the number of the mixture' contributors constitutes the next step [87]. The maximum allele count (MAC) is a common practice to estimate the number of contributors in forensic laboratories and defines that the number of contributors cannot be less than half of the maximum number of alleles present in a loci [88]. However, this estimation is subjective and prone to errors (under- or overestimation of the real number of mixture donors).

Afterwards, an estimation of the mixture contributors' ratio would be performed. Contributors can be either in equal (1:1) or unequal proportions (major/minor contributors), which should be reflected in the height of the peaks (corresponding to the DNA amount of each contributor) throughout all loci [87]. Combining these estimates with the qualitative and quantitative information of the peaks, the determination of all possible genotype combinations could be attempted.

Finally, and only at this stage, a comparison between the mixture and the reference samples profile – victim and/or person of interest (POI) – should be executed,

avoiding a possible biased interpretation. If POI's genotype matches to one of the genotypes considered possible to be part of the mixture, there is an evidence suggesting that the individual cannot be excluded from being one of the mixture contributors [87]. However, with the appearance of statistical analysis software, some of the steps above-mentioned loss some of the relevance they used to have.

1.2.1.1. Biological and technical artifacts

During the amplification of STR alleles in PCR reaction several biological artifacts can be generated.

When copying the DNA template strand, the Taq polymerase (DNA polymerase) usually adds a non-template/extra nucleotide (adenine) to the 3'-end of the PCR product, making it one bp longer than the target sequence. However, the adenylation is primer-specific and therefore different loci have different adenylation properties, which may lead to the formation of +A and -A peaks where the peaks become broader, resulting in a split peak (figure 6). To prevent this from happening, some solutions have been pointed out, such as including a final extension step to the STR protocol or modifying the sequence of reverse primers [89, 90]. Too much DNA template in the PCR reaction can also result in an incomplete adenylation because there is not enough Taq polymerase to go around, being one of the reasons why it is so important to quantify the DNA before proceeding with its amplification.

Stutter peaks – the most encountered artifact in an epg – are another PCR product artifact that results from a slipped-strand mispairing. During the PCR extension phase the DNA polymerase slippage separates the template and extending strand. When the two strands re-anneal, one of them looped out and the other aligns one repeat unit in front of the supposed. If the loop occur in the template strand one repeat unit is deleted in the new strand, but if the loop happens in the extending strand it will result in the addition of one repeat unit to the new strand (less common). Considering single-source samples, this artifact can be easily identified by its size and position; however, when analyzing mixed-source samples, it becomes difficult to differentiate from a minor contributor allele [91, 92]. However, an advantage associated to stutters peaks is that they facilitate the identification of other artifacts that appear in the epg, such as pull-ups or spikes, because only (true) alleles contain the stutter peaks (figure 6).

Pull-ups, spikes, and dye-blobs are artifacts generated during the STR separation and detection stage, namely during CE.

The pull-up artifact reflects a limitation of the CE instrument. When an excessive amount of DNA is amplified, the range of detection of the CE instrument is exceeded and it is unable to properly deconvolute the dye colors used to label the different alleles. Due to spectral overlap, these off-scale peaks cause a color bleeding from one spectral channel into another resulting in a pull-up peak, which can be identified by appearing in the channel above or below the position of the saturated data (figure 6). A previous DNA quantification (and in this case, a DNA dilution) would minimize this type of artifact [12, 93].

Air bubbles in CE capillary, crystal formation in the polymer or contamination of the polymer by the fluorescent material generates fluctuation in voltage during electrophoresis. This fluctuation creates an analytical artifact – spike – that generally appears at the same data point for all the dye sets [93].

When the fluorescent dye disassociates from the labeled primer, the released residual dye molecule is detected in CE producing an artifact in the epg called dye-blobs. To solve this problem the PCR products should by filtrated to efficiently remove the residual dye molecules. Nevertheless, due to the predictable position and wider base peak, dye-blobs can be easily identified in the STR profile (figure 6) [94].

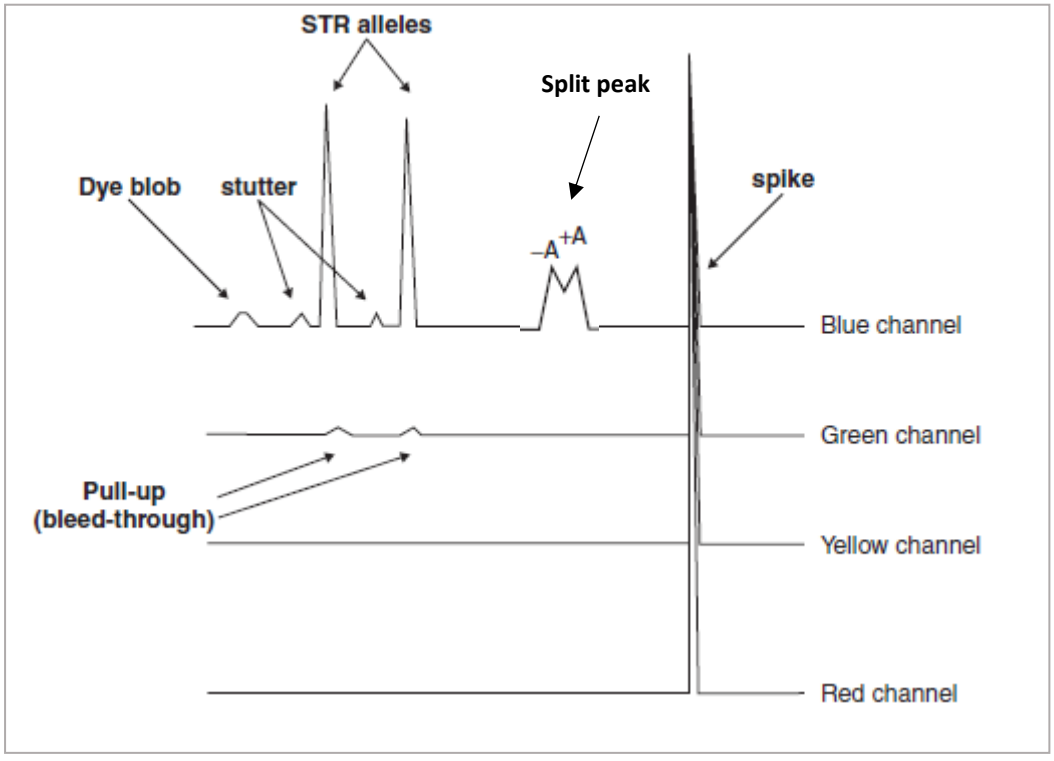


Figure 6: Representation of biological and technical artifacts (Adapted from J.M. Butler [12]).

1.2.1.2. Low-template-DNA profiles

The use of low-template-DNA (LT-DNA) has the purpose of extending the range of samples that may be analyzed with DNA testing. To produce a DNA profile with few cells, a DNA profiling technique called low copy number (LCN) [95, 96] can be applied and, for that, the number of PCR cycles is increased to generate more amplified product, compensating the low starting template.

However, low DNA levels are prone to sporadic contamination and have several disadvantages associated, mainly derived from stochastic effects, like drop-in, drop-out and elevated heterozygotic imbalance. Additionally, LT-DNA profiles have also associated epg peaks with low height and stutter peaks with highly variable heights [97].

Usually, in a heterozygotic locus the two alleles have nearly the same height; however, in LT-DNA samples the two alleles may have substantial different heights. This heterozygote imbalance results from a preferential amplification of one of the alleles. In some situations, the less amplified allele had a height below the threshold limit and is considered baseline noise [95]. This stochastic effect is a major concern not only in LT-DNA but also in degraded DNA and mixture samples analysis, as peak imbalance make the deconvolution of the mixture contributors more difficult [93].

A drop-in allele corresponds to a spurious allele in the problem sample profile, i.e., an allele that shows up in the problem sample profile but cannot be explained by any of the contributors of the sample. On the other hand, when an allele present in the contributor profile is not reported in the problem sample profile is called a drop-out allele [97]. Both cases generate discordances between the mixture sample and the contributor profiles, which can lead to misinterpretations and, consequently, misleading conclusions. So, drop-in and drop-out phenomena should be modeled for the sake of the accuracy of the analysis [98, 99].

Nowadays, there are kits capable to amplify and type LT-DNA without the need of increasing the number of PCR cycles (and consequently the stochastic effects), being the discontinuation of the LCN technique foreseen [100].

1.2.1.3. Degraded samples

In forensic casework is not unusual to find highly degraded DNA samples. The extent of DNA degradation will depend on two main factors. The first is related with the environmental conditions to which the biological material was exposed, such as, temperature, humidity, pH, ultraviolet radiation, chemical properties of soil,

microorganism contamination, among others. The second factor is the time of exposure to these conditions, the longer samples are exposed, the more degraded they are expected to be [101, 102].

During the degradation process, several chemical reactions affect the DNA molecule stability resulting in bases loss, bases modification and breakage of the molecule [102]. This leads to loss of genetic information, reduction in the size of DNA fragments and subsequent failure of the STR typing method. A strong peak imbalance is a typical feature of this type of profile, since there is an over amplification of the smaller loci and a decrease in the successful amplification with the increasing size of the alleles (figure 7) [103].

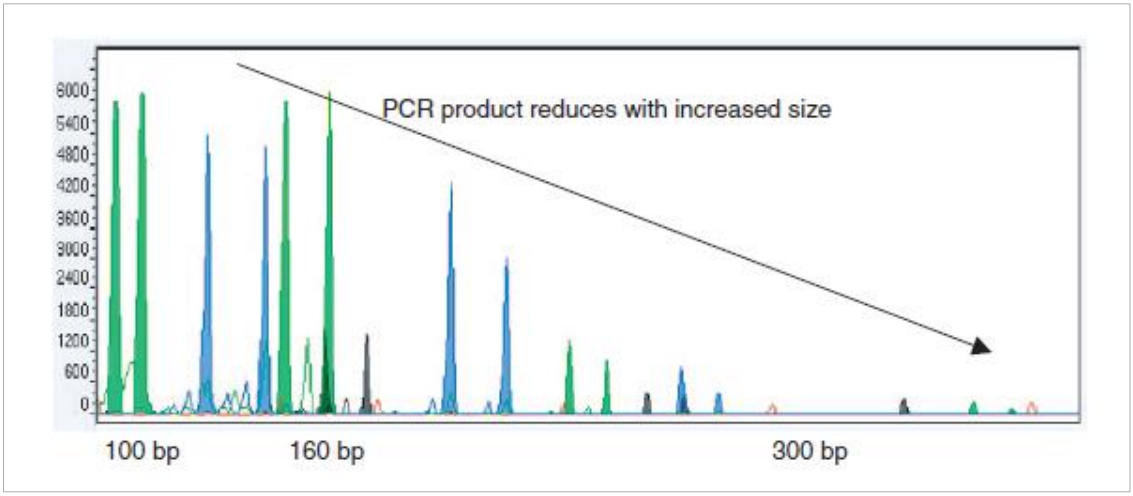


Figure 7: Representation of a typical degraded profile with the characteristic gradual reduction in PCR product as the size of the amplicon increases (From W. Goodwin et al. [7]).

Several alternatives were developed in order to achieve a better analysis of extremely degraded DNA material [102], such as, mini-STRs [104] (where primers are positioned closer to the core repeats of the STRs, generating smaller lengths of the amplicons), SNPs [105] and INDELs [50]. Having a reduced amplicon size, are less prone to be fragmented and therefore more able to deliver a complete DNA profile.

1.3. Forensic Samples: Quantifying the Genetic Evidence

The generally accepted approach for the quantification of the proof is the calculation of a Likelihood Ratio (LR) [87], which consists in a comparison between the probability of observing the evidence (*E*) assuming two opposite, alternative and mutually exclusive hypotheses (H1 and H2):

$$LR = \frac{\mathrm{P}\,(E|\mathrm{H1})}{\mathrm{P}\,(E|\mathrm{H2})}.$$

LR computation to quantify the genetic evidence derives from Bayes' Theorem:

Posterior odds = LR x Prior odds, i.e., $\frac{\mathrm{P}\,(\mathrm{H1}|E)}{\mathrm{P}\,(\mathrm{H2}|E)} = \frac{\mathrm{P}\,(E|\mathrm{H1})}{\mathrm{P}\,(E|\mathrm{H2})} \times \frac{\mathrm{P}\,(\mathrm{H1})}{\mathrm{P}\,(\mathrm{H2})}$. Indeed, considering equal prior odds – hypotheses odds before the analysis of DNA evidence – the ratio between the probabilities of the evidence given the hypotheses equates the LR which depends on the frequency of the alleles in the population [106]. In criminal context, hypotheses H1 and H2 are typically defined as follows: "POI is contributor of the mixture sample.", and "POI is neither a contributor of the mixture, nor genetically related to any contributor.", where POI is the donor of the reference sample.

If the obtained LR value is greater than one it will support H1, while if it is less than one it favors H2. A common mistake in the interpretation and later communication of this value is to state that it represents the number of times that one hypothesis is more likely than the other. So, to avoid this mistake – known as fallacy of the transposed conditional [107] – the LR value should be reported as follows: "The observed evidence is *n* times more likely assuming one hypothesis than assuming the alternative".

1.3.1. Statistical Models

To perform a DNA mixture analysis, there are three different approaches, namely, binary (or traditional), semi-continuous (or qualitative) and continuous (or quantitative) approach. The latter two allow a quantification of the evidence.

The binary interpretation consists in assigning a value of zero (genotype excluded) or one (genotype included) to the probability of the profile belonging to the problem sample under analysis, given the profiles considered possible [108]. The subjectivity of expert's opinion, the difficulty to apply the reasoning to problem samples with more than two contributors and the fact that stochastic effects and artifacts are not considered, resulted in their gradual replacement by software-based probabilistic genotyping (PG) – semi-continuous and continuous methods [109].

Software-based PGs were developed in order to minimize the impact of the difficulties raised in 1.2.1. and quantify the weight of the genetic evidence with a robust and scientifically supported statistical approach. However, it is noteworthy that PG software are an informatics tool to assist in the expert interpretation and as such, the

expert must always critically evaluate not only the DNA profile before analyzing it in the software, but also the produced results [110].

The semi-continuous method is also called qualitative because it is only based in the qualitative information of the epg (alleles observed in the profile). This approach has simpler algorithms and computations, being easier to use, implement and, consequently, discuss results in court comparatively to the continuous method [110, 111]. Several computer tools have been created based on this approach, like *Lab Retriever* [112] or *LRmix Studio* [113].

On the other hand, there is the continuous method, also known as quantitative model, which depends not only on the qualitative information of the epg (alleles observed in the profile) but also on the quantitative information (height of the detected allele peaks). This constitutes a more complex approach, making the results more sensitive to artifacts and stochastic effects [111]. *EuroForMix* [114] and *STRmix*^{TM} [115] are two examples of quantitative informatic tools available.

Despite the above-mentioned advantages inherent to the qualitative methods, these approaches do not consider the information regarding peak heights when produce the possible genotypes and so, also do not model artefacts that may be present on the epg. Oppositely, quantitative models take into account a large amount of data and information, being considered in several publications as more efficient in distinguishing between non-contributors from contributors and as such, a preferred approach for the analysis of complex DNA mixtures, becoming the main focus of this work [110, 116].

1.3.2. Software Parameters: Impact on the Quantification of the Evidence

Before performing any computation, it is necessary for the expert to establish and introduce the values determined either empirically or based on values presented in the literature, for each parameter of the software, so that the computation of the LR value is as accurate as possible.

1.3.2.1. Number of Contributors

Considering that the number of contributors of a mixture is usually unknown, an estimate needs to be made (as previously stated in 1.2.1.4.), since the expert is required to fill in a parameter called “Number of Contributors” for the software proceeding with the analysis. This estimate can be hindered by the various artifacts and stochastic effects

that appear on the epg (already described in 1.2.1.) and also, by the unbalanced profile resulted from an asymmetry caused by the shared alleles between the mixture contributors [87].

Several studies have looked at the impact that this parameter may have on the global LR value, using either mocked [117, 118] or real casework mixtures samples profiles [1]. In all of them is stated that, a wrong estimate of the number of contributors, can either have no significant effect or it can decrease the LR value, reaching in some cases values below one. Benschop et al. [118] and Figueiredo [1], also concluded that the higher the number of estimated contributors, the lower the computed LR values (less powerful probative value achieved).

1.3.2.2. Threshold Detection

The threshold detection is an RFU value introduced in the peak detection software, for distinguishing true alleles from the baseline noise, considering as true alleles only peaks higher than the define threshold. The baseline noise consists in non-reproducible peaks, resulting from electronic fluctuations, or air bubbles and crystals in the polymer in CE capillary, or from low level sample contamination [93].

There is no standard rule for determining the threshold detection value, which should be used. However, it should always be taken into account that, a value that is too high may result in loss of information due to the non-detection of alleles with smaller heights, affecting the global LR computed value [1]. On the other hand, a value that is too low may result in the incorrect assignment of the peaks, that is, baseline noise being considered true alleles. The determination of a threshold detection should be part of the internal validation procedure of any laboratory, and there are several methods that can be used [119].

1.3.2.3. Drop-in: Frequency and distribution

As previously mentioned in 1.2.1.2., a drop-in allele corresponds to a spurious allele in the sample profile that can lead to misinterpretation. So, the informatics tools for statistical analysis of mixture samples may consider the drop-in frequency value (in both quantitative and qualitative models) and the distribution of drop-in parameters (only in qualitative models) when computing LR values.

The drop-in frequency is laboratory-specific and usually is estimated considering the amount of negative controls in which an additional allelic component appears in the epg, a no-reproducible and unexplained peak. A negative control is an additional tube

not containing any type of biological sample that is analyzed at the same time as the samples [120]. The higher the drop-in frequency, the less likely that an allele is considered to belong to a mixture contributor.

Three different drop-in frequency values were already analyzed to measure the impact that this parameter may have on the global LR values [1]. None of the considered values showed a substantial impact, with the greatest being observed when a null drop-in frequency was assumed.

The information of the drop-in peaks height is used to estimate the distribution of drop-in parameters, which can be modelled by different statistical distributions [121, 122].

1.3.2.4. Drop-out

An allele drop-out is a stochastic phenomenon, which corresponds to an allele present in the contributor' profile but absent in the mixture profile for which he/she contributed, as already referred in 1.2.1.2.

Whereas qualitative software does not use the peak heights information for computing the LR value, both drop-out and drop-in probability may be incorporated, such as in the quantitative counterparts [123-125]. Depending on the software, parameters related to this phenomenon may have to be introduced by the user, or in case of quantitative programs could be directly estimated through the peaks height.

1.3.2.5. Co-ancestry Coefficient

The coefficient of co-ancestry (F_{ST}) indicates the probability of pair of individuals sharing identical by descent (IBD) alleles (i.e., derived from the same common ancestor) at a population-level. This empiric parameter can be interpreted as a measure of relatedness (shared ancestry) within the subpopulation [126].

For this reason, F_{ST} is crucial to correctly calculate the profile frequencies and evidence quantification. A non-inclusion or the use of a non-suitable value in this parameter will have an impact in LR value computation, especially when the evidence samples contains rare alleles matching with the reference sample under analysis [1].

Given the difficulty to determine its value in actual populations, many forensic laboratories use already assigned values for similar populations [127].

2. Aims

In order to overcome the multifactorial complexity inherent to the analysis and interpretation of identification cases involving mixtures, various computer tools were developed. Nowadays, there are indeed several software based on qualitative or quantitative statistical models that enable the quantification of the genetic proof. Qualitative models rely on a simplified approach of presence/absence of alleles, while quantitative ones also consider the DNA quantity present in the analyzed samples. Since quantitative models take into account more information of the electropherogram than qualitative ones, they have been considered more accurate and efficient, and therefore the preferred approach.

The main goal of this dissertation is to compare the results obtained by two widely used quantitative software: EuroForMix v.1.9.3. and STRmix^{TM} v.2.7, through the analysis of real casework samples under the framework of forensic identification problems. For this work, mixture profiles recovered from crime scenes and reference samples associated from former *Laboratório de Polícia Cientifica da Polícia Judiciária* cases were used. An immediate consequence of the use of this type of data is that the composition of the mixture samples is unknown, carrying a higher level of complexity than mock ones. Mixture samples used in this work were estimated to have two or three contributors.

Despite of being both quantitative, the programs considered in this work differ in several features, such as in the modelling of drop-in, drop-out, population co-ancestry, or requirement of including stutters in the analysis. For some of these features, the user is able to choose the most adequate parameter values considering the laboratory and/or the population in question. Thus, to understand the impact on the quantification of the proof, several software parameters were varied and resulting values compared, both in an inter- and intra- software analysis. Also, the impact that the underestimation (in the case of mixtures with three estimated contributors) and overestimation (in mixtures with both two and three estimated contributors) of the number of contributors may have on the global LR value was analyzed.

3. Material and Methods

3.1. STRmix™ v.2.7 Implementation

Currently, there are several computer solutions for the statistical analysis of mixture and reference samples, based on either a qualitative or quantitative model. Those following the quantitative (or continuous) model, which is based both on the qualitative (observed alleles) and quantitative (height of allele peaks) information of the epg, are considered more efficient and therefore the preferred approach for this type of analysis [111]. This was the motto for the *Laboratório de Polícia Científica da Polícia Judiciária* (LPC-PJ) to recently acquire the quantitative software STRmix™ v.2.7 [115], developed by the Institute of Environmental Science and Research (ESR) from New Zealand and Forensic Science South Australia (FSSA).

Facing this new acquisition, the first step carried out was the implementation of STRmix™ v.2.7 software, modeling the following parameters according to the guide provided by the manufacturer:

- Analytical/detection threshold(s);
- Expected stutter ratios;
- CE instrument's saturation limit;
- Drop-in parameters;
- Allele and stutter peak height variance prior distributions;
- Locus Specific Amplification Efficiency (LSAE) variance prior distribution;
- Parameters for all relevant populations including allele frequencies and theta (F_{ST}) value.

The process of implementation was carried out considering the laboratory and population specificities and it is described in Appendix I. Nevertheless, as the main goal of this work lies in the comparison between two quantitative software (STRmix™ v.2.7 and EuroForMix v.1.9.3) considering some data previously obtained [1], the same parameter values as before were considered to allow comparison between analyses.

3.2. Data

The complexity, uniqueness, and inability to predict and replicate real casework samples were the reasons why this type of data was chosen to develop this work. The

drawback of this approach is that inference on which software produced more accurate results cannot be performed as the composition of the mixtures is unknown.

Resorting to evidences from LPC-PJ former cases, mixture samples (with two or three estimated contributors) with at least one reference (single profile) associated were selected. The associated references were either from sampled individuals, that were considered a possible donor and could not be excluded from the mixture, or single-source problem sample profiles obtained in the same case of the analyzed mixture and that could not also be excluded from being from one of the mixture contributors. The samples were previous amplified in the context of the respective casework using the GlobalFiler™ PCR Amplification Kit and GlobalFiler™ Express PCR Amplification Kit (Applied Biosystems™), both 24-locus STR kits. In this work, since the three gender markers were not considered (Y-indel, amelogenin, and DYS391), only 21 out of 24 loci were used.

The total of 158 mixture/reference sample pairs (79 mixtures with two and 79 mixtures with three estimated contributors) used in this thesis, were previously selected and analyzed by Carolina Figueiredo considering computations performed by EuroForMix v.1.9.3 (quantitative) and LRmix Studio v.2.1.3 (qualitative) software [1].

Therefore, it was necessary to recover the .fsa/.hid files of those mixtures and corresponding reference profiles in the typing software GeneMapper™ ID-X, in order to export .txt files with STRmix™ table format, following the recommendations specified in the STRmix™ v.2.7 Operation Manual, provided by the manufacturer.

3.3. Statistical Analysis: Quantification of the evidence

In this dissertation, the quantification of the evidence computed by STRmix™ v.2.7 and EuroForMix v.1.9.3 for the same mixture/reference pairs was compared. In table 1 are described the main differences between the two software.

STRmix (http://strmix.esr.cri.nz/) is a commercial software based on a Bayesian approach using Markov Chain Monte Carlo (MCMC) for quantitative DNA mixtures interpretation, developed by D. Taylor, J.A. Bright and J. Buckleton [128]. On the other hand, EuroForMix (http://www.euroformix.com/) is a quantitative open-source software, programmed by Ø. Bleka [114] and working in R [129]. It involves maximization (frequentistic) or integration (Bayesian) approaches over the likelihood ratio. The “Continuous LR” mode (i.e. involving a Maximum Likelihood Estimation (MLE) methodology) was employed.

Table 1: Comparison between EuroForMix v.1.9.3 and STRmix™ v.2.7 software properties (Adapted from [114]).

Properties	EuroForMix	STRmix™
Calibration[1]	Possible	Required
Drop-in distribution	Exponential	Gamma or Uniform
Peak height distribution	Gamma	Log-normal
Inference approach	Bayesian or Maximum Likelihood Estimation (MLE)	Bayesian
Problem samples files with stutter	Possible	Required

For each mixture/reference sample pair, the quantification of the evidence was computed through STRmix™ v.2.7 and EuroForMix v.1.9.3, comparing the probability of the observations assuming the following alternative hypotheses: "The POI is a contributor of the mixture" and "The POI is unrelated to any contributor of the mixture". In all the cases the reference sample was assumed as belonging to POI.

All LR values were computed using the allelic frequencies of the National Institute of Standards and Technology (NIST) database concerning the Caucasian population (Appendix II – table A1).

3.3.1. Analysis of the global LR values

To compare the results obtained through the informatic tools under analysis, it was necessary to maintain the same conditions in both computations (table 3 in 3.3.2. – column 4.1.). Since STRmix™ analyses require the inclusion of stutters in problem samples files, the repetition of EuroForMix calculations was needed, as stutters were previously disregarded in [1]. This allowed to compare the influence on the LR result of considering stutters or not in EuroForMix computations.

When for one of the programs a null LR value was obtained for a specific case, the mixture/reference pair in question was re-analyzed, in both programs, after the removal of the marker(s) for which LR=0. In these cases, the final LR value is denoted as $LR_{<21}$, as less than 21 markers were considered in the analysis.

The inter-software comparison consisted of computing the difference between the LR values (log_{10} scale) obtained in both software, for the same mixture/reference pair

[1] Incorporation of specific-laboratory' validation data to determine some of the parameters involved and consequently modeled.

and set of markers. For each mixture/reference pair, these differences were computed considering not only the global LR value, but also the per marker analysis. To understand if there was trend to the LR value to be higher in a specific software, a chi-square test (α=0.05) was computed through Microsoft® Excel®, considering N/2 as expected value (N corresponds to the number of cases analyzed). Also in Microsoft® Excel®, a test-t (α=0.05) was carry out to see if the LR values computed for cases with mixtures with two estimated contributors were higher than those computed for cases with mixtures with three.

3.3.2. Weighing the impact of parameters' variation

In both software computations, the impact of several parameters: Number of contributors, threshold detection, drop-in, F_{ST} and stutters, was considered. For each parameter, different conditions/values were tested in order to understand what kind of impact these may have on the global LR value and if that impact is similar in the two different quantitative software under analysis.

Prior to any computation, the user must introduce his/her estimation of the number of contributors of the mixture under analysis, given his/her examination of the mixture epg. Since, the quantity and quality of DNA in real casework samples are usually low, the estimation of the number of contributors may not be accurate, relying on the expert's opinion. For this reason, computations considering different numbers of contributors than those initially estimated were considered: +1 and ±1 for mixtures with two and three estimated contributors, respectively.

Besides the number of contributors, there are several parameters whose values should also be introduced by the user. Those analyzed in this dissertation are presented in table 2, as well as the respective tested values. Most of the parameter values were previously selected [1], the only defined in this work correspond to the "Drop-in parameters' distribution" of STRmix™ software. The drop-in modeling in EuroForMix and STRmix™ software is done differently, since in EuroForMix the drop-in is modelled using a Lambda distribution (λ) while, in STRmix™ it is used either a Gamma (ɣ) or Uniform distribution. If limited observations of drop-in have been made or if the dataset is limited in size, the STRmix™ software may not be able to develop a reliable Gamma model. So, instead of determining the parameters (α and β) of the Gamma distribution, the use of a Uniform distribution is recommended by the STRmix™ v.2.7 Implementation and Validation Guide.

That said, in this project both distributions that can be considered in STRmix™ software were tested. The Gamma distribution was considered the “default” condition, for which the software default values of parameters α and β were used (0.1 and 0.1, respectively), while Uniform distribution was considered the "variation" condition.

Table 2: Default and varied values introduced in EuroForMix v.1.9.3 [1] and STRmix™ v.2.7 for each analyzed parameter.

Parameters	Default	Variation
Threshold detection	100	150
Drop-in frequency	0.05	0.00 0.10
Drop-in parameters' distribution	EuroForMix (λ): 0.01 STRmix™ (ɣ): (0.1,0.1)	EuroForMix (λ): 0.05 STRmix™: Uniform
Co-ancestry Coefficient (F_{ST})	0.010	0.000 0.015 0.030

Finally, the presence/absence of stutters in mixture samples profiles under analysis was tested. For this, EuroForMix LR values computed for each pair mixture/reference sample with and without stutters [1] were compared. As previously mentioned, this analysis was not possible considering STRmix™, since it requires the inclusion of stutters in the mixture samples profiles to perform a LR value computation.

To verify the effect that each parameter – Number of contributors, Drop-in, F_{ST}, Threshold detection and Stutters – may have on the global LR value, the LR values were computed varying only one parameter at a time, as outlined in table 3. A total of 1,856 LR values were computed and the impact of each parameter within and between software was evaluated.

In the intra-software analysis, a comparison between the LR value computed under the default and varied conditions was performed, for each mixture/reference sample pair. This comparison consisted in the subtraction of the two LR values ($\log_{10}$ scale). Like before, to infer a possible trend regarding the LR value increase or decrease, when the parameter value was varied in each software, a chi-square test (α=0.05) was performed in Microsoft® Excel®, considering N/2 as expected value. N corresponds to the number of cases analyzed. Afterwards, the range of differences obtained in both software for each varied parameter was compared, in order to understand in which software the parameter under study had more impact, i.e., which software was more sensitive to a parameter value variation.

Table 3: Parameter values used during the computation of the LRs analyzed throughout this dissertation, as well as the specific "Results and Discussion" chapters where those LR values are analyzed.

Data		Parameters values						4. Results and Discussion Chapters						
		Number of contributors	Threshold Detection	Drop-in		F_{ST}	Stutters	4.1. Analysis of the global LR values	4.2. Weighing the impact on parameters' variation (intra software analysis)					
				Frequency	Parameters' distribution				4.2.1. Number of estimated contributors	4.2.2. Threshold Detection	4.2.3. Drop-in		4.2.4. F_{ST}	4.2.5. Stutters
											4.2.3.1. Frequency	4.2.3.2. Parameters' distribution		
EuroForMix v.1.9.3	*	Estimated	100	0.05	λ = 0.01	0.010	No		X	X	X	X	X	X
		Estimated	100	0.05	λ = 0.01	0.010	**Yes**	X						X
	*	**Estimated +1**	100	0.05	λ = 0.01	0.010	No		X					
	*	**Estimated -1**	100	0.05	λ = 0.01	0.010	No		X					
	*	Estimated	**150**	0.05	λ = 0.01	0.010	No			X				
	*	Estimated	100	**0.00**	λ = 0.01	0.010	No				X			
	*	Estimated	100	**0.10**	λ = 0.01	0.010	No				X			
	*	Estimated	100	0.05	**λ = 0.05**	0.010	No					X		
	*	Estimated	100	0.05	λ = 0.01	**0.000**	No						X	
	*	Estimated	100	0.05	λ = 0.01	**0.015**	No						X	
	*	Estimated	100	0.05	λ = 0.01	**0.030**	No						X	
STRmix ™ v.2.7		Estimated	100	0.05	ɣ = 0.1, 0.1	0.010	Yes	X	X	X	X	X	X	
		Estimated +1	100	0.05	ɣ = 0.1, 0.1	0.010	Yes		X					
		Estimated -1	100	0.05	ɣ = 0.1, 0.1	0.010	Yes		X					
		Estimated	**150**	0.05	ɣ = 0.1, 0.1	0.010	Yes			X				
		Estimated	100	**0.00**	ɣ = 0.1, 0.1	0.010	Yes				X			
		Estimated	100	**0.10**	ɣ = 0.1, 0.1	0.010	Yes				X			
		Estimated	100	0.05	**Uniform**	0.010	Yes					X		
		Estimated	100	0.05	ɣ = 0.1, 0.1	**0.000**	Yes						X	
		Estimated	100	0.05	ɣ = 0.1, 0.1	**0.015**	Yes						X	
		Estimated	100	0.05	ɣ = 0.1, 0.1	**0.030**	Yes						X	

* Computed by Carolina Figueiredo [1].

4. Results and Discussion

4.1. Analysis of the global LR values

For each mixture/reference pair of samples, LR values were computed through the two quantitative software under analysis – EuroForMix v.1.9.3 and STRmix™ v.2.7, for the same set of markers (comprised by 21 STRs in most of the cases). These computations were performed under the same conditions (default values presented in table 2, section 3.3.2.). In this sub-chapter, global LR values (i.e. considering the total set of markers) obtained by each pair of samples through the two software are compared. An example of how these values were analyzed is illustrated in Box 1.

Box 1

Illustrative example of the comparison made between LR values computed by STRmix™ and EuroForMix for the mixture/reference pair 1847.17-3R2 (JC1) (two estimated contributors).

Software	LR	Log_{10}(LR)	Dif. = log_{10}(LR STRmix™) – log_{10}(LR EuroForMix)	Absolute value (Dif.)
STRmix™	2.23E+21	21.34805	3.26373	3.26373
EuroForMix	1.21E+18	18.08432		

The values with bigger discrepancies between STRmix™ and EuroForMix analyzes, will be referred to as Outliers (Out.). Throughout this sub-chapter, outliers correspond to the decile of cases showing greater differences when analyzed by one or another software.

In STRmix™ software null LR values were achieved for some mixture/reference pairs, namely, in 15% and 9% of cases with mixtures with two and three estimated contributors, respectively. These specific situations and the reasons that may have led to these events will be analyzed in greater detail later in this sub-chapter. As already mentioned in section 3.3.1., these mixture/reference pairs were re-analyzed, in both programs, removing the marker(s) for which LR equated zero in STRmix™. For these cases the total LR value is denoted as $LR_{<21}$, since less than 21 markers were considered. This was also the case of some mixtures where the information from the complete set of 21 markers was not possible to be retrieved. These situations will be highlighted in all the figures of the subsequent analyzes with different symbols,

depending on the number of markers that were analyzed, in order to stand-out the comparisons where different sets of markers were considered.

All the LR values analyzed in this sub-chapter are presented in the tables B2, B3, B5 and B6 of Appendix III.

Table 4 shows the proportions of the differences calculated between the LR values (log_{10} scale) computed by the two quantitative software for each pair of problem sample (with two or three estimated contributors)/reference sample.

Table 4: Differences between the LR values (log_{10} scale) computed by STRmix™ v.2.7 and EuroForMix v.1.9.3 for cases with mixtures with two and three estimated contributors, and the maximum, mean and median values of these differences.

X = ABS [Log_{10}(LR STRmix™) – Log_{10}(LR EuroForMix)]	**Estimated Number of Contributors**	
	2 (N=79)	**3 (N=79)**
0 < X < 2	51%	51%
2 < X < 4	27%	16%
4 < X < 6	10%	16%
6 < X < 8	9%	9%
8 < X < 10	4%	4%
X > 10	0%	4%
Maximum	9.54	28.06
Mean	2.61	3.31
Median	1.78	2.00

In cases with mixtures with two estimated contributors none showed a difference greater than ten units in a log_{10} scale, 9.54 being the highest difference reached between EuroForMix and STRmix™ software values (1.52E+12 and 5.20E+21, respectively, for the mixture/reference pair 9233.6-9.1 (LCGS1), 21 STRs analyzed). Contrarily, 4% of the cases involving mixtures with three estimated contributors showed differences greater than ten units in a log_{10} scale, reaching the maximum difference of 28.06 units between the values computed by EuroForMix and STRmix™ (1.34E+20 and 1.16E-08, respectively, for the mixture/reference pair 10814.16-2 (CMSA), 20 STRs analyzed) – explored in more detail in the per marker analysis below.

From the distribution of the LR values computed by EuroForMix v.1.9.3 and STRmix™ v.2.7 for each mixture (with two or three estimated contributors)/reference pair (figure 8), it can be seen that the use of different software may result in strikingly different global LR values, even if both consider DNA quantity in problem sample.

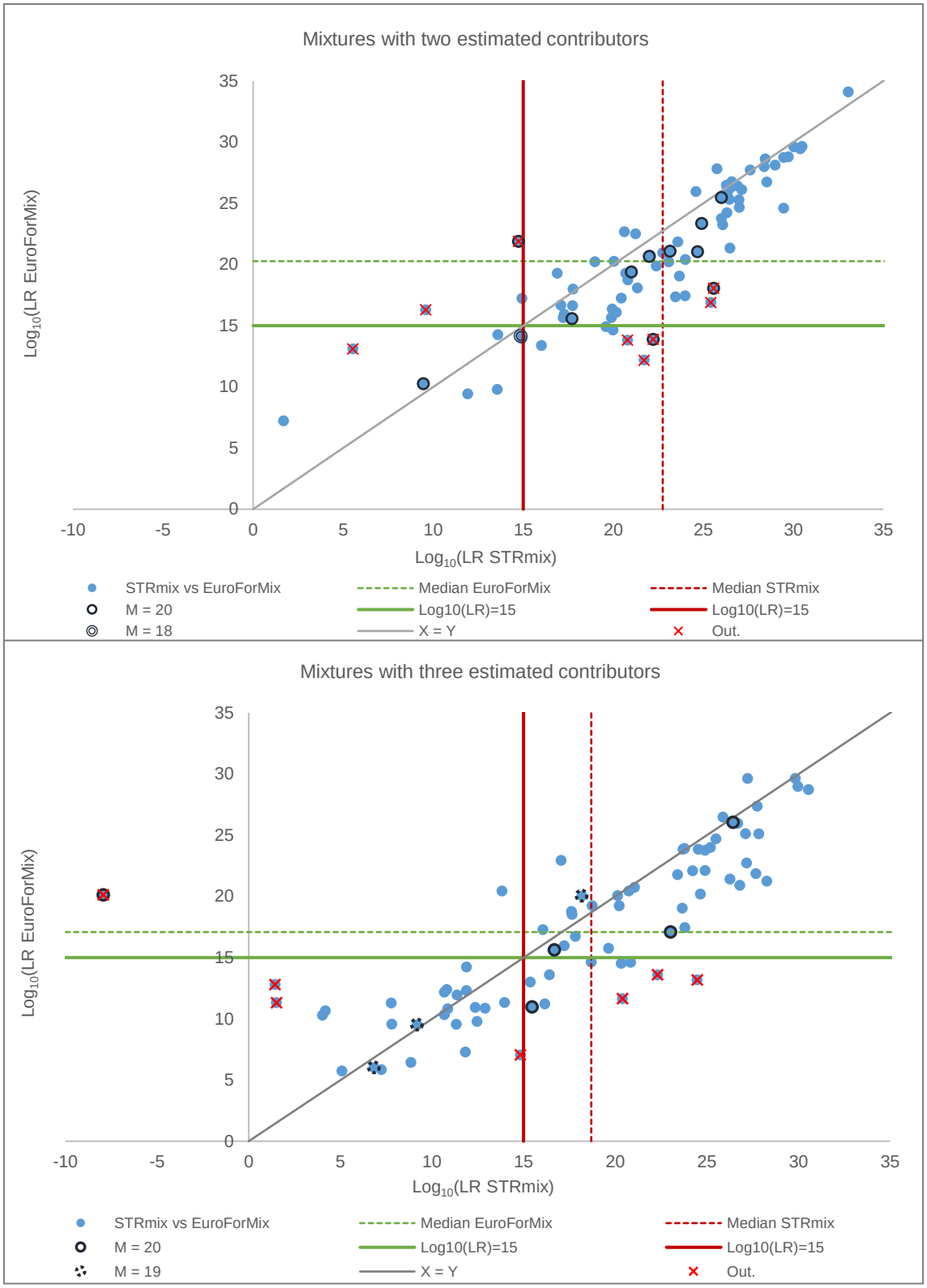


Figure 8: Values of LR (log_{10} scale) computed by STRmix™ v.2.7 (x axis) and by EuroForMix v.1.9.3 (y axis) for the same mixture/reference samples pair, with two (upper plot) and three estimated contributors (lower plot). The mixture/reference pairs that are highlighted with a continuous, dashed, or double continuous line circle correspond to the cases where less than 21 markers were analyzed. The outliers (Out.) represent the cases in the decile with bigger discrepancy between software and are highlighted with an X. The median of the LR values (log_{10} scale) of STRmix™ and EuroForMix is shown in red and green dashed lines, respectively.

With this analysis, it was possible to verify a trend for the LR values computed by STRmix™ to be higher than those computed by EuroForMix. Chi-square test (α=0.05) supported this trend for both cases with mixtures with two (p-value= 1.14E-05) and three (p-value=1.10E-03) estimated contributors.

Throughout figure 8, it was also possible to ascertain that in cases with mixtures with two estimated contributors LR values are higher than those obtained for mixtures with three estimated contributors. This was supported by the t-test (α=0.05) for both STRmix™ (p=3.41E-04) and EuroForMix (p=4.13E-04). On the other hand, LR values corresponding to mixtures with three estimated contributors showed to be more disperse. This trend is corroborated by the standard deviation values obtained, for cases with mixtures with two and three estimated contributors, respectively, in STRmix™, 5.89 and 7.97, and in EuroForMix, 5.64 and 6.39. This dispersion as well as lower LR values may be a consequence of the higher complexity associated with the higher number of contributors.

Additionally, thresholds considering median and Log_{10} (LR) = 15 values were used in order to better situate the LR values, namely the outliers. As illustrated in figure 8, each one of these thresholds divide the figure into four quadrants. For each of the thresholds considered, in the first quadrant are represented the mixture/reference pairs showing a high LR when using EuroForMix, contrarily to what occurs when considering STRmix™. In the fourth quadrant are represented the pairs showing the opposite trend.

The outliers present in the first and fourth quadrants correspond to the 10% of cases showing greater differences, for which only one of the obtained LR values (computed by EuroForMix or STRmix™) surpasses the defined threshold. Its proportion when considered each threshold is represented in table 5, for both cases with mixtures with two and three estimated contributors.

Table 5: Proportion of outliers present in the first and fourth quadrant when the Median and Log_{10}(LR)=15 thresholds are taking into account, for mixtures with two and three estimated contributors.

Thresholds	**Estimated Number of Contributors**	
	2	**3**
Median	25% **(N=12)**	29% **(N=14)**
Log_{10}(LR)=15	63% **(N=8)**	29% **(N=14)**

During the analysis of the presented data, two distinct and unusual situations stood out and therefore, were analyze in more detail.

The first situation, briefly mentioned at the beginning of this sub-chapter, consists of the mixture/reference pairs for which the global LR value computed by STRmix™ for the total set of 21 markers equated zero. This occurred in both cases with mixtures with two (12 out of the 79) and three estimated contributors (7 out of 79) analyzed.

The two main reasons that led to the computation of a null LR value were the lack of alleles in the mixture that were part of the reference sample analyzed and the relative height of the peaks.

The relative height of the peaks constitutes a reason to a null LR value computation since, STRmix™ first performs the deconvolution of the mixture in the most likely profile combinations through the relative height of the peaks analysis, and only after does the correspondence between the reference sample under analysis with one of those possible profiles. So, even when all reference alleles are in the mixture, a null LR can still be achieved for a marker.

The second situation that stood-out was two mixture/reference pairs in which the reference sample has no genetic information for one marker (mixture/reference pair 14002.16-1 (MPNG1) and 20008.17-1 (RMRO1)). Interestingly, the programs act differently, as STRmix™ does not compute an LR value for that marker (leaving this computation blank excluding it from the global LR value), contrarily to EuroForMix. In these situations, under the assumption that genotypes are independent between markers, assuming Hardy-Weinberg equilibrium (HWE) and considering the co-ancestry coefficient (F_{ST}) EuroForMix takes into account the probability of the individual exhibiting certain genotypes, considering the frequency of the alleles in the population [114].

4.1.1. Analysis per marker of the LR values

To understand more deeply the differences between the global LR values obtained by the two software, a per marker analysis was performed for each mixture/reference pair (figure 9 and figure 11), as demonstrated in Box 2.

Box 2

Illustrative example of the comparison made between the LR values computed by STRmix™ and EuroForMix for the mixture/reference pair 243.17-1FM (JRA) (two estimated contributors) for the marker D3S1358, with the profile (heights in parentheses):

- Mixture: **14** (117.6), **15** (121.71), **16** (125.73)
- Reference: **15** (121.48), **16** (125.56)

Software	LR	Log_{10}(LR)	Dif. = log_{10}(LR STRmix™) – log_{10}(LR EuroForMix)	Absolute value (Dif.)
STRmix™	3.9938	0.6014	-0.1003	0.1003
EuroForMix	5.0318	0.7017		

For this analysis, only markers for which a non-null LR was obtained were considered. All the LR values computed for each marker are presented in tables B2, B3, B5 and B6 of Appendix III.

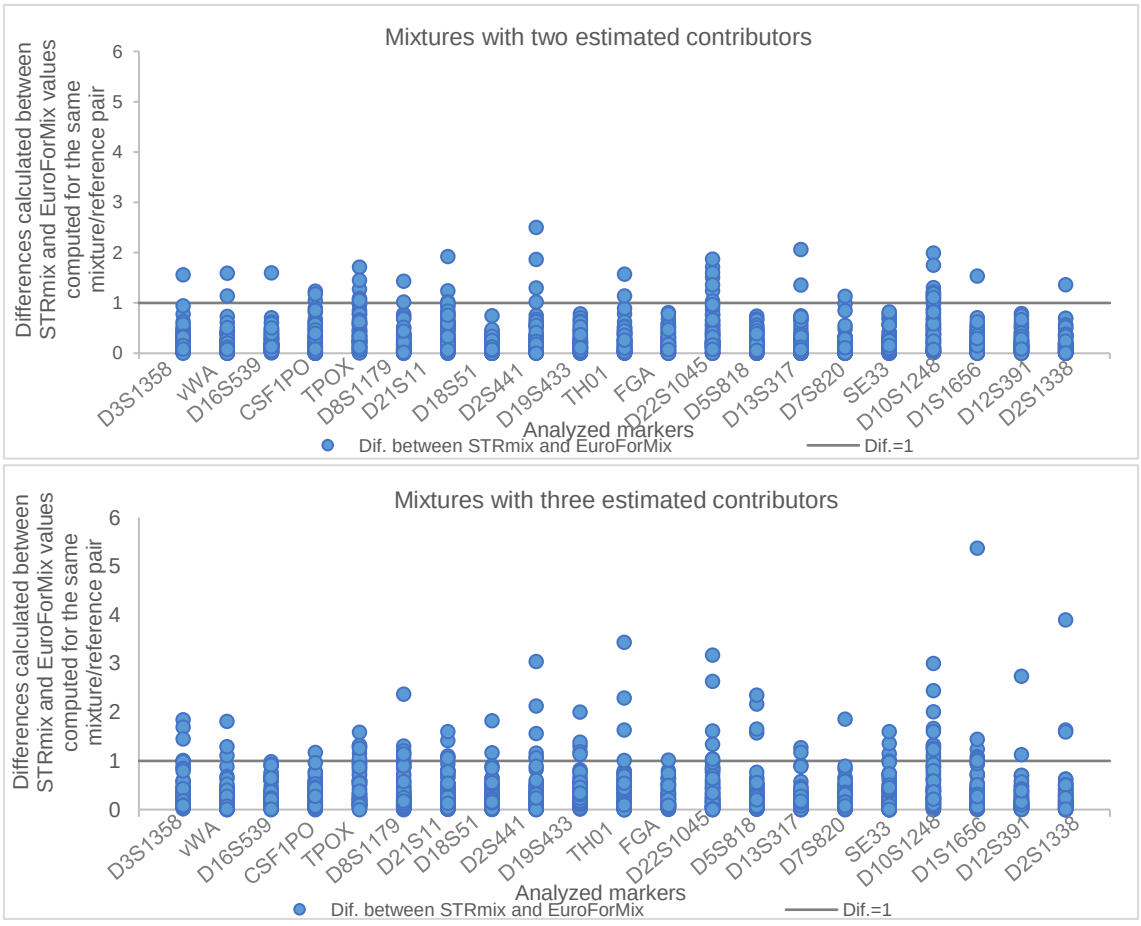


Figure 9: Distribution of the differences between the LR (log_{10} scale) computed by STRmix™ v.2.7 and EuroForMix v.1.9.3 (y axis) for each analyzed marker (x axis) for all mixture/reference pairs, for both cases with mixtures with two (upper plot) and three estimated contributors (lower plot).

Through figure 9 it is possible to verify that the computed differences in cases with mixtures with two estimated contributors tend to be less than those computed in cases with mixtures with three estimated contributors. This trend is supported by the t-test (α=0.05) with a p-value of 1.31E-09 and also by the median values obtained, 0.17 and 0.21, for cases with mixtures with two and three estimated contributors, respectively.

For a more objective analysis of figure 9, a line corresponding to the computed differences equal to one unit in a $\log_{10}$ scale was added, for both cases with mixtures with two and three estimated contributors, allowing to easily identify in which markers the values computed by STRmix™ and EuroForMix were more similar.

In cases involving mixtures with two estimated contributors, in the markers D18S51, D19S433, FGA, D5S818, SE33 and D12S391 only differences less than one $\log_{10}$ unit were computed. However, in the cases with mixtures with three estimated contributors such small difference only occurred in the marker D16S539.

On the opposite side, the marker D10S1248 showed the lowest proportion of cases for which the difference between the values computed by the two software was less than one unit in a $\log_{10}$ scale, in both cases with mixtures with two and three estimated contributors.

In table 6 are presented the largest, the smallest and the amplitude of the differences that were calculated between the LR values ($\log_{10}$ scale) computed by STRmix™ and EuroForMix for each mixture/reference pair in a per marker analysis. The smallest differences between the values computed by the two software were reached for markers CSF1PO – with a difference of 1.65E-04 units, in a $\log_{10}$ scale, for the mixture with two estimated contributors/reference pair 1843.17-1FIXACAO (FN1) – and TH01 – with a computed difference of 2.74E-04 units for the mixture with three estimated contributors/reference pair 5396.16-1CABO (JJCC).

On the other hand, the maximum difference achieved in cases with mixtures with two estimated contributors was 2.51 units in a $\log_{10}$ scale where STRmix™ computed a LR value of 4.18E-02 and EuroForMix of 1.34E+01 and occurred on marker D2S441. Whereas, in cases with mixtures with three estimated contributors the maximum difference doubled to 5.38 units with a computed LR value of 2.90E-04 in STRmix™ and 6.88E+01 in EuroForMix on the marker D1S1656. These differences were computed for the mixture/reference pairs 12818.17-7 (1) and 10814.16-2 (CMSA), respectively, whose profiles are showed in figure 10.

It should be noted that, for both cases, a null global LR value was initially computed by STRmix™ software.

Table 6: Layout of the largest, smallest and amplitude values of the differences calculated between the LR values (log_{10} scale) computed by both STRmix™ v.2.7 and EuroForMix v.1.9.3 for each marker, for cases with mixtures with two and three estimated contributors.

Marker	Estimated Number of Contributors					
	2			3		
	Maximum difference	Minimum difference	Amplitude	Maximum difference	Minimum difference	Amplitude
D3S1358	1.5601	0.0019	1.5582	1.8477	0.0211	1.8266
vWA	1.5917	0.0050	1.5867	1.8127	0.0017	1.8110
D16S539	1.6012	0.0079	1.5933	0.9869	0.0004	0.9865
CSF1PO	1.2398	0.0002	1.2397	1.1773	0.0025	1.1748
TPOX	1.7135	0.0082	1.7053	1.5898	0.0171	1.5727
D8S1179	1.4345	0.0043	1.4302	2.3759	0.0104	2.3655
D21S11	1.9275	0.0008	1.9267	1.6028	0.0053	1.5976
D18S51	0.7470	0.0007	0.7464	1.8309	0.0034	1.8275
D2S441	2.5058	0.0048	2.5010	3.0443	0.0011	3.0432
D19S433	0.7831	0.0015	0.7816	2.0081	0.0106	1.9975
TH01	1.5758	0.0006	1.5752	3.4381	0.0003	3.4378
FGA	0.8140	0.0035	0.8106	1.0189	0.0043	1.0145
D22S1045	1.8724	0.0035	1.8690	3.1784	0.0048	3.1736
D5S818	0.7412	0.0018	0.7394	2.3545	0.0099	2.3447
D13S317	2.0652	0.0008	2.0644	1.2773	0.0065	1.2708
D7S820	1.1389	0.0013	1.1376	1.8613	0.0005	1.8607
SE33	0.8262	0.0003	0.8259	1.6042	0.0009	1.6033
D10S1248	1.9926	0.0184	1.9743	3.0079	0.0102	2.9977
D1S1656	1.5381	0.0076	1.5305	5.3759	0.0043	5.3715
D12S391	0.7894	0.0022	0.7872	2.742	0.0040	2.7380
D2S1338	1.3647	0.0007	1.3640	3.9001	0.0027	3.8974

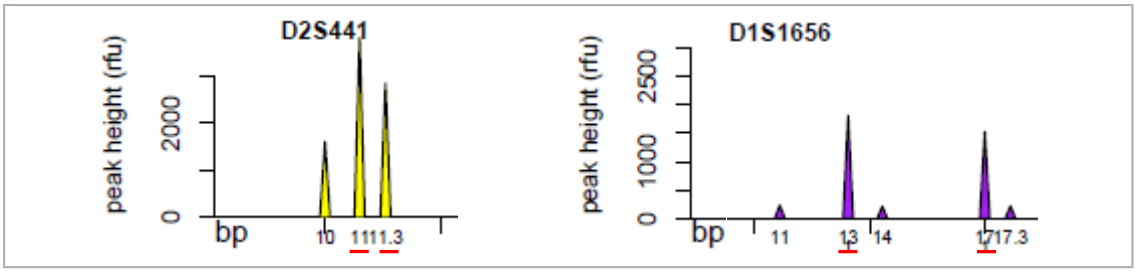


Figure 10: Reference and mixture profiles in the markers where the maximum difference between the LR value computed by STRmix™ and EuroForMix was achieved, namely, in D2S441 marker (left plot) for the mixture (with two estimated contributors)/reference pair 12818.17-1 (1) and in D1S1656 marker (right plot) for the mixture (with three estimated contributors)/reference pair 10814.16-2 (CMSA). The reference profile is underlined in red.

Figure 9 also allows the visualization of the amplitude of the computed differences for each marker presented in table 6. The smallest amplitude was observed on markers D5S818 and D16S539, with a variation of 0.74 and 0.99 units in a log_{10} scale, for cases with mixtures with two and three estimated contributors, respectively. In contrast, the markers that presented the largest amplitude of values were the same for which the maximum differences were computed – D2S441 and D1S1656 –, with a variation of 2.50 and 5.37 units in the log_{10} scale, for cases with mixtures with two and three estimated contributors, respectively.

In order to understand if the differences between the global LR values computed by STRmix™ and EuroForMix were due to an accumulation of small differences in all (or almost all) markers or to large differences in one (or few) marker(s), a comparison between the differences in global LR values and per marker differences was computed (figure 11) , as illustrated in Box 3.

Box 3

Illustrative example of the comparison made in figure 11, for the mixture/reference pair 16839.17-1.9 (BZ1) (three estimated contributors):

- 21 points, representing the 21 markers, are associated with the mixture/ reference pair;
- All points have the same x-axis coordinate (9.79205), which corresponds to the difference calculated between the global LR values computed by STRmix™ and EuroForMix (log_{10} scale);
- Each point y-axis coordinate represents the differences found for each marker between the values computed in both software.

For example, in this mixture/reference pair, the markers D5S818 and D2S441 have the following coordinates (9.792, 2.170) and (9.792, 3.044), respectively.

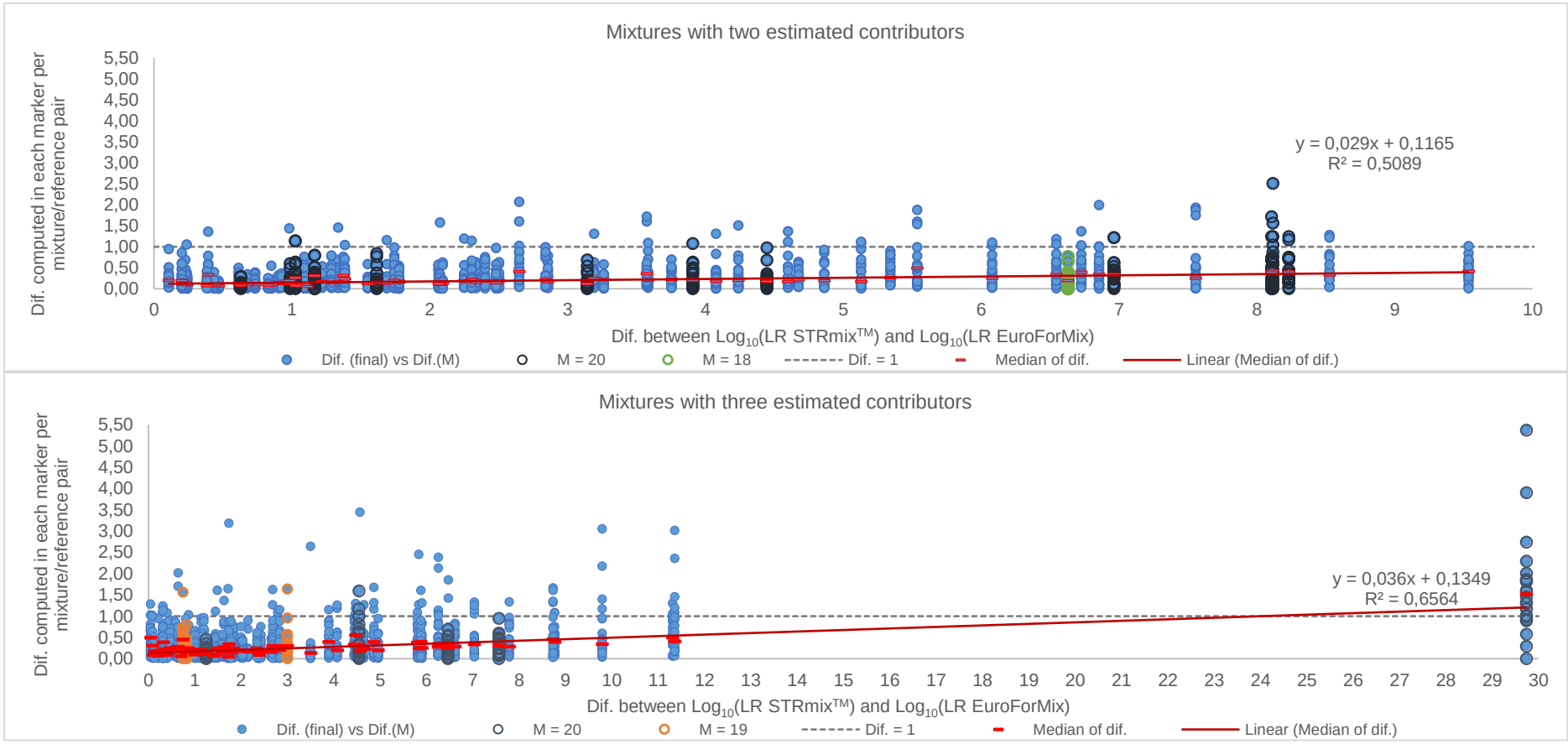


Figure 11: Comparison between the differences found for global LR values computed by STRmix™ v.2.7 and EuroForMix v.1.9.3 (log_{10} scale, x axis) and the differences calculated in a per marker analysis, for each mixture/reference pair, for both cases with mixtures with two (upper plot) and three estimated contributors (lower plot). For each mixture/reference pair the median of markers' differences is highlighted with a red dash. The dark red line represents the linear regression of these medians. The set of differences computed for the mixture/reference pairs for which less than 21 markers were analyzed are highlighted with a dark blue, orange and green continuous line circle.

In both set of cases, there is a positive linear correlation between the difference in the global LR value (log_{10} scale) computed by EuroForMix and STRmix^{TM} and the median of the per marker differences for each mixture/reference pair. As the difference between the global LR value computed by STRmix^{TM} and EuroForMix increases, the median of the differences between markers for each mixture/reference pair also increases. This positive correlation is stronger in cases with mixtures with three estimated contributors (R^2= 0.6564) than in those with two (R^2= 0.5089) – figure 11.

A situation that stands-out in figure 11 is the mixture (with three estimated contributors) /reference pair 10814.16-2 (CMSA) since it is the only one with a median of differences higher than one unit in a log_{10} scale. This higher median value reflects higher per marker differences comparing to the other pairs, what makes sense, since is the mixture/reference pair that reached the biggest difference calculated for the global value LR (28.06 units). The markers that reached the greatest differences in this situation were D1S1656, D2S1338 and D12S391, with the computed differences of 5.375, 3.900, and 2.742 units (log_{10} scale), respectively. It should also be noted that for the SE33 marker, a null LR value was initially computed in STRmix^{TM} software and therefore it was removed from the both analyses as has been mentioned. To see in greater detail this mixture/reference pair, the epg is illustrated in the Appendix VI figure C1.

Most of the computed differences showed to be of less than one unit in a log_{10} scale: 97% and 95% of the computed differences for mixtures with two and three estimated contributors, respectively.

The correlation existing between the differences of the global LR values and the number of markers that differed more than one unit in a log_{10} scale for each mixture/reference pair was performed, as illustrated in figure 12. As can be seen in the figure, there are situations where all the markers show differences smaller than one unit in a log_{10} scale but the global LR value presents differences up to 6.63 and 7.56 units both in cases involving mixtures with two and three estimated contributors, respectively. In these specific situations, the difference computed for the global LR value results from the combination of small differences in several markers.

Contrasting with those situations, there are cases where the global LR value presents a small difference (less than one unit in a log_{10} scale), despite more than one marker showed differences greater than one unit in a log_{10} scale. This situation is consequence of computed differences going in opposite directions, i.e., a value computed by STRmix^{TM} in a marker is higher than the one computed by EuroForMix,

while in another marker the opposite situation occurs balancing the computed difference in the global LR value.

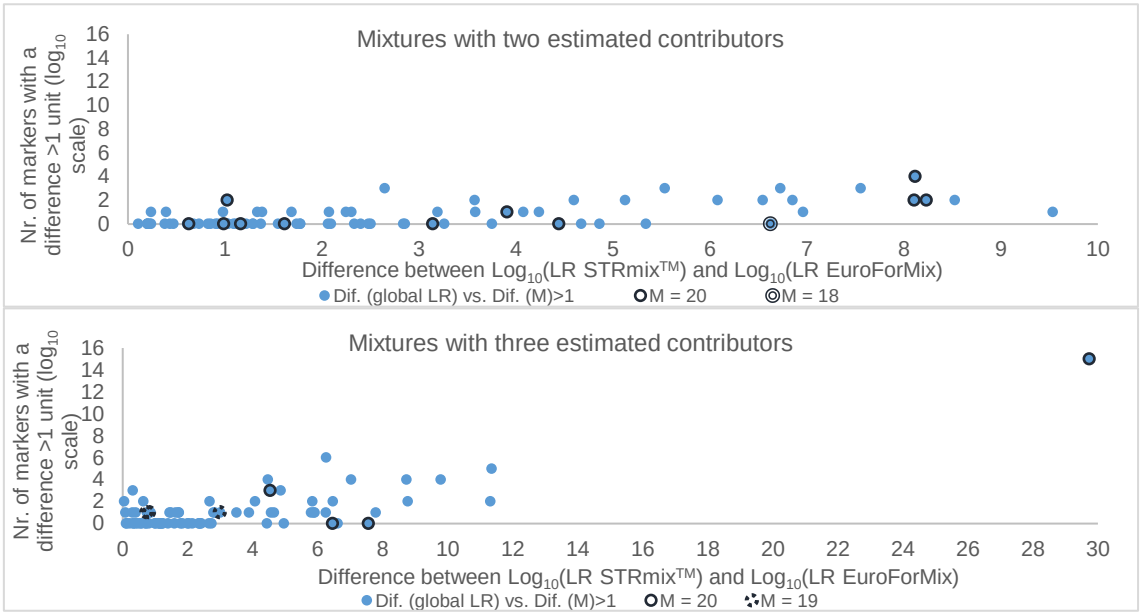


Figure 12: Comparison between the differences of the global LR values computed by STRmix™ v.2.7 and EuroForMix v.1.9.3 (log_{10} scale, x axis) and the number of markers for which the difference of the LR values (log_{10} scale) was greater than one unit in a log_{10} scale. The mixture/reference pairs that are highlighted with a continuous, dashed, or double continuous line circle correspond to the cases where less than 21 markers were analyzed.

Thus, simultaneously analyzing both figures 11 and 12, it becomes clear that the discrepancies between the global LR values computed by both software may result from an accumulation of small differences in a large set of markers and not of a large difference in a single (or small set of) marker(s).

Finally, a more thorough review was performed on the cases whose analysis through STRmix™ resulted in a null LR. As already referred in section 3.3.1. and in the beginning of the section 4.1.1., these mixture/reference pairs were re-analyzed, in both programs, disregarding the markers for which LR equated zero.

Proceeding in the per marker analysis, all those mixture/reference pairs were analyzed in more detail, in order to understand the impact that the removal of the markers for which LR equated zero had on the LR of the remaining markers and if STRmix™ and EuroForMix software behaved similarly. Indeed, both software consider the whole information of a mixture, not analyzing independently markers' information.

The results obtained for each of the remaining markers (those with a non-null LR value) before and after markers with null LR values have been removed were compared and are presented in the tables B2, B3, B5 and B6 of Appendix III following the mixture/reference pairs with two LR values, LR_{21} and $LR_{<21}$, respectively.

An example of the analysis carried out is illustrated in Box 4.

Box 4

Illustrative example of the comparison made between the LR values computed for the markers with a non-null value before and after the removal of the marker(s) with a null LR value for the mixture/reference pair 17065.17-1 (SSC1) (two estimated contributors). The illustrated markers and the observed profiles (peak heights in parentheses) were as follows:

D22S1045

- Mixture: **14** (106.59), **15** (109.53), **16** (112.53), **17** (115.54), **18** (118.54)
- Reference: **16** (112.17), **17** (115.21)

D13S317

- Mixture: **10** (218.68), **11** (222.61), **12** (226.63)
- Reference: **11**(222.78), **12** (226.75)

D2S1338

- Mixture: **19** (312.68), **19.3** (316.77), **21** (320.79), **25** (336.91)
- Reference: **21** (321.67)

Software		Markers (values in log_{10} scale) D22S1045	D13S317	D2S1338
STRmix™				
(After removal)	LR_{21}	1.082	0.739	[a]
(Before removal)	$LR_{<21}$	1.082	0.743	-
	Dif.	0.000	-0.004	-
	ABS (Dif.)	0.000	0.004	-
EuroForMix				
(After removal)	LR_{21}	0.905	0.702	0.581
(Before removal)	$LR_{<21}$	1.005	0.697	-
	Dif.	-0.100	0.005	-
	ABS (Dif.)	0.100	0.005	-

[a] Null LR value computed.

After calculating the difference between the two values computed by the software – before and after the removal of the markers for which a null LR value was computed – , it was visible that the largest discrepancies occur in cases with mixtures with two estimated contributors. As showed in table 7, in these cases, STRmix™ software reached a maximum difference of 2.72 units (log_{10} scale) and the EuroForMix of 1.27. In the case of mixtures with three estimated contributors, these values decrease to 0.45 and 1.03, respectively.

Table 7: Mean and maximum per marker differences between the two computed values for each marker, before and after the removal of the markers for which LR equated zero in the STRmix™ analysis, for both mixtures with two and three estimated contributors in both STRmix™ v.2.7 and EuroForMix v.1.9.3.

Analysis		Estimated Number of Contributors	
		2 N=238	3 N=138
Maximum	**STRmix™**	2.72	0.45
	EuroForMix	1.27	1.03
Mean	**STRmix™**	0.08	0.05
	EuroForMix	0.09	0.10

In mixtures with two estimated contributors, the average value of the calculated differences was similar between EuroForMix and STRmix™ (0.09 and 0.08, respectively). However, the average in EuroForMix remains similar for the mixtures with three estimated contributors at 0.10, while in STRmix™ it decreases to 0.05 (table 7).

This analysis shows that, considering STRmix™ software, when one or more markers are removed there is no trend for LR values (re)computed in each of the remaining markers to be higher or lower than those computed when none is removed. The absence of a trend is supported by the chi-square test (α=0.05) for both cases with mixtures with two and three estimated contributors (p-value=1.54E-01 and 4.96E-01, respectively). On the other hand, when considering EuroForMix software, a trend for LR values (re)computed to be higher than those computed when none marker is removed was verified and supported by the chi-square test (α=0.05), for both cases with mixtures with two and three estimated contributors (p-value= 2.87E-03 and 3.80E-03, respectively).

4.2. Weighing the impact on parameters' variation

In this sub-chapter, the impact of the variation of values/conditions of software parameters (number of contributors, threshold detection, drop-in and F_{ST}, stutters) on the global LR value computation was analyzed.

For both STRmix™ v.2.7. and EuroForMix v.1.9.3, an intra-software analysis was performed by comparing the LR values computed under the default and varied conditions (see table 2 of section 3.3.2.), for each mixture/reference sample pair, varying a single parameter at a time. Then, a comparison between the differences found in each software was carried out.

4.2.1. Impact of the estimated number of contributors

During the examination of the mixture's epg, the expert must estimate the number of contributors of the mixture under analysis, as this is a parameter which is needed to be introduced later in the software, as referred in section 3.3.2.

Since the quantity and quality of DNA in real casework samples are usually low, the estimation of the number of contributors may not be accurate. For that reason, the impact of a possible underestimation and overestimation of the number of contributors estimated by epg observation was performed and analyzed in both software.

It should be noted that the number of contributors estimated for the mixtures samples under analysis were previously determined during the EuroForMix v.1.9.3 values computations [1], and for that reason these maintained during the STRmix^{TM} v.2.7 values computations, allowing the comparison.

The conditions of the other parameters used in this analysis are specified in table 2 of section 3.3.2.

4.2.1.1. Overestimating the number of contributors

The comparison and distribution of the computed LR values, in both EuroForMix v.1.9.3 [1] and STRmix^{TM} v.2.7, when the number of contributors is overestimated considering three and four contributors, for cases with mixtures for which two and three contributors were estimated, respectively, are outlined in figure 13. The differences greater than four units in a $\log_{10}$ scale were titled as outliers and highlighted in the same figure.

An illustrative example of the analysis performed in each mixture/reference pair considered in this sub-section described in greater detail in Box 5.

All LR values analyzed in this subsection are presented in the tables B1, B3, B4, B6 – initial estimate number of contributors –, B7, B8 – overestimating two contributors' mixtures – B9, and B10 – overestimating three contributors' mixtures – of Appendix III. For the mixture/reference pairs which a null LR value was initially computed by STRmix^{TM} software, two LR values (LR_{21} and $LR_{<21}$) are presented in the tables B1, B3, B4 and B6 of which the $LR_{<21}$ values were utilized. In the remaining tables corresponding to the STRmix^{TM} software (namely, tables B8 and B10), for the pairs in question, only the $LR_{<21}$ values are presented.

Box 5

Illustrative example of the comparison made between LR values computed by STRmix™ considering the initial estimation and the overestimation of the number of mixture contributors, for the mixture/reference pair 13027.17-1R2FF (1R1FF) (two initial estimated contributors).

Number of contributors	LR	Log_{10}(LR)	Dif. = log_{10}(LR initial) – log_{10}(LR overestimation)	Absolute value (Dif.)
2 (initial)	3.80E+09	9.57978	3.07557	3.07557
3 (overestimation)	3.19E+06	6.50421		

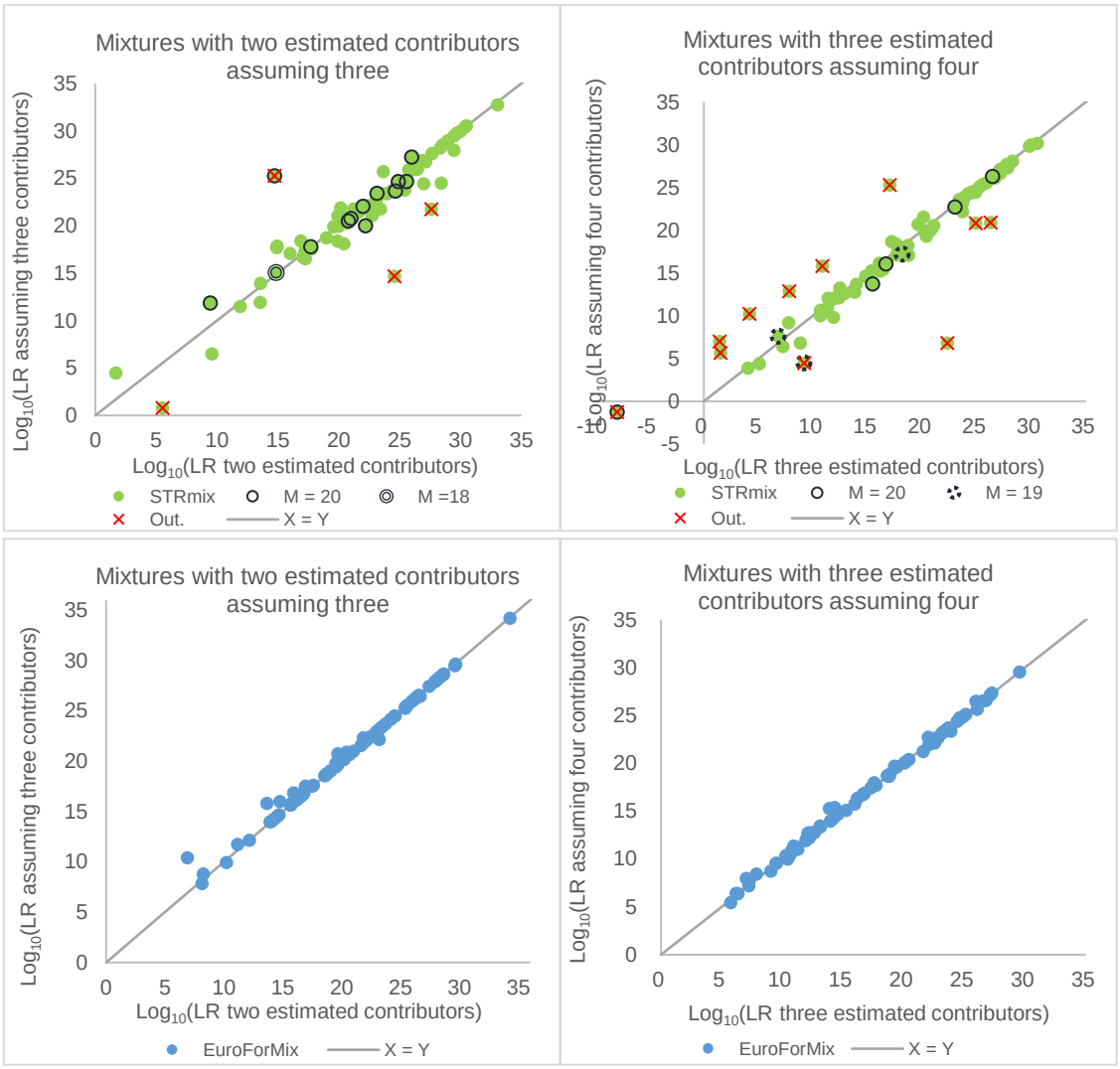


Figure 13: Values of LR (log_{10} scale) computed by STRmix™ v.2.7 in green (uppers plots) and EuroForMix v.1.9.3 [1] in blue (lowers plots) for the same mixture/reference pairs, when overestimating the number of contributors, in mixtures with two (left plots) and three estimated contributors (right plots), assuming three and four contributors, respectively. The mixture/reference pairs that are highlighted with a continuous, dashed, or double continuous line circle correspond to the cases where less than 21 markers were analyzed. The outliers (Out.) are highlighted with an X representing the biggest discrepancy between analyzes (greater than four units in a log_{10} scale).

Although it is not clear from figure 13 if there is a trend for the LR values computed, in either STRmix™ or EuroForMix, to increase or decrease when the number of contributors is overestimated, through the application of Chi-square test (α=0.05) it was possible to verify that, indeed, there is a trend.

For the LR values computed by STRmix™, the Chi-square test (α=0.05) showed a trend for the LR values to be lower when overestimating the number of contributors, for both cases with mixtures with two (p-value= 4.91E-03) and three (p-value=8.22E-05) estimated contributors. On the other side, for the LR values computed by EuroForMix software the opposite trend was verified. Chi-square test (α=0.05) supported this trend (i.e., LR values tend to be higher when the number of contributors is overestimated) only for cases with mixtures with two estimated contributors (p-value= 9.66E-03), since for the cases with mixtures with three estimated contributors no evidence on the increasing or decreasing of the global LR value was observed (p-value= 7.36E-01).

Table 8: Differences between the LR values (log_{10} scale) obtained under the condition of overestimation of the number of contributors (from two to three and from three to four) and the initial estimate, computed by EuroForMix v.1.9.3 [1] and STRmix™ v.2.7. The maximum, mean and median values of these differences are also presented.

X = ABS [Log_{10}(LR initial) – Log_{10}(LR overestimation)]	**Number of estimated contributors**			
	2		**3**	
	Number of considered contributors			
	3		**4**	
	(N=79)		**(N=79)**	
	EuroForMix	**STRmix™**	**EuroForMix**	**STRmix™**
0 < X < 1	94%	67%	97%	56%
1 < X < 2	4%	15%	3%	10%
2 < X < 3	1%	10%	0%	2%
3 < X < 4	1%	3%	0%	0%
X > 4	0%	5%	0%	11%
Maximum	3.52	10.52	1.41	15.51
Mean	0.19	1.10	0.20	1.36
Median	0.01	0.30	0.11	0.52

Regarding the differences computed for the EuroForMix values, the great majority were within zero and one unit in the log_{10} scale, namely, 94% for mixtures of two analyzed as three and 97% for three overestimated as four (table 8). However, in the STRmix™ software those percentages drastically decreased to 67% and 56%, respectively, reflecting a greater dispersion of dots observed in the STRmix™ graphs (figure 13), and so, a greater sensitivity on the part of STRmix™ to the overestimation of the number of contributors.

Another evidence of the STRmix™ higher sensitivity, was the outliers found in the software computations, highlighted in figure 13 corresponding to 5% and 11% of the cases with mixtures with two and three estimated contributors showing differences greater than four units in a log_{10} scale. Those outliers resulted indiscriminately from either the decrease or increase of the global LR value. The decrease of the global LR value can be associated with the increase in the number of possible combinations of genotypes created with the consideration of one more contributor than initially considered. However, there are cases where the global LR value computed under the overestimation condition increases comparing to the computed for the initial estimation. These cases can constitute situations whose value used in the overestimation of the number of contributors is more likely than initially estimated, thus resulting in the computation of a higher global LR value.

4.2.1.2. Underestimating the number of contributors

Figure 14 depicts the LR values computed by EuroForMix v.1.9.3 [1] and STRmix™ v.2.7, under the condition of underestimation of the number of contributors for cases with mixtures with three estimated contributors, comparing those with the LR values computed for the initial estimate. As before, the cases with greater discrepancies between the two computed values (more than four units in the log_{10} scale) are designated as “outliers” and are highlighted in the figure. An illustrative example of the analysis performed for each mixture/reference pair considered in this subsection is described in more detail in Box 6 below.

Box 6

Illustrative example of the comparison made between the LR value computed by STRmix™ considering the initial estimation of three contributors and assuming two, for the mixture/reference pair 12179.17-14R6 (MAM1).

Number of contributors	LR	Log_{10}(LR)	Dif. = log_{10}(LR initial) – log_{10}(LR underestimation)	Absolute value (Dif.)
3 (initial)	4.78E+10	10.67928	3.06690	3.06690
2 (underestimation)	4.10E+07	7.61238		

All the LR values analyzed in this subsection are presented in tables B4, B6 – initial estimate number of contributors –, B11, and B12 – underestimating three contributors’ mixtures – of Appendix III. For the mixture/reference pairs which a null LR value was initially computed by STRmix™ software, two LR values (LR_{21} and $LR_{<21}$) are presented in the tables B6 of which the $LR_{<21}$ values were utilized in this subsection to

enable comparison. In table B12, that also corresponds to the STRmix™, only the $LR_{<21}$ values are presented for the pairs in question.

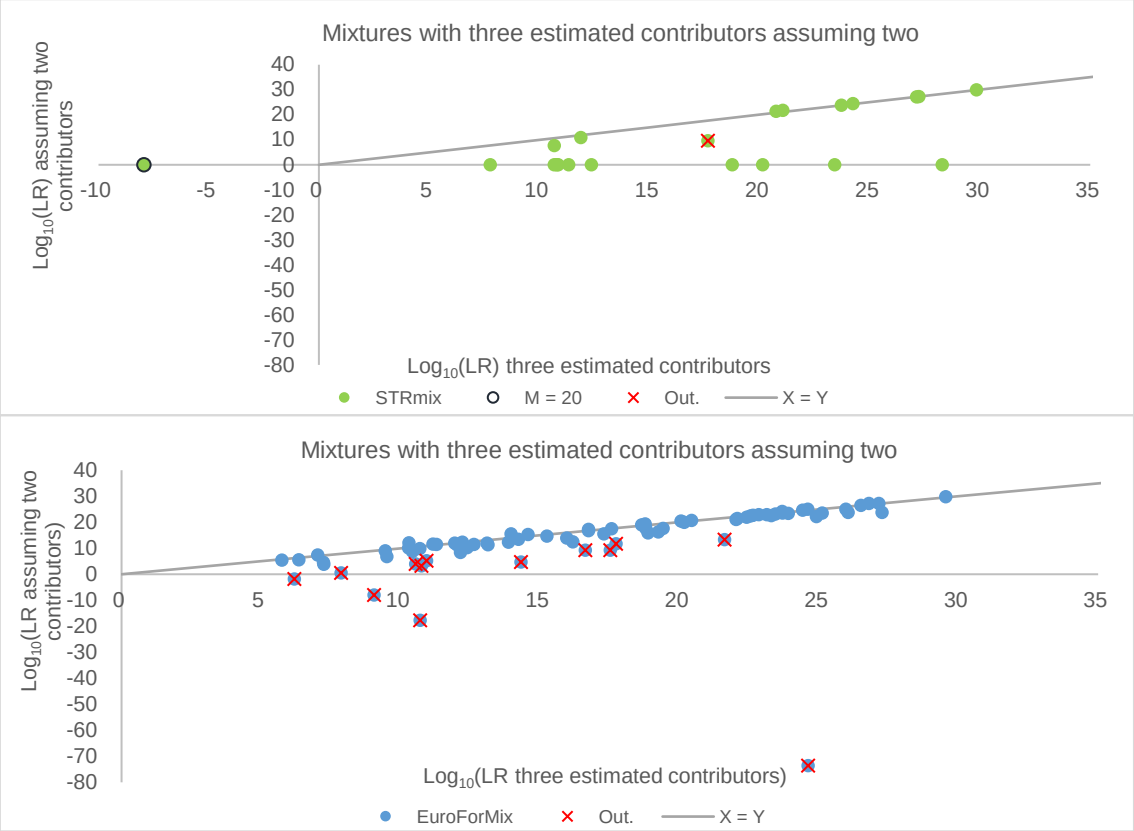


Figure 14: Values of LR (log_{10} scale) computed by STRmix™ v.2.7 in green (upper plot) and EuroForMix v.1.9.3 [1] in blue (lower plot) for the same mixture/reference pairs, when underestimating the number of contributors in cases with mixtures with three estimated contributors, assuming two contributors. The pairs that are highlighted with a continuous line circle correspond to the cases where less than 21 markers were analyzed. The outliers (Out.) are highlighted with an X representing the cases showing biggest discrepancy between analyzes (greater than four units in a log_{10} scale).

For 87% of the STRmix™ computations, comparisons were not performed, namely, 14% of the cases for which a null LR value was computed, and 73% of the cases for which the software was unable to perform any calculations, presenting the following error message "The evidence cannot be explained given the parameters you have chosen" – table 9.

Table 9: Proportions of the different results obtained when the number of contributors was underestimated, in mixtures with three estimated contributors in both EuroForMix v.1.9.3 [1] and STRmix™ v.2.7.

	EuroForMix (N=79)	**STRmix™ (N=79)**
Error message	0%	73%
Null LR value	0%	14%
Non-null LR value	100%	13%

Table 10: Proportions of the non-null LR values computed by EuroForMix v.1.9.3 [1] and STRmix™ v.2.7 that resulted in an increase and/or decrease in the global LR value when the number of contributors was underestimated in mixtures with three estimated contributors.

LR variation	EuroForMix (N=79)	STRmix™ (N=10)
Increase	27%	60%
Decrease	73%	40%

Through figure 14 and table 10 it is noteworthy that for the cases for which STRmix™ retrieved a non-null value there is no evidence of trend for LR values, computed under the underestimation conditions, to increase or decrease comparatively to the LR values computed for the initial estimated number of contributors. The absence of a trend is supported by the chi-square test (α=0.05) with a p-value of 5.27E-01.

On the opposite side, for EuroForMix software, through which all computations retrieved a non-null LR, there is indeed a trend for LR values computed, assuming only two contributors, to be lower than those computed for the initial three contributors estimated. Chi-square test (α=0.05) supported this trend with a p-value of 3.14E-05.

The global LR value decrease verified in EuroForMix when the number of contributors was underestimated, may be a result of mixture sample alleles (that correspond to some alleles of the reference sample under analysis) with a low peak height. Comparatively to the other peak alleles height in the same marker, those low peak height may be considered by the software to be stutter or even non-specific peak. This evaluation comprises a way for the software to be able to make compatible the mixture sample peaks under analysis with the number of contributors introduced by the user, resulting in the computation of a lower LR value. However, in some cases, the software just cannot justify the presence of so many peaks per marker (considering the number of contributors proposed) resulting in the computation of an LR value lower than one ($\log_{10}$ scale).

A distribution of the differences obtained between the LR values computed when underestimating the number of contributors and when considering the initial estimate is represented in table 11, for both EuroForMix and STRmix™ software.

Table 11: Differences between the LR values(log_{10} scale) obtained under the condition of underestimation the number of contributors (two) and the initial estimate (three), computed by EuroForMix v.1.9.3 [1] and STRmix™ v.2.7, as well as, the maximum, mean and median values of these differences.

X = ABS [Log_{10}(LR initial) – Log_{10}(LR underestimation)]	**Number of estimated contributors**	
	3	
	Number of considered contributors	
	2	
	EuroForMix (N=79)	**STRmix™ (N=10)**
0 < X < 1	52%	70%
1 < X < 2	16%	10%
2 < X < 3	9%	0%
3 < X < 4	6%	10%
X > 4	16%	10%
Maximum	98.22	8.06
Mean	3.66	1.37
Median	0.89	0.59

Table 11 shows that although 52% and 70% of EuroForMix and STRmix™ computed differences were within one unit in a log_{10} scale, both software registered cases with computed differences greater than four units, namely, 16% and 10% of the cases, respectively. However, it should be bearing in mind that the number of cases considered in STRmix™ is much lower than that considered in EuroForMix, and as such, comparison between software must be taken with care.

Contrarily to what happened in the overestimation analysis, several outliers – mixture/reference pairs with a computed difference greater than four units in a log_{10} scale – were highlighted in EuroForMix values. In some of those outliers, a negative log_{10}(LR) value was computed under the underestimation condition, constituting a situation that only occurred in this software computations. An outlier, that constitutes this set of mixture/reference pairs, and clearly stands-out the most, corresponds to the maximum computed difference: 98.22 units in a log_{10} scale reached in the mixture/reference pair 4548.16-PC9.9 (PC9.8) whose computed LR values were 4.02E+24 and 2.44E-74 for the initial estimate and underestimation, respectively (table 11). This particular situation has analyzed in great detail by Figueiredo ([1] – subsection 3.1.2.2.).

So, even though the impact of underestimation and consequent software sensitivity was reflected in EuroForMix with the presence of several outliers, it is safe to say that, when underestimating the number of contributors, the STRmix™ software can be even more sensitive than EuroForMix, since in the 73% of STRmix™ computation an

error message appeared reflecting the inability to compute a value in those situations and, additionally, in 14% of the cases a null LR value was computed.

4.2.2. Impact of Threshold detection

To separate true peak alleles from baseline noise, a threshold value is needed to be established and introduced in the peak detection software.

The values of LR (log_{10} scale) computed by EuroForMix v.1.9.3 [1] and STRmix™ v.2.7 when the threshold value was changed from 100 RFU (default value) to 150 RFU (varied value – table 2 of section 3.3.2.), for cases with mixtures with two and three estimated contributors are illustrated in figure 15. The greater discrepancies found between the two computed LR values (greater than four units on the log_{10} scale) are designated as “outliers” and highlighted in the figure.

An example of how these values were analyzed is illustrated in Box 7.

Box 7

Illustrative example of the comparison made between LR value computed by STRmix™ when the threshold detection value was change from 100 RFU to 150 RFU, for the mixture/reference pair 13027.17-1R2FF (1R1FM) (two estimated contributors).

Threshold detection (RFU)	LR	Log_{10}(LR)	Dif. = log_{10}(LR 100 RFU) – log_{10}(LR 150 RFU)	Absolute value (Dif.)
100 (default)	3.91E+24	24.59222	-1.84378	1.84378
150	2.73E+26	26.43600		

All the computed LR values analyzed in this section are presented in tables B1, B3, B4, B6, – default threshold detection value considered – ($LR_{<21}$ values from tables B3 and B6 were used), B13, B14, B15, and B16 – varied threshold detection value –of Appendix III.

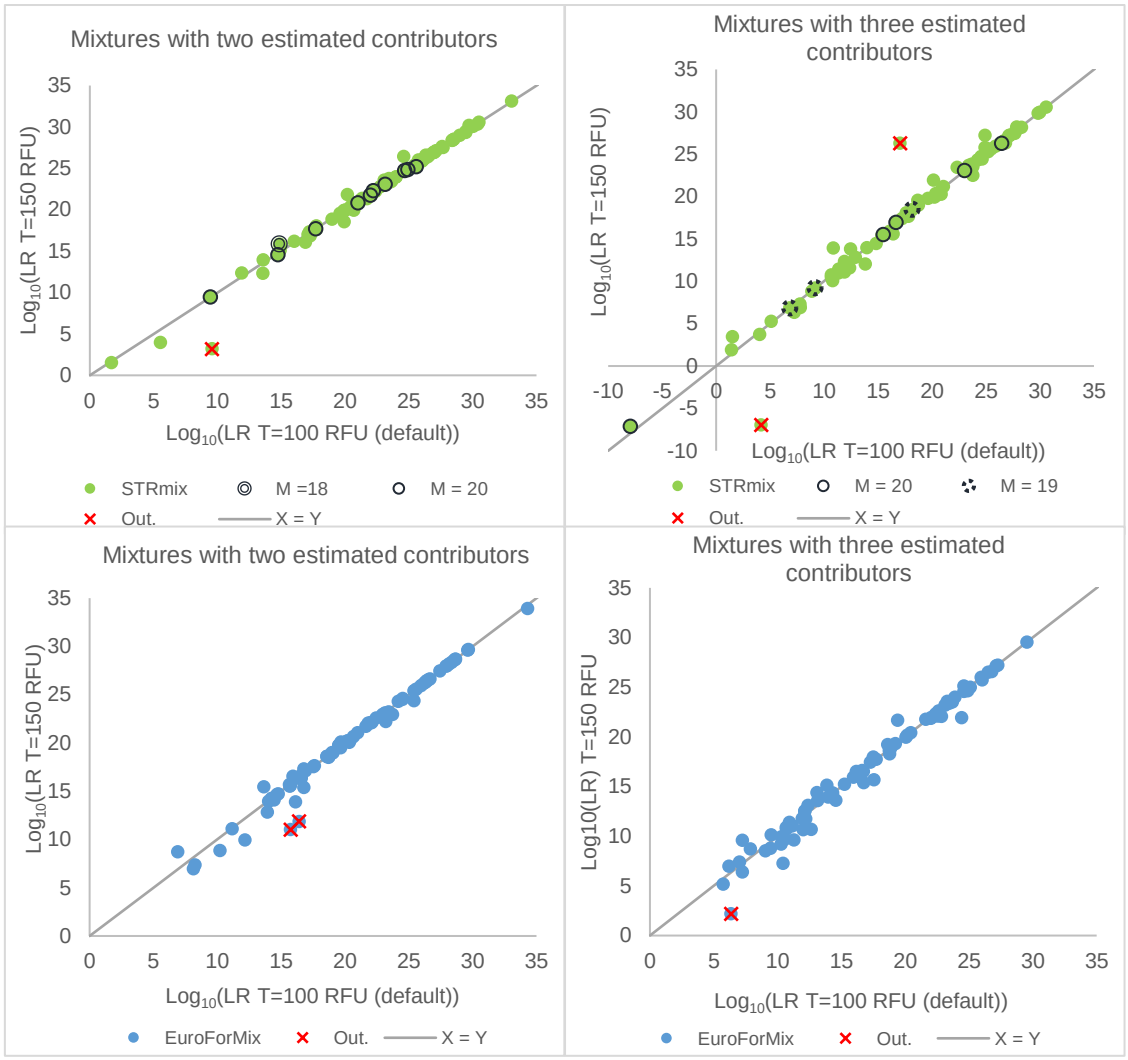


Figure 15: Values of LR (log_{10} scale) computed by STRmix™ v.2.7 in green (uppers plots) and EuroForMix v.1.9.3 [1] in blue (lowers plots) and for the same mixture/reference pairs, with two (left plots) and three estimated contributors (right plots). The mixture/reference pairs that are highlighted with a continuous, dashed, or double continuous line circle correspond to cases where less than 21 markers were analyzed. The outliers, where the discrepancy between values is greater than four units in a log_{10} scale, are highlighted with an X.

Regarding a possible trend to increase or decrease the LR value computed by the STRmix™ software when a threshold detection of 150 RFU is considered, the Chi-square test (α=0.05) didn´t show evidence of a trend, neither in cases with mixtures with two (p-value= 5.74E-01) nor with three estimated contributors (p-value= 4.31E-01). On the other hand, even though not evident from figure 15, there is a trend for LR values computed in the EuroForMix with a threshold detection of 150 RFU to be higher than those computed with a threshold detection of 100 RFU, as supported by Chi-square test (α=0.05), in both cases with mixtures with two and three estimated contributors (p-value= 9.66E-03, for both cases).

In EuroForMix, the greatest discrepancy obtained in both cases with mixtures with two and three estimated contributors have the same order of magnitude (4.75 and

4.18 in a log_{10} scale, for the mixture/reference pairs 1793.17-2 (1) and 8356.16-8.2FF (DPMF), respectively). However, the same does not happen in the STRmix™, where the greatest discrepancy occurred in mixtures with three estimated contributors with a difference of 11.14 units in a log_{10} scale (for the mixture/reference pair 6568.17-9 (RFAS2)), a value higher than the 6.38 achieved in mixtures with two estimated contributors (for the pair 13027.17-1R2FF (1R1FF)) – table 12.

Table 12: Differences between the LR values(log_{10} scale) computed considering the threshold detection equal to 100 RFU and 150 RFU by EuroForMix v.1.9.3 [1] and STRmix™ v.2.7 for samples with two and three estimated contributors, and the maximum, mean and median values of these differences.

X = ABS [Log_{10}(LR default) – Log_{10}(LR variation)]	**Estimated Number of Contributors**			
	2 (N=79)		**3 (N=79)**	
	EuroForMix	**STRmix™**	**EuroForMix**	**STRmix™**
0 < X < 1	86%	91%	84%	87%
1 < X < 2	9%	8%	10%	8%
2 < X < 3	3%	0%	4%	1%
3 < X < 4	0%	0%	1%	1%
X > 4	3%	1%	1%	3%
Maximum	4.75	6.38	4.18	11.14
Mean	0.41	0.32	0.56	0.67
Median	0.07	0.09	0.29	0.21

As can be seen in both figure 15 and table 12, a low number of cases presents a large discrepancy between values. In mixtures with two estimated contributors, only 14% and 9% of the cases computed by EuroForMix and STRmix™, respectively, difference higher than one unit (log_{10} scale) was found. In mixtures with three estimated contributors, these percentages increased to 16% and 13%, respectively.

Focusing only on outliers, almost all of them correspond to a decrease of the global LR value when the threshold detection value increase to 150 RFU. This decrease was caused by the disregarding of some alleles that matched to the reference sample – as it happens in outliers detected in EuroForMix [1] – and/or by the new relative height of the peaks resulting from the change in the height of the alleles present in the mixture sample – as it happens in STRmix™. However, for one of them, increasing the threshold detection led to an increase of the global LR value. In this situation, no alleles matching with the reference sample were eliminated, but alleles matching with the other possible contributors of the mixture were. This resulted in a reduction of the proportion of the other mixture contributors in relation to the reference sample.

4.2.3. Impact of Drop-in

4.2.3.1. Drop-in frequency

To understand the impact that drop-in frequency may have on the global LR value, all the other parameters conditions were maintained as detailed in table 2 section 3.3.2, and two different drop-in frequency values were considered. A comparison between the default drop-in frequency value used (0.05), and the two varied values tested, namely, 0.00 and 0.10, corresponding to a null drop-in frequency value and the double of the determine default value, respectively, was performed.

The LR values (log_{10} scale) computed by EuroForMix v.1.9.3 [1] and STRmix™ v.2.7 under the both above-mentioned conditions (frequency value equal to 0.00 and 0.10) and the LR values (log_{10} scale) computed under de default conditions (frequency value equal to 0.05), for cases with mixtures with two and three estimated contributors, are illustrated in figure 16 and 17. The greatest discrepancy observed between the two compared values (greater than four units on the log_{10} scale) are highlighted and titled as "outliers" in both figures.

An example of how these values were analyzed is illustrated in Box 8.

Box 8

Illustrative example of the comparison made between LR values computed by STRmix™ considering the drop-in frequency values: 0.05 (default), 0.00 and 0.10 (varied), for the mixture/reference pair 243.17-1FM (JRA) (two estimated contributors).

Drop-in frequency		**LR**	**Log_{10}(LR)**	**Dif. = log_{10}(LR default) – log_{10}(LR variation)**	**Absolute value (Dif.)**
Default	**0.05**	3.91E+24	24.59222	-	-
Variation	**0.00**	4.43E+21	21.64622	2.94600	2.94600
	0.10	4.24E+23	23.62770	0.96452	0.96452

All LR values analyzed in this subsection are presented in tables B1, B3, B4, B6 – default drop-in frequency value considered – ($LR_{<21}$ values from tables B3 and B6 were used), B21, B22, B23, B24 – null drop-in frequency value – B25, B26, B27 and B28 – frequency value equal to 0.10 – of Appendix III.

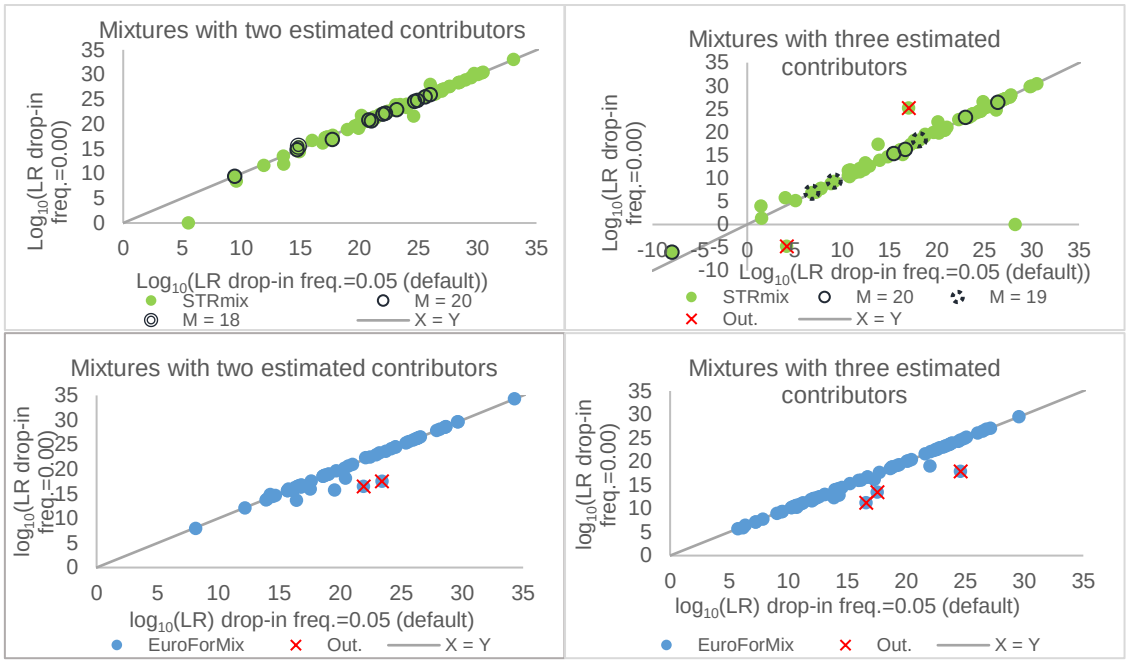


Figure 16: Values of LR (log_{10} scale) computed by STRmix™ v.2.7 in green (uppers plots) and EuroForMix v.1.9.3 [1] in blue (lowers plots) for the same mixture/reference pairs, with two (left plots) and three estimated contributors (right plots), under the conditions drop-in frequency=0.05 (default value) and drop-in frequency=0.00 (varied value). The mixture/reference pairs that are highlighted with a continuous, dashed, or double continuous line circle correspond to the cases where less than 21 markers were analyzed. The outliers, where the discrepancy between values is greater than four units in a log_{10} scale, are highlighted with an X.

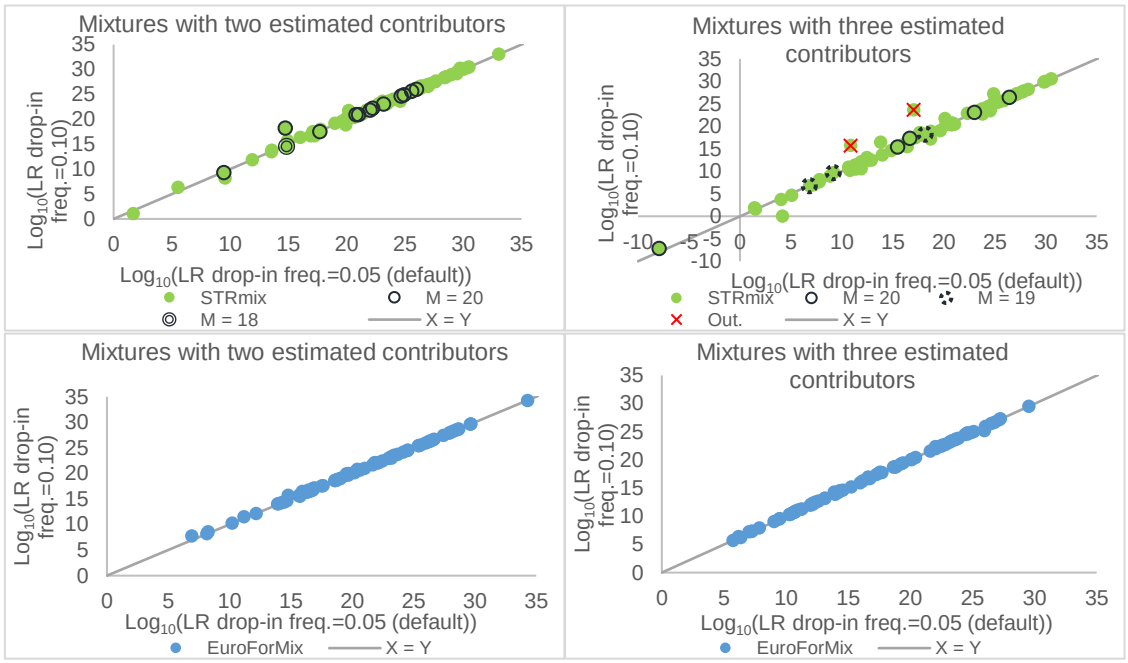


Figure 17: Values of LR (log_{10} scale) computed by STRmix™ v.2.7 in green (uppers plots) and EuroForMix v.1.9.3 [1] in blue (lowers plots) for the same mixture/reference pairs, with two (left plots) and three estimated contributors (right plots), under the conditions drop-in frequency=0.05 (default value) and drop-in frequency=0.10 (varied value). The mixture/reference pairs that are highlighted with a continuous, dashed, or double continuous line circle correspond to cases where less than 21 markers were analyzed. The outliers, where the discrepancy between values is greater than four units in a log_{10} scale, are highlighted with an X.

Analyzing both figures, it is difficult to affirm that there is a trend towards an increase or decrease in the global LR value for both new drop-in frequency conditions considered (0.00 and 0.10) comparatively to those computed under the default drop-in frequency value (0.05). The absence of a trend was supported by the chi-square test (α=0.05) in both STRmix™ and EuroForMix computations for the drop-in frequency value equal to 0.00 for both cases with mixtures with two (p-value=2.58E-01 and 1.15E-01) and three estimated contributors (p-value=4.97E-01 and 4.96E-02), respectively; and for the drop-in frequency equal to 0.10 for both cases with mixtures with two (p-value=2.16E-01 and 4.31E-01) and three estimated contributors (p-value=2.58E-01 and 5.58E-02), respectively.

In STRmix™ software, outliers were only found for cases with mixtures with three estimated contributors, under both considered conditions – drop-in frequency equal to 0.00 and 0.10. Although there was no evidence of trend to global LR values increase or decrease in either condition, in almost all outliers found, an increase on the global LR value occurred. In EuroForMix, outliers were only found when the drop-in frequency is considered null, for both cases with mixtures with two and three estimated contributors. But, contrarily to what happened in the STRmix™, a decrease on the global LR value occurred in all the found outliers.

In general, the two drop-in frequency values tested did not have a great impact on the global LR values of EuroForMix nor STRmix™ software, since the majority of the computed differences were within one unit in a $\log_{10}$ scale, as demonstrated in table 13.

Table 13: Differences between the LR values ($\log_{10}$ scale) computed considering the varied values of drop-in frequency (0.00 and 0.10) and the default value (0.05) by EuroForMix v.1.9.3 [1] and STRmix™ v.2.7 for cases with mixtures with two and three estimated contributors.

X = ABS [$\log_{10}$(LR default) – $\log_{10}$(LR variation)]	**Estimated Number of Contributors**							
	2				**3**			
	EuroForMix		**STRmix™**		**EuroForMix**		**STRmix™**	
	0.00 (N=58)	**0.10 (N=79)**	**0.00 (N=78)**	**0.10 (N=79)**	**0.00 (N=75)**	**0.10 (N=79)**	**0.00 (N=78)**	**0.10 (N=78)**
0 < X < 1	90%	100%	92%	95%	91%	100%	85%	88%
1 < X < 2	2%	0%	4%	4%	4%	0%	9%	6%
2 < X < 3	3%	0%	4%	0%	1%	0%	3%	3%
3 < X < 4	2%	0%	0%	1%	0%	0%	1%	0%
X > 4	3%	0%	0%	0%	4%	0%	3%	3%
Maximum	5.89	0.96	2.95	3.48	6.71	0.76	8.90	6.63
Mean	0.42	0.10	0.31	0.26	0.31	0.09	0.60	0.50
Median	0.02	0.01	0.09	0.09	0.06	0.05	0.16	0.17

Comparing all the computed differences analyzed in this sub-section (figure 16, 17 and table 13), is clear that this parameter has a different impact in both software. The impact cannot be only measured by the percentage of outliers found in each software, but also by the percentage of mixture/reference pairs for which no comparisons were performed.

In STRmix™ software, for 1% of the situations computed for a null drop-in frequency, in both cases with mixtures with two and three estimated contributors, a null LR value was obtained, and no comparison was made. The same happened for 1% of the cases with mixtures with two estimated contributors when a drop-in frequency value of 0.10 was considered.

In EuroForMix software, when the null drop-in frequency was used, in 27% and 5% of cases with mixtures with two and three estimated contributors, respectively, no comparison was performed. The software did not compute any LR value for these cases and the following error message appeared instead “The specified model could not explain the data”.

When the drop-in frequency was considered null, the probability of drop-in peak being treated by both software as true peak alleles increases. In some mixture/reference pairs’ markers, the maximum number of peaks may have been exceeded considering the number of contributors defined. Even when the number of peaks has not been exceeded, the software can infer, based on the relative height of the peaks, that more alleles are presented than would be expected, taking into account the number of contributors in question. Both situations resulted in either a computation of null LR values – as happened in STRmix™ – or not computing a value at all – as in EuroForMix.

On the opposite side, when the drop-in frequency value was doubled, leaded to an increase in the probability of some peaks being considered drop-in. Those peaks may belong to either the reference sample under analysis – resulting in a decrease on the global LR value – or to another contributor present in the mixture – increase the global LR value of the reference under analysis, as verified in STRmix™ software computations.

That said, it can be concluded that drop-in frequency parameter had a bigger impact in EuroForMix software than in STRmix™ when a null drop-in frequency is considered. Contrarily to what happens when doubling the drop-in frequency, where STRmix™ shows to be more sensitive to variation than EuroForMix.

4.2.3.2. Drop-in parameters' distribution

In both software drop-in modelling relies on statistical distributions which, besides frequency, depend on other parameters. However, it should be noted that, even though both software under analysis are quantitative, the drop-in modeling is computed differently. In EuroForMix the drop-in is modelled using a Lambda distribution (λ) while, in STRmix™ it is used either a Gamma (ɣ) or a Uniform distribution, as mentioned in section 3.3.2.

So, to understand the impact that drop-in parameters' distribution may have on the global LR value, the default value (λ=0.01 for EuroForMix [1] and ɣ=(0.1,0.1) for STRmix™) and a varied value (λ=0.05 [1] and Uniform, respectively) were considered and compared in both software (figure 18). The other parameters conditions were maintained as detailed in table 2 of section 3.3.2.

As before, greater discrepancies between the two computed values (greater than four units on the $\log_{10}$ scale) are designated as "outliers" and highlighted in the figure.

An example of how these values were analyzed is illustrated in Box 9.

Box 9

Illustrative example of the comparison made between LR value computed by STRmix™ considering the default and the varied drop-in parameters' distribution value, for the mixture/ reference pair 20601.16-1 (AMM) (two estimated contributors).

Drop-in parameters' distribution	LR	Log_{10}(LR)	Dif. = $\log_{10}$(LR default) – $\log_{10}$(LR variation)	Absolute value (Dif.)
Gamma (0.1, 0.1) (default)	1.51E+20	20.17898	-1.42937	1.42937
Uniform (variation)	4.06E+21	21.60834		

All LR values analyzed in this subsection are presented in tables B1, B3, B4, B6 – default drop-in parameters' distribution values – ($LR_{<21}$ values from tables B3 and B6 were used), B17, B19 – EuroForMix λ varied value – B18 and B20 – STRmix™ Uniform distribution (variation) – of Appendix III.

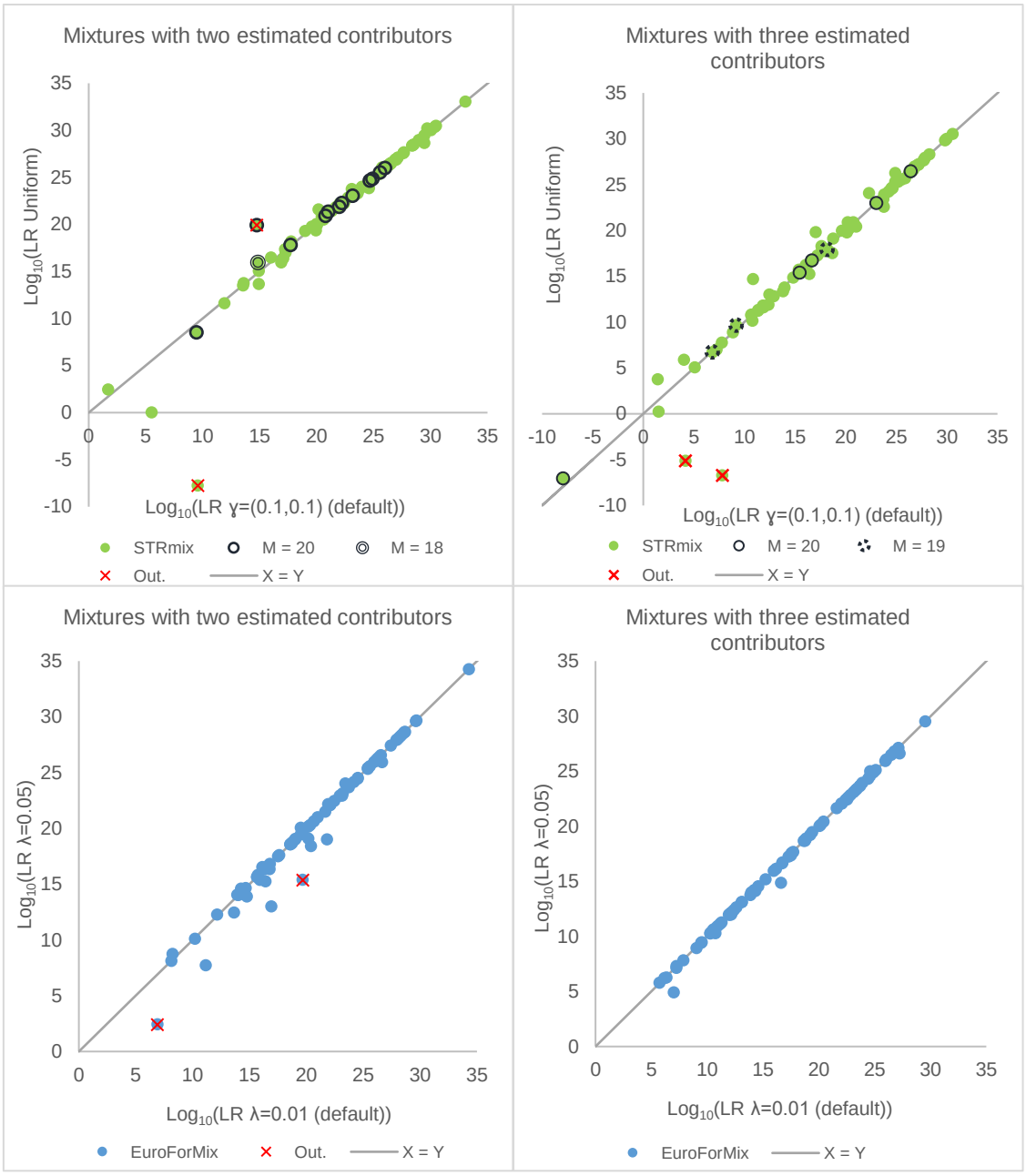


Figure 18: Values of LR (log_{10} scale) computed for the same mixture/reference pairs, with two (left plots) and three estimated contributors (right plots) in STRmix™ v.2.7 (in green – uppers plots) under the conditions γ=(0.1,0.1) (default) and Uniform (varied); and in EuroForMix v.1.9.3 [1] (in blue – lowers plots) under the conditions of λ=0.01 (default value) and λ=0.05 (varied value). The mixture/reference pairs that are highlighted with a continuous, dashed, or double continuous line circle correspond to the cases where less than 21 markers were analyzed. The outliers, where the discrepancy between values is greater than four units in a log_{10} scale, are highlighted with a X.

As confirmed by the chi-square test (α=0.05), there is no evidence of trend to an increase or decrease of the global LR value in either STRmix™ or EuroForMix software, for both cases with mixtures with two (p-value=3.11E-01 and 4.97E-01) and three estimated contributors (p-value=3.25E-02 and 7.36E-01), respectively.

Coincidentally, almost all outliers – computed differences greater than four units in a log_{10} scale – correspond to mixture/reference pairs where a decrease in the global LR value occurred. In fact, in STRmix™ outliers the LR drooped to values bellow one. Probably a consequence of unattributed peaks that could no longer be explained by drop-in.

The computed differences between the default and the varied value, in STRmix™ and EuroForMix software, for both cases with mixtures with two and three estimated contributors, were explored in more detail in table 14.

Table 14: Differences between the LR values (log_{10} scale) computed in EuroForMix v.1.9.3 [1] under the default and varied drop-in parameters' distribution condition (λ=0.01 and 0.05, respectively) and in STRmix™ v.2.7 under the default and varied condition (ɣ=(0.1,0.1) and Uniform, respectively), for samples with two and three estimated contributors. The maximum, mean and median values of these differences are also presented.

X = ABS [Log_{10}(LR default) – Log_{10}(LR variation)]	**Estimated Number of Contributors**			
	2		**3**	
	EuroForMix (N=79)	**STRmix™ (N=78)**	**EuroForMix (N=79)**	**STRmix™ (N=79)**
0 < X < 1	89%	94%	97%	85%
1 < X < 2	5%	4%	1%	9%
2 < X < 3	1%	0%	1%	3%
3 < X < 4	3%	0%	0%	1%
X > 4	3%	3%	0%	3%
Maximum	4.49	17.33	2.09	14.54
Mean	0.39	0.50	0.10	0.70
Median	0.02	0.09	0.03	0.15

Although this table reinforce the information already seen in figure 18, it also allows to understand that, even though most of the computed differences were within one unit in a log_{10} scale, both software registered cases with computed differences greater than four units. In both cases with mixtures with two and three estimated contributors, the maximum computed differences were much bigger for STRmix™ values (17.33 units in a log_{10} scale for the mixture/reference pair 13027.17-1R2FF (1R1FF) and 14.54 units for the pair 8410.16-2R1 (2R2), respectively) than those computed for EuroForMix values (4.49 units for the mixture (with two estimated contributor)/reference pair 19799.17-1 (TFPA1)). This reflects a greater sensitivity in the STRmix™ software.

4.2.4. Impact of Co-ancestry coefficient (F_{ST})

The impact that co-ancestry coefficient (F_{ST}) parameter may have on the LR value, was evaluated through the comparison between the default value (0.010) and three varied values (0.000, 0.015 and 0.030), for both cases with mixtures with two and three estimated contributors in EuroForMix v.1.9.3 [1] and STRmix™ v.2.7 software (figure 19).

An example of how these values were analyzed is illustrated in Box 10.

Box 10

Illustrative example of the comparison made between LR value computed by STRmix™ considering the F_{ST} values: 0.010 (default), 0.000, 0.015 and 0.030 (varied), for the mixture/reference pair 243.17-1FM (JRA) (two estimated contributors).

F_{ST}		LR	Log_{10}(LR)	Dif. = log_{10}(LR default) – log_{10}(LR variation)	Absolute value (Dif.)
Default	0.010	5.83E+17	17.76574	-	-
Variation	0.000	1.51E+20	20.18013	-2.41438	2.41438
	0.015	7.65E+16	16.88364	0.88210	0.88210
	0.030	4.05E+15	15.60706	2.15868	2.15868

All LR values analyzed in this section are presented in tables B1, B3, B4, B6, – default value – ($LR_{<21}$ values from tables B3 and B6 were used), B29, B30, B31, B32 – null F_{ST} value –, B33, B34, B35, B36 – F_{ST} equal to 0.015 – B37, B38, B39 and B40 – F_{ST} equal to 0.030 – of Appendix III.

Through the figure 19 analysis, and as expected for cases where the hypothesis of the individual being a mixture contributor is supporting, an inverse proportional relationship between the F_{ST} and LR values is verified in both software. Increasing the F_{ST} value resulted in a decrease of the global LR value.

This trend was confirmed by Chi-square test (α=0.05) for STRmix™, for the comparisons between the F_{ST} values 0.000 and 0.010; 0.015 and 0.010; 0.030 and 0.010; and 0.015 and 0.030, in both cases with mixtures with two (p-value= 1.26E-17; 3.75E-15; 7.61E-18 and 5.91E-16, respectively) and three estimated contributors (p-value= 4.77E-14; 2.48E-09; 4.77E-14 and 1.36E-12, respectively). For EuroForMix computed values, the Chi-square test (α=0.05) also proved this trend (p-value= 6.21E-19) for all the considered comparisons.

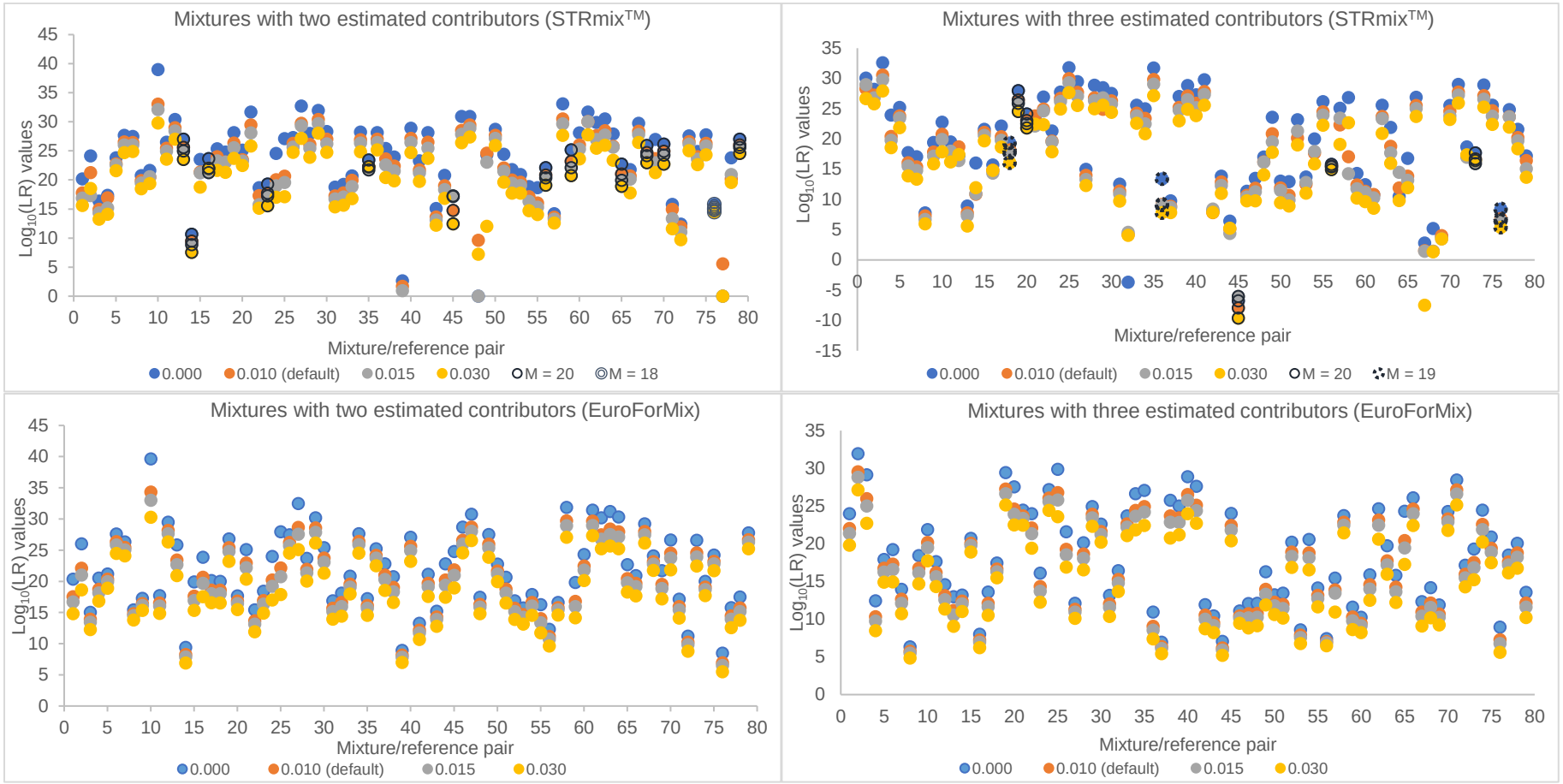


Figure 19: Values of LR (log_{10} scale) computed for the same mixture/reference sample pairs, with two (left plots) and three estimated contributors (right plots) in STRmix™ v.2.7 (uppers plots) and in EuroForMix v.1.9.3 [1] (lowers plots) for the F_{ST} default value (0.010) and all F_{ST} varied values considered (0.000, 0.015 and 0.030). Each group of four vertically placed dots concerns the analysis of the same mixture/reference sample pair. The mixture/reference pairs that are highlighted with a continuous, dashed, or double continuous line circle correspond to the cases where less than 21 markers were analyzed.

The obtained results were congruent with the expected results. The higher the value of the F_{ST} parameter, greater the probability of a matched allele between the problem mixture and the reference sample under analysis being an IBD allele, i.e., an allele shared through identity by descent from a common ancestor, resulting in lower LR values, as observed in figure 19. In order to better understand these values, a summary of the computed differences between the default and varied values for STRmix™ and EuroForMix, for both cases with mixtures with two and three estimated contributors, is presented in table 15.

Table 15: Differences between the LR values (log_{10} scale) computed considering the varied F_{ST} values (0.000, 0.015 and 0.030) and the default F_{ST} value (0.010) by EuroForMix v.1.9.3 [1] and STRmix™ v.2.7 for cases with mixtures with two and three estimated contributors.

X = ABS [Log_{10}(LR default=0.010) – Log_{10}(LR variation)]	EuroForMix			STRmix™		
	0.000 (N=79)	0.015 (N=79)	0.030 (N=79)	0.000 (N=77)	0.015 (N=77)	0.030 (N=78)
Two estimated contributors						
0 < X < 1	15%	94%	0%	16%	82%	6%
1 < X < 2	54%	6%	49%	60%	16%	33%
2 < X < 3	22%	0%	43%	18%	1%	50%
3 < X < 4	6%	0%	5%	3%	1%	9%
X > 4	3%	0%	3%	4%	0%	1%
Maximum	5.81	1.39	4.24	6.48	3.94	12.57
Mean	1.76	0.61	2.08	1.72	0.74	2.25
Median	1.49	0.58	2.01	1.49	0.63	2.16
Three estimated contributors						
	(N=79)	(N=79)	(N=79)	(N=79)	(N=79)	(N=79)
0 < X < 1	24%	99%	6%	20%	86%	14%
1 < X < 2	57%	1%	52%	57%	10%	48%
2 < X < 3	15%	0%	38%	11%	4%	33%
3 < X < 4	4%	0%	4%	6%	0%	3%
X > 4	0%	0%	0%	5%	0%	3%
Maximum	3.86	1.01	3.25	9.76	2.81	9.03
Mean	1.51	0.55	1.88	1.79	0.66	1.86
Median	1.45	0.55	1.86	1.49	0.55	1.83

Combining both figure 19 and table 15 information, namely, data distribution, percentages of computed differences and the maximum difference values achieved, at first glance the impact of the F_{ST} parameter it seems to be similar in both software. However, there are some factors that may indicate a slightly higher sensitivity to F_{ST} by the STRmix™ software such as higher percentages of cases in which a difference greater than four units in a log_{10} scale was computed, associated with higher maximum difference values reached.

4.2.5. Impact of stutters in EuroForMix

A stutter peak is the most common profile artifact. Their identification and possible elimination during the epg analysis is of expert's choice and responsibility.

Contrarily to STRmix™ V.2.7, which requires the consideration of stutters in the sample profiling, in EuroForMix v.1.9.3 stutters can be, or not, considered in the analysis. To evaluate the impact that stutters may have on the global LR value, LR values (log_{10} scale) considering a set of markers were computed in EuroForMix for each mixture (with two or three estimated contributors) /reference pair, assuming the presence and absence of stutters [1]. For each analyzed pair, both LR values were compared as illustrated in Box 11. Results are shown in figure 20; the greatest discrepancies observed between the two compared values (greater than four units on the log_{10} scale) are highlighted and titled as "outliers".

Box 11

Illustrative example of the comparison made between LR value computed with and without stutters by EuroForMix software for the mixture/reference pair 3053.17-3.1R2 (EAD1) (two estimated contributors).

Stutters	LR	Log_{10}(LR)	Dif. = log_{10}(LR with) – log_{10}(LR without)	Absolute value (Dif.)
With	8.69E+15	15.93881	2.28959	2.28959
Without	4.46E+13	13.64922		

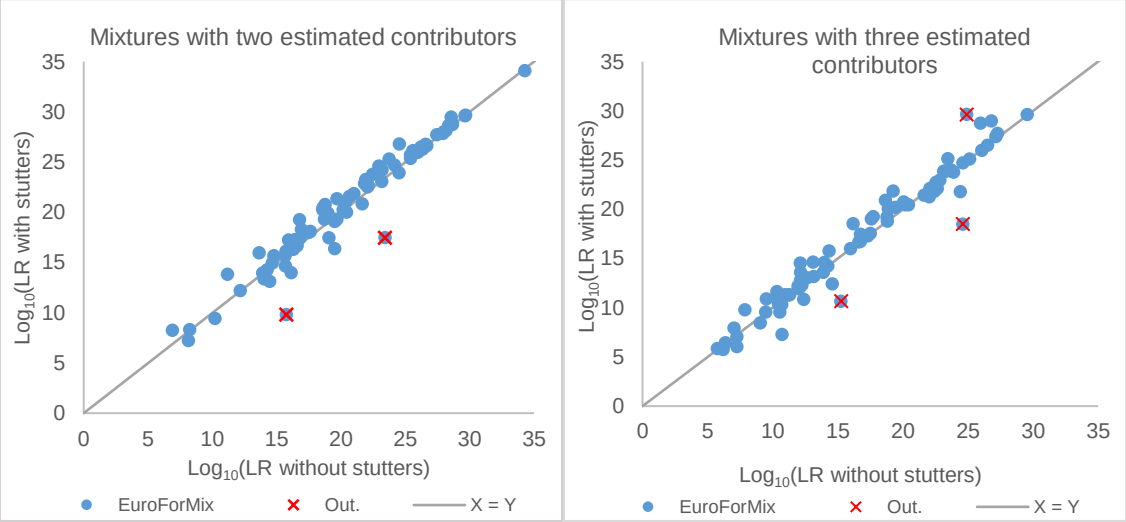


Figure 20: Values of LR (log_{10} scale) computed in EuroForMix v.1.9.3 without (x axis) and with stutters [1] (y axis), for the same mixture /reference samples pair, with two (left plot) and three estimated contributors (right plot). The outliers (Out.) are highlighted with an X representing the biggest discrepancy between analyzes (greater than four units in a log_{10} scale).

The LR values analyzed in this section were computed under the default conditions for all the other parameters (table 2 of section 3.3.2.) and are presented in tables B1, B2, B4 and B5 (LR_{21} values from tables B2 and B5 were used) of Appendix III.

From figure 20 it seems that the LR values obtained with stutters tend to be higher than those without. This trend is supported by Chi-square test (α=0.05) in both cases with mixtures with two (p-value = 1.10E-03) and three estimated contributors (p-value = 2.38E-03).

In section 4.1.1. was shown that for the cases with mixtures with a lower number of contributors a higher LR value was computed. This trend was also verified when stutters are not considered, as supported through a t-test (α=0.05, p-value=5.09E-04), for cases with mixtures with two and three estimated contributors.

Table 16: Proportion of differences between the LR values (log_{10} scale) computed in EuroForMix v.1.9.3 with and without stutters [1], for samples with two and three estimated contributors. The maximum, mean and median values of these differences are also presented.

X = ABS [Log_{10}(LR with stutters) – Log_{10}(LR without stutters)]	**Estimated Number of Contributors**	
	2 (N=79)	**3 (N=79)**
0 < X < 1	70%	70%
1 < X < 2	20%	15%
2 < X < 3	6%	10%
3 < X < 4	1%	1%
X > 4	3%	4%
Maximum	5.96	6.12
Mean	0.87	0.91
Median	0.53	0.46

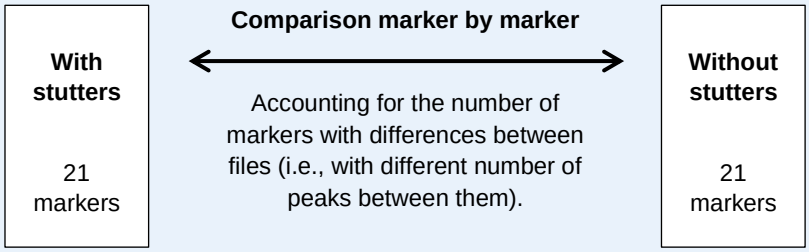
As shown in table 16, 70% of the cases did not reach differences greater than one unit (log_{10} scale) in both cases with mixtures with two and three estimated contributors. Nevertheless, in 3% and 4%, respectively, differences with more than four units were computed, reaching the maximum value of 5.96 units in mixtures with two (for the mixture/reference pair 1816.17-2FF (SC1)) and 6.12 units in mixtures with three estimated contributors (for the mixture/reference pair 4548.16-PC9.9 (PC9.8)). Those mixture/reference pairs that achieved a difference higher than four units (log_{10} scale) were flagged and titled outliers in figure 20.

This comparison allows us to assume that the inclusion of stutters may have a strong impact on the global LR value.

In order to understand if there is a correlation between the differences observed in figure 20 and the number of markers presenting differences between both analyzes (with and without stutters), a thorough analysis of the two .txt files (with and without stutters) of each mixture/reference pair was made and the number of markers with different number of peaks was registered, as illustrated in Box 12. Then, a correspondence between the differences obtained for the global LR value and the number of markers containing changes between .txt files, for each mixture/reference pair, in both cases with mixtures with two and three estimated contributors, was performed and analyzed (figure 21).

Box 12

Illustrative example of the comparison made between .txt files used for the EuroForMix LR value computation, with and without stutters, for the mixture/reference pair 1087.17-4 (PMCC1) (two estimated contributors):



In this mixture/reference pair, only one marker (D7S820) shows differences between the .txt files used to calculate the global LR values, and so, it is illustrated below (peaks heights in parentheses):

- Mixture with stutters: **27** (103), **28** (1058), **29** (783), **30** (120), **32.2** (380)
- Mixture without stutters: **28** (1058), **29** (783), **30** (120), **32.2** (380)

For this pair of samples, the difference between the global LRs equated 0.63520 ($\log_{10}$ scale), and therefore this case is represented by the point with the coordinates (20.33567, 20.97087) in figure 21.

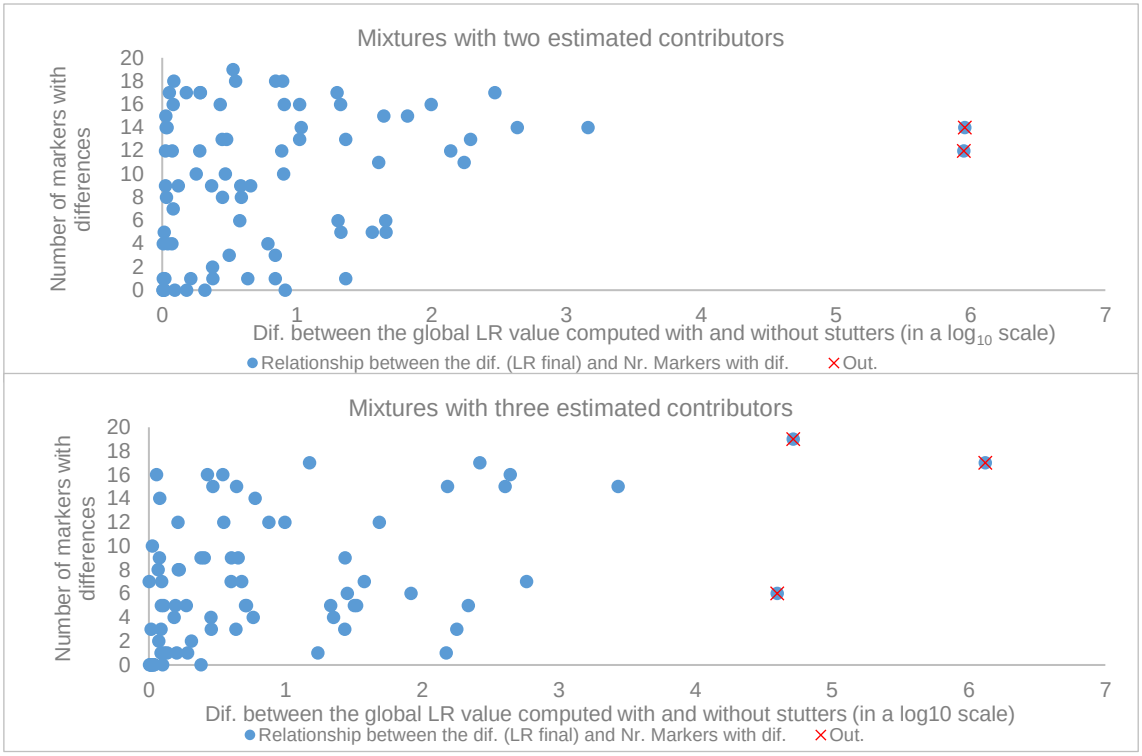


Figure 21: Comparison between the number of markers that presented modifications between the analysis with and without stutters (x axis) and the differences found for LRs values (in a log_{10} scale) computed in EuroForMix with and without stutters (y axis), for the same mixture sample/reference sample pair, with two (upper plot) and three estimated contributors (lower plot).The outliers (Out.) highlighted in figure 20 are also highlighted in this figure with an X.

Considering the data dispersion in figure 21, it seems that there is no direct relationship between the differences computed for the global LR values and the number of markers containing variations between the analyzes with and without stutters.

Although, in mixtures with two estimated contributors, outliers do have a high number of markers with differences, it is in a mixture/reference pair in in which the difference computed did not exceed one unit on the log_{10} scale that the maximum number of markers with differences is reached (19 out of 21). On the other hand, one of the three outliers in mixtures with three estimated contributors presents a low number of markers with differences between the two analyzes (6 out of 21).

This allows to conclude that the presence of a high number of markers with differences does not necessarily lead to a great discrepancy between the two analyzes for the mixture/reference pairs in question. Indeed, a balance between the differences computed for the markers that presented differences between .txt files (with and without stutters) may occur, i.e., for example, in one marker the computed LR value is greater for the analysis with stutters, while in another marker the computed LR value is greater for the analysis without stutters, resulting in a situation with a high number of markers with differences but with a low difference when considering a global LR value.

5. Conclusions

The interpretation of the biological evidence is currently part of the routine of criminal investigations and legal proceedings, being increasingly crucial in trials. Therefore, an extreme caution is required in this forensic field, especially when interpreting complex DNA mixture profiles from samples collected at crime scenes.

After the samples processing – DNA extraction and purification; DNA quantification; DNA amplification; STR separation and detection; and STR genotyping – the STR profile is interpreted by the expert through the epg analysis. At this stage, two crucial decisions are made for profiling analysis in the software, namely, it is decided about the presence of not allelic peaks (artifacts or stochastic effects), as well as the estimation of the number of contributors of the mixture. Lastly, the weight of the DNA evidence (constituted by the mixture sample and the corresponding reference) is quantified through a LR value computed in a statistical analysis software. For this end, since quantitative model's software consider more information of the epg than qualitative ones, they are considered more efficient and therefore the preferred approach to perform this analysis, as already mentioned throughout this dissertation.

In this work we considered two quantitative software: STRmix™ v.2.7 and EuroForMix v.1.9.3. To statistically evaluate the genetic evidence, these programs model the peak height information (peaks alleles, allele drop-in, allele drop-out, peak balance and stutter peaks) and incorporate the F_{ST}-correction. For that, several parameters are considered, whose values are or can be entered by the user. So, it is fundamental to understand the impact that these software parameters can have on the global LR value computation. In this project were analyzed the estimation of the number of contributors, threshold detection, drop-in, co-ancestry coefficient (F_{ST}) and presence/absence of stutters. LR values were computed in both programs under the previously established default and varied conditions [1], varying a single parameter at a time, for each real casework mixture/reference pairs with two and three estimated contributors.

The first approach was to compare the two software under the default parameter conditions. Since STRmix™ software required the inclusion of the stutters in the mixture sample files, they were also included in the EuroForMix analysis. Generally, STRmix™ values showed to be higher than those computed by EuroForMix. It was also verified that the accumulation of small differences in the LR of each marker resulted in substantial discrepancies in the global LR. Indeed, 13% and 17% of the cases with mixtures with two and three estimated contributors, respectively, presented differences of more than

six units (log_{10} scale) after the total set markers was analyzed. At this point, it is noteworthy that the proportion of cases in these conditions were not greater because for the same mixture/reference pair there were markers where the LR was greater when computed with STRmix™ than when EuroForMix was used, occurring the opposite situation for others. This resulted in smoother global LR differences. Nevertheless, and as expected, the found differences were smaller than those observed when a qualitative and a quantitative models were compared - 46% and 53% of cases with mixtures with two and three estimated contributors, respectively, showed differences greater than six units (log_{10} scale) [1].

In both STRmix™ and EuroForMix, the LR values computed for cases with mixtures with two estimated contributors were higher compared to the computed for cases with mixtures with three. This trend was also verified when no stutters were considered.

Focusing on the presence/absence of stutters (only measured in EuroForMix), computed LR values showed to be higher when stutters were considered. Differences greater than four units (log_{10} scale) were found in both cases with mixtures with two (3%) and three (4%) estimated contributors.

A trend was also verified when different values for the F_{ST} parameter were analyzed. In this parameter variation, differences greater than four units (log_{10} scale) were observed, reaching a maximum proportion of cases (5%) for a null F_{ST} value in STRmix™ computation. In both software, the increase in the F_{ST} value resulted in a decrease of the computed global LR value, as expected for cases where the hypothesis of the individual being a mixture contributor is supporting. That is, the higher the F_{ST} value, the higher the probability of a matched allele between the problem and the reference sample being an allele shared through identity by descent from a common ancestor, resulting in lower LR values.

On the opposite side, no trend was showed when the drop-in values were varied (in both frequency and distribution), neither in STRmix™ nor in EuroForMix software. However, discrepancies greater than four units (log_{10} scale) were also verified, varying between 0% and 4% when the frequency value was tested, and between 0% and 3% when the distribution condition was varied.

In the threshold detection parameter, only a trend was observed for the LR values computed in EuroForMix. Considering the analyzed data, when the threshold detection was increased from 100 RFU to 150 RFU, the EuroForMix values decreased. The

proportion of cases where the global LR differs in more than four units (log_{10} scale) varied between 1% and 3%, in both software.

When the computed LR values were compared the variation of these parameters revealed a lower impact than the one obtained for under- and overestimation of the number of contributors. Nevertheless, the proportion of mixture/reference pairs which differed in more than four units (log_{10} scale) and the modest dataset size (79 mixture/reference pair with two and 79 with three estimated contributors) show that the impact of these parameters on the weight of the evidence should not be overlooked.

Undeniably, the variation of the estimate of the number of contributors reflected a greater impact on the global LR value. When the number of contributors was overestimated (i.e. considered three and four contributors in mixtures for which two and three contributors were estimated, respectively), software showed opposite trends. In STRmix™ a trend for the global LR value decreasing was verified and discrepancies greater than four units (log_{10} scale) between LR values were found, in both cases with mixtures with two (5%) and three initially estimated contributors (11%). On the other hand, in EuroForMix, only discrepancies lower than four units (log_{10} scale) were observed, global LR values increasing for cases with two initially estimated contributors. When underestimation was considered (i.e. mixtures with three estimated contributors analyzed assuming two), a greater impact was verified in EuroForMix computations than in case of overestimation - 16% of the cases showing differences greater than four units (log_{10} scale). It was also observed a trend for global LR values decreasing. However, in both conditions (over- and underestimation of the number of contributors) a greater sensitivity was evident in the STRmix™ software compared to EuroForMix. Indeed, STRmix™ showed greater proportion of cases differing in more than four units (log_{10} scale) when overestimating the number of contributors; and retrieved null LR values (14%) or didn't proceed with the computations claiming incongruence between profiles, parameter values and number of contributors, in several cases (73%) when the number of contributors was underestimated. The variation of this parameter was, without a doubt, the one that had the greatest impact in both software.

So, even though software based on probabilistic genotyping methods are a useful tool in the interpretation of complex DNA mixture profiles, it should be remembered that they are only a tool to assist the expert's assessment of this type of profiles. The expert will always have a crucial and irreplaceable role in the profile interpretation process, from the mixture sample epg analysis (decisions about the presence of non-allelic peaks and estimation of the number of contributors) to the evaluation of computed LR value. This

work also shows the pertinence of validating software for forensic use either by the developer and the user.

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Appendices

Appendix I: STRmix™ v.2.7 Implementation

As already referred in sub-chapter 3.1., the parameters values determined in the implementation phase were not used in the context of this dissertation.

Empirical observations suggest that the analytical threshold, expected stutter ratios, saturation limit of CE instruments and variance prior distributions do not substantially differ between laboratories using the same multiplex kit(s), Polymerase Chain Reaction (PCR) protocol and CE instruments. This supports the use of the same parameter values in laboratories operating under the same conditions [1].

1.1. Analytical/Detection Threshold(s)

The analytical/detection threshold is defined by the value from which a true DNA signal is distinguished from a noise signal, which must be the same as that used in the software from which the samples are exported.

In this case, the value considered is 100 RFU, since it is the value used in GeneMapper™ ID-X, software from which the laboratory exports the sample files.

1.2. Expected Stutter Ratios

As mentioned earlier, it is not expected that the value of the expected stutter ratios differs substantially between laboratories using the same kits and the same PCR conditions, namely, the number of cycles [1, 2].

In STRmix™ v.2.7 root directory exists a Stutters sub-folder with Excel files containing expected stutter ratios for different combination of kits and CE instruments. So, no calculations were performed for this parameter, and values concerning the kit and the CE instrument currently used by the LPC-PJ (GlobalFiler and 3500, respectively) were considered.

1.3. Drop-in Parameters

For each set of analyzed samples, an additional tube not containing any type of biological sample (negative control) followed the same procedure as the tubes with the samples, allowing the verification of a possible contamination. However, in some cases, appear an additional allelic component in the electropherogram, a no-reproducible and unexplained peak, called drop-in allele.

Drop-in parameters are dependent on PCR conditions, namely, the number of cycles. However, unlike the other parameters, they need to be defined specifically for each laboratory [1].

For this purpose, all the negative controls of the existing projects in GeneMapper™ ID-X were analyzed, making a total of 2,507 loci in which two drop-in events were found with heights of 104 and 110 RFU.

These values were then inserted into an Excel sheet provided on the software support website, shared in the STRmix™ v.2.7 implementation and validation guide. The following values for the drop-in parameters were calculated:

- Drop-in cap: 100;
- Drop-in frequency: 0.0008.

1.4. CE instrument's saturation limit

Saturation of CE instruments may depend on the CE model and not exactly on the laboratory, therefore, it was considered the commonly observed value for 3500 instruments (currently used by the LPC-PJ) of 30,000 RFU [1].

1.5. LSAE, allele and stutter peak height variance prior distributions

As mentioned initially, the same values of different parameters can be used by different laboratories working according to the same requirements.

For these parameters, no calculations were made, and the values shown in the table provided in the STRmix™ Operational Manual v.2.7 were used, namely:

- Allele Variance (mode): 6.636, 1.520 (10.538);
- Stutter Variance k2 (mode): 3.371, 5.783 (13.711);
- Forward Stutter k2 (mode): 3.521, 2.221 (5.599);
- (0, -2) Stutter k2 (mode): 1.578, 1.150 (0.665);
- (-2, 0) Stutter k2 (mode): 3.490, 5.165 (12.861);
- LSAE mean: 0.0055.

1.6. Parameters for the relevant population including allele frequencies and theta (F_{ST}) value

Regarding to the population allele frequencies database, it was necessary to create and add a new one to the list already existing in STRmix™ v.2.7, with the allele frequencies used by the laboratory provided in Appendix II (table A1).

Another parameter related to the population was the establishment of the population size and number of children per family. To ensure a more conservative LR value, the STRmix™ manufacturer advised that the value attributed to the population size must be inferior to the real one and the number of children per family superior. So, the values of 10,100,000 individuals (inferior to 10,276,617 [3]) and two children per family (superior to 1.41 [4]) were assigned.

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Appendix II: Population Allele Frequency Database

Table A1: Allele frequency of 21 autosomal markers in the National Institute of Standards and Technology (NIST) database for the Caucasian population.

Allele	CSF1PO	D10S1248	D12S391	D13S317	D16S539	D18S51	D19S433	D1S1656	D21S11	D22S1045	D2S1338	D2S441	D3S1358	D5S818	D7S820	D8S1179	FGA	SE33	TH01	TPOX	vWA
5																			0.001385042	0.001385042	
6																			0.235457064	0.001385042	
6.3																					
7														0.002770083	0.027700831				0.193905817		
8	0.005540166			0.120498615	0.01800554									0.005540166	0.144044321	0.013850416			0.095567867	0.524930748	
8.1															0.001385042						
9	0.013850416			0.077562327	0.106648199							0.001385042		0.041551247	0.167590028	0.005540166			0.119113573	0.127423823	
9.1												0.001385042									
9.3																			0.344875346		
10	0.220221607			0.047091413	0.056786704	0.008310249	0.001385042	0.002770083				0.210526316		0.055401662	0.256232687	0.102493075			0.008310249	0.049861496	
10.1																					
10.2																					
10.3																					
11	0.308864266	0.001385042		0.325484765	0.314404432	0.009695291	0.005540166	0.077562327		0.139889197		0.343490305	0.001385042	0.355955679	0.20498615	0.076177285		0.001385042	0.001385042	0.252077562	
11.2																					
11.3												0.060941828									
12	0.360110803	0.031855956		0.268698061	0.314404432	0.113573407	0.070637119	0.11634349		0.012465374		0.047091413		0.387811634	0.159279778	0.167590028		0.006925208		0.041551247	0.001385042
12.2							0.001385042														
12.3												0.004155125									
13	0.081717452	0.307479224		0.11634349	0.163434903	0.123268698	0.254847645	0.066481994		0.006925208		0.029085873	0.001385042	0.14265928	0.034626039	0.329639889		0.016620499		0.001385042	0.001385042
13.2							0.006925208														
13.3																					
13.4																					
14	0.009695291	0.297783934		0.042936288	0.026315789	0.13434903	0.361495845	0.078947368		0.056786704		0.24099723	0.106648199	0.006925208	0.004155125	0.166204986		0.024930748			0.092797784
14.2						0.001385042	0.023545706											0.002770083			
14.3								0.002770083													
15		0.1966759	0.031855956	0.001385042		0.170360111	0.156509695	0.149584488		0.32132964	0.001385042	0.059556787	0.272853186	0.001385042		0.103878116		0.040166205			0.105263158
15.2							0.03601108														
15.3								0.058171745													
15.4																					
16		0.132963989	0.022160665			0.146814404	0.056786704	0.135734072		0.382271468	0.037396122	0.001385042	0.238227147			0.033240997		0.040166205			0.200831025
16.2						0.001385042	0.015235457											0.001385042			
16.3								0.060941828													
17		0.027700831	0.127423823			0.138504155	0.006925208	0.047091413		0.074792244	0.185595568		0.210526316			0.001385042		0.06232687			0.283933518
17.1																					
17.2							0.001385042														
17.3			0.020775623					0.132963989										0.001385042			
18		0.001385042	0.171745152			0.077562327		0.005540166		0.005540166	0.073407202		0.150969529				0.024930748	0.072022161			0.202216066
18.1																					
18.2							0.001385042														
18.3			0.024930748					0.049861496										0.001385042			
19		0.002770083	0.12465374			0.040166205					0.120498615		0.016620499				0.049861496	0.072022161			0.103878116
19.1																					
19.2																		0.004155125			
19.3			0.004155125					0.015235457													
19.4																					

20	0.110803324	0.01800554	0.156509695	0.001385042	0.123268698	0.058171745	0.006925208
20.1							
20.2						0.009695291	
20.3							
21	0.128808864	0.009695291	0.037396122		0.17867036	0.024930748	0.001385042
21.2					0.005540166	0.023545706	
21.3							
22	0.095567867	0.006925208	0.034626039		0.20498615	0.013850416	
22.2					0.012465374	0.037396122	
22.3							
23	0.069252078		0.105263158		0.152354571	0.002770083	
23.2					0.002770083	0.03601108	
23.3							
24	0.047091413		0.114958449		0.13434903	0.001385042	
24.2					0.001385042	0.022160665	
24.3							
25	0.016620499		0.102493075		0.078947368		
25.2		0.001385042				0.041551247	
26	0.002770083		0.030470914		0.026315789		
26.2						0.041551247	
27	0.001385042	0.022160665			0.004155125		
27.2						0.094182825	
27.3							
28		0.159279778					
28.2						0.076177285	
28.3						0.001385042	
29		0.202216066					
29.2		0.002770083				0.055401662	
29.3							
30		0.282548476					
30.2		0.029085873				0.056786704	
30.3							
31		0.072022161				0.002770083	
31.2		0.09833795				0.023545706	
32		0.005540166				0.001385042	
32.2		0.090027701				0.012465374	
33		0.001385042				0.001385042	
33.1							
33.2		0.026315789				0.004155125	
34						0.008310249	
34.2		0.004155125				0.001385042	
35		0.001385042					
36		0.001385042					

Appendix III: Log_{10} of LR Values Computed by EuroForMix v.1.9.3 and STRmix™ v.2.7

Table B1: Log_{10} values of the global LRs computed by EuroForMix v.1.9.3 without stutters[1], for mixtures with two estimated contributors.

Mixture (Reference)	Log_{10} (LR)
243.17-1FM (JRA)	17.5242783396992
243.17-1FM (MM)	22.0784630573999
913.17-1.3 (ASML1)	13.9205724472488
913.17-1.3 (PMRP1)	18.7125018516594
1087.17-4 (PMCC1)	20.3356691709480
1182.17-2L2FM (MD1)	26.3518860844247
1383.17-1CABO (AMAD1)	25.4177235012620
1383.17-1CABO (AMBC1)	14.7768432237745
1793.17-2 (1)	16.4136370228149
1793.17-2 (3)	34.2998809963809
1799.17-1 (2)	16.5291234746973
1816.17-2FF (EVM1)	28.1703726983469
1816.17-2FF (SC1)	23.4228494483054
1843.17-1FIXACAO (FN1)	8.2531688614244
1847.17-3R2 (JC1)	17.6148758658441
1847.17-3R2 (MC1)	20.6586914586542
2572.17-4CABO (IOSS)	18.5940843148801
2572.17-4CABO (LMVG1)	18.5804198401146
2799.17-2FM (1FF)	25.3990952221238
2921.17-2 (JAVC2)	16.7962994010766
2921.17-2 (TFTS1)	22.9454491766520
3053.17-3.1R2 (EAD1)	13.6492156959327
3053.17-3.1R2 (MMM1)	16.9220436190151
3732.17-2.1FM (ASSC1)	20.1812960467766
3732.17-2.1FM (IST1)	22.1311300408903
3929.16-1 (2)	26.2007430030690
5258.17-5 (1)	28.6344376974011
5700.16-5 (AGT)	21.9215326315776
5700.16-5 (TMAS)	28.5564802929045
5707.17-6R1 (MAGDC1)	23.7327387475283
5709.17-6R2 (CMDF1)	15.6645343141757
5709.17-6R2 (MJLF1)	16.5812180988184
5773.17-4 (5FM)	19.5247143933286
5773.17-4 (17FDC1)	26.3986497858739
6010.17-1 (AAM1)	16.1332235256782
6472.17-1FM (PSBM2)	24.1757824146097
7241.17-11R2FF (ASJ1)	21.0079579548889
7241.17-11R2FF (MCPSJ1)	19.0018563579077
7385.16-3 (2)	8.1463915938754
7588.17-1R1FF (3)	25.5865246614675
9233.16-9.1 (LCGS1)	12.1656367230092
9233.16-9.1 (VMTJ2)	19.6882931048964
10223.17-3LAM (IM2)	14.2619881360925
10223.17-3LAM (VMPM1)	20.1867599585034
12818.17-7 (1)	21.8310005151426
13017.17-25.2 (AJAN1)	26.5698325813616
13017.17-25.2 (MJCR1)	28.6793685609202
13027.17-1R2FF (1R1FF)	16.2979118808928
13027.17-1R2FF (1R1FM)	25.9695033924259
13034.16-2CABO (2LAM)	21.6599192997595
13252.17-8 (FTMR1)	18.7661783034101
13252.17-8 (LIOR1)	15.6717415723401
13740.17-1R1FF (1R2FF)	14.6722449424754
13940.17-2 (DMC1)	16.5773077688830
13940.17-2 (NMFM1)	14.0241304270880
14002.16-1 (MPNG1)	11.1680415794699
14552.16-1FM (LMRR1)	15.7552477353469
14552.16-1FM (1FF)	29.6820202398449
15150.17-1 (DASS1)	16.7768754025122
15150.17-1 (RJABO2)	22.4572006796733
16126.17-3.3 (1)	29.6297484916951
16537.17-1 (AJMC1)	27.4370800056065
16537.17-1 (ASLS1)	28.3591108648401
16672.17-4R2 (4R1)	27.9180409222925
16672.17-4R2 (AMC1)	20.4217795929546
16913.17-3 (NMSAOM1)	19.6753375586306
17065.17-1 (3)	27.9851306026269
17065.17-1 (SSC1)	23.1578862777045
17222.17-3R2FF (3R1)	19.5173942235008
17222.17-3R2FF (PM1)	24.5152984025571
18119.17-2 (LZ1)	15.9308502566077
19187.16-4CABO (RGCF)	10.2187182993567
19724.16-6 (ENP1)	24.5391865441215
19724.16-6 (13)	19.0551997547383
19724.16-8 (BMAP)	23.1990618943153
19799.17-1 (TFPA1)	6.9105685126814
20601.16-1 (HMNM1)	14.4626335252475
20601.16-1 (AMM)	15.7249745238029
20628.16-1CABO (AMP)	26.6695729126876

[1] Computed by Figueiredo C: Forensic DNA mixtures: Analysis and comparison of software results. Faculdade de Ciências da Universidade do Porto; 2018.

Table B2: Log_{10} values of the LRs (per markers and global) computed by EuroForMix v.1.9.3 with stutters, for mixtures with two estimated contributors. The markers that have been removed to allow comparison with STRmix™ values are referenced with an "X".

Mixture (Reference)		Log_{10} (LR)	D3S1358	vWA	D16S539	CSF1PO	TPOX	D8S1179	D21S11	D18S51	D2S441	D19S433	TH01	FGA	D22S1045	D5S818	D13S317	D7S820	SE33	D10S1248	D1S1656	D12S391	D2S1338
243.17-1FM (JRA)	LR_{21}	**18.003716049638**	0.70172	0.77430	0.24573	1.06421	-0.59201	2.03033	0.26121	2.13264	0.06852	0.66605	0.65121	0.60110	0.80651	0.84251	0.91715	1.02557	1.78489	0.50217	1.00861	1.44662	1.06466
243.17-1FM (MM)	LR_{21}	**22.524744358999**	0.88326	2.05057	0.69306	-0.22115	1.51094	0.88056	1.06720	2.08216	0.28942	0.47013	1.22628	0.46960	1.68514	1.46280	0.58968	0.82970	1.87789	1.27903	0.84172	1.80488	0.75185
913.17-1.3 (ASML1)	LR_{21}	**13.945686344540**	0.68324	0.89995	-0.11878	-0.36089	-0.26442	1.09454	0.79188	0.57764	0.45526	0.60723	0.35976	1.51542	0.51991	0.44324	0.89012	0.81386	1.77922	0.34783	0.94111	1.38532	0.58425
913.17-1.3 (PMRP1)	LR_{21}	**19.296490904619**	0.89690	1.29678	0.37476	1.40283	0.47967	1.51599	1.10063	1.38671	0.46490	-0.09009	0.45410	0.52003	1.66171	0.35820	0.76903	1.20575	1.70011	0.41595	1.63169	0.37898	1.37187
1087.17-4 (PMCC1)	LR_{21}	**20.970874046132**	1.05916	0.77072	0.78225	0.70869	0.26579	0.85152	1.10204	1.22221	0.99268	0.68619	0.73757	1.46274	0.54435	0.16757	1.15766	1.11687	2.18984	0.36809	1.59160	1.69573	1.49761
1182.17-2L2FM (MD1)	LR_{21}	**26.270951515714**	1.81556	1.41913	0.98579	1.96741	0.55053	0.94537	0.91861	1.33147	1.14224	0.66109	0.77546	1.45379	1.26199	0.58743	1.22811	1.11584	2.10374	1.59545	1.65764	1.43833	1.31597
1383.17-1CABO (AMAD1)	LR_{21}	**25.342114768238**	1.16839	1.31353	0.97054	1.39252	0.84460	0.94862	1.02257	2.11420	0.97014	1.24869	0.87135	1.40339	0.61588	0.93825	0.76736	1.05443	2.29038	0.72940	1.64602	1.31900	1.71284
1383.17-1CABO (AMBC1)	LR_{21}	**15.664074162217**	0.48397	1.09946	0.30209	-0.46093	0.42684	1.42222	0.41338	1.47495	0.74160	0.81376	0.00215	0.88006	-0.74498	0.34820	0.07318	1.17406	2.28065	0.59695	1.03458	1.75897	1.54292
1793.17-2 (1)	LR_{21}	**17.253315418255**	1.03412	1.26797	1.11172	0.30617	-0.58103	0.69334	1.31864	0.00034	0.69162	0.98788	0.82872	0.65421	1.58011	0.85573	1.72009	0.85122	0.28694	-0.35504	1.43676	1.35019	1.21363
1793.17-2 (3)	LR_{21}	**34.087267211476**	2.34248	1.83334	0.98418	0.70854	2.24442	0.91795	1.19544	1.47088	0.87567	1.51324	1.90096	2.44020	1.27389	2.93834	0.84886	1.14018	1.89261	2.58887	1.57597	1.54038	1.86088
1799.17-1 (2)	LR_{21}	**16.896395414641**	0.69913	0.84633	1.79030	-0.07052	-1.34690	0.62650	1.25853	1.06633	0.50309	1.23063	0.65805	0.68505	0.51057	0.20045	1.02700	1.01360	2.10670	-0.18761	1.86327	1.30865	1.10724
1816.17-2FF (EVM1)	LR_{21}	**28.134594784396**	0.87541	1.06869	0.96966	0.97995	1.13842	1.46305	1.15420	1.46792	0.83383	1.63323	2.42727	1.61646	0.80101	0.93532	1.17273	1.06308	1.80394	1.94633	1.85975	1.62114	1.30322
1816.17-2FF (SC1)	LR_{21}	**17.465962323005**	0.63151	0.38953	0.32411	1.82195	-0.27668	1.19549	0.81831	1.28488	1.51183	1.52530	0.50464	0.73994	1.01750	0.35068	0.24786	0.36014	-0.58455	0.62911	1.39994	2.78093	0.79353
	$LR_{<21}$	**18.062803715214**	0.66973	0.39969	0.31664	1.82621	-0.38624	1.20394	0.82426	1.29710	1.52278	1.54514	0.48593	0.72771	1.05394	0.35494	0.22555	0.36424	X	0.60583	1.39330	2.82718	0.80496
1843.17-1FIXACAO (FN1)	LR_{21}	**8.295255681973**	0.41746	0.58592	0.15454	0.23423	0.27588	0.39988	1.49479	0.95938	0.61566	-0.03340	0.60945	0.96164	0.57317	0.58298	0.15229	1.04793	-1.75876	0.52887	0.99842	-0.25600	-0.24905
	$LR_{<21}$	**10.270750713179**	0.45453	0.62785	0.23129	0.23345	0.22512	0.46900	1.62985	0.97920	0.71382	0.02760	0.67696	0.99331	0.59743	0.59784	0.21803	0.99593	X	0.99331	0.94158	-0.39525	-0.33901
1847.17-3R2 (JC1)	LR_{21}	**18.084320389779**	0.55976	0.59488	0.52580	0.32906	0.11941	0.93222	1.29323	1.94689	0.16795	0.76229	1.04066	0.79530	-0.15543	0.69443	0.47924	0.67047	1.93826	1.50667	1.08590	1.62526	1.17206
1847.17-3R2 (MC1)	LR_{21}	**17.559906208162**	0.28355	0.78526	0.71592	2.54140	0.68931	0.78389	0.45528	1.49332	1.51005	0.15337	1.27810	2.17883	-2.93231	0.53364	0.64768	1.43315	1.52265	0.95214	1.00856	0.72677	0.79933
	$LR_{<21}$	**20.664239537220**	0.43954	0.92611	0.65056	2.44243	0.05367	0.61127	0.59731	1.57744	1.63616	0.27408	1.24136	2.22681	X	0.55512	0.44315	1.54740	1.61739	2.22681	0.96111	0.92178	0.96970
	$*LR_{21}$	**21.561320913696**	0.43326	0.92572	0.6542	2.45291	0.07767	0.60058	0.58355	1.56948	1.65136	0.27449	1.25507	2.22654	0.89846	0.54817	0.44103	1.54692	1.61586	0.96129	0.95479	0.91594	0.97403
2572.17-4CABO (IOSS)	LR_{21}	**20.415271146644**	1.01224	1.74462	0.83219	-0.14053	-0.20687	0.25237	1.27609	1.48116	1.38966	0.63407	1.20037	1.41324	0.35598	0.66656	1.43377	1.19470	1.64277	-0.18758	1.86657	0.95600	1.59789
2572.17-4CABO (LMVG1)	LR_{21}	**20.225987871568**	0.75011	1.00028	0.40351	-0.01876	-0.40550	0.72649	1.29510	1.42244	0.83339	0.73850	1.40014	1.65188	0.18262	0.31962	1.70037	1.66864	1.77925	0.56228	1.99144	0.95042	1.27377
2799.17-2FM (1FF)	LR_{21}	**25.716396830005**	1.00879	1.37924	0.87194	0.97128	1.24347	0.77026	1.08883	2.21315	0.74365	1.66969	1.10600	1.66068	0.82535	0.68188	0.71730	1.59100	1.76959	1.14201	1.85639	1.83129	0.57458
2921.17-2 (JAVC2)	LR_{21}	**17.372060101678**	0.73376	1.06427	0.89926	-0.40543	0.43435	0.46913	1.53788	1.18667	1.24486	0.52079	0.63598	0.93436	0.35832	1.50392	1.06235	1.07454	0.91942	-0.41711	1.29823	0.94759	1.36894
2921.17-2 (TFTS1)	LR_{21}	**24.605279968959**	0.92074	1.82446	1.20278	0.30714	0.00056	1.01767	1.52148	1.26351	0.75687	1.11778	1.01571	2.02235	0.99541	2.08737	1.00943	1.64299	1.49616	0.18875	1.53085	1.00311	1.68013
3053.17-3.1R2 (EAD1)	LR_{21}	**15.938805407212**	0.79090	2.16033	0.91608	-0.06220	-1.59495	0.98369	0.95750	1.40892	0.69804	0.22945	0.96986	-0.04457	0.15595	0.83328	1.17875	0.83664	1.66539	-0.54038	1.65869	0.91663	1.82080
3053.17-3.1R2 (MMM1)	LR_{21}	**14.566576262750**	0.63689	0.43452	0.51697	0.85343	1.44621	0.71971	0.56448	-2.06675	0.62098	1.68848	0.23705	1.29618	0.67980	0.67437	0.67183	0.73349	1.49867	0.32358	0.92502	0.79123	1.32045
	$LR_{<21}$	**16.972510930366**	0.76957	0.61126	0.53606	0.72085	0.55315	0.81651	0.75186	X	0.71275	1.85050	0.41008	1.19015	0.50021	0.71121	0.77192	0.84109	1.72570	1.19015	1.16569	0.91780	1.47867
	$*LR_{21}$	**18.285583918224**	0.77131	0.61405	0.53245	0.72299	0.54889	0.82053	0.74925	1.31517	0.71155	1.84175	0.40387	1.19853	0.49724	0.70652	0.77106	0.83947	1.73402	-0.07012	1.17481	0.92028	1.48197
3732.17-2.1FM (ASSC1)	LR_{21}	**20.267310523943**	0.62986	0.51222	0.76876	0.37256	-0.01279	1.16619	1.02974	1.26480	2.33285	0.37230	0.85753	0.60691	0.65780	1.50697	0.59446	0.87994	2.32586	0.32761	1.28357	1.08064	1.70953
3732.17-2.1FM (IST1)	LR_{21}	**22.677055402593**	0.42291	1.69469	0.35017	0.42092	2.10898	1.07055	1.60776	1.17451	0.18060	2.17288	0.76287	1.95574	1.07919	-0.04302	0.96573	0.87316	2.06724	0.21053	1.38150	0.85100	1.36915
3929.16-1 (2)	LR_{21}	**26.479727588542**	1.15827	1.00835	1.17128	0.75055	0.43403	0.92353	1.03664	1.36265	1.57422	2.61253	0.79772	1.37264	1.02447	1.34925	1.10263	1.15050	2.06717	0.71921	1.94782	1.50711	1.40917
5258.17-5 (1)	LR_{21}	**28.815336662235**	0.56057	0.73992	0.87340	1.59360	1.12936	1.30428	2.04082	1.81044	0.68314	2.33282	1.17100	1.28609	1.03343	1.02397	1.73576	1.32398	1.99919	1.23404	1.60156	1.50380	1.83417
5700.16-5 (AGT)	LR_{21}	**23.245849817647**	1.08697	1.31229	0.55207	0.56843	-0.46717	1.89545	1.68524	1.34816	1.68335	0.12815	1.05028	0.82687	-0.17345	1.92539	0.04285	1.02807	1.91139	0.96659	3.16622	1.42531	1.28339
5700.16-5 (TMAS)	LR_{21}	**29.461694745268**	1.32450	1.39117	1.45269	1.24112	0.95910	1.85679	2.15310	1.31612	1.07455	0.77778	1.59261	1.28576	0.54227	1.34526	0.65659	1.08193	2.72104	1.64388	1.58926	1.65533	1.80084
5707.17-6R1 (MAGDC1)	LR_{21}	**25.291683186245**	1.05570	1.09915	0.97593	0.59877	0.96554	1.16366	1.50433	2.54725	0.75379	0.66786	1.06665	0.65198	1.37073	1.74534	1.93619	1.28699	2.02012	0.12096	0.87634	0.77124	2.11318
5709.17-6R2 (CMDF1)	LR_{21}	**15.672318404407**	0.87134	0.67611	1.22237	0.49182	0.32339	0.56412	0.16345	1.03292	0.49295	0.23428	0.59928	0.82319	0.43132	0.27177	0.42359	0.79086	1.69372	1.21679	0.91821	1.80628	0.62457
5709.17-6R2 (MJLF1)	LR_{21}	**16.654207440809**	0.49013	0.62802	0.47982	0.34869	0.00639	0.59294	0.49971	1.07012	0.85828	1.80180	0.06371	0.85767	0.46060	0.46749	0.76968	0.74962	1.81658	0.50685	0.93155	1.64039	1.61419
5773.17-4 (5FM)	LR_{21}	**16.363427404147**	1.39615	0.66221	-0.10813	0.21616	-0.17042	0.60820	0.61337	0.77218	0.48940	0.81193	-0.15543	2.83026	-1.02957	0.25327	0.48825	1.34924	1.89145	1.29238	1.21758	0.97239	1.96255
5773.17-4 (17FDC1)	LR_{21}	**26.429003360625**	1.07963	1.31597	1.47491	0.79024	0.85291	1.55650	0.92146	1.53830	0.88232	2.06082	0.86336	1.18510	0.80748	0.93817	1.15862	1.11716	1.97965	1.06559	1.57747	1.74136	1.52201
6010.17-1 (AAM1)	LR_{21}	**13.991391232344**	0.59742	0.57801	0.39078	-0.07611	1.01434	1.58975	1.99010	1.21398	0.73512	0.46636	0.86599	1.20913	-0.54502	0.30956	0.64590	0.88074	-1.06508	0.55069	1.05808	1.55930	0.02235
	$LR_{<21}$	**13.885864050308**	0.62619	0.57609	0.48710	-0.08516	0.95154	1.69864	1.96301	1.09438	0.78242	0.48425	0.98757	1.13162	-0.57967	0.30101	0.64649	0.82809	-0.97636	1.13162	1.05427	1.52833	X
6472.17-1FM (PSBM2)	LR_{21}	**24.672680015735**	1.01387	1.07655	0.89892	0.23658	-0.36115	1.32553	1.63234	1.40112	0.93793	1.57568	0.96810	1.13963	1.19285	1.48444	1.22095	1.21608	2.21644	0.78082	1.80049	1.64045	1.27506
7241.17-11R2FF (ASJ1)	LR_{21}	**21.849082377982**	1.13437	1.13101	0.79605	0.11597	1.47046	1.23618	0.69473	1.11863	1.19094	0.04220	1.75650	1.16019	1.06270	1.65971	0.76889	1.21453	1.21877	0.73914	0.92465	1.28070	1.13276
7241.17-11R2FF (MCPSJ1)	LR_{21}	**19.895322990479**	1.12820	1.05030	0.31360	0.30265	-0.11042	1.29422	1.09728	1.12566	1.47678	1.75722	0.35273	1.14090	0.58584	0.76184	0.25425	1.02043	1.70823	0.52532	1.62767	1.31084	1.17178
7385.16-3 (2)	LR_{21}	**7.233012934418**	0.51730	1.09386	-0.10631	-0.26012	-0.12424	0.39840	0.68975	0.70701	0.44312	0.42011	0.50810	0.11130	-0.16942	0.16418	0.48983	0.53155	0.75850	-0.07039	0.09333	0.59851	0.43865
7588.17-1R1FF (3)	LR_{21}	**26.113518344873**	1.26016	1.27282	1.17790	0.76585	0.42151	1.10994	0.91560	1.43934	1.29143	1.81619	2.27144	1.25362	0.76305	0.59606	0.78260	1.04596	2.39165	0.89327	1.58065	1.52422	1.54024

9233.16-9.1 (LCGS1)	LR_{21}	**12.180534980206**	0.42403	0.30185	0.37636	0.20257	-0.64386	0.65045	0.80785	0.93845	0.00395	0.35954	1.76634	1.36058	0.05807	0.12922	0.37728	0.72645	1.42788	-0.21992	1.47286	0.65011	1.01048
9233.16-9.1 (VMTJ2)	LR_{21}	**21.350010350582**	0.14117	0.93180	0.46549	0.60745	0.21682	1.37333	1.22801	1.27518	0.22994	0.69423	1.30809	0.79503	1.45214	1.48056	1.06752	1.13681	1.66427	0.21362	1.88814	1.37758	1.80285
10223.17-3LAM (IM2)	LR_{21}	**14.269688403557**	1.13643	0.99343	1.20389	0.90279	0.12491	0.09021	0.33296	0.78065	0.23698	0.74622	0.71944	0.90962	0.76787	0.16429	0.29679	0.70004	1.13073	0.67550	1.14856	0.69577	0.51260
10223.17-3LAM (VMPM1)	LR_{21}	**20.207464629481**	1.13646	0.99110	0.68430	0.89221	0.40207	0.69816	1.65671	1.74631	0.58707	0.35278	0.16592	2.51640	0.76487	0.54871	1.09537	0.45416	1.46382	0.72256	0.99123	0.76137	1.57586
12818.17-7 (1)	LR_{21}	**22.862586401124**	2.19116	1.69330	0.88099	2.40058	0.27605	1.16482	1.14549	1.46008	1.12678	0.54704	0.52268	0.52956	1.12033	0.16600	0.42335	0.95689	1.49642	0.94750	0.97333	1.40998	1.43024
	$LR_{<21}$	**21.902718559614**	2.17054	1.67049	0.89963	2.39965	0.40749	1.13952	1.09607	1.42530	1.11135	0.53236	0.53432	0.51976	1.12124	0.15094	0.41537	0.94214	1.50075	0.51976	X	1.43916	1.43768
13017.17-25.2 (AJAN1)	LR_{21}	**26.749857762486**	1.06878	0.79378	0.98752	0.62942	0.10945	1.09094	2.38186	1.49762	0.74420	2.34973	0.74664	1.17397	1.35230	2.11358	1.14269	0.92222	2.31028	0.69812	1.76931	1.42270	1.44475
13017.17-25.2 (MJCR1)	LR_{21}	**28.733395980635**	0.85771	1.30251	0.97053	2.13745	0.48070	0.93919	1.92612	1.35054	1.24730	1.49985	0.98373	1.27560	1.31621	0.99974	1.08367	1.98809	2.30615	0.73572	1.72248	1.65949	1.95062
13027.17-1R2FF (1R1FF)	LR_{21}	**16.306741240909**	0.98822	0.56452	1.93652	0.14497	-0.11759	0.98749	1.86485	2.50060	0.44902	0.36699	0.83474	0.84942	0.98620	0.35783	-0.43573	-0.33021	0.66502	1.17374	1.07742	0.95985	0.48288
13027.17-1R2FF (1R1FM)	LR_{21}	**25.964772961341**	1.34281	1.31676	0.76529	0.39969	0.01895	1.09892	1.63250	2.39744	0.82165	1.13758	1.47088	2.19266	0.16989	1.34157	0.84903	0.91825	2.09008	0.82915	1.42758	1.50039	2.24371
13034.16-2CABO (2LAM)	LR_{21}	**20.821011585759**	1.15209	1.20393	1.35298	0.21774	0.78398	1.87341	0.69136	1.48409	1.04009	1.08610	0.71871	0.75210	0.38424	0.29080	0.82365	1.05497	1.87677	-1.20577	1.60641	1.77773	1.85560
13252.17-8 (FTMR1)	LR_{21}	**20.762818252297**	0.77765	1.03364	1.04302	0.58430	0.13386	1.02702	0.96015	1.25154	0.85444	0.80049	0.85883	1.27050	-0.05112	0.28802	1.10684	0.33665	3.02735	1.06051	1.39605	1.95722	1.04588
13252.17-8 (LIOR1)	LR_{21}	**14.652328661959**	0.34439	0.76592	0.82390	-0.36496	0.13658	0.36490	0.25568	1.07634	0.33658	0.58645	0.53798	0.65402	0.30274	0.69852	0.84145	0.71731	1.77440	0.51410	1.47957	1.89375	0.91271
13740.17-1R1FF (1R2FF)	LR_{21}	**14.924829107993**	0.61324	0.83662	0.60489	0.27238	0.25707	1.21753	0.52146	0.95552	1.19742	0.72299	0.86862	0.86227	0.33439	0.54304	0.54200	0.41748	0.92012	0.51796	0.93920	1.05852	0.72212
13940.17-2 (DMC1)	LR_{21}	**16.696391975322**	1.18415	0.92335	0.10493	0.62064	-0.20159	1.05065	1.44568	1.16355	1.04410	1.12889	1.37519	0.59284	1.00366	0.85182	-0.00139	0.52354	1.26068	0.34605	1.18280	0.82147	0.27537
13940.17-2 (NMFM1)	LR_{21}	**13.367720600820**	0.71757	0.46535	0.66885	0.47318	0.02063	0.68475	0.62843	0.96023	-0.13526	0.32495	0.61359	1.00412	-0.66589	0.81690	0.90552	0.31804	2.66260	-0.13106	0.97179	0.34527	1.71816
14002.16-1 (MPNG1)	LR_{21}	**13.835841407327**	0.73370	0.45672	0.03694	-0.20706	-0.36048	1.43469	0.82438	0.52629	0.63948	0.49766	0.79119	0.46001	0.71677	0.23267	0.34860	0.71682	1.88887	-0.29111	1.60979	1.58355	1.19637
	*LR_{21}	**13.803802770133**	0.73301	0.45640	0.03657	-0.20721	-0.39355	1.43450	0.82311	0.52641	0.63996	0.49632	0.79229	0.45925	0.71744	0.23302	0.34889	0.71683	1.88939	-0.28882	1.60916	1.58407	1.19674
14552.16-1FM (LMRR1)	LR_{21}	**9.804873995909**	0.63683	0.87736	0.35003	0.11118	-0.46271	0.00296	0.01840	-0.06229	0.29251	0.79831	-0.01473	0.79374	0.34059	0.19234	0.28998	0.93271	0.95413	-0.03922	1.56324	0.38569	1.84383
14552.16-1FM (1FF)	LR_{21}	**29.658030713789**	1.05792	1.31358	1.64967	1.19248	0.86598	3.13973	1.35646	1.29202	0.77157	2.26631	1.06033	1.43293	1.77358	0.79057	1.09361	1.12158	2.00238	0.90485	1.67742	1.32044	1.57464
15150.17-1 (DASS1)	LR_{21}	**19.247710106783**	0.29700	-1.69842	0.98594	-0.07820	-0.59446	1.29067	2.43067	0.89606	1.05371	2.26054	0.42286	0.94012	0.18991	0.41133	2.06084	0.76524	1.73867	0.80137	2.02685	1.53387	1.51311
	$LR_{<21}$	**21.104648088798**	0.37597	X	0.94296	-0.34035	-0.78086	1.33470	2.46996	0.91465	1.19077	2.35977	0.53048	1.00407	0.24560	0.46120	2.14431	0.81994	1.77279	1.00407	2.03644	1.55344	1.57866
15150.17-1 (RJABO2)	LR_{21}	**23.754656639504**	1.04685	1.44683	0.79256	1.08285	0.52968	2.23136	1.62560	1.07066	0.63600	0.92411	0.24653	1.17228	0.84115	0.57351	0.96529	0.99153	2.25925	-0.28128	2.24849	1.56852	1.78287
16126.17-3.3 (1)	LR_{21}	**29.602042096820**	0.98055	1.33799	0.97116	0.78970	0.56932	0.93611	2.20304	1.92829	1.32872	1.07536	0.89250	1.63138	1.03147	0.98185	1.10266	1.73906	2.65116	1.94815	2.03285	2.08223	1.38849
16537.17-1 (AJMC1)	LR_{21}	**27.719769196134**	0.66737	1.72137	1.15859	2.25945	1.26540	0.91853	1.92516	1.68305	1.64234	0.55495	0.92701	1.26514	0.67124	0.38325	1.26364	0.85928	1.89881	2.57370	1.15499	1.48986	1.43664
16537.17-1 (ASLS1)	LR_{21}	**28.640790692609**	0.56199	1.95191	0.95923	1.83416	0.42258	0.91675	1.14719	1.40728	0.88446	1.58788	1.28173	2.69728	0.56664	1.97654	1.52316	0.96159	2.18215	0.77382	1.35697	1.51806	2.12940
16672.17-4R2 (4R1)	LR_{21}	**27.836973535824**	0.83968	1.01366	1.46940	0.97293	0.51777	1.78006	1.72646	1.43575	1.42602	0.72178	-0.20392	2.30337	0.83298	1.91229	0.74387	1.30352	2.85903	0.73106	1.69338	2.29128	1.46659
16672.17-4R2 (AMC1)	LR_{21}	**19.991708015011**	0.63330	0.38399	0.10254	1.30656	0.18599	0.71158	0.71242	0.95149	0.67952	2.22903	-0.58118	0.73397	1.30905	0.60051	1.11691	1.20760	2.30601	0.61776	2.30322	1.65934	0.82210
	$LR_{<21}$	**19.402610852923**	0.64541	0.40762	0.08020	1.29786	0.20404	0.67738	0.72456	0.96364	0.68148	2.24315	-0.56342	0.77586	1.29595	X	1.08807	1.19247	2.29936	0.77586	2.27649	1.67961	0.84908
16913.17-3 (NMSAOM1)	LR_{21}	**19.302094849617**	0.58189	1.15589	0.94230	0.60801	0.46744	1.28075	0.67403	1.46000	0.46264	1.77543	1.13329	0.93971	0.39573	0.49699	0.90869	0.91415	1.85547	-0.14395	1.34535	1.23587	0.81240
17065.17-1 (3)	LR_{21}	**28.002949470201**	1.15136	1.39587	1.41832	1.22782	0.57537	1.42430	1.35512	1.35989	0.76860	1.62136	0.87840	1.34837	2.01017	0.55698	1.25183	1.14278	2.12831	0.72866	1.73938	2.02571	1.89434
17065.17-1 (SSC1)	LR_{21}	**23.065206550334**	0.83647	1.67022	0.72521	1.04493	0.57045	0.71780	1.17390	1.56928	0.54533	0.72189	1.29454	1.47948	1.45705	0.13971	0.46574	0.87821	2.43584	0.40643	1.77608	1.15069	2.00596
	LR_{21}	**21.049067955459**	0.84514	1.68603	0.72823	1.03368	0.56299	0.70451	1.17888	1.59312	0.54132	0.72985	1.31097	1.46479	1.48127	0.13849	0.45658	0.88354	2.43026	1.46479	1.80078	1.14236	X
17222.17-3R2FF (3R1)	LR_{21}	**19.069130047728**	1.83372	0.94537	0.78220	0.01577	-0.16874	0.50471	1.43474	1.08396	1.67563	0.90783	0.75993	1.14652	0.05508	0.65293	1.08808	0.96385	2.02979	0.17334	2.08491	1.24764	-0.14811
17222.17-3R2FF (PM1)	LR_{21}	**23.927314066510**	1.05962	0.85386	1.15729	2.24996	0.35033	1.20183	1.05158	1.16876	1.21875	1.43819	1.11597	1.35380	0.90542	0.88483	0.70157	1.62668	1.21963	0.68169	1.36562	1.74051	0.58138
	$LR_{<21}$	**23.368506810215**	1.06843	0.80491	1.18665	2.20443	0.39928	1.25534	1.00869	1.12400	1.18534	1.46530	1.13239	1.30237	1.00530	0.91391	0.69678	1.61476	1.15058	1.30237	1.31321	1.69001	X
18119.17-2 (LZ1)	LR_{21}	**17.237163183832**	0.47594	1.30644	1.33484	0.54069	-0.10449	0.75878	1.20634	0.95844	0.50269	1.48364	0.87189	0.85839	0.24504	-0.11103	1.22183	0.84117	1.30603	-0.25783	1.13016	1.22317	1.44504
19187.16-4CABO (RGCF)	LR_{21}	**9.433092628097**	0.20439	0.87019	0.36257	0.37626	-0.54741	0.42081	0.31917	1.02089	0.88320	0.08199	0.26540	0.55857	0.00471	0.10718	0.97454	0.59173	-0.03478	0.52917	1.14242	1.44362	-0.65936
19724.16-6 (ENP1)	LR_{21}	**26.781560245875**	1.44478	1.18023	0.24731	0.02805	0.67325	0.80147	1.00079	1.97580	0.88043	2.16244	1.55516	1.87089	1.89954	1.11422	1.37416	1.18344	1.25934	0.53959	1.99756	1.61582	1.97729
19724.16-6 (13)	LR_{21}	**17.448307673578**	1.19622	0.82228	0.14163	-0.54965	-1.90294	1.06798	2.31541	1.27892	0.58449	0.52583	0.87170	2.07605	0.40275	0.46037	0.88262	1.12388	1.49226	0.08902	1.33248	1.17940	2.05759
19724.16-8 (BMAP)	LR_{21}	**24.219469568872**	1.85669	0.78089	0.86234	0.69642	0.10729	1.34788	1.44179	1.25398	0.84049	1.52535	1.11667	1.33122	1.16308	1.13432	1.05958	0.43165	1.73831	0.88876	1.73536	1.37820	1.52920
19799.17-1 (TFPA1)	LR_{21}	**8.236989241120**	0.19203	0.61433	0.19358	0.14788	1.49984	1.17920	0.79048	-0.56005	0.36114	0.93672	0.18902	0.69370	0.78750	0.33398	-0.33568	1.30182	1.83580	1.53464	-3.98676	-0.53002	1.05785
	$LR_{<21}$	**14.151807937381**	0.35124	0.79635	0.20630	0.16448	1.42804	0.92756	0.93307	X	0.54056	1.18374	0.28302	0.66077	0.97776	0.52513	-0.69635	1.32240	1.86468	0.66077	X	X	1.12243
20601.16-1 (HMNM1)	LR_{21}	**13.100816344467**	0.68104	0.73763	0.54693	1.32297	-0.15185	0.60767	-0.68414	0.82584	0.88015	1.03038	0.67779	1.16870	0.28990	0.30593	0.93092	0.06911	0.61022	0.17193	1.18920	1.26108	0.62941
20601.16-1 (AMM)	LR_{21}	**16.102063740722**	0.84954	0.84157	0.78091	0.91305	-0.03963	0.32512	1.45498	1.26727	-0.51368	0.69902	0.49965	1.19637	0.01125	0.24146	0.63739	0.49068	2.43586	0.33342	1.10061	1.59350	0.98372
20628.16-1CABO (AMP)	LR_{21}	**26.636796259539**	1.33555	1.02979	1.14189	0.76245	0.49662	0.92778	1.80127	1.48362	1.15162	0.71870	0.78666	1.30249	0.62679	1.93709	1.51341	1.21427	2.15052	1.09184	1.58541	1.74099	1.83803
	$LR_{<21}$	**25.483900941791**	1.32880	1.03144	1.14583	0.78432	0.52044	0.92866	1.79356	1.47830	X	0.71721	0.78475	1.29709	0.62256	1.93181	1.50958	1.21177	2.15521	1.29709	1.57969	1.74354	1.83298

*Values computed in order to allow comparison of those mixture/reference pairs in section 4.2.1., since there is a difference in one marker between the reference sample files used in the analyzes with and without stutters. In no other analysis did this difference have an impact.

Table B3: Log_{10} values of the LRs (per markers and global) computed by STRmix™ v.2.7 with stutters, for mixtures with two estimated contributors. The "-" represent the null LRs values (markers and global) and the "X" refer to the markers that have been removed to allow comparison. The blank cell corresponds to the marker for which STRmix™ did not compute any value.

Mixture (Reference)		Log_{10} (LR)	D3S1358	vWA	D16S539	CSF1PO	TPOX	D8S1179	D21S11	D18S51	D2S441	D19S433	TH01	FGA	D22S1045	D5S818	D13S317	D7S820	SE33	D10S1248	D1S1656	D12S391	D2S1338
243.17-1FM (JRA)	LR_{21}	**17.765743041421**	0.60139	0.78849	0.37396	0.01364	-0.21312	1.89904	0.37603	2.01528	0.04001	0.69853	0.64309	0.75759	0.87858	0.73983	0.84114	0.80749	1.61131	0.55393	0.97345	1.39803	0.96807
243.17-1FM (MM)	LR_{21}	**21.2328691051326**	0.83724	2.15143	0.55957	0.00924	1.49024	0.68147	1.21299	1.88975	0.33796	0.66302	0.84584	0.69700	1.42403	1.40144	0.46928	0.50117	1.52800	1.05127	0.93213	1.94663	0.60313
913.17-1.3 (ASML1)	LR_{21}	**14.9269132406465**	0.71022	1.04336	-0.26450	-0.01377	0.29212	-0.33999	0.78760	0.38338	0.72209	0.81182	0.56991	1.50375	1.00612	0.61635	0.74593	1.00937	2.04187	0.96834	0.76610	0.87966	0.68715
913.17-1.3 (PMRP1)	LR_{21}	**16.8938948587436**	0.71043	1.04552	0.56202	1.07181	0.57719	1.40489	1.02235	0.63968	0.49454	0.38184	0.64940	0.62673	1.00527	0.36337	0.83487	1.02173	1.11193	-0.27793	1.71481	0.63328	1.30023
1087.17-4 (PMCC1)	LR_{21}	**22.7475050274658**	0.70268	0.83513	0.77438	0.85153	0.58074	1.04867	1.64596	1.40140	0.80518	0.76557	1.14625	1.47489	0.56166	0.52533	1.06292	0.79837	2.23211	0.88541	1.64814	1.69794	1.30324
1182.17-2L2FM (MD1)	LR_{21}	**26.5116026492278**	1.91058	1.32399	1.13322	1.73418	0.63604	0.87715	1.01047	1.32926	1.21296	0.81335	1.07221	1.37847	1.03810	0.87207	1.22886	1.00826	2.29119	1.33680	1.56756	1.37902	1.35786
1383.17-1CABO (AMAD1)	LR_{21}	**26.4529511754639**	1.32683	1.22552	1.13075	1.44309	0.87370	0.90532	1.63616	1.91847	1.00221	1.25725	0.90888	1.54829	0.70323	0.92793	0.75693	1.11671	2.34294	0.78277	1.57739	1.26769	1.80096
1383.17-1CABO (AMBC1)	LR_{21}	**19.9023673715751**	0.54753	1.55224	0.50457	-0.48576	0.77806	1.78945	0.68007	1.47038	0.81464	0.92578	-0.78675	1.16050	0.76092	0.54474	0.76011	1.20658	2.41078	1.02432	1.10816	1.75300	1.38306
1793.17-2 (1)	LR_{21}	**20.4451525513000**	0.92803	1.02263	1.49545	0.46084	0.04860	0.96982	0.97688	0.05877	0.71050	1.09992	1.00156	1.11744	1.94982	0.66447	1.92148	0.65565	0.71355	0.95328	1.72272	0.96299	1.01081
1793.17-2 (3)	LR_{21}	**33.0541149005106**	2.60845	1.55145	1.02259	0.77263	1.93285	0.88847	1.73859	1.37299	0.88044	1.50169	1.64542	2.66733	1.01317	2.66072	0.76163	1.00813	1.79165	2.46337	1.45054	1.49177	1.83022
1799.17-1 (2)	LR_{21}	**25.4233441936328**	0.91871	0.90375	2.13427	0.74689	-0.07061	1.40834	1.47001	1.39592	0.85040	1.27045	0.94047	1.03407	0.75345	0.94163	0.98580	1.31010	2.33391	1.02633	1.65183	1.74112	1.67651
1816.17-2FF (EVM1)	LR_{21}	**28.9864358096792**	0.76139	1.07835	1.06006	1.08661	1.16891	1.59607	1.69692	1.56690	0.86353	1.49821	2.34240	1.50825	1.01878	0.91329	1.12992	1.06179	1.80426	1.75333	2.02416	1.72002	1.33331
1816.17-2FF (SC1)	LR_{21}	-	0.51617	1.12522	0.77289	1.82405	1.43680	1.11468	2.05926	1.43849	1.73947	2.19857	0.91689	1.25266	1.01402	0.80724	0.72007	0.11518	-	1.00509	1.43033	2.59563	1.48945
	$LR_{<21}$	**25.5721626826463**	0.51617	1.12522	0.77289	1.82405	1.43680	1.11468	2.05926	1.43849	1.73947	2.19857	0.91689	1.25266	1.01402	0.80724	0.72007	0.11518	X	1.00509	1.43033	2.59563	1.48945
1843.17-1FIXACAO (FN1)	LR_{21}	-	0.64622	0.19371	0.65968	0.23406	0.43718	0.66076	2.29546	0.65474	0.92791	-0.39392	0.61005	0.90975	0.91861	0.21291	0.02354	0.94310	-	0.01912	1.18949	-1.04538	-0.63695
	$LR_{<21}$	**9.4600103145409**	0.64622	0.19371	0.65968	0.23406	0.43718	0.66076	2.29546	0.65474	0.92791	-0.39392	0.61005	0.90975	0.91861	0.21291	0.02354	0.94310	X	0.01912	1.18949	-1.04538	-0.63695
1847.17-3R2 (JC1)	LR_{21}	**21.3480516130684**	0.90233	0.50217	0.54827	0.50303	0.38189	1.23691	1.57163	2.15827	0.41209	0.76081	0.80165	1.04650	-0.01981	0.77848	0.34891	0.72024	2.05937	1.84948	1.66494	1.97289	1.14802
1847.17-3R2 (MC1)	LR_{21}	-	0.64322	0.89720	0.54296	1.86480	0.81737	1.00911	1.42852	1.42308	1.45168	0.32143	1.24326	1.97124	-	0.74159	0.37905	1.74587	1.67007	1.03997	1.27121	0.89533	0.64768
	$LR_{<21}$	**22.0046222657008**	0.64322	0.89720	0.54296	1.86480	0.81737	1.00911	1.42852	1.42308	1.45168	0.32143	1.24326	1.97124	X	0.74159	0.37905	1.74587	1.67007	1.03997	1.27121	0.89533	0.64768
2572.17-4CABO (IOSS)	LR_{21}	**23.9985731728215**	1.17736	1.89287	1.22920	0.76242	0.88146	0.42890	1.29316	1.58123	1.61812	0.77090	1.03197	1.47615	0.62044	0.90618	1.66415	1.04411	1.85050	0.18304	1.59185	1.09510	0.89948
2572.17-4CABO (LMVG1)	LR_{21}	**23.0834667854739**	0.81829	1.24443	0.71779	0.61000	0.37330	0.88704	1.20504	1.44917	0.94310	0.90649	1.21309	1.79170	0.61414	0.59519	1.90356	1.65227	1.91904	0.66426	1.67958	1.10954	0.78642
2799.17-2FM (1FF)	LR_{21}	**26.3298248443129**	1.10377	1.22029	1.04833	1.01907	1.12401	0.78093	1.58207	1.82596	0.75539	1.96919	0.94729	1.60009	0.98404	0.85994	0.61918	1.53377	1.89316	1.12366	1.66768	1.95774	0.71427
2921.17-2 (JAVC2)	LR_{21}	**23.4515101179343**	0.71404	1.34584	1.02449	0.22647	1.45924	0.85145	1.38817	0.93555	1.58409	0.76661	0.99638	1.38258	0.92664	1.42015	1.11551	0.97568	1.72185	0.67585	1.41817	1.18752	1.33526
2921.17-2 (TFTS1)	LR_{21}	**29.4673712876475**	0.87831	1.95566	1.01242	0.66683	0.85333	1.38543	2.44515	1.43436	0.82872	1.32327	1.11588	2.24694	1.01666	1.92320	1.20712	1.57314	1.84379	0.83783	1.64603	1.60583	1.66746
3053.17-3.1R2 (EAD1)	LR_{21}	**17.2744349700740**	0.60133	2.08824	0.79420	-0.15268	-0.14232	1.29409	0.87077	1.22835	0.68277	0.31846	0.74309	0.45644	0.55097	0.92006	1.07085	0.70199	1.53778	0.14464	1.50087	0.74331	1.32123
3053.17-3.1R2 (MMM1)	LR_{21}	-	0.60621	0.65030	0.68507	0.84504	0.75839	0.82754	0.92840	-	0.69656	1.82323	0.65907	1.14126	0.56028	0.72217	0.78711	0.69752	1.43843	0.27960	1.46100	0.92435	1.21783
	$LR_{<21}$	**17.7093462950939**	0.60621	0.65030	0.68507	0.84504	0.75839	0.82754	0.92840	X	0.69656	1.82323	0.65907	1.14126	0.56028	0.72217	0.78711	0.69752	1.43843	0.27960	1.46100	0.92435	1.21783
3732.17-2.1FM (ASSC1)	LR_{21}	**20.0403253791997**	0.77634	0.36751	0.78804	0.39589	0.07693	1.20512	1.28630	1.31794	2.31355	0.43903	0.57786	0.89265	0.27024	0.82177	0.32617	0.82366	2.48420	0.79051	1.06629	1.42914	1.59122
3732.17-2.1FM (IST1)	LR_{21}	**20.6129003591238**	0.35168	1.66188	0.63976	0.52744	1.67390	1.28814	1.16113	1.27782	0.12339	1.62997	0.77217	2.04759	0.53647	-0.50521	0.62192	0.78037	2.09110	0.76898	1.39394	0.96939	0.80107
3929.16-1 (2)	LR_{21}	**26.2774029040768**	1.34602	1.12362	1.00852	0.88594	0.63924	0.88786	1.64588	1.39373	1.32226	2.14504	1.07280	1.34873	1.04415	1.22668	0.97670	1.02845	1.87049	0.79392	1.76788	1.36659	1.38295
5258.17-5 (1)	LR_{21}	**29.7211508437497**	0.87997	0.87331	1.01515	1.81608	1.36329	1.54050	2.31165	1.50977	0.70664	2.42297	1.23757	1.43766	0.83509	0.89006	1.88210	1.14650	1.99411	1.30218	1.48762	1.42272	1.64621
5700.16-5 (AGT)	LR_{21}	**26.0856472882969**	0.97125	1.14404	0.83432	0.84393	0.51714	1.67738	2.41581	1.39664	1.36670	0.91121	0.81364	1.13991	0.69719	1.83608	0.16741	0.99106	1.95573	0.93532	2.86756	1.25229	1.35104
5700.16-5 (TMAS)	LR_{21}	**30.3862313505795**	1.65885	1.40797	1.61819	1.21189	1.23757	2.00376	2.17906	1.26578	1.23472	1.13437	1.32913	1.51988	0.37960	1.22266	0.73360	0.98257	2.68168	1.34988	1.69367	1.71477	1.82666
5707.17-6R1 (MAGDC1)	LR_{21}	**26.9811750668257**	1.07649	1.26271	0.91996	0.68066	1.12882	1.10449	1.45358	2.48394	0.76133	0.78738	0.93092	1.23596	1.39289	1.51332	1.84970	0.99847	1.85423	1.27024	1.04080	0.91685	2.31842
5709.17-6R2 (CMDF1)	LR_{21}	**17.2230803978312**	1.09681	0.79277	1.24507	0.54125	0.27875	0.68467	0.74636	0.97291	0.76119	0.28592	0.43984	0.85190	0.58165	0.27809	0.38979	0.66014	1.42001	1.19081	1.17653	2.01381	0.81484
5709.17-6R2 (MJLF1)	LR_{21}	**17.7449732360353**	0.59447	0.59593	0.74888	0.55201	0.29243	0.49170	0.39277	1.08938	1.61541	1.23807	0.56415	0.85111	0.55687	0.49104	0.60903	0.67008	1.55317	0.78837	0.93942	1.67581	1.43490
5773.17-4 (5FM)	LR_{21}	**19.9380741947804**	1.34608	0.79460	-1.70930	0.55267	0.31580	0.67492	1.15609	0.86516	0.83478	1.01891	0.24276	2.22717	0.68344	0.37783	0.88515	1.18656	2.30395	1.69469	1.65779	1.22727	1.60172
5773.17-4 (17FDC1)	LR_{21}	**26.8987306650711**	1.00255	1.19816	1.61818	0.79223	0.86721	1.48982	0.98696	1.53898	0.86799	1.95527	0.90588	1.20126	0.99520	0.92330	1.17754	1.01094	2.04914	1.19758	1.67991	1.79179	1.64886
6010.17-1 (AAM1)	LR_{21}	-	0.86086	0.94130	1.09930	0.37203	1.45725	1.55525	2.11714	1.37265	0.39534	0.67772	1.29719	1.90119	0.69888	0.07232	1.39585	1.10718	-0.32895	1.71769	1.20447	2.30827	-
	$LR_{<21}$	**22.2228724770698**	0.86086	0.94130	1.09930	0.37203	1.45725	1.55525	2.11714	1.37265	0.39534	0.67772	1.29719	1.90119	0.69888	0.07232	1.39585	1.10718	-0.32895	1.71769	1.20447	2.30827	X
6472.17-1FM (PSBM2)	LR_{21}	**27.0073209529227**	0.75959	1.22422	1.15697	0.80587	0.26762	1.15415	2.07809	1.44003	0.89173	1.70685	1.07048	1.20412	1.39986	1.26124	1.11667	1.06296	2.19338	1.33957	1.78376	1.69299	1.39714
7241.17-11R2FF (ASJ1)	LR_{21}	**23.5914986845058**	1.24591	0.91002	1.23459	0.22248	0.49229	1.21764	1.47757	1.16915	1.11049	0.75265	1.83723	1.15354	0.52622	1.38908	0.88493	1.17006	1.78364	0.93876	1.31643	1.40364	1.35520
7241.17-11R2FF (MCPSJ1)	LR_{21}	**22.3982873053574**	1.10934	1.03651	0.50040	0.58269	0.48184	1.21696	1.14610	1.16856	1.60254	1.53177	0.97903	1.11113	0.80181	0.83024	0.50485	0.89105	1.74271	0.89876	1.82087	1.07911	1.36205
7385.16-3 (2)	LR_{21}	**1.6974385908880**	1.29380	-0.49786	-0.05603	-0.44261	0.00389	0.90235	0.12343	0.75753	-0.12261	0.31277	0.28165	-0.27990	-2.04187	0.64855	-0.06828	0.39716	0.67104	0.91508	-1.44477	0.07000	0.27411

7588.17-1R1FF (3)	LR_{21}	**27.1407593708704**	1.27880	1.26658	1.03981	0.77051	0.63741	1.07799	1.00587	1.48770	1.31309	1.52332	2.19510	1.30893	0.99422	0.63980	0.73350	1.09008	2.28133	0.99784	1.78474	2.10133	1.61281
9233.16-9.1 (LCGS1)	LR_{21}	**21.7156022712819**	0.93660	0.56445	0.99718	0.54916	0.19673	0.90933	1.45179	1.29688	0.67889	0.77732	1.83382	1.67342	0.71062	0.66532	0.55897	0.72079	2.12054	0.78880	1.84834	1.14907	1.28762
9233.16-9.1 (VMTJ2)	LR_{21}	**26.4784654851313**	1.08497	0.95768	1.05971	0.73392	1.30356	1.36751	1.63957	1.44052	0.26825	0.67911	1.19340	1.32329	1.65586	1.53035	1.07273	1.00647	2.35539	1.32722	1.47669	1.44646	1.55583
10223.17-3LAM (IM2)	LR_{21}	**13.5918322952780**	1.00766	0.94188	0.88197	0.78469	0.31178	0.42702	0.37313	0.72660	0.28782	0.75988	0.45746	0.82315	0.88268	0.15005	0.27402	0.64903	1.03603	0.80391	1.04536	0.56838	0.39938
10223.17-3LAM (VMPM1)	LR_{21}	**18.9876260506124**	1.01920	1.04348	0.51887	1.04630	0.60920	0.92751	1.37372	1.72735	0.55782	0.64271	0.21000	1.98698	0.98094	0.47110	0.98454	0.27717	1.42570	0.44036	0.65851	0.86844	1.21772
12818.17-7 (1)	LR_{21}	**-**	0.63105	1.25506	0.76925	1.16074	0.84519	0.40152	1.43393	1.88072	-1.37900	-0.08934	0.73477	0.96152	0.07737	-0.26668	0.56580	1.07243	1.55969	0.07078	-	1.51882	1.54292
	$LR_{<21}$	**14.7465252224929**	0.63105	1.25506	0.76925	1.16074	0.84519	0.40152	1.43393	1.88072	-1.37900	-0.08934	0.73477	0.96152	0.07737	-0.26668	0.56580	1.07243	1.55969	0.07078	X	1.51882	1.54292
13017.17-25.2 (AJAN1)	LR_{21}	**28.5279133240549**	1.26541	0.98040	1.14461	0.80284	0.60053	1.10123	2.11830	1.52054	0.84311	2.51880	1.20572	1.17745	1.04980	2.11183	1.18307	0.86616	2.34294	0.90452	1.84048	1.29946	1.65065
13017.17-25.2 (MJCR1)	LR_{21}	**29.4680222264941**	0.75931	1.37286	1.03973	1.75558	0.63658	1.09733	1.92696	1.34594	1.60256	1.75062	1.03667	1.40751	1.45173	0.98567	0.97621	2.06644	2.10298	0.77981	1.78380	1.75315	1.83663
13027.17-1R2FF (1R1FF)	LR_{21}	**9.5797835966168**	1.05960	0.44957	1.49289	0.26858	0.32652	-0.03326	0.83464	2.22389	0.31184	0.12405	0.85801	0.03539	0.38718	0.10673	0.23742	-0.09648	0.08938	0.78229	0.71771	0.28569	-0.88183
13027.17-1R2FF (1R1FM)	LR_{21}	**24.5922211842264**	1.73784	0.95753	0.29533	0.59726	0.62291	0.77484	1.30807	2.41627	0.62685	0.89512	0.93323	1.98271	0.92457	1.12532	0.90103	0.71404	1.77530	1.29898	1.54253	1.44243	1.72004
13034.16-2CABO (2LAM)	LR_{21}	**27.6754392030515**	1.04763	1.14173	1.05911	0.69144	1.56617	1.79354	1.69433	1.48293	0.81785	1.22047	1.09279	1.34969	0.95569	0.94933	0.74708	2.04301	2.15091	0.78688	1.52226	1.37020	2.19240
13252.17-8 (FTMR1)	LR_{21}	**22.0506890277589**	0.86951	0.84727	1.08019	0.66380	0.39442	1.12284	1.49397	1.23462	0.88803	0.78357	0.70449	0.96824	0.71462	0.84849	0.98580	0.82296	2.24022	0.69894	1.33106	2.16409	1.19354
13252.17-8 (LIOR1)	LR_{21}	**19.9929730300616**	0.74166	0.85172	1.08019	0.08343	0.40002	1.07041	0.87776	0.97199	0.83879	0.78717	-0.35466	1.19471	1.08860	0.91020	0.98580	0.86997	1.45870	1.32087	1.67843	2.14454	0.99272
13740.17-1R1FF (1R2FF)	LR_{21}	**19.6004501216460**	0.91263	1.02407	0.74431	0.48683	0.38609	1.44514	1.15281	1.04681	1.77942	1.19092	1.00398	1.03595	0.70438	0.78490	0.58063	0.28921	1.15070	0.43099	1.39007	1.01460	1.04599
13940.17-2 (DMC1)	LR_{21}	**17.0901874875754**	1.64605	0.53865	-0.22909	0.72931	-0.76968	1.12538	2.04356	1.10113	1.59105	1.33864	1.21854	-0.19067	1.41848	0.92377	-1.35927	0.52772	1.41739	0.91428	1.48728	0.96648	0.65116
13940.17-2 (NMFM1)	LR_{21}	**16.0174507295105**	1.20388	-0.14828	0.62514	0.67289	0.25933	0.47744	0.48050	0.82046	0.88369	0.75835	1.09934	1.32195	0.93289	0.92377	-1.15968	-0.53396	2.70424	0.75092	1.67852	0.74702	1.51908
14002.16-1 (MPNG1)	LR_{21}	**20.7990716172391**	1.16847	0.87545	0.35422		0.06356	1.78400	1.34665	0.64856	0.87346	1.11992	0.82623	0.88563	1.04735	0.63926	0.63831	0.82238	1.96912	0.92750	2.05626	1.88312	0.86959
14552.16-1FM (LMRR1)	LR_{21}	**13.5588525116985**	0.36237	1.29916	0.72731	0.36133	-0.01657	0.69490	0.12775	0.15284	0.24272	0.83110	0.01941	0.55978	0.48031	0.70294	0.31182	0.99499	0.96522	0.44520	2.08536	0.58203	1.62888
14552.16-1FM (1FF)	LR_{21}	**30.4857214264816**	1.16823	1.22577	1.78690	1.30224	0.87420	3.15324	1.45764	1.30094	0.79570	2.51880	1.12723	1.56461	1.68969	0.84468	1.14545	1.01136	2.03334	0.92429	1.65185	1.23442	1.67515
15150.17-1 (DASS1)	LR_{21}	**-**	-0.08259	-	1.14566	-0.08818	0.00732	1.36365	2.24991	1.33054	1.68951	2.17545	0.08135	1.17912	0.65916	0.47496	2.17924	0.54406	1.66207	1.87825	1.52966	1.50092	1.67619
	$LR_{<21}$	**23.1562461903973**	-0.08259	X	1.14566	-0.08818	0.00732	1.36365	2.24991	1.33054	1.68951	2.17545	0.08135	1.17912	0.65916	0.47496	2.17924	0.54406	1.66207	1.87825	1.52966	1.50092	1.67619
15150.17-1 (RJABO2)	LR_{21}	**26.0051375959089**	1.09649	1.51355	1.00651	1.37892	0.88558	2.16155	1.39314	1.27823	1.19030	1.16167	0.20317	1.28625	0.65658	0.55564	1.13663	0.81437	2.04809	0.90746	2.04100	1.53672	1.75334
16126.17-3.3 (1)	LR_{21}	**30.0372670945687**	0.92462	1.17574	1.07419	0.77717	0.63473	1.10223	2.03326	1.83086	1.42504	1.20992	1.28666	1.61874	1.05480	0.98566	1.15746	1.75050	2.62095	1.75481	2.11631	1.90709	1.59650
16537.17-1 (AJMC1)	LR_{21}	**27.6123493449457**	0.64078	1.80443	1.07540	1.75552	1.48982	1.08225	2.28756	1.64474	1.32162	0.79036	1.15085	1.54507	-0.26947	0.72822	1.13789	1.04825	1.69990	2.60598	1.28106	1.19050	1.60164
16537.17-1 (ASLS1)	LR_{21}	**28.4363694047128**	0.33688	1.83033	1.03810	1.59326	0.65551	1.07350	1.66345	1.43989	0.86304	1.48433	1.02723	2.49932	0.70662	1.72604	1.54533	0.97178	2.17149	0.79390	1.32504	1.56258	2.12872
16672.17-4R2 (4R1)	LR_{21}	**25.7616347034453**	0.75919	1.06536	1.57484	1.06506	0.64777	1.58204	1.64666	1.53083	1.14054	0.83110	-1.77976	1.96326	0.95988	1.64784	0.74740	1.37460	2.99188	0.77892	1.53007	2.22363	1.48054
16672.17-4R2 (AMC1)	LR_{21}	**-**	1.26548	-0.75496	0.21945	1.92652	0.26630	1.10285	1.00048	1.17780	0.79305	2.31852	-1.72074	1.12202	1.08182	-	1.49627	1.18656	2.28937	1.19620	2.13229	1.72463	1.19126
	$LR_{<21}$	**21.0151081606458**	1.26548	-0.75496	0.21945	1.92652	0.26630	1.10285	1.00048	1.17780	0.79305	2.31852	-1.72074	1.12202	1.08182	X	1.49627	1.18656	2.28937	1.19620	2.13229	1.72463	1.19126
16913.17-3 (NMSAOM1)	LR_{21}	**20.6867077521827**	0.55057	1.00264	0.92118	0.47129	0.81222	1.21195	1.38139	1.23203	0.61701	1.53194	0.61619	1.35166	0.86306	0.42930	0.93225	0.65754	1.51564	0.89230	1.48753	1.01712	1.19193
17065.17-1 (3)	LR_{21}	**28.3853023398563**	1.32650	1.43482	1.31014	1.33712	0.64645	1.36607	1.45384	1.38331	0.78869	1.43716	0.92105	1.32265	1.60032	0.64009	1.25777	1.21237	2.06371	0.77982	1.73176	2.29918	2.07247
17065.17-1 (SSC1)	LR_{21}	**-**	0.78817	1.62833	0.94585	1.60633	0.80500	1.09043	2.01586	1.53344	0.69912	0.79844	1.17228	1.62490	1.28724	0.22324	0.83648	0.82300	2.58809	1.16729	1.76591	1.27994	-
	LR_{21}	**24.6793097669857**	0.78817	1.62833	0.94585	1.60633	0.80500	1.09043	2.01586	1.53344	0.69912	0.79844	1.17228	1.62490	1.28724	0.22324	0.83648	0.82300	2.58809	1.16729	1.76591	1.27994	X
17222.17-3R2FF (3R1)	LR_{21}	**23.6682927104482**	1.71543	1.01778	0.84797	0.54118	0.61190	1.02123	1.35284	1.26991	1.56940	0.93588	1.02036	1.09339	1.41967	0.83801	1.36739	1.02698	2.04895	1.28641	1.65267	1.34912	-0.31818
17222.17-3R2FF (PM1)	LR_{21}	**-**	0.92663	1.13900	0.94790	2.16935	0.62056	1.13274	1.64502	1.22768	1.32042	1.31511	1.10704	1.16749	1.08182	0.83824	0.74341	1.70504	1.34629	1.16926	1.51981	1.79233	-
	$LR_{<21}$	**24.9151095049392**	0.92663	1.13900	0.94790	2.16935	0.62056	1.13274	1.64502	1.22768	1.32042	1.31511	1.10704	1.16749	1.08182	0.83824	0.74341	1.70504	1.34629	1.16926	1.51981	1.79233	X
18119.17-2 (LZ1)	LR_{21}	**14.9324483962679**	-0.10907	1.32607	0.84559	0.85968	0.56326	0.78725	1.04001	0.48224	0.08629	1.03763	0.92637	1.01233	0.06577	0.08382	1.21743	-0.29768	1.58045	0.02015	1.10476	0.99552	1.30460
19187.16-4CABO (RGCF)	LR_{21}	**11.9150514155866**	-0.13280	0.86302	0.63074	0.95084	-0.30998	0.75836	0.22626	1.14201	0.64434	0.13085	0.36515	0.62153	0.97274	0.55828	0.97278	0.51504	0.01536	0.90280	1.49711	1.30099	-0.71039
19724.16-6 (ENP1)	LR_{21}	**26.5798978696031**	1.32029	1.14404	0.42775	0.88213	0.44999	1.11002	1.02555	1.63691	0.85016	1.94287	1.10565	1.52674	1.70400	0.92419	1.40216	0.85152	1.84749	0.76498	1.86363	1.76043	2.03941
19724.16-6 (13)	LR_{21}	**23.9939033417933**	1.28321	1.33375	0.51352	0.62896	-0.84722	1.41804	2.13223	1.53344	0.75312	0.83110	0.86301	1.59922	1.07070	0.53519	1.21269	0.93756	2.31842	0.67783	1.96232	1.52139	1.71542
19724.16-8 (BMAP)	LR_{21}	**26.3127272837781**	1.91829	0.57287	1.06239	0.67595	0.73118	1.35216	1.64329	1.25147	0.79909	1.57635	1.10527	1.48711	1.16885	0.97127	1.16119	0.98782	2.30339	1.02465	1.86140	1.21764	1.44107
19799.17-1 (TFPA1)	LR_{21}	**-**	0.51077	0.73943	0.59155	0.18182	1.12691	0.99901	1.55022	-	0.54225	1.05990	0.54676	0.81381	0.90456	0.53382	-0.98284	1.01490	1.91587	1.78032	-	-	1.03663
	$LR_{<21}$	**14.8657315593765**	0.51077	0.73943	0.59155	0.18182	1.12691	0.99901	1.55022	X	0.54225	1.05990	0.54676	0.81381	0.90456	0.53382	-0.98284	1.01490	1.91587	1.78032	X	X	1.03663
20601.16-1 (HMNM1)	LR_{21}	**5.5436583735350**	0.83597	0.69383	1.05415	0.85372	-0.48645	0.38382	-2.61165	0.69767	-0.98754	0.49938	0.64350	1.16450	-0.03495	0.25631	0.20696	0.06390	0.36161	-1.57840	1.47496	1.41711	0.63518
20601.16-1 (AMM)	LR_{21}	**20.1789769472932**	0.84763	0.83655	0.83644	0.51424	0.29743	0.76813	1.79012	1.20734	0.79011	1.06833	0.60344	1.01783	0.17875	0.63417	0.75872	0.47945	2.33506	1.15912	0.95393	1.87602	1.22619
20628.16-1CABO (AMP)	LR_{21}	**-**	1.41967	1.10917	0.92531	0.84590	0.59384	0.87749	1.84644	1.31725	-	0.83110	0.96388	1.37477	0.36371	1.70780	1.64864	1.10609	1.85890	1.06922	1.13814	1.82606	1.63349
	$LR_{<21}$	**26.0080896024047**	1.41967	1.10917	1.00860	0.84843	0.62323	0.90374	1.86591	1.56426	X	0.83110	1.05369	1.37477	0.70804	1.87856	1.58652	1.10609	1.99426	1.16979	1.28726	1.82606	1.84894

Table B4: Log_{10} values of the global LRs computed by EuroForMix v.1.9.3 without stutters[1], for mixtures with three estimated contributors.

Mixture (Reference)	**Log_{10} (LR)**
245.17-2.1 (MABS)	22.025242594612
245.17-2.1 (OCF)	29.540851585487
428.17-10 (LHIF)	25.9617521662695
1305-17-3 (PBS1)	10.3040607689126
1305-17-3 (RDS1)	16.7418187946501
1533.17-4 (EIJB1)	17.2919420237485
2193.16-3 (MNTB)	12.6280652834578
2193.16-3 (MHMB)	5.74528211816608
2793.17-1R3 (FJCM1)	16.7360138686195
3053.17-5R2 (MHR2)	20.1680203311183
3053.17-5R2 (CDS1)	16.1772645737313
3357.17-12.2 (9)	13.1007372271444
3665.17-26 (SL2)	11.1626427793288
3675.17-1 (AJRG1)	12.392971624218
3675.17-1 (ORG1)	20.0564024946498
3841.17-7 (3)	7.24105824564174
3958.17-1R2FF (LGS1)	12.1108110875209
4406.17-6 (CVG)	16.6197588094763
4406.17-6 (NGP)	27.2529753237408
4548.16-PC9.9 (PC9.8)	24.6046933544984
4702.17-1 (CSP1)	23.6833942448028
4980.17-11 (JAMR1)	22.0773264618335
5008.17-1R1 (1R2)	14.3134013077989
5008.17-1R1 (2R1)	26.0436845150884
5008.17-3CABO (3LAM)	26.7856896916695
5008.17-3CABO (4R2)	19.2405098847836
5374.16-9 (BMEB1)	11.2884983182941
5396.16-1CABO (JJCC)	18.6451538701864
6561.17-2BIO (FMGV1)	23.8930533883437
6561.17-2BIO (JAPG1)	21.61403251922
6568.17-9 (DFSDN1)	12.0225570771193
6568.17-9 (RFAS2)	15.2492149493157
6978.17-4R2 (7FF)	22.6308135065466
6978.17-4R2 (JAB1)	24.4149152646666
7245.17-1R1 (1R2)	24.9072082570914
7582.17-1 (FMBSC)	9.04900110874182
8356.16-8.2FF (DPMF)	6.35811993068392
8356.16-8.2FF (HVF)	23.6901017029986
8371.16-1R1 (JARR1)	23.4394241366229
8393.17-2FF (JPB2)	26.4985356592412
8393.17-2FF (TFB2)	25.1153838762474
8410.16-2R1 (2R2)	10.5467044435969
10175.16-4 (5)	9.51368011162453
10278.16-2 (1)	6.19262068892204
10814.16-2 (CMSA)	22.4043448648466
10814.16-2 (FMRG)	10.4289758273253
11021.17-20LAM (MABSC1)	10.7048676962376
11021.17-20LAM (MGSF1)	10.7461423628535
11021.17-20LAM (MSSF1)	13.9582054600881
12179.17-14R6 (GCG1)	12.2233102403254
12179.17-14R6 (MAM1)	11.9412695678434
12946.17-3.1 (2)	18.8741897951599
13020.17-1LAM (1CABO)	7.86571847711734
13046.17-1R1 (2R1)	18.7951805911863
13253.17-4 (3)	13.1328401553289
13367.17-5 (SMCP1)	7.02779657615023
14005.17-1R1FF (1R2FM)	13.8752009459686
14005.17-1R1FF (2R1FF)	22.841910169194
14281.17-6R1 (6R2)	10.2866023147339
14281.17-6R1 (MGGS1)	9.45870284985563
14503.17-1 (MRER1)	14.5728190111245
14828.17-2FF (1FF)	23.1252270845659
14828.17-2FF (FLEP1)	17.7214518434267
14942.17-2LAM (3R1)	14.2228484565367
14942.17-2LAM (NMLC1)	20.4295679053781
15014.17-1 (2)	24.5932994777537
16839.17-1.9 (BZ1)	10.9321359276071
16839.17-1.9 (JW1)	12.1450313544242
16839.17-1.9 (QJ1)	10.6951221369783
18094.16-2 (IMSS)	23.2916105884955
18094.16-2 (CCM)	27.1424318983886
18690.17-2R1 (1R1)	15.9600914820904
18690.17-2R1 (CFB2)	17.5177734055256
19364.16-4M1 (MPPA1)	22.5401959420317
19364.16-4M1 (HJDC)	19.4146044123045
20008.17-1 (RMRO1)	7.25374508186393
20880.15-2R2 (1)	17.5680591488719
23308.16-6CABO (AFM)	18.7637005142594
23308.16-6CABO (MARCC)	12.1473305589433

[1]Computed by Figueiredo C: Forensic DNA mixtures: Analysis and comparison of software results. Faculdade de Ciências da Universidade do Porto; 2018.

Table B5: Log_{10} values of the LRs (by markers and global) computed by EuroForMix v.1.9.3 with stutters, for mixtures with three estimated contributors. The markers that have been removed to allow comparison with STRmix™ values are referenced with an "X".

Mixture (Reference)		Log_{10} (LR)	D3S1358	vWA	D16S539	CSF1PO	TPOX	D8S1179	D21S11	D18S51	D2S441	D19S433	TH01	FGA	D22S1045	D5S818	D13S317	D7S820	SE33	D10S1248	D1S1656	D12S391	D2S1338
245.17-2.1 (MABS)	LR_{21}	**21.246277801342**	1.07777	1.43941	0.61820	-0.08170	-0.20177	0.79897	1.72786	1.65332	1.49666	1.06667	1.10274	0.77577	0.47199	1.02791	0.88465	0.80501	2.06220	-0.19456	1.10712	1.62537	1.98273
245.17-2.1 (OCF)	LR_{21}	**29.62090859878**	1.07211	0.93131	1.14812	0.79002	2.86663	1.22073	1.80963	1.55381	0.77824	2.10399	1.02464	1.99687	1.29566	0.80327	0.75164	1.16542	1.94827	1.06786	2.03289	1.34001	1.91977
428.17-10 (LHIF)	LR_{21}	**28.725729787778**	1.19319	1.17973	0.87494	1.62642	0.96347	0.75874	1.04131	1.39497	1.50009	1.74570	1.28552	2.59805	0.19384	2.61327	0.88015	1.34751	1.93859	0.48084	2.20035	1.40146	1.50759
1305-17-3 (PBS1)	LR_{21}	**11.633992929905**	0.24475	0.37584	0.60073	-0.02964	-0.36113	0.58013	0.97080	0.70875	-0.03507	-0.14173	0.40238	1.83273	0.52041	0.55247	0.39671	0.67983	1.71842	0.04976	0.75387	1.15123	0.66274
1305-17-3 (RDS1)	LR_{21}	**15.729141191005**	0.63543	0.87124	0.58272	0.27184	0.45057	1.46511	0.97108	0.81363	1.02279	0.73481	-1.13961	0.78839	0.51440	0.57403	1.03727	0.62988	1.10531	1.19528	1.54270	1.16515	0.49710
1533.17-4 (EIJB1)	LR_{21}	**17.276084323526**	0.65372	0.34218	1.57566	0.88224	-0.02816	0.98649	0.92573	0.97453	1.36825	1.23802	0.59043	0.68951	0.33936	0.21174	0.75300	0.47388	2.07564	-0.25389	1.37831	0.94358	1.15584
2193.16-3 (MNTB)	LR_{21}	**13.0095854175**	0.77933	0.64049	1.14024	-0.09223	0.11152	0.54729	1.13027	1.11900	-0.26771	1.23610	-0.36971	0.21388	-0.25365	0.49025	0.95150	0.59880	1.22154	0.08356	1.26794	1.70198	0.75919
2193.16-3 (MHMB)	LR_{21}	**5.847435571727**	0.38087	0.11404	0.10240	0.04866	-0.26163	0.58875	0.75444	0.09854	0.59188	-0.01975	0.52254	-0.12745	0.52033	0.43225	0.01433	0.22254	0.28438	-0.10258	0.95908	0.29802	0.42579
2793.17-1R3 (FJCM1)	LR_{21}	**16.733292048839**	0.73403	2.17535	0.49237	0.01073	-0.14552	0.37894	0.94091	1.28939	0.24822	1.25681	0.14585	1.09964	2.13000	0.63963	0.52314	0.90469	0.91701	0.19877	1.24904	0.97807	0.56623
3053.17-5R2 (MHR2)	LR_{21}	**20.442669253036**	0.60235	0.58916	1.10096	0.69887	0.21376	2.13070	0.69852	1.22031	0.55454	1.38814	0.59558	1.05040	0.70254	0.24273	1.35870	1.42578	2.29723	0.50440	1.56196	1.01916	0.48688
3053.17-5R2 (CDS1)	LR_{21}	**18.514599660001**	0.72950	0.30011	-0.05289	0.54248	-0.24949	0.83108	1.08780	1.17994	0.19553	1.80232	-0.02381	2.19019	1.00406	0.65609	1.01047	1.78990	2.42799	-0.13648	1.53987	0.76870	0.92123
3357.17-12.2 (9)	LR_{21}	**14.621681399089**	0.56787	1.05577	0.49571	-0.39617	-0.61068	0.67633	1.34429	1.66540	0.44803	0.29299	0.64585	2.06464	0.34941	0.64395	0.95966	0.79856	1.34124	-0.44795	1.24547	0.93157	0.54974
3665.17-26 (SL2)	LR_{21}	**11.274330383985**	0.34170	0.36523	0.07619	0.08447	0.30122	0.08941	0.24855	1.62568	1.07856	0.24970	0.25726	0.32618	1.61833	0.23246	0.85044	0.19657	2.02475	0.38678	-0.46999	0.77952	0.61130
3675.17-1 (AJRG1)	LR_{21}	**10.816702239596**	0.63749	0.68902	0.26060	0.52241	0.49402	0.02994	0.29772	0.20927	0.15698	0.63325	0.98809	0.81241	0.65212	0.32441	0.55067	0.43757	1.05814	0.66796	0.10837	0.71925	0.56703
3675.17-1 (ORG1)	LR_{21}	**20.735115673938**	1.04528	1.20938	0.62658	0.57929	0.42691	0.15094	0.95070	1.45747	0.75421	1.07381	0.83742	1.33266	0.90359	1.02558	1.13920	0.81441	1.93939	0.41528	1.44275	1.33437	1.27591
3841.17-7 (3)	LR_{21}	**7.045956386824**	0.30000	0.31230	0.22299	0.14189	0.22989	0.05416	0.18890	0.36306	-0.18085	0.57516	0.22338	1.24956	0.51564	0.08180	0.09192	0.24613	1.20150	-0.24365	0.70073	0.48284	0.28859
3958.17-1R2FF (LGS1)	LR_{21}	**14.533014626603**	0.84483	0.58962	0.56099	-0.08157	-0.29641	0.40395	0.67385	0.48201	0.86855	0.84438	-0.05428	0.53837	0.70947	0.19877	0.74516	0.56639	1.58797	0.62834	1.37492	2.22060	1.12711
4406.17-6 (CVG)	LR_{21}	**15.181765086879**	0.88930	0.82542	0.82800	0.10551	-0.40860	0.86010	0.97219	1.14742	0.73579	1.79387	1.22683	0.84587	0.43457	0.91803	-2.65722	0.91356	2.34082	-1.45782	1.68709	2.27216	0.90887
	$LR_{<21}$	**20.043600139016**	0.92878	0.94111	1.09691	-0.12738	-0.48919	0.60264	0.95538	1.43857	0.68854	1.74017	1.28120	1.10075	0.56227	0.78370	X	1.03024	2.54660	X	1.67123	2.50202	0.79005
4406.17-6 (NGP)	LR_{21}	**27.68316902588**	0.94923	1.11994	1.32098	0.69429	2.06001	0.94323	1.16249	1.28953	1.04856	2.37365	1.01050	1.36696	0.85671	0.93794	1.42369	0.95068	2.18400	0.52179	2.18973	1.65956	1.61972
	$LR_{<21}$	**26.056066623359**	0.96132	1.12796	1.32083	0.69179	2.04380	0.94745	1.16632	1.26343	1.06144	2.39278	1.01628	1.33743	0.83890	0.94998	1.42289	0.95518	2.19784	1.33743	2.20465	1.65322	X
4548.16-PC9.9 (PC9.8)	LR_{21}	**18.483461839374**	-0.33013	0.62006	1.87772	1.02597	0.13617	1.36946	1.26251	-0.13100	0.20062	0.94651	1.46783	0.94816	1.18096	1.07799	0.90734	0.66594	1.36892	0.69643	1.16354	0.81427	1.21419
	$LR_{<21}$	**17.087071447212**	-0.28208	0.63167	1.86468	1.00592	0.15862	1.31150	1.27375	-0.07541	0.24697	0.95958	1.43595	0.96432	1.13673	1.06318	0.91982	0.64443	X	0.96432	1.10079	0.83082	1.21980
4702.17-1 (CSP1)	LR_{21}	**23.899831916364**	0.94700	1.06251	1.29066	0.60973	0.50107	0.84598	1.20537	1.69667	1.40576	0.84522	1.31766	1.44372	0.52434	0.56812	1.17002	1.01214	1.90457	0.97039	1.83058	1.48217	1.26613
4980.17-11 (JAMR1)	LR_{21}	**22.114507251029**	1.11301	0.90065	-0.26847	1.57771	-0.39950	1.15953	1.13082	1.11357	1.21252	1.77950	1.14003	1.40337	0.52675	0.41025	1.37639	1.61980	2.07324	0.67936	1.48868	1.21378	0.86351
5008.17-1R1 (1R2)	LR_{21}	**15.749396121527**	1.41424	0.53922	0.21935	-0.14041	0.00366	-0.06520	0.66471	1.87181	0.45016	2.46363	1.36962	0.90292	-1.36278	1.72724	0.38207	0.93700	0.68571	0.14813	1.79890	0.68028	1.05912
5008.17-1R1 (2R1)	$LR_{<21}$	**25.966348022267**	0.93128	1.18773	0.69679	1.64702	0.12515	0.88230	1.76795	1.51648	0.92994	0.33430	1.41353	1.84759	1.57288	0.15624	1.26211	0.93436	1.97899	1.55088	1.34134	2.30011	1.58941
5008.17-3CABO (3LAM)	LR_{21}	**28.970970111009**	1.08854	1.23145	0.23085	1.86580	0.61174	1.65777	2.95233	1.60347	0.82502	1.52852	0.54277	1.46832	1.23885	2.54540	0.64216	1.32702	1.92675	1.34302	1.49704	1.23226	1.61188
5008.17-3CABO (4R2)	LR_{21}	**21.847168954758**	1.07048	1.33613	0.73390	0.09616	-1.34136	2.21742	1.60534	1.60740	1.63112	1.31426	0.91896	1.45679	0.49649	1.59428	1.27488	0.56856	2.49830	-1.52866	2.25858	0.90245	1.13570
5374.16-9 (BMEB1)	LR_{21}	**11.315847472114**	0.53937	0.01599	0.15274	0.47255	-0.11942	0.11294	1.00504	0.54487	0.70463	0.18598	0.38713	0.52718	0.90070	0.84781	-0.10140	0.65158	1.21119	0.67163	0.45372	1.53665	0.61498
5396.16-1CABO (JJCC)	LR_{21}	**20.8995443847**	0.71049	1.10636	0.46130	0.65529	0.48941	1.72489	1.07198	1.31796	0.46051	1.33398	1.33920	0.97969	0.25131	0.71383	1.33013	0.79648	1.48225	-0.37933	1.28268	1.33879	2.43234
6561.17-2BIO (FMGV1)	LR_{21}	**23.760202891059**	1.19237	1.23166	0.91174	0.63510	0.48027	-0.22748	1.11475	1.68311	1.52873	1.41352	0.48227	1.53583	0.83728	1.80862	0.71756	0.88953	2.07823	0.46800	2.00155	1.52973	1.44781
6561.17-2BIO (JAPG1)	LR_{21}	**21.408881704623**	0.89967	1.00680	1.17862	0.26284	-0.34458	0.90798	0.94380	2.21935	1.09239	1.10527	0.40570	1.11039	0.71064	0.38352	1.35767	1.00854	2.41748	-0.48474	0.99531	1.74919	2.48304
6568.17-9 (DFSDN1)	LR_{21}	**11.930740551371**	0.29516	0.58470	0.59336	0.20736	0.66173	0.69835	0.84369	0.00130	0.72329	0.49002	0.92440	0.65996	0.23856	0.20761	0.52213	-1.10314	1.18786	0.19151	0.81909	1.33424	0.84954
6568.17-9 (RFAS2)	LR_{21}	**10.650116761646**	1.28928	0.76917	0.53373	0.96198	-0.03055	0.34527	-0.58194	1.24192	0.81485	0.42646	1.01363	1.07120	0.26728	-0.10713	0.36319	0.40651	1.37578	0.77967	-2.94339	0.57762	1.07560
6978.17-4R2 (7FF)	LR_{21}	**22.089578618836**	0.84480	1.38266	0.92998	0.88452	0.50863	2.24184	1.24860	1.28840	1.36347	-0.75070	0.87664	1.10764	0.41968	0.59127	1.17373	1.14212	2.34053	0.13134	1.64981	1.55107	1.16356
6978.17-4R2 (JAB1)	LR_{21}	**21.770670525549**	1.15094	2.23925	0.24956	0.12164	-0.00517	2.46421	0.89838	1.35652	1.07269	0.78334	1.18766	0.84001	-0.12433	0.94874	1.32820	0.69488	1.40541	0.88112	2.03576	1.46695	0.77491
7245.17-1R1 (1R2)	LR_{21}	**29.62327075679**	0.87383	1.19014	1.14216	2.15807	0.57476	1.41394	1.49048	2.01525	1.41476	1.59195	1.18955	1.23397	2.19545	0.93691	1.69663	1.13841	1.79082	0.91678	1.53975	1.43690	1.68275
7582.17-1 (FMBSC)	LR_{21}	**8.445067683689**	0.56722	0.29420	0.10106	-0.18020	0.20386	-0.23137	0.15665	0.55688	-0.03411	0.54563	1.29623	0.91192	-0.66840	0.15865	0.11530	0.71361	2.04895	0.53554	0.62069	0.21248	0.52029
	$LR_{<21}$	**9.510256031334**	0.61799	0.29596	0.12225	-0.21699	0.22252	X	0.20861	0.61273	-0.09531	0.45799	1.32017	0.85058	X	0.16832	0.11927	0.76046	2.15472	0.85058	0.66152	0.22115	0.46524
8356.16-8.2FF (DPMF)	LR_{21}	**6.431609730544**	0.61207	0.76519	-0.51232	-0.33003	-0.63084	0.62761	0.64342	-0.16773	0.33521	0.19305	0.08245	0.77908	0.05088	0.31237	0.55083	0.48192	0.34524	-0.00321	0.60473	0.74324	0.94845
8356.16-8.2FF (HVF)	LR_{21}	**24.001419980631**	1.34973	1.18077	1.26986	-0.67788	-0.59810	0.96205	0.89332	1.36627	1.15575	2.16013	1.87952	1.52706	2.03124	1.06331	2.01970	0.59417	1.71067	-0.16679	1.96530	1.10058	1.21475
8371.16-1R1 (JARR1)	LR_{21}	**25.126060279112**	0.85345	1.03203	1.12554	0.25334	0.52209	1.63838	1.45066	2.01366	0.89173	1.51649	1.49656	1.14150	0.47440	0.61887	1.43662	1.23404	1.35402	0.40303	2.15761	1.41617	2.09586
8393.17-2FF (JPB2)	LR_{21}	**26.479653713799**	1.09304	1.44266	1.26536	1.99733	0.00095	1.42855	0.68481	1.47100	0.81922	0.34165	1.08267	2.04857	1.16590	0.47087	0.81459	0.97545	2.48765	1.81086	1.64945	2.31765	1.11142
8393.17-2FF (TFB2)	LR_{21}	**25.10442499717**	0.93055	1.62846	0.42557	0.42153	1.07044	1.00625	2.27438	2.22329	0.84597	0.21597	0.58969	0.67552	1.08320	0.75811	1.07419	1.48090	2.56708	1.08178	1.77405	1.96539	1.01210
8410.16-2R1 (2R2)	LR_{21}	**9.551264477066**	0.20231	0.14555	0.31928	-0.31681	-0.11783	-0.08917	0.95872	0.50791	0.80387	0.90191	0.54362	0.66149	0.00141	-0.13751	0.31850	0.04619	1.43640	0.74721	0.76963	1.06661	0.78200
10175.16-4 (5)	LR_{21}	**10.866596715077**	0.63885	-0.11289	0.21018	-0.96567	0.08561	0.38805	0.45716	1.02746	0.90926	0.17922	0.60524	1.02818	0.54621	0.24885	0.19670	0.78771	1.26728	-0.07577	1.56604	1.23696	0.64198

10278.16-2 (1)	LR_{21}	**5.737312510137**	-0.02101	0.74579	0.16983	0.08889	-0.05089	1.33687	0.01781	0.52575	0.66586	-0.17899	-0.21501	0.71010	-0.02088	0.12823	0.15435	0.49202	1.00219	-0.21065	0.93399	-1.13143	0.59448
10814.16-2 (CMSA)	LR_{21}	**21.801916122278**	0.93337	1.47821	0.73789	0.74332	1.31921	0.85715	-1.23176	-1.59769	1.19667	1.49417	2.02867	1.04907	0.41245	1.01206	1.19370	1.75836	1.67521	0.72041	1.83751	2.45165	1.73227
	$LR_{<21}$	**20.125499678538**	0.93571	1.47355	0.72441	0.73115	1.26209	0.85144	-1.13615	-1.48594	1.19347	1.47758	1.98896	1.04122	0.41300	0.99275	1.17230	1.74768	X	1.04122	1.84486	2.45589	1.73308
10814.16-2 (FMRG)	LR_{21}	**10.335559165459**	0.39254	0.76907	0.56993	0.24239	-0.15931	0.36652	0.96734	0.83945	0.61130	-0.10571	0.02844	0.49849	0.78281	0.55524	0.75303	-0.44209	1.49711	0.31566	1.11385	0.97127	-0.23175
11021.17-20LAM (MABSC1)	LR_{21}	**7.269168405586**	0.05607	0.56104	0.29066	0.45322	0.73105	0.41561	0.10997	0.02664	0.82543	0.10886	-2.87807	0.96112	0.37836	0.11514	0.71696	0.19090	1.29161	0.29512	0.80148	1.06741	0.75057
11021.17-20LAM (MGSF1)	LR_{21}	**11.215795678833**	0.13909	1.37974	1.08315	-0.15781	-0.54600	-0.04913	0.55651	0.47568	0.75137	0.48966	0.08025	0.96115	0.10346	0.04431	0.28852	0.37112	1.83622	0.13568	0.97680	1.31854	0.97748
11021.17-20LAM (MSSF1)	LR_{21}	**14.601122980816**	0.74747	0.52158	0.39618	0.28123	0.09973	0.69113	0.38614	0.79842	1.10046	0.39391	0.24557	0.67033	0.58082	0.30032	0.25813	0.58789	0.69102	1.55641	1.30468	1.58568	1.40403
12179.17-14R6 (GCG1)	LR_{21}	**12.29073997485**	0.50227	0.32835	0.72558	0.47775	-0.12515	1.23641	0.68292	1.03003	-0.92955	0.10977	0.34153	1.15245	0.72244	0.52140	0.18051	0.88433	1.90600	0.71213	1.24435	1.05672	-0.46949
12179.17-14R6 (MAM1)	LR_{21}	**12.164633655318**	0.73749	0.17883	0.63034	0.42900	0.74415	0.95940	0.16272	0.80043	0.64702	0.26856	0.62428	-0.48916	0.57814	0.48693	0.41112	0.59338	1.27432	0.67455	1.75731	0.89338	-0.19755
12946.17-3.1 (2)	LR_{21}	**20.049727647164**	-0.08339	0.49523	0.60394	0.79489	0.69323	0.39686	1.84009	1.84135	0.44994	1.50311	0.55549	0.63505	0.44186	0.51931	1.02845	1.25161	2.69744	-0.20656	1.60090	1.43787	1.55307
13020.17-1LAM (1CABO)	LR_{21}	**9.784966749287**	0.53057	0.85812	0.22636	-1.04668	-0.06381	0.57364	0.58299	0.89397	0.65286	0.46834	0.70898	0.67291	-0.92358	0.51538	0.12168	0.74489	1.32525	-0.41527	1.58487	0.74753	1.02598
13046.17-1R1 (2R1)	LR_{21}	**18.769284844306**	0.66298	2.07796	0.36534	0.69227	1.02762	0.57417	0.67195	0.84341	0.62033	0.55536	0.54161	0.33939	-0.06556	0.26894	0.66881	0.78421	2.07202	0.94986	1.28562	1.81741	2.01558
13253.17-4 (3)	LR_{21}	**13.170962322155**	0.58711	1.15827	0.57232	-0.04523	0.71337	0.63813	-0.05742	0.56154	1.39329	0.61974	0.36045	0.70881	-0.17962	0.22987	0.81298	0.78720	0.95343	0.16141	1.30203	1.27949	0.61381
13367.17-5 (SMCP1)	LR_{21}	**7.907517728392**	0.34007	0.47864	0.15738	0.73211	0.36987	0.14722	1.45699	0.18298	0.41666	0.24900	0.69306	0.42320	0.16320	0.64663	0.92283	0.26142	1.60417	-0.30961	0.87150	0.78298	-2.68278
	$LR_{<21}$	**10.975305801497**	0.38857	0.53800	0.01281	0.67611	0.18019	0.14248	1.62951	0.10408	0.46549	0.35541	0.78455	0.40023	0.19694	0.74918	1.11137	0.22187	1.66892	0.40023	1.03586	0.91803	X
14005.17-1R1FF (1R2FM)	LR_{21}	**13.590913989632**	0.60923	0.50170	0.23112	-0.49216	-0.83897	0.14306	2.60798	0.74341	0.83851	0.82872	0.28411	2.33505	0.09375	-0.91644	1.45547	0.86734	1.07582	-0.63392	1.18441	1.13868	1.53404
14005.17-1R1FF (2R1FF)	LR_{21}	**22.931700990449**	1.08779	1.22080	0.70580	0.59064	0.52525	1.11119	1.66513	1.54702	1.37908	1.41251	0.89564	0.76432	1.27012	1.03743	0.86052	1.15697	1.79816	0.87512	1.38252	0.76192	0.88375
14281.17-6R1 (6R2)	LR_{21}	**10.924236770759**	1.26933	0.03118	0.41563	0.18031	-0.43502	0.39389	0.34999	0.67547	0.58994	1.49974	-0.17369	0.53588	-0.03745	0.43318	0.34101	0.24076	1.37933	0.09213	1.48824	1.55158	0.10280
14281.17-6R1 (MGGS1)	LR_{21}	**9.547341911622**	0.33011	0.50774	0.27369	0.31824	0.29019	0.46509	0.84663	0.93037	0.59494	0.11982	0.42403	0.65630	0.79955	0.18668	0.52375	0.23707	1.32700	0.16178	0.65244	-0.43166	0.33358
14503.17-1 (MRER1)	LR_{21}	**12.395770608518**	0.56906	1.05830	0.59447	0.51776	0.30087	0.74748	0.82503	0.83712	0.77595	1.58150	0.41507	0.72092	0.40942	-0.01999	0.92437	0.56991	1.28718	-2.08075	0.57195	0.61184	1.17831
14828.17-2FF (1FF)	LR_{21}	**23.841213189931**	1.07165	1.05094	0.44544	0.53480	0.61772	1.38801	1.35142	1.72390	0.60455	1.52698	0.93213	1.59253	0.74551	1.43455	1.40111	1.33583	1.75189	0.68144	1.56609	1.93386	0.15087
14828.17-2FF (FLEP1)	LR_{21}	**19.225574511092**	-0.04470	0.41767	0.31865	0.82890	-0.40043	1.24283	1.24633	1.31738	1.99213	0.84895	0.74228	1.20899	0.25701	1.14803	1.59276	1.05429	2.28239	0.03396	1.90953	1.20343	0.02518
14942.17-2LAM (3R1)	LR_{21}	**14.228219881578**	0.20145	0.20425	1.04789	1.42647	-0.44483	0.08491	0.60962	1.13029	1.03823	0.26570	0.79759	0.49839	0.62173	0.17517	0.41350	0.84283	1.50634	0.97511	1.22977	0.77222	0.83160
14942.17-2LAM (NMLC1)	LR_{21}	**20.442877585104**	0.36801	0.80078	0.38213	0.36259	0.85628	1.62248	1.72738	1.33191	0.76658	0.36725	1.02171	1.49675	1.65125	0.82609	0.44870	0.92043	1.35000	0.28353	0.93266	1.85214	1.07424
15014.17-1 (2)	LR_{21}	**24.702290513837**	0.98269	1.54975	0.50464	-0.05556	1.28636	0.67254	0.63847	1.35194	1.77528	1.53324	0.82412	1.21094	0.82088	1.08391	1.26240	1.37510	2.29098	-0.00401	2.23480	1.26370	2.10011
16839.17-1.9 (BZ1)	LR_{21}	**11.313188087447**	0.63079	0.69685	0.34057	0.67231	0.10293	0.04586	0.62607	1.36029	-0.22753	1.14346	1.02593	-0.12909	-0.21134	0.10696	0.54877	0.24278	1.32548	0.06794	1.31596	0.49427	1.13395
16839.17-1.9 (JW1)	LR_{21}	**12.797917653524**	0.29989	0.47920	0.00376	0.72169	0.03457	1.74485	0.71230	0.46408	0.33458	0.44616	0.71793	1.30137	0.38246	0.25795	0.48004	0.15428	1.73280	0.15997	0.83148	0.34098	1.19759
16839.17-1.9 (QJ1)	LR_{21}	**10.288648540677**	0.35051	-0.01095	0.25907	0.07607	0.09690	0.79642	0.66243	0.27041	0.11937	0.44007	0.98992	0.56469	0.31098	2.01563	0.50378	-0.12342	1.20365	-0.03148	0.35989	0.64934	0.78538
18094.16-2 (IMSS)	LR_{21}	**23.840865009379**	1.03825	1.11047	1.60320	0.75725	0.24763	0.87541	1.28309	1.80495	0.86485	0.55353	0.91226	1.41278	0.83639	0.83697	0.87137	1.03632	1.82679	1.05317	1.65492	1.73736	1.52389
18094.16-2 (CCM)	LR_{21}	**27.354784273429**	1.09645	1.01588	0.97920	1.25359	0.48987	1.84946	1.28018	1.37251	1.26335	1.06710	1.20025	1.30288	1.02231	0.57019	1.85826	1.03066	2.23476	1.79873	1.69028	1.50456	1.47432
18690.17-2R1 (1R1)	LR_{21}	**17.535830066048**	0.38792	0.93433	0.34896	0.66047	0.61605	1.17178	0.41930	1.06389	1.29587	1.29646	-0.10041	1.57047	0.43356	0.65429	1.07792	0.98411	1.84522	-0.14731	1.07051	0.73837	1.21408
18690.17-2R1 (CFB2)	LR_{21}	**10.223041398087**	0.31555	0.96442	0.34246	0.58264	1.53466	1.03952	0.34721	0.54556	1.12384	0.90896	-0.25978	1.22591	0.37440	0.40871	0.91444	0.78902	-3.43939	0.48413	0.95276	0.38209	0.68596
	$LR_{<21}$	**15.623008221885**	0.39118	0.93872	0.32008	0.62553	0.79372	1.22290	0.40774	0.96898	1.24554	1.26215	-0.07427	1.51744	0.43228	0.64570	1.03342	0.93519	X	1.51744	1.08372	0.68858	1.13850
19364.16-4M1 (MPPA1)	LR_{21}	**22.72511282247**	0.90185	0.89039	-0.13147	0.69886	0.33367	1.11204	1.51190	2.79049	0.46831	0.44466	0.70949	2.67574	0.04308	0.68824	0.83412	1.01463	2.64001	0.38210	1.75527	1.43927	1.52248
19364.16-4M1 (HJDC)	LR_{21}	**20.177965012961**	0.03062	0.09694	0.37289	0.30280	0.10844	0.88603	-0.39475	2.31061	1.43003	0.93473	1.06324	1.66980	0.10961	1.93261	-0.49027	-0.00696	2.80233	0.23094	1.53669	1.85341	2.39824
20008.17-1 (RMRO1)	LR_{21}	**6.016313795590**	1.31767	0.35758	0.39801	-1.75069	-0.06709	0.58011	0.43291	0.49639	0.05136	0.78072	0.01141	0.78894	0.47353	0.31756	0.35435	0.15865	0.68726	0.46046	0.98873	0.60261	-1.42415
20880.15-2R2 (1)	LR_{21}	**19.020057262535**	1.35794	1.27776	0.59143	0.29501	-0.17206	0.46771	1.11466	1.06315	0.84429	0.72737	1.22629	0.89421	0.57672	0.46663	1.10699	0.36352	1.88100	0.19035	1.52250	1.75044	1.47416
23308.16-6CABO (AFM)	LR_{21}	**19.219743822399**	0.93995	0.71184	0.98163	0.08294	0.16510	0.54345	0.58684	1.37218	1.43112	0.65174	-0.05275	1.20340	0.85994	0.98456	0.77497	0.86336	1.62348	1.57732	1.42690	1.17700	1.31477
23308.16-6CABO (MARCC)	LR_{21}	**13.582392892884**	0.48359	0.37051	-0.43055	-0.14535	-0.31547	-0.28778	1.71268	1.96686	0.40594	-0.03850	0.51792	1.07626	0.52580	0.57056	0.21567	1.29672	2.22575	0.04527	1.35035	0.55213	1.48405

Table B6: Log_{10} values of the LRs (per markers and global) computed by STRmix™ v.2.7 with stutters, for mixtures with three estimated contributors. The "-" represent the null LRs values (markers and global) and the "X" refer to the markers that have been removed to allow comparison. The blank cells correspond to the marker for which STRmix™ did not compute any value.

Mixture (Reference)		Log_{10} (LR)	D3S1358	vWA	D16S539	CSF1PO	TPOX	D8S1179	D21S11	D18S51	D2S441	D19S433	TH01	FGA	D22S1045	D5S818	D13S317	D7S820	SE33	D10S1248	D1S1656	D12S391	D2S1338
245.17-2.1 (MABS)	LR_{21}	**28.2805328444514**	0.92054	1.88837	0.95169	0.45602	1.12057	1.29837	1.64578	1.54712	1.10711	1.25154	1.24966	1.13373	1.51457	1.40121	1.00100	1.02366	2.02280	0.95023	2.35251	1.66360	1.78044
245.17-2.1 (OCF)	LR_{21}	**27.2298353665573**	1.00368	0.92030	0.99651	0.78755	2.26986	1.13504	1.78931	1.55970	0.80600	1.76618	0.94362	1.79470	1.04821	0.86752	0.74348	1.18113	1.80075	1.18259	1.81985	1.18966	1.62422
428.17-10 (LHIF)	LR_{21}	**30.5634918222689**	0.95000	1.16770	1.06198	1.81301	1.68632	0.88750	1.39078	1.34809	1.13373	1.65498	1.16670	2.72352	0.95299	1.99348	0.99000	1.30655	2.33017	0.74038	1.49687	1.75126	2.01749
1305-17-3 (PBS1)	LR_{21}	**20.4040122261822**	0.84441	0.63631	0.97933	0.43897	0.21149	0.96913	1.72124	0.82918	1.04230	0.40454	0.83385	1.90844	0.58288	0.85153	0.57810	0.82602	2.13994	1.11341	1.29594	1.44264	0.75437
1305-17-3 (RDS1)	LR_{21}	**17.4502028542234**	0.67700	0.91572	0.58228	0.20920	0.31633	1.48355	1.02975	0.81025	1.08131	0.76537	0.49763	0.81934	0.54494	0.61771	1.05864	0.64107	1.00620	1.10661	1.60534	1.21288	0.46906
1533.17-4 (EIJB1)	LR_{21}	**16.0677773586333**	0.47144	0.43610	0.92675	1.08189	0.16011	1.01620	1.07078	0.70581	1.35185	0.96079	0.58148	0.62007	0.48299	0.30242	0.76206	0.51124	1.66842	-0.09388	1.03266	0.75890	1.25974
2193.16-3 (MNTB)	LR_{21}	**15.3741799096546**	0.96211	0.80589	1.25010	0.13574	0.30969	0.53686	1.09426	1.02449	0.18904	1.62660	-0.41814	0.43388	-0.18512	0.33104	0.90988	0.90377	1.18853	0.30514	1.52284	1.70697	0.74061
2193.16-3 (MHMB)	LR_{21}	**7.2494185072360**	0.55468	0.08707	0.14675	0.10514	-0.18063	0.55112	1.22420	0.15963	0.64149	0.04206	0.45416	-0.14556	0.40303	0.39498	0.21529	0.24482	0.27492	0.12447	1.20930	0.21508	0.52746
2793.17-1R3 (FJCM1)	LR_{21}	**17.8307297754283**	1.12694	2.02181	0.72382	0.29079	0.16794	0.59780	0.82234	1.00048	0.06427	1.54014	0.75334	1.01762	2.18946	0.57833	0.36756	0.52393	1.17365	0.23485	1.03447	0.98882	0.61234
3053.17-5R2 (MHR2)	LR_{21}	**20.7457304247981**	0.40231	0.58366	0.87631	0.71128	0.79960	2.05053	1.77919	1.02049	0.51884	1.17728	0.45773	0.91024	0.62146	0.44931	1.11734	1.06062	1.59631	1.13030	1.47637	1.40377	0.60278
3053.17-5R2 (CDS1)	LR_{21}	**17.6483795293954**	0.28901	0.13043	0.15317	0.66228	0.77735	0.71896	1.21101	0.95317	0.44202	1.51615	0.27224	1.53334	0.82697	0.68311	0.75099	1.47769	1.72749	0.64895	1.30561	0.90733	0.66107
3357.17-12.2 (9)	LR_{21}	**18.6967145121385**	0.49947	0.81134	0.75554	0.78114	0.00788	1.28780	1.16008	1.46811	0.49132	0.43033	0.60006	1.78287	0.67075	0.59784	0.97635	0.64945	1.59754	0.80312	1.17123	1.07679	1.07773
3665.17-26 (SL2)	LR_{21}	**7.7739472650097**	0.04044	0.00268	0.11807	0.14684	0.38254	0.27814	0.29409	1.47573	1.07405	0.11384	0.25440	0.34169	-1.01641	0.39540	0.68183	0.42321	1.83605	0.16917	-0.48216	0.70058	0.54371
3675.17-1 (AJRG1)	LR_{21}	**10.8618568757359**	1.14101	0.32826	0.17345	0.54471	0.60660	0.31364	0.79065	0.86393	0.34394	0.18924	0.18424	1.03350	1.17155	0.84813	-0.72665	1.07328	0.03491	0.18517	0.83366	0.01662	0.91209
3675.17-1 (ORG1)	LR_{21}	**21.0588054866759**	1.31796	1.10779	0.78912	0.59869	0.63931	0.00826	0.93701	1.37188	0.75533	1.16932	0.70342	1.48654	0.92253	0.90374	1.16761	0.84835	1.75504	0.54676	1.37992	1.31898	1.33125
3841.17-7 (3)	LR_{21}	**14.8338416824638**	0.75618	1.20080	0.15543	0.17866	0.34530	1.01737	0.31127	0.76349	0.64560	0.86260	0.94326	2.04918	-0.27003	0.17313	0.33806	0.45894	1.37938	1.08600	1.14746	0.72782	0.56400
3958.17-1R2FF (LGS1)	LR_{21}	**20.3366398186417**	0.74797	0.99057	0.94799	0.25821	0.50522	0.87161	1.34118	0.73527	0.98582	1.10752	0.72318	0.82928	1.12872	0.63054	1.12225	0.25544	1.42786	1.71182	0.43454	2.46497	1.11671
4406.17-6 (CVG)	LR_{21}	**-**	0.59820	0.80156	0.90810	0.65870	0.57447	0.58405	1.14211	1.35345	0.65060	1.41083	1.15109	1.39948	0.84608	0.79567	-	1.00659	1.99603	-	1.62862	2.07298	-0.53804
	$LR_{<21}$	**18.1812145484904**	0.57160	0.80442	0.88540	0.67590	0.54750	0.56185	1.23284	1.31637	0.58237	1.41306	1.07940	1.35284	0.75910	0.60275	X	0.95977	1.99773	X	1.50137	2.06251	-0.72557
4406.17-6 (NGP)	LR_{21}	**-**	0.75801	1.06659	1.19775	0.77193	2.06670	0.88178	1.62432	1.52525	1.01957	2.01687	0.93756	1.60401	1.06206	0.96544	1.38917	0.82499	1.88359	0.79585	2.35946	1.55489	-
	$LR_{<21}$	**26.4423700056868**	0.75784	1.06119	1.20060	0.77388	2.09356	0.88045	1.61589	1.55894	1.01343	2.01812	0.94400	1.62190	1.07617	0.96299	1.38933	0.83356	1.94325	0.79575	2.33772	1.56380	X
4548.16-PC9.9 (PC9.8)	LR_{21}	**-**	0.69277	0.83050	2.06465	0.80396	1.72596	1.14731	2.07434	0.99531	0.61542	1.57187	0.84799	0.85508	2.17817	0.76114	0.79679	0.92925	-	0.71163	1.29839	1.51235	0.61691
	$LR_{<21}$	**23.0206926786820**	0.67161	0.84692	2.06483	0.81939	1.72596	1.14848	2.07751	1.03735	0.54342	1.58008	0.85351	0.87655	2.17765	0.75990	0.78053	0.88048	X	0.71963	1.32102	1.51613	0.61974
4702.17-1 (CSP1)	LR_{21}	**23.7916906490201**	0.82653	1.08343	1.25363	0.71122	0.63808	0.93420	1.40916	1.65824	1.23449	1.01845	0.98515	1.53872	0.48219	0.61407	1.14098	0.85369	1.83983	0.92829	1.77460	1.48633	1.38037
4980.17-11 (JAMR1)	LR_{21}	**24.9064697276433**	1.20058	0.72094	0.71842	1.91160	0.52546	1.53793	1.31643	1.00762	0.85631	2.05732	1.01858	1.17829	0.98692	0.43033	1.47551	2.01858	2.26795	0.92913	0.40021	1.27782	1.07052
5008.17-1R1 (1R2)	LR_{21}	**19.6427612032653**	1.25402	0.54830	0.13647	0.39609	0.89141	0.80481	1.45016	1.60217	-0.05112	2.16501	0.97764	1.42881	-0.59171	1.66260	0.51463	1.43167	1.83409	0.52627	1.44949	0.78406	0.42788
5008.17-1R1 (2R1)	$LR_{<21}$	**26.6932167489510**	0.91015	1.06767	0.82000	2.08757	0.64332	1.11647	2.02020	1.60324	0.41629	0.81455	1.05565	1.76840	1.34531	0.64274	1.11371	1.08282	2.06599	1.40608	1.71563	1.79109	1.20634
5008.17-3CABO (3LAM)	LR_{21}	**29.9757396118965**	1.16158	1.23543	0.83042	1.76865	0.80974	1.57763	2.86339	1.54040	0.85680	1.45142	0.92133	1.34932	1.68092	1.88955	0.73690	1.19254	2.18387	1.48800	1.64393	1.15921	1.63473
5008.17-3CABO (4R2)	LR_{21}	**27.6837222824514**	0.76114	1.27955	1.42762	0.87503	-0.07495	2.18560	1.73732	1.48174	1.56308	1.70714	0.97493	1.78503	1.08540	1.83322	1.11737	0.83881	2.28366	0.91675	2.23480	0.31222	1.35828
5374.16-9 (BMEB1)	LR_{21}	**13.9711041385599**	0.69911	0.21595	0.12503	0.42830	0.16101	0.18718	1.45309	0.65538	0.65446	0.46022	0.43789	0.48718	1.13395	0.77762	0.15848	0.34286	1.26304	0.89852	0.93631	1.73204	0.76354
5396.16-1CABO (JJCC)	LR_{21}	**26.8033068620087**	0.84198	1.30229	0.67845	1.17632	0.90820	1.59221	1.32467	1.57477	1.02502	2.15606	1.33947	1.34248	1.07726	0.95803	1.07595	0.91137	1.70929	0.92435	1.47425	1.40873	2.00212
6561.17-2BIO (FMGV1)	LR_{21}	**24.9024706759913**	1.13574	1.05664	0.99453	0.83330	0.98265	0.71489	1.48840	1.41729	1.61583	1.24015	1.12633	1.53150	0.45672	1.35007	0.57928	0.79134	1.86122	1.32048	1.64198	1.50698	1.25717
6561.17-2BIO (JAPG1)	LR_{21}	**26.2741347478790**	0.50940	1.02588	1.02403	0.84989	0.81214	2.21646	1.11929	1.68399	1.01490	1.18605	1.16426	1.25479	0.77281	0.90267	1.38369	1.66983	2.34042	1.18738	0.60325	1.62929	1.92372
6568.17-9 (DFSDN1)	LR_{21}	**11.3760474520415**	0.36082	0.75716	0.73628	0.15625	0.47783	0.42032	0.69616	0.89992	0.82272	0.65363	0.60021	0.75607	0.29206	-0.04575	0.39981	-0.26538	0.95874	0.38741	0.37952	1.24324	0.68905
6568.17-9 (RFAS2)	LR_{21}	**4.1797815158370**	-0.55841	0.08721	0.84286	0.66435	-0.27187	-0.38822	0.83838	1.60004	0.41350	0.32928	0.27556	0.59459	-0.07784	-0.11699	0.06382	0.37061	1.45133	0.08575	-3.03283	0.09398	0.91467
6978.17-4R2 (7FF)	LR_{21}	**24.2364112877440**	0.75520	1.19780	1.13159	1.06315	0.63296	2.46030	1.30878	1.48103	1.59387	-1.44009	0.90684	1.21275	0.47379	0.65286	1.21018	1.18648	2.50998	1.02280	1.88514	1.61340	1.37765
6978.17-4R2 (JAB1)	LR_{21}	**23.4059948411918**	1.26250	1.97395	0.42402	0.56173	0.25066	2.81192	1.70023	1.67360	0.86100	-0.01480	1.07033	0.51211	0.72641	0.92018	1.54463	1.13133	0.04230	1.75331	1.99644	1.29168	0.91243
7245.17-1R1 (1R2)	LR_{21}	**29.8354686124927**	0.75610	1.12336	1.05827	1.73695	0.63823	1.35493	2.42875	1.80389	1.13392	1.64409	1.33474	1.30179	2.23830	0.91959	1.84693	1.21812	1.79634	0.90656	1.48524	1.49395	1.61542
7582.17-1 (FMBSC)	LR_{21}	**-**	0.82470	-0.30249	0.07159	-0.01541	0.11025	-	-0.51118	0.78224	-1.47178	0.54175	2.08418	1.49541	-	0.60505	0.26105	0.59470	1.37005	1.16280	0.93313	0.52260	1.17135
	$LR_{<21}$	**9.1903036782676**	0.78025	-0.34311	-0.01966	-0.01112	0.10887	X	-0.57255	0.77347	-1.59594	0.09496	1.95810	1.47630	X	0.68053	0.28592	0.54520	1.31553	1.18438	0.84464	0.54034	1.14420
8356.16-8.2FF (DPMF)	LR_{21}	**8.8577906766096**	0.24846	0.50189	-0.54046	0.09614	0.11651	1.07598	1.19089	-0.18039	0.48339	0.35127	-0.05730	0.65322	0.40099	0.39150	0.40264	0.51000	0.03048	0.55313	1.00471	0.75975	0.86495
8356.16-8.2FF (HVF)	LR_{21}	**25.2022430376248**	1.18941	1.03092	1.04123	0.02812	0.36203	1.06985	1.15634	1.23429	1.17219	1.87345	1.39074	1.37061	2.23147	0.92473	1.79669	0.63178	1.55086	0.71035	2.20461	1.17120	1.06141
8371.16-1R1 (JARR1)	LR_{21}	**27.1220191720800**	0.77517	0.90594	1.04450	0.70704	0.86520	1.47390	1.48671	2.18896	0.79860	1.63582	0.99348	1.19000	0.72166	0.63663	1.23480	1.18704	2.10161	0.79219	2.33510	1.67778	2.36992
8393.17-2FF (JPB2)	LR_{21}	**25.8893969566555**	0.89165	1.19780	1.49420	1.74027	0.85365	1.11541	1.02301	1.36734	0.87234	0.59834	1.12830	1.73851	1.02280	0.65009	0.74475	1.46776	2.23050	1.35488	1.35946	1.61575	1.42259

8393.17-2FF (TFB2)	LR_{21}	**27.8393271808320**	0.55736	1.50787	1.09124	0.71583	1.90832	0.94397	2.67353	1.84507	0.87279	0.78745	0.12856	1.33941	1.02272	0.96242	1.11787	2.00749	2.56619	0.78283	1.60635	1.90414	1.49791
8410.16-2R1 (2R2)	LR_{21}	**7.8151126581898**	0.11714	0.48481	0.54057	0.30542	0.47041	0.77586	0.71084	0.69319	0.68712	1.29414	-0.00008	0.46204	-3.17699	-0.04551	0.55817	0.43274	0.78407	0.92807	0.38920	0.69613	0.70776
10175.16-4 (5)	LR_{21}	**12.9009676239191**	0.89728	0.05092	0.36635	-0.76772	0.18387	0.50474	0.45189	0.79521	1.19184	0.47097	0.26067	1.25508	0.98326	0.44959	0.28490	0.64191	1.30636	0.31190	1.72266	0.82676	0.71251
10278.16-2 (1)	LR_{21}	**5.0953088613854**	-1.71899	0.80819	0.29387	0.14442	0.03222	1.01085	0.54379	0.80069	0.78544	0.16959	0.03782	1.37326	0.56309	0.11391	-0.12136	0.48673	1.15948	-2.22003	1.67093	-1.46042	0.62185
10814.16-2 (CMSA)	LR_{21}	**-**	-0.53374	-0.29348	-0.16973	0.18839	0.00642	-0.10102	0.36553	0.19254	0.06277	-0.45563	-0.28577	0.06573	0.13456	-0.61660	0.28171	-0.10803	-	-0.63052	-3.09574	-0.46438	-2.28907
	$LR_{<21}$	**-7.9339351025403**	-0.51651	-0.33449	-0.15446	0.16994	0.01853	-0.13390	0.37107	0.23322	0.02987	-0.51392	-0.26374	0.03019	0.12044	-0.56618	0.27763	-0.10292	X	-0.60220	-3.53834	-0.29037	-2.16781
10814.16-2 (FMRG)	LR_{21}	**10.6832722363159**	0.54531	0.73665	0.31040	-0.01581	0.06055	0.63456	1.25217	0.80046	0.68842	0.02735	0.20426	0.58537	0.22425	0.70427	0.55158	-0.64474	1.37630	0.73523	1.36401	1.04650	-0.50379
11021.17-20LAM (MABSC1)	LR_{21}	**11.8360328001503**	-0.53081	0.89537	0.40447	0.33530	0.40591	0.66886	0.51837	-0.05790	1.05484	0.24944	0.56003	1.02485	0.38614	0.10490	0.85286	0.00329	1.54183	0.35564	1.29338	1.22863	0.54059
11021.17-20LAM (MGSF1)	LR_{21}	**16.1740016264024**	0.20472	1.38437	1.27804	0.42017	0.39189	0.29223	0.52673	0.56753	0.87908	0.80271	0.67000	1.02135	0.23613	0.42402	0.86370	0.73174	1.87443	-0.12661	1.21442	1.43551	1.08185
11021.17-20LAM (MSSF1)	LR_{21}	**20.8525348869419**	1.02682	0.99041	0.52961	0.40329	0.41712	0.91042	1.48938	0.71680	1.15299	0.69461	0.33905	1.18974	0.48460	0.80718	0.53783	1.10212	0.62857	2.30754	1.48760	2.07118	1.56568
12179.17-14R6 (GCG1)	LR_{21}	**11.8891896120471**	0.82180	0.21840	0.85238	0.58286	-0.28995	1.69419	0.91411	1.19753	-1.99727	-0.02707	0.61950	1.26977	-0.13862	0.57519	0.65391	1.06187	1.91984	0.95963	0.93071	0.83840	-0.76800
12179.17-14R6 (MAM1)	LR_{21}	**10.6792825017390**	0.49722	0.44199	0.21021	0.32226	0.48647	0.94675	0.55340	1.05515	0.63088	0.14582	0.19642	0.02284	0.28439	0.27346	0.26752	0.66903	-0.32984	1.07416	1.85160	1.07940	0.00009
12946.17-3.1 (2)	LR_{21}	**20.1358002833021**	0.92774	0.65048	0.65105	0.62819	0.82586	0.58636	1.69472	1.21093	0.28160	1.10096	0.63623	1.26759	0.62239	0.56909	1.33098	0.86385	1.69982	0.42063	1.17017	1.79747	1.19967
13020.17-1LAM (1CABO)	LR_{21}	**12.4667045440307**	0.97467	0.82249	0.84618	-1.80077	0.43886	0.70146	1.07044	1.09527	0.86438	0.73897	1.00471	1.10175	-2.54123	0.83857	-0.76569	0.93149	1.32948	0.84784	1.80619	1.02763	1.13395
13046.17-1R1 (2R1)	LR_{21}	**17.6258369923234**	0.60979	1.83603	0.47144	0.50406	1.14000	0.74013	0.97818	0.94689	0.57672	0.54476	-0.04007	0.39594	-0.13485	0.30878	0.72018	0.73077	2.09015	0.55125	1.46100	1.69227	1.50239
13253.17-4 (3)	LR_{21}	**24.4828021477205**	0.93018	1.52642	1.05396	0.45627	1.32703	1.51376	-0.00644	0.88395	2.28845	1.91834	1.09015	1.03015	0.72025	0.64986	1.15241	1.37122	1.92844	0.77696	2.35372	1.35299	0.16474
13367.17-5 (SMCP1)	LR_{21}	**-**	-0.07711	0.38995	0.75009	1.02090	0.57079	1.10387	1.80974	0.71108	0.13567	0.82467	0.84538	0.87056	0.04466	0.89848	1.17091	0.03719	1.65581	0.06974	1.30036	1.25765	-
	$LR_{<21}$	**15.4699397747863**	-0.03551	0.36139	0.75935	0.98633	0.60386	1.09430	1.81080	0.67655	0.15561	0.82268	0.84781	0.87053	0.07679	0.89273	1.17551	0.01098	1.68172	0.12636	1.29294	1.25916	X
14005.17-1R1FF (1R2FM)	LR_{21}	**22.3223433611487**	0.70090	0.95708	0.96925	0.47679	0.47929	0.84282	2.07258	1.23596	0.71892	0.78680	0.48252	2.37230	1.43772	0.73905	1.19535	0.89141	1.44489	0.96963	1.49420	1.02465	1.03028
14005.17-1R1FF (2R1FF)	LR_{21}	**17.0510366951412**	0.85335	0.74766	0.81419	0.18707	0.54238	1.26604	2.32642	1.12759	1.09293	0.63971	1.02214	0.70190	0.73250	0.62761	0.46431	0.26262	1.37751	0.96923	1.30554	0.70717	-0.71679
14281.17-6R1 (6R2)	LR_{21}	**12.3690487889403**	1.84863	-1.07876	0.32564	0.19728	-0.32939	0.35576	0.44326	0.59120	0.55564	1.81265	0.34380	0.81004	0.45411	0.64214	0.35415	0.25653	1.40214	0.23972	1.40766	1.66004	0.07682
14281.17-6R1 (MGGS1)	LR_{21}	**11.3323172445410**	0.25152	0.50942	0.42718	0.37845	0.31105	0.54906	0.87760	0.95444	0.81395	0.35801	0.17531	0.67655	1.67441	0.64082	0.45494	0.06254	1.18879	0.52998	0.18817	-0.02605	0.33624
14503.17-1 (MRER1)	LR_{21}	**10.8063292370589**	0.42723	0.84101	0.64166	0.47962	0.24655	0.56878	0.86953	0.78191	0.66792	1.01645	0.27850	0.40209	0.56418	0.11684	0.64335	0.44868	0.95482	-2.00010	0.69026	0.85180	1.31528
14828.17-2FF (1FF)	LR_{21}	**23.7108363608637**	1.26839	1.13392	0.46343	0.46789	0.93900	1.29964	1.23500	1.51310	0.80729	1.64104	0.90374	1.17003	0.92765	1.18794	1.20766	1.17513	1.25234	0.91464	1.57693	2.04603	0.58002
14828.17-2FF (FLEP1)	LR_{21}	**18.7579726804139**	0.24045	0.30246	0.46619	0.53743	0.29466	1.00415	1.08052	0.91772	1.86773	0.97731	0.58111	0.86770	0.87748	0.80008	1.39226	0.83467	2.03423	0.50301	1.64860	1.09538	0.43481
14942.17-2LAM (3R1)	LR_{21}	**11.8828659197216**	0.52103	0.14482	1.10755	0.89757	-0.01837	-0.08930	0.95850	0.82539	0.59006	0.36886	0.83945	0.42609	0.18915	-0.00815	0.16104	0.73809	0.90396	0.73699	0.85935	0.92486	0.80592
14942.17-2LAM (NMLC1)	LR_{21}	**13.8271430190857**	0.20739	0.69075	-0.27204	0.07936	0.74889	1.06258	1.39349	0.81500	0.98868	0.23160	0.80416	0.96265	0.82582	0.05998	0.48601	0.89772	1.30110	-0.06965	0.41817	1.28206	0.91345
15014.17-1 (2)	LR_{21}	**25.5082198790747**	0.93359	1.46878	0.65199	-0.37288	1.14183	1.05953	0.88053	1.28110	1.30060	1.80430	0.89459	1.30582	1.01364	1.20328	1.12685	1.19893	2.39936	0.92665	2.40466	1.20477	1.68029
16839.17-1.9 (BZ1)	LR_{21}	**1.5211380837040**	0.75087	0.43209	-0.25043	1.12388	0.31275	-1.11781	0.84574	1.33037	-3.27183	-0.24671	0.96230	-0.37760	-0.66837	-2.06257	0.37925	-0.04024	1.19607	1.00013	0.36737	0.06506	0.79084
16839.17-1.9 (JW1)	LR_{21}	**1.4402949710949**	1.20992	0.41908	-0.76193	0.36840	0.28468	0.66813	0.30494	0.28778	0.59327	-0.74239	1.16262	0.67915	-0.58981	-2.09657	0.63895	-0.20583	1.48786	-2.84796	-0.61549	0.16906	1.02645
16839.17-1.9 (QJ1)	LR_{21}	**4.0290995668235**	1.20396	0.30201	-0.08582	0.45556	0.29092	-1.57947	0.37574	0.46706	-2.00900	-0.69527	-0.02100	0.41867	-0.72520	1.81397	0.28917	0.21635	1.56998	0.76852	-0.64768	0.53162	1.08902
18094.16-2 (IMSS)	LR_{21}	**24.5450100614051**	0.72622	1.03096	1.62124	0.90055	0.80741	0.69516	1.26072	1.74825	1.03419	0.73803	0.88747	1.44587	0.73823	0.78893	1.21211	0.97902	1.84429	1.10857	1.67222	1.74139	1.56422
18094.16-2 (CCM)	LR_{21}	**27.7580257545744**	0.99057	1.10571	1.13830	1.39229	0.63954	1.78352	1.29066	1.39993	1.30580	1.20621	1.35324	1.37003	1.02706	0.65383	1.79918	1.11879	2.32422	1.49474	1.51738	1.36528	1.48171
18690.17-2R1 (1R1)	LR_{21}	**17.2237035635225**	0.52790	0.83403	0.71890	0.27699	0.70965	-0.04060	1.19921	0.86772	1.42384	0.83594	0.36346	0.82615	0.60573	0.27768	0.64552	0.98356	1.33979	1.08565	1.07485	1.86738	0.80033
18690.17-2R1 (CFB2)	LR_{21}	**-**	0.68789	0.62586	0.72537	0.87781	1.10860	1.13367	0.43715	1.19893	1.43183	1.17978	0.33624	1.70315	0.61531	0.84136	1.11959	0.91059	-	0.32255	0.86306	0.60581	0.68098
	$LR_{<21}$	**16.6824429309240**	0.74930	0.43754	0.58400	0.79420	0.98229	0.95289	0.30918	1.07824	1.45343	1.20564	0.42843	1.61325	0.63233	0.93909	1.04505	0.81043	X	0.30389	0.94186	0.48650	0.93487
19364.16-4M1 (MPPA1)	LR_{21}	**27.1688803424136**	1.88668	1.28921	0.79856	0.77154	0.87993	1.24182	1.83287	1.93399	0.82194	0.78795	1.14761	2.59296	0.74073	0.98773	1.11180	1.09072	2.23195	0.28212	1.48246	1.40104	1.85526
19364.16-4M1 (HJDC)	LR_{21}	**24.6504920833547**	0.87683	1.39062	1.28341	0.65496	1.15842	1.78393	-1.45583	1.74929	1.52230	1.26541	1.10044	1.36793	0.74375	2.48979	0.68937	0.30925	2.06915	0.45073	1.50416	1.80134	1.89531
20008.17-1 (RMRO1)	LR_{21}	**6.8380048582376**	0.52389	0.38050	0.60874	-1.28726		0.33268	0.69736	0.63707	-0.26464	0.95769		0.99646	0.63543	0.57619	0.36088	-0.00330	0.69411	0.57430	1.07525	0.59201	-1.24936
20880.15-2R2 (1)	LR_{21}	**23.6736842898677**	1.54442	1.00449	0.79975	0.67082	1.09103	1.04427	1.64260	1.29010	0.83544	0.96257	1.11481	1.39294	0.23348	0.62858	1.18293	0.22502	2.38455	0.77978	1.83992	1.65316	1.35299
23308.16-6CABO (AFM)	LR_{21}	**20.2228204813222**	1.03655	0.63949	0.96735	0.52589	0.54279	0.72175	1.13504	1.17108	1.18865	0.95738	0.49087	1.12885	0.83596	0.91600	0.63218	1.01389	1.21331	1.21203	1.48588	1.33654	1.07137
23308.16-6CABO (MARCC)	LR_{21}	**16.4127628522751**	0.39613	0.35635	0.22227	0.13277	0.55855	0.85562	1.58434	1.81040	1.00830	0.30602	0.41809	0.98566	0.53116	0.36734	0.03878	1.21595	1.77169	-0.17335	1.61709	0.94020	1.46942

Table B7: Log_{10} values of the global LRs computed by EuroForMix v.1.9.3 without stutters[1], for mixtures with two estimated contributors assuming three contributors.

Mixture (Reference)	Log_{10} (LR)
243.17-1FM (JRA)	17.5447869913859
243.17-1FM (MM)	22.0866654611822
913.17-1.3 (ASML1)	13.9929901445859
913.17-1.3 (PMRP1)	18.7226601254657
1087.17-4 (PMCC1)	20.7181319167464
1182.17-2L2FM (MD1)	26.3529724427548
1383.17-1CABO (AMAD1)	25.2823066891299
1383.17-1CABO (AMBC1)	16.0127305654672
1793.17-2 (1)	16.6794842260548
1793.17-2 (3)	34.2231738730912
1799.17-1 (2)	16.5330656155458
1816.17-2FF (EVM1)	28.1714838538683
1816.17-2FF (SC1)	23.4180491858356
1843.17-1FIXACAO (FN1)	8.7971426701986
1847.17-3R2 (JC1)	17.6148742744335
1847.17-3R2 (MC1)	20.6587279185337
2572.17-4CABO (IOSS)	18.5941836055967
2572.17-4CABO (LMVG1)	18.5804228645739
2799.17-2FM (1FF)	25.3930913439311
2921.17-2 (JAVC2)	16.8082894078063
2921.17-2 (TFTS1)	22.947236653785
3053.17-3.1R2 (EAD1)	15.8335908769822
3053.17-3.1R2 (MMM1)	17.5348931917694
3732.17-2.1FM (ASSC1)	20.1804991721381
3732.17-2.1FM (IST1)	22.1353250138282
3929.16-1 (2)	26.2024777856494
5258.17-5 (1)	28.634438309594
5700.16-5 (AGT)	21.922031373539
5700.16-5 (TMAS)	28.5552666785397
5707.17-6R1 (MAGDC1)	23.7254238134288
5709.17-6R2 (CMDF1)	15.6643208018385
5709.17-6R2 (MJLF1)	16.5818412821945
5773.17-4 (5FM)	19.4718434838888
5773.17-4 (17FDC1)	26.399365583987
6010.17-1 (AAM1)	16.1274283431877
6472.17-1FM (PSBM2)	24.1824430968078
7241.17-11R2FF (ASJ1)	21.0079617962763
7241.17-11R2FF (MCPSJ1)	19.0018538328098
7385.16-3 (2)	7.86023189769177
7588.17-1R1FF (3)	25.5897907047968
9233.16-9.1 (LCGS1)	12.1706390452205
9233.16-9.1 (VMTJ2)	20.7449769311586
10223.17-3LAM (IM2)	14.235309326221
10223.17-3LAM (VMPM1)	20.1883433718639
12818.17-7 (1)	22.3369182732166
13017.17-25.2 (AJAN1)	26.5700755082624
13017.17-25.2 (MJCR1)	28.6794111186366
13027.17-1R2FF (1R1FF)	16.3008892121811
13027.17-1R2FF (1R1FM)	25.9700610848057
13034.16-2CABO (2LAM)	21.5723297975121
13252.17-8 (FTMR1)	18.7669936473984
13252.17-8 (LIOR1)	15.6689821250698
13740.17-1R1FF (1R2FF)	14.6908853252983
13940.17-2 (DMC1)	16.5765281106079
13940.17-2 (NMFM1)	14.0140249879823
14002.16-1 (MPNG1)	11.7350926949956
14552.16-1FM (LMRR1)	15.8170911669194
14552.16-1FM (1FF)	29.6824443042962
15150.17-1 (DASS1)	16.7884237009908
15150.17-1 (RJABO2)	22.469433921609
16126.17-3.3 (1)	29.5181198254786
16537.17-1 (AJMC1)	27.4475876431275
16537.17-1 (ASLS1)	28.3572067678286
16672.17-4R2 (4R1)	27.9203622330061
16672.17-4R2 (AMC1)	20.9040361821174
16913.17-3 (NMSAOM1)	19.6713177944255
17065.17-1 (3)	27.974034297632
17065.17-1 (SSC1)	23.1573307293109
17222.17-3R2FF (3R1)	19.8162869602637
17222.17-3R2FF (PM1)	24.5231469164306
18119.17-2 (LZ1)	16.8572453444226
19187.16-4CABO (RGCF)	9.95391737156788
19724.16-6 (ENP1)	24.5142826760684
19724.16-6 (13)	19.0606877584941
19724.16-8 (BMAP)	22.1738627248116
19799.17-1 (TFPA1)	10.4270816200413
20601.16-1 (HMNM1)	14.4710993417691
20601.16-1 (AMM)	15.7198691682836
20628.16-1CABO (AMP)	26.47159498923

[1] Computed by Figueiredo C: Forensic DNA mixtures: Analysis and comparison of software results. Faculdade de Ciências da Universidade do Porto; 2018.

Table B8: Log_{10} values of the global LRs computed by STRmix™ v.2.7 with stutters, for mixtures with two estimated contributors assuming three contributors.

Mixture (Reference)	Log_{10} (LR)
243.17-1FM (JRA)	17.5696430653593
243.17-1FM (MM)	21.7793439210373
913.17-1.3 (ASML1)	17.690506179636
913.17-1.3 (PMRP1)	18.3856956254106
1087.17-4 (PMCC1)	21.0664750137541
1182.17-2L2FM (MD1)	26.4849827819306
1383.17-1CABO (AMAD1)	26.3567713616696
1383.17-1CABO (AMBC1)	18.3927672786556
1793.17-2 (1)	18.0873554300540
1793.17-2 (3)	32.7550817349541
1799.17-1 (2)	23.7513484007654
1816.17-2FF (EVM1)	28.9476248478251
1816.17-2FF (SC1)	24.6740707956937
1843.17-1FIXACAO (FN1)	11.8725524949666
1847.17-3R2 (JC1)	21.1741761469922
1847.17-3R2 (MC1)	22.0489853025707
2572.17-4CABO (IOSS)	23.379341782999
2572.17-4CABO (LMVG1)	22.6217473462648
2799.17-2FM (1FF)	25.9562548964323
2921.17-2 (JAVC2)	21.7479630662528
2921.17-2 (TFTS1)	27.9558752788656
3053.17-3.1R2 (EAD1)	16.505434890597
3053.17-3.1R2 (MMM1)	17.7902710861882
3732.17-2.1FM (ASSC1)	20.0080463061583
3732.17-2.1FM (IST1)	20.6949121673286
3929.16-1 (2)	26.2713303710662
5258.17-5 (1)	29.7561414458833
5700.16-5 (AGT)	26.0862886290217
5700.16-5 (TMAS)	30.3938032576551
5707.17-6R1 (MAGDC1)	24.4333056987081
5709.17-6R2 (CMDF1)	17.2680160207819
5709.17-6R2 (MJLF1)	17.7393428750954
5773.17-4 (5FM)	21.0418662027213
5773.17-4 (17FDC1)	26.8715554233185
6010.17-1 (AAM1)	20.0071501053667
6472.17-1FM (PSBM2)	26.8228412370935
7241.17-11R2FF (ASJ1)	23.3747666702852
7241.17-11R2FF (MCPSJ1)	22.1294320741556
7385.16-3 (2)	4.46284703583167
7588.17-1R1FF (3)	26.7447544203199
9233.16-9.1 (LCGS1)	21.5114154072088
9233.16-9.1 (VMTJ2)	25.9852108452241
10223.17-3LAM (IM2)	13.9241500125137
10223.17-3LAM (VMPM1)	18.7181278520753
12818.17-7 (1)	25.2669603985977
13017.17-25.2 (AJAN1)	28.5310699768219
13017.17-25.2 (MJCR1)	29.464861980766
13027.17-1R2FF (1R1FF)	6.5042125197822
13027.17-1R2FF (1R1FM)	14.6639457946636
13034.16-2CABO (2LAM)	27.6222762086546
13252.17-8 (FTMR1)	22.1693216836818
13252.17-8 (LIOR1)	19.9505546949946
13740.17-1R1FF (1R2FF)	19.8924897422147
13940.17-2 (DMC1)	16.698509408026
13940.17-2 (NMFM1)	17.0985052832013
14002.16-1 (MPNG1)	20.514056070897
14552.16-1FM (LMRR1)	11.9097966430143
14552.16-1FM (1FF)	30.5285053391464
15150.17-1 (DASS1)	23.4378456533908
15150.17-1 (RJABO2)	25.8823366635374
16126.17-3.3 (1)	29.9662872556953
16537.17-1 (AJMC1)	21.7535753993107
16537.17-1 (ASLS1)	24.5101426994026
16672.17-4R2 (4R1)	25.9049318273957
16672.17-4R2 (AMC1)	20.7772165120434
16913.17-3 (NMSAOM1)	20.2753804675274
17065.17-1 (3)	28.2142343490256
17065.17-1 (SSC1)	23.6558680512486
17222.17-3R2FF (3R1)	25.7003142347476
17222.17-3R2FF (PM1)	24.6590600722409
18119.17-2 (LZ1)	17.853375716612
19187.16-4CABO (RGCF)	11.4851249265598
19724.16-6 (ENP1)	26.5561577118072
19724.16-6 (13)	23.4294131072925
19724.16-8 (BMAP)	26.2922117533319
19799.17-1 (TFPA1)	15.0662140754712
20601.16-1 (HMNM1)	0.79619954051265
20601.16-1 (AMM)	21.8799097770925
20628.16-1CABO (AMP)	27.2512974636776

Table B9: Log_{10} values of the global LRs computed by EuroForMix v.1.9.3 without stutters[1], for mixtures with three estimated contributors assuming four contributors.

Mixture (Reference)	Log_{10}(LR)
245.17-2.1 (MABS)	22.7355937472334
245.17-2.1 (OCF)	29.5288116940737
428.17-10 (LHIF)	26.497793900055
1305-17-3 (PBS1)	10.379701038577
1305-17-3 (RDS1)	16.8729824154547
1533.17-4 (EIJB1)	17.4365233277449
2193.16-3 (MNTB)	12.748167864568
2193.16-3 (MHMB)	5.45037439820669
2793.17-1R3 (FJCM1)	16.8041343915283
3053.17-5R2 (MHR2)	20.1401789023699
3053.17-5R2 (CDS1)	16.3647502217099
3357.17-12.2 (9)	13.4701791449842
3665.17-26 (SL2)	11.2322001421802
3675.17-1 (AJRG1)	12.77470062313
3675.17-1 (ORG1)	20.049915905798
3841.17-7 (3)	7.21804986952302
3958.17-1R2FF (LGS1)	12.7124207819619
4406.17-6 (CVG)	16.7214118702804
4406.17-6 (NGP)	27.3526443280155
4548.16-PC9.9 (PC9.8)	24.7478395980856
4702.17-1 (CSP1)	23.6846689269804
4980.17-11 (JAMR1)	21.9722491933022
5008.17-1R1 (1R2)	15.3725889966463
5008.17-1R1 (2R1)	25.6570795079022
5008.17-3CABO (3LAM)	26.5859930854643
5008.17-3CABO (4R2)	19.6899322974784
5374.16-9 (BMEB1)	11.0188223414441
5396.16-1CABO (JJCC)	18.6966981048863
6561.17-2BIO (FMGV1)	23.3454851522092
6561.17-2BIO (JAPG1)	21.2300735720128
6568.17-9 (DFSDN1)	12.1392936610562
6568.17-9 (RFAS2)	15.0795726001187
6978.17-4R2 (7FF)	22.6272631342461
6978.17-4R2 (JAB1)	24.3912500522444
7245.17-1R1 (1R2)	24.8780511027344
7582.17-1 (FMBSC)	8.7350167908079
8356.16-8.2FF (DPMF)	6.38245239110087
8356.16-8.2FF (HVF)	23.6855214869792
8371.16-1R1 (JARR1)	23.4203536121748
8393.17-2FF (JPB2)	26.5092644288682
8393.17-2FF (TFB2)	25.1390020194361
8410.16-2R1 (2R2)	10.2762469957288
10175.16-4 (5)	9.57233129769482
10278.16-2 (1)	6.42386437354889
10814.16-2 (CMSA)	22.3509093118930
10814.16-2 (FMRG)	10.0089117180719
11021.17-20LAM (MABSC1)	10.703426806061
11021.17-20LAM (MGSF1)	10.8564292231137
11021.17-20LAM (MSSF1)	13.9690222674379
12179.17-14R6 (GCG1)	12.2169545901176
12179.17-14R6 (MAM1)	11.9373613208878
12946.17-3.1 (2)	18.8661148031029
13020.17-1LAM (1CABO)	8.43245939182014
13046.17-1R1 (2R1)	18.628183714267
13253.17-4 (3)	13.3549904204272
13367.17-5 (SMCP1)	7.97719500694893
14005.17-1R1FF (1R2FM)	15.2851179036809
14005.17-1R1FF (2R1FF)	22.6604493932521
14281.17-6R1 (6R2)	10.2591293716342
14281.17-6R1 (MGGS1)	9.53255628098816
14503.17-1 (MRER1)	14.6937751664215
14828.17-2FF (1FF)	23.1236505599392
14828.17-2FF (FLEP1)	17.709394578312
14942.17-2LAM (3R1)	14.2621787237666
14942.17-2LAM (NMLC1)	20.4178705583294
15014.17-1 (2)	24.5898905373305
16839.17-1.9 (BZ1)	11.3597782064772
16839.17-1.9 (JW1)	12.1707289723221
16839.17-1.9 (QJ1)	10.6167394637407
18094.16-2 (IMSS)	23.2834073506895
18094.16-2 (CCM)	27.1423587692097
18690.17-2R1 (1R1)	15.7513799699707
18690.17-2R1 (CFB2)	17.7812741585797
19364.16-4M1 (MPPA1)	22.1423257097853
19364.16-4M1 (HJDC)	19.6079995623135
20008.17-1 (RMRO1)	7.57493380867569
20880.15-2R2 (1)	17.9820954022089
23308.16-6CABO (AFM)	18.7565207046892
23308.16-6CABO (MARCC)	12.6481173223544

[1]Computed by Figueiredo C: Forensic DNA mixtures: Analysis and comparison of software results. Faculdade de Ciências da Universidade do Porto; 2018.

Table B10: Log_{10} values of the global LRs computed by STRmix™ v.2.7 with stutters, for mixtures with three estimated contributors assuming four contributors.

Mixture (Reference)	Log_{10}(LR)
245.17-2.1 (MABS)	28.1108926008022
245.17-2.1 (OCF)	27.2184567264005
428.17-10 (LHIF)	30.194363200335
1305-17-3 (PBS1)	19.3024175191506
1305-17-3 (RDS1)	23.6700602174731
1533.17-4 (EIJB1)	16.1338581252033
2193.16-3 (MNTB)	15.2652896258608
2193.16-3 (MHMB)	6.39925826116692
2793.17-1R3 (FJCM1)	17.5970366649777
3053.17-5R2 (MHR2)	19.9719759088495
3053.17-5R2 (CDS1)	17.1059867955215
3357.17-12.2 (9)	18.2469661065587
3665.17-26 (SL2)	9.21015793765324
3675.17-1 (AJRG1)	15.8299338468024
3675.17-1 (ORG1)	20.5433974725754
3841.17-7 (3)	14.6219651911326
3958.17-1R2FF (LGS1)	19.9012021374367
4406.17-6 (CVG)	17.2051231292037
4406.17-6 (NGP)	26.2927211377745
4548.16-PC9.9 (PC9.8)	22.7550970009429
4702.17-1 (CSP1)	23.8299274220902
4980.17-11 (JAMR1)	24.4357169882208
5008.17-1R1 (1R2)	20.7091427076228
5008.17-1R1 (2R1)	26.1121691480017
5008.17-3CABO (3LAM)	29.9908004358526
5008.17-3CABO (4R2)	27.4839864647193
5374.16-9 (BMEB1)	13.6874040947495
5396.16-1CABO (JJCC)	26.6169793602044
6561.17-2BIO (FMGV1)	20.8360708089151
6561.17-2BIO (JAPG1)	20.9295823940448
6568.17-9 (DFSDN1)	12.0514612443242
6568.17-9 (RFAS2)	10.2382970678754
6978.17-4R2 (7FF)	24.3158864157085
6978.17-4R2 (JAB1)	23.6017667435704
7245.17-1R1 (1R2)	29.8271559510597
7582.17-1 (FMBSC)	4.48132794815258
8356.16-8.2FF (DPMF)	6.81034679098138
8356.16-8.2FF (HVF)	24.9975873192567
8371.16-1R1 (JARR1)	27.1099158630238
8393.17-2FF (JPB2)	25.5774917998372
8393.17-2FF (TFB2)	27.3145413291299
8410.16-2R1 (2R2)	12.8930512233535
10175.16-4 (5)	12.6009184694091
10278.16-2 (1)	4.38288116718144
10814.16-2 (CMSA)	-1.25344363858963
10814.16-2 (FMRG)	10.0282458165725
11021.17-20LAM (MABSC1)	11.9625066589949
11021.17-20LAM (MGSF1)	15.2367135633656
11021.17-20LAM (MSSF1)	20.1531438565137
12179.17-14R6 (GCG1)	12.0400482415475
12179.17-14R6 (MAM1)	10.6383394744107
12946.17-3.1 (2)	21.5374664810803
13020.17-1LAM (1CABO)	13.2351495364732
13046.17-1R1 (2R1)	18.4361308294297
13253.17-4 (3)	24.3775794208949
13367.17-5 (SMCP1)	13.7487460469755
14005.17-1R1FF (1R2FM)	6.81436747643434
14005.17-1R1FF (2R1FF)	25.2930972556916
14281.17-6R1 (6R2)	12.0857185951654
14281.17-6R1 (MGGS1)	10.9550476202448
14503.17-1 (MRER1)	10.3339508043872
14828.17-2FF (1FF)	22.1848617089934
14828.17-2FF (FLEP1)	17.072874596811
14942.17-2LAM (3R1)	9.83520845902107
14942.17-2LAM (NMLC1)	12.7464940813426
15014.17-1 (2)	25.3437432950101
16839.17-1.9 (BZ1)	5.64806712944893
16839.17-1.9 (JW1)	6.98909814597636
16839.17-1.9 (QJ1)	3.85503431667588
18094.16-2 (IMSS)	24.4794457366434
18094.16-2 (CCM)	27.7287838047095
18690.17-2R1 (1R1)	18.6691680603875
18690.17-2R1 (CFB2)	16.0848264166974
19364.16-4M1 (MPPA1)	26.6690936311702
19364.16-4M1 (HJDC)	24.5008262973417
20008.17-1 (RMRO1)	7.61158524625395
20880.15-2R2 (1)	23.0922994765743
23308.16-6CABO (AFM)	19.8514418146721
23308.16-6CABO (MARCC)	15.4096795700604

Table B11: Log_{10} values of the global LRs computed by EuroForMix v.1.9.3 without stutters[1], for mixtures with three estimated contributors assuming two contributors.

Mixture (Reference)	Log_{10} (LR)
243.17-1FM (JRA)	20.9750142284302
243.17-1FM (MM)	29.7665120083201
913.17-1.3 (ASML1)	24.9947854697638
913.17-1.3 (PMRP1)	12.1048552718317
1087.17-4 (PMCC1)	17.249691976518
1182.17-2L2FM (MD1)	15.4844121266544
1383.17-1CABO (AMAD1)	11.4083597627895
1383.17-1CABO (AMBC1)	5.43528109604087
1793.17-2 (1)	16.7354313373038
1793.17-2 (3)	19.9850437805947
1799.17-1 (2)	12.4616490068978
1816.17-2FF (EVM1)	11.8978514527524
1816.17-2FF (SC1)	11.574164334213
1843.17-1FIXACAO (FN1)	10.1948277973836
1847.17-3R2 (JC1)	20.364555022494
1847.17-3R2 (MC1)	4.56190243900404
2572.17-4CABO (IOSS)	10.5823397688542
2572.17-4CABO (LMVG1)	9.16505653754365
2799.17-2FM (1FF)	23.6919302779036
2921.17-2 (JAVC2)	-73.6120992499896
2921.17-2 (TFTS1)	24.1396123251651
3053.17-3.1R2 (EAD1)	21.4618897733827
3053.17-3.1R2 (MMM1)	4.6725310109408
3732.17-2.1FM (ASSC1)	23.6826344324439
3732.17-2.1FM (IST1)	27.151774903459
3929.16-1 (2)	16.2650567388826
5258.17-5 (1)	11.422978525856
5700.16-5 (AGT)	18.983305988701
5700.16-5 (TMAS)	23.4140497242138
5707.17-6R1 (MAGDC1)	13.255857142384
5709.17-6R2 (CMDF1)	11.2921476894414
5709.17-6R2 (MJLF1)	14.5996254245466
5773.17-4 (5FM)	22.6646621684467
5773.17-4 (17FDC1)	24.5750873201305
6010.17-1 (AAM1)	22.1810762611953
6472.17-1FM (PSBM2)	-8.02567064574846
7241.17-11R2FF (ASJ1)	5.46647601206326
7241.17-11R2FF (MCPSJ1)	23.4998337272144
7385.16-3 (2)	23.0950447638211
7588.17-1R1FF (3)	26.471589768014
9233.16-9.1 (LCGS1)	23.5474790829288
9233.16-9.1 (VMTJ2)	3.96751918944793
10223.17-3LAM (IM2)	6.77261177153036
10223.17-3LAM (VMPM1)	-1.84634302228096
12818.17-7 (1)	21.8627990008954
13017.17-25.2 (AJAN1)	8.66435496796194
13017.17-25.2 (MJCR1)	-17.7016911890842
13027.17-1R2FF (1R1FF)	3.20167437998602
13027.17-1R2FF (1R1FM)	15.4821519650363
13034.16-2CABO (2LAM)	12.2328488932812
13252.17-8 (FTMR1)	11.9457654547225
13252.17-8 (LIOR1)	15.8517998451953
13740.17-1R1FF (1R2FF)	0.46531357219615
13940.17-2 (DMC1)	17.6028802799993
13940.17-2 (NMFM1)	11.3467085405989
14002.16-1 (MPNG1)	7.41832173741204
14552.16-1FM (LMRR1)	12.2752939817767
14552.16-1FM (1FF)	22.8534515924476
15150.17-1 (DASS1)	10.0410953552013
15150.17-1 (RJABO2)	9.00209776364961
16126.17-3.3 (1)	15.3060046274073
16537.17-1 (AJMC1)	22.909043454667
16537.17-1 (ASLS1)	11.6921686137674
16672.17-4R2 (4R1)	13.4298034008432
16672.17-4R2 (AMC1)	20.6474157692262
16913.17-3 (NMSAOM1)	24.9720244064032
17065.17-1 (3)	5.16958958877412
17065.17-1 (SSC1)	8.40875372979695
17222.17-3R2FF (3R1)	9.88030396872198
17222.17-3R2FF (PM1)	22.4996613214218
18119.17-2 (LZ1)	27.2350779212919
19187.16-4CABO (RGCF)	13.9053579367883
19724.16-6 (ENP1)	9.25017424283231
19724.16-6 (13)	22.3652551416635
19724.16-8 (BMAP)	17.5761990227146
19799.17-1 (TFPA1)	3.83467099213571
20601.16-1 (HMNM1)	17.439792621267
20601.16-1 (AMM)	19.2477555948825
20628.16-1CABO (AMP)	11.7876564901038

[1] Computed by Figueiredo C: Forensic DNA mixtures: Analysis and comparison of software results. Faculdade de Ciências da Universidade do Porto; 2018.

Table B12: Log10 values of the global LRs computed by STRmixTM v.2.7 with stutters, for mixtures with three estimated contributors assuming two contributors. The "-" represent the null LRs values (markers and global) and for that reason it was not possible to calculate a Log10 value.

Mixture (Reference)	Log_{10} (LR)
243.17-1FM (JRA)	-
243.17-1FM (MM)	27.287913647076
913.17-1.3 (ASML1)	Evidence cannot be explained given the parameters you have chosen
913.17-1.3 (PMRP1)	Evidence cannot be explained given the parameters you have chosen
1087.17-4 (PMCC1)	Evidence cannot be explained given the parameters you have chosen
1182.17-2L2FM (MD1)	Evidence cannot be explained given the parameters you have chosen
1383.17-1CABO (AMAD1)	Evidence cannot be explained given the parameters you have chosen
1383.17-1CABO (AMBC1)	Evidence cannot be explained given the parameters you have chosen
1793.17-2 (1)	Evidence cannot be explained given the parameters you have chosen
1793.17-2 (3)	21.3327817198629
1799.17-1 (2)	9.58904434351819
1816.17-2FF (EVM1)	Evidence cannot be explained given the parameters you have chosen
1816.17-2FF (SC1)	-
1843.17-1FIXACAO (FN1)	-
1847.17-3R2 (JC1)	21.6789460895454
1847.17-3R2 (MC1)	Evidence cannot be explained given the parameters you have chosen
2572.17-4CABO (IOSS)	Evidence cannot be explained given the parameters you have chosen
2572.17-4CABO (LMVG1)	Evidence cannot be explained given the parameters you have chosen
2799.17-2FM (1FF)	Evidence cannot be explained given the parameters you have chosen
2921.17-2 (JAVC2)	Evidence cannot be explained given the parameters you have chosen
2921.17-2 (TFTS1)	Evidence cannot be explained given the parameters you have chosen
3053.17-3.1R2 (EAD1)	Evidence cannot be explained given the parameters you have chosen
3053.17-3.1R2 (MMM1)	Evidence cannot be explained given the parameters you have chosen
3732.17-2.1FM (ASSC1)	Evidence cannot be explained given the parameters you have chosen
3732.17-2.1FM (IST1)	Evidence cannot be explained given the parameters you have chosen
3929.16-1 (2)	Evidence cannot be explained given the parameters you have chosen
5258.17-5 (1)	Evidence cannot be explained given the parameters you have chosen
5700.16-5 (AGT)	Evidence cannot be explained given the parameters you have chosen
5700.16-5 (TMAS)	Evidence cannot be explained given the parameters you have chosen
5707.17-6R1 (MAGDC1)	Evidence cannot be explained given the parameters you have chosen
5709.17-6R2 (CMDF1)	Evidence cannot be explained given the parameters you have chosen
5709.17-6R2 (MJLF1)	Evidence cannot be explained given the parameters you have chosen
5773.17-4 (5FM)	24.4213241774639
5773.17-4 (17FDC1)	-
6010.17-1 (AAM1)	29.8483430948274
6472.17-1FM (PSBM2)	Evidence cannot be explained given the parameters you have chosen
7241.17-11R2FF (ASJ1)	Evidence cannot be explained given the parameters you have chosen
7241.17-11R2FF (MCPSJ1)	Evidence cannot be explained given the parameters you have chosen
7385.16-3 (2)	27.0881715398644
7588.17-1R1FF (3)	Evidence cannot be explained given the parameters you have chosen
9233.16-9.1 (LCGS1)	Evidence cannot be explained given the parameters you have chosen
9233.16-9.1 (VMTJ2)	Evidence cannot be explained given the parameters you have chosen
10223.17-3LAM (IM2)	Evidence cannot be explained given the parameters you have chosen
10223.17-3LAM (VMPM1)	Evidence cannot be explained given the parameters you have chosen
12818.17-7 (1)	-
13017.17-25.2 (AJAN1)	-
13017.17-25.2 (MJCR1)	Evidence cannot be explained given the parameters you have chosen
13027.17-1R2FF (1R1FF)	Evidence cannot be explained given the parameters you have chosen
13027.17-1R2FF (1R1FM)	Evidence cannot be explained given the parameters you have chosen
13034.16-2CABO (2LAM)	10.8884378587872
13252.17-8 (FTMR1)	7.61238115323532
13252.17-8 (LIOR1)	-
13740.17-1R1FF (1R2FF)	Evidence cannot be explained given the parameters you have chosen
13940.17-2 (DMC1)	Evidence cannot be explained given the parameters you have chosen
13940.17-2 (NMFM1)	Evidence cannot be explained given the parameters you have chosen
14002.16-1 (MPNG1)	Evidence cannot be explained given the parameters you have chosen
14552.16-1FM (LMRR1)	Evidence cannot be explained given the parameters you have chosen
14552.16-1FM (1FF)	Evidence cannot be explained given the parameters you have chosen
15150.17-1 (DASS1)	-
15150.17-1 (RJABO2)	-
16126.17-3.3 (1)	-
16537.17-1 (AJMC1)	23.7891363200687
16537.17-1 (ASLS1)	-
16672.17-4R2 (4R1)	Evidence cannot be explained given the parameters you have chosen
16672.17-4R2 (AMC1)	Evidence cannot be explained given the parameters you have chosen
16913.17-3 (NMSAOM1)	Evidence cannot be explained given the parameters you have chosen
17065.17-1 (3)	Evidence cannot be explained given the parameters you have chosen
17065.17-1 (SSC1)	Evidence cannot be explained given the parameters you have chosen
17222.17-3R2FF (3R1)	Evidence cannot be explained given the parameters you have chosen
17222.17-3R2FF (PM1)	Evidence cannot be explained given the parameters you have chosen
18119.17-2 (LZ1)	Evidence cannot be explained given the parameters you have chosen
19187.16-4CABO (RGCF)	Evidence cannot be explained given the parameters you have chosen
19724.16-6 (ENP1)	Evidence cannot be explained given the parameters you have chosen
19724.16-6 (13)	Evidence cannot be explained given the parameters you have chosen
19724.16-8 (BMAP)	Evidence cannot be explained given the parameters you have chosen
19799.17-1 (TFPA1)	Evidence cannot be explained given the parameters you have chosen
20601.16-1 (HMNM1)	Evidence cannot be explained given the parameters you have chosen
20601.16-1 (AMM)	Evidence cannot be explained given the parameters you have chosen
20628.16-1CABO (AMP)	Evidence cannot be explained given the parameters you have chosen

Table B13: Log_{10} values of the global LRs computed by EuroForMix v.1.9.3 without stutters[1], for mixtures with two estimated contributors with threshold limit T=150.

Mixture (Reference)	**Log_{10} (LR)**
243.17-1FM (JRA)	17.52887618
243.17-1FM (MM)	22.07177147
913.17-1.3 (ASML1)	12.83121333
913.17-1.3 (PMRP1)	18.49356781
1087.17-4 (PMCC1)	20.05135473
1182.17-2L2FM (MD1)	26.31967972
1383.17-1CABO (AMAD1)	25.37521929
1383.17-1CABO (AMBC1)	14.72566263
1793.17-2 (1)	11.85076691
1793.17-2 (3)	33.89820425
1799.17-1 (2)	16.38509631
1816.17-2FF (EVM1)	28.16354756
1816.17-2FF (SC1)	23.21769501
1843.17-1FIXACAO (FN1)	7.337316721
1847.17-3R2 (JC1)	17.6182739
1847.17-3R2 (MC1)	20.6369327
2572.17-4CABO (IOSS)	18.57982191
2572.17-4CABO (LMVG1)	18.59167528
2799.17-2FM (1FF)	24.37133956
2921.17-2 (JAVC2)	15.36718875
2921.17-2 (TFTS1)	22.93326419
3053.17-3.1R2 (EAD1)	15.43984674
3053.17-3.1R2 (MMM1)	17.08446827
3732.17-2.1FM (ASSC1)	20.18195315
3732.17-2.1FM (IST1)	22.12915748
3929.16-1 (2)	26.17246241
5258.17-5 (1)	28.63447137
5700.16-5 (AGT)	22.03084129
5700.16-5 (TMAS)	28.55980519
5707.17-6R1 (MAGDC1)	22.92311655
5709.17-6R2 (CMDF1)	15.66024302
5709.17-6R2 (MJLF1)	16.34580881
5773.17-4 (5FM)	19.75082936
5773.17-4 (17FDC1)	26.41875299
6010.17-1 (AAM1)	13.89192971
6472.17-1FM (PSBM2)	24.28187797
7241.17-11R2FF (ASJ1)	21.05768698
7241.17-11R2FF (MCPSJ1)	18.99483258
7385.16-3 (2)	6.941971525
7588.17-1R1FF (3)	25.56053166
9233.16-9.1 (LCGS1)	9.945443874
9233.16-9.1 (VMTJ2)	20.07991331
10223.17-3LAM (IM2)	14.25748994
10223.17-3LAM (VMPM1)	20.19435496
12818.17-7 (1)	22.05012082
13017.17-25.2 (AJAN1)	26.56279071
13017.17-25.2 (MJCR1)	28.67948304
13027.17-1R2FF (1R1FF)	16.3344708
13027.17-1R2FF (1R1FM)	25.93496766
13034.16-2CABO (2LAM)	21.70960345
13252.17-8 (FTMR1)	18.59531233
13252.17-8 (LIOR1)	15.49174541
13740.17-1R1FF (1R2FF)	14.64722238
13940.17-2 (DMC1)	16.64556055
13940.17-2 (NMFM1)	13.93211393
14002.16-1 (MPNG1)	11.0949838
14552.16-1FM (LMRR1)	11.00057169
14552.16-1FM (1FF)	29.67543567
15150.17-1 (DASS1)	17.29365242
15150.17-1 (RJABO2)	22.57358903
16126.17-3.3 (1)	29.6090563
16537.17-1 (AJMC1)	27.43326148
16537.17-1 (ASLS1)	28.35783268
16672.17-4R2 (4R1)	27.93659444
16672.17-4R2 (AMC1)	20.28513072
16913.17-3 (NMSAOM1)	19.47387902
17065.17-1 (3)	27.99185139
17065.17-1 (SSC1)	23.09697522
17222.17-3R2FF (3R1)	19.70326641
17222.17-3R2FF (PM1)	24.50865229
18119.17-2 (LZ1)	16.5283751
19187.16-4CABO (RGCF)	8.825227757
19724.16-6 (ENP1)	24.58048768
19724.16-6 (13)	18.94451018
19724.16-8 (BMAP)	22.2045179
19799.17-1 (TFPA1)	8.719352039
20601.16-1 (HMNM1)	14.0682714
20601.16-1 (AMM)	15.588538
20628.16-1CABO (AMP)	26.61808864

[1] Computed by Figueiredo C: Forensic DNA mixtures: Analysis and comparison of software results. Faculdade de Ciências da Universidade do Porto; 2018.

Table B14: Log_{10} values of the global LRs computed by STRmix™ v.2.7 with stutters, for mixtures with two estimated contributors with threshold limit T=150.

Mixture (Reference)	Log_{10} (LR)
243.17-1FM (JRA)	18.0461828907409
243.17-1FM (MM)	21.2134380626238
913.17-1.3 (ASML1)	15.1280436738265
913.17-1.3 (PMRP1)	16.0852192010449
1087.17-4 (PMCC1)	22.77102127989
1182.17-2L2FM (MD1)	26.5738227563297
1383.17-1CABO (AMAD1)	26.4817435204204
1383.17-1CABO (AMBC1)	19.9215564277264
1793.17-2 (1)	20.3669270065877
1793.17-2 (3)	33.1377654200573
1799.17-1 (2)	25.3550490317763
1816.17-2FF (EVM1)	29.0112743289047
1816.17-2FF (SC1)	25.2224042910825
1843.17-1FIXACAO (FN1)	9.46809613512106
1847.17-3R2 (JC1)	21.4042348666534
1847.17-3R2 (MC1)	21.7882885988986
2572.17-4CABO (IOSS)	23.9659679801934
2572.17-4CABO (LMVG1)	23.5853027755217
2799.17-2FM (1FF)	26.6265046084593
2921.17-2 (JAVC2)	23.7812238463513
2921.17-2 (TFTS1)	29.3638563192951
3053.17-3.1R2 (EAD1)	16.8686444383948
3053.17-3.1R2 (MMM1)	17.722296555286
3732.17-2.1FM (ASSC1)	19.9523564773238
3732.17-2.1FM (IST1)	20.6853296349724
3929.16-1 (2)	26.2800089531082
5258.17-5 (1)	30.2213359795338
5700.16-5 (AGT)	25.9687117101179
5700.16-5 (TMAS)	30.3793599144876
5707.17-6R1 (MAGDC1)	26.9401577450345
5709.17-6R2 (CMDF1)	17.3211632967607
5709.17-6R2 (MJLF1)	17.6300310313617
5773.17-4 (5FM)	18.5529965499795
5773.17-4 (17FDC1)	26.932661444864
6010.17-1 (AAM1)	22.3250638935649
6472.17-1FM (PSBM2)	26.9624072223037
7241.17-11R2FF (ASJ1)	23.4003652733499
7241.17-11R2FF (MCPSJ1)	22.2428394686728
7385.16-3 (2)	1.56489084517638
7588.17-1R1FF (3)	27.1438263908396
9233.16-9.1 (LCGS1)	21.34519723193
9233.16-9.1 (VMTJ2)	26.40119368463
10223.17-3LAM (IM2)	13.9661041705109
10223.17-3LAM (VMPM1)	18.8647957709944
12818.17-7 (1)	14.5783985051725
13017.17-25.2 (AJAN1)	28.5377057860805
13017.17-25.2 (MJCR1)	29.4649959786189
13027.17-1R2FF (1R1FF)	3.19750109614326
13027.17-1R2FF (1R1FM)	26.4360035356699
13034.16-2CABO (2LAM)	27.5202345444822
13252.17-8 (FTMR1)	22.0191994010553
13252.17-8 (LIOR1)	19.9787190551254
13740.17-1R1FF (1R2FF)	19.560993989868
13940.17-2 (DMC1)	17.0287338793493
13940.17-2 (NMFM1)	16.190107488314
14002.16-1 (MPNG1)	20.7512251988407
14552.16-1FM (LMRR1)	12.3311640079514
14552.16-1FM (1FF)	30.5894357358397
15150.17-1 (DASS1)	23.0790364570875
15150.17-1 (RJABO2)	25.88107066423
16126.17-3.3 (1)	30.0757293997409
16537.17-1 (AJMC1)	27.642375475799
16537.17-1 (ASLS1)	28.4363376022463
16672.17-4R2 (4R1)	26.046573197662
16672.17-4R2 (AMC1)	20.8326940870465
16913.17-3 (NMSAOM1)	19.970449160529
17065.17-1 (3)	28.3988597384043
17065.17-1 (SSC1)	24.7433607934204
17222.17-3R2FF (3R1)	23.5206276186193
17222.17-3R2FF (PM1)	24.8659326681932
18119.17-2 (LZ1)	15.6543209617037
19187.16-4CABO (RGCF)	12.3852129070845
19724.16-6 (ENP1)	26.5708347064242
19724.16-6 (13)	23.9807576155614
19724.16-8 (BMAP)	26.3708090565455
19799.17-1 (TFPA1)	15.8776736340151
20601.16-1 (HMNM1)	3.98590676176562
20601.16-1 (AMM)	21.8451104482508
20628.16-1CABO (AMP)	26.02633530733

Table B15: Log_{10} values of the global LRs computed by EuroForMix v.1.9.3 without stutters[1], for mixtures with three estimated contributors with threshold limit T=150.

Mixture (Reference)	Log_{10} (LR)
245.17-2.1 (MABS)	21.84919616
245.17-2.1 (OCF)	29.53513407
428.17-10 (LHIF)	25.96829913
1305-17-3 (PBS1)	9.923733597
1305-17-3 (RDS1)	15.38363892
1533.17-4 (EIJB1)	17.45195972
2193.16-3 (MNTB)	10.68782169
2193.16-3 (MHMB)	5.172058594
2793.17-1R3 (FJCM1)	16.51908093
3053.17-5R2 (MHR2)	20.15049101
3053.17-5R2 (CDS1)	16.51233727
3357.17-12.2 (9)	14.38264995
3665.17-26 (SL2)	11.01429342
3675.17-1 (AJRG1)	13.09684142
3675.17-1 (ORG1)	19.96500585
3841.17-7 (3)	6.391317331
3958.17-1R2FF (LGS1)	11.80850765
4406.17-6 (CVG)	16.61883816
4406.17-6 (NGP)	27.19195325
4548.16-PC9.9 (PC9.8)	25.10626569
4702.17-1 (CSP1)	23.62475385
4980.17-11 (JAMR1)	21.95369455
5008.17-1R1 (1R2)	14.34719649
5008.17-1R1 (2R1)	25.73117441
5008.17-3CABO (3LAM)	26.56786443
5008.17-3CABO (4R2)	19.31020873
5374.16-9 (BMEB1)	9.617311665
5396.16-1CABO (JJCC)	19.23082811
6561.17-2BIO (FMGV1)	23.98710978
6561.17-2BIO (JAPG1)	21.75055479
6568.17-9 (DFSDN1)	10.64001936
6568.17-9 (RFAS2)	15.20884493
6978.17-4R2 (7FF)	22.61060985
6978.17-4R2 (JAB1)	21.91264873
7245.17-1R1 (1R2)	24.61912305
7582.17-1 (FMBSC)	8.519077564
8356.16-8.2FF (DPMF)	2.183102678
8356.16-8.2FF (HVF)	23.49363958
8371.16-1R1 (JARR1)	23.38445029
8393.17-2FF (JPB2)	26.48378674
8393.17-2FF (TFB2)	24.97789065
8410.16-2R1 (2R2)	9.66936825
10175.16-4 (5)	10.13564864
10278.16-2 (1)	6.969899374
10814.16-2 (CMSA)	22.29895422
10814.16-2 (FMRG)	7.268627196
11021.17-20LAM (MABSC1)	10.70345255
11021.17-20LAM (MGSF1)	10.84239852
11021.17-20LAM (MSSF1)	13.94174013
12179.17-14R6 (GCG1)	11.74304197
12179.17-14R6 (MAM1)	11.77425251
12946.17-3.1 (2)	18.8969204
13020.17-1LAM (1CABO)	8.704997447
13046.17-1R1 (2R1)	18.26542072
13253.17-4 (3)	13.58785226
13367.17-5 (SMCP1)	7.385519464
14005.17-1R1FF (1R2FM)	15.11385373
14005.17-1R1FF (2R1FF)	22.05633222
14281.17-6R1 (6R2)	9.194840664
14281.17-6R1 (MGGS1)	8.775212259
14503.17-1 (MRER1)	13.61465363
14828.17-2FF (1FF)	23.19050318
14828.17-2FF (FLEP1)	17.71695935
14942.17-2LAM (3R1)	14.22142157
14942.17-2LAM (NMLC1)	20.41136173
15014.17-1 (2)	24.57962319
16839.17-1.9 (BZ1)	11.39324672
16839.17-1.9 (JW1)	12.54236598
16839.17-1.9 (QJ1)	10.855135
18094.16-2 (IMSS)	23.57907042
18094.16-2 (CCM)	27.14006611
18690.17-2R1 (1R1)	15.91257528
18690.17-2R1 (CFB2)	17.95329608
19364.16-4M1 (MPPA1)	22.090888
19364.16-4M1 (HJDC)	21.6635693
20008.17-1 (RMRO1)	9.583303734
20880.15-2R2 (1)	15.67311566
23308.16-6CABO (AFM)	18.60207049
23308.16-6CABO (MARCC)	12.49463606

[1] Computed by Figueiredo C: Forensic DNA mixtures: Analysis and comparison of software results. Faculdade de Ciências da Universidade do Porto; 2018.

Table B16: Log_{10} values of the global LRs computed by STRmix™ v.2.7 with stutters, for mixtures with three estimated contributors with threshold limit T=150.

Mixture (Reference)	Log_{10}(LR)
245.17-2.1 (MABS)	28.2037126406077
245.17-2.1 (OCF)	27.2275010649714
428.17-10 (LHIF)	30.5878145972397
1305-17-3 (PBS1)	20.1483866876668
1305-17-3 (RDS1)	23.5323912538315
1533.17-4 (EIJB1)	15.9036108279281
2193.16-3 (MNTB)	15.427810572676
2193.16-3 (MHMB)	6.34220547927634
2793.17-1R3 (FJCM1)	17.6823436687699
3053.17-5R2 (MHR2)	20.6136938618146
3053.17-5R2 (CDS1)	17.7957549225188
3357.17-12.2 (9)	19.5792461104542
3665.17-26 (SL2)	7.32471447656067
3675.17-1 (AJRG1)	13.9644434944715
3675.17-1 (ORG1)	21.2104255416311
3841.17-7 (3)	14.461888526344
3958.17-1R2FF (LGS1)	20.3759743661762
4406.17-6 (CVG)	18.4855936740224
4406.17-6 (NGP)	26.2980151661527
4548.16-PC9.9 (PC9.8)	23.1045895271794
4702.17-1 (CSP1)	22.5303021744853
4980.17-11 (JAMR1)	25.8155777483243
5008.17-1R1 (1R2)	19.786424868913
5008.17-1R1 (2R1)	26.6033717491009
5008.17-3CABO (3LAM)	29.9685016274848
5008.17-3CABO (4R2)	27.4539143212378
5374.16-9 (BMEB1)	13.9779978099587
5396.16-1CABO (JJCC)	26.3503449482491
6561.17-2BIO (FMGV1)	27.2471136417709
6561.17-2BIO (JAPG1)	26.2386231053847
6568.17-9 (DFSDN1)	11.4559406414525
6568.17-9 (RFAS2)	-6.95683427979255
6978.17-4R2 (7FF)	24.3258029087436
6978.17-4R2 (JAB1)	23.6962340350258
7245.17-1R1 (1R2)	29.8340581104046
7582.17-1 (FMBSC)	9.23317385538094
8356.16-8.2FF (DPMF)	8.83916368291465
8356.16-8.2FF (HVF)	25.3247144765607
8371.16-1R1 (JARR1)	27.1735358950099
8393.17-2FF (JPB2)	25.9455424384577
8393.17-2FF (TFB2)	28.2160338778187
8410.16-2R1 (2R2)	6.92165526757323
10175.16-4 (5)	12.848250714677
10278.16-2 (1)	5.27982658179401
10814.16-2 (CMSA)	-7.08902040854576
10814.16-2 (FMRG)	10.5172222980279
11021.17-20LAM (MABSC1)	11.7451919415577
11021.17-20LAM (MGSF1)	15.8740931561188
11021.17-20LAM (MSSF1)	20.3107994838344
12179.17-14R6 (GCG1)	12.3721937192757
12179.17-14R6 (MAM1)	10.763068428634
12946.17-3.1 (2)	21.9651781741437
13020.17-1LAM (1CABO)	13.8508054677167
13046.17-1R1 (2R1)	18.0928960109219
13253.17-4 (3)	24.5383977686857
13367.17-5 (SMCP1)	15.5250577708577
14005.17-1R1FF (1R2FM)	23.4688197748231
14005.17-1R1FF (2R1FF)	26.286186916941
14281.17-6R1 (6R2)	11.6194168430094
14281.17-6R1 (MGGS1)	10.9971241556592
14503.17-1 (MRER1)	10.0955877469187
14828.17-2FF (1FF)	23.8331343571152
14828.17-2FF (FLEP1)	19.0090257420869
14942.17-2LAM (3R1)	11.0961797847148
14942.17-2LAM (NMLC1)	12.0623563180854
15014.17-1 (2)	25.6505697694640
16839.17-1.9 (BZ1)	3.48960696626772
16839.17-1.9 (JW1)	1.93919965405252
16839.17-1.9 (QJ1)	3.73175793787546
18094.16-2 (IMSS)	24.7554861024574
18094.16-2 (CCM)	27.7846957295444
18690.17-2R1 (1R1)	17.414939939418
18690.17-2R1 (CFB2)	16.9690476310961
19364.16-4M1 (MPPA1)	27.2284773544451
19364.16-4M1 (HJDC)	24.4405312703999
20008.17-1 (RMRO1)	6.88138465677057
20880.15-2R2 (1)	23.4805674250017
23308.16-6CABO (AFM)	19.9519976884757
23308.16-6CABO (MARCC)	15.6081728920617

Table B17: Log_{10} values of the global LRs computed by EuroForMix v.1.9.3 with stutters[1], for mixtures with two estimated contributors with λ=0.05.

Mixture (Reference)	Log_{10} (LR)
243.17-1FM (JRA)	17.5254944993951
243.17-1FM (MM)	22.0775741564395
913.17-1.3 (ASML1)	14.0642857458723
913.17-1.3 (PMRP1)	18.6525439634993
1087.17-4 (PMCC1)	20.2982599442718
1182.17-2L2FM (MD1)	26.3542566158969
1383.17-1CABO (AMAD1)	25.418126650892
1383.17-1CABO (AMBC1)	13.9060634198487
1793.17-2 (1)	15.2642941169745
1793.17-2 (3)	34.2793938328464
1799.17-1 (2)	16.5470269296182
1816.17-2FF (EVM1)	28.1710269753445
1816.17-2FF (SC1)	24.0527482073615
1843.17-1FIXACAO (FN1)	8.76195199427449
1847.17-3R2 (JC1)	17.6148301380946
1847.17-3R2 (MC1)	20.6589350261577
2572.17-4CABO (IOSS)	18.5943954867273
2572.17-4CABO (LMVG1)	18.5804299297185
2799.17-2FM (1FF)	25.343963192097
2921.17-2 (JAVC2)	16.822816246839
2921.17-2 (TFTS1)	22.9475807386936
3053.17-3.1R2 (EAD1)	12.4787698346001
3053.17-3.1R2 (MMM1)	13.0089606561544
3732.17-2.1FM (ASSC1)	20.1812967640596
3732.17-2.1FM (IST1)	22.1311290550811
3929.16-1 (2)	26.200369954818
5258.17-5 (1)	28.6344443204762
5700.16-5 (AGT)	22.2018665784344
5700.16-5 (TMAS)	28.5658020555617
5707.17-6R1 (MAGDC1)	23.699864079348
5709.17-6R2 (CMDF1)	15.663605210442
5709.17-6R2 (MJLF1)	16.5838569838335
5773.17-4 (5FM)	20.0811829278284
5773.17-4 (17FDC1)	26.4038160106212
6010.17-1 (AAM1)	16.5591520523733
6472.17-1FM (PSBM2)	24.1663748212081
7241.17-11R2FF (ASJ1)	21.0079625086546
7241.17-11R2FF (MCPSJ1)	19.0018570075869
7385.16-3 (2)	8.13034034938286
7588.17-1R1FF (3)	25.5800414622538
9233.16-9.1 (LCGS1)	12.2904979034139
9233.16-9.1 (VMTJ2)	15.3830836827866
10223.17-3LAM (IM2)	14.6244114134086
10223.17-3LAM (VMPM1)	19.1067241411975
12818.17-7 (1)	19.0184739896535
13017.17-25.2 (AJAN1)	26.5706551310306
13017.17-25.2 (MJCR1)	28.6795583675699
13027.17-1R2FF (1R1FF)	16.3322119234964
13027.17-1R2FF (1R1FM)	25.9785769687535
13034.16-2CABO (2LAM)	21.5042076942674
13252.17-8 (FTMR1)	18.7672965319915
13252.17-8 (LIOR1)	15.6621431962292
13740.17-1R1FF (1R2FF)	14.6683111830601
13940.17-2 (DMC1)	16.5980330945384
13940.17-2 (NMFM1)	14.0334842663352
14002.16-1 (MPNG1)	7.73773385488408
14552.16-1FM (LMRR1)	15.8387891214786
14552.16-1FM (1FF)	29.6839597904106
15150.17-1 (DASS1)	16.3596233033866
15150.17-1 (RJABO2)	22.4888297433281
16126.17-3.3 (1)	29.6337685469546
16537.17-1 (AJMC1)	27.4392177839674
16537.17-1 (ASLS1)	28.3596453342081
16672.17-4R2 (4R1)	27.9310404270672
16672.17-4R2 (AMC1)	18.4343877851703
16913.17-3 (NMSAOM1)	19.6779241088863
17065.17-1 (3)	27.99314104607
17065.17-1 (SSC1)	22.9351736237908
17222.17-3R2FF (3R1)	19.4767935865747
17222.17-3R2FF (PM1)	24.4633343871714
18119.17-2 (LZ1)	15.3860771317756
19187.16-4CABO (RGCF)	10.1326639048464
19724.16-6 (ENP1)	24.5477370238316
19724.16-6 (13)	19.0797093286423
19724.16-8 (BMAP)	23.1529241061781
19799.17-1 (TFPA1)	2.42299087070464
20601.16-1 (HMNM1)	14.4922029050714
20601.16-1 (AMM)	15.706512103313
20628.16-1CABO (AMP)	25.9605295421859

[1] Computed by Figueiredo C: Forensic DNA mixtures: Analysis and comparison of software results. Faculdade de Ciências da Universidade do Porto; 2018.

Table B18: Log_{10} values of the global LRs computed by STRmix™ v.2.7 with stutters, for mixtures with two estimated contributors with drop-in Uniform distribution. The "-" represent the null LRs values and for that reason it was not possible to calculate a Log_{10} value.

Mixture (Reference)	Log_{10} (LR)
243.17-1FM (JRA)	18.2062590352093
243.17-1FM (MM)	21.4944607193908
913.17-1.3 (ASML1)	15.0890215007950
913.17-1.3 (PMRP1)	15.9632682515262
1087.17-4 (PMCC1)	22.8542392221253
1182.17-2L2FM (MD1)	26.5091083925838
1383.17-1CABO (AMAD1)	26.4523385438460
1383.17-1CABO (AMBC1)	19.8640243036114
1793.17-2 (1)	20.8745397970710
1793.17-2 (3)	33.0772588636929
1799.17-1 (2)	25.3212047568544
1816.17-2FF (EVM1)	28.9799306041087
1816.17-2FF (SC1)	25.5324103732534
1843.17-1FIXACAO (FN1)	8.54071728801072
1847.17-3R2 (JC1)	21.4432160341658
1847.17-3R2 (MC1)	21.877071729106
2572.17-4CABO (IOSS)	23.985192871319
2572.17-4CABO (LMVG1)	23.781403489496
2799.17-2FM (1FF)	26.323540846098
2921.17-2 (JAVC2)	23.226032503345
2921.17-2 (TFTS1)	28.6836772988187
3053.17-3.1R2 (EAD1)	17.0330214446829
3053.17-3.1R2 (MMM1)	17.828124753286
3732.17-2.1FM (ASSC1)	19.9680577856946
3732.17-2.1FM (IST1)	20.5285696400129
3929.16-1 (2)	26.278730742747
5258.17-5 (1)	30.225412672866
5700.16-5 (AGT)	26.1064628837961
5700.16-5 (TMAS)	30.382341290824
5707.17-6R1 (MAGDC1)	26.9497509553911
5709.17-6R2 (CMDF1)	17.3637059728547
5709.17-6R2 (MJLF1)	17.7559738939978
5773.17-4 (5FM)	19.3744367149817
5773.17-4 (17FDC1)	26.9013602262447
6010.17-1 (AAM1)	22.2842276395935
6472.17-1FM (PSBM2)	26.9135330590988
7241.17-11R2FF (ASJ1)	23.3125158556634
7241.17-11R2FF (MCPSJ1)	22.2338334148844
7385.16-3 (2)	2.46422119753445
7588.17-1R1FF (3)	27.1232961726453
9233.16-9.1 (LCGS1)	21.8719405292931
9233.16-9.1 (VMTJ2)	26.4513411705978
10223.17-3LAM (IM2)	13.7803389182933
10223.17-3LAM (VMPM1)	19.3154875277508
12818.17-7 (1)	19.9313103685944
13017.17-25.2 (AJAN1)	28.5203131877761
13017.17-25.2 (MJCR1)	29.4663633682610
13027.17-1R2FF (1R1FF)	-7.74683167409856
13027.17-1R2FF (1R1FM)	23.8727038962168
13034.16-2CABO (2LAM)	27.6763917843913
13252.17-8 (FTMR1)	22.2517355304378
13252.17-8 (LIOR1)	20.0617162931599
13740.17-1R1FF (1R2FF)	19.7905384872419
13940.17-2 (DMC1)	16.3947492807005
13940.17-2 (NMFM1)	16.4936531956769
14002.16-1 (MPNG1)	20.928155079859
14552.16-1FM (LMRR1)	13.5436832130 73
14552.16-1FM (1FF)	30.4944607193908
15150.17-1 (DASS1)	23.0668847431298
15150.17-1 (RJABO2)	25.9958500952539
16126.17-3.3 (1)	30.0417873189718
16537.17-1 (AJMC1)	27.5917989457305
16537.17-1 (ASLS1)	28.4236062707212
16672.17-4R2 (4R1)	26.054689642950
16672.17-4R2 (AMC1)	21.3500346963401
16913.17-3 (NMSAOM1)	20.7155437506051
17065.17-1 (3)	28.3834203732457
17065.17-1 (SSC1)	24.6683579569178
17222.17-3R2FF (3R1)	23.6312915363253
17222.17-3R2FF (PM1)	24.8534304968247
18119.17-2 (LZ1)	13.6793097669857
19187.16-4CABO (RGCF)	11.6521012295195
19724.16-6 (ENP1)	26.577100988801
19724.16-6 (13)	24.0022956825549
19724.16-8 (BMAP)	26.3052008452764
19799.17-1 (TFPA1)	15.9646225694356
20601.16-1 (HMNM1)	-
20601.16-1 (AMM)	21.6083441480519
20628.16-1CABO (AMP)	26.0122887398346

Table B19: Log_{10} values of the global LRs computed by EuroForMix v.1.9.3 without stutters[1], for mixtures with three estimated contributors with λ=0.05.

Mixture (Reference)	Log_{10}(LR)
245.17-2.1 (MABS)	22.0674920391912
245.17-2.1 (OCF)	29.5398519553356
428.17-10 (LHIF)	25.9510111552486
1305-17-3 (PBS1)	10.3300809831859
1305-17-3 (RDS1)	16.724891305801
1533.17-4 (EIJB1)	17.249376437844
2193.16-3 (MNTB)	12.6484272032992
2193.16-3 (MHMB)	5.79598711158092
2793.17-1R3 (FJCM1)	16.6576533110778
3053.17-5R2 (MHR2)	20.1457407459469
3053.17-5R2 (CDS1)	16.1366977687587
3357.17-12.2 (9)	13.1427440198473
3665.17-26 (SL2)	11.1470862435304
3675.17-1 (AJRG1)	12.3883780425645
3675.17-1 (ORG1)	20.050886215542
3841.17-7 (3)	7.16519751459179
3958.17-1R2FF (LGS1)	12.035571597026
4406.17-6 (CVG)	14.889780665962
4406.17-6 (NGP)	26.621719004364
4548.16-PC9.9 (PC9.8)	25.0077135365962
4702.17-1 (CSP1)	23.6866923073517
4980.17-11 (JAMR1)	22.0780472162997
5008.17-1R1 (1R2)	14.1398643753548
5008.17-1R1 (2R1)	26.0681415538205
5008.17-3CABO (3LAM)	26.8190836076285
5008.17-3CABO (4R2)	19.2104213766701
5374.16-9 (BMEB1)	11.2696103271004
5396.16-1CABO (JJCC)	18.6962223519487
6561.17-2BIO (FMGV1)	23.956213926734
6561.17-2BIO (JAPG1)	21.6505975016176
6568.17-9 (DFSDN1)	11.9590412163132
6568.17-9 (RFAS2)	15.2100490537093
6978.17-4R2 (7FF)	22.6197528211042
6978.17-4R2 (JAB1)	24.3188045366602
7245.17-1R1 (1R2)	24.9039989277148
7582.17-1 (FMBSC)	8.9656977644017
8356.16-8.2FF (DPMF)	6.27419838738382
8356.16-8.2FF (HVF)	23.6601522476313
8371.16-1R1 (JARR1)	23.4306529589725
8393.17-2FF (JPB2)	26.5036887748935
8393.17-2FF (TFB2)	25.1155161179106
8410.16-2R1 (2R2)	10.6106610317142
10175.16-4 (5)	9.47932182830807
10278.16-2 (1)	6.22420469986178
10814.16-2 (CMSA)	22.4140883649271
10814.16-2 (FMRG)	10.4410661187906
11021.17-20LAM (MABSC1)	10.7010830468139
11021.17-20LAM (MGSF1)	10.3059937660905
11021.17-20LAM (MSSF1)	14.0170353273261
12179.17-14R6 (GCG1)	12.1503236253325
12179.17-14R6 (MAM1)	11.9846844655538
12946.17-3.1 (2)	18.8967349607636
13020.17-1LAM (1CABO)	7.84243735757224
13046.17-1R1 (2R1)	18.7630969124874
13253.17-4 (3)	13.1345971081092
13367.17-5 (SMCP1)	4.93769207922938
14005.17-1R1FF (1R2FM)	13.7571461054837
14005.17-1R1FF (2R1FF)	22.8378579188677
14281.17-6R1 (6R2)	10.2760217694561
14281.17-6R1 (MGGS1)	9.43423597205009
14503.17-1 (MRER1)	14.5532033297932
14828.17-2FF (1FF)	23.1199354361087
14828.17-2FF (FLEP1)	17.676773563446
14942.17-2LAM (3R1)	14.2218080810089
14942.17-2LAM (NMLC1)	20.4365530077519
15014.17-1 (2)	24.5757343722343
16839.17-1.9 (BZ1)	10.9466520947809
16839.17-1.9 (JW1)	12.1649466759611
16839.17-1.9 (QJ1)	10.6708144645473
18094.16-2 (IMSS)	23.2836373843815
18094.16-2 (CCM)	27.1359228564272
18690.17-2R1 (1R1)	15.9748280969942
18690.17-2R1 (CFB2)	17.3717286933158
19364.16-4M1 (MPPA1)	22.4544219606305
19364.16-4M1 (HJDC)	19.496051850141
20008.17-1 (RMRO1)	7.28705968866933
20880.15-2R2 (1)	17.5719212118275
23308.16-6CABO (AFM)	18.6779048868038
23308.16-6CABO (MARCC)	12.005902031354

[1] Computed by Figueiredo C: Forensic DNA mixtures: Analysis and comparison of software results. Faculdade de Ciências da Universidade do Porto; 2018.

Table B20: Log_{10} values of the global LRs computed by STRmix™ v.2.7 with stutters, for mixtures with three estimated contributors with drop-in Uniform distribution.

Mixture (Reference)	Log_{10}(LR)
245.17-2.1 (MABS)	28.3081160158656
245.17-2.1 (OCF)	27.2303467224175
428.17-10 (LHIF)	30.5543882211507
1305-17-3 (PBS1)	20.4106085425684
1305-17-3 (RDS1)	23.9310966560155
1533.17-4 (EIJB1)	16.2253609803727
2193.16-3 (MNTB)	15.7259197956484
2193.16-3 (MHMB)	7.016029963076
2793.17-1R3 (FJCM1)	17.760723972142
3053.17-5R2 (MHR2)	20.9017143543254
3053.17-5R2 (CDS1)	18.1947917577219
3357.17-12.2 (9)	17.5511571164409
3665.17-26 (SL2)	7.79496181743753
3675.17-1 (AJRG1)	14.7182358824283
3675.17-1 (ORG1)	20.4486135780856
3841.17-7 (3)	14.8851858834841
3958.17-1R2FF (LGS1)	20.16767171623
4406.17-6 (CVG)	17.9442309057952
4406.17-6 (NGP)	26.4676968790276
4548.16-PC9.9 (PC9.8)	23.016029963076
4702.17-1 (CSP1)	22.6119780759939
4980.17-11 (JAMR1)	25.3305963821648
5008.17-1R1 (1R2)	19.9878494163606
5008.17-1R1 (2R1)	26.6380997148397
5008.17-3CABO (3LAM)	29.993493544769
5008.17-3CABO (4R2)	27.6374396927037
5374.16-9 (BMEB1)	13.7812382205378
5396.16-1CABO (JJCC)	26.9874249231685
6561.17-2BIO (FMGV1)	26.275057846121
6561.17-2BIO (JAPG1)	26.2719344938178
6568.17-9 (DFSDN1)	11.3595509167633
6568.17-9 (RFAS2)	-5.12158736630087
6978.17-4R2 (7FF)	24.2528287680406
6978.17-4R2 (JAB1)	23.1626838658779
7245.17-1R1 (1R2)	29.845284126348
7582.17-1 (FMBSC)	9.68043523556175
8356.16-8.2FF (DPMF)	8.89062777647295
8356.16-8.2FF (HVF)	25.3445690996885
8371.16-1R1 (JARR1)	27.1288191421945
8393.17-2FF (JPB2)	25.7242021152189
8393.17-2FF (TFB2)	27.9309897602759
8410.16-2R1 (2R2)	-6.72312477886845
10175.16-4 (5)	12.837462171486
10278.16-2 (1)	5.07055501583503
10814.16-2 (CMSA)	-7.01306711417912
10814.16-2 (FMRG)	10.7274192470595
11021.17-20LAM (MABSC1)	11.8334276227297
11021.17-20LAM (MGSF1)	16.1022621494943
11021.17-20LAM (MSSF1)	20.7140110484215
12179.17-14R6 (GCG1)	11.7379793866908
12179.17-14R6 (MAM1)	10.829625353358
12946.17-3.1 (2)	19.8069596466035
13020.17-1LAM (1CABO)	13.0206512680043
13046.17-1R1 (2R1)	18.3151303171836
13253.17-4 (3)	24.4999893343342
13367.17-5 (SMCP1)	15.4256646196831
14005.17-1R1FF (1R2FM)	24.0957619594775
14005.17-1R1FF (2R1FF)	19.8416472359922
14281.17-6R1 (6R2)	11.9232336534832
14281.17-6R1 (MGGS1)	11.2367639221878
14503.17-1 (MRER1)	10.1796379521578
14828.17-2FF (1FF)	23.4130481693179
14828.17-2FF (FLEP1)	19.147614498562
14942.17-2LAM (3R1)	11.6212178390672
14942.17-2LAM (NMLC1)	13.3908997971735
15014.17-1 (2)	25.557073894366
16839.17-1.9 (BZ1)	0.25524837696186
16839.17-1.9 (JW1)	3.79051738261732
16839.17-1.9 (QJ1)	5.91034687995707
18094.16-2 (IMSS)	24.6580018516186
18094.16-2 (CCM)	27.7557300667124
18690.17-2R1 (1R1)	17.3008345191616
18690.17-2R1 (CFB2)	16.7350077292951
19364.16-4M1 (MPPA1)	27.1993711613915
19364.16-4M1 (HJDC)	24.634094196616
20008.17-1 (RMRO1)	6.75250940078884
20880.15-2R2 (1)	23.4090196379315
23308.16-6CABO (AFM)	20.9200450209477
23308.16-6CABO (MARCC)	15.2480959310941

Table B21: Log_{10} values of the global LRs computed by EuroForMix v.1.9.3 without stutters[1], for mixtures with two estimated contributors with drop-in=0.

Mixture (Reference)	Log_{10} (LR)
243.17-1FM (JRA)	16.022015897344
243.17-1FM (MM)	22.3366584871591
913.17-1.3 (ASML1)	13.7783877569933
913.17-1.3 (PMRP1)	18.7669517798618
1087.17-4 (PMCC1)	20.2474128781511
1182.17-2L2FM (MD1)	26.3622121433798
1383.17-1CABO (AMAD1)	model couldn't explain the data
1383.17-1CABO (AMBC1)	model couldn't explain the data
1793.17-2 (1)	13.7088465940449
1793.17-2 (3)	34.3484408968761
1799.17-1 (2)	16.5471259356165
1816.17-2FF (EVM1)	28.1789326568952
1816.17-2FF (SC1)	17.5303987264437
1843.17-1FIXACAO (FN1)	model couldn't explain the data
1847.17-3R2 (JC1)	17.6148301368338
1847.17-3R2 (MC1)	20.6589350262269
2572.17-4CABO (IOSS)	18.594395486693
2572.17-4CABO (LMVG1)	18.5804299297346
2799.17-2FM (1FF)	25.3844109543824
2921.17-2 (JAVC2)	16.8372047233068
2921.17-2 (TFTS1)	22.952106501048
3053.17-3.1R2 (EAD1)	model couldn't explain the data
3053.17-3.1R2 (MMM1)	model couldn't explain the data
3732.17-2.1FM (ASSC1)	model couldn't explain the data
3732.17-2.1FM (IST1)	model couldn't explain the data
3929.16-1 (2)	26.2085642177085
5258.17-5 (1)	28.6344443204716
5700.16-5 (AGT)	16.495974452652
5700.16-5 (TMAS)	28.5606636734037
5707.17-6R1 (MAGDC1)	23.6984228207875
5709.17-6R2 (CMDF1)	15.663560624651
5709.17-6R2 (MJLF1)	16.5839277310566
5773.17-4 (5FM)	15.7895646280208
5773.17-4 (17FDC1)	26.4054892463734
6010.17-1 (AAM1)	15.7567548472069
6472.17-1FM (PSBM2)	24.1972052926873
7241.17-11R2FF (ASJ1)	21.0079625061374
7241.17-11R2FF (MCPSJ1)	19.0018570062862
7385.16-3 (2)	8.00116642257523
7588.17-1R1FF (3)	25.5956834841593
9233.16-9.1 (LCGS1)	12.1481744608365
9233.16-9.1 (VMTJ2)	model couldn't explain the data
10223.17-3LAM (IM2)	14.9017238384343
10223.17-3LAM (VMPM1)	model couldn't explain the data
12818.17-7 (1)	model couldn't explain the data
13017.17-25.2 (AJAN1)	26.5706551310571
13017.17-25.2 (MJCR1)	28.6795583648966
13027.17-1R2FF (1R1FF)	16.3322763512718
13027.17-1R2FF (1R1FM)	25.9785937892886
13034.16-2CABO (2LAM)	model couldn't explain the data
13252.17-8 (FTMR1)	18.7660715556647
13252.17-8 (LIOR1)	15.6630946069865
13740.17-1R1FF (1R2FF)	14.6660162487919
13940.17-2 (DMC1)	16.5736537615653
13940.17-2 (NMFM1)	13.9546013045637
14002.16-1 (MPNG1)	model couldn't explain the data
14552.16-1FM (LMRR1)	15.9704930280439
14552.16-1FM (1FF)	29.6874814074747
15150.17-1 (DASS1)	16.3575070044738
15150.17-1 (RJABO2)	22.4889690621324
16126.17-3.3 (1)	29.6440004303717
16537.17-1 (AJMC1)	model couldn't explain the data
16537.17-1 (ASLS1)	model couldn't explain the data
16672.17-4R2 (4R1)	27.9311289762029
16672.17-4R2 (AMC1)	18.1798774037805
16913.17-3 (NMSAOM1)	19.6700105797952
17065.17-1 (3)	model couldn't explain the data
17065.17-1 (SSC1)	model couldn't explain the data
17222.17-3R2FF (3R1)	model couldn't explain the data
17222.17-3R2FF (PM1)	24.5571694914213
18119.17-2 (LZ1)	model couldn't explain the data
19187.16-4CABO (RGCF)	model couldn't explain the data
19724.16-6 (ENP1)	24.5477374905591
19724.16-6 (13)	19.0797098446316
19724.16-8 (BMAP)	23.3686990941879
19799.17-1 (TFPA1)	model couldn't explain the data
20601.16-1 (HMNM1)	14.4974686929893
20601.16-1 (AMM)	15.7027610144173
20628.16-1CABO (AMP)	model couldn't explain the data

[1] Computed by Figueiredo C: Forensic DNA mixtures: Analysis and comparison of software results. Faculdade de Ciências da Universidade do Porto; 2018.

Table B22: Log_{10} values of the global LRs computed by STRmix™ v.2.7 with stutters, for mixtures with two estimated contributors with drop-in=0. The "-" represent the null LRs values and for that reason it was not possible to calculate a Log_{10} value.

Mixture (Reference)	Log_{10} (LR)
243.17-1FM (JRA)	17.5464069252423
243.17-1FM (MM)	21.4744785104083
913.17-1.3 (ASML1)	14.9694438703263
913.17-1.3 (PMRP1)	16.2329453127452
1087.17-4 (PMCC1)	22.7993681228311
1182.17-2L2FM (MD1)	26.5049870873452
1383.17-1CABO (AMAD1)	26.4522925616177
1383.17-1CABO (AMBC1)	19.8060849616736
1793.17-2 (1)	20.9940750771458
1793.17-2 (3)	33.1006806447251
1799.17-1 (2)	25.449725174949
1816.17-2FF (EVM1)	28.9830034873119
1816.17-2FF (SC1)	25.5068836911289
1843.17-1FIXACAO (FN1)	9.48623206085188
1847.17-3R2 (JC1)	21.1645312963054
1847.17-3R2 (MC1)	22.052540045934
2572.17-4CABO (IOSS)	23.3990330541069
2572.17-4CABO (LMVG1)	23.9362573124073
2799.17-2FM (1FF)	26.0376654933508
2921.17-2 (JAVC2)	23.960199556110
2921.17-2 (TFTS1)	29.4334818083930
3053.17-3.1R2 (EAD1)	17.4258601450778
3053.17-3.1R2 (MMM1)	16.9144277860439
3732.17-2.1FM (ASSC1)	19.8443777550432
3732.17-2.1FM (IST1)	20.5972013888491
3929.16-1 (2)	26.2758179278775
5258.17-5 (1)	30.2210489116929
5700.16-5 (AGT)	26.1408221801093
5700.16-5 (TMAS)	30.3772333767527
5707.17-6R1 (MAGDC1)	26.6970548922726
5709.17-6R2 (CMDF1)	17.3322162058783
5709.17-6R2 (MJLF1)	17.7804901312757
5773.17-4 (5FM)	19.1978592317381
5773.17-4 (17FDC1)	26.9013329736589
6010.17-1 (AAM1)	22.2163770579882
6472.17-1FM (PSBM2)	26.9208326511534
7241.17-11R2FF (ASJ1)	23.6758516341360
7241.17-11R2FF (MCPSJ1)	22.6113515032548
7385.16-3 (2)	-0.52215552366124
7588.17-1R1FF (3)	27.1295932283679
9233.16-9.1 (LCGS1)	21.9493314461376
9233.16-9.1 (VMTJ2)	26.1563674001335
10223.17-3LAM (IM2)	11.9437417658313
10223.17-3LAM (VMPM1)	18.9133316238067
12818.17-7 (1)	14.8550525079096
13017.17-25.2 (AJAN1)	28.5271012090571
13017.17-25.2 (MJCR1)	29.4521699185354
13027.17-1R2FF (1R1FF)	8.518749275295
13027.17-1R2FF (1R1FM)	21.6462174200111
13034.16-2CABO (2LAM)	27.6358555527964
13252.17-8 (FTMR1)	22.2962921509949
13252.17-8 (LIOR1)	20.1099158630238
13740.17-1R1FF (1R2FF)	19.6437388217436
13940.17-2 (DMC1)	17.2637070646074
13940.17-2 (NMFM1)	16.7230860771628
14002.16-1 (MPNG1)	20.8674203434298
14552.16-1FM (LMRR1)	13.5306990418449
14552.16-1FM (1FF)	30.4883250503577
15150.17-1 (DASS1)	22.9354871124809
15150.17-1 (RJABO2)	28.0327798791912
16126.17-3.3 (1)	30.0389776223327
16537.17-1 (AJMC1)	27.6100316846826
16537.17-1 (ASLS1)	28.4253548576655
16672.17-4R2 (4R1)	25.9853905433738
16672.17-4R2 (AMC1)	20.658288111559
16913.17-3 (NMSAOM1)	20.6117339263245
17065.17-1 (3)	28.3846401008263
17065.17-1 (SSC1)	24.6254256409328
17222.17-3R2FF (3R1)	23.73745504909
17222.17-3R2FF (PM1)	24.8236176661205
18119.17-2 (LZ1)	14.4793305277077
19187.16-4CABO (RGCF)	11.6992131411739
19724.16-6 (ENP1)	26.5353194425979
19724.16-6 (13)	24.0236639181978
19724.16-8 (BMAP)	26.2664668954402
19799.17-1 (TFPA1)	15.5005246277602
20601.16-1 (HMNM1)	-
20601.16-1 (AMM)	21.7799930907874
20628.16-1CABO (AMP)	25.9843008811396

Table B23: Log_{10} values of the global LRs computed by EuroForMix v.1.9.3 without stutters[1], for mixtures with three estimated contributors with drop-in=0.

Mixture (Reference)	Log_{10}(LR)
245.17-2.1 (MABS)	19.0710700399011
245.17-2.1 (OCF)	29.5513162625343
428.17-10 (LHIF)	model couldn't explain the data
1305-17-3 (PBS1)	10.2632920751357
1305-17-3 (RDS1)	16.7118013819817
1533.17-4 (EIJB1)	16.2225108027638
2193.16-3 (MNTB)	12.5585751961319
2193.16-3 (MHMB)	5.76712094658752
2793.17-1R3 (FJCM1)	16.7870126065989
3053.17-5R2 (MHR2)	20.1858687093776
3053.17-5R2 (CDS1)	16.0728824931787
3357.17-12.2 (9)	13.0106684299538
3665.17-26 (SL2)	11.0844727630411
3675.17-1 (AJRG1)	12.2572820999834
3675.17-1 (ORG1)	20.0695374753902
3841.17-7 (3)	7.14418979880512
3958.17-1R2FF (LGS1)	12.1296008029935
4406.17-6 (CVG)	11.2244756779254
4406.17-6 (NGP)	model couldn't explain the data
4548.16-PC9.9 (PC9.8)	17.8944599359111
4702.17-1 (CSP1)	23.6913300344647
4980.17-11 (JAMR1)	22.1358392177973
5008.17-1R1 (1R2)	12.8986382376625
5008.17-1R1 (2R1)	26.1277459646145
5008.17-3CABO (3LAM)	26.8817145104749
5008.17-3CABO (4R2)	19.189348512282
5374.16-9 (BMEB1)	11.2746295743153
5396.16-1CABO (JJCC)	18.5191177376367
6561.17-2BIO (FMGV1)	23.9707541525397
6561.17-2BIO (JAPG1)	21.655759471706
6568.17-9 (DFSDN1)	11.6594580569175
6568.17-9 (RFAS2)	15.3100694485268
6978.17-4R2 (7FF)	22.6214815548687
6978.17-4R2 (JAB1)	24.3310597198026
7245.17-1R1 (1R2)	24.9173210667018
7582.17-1 (FMBSC)	8.98847905581167
8356.16-8.2FF (DPMF)	6.46678176885267
8356.16-8.2FF (HVF)	23.6855298876219
8371.16-1R1 (JARR1)	23.4376120079873
8393.17-2FF (JPB2)	26.5217806801114
8393.17-2FF (TFB2)	25.2036101806084
8410.16-2R1 (2R2)	10.5118309625126
10175.16-4 (5)	9.43200708572459
10278.16-2 (1)	5.91715409376371
10814.16-2 (CMSA)	22.4043029585844
10814.16-2 (FMRG)	10.4456844276186
11021.17-20LAM (MABSC1)	10.7010685463623
11021.17-20LAM (MGSF1)	10.3040797967328
11021.17-20LAM (MSSF1)	14.0172923382333
12179.17-14R6 (GCG1)	12.1903142518501
12179.17-14R6 (MAM1)	11.9048905795015
12946.17-3.1 (2)	18.9055913520227
13020.17-1LAM (1CABO)	7.78974233587604
13046.17-1R1 (2R1)	18.8601324338963
13253.17-4 (3)	13.0070053568896
13367.17-5 (SMCP1)	model couldn't explain the data
14005.17-1R1FF (1R2FM)	12.3495955359909
14005.17-1R1FF (2R1FF)	22.9496782013873
14281.17-6R1 (6R2)	10.2481284307034
14281.17-6R1 (MGGS1)	9.37373974482916
14503.17-1 (MRER1)	14.5216995526133
14828.17-2FF (1FF)	23.1290442951909
14828.17-2FF (FLEP1)	17.7044368010534
14942.17-2LAM (3R1)	14.2306298011007
14942.17-2LAM (NMLC1)	20.4497767170836
15014.17-1 (2)	24.6165754313326
16839.17-1.9 (BZ1)	10.8152106214486
16839.17-1.9 (JW1)	12.0682371817328
16839.17-1.9 (QJ1)	10.6219138895666
18094.16-2 (IMSS)	23.2709825863281
18094.16-2 (CCM)	27.1470325086393
18690.17-2R1 (1R1)	15.9869834955959
18690.17-2R1 (CFB2)	model couldn't explain the data
19364.16-4M1 (MPPA1)	22.6092388458549
19364.16-4M1 (HJDC)	19.3404903406444
20008.17-1 (RMRO1)	7.14826173740838
20880.15-2R2 (1)	13.4999260118566
23308.16-6CABO (AFM)	18.7521608649353
23308.16-6CABO (MARCC)	11.9498931957151

[1] Computed by Figueiredo C: Forensic DNA mixtures: Analysis and comparison of software results. Faculdade de Ciências da Universidade do Porto; 2018.

Table B24: Log_{10} values of the global LRs computed by STRmix™ v.2.7 with stutters, for mixtures with three estimated contributors with drop-in=0. The "-" represent the null LRs values and for that reason it was not possible to calculate a Log_{10} value.

Mixture (Reference)	Log_{10}(LR)
245.17-2.1 (MABS)	-
245.17-2.1 (OCF)	27.2298097829525
428.17-10 (LHIF)	30.489453690087
1305-17-3 (PBS1)	20.3560832491473
1305-17-3 (RDS1)	23.9635517335741
1533.17-4 (EIJB1)	16.0668475109739
2193.16-3 (MNTB)	15.4648024128913
2193.16-3 (MHMB)	6.97027247251535
2793.17-1R3 (FJCM1)	17.8215135284048
3053.17-5R2 (MHR2)	20.4180525782375
3053.17-5R2 (CDS1)	17.9302509517388
3357.17-12.2 (9)	19.0752549005329
3665.17-26 (SL2)	7.84229713432807
3675.17-1 (AJRG1)	11.8684857361807
3675.17-1 (ORG1)	21.0348289156558
3841.17-7 (3)	14.6666022105401
3958.17-1R2FF (LGS1)	20.3638375288361
4406.17-6 (CVG)	18.3105233839515
4406.17-6 (NGP)	26.4639079129385
4548.16-PC9.9 (PC9.8)	23.1851737123573
4702.17-1 (CSP1)	23.8851745690176
4980.17-11 (JAMR1)	25.1362765356603
5008.17-1R1 (1R2)	19.9104002639112
5008.17-1R1 (2R1)	26.675274120888
5008.17-3CABO (3LAM)	29.963324962741
5008.17-3CABO (4R2)	27.5811301057189
5374.16-9 (BMEB1)	13.9157479755368
5396.16-1CABO (JJCC)	26.9106937584209
6561.17-2BIO (FMGV1)	26.5773998759334
6561.17-2BIO (JAPG1)	24.8243146165676
6568.17-9 (DFSDN1)	11.5154631883733
6568.17-9 (RFAS2)	-4.71780854372444
6978.17-4R2 (7FF)	24.2162187008371
6978.17-4R2 (JAB1)	23.1995083488968
7245.17-1R1 (1R2)	29.8385531661624
7582.17-1 (FMBSC)	9.3700131875541
8356.16-8.2FF (DPMF)	8.84998418209427
8356.16-8.2FF (HVF)	25.3644571851188
8371.16-1R1 (JARR1)	27.1191568746903
8393.17-2FF (JPB2)	25.7923566643374
8393.17-2FF (TFB2)	28.0657290594623
8410.16-2R1 (2R2)	7.84636804368367
10175.16-4 (5)	12.7061457411211
10278.16-2 (1)	5.19203750271325
10814.16-2 (CMSA)	-5.9661341326521
10814.16-2 (FMRG)	11.710802552446
11021.17-20LAM (MABSC1)	12.1410733262675
11021.17-20LAM (MGSF1)	16.2088711382469
11021.17-20LAM (MSSF1)	20.4586680597649
12179.17-14R6 (GCG1)	11.447654084488
12179.17-14R6 (MAM1)	10.5848737534598
12946.17-3.1 (2)	22.2058807298875
13020.17-1LAM (1CABO)	13.3380578754198
13046.17-1R1 (2R1)	18.2010965650395
13253.17-4 (3)	24.5009496472545
13367.17-5 (SMCP1)	15.3596495872799
14005.17-1R1FF (1R2FM)	22.7215385809253
14005.17-1R1FF (2R1FF)	25.192651070668
14281.17-6R1 (6R2)	11.927796235039
14281.17-6R1 (MGGS1)	11.2253609803727
14503.17-1 (MRER1)	10.3898214629105
14828.17-2FF (1FF)	23.879113090301
14828.17-2FF (FLEP1)	19.4961821292573
14942.17-2LAM (3R1)	11.7133561178102
14942.17-2LAM (NMLC1)	17.3508099109364
15014.17-1 (2)	25.5340515026517
16839.17-1.9 (BZ1)	1.35926616460675
16839.17-1.9 (JW1)	4.02636981157372
16839.17-1.9 (QJ1)	5.84257803917362
18094.16-2 (IMSS)	24.6443499488957
18094.16-2 (CCM)	27.7375424826637
18690.17-2R1 (1R1)	17.3443922736851
18690.17-2R1 (CFB2)	16.2592354021987
19364.16-4M1 (MPPA1)	27.1984371353256
19364.16-4M1 (HJDC)	24.5455174076015
20008.17-1 (RMRO1)	6.93841964579319
20880.15-2R2 (1)	23.5574350139981
23308.16-6CABO (AFM)	19.8223054098232
23308.16-6CABO (MARCC)	15.160318437984

Table B25: Log_{10} values of the global LRs computed by EuroForMix v.1.9.3 without stutters[1], for mixtures with two estimated contributors with drop-in=0.10.

Mixture (Reference)	Log_{10} (LR)
243.17-1FM (JRA)	17.5281104540128
243.17-1FM (MM)	22.0745331445602
913.17-1.3 (ASML1)	14.0567587088656
913.17-1.3 (PMRP1)	18.6680603707635
1087.17-4 (PMCC1)	20.4231530229416
1182.17-2L2FM (MD1)	26.3418064089216
1383.17-1CABO (AMAD1)	25.4054932588082
1383.17-1CABO (AMBC1)	15.7350376934665
1793.17-2 (1)	16.7329855441534
1793.17-2 (3)	34.2559635821639
1799.17-1 (2)	16.5093471835403
1816.17-2FF (EVM1)	28.1618716402713
1816.17-2FF (SC1)	23.5833579175155
1843.17-1FIXACAO (FN1)	8.56293832599103
1847.17-3R2 (JC1)	17.6149266429607
1847.17-3R2 (MC1)	20.6584208357291
2572.17-4CABO (IOSS)	18.593738607965
2572.17-4CABO (LMVG1)	18.580408651762
2799.17-2FM (1FF)	25.4161014015559
2921.17-2 (JAVC2)	16.7516592740055
2921.17-2 (TFTS1)	22.9386677409409
3053.17-3.1R2 (EAD1)	16.2079486845375
3053.17-3.1R2 (MMM1)	17.1686203270444
3732.17-2.1FM (ASSC1)	20.1812952051712
3732.17-2.1FM (IST1)	22.1311311413194
3929.16-1 (2)	26.1925655660681
5258.17-5 (1)	28.6344303412099
5700.16-5 (AGT)	22.1080134432871
5700.16-5 (TMAS)	28.5503784967766
5707.17-6R1 (MAGDC1)	23.7713224134557
5709.17-6R2 (CMDF1)	15.665605670552
5709.17-6R2 (MJLF1)	16.578210284904
5773.17-4 (5FM)	19.6935429143138
5773.17-4 (17FDC1)	26.3917031860498
6010.17-1 (AAM1)	16.3293416269065
6472.17-1FM (PSBM2)	24.155538314396
7241.17-11R2FF (ASJ1)	21.0079528977641
7241.17-11R2FF (MCPSJ1)	19.0018556344345
7385.16-3 (2)	8.23727703955506
7588.17-1R1FF (3)	25.5644390680055
9233.16-9.1 (LCGS1)	12.1694557584518
9233.16-9.1 (VMTJ2)	20.0099879903935
10223.17-3LAM (IM2)	14.2563911024993
10223.17-3LAM (VMPM1)	20.1963367176565
12818.17-7 (1)	22.1356877192713
13017.17-25.2 (AJAN1)	26.5689190678
13017.17-25.2 (MJCR1)	28.6791579130504
13027.17-1R2FF (1R1FF)	16.2617553186872
13027.17-1R2FF (1R1FM)	25.9605564187752
13034.16-2CABO (2LAM)	21.6598899962642
13252.17-8 (FTMR1)	18.7679182977548
13252.17-8 (LIOR1)	15.6754645546252
13740.17-1R1FF (1R2FF)	14.6743921883035
13940.17-2 (DMC1)	16.575556760344
13940.17-2 (NMFM1)	14.0813232263226
14002.16-1 (MPNG1)	11.5525427828554
14552.16-1FM (LMRR1)	15.5218558700953
14552.16-1FM (1FF)	29.6764533324753
15150.17-1 (DASS1)	17.0721013058596
15150.17-1 (RJABO2)	22.4266496813986
16126.17-3.3 (1)	29.6156790222629
16537.17-1 (AJMC1)	27.4347659828724
16537.17-1 (ASLS1)	28.3585360394092
16672.17-4R2 (4R1)	27.9052465264041
16672.17-4R2 (AMC1)	20.8206012220341
16913.17-3 (NMSAOM1)	19.6803615843396
17065.17-1 (3)	27.9811672094055
17065.17-1 (SSC1)	23.2194069003935
17222.17-3R2FF (3R1)	19.9552025515314
17222.17-3R2FF (PM1)	24.4846244936777
18119.17-2 (LZ1)	16.4654686399900
19187.16-4CABO (RGCF)	10.2905831372947
19724.16-6 (ENP1)	24.5299490395586
19724.16-6 (13)	19.0282402520187
19724.16-8 (BMAP)	23.0037064746231
19799.17-1 (TFPA1)	7.79974950049863
20601.16-1 (HMNM1)	14.4243171262311
20601.16-1 (AMM)	15.7491075905695
20628.16-1CABO (AMP)	26.6662943858857

[1] Computed by Figueiredo C: Forensic DNA mixtures: Analysis and comparison of software results. Faculdade de Ciências da Universidade do Porto; 2018.

Table B26: Log_{10} values of the global LRs computed by STRmix™ v.2.7 with stutters, for mixtures with two estimated contributors with drop-in=0.10.

Mixture (Reference)	Log_{10} (LR)
243.17-1FM (JRA)	17.9767900122898
243.17-1FM (MM)	21.1670809196733
913.17-1.3 (ASML1)	14.6450093951416
913.17-1.3 (PMRP1)	16.6845401715365
1087.17-4 (PMCC1)	23.110353982664
1182.17-2L2FM (MD1)	26.5079233034919
1383.17-1CABO (AMAD1)	26.4599801970317
1383.17-1CABO (AMBC1)	19.7565904707011
1793.17-2 (1)	20.3673186409297
1793.17-2 (3)	33.0980550396692
1799.17-1 (2)	25.3320342770275
1816.17-2FF (EVM1)	28.9802216008829
1816.17-2FF (SC1)	25.6033176226402
1843.17-1FIXACAO (FN1)	9.28724171117835
1847.17-3R2 (JC1)	21.0540382106849
1847.17-3R2 (MC1)	21.8577304173538
2572.17-4CABO (IOSS)	24.0053092368485
2572.17-4CABO (LMVG1)	23.6422765161117
2799.17-2FM (1FF)	26.6775430811884
2921.17-2 (JAVC2)	23.0483252509312
2921.17-2 (TFTS1)	29.1453828919749
3053.17-3.1R2 (EAD1)	16.6826413871962
3053.17-3.1R2 (MMM1)	17.4980209275822
3732.17-2.1FM (ASSC1)	19.9685903414369
3732.17-2.1FM (IST1)	20.4834731816212
3929.16-1 (2)	26.2763009245708
5258.17-5 (1)	30.2416460780014
5700.16-5 (AGT)	26.0792536224301
5700.16-5 (TMAS)	30.3883499078704
5707.17-6R1 (MAGDC1)	26.6005046066455
5709.17-6R2 (CMDF1)	17.2867707367141
5709.17-6R2 (MJLF1)	17.6475785542125
5773.17-4 (5FM)	18.9044937442691
5773.17-4 (17FDC1)	26.9027315461672
6010.17-1 (AAM1)	22.1939867630857
6472.17-1FM (PSBM2)	27.0000868502116
7241.17-11R2FF (ASJ1)	23.431588895528
7241.17-11R2FF (MCPSJ1)	22.4859910027707
7385.16-3 (2)	1.06099985321829
7588.17-1R1FF (3)	27.1351008337657
9233.16-9.1 (LCGS1)	21.8058269662885
9233.16-9.1 (VMTJ2)	26.6612256602701
10223.17-3LAM (IM2)	13.8098155027099
10223.17-3LAM (VMPM1)	19.1725445543724
12818.17-7 (1)	18.2300911197487
13017.17-25.2 (AJAN1)	28.5307118379817
13017.17-25.2 (MJCR1)	29.4523385438460
13027.17-1R2FF (1R1FF)	8.20115122765526
13027.17-1R2FF (1R1FM)	23.6277037373379
13034.16-2CABO (2LAM)	27.6982310754491
13252.17-8 (FTMR1)	22.1655707406329
13252.17-8 (LIOR1)	20.1997003386295
13740.17-1R1FF (1R2FF)	19.6111389003956
13940.17-2 (DMC1)	17.5368613330745
13940.17-2 (NMFM1)	16.376978220308
14002.16-1 (MPNG1)	20.9292247271218
14552.16-1FM (LMRR1)	13.4803950460168
14552.16-1FM (1FF)	30.4940571452217
15150.17-1 (DASS1)	23.0692609862847
15150.17-1 (RJABO2)	25.9656061640404
16126.17-3.3 (1)	30.0417478717233
16537.17-1 (AJMC1)	27.5589004814872
16537.17-1 (ASLS1)	28.4187320568733
16672.17-4R2 (4R1)	26.0509980791734
16672.17-4R2 (AMC1)	20.9599900763014
16913.17-3 (NMSAOM1)	20.4085621736929
17065.17-1 (3)	28.3839230289522
17065.17-1 (SSC1)	24.6558104944953
17222.17-3R2FF (3R1)	23.6683299953454
17222.17-3R2FF (PM1)	24.9003671286565
18119.17-2 (LZ1)	15.7299661982037
19187.16-4CABO (RGCF)	11.8546824696375
19724.16-6 (ENP1)	26.5612326066603
19724.16-6 (13)	23.9801715996865
19724.16-8 (BMAP)	26.2054479770517
19799.17-1 (TFPA1)	14.5404796371212
20601.16-1 (HMNM1)	6.361690069638
20601.16-1 (AMM)	21.7758797508436
20628.16-1CABO (AMP)	26.0204524417688

Table B27: Log_{10} values of the global LRs computed by EuroForMix v.1.9.3 without stutters[1], for mixtures with three estimated contributors with drop-in=0.10.

Mixture (Reference)	Log_{10}(LR)
245.17-2.1 (MABS)	22.3698708507426
245.17-2.1 (OCF)	29.5320492696476
428.17-10 (LHIF)	25.2039717561838
1305-17-3 (PBS1)	10.3462332469259
1305-17-3 (RDS1)	16.7714175272377
1533.17-4 (EIJB1)	17.4304236778874
2193.16-3 (MNTB)	12.6985500381046
2193.16-3 (MHMB)	5.72249427759447
2793.17-1R3 (FJCM1)	16.7077072334432
3053.17-5R2 (MHR2)	20.1527029629946
3053.17-5R2 (CDS1)	16.2750066017817
3357.17-12.2 (9)	13.1830299979257
3665.17-26 (SL2)	11.2275221421051
3675.17-1 (AJRG1)	12.5197052506691
3675.17-1 (ORG1)	20.0433296853715
3841.17-7 (3)	7.32297562175103
3958.17-1R2FF (LGS1)	12.0958133694962
4406.17-6 (CVG)	16.9606993468799
4406.17-6 (NGP)	27.3303474054781
4548.16-PC9.9 (PC9.8)	24.7893204637684
4702.17-1 (CSP1)	23.67499168451
4980.17-11 (JAMR1)	22.0293369669224
5008.17-1R1 (1R2)	14.5024624888222
5008.17-1R1 (2R1)	25.9687300903085
5008.17-3CABO (3LAM)	26.6924011124071
5008.17-3CABO (4R2)	19.2882528262011
5374.16-9 (BMEB1)	11.3043878745063
5396.16-1CABO (JJCC)	18.7552718939223
6561.17-2BIO (FMGV1)	23.8206694729148
6561.17-2BIO (JAPG1)	21.572647226019
6568.17-9 (DFSDN1)	12.147695801655
6568.17-9 (RFAS2)	15.2108184483453
6978.17-4R2 (7FF)	22.6413853461963
6978.17-4R2 (JAB1)	24.5006254301133
7245.17-1R1 (1R2)	24.8896223781465
7582.17-1 (FMBSC)	9.09411482852175
8356.16-8.2FF (DPMF)	6.24939306764942
8356.16-8.2FF (HVF)	23.6913512409306
8371.16-1R1 (JARR1)	23.4422382321638
8393.17-2FF (JPB2)	26.4760626088583
8393.17-2FF (TFB2)	25.0188328371321
8410.16-2R1 (2R2)	10.5906788627885
10175.16-4 (5)	9.58709518115208
10278.16-2 (1)	6.3953144566958
10814.16-2 (CMSA)	22.4039288864386
10814.16-2 (FMRG)	10.4070714078591
11021.17-20LAM (MABSC1)	10.7077837224279
11021.17-20LAM (MGSF1)	10.9018864045509
11021.17-20LAM (MSSF1)	13.9186630824799
12179.17-14R6 (GCG1)	12.2572463751294
12179.17-14R6 (MAM1)	11.9692279593833
12946.17-3.1 (2)	18.8464801348672
13020.17-1LAM (1CABO)	7.94539397912868
13046.17-1R1 (2R1)	18.7444582839422
13253.17-4 (3)	13.2363700462507
13367.17-5 (SMCP1)	7.2396307948417
14005.17-1R1FF (1R2FM)	14.284657509073
14005.17-1R1FF (2R1FF)	22.7466811356351
14281.17-6R1 (6R2)	10.3227020747207
14281.17-6R1 (MGGS1)	9.52788341287911
14503.17-1 (MRER1)	14.6200516794913
14828.17-2FF (1FF)	23.1224814884274
14828.17-2FF (FLEP1)	17.7402399108734
14942.17-2LAM (3R1)	14.2169730880181
14942.17-2LAM (NMLC1)	20.411853424775
15014.17-1 (2)	24.5698868706224
16839.17-1.9 (BZ1)	11.0395074980971
16839.17-1.9 (JW1)	12.2156703651776
16839.17-1.9 (QJ1)	10.763552839785
18094.16-2 (IMSS)	23.3143866772915
18094.16-2 (CCM)	27.1385688755908
18690.17-2R1 (1R1)	15.9376036105069
18690.17-2R1 (CFB2)	17.6976972298461
19364.16-4M1 (MPPA1)	22.4730799540847
19364.16-4M1 (HJDC)	19.4815428806243
20008.17-1 (RMRO1)	7.34996759000941
20880.15-2R2 (1)	17.7970834871966
23308.16-6CABO (AFM)	18.7764157057559
23308.16-6CABO (MARCC)	12.3324734563863

[1] Computed by Figueiredo C: Forensic DNA mixtures: Analysis and comparison of software results. Faculdade de Ciências da Universidade do Porto; 2018.

Table B28: Log_{10} values of the global LRs computed by STRmix™ v.2.7 with stutters, for mixtures with three estimated contributors with drop-in=0.10. The "-" represent the null LRs values and for that reason it was not possible to calculate a Log_{10} value.

Mixture (Reference)	Log_{10}(LR)
245.17-2.1 (MABS)	28.2605960423019
245.17-2.1 (OCF)	27.2255418771872
428.17-10 (LHIF)	30.5716768627958
1305-17-3 (PBS1)	20.5163237938505
1305-17-3 (RDS1)	23.8711232313563
1533.17-4 (EIJB1)	15.9581862794642
2193.16-3 (MNTB)	15.2289903108407
2193.16-3 (MHMB)	7.00199317382353
2793.17-1R3 (FJCM1)	18.0569810366681
3053.17-5R2 (MHR2)	20.3372395625437
3053.17-5R2 (CDS1)	18.587486465411
3357.17-12.2 (9)	17.2224042910825
3665.17-26 (SL2)	7.63971552916208
3675.17-1 (AJRG1)	15.7331892374079
3675.17-1 (ORG1)	20.4411922252776
3841.17-7 (3)	14.6512586254188
3958.17-1R2FF (LGS1)	20.4894944219422
4406.17-6 (CVG)	18.263517716092
4406.17-6 (NGP)	26.4470339294748
4548.16-PC9.9 (PC9.8)	23.1014377351388
4702.17-1 (CSP1)	22.731072784454
4980.17-11 (JAMR1)	25.2427401446056
5008.17-1R1 (1R2)	19.0629202637327
5008.17-1R1 (2R1)	26.6501034442255
5008.17-3CABO (3LAM)	29.9844958089745
5008.17-3CABO (4R2)	27.638509224058
5374.16-9 (BMEB1)	13.6380897219845
5396.16-1CABO (JJCC)	26.835240193399
6561.17-2BIO (FMGV1)	27.2636834005572
6561.17-2BIO (JAPG1)	26.2393995931158
6568.17-9 (DFSDN1)	10.4855936740224
6568.17-9 (RFAS2)	-
6978.17-4R2 (7FF)	24.2816468578675
6978.17-4R2 (JAB1)	23.4310419453359
7245.17-1R1 (1R2)	29.8429959389206
7582.17-1 (FMBSC)	9.69538535050001
8356.16-8.2FF (DPMF)	8.90518041874631
8356.16-8.2FF (HVF)	25.342955351796
8371.16-1R1 (JARR1)	27.147614498562
8393.17-2FF (JPB2)	25.7723510499534
8393.17-2FF (TFB2)	27.9103628958323
8410.16-2R1 (2R2)	8.15035725799852
10175.16-4 (5)	12.5002639262009
10278.16-2 (1)	4.69474555426545
10814.16-2 (CMSA)	-7.14298127401419
10814.16-2 (FMRG)	10.7335583580496
11021.17-20LAM (MABSC1)	11.7688008387025
11021.17-20LAM (MGSF1)	15.9811705314684
11021.17-20LAM (MSSF1)	20.7507243313102
12179.17-14R6 (GCG1)	12.1687625756224
12179.17-14R6 (MAM1)	10.9562068619149
12946.17-3.1 (2)	21.7265805182017
13020.17-1LAM (1CABO)	13.0685198060009
13046.17-1R1 (2R1)	18.2027606873932
13253.17-4 (3)	24.5085162522669
13367.17-5 (SMCP1)	15.45039538856
14005.17-1R1FF (1R2FM)	22.8665767722718
14005.17-1R1FF (2R1FF)	23.6769678142948
14281.17-6R1 (6R2)	12.2771276712299
14281.17-6R1 (MGGS1)	11.445868746564
14503.17-1 (MRER1)	10.2377196319963
14828.17-2FF (1FF)	23.7549824929448
14828.17-2FF (FLEP1)	18.8815672389297
14942.17-2LAM (3R1)	10.5477008813547
14942.17-2LAM (NMLC1)	16.5167864913926
15014.17-1 (2)	25.5520351691576
16839.17-1.9 (BZ1)	1.61835147361624
16839.17-1.9 (JW1)	1.91372910372857
16839.17-1.9 (QJ1)	3.77310595612914
18094.16-2 (IMSS)	23.4699397747863
18094.16-2 (CCM)	27.7504158177774
18690.17-2R1 (1R1)	17.496459138121
18690.17-2R1 (CFB2)	17.3500502142005
19364.16-4M1 (MPPA1)	27.2287595554356
19364.16-4M1 (HJDC)	24.1644420852095
20008.17-1 (RMRO1)	6.78970759785856
20880.15-2R2 (1)	23.3928727454021
23308.16-6CABO (AFM)	20.4130146123342
23308.16-6CABO (MARCC)	15.4674008969525

Table B29: Log_{10} values of the global LRs computed by EuroForMix v.1.9.3 without stutters[1], for mixtures with two estimated contributors with F_{ST}=0.

Mixture (Reference)	Log_{10} (LR)
243.17-1FM (JRA)	20.3433241819293
243.17-1FM (MM)	25.9849873391053
913.17-1.3 (ASML1)	15.0132128190861
913.17-1.3 (PMRP1)	20.5254814463071
1087.17-4 (PMCC1)	21.1869195982034
1182.17-2L2FM (MD1)	27.569629881181
1383.17-1CABO (AMAD1)	26.3211669023398
1383.17-1CABO (AMBC1)	15.4234691836023
1793.17-2 (1)	17.2564413601559
1793.17-2 (3)	39.620566077284
1799.17-1 (2)	17.6769099351866
1816.17-2FF (EVM1)	29.4801886690164
1816.17-2FF (SC1)	25.8228802484304
1843.17-1FIXACAO (FN1)	9.39951548415361
1847.17-3R2 (JC1)	19.9068228506593
1847.17-3R2 (MC1)	23.866789076246
2572.17-4CABO (IOSS)	20.0958106192044
2572.17-4CABO (LMVG1)	19.960853207978
2799.17-2FM (1FF)	26.8115477460904
2921.17-2 (JAVC2)	17.6551152276905
2921.17-2 (TFTS1)	25.062273258486
3053.17-3.1R2 (EAD1)	15.4094542756268
3053.17-3.1R2 (MMM1)	18.4105787437575
3732.17-2.1FM (ASSC1)	23.9689803862638
3732.17-2.1FM (IST1)	27.9445914271863
3929.16-1 (2)	27.4317983004395
5258.17-5 (1)	32.4729580002972
5700.16-5 (AGT)	23.6677378478977
5700.16-5 (TMAS)	30.1848174383332
5707.17-6R1 (MAGDC1)	25.4085273701586
5709.17-6R2 (CMDF1)	16.8640366743317
5709.17-6R2 (MJLF1)	18.1115092979872
5773.17-4 (5FM)	20.799152058938
5773.17-4 (17FDC1)	27.6065298118165
6010.17-1 (AAM1)	17.2037861508964
6472.17-1FM (PSBM2)	25.2117676804851
7241.17-11R2FF (ASJ1)	22.7968654276176
7241.17-11R2FF (MCPSJ1)	20.7082578996951
7385.16-3 (2)	8.92483592611319
7588.17-1R1FF (3)	27.0749966715466
9233.16-9.1 (LCGS1)	13.2665817259819
9233.16-9.1 (VMTJ2)	21.1167892329666
10223.17-3LAM (IM2)	15.1720288208381
10223.17-3LAM (VMPM1)	22.7982576610498
12818.17-7 (1)	24.7653801038172
13017.17-25.2 (AJAN1)	28.6857082470835
13017.17-25.2 (MJCR1)	30.7370019963601
13027.17-1R2FF (1R1FF)	17.4443730878051
13027.17-1R2FF (1R1FM)	27.5101841183751
13034.16-2CABO (2LAM)	22.7672051500665
13252.17-8 (FTMR1)	20.6467599815378
13252.17-8 (LIOR1)	16.8528736648334
13740.17-1R1FF (1R2FF)	15.7090564391032
13940.17-2 (DMC1)	17.8845883387204
13940.17-2 (NMFM1)	16.2497027596903
14002.16-1 (MPNG1)	12.2691499676369
14552.16-1FM (LMRR1)	16.6049586461177
14552.16-1FM (1FF)	31.8499101667162
15150.17-1 (DASS1)	19.8258823441136
15150.17-1 (RJABO2)	24.2919911934343
16126.17-3.3 (1)	31.3970522378978
16537.17-1 (AJMC1)	30.1663825738338
16537.17-1 (ASLS1)	31.1988818021809
16672.17-4R2 (4R1)	30.3034938087511
16672.17-4R2 (AMC1)	22.665506196564
16913.17-3 (NMSAOM1)	20.8914276895881
17065.17-1 (3)	29.2307852813879
17065.17-1 (SSC1)	24.0705281846925
17222.17-3R2FF (3R1)	21.6852873655813
17222.17-3R2FF (PM1)	26.6073281865809
18119.17-2 (LZ1)	17.1168122307708
19187.16-4CABO (RGCF)	11.198739273886
19724.16-6 (ENP1)	26.5903698376527
19724.16-6 (13)	19.9644541753243
19724.16-8 (BMAP)	24.1803522374129
19799.17-1 (TFPA1)	8.45336656249504
20601.16-1 (HMNM1)	15.7826685266352
20601.16-1 (AMM)	17.4551356667036
20628.16-1CABO (AMP)	27.7533992589309

[1] Computed by Figueiredo C: Forensic DNA mixtures: Analysis and comparison of software results. Faculdade de Ciências da Universidade do Porto; 2018.

Table B30: Log_{10} values of the global LRs computed by STRmix™ v.2.7 with stutters, for mixtures with two estimated contributors with F_{ST}=0. The "-" represent the null LRs values and for that reason it was not possible to calculate a Log_{10} value.

Mixture (Reference)	Log_{10} (LR)
243.17-1FM (JRA)	20.1801258751641
243.17-1FM (MM)	24.1406651399767
913.17-1.3 (ASML1)	16.3310221710418
913.17-1.3 (PMRP1)	17.3278899816485
1087.17-4 (PMCC1)	23.7683642688411
1182.17-2L2FM (MD1)	27.6461978041808
1383.17-1CABO (AMAD1)	27.4590455167946
1383.17-1CABO (AMBC1)	20.7069822033747
1793.17-2 (1)	21.6384093793598
1793.17-2 (3)	38.9684502584917
1799.17-1 (2)	26.4798055677094
1816.17-2FF (EVM1)	30.3892547068487
1816.17-2FF (SC1)	27.0197807304036
1843.17-1FIXACAO (FN1)	10.625559372876
1847.17-3R2 (JC1)	23.5105450102066
1847.17-3R2 (MC1)	23.642642554376
2572.17-4CABO (IOSS)	25.3354177792535
2572.17-4CABO (LMVG1)	24.780259690476
2799.17-2FM (1FF)	28.117304446641
2921.17-2 (JAVC2)	25.1110944105093
2921.17-2 (TFTS1)	31.6553401619386
3053.17-3.1R2 (EAD1)	18.6691122396704
3053.17-3.1R2 (MMM1)	19.2429387700296
3732.17-2.1FM (ASSC1)	24.5375672571527
3732.17-2.1FM (IST1)	27.0965972083579
3929.16-1 (2)	27.277494609611
5258.17-5 (1)	32.7170710626284
5700.16-5 (AGT)	28.0019067040409
5700.16-5 (TMAS)	31.9678333561786
5707.17-6R1 (MAGDC1)	28.3213912783117
5709.17-6R2 (CMDF1)	18.7401257369657
5709.17-6R2 (MJLF1)	19.2215446370272
5773.17-4 (5FM)	20.6764741211691
5773.17-4 (17FDC1)	28.2235997646497
6010.17-1 (AAM1)	23.4133668314093
6472.17-1FM (PSBM2)	28.1260339480518
7241.17-11R2FF (ASJ1)	25.4015556182629
7241.17-11R2FF (MCPSJ1)	23.9561780386541
7385.16-3 (2)	2.63004121137135
7588.17-1R1FF (3)	28.9011748749285
9233.16-9.1 (LCGS1)	23.2507614479797
9233.16-9.1 (VMTJ2)	28.1483866876668
10223.17-3LAM (IM2)	15.0776585490841
10223.17-3LAM (VMPM1)	20.7945507812986
12818.17-7 (1)	17.1231326643109
13017.17-25.2 (AJAN1)	30.9023347440221
13017.17-25.2 (MJCR1)	30.922003628674
13027.17-1R2FF (1R1FF)	-
13027.17-1R2FF (1R1FM)	24.3324990549182
13034.16-2CABO (2LAM)	28.7086503101983
13252.17-8 (FTMR1)	24.4261207087466
13252.17-8 (LIOR1)	21.7607465753609
13740.17-1R1FF (1R2FF)	20.9096041626616
13940.17-2 (DMC1)	18.8217951062246
13940.17-2 (NMFM1)	18.6543690909753
14002.16-1 (MPNG1)	22.0762762554042
14552.16-1FM (LMRR1)	14.1863629403947
14552.16-1FM (1FF)	33.0896225515843
15150.17-1 (DASS1)	25.1465621131576
15150.17-1 (RJABO2)	28.0751087964165
16126.17-3.3 (1)	31.642642554376
16537.17-1 (AJMC1)	29.8755242639493
16537.17-1 (ASLS1)	30.5020035446566
16672.17-4R2 (4R1)	27.8721562727483
16672.17-4R2 (AMC1)	22.7062226263013
16913.17-3 (NMSAOM1)	21.7829596780942
17065.17-1 (3)	29.7318545784044
17065.17-1 (SSC1)	25.897429139838
17222.17-3R2FF (3R1)	26.9345438982881
17222.17-3R2FF (PM1)	26.1582418379809
18119.17-2 (LZ1)	15.7579802628339
19187.16-4CABO (RGCF)	12.3889178451569
19724.16-6 (ENP1)	27.573138599605
19724.16-6 (13)	24.8726456712128
19724.16-8 (BMAP)	27.7648408937424
19799.17-1 (TFPA1)	15.8007857903278
20601.16-1 (HMNM1)	-
20601.16-1 (AMM)	23.7866804531966
20628.16-1CABO (AMP)	26.995941286249

Table B31: Log_{10} values of the global LRs computed by EuroForMix v.1.9.3 without stutters[1], for mixtures with three estimated contributors with F_{ST}=0.

Mixture (Reference)	Log_{10}(LR)
245.17-2.1 (MABS)	23.9694579808526
245.17-2.1 (OCF)	31.9406486494309
428.17-10 (LHIF)	29.1410668614927
1305-17-3 (PBS1)	12.4154631040211
1305-17-3 (RDS1)	17.9217280436288
1533.17-4 (EIJB1)	19.2277910513451
2193.16-3 (MNTB)	13.9601584593493
2193.16-3 (MHMB)	6.3249104731975
2793.17-1R3 (FJCM1)	18.4299924652993
3053.17-5R2 (MHR2)	21.8837390657432
3053.17-5R2 (CDS1)	17.6279443375506
3357.17-12.2 (9)	14.5604543614473
3665.17-26 (SL2)	12.9745019660312
3675.17-1 (AJRG1)	13.2005668766514
3675.17-1 (ORG1)	20.711466826892
3841.17-7 (3)	7.99062840288268
3958.17-1R2FF (LGS1)	13.5753999328471
4406.17-6 (CVG)	17.4396585049923
4406.17-6 (NGP)	29.4156688137829
4548.16-PC9.9 (PC9.8)	27.5294924033180
4702.17-1 (CSP1)	24.4487764999717
4980.17-11 (JAMR1)	23.9616915390826
5008.17-1R1 (1R2)	16.0819401193476
5008.17-1R1 (2R1)	27.1836165964101
5008.17-3CABO (3LAM)	29.8663866866837
5008.17-3CABO (4R2)	21.5617431098299
5374.16-9 (BMEB1)	12.0939824900787
5396.16-1CABO (JJCC)	20.1371953283658
6561.17-2BIO (FMGV1)	24.9158658555855
6561.17-2BIO (JAPG1)	22.6086975781026
6568.17-9 (DFSDN1)	13.1319958150016
6568.17-9 (RFAS2)	16.4101324664474
6978.17-4R2 (7FF)	23.6948761941669
6978.17-4R2 (JAB1)	26.632587303076
7245.17-1R1 (1R2)	27.0523475276996
7582.17-1 (FMBSC)	10.930430945974
8356.16-8.2FF (DPMF)	6.94796249151406
8356.16-8.2FF (HVF)	25.7381931796771
8371.16-1R1 (JARR1)	24.9847642381139
8393.17-2FF (JPB2)	28.8853239447066
8393.17-2FF (TFB2)	27.5967918381771
8410.16-2R1 (2R2)	11.9165354121822
10175.16-4 (5)	10.4428782532844
10278.16-2 (1)	7.05393982143616
10814.16-2 (CMSA)	24.0134289563887
10814.16-2 (FMRG)	11.092412582952
11021.17-20LAM (MABSC1)	12.0437063103234
11021.17-20LAM (MGSF1)	12.1028793661966
11021.17-20LAM (MSSF1)	16.2802577441369
12179.17-14R6 (GCG1)	13.2211945477801
12179.17-14R6 (MAM1)	13.4253797108382
12946.17-3.1 (2)	20.1869107830963
13020.17-1LAM (1CABO)	8.55878291851669
13046.17-1R1 (2R1)	20.5437491886073
13253.17-4 (3)	14.1365834705601
13367.17-5 (SMCP1)	7.42590554294029
14005.17-1R1FF (1R2FM)	15.4254922109792
14005.17-1R1FF (2R1FF)	23.7332142472121
14281.17-6R1 (6R2)	11.5812777924233
14281.17-6R1 (MGGS1)	10.2566870315856
14503.17-1 (MRER1)	15.8750319121246
14828.17-2FF (1FF)	24.6374554096918
14828.17-2FF (FLEP1)	19.7195972111505
14942.17-2LAM (3R1)	15.7974052915111
14942.17-2LAM (NMLC1)	24.2943635325701
15014.17-1 (2)	26.0923510556966
16839.17-1.9 (BZ1)	12.3091853698949
16839.17-1.9 (JW1)	14.1637415648377
16839.17-1.9 (QJ1)	11.8818670385455
18094.16-2 (IMSS)	24.2595402149578
18094.16-2 (CCM)	28.4259254505001
18690.17-2R1 (1R1)	17.1616648617795
18690.17-2R1 (CFB2)	19.2848406436482
19364.16-4M1 (MPPA1)	24.4427613484511
19364.16-4M1 (HJDC)	20.8785097963301
20008.17-1 (RMRO1)	8.95391975867455
20880.15-2R2 (1)	18.4971214307324
23308.16-6CABO (AFM)	20.0525100008918
23308.16-6CABO (MARCC)	13.5484121693056

[1] Computed by Figueiredo C: Forensic DNA mixtures: Analysis and comparison of software results. Faculdade de Ciências da Universidade do Porto; 2018.

Table B32: Log_{10} values of the global LRs computed by STRmix™ v.2.7 with stutters, for mixtures with three estimated contributors with F_{ST}=0.

Mixture (Reference)	Log_{10}(LR)
245.17-2.1 (MABS)	30.0539231505486
245.17-2.1 (OCF)	28.1967011124334
428.17-10 (LHIF)	32.5723910736011
1305-17-3 (PBS1)	23.9334518544525
1305-17-3 (RDS1)	25.2198463860244
1533.17-4 (EIJB1)	17.725878977347
2193.16-3 (MNTB)	17.070370390367
2193.16-3 (MHMB)	7.76002268821941
2793.17-1R3 (FJCM1)	19.413819265173
3053.17-5R2 (MHR2)	22.7593429464478
3053.17-5R2 (CDS1)	19.5144016351376
3357.17-12.2 (9)	17.2108266386783
3665.17-26 (SL2)	8.89401128489268
3675.17-1 (AJRG1)	16.0021660617565
3675.17-1 (ORG1)	21.5584205450013
3841.17-7 (3)	15.6897172058652
3958.17-1R2FF (LGS1)	22.1034958441098
4406.17-6 (CVG)	19.3256593098016
4406.17-6 (NGP)	27.9442111532405
4548.16-PC9.9 (PC9.8)	24.0984014222701
4702.17-1 (CSP1)	23.417654340806
4980.17-11 (JAMR1)	26.9103468799571
5008.17-1R1 (1R2)	21.3127484209296
5008.17-1R1 (2R1)	27.745629022467
5008.17-3CABO (3LAM)	31.7813891207787
5008.17-3CABO (4R2)	29.4633254984367
5374.16-9 (BMEB1)	14.979047326948
5396.16-1CABO (JJCC)	28.8670194090185
6561.17-2BIO (FMGV1)	28.4411764999411
6561.17-2BIO (JAPG1)	27.5014974456141
6568.17-9 (DFSDN1)	12.5438570500706
6568.17-9 (RFAS2)	-3.70838698306012
6978.17-4R2 (7FF)	25.5757649805367
6978.17-4R2 (JAB1)	24.9932113091314
7245.17-1R1 (1R2)	31.7160785034834
7582.17-1 (FMBSC)	13.3943465968683
8356.16-8.2FF (DPMF)	9.74085986938845
8356.16-8.2FF (HVF)	27.0266966559782
8371.16-1R1 (JARR1)	28.8223511769931
8393.17-2FF (JPB2)	27.2847464695777
8393.17-2FF (TFB2)	29.7957410208692
8410.16-2R1 (2R2)	8.13874466394889
10175.16-4 (5)	13.8161153031645
10278.16-2 (1)	6.40072789773712
10814.16-2 (CMSA)	-6.76853040956932
10814.16-2 (FMRG)	11.3461377301604
11021.17-20LAM (MABSC1)	13.4838439469213
11021.17-20LAM (MGSF1)	17.0034174452022
11021.17-20LAM (MSSF1)	23.5794634722014
12179.17-14R6 (GCG1)	13.0240749873074
12179.17-14R6 (MAM1)	12.9120785083192
12946.17-3.1 (2)	23.1784301399477
13020.17-1LAM (1CABO)	13.6894686927077
13046.17-1R1 (2R1)	20.0056523153551
13253.17-4 (3)	26.1503265364987
13367.17-5 (SMCP1)	15.7635702391474
14005.17-1R1FF (1R2FM)	25.0516540841133
14005.17-1R1FF (2R1FF)	26.8153186881259
14281.17-6R1 (6R2)	14.2846111823698
14281.17-6R1 (MGGS1)	12.4299621113954
14503.17-1 (MRER1)	10.7494502979937
14828.17-2FF (1FF)	25.5680021375046
14828.17-2FF (FLEP1)	21.9002797146811
14942.17-2LAM (3R1)	10.4918937287927
14942.17-2LAM (NMLC1)	16.7800651608974
15014.17-1 (2)	26.8718180326115
16839.17-1.9 (BZ1)	2.76599620055494
16839.17-1.9 (JW1)	5.1773344555057
16839.17-1.9 (QJ1)	3.82763416359034
18094.16-2 (IMSS)	25.5365836915167
18094.16-2 (CCM)	28.9817416138375
18690.17-2R1 (1R1)	18.687493288745
18690.17-2R1 (CFB2)	17.6854998990941
19364.16-4M1 (MPPA1)	28.8922504752983
19364.16-4M1 (HJDC)	25.5722208343653
20008.17-1 (RMRO1)	8.4165739436962
20880.15-2R2 (1)	24.8340899289481
23308.16-6CABO (AFM)	21.5658950220301
23308.16-6CABO (MARCC)	17.1999196515906

Table B33: Log_{10} values of the global LRs computed by EuroForMix v.1.9.3 without stutters[1], for mixtures with two estimated contributors with F_{ST}=0.015.

Mixture (Reference)	Log_{10} (LR)
243.17-1FM (JRA)	16.6799674861257
243.17-1FM (MM)	20.9901782381082
913.17-1.3 (ASML1)	13.450155523163
913.17-1.3 (PMRP1)	18.1536345714969
1087.17-4 (PMCC1)	19.9469685599633
1182.17-2L2FM (MD1)	25.8285963519747
1383.17-1CABO (AMAD1)	25.0345168302783
1383.17-1CABO (AMBC1)	14.495062050572
1793.17-2 (1)	16.0952276779
1793.17-2 (3)	33.0060415666093
1799.17-1 (2)	16.0427155358882
1816.17-2FF (EVM1)	27.6352904641125
1816.17-2FF (SC1)	22.6580092369053
1843.17-1FIXACAO (FN1)	7.84534235593516
1847.17-3R2 (JC1)	16.9123723695636
1847.17-3R2 (MC1)	19.6914327281667
2572.17-4CABO (IOSS)	18.0048772259975
2572.17-4CABO (LMVG1)	17.9954597666249
2799.17-2FM (1FF)	24.7839591367364
2921.17-2 (JAVC2)	16.4244767830072
2921.17-2 (TFTS1)	22.1673226426381
3053.17-3.1R2 (EAD1)	13.1199007455496
3053.17-3.1R2 (MMM1)	16.3307830186246
3732.17-2.1FM (ASSC1)	19.1699135061133
3732.17-2.1FM (IST1)	20.7419460744105
3929.16-1 (2)	25.7123866365834
5258.17-5 (1)	27.5223668123522
5700.16-5 (AGT)	21.3526255530379
5700.16-5 (TMAS)	27.8678795620526
5707.17-6R1 (MAGDC1)	23.0426954466951
5709.17-6R2 (CMDF1)	15.1619495913711
5709.17-6R2 (MJLF1)	15.9503881892942
5773.17-4 (5FM)	19.0657335848668
5773.17-4 (17FDC1)	25.869030161823
6010.17-1 (AAM1)	15.6758876328994
6472.17-1FM (PSBM2)	23.7092962880747
7241.17-11R2FF (ASJ1)	20.2894701967355
7241.17-11R2FF (MCPSJ1)	18.3151543975157
7385.16-3 (2)	7.81158074228095
7588.17-1R1FF (3)	24.9120288367475
9233.16-9.1 (LCGS1)	11.7288955596138
9233.16-9.1 (VMTJ2)	19.0856903386427
10223.17-3LAM (IM2)	13.8554183454446
10223.17-3LAM (VMPM1)	19.3550862783939
12818.17-7 (1)	20.9363533961741
13017.17-25.2 (AJAN1)	25.9536484099928
13017.17-25.2 (MJCR1)	28.0326044313431
13027.17-1R2FF (1R1FF)	15.8550861407943
13027.17-1R2FF (1R1FM)	25.3529441589635
13034.16-2CABO (2LAM)	21.1771229256506
13252.17-8 (FTMR1)	18.1048726740127
13252.17-8 (LIOR1)	15.1640710881024
13740.17-1R1FF (1R2FF)	14.232718960326
13940.17-2 (DMC1)	16.0051937061788
13940.17-2 (NMFM1)	13.3330063157685
14002.16-1 (MPNG1)	10.7126318514002
14552.16-1FM (LMRR1)	15.4205754671109
14552.16-1FM (1FF)	28.9021147575335
15150.17-1 (DASS1)	15.9502381066734
15150.17-1 (RJABO2)	21.7622330424408
16126.17-3.3 (1)	28.951674146114
16537.17-1 (AJMC1)	26.735669536985
16537.17-1 (ASLS1)	27.5161790176662
16672.17-4R2 (4R1)	27.0942824148137
16672.17-4R2 (AMC1)	19.7527680363623
16913.17-3 (NMSAOM1)	19.131988015425
17065.17-1 (3)	27.4590090475577
17065.17-1 (SSC1)	22.7618416740393
17222.17-3R2FF (3R1)	18.8193142491365
17222.17-3R2FF (PM1)	23.7183586173611
18119.17-2 (LZ1)	15.4161170019236
19187.16-4CABO (RGCF)	9.80953489498101
19724.16-6 (ENP1)	23.9087718720635
19724.16-6 (13)	18.6729810120667
19724.16-8 (BMAP)	22.7759931872382
19799.17-1 (TFPA1)	6.47728170773975
20601.16-1 (HMNM1)	13.9171968776543
20601.16-1 (AMM)	15.1330636410104
20628.16-1CABO (AMP)	26.2467434158182

[1] Computed by Figueiredo C: Forensic DNA mixtures: Analysis and comparison of software results. Faculdade de Ciências da Universidade do Porto; 2018.

Table B34: Log_{10} values of the global LRs computed by STRmix™ v.2.7 with stutters, for mixtures with two estimated contributors with F_{ST}=0.015. The "-" represent the null LRs values and for that reason it was not possible to calculate a Log_{10} value.

Mixture (Reference)	Log_{10} (LR)
243.17-1FM (JRA)	16.8836444036635
243.17-1FM (MM)	17.2942457161381
913.17-1.3 (ASML1)	14.3356785023566
913.17-1.3 (PMRP1)	15.1805272829134
1087.17-4 (PMCC1)	22.5433726166886
1182.17-2L2FM (MD1)	26.0045792939022
1383.17-1CABO (AMAD1)	26.0198637139678
1383.17-1CABO (AMBC1)	19.4598597061048
1793.17-2 (1)	20.5375420653268
1793.17-2 (3)	32.0752914188833
1799.17-1 (2)	24.9254461759833
1816.17-2FF (EVM1)	28.4169565453903
1816.17-2FF (SC1)	24.9574348757596
1843.17-1FIXACAO (FN1)	8.85424529706612
1847.17-3R2 (JC1)	21.2024065726394
1847.17-3R2 (MC1)	21.2683673254215
2572.17-4CABO (IOSS)	23.2791191687201
2572.17-4CABO (LMVG1)	23.0340265237751
2799.17-2FM (1FF)	25.5174994019984
2921.17-2 (JAVC2)	23.2334022778119
2921.17-2 (TFTS1)	28.1033589398666
3053.17-3.1R2 (EAD1)	15.7514099886239
3053.17-3.1R2 (MMM1)	17.2438810022183
3732.17-2.1FM (ASSC1)	18.9988998426742
3732.17-2.1FM (IST1)	19.5356738034258
3929.16-1 (2)	25.6162654052817
5258.17-5 (1)	29.3280532502527
5700.16-5 (AGT)	25.4599500774338
5700.16-5 (TMAS)	29.7024994666071
5707.17-6R1 (MAGDC1)	26.1965630351481
5709.17-6R2 (CMDF1)	16.7273785694515
5709.17-6R2 (MJLF1)	17.0704442499729
5773.17-4 (5FM)	18.8347702876381
5773.17-4 (17FDC1)	26.329397879361
6010.17-1 (AAM1)	21.7163372878895
6472.17-1FM (PSBM2)	26.4517710891584
7241.17-11R2FF (ASJ1)	22.5887533664283
7241.17-11R2FF (MCPSJ1)	21.533149012806
7385.16-3 (2)	0.92620863861472
7588.17-1R1FF (3)	26.4544789842650
9233.16-9.1 (LCGS1)	21.2200034261569
9233.16-9.1 (VMTJ2)	25.4425581544959
10223.17-3LAM (IM2)	13.1107243543809
10223.17-3LAM (VMPM1)	18.3262948878185
12818.17-7 (1)	17.2329961103922
13017.17-25.2 (AJAN1)	27.8626083639649
13017.17-25.2 (MJCR1)	28.8595285664436
13027.17-1R2FF (1R1FF)	-
13027.17-1R2FF (1R1FM)	23.0386201619497
13034.16-2CABO (2LAM)	27.1367205671564
13252.17-8 (FTMR1)	21.475177060761
13252.17-8 (LIOR1)	19.406982764901
13740.17-1R1FF (1R2FF)	19.0157368744775
13940.17-2 (DMC1)	16.3000299678823
13940.17-2 (NMFM1)	15.3240147980363
14002.16-1 (MPNG1)	20.3516417261935
14552.16-1FM (LMRR1)	13.2239110868723
14552.16-1FM (1FF)	29.6310478529774
15150.17-1 (DASS1)	22.1016439854903
15150.17-1 (RJABO2)	25.2916795839828
16126.17-3.3 (1)	30.0371475036326
16537.17-1 (AJMC1)	26.9534794113221
16537.17-1 (ASLS1)	27.6808520075336
16672.17-4R2 (4R1)	25.6290118234547
16672.17-4R2 (AMC1)	19.9053154630834
16913.17-3 (NMSAOM1)	20.0958664534785
17065.17-1 (3)	27.8209301471806
17065.17-1 (SSC1)	24.1768144806748
17222.17-3R2FF (3R1)	22.9205302866346
17222.17-3R2FF (PM1)	24.254886293889
18119.17-2 (LZ1)	13.3100557377509
19187.16-4CABO (RGCF)	11.0403649558601
19724.16-6 (ENP1)	26.1436392352745
19724.16-6 (13)	23.5721626826463
19724.16-8 (BMAP)	25.8034639441243
19799.17-1 (TFPA1)	15.0790364570875
20601.16-1 (HMNM1)	-
20601.16-1 (AMM)	20.9148929505773
20628.16-1CABO (AMP)	25.5823463579299

Table B35: Log_{10} values of the global LRs computed by EuroForMix v.1.9.3 without stutters[1], for mixtures with three estimated contributors with F_{ST}=0.015.

Mixture (Reference)	Log_{10}(LR)
245.17-2.1 (MABS)	21.3527923833745
245.17-2.1 (OCF)	28.8104063584401
428.17-10 (LHIF)	24.972048174698
1305-17-3 (PBS1)	9.72618133296293
1305-17-3 (RDS1)	16.2242104523014
1533.17-4 (EIJB1)	16.5756152777644
2193.16-3 (MNTB)	12.0823881247705
2193.16-3 (MHMB)	5.49050226554324
2793.17-1R3 (FJCM1)	16.1214798741865
3053.17-5R2 (MHR2)	19.4766825322919
3053.17-5R2 (CDS1)	15.6354938410592
3357.17-12.2 (9)	12.5714285810426
3665.17-26 (SL2)	10.52342333164
3675.17-1 (AJRG1)	12.0209194232745
3675.17-1 (ORG1)	19.7492528844713
3841.17-7 (3)	6.9384345479999
3958.17-1R2FF (LGS1)	11.6270057012368
4406.17-6 (CVG)	16.2876170348336
4406.17-6 (NGP)	26.6065307418187
4548.16-PC9.9 (PC9.8)	23.9060152200734
4702.17-1 (CSP1)	23.3411037623852
4980.17-11 (JAMR1)	21.3064722797391
5008.17-1R1 (1R2)	13.6774197375943
5008.17-1R1 (2R1)	25.5676425427905
5008.17-3CABO (3LAM)	25.8031124939390
5008.17-3CABO (4R2)	18.5279049581313
5374.16-9 (BMEB1)	10.9466934310133
5396.16-1CABO (JJCC)	18.0420406452404
6561.17-2BIO (FMGV1)	23.4444448486638
6561.17-2BIO (JAPG1)	21.204965283136
6568.17-9 (DFSDN1)	11.5483436006294
6568.17-9 (RFAS2)	14.7885016629308
6978.17-4R2 (7FF)	22.1841359317344
6978.17-4R2 (JAB1)	23.6286282996609
7245.17-1R1 (1R2)	24.1833077536308
7582.17-1 (FMBSC)	8.52440178766854
8356.16-8.2FF (DPMF)	6.09497918053937
8356.16-8.2FF (HVF)	22.8443577454766
8371.16-1R1 (JARR1)	22.8045350452566
8393.17-2FF (JPB2)	25.7408896459652
8393.17-2FF (TFB2)	24.3752196058154
8410.16-2R1 (2R2)	9.99052595155536
10175.16-4 (5)	9.13630454474529
10278.16-2 (1)	5.89304170395815
10814.16-2 (CMSA)	21.8072146510419
10814.16-2 (FMRG)	10.1460411468255
11021.17-20LAM (MABSC1)	10.1598978101176
11021.17-20LAM (MGSF1)	10.2475678147413
11021.17-20LAM (MSSF1)	13.3013126503601
12179.17-14R6 (GCG1)	11.775491636042
12179.17-14R6 (MAM1)	11.4030252440401
12946.17-3.1 (2)	18.3044078184345
13020.17-1LAM (1CABO)	7.55693158289534
13046.17-1R1 (2R1)	18.1248478607836
13253.17-4 (3)	12.7026397870965
13367.17-5 (SMCP1)	6.86217530925384
14005.17-1R1FF (1R2FM)	13.4416222859251
14005.17-1R1FF (2R1FF)	22.4480739893468
14281.17-6R1 (6R2)	9.78616802827511
14281.17-6R1 (MGGS1)	9.10655337701301
14503.17-1 (MRER1)	13.9893600024679
14828.17-2FF (1FF)	22.4422282386593
14828.17-2FF (FLEP1)	17.1766612714213
14942.17-2LAM (3R1)	13.629732616532
14942.17-2LAM (NMLC1)	19.417216741588
15014.17-1 (2)	23.9706641124003
16839.17-1.9 (BZ1)	10.3865732647532
16839.17-1.9 (JW1)	11.5416227391041
16839.17-1.9 (QJ1)	10.2545005915717
18094.16-2 (IMSS)	22.8655270395792
18094.16-2 (CCM)	26.586907359373
18690.17-2R1 (1R1)	15.4658726536451
18690.17-2R1 (CFB2)	16.8354644253576
19364.16-4M1 (MPPA1)	21.8584850207286
19364.16-4M1 (HJDC)	18.8491064331911
20008.17-1 (RMRO1)	6.74953550914925
20880.15-2R2 (1)	17.1655062585449
23308.16-6CABO (AFM)	18.1977612334709
23308.16-6CABO (MARCC)	11.5820654526017

[1] Computed by Figueiredo C: Forensic DNA mixtures: Analysis and comparison of software results. Faculdade de Ciências da Universidade do Porto; 2018.

Table B36: Log_{10} values of the global LRs computed by STRmix™ v.2.7 with stutters for mixtures with three estimated contributors with F_{ST}=0.015.

Mixture (Reference)	Log_{10}(LR)
245.17-2.1 (MABS)	28.9651264105161
245.17-2.1 (OCF)	26.7956019798942
428.17-10 (LHIF)	29.7586418580119
1305-17-3 (PBS1)	19.7472253086786
1305-17-3 (RDS1)	23.4280375530353
1533.17-4 (EIJB1)	15.5029321374316
2193.16-3 (MNTB)	14.796428618926
2193.16-3 (MHMB)	6.66839523621408
2793.17-1R3 (FJCM1)	17.1434519990216
3053.17-5R2 (MHR2)	19.8886848466597
3053.17-5R2 (CDS1)	17.9384096365863
3357.17-12.2 (9)	16.4344092075875
3665.17-26 (SL2)	7.30931071578818
3675.17-1 (AJRG1)	10.9308166351797
3675.17-1 (ORG1)	20.5707647003284
3841.17-7 (3)	14.3148148872107
3958.17-1R2FF (LGS1)	19.786971352216
4406.17-6 (CVG)	17.7534221792904
4406.17-6 (NGP)	25.864374600967
4548.16-PC9.9 (PC9.8)	22.5376554170374
4702.17-1 (CSP1)	22.1242759320063
4980.17-11 (JAMR1)	24.6315147926767
5008.17-1R1 (1R2)	19.4832305869021
5008.17-1R1 (2R1)	26.1993986023596
5008.17-3CABO (3LAM)	29.2936497792158
5008.17-3CABO (4R2)	27.0455185628845
5374.16-9 (BMEB1)	13.2706788361447
5396.16-1CABO (JJCC)	26.3183764152228
6561.17-2BIO (FMGV1)	26.7632107920171
6561.17-2BIO (JAPG1)	25.7455978169859
6568.17-9 (DFSDN1)	10.9024543664012
6568.17-9 (RFAS2)	4.56135186591029
6978.17-4R2 (7FF)	23.8028763024247
6978.17-4R2 (JAB1)	22.483729899
7245.17-1R1 (1R2)	29.0651687517057
7582.17-1 (FMBSC)	9.06729408631598
8356.16-8.2FF (DPMF)	8.6793461179855
8356.16-8.2FF (HVF)	24.762866042462
8371.16-1R1 (JARR1)	26.4676229024178
8393.17-2FF (JPB2)	25.1664893183259
8393.17-2FF (TFB2)	27.3188143487607
8410.16-2R1 (2R2)	8.38205308211531
10175.16-4 (5)	12.2785935682411
10278.16-2 (1)	4.37316955890372
10814.16-2 (CMSA)	-6.03764960888633
10814.16-2 (FMRG)	10.3966177425827
11021.17-20LAM (MABSC1)	11.2506151469906
11021.17-20LAM (MGSF1)	16.1317790093692
11021.17-20LAM (MSSF1)	19.4967082951215
12179.17-14R6 (GCG1)	11.460130763696
12179.17-14R6 (MAM1)	9.91336873732877
12946.17-3.1 (2)	21.3226327116922
13020.17-1LAM (1CABO)	12.7940416721283
13046.17-1R1 (2R1)	17.895433596649
13253.17-4 (3)	23.952990904645
13367.17-5 (SMCP1)	15.3675422735206
14005.17-1R1FF (1R2FM)	23.4502183062
14005.17-1R1FF (2R1FF)	14.241421951712
14281.17-6R1 (6R2)	11.7538893314598
14281.17-6R1 (MGGS1)	11.1611582922062
14503.17-1 (MRER1)	10.2472611268805
14828.17-2FF (1FF)	23.3548764225162
14828.17-2FF (FLEP1)	17.6902492556891
14942.17-2LAM (3R1)	14.4519245284201
14942.17-2LAM (NMLC1)	13.1368156577268
15014.17-1 (2)	25.0163228540138
16839.17-1.9 (BZ1)	1.4432473369251
16839.17-1.9 (JW1)	1.4416637207988
16839.17-1.9 (QJ1)	3.48089762693439
18094.16-2 (IMSS)	23.8039825943946
18094.16-2 (CCM)	27.2295794626656
18690.17-2R1 (1R1)	16.9649051691280
18690.17-2R1 (CFB2)	15.8951185440351
19364.16-4M1 (MPPA1)	26.5389756722732
19364.16-4M1 (HJDC)	23.7570238338683
20008.17-1 (RMRO1)	6.51172297648198
20880.15-2R2 (1)	23.5980514682958
23308.16-6CABO (AFM)	19.6955954887587
23308.16-6CABO (MARCC)	15.0482863931061

Table B37: Log_{10} values of the global LRs computed by EuroForMix v.1.9.3 without stutters[1], for mixtures with two estimated contributors with F_{ST}=0.03.

Mixture (Reference)	Log_{10} (LR)
243.17-1FM (JRA)	14.8093778825503
243.17-1FM (MM)	18.6249904118688
913.17-1.3 (ASML1)	12.2514819771221
913.17-1.3 (PMRP1)	16.821522155517
1087.17-4 (PMCC1)	18.9006161839886
1182.17-2L2FM (MD1)	24.4790061348637
1383.17-1CABO (AMAD1)	24.0628320511216
1383.17-1CABO (AMBC1)	13.7725279516136
1793.17-2 (1)	15.325173353799
1793.17-2 (3)	30.2531210166921
1799.17-1 (2)	14.8226342389697
1816.17-2FF (EVM1)	26.2921771005641
1816.17-2FF (SC1)	20.9011998314001
1843.17-1FIXACAO (FN1)	6.86791226116805
1847.17-3R2 (JC1)	15.3111575679128
1847.17-3R2 (MC1)	17.5272413198569
2572.17-4CABO (IOSS)	16.570206031254
2572.17-4CABO (LMVG1)	16.5270649370398
2799.17-2FM (1FF)	23.182387103985
2921.17-2 (JAVC2)	15.4707862304408
2921.17-2 (TFTS1)	20.346248910121
3053.17-3.1R2 (EAD1)	11.8798303851637
3053.17-3.1R2 (MMM1)	14.8792014666084
3732.17-2.1FM (ASSC1)	17.0114362868769
3732.17-2.1FM (IST1)	17.8898389384577
3929.16-1 (2)	24.5009287597008
5258.17-5 (1)	25.0571632141911
5700.16-5 (AGT)	20.0359514047481
5700.16-5 (TMAS)	26.130296188310
5707.17-6R1 (MAGDC1)	21.3100561274136
5709.17-6R2 (CMDF1)	13.9052291771611
5709.17-6R2 (MJLF1)	14.3982095140471
5773.17-4 (5FM)	17.9662364877812
5773.17-4 (17FDC1)	24.4965144865754
6010.17-1 (AAM1)	14.5233461478372
6472.17-1FM (PSBM2)	22.4747751310189
7241.17-11R2FF (ASJ1)	18.5302867361981
7241.17-11R2FF (MCPSJ1)	16.6166472161258
7385.16-3 (2)	6.96162396786707
7588.17-1R1FF (3)	23.1912777615999
9233.16-9.1 (LCGS1)	10.656644175901
9233.16-9.1 (VMTJ2)	17.5602698495699
10223.17-3LAM (IM2)	12.787919763355
10223.17-3LAM (VMPM1)	17.427179862917
12818.17-7 (1)	18.9138862107304
13017.17-25.2 (AJAN1)	24.5724620785422
13017.17-25.2 (MJCR1)	26.5149300509974
13027.17-1R2FF (1R1FF)	14.777274386367
13027.17-1R2FF (1R1FM)	23.8284099429445
13034.16-2CABO (2LAM)	19.9324631583527
13252.17-8 (FTMR1)	16.5168340257534
13252.17-8 (LIOR1)	13.8633294322201
13740.17-1R1FF (1R2FF)	13.1131920567228
13940.17-2 (DMC1)	14.5291384780887
13940.17-2 (NMFM1)	11.7355402549635
14002.16-1 (MPNG1)	9.58805412427605
14552.16-1FM (LMRR1)	14.5941580262717
14552.16-1FM (1FF)	27.0738219087603
15150.17-1 (DASS1)	14.1160480661896
15150.17-1 (RJABO2)	20.1068865245545
16126.17-3.3 (1)	27.3168044353041
16537.17-1 (AJMC1)	25.1954673998742
16537.17-1 (ASLS1)	25.65432449991
16672.17-4R2 (4R1)	25.2073764125459
16672.17-4R2 (AMC1)	18.2499646135819
16913.17-3 (NMSAOM1)	17.663271869617
17065.17-1 (3)	26.1405362752969
17065.17-1 (SSC1)	21.7463376796579
17222.17-3R2FF (3R1)	17.1632041351038
17222.17-3R2FF (PM1)	21.8156214563936
18119.17-2 (LZ1)	14.0941706822495
19187.16-4CABO (RGCF)	8.78559455048141
19724.16-6 (ENP1)	22.4483826593312
19724.16-6 (13)	17.7159663401803
19724.16-8 (BMAP)	21.6865070715735
19799.17-1 (TFPA1)	5.48613748775888
20601.16-1 (HMNM1)	12.5631512639588
20601.16-1 (AMM)	13.733995044499
20628.16-1CABO (AMP)	25.2058500991243

[1] Computed by Figueiredo C: Forensic DNA mixtures: Analysis and comparison of software results. Faculdade de Ciências da Universidade do Porto; 2018.

Table B38: Log_{10} values of the global LRs computed by STRmix™ v.2.7 with stutters, for mixtures with two estimated contributors with F_{ST}=0.03. The "-" represent the null LRs values and for that reason it was not possible to calculate a Log_{10} value.

Mixture (Reference)	Log_{10} (LR)
243.17-1FM (JRA)	15.6070580790068
243.17-1FM (MM)	18.515277603768
913.17-1.3 (ASML1)	13.2096758345711
913.17-1.3 (PMRP1)	14.0956225950216
1087.17-4 (PMCC1)	21.5903401790322
1182.17-2L2FM (MD1)	24.7067945663214
1383.17-1CABO (AMAD1)	24.8963112215814
1383.17-1CABO (AMBC1)	18.4621133668836
1793.17-2 (1)	19.3537431707539
1793.17-2 (3)	29.7855077880892
1799.17-1 (2)	23.5670028265248
1816.17-2FF (EVM1)	27.0161136663589
1816.17-2FF (SC1)	23.5054755771
1843.17-1FIXACAO (FN1)	7.53844805171
1847.17-3R2 (JC1)	18.7456680261656
1847.17-3R2 (MC1)	21.9673654218562
2572.17-4CABO (IOSS)	21.6304990650066
2572.17-4CABO (LMVG1)	21.3065751280964
2799.17-2FM (1FF)	23.7036696085611
2921.17-2 (JAVC2)	22.4601157093783
2921.17-2 (TFTS1)	25.8374432283069
3053.17-3.1R2 (EAD1)	15.1086326655805
3053.17-3.1R2 (MMM1)	15.5632318285210
3732.17-2.1FM (ASSC1)	17.0272272540673
3732.17-2.1FM (IST1)	17.0895518828865
3929.16-1 (2)	24.7183272717426
5258.17-5 (1)	27.1247975679605
5700.16-5 (AGT)	23.8626798665003
5700.16-5 (TMAS)	28.0345883537136
5707.17-6R1 (MAGDC1)	24.7535983776521
5709.17-6R2 (CMDF1)	15.3396700242445
5709.17-6R2 (MJLF1)	15.6265661828561
5773.17-4 (5FM)	16.7809218784848
5773.17-4 (17FDC1)	24.8499351009526
6010.17-1 (AAM1)	22.2698187951911
6472.17-1FM (PSBM2)	25.1418572232384
7241.17-11R2FF (ASJ1)	20.4209618811209
7241.17-11R2FF (MCPSJ1)	19.8350814983157
7385.16-3 (2)	-0.19651557109213
7588.17-1R1FF (3)	24.6833622828603
9233.16-9.1 (LCGS1)	19.7352634693088
9233.16-9.1 (VMTJ2)	23.7095074008516
10223.17-3LAM (IM2)	12.2051772873883
10223.17-3LAM (VMPM1)	16.8166389448985
12818.17-7 (1)	12.4520012277266
13017.17-25.2 (AJAN1)	26.3941538768821
13017.17-25.2 (MJCR1)	27.3615200802763
13027.17-1R2FF (1R1FF)	7.21415478605354
13027.17-1R2FF (1R1FM)	12.0271456657743
13034.16-2CABO (2LAM)	25.8926899573746
13252.17-8 (FTMR1)	19.5902509350912
13252.17-8 (LIOR1)	17.7313711605686
13740.17-1R1FF (1R2FF)	17.7044250826665
13940.17-2 (DMC1)	14.6723195687285
13940.17-2 (NMFM1)	14.033745336014
14002.16-1 (MPNG1)	19.0865733656206
14552.16-1FM (LMRR1)	12.5566522082644
14552.16-1FM (1FF)	27.6341849551023
15150.17-1 (DASS1)	20.715618990027
15150.17-1 (RJABO2)	23.6014841695732
16126.17-3.3 (1)	27.7316129367487
16537.17-1 (AJMC1)	25.4316531973466
16537.17-1 (ASLS1)	25.9737972597741
16672.17-4R2 (4R1)	23.3908997971735
16672.17-4R2 (AMC1)	18.8854290732434
16913.17-3 (NMSAOM1)	17.7806628816686
17065.17-1 (3)	26.4377822619906
17065.17-1 (SSC1)	22.9580619329682
17222.17-3R2FF (3R1)	21.2324370092206
17222.17-3R2FF (PM1)	22.7172043431211
18119.17-2 (LZ1)	11.5607074765515
19187.16-4CABO (RGCF)	9.68055305949454
19724.16-6 (ENP1)	25.0255516227825
19724.16-6 (13)	22.6247872752921
19724.16-8 (BMAP)	24.3042103864352
19799.17-1 (TFPA1)	14.4468942724719
20601.16-1 (HMNM1)	-
20601.16-1 (AMM)	19.5707413624553
20628.16-1CABO (AMP)	24.5316883497568

Table B39: Log_{10} values of the LRs computed by EuroForMix v.1.9.3 without stutters[1], for mixtures with three estimated contributors with F_{ST}=0.03.

Mixture (Reference)	Log_{10}(LR)
245.17-2.1 (MABS)	19.7833002321213
245.17-2.1 (OCF)	27.1386281103015
428.17-10 (LHIF)	22.7130837108488
1305-17-3 (PBS1)	8.47538381868989
1305-17-3 (RDS1)	14.8903864897646
1533.17-4 (EIJB1)	14.9209084433591
2193.16-3 (MNTB)	10.7303435509263
2193.16-3 (MHMB)	4.8351390386092
2793.17-1R3 (FJCM1)	14.6700576348241
3053.17-5R2 (MHR2)	17.7347788276833
3053.17-5R2 (CDS1)	14.3027147288129
3357.17-12.2 (9)	11.3170748366145
3665.17-26 (SL2)	9.04768688174318
3675.17-1 (AJRG1)	11.0144477873315
3675.17-1 (ORG1)	18.9003227297441
3841.17-7 (3)	6.19957986705504
3958.17-1R2FF (LGS1)	10.507427526059
4406.17-6 (CVG)	15.4823103528079
4406.17-6 (NGP)	25.136380841575
4548.16-PC9.9 (PC9.8)	22.4807635146267
4702.17-1 (CSP1)	22.4436328848961
4980.17-11 (JAMR1)	19.4053718936911
5008.17-1R1 (1R2)	12.2339793061588
5008.17-1R1 (2R1)	24.3936224314727
5008.17-3CABO (3LAM)	23.5660637399181
5008.17-3CABO (4R2)	16.8868511470671
5374.16-9 (BMEB1)	10.0910111352479
5396.16-1CABO (JJCC)	16.5313997843148
6561.17-2BIO (FMGV1)	22.2924291220437
6561.17-2BIO (JAPG1)	20.2009130956124
6568.17-9 (DFSDN1)	10.3512000419634
6568.17-9 (RFAS2)	13.640165784147
6978.17-4R2 (7FF)	21.0537617374458
6978.17-4R2 (JAB1)	21.8226409271763
7245.17-1R1 (1R2)	22.4127362381008
7582.17-1 (FMBSC)	7.38014865734064
8356.16-8.2FF (DPMF)	5.39686706410931
8356.16-8.2FF (HVF)	20.74641375711
8371.16-1R1 (JARR1)	21.1723585014036
8393.17-2FF (JPB2)	23.985599280582
8393.17-2FF (TFB2)	22.7139565657806
8410.16-2R1 (2R2)	8.70240358925401
10175.16-4 (5)	8.21689847207146
10278.16-2 (1)	5.20642096148889
10814.16-2 (CMSA)	20.370068946324
10814.16-2 (FMRG)	9.43247724808593
11021.17-20LAM (MABSC1)	8.84272454600353
11021.17-20LAM (MGSF1)	9.10254094346453
11021.17-20LAM (MSSF1)	11.8611737254203
12179.17-14R6 (GCG1)	10.6138592214417
12179.17-14R6 (MAM1)	10.1276863598711
12946.17-3.1 (2)	16.8452788452949
13020.17-1LAM (1CABO)	6.7493197297683
13046.17-1R1 (2R1)	16.5341924403296
13253.17-4 (3)	11.6183604279373
13367.17-5 (SMCP1)	6.45711346748265
14005.17-1R1FF (1R2FM)	10.928966489028
14005.17-1R1FF (2R1FF)	21.4215285006772
14281.17-6R1 (6R2)	8.591831654112
14281.17-6R1 (MGGS1)	8.19378481405389
14503.17-1 (MRER1)	12.5089378214113
14828.17-2FF (1FF)	20.5862057448192
14828.17-2FF (FLEP1)	15.9449664473895
14942.17-2LAM (3R1)	12.2181387158704
14942.17-2LAM (NMLC1)	17.2604718959591
15014.17-1 (2)	22.4222734057976
16839.17-1.9 (BZ1)	9.08022621039987
16839.17-1.9 (JW1)	10.1775513340394
16839.17-1.9 (QJ1)	9.21487670277837
18094.16-2 (IMSS)	21.7457763952241
18094.16-2 (CCM)	25.1474259450167
18690.17-2R1 (1R1)	14.2678784359099
18690.17-2R1 (CFB2)	15.2108871243127
19364.16-4M1 (MPPA1)	20.2477793040358
19364.16-4M1 (HJDC)	17.466267854245
20008.17-1 (RMRO1)	5.60802690493763
20880.15-2R2 (1)	16.1402994525396
23308.16-6CABO (AFM)	16.7407874921522
23308.16-6CABO (MARCC)	10.2067673562001

[1] Computed by Figueiredo C: Forensic DNA mixtures: Analysis and comparison of software results. Faculdade de Ciências da Universidade do Porto; 2018.

Table B40: Log_{10} values of the LRs computed by STRmix™ v.2.7 with stutters, for mixtures with three estimated contributors with F_{ST}=0.03.

Mixture (Reference)	Log_{10}(LR)
245.17-2.1 (MABS)	26.657275814173
245.17-2.1 (OCF)	25.7680532226793
428.17-10 (LHIF)	27.9388761012532
1305-17-3 (PBS1)	18.5295330123232
1305-17-3 (RDS1)	21.8361531498292
1533.17-4 (EIJB1)	13.8657374756711
2193.16-3 (MNTB)	13.3425608434508
2193.16-3 (MHMB)	5.95362923887213
2793.17-1R3 (FJCM1)	15.8819435723847
3053.17-5R2 (MHR2)	17.8655125997966
3053.17-5R2 (CDS1)	16.1994809148624
3357.17-12.2 (9)	17.4275185663644
3665.17-26 (SL2)	5.59409407758012
3675.17-1 (AJRG1)	11.9295772865907
3675.17-1 (ORG1)	19.6623516708872
3841.17-7 (3)	14.777752964533
3958.17-1R2FF (LGS1)	18.6425139814895
4406.17-6 (CVG)	16.0374834274188
4406.17-6 (NGP)	24.5117898105539
4548.16-PC9.9 (PC9.8)	21.7947180293802
4702.17-1 (CSP1)	22.4515254735246
4980.17-11 (JAMR1)	22.3431721787289
5008.17-1R1 (1R2)	17.8460772000652
5008.17-1R1 (2R1)	24.9426627235847
5008.17-3CABO (3LAM)	27.645687481363
5008.17-3CABO (4R2)	25.5393145187458
5374.16-9 (BMEB1)	12.2802595886861
5396.16-1CABO (JJCC)	24.973026198314
6561.17-2BIO (FMGV1)	25.5789484916621
6561.17-2BIO (JAPG1)	24.4060118934125
6568.17-9 (DFSDN1)	9.71391874621177
6568.17-9 (RFAS2)	4.05219358043347
6978.17-4R2 (7FF)	22.5737416415203
6978.17-4R2 (JAB1)	20.8559550484597
7245.17-1R1 (1R2)	27.140979163477
7582.17-1 (FMBSC)	7.806118897028
8356.16-8.2FF (DPMF)	7.81458717181344
8356.16-8.2FF (HVF)	22.9647073686535
8371.16-1R1 (JARR1)	24.8971430505796
8393.17-2FF (JPB2)	23.8486385793266
8393.17-2FF (TFB2)	25.5717903271478
8410.16-2R1 (2R2)	7.84614528730869
10175.16-4 (5)	10.9974650221534
10278.16-2 (1)	5.2146849307506
10814.16-2 (CMSA)	-9.61980685426881
10814.16-2 (FMRG)	9.73961980573443
11021.17-20LAM (MABSC1)	9.74383105512765
11021.17-20LAM (MGSF1)	14.0460657302307
11021.17-20LAM (MSSF1)	17.7859559067136
12179.17-14R6 (GCG1)	9.43463276617414
12179.17-14R6 (MAM1)	8.91979957273922
12946.17-3.1 (2)	18.9771289005807
13020.17-1LAM (1CABO)	11.0489853025707
13046.17-1R1 (2R1)	15.8662046084464
13253.17-4 (3)	22.2619524328441
13367.17-5 (SMCP1)	14.9218372821112
14005.17-1R1FF (1R2FM)	19.0802295248849
14005.17-1R1FF (2R1FF)	22.6447437685884
14281.17-6R1 (6R2)	10.19794183649
14281.17-6R1 (MGGS1)	9.63729955896163
14503.17-1 (MRER1)	8.53539540140561
14828.17-2FF (1FF)	20.8920556257957
14828.17-2FF (FLEP1)	15.9497655821228
14942.17-2LAM (3R1)	9.79791123241847
14942.17-2LAM (NMLC1)	11.9427667847898
15014.17-1 (2)	23.6902847025126
16839.17-1.9 (BZ1)	-7.50732340577329
16839.17-1.9 (JW1)	1.32872608519878
16839.17-1.9 (QJ1)	3.4701163531510
18094.16-2 (IMSS)	23.2175892149651
18094.16-2 (CCM)	25.9344529994427
18690.17-2R1 (1R1)	17.3639878297485
18690.17-2R1 (CFB2)	16.4035151549893
19364.16-4M1 (MPPA1)	25.2655017700392
19364.16-4M1 (HJDC)	22.4092058741896
20008.17-1 (RMRO1)	5.38490869783028
20880.15-2R2 (1)	21.9374677396434
23308.16-6CABO (AFM)	18.3565230023418
23308.16-6CABO (MARCC)	13.6544364629961

Appendix IV: Mixture/reference pair 10814.16-2 (CMSA) electropherogram (three estimated contributors)

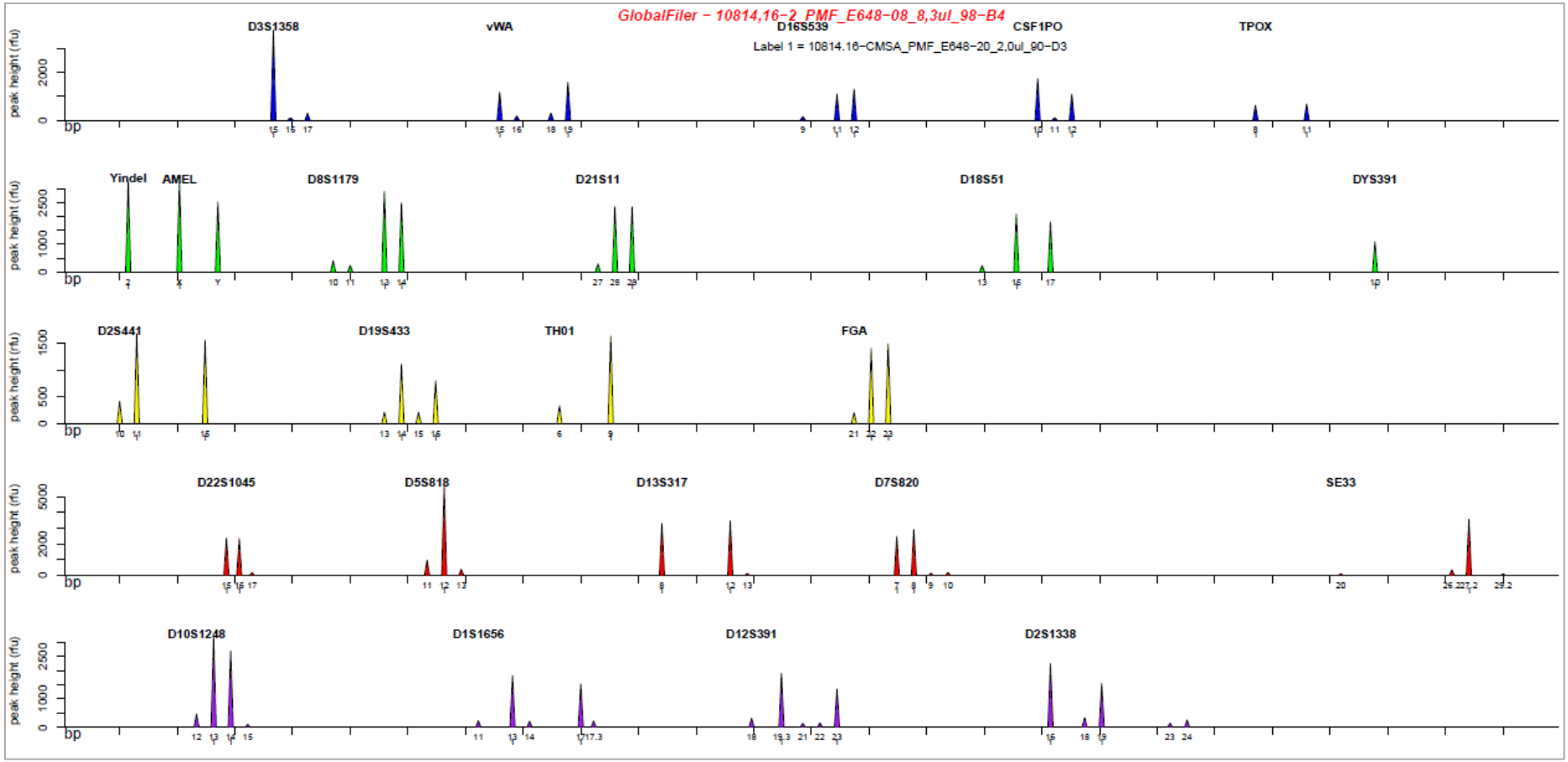


Figure C1: Electropherogram of mixture 10814.16-2 with stutters, in which the reference sample 10814.16-CMSA profile is marked for 24 markers. It should be noted that the Yindel, AMEL and DYS391 markers were ignored in this dissertation.