

# FORENSIC BIOLOGY PROTOCOLS FOR FORENSIC STR ANALYSIS

Usage of the “Y-Mix Database Filter”		
Status: Published		Document ID: 5787
DATE EFFECTIVE 04/25/2022	APPROVED BY Nuclear DNA Technical Leader	PAGE 1 OF 5

## Usage of the “Y-Mix Database Filter”

### 1 Procedure

- 1.1 Open the [Y mixture database](#) filter
- 1.2 Excel window will open. **If the following message appears**, enable the content by choosing Options→ Enable this content→ OK



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1.3 Using drop-down menu, enter all of the alleles of the single source, deconvoluted donor, or mixture into the loci columns within the “Profile” worksheet.

**Note:** The order of loci in the Y-STR Mixture Tool is different from the Y-STR kit order. Please carefully enter these loci as they cannot be copied and pasted.

View the instructions.

View the updates.

View the DB composition.

**Y-Mix Database Filter 4.3**

BETA091620spm

Clear the filtered list.

Clear your profile.

Y-STR Profile	DYS 387S1	DYS 19	DYS 385	DYS 389I	DYS 389II	DYS 390	DYS 391	DYS 392	DYS 393	DYS 437	DYS 438	DYS 439	DYS 448	DYS 449	DYS 456	DYS 458	DYS 460	DYS 481	DYS 518	DYS 533	DYS 549	DYS 570	DYS 576	DYS 627	DYS 635	DYS 643	YGATA H4
Allele 1		16	14	12																		18	18		21	12	13
Allele 2			20																								
Allele 3																											
Allele 4																											
Allele 5																											
Allele 6																											
Allele 7																											
Allele 8																											
Allele 9																											
Allele 10																											
Allele 11																											
Allele 12																											
Allele 13																											
Allele 14																											
Allele 15																											

1.3.1 Null allele: A sample believed to contain a legitimate null allele due to mutation will be represented by a “0” allele at that locus. To include haplotypes with “0” alleles, you must manually enter “0” as an allele at that locus.

1.3.2 Drop Out: If drop out is suspected at any locus in the profile, the locus should be left blank. **Drop out may be indicated at locations where:**

1.3.2.1 Visible peaks are present below analytical threshold

1.3.2.2 One or more donors within a sample do not meet the between locus stochastic threshold

1.3.2.3 A mixture where there are not distinct alleles for each contributor

1.3.2.4 A single peak for a donor is present below the within locus stochastic threshold (DYS385 a/b)

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1.3.3 If an allele in the evidence profile is not present in the list below the table, enter it as a “New Variant” prior to entering it into the table (see red arrow below or the Instructions tab).

View the instructions.

View the updates.

View the DB composition.

**Y-Mix Database Filter 4.3**

BETA091620spm

Clear the filtered list.

Clear your profile.

Y-STR Profile	D19S11	DYS19	DYS385	DYS389I	DYS389II	DYS390	DYS391	DYS392	DYS393	DYS437	DYS438	DYS439	DYS448	DYS449	DYS456	DYS458	DYS460	DYS481	DYS518	DYS533	DYS549	DYS570	DYS576	DYS627	DYS635	DYS643	Y-GATA H4	
Allele 1		16	14	12																			18	18		21	12	13
Allele 2			20																									

**Database Source:**  
<https://yhrd.org/>  
R63 (US with subpopulations)

Upper Confidence Interval:  
Clopper and Pearson approach  
(Biometrika 1934)

Database	x	N	x/N	1 in...	95% UCI	1 in...
African American						
Asian						
Caucasian						
Hispanic						
Native American						
<b>Combined</b>						

Limit database to samples with all the loci entered above? Yes

Treat this profile as a single source sample? Yes

Single-source only: Allow for dropped alleles at multicopy loci? No

Desired UCI 95.0%

Use (x+1) / (N+1)? No

↓

New Variant:	D19S11	DYS19	DYS385	DYS389I	DYS389II	DYS390	DYS391	DYS392	DYS393	DYS437	DYS438	DYS439	DYS448	DYS449	DYS456	DYS458	DYS460	DYS481	DYS518	DYS533	DYS549	DYS570	DYS576	DYS627	DYS635	DYS643	Y-GATA H4
Observed Alleles:	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

1.4 In the center of the screen, ensure the following options are selected (see red arrows in diagram below):

1.4.1 Where it says: “Limit database to samples with all the loci entered above”, choose **YES**

1.4.2 Where it says: “Treat this profile as a single source sample”:

1.4.2.1 For a single source sample or deconvoluted donor profile: choose **YES**

1.4.2.1.1 Single source only: Allow for dropped alleles at multicopy loci: choose **NO**

1.4.2.2 For a mixed profile: choose **NO**

1.4.3 The desired Upper Confidence Interval (Desired UCI) should be set to **95%**.

1.4.4 Where it says: Use (x+1) / (N+1), choose **NO**

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Database Source:  
<https://yhrd.org/>  
R63 (US with subpopulations)

Upper Confidence Interval:  
Clopper and Pearson approach  
(Biometrika 1934)

Database	x	N	x/N	1 in...	95% UCI	1 in...
African American						
Asian						
Caucasian						
Hispanic						
Native American						
<b>Combined</b>						

Limit database to samples with all the loci entered above?	Yes	Desired UCI	95.0%
Treat this profile as a single source sample?	Yes	Use (x+1) / (N+1)?	No
Single-source only: Allow for dropped alleles at multicopy loci?	No		

Database Source:  
<https://yhrd.org/>  
R63 (US with subpopulations)

Upper Confidence Interval:  
Clopper and Pearson approach  
(Biometrika 1934)

Database	x	N	x/N	1 in...	95% UCI	1 in...
African American						
Asian						
Caucasian						
Hispanic						
Native American						
<b>Combined</b>						

Limit database to samples with all the loci entered above?	Yes	Desired UCI	95.0%
Treat this profile as a single source sample?	No	Use (x+1) / (N+1)?	No

- 1.5 Click on the macro button “Compare the profile to the database.” (see green arrow below). This will filter the database, leaving only those haplotype(s) that would be included as possible contributors to your evidence.

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1.6 Summary of results. The website reports the number of times the haplotype was observed in the database (x), the database size (N), sample frequencies (x/N), and the upper bound of the 95% confidence interval (UCIs). See screenshot below.

View the instructions.
View the updates.
View the DB composition.

**Y-Mix Database Filter 4.3**  
BETA091620spm

Clear the filtered list.
Clear your profile.

Y-STR Profile	DYS 387S1	DYS 19	DYS 385	DYS 389I	DYS 389II	DYS 390	DYS 391	DYS 392	DYS 393	DYS 437	DYS 438	DYS 439	DYS 448	DYS 449	DYS 456	DYS 458	DYS 460	DYS 481	DYS 518	DYS 533	DYS 549	DYS 570	DYS 576	DYS 627	DYS 635	DYS 643	DYS 643	YGATA H4
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[Compare the profile to the database.](#)

**Database Source:**  
<https://yhrd.org/>  
 R63 (US with subpopulations)

**Upper Confidence Interval:**  
 Clopper and Pearson approach  
 (Biometrika 1934)

Database	x	N	x/N	1 in...	95% UCI	1 in...
African American	0	3,278	0		0.000913473	1,095
Asian	0	3,149	0		0.000950876	1,052
Caucasian	0	3,611	0		0.000829269	1,206
Hispanic	0	3,157	0		0.000948467	1,054
Native American	0	3,168	0		0.000945176	1,058
<b>Combined</b>	<b>0</b>	<b>16,363</b>	<b>0</b>		<b>0.000183063</b>	<b>5,463</b>

Limit database to samples with all the loci entered above? Yes

Treat this profile as a single source sample? Yes

Single-source only: Allow for dropped alleles at multicopy loci? No

Desired UCI 95.0%

Use (x+1) / (N+1)? No

- 1.7 Print the screen by selecting “Print” from the printer menu at the top of the page and selecting a printer.
- 1.8 Verify on the printout that the Y-haplotype alleles were correctly entered into the website.
- 1.9 Report the 95% upper-bound confidence statistic from the African American, Asian, Caucasian, and Hispanic ethnic groups, and truncate to three significant figures (the “1 in...” column furthest to the right)
- 1.10 If both autosomal and Y-STRs are typed, the results are reported separately.