

EUROPEAN DNA PROFILING GROUP (EDNAP) MEETING

Rome, Italy

8 November 2016

Host: Vince Pascali
Chairman: Niels Morling

A list of participants is attached.

Welcome

Vince Pascali welcomed members to Rome.

Presentation

What is inside a mixture?

Vince Pascali

Vince Pascali presented research on biostatistics analysis of mixtures of DNA from two or more individuals. The data will be published elsewhere.

Update on exercises

A SNaPshot based method targeting 18 common mtDNA mutations

Arnoud Kal

The manuscript is in press (presentation attached).

Second exercise on methylated DNA and age

David Ballard

David Ballard presented the results of the second collaborative EDNAP exercise on age estimation by means of measurements of methylation of selected DNA positions (presentation attached).

Exercise on mRNA typing with NGS

Cordula Haas

Cordula Haas gave an update of the NGS based study of discrimination between various tissues and body fluids (presentation attached).

Updates from other groups

High quality DNA sequence database - STRidER

Ingo Bastisch

Ingo Bastisch informed about the update of the advice on formulas on the website, <http://strider.online>. Colleagues are invited to submit data to the database. In the near future, STRidER will be used as a screening tool and repository for population genetic information that is sent to Forensic Science International: Genetics.

EUROFORGEN-NoE – General update

Peter Schneider

Peter Schneider gave an update concerning the project (presentation attached).

EDNAP website update (www.isfg.org/EDNAP)

Peter Schneider

Members are encouraged to visit the website. Suggestions are welcome.

Future activities

Niels Morling

At the next EDNAP meeting, Cordula Haas will suggest a follow-up exercise on mRNA typing with NGS.

Next meeting

Niels Morling

The next EDNAP meeting will be held 25 April 2017 in Vilnius, Lithuania in connection with the meetings of CODIS users and the DNA Working Group of ENFSI. The meetings will be organised by Gintautas Šinkūnas (gintautas.sinkunas@vrm.lt).

If you are willing to host the EDNAP meeting in the autumn of 2017, please contact Niels Morling.

Any other business

Niels Morling

There was no other business.

Closing of the meeting

The meeting closed with sincere thanks to Vince Pascal, Francesca Brisighelli and all other colleagues, who helped to organise the meeting.

Attachments are found at the EDNAP website <http://www.isfg.org/EDNAP/Meetings>:

- Agenda
- List of participants
- Presentations
 - Arnoud Kal: Report on mtDNA SNP typing
 - David Ballard: Report on methylated DNA and age determination
 - Cordula Haas: Report on mRNA NGS
 - Peter Schneider: Report on EUROFORGEN-NoE.

AGENDA FOR THE EDNAP MEETING

ROME – 8 NOVEMBER 2016

DRAFT

Expected duration: 09.00 - 17.00

Coffee: 10.15 – Lunch: 12.30-13.30 – Coffee: 15.15

Host: Vince Pascali
Chairman: Niels Morling

Welcome	Vince Pascali
What is inside a mixture?	Vince Pascali
Validation of software – ENFSI – draft	Peter Gill
Education, competence, certification, accreditation - ENFSI	Niels Morling
Update on activities concerning	
mtDNA SNP screening – two PCRs, 18 SNPs	Arnoud Kal
Methylated DNA and age exercise	David Ballard
Exercise on mRNA typing with MPS	Cordula Haas
Updates from other groups	
High quality DNA sequence database	Walther Parson
EUROFORGEN-NoE	Peter Schneider
Future activities	Niels Morling
EDNAP meeting 25 April 2017 in Vilnius, Lithuania	
EDNAP meeting in the fall of 2017 – where? Please suggest	
Any other business	Niels Morling

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Ministry of Justice

Final Update Exercise mtDNA SNaPshot

8 November 2016, Rome



A control region-based mtDNA SNaPshot selection tool, integrated into a mini amplicon sequencing method

- Targets 18 SNPs in HVS I - II - III

- Degenerate bases in 3' part
primer to cover SNPs at primer
binding site positions

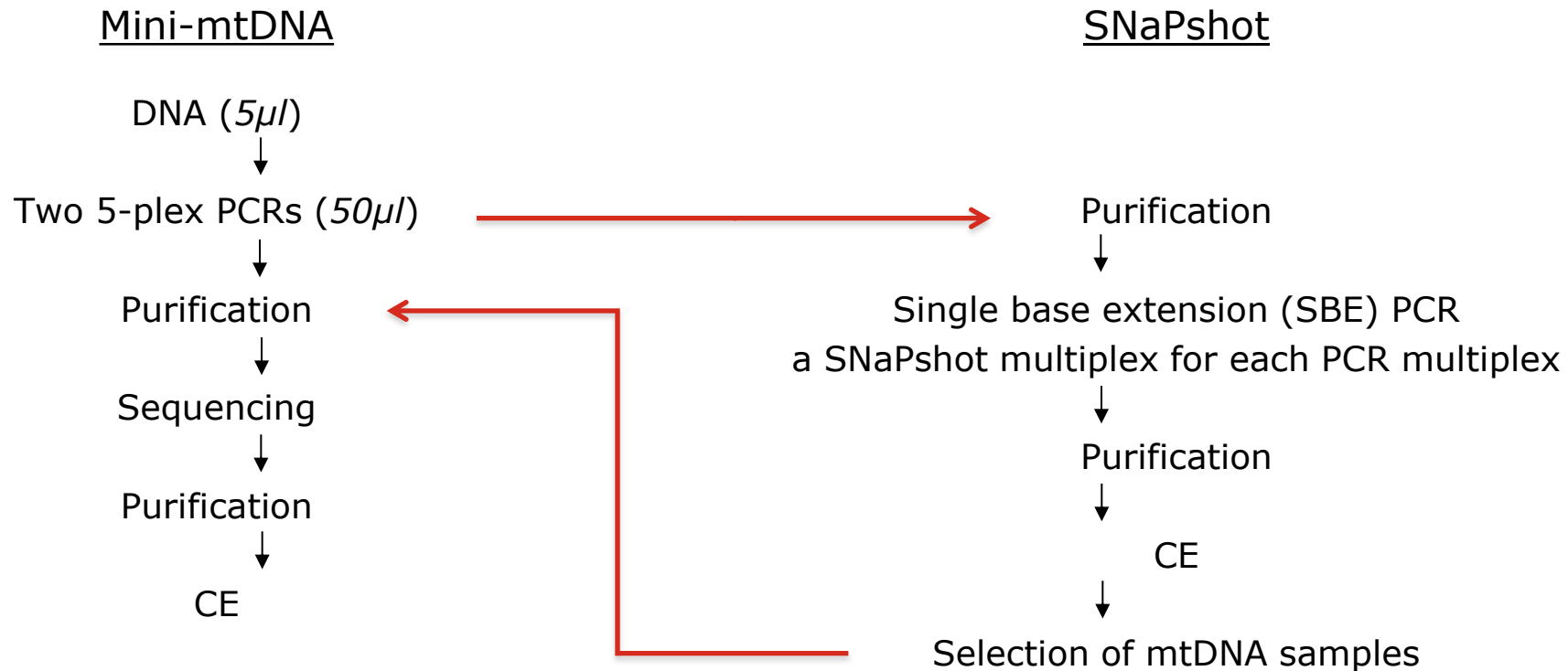
- Two SNaPshot multiplexes for PCR
products of mini amplicon mtDNA
multiplexes (Eichmann et al 2008)

SNP	Base change	Frequency	Haplogroup
73	A>G	0.5551	HV / H / V
146	T>C - T>a	0.0933 - 0.0001	
150	C>T - C>g	0.1028 - 0.0001	
152	T>C	0.2007	
182	C>T	0.0088	
185	G>A - G>t - G>c	0.0541 - 0.0031 - 0.0004	M / J K
195	T>C - T>a	0.1986 - 0.0002	
489	T>C	0.1351	
497	C>T	0.0419	
16126	T>C	0.1799	
16129	G>A - G>c	0.0689 - 0.0111	
16223	C>T	0.1405	
16270	C>T	0.0876	
16278	C>T	0.0646	
16294	C>T - C>a - C>g	0.1071 - 0.0003 - 0.0002	
16311	T>C	0.1676	
16362	T>C	0.0743	
16519	T>C	0.6642	

2



Same PCR product for sequencing and SNaPshot

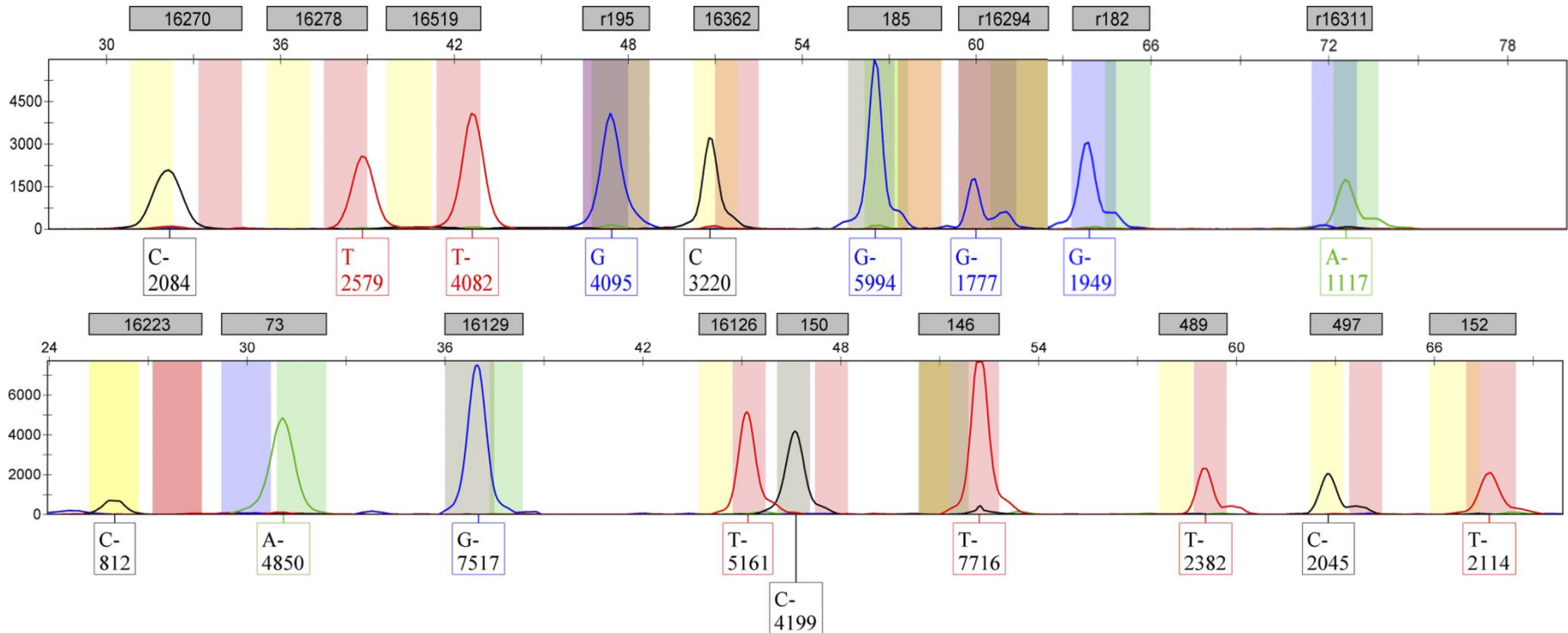


Example: Case with 30 hairs → 600 sequencing reactions

SNaPshot: Selection of 3 hair samples → 60 sequencing reactions



Optimised SNaPshot assay

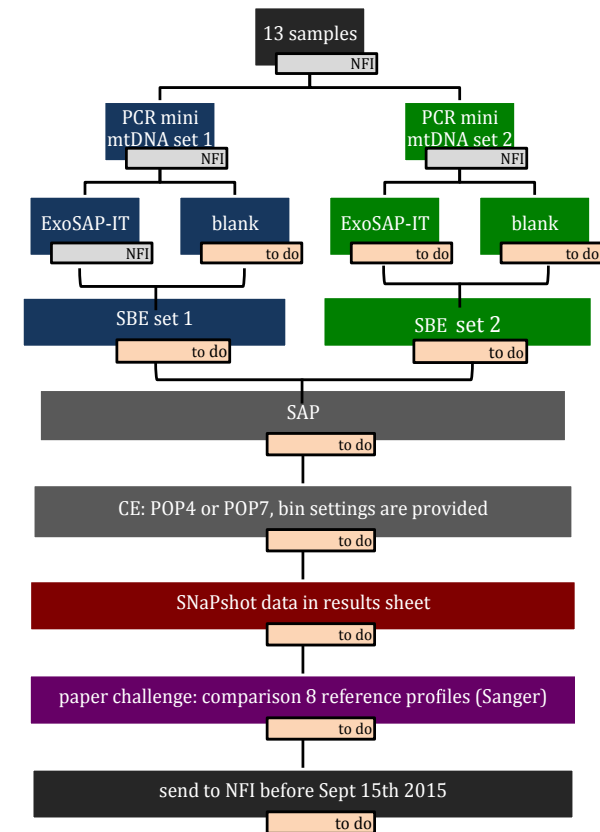


- SNP number preceded by 'r': reverse primer
- Allele call followed by '-': rCRS allele



EDNAP Exercise: 3 parts – 14 labs (excl NFI)

- ① SNaPshot assays on 13 samples for which PCR products are provided
- ② Paper challenge: compare results 1 to list of 8 references given in standard nomenclature
- ③ Optional: NGS full mtDNA analysis of 2 samples
 - » Commercial control DNA sample (cell line)
 - » Sample with heteroplasmy





Warsaw meeting april 2016

Draft manuscript almost finished



Forensic Science International: Genetics 26 (2017) 77–84



Contents lists available at ScienceDirect

Forensic Science International: Genetics

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



A collaborative EDNAP exercise on SNaPshot™-based mtDNA control region typing



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MPS data in Supplemental Materials

In summary, four laboratories submitted two samples to MPS using two different platforms. Some differences were reported, but these were observed to be calling errors when the data were re-analysed through the same software. Although the average read coverage varied markedly between the four laboratories, the ratio between the two bases at a heteroplasmic position was similar for all four laboratories. MPS appeared to generate reliable mtDNA typing results.



Big THANK YOU ALL!!



Methylated DNA & Age Exercise



David Ballard

EDNAP, Rome 2016

KING'S
College
LONDON

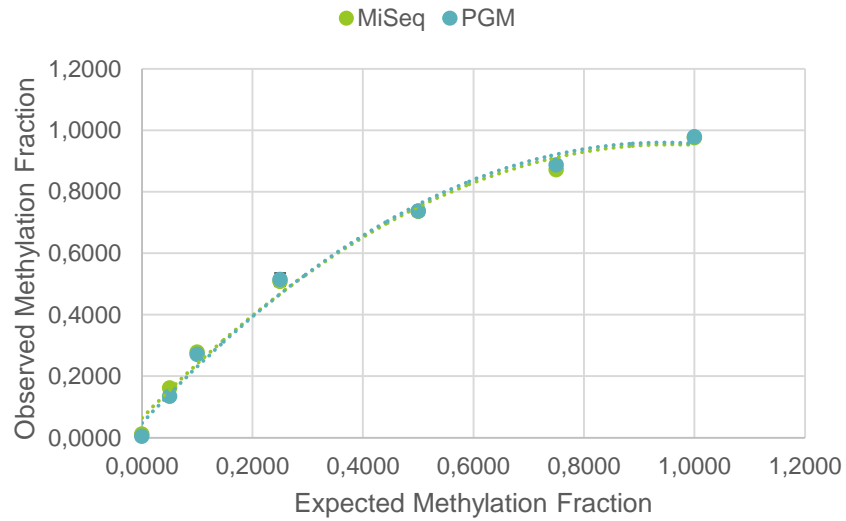
EDNAP EXERCISE

Part 1

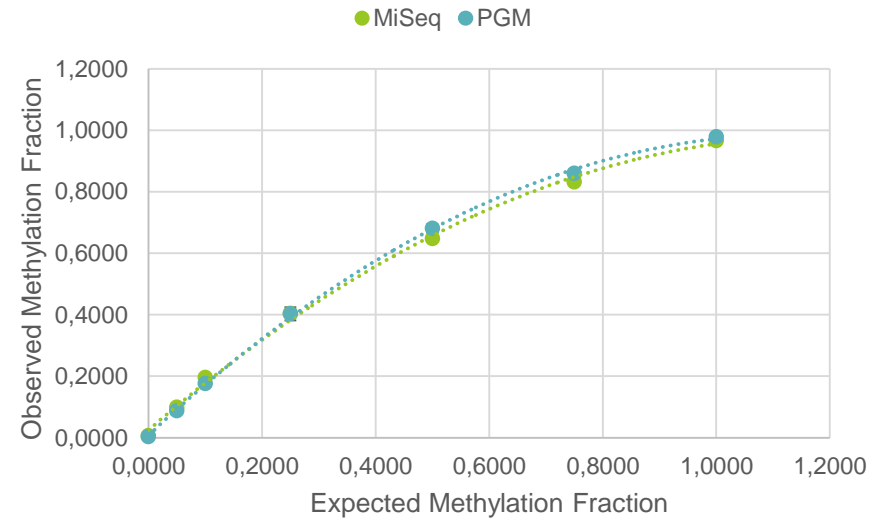
Part 1

- Results now received from 15 laboratories
 - 8 MiSeq only
 - 5 PGM only
 - 2 MiSeq and PGM
- 7 Methylation standards between 0-100% sent out to all labs

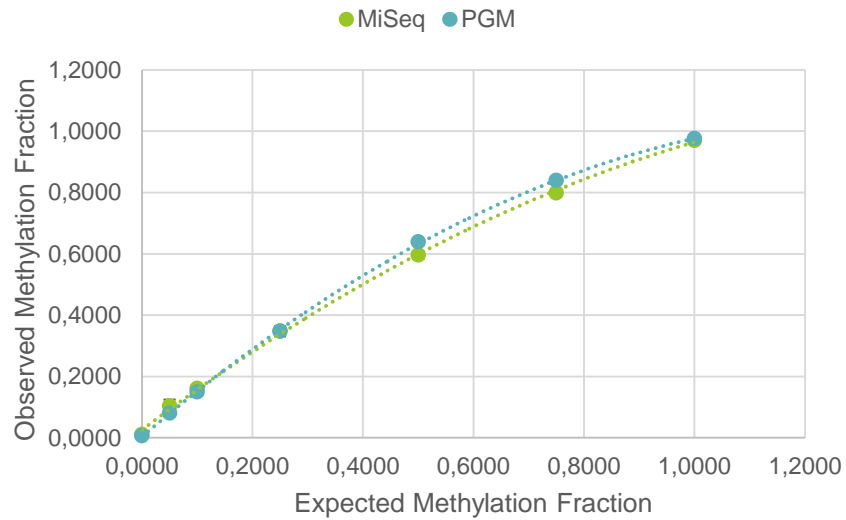
CpG 1



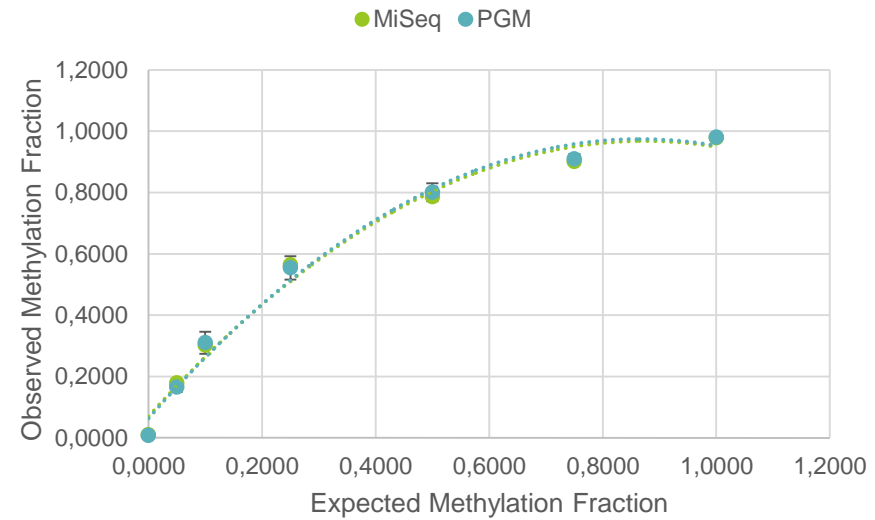
CpG 2



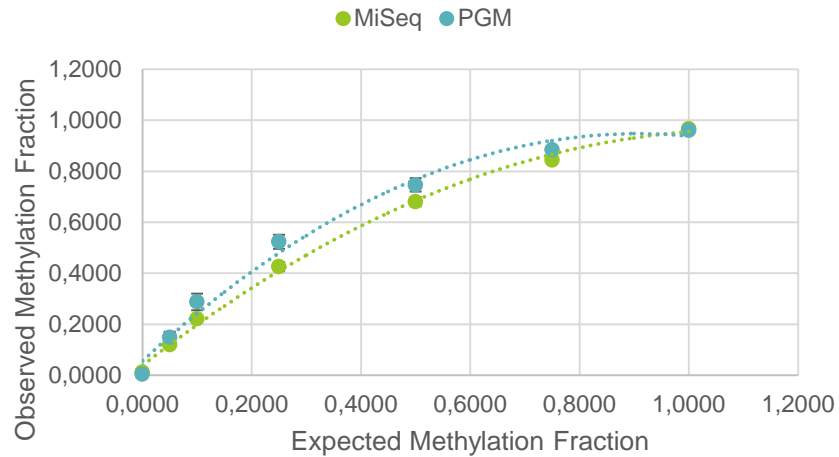
CpG 3



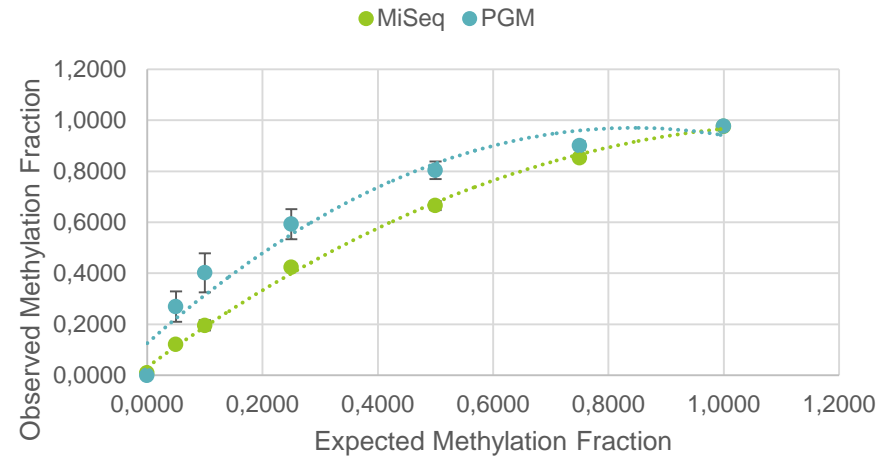
CpG 4



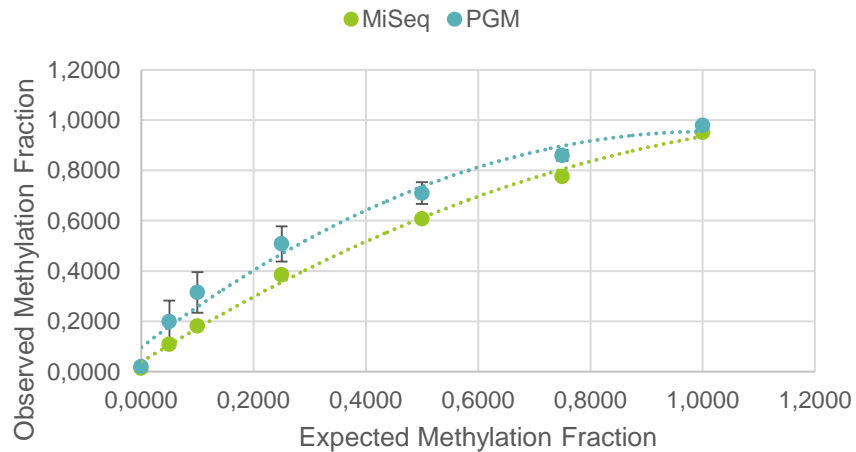
CpG 5



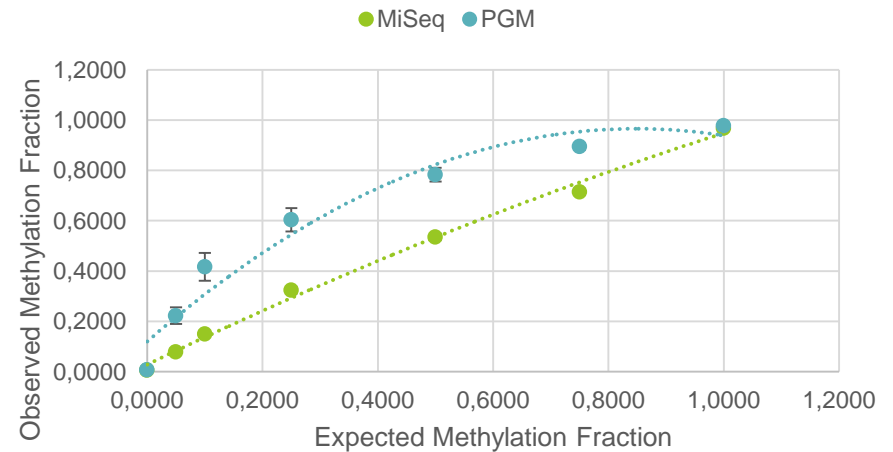
CpG 6



CpG 7



CpG 8



EDNAP EXERCISE

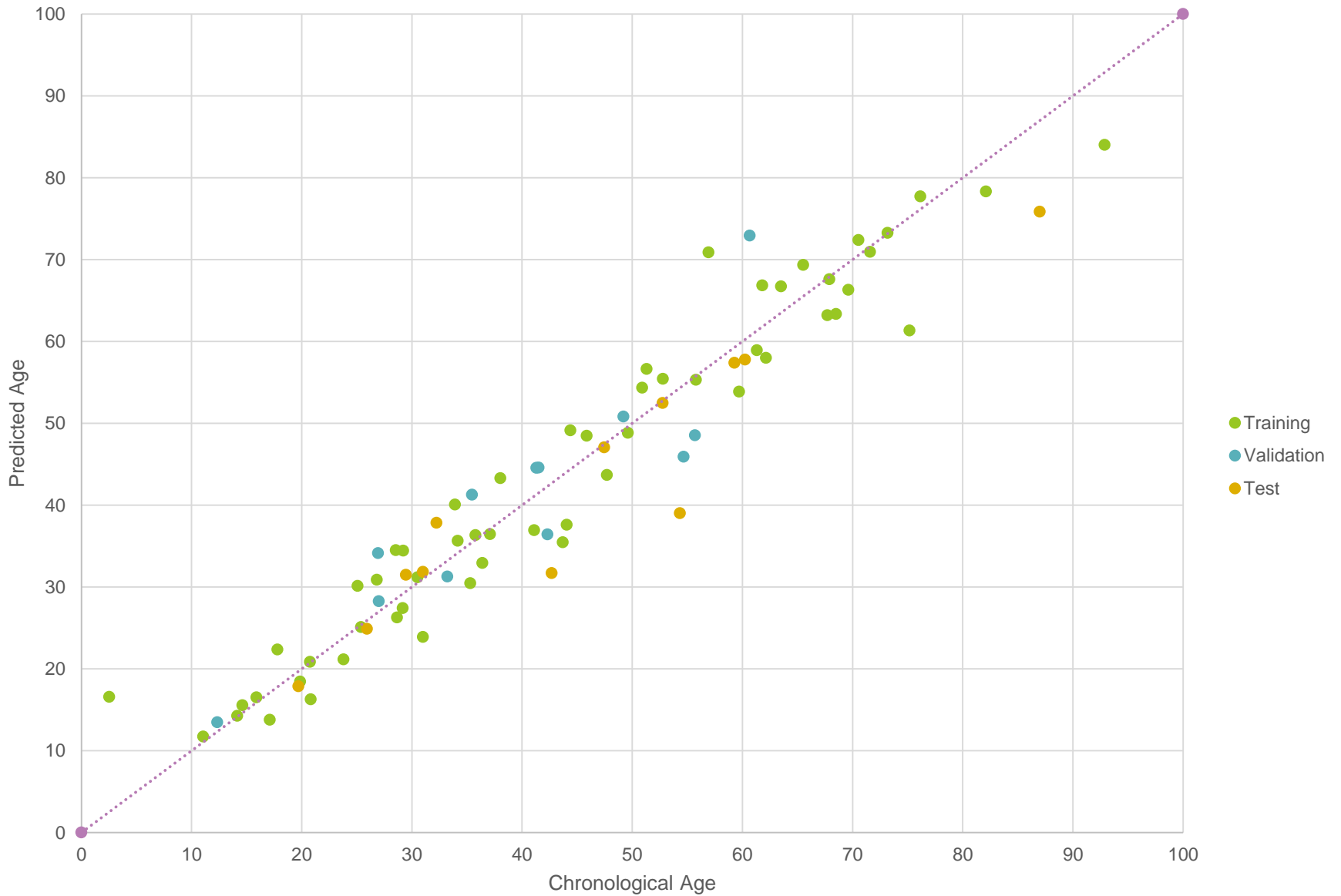
Part 2

Part 2

- Results now received from 12/15 laboratories
- Samples sent:
 - 7 blood stains
 - 2 methylation standards
- Also possible to analyse 3-6 samples unique to the laboratory

ANN Based Prediction Model

Methylation Age Predictions

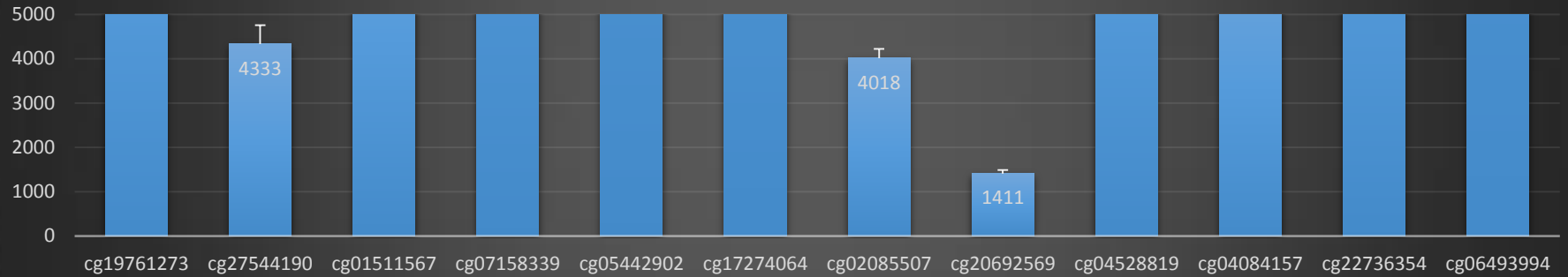


Stain D

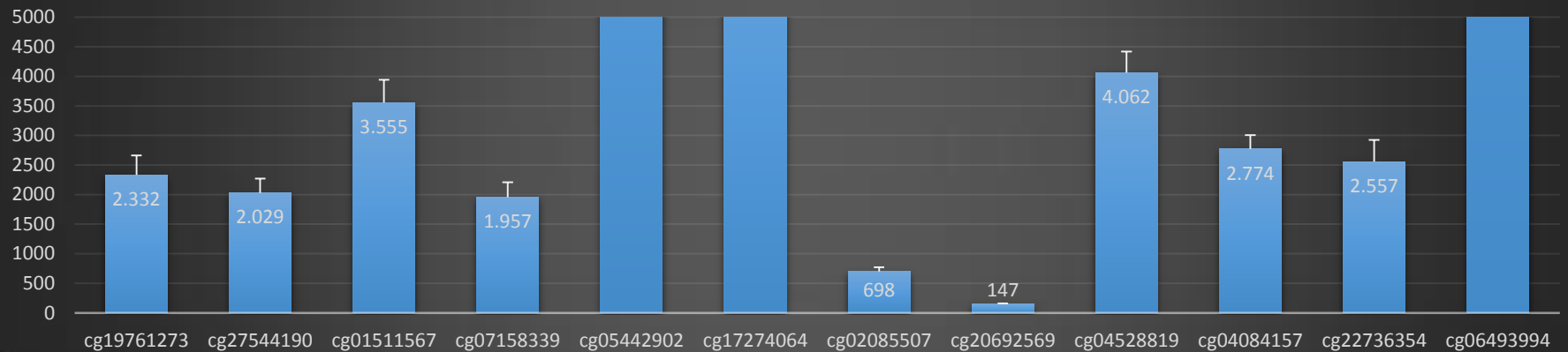
- Actual age 47
 - Prediction KCL – 48.8
 - MiSeq Lab 13 - 50.6
 - MiSeq Lab 14 - 49.55
 - MiSeq Lab 3 - 48.3
 - MiSeq Lab 10 - 47.5
 - MiSeq Lab 12 - 44.35

Lower read numbers lead to less accurate predictions

Average Reads – Lab 13



Average Reads – Lab 12



Stain D

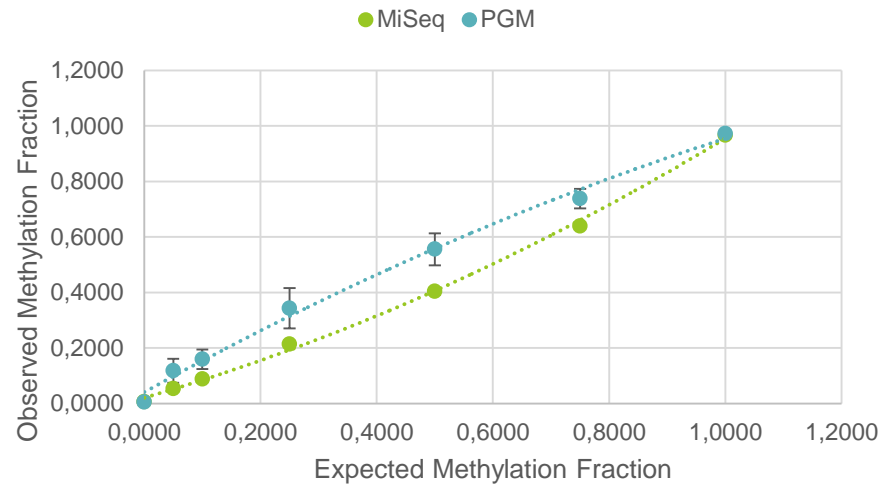
- Actual age 47
 - Prediction KCL – 48.8
 - MiSeq Lab 13 - 50.6
 - MiSeq Lab 14 - 49.55
 - MiSeq Lab 3 - 48.3
 - MiSeq Lab 10 - 47.5
 - MiSeq Lab 12 - 44.35
 - MiSeq Lab 11 - 42.2

Stain D

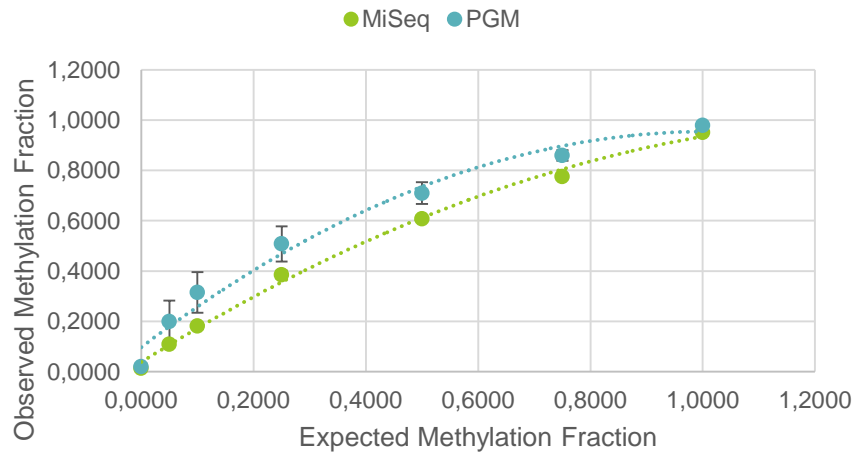
- Actual age 47
 - Prediction KCL – 48.8
 - PGM Lab 9 - 46.9 (48.6)

Normalisation of PGM values to MiSeq values

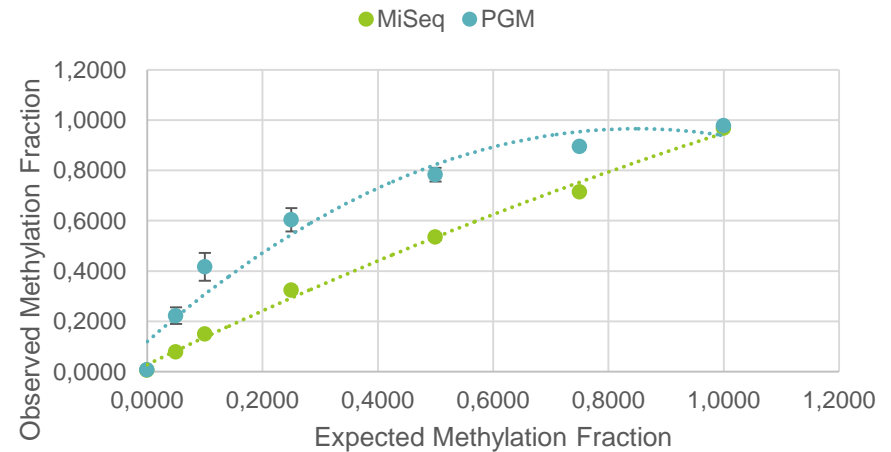
CpG 9



CpG 6



CpG 8

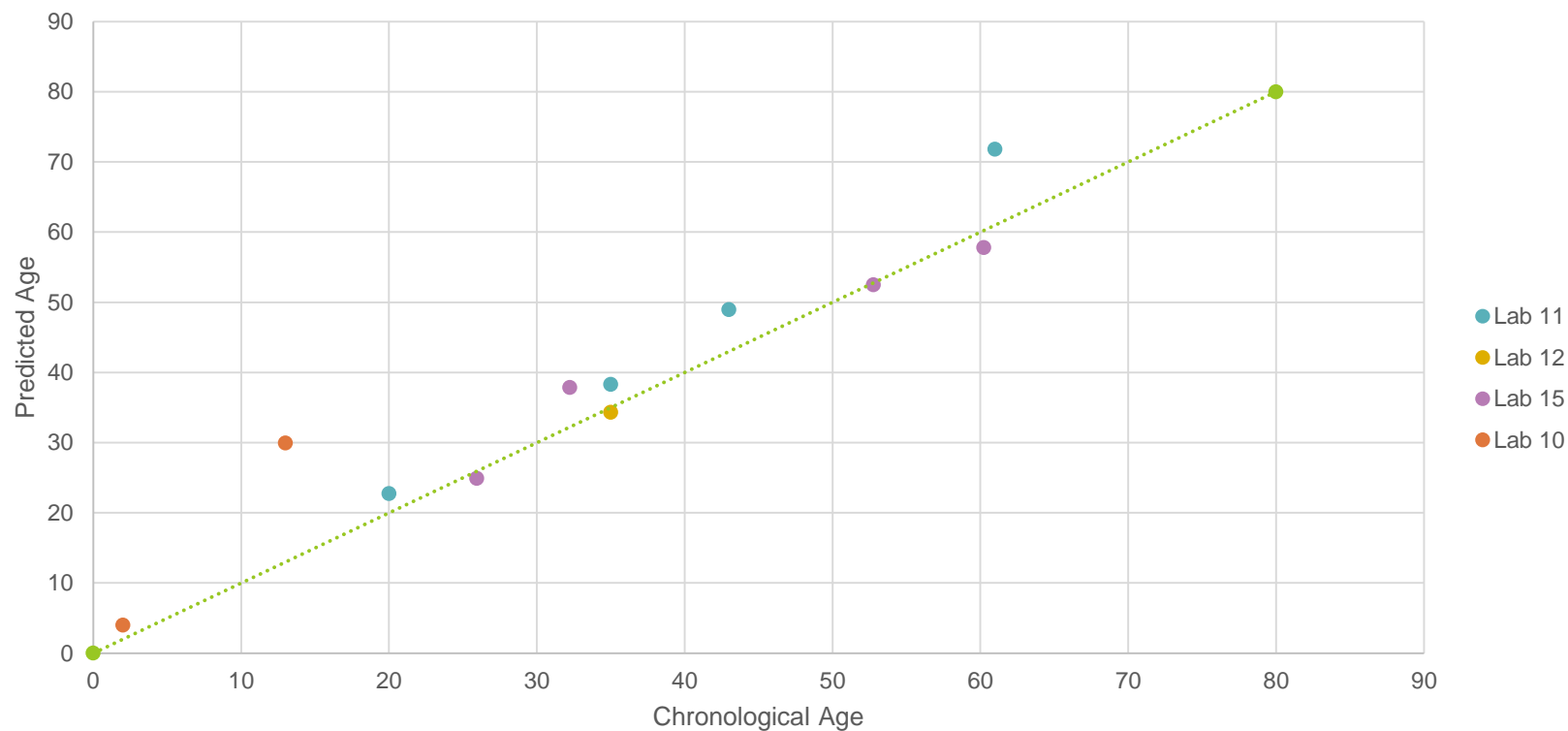


Stain D

- Actual age 47
 - Prediction KCL – 48.8
 - PGM Lab 9 - 46.9 (48.6)
 - PGM Lab 8 - 66.4 (47.6)
 - PGM Lab 16 - 55.35 (42.8)
 - PGM Lab 11 - 57.65 (33.8)
 - PGM Lab 2 - 50.15 (27.4)

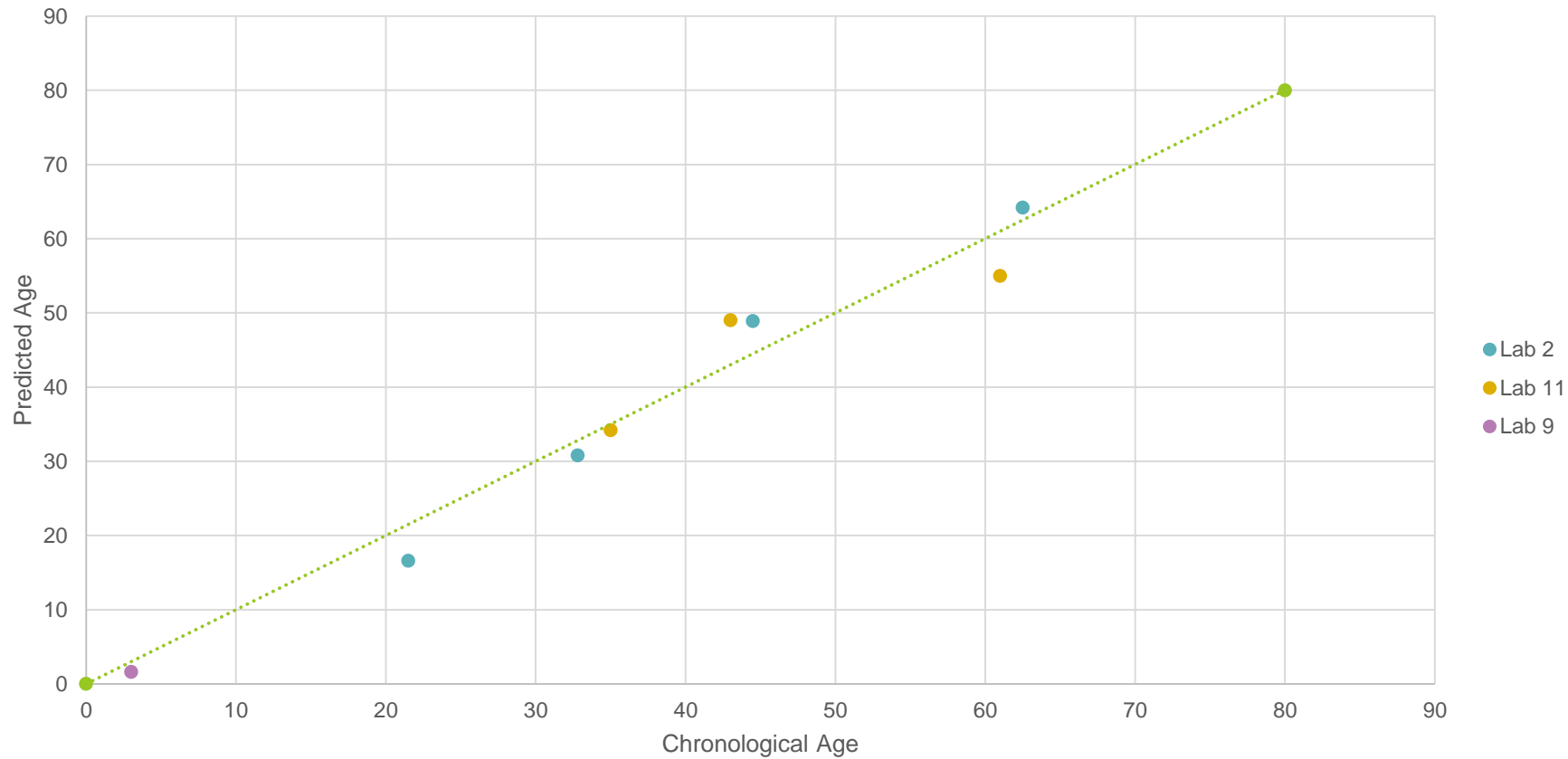
Blind age predictions of extra MiSeq results

MiSeq - Venus Blood



Blind age predictions of extra PGMresults


PGM - Venus Blood



Acknowledgments

- Anastasia Aliferi
- Athina Vidaki
- Denise Syndercome Court
- Leon Barron



A photograph of a grand staircase with a large stone statue of King Charles I in the foreground, seen from behind. The statue is wearing a long, flowing robe. In the background, another statue of a woman in classical attire stands near a doorway. The staircase has ornate balustrades with turned balusters.

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EUROFORGEN / EDNAP

mRNA NGS exercise 1

Assay for body fluid/tissue identification

Cordula Haas / Sabrina Ingold / Guro Dorum
Erin Hanson / Jack Ballantyne

8. November 2016, Rome

Association of a Body Fluid with a DNA Profile by Targeted RNA/DNA Deep Sequencing

Cordula Haas*, Sabrina Ingold*, Erin Hanson°, Jack Ballantyne°

*University of Zurich, °University of Central Florida

1. set up a targeted mRNA/miRNA NGS approach for body fluid/tissue identification
→ establish a probabilistic approach to call/predict the presence of a body fluid
2. select a set of SNPs for each body fluid/tissue, that discriminates individuals the most
→ assign a body fluid to a specific individual
3. combine the RNA analysis with gDNA STR sequencing, allowing simultaneous human individual identification and forensic tissue identification

1A. targeted mRNA NGS approach for body fluid/tissue identification (MiSeq)

- Illumina DesignStudio
- TruSeq Targeted RNA Custom Panel
- TruSeq Targeted RNA Index Kit
- Illumina MiSeq
- Bioinformatics pipeline
- 66 mRNA biomarkers evaluated
- TOP6: 33 biomarkers
- blood, semen, saliva, vaginal secretions, menstrual blood, skin

Body fluid/tissue	Gene Name	TOP1 30plex	TOP2 50plex	TOP3 55plex	TOP4 47plex	TOP5 38plex	TOP6 33plex
Blood	BD1						
	BD2						
	BD3						
	BD4						
	BD5						
	BD6						
	BD7						
	BD8						
	BD9						
	BD2 - cSNP						
Semen	SE1						
	SE2						
	SE3						
	SE4						
	SE5						
	SE6						
	SE7						
	SE7 - cSNP						
Saliva	SA1						
	SA2						
	SA3						
	SA4						
	SA5						
	SA6						
	SA7						
	SA8						
	SA9						
	SA10						
	SA11						
	SA12						
	SA13						
	SA14						
	SA15						
	SA16						
	SA17						
	SA18						
Vaginal	VS1						
	VS2						
	VS3						
	VS4						
	VS5						
	VS6						
	VS7						
	VS8						
	VS9						
	VS10						
Menstrual	MB1						
	MB2						
	MB3						
	MB4						
	MB5						
	MB6						
Skin	SK1						
	SK2						
	SK3						
	SK4						
	SK5						
	SK6						
	SK7						
	SK8						
	SK9						
	SK10						
	SK11						
	SK12						
	SK13						
Housekeeping	HKG1						
	HKG2						
	HKG3						

1B. targeted mRNA NGS approach for body fluid/tissue identification (PGM)

- Ion AmpliSeq Designer
- AmpliSeq RNA library preparation kits
- IonTorrent PGM
- Bioinformatics pipeline
- BFP0: same 33 mRNA biomarkers
- BFP3: 29 markers

Body fluid	Gene	BFP0 (33plex)	BFP1 (61plex)	BFP2 (37plex)	BFP3 (29plex)
Blood	B1				
	B2				
	B3				
	B4				
	B5				
	B6				
	B7				
	B8				
Semen	Se1				
	Se2				
	Se3				
	Se4				
	Se5				
	Se6				
	Se7				
Saliva	Sa1				
	Sa2				
	Sa3				
	Sa4				
	Sa5				
	Sa6				
	Sa7				
	Sa8				
	Sa9				
	Sa10				
	Sa11				
	Sa12				
	Sa13				
	Sa14				
	Sa15				
	Sa16				
	Sa17				
Vaginal	V1				
	V2				
	V3				
	V4				
	V5				
	V6				
	V7				
	V8				
	V9				
	V10				
	V11				
Menstrual Blood	M1				
	M2				
	M3				
	M4				
	M5				
	M6				
Skin	Sk1				
	Sk2				
	Sk3				
	Sk4				
	Sk5				
	Sk6				
	Sk7				
	Sk8				
	Sk9				
	Sk10				
	Sk11				
	Sk12				

targeted mRNA NGS approach for the identification of blood, saliva, semen, vaginal secretion, menstrual blood, skin

RNA extraction (manual or kit), DNase treatment, quantification

Protocols for PGM and MiSeq provided by UZH

Primerpools for PGM and MiSeq provided by UZH

Laboratories analysed 8/16 samples provided by UZH and 0/8 own body fluid samples

Results (BAM/FASTQ files) collected and evaluated by UZH

Participating laboratories:

Cellmark, UK	PGM	No data yet
Coimbra, Portugal	S5	
Cologne, Germany	PGM	Auckland, New Zealand
Copenhagen, Denmark	MiSeq	Glasgow, Scotland
Innsbruck, Austria	MiSeq	Münster, Germany
Krakow, Poland	PGM	Santiago de Compostela, Spain
London, UK	MiSeq	
Lyon, France	FGx	
NFI, Netherlands	FGx	
NIPH, Oslo	PGM	
NIST, USA	MiSeq	
Orlando, Florida, USA	MiSeq/S5	
Rome, Italy	FGx	
Rotterdam, Netherlands	PGM	
Zurich, Switzerland	MiSeq/PGM	

Collaborative exercise mRNA NGS part 1

Provided stains:

single stains

stain number	MiSeq/FGx	PGM/S5
11	blood on swab	
12	blood on swab	blood on swab
13	blood on cotton pad	
14	blood on cotton pad	
15	saliva on swab	saliva on swab
16	buccal swab	buccal swab
17	semen on swab	semen on swab
18	semen on swab	
19	vaginal secretion on swab	vaginal secretion on swab
20	menstrual blood on swab	
21	menstrual blood on swab	menstrual blood on swab
22/23	skin swab	skin swab

mixed stains

stain number	MiSeq/FGx		PGM/S5	
24	vaginal	semen	vaginal	semen
25	blood	saliva		
26	menstrual	semen		
27/28	skin swab	saliva		

Summary Questionnaire

- Delivery time Fedex (samples+primers): 17 labs within 1-4 days (max: 16 days to Italy)
- 2 labs: primers were not immediately stored at -20°C (1-3 weeks at room temp)
- 4x manual RNA extraction (recommended), 11x RNA extraction kit (Rneasy, EZ1 RNA Universal Tissue Kit, mirVana)
- 11x RNA quantification (Qubit, RiboGreen, Nanodrop, Quantus)
- RT (Illumina): 7x ProtoScript II Reverse Transcriptase, 2x others (Retroscript, RT2 First Strand Kit)
RT (PGM): included in library kit

Collaborative exercise mRNA NGS part 1

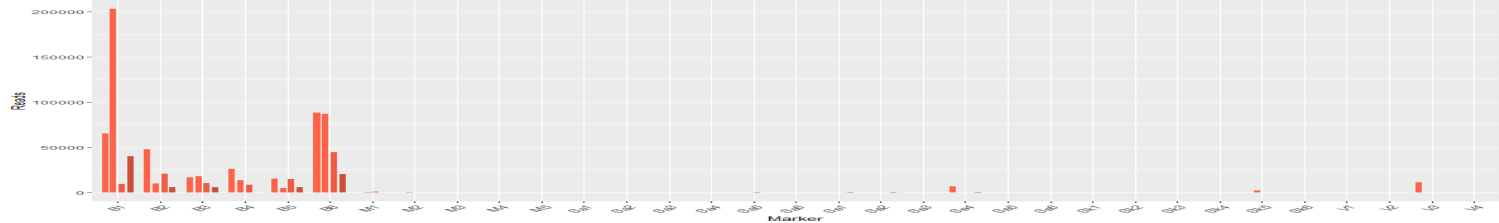
Results:

RNA quants

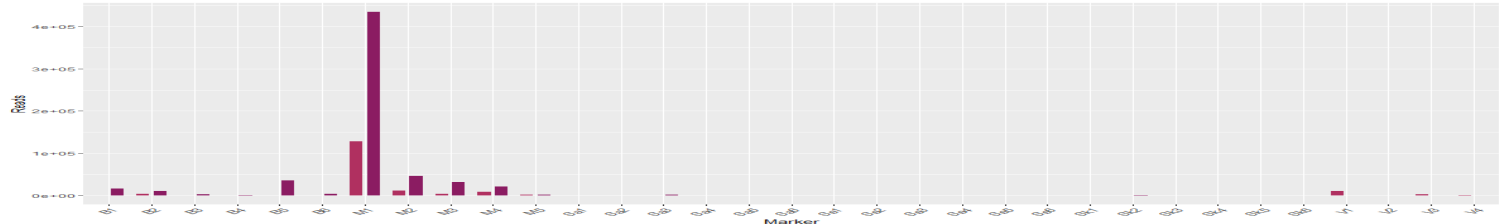
	extr method	quant method	s11	s12	s13	s14	s15	s16	s17	s18	s19	s20	s21	s 22/23	s24	s25	s26	s 27/28
Lab_1	Kit	Qubit	undet	undet	undet	undet	16.5	24.6	4	undet	23.2	71	29.4	undet	128	6.1	31.4	undet
Lab_2	Kit	Qubit	undet	undet	undet	undet	2.63	3.05	undet	undet	2.3	undet	4.76	undet	20.5	undet	11.5	undet
Lab_3	Kit	Nanodrop	3.8	4	2.2	2.1	30.1	130.4	15.4	3.9	62.2	86.9	39.6	2.7	127.2	10.9	30.1	7.2
Lab_4	Kit	Qubit	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Lab_5	Kit	Qubit	<0.5	0.81	1.04	0.76	4.44	15.2	2.17	1.22	9.19	44.6	9.63	0.5	>60	0.69	51	0.87
Lab_6	manual	Quantus	29.35	34.6	43.3	57.25	26.9	190	24	61	259.5	234.5	69.6	11	377.5	74.85	212.5	36.9
Lab_7	manual	Quant-iT RiboGreen	23	25.2	64.3	79.9	18	119	33.7	68.2	334.8	471.3	44.7	undet	525	50	392.4	16.6
Lab_8	Kit	no quant	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Lab_9	Kit	Qubit	undet	undet	undet	undet	10	10	undet	undet	3.3	9.7	2.7	undet	32	undet	21.5	undet
Lab_10	Kit	no quant		-			-	-	-		-		-	-	-			
Lab_11	Kit	no quant		-			-	-	-		-		-	-	-			
Lab_12	Kit	Qubit/ Nanodrop*		4.8			5.5	8	3.8*		11.6		4.4	4.7*	9.6			
Lab_13	Kit	Qubit		undet			undet	56	undet		12.9		9.02	undet	54.8			
Lab_14	manual	Qubit		16.2			8.2	15.6	5.6		65		39.3	2.4	129			
Lab_15	manual	Nanodrop		117.7			223	143.7	107.7		436		107.7	66.25	477.4			

Results Illumina MiSeq / FGx

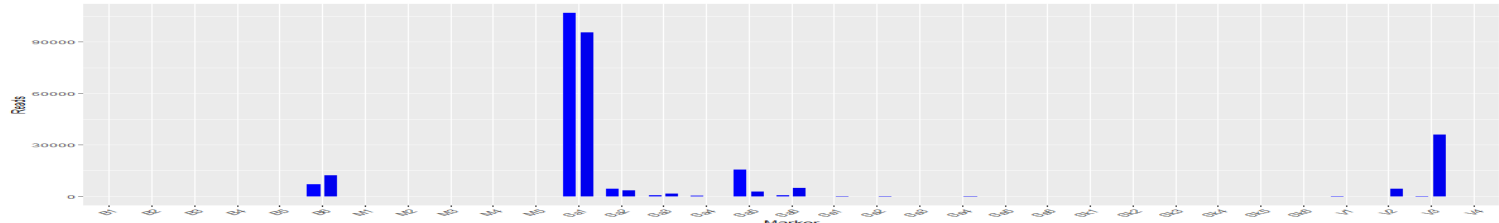
Blood
(n=4)



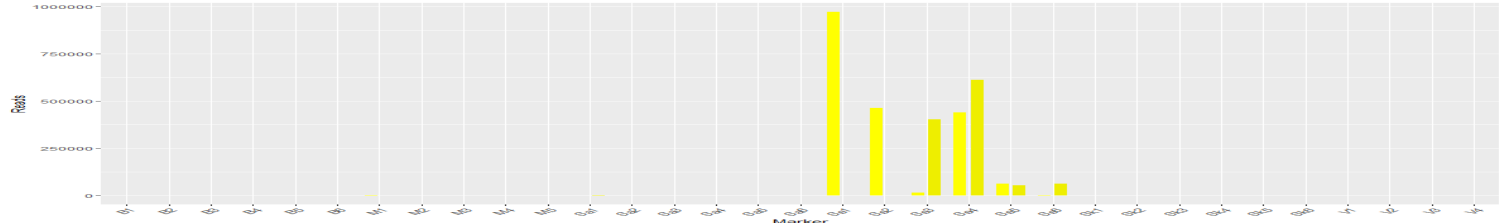
Menstrual
blood
(n=2)



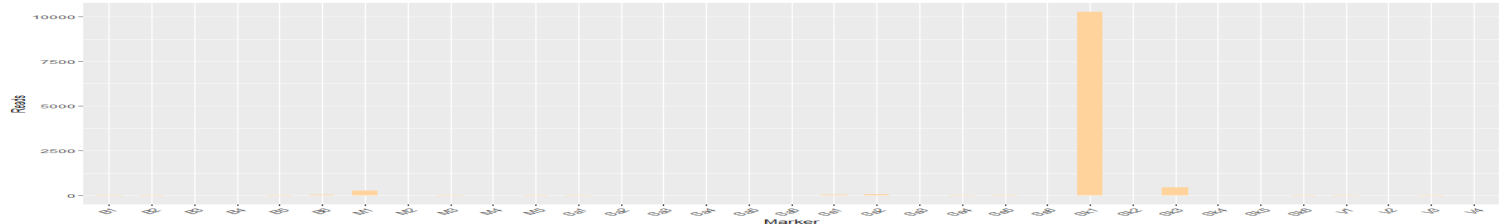
Saliva
(n=2)



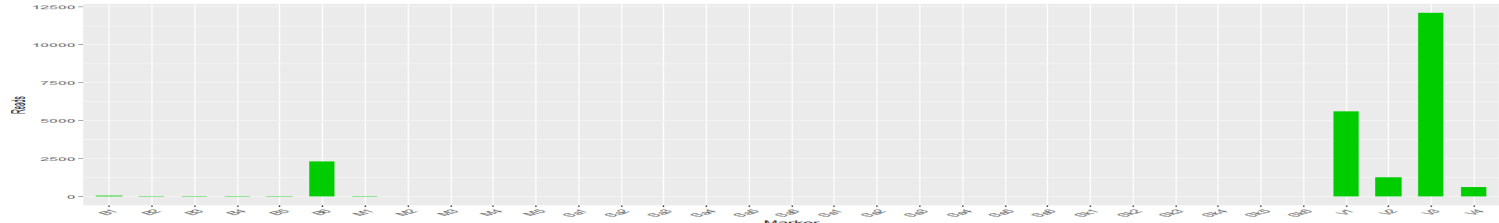
Semen
(n=2)



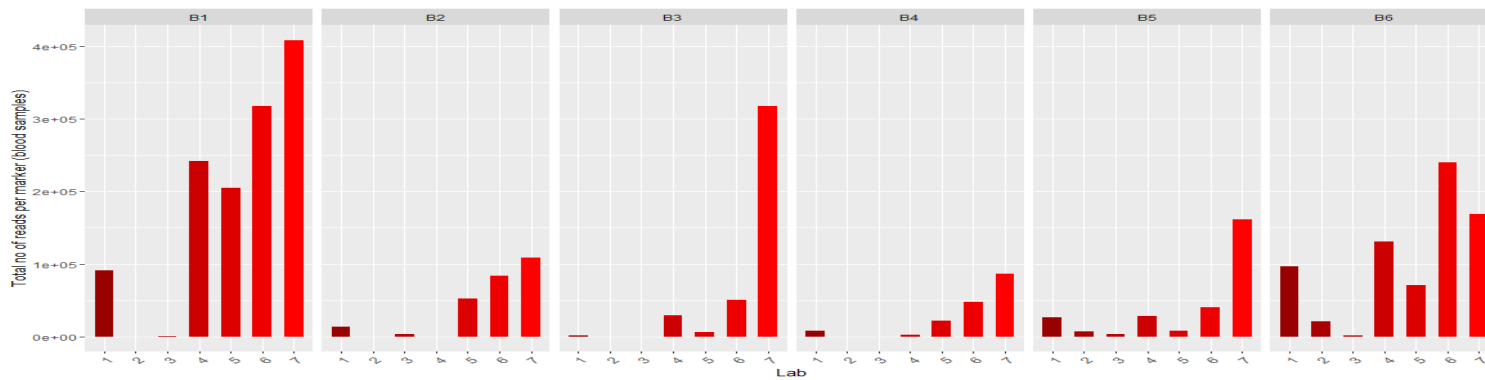
Skin
(n=1)



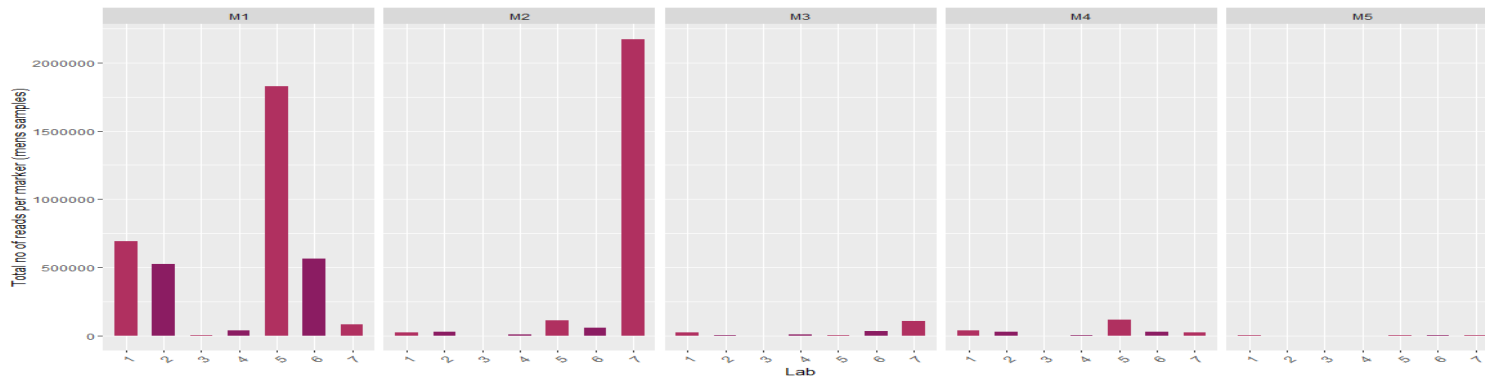
Vaginal
secretion
(n=1)



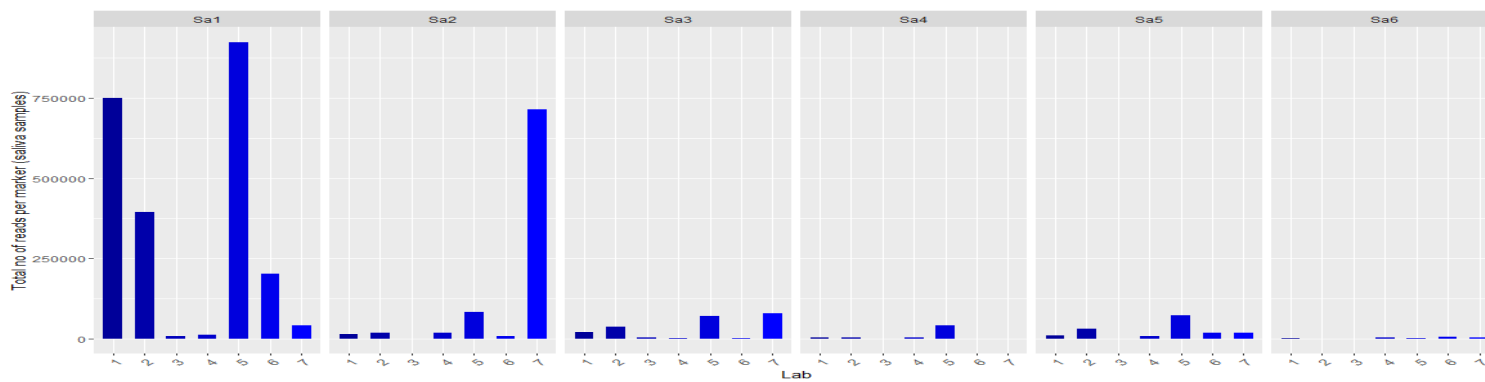
Blood
(n=4)



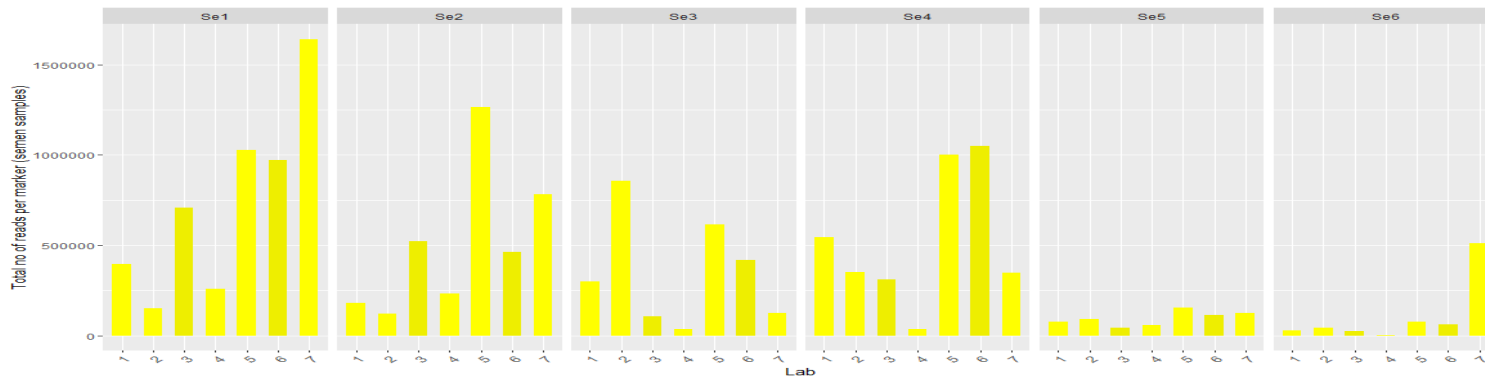
Menstrual
blood
(n=2)



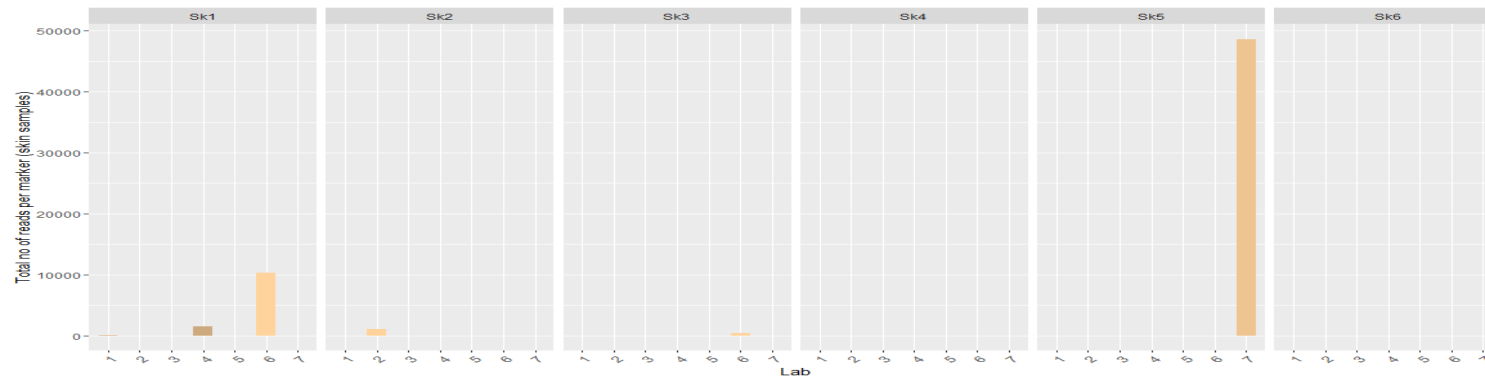
Saliva
(n=2)



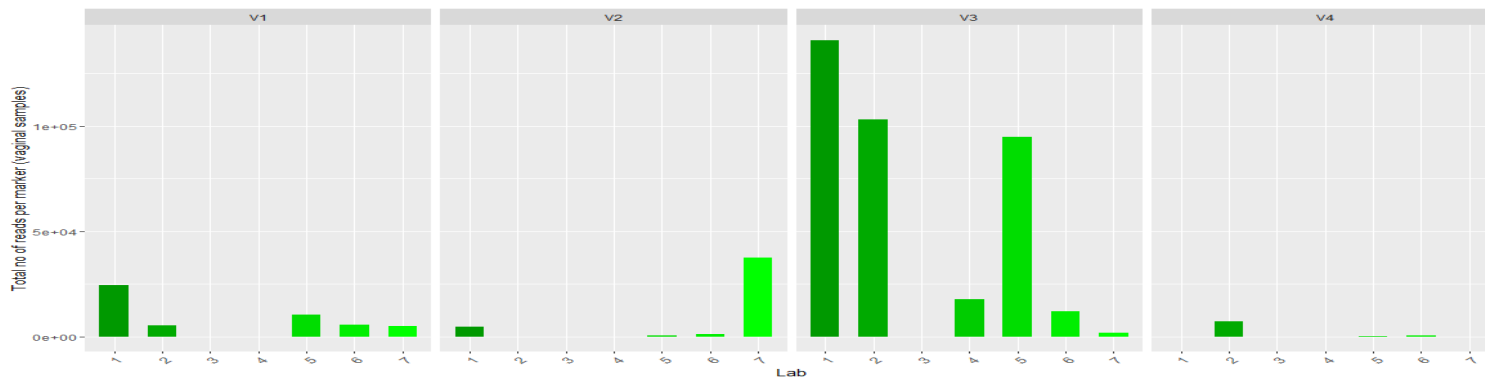
Semen
(n=2)

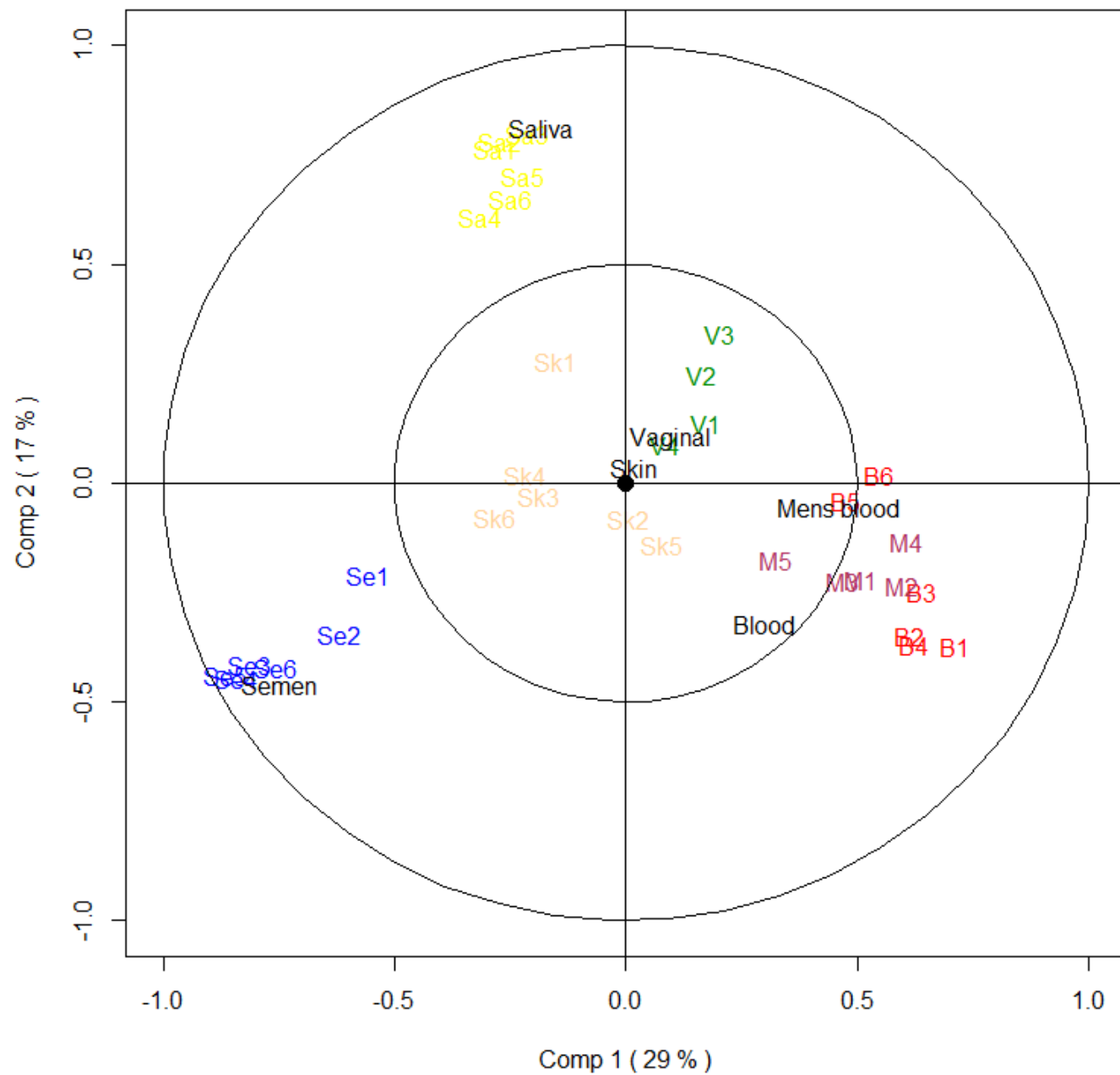


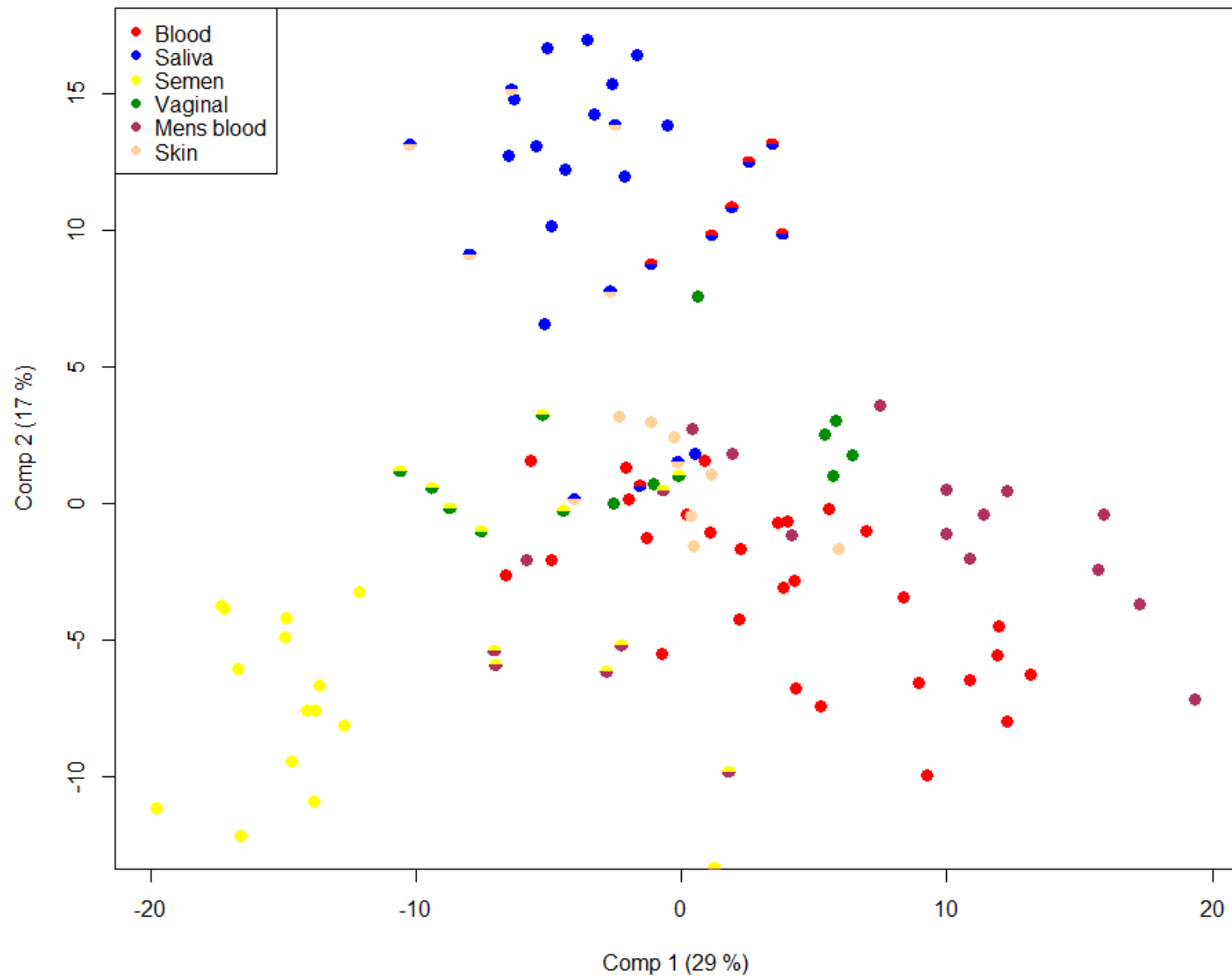
Skin
(n=1)



Vaginal
secretion
(n=1)

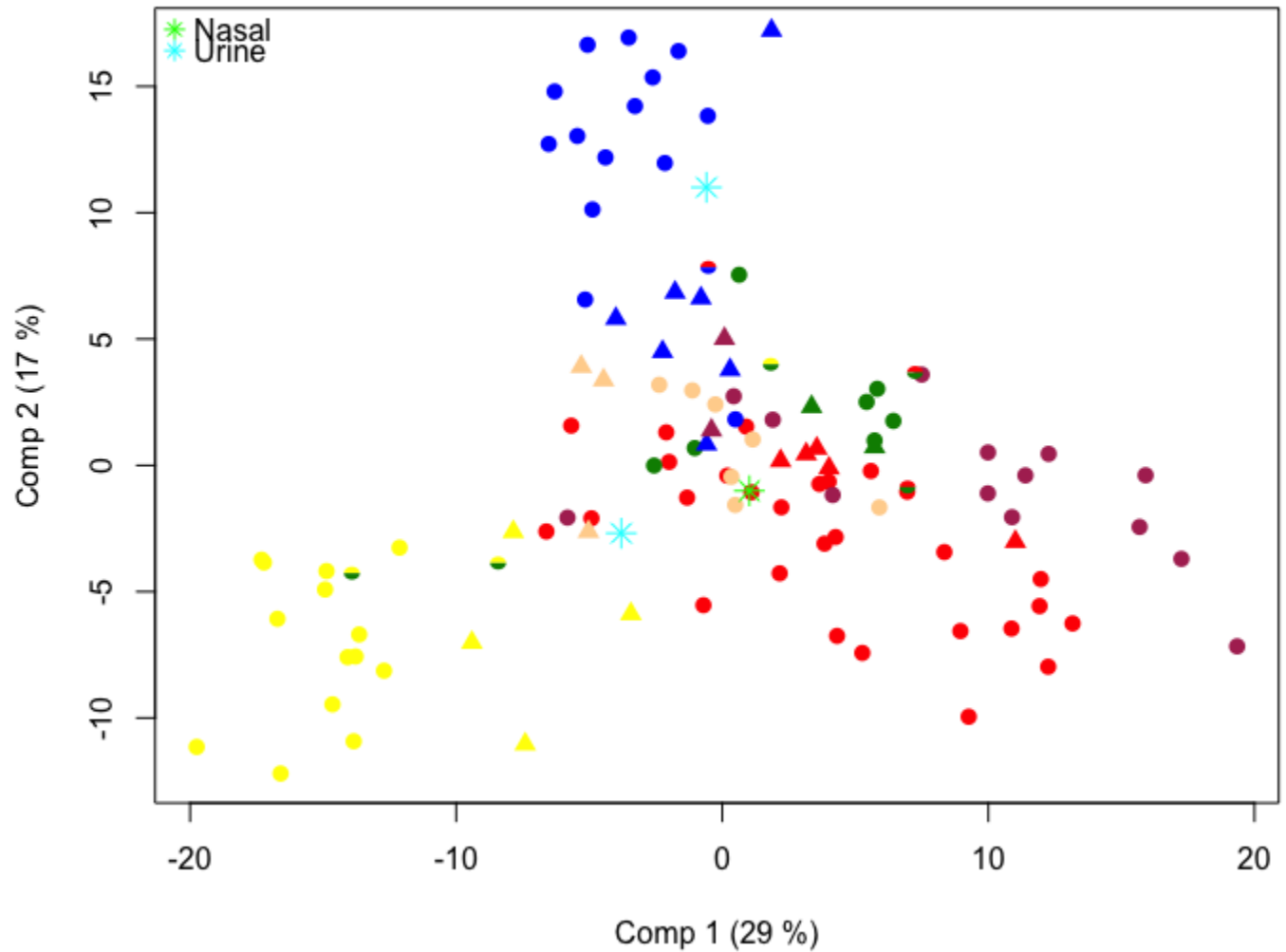






5x blood
2x mens
7x saliva
4x semen
3x skin
2x vag
1x nasal
2x urine

4x vag/semen
1x vag/blood
1x blood/saliva

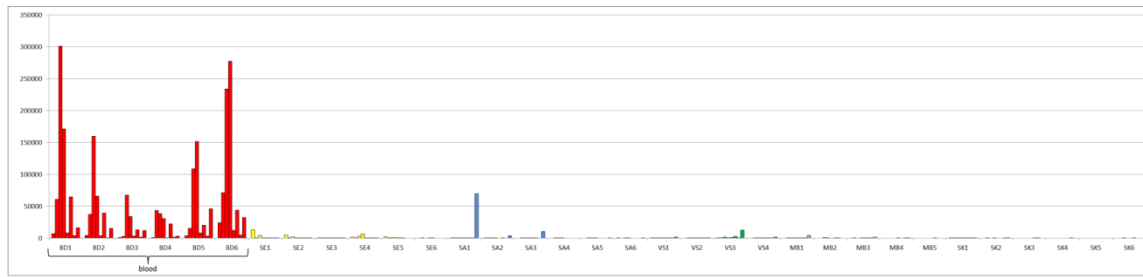


Results IonTorrent PGM / S5

→ not analyzed yet...

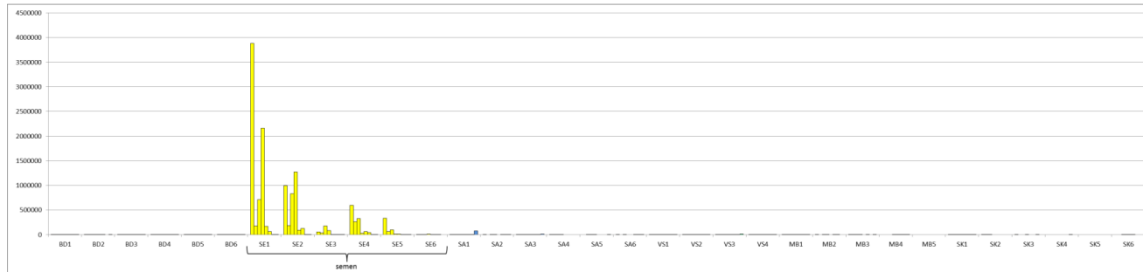


Blood
(n=8)

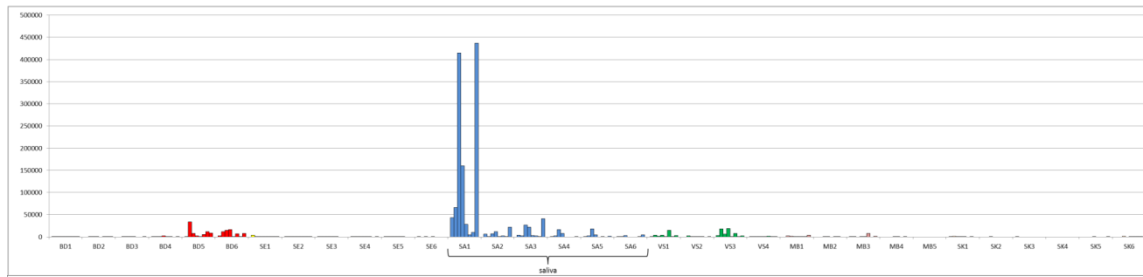


Illumina
MiSeq

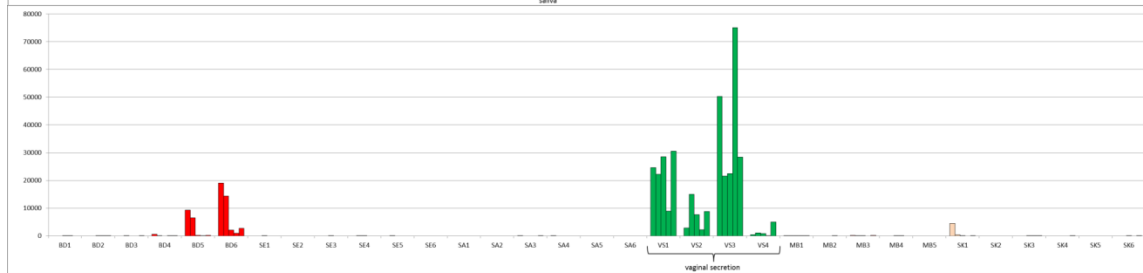
Semen
(n=8)



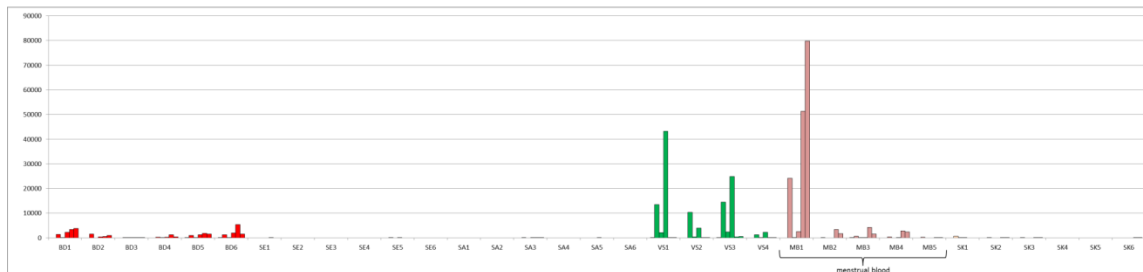
Saliva
(n=8)



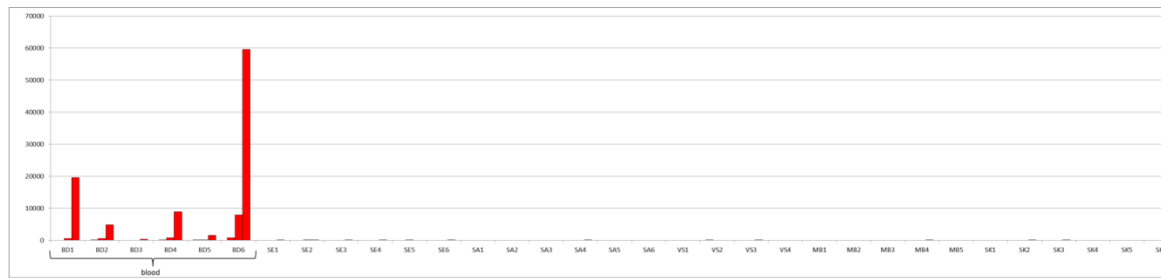
Vaginal
secretion
(n=8)



Menstrual
blood
(n=8)

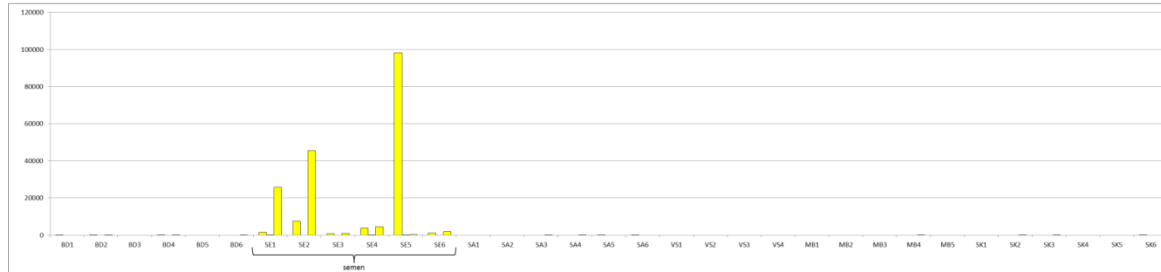


Blood
(n=3)

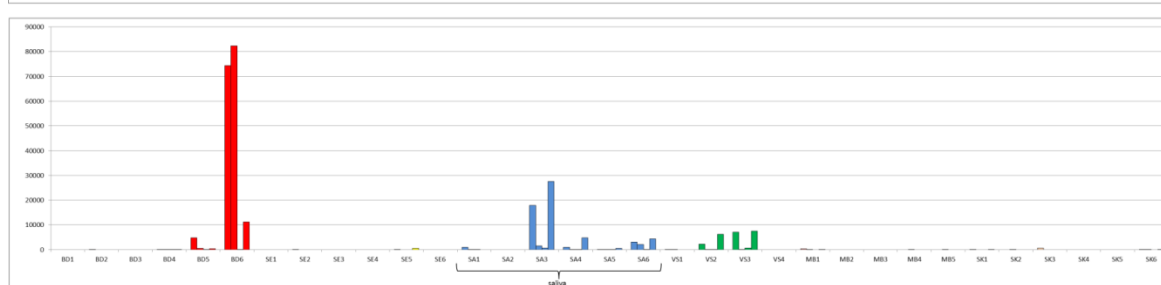


IonTorrent
PGM

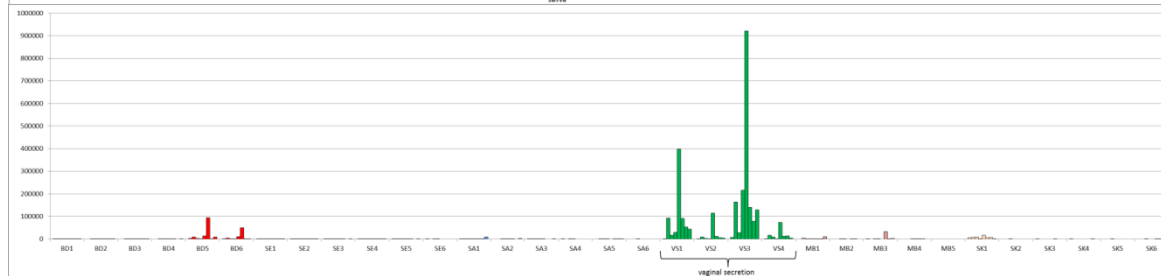
Semen
(n=3)



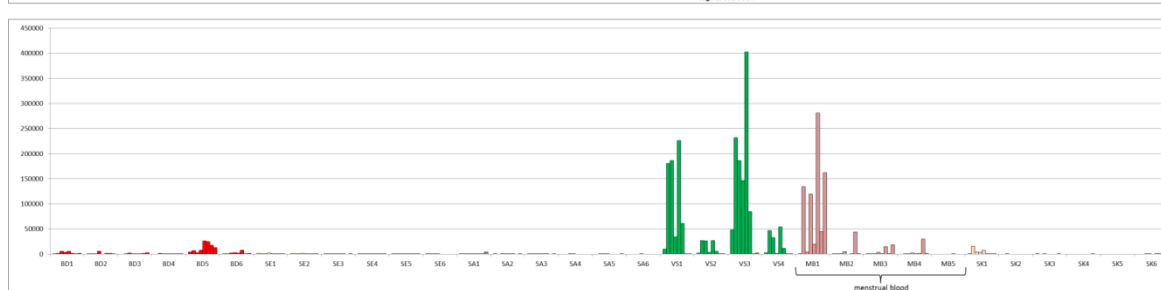
Saliva
(n=4)



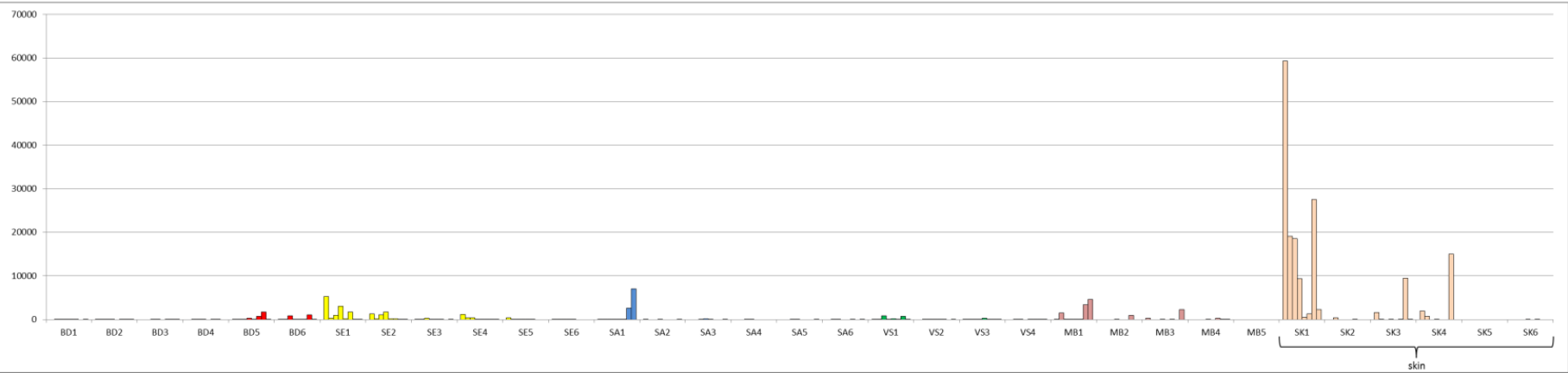
Vaginal
secretion
(n=5)



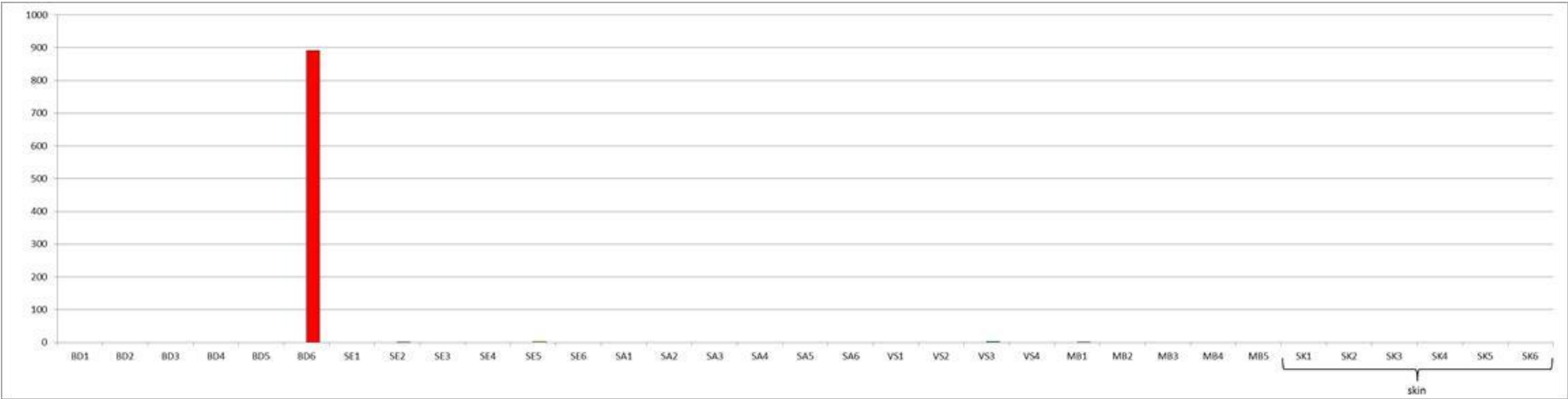
Menstrual
blood
(n=6)



Illumina MiSeq
 Skin (n=8)



IonTorrent PGM
 Skin (n=2)



Technical challenges:

- no target region / manifest-files provided
- plan run / sequencing mode

Conclusion:

- 7/9 MiSeq labs successfully implemented the mRNA NGS approach
- MiSeq-assay satisfying, PGM-assay needs some optimization
- PGM protocol is more lab-work
- manual RNA-extraction!

2. Body fluid/tissue specific SNPs

→ associate specific mRNA transcripts to an individual (on mRNA)

- 35 cSNPs
- Illumina MiSeq (and IonTorrent PGM)

→ estimate RNA-SNP allele frequency by testing of population samples (on DNA)

- 35 cSNPs
- Illumina MiSeq (and IonTorrent PGM)

- 11/2016 Presentation of results of Collaborative exercise, part 1 (mRNA)
- 04/2017 Submission of a manuscript on part 1
- 04/2017 Suggestion for Collaborative exercise, part 2 (cSNPs)
- 06/2017 Shipment of samples, primers, protocols
- 10/2017 Submission of results

Thanks for participating!

EUROFORGEN-NoE Update: EDNAP Meeting Rome 2016

Peter M. Schneider
Institute of Legal Medicine
University of Cologne (Germany)

Overview on recent activities

- **Conferences**
 - EUROFORGEN Conference in Venice
 - Security Research and Innovation (SRIE) in The Hague
- **Dissemination activities**
 - A new guide explaining our science
- **The Training Academy**
 - For online learning
- **The end of funding ... but not of EUROFORGEN**
 - Sustaining the network structures

EUROFORGEN Conference Venice 2016

International Dissemination Conference - “Forensic DNA analysis in the light of the new security needs”

The European Forensic Genetics Network of Excellence - EUROFORGEN-NoE - held its International Dissemination Conference “Forensic DNA analysis in the light of the new security needs” on **23rd June 2016 in Venice**, in connection with the **Intersocietal Symposium of the International Academy of Legal Medicine (IALM)**.



ISSUE 3/2016

NEWSLETTER
European Forensic Genetics
Network of Excellence



Dear colleagues,

On June 23rd 2016, the EUROFORGEN Network of Excellence has held the International Dissemination Conference “Forensic DNA analysis in the light of the new security needs” in Venice, Italy, in connection with the Intersocietal Symposium of the International Academy of Legal Medicine (IALM). Experts from science, social studies and law joined a number of consortium speakers to discuss current challenges and perspectives in forensic genetics. With this newsletter we would like to inform you about the major topics addressed and discussed in three sessions and a round table.

Welcome Address

The coordinator of the EUROFORGEN network, Peter M. Schneider (Institute of Legal Medicine, University of Cologne) welcomed the conference speakers and about 100 participants from all over Europe. He presented an overview about the research and networking activities carried out within the EU-funded project. In addition to an array of molecular genetic research activities, such as human body fluid and tissue identification in crime scene samples using mRNA/miRNA typing and methylation analysis, prediction of biogeographic ancestry using a newly developed “Global AIMs” genotyping panel, as well as hair morphology features using massively parallel sequencing, and new software for STR system validation as well as advanced mixture interpretation methods, he pointed out numerous other successful activities carried out during the five year funding period 2012-2016. These include:

- the establishment of a network of more than 200 European forensic laboratories and organizations forming the “European Virtual Institute of Research in Forensic Genetics”, with a central website offering

privileged access to publications and educational resources,

- an ongoing short term fellowship program to support lab exchange visits among all network participants,
- a series of three very popular “Train the Trainers” workshops in Copenhagen addressing the most recent progress in forensic biostatistics, and resulting in more than 20 subsequent satellite training workshops at the local level across Europe,
- support for organizing several training workshops on DNA interpretation methods for members of police organizations by the European Police College (CEPOL) in Avila, Spain,
- additional research addressing ethical and legal aspects and the societal dimension of forensic genetics, leading to several in depth publications openly available from the EUROFORGEN homepage.

P. Schneider encouraged all attending colleagues to join the network and to contribute to the research activities. He also announced the EUROFORGEN network structures will be maintained beyond the end of EC funding to serve as an information platform about research and education, as well as to offer additional training opportunities for the forensic genetics community.



Speakers M. Wienroth, E. Murphy, P. Schneider, S. Chu (left to right)

Session I: FROM CRIME SCENE TO COURT ROOM – addressing evidence challenges and advanced interpretation methods, and the interpretation debate on miscarriages of justice

The first invited speaker was John M. Butler (National Institute of Standards and Technology, Gaithersburg, MD, USA), one of the best known scientists in the field, to discuss “Challenges in Forensic Genetics”. He is the author of a series of most popular textbooks covering all aspects on the use of DNA analysis in the forensic context. In spite of the high marks given to nuclear DNA analysis by the 2009 landmark report from the U.S. National Academy of Sciences

- **Panel Discussion on Forensics**

- CHAIR: Michele Socco (DG Home, EC)
- Arie Ijzerman (Chair of the COSI)
 - COSI = Standing Committee on Internal Security
- Jan de Kinder (Chair of ENFSI)
- Dominique Saint-Dizier (Head, Institute of Criminalistics, France)
- Peter M. Schneider (Coordinator EUROFORGEN-NoE)



Security Research & Innovation Event 2016
powered by The Hague Security Delta

1 & 2 June 2016
The Hague, The Netherlands

About | Conference

What are the challenges today and tomorrow?

Challenges exist at several levels:

- the **crime scene** with forensic evidence
- the adequate **interpretation of evidence**
- searching integrated forensic databases (such as DNA)
 - **Lack of transnational, powerful interconnected database systems**
- acceptance of **new technologies** in society and legislation
- the **diversity of legal systems** across Europe

For the time being, the challenges of today will stay with us until tomorrow, as there is a constant **stream of technological innovation** suitable for **forensic casework**, searching **missing persons**, and identifying **victims of disaster and war**.

What are the answers?

There is a **lack of high level scientific and technological research** in particular in the field of new forensic genetic applications such as:

- reliable and validated **prediction of externally visible characteristics** beyond pigmentation, age prediction and ancestry,
- the transition from standard DNA analysis to sequence-based typing using **Massively Parallel Sequencing (MPS)** for DNA Databasing, Missing Persons and Disaster Victim identification (DVI),
 - **highly focused optimization of platforms, DNA targets, and work flow tailored for specific applications,**
- the early assessment of **direct DNA sequencing** using long read single molecule sequencing,

What are the answers?

- transition / extension of **National DNA Databases** to accept MPS-based DNA data,
 - providing suitable **training for casework analysts** to understand the scope of new technologies and probabilistic genotyping for **adequate courtroom presentation**,
 - ensuring **genetic privacy** by using smart filtering of the accumulated data
 - **due to considerable heterogeneity regarding the acceptance of genotyping in various legal systems across Europe**,
- ... as a prerequisite for the development and introduction of reliable forensic tests and applications, and for obtaining acceptance of these advanced typing technologies in by **legislators**, in the **courtroom** and by **society**.

What is the role for the EU?

Real progress requires **activities at all levels**, and including all players

in the forensic arena:

- **EFSA 2020** serving as framework and reference for all activities
- **Horizon 2020** focusing on funding high level basic and applied research projects aiming to achieve real scientific progress (to avoid falling behind the US NIJ level of funding)
- **ISF** supporting the practical implementation of new forensic technologies at the practical casework level
- **CEPOL, EJTN, Europol, Eurojust** establishing a cross cutting training network involving academic professionals, as well as all stake holders and end users
- **Other EC funding** providing support for ethical, legal and societal research to understand public concerns and the political processes required for adopting new legislation

What is the role for the EU?

- **EU legislative initiatives:** Priorization of centralized resources and operational systems whenever possible to address current limitations relating to separate national jurisdictions and legal systems.
 - Support and promotion of mechanisms for cross border data exchange anchored in appropriate policies and data protection.
 - Establish policy mechanisms and fund operation of forensic elimination databases.
- **Strengthening human rights applications** of forensic investigations to give visibility and effect to benefits derived from effective workflows **safeguarding the rule of law and human rights**.

The “wish list”

- Involve relevant **advisors from all fields of expertise** in forensics for drafting topics for new calls in H2020:
 - academic researchers, police investigators & scientists, technology developers, legal experts, social scientists
- Consider a more prominent role for the **ICMP (International Commission of Missing Persons)** as a high-profile collaborating international institution based in Europe, to strengthen the **expertise in the forensic arena** and serve as a **protected data repository** able to bridge gaps in operational data exchange.



„Making Sense of Forensic Genetics“ Guide

- **Collaboration with the non-profit charity „Sense about Science“**
- **Production of brochure and a series of media and public relation events for launch**
- **To address public misconceptions and explain the basics**



Who we are What we are doing Campaigns & news



<http://senseaboutscience.org/>

Sense about Science is an independent campaigning charity that challenges the misrepresentation of science and evidence in public life. We advocate openness and honesty about research findings, and work to ensure the public interest in sound science and evidence is recognised in public discussion and policy making.

The EUROFORGEN Online Training Academy:

- **Online lectures on basic and advanced topics in forensic genetics**
- **WEBEX-based interactive presentations with Q & A session**
- **Participants need to register and can obtain a certificate for successful participation, after submitting their answers to a web-based questionnaire**
- **Presentations will be recorded for individual viewing accessible to members of the “Virtual Institute”**
- **At least 3 lectures this year, more lectures scheduled for 2017**

WP5: Education, Training and Career Development



GO

About EUROFORGEN-NoE

The Group

The Project

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[Online resources](#)

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Course

Course title	WEBINAR: Relationship Inference with Familias
Subject	The aim of this webinar is to educate/train DNA experts in statistical methods of relationship testing as well as the new development on the Familias software
Institute	EUROFORGEN-NoE
Country	Online
Timeperiod	09.11.2016
Month	4
Email Address	@ euroforgen-webinars(at)eurtd.com
Homepage address	http://www.euroforgen.eu/webinar-registration/



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Newsletter (3/2016)



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The Virtual Institute of Research for Forensic Genetics



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European landscape in forensic genetics

Directory of Forensic Genetic Research Laboratories in Europe

European Virtual Institute of Research in Forensic Genetics

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European Virtual Institute of Research in Forensic Genetics - access query

You are interested in becoming a member of the European Virtual Institute of Research in Forensic Genetics?

If you are a scientist working at a forensic genetics laboratory, or a professional working in an institution of the justice system, you are invited to join the Virtual Institute. Please see our Newsletter 3/2014 for further details.

Please enter your personal contact data, and the data of your institution below. We will verify your request and come back to you in the following days.

One requirement to get access to the EUROFORGEN-NoE Virtual Institute of Research in Forensic Genetics is the participation of your institution by submitting the EUROFORGEN-NoE [questionnaire](#).

Your EUROFORGEN-NoE team.



EU
wit

The end of funding ... ?

... but not of our network!

- **The EC-funded project will end on Dec 31, 2016**
- **EUROFORGEN will associate with the ISFG to**
 - Maintain the Virtual Institute of Research
 - add more content for the website for training and education
 - Continue the online Training Academy
 - Collaborate with other stakeholders (ENFSI, CEPOL)
- **The EUROFORGEN Summer School will be organized to offer high level training with experts colleagues and scientists as teachers**
 - The first Summer School is scheduled for **July 17-21, 2017**, to take place in **Santiago de Compostela, Spain**



EUROFORGEN

EUROFORGEN - European Forensic Genetics Network of Excellence

Public group

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RECENT ACTIVITY



Peter Schneider
Yesterday at 00:47

Interesting wrap-up on the pros and cons of releasing proprietary codes for "probabilistic genotyping" software to the defense - in any case, I find it worrisome when a decisive verdict hinges on the outcome of a complex expert system: are we going from RoboCop to RoboJudge?



Where Traditional DNA Testing Fails, Algorithms Take Over

Powerful software is solving more crimes and raising new questions about due process.

PROPUBICA.ORG | BY LAUREN KIRCHNER

ADD MEMBERS

Enter name or email address...

MEMBERS 362 members (5 new)



SUGGESTED MEMBERS See More

	Christoph Doeppes	Add
	Christina Strobl	Add
	Henriette Tietze	Add

DESCRIPTION Edit

The EUROFORGEN Network of Excellence is creating the Europe... See more

TAGS Edit

Forensic DNA · Science · Genetics

CREATE NEW GROUPS

Groups make it easier than ever to share with friends, family and teammates.

Create group

MORE WAYS TO CREATE





Thank you for
your attention!



Please do not forget to join
our Facebook group!
... already **362** members!