

FORENSIC BIOLOGY PROTOCOLS FOR FORENSIC STR ANALYSIS

Usage of the “Y-Mix Database Filter”		Document ID: 5787
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Usage of the “Y-Mix Database Filter”

1 Procedure

1.1 Open the [Y mixture database filter](#)

1.2 Excel window will open. Enable the content by choosing Options→ Enable this content→ OK

The screenshot displays the Microsoft Excel interface with the 'Y-Mix Database Filter 3.0.1' spreadsheet open. A 'Security Alert - Macro' dialog box is centered on the screen, warning that macros are disabled and asking the user to either help protect from unknown content (recommended) or enable the content. The spreadsheet background shows a 'Y-STR Profile' section with columns for various STR markers (DYS 387S1, 19, 385, 388I, 388II, 390, 391, 392, 393, 437, 438, 439, 446, 445, 456, 458, 460, 461, 518, 533, 549, 570, 576, 627, 636, 643, 14) and rows for Allele 1 through Allele 15. Below this is a 'Database Source' section with the URL 'www.usstrdatabase.org' and 'Release 4.1 (Sept. 20, 2015)'. The 'Upper Confidence Interval' is set to 'Clopper and Pearson approach (Biometrika 1934)'. A 'Limit data' section is also visible. At the bottom, there is a 'New Variant' section with a table of observed alleles and their frequencies across the various STR markers.

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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.

The screenshot shows the 'Y-Mix Database Filter 3.0.1' spreadsheet. The main grid has columns for loci: D1F1, D1S1, D2S1, D3S1, D4S1, D5S1, D6S1, D7S1, D8S1, D9S1, D10S1, D11S1, D12S1, D13S1, D14S1, D15S1, D16S1, D17S1, D18S1, D19S1, D20S1, D21S1, D22S1, D23S1, D24S1, D25S1, D26S1, D27S1, D28S1, D29S1, D30S1, D31S1, D32S1, D33S1, D34S1, D35S1, D36S1, D37S1, D38S1, D39S1, D40S1, D41S1, D42S1, D43S1, D44S1, D45S1, D46S1, D47S1, D48S1, D49S1, D50S1, D51S1, D52S1, D53S1, D54S1, D55S1, D56S1, D57S1, D58S1, D59S1, D60S1, D61S1, D62S1, D63S1, D64S1, D65S1, D66S1, D67S1, D68S1, D69S1, D70S1, D71S1, D72S1, D73S1, D74S1, D75S1, D76S1, D77S1, D78S1, D79S1, D80S1, D81S1, D82S1, D83S1, D84S1, D85S1, D86S1, D87S1, D88S1, D89S1, D90S1, D91S1, D92S1, D93S1, D94S1, D95S1, D96S1, D97S1, D98S1, D99S1, D100S1. The 'Database Source' is 'www.usystrdatabase.org Release 4.1 (Sept. 20, 2015)'. The 'Upper Confidence Interval' is 'Clopper and Pearson approach (Biometrika 1934)'. The 'Limit database to samples with all the loci entered above?' is set to 'No'. The 'Desired UCI' is '95.0%'. The 'New Variant' section shows observed allele counts for various loci.

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 (i.e., there are visible peaks below analytical threshold that are unambiguously attributable to a contributor), the locus should be left blank.

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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).

Y-Mix Database Filter 3.0.1
BETA 10/15/2011

Y-STR Profile

38751	DYS 19	DYS 385	DYS 389	DYS 390	DYS 391	DYS 392	DYS 393	DYS 437	DYS 438	DYS 439	DYS 448	DYS 449	DYS 458	DYS 459	DYS 460	DYS 461	DYS 518	DYS 533	YGATA 543	DYS 570	DYS 578	DYS 627	DYS 635	DYS 643	YGATA 44	
Allele 1	33		10																							
Allele 2	36		12																							

Database Source:
www.usisrtdatabase.org
Release 4.1 (Sept. 20, 2015)

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

Limit database to samples with all the loci entered above? **Yes**
Treat this profile as a single source sample? **No**

Desired UCI: **95.0%**

Observed Alleles:

38751	DYS 19	DYS 385	DYS 389	DYS 390	DYS 391	DYS 392	DYS 393	DYS 437	DYS 438	DYS 439	DYS 448	DYS 449	DYS 458	DYS 459	DYS 460	DYS 461	DYS 518	DYS 533	YGATA 543	DYS 570	DYS 578	DYS 627	DYS 635	DYS 643	YGATA 44
New Variant:	29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Average: 220.4693878 Count: 56 Sum: 10803 75%

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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**

1.4.2.2 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**

Y-Mix Database Filter 3.1
BETA 041017spm

Y-STR Profile	DYS 385T	DYS 385	DYS 389I	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	32		10																						
Allele 2	34		12																						

Database Source: www.usysdbdatabase.org
Release 4.2 (Feb. 18, 2017)

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						
	Combined						

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

Treat this profile as a single source sample? **No**

Desired UCI Use $(x+1) / (N+1)$? **95.0%**

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

New Variant:	DYS 385T	DYS 385	DYS 389I	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
Observed Alleles:	23	0	0	0	0	0	0	0	0	0	0	0	24	0	0	3	0	33	7	<7	0	0	14	0	0
	32	6	7	9	24	16	6	7	9	11	1	8	14	25	11	10	10	13	33.2	6	7	11	8	14.2	12
	33	<10	9	10	25	19	6	8	10	12	<8	9	15	26	12	11	11	16	24	9	9	12	11	15	17
	34	10	9	11	26	20	<7	9	11	<13	6	9	<16	27	<13	12	12	17	34.2	10	10	13	12	16	18
	35	11	10	12	27	20.1	7	10	12	13	8.2	10	16	28	13	13	13	18	35	10.1	11	14	13	17	<19
	36	12	10.2	13	28	21	8	10.2	13	14	9	10.1	16.2	29	14	<14	13	36	11	11.1	15	14	18	19	11
	37	13	11	14	28.3	21.1	9	11	14	14.3	10	11	<17	30	14.3	14	20	37	12	12	16	15	19.2	<20	
	37.2	13.2	11.2	15	29	22	10	11.1	15	15	11	12	17	31	15	14.1	21	38.1	13	13	17	16	19	20	
	38	14	11.3	16	30	23	11	12	16	16	12	13	17.2	32	16	14.2	22	37.2	14	14	17.3	17	19.2	21	
	39	14.1	12		31	24	12	13	17	17	13	14	17.4	33	17	15	23	38	15	15	18	17.2	20	21.3	

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.

Y-Mix Database Filter 3.1
BETA 04/07/19pm

Database	x	N	x/N	1 in...	95% UCI	1 in...
African American	0	560	0		0.005335239	187
Asian	0	332	0		0.000982702	111
Caucasian	0	576	0		0.005187423	193
Hispanic	0	387	0		0.007711027	130
Native American	0	239	0		0.012456216	80
Combined	0	2,094	0		0.001429604	699

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

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