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The landscape of timely RNA host-response testing for management of infection, sepsis, or acute inflammation: a systematic review and meta-analysis

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Systematic Review

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Abstract

Background

RNA-based host-response assays aim to distinguish infectious and inflammatory conditions by measuring predefined transcript signatures in whole blood. While numerous signatures have been described, the extent to which these platforms have progressed to clinically-deployable, timely diagnostics remains unclear.

Methods

We conducted a systematic review of studies published between 1 January 2013 and 30 June 2025 evaluating RNA-based host-response tests capable of returning results within 24 hours. Eligible studies assessed diagnostic or prognostic performance in human patients with suspected infection or acute inflammation. Discovery-only transcriptomic studies were excluded. Where ≥ 5 independent studies evaluated the same platform, meta-analysis using a hierarchical summary receiver operating characteristic (HSROC) model was performed.

Results

Seventy-four studies met inclusion criteria. Most were observational cohort or case-control diagnostic accuracy studies. Platforms were predominantly reverse transcription-quantitative polymerase chain reaction-based. Reported AUROCs frequently exceeded 0.80 across tuberculosis, bacterial–viral discrimination, and sepsis. The median time to result reported in 31 studies was a clinically-relevant 60 minutes. Only the Cepheid Xpert MTB-HR assay had sufficient independent evaluations for meta-analysis, with analyses performed separately by transcript configuration. The TBP-based configuration demonstrated pooled sensitivity 0.83 (95% CI 0.73–0.90) and specificity 0.76 (95% CI 0.66–0.84), with substantial heterogeneity. No randomised trials assessing clinical implementation or patient-centred outcomes for acute infection were identified.

Conclusions

RNA-based host-response diagnostics show promising diagnostic discrimination and have progressed beyond discovery-phase research. However, evidence is dominated by early-phase observational validation, with limited demonstration of clinical utility or impact on patient outcomes. Pragmatic prospective studies and randomised implementation trials are needed to determine whether these technologies improve real-world clinical decision-making.

1 Background

Timely and accurate identification of serious infection is critical for patient outcomes, especially in life-threatening conditions including sepsis. However, identification of the subset of patients with critical illness is difficult as they comprise a small proportion of patients presenting to the Emergency Department (ED) with acute febrile illness, accounting for between 5–20% of paediatric presentations(1–3), and ~ 5% of ED visits in adults, rising to 15% in the geriatric population(4). The number with serious bacterial infection is variable, between 1.5% – 7% in children (5, 6), and up to 50% in the elderly population(7). Especially in the paediatric population where the risks are lower, despite a decrease in reported cases of bacteraemia over time(8), the number of short but unplanned hospital admissions continues to increase(9–11). Early recognition and appropriate treatment therefore are important for both the outcomes of those with serious infections, as well as reducing unnecessary burdens for those with less severe infections.

Diagnostic tools can help classify patients presenting with fever. Traditional pathogen-focused diagnostics can be slow and insensitive, such as microbiological cultures, or faster and non-specific such as viral polymerase chain reaction (PCR) tests on throat swabs(12). Conventional biomarkers like C-reactive protein (CRP) and procalcitonin may provide some help in determining those with more severe infection. But it takes 4–6 hours for CRP concentrations to rise, with peak concentrations reached after 36–48 hours(13), frequently only permitting a diagnosis to be made retrospectively once treatment has started. Both CRP and procalcitonin lack sufficient specificity to distinguish bacterial infection from self-limiting viral infections or sterile inflammation in many scenarios.

In contrast, host-response gene-expression diagnostics aim to detect the body's immune reaction to infection rather than the pathogen itself. This technique has become feasible in recent years by the increased speed and reduction in cost of sequencing technologies. By measuring changes in host gene expression (RNA transcripts), these tests can potentially identify an infection even when direct pathogen tests are negative and help discern the cause of inflammation(14). RNA-based hokst response assays leverage the principle that infectious and non-infectious causes of systemic inflammation elicit distinguishable gene expression signatures in blood cells or tissues. These changes are detectable very early after symptom onset(15). Much research has been done on discovering signatures for infection(16), which can include TB(17, 18), bacterial/viral discrimination(19, 20), and even multi-class signatures to distinguish a number of infectious or acute inflammatory conditions(17, 21).

However, despite the promising results of the accuracy of these RNA signatures, and the significant resources spent deriving these signatures, this RNA-based technology does not appear to have been matched in increased availability of diagnostic tests for frontline clinicians(22). Whilst some prior reviews have examined the performance of host gene-expression signatures(23), these have focussed on the RNA signatures themselves – often derived and validated on whole-genome RNASeq, which is expensive and cumbersome both from sequencing and its analysis, limiting its use in acute conditions.

Given the growing body of evidence that host RNA expression signatures can diagnose important infections or inflammatory conditions, a systematic review is warranted to assess how these signatures could be used to inform clinical practice. This systematic review therefore examines the current clinically-relevant application of RNA signatures in an acute febrile setting: where the host-response is analysed using a platform that allows timely results to effect acute clinical decision making. This will help clarify the current state of evidence, which platforms can be used to translate known RNA-based signatures in a clinically-relevant fashion, and their accuracy in diagnosing infections or acute inflammatory conditions.

2 Methods

2.1 Objective

The primary objective of this systematic review is to determine the accuracy of timely RNA-based host response tests in managing infections or acute inflammatory conditions.

2.2 Protocol and registration

This systematic review was prospectively registered with PROSPERO (CRD420251128323, available from www.crd.york.ac.uk/PROSPERO/view/CRD420251128323). It was conducted in accordance with a pre-specified protocol, that is also available on the PROSPERO database(24). Full details are available in the protocol, with a summary of the methods below.

2.3 Eligibility criteria

Population: We included studies involving human participants of any age (neonates, children, or adults) presenting with suspected or confirmed infection or acute inflammatory illness. Studies limited to animal models, healthy volunteers, or populations with unrelated chronic conditions were excluded.

Index test: Eligible studies evaluated tests that incorporated measurement of RNA transcripts produced by the human host and were intended for diagnostic or prognostic use in infection or acute inflammatory conditions. Tests were required to be clinically deployable through being 'timely', i.e. capable of delivering results within 24 hours. Studies relying on platforms that were not timely, such as whole-transcriptome approaches (e.g. RNAseq), and discovery-only analyses without validation on non-discovery samples were therefore excluded. If both discovery and validation results were included in the paper, only the clinically-relevant validation results were included.

Comparator (reference standard): Acceptable reference standards included microbiological testing, adjudicated clinical diagnosis, conventional diagnostic assays, other biomarker platforms, or standard clinical assessment and usual care.

Outcomes: The primary outcomes were measures of diagnostic accuracy of RNA-based host-response tests, including area under the receiver-operator curve (AUROC). Prognostic outcomes were also extracted when available. Secondary outcomes included reported test turnaround time, cost, and any measures of clinical impact or utility, such as effects on antibiotic prescribing or patient management.

2.4 Search Strategy

A comprehensive literature search was conducted in MEDLINE (via Ovid/PubMed), Embase (via Ovid), and Web of Science Core Collection. These databases were selected to ensure broad coverage of biomedical, diagnostic, and translational research literature. Searches were limited to studies published from 1 January 2013 to 30 June 2025 to capture contemporary research relevant to host RNA diagnostic platforms, with no geographic or setting restrictions. Reference lists of prior reviews were hand-searched to identify additional studies.

The search strategy was developed in consultation with an information specialist and combined controlled vocabulary terms and free-text keywords representing five core concepts: (1) infection or inflammation, (2) host RNA or gene expression, (3) rapid or timely diagnostics, (4) diagnostic test or assay platforms, and (5) diagnostic or prognostic intent. Detailed search strategies for each database are provided in Appendix A of the protocol(24).

2.5 Study Selection

Outputs from searches were transferred to Covidence [Covidence systematic review software, Veritas Health Innovation, Melbourne, Australia. Available at www.covidence.org]. Following automated de-duplication, two reviewers independently screened titles and abstracts against the eligibility criteria. Full-text articles were retrieved for all records deemed potentially eligible. Two reviewers independently assessed full-text articles for inclusion, documenting reasons for exclusion. Disagreements at either stage were resolved by discussion and consensus; if consensus could not be reached, a third reviewer adjudicated.

2.6 Data extraction and assessment of bias

One reviewer manually extracted data using a pre-designed Excel template, capturing study design and setting, participant characteristics, details of the RNA-based host response test (including gene targets, platform, sample type, and testing context), reference standards, diagnostic and prognostic performance measures, test turnaround time. The reviewer used QUADAS-2 to assess risk of bias across patient selection, index test, reference standard and flow/timing, rating each domain as low, high or unclear(25).The extracted data and QUADAS-2 assessment were then compared against results generated by an AI-assisted extraction tool (Elicit: The AI Research Assistant; https://elicit.com). Any discrepancies between the reviewer's extraction or QUADAS-2 assessment and the AI-generated output were identified and manually reviewed, and resolved following adjudication from a second reviewer.

2.7 Data synthesis

During study identification and data extraction, RNA-based host-response tests meeting the eligibility criteria were catalogued by outcome, test platform, and transcript configuration. Meta-analysis of diagnostic accuracy was undertaken where at least five independent studies evaluated the same index test

configuration. Tests that did not meet this criterion were summarised narratively.

For studies included in meta-analyses, true positive, false positive, false negative, and true negative values were extracted or derived (using RevMan v5.4). Sensitivity and specificity were synthesised using a bivariate random-effects model within a hierarchical summary receiver operating characteristic (HSROC) framework, allowing joint modelling of sensitivity and specificity while accounting for between-study variability and potential threshold effects. For each eligible test configuration, pooled estimates of sensitivity and specificity with 95% confidence intervals were generated and presented using forest plots. A hierarchical summary receiver operating characteristic (HSROC) model was used to synthesise sensitivity and specificity estimates. This approach jointly models sensitivity and specificity while accounting for between-study heterogeneity and variation in diagnostic thresholds. Because included studies used predefined or data-derived cut-offs that were not identical, threshold effects were anticipated and accommodated within the HSROC framework. Studies evaluating the same assay configuration were pooled within a single model, while distinct assay configurations were analysed separately. Statistical analyses were carried out using Stata v19.5.

3 Results

A total of 3,545 studies were initially identified, which after de-duplication, screening, and assessment, 76 studies were eligible for inclusion. Two studies were subsequently excluded to avoid duplication of results: one(26) reported the same results as the main included paper(27), and another was preliminary results of a trial when the paper with the full results was included. This left 74 included papers as detailed in PRISMA diagram in Fig. 1. Thirty tests were aimed at diagnosing tuberculosis (TB), 14 studies testing distinguishing bacterial or viral infection, and 13 studies examining a test diagnosing sepsis.

Two signature–test combinations, representing different versions of the 3-transcript Xpert MTB-HR assay for TB, had five or more independent evaluations and were therefore eligible for meta-analysis.

A summary of all the area under the receiver-operator curve (AUROC) results of the 74 studies are shown in Fig. 2.

3.1 Bacterial/Viral discrimination

Fourteen studies evaluated RNA-based host response tests for distinguishing bacterial from viral infection, enrolling 3,160 participants across ten countries, as shown in Table 1(28–41). Most studies recruited patients presenting to emergency departments with acute febrile illness, suspected infection, or respiratory symptoms. Study populations included adults only (n = 6 studies), children only (n = 4), or both age groups (n = 4). The majority employed prospective observational designs with validation cohorts. Reference standards varied considerably: eight studies used clinical adjudication by expert panels, five relied primarily on microbiological confirmation, and one employed a hybrid approach.

Diagnostic performance varied substantially across studies and appeared strongly influenced by study population characteristics and reference standard stringency. The highest AUROC values approached or achieved perfect discrimination in carefully selected pre-tested cohorts with microbiologically confirmed diagnoses, unlikely to reflect their real-world use. Pennisi et al. (2021) reported perfect classification (AUROC 1.0, sensitivity 92.2%, specificity 100%) in 24 severity-matched paediatric patients with definite bacterial (n = 12) or viral (n = 12) infections(38). Xu et al. achieved near-perfect performance (AUROC 0.986, 95% CI 0.968-1.0) in 390 Chinese participants under 85 years with microbiologically confirmed bacterial or viral fever(41). Gomez-Carballa et al. reported AUROC 0.922 in 35 febrile children(30).

Commercial platforms evaluated in larger, more heterogeneous emergency department cohorts showed good but more modest performance. The BioFire HR-B/V test achieved AUROC 0.85 (95% CI 0.81–0.89, sensitivity 86.4%, specificity 71.9%) for bacterial versus viral discrimination in 616 febrile emergency department patients(32), and similar performance (AUROC 0.85, 95% CI 0.78–0.90) in 209 adults with suspected sepsis or acute respiratory infection(40). The IMX-BVN-2 panel demonstrated variable performance across validation cohorts: AUROC 0.82 (95% CI 0.77–0.86) in 319 German emergency department patients(28), but lower AUROC 0.71 (95% CI 0.65–0.77) in 602 Australian adults with influenza-like symptoms(39). Multi-country validation by Ko et al. showed AUROC 0.84 (95% CI 0.76–0.90) across 101 patients from the USA, Sri Lanka, Tanzania, Cambodia, and Australia(33). For viral versus non-viral classification, performance was generally higher, with BioFire-based platforms consistently achieving AUROCs of 0.89–0.91 across multiple studies.

Performance varied notably by population characteristics and clinical setting. Studies in well-defined paediatric cohorts with microbiological confirmation generally outperformed those in undifferentiated adult emergency presentations. Mahle et al. observed reduced accuracy in immunocompromised adults (AUROC 0.78 for bacterial vs non-bacterial, 0.82 for viral vs non-viral). Li et al. (2021) reported AUROC 0.841 in 200 patients with undifferentiated fever. The TriVerity test achieved AUROC 0.77 (95% CI 0.70–0.84) for bacterial infection and 0.82 (95% CI 0.75–0.88) for viral infection in 169 hospitalized adults with acute respiratory illness(29). Iglesias-Ussel et al. (2024) demonstrated perfect agreement (AUROC 1.0) between the Biomeme platform and BioFire HR-B/V in 82 emergency department patients(31).

3.2 Sepsis

Thirteen reports evaluated RNA-based host-response tests for the diagnosis or stratification of sepsis across predominantly adult critical care and emergency populations, with one paediatric study, as shown in Table 2(26, 42–53). Most cohorts were prospective validation studies, and the majority evaluated commercially developed tests, most commonly SeptiCyte RAPID or LAB, as well as TriVerity (formerly known as InSep), which examined multigene signatures comprising between 2–29 transcripts.

For sepsis diagnosis, host-response testing distinguished sepsis from non-infectious inflammation or SIRS with AUROCs ranging from 0.71 to 0.92 in adult cohorts. Large ICU validation studies of SeptiCyte RAPID reported AUROCs of 0.82 in 419 patients with sepsis versus SIRS(26) and 0.82 in 447 ICU patients(49). SeptiCyte LAB achieved an AUROC of 0.88 in 308 ICU patients(48) and 0.73 in ventilated ICU admissions(45).

Multigene classifiers reported similar discrimination, including a 29-gene panel in ICU patients (AUROC 0.84)(43), an 11-gene SepsisMetaScore in trauma patients (AUROC 0.92)(51), and 7–8 gene signatures in suspected sepsis cohorts with AUROCs between 0.81 and 0.91(42, 47).

In emergency department populations, AUROCs of 0.76 for TriVerity(46) and 0.86 for SeptiCyte RAPID in mixed ED and ICU cohorts were reported(44). Post-operative cohorts demonstrated lower discrimination between infectious and sterile inflammation (AUROC 0.71)(52).

Severity stratification was reported in several studies. SeptiCyte RAPID predicted critical illness or intensive care admission with an AUROC of 0.86 in ED and ICU patients(44), and an AUROC of 0.66 for COVID-19 severity(50).

Paediatric evidence was limited to one prospective ICU study with two cohorts evaluating SeptiCyte LAB in children with severe sepsis versus non-infectious inflammation (post-cardiac bypass), reporting AUROCs of 0.95 in a smaller validation cohort in initially of 64 participants(53).

3.3 Other conditions and prognostic applications

Seventeen papers evaluated timely RNA-based host-response tests in acute infectious or inflammatory presentations beyond tuberculosis, bacterial–viral discrimination, and sepsis, as shown in Table 3(54–70). Adult and paediatric populations were included across emergency, inpatient, intensive care, outpatient, and surgical cohorts, with some reports including healthy or non-infectious comparator groups.

For acute viral illness, host-response testing distinguished viral from non-viral presentations, with reported AUROCs ranging from 0.92 to 1.00(66, 67, 69). In respiratory viral infection cohorts, AUROCs of 0.92 and 0.94 were reported(67, 69), while an influenza-specific cohort reported complete separation of PCR-confirmed influenza and influenza-negative illness (AUROC 1.00)(66).

Bacterial infection was classified with AUROCs between 0.83 and 0.97 in hospitalised cohorts(58, 70), including two-gene bacterial classifiers reporting AUROCs above 0.90(58). Persistent infection following bloodstream infection was identified with AUROCs of 0.85 to 1.00 in candidemia(61) and up to 0.86 in Gram-negative bacteraemia, with lower discrimination reported for Staphylococcus aureus(62). In paediatric populations, host-response testing distinguished severe pneumonia (AUROC 0.83)(70), MIS-C (AUROC 0.93)(56), Kawasaki disease (AUROC 0.96)(57), and septic shock subgroups (AUROC 0.98)(68).

Three of these papers, which included both adult and paediatric populations, focused on prognostic stratification. In COVID-19 and general intensive care populations, RNA-based host-response tests demonstrated AUROCs ranging from 0.68 to 0.89(54, 60), with higher discrimination reported in septic shock subgroups (AUROC 0.98)(68).

3.4 Tuberculosis [TB]

The largest number of studies, with thirty studies, evaluated rapid RNA-based host-response assays for TB diagnostics, as shown in Table 4(71–100). The evaluated tests were assessed for diagnostic accuracy or severity prediction, most commonly to discriminate active TB from latent infection (LTBI) or healthy controls. The studies included adult and paediatric populations which were recruited from hospitals, healthcare clinics, community settings, HIV-positive, or incarcerated populations, and were assessed against healthy, non-infectious, or alternative disease comparator groups. The studies evaluated samples including venous, capillary, dried blood spots, PAXgene, fingerstick, EDTA blood, Tempus RNA, RNAlater, whole blood, and serum samples. The test technology platforms included reverse transcription quantitative polymerase chain reaction (RT-qPCR) and dual-colour reverse transcriptase multiplex ligation-dependent probe amplification systems (dc-RT-MLPA). Where reported, turnaround times ranged from under one hour to within 24 hours, depending on platform.

For diagnostic accuracy, the RNA-based host response test assessed adult populations with active TB from healthy controls with an AUROC ranging from 0.82 to 0.97(71–73, 75–77, 83, 87, 88, 92, 98). Furthermore, host response testing differentiated active TB in adults from non-active TB with lower AUROCs of 0.77 and 0.746 (93, 99). In addition, host-response testing demonstrated variable performance in differentiating active tuberculosis in adults from other diseases, with AUROC values ranging from 0.68 to 0.98(79–82, 84, 89, 94, 96, 98). In HIV positive adult populations, host response testing differentiated TB from other diseases with AUROCs of 0.97, 0.88, and 0.886 (74, 86, 95).

In paediatric populations, host response testing differentiated TB from non-TB (AUROC 0.94 and 0.65)(78, 90), TB meningitis (AUROC 0.89)(91), and tuberculosis-associated Immune Reconstitution Inflammatory Syndrome (IRIS) in HIV positive children (AUROC 0.71 and 0.655)(85). Finally, the host response-based testing assessed TB severity in a paediatric population with an AUROC of 0.67(97).

3.5 Meta analysis: Cepheid Xpert MTB-HR

The Cepheid Xpert MTB-HR assay was initially developed as a three-transcript host-response test incorporating *GBP5*, *DUSP3*, and *KLF2*. In later iterations, the *KLF2* transcript was replaced with *TBP*. At least five independent studies evaluated each version of the assay, allowing separate meta-analyses to be conducted for the TBP-based and KLF2-based Xpert MTB-HR tests.

TBP-based Xpert MTB-HR

Based on six studies with a combined number of participants of n = 5146, the TBP-based Xpert MTB-HR demonstrated a pooled sensitivity of 0.83 (95% CI 0.73–0.90) and a pooled specificity of 0.76 (95% CI 0.66–0.84) (Fig. 3). Individual study estimates showed substantial variability, with sensitivity ranging from approximately 0.63 to 0.93 and specificity from approximately 0.63 to 0.87. Statistical heterogeneity was high for both sensitivity and specificity (I^2 >90%). HSROC analysis for the TBP-based assay showed a summary area under the curve (AUC) of 0.86 (95% CI 0.83–0.89), and HSROC prediction regions were broad, but study-level estimates were distributed along the ROC curve, consistent with variation in operating thresholds across settings.

KLF2-based Xpert MTB-HR

Five studies with a combined number of participants of n = 2383 evaluated the KLF2-based Xpert MTB-HR. The pooled sensitivity was 0.71 (95% CI 0.58–0.82), while the pooled specificity was 0.81 (95% CI 0.69–0.89) (Fig. 3). Study-level estimates again varied considerably, with sensitivity ranging from approximately 0.42 to 0.81 and specificity from approximately 0.70 to 0.93. High heterogeneity was observed for both outcomes (I^2 >90%). HSROC analysis yielded a lower AUC of 0.83 (95% CI 0.79–0.86) (Fig. 3). The prediction region was broad, suggesting substantial between-study variability not clearly aligned with a simple sensitivity–specificity trade-off.

Formal assessment of publication bias was not performed, as statistical methods for detecting publication bias in diagnostic test accuracy meta-analyses are limited and unreliable, particularly with small numbers of studies. No formal statistical comparison between the TBP- and KLF2-based assays was performed.

3.6 Test technologies

Reverse transcription quantitative PCR technology is used in the majority of the tests published, as shown in Supplementary Table 3. Other technologies used were digital-chemiluminescence reverse transcription multiplex Ligation-dependent Probe Amplification(78), LAMP(45, 46), digital droplet PCR(47), and Nanostring Ncounter (28, 33, 39, 54, 60, 63, 68). There were novel technologies reported to analyse the transcripts in a point-of-care manner, which included a platform using giant magnetoresistive biosensors to provide the results(66), an ISFET-based Lab-on-Chip with RT-LAMP(37), a PREDICT microfluidic lab-on-a-chip device using ddPCR(47), and a Biomeme M1/Franklin device which uses a RT-qPCR base to provide results(31).

The number of RNA transcripts per test ranged from 1-100, with the median being four transcripts per test, as shown in Supplementary Fig. 1A. There was no significant relationship between the year published and the number of transcripts in a test, nor the reported AUC and the number of transcripts in a test (Supplementary Fig. 1B and C).

As part of the test technology assessment whether these tests were potentially clinically useful, we collected any reported data on the cost and the turnaround time of the tests. Only three tests reported the planned or likely cost of the tests, which ranged between GBP10(37), USS35(64), and USD100(68). In the 31 studies which reported a turnaround time for the test, times ranged from 25 minutes up to one day, with the median reported turnaround time was 60 minutes (Supplementary Table 1). No tests used an 'electricity free' testing technology such as a lateral flow test, which may limit the environment these tests could be used in, particularly with reference to low- and middle-income country settings.

3.7 Quality of studies [QUADAS-2]

The quality assessment for each of the studies is included in Supplementary Table 4. Partially reflecting the fact that many of the studies are case control studies, 51 of the studies were rated as high risk of bias for their patient selection. Twenty-three studies were rated as high risk for the index test, frequently due to no pre-specified cut-off being used for the index test. Only three studies were rated as low risk across all domains.

4 Discussion

This systematic review set out to determine whether RNA-based host-response tests have progressed from discovery-phase research into potentially clinically-deployable tools capable of influencing timely management of infection or acute inflammation. Overall, the findings are encouraging from a diagnostic accuracy perspective. Across 74 included studies, many platforms demonstrated moderate to high discriminatory performance, frequently with AUROCs exceeding 0.80, and in selected cohorts approaching near-perfect classification. Importantly, these signatures were not confined to laboratory-based RNA sequencing but were translated onto clinically relevant platforms, most commonly RT-qPCR, including cartridge-based and point-of-care technologies. Several studies demonstrated feasibility using whole blood collected in routine clinical formats, including fresh venous samples and fingerstick blood, with median reported turnaround times of approximately 60 minutes. These characteristics suggest that RNA-based host-response testing is technically capable of delivering results within a timeframe compatible with emergency and acute care decision-making. However, despite these promising performance metrics and technological advances, the evidence base remains largely confined to diagnostic validation studies rather than trials demonstrating real-world clinical impact.

Despite encouraging diagnostic discrimination, this performance has not yet translated into evidence of clinical implementation or patient benefit. The overwhelming majority of included studies were observational diagnostic accuracy studies, frequently conducted in case–control or enriched cohorts rather than pragmatic, consecutive "all-comer" populations. Only one randomised controlled trial involving a host-response RNA signature was identified(93), and in that study the randomised component related to biomarker-guided preventive therapy for tuberculosis rather than acute diagnostic decision-making. No study within this review demonstrated that use of an RNA-based host-response test altered immediate patient management, reduced unnecessary antibiotic prescribing, shortened hospital stays, or improved clinical outcomes. This is consistent with previous studies and reviews, which have reported the identification of more than 250 candidate biomarkers over the past decade, but approximately one third were evaluated in only a single study, with limited robust validation and little demonstrable clinical impact(101). With only a handful of platforms commercially available, the field remains in the earlier stages of validation and development, with limited progression into implementation or effectiveness research. This is likely to suggest significant hurdles, and bridging this gap will require prospective pragmatic studies and interventional trials designed not merely to confirm discrimination, but to evaluate whether acting on test results meaningfully changes clinical decision-making and patient outcomes.

It is notable that the platforms which have progressed furthest, namely Xpert MTB-HR for tuberculosis disease and SeptiCyte for sepsis, target clinical syndromes in which existing diagnostics are inherently limited. In tuberculosis, confirmation usually depends on detecting *Mycobacterium tuberculosis* in sputum or other specimens, which is difficult in paucibacillary disease, extrapulmonary TB, young children, or individuals unable to produce sputum. A blood-based host-response assay offers a conceptual advantage because it measures the systemic immune response rather than requiring direct pathogen

detection, and meets an urgent requirement for non-sputum TB-detection(102). The meta-analysis of Xpert MTB-HR stratified by different transcripts, unlike a previous review(103), demonstrated encouraging performance for the updated TBP-transcript configuration, with improved pooled sensitivity compared with the earlier KLF2-based version. However, this improvement followed modification of a prototype assay and substantial heterogeneity remained. Several TB studies explicitly assessed performance against the WHO target product profile benchmarks(104), but real-world evaluation in a large pragmatic lower- and middle- income country paediatric study of the device did not reproduce the higher accuracy estimates reported in likely higher-income cohorts(90). SeptiCyte has achieved commercial availability and multiple prospective validations in sepsis, another condition lacking a definitive diagnostic gold standard. Nevertheless, even in this setting the evidence remains focused on diagnostic discrimination rather than interventional impact. The authors understand that the Xpert MTB-HR is not progressing toward widespread implementation, suggesting that significant translational barriers remain.

Several biological and methodological limitations within the current evidence base likely contribute to the variability observed across studies and the slow progression toward implementation. Host transcriptomic responses are influenced by age, immunological status, comorbidities, coinfection, and timing of sampling, and there is substantial overlap between infectious and non-infectious inflammatory pathways(105, 106). This biological complexity makes consistent discrimination challenging in heterogeneous real-world populations, particularly in settings such as post-operative care, trauma, or chronic inflammatory disease. However, as reflected by the lower quality scores, many studies were conducted in enriched or case control cohorts rather than consecutive unselected populations, which may inflate apparent performance(107, 108). Operational thresholds were frequently absent, post hoc defined, or modified between discovery and validation phases. In many cases only AUROC values were reported, without prespecified cut-offs or stable decision bands that could be applied consistently in clinical practice. Reference standards also varied widely, ranging from microbiological confirmation to expert adjudication or composite definitions, each with inherent limitations. Together, this combination of biological variability and methodological inconsistency contributes to substantial between-study heterogeneity and highlights how early the field remains in the translational pathway toward robust, standardised clinical implementation.

A further gap relates to implementation and clinical utility rather than analytical performance. Reported turnaround times, where provided, had a median of approximately 60 minutes, placing many platforms within a useful timeframe such as the ‘golden hour’ in sepsis(109). Although we allowed up to 24 hours for the results to be available, these tests seem well placed for near point-of-care timeframe of under one hour, likely in an Emergency Department setting, allowing decision for admission and/or treatment. Limited cost data were available, but the few studies reporting projected costs suggested figures that may be feasible in high-income settings. However, no included study undertook formal implementation research or economic evaluation of introducing these assays into routine clinical workflows. Diagnostic accuracy alone does not guarantee clinical usefulness. How results are reported, whether they are presented as binary classifications, probability scores, or risk bands, and how clinicians interpret and act upon those results are central to successful adoption(110). Without studies examining test-guided decision algorithms, antimicrobial stewardship outcomes, workflow integration, and cost-effectiveness, it remains uncertain whether these platforms would meaningfully improve care in real-world settings. Addressing these questions will be essential if RNA-based host-response diagnostics are to move beyond validation studies toward demonstrable clinical impact.

This review has several strengths. It was prospectively registered and conducted according to a predefined protocol, and it focused specifically on potentially clinically-deployable RNA-based host-response assays capable of returning results within 24 hours, thereby excluding discovery-only transcriptomic studies unlikely to influence acute care. Meta-analysis was undertaken only where sufficient independent evaluations of the same assay were available, avoiding inappropriate pooling across heterogeneous signatures. However, the underlying evidence base was highly variable in design, population, reference standards, and reporting. Many studies did not provide complete 2×2 data or prespecified operational thresholds, limiting quantitative synthesis and reflecting the early stage of translational development. Substantial heterogeneity was observed even within pooled analyses. As with most diagnostic accuracy reviews, publication bias could not be formally assessed, and conclusions regarding clinical impact are constrained by the predominance of observational validation studies rather than interventional trials.

5 Conclusion

Despite substantial investment in the discovery and validation of RNA-based host-response signatures, no platform identified in this review has yet demonstrated a change in acute patient management or improved outcomes within a randomised implementation trial. Diagnostic discrimination is frequently encouraging, and several assays now operate within clinically relevant turnaround times. However, translation into routine care remains limited. Moving from validation to clinical utility will require pragmatic prospective studies, test-guided interventional trials, health economic evaluation, and integration into decision-making pathways. To date, this phase of development appears underrepresented relative to discovery research. Sustained progress will depend on coordinated engagement between academic investigators, healthcare systems, and industry partners to determine whether these biologically plausible technologies can deliver measurable benefit in real-world clinical practice.

Declarations

Ethics approval and consent to participate

Not applicable. This systematic review and meta-analysis used only aggregate data from previously published studies. No participants were recruited, no new human samples or data were collected, and no identifiable participant-level information was accessed. Therefore, institutional ethics committee or institutional review board approval and informed consent to participate were not required. The review was conducted and reported in accordance with the PRISMA 2020 statement and its registered PROSPERO protocol (CRD420251128323).

Competing Interests

JH and RR have received a grant from PACE for developing and testing an RNA-based lateral flow transcript test.

Author Contribution

This systematic review was conceptualised by JPS and JH; Methodology by JPS; Data curation and data analysis by GC, EK, CP, ES, and JPS; Writing – original draft by GC, EK, CP, ES, and JPS; Writing – review and editing by JH, RR, RA, and JPS.

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Tables

Table 1

Study characteristics and diagnostic performance of RNA-based host response tests distinguishing bacterial form viral infections (n = 14) Number of pa
discovery work that are not included here. Where countries say 'multiple' more than one country was involved, and full list is in Supplementary Table

Paper	Countr(ies)	Test name	No of trans-cripts	Discovery or validation	Design	Age	Population	No of patients	Test results given as	Controls
Bauer et al., 2021(28)	Germany	IMX-BVN-2	29	Both	Prospective observational cohort	Adult	ED presentations with suspected infection	319	IMX-BVN-2 score	Infectio not bein tested
Dedeoglu et al., 2024(29)	UK	TriVerity test	29	Validation	Retrospective observational cohort	Adult	Adults hospitalised with ARI	169	1–50 banded severity score,	Others i group w the othe infectio
Gomez-Carballa, 2019(30)	Spain	-	2	Validation	Prospective case-control	Paediatric	Febrile children with confirmed bacterial or viral infections	35	Disease risk score	Healthy controls Others v other ty infectio
Iglesias-Ussel et al., 2024(31)	United States	Biomeme HR-B/V test	22	Both	Prospective observational cohort	Both	ED patients with confirmed or suspected infections	82	Probability scores	Others i cohort
Ko et al., 2023(33)	Multiple;	Global Fever	27	Both	Prospective observational cohort	Both	Patients with acute febrile illness	101	Probability score	Others i cohort
Ko, 2022(32)	United States	BioFire system; HR-B/V	45	Validation	Prospective observational cohort	Both	Febrile ED patients	616	Probability score	Others i cohort
Li et al., 2021(34)	United Kingdom	-	3	Both	Prospective observational cohort	Both	Presented to ED with undifferententiated fever	200	FS-PLS score	Others i group (includi probabl
Lydon et al., 2019(35)	United States	-	41	Validation	Prospective observational cohort	Both	ED presentations with respiratory illnesses	255	Probability score	Others i group
Mahle, 2021(36)	United States		81	Validation	Prospective observational cohort	Adult	Adults presenting to ED with infection, immunocompromised	134	Probability scores	Non-infe patients (non-infectio illness)

Paper	Countr(ies)	Test name	No of trans-cripts	Discovery or validation	Design	Age	Population	No of patients	Test results given as	Controls
Pennisi et al., 2021(38)	United Kingdom	-	2	Validation	Retrospective case-control	Paediatric	Febrile children with bacterial/viral infections	24	Probability score	Others i cohort
Pennisi et al., 2022(37)	United Kingdom	-	2	Validation	Case-control (unclear if pro- or retro-spective)	Not mentioned	Not mentioned	24	Probability score	Others v the othe diagnos
Shojaei et al., 2023(39)	Australia	IMX-BVN-2	29	Validation	Prospective observational cohort	Adult	Adults attending acute healthcare with flu-like symptoms	602	Bacterial/ Viral score 0–1	Others r the bact or viral g
Tsalik et al., 2021(40)	USA	BioFire system Film Array	45	Both	Prospective observational cohort	Adult	Adults attending ED with suspected sepsis or acute respiratory infection	209	P(Bacterial) and P(Viral)	ED presenta with nor infectiou cause
Xu et al., 2021(41)	China	-	2	Both	Both pro- and retrospective observational cohort	Both	< 85 years old with fever and bacterial/ viral infection	390	Score 0–1	Others i cohort

Table 2

Study characteristics and diagnostic performance of RNA-based host response tests diagnosing sepsis (n = 13) Number of patients is the number relevant
not included here. Where countries say 'multiple' more than one country was involved, and full list is in Supplementary Table 3. AUROC: area under the receiv
syndrome; SOFA: Sequential Organ Failure Assessment;

Paper	Countr(ies)	Test name	No of trans-cripts	Discovery or validation	Design	Age	Population	No of patients	Test results given as	Control
Balk et al., 2024(27)	United States	SeptiCyte RAPID	2	Validation	Both pro- and retrospective observational cohort	Adult	Patients in ITU with SEPSIS-2 or SEPSIS-3	419	Bands 1–5	SIRS al
Bauer et al., 2016(42)	Multiple: Germany, Greece	-	7	Both	Both pro- and retrospective observational cohort	Adult	Patients in ITU with SEPSIS-2 or SEPSIS-3	246	Genetic score	Patient without sepsis
Brakenridge et al., 2022(43)	United States	Inflammatix	29	Validation	Prospective observational cohort	Adult	Patients in ITU	200	Probability	Other IT patient
Gravrand et al., 2023(44)	France	SeptiCyte RAPID	2	Validation	Prospective observational cohort	Adult	ED and ITU patients	94	SeptiCyte Score	Dischar or thos not admitte to ITU
Koster-Brouwer et al., 2018(45)	Netherlands	SeptiCyte RAPID	4	Validation	Prospective observational cohort	Adult	ICU admissions requiring ventilation	467	SeptiCyte Lab Score (1–10)	Non-infecte ITU patient
Lu et al., 2025(46)	Netherlands	TriVerity	29	Validation	Prospective observational cohort	Adult	Patients visiting ED	60	5 bands	Other E patient
Malic et al., 2025(47)	Not stated	-	8	Both	Both pro- and retrospective observational cohort	Adult	Patients with suspected sepsis	248	Positive/negative	Other E patient
		-	8	Validation	Prospective observational cohort	Adult	Patients with suspected sepsis	30	Positive/negative	Other E patient
		PREDICT	8	Validation	Prospective observational cohort	Adult	Patients with suspected sepsis	30	Positive/negative	Other E patient
McHugh et al., 2015(48)	Netherlands	SeptiCyte LAB	4	Both	Prospective case-control	Adult	Patients in ITU	308	SeptiCyte Lab Score (0–10)	Not indicate
Miller et al., 2018(49)	Multiple: Netherlands and United States	SeptiCyte RAPID	4	Validation	Prospective observational cohort	Adult	Patients in ITU	447	SeptiCyte Lab Score (1–10)	SIRS al
Montero et al., 2023(50)	Spain	SeptiCyte RAPID	2	Validation	Retrospective observational cohort	Adult	Admitted to hospital with signs of COVID	146	SeptiCyte Score	Other COVID patient
Thair et al., 2021(51)	Germany	Sepsis MetaScore	11	Validation	Prospective observational cohort	Adult	Patients in ITU with blunt traumatic injury	51	SepsisMetaScore	Patient with no infectio
von der Forst et al., 2025(52)	Germany	SeptiCyte RAPID	2	Validation	Prospective observational cohort	Adult	Patients in ITU following elective major abdominal surgery	59	SeptiScore (Band 1–4)	Non-infectio SIRS
Zimmerman et al., 2017(53)	USA	SeptiCyte LAB	4	Validation	Prospective case-control	Paediatric	Patients in ITU with 'Clinical Severe	64	SeptiCyte Lab Score (1–10)	Childre post cardiac bypass

Paper	Countr(ies)	Test name	No of trans-cripts	Discovery or validation	Design	Age	Population	No of patients	Test results given as	Control
							Sepsis Syndrome'			without infectio

Table 3

Study characteristics and diagnostic performance of RNA-based host response tests diagnosing other infections, and prognosis (n = 17) Number of patie
work that are not included here. Where countries say 'multiple' more than one country was involved, and full list is in Supplementary Table 3. AUROC: are

Paper	Type	Countr(ies)	Test name	No of trans-cripts	Discovery or validation	Design	Age	Population	No of patients	Test res given as
Lei, 2021(58)	Bacterial only	China	-	2	Both	Retrospective case-control	Adult	one tertiary hospital in China.	264	Ct value
Peri et al., 2024(62)	Bacterial only	Australia	SeptiCyte RAPID	2	Validation only	Prospective observational cohort	Adult	Hospitalised patients with bacteraemia	86	SeptiCyt Score
Ram-Mohan et al., 2022(63)	Bacterial only	USA	MX-BVN-3 and IMX-SEV-3	29	Validation only	Prospective observational cohort	Adult	COVID-19 patients presenting to ED	161	4 bands viral/bac
Peri et al., 2024(61)	Candidemia	Australia	SeptiCyte RAPID	2	Validation only	Prospective observational cohort	Adult	Hospitalised patients with candidemia on blood culture	10	SeptiCyt Score
McClain et al., 2021(59)	Viral only	USA	-	36	Validation only	Prospective observational cohort	Adult	Students with URTIs and close contacts	1465	Probabi score
Tsalik et al., 2019(67)	Viral only	USA	Qvella's FAST HR	10	Both	Retrospective observational cohort	Adult	Adults with known bacterial/viral	128	Probabi score
Zaas et al., 2013(69)	Viral only	USA	-	48	Both	Retrospective case-control	Both	Microbiologically-proven infection, or healthy controls	102	Probabi having a infectior
de Olazarra et al., 2023(66)	Influenza	USA	-	4	Validation only	Retrospective case-control	Adult	Symptomatic patients tested for influenza	20	Express levels
Fillerova et al., 2017(55)	Joint infection	Czech Republic	-	3	Both	Prospective observational cohort	Adult	patients undergoing revision surgery after TJA	10	Probabi
Sangwichian et al., 2020(64)	Melioidosis	USA	-	2	Both	Retrospective observational cohort	Adult	Adults admitted with SIRS or healthy blood donor controls	42	binary (I melioido or unlike
Zhou et al., 2022(70)	Pneumonia	China	-	1	Validation only	Retrospective observational cohort	Paediatric	Children with pneumonia, healthy children	288	Ct value
Jackson et al., 2023(56)	MIS-C	Multiple;	-	5	Both	Prospective case-control	Paediatric	Children presenting with MIS-C	194	Disease score
Kuiper et al., 2023(57)	Kawasaki Disease	Multiple;	KiDs-GEP	14	Both	Retrospective case-control	Paediatric	Children presenting with fever	83	Classifie score
Seitzman 2024(65)	Conjunctivitis	Multiple	n/a	1	Both	Prospective observational cohort	Adult	Adults with conjunctivitis	164	Ct value
Buturovic et al., 2022(54)	Prognosis	Multiple	CoVerity	6	Both	Both pro- and retrospective observational cohort	Adult	COVID-19 patients	197	6-mRNA score
Moore et al., 2021(60)	Prognosis	USA	-	11	Validation only	Prospective observational cohort	Adult	ICU patients < 24 hours from ED	70	Score

Paper	Type	Countr(ies)	Test name	No of trans-cripts	Discovery or validation	Design	Age	Population	No of patients	Test res given as
Wong et al., 2015(68)	Prognosis	USA	-	100	Both	Prospective observational cohort	Paediatric	Children admitted to PICU with septic shock	132	Gene Express Score

Table 4
Study characteristics and diagnostic performance of RNA-based host response tests diagnosing

Paper	Countr(ies)	Test name	No of trans-cripts	Discovery or validation	Design	Age	Population	No of patients	Test results given as	Controls
Bayaa et al., 2021(71)	Multiple;	RISK6	6	Validation	Prospective nested case control	Adult	Adults with TB, LTB, and healthy donors	238	RISK6 Score	Healthy Donc (HD)
Blauenfeldt et al., 2014(72)	Multiple;	-	3	Both	Prospective case-control	Adult	Adults with TB, LTB, and healthy donors	152	Log-fold change	Healthy Controls
Crowder et al., 2024(73)	Multiple;	Xpert® MTB HR	4	Validation	Prospective observational cohort	Adult	≥ 2 weeks of cough at primary health centre	1392	TB score	No TB detected
Darboe et al., 2019(74)	South Africa	ACS COR signature	11	Validation	Retrospective Mixed	Adult	HIV-infected and uninfected adults (Diagnostic cohort)	100	ACS COR score	HIV negative
De Araujo et al., 2016(75)	Brazil	-	3	Validation	Both pro- and retrospective observational cohort	Adult	Adults with TB, LTB, and healthy donors	129	-	Healthy and LTBI contacts
Ding et al., 2024(76)	China	-	2	Both	Prospective case control	-	Hospital patients	18	-	Healthy controls
Folkesson et al., 2025(77)	Sweden	Xpert® MTB HR	4	Validation	Prospective observational cohort	Adult	Individuals with presumed TB	307	TB score	Suspected TI with negative tests
Gjoen et al., 2017(78)	India	-	10	Both	Prospective case-control	Paediatric	Children evaluated for TB	107	-	Household contacts; symptomatic non-TB children
			7							
Gliddon et al., 2021(79)	Multiple: South Africa, Malawi	-	4	Both	Retrospective case-control	Adult	Adults with active TB, other respiratory diseases, and LTBI	40	Disease risk score	Other diagnosis
Gong et al., 2021(80)	China	-	4	Both	Both pro- and retrospective case-control	Adult	TB patients, pulmonary lung cancer patients, pneumonia patients, and healthy controls	126	TB score	Lung cancer, pneumonia patients
Gupta-Wright et al., 2024(81)	Multiple;	Xpert® MTB HR	4	Validation	Prospective observational cohort	Adult	Outpatients with presumed TB	1499	TB score	Participants with negative microbiologi results
Halliday et al., 2021(82)	United Kingdom	Anderson	51	Validation	Prospective observational cohort	Adult	Adults presenting with suspected active TB	628	-	Other diagnosis
		Kaforou	44							
		Sweeney	3							
Ji et al., 2024(83)	China	Xpert® MTB HR	3	Validation	Prospective observational cohort	Adult	Adults presenting at the hospital with suspected active TB	297	TB score	Negative microbiology
Li, 2023(84)	China	Xpert® MTB HR	3	Validation	Prospective case-control	Adult	TB patients, other respiratory diseases (ORD) patients, and healthy controls	590	TB score	Other diagnoses or healthy

Paper	Countr(ies)	Test name	No of trans-cripts	Discovery or validation	Design	Age	Population	No of patients	Test results given as	Controls
							presenting to a primary care			
Mbandi et al., 2022(85)	Multiple;	RISK6	6	Validation	Prospective case-control	Paediatric	HIV+ children who had BCG starting ART	90	-	Starting ART without subsequent IRIS
		Sweeney3	3							
Mendelsohn et al., 2021(86)	South Africa	RISK11	11	Validation	Prospective observational cohort	Adult	HIV+ adults from communities	861	-	No incident T
Mendelsohn et al., 2022(87)	South Africa	**9 signatures**		Validation	Prospective observational cohort	Adult	Case-control and community volunteers	3784	-	Community controls
Moreira et al., 2021(88)	Brazil	Xpert® MTB HR	3	Validation	Retrospective case-control	Adult	Incarcerated men	300	TB score	Negative testing
Muwanga et al., 2024(89)	Multiple;	**20 signatures**		Validation	Prospective case-control	Adult	Individuals presenting with respiratory symptoms at primary healthcare clinics	579	-	Other diagnoses
Olbrich et al., 2024(90)	Multiple;	Xpert® MTB HR	3	Validation	Prospective observational cohort	Paediatric	Children with presumptive TB	639	TB score	Other diagnoses
Pan et al., 2017(91)	China	-	1	Validation	Prospective case-control	Paediatric	Paediatric patients with confirmed TB meningitis	242	-	Control grou
Penn-Nicholson et al., 2020(92)	South Africa	RISK6	6	Both	Both pro- and retrospective observational cohort	Adult	TB patients and healthy controls	293 + 194	-	Controls
Scriba, 2021(93)	South Africa	RISK11	11	Validation	Prospective RCT Cohort[2]	Adult	Adult community volunteers	2923	RISK11 score	Those withou active TB at baseline
Seifert et al., 2024(94)	Multiple;	Xpert® MTB HR	3	Validation	Prospective observational cohort	Both	Patients presenting with TB-like symptoms at hospitals in Pakistan	497	TB score	Other diagnoses
Sodersten et al., 2021(95)	Multiple;	Xpert® MTB HR	3	Validation	Retrospective nested case-control	Adult	Adult inpatients living with HIV	201	TB score	No TB detected
Sutherland et al., 2025(96)	Multiple;	Xpert® MTB HR	3	Validation	Prospective observational cohort	Adults[1]	Adults presenting with symptoms compatible with TB	1154	TB score	Other diagnoses
Sweetser et al., 2025(97)	Multiple;	Xpert® MTB HR	3	Validation	Prospective observational Cohort	Paediatric	Children with microbiologically or clinically diagnosed TB	106	TB score	Non-severe T
Warsinske et al., 2018(98)	Brazil		3	Validation	Prospective nested case-control	Adult	Adult inmates undergoing screening	81		Consecutive non-TB controls
	South Africa		3	Validation	Prospective nested case-control	Adult	HIV-negative adults starting TB treatment and controls	138		Healthy controls or patients with other lung diseases

Paper	Countr(ies)	Test name	No of trans-cripts	Discovery or validation	Design	Age	Population	No of patients	Test results given as	Controls
Wu et al., 2023(99)	China	Xpert® MTB HR	3	Validation	Prospective observational cohort	Adults[1]	TB patients, LTBI patients, other pulmonary diseases patients, and healthy volunteers;	653	TB score	Non-active TI
Zhang et al., 2013(100)	China	-	6	Both	Retrospective case-control	Adult	TB patients and Healthy controls	218	Numeric score	Other lung pathologies

Number of patients is the number relevant to this systematic review – there may be other patients in discovery work that are not included here. Where countries say 'multiple' more than one country was involved, and full list is in Supplementary Table 3. AUROC: area under the receiver-operator curve;[1]These include patients > 12 years, who were not considered paediatric patients in the countries they were treated. [2]Although this was a randomized trial, the results shown here are from the baseline only, so these results were observational only. ATB – active TB; CSF – cerebrospinal fluid; ORD – other respiratory disease; TBM – TB meningitis.

Figures

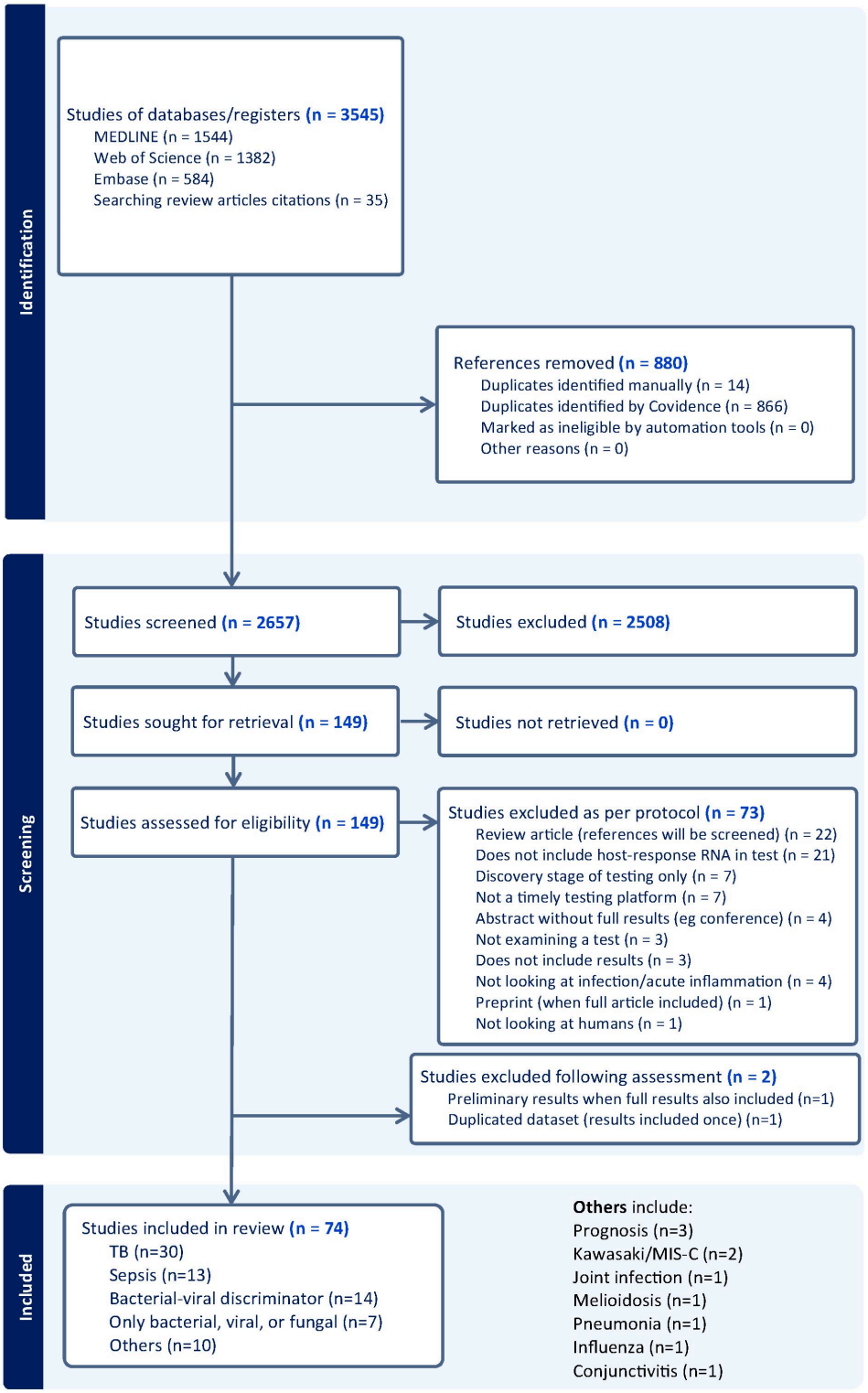


Figure 1

PRISMA diagram

The PRISMA flow chart detailing the outcome of the searches is shown. 76 studies were found to meet the protocol requirements, with two studies excluded post-assessment to avoid duplication of the results – the first or the main publication of these studies were included in the review once.

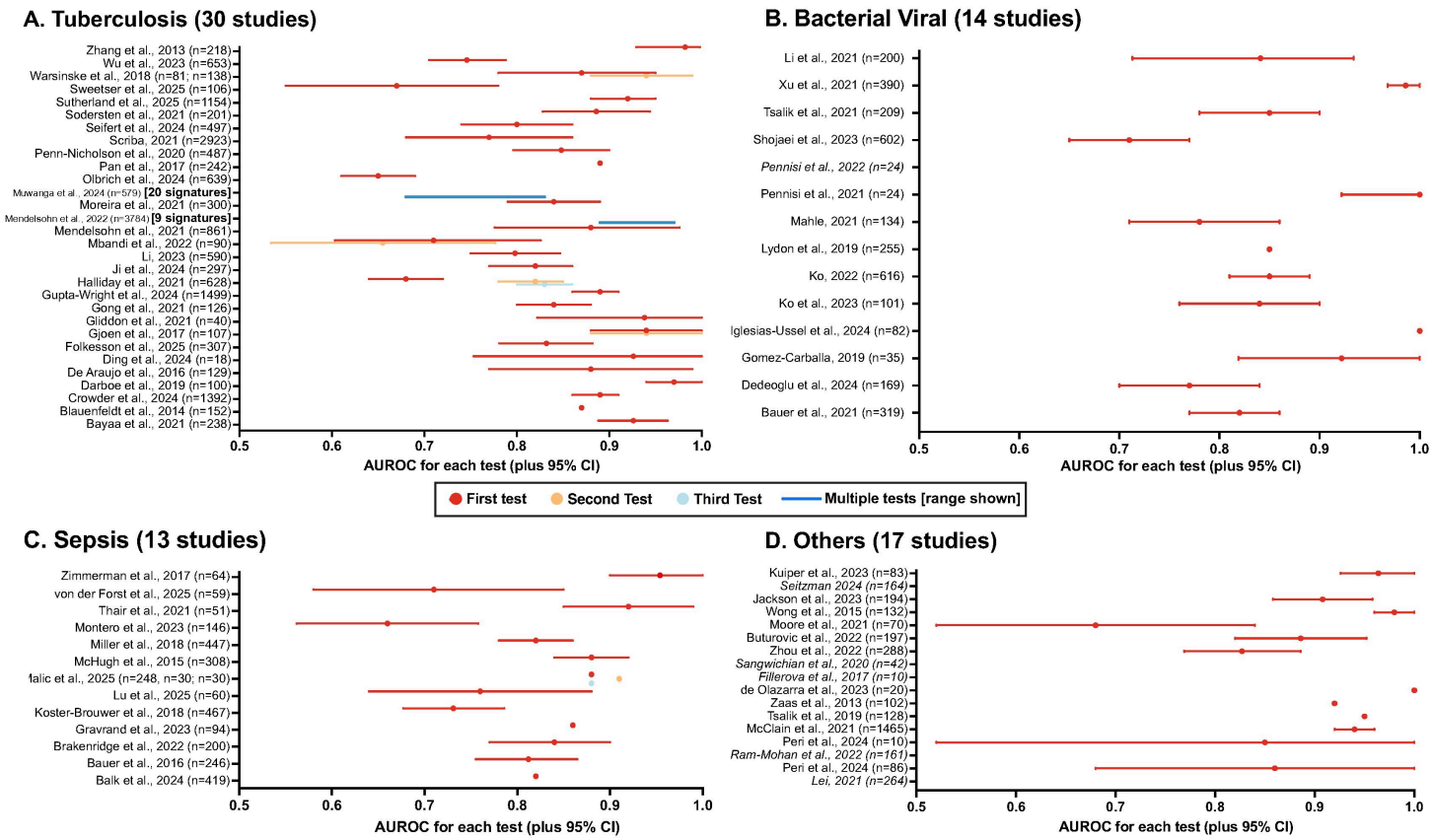


Figure 2

Reported accuracy across the 74 papers

The point estimate for the area under the receiver operator characteristic curve (AUROC) is shown for each of the studies, along with the 95% confidence intervals, where available. Where more than 3 tests were included in the paper, they are displayed as a range of the point estimate for all the tests, with full details shown in Supplementary Table 2.

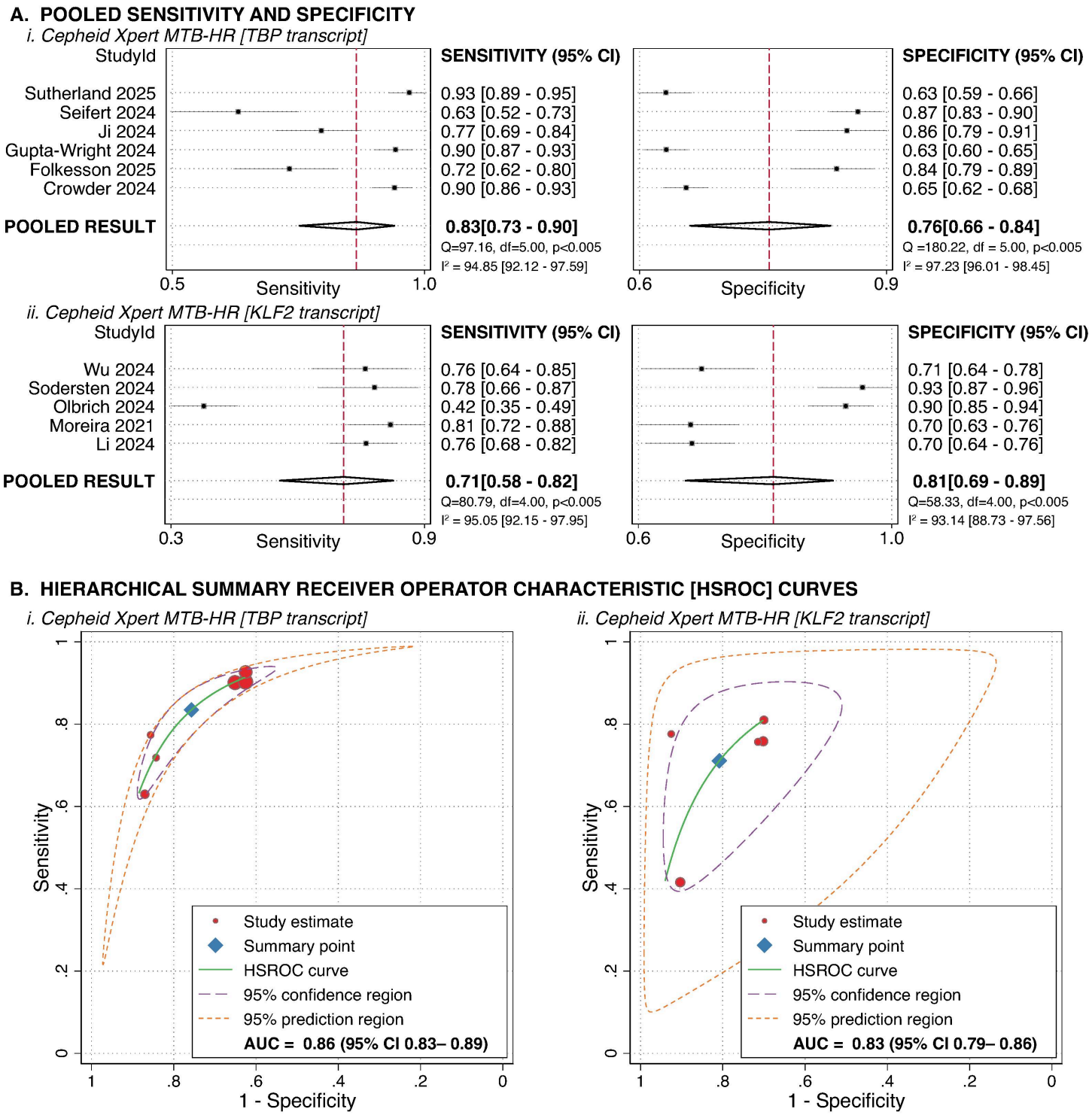


Figure 3

Meta-analysis results showing A) Pooled sensitivities and specificities for the Cepheid MTB-HR tests; B) Hierarchical summary receiver operator characteristic (HSROC) curves

Results of the pooled sensitivities and specificities, split by the transcript of the Cepheid Xpert MTB-HR test are shown. The HSROC curves, along with the area under the curve (AUC) are shown below.

Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- SturgeonSupplementalBMCID.docx