

October 10, 2002

Participant
Centers for Disease Control and Prevention (CDC)
Mycobacterium tuberculosis Nucleic Acid Amplification Testing
Performance Evaluation Program

Subject: Analyses of Participant Laboratory Results for the June 2002 Shipment

Dear Participant:

Enclosed are analyses of laboratory test results reported to the Centers for Disease Control and Prevention (CDC) by participant laboratories for the June 2002 shipment of samples for the CDC *M. tuberculosis* Nucleic Acid Amplification (*M.tb* NAA) Testing Performance Evaluation Program. Participant laboratories received five individual samples. Testing results were received from 83 of 89 (93%) enrolled laboratories that received this shipment.

The enclosed aggregate report is prepared in a format that will allow laboratories to compare their results with those obtained by other participants for the same sample using the same *M.tb* NAA test method.

We encourage you to circulate this report to all personnel involved with *M.tb* NAA testing, interpreting, or reporting. If you have any comments or suggestions on the format selected for the results, or questions regarding this report, you may call Laurina Williams at (770) 488-8130.

Sincerely yours,

Laurina O. Williams, Ph.D.
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Division of Laboratory Systems
Public Health Practice Program Office

Enclosures

Analyses of the June 17, 2002 Performance Evaluation Results for *M. tuberculosis* Nucleic Acid Amplification Testing Reported to the Centers for Disease Control and Prevention

This report is an analysis of laboratory test results reported to the Centers for Disease Control and Prevention (CDC) by participant laboratories for the samples containing *M. tuberculosis* or other mycobacteria shipped in June 2002. Testing results were received from 83 of 89 (93%) laboratories participating in this shipment. The *M.tb* NAA Performance Evaluation Program provides laboratories with assessment and evaluation of test methods and results. To maintain participant confidentiality, the CDC analyzes only participant data from which all laboratory identifiers have been removed by the contractor, Wisconsin State Laboratory of Hygiene.

Participant laboratories received five individual samples. Participants were requested to test the samples without the decontamination and concentration routinely performed on respiratory specimens prior to *M.tb* NAA testing. The specimen decontamination/concentration preparation steps for *M.tb* NAA testing were eliminated to allow this program to specifically assess *M.tb* NAA testing procedures (2,6).

Experiments were performed to document sample viability and test reactivity. Due to specific concerns of cross-contamination between *M.tb* NAA-positive and *M.tb* NAA-negative test samples, the negative samples were produced in a separate area. Additionally, 10% of both positive and negative samples were randomly selected and tested by the contractor to validate *M.tb* NAA test results. The test samples were also tested by five reference laboratories before shipping.

Figure 1 shows the laboratory classification represented by 79 participants. Participants consisted of 36 hospitals, 28 health departments, 12 independents, and 3 other types of laboratories.

Figure 2 provides the distribution of the volume of specimens tested with *M.tb* NAA by participating laboratories during the 3 months prior to reporting results.

Figure 3 provides a breakdown of the *M.tb* NAA test procedures reported by the participating laboratories. Participants were asked to check all of the test methods used. All of the participants (6/6) reporting the use of In-house and "Other" *M.tb* NAA test procedures used methods based on polymerase chain reaction (PCR). Although the CDC does not recommend the use of non-FDA cleared *M.tb* NAA test procedures (3,5), laboratories using In-house methods are encouraged to participate in this evaluation program to assess performance (2).

Figure 4 lists the biosafety levels reported by participant laboratories. All laboratories should routinely consult the CDC/NIH manual, Biosafety in Microbiological and Biomedical Laboratories (4th edition), for recommendations and for determining their correct biosafety level.

Participants were also asked to provide information on specific quality control practices related to the prevention of cross-contamination and subsequent false positives with NAA testing.

Figure 5 provides the participant laboratory responses to a question about whether the biological safety cabinet (BSC) used for *M.tb* NAA testing is used for other purposes. One concern is that 16% (13/82) of participant laboratories indicated that they process *M.tb* specimens in the same BSC that is used for *M.tb* NAA testing. Among the 28% (23/82) of participants that indicated "Other" uses for the *M.tb* NAA testing BSC, 12 performed *M.tb* culture work (biochemicals, drug susceptibility testing, Accuprobe® identification, etc.), 8 performed mycology, and 5 performed other microbiology or clinical specimen work. One laboratory reported using the same BSC for bioterrorism-related work and other procedures. Laboratories should be aware of recommendations (4) to perform specimen processing and NAA testing in separate work areas with separate equipment.

Figure 6 provides participant responses to a question on the use of uni-directional workflow for *M.tb* NAA testing. In addition to recommendations (4) that emphasize considerations of laboratory design for NAA testing, both manufacturers (Roche Amplicor® and Gen-Probe® MTD) recommend the use of unidirectional workflow. It is concerning that 12% (10/83) responding laboratories reported that unidirectional workflow is not being used, or that they do not know if unidirectional workflow is used.

Separate figures and tables are provided to show either the qualitative or quantitative results reported for each sample by the participant laboratories. Quantitative results for the In-house methods could not be presented in a consistent format since participants used a variety of detection systems and test interpretation criteria. The Roche Amplicor® test has interpretive criteria for quantitative results that reflect some probability that the sample is positive but are below the recommended threshold for positivity. The result form and this report use the term "equivocal" for Roche Amplicor®, to reflect the manufacturer's recommendation for reporting indeterminate quantitative test results.

Figure 7 provides a summary of the participant qualitative results reported for all five samples by test method. The aggregate participant qualitative results are indicated for the 3 positive and 2 negative samples. The combined analytical sensitivity of all methods was 97.2% (242/249) for the 3 positive samples: 100% (183/183) sensitivity for Gen-Probe® MTD; 93.8% (45/48) sensitivity for Roche Amplicor®; 77.8% (14/18) sensitivity for In-house methods. The combined analytical specificity of all methods was 98.8% (164/166) for the 2 negative samples: 99.2% (121/122) specificity for Gen-Probe®; 96.9% (31/32) specificity for Roche Amplicor®; 100% (12/12) specificity for In-house methods. Sample TB02-06-1 contained 3×10^5 theoretical cells/ml. of *M. bovis*. Sample TB02-06-3 was a blank sample containing no organisms.

Figure 8 is graphical representation of the quantitative results reported for each sample by participant laboratories using the Gen-Probe® MTD test. The indentation in each box-plot indicates the median value. The shaded area within the box represents the results between the 25th percentile and 75th percentile of the data. The bracketed areas designate either 1.5 times the interquartile range of the data or the most extreme data point on either side of the median, whichever is the least distance from the median. Each value reported which was outside these ranges is signified by one of the solid lines drawn outside the brackets. For the positive samples, TB02-06-1, TB02-06-2, and TB02-06-4, the median values of all data were 2,730,897, 2,672,263,

and 2,716,287 relative light units (RLU), respectively. The median value for the negative sample containing *M. gordonae*, TB02-06-5, was 2,520 RLU. For the sample containing no organism (blank), TB02-06-3, the median value was 2,372.

Figure 9 is a graphical representation of all quantitative results reported for each sample by participant laboratories using the Roche Amplicor® test. The solid line through each set of data represents the median value for each sample. The shaded band represents the equivocal range. The median value was 3.000 (A₄₅₀) for all the positive samples, TB02-06-1, TB02-06-2, and TB02-06-4. The median value for the sample containing no organisms (blank), TB02-06-3, was 0.054 (A₄₅₀). The median value for the sample containing *M. gordonae*, TB02-06-5, was 0.054 (A₄₅₀).

Tables 1-5 provide the qualitative results reported for individual samples by participants. In most instances the laboratories used the manufacturer's recommended interpretations of quantitative test results. Results for sample TB02-06-1, containing *M. bovis*, were similar to typical results for *M.tb*-positive samples. All results for the blank sample containing no organisms, TB02-06-3, were interpreted as negative. Thus, there was no evidence of cross-contamination. The four false-negative and three equivocal interpretations reported for positive samples appeared to be random. The one false positive and one equivocal interpretation reported for sample TB02-06-5, containing *M. gordonae*, also appeared to be random. Overall, composite results for all samples were relatively accurate and indicate that laboratories performed very well.

References

1. CDC. Update: Nucleic Acid Amplification Tests for Tuberculosis. MMWR 2000; 49:593-594.
2. CDC. Nucleic acid amplification tests for tuberculosis. MMWR 1996; 45:950-951.
3. CDC. Notice to Readers. Diagnosis of tuberculosis by Nucleic Acid Amplification methods applied to clinical specimens. MMWR 1993; 42:686.
4. NCCLS - Molecular Diagnostic Methods for Infectious Diseases; Approved Guidelines (NCCLS Document MM3-A, 1995).
5. Noordhoek GT, van Embden JDA, Kolk AHJ. Reliability of nucleic acid amplification for detection of *Mycobacterium tuberculosis*: an international collaborative quality control study among 30 laboratories. J. Clin. Microbiol. 1996; 34:2522-2525.
6. Noordhoek GT, Kolk AHJ, Bjune G, Catty D, Dale JW, Fine PEM, Godfrey-Faussett P, Cho S-N, Shinnick T, Svenson SB, Wilson S, van Embden JDA. Sensitivity and specificity of PCR for detection of *Mycobacterium tuberculosis*: A blind comparison study among seven laboratories. J. Clin. Microbiol. 1994;32:277-285.
7. CDC. Multiple misdiagnoses of tuberculosis resulting in laboratory error-Wisconsin, 1996. MMWR 1997; 46:797-801.

Figure 1. Primary Classification of Participating Laboratories

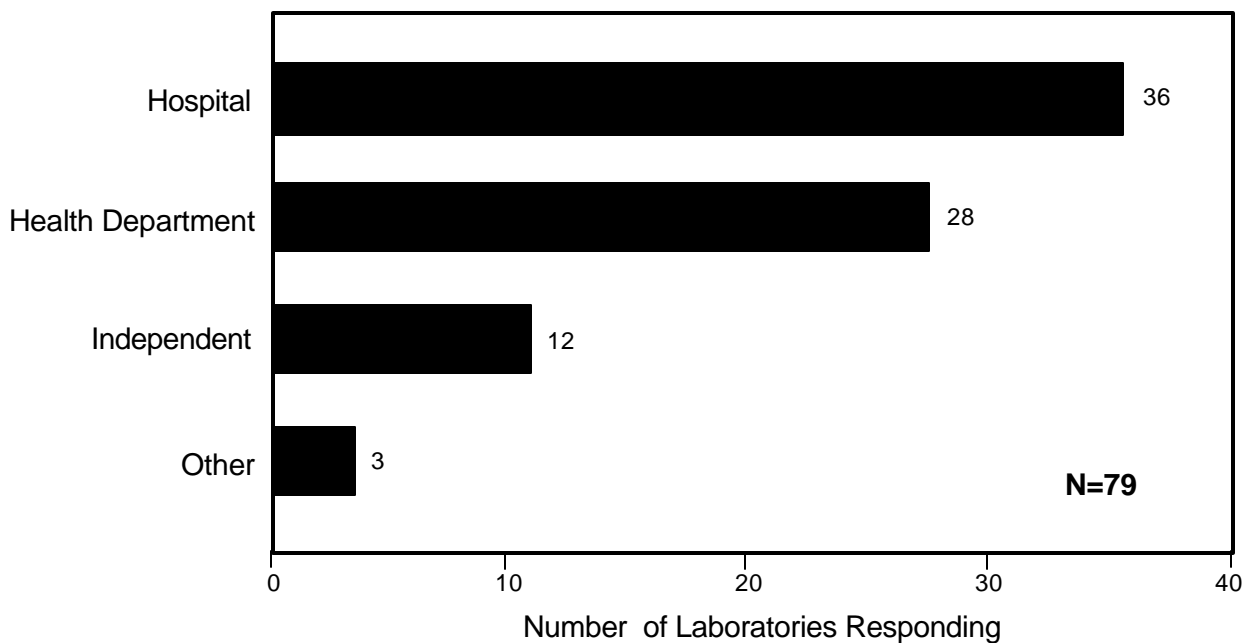
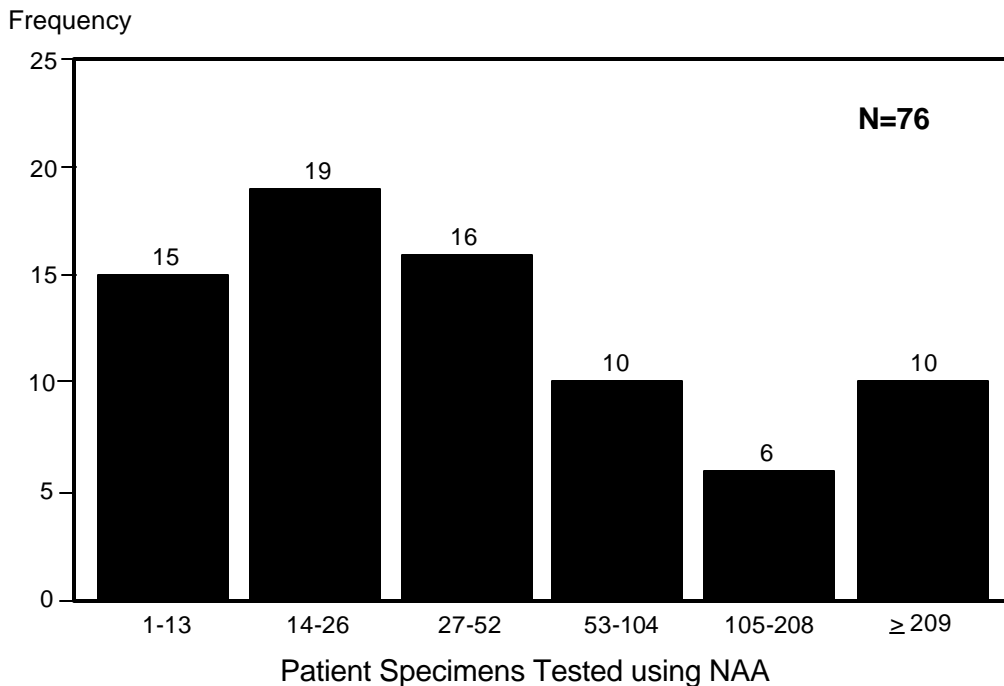


Figure 2. Number of Patient Specimens Tested for *M.tb* Using TB NAA during the Previous Quarter.*



*See explanation in the analysis.

Figure 3. Amplification Procedure Used for Direct Detection of *M.tb*

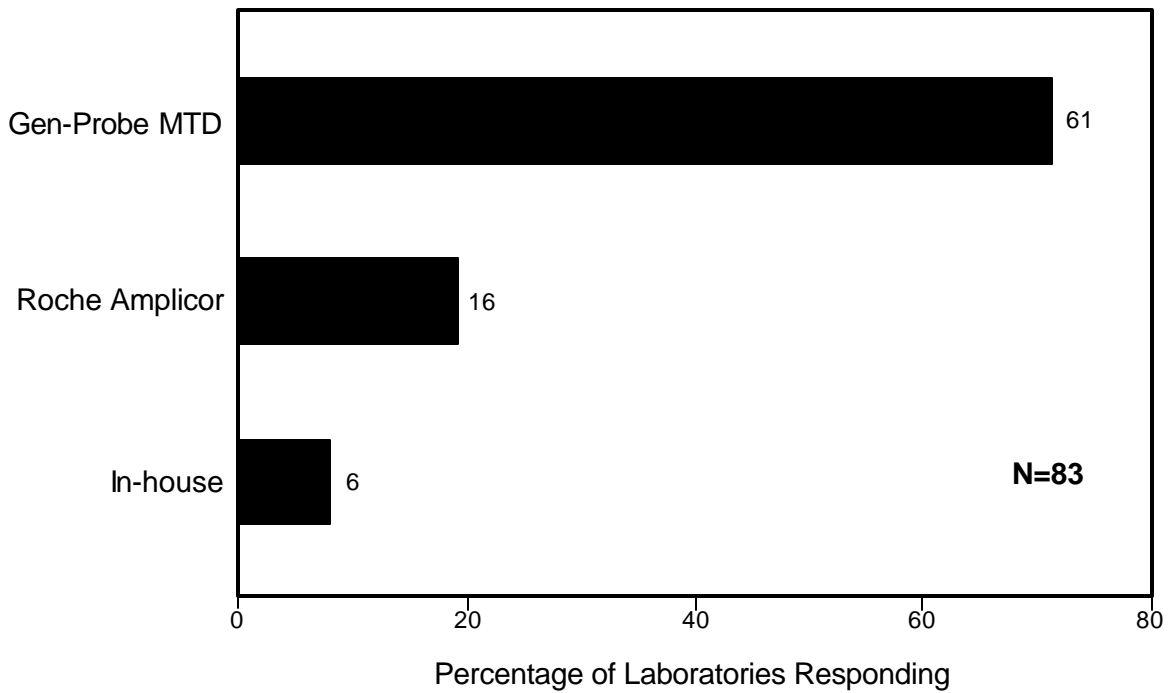


Figure 4. Biosafety Levels of Participant Laboratories

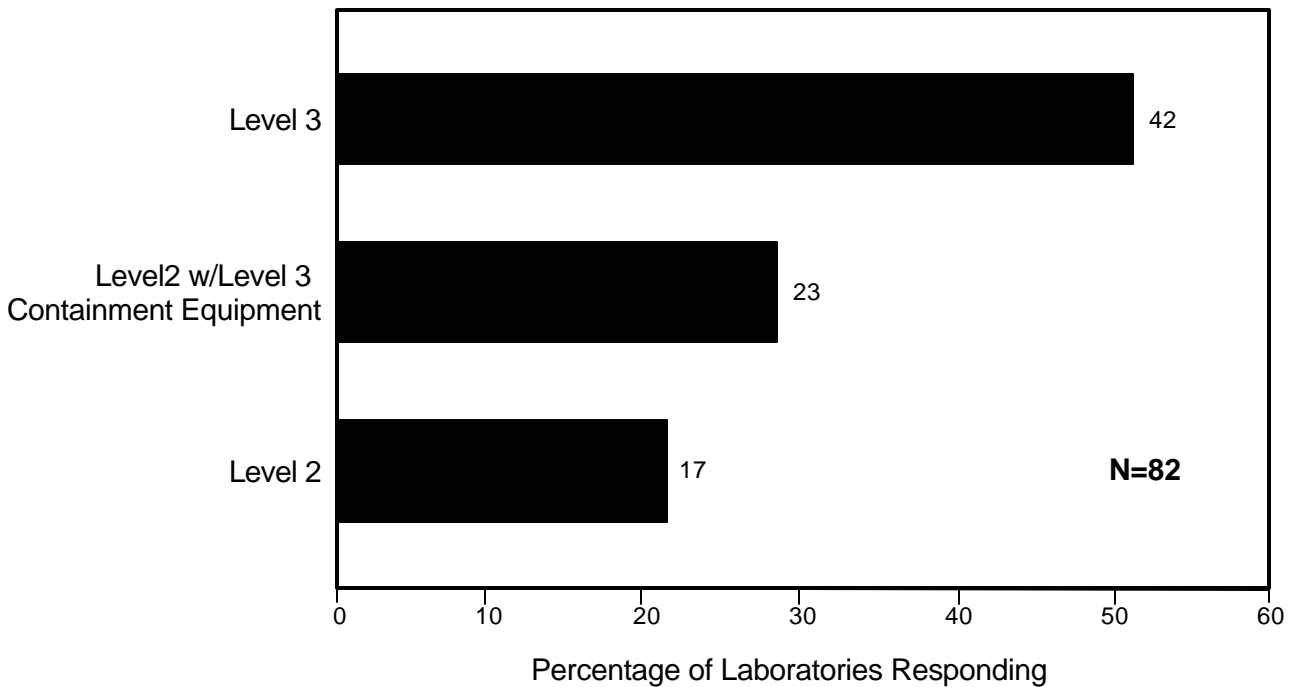


Figure 5. Is the Biological Safety Cabinet that is Used for TB NAA Testing Used for Other Purposes?

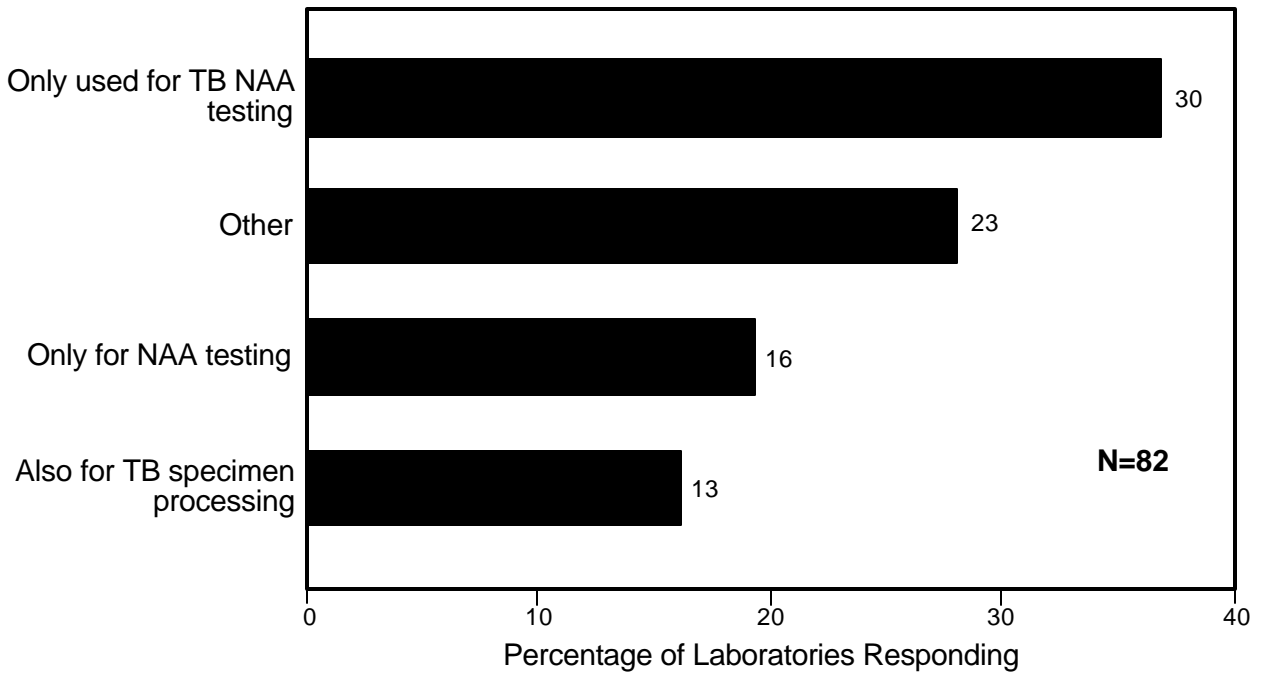


Figure 6. Use of Uni-directional Workflow by Participating Laboratories

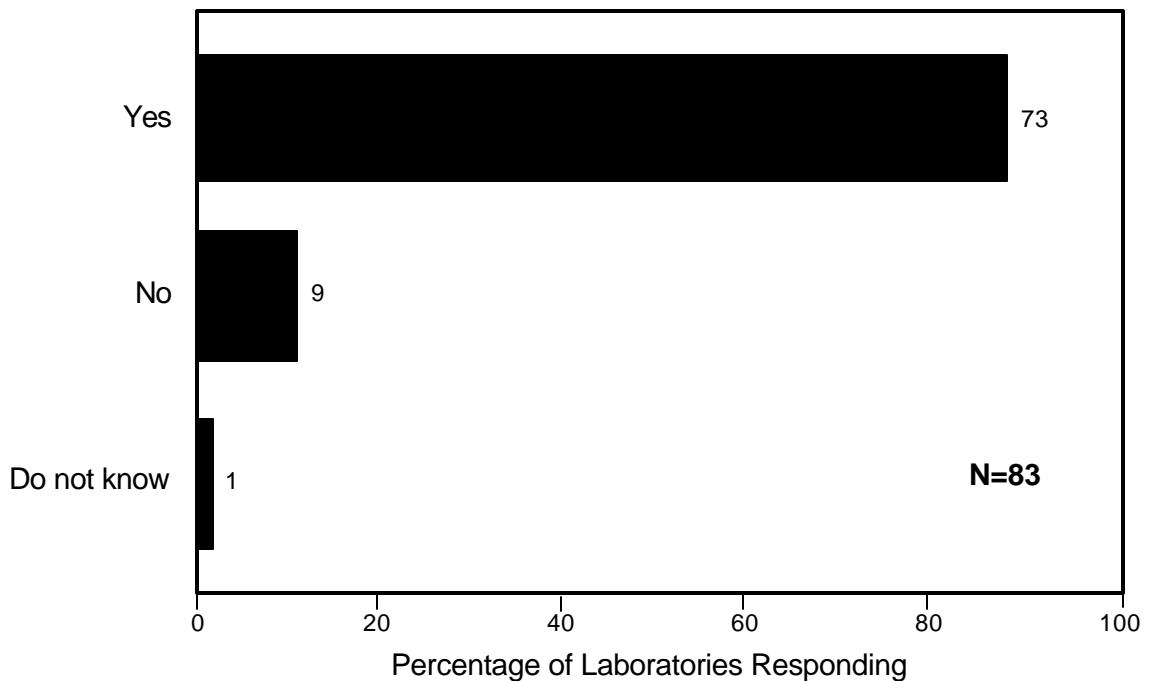
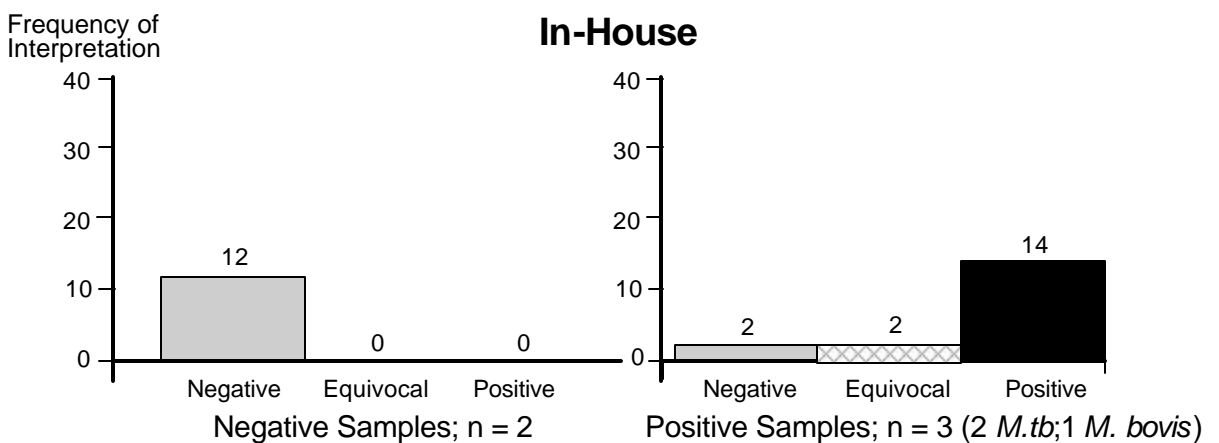
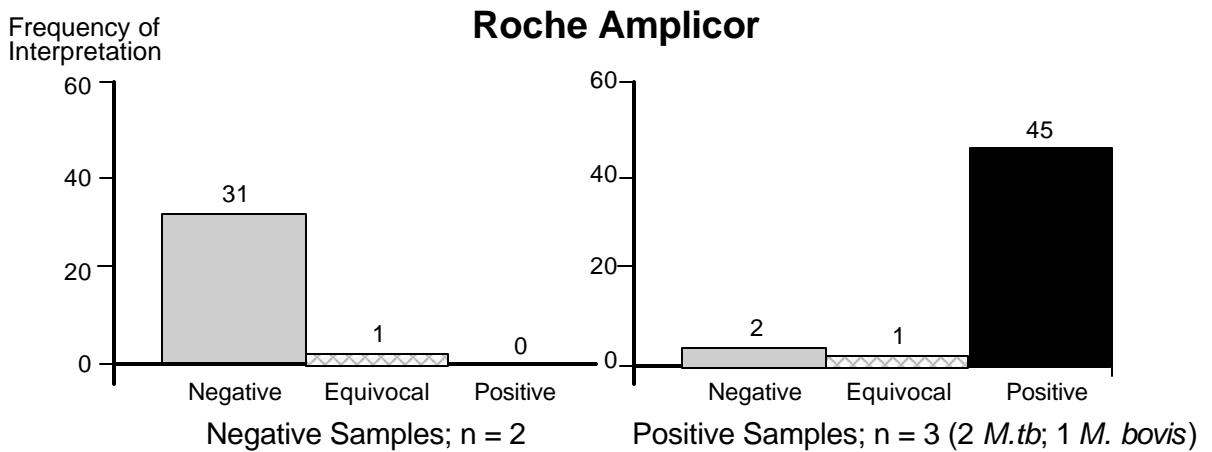
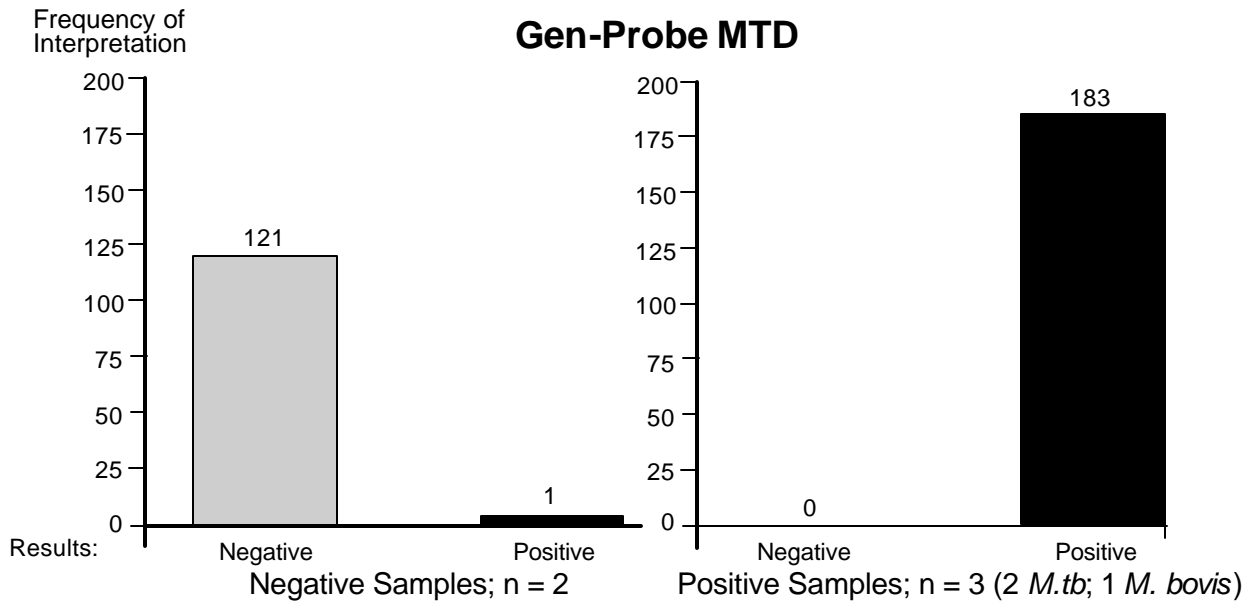
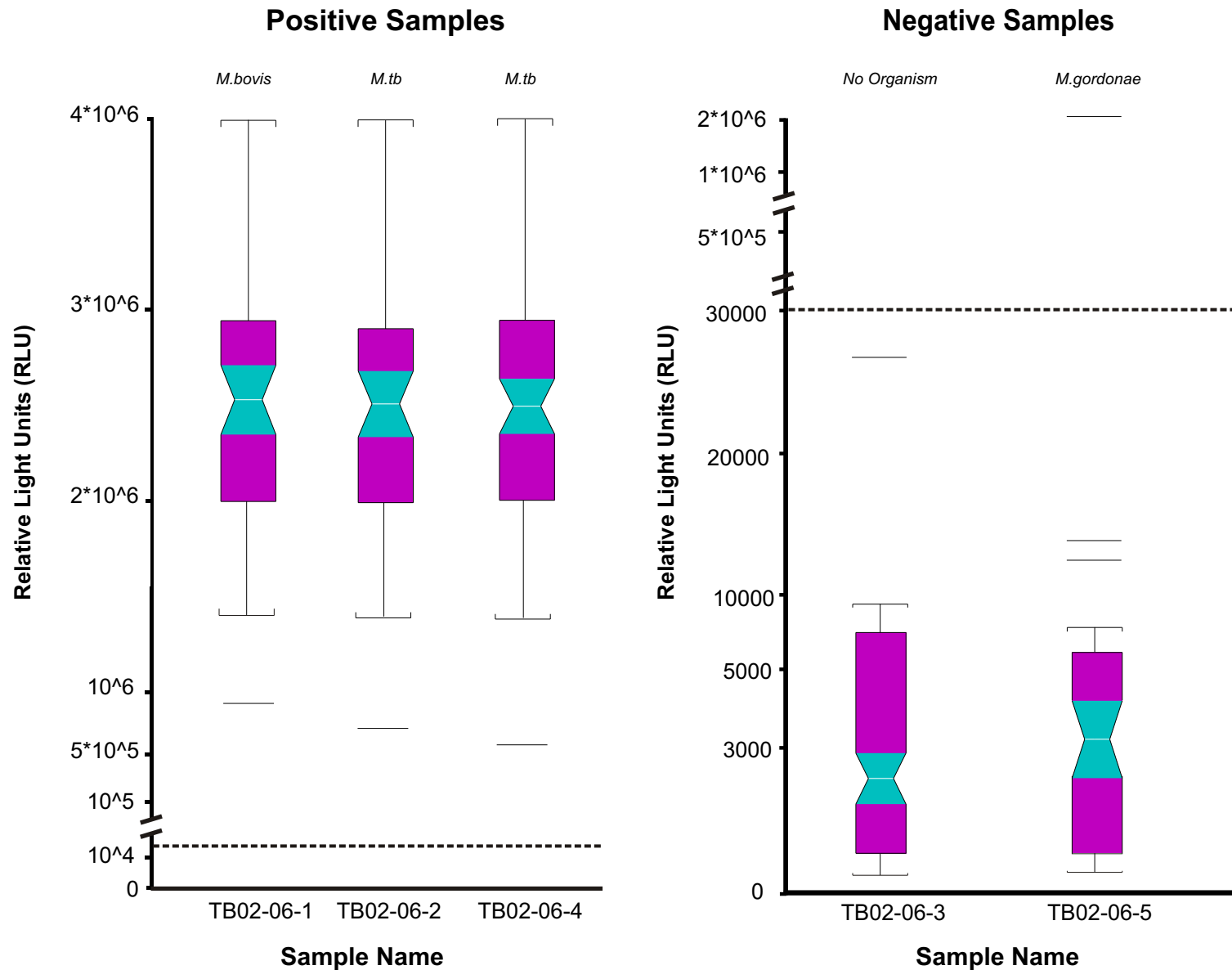


Figure 7. Frequency of TB NAA Qualitative Test Results by Sample Type for the Gen-Probe MTD, Roche Amplicor, and In-House Methods



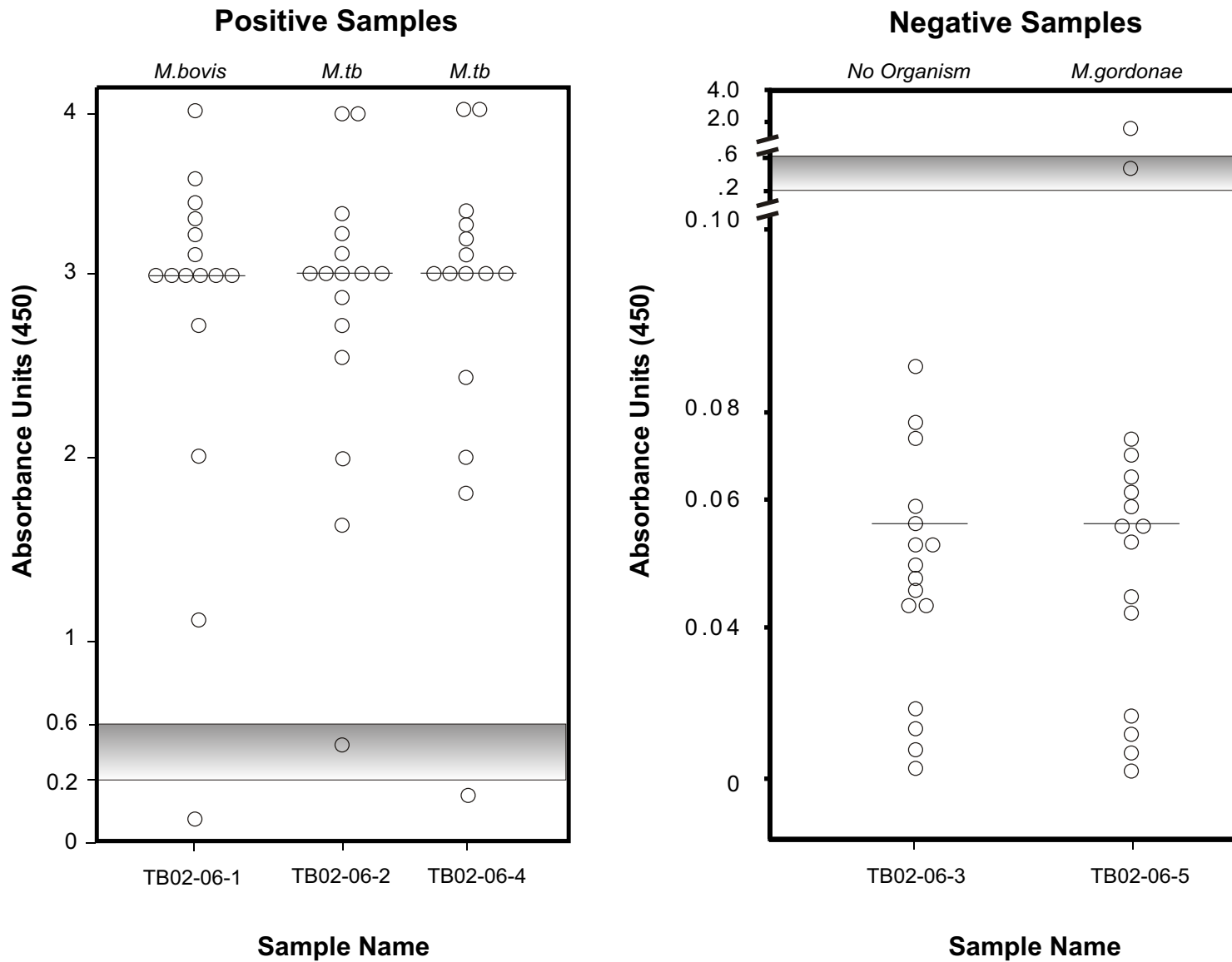
Test Result Interpretations: Negative Equivocal Positive

Figure 8. Quantitative Results for GenProbe[®] MTD



Note: Dashed line (---) represents cut-off between positive and negative values (30,000 RLUs).

Figure 9. Quantitative Results for Roche Amplicor[®]



Note: Shaded areas represent equivocal range.

The following tables summarize qualitative results reported by participant laboratories for the June 2002 shipment of samples for the *M. tb.* NAA testing performance evaluation program.

Table 1. Sample TB02-06-1 contained *Mycobacterium bovis*

Test Methods	No. Tests Performed	Positive		Equivocal		Negative	
		No.	%	No.	%	No.	%
Gen-Probe	61	61	100.0	0	0.0	0	0.0
In-house	6	3	50.0	2	33.3	1	16.7
Roche	16	15	93.8	0	0.0	1	6.3
All methods	83	79	95.2	2	2.4	2	2.4

Table 2. Sample TB02-06-2 contained *Mycobacterium tuberculosis*

Test Methods	No. Tests Performed	Positive		Equivocal		Negative	
		No.	%	No.	%	No.	%
Gen-Probe	61	61	100.0	0	0.0	0	0.0
In-house	6	5	83.3	0	0.0	1	16.7
Roche	16	15	93.8	1	6.3	0	0.0
All methods	83	81	97.6	1	1.2	1	1.2

Table 3. Sample TB02-06-3 contained no organism

Test Methods	No. Tests Performed	Positive		Equivocal		Negative	
		No.	%	No.	%	No.	%
Gen-Probe	61	0	0.0	0	0.0	61	100.0
In-house	6	0	0.0	0	0.0	6	100.0
Roche	16	0	0.0	0	0.0	16	100.0
All methods	83	0	0.0	0	0.0	83	100.0

Table 4. Sample TB02-06-4 contained *Mycobacterium tuberculosis*

Test Methods	No. Tests Performed	Positive		Equivocal		Negative	
		No.	%	No.	%	No.	%
Gen-Probe	61	61	100.0	0	0.0	0	0.0
In-house	6	6	100.0	0	0.0	0	0.0
Roche	16	15	93.8	0	0.0	1	6.3
All methods	83	82	98.8	0	0.0	1	1.2

Table 5. Sample TB02-06-5 contained *Mycobacterium gordonae*

Test Methods	No. Tests Performed	Positive		Equivocal		Negative	
		No.	%	No.	%	No.	%
Gen-Probe	61	1	1.6	0	0.0	60	98.4
In-house	6	0	0.0	0	0.0	6	100.0
Roche	16	0	0.0	1	6.3	15	93.8
All methods	83	1	1.2	1	1.2	81	97.6