AGENDA FOR THE EDNAP MEETING

OSLO, NORWAY

3 OCTOBER 2023

Registration: 08.00 – 08.30

Expected duration: 08.30 - 17.30

Coffee: 11.00-11.30 – Lunch: 13.00-14.00 – Coffee: 15.30-16.00

Hosts: Solveig Jacobsen and Ane Elida Fonneløp

Chairman: Denise Syndercombe Court

Welcome	Solveig Jacobsen & Ane Elida Fonneløp
Special session with Walther Parson on Teams	
The future of EDNAP	Walther Parson & Niels Morling
Update on activities	
mtDNA quantification exercise	Arnoud Kal
Methylated DNA and age exercise	Denise S. Court
Exercise no. four on cSNPs (vaginal secretion, menstrual blood, and skin)	Cordula Haas
The series of exercises relating to DNA transfer	Baas Kokshoorn
Updates from other groups	
ENFSI	Sander Kneppers
Presentations	
Exhaustive propositions	Peter Gill
Future activities	
Suggestion for a Paper Exercise on Estimating Biogeographic Ancestry from DNA	Chris Phillips, Marta Diepenbroek & Walther Parson
Next EDNAP meeting	Niels Morling
Any other business	Niels Morling

EUROPEAN DNA PROFILING GROUP (EDNAP) MEETING

Oslo, Norway

3 October 2023

Host: Ane Elida Fonneløp and Solveig Jacobsen.
Chairman: Denise Syndercombe Court.

A list of participants is attached.

Welcome
Ane Elida Fonneløp welcomed members to Oslo.

The future of EDNAP Walther Parson and Niels Morling on Teams

Walther Parson had circulated considerations (attached) and a draft of EDNAP terms of references (TOR) (attached). Walther Parson presented his considerations (attached). The suggestions were discussed.

EDNAP secretary Niels Morling announced he will retire as Professor of Forensic Genetics at the University of Copenhagen in 2024 and as secretary of EDNAP.

Members discussed the suggestions and made the following decisions:

- EDNAP's core principles of exploring forensic genetics research through joint exercises, publication, and driving the development of future ideas were reiterated.
- The decline in research activity, the changed role of EDNAP during the last years, and the need for adjusting the organization of EDNAP was aggreed.
- EDNAP will continue as a working group under the International Society for Forensic Genetics.
- Membership of EDNAP will change from country and laboratory representation to personal membership of active researchers in forensic genetics.
- EDNAP will continue twice-yearly meetings with an in-person meeting aligned with ENFSI meetings.
- A possible move to online meetings for the second meeting will be made at the next meeting in 2024.
- Additional online meetings relating to collaborative research will be arranged if required.
- The EDNAP organization will be updated with two co-chairs elected by voting to lead with terms to be decided.
- Other platforms for collaboration and communications will be established to facilitate sharing ideas for new exercises and discussions of ongoing exercises available for all members so that meetings provide better opportunities for discussions and decisions.
- Emphasis on timely group publications and looking for funding opportunities.

An interim group to debate ideas discussed about future directions and present a suggestion for Terms of References at the next EDNAP meeting (29 May 2024, cf. below) was established with the following members: Cordula Haas, Niels Morling, Geraldine O'Donnell, Walther Parson, Vince Pascali, Chris Phillips, and Bo Simonsen.

Update on exercises

mtDNA quantification exercise Arnoud Kaal

Arnoud Kaal reported that the previous exercise demonstrated that the methodology provided too much variability for casework. The results will not be published. The methodology used by NFI has changed. Members use mtDNA analyses without the ability to quantify mtDNA and would welcome a new exercise in this area.

Second exercise on methylated DNA and age Denise Syndercombe Court

A two-part exercise was completed some years ago. The work has been presented at meetings. The results of the exercise remain relevant. The organisers commit to publishing the data.

Exercise no. 4 on mRNA typing with MPS Cordula Haas

Cordula Haas recapitulated the results of EDNAP mRNAMPS Exercise no. 3 (2021/2022) and a recent article on mRNA typing of mixtures. The results of Exercise no. 4 were presented (attached). The results are encouraging in many cases apart from skin. Some laboratories produced no results. Discussions between the organisers and participants are going on to understand the reasons. Some results are still waiting to be submitted. An updated report will be presented at the next EDNAP meeting and published when complete.

The series of exercises relating to DNA transfer Roland van Oorschot

Roland van Oorshot had sent an update on the exercise (attached). Data on over 1,000 tool handles and 1,000 glove samples have been submitted from 17 laboratories. Data are expected shortly from four more laboratories.

Updates from other groups

ENFSI Sander Kneppers

Sander Kneppers reported from the ENFSI DNA Expert Working Group (attached).

Presentations

Y-chromosome evidence in a criminal case - interpretation Arnoud Kal and Peter Gill

Arnoud Kal presented the case circumstances that led to a court appointing six international forensic genetic and statistical experts to assist with the interpretation of partial Y-STR evidence obtained from a stain with the potential not to be able to exclude the suspect's brother. Peter Gill outlined the different statistical evidence assessments presented to the court, subsequently leading to a conviction (attached).

Exhaustive propositions – DNA mixtures Peter Gill

Peter Gill presented a case in which the DNA mixture of a stain was compared to the DNA of family members (attached). The LR results of traditional mixture approaches concerning single individuals' potential contributions to the stain were compared to those using exhaustive propositions. Different conclusions were reached with the two methods, highlighting the importance of using exhaustive propositions, particularly with related individuals. The calculations can be done with the open-source tool EFMex.

Future activities

Biogeographical ancestry – proposition of a paper exercise — Chris Phillips, Marta Diepenbroek, and Walther Parson

Chris Phillips circulated in August 2023 by e-mail a suggestion for a collaborative paper exercise on biogeographical ancestry – BGA (attached). At the meeting, Chris Phillips presented the proposition in detail (attached). The plans were discussed and welcomed by members. A plan for the exercise will be ready before the end of November.

Next meeting — Denise Syndercombe Court

It was decided to organize an in-person meeting in Copenhagen on 29 May 2024. Niels Morling, secretary of EDNAP and meeting chair since 1996, will retire as Professor of Forensic Genetics at the University of Copenhagen in the spring of 2024 and leave EDNAP. On 30 May 2024, a symposium is planned by the University of Copenhagen to honour Niels Morling's contribution to Forensic Genetics in Denmark.

Any other business — Denise Syndercombe Court

There was no other business.

Closing of the meeting — Denise Syndercombe Court

The meeting closed with sincere thanks to Ane Elida Fonneløp and Solveig Jacobsen, who organised the meeting.

The minutes and attachments are found at the EDNAP website:
http://www.isfg.org/EDNAP/Meetings, including:

- Agenda.
- List of participants.
- Group photo.
- Minutes.
- Presentations.
  - Walther Parson: Considerations of EDNAP's future.
  - Walther Parson: Draft of Terms of References.
  - Walther Parson: Presentation of considerations.
  - Cordula Haas: Update on collaborative exercises on mRNA MPS.
  - Roland van Oorshot: Update on the series of exercises relating to DNA transfer.
  - Sander Kneppers: Report from the ENFSI DNA Expert Working Group.
  - Peter Gill: Interpretation of Y-chromosome evidence.
  - Peter Gill: Exhaustive propositions – DNA mixtures.
  - Chris Phillips: Biogeographical ancestry – proposition of a paper exercise (document).
  - Chris Phillips: Biogeographical ancestry – proposition of a paper exercise (slides).

EDNAP considerations
Walther Parson, June 29 2023
Update Aug 18 2023

1. **Mission statement**
   EDNAP is an informal group of scientists and practitioners to develop research ideas and brainstorm new research projects and topics of interest. EDNAP should be flexible in inviting non-members to participate in projects and meetings.

2. **Membership**
   We need to discuss membership criteria: are they based on representing institutions or individuals? Maybe refine definitions to allow continuation of this group.

3. **Collaborative exercises:**
   The scientific content in our joint exercises is becoming increasingly difficult to understand (and discuss) in the short timeframe available to us at our annual meetings. The exercises are more complex and require more scientific input compared to earlier times, e.g., when STRs were investigated. (this is a positive development as our main goal is to advance research and application in forensic genetics).

   I would like to propose that we **change** the way how we plan and discuss the details of collaborative projects, as the time available at meetings is usually limited and therefore discussions are rare or based on spontaneous thoughts only.

   We would benefit from more in-depth preparations **before** meeting in person. This can be achieved by sharing common research plans in advance, giving participants more time to reflect on the proposed exercise. EDNAP members can also discuss internally with colleagues, ask questions and make comments/suggestions, which will lead to more fruitful plannings.

   Similarly, we would benefit if the experimental results were communicated to all EDNAP members, not just the participants of a particular exercise, prior to our personal meetings. This would give us more time to process the information and better engage in the discussions.

   Thus, EDNAP meetings would become real work meetings where specific content is produced that the leading laboratory can take back home for further work.

   We have lost publications in the past, which is unfortunate, as a lot of work went into preparing the exercises, performing the experiments and analysing the data. The new procedure outlined above should help avoiding this in the future.

4. **Updates/presentations at EDNAP meetings**
   We have witnessed a significant redundancy of presentations and updates at EDNAP meetings and the following ENFSI meetings (and yes, I have held many of them). We hear the same content 2-3 times during the week of these meetings. The vast majority of EDNAP members are also ENFSI members or have representatives of their institutes

in ENFSI. Therefore, this information is not lost when reduced to ENFSI, which I believe makes for a better audience for this content.

EDNAP should focus on its original mandate, exploring new research and driving development (in contrast to ENFSI, which is more concerned with other duties, such as, amongst many others, implementation and harmonisation of new technology). The above joint exercises would be an important step towards achieving this goal.

5. **EDNAP Status**
   EDNAP, as a group of active forensic geneticists, is getting older. The positive aspect of this is an increasing level of experience and expertise, but we lack the involvement of younger researchers who can contribute to the science while learning from those with experience. I would like to see EDNAP open up to more guests/members to either suggest or participate in specific exercises, thus capitalizing on EDNAP's established strengths. EDNAP would benefit from "fresh blood" and research ideas that may not be covered by the currently participating EDNAP labs. Many of the most recent and exciting developments in forensic genetics have taken place in laboratories outside of the current EDNAP membership and this gap in participants of a collaborative R&D group should be addressed.

6. **Chair persons**
   I propose to follow the successful concept of the ENFSI sub-groups and to have two EDNAP chairs and a secretary role, who support each other in the administration of EDNAP and the planning of the meeting agendas. This has worked very well for ENFSI subgroups in the past decade. The new chair persons could learn from Niels' vast experience in chairing this group for almost three decades.

   Because of their outstanding research work and dedication to our field and EDNAP, I would like to propose Cordula Haas (Zürich) and Bo Simonsen (Copenhagen) as possible candidates for chairs. This is of course open for further nominations.

Additional comments to be considered at next in person meeting(s)

We should have an annual main meeting and - depending on needs - an additional meeting. We should discuss whether or not we continue to meet together with ENFSI, which is currently scheduled to meetings in September/October.

The IFSG Board is supporting this initiative of discussing the future of EDNAP and considers inviting EDNAP to present their work at the upcoming ISFG2024 meeting.

A prior commitment from those making exercise proposals to publish the results for the benefit of the community as a whole 6-15 months after completion.

To consider submissions for membership as well as making invitations by mutual agreement at each meeting - optimally a 'hybrid' model which identifies the most active labs not yet in EDNAP.

Please add more ….

EDNAP – The European DNA Profiling Group

Terms of References

EDNAP was formally established at the 14th Congress of the ISFG (International Society for Forensic Genetics) in Mainz in 1991, where EDNAP was accepted as a working group.

1. Aims of EDNAP is to serve as a forum for experts and information to explore new research and to drive development in the field of forensic genetics. Therefore, EDNAP
    a. Supports collaborative exercises, workshops and in-depth discussions of research results and research ideas, presentations etc.
    b. Organizes at minimum one annual scientific meeting for its members. Such meetings will be held after consultation with the Society for Forensic Genetics. As a rule, one annual meeting takes place in cooperation with the ENFSI Expert DNA WG in in-person meetings. Additional meetings can be decided by the board.
    c. Strives to act as an informal scientific environment and in the spirit for helping each other in research-related questions.

2. Membership of EDNAP is open for representatives from forensic genetics laboratories, who are members of the International Society for Forensic Genetics.
    a. It is intended that each European country should be represented by laboratories with high scientific expertise in forensic DNA technology.
    b. Members must be qualified experts in the field of forensic genetics, i.e., biologists, molecular biologists, or equivalent, who have knowledge, expertise, and experience in methods and practice of forensic genetic identification.
    c. Membership is acknowledged by the members of EDNAP and should be obtained by application to the board. New members are acknowledged by vote of members at an in-person meeting. The vote is decided by a simple majority vote of the members present.
    d. The board can invite guests to participate in EDNAP activities and meetings, and/or to suggest or participate in specific exercises and activities.
    e. Applications for membership must be sent in writing to the board.
    f. Anyone considered as member of EDNAP must disclose any commercial interest they may have relevant for the field of EDNAP, which will then be disseminated to the entire group.

3. EDNAP is administered by a board. The board
    a. Represents the EDNAP.
    b. Is responsible for organizing the meetings of the group.
    c. Prepares annual statements from the board and distributes them to the members of EDNAP and the forensic community.

4. Elections of the board
    a. The board consists of two co-chairs and the secretary.
    b. The board is elected every two years by the members. Re-election is possible.
    c. The elections take place during the annual meeting in connection to the ENFSI Expert DNA WG in-person meeting. Election is decided by a simple majority vote of the members present.

5. All EDNAP member labs have a vote at any general meeting of the group.
    a. Any general meeting must be announced at least 6 weeks in advance dating from the notification. At a general meeting, decisions are taken by simple majority vote of the member labs present, except in the case of changes in the constitution, where a two-thirds majority of the votes of the members present must be obtained.
    b. An extraordinary general meeting shall be called by the Board if there is an important reason or when it is desired by at least 20% its members.

6. Membership fee
    a. There is no membership fee in addition to the membership fee of the ISFG.
    b. Lack of ISFG membership payment results in loss of ENDAP membership.
    c. All meetings will be self-financing from the registration fees payable by those attending.
    d. EDNAP does not provide financial support for travel, subsistence, and accommodation costs.

7. Dissolution of the EDNAP
    a. Dissolution of the EDNAP can be decided by resolution where a two-thirds majority of the votes of the members present must be obtained at two consecutive meetings.
    b. If the ISFG is dissolved, the EDNAP will also be dissolved.

The Future of EDNAP

2005

Dr. Walther Parson
Institute of Legal Medicine, Medical University of Innsbruck, Austria
Forensic Science Program, Penn State University, PA, USA
walther.parson@i-med.ac.at

Aims of EDNAP

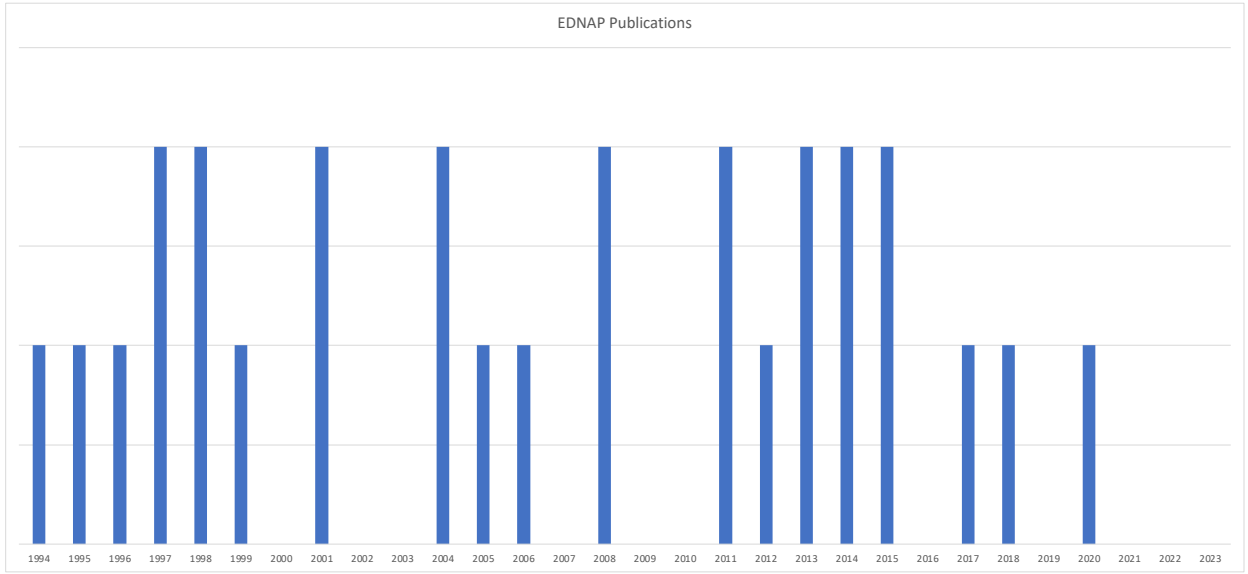
“Harmonization of DNA technology for crime investigations by collaborative exercises”

Total of 33 peer-reviewed publications since 1991

Decline in output since mid 2010s - reasons?

Too busy with routine work?

Covid?



A. Carracedo

Challenges

Change in technological landscape - move to MPS methods

Not all labs have opportunities/interest to work with MPS

That limits the number of labs participating in MPS-based exercises

Also, MPS –based exercises are more complex, huge amounts of data

We are observing that some organizing labs struggle with data interpretation

How can we address this situation?

Are we still able to work in the way that one lab organizes the exercise, collects and analyses/interprets data alone?

Review our collaboration and communication

We discuss new exercises and results of ongoing exercises almost exclusively at our meetings; This is a short time frame; I see elements of ad hoc, unprepared conversations due to the lack of preparation time

I cannot understand new (complex) data from a 15 min presentation and provide useful comments; instead, I would prefer to see suggestions for new exercises or results of ongoing exercises in **advance** to have a chance to digest and develop an opinion

In earlier times we were all more or less on the same technological level (e.g., STRs), so we could all contribute ad hoc; these times have changed; technologies and data are very complex now

We could improve our conversations by exchanging research ideas/results in advance

We could allow for more time for discussions during our meetings

We could allow for other (prepared) presentations on the topic from colleagues

Move from ad hoc to more prepared conversations (still allow for spontaneous ideas, …)

Higher quality discussions, trouble shooting, results interpretation

Review our EDNAP meeting agendas

>50% of our EDNAP meeting topics are updates and lectures

The same updates and lectures are provided during the ENFSI DNA WG meetings, some even twice (in subgroups and at the main ENFSI DNA WG meeting)

The majority of EDNAP members are also ENFSI DNA WG members

EDNAP – ENFSI DNA WG

EDNAP	ENFSI DNA WG
Recognized ISFG working group	Recognized monopoly organization by EU
“promoting scientific knowledge“	“improving the mutual exchange of information”
Accessible to any ISFG member	Formal application and voting
Forensic genetic researchers and practitioners	Bring together recognized organizations (e.g., 17025 in accordance with Council Framework Decision 2009/905JHA)
	Establish quality assurance guidelines for DNA profiling and reporting
	Reviewing and revising guidelines and BPMs for DNA profiling and reporting
	Disseminate to EU forensic DNA community guidelines and BPMs for DNA profiling and reporting
	Support colleagues by education and training
Collaborate with ENFSI	Support organization of collaborative exercises together with EDNAP to harmonize procedures in European labs

Review our meeting agendas

We meet in the same week as the ENFSI DNA WG because this reduces traveling costs and time, which makes sense

Many EDNAP members are also ENFSI DNA WG members; thus, most of us hear lectures/updates twice, some of us three times

Not effective

As a consequence there is a risk of adopting ENFSI content in EDNAP

It should be the other way round

Meeting fallacy

We should meet because we work together

We should not work together because we have the meeting

Evolution of EDNAP

Change of our collaboration style

Colleagues that have **new research questions/suggestions** should be able to get in contact with the EDNAP group directly/immediately, not only at the meeting

Discussions of new collaboration ideas could happen when they occur and well before the meeting

This would give participants the opportunity to contribute to discussions at the meeting in a better prepared way

Colleagues that plan to present **ongoing exercise results** should send results well ahead of the meeting to allow for more meaningful discussions

Particularly **problems, limitations** that arise during the analyses should be shared when they arise to allow for better troubleshooting

Evolution of EDNAP

Focus more on EDNAP members' practical experiences (at court)

We encounter limitations/errors/pitfalls in our practical work on a regular basis

<u>Current cold case investigation</u>

Low-level Y-STR contribution in mixture with DNA matching the victim (dominant)

Parallel Y-STR analyses were performed

Consensus Y-STR profiles?

Lack of PG methods for Y

(even more so for mtDNA)

Can we discuss such issues @EDNAP?

Evolution of EDNAP

Change static EDNAP membership rules

EDNAP members are aging and we lack “fresh blood”

On a positive note, this group has a lot of experience

On the other hand, there are young forensic scientists with ideas that seek for partners and for collaboration

EDNAP should open to new (temporary) members as long this is possible to handle for our labs (exercises) and meetings

Evolution of EDNAP

Suggestion to invite and involve young scientists for mutual research (see suggestion for new collaborative exercise BGA)

Evolution of EDNAP

Should take advantage of precious resources, but also give younger colleagues the chance to take responsibilities and shape EDNAP

Evolution of EDNAP

As ISFG working group we should have elections for chairmen

Co-chairmanships have proven useful in ENFSI DNA WG subgroups

Suggestion for future EDNAP co-chairs

Cordula Haas

Bo Thisted Simonsen

EDNAP/ENFSI Rome 2018

University of Zurich[UZH]

Zurich Institute of Forensic Medicine

NATIONAL CENTER FOR FORENSIC SCIENCE

EDNAP mRNA MPS collaborative exercise 4 - IonTorrent S5 and Illumina MiSeq (BFID-cSNP-6F)

Cordula Haas, Nadescha Hänggi, Rob Lagace, Erin Hanson, Jack Ballantyne

EDNAP Meeting, 3. October 2023, Oslo

EUROFORGEN Network of Excellence

EUROFORGEN-NoE is funded by the European Commission within the 7th Framework Programme

Recap EDNAP mRNA MPS Exercise 3 – 2021/2022

- BFID-cSNP-BSS RNA and DNA assays
  – identification of blood, saliva, semen, vaginal secretion, menstrual blood, skin
  – including cSNPs to associate specific mRNA transcripts to an individual (blood, saliva, semen)
- IonTorrent S5
- 6 participants
- 16 stains provided by Zurich
  8 own single source and/or mixed body fluid stains
  up to 8 own reference DNA samples (for assignment with donor)
- BFID: 13/16 of the provided stains were predicted correctly (one body fluid missing (2), skin difficult (1))
  21/32 (65%) of own stains could be predicted
- cSNP: performance dependent on how many reads per RNA cSNP were detected
  some labs did not analyze reference persons?

International Journal of Legal Medicine (2023) 137:13–32
https://doi.org/10.1007/s00414-022-02908-9

ORIGINAL ARTICLE

Targeted S5 RNA sequencing assay for the identification and direct association of common body fluids with DNA donors in mixtures

Erin Hanson[1,2] · Guro Dørum[3] · Manuel Zamborlin[3] · Shouyu Wang[3] · Mario Gysi[3] · Sabrina Ingold[3] · Robert Lagace[4] · Chantal Roth[4] · Cordula Haas[3] · Jack Ballantyne[1,2]

BFID-cSNP-BSS blood, semen, saliva
BFID-cSNP-6F 6 fluids/tissue

EDNAP mRNA MPS Exercise 4 – 2022/2023

- **BFID-cSNP-6F RNA assay**

  - Identification of blood, saliva, semen, vaginal secretion, menstrual blood, skin

  - Including cSNPs in all bodyfluids

- **BFID-cSNP-6F DNA assay**

  - For reference persons: donor genotypes

		BFID-cSNP-BSS	BFID-cSNP-6F
BD	ANK1	2	2
	CD3G	1	1
	SPTB	4	4
SE	PRM1	1	1
	SEMG2	1	1
	KLK3	2	2
	TGM4	4	4
SA	HTN3	3	3
	PRB4	1	1
	PRH2	1	1
	MUC7	1	1
	STATH		
VS	CYP2A6		1
	MUC22		7
	CYP2B7P1		
MB	MMP10		2
	MMP3		1
	COL6A3		5
	COL12A1		3
	LEFTY2		
SK	LCE1C		3
	COL17A1		1
	IL37		2
Total		19 genes (BFID) 23 cSNPs (11 genes) *cSNP microhaps:* *3 bi-local, 1 tri-local*	23 genes (BFID) 46 cSNPs (20 genes) *cSNP microhaps:* *8 bi-local, 3 tri-local*

EDNAP mRNA MPS Exercise 4

- 16 dried stains
- 8 own stains and up to 8 own donor samples (reference)
- 2 primer pools (RNA/DNA)

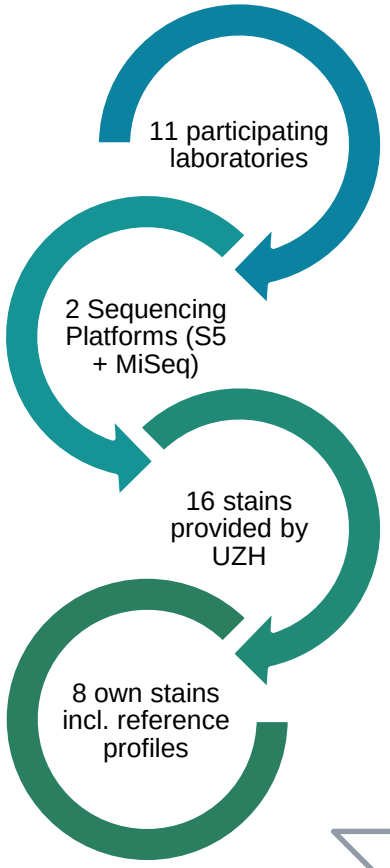
- DNA/RNA co-extraction
- STR-analysis of stains (CE)
- mRNA profiling of stain with BFID-cSNP-6F RNA assay
- DNA cSNP-typing of reference persons with BFID-cSNP-6F DNA assay

- Sequencing on IonTorrent S5 and Illumina MiSeq platforms

Stain N°	BF/T	Amount	Stain Provided
1	SK	1 swab	1 swab
2	BL-MB	1 swab + 25ul	1/4 swab
3	SA-VAG	1 swab + 25ul	1/4 swab
4	SE-MB	1 swab + 25ul	1/4 swab
5	BL-SE	25ul + 25ul	part of T-Shirt
6	SE-SE	25ul + 25ul	1 swab
7	SA-MB	1 swab + 50ul	1/4 swab
8	SA-SK	1 swab + 25ul	1 swab
9	VAG	cotton part of a slip	a piece of it
10	MB	menstrual pad	a part of it
11	SE	50ul	part of a glove (latex)
12	BL	20ul	part of a T-Shirt
13	SA-SE	50ul + 10ul	artificial cotton
14	VAG-BL	1 swab + 25ul	1/4 swab
15	SA	50ul	stockings (nylon)
16	VAG-SE	1 swab + 25ul	1/4 swab

Light blue: single donor, low input
Dark blue: single donor, high input
Orange: mixtures

EDNAP mRNA MPS Exercise 4



RNA + DNA Extraction → Reverse Transcription → Library preparation (automated or manual) → Sequencing: S5/MiSeq → Data Analysis

Participatinig Laboratories

6x S5
3x MiSeq
2x both sequencing platforms

- Netherlands Forensic Institute, Ministry of Justice and Security, Netherlands
- National Forensic Center, Swedish Police Authority, Sweden
- Department of Analytical, Environmental and Forensic Sciences, King's College London, UK
- Institute of Forensic Medicine, University of Zurich, Switzerland
- Department of Forensic Medicine, University of Copenhagen, Denmark
- Institute of Forensic Medicine, University Medical Center Cologne, University of Cologne, Germany
- National Center for Forensic Science, University of Central Florida (UCF), USA
- Institute of Forensic Sciences, DNA department, Bavarian State Criminal Police Office, Germany
- Departement of Forensic Sciences, Oslo University Hospital, Norway
- Institute of Legal Medicine, Innsbruck Medical University, Austria
- Instituto Nacional de Medicina Legal, I.P., Ministry of Justice, Portugal

Methods & Quantification Results

Laboratory Methods: Extraction & Reverese Transcription

- DNA extraction of reference samples: any Kit
- DNA quantification: e.g. Quantifiler® Trio DNA Quantification Kit
- DNA/RNA co-extraction of stains (recommended: NFI DNA/RNA co-extraction protocol)
- DNAse treatment: TURBO DNA-free Kit
- RNA quantification (recommended)
- Reverse Transcription (RNA): SuperScript™ IV VILO™ Master Mix

Laboratory Methods: Library Preparation & Sequencing

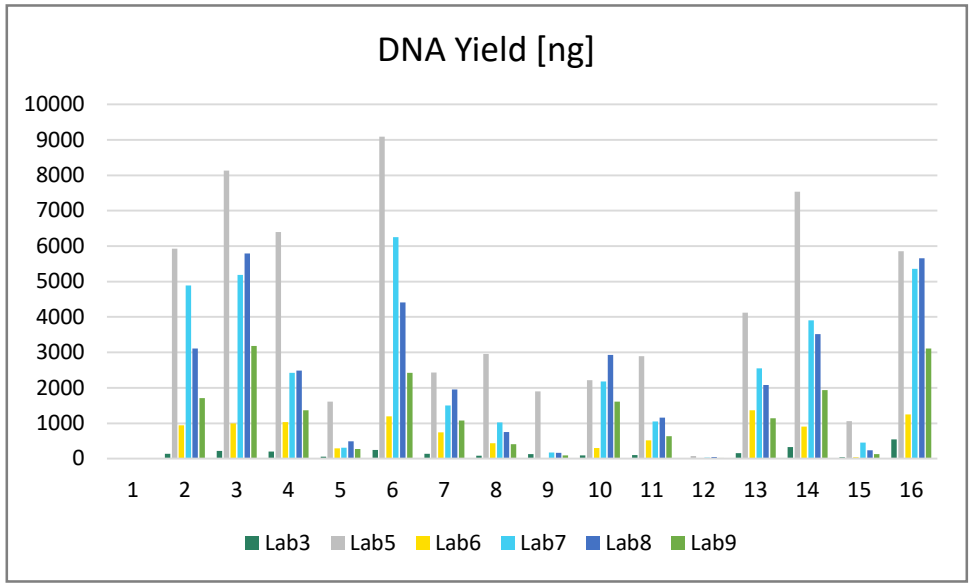
S5:

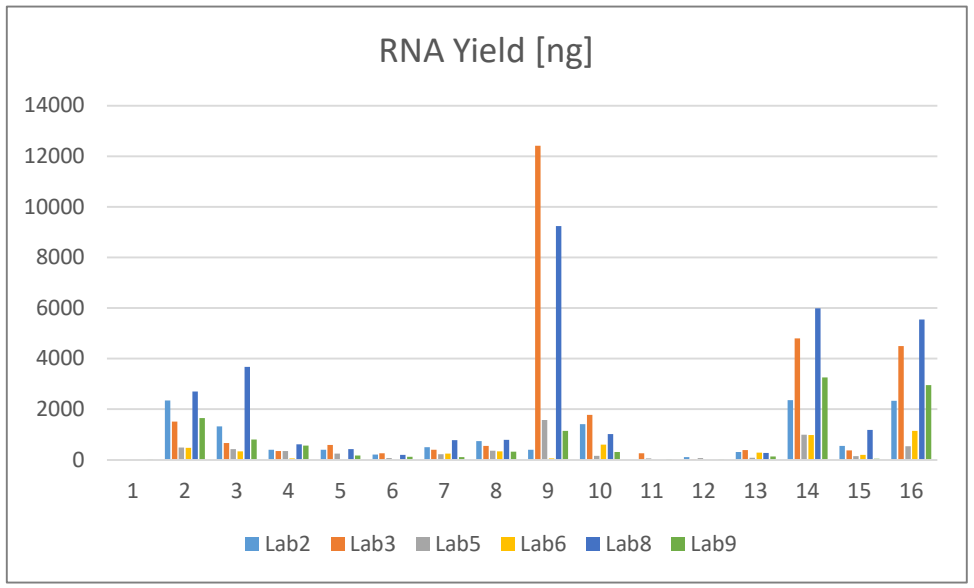
- **Manual** library preparation (RNA and DNA): Ion AmpliSeq™ library Kit 2.0 or Precision ID Library Kit
- **Automated** library preparation on IonChef (RNA and DNA): Precision ID DL8 kit or Ion AmpliSeq™ Kit for Chef DL8
- Ion Chef template preparation and Ion S5 sequencing
  - Ion S5™ Precision ID Chef & Sequencing Kit or Ion 510™ & Ion 520™ & Ion 530™ Kit – Chef
  - 2x 520 chips

MiSeq:

- AmpliSeq library PLUS for Illumina
- MiSeq FGx Reagent Micro Kit
- 2x Micro Flow Cells

Quantification results





Light blue: single donor, low input
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Orange: mixtures

Stain N°	BF/T	Amount	Stain Provided
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3	SA-VAG	1 swab + 25ul	1/4 swab
4	SE-MB	1 swab + 25ul	1/4 swab
5	BL-SE	25ul + 25ul	part of T-Shirt
6	SE-SE	25ul + 25ul	1 swab
7	SA-MB	1 swab + 50ul	1/4 swab
8	SA-SK	1 swab + 25ul	1 swab
9	VAG	cotton part of a slip	a piece of it
10	MB	menstrual pad	a part of it
11	SE	50ul	part of a glove (latex)
12	BL	20ul	part of a T-Shirt
13	SA-SE	50ul + 10ul	artificial cotton
14	VAG-BL	1 swab + 25ul	1/4 swab
15	SA	50ul	stockings (nylon)
16	VAG-SE	1 swab + 25ul	1/4 swab

Data Analysis Methods

- Ion Torrent's TMAP alignment program > aligned BAM/BAI Files

- multiple sequence alignment algorithm:
  - all SNPs positions of the targeted microhaplotype need to be present
  - removes contaminating genomic DNA (alignment gap parameters)
  - the sequences are phased and the microhaplotype genotypes identified
  → sequence coverage and cSNP genotypes

- Body fluid identification:
  - Threshold (0.5% of total reads) to identify sporradic reads
  (put back to zero in mh counts corrected)

- Assignment of body fluids with donors:
  - Comparison of cSNP genotypes based on RNA-Seq with DNA references (DNA genotypes)

Results of Body Fluid Identification for stains 1-16

BFID – Stains 1-4

Actual Body Fluids: SK MB-BL VAG-SA MB-SE

Markers	1-Lab1-S5	1-Lab2-S5	1-Lab3-S5	1-Lab4-S5	1-Lab5-S5	1-Lab6-MiSeq	1-Lab7-MiSeq	1-Lab8-S5	1-Lab9-S5	1-Lab10-MiSeq	1-Lab11-MiSeq	2-Lab1-S5	2-Lab2-S5	2-Lab3-S5	2-Lab4-S5	2-Lab5-S5	2-Lab6-MiSeq	2-Lab7-MiSeq	2-Lab8-S5	2-Lab9-S5	2-Lab10-MiSeq	2-Lab11-MiSeq	3-Lab1-S5	3-Lab2-S5	3-Lab3-S5	3-Lab4-S5	3-Lab5-S5	3-Lab6-MiSeq	3-Lab7-MiSeq	3-Lab8-S5	3-Lab9-S5	3-Lab10-MiSeq	3-Lab11-MiSeq	4-Lab1-S5	4-Lab2-S5	4-Lab3-S5	4-Lab4-S5	4-Lab5-S5	4-Lab6-MiSeq	4-Lab7-MiSeq	4-Lab8-S5	4-Lab9-S5	4-Lab10-MiSeq	4-Lab11-MiSeq
Blood_01_ANK1	NA	0	5	NA	12	0	0	0	0	0	0	0	0	321	0	5633	0	1795	5513	0	720	0	NA	0	0	0	0	0	0	0	0	0	0	0	0	0	4704	0	0	6629	21889	0	0
Blood_02_ANK1	NA	0	0	NA	0	0	0	0	0	0	0	0	0	412	0	10359	0	2307	0	0	844	0	NA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Blood_03_CD3G	NA	0	0	NA	10	0	0	0	0	0	0	0	2253	687	0	9569	3918	4382	0	0	1562	0	NA	0	0	0	0	0	0	0	0	0	0	77	0	0	0	2286	0	0	0	0	0
Blood_04_SPTB	NA	0	0	NA	8	0	0	0	0	0	0	0	0	279	0	6374	0	1475	0	0	474	0	NA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Blood_05_SPTB	NA	0	0	NA	20	0	0	0	0	0	0	0	0	375	0	13410	0	3243	0	0	711	0	NA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2705	7283	21865	0	0
Blood_06_SPTB	NA	0	0	NA	0	0	0	0	0	0	0	0	0	154	0	0	0	0	0	0	0	0	NA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Menstrual_01_LEFTY2	NA	5	0	NA	12	0	0	0	56	0	0	0	4198	313	0	17765	0	4878	5985	33783	948	1071	NA	0	0	0	0	0	0	0	0	0	0	0	13	0	0	0	0	0	7416	0	0	0
Menstrual_02_MMP10	NA	0	0	NA	0	0	0	0	265	0	0	0	11358	2857	0	31346	0	7551	8001	162249	2086	1244	NA	251	0	0	0	0	0	0	0	0	0	489	21	0	0	0	0	23557	0	0	8591
Menstrual_03_COL12A1	NA	0	0	NA	0	0	0	0	0	0	0	0	3002	117	0	6135	1769	1822	0	0	0	0	NA	0	0	0	0	0	0	0	0	0	0	258	0	1464	2079	20821	24308	16763	59065	58769	30	10037
Menstrual_04_COL12A1	NA	0	6	NA	7	0	0	0	0	0	0	434	3567	208	0	6292	1541	1724	0	0	398	0	NA	0	0	0	0	0	0	0	0	0	0	129	0	697	4287	19272	19378	8015	38069	26982	24	8665
Menstrual_05_COL12A1	NA	5	0	NA	7	0	0	0	0	0	0	810	2192	135	0	0	0	0	0	0	0	0	NA	0	0	0	0	0	0	0	0	0	0	167	17	775	0	14735	13770	11929	42584	28989	7	6396
Menstrual_06_COL6A3	NA	0	5	NA	10	0	0	0	0	0	0	1275	0	114	0	7062	0	3428	0	0	512	0	NA	0	0	0	0	0	0	0	0	0	0	105	10	539	5895	20133	3615	9617	37393	20513	7	4693
Menstrual_07_COL6A3	NA	0	0	NA	14	0	0	0	0	0	0	570	0	0	0	0	0	1761	0	0	0	0	NA	0	0	0	0	0	0	0	0	0	0	123	13	0	0	0	0	4259	24256	14235	0	1729
Menstrual_08_COL6A3	NA	0	0	NA	0	0	0	0	0	0	0	0	2509	223	0	0	0	0	0	14239	0	0	NA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	18822	0	0	2841
Menstrual_09_COL6A3	NA	0	24	NA	52	9	0	6	60	0	0	52213	31632	1789	1287	93342	31019	32626	39331	62984	11196	7991	NA	0	0	32	0	0	0	0	0	0	0	1089	19	3344	104795	101840	53672	61274	96767	49117	111	28518
Menstrual_10_MMP3	NA	0	0	NA	84	0	0	22	79	0	0	0	4228	1037	0	35155	4980	8720	12768	65708	2205	1502	NA	0	0	0	0	0	0	0	0	0	0	1580	76	2871	0	0	35018	3746	403038	11386	19	95083
Saliva_01_HTN3	NA	0	0	NA	65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	NA	255	215	0	74	0	14464	33244	2536	311	2971	0	0	0	0	0	0	0	0	0	0	0
Saliva_02_MUC7	NA	14	0	NA	25	0	0	0	26	0	0	0	0	0	0	0	0	0	0	0	0	0	NA	4096	3228	56	7867	53	38309	83342	110030	1576	6978	0	0	0	0	0	0	0	0	0	0	0
Saliva_03_PRB4	NA	0	0	NA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	NA	0	0	0	0	0	2418	3064	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Saliva_04_PRH2	NA	0	0	NA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	NA	2327	1632	0	560	51	8824	33033	60076	329	3107	0	0	0	0	0	0	0	0	0	0	0
Saliva_05_STATH	NA	5	0	NA	26	0	0	0	31	0	0	0	0	0	0	0	0	0	0	0	0	0	NA	3396	5376	37	950	191	17723	71103	60206	3279	10273	0	0	0	0	0	0	0	0	0	0	0
Semen_01_KLK3	NA	0	0	NA	36	0	0	0	16	0	0	0	0	0	0	0	0	0	0	0	0	0	NA	0	149	0	0	0	0	0	0	0	0	248	0	10369	0	26866	15278	20662	78645	354027	51	10586
Semen_02_PRM1	NA	43	25	NA	457	0	0	7	0	7	0	0	0	0	0	0	0	0	0	0	0	0	NA	738	542	3067	193	54	4975	6580	2711	199	723	2507	252	22187	121505	281910	41608	27082	17239	67441	297	3155
Semen_03_SEMG2	NA	0	0	NA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	NA	0	0	0	0	0	0	0	0	0	0	147	0	0	0	0	0	0	0	0	0	0
Semen_04_TGM4	NA	0	0	NA	147	0	0	0	28	0	0	0	0	0	0	0	0	0	0	0	0	0	NA	273	240	540	444	9	1641	0	2438	158	0	484	44	26118	157978	296304	84243	79531	149847	722251	512	25472
Semen_05_TGM4	NA	0	0	NA	116	0	0	0	20	0	0	0	0	0	0	0	0	0	0	0	0	0	NA	237	193	0	291	0	0	3957	3299	69	0	451	0	30990	0	15516	88828	50877	186620	469453	257	28737
Semen_06_TGM4	NA	0	0	NA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	NA	0	0	0	0	0	0	0	0	0	0	80	0	0	0	0	0	0	18890	0	0	1664
Skin_01_COL17A1	NA	0	0	NA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	NA	0	0	0	258	0	0	3191	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Skin_02_IL37	NA	0	0	NA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	NA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Skin_03_LCE1C	NA	0	0	NA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	NA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Vaginal_01_CYP2A6	NA	0	0	NA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	NA	408	261	0	464	0	1701	7923	3487	139	740	0	14	0	0	0	0	0	0	0	0	0
Vaginal_02_CYP2B7P1	NA	76	0	NA	25	0	0	0	257	63	0	2438	32825	1020	0	44624	13103	11869	52178	144942	2135	9667	NA	4955	3272	19	1108	387	50077	87490	84696	1415	13568	0	335	0	0	0	2290	6935	0	28887	0	0
Vaginal_03_MUC22	NA	81	0	NA	79	0	0	0	808	497	0	15216	183076	5815	0	321642	90987	83476	446572	804553	40209	95493	NA	9486	3248	0	1618	205	46528	109203	53842	3068	19791	114	277	0	0	0	3363	25964	8006	42563	9	3027
Vaginal_04_MUC22	NA	131	5	NA	114	0	0	0	1287	122	0	5295	123521	5796	0	206483	88909	61434	267380	801315	12157	38014	NA	1874	1065	0	0	250	30115	70883	36149	761	7131	275	698	0	0	0	4699	11003	9415	23603	0	1721
Vaginal_05_MUC22	NA	14	0	NA	0	0	0	0	109	49	0	1687	18497	484	0	28872	7281	8220	32351	86202	1786	5408	NA	1272	469	0	0	108	16939	22053	10201	268	3755	0	51	0	0	0	0	5987	0	10997	0	0
gDNAPRM1_01_gDNA	NA	0	0	NA	0	0	0	0	0	0	0	1033	0	0	0	0	0	0	0	0	0	0	NA	0	0	0	0	0	0	0	0	0	0	1994	0	0	0	0	0	0	0	0	0	0

Predicted Body Fluids: ? MB/ MB-BL VAG-SA(-SE) MB-SE

BFID – Stains 5-8

Actual Body Fluids: SE-BL SE-SE MB-SA SA-SK

Markers	5-Lab1-S5	5-Lab2-S5	5-Lab3-S5	5-Lab4-S5	5-Lab5-S5	5-Lab6-MiSeq	5-Lab7-MiSeq	5-Lab8-S5	5-Lab9-S5	5-Lab10-MiSeq	5-Lab11-MiSeq	6-Lab1-S5	6-Lab2-S5	6-Lab3-S5	6-Lab4-S5	6-Lab5-S5	6-Lab6-MiSeq	6-Lab7-MiSeq	6-Lab8-S5	6-Lab9-S5	6-Lab10-MiSeq	6-Lab11-MiSeq	7-Lab1-S5	7-Lab2-S5	7-Lab3-S5	7-Lab4-S5	7-Lab5-S5	7-Lab6-MiSeq	7-Lab7-MiSeq	7-Lab8-S5	7-Lab9-S5	7-Lab10-MiSeq	7-Lab11-MiSeq	8-Lab1-S5	8-Lab2-S5	8-Lab3-S5	8-Lab4-S5	8-Lab5-S5	8-Lab6-MiSeq	8-Lab7-MiSeq	8-Lab8-S5	8-Lab9-S5	8-Lab10-MiSeq	8-Lab11-MiSeq
Blood_01_ANK1	0	0	824	1176	11124	0	2468	14568	0	0	2159	0	0	0	0	0	0	0	0	0	0	0	8965	1458	0	2039	0	0	98	12276	90	0	1078	0	0	0	0	0	0	0	0	0	0	0	0
Blood_02_ANK1	0	0	406	0	0	0	0	0	0	0	1877	0	0	0	0	0	0	0	0	0	0	0	5068	0	0	0	2491	0	0	0	0	0	764	0	0	0	0	0	0	0	0	0	0	0	0
Blood_03_CD3G	0	0	343	0	0	0	0	6489	0	0	1135	0	0	0	0	0	0	0	0	0	0	0	21849	0	0	0	0	0	0	5334	0	0	1212	0	0	0	0	0	0	0	0	0	0	0	0
Blood_04_SPTB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4981	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Blood_05_SPTB	0	0	498	0	16420	0	3678	15311	0	0	1681	0	0	0	0	0	0	0	0	0	0	0	7920	221	0	377	0	0	37	10647	0	0	783	0	0	0	0	0	0	0	0	0	0	0	0
Blood_06_SPTB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Menstrual_01_LEFTY2	0	0	0	0	0	0	0	0	32	0	0	0	0	0	0	0	0	0	0	0	0	0	8584	0	0	0	2331	0	79	4672	0	0	957	0	0	0	0	0	0	0	0	0	0	0	0
Menstrual_02_MMP10	0	0	0	0	0	0	0	0	191	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78	0	0	0	4635	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Menstrual_03_COL12A1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9021	132	6331	315	1789	1930	56	9544	17	9718	1426	0	0	0	0	0	0	0	0	0	0	0	0
Menstrual_04_COL12A1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6225	355	3497	811	1416	1393	103	6563	11	5840	938	0	0	0	0	0	0	0	0	0	0	0	0
Menstrual_05_COL12A1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6110	103	4007	348	0	0	0	9294	0	6437	1064	0	0	0	0	0	0	0	0	0	0	0	0
Menstrual_06_COL6A3	0	0	0	0	0	0	0	0	15	0	0	0	0	0	0	0	0	0	0	0	0	0	5505	392	3749	1040	2063	0	37	8456	28	5144	793	0	0	0	0	0	0	0	0	0	0	0	0
Menstrual_07_COL6A3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5880	0	1987	0	0	0	0	0	0	2194	0	0	0	0	0	0	0	0	0	0	0	0	0
Menstrual_08_COL6A3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Menstrual_09_COL6A3	0	0	361	0	0	0	0	0	55	0	0	0	0	0	0	0	0	0	0	0	0	0	31854	6427	20046	16496	11935	7094	2217	49647	337	60872	6952	0	0	0	0	0	0	0	0	0	0	0	0
Menstrual_10_MMP3	0	0	0	0	0	0	0	0	63	0	0	0	0	0	0	0	0	0	0	0	0	0	72151	0	19206	0	47399	21320	225	11343	0	14652	13094	0	0	0	0	0	0	0	0	0	0	0	0
Saliva_01_HTN3	0	648	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	56518	0	0	0	39397	9033	112	0	0	0	0	0	18374	8476	0	297292	9908	58251	16970	0	19177	2623
Saliva_02_MUC7	0	2287	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	49166	575	3898	2857	22935	4029	336	35132	101	3685	3893	53464	60797	6948	97443	195674	6908	62986	272960	48381	14742	26264
Saliva_03_PRB4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2065	0	0	0	0	0	0
Saliva_04_PRH2	0	134	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	13118	104	2684	364	11808	3745	685	13717	31	1605	1812	27922	8719	1949	8374	14278	5237	23009	42794	7652	2221	4822
Saliva_05_STATH	0	1040	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97026	1857	22617	11569	89615	28858	2143	88416	156	40365	11629	170883	61813	18933	173421	194849	40414	87955	264098	77399	65193	40959
Semen_01_KLK3	0	0	1567	0	55805	1159	8992	50558	40	0	6725	0	0	1448	16239	13603	3191	3997	0	133	0	0	0	0	0	0	0	0	0	0	53	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Semen_02_PRM1	122757	162	37593	189044	668116	135890	331246	710492	545	5	137352	3552	52653	31690	419109	190074	300188	386319	806268	9639	87	132207	0	0	0	0	0	0	0	0	53	0	0	2100	0	0	0	0	0	0	0	0	0	0	0
Semen_03_SEMG2	0	0	2432	0	0	836	14274	11327	0	0	9922	0	0	729	0	15476	11187	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Semen_04_TGM4	0	0	5691	29794	137982	4158	21133	93845	95	0	16587	0	0	2909	23898	16363	6548	8627	0	344	6	2212	0	0	0	0	0	0	0	0	160	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Semen_05_TGM4	0	0	7047	0	149178	5231	20436	101696	39	0	15900	0	0	1879	8661	17001	8433	4856	0	158	0	0	0	0	0	0	0	0	0	0	68	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Semen_06_TGM4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Skin_01_COL17A1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Skin_02_IL37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Skin_03_LCE1C	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Vaginal_01_CYP2A6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5780	0	0	0	0	1673	0	30091	0	0	3464	0	0	0	0	0	0	0	0	0	0	0	0
Vaginal_02_CYP2B7P1	0	22	0	0	0	0	0	0	220	0	0	0	0	0	0	0	0	0	0	86	0	0	251636	876	1650	2314	6452	35878	462	189151	126	1884	36276	0	0	0	0	0	0	0	0	0	0	0	0
Vaginal_03_MUC22	0	0	0	0	0	0	0	0	586	0	0	0	287	0	0	0	0	0	0	103	0	0	82348	386	1215	959	17743	29596	305	129199	104	2603	33101	0	0	0	0	0	0	0	0	0	0	0	0
Vaginal_04_MUC22	0	31	0	0	0	0	0	0	806	0	0	0	507	0	0	0	0	0	0	127	0	0	126764	92	1345	0	8703	33434	278	67606	240	1110	15827	0	0	0	0	0	0	0	0	0	0	0	0
Vaginal_05_MUC22	0	0	0	0	0	0	0	0	70	0	0	0	0	0	0	0	0	0	0	0	0	0	51085	205	0	659	3338	9149	104	47130	25	0	9659	0	0	0	0	0	0	0	0	0	0	0	0
gDNAPRM1_01_gDNA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	11660	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Predicted Body Fluids: SE-BL SE MB-SA SA

BFID – Stains 9-12

Predicted Body Fluids: VAG MB SE BL

Markers	9-Lab1-SS	9-Lab2-SS	9-Lab3-SS	9-Lab4-SS	9-Lab5-SS	9-Lab6-MiSeq	9-Lab7-MiSeq	9-Lab8-SS	9-Lab9-SS	9-Lab10-MiSeq	9-Lab11-MiSeq	10-Lab1-SS	10-Lab2-SS	10-Lab3-SS	10-Lab4-SS	10-Lab5-SS	10-Lab6-MiSeq	10-Lab7-MiSeq	10-Lab8-SS	10-Lab9-SS	10-Lab10-MiSeq	10-Lab11-MiSeq	11-Lab1-SS	11-Lab2-SS	11-Lab3-SS	11-Lab4-SS	11-Lab5-SS	11-Lab6-MiSeq	11-Lab7-MiSeq	11-Lab8-SS	11-Lab9-SS	11-Lab10-MiSeq	11-Lab11-MiSeq	12-Lab1-SS	12-Lab2-SS	12-Lab3-SS	12-Lab4-SS	12-Lab5-SS	12-Lab6-MiSeq	12-Lab7-MiSeq	12-Lab8-SS	12-Lab9-SS	12-Lab10-MiSeq	12-Lab11-MiSeq
Blood_01_ANK1	0	0	0	5	28	0	0	0	0	0	0	234	22124	40606	18331	13114	7770	8480	25189	0	1924	2108	0	0	0	0	0	0	0	0	0	0	0	2451	153	963	7928	2852	33	4778	1900	161	0	57
Blood_02_ANK1	0	0	0	0	31	0	0	0	0	0	0	0	24524	0	0	14299	0	6491	17390	0	2312	2476	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Blood_03_CD3G	0	0	0	0	31	0	0	0	0	0	0	0	10202	15446	0	7135	14020	2352	23051	0	1509	2008	0	0	0	0	0	0	0	0	0	0	0	913	0	0	989	0	58	181	0	0	0	0
Blood_04_SPTB	0	0	0	0	0	0	0	0	0	0	0	0	10360	0	0	3112	0	2517	11462	0	928	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Blood_05_SPTB	0	0	0	0	52	0	0	0	0	0	0	36	33402	44543	4526	24822	9180	12176	29379	0	2416	1773	0	0	0	0	0	0	0	0	0	0	0	1215	8	0	7213	82	11	4819	56	0	0	0
Blood_06_SPTB	0	0	0	0	0	0	0	0	0	0	0	0	4289	0	0	0	0	1459	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Menstrual_01_LEFTY2	0	0	0	0	65	0	0	0	68	0	0	0	30616	12532	0	12362	0	6254	28919	8	2668	2714	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	13	0	0
Menstrual_02_MMP10	0	0	0	0	48	0	0	0	447	0	0	0	97336	0	0	0	0	16505	124347	75	9073	18008	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	50	0	0
Menstrual_03_COL12A1	0	0	0	9	47	0	0	0	0	0	0	80	42640	89195	22701	31646	76300	10076	52577	0	3981	5473	0	0	0	0	0	0	0	0	0	0	0	0	0	31	0	0	0	0	0	0	0	0	0
Menstrual_04_COL12A1	0	0	0	0	40	0	0	0	0	0	0	122	24523	78098	22385	20372	55608	7936	35354	8	2469	4606	0	0	0	0	0	0	0	0	0	0	0	0	0	13	0	0	0	0	0	0	0	0	0
Menstrual_05_COL12A1	0	0	0	0	34	0	0	0	0	0	0	160	26586	48810	13232	13234	46688	7317	38846	6	2423	2742	0	0	0	0	0	0	0	0	0	0	0	0	0	31	0	0	0	0	51	0	0	0	0
Menstrual_06_COL6A3	0	0	0	5	62	0	0	0	0	0	0	429	21393	53695	57990	16397	20024	8773	30719	0	2847	1884	0	0	0	0	0	0	0	0	0	0	0	44	0	34	0	0	0	0	55	9	0	0	0
Menstrual_07_COL6A3	0	0	0	0	39	0	0	0	31	0	0	0	21517	19016	2698	13912	8446	4554	18668	6	1168	778	0	0	0	0	0	0	0	0	0	0	0	0	0	19	0	0	0	0	0	0	0	0	0
Menstrual_08_COL6A3	0	0	0	0	0	0	0	0	0	0	0	0	16857	0	0	5310	0	1830	20315	0	542	1496	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Menstrual_09_COL6A3	0	0	0	44	162	33	0	0	76	0	0	5733	90434	198475	275381	56107	152888	36042	100574	30	18559	13715	0	0	0	0	0	0	0	0	30	0	0	172	8	207	536	88	0	689	163	18	0	9
Menstrual_10_MMP3	0	0	0	0	306	0	0	0	86	0	0	0	172781	5188	0	177014	111654	79125	613365	21	47401	77080	0	0	0	0	0	0	0	0	0	0	0	0	0	107	0	109	0	0	41	19	0	0
Saliva_01_HTN3	0	0	0	0	202	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	27	13	0	107	0	0	0	0	0	0	0
Saliva_02_MUC7	0	0	0	0	152	0	0	0	26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	107	54	0	49	0	0	186	48	0	0	0
Saliva_03_PRB4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Saliva_04_PRH2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	8	14	0	0	0	0	26	14	0	0	0
Saliva_05_STATH	0	0	456	0	94	0	0	0	0	116	0	0	0	0	0	0	0	0	0	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66	121	0	150	0	0	242	21	0	0	0
Semen_01_KLK3	0	0	0	0	55	0	0	0	38	0	0	0	0	0	0	0	0	0	0	19	0	0	0	0	460	0	0	0	0	0	144	0	0	0	0	0	0	0	0	0	0	33	0	0	0
Semen_02_PRM1	25	0	0	0	585	28	0	0	0	0	0	0	0	0	0	0	0	0	0	8	0	0	14378	24010	21993	393470	185478	19616	280066	525001	4365	328	12970	0	12	77	177	112	0	0	55	32	0	0	0
Semen_03_SEMG2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Semen_04_TGM4	0	0	0	0	231	41	0	0	87	0	0	0	0	0	0	0	0	0	0	47	0	0	0	0	4021	0	1371	0	0	0	342	17	0	0	0	15	0	32	0	0	0	111	0	0	0
Semen_05_TGM4	0	0	0	0	122	41	0	0	39	0	0	0	0	0	0	0	0	0	0	31	0	0	0	0	364	0	0	0	0	0	181	0	0	0	0	13	0	0	0	0	0	58	0	0	0
Semen_06_TGM4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Skin_01_COL17A1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Skin_02_IL37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Skin_03_LCE1C	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Vaginal_01_CYP2A6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	184	0	0	0	0
Vaginal_02_CYP2B7P1	193	14129	8638	0	105	1153	5090	190712	367	2355	28674	0	0	0	0	4154	18515	2238	0	123	0	0	0	837	0	0	0	0	0	0	98	0	0	0	42	88	0	66	0	0	1089	239	0	0	0
Vaginal_03_MUC22	991	18103	31042	0	315	2068	13174	277425	1400	11026	64683	0	4128	8081	0	4048	43138	2295	6969	275	880	950	0	617	0	0	0	0	0	0	127	0	0	0	36	98	0	149	0	0	321	270	0	0	0
Vaginal_04_MUC22	526	12887	12675	0	426	1736	6479	361550	1951	3786	49084	0	0	0	0	13910	25265	2285	6018	437	0	0	0	1299	0	0	0	0	0	0	225	0	0	0	49	93	0	123	0	0	381	536	0	0	0
Vaginal_05_MUC22	89	3549	1405	0	36	186	1555	58277	102	534	6414	0	0	3493	0	3954	18646	1497	0	39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6	15	0	0	0	0	110	52	0	0	0
gDNAPRM1_01_gDNA	28	0	279	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Predicted Body Fluids: VAG MB SE Difficult, BL?

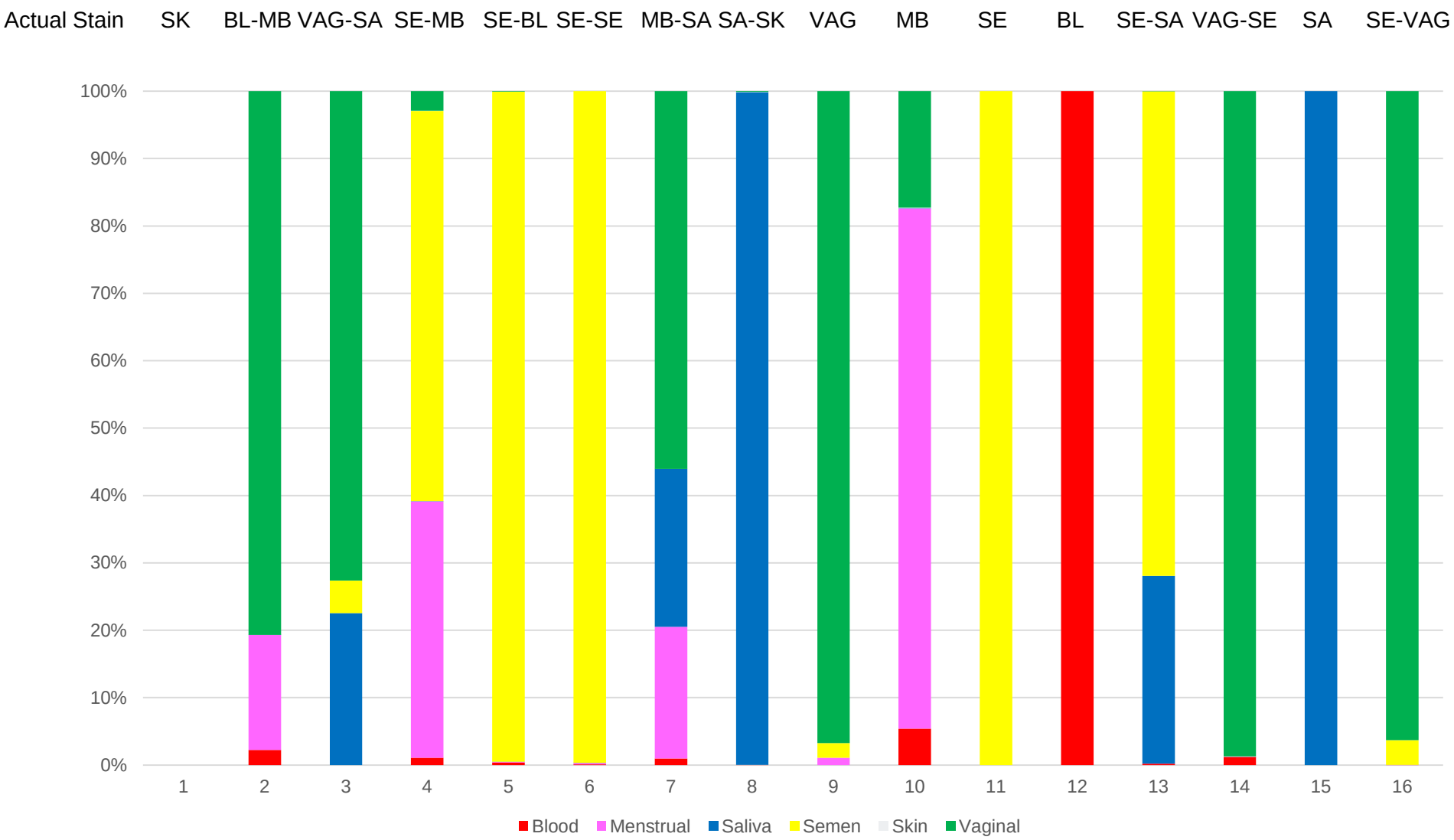
BFID – Stains 13-16

Predicted Body Fluids: SA-SE VAG-BL SA SE-VAG

Markers	13-Lab1-SS	13-Lab2-SS	13-Lab3-SS	13-Lab4-SS	13-Lab5-SS	13-Lab6-MiSeq	13-Lab7-MiSeq	13-Lab8-SS	13-Lab9-SS	13-Lab10-MiSeq	13-Lab11-MiSeq	14-Lab1-SS	14-Lab2-SS	14-Lab3-SS	14-Lab4-SS	14-Lab5-SS	14-Lab6-MiSeq	14-Lab7-MiSeq	14-Lab8-SS	14-Lab9-SS	14-Lab10-MiSeq	14-Lab11-MiSeq	15-Lab1-SS	15-Lab2-SS	15-Lab3-SS	15-Lab4-SS	15-Lab5-SS	15-Lab6-MiSeq	15-Lab7-MiSeq	15-Lab8-SS	15-Lab9-SS	15-Lab10-MiSeq	15-Lab11-MiSeq	16-Lab1-SS	16-Lab2-SS	16-Lab3-SS	16-Lab4-SS	16-Lab5-SS	16-Lab6-MiSeq	16-Lab7-MiSeq	16-Lab8-SS	16-Lab9-SS	16-Lab10-MiSeq	16-Lab11-MiSeq
Blood_01_ANK1	NA	0	12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Blood_02_ANK1	NA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Blood_03_CD3G	NA	0	9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	7	0	0	0	0	0	0	0	0	0	0	0	0
Blood_04_SPTB	NA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Blood_05_SPTB	NA	0	12	0	0	0	0	0	0	0	0	0	1511	0	0	0	0	0	0	0	0	0	0	0	0	7	0	0	0	0	0	5	0	0	0	0	0	0	0	0	0	0	0	0
Blood_06_SPTB	NA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Menstrual_01_LEFTY2	NA	0	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	0	0	0	0	0	0	0	0	0	0	0	0
Menstrual_02_MMP10	NA	0	0	0	0	0	0	0	68	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	42	5	0	0	0	0	0	0	0	0	0	0	0	0
Menstrual_03_COL12A1	NA	0	23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Menstrual_04_COL12A1	NA	0	24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Menstrual_05_COL12A1	NA	0	27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6	0	0	0	24	0	0	0	0	0	0	0	0	0	0	0	0	0
Menstrual_06_COL6A3	NA	0	27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	26	0	0	0	0	0	0	0	0	0	0	0	0	0
Menstrual_07_COL6A3	NA	0	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Menstrual_08_COL6A3	NA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Menstrual_09_COL6A3	NA	0	59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	8	0	22	0	0	0	36	37	0	0	0	0	0	0	0	0	0	0	0	0
Menstrual_10_MMP3	NA	0	0	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6	0	0	0	0	9	0	0	0	0	0	0	0	0	0	0	0	0
Saliva_01_HTN3	NA	0	0	0	37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	8	0	0	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Saliva_02_MUC7	NA	0	38	0	358	22025	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1353	19	128	0	10	0	94	0	26	0	0	0	0	0	0	0	0	0	0	0	0	0
Saliva_03_PRB4	NA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Saliva_04_PRH2	NA	0	10	0	0	2988	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	420	0	43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Saliva_05_STATH	NA	0	13	106	215	56763	0	0	0	0	227	106	0	0	0	0	0	0	0	0	0	0	1842	26	115	0	16	7	0	1696	0	0	137	0	0	0	0	0	0	0	0	0	0	0
Semen_01_KLK3	NA	0	0	0	0	4977	0	0	102	0	403	0	0	0	0	0	0	0	0	0	0	0	0	0	14	0	18	0	0	0	210	0	0	0	2324	0	0	10858	0	0	0	65208	0	0
Semen_02_PRM1	NA	0	73	13425	3357	191555	272955	184079	98	0	34758	13425	0	0	0	0	0	0	0	0	0	0	31	0	96	17	192	0	0	44	134	0	0	43758	34056	4520	25461	93905	13431	30372	29848	118668	1088	4692
Semen_03_SEMG2	NA	0	0	0	37	9701	0	0	156	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6	0	11	0	0	0	94	0	0	0	4342	936	0	43507	6477	0	5935	159701	0	1365
Semen_04_TGM4	NA	0	5	0	376	3196	0	2809	128	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	8	0	96	0	0	0	456	0	0	0	0	0	0	0	0	0	0	19166	0	0
Semen_05_TGM4	NA	0	0	0	0	3547	0	0	58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6	0	13	0	0	0	201	0	0	0	0	0	0	9486	0	0	0	22718	0	0
Semen_06_TGM4	NA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Skin_01_COL17A1	NA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Skin_02_IL37	NA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Skin_03_LCE1C	NA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5475	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Vaginal_01_CYP2A6	NA	9	0	0	0	0	0	0	0	0	0	2236	1058	0	8062	0	1599	5730	5521	0	0	0	0	0	0	0	8	0	0	0	33	0	0	0	1967	1304	0	9205	0	0	6629	0	0	0
Vaginal_02_CYP2B7P1	NA	129	140	0	107	0	0	0	972	0	0	49786	24848	65255	92168	111402	45029	136295	200364	3304	27274	0	10	33	31	116	0	0	0	874	7	0	0	55212	21727	35999	126499	118847	51129	136670	535554	6914	24925
Vaginal_03_MUC22	NA	184	87	0	381	0	0	0	1036	0	0	136536	49507	349726	391668	215926	154060	362296	308510	17601	90357	0	5	47	150	297	0	0	0	786	127	0	0	144948	58692	392311	654377	232961	127622	426878	966574	52355	89642
Vaginal_04_MUC22	NA	221	101	0	324	0	0	0	2135	0	0	74606	36921	75252	153501	197972	92265	311384	307038	7169	50461	0	9	35	42	238	0	0	0	1541	30	0	0	72064	37193	80189	327618	186997	89854	263711	1032219	15554	38831
Vaginal_05_MUC22	NA	25	12	0	44	0	0	0	182	0	0	16600	6370	39616	39196	34591	21248	36495	57011	1106	8562	0	0	7	30	41	0	0	0	146	9	0	0	17763	8781	53159	77644	45206	23724	65351	204746	4187	9885
gDNAPRM1_01_gDNA	NA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Predicted Body Fluids: Difficult, SA-SE? VAG-BL Difficult, SA? SE-VAG

Percentage of Reads per Stain (Lab 6)



Assignment of Body Fluids with Donors – stains 1-16

Single Donor Stains

Stain 1	COL17A1	IL37.0	IL37.1	IL37.2	LCE1C.0	LCE1C.1	LCE1C.2	LCE1C.3
SK	rs805701	rs3811046_rs3811047	rs3811046	rs3811047	rs36107483_rs2006940_rs17624493	rs36107483	rs2006940	rs17624493
IonCode_133		TG	T/T	G/G	GCA/ATG	G/A	C/T	A/G
Lab1 S5 - Genotype								
Lab1 S5 - Read Counts								
Lab2 S5 - Genotype								
Lab2 S5 - Read Counts								
Lab3 S5 - Genotype	A/G							
Lab3 S5 - Read Counts	34\24							
Lab4 S5 - Genotype								
Lab4 S5 - Read Counts								
Lab5 S5 - Genotype								
Lab5 S5 - Read Counts								
Lab6 MiSeq - Genotype								
Lab6 MiSeq - Read Counts								
Lab7 MiSeq - Genotype								
Lab7 MiSeq - Read Counts								
Lab8 S5 - Genotype								
Lab8 S5 - Read Counts								
Lab9 S5 - Genotype								
Lab9 S5 - Read Counts								
Lab10 MiSeq - Genotype								
Lab10 MiSeq - Read Counts								
Lab11 MiSeq - Genotype								
Lab11 MiSeq - Read Counts								

Stain 1 (SK):
- low input
- extremely difficult, even at BFID level
- sample donor = bad shedder?

Stain 9	CYP2A6	MUC22.0	MUC22.1	MUC22.2	MUC22.3	MUC22.4	MUC22.5	MUC22.6	MUC22.7	MUC22.8	MUC22.9
VAG	rs8192721	rs12110470_rs12110785	rs12110470	rs12110785	rs3869098_rs4248153	rs3869098	rs4248153	rs1419664_rs3094672	rs1419664	rs3094672	rs10947121
IonCode_135	C/C	GT	G/G	T/T	AA/GA	A/G	A/A	CT/TA/TC	C/T	T/A	T/T
Lab1 S5 - Genotype		GT/GT	G/G	T/T	CGA/CAA	G/A	A/A	ACT/ATA	C/T	T/A	T/T
Lab1 S5 - Read Counts		89	89\89	89\89	795\196	795\196	795\795	436\90	436\90	436\90	89\89
Lab2 S5 - Genotype		GT/GT	G/G	T/T	CGA/CAA	G/A	A/A	ACT/ATA	C/T	T/A	T/T
Lab2 S5 - Read Counts		3549	3549\3549	3549\3549	14414\3689	14414\3689	14414\14414	11106\1781	11106\1781	11106\1781	3549\3549
Lab3 S5 - Genotype		GT/GT	G/G	T/T	CGA/CAA	G/A	A/A	ACT/ATA	C/T	T/A	T/T
Lab3 S5 - Read Counts		1405	1405\1405	1405\1405	25071\5971	25071\5971	25071\25071	10941\1734	10941\1734	10941\1734	1405\1405
Lab4 S5 - Genotype											
Lab4 S5 - Read Counts											
Lab5 S5 - Genotype		GT/GT	G/G	T/T	CAA/CGA	A/G	A/A	ACT/ATA	C/T	T/A	T/T
Lab5 S5 - Read Counts		36	36\36	36\36	295\20	295\20	295\295	417\9	417\9	417\9	36\36
Lab6 MiSeq - Genotype		GT/GT	G/G	T/T	CGA/CAA	G/A	A/A	ACT/ATA	C/T	T/A	T/T
Lab6 MiSeq - Read Counts		186	186\186	186\186	1734\334	1734\334	1734\1734	1535\201	1535\201	1535\201	186\186
Lab7 MiSeq - Genotype		GT/GT	G/G	T/T	CGA/CAA	G/A	A/A	ACT/ATA	C/T	T/A	T/T
Lab7 MiSeq - Read Counts		1555	1555\1555	1555\1555	10164\3010	10164\3010	10164\10164	4967\1512	4967\1512	4967\1512	1555\1555
Lab8 S5 - Genotype		GT/GT	G/G	T/T	CGA/CAA	G/A	A/A	ACT/ATA	C/T	T/A	T/T
Lab8 S5 - Read Counts		58277	58277\58277	58277\58277	222689\54736	222689\54736	222689\222689	299443\62107	299443\62107	299443\62107	58277\58277
Lab9 S5 - Genotype		GT/GT	G/G	T/T	CAA/CGA	A/G	A/A	ACT	C/C	T/T	T/T
Lab9 S5 - Read Counts		102	102\102	102\102	955\445	955\445	955\955	1951	1951\1951	1951\1951	102\102
Lab10 MiSeq - Genotype		GT/GT	G/G	T/T	CGA/CAA	G/A	A/A	ACT/ATA	C/T	T/A	T/T
Lab10 MiSeq - Read Counts		534	534\534	534\534	9022\2004	9022\2004	9022\9022	3248\538	3248\538	3248\538	534\534
Lab11 MiSeq - Genotype		GT/GT	G/G	T/T	CGA/CAA	G/A	A/A	ACT/ATA	C/T	T/A	T/T
Lab11 MiSeq - Read Counts		6414	6414\6414	6414\6414	53448\11235	53448\11235	53448\53448	40193\8891	40193\8891	40193\8891	6414\6414

Stain 9 (VAG):
- high input
- rather high number of reads in most markers
- RNA cSNP genotype reflects donor genotype

Single Donor Stains

Stain 11	KLK3.0	KLK3.1	KLK3.2	PRM1	SEMG2	TGM4.0	TGM4.1	TGM4.2	TGM4.3
SE	rs11573_rs1135766	rs11573	rs1135766	rs737008	rs2233896	rs1995640	rs1995641	rs3749195	rs9876921
IonCode_144	A/A	G/G	G/G	T/T	T/T	AG	A/A	G/G	T/T
Lab1 S5 - Genotype				G/T					
Lab1 S5 - Read Counts				7344\7034					
Lab2 S5 - Genotype				G/T					
Lab2 S5 - Read Counts				12581\11429					
Lab3 S5 - Genotype	CTA/CCG	T/C	A/G	T/G		C/T	G/A		
Lab3 S5 - Read Counts	236\224	236\224	236\224	11555\10438		3811\210	325\39		
Lab4 S5 - Genotype	CTA	T/T	A/A	T/G		T/T	A/G		
Lab4 S5 - Read Counts	47	47\47	47\47	203857\189613		94\94	51\50		
Lab5 S5 - Genotype	CTA/CCG	T/C	A/G	T/G		C/C	G/A		
Lab5 S5 - Read Counts	445\119	445\119	445\119	92794\92684		1371\1371	51\13		
Lab6 MiSeq - Genotype				T/G					
Lab6 MiSeq - Read Counts				10051\9565					
Lab7 MiSeq - Genotype	CCG/CTA	C/T	G/A	T/G		C/C	G/A		
Lab7 MiSeq - Read Counts	304\163	304\163	304\163	143176\136890		911\911	361\83		
Lab8 S5 - Genotype	CTA/CCG	T/C	A/G	G/T		C/T			
Lab8 S5 - Read Counts	14\6	14\6	14\6	267823\257178		37\33			
Lab9 S5 - Genotype	CCG	C/C	G/G	G/T	C/C	C/T	G/A		
Lab9 S5 - Read Counts	144	144\144	144\144	2557\1808	7\7	179\163	92\89		
Lab10 MiSeq - Genotype				G/T		C/C			
Lab10 MiSeq - Read Counts				166\162		17\17			
Lab11 MiSeq - Genotype				T/G		C/T			
Lab11 MiSeq - Read Counts				6541\6429		32\7			

Stain 11 (SE):
- high input
- difficult carrier material (latex glove)
- high number of reads, especially in PRM1
- RNA cSNP genotype mostly reflects donor genotype

Stain 12	ANK1.0	ANK1.1	CD3G	SPTB.0	SPTB.1	SPTB.2	SPTB.3	SPTB.4
BL	rs504574	rs7816734	rs3753059	rs1741488_rs1741487	rs1741488	rs1741487	rs229592	rs229586
IonCode_142	C/C	G/G	T/T	CA/TG	C/T	A/G	A/G	C/C
Lab1 S5 - Genotype	C/C	G/G	T/T	ACA	C/C	A/A		C/C
Lab1 S5 - Read Counts	2451\2451	5\5	913\913		8 8\8	8\8		1215\1215
Lab2 S5 - Genotype	C/C							C/C
Lab2 S5 - Read Counts	153\153							8\8
Lab3 S5 - Genotype	C/C							C/C
Lab3 S5 - Read Counts	963\963							9\9
Lab4 S5 - Genotype	C/C		T/T	ATG	T/T	G/G		C/C
Lab4 S5 - Read Counts	7928\7928		989\989		9 9\9	9\9		7213\7213
Lab5 S5 - Genotype	C/C		T/T					C/C
Lab5 S5 - Read Counts	2852\2852		5\5					82\82
Lab6 MiSeq - Genotype	C/C		T/T					C/C
Lab6 MiSeq - Read Counts	33\33		58\58					11\11
Lab7 MiSeq - Genotype	C/C		T/T	ATG	T/T	G/G		C/C
Lab7 MiSeq - Read Counts	4778\4778		181\181		5 5\5	5\5		4819\4819
Lab8 S5 - Genotype	C/C	G/G	T/T					C/C
Lab8 S5 - Read Counts	1900\1900	19\19	24\24					56\56
Lab9 S5 - Genotype	C/C							
Lab9 S5 - Read Counts	161\161							
Lab10 MiSeq - Genotype								
Lab10 MiSeq - Read Counts								
Lab11 MiSeq - Genotype	C/C							
Lab11 MiSeq - Read Counts	57\57							

Stain 12 (BL):
- low input
- low number of reads
- RNA cSNP genotype largely reflects donor genotype

Single Donor Stains

Stain 10 (MB):

- high input
- overall high number of reads in all bodyfluid-specific markers
- not every lab detected the same components
- RNA cSNP genotype reflects donor genotype
- some dropouts → inhibition due to high input?

Stain 10	MMP10.0	MMP10.1	COL12A1.0	COL12A1.1	COL12A1.2	COL6A3.0	COL6A3.1	COL6A3.2	COL6A3.3	COL6A3.4	COL6A3.5	MMP3	CYP2A6	MUC22.0	MUC22.1	MUC22.2	MUC22.3	MUC22.4	MUC22.5	MUC22.6	MUC22.7	MUC22.8	MUC22.9
MB	rs17860950	rs17860949	rs240736	rs594012	rs970547	rs11131296_rs2270669	rs1131296	rs2270669	rs4433949	rs34558385	rs3790993	rs679620	rs8192721	rs12110470_rs12110785	rs12110470	rs12110785	rs3869098_rs4248153	rs3869098	rs4248153	rs1419664_rs3094672	rs1419664	rs3094672	rs10947121
IonCode_135	A/A	G/G	G/G	T/T	T/T	AG	A/A	G/G	T/T	G/G	G/G	T/C	C/C	GT	G/G	T/T	AA/GA	A/G	A/A	CT/TA/TC	C/T	T/A	T/T
Lab1 S5 - Genotype			G/G	T/T	T/T		A/A	G/G			G/G												
Lab1 S5 - Read Counts			80\80	122\122	160\160		429\429	21\21			5733\5733												
Lab2 S5 - Genotype	A/A	G/G	G/G	T/T	T/T		A/A	G/G	T/T	G/G	G/C	T/C		GT/GT	G/G	T/T	CGA/CAA	G/A	A/A	ACT/ATA	C/T	T/A	T/T
Lab2 S5 - Read Counts	97336\97336	97336\97336	42640\42640	24523\24523	26586\26586		21393\21393	21517\21517	16857\16857	16857\16857	85164\5270	87330\79382		1920	1920\1920	1920\1920	2893\1235	2893\1235	2893\2893	2601\701	2601\701	2601\701	1920\1920
Lab3 S5 - Genotype			G/G	T/T	T/T		A/A	G/G	T/T	G/G	G/C	C/T		GT/GT	G/G	T/T	CGA/CAA	G/A	A/A	ACT/ATA	C/T	T/A	T/T
Lab3 S5 - Read Counts			89195\89195	78098\78098	48810\48810		53695\53695	19016\19016	11\11	11\11	170788\27687	2998\2190		1920	1920\1920	1920\1920	2893\1235	2893\1235	2893\2893	2601\701	2601\701	2601\701	1920\1920
Lab4 S5 - Genotype			G/G	T/T	T/T		A/A	G/G			G/G	C/T											
Lab4 S5 - Read Counts			22701\22701	22385\22385	13232\13232		57990\57990	2698\2698			275381\275381	105\35											
Lab5 S5 - Genotype	A/A	G/G	G/G	T/T	T/T		A/A	G/G	T/T	G/G	G/G	C/T		GT/GT	G/G	T/T	CGA/CAA	G/A	A/A	ACT/ATA	C/T	T/A	T/T
Lab5 S5 - Read Counts	1994\1994	1994\1994	31646\31646	20372\20372	13234\13234		16397\16397	13912\13912	5310\5310	5310\5310	56107\56107	92599\84415		3954	3954\3954	3954\3954	2474\1574	2474\1574	2474\2474	10196\3714	10196\3714	10196\3714	3954\3954
Lab6 MiSeq - Genotype	A/A	G/G	G/G	T/T	T/T		A/A	G/G	T/T	G/G	G/G	C/T	C/T	GT/GT	G/G	T/T	CGA/CAA	G/A	A/A	ACT/ATA		T/A	T/T
Lab6 MiSeq - Read Counts	108\108	108\108	76300\76300	55608\55608	46688\46688		20024\20024	8446\8446	391\391	391\391	152888\152888	62950\48704	17009\8256	18646	18646\18646	18646\18646	30610\12528	30610\12528	30610\30610	17009\8256		17009\8256	18646\18646
Lab7 MiSeq - Genotype	A/A	G/G	G/G	T/T	T/T		A/A	G/G	T/T	G/G	G/G	C/T	C/T	GT/GT	G/G	T/T	CGA/CAA	G/A	A/A	ACT/ATA		T/A	T/T
Lab7 MiSeq - Read Counts	16505\16505	16505\16505	10076\10076	7936\7936	7317\7317		8773\8773	4554\4554	1830\1830	1830\1830	36042\36042	42682\36443	1505\780	1497	1497\1497	1497\1497	1880\415	1880\415	1880\1880	1505\780		1505\780	1497\1497
Lab8 S5 - Genotype	A/A	G/G	G/G	T/T	T/T		A/A	G/G	T/T	G/G	G/G	C/T		GT/GT	G/G	T/T	CGA/CAA	G/A	A/A	ACT/ATA	C/T	T/A	T/T
Lab8 S5 - Read Counts	124347\124347	124347\124347	52577\52577	35354\35354	38846\38846		30719\30719	18668\18668	20315\20315	20315\20315	100574\100574	308239\305126		1800	1800\1800	1800\1800	6003\966	6003\966	6003\6003	4342\1676	4342\1676	4342\1676	1800\1800
Lab9 S5 - Genotype	A/A	A/G		T/T	T/T			G/G			G/G	T/C											
Lab9 S5 - Read Counts	42\42	42\33		8\8	6\6			6\6			30\30	13\8											
Lab10 MiSeq - Genotype	A/A	G/G	G/G	T/T	T/T		A/A	G/G	T/T	G/G	G/G	C/T		GT/GT	G/G	T/T	CGA/CAA	G/A	A/A	ATA/ACT	T/C	A/T	T/T
Lab10 MiSeq - Read Counts	9073\9073	9073\9073	3981\3981	2469\2469	2423\2423		2847\2847	1168\1168	542\542	542\542	18559\18559	25099\22302		160	160\160	160\160	605\275	605\275	605\605	104\81	104\81	104\81	160\160
Lab11 MiSeq - Genotype	A/A	G/G	G/G	T/T	T/T		A/A	G/G	T/T	G/G	G/G	C/T		GT/GT	G/G	T/T	CGA/CAA	G/A	A/A	ACT/ATA	C/T	T/A	T/T
Lab11 MiSeq - Read Counts	18008\18008	18008\18008	5473\5473	4606\4606	2742\2742		1884\1884	778\778	1496\1496	1496\1496	13715\13715	40623\36457		256	256\256	256\256	743\207	743\207	743\743	357\112	357\112	357\112	256\256

Stain 10	ANK1.0	ANK1.1	CD3G	SPTB.0	SPTB.1	SPTB.2	SPTB.3	SPTB.4	COL17A1	IL37.0	IL37.1	IL37.2	LCE1C.0	LCE1C.1	LCE1C.2	LCE1C.3
MB	rs504574	rs7816734	rs3753059	rs1741488_rs1741487	rs1741488	rs1741487	rs229592	rs229586	rs805701	rs3811046_rs3811047	rs3811046	rs3811047	rs36107483_rs2006940_rs7624693	rs36107483	rs2006940	rs17624493
IonCode_135	C/C	A/A	T/T	CA	C/C	A/A	A/A	C/C	A/G	TG	T/T	G/G	ACG	A/A	C/C	G/G
Lab1 S5 - Genotype	C/C	A/A	T/T	ACA	C/C	A/A	A/A	C/C								
Lab1 S5 - Read Counts	13114\13114	14299\14299	7135\7135	3112	3112\3112	3112\3112	996\996	24822\24822								
Lab2 S5 - Genotype																
Lab2 S5 - Read Counts																
Lab3 S5 - Genotype																
Lab3 S5 - Read Counts																
Lab4 S5 - Genotype	C/C		T/T					C/C								
Lab4 S5 - Read Counts	18331\18331		147\147					4526\4526								
Lab5 S5 - Genotype	C/C	A/A	T/T	ACA	C/C	A/A	A/A	C/C								
Lab5 S5 - Read Counts	13114\13114	14299\14299	7135\7135	3112	3112\3112	3112\3112	996\996	24822\24822								
Lab6 MiSeq - Genotype	C/C	A/A	T/T	ACA	C/C	A/A	A/A	C/C								
Lab6 MiSeq - Read Counts	7770\7770	1125\1125	14020\14020	1100	1100\1100	1100\1100	24\24	9180\9180								
Lab7 MiSeq - Genotype	C/C	A/A	T/T	ACA/TCA	C/C	A/A	A/A	C/C								
Lab7 MiSeq - Read Counts	8480\8480	6491\6491	2352\2352	2441\76	2441\2441	2441\2441	1459\1459	12176\12176								
Lab8 S5 - Genotype	C/C	A/A	T/T	ACA	C/C	A/A	A/A	C/C								
Lab8 S5 - Read Counts	25189\25189	17390\17390	23051\23051	11462	11462\11462	11462\11462	4295\4295	29379\29379								
Lab9 S5 - Genotype																
Lab9 S5 - Read Counts																
Lab10 MiSeq - Genotype	C/C	A/A	T/T	ACA	C/C	A/A	A/A	C/C	A/A							
Lab10 MiSeq - Read Counts	1924\1924	2312\2312	1509\1509	928	928\928	928\928	277\277	2416\2416	20\20							
Lab11 MiSeq - Genotype	C/C	A/A	T/T	ACA	C/C	A/A	A/A	C/C								
Lab11 MiSeq - Read Counts	2108\2108	2476\2476	2008\2008	618	618\618	618\618	337\337	1773\1773								

Single Donor Stains

Stain 15	HTN3.0	HTN3.1	HTN3.2	MUC7	PRB4	PRH2	HTN3
SA	rs1849937_rs1136515	rs1849937	rs1136515	rs2306948	rs1052808	rs10772391	rs75067954
IonCode_147	CT/CC	C/C	T/C	C/C	G/G	C/C	C/C
Lab1 S5 - Genotype				C/C		C/C	
Lab1 S5 - Read Counts				1353\1353		420\420	
Lab2 S5 - Genotype		C/C	T/T	C/C			C/C
Lab2 S5 - Read Counts		8\8	8\8	19\19			8\8
Lab3 S5 - Genotype				C/T		C/C	
Lab3 S5 - Read Counts				79\49		43\43	
Lab4 S5 - Genotype							
Lab4 S5 - Read Counts							
Lab5 S5 - Genotype	CT/CT	C/C	T/T	C/C			C/C
Lab5 S5 - Read Counts	6	6\6	6\6	10\10			6\6
Lab6 MiSeq - Genotype							
Lab6 MiSeq - Read Counts							
Lab7 MiSeq - Genotype				C/C			
Lab7 MiSeq - Read Counts				94\94			
Lab8 S5 - Genotype							
Lab8 S5 - Read Counts							
Lab9 S5 - Genotype				C/T		C/C	
Lab9 S5 - Read Counts				16\10		6\6	
Lab10 MiSeq - Genotype							
Lab10 MiSeq - Read Counts							
Lab11 MiSeq - Genotype							
Lab11 MiSeq - Read Counts							

Stain 15 (SA):

- high input
- difficult carrier material (nylon stockings)
- low number of reads overall

Mixed Stains

A mixed stain can contain…

…two different body fluids from the same donor

…two different body fluids from two different donors

…the same type of body fluid from two different donors

Stain 16 (VAG-SE):

- rather high number of reads in several markers
- RNA cSNP genotype mostly reflects donor genotypes

Stain 16	CYP2A6	MUC22.0	MUC22.1	MUC22.2	MUC22.3	MUC22.4	MUC22.5	MUC22.6	MUC22.7	MUC22.8	MUC22.9	KLK3.0	KLK3.1	KLK3.2	PRM1	SEMG2	TGM4.0	TGM4.1	TGM4.2	TGM4.3	COL17A1	IL37.0	IL37.1	IL37.2	LCE1C.0	LCE1C.1	LCE1C.2	LCE1C.3
VAG-SE	rs8192721	rs12110470_rs12110785	rs12110470	rs12110785	rs3869098_rs4248153	rs3869098	rs4248153	rs1419664_rs3094672	rs1419664	rs3094672	rs10947121	rs11573_rs1135766	rs11573	rs1135766	rs737008	rs2233896	rs1995640	rs1995641	rs3749195	rs9876921	rs805701	rs3811046_rs3811047	rs3811046	rs3811047	rs80357061_rs2076485	rs36107483	rs2006940	rs17624493
IonCode_135	CT/CC	C/C	T/C	C/C	G/G	C/C	C/C	CA/TA/CC/TC	C/T	A/A	C/T	TA/CG	T/C	A/G	T/T	C/A	T/T	A/A	T/T	A/A	A/G	TG	T/T	G/G	ACG	A/A	C/C	G/G
IonCode_145	TC/CT	T/C	C/T	C/C	G/G	C/C	C/C	TA/TT/TC	T/T	A/T	C/T	TA	T/T	A/A	T/T	C/C	T/T	A/A	C/T	G/A	A/A	TG	T/T	G/G	ACG/GCA	A/G	C/C	G/A
Lab1 S5 - Genotype																												
Lab1 S5 - Read Counts																												
Lab2 S5 - Genotype		GT/GT	G/G	T/T	CGA/CAA	G/A	A/A	ACT/ATA	C/T	T/A	T/T	CTA	T/T	A/A	T/T	C/C	T/T	A/A	T/C	A/G								
Lab2 S5 - Read Counts		17763	17763\17763	17763\17763	109405\35543	109405\35543	109405\109405	58412\13652	58412\13652	58412\13652	17763\17763	2324	2324\2324	2324\2324	34056\34056	4342\4342	1206\1206	1561\1561	252\107	252\107								
Lab3 S5 - Genotype		GT/GT	G/G	T/T	CGA/CAA	G/A	A/A	ACT/ATA	C/T	T/A	T/T	CTA	T/T	A/A	T/T	C/C	T/T	A/A										
Lab3 S5 - Read Counts		8781	8781\8781	8781\8781	46234\12458	46234\12458	46234\46234	30237\6956	30237\6956	30237\6956	8781\8781	396	396\396	396\396	4520\4520	936\936	232\232	397\397										
Lab4 S5 - Genotype		GT/GT	G/G	T/T	CGA/CAA	G/A	A/A	ACT/ATA	C/T	T/A	T/T	CTA	T/T	A/A	T/T	C/C	T/T	A/A										
Lab4 S5 - Read Counts		53159	53159\53159	53159\53159	305197\87114	305197\87114	305197\305197	60152\20037	60152\20037	60152\20037	53159\53159	1575	1575\1575	1575\1575	25461\25461	332\332	759\759	635\635										
Lab5 S5 - Genotype		GT/GT	G/G	T/T	CGA/CAA	G/A	A/A	ACT/ATA	C/T	T/A	T/T	CTA	T/T	A/A	T/T	C/C	T/T	A/A	T/C	A/G								
Lab5 S5 - Read Counts		77644	77644\77644	77644\77644	524265\130112	524265\130112	524265\524265	260506\67112	260506\67112	260506\67112	77644\77644	10858	10858\10858	10858\10858	93905\93905	43507\43507	6143\6143	9486\9486	1198\459	1198\459								
Lab6 MiSeq - Genotype		GT/GT	G/G	T/T	CGA/CAA	G/A	A/A	ACT/ATA	C/T	T/A	T/T	CTA	T/T	A/A	T/T	C/C	T/T	A/A	C/T	G/A								
Lab6 MiSeq - Read Counts		45206	45206\45206	45206\45206	188029\44932	188029\44932	188029\188029	152850\34147	152850\34147	152850\34147	45206\45206	912	912\912	912\912	13431\13431	6477\6477	648\648	876\876	102\78	102\78								
Lab7 MiSeq - Genotype		GT/GT	G/G	T/T	CGA/CAA	G/A	A/A	ACT/ATA	C/T	T/A	T/T	CTA	T/T	A/A	T/T	C/C	T/T	A/A	C/T	G/A								
Lab7 MiSeq - Read Counts		23724	23724\23724	23724\23724	102456\25166	102456\25166	102456\102456	74240\15614	74240\15614	74240\15614	23724\23724	433	433\433	433\433	30372\30372	1587\1587	1027\1027	525\525	72\5	72\5								
Lab8 S5 - Genotype		GT/GT	G/G	T/T	CGA/CAA	G/A	A/A	ACT/ATA	C/T	T/A	T/T	CTA	T/T	A/A	T/T	C/C	T/T	A/A	C/T	G/A								
Lab8 S5 - Read Counts		65351	65351\65351	65351\65351	351541\75337	351541\75337	351541\351541	217045\46666	217045\46666	217045\46666	65351\65351	4009	4009\4009	4009\4009	29848\29848	5935\5935	1793\1793	1811\1811	44\13	44\13								
Lab9 S5 - Genotype		GT/GT	G/G	T/T	CGA/CAA	G/A	A/A	ACT/ATA	C/T	T/A	T/T	CTA	T/T	A/A	T/T	C/C	T/T	A/A	T/C	A/G								
Lab9 S5 - Read Counts		204746	204746\204746	204746\204746	789016\177558	789016\177558	789016\789016	855675\176544	855675\176544	855675\176544	204746\204746	65208	65208\65208	65208\65208	118668\118668	159701\159701	19166\19166	22718\22718	6120\4934	6120\4934								
Lab10 MiSeq - Genotype		GT/GT	G/G	T/T	CGA/CAA	G/A	A/A	ACT/ATA	C/T	T/A	T/T	CTA	T/T	A/A	T/T	C/C	T/T	A/A	C/C	G/G	G/G							
Lab10 MiSeq - Read Counts		4187	4187\4187	4187\4187	42483\9872	42483\9872	42483\42483	12524\3030	12524\3030	12524\3030	4187\4187	100	100\100	100\100	1088\1088	350\350	31\31	58\58	6\6	6\6	14\14							
Lab11 MiSeq - Genotype		GT/GT	G/G	T/T	CGA/CAA	G/A	A/A	ACT/ATA	C/T	T/A	T/T	CTA	T/T	A/A	T/T	C/C	T/T	A/A	T/T	A/A								
Lab11 MiSeq - Read Counts		9885	9885\9885	9885\9885	72897\16745	72897\16745	72897\72897	31746\7085	31746\7085	31746\7085	9885\9885	399	399\399	399\399	4692\4692	1365\1365	293\293	193\193	6\6	6\6								

Mixed Stains

Stain 3	HTN3	HTN3	HTN3	MUC7	PRB4	PRH2	HTN3	CYP2A6	MUC22	MUC22	MUC22	MUC22	MUC22	MUC22	MUC22	MUC22	MUC22	MUC22
SA-VAG	rs1849937_rs1136515	rs1849937	rs1136515	rs2306948	rs1052808	rs10772391	rs75067954	rs8192721	rs12110470_rs12110785	rs12110470	rs12110785	rs3869098_rs4248153	rs3869098	rs4248153	rs1419664_rs3094672	rs1419664	rs3094672	rs10947121
IonCode_135	TC	T/T	C/C	C/T	G/G	C/C	C/C	C/C	GT	G/G	T/T	AA/GA	A/G	A/A	CT/TA/TC	C/T	T/A	T/T
IonCode_136	CT/CC	C/C	T/C	C/C	G/C	C/C	C/C	C/C	TC/GT	T/G	C/T	AA/GG	A/G	A/G	CA/CC	C/C	A/C	T/C
Lab1 S5 - Genotype																		
Lab1 S5 - Read Counts																		
Lab2 S5 - Genotype	TC/CT	T/C	C/T	C/T	G/G	C/C	C/C		TC/GT	T/G	C/T	CAA/CGG	A/G	A/G	ACA/ACT	C/C	A/T	C/T
Lab2 S5 - Read Counts	204\51	204\51	204\51	2185\1911	15\15	2327\2327	204\204		672\600	672\600	672\600	5858\3628	5858\3628	5858\3628	1600\274	1600\1600	1600\274	672\600
Lab3 S5 - Genotype	TC/TC	T/T	C/C	C/T		C/C	C/C		TC/GT	T/G	C/T	CGG/CAA	G/A	G/A	ACA	C/C	A/A	C/T
Lab3 S5 - Read Counts	215		215\215	1724\1504		1632\1632	215\215		269\200	269\200	269\200	1700\1548	1700\1548	1700\1548	1065	1065\1065	1065\1065	269\200
Lab4 S5 - Genotype																		
Lab4 S5 - Read Counts																		
Lab5 S5 - Genotype	TC/CC	T/C	C/C	T/C		C/C	C/C					CAA/CGG	A/G	A/G	ACT	C/C	T/T	
Lab5 S5 - Read Counts	42\17\15	42\17	42\42	4405\3462		560\560	42\42					950\668	950\668	950\668	19	19\19	19\19	
Lab6 MiSeq - Genotype				C/T		C/C			TC/GT	T/G	C/T	CAA/CGG	A/G	A/G	ACA	C/C	A/A	C/T
Lab6 MiSeq - Read Counts				34\19		51\51			76\32	76\32	76\32	103\102	103\102	103\102	250	250\250	250\250	76\32
Lab7 MiSeq - Genotype	TC/TC	T/T	C/C	C/T	G/G	C/C	C/C		TC/GT	T/G	C/T	CAA/CGG	A/G	A/G	ACA	C/C	A/A	C/T
Lab7 MiSeq - Read Counts		14464\14464	14464\14464	21108\17201	2418\2418	8824\8824	14464\14464		8858\8081	8858\8081	8858\8081	27716\18812	27716\18812	27716\18812	30115	30115\30115	30115\30115	8858\8081
Lab8 S5 - Genotype	TC/TC	T/T	C/C	C/T	G/G	C/C	C/C		TC/GT	T/G	C/T	CGG/CAA	G/A	G/A	ACA	C/C	A/A	C/T
Lab8 S5 - Read Counts	33244	33244\33244	33244\33244	47296\36046	3064\3064	33033\33033	33244\33244		11954\10099	11954\10099	11954\10099	57295\51908	57295\51908	57295\51908	70883	70883\70883	70883\70883	11954\10099
Lab9 S5 - Genotype	TC/TC	T/T	C/C	C/T	G/G	C/C	C/C		TC/GT	T/G	C/T	CAA/CGG	A/G	A/G	ACA	C/C	A/A	C/T
Lab9 S5 - Read Counts	2536	2536\2536	2536\2536	68781\41249	298\298	60076\60076	2536\2536		6614\3587	6614\3587	6614\3587	30194\23648	30194\23648	30194\23648	36149	36149\36149	36149\36149	6614\3587
Lab10 MiSeq - Genotype	TC/TC	T/T	C/C	C/T	G/G	C/C	C/C		TC/GT	T/G	C/T	CAA/CGG	A/G	A/G	ACA	C/C	A/A	C/T
Lab10 MiSeq - Read Counts	311	311\311	311\311	1017\559	5\5	329\329	311\311		197\71	197\71	197\71	1740\1328	1740\1328	1740\1328	761	761\761	761\761	197\71
Lab11 MiSeq - Genotype	TC/TC	T/T	C/C	C/T	G/G	C/C	C/C		GT/TC	G/T	T/C	CAA/CGG	A/G	A/G	ACA	C/C	A/A	T/C
Lab11 MiSeq - Read Counts	2971	2971\2971	2971\2971	3854\3124	268\268	3107\3107	2971\2971		1978\1777	1978\1777	1978\1777	9956\9835	9956\9835	9956\9835	7131	7131\7131	7131\7131	1978\1777

Stain 3 (SA-VAG):
- high number of reads
- RNA cSNP genotype mostly reflects donor genotypes

Stain 5	ANK1.0	ANK1.1	CD3G	SPTB.0	SPTB.1	SPTB.2	SPTB.3	SPTB.4	KLK3.0	KLK3.1	KLK3.2	PRM1	SEMG2	TGM4.0	TGM4.1	TGM4.2	TGM4.3
SE-BL	rs504574	rs7816734	rs3753059	rs1741488_rs1741487	rs1741488	rs1741487	rs229592	rs229586	rs11573_rs1135766	rs11573	rs1135766	rs737008	rs2233896	rs1995640	rs1995641	rs3749195	rs9876921
IonCode_144	C/G	G/G	T/C	CA	C/C	A/A	G/G	T/T	CG	C/C	G/G	G/T	C/C	C/T	G/A	T/C	G/A
Lab1 S5 - Genotype	G/C											T/G		C/C			
Lab1 S5 - Read Counts	11\6											63292\59465		95\95			
Lab2 S5 - Genotype												T/G					
Lab2 S5 - Read Counts												89\73					
Lab3 S5 - Genotype	C/G	G/G	T/C	ACA/ATG	C/T	A/G	A/A	C/C	CTA/CCG	T/C	A/G	G/T	A/A	C/T	G/A	C/C	G/G
Lab3 S5 - Read Counts	437\387	406\406	217\126	103\79	103\79	103\79	19\19	498\498	815\752	815\752	815\752	19482\18111	2432\2432	5407\284	6388\659	155\155	155\155
Lab4 S5 - Genotype	G/C							C/C	CCG/CTA	C/T	G/A	T/G		C/T	G/A		
Lab4 S5 - Read Counts	722\454							119\119	260\225	260\225	260\225	100461\88583		28785\1009	218\10		
Lab5 S5 - Genotype	C/G	G/G	T/C	ACA/ATG	C/T	A/G	A/A	C/C	CCG/CTA	C/T	G/A	T/G	A/A	C/T	G/A	C/C	G/G
Lab5 S5 - Read Counts	6265\4859	1153\1153	2673\2491	1283\384	1283\384	1283\384	17\17	16420\16420	34553\21252	34553\21252	34553\21252	350005\318111	3185\3185	132496\5486	140483\8695	7\7	7\7
Lab6 MiSeq - Genotype	G/G	G/G	C/C	ACA/ATG	C/T	A/G		C/C	CCG/CTA	C/T	G/A	T/G	A/A	C/C	G/A	C/C	G/G
Lab6 MiSeq - Read Counts	98\98	7\7	44\44	144\30	144\30	144\30		273\273	737\422	737\422	737\422	72444\63446	836\836	4158\4158	4997\234	25\25	25\25
Lab7 MiSeq - Genotype	CTA/CCG	T/C	A/G	T/G	C/A	C/T	G/A										
Lab7 MiSeq - Read Counts	2810\1187	2810\1187	2810\1187	304046\82273	563\64	7245\1382	3229\1627										
Lab8 S5 - Genotype	C/G	G/G	T/C	ACA/ATG	C/T	A/G	A/A	C/C	CCG/CTA	C/T	G/A	T/G	A/A	C/T	G/A	C/T	G/A
Lab8 S5 - Read Counts	7602\6966	4323\4323	3430\3059	2120\2021	2120\2021	2120\2021	481\481	15311\15311	29242\21316	29242\21316	29242\21316	384147\326345	11327\11327	89728\4117	96140\5556	893\88	893\88
Lab9 S5 - Genotype		G/G						C/C	CCG	C/C	G/G	G/T	C/C	T/C	A/G		
Lab9 S5 - Read Counts		6\6						5\5	40	40\40	40\40	303\242	10\10	60\35	24\15		
Lab10 MiSeq - Genotype												G/G					
Lab10 MiSeq - Read Counts												5\5					
Lab11 MiSeq - Genotype	C/G	G/G	C/T	ATG/ACA	T/C	G/A	A/A	C/C	CCG/CTA	C/T	G/A	T/G	A/A	C/T	G/A	C/T	G/A
Lab11 MiSeq - Read Counts	1087\1072	1877\1877	601\534	257\145	257\145	257\145	159\159	1681\1681	3476\3249	3476\3249	3476\3249	72229\65123	9922\9922	15837\750	14923\977	464\24	464\24

Stain 5 (BL-SE):
- high number of reads for most labs
- RNA cSNP genotype mostly reflects donor genotypes

Mixed Stains

Stain 13	HTN3.0	HTN3.1	HTN3.2	MUC7	PRB4	PRH2	HTN3	KLK3.0	KLK3.1	KLK3.2	PRM1	SEMG2	TGM4.0	TGM4.1	TGM4.2	TGM4.3
SA-SE	rs1849937_rs1136515	rs1849937	rs1136515	rs2306948	rs1052808	rs10772391	rs75067954	rs11573_rs1135766	rs11573	rs1135766	rs737008	rs2233896	rs1995640	rs1995641	rs3749195	rs9876921
IonCode_145	TC/CT	T/C	C/T	C/C	G/G	C/C	C/C	TA	T/T	A/A	T/T	C/C	T/T	A/A	C/T	G/A
IonCode_146	CC/CT	C/C	C/T	C/C	C/G	C/C	C/C	TA/CG	T/C	A/G	T/T	C/C	C/T	G/A	T/C	G/A
Lab1 S5 - Genotype																
Lab1 S5 - Read Counts																
Lab2 S5 - Genotype																
Lab2 S5 - Read Counts																
Lab3 S5 - Genotype				C/T		C/C					T/T		T/T			
Lab3 S5 - Read Counts				23\15		10\10					73\73		5\5			
Lab4 S5 - Genotype											T/T					
Lab4 S5 - Read Counts											13425\13425					
Lab5 S5 - Genotype	CT/CT	C/C	T/T	C/C			C/C	CCG/CTA	C/T	G/A	T/T	C/C	T/C	G/A		
Lab5 S5 - Read Counts	37	37\37	37\37	358\358			37\37	7\6	7\6	7\6	3357\3357	37\37	355\21	10\8		
Lab6 MiSeq - Genotype	CT/CC	C/C	T/C	C/C		C/C	C/C	CTA	T/T	A/A	T/T	C/C	T/T	A/A		
Lab6 MiSeq - Read Counts	400\296	400\400	400\296	22025\22025		2988\2988	400\400	4977	4977\4977	4977\4977	191555\191555	9701\9701	3196\3196	3547\3547		
Lab7 MiSeq - Genotype				C/C		C/C		CTA	T/T	A/A	T/T		T/T			
Lab7 MiSeq - Read Counts				141\141		5\5		37	37\37	37\37	272955\272955		365\365			
Lab8 S5 - Genotype				C/C		C/C		CTA/TTA	T/T	A/A	T/T	C/C	T/T	A/A		
Lab8 S5 - Read Counts				316\316		7\7		257\60	257\257	257\257	184079\184079	7\7	2809\2809	14\14		
Lab9 S5 - Genotype				C/C				CTA/CCG	T/C	A/G	T/T	C/C	T/C	A/G		
Lab9 S5 - Read Counts				5\5				70\32	70\32	70\32	98\98	156\156	84\44	39\19		
Lab10 MiSeq - Genotype																
Lab10 MiSeq - Read Counts																
Lab11 MiSeq - Genotype				C/C				CTA	T/T	A/A	T/T	C/C	T/T	A/A		
Lab11 MiSeq - Read Counts				141\141				403	403\403	403\403	34758\34758	8\8	171\171	59\59		

Stain 13 (SA-SE):

- high number of reads in a few markers
- RNA cSNP genotype reflects donor genotypes in markers with high coverage

Stain 14 (VAG-BL):

- high number of reads in most markers
- RNA cSNP genotype reflects donor genotypes

Stain 14	CYP2A6	MUC22.0	MUC22.1	MUC22.2	MUC22.3	MUC22.4	MUC22.5	MUC22.6	MUC22.7	MUC22.8	MUC22.9	ANK1.0	ANK1.1	CD3G	SPTB.0	SPTB.1	SPTB.2	SPTB.3	SPTB.4	COL17A1	IL37.0	IL37.1	IL37.2	LCE1C.0	LCE1C.1	LCE1C.2	LCE1C.3
VAG-BL	rs8192721	rs12110470_rs12110785	rs12110470	rs12110785	rs3869098_rs4248153	rs3869098	rs4248153	rs1419664_rs3094672	rs1419664	rs3094672	rs10947121	rs504574	rs7816734	rs3753059	rs1741488_rs1741487	rs1741488	rs1741487	rs229592	rs229586	rs805701	rs3811046_rs3811047	rs3811046	rs3811047	rs1837093_rs2056582_rs1702493	rs36107483	rs2006940	rs17624493
IonCode_139	C/C	GT		T/T	AA/GA	A/G	A/A	CT/CA/CC	C/C	T/A	T/T	C/G	G/G	T/T	CA	C/C	A/A	A/A	C/T	G/G	TG/GA	T/G	G/A	ACG/GCA	A/G	C/C	G/A
IonCode_147	C/C	TC/TT	T/T	C/T	GG/AG	G/A	G/G	CA/TA/CC/TC	C/T	A/A	C/T	G/C	G/G	T/T	CA/TG	C/T	A/G	A/G	C/C	A/G	GA	G/G	A/A	ATG	A/A	T/T	G/G
Lab1 S5 - Genotype																											
Lab1 S5 - Read Counts																											
Lab2 S5 - Genotype		GT/GT	G/G	T/T	CAA/CGA	A/G	A/A	ACT/ACA	C/C	T/A	T/T	C/G	G/G	T/T	ATG/ACA	T/C	G/A	G/A	C/C								
Lab2 S5 - Read Counts		16600	16600\16600	16600\16600	76026\60510	76026\60510	76026\76026	38149\36457	38149\38149	38149\36457	16600\16600	530\375	868\868	413\413	244\228	244\228	244\228	304\60	1511\1511								
Lab3 S5 - Genotype		GT/GT	G/G	T/T	CAA/CGA	A/G	A/A	ACA/ACT	C/C	A/T	T/T	C/G	G/G	T/T	ATG/ACA	T/C	G/A	G/A	C/C								
Lab3 S5 - Read Counts		6370	6370\6370	6370\6370	25976\23531	25976\23531	25976\25976	18803\18118	18803\18803	18803\18118	6370\6370	84\18	421\421	326\326	82\20	82\20	82\20	31\11	312\312								
Lab4 S5 - Genotype		GT/GT	G/G	T/T	CGA/CAA	G/A	A/A	ACA/ACT	C/C	A/T	T/T	C/G	G/G	T/T	ATG/ACA/AAG	T/C	G/A		C/C								
Lab4 S5 - Read Counts		39616	39616\39616	39616\39616	179565\170161	179565\170161	179565\179565	39416\35836	39416\39416	39416\35836	39616\39616	798\682	56\56	1055\1055	99\64\8	99\64	99\64		1604\1604								
Lab5 S5 - Genotype		GT/GT	G/G	T/T	CAA/CGA	A/G	A/A	ACT/ACA	C/C	T/A	T/T	C/C	G/G	T/T	ACA	C/C	A/A	G/G	C/C								
Lab5 S5 - Read Counts		39196	39196\39196	39196\39196	200156\191512	200156\191512	200156\200156	79575\73926	79575\79575	79575\73926	39196\39196	932\932	1226\1226	1665\1665	735	735\735	735\735	479\479	2034\2034								
Lab6 MiSeq - Genotype		GT/GT	G/G	T/T	CGA/CAA	G/A	A/A	ACA/ACT	C/C	A/T	T/T	G/C	G/G	T/T	ATG/ACA	T/C	G/A	G/A	C/T								
Lab6 MiSeq - Read Counts		18646	18646\18646	18646\18646	30610\12528	30610\12528	30610\30610	17009\8256	17009\8256	17009\8256	18646\18646	7770\7770	1125\1125	14020\14020	1100	1100\1100	1100\1100	24\24	9180\9180								
Lab7 MiSeq - Genotype		GT/GT	G/G	T/T	CGA/CAA	G/A	A/A	ACT/ACA	C/C	T/A	T/T	G/C	G/G	T/T	ACA/ATG	C/T	A/G	G/A	C/C								
Lab7 MiSeq - Read Counts		21248	21248\21248	21248\21248	77165\76895	77165\76895	77165\77165	46196\46069	46196\46196	46196\46069	21248\21248	299\175	274\274	485\485	177\22	177\22	177\22	21\19	588\588								
Lab8 S5 - Genotype		GT/GT	G/G	T/T	CGA/CAA	G/A	A/A	ACT/ACA	C/C	T/A	T/T	C/G	G/G	T/T	ACA/ATG	C/T	A/G	A/A	C/C								
Lab8 S5 - Read Counts		36495	36495\36495	36495\36495	187101\175195	187101\175195	187101\187101	158341\153043	158341\158341	158341\153043	36495\36495	1263\261	189\189	2392\2392	248\231	248\231	248\231	253\253	661\661								
Lab9 S5 - Genotype		GT/GT	G/G	T/T	CAA/CGA	A/G	A/A	ACT/ACA	C/C	T/A	T/T	G/C	G/G	T/T	ACA	C/C	A/A	G/G	C/C								
Lab9 S5 - Read Counts		57011	57011\57011	57011\57011	154560\153950	154560\153950	154560\154560	157605\149433	157605\157605	157605\149433	57011\57011	378\364	550\550	1372\1372	301	301\301	301\301	181\181	2274\2274								
Lab10 MiSeq - Genotype		GT/GT	G/G	T/T	CAA/CGA	A/G	A/A	ACA/ACT	C/C	A/T	T/T	G/C	G/G	T/T	ACA	C/C	A/A		C/C		TGC	T/T	G/G				
Lab10 MiSeq - Read Counts		1106	1106\1106	1106\1106	8971\8630	8971\8630	8971\8971	3612\3557	3612\3612	3612\3557	1106\1106	16\16	26\26	49\49	6	6\6	6\6		24\24		23	23\23	23\23				
Lab11 MiSeq - Genotype		GT/GT	G/G	T/T	CGA/CAA	G/A	A/A	ACA/ACT	C/C	A/T	T/T	C/G	G/G	T/T	ATG/ACA	T/C	G/A	A/A	C/C								
Lab11 MiSeq - Read Counts		8562	8562\8562	8562\8562	45238\45119	45238\45119	45238\45238	26448\24013	26448\26448	26448\24013	8562\8562	102\42	133\133	77\77	35\31	35\31	35\31	13\13	53\53								

Mixed Stains

Stain 6	KLK3.0	KLK3.1	KLK3.2	PRM1	SEMG2	TGM4.0	TGM4.1	TGM4.2	TGM4.3
SE-SE	rs11573_rs1135766	rs11573	rs1135766	rs737008	rs2233896	rs1995640	rs1995641	rs3749195	rs9876921
IonCode_144	CG/TA	C/T	G/A	G/T	A/A	C/T	G/A	T/C	A/G
IonCode_145	TA	T/T	A/A	T/T	C/C	T/T	A/A	C/T	G/A
Lab1 S5 - Genotype				T/G					
Lab1 S5 - Read Counts				2975\577					
Lab2 S5 - Genotype	CTA	T/T	A/A	T/G		C/T			
Lab2 S5 - Read Counts	5	5\5	5\5	40237\12416		96\45			
Lab3 S5 - Genotype	CTA/CCG	T/C	A/G	T/G	C/A	C/T	G/A		
Lab3 S5 - Read Counts	1053\395	1053\395	1053\395	23590\8100	667\62	2122\787	1370\509		
Lab4 S5 - Genotype	CTA/CCG	T/C	A/G	T/G	C/A	C/T	G/A		
Lab4 S5 - Read Counts	12796\3443	12796\3443	12796\3443	322793\96316	298\13	15124\8774	5563\3098		
Lab5 S5 - Genotype	CTA/CCG	T/C	A/G	T/G	C/A	C/T	G/A	C/T	G/A
Lab5 S5 - Read Counts	8725\4878	8725\4878	8725\4878	137666\52408	12588\2888	14487\1876	10424\6577	283\91	283\91
Lab6 MiSeq - Genotype	CTA/CCG	T/C	A/G	T/G	C/A	C/T	G/A	C/C	G/G
Lab6 MiSeq - Read Counts	2502\689	2502\689	2502\689	238139\62049	10142\1045	4669\1879	5790\2643	17\17	17\17
Lab7 MiSeq - Genotype	CTA/CCG	T/C	A/G	T/G	C/A	C/T	G/A		
Lab7 MiSeq - Read Counts	2810\1187	2810\1187	2810\1187	304046\82273	563\64	7245\1382	3229\1627		
Lab8 S5 - Genotype	CTA/CCG	T/C	A/G	T/G	C/C	C/T	A/G		
Lab8 S5 - Read Counts	83\16	83\16	83\16	605400\200868	10\10	1580\1105	15\15		
Lab9 S5 - Genotype	CCG	C/C	G/G	T/G		T/C	G/A	T/T	A/A
Lab9 S5 - Read Counts	133	133\133	133\133	6377\3262		191\153	81\77	55\55	55\55
Lab10 MiSeq - Genotype				T/G		C/C			
Lab10 MiSeq - Read Counts				66\21		6\6			
Lab11 MiSeq - Genotype	CTA/CCG	T/C	A/G	T/G	A/C	T/C	A/G		
Lab11 MiSeq - Read Counts	95\9	95\9	95\9	100545\31662	14\10	1115\1097	19\8		

Stain 6 (SE-SE):
- rather high number of reads in several markers
- RNA cSNP genotype mostly reflects sum of donor genotypes

Stain 8	HTN3.0	HTN3.1	HTN3.2	MUC7	PRB4	PRH2	HTN3	COL17A1	IL37.0	IL37.1	IL37.2	LCE1C.0	LCE1C.1	LCE1C.2	LCE1C.3
SA-SK	rs1849937_rs1136515	rs1849937	rs1136515	rs2306948	rs1052808	rs10772391	rs75067954	rs805701	rs3811046_rs3811047	rs3811046	rs3811047	rs36107483_rs2006940_rs17624493	rs36107483	rs2006940	rs17624493
IonCode_138	CC/CT	C/C	C/T	C/C	G/G	C/C	C/C	A/G	TG	T/T	G/G	ACG/GCA	A/G	C/C	G/A
IonCode_131	CT	C/C	T/T	C/C	G/G	C/C	C/C	A/A	TG	T/T	G/G	ACG	A/A	C/C	G/G
Lab1 S5 - Genotype	CT/CT	C/C	T/T	C/C		C/C	C/C					ACG	A/A	C/C	G/G
Lab1 S5 - Read Counts	624	624\624	624\624	53464\53464		27922\27922	624\624					6	6\6	6\6	6\6
Lab2 S5 - Genotype	CT/CT	C/C	T/T	C/C	G/G	C/C	C/C	A/A				ACG/GCG	A/G	C/C	G/G
Lab2 S5 - Read Counts	18374	18374\18374	18374\18374	60797\60797	102\102	8719\8719	18374\18374	143\143				28\8	28\8	28\28	28\28
Lab3 S5 - Genotype	CT/CG	C/C	T/G	C/C	G/G	C/C	C/C	A/A							
Lab3 S5 - Read Counts	8018\458	8018\8018	8018\458	6948\6948	71\71	1949\1949	8018\8018	8\8							
Lab4 S5 - Genotype	CT/CT	C/C	T/T	C/C		C/C	C/C	A/A	TGC	T/T	G/G				
Lab4 S5 - Read Counts	221	221\221	221\221	97443\97443		8374\8374	221\221	525\525	5	5\5	5\5				
Lab5 S5 - Genotype	CT/CT	C/C	T/T	C/C	G/G	C/C	C/C		GAC	G/G	A/A	ACG	A/A	C/C	G/G
Lab5 S5 - Read Counts	297292	297292\297292	297292\297292	195674\195674	1941\1941	14278\14278	297292\297292		288	288\288	288\288	72	72\72	72\72	72\72
Lab6 MiSeq - Genotype	CT/CT	C/C	T/T	C/C	G/G	C/C	C/C	A/A							
Lab6 MiSeq - Read Counts	9908	9908\9908	9908\9908	6908\6908	303\303	5237\5237	9908\9908	13\13							
Lab7 MiSeq - Genotype	CT/CT	C/C	T/T	C/C	G/G	C/C	C/C		GAC	G/G	A/A	ACG/GCG	A/G	C/C	G/G
Lab7 MiSeq - Read Counts	58251	58251\58251	58251\58251	62986\62986	2065\2065	23009\23009	58251\58251		79	79\79	79\79	19\7	19\7	19\19	19\19
Lab8 S5 - Genotype	CT/CT	C/C	T/T	C/C	G/G	C/C	C/C	A/A				GCG/ACG	G/A	C/C	G/G
Lab8 S5 - Read Counts	16970	16970\16970	16970\16970	272960\272960	42\42	42794\42794	16970\16970	434\434				82\69	82\69	82\82	82\82
Lab9 S5 - Genotype				C/C	G/G	C/C		A/A							
Lab9 S5 - Read Counts				48381\48381	61\61	7652\7652		123\123							
Lab10 MiSeq - Genotype	CT/CT	C/C	T/T	C/C	G/G	C/C	C/C								
Lab10 MiSeq - Read Counts	19177	19177\19177	19177\19177	14742\14742	86\86	2221\2221	19177\19177								
Lab11 MiSeq - Genotype	CT/CT	C/C	T/T	C/C	G/G	C/C	C/C	A/A							
Lab11 MiSeq - Read Counts	2623	2623\2623	2623\2623	26264\26264	5\5	4822\4822	2623\2623	82\82							

Stain 8 (SA-SK):
- rather high number of reads in several saliva markers
- RNA cSNP genotype reflects saliva donor genotype

Mixed Stains

Stain 4 (SE-MB):

- rather high number of reads in most markers
- not every lab detected the same components
- RNA cSNP genotype reflects donor genotypes

Stain 4	KLK3.0	KLK3.1	KLK3.2	PRM1	SEMG2	TGM4.0	TGM4.1	TGM4.2	TGM4.3	MMP10.0	MMP10.1	COL12A1.0	COL12A1.1	COL12A1.2	COL6A3.0	COL6A3.1	COL6A3.2	COL6A3.3	COL6A3.4	COL6A3.5	MMP3
SE-MB	rs11573_rs1135766	rs11573	rs1135766	rs737008	rs2233896	rs1995640	rs1995641	rs3749195	rs9876921	rs17860950	rs17860949	rs240736	rs594012	rs970547	rs1131296_rs2270669	rs1131296	rs2270669	rs4433949	rs34558385	rs3790993	rs679620
IonCode_135	TA/CG	T/C	A/G	G/T	C/A	T/T	A/A	T/T	A/A	A/A	G/G	G/G	T/T	T/T	AG	A/A	G/G	T/T	G/G	G/G	T/C
IonCode_143	CG	C/C	G/G	G/T	C/C	C/T	G/A	T/C	G/A	A/A	G/G	A/A	T/T	T/T	GG	G/G	G/G	C/C	G/G	G/C	T/T
Lab1 S5 - Genotype	CCG	C/C	G/G	T/G	C/C	T/C	G/A	T/C	A/G	A/A	G/G	G/G	T/T	T/T		A/A	G/G	T/T	G/G	G/G	C/T
Lab1 S5 - Read Counts	248	248\248	248\248	1375\1132	147\147	248\236	287\164	70\10	70\10	489\489	489\489	258\258	129\129	167\167		105\105	123\123	36\36	36\36	1089\1089	881\699
Lab2 S5 - Genotype				T/G		T/C				A/A	G/G			T/T		A/A	G/G			G/G	C/T
Lab2 S5 - Read Counts				134\118		27\17				21\21	21\21			17\17		10\10	13\13			19\19	54\22
Lab3 S5 - Genotype	CCG/CCC	C/C	G/C	T/G	C/C	T/C	A/G	T/C	A/G	A/A	G/G	G/G	T/T	T/T		A/A	G/G	T/T	G/G	G/C	C/T
Lab3 S5 - Read Counts	10140\229	10140\10140	10140\229	11920\10267	497\497	14260\11858	16870\14120	66\55	66\55	8\8	8\8	1464\1464	697\697	775\775		539\539	341\341	26\26	26\26	3086\258	1587\1284
Lab4 S5 - Genotype	CCG	C/C	G/G	T/G		T/C	A/G					G/G	T/T	T/T		A/A	G/G			G/C	T/C
Lab4 S5 - Read Counts	1914	1914\1914	1914\1914	63263\58242		80142\77836	248\204					2079\2079	4287\4287	899\899		5895\5895	54\54			102549\2246	69\52
Lab5 S5 - Genotype	CCG/CCC	C/C	G/C	T/G	C/C	T/C	A/G	T/C	A/G	A/A	G/G	G/G	T/T	T/T		A/A	G/G	T/T	G/G	G/C	C/T
Lab5 S5 - Read Counts	10140\229	26866\26866	26866\26866	146367\135543		160044\136260	8883\6633					20821\20821	19272\19272	14735\14735		20133\20133	3686\3686			101840\101840	183\10
Lab6 MiSeq - Genotype	CCG	C/C	G/G	T/G	C/C	T/C	A/G	T/C	A/G	A/A	G/G	G/G	T/T	T/T		A/A	G/G	T/T	G/G	G/G	C/T
Lab6 MiSeq - Read Counts	15278	15278\15278	15278\15278	22643\18965	808\808	46860\37383	49510\39318	13\8	13\8	7\7	7\7	24308\24308	19378\19378	13770\13770		3615\3615	1548\1548	73\73	73\73	53672\53672	20319\14699
Lab7 MiSeq - Genotype		C/C	G/G	T/G	C/C	T/C	A/G					G/G	T/T	T/T		A/A	G/G			G/G	C/T
Lab7 MiSeq - Read Counts	20662	20662\20662	20662\20662	14108\12974	55\55	42666\36865	27439\23438					16763\16763	8015\8015	11929\11929		9617\9617	4259\4259			61274\61274	2313\1433
Lab8 S5 - Genotype	CCG	C/C	G/G	T/G	C/C	T/C	A/G	T/C	A/G	A/A	G/G	G/G	T/T	T/T		A/A	G/G	T/T	G/G	G/G	C/T
Lab8 S5 - Read Counts	78645	78645\78645	78645\78645	8828\8411	4201\4201	79387\70460	108229\78391	10311\8579	10311\8579	23557\23557	23557\23557	59065\59065	38069\38069	42584\42584		37393\37393	24256\24256	18822\18822	18822\18822	96767\96767	208352\194686
Lab9 S5 - Genotype	CCG	C/C	G/G	G/T	C/C	T/C	A/G	T/C	A/G	A/A	A/G	G/G	T/T	T/T		A/A	G/G	T/T	G/G	G/G	C/T
Lab9 S5 - Read Counts	354027	354027\354027	354027\354027	34014\33427	751\751	396686\325565	251693\217760	68\35	68\35	16\16	16\16	58769\58769	26982\26982	28989\28989		20513\20513	14235\14235	110\110	110\110	49117\49117	6738\4648
Lab10 MiSeq - Genotype	CCG	C/C	G/G	T/G		T/C	A/G					G/G	T/T	T/T		A/A				G/G	C/T
Lab10 MiSeq - Read Counts	51	51\51	51\51	162\135		269\243	152\105					30\30	24\24	7\7		7\7				111\111	10\9
Lab11 MiSeq - Genotype	CCG	C/C	G/G	T/G	C/C	T/C	A/G	T/C	A/G	A/A	G/G	G/G	T/T	T/T		A/A	G/G	T/T	G/G	G/G	C/T
Lab11 MiSeq - Read Counts	10586	10586\10586	10586\10586	1631\1524	982\982	14013\11459	15973\12764	932\732	932\732	8591\8591	8591\8591	10037\10037	8665\8665	6396\6396		4693\4693	1729\1729	2841\2841	2841\2841	28518\28518	50624\44459

Stain 4	CYP2A6	MUC22.0	MUC22.1	MUC22.2	MUC22.3	MUC22.4	MUC22.5	MUC22.6	MUC22.7	MUC22.8	MUC22.9	ANK1.0	ANK1.1	CD3G	SPTB.0	SPTB.1	SPTB.2	SPTB.3	SPTB.4
SE-MB	rs8192721	rs12110470_rs12110785	rs12110470	rs12110785	rs3869098_rs4248153	rs3869098	rs4248153	rs1419664_rs3094672	rs1419664	rs3094672	rs10947121	rs504574	rs7816734	rs3753059	rs1741488_rs1741487	rs1741488	rs1741487	rs229592	rs229586
IonCode_135	C/C	GT	G/G	T/T	AA/GA	A/G	A/A	CT/TA/TC	C/T	T/A	T/T	C/C	A/A	T/T	CA	C/C	A/A	A/A	C/C
IonCode_143	C/C	GT/TC	G/T	T/C	AA/GG	A/G	A/G	CT/CA/CC	C/C	T/A	C/T	C/G	G/G	T/C	CA	C/C	A/A	G/G	T/T
Lab1 S5 - Genotype		GT/GT	G/G	T/T	CGA/CAA	G/A	A/A	ACT/ATA	C/T	T/A	T/T			T/T					C/C
Lab1 S5 - Read Counts		48	48\48	48\48	104\10	104\10	104\104	239\36	239\36	239\36	48\48			77\77					51\51
Lab2 S5 - Genotype		GT/GT	G/G	T/T	CAA/CGA	A/G	A/A	ACT/ACA/ATA	C/C	T/A	T/T	C/C	A/A		ACA	C/C	A/A		
Lab2 S5 - Read Counts		51	51\51	51\51	148\129	148\129	148\148	373\311\14	373\373	373\311	51\51	5\5	5\5		7	7\7	7\7		
Lab3 S5 - Genotype		GT/GT	G/G	T/T	CGA/CAA	G/A	A/A	ACT/ATA	C/T	T/A	T/T	C/G	A/G	T/C	ACA	C/C	A/A		C/C
Lab3 S5 - Read Counts		207	207\207	207\207	199\71	199\71	199\199	367\106	367\106	367\106	207\207	241\75	115\38	205\5	78	78\78	78\78		324\324
Lab4 S5 - Genotype		GT/GT	G/G	T/T	CGA/CAA	G/A	A/A				T/T	C/G		T/T					C/C
Lab4 S5 - Read Counts		39	39\39	39\39	74\6	74\6	74\74				39\39	1264\27		9\9					100\100
Lab5 S5 - Genotype	C/G	A/G	T/C	ACA	C/C	A/A		C/C	G/G	T/T	CGA/CAA	G/A	A/A	ACT/ATA	C/T	T/A	T/T		
Lab5 S5 - Read Counts	4394\310		70\8					1948\1948	1151\1151	1151\1151	898\153	898\153	898\898	124\61	124\61	124\61	1151\1151		
Lab6 MiSeq - Genotype		GT/GT	G/G	T/T	CGA/CAA	G/A	A/A	ACT/ATA	C/T	T/A	T/T	C/G	A/G	T/C	ACA	C/C	A/A		C/C
Lab6 MiSeq - Read Counts		1256	1256\1256	1256\1256	2678\685	2678\685	2678\2678	3625\1074	3625\1074	3625\1074	1256\1256	811\46	98\20	2216\70	115	115\115	115\115		932\932
Lab7 MiSeq - Genotype		GT/GT	G/G	T/T	CGA/CAA	G/A	A/A	ACT/ATA	C/T	T/A	T/T								
Lab7 MiSeq - Read Counts		5987	5987\5987	5987\5987	20181\5783	20181\5783	20181\20181	8371\2632	8371\2632	8371\2632	5987\5987								
Lab8 S5 - Genotype		GT/GT	G/G	T/T	CGA/CAA	G/A	A/A	ACT/ATA	C/T	T/A	T/T	C/C	A/G	T/T	ACA	C/C	A/A	A/A	C/C
Lab8 S5 - Read Counts		2465	2465\2465	2465\2465	6392\1614	6392\1614	6392\6392	7231\2184	7231\2184	7231\2184	2465\2465	6629\6629	3890\120	4689\4689	2053	2053\2053	2053\2053	780\780	7283\7283
Lab9 S5 - Genotype		GT/GT	G/G	T/T	CGA/CAA	G/A	A/A	ACT/ATA	C/T	T/A	T/T	C/C	A/A	T/T	ACA	C/C	A/A	A/A	C/C
Lab9 S5 - Read Counts		10997	10997\10997	10997\10997	34816\7747	34816\7747	34816\34816	18057\5546	18057\5546	18057\5546	10997\10997	21889\21889	1041\1041	8037\8037	2101	2101\2101	2101\2101	57\57	21865\21865
Lab10 MiSeq - Genotype		GT/GT	G/G	T/T	CGA/CAA	G/A	A/A				T/T	C/G		T/T					C/C
Lab10 MiSeq - Read Counts		39	39\39	39\39	74\6	74\6	74\74				39\39	1264\27		9\9					100\100
Lab11 MiSeq - Genotype		GT/GT	G/G	T/T	CGA/CAA	G/A	A/A	ACT/ATA	C/T	T/A	T/T	C/C	A/G	T/T	ACA/AGA	C/G	A/A	A/A	C/C
Lab11 MiSeq - Read Counts		346	346\346	346\346	2514\513	2514\513	2514\2514	1236\485	1236\485	1236\485	346\346	1037\1037	906\36	1053\1053	208\6	208\6	208\208	126\126	790\790

Mixed Stains

Stain 2 (BL-MB):

- rather high number of reads in most markers
- not every lab detected the same components
- RNA cSNP genotype reflects donor genotypes > blood reflects sum of donor genotypes (only 1 discriminating cSNP: ANK1.0)

Stain 2	ANK1.0	ANK1.1	CD3G	SPTB.0	SPTB.1	SPTB.2	SPTB.3	SPTB.4	MMP10.0	MMP10.1	COL12A1.0	COL12A1.1	COL12A1.2	COL6A3.0	COL6A3.1	COL6A3.2	COL6A3.3	COL6A3.4	COL6A3.5	MMP3
BL-MB	rs504574	rs7816734	rs3753059	rs1741488_rs1741487	rs1741488	rs1741487	rs229592	rs229586	rs17860950	rs17860949	rs240736	rs594012	rs970547	rs1131296_rs2270669	rs1131296	rs2270669	rs4433949	rs34558385	rs3790993	rs679620
IonCode_134	G/C	G/G	T/T	CA/TG	C/T	A/G	G/A	C/C	A/A	G/A	A/A	T/T	T/T	AG/GG	A/G	G/G	C/T	G/G	G/G	C/T
IonCode_142	C/C	G/G	T/T	CA/TG	C/T	A/G	A/G	C/C	A/A	G/G	A/A	A/T	T/T	GG	G/G	G/G	C/C	G/A	C/C	T/C
Lab1 S5 - Genotype	C/G	G/G	T/T	ATG/ACA	T/C	G/A		C/C			A/A	T/T	T/T		A/G	G/G			G/G	C/T
Lab1 S5 - Read Counts	233\112	5\5	357\357	17\16	17\16	17\16		196\196			348\348	434\434	810\810		775\473	570\570			52213\52213	22\12
Lab2 S5 - Genotype	C/G	G/G	T/T	ACA/ATG	C/T	A/G	G/A	C/C	A/A	A/G	A/A	T/T	T/T		G/A	G/G	C/T	G/G	G/C	T/C
Lab2 S5 - Read Counts	608\89	1697\1697	2253\2253	551\406	551\406	551\406	241\223	1912\1912	6924\6924	6924\4434	3002\3002	3567\3567	2192\2192		1168\963	1932\1932	1486\1023	1486\1486	30494\1138	2113\1990
Lab3 S5 - Genotype	C/C	G/G	T/T	ATG/ACA	T/C	G/A	G/A	C/C	A/A	A/G	A/A	T/T	T/T		A/A	G/G	T/C	G/G	G/G	C/T
Lab3 S5 - Read Counts	5\5	412\412	687\687	144\135	144\135	144\135	109\45	375\375	1589\1589	1589\1268	117\117	6\6	135\135		5\5	73\73	141\82	141\141	24\24	585\452
Lab4 S5 - Genotype	C/C																		G/G	
Lab4 S5 - Read Counts	6\6																		1287\1287	
Lab5 S5 - Genotype	C/G	G/G	T/T	ATG/ACA	T/C	G/A	G/A	C/C	A/A	A/G	A/A	T/T	T/T		A/G	G/G	T/C	G/G	G/G	C/T
Lab5 S5 - Read Counts	4390\1243	10359\10359	9569\9569	3356\3018	3356\3018	3356\3018	947\881	13410\13410	17120\17120	17120\14226	6135\6135	6292\6292	3414\3414		3645\3417	4134\4134	1375\558	1375\1375	93342\93342	21460\13695
Lab6 MiSeq - Genotype	C/G	G/G	T/T	ACA/ATG	C/T	A/G	G/A	C/C	A/A	A/G	A/A	T/T	T/T		G/A	G/G	C/T	G/G	G/G	C/T
Lab6 MiSeq - Read Counts	489\77	464\464	3918\3918	118\88	118\88	118\88	12\7	391\391	32\32	32\27	1769\1769	1541\1541	966\966		338\297	265\265	74\68	74\74	31019\31019	2830\2150
Lab7 MiSeq - Genotype	C/G	G/G	T/T	ACA/ATG	C/T	A/G	G/A	C/C	A/A	A/G	A/A	T/T	T/T		A/G	G/G	T/C	G/G	G/G	C/T
Lab7 MiSeq - Read Counts	1622\173	2307\2307	4382\4382	758\717	758\717	758\717	303\227	3243\3243	4620\4620	4620\2931	1822\1822	1724\1724	1032\1032		1764\1664	1761\1761	433\221	433\433	32626\32626	5302\3418
Lab8 S5 - Genotype	C/G	G/G	T/T	ACA	C/C	A/A	G/A	C/C	A/A	A/G	A/A	T/T	T/T		G/A	G/G	C/T	G/G	G/G	C/T
Lab8 S5 - Read Counts	4728\4728	4728\4728	4728\4728	4728\4728	4728\4728	4728\4728	4728\4728	4728\4728	4728\4728	4728\4728	4728\4728	4728\4728	4728\4728	4728\4728	4728\4728	4728\4728	4728\4728	4728\4728	4728\4728	4728\4728
Lab9 S5 - Genotype	C/G	G/G	T/T	ATG/ACA	T/C	G/A	G/A	C/C	A/A	A/G	A/A	T/T	T/T		A/G	G/G	C/T	G/G	G/G	C/T
Lab9 S5 - Read Counts	5415\1435	9522\9522	5460\5460	4454\2023	4454\2023	4454\2023	1862\770	6457\6457	96040\96040	96040\66209	7305\7305	8578\8578	7746\7746		5107\4647	8302\8302	7374\6464	7374\7374	62984\62984	33053\32655
Lab10 MiSeq - Genotype	C/G	G/G	T/T	ATG/ACA	T/C	G/A	A/G	C/C	A/A	A/G	A/A	T/T	T/T		A/G	G/G	C/T	G/G	G/G	C/T
Lab10 MiSeq - Read Counts	607\113	844\844	1562\1562	242\232	242\232	242\232	134\108	711\711	1245\1245	1245\841	161\161	398\398	331\331		265\247	255\255	54\34	54\54	11196\11196	1217\988
Lab11 MiSeq - Genotype	C/G	G/G	T/T	ACA/ATG	C/T	A/G	A/G	C/C	A/A	A/G	A/A	T/T	T/C		G/A	G/G	T/C	G/G	G/G	C/T
Lab11 MiSeq - Read Counts	223\20	276\276	393\393	43\39	43\39	43\39	45\11	152\152	726\726	726\518	338\338	556\556	272\6		196\145	149\149	108\42	108\108	7991\7991	961\541

Stain 2	CYP2A6	MUC22.0	MUC22.1	MUC22.2	MUC22.3	MUC22.4	MUC22.5	MUC22.6	MUC22.7	MUC22.8	MUC22.9
BL-MB	rs8192721	rs12110470_rs12110785	rs12110470	rs12110785	rs3869098_rs4248153	rs3869098	rs4248153	rs1419664_rs3094672	rs1419664	rs3094672	rs10947121
IonCode_134	T/T	GT	G/G	T/T	AA	A/A	A/A	CT	C/C	T/T	T/T
IonCode_142	C/C	GT/TT	G/T	T/T	GG	G/G	G/G	TA/CA/CC/TC	T/C	A/A	C/C
Lab1 S5 - Genotype		GT/GT	G/G	T/T	CAA	A/A	A/A	ACT	C/C	T/T	T/T
Lab1 S5 - Read Counts		1687	1687\1687	1687\1687	15216	15216\15216	15216\15216	5295	5295\5295	5295\5295	1687\1687
Lab2 S5 - Genotype		GT/GT	G/G	T/T	CAA	A/A	A/A	ACT	C/C	T/T	T/T
Lab2 S5 - Read Counts		18497	18497\18497	18497\18497	183076	183076\183076	183076\183076	123521	123521\123521	123521\123521	18497\18497
Lab3 S5 - Genotype		GT/GT	G/G	T/T	CAA	A/A	A/A	ACT	C/C	T/T	T/T
Lab3 S5 - Read Counts		484	484\484	484\484	5815	5815\5815	5815\5815	5	5\5	5\5	484\484
Lab4 S5 - Genotype											
Lab4 S5 - Read Counts											
Lab5 S5 - Genotype	G/G	T/T	CAA	A/A	A/A	ACT	C/C	T/T	T/T		
Lab5 S5 - Read Counts	28872\28872	28872\28872	321642	321642\321642	321642\321642	206483	206483\206483	206483\206483	28872\28872		
Lab6 MiSeq - Genotype		GT/GT	G/G	T/T	CAA	A/A	A/A	ACT	C/C	T/T	T/T
Lab6 MiSeq - Read Counts		7281	7281\7281	7281\7281	90987	90987\90987	90987\90987	88909	88909\88909	88909\88909	7281\7281
Lab7 MiSeq - Genotype		GT/GT	G/G	T/T	CAA	A/A	A/A	ACT	C/C	T/T	T/T
Lab7 MiSeq - Read Counts		8220	8220\8220	8220\8220	83476	83476\83476	83476\83476	61434	61434\61434	61434\61434	8220\8220
Lab8 S5 - Genotype		GT/GT	G/G	T/T	CAA	A/A	A/A	ACT	C/C	T/T	T/T
Lab8 S5 - Read Counts	4728\4728	4728\4728	4728\4728	4728\4728	4728\4728	4728\4728	4728\4728	4728\4728	4728\4728	4728\4728	4728\4728
Lab9 S5 - Genotype		GT/GT	G/G	T/T	CAA	A/A	A/A	ACT	C/C	T/T	T/T
Lab9 S5 - Read Counts		86202	86202\86202	86202\86202	804553	804553\804553	804553\804553	801315	801315\801315	801315\801315	86202\86202
Lab10 MiSeq - Genotype		GT/GT	G/G	T/T	CAA	A/A	A/A	ACT	C/C	T/T	T/T
Lab10 MiSeq - Read Counts		1786	1786\1786	1786\1786	40209	40209\40209	40209\40209	12157	12157\12157	12157\12157	1786\1786
Lab11 MiSeq - Genotype		GT/GT	G/G	T/T	CAA	A/A	A/A	ACT	C/C	T/T	T/T
Lab11 MiSeq - Read Counts		5408	5408\5408	5408\5408	95493	95493\95493	95493\95493	38014	38014\38014	38014\38014	5408\5408

Results for the Body Fluid Identification for the Own Stains (up to 8 per laboratory)

BFID RNA Results – Laboratory 2 (S5) Stains 1-8

- mh counts: raw data, used to calculate the 0.5% threshold for correction
- mh counts corrected: everything below the 0.5% threshold set to 0

	own-1	own-1-corrected	own-2	own-2-corrected	own-3	own-3-corrected	own-4	own-4-corrected	own-5	own-5-corrected	own-6	own-6-corrected	own-7	own-7-corrected	own-8	own-8-corrected
	counts	counts corrected	counts	counts corrected	counts	counts corrected	counts	counts corrected	counts	counts corrected	counts	counts corrected	counts	counts corrected	counts	counts corrected
Blood_01_ANK1	5	0	97	0	0	0	9	0	101	0	0	0	5	0	11	11
Blood_02_ANK1	0	0	0	0	0	0	0	0	166	0	0	0	0	0	0	0
Blood_03_CD3G	0	0	0	0	0	0	0	0	71	0	0	0	0	0	0	0
Blood_04_SPTB	0	0	0	0	0	0	0	0	110	0	0	0	0	0	0	0
Blood_05_SPTB	0	0	153	153	0	0	0	0	307	0	0	0	0	0	0	0
Blood_06_SPTB	0	0	0	0	0	0	0	0	101	0	0	0	0	0	0	0
Menstrual_01_LEFTY2	0	0	3692	3692	0	0	5	0	20369	20369	7	0	46	0	0	0
Menstrual_02_MMP10	0	0	33	0	9	0	41	0	143698	143698	41	0	503	503	14	14
Menstrual_03_COL12A1	0	0	0	0	0	0	0	0	5039	5039	0	0	80	0	0	0
Menstrual_04_COL12A1	0	0	0	0	0	0	0	0	3870	3870	0	0	13	0	14	14
Menstrual_05_COL12A1	0	0	0	0	0	0	0	0	3593	3593	0	0	11	0	0	0
Menstrual_06_COL6A3	0	0	0	0	0	0	0	0	4994	4994	0	0	11	0	8	8
Menstrual_07_COL6A3	0	0	0	0	0	0	0	0	6582	6582	0	0	36	0	0	0
Menstrual_08_COL6A3	0	0	0	0	0	0	0	0	12861	12861	0	0	22	0	0	0
Menstrual_09_COL6A3	0	0	0	0	0	0	0	0	34566	34566	0	0	43	0	0	0
Menstrual_10_MMP3	0	0	24239	24239	120	0	0	0	40599	40599	77	0	73	0	0	0
Saliva_01_HTN3	0	0	0	0	76	0	34	0	0	0	122087	122087	28	0	27	27
Saliva_02_MUC7	0	0	0	0	15037	15037	20	0	0	0	15833	15833	12	0	115	115
Saliva_03_PRB4	0	0	0	0	5	0	8	0	0	0	1597	1597	15	0	19	19
Saliva_04_PRH2	0	0	0	0	0	0	0	0	17	0	19913	19913	0	0	0	0
Saliva_05_STATH	0	0	0	0	95462	95462	79	0	0	0	74120	74120	7	0	540	540
Semen_01_KLK3	0	0	0	0	0	0	746	746	0	0	0	0	0	0	0	0
Semen_02_PRM1	7383	7383	0	0	13	0	23750	23750	0	0	24	0	183	0	21	21
Semen_03_SEMG2	0	0	0	0	0	0	36	0	0	0	0	0	0	0	0	0
Semen_04_TGM4	0	0	0	0	0	0	5043	5043	0	0	0	0	24	0	0	0
Semen_05_TGM4	0	0	0	0	0	0	55	0	0	0	0	0	0	0	0	0
Semen_06_TGM4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Skin_01_COL17A1	0	0	0	0	0	0	0	0	51	0	43	0	63	0	0	0
Skin_02_IL37	0	0	0	0	0	0	0	0	28	0	0	0	0	0	0	0
Skin_03_LCE1C	0	0	102	0	24	0	12	0	202	0	8	0	50	0	18	18
Vaginal_01_CYP2A6	0	0	0	0	0	0	15	0	450	0	0	0	1353	1353	0	0
Vaginal_02_CYP2B7P1	0	0	1439	1439	0	0	31	0	11079	11079	5	0	2305	2305	0	0
Vaginal_03_MUC22	0	0	0	0	0	0	239	239	688	0	15	0	80816	80816	18	18
Vaginal_04_MUC22	0	0	0	0	0	0	72	0	771	0	0	0	5613	5613	0	0
Vaginal_05_MUC22	0	0	0	0	0	0	10	0	375	0	0	0	2751	2751	0	0
gDNAPRM1_01_gDNA	0	0	0	0	79	0	63	0	28	0	8	0	175	0	147	147
Tot. # of reads	7388	7383	29755	29523	110825	110499	30268	29778	290716	287250	233778	233550	94238	93341	952	952
0.5% threshold	36.94		148.775		554.125		151.34		1453.58		1168.89		471.19		4.76	
0.15% threshold	11.082		44.6325		166.2375		45.402		436.074		350.667		141.357		1.428	

Predicted Body Fluids: SE? MB? SA? VAG-SE? MB? SA? VAG? ?

BFID RNA Results – Laboratory 3 (S5) Stains 1-9

- mh counts: raw data, used to calculate the 0.5% threshold for correction
- mh counts corrected: everything below the 0.5% threshold set to 0

Markers	own-1	own-1-corrected	own-2	own-2-corrected	own-3	own-3-corrected	own-4	own-4-corrected	own-5	own-5-corrected	own-6	own-6-corrected	own-7	own-7-corrected	own-8	own-8-corrected	own-9	own9-corrected
	counts	counts corrected	counts	counts corrected	counts	counts corrected	counts	counts corrected	counts	counts corrected	counts	counts corrected	counts	counts corrected	counts	counts corrected	counts	counts corrected
Blood_01_ANK1	527	0	6	0	531	0	0	0	0	0	148	0	0	0	42	42	4815	4815
Blood_02_ANK1	529	0	65	0	0	0	0	0	0	0	54	0	0	0	0	0	4312	4312
Blood_03_CD3G	812	812	0	0	176	0	0	0	0	0	36	0	0	0	21	21	3480	3480
Blood_04_SPTB	217	0	20	0	0	0	0	0	0	0	0	0	0	0	0	0	3111	3111
Blood_05_SPTB	940	940	15	0	343	0	0	0	0	0	0	0	0	0	47	47	7938	7938
Blood_06_SPTB	13	0	0	0	0	0	0	0	31	0	0	0	0	0	0	0	193	193
Menstrual_01_LEFTY2	0	0	239	0	0	0	0	0	0	0	0	0	0	0	16	16	0	0
Menstrual_02_MMP10	0	0	653	653	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Menstrual_03_COL12A1	0	0	14	0	0	0	6	0	0	0	0	0	0	0	86	86	0	0
Menstrual_04_COL12A1	0	0	494	494	28	0	5	0	0	0	83	0	0	0	60	60	0	0
Menstrual_05_COL12A1	0	0	95	0	0	0	0	0	40	0	29	0	0	0	59	59	0	0
Menstrual_06_COL6A3	17	0	186	0	11	0	5	0	0	0	0	0	0	0	74	74	52	0
Menstrual_07_COL6A3	12	0	61	0	7	0	0	0	0	0	0	0	0	0	29	29	17	0
Menstrual_08_COL6A3	0	0	66	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Menstrual_09_COL6A3	30	0	1961	1961	185	0	10	0	0	0	0	0	0	0	188	188	151	151
Menstrual_10_MMP3	0	0	1406	1406	0	0	0	0	0	0	0	0	0	0	5	5	0	0
Saliva_01_HTN3	146	0	9	0	0	0	0	0	22792	22792	0	0	0	0	9	9	0	0
Saliva_02_MUC7	38094	38094	23	0	23	0	76	0	7251	7251	0	0	5513	5513	16	16	0	0
Saliva_03_PRB4	101	0	0	0	0	0	0	0	1397	1397	0	0	0	0	0	0	0	0
Saliva_04_PRH2	25953	25953	0	0	0	0	10	0	11590	11590	0	0	5	0	0	0	0	0
Saliva_05_STATH	48034	48034	0	0	0	0	88	0	16684	16684	11	0	6642	6642	20	20	0	0
Semen_01_KLK3	0	0	0	0	0	0	0	0	461	461	16946	16946	0	0	13	13	0	0
Semen_02_PRM1	0	0	5	0	0	0	0	0	18009	18009	20042	20042	18	0	49	49	0	0
Semen_03_SEMG2	0	0	0	0	0	0	0	0	264	0	1995	1995	0	0	0	0	0	0
Semen_04_TGM4	0	0	0	0	0	0	0	0	84	0	25676	25676	0	0	64	64	0	0
Semen_05_TGM4	0	0	0	0	0	0	0	0	219	0	29298	29298	0	0	35	35	0	0
Semen_06_TGM4	0	0	0	0	0	0	0	0	67	0	398	0	0	0	0	0	0	0
Skin_01_COL17A1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	55	0
Skin_02_IL37	0	0	0	0	0	0	0	0	0	0	25	0	0	0	0	0	0	0
Skin_03_LCE1C	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Vaginal_01_CYP2A6	0	0	147	0	1008	1008	206	206	0	0	0	0	0	0	0	0	0	0
Vaginal_02_CYP2B7P1	0	0	3398	3398	40381	40381	9794	9794	0	0	1524	1524	8	0	10	10	0	0
Vaginal_03_MUC22	0	0	57423	57423	47667	47667	12053	12053	9	0	3692	3692	13	0	23	23	0	0
Vaginal_04_MUC22	15	0	24608	24608	15699	15699	774	774	7	0	1810	1810	0	0	12	12	0	0
Vaginal_05_MUC22	0	0	2975	2975	15438	15438	3335	3335	0	0	166	0	0	0	6	6	0	0
gDNAPRM1_01_gDNA	7	0	0	0	0	0	0	0	136	0	239	0	0	0	0	0	9	0
Tot. # of reads	115447	113833	93869	92918	121497	120193	26362	26162	79041	78184	102172	100983	12199	12155	884	884	24133	24000
0.5% threshold	577.235		469.345		607.485		131.81		395.205		510.86		60.995		4.42		120.665	
0.15% threshold	173.1705		140.8035		182.2455		39.543		118.5615		153.258		18.2985		1.326		36.1995	

Predicted Body Fluids:	SA-BL?	MB?	MB?	VAG?	SA-SE?	VAG-SE?	SA?	?	BL?

BFID RNA Results – Laboratory 6 (MiSeq) Stains 1-8

- mh counts: raw data, used to calculate the 0.5% threshold for correction
- mh counts corrected: everything below the 0.5% threshold set to 0

Markers	own-1	own-1-corrected	own-2	own-2-corrected	own-3	own-3-corrected	own-4	own-4-corrected	own-5	own-5-corrected	own-6	own-6-corrected	own-7	own-7-corrected	own-8	own-8-corrected
	counts	counts corrected	counts	counts corrected	counts	counts corrected	counts	counts corrected	counts	counts corrected	counts	counts corrected	counts	counts corrected	counts	counts corrected
Blood_01_ANK1	20	0	30	0	11	0	10	0	1124	0	710	0	6853	6853	16686	16686
Blood_02_ANK1	0	0	18	0	17	0	15	0	435	0	372	0	7017	7017	27735	27735
Blood_03_CD3G	524	524	995	995	415	0	538	0	2844	2844	631	0	16704	16704	41578	41578
Blood_04_SPTB	16	0	21	0	7	0	9	0	488	0	408	0	4533	4533	16190	16190
Blood_05_SPTB	0	0	5	0	13	0	7	0	1056	0	651	0	7294	7294	19863	19863
Blood_06_SPTB	0	0	0	0	0	0	0	0	18	0	21	0	646	0	5146	5146
Menstrual_01_LEFTY2	0	0	0	0	0	0	0	0	9	0	0	0	44	0	92	0
Menstrual_02_MMP10	34	0	47	0	6	0	0	0	57	0	0	0	488	0	7394	7394
Menstrual_03_COL12A1	48	0	29	0	0	0	0	0	15338	15338	181	0	24367	24367	2181	2181
Menstrual_04_COL12A1	44	0	28	0	0	0	0	0	12179	12179	57	0	24208	24208	2048	2048
Menstrual_05_COL12A1	135	0	326	0	0	0	5	0	9857	9857	2635	2635	20486	20486	1453	1453
Menstrual_06_COL6A3	18	0	55	0	13	0	0	0	1071	0	16	0	12655	12655	725	0
Menstrual_07_COL6A3	10	0	27	0	0	0	0	0	432	0	5	0	5283	5283	312	0
Menstrual_08_COL6A3	42	0	82	0	15	0	10	0	226	0	6	0	9761	9761	1405	1405
Menstrual_09_COL6A3	241	0	265	0	107	0	186	0	8097	8097	198	0	82683	82683	4933	4933
Menstrual_10_MMP3	764	764	1257	1257	0	0	0	0	41848	41848	478	0	206112	206112	62824	62824
Saliva_01_HTN3	0	0	0	0	34	0	24	0	0	0	0	0	0	0	0	0
Saliva_02_MUC7	0	0	0	0	111	0	160	0	16	0	33	0	0	0	0	0
Saliva_03_PRB4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Saliva_04_PRH2	6	0	10	0	54	0	53	0	27	0	129	0	0	0	0	0
Saliva_05_STATH	0	0	0	0	267	0	355	0	19	0	30	0	0	0	0	0
Semen_01_KLK3	9299	9299	10024	10024	0	0	0	0	51736	51736	70049	70049	58	0	53	0
Semen_02_PRM1	13056	13056	15394	15394	0	0	0	0	62074	62074	79500	79500	48	0	92	0
Semen_03_SEMG2	24512	24512	39002	39002	0	0	5	0	40846	40846	76308	76308	6	0	15	0
Semen_04_TGM4	3970	3970	4056	4056	0	0	0	0	18614	18614	23664	23664	15	0	70	0
Semen_05_TGM4	3707	3707	4477	4477	0	0	0	0	20482	20482	28539	28539	27	0	132	0
Semen_06_TGM4	871	871	1234	1234	0	0	0	0	78	0	165	0	0	0	21	0
Skin_01_COL17A1	0	0	0	0	244	0	286	0	40	0	49	0	55	0	83	0
Skin_02_IL37	0	0	11	0	0	0	0	0	14	0	20	0	10	0	11	0
Skin_03_LCE1C	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Vaginal_01_CYP2A6	68	0	113	0	1349	1349	2028	2028	0	0	0	0	0	0	19	0
Vaginal_02_CYP2B7P1	596	596	753	753	33945	33945	47857	47857	207	0	195	0	467	0	1059	0
Vaginal_03_MUC22	643	643	411	411	77013	77013	96223	96223	617	0	470	0	1987	0	5173	5173
Vaginal_04_MUC22	184	0	211	0	53400	53400	66852	66852	415	0	277	0	1326	0	4493	4493
Vaginal_05_MUC22	71	0	72	0	17334	17334	24996	24996	270	0	83	0	680	0	1551	1551
gDNAPRM1_01_gDNA	0	0	5	0	0	0	0	0	14	0	29	0	0	0	0	0
Tot. # of reads	58879	57942	78958	77603	184355	183041	239619	237956	290548	283915	285909	280695	433813	427956	223337	220653
0.5% threshold	294.395		394.79		921.775		1198.095		1452.74		1429.545		2169.065		1116.685	
0.15% threshold	88.3185		118.437		276.5325		359.4285		435.822		428.8635		650.7195		335.0055	
Predicted Body Fluids:	MB-SE?		MB-SE?		VAG?		VAG?		MB-SE?		MB-SE?		MB?		MB?	

Assignment of Body Fluids with a Donor: Own Stains (8 per laboratory)

Assignment of Body Fluid with Donor – Own Stains Laboratory 2 (S5) Stains 5-7

- Matching RNA + DNA genotype in green
- Supposed donor in light blue

own-5	MMP10.0	MMP10.1	COL12A1.0	COL12A1.1	COL12A1.2	COL6A3.0	COL6A3.1	COL6A3.2	COL6A3.3	COL6A3.4	COL6A3.5	MMP3	CYP2A6	MUC22.0	MUC22.1	MUC22.2	MUC22.3	MUC22.4	MUC22.5	MUC22.6	MUC22.7	MUC22.8	MUC22.9
MB (?)	rs17860950	rs17860949	rs240736	rs594012	rs970547	rs1131296_rs2270669	rs1131296	rs2270669	rs4433949	rs34558385	rs3790993	rs679620	rs8192721	rs12110470_rs12110785	rs12110470	rs12110785	rs3869098_rs4248153	rs3869098	rs4248153	rs1419664_rs3094672	rs1419664	rs3094672	rs10947121
RNA Genotype S5	A/A	G/G	A/A	T/T	T/T		G/A	C/G	C/T	G/G	C/G	C/T		GT/GT	G/G	T/T	CGG/CAA	G/A	G/A	ACA/ATA	C/T	A/A	C/T
Read Counts S5	143698\143	143698\143	5039\5039	3870\3870	3593\3593		2860\2134	3299\3283	6654\6207	6654\6654	17333\1723	23122\1647		204\171	204\204	204\204	452\236	452\236	452\236	420\351	420\351	420\420	204\171
Donor genotype 1		G/G										C/T											
Donor genotype 2		G/G										C/T											
Donor genotype 3	A/A	G/G	A/A	T/T	T/T	AG/GC	A/G	G/C	C/T	G/G	C/G	C/T	C/C	GT/TC	G/T	T/C	GG	G/G	G/G	CA	C/C	A/A	C/C
Donor genotype 4	A/A	G/G	A/A	T/A	T/T	AG/GC	A/G	G/C	T/C	G/G	C/G	C/C	C/C	GT	G/G	T/T	GG/AA	G/A	G/A	TA/CA/CC/	T/C	A/A	T/T
Donor genotype 5	A/A	G/G	A/A	T/T	T/T	AG/GC	A/G	G/C	C/T	G/G	C/G	T/C	C/C	GT	G/G	T/T	AA/GG	A/G	A/G	TA/CA/TC/	T/C	A/A	C/T
Donor genotype 6	A/A	G/G	G/G	T/T	T/T	GG	G/G	G/G	C/C	A/A	C/C	T/C	C/C	GT	G/G	T/T	GG	G/G	G/G	CA/CC	C/C	A/C	C/C
Donor genotype 7	A/A	G/G	A/A	T/T	T/T	AG/GC	A/G	G/C	C/T	G/G	C/G	C/T	C/C	GT/TC	G/T	T/C	GG	G/G	G/G	CA/CC	C/C	A/C	C/C
Donor genotype 8																							

own-6	HTN3.0	HTN3.1	HTN3.2	MUC7	PRB4	PRH2	HTN3
SA (?)	rs1849937_rs1136515	rs1849937	rs1136515	rs2306948	rs1052808	rs10772391	rs75067954
RNA Genotype S5	CC/CC	C/C	C/C	C/C	C/G	C/T	C/C
Read Counts S5	122087	122087\122	122087\122	15833\1583	1130\467	11299\8614	122087\122087
Donor genotype 1	CC	C/C	C/C	C/C			
Donor genotype 2	CT	C/C	T/T	C/C			
Donor genotype 3	CC	C/C	C/C	T/T	C/G	C/T	C/C
Donor genotype 4	CC	C/C	C/C	C/C	C/G	T/C	C/C
Donor genotype 5	CT	C/C	T/T	C/C	C/G	T/C	C/C
Donor genotype 6	CC	C/C	C/C	T/T	G/G	C/C	C/C
Donor genotype 7	CT/CC	C/C	T/C	T/C	C/G	T/C	C/C
Donor genotype 8	CC	C/C	C/C	C/C			

own-7	MMP10.0	MMP10.1	COL12A1.0	COL12A1.1	COL12A1.2	COL6A3.0	COL6A3.1	COL6A3.2	COL6A3.3	COL6A3.4	COL6A3.5	MMP3	CYP2A6	MUC22.0	MUC22.1	MUC22.2	MUC22.3	MUC22.4	MUC22.5	MUC22.6	MUC22.7	MUC22.8	MUC22.9
VAG (?)	rs17860950	rs17860949	rs240736	rs594012	rs970547	rs1131296_rs2270669	rs1131296	rs2270669	rs4433949	rs34558385	rs3790993	rs679620	rs8192721	rs12110470_rs12110785	rs12110470	rs12110785	rs3869098_rs4248153	rs3869098	rs4248153	rs1419664_rs3094672	rs1419664	rs3094672	rs10947121
RNA Genotype S5	A/A	G/G	A/A	T/T	T/T		G/G	C/G	C/T	G/G	C/G	C/T		GT/GT	G/G	T/T	CGG/CAA	G/A	G/A	ACA/ATA	C/T	A/A	C/T
Read Counts S5	503\503	503\503	80\80	13\13	11\11		6\6	19\17	14\8	14\14	23\20	46\27		1505\1246	1505\1505	1505\1505	42148\3866	42148\3866	42148\3866	3387\2226	3387\2226	3387\3387	1505\1246
Donor genotype 1		G/G										C/T											
Donor genotype 2		G/G										C/T											
Donor genotype 3	A/A	G/G	A/A	T/T	T/T	AG/GC	A/G	G/C	C/T	G/G	C/G	C/T	C/C	GT/TC	G/T	T/C	GG	G/G	G/G	CA	C/C	A/A	C/C
Donor genotype 4	A/A	G/G	A/A	T/A	T/T	AG/GC	A/G	G/C	T/C	G/G	C/G	C/C	C/C	GT	G/G	T/T	GG/AA	G/A	G/A	TA/CA/CC/	T/C	A/A	T/T
Donor genotype 5	A/A	G/G	A/A	T/T	T/T	AG/GC	A/G	G/C	C/T	G/G	C/G	T/C	C/C	GT	G/G	T/T	AA/GG	A/G	A/G	TA/CA/TC/	T/C	A/A	C/T
Donor genotype 6	A/A	G/G	G/G	T/T	T/T	GG	G/G	G/G	C/C	A/A	C/C	T/C	C/C	GT	G/G	T/T	GG	G/G	G/G	CA/CC	C/C	A/C	C/C
Donor genotype 7	A/A	G/G	A/A	T/T	T/T	AG/GC	A/G	G/C	C/T	G/G	C/G	C/T	C/C	GT/TC	G/T	T/C	GG	G/G	G/G	CA/CC	C/C	A/C	C/C
Donor genotype 8	A/A																						C/C

Assignment of Body Fluid with Donor – Own Stains Laboratory 3 (S5) Stains 5,6

- Matching RNA + DNA genotype in green
- Supposed donor in light blue

own-5	HTN3.0	HTN3.1	HTN3.2	MUC7	PRB4	PRH2	HTN3	KLK3.0	KLK3.1	KLK3.2	PRM1	SEMG2	TGM4.0	TGM4.1	TGM4.2	TGM4.3
SA-SE?	rs1849937_rs1136515	rs1849937	rs1136515	rs2306948	rs1052808	rs10772391	rs75067954	rs11573_rs1135766	rs11573	rs1135766	rs737008	rs2233896	rs1995640	rs1995641	rs3749195	rs9876921
RNA Genotype S5	CC/CT	C/C	C/T	C/C	G/G	C/C	C/C	CCG/CTA	C/T	G/A	T/T	A/C	T/T	A/A	T/T	A/A
Read Counts S5	11273\10886\633	11273\11273	11273\10886	7251\7251	1397\1397	11590\11590	11273\11273	298\163	298\163	298\163	18009\18009	141\123	84\84	219\219	67\67	67\67
Donor genotype 1	CT/CC	C/C	T/C	C/C	G/G	C/C	C/C	TA	T/T	A/A	G/G	C/C	C/T	G/A	T/T	A/A
Donor genotype 2	CT	C/C	T/T	C/C	G/G	C/C	C/C	TA/CG	T/C	A/G	T/G	C/C	T/T	A/A	T/T	A/A
Donor genotype 3	CT/TC	C/T	T/C	C/C	G/C	C/T	C/C	TA/CG	T/C	A/G	T/G	C/C	C/T	G/A	C/T	G/A
Donor genotype 4	CC/CT	C/C	C/T	C/C	G/G	C/C	C/C	CG	C/C	G/G	T/G	C/C	C/C	G/G	C/C	G/G
Donor genotype 5	TC	T/T	C/C	C/T	G/G	C/C	C/C	TA/CG	T/C	A/G	G/T	C/A	T/T	A/A	T/T	A/A
Donor genotype 6	CT/CC	C/C	T/C	C/C	G/C	C/C	C/C	CG/TA	C/T	G/A	G/T	C/C	C/T	G/A	C/T	G/A
Donor genotype 7	CC/CT	C/C	C/T	C/C	G/G	C/C	C/C	TA/CG	T/C	A/G	T/T	C/C	C/C	G/G	T/C	G/A
Donor genotype 8	TC/CT	T/C	C/T	C/C	G/G	C/C	C/C	CG	C/C	G/G	T/T	C/C	T/C	A/G	T/T	A/A
Donor genotype 9	CT/CC	C/C	T/C	C/C	G/G	C/C	C/C	TA/CG	T/C	A/G	T/G	C/A	C/T	A/G	T/C	G/A
Donor genotype 10	CT	C/C	T/T	C/C	G/G	T/C	C/C	TA	T/T	A/A	T/G	C/C	C/C	G/G	C/C	G/G
Donor genotype 11	CC/TC	C/T	C/C	C/C	G/G	C/C	C/C	TA	T/T	A/A	G/T	C/C	C/T	G/A	C/T	G/A
Donor genotype 12	CC/CT	C/C	C/T	C/C	C/G	T/C	C/C	TA	T/T	A/A	T/T	C/C	C/T	G/A	C/T	G/A
Donor genotype 13	CC/CT	C/C	C/T	C/C	G/G	C/C	C/C	CG	C/C	G/G	G/T	C/C	C/T	G/A	T/C	G/A
Donor genotype 14	CC/CT	C/C	C/T	C/C	G/G	C/C	C/C	CG/TA	C/T	G/A	G/T	A/A	C/T	G/A	T/C	A/G
Donor genotype 15	TC/CT	T/C	C/T	C/C	G/G	C/C	C/C	TA	T/T	A/A	T/T	C/C	T/T	A/A	C/T	G/A
Donor genotype 16	CC/CT	C/C	C/T	C/C	C/G	C/C	C/C	TA/CG	T/C	A/G	T/T	C/C	C/T	G/A	T/C	G/A
Donor genotype 17	CT/CC	C/C	T/C	C/C	G/G	C/C	C/C	TA/CG	T/C	A/G	T/T	C/A	T/T	A/A	T/T	A/A
Donor genotype 18	CC/CT	C/C	C/T	C/C	G/G	C/C	C/C	CG/TA	C/T	G/A	G/T	A/A	T/T	A/A	T/T	A/A

own-6	CYP2A6	MUC22.0	MUC22.1	MUC22.2	MUC22.3	MUC22.4	MUC22.5	MUC22.6	MUC22.7	MUC22.8	MUC22.9	KLK3.0	KLK3.1	KLK3.2	PRM1	SEMG2	TGM4.0	TGM4.1	TGM4.2	TGM4.3
VAG-SE?	rs8192721	rs12110470_rs12110785	rs12110470	rs12110785	rs3869098_rs4248153	rs3869098	rs4248153	rs1419664_rs3094672	rs1419664	rs3094672	rs10947121	rs11573_rs1135766	rs11573	rs1135766	rs737008	rs2233896	rs1995640	rs1995641	rs3749195	rs9876921
RNA Genotype S5		GT/GT	G/G	T/T	CGA/CAA	G/A	A/A	ACT/ATA	C/T	T/A	T/T	CCG/CCC	C/C	G/C	T/G	C/C	T/C	A/G	T/C	A/G
Read Counts S5		166	166\166	166\166	3139\553	3139\553	3139\3139	1727\83	1727\83	1727\83	166\166	16542\404	16542\16542	16542\404	10592\9450	1995\1995	14146\11530	16461\12837	222\176	222\176
Donor genotype 1	C/C	GT	G/G	T/T	AA/AG	A/A	A/G	CT/CA/CC	C/C	T/A	T/T	TA	T/T	A/A	G/G	C/C	C/T	G/A	T/T	A/A
Donor genotype 2	C/C	TC	T/T	C/C	GG	G/G	G/G	CA/CC	C/C	A/C	C/C	TA/CG	T/C	A/G	T/G	C/C	T/T	A/A	T/T	A/A
Donor genotype 3	T/T	GT	G/G	T/T	AA/GG	A/G	A/G	CA/TA/CC	C/T	A/A	C/T	TA/CG	T/C	A/G	T/G	C/C	C/T	G/A	C/T	G/A
Donor genotype 4	T/T	GT	G/G	T/T	AA	A/A	A/A	CT	C/C	T/T	T/T	CG	C/C	G/G	T/G	C/C	C/C	G/G	C/C	G/G
Donor genotype 5	C/C	GT	G/G	T/T	AA/GA	A/G	A/A	CT/TA/TC	C/T	T/A	T/T	TA/CG	T/C	A/G	G/T	C/A	T/T	A/A	T/T	A/A
Donor genotype 6	C/C	TC/GT	T/G	C/T	AA/GG	A/G	A/G	CA/CC	C/C	A/C	T/C	CG/TA	C/T	G/A	G/T	C/C	C/T	G/A	C/T	G/A
Donor genotype 7	C/C	GT	G/G	T/T	GG	G/G	G/G	CA/CC	C/C	A/C	C/C	TA/CG	T/C	A/G	T/T	C/C	C/C	G/G	T/C	G/A
Donor genotype 8	C/C	GT	G/G	T/T	GG/AA/GA	G/A	G/A	CT/CA/CC	C/C	T/A	C/T	CG	C/C	G/G	T/T	C/C	T/C	A/G	T/T	A/A
Donor genotype 9	C/C	GT	G/G	T/T	AA/GA	A/G	A/A	CT/CA/CC	C/C	T/A	T/T	TA/CG	T/C	A/G	T/G	C/A	C/T	A/G	T/C	G/A
Donor genotype 10	C/C	GT/TC	G/T	T/C	GG/AA	G/A	G/A	CA/CC/CT	C/C	A/C	T/C	TA	T/T	A/A	T/G	C/C	C/C	G/G	C/C	G/G
Donor genotype 11	C/C	GT/TC	G/T	T/C	GG	G/G	G/G	CA/CC	C/C	A/C	C/C	TA	T/T	A/A	G/T	C/C	C/T	G/A	C/T	G/A
Donor genotype 12	C/C	GT/TT	G/T	T/T	GG	G/G	G/G	TA/CA/CC/TC	T/C	A/A	C/C	TA	T/T	A/A	T/T	C/C	C/T	G/A	C/T	G/A
Donor genotype 13	C/C	GT/TC	G/T	T/C	AA/GG	A/G	A/G	CT/CA/CC	C/C	T/A	C/T	CG	C/C	G/G	G/T	C/C	C/T	G/A	T/C	G/A
Donor genotype 14	C/T	GT	G/G	T/T	AA	A/A	A/A	CA/TA/TC	C/T	A/A	T/T	CG/TA	C/T	G/A	G/T	A/A	C/T	G/A	T/C	A/G
Donor genotype 15	C/C	TT/GT	T/G	T/T	GG/AA	G/A	G/A	TA/TT/TC	T/T	A/T	C/T	TA	T/T	A/A	T/T	C/C	T/T	A/A	C/T	G/A
Donor genotype 16	C/C	GT	G/G	T/T	AA/GG	A/G	A/G	CA/CC	C/C	A/C	T/T	TA/CG	T/C	A/G	T/T	C/C	C/T	G/A	T/C	G/A
Donor genotype 17	C/C	TC/TT	T/T	C/T	GG/AG	G/A	G/G	CA/TA/CC/TC	C/T	A/A	C/T	TA/CG	T/C	A/G	T/T	C/A	T/T	A/A	T/T	A/A
Donor genotype 18	C/C	GT/TC	G/T	T/C	GG/AA	G/A	G/A	CT/CA/CC	C/C	T/A	T/C	CG/TA	C/T	G/A	G/T	A/A	T/T	A/A	T/T	A/A

Assignment of Body Fluid with Donor – Own Stains Laboratory 6 (MiSeq) Stain 5

- Matching RNA + DNA genotype in green
- Supposed donor in light blue

2 person mixture: MB-SE
Who are the contributors?

	Blood								Menstrual												Semen								
own 5	ANK1.0	ANK1.1	CD3G	SPTB.0	SPTB.1	SPTB.2	SPTB.3	SPTB.4	MMP10.0	MMP10.1	COL12A1.0	COL12A1.1	COL12A1.2	COL6A3.0	COL6A3.1	COL6A3.2	COL6A3.3	COL6A3.4	COL6A3.5	MMP3	KLK3.0	KLK3.1	KLK3.2	PRM1	SEMG2	TGM4.0	TGM4.1	TGM4.2	TGM4.3
RNA Genotype	C/C	G/G	T/T	CA/TG	C/T	A/G	A/A	C/C	A/G	G/G	A/A	T/T	T/C		G/G	C/G	C/C	G/G	C/G	T/C	CG/TA	C/T	G/A	T/G	C/C	T/T	A/A	T/T	A/A
Coverage	1124\1124	435\435	2844\2844	475\13	475\13	475\13	18\18	1056\1056	47\10	47\47	15338\15338	12179\12179	5336\4521		1071\1071	241\191	226\226	226\226	4523\3574	22428\19420	27943\23793	27943\23793	27943\23793	33370\28704	40846\40846	18614\18614	20482\20482	78\78	78\78
Donor genotype 1	C/G	G/G	T/T	TG	T/T	G/G	A/G	C/C	A/A	A/G	A/G	T/T	T/T	AG	A/A	G/G	T/T	G/G	G/G	T/C	CG/TA	C/T	G/A	G/T	C/C	T/T	A/A	T/T	A/A
Donor genotype 2	G/C	G/A	T/T	CA	C/C	A/A	A/G	C/T	A/A	A/A	A/A	T/T	T/T	GC/AG	G/A	C/G	C/T	G/G	G/C	T/C	TA/CG	T/C	A/G	T/T	C/C	C/C	G/G	C/C	G/G
Donor genotype 3	C/C	G/G	T/T	CA	C/C	A/A	A/G	C/C	A/A	G/G	A/G	T/T	T/T	GC/AG	G/A	C/G	T/C	G/G	C/G	T/T	TA/CG	T/C	A/G	T/T	C/C	C/C	G/G	C/C	G/G
Donor genotype 4	C/C	G/A	T/T	TG	T/T	G/G	G/G	T/C	A/A	G/G	A/A	T/A	C/C	AG/GG	A/G	G/G	T/C	G/G	G/G	T/C	CG/TA	C/T	G/A	T/G	C/C	T/T	A/A	T/T	A/A
Donor genotype 5	G/G	G/G	T/T	CA	C/C	A/A	A/A	C/C	A/A	G/G	G/A	T/T	T/T	AG/GC	A/G	G/C	C/T	G/G	C/G	C/T	CG/TA	C/T	G/A	T/T	C/C	T/C	A/G	C/T	G/A
Donor genotype 6	C/G	G/G	T/T	CA	C/C	A/A	A/A	C/C	A/A	G/G	G/G	A/T	C/T	GG	G/G	G/G	C/C	G/A	C/C	T/C	TA	T/T	A/A	T/T	C/A	C/T	A/G	T/T	A/A
Donor genotype 7	C/C	G/G	T/T	CA	C/C	A/A	A/A	C/C	A/G	G/G	A/A	T/T	C/T	GC/GG	G/G	C/G	C/C	G/G	C/G	T/C	CG/TA	C/T	G/A	T/T	A/A	T/C	A/G	C/T	A/G
Donor genotype 8	C/G	G/G	C/T	CA	C/C	A/A	A/A	C/C	A/A	G/A	A/G	A/T	C/T	AG/GG	A/G	G/G	C/T	G/G	G/C	T/T	CG	C/C	G/G	T/T	A/C	C/T	G/A	T/C	G/A

Conclusions and Outlook

Conclusions

Stain 1-16:

BFID

- 11/16 stains were predicted correctly
  0/2 low input stains correctly predicted
- 5/16 stains could not be predicted
  1/5 one body fluid was missing
  1/5 skin generally difficult
- Difficulties arise because of various (misleading) reads in stains with low number of total reads

cSNPs

- Performance dependent on how many markers are detected per body fluid

Own Stains of the Laboratories:

BFID

- Overall we could predict 41/62 stains (74%)

cSNPs

- performance dependent on how many reads per RNA cSNP were detected
  → the more, the more accurate/complete the reflection of DNA genotypes

Summary and Outlook

- overall promising results ☺
- not all participants followed the recommendations
- also labs with little RNA experience had good results
- results comparable between laboratories
- panels worked well on both sequencing platforms

- inclusion of last incoming results
- get bodyfluid/donor info from participants on own stains
- data analysis
- comparison with Cologne cSNP panel (31 body fluid markers, 80 cSNPs)

→ write manuscript on exercises 3 and 4 (draft in winter 2023/2024)

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Cc: Bianca Szkuta; b.kokshoorn@nfi.nl
Emne: Update: EDNAP DNA transfer exercise - casefile data

OFFICIAL: Sensitive

Hi All

A brief update:

Thank you very much to all those who made the significant effort to complete the datasheets as best they could for the number of samples they could.
Also thank you for the communications and efforts from those who have committed to submit data soon but are still in the process of collecting the data.

The current states is:

- Submissions received from 17 labs.
- 15 labs submitted data for tool handles and gloves; 1 lab submitted data for tool handles only; 1 lab submitted data for gloves only.
- From these labs, data received from a total of 1333 tool handle samples and 1187 glove samples.
- One lab that has submitted data, will be topping it up with data from additional samples soon.
- Awaiting submissions from 4 additional labs – expected to receive between September and November.
- Of the labs that had initially expressed an interest to participate, most apologised for not being able to participate due to limitations in available resources, reiterated their positive view of the value of this study, looked forward to seeing the outcomes, and expressed their desire to be considered for any future other studies of this type.
- Some initial collating has commenced, however awaiting final submissions before commencing analyses.

Niels, you are welcome to summarise this during your upcoming EDNAP meeting.

Kind regards
Bianca, Bas & Roland

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Update ENFSI DNA Expert Working Group activities

Sander Kneppers
Chair ENFSI DNA Expert Working Group

Netherlands Forensic Institute
Division Biological Traces

ENFSI DNA Working group Steering Committee

* Chair	Sander Kneppers, NFI, the Netherlands
* Vice chair	Livia Zatkalikova, Ministry of Interior, Slovakia
* Secretary	Astrid Quak, NFI, the Netherlands
* Treasurer	Ingo Bastisch, BKA, Germany
* QCLG	Stavroulla Xenophontos, Inst. of Neurology & Genetics, Cyprus
* E&T	Paula di Simone, National Police, Italy
* Webmaster	Fabrice Noël, NICC Belgium
* EDNAP	Niels Morling, Univ. Copenhagen, Denmark

DNA working group subgroups

* Group A: Quality Assurance
  * Stavroulla Xenophontos
  * Heli Autere
* Group B: DNA Analysis Methods & Interpretation
  * Antonio Alonso
  * Walther Parson
* Group C: DNA Database and Legislation
  * Igor Obleščuk
  * Emilia Lindberg
* Group D: Automation, Expert Systems and Artificial Intelligence
  * Christina Forsberg
  * Shazia Khan
* Group E: Forensic Biology and Casework
  * Ricky Ansell
  * Arnoud Kal

Release documents ENFSI

* Annual Report
* Vision of the European Forensic Science Area 2030
  * “Improving the Reliability and Validity of Forensic Science and Fostering the Implementation of Emerging Technologies”
* Reporting and planning cycle DNA EWG

ENFSI Strategic Plan 2023-2026 is composed of three main themes and the Action Plan makes it operational on time-specific basis

Contribute to the establishment of European Forensic Science Area 2.0

Planning, monitoring, implementation

Strengthening the network through professionalization

Development, enhancement, raising the profile

Consolidate and improve cooperation within ENFSI

Review, identify, enhance

Deliver

Strategic plan 2023 - 2026

Contribute to the establishment of the European Forensic Science Area 2.0 through the implementation of the Action Plan

This shall be realized through ENFSI's involvement in the EU-funded Direct Award initiative and encouragement towards project execution within the ENFSI forensic community, Expert Working Groups and Standing Committees.

A. Meeting the future
B. Strengthening the impact of forensic results
C. Demonstrating reliability in forensic results

Strategic Plan 2023-2026

- Meeting the future
  - Biometics
  - Digitalization
  - Artificial Intelligence
  - New tools and emerging technologies

Strategic Plan 2023-2026

- Strengthening the impact of forensic results
  - Forensic examination and interpretation
  - Forensic data sharing
  - Multidisciplinary approaches

Strategic Plan 2023-2026

A. Demonstrating reliability in forensic results
   - Fundamentals in Forensic Science
   - Forensic Human Factors
   - Quality and competence assurance

2. **Strengthening the network through professionalization**

This shall be achieved through identification of operational areas which are not presently covered (role gap analysis) in ENFSI, with a view to ensure the smooth management of the Network and fulfillment of its mission and goals in an even more structured and efficient way.

2. **Strengthen and improve cooperation within ENFSI**

The ENFSI Working Groups will be encouraged to cooperate in research, training and proficiency testing. Direct awards will be discussed with the EU and other stakeholders to reach scientific goals, as identified, among others, in the Action Plans

ENFSI Action Plan 2023-2024 Highlights

Scientific goals:

- Execution of ENFSI Strategic Plan 2023-2026 is ensured
- ENFSI Vision 2023 and EFSA 2.0 are implemented

Organizational and corporate goals:

- Network is strengthened internally and externally
- Development through strategic coherence

RDSC Status Report

Current Membership of the R&D Standing Committee

Name	Function	Affiliation
Christa Dern	Member	BKA, Germany
Lisa Burke	Member	Metropolitan Police, UK
Emil Hjalmarson	Member	NFC, Sweden
Didier Meuwly	member	NFI, Netherlands
Bart Nys	member, Chairman	NICC, Belgium
Brid McBride	member	FSI, Ireland
Chris Porter	Board liaison	Metropolitan Police, UK
Jose Lopez	Member	Policia, Spain
Laura Aalberg	Member	NBI, Finland

Public review of ENFSI documents

* proper, balanced and agreed content of these documents for the target groups (forensic community)
* a transparent and documented, public reviewing process is needed > practicable procedure for public review of ENFSI documents

* OSAC requirement that only documents which went through an SDO assessment (standardizing body like ASTM or ISO) will be listed in the OSAC registry

Overview of recently completed and developing ENFSI DNA EWG documents

Document Title	Stage	Responsible Task Force
BPM on Human Forensic Biology & DNA Profiling (New)	Published	2
ENFSI Guideline for Internal Validation / Verification of Various Aspects of the DNA Profiling Process (Revision)	QCC Review	4 & others
ENFSI Guideline for the Minimization of DNA Contamination in DNA Laboratories (Revision)	Public Review	3
ENFSI Guideline for the Validation of Probabilistic Genotyping Software Revision & change from BPM to a Guideline	Starting soon	2
ENFSI Quality Assurance Guideline Revision & change from Programme to Guideline	Revision in progress	2 & 3

Whitepaper

EWG Name	DNA
Subject Area	Forensic Biological Trace profiling
Represented by	Alexander Kneppers
Date	December 2020

1. Description of the forensic field – State of Art

The ENFSI DNA Working Group provides a forum for implementation and improvement of DNA analysis in casework as well as validation of methods and software. It considers all aspects of DNA case analysis and case reporting. Focusing on casework requirements, the group aims to:

- Promote quality management systems and the development of best practices laid down in manuals (BPMs) and guidelines.
- Develop uniform guidelines, which members can conform to and achieve.
- Exchange information and expertise.
- Collaborate with regard to the reporting and interpretation of DNA evidence and develop and improve the interpretation of DNA analyses.
- Promote and collaborate with research activities amongst members and together with industry and academic partners.
- Support colleagues by providing education and training.
- Assess the need and create pan-European intelligence/knowledge databases.
- Disseminate and implement newly developed methods.
- Support the organization of collaborative exercises in all aspects of forensic DNA casework, aiming to harmonize procedures within European forensic DNA laboratories.

The field of forensic biological trace profiling is an ever evolving field due to the rapidly changing possibilities in molecular biology including the DNA and RNA typing methods. For the characterization of body fluids using presumptive tests many of the laboratories have incorporated these tests in their daily routine for stain searching. DNA extraction has more and more shifted from the hazardous phenol/chloroform extraction and Chelex extraction to extraction methods based on silica columns or more recent the magnetic beads extraction methods. The big advantage of these methods is that these can be (semi) automated to the needs of the laboratory. Many of the laboratories nowadays use these automation solutions to be able to handle more samples within the laboratory and to prevent the contamination of the traces by laboratory personnel. Although not required in all countries, most laboratories use molecular quantification methods to determine the concentration of the DNA extract before proceeding to the PCR typing stage. By doing so laboratories are more efficient in the DNA profiling and can perform more sensitive analysis on trace samples containing low amounts of human material. Furthermore cut-off values on DNA concentrations are used to prevent samples from continuing in the DNA profiling process that will not lead to usable DNA profiles

Education and Training

ANNEX 3 - TRAINING CATALOGUE OF GRANTED ACTIVITIES 2022

86/2022: Analysis of Complex DNA Profiles	**Cat. 9**	**Forensics**

Duration	4 days
Minimum number of participants	26
Maximum budget	EUR 25,000

In cooperation with ENFSI - DNA Working Group which may provide experts for the course development.

E&T Liaison Paola Di Simone
Trainings organized in the last three years:

E&T

9-11th DECEMBER 2020 - Online ENFSI training course
"DNA mixture analysis and statistical interpretation"

Hosted by: *Netherlands Forensic Institute*

Training details

The training will include online support with installation and data format checking for EuroForMix, CaseSolver and/or DNAxs, DNAStatistX; introduction to DNA mixtures and likelihood ratio principles; introduction and functionality of EuroForMix, DNAxs, DNAStatistX software. A demonstration will be given after which various hands-on exercises will be performed by participants; complex case management using Case Solver software; how to write a statement.

Learning outcomes

- Get familiar to perform a statistical evaluation of DNA mixtures with different software .
- Be able to use different software on own cases.

Target Group

Law enforcement forensic experts – experienced reporting officers who deal routinely with DNA profiling evidence and are required to interpret complex mixtures in casework.

Number of participants: max 30 persons.

Possible selection (one per Institute) if more requests are received.

Presenters:

Peter Gill

Corina Benschop

Øyvind Bleka

Deadline, final program and more details will be given shortly by the ENFSI DNA EWG.

Costs: no workshop fee (training sponsored by ENFSI) nor software costs required

December 2020: Training on
"DNA Mixture Analysis and statistical interpretation"
More than 33 participants
VIDEO ON EPE Platform

E&T

14-15th DECEMBER 2021 - Online ENFSI training course
"Kinship statistics using Familias"

Hosted by: *Netherlands Forensic Institute*

Training details

The workshop provides the necessary background for relationship testing using autosomal markers. Statistical methods are introduced and the likelihood ratio based approach is emphasized. The freely available software *Familias* is presented and used in hands-on exercises.

Selected chapters of the tutorial https://familias.name/tutorial/familias_tutorial_english.pdf will be presented.

Learning outcomes

- Get familiar with statistical evaluation of relationship test.
- Be able to use *Familias* software on own cases.

Target Group

Law enforcement forensic experts – experienced reporting officers who deal routinely with DNA profiling evidence and are required to interpret relationship in casework.

Number of participants: max 25 persons.

Possible selection (one per Institute) if more requests are received.

Presenter:

Thore Egeland

Deadline, final program and more details will be given shortly by the ENFSI DNA

Costs: no workshop fee,

training sponsored by ENFSI nor software costs required

December 2021: Training on
"Kinship statistics using Familias"
37 participants

E&T

17-18th NOVEMBER 2022 - 2^ Online ENFSI Training on
"Kinship statistics using Familias"

Hosted by: *Netherlands Forensic Institute*

Training details

The workshop provides the necessary background for relationship testing using autosomal markers. Statistical methods are introduced and the likelihood ratio based approach is emphasized. The freely available software *Familias* is presented and used in hands-on exercises.

Selected chapters of the tutorial https://familias.name/tutorial/familias_tutorial_english.pdf will be presented.

Learning outcomes

- Get familiar with statistical evaluation of relationship test.
- Be able to use *Familias* software on own cases.

Target Group

Law enforcement forensic experts – experienced reporting officers who deal routinely with DNA profiling evidence and are required to interpret relationship in casework.

Number of participants: max 25 persons.

Possible selection (one per Institute) if more requests are received.

Presenter:

Thore Egeland

Deadline, final program and more details will be given shortly by the ENFSI DNA WG.

Costs: no workshop fee, training sponsored by ENFSI nor software costs required

November 2022: second training on
"Kinship statistics using Familias"
More than 22 participants
VIDEO ON EPE Platform

Short Term Fellowships of the ENFSI DNA Working Group

* Financial support for travel and accommodation of up to EUR 1000 for a maximum of one week
* Two rounds per year (January/June)

* First three fellowship awarded

Monopoly 2018 AFORE
(Accreditation of Forensic Laboratories in Europe)

- "Accreditation of Forensic Laboratories in Europe" (AFORE)
  - kick off meeting AFORE planned in Oslo on the 16th and 17th January 2020
    - Accreditation of Scene of Crime Services
    - Training of Forensic Personnel in Accreditation Matters
    - Training of Technical Experts
    - Production of New and/or Updated Best Practice Manuals
      - BPM on Digital Image Authentication
      - BPM on Forensic Examination on Fibres
      - BPM on Forensic Examination of Gunshot Residues
      - BPM on Forensic Handwriting Examination
      - BPM on Forensic Voice Comparison
      - BPM on Human DNA Analysis (Application for funding (40K EUR))
      - BPM on Glass or BPM on Paint

Horizon 2020

Competency, Education, Research, Testing, Accreditation, and Innovation in Forensic Science (CERTAIN-FORS)

React project (Recovery; Activity)

Establishment of a trace DNA transfer rate repository & Bayes Net(s) to calculate LRs

Multidisciplinary CE's in the year 2022/2023

covering at least 3 forensic disciplines each time (e.g document examination, handwriting examinations, DNA, fingerprint, explosives, fibres/textiles).To identify best practices in examining certain types of exhibits.

ENFSI Meetings

- QCLG meeting, October, Turkey
- Annual ENFSI joint meeting (board/EWG chairs/Standing Committees), November, Spain
- DNA EWG Steering committee online meetings every two months
- annual DNA working group meeting and CODIS/EDNAP meetings
  - Oslo October 2023 50th
    - Local organizer
      - Solveig Jacobsen and Ane Elida Fonnelop
      - Oslo University Hospital
  - Next hosts for the annual DNA working group meeting
    - 2024 – Spain 1 to 4 October
      - Lydia Camps
      - Scientific Police Division (CME; Mossos d'Esquadra)
    - 2025 –Luxemburg Q2
      - Elizabet Petkovski
      - Forensic Genetics Department of the National Laboratory of Health
- EAFS
  - 26th – 30th May 2025, EAFS (Dublin)

ENFSI EUROPEAN NETWORK OF FORENSIC SCIENCE INSTITUTES

EAFS | STOCKHOLM 2022

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www. ENFSI.EU

Welcome to ENFSI!

The European Network of Forensic Science Institutes (ENFSI) was founded in 1995 with the purpose of improving the mutual exchange of information in the field of forensic science. This, as well as improving the quality of forensic science delivery in Europe have become the main issues of the network. Besides the general work in the fields of quality and competence management, research and development and education and training, different forensic expertizes are dealt with by 17 different Expert Working Groups. ENFSI therefore has been recognized as the monopoly organization in the field of forensic science by the European Commission.

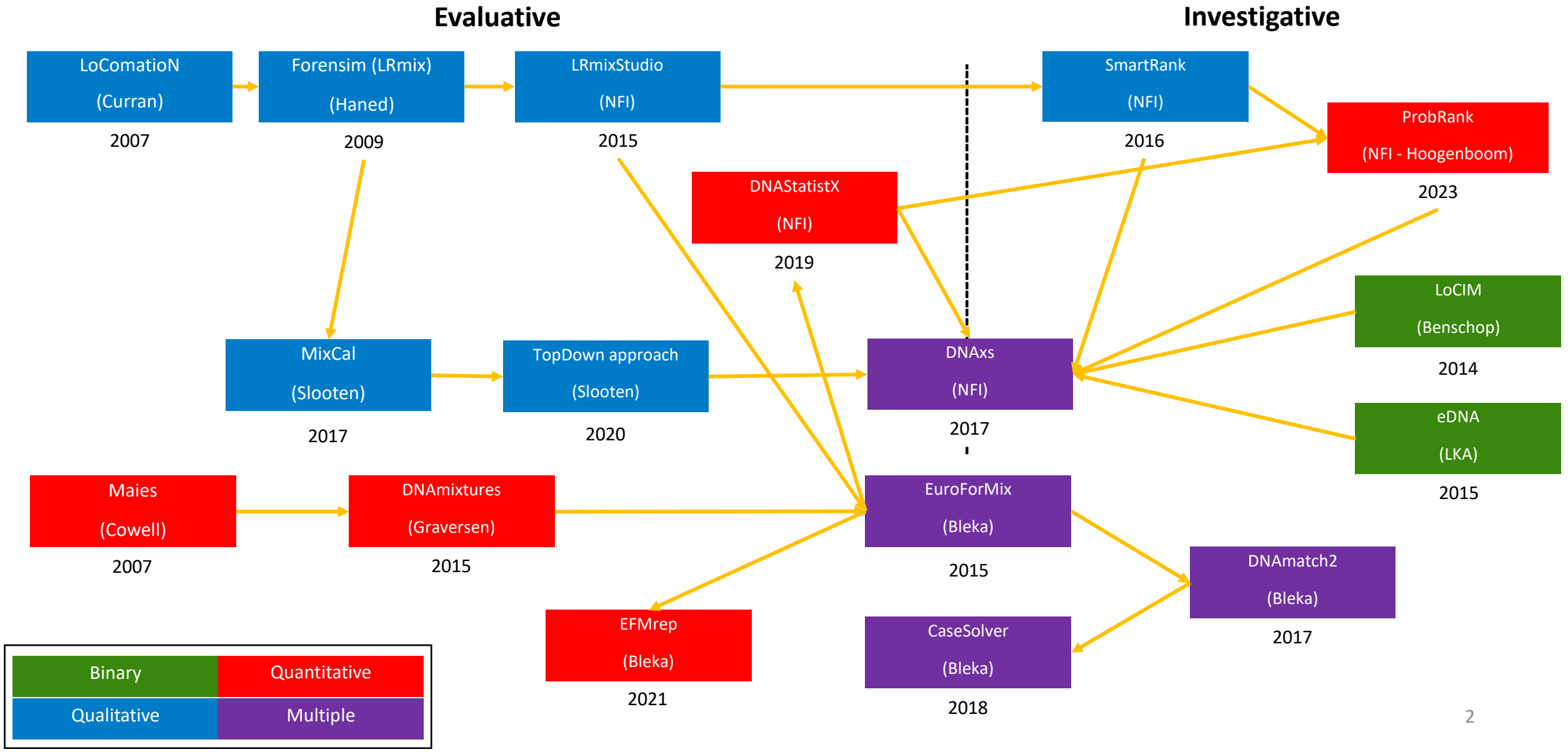
Members RESET MAP

Search in members

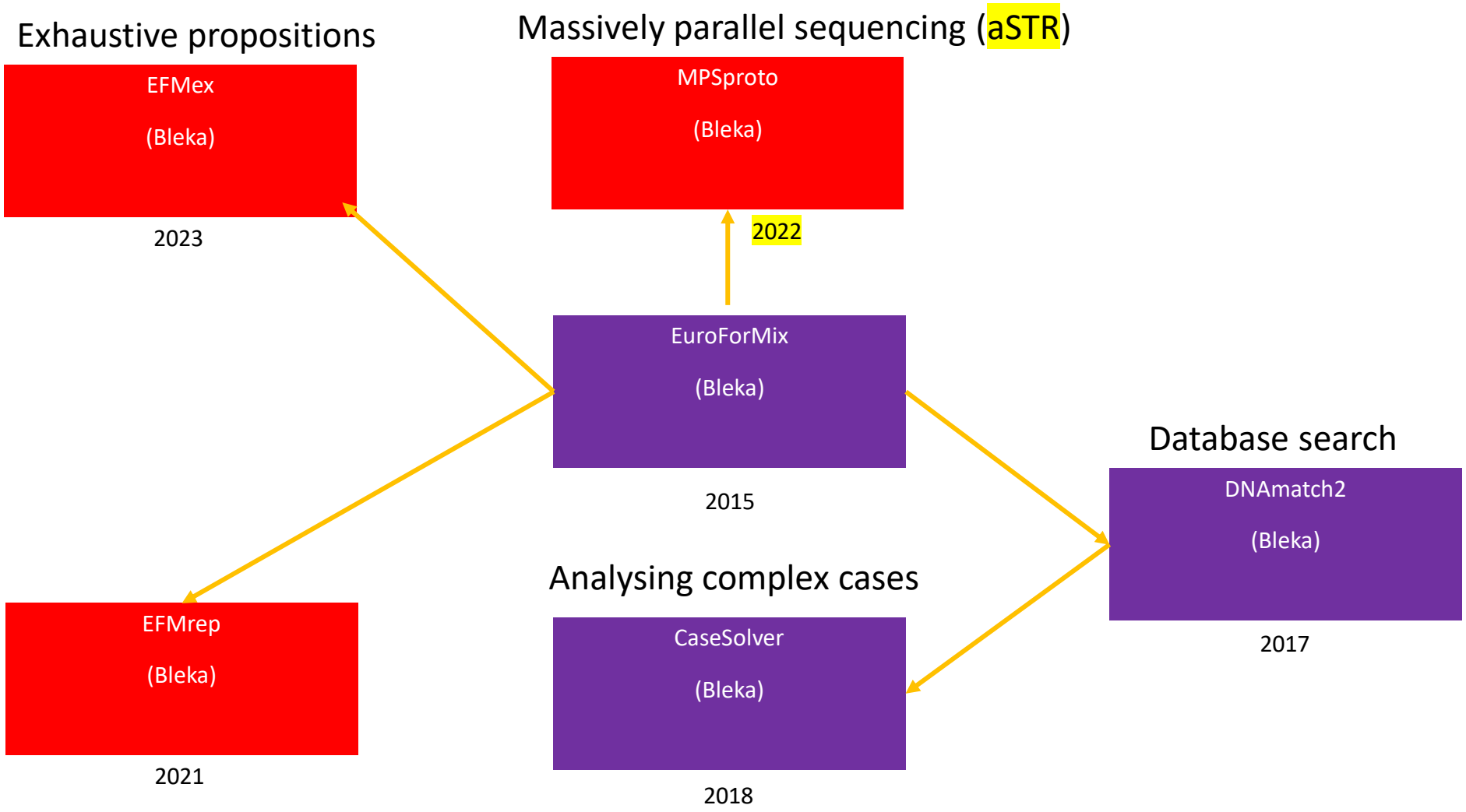
ENFSI DNA EWG meeting September 2022 Lisbon

Two suspects problem

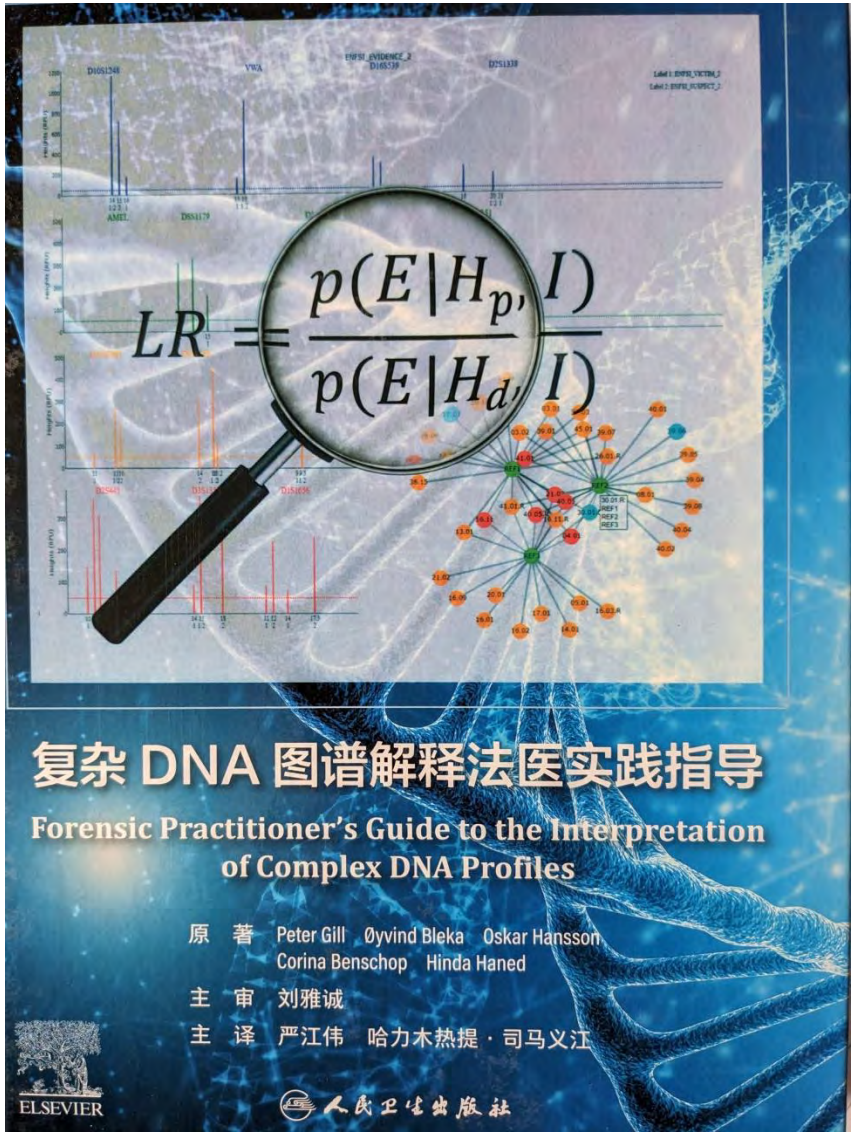
Overview of software (NFI and OUS) and how this has evolved over time (thanks to Corina Benschop for slide)



EuroForMix family

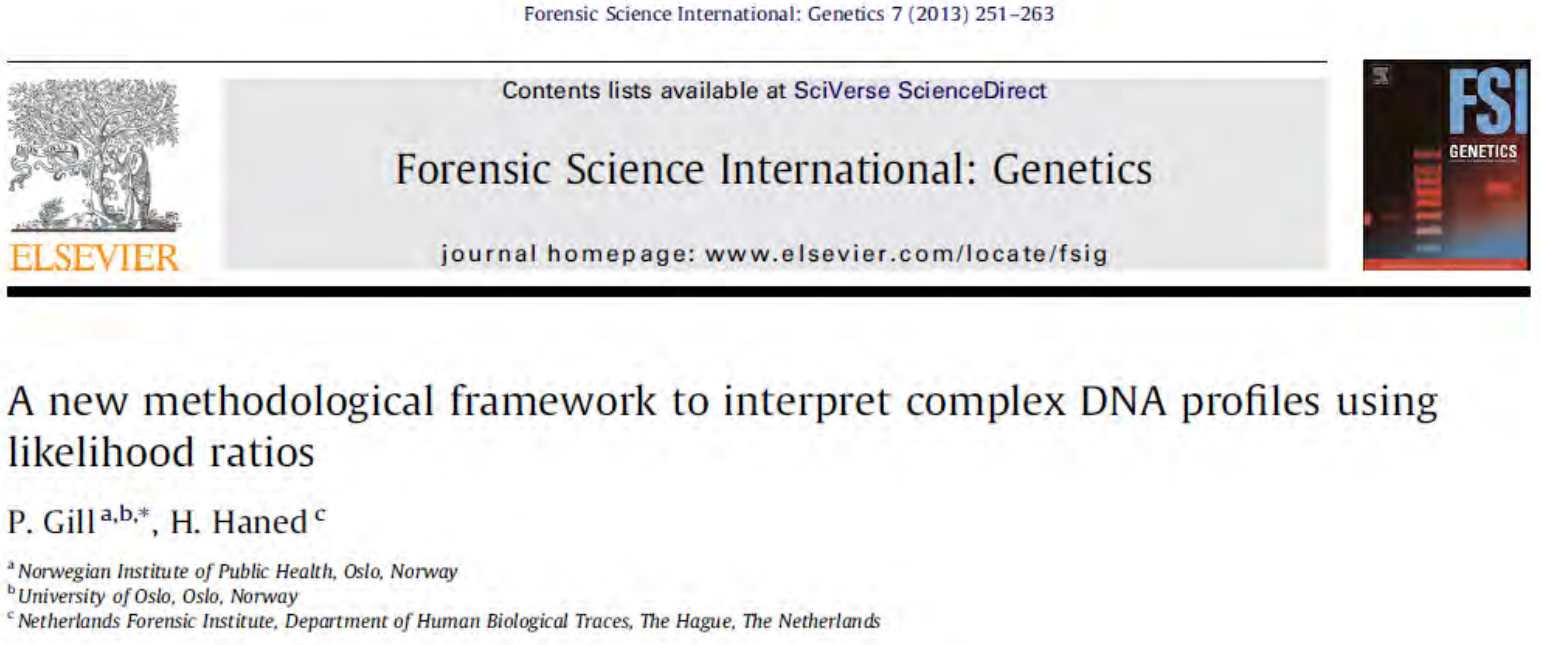


Chinese version of our book is now available



The early work described in our book section 6.2, page 167

- From Gill, P., and H. Haned. "A new methodological framework to interpret complex DNA profiles using likelihood ratios." *Forensic Science International: Genetics* 7.2 (2013): 251-263.



Forensic Science International: Genetics 7 (2013) 251–263

Contents lists available at SciVerse ScienceDirect

Forensic Science International: Genetics

journal homepage: www.elsevier.com/locate/fsig

A new methodological framework to interpret complex DNA profiles using likelihood ratios

P. Gill [a,b,*], H. Haned [c]

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[c] Netherlands Forensic Institute, Department of Human Biological Traces, The Hague, The Netherlands

The case circumstances

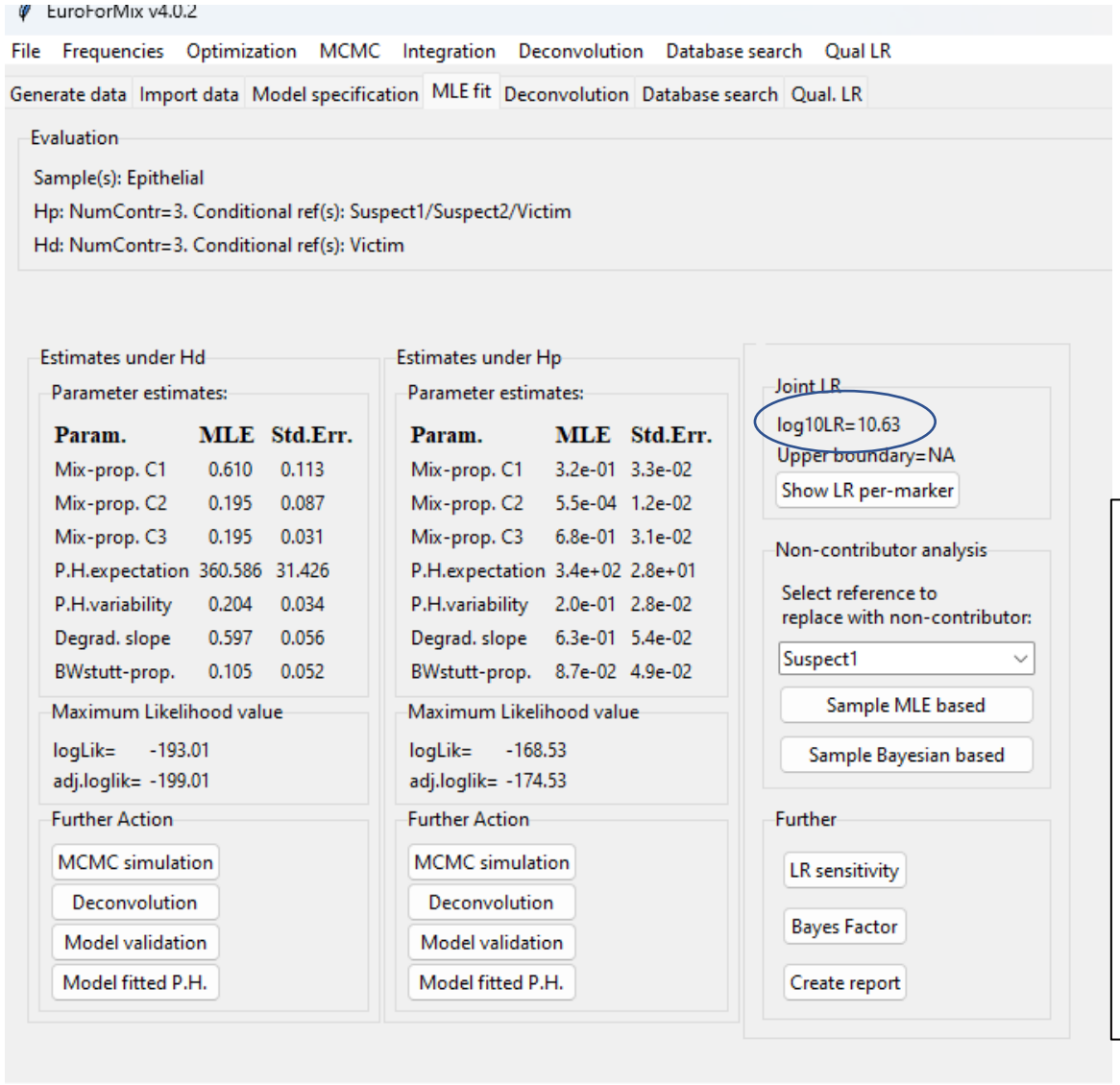
- A female victim has been assaulted. Two suspects S_1 and S_2 were arrested and accused of the assault
- Both suspects deny the offence, stating that they were not in the vicinity of the crime event at the time of occurrence and they had never met the victim
- The evidence is a swab taken from an exposed area of skin of the victim where she had been repeatedly struck and bruised

What propositions should be tested

- Prosecution contend that both suspects were responsible for the assault: Hp=S1+S2+V
- Defence contend that neither suspect was present and they were elsewhere at the time of the assault, therefore the crime was committed by unknown (U) individual(s): Hd=U+U+V

- Hence the LR is calculated as $LR = \frac{S_1+S_2+V}{U+U+V}$

Calculation with EFM (Fst=0.01, AT=50RFU)



$$LR = \frac{S_1+S_2+V}{U+U+V} = 10^{10.63}$$

A statement may follow:

The evidence is 10^{10} times more likely if S1 and S2 are contributors rather than if two unknown individuals are contributors

But this may be misleading

Let's take a closer look at the evidence

- In our original paper, for this example, we showed that if S_1 and S_2 are considered separately, then the results gave a much lower LR for S_2 when the following propositions were considered:

- Suspect 1: $LR = \frac{S_1+U+V}{U+U+V} = 10^{10.63}$

- Suspect 2: $LR = \frac{S_2+U+V}{U+U+V} = 1$ (evidence does not support proposition that S2 is a donor)

- Note that the LR is the same when the numerator is S_1S_2V (previous slide) and S_1UV, which indicates that S_2 does not provide any contribution to the magnitude of the LR in the former, whilst noting that in the second calculation the LR is neutral

- Our original recommendation was to always split the LR calculations to reflect the individual contributions by multiple PoIs, ensuring that the propositions were balanced, meaning that the denominator only had one extra U compared to the numerator

We can assign the various exhaustive alternatives to propositions

Hp (S_1)	Hd(S_1 not present)	Hp(S_2)	Hd(S_2 not present)
S_1+S_2+V	S_2+U+V	S_1+S_2+V	S_1+U+V
S_1+U+V	$U+U+V$	S_2+U+V	$U+U+V$

Either the likelihoods can be calculated with EFM for Hp and Hd separately, or a likelihood ratio for each alternative can be calculated by applying *U+U+V* in every denominator. *The following slide shows method in greater detail*

Slooten paper

Forensic Science International: Genetics 56 (2022) 102592

Contents lists available at ScienceDirect

Forensic Science International: Genetics

journal homepage: www.elsevier.com/locate/fsigen

Research paper

The comparison of DNA mixture profiles with multiple persons of interest

K. Slooten [a,b]

[a] Netherlands Forensic Institute
[b] VU University Amsterdam

Hicks et al paper

Forensic Science International: Genetics 52 (2021) 102481

Contents lists available at ScienceDirect

Forensic Science International: Genetics

journal homepage: www.elsevier.com/locate/fsigen

Forensic Population Genetics - Research Paper

Comparing multiple POI to DNA mixtures

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[g] School of Biological Sciences, Flinders University, GPO Box 2100, Adelaide 5001, SA, Australia

Spreadsheet to help with calculations

- Thanks to Klaas Slooten (NFI) for spreadsheet to help calculations
- Spreadsheet “Evaluation multiple PoI_1.0_PG.xlsx” available at the book’s website
- Either two person or three known persons are accommodated
- The worked example is shown

Worksheet (Two persons)

- Note that we use the two person spreadsheet – this is OK for our victim conditioned samples

Hypotheses listed here to include victim in our example:

Insert LRs here for each test

Person 1	P1				
Person 2	P2				
					RESCALE: LR with regards to
Hypothesis H	donor 1	donor 2	$Log_{10}(LR_{H,Huu})$	$LR_{H,Huu}$	*H2u*
H_{12}	P1	P2	10.63	4.27E+10	*2.28E+10*
H_{1u}	P1	*U*	10.63	4.27E+10	*2.28E+10*
H_{2u}	*U*	P2	2.73E-01	1.87E+00	*1.00E+00*
H_{uu}	*U*	*U*	0	1.00E+00	*5.34E-01*
LR with uniform prior		numeric	log_{10}		
regarding P1		2.97E+10	10.47	*(H12+H1u)/(H2u+Huu)*	
regarding P2		1.00E+00	0.00	*(H12+H2u)/(H1u+Huu)*	
regarding P1 and/or P2		2.84E+10	10.45	*(H12+H1u+H2u)/Huu*	

Results listed here

Worksheet 3 person example

- See 3-person example worksheet.
- This uses the same data, except we do not condition on the victim (P3) this time. ie, we consider all three- person combinations

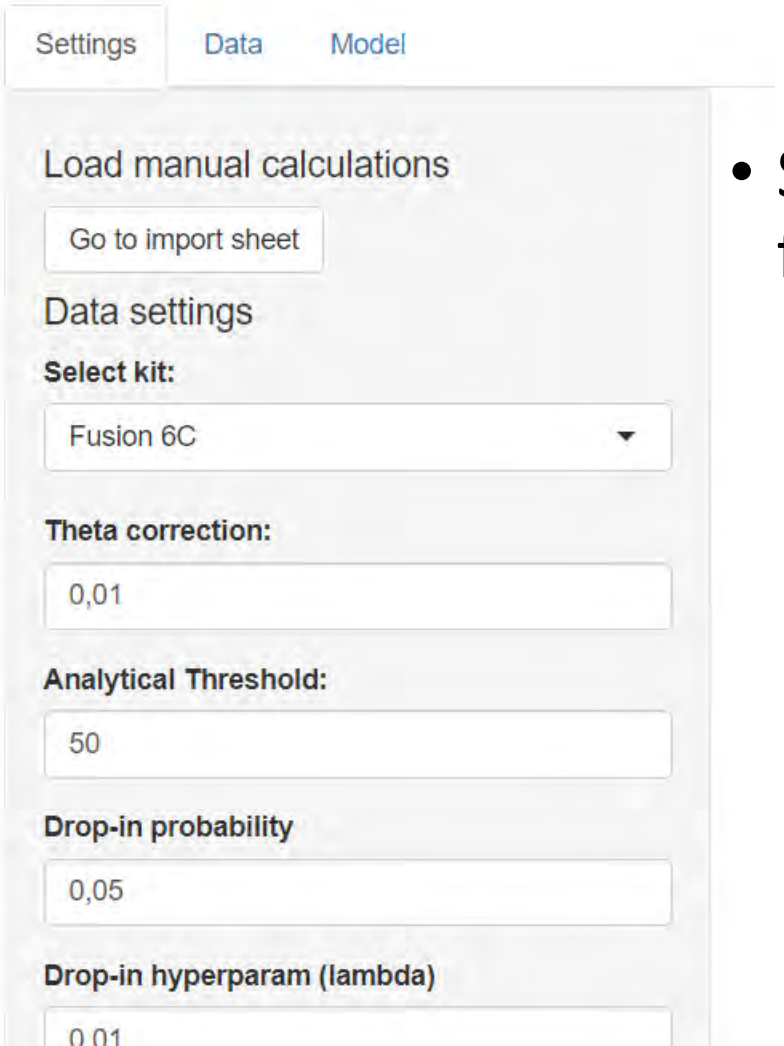
Hypothesis H	donor 1	donor 2	donor 3	$Log_{10}(LR_{H,Huuu})$	$LR_{H,Huuu}$
H_{123}	P1	P2	P3	21.31	2.04E+21
H_{12u}	P1	P2	*U*	8.002	1.00E+08
H_{13u}	P1	*U*	P3	21.31	2.04E+21
H_{23u}	*U*	P2	P3	10.94	8.71E+10
H_{1uu}	P1	*U*	*U*	7.984	9.64E+07
H_{2uu}	*U*	P2	*U*	-0.05492	8.81E-01
H_{3uu}	*U*	*U*	P3	10.67	4.68E+10
H_{uuu}	*U*	*U*	*U*	0	1.00E+00

LR with uniform prior		numeric	log_{10}
regarding P1		3.05E+10	10.48
regarding P2		1.00E+00	0.00
regarding P3		2.07E+13	13.32

Using EFMex() written by Oyvind Bleka

- Program written in ShinyR()
- Open R v.4.3.1
- Load euroformix v. 4.0.7
- From the local directory (see workshop folder)
  - Load file “EFMex_0.7.tar.gz” (or latest version)
- Then in the consol type commands
  - library(EFMex)
  - app()
  - And the screen will appear in your browser window (next slide)

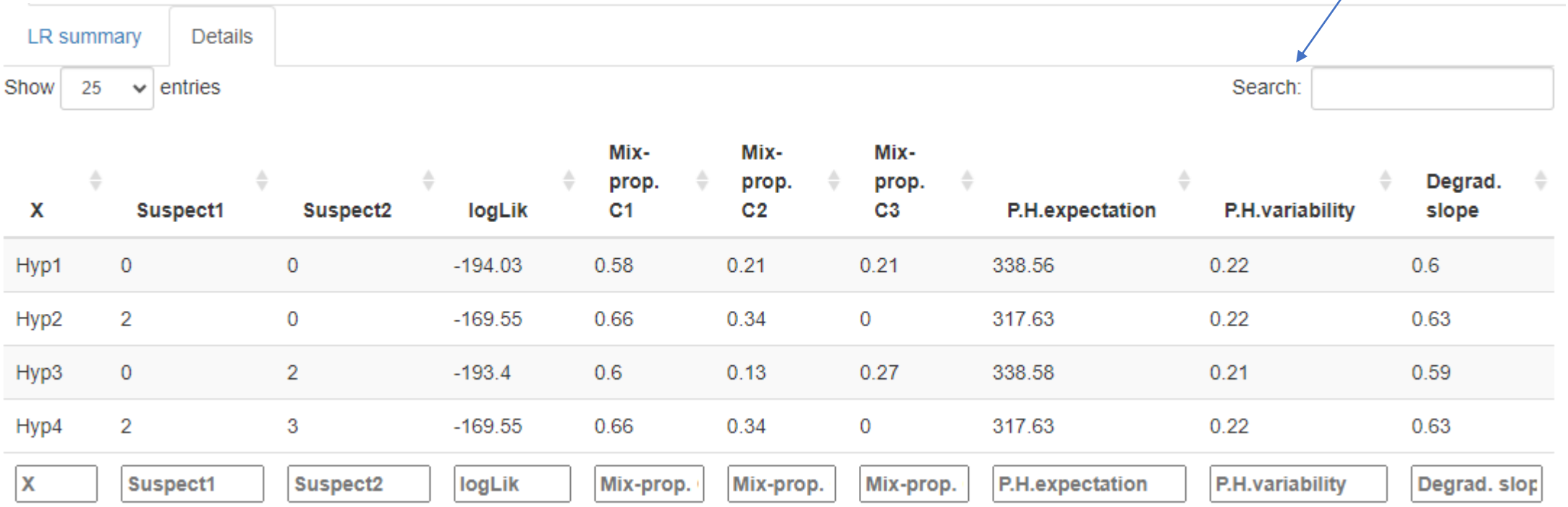
Open EFMex v. 0.7



- Step 1: Set the kit and other settings same as for EFM

“Details” tab shows calculations from euroformix

To select a given hypothesis (X)



LR summary | Details

Show 25 entries

Search:

X	Suspect1	Suspect2	logLik	Mix-prop. C1	Mix-prop. C2	Mix-prop. C3	P.H.expectation	P.H.variability	Degrad. slope
Hyp1	0	0	-194.03	0.58	0.21	0.21	338.56	0.22	0.6
Hyp2	2	0	-169.55	0.66	0.34	0	317.63	0.22	0.63
Hyp3	0	2	-193.4	0.6	0.13	0.27	338.58	0.21	0.59
Hyp4	2	3	-169.55	0.66	0.34	0	317.63	0.22	0.63
X	Suspect1	Suspect2	logLik	Mix-prop.	Mix-prop.	Mix-prop.	P.H.expectation	P.H.variability	Degrad. slop

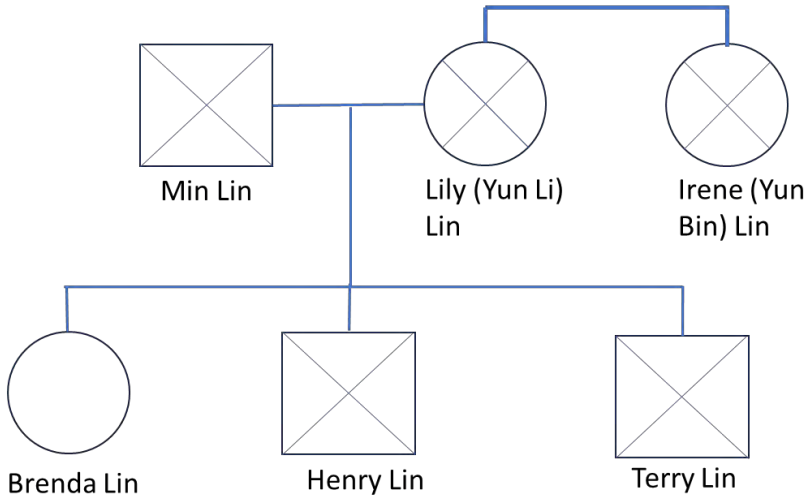
Queen v. Xie (Melbourne Australia, 2017)

- In the early hours of 18 July 2009 in North Epping, New South Wales, newsagent proprietor Min Lin, age 45; his wife, Yun Lin, 43; their sons, Henry (12) and Terry (9); and Yun Lin's sister, Irene Lin (39), were bludgeoned to death.[2] Kathy Lin, sister of Min Lin, and her husband Lian Bin "Robert" Xie discovered the bodies when they went to the house at around 9:00 am to see why the newsagency run by the Lin family was not open.
- Forensic analysts also determined that the killings had been started with a hammer-like object
- The weapon was never recovered
- Ten months after the crime event, investigators discovered a brown stain in the garage of the defendant which was subsequently tested for DNA
- It was alleged that the weapon had been removed from the crime scene to the defendant’s garage

Evidence: stain 91

- Evidence was a brown stain that was found in garage of the defendant

Family tree



- Family tree illustrated
- X indicates victims
- Note that Brenda is not a victim and was absent when the crime occurred but it is a question whether her DNA is present as this affects relevance of the evidence

Activity level propositions – Let's start here to give perspective to the case

- **List the alternatives**
- Defendant assaulted the victims and removed the weapon to the garage before disposing of it
- Defendant had nothing to do with the crime. Two of the children Henry and Terry used to play regularly together in the garage. All victims are related to each other
- Common ground: Henry and Terry used to play together in the garage.
  a) They may have bled at the crime scene because of an accident
  b) If their DNA is present, the body fluid is not known

Should we condition the LR under both propositions?

- Conditioning the LR under both propositions is allowed where there is common ground between prosecution and defence
- But there is a dispute on how the DNA was transferred.
- The cell type is unknown – could be skin cells or could be blood – defence can propose that Henry had an accident in the garage which led to him bleeding for example
- We can condition on Henry and Terry

Results of tests

- A conventional test evaluates propositions of the kind:

$$LR = \frac{S_1 UU}{UUU}$$

- A conditioned test evaluates propositions of the kind:

$$LR = \frac{S_1 S_2 U}{S_1 UU}$$

- An exhaustive test was described in a previous lecture (we can also condition the exhaustive test)

Results

- We show both conventional vs Exhaustive conditioning out of interest
- The values are log 10, so $10^{0.08} = 1.2$
- Anything below 0 is support for Hd and anything above zero is support for Hp

EuroForMix			Lily		Irene		
with conditioning	**Henry Lin**	**Terry Lin**	**Yun Li Lin**	**Min Lin**	**Yun Bin Lin**	**Brenda Lin**	**No of contributors**
log10LR conventional	**NA**	**NA**	**-0.31**	**7.72**	**5.64**	**0.16**	5
log10LR exhaustive	**NA**	**NA**	**0.08**	**10.49**	**7.62**	**-2.54**	5
without conditioning							
log10LR conventional	**10.03**	**15.15**	**5.46**	**12.16**	**7.66**	**8.71**	4
log10LR exhaustive	**3.32**	**9.44**	**-3.32**	**8.38**	**7.79**	**-6.99**	4
True allele (trial reported)	**9.34**	**16.70**	**2.46**	**5.35**	**4.45**	**1.84**	3

We can see that the choice of model has a big impact on the results, but at the trial, the conventional method was used (software called true allele was used)

Questions under examination at trial

EuroForMix			Lily		Irene		
with conditioning	**Henry Lin**	**Terry Lin**	**Yun Li Lin**	**Min Lin**	**Yun Bin Lin**	**Brenda Lin**	**No of contributors**
log10LR conventional	**NA**	**NA**	**-0.31**	**7.72**	**5.64**	**0.16**	5
log10LR exhaustive	**NA**	**NA**	**0.08**	**10.49**	**7.62**	**-2.54**	5
without conditioning							
log10LR conventional	**10.03**	**15.15**	**5.46**	**12.16**	**7.66**	**8.71**	4
log10LR exhaustive	**3.32**	**9.44**	**-3.32**	**8.38**	**7.79**	**-6.99**	4
True allele (trial reported)	**9.34**	**16.70**	**2.46**	**5.35**	**4.45**	**1.84**	3

- Does the evidence support the proposition that Irene and Lily Lin are donors?
- Consider this response from prosecution witness:
  "…there's no possibility that both of them are not in there; it means either one of them is there or both of them is there and it's more likely that if there is only one there that it would be Irene, as opposed to Lily"
- *What do we think of such a statement?*

Statement from from an Australian newspaper June, 2017 (copied to Cybergenetics website)

- *Police found "Stain 91", a small bloodstain, on the floor of Robert Xie's garage. Cybergenetics ran TrueAllele software on the DNA mixture, finding match statistics to* ***"at least four victims beaten to death by Xie."*** *These computer results "would forensically connect Xie to the murders of five of his wife's family."*

- If we condition on Henry/Terry, the evidence supports proposition that 2 victims are donors
- Consider the limitations of sub-source reporting
  - Does it imply that blood was present from all the donors?
  - Does it have any impact on the activity level?

ENFSI BPM recommendations on reporting two or more suspects in a case

https://enfsi.eu/wp-content/uploads/2022/12/ENFSI-DNA-BPM-03.pdf

APPROVED BY ENFSI BOARD ON 29.11.2022

A2.4 Example of Reporting when There are Multiple Persons of Interest

The DNA mixture from the item is in our opinion from 3 persons. The DNA profiles of person A and person B are compatible with this DNA profile for all 16 loci available. To determine the value of these compatibilities, we have considered the probability of the results given the proposition that Person A contributed to the mixture, with or without Person B, and the probability of the results given the alternative proposition that unknown persons contributed to the mixture, with or without the person B. We proceeded in the same way for the person B.

The ratio of these probabilities is called the likelihood ratio. In order to determine the latter, we have used the software ZZZ and the genetic characteristics of the population XXX (Publication/s), as well as an Fst correction of 1% to take into account the population sub-structure.

For person A, we assigned a likelihood ratio of the order of one billion. This means that it is of the order of a billion times more probable to observe the results if person A contributed to the DNA mixture derived from item YYY than not.
For person B, we assigned a likelihood ratio of the order of one million. This means that it is of the order of a million times more probable to observe the analytical results if person B contributed to the DNA mixture highlighted derived from item YYY than not.

To assign the probability, for example, that a person is the source of all or part of the DNA derived from an item, the DNA results must be combined with the other information of the case. This is generally not considered to be the domain of the forensic DNA expert.

Reporting

- The DNA mixture from the item is in my opinion from 5 persons. The DNA profiles of Min Lin and Irene Lin are compatible. To determine the value of these compatibilities, I have considered the probability of the results given the proposition that Terry, Henry and Min Lin contributed to the mixture, with or without Lily, Irene and Brenda, and the alternative proposition that Terry, Henry and an unknown person contributed to the mixture, with or without Lily, Irene and Brenda.
- For Min Lin, we assign a likelihood ratio of the order of the order of 10 billion. This means that it is 10 billion times more likely to observe the results if he is a contributor than he is not.

EuroForMix			Lily		Irene		
with conditioning	Henry Lin	Terry Lin	Yun Li Lin	Min Lin	Yun Bin Lin	Brenda Lin	No of contributors
log10LR conventional	NA	NA	-0.31	7.72	5.64	0.16	5
log10LR exhaustive	NA	NA	0.08	10.49	7.62	-2.54	5

Reporting – go through the list and report each individual in turn in the same way – abbreviated version follows

For Lily Lin (log10)LR=0.08, we can describe this as neutral evidence that supports neither proposition.

For Brenda Lin (log10)LR=-2.54, the evidence is of the order of 300 times more likely if Terry, Henry and an unknown person are contributors rather than Terry, Henry and Brenda Lin are contributors (i.e. the evidence supports the proposition that she is not present as a donor)

EuroForMix			Lily		Irene		
with conditioning	Henry Lin	Terry Lin	Yun Li Lin	Min Lin	Yun Bin Lin	Brenda Lin	No of contributors
log10LR conventional	NA	NA	-0.31	7.72	5.64	0.16	5
log10LR exhaustive	NA	NA	0.08	10.49	7.62	-2.54	5

Summary

- Statement writing follows a format that can be used for all cases
- The choice of propositions must be consistent with case circumstances, and reflect your understanding. It is useful to include a caveat to that effect
- Choice of model has a big effect on the results
- Consider exhaustive models when multiple persons of interest are present – especially important when there are shared alleles, such as found in related individuals.

References

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- Hicks T, Kerr Z, Pugh S, et al. Comparing multiple POI to DNA mixtures. *Forensic Sci Int Genet*. 2021;52:102481. doi:10.1016/j.fsigen.2021.102481
- Slooten K. The comparison of DNA mixture profiles with multiple persons of interest. *Forensic Sci Int Genet*. 2022;56:102592. doi:10.1016/j.fsigen.2021.102592
- Buckleton, J., Taylor, D., Bright, J. A., Hicks, T., & Curran, J. (2021). When evaluating DNA evidence within a likelihood ratio framework, should the propositions be exhaustive?. Forensic Science International: Genetics, 50, 102406.

Oslo University Hospital

A framework to evaluate evidence given alternative propositions

Peter Gill

Before

Birgitte-saken

Åtte sakkyndige skal forklare seg om påtalemyndighetens kronbevis, funnet av et Y-kromosom på strømpebuksen til Birgitte Tengs. Fra venstre: Jonathan Whitaker fra Storbritannia, Peter Gill fra Storbritannia, Mikkel Meyer Andersen fra Danmark, Ate Kloosterman fra Nederland, Walther Parson fra Østerrike og de norske DNA-ekspertene Gro Bjørnstad og Bente Mevåg. Arnoud Kal fra Nederland satt i vitneboksen da bildet ble tatt.

JON INGEMUNDSEN

Fant mer på strømpebuksen som kan knytte tiltalte til drapet

After

Presentation of evidence in court

- Presentation of evidence follows a structure
- The methods described here were developed more than 20 years ago and are recommended by scientific bodies such as the European Network of Forensic Science Institutes (ENFSI)
- The interaction between the scientist and the court must follow strict guidelines, otherwise there are risks of miscarriages of justice
- The framework described applies to all scientific evidence (DNA is used here as an example)

Case circumstances

- Murder of a young girl late 1990s
- Brutally assaulted/murdered. Struck on head with 23kg rock and while unconscious her tights/pants had been rolled down to her ankles
- Heavily blood stained material – victim's blood
- Evidence is a DNA profile from the top of tights A-12-F
- C 5pg/ul recovery of male DNA
- This is an appeal – defendant had been found guilty at first trial in Haugesund

International Society of Forensic Genetics Recommendation 1 – likelihood ratio

- ”The value of DNA and biological results is given by assigning a likelihood ratio. This implies the formulation of at least two mutually exclusive propositions. Assumptions regarding the model and the background information (i.e., case information and data) used should be disclosed.”
- A prosecution and alternative defence proposition must be proposed

  ”These should be formulated from the framework of circumstances of the case and through dialogue between parties in the criminal justice system.”

What is a likelihood ratio?

LR is a measure for Weight of Evidence

- Given **observed** data (E) and alternative **propositions (hypotheses)** for prosecution (Hp) and defence (Hd)
- LR gives a weight of whether the data supports Hp or Hd.
- LR=1 means that data support neither of the hypotheses (Hp nor Hd)
- LR greater than 1 means that data supports that Hp is true
- LR less than 1 means that data supports that Hd is true

Meaning of LR (same DNA result, different propositions)

- The LR does not tell us if a proposition is true or not
- It evaluates the strength of the evidence in support of a given proposition.
- Likelihood ratios are very flexible and they reflect the alternative views of the prosecution and defence respectively.
- Wording is extremely important. Must be concise and must explain the points of view that are contended
- Suppose we have a DNA mixture of a victim and a suspect.
- The prosecution say: “the DNA has come from the suspect and the victim”
- The defence say: the DNA has come from an unknown individual unrelated to the suspect and the victim.

In a statement to the court, the scientist says:

- I have considered two alternatives:

  Hp: Mr X and Ms V are contributors to the evidence

  Hd: Ms V and an unknown person, unrelated to Mr X are contributors to the evidence.

Hypothetical conclusion:

- The evidence is 1 million times more likely **if** the first proposition is true rather than **if** the second proposition is true.

The evidence provides extremely strong support for the proposition that Mr X contributed to the crime stain.

- The scientist must not say:

"it is more likely **that** the DNA came from Mr X" because this is known as the prosecutors fallacy, resulting in mis-trials in the UK.

This wording gives the probability of the proposition *given* the evidence.

Propositions (summary)

- In court, scientists do not evaluate propositions
- We ask: what is the probability of the *evidence* given the *proposition (or if a proposition is true*) *?*
- The scientist cannot tell the court how likely a proposition is given the evidence
- Propositions are provided by the mandating authorities and are based on the case circumstances
- The propositions should be set before the results are known to prevent unconscious bias

Beyond the DNA profile

- Often in court, the origin of the DNA profile is not the issue.
- Rather it is ‘how’, ‘why’ or ‘when’ did the DNA profile become evidential
- In particular, there is considerable interest in the ‘activity’ that led to the transfer of the DNA profile
- Was it direct, or indirect (innocent transfer)

What a DNA profile does not do

- The presence of a DNA profile does not tell us anything about how, why or when it became evidence
- To assist with the interpretation we can use the ‘hierarchy of propositions’ framework

Hierarchy of Propositions

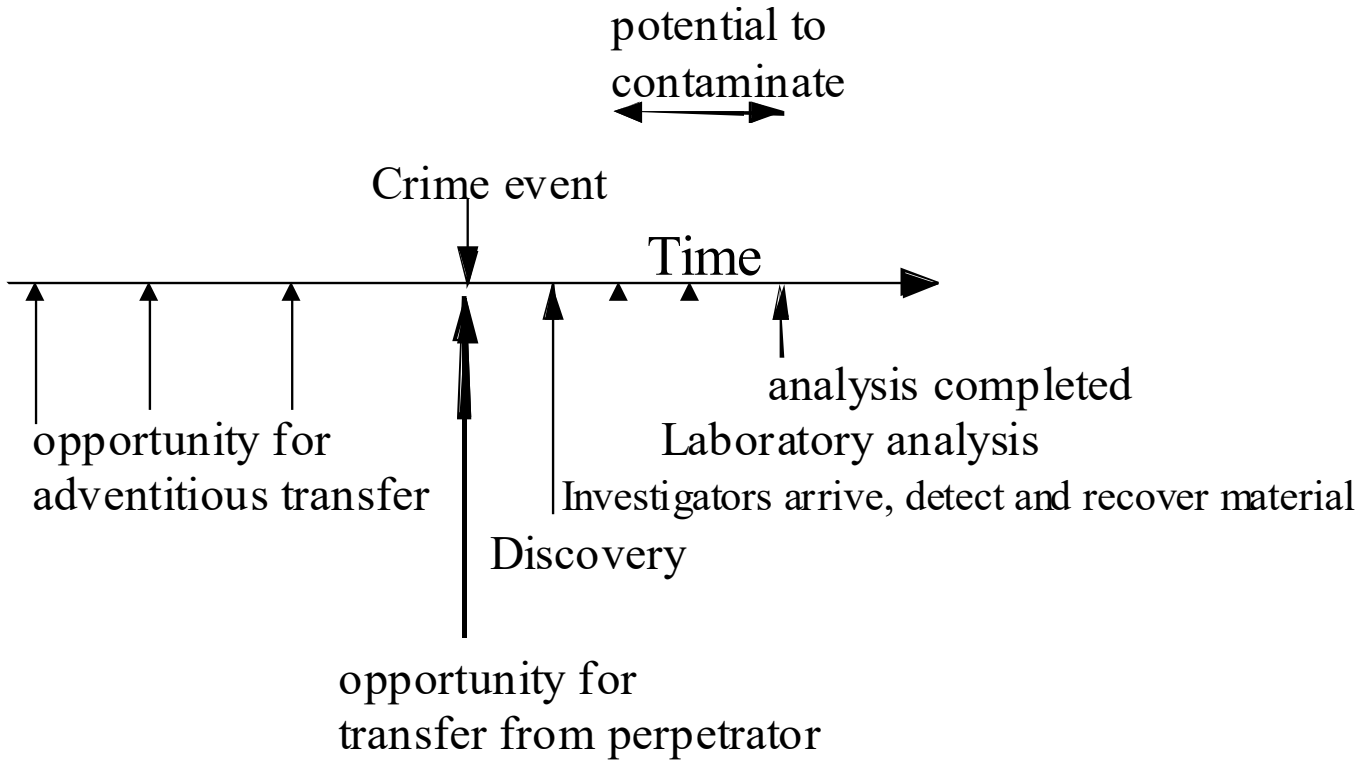
- LEVEL 3 - THE OFFENCE LEVEL:
  - Was a crime committed by the defendant or an unrelated person?
  - The forensic scientist would rarely consider evidence at this level.
- LEVEL 2 - THE ACTIVITY LEVEL:
  - Did the defendant / unrelated person take part in a connected activity?
  - Scientists may report cases at level 2 if given background information.
- LEVEL 1 - THE SOURCE LEVEL:
  - Does the profile from a body fluid stain or cell type match the suspect / unrelated person?
  - Scientists must have relevant background info.
- SUB-LEVEL 1 - SUB SOURCE LEVEL:
  - Low quant value, degraded/ small stains, no background information.
  - No association made between body fluid & DNA profile obtained.

Carry over of the strength of evidence

- The strength of evidence of the DNA profile at sub-source level has nothing to do with the activity level
- i.e. it is wrong to apply a statistic of 1 in 1 billion to an ‘activity’ e.g. handling an object like a knife.
- This mistake is often known as the CSI effect
- For example
  - Suppose the evidence to support a proposition is ‘1 in 1 billion’
  - This statistic refers to the strength of the evidence at sub-source level only
  - With low level samples of DNA we cannot apply the same statistic to the source level: e.g. is the DNA from blood?
  - We cannot apply the same statistic to the activity level: e.g. ‘did the suspect assault the victim’?

How did the DNA become evidential?

- Essentially, the method of transfer is often unknown and the purpose of the scientist is to explain limitations of the evidence

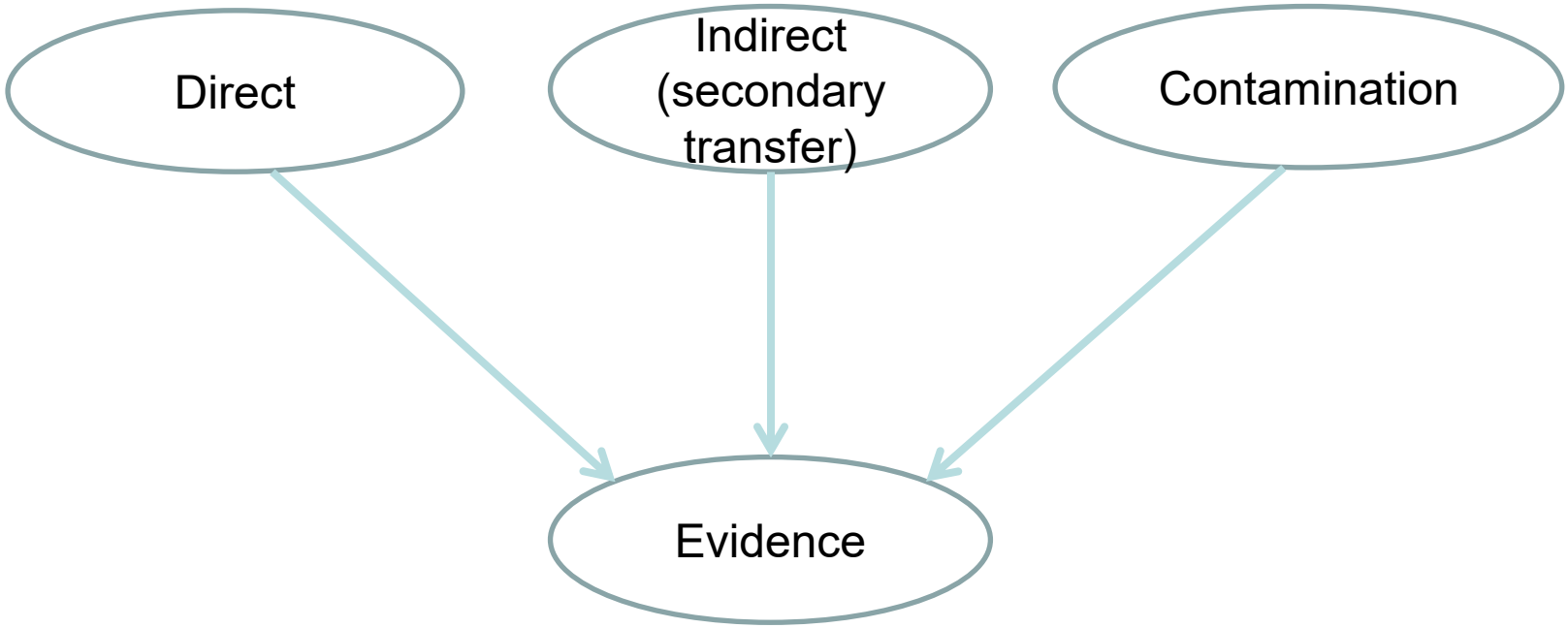


Confirmation Bias

- A well known psychological effect: **Confirmation bias**, also called **confirmatory bias** is the tendency to search for, interpret, favour, and recall information in a way that confirms one's pre-existing beliefs or hypotheses, while giving disproportionately less consideration to alternative possibilities.

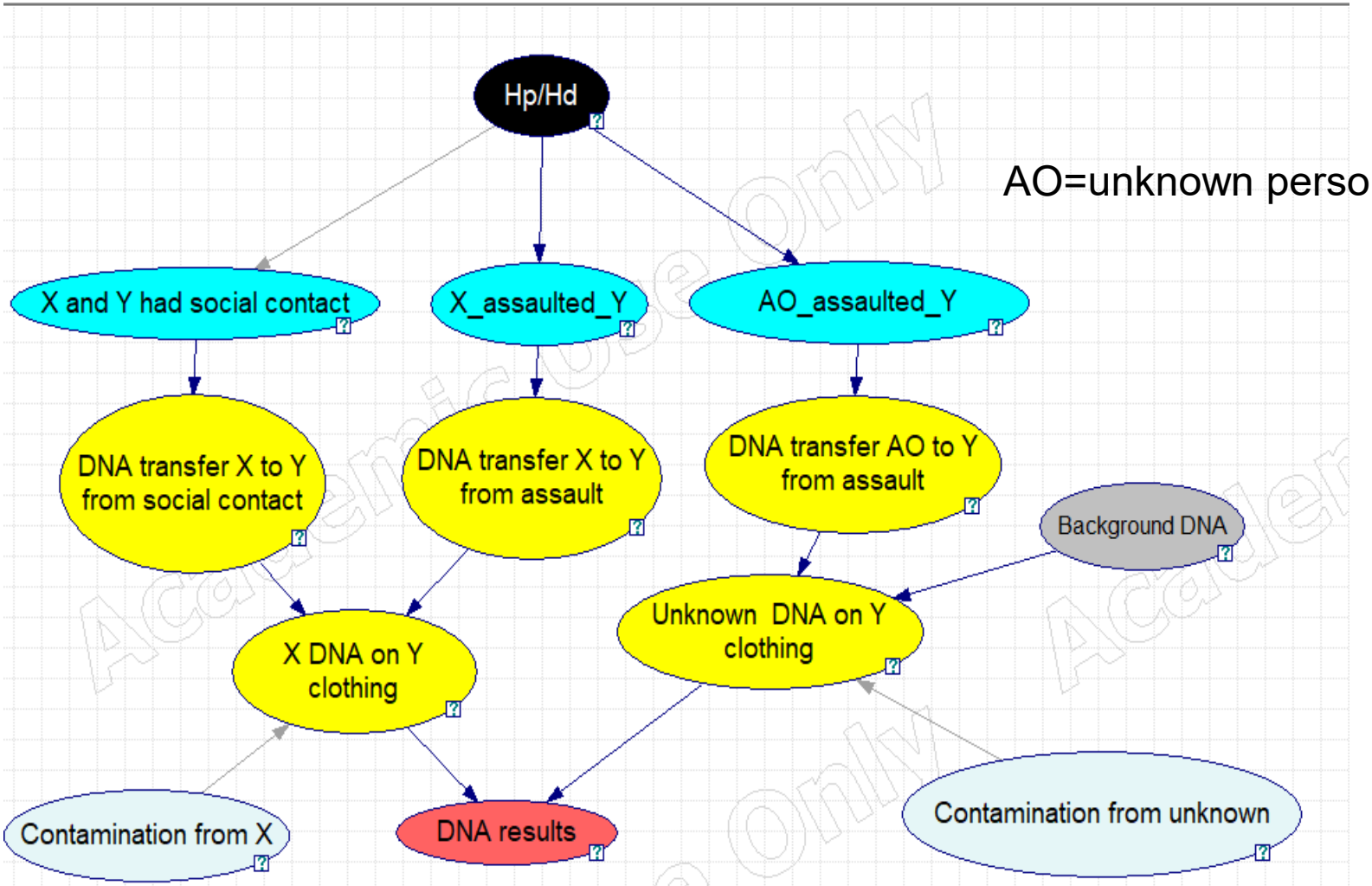
Modes of transfer of DNA profiles

- There are three different routes to transfer a DNA profile



- Transfers propagated by different individuals can occur at different times.

Bayesian Network describes all possible routes of DNA transfer given alternative propositions



AO=unknown person

Conclusion

- It is difficult to describe an experimental design to satisfy the defence proposition – especially timings etc
- Prosecution proposition is not an issue
- Indicates multiple kinds of experiments should be carried out and sensitivity analysis is needed
- Position of the defence is that *HE WASN'T THERE*, and they don't have to put forward any proposition

- It is still useful to discuss activity level in court because otherwise the court may carry over the subsource LR to activity and this would have disastrous consequences
- A major frustration is inability to provide a weight of evidence calculation
- So it is necessary to run through all of the possible transfer mechanisms and the court has to make its mind up
- This was an appeal court hearing. At trial the defendant was found guilty. The court ruled that the alternative propositions were very unlikely

Summary of key considerations to interpret evidence

- Appreciation of hierarchy of propositions places evidence into context
- Avoidance of the '*association fallacy*' where a DNA profile may be inappropriately associated with something else, like a body fluid or activity
- Recognition that '*confirmation bias*' can have a significant effect on the objective interpretation of evidence

Suggestion for an EDNAP Paper Exercise on Estimating Biogeographic Ancestry from DNA

Dear colleagues,

Some years ago, the EDNAP group discussed organizing a collaborative exercise on estimating biogeographic ancestry (BGA) from the DNA of unknown samples. There was general interest amongst members, however discussions revealed that such exercises would be costly and difficult to harmonize, as many laboratories use different marker panels and genotyping technologies. Based on previous experience the laboratory part is not as challenging as the interpretational part. This is why we would like to suggest an **alternative approach** by providing detailed analysis results comprising the full range of current BGA panels and population analysis software - thus avoiding redundant and expensive DNA analyses.

We suggest sharing the results of nine samples of known origin (to the level of the volunteer's grandparents) that were already genotyped in Munich and Innsbruck. Some of these samples are straightforward to interpret, others show more difficult backgrounds with mixed ancestries.

The provision of genotypes is not possible, as it would require explicit permission to share those; however, we can provide the analysis results obtained after applying the most widely used BGA marker panels and analysis tools:

1) AmpliSeq™ PhenoTrivium Panel (PT)
2) VISAGE Basic Tool (BT),
3) VISAGE Enhanced Tool (ET)
4) Precision ID mtDNA Whole Genome Panel

For this **paper exercise**, participants are provided with the following data:

- p-values for eye, hair and skin colour predictions obtained with HIrisPlex-S markers and the Erasmus HPS Webtool
- PCA analysis results using SNIPPER for PT, BT, ET
- STRUCTURE genetic cluster analysis results for PT, BT, ET
- Thermo Fisher CONVERGE admixture analysis results for PT
- GenoGeographer ancestry analysis results for PT, BT, ET
- PCA analysis with SNIPPER of the 16 X-SNP sub-set for ET
- paternal lineage based on Y-SNP sub-sets for PT and ET
- maternal lineage based on haplogroup assignments made with EMPOP

Participants are invited to pick their preferred dataset(s) for BGA estimations. There are no specific interpretation requirements. The participants are free to choose how to provide their BGA assessments in the form of a report to investigators which they currently provide, or envisage they would do at a future date.

The goal of this exercise is to have a benchmark of currently applied verbal assessments of BGA. This could serve as basis for further collaborative work towards harmonization of BGA reporting in forensic genetics.

This collaborative project is organized by Santiago the Compostela (Chris Phillips), Munich (Marta Diepenbroek) and Innsbruck (Walther Parson).

This suggestion is open for discussion and comments. Please feel free to provide responses before the Meeting in Oslo (Oct 03 2023) so that we can have a more informed discussion at the upcoming EDNAP meeting in Oslo.

Santiago, Munich, Innsbruck 18.08.2023
Chris, Marta, Walther

Examining ancestry analysis within a collaborative exercise framework

Examining ancestry analysis within a collaborative exercise framework

- BGA is an important part of forensic genetic research and practice - different rules in EU

genes

MDPI

Converge

Article

Evaluation of the Ion AmpliSeq™ PhenoTrivium Panel: MPS-Based Assay for Ancestry and Phenotype Predictions Challenged by Casework Samples

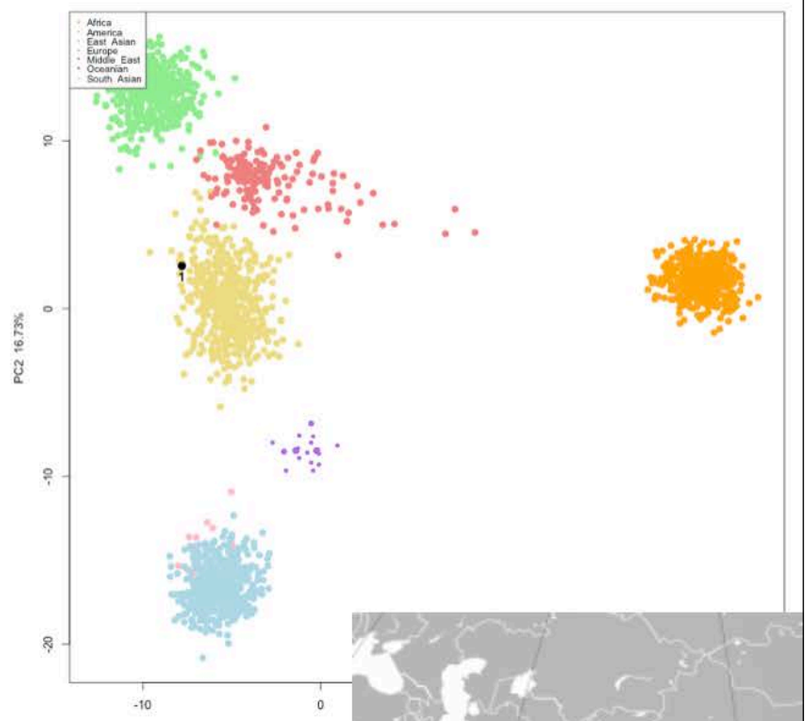
Marta Diepenbroek [1,*], Birgit Bayer [1], Robert Lagacé [2] and Katja Anslinger [1]

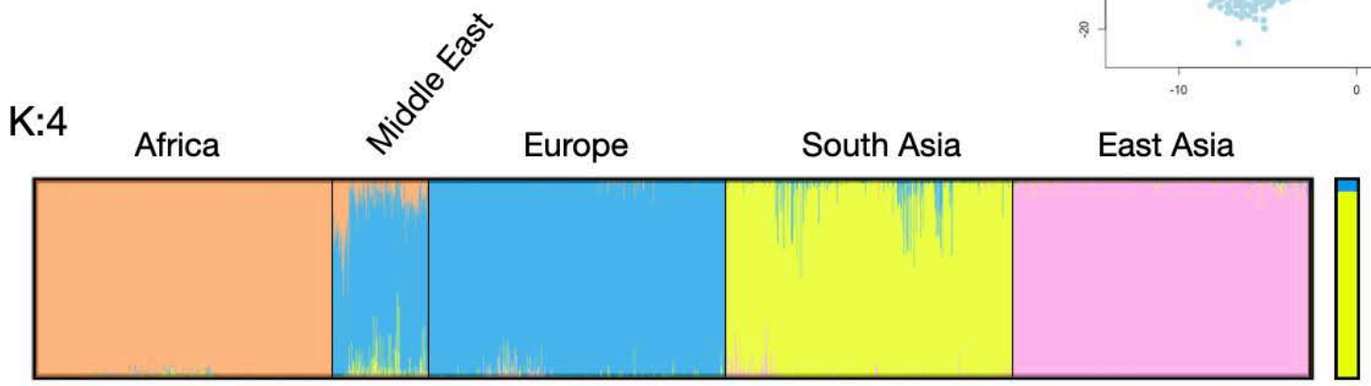
Casework example from USC

- Murder of a European in a region of the world where Middle East and South Asian individuals form the major demographic components

- PCA analysis used 7 reference population groups but STRUCTURE was kept simple and tested 5

- The PCA position in the South Asian cluster and a separate CE-based skin colour test was used to add geographic detail to the ancestry inference

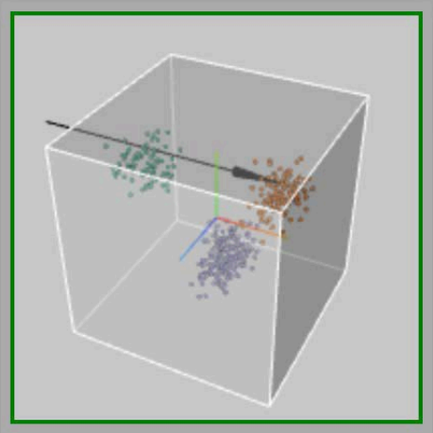




Skin colour

Pigmentation phenotype SNP analysis gave: **This profile is 151,097 times more likely White than Intermediate, and 744,240,654 times more likely White than Black.** This can be interpreted to strongly indicate pale skin.

USC UNIVERSIDADE DE SANTIAGO DE COMPOSTELA



The Snipper 3

app suite

Snipper v3

Examining ancestry analysis within a collaborative exercise framework

- BGA is an important part of forensic genetic research and practice - different rules in EU
- Genotyping SNPs is technically complex and data can be difficult to assess

The 2015 EDNAP Ancestry Exercise

CE

Genotyping <u>dedicated</u> ancestry informative marker sets (SNPs or Indels)

MPS (excluding ForenSeq)

↓

Converge

Analysing the genotype data with an array of statistical tools

Bayes / PCA / STRUCTURE

GenoGeographer

↓

Evaluating the statistical results to analyse the ancestry patterns in the sample

Standardised reference population data (VCFs)

The proposed 2023 EDNAP Ancestry Exercise

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- Genotyping SNPs is technically complex and data can be difficult to assess.

The 2015 EDNAP Ancestry Exercise

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Genotyping <u>dedicated</u> ancestry informative marker sets (SNPs or Indels)

MPS

(excludes ForenSeq)

ISFG Summer Schools 2021, 2023

Converge

Analysing the genotype data with an array of statistical tools

Bayes / PCA / STRUCTURE

GenoGeographer

Evaluating the statistical results to analyse the ancestry patterns in the sample

Standardised reference population data (VCFs)

The proposed 2023 EDNAP Ancestry Exercise

The 2015 EDNAP Ancestry Exercise

- EDNAP already successfully undertook a ‘wet’ ancestry analysis exercise for a SNaPshot 34-plex SNP set and a direct PCR-to-CE 46-plex Indel set, sponsored by EUROFORGEN and primarily looking at ease-of-use with CE and mixed DNA detection

Forensic Science International: Genetics 19 (2015) 56–67

Contents lists available at ScienceDirect

Forensic Science International: Genetics

journal homepage: www.elsevier.com/locate/fsig

Forensic ancestry analysis with two capillary electrophoresis ancestry informative marker (AIM) panels: Results of a collaborative EDNAP exercise

C. Santos[a,1], M. Fondevila[a,1], D. Ballard[b,1], R. Banemann[c], A.M. Bento[d], C. Børsting[e,1], W. Branicki[f,2], F. Brisighelli[g], M. Burrington[h], T. Capal[i], L. Chaitanya[j], R. Daniel[k], V. Decroyer[l], R. England[m], K.B. Gettings[n], T.E. Gross[o,1], C. Haas[p], J. Harteveld[q], P. Hoff-Olsen[r], A. Hoffmann[c], M. Kayser[j], P. Kohler[r,2], A. Linacre[s], M. Mayr-Eduardoff[t,1], C. McGovern[m], N. Morling[e,l,1], G. O'Donnell[h], W. Parson[t,u], V.L. Pascali[g], M.J. Porto[d], A. Roseth[r], P.M. Schneider[o,1], T. Sijen[q], V. Stenzl[i], D. Syndercombe Court[b,1], J.E. Templeton[s], M. Turanska[v], P.M. Vallone[n], R.A.H.van Oorschot[k], L. Zatkalikova[v], The EUROFORGEN-NoE Consortium, Á. Carracedo[a,1], C. Phillips[a,1,*]

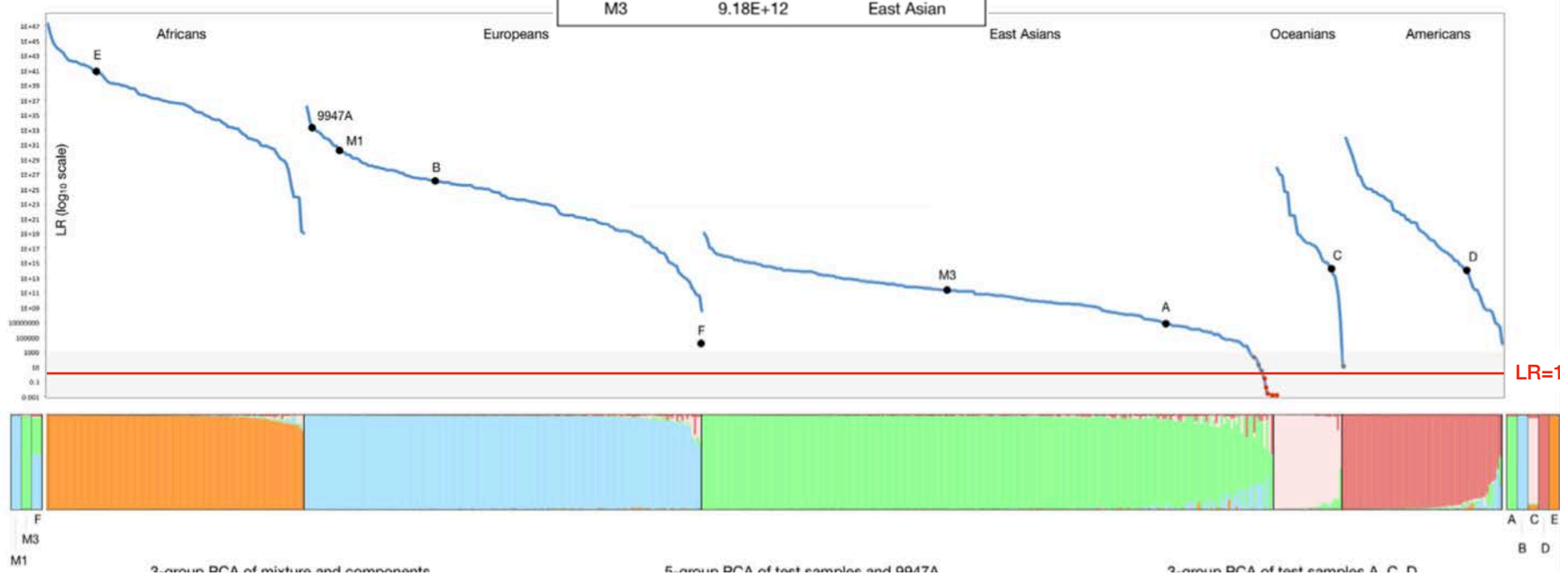
Five samples of known ancestry, 9947A universal control, 1:3 mixed DNA F (M1:M3)

Sample	Lowest LR	Assignment
9947A	4.11E+33	European
A	1.25E+07	East Asian
B	9.22E+27	European
C	1.54E+14	Oceanian
D	8.07E+13	American
E	1.78E+41	African
F	6,487	European
M1	1.82E+30	European
M3	9.18E+12	East Asian

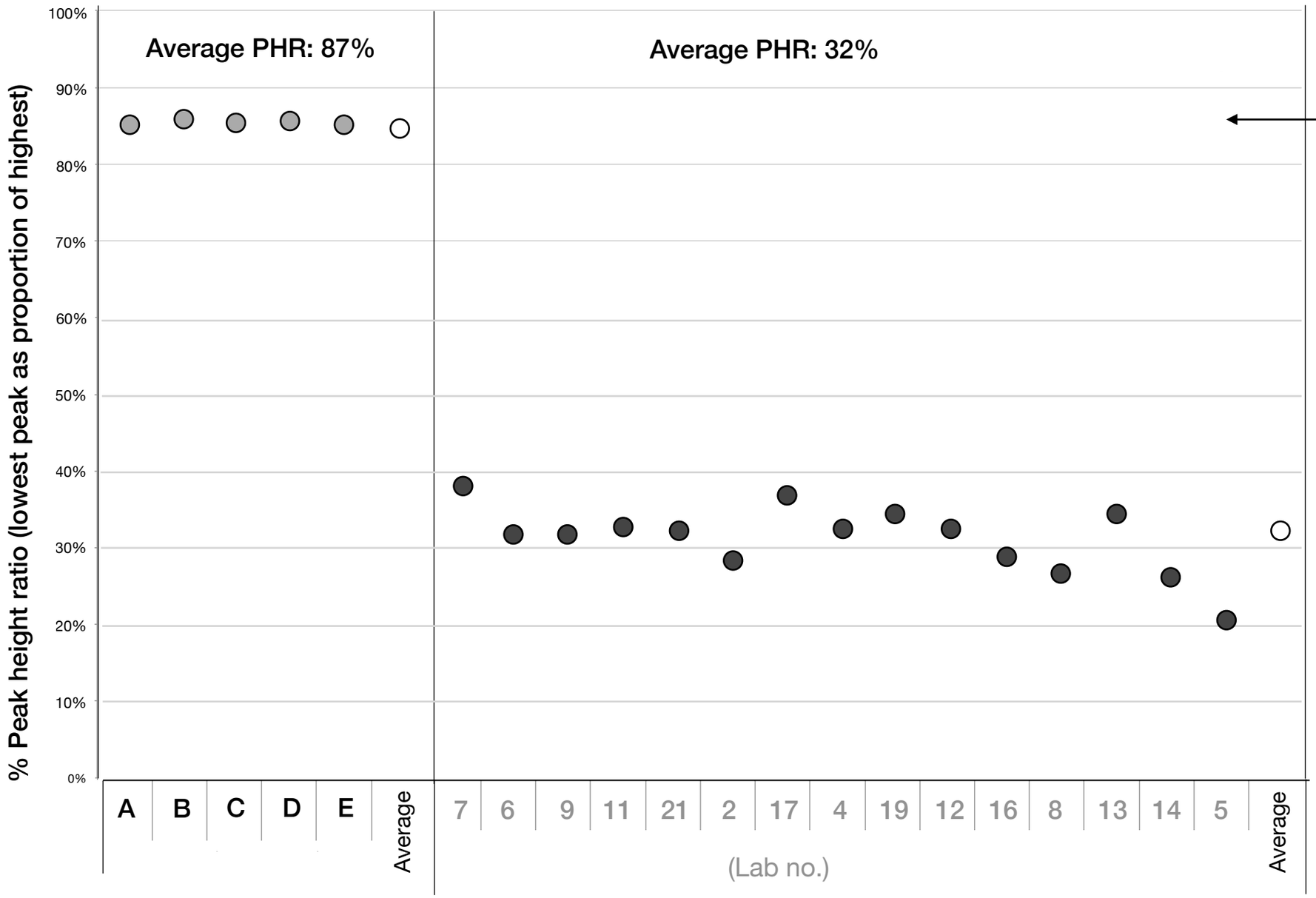
Likelihood ratio tests

PCA tests (shown in slide 11)

STRUCTURE



Indel peak height ratios indicated mixed DNA successfully for all labs



Average Indel peak height ratios of 87% vs 32% provided clear indications to all labs that F was mixed

- PHR of single donor samples
- PHR of single donor samples
- Average PHR

Examining ancestry analysis within a collaborative exercise framework

- BGA is an important part of forensic genetic research and practice - different rules in EU

- Genotyping SNPs is technically complex and data can be difficult to assess

- The field has developed diverse tools for genotyping ancestry-informative markers over the past decade, but there has been little attempt to harmonise the process of population data analysis and its interpretation to infer a likely ancestry for a forensic DNA sample

- Two blind-trial collaborative exercises on BGA were conducted several years ago indicating only some differences in technical aspects, but a wide variety of approaches in marker choice and the interpretation of the genetic findings

#1 African ancestry #2 D: East Asian ancestry #2 I: German-Nepalese (♀) parental co-ancestry

- Some discussion at Riga 2019 whether EDNAP should do something similar, but further collaborative exercises in EDNAP have not been initiated for two main reasons:

  - The lab work is complex and expensive, but reliable (high genotyping concordance), so little further progress can be achieved here through a collaborative exercise

  - There is limited shared knowledge and consensus on the interpretation of BGA results, so a lot could be achieved here - although difficult to standardise population analysis tools

A proposed ancestry (BGA) analysis exercise

- Four years after the Riga meeting we propose an exercise that focuses on interpretation and to some extent has constraints on the population analysis part of the BGA process:

The What:

9 donor individuals
(3 females, 6 males)

Donors have known ancestry
(self declared, 2 generations back)

Donors have known appearance
(eye, hair and skin color pictures)

DNA collected based on LMU Munich Ethics commission agreement

No genotypes shared (privacy issues) – so, all data is pre-analyzed

Fully a paper exercise

MPS panels:

- AmpliSeq™ PhenoTrivium Panel (PT)
- VISAGE AmpliSeq Basic Tool (BT)
- VISAGE AmpliSeq Enhanced Tool (ET)
- Precision ID mtDNA Whole Genome Panel

Markers:

- 41 appearance SNPs – HIrisPlex-S
- 163 BGA SNPs – PT (Precision ID Ancestry)
- 115 BGA SNPs – BT
- 104 BGA SNPs – ET
- 116 Y-SNPs - PT
- 85 Y-SNPs – ET
- 16 X-SNPs – ET
- Whole mitochondrial genomes

A proposed ancestry (BGA) analysis exercise

- Four years after the Riga meeting we propose an exercise that focuses on interpretation and to some extent has constraints on the population analysis part of the BGA process:

The How:

Statistical Tools:

- Calculated p-values for eye, hair and skin color obtained with Erasmus HPS Webtool

- PCA analysis results using SNIPPER for three different SNP sets and specific K values (PT, BT, ET)

- STRUCTURE admixture analysis results for three different SNP sets and specific K values (PT, BT, ET)

- CONVERGE admixture analysis results with different K values (PT)

- GenoGeographer ancestry analysis results for three different SNP sets (PT, BT, ET)

- PCA analysis with SNIPPER for the 16 X-SNPs (ET)

- Paternal lineage (most derived within PT and ET)

- Maternal lineage (mtDNA haplogroup assignment using EMPOP)

A proposed ancestry (BGA) analysis exercise

- Four years after the Riga meeting we propose an exercise that focuses on interpretation and to some extent has constraints on the population analysis part of the BGA process:

The Why:

- 'One for all, all for one': combining different markers and software to obtain the best possible BGA prediction

- Dealing with potentially challenging samples (in terms of patterns of variation) which could be a regular occurrence

- Lab work is complex and expensive: little foreground can be achieved through running a 'wet' genotyping exercise

- Limited knowledge and harmonization of the interpretation of results : a lot can be achieved with a clear need for improvement

- Results could be used as a benchmark for further research and be a first step to create interpretative guidelines

genes

MDPI

Article

Evaluation of the Ion AmpliSeq™ PhenoTrivium Panel: MPS-Based Assay for Ancestry and Phenotype Predictions Challenged by Casework Samples

Marta Diepenbroek [1,*], Birgit Bayer [1], Kristina Schwender [1], Roberta Schiller [1], Jessica Lim [2], Robert Lagacé [2] and Katja Anslinger [1]

genes

MDPI

Article

Development and Evaluation of the Ancestry Informative Marker Panel of the VISAGE Basic Tool

María de la Puente [1], Jorge Ruiz-Ramírez [1], Adrián Ambroa-Conde [1], Catarina Xavier [2], Jacobo Pardo-Seco [3], Jose Álvarez-Dios [4], Ana Freire-Aradas [1], Ana Mosquera-Miguel [1], Theresa E. Gross [5,6], Elaine Y. Y. Cheung [5], Wojciech Branicki [7], Michael Nothnagel [8,9], Walther Parson [2,10], Peter M. Schneider [5], Manfred Kayser [11], Ángel Carracedo [1,12], Maria Victoria Lareu [1], Christopher Phillips [1,*] and on behalf of the VISAGE Consortium †

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Contents lists available at ScienceDirect

Forensic Science International: Genetics

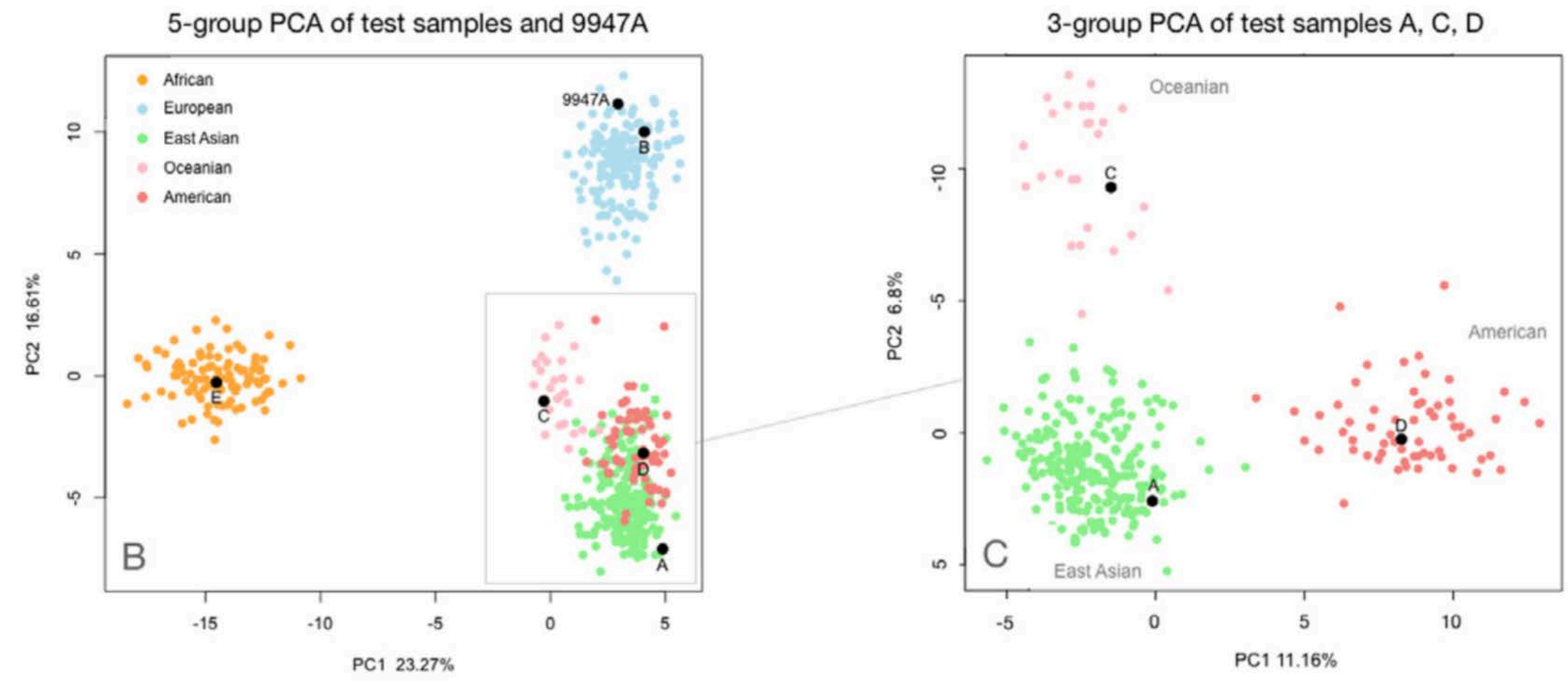
journal homepage: www.elsevier.com/locate/fsigen

Development and evaluations of the ancestry informative markers of the VISAGE Enhanced Tool for Appearance and Ancestry☆

J. Ruiz-Ramírez [a,1], M. de la Puente [a,*,1], C. Xavier [b], A. Ambroa-Conde [a], J. Álvarez-Dios [c], A. Freire-Aradas [a], A. Mosquera-Miguel [a], A. Ralf [d], C. Amory [b], M.A. Katsara [e], T. Khellaf [e], M. Nothnagel [e,f], E.Y.Y. Cheung [g], T.E. Gross [g], P.M. Schneider [g], J. Uacyisrael [h], S. Oliveira [i], M.d.N. Klautau-Guimarães [i], C. Carvalho-Gontijo [i], E. Pośpiech [j], W. Branicki [k], W. Parson [b,l], M. Kayser [d], A. Carracedo [m,n], M.V. Lareu [a], C. Phillips [a,*,1], on behalf of the VISAGE Consortium [2]

Restricted population comparisons in PCA

- Four years after the Riga meeting we propose an exercise that focuses on interpretation and to some extent has constraints on the population analysis part of the BGA process:
  - Agreement with sample donor's informed consent not to share genotypes beyond lead labs
  - For this exercise we decided to restrict the choice of K-values and population groupings in STRUCTURE which takes some aspects of choice of population data analysis from participants
  - Santiago now uses a nested approach for some **PCA** and all STRUCTURE analyses, i.e. begin with a general analysis of all possible ancestries then drill down to most likely ancestries



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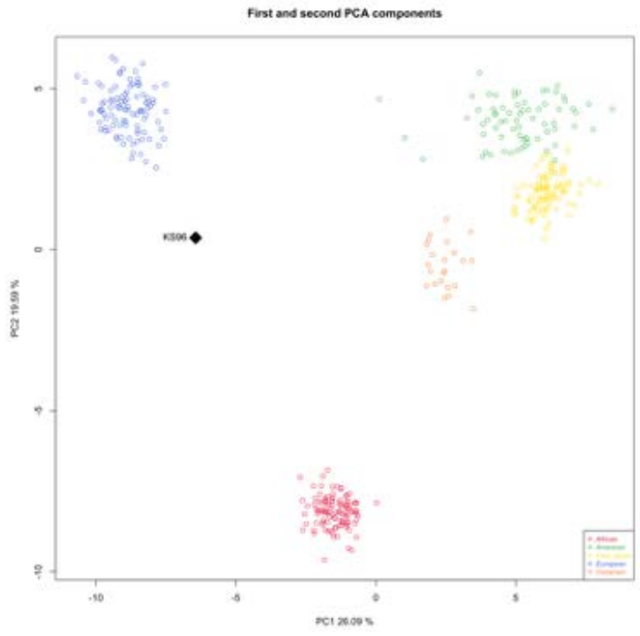
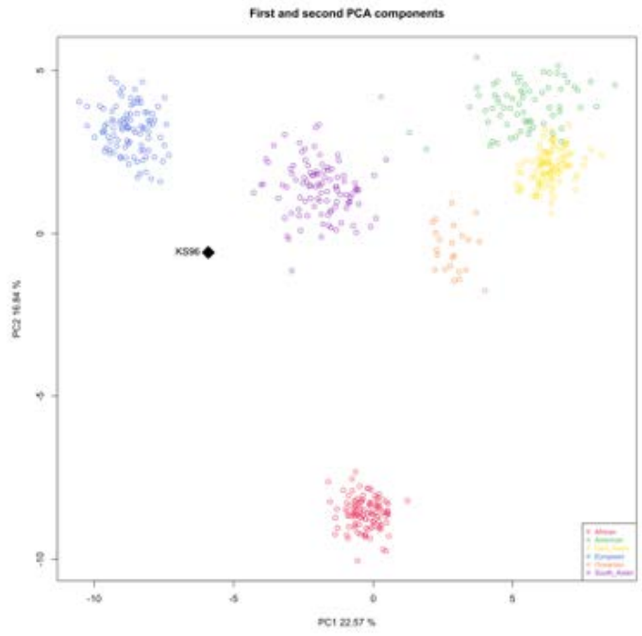
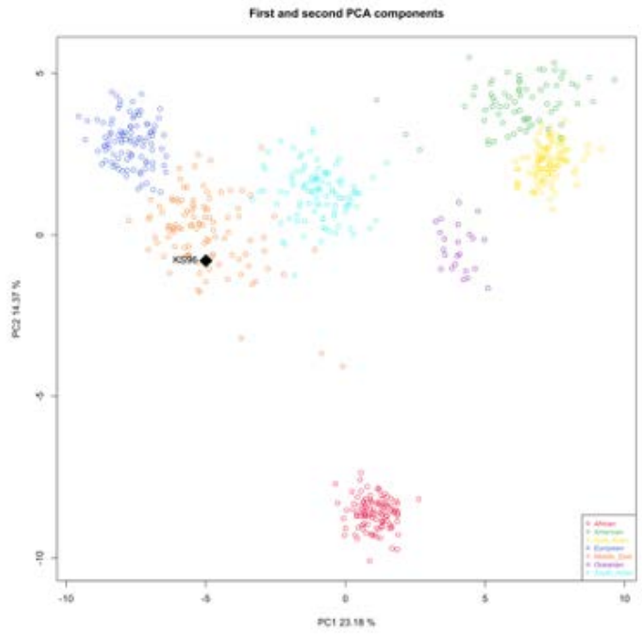
5 Clusters



6 Clusters



7 Clusters



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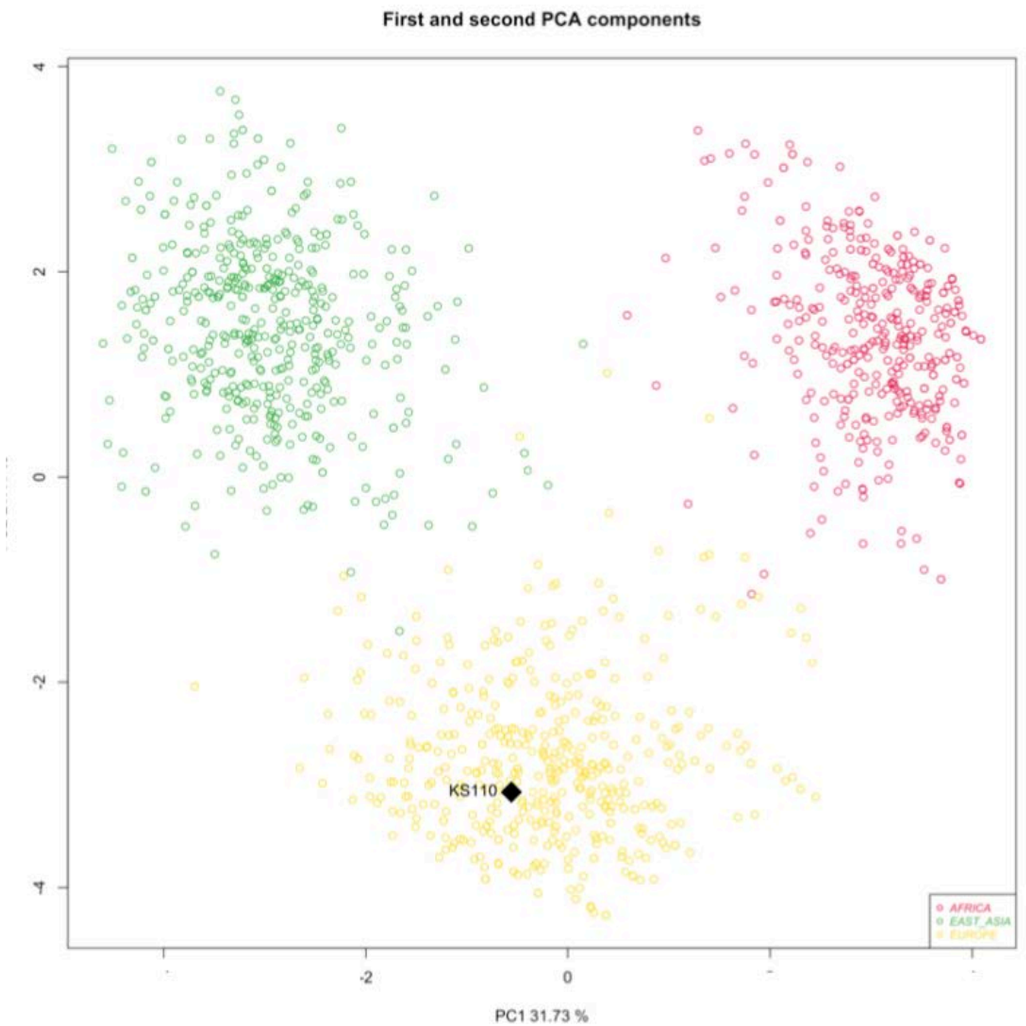
X-SNP variation is less well separated in PCA: so AFR-EUR-EAS reference clusters are used mainly

AFR-EUR-AMR reference clusters are also applied to samples indicating admixed American backgrounds



Restricted population comparisons in STRUCTURE

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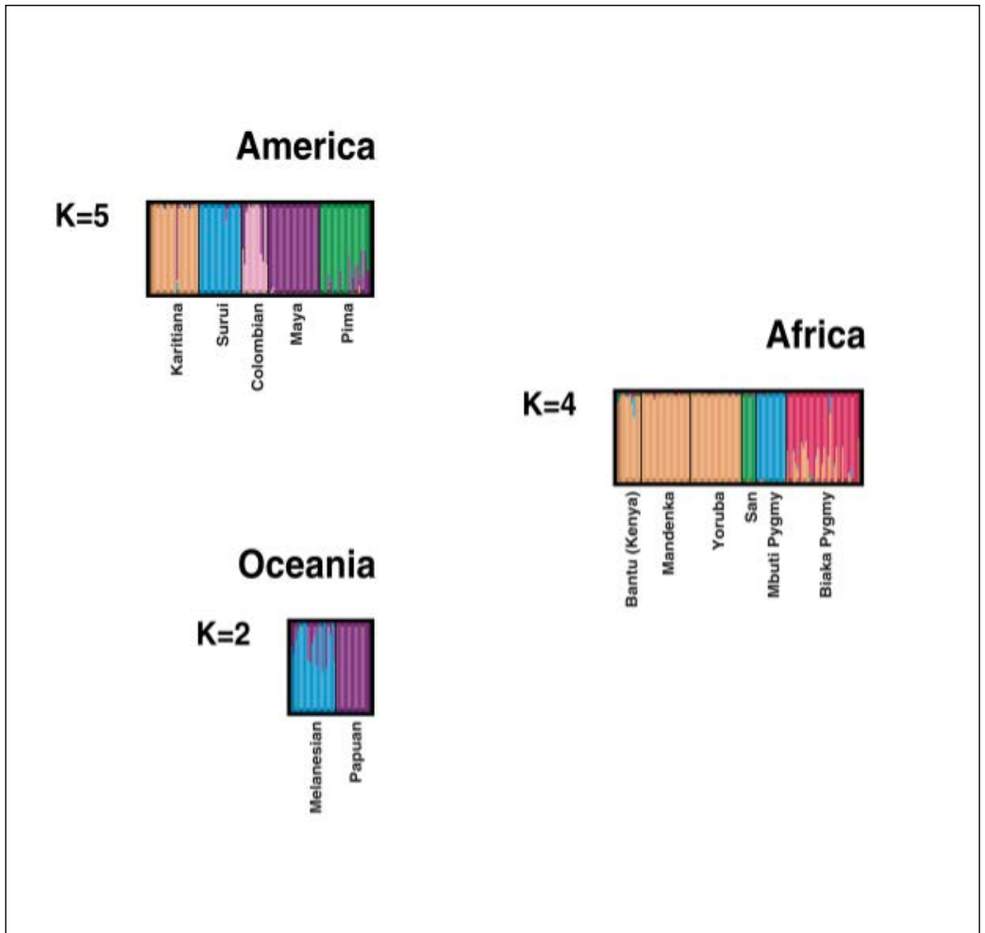
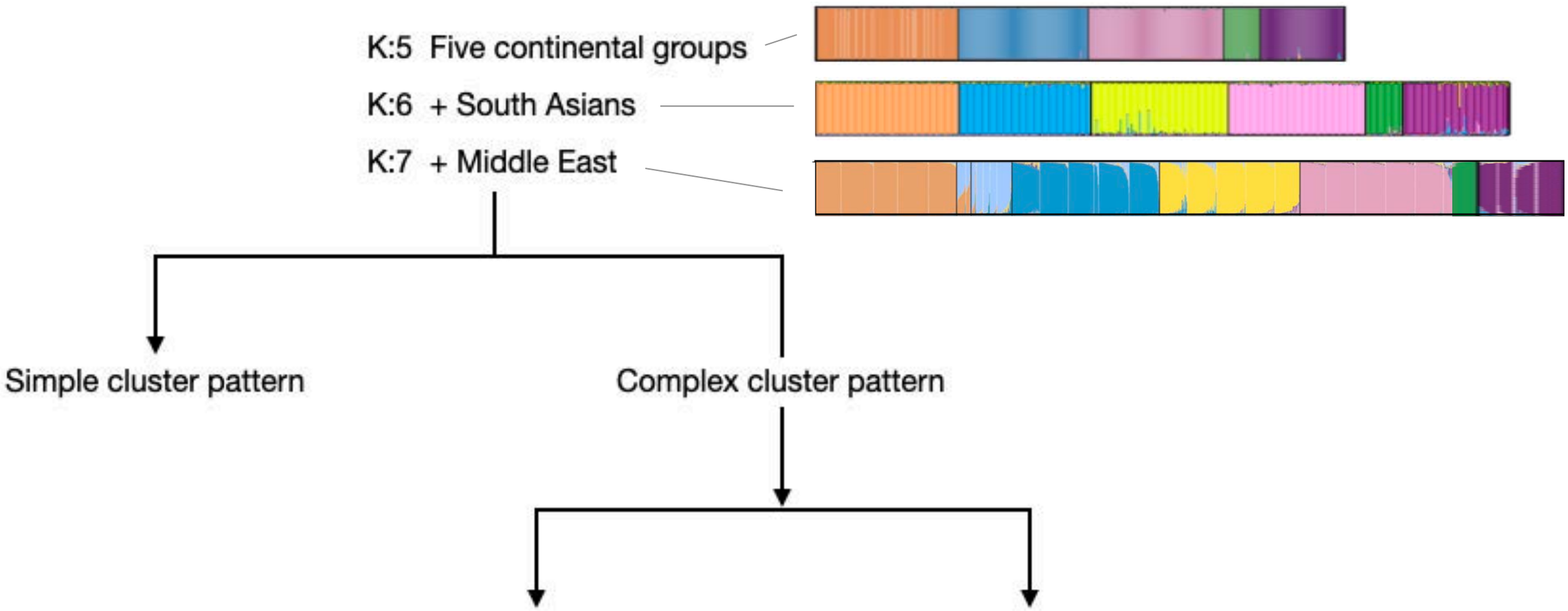


Genetic Structure of Human Populations

Noah A. Rosenberg,[1]* Jonathan K. Pritchard,[2] James L. Weber,[3]
Howard M. Cann,[4] Kenneth K. Kidd,[5] Lev A. Zhivotovsky,[6]
Marcus W. Feldman[7]

A nested STRUCTURE approach performs an 'open' analysis with all possibilities then follows with reduced populations and applies K values appropriate for those selected populations

Restricted population comparisons in STRUCTURE



Avoids ambiguous identification of co-ancestry components from closely related populations

Confines the analysis of closely related populations to those from the target region and adjoining areas

Discussion Points

During morning discussions on the future of EDNAP it was agreed that the expression of interest in the ancestry exercise by labs outside the current membership was a positive sign and we could look at ways to disseminate ideas for possible collaborations more widely. This would need to be done carefully to avoid a too large uptake of participators.

The restrictions on K-value choice in STRUCTURE and reference population data selections in PCA and STRUCTURE were accepted as a necessary constraint on the ability of participants to shape these ancestry analyses. The USC nested approach therefore provides a level of interpretation of the initial findings obtained with a full range of populations that participants might apply themselves in a casework scenario.

Kris, NFI, presented on the details of ForAPP (Forensic Ancestry Prediction Pipeline) - in development, soon to be released (?). It was suggested that if there is a way to upload the genotypes anonymously (i.e. undisclosed data listed on the ForAPP portal) for each donor and multiplex used, this should be pursued by the exercise organisers and Kris, if possible.

Vania, Copenhagen, suggested that GenoGeographer requires careful adjustment of analysis parameters, and the data generated for the donor/multiplex combinations have already been largely pre-set by the organisers. Copenhagen and the organisers will aim to hold discussions to possibly resolve this restriction on user choice and interpretative decision making when applying GenoGeographer