Part II:

Internal Validation of STRmix™ V2.3

District of Columbia

Department of Forensic Science

Forensic Science Laboratory

Forensic Biology Unit

STRmix™ internal validation

This document describes the internal validation of STRmix™ V2.3 at the Department of Forensic Sciences Laboratory, Washington DC (DFS). STRmix™ has previously been subjected to developmental validation. This involved, in part, the complete 'by hand' confirmation of the calculations behind the software. The results of the developmental validation are included in the STRmix™ User's Manual. In addition, a summary of the developmental validation is discussed in Taylor et al. [1]. A list of all papers describing the theory behind different aspects of STRmix™ is provided in Appendix 1 of this document.

Internal validation describes the activities DFS has undertaken in-house before the implementation of STRmix™ into routine casework. This document follows the internal validation section of the SWGDAM Guidelines for the Validation of Probabilistic Genotyping Systems [10]. This included the examination of known and non-probative evidence samples, and investigations into reproducibility and precision, sensitivity and stochastic studies, and mixture studies. The section where specific SWGDAM guidelines are discussed in this document is cross referenced in Appendix 2.

The results of all experiments related to the internal validation of STRmix™ at DFS Laboratory are retained within the laboratory's quality system.

STRmix™ parameters

The parameters described in the document "Estimation of STRmix™ Parameters" for DFS were used for all internal validation checks presented in this report. All other run parameters have been optimised by the STRmix™ developers.

Section A: Single source profiles

Inspection of weights

This section covers the following standards:

> 4.1.5. Single-source specimens
>
> 4.2.1.2. For single-source specimens with high quality results, genotypes derived from non-probabilistic analyses of profiles above the stochastic threshold should be in complete concordance with the results of probabilistic methods.

Within this section we demonstrate how the weights assigned by STRmix™ to different genotype combinations are appropriate. The weights can be used as a diagnostic of the deconvolution process and should be intuitively correct, where the most supported genotypes have the highest weights.

A dilution series of two single source profiles where the peak heights ranged from above the level where dropout is observed to below was constructed. Profiles were amplified using AmpFlSTR® Identifiler™ Plus following DFS Laboratory's standard operating procedure for amplification (FBS12-PCR Amplification Using the Identifiler™ Plus Kit). The template DNA in nanograms for the serial dilution was: 0.025, 0.05, 0.1, 0.2, and 0.4 ng. The profiles were analysed following DFS Laboratory's standard operating procedure for analysis (FBS14- Data Analysis Using GeneMapper® ID-X). The 0.025 ng sample for STRMIX01 did not produce any data and was not further evaluated because it did not meet the two locus minimum for running STRmix™. Some low AT samples were originally

analyzed using slightly lower analytical thresholds in blue, yellow and red. All samples were reviewed and reanalyzed if an allele or stutter peak should not have been detected.

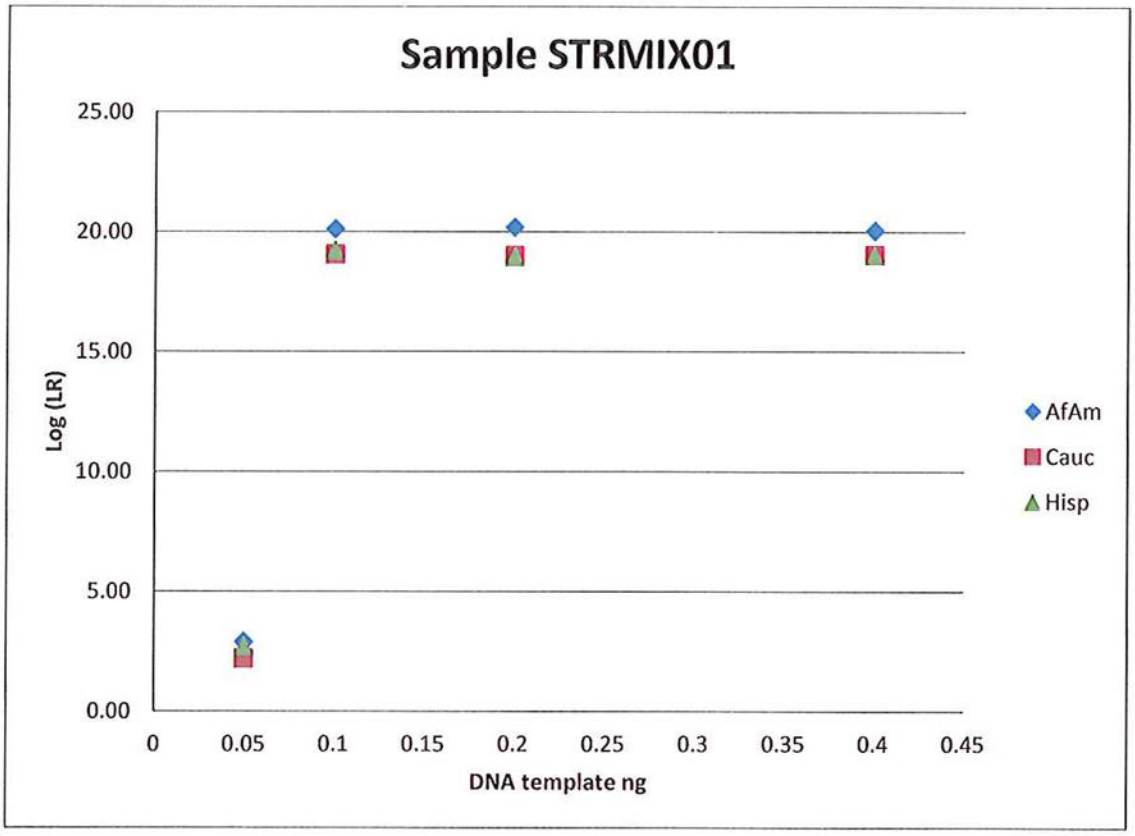
The profiles were interpreted in STRmix™ using the propositions:

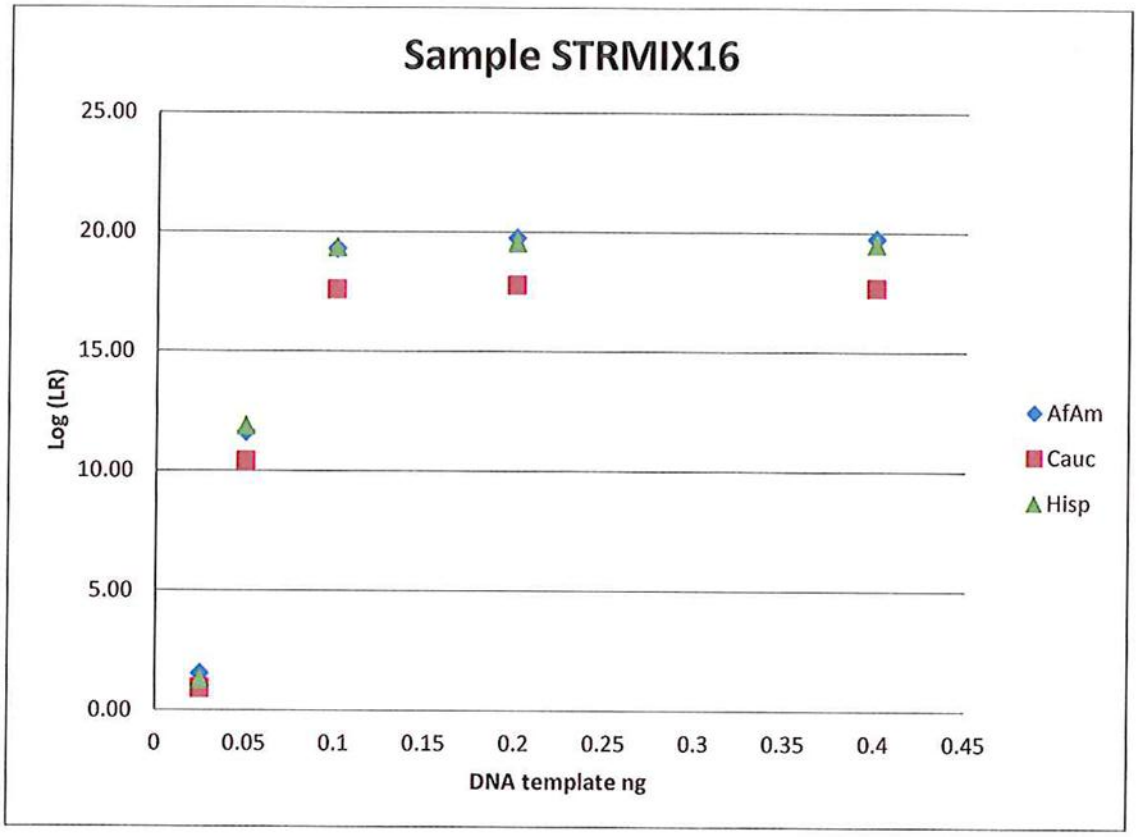
H_p: The DNA originated from the person of interest

H_d: The DNA originated from an unknown individual

The Likelihood Ratio (*LR*) was calculated for the known contributor using the DFS Laboratory Caucasian, African American and Hispanic allele frequencies and an F_{ST} (θ) of 0.01 and 99.0% 1-sided lower HPD. A plot of log(*LR*) versus input DNA is provided in Figure 1 for both samples.

Figure 1: Plot of log(LR) versus input DNA amount (ng)





Inspection of the plots shows the *LR* progressing from the value for the single source *LR* calculated for a full profile at >0.2 ng towards *LR* = 1 as the DNA template decreases. As expected, the weights for genotypes considering dropout increased as template drops. In addition, the DNA amounts from the STRmix™ output (*t* or template mass parameter) declined steadily in line with peak heights (data not shown).

Reproduction of single source LR

There is a small subset of profiles where the 'answer' is known or can be estimated easily [2]. These include single source profiles where the weight is one (or 100%) for one genotype at each locus. The *LR* was calculated 'by hand' using Microsoft Excel at each locus for five single source profiles analysed using three allele frequency databases and the individual locus *LR*s compared with the STRmix™ results using an F_{ST} (or θ) of 0.01.

When θ > 0, the Balding and Nichols [3] formulae (or equations 4.10 from NRCII [4]) are applied. For single source profiles:

$$\frac{2\left[\theta+(1-\theta)p_i\right]\left[\theta+(1-\theta)p_j\right]}{(1+\theta)(1+2\theta)} \quad \text{for heterozygote loci} \qquad [1]$$

$$\frac{\left[3\theta+(1-\theta)p_i\right]\left[2\theta+(1-\theta)p_i\right]}{(1+\theta)(1+2\theta)} \quad \text{for homozygote loci} \qquad [2]$$

Where p_i is the allele frequency for allele i, p_j the allele frequency for allele j and θ is the F_{ST} value. The allele frequencies used within equations 1 and 2 are posterior mean frequencies. These are calculated using the following equation:

$$\frac{x_i + \frac{1}{k}}{N_a + 1} \qquad [3]$$

Where for the given locus, x_i is the number of observations of allele i in a database, N_a is the number of alleles in that database and k is the number of allele designations with non-zero observations in the database at that locus.

The 'by hand' calculated and STRmix™ results for one of the five single source profiles for the three different sub populations are given in Table 1. Small differences in the locus *LR*s are due to rounding in the STRmix™ file.

Table 1: 'By hand' (Excel) calculation of *LR* versus STRmix™ results for one single source profile (STRMIX16 0.2 ng) with a theta of 0.01

Subpopulation	Hispanic		Caucasian		African American	
Locus	Excel	STRmix™	Excel	STRmix™	Excel	STRmix™
D8S1179	113.0	113	47.3	47.3	150.3	150
D21S11	77.5	77.5	28.3	28.3	16.2	16.2
D7S820	24.4	24.4	14.8	14.8	17.1	17.1
CSF1PO	4.4	4.42	4.7	4.74	8.1	8.08
D3S1358	30.6	30.6	24.5	24.5	21.8	21.8
TH01	7.1	7.12	7.7	7.67	9.5	9.49
D13S317	20.4	20.4	12.9	12.9	50.2	50.2
D16S539	5.5	5.54	5.1	5.11	8.2	8.18
D2S1338	35.8	35.8	30.7	30.7	38.0	38
D19S433	58.0	58	34.0	34	50.2	50.2
vWA	29.5	29.5	22.1	22.1	29.9	29.9
TPOX	3.7	3.68	3.6	3.6	6.3	6.31
D18S51	43.9	43.9	45.6	45.6	76.1	76.1
D5S818	10.4	10.4	7.4	7.38	6.9	6.95
FGA	27.0	27	27.9	27.9	18.1	18.2
Total	6.440E19	6.440E19	9.140E17	9.140E17	9.85E+19	9.85E+19

The results in Table 1 show that STRmix™ is giving the expected answer based on the population genetic model being used.

Section B: Use of peak heights

This section covers the following standard:

4.1.4. Allelic peak height, to include off-scale peaks

STRmix™ is a fully continuous model that uses peak heights to inform the genotype combinations of contributors to profiles. As template decreases dropout starts to be considered. As the weights for

genotypes considering dropout increase, the weights for genotype combinations for the *true* contributors decrease and subsequently the LR decreases. This can be observed in Figure 1 (and later in Figure 3). This is the expected result.

STRmix™ treats all peaks that are greater than the saturation threshold (calculated as 7000 rfu for DFS laboratory's Applied Biosystems 3130xl data) qualitatively and not quantitatively. It is not recommended that saturated profiles are interpreted within STRmix™ as a profile that exceeds the saturation threshold is likely to have higher stutter peak heights than expected by STRmix™.

A number of single source samples were amplified with deliberately high input amounts of DNA (2, 4 and 8 ng). The profiles were interpreted in STRmix™ and the weights were reviewed. All profiles were interpreted correctly, with weights = 1 for the known genotype combination.

Section C: Weights

This section covers the following standard:

> 4.2.1.3. Generally, as the analyst's ability to deconvolute a complex mixture decreases, so do the weightings of individual genotypes within a set determined by the software.

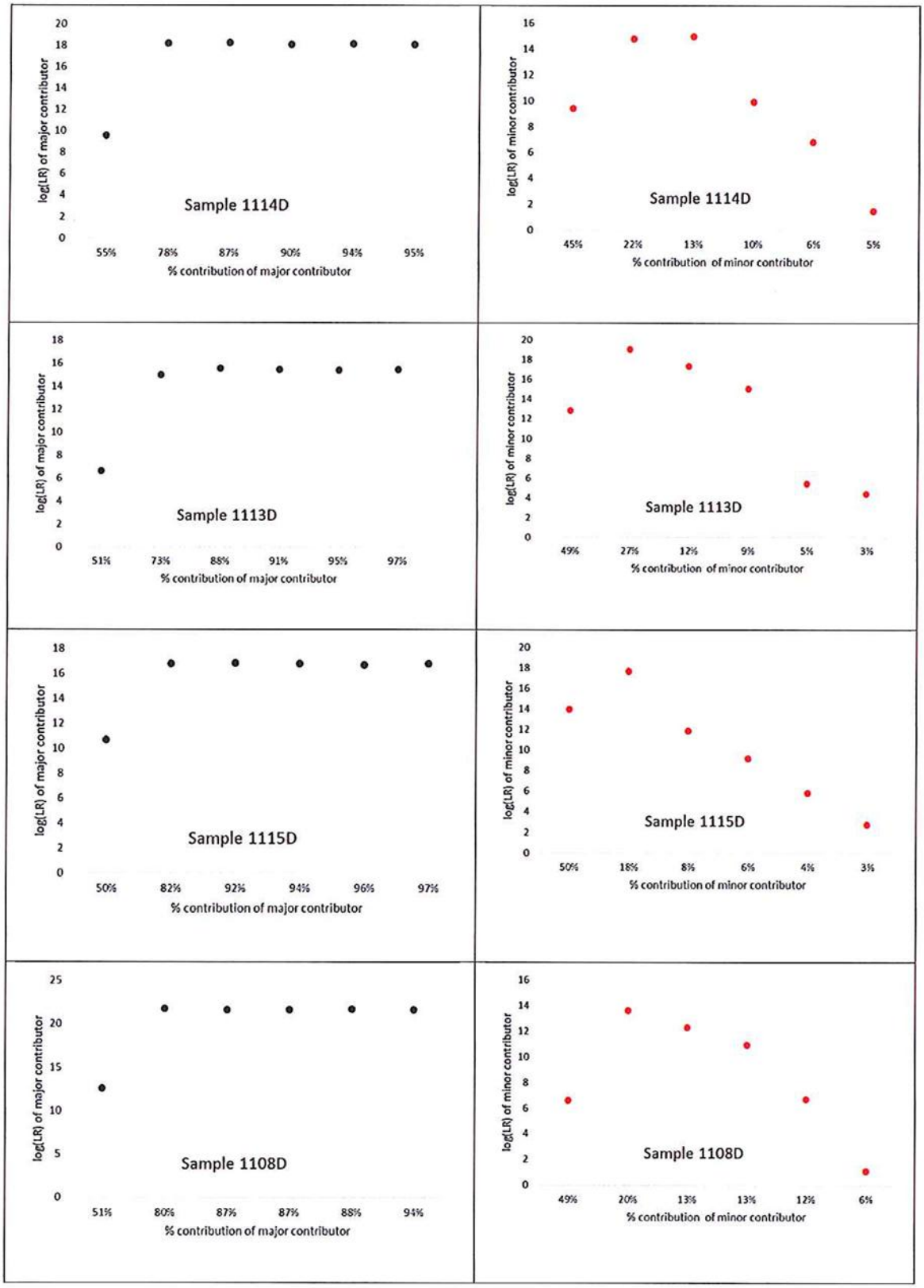
The weights are described as the primary output from STRmix™. They can be used as a diagnostic of the deconvolution process and should be intuitively correct, where the most supported genotypes have the highest weights.

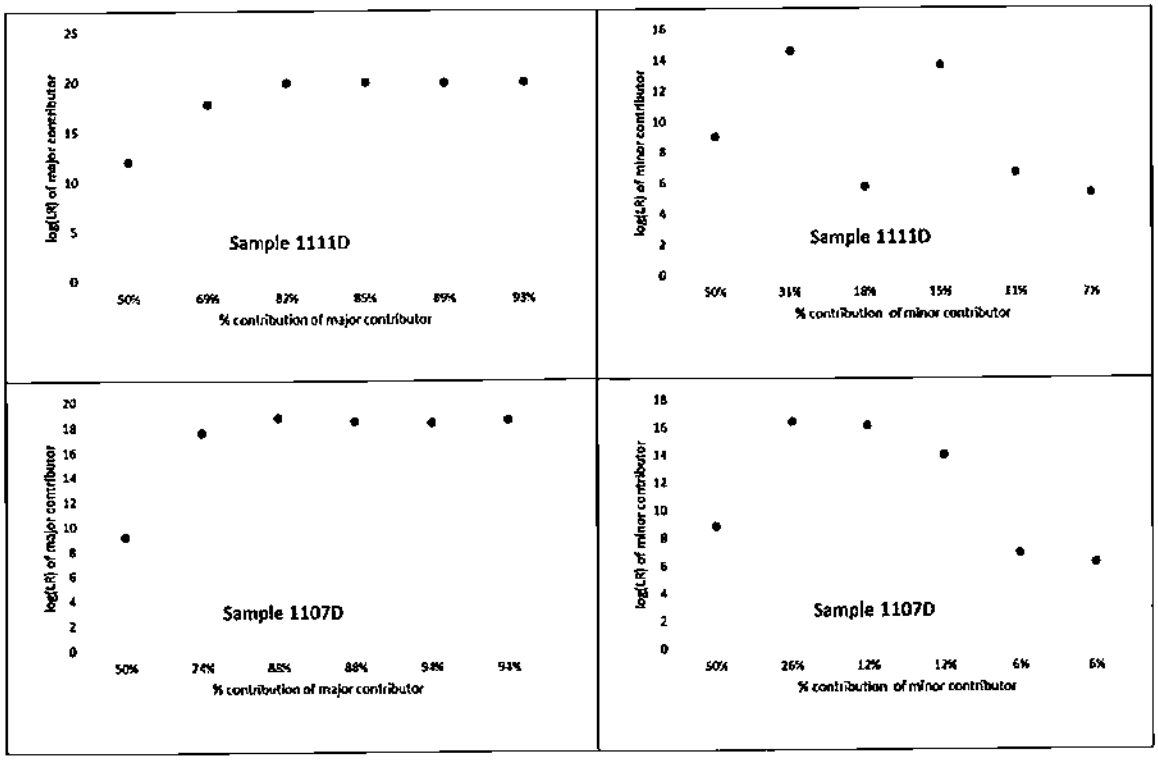
Twelve two person mixture series were constructed in the following ratios 20:1, 15:1, 10:1, 7:1, 3:1 and 1:1. For one set of six, the total amount of DNA in the profiles was approximately 500 pg DNA and for the second set of six, it was approximately 1 ng. The profiles were interpreted in STRmix™ under the following propositions and a *LR* calculated for the Caucasian, African American and Hispanic sub populations:

> H_p: The DNA originated from the person of interest (known major or minor) and an unknown individual
>
> H_d: The DNA originated from two unknown individuals

A plot of log(*LR*) for six of the twelve mixture series considering both the major and minor for the Caucasian sub population is provided in Figure 2.

Figure 2: Log(*LR*) versus mixture proportion considering both the major and minor for the Caucasian sub population





Inspection of Figure 2 shows that the mixture proportions in the STRmix™ output changed appropriately as the mixture ratios varied. The log(*LR*) decreases by approximately half (~10 orders of magnitude) for the 1:1 mixtures when compared to the single source *LR* calculated for the major contributor. The decrease starts where it is reasonable for alleles from a major and minor to be confused, when major < 80% of the mixture proportion. The *LR* for the minor contributor reduces as the amount of DNA template from them also reduces. This is most evident for the 1:20 mixture which produced mixture proportions of around 3 to 7% for the minor.

Section D: Sensitivity and specificity and mixtures

This section covers the following standards:

4.1.2. Hypothesis testing with contributors and non-contributors

4.1.6. Mixed specimens

4.1.6.1. Various contributor ratios (e.g., 1:1 through 1:20, 2:2:1, 4:2:1, 3:1:1, etc)

4.1.6.2. Various total DNA template quantities

4.1.6.3. Various numbers of contributors. The number of contributors evaluated should be based on the laboratory's intended use of the software. A range of contributor numbers should be evaluated in order to define the limitations of the software.

4.1.6.5. Sharing of alleles among contributors

4.1.7. Partial profiles, to include the following:

4.1.7.1. Allele and locus drop-out

4.1.13. Sensitivity, specificity and precision, as described for Developmental Validation

A demonstration of sensitivity and specificity for a range of DFS Identifiler™ Plus mixtures was undertaken as per Taylor [5]. With respect to interpretation methods, sensitivity is defined as the ability of the software to reliably resolve the DNA profile of known contributors within a mixed DNA profile for a range of starting DNA templates. The log(*LR*) for known contributors (H_p true) should be high and should trend to 0 as less information is present within the profile. Information includes amount of DNA from the contributor of interest, conditioning profiles (for example the victim's profile on intimate samples), replicates and decreasing numbers of contributors. Specificity is defined as ability of the software to reliably exclude known non contributors (H_d true) within a mixed DNA profile for a range of starting DNA templates. The log(*LR*) should trend upwards to 0 as less information is present within the profile.

Specificity and sensitivity were tested by calculating the *LR* for a number of one, two, three and four person profiles for both known contributors and known non-contributors. The plots in [6] have been reproduced for DFS's Identifiler™ Plus data. A summary of the profiles analysed for the sensitivity and specificity plots are in Appendix 3.

These profiles represent typical profiles encountered by the laboratory. The profiles are of varying DNA quantity and mixture proportions. The contributors include homozygote and heterozygote alleles and there are varying amounts of allele sharing across the different loci (standard 4.1.6.5). Given the template amounts, allele and/or locus dropout was expected to occur within the profiles containing the lower DNA amounts (standard 4.1.7.1).

Each profile was interpreted in STRmix™ and compared to the known contributors and 300 known non-contributors using the Database Search function within STRmix™. The non-contributors consisted of the DFS FBU Staff and Visitor QA database.

The propositions considered were:

H_p: The DNA originated from the database individual and N-1 unknown individuals

H_d: The DNA originated from N unknown individuals

Plots of log(*LR*) versus average peak height (APH) per contributor for the one, two, three and four contributor mixtures are given in Figure 3. Exclusions (*LR*=0) are plotted as log(*LR*)=-30. The per contributor APH for H_d true contributors is taken as the lowest of the known contributors. The APH per known contributor is taken from the unmasked and unshared alleles. The results of all comparisons are provided in Figure 3.

Inspection of the plots in Figure 3 shows that the addition of more relevant information such as DNA template (and addition of assumed contributors, refer to Figure 4) improves the performance of STRmix™. The *LR* distributions for H_p true and H_d true were very well separated at high template for two person mixtures and all single source profiles. As the number of contributors increased and the template lowered the two distributions converged on log(*LR*) = 0. At high template STRmix™

correctly and reliably gave a high *LR* for true contributors and a low *LR* for false contributors. At low template or high contributor number STRmix™ correctly and reliably reported that the analysis of the sample tends towards uninformative or inconclusive.

The plots in Figure 3 can help inform the limits of STRmix™, particularly the lower limit of DNA where an H_p true hypothesis results in a *LR* greater than 1 and the limit where false positives may arise (a *LR* greater than 1 where H_d is true).

Section E: Alternate propositions

This section covers the following standard:

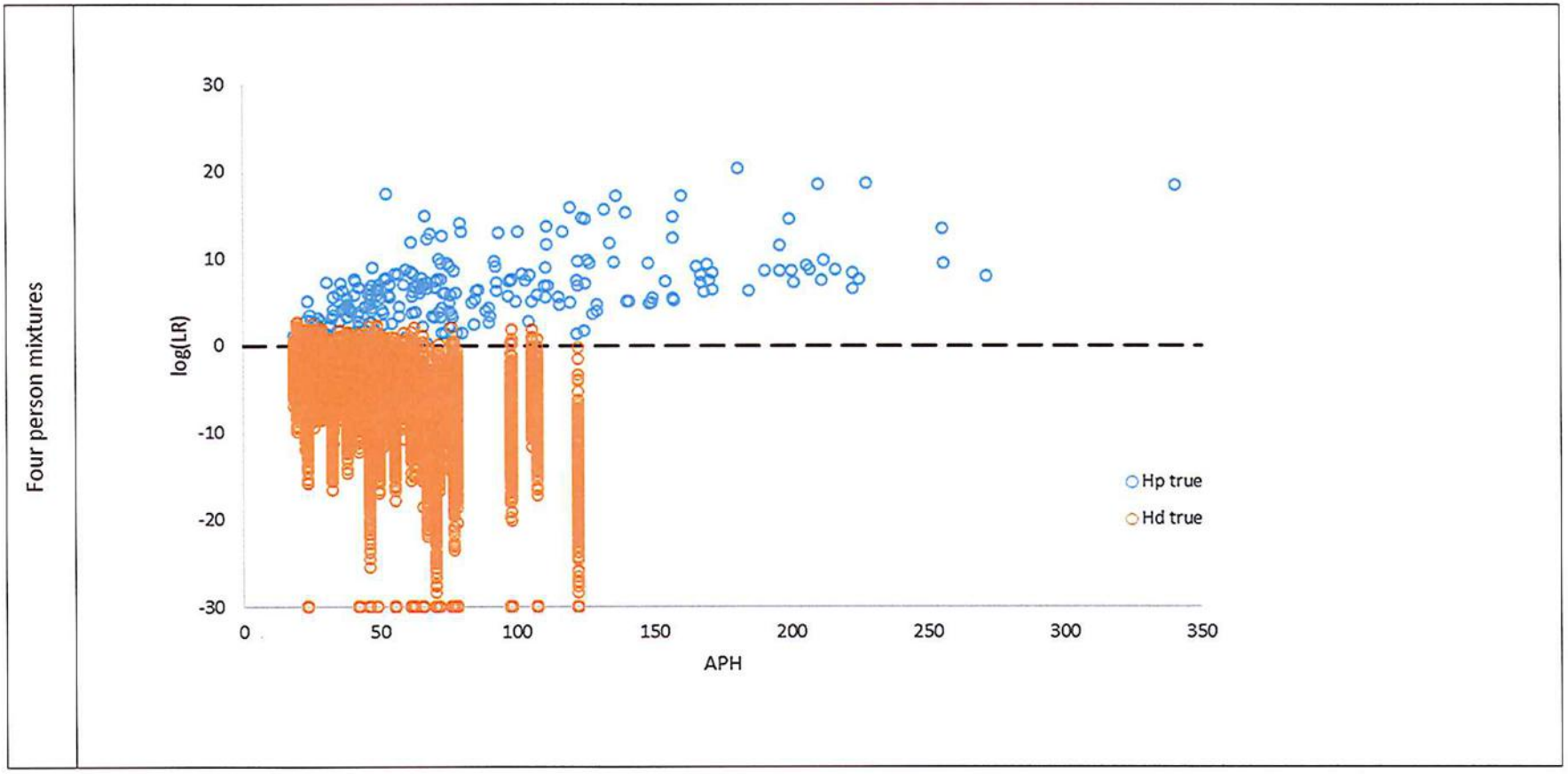
> 4.1.2.1. The laboratory should evaluate more than one set of hypotheses for individual evidentiary profiles to aid in the development of policies regarding the formulation of hypotheses. For example, if there are two persons of interest, they may be evaluated as co-contributors and, alternatively, as each contributing with an unknown individual. The hypotheses used for evaluation of casework profiles can have a significant impact on the results obtained.

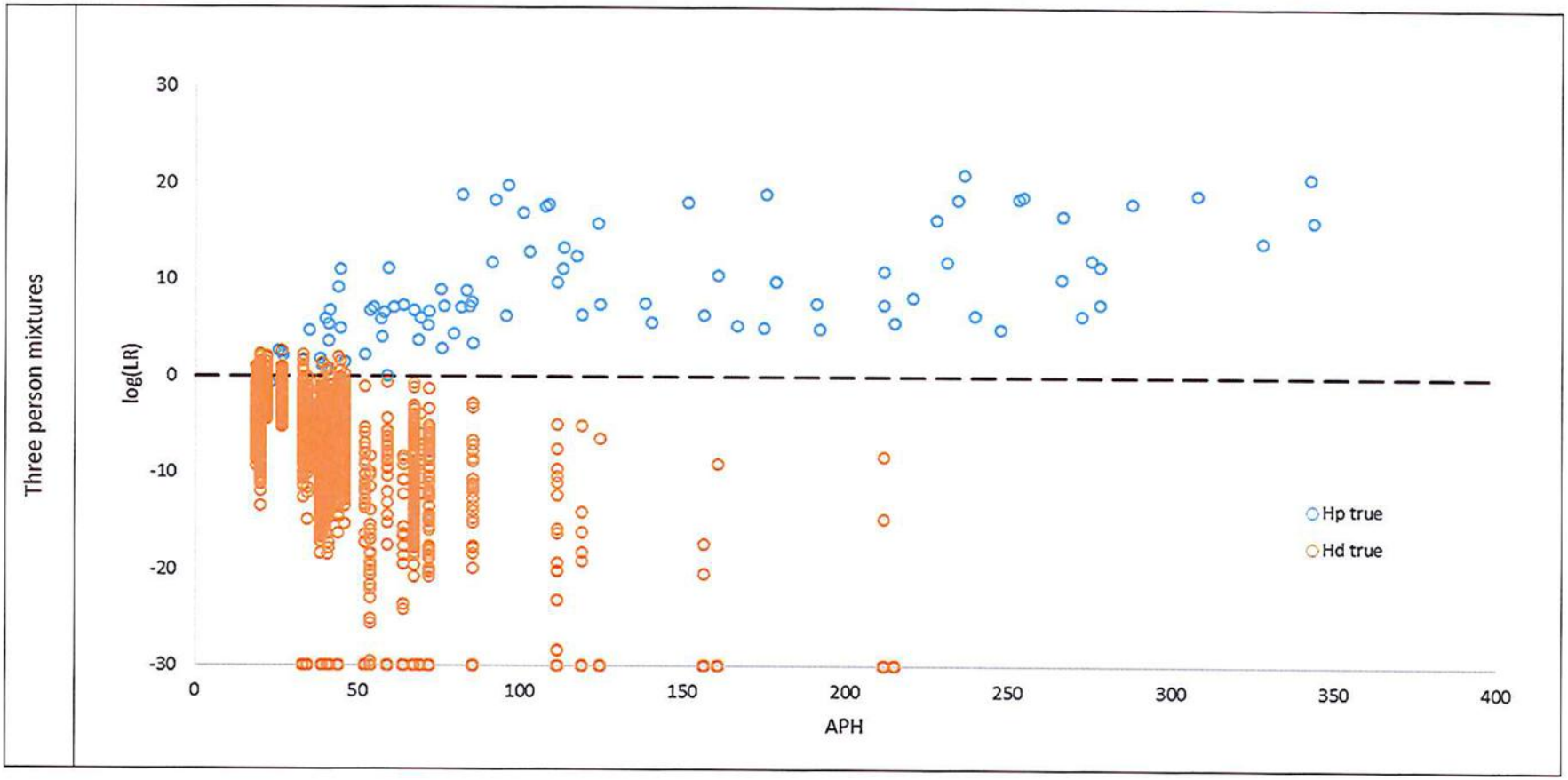
In an extension of the sensitivity and specificity experiments in section D, alternate propositions were trialled for the four person mixtures with 0.5 ng input DNA. The profiles were reinterpreted in STRmix™ with alternate propositions. In these interpretations assume one of the contributors is a known under both H_p and H_d. The different propositions being considered are:

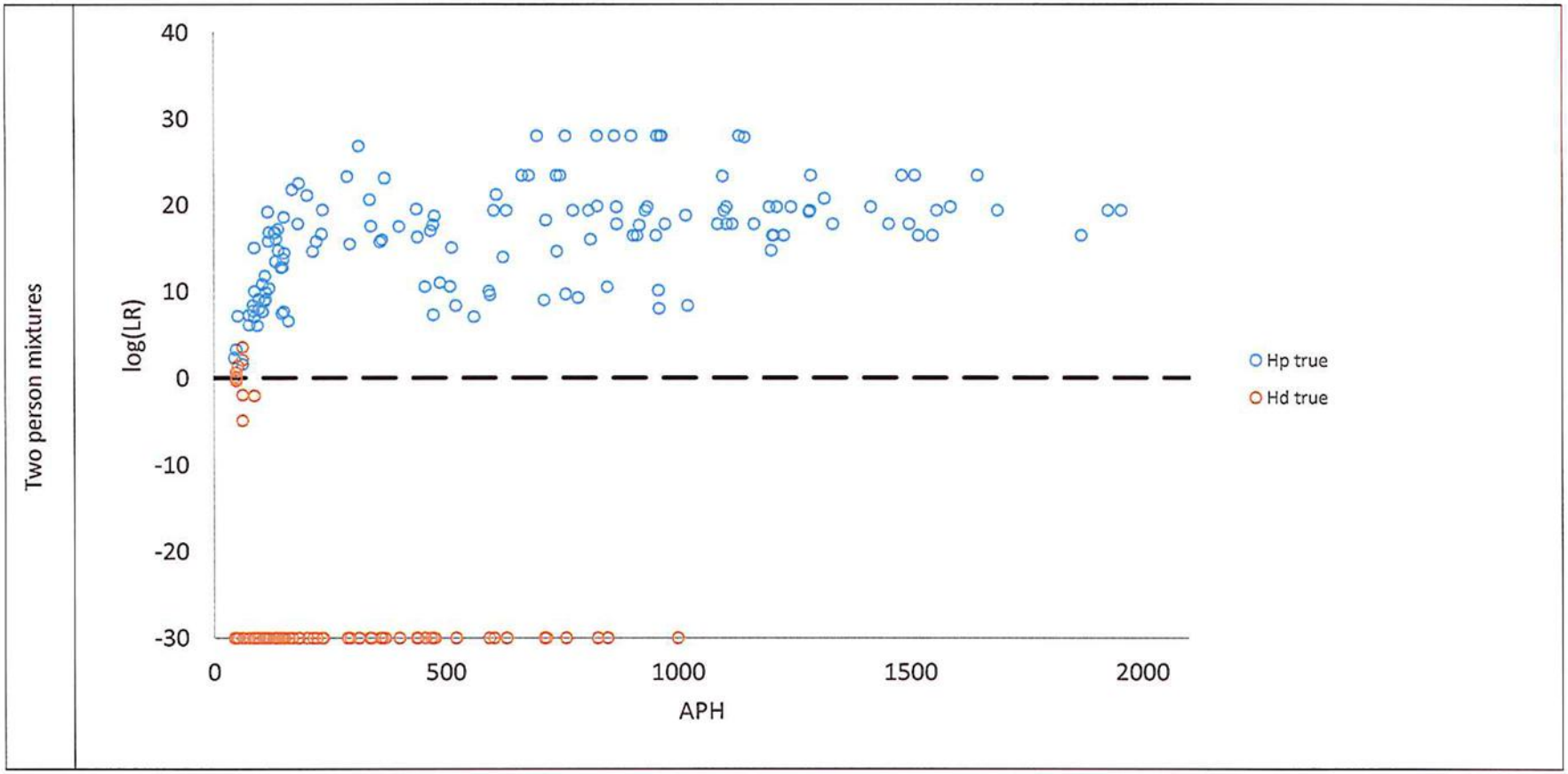
> H_p: The DNA originated from the known individual, the database individual and 2 unknown individuals
>
> H_d: The DNA originated from the known individual and three unknown individuals

In Figure 4, the original log(LR) values for the 0.5 ng four person mixture series are plotted versus APH (top pane) above the results with an assumed contributor (bottom pane).

Figure 3: Log(*LR*) versus APH for four, three, two and one person mixtures amplified by the DFS laboratory.




Three person mixtures
log(LR)
30
20
10
0
-10
-20
-30
0
50
100
150
200
250
300
350
400
APH
Hp true
Hd true


Two person mixtures
log(LR)
40
30
20
10
0
-10
-20
-30
0
500
1000
1500
2000
APH
Hp true
Hd true

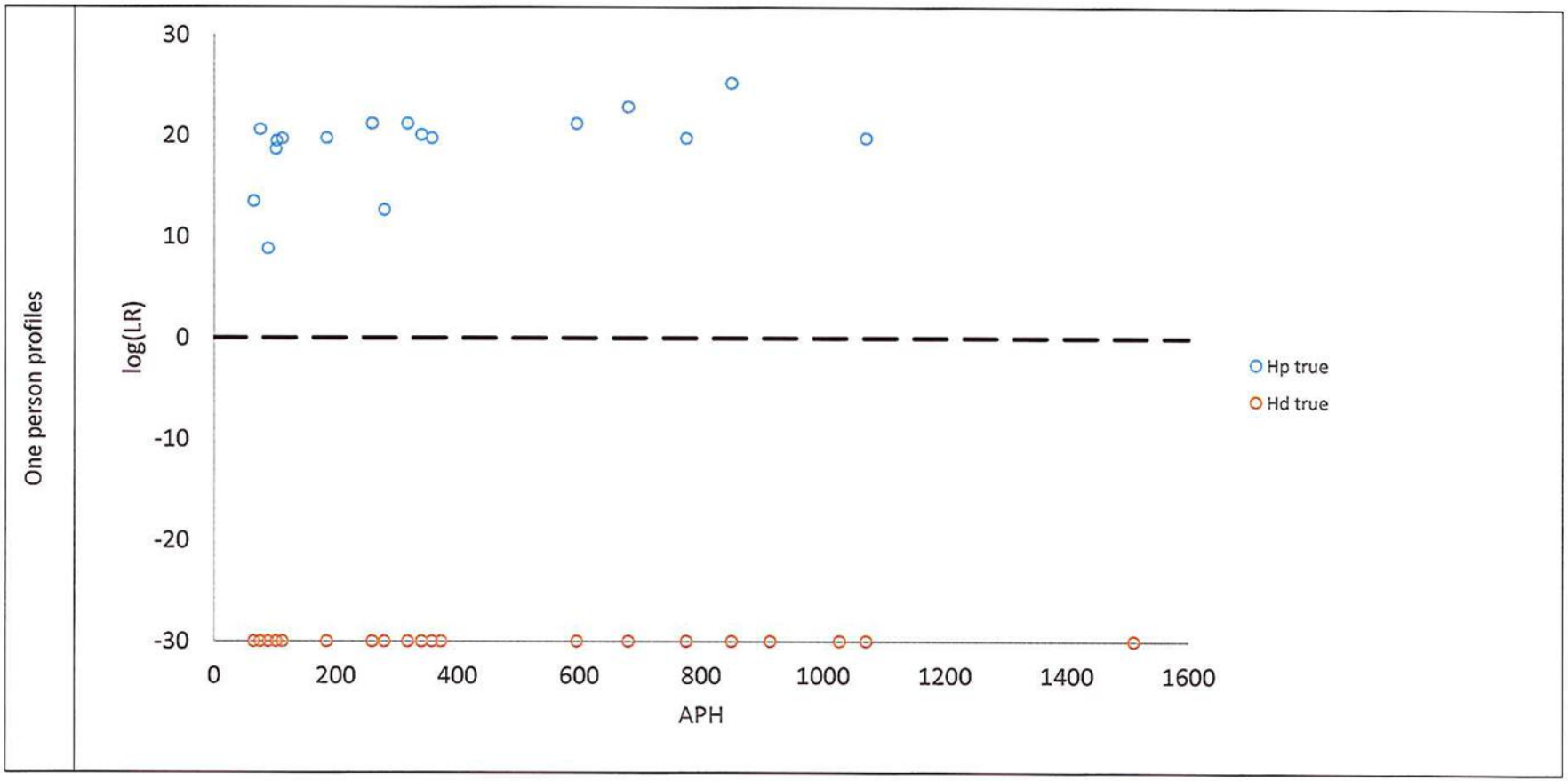
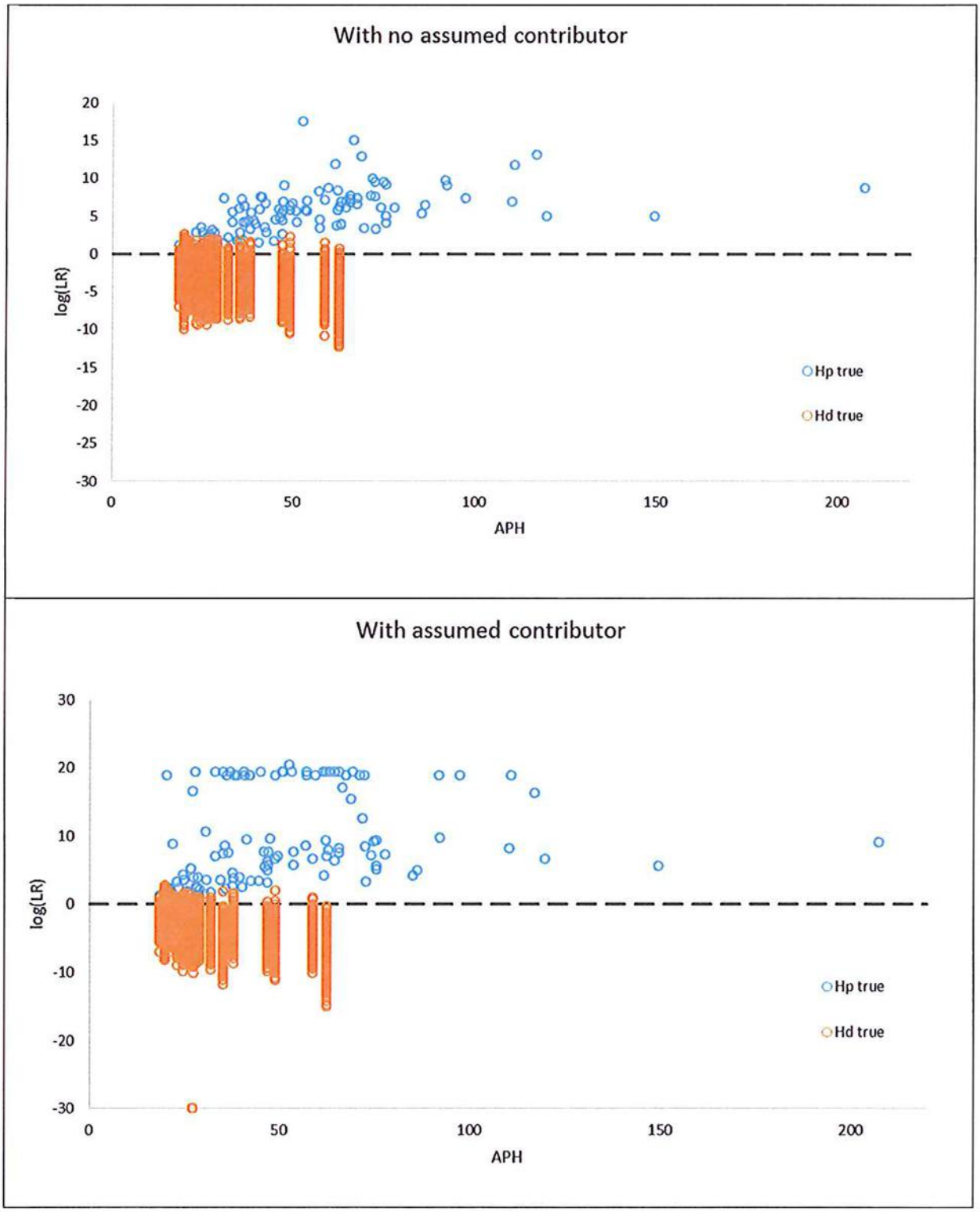

One person profiles
log(LR)
30
20
10
0
-10
-20
-30
0
200
400
600
800
1000
1200
1400
1600
APH
Hp true
Hd true

Figure 4: Plot of log(LR) versus APH for four person mixtures (top) and four person mixtures assuming one contributor (bottom)



Inspection of the plot in Figure 4 indicates that, as expected, the addition of correct conditioning profiles (known contributors under both H_p and H_d) further improves the performance shown in Figure 3. While some contributors remained at an uninformative or inconclusive LR, many of the true contributors resulted in higher LRs and some false contributors resulted in full exclusions.

Section F: Assigning number of contributors

This section covers the following standard:

> 4.1.6.4. If the number of contributors is input by the analyst, both correct and incorrect values (i.e., over- and under-estimating) should be tested.

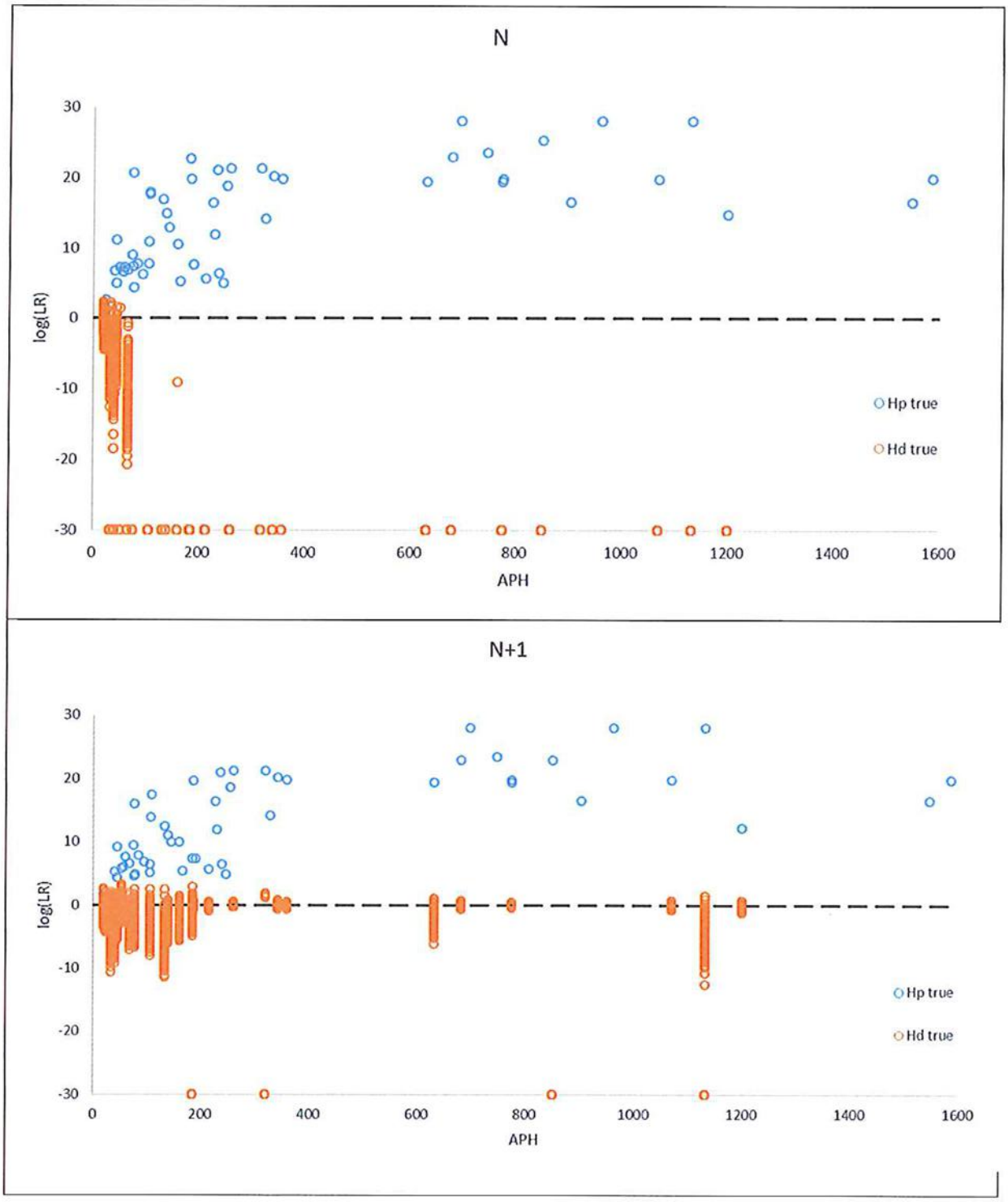
The effect of the uncertainty in the number of contributors within STRmix™ has previously been reported for a number of profiles with *N* and *N*+1 assumed contributors, where *N* is the number of contributors [3, 4]. The inclusion of an additional contributor beyond that present in the profile had the effect of lowering the *LR* for trace contributors within the profile. STRmix™ adds the additional (unseen) profile at trace levels which interacts with the known trace contribution, diffusing the genotype weights and lowering the *LR*. There was no significant effect on the *LR* of the major or minor contributor within the profiles.

The effect was tested by both increasing and decreasing the number of contributors compared with the known (*N*+1 and *N*-1 trials). The true number of contributors to a profile is always unknown. Analysts are likely to add contributors in the presence of an artefact, high stutter, or forward stutter peaks. The assumption of one fewer contributor than that actually present may be made when contributors are at very low levels and dropping out (or visible below the analytical threshold), in constructed profiles where DNA is from individuals with similar profiles at the same concentrations, or family scenarios, such as DNA from a father, mother and their child where the child was the minor contributor.

Addition of one contributor

Ten each of one, two and three person mixtures were interpreted as two, three and four person profiles, respectively. The *LR* for both the known contributors and 300 known non-contributors (as for the specificity and sensitivity studies, Section D) were calculated. The *LR* was compared for the known contributors and known non-contributors under the assumption of *N* and *N*+1 contributors. A plot of log(*LR*) versus APH for the original (assuming *N*) and *N*+1 interpretations is provided in Figure 5. Note that there are many more non-zero *LR*s for non-contributors assuming *N*+1 contributors, whereas assuming *N* most are exclusions (plotted as log(*LR*)=-30). Also note that as for Figures 3 and 4, the H_d true log(*LR*) values have been plotted against the minimum APH for a known contributor to the mixture. When assuming N+1 the additional contributor is likely to be at trace levels. The *x*-axis is intended to reflect this.

Figure 5: log(*LR*) versus APH for values for the known and non-contributors for thirty profiles assuming the correct number of contributors (top pane) and N+1 contributors (bottom pane)



Subtraction of one contributor

Eight three contributor profiles were selected that had no more than four alleles per locus. In addition, eight four contributors were selected with no more than five alleles at a locus. Each of these profiles were interpreted assuming two or three contributors, respectively (*N*-1). The *LR* for both the known contributors

and 300 known non-contributors (as for the specificity and sensitivity studies, Section D) were calculated. The propositions considered were:

H_p: The DNA originated from the person of interest (either a known contributor or one of 300 unknown contributors) and N-2 unknown individuals

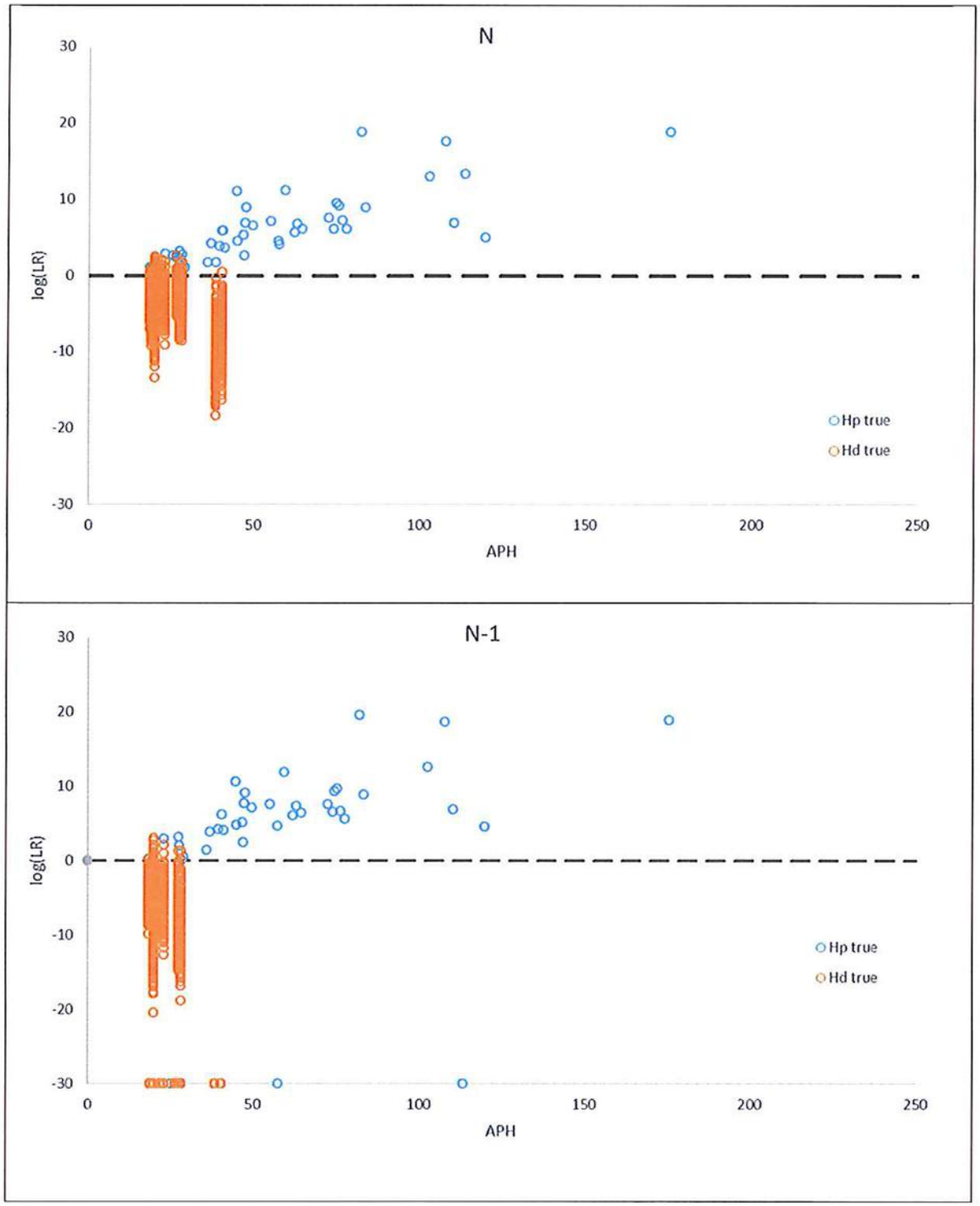
H_d: The DNA originated from N-1 unknown individuals

A summary of the original log(LR) assuming the correct number of contributors (N) and after assuming N-1 is given in Table 2. Significant differences in the log(LR) (defined as > 1 order of magnitude where log(LR)>0) have been highlighted in this table. Inspection of the values in Table 2 shows that as expected there is no significant effect on the LR for most of the contributors and any effect on mid or low level contributors is to lower the LR.

Table 2: Log(*LR*) values for three and four person mixtures assuming *N* and *N*-1 contributors

Sample	N	reference	log(LR) N	log(LR) N-1
	3	A.fsa	11.03	10.58
	3	B.fsa	2.21	0.84
1_B06_Mix_A_20_1_1_0045_004.fsa	3	D.fsa	0.04	-1.65
	3	A.fsa	3.64	4.17
	3	B.fsa	12.94	12.66
1_C06_Mix_A_20_10_1_0045_006.fsa	3	D.fsa	-0.27	-30.00
	3	A.fsa	11.12	11.91
	3	B.fsa	0.79	-0.15
1_D06_Mix_A_10_1_1_0045_008.fsa	3	D.fsa	-0.77	-2.40
	3	C.fsa	17.54	18.62
	3	E.fsa	2.56	-30.00
1_D07_Mix_B_20_1_1_0046_007.fsa	3	F.fsa	-0.66	-30.00
	3	A.fsa	7.22	6.74
	3	B.fsa	13.28	-30.00
1_E06_Mix_A_10_5_1_0045_010.fsa	3	D.fsa	1.70	-30.00
	3	C.fsa	7.10	7.65
	3	E.fsa	18.79	19.58
1_E07_Mix_B20_10_1_0046_009.fsa	3	F.fsa	-7.72	-30.00
	3	A.fsa	8.87	8.95
	3	B.fsa	5.85	-30.00
1_F06_Mix_A_5_1_1_0045_012.fsa	3	D.fsa	4.08	-30.00
	3	C.fsa	18.87	18.89
	3	E.fsa	2.11	-30.00
2_D07_Mix_B_20_1_1_0049_007.fsa	3	F.fsa	2.36	-30.00
	4	A.fsa	3.89	4.26
	4	B.fsa	9.12	9.69
	4	D.fsa	1.07	0.34
1_A02_Mix_A_5_5_1_1_0043_002.fsa	4	G.fsa	0.36	-0.47
	4	A.fsa	2.14	2.01
	4	B.fsa	6.84	7.70
	4	D.fsa	6.59	7.10
1_B02_Mix_A_5_5_5_1_0043_004.fsa	4	G.fsa	0.07	-1.15
	4	A.fsa	6.10	6.49
	4	B.fsa	8.95	9.13
	4	D.fsa	4.96	4.56
1_D02_Mix_A_5_2_2_1_0043_008.fsa	4	G.fsa	1.57	-1.29
	4	A.fsa	4.19	3.86
	4	B.fsa	9.44	9.37
	4	D.fsa	6.10	5.64
1_E03_Mix_A_2_2_2_1_0044_009.fsa	4	G.fsa	2.76	0.03
	4	A.fsa	4.49	4.73
	4	B.fsa	7.59	7.65
	4	D.fsa	5.33	5.20
1_F01_Mix_A_10_5_5_2_0043_011.fsa	4	G.fsa	2.84	2.92
	4	A.fsa	4.51	4.80
	4	B.fsa	6.07	6.53
	4	D.fsa	6.90	6.95
1_G02_Mix_A_3_2_2_1_0043_014.fsa	4	G.fsa	3.17	3.18
	4	A.fsa	5.67	6.09
	4	B.fsa	2.61	2.52
	4	D.fsa	1.03	0.56
1_H01_Mix_A_5_1_1_1_0043_015.fsa	4	G.fsa	1.56	1.26
	4	A.fsa	5.84	6.22
	4	B.fsa	6.80	7.43
	4	D.fsa	1.74	1.46
2_D01_Mix_A_10_10_10_1_0047_007.fsa	4	G.fsa	-1.38	-2.46

Figure 6: log(*LR*) versus APH for values for the known and non-contributors for 16 profiles assuming the correct number of contributors (top pane) and N-1 contributors (bottom pane)



Section G: Drop-in

This section covers the following standard:

4.1.8. Allele drop-in

Drop-in has not been observed in DFS 28 cycle Identifiler™ Plus profiles and therefore is not enabled within STRmix™.

Section H: Forward and reverse stutter

This section covers the following standard:

4.1.9. Forward and reverse stutter

STRmix™ implements a 'per allele' back stutter model. This is alternatively based on the longest uninterrupted stretch (LUS) of common repeats in the allele or the allele designation itself. Stutter peak labels are retained at analysis and within the STRmix™ input file. The modelling of stutter peaks can be seen in the interpretation of single source profiles where stutter peaks are retained at interpretation. As part of the Markov Chain Monte Carlo (MCMC) process they are considered as alleles in the genotype but those combinations are not accepted and therefore receive no weight. In mixed DNA profiles, where the minor contributor is of a similar height as the stutter peaks they start to be considered as minor alleles. This is as expected.

STRmix™ does not currently model forward (*N*+4) stutter peaks. The DFS laboratory has a validated forward stutter filter activated within GeneMapper ID-X. In theory, if a forward stutter peak is higher than the filter and retained within the STRmix™ input file it may cause an exclusionary *LR* if that allele is modelled as having originated from the person of interest. By the same mechanism, if a person of interest appeared to correspond at a minor contribution within a mixture then removing a peak in a forward stutter could also result in either a reduced *LR* or an exclusion at that particular loci. Both of these expected results have been observed in internal validation trials at DFS Laboratory. A review of the profile after deconvolution, and provided there is no issue of non-concordance, the option of ignoring that locus could be a mechanism of providing an *LR* in this scenario.

Section I: Intra-Locus peak height

This section covers the following standard:

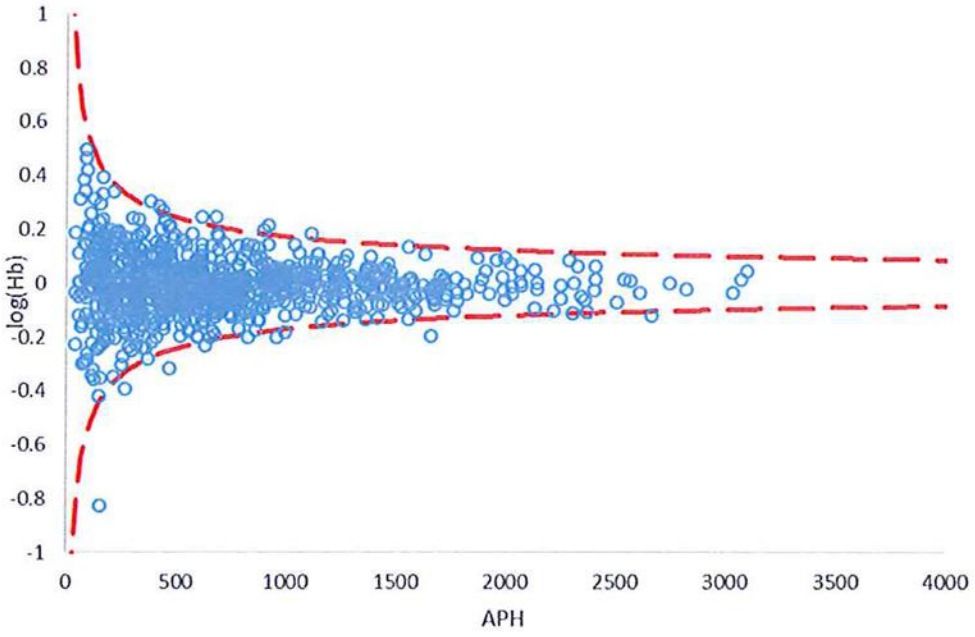
4.1.10. Intra-locus peak height variance

STRmix™ models the variability of single peaks. The variance of this model is determined by directly modelling laboratory data. This is undertaken within STRmix™ using the Model Maker function. Traditionally we investigate heterozygote balance (*Hb*), which can be thought of as the variability of two alleles at a heterozygous locus. A plot of log(*Hb*) versus average peak height (APH) of a locus demonstrates that the variability in *Hb* decreases as APH increases. The performance of Model Maker is checked by plotting the bounds informed by the Model Maker results (refer to the DFS Laboratory Part I: Estimation of STRmix™ Parameters report for further details).

The plot of log(*Hb*) versus APH and the expected 95% bounds (plotted as dotted lines) calculated by $\pm\sqrt{2}\times 1.96\times\sqrt{\frac{c^2}{APH}}$ where c^2 = 3.84, the 50th percentile from the gamma distribution, determined for

the DFS Laboratory Identifiler™ Plus data determined by Model Maker. The plot of log(*Hb*) versus APH is given in Figure 7.

Figure 7: Plot of log(*Hb*) versus APH For DFS Laboratory Identifiler™ Plus data



Section J: Inter-Locus peak heights

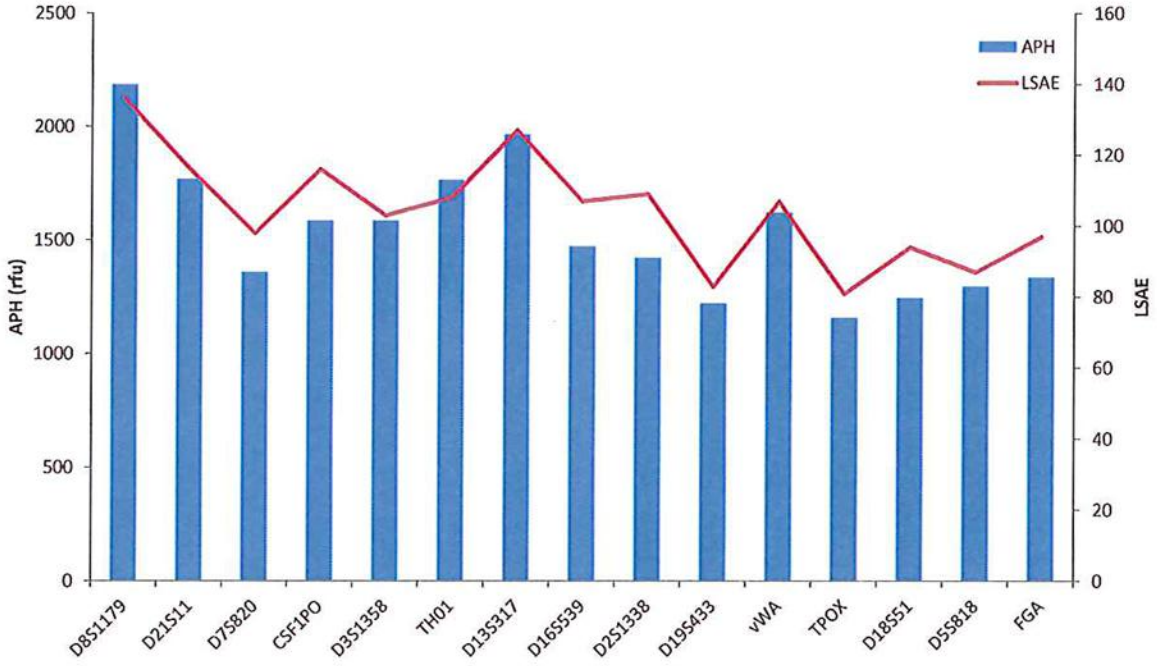
This section covers the following standard:

4.1.11. Inter-locus peak height variance

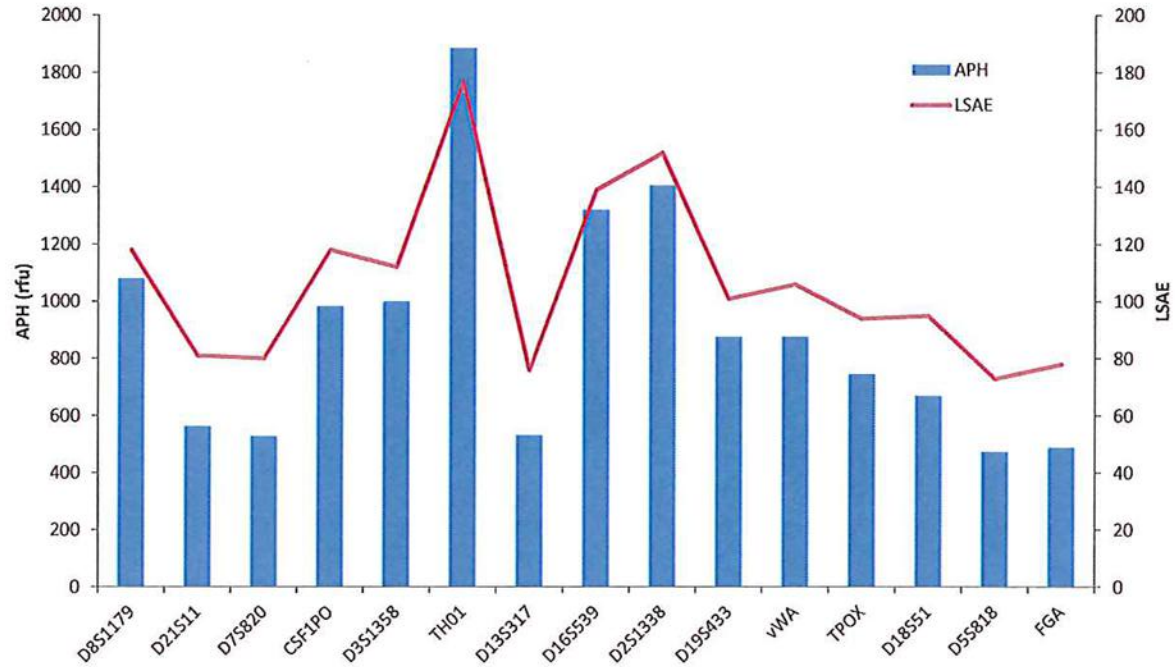
Inter locus peak variance is modelled in STRmix™ using locus specific amplification efficiencies (LSAE). The LSAE model reflects the observation that even after template DNA amount, degradation and variation in peak height within loci are modelled, the peak heights between loci are still more variable than predicted. The variance of this model is determined by directly modelling laboratory data. LSAE values for each STRmix™ interpretation appear within the results. We can demonstrate the relationship of LSAE values to average peak heights (APH) via a simple plot. The LSAE values should mimic the average peaks heights of the locus. This is demonstrated for one single source Identifiler™ Plus profile and one inhibited profile in Figure 8.

Figure 8: Plot of APH and LSAE value for each locus for a single source Identifiler™ Plus profile without inhibition (top pane) and with inhibition (bottom pane)

1_E01_STRMix01_0.8_0037_009



1_H04_1410088-0.5-2_022_016



Section K: Challenge testing

This section covers the following standard:

> 4.1.14. Additional challenge testing (e.g., the inclusion of non-allelic peaks such as bleedthrough and spikes in the typing results)

STRmix™ requires that only numeric values are retained within the input file. Any values that are not numeric (such as OL alleles not removed at analysis) will cause STRmix™ to halt the interpretation. The presence of a non-allelic peak (or peaks) that has sized within an allelic bin position and is retained within the input file can cause a number of results depending on the scenario. These include:

- An exclusionary *LR*. If the artefact is modelled as having originated from the person of interest (for example if the peak is of a similar height to the alleles corresponding to the person of interest in a mixed DNA profile) this may result in an exclusion.
- No effect. If drop-in is observed within a laboratory, the artefact may be modelled as a drop-in peak if it less than the drop-in height threshold.
- Failure to interpret. If an artefact within an allelic bin is retained in a profile it may artificially increase the minimum number of contributors within the profile. For example an artefact at a heterozygous locus in a single source profile (not modelled as stutter or drop-in) will increase the minimum number of contributors by one. STRmix™ will not proceed assuming only one contributor.

Each of these expected outcomes was demonstrated by editing an input file and calculating a *LR* within STRmix™. A summary of the effect is in the following table.

Table 3: A list of effects obtained from various scenarios where input files included one or more peaks which should have been removed.

Sample and artifact	STRmix error message
Sample A06: Two peaks that were deemed pull-up, 32.2 and 33.2, at FGA were not edited out of the STRmix input file.	Sample A06: Locus 15 in evidence cannot be explained given the parameters you have chosen. STRmix will now exit.
Sample A08: Two peaks that were deemed pull-up, 20.2 and 32.2, at FGA were not edited out of the STRmix input file.	Sample A08: produced a run report with the correct allele calls for the major contributor, however the pull up peaks at the non-edited loci were deemed to be the minor contributor's alleles by the software program.
Sample B01: One peak that was deemed pull-up, 17, at D5S818 was not edited out of the STRmix input file. In addition one peak that was deemed pull-up, 20.2, at FGA was not edited out of the STRmix input file.	Sample B01: Locus 14 in evidence cannot be explained given the parameters you have chosen. STRmix will now exit.
Sample C01: Two peaks (6.3 and 7.3, both minus A), at TH01 were not edited out of the STRmix input file. One peak deemed N+4, 14, at D16S539 was not edited out of the STRmix input file. One peak deemed N-8, 22, at D2S1338 was not edited out of the STRmix input file. One peak deemed pull-up, 17, at vWA was not edited out of the	Sample C01: Locus 6 in evidence cannot be explained given the parameters you have chosen. STRmix will now exit.

STRmix input file.	
Sample E01: One peak deemed N+4, 14, at D16S539 was not edited out of the STRmix input file.*	Sample E01: Warning an error occurred while executing analysis.
Sample G06: One peak deemed an off-ladder, OL, at TPOX was not edited out of the STRmix input file.	Sample G06: Analysis completed by software. Evidence input section shows loci after TPOX are blank. TPOX locus includes allele prior to OL, no height associated with allele. Software gives weight of 1 to both contributors for 8,8 homozygote.
1_E07_MixB_20_10_1_0046_009 from 0.5ng 3-person mixture study: One peak, 13.3 at TH01, designated a spike was not edited out of input file.	1_E07_MixB_20_10_1_0046_009 from 0.5ng 3-person mixture study: STRmix analysis completed normally. TH01 locus resulted in inaccurate LR favouring H_d.

*The N+4 peak was observed just below the analytical threshold. It was included in the chart as an example of the type of result which would be obtained from this type of occurrence.

Section L: Casework profiles

This section covers the following standards:

4.2. Laboratories with existing interpretation procedures should compare the results of probabilistic genotyping and of manual interpretation of the same data, notwithstanding the fact that probabilistic genotyping is inherently different from and not directly comparable to binary interpretation. The weights of evidence that are generated by these two approaches are based on different assumptions, thresholds and formulae. However, such a comparison should be conducted and evaluated for general consistency.

4.2.1. The laboratory should determine whether the results produced by the probabilistic genotyping software are intuitive and consistent with expectations based on non-probabilistic mixture analysis methods.

4.2.1.1. Generally, known specimens that are included based on non-probabilistic analyses would be expected to also be included based on probabilistic genotyping.

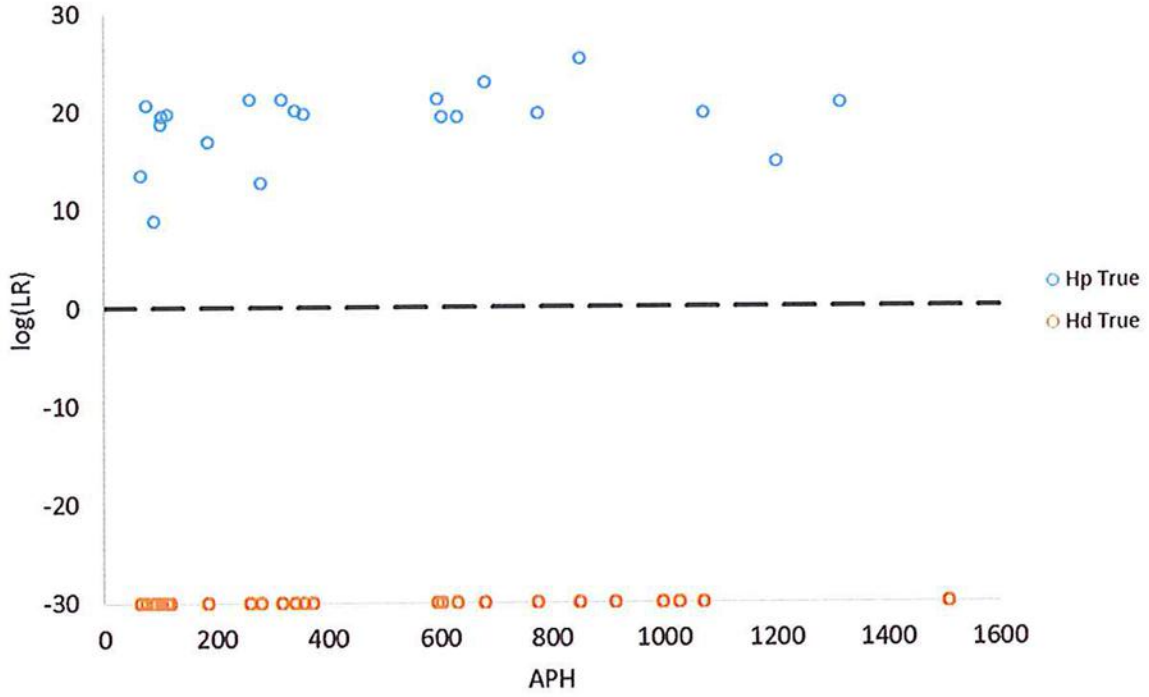
4.1.7. Partial profiles, to include the following:

4.1.7.2. DNA degradation

4.1.7.3. Inhibition

Twenty five inhibited, degraded and mock forensic samples were interpreted and compared to both known contributors and 300 known non-contributors. The profiles were single source and two person mixtures. The known contributors had previously been included using DFS validated non-probabilistic methods. A plot of log(LR) versus APH for the known and non-contributor comparisons are provided in Figure 9. All non-contributors were excluded with LR=0.

Figure 9: Plot of log(LR) versus APH for inhibited, degraded and mock forensic samples



Section M: Precision

This section covers the following standard:

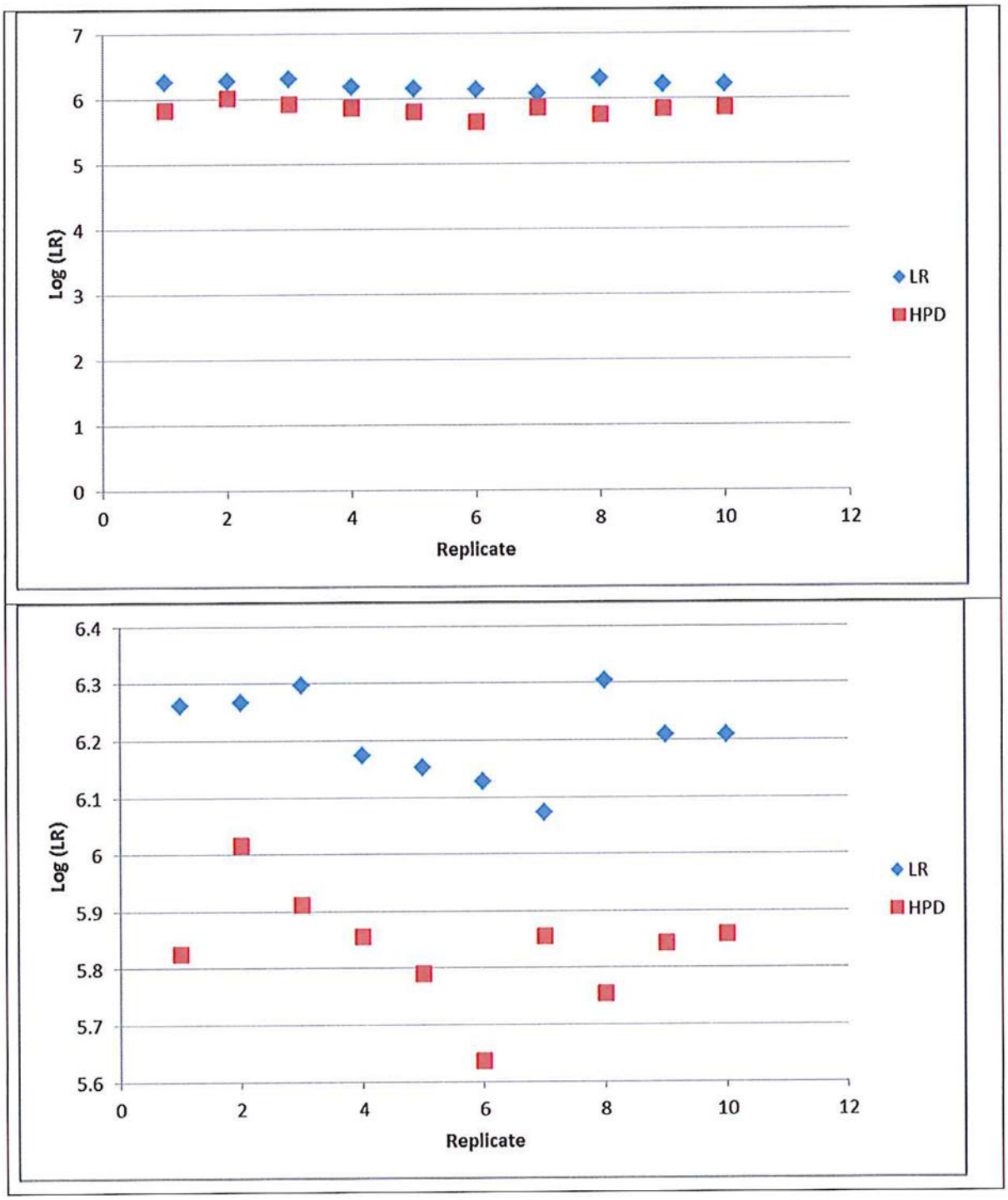
4.1.13. Sensitivity, specificity and precision, as described for Developmental Validation

Refer to section D above for details of sensitivity and specificity tests.

The MCMC process is used to generate the weights within STRmix™ for different genotype combinations. This is a sampling procedure and therefore the weights will vary slightly between each run. The variability in *LR*s between replicate interpretations has previously been explored [6]. The MCMC process was shown to be a small source of variability compared with other lab variables including the polymerase chain reaction (PCR) and capillary electrophoresis (CE) process. The variability due to the size of the allele frequency database and the MCMC process is taken into account within STRmix™ V2.3 using the highest posterior density (HPD) method [7-9] (a type of confidence interval).

The extent of STRmix™ run variability was investigated by DFS Laboratory by interpreting one of the mixed DNA profiles from Section D (1_B07_Mix_A_3_1_1_0046_003.fsa) where there was ambiguity in the genotype combinations, ten times. A plot of log(*LR*) from the DFS Identifiler Caucasian database for each replicate is given in Figure 10. The blue circles indicate the *LR* values and the red circles are the lower 99% bound of the HPD.

Figure 10: Plot of replicate log(*LR*) demonstrating reproducibility of STRmix™ (top pane) and zoom of Y axis (bottom pane)

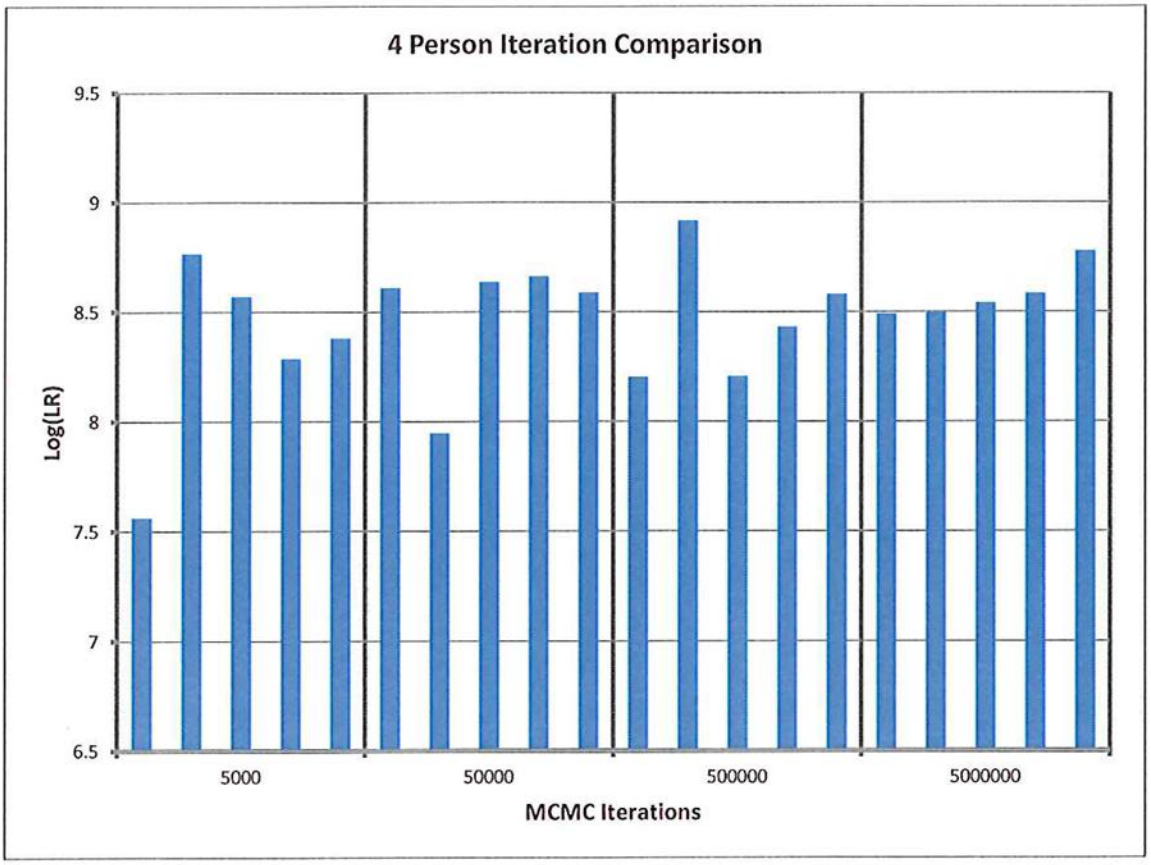


Inspection of Figure 10 shows that the *LR*s are very reproducible and that the lower 99% bound of the HPD is always below the *LR* values.

Parameters within STRmix™ that affect run variability include the number of iterations and the RWSD (random walk standard deviation). The default number of iterations is set to 100,000 burn-in and 400,000 post burn-in. These will be suitable for many different types of profiles. Decreasing the number of

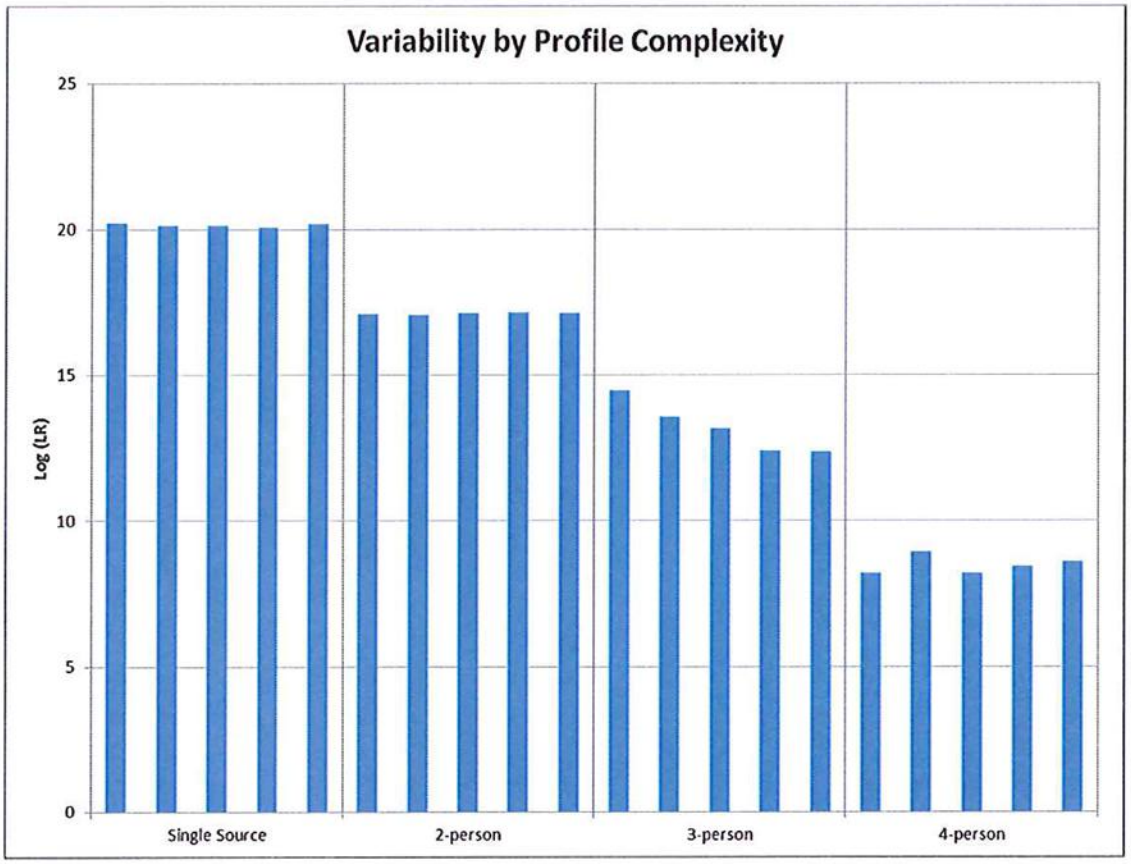
iterations may mean that STRmix™ has not converged and more variability is expected. Increasing the number of iterations may mean convergence is achieved (if it hasn't already) and will certainly mean higher run times. Four samples (single source, two person mixture, three person mixture and four person mixture) were interpreted using four different sets of iterations (total 5000, 50,000, 500,000 and 5,000,000) five times each. A plot of log(*LR*) for each replicate of the four person mixture is given in Figure 11.

Figure 11: Log(*LR*) using HPD of the Identifiler African American database is plotted below for a complex four person mixture interpreted five times in STRmix™ using different numbers of iterations



Data was also compiled to demonstrate that variability will increase as the complexity of the mixture increases. Refer to the figure below for the Log(*LR*) using HPD of the Identifiler African American database for a single source, two person, three person and four person mixtures interpreted five times in STRmix™ using the recommended 500,000 iterations.

Figure 12: Log(LR) using HPD of the African American database for single source, two person, three person and four person mixtures at 500,000 iterations.



Section N: NIST SRM 2391c – NIST D

As a part of the required annual testing of the NIST SRM 2391c, a mixture sample (NIST D) was run through STRmix™ to verify concordance between the software and expected results from other laboratories. Results, including the deconvolution, comparison and likelihood ratio calculation, were reviewed and determined to be accurate and appropriate.

For details regarding the testing in this section, please see the "NIST 2015" folder located with the Forensic Biology Unit's Quality Assurance documents.

Conclusion

This document describes the DFS Laboratory's internal validation activities for STRmix™ V2.3. It has been shown that STRmix™ V2.3 is suited for its intended use for the interpretation of profiles generated from crime scene samples.

Based on the studies conducted for this validation, two overall recommendations are made for the implementation of STRmix™ V2.3 at the DFS Forensic Biology Unit: 1) the use of a verbal scale for evidence interpretation published in Essential Mathematics and Statistics for Forensic Science by Craig Adam (2010) on page 289 in order to provide context to the likelihood ratio; and 2) the high AT GMID-X analysis method described in the Parameters portion of the validation will be used for all samples, regardless of peak height, as the variance values used in Model Maker are based on this analysis method. Also this method will provide a more efficient approach to data analysis in case processing.

The following summary lists the limitations of the software and recommendations for use in forensic DNA casework. This section is designed to help provide documentation for the connection of validation to standard operating procedures and analyst training.

Section A: Single source profiles

Likelihood ratios for known contributors decrease with lower templates. Therefore, STRmix™ is giving more weight to possible genotypes that include dropout. Additionally, the likelihood ratios calculated by STRmix™ were verified with the published formulas using Microsoft Excel.

Section B: Use of peak heights

If a single source sample is saturated (peaks above 7000 rfu), STRmix™ will correctly interpret the profile qualitatively.

LIMITATION: Because STRmix™ uses stutter and allele peak heights, mixed samples will not be properly interpreted if peak heights are saturated.

RECOMMENDATION: Where practicable, mixed samples which are saturated should be reamplified at a lower template and run.

Section C: Weights

STRmix™ appropriately decreased the likelihood ratio/weights as the ability to define a contributor decreased. With two person mixtures, a decrease in likelihood ratio was observed when the major contributor was 80% or less and when the minor contributor was 3-7%.

Section D: Sensitivity and specificity and mixtures

Sensitivity – The ability of the software to reliably resolve the DNA profile of known contributors within a mixed DNA profile for a range of starting DNA templates.

Specificity – The ability of the software to reliably exclude known non-contributors within a mixed DNA profile for a range of starting DNA templates.

LIMITATION: Based on the samples run, false inclusions and exclusions can occur with low level contributors in two, three and four person mixtures. Regardless of the template quantity, no false inclusions or exclusions were observed for single source samples. Because validation samples are specifically chosen to create mixtures with varying alleles, it is expected for casework samples to show a slightly larger range of false inclusions and exclusions.

RECOMMENDATION: Prior to implementation in casework, all analysts will be required to read the STRmix™ validation and understand the potential for false inclusions and false exclusions at low APH.

Section E: Alternate propositions

Assuming a known contributor can improve the performance of the software especially at lower template amounts. It is critical that any assumptions made while interpreting a profile are clearly documented.

Section F: Assigning number of contributors

Adding a contributor lowered the likelihood ratio for trace contributors but had no significant effect on the major. There were some false inclusions, however, the likelihood ratios were within the general values observed in Section D.

Subtracting a contributor slightly lowered the likelihood ratio and led to false exclusions. This situation is of lesser concern in forensics because it favors the defendant. Additionally, the correct likelihood ratios were within the values observed in Section D.

LIMITATION: The true number of contributors is never known for evidence profiles. Incorrectly assuming a number of contributors which is above or below the correct number of contributors may lead to slightly lower likelihood ratios and false inclusions/exclusions (values above one/values below one).

RECOMMENDATION: Evidence profiles will be carefully evaluated to determine number of contributors. If an analyst cannot be confident in assigning the number of contributors to a profile, multiple propositions may be calculated or the entire profile may be deemed inconclusive.

Section G: Drop-in (N/A)

Section H: Forward and reverse stutter

STRmix™ correctly models reverse stutter but not forward stutter. A true stutter peak above the expected value may produce a false exclusion and true alleles eliminated due to stutter position may result in either a reduced likelihood ratio or an exclusion. For examples of this, see Section K.

Section I: Intra-Locus peak height

Model maker results were verified with regard to heterozygote balance and approximate peak height. As expected, heterozygote balance is more variable at lower peak heights.

Section J: Inter-Locus peak height

Model maker results were verified for locus specific amplification efficiencies (LSAE). Average peak heights for a profile with and without inhibition were compared to LSAE results to demonstrate concordance.

Section K: Challenge testing

Five of seven samples with artifacts that were left in imported text files produced software error messages or clear indications of an error during the interpretation. However, two of seven produced results which may lead to false exclusion. All of the seven samples contained artifacts which were easily identified but could be missed during analysis. During validation, it was determined that most of the time software errors are due to user errors during analysis.

LIMITATION: Artifacts or peaks in stutter position should be closely evaluated and carefully eliminated. Errors in the text files may result in STRmix™ errors or false exclusions.

RECOMMENDATION: During review of STRmix™ results, weights and likelihood ratios should be carefully evaluated to make sure they are intuitively correct. If one locus produces a significantly different result than all others, re-evaluate the locus to determine if stutter may be an issue. If a peak in stutter position is unable to be identified as stutter, the profile can be re-run by ignoring that locus. If a peak in stutter position is identified as stutter, the text file can be corrected and profile re-run. Extreme caution should be used for profiles where the minor contributor peak heights are at or around stutter peak heights.

Section L: Casework profiles

25 inhibited, degraded and mock casework samples were interpreted and compared. Concordant results were obtained for known contributors and non-contributors when compared to historic DFS interpretation methods.

Section M: Precision

A three person mixture with ambiguity in the genotype combinations was run ten times. As expected, STRmix™ did not give the same likelihood ratio each time, however, the variability was low (within a factor of two). Additionally, the highest posterior density (HPD) was always lower than the likelihood ratio demonstrating its ability to account for sampling variation in the allele frequency database. Its variability was also low (within a factor of two).

A single source, two person, three person and four person mixture were all run at different iterations. Lower iterations produced more variability than higher iterations, but higher iterations had significantly longer run times.

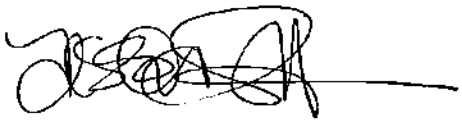
LIMITATION: Variability in the likelihood ratio is not only affected by the complexity of the profile, but also the chosen number of iterations.

RECOMMENDATION: Run all samples at the default setting of 500,000 total iterations (100,000 burn-in). This will result in the least amount of variability with a reasonable run time. Lowering the number of iterations may be used for single source profiles with good peak heights where variability is expected to be extremely low. Raising the iterations may be needed for highly complex profiles to reduce variability, however run times will be significant. It is recommended to obtain technical leader approval for iterations other than 500,000.

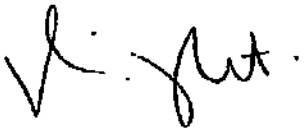
Section N: NIST SRM 2391c – NIST D

A mixture sample from the NIST SRM 2391c produced accurate and appropriate results.

Signatures



Jessica Skillman, Forensic Scientist III, DFS Laboratory STRmix™ implementation manager



Jo-Anne Bright, STRmix™ Technical Development team

This work has been reviewed and it has been determined that STRmix™ V2.3 is suitable for its intended use for interpretation of crime profiles at DFS Laboratory. The project work has met the validation requirements as required by DFS standard operating procedures, ISO/IEC 17025 and the guidelines published by SWGDAM.

Susan Welti, DFS Laboratory FBU Technical Leader

Additional support for this validation was provided by Andrew Feiter (Forensic Scientist I) and Yoelia Perez (Forensic Scientist Technician).

References

[1] Taylor D, Bright J-A, Buckleton JS. The interpretation of single source and mixed DNA profiles Forensic Science International: Genetics. 2013;7:516-28.

[2] Bright J-A, Evett IW, Taylor D, Curran JM, Buckleton J. A series of recommended tests when validating probabilistic DNA profile interpretation software. Forensic Science International: Genetics. 2015;14:125-31.

[3] Balding DJ, Nichols RA. DNA profile match probability calculation: how to allow for population stratification, relatedness, database selection and single bands. Forensic Science International. 1994;64:125-40.

[4] National Research Council II. National Research Council Committee on DNA Forensic Science, The Evaluation of Forensic DNA Evidence. Washington, D.C.: National Academy Press; 1996.

[5] Taylor D. Using continuous DNA interpretation methods to revisit likelihood ratio behaviour. Forensic Science International: Genetics. 2014;11:144-53.

[6] Bright J-A, Stevenson KE, Curran JM, Buckleton JS. The variability in likelihood ratios due to different mechanisms. Forensic Science International: Genetics. 2015;14:187-90.

[7] Taylor D, Bright J-A, Buckleton J, Curran J. An illustration of the effect of various sources of uncertainty on DNA likelihood ratio calculations. Forensic Science International: Genetics. 2014;11:56-63.

[8] Triggs CM, Curran JM. The sensitivity of the Bayesian HPD method to the choice of prior. Science & Justice. 2006;46:169-78.

[9] Curran JM, Buckleton JS. An investigation into the performance of methods for adjusting for sampling uncertainty in DNA likelihood ratio calculations. Forensic Science International: Genetics. 2011;5:512-6.

[10] Scientific Working Group on DNA Analysis Methods, Guidelines for the Validation of Probabilistic Genotyping Systems, 06/15/2015.

APPENDIX 1: List of papers that support STRmix™

The following is a list of papers that directly support STRmix™.

1. D. Taylor, J.-A. Bright and J.S. Buckleton, The interpretation of single source and mixed DNA profiles. Forensic Science International: Genetics, 2013 7(5): 516-528 **(Core maths paper)**
2. J.-A. Bright, D. Taylor, J.M. Curran and J.S. Buckleton, Developing allelic and stutter peak height models for a continuous method of DNA interpretation. Forensic Science International: Genetics, 2013. 7(2): 296-304 **(Core models paper)**
3. J.-A. Bright, D. Taylor, J.M. Curran and J.S. Buckleton, Degradation of forensic DNA profiles, Australian Journal of Forensic Sciences, 2013. 45(4): 445-449
4. D. Taylor. Using continuous DNA interpretation methods to revisit likelihood ratio behaviour. Forensic Science International: Genetics, 2014. 11: 144-153
5. J.-A. Bright, D. Taylor, J.M. Curran and J.S. Buckleton, Searching mixed DNA profiles directly against profile databases. Forensic Science International: Genetics, 2014. 9: 102-110
6. D. Taylor, J.-A. Bright, J.S. Buckleton, J. Curran, An illustration of the effect of various sources of uncertainty on DNA likelihood ratio calculations. Forensic Science International: Genetics, 2014. 11: 56–63
7. J.-A. Bright, J.M. Curran and J.S. Buckleton, The effect of the uncertainty in the number of contributors to mixed DNA profiles on profile interpretation. Forensic Science International: Genetics, 2014. 12: 208-214
8. J.-A. Bright, K.E. Stevenson, J.M. Curran and J.S. Buckleton, The variability in likelihood ratios due to different mechanisms. Forensic Science International: Genetics, 2015. 14:187-190
9. D .Taylor, J.-A. Bright and J.S. Buckleton, Considering relatives when assessing the evidential strength of mixed DNA profiles. Forensic Science International: Genetics, 2014. 13: 259-263
10. D. Taylor, J.-A. Bright and J.S. Buckleton. Interpreting forensic DNA profiling evidence without specifying the number of contributors. Forensic Science International: Genetics, 2014. 13: 269-280

The following is a subset of other papers that support the theory within STRmix™:

1. J.-A. Bright, J.M. Curran. Investigation into stutter ratio variability between different laboratories. Forensic Science International: Genetics, 2014. 13: 79-81
2. C. Brookes, J.-A. Bright, S.A. Harbison, and J.S. Buckleton, Characterising stutter in forensic STR multiplexes. Forensic Science International: Genetics, 2012. 6(1): 58-63
3. H. Kelly, J.-A. Bright, J.M. Curran, and J.S. Buckleton Identifying and modelling the drivers of stutter in forensic DNA profiles. Australian Journal of Forensic Sciences, 2014. 46(2): 194-203
4. J.-A. Bright, S. Neville, J.M. Curran, and J.S. Buckleton. Variability of mixed DNA profiles separated on a 3130 and 3500 capillary electrophoresis instrument. Australian Journal of Forensic Sciences, 2014. 46(3): 304-312
5. J.-A. Bright, K.E. Stevenson, M.D. Coble, C.R. Hill, J.M. Curran, and J.S. Buckleton Bright, Characterising the STR locus D6S1043 and examination of its effect on stutter rates. Forensic Science International: Genetics, 2014. 8(1): p. 20-23.
6. D. Taylor, J.S. Buckleton. Do low template DNA profiles have useful quantitative data? Forensic Science International: Genetics, 2015. 16: 13-16.

The following is a subset of other papers that support the validation and use of STRmix™:

1. J.-A. Bright, I.W. Evett, D. Taylor, J.M. Curran and J.S. Buckleton, A series of recommended tests when validating probabilistic DNA profile interpretation software. Forensic Science International: Genetics, 2015. 14: 125-131
2. T.W. Bille, S.M. Weitz, M.D. Coble, J.S. Buckleton, J.-A. Bright. Comparison of the performance of different models for the interpretation of low level mixed DNA profiles. ELECTROPHORESIS. 2014;35:3125-33.
3. S.J. Cooper, C.E. McGovern, J.-A. Bright, D. Taylor, J.S. Buckleton. Investigating a common approach to DNA profile interpretation using probabilistic software. Forensic Science International: Genetics, 2014. 16: 121-131.

APPENDIX 2: Cross reference for document sections and SWGDAM recommendations

Standard	Text	Refer section
4.1	Test the system using representative data	Preamble
4.1.1	Specimens with known contributors	Preamble
4.1.2	Hypothesis testing with contributors and non-contributors	D
4.1.2.1	More than one set of hypotheses	E
4.1.3	Variable DNA typing conditions	Preamble
4.1.4	Allelic peak height, to include off-scale peaks	B
4.1.5	Single-source specimens	A
4.1.6	Mixed specimens	D
4.1.6.1	Various contributor ratios	D
4.1.6.2	Various total DNA template quantities	D
4.1.6.3	Various numbers of contributors	D
4.1.6.4	Both correct and incorrect number of contributors (i.e., over- and under-estimating)	F
4.1.6.5	Sharing of alleles among contributors	D
4.1.7	Partial profiles	D
4.1.7.1	Allele and locus drop-out	D
4.1.7.2	DNA degradation	L
4.1.7.3	Inhibition	L
4.1.8	Allele drop-in	G
4.1.9	Forward and reverse stutter	H
4.1.10	Intra-locus peak height variance	I
4.1.11	Inter-locus peak height variance	J
4.1.12	In-house parameters	Preamble
4.1.13	Sensitivity, specificity and precision	D and M
4.1.14	Additional challenge testing	K
4.2	Compare the results of probabilistic genotyping and of manual interpretation	L
4.2.1	Intuitive and consistent with expectations	L
4.2.1.1	Known specimens that are included based on non-probabilistic analyses would be expected to also be included based on probabilistic genotyping	L
4.2.1.2	Concordance of single-source specimens with high quality results	A
4.2.1.3	Generally, as the analyst's ability to deconvolute a complex mixture decreases, so does the weighting of a genotype set determined by the software	C

APPENDIX 3: Summary of profiles analysed as part of the sensitivity and specificity plots, Section D

Single source profiles

	Sample	Reference	log(LR)	APH
Single source profiles	1_B02_14-01513-MARROW_10_0462_004.fsa	1_F07_14-01513-BLOOD_0465_011.fsa	21.21	597
	1_B03_14-01553-TOOTH_0463_003.fsa	1_H07_14-01553-BLOOD_0465_015.fsa	21.21	261
	1_B05_14-01553-BONE_10_0464_003.fsa	1_H07_14-01553-BLOOD_0465_015.fsa	20.62	77
	1_C02_14-01513-MARROW_100_0462_006.fsa	1_F07_14-01513-BLOOD_0465_011.fsa	8.81	90
	1_C04_14-01450-BONE_10_0463_006.fsa	1_E07_14-01450-BLOOD_0465_009.fsa	18.68	102
	1_C06_1410088-0.0625-3_0023_006.fsa	1_B04_NL-1.0-3_0600_004.fsa	19.70	113
	1_D02_14-01553-MARROW_0462_008.fsa	1_H07_14-01553-BLOOD_0465_015.fsa	21.21	319
	1_D04_1410088-1.0-1_0022_008.fsa	1_B04_NL-1.0-3_0600_004.fsa	19.74	1071
	1_D05_1410088-0.25-2_0023_007.fsa	1_B04_NL-1.0-3_0600_004.fsa	19.74	359
	1_E02_14-01450-TOOTH_0462_010.fsa	1_E07_14-01450-BLOOD_0465_009.fsa	20.09	342
	1_E06_1410088-0.03125-2_0023_010.fsa	1_B04_NL-1.0-3_0600_004.fsa	13.51	66
	1_G02_14-01524-TOOTH_0462_014.fsa	1_G07_14-01524-BLOOD_0465_013.fsa	19.46	104
	1_G03_14-01524-TISSUE_0463_013.fsa	1_G07_14-01524-BLOOD_0465_013.fsa	12.67	281
	1_H04_1410088-0.5-2_0022_016.fsa	1_B04_NL-1.0-3_0600_004.fsa	19.74	776
	1_H05_1410088-0.125-3_0023_015.fsa	1_B04_NL-1.0-3_0600_004.fsa	16.91	186
	2_B01_10-573-JS-COMP-3-1_1313_003.fsa	1_C03_10-573-JS-COMP-2_1312_005.fsa	22.85	681
	5_F01_15-582-JS-4_0612_011.fsa	1_C01_15-582-JS-2_0620_005.fsa	25.25	851

Two person mixtures

	Sample	Reference	log(LR)	APH
Two person mixtures	1_A02_1108D_1113D_1_15_R2_0299_002.fsa	1_A04_1000D_1113D.fsa	16.48	905.17
	1_A02_1108D_1113D_1_15_R2_0299_002.fsa	1_A04_1001D_1108D.fsa	7.12	52.50
	1_A02_1113D_1108D_1_15_R2_0293_002.fsa	1_A04_1001D_1108D.fsa	27.99	698.00
	1_A02_1113D_1108D_1_15_R2_0293_002.fsa	1_A04_1000D_1113D.fsa	7.68	106.71
	1_A06_1001D_1000D_1_7_R2_0792_002.fsa	1_A04_1001D_1108D.fsa	22.50	184.14
	1_A06_1001D_1000D_1_7_R2_0792_002.fsa	1_A04_1000D_1113D.fsa	16.48	1549.08
	1_A06_1004D_1005D_1_7_R2_0797_002.fsa	1_C07_1004D_1111D.fsa	17.80	182.83
	1_A06_1004D_1005D_1_7_R2_0797_002.fsa	1_D04_1005D_1115D.fsa	17.79	1086.97
	1_A06_1107D_1114D_1_7_R2_0295_002.fsa	1_A04_1003D_1114D.fsa	19.36	809.67
	1_A06_1107D_1114D_1_7_R2_0295_002.fsa	1_C07_1002D_1107D.fsa	16.07	135.15
	1_A06_1114D_1107D_1_7_R2_0301_002.fsa	1_C07_1002D_1107D.fsa	19.77	869.30
	1_A06_1114D_1107D_1_7_R2_0301_002.fsa	1_A04_1003D_1114D.fsa	17.19	139.50
	1_A08_1002D_1003D_1_20_R2_0793_002.fsa	1_A04_1003D_1114D.fsa	19.36	1927.33

	1_A08_1002D_1003D_1_20_R2_0793_002.fsa	1_C07_1002D_1107D.fsa	9.09	112.93
	1_A08_1005D_1004D_1_20_R2_0798_002.fsa	1_C07_1004D_1111D.fsa	23.42	1287.29
	1_A08_1005D_1004D_1_20_R2_0798_002.fsa	1_D04_1005D_1115D.fsa	6.03	94.93
	1_A08_1111D_1115D_1_20_R2_0296_002.fsa	1_D04_1005D_1115D.fsa	17.79	973.70
	1_A08_1111D_1115D_1_20_R2_0296_002.fsa	1_C07_1004D_1111D.fsa	3.26	49.00
	1_A08_1115D_1111D_1_20_R2_0302_002.fsa	1_C07_1004D_1111D.fsa	23.42	665.63
	1_A08_1115D_1111D_1_20_R2_0302_002.fsa	1_D04_1005D_1115D.fsa	6.08	77.28
	1_A10_1002D_1003D_1_1_R2_0794_002.fsa	1_C07_1002D_1107D.fsa	10.51	849.45
	1_A10_1002D_1003D_1_1_R2_0794_002.fsa	1_A04_1003D_1114D.fsa	10.11	959.17
	1_A10_1005D_1004D_1_1_R2_0799_002.fsa	1_C07_1004D_1111D.fsa	13.97	624.63
	1_A10_1005D_1004D_1_1_R2_0799_002.fsa	1_D04_1005D_1115D.fsa	8.35	523.07
	1_A10_1111D_1115D_1_1_R2_0297_002.fsa	1_C07_1004D_1111D.fsa	20.63	337.13
	1_A10_1111D_1115D_1_1_R2_0297_002.fsa	1_D04_1005D_1115D.fsa	15.06	514.10
	1_A10_1115D_1111D_1_1_R2_0303_002.fsa	1_C07_1004D_1111D.fsa	15.99	363.58
	1_A10_1115D_1111D_1_1_R2_0303_002.fsa	1_D04_1005D_1115D.fsa	11.00	489.00
	1_B01_14-575-JS-3-1EF_0462_003.fsa	1_B07_14-575-JS-1_0465_003.fsa	14.74	1202.00
	1_C03_1000D_1001D_1_3_R2_0791_005.fsa	1_A04_1001D_1108D.fsa	27.86	1145.29
	1_C03_1000D_1001D_1_3_R2_0791_005.fsa	1_A04_1000D_1113D.fsa	16.29	440.25
	1_C03_1003D_1002D_1_3_R2_0796_005.fsa	1_C07_1002D_1107D.fsa	19.17	1283.35
	1_C03_1003D_1002D_1_3_R2_0796_005.fsa	1_A04_1003D_1114D.fsa	18.74	476.83
	1_C03_1108D_1113D_1_3_R2_0300_005.fsa	1_A04_1001D_1108D.fsa	23.31	288.57
	1_C03_1108D_1113D_1_3_R2_0300_005.fsa	1_A04_1000D_1113D.fsa	16.03	813.42
	1_C03_1113D_1108D_1_3_R2_0294_005.fsa	1_A04_1001D_1108D.fsa	27.99	759.21
	1_C03_1113D_1108D_1_3_R2_0294_005.fsa	1_A04_1000D_1113D.fsa	14.61	214.58
	1_C05_1001D_1000D_1_15_R2_0792_005.fsa	1_A04_1000D_1113D.fsa	16.48	1870.08
	1_C05_1004D_1005D_1_15_R2_0797_005.fsa	1_D04_1005D_1115D.fsa	17.79	1499.33
	1_C05_1004D_1005D_1_15_R2_0797_005.fsa	1_C07_1004D_1111D.fsa	16.82	120.20
	1_C05_1107D_1114D_1_15_R2_0295_005.fsa	1_A04_1003D_1114D.fsa	19.36	1285.83
	1_C05_1107D_1114D_1_15_R2_0295_005.fsa	1_C07_1002D_1107D.fsa	7.74	86.50
	1_C05_1114D_1107D_1_15_R2_0301_005.fsa	1_C07_1002D_1107D.fsa	19.77	1214.05
	1_C05_1114D_1107D_1_15_R2_0301_005.fsa	1_A04_1003D_1114D.fsa	7.45	148.13
	1_C09_1002D_1003D_1_7_R2_0794_005.fsa	1_C07_1002D_1107D.fsa	19.43	235.85
	1_C09_1002D_1003D_1_7_R2_0794_005.fsa	1_A04_1003D_1114D.fsa	19.36	1955.50
	1_C09_1005D_1004D_1_7_R2_0799_005.fsa	1_C07_1004D_1111D.fsa	23.42	1483.71
	1_C09_1005D_1004D_1_7_R2_0799_005.fsa	1_D04_1005D_1115D.fsa	16.63	233.37
	1_C09_1111D_1115D_1_7_R2_0297_005.fsa	1_D04_1005D_1115D.fsa	17.79	1118.77
	1_C09_1111D_1115D_1_7_R2_0297_005.fsa	1_C07_1004D_1111D.fsa	12.82	149.05
	1_C09_1115D_1111D_1_7_R2_0303_005.fsa	1_C07_1004D_1111D.fsa	23.42	680.42
	1_C09_1115D_1111D_1_7_R2_0303_005.fsa	1_D04_1005D_1115D.fsa	7.65	151.79
	1_D02_1108D_1113D_1_10_R2_0299_008.fsa	1_A04_1001D_1108D.fsa	21.78	169.92
	1_D02_1108D_1113D_1_10_R2_0299_008.fsa	1_A04_1000D_1113D.fsa	16.48	1207.83
	1_D02_1113D_1108D_1_10_R2_0293_008.fsa	1_A04_1001D_1108D.fsa	27.99	901.21
	1_D02_1113D_1108D_1_10_R2_0293_008.fsa	1_A04_1000D_1113D.fsa	11.77	111.40
	1_D06_1001D_1000D_1_3_R2_0792_008.fsa	1_A04_1001D_1108D.fsa	26.85	313.79
	1_D06_1001D_1000D_1_3_R2_0792_008.fsa	1_A04_1000D_1113D.fsa	16.48	1229.33
	1_D06_1004D_1005D_1_3_R2_0797_008.fsa	1_C07_1004D_1111D.fsa	23.11	369.25
	1_D06_1004D_1005D_1_3_R2_0797_008.fsa	1_D04_1005D_1115D.fsa	17.65	918.33
	1_D06_1107D_1114D_1_3_R2_0295_008.fsa	1_A04_1003D_1114D.fsa	19.32	1100.58

	1_D06_1107D_1114D_1_3_R2_0295_008.fsa	1_C07_1002D_1107D.fsa	15.74	359.50
	1_D06_1114D_1107D_1_3_R2_0301_008.fsa	1_C07_1002D_1107D.fsa	18.79	1018.00
	1_D06_1114D_1107D_1_3_R2_0301_008.fsa	1_A04_1003D_1114D.fsa	17.51	400.83
	1_D08_1002D_1003D_1_15_R2_0793_008.fsa	1_A04_1003D_1114D.fsa	19.36	2102.17
	1_D08_1002D_1003D_1_15_R2_0793_008.fsa	1_C07_1002D_1107D.fsa	6.54	161.67
	1_D08_1005D_1004D_1_15_R2_0798_008.fsa	1_C07_1004D_1111D.fsa	23.42	1646.21
	1_D08_1005D_1004D_1_15_R2_0798_008.fsa	1_D04_1005D_1115D.fsa	10.38	119.59
	1_D08_1111D_1115D_1_15_R2_0296_008.fsa	1_D04_1005D_1115D.fsa	17.79	1455.17
	1_D08_1111D_1115D_1_15_R2_0296_008.fsa	1_C07_1004D_1111D.fsa	8.88	109.81
	1_D08_1115D_1111D_1_15_R2_0302_008.fsa	1_C07_1004D_1111D.fsa	23.42	739.63
	1_D08_1115D_1111D_1_15_R2_0302_008.fsa	1_D04_1005D_1115D.fsa	7.62	105.22
	1_F01_1108D_1113D_1_20_R2_0299_011.fsa	1_A04_1000D_1113D.fsa	16.48	914.00
	1_F01_1108D_1113D_1_20_R2_0299_011.fsa	1_A04_1001D_1108D.fsa	8.39	85.00
	1_F01_1113D_1108D_1_20_R2_0293_011.fsa	1_A04_1001D_1108D.fsa	27.99	827.14
	1_F01_1113D_1108D_1_20_R2_0293_011.fsa	1_A04_1000D_1113D.fsa	1.57	62.50
	1_F03_1000D_1001D_1_1_R2_0791_011.fsa	1_A04_1001D_1108D.fsa	18.22	717.07
	1_F03_1000D_1001D_1_1_R2_0791_011.fsa	1_A04_1000D_1113D.fsa	8.03	960.25
	1_F03_1003D_1002D_1_1_R2_0796_011.fsa	1_C07_1002D_1107D.fsa	9.69	759.55
	1_F03_1003D_1002D_1_1_R2_0796_011.fsa	1_A04_1003D_1114D.fsa	9.28	786.08
	1_F03_1108D_1113D_1_1_R2_0300_011.fsa	1_A04_1001D_1108D.fsa	17.72	473.93
	1_F03_1108D_1113D_1_1_R2_0300_011.fsa	1_A04_1000D_1113D.fsa	7.08	562.25
	1_F03_1113D_1108D_1_1_R2_0294_011.fsa	1_A04_1001D_1108D.fsa	17.03	468.36
	1_F03_1113D_1108D_1_1_R2_0294_011.fsa	1_A04_1000D_1113D.fsa	7.29	474.33
	1_F05_1001D_1000D_1_10_R2_0792_011.fsa	1_A04_1001D_1108D.fsa	16.77	131.44
	1_F05_1001D_1000D_1_10_R2_0792_011.fsa	1_A04_1000D_1113D.fsa	16.48	1204.92
	1_F05_1004D_1005D_1_10_R2_0797_011.fsa	1_D04_1005D_1115D.fsa	17.79	1106.60
	1_F05_1004D_1005D_1_10_R2_0797_011.fsa	1_C07_1004D_1111D.fsa	15.80	118.55
	1_F05_1107D_1114D_1_10_R2_0295_011.fsa	1_A04_1003D_1114D.fsa	19.36	775.33
	1_F05_1107D_1114D_1_10_R2_0295_011.fsa	1_C07_1002D_1107D.fsa	10.82	106.00
	1_F05_1114D_1107D_1_10_R2_0301_011.fsa	1_C07_1002D_1107D.fsa	19.77	935.45
	1_F05_1114D_1107D_1_10_R2_0301_011.fsa	1_A04_1003D_1114D.fsa	15.03	88.00
	1_F09_1002D_1003D_1_3_R2_0794_011.fsa	1_C07_1002D_1107D.fsa	19.52	438.15
	1_F09_1002D_1003D_1_3_R2_0794_011.fsa	1_A04_1003D_1114D.fsa	19.36	1558.67
	1_F09_1005D_1004D_1_3_R2_0799_011.fsa	1_C07_1004D_1111D.fsa	23.33	1097.67
	1_F09_1005D_1004D_1_3_R2_0799_011.fsa	1_D04_1005D_1115D.fsa	17.54	339.90
	1_F09_1111D_1115D_1_3_R2_0297_011.fsa	1_C07_1004D_1111D.fsa	21.09	202.00
	1_F09_1111D_1115D_1_3_R2_0297_011.fsa	1_D04_1005D_1115D.fsa	17.79	870.00
	1_F09_1115D_1111D_1_3_R2_0303_011.fsa	1_C07_1004D_1111D.fsa	21.21	610.38
	1_F09_1115D_1111D_1_3_R2_0303_011.fsa	1_D04_1005D_1115D.fsa	15.47	294.57
	1_G02_1108D_1113D_1_7_R2_0299_014.fsa	1_A04_1001D_1108D.fsa	19.17	117.58
	1_G02_1108D_1113D_1_7_R2_0299_014.fsa	1_A04_1000D_1113D.fsa	16.48	954.08
	1_G02_1113D_1108D_1_7_R2_0293_014.fsa	1_A04_1001D_1108D.fsa	27.99	864.86
	1_G02_1113D_1108D_1_7_R2_0293_014.fsa	1_A04_1000D_1113D.fsa	13.46	134.36
	1_G04_1001D_1000D_1_20_R2_0791_014.fsa	1_A04_1000D_1113D.fsa	16.48	1519.33
	1_G04_1001D_1000D_1_20_R2_0791_014.fsa	1_A04_1001D_1108D.fsa	9.13	97.86
	1_G04_1004D_1005D_1_20_R2_0796_014.fsa	1_D04_1005D_1115D.fsa	17.79	1334.97
	1_G04_1107D_1114D_1_20_R2_0294_014.fsa	1_A04_1003D_1114D.fsa	19.36	931.33
	1_G04_1107D_1114D_1_20_R2_0294_014.fsa	1_C07_1002D_1107D.fsa	2.32	45.00
	1_G04_1114D_1107D_1_20_R2_0300_014.fsa	1_C07_1002D_1107D.fsa	19.77	1105.65

	1_G04_1114D_1107D_1_20_R2_0300_014.fsa	1_A04_1003D_1114D.fsa	7.00	88.00
	1_G06_1001D_1000D_1_1_R2_0792_014.fsa	1_A04_1001D_1108D.fsa	19.85	827.93
	1_G06_1001D_1000D_1_1_R2_0792_014.fsa	1_A04_1000D_1113D.fsa	8.35	1022.00
	1_G06_1004D_1005D_1_1_R2_0797_014.fsa	1_C07_1004D_1111D.fsa	14.63	740.54
	1_G06_1004D_1005D_1_1_R2_0797_014.fsa	1_D04_1005D_1115D.fsa	9.00	713.23
	1_G06_1107D_1114D_1_1_R2_0295_014.fsa	1_A04_1003D_1114D.fsa	10.59	511.00
	1_G06_1107D_1114D_1_1_R2_0295_014.fsa	1_C07_1002D_1107D.fsa	10.56	456.55
	1_G06_1114D_1107D_1_1_R2_0301_014.fsa	1_C07_1002D_1107D.fsa	10.02	594.55
	1_G06_1114D_1107D_1_1_R2_0301_014.fsa	1_A04_1003D_1114D.fsa	9.62	596.58
	1_G08_1002D_1003D_1_10_R2_0793_014.fsa	1_A04_1003D_1114D.fsa	19.36	1689.25
	1_G08_1002D_1003D_1_10_R2_0793_014.fsa	1_C07_1002D_1107D.fsa	18.56	152.25
	1_G08_1005D_1004D_1_10_R2_0798_014.fsa	1_C07_1004D_1111D.fsa	23.42	1510.92
	1_G08_1005D_1004D_1_10_R2_0798_014.fsa	1_D04_1005D_1115D.fsa	13.70	151.10
	1_G08_1111D_1115D_1_10_R2_0296_014.fsa	1_D04_1005D_1115D.fsa	17.79	1165.33
	1_G08_1111D_1115D_1_10_R2_0296_014.fsa	1_C07_1004D_1111D.fsa	9.88	112.79
	1_G08_1115D_1111D_1_10_R2_0302_014.fsa	1_C07_1004D_1111D.fsa	23.42	747.75
	1_G08_1115D_1111D_1_10_R2_0302_014.fsa	1_D04_1005D_1115D.fsa	14.74	139.96
	2_A02_1000D_1001D_1_15_R2_0800_002.fsa	1_A04_1001D_1108D.fsa	27.99	956.43
	2_A02_1000D_1001D_1_15_R2_0800_002.fsa	1_A04_1000D_1113D.fsa	7.96	98.13
	2_A02_1003D_1002D_1_15_R2_0801_002.fsa	1_C07_1002D_1107D.fsa	19.77	1416.80
	2_D01_10-573-JS-COMP-4-1EF1_1313_007.fsa	1_B03_10-573-JS-COMP-1_1312_003.fsa	19.36	605.00
	2_D02_1000D_1001D_1_10_R2_0800_008.fsa	1_A04_1001D_1108D.fsa	27.99	1132.79
	2_D02_1000D_1001D_1_10_R2_0800_008.fsa	1_A04_1000D_1113D.fsa	12.78	145.75
	2_D02_1003D_1002D_1_10_R2_0801_008.fsa	1_C07_1002D_1107D.fsa	19.77	1587.75
	2_D02_1003D_1002D_1_10_R2_0801_008.fsa	1_A04_1003D_1114D.fsa	16.82	133.00
	2_F01_1000D_1001D_1_20_R2_0800_011.fsa	1_A04_1001D_1108D.fsa	27.99	963.21
	2_F01_1000D_1001D_1_20_R2_0800_011.fsa	1_A04_1000D_1113D.fsa	7.24	76.67
	2_F01_1003D_1002D_1_20_R2_0801_011.fsa	1_C07_1002D_1107D.fsa	19.77	1244.55
	2_F01_1003D_1002D_1_20_R2_0801_011.fsa	1_A04_1003D_1114D.fsa	9.99	88.50
	2_F01_10-573-JS-COMP-4-1EF2_1313_011.fsa	1_B03_10-573-JS-COMP-1_1312_003.fsa	19.36	632.00
	2_G02_1000D_1001D_1_7_R2_0800_014.fsa	1_A04_1001D_1108D.fsa	27.99	966.36
	2_G02_1000D_1001D_1_7_R2_0800_014.fsa	1_A04_1000D_1113D.fsa	14.43	153.42
	2_G02_1003D_1002D_1_7_R2_0801_014.fsa	1_C07_1002D_1107D.fsa	19.77	1197.90
	2_G02_1003D_1002D_1_7_R2_0801_014.fsa	1_A04_1003D_1114D.fsa	15.76	222.33
	5_B01_15-582-JS-3EF_0612_003.fsa	1_B01_15-582-JS-1_0620_003.fsa	20.75	1317.00

Three person mixtures

	Sample	Reference	log(LR)	APH
Three person mixtures	1_A08_Mix_B_5_2.5_1_0042_002.fsa	C.fsa	4.885	192
	1_A08_Mix_B_5_2.5_1_0042_002.fsa	E.fsa	18.053	288
	1_A08_Mix_B_5_2.5_1_0042_002.fsa	F.fsa	6.347	119
	1_A08_Mix_B_5_2.5_1_0046_002.fsa	C.fsa	4.332	79
	1_A08_Mix_B_5_2.5_1_0046_002.fsa	E.fsa	17.818	109
	1_A08_Mix_B_5_2.5_1_0046_002.fsa	F.fsa	1.520	33
	1_B06_Mix_A_20_1_1_0041_004.fsa	A.fsa	18.639	255

	1_B06_Mix_A_20_1_1_0041_004.fsa	B.fsa	4.902	45
	1_B06_Mix_A_20_1_1_0041_004.fsa	D.fsa	6.550	58
	1_B06_Mix_A_20_1_1_0045_004.fsa	A.fsa	11.032	45
	1_B06_Mix_A_20_1_1_0045_004.fsa	B.fsa	2.210	20
	1_B06_Mix_A_20_1_1_0045_004.fsa	D.fsa	0.039	20
	1_B07_Mix_A_3_1_1_0042_003.fsa	A.fsa	7.537	191
	1_B07_Mix_A_3_1_1_0042_003.fsa	B.fsa	10.430	161
	1_B07_Mix_A_3_1_1_0042_003.fsa	D.fsa	6.292	240
	1_B07_Mix_A_3_1_1_0046_003.fsa	A.fsa	6.816	68
	1_B07_Mix_A_3_1_1_0046_003.fsa	B.fsa	8.905	76
	1_B07_Mix_A_3_1_1_0046_003.fsa	D.fsa	6.191	96
	1_B08_Mix_B_3_1_1_0042_004.fsa	C.fsa	4.868	248
	1_B08_Mix_B_3_1_1_0042_004.fsa	E.fsa	16.308	228
	1_B08_Mix_B_3_1_1_0042_004.fsa	F.fsa	5.598	215
	1_B08_Mix_B_3_1_1_0046_004.fsa	C.fsa	5.271	72
	1_B08_Mix_B_3_1_1_0046_004.fsa	E.fsa	16.958	101
	1_B08_Mix_B_3_1_1_0046_004.fsa	F.fsa	0.022	59
	1_C06_Mix_A_20_10_1_0041_006.fsa	A.fsa	11.852	231
	1_C06_Mix_A_20_10_1_0041_006.fsa	B.fsa	14.025	328
	1_C06_Mix_A_20_10_1_0041_006.fsa	D.fsa	6.723	41
	1_C06_Mix_A_20_10_1_0045_006.fsa	A.fsa	3.644	41
	1_C06_Mix_A_20_10_1_0045_006.fsa	B.fsa	12.936	103
	1_C06_Mix_A_20_10_1_0045_006.fsa	D.fsa	-0.267	19
	1_C07_Mix_A_3_1.5_1_0042_005.fsa	A.fsa	7.403	212
	1_C07_Mix_A_3_1.5_1_0042_005.fsa	B.fsa	11.511	278
	1_C07_Mix_A_3_1.5_1_0042_005.fsa	D.fsa	6.300	273
	1_C07_Mix_A_3_1.5_1_0046_005.fsa	A.fsa	6.041	69
	1_C07_Mix_A_3_1.5_1_0046_005.fsa	B.fsa	11.183	113
	1_C07_Mix_A_3_1.5_1_0046_005.fsa	D.fsa	7.056	82
	1_C08_Mix_B_3_1.5_1_0042_006.fsa	C.fsa	4.994	175
	1_C08_Mix_B_3_1.5_1_0042_006.fsa	E.fsa	18.311	234
	1_C08_Mix_B_3_1.5_1_0042_006.fsa	F.fsa	7.390	125
	1_C08_Mix_B_3_1.5_1_0046_006.fsa	C.fsa	2.802	76
	1_C08_Mix_B_3_1.5_1_0046_006.fsa	E.fsa	18.205	92
	1_C08_Mix_B_3_1.5_1_0046_006.fsa	F.fsa	2.141	52
	1_D06_Mix_A_10_1_1_0041_008.fsa	A.fsa	16.760	267
	1_D06_Mix_A_10_1_1_0041_008.fsa	B.fsa	5.323	41
	1_D06_Mix_A_10_1_1_0041_008.fsa	D.fsa	7.204	85
	1_D06_Mix_A_10_1_1_0045_008.fsa	A.fsa	11.124	59
	1_D06_Mix_A_10_1_1_0045_008.fsa	B.fsa	0.790	19
	1_D06_Mix_A_10_1_1_0045_008.fsa	D.fsa	-0.766	23
	1_D07_Mix_B_20_1_1_0042_007.fsa	C.fsa	18.870	308
	1_D07_Mix_B_20_1_1_0042_007.fsa	E.fsa	9.161	44
	1_D07_Mix_B_20_1_1_0042_007.fsa	F.fsa	3.743	69
	1_D07_Mix_B_20_1_1_0046_007.fsa	C.fsa	17.544	108
	1_D07_Mix_B_20_1_1_0046_007.fsa	E.fsa	2.561	26
	1_D07_Mix_B_20_1_1_0046_007.fsa	F.fsa	-0.658	22
	1_E06_Mix_A_10_5_1_0041_010.fsa	A.fsa	10.885	212
	1_E06_Mix_A_10_5_1_0041_010.fsa	B.fsa	16.195	344

	1_E06_Mix_A_10_5_1_0041_010.fsa	D.fsa	6.642	72
	1_E06_Mix_A_10_5_1_0045_010.fsa	A.fsa	7.223	77
	1_E06_Mix_A_10_5_1_0045_010.fsa	B.fsa	13.279	114
	1_E06_Mix_A_10_5_1_0045_010.fsa	D.fsa	1.702	39
	1_E07_Mix_B20_10_1_0042_009.fsa	C.fsa	5.215	167
	1_E07_Mix_B20_10_1_0042_009.fsa	E.fsa	20.973	236
	1_E07_Mix_B20_10_1_0042_009.fsa	F.fsa	0.881	33
	1_E07_Mix_B20_10_1_0046_009.fsa	C.fsa	7.097	55
	1_E07_Mix_B20_10_1_0046_009.fsa	E.fsa	18.788	82
	1_E07_Mix_B20_10_1_0046_009.fsa*	F.fsa	-7.718	20
	1_F06_Mix_A_5_1_1_0041_012.fsa	A.fsa	9.782	178
	1_F06_Mix_A_5_1_1_0041_012.fsa	B.fsa	9.730	111
	1_F06_Mix_A_5_1_1_0041_012.fsa	D.fsa	5.565	140
	1_F06_Mix_A_5_1_1_0045_012.fsa	A.fsa	8.872	84
	1_F06_Mix_A_5_1_1_0045_012.fsa	B.fsa	5.852	40
	1_F06_Mix_A_5_1_1_0045_012.fsa	D.fsa	4.084	58
	1_F07_Mix_B_10_1_1_0042_011.fsa	C.fsa	18.420	253
	1_F07_Mix_B_10_1_1_0042_011.fsa	E.fsa	19.809	97
	1_F07_Mix_B_10_1_1_0042_011.fsa	F.fsa	6.791	54
	1_F07_Mix_B_10_1_1_0046_011.fsa	C.fsa	12.502	117
	1_F07_Mix_B_10_1_1_0046_011.fsa	E.fsa	4.693	35
	1_F07_Mix_B_10_1_1_0046_011.fsa	F.fsa	-1.088	34
	1_G06_Mix_A_5_2.5_1_0041_014.fsa	A.fsa	8.203	221
	1_G06_Mix_A_5_2.5_1_0041_014.fsa	B.fsa	12.099	275
	1_G06_Mix_A_5_2.5_1_0041_014.fsa	D.fsa	6.352	156
	1_G06_Mix_A_5_2.5_1_0045_014.fsa	A.fsa	5.854	57
	1_G06_Mix_A_5_2.5_1_0045_014.fsa	B.fsa	11.798	92
	1_G06_Mix_A_5_2.5_1_0045_014.fsa	D.fsa	1.357	46
	1_G07_Mix_B_10_5_1_0042_013.fsa	C.fsa	7.561	278
	1_G07_Mix_B_10_5_1_0042_013.fsa	E.fsa	20.622	343
	1_G07_Mix_B_10_5_1_0042_013.fsa	F.fsa	7.346	64
	1_G07_Mix_B_10_5_1_0046_013.fsa	C.fsa	7.518	138
	1_G07_Mix_B_10_5_1_0046_013.fsa	E.fsa	17.972	151
	1_G07_Mix_B_10_5_1_0046_013.fsa	F.fsa	1.076	39
	1_H07_Mix_B_5_1_1_0042_015.fsa	C.fsa	10.169	266
	1_H07_Mix_B_5_1_1_0042_015.fsa	E.fsa	15.865	124
	1_H07_Mix_B_5_1_1_0042_015.fsa	F.fsa	3.418	86
	1_H07_Mix_B_5_1_1_0046_015.fsa	C.fsa	7.617	85
	1_H07_Mix_B_5_1_1_0046_015.fsa	E.fsa	7.134	61
	1_H07_Mix_B_5_1_1_0046_015.fsa	F.fsa	0.524	41
	2_D07_Mix_B_20_1_1_0049_007.fsa	C.fsa	18.873	176
	2_D07_Mix_B_20_1_1_0049_007.fsa	E.fsa	2.108	27
	2_D07_Mix_B_20_1_1_0049_007.fsa	F.fsa	2.357	27

*Note that there was no evidence of the third contributor to this profile and F.fsa would be excluded visually.

Four person mixtures

	Sample	Reference	log(LR)	APH
Four person mixtures	1_A02_Mix_A_5_5_1_1_0039_002.fsa	A.fsa	7.48	122
	1_A02_Mix_A_5_5_1_1_0039_002.fsa	B.fsa	13.48	256
	1_A02_Mix_A_5_5_1_1_0039_002.fsa	D.fsa	2.14	66
	1_A02_Mix_A_5_5_1_1_0039_002.fsa	G.fsa	6.27	86
	1_A02_Mix_A_5_5_1_1_0043_002.fsa	A.fsa	3.89	40
	1_A02_Mix_A_5_5_1_1_0043_002.fsa	B.fsa	9.12	76
	1_A02_Mix_A_5_5_1_1_0043_002.fsa	D.fsa	1.07	19
	1_A02_Mix_A_5_5_1_1_0043_002.fsa	G.fsa	0.36	20
	1_A04_Mix_B_10_5_2_1_0040_002.fsa	C.fsa	8.63	191
	1_A04_Mix_B_10_5_2_1_0040_002.fsa	E.fsa	15.89	120
	1_A04_Mix_B_10_5_2_1_0040_002.fsa	F.fsa	-0.23	35
	1_A04_Mix_B_10_5_2_1_0040_002.fsa	G.fsa	-0.40	23
	1_A04_Mix_B_10_5_2_1_0044_002.fsa	C.fsa	6.50	68
	1_A04_Mix_B_10_5_2_1_0044_002.fsa	E.fsa	7.37	41
	1_A04_Mix_B_10_5_2_1_0044_002.fsa	F.fsa	-1.82	23
	1_A04_Mix_B_10_5_2_1_0044_002.fsa	G.fsa	-2.00	20
	1_A06_Mix_B_2_2_2_1_0041_002.fsa	C.fsa	1.40	73
	1_A06_Mix_B_2_2_2_1_0041_002.fsa	E.fsa	14.73	157
	1_A06_Mix_B_2_2_2_1_0041_002.fsa	F.fsa	4.74	129
	1_A06_Mix_B_2_2_2_1_0041_002.fsa	G.fsa	3.91	72
	1_A06_Mix_B_2_2_2_1_0045_002.fsa	C.fsa	1.45	22
	1_A06_Mix_B_2_2_2_1_0045_002.fsa	E.fsa	1.78	20
	1_A06_Mix_B_2_2_2_1_0045_002.fsa	F.fsa	0.16	20
	1_A06_Mix_B_2_2_2_1_0045_002.fsa	G.fsa	-0.20	20
	1_B01_Mix_A_10_1_1_1_0039_003.fsa	A.fsa	18.68	228
	1_B01_Mix_A_10_1_1_1_0039_003.fsa	B.fsa	7.40	71
	1_B01_Mix_A_10_1_1_1_0039_003.fsa	D.fsa	2.17	42
	1_B01_Mix_A_10_1_1_1_0039_003.fsa	G.fsa	6.99	50
	1_B02_Mix_A_5_5_5_1_0039_004.fsa	A.fsa	5.81	76
	1_B02_Mix_A_5_5_5_1_0039_004.fsa	B.fsa	9.84	212
	1_B02_Mix_A_5_5_5_1_0039_004.fsa	D.fsa	7.98	272
	1_B02_Mix_A_5_5_5_1_0039_004.fsa	G.fsa	2.42	51
	1_B02_Mix_A_5_5_5_1_0043_004.fsa	A.fsa	2.14	28
	1_B02_Mix_A_5_5_5_1_0043_004.fsa	B.fsa	6.84	47
	1_B02_Mix_A_5_5_5_1_0043_004.fsa	D.fsa	6.59	50
	1_B02_Mix_A_5_5_5_1_0043_004.fsa	G.fsa	0.07	20
	1_B03_Mix_A_1_1_1_1_0040_003.fsa	A.fsa	5.80	108
	1_B03_Mix_A_1_1_1_1_0040_003.fsa	B.fsa	8.33	223
	1_B03_Mix_A_1_1_1_1_0040_003.fsa	D.fsa	6.24	185
	1_B03_Mix_A_1_1_1_1_0040_003.fsa	G.fsa	9.63	122
	1_B03_Mix_A_1_1_1_1_0044_003.fsa	A.fsa	2.77	35
	1_B03_Mix_A_1_1_1_1_0044_003.fsa	B.fsa	9.01	92
	1_B03_Mix_A_1_1_1_1_0044_003.fsa	D.fsa	4.96	76
	1_B03_Mix_A_1_1_1_1_0044_003.fsa	G.fsa	5.60	54
	1_B04_Mix_B_10_5_5_2_0040_004.fsa	C.fsa	8.58	201
	1_B04_Mix_B_10_5_5_2_0040_004.fsa	E.fsa	13.99	79
	1_B04_Mix_B_10_5_5_2_0040_004.fsa	F.fsa	2.09	76

	1_B04_Mix_B_10_5_5_2_0040_004.fsa	G.fsa	-0.82	50
	1_B04_Mix_B_10_5_5_2_0044_004.fsa	C.fsa	7.31	68
	1_B04_Mix_B_10_5_5_2_0044_004.fsa	E.fsa	2.58	27
	1_B04_Mix_B_10_5_5_2_0044_004.fsa	F.fsa	-0.21	38
	1_B04_Mix_B_10_5_5_2_0044_004.fsa	G.fsa	-0.76	28
	1_B05_Mix_B_5_2_2_1_0041_003.fsa	C.fsa	9.18	206
	1_B05_Mix_B_5_2_2_1_0041_003.fsa	E.fsa	12.53	73
	1_B05_Mix_B_5_2_2_1_0041_003.fsa	F.fsa	1.35	122
	1_B05_Mix_B_5_2_2_1_0041_003.fsa	G.fsa	4.74	38
	1_B05_Mix_B_5_2_2_1_0045_003.fsa	C.fsa	8.65	60
	1_B05_Mix_B_5_2_2_1_0045_003.fsa	E.fsa	1.84	29
	1_B05_Mix_B_5_2_2_1_0045_003.fsa	F.fsa	-2.16	24
	1_B05_Mix_B_5_2_2_1_0045_003.fsa	G.fsa	-1.63	20
	1_C01_Mix_A_10_10_1_1_0039_005.fsa	A.fsa	8.22	102
	1_C01_Mix_A_10_10_1_1_0039_005.fsa	B.fsa	14.54	200
	1_C01_Mix_A_10_10_1_1_0039_005.fsa	D.fsa	2.19	25
	1_C01_Mix_A_10_10_1_1_0039_005.fsa	G.fsa	1.48	74
	1_C01_Mix_A_10_10_1_1_0043_005.fsa	A.fsa	5.61	51
	1_C01_Mix_A_10_10_1_1_0043_005.fsa	B.fsa	13.10	117
	1_C01_Mix_A_10_10_1_1_0043_005.fsa	D.fsa	0.67	28
	1_C01_Mix_A_10_10_1_1_0043_005.fsa	G.fsa	-2.38	21
	1_C02_Mix_A_5_2_1_1_0039_006.fsa	A.fsa	6.07	73
	1_C02_Mix_A_5_2_1_1_0039_006.fsa	B.fsa	9.84	126
	1_C02_Mix_A_5_2_1_1_0039_006.fsa	D.fsa	3.94	89
	1_C02_Mix_A_5_2_1_1_0039_006.fsa	G.fsa	6.81	63
	1_C02_Mix_A_5_2_1_1_0043_006.fsa	A.fsa	4.14	33
	1_C02_Mix_A_5_2_1_1_0043_006.fsa	B.fsa	7.18	36
	1_C02_Mix_A_5_2_1_1_0043_006.fsa	D.fsa	1.83	21
	1_C02_Mix_A_5_2_1_1_0043_006.fsa	G.fsa	1.13	21
	1_C03_Mix_A_2_1_1_1_0040_005.fsa	A.fsa	7.22	167
	1_C03_Mix_A_2_1_1_1_0040_005.fsa	B.fsa	7.60	98
	1_C03_Mix_A_2_1_1_1_0040_005.fsa	D.fsa	5.45	157
	1_C03_Mix_A_2_1_1_1_0040_005.fsa	G.fsa	8.95	111
	1_C03_Mix_A_2_1_1_1_0044_005.fsa	A.fsa	3.91	63
	1_C03_Mix_A_2_1_1_1_0044_005.fsa	B.fsa	6.39	86
	1_C03_Mix_A_2_1_1_1_0044_005.fsa	D.fsa	5.26	85
	1_C03_Mix_A_2_1_1_1_0044_005.fsa	G.fsa	7.06	59
	1_C04_Mix_B_10_5_5_5_0040_006.fsa	C.fsa	7.43	155
	1_C04_Mix_B_10_5_5_5_0040_006.fsa	E.fsa	12.18	68
	1_C04_Mix_B_10_5_5_5_0040_006.fsa	F.fsa	2.75	105
	1_C04_Mix_B_10_5_5_5_0040_006.fsa	G.fsa	6.23	93
	1_C04_Mix_B_10_5_5_5_0044_006.fsa	C.fsa	6.64	42
	1_C04_Mix_B_10_5_5_5_0044_006.fsa	E.fsa	3.50	25
	1_C04_Mix_B_10_5_5_5_0044_006.fsa	F.fsa	-0.49	38
	1_C04_Mix_B_10_5_5_5_0044_006.fsa	G.fsa	4.74	46
	1_C05_Mix_B_3_1_1_1_0041_005.fsa	C.fsa	7.23	201
	1_C05_Mix_B_3_1_1_1_0041_005.fsa	E.fsa	13.03	80
	1_C05_Mix_B_3_1_1_1_0041_005.fsa	F.fsa	-0.72	77
	1_C05_Mix_B_3_1_1_1_0041_005.fsa	G.fsa	6.44	46

	1_C05_Mix_B_3_1_1_1_0045_005.fsa	C.fsa	7.57	41
	1_C05_Mix_B_3_1_1_1_0045_005.fsa	E.fsa	-1.13	24
	1_C05_Mix_B_3_1_1_1_0045_005.fsa	F.fsa	-1.89	20
	1_C05_Mix_B_3_1_1_1_0045_005.fsa	G.fsa	1.35	21
	1_D01_Mix_A_10_10_10_1_0039_007.fsa	A.fsa	3.72	52
	1_D01_Mix_A_10_10_10_1_0039_007.fsa	B.fsa	11.71	134
	1_D01_Mix_A_10_10_10_1_0039_007.fsa	D.fsa	4.96	84
	1_D01_Mix_A_10_10_10_1_0039_007.fsa	G.fsa	0.26	68
	1_D02_Mix_A_5_2_2_1_0039_008.fsa	A.fsa	8.12	167
	1_D02_Mix_A_5_2_2_1_0039_008.fsa	B.fsa	7.21	93
	1_D02_Mix_A_5_2_2_1_0039_008.fsa	D.fsa	6.18	168
	1_D02_Mix_A_5_2_2_1_0039_008.fsa	G.fsa	6.35	49
	1_D02_Mix_A_5_2_2_1_0043_008.fsa	A.fsa	6.10	65
	1_D02_Mix_A_5_2_2_1_0043_008.fsa	B.fsa	8.95	48
	1_D02_Mix_A_5_2_2_1_0043_008.fsa	D.fsa	4.96	120
	1_D02_Mix_A_5_2_2_1_0043_008.fsa	G.fsa	1.57	20
	1_D03_Mix_A_2_2_1_1_0040_007.fsa	A.fsa	5.11	100
	1_D03_Mix_A_2_2_1_1_0040_007.fsa	B.fsa	9.37	170
	1_D03_Mix_A_2_2_1_1_0040_007.fsa	D.fsa	4.89	149
	1_D03_Mix_A_2_2_1_1_0040_007.fsa	G.fsa	8.20	56
	1_D03_Mix_A_2_2_1_1_0044_007.fsa	A.fsa	1.59	27
	1_D03_Mix_A_2_2_1_1_0044_007.fsa	B.fsa	6.99	65
	1_D03_Mix_A_2_2_1_1_0044_007.fsa	D.fsa	3.25	73
	1_D03_Mix_A_2_2_1_1_0044_007.fsa	G.fsa	4.43	38
	1_D04_Mix_B_5_1_1_1_0040_008.fsa	C.fsa	17.18	160
	1_D04_Mix_B_5_1_1_1_0040_008.fsa	E.fsa	7.73	53
	1_D04_Mix_B_5_1_1_1_0040_008.fsa	F.fsa	3.89	43
	1_D04_Mix_B_5_1_1_1_0040_008.fsa	G.fsa	4.01	47
	1_D04_Mix_B_5_1_1_1_0044_008.fsa	C.fsa	9.68	92
	1_D04_Mix_B_5_1_1_1_0044_008.fsa	E.fsa	0.56	24
	1_D04_Mix_B_5_1_1_1_0044_008.fsa	F.fsa	-1.79	30
	1_D04_Mix_B_5_1_1_1_0044_008.fsa	G.fsa	1.49	26
	1_D05_Mix_B_3_2_1_1_0041_007.fsa	C.fsa	7.46	211
	1_D05_Mix_B_3_2_1_1_0041_007.fsa	E.fsa	14.70	124
	1_D05_Mix_B_3_2_1_1_0041_007.fsa	F.fsa	-1.48	71
	1_D05_Mix_B_3_2_1_1_0041_007.fsa	G.fsa	5.09	24
	1_D05_Mix_B_3_2_1_1_0045_007.fsa	C.fsa	7.32	98
	1_D05_Mix_B_3_2_1_1_0045_007.fsa	E.fsa	9.94	72
	1_D05_Mix_B_3_2_1_1_0045_007.fsa	F.fsa	-1.38	38
	1_D05_Mix_B_3_2_1_1_0045_007.fsa	G.fsa	1.22	29
	1_E01_Mix_A_10_5_2_1_0039_009.fsa	A.fsa	9.41	148
	1_E01_Mix_A_10_5_2_1_0039_009.fsa	B.fsa	12.40	157
	1_E01_Mix_A_10_5_2_1_0039_009.fsa	D.fsa	5.73	97
	1_E01_Mix_A_10_5_2_1_0039_009.fsa	G.fsa	2.60	46
	1_E01_Mix_A_10_5_2_1_0043_009.fsa	A.fsa	7.68	66
	1_E01_Mix_A_10_5_2_1_0043_009.fsa	B.fsa	8.27	62
	1_E01_Mix_A_10_5_2_1_0043_009.fsa	D.fsa	2.74	43
	1_E01_Mix_A_10_5_2_1_0043_009.fsa	G.fsa	2.14	26
	1_E02_Mix_A_3_1_1_1_0039_010.fsa	A.fsa	8.29	172

	1_E02_Mix_A_3_1_1_1_0039_010.fsa	B.fsa	7.49	103
	1_E02_Mix_A_3_1_1_1_0039_010.fsa	D.fsa	4.00	129
	1_E02_Mix_A_3_1_1_1_0039_010.fsa	G.fsa	8.53	77
	1_E02_Mix_A_3_1_1_1_0043_010.fsa	A.fsa	5.77	53
	1_E02_Mix_A_3_1_1_1_0043_010.fsa	B.fsa	6.76	66
	1_E02_Mix_A_3_1_1_1_0043_010.fsa	D.fsa	4.00	76
	1_E02_Mix_A_3_1_1_1_0043_010.fsa	G.fsa	6.25	49
	1_E03_Mix_A_2_2_2_1_0040_009.fsa	A.fsa	3.58	77
	1_E03_Mix_A_2_2_2_1_0040_009.fsa	B.fsa	9.02	166
	1_E03_Mix_A_2_2_2_1_0040_009.fsa	D.fsa	6.52	223
	1_E03_Mix_A_2_2_2_1_0040_009.fsa	G.fsa	8.07	105
	1_E03_Mix_A_2_2_2_1_0044_009.fsa	A.fsa	4.19	37
	1_E03_Mix_A_2_2_2_1_0044_009.fsa	B.fsa	9.44	75
	1_E03_Mix_A_2_2_2_1_0044_009.fsa	D.fsa	6.10	78
	1_E03_Mix_A_2_2_2_1_0044_009.fsa	G.fsa	2.76	28
	1_E04_Mix_B_5_5_1_1_0040_010.fsa	C.fsa	6.87	112
	1_E04_Mix_B_5_5_1_1_0040_010.fsa	E.fsa	18.54	210
	1_E04_Mix_B_5_5_1_1_0040_010.fsa	F.fsa	2.48	55
	1_E04_Mix_B_5_5_1_1_0040_010.fsa	G.fsa	3.26	70
	1_E04_Mix_B_5_5_1_1_0044_010.fsa	C.fsa	5.76	49
	1_E04_Mix_B_5_5_1_1_0044_010.fsa	E.fsa	17.43	53
	1_E04_Mix_B_5_5_1_1_0044_010.fsa	F.fsa	-3.09	26
	1_E04_Mix_B_5_5_1_1_0044_010.fsa	G.fsa	-4.21	20
	1_E05_Mix_B_3_2_2_1_0041_009.fsa	C.fsa	5.06	141
	1_E05_Mix_B_3_2_2_1_0041_009.fsa	E.fsa	15.31	140
	1_E05_Mix_B_3_2_2_1_0041_009.fsa	F.fsa	1.67	125
	1_E05_Mix_B_3_2_2_1_0041_009.fsa	G.fsa	3.18	33
	1_E05_Mix_B_3_2_2_1_0045_009.fsa	C.fsa	4.14	36
	1_E05_Mix_B_3_2_2_1_0045_009.fsa	E.fsa	5.50	33
	1_E05_Mix_B_3_2_2_1_0045_009.fsa	F.fsa	1.67	45
	1_E05_Mix_B_3_2_2_1_0045_009.fsa	G.fsa	2.15	32
	1_F01_Mix_A_10_5_5_2_0039_011.fsa	A.fsa	7.33	161
	1_F01_Mix_A_10_5_5_2_0039_011.fsa	B.fsa	7.70	205
	1_F01_Mix_A_10_5_5_2_0039_011.fsa	D.fsa	6.51	247
	1_F01_Mix_A_10_5_5_2_0039_011.fsa	G.fsa	4.08	78
	1_F01_Mix_A_10_5_5_2_0043_011.fsa	A.fsa	4.49	57
	1_F01_Mix_A_10_5_5_2_0043_011.fsa	B.fsa	7.59	73
	1_F01_Mix_A_10_5_5_2_0043_011.fsa	D.fsa	5.33	47
	1_F01_Mix_A_10_5_5_2_0043_011.fsa	G.fsa	2.84	23
	1_F02_Mix_A_3_2_1_1_0039_012.fsa	A.fsa	6.42	171
	1_F02_Mix_A_3_2_1_1_0039_012.fsa	B.fsa	9.38	256
	1_F02_Mix_A_3_2_1_1_0039_012.fsa	D.fsa	3.64	128
	1_F02_Mix_A_3_2_1_1_0039_012.fsa	G.fsa	7.53	98
	1_F02_Mix_A_3_2_1_1_0043_012.fsa	A.fsa	4.11	51
	1_F02_Mix_A_3_2_1_1_0043_012.fsa	B.fsa	7.16	66
	1_F02_Mix_A_3_2_1_1_0043_012.fsa	D.fsa	3.74	62
	1_F02_Mix_A_3_2_1_1_0043_012.fsa	G.fsa	3.28	38
	1_F03_Mix_B_10_1_1_1_0040_011.fsa	C.fsa	18.35	341
	1_F03_Mix_B_10_1_1_1_0040_011.fsa	E.fsa	7.66	52

	1_F03_Mix_B_10_1_1_1_0040_011.fsa	F.fsa	0.54	38
	1_F03_Mix_B_10_1_1_1_0040_011.fsa	G.fsa	2.38	85
	1_F03_Mix_B_10_1_1_1_0044_011.fsa	C.fsa	11.67	111
	1_F03_Mix_B_10_1_1_1_0044_011.fsa	E.fsa	-1.43	20
	1_F03_Mix_B_10_1_1_1_0044_011.fsa	F.fsa	-2.09	22
	1_F03_Mix_B_10_1_1_1_0044_011.fsa	G.fsa	1.22	20
	1_F04_Mix_B_5_5_5_1_0040_012.fsa	C.fsa	5.08	141
	1_F04_Mix_B_5_5_5_1_0040_012.fsa	E.fsa	15.62	132
	1_F04_Mix_B_5_5_5_1_0040_012.fsa	F.fsa	4.67	116
	1_F04_Mix_B_5_5_5_1_0040_012.fsa	G.fsa	3.51	33
	1_F04_Mix_B_5_5_5_1_0044_012.fsa	C.fsa	3.37	57
	1_F04_Mix_B_5_5_5_1_0044_012.fsa	E.fsa	14.95	67
	1_F04_Mix_B_5_5_5_1_0044_012.fsa	F.fsa	1.30	31
	1_F04_Mix_B_5_5_5_1_0044_012.fsa	G.fsa	-0.42	20
	1_F05_Mix_B_1_1_1_1_0041_011.fsa	C.fsa	3.36	91
	1_F05_Mix_B_1_1_1_1_0041_011.fsa	E.fsa	13.65	111
	1_F05_Mix_B_1_1_1_1_0041_011.fsa	F.fsa	5.24	158
	1_F05_Mix_B_1_1_1_1_0041_011.fsa	G.fsa	6.66	71
	1_F05_Mix_B_1_1_1_1_0045_011.fsa	C.fsa	0.56	21
	1_F05_Mix_B_1_1_1_1_0045_011.fsa	E.fsa	8.18	57
	1_F05_Mix_B_1_1_1_1_0045_011.fsa	F.fsa	1.40	40
	1_F05_Mix_B_1_1_1_1_0045_011.fsa	G.fsa	1.02	20
	1_G01_Mix_A_10_5_5_5_0039_013.fsa	A.fsa	6.90	122
	1_G01_Mix_A_10_5_5_5_0039_013.fsa	B.fsa	7.14	125
	1_G01_Mix_A_10_5_5_5_0039_013.fsa	D.fsa	5.39	150
	1_G01_Mix_A_10_5_5_5_0039_013.fsa	G.fsa	9.48	127
	1_G01_Mix_A_10_5_5_5_0043_013.fsa	A.fsa	3.39	69
	1_G01_Mix_A_10_5_5_5_0043_013.fsa	B.fsa	7.01	54
	1_G01_Mix_A_10_5_5_5_0043_013.fsa	D.fsa	4.38	47
	1_G01_Mix_A_10_5_5_5_0043_013.fsa	G.fsa	5.78	47
	1_G02_Mix_A_3_2_2_1_0039_014.fsa	A.fsa	5.60	111
	1_G02_Mix_A_3_2_2_1_0039_014.fsa	B.fsa	9.50	136
	1_G02_Mix_A_3_2_2_1_0039_014.fsa	D.fsa	7.52	171
	1_G02_Mix_A_3_2_2_1_0039_014.fsa	G.fsa	5.02	106
	1_G02_Mix_A_3_2_2_1_0043_014.fsa	A.fsa	4.51	45
	1_G02_Mix_A_3_2_2_1_0043_014.fsa	B.fsa	6.07	74
	1_G02_Mix_A_3_2_2_1_0043_014.fsa	D.fsa	6.90	110
	1_G02_Mix_A_3_2_2_1_0043_014.fsa	G.fsa	3.17	28
	1_G03_Mix_B_10_10_1_1_0040_013.fsa	C.fsa	8.77	216
	1_G03_Mix_B_10_10_1_1_0040_013.fsa	E.fsa	20.36	181
	1_G03_Mix_B_10_10_1_1_0040_013.fsa	F.fsa	1.23	22
	1_G03_Mix_B_10_10_1_1_0040_013.fsa	G.fsa	0.08	54
	1_G03_Mix_B_10_10_1_1_0044_013.fsa	C.fsa	7.64	71
	1_G03_Mix_B_10_10_1_1_0044_013.fsa	E.fsa	12.85	69
	1_G03_Mix_B_10_10_1_1_0044_013.fsa	F.fsa	-4.78	21
	1_G03_Mix_B_10_10_1_1_0044_013.fsa	G.fsa	-2.60	25
	1_G04_Mix_B_5_2_1_1_0040_014.fsa	C.fsa	11.45	196
	1_G04_Mix_B_5_2_1_1_0040_014.fsa	E.fsa	13.00	94
	1_G04_Mix_B_5_2_1_1_0040_014.fsa	F.fsa	0.92	60

	1_G04_Mix_B_5_2_1_1_0040_014.fsa	G.fsa	4.08	39
	1_G04_Mix_B_5_2_1_1_0044_014.fsa	C.fsa	9.42	72
	1_G04_Mix_B_5_2_1_1_0044_014.fsa	E.fsa	7.27	31
	1_G04_Mix_B_5_2_1_1_0044_014.fsa	F.fsa	-3.21	21
	1_G04_Mix_B_5_2_1_1_0044_014.fsa	G.fsa	-2.80	26
	1_G05_Mix_B_2_1_1_1_0041_013.fsa	C.fsa	7.56	225
	1_G05_Mix_B_2_1_1_1_0041_013.fsa	E.fsa	13.14	101
	1_G05_Mix_B_2_1_1_1_0041_013.fsa	F.fsa	1.39	78
	1_G05_Mix_B_2_1_1_1_0041_013.fsa	G.fsa	2.63	90
	1_G05_Mix_B_2_1_1_1_0045_013.fsa	C.fsa	3.52	42
	1_G05_Mix_B_2_1_1_1_0045_013.fsa	E.fsa	5.92	35
	1_G05_Mix_B_2_1_1_1_0045_013.fsa	F.fsa	-3.73	27
	1_G05_Mix_B_2_1_1_1_0045_013.fsa	G.fsa	2.84	25
	1_H01_Mix_A_5_1_1_1_0039_015.fsa	A.fsa	8.56	196
	1_H01_Mix_A_5_1_1_1_0039_015.fsa	B.fsa	6.58	65
	1_H01_Mix_A_5_1_1_1_0039_015.fsa	D.fsa	3.24	77
	1_H01_Mix_A_5_1_1_1_0039_015.fsa	G.fsa	8.48	62
	1_H01_Mix_A_5_1_1_1_0043_015.fsa	A.fsa	5.67	62
	1_H01_Mix_A_5_1_1_1_0043_015.fsa	B.fsa	2.61	47
	1_H01_Mix_A_5_1_1_1_0043_015.fsa	D.fsa	1.03	29
	1_H01_Mix_A_5_1_1_1_0043_015.fsa	G.fsa	1.56	20
	1_H03_Mix_B_10_10_10_1_0040_015.fsa	C.fsa	4.32	90
	1_H03_Mix_B_10_10_10_1_0040_015.fsa	E.fsa	17.21	136
	1_H03_Mix_B_10_10_10_1_0040_015.fsa	F.fsa	5.53	116
	1_H03_Mix_B_10_10_10_1_0040_015.fsa	G.fsa	-1.15	41
	1_H03_Mix_B_10_10_10_1_0044_015.fsa	C.fsa	4.32	39
	1_H03_Mix_B_10_10_10_1_0044_015.fsa	E.fsa	5.87	46
	1_H03_Mix_B_10_10_10_1_0044_015.fsa	F.fsa	1.69	35
	1_H03_Mix_B_10_10_10_1_0044_015.fsa	G.fsa	-3.75	20
	1_H05_Mix_B_2_2_1_1_0041_015.fsa	C.fsa	4.30	73
	1_H05_Mix_B_2_2_1_1_0041_015.fsa	E.fsa	14.57	125
	1_H05_Mix_B_2_2_1_1_0041_015.fsa	F.fsa	1.39	80
	1_H05_Mix_B_2_2_1_1_0041_015.fsa	G.fsa	6.49	49
	1_H05_Mix_B_2_2_1_1_0045_015.fsa	C.fsa	5.38	38
	1_H05_Mix_B_2_2_1_1_0045_015.fsa	E.fsa	6.25	37
	1_H05_Mix_B_2_2_1_1_0045_015.fsa	F.fsa	-2.08	22
	1_H05_Mix_B_2_2_1_1_0045_015.fsa	G.fsa	0.84	21
	2_B01_Mix_A_10_1_1_1_0047_003.fsa	A.fsa	11.82	61
	2_B01_Mix_A_10_1_1_1_0047_003.fsa	B.fsa	-0.62	25
	2_B01_Mix_A_10_1_1_1_0047_003.fsa	D.fsa	-0.43	20
	2_B01_Mix_A_10_1_1_1_0047_003.fsa	G.fsa	0.14	20
	2_D01_Mix_A_10_10_10_1_0047_007.fsa	A.fsa	5.84	41
	2_D01_Mix_A_10_10_10_1_0047_007.fsa	B.fsa	6.80	63
	2_D01_Mix_A_10_10_10_1_0047_007.fsa	D.fsa	1.74	36
	2_D01_Mix_A_10_10_10_1_0047_007.fsa	G.fsa	-1.38	20
	2_D03_Mix_A_2_2_1_1_0048_007.fsa	A.fsa	3.81	63
	2_D03_Mix_A_2_2_1_1_0048_007.fsa	B.fsa	8.69	207
	2_D03_Mix_A_2_2_1_1_0048_007.fsa	D.fsa	4.96	150
	2_D03_Mix_A_2_2_1_1_0048_007.fsa	G.fsa	6.16	63