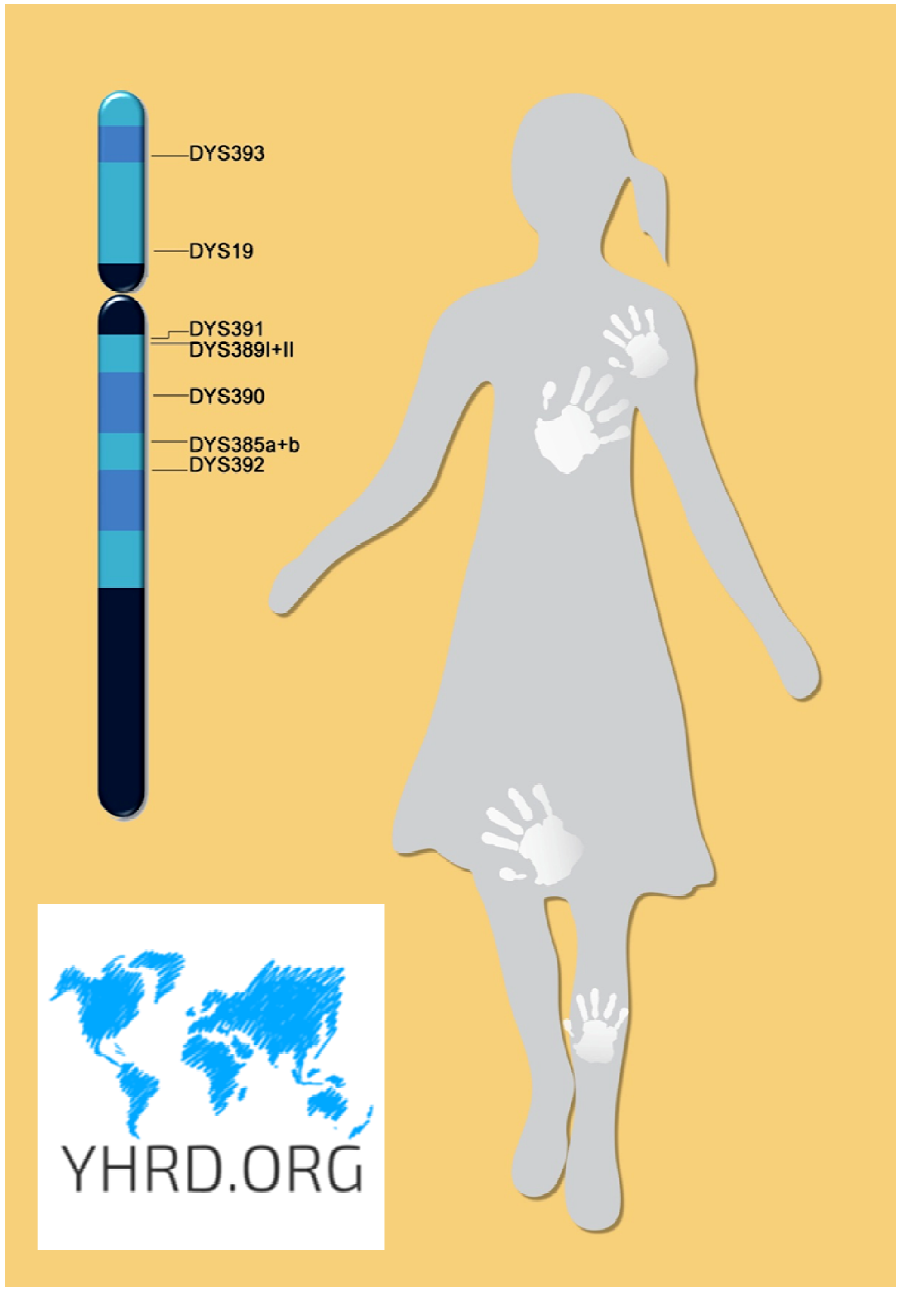

Stretching the boundaries of Y chromosome analysis – Use of the YHRD database and its tools in forensic casework

Lutz Roewer

Dept. Forensic Genetics

Institute of Legal Medicine and Forensic Sciences

Charité – Universitätsmedizin Berlin

Germany

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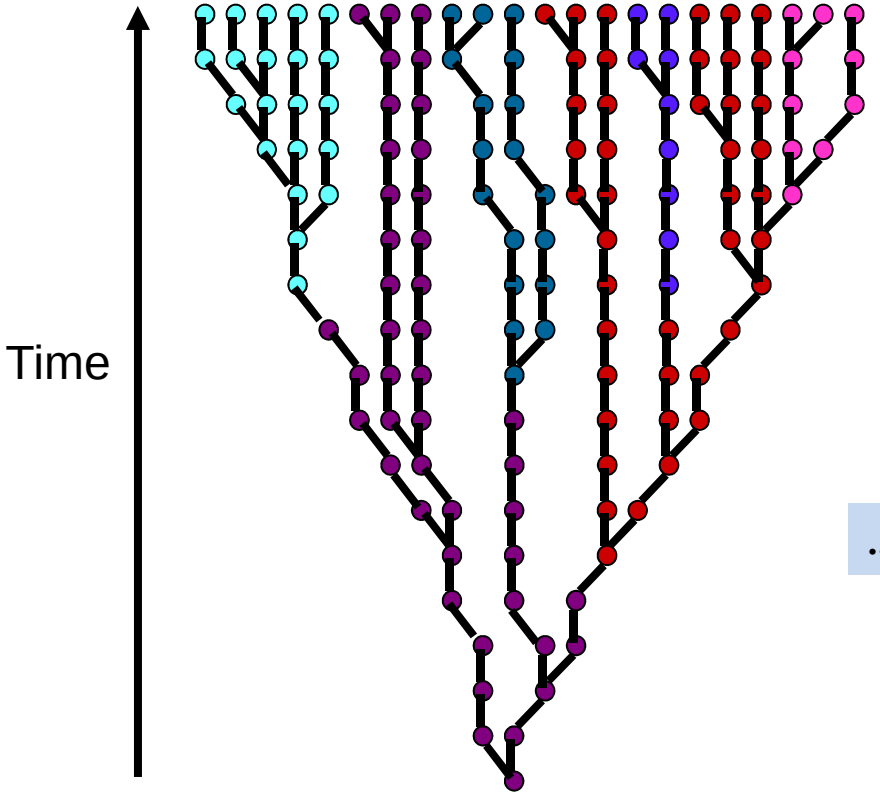
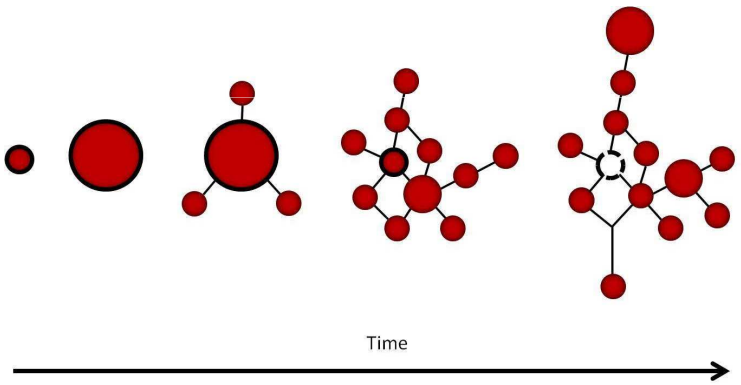
A Y chromosomal haplotype – a time capsule

SNP-typed chromosomes are connected to a tree and …





…STR-typed chromosomes to a cluster (network)

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The expansions detected with Y-SNPs- when and where ?

250 kya

80 kya

47-52kya

<10 kya

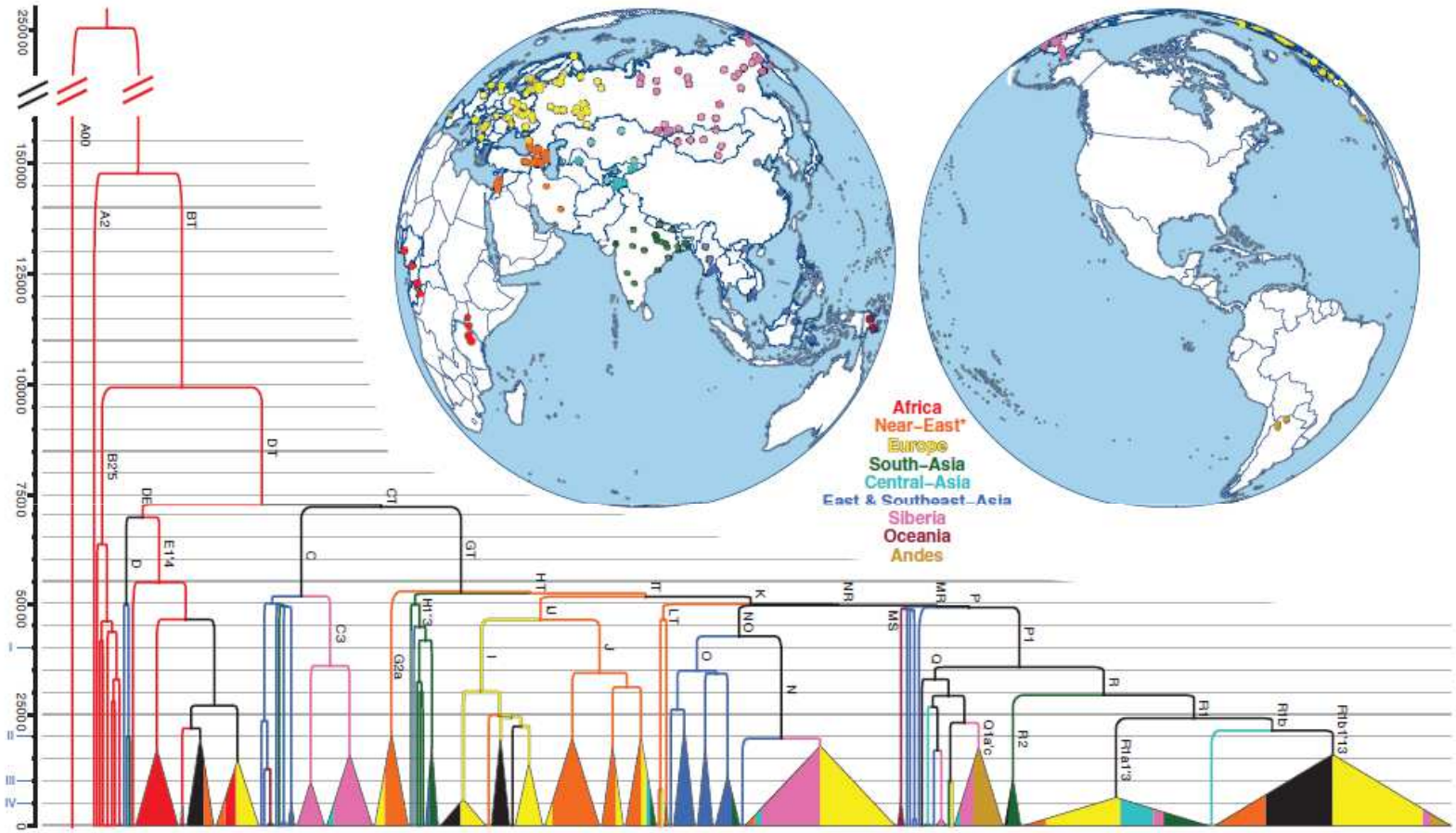

Figure 1. The phylogenetic tree of 456 whole Y chromosome sequences and a map of sampling locations. The phylogenetic tree is reconstructed using BEAST. Clades coalescing within 10% of the overall depth of the tree have been collapsed. Only main haplogroup labels are shown (details are provided in Supplemental Information 6). Colors indicate geographic origin of samples (Supplemental Table S1), and fill proportions of the collapsed clades represent the proportion of samples from a given region. Asterisk (*) marks the inclusion of samples from Caucasus area. Personal Genomes Project (http://www.personalgenomes.org) samples of unknown and mixed geographic/ethnic origin are shown in black. The proposed structure of Y chromosome haplogroup naming (Supplemental Table S5) is given in Roman numbers on the *y*-axis.

Karmin et al. 2015

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The database switch

- Decommission of USYSTR (June 30, 2019)
- US data uploaded to YHRD (Release 58, Sept 2018)
- SWGDAM compliant functionality (Release 59, Nov 2018)
- US forensic labs switch to YHRD (2019)

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Prosecution rests in Mentor-on-the-Lake murder retrial

T., 34, was convicted in 2012 and sentenced to death for the 2010 murder of M. outside of Mario's Lakeway Lounge. The Ohio Supreme Court overturned his conviction, however, and ordered a new trial.

News-Herald.com

Using Y-STR testing, … the Ohio Bureau of Criminal Investigations. detected a single male DNA profile that was consistent with T. That male profile was compared to the profiles of the other 48 men who had DNA swabs submitted in the M. investigation.

(…)

The U.S. Y-STR database is now defunct, [BCI] said. BCI now uses the YHRD database. [BCI] said the switched happened because the prior database was decommissioned on Jan. 30, 2019.
"Not for errors, not for mistakes, simply for a term of resources," [BCI] said. "There was a larger database that could incorporate all of this data. That data was moved to the new database and we're now using it."

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YHRD - some facts

- established 1999 at Charité in Berlin, Germany
- close to 300,000 Y-STR profiles, 10% typed for Y-SNPs
- Up to 29 STRs and >500 phylogenetic Y-SNPs
- 135 countries represented
- 480 submitting forensic and academic institutions
- 570 population papers published
- On average 10,000 hits and 700 unique users per day

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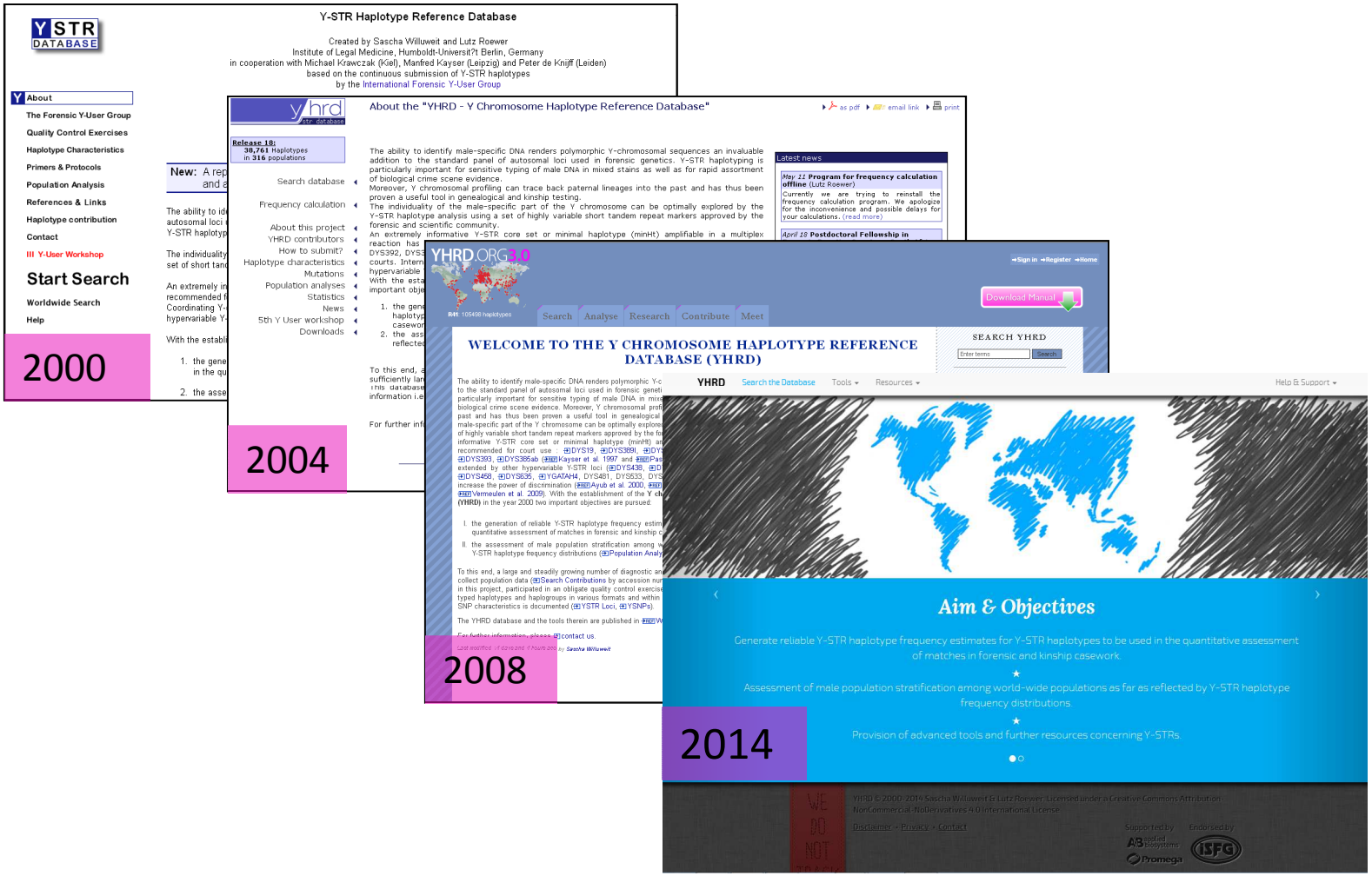
https://yhrd.org



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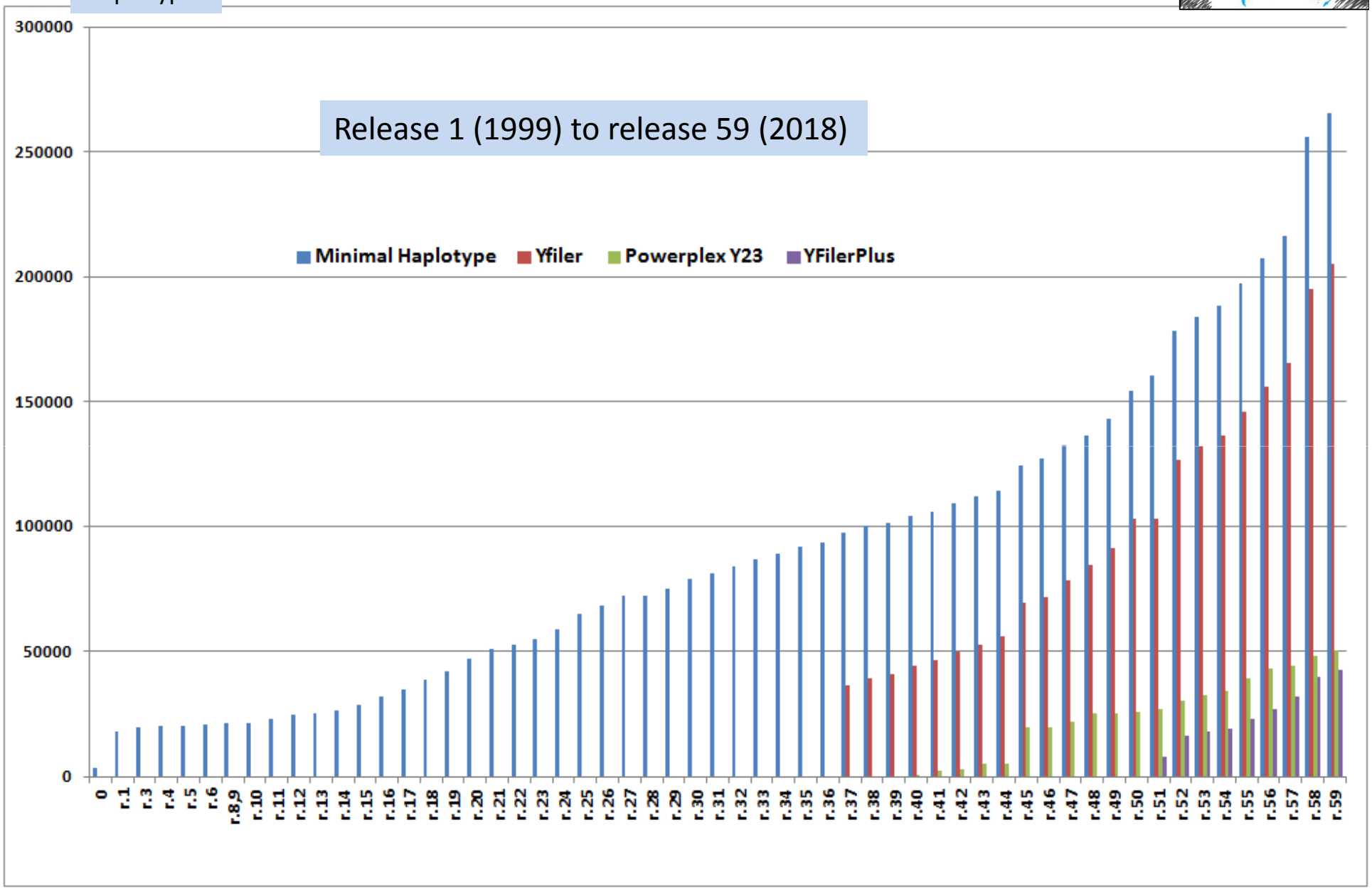
Haplotypes



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Lab Network YHRD

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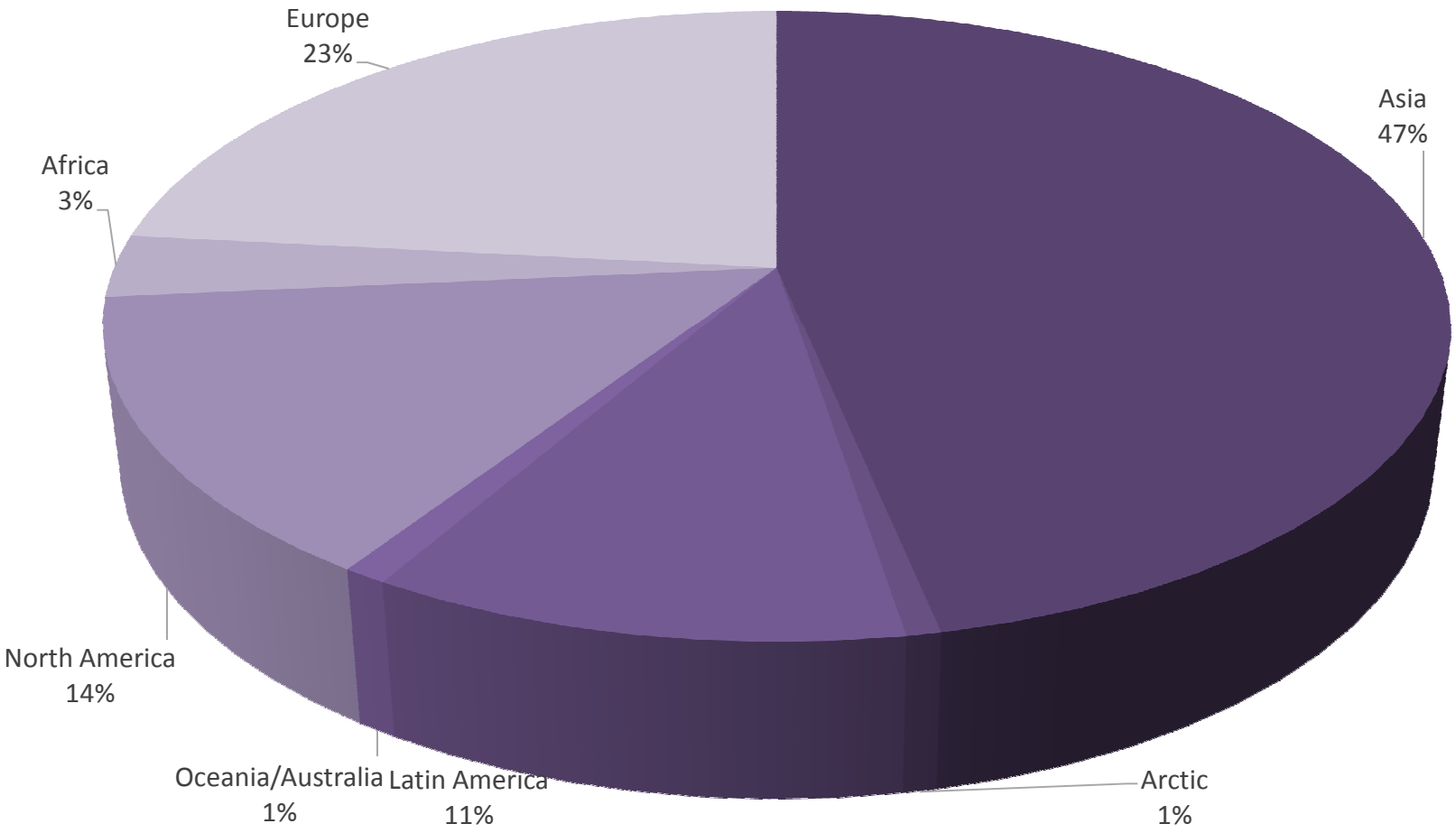
YHRD composition (continents)



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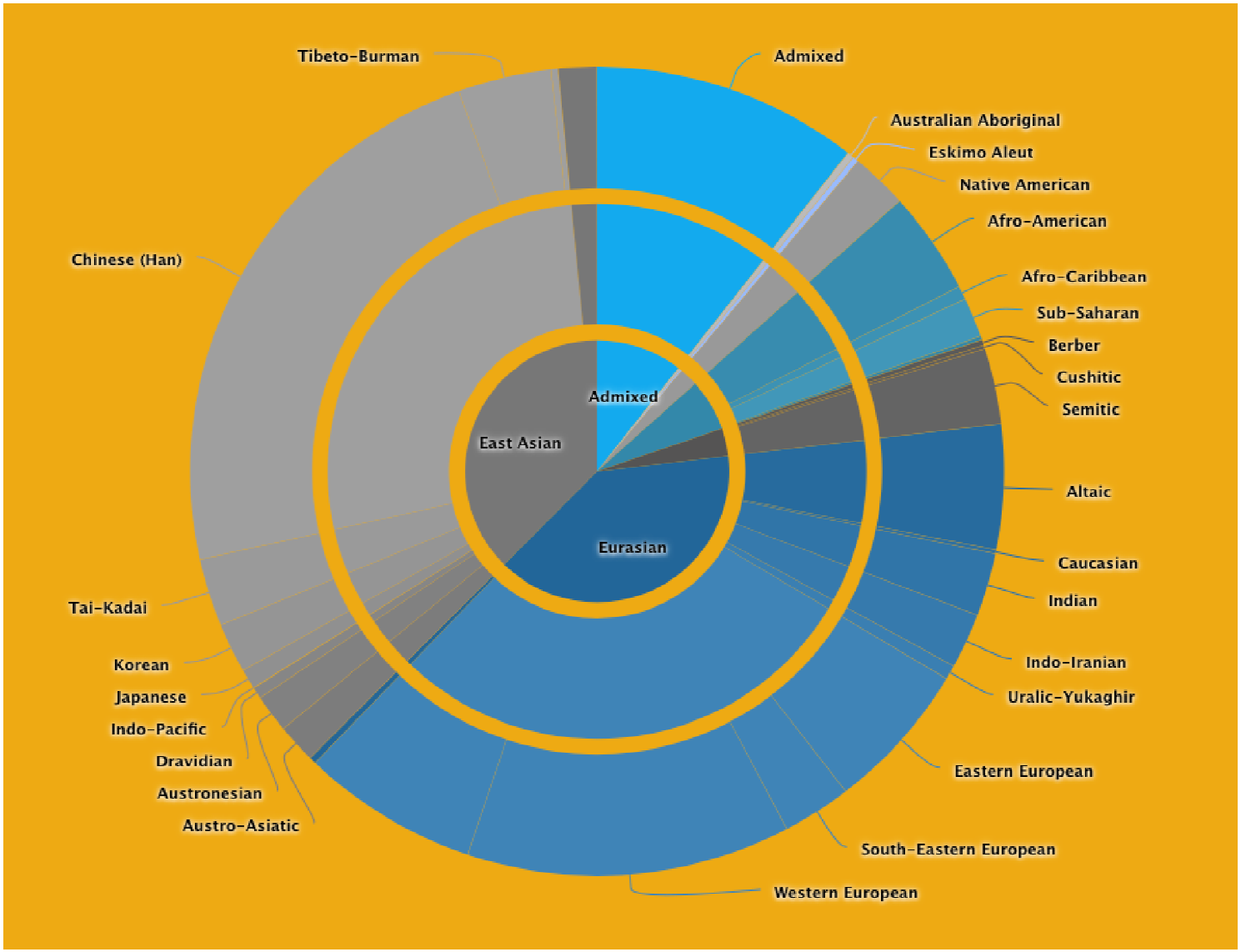
YHRD composition (metapopulations)



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YHRD - Six datasets

Name	Description	Loci
Minimal	YHRD Core Loci	DYS19 DYS389I DYS389II DYS390 DYS391 DYS392 DYS393 DYS385
PowerPlex Y	Promega PowerPlex® Y	DYS391 DYS389I DYS439 DYS389II DYS438 DYS437 DYS19 DYS392 DYS393 DYS390 DYS385
Yfiler	Applied Biosystems AmpFLSTR® Yfiler®	DYS456 DYS389I DYS390 DYS389II DYS458 DYS19 DYS385 DYS393 DYS391 DYS439 DYS635 DYS392 YGATAH4 DYS437 DYS438 DYS448
PowerPlex Y23	Promega PowerPlex® Y23	DYS576 DYS389I DYS448 DYS389II DYS19 DYS391 DYS481 DYS549 DYS533 DYS438 DYS437 DYS570 DYS635 DYS390 DYS439 DYS392 DYS643 DYS393 DYS458 DYS385 DYS456 YGATAH4
Yfiler Plus	Applied Biosystems AmpFLSTR® Yfiler® Plus	DYS576 DYS389I DYS635 DYS389II DYS627 DYS460 DYS458 DYS19 YGATAH4 DYS448 DYS391 DYS456 DYS390 DYS438 DYS392 DYS518 DYS570 DYS437 DYS385 DYS449 DYS393 DYS439 DYS481 DYF387S1 DYS533
Maximal	YHRD Max Loci	DYS19 DYS389I DYS389II DYS390 DYS391 DYS392 DYS393 DYS385 DYS438 DYS439 DYS437 DYS448 DYS456 DYS458 DYS635 YGATAH4 DYS481 DYS533 DYS549 DYS570 DYS576 DYS643 DYF387S1 DYS449 DYS460 DYS518 DYS627

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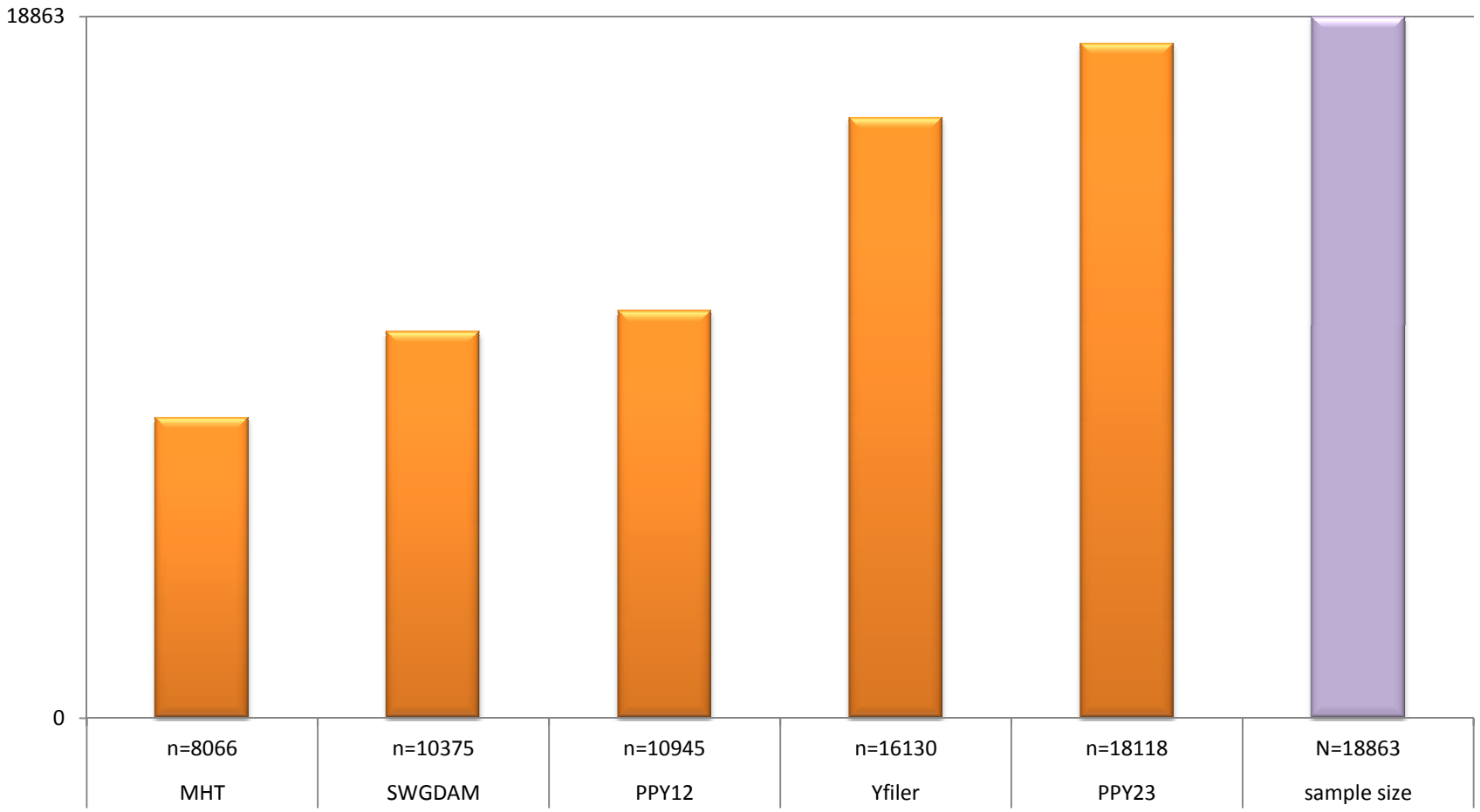
Increasing discrimination capacity (DC)



Purps et al. 2015

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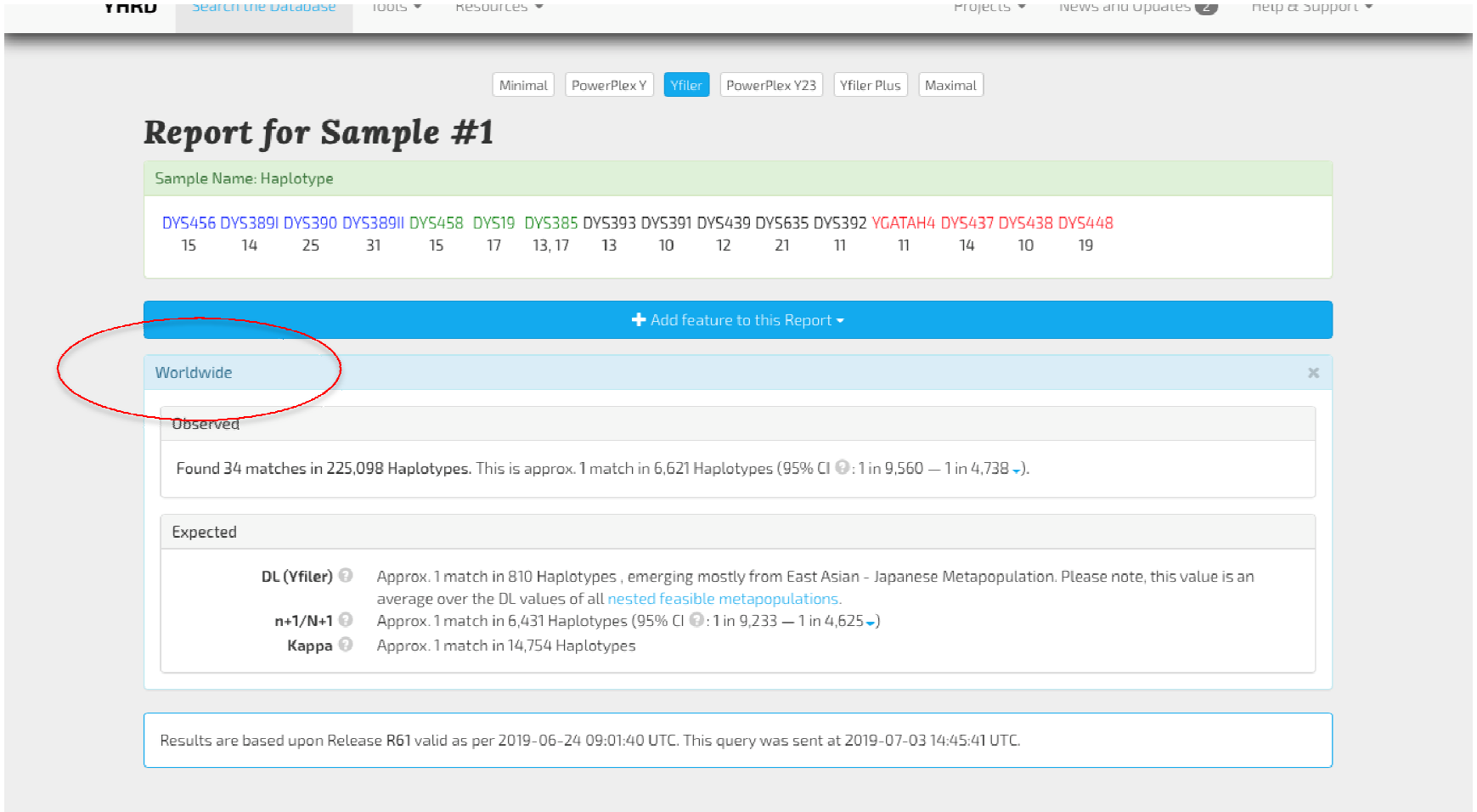
Search 17 loci



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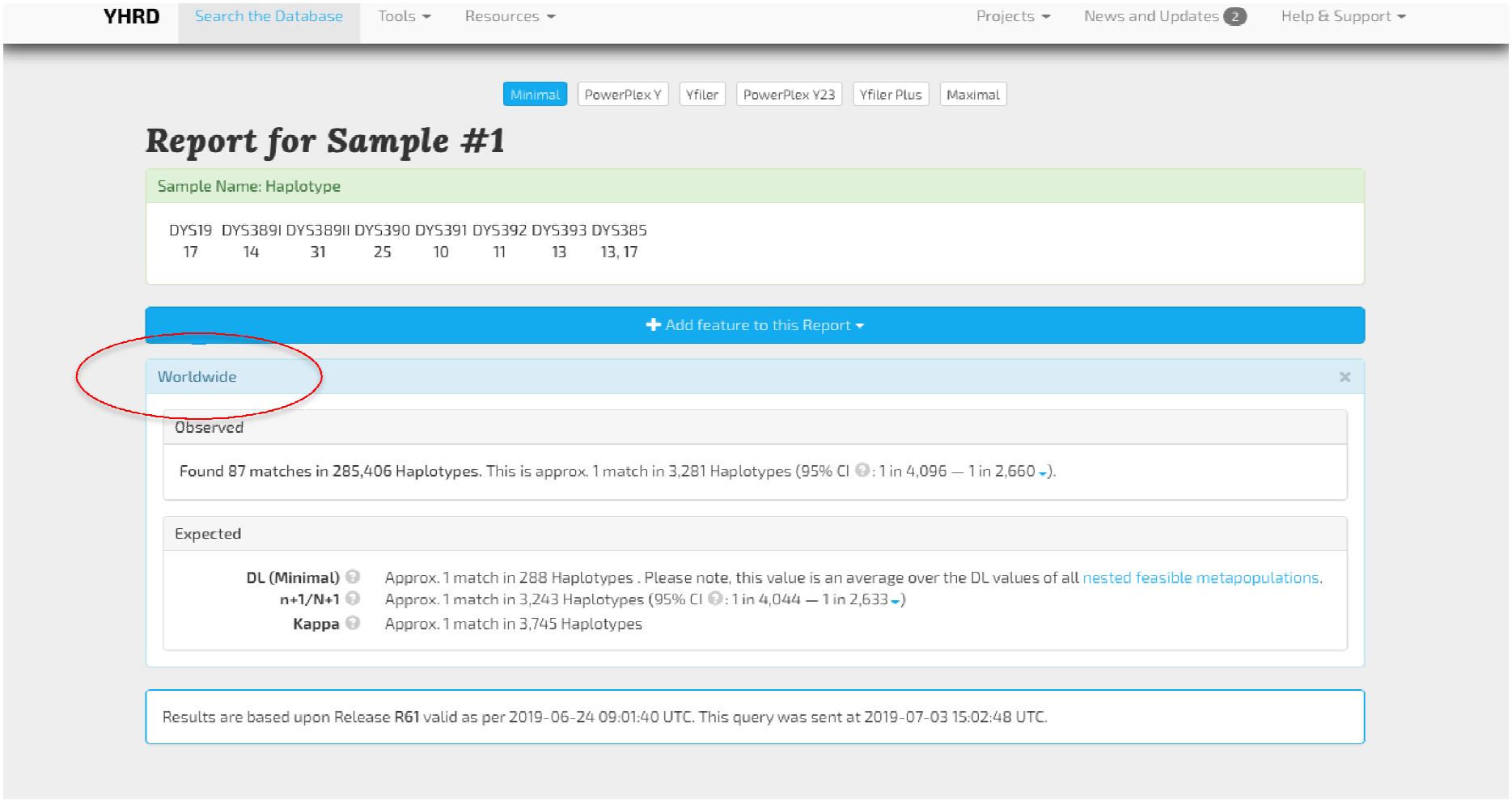
Switch to lower resolution



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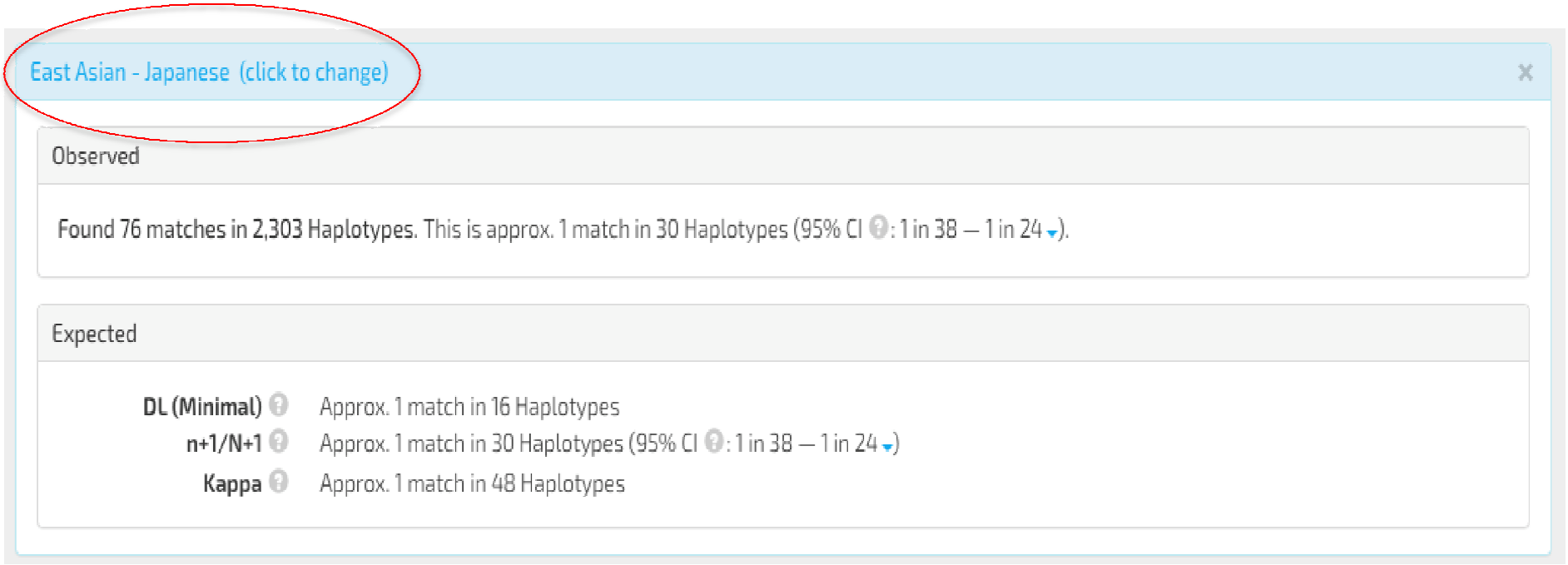
Search in metapopulation



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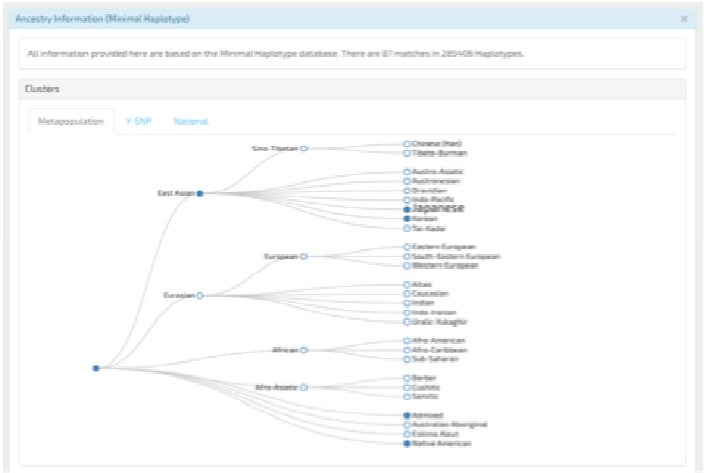
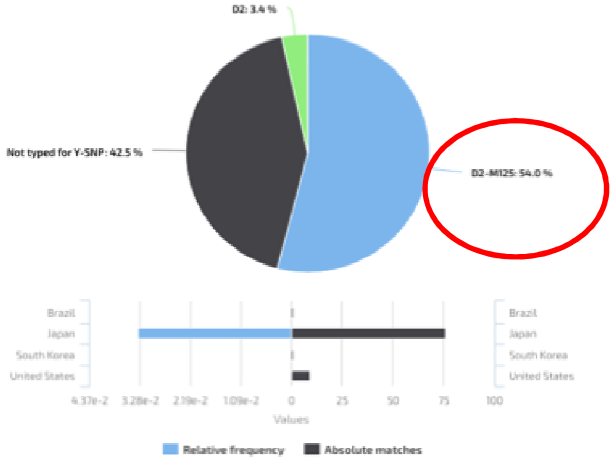
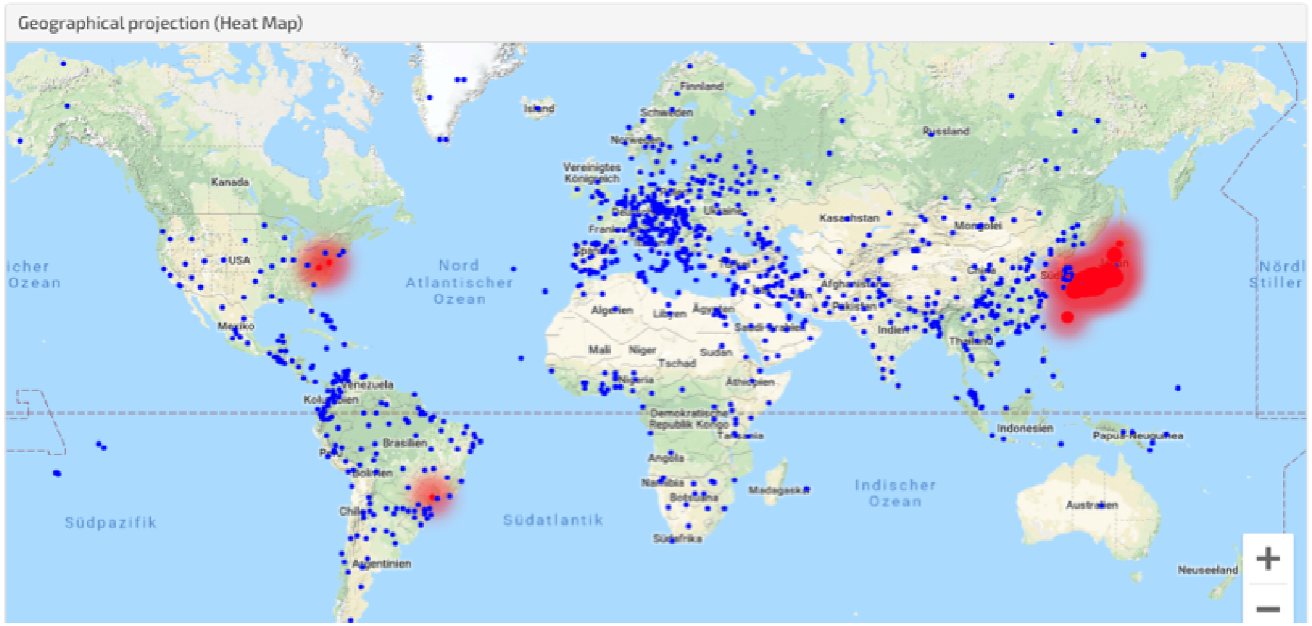
Add ancestry information to your searched haplotype







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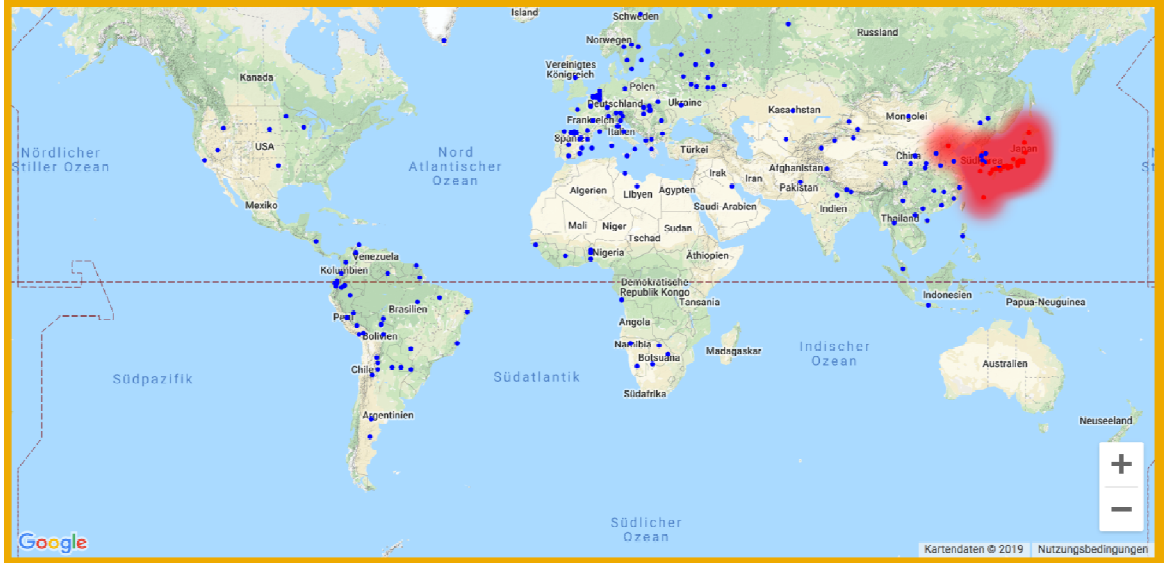
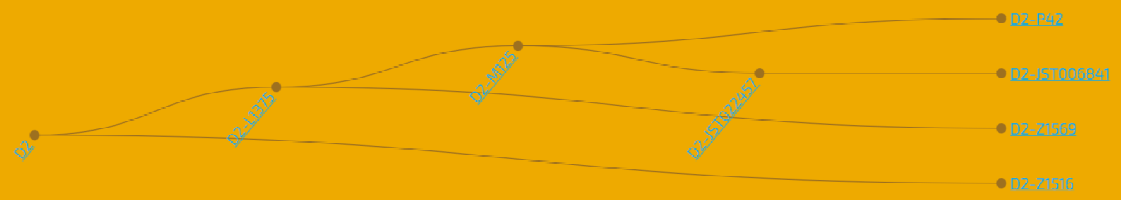
Haplogroup D2

The Y-SNP branch D2 is defined by M179, M55, M57, Page31. Additionaly, all downstream markers CTS2098, CTS504, CTS583, CTS7590, CTS9508, JST006841, JST022457, L1375, M116, M125, P42, Page3, Z1516, Z1520, Z1569, Z1576, Z1627 are defining this branch as well. For further information on a marker, please see marker details at Phylotree Y or consult the Y-SNP tree there.

Please note, that colours on the map only reflect a haplogroup distribution from the SNP-typed samples which were submitted to the YHRD.





Y-SNP marker	Haplogroup	Minimal	PowerPlex Y	Yfiler	PowerPlex Y23	Yfiler Plus	Maximal
CTS2098	D2-Z1516	0 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes
CTS504	D2-Z1569	0 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes
CTS583	D2-Z1516	0 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes

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YHRD lexicography

1. Create a **geoposition** with latitude, longitude (map)
2. Attach a **population** name
3. Assign population to a **continent**
4. Assign population to a **national database**
5. Assign population to a **metapopulation**
6. Create a **contribution** to this population
7. Attach a **contributor** to this contribution
8. Upload a validated **submission** to this contribution
9. Issue a unique **accession nr.** to this submission
10. Unlock all new submissions and create a new **release**

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Check for file type support
- Format "Excelx" is supported at YHRD

Check for unexpected columns at sheet "YHRD_RJ"
- All columns are known Y-STR markers, known Y-SNPs or other known named columns.

Check detected dataset
- Dataset "PowerPlex Y23" is detected.

Check for at least one haplotype
- 201 haplotypes are not empty.

Check for blank haplotypes
- No haplotypes are empty.

Check for any additional marker
- No additional marker was found.

Check for missing/empty markers
- No marker was missing/empty.

Check for nomenclature consistency
- All alleles are valid.

Check for unobserved alleles (regarding the current state of the YHRD)
- All alleles are known to us.

Check for null alleles
- At marker DYS392 there is a null-allele found at 47_P.

Check for alleles beyond reasonable range (regarding the current state of the YHRD)
- All alleles are within the range.

Check presence of population name
- We found population name Rio de Janeiro, Brazil [Admixed]

Check for additional samples
- All samples are assigned only to "Rio de Janeiro, Brazil [Admixed]"

Check required minimal number haplotypes
- We found 201 haplotypes.

Oh well.. you may proceed with your file, but be advised to review the issues above. Or download your file as Excel sheet with the modifications we did.

Validation of the submission file
https://yhrd.org/pages/tools/validator

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Release History

Release 55 - 2017/Oct/20

- Contribution YA003031 (Stuttgart, Germany [German]): replace 1154 => 2409
- Contribution YA003115 (London, United Kingdom [British European]): replace 299 => 1222
- Contribution YA003116 (London, United Kingdom [British Afro Caribbean]): replace 295 => 1156
- Contribution YA003117 (London, United Kingdom [British Indian, Pakistani, Bangladeshi, Sri Lankan]): replace 263 => 510
- Contribution YA003118 (Ireland [Irish]): replace 177 => 766
- Contribution YA003793 (Xuanwei, China [Han]): replace 145 => 258
- Contribution YA004263 (Shanghai, China [Han]): new 0 => 843
- Contribution YA004264 (Zacatecas, Mexico [Admixed]): new 0 => 130
- Contribution YA004265 (Swat and Dir District, Pakistan [Gujjar]): new 0 => 20
- Contribution YA004266 (Swat and Dir District, Pakistan [Kohistani]): new 0 => 20
- Contribution YA004267 (Swat and Dir District, Pakistan [Tharklani, Pashtun]): new 0 => 20
- Contribution YA004268 (Swat and Dir District, Pakistan [Uthmankheil, Pashtun]): new 0 => 20
- Contribution YA004269 (Swat and Dir District, Pakistan [Yousafzai, Pashtun]): new 0 => 20
- Contribution YA004270 (Saudi Arabia Central [Arab]): new 0 => 125
- Contribution YA004271 (Saudi Arabia East [Arab]): new 0 => 110
- Contribution YA004272 (Saudi Arabia North [Arab]): new 0 => 106
- Contribution YA004273 (Saudi Arabia South [Arab]): new 0 => 140
- Contribution YA004274 (Saudi Arabia West [Arab]): new 0 => 116
- Contribution YA004276 (Rio de Janeiro, Brazil [Admixed]): new 0 => 592
- Contribution YA004277 (Inner Mongolia, China [Daur]): new 0 => 200
- Contribution YA004278 (Bahrain [Bahraini]): new 0 => 156
- Contribution YA004279 (Hainan, China [Han]): new 0 => 473
- Contribution YA004280 (Shenzhen, China [Han]): new 0 => 136
- Contribution YA004281 (Hainan, China [Han]): new 0 => 280
- Contribution YA004282 (Rio de Janeiro, Brazil [Admixed]): new 0 => 75
- Contribution YA004283 (Netrokona, Bangladesh [Hajong]): new 0 => 89
- Contribution YA004284 (Cox's Bazar, Bangladesh [Rakhine]): new 0 => 110
- Contribution YA004285 (Bandarban, Bangladesh [Marma]): new 0 => 107
- Contribution YA004287 (Ljubljana, Slovenia [Slovenian]): new 0 => 201
- Contribution YA004288 (Guanzhong, China [Han]): new 0 => 132
- Contribution YA004289 (Yanbian, China [Korean]): new 0 => 347
- Contribution YA004290 (Germany [Romanian]): new 0 => 42
- Contribution YA004291 (Germany [Afghan]): new 0 => 32
- Contribution YA004292 (Nordrhein-Westfalen [German]): new 0 => 53
- Contribution YA004293 (Hessen [German]): new 0 => 20
- Contribution YA004294 (Bayern [German]): new 0 => 73
- Contribution YA004295 (Brandenburg [German]): new 0 => 31
- Contribution YA004296 (Sachsen [German]): new 0 => 23
- Contribution YA004297 (Niedersachsen [German]): new 0 => 31
- Contribution YA004298 (Rheinland-Pfalz [German]): new 0 => 34
- *Former database sizes: minimal=188209, y12=149141, yfiler=136443, y23=34133, yfilerplus=18921, ymax=1538, ysnp=20495*
- *New database sizes: minimal=197104, y12=158814, yfiler=145818, y23=39415, yfilerplus=22833, ymax=2849, ysnp=20495*

https://yhrd.org/pages/resources/release_history

Release 54 - 2017/Jun/06

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Tools

https://yhrd.org/mixture

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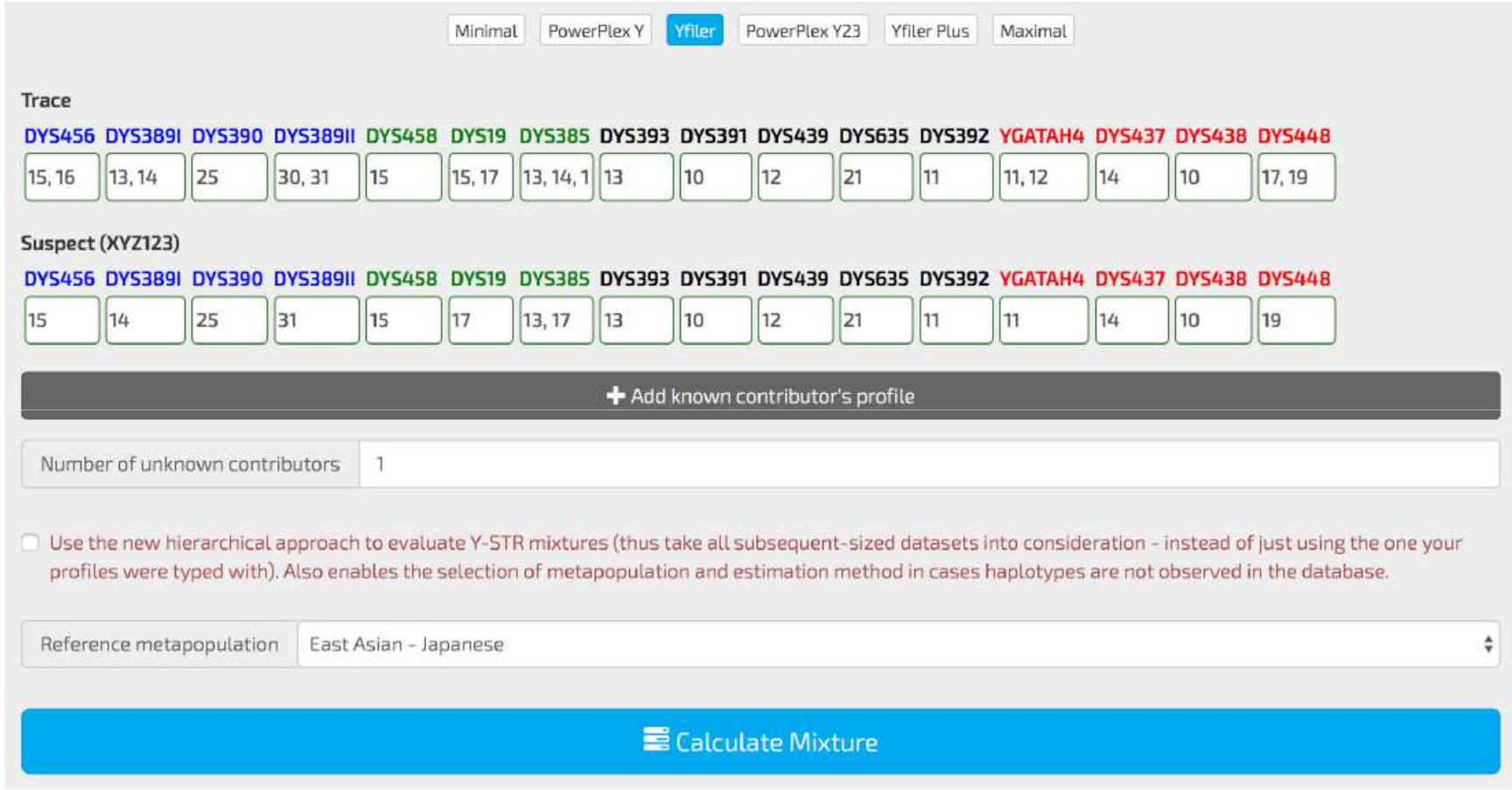
Mixture analysis – options and confirmation



Mixture analysis – results

Mixture Calculation Result

Congratulations! Your job has been successfully processed. It took less than a minute.

Name	Role	DYS456	DYS389I	DYS390	DYS389II	DYS458	DYS19	DYS385	DYS393	DYS391	DYS439
Trace A	Trace	15, 16	13, 14	25	30, 31	15	15, 17	13, 14, 17	13	10	12
XYZ123	Suspect	15	14	25	31	15	17	13, 17	13	10	12

Given the Haplotypes above and that there is 1 additional unknown contributor, the likelihood of the donorship of the suspect is approx. 15 times more likely than the non-donorship. This calculation is based on 1909 haplotypes (Yfiler) in the East Asian - Japanese Metapopulation.

Wolf et al. (2005) Forensic interpretation of Y-chromosomal mixtures. Forensic Science International 152: 209-13

Tools

https://yhrd.org/kinship

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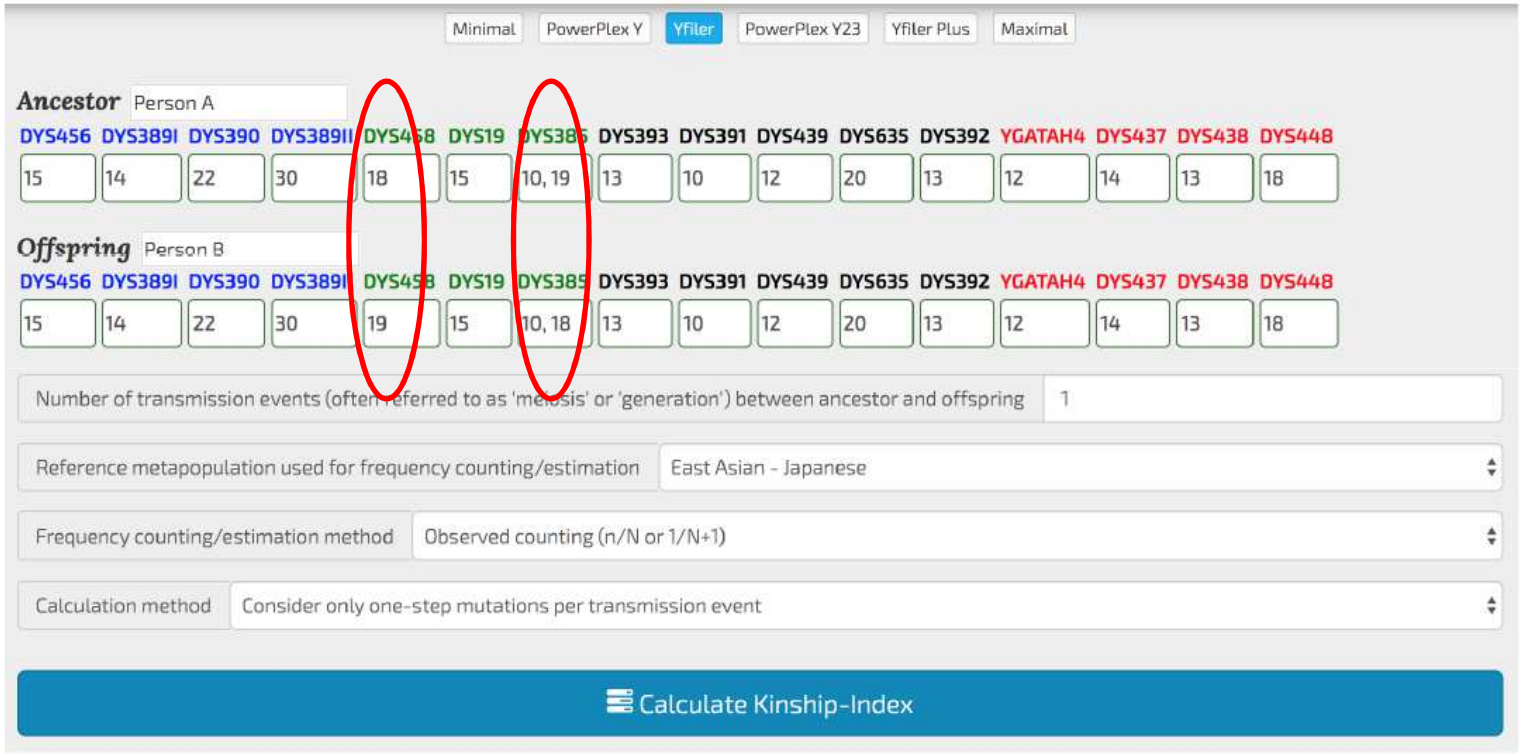
Kinship tool (results in LR)



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Kinship tool (LR)

Result

The likelihood ratio of patrilineal non-relationship versus relationship (1/LR) is approx. **982**.

Additional information:

- Japanese Metapopulation is used.
- Markers to consider for calculation: DYS456, DYS389I, DYS390, DYS389II, DYS458, DYS19, DYS385, DYS393, DYS391, DYS439, DYS635, DYS392, YGATAH4, DYS437, DYS438, DYS448.
- There's a 1-step difference between the ancestor and the offspring at DYS458.
- There's a 1-step difference between the ancestor and the offspring at DYS385.
- Consider 1 transmission event

Rolf et al. (2001) Paternity testing using Y-STR haplotypes: assigning a probability for paternity in cases of mutations. Int J Legal Med 115(1) 12-5.

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Strategic applications

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Use of Y‘s for investigation

- An **investigative tool** is used by law enforcement agencies to identify likely suspects
- Cold case investigation
- Y is used to identify (distant) patrilineal relatives
- Y is used to infer surnames
- Y is used to predict (biogeographical) ancestry
- → Y-based mass screenings
- efficient strategy in Holland and now Germany (recent cases solved: Vaatstra, van Doorn, Verstappen)

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Reconstruct the ancestry of an unknown (recent casework)

Nearly completely sceletonized man found in a trolley

Contradictory results of 3 commonly used methods in police investigations!

1) Isotope analysis - resident of South America (explicitly: Bolivien) - misleading
2) Facial reconstruction - misleading
3) Ancestry inference using Y chromosome DNA - Fertile Crescent, **Turkey**, Caucasus

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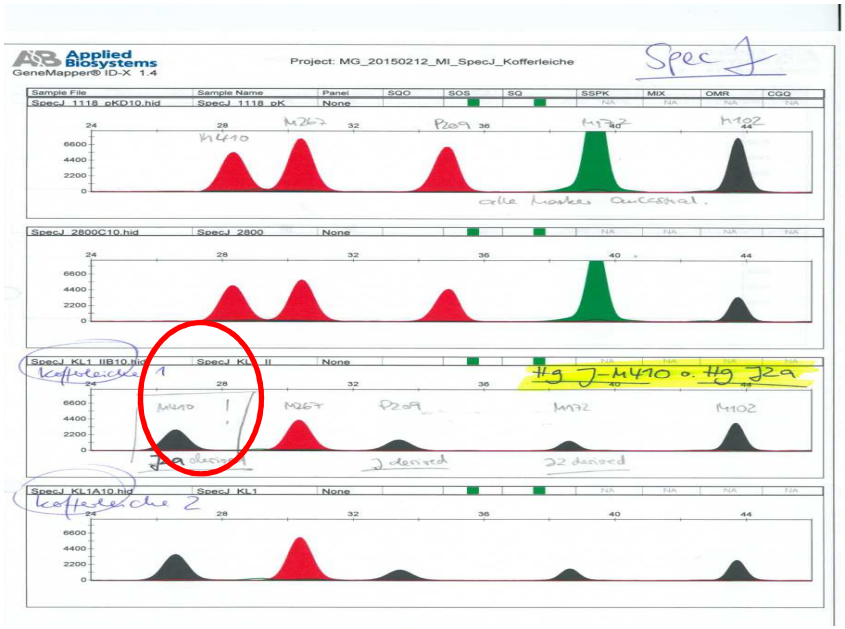
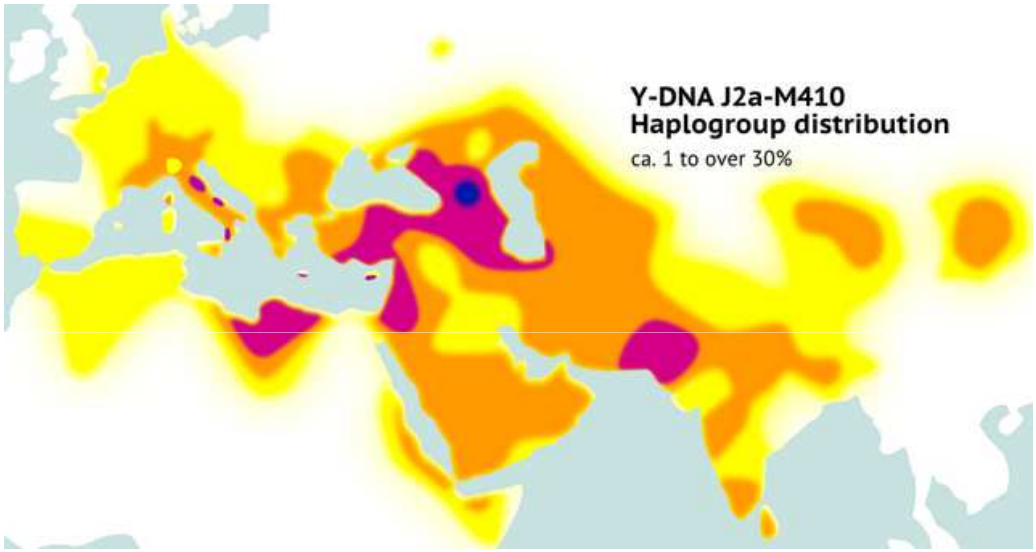
Haplogroup detected with SNaPshot assay: hg J2a (M210)



Geppert et al. 2010 (37 Y-SNPs)



Semino et al. 2004 (n = 2400)

Person identified, born in Istambul (Turkey), lived (and died) in Germany

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Use of Y-STRs as evidence

- An **evidence** needs to be sufficiently useful to prove something important in a trial.
- **probative value** of the proposed evidence must be weighed by the trial judge against prejudicing in the minds of jurors toward the opposing party or criminal defendant
- What is the evidentiary strength of Y profiles (especially in sexual assualt cases)?

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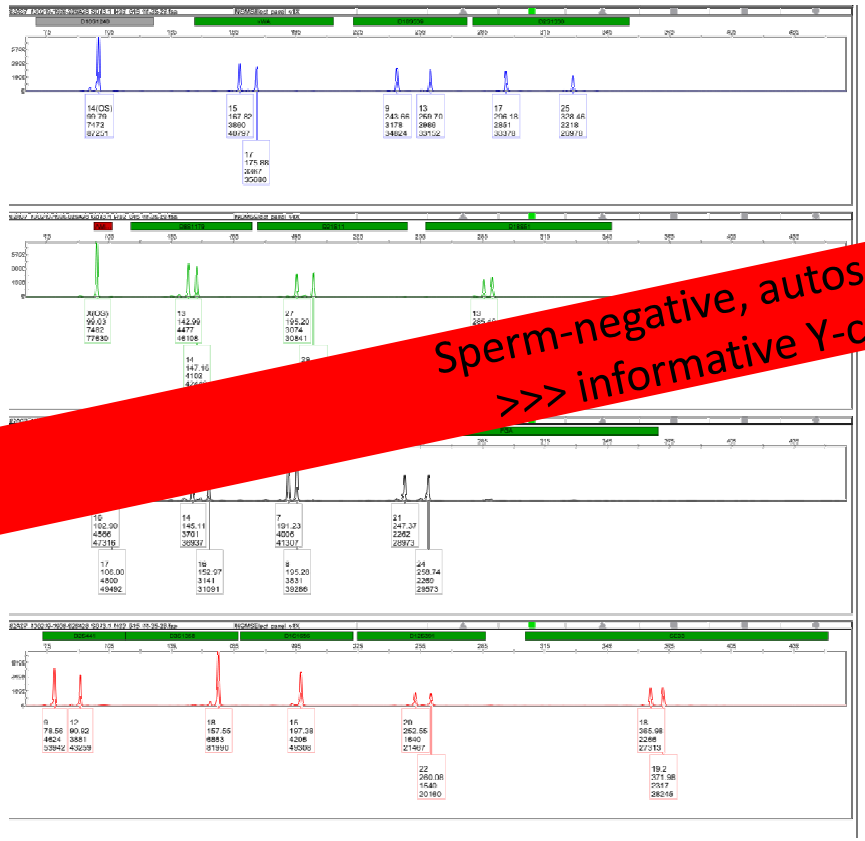
Casework example

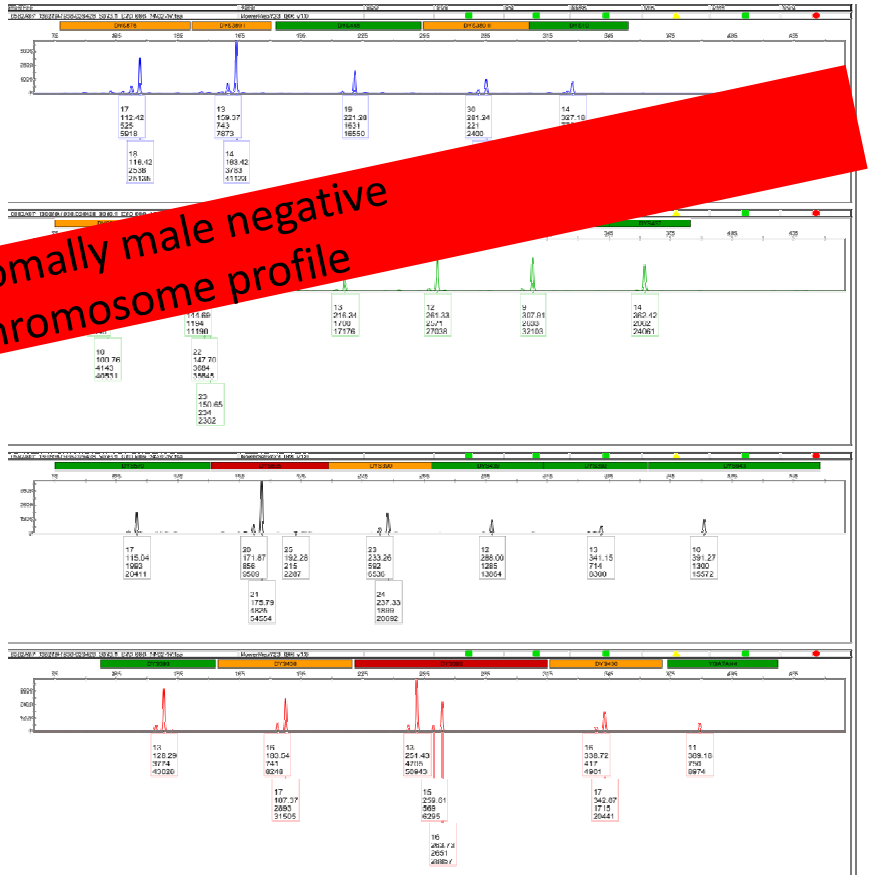
Delict: Rape (§177)

Evidence: Cut-out of the slip of the victim, sperm pretest

Autosomal profile



Y-chromosomal profile



Sperm-negative, autosomally male negative
>>> informative Y-chromosome profile

- Sperm negative
- Autosomal STR, Amelogenin - ♂negative

- Y-chromosomal mixed profile (major, minor components)

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Random match probability.

- By counting
- By extrapolation (Discrete Laplace)

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Discrete Laplace Method

Andersen et al. 2013

- **Assumptions**
  - The population sample is characterized by a substructure of haplotype clusters, which are built by closely related haplotypes
  - Each of these clusters can be described by an ancestral haplotype (*haplotype center*) and the distribution of alleles
  - Allelic distributions are assessed using a suitable population sample
  - For each marker allele the distance to the ancestral haplotypes is determined and with DL parameters the frequency is estimated

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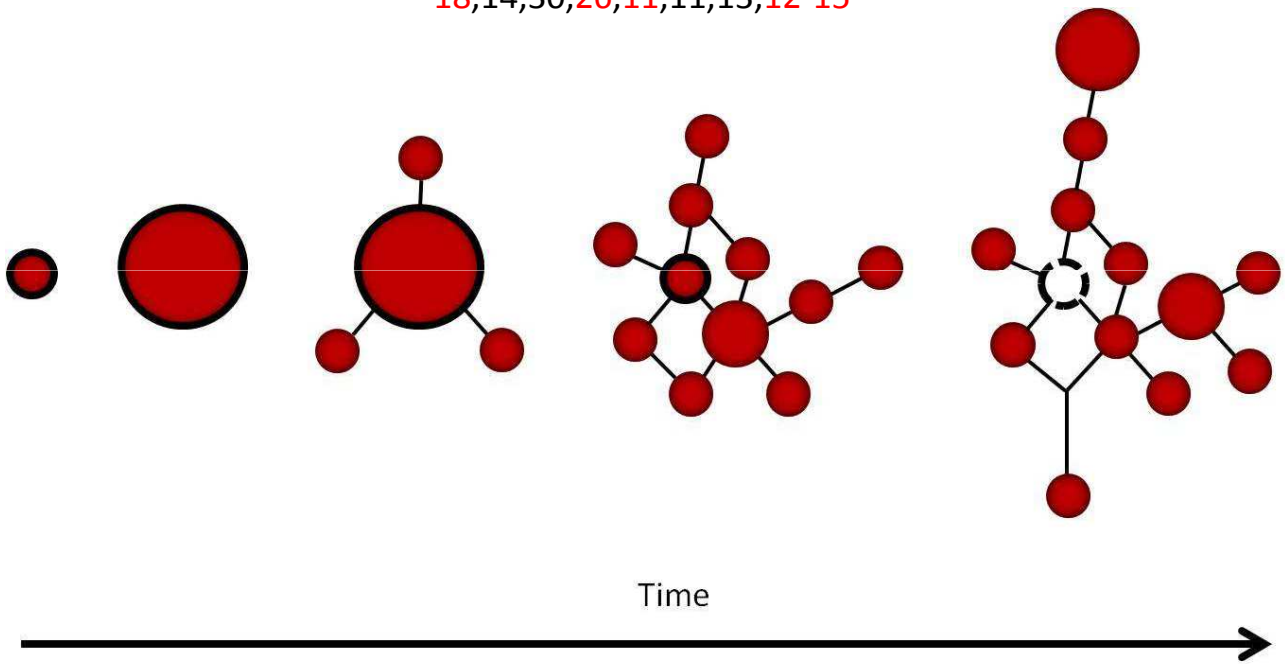
<u>17,13,30,25,10,11,13,10-14</u>
16,13,30,25,10,11,13,10-14
17,13,31,25,10,11,13,10-14
17,13,30,24,10,11,13,10-14
16,13,31,25,10,11,13,11-14
17,14,29,25,10,11,13,10-15
15,13,29,26,10,12,13,10-14
17,14,31,25,10,11,14,11-14
18,14,30,26,11,11,13,12-15

Y-STRs: $\mu = 10^{-4}$ to 10^{-2}



Schematic representation of a Y-STR cluster and ist evolution from an ancestral haplotype (center).

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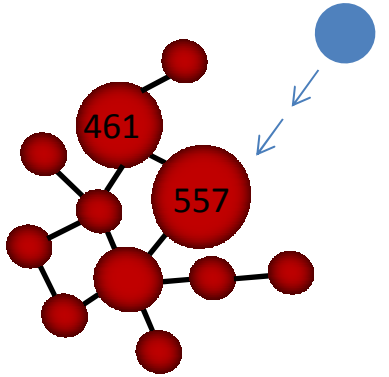
DL vs. counting

Trace haplotype



Example profile:

13,12,28,23,**10**,14,13,13-13

0 matches to YHRD metapopulations:

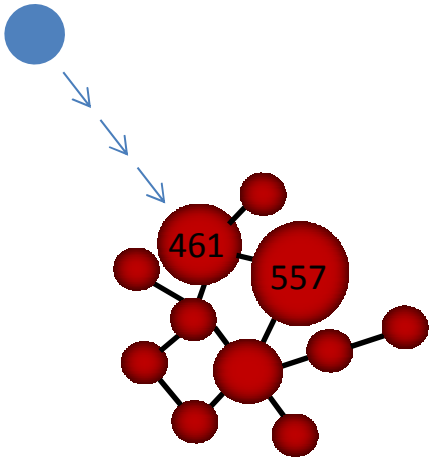
0 /36.656 Western European

0 / 59.580 Chinese (Han)

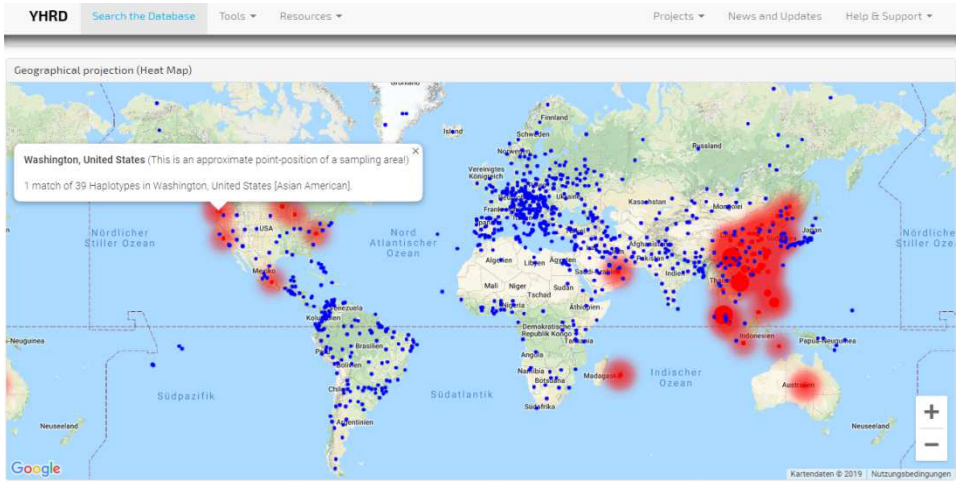
DL = 1/195.849 Western European

DL = 1/7.706 Chinese (Han)

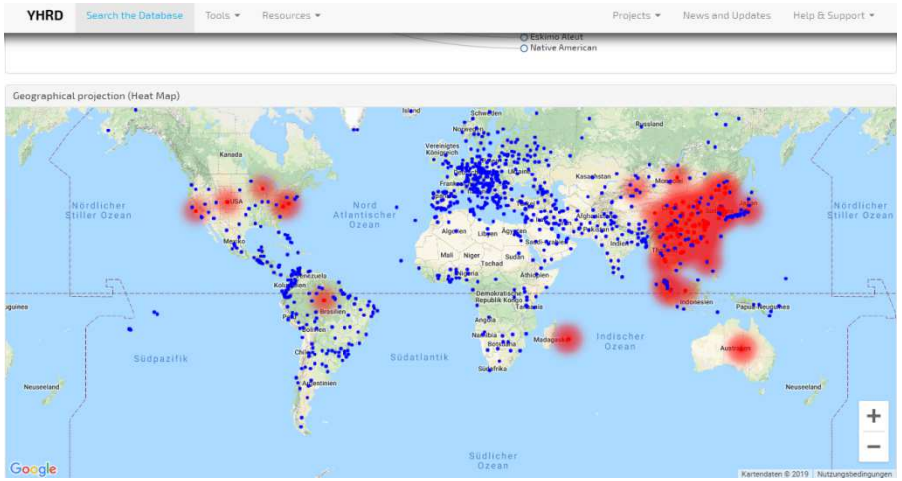
Trace haplotype



15,12,28,23,10,14,13,13-13 (557 matches/YHRD)



15,12,28,23,**11**,14,13,13-13 (461 matches/YHRD)



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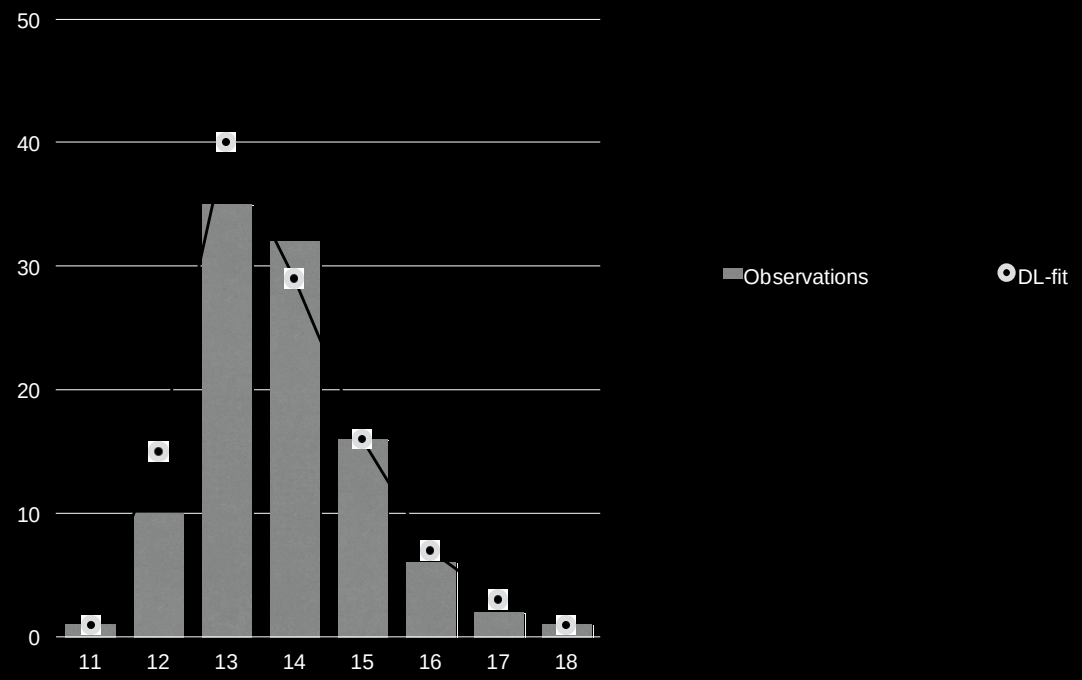
Discrete Laplace

- Allele distribution within a *cluster*

→ Double exponential distribution (Discrete Laplace distribution)



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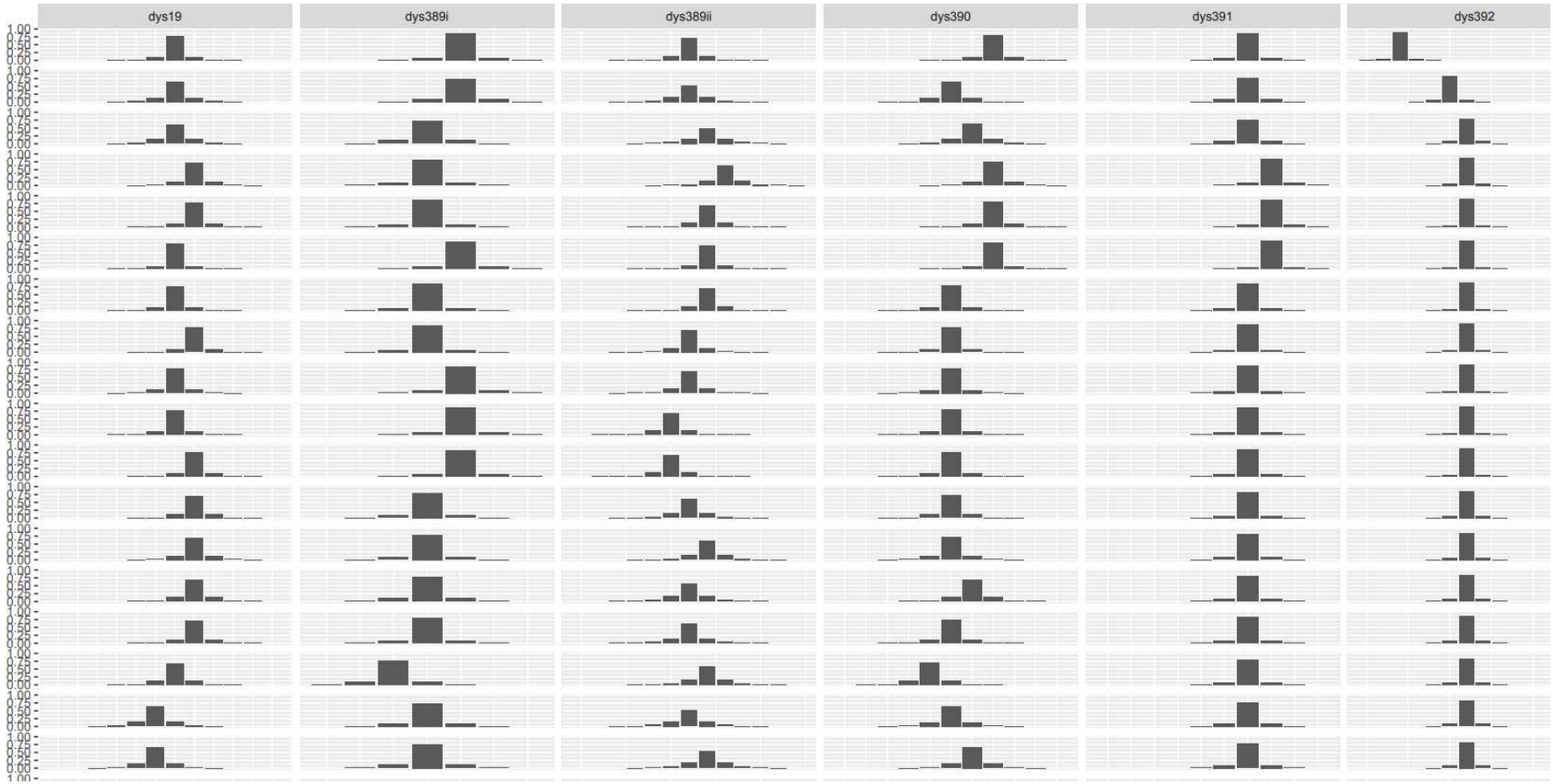
DL center distribution for Yfiler (excl. DYS385)
Metapopulation: Han Chinese



https://yhrd.org

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The figure illustrates the principle difference between naive counting and model-based computation

PPY23 (n=62.737 in YHRD)
15,13,21,31,15,10,28,12,11,11,14,19,21,21,11,11,13,13,17,16-17,15,11
Reduce to Yfiler (n=225.098 in YHRD)
15,13,21,31,17,15,16-17,13,10,11,21,11,11,14,11,21

Reference population (YHRD)	Size (N)**	counts	Frequency	Discrete Laplace (DL)
USA (National database)	29.275	3	1/9.758	*
African American MP	7.218	3	1/2.406	1/12.091
African MP	11.949	3	1/3.983	1/10.297
East Asian MP	99.124	0	1/99.125	1/114.445.555
European MP	52.509	0	1/52.510	1/58.609.616

* DL feasible only for Metapopulations

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Reporting LR*

Proposition A: The haplotype profile observed in the trace is derived from person X or a closely related patrilineal relative to person X.
Proposition B: The haplotype profile observed in the trace originates from a person of the **African American metapopulation** which is not paternally related to person X.

The 17 matching alleles detected in the trace are approx. 12,091 times more likely to be observed based on proposition A than on proposition B.

** Wording according to the **German reporting guidelines for Y-STR results** (2018)*

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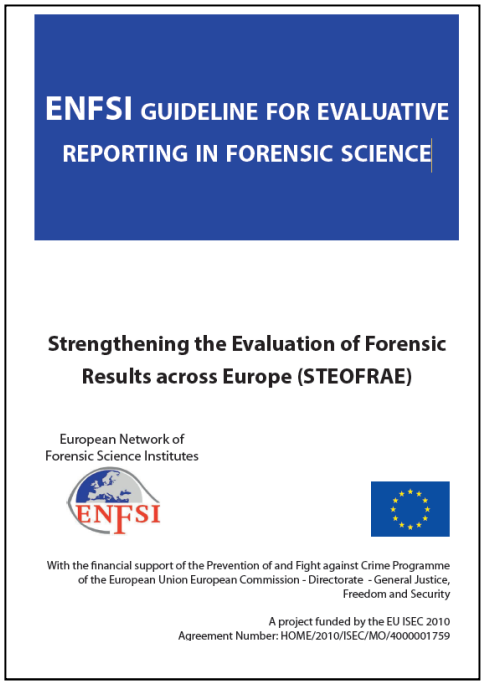
Values* of likelihood ratio	Verbal equivalent (two options of phrasing are suggested)
1	The forensic findings do not support one proposition over the other. The forensic findings provide no assistance in addressing the issue.
2 - 10	The forensic findings provide weak support** for the first proposition relative to the alternative. The forensic findings are slightly more probable given one proposition relative to the other.
10 - 100	...provide moderate support for the first proposition rather than the alternative …are more probable given…proposition...than proposition...
100 - 1000	...provide moderately strong suppor tfor the first proposition rather than the alternative …are appreciably more probable given… proposition...than proposition...
1000 - 10,000	...provide strong support for the first proposition rather than the alternative …are much more probable given… proposition...than proposition...
10,000 - 1,000,000	...provide very strong support for the first proposition rather than the alternative …are far more probable given… proposition...than proposition...
1,000,000 and above	...provide extremely strong support for the first proposition rather than the alternative …are exceedingly more probable given… proposition...than proposition...



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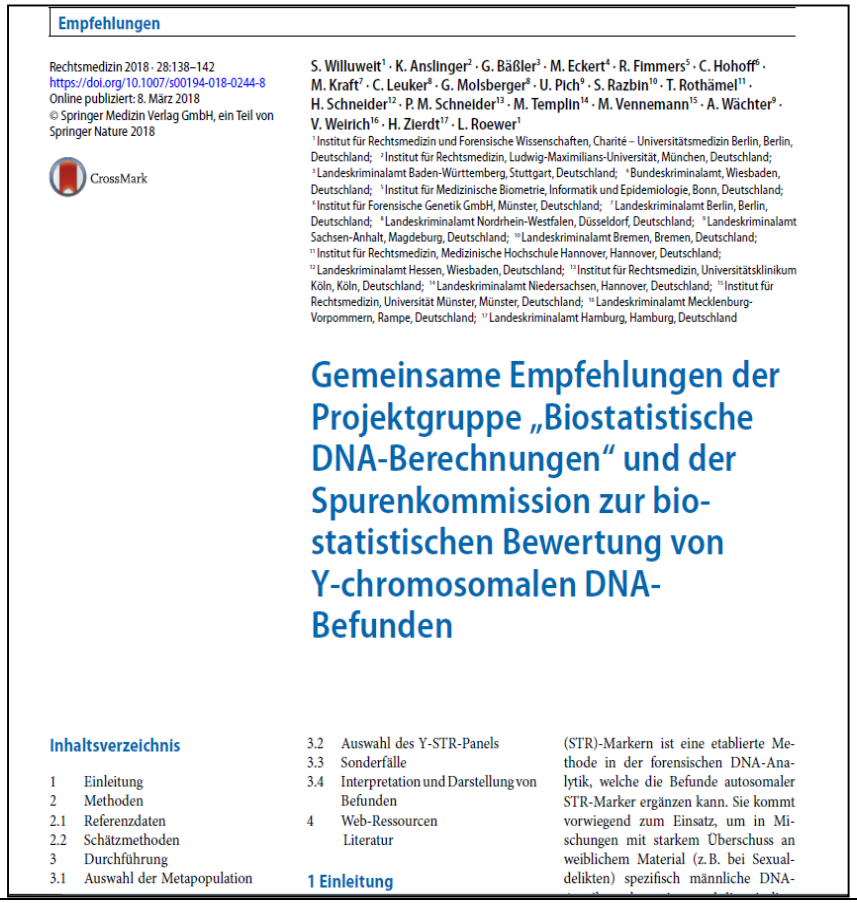

Empfehlungen

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Gemeinsame Empfehlungen der Projektgruppe „Biostatistische DNA-Berechnungen“ und der Spurenkommission zur biostatistischen Bewertung von Y-chromosomalen DNA-Befunden

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3.3 Sonderfälle
3.4 Interpretation und Darstellung von Befunden
4 Web-Ressourcen
Literatur

1 Einleitung

(STR)-Markern ist eine etablierte Methode in der forensischen DNA-Analytik, welche die Befunde autosomaler STR-Marker ergänzen kann. Sie kommt vorwiegend zum Einsatz, um in Mischungen mit starkem Überschuss an weiblichem Material (z. B. bei Sexualdelikten) spezifisch männliche DNA-

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Y-chromosomale STR-Analyse in der forensischen Praxis

Zusammenfassung
Hauptanwendungsgebiet der Y-chromosomalen DNA-Analysen ist die Identifizierung männlicher Spurenleger in Mischungen weiblicher und männlicher DNA, wie sie v. a. bei Sexualstraftaten auftreten. Die Y-STR-Analyse (Y-STR: „Y-chromosomal short tandem repeat“) dient zur Sicherung von DNA-Beweisen, wenn die konventionelle autosomale STR-Analyse ergebnislos bleibt. Im Zuge des novellierten § 81 StPO können Y-STRs zum Nachweis der Verwandtschaft zwischen männlichen Personen ersten bis dritten Grades genutzt werden. Wie für jede DNA-Identifizierung ist für Y-STR-Ergebnisse die biosta-

[German guidelines for the interpretation of Y-STR results published 2018 in: Rechtsmedizin 28(2) 138-42]

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