

2014 SWGDAM Compliant YHRD User's Guide

Release 59, November 1, 2018

Overview

Section 1: How to search a Y-STR Haplotype

Section 2: How to search a Y-STR Haplotype with reduced loci

Section 3: How to check the current state of the database

Section 4: How to check release history

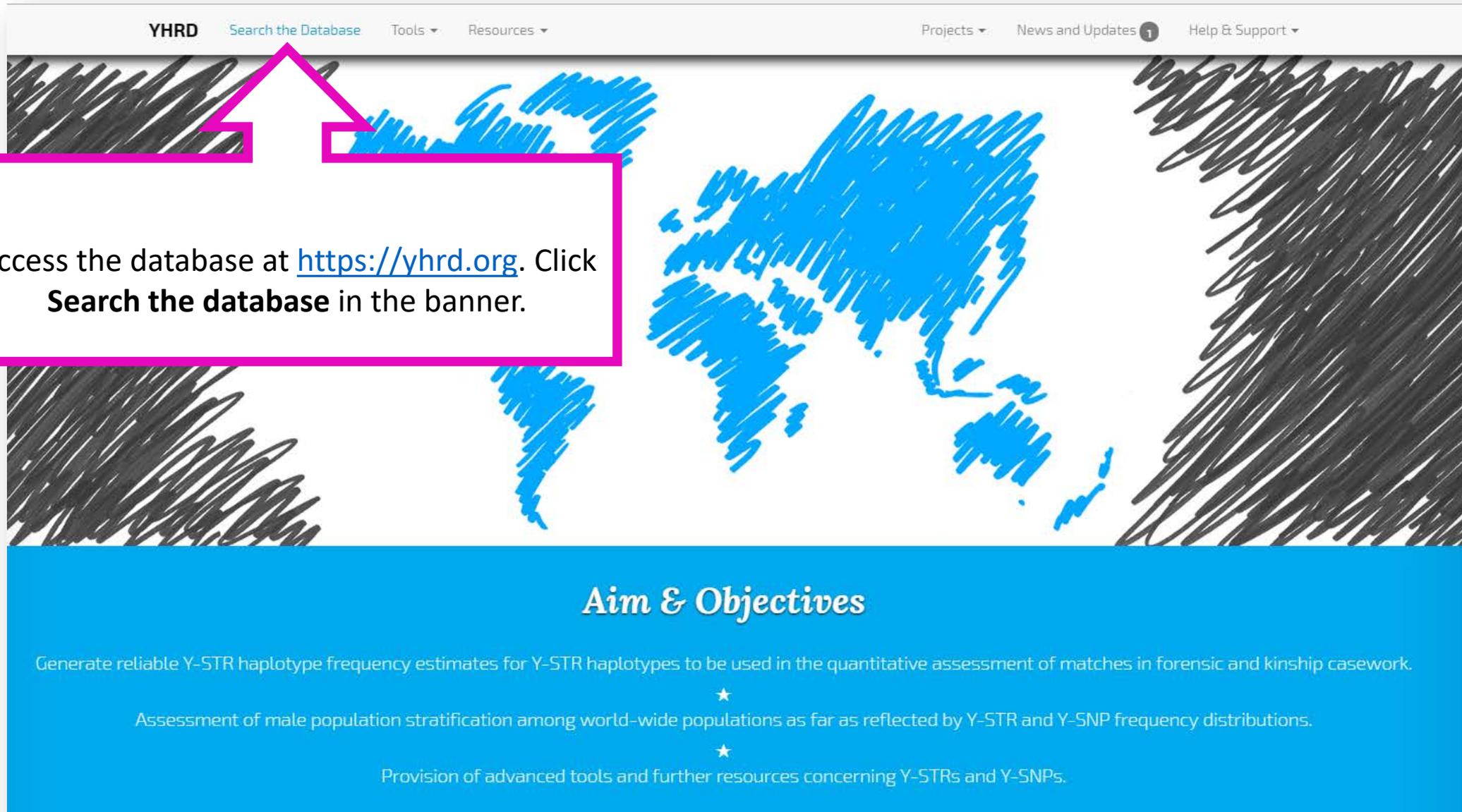
Section 5: How to obtain locus information

Section 1

How to search a Y-STR haplotype

Entry of the haplotypes can be performed manually or through a properly formatted spreadsheet. Searches can be performed individually or in batches.

How to search a Y-STR Haplotype



The image shows a screenshot of the YHRD (Y-Chromosome Haplotype Reference Database) website. The navigation bar at the top includes 'YHRD', 'Search the Database', 'Tools', 'Resources', 'Projects', 'News and Updates', and 'Help & Support'. A pink callout box with a border and arrows points to the 'Search the Database' link in the navigation bar. Below the navigation bar is a world map with blue scribbles over the continents. At the bottom of the page, there is a blue section titled 'Aim & Objectives' containing three bullet points.

Access the database at <https://yhrd.org>. Click **Search the database** in the banner.

Aim & Objectives

- Generate reliable Y-STR haplotype frequency estimates for Y-STR haplotypes to be used in the quantitative assessment of matches in forensic and kinship casework.
- ★ Assessment of male population stratification among world-wide populations as far as reflected by Y-STR and Y-SNP frequency distributions.
- ★ Provision of advanced tools and further resources concerning Y-STRs and Y-SNPs.

How to search a Y-STR Haplotype



Search using your Excel-, OpenOffice- or CSV-spreadsheet OR your Applied Biosystems® GeneMapper® ID/ID-X or ABI PRISM® Genotyper® export-file

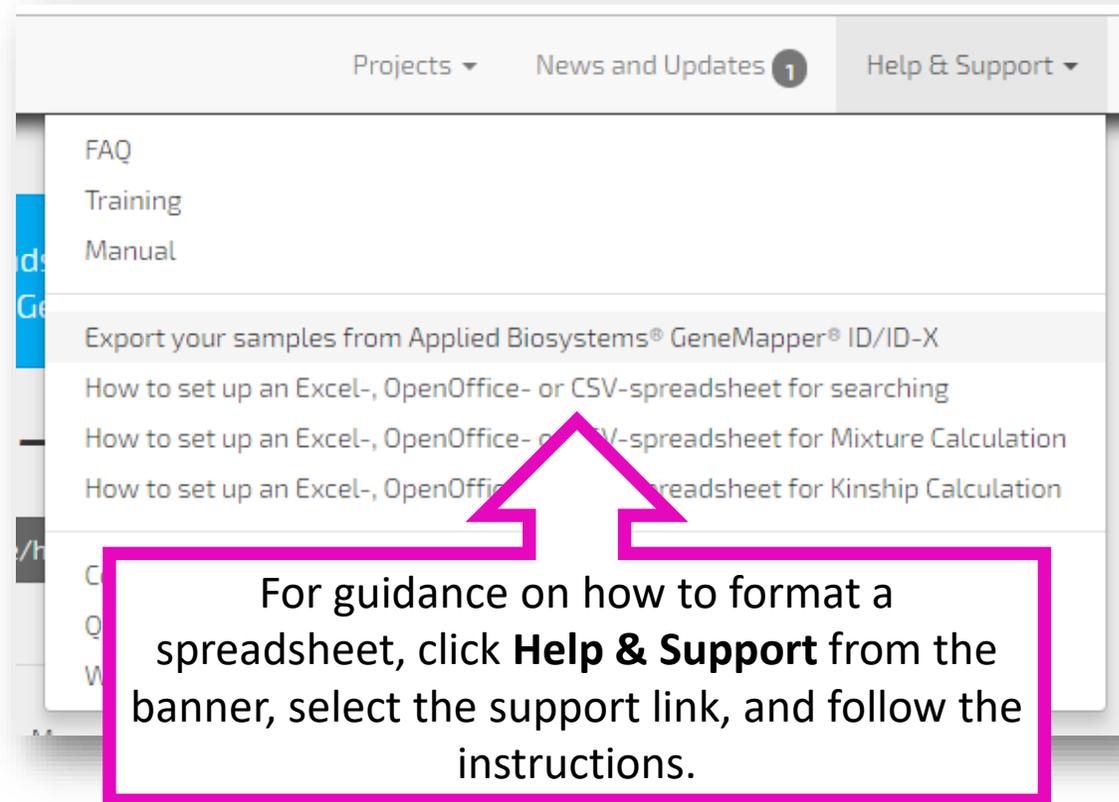
— or —



Manually enter the haplotype/haplotypes to search for

Choose your data entry option. Manually enter a haplotype or import haplotype(s) from a spreadsheet.

How to search a Y-STR Haplotype



Projects ▾ News and Updates **1** Help & Support ▾

- FAQ
- Training
- Manual
- Export your samples from Applied Biosystems® GeneMapper® ID/ID-X
- How to set up an Excel-, OpenOffice- or CSV-spreadsheet for searching
- How to set up an Excel-, OpenOffice- or CSV-spreadsheet for Mixture Calculation
- How to set up an Excel-, OpenOffice- or CSV-spreadsheet for Kinship Calculation

For guidance on how to format a spreadsheet, click **Help & Support** from the banner, select the support link, and follow the instructions.

How to search a Y-STR Haplotype

YHRD Search the Database Tools Resources Projects News and Updates 1 Help & Support

Minimal PowerPlex Y **Yfiler** PowerPlex Y23 Yfiler Plus Maximal

Manual input

DYS456 14 **DYS389I** 12 **DYS390** 23 **DYS389II** 28 **DYS458** 15 **DYS19** 14 **DYS385** 14, 15 **DYS393** 13 **DYS391** 10 **DYS439** 11 **DYS635** 22 **DYS392** 11 **YGATAH4** 11 **DYS437** 16 **DYS438** 10 **DYS448** 20

Search

To manually enter a haplotype, select the appropriate Y-STR multiplex to organize the loci, then enter each allele. Click **Search**.

How to search a Y-STR Haplotype

The screenshot shows the YHRD search interface. At the top, there are navigation links: "YHRD", "Search the Database", "Tools", "Resources", "Projects", "News and Updates", and "Help & Support". Below this, there are filter buttons: "Minimal", "PowerPlex Y", "Yfiler", "PowerPlex Y23", "Yfiler Plus", and "Maximal". The main content area displays four haplotypes, each with a checkbox and a list of loci and their corresponding values. The loci are color-coded: blue for DYS456, DYS389I, DYS390, DYS389II; green for DYS458, DYS19, DYS385; red for YGATAH4, DYS437, DYS438, DYS448; and black for DYS393, DYS391, DYS439, DYS635, DYS392. The values are shown in small boxes below each locus name.

Haplotype	DYS456	DYS389I	DYS390	DYS389II	DYS458	DYS19	DYS385	DYS393	DYS391	DYS439	DYS635	DYS392	YGATAH4	DYS437	DYS438	DYS448
<input checked="" type="checkbox"/> 1001	16	13	24	29	17	14	11, 14	13	11	11	23	13	12	15	12	19
<input type="checkbox"/> 1002	15	13	23	30	15	14	14, 19	12	8	11	21	11	11	14	9	20
<input type="checkbox"/> 1003	15	14	25	31	16	13	14, 18	14	10	11	22	14	11	14	11	19
<input type="checkbox"/> 1004	12	22	29	17	15	14, 15	13	10	12	20	11	12	17	8	20	

At the bottom of the interface is a large blue button labeled "Search".

To perform multiple searches simultaneously, check each haplotype.

If using a spreadsheet for entry, YHRD will detect the kit used to generate the data based on the loci present. Each haplotype can be searched individually or together as a batch. Click **Search** when all desired haplotypes are selected.

How to search a Y-STR Haplotype

The screenshot displays the YHRD search results for Sample #1. At the top, there are tabs for Sample #1, Sample #2, Sample #3, and Sample #4. A pink box with arrows pointing to these tabs contains the text: "If you performed a batch search, select each sample tab to view search results." Below the tabs is the "Report for Sample #1" section, which includes the sample name "1001" and a list of Y-STR markers with their corresponding repeat counts: **DYS456** 16, **DYS389I** 13, **DYS390** 24, **DYS389II** 29, **DYS458** 17, **DYS19** 14, **DYS385** 11,14, **DYS393** 13, **DYS391** 11, **DYS439** 11, **DYS635** 23, **DYS392** 13, **YGATAH4** 12, **DYS437** 15, **DYS438** 12, and **DYS448** 19. A blue bar below the markers contains the text "+ Add feature to this Report". The main search results are displayed in a "Worldwide" panel, which includes an "Observed" section stating "Found 46 matches in 20,059 Haplotypes. This is approx. 1 match in 4,458 Haplotypes (95% CI ⚙: 1 in 5,938 — 1 in 3,342)" and an "Expected" section with three metrics: **DL (Yfiler)** (Approx. 1 match in 6,509 Haplotypes), **n+1/N+1** (Approx. 1 match in 4,863 Haplotypes), and **Kappa** (Approx. 1 match in 10,090 Haplotypes). A pink box with an arrow pointing to the "Worldwide" panel contains the text: "YHRD automatically searches each haplotype against the Worldwide database. See next slide for U.S. database searches."

Minimal

Sample #1 Sample #2 Sample #3 Sample #4

Report for Sample #1

Sample Name: 1001

DYS456 **DYS389I** **DYS390** **DYS389II** **DYS458** **DYS19** **DYS385** **DYS393** **DYS391** **DYS439** **DYS635** **DYS392** **YGATAH4** **DYS437** **DYS438** **DYS448**

16 13 24 29 17 14 11,14 13 11 11 23 13 12 15 12 19

+ Add feature to this Report

Worldwide

Observed

Found 46 matches in 20,059 Haplotypes. This is approx. 1 match in 4,458 Haplotypes (95% CI ⚙: 1 in 5,938 — 1 in 3,342).

Expected

- DL (Yfiler)** ⚙ Approx. 1 match in 6,509 Haplotypes . Please note, this value is an average over the DL values of all [nested feasible metapopulations](#).
- n+1/N+1** ⚙ Approx. 1 match in 4,863 Haplotypes (95% CI ⚙: 1 in 5,938 — 1 in 3,342)
- Kappa** ⚙ Approx. 1 match in 10,090 Haplotypes

If you performed a batch search, select each sample tab to view search results.

YHRD automatically searches each haplotype against the Worldwide database. See next slide for U.S. database searches.

How to search a Y-STR Haplotype

Sample #1 Sample #2 Sample #3 Sample #4

Report for Sample #1

Sample Name: 1001

DYS456 DYS389I DYS390 DYS389II DYS458 DYS19 DYS385 DYS393 DYS391 DYS439 DYS635 DYS392 YGATAH4 DYS437 DYS438 DYS448

16 13 24 29 17 14 11, 14 13 11 11 23 13 12 15 12 19

+ Add feature to this Report ▾

- Metapopulation
- National Database
- National Database (with Subpopulations, 2014 SWGDAM-compliant)
- Ancestry Information (Minimum Haplotype)
- Ancestry Information (Yfiler Haplotype)
- Ancestry Information (1-Step-Neighbor)
- Expected

DL (Yfiler) ⓘ	Approx. 1 match in 1,509 Haplotypes . Please
n+1/N+1 ⓘ	Approx. 1 match in 4,387 Haplotypes (95%)
Kappa ⓘ	Approx. 1 match in 10,098 Haplotypes

To search against the U.S. database, click **Add feature to this Report** to view the dropdown menu, then select **National Database (with Subpopulations, 2014 SWGDAM-compliant)**.

How to search a Y-STR Haplotype

The results of the search against the **National Database (with Subpopulations) – United States** is now included in the results panel. This database contains the U.S. Y-STR Database samples.

DL (Yfiler) Approx. 1 match in 2,662 Haplotypes. Please note, this value is an average over the DL values of all nested feasible metapopulations.
n+1/N+1 Approx. 1 match in 1,342 Haplotypes (95% UCI : 1 in 5,938 — 1 in 3,342)
Kappa Approx. 1 match in 1,098 Haplotypes

National Database (with Subpopulations) - United States (click to change)

Observed

Found 2 matches in 7,118 Haplotypes in United States (African American). This is approx. 1 match in 3,559 Haplotypes (95% UCI : 1 in 1,131) in United States (African American).
Found no match in 4,083 Haplotypes (95% UCI : 1 in 1,363) in United States (Asian).
Found 6 matches in 8,483 Haplotypes in United States (Caucasian). This is approx. 1 match in 1,414 Haplotypes (95% UCI : 1 in 717) in United States (Caucasian).
Found 2 matches in 6,012 Haplotypes in United States (Hispanic). This is approx. 1 match in 3,006 Haplotypes (95% UCI : 1 in 955) in United States (Hispanic).
Found 1 match in 3,581 Haplotypes (95% UCI : 1 in 755) in United States (Native American).
Found 11 matches in 29,277 Haplotypes in United States (Overall). This is approx. 1 match in 2,662 Haplotypes (95% UCI : 1 in 1,608) in United States (Overall).

Theta-corrected Match Probability

Given a theta-value of 6.0×10^{-05} and a 95% UCI of the combined Haplotype frequency of 1 in 1515 (10 matches in 25696 Haplotypes at U.S. subpopulations without Native American), the corrected Match Probability is 1 in 1389.
Given a theta-value of 4.0×10^{-04} and a 95% UCI of the combined Haplotype frequency of 1 in 1608 (11 matches in 29277 Haplotypes at U.S. subpopulations with Native American), the corrected Match Probability is 1 in 979.

Expected n+1/N+1

Expected Kappa

How to search a Y-STR Haplotype

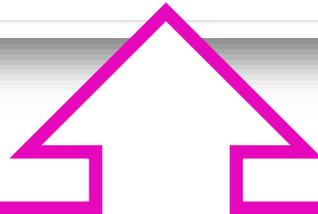
National Database (with Subpopulations) - United States (click to change) ✕

Observed

Found 2 matches in 7,118 Haplotypes in United States (African American). This is approx. 1 match in 3,559 Haplotypes (95% UCI ⓘ: 1 in 1,131 ↘) in United States (African American).
Found no match in 4,083 Haplotypes (95% UCI ⓘ: 1 in 1,363 ↘) in United States (Asian).
Found 6 matches in 8,483 Haplotypes in United States (Caucasian). This is approx. 1 match in 1,414 Haplotypes (95% UCI ⓘ: 1 in 717 ↘) in United States (Caucasian).
Found 2 matches in 6,012 Haplotypes in United States (Hispanic). This is approx. 1 match in 3,006 Haplotypes (95% UCI ⓘ: 1 in 955 ↘) in United States (Hispanic).
Found 1 match in 3,581 Haplotypes (95% UCI ⓘ: 1 in 755 ↘) in United States (Native American).
Found 11 matches in 29,277 Haplotypes in United States (Overall). This is approx. 1 match in 2,662 Haplotypes (95% UCI ⓘ: 1 in 1,608 ↘) in United States (Overall).

Theta-corrected Match Probability ⓘ

Given a theta-value of 6.0×10^{-05} and a 95% UCI ⓘ of the combined Haplotype frequency of 1 in 1515 (10 matches in 25696 Haplotypes at U.S. subpopulations without Native American), the corrected Match Probability is 1 in 1389.
Given a theta-value of 4.0×10^{-04} and a 95% UCI ⓘ of the combined Haplotype frequency of 1 in 1608 (11 matches in 29277 Haplotypes at U.S. subpopulations with Native American), the corrected Match Probability is 1 in 979.



The **Observed** results box includes the observed haplotype frequencies and 1-sided 95% upper confidence interval profile probabilities for each subpopulation (African American, Asian, Caucasian, Hispanic, Native American, and Overall). The **Theta-corrected Match Probability** results box provides two combined theta-corrected match probabilities (with and without the Native American population).

Note: in this particular search, haplotypes from the Native American population were included in the database. As of November 2018, no Native American population samples are present in the 'maximal' database.

How to search a Y-STR Haplotype

Worldwide

Back Alt+Left Arrow
Forward Alt+Right Arrow
Reload Ctrl+R
Save as... Ctrl+S
Print... Ctrl+P
Cast...
Translate to English
View page source Ctrl+U
Inspect Ctrl+Shift+I

Haplotypes. This is approx. 1 match in 4,458 Haplotypes

Approx. 1 match in 6,509 Haplotypes . Please note, this is

Approx. 1 match in 4,363 Haplotypes (95% CI 1 in 5,9

Approx. 1 match in 10,098 Haplotypes

To save search results, right click anywhere on the page or **Ctrl + P** and select **print**. You will have the option to save as a pdf or print results.

National Database (with Subpopulations) - United States (click to change)

Observed

Found 2 matches in 7,118 Haplotypes in United States (African American). This is approx. 1 match in 3,559 Haplotypes (95% UCI 1 in 1,131) in United States (African American).
Found no match in 4,083 Haplotypes (95% UCI 1 in 1,363) in United States (Asian).
Found 6 matches in 8,483 Haplotypes in United States (Caucasian). This is approx. 1 match in 1,414 Haplotypes (95% UCI 1 in 717) in United States (Caucasian).
Found 2 matches in 6,012 Haplotypes in United States (Hispanic). This is approx. 1 match in 3,006 Haplotypes (95% UCI 1 in 955) in United States (Hispanic).
Found 1 match in 3,581 Haplotypes (95% UCI 1 in 755) in United States (Native American).

Found 11 matches in 29,277 Haplotypes in United States (Overall). This is approx. 1 match in 2,662 Haplotypes (95% UCI 1 in 1,608) in United States (Overall).

Theta-corrected Match Probability

Given a theta-value of 6.0×10^{-05} and a 95% UCI of the combined Haplotype frequency of 1 in 1515 (10 matches in 25696 Haplotypes at U.S. subpopulations without Native American), the corrected Match Probability is 1 in 1389.
Given a theta-value of 4.0×10^{-04} and a 95% UCI of the combined Haplotype frequency of 1 in 1608 (11 matches in 29277 Haplotypes at U.S. subpopulations with Native American), the corrected Match Probability is 1 in 979.

Expected $n+1/N+1$

Expected Kappa

How to search a Y-STR Haplotype

Report for Sample #1

Sample Name: Maximal Profile

DYS19 14 DYS389I 12 DYS389II 28 DYS390 23 DYS391 10 DYS392 11 DYS393 13 DYS385 14,15 DYS438 10 DYS439 11 DYS437 16 DYS448 20 DYS456 14 DYS458 15 DYS635 22 YGATAH4 11 DYS481 25 DYS533 11 DYS549 12 DYS570 19 DYS576 16 DYS643 12 DYF38751 37,37 DYS449 28 DYS460 10 DYS518 40 DYS627 19

This search of a maximal haplotype (29 loci) provides an example that does not return results from the Native American population because no Native American haplotypes exist in the maximal population database. Also note that because the number of loci in the searched haplotype exceeds 22 loci, theta-corrected match probabilities are not provided (refer to Appendix 1 of the 2014 SWGDAM *Interpretation Guidelines for Y-Chromosome STR Typing*).

DL (Yfiler) Approx. 1 match in 2,646 Haplotypes. Please note, this value is an average over the DL values of all the populations.
n+1/N+1 Approx. 1 match in 2,759 Haplotypes (95% CI : 1 in 22,772 — 1 in 990).
Kappa Approx. 1 match in 139,595 Haplotypes.

National Database (with Subpopulations) - United States (click to change)

Observed

Found no match in 242 Haplotypes (95% UCI : 1 in 81) in United States (African American).
Found no match in 2 Haplotypes (95% UCI : 1 in 1) in United States (Asian).
Found 1 match in 229 Haplotypes (95% UCI : 1 in 49) in United States (Caucasian).
Found no match in 102 Haplotypes (95% UCI : 1 in 35) in United States (Hispanic).
There are no Haplotypes in United States (Native American).
Found 1 match in 575 Haplotypes (95% UCI : 1 in 122) in United States (Overall).

Expected n+1/N+1

Expected Kappa

Section 2

How to search a Y-STR haplotype with reduced loci

Per the 2014 SWGDAM Y-STR Interpretation Guidelines, it is acceptable to perform additional searches of the population database using reduced locus sets in an attempt to obtain the maximal discrimination potential for that combination of evidence and population database profiles. This section describes how to perform reduced loci searches using YHRD.

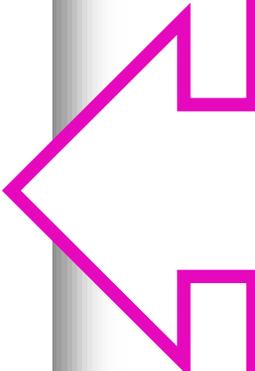
How to search a Y-STR Haplotype with reduced loci

YHRD Reduced Locus Search Instructions

Underlined text represents an example for illustration purposes. In the example spreadsheet accompanying these instructions, the corresponding cells are as follows: $x_1 = G4$, $n_1 = H4$; $x_2 = G8$, $n_2 = H8$ and $H11$, $x_3 = G9$, $x_4 = G10$, $x_5 = G11$.

Note: this procedure requires calculations outside of the YHRD website.

1. Search the full multiplex haplotype (PP Y23) in YHRD against the Worldwide and US National Database. Record x_1 , n_1 , 1 in (x/n), and 1 in (95% UCI) values.
2. Within the YHRD report results page, select the next smallest multiplex (Yfiler) to search the haplotype with a reduced number of loci. Record x_2 and n_2 .
3. Next, reselect the full multiplex haplotype within the YHRD report results page to search the reduced number of loci against the dataset for the larger multiplex (Yfiler loci against PP Y23 dataset). Record the number of matches (x_3).
4. Subtract the number of matches (x_3) obtained from the third search (PP Y23 dataset with Yfiler loci) from the number of matches (x_2) obtained from the second search (Yfiler). The value obtained (x_4) represents the number of haplotypes from the smaller dataset (Yfiler) that are excluded from the larger dataset (PP Y23) and are representative of that multiplex only (Just Yfiler). Note: haplotypes are excluded because they were tested with the larger multiplex and did not match at the additional loci.
5. To obtain the total number of matches from both datasets, add the number of matches (x_1) observed from the original full multiplex haplotype (PP Y23) to the number of matches (x_4) calculated in the previous step (Just Yfiler). Record this value (x_5). Use the n_2 from the larger dataset (from search in step 2) to calculate the frequency estimate (1 in x/n) and the profile probability (1 in 95% UCI).
6. The process from step 2 through step 5 can be repeated for all existing smaller multiplexes (PPY and Minimal). Combine the number of matches observed with each dataset (Total PPY = PPY23 + Just Yfiler + Just PPY; Total Minimal = PPY23 + Just Yfiler + Just PPY + Just Minimal) to calculate new frequency estimates and profile probabilities.
7. Determine the most and least discriminatory profile probabilities and report per your laboratory's guidelines.



These instructions guide the user through the entire process. The following slides will illustrate these steps with an example. Note: these instructions refer to items on a spreadsheet that is shown in the next slide.

How to search a Y-STR Haplotype with reduced loci

A spreadsheet is recommended to record values obtained from reduced locus searches. Note: cells in this spreadsheet are referenced in the previous slide.

	A	B	C	D	E	F	G	H	I	J
1			Worldwide				US (SWGAM Total)			
2			PPY23 or YFP loci				PPY23 or YFP loci			
3			x	n	1 in (x/n)	1 in (95% UCI)	x	n	1 in (x/n)	1 in (95% UCI)
4		PPY23 or YFP profiles	2	50692	25,346	8,052	2	5717	2,859	908
5										
6			Yfiler loci				Yfiler loci			
7			x	n	1 in (x/n)	1 in (95% UCI)	x	n	1 in (x/n)	1 in (95% UCI)
8		Yfiler profiles	26	205059			12	29277		
9		PPY23 or YFP profiles	10				5			
10		Just Yfiler	16				7			
11		Total Yfiler	18	205059	11,392	7,683	9	29277	3,253	1,864
12										
13			PPY loci				PPY loci			
14			x	n	1 in (x/n)	1 in (95% UCI)	x	n	1 in (x/n)	1 in (95% UCI)
15		PPY profiles	732	224657			233	35864		
16		Yfiler profiles	646				189			
17		Just PPY	86				44			
18		Total PPY	104	224657	2,160	1,835	53	35864	677	538
19										
20			Minimal loci				Minimal loci			
21			x	n	1 in (x/n)	1 in (95% UCI)	x	n	1 in (x/n)	1 in (95% UCI)
22		Minimal profiles	1906	265324			576	40923		
23		PPY profiles	1569				503			
24		Just Minimal	337				73			
25		Total Minimal	441	265324	602	556	126	40923	325	280
26										
27										
28		Notes:	= a cell in which you'll enter search results							
29			Total Yfiler = Just Yfiler + (PPY23 or YFP)							
30			Total PPY = Just PPY + Total Yfiler = Just PPY + Just Yfiler + (PPY23 or YFP)							
31			Total Minimal = Just Minimal + Total PPY = Just Minimal + Just PPY + Just Yfiler + (PPY23 or YFP)							
32			Per YHRD Search Instructions, G4 = X1; H4 = n1; G8 = X2; H8 & H11 = n2; G9 = X3; G10 = X4; G11 = X5							

How to search a Y-STR Haplotype with reduced loci

The screenshot shows the YHRD search interface. At the top, there are navigation links: YHRD, Search the Database, Tools, Resources, Projects, News and Updates (with a notification badge), and Help & Support. Below this, there are filter buttons for different marker sets: Minimal, PowerPlex Y, Yfiler, PowerPlex Y23 (highlighted in blue), Yfiler Plus, and Maximal. A checkbox labeled 'C' is checked. Below the checkbox, a row of Y-STR loci is displayed with their corresponding allele values in input boxes. The loci and their values are: DYS576 (17), DYS389I (13), DYS448 (19), DYS389II (29), DYS19 (14), DYS391 (11), DYS481 (22), DYS549 (13), DYS533 (12), DYS438 (12), DYS437 (15), DYS570 (17), DYS635 (23), DYS390 (23), DYS439 (12), DYS392 (13), DYS643 (10), DYS393 (13), DYS458 (16), DYS385 (11, 14), DYS456 (15), and YGATAH4 (12). A large blue 'Search' button is positioned below the input boxes.

Follow the instructions in Section 1 to enter the complete Y-STR haplotype and click **Search**.

How to search a Y-STR Haplotype with reduced loci

Minimal PowerPlex Y Yfiler PowerPlex Y23 Yfiler Plus Maximal

Report for Sample #1

Sample Name: C

DYS576	DYS389I	DYS448	DYS389II	DYS19	DYS391	DYS481	DYS549	DYS533	DYS438	DYS437	DYS570	DYS635	DYS390	DYS439	DYS392	DYS643	DYS393	DYS458	DYS385	DYS456	YGATAH4
17	13	19	29	14	11	22	13	12	12	15	17	23	23	12	13	10	13	16	11,14	15	12

In this example, the PP Y23 haplotype has been observed 2 times (x_1) in the National Database (with Subpopulations) – United States (out of 5,717 haplotypes; n_1) and has a 1 in 908 profile probability. Now that the entire database has been searched with the complete Y-STR haplotype, select the next smallest multiplex that has fewer loci than your Y-STR haplotype and search again (next slide).

Note: A more discriminating set of loci gives a less discriminating frequency estimate than a less discriminating set of loci, simply because there were fewer database profiles typed with the more discriminating set.

National Database (with Subpopulations) - United States (click to change)

Observed

- Found no match in 1,356 Haplotypes (95% UCI 1 in 453) in United States (African American).
- Found no match in 708 Haplotypes (95% UCI 1 in 237) in United States (Asian).
- Found 2 matches in 1,549 Haplotypes in United States (Caucasian). This is approx. 1 match in 775 Haplotypes (95% UCI 1 in 237) in United States (Caucasian).
- Found no match in 1,223 Haplotypes (95% UCI 1 in 409) in United States (Hispanic).
- Found no match in 881 Haplotypes (95% UCI 1 in 295) in United States (Native American).
- Found 2 matches in 5,717 Haplotypes in United States (Overall). This is approx. 1 match in 2,859 Haplotypes (95% UCI 1 in 908) in United States (Overall).

Theta-corrected Match Probability

- Given a theta-value of 2.0×10^{-5} and a 95% UCI of the combined Haplotype frequency of 1 in 768 (2 matches in 4836 Haplotypes at U.S. subpopulations without Native American), the corrected Match Probability is 1 in 756.
- Given a theta-value of 3.0×10^{-4} and a 95% UCI of the combined Haplotype frequency of 1 in 908 (2 matches in 5717 Haplotypes at U.S. subpopulations with Native American), the corrected Match Probability is 1 in 714.

How to search a Y-STR Haplotype with reduced loci

The screenshot shows a web interface for a Y-STR haplotype search. At the top, there are tabs for different search methods: Minimal, PowerPlex Y, Yfiler (selected), PowerPlex Y23, Yfiler Plus, and Maximal. Below this, a report for 'Sample #1' is displayed, showing the sample name and a list of loci with their repeat counts. A blue bar with a '+ Add feature to this Report' button is visible. Below the bar, there are two panels: 'Worldwide' and 'National Database (with Subpopulations) - United States'. The 'Worldwide' panel shows 'Observed' results (26 matches in 205,059 Haplotypes) and 'Expected' results for various markers (DL, n+1/N+1, Kappa). The 'National Database' panel shows 'Observed' results for various subpopulations and an overall result. A callout box with a pink border and arrow points to the 'Yfiler' tab, containing the following text:

To reduce the number of loci in the previously searched haplotype, click on the next smallest multiplex (do not return to the **Search the Database** tab). The reduced locus haplotype will be displayed and the search results will automatically be updated to reflect a reduced locus search.

How to search a Y-STR Haplotype with reduced loci

Minimal PowerPlex Y **Yfiler** PowerPlex Y23 Yfiler Plus Maximal

Report for Sample #1

Sample Name: C

DYS456 15 DYS389I 13 DYS390 23 DYS389II 29 DYS458 16 DYS19 14 DYS385 11,14 DYS393 13 DYS391 11 DYS439 12 DYS635 23 DYS392 13 **YGATAH4 12** **DYS437 15** **DYS438 12** **DYS448 19**

+ Add feature to this Report ▾

Worldwide

Observed

Found 26 matches in 205,059 Haplotypes. This is approx. 1 match in 7,887 Haplotypes (95% CI ⓘ: 1 in 11,524 — 1 in 5,383 ▾).

Expected

- DL (Yfiler)** ⓘ Approx. 1 match in 14,961 Haplotypes. Please note, this value is an average over the DL values of all [nested feasible metapopulations](#).
- n+1/N+1** ⓘ Approx. 1 match in 7,595 Haplotypes (95% CI ⓘ: 1 in 11,524 — 1 in 5,383 ▾)
- Kappa** ⓘ Approx. 1 match in 17,578 Haplotypes

National Database (with Subpopulations) - United States (click to change)

Observed

Found no match in 7,118 Haplotypes (95% UCI ⓘ: 1 in 2,377 ▾) in United States (African American).
Found no match in 4,083 Haplotypes (95% UCI ⓘ: 1 in 1,363 ▾) in United States (Asian).
Found 7 matches in 8,483 Haplotypes in United States (Caucasian). This is approx. 1 match in 1,212 Haplotypes (95% UCI ⓘ: 1 in 645 ▾) in United States (Caucasian).
Found 4 matches in 6,012 Haplotypes in United States (Hispanic). This is approx. 1 match in 1,503 Haplotypes (95% UCI ⓘ: 1 in 657 ▾) in United States (Hispanic).
Found 1 match in 3,581 Haplotypes (95% UCI ⓘ: 1 in 755 ▾) in United States (Native American).
Found 12 matches in 29,277 Haplotypes in United States (Overall). This is approx. 1 match in 2,440 Haplotypes (95% UCI ⓘ: 1 in 1,506 ▾) in United States (Overall).

Theta-corrected Match Probability ⓘ

Given a theta-value of 6.0×10^{-05} and a 95% UCI ⓘ of the combined Haplotype frequency of 1 in 1411 (11 matches in 25696 Haplotypes at U.S. subpopulations without Native American), the corrected Match Probability is 1 in 1,411.

Given a theta-value of 4.0×10^{-04} and a 95% UCI ⓘ of the combined Haplotype frequency of 1 in 1506 (12 matches in 29277 Haplotypes at U.S. subpopulations with Native American), the corrected Match Probability is 1 in 1,506.

In this reduced locus search using just the Yfiler loci, the haplotype has been observed 12 times (x_2) out of 29,277 haplotypes (n_2) in the National Database (with Subpopulations) – United States.

See the next slide to determine how many of these 12 observations, based on Yfiler loci, are present in the PP Y23 database.

How to search a Y-STR Haplotype with reduced loci

Minimal PowerPlex Y Yfiler **PowerPlex Y23** Yfiler Plus Maximal

Report for Sample #1

Sample Name: C

DYS576	DYS389I	DYS448	DYS389II	DYS19	DYS391	DYS481	DYS549	DYS533	DYS438	DYS437	DYS570	DYS635	DYS390	DYS439	DYS392
.	13	.	29	14	11	.	.	.	12	15	.	.	23	12	13
DYS643	DYS393	DYS458	DYS385	DYS456	YGATAH4										
.	13	.	11, 14	.	.										

To search the PP Y23 database without the additional loci beyond the Yfiler multiplex, select the **PowerPlex Y23** button (do not return to the **Search the Database** tab). Note that the haplotype displays all of the alleles present in the Yfiler multiplex but the additional loci in the PP Y23 multiplex are represented by a dot. The search results will automatically be updated to reflect a search of the PP Y23 dataset using the Yfiler haplotype.

How to search a Y-STR Haplotype with reduced loci

Minimal PowerPlex Y Yfiler **PowerPlex Y23** Yfiler Plus Maximal

Report for Sample #1

Sample Name: C

DYS576 13 DYS389I 19 DYS448 29 DYS389II 29 DYS19 14 DYS391 11 DYS481 - DYS549 - DYS533 - DYS438 12 DYS437 15 DYS570 - DYS635 23 DYS390 23 DYS439 12 DYS392 13 DYS643 - **DYS393 13** **DYS458 16** **DYS385 11,14** **DYS456 15** **YGATAH4 12**

+ Add feature to this Report

Worldwide

Observed
Found 10 matches in 50,692 Haplotypes. This is approx. 1 match in 5,069 Haplotypes (95% UCI: 1 in 9,231 — 1 in 2,757).

Expected

- DL (Yfiler)** Approx. 1 match in 14,961 Haplotypes. Please note, this value is an average over the DL values of all nested feasible metapopulations.
- n+1/N+1** Approx. 1 match in 4,608 Haplotypes (95% UCI: 1 in 9,231 — 1 in 2,757)
- Kappa** Approx. 1 match in 38,084 Haplotypes

National Database (with Subpopulations) - United States (click to change)

Observed

Found no match in 1,356 Haplotypes (95% UCI: 1 in 453) in United States (African American).
Found no match in 708 Haplotypes (95% UCI: 1 in 237) in United States (Asian).
Found 3 matches in 1,549 Haplotypes in United States (Caucasian). This is approx. 1 match in 516 Haplotypes (95% UCI: 1 in 200) in United States (Caucasian).
Found 2 matches in 1,223 Haplotypes in United States (Hispanic). This is approx. 1 match in 612 Haplotypes (95% UCI: 1 in 195) in United States (Hispanic).
Found no match in 881 Haplotypes (95% UCI: 1 in 295) in United States (Native American).

Found 5 matches in 5,717 Haplotypes in United States (Overall). This is approx. 1 match in 1,143 Haplotypes (95% UCI: 1 in 544) in United States (Overall).

Theta-corrected Match Probability

Given a theta-value of 6.0×10^{-05} and a 95% UCI of the combined Haplotype frequency of 1 in 460 (5 matches in 4836 Haplotypes at U.S. subpopulations without Native American), the corrected Match Probability is 1 in 1,143.

Given a theta-value of 4.0×10^{-04} and a 95% UCI of the combined Haplotype frequency of 1 in 544 (5 matches in 5717 Haplotypes at U.S. subpopulations with Native American), the corrected Match Probability is 1 in 1,143.

The Yfiler haplotype searched against the PP Y23 dataset has been observed 5 times (x_3) in the National Database (with Subpopulations) – United States (out of 5,717 haplotypes).

A user will subtract the number of matches from this search (x_3) from the number of matches obtained from second search (x_2). This new value, x_4 , represents the number of haplotypes from the smaller dataset (Yfiler) that are excluded from the larger dataset (PP Y23) and are representative of that multiplex only (Just Yfiler).

How to search a Y-STR Haplotype with reduced loci

	A	B	C	D	E	F	G	H	I	J
1			Worldwide				US (SWGDM Total)			
2			PPY23 or YFP loci				PPY23 or YFP loci			
3			x	n	1 in (x/n)	1 in (95% UCI)	x	n	1 in (x/n)	1 in (95% UCI)
4		PPY23 or YFP profiles	2	50692	25,346	8,052	2	5717	2,859	908
5										
6			Yfiler loci				Yfiler loci			
7			x	n	1 in (x/n)	1 in (95% UCI)	x	n	1 in (x/n)	1 in (95% UCI)
8		Yfiler profiles	26	205059			12	29277		
9		PPY23 or YFP profiles	10				5			
10		Just Yfiler	16				7			
11		Total Yfiler	18	205059	11,392	7,683	9	29277	3,253	1,864
12										

To obtain the total number of matches from both datasets, add the number of matches observed from the first search using the full multiplex haplotype ($x_1 = 2$) to the number of matches calculated in the previous step (Just Yfiler, $x_4 = 7$). Record this value ($x_5 = 9$). Use the n_2 (29,277) from the larger dataset to calculate the frequency estimate (1 in x/n) and the profile probability (1 in 95% UCI).

How to search a Y-STR Haplotype with reduced loci

Minimal **PowerPlex Y** Yfiler PowerPlex Y23 Yfiler Plus Maximal

Report for Sample #1

Sample Name: C

DYS391	DYS389I	DYS439	DYS389II	DYS438	DYS437	DYS19	DYS392	DYS393	DYS390	DYS385
11	13	12	29	12	15	14	13	13	23	11, 14



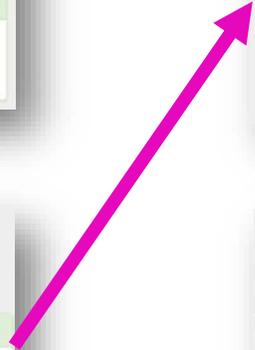
Minimal PowerPlex Y **Yfiler** PowerPlex Y23 Yfiler Plus Maximal

Report for Sample #1

Sample Name: C

DYS456	DYS389I	DYS390	DYS389II	DYS458	DYS19	DYS385	DYS393	DYS391	DYS439	DYS635	DYS392	YGATAH4	DYS437	DYS438
.	13	23	29	.	14	11, 14	13	11	12	.	13	.	15	12

DYS448
.



Minimal **PowerPlex Y** Yfiler PowerPlex Y23 Yfiler Plus Maximal

Report for Sample #1

Sample Name: C

DYS19	DYS389I	DYS389II	DYS390	DYS391	DYS392	DYS393	DYS385
14	13	29	23	11	13	13	11, 14



Minimal **PowerPlex Y** Yfiler PowerPlex Y23 Yfiler Plus Maximal

Report for Sample #1

Sample Name: C

DYS391	DYS389I	DYS439	DYS389II	DYS438	DYS437	DYS19	DYS392	DYS393	DYS390	DYS385
11	13	.	29	.	.	14	13	13	23	11, 14



Continue to perform reduced locus searches by selecting the next smallest multiplex (PP Y), record new values (x and n), then search the previous multiplex (Yfiler) again, record new value (x), and calculate new frequency estimates and profile probabilities. Repeat until all multiplexes (Minimal) have been searched.

How to search a Y-STR Haplotype with reduced loci

Once all datasets are searched and new frequency estimates and profile probabilities are calculated, the profile probabilities can be compared to determine the most and least discriminatory probabilities.

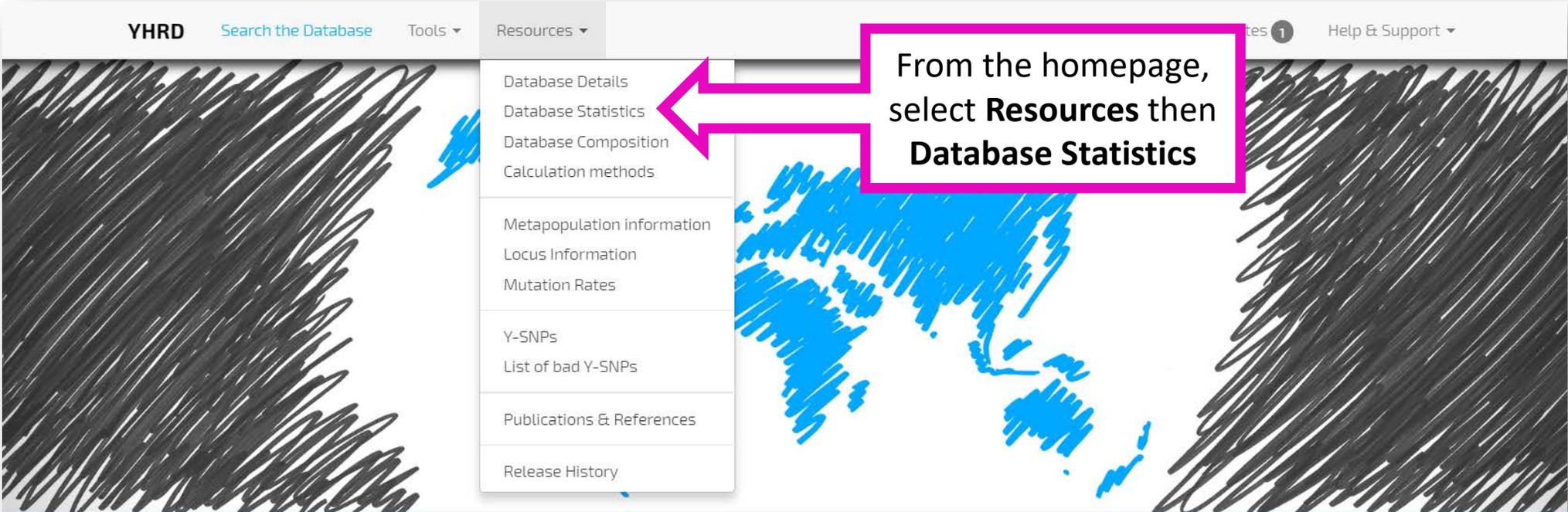
	A	B	C	D	E	F	G	H	I	J
1			Worldwide				US (SWGDM Total)			
2			PPY23 or YFP loci				PPY23 or YFP loci			
3			x	n	1 in (x/n)	1 in (95% UCI)	x	n	1 in (x/n)	1 in (95% UCI)
4		PPY23 or YFP profiles	2	50692	25,346	8,052	2	5717	2,859	908
5										
6			Yfiler loci				Yfiler loci			
7			x	n	1 in (x/n)	1 in (95% UCI)	x	n	1 in (x/n)	1 in (95% UCI)
8		Yfiler profiles	26	205059			12	29277		
9		PPY23 or YFP profiles	10				5			
10		Just Yfiler	16				7			
11		Total Yfiler	18	205059	11,392	7,683	9	29277	3,253	1,864
12										
13			PPY loci				PPY loci			
14			x	n	1 in (x/n)	1 in (95% UCI)	x	n	1 in (x/n)	1 in (95% UCI)
15		PPY profiles	732	224657			233	35864		
16		Yfiler profiles	646				189			
17		Just PPY	86				44			
18		Total PPY	104	224657	2,160	1,835	53	35864	677	538
19										
20			Minimal loci				Minimal loci			
21			x	n	1 in (x/n)	1 in (95% UCI)	x	n	1 in (x/n)	1 in (95% UCI)
22		Minimal profiles	1906	265324			576	40923		
23		PPY profiles	1569				503			
24		Just Minimal	337				73			
25		Total Minimal	441	265324	602	556	126	40923	325	280
26										
27										
28		Notes:	= a cell in which you'll enter search results							
29			Total Yfiler = Just Yfiler + (PPY23 or YFP)							
30			Total PPY = Just PPY + Total Yfiler = Just PPY + Just Yfiler + (PPY23 or YFP)							
31			Total Minimal = Just Minimal + Total PPY = Just Minimal + Just PPY + Just Yfiler + (PPY23 or YFP)							
32			Per YHRD Search Instructions, G4 = X1; H4 = n1; G8 = X2; H8 & H11 = n2; G9 = X3; G10 = X4; G11 = X5							

Section 3

How to check the current state and composition of the database

The number of haplotypes in the databases can be verified. The composition and contributing laboratory of each metapopulation and national database haplotypes are available for review.

How to check the current state of the database



YHRD Search the Database Tools Resources Help & Support

- Database Details
- Database Statistics
- Database Composition
- Calculation methods
- Metapopulation information
- Locus Information
- Mutation Rates
- Y-SNPs
- List of bad Y-SNPs
- Publications & References
- Release History

From the homepage, select **Resources** then **Database Statistics**

Aim & Objectives

Generate reliable Y-STR haplotype frequency estimates for Y-STR haplotypes to be used in the quantitative assessment of matches in forensic and kinship casework.

★

Assessment of male population stratification among world-wide populations as far as reflected by Y-STR and Y-SNP frequency distributions.

★

Provision of advanced tools and further resources concerning Y-STRs and Y-SNPs.

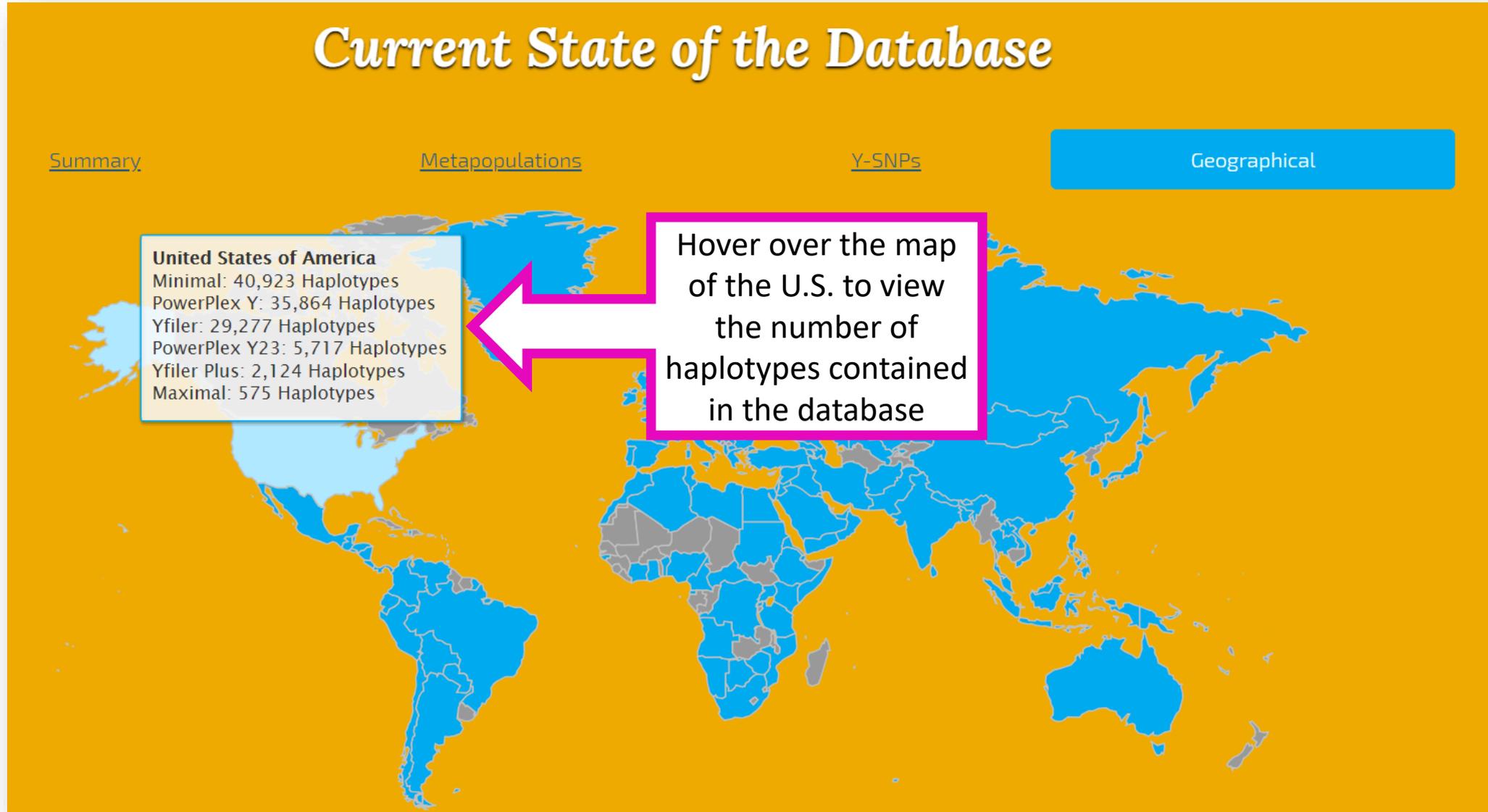
How to check the current state of the database

Current State of the Database

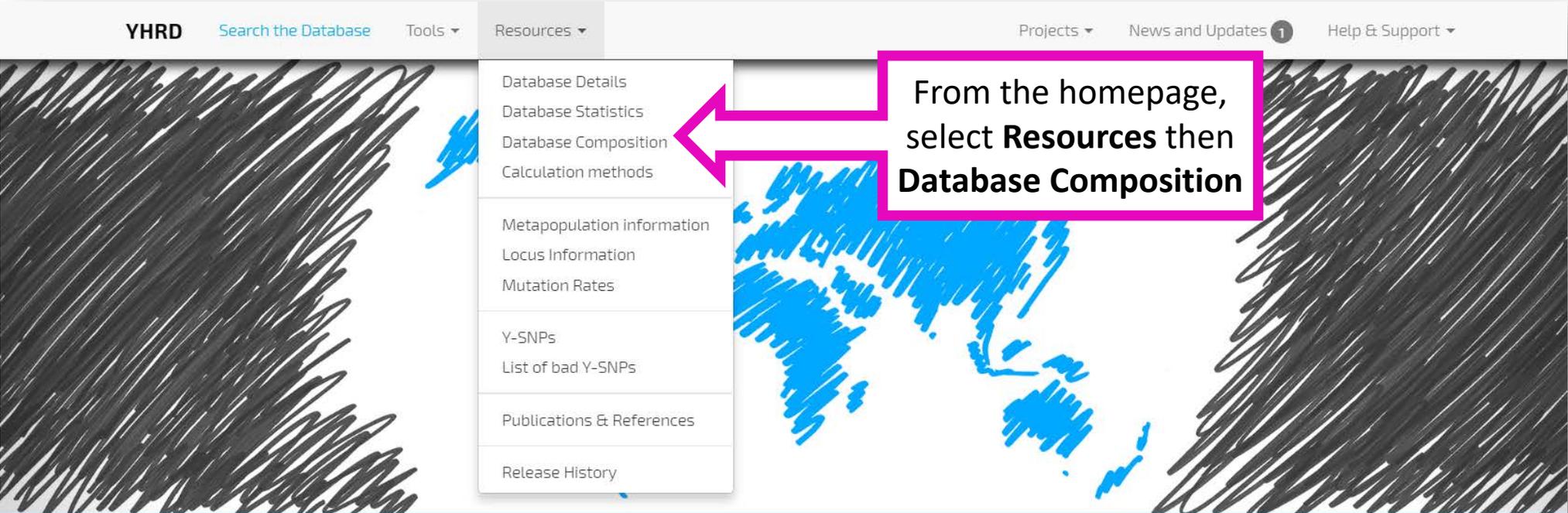
Click on
Geographical link

Summary		Metapopulations	Y-SNPs	Geographical		
Dataset	Y-STR loci		Number of haplotypes	Number of population samples	Number of national databases	Number of metapopulations
Minimal	DYS19, DYS389I , DYS389II , DYS390 , DYS391 , DYS392 , DYS393 , DYS385		265,324	1251	135	33
PowerPlex Y	DYS391 , DYS389I , DYS439 , DYS389II , DYS438 , DYS437 , DYS19 , DYS392 , DYS393 , DYS390 , DYS385		224,657	1025	126	32
Yfiler	DYS456 , DYS389I , DYS390 , DYS389II , DYS458 , DYS19 , DYS385 , DYS393 , DYS391 , DYS439 , DYS635 , DYS392 , YGATAH4 , DYS437 , DYS438 , DYS448		205,059	940	119	32
PowerPlex Y23	DYS576 , DYS389I , DYS448 , DYS389II , DYS19 , DYS391 , DYS481 , DYS549 , DYS533 , DYS438 , DYS437 , DYS570 , DYS635 , DYS390 , DYS439 , DYS392 , DYS643 , DYS393 , DYS458 , DYS385 , DYS456 , YGATAH4		50,692	307	67	28
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		42,506	209	49	30
Maximal	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		5,516	40	14	18

How to check the current state of the database



How to check the composition of the database



The screenshot shows the YHRD website interface. The top navigation bar includes 'YHRD', 'Search the Database', 'Tools', 'Resources', 'Projects', 'News and Updates', and 'Help & Support'. The 'Resources' dropdown menu is open, listing several options. A pink box highlights the 'Resources' menu, and a pink arrow points to 'Database Composition'.

From the homepage, select **Resources** then **Database Composition**

Aim & Objectives

Generate reliable Y-STR haplotype frequency estimates for Y-STR haplotypes to be used in the quantitative assessment of matches in forensic and kinship casework.

★

Assessment of male population stratification among world-wide populations as far as reflected by Y-STR and Y-SNP frequency distributions.

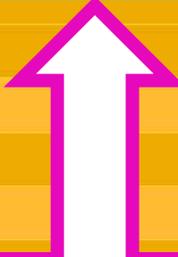
★

Provision of advanced tools and further resources concerning Y-STRs and Y-SNPs.

How to check the composition of the database

Database Composition

National	<u>Metapopulation</u>	<u>Y-SNPS</u>	<u>Loci</u>			
National Database	Minimal	PowerPlex Y	Yfiler	PowerPlex Y23	Yfiler Plus	Maximal
Afghanistan	743 Haplotypes	743 Haplotypes	743 Haplotypes	0 Haplotypes	260 Haplotypes	0 Haplotypes
Albania	494 Haplotypes	396 Haplotypes	322 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes
Algeria	166 Haplotypes	166 Haplotypes	166 Haplotypes	0 Haplotypes	64 Haplotypes	0 Haplotypes
Angola	309 Haplotypes	309 Haplotypes	71 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes
Argentina	5354 Haplotypes	3704 Haplotypes	2901 Haplotypes	1417 Haplotypes	0 Haplotypes	0 Haplotypes
Armenia	100 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes
Australia	2257 Haplotypes	2257 Haplotypes	2256 Haplotypes	0 Haplotypes	1136 Haplotypes	0 Haplotypes
Austria	1877 Haplotypes	1516 Haplotypes	1516 Haplotypes	259 Haplotypes	436 Haplotypes	0 Haplotypes
Azerbaijan	119 Haplotypes	47 Haplotypes	47 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes
Bahamas	427 Haplotypes	427 Haplotypes	427 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes
Bahrain	156 Haplotypes	156 Haplotypes	156 Haplotypes	0 Haplotypes	156 Haplotypes	0 Haplotypes
Bangladesh	1189 Haplotypes	1189 Haplotypes	1189 Haplotypes	132 Haplotypes	0 Haplotypes	0 Haplotypes
Belarus	489 Haplotypes	414 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes
Belgium	1628 Haplotypes	1503 Haplotypes	1168 Haplotypes	728 Haplotypes	169 Haplotypes	169 Haplotypes
Belize	157 Haplotypes	157 Haplotypes	157 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes
Benin	234 Haplotypes	234 Haplotypes	234 Haplotypes	51 Haplotypes	0 Haplotypes	0 Haplotypes

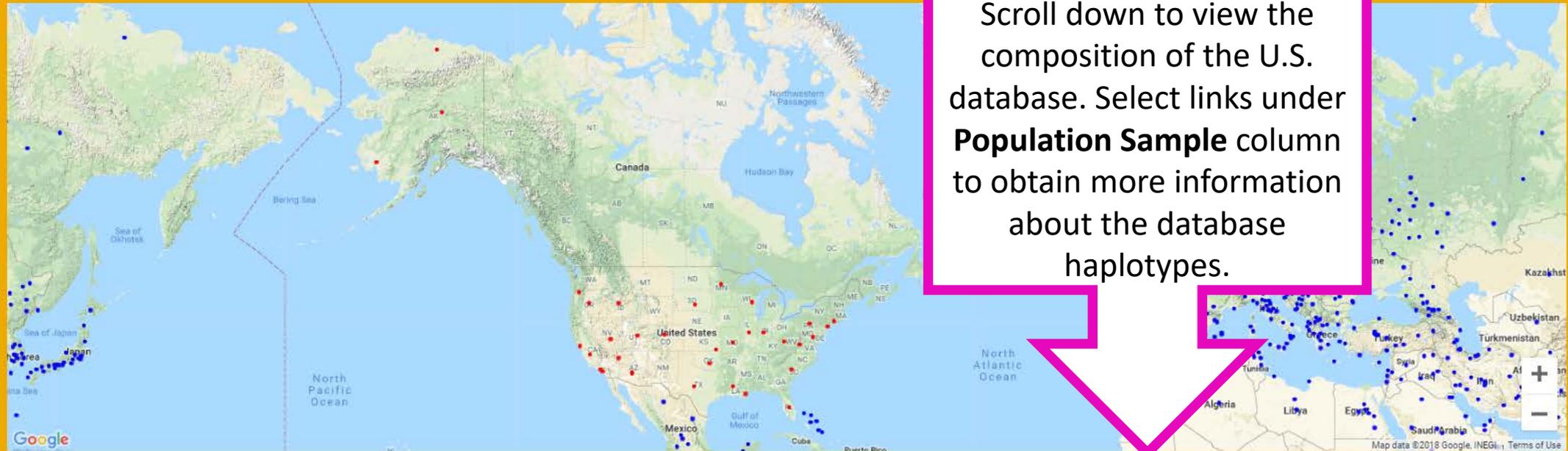


Select the **National** Database, then scroll to the link to the **United States** database

How to check the composition of the database

Information on the National Database "United States"

The National Database "United States" consists of 40923 minimal haplotypes.



Scroll down to view the composition of the U.S. database. Select links under **Population Sample** column to obtain more information about the database haplotypes.

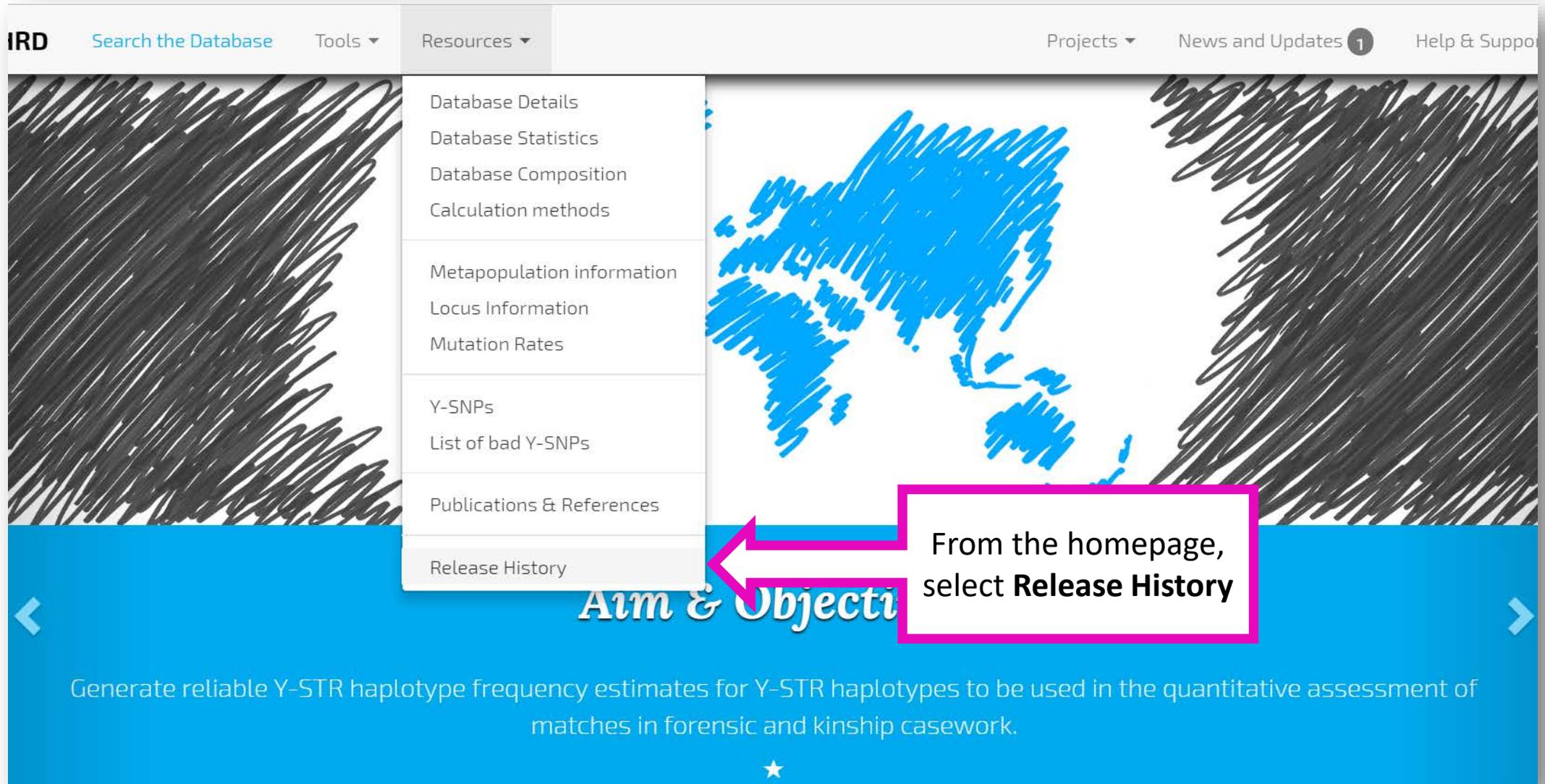
Population Sample	Minimal	PowerPlex Y	Yfiler	PowerPlex Y23	Yfiler Plus	Maximal
Cajun, United States (European American)	22 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes
Connecticut, United States (Hispanic American)	53 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes
Florida, United States (African American)	863 Haplotypes	815 Haplotypes	797 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes
Florida, United States (European American)	998 Haplotypes	976 Haplotypes	854 Haplotypes	0 Haplotypes	1 Haplotypes	0 Haplotypes
Florida, United States (Hispanic American)	279 Haplotypes	256 Haplotypes	254 Haplotypes	195 Haplotypes	0 Haplotypes	0 Haplotypes
Illinois, United States (African American)	310 Haplotypes	198 Haplotypes	198 Haplotypes	172 Haplotypes	7 Haplotypes	0 Haplotypes
Illinois, United States (European American)	253 Haplotypes	253 Haplotypes	253 Haplotypes	162 Haplotypes	19 Haplotypes	0 Haplotypes
Illinois, United States (Hispanic American)	103 Haplotypes	103 Haplotypes	103 Haplotypes	94 Haplotypes	2 Haplotypes	0 Haplotypes
Indiana, United States (African American)	37 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes
Indiana, United States (European American)	34 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes
Louisiana, United States (African American)	1554 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes

Section 4

How to check release history

The current release version and information about the contributed haplotypes can be reviewed.

How to check release history



The screenshot displays the IRD website interface. At the top, there is a navigation bar with the following elements: 'IRD', 'Search the Database', 'Tools', 'Resources', 'Projects', 'News and Updates' (with a notification badge '1'), and 'Help & Support'. The 'Resources' dropdown menu is open, showing a list of options: 'Database Details', 'Database Statistics', 'Database Composition', 'Calculation methods', 'Metapopulation information', 'Locus Information', 'Mutation Rates', 'Y-SNPs', 'List of bad Y-SNPs', 'Publications & References', and 'Release History'. A pink arrow points from a text box to the 'Release History' option. The background features a world map with blue scribbles over the continents. Below the navigation bar, there is a blue banner with the text 'Aim & Objecti' and a star icon. The main content area contains the text: 'Generate reliable Y-STR haplotype frequency estimates for Y-STR haplotypes to be used in the quantitative assessment of matches in forensic and kinship casework.'

From the homepage, select **Release History**

Aim & Objecti

Generate reliable Y-STR haplotype frequency estimates for Y-STR haplotypes to be used in the quantitative assessment of matches in forensic and kinship casework.

★

How to check release history

YHRD Search the Database Tools Resources Projects News and Updates 1 Help & Support

Release History

Release 59 - 2018/Nov/01

- Contribution [YA002987](#) (Buenos Aires, Argentina [European]): replace 623 => 623
- Contribution [YA003143](#) (Finland [Finnish]): replace 913 => 956
- Contribution [YA004312](#) (Balochistan, Pakistan [Hazara]): replace 153 => 153
- Contribution [YA004400](#) (Madhya Pradesh, India [Indian]): replace 365 => 777
- Contribution [YA004476](#) (California, United States [European American]): replace 301 => 235
- Contribution [YA004477](#) (California, United States [African American]): replace 308 => 236
- Contribution [YA004478](#) (California, United States [Hispanic American]): replace 281 => 198
- Contribution [YA004480](#) (California, United States [Asian American]): replace 329 => 234
- Contribution [YA004487](#) (Hulun Buir, China [Han]): new 0 => 402
- Contribution [YA004488](#) (Fuzhou,China [Danmin]): new 0 => 87
- Contribution [YA004489](#) (Xinjiang, China [Xibe]): new 0 => 120
- Contribution [YA004490](#) (Kizilsu Kirghiz, China [Kyrgyz]): new 0 => 248
- Contribution [YA004491](#) (Yongchang, China [Liqian]): new 0 => 90
- Contribution [YA004492](#) (Nujiang, China [Lisu]): new 0 => 27
- Contribution [YA004493](#) (Gansu, China [Yugur]): new 0 => 135
- Contribution [YA004494](#) (Kanas, China [Tuva]): new 0 => 143
- Contribution [YA004495](#) (Urumqi, China [Uighur]): new 0 => 405
- Contribution [YA004496](#) (Turpan, China [Uighur]): new 0 => 485
- Contribution [YA004497](#) (Lijiang, China [Mosuo]): new 0 => 59
- Contribution [YA004498](#) (Taijiang, China [Miao]): new 0 => 290
- Contribution [YA004499](#) (Lhasa, China [Tibetan]): new 0 => 2016
- Contribution [YA004500](#) (Wuhan, China [Han]): new 0 => 274
- Contribution [YA004501](#) (Tianjin, China [Han]): new 0 => 214
- Contribution [YA004502](#) (Zhengzhou, China [Han]): new 0 => 2199
- Contribution [YA004503](#) (Afghanistan [Hazara]): new 0 => 260
- Contribution [YA004505](#) (Changzhou, China [Han]): new 0 => 1550
- Contribution [YA004506](#) (Jieyang, China [Han]): new 0 => 293
- Contribution [YA004507](#) (Piauí, Brazil [Admixed]): new 0 => 42
- Contribution [YA004508](#) (Ceará, Brazil [Admixed]): new 0 => 38
- Contribution [YA004509](#) (Rio Grande do Norte, Brazil [Admixed]): new 0 => 19
- Contribution [YA004510](#) (Tolima/Huila, Colombia [Colombian]): new 0 => 83
- Contribution [YA004511](#) (Rio Grande do Sul, Brazil [Admixed]): new 0 => 211
- Contribution [YA004512](#) (Guizhou, China [Yi]): new 0 => 217
- Contribution [YA004513](#) (Sichuan, China [Yi]): new 0 => 227
- Contribution [YA004514](#) (Yunnan, China [Yi]): new 0 => 66
- Contribution [YA004515](#) (Eastern Botswana, Botswana [Bantu]): new 0 => 3

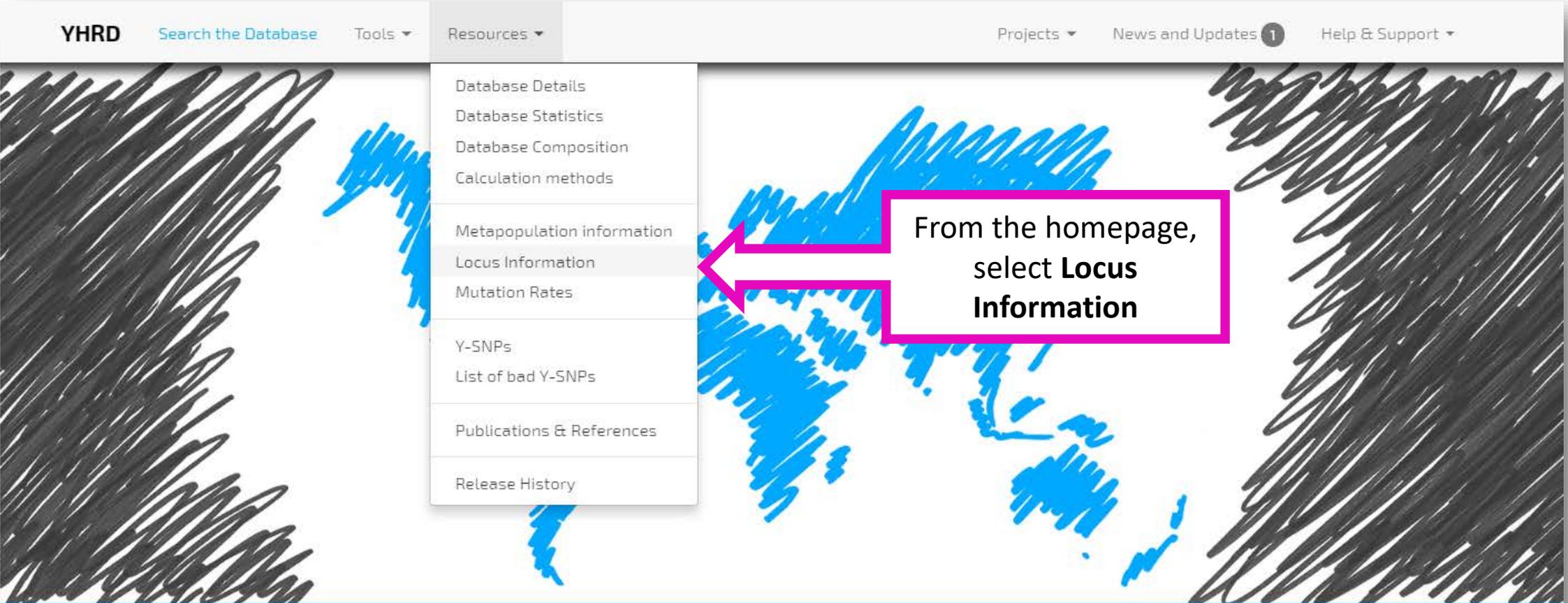
The most current release version is displayed first followed by previous release versions. Links to information about the contributed haplotypes for each release are provided.

Section 5

How to obtain locus information

The loci comprising each dataset can be reviewed. Additional information about each locus is available and includes mutation rate, observed alleles, number of null allele observations, and allelic distribution.

How to obtain locus information



The image shows a screenshot of the YHRD (Y-Chromosome Haplotype Reference Database) website. The navigation bar at the top includes 'YHRD', 'Search the Database', 'Tools', 'Resources', 'Projects', 'News and Updates' (with a notification badge '1'), and 'Help & Support'. The 'Resources' dropdown menu is open, listing several options: 'Database Details', 'Database Statistics', 'Database Composition', 'Calculation methods', 'Metapopulation information', 'Locus Information', 'Mutation Rates', 'Y-SNPs', 'List of bad Y-SNPs', 'Publications & References', and 'Release History'. The 'Locus Information' option is highlighted in grey. A pink rectangular box with a white border contains the text 'From the homepage, select **Locus Information**'. A pink arrow points from this box to the 'Locus Information' option in the dropdown menu. The background of the website features a stylized world map with blue and black scribbles.

From the homepage, select **Locus Information**

Aim & Objectives

How to obtain locus information

Locus Information

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, DYS387S1, 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, DYS387S1, DYS449, DYS460, DYS518, DYS627

(Click on a locus to get more information.)

Click on any locus to obtain additional information

How to obtain locus information

Locus Information on DYS449

Mutation rate

9.44e-03 (20 in 2118) based on [Ballantyne2010](#), [LiYuan2018](#)

Observed alleles

22, 23, 24, 25, 26, 26.2, 27, 27.2, 28, 28.2, 29, 29.1, 29.2, 30, 30.1, 30.2, 31, 31.1, 31.2, 32, 32.2, 33, 33.2, 34, 34.1, 34.2, 35, 35.1, 36, 37, 38, 39, 40, 41, 42

NULL alleles

9 NULL allele observations.

Allelic distribution



To view all available alleles, click through each option.

To view the counts and database percentage of a particular allele, hover over the allele's bar.