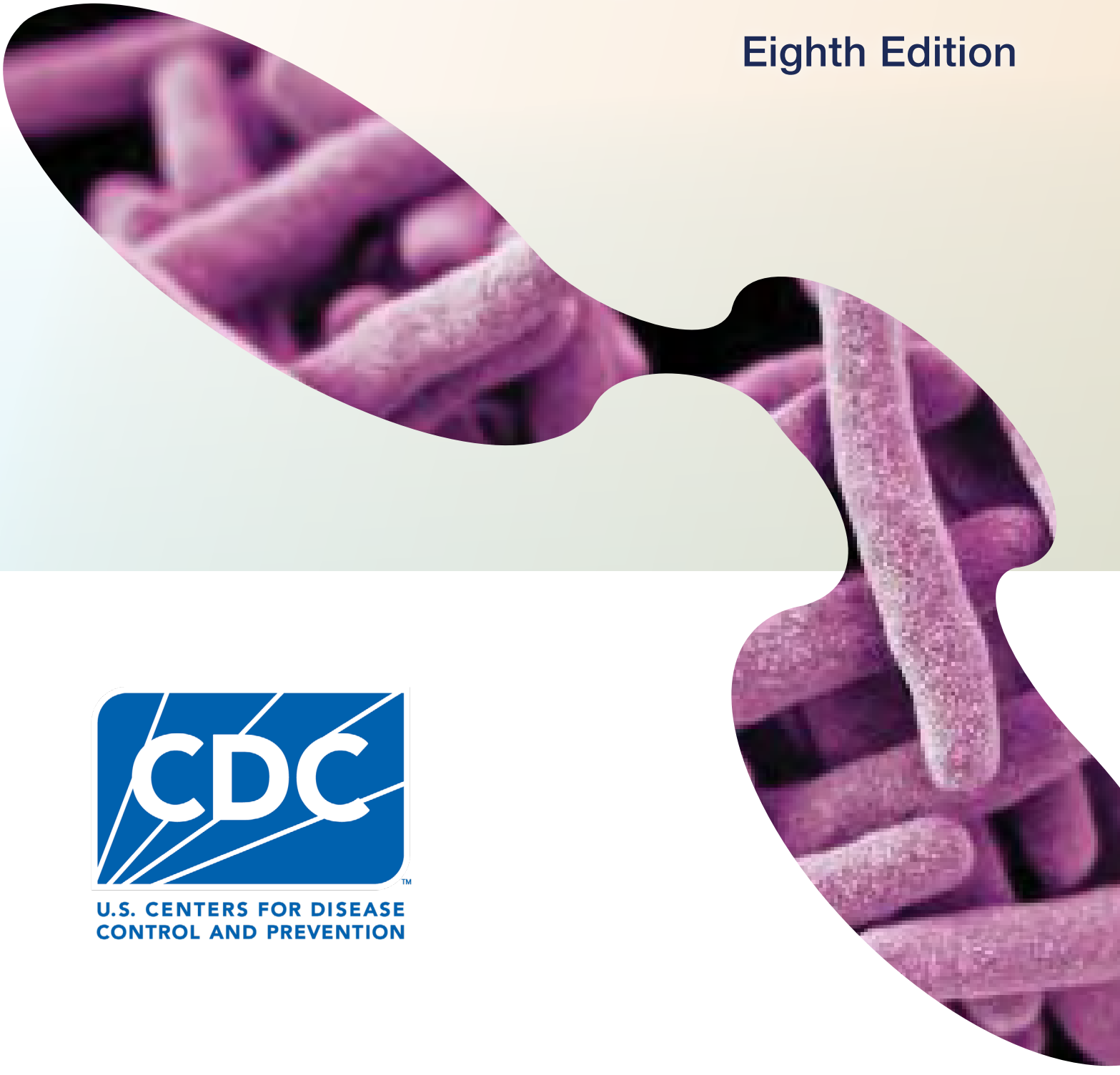
2026

Tuberculosis Laboratory Aggregate Report

Eighth Edition



U.S. CENTERS FOR DISEASE CONTROL AND PREVENTION

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Note on Accessibility: Find descriptions and explanations of figures in **Appendix B: Explanation of Figures for Accessibility (page 34)**.

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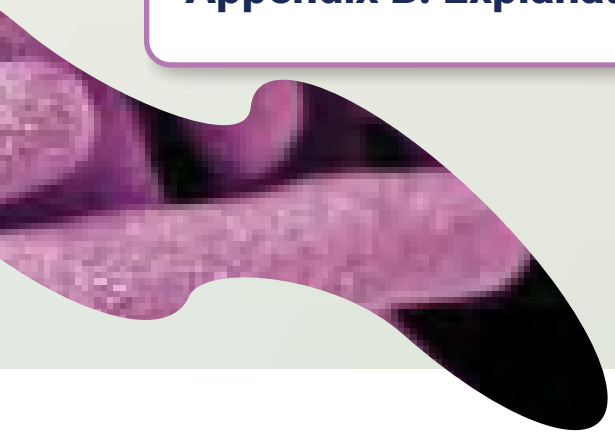

Executive Summary

The *Tuberculosis Laboratory Aggregate Report: Eighth Edition* summarizes national PHL data on workload, *Mycobacterium tuberculosis* complex (MTBC) culture positivity, TAT performance, and testing practices across 2022–2024, with updated TB testing methods reported for 2025. Self-reported data highlight continued growth in testing volume and expansion of molecular capabilities with mixed progress in meeting performance benchmarks.

PHL self-reported workload volume and TAT benchmark data suggest:

- **Sustained workload growth:** From 2022 to 2024, 44 of 58 CoAg funded PHLs experienced an increase in workload volume. In 2024, PHLs processed over 30,000 additional patient specimens than in 2022, with a 24% increase in MTBC culture-positive patients and a 44% rise in nucleic acid amplification test (NAAT) volume. Molecular drug susceptibility testing by sequencing (molecular DST) workloads more than doubled, reflecting expanded capacity.
- **Rapid expansion of sequencing:** In-house molecular DST using sequencing methods more than doubled from 2022 to 2024 (115% increase), reflecting increased adoption and expanded capacity of sequencing-based resistance detection.
- **Mixed TAT performance:** In 2024, targets were met for NAAT reporting and interferon-gamma release assay (IGRA) reporting. Specimen receipt within one day of collection, acid-fast bacilli (AFB) reporting within one day of receipt, MTBC identification within 21 days, and growth-based drug susceptibility testing (DST) within 17 days of identification remain below national targets.
- **Evolving diagnostic practices:** Matrix-assisted laser desorption ionization-time of flight (MALDI-TOF) is now the most common primary identification method from culture, while Cepheid Xpert® MTB/RIF and laboratory developed real-time polymerase chain reaction (PCR) account for the majority of NAAT use for direct detection in 2025.
- **Shifts in DST approaches:** More PHLs added fluoroquinolones to initial DST panels and implemented molecular sequencing-based DST, though variability in practices remained.

Laboratories are encouraged to review the details of each section in this report for more in-depth assessments and comparisons.

Introduction

About This Report

CDC's Tuberculosis (TB) Elimination and Laboratory Strengthening Cooperative Agreement[1] (CoAg), PS-20-2001/PS-25-2003, provides laboratory strengthening support to 58 state, local, and territorial public health laboratories (PHLs). Awardees submit Annual Performance Reports (APRs), in which PHLs self-report progress and challenges across three focus areas: (1) availability of high-quality, timely core TB laboratory services; (2) advancement of laboratory efficiency and quality assurance through the use of laboratory-specific data; and (3) communication and collaboration with partners to ensure optimal use of laboratory services and timely information exchange. In addition, PHLs report TB testing methods and algorithms, laboratory workload volume, and turnaround time (TAT) performance data.

These data are compiled and presented in the *Tuberculosis Laboratory Aggregate Report: Eighth Edition*. The purpose of this report is to support PHLs in assessing progress toward national TB testing benchmarks and to facilitate peer comparison among laboratories with similar testing or specimen volumes, methodologies, or geographic characteristics. Laboratories are encouraged to routinely monitor and evaluate TB workload and TAT indicators, with the goal of improving performance by establishing realistic, incremental, laboratory-specific objectives and goals. Laboratory practices should also be reviewed to identify opportunities for quality improvement and to evaluate the effectiveness of implemented changes.

For questions regarding CDC TB CoAg requirements or laboratory-specific data, please contact your Laboratory Capacity Team (LCT) consultant.

Technical Notes

Unless otherwise specified, all data and information presented in the tables and figures originate from APRs submitted to CDC by U.S. PHLs receiving TB Elimination and Laboratory Strengthening CoAg funding.

- One laboratory did not report 2024 TAT data in time for publication; therefore, analyses include TAT data from 57 PHLs.
- For **Table 4 (page 24)**, PHLs were asked to describe their NAAT algorithms for inclusion.
- For **Figures 11–16**, data on testing methods were as reported from APR narratives.

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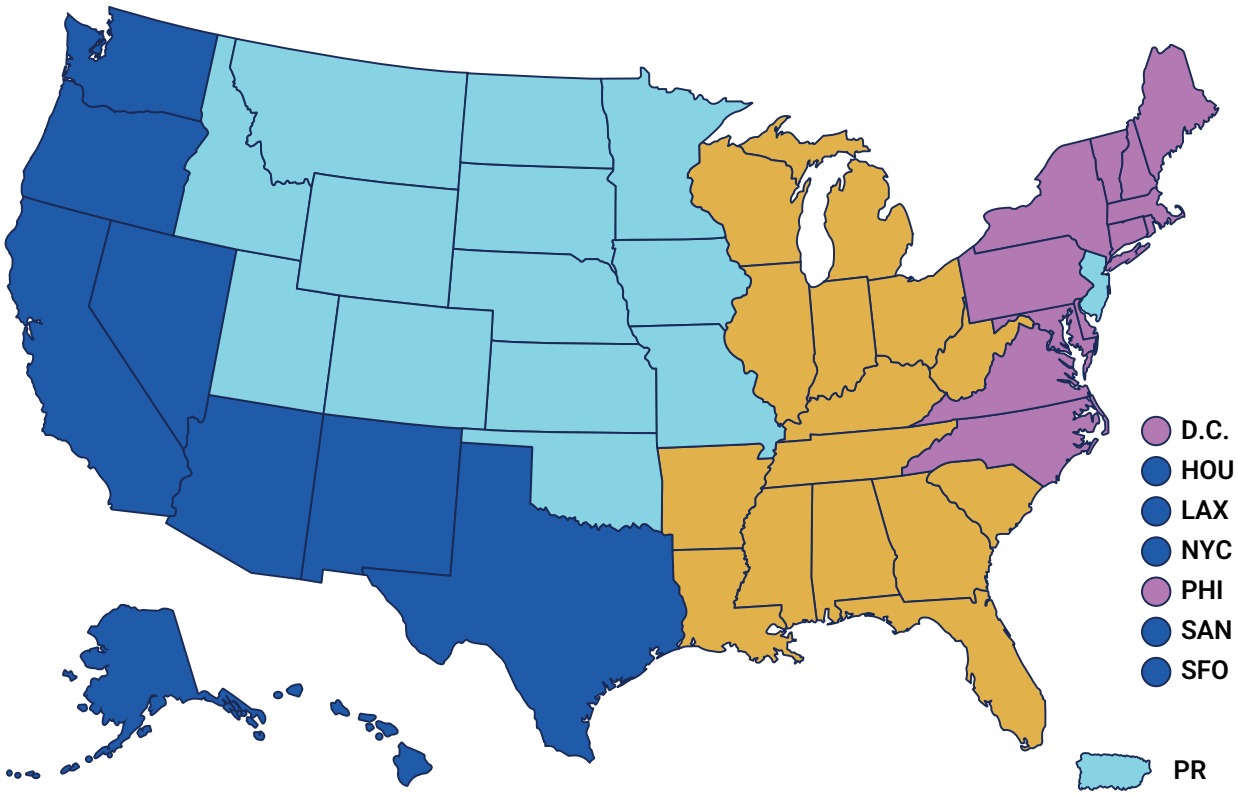


Location Abbreviations

D.C.: District of Columbia
HOU: Houston, TX
LAX: Los Angeles, CA
NYC: New York City, NY
PHI: Philadelphia, PA
PR: Puerto Rico
SAN: San Diego, CA
SFO: San Francisco, CA

Acronyms and Abbreviations

AFB .....Acid-fast bacilli

AP.....Agar proportion

APR.....Annual Performance Report for the CDC TB Elimination and Laboratory Cooperative Agreement

BACTEC™ MGIT™.....Mycobacterial Growth Indicator Tube; a commercial non-radiometric broth-based mycobacterial culture system by Becton Dickinson and Co.

CoAg....CDC TB Elimination and Laboratory Cooperative Agreement

CDC.....U.S. Centers for Disease Control and Prevention

Deeplex® Myc-TB.....A commercial targeted next generation sequencing assay by GenoScreen that identifies MTBC, detects mutations associated with resistance, and provides reportable interpretation.

DST .....Drug susceptibility testing; inoculation of bacteria in/on media containing a particular drug for determination of susceptibility or resistance based on growth.

HPLC....High performance liquid chromatography; analytical technique for the identification of mycobacteria species based on differences in cell wall mycolic acids.

ID .....Identification from culture growth

IGRA.....Interferon-gamma release assay; whole-blood test used to measure a person's immune reactivity to MTBC.

In-house.....Testing performed at the public health laboratory

INNO-LiPA® .....A commercial line probe assay by Fujirebio that identifies MTBC.

LCT.....Laboratory Capacity Team

MALDI-TOF .....Matrix-assisted Laser Desorption Ionization-Time of Flight; a mass-spectrometry based assay for bacterial identification based on time of flight of proteins and peptides.

MTBC ..*Mycobacterium tuberculosis* complex

NAAT ...Nucleic acid amplification test; in this report, generic terminology for molecular methods used for direct detection of MTBC in clinical specimens.

National DST Reference Center for MTBC ..... National PHL Drug Susceptibility Testing Reference Center for *Mycobacterium tuberculosis* complex, currently awarded to the California Microbial Diseases Laboratory

PHLs....Public health laboratories

PRA.....PCR restriction analysis; analysis of amplified DNA fragments produced by the cleaving of DNA by restriction enzymes.

QuantiFERON®.A commercial IGRA blood test by QIAGEN that is used to aid in diagnosis of TB infection.

tNGS ....Targeted next generation sequencing

TAT.....Turnaround time

TB.....Tuberculosis

Trek Sensititre®.....A commercial broth microdilution plate by ThermoScientific for determination of minimum inhibitory concentration (MIC) of 12 antituberculosis drugs, simultaneously.

T-SPOT®.TB.....A commercial IGRA blood test by Revvity used to aid in diagnosis of TB infection.

WGS.....Whole genome sequencing

Xpert® MTB/RIF .....A commercial molecular assay by Cepheid®, Inc. for direct detection of MTBC and mutations associated with rifampin resistance.

Laboratory Workload

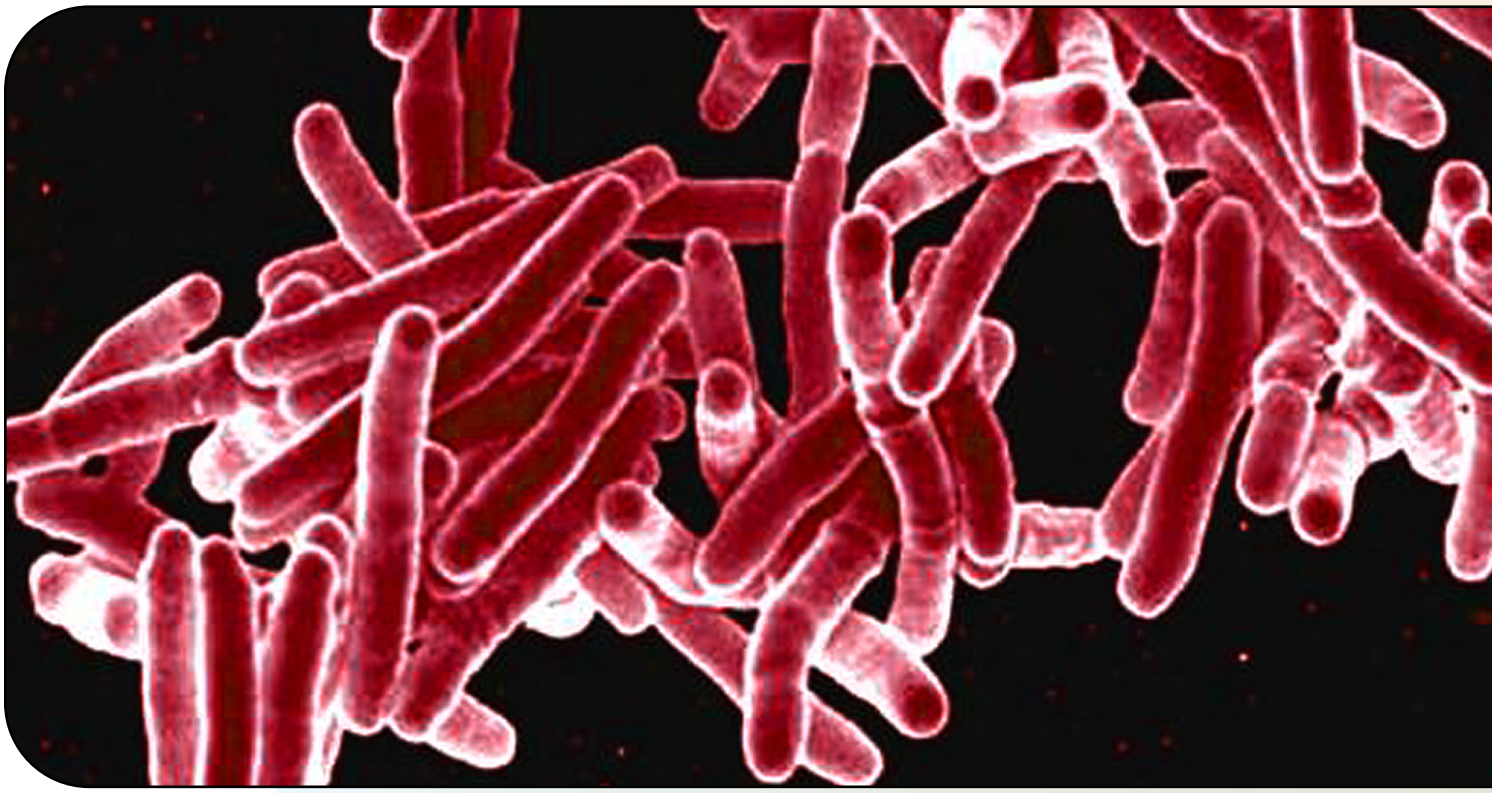
Table 1. National Workload Data Among 58 PHLs, 2022–2024

Key Workload Data Indicator Number and Description	Total Number (Range: Min. – Max.)			Three-Year Change Total # (% change)
	2022	2023	2024	
Acid-Fast Bacilli (AFB) Smear & Culture Testing				
1. Clinical specimens[a] processed for smear and culture	161,772 (5–17,214)	188,486 (6–19,233)	192,063 (27–19,787)	30,291 (18.7%)
2. Patients for whom a clinical specimen was processed	65,049 (3–9,952)	76,961 (2–12,069)	75,682 (5–8,598)	10,633 (16.3%)
2a. Patients culture positive for MTBC	3,170 (0–425)	3,550 (0–608)	3,932 (2–564)	762 (24.0%)
2b. MTBC culture positive patients that were NAAT positive	1,932 (0–297)	2,239 (0–419)	2,480 (1–391)	548 (28.4%)
Nucleic Acid Amplification Testing (NAAT)				
3. Patients for whom a clinical specimen was tested by NAAT[b]	17,201 (1–3,449)	22,273 (1–3,795)	24,826 (5–4,140)	7,625 (44.3%)
3a. Patients for whom a clinical specimen was NAAT positive for MTBC[b]	2,558 (0–376)	3,134 (0–456)	3,244 (1–422)	686 (26.8%)
Referred Isolates				
4. Patients for whom a reference isolate was submitted to rule out or confirm identification (ID) of MTBC	10,084 (0–1,720)	11,445 (0–1,442)	12,655 (0–1,614)	2,571 (25.5%)
4a. Patients for whom a reference isolate was identified as MTBC	3,067 (0–643)	3,843 (0–693)	3,964 (0–778)	897 (29.2%)
First-Line Drug Susceptibility Testing (DST)				
5. Patients for whom first-line DST was performed/referred	5,430 (0–586)	6,334 (0–853)	6,537 (2–817)	1,107 (20.4%)
Molecular DST by Sequencing				
6. Patients for whom in-house molecular DST by sequencing was performed[c]	1,869 (59–678)	2,262 (75–830)	4,024 (12–1,232)	2,155 (115.3%)
6a. Patients for whom in-house molecular DST by sequencing directly from a specimen was performed[c]	436 (22–278)	537 (30–294)	1,013 (28–332)	577 (132.3%)
6b. Patients for whom in-house molecular DST by sequencing of an isolate was performed[c]	1,503 (31–640)	1,765 (40–693)	3,180 (12–999)	1,677 (111.6%)
Genotyping				
7. Patients for whom an MTBC isolate was referred to another laboratory for genotyping or FASTQ files from in-house whole genome sequencing (WGS) were provided to CDC for genotyping analysis	5,783 (0–949)	7,882 (0–1,263)	8,958 (2–1,150)	3,175 (54.9%)
Interferon-Gamma Release Assay (IGRA)				
8. IGRA performed in-house	95,606 (0–37,002)	108,131 (20–38,274)	114,185 (43–41,208)	18,579 (19.4%)

a Processed and cultured, not including isolates referred from other laboratories.
b Includes sediments received only for NAAT.
c Laboratories may have tested patient samples as both specimen and isolates.

Overall, national laboratory workload volumes increased between 2022-2024, following the pandemic years of 2020–2022. Nearly all workload indicators showed year-over-year growth (**Table 1**):

- In 2024, PHLs processed more than 30,000 additional patient specimens than in 2022, and the number of patients that were MTBC culture-positive increased by 24%, from 3,170 in 2022 to 3,932 in 2024.
- NAAT workload volume increased sharply, with a 44.3% increase in patients with a specimen tested (from 17,201 to 24,826) and a 26.8% increase in patients with specimens that were NAAT-positive (from 2,558 to 3,244).
- From 2022 to 2024, increased workload volume for in-house molecular DST was observed:
  - Overall, molecular DST performed from patient specimens increased by 115.3% (from 1,869 to 4,024).
  - Sequencing performed directly from specimens increased by 132.3%, and sequencing from patient isolates increased by 111.6%, reflecting expanded PHL sequencing capacity and integration into routine workflows.



M. tuberculosis pink bacilli on electron microscope

Table 2. Mean and Range for PHL Key Workload Indicators, Stratified by Category of Number of Clinical Specimens Processed by 58 PHLs, 2024

Key Workload Data Indicator Number and Description	Clinical Specimens Processed by Each PHL Mean (Range: Min. – Max.)				
	1–1,000 Specimens (17 [29.3%])[a]	1,001–2,000 Specimens (11 [19%])[a]	2,001–4,000 Specimens (13 [22.4%])[a]	4,001–8,000 Specimens (12 [20.7%])[a]	>8,000 Specimens (5 [8.6%])[a]
1. Clinical specimens processed for smear and culture	649 (27–979)	1,615 (1,063–1,974)	2,432 (2,019–3,603)	5,006 (4,037–6,012)	14,317 (8,154–19,787)
2. Patients for whom a clinical specimen was processed	209 (5–362)	775 (371–1,006)	971 (523–1,496)	1,897 (817–3,352)	5,647 (3,526–8,598)
2a. Patients culture positive for MTBC	21 (2–65)	57 (5–318)	56 (11–135)	77 (21–149)	258 (40–564)
2b. MTBC culture positive patients that were NAAT positive	14 (1–38)	45 (3–298)	33 (6–68)	43 (2–94)	159 (27–391)
3. Patients for whom a clinical specimen was tested by NAAT	110 (5–323)	265 (38–974)	289 (51–568)	492 (99–1,071)	2,078 (417–4,140)
3a. Patients for whom a clinical specimen was NAAT positive for MTBC	26 (1–136)	51 (3–310)	38 (7–74)	52 (2–108)	226 (59–422)
4. Patients for whom a reference isolate was submitted to rule out or confirm ID of MTBC	47 (0–303)	230 (0–1,340)	178 (0–738)	248 (0–543)	809 (4–1,614)
4a. Patients for whom a reference isolate was identified as MTBC	19 (0–107)	110 (0–778)	83 (0–688)	58 (0–142)	130 (4–300)
5. Patients for whom first-line DST was performed/referred	42 (2–274)	83 (5–249)	142 (11–817)	116 (21–258)	337 (86–776)
6. Patients for whom in-house molecular DST by sequencing was performed	444 (12–1,232) [3][b]	1,055 (1,055) [1][b]	90 (90) [1][b]	N/A (N/A) [0][b]	774 (549–999) [2][b]
6a. Patients for whom in-house molecular DST by sequencing directly from a specimen was performed	155 (28–282) [2][b]	323 (323) [1][b]	48 (48) [1][b]	N/A (N/A) [0][b]	332 (332) [1][b]
6b. Patients for whom in-house molecular DST by sequencing of an isolate was performed	340 (12–950) [3][b]	779 (779) [1][b]	42 (42) [1][b]	N/A (N/A) [0][b]	669 (339–999) [2][b]

a (Number of PHLs [% of total])
b [# PHLs that perform this testing]

Note: MTBC: *Mycobacterium tuberculosis* complex, NAAT: nucleic acid amplification test, ID: identification, DST: drug susceptibility testing, IGRA: interferon-gamma release assay

United States PHLs receive varying volumes of clinical specimens for TB testing. To facilitate meaningful comparisons of testing volume, the 58 CoAg PHLs were categorized into five groups based on the number of clinical specimens processed and key workload indicators; mean values and ranges are also presented (**Table 2**). Because not all PHLs perform molecular DST, the analysis was limited to laboratories that conduct this testing in-house from patient specimens or isolates, as indicated in the table.

Figure 1. Culture Positivity by Site, Stratified by Category of Number of Clinical Specimens Processed, 2024

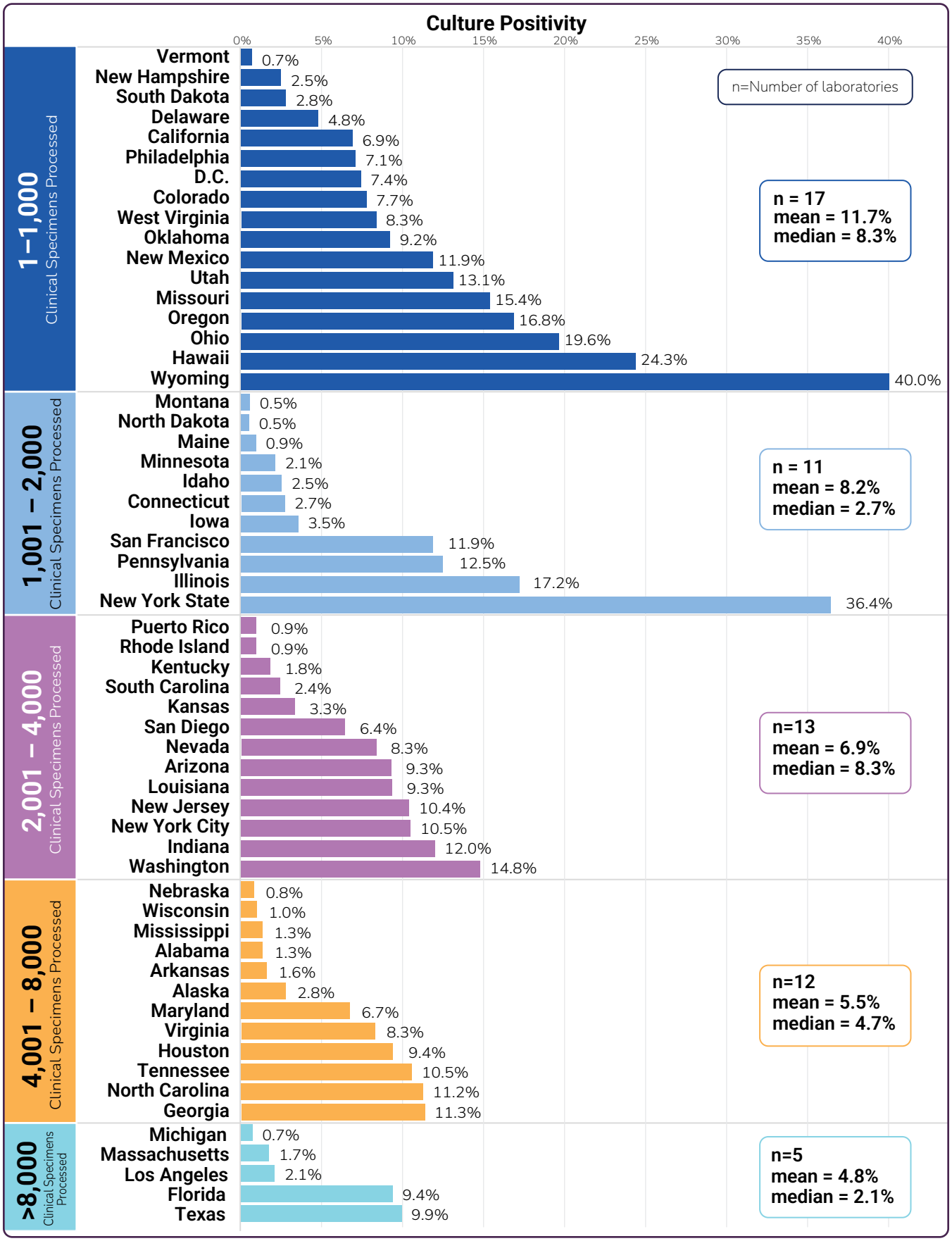
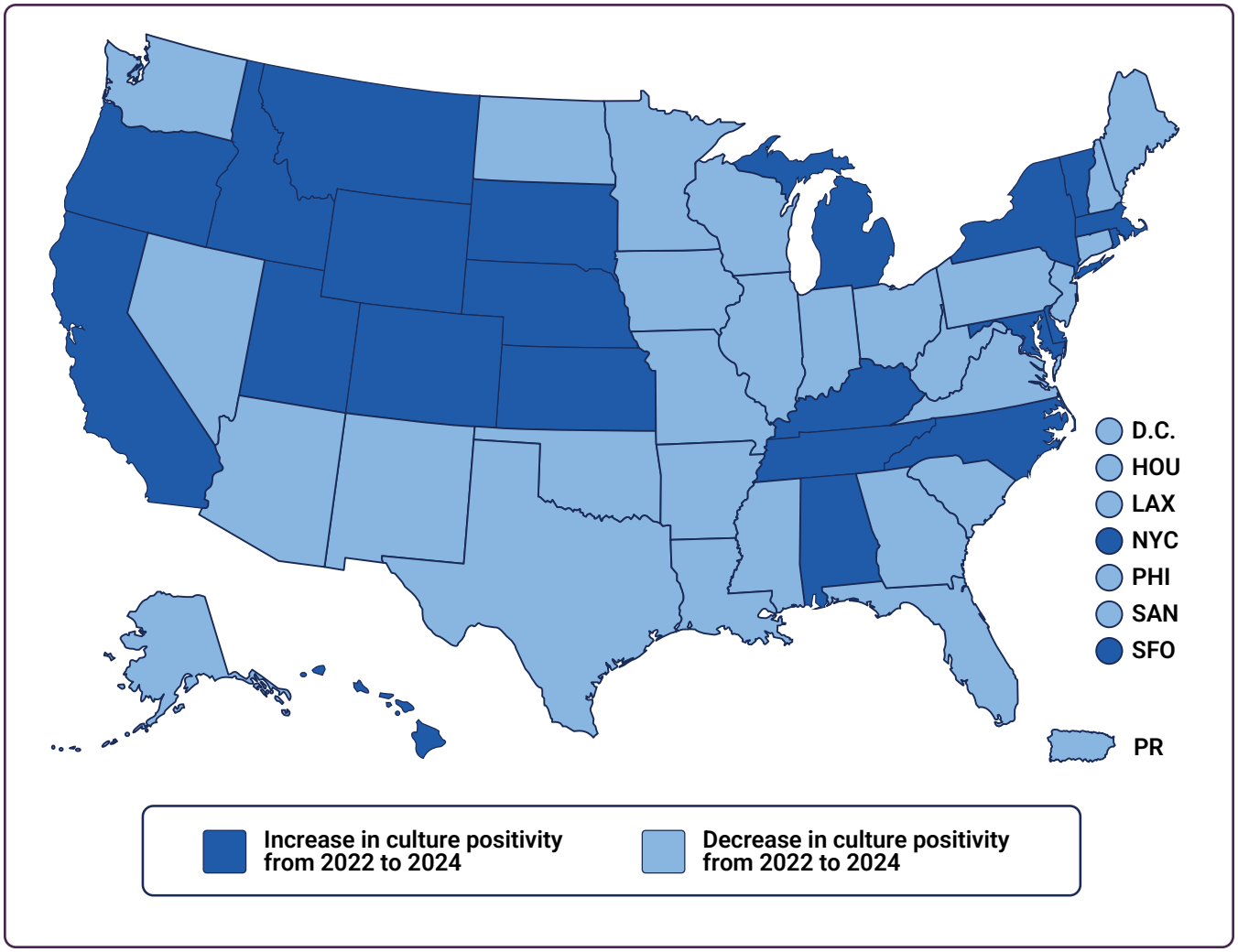


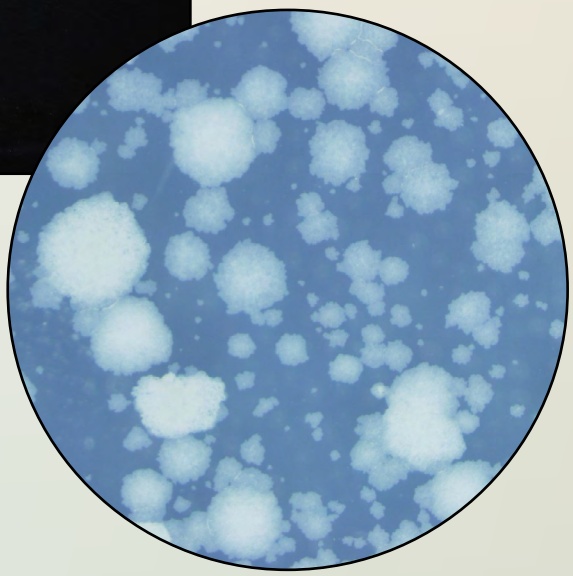
Figure 2. Change in MTBC Culture Positivity Among PHLs, 2022–2024



Culture positivity, defined as the percentage of patients with MTBC positive cultures among all patients with a processed specimen, varied widely across PHLs in 2024. MTBC culture positivity ranged from 0.5% to 40%, with substantial variability observed within each specimen volume category (**Figure 1, page 11**). PHLs processing fewer than 2,000 specimens (n=28) had a higher mean culture positivity (10.3%) compared with those processing more than 2,000 specimens (6.0%, n=30).

These differences reflect variation in local patient populations and testing patterns. PHLs serving as primary diagnostic laboratories often receive high volumes of specimens from patients undergoing initial TB evaluation, contributing to lower culture positivity. In contrast, reference laboratories receiving specimens after TB diagnosis may show higher positivity.

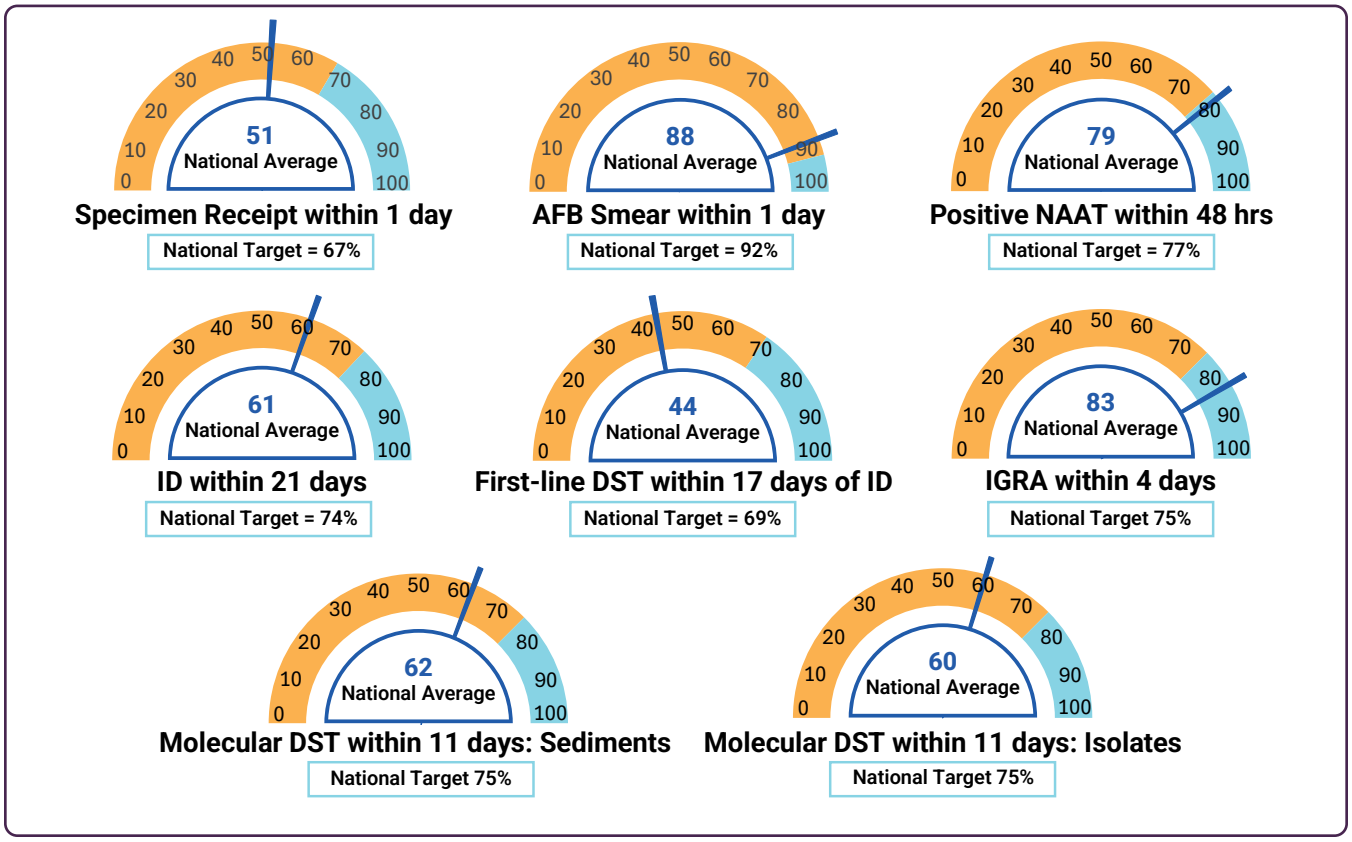
Between 2022 and 2024, most PHLs (n=34) experienced a decrease in culture positivity, while 24 reported an increase (**Figure 2**). Monitoring shifts over time helps identify changes in TB burden or testing practices. Larger fluctuations, especially in lower volume PHLs, may stem from small changes in MTBC positive cultures, variations in testing volume, or laboratory factors such as contamination, specimen collection concerns, or issues with reagents, media or equipment. When notable changes occur, PHLs should communicate with their jurisdictional TB Program and, when appropriate, submitting facilities.



M. tuberculosis on 7H11 agar plate
(Source: APHL)

Turnaround Times

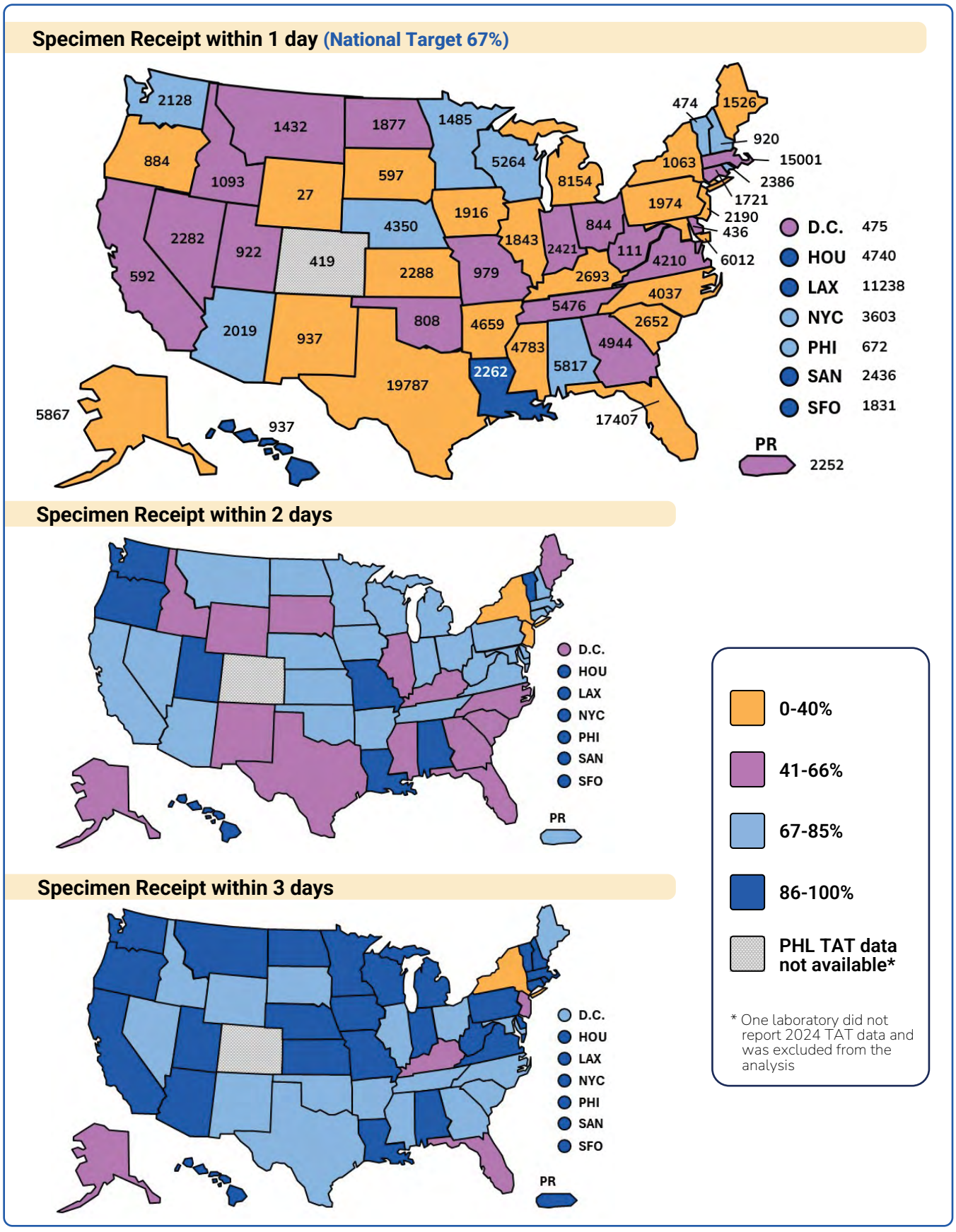
Figure 3. Turnaround Time Indicators and National Averages Among PHLs, 2024



In 2024, national averages for two of eight TAT benchmarks exceeded national targets: positive NAAT TAT within 48 hours (79%) and IGRA result within 4 days (83%).

- The NAAT TAT benchmark was revised prior to collection of 2024 data with the new 2025–2029 Notice of Funding Opportunity application. It was updated to emphasize timely reporting of positive results rather than both timely reporting *and* testing algorithm. Following this change, the national average for NAAT TAT increased and exceeded the national target for the first time.
- Three new TAT benchmarks were introduced for 2024 data: reporting IGRA results within 4 days of specimen collection, reporting molecular DST results within 11 days for sediments, and reporting molecular DST results within 11 days for isolates.
  - National performance for reporting IGRA results within 4 days of specimen collection (83%) exceeded the national target of 75%.
  - Among laboratories performing molecular DST, national averages were close to the national target of 75% for both sediments (62%) and isolates (60%).
- National averages for four longstanding TAT benchmarks—specimen receipt within 1 day of collection, AFB smear results reported within 1 day, identification (ID) of MTBC from initial diagnostic specimen reported within 21 days of specimen receipt, and growth-based DST results reported within 17 days of ID of MTBC remained below their respective national targets.

Figure 4. Maps of Percentage of Specimens Received within 1, 2, and 3 Days from Specimen Collection, with Total Number of Specimens Received by PHL, 2024



Specimen receipt within one day of collection remains a challenge for many PHLs (**Figure 4**). In 2024, PHLs reported a broad range in the number of specimens received (27–19,787 specimens) as well as in the percentage of specimens received within 1 day of specimen collection (4%–96%). Variation in specimen receipt TAT reflects differences in specimen collection practices and transportation logistics. Local PHLs typically serve submitters within a smaller geographic area, which may contribute to shorter transport times and more rapid specimen receipt.

- In 2024, 17 PHLs (29%), including 11 state PHLs (19%) and 6 local PHLs (10%), met or exceeded the national target of 67% for specimen receipt within 1 day of collection. This represents a decrease in the number of state PHLs meeting or exceeding the national target compared with 2022, when 13 state PHLs (22%) and 6 local PHLs (10%) met the target.

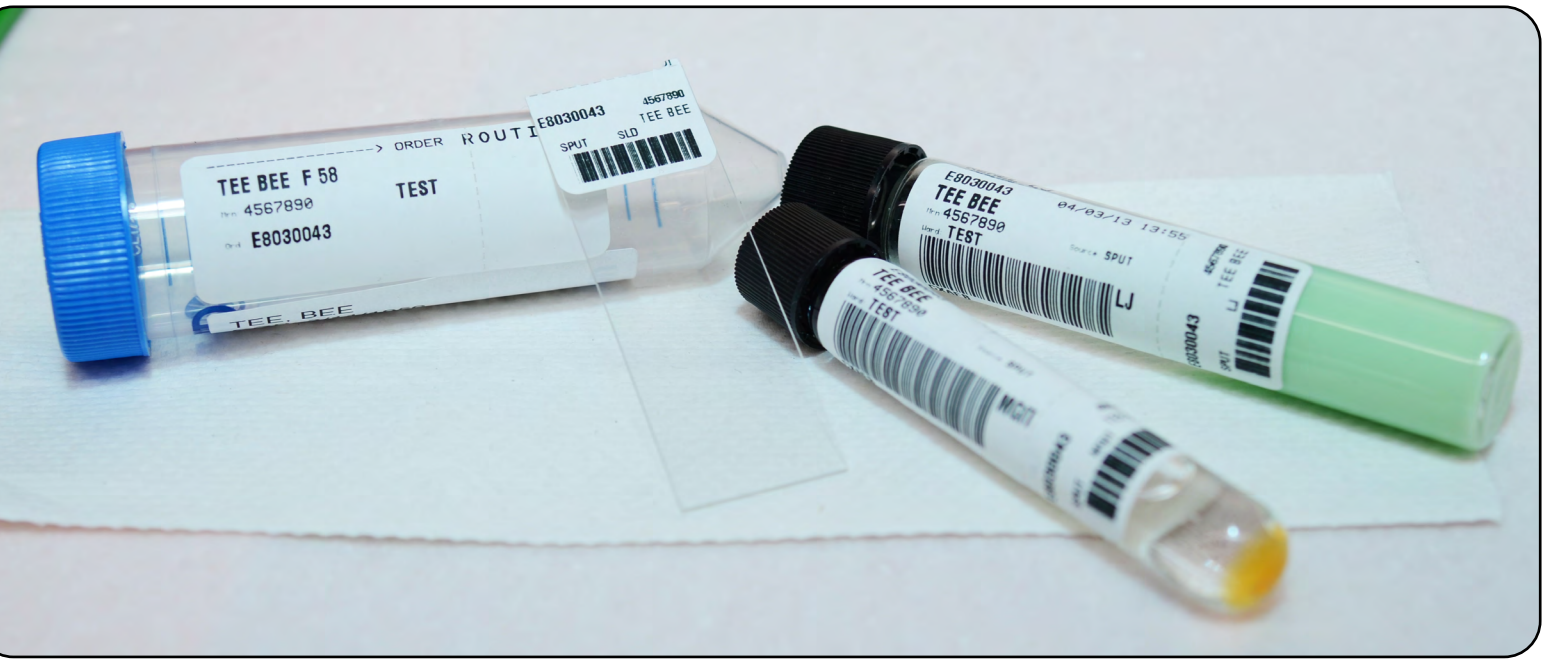
  The 17 PHLs that met or exceeded the national target in 2024 processed as few as 474 specimens to as many as 11,238 specimens.

- Nineteen PHLs (33%) reported specimen receipt within 1 day of collection for 41–66% of specimens. These PHLs processed between 111 and 15,001 specimens in 2024.

  Four of these 19 PHLs reported specimen receipt TATs at the upper end of this range (60%–66%), approaching the national target.

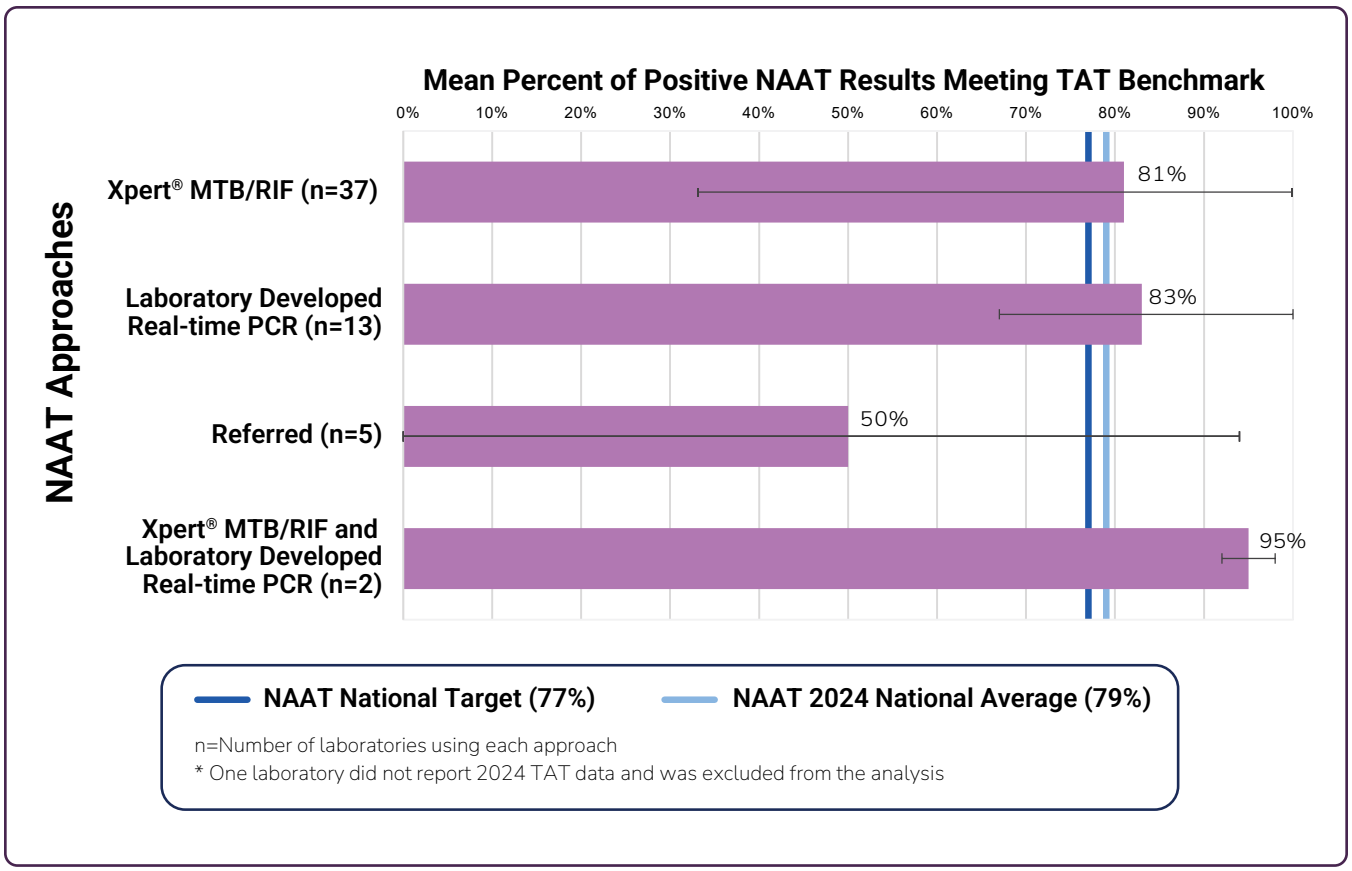
- Specimen receipt TAT improved by day 3, as illustrated in the maps by the increasing number of states with higher percentages of specimens received by day 2 and day 3.

  On average, 51% of specimens were received by day 1, 73% by day 2, and 85% by day 3.



Common testing materials and media (Source: APHL)

Figure 5. Mean Percentage of Patients with a Positive NAAT Result Reported within 48 hours of Specimen Receipt, by NAAT Approach, 2024

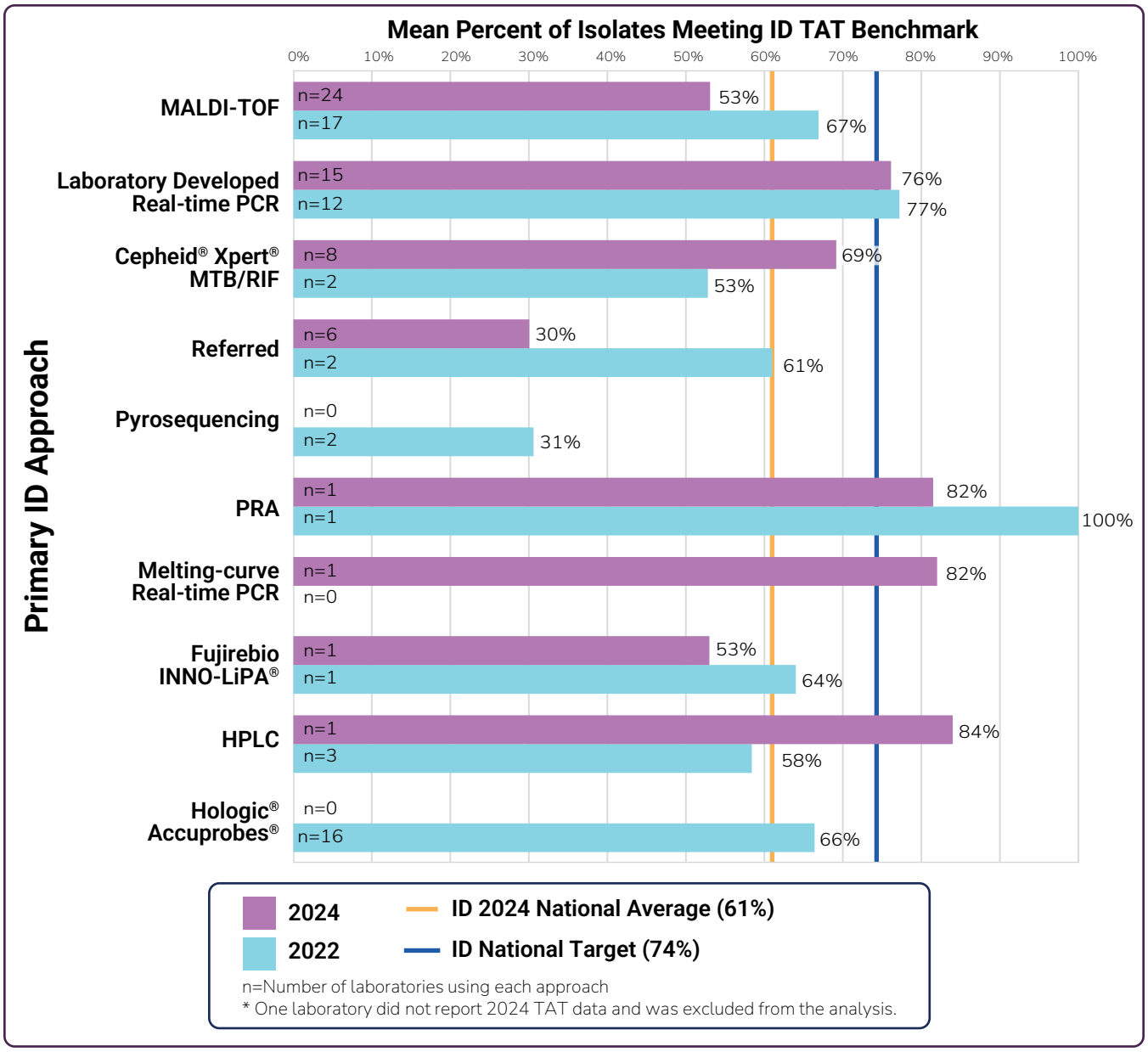


The NAAT TAT indicator measures the proportion of patients for whom a positive NAAT result for MTBC was reported within 48 hours of specimen receipt. In 2024, this indicator was evaluated across the different NAAT approaches used by laboratories. Although the national target provides a common benchmark, performance varied by testing approach, as illustrated by the range bars.

Laboratories performing NAAT in-house reported higher proportions of positive NAAT results within 48 hours of specimen receipt compared to laboratories who referred testing. However, variability was observed among laboratories using the same testing approach, suggesting that differences in workflows or testing practices may influence timeliness. Laboratories that relied on referral testing showed that additional steps in the referral process may be associated with longer TATs.

These findings highlight the importance of reviewing NAAT pathways to identify opportunities for improvement. Review of cases in which NAAT results were not reported within 48 hours may help laboratories and TB Programs identify workflow or algorithm adjustments that could support more timely detection of MTBC and reporting of results. Note: Data presented in this report reflect NAAT results reported by TB CoAg supported PHLs and do not represent all NAAT performed nationally.

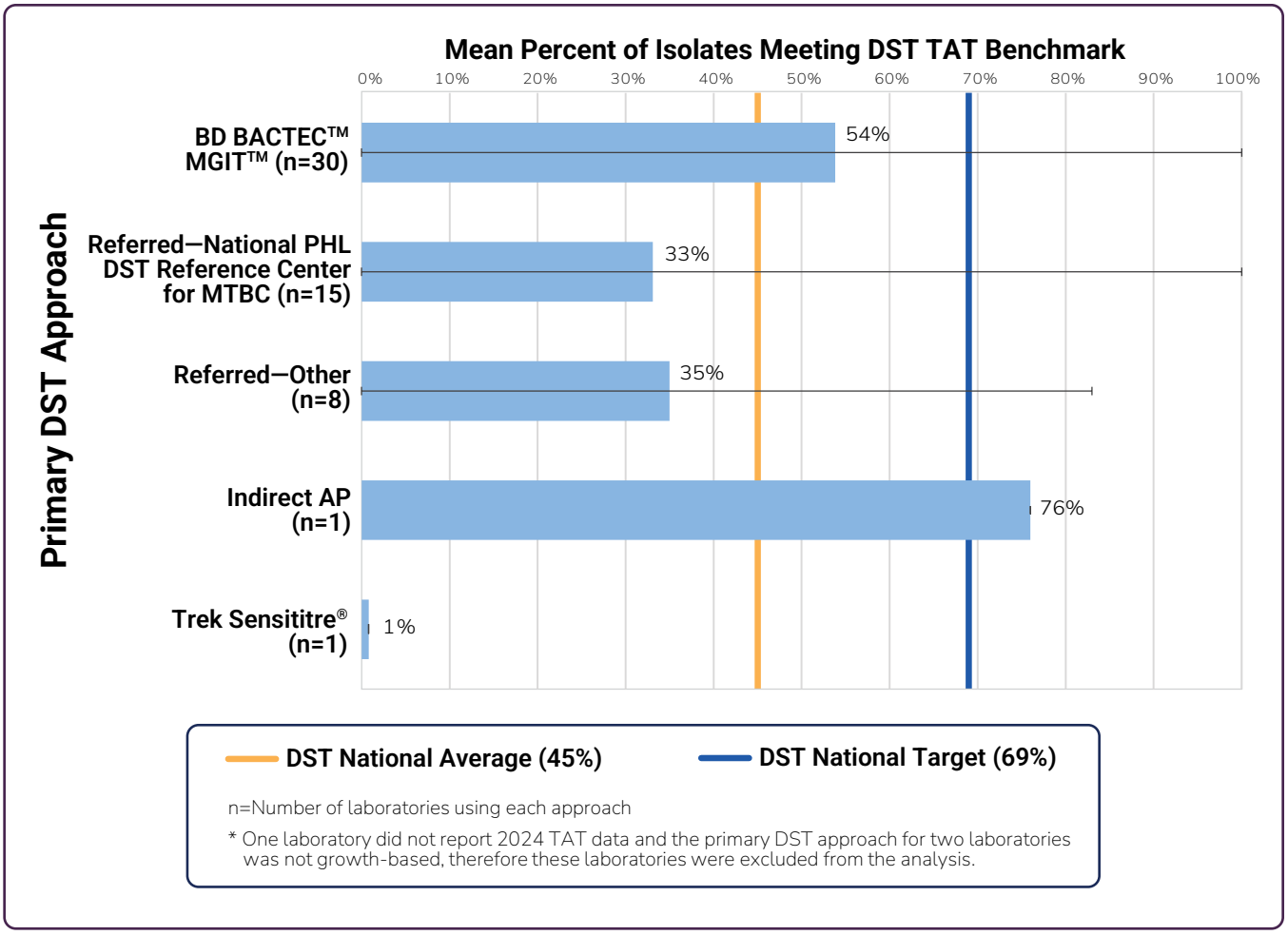
Figure 6. Comparison of MTBC Identification (ID) Approach by Mean Percentage of Isolates Meeting the Identification Turnaround Time Benchmark, 2022–2024



Primary methods used by PHLs for MTBC identification (ID) changed between 2022 and 2024. Laboratories that reported using Hologic® AccuProbe® or pyrosequencing in 2022 reported validating new ID methods or transitioning to referral-based identification by 2024. During this period, the mean percentage of MTBC isolates identified within 21 days decreased for most primary ID approaches.

- Laboratories using high-performance liquid chromatography (HPLC) and Cepheid® Xpert® MTB/RIF as primary ID methods from culture showed increases in the mean percentage of MTBC isolates identified within 21 days from 2022 to 2024.
- hsp65 nested PCR-restriction analysis (PRA) and real-time PCR exceeded the national target in both years. In addition, two laboratories using HPLC and melting-curve real-time PCR met or exceeded the national target in 2024.

Figure 7. Mean Percentage of Isolates with Growth-based Rifampin DST Results Reported within 17 Days of ID*, by Primary DST Approach, 2024

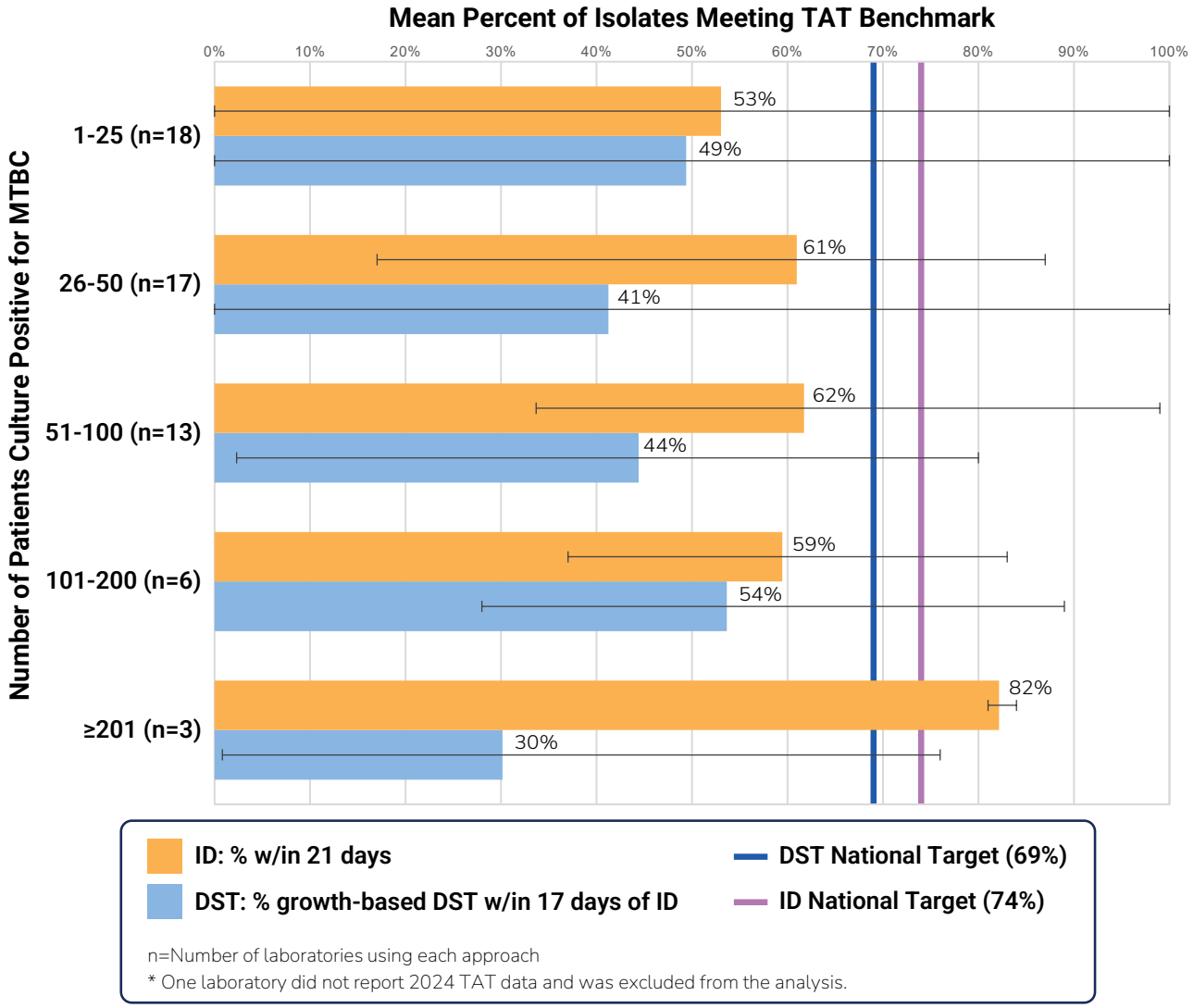


In 2024, all PHLs that identified MTBC from culture growth (n=58) reported that first-line DST was performed (measured by rifampin); however, one laboratory did not report drug susceptibility testing TAT data.

- Among reporting PHLs, the percentage of MTBC isolates with growth-based DST completed within 17 days of ID ranged from 0% to 100%.
- The single laboratory using indirect agar proportion (AP) had a mean percentage above the national target of 69%.
- The most reported DST approach was the BD BACTEC™ MGIT™ (n=30), with a mean of 54% of isolates completing growth-based DST within 17 days of ID.

Continued monitoring of growth-based DST turnaround times and frequent review of testing approaches may support improvements in timely DST reporting.

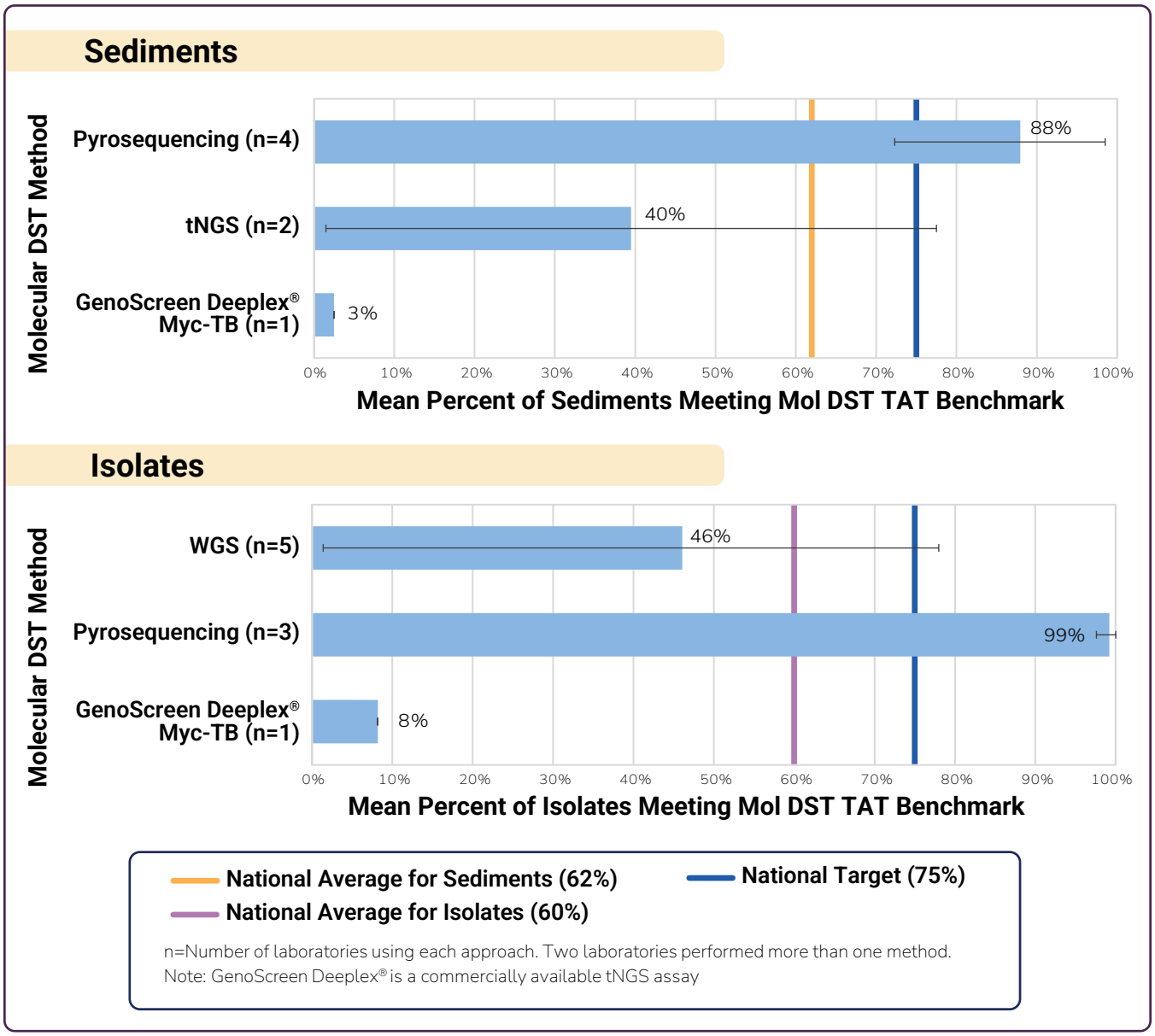
Figure 8. Mean Percentage of MTBC Identified* from Culture within 21 Days of Specimen Receipt and Growth-based DST* Performed within 17 Days of ID, by Number of MTBC Culture Positive Patients, 2024



In **Figure 8**, PHLs were grouped according to the number of patients with cultures positive for MTBC, ranging from 2 to 564 patients. For each group, the mean percentage of isolates meeting recommended TATs was assessed for ID (ID reported within 21 days from specimen receipt) and growth-based DST (DST results reported within 17 days of ID).

- The three laboratories with ≥201 MTBC culture-positive patients had a mean percentage of MTBC isolates identified within 21 days of 82%, exceeding the national target of 74% with individual laboratory percentages ranging from 81% to 84%. In contrast, the mean percentage of isolates in this group with growth-based DST reported within 17 days of ID was 30%, below the national target of 69%, with individual laboratory percentages ranging from 1% to 76%.
- Across all PHL groups, none met or exceeded the national target for growth-based DST within 17 days of ID.

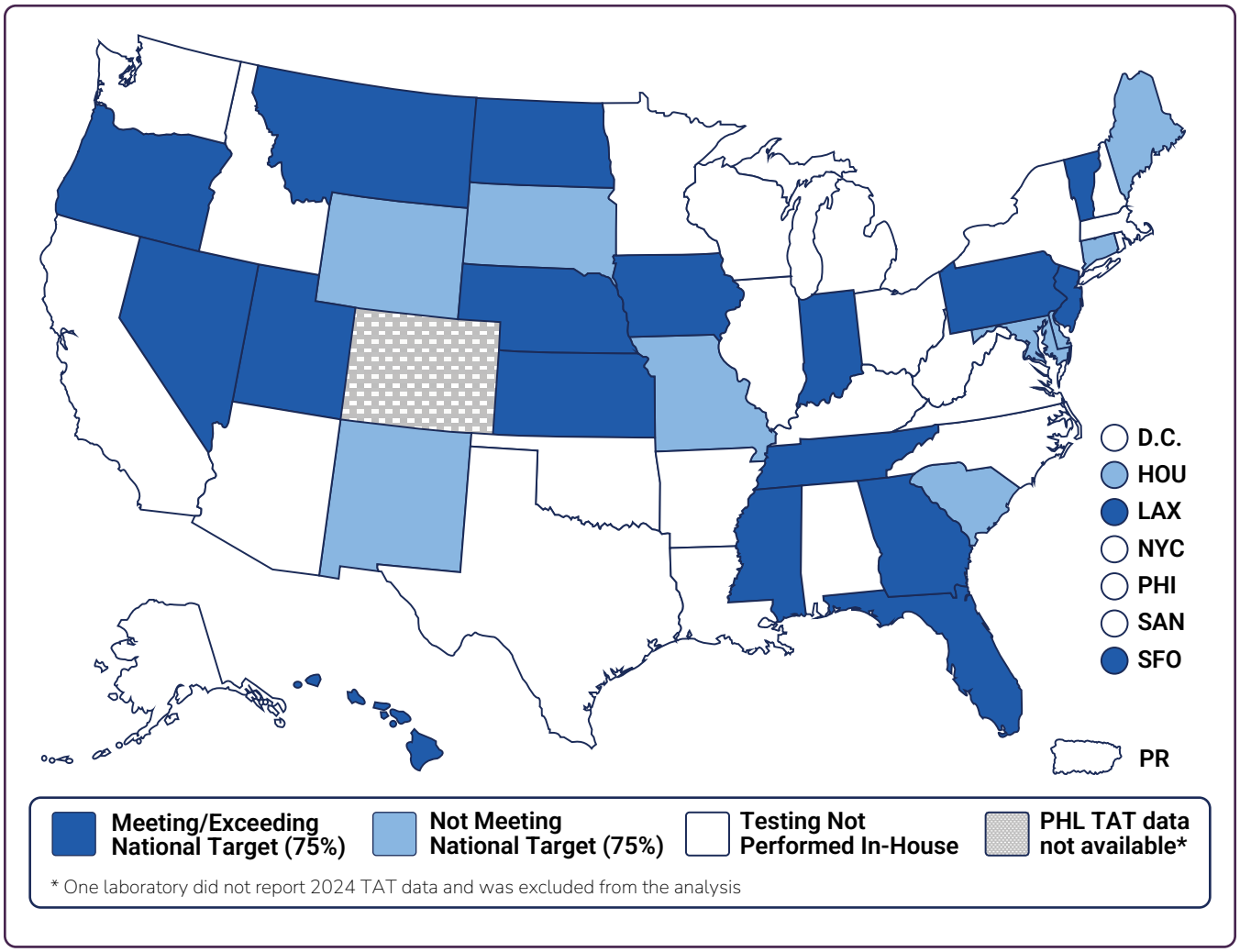
Figure 9. Mean Percentage of Sediments and Isolates with In-house Molecular DST Results Reported within 11 Days of Specimen Receipt or ID, by Molecular DST Method, 2024



In 2024, seven PHLs reported in-house molecular DST TAT data; two laboratories reported data for more than one sequencing method.

- Laboratories performing pyrosequencing had a mean percentage exceeding the national target of 75% for both sediments (88%) and isolates (99%).
- Laboratories using newer molecular sequencing methods, including GenoScreen Deeplex® Myc-TB, in-house developed targeted next generation sequencing (tNGS), and whole genome sequencing (WGS), had a mean percentage below the national target.

Figure 10. Map of Reported PHL Interferon Gamma Release Assay (IGRA) Use and TAT Performance, 2024



The national target for the interferon-gamma release assay (IGRA) TAT indicator is defined as ≥75% of IGRA results reported within 4 days of specimen collection among laboratories performing in-house IGRA testing. In 2024, this indicator was implemented and reported by PHLs for the first time.

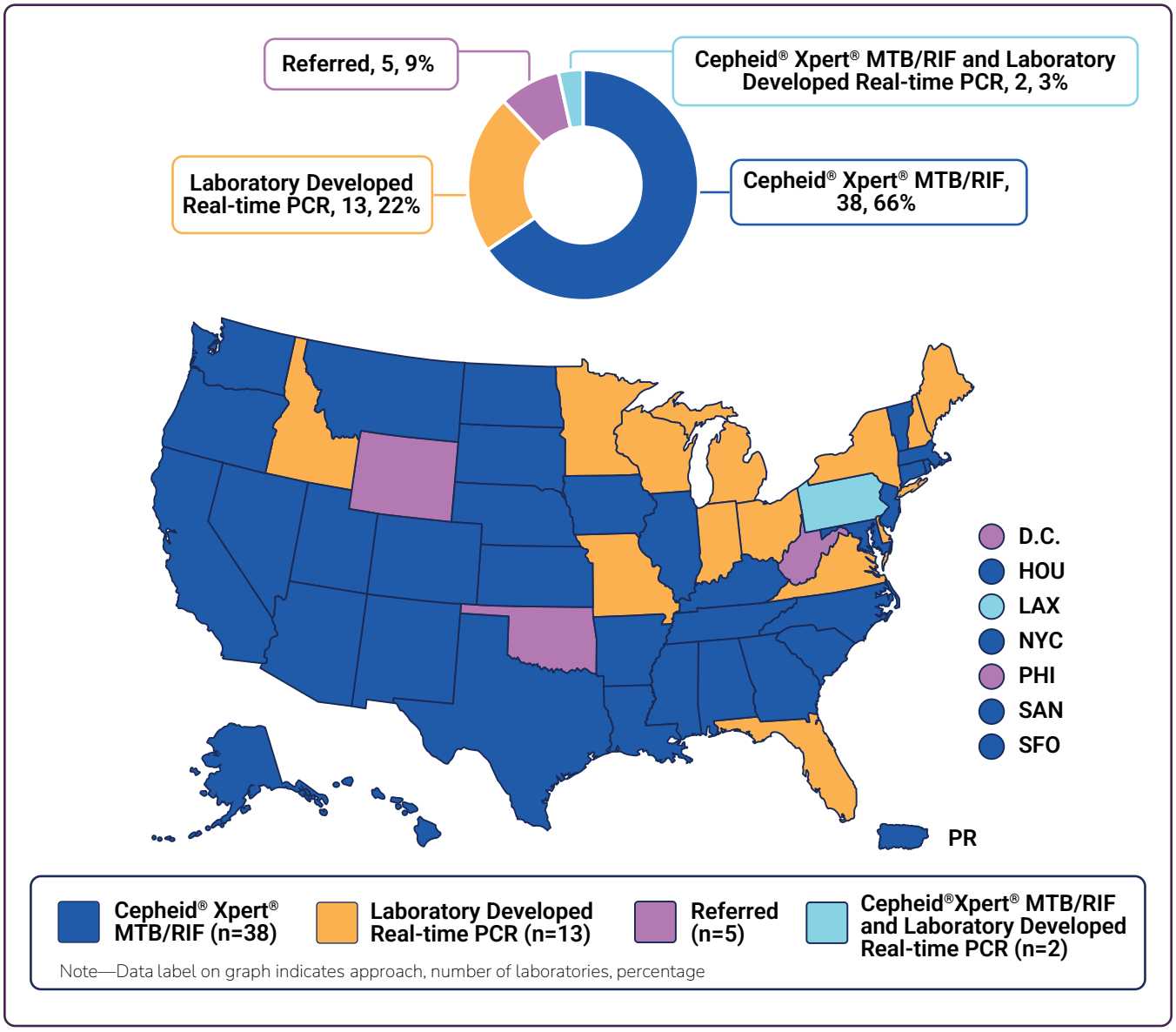
Among the 57 PHLs reporting IGRA data in 2024, 51% (29) reported performing IGRA in-house. Of these, 66% (19) met or exceeded the national TAT target. The national average IGRA TAT, calculated as the mean percentage of laboratories performing in-house IGRAs with results reported within 4 days of specimen collection, was 83%.

Methods in Public Health Laboratories, 2025

Methods performed by PHLs or accessed through referral in 2025 for NAAT, ID, growth-based DST, molecular DST, and IGRA are presented in **Figures 11–16.**

NAAT Methods

Figure 11. NAAT Approaches for Pulmonary Specimens, 2025 (n=58)



Performing NAAT is essential for the rapid detection of MTBC, enabling timely treatment decisions and public health intervention. Cepheid® Xpert® MTB/RIF was the most used approach, reported by 38 of 58 PHLs (66%), followed by laboratory developed real-time PCR assays used by 13 of 58 PHLs (22%). Together, these two approaches accounted for 88% of NAAT performed by PHLs in 2025. An additional five PHLs (9%) referred NAAT to another facility. Two PHLs (3%) performed Cepheid® Xpert® MTB/RIF and laboratory developed real-time PCR assay, depending on submission criteria. No laboratories reported using pyrosequencing in 2025.

Table 3. NAAT Approach for Extrapulmonary Specimens, 2025 (n=15)

Extrapulmonary NAAT Approach	PHL
Laboratory Developed Real-time PCR	DE, FL, IN, LAX, MI, NM, NY, OH, PA, WI
Cepheid® Xpert® MTB/RIF	AL, AR, HI, MT, SD

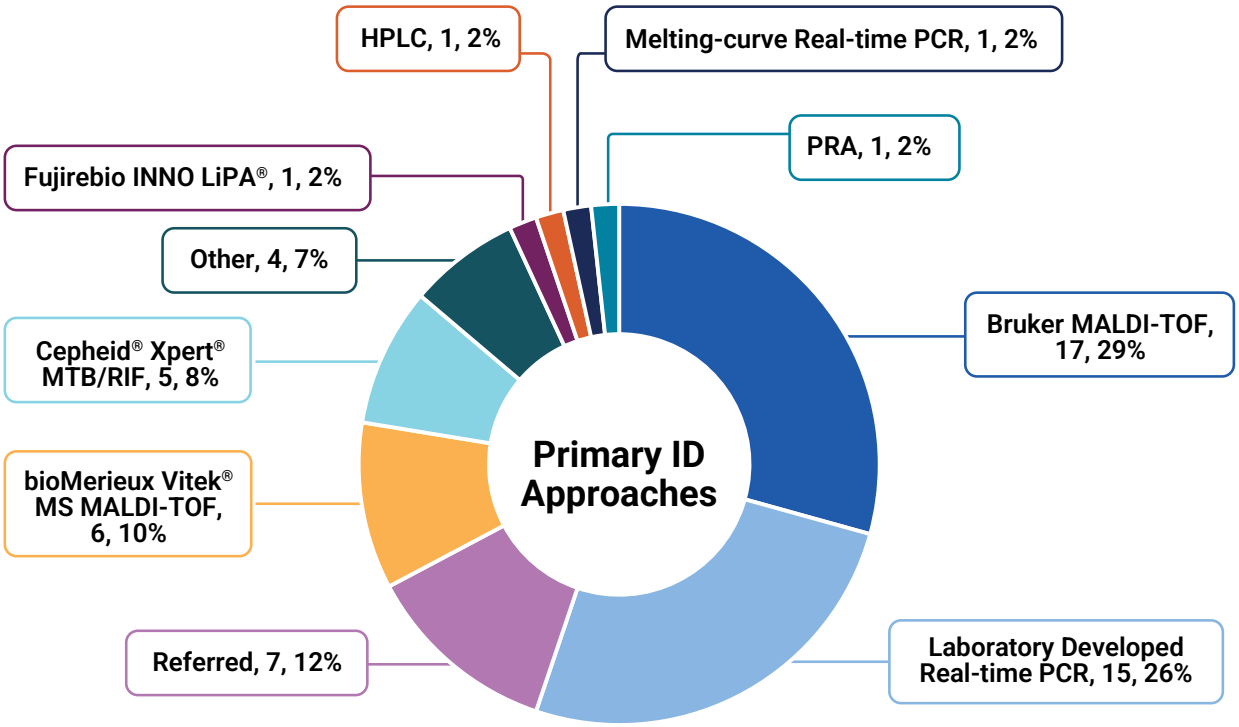
Nucleic acid amplification testing for extrapulmonary specimens was performed by a subset of PHLs in 2025 (**Table 3**). In total, 15 PHLs reported performing NAAT for extrapulmonary specimens. Real-time PCR was the most reported approach, reported by 10 laboratories (67%), while five laboratories (33%) used the Cepheid® Xpert® MTB/RIF assay.

Table 4. NAAT Algorithm by PHL, 2025

NAAT Algorithms	PHL
New AFB smear positive patients tested (routinely only first smear positive specimen); AFB smear negative patients tested by request only	AK, CT, GA, KS, KY, MI, MN, MS, ND, NE, NJ, NV, NYC, OK, OR, PR, SC, TN, TX, WA
New AFB smear positive patients tested (automatically >1 specimen per patient); AFB smear negative patients by request only	AL, IN, ME, NC, NH, UT, VT, WI
Testing per request only	HI, HOU, ID, LAX, MT, PHI, RI, SFO
Combination of submitter location/type, AFB smear status, or upon request	AR, AZ, CA, DE, IA, MA
Regardless of AFB smear status, NAAT automatically performed on >1 specimen from new patients	CO, IL, SAN, WY
Regardless of AFB smear status, NAAT only routinely performed on 1 specimen from new patients	LA, MO, OH, PA
Testing per request; if NAAT not ordered, performed on certain specimen types and/or automatically on new AFB smear positive	DC, FL, MD, SD
All specimens regardless of AFB smear status except patients previously positive for MTBC within a specified timeframe	NM, VA
All specimens tested by NAAT regardless of AFB smear status and previous positivity	NY, WV

Identification Methods

Figure 12. Primary ID Approaches, 2025 (n=58)



Note—Data label indicates approach, number of laboratories, percentage

Primary ID approaches used by PHLs are shown in **Figure 12**. In 2025, 23 of 58 PHLs (40%) reported using MALDI-TOF as their primary method of TB identification. Among these, most used the Bruker MALDI-TOF platform (17/58, 29%) while six (10%) used the bioMérieux Vitek® MS MALDI-TOF system. After Bruker MALDI-TOF, the next most reported primary ID method was laboratory developed real-time PCR (15/58, 26%), followed by referral to another laboratory (7/58, 12%). Five PHLs (9%) reported using Cepheid® Xpert® MTB/RIF as their primary ID method.

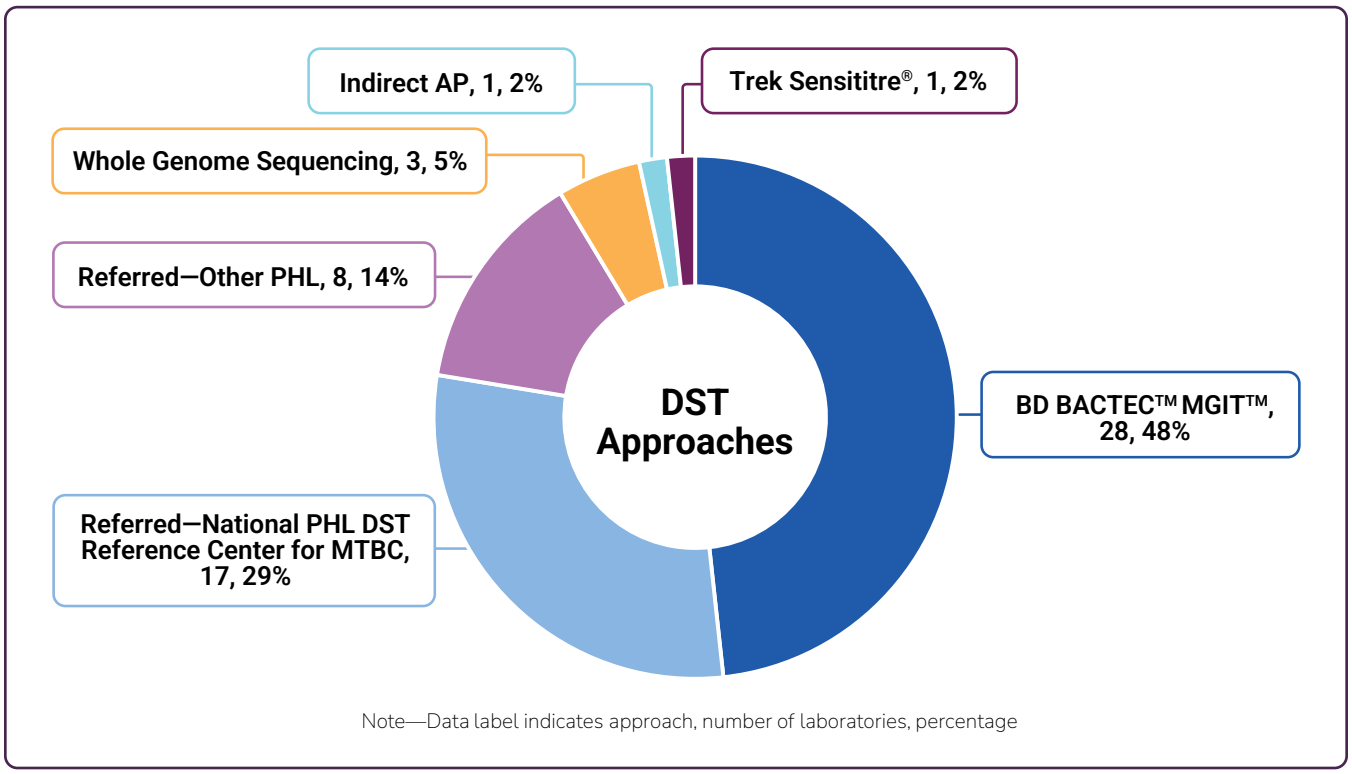
Four PHLs (7%) used a combination approach based on prior results or patient history (e.g., new verses previously known TB patients). Four additional PHLs each reported using a single alternative method as their primary ID approach: Fujirebio INNO-LiPA® (1/58, 2%), high-performance liquid chromatography (HPLC) (1/58, 2%), melting-curve real-time PCR (1/58, 2%), and PCR-restriction enzyme analysis (PRA) (1/58, 2%).

Discontinuation of the Hologic® AccuProbe® in 2022 and the Qiagen® PyroMark® Q96 reagents in 2025 contributed to increased use of MALDI TOF, real time PCR, and Xpert® MTB/RIF for ID.

Additionally, not all PHLs reported a secondary culture-based ID method. In 2025, 26 of 58 PHLs (45%) did not utilize a secondary culture ID approach, while 32 (55%) had a validated secondary method in place. Reported secondary approaches included Cepheid® Xpert® MTB/RIF, Fujirebio INNO-LiPA®, MALDI-TOF, laboratory developed real-time PCR, and sequencing.

Drug Susceptibility Testing Methods

Figure 13. First-line DST Approaches, 2025 (n=58)



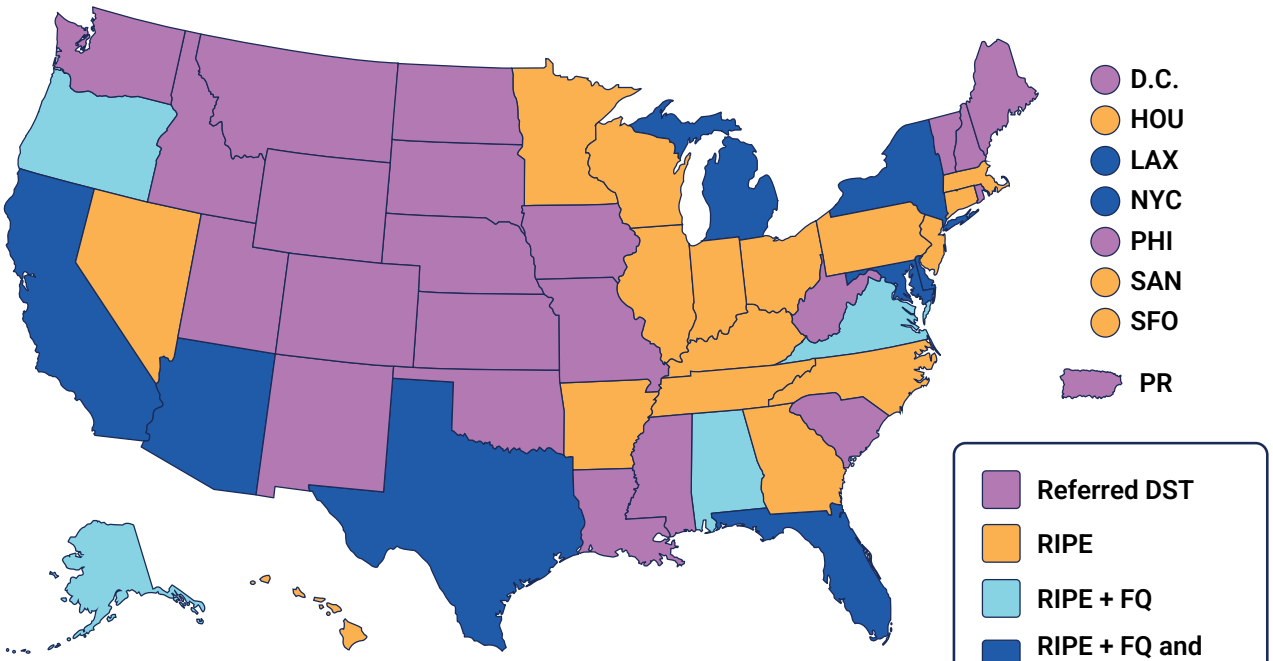
Note—Data label indicates approach, number of laboratories, percentage

First-line DST approaches are presented in **Figure 13**. Among those performing DST in-house, the most used DST method was the BD BACTEC™ MGIT™ system, reported by 28 of 58 PHLs (48%).

In 2025, seventeen PHLs (29%), primarily those performing fewer than 50 DSTs per year, utilized the National PHL DST Reference Center.[2] Eight PHLs (14%) referred DST to another laboratory other than the National PHL DST Reference Center. For some, referral is their normal practice; for others, it was a temporary arrangement due to circumstances such as BSL-3 renovations or other service interruptions.

Three PHLs (5%) reported performing whole genome sequencing (WGS) for DST. One PHL (2%) used indirect agar proportion (AP), and one PHL (2%) reported using the Trek Sensititre® system as its primary DST method.

Figure 14. Map of PHL DST Approaches and Drug Panels, 2025 (n=58)



Note—DST: drug susceptibility testing; RIPE: rifampin, isoniazid, pyrazinamide, and ethambutol; FQ: fluoroquinolone; Pyrazinamide was unavailable for much of 2025 due to a manufacturer recall.

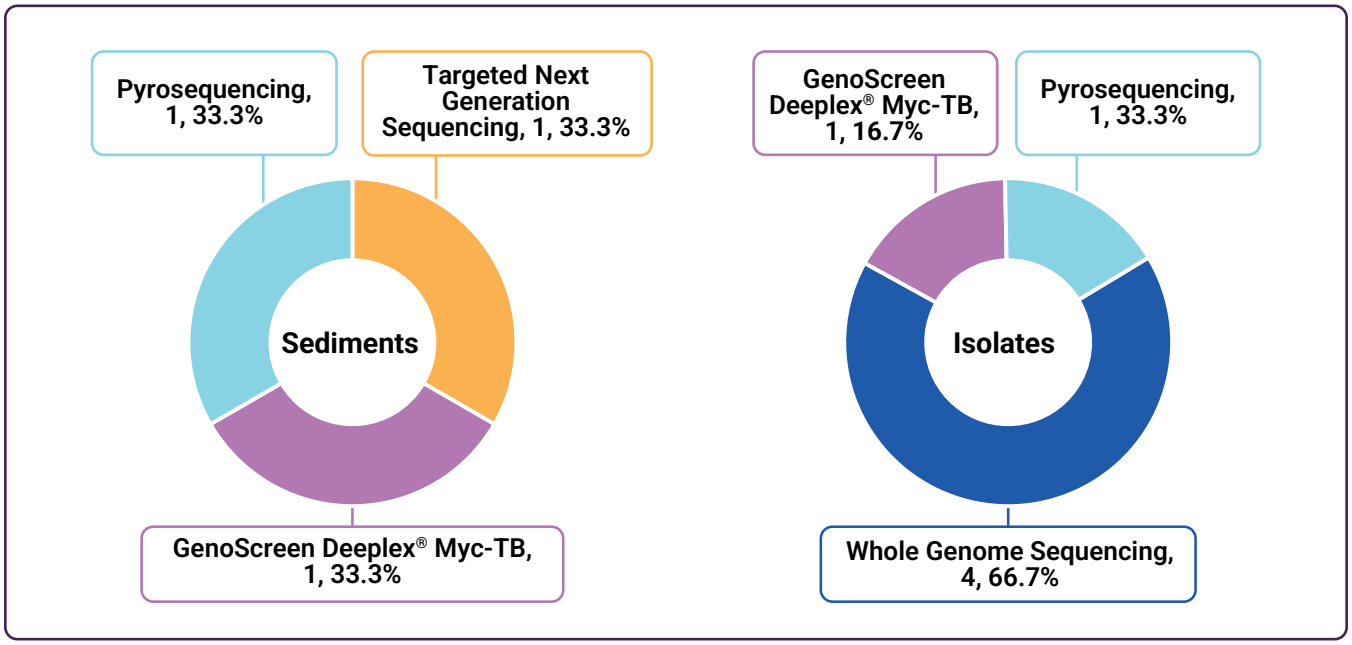
PHLs ensure access to DST services through a variety of approaches. In 2025, 25 PHLs (43%) referred DST to another laboratory, while 19 (33%) performed rifampin, isoniazid, pyrazinamide, and ethambutol (RIPE) DST exclusively in-house.

An increasing number of PHLs have incorporated fluoroquinolone (FQ) testing into their initial drug panels. Four PHLs (7%) performed an initial DST panel of both RIPE plus FQ, and 10 PHLs (17%) performed RIPE plus FQ along with additional second-line DST. Drugs included in second-line DST panels varied by laboratory.

Table 5. Growth-based Second-line DST by PHL, 2025

Growth-based Second-line DST Method	PHL
Indirect Agar Proportion	AZ, MD, MI, NY, NYC, TX
BD BACTEC™ MGIT™	CA, LAX, NY
Trek Sensititre®	FL

Figure 15. Molecular DST Methods from Sediments and Isolates in PHLs, 2025



Public health laboratory methods for molecular sequencing-based DST are shown in **Figure 15** and are stratified by testing performed on primary specimens (sediments) versus cultured isolates. Use of molecular DST continues to increase, offering faster turnaround times in many cases and complementing growth-based DST, particularly when discrepancies arise.

Table 6. Genotyping Pathway for National Surveillance, 2025

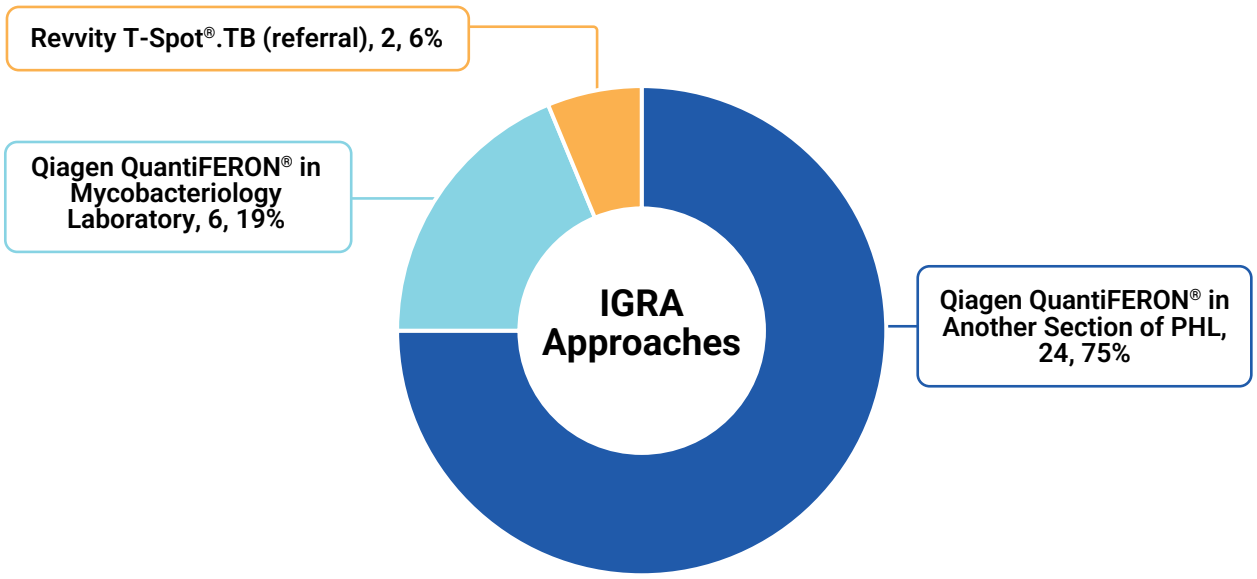
Genotyping Pathway	PHL
FastQ file Submission to CDC	AZ, CA[a] (SFO), FL,[a] NY (NYC)
Direct Submission of isolates to National TB Molecular Surveillance Center (NTMSC)	AK, AL, AR, CT, DC, GA, HI, IL, IN, LA, LAX, MA, MD, MI, MN, MO, NC, NJ, NV, OH, OR, PA (PHI), SAN, TN, TX (HOU), VA, WA, WI, WV
FastQ file Submission to CDC by the National PHL DST Reference Center[b]	CO, DE, IA, ID, KS, KY, ME, MS, MT, ND, NE, NH, NM, OK, PR, RI, SC, SD, UT, VT, WY

a PHLs transitioned from submission of isolates to the NTMSC to submission of FastQ files to CDC in 2025.
b National PHL DST Reference Center performs whole genome sequencing, submitting FastQ file data to CDC for national surveillance on behalf of the PHLs.

Public health laboratories play a vital role in ensuring universal genotyping of MTBC isolates nationwide. These pathways include direct submission of isolates to the National TB Molecular Surveillance Center (NTMSC), and submission of FastQ files from WGS performed either by individual PHLs or the National PHL DST Reference Center to CDC.

Interferon-gamma Release Assay Methods

Figure 16. IGRA Approaches in PHLs, 2025 (n=32)



Note—Data label indicates approach, number of laboratories, percentage

PHLs' IGRA approaches for 2025 are shown in **Figure 16**. IGRA testing was not offered by all PHLs. Among the 32 laboratories that performed IGRA testing, most (24/32, 75%) conducted Qiagen® QuantiFERON® testing in a laboratory section outside of mycobacteriology. An additional six PHLs (19%) performed QuantiFERON® testing within the mycobacteriology laboratory.

Two PHLs (6%) did not perform IGRA testing on site and instead referred testing for Revvity T-Spot™.TB. Overall, QuantiFERON® remained the predominant IGRA method among funded PHLs in 2025, and referral-based IGRA testing was used infrequently.

Table 7. IGRA Approaches by PHL, 2025

IGRA Approach	PHL
Qiagen® QuantiFERON® in Another Section of PHL	CO, CT, FL, GA, HI, IA, KS, LAX, ME, MO, MS, MT, ND, NE, NJ, NM, NV, OR, PA, SFO, SC, SD, VT, WY
Qiagen® QuantiFERON® in Mycobacteriology Laboratory	DE, HOU, IN, MD, NH, TN
Revvity T-Spot™TB (referral)	AR, LA

References

1 CDC. TB Elimination and Laboratory Cooperative Agreement Funding | Information for Tuberculosis Programs. Atlanta, GA. 2025. www.cdc.gov/tb-programs/php/funding/elimination-and-laboratory-co-operative-agreement.html

2 Association of Public Health Laboratories. National Public Health Laboratory Drug Susceptibility Testing Reference Center. Bethesda, MD. 2026. aphl.org/focus-areas/infectious-diseases/major-work/tuberculosis

Appendix A: Additional Resources

Informational Resources

- CDC TB Website www.cdc.gov/tb/
- CDC Molecular Detection of Drug Resistance (MDDR) Service
  www.cdc.gov/tb/php/laboratory-information/mddr-user-guide.html
- *Continuity of Operations Plan Toolkit for Public Health Mycobacteriology Laboratories: 2023*
  stacks.cdc.gov/view/cdc/131520
- CDC False-Positive Investigation Toolkit
  www.cdc.gov/tb/php/false-positive-investigation-toolkit/index.html
- *Biosafety in Microbiological and Biomedical Laboratories* (BMBL), 6th Edition (2020)
  www.cdc.gov/labs/bmbl/index.html
- *Guide to the Application of Genotyping to Tuberculosis Prevention and Control*
  stacks.cdc.gov/view/cdc/11437
- *Interim Guidance: 4-Month Rifapentine-Moxifloxacin Regimen for the Treatment of Drug-Susceptible Pulmonary Tuberculosis — United States, 2022* | MMWR
  www.cdc.gov/mmwr/volumes/71/wr/mm7108a1.htm
- CDC Model Performance Evaluation Program
  www.cdc.gov/tb/php/laboratory-information/model-performance-evaluation-program.html
- APHL TB Website
  aphl.org/TB
- APHL *Issues in Mycobacterium tuberculosis Complex Drug Susceptibility Testing: Fluoroquinolones*
  https://aphl.org/docs/default-source/technical/ID-MTBC-DST-FQ.pdf
- APHL *TB Next Generation Sequencing and Molecular Drug Susceptibility Testing*
  https://aphl.org/docs/default-source/technical/ID-TB-NGS-Mutations.pdf

Articles of Interest

Laboratory Practices

- Hioki, T., et al., *Xpert MTB/RIF probe reactivity to non-tuberculosis mycobacteria cultured in MGIT broth samples.* J Infect Chemother, 2026. 32(1): p. 102891.
- Dugdale, C.M., et al., *Second Time's the Charm? Assessing the Sensitivity and Yield of Inpatient Diagnostic Algorithms for Pulmonary Tuberculosis in a Low-Prevalence Setting.* Open Forum Infect Dis, 2024. 11(6): p. ofae253.
- Yildirim, K., et al., *The Effect of Inoculum Size on Antimicrobial Susceptibility Testing of* Mycobacterium tuberculosis. Microbiol Spectr, 2023. 11(3): p. e0031923.

Drug Resistance

- Yu, H.J., et al., *Performance Evaluation of the BACTEC MGIT 960 System for Rifampin Drug-Susceptibility Testing of Mycobacterium tuberculosis Using the Current WHO Critical Concentration.* J Clin Microbiol, 2023. 61(1): p. e0108622.
- Wang, W., et al., *Association between the rifampicin resistance mutations and rifabutin susceptibility in Mycobacterium tuberculosis: A meta-analysis.* J Glob Antimicrob Resist, 2025. 40: p. 53-61.
- Maghradze, N., et al., *Linking genetic and phenotypic bedaquiline resistance in Mycobacterium tuberculosis strains from Georgia.* PLoS One, 2025. 20(7): p. e0326794.
- Chan, H.H., Y.C. Wang, and R. Jou, *A simplified pyrazinamidase test for Mycobacterium tuberculosis pyrazinamide antimicrobial susceptibility testing.* J Clin Microbiol, 2024. 62(12): p. e0122724.

Next Generation Sequencing

- Conceição, E.C., et al., *Mycobacterium tuberculosis cultured in MGIT media for whole-genome sequencing application: a systematic literature review and meta-analysis.* Microb Genom, 2025. 11(11).
- Colman, R.E., et al., *Evaluating culture-free targeted next-generation sequencing for diagnosing drug-resistant tuberculosis: a multicentre clinical study of two end-to-end commercial workflows.* Lancet Infect Dis, 2025. 25(3): p. 325-334.
- Ng, J.H.J., et al., *The Next Frontier in Tuberculosis Investigation: Automated Whole Genome Sequencing for Mycobacterium tuberculosis Analysis.* Int J Mol Sci, 2024. 25(14).
- Mohr, V., et al., *Use of Whole Genome Sequencing for Mycobacterium tuberculosis Complex Antimicrobial Susceptibility Testing.* Methods Mol Biol, 2024. 2833: p. 185-193.

Other Resources

- Rigouts, L., et al., *Successful Mycobacterium tuberculosis culture isolation from tongue swabs: Results from both experimentally infected and clinical swabs from pulmonary tuberculosis patients.* Diagn Microbiol Infect Dis, 2024. 110(2): p. 116423.
- Tomasello, G., et al., *Evaluation of MetaSystems Automated Fluorescent Microscopy System for the Machine-Assisted Detection of Acid-Fast Bacilli in Clinical Samples.* J Clin Microbiol, 2022. 60(10): p. e0113122.

- Saukkonen, J.J., et al., *Updates on the Treatment of Drug-Susceptible and Drug-Resistant Tuberculosis: An Official ATS/CDC/ERS/IDSA Clinical Practice Guideline*. Am J Respir Crit Care Med, 2025. 211(1): p. 15-33.
- Shah, M., et al., *NTCA Guidelines for Respiratory Isolation and Restrictions to Reduce Transmission of Pulmonary Tuberculosis in Community Settings*. Clin Infect Dis, 2024.
- Marshall, J.E., et al., *Nontuberculous mycobacteria testing and culture positivity in the United States*. BMC Infect Dis, 2024. 24(1): p. 288.
- Huang, Z., et al., *CRISPR detection of circulating cell-free Mycobacterium tuberculosis DNA in adults and children, including children with HIV: a molecular diagnostics study*. Lancet Microbe, 2022. 3(7): p. e482-e492.

Technical Resources

- Clinical and Laboratory Standards Institute (CLSI). *Laboratory Detection and Identification of Mycobacteria*, 2nd ed. CLSI guideline M48. CLSI, Wayne, PA; 2018. clsi.org/
- CLSI. *Susceptibility Testing of Mycobacteria, Nocardia spp., and Other Aerobic Actinomycetes*; 3rd ed. CLSI standard M24. CLSI, Wayne, PA; 2018. clsi.org/
- CLSI. *Performance Standards for Susceptibility Testing of Mycobacteria, Nocardia spp., and Other Aerobic Actinomycetes*. 2nd edition. CLSI supplement M24S. CLSI, Wayne, PA; 2023. clsi.org/
- World Health Organization (WHO). *Catalogue of Mutations in Mycobacterium tuberculosis Complex and their Association with Drug Resistance*, 2nd ed. Geneva: World Health Organization; 2023. Licence: CC BY-NC-SA 3.0 IGO. https://www.who.int/publications/i/item/9789240082410
- WHO. *Technical Report on Critical Concentrations for Drug Susceptibility Testing of Isoniazid and the Rifamycins (rifampicin, rifabutin and rifapentine)*. Geneva: World Health Organization; 2021. Licence: CC BY-NC-SA 3.0 IGO. https://www.who.int/publications/i/item/9789240017283
- WHO. *Technical Report on Critical Concentrations for Drug Susceptibility Testing of Medicines used in the Treatment of Drug-Resistant Tuberculosis*. Geneva: World Health Organization; 2018 (WHO/CDS/TB/2018.5). Licence: CC BY-NC-SA 3.0 IGO. https://www.who.int/publications/i/item/WHO-CDS-TB-2018.5
- WHO. *The Use of Next-generation Sequencing for the Surveillance of Drug-resistant Tuberculosis: An Implementation Manual*. Geneva: World Health Organization; 2023. Licence: CC BY-NC-SA 3.0 IGO. https://www.who.int/publications/i/item/9789240078079
- WHO. *Use of Targeted Next-generation Sequencing to Detect Drug-resistant Tuberculosis: Rapid Communication, July 2023*. Geneva: World Health Organization; 2023. Licence: CC BY-NC-SA 3.0 IGO. https://iris.who.int/server/api/core/bitstreams/18b79164-04da-4a25-90ec-ccf944c57164/content
- WHO. Consolidated Guidelines on Tuberculosis. Module 3: Diagnosis – Rapid Diagnostics for Tuberculosis Detection, Third Edition. Geneva: World Health Organization; 2024. Licence: CC BY-NC-SA 3.0 IGO. https://www.who.int/publications/i/item/9789240089488

Appendix B: Explanation of Figures for Accessibility

Laboratory Capacity Team Contact Details (page 6): Map of the U.S. divided by LCT consultant. Each consultant is assigned a color:

- Stephanie Johnston, MS (Dark Blue)—Alaska, Arizona, California, Hawaii, Nevada, New Mexico, Oregon, Texas, Washington; Houston, TX; Los Angeles, CA; New York City, NY; San Diego, CA; San Francisco, CA
- Monica Youngblood, MPH, M(ASCP) (Teal)—Colorado, Idaho, Iowa, Kansas, Minnesota, Missouri, Montana, Nebraska, New Jersey, North Dakota, Oklahoma, Puerto Rico, South Dakota, Utah, Wyoming
- Cortney Stafford, MPH, MT(ASCP) (Yellow)—Alabama, Arkansas, Florida, Georgia, Illinois, Indiana, Kentucky, Louisiana, Michigan, Mississippi, Ohio, South Carolina, Tennessee, West Virginia, Wisconsin
- Stephanie Swint, MPH, MLS(AMT) (Purple)—Connecticut, Delaware, Maine, Maryland, Massachusetts, New Hampshire, New York, North Carolina, Pennsylvania, Rhode Island, Vermont, Virginia; District of Columbia; Philadelphia, PA

Figure 1 (page 11): PHLs' 2024 culture positivity, categorized by number of clinical specimens processed, is presented in a horizontal bar graph. PHLs who processed 1–1,000 specimens are displayed as dark blue. PHLs who processed 1,001–2,000 specimens are displayed as light blue. PHLs who processed 2,001–4,000 specimens are displayed as purple. PHLs who processed 4,001–8,000 specimens are displayed as yellow. PHLs who processed >8,000 specimens are displayed as teal.

Figure 2 (page 12): Map of U.S. indicating change in MTBC culture positivity among PHLs from 2022 to 2024. Each level is assigned a color.

- Increase in culture positivity (Dark Blue)—Alabama, California, Colorado, Delaware, Hawaii, Idaho, Kansas, Kentucky, Maryland, Massachusetts, Michigan, Montana, Nebraska, New York, New York City, North Carolina, Oregon, Rhode Island, San Francisco, South Dakota, Tennessee, Utah, Vermont, Wyoming.
- Decrease in culture positivity (Light Blue)—Alaska, Arizona, Arkansas, Connecticut, D.C., Florida, Georgia, Houston, Illinois, Indiana, Iowa, Los Angeles, Louisiana, Maine, Minnesota, Mississippi, Missouri, Nevada, New Hampshire, New Jersey, New Mexico, North Dakota, Ohio, Oklahoma, Pennsylvania, Philadelphia, Puerto Rico, San Diego, South Carolina, Texas, Virginia, West Virginia, Washington, Wisconsin.

Figure 3 (page 14): Dashboard with gauge graphs presenting the 2024 national averages for eight turnaround time indicators. Each gauge graph ranges from 0% to 100%, by increments of 10%, and the dial indicates the national average for that turnaround time indicator.

Figure 4 (page 15): Maps of U.S. divided by groupings of TAT for specimen receipt within one, two, and three days from specimen collection. Each level of specimen receipt is assigned a color. Number of specimens processed in 2024 is included for each site on the specimen receipt within one day map.

- Specimen receipt within one day:
  - 0–40% (Yellow)—Alaska, Arkansas, Florida, Illinois, Iowa, Kansas, Kentucky, Maine, Maryland, Michigan, Mississippi, New Jersey, New Mexico, New York, North Carolina, Oregon, Pennsylvania, South Carolina, South Dakota, Texas, Wyoming.
  - 41–66% (Purple)—California, Connecticut, D.C., Delaware, Georgia, Idaho, Indiana, Massachusetts, Missouri, Montana, Nevada, North Dakota, Ohio, Oklahoma, Puerto Rico, Tennessee, Utah, Virginia, West Virginia.
  - 67–85% (Light Blue)—Alabama, Arizona, Minnesota, Nebraska, New Hampshire, New York City, Philadelphia, Rhode Island, Vermont, Washington, Wisconsin.
  - 86–100% (Dark Blue)—Hawaii, Houston, Los Angeles, Louisiana, San Diego, San Francisco.
  - PHL TAT data not available (Grey, hatched)—Colorado.
- Specimen receipt within two days:
  - 0–40% (Yellow)—New Jersey, New York.
  - 41–66% (Purple)—Alaska, D.C., Florida, Georgia, Idaho, Illinois, Kentucky, Maine, Mississippi, New Mexico, North Carolina, South Carolina, South Dakota, Texas, Wyoming.
  - 67–85% (Light Blue)—Arizona, Arkansas, Connecticut, California, Delaware, Indiana, Iowa, Kansas, Maryland, Massachusetts, Michigan, Minnesota, Montana, Nebraska, Nevada, New Hampshire, North Dakota, Ohio, Oklahoma, Pennsylvania, Puerto Rico, Rhode Island, Tennessee, Virginia, West Virginia, Wisconsin.
  - 86–100% (Dark Blue)—Alabama, Hawaii, Houston, Los Angeles, Louisiana, Missouri, New York City, Oregon, Philadelphia, San Diego, San Francisco, Utah, Vermont, Washington.
  - PHL TAT data not available (Grey, hatched)—Colorado.
- Specimen receipt within three days:
  - 0–40% (Yellow)—New York
  - 41–66% (Purple)—Alaska, Florida, Kentucky, New Jersey.
  - 67–85% (Light Blue)—Arkansas, D.C., Georgia, Idaho, Illinois, Maine, Maryland, Mississippi, Nevada, New Mexico, North Carolina, Ohio, Oklahoma, South Carolina, South Dakota, Tennessee, Texas, Wyoming.
  - 86–100% (Dark Blue)—Alabama, Arizona, California, Connecticut, Delaware, Hawaii, Houston, Indiana, Iowa, Kansas, Los Angeles, Louisiana, Massachusetts, Michigan, Minnesota, Missouri, Montana, Nebraska, New Hampshire, New York City, North Dakota, Oregon, Pennsylvania, Philadelphia, Puerto Rico, Rhode Island, San Diego, San Francisco, Utah, Vermont, Virginia, Washington, West Virginia, Wisconsin.
  - PHL TAT data not available (Grey, hatched)—Colorado.

Figure 5 (page 17): 2024 NAAT TAT data, grouped by testing approach, are displayed in a horizontal bar graph. The vertical y-axis contains a list of NAAT approaches with the number of laboratories using the particular NAAT approach. The horizontal x-axis is the mean percentage of NAAT positive result meeting TAT benchmark, ranging from 0% to 100%, by increments of 10%. There are 4 horizontal bars with each bar representing the average NAAT TAT for PHLs using that testing algorithm; each bar includes a small thin line representing the range.

Figure 6 (page 18): Comparison of MTBC ID approaches used by PHLs during 2022 and 2024 are presented in a clustered bar graph, grouped by approach. The horizontal y-axis is the mean percentage of isolates meeting ID TAT benchmark, ranging from 0% to 100%, by increments of 10% and the horizontal x-axis is ID approaches with two clustered bars for each approach. The clustered bars represent years; 2022 is displayed as medium teal and 2024 is displayed as purple.

Figure 7 (page 19): 2024 turnaround times for growth-based DST, divided by primary DST method, is presented in a horizontal bar graph. The vertical y-axis contains 5 groupings of PHLs by primary DST methods and the horizontal x-axis is the mean percentage of isolates meeting growth-based DST TAT benchmark ranging from 0% to 100%, by increments of 10%. Each of the 5 groups has a horizontal bar representing the average percentage of DST performed within 17 days of ID, by approach; each bar includes a small thin line representing the range.

Figure 8 (page 20): 2024 turnaround times for ID and DST, divided into groups by number of MTBC positive patients, is presented in a horizontal bar graph. The vertical y-axis contains 5 groupings of PHLs by number of MTBC positive patients and the horizontal x-axis is the mean percentage of isolates meeting TAT benchmark ranging from 0% to 100%, by increments of 10%. Each of the 5 groups have two horizontal bars representing the average percentage of MTBC identified within 21 days and DST performed within 17 days of ID; each bar includes a small thin line representing the range.

Figure 9 (page 21): 2024 turnaround times for molecular DST, divided by molecular DST method, are presented in two horizontal bar graphs, for sediment source on top and isolate source on bottom. The vertical y-axis contains 3 groupings of PHLs by molecular DST methods and the horizontal x-axis is the mean percentage of sediments or isolates meeting molecular DST TAT benchmark ranging from 0% to 100%, by increments of 10%. Each of the 3 groups has a horizontal bar representing the average percentage of molecular DST reported within 11 days of specimen receipt or ID, by approach; each bar includes a small thin line representing the range.

Figure 10 (page 22): Map of U.S. indicating 2024 data for interferon gamma release assay use and TAT performance. Each level is assigned a color.

- Meeting/exceeding national target (≥75%) (Dark Blue)—Florida, Georgia, Hawaii, Indiana, Iowa, Kansas, Los Angeles, Mississippi, Montana, Nebraska, Nevada, New Jersey, North Dakota, Oregon, Pennsylvania, San Francisco, Tennessee, Utah, Vermont
- Not meeting national target (<75%) (Light Blue)—Connecticut, Delaware, Houston, Maine, Maryland, Missouri, New Mexico, South Carolina, South Dakota, Wyoming.
- Testing not performed in-house (White)— Alaska, Alabama, Arkansas, Arizona, California, D.C., Idaho, Illinois, Kentucky, Louisiana, Massachusetts, Michigan, Minnesota, New Hampshire, New York, New

York City, North Carolina, Ohio, Oklahoma, Philadelphia, Puerto Rico, Rhode Island, San Diego, Texas, Virginia, Washington, West Virginia, Wisconsin.

- PHL TAT data not available (Grey, dotted)—Colorado

Figure 11 (page 23): Dual figure with doughnut graph and U.S. Map.

- NAAT approaches used by PHLs during 2025 are presented in a doughnut chart. The largest slice represents the 38 PHLs that performed Cepheid® Xpert® MTB/RIF. The following three slices represent: 13 PHLs that performed laboratory developed real-time PCR, 5 PHLs that referred testing, and 2 PHLs that performed both Xpert® MTB/RIF and laboratory developed real-time PCR.
- Map of U.S. divided by NAAT approach for pulmonary specimens in 2025. Each NAAT approach is assigned a color.
    - Performs Cepheid® Xpert® MTB/RIF (Dark blue)—Alabama, Alaska, Arizona, Arkansas, California, Colorado, Connecticut, Georgia, Hawaii, Houston, Illinois, Iowa, Kansas, Kentucky, Louisiana, Maryland, Massachusetts, Mississippi, Montana, Nebraska, Nevada, New Jersey, New Mexico, New York City, North Carolina, North Dakota, Oregon, Puerto Rico, Rhode Island, San Diego, San Francisco, South Carolina, South Dakota, Tennessee, Texas, Utah, Vermont, Washington.
    - Performs laboratory developed real-time PCR (Yellow)—Delaware, Florida, Idaho, Indiana, Maine, Michigan, Minnesota, Missouri, New Hampshire, New York, Ohio, Virginia, Wisconsin.
    - Referred DST (Purple)—D.C., Oklahoma, Philadelphia, West Virginia, Wyoming.
    - Performs Cepheid® Xpert® MTB/RIF and laboratory developed real-time PCR (Teal)—Los Angeles, Pennsylvania.

Figure 12 (page 25): Primary ID methods used by PHLs in 2025 are presented in a doughnut chart. The largest slice represents the 17 PHLs that performed Bruker MALDI-TOF. The following eight slices represent: 15 PHLs that performed laboratory developed real-time PCR, 7 PHLs that referred testing, 6 PHLs that performed bioMerieux Vitek® MALDI-TOF, 5 PHLs that performed Cepheid® Xpert® MTB/RIF assay, 4 PHLs that performed other methods, 1 public health laboratory that performed Fujirebio INNP-LiPA®, 1 public health laboratory that performed HPLC, 1 public health laboratory that performed melting-curve real-time PCR, and 1 public health laboratory that performed PRA.

Figure 13 (page 26): The first-line DST approaches for initial drug panel used by PHLs in 2023 are presented in a doughnut chart. The largest slice represents the 29 PHLs that perform DST using BD BACTEC™ MGIT™. The next five slices represent 17 PHLs that referred testing to the National PHL DST Reference Center for MTBC, 7 PHLs that referred testing to another PHL, 3 PHLs that performed whole genome sequencing, 1 public health laboratory that performed indirect agar proportion, and 1 public health laboratory that performed Thermoscientific Sensititre®.

Figure 14 (page 27). Map of U.S. divided by DST approaches and drug panels in 2025. Each DST approach and drug panel is assigned a color.

- Referred DST (Purple)—Colorado, D.C., Idaho, Iowa, Kansas, Louisiana, Maine, Mississippi, Missouri, Montana, Nebraska, New Hampshire, New Mexico, North Dakota, Oklahoma, Philadelphia, Puerto Rico, Rhode Island, South Carolina, South Dakota, Utah, Vermont, West Virginia, Wyoming, Washington.
- Performs RIPE (Yellow)— Arkansas, Connecticut, Georgia, Hawaii, Houston, Illinois, Indiana, Kentucky, Massachusetts, Minnesota, Nevada, New Jersey, North Carolina, Ohio, Pennsylvania, San Diego, San Francisco, Tennessee, Wisconsin.
- Performs RIPE & FQ (Teal)—Alabama, Alaska, Oregon, Virginia.
- Performs RIPE & FQ and Second-line Drugs (Dark Blue)—Arizona, California, Delaware, Florida, Los Angeles, Maryland, Michigan, New York, New York City, Texas.

Figure 15 (page 28): Molecular testing for detection of drug resistance used by PHLs in 2025 are presented in two doughnut charts, separated as sediments on left and isolates on right. For the sediment source doughnut chart, 1 public health laboratory performed targeted next generation sequencing, 1 public health laboratory performed GenoScreen Deeplex® Myc-TB assay, and 1 public health laboratory performed pyrosequencing. For the isolate source doughnut chart, 4 public health laboratories performed whole genome sequencing, 1 public health laboratory performed GenoScreen Deeplex® Myc-TB assay, and 1 public health laboratory performed pyrosequencing.

Figure 16 (page 29): The IGRA methods used by PHLs in 2025 are presented in a doughnut chart. The largest slice represents the 24 PHLs that perform Qiagen QuantiFERON® in another section of the PHL. The other two slices represent 6 PHLs that perform Qiagen QuantiFERON® in the mycobacteriology section of the PHL and 2 PHLs that refer for Revvity T-Spot®.TB.

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