Usage of the "Y-Mix Database Filter"		
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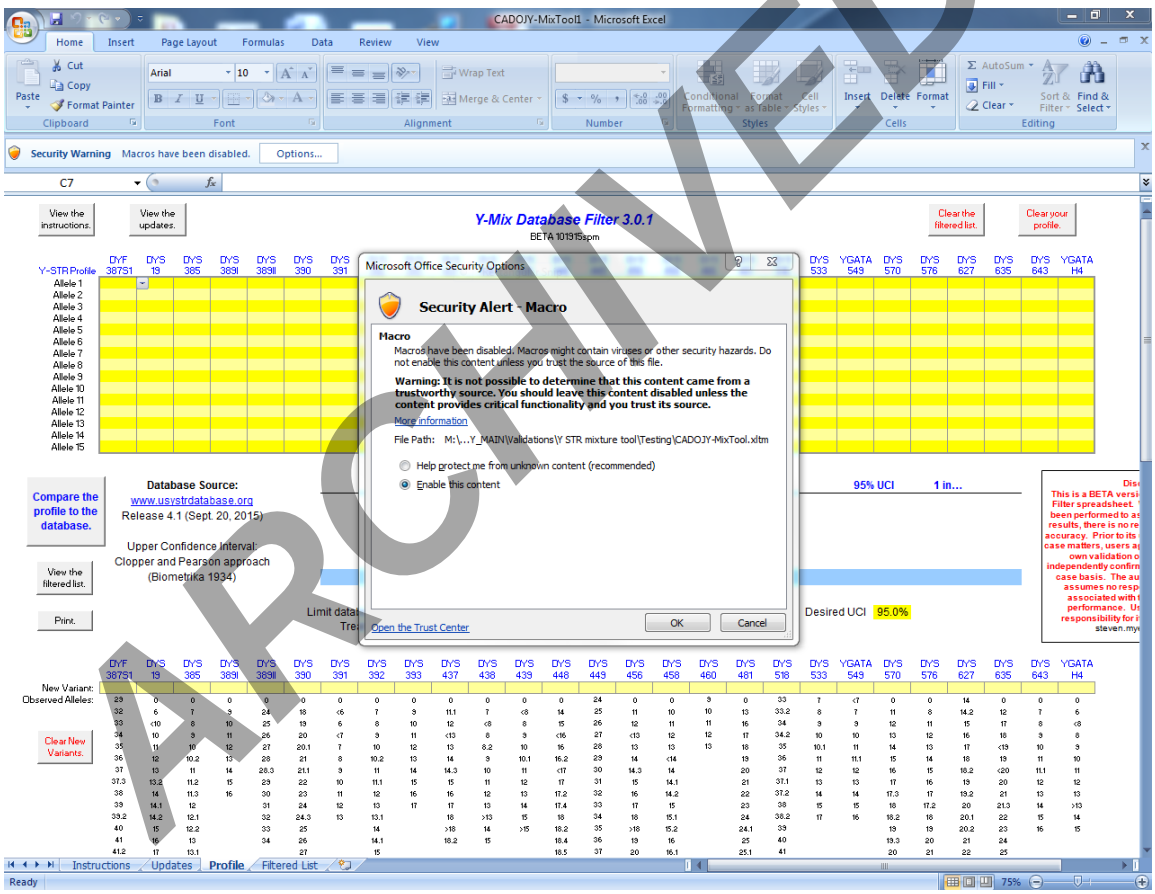
1 Procedure

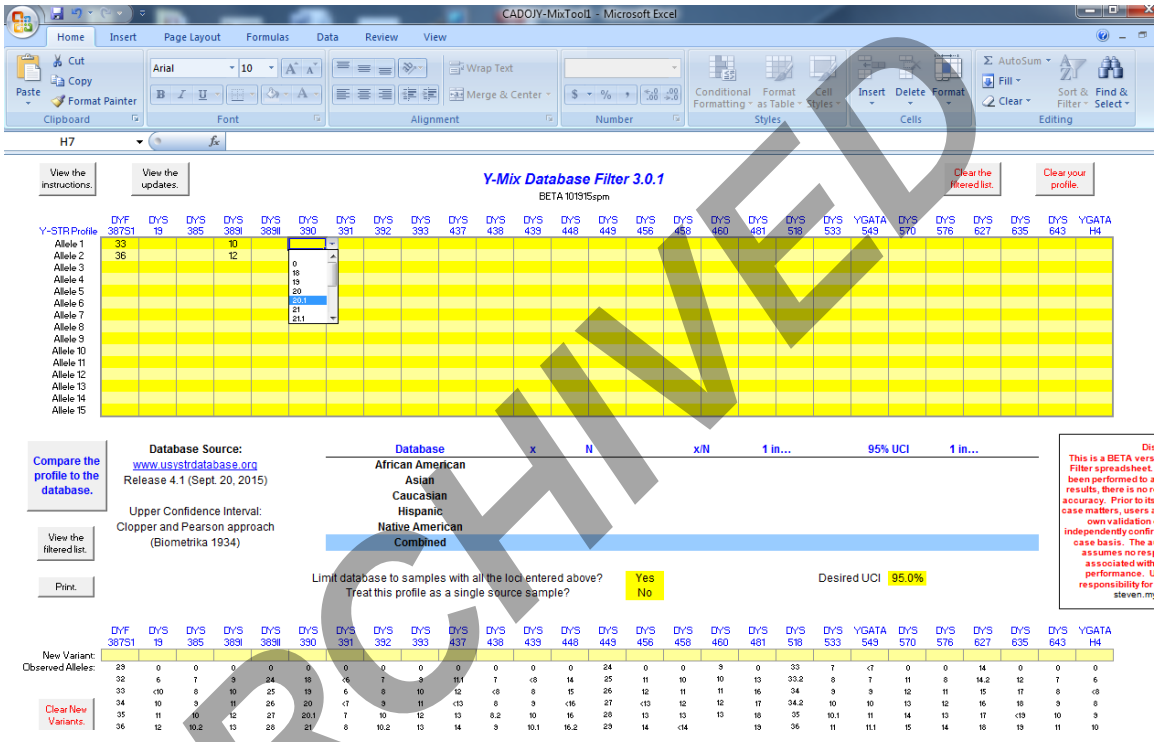
1.1 Open the Y mixture database filter

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



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.

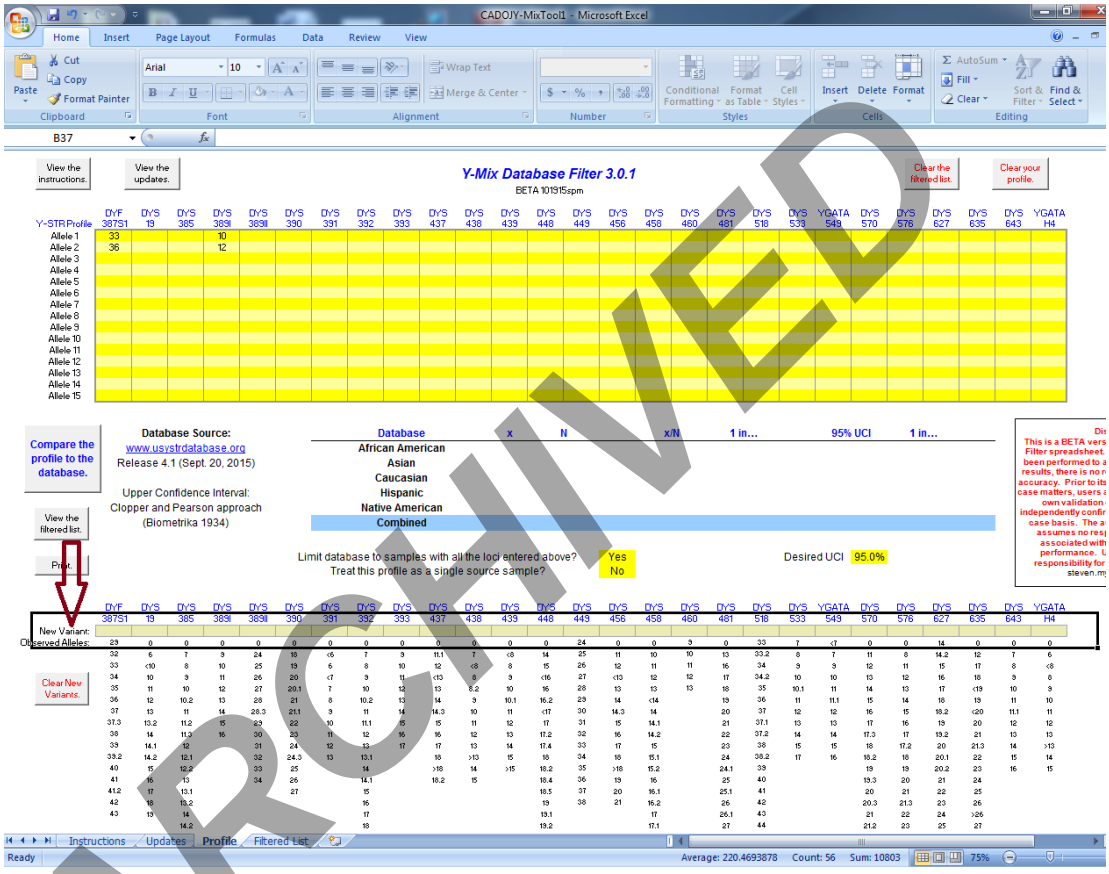
Note: The order of loci in the Y-STR Mixture Tool is different from the Y-STR kit order. Please carefully enter these loci as they cannot be copied and pasted.



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.

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).



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**

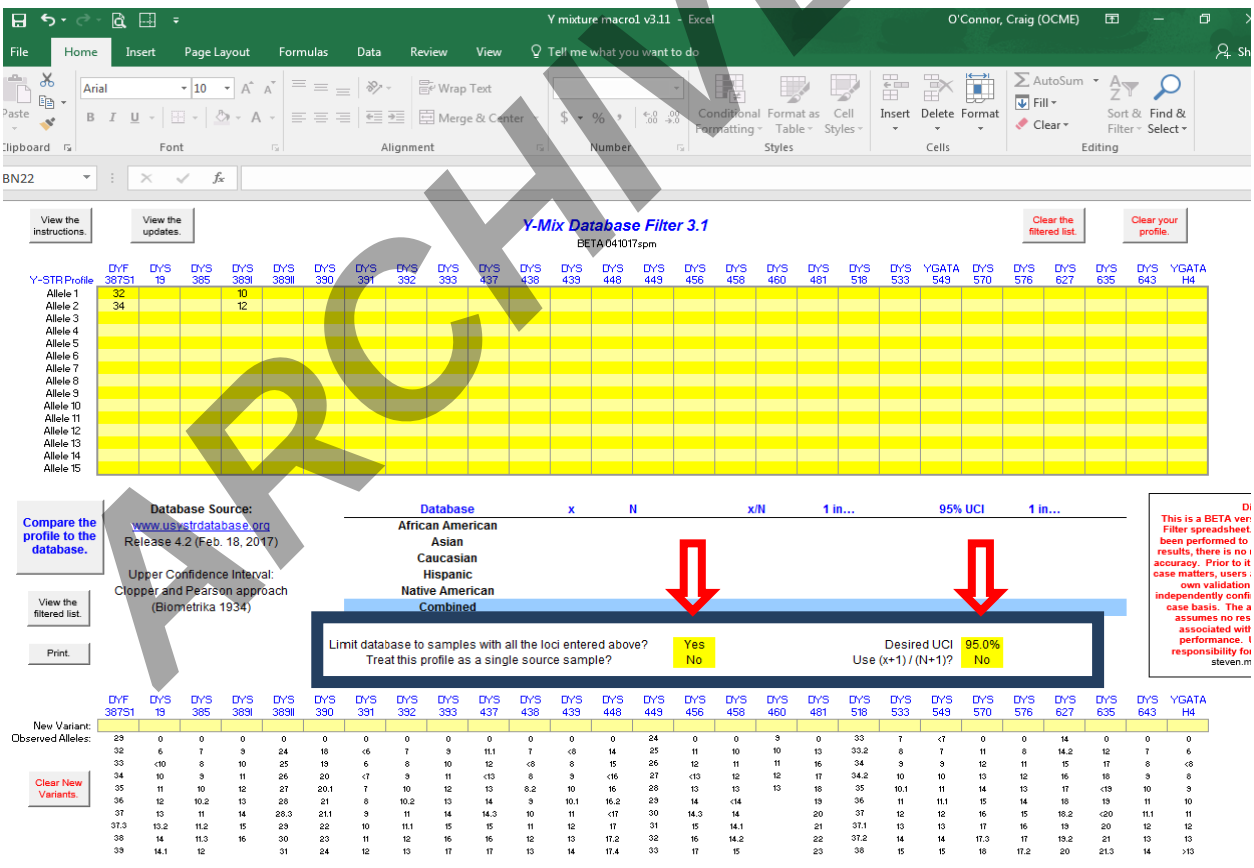
1.4.2 Where it says: "Treat this profile as a single source sample":

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**

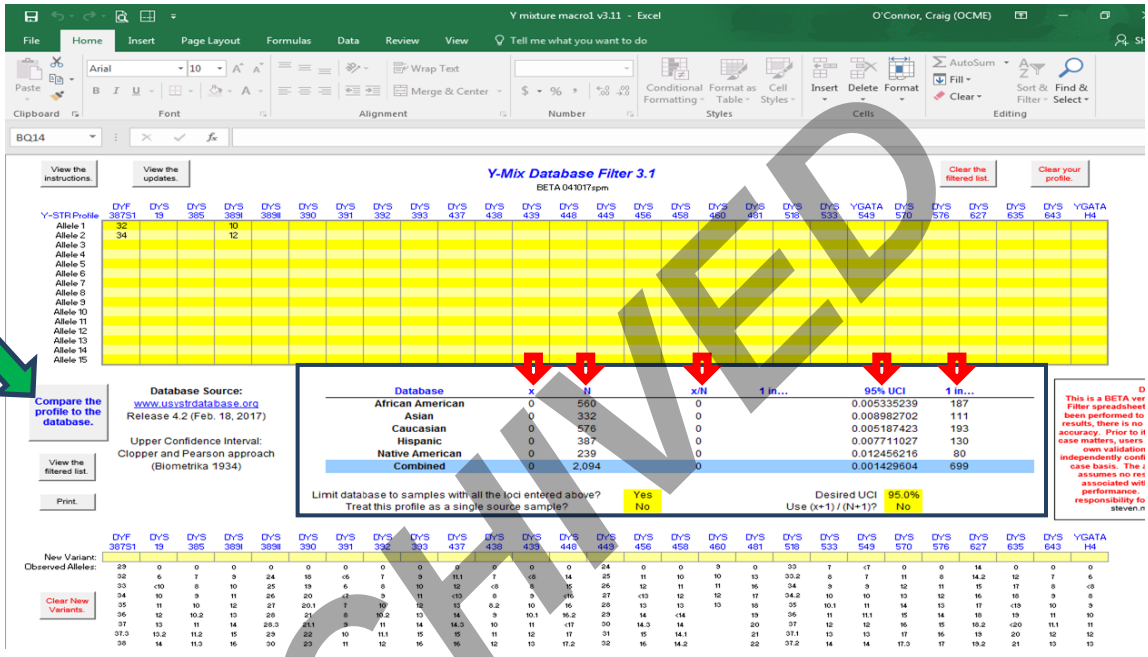
1.4.3 The desired Upper Confidence Interval (Desired UCI) should be set to **95%**.

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



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.

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.



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.