CaseSolver

Version 1.8

by Øyvind Bleka, Oslo University Hospital

Many new features added

- New module: **Weight of evidence (WoE)**
  - Configure hypotheses as wanted (suggested from Matches table)
  - Supports evaluation of replicates (same as EuroForMix)
  - Fst/theta correction applied
  - Model validation performed and number of failed alleles summarized
  - Optional to conduct alternative LRs based on MCMC (addition to MLE):
    - BayesLR, ConsLR (quantile set as 5% by default).
  - Obtain suggested statements for each designed hypothesis sets
    - Can be edited in text editor
    - Statement formula can be easily be changed in Language spreadsheet
  - Other functionalities (for selected hypothesis set):
    - LR per marker
    - Model validation plot
    - ExpectedPH plot
    - Parameter estimates (Pie chart for mixture proportions)
  - All this is optional to add to report

- **Model extensions** (adopts EuroForMix version 3)
  - Possible to apply Forward stutters
  - Per-marker settings for Analytical threshold, Drop-in model and Fst.

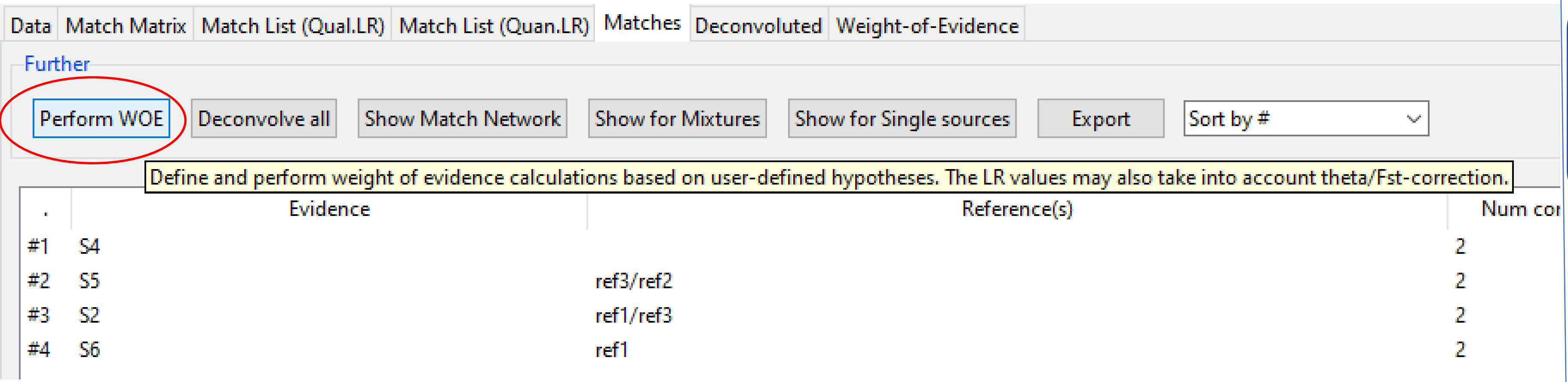
- New **exported report** possibilities:
    - In addition to HTML we user can optionally export as Word (DOCX or DOC).
    - Possible to reorganize report by changing the priority of report items.
    - Change graphical settings for images in report
- “Unknowns” and deconvoluted profiles are now separated out as “Extracted profiles” instead of “References” in the report.
- Tables in report will now be sorted similar as specified in GUI.
- Added **deconvolution features**:
    - Suggested deconvolved profile can be visualized in ExpPH plot.
    - Sort deconvolved profiles by similarity (performs hierarchical clustering)
    - Show RatioToNext values (used as quantification of deconvolution certainty)
        - Can also be added to report

- Dynamically adjust height of Evidence table vs Reference table (import data)
- Added tooltip for all buttons
    - explaining, in selected language, what operation it performs

Details follows

Weight-of-evidence module

Specifying hypothesis sets

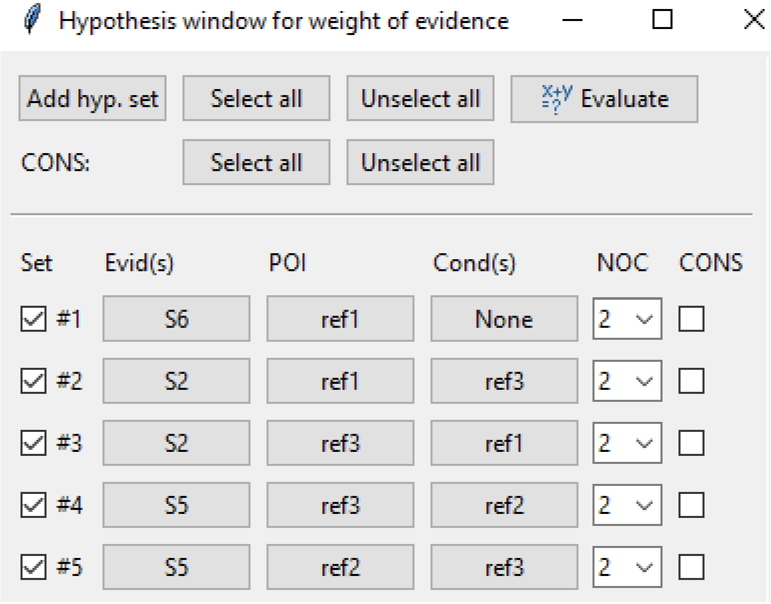


Define and perform weight of evidence calculations based on user-defined hypotheses. The LR values may also take into account theta/Fst-correction.

.	Evidence	Reference(s)	Num cor
#1	S4		2
#2	S5	ref3/ref2	2
#3	S2	ref1/ref3	2
#4	S6	ref1	2

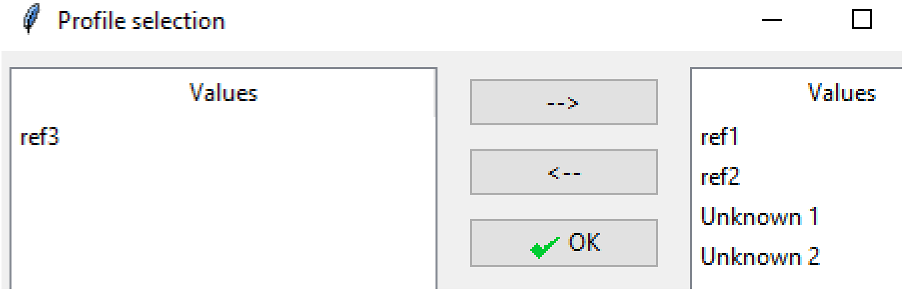
In relation to Hp/Hd:
Hp: POI + Cond(s) + #Uhp unknowns
Hd: Conds(s) + #Uhd unknowns

#Uhp = NOC - #conds - 1
#Uhd = NOC - #conds



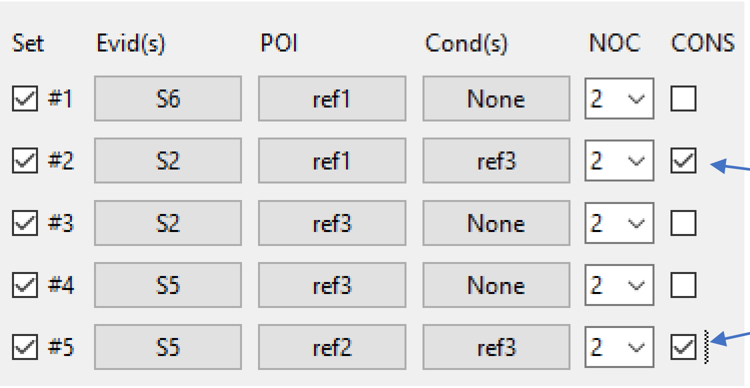
Set	Evid(s)	POI	Cond(s)	NOC	CONS
☑ #1	S6	ref1	None	2	☐
☑ #2	S2	ref1	ref3	2	☐
☑ #3	S2	ref3	ref1	2	☐
☑ #4	S5	ref3	ref2	2	☐
☑ #5	S5	ref2	ref3	2	☐

Easy to change profiles in hypothis set:



Values	Values
ref3	ref1
	ref2
	Unknown 1
	Unknown 2

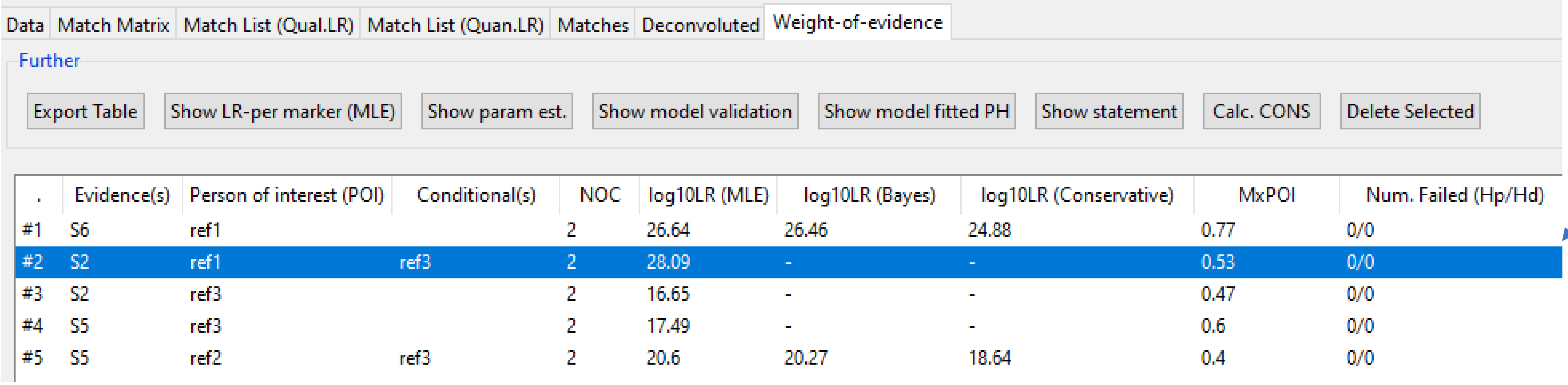
Weight-of-evidence results



Set	Evid(s)	POI	Cond(s)	NOC	CONS
☑ #1	S6	ref1	None	2	☐
☑ #2	S2	ref1	ref3	2	☑
☑ #3	S2	ref3	None	2	☐
☑ #4	S5	ref3	None	2	☐
☑ #5	S5	ref2	ref3	2	☑

Performs MCMC simulations for selected sets for the calculation of

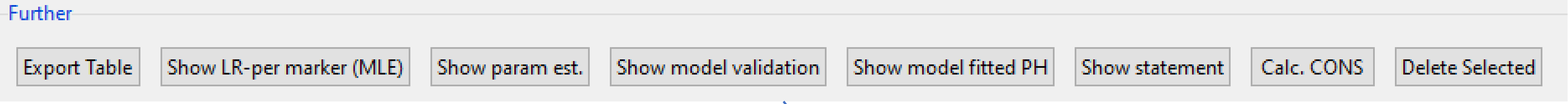
- Bayesian LR
- Conservative LR (5% quantile)

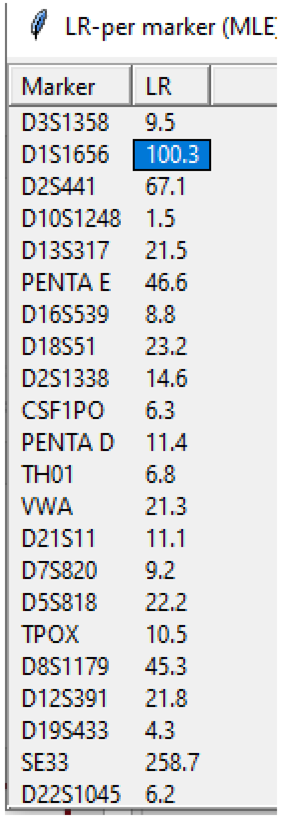


.	Evidence(s)	Person of interest (POI)	Conditional(s)	NOC	log10LR (MLE)	log10LR (Bayes)	log10LR (Conservative)	MxPOI	Num. Failed (Hp/Hd)
#1	S6	ref1		2	26.64	26.46	24.88	0.77	0/0
#2	S2	ref1	ref3	2	28.09	-	-	0.53	0/0
#3	S2	ref3		2	16.65	-	-	0.47	0/0
#4	S5	ref3		2	17.49	-	-	0.6	0/0
#5	S5	ref2	ref3	2	20.6	20.27	18.64	0.4	0/0

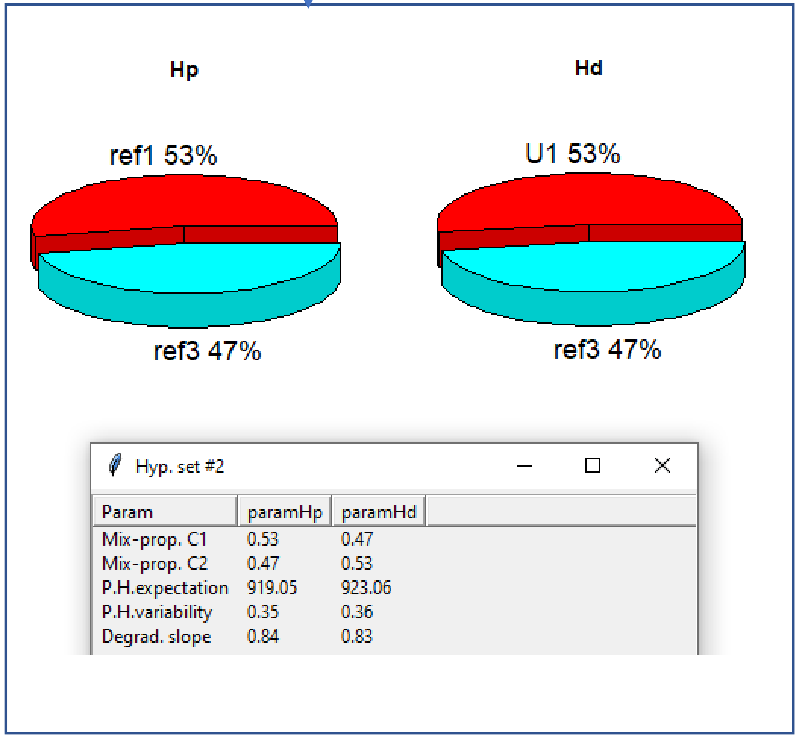
Select row for further functionalities

Further information (WOE)



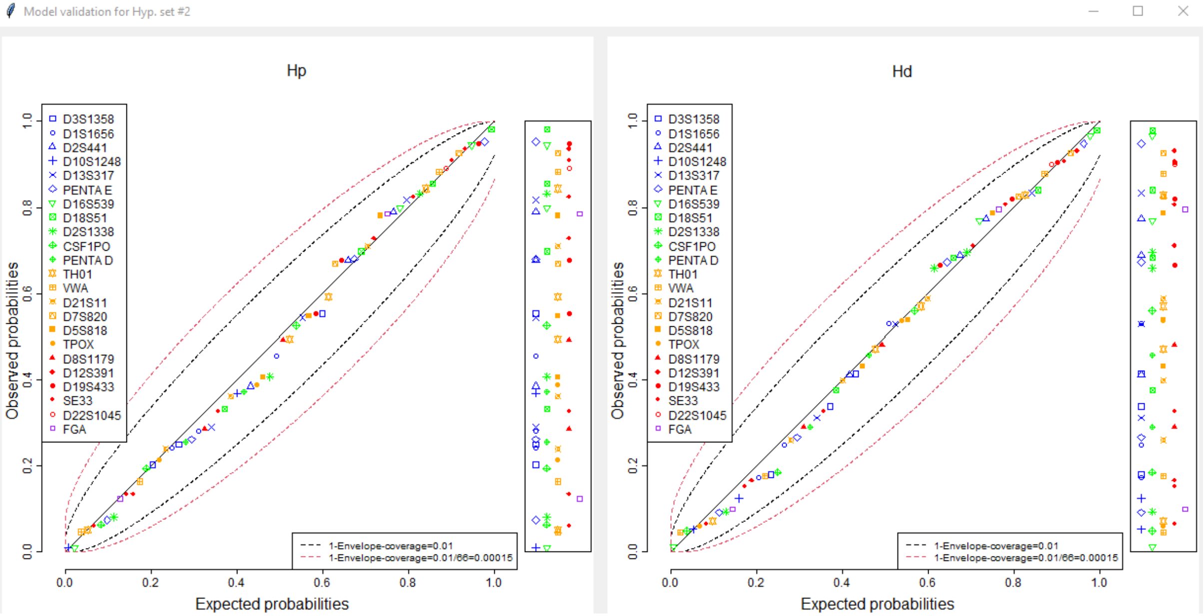


Marker	LR
D3S1358	9.5
D1S1656	100.3
D2S441	67.1
D10S1248	1.5
D13S317	21.5
PENTA E	46.6
D16S539	8.8
D18S51	23.2
D2S1338	14.6
CSF1PO	6.3
PENTA D	11.4
TH01	6.8
VWA	21.3
D21S11	11.1
D7S820	9.2
D5S818	22.2
TPOX	10.5
D8S1179	45.3
D12S391	21.8
D19S433	4.3
SE33	258.7
D22S1045	6.2



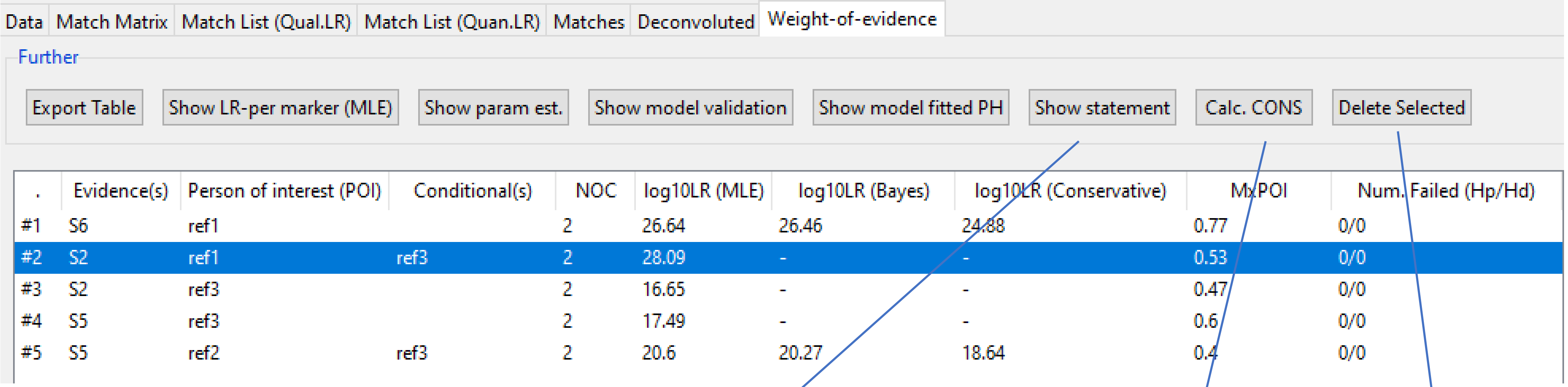
Param	paramHp	paramHd
Mix-prop. C1	0.53	0.47
Mix-prop. C2	0.47	0.53
P.H.expectation	919.05	923.06
P.H.variability	0.35	0.36
Degrad. slope	0.84	0.83

Uses signif level=0.01

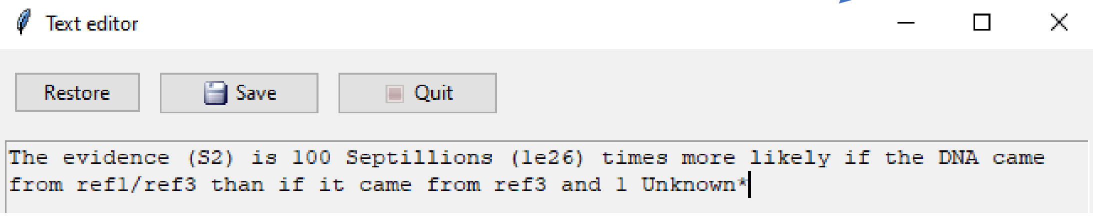


Number of points outside the red envelop lines indicated in the “Num.Failed (Hp/Hd)” column

Further information (WOE)



.	Evidence(s)	Person of interest (POI)	Conditional(s)	NOC	log10LR (MLE)	log10LR (Bayes)	log10LR (Conservative)	MxPOI	Num. Failed (Hp/Hd)
#1	S6	ref1		2	26.64	26.46	24.88	0.77	0/0
#2	S2	ref1	ref3	2	28.09	-	-	0.53	0/0
#3	S2	ref3		2	16.65	-	-	0.47	0/0
#4	S5	ref3		2	17.49	-	-	0.6	0/0
#5	S5	ref2	ref3	2	20.6	20.27	18.64	0.4	0/0



```
The evidence (S2) is 100 Septillions (1e26) times more likely if the DNA came
from ref1/ref3 than if it came from ref3 and 1 Unknown*
```

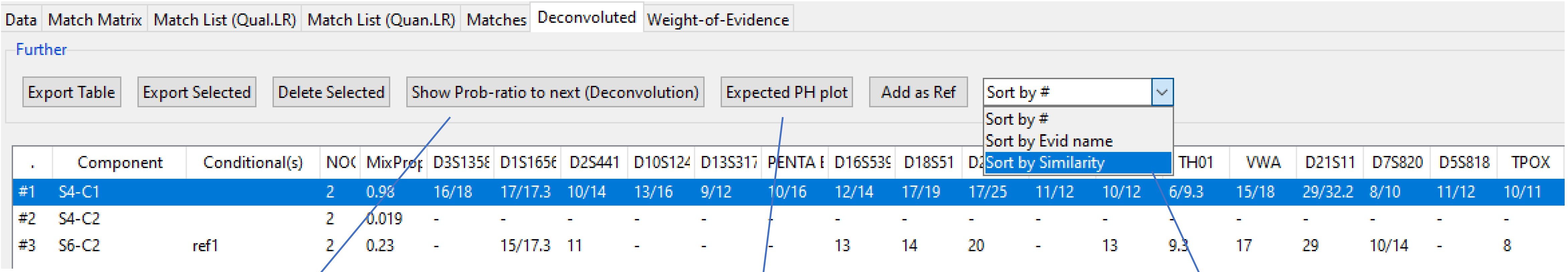
Possible to modify text before exporting to report

Delete row (hypothesis set)

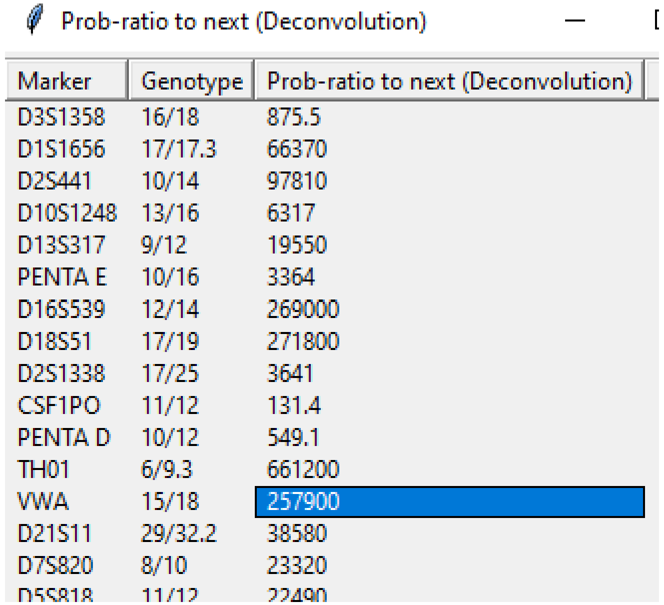
(Re-)Calculate Bayes/Cons LR for selected hypothesis (avoiding MLE recalculation)

Notice that it is possible to perform more WOE results afterwards!

Deconvolution

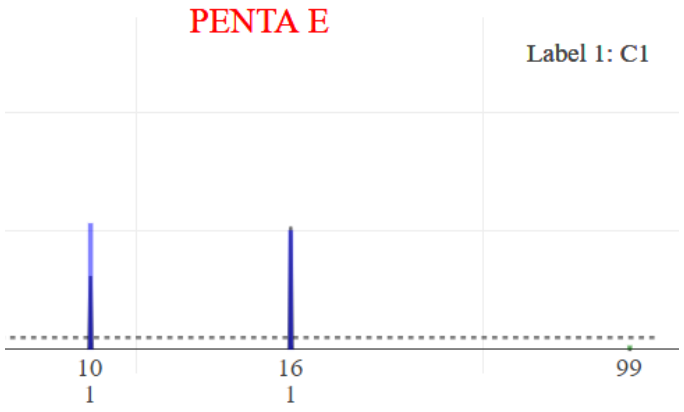


.	Component	Conditional(s)	NO(	MixProp	D3S135	D1S165	D2S441	D10S124	D13S317	PENTA E	D16S53	D18S51	D2			TH01	VWA	D21S11	D7S820	D5S818	TPOX
#1	S4-C1		2	0.98	16/18	17/17.3	10/14	13/16	9/12	10/16	12/14	17/19	17/25	11/12	10/12	6/9.3	15/18	29/32.2	8/10	11/12	10/11
#2	S4-C2		2	0.019	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
#3	S6-C2	ref1	2	0.23	-	15/17.3	11	-	-	-	13	14	20	-	13	9.3	17	29	10/14	-	8



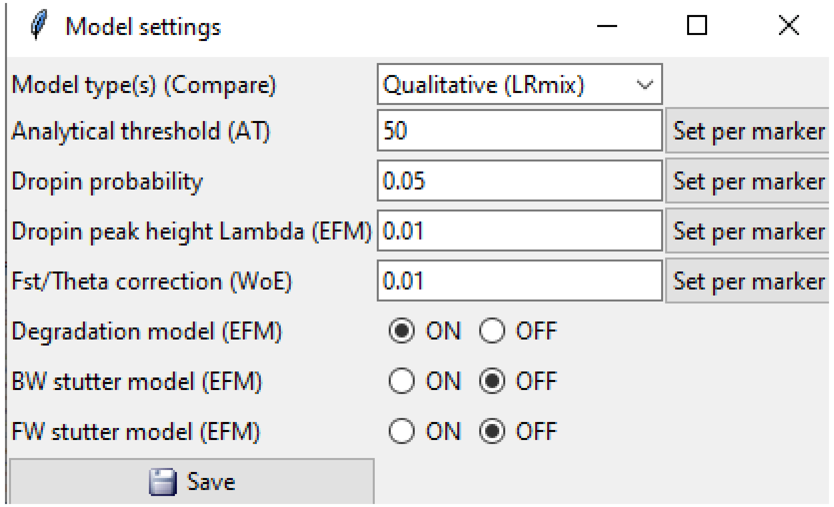
Marker	Genotype	Prob-ratio to next (Deconvolution)
D3S1358	16/18	875.5
D1S1656	17/17.3	66370
D2S441	10/14	97810
D10S1248	13/16	6317
D13S317	9/12	19550
PENTA E	10/16	3364
D16S539	12/14	269000
D18S51	17/19	271800
D2S1338	17/25	3641
CSF1PO	11/12	131.4
PENTA D	10/12	549.1
TH01	6/9.3	661200
VWA	15/18	257900
D21S11	29/32.2	38580
D7S820	8/10	23320
D5S818	11/12	22490

Alleles of extracted component is shown in EPG together with other conditionals

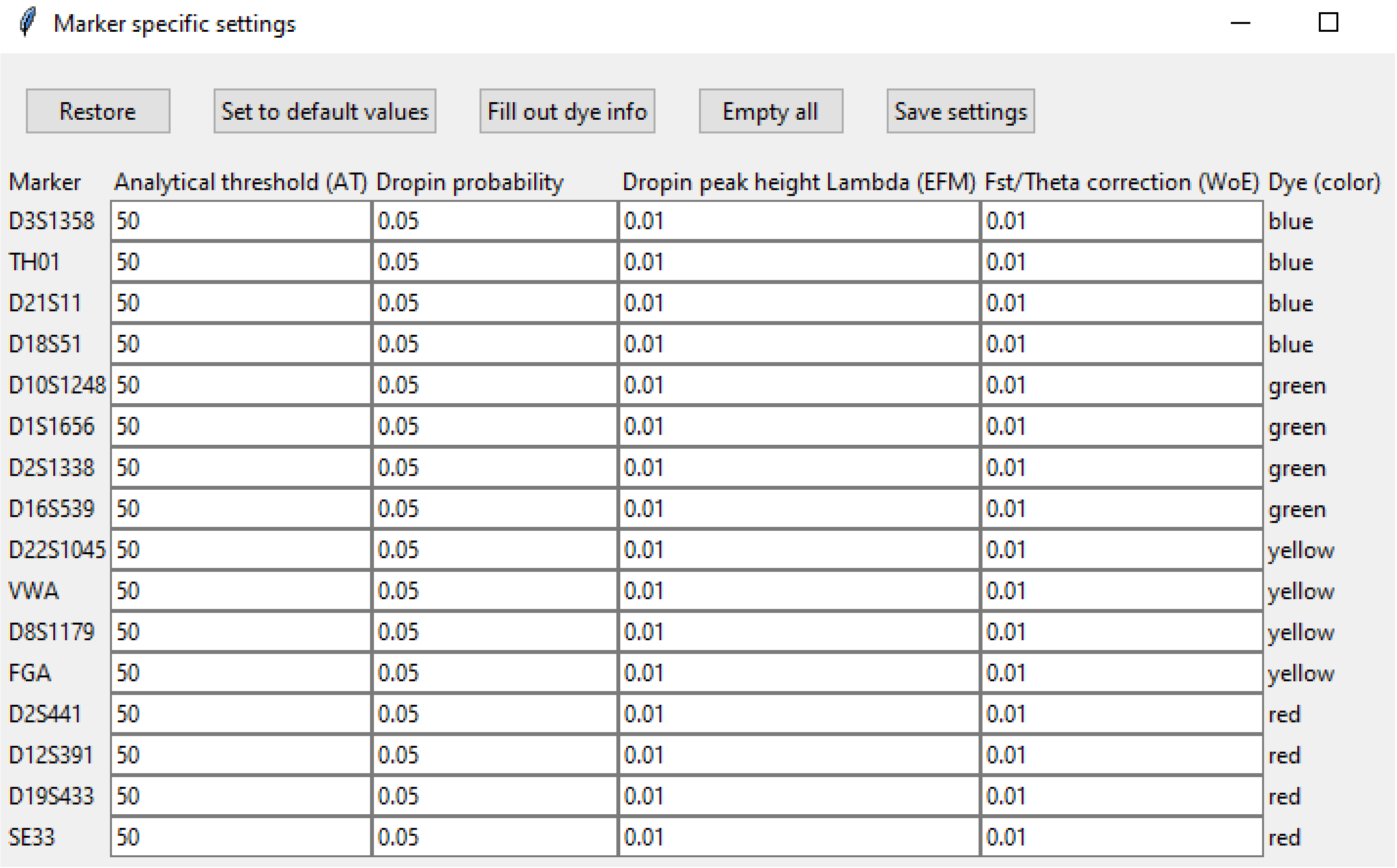


Sort by Similarity to easily structure many deconvolved profiles!

Selecting marker specific settings

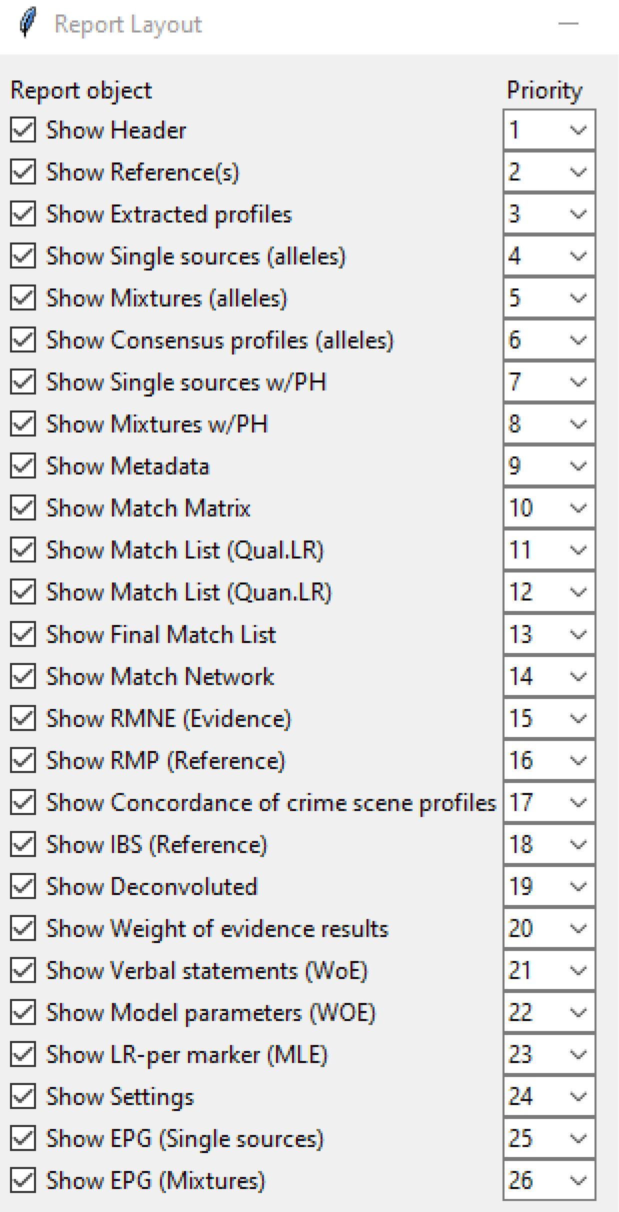


Model type(s) (Compare)	Qualitative (LRmix)
Analytical threshold (AT)	50
Dropin probability	0.05
Dropin peak height Lambda (EFM)	0.01
Fst/Theta correction (WoE)	0.01
Degradation model (EFM)	● ON ○ OFF
BW stutter model (EFM)	○ ON ● OFF
FW stutter model (EFM)	○ ON ● OFF



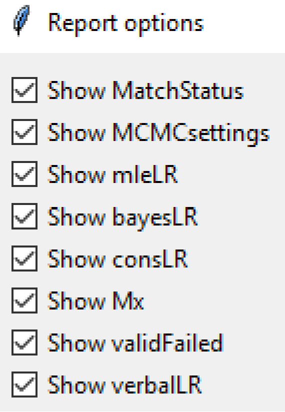
Marker	Analytical threshold (AT)	Dropin probability	Dropin peak height Lambda (EFM)	Fst/Theta correction (WoE)	Dye (color)
D3S1358	50	0.05	0.01	0.01	blue
TH01	50	0.05	0.01	0.01	blue
D21S11	50	0.05	0.01	0.01	blue
D18S51	50	0.05	0.01	0.01	blue
D10S1248	50	0.05	0.01	0.01	green
D1S1656	50	0.05	0.01	0.01	green
D2S1338	50	0.05	0.01	0.01	green
D16S539	50	0.05	0.01	0.01	green
D22S1045	50	0.05	0.01	0.01	yellow
VWA	50	0.05	0.01	0.01	yellow
D8S1179	50	0.05	0.01	0.01	yellow
FGA	50	0.05	0.01	0.01	yellow
D2S441	50	0.05	0.01	0.01	red
D12S391	50	0.05	0.01	0.01	red
D19S433	50	0.05	0.01	0.01	red
SE33	50	0.05	0.01	0.01	red

Report settings



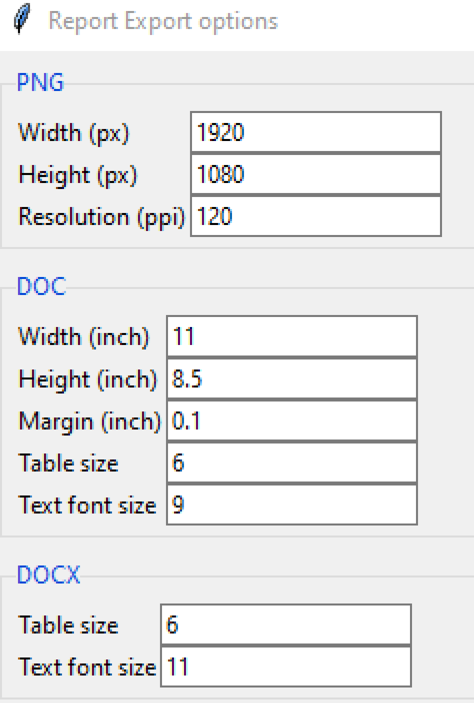
Report Layout

Report object	Priority
☑ Show Header	1
☑ Show Reference(s)	2
☑ Show Extracted profiles	3
☑ Show Single sources (alleles)	4
☑ Show Mixtures (alleles)	5
☑ Show Consensus profiles (alleles)	6
☑ Show Single sources w/PH	7
☑ Show Mixtures w/PH	8
☑ Show Metadata	9
☑ Show Match Matrix	10
☑ Show Match List (Qual.LR)	11
☑ Show Match List (Quan.LR)	12
☑ Show Final Match List	13
☑ Show Match Network	14
☑ Show RMNE (Evidence)	15
☑ Show RMP (Reference)	16
☑ Show Concordance of crime scene profiles	17
☑ Show IBS (Reference)	18
☑ Show Deconvoluted	19
☑ Show Weight of evidence results	20
☑ Show Verbal statements (WoE)	21
☑ Show Model parameters (WOE)	22
☑ Show LR-per marker (MLE)	23
☑ Show Settings	24
☑ Show EPG (Single sources)	25
☑ Show EPG (Mixtures)	26



Report options

☑ Show MatchStatus
☑ Show MCMCsettings
☑ Show mleLR
☑ Show bayesLR
☑ Show consLR
☑ Show Mx
☑ Show validFailed
☑ Show verbalLR



Report Export options

PNG

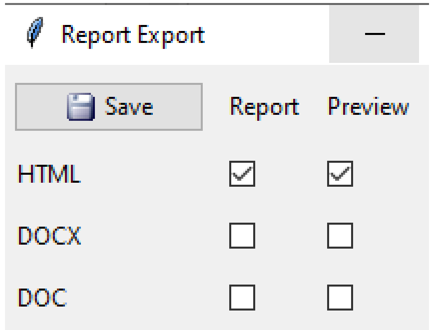
Width (px): 1920
Height (px): 1080
Resolution (ppi): 120

DOC

Width (inch): 11
Height (inch): 8.5
Margin (inch): 0.1
Table size: 6
Text font size: 9

DOCX

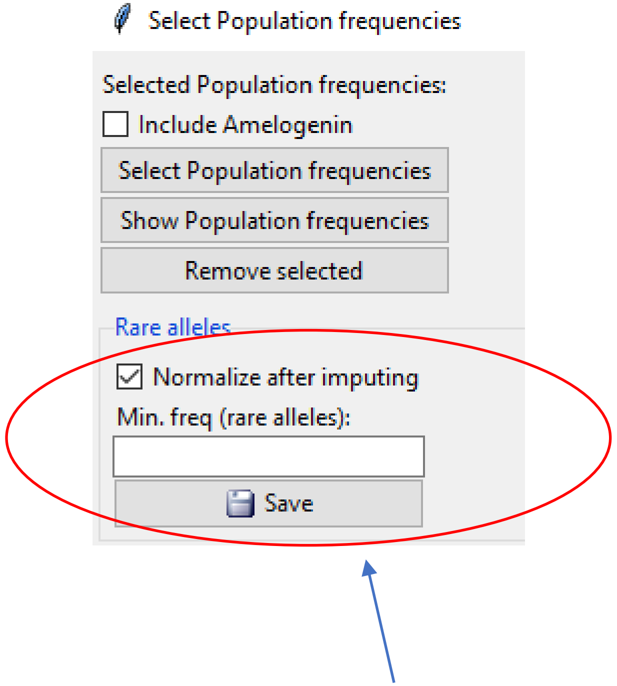
Table size: 6
Text font size: 11



Report Export

Save	Report	Preview
HTML	☑	☑
DOCX	☐	☐
DOC	☐	☐

Other added settings



Select Population frequencies

Selected Population frequencies:

☐ Include Amelogenin

Rare alleles

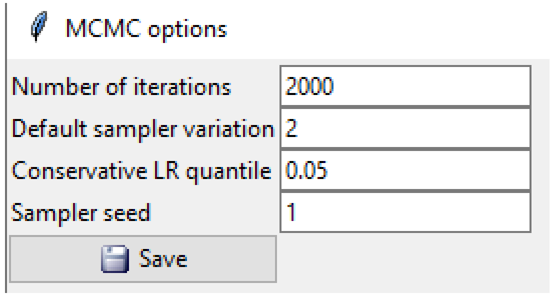
☑ Normalize after imputing

Min. freq (rare alleles):

Similar as in EuroForMix

MCMC settings used for quantifying Weight-of-evidence results:

- ConsLR
- BayesLR

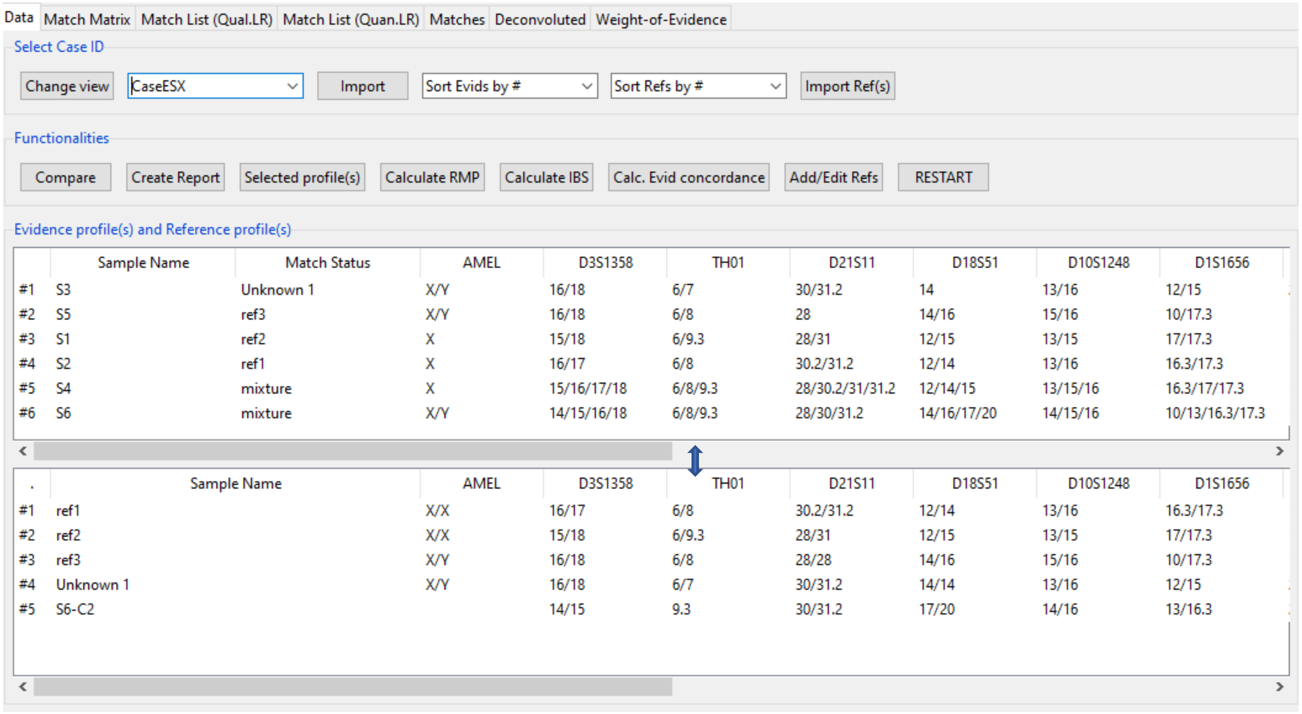


MCMC options

Number of iterations	2000
Default sampler variation	2
Conservative LR quantile	0.05
Sampler seed	1

Sliding adjustment between two tables

Adjust table windows between evidence and reference profiles



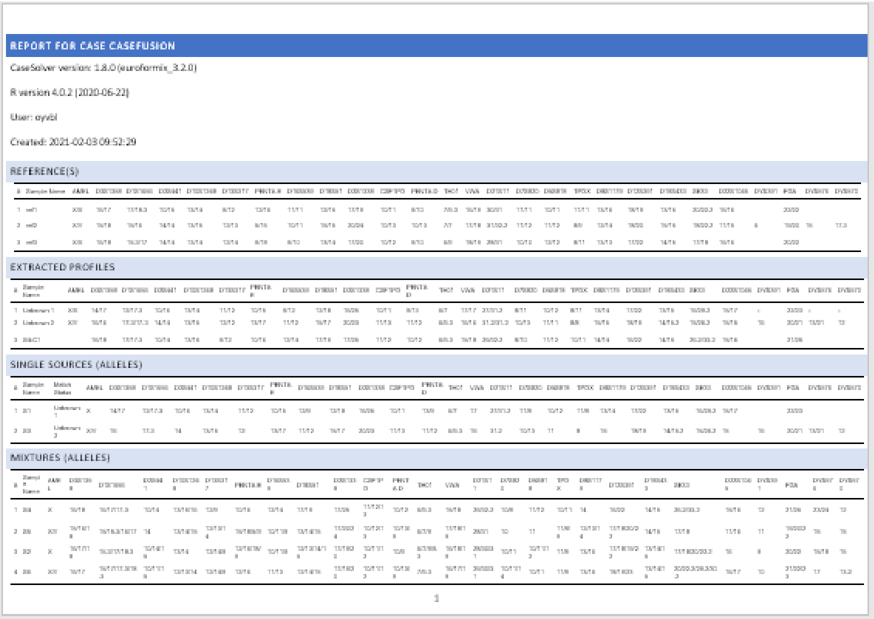
	Sample Name	Match Status	AMEL	D3S1358	TH01	D21S11	D18S51	D10S1248	D1S1656
#1	S3	Unknown 1	X/Y	16/18	6/7	30/31.2	14	13/16	12/15
#2	S5	ref3	X/Y	16/18	6/8	28	14/16	15/16	10/17.3
#3	S1	ref2	X	15/18	6/9.3	28/31	12/15	13/15	17/17.3
#4	S2	ref1	X	16/17	6/8	30.2/31.2	12/14	13/16	16.3/17.3
#5	S4	mixture	X	15/16/17/18	6/8/9.3	28/30.2/31/31.2	12/14/15	13/15/16	16.3/17/17.3
#6	S6	mixture	X/Y	14/15/16/18	6/8/9.3	28/30/31.2	14/16/17/20	14/15/16	10/13/16.3/17.3

.	Sample Name	AMEL	D3S1358	TH01	D21S11	D18S51	D10S1248	D1S1656
#1	ref1	X/X	16/17	6/8	30.2/31.2	12/14	13/16	16.3/17.3
#2	ref2	X/X	15/18	6/9.3	28/31	12/15	13/15	17/17.3
#3	ref3	X/Y	16/18	6/8	28/28	14/16	15/16	10/17.3
#4	Unknown 1	X/Y	16/18	6/7	30/31.2	14/14	13/16	12/15
#5	S6-C2		14/15	9.3	30/31.2	17/20	14/16	13/16.3

Report

Export as word file (editable)

Based on word-template found in installation folder (**reportTemplate.docx**)



REPORT FOR CASE CASEFUSION

CaseSolver version: 1.8.0 (euroformix_3.2.0)

R version 4.0.2 (2020-06-22)

User: oyvbl

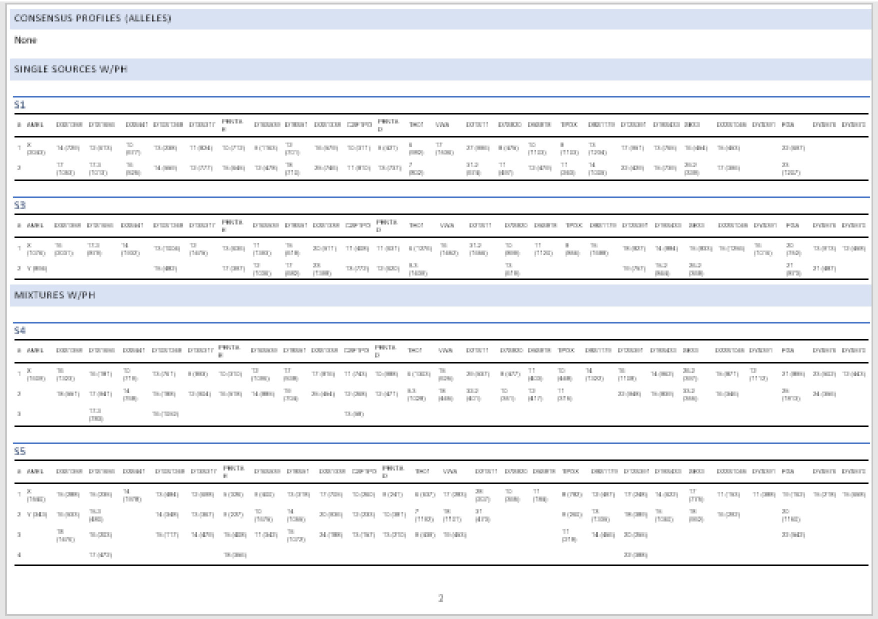
Created: 2021-02-03 09:52:29

REFERENCE(S)

EXTRACTED PROFILES

SINGLE SOURCES (ALLELES)

MIXTURES (ALLELES)



CONSENSUS PROFILES (ALLELES)

None

SINGLE SOURCES W/PH

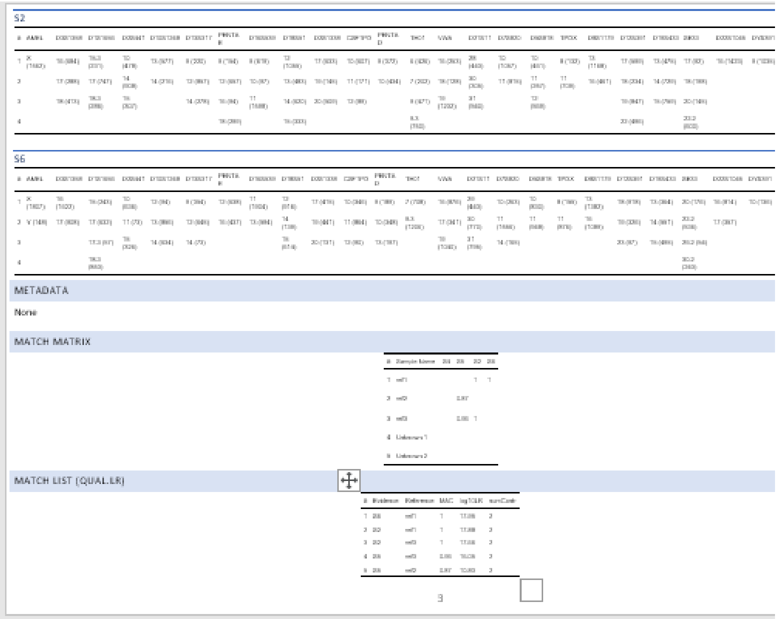
S1

S3

MIXTURES W/PH

S4

S5



S2

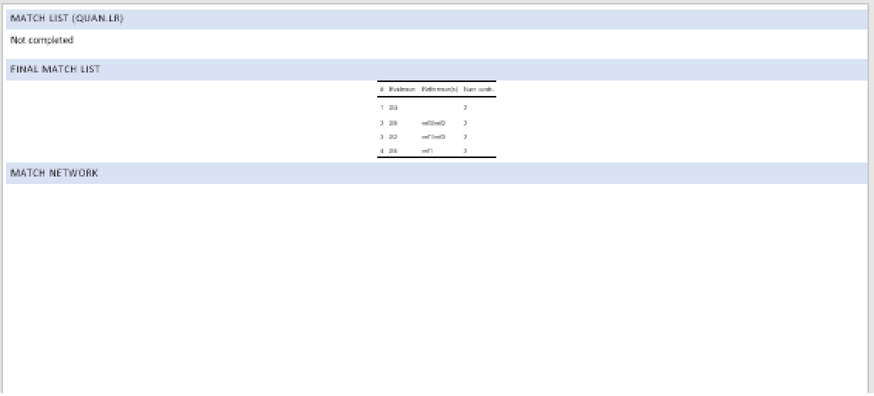
S6

METADATA

None

MATCH MATRIX

MATCH LIST (QUAL.LR)

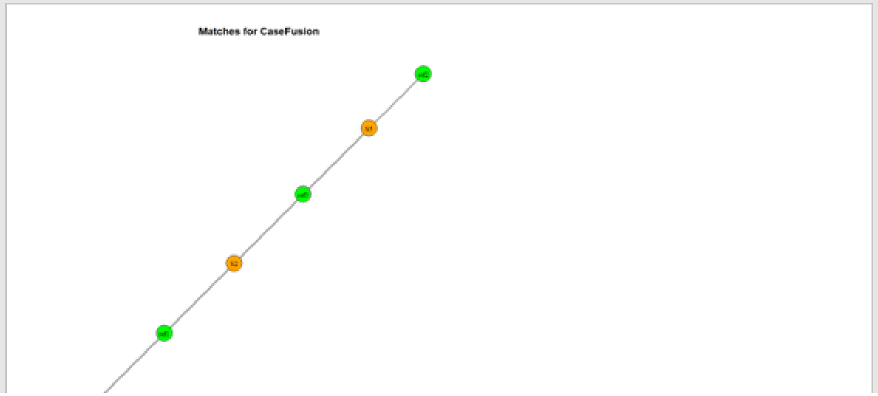


MATCH LIST (QUAN.LR)

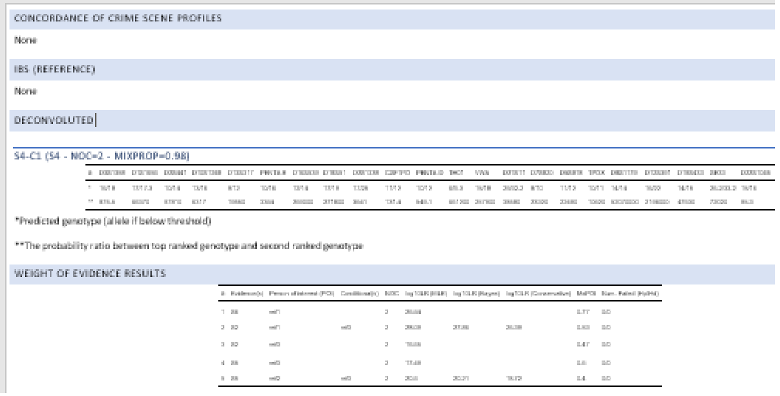
Not completed

FINAL MATCH LIST

MATCH NETWORK



Matches for CaseFusion



CONCORDANCE OF CRIME SCENE PROFILES

None

IBS (REFERENCE)

None

DECONVOLUTED

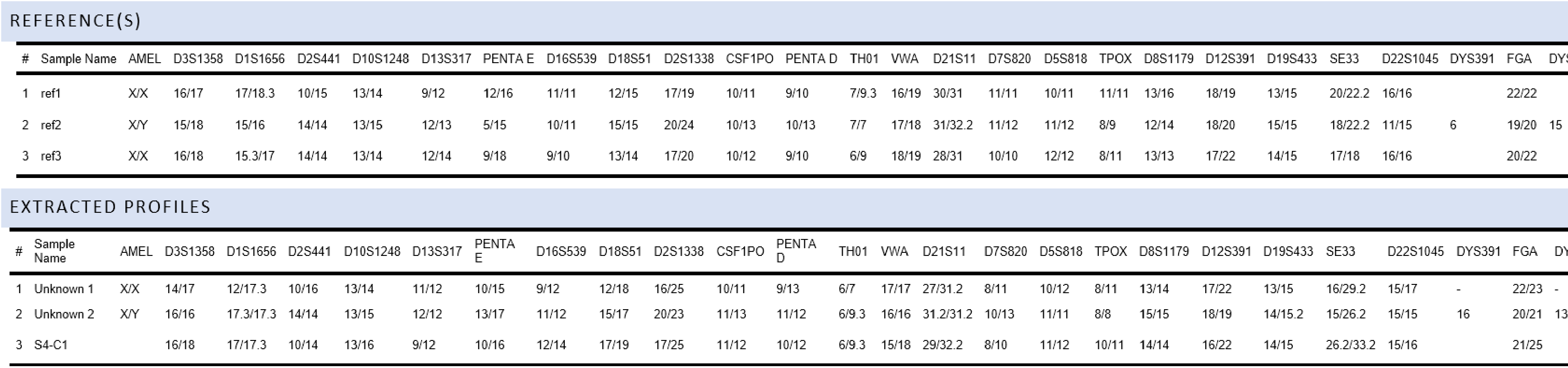
S4-C1 (S4 - NOC=2 - MIXPROP=0.98)

*Predicted genotype (allele if below threshold)

**The probability ratio between top ranked genotype and second ranked genotype

WEIGHT OF EVIDENCE RESULTS

References (known) vs extracted (unknown)



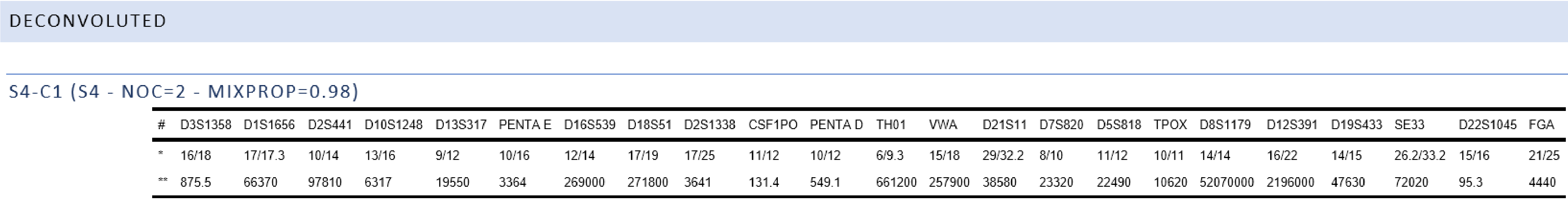
REFERENCE(S)

#	Sample Name	AMEL	D3S1358	D1S1656	D2S441	D10S1248	D13S317	PENTA E	D16S539	D18S51	D2S1338	CSF1PO	PENTA D	TH01	VWA	D21S11	D7S820	D5S818	TPOX	D8S1179	D12S391	D19S433	SE33	D22S1045	DYS391	FGA	DY
1	ref1	X/X	16/17	17/18.3	10/15	13/14	9/12	12/16	11/11	12/15	17/19	10/11	9/10	7/9.3	16/19	30/31	11/11	10/11	11/11	13/16	18/19	13/15	20/22.2	16/16		22/22	
2	ref2	X/Y	15/18	15/16	14/14	13/15	12/13	5/15	10/11	15/15	20/24	10/13	10/13	7/7	17/18	31/32.2	11/12	11/12	8/9	12/14	18/20	15/15	18/22.2	11/15	6	19/20	15
3	ref3	X/X	16/18	15.3/17	14/14	13/14	12/14	9/18	9/10	13/14	17/20	10/12	9/10	6/9	18/19	28/31	10/10	12/12	8/11	13/13	17/22	14/15	17/18	16/16		20/22	

EXTRACTED PROFILES

#	Sample Name	AMEL	D3S1358	D1S1656	D2S441	D10S1248	D13S317	PENTA E	D16S539	D18S51	D2S1338	CSF1PO	PENTA D	TH01	VWA	D21S11	D7S820	D5S818	TPOX	D8S1179	D12S391	D19S433	SE33	D22S1045	DYS391	FGA	DY
1	Unknown 1	X/X	14/17	12/17.3	10/16	13/14	11/12	10/15	9/12	12/18	16/25	10/11	9/13	6/7	17/17	27/31.2	8/11	10/12	8/11	13/14	17/22	13/15	16/29.2	15/17	-	22/23	-
2	Unknown 2	X/Y	16/16	17.3/17.3	14/14	13/15	12/12	13/17	11/12	15/17	20/23	11/13	11/12	6/9.3	16/16	31.2/31.2	10/13	11/11	8/8	15/15	18/19	14/15.2	15/26.2	15/15	16	20/21	13
3	S4-C1		16/18	17/17.3	10/14	13/16	9/12	10/16	12/14	17/19	17/25	11/12	10/12	6/9.3	15/18	29/32.2	8/10	11/12	10/11	14/14	16/22	14/15	26.2/33.2	15/16		21/25	

Deconvolution results



DECONVOLUTED

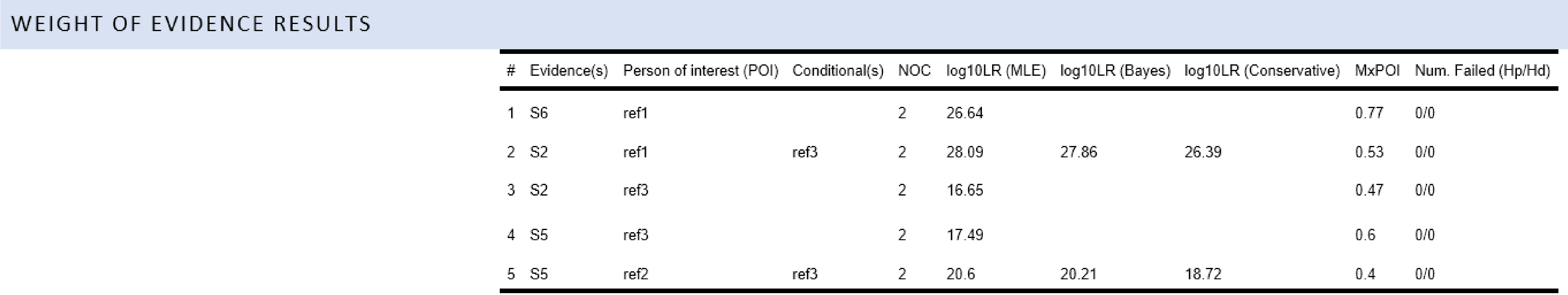
S4-C1 (S4 - NOC=2 - MIXPROP=0.98)

#	D3S1358	D1S1656	D2S441	D10S1248	D13S317	PENTA E	D16S539	D18S51	D2S1338	CSF1PO	PENTA D	TH01	VWA	D21S11	D7S820	D5S818	TPOX	D8S1179	D12S391	D19S433	SE33	D22S1045	FGA
*	16/18	17/17.3	10/14	13/16	9/12	10/16	12/14	17/19	17/25	11/12	10/12	6/9.3	15/18	29/32.2	8/10	11/12	10/11	14/14	16/22	14/15	26.2/33.2	15/16	21/25
**	875.5	66370	97810	6317	19550	3364	269000	271800	3641	131.4	549.1	661200	257900	38580	23320	22490	10620	52070000	2196000	47630	72020	95.3	4440

*Predicted genotype (allele if below threshold)

**The probability ratio between top ranked genotype and second ranked genotype

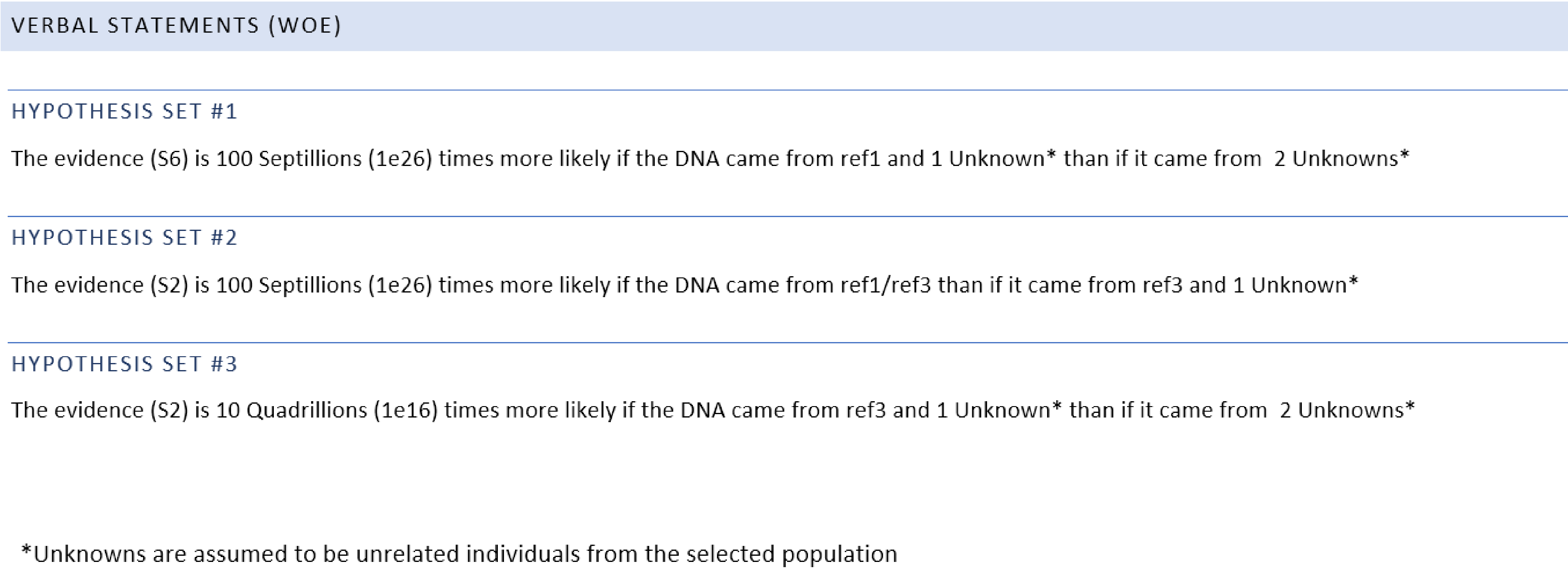
Weight of evidence results: Table



WEIGHT OF EVIDENCE RESULTS

#	Evidence(s)	Person of interest (POI)	Conditional(s)	NOC	log10LR (MLE)	log10LR (Bayes)	log10LR (Conservative)	MxPOI	Num. Failed (Hp/Hd)
1	S6	ref1		2	26.64			0.77	0/0
2	S2	ref1	ref3	2	28.09	27.86	26.39	0.53	0/0
3	S2	ref3		2	16.65			0.47	0/0
4	S5	ref3		2	17.49			0.6	0/0
5	S5	ref2	ref3	2	20.6	20.21	18.72	0.4	0/0

Weight of evidence: Verbal statements



VERBAL STATEMENTS (WOE)

HYPOTHESIS SET #1

The evidence (S6) is 100 Septillions (1e26) times more likely if the DNA came from ref1 and 1 Unknown* than if it came from 2 Unknowns*

HYPOTHESIS SET #2

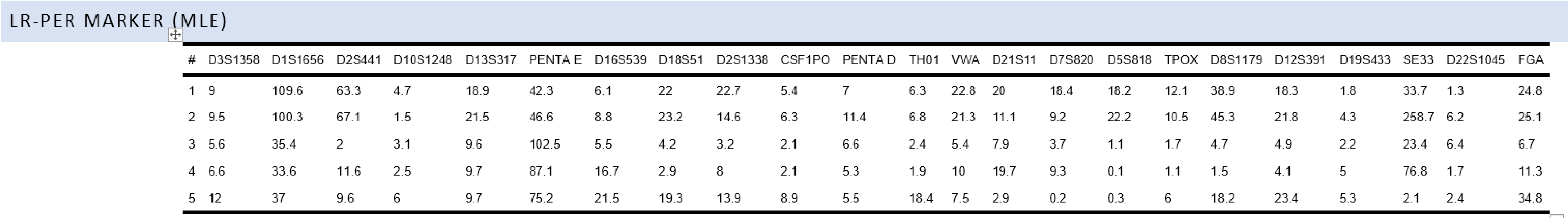
The evidence (S2) is 100 Septillions (1e26) times more likely if the DNA came from ref1/ref3 than if it came from ref3 and 1 Unknown*

HYPOTHESIS SET #3

The evidence (S2) is 10 Quadrillions (1e16) times more likely if the DNA came from ref3 and 1 Unknown* than if it came from 2 Unknowns*

*Unknowns are assumed to be unrelated individuals from the selected population

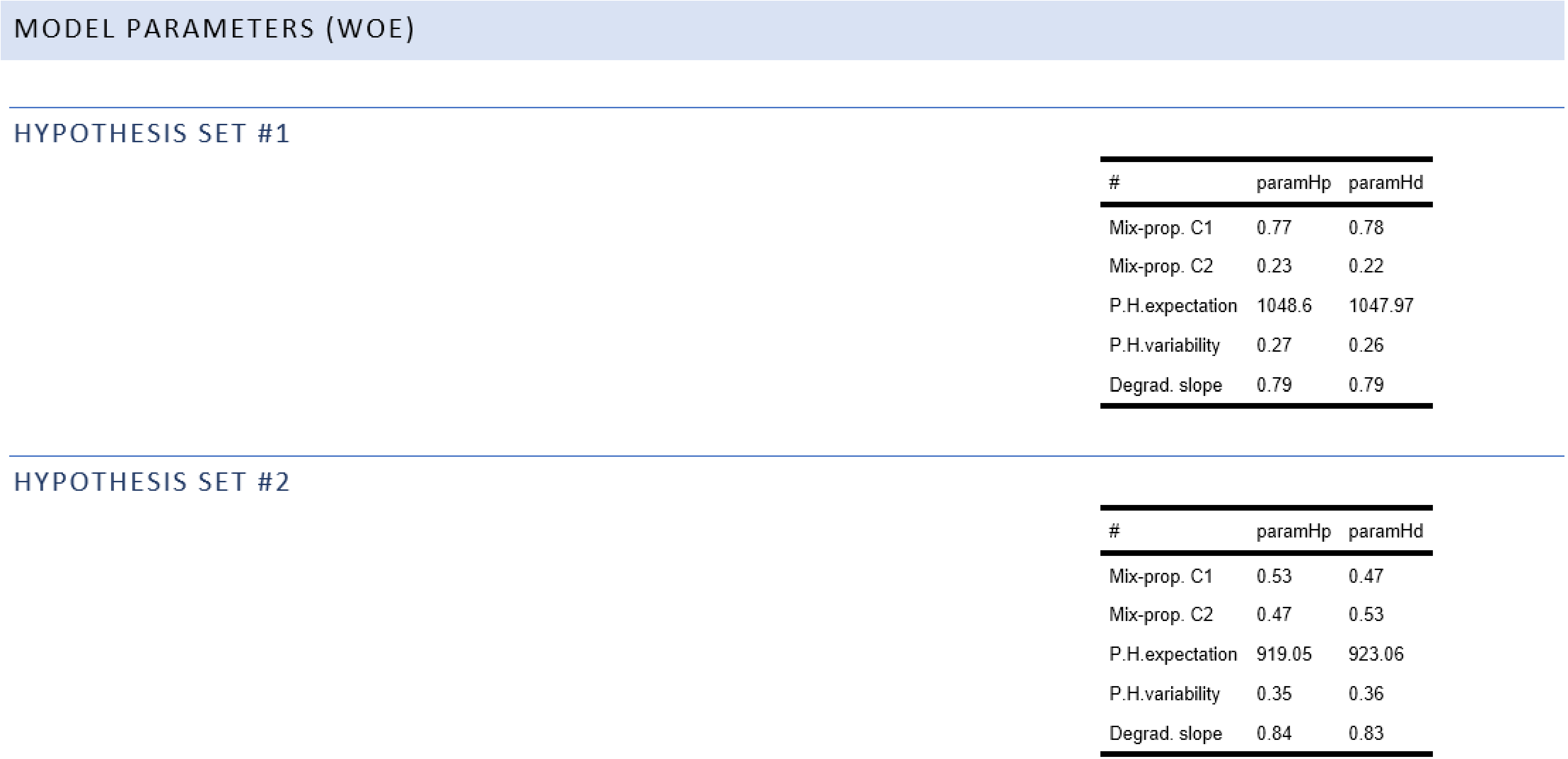
Weight of evidence: LR-per marker



LR-PER MARKER (MLE)

#	D3S1358	D1S1656	D2S441	D10S1248	D13S317	PENTA E	D16S539	D18S51	D2S1338	CSF1PO	PENTA D	TH01	VWA	D21S11	D7S820	D5S818	TPOX	D8S1179	D12S391	D19S433	SE33	D22S1045	FGA
1	9	109.6	63.3	4.7	18.9	42.3	6.1	22	22.7	5.4	7	6.3	22.8	20	18.4	18.2	12.1	38.9	18.3	1.8	33.7	1.3	24.8
2	9.5	100.3	67.1	1.5	21.5	46.6	8.8	23.2	14.6	6.3	11.4	6.8	21.3	11.1	9.2	22.2	10.5	45.3	21.8	4.3	258.7	6.2	25.1
3	5.6	35.4	2	3.1	9.6	102.5	5.5	4.2	3.2	2.1	6.6	2.4	5.4	7.9	3.7	1.1	1.7	4.7	4.9	2.2	23.4	6.4	6.7
4	6.6	33.6	11.6	2.5	9.7	87.1	16.7	2.9	8	2.1	5.3	1.9	10	19.7	9.3	0.1	1.1	1.5	4.1	5	76.8	1.7	11.3
5	12	37	9.6	6	9.7	75.2	21.5	19.3	13.9	8.9	5.5	18.4	7.5	2.9	0.2	0.3	6	18.2	23.4	5.3	2.1	2.4	34.8

Weight of evidence: Model parameters



MODEL PARAMETERS (WOE)

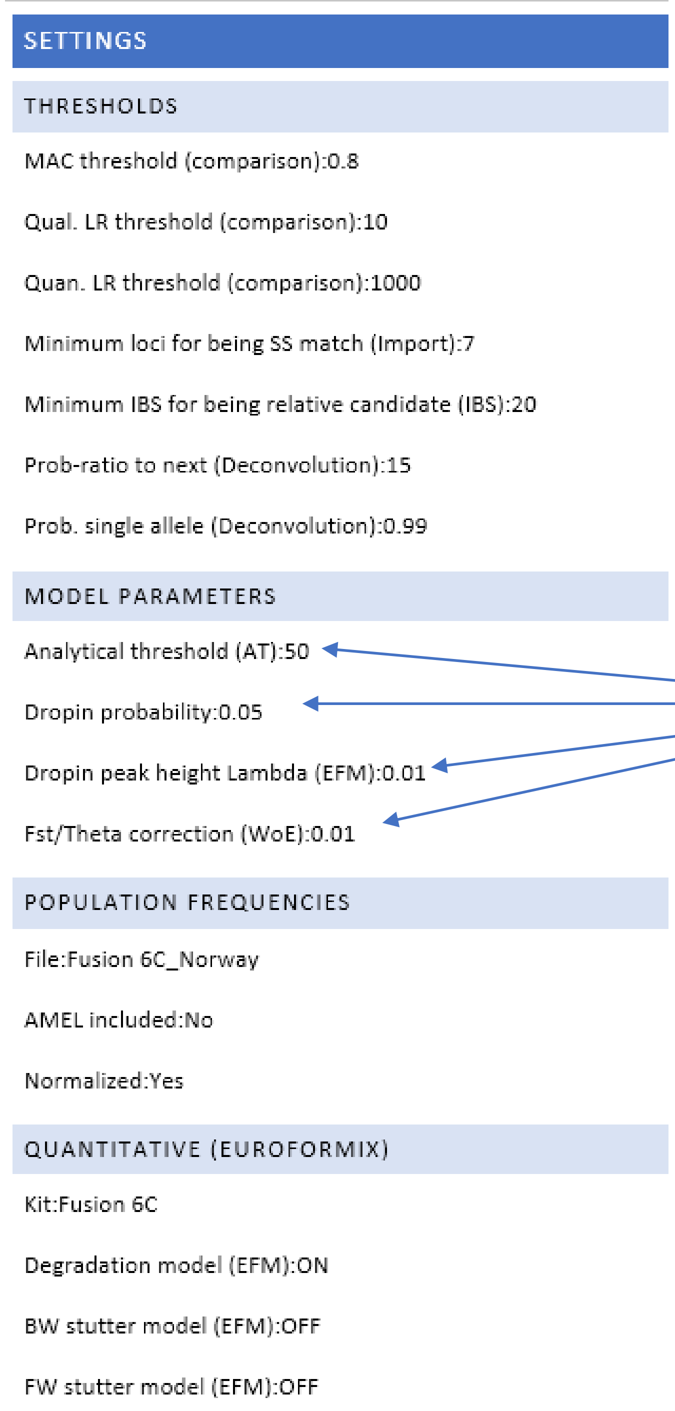
HYPOTHESIS SET #1

#	paramHp	paramHd
Mix-prop. C1	0.77	0.78
Mix-prop. C2	0.23	0.22
P.H.expectation	1048.6	1047.97
P.H.variability	0.27	0.26
Degrad. slope	0.79	0.79

HYPOTHESIS SET #2

#	paramHp	paramHd
Mix-prop. C1	0.53	0.47
Mix-prop. C2	0.47	0.53
P.H.expectation	919.05	923.06
P.H.variability	0.35	0.36
Degrad. slope	0.84	0.83

Settings



SETTINGS

THRESHOLDS

MAC threshold (comparison):0.8

Qual. LR threshold (comparison):10

Quan. LR threshold (comparison):1000

Minimum loci for being SS match (Import):7

Minimum IBS for being relative candidate (IBS):20

Prob-ratio to next (Deconvolution):15

Prob. single allele (Deconvolution):0.99

MODEL PARAMETERS

Analytical threshold (AT):50

Dropin probability:0.05

Dropin peak height Lambda (EFM):0.01

Fst/Theta correction (WoE):0.01

POPULATION FREQUENCIES

File:Fusion 6C_Norway

AMEL included:No

Normalized:Yes

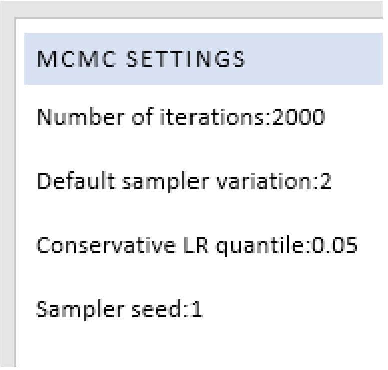
QUANTITATIVE (EUROFORMIX)

Kit:Fusion 6C

Degradation model (EFM):ON

BW stutter model (EFM):OFF

FW stutter model (EFM):OFF



MCMC SETTINGS

Number of iterations:2000

Default sampler variation:2

Conservative LR quantile:0.05

Sampler seed:1

Will show for each marker if specified