Analysis/Review of Male Screen Batch Paperwork Workflow

- DNA QR-22b,32 Dilution Factor and DNA QR-313 Male Screen Concentration Worksheets will flag samples needing microcon concentration. Individuals performing the male screen will not need DNA Analyst's sign-offs during the process. (see DNA SOP 34).

-Once the male screen batch is completed, it along with the associated case jackets will be handed off to a qualified DNA Analyst as per the rotation.

-It will be the responsibility of the DNA Analyst to review the male screen batch and case jacket information and create DNA requests in JusticeTrax for all cases in the batch.

1. Review male screen batch paperwork to determine which screened samples are positive, inconclusive, or negative (see SOP 34).

    a) For screened samples that are positive or inconclusive (low quantity of human DNA) in the 1st quant run, make notes in the "Comments" section of the 1st DNA QR-24. Initial and date your comments.

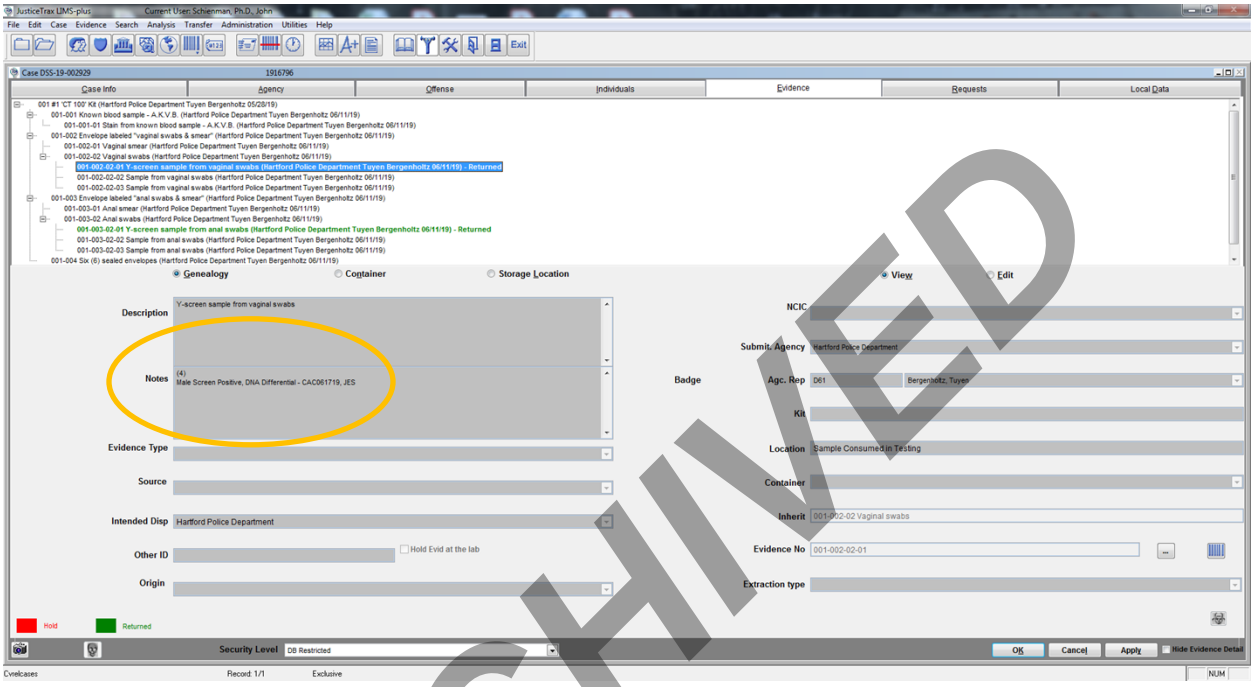
    b) For screened samples that are positive, inconclusive (SA value failed to concentrate), or negative after microcon concentration, make notes on the DNA QR-313. Initial and date your notes.

    c) Make sure the Lot #s are correct and the Pos control has passed (value in the Reagent Lot Log). Initial all sheets in the male screen batch.

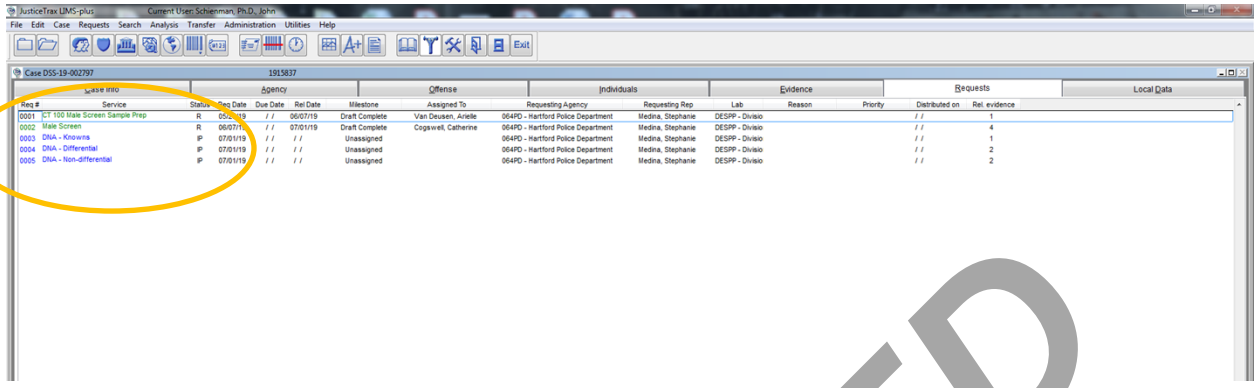
2. Review the case jacket information to determine what type of testing, i.e. Differential vs. Non-Differential (with or without DTT) or NFT (no further testing) for male screen negative cases, is needed for each sample. In general, most samples will be a Differential, unless it is clear that the contact is touch or saliva only. If the victim was drugged/intoxicated during the assault or a young minor, a differential should be done. There may be situations where maximizing the amount of DNA extracted is desirable, but there is a remote possibility of the presence of semen. For these situations, a Non-Differential with the addition of DTT could be performed. Make case management aware of these situations.

3. In JusticeTrax, for each male screened sample, type in the results in the Notes section of the Evidence tab: Male Screen Result, DNA Test Type, male screen batch, DNA Analyst Initials. The (#) already present in the Notes is the number of swabs for that item. These notes will aid Case Management in fielding

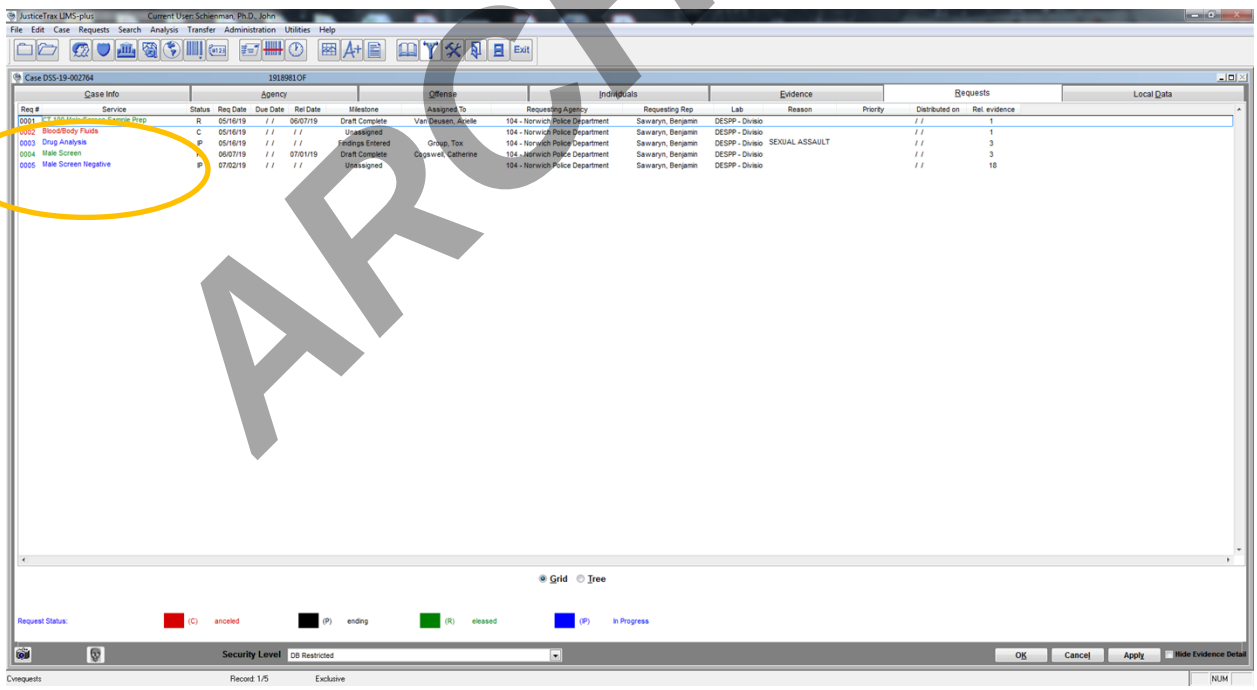
phone calls regarding DNA testing and modifying a "DNA – Consumption" request when permission for testing is received.



4. Under the Requests tab, add the appropriate DNA requests and related evidence, including DNA Knowns, but do not add these to the casework knowns spreadsheet at this time. Don't print the barcode for the request. There will be 3 sub-items for every sample; the already consumed Y-screen sample, one in "Freezer Storage – DNA Sample", and one in "Freezer Storage". Make sure to choose the one in "Freezer Storage – DNA Sample" as related evidence for the DNA request. The one in "Freezer Storage" is for serology testing upon request. In some cases, the victim's known sample will be the oral swab from the kit. **Check to see if a suspect has been arrested in the case, if so use the "DNA – Consumption" request in JusticeTrax.** When the permission to test is received, case management will modify the request(s) to match the evidence notes and Evidence Transfer Sheet.



For cases with only negative male screen samples, we will be reporting out the negative results. A request still needs to be added, "Male Screen Negative", so the request can track the draft complete, technical review, and administrative review process. The samples that are in "Freezer Storage – DNA Sample" will need to be transferred to "Freezer Storage" both physically and in JusticeTrax. These will be added into batches with cases that are positive and will be moved to freezer storage by the processing analyst. CM will add a note to the batch sheet to alert the analyst.



5. On the evidence transfer sheet in the case jacket, hand-write the DNA request type in the "Evidence Type" column for each sample, i.e. DNA Differential. Also, under the "Notes" column hand-write the male screen results, e.g. Male Screen Positive, Inconclusive, or Negative. Initial and date these hand-written additions.

6. Fill out DNA QR-4E and hand off to another analyst on the rotation for TR/AR.

7. When TR is done, make copies of the Male Screen batch paperwork (DNA QR-4E, the first DNA QR-24, and DNA QR 313, if applicable) for each case jacket in the set and add the case number to each worksheet.

8. Give the set of cases to Case Management. Scan the male screen batch paperwork and save to U-Drive. File the original Male-Screen batch paperwork in the casework batch paperwork filing cabinets.

Process Post Male-Screen

1. Once the samples have been extracted, the quant results need to be evaluated to determine which samples will go on for amplification or be halted. For any non-interpreting analyst that is processing the batch, give paperwork and case jackets to an interpreting analyst as per the rotation list to make this evaluation. The interpreting analyst will analyze the quant data, fill in the halt at quant sheet, create the amp sheet(s), print out the staff search sheet(s), add the appropriate known(s) to the casework knowns spreadsheet, and eventually own the batch.

2. Samples will follow the process outlined on the flow chart in DNA SOP-34. Things to consider:
   a. How many suspects are alleged in the narrative? Was there a consensual partner that could be a contributor? Typically 1 sample will be sent on but if there are more potential males contributing, you will want to send on more samples.
   b. Is the most probative sample not the most positive? If you have a probative sample (ex: vaginal swab) that has a male value and the ratio is sufficient but the M:F ratio is close to 1:50, you may develop a minor male but it may not be sufficient for CODIS. If this is the case, you may also want to send a sample that although not as probative, would give a potential CODIS eligible profile (ex: Dried secretion swab of neck).
   c. Are multiple orifice swabs positive for male DNA? Vaginal penetration and Anal penetration are legally different charges. If both are positive for male DNA and the ratios are sufficient,

then both should be sent. Keep in mind item 2b above and send a third sample if necessary to develop a CODIS eligible profile.

d. If the B fraction of a sample is being amplified, the A fraction will also need to be amplified for QA purposes. This is regardless of the ratio of M:F DNA in the A fraction. If the A fraction of a sample is being amplified and the B fraction does not meet the criteria, then it does NOT need to be amplified.

e. Y-STR testing is to be done on samples where a known for the suspect is already at the laboratory and the male quant value is positive. You may not need Y-STR testing if you already have samples that may generate Autosomal profiles. If you have a vaginal sample going for autosomal testing and an anal sample that is eligible for Y-STR testing then it's a good idea to amplify it. However, if you have a vaginal sample that is going for autosomal testing and a touched sample eligible for Y-STR testing, you may choose not to amplify the touched sample for Y-STR testing. If doing Y-STR testing, the chosen sample(s) may need to be concentrated first (target of 0.5ng of male DNA), but keep in mind that if it is an A fraction then it needs to be sent to Autosomal **AND** Y-STR testing for QA purposes. Amplify for autosomal DNA first, and then perform the concentration for Y-STR testing. If the sample being amplified for Y-STR is a B fraction, then the A fraction will need to be amplified for Autosomal loci.

3. QR-48 includes 3 columns. This QR will assist the analyst in writing reports. The 3 columns are:
    a. Highest quant target >0ng/ul?—answer Y or N, as some samples are undet. for all targets
    b. Male DNA present?—if answer to (a.) is no, mark as N/A or leave blank
    c. M:F ratio >1:50?—if answer to (a. or b.) is no, mark as N/A or leave blank

4. Once you have determined which cases will have samples moving on to amplification (either autosomal and/or Y-STR), add any knowns to the knowns spreadsheet for processing. If a case has no samples moving on for amplification and it contains a non-kit submitted known, add that to the spreadsheet for itemization and retaining only. Remember to indicate if a known also needs Y-STR testing. Do not cancel any known requests. If a case is halted at quant, the known assignment will still be closed out as usual.

5. Report wording is contained within the flow chart in DNA SOP-34 and will indicate specific reasons why a sample was halted. Also refer to DNA SOP-6.