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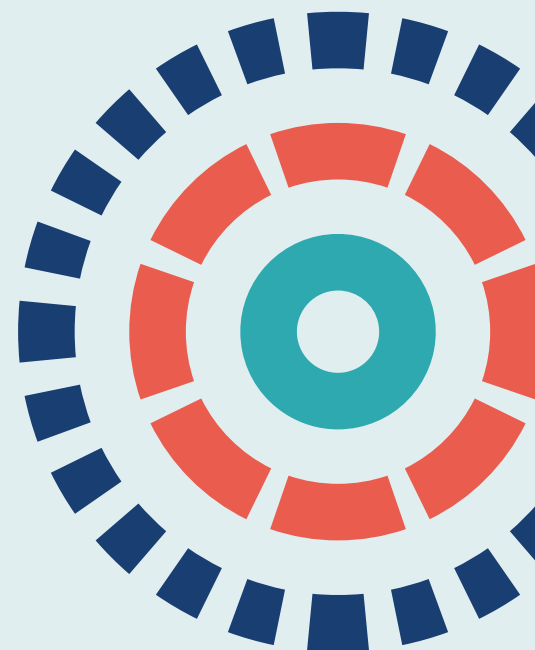
## Efficacy and Mechanism Evaluation

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# New technologies for diagnosing active TB: the VANTDET diagnostic accuracy study

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**Declared competing interests of authors:** Alice Halliday has a patent pending entitled 'A cellular immune signature for risk stratification of latent tuberculosis infection'. Robert Parker reports having the following patents pending: 1719853.2 and 2017904359. Lachlan Coin reports having the following patents pending: WO2014067943A1 and US20150284780A1. In addition, Lachlan Coin has one patent issued: EP2914740B1. Jon Deeks reports grants from National Institute for Health Research (NIHR) during the conduct of the study and receipt of a NIHR Senior Investigator Emeritus award and that he is supported by the NIHR Biomedical Research Centre, University Hospitals Birmingham NHS Foundation Trust and University of Birmingham. Peter White reports grants from the Medical Research Council and the NIHR during the conduct of the study, and grants from Otsuka Pharmaceutical (Tokyo, Japan) outside the submitted work. Onn Min Kon is chairperson of the UK Joint Tuberculosis Committee. Ajit Lalvani reports issued patents underpinning interferon gamma release assays (IGRAs) and next-generation IGRAs, some of which were assigned by the University of Oxford to Oxford Immunotec Global plc (Abingdon, UK), resulting in royalty entitlements for the University of Oxford and Ajit Lalvani. Ajit Lalvani is also inventor of issued and pending unlicensed patents underpinning flow-cytometric diagnosis of tuberculosis.

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# Abstract

## New technologies for diagnosing active TB: the VANTDET diagnostic accuracy study

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**Background:** Tuberculosis (TB) is a devastating disease for which new diagnostic tests are desperately needed.

**Objective:** To validate promising new technologies [namely whole-blood transcriptomics, proteomics, flow cytometry and quantitative reverse transcription-polymerase chain reaction (qRT-PCR)] and existing signatures for the detection of active TB in samples obtained from individuals with suspected active TB.

**Design:** Four substudies, each of which used samples from the biobank collected as part of the interferon gamma release assay (IGRA) in the Diagnostic Evaluation of Active TB study, which was a prospective cohort of patients recruited with suspected TB.

**Setting:** Secondary care.

**Participants:** Adults aged  $\geq 16$  years presenting as inpatients or outpatients at 12 NHS hospital trusts in London, Slough, Oxford, Leicester and Birmingham, with suspected active TB.

**Interventions:** New tests using genome-wide gene expression microarray (transcriptomics), surface-enhanced laser desorption ionisation time-of-flight mass spectrometry/liquid chromatography–mass spectrometry (proteomics), flow cytometry or qRT-PCR.

**Main outcome measures:** Area under the curve (AUC), sensitivity and specificity were calculated to determine diagnostic accuracy. Positive and negative predictive values were calculated in some cases. A decision tree model was developed to calculate the incremental costs and quality-adjusted life-years of changing from current practice to using the novels tests.

**Results:** The project, and four substudies that assessed the previously published signatures, measured each of the new technologies and performed a health economic analysis in which the best-performing tests were evaluated for cost-effectiveness. The diagnostic accuracy of the transcriptomic tests ranged from an AUC of 0.81 to 0.84 for detecting all TB in our cohort. The performance for detecting culture-confirmed TB or pulmonary TB was better than for highly probable TB or extrapulmonary tuberculosis (EPTB), but was not high enough to be clinically useful. None of the previously described serum proteomic signatures for active TB provided good diagnostic accuracy, nor did the candidate rule-out tests. Four out of six previously described cellular immune signatures provided a reasonable level of diagnostic accuracy (AUC = 0.78–0.92) for discriminating all TB from those with other disease and latent TB infection in human immunodeficiency virus-negative TB suspects. Two of these assays may be useful in the IGRA-positive population and can provide high positive predictive value. None of the new tests for TB can be considered cost-effective.

**Limitations:** The diagnostic performance of new tests among the HIV-positive population was either underpowered or not sufficiently achieved in each substudy.

**Conclusions:** Overall, the diagnostic performance of all previously identified 'signatures' of TB was lower than previously reported. This probably reflects the nature of the cohort we used, which includes the harder to diagnose groups, such as culture-unconfirmed TB or EPTB, which were under-represented in previous cohorts.

**Future work:** We are yet to achieve our secondary objective of deriving novel signatures of TB using our data sets. This was beyond the scope of this report. We recommend that future studies using these technologies target specific subtypes of TB, specifically those groups for which new diagnostic tests are required.

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## List of abbreviations

AIDS	acquired immunodeficiency syndrome	HPRU	Health Protection Research Unit
AUC	area under the curve	IDEA	IGRA in the Diagnostic Evaluation of Active TB
<i>BATF2</i>	basic leucine zipper atf-like transcription factor 2	IFN $\gamma$	interferon gamma
BCG	bacillus Calmette–Guérin	IGRA	interferon gamma release assay
BMI	body mass index	IL-2	interleukin 2
CD3	cluster of differentiation 3	IMAC	immobilised metal affinity chromatography
CD4	cluster of differentiation 4	ISAB	Independent Scientific Advisory Board
CD8	cluster of differentiation 8	LC–MS	liquid chromatography–mass spectrometry
CD27	cluster of differentiation 27	LDA	linear discriminant analysis
cDNA	complementary deoxyribonucleic acid	LTBI	latent tuberculosis infection
CFP-10	culture filtrate antigen	MFI	median fluorescence intensity
CI	confidence interval	MSD	Meso Scale Discovery
<i>CXCL9</i>	chemokine (C-X-C motif) ligand 9	<i>Mtb</i>	<i>Mycobacterium tuberculosis</i>
<i>CXCL10</i>	chemokine (C-X-C motif) ligand 10	m/z	mass-to-charge ratio
DRS	disease risk score	NICE	National Institute for Health and Care Excellence
ECRR	ESAT-6, CFP-10, Rv3615c and Rv3879c	NIHR	National Institute for Health Research
ELISA	enzyme-linked immunosorbent assay	NPV	negative predictive value
EPTB	extrapulmonary tuberculosis	OD	other disease
ESAT-6	6-kDa early secretory antigenic target	PBMC	peripheral blood mononuclear cell
FACS	fluorescence-activated cell sorting	PBS	phosphate-buffered saline
FDR	false discovery rate	PCR	polymerase chain reaction
HC	healthy control	PHA	phytohaemagglutinin
HIV	human immunodeficiency virus	PMA	phorbol 12-myristate 13-acetate
HIV–	human immunodeficiency virus negative	PPD	purified protein derivative
HIV+	human immunodeficiency virus positive	PPI	patient and public involvement
HLA-DR	human leucocyte antigen – antigen D related	PPV	positive predictive value
		PTB	pulmonary tuberculosis
		QC	quality control



## LIST OF ABBREVIATIONS

QFT-GIT	QuantiFERON® GOLD In-Tube	SVML	support vector machine learning
qRT-PCR	quantitative reverse transcription-polymerase chain reaction	TB	tuberculosis
RD1	region of difference 1	TBS	tuberculosis score
RNA	ribonucleic acid	TEAB	triethylammonium bicarbonate
RNase	ribonuclease	T <sub>EFF</sub>	differentiation T effector cells
ROC	receiver operating characteristic	TNF- $\alpha$	tumour necrosis factor alpha
SELDI-TOF	surface-enhanced laser desorption ionisation time-of-flight mass spectrometry	TST	tuberculin skin test
SERPINA1	serpin family A member 1	VANTDET	Validation of New Technologies for the Diagnostic Evaluation of active Tuberculosis
SMG	Study Management Group	v/v	volume/volume
		WHO	World Health Organization

## Plain English summary

Globally, tuberculosis (TB) is the most deadly infectious disease, with 10 million cases each year, resulting in 1.3 million deaths. TB is caused by a bacterium that is transmitted from an individual with TB disease of the lungs to another person by coughing. There are several diagnostic tests for TB, most of which detect the presence of the bacteria in clinical samples. However, these tests fail to detect all TB patients, particularly when there is a small number of bacteria present at the site of disease and/or it is difficult to get a sample. This means that some wait a long time for a final diagnosis and incur a delay before starting treatment, or else are given TB treatment without a clear diagnosis. New and improved diagnostic tests that allow for the rapid detection of all active TB cases would greatly improve patient care.

Recently, scientists have found several new approaches to testing for TB disease that use new technologies to measure the immune response in blood samples. In previous studies, these new technologies were able to distinguish between TB and other diseases that appear clinically similar to TB. In this project we aimed to validate these new technologies using samples from patients with the full range of TB disease, including those who test negative on the current tests. Overall, we found that the new technologies worked less well than previously reported. Importantly, they were unable to detect all of the TB patients who tested positive on the current tests. Owing to the poor accuracy for diagnosing all TB patients, and the high cost of these new tests, we found that none of the new tests would be cost-effective for use on all individuals who have suspected TB. However, in the hard-to-diagnose patient groups, for whom there are currently no rapid tests available, some of the new tests may be useful if used alongside existing tests.



# Scientific summary

## Background

Tuberculosis (TB) is an important global disease, with millions of cases reported, including 1.3 million deaths, annually. In order to reduce the burden of TB disease, new tools are needed, including improved diagnostic tests. The currently available toolkit lacks a test that can detect all cases of TB with high accuracy and speed. The gold-standard tests for active TB are those that detect the causative bacteria, *Mycobacterium tuberculosis* (*Mtb*), but these have limitations. The smear test is quick but lacks sensitivity for all TB cases and does not achieve 100% specificity; *Mtb* culture is more sensitive than the smear test and has greater specificity, but lacks speed. The new nucleic acid amplification tests are an improvement on current tests; they have a greater sensitivity than smear, are rapid and provide information about drug sensitivity. However, these tests are unable to detect culture-negative TB cases. There are two major clinical unmet needs for active TB diagnostics: a triage rule-out test for TB and a rule-in test for hard-to-diagnosis TB cases (including culture-negative TB).

There has recently been an explosion in the discovery of biomarkers for TB based on measurements of a wide range of host responses using genome-wide gene expression microarrays, proteomic techniques and characterisation of functional T-cell subsets by flow cytometry. The resulting biomarker and cellular immunological signatures have high diagnostic sensitivity and specificity for active TB and distinguish active from latent infection. The feasibility of these novel approaches for diagnosis of TB has now been established and the apparent accuracy of the signatures has the potential to revolutionise TB diagnosis. In addition to the above, we have recently developed a highly sensitive whole-blood molecular test that can reliably rule out the diagnosis of TB based on measurement of interferon gamma (IFN $\gamma$ )-dependent chemokine release in response to *Mtb*-specific antigens.

Thus, there are a number of new, promising biomarkers that now need urgent prospective and rigorous validation in routine clinical practice.

## Aim

To validate promising new technologies [namely whole-blood transcriptomics, proteomics, flow cytometry and quantitative reverse transcription-polymerase chain reaction (qRT-PCR)] and existing signatures for detection of active TB in samples obtained from individuals suspected of active TB.

## Objectives

### Primary objectives

- To define the role of previously identified whole-blood gene expression signatures in the diagnostic evaluation of active TB using host transcriptomic microarray.
- To define the role of previously identified serum proteomic signatures in the diagnostic evaluation of active TB using liquid chromatography–mass spectrometry (LC–MS) and expanded to surface-enhanced laser desorption ionisation time-of-flight mass spectrometry (SELDI-TOF).
- To define the role of previously established cellular immunological signatures in the diagnostic evaluation of active TB using flow cytometry.
- To validate our candidate-stimulated whole-blood chemokine-based quantitative reverse transcription-polymerase chain reaction assay for rapid patient triage by excluding the diagnosis of active TB.

## Secondary objectives

- To evaluate the use of the previously identified tests in the diagnosis of key subpopulations of active TB, namely human immunodeficiency virus positive/human immunodeficiency virus negative (HIV–), culture-confirmed/highly probable TB and pulmonary tuberculosis (PTB)/extrapulmonary tuberculosis (EPTB).
- To define optimal diagnostic algorithms that delineate the role of these new tests in the routine diagnostic assessment of patients with suspected active TB in the NHS.
- To assess the cost-effectiveness of the best-performing novel tests validated in this study for the diagnostic work-up of TB patients in routine NHS practice.
- To identify novel signatures of active TB (using the same technologies described in the primary objectives), selected to provide optimal diagnostic performance (i.e. beyond those previously proposed).

## Methods

This project used the biobank of samples from the interferon gamma release assay (IGRA) in the Diagnostic Evaluation of Active TB (IDEA) study, in which individuals with suspected TB were recruited as part of routine clinical practice in 12 hospital sites in England (2011–14). The Validation of New Technologies for the Diagnostic Evaluation of active Tuberculosis (VANTDET) study comprised four laboratory subprojects, each evaluating proposed tests using the following new technologies/approaches: transcriptomics, proteomics, flow cytometry and candidate rule-out tests. For each of the subprojects, the reference standard used was the final diagnosis as allocated in the IDEA study, in which clinicians used the Dosanjh classification to stratify patients based on the diagnostic and clinical data available (excluding the IGRA results) into the following groups: culture-confirmed TB, highly probable TB, clinically indeterminate TB and active TB excluded. Signatures were first assessed according to their ability to detect all active TB cases (i.e. culture-confirmed TB and highly probable TB combined), from the TB excluded group [other diseases (ODs)]. Subanalyses assessing the performance of tests/signatures for specific types of TB (i.e. culture-confirmed TB, highly probable TB, PTB and EPTB) were also performed.

For the validation of transcriptomic signatures from whole-blood samples, a total of 628 individuals were selected who reflected the full IDEA study cohort and were profiled using genome-wide gene expression microarray using the Illumina platform. For validation of proteomic signatures, we were restricted to a total of 90 individuals for SELDI-TOF analysis owing to the lack of consumable supply; meanwhile, 166 individuals infected with HIV, from the IDEA study cohort were profiled using LC-MS. For both of these 'omic' approaches, signatures were evaluated for their discriminatory ability by calculating the score as previously described, using raw expression/abundance data, or using linear discriminant analysis (LDA).

To validate previously reported cellular immune signatures for discrimination of active TB from individuals with latent tuberculosis infection (LTBI) and ODs, we took a nested case-control approach to select the cohort. Peripheral blood mononuclear cells (PBMCs) from 184 individuals were stimulated with *Mtb* antigens overnight, stained with antibodies for functional and phenotypic markers, and enumerated using flow cytometry.

For validation of candidate rule-out tests, we took a GO/NO-GO approach to select the cohort. The GO/NO-GO cohort of 100 patients was selected to artificially inflate the proportion of individuals with TB who are negative with standard IGRA tests. If high test accuracy was achieved using this cohort, we planned to carry out the tests on remaining samples. We developed protocols to evaluate the performance of two candidate immune-based rule-out tests: either using qRT-PCR to detect IFN $\gamma$ -dependent target genes in *Mtb*-stimulated PBMCs or using Meso Scale Discovery to detect chemokines in QuantiFERON® GOLD In-Tube supernatants (QIAGEN, Hilden, Germany).

For the health economic analysis, the best-performing tests were evaluated. Costs were estimated based on similar assays currently available in NHS practice. Decision tree models were developed to calculate the incremental costs and incremental health utilities [quality-adjusted life-years (QALYs)] of changing from current practice to using the candidate test as either rule-in or initial rule-out of active TB. The models were parameterised using the IDEA study clinical patient records and relevant current literature.

## Results

The project and four substudies assessed each of the new technologies and evaluated the performance of previously published signatures. In addition, best-performing tests were evaluated for cost-effectiveness in a health economic analysis.

### *Principal findings in the transcriptomic substudy*

We assessed six previously reported gene expression signatures, using LDA. Three of these signatures could also be valued using the score methods as previously described. For all TB, the optimal diagnostic accuracy for all signatures ranged from an area under the curve (AUC) = 0.81–0.84; inclusion of HIV-infected individuals in the validation cohort reduced diagnostic accuracy. The diagnostic accuracy for detecting culture-confirmed TB or PTB was better than for highly probable TB or EPTB.

### *Principal findings in the proteomics substudy*

We assessed the performance of one four-protein signature using SELDI-TOF and LC–MS, and three additional previously reported proteomic signatures using LC–MS. The optimal performance for the four-protein signature was found using SELDI-TOF, for which the AUC for detecting culture-confirmed TB was 0.74. Using LDA, the performance of all signatures for detecting all TB cases using LC–MS ranged from AUC 0.62 to 0.68.

### *Principal findings in the cellular immune signatures substudy*

Four of six previously described cellular immune signatures provided a reasonable level of diagnostic accuracy (AUC = 0.78–0.92) for discriminating all TB from those with ODs/LTBI in HIV– TB suspects. Two of these assays may be useful in the IGRA-positive population and can provide high positive predictive value (PPV).

### *Principal findings in the candidate rule-out test substudy*

Improved diagnostic accuracy for all TB over IGRA was achieved using the qRT-PCR detection of chemokine (C-X-C motif) ligand 9 (CXCL9), chemokine (C-X-C motif) ligand 10 (CXCL10) or basic leucine zipper atf-like transcription factor 2. None of the tests was able to provide > 95% sensitivity and > 65% specificity for active TB and, therefore, would not be suitable for a rule-out test. The assay also resulted in a high failure rate and is complex. CXCL9 may provide good discriminatory ability for TB and LTBI in the T-SPOT.TB (Oxford Immunotec Global plc, Abingdon, UK) test-positive population.

None of the evaluated new tests for TB can be considered cost-effective for use in detecting all TB patients with their current cost and diagnostic performance.

## Conclusions

None of the previously reported signatures using new technologies was able to provide diagnostic accuracy at a level that could be considered clinically useful for either all TB cases or for culture-positive TB. However, in specific patient groups, there may be a use for the best-performing new tests. Specifically, although the diagnostic accuracy for detection of highly probable TB was suboptimal (AUC = 0.8), the Sweeney *et al.* four-gene transcriptomic signature may be useful in this microbiologically unconfirmed population (Sweeney TE, Braviak L, Tato CM, Khatri P. Genome-wide expression for diagnosis of pulmonary tuberculosis: a multicohort analysis. *Lancet Respir Med* 2016;**4**:213–24), as it could provide a

high negative predictive value (0.95) and a result quickly. We identified two cellular-immune signatures that could provide a high PPV (0.88–0.95) for all TB, and for culture-confirmed TB, which may be useful in the IGRA-positive population of TB suspects.

In general, the performance of all signatures we evaluated was suboptimal compared with previous publications, probably as a result of the heterogeneous cohort of TB and OD patients included in this study, which reflects the full complexity of TB and its differential diagnoses presenting in real-life clinical settings. The secondary objective of defining novel signatures for active TB using the data sets generated is outstanding, but will build the bases for future studies. We recommend that future studies investigating blood-based tests for TB using these technologies focus on specific subgroups of TB patients and the OD they are clinically confused with. In particular, new tests for culture-negative TB and EPTB are needed most.

## Funding

This project was funded by the Efficacy and Mechanism Evaluation (EME) programme, a MRC and NIHR partnership.

# Chapter 1 Introduction

## Background: tuberculosis

Tuberculosis (TB) is a devastating disease, with approximately 10 million cases worldwide each year.<sup>1</sup> Globally, it is one of the top 10 causes of death and is the leading cause of death from a single infectious agent, ahead of human immunodeficiency virus (HIV)/acquired immunodeficiency syndrome (AIDS).<sup>1</sup> Important characteristics of the current global epidemic are the interaction with the HIV/AIDS epidemic (with HIV/TB co-infection driving increased mortality) and the increasing rates of multidrug-resistant TB cases. The areas with the greatest TB burden are in south-east Asia, Africa and the Western Pacific World Health Organization (WHO) regions. England has among the highest rates of TB in Western Europe, with 5664 notifications and a rate of 10.2 cases per 100,000 people in 2016.<sup>2</sup> The majority of TB cases in Europe occur in large cities (especially London, Birmingham and Leicester in England), and the disease disproportionately affects immigrants and socially marginalised and socioeconomically disadvantaged groups.

Tuberculosis is caused by the bacterium *Mycobacterium tuberculosis* (*Mtb*), and is transmitted from person to person via the aerosol route by droplet particles that are produced when an individual with the pulmonary form of TB coughs. On exposure to an uninfected individual, a number of eventualities can occur. Approximately 50% of exposed individuals resist the infection; the remainder become infected, as identified by the detection of peripheral cellular immune responses to *Mtb* antigens. The majority of infected individuals will develop prolonged but controlled latent infection of *Mtb* [i.e. latent tuberculosis infection (LTBI)]. It is estimated that between one-quarter and one-third of the world's population has LTBI.<sup>3</sup> In a small proportion of infected individuals, the immune response can lose control of *Mtb* replication, and in such cases TB disease will develop. In most cases this development to active TB occurs within the first 6 months after initial infection,<sup>4</sup> although progression from LTBI to active TB (also known as reactivation) can occur at any time during an individual's lifetime. Active TB can manifest in many forms and can infect any organ of the body. Owing to the mode of transmission, pulmonary tuberculosis (PTB) is the typical form of TB; however, extrapulmonary tuberculosis (EPTB) is becoming increasingly common, particularly in cases of reactivation from LTBI.

Reduction of TB cases and working towards elimination of TB as a public health issue are nationally and internationally agreed as public health priorities at the level of the UK, European Union and WHO.<sup>1,5</sup> Although global TB incidence is declining by around 2% per year, improved reduction rates are required to progress towards elimination. Internationally agreed targets for improved global TB control, such as in the sustainable development goals or the WHO's *End TB Strategy*,<sup>6</sup> require that TB incidence rates fall by up to 5% per year, which is not achievable with existing tools. New innovative methods for TB prevention, diagnosis and treatment are urgently needed, and the WHO's global plan calls for researchers and industry to deliver an improved, fit-for-purpose anti-TB toolkit, with major emphasis on the need for new diagnostic tests.<sup>7</sup> Prompt and accurate diagnosis and treatment of TB are essential to improve individual patient outcomes, as well as to prevent onward transmission in the community with its attendant health and social care costs. However, the currently available diagnostic toolkit lacks the ability to provide results with clinically acceptable speed and diagnostic accuracy.

## Current diagnostic tests for tuberculosis

Currently available tests recommended by the National Institute for Health and Care Excellence (NICE) for diagnosis of active TB in the UK comprise smear microscopy, *Mtb* culture, radiography and nucleic acid amplification tests.<sup>8</sup> Smear microscopy is rapid but has low sensitivity, whereas radiography has low specificity. *Mtb* culture is the current microbiological gold standard, but is limited by its lack of speed



(requiring 2–6 weeks to generate a result), and it is only moderately sensitive. Importantly, both smear microscopy and *Mtb* culture suffer from reduced sensitivity in a number of key ‘hard-to-diagnose’ patient populations, including those with EPTB or HIV co-infection.

Nucleic acid amplification tests have been a major advancement in TB diagnostics, and the Xpert® MTB/RIF test (Cepheid Inc., Sunnyvale, CA, USA) now performs with higher sensitivity than smear microscopy and provides a result on the same day. The Xpert MTB/RIF test is a substantial improvement on conventional microbiological tests, especially now that the improved Xpert MTB/RIF Ultra has shown greater sensitivity in the smear-negative culture-positive population of TB cases (64% compared with 46% with conventional Xpert).<sup>9</sup> However, culture-negative TB cases (another key ‘hard-to-diagnose’ patient subgroup) are mostly falsely negative when tested by Xpert. As with microscopy and culture, sensitivity of the Xpert (and Ultra) is also lower in people with EPTB and HIV co-infection. Furthermore, the Xpert is expensive and its cost-effectiveness within routine NHS practice is unknown. Thus, within the UK setting, culture remains the gold standard.

The tuberculin skin test (TST) and interferon gamma release assays (IGRAs) are immunological tests recommended by NICE for the diagnosis of LTBI.<sup>8,10</sup> Although these tests can be used to detect *Mtb* infection, none is able to discriminate between LTBI and active TB disease, and all lack sufficient diagnostic sensitivity to exclude a suspected diagnosis of TB.<sup>11,12</sup> IGRAs have improved specificity for *Mtb* infection over the TST, which is compromised by poor specificity owing to cross-reactive responses to the test in bacillus Calmette–Guérin (BCG)-vaccinated or non-*Mtb*-exposed individuals.<sup>13</sup> There are two main types of IGRA: the QuantiFERON® GOLD In-Tube (QFT-GIT) (QIAGEN, Hilden, Germany) and the T-SPOT.*TB* test.<sup>12,14</sup> Therefore, although the IGRA and TST tests are recommended for detection of LTBI, the utility of IGRAs in the diagnostic work-up of active TB is not currently recommended. However, should there be an upgrade to these immunological tests whereby the sensitivity for all active TB was increased to > 95%, then they would have the potential to be used as triage tests to rule out active TB. The IGRA in the Diagnostic Evaluation of Active TB (IDEA) study,<sup>12,14</sup> which provided the cohort and biobank samples for the Validation of New Technologies for the Diagnostic Evaluation of active Tuberculosis (VANTDET) study, was an observational prospective cohort study that sought to define the role of commercially available IGRAs, as well as a second-generation IGRA, in the diagnosis of active TB. The IDEA study found that, although the T-SPOT.*TB* had significantly greater sensitivity for active TB than QFT-GIT (81.4% and 67.3%, respectively), neither test had sufficient sensitivity to rule out a diagnosis of active TB. However, the second-generation IGRA had a sensitivity of 94% for culture-confirmed TB and 89% for all TB, providing the first proof of principle that an immune-based test has the potential to practically serve as a rule-out test.<sup>12,14</sup> Such a test would significantly reduce the time to diagnosis of patients for whom TB is a suspected condition on initial assessment, but are diagnosed with another disease by the end of diagnostic work-up.

Interferon gamma release assays and the TST are widely used to detect LTBI in those at high risk of having the infection, such as those who have recently been exposed to an active case of PTB. A recent large prospective cohort study investigating the predictive power of the IGRA and TSTs for detecting progression to active TB disease (among new-entrant migrants and recent close contacts of TB cases) in the UK found that these tests provide high negative predictive power but very low positive predictive power for identifying those who will progress to active TB.<sup>15</sup> Despite culture being the gold standard microbiological test for active TB in the UK and elsewhere, it is standard practice to commence treatment for clinically suspected TB cases before a positive culture result has confirmed TB. Globally, although a large proportion of cases of TB are diagnosed based on a positive sputum smear microscopy test, the sensitivity of smear for all TB cases (especially in EPTB, childhood TB and with HIV co-infection) is low and, therefore, a large proportion of patients are diagnosed clinically and treated without a definitive diagnosis. The unique epidemiology of TB in the UK (i.e. high rate of culture-negative TB cases and high proportion of active cases with EPTB)<sup>2</sup> means that a large proportion of patients’ treatment is initiated despite the lack of microbiological confirmation and, as such, the need for tests to detect these hard-to-diagnose groups of patients is greater.

## Clinical unmet needs

Globally, there is a need for improved diagnostic tests for both active TB and LTBI. As identified by the New Diagnostic Working Group (WHO and Stop TB Partnership), there is a need for a rapid non-sputum-based biomarker test for detecting active TB.<sup>16</sup> A fast, highly sensitive test for all types of active TB, with improved sensitivity over the current microbiological tests (which provide high specificity but low sensitivity), would improve triage of TB suspects and increase the speed at which patients start appropriate treatment.

In high-income, low-incidence settings, such as in the UK, a high proportion of new cases of active TB are a result of reactivation from LTBI. For this reason, a major priority for TB control programmes in these settings is to identify individuals with LTBI and to offer prophylactic treatment to those at highest risk of progression to active TB.<sup>17</sup> Although IGRAs and TST provide high sensitivity for these individuals, an independent or follow-on test with improved specificity would enable us to reduce the number needed to treat to prevent subsequent cases of progression to active TB.

Therefore, the major clinical unmet needs for improved TB diagnostics in the UK are as follows:

- a triage rule-out test for active TB
- a rapid, accurate test for identifying 'highly probable' TB, where a clinical diagnosis cannot be confirmed by culture
- a sensitive test to predict those at increased risk of progressing to active TB from exposure and/or positive test for LTBI.

## Rationale for the VANTDET study

### Blood-based tests: the rationale and technological approaches

The low sensitivity of microbiological diagnostic tools for TB reflects the low bacterial load in a high proportion of clinical samples from TB cases. Therefore, host-derived biomarkers, such as molecular transcriptomic or proteomic signatures, have been proposed as an approach that may have improved sensitivity for TB diagnosis.<sup>18–20</sup> The pursuit of TB biomarkers has been reinvigorated by the developments in high-throughput transcriptomic, proteomic and cellular immune technology platforms, and parallel advances in computational analytical methodologies. The past 18 or so years have seen a wealth of publications in this field, particularly in the development of transcriptomic biomarkers for active TB,<sup>18,20</sup> in which promising test accuracy has been demonstrated in large, multisite international cohorts of TB cases and controls. In addition, serum proteomic profiling has led to blood-based biomarkers of TB with promising test accuracies.<sup>19,21</sup>

Currently available immune-based tests have shown promise of greater sensitivity for detecting active TB when compared with microbiological tests, leading to speculation that development of newer, more sophisticated, immunological assays might lead to more accurate immune-based tests for TB. Several strategies for improving either sensitivity or specificity for TB have been proposed, including using different/additional antigens for stimulation,<sup>22</sup> measurement of additional/alternative analytes [to interferon gamma (IFN $\gamma$ )],<sup>23,24</sup> and/or measurement of cellular phenotype.<sup>25</sup> Measurement of additional or alternative analytes has been shown to improve both sensitivity and specificity for active TB in case-control studies. The measurement of phenotype and function, so far using only flow cytometric technology, has been shown in multiple studies to improve specificity by discriminating between active TB and LTBI.<sup>24,25</sup>

### Technologies

In the light of the above developments in the field of blood-based diagnostic tests for TB, we sought to validate the following approaches for the diagnostic evaluation of active TB: transcriptomics, proteomics, flow cytometry and chemokine quantitative reverse transcription-polymerase chain reaction (qRT-PCR) (*Table 1*).

**TABLE 1** Details of technologies to be assessed in the VANTDET study

Blood sample type	Field	Technology to be tested in VANTDET
RNA (whole blood)	Transcriptomics	Illumina microarray
Serum	Proteomics	SELDI-TOF
PBMC	Cellular immunology	Flow cytometry
Improved immune-based tests for rule-out of active TB		

PBMC, peripheral blood mononuclear cell; RNA, ribonucleic acid; SELDI-TOF, surface-enhanced laser desorption ionisation time-of-flight mass spectrometry.

### The need for a real-life clinical cohort of active tuberculosis suspects

A large proportion of reported cases of TB are diagnosed without confirmation from standard tests. Furthermore, most studies of new diagnostic approaches fail to include individuals who lack culture confirmation (or those negative with other microbiological tests, such as Xpert, smear microscopy), despite the fact that those with a negative culture results are the very population in whom a new diagnostic test would be most beneficial. This is why, when validating new diagnostics for active TB, we require a representative spectrum of patients, including those with a culture-negative status. We have therefore used the samples collected as part of the IDEA study, a National Institute for Health Research (NIHR) Health Technology Assessment-funded, prospective, multicentre UK cohort study of > 1000 adults presenting with suspected active TB at NHS outpatient or inpatient services at 13 participating NHS hospitals in London, Birmingham and Leicester.<sup>12</sup> Patients with suspected TB were prospectively recruited into the IDEA study at the point of initial diagnostic work-up in secondary care in routine clinical practice, before a diagnosis was confirmed. The new diagnostic tests for ruling in active TB were evaluated against the composite reference standard to allow for the inclusion of clinically diagnosed TB patients in the TB disease group. Within the VANTDET study, we also evaluated two candidate approaches for a triage rule-out test, which aim to improve on the sensitivity of the current IGRA tests.

### Study scope

The scope of the VANTDET study is specifically to address the needs for new diagnostic tests for active TB in individuals for whom there is a clinical suspicion of the condition (i.e. a triage rule-out test for active TB and a rapid, accurate test for identifying 'highly probable' TB, where a clinical diagnosis cannot be confirmed by culture). Although a triage test for active TB may potentially have a use in other settings, such as in contact clinics or for screening new patients from high-incidence areas, this is beyond the scope of this study.

### Aim

To validate promising new technologies (namely whole-blood transcriptomics, proteomics, flow cytometry and a chemokine qRT-PCR), and existing signatures for detection of active TB in samples obtained from individuals suspected of having active TB.

## Research objectives

### Primary objectives

1. To define the role of previously identified whole-blood gene expression signatures in the diagnostic evaluation of active TB using host transcriptomic microarray.
2. To define the role of previously identified serum proteomic signatures in the diagnostic evaluation of active TB using mass spectrometry and surface-enhanced laser desorption ionisation time-of-flight mass spectrometry (SELDI-TOF).

3. To define the role of previously established cellular immunological signatures in the diagnostic evaluation of active TB using flow cytometry.
4. To validate our candidate-stimulated whole-blood chemokine-based qRT-PCR assay for rapid patient triage by excluding the diagnosis of active TB.

### *Secondary objectives*

5. To evaluate the use of the previously identified tests in the diagnosis of key subpopulations of active TB, namely human immunodeficiency virus-positive (HIV+) patients/human immunodeficiency virus-negative (HIV-) patients, patients with culture-confirmed TB/highly probable TB and patients with PTB/EPTB.
6. To define optimal diagnostic algorithms that delineate the role of these new tests in the routine diagnostic assessment of patients with suspected active TB in the NHS.
7. To assess the cost-effectiveness of the best-performing novel tests validated in this study for the diagnostic work-up of TB patients in routine NHS practice.
8. To identify novel signatures of active TB (using the same technologies described in the *Primary objectives*), selected to provide optimal diagnostic performance (i.e. beyond those previously proposed).



## Chapter 2 Study overview, management and general methodology

This study consists of four substudies each addressing the main technologies to be assessed in primary objectives 1–4. The substudies are outlined in detail in *Chapters 3–6*; the secondary objectives (5–8) are addressed within these same chapters, in the context of each of the technologies being assessed. The health economic assessment is presented in *Chapter 7* for all of the best-performing tests. The reporting of each of the subprojects adheres to the standards for the reporting of diagnostic accuracy studies (STARD) guideline.

The biobank of blood samples that were collected and stored as part of the IDEA study<sup>12</sup> were used for the four subprojects. However, the criteria for cohort selection, sample processing, technical methodology and analytical approach differed between these subprojects. Detailed methodology and rationale can be found in the chapter corresponding to each subproject. This chapter summarises the main features of the overall study cohort (i.e. the IDEA study cohort), as well as the overarching methodology and approach for study management.

### Study management structure

#### Overview of study design

The original protocol specified the link between the IDEA study and the VANTDET study, as well as the processes and samples for each VANTDET substudy (*Figure 1*). In the IDEA study, additional blood was taken to allow for long-term storage of PAXGene® (Beckton, Dickinson Biosciences, NJ, USA), serum and peripheral blood mononuclear cell (PBMC) samples. These samples, coupled with clinical data, provided the biobank for the VANTDET study.

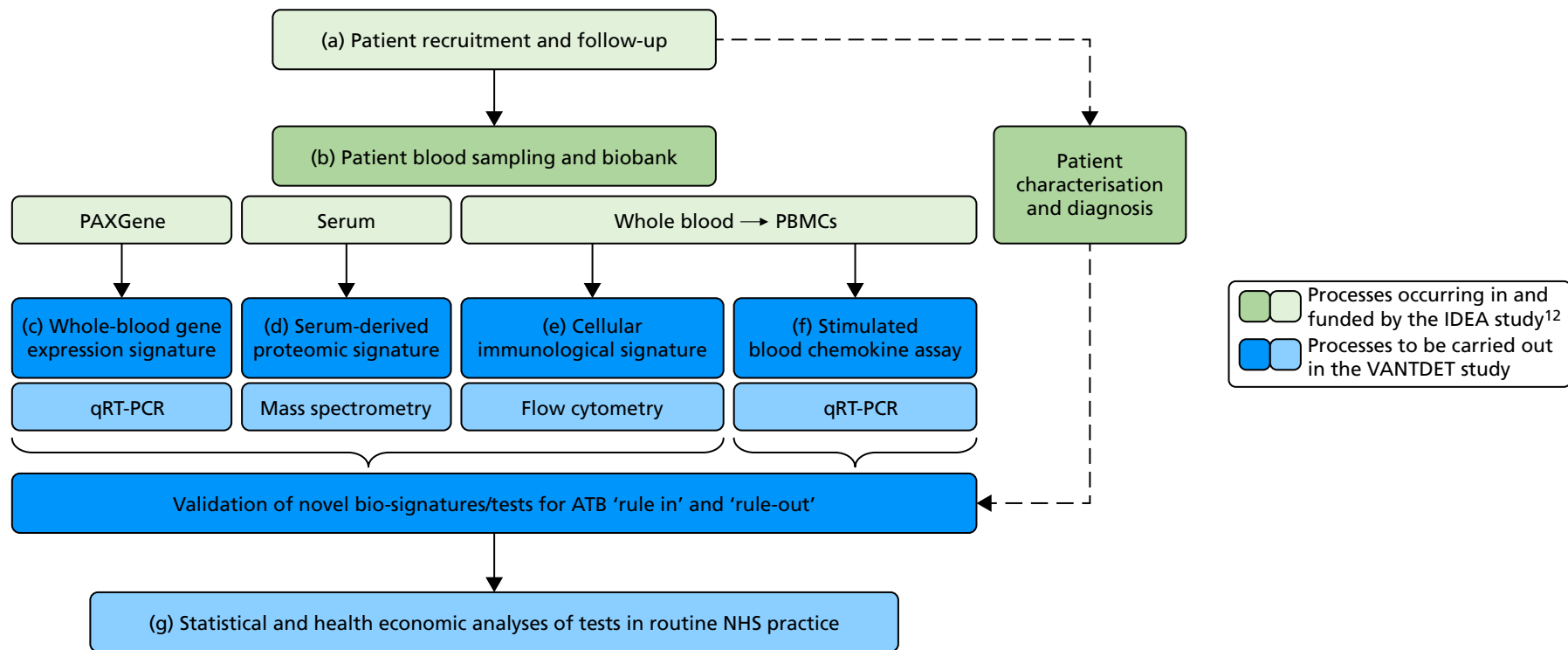
#### General management and task allocation

The VANTDET study required a relatively simple management structure and a less rigorous monitoring process because there was no patient recruitment. The chief investigator (AL) and interim chief investigator (PB led the project from May 2015 to May 2016) provided general oversight of the study. Each of the four subprojects was managed by a laboratory scientist [three research associates (AH, LH and RP) and a laboratory technician (MTW)], who all worked within the TB research centre laboratory at St Mary's Campus, Imperial College London. Data processing and analysis support was provided by a bioinformatician (PJ), and laboratory and analytical support was provided by a research MSc student/technician (TM) and other TB research group members (AB, VM and AF). These individuals constituted the main research team. The SELDI-TOF proteomic validation work was performed by a research associate (SH) and was overseen by a co-investigator (ML) and the chief investigator (AL). A research associate (NG) and co-investigator (PW) in the Department of Infection Disease Epidemiology (also based at the St Mary's Campus in Imperial College London) were responsible for the health economic analysis that was done at the end of the project and involved discussion with the main research team. Medical statisticians (YT and JD) provided advice on study design, cohort selection, analytical protocols and presentation of data.

#### Management and oversight meetings

##### Study Management Group

The Study Management Group (SMG) included the chief investigators, post-doctoral research associates and technicians. The SMG met regularly (at least fortnightly in laboratory meetings), to report on progress, share/discuss results, discuss methodology, etc.



**FIGURE 1** Proposed VANTDET study design and link with the IDEA study. ATB, active tuberculosis.

## Wider Study Management Group

The wider SMG consisted of members of the SMG and statisticians from the University of Birmingham: Dr Yemisi Takwoingi and Dr Jon Deeks. The group met three times (22 September 2015, 3 February 2016 and 18 May 2016) to discuss the statistical approaches taken for each of the objectives/substudies and established the need for an Independent Scientific Advisory Board (ISAB).

## Independent Scientific Advisory Board

The ISAB consisted of three independent members: Professor Sanjeev Krishna, Dr Mahdad Noursadeghi and Dr David Connell. The ISAB and SMG met once (15 July 2016) to discuss overall study design and research plans for each objective.

## Issues and problems

The SELDI-TOF arrays required to validate the SELDI-TOF signatures were discontinued by the manufacturer. Initially, an alternative supplier was sought, but unfortunately was not found. Hence, this platform will not be available for future diagnostic tests. We are performing an analysis using the remaining stock from the manufacture ( $n = 90$ ) and are performing liquid chromatography–mass spectrometry (LC–MS) to identify serum biomarkers and will develop enzyme-linked immunosorbent assay (ELISA) tests.

## Changes to study protocol and management plan

The study protocol and management plan documents were changed once, in October 2016. The comments below are taken from the progress report that followed the updates in March 2017.

## Protocol

The changes included updated methods for the validation of cellular immunological signatures and candidate rule-out tests for active TB, based on new literature and results from the IDEA study. Furthermore, there were changes in the sample size for both the cellular immune signature validation and the proteomic signature validation.

## Cellular immune signature validation

Additional cellular immune signatures identified since conception of the VANTDET study and protocol also show promise in their ability to discriminate between active TB and LTBI. These new signatures were tested in-house in preliminary experiments, before the laboratory was protocol updated, and optimised so that these additional signatures could be identified within the flow cytometry panel we used on the cohort. These signatures included those which measure the proportion of *Mtb*-specific cluster of differentiation 4 (CD4)<sup>+</sup> IFN $\gamma$ <sup>+</sup> cells with an activation phenotype<sup>26</sup> or the levels of cluster of differentiation 27 (CD27) as a ratio or in combination with CD45RA expression.<sup>27,28</sup>

## Candidate 'rule-out' tests

In a draft final report, the IDEA study identified that the use of four antigens [6-kDa early secretory antigenic target (ESAT-6), culture filtrate antigen (CFP-10), Rv3615c and Rv3879c (ECRR)] combined in the T-SPOT.*TB* assay provided the highest sensitivity for active TB.<sup>12</sup> Use of all four of these antigens was therefore included in the assay for validation of a rule-out test for TB.

## Study population and sample sizes

### Proteomic signature

For the proteomics experiments, samples were chosen at random from the IDEA study cohort (HIV–) and the first 90 were analysed using both SELDI-TOF and LC–MS, techniques, with the sensitivity and specificity of signatures compared with the landmark studies. The Hamilton and Levin unpublished SELDI-TOF signature (Hamilton MS and Levin M, Imperial College London, London, UK, 2016–18) is currently being adapted into an ELISA-based test; should the SELDI-TOF signature be validated in the IDEA study cohort ( $n = 90$ , sensitivity > 85%), we planned to validate the ELISA test on the entire IDEA (HIV–/+ ) study cohort



to provide confidence intervals (CIs) < 5% for active TB compared with other disease (OD). For LC–MS, a total of 200 samples (HIV–/+) were analysed and this data set was used to explore the diagnostic performance of both previously identified and novel protein markers.

### Cellular immunological signature

Using a nested case–control approach, 82 active TB patients were randomly selected (but enriched for those with HIV infection), to add to the approximately 82 LTBI patients, to provide a final cohort of 164 individuals. Although smaller than the ideal sample size, this will still be more than sufficient to provide enough power to demonstrate 95% sensitivity and specificity.

### Molecular rule-out test

In order for the molecular test to be used to rule out TB, it must have extremely high sensitivity and, therefore, must provide a positive result for those individuals who are infected with *Mtb* but who fail to test positive in the most sensitive of the currently available tests for *Mtb* infection (the T-SPOT.*TB*). We therefore selected an initial cohort of 100 individuals recruited into the IDEA study, selected at random, but conforming to the following criteria: 25 individuals with active TB and a positive T-SPOT.*TB* result; 25 individuals with active TB and a negative T-SPOT.*TB* result; 25 individuals with ODs with a positive T-SPOT.*TB* result; and 25 individuals with a negative T-SPOT.*TB* result. The new protocol stipulated that, once this initial cohort was tested using the molecular rule-out test, the results would be analysed to test the performance of the assay in ruling out active TB. If the results were promising (i.e. > 95% sensitivity is demonstrated), we would continue to assay the rest of the available PBMC samples from the IDEA study cohort, in order to maximise the confidence of our findings. However, in the event of obtaining less promising results, the full cohort of PBMCs would not be analysed.

### Management plan

An updated management plan that reflected the changes in timelines, sample sizes, protocols and experimental approaches was submitted to the NIHR Efficacy and Mechanism Evaluation board in October 2016. The new end-of-study date of 31 December 2017 was agreed. No further changes to the management plan were made during the course of the project.

### Study cohorts

Although the focus of this study project was to evaluate all four novel technologies in the diagnostic evaluation of all TB, each required a slightly different approach to selecting a final study cohort from the full IDEA study cohort. The details of the inclusion criteria are presented in each substudy chapter. The inclusion criteria, as well as the sample size calculations, were agreed by the study oversight groups and the ISAB.

### The IDEA study cohort and biobank

The IDEA study cohort is described in detail in the IDEA Health Technology Assessment report<sup>12</sup> and recent manuscript.<sup>14</sup> In summary, 1060 adults (aged  $\geq 16$  years) with suspected active TB were prospectively recruited to 12 NHS hospital sites in London, Slough, Oxford, Leicester and Birmingham. Because the proportion of HIV+ patients recruited within the main study cohort of active TB suspects was low, an extended study was performed to increase the number of HIV+ patients. The HIV infection rate in the full cohort was 22.9%, but in the main study it was 16%.

In the main cohort, 845 individuals were included in the final analysis. Of these, 363 (43%) had active TB, of which 261 cases (72%) were confirmed by culture. This represents the rate of TB in the full cohort of TB suspects recruited in the IDEA study, a population that is reflective of all TB suspects in areas with high TB rates in England. TB was excluded in 52% of patients and the remaining 5.1% were clinically indeterminate. For a more detailed description of the full IDEA study cohort, including demographic and clinical characteristics, please refer to the publications and reports from this study.<sup>12</sup>

### Reference standard

For the validation of signatures for the detection of active TB, a composite reference standard was used, the Dosanjh categorisation,<sup>11</sup> by which patients are divided into four possible groups: definite TB, highly probable TB, clinically indeterminate and non-TB (Table 2). Importantly, this allows for inclusion of the full spectrum of TB cases, including those lacking microbiological confirmation (Dosanjh category 2).

Categorisation of patients was performed by a clinical panel of four respiratory medicine and infectious disease clinicians specialising in TB. These clinicians had access to anonymised diagnostic and follow-up (up to 12 months post recruitment) clinical details for each patient, including response to treatment, while remaining blind to final IGRA results, as outlined in the IDEA study protocol. It should be noted that not all individuals in Dosanjh category 2 were culture negative; some individuals did not have a culture test done or the test failed. This group should therefore be considered as 'culture unconfirmed' rather than 'culture negative', given that, for active TB to be excluded, a definitive diagnosis of another condition is required. Therefore, in this report, we refer to the 'active TB excluded' group (i.e. Dosanjh category 4) as OD.

### Patient groups used for main and subgroup analyses

The primary analysis for determining test accuracies and other diagnostic accuracy parameters of previously described tests/signatures was to assess their performance in detecting all TB (i.e. Dosanjh categories 1 and 2 combined), against all OD within each cohort. Given the uncertainty over the correct final diagnosis of those who were categorised as 'clinically indeterminate' (Dosanjh category 3) by the clinical panel in the IDEA study, these patients have been excluded from each of the VANTDET substudies (as was the case with the IDEA study).

**TABLE 2** Dosanjh categorisation for the diagnosis of active TB suspects, as from Dosanjh *et al.*<sup>11</sup>

Diagnostic category	Criteria
1: Culture-confirmed TB	Microbiological culture of <i>Mtb</i> AND suggestive clinical and radiological findings
2: Highly probable TB	Clinical and radiological features highly suggestive of TB unlikely to be caused by OD AND a decision to treat made by a clinician AND appropriate response to therapy AND histological support if available
3: Clinically indeterminate	Final diagnosis of TB neither highly probable nor reliably excluded
4: Active TB excluded: subclassification	
4A: inactive TB	History of prior episode OR stable CXR changes AND TST positive <sup>a</sup> (if done) AND bacteriologically negative (if done) AND no clinical evidence of active disease
4B: one or more risk factors for TB exposure, <sup>b</sup> TST positive <sup>a</sup>	TST positive <sup>a</sup> AND bacteriologically negative (if done) AND no clinical evidence of active disease
4C: one or more risk factors for TB exposure, <sup>b</sup> TST negative <sup>a</sup>	History of TB exposure AND TST negative (if done)
4D: no risk factors for TB exposure, <sup>b</sup> TST negative	No history of TB exposure AND TST negative (if done)

CXR, chest radiography.

a A TST using the Mantoux test with a threshold of  $\geq 15$  mm was considered positive.

b Risk factors for TB exposure: recent exposure to active TB patient, born in country of high prevalence or belonging to an ethnic group with a high prevalence of TB (Incidence  $> 100/100,000$ , Rose *et al.*<sup>29</sup>).

Table from the *Annals of Internal Medicine*, Dosanjh DP, *et al.*,<sup>11</sup> improved diagnostic evaluation of suspected tuberculosis, Volume no. 148, Issue no. 5, pages 325–36. © 2008 American College of Physicians. All Rights Reserved. Reprinted with modifications, with the permission of American College of Physicians, Inc.

In each substudy (with the exception of the candidate rule-out tests), subgroup analyses were also performed, which included determining diagnostic performance for detecting either culture-confirmed (Dosanjh category 1) or highly probable (Dosanjh category 2) TB, as well as for either PTB or EPTB. In these cases, the PTB group included individuals who had pulmonary involvement as well as those who had pulmonary and extrapulmonary involvement. Those with extrapulmonary involvement only were classified as EPTB.

### Prevalence data

Within this report, we have calculated prevalence values for active TB groups in various parent populations using the data from the final IDEA study [both the 'main study' and the 'HIV cohort',<sup>12</sup> without exclusion of the 'clinically indeterminate' population (Dosanjh category 3)]. The prevalence values are given in *Appendices 1 and 2* (see *Table 23*).

## Patient and public engagement and involvement

The TB research centre where the laboratory team of the VANTDET study is based is associated with the Health Protection Research Unit (HPRU) in Respiratory Infections, and both are led by the VANTDET study's chief investigator, Professor Ajit Lalvani. The HPRU conducts an extensive patient and public involvement (PPI) and engagement programme, which has been recognised within the Imperial College London as an exemplar of good practice (see our case studies in the Imperial Patient Experience Research Centre<sup>30,31</sup>). The TB research centre team, including the VANTDET study researchers AH, MTW, LH, TM and RP, are frequently requested to run public engagement events.

For the IDEA study, Ms Nisha Karnani (a lay member) was appointed as the patient representative for the duration of the study. She was consulted at key points during the study and was invited to Study Steering Committee meetings and the IDEA study presentation at the end of the study.

The HPRU conducts quarterly symposium series, in which the VANTDET study team has disseminated and discussed project findings to a wide audience, including the HPRU in Respiratory Infections, the ISAB, patient representatives, collaborators and colleagues. Members of the management board have an excellent track record in active engagement with patients and public:

- Professor Ajit Lalvani was a key member on the panel at the Engagement to End TB event at the University of East London. This was part of the Voices for London Festival, which was attended by community members of East London.
- The VANTDET study team has participated in several public engagement events to showcase the TB research we are involved in. We also, along with other TB research centre members, received specific public engagement funding to develop and evaluate an animation film and LTBI diagnostics and treatment. This film was evaluated with screening and focus groups events for community groups, members of the public and other institutions involved in public engagement. These included the Imperial Festival (May 2017), Bromley by Bow Unity Festival (East London, July 2017), screening of the LTBI film at the Midaye Somali Women's Group (White City, December 2017) and Let's Talk about Tuberculosis (White City, December 2017).

The team has also published their research work in various online articles for a wider public audience:

- *Tuberculosis in England: How Research at Imperial is Supporting the National Strategy.*<sup>32</sup>
- *Increasing Awareness About Latent Tuberculosis Infection.*<sup>33</sup>
- *Multilingual White City Residents Help Imperial Raise Awareness of TB Research.*<sup>34</sup>
- *Case Study #6: Evaluating a TB Awareness Animation.*<sup>35</sup>

The HPRU in Respiratory Infections and TB research centre have established their first patient and public panel that comprises seven members of the public directly or indirectly affected by, or interested in, our research areas and both with and without previous experience of PPI. The role of the panel is to support the delivery of effective PPI and engagement approaches and activities within the HPRU. The panel advises on different PPI avenues available for disseminating our findings (e.g. charity/voluntary organisation websites and blogs), and also help to distribute findings within their informal networks.

### **Statistical analysis and presentation of data**

For statistical analyses, R software (version 3.4.2; The R Foundation for Statistical Computing, Vienna, Austria) or Prism (version 7.04; GraphPad Software Inc., CA, USA) was used as indicated in the *Methods* sections of *Chapters 3–6*. For all technologies and data sets, the outcome of signature performance was presented in a dot plot, box-and-whisker plot and/or a receiver operating characteristic (ROC) curve, all generated using Prism software. ROC curve analysis was used to estimate diagnostic accuracy.

### **Blinding**

All individuals carrying out experiments and determining index test results were blind to clinical data, reference standard results and all other patient-specific information. Only study ID was known.

### **Defining the cut-off points**

In each substudy, multiple methods for defining test cut-off points were used, depending on the proposed use of the test. For those tests being assessed as rule-in tests, specificity was set at > 90%. For those being assessed as rule-out tests, sensitivity was set at > 95%. For a balanced approach, either the cut-off point with the optimal Youden value was given (for transcriptomic and proteomic tests) or, for the cellular immune signatures, the cut-off point in which sensitivity was equal to specificity was used (in line with standard practice in the respective field of study).



# Chapter 3 Transcriptomics

## Introduction

Several studies have demonstrated that whole-blood gene expression profiles have the potential to be used for diagnostic tests for active TB, in adults and children. In 2010, Berry *et al.*<sup>18</sup> demonstrated that differential transcriptional patterns in peripheral blood can be harnessed to differentiate TB from other conditions and a whole-blood 86-transcript signature distinguished active TB from other inflammatory and infectious diseases. A major milestone was reached by a study that showed that a 44-blood transcript signature was able to differentiate active TB from ODs using a cohort from a high-burden setting.<sup>20</sup> Anderson *et al.*<sup>36</sup> used a similar approach to identify a 51-gene signature that could distinguish TB from ODs in a cohort of children, all of whom had suspected TB at recruitment. This study has particular strengths in the approach to study design, as highly probable TB cases were also included and the OD group included a wide variety of differential diagnoses that present in a real-life clinical setting. Such a study in adults has yet to be used for validation of transcriptomic signatures for TB diagnosis. Maertzdorf *et al.*<sup>37</sup> identified a four-gene signature (guanylate-binding protein 1, inhibitor of DNA binding 3, interferon-induced transmembrane protein 3 and purinergic receptor, *P2RY14*) that distinguished subjects with active TB from healthy controls (HCs) and those with LTBI with high accuracy. Similarly, a combination of four genes [cluster of differentiation 177 (CD177), Charcot–Leyden crystal galectin, haptoglobin (HP) and immunoglobulin J chain] was identified using support vector machine learning (SVML) and was shown to accurately classify active TB (including EPTB) from non-TB febrile patients.<sup>38</sup>

Most recently, Sweeney *et al.*<sup>39</sup> used a meta-analysis approach to derive a TB risk score from three genes (dual-specificity phosphatase 3, guanylate-binding protein 5 and Krüppel-like factor 2), which was able to distinguish active TB from ODs with high accuracy. The important characteristics and diagnostic classification of TB are summarised in *Table 29* for the five studies and the meta-analysis.

The aim of this substudy is to define the role of previously identified whole-blood gene-expression signatures in the diagnostic evaluation of active TB using host transcriptomic microarray.

## Methods

### Inclusion criteria

The inclusion criteria were definite diagnosis of either active TB (Dosanjh categories 1 or 2) or OD (Dosanjh category 4); consent given for genetic analysis; and PAXGene sample available. Those with a clinically indeterminate diagnosis (Dosanjh category 3) were excluded. Among HIV+ participants in the IDEA study, all active TB cases were selected and a similar number of participants with ODs were randomly selected for the microarray assay analysis.

### Ribonucleic acid extraction and quality control

For whole-blood ribonucleic acid (RNA), 2.5 ml of blood was collected into PAXGene tubes and was frozen at  $-80^{\circ}\text{C}$  as part of the IDEA study protocol.<sup>12</sup> RNA was extracted from PAXGene tube samples using the PAXGene Blood RNA Kit (PreAnalytiX, Hombrechtikon, Switzerland), in accordance with the manufacturer's instructions. RNA quality control (QC) was performed using both the NanoDrop 8000 (Thermo Fisher Scientific, Waltham, MA, USA) and the Agilent 2100 Bioanalyzer (Agilent, CA, USA) instruments.

### Whole genome-wide microarray

Illumina gene expression microarray platforms were used in this study (Illumina, San Diego, CA, USA). The detailed protocol has been published.<sup>40</sup> Briefly, a total of 100 ng of RNA in 11  $\mu\text{l}$  of ribonuclease

(RNase)-free water was used for synthesising first-strand complementary deoxyribonucleic acid (cDNA), using a master mix containing 1 µl of T7 oligo(dT) primer, 2 µl of 10× first-strand buffer, 4 µl of deoxyribonucleotide triphosphate mix, 1 µl of RNase inhibitor and 1 µl of ArrayScript. Next, a second-strand cDNA was synthesised using 80 µl of master mix (i.e. 63 µl of nuclease-free water, 10 µl of 10× second-strand buffer, 4 µl of deoxyribonucleotide triphosphate mix, 2 µl of DNA polymerase and 1 µl of RNase H). After purification, 17.5 µl of cDNA was in vitro transcribed to synthesise antisense RNA using an in vitro transcription master mix (i.e. 2.5 µl of T7 10 × reaction buffer, 2.5 µl of T7 enzyme mix and 2.5 µl of biotin-NTP mix). Next, a total of 750 ng of complementary RNA was used for array hybridisation to the Illumina Human HT12-v4 beadchips (Illumina, San Diego, CA, USA), in accordance with the manufacturer's protocol. Finally, the beadchip was scanned on the Illumina BeadArray Reader (Illumina, San Diego, CA, USA). The gene expression data were extracted from images collected from Illumina BeadArray Reader.

### **Microarray quality control and normalisation**

A raw probe intensity signal for approximately 47,000 transcripts was acquired from the arrays using Beadstudio software (Illumina, San Diego, CA, USA) and normalised using the Lumi R package (Bioconductor, WA, USA).<sup>41</sup> First, the raw data were  $\log_2$ -transformed using lumi.T function, and robust spline normalisation was applied using lumi.N.<sup>42</sup> Next, transcripts that were not expressed in any samples (Illumina detection  $p$ -value > 0.01) were removed from further analysis. Finally, principal component analysis was used to remove outliers.

### **Statistical analysis**

#### **Calculation of signatures scores**

Those published signatures for which the gene expression levels of selected target genes were combined to give a score were calculated as previously described.<sup>20,36,39</sup>

#### **Linear discriminant analysis**

Linear discriminant analysis (LDA) is a supervised classification approach. It was used to model the linear combination of candidate transcripts from previously reported signatures as a function of sample type (i.e. TB or OD). LDA is based on the assumptions of multivariate normal distribution of the explanatory variables (candidate transcripts) and these variables have the same covariance matrix for classification categories (sample types) considered.

#### **Testing trained models**

For the Roe *et al.*<sup>38</sup> signature, the original trained support vector machine model was available. Therefore, classification performance of this model was assessed, in addition to the leave-one-out LDA model on the full cohort, and performance was reported. Support vector machine is a machine-learning algorithm that used preselected variables to perform a binary classification of input samples; in our case two classes were active, TB and OD.

#### **Receiver operating characteristic curve analysis and defining cut-off points**

Test values (i.e. score, probability or otherwise) for the different signatures in diagnostic evaluation of the key patient groups were assessed for discriminatory ability using ROC analysis, performed using either Prism or R software. Three alternative approaches were used for selecting the cut-off point. To prioritise sensitivity, the cut-off point providing > 95% was given and, to prioritise specificity, the cut-off point providing > 90% specificity was given. To optimise both sensitivity and specificity, the maximum Youden index (i.e. sensitivity + specificity – 1) was used to select the cut-off point.<sup>43</sup>

#### **Calculation of predictive values**

To determine the predictive value of tests in given populations in which TB prevalence is known (or assumed), we calculated the positive predictive value (PPV) and negative predictive value (NPV).

## Results

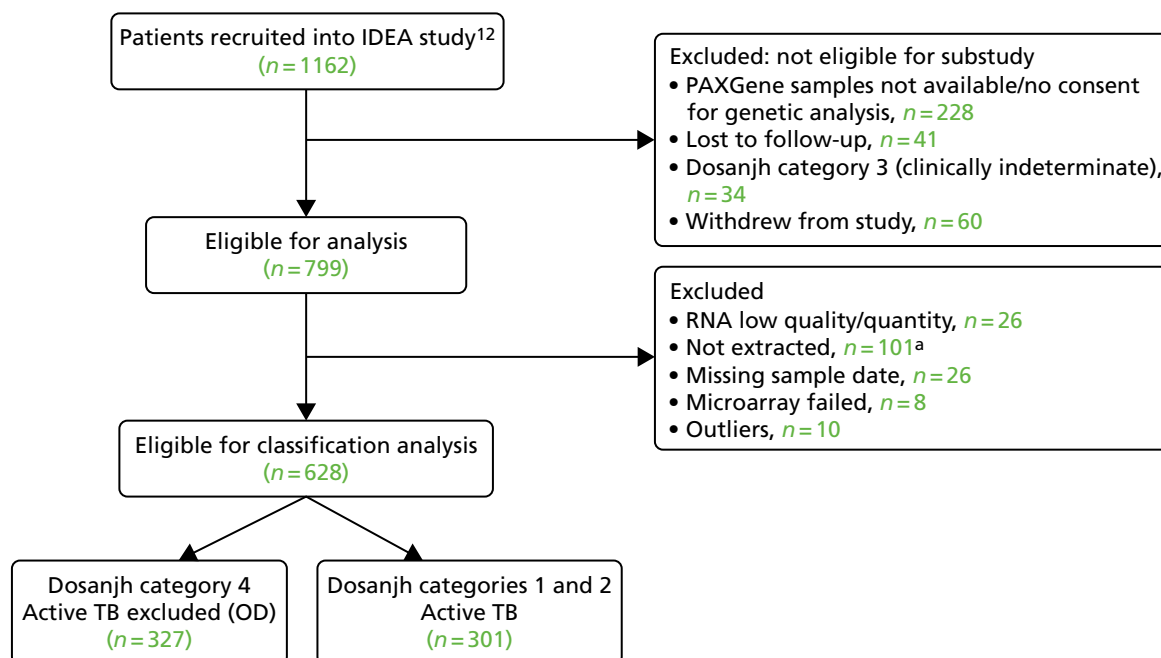
### Final cohort

The study flow chart in *Figure 2* shows the final cohort selected from the total IDEA study cohort. In the IDEA study, 288 patients did not give consent for a PAXGene sample to be taken or for genetic analysis. Of the 799 patients who were eligible for the transcriptomic substudy, 628 patients were selected for RNA extraction, had sufficient RNA, were used in microarray analysis and had passed the RNA and microarray QC checks.

The main demographic characteristics of the transcriptomics validation cohort are presented in *Table 3*. Of all TB cases included, 29.6% were culture unconfirmed (highly probable TB/Dosanjh category 2), which reflects the proportion of this group in the full IDEA study cohort of TB patients (in which 28.1% of TB cases were highly probable). As in the overall IDEA study cohort, significant differences were observed between patients groups, with TB patients being younger, weighing less and having lower body mass index (BMI), and more likely to be of Indian subcontinent ethnicity (includes Indian, Bangladeshi, Pakistani and Sri Lankan).

The main clinical features of the transcriptomic signatures validation cohort are presented in *Table 4*. There was a higher proportion of HIV+ individuals in the highly probable TB group than in the culture-confirmed TB and OD groups. Because the number of HIV+ OD cases was higher in the overall IDEA study cohort, the HIV+ rate we reported within this subcohort does not reflect the parent population. However, all HIV+ TB patients were included. The higher proportion of HIV-infected individuals in the highly probable TB group than in the culture-confirmed TB group reflects the comparatively paucibacillary nature of active TB and HIV co-infected cases.

The distribution of type and severity of TB, and distribution of alternative diagnoses in the OD group, are presented in *Appendix 1*.



**FIGURE 2** Study flow chart for validation of transcriptomics signatures. a, 101 samples from OD patients who were HIV+ were excluded. From the full cohort of 1162 patients recruited into the IDEA study, 628 were selected for RNA extraction. Of note, the rate of active TB among the HIV+ cohort of patients in IDEA study was low ( $\approx 14\%$ ). Therefore, all of the eligible HIV+ active TB cases ( $n = 20$ ) were selected for cohort inclusion, with a similar number of HIV+ OD participants ( $n = 25$ ) randomly selected from the 146 HIV+ participants available.



**TABLE 3** Demographic characteristics of transcriptomic validation cohort ( $n = 628$ ) of patients selected from the IDEA study cohort

Demographic characteristic	Culture-confirmed TB (Dosanjh category 1) ( $N = 212$ )	Highly probable TB (Dosanjh category 2) ( $N = 89$ )	OD (Dosanjh category 4) ( $N = 327$ )	$p$ -value overall <sup>a</sup>
Age (years), median (range)	32.0 (16.0–81.0)	36.0 (18.0–76.0)	43.0 (17.0–87.0)	< 0.001
Male, $n$ (%)	149 (70.3)	45 (50.6)	189 (57.8)	0.001
Ethnic origin, $n$ (%)				< 0.001
Asian	12 (5.66)	3 (3.37)	12 (3.67)	
Black	36 (17.00)	17 (19.10)	62 (19.00)	
Hispanic	1 (0.47)	0 (0.00)	1 (0.31)	
Indian subcontinent	139 (65.60)	61 (68.50)	150 (45.90)	
Middle Eastern	3 (1.42)	0 (0.00)	11 (3.36)	
Mixed	2 (0.94)	0 (0.00)	7 (2.14)	
Unable/unwilling to respond	0 (0.00)	0 (0.00)	1 (0.31)	
White	19 (8.96)	8 (8.99)	83 (25.4)	
Height (m), median (range)	1.69 (1.37–1.96)	1.67 (1.47–1.98)	1.70 (1.32–1.96)	0.305
Height missing, $n$ (%)	94 (44.3)	33 (37.1)	106 (32.4)	
Weight (kg), median (range)	63.1 (34.7–1270)	63.0 (40.4–1160)	68.7 (41.4–1400)	< 0.001
Weight missing, $n$ (%)	6 (2.8)	4 (4.5)	24 (7.3)	
BMI (kg/m <sup>2</sup> ), median (range)	22.6 (15.7–48.5)	22.5 (15.6–42.2)	24.4 (14.8–47.2)	0.005
BMI missing, $n$ (%)	96 (45.3)	36 (40.4)	114 (34.9)	

<sup>a</sup> Where the data were categorical, a chi-squared test was used to compare characteristics between groups; where the data were continuous, the groups were compared using a Kruskal–Wallis test. The full cohort is divided into the three diagnostic categories as outlined in the Dosanjh reference standard [i.e. culture-confirmed TB, highly probable TB and active TB excluded (referred to here as ‘OD’)].

**TABLE 4** Clinical characteristics of transcriptomics validation cohort, stratified by patient final diagnosis

Clinical characteristic	Culture-confirmed TB (Dosanjh category 1) ( $N = 212$ )	Highly probable TB (Dosanjh category 2) ( $N = 89$ )	OD (Dosanjh category 4) ( $N = 327$ )	$p$ -value overall <sup>a</sup>
Clinical setting, $n$ (%)				0.74
Unknown	1 (0.47)	1 (1.12)	1 (0.31)	
Inpatient	68 (32.1)	31 (34.8)	103 (31.5)	
Outpatient	143 (67.5)	57 (64.0)	223 (68.2)	
BCG vaccinated yes, $n$ (%)	126 (59.4)	46 (51.7)	191 (58.4)	0.439
BCG scar visible, $n$ (%)				0.632
Missing	49 (23.1)	19 (21.3)	75 (22.9)	
No	13 (6.13)	4 (4.49)	16 (4.89)	
Unsure	10 (4.72)	8 (8.99)	30 (9.17)	
Yes	140 (66.0)	58 (65.2)	206 (63.0)	
HIV+, $n$ (%)	9 (4.2)	11 (12.4)	25 (7.6)	0.04
TB contact no, $n$ (%)	160 (75.5)	72 (80.9)	257 (78.6)	0.527

<sup>a</sup> Where the data were categorical, a chi-squared test was used to compare characteristics between groups; where the data were continuous, the groups were compared using a Kruskal–Wallis test.

### Diagnostic accuracy analysis

There were no missing data for any of the genes for the validation of published signatures.

### Performance of 'score'-based signatures in diagnosing active tuberculosis

Three of the published signatures presented a score [referred to in the publications as either disease risk score (DRS) or tuberculosis score (TBS), as previously described<sup>20,36,39</sup>], which is calculated using the expression levels of signature genes. We were able to apply the same score-based approach to testing these gene signatures within the signatures in our cohort. Cross-tabulation of the score value distributions against diagnostic categories according to the reference standard (Dosanjh criteria) is shown in *Table 26* in *Appendix 3*.

### Analysis of performance of score-based signatures in the full cohort

The distribution of score values in TB and OD cases in the overall cohort, as well as within either the HIV+ or HIV- cohort, is shown in *Figure 16* in *Appendix 3* (the ROC curves showing diagnostic performance are also shown).

The TB group had significantly higher score values than the OD group for all three signatures when assessed within the full transcriptomic cohort, with the difference being lowest for the Anderson *et al.*<sup>36</sup> DRS. The Kaforou *et al.*<sup>20</sup> 44-gene signature and the Sweeney *et al.*<sup>39</sup> three-gene signature performed comparably, and both performed better than the Anderson *et al.*<sup>36</sup> signature in the overall and HIV+ cohorts, with area under the curve (AUC) values between 0.82 (95% CI 0.78 to 0.85) and 0.84 (95% CI 0.80 to 0.86).

Interestingly, although the scores were all significantly higher in the TB groups than in the OD group within the HIV- population, there were no significant differences between scores in these groups within the HIV+ population (*Table 5* and *Figure 16c* in *Appendix 3*). This was reflected in a poor diagnostic performance (AUC = 0.50–0.69) for all three signatures in the HIV+ population, and the observation that, when the HIV+ population was excluded from the overall cohort, the AUC for each signature improved slightly (see *Table 5*).

**TABLE 5** Performance of published gene expression score signatures in full cohort, stratified by HIV infection status

Signature (reference)	HIV	TB (n)	OD (n)	AUC, % (95% CI)	Cut-off point	Sensitivity, % (95% CI)	Specificity, % (95% CI)	PPV	NPV
DRS (Anderson <i>et al.</i> <sup>36</sup> )	–	281	302	0.70 (0.66 to 0.75)	> 86.0 <sup>a</sup>	95.0 (91.8 to 97.3)	23.8 (19.2 to 29.1)	0.48	0.86
					> 100.6 <sup>b</sup>	30.3 (24.9 to 36.0)	90.0 (86.1 to 93.2)	0.70	0.63
					> 91.4 <sup>c</sup>	75.4 (70.0 to 80.4)	53.6 (47.8 to 59.4)	0.55	0.74
	+	20	25	0.50 (0.33 to 0.68)	< 105.6 <sup>a</sup>	95.0 (75.1 to 99.9)	8.0 (0.98 to 26.0)	0.44	0.68
					< 84.2 <sup>b</sup>	5.0 (0.13 to 24.9)	92.0 (74.0 to 99.0)	0.32	0.56
					> 97.9 <sup>c</sup>	70.0 (45.7 to 88.1)	44.0 (24.4 to 65.0)	0.49	0.66
	–/+	301	327	0.68 (0.64 to 0.72)	> 86.0 <sup>a</sup>	95.0 (91.9 to 97.2)	22.9 (18.5 to 27.9)	0.48	0.86
					> 100.8 <sup>b</sup>	28.2 (23.2 to 33.7)	90.2 (86.5 to 93.2)	0.68	0.62
					> 91.4 <sup>c</sup>	75.4 (70.2 to 80.2)	52.0 (46.4 to 57.5)	0.54	0.74

continued

**TABLE 5** Performance of published gene expression score signatures in full cohort, stratified by HIV infection status (continued)

Signature (reference)	HIV	TB (n)	OD (n)	AUC, % (95% CI)	Cut-off point	Sensitivity, % (95% CI)	Specificity, % (95% CI)	PPV	NPV				
DRS (Kaforou <i>et al.</i> <sup>20</sup> )	-	281	302	0.83 (0.79 to 0.86)	> 101.1 <sup>a</sup>	95.0 (91.8 to 97.3)	32.8 (27.5 to 38.3)	0.52	0.90				
					> 113.4 <sup>b</sup>	57.0 (51.0 to 62.8)	90.4 (86.5 to 93.5)	0.82	0.74				
					> 108.6 <sup>c</sup>	74.7 (69.2 to 79.7)	78.8 (73.8 to 83.3)	0.73	0.81				
	+	20	25	0.69 (0.53 to 0.85)	> 104.3 <sup>a</sup>	95.0 (75.1 to 99.9)	36.0 (18 to 57.5)	0.53	0.91				
					> 124.2 <sup>b</sup>	35.0 (15.4 to 59.2)	92.0 (74.0 to 99.0)	0.77	0.65				
					> 120.2 <sup>d</sup>	45.0 (23.0 to 68.5)	88.0 (68.8 to 97.5)	0.74	0.68				
					> 113.2 <sup>d</sup>	65.0 (40.8 to 84.6)	68.0 (46.5 to 85.05)	0.61	0.72				
					-/+	301	327	0.82 (0.78 to 0.85)	> 101.1 <sup>a</sup>	95.0 (91.9 to 97.2)	31.8 (26.8 to 37.2)	0.51	0.89
									> 114.7 <sup>b</sup>	53.2 (47.4 to 58.9)	90.2 (86.5 to 93.2)	0.80	0.72
> 108.6 <sup>c</sup>	74.4 (69.1 to 79.3)	76.8 (71.8 to 81.2)	0.71	0.80									
TBS (Sweeney <i>et al.</i> <sup>39</sup> )	-	281	302	0.84 (0.81 to 0.87)	> -4.05 <sup>a</sup>	95.0 (91.8 to 97.3)	34.4 (29.1 to 40.1)	0.52	0.90				
					> -2.60 <sup>b</sup>	56.2 (50.2 to 62.1)	90.0 (86.1 to 93.2)	0.81	0.7				
					> -3.2 <sup>c</sup>	79.4 (74.2 to 83.9)	76.8 (71.7 to 81.5)	0.72	0.83				
	+	20	25	0.64 (0.47 to 0.81)	> -4.51 <sup>a</sup>	95.0 (75.1 to 99.9)	0.0 (0.0 to 13.7)	0.42	0				
					> -1.69 <sup>b</sup>	15.0 (3.2 to 37.9)	92.0 (74.0 to 99.0)	0.59	0.59				
					> -2.49 <sup>c</sup>	55.0 (31.5 to 76.9)	80.0 (59.3 to 93.1)	0.67	0.70				
	-/+	301	327	0.83 (0.80 to 0.86)	> -4.1 <sup>a</sup>	95.0 (91.9 to 97.2)	29.4 (24.5 to 34.6)	0.50	0.89				
					> -2.5 <sup>b</sup>	55.2 (49.3 to 60.9)	90.2 (86.5 to 93.2)	0.81	0.73				
					> -3.2 <sup>c</sup>	78.4 (73.3 to 82.9)	75.5 (70.5 to 80.1)	0.71	0.83				

-, negative; +/-, negative and positive; +, positive.

a To provide sensitivity > 95%.

b To provide specificity > 90%.

c To provide the optimal Youden index.

d When two cut-off values gave the optimal Youden index, both are given.

The full diagnostic performance of the 'score'-based signatures in full, HIV+ and HIV- populations is also presented in *Table 5*, including a range of sensitivity and specificity values selected by varying the cut-off values for each score-based test based on predefined criteria. The PPVs and NPVs are also given.

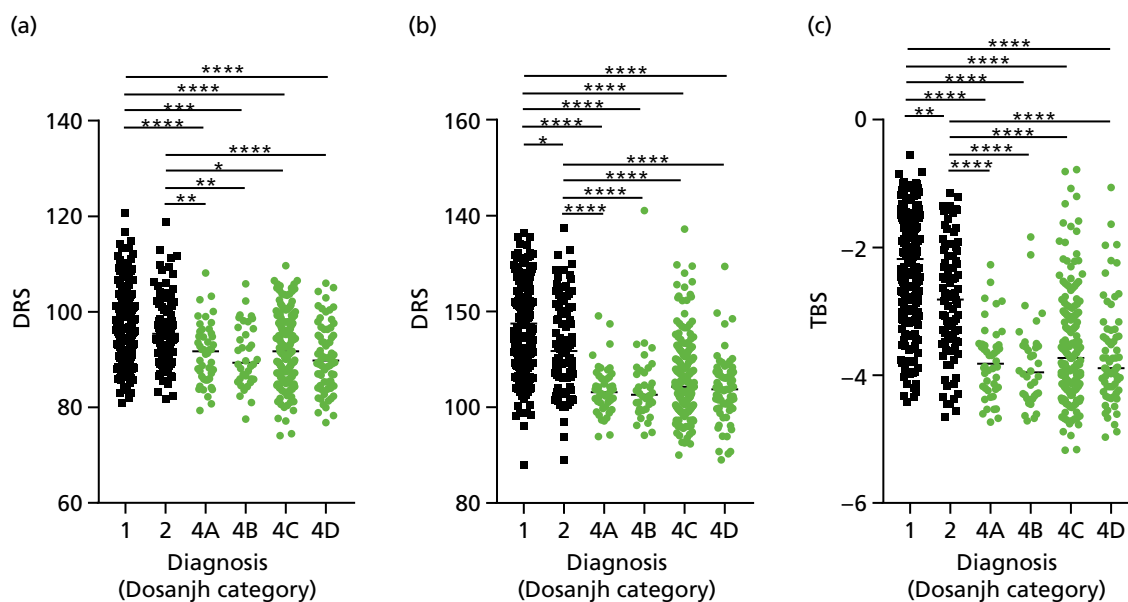
The poor performance of these signatures within the HIV+ population suggests that these signatures are unable to detect TB in this population. However, the variability in the diagnostic accuracy scores demonstrates uncertainty in the estimates and reflects the small numbers of patients.

### The performance of score signatures by Dosanjh classification

By comparing the 'score' signature results between Dosanjh categories, we can ascertain the effect of culture status within the TB group, and the likelihood of LTBI within the OD group (*Figure 3*).

In all cases, the score signatures were higher (significantly so in the case of the Kaforou *et al.*<sup>20</sup> and Sweeney *et al.*<sup>39</sup> signatures) in the culture-confirmed TB cases (Dosanjh category 1) than the highly probable TB cases (Dosanjh category 2) and, as a result, the diagnostic accuracy (AUC values) for culture-confirmed TB was slightly better than for highly probable TB for all score signatures (see *Appendix 4*). The maximum AUC for the detection of culture-confirmed TB was 0.86 (95% CI 0.83 to 0.89) using the Sweeney *et al.*<sup>39</sup> TBS, [the Kaforou *et al.*<sup>20</sup> DRS gave similar performance AUC of 0.85 (95% CI 0.81 to 0.88)] (see *Table 27*). For distinguishing highly probable TB from OD, the highest AUC achieved was 0.75 (95% CI 0.70 to 0.81), again with the Sweeney *et al.*<sup>39</sup> TBS.

No differences were observed in score signatures between the subgroups of OD patients in Dosanjh category 4, suggesting that neither previous history of TB or inactive TB (not to be confused with diagnosed LTBI) nor stratified risk of LTBI within the OD population affected the outcome of these score signatures. In fact, the highest AUCs were reported when the 4A and 4B groups (highest risk of having LTBI) were classified from all TB cases (see *Figure 17b*), the opposite of what was expected. The full diagnostic accuracy data are shown in *Table 27* in *Appendix 3*, including additional analyses with the HIV+ patients excluded from the cohort. As expected, given the poor diagnostic performance within the HIV+ population, removing this group of patients resulted in slightly improved diagnostic performance (see *Figure 17*).



**FIGURE 3** The performance of previously published score signatures, stratified by Dosanjh category. (a) Anderson *et al.*;<sup>36</sup> (b) Kaforou *et al.*;<sup>20</sup> and (c) Sweeney *et al.*<sup>39</sup> Statistical differences between score values between groups were determined using the Kruskal–Wallis with Dunn's post hoc test for multiple comparisons. \* $p < 0.05$ ; \*\* $p < 0.005$ ; \*\*\* $p < 0.0005$ ; \*\*\*\* $p < 0.0001$ .

## The performance of score signatures in detecting pulmonary or extrapulmonary tuberculosis

The clinical presentation, management and outcome of PTB and EPTB are different, and the latter is typically harder to diagnose as a result of several factors (e.g. difficulty of obtaining biopsy samples). Therefore, we wished to compare the score values in these groups and determine the diagnostic performance in either of these subclassifications of TB. As with the previous analyses, the Kaforou *et al.*<sup>20</sup> and Sweeney *et al.*<sup>39</sup> score signatures performed similarly when classifying either PTB or EPTB, whereas the Anderson *et al.*<sup>36</sup> signature had lower AUC values (see *Figure 18* in *Appendix 3*). The optimal performance for diagnosing either PTB or EPTB was comparable, with highest AUCs being 0.85 (95% CI 0.81 to 0.89; achieved by both the Kaforou *et al.*<sup>20</sup> DRS and the Sweeney *et al.*<sup>39</sup> TBS) and 0.84 (95% CI 0.80 to 0.87; achieved by the Sweeney *et al.*<sup>39</sup> TBS), respectively.

In addition, we stratified the OD group by the most prevalent disease types, so that we could identify any differences within this heterogeneous population of TB suspects with a wide array of ODs. Interestingly, sarcoidosis was the only condition within the OD group that consistently did not differ significantly from either type of TB (PTB or EPTB) across all three signatures (see *Figure 18b* and *18c*), suggesting that this specific differential diagnosis is a major confounding factor for the optimal performance of these score-based signatures in a real-life clinical setting.

## Performance of score signatures in detecting tuberculosis in smear-negative tuberculosis suspects

Among those in the IDEA study population tested for acid-fast bacilli (76% of IDEA study cohort), using smear microscopy, the test provided high specificity (96.7%) and poor sensitivity (23%) for all TB. Therefore, smear microscopy functions as a reliable cheap and fast rule-in test for (mostly) PTB in the UK setting, and a positive result indicates high bacterial burden. This allows clinicians to start treatment for this important infectious subgroup of TB patients very quickly. However, there is currently no rapid and reliable rule-in or rule-out test with which to identify TB in the  $\approx 77\%$  of smear-negative (paucibacillary) TB suspects who present in secondary care, as culture confirmation can take several weeks. We therefore assessed the performance of the score signatures within this smear-negative population of TB suspects and, using the prevalence data from the IDEA study as the pre-test probability, calculated the PPVs and NPVs for these tests. In *Table 6* we present the performance of these scores in the smear-negative population of TB suspects.

These results demonstrate that the performance of the Sweeney *et al.*<sup>39</sup> and Kaforou *et al.*<sup>20</sup> transcriptomic signatures in the smear-negative population of TB suspects is sufficient to provide a high NPV (89–90%) for culture-positive TB in a UK-like setting, in which the prevalence of culture-positive TB in smear-negative TB suspects was 33%.

## Analysis of Roe *et al.* signatures using published method

We obtained the SVMML model from Roe *et al.*<sup>38</sup> and validated the signature using the approach proposed in their publication. The performance of this model for discriminating TB cases from patients with ODs in our cohort was very poor with an AUC of 0.59 (95% CI 0.54 to 0.63). Although sensitivity for TB was high using this model [296 of 301 cases correctly classified, sensitivity of 98.3% (95% CI 96.2% to 99.3%)], specificity was very low [10/327 cases correctly classified as fever; specificity of 3.1% (95% CI 1.7% to 5.5%)].

## Analysis of all previously reported signatures using linear discriminant analysis

To allow for a fair and comparable validation of all six transcriptomic signatures in our cohort (i.e. including those in which the published method of diagnostic assessment was not reproducible),<sup>18,37</sup> we applied a LDA approach to assess the accuracy of each signature to each of the predefined comparisons we selected for validation analyses. Furthermore, this approach determined the optimal performance of each gene set from the selected signatures within our cohort, without the introduction of learning bias. Thus, the findings using this approach should be reproducible in a new, similarly designed cohort.

**TABLE 6** Performance of score signatures in the detection of subgroups of TB cases within the smear-negative population of TB suspects

Performance characteristic	Signature		
	Anderson <i>et al.</i> <sup>36</sup>	Kaforou <i>et al.</i> <sup>20</sup>	Sweeney <i>et al.</i> <sup>39</sup>
<i>Performance in smear-negative TB (Dosanjh categories 1 and 2) (n = 198 TB vs. n = 244 OD)</i>			
<i>Prevalence of TB in all smear-negative TB suspects = 46% (from overall IDEA study population)</i>			
AUC, % (95% CI)	0.67 (0.61 to 0.71)	0.79 (0.75 to 0.83)	0.80 (0.76 to 0.84)
Cut-off point (Youden index) <sup>a</sup>	> 91.78	> 107.5	> -3.241
Sensitivity, % (95% CI)	72.2 (65.43 to 78.34)	77.3 (70.8 to 82.9)	78.3 (71.9 to 83.8)
Specificity, % (95% CI)	50.8 (44.4 to 57.3)	71.3 (65.2 to 76.0)	74.2 (68.2 to 79.55)
PPV/NPV	0.56/0.68	0.69/0.79	0.72/0.80
<i>Performance in smear-negative culture-confirmed (Dosanjh category 1) TB (n = 139 TB vs. n = 244 OD)</i>			
<i>Prevalence of culture-confirmed TB = 33%</i>			
AUC, % (95% CI)	0.66 (0.61 to 0.72)	0.81 (0.77 to 0.86)	0.82 (0.78 to 0.87)
Cut-off point (Youden index) <sup>a</sup>	> 91.78	> 107.5	> -3.233
Sensitivity, % (95% CI)	72.7 (64.5 to 79.9)	82.0 (74.6 to 88.0)	82.7 (75.4 to 88.6)
Specificity, % (95% CI)	50.8 (44.4 to 57.3)	71.3 (65.2 to 76.9)	74.2 (68.2 to 79.6)
PPV/NPV	0.42/0.79	0.58/0.89	0.61/0.90
<i>Performance in detecting smear-negative and culture-negative (Dosanjh category 2) TB (n = 59 TB vs. n = 244 OD)</i>			
<i>Prevalence of culture-unconfirmed TB in smear-negative TB suspects = 13%</i>			
AUC, % (95% CI)	0.65 (0.58 to 0.73)	0.74 (0.67 to 0.81)	0.75 (0.68 to 0.82)
Cut-off point (Youden index) <sup>a</sup>	> 92.41	> 109.5	> -3.467
Sensitivity, % (95% CI)	71.2 (57.9 to 82.2)	62.7 (49.2 to 75.0)	74.6 (61.7 to 85.0)
Specificity, % (95% CI)	52.9 (46.4 to 59.3)	76.2 (70.4 to 81.4)	68.9 (62.6 to 74.6)
PPV/NPV	0.18/0.92	0.28/0.93	0.26/0.95

<sup>a</sup> The optimal score cut-off values for providing optimal sensitivity and specificity were calculated using the Youden index.

### Assessment in the full cohort

For the distribution of these signatures by probability as calculated by LDA in the full cohort, and diagnostic performance for detecting all TB cases (including stratification by HIV infection status), see *Figure 19* in *Appendix 5*.

Interestingly, in contrast to the score values, where the Anderson *et al.*<sup>36</sup> DRS underperformed compared with the Kaforou *et al.*<sup>20</sup> and Sweeney *et al.*<sup>39</sup> signatures (although no formal statistical comparison was made), the six signatures performed with similar accuracy when assessed using the LDA approach, with AUCs between 0.81 and 0.84 for detecting all TB cases in the full cohort. The accuracy marginally increased to AUC = 0.85 when HIV+ cases were excluded. The performance in the HIV+ population could be assessed only for these signatures using this method,<sup>37–39</sup> as the other signatures used a larger set of genes and, in all cases, the performance was poor and highly variable, with no significant differences between probability scores.

### Performance in detecting culture-confirmed or highly probable tuberculosis

The performance of all six signatures at detecting either culture-confirmed (Dosanjh category 1) or highly probable (Dosanjh category 2) TB was assessed using the LDA approach (see *Table 30* in *Appendix 5*). For detecting culture-confirmed TB, the performance of all six signatures was comparable, with AUCs between 0.84 and 0.87. However, for detecting highly probable TB, there was a wide range in performance, with the Sweeney *et al.*<sup>39</sup> signature providing the highest test accuracy (AUC = 0.80).

### Performance in detecting either pulmonary tuberculosis or extrapulmonary tuberculosis

When the six signatures were compared using LDA for the detection of either PTB or EPTB, comparable test accuracies were found for all signatures, with detection of PTB being marginally more accurate (maximum AUC = 0.86) than detection of EPTB (maximum AUC = 0.85) (see *Table 32* in *Appendix 5*).

### Derivation of novel signatures

To address our secondary objective to derive novel transcriptomic signatures for the detection of TB, we plan to split the validation cohort into a training set and a test set (80% : 20% split), and to use a variable selection method to identify our candidate genes within the training set, train them and finally test their performance on the remaining 20%. We are in the process of carrying out this analysis, but it did not fit within the scope of this report and will therefore be published elsewhere.

## Discussion

In this study, we have shown that none of the previously identified transcriptomic signatures for detecting active TB is sufficiently accurate for the detection of all TB in this clinically relevant cohort. Indeed, the signatures are not sufficiently accurate to detect any of the major subgroups of TB, even when considering the culture-confirmed TB cases alone, which are typically the most straightforward to identify. Their performance was much lower than previously reported, which probably reflects differences in study cohorts, as most of the previous studies did not include the full spectrum of TB types and their differential diagnoses.

Assessment of the previously proposed signatures in an unbiased and reproducible way by using summary scores<sup>20,36,39</sup> or a SVM model as previously reported,<sup>38</sup> or by applying a LDA approach, allowed us to assess performance in key patient groups in our validation cohort. Although diagnostic performance among culture-confirmed TB cases was greater than for highly probable TB cases, neither group could be accurately distinguished from the OD group. For highly probable TB, the Sweeney *et al.*<sup>39</sup> signature performed better than other published signatures, although only marginally so, and no statistical comparison was made. It is of note that the Anderson *et al.*<sup>36</sup> TBS underperformed when compared with the Kaforou *et al.*<sup>20</sup> DRS, whereas when the signatures were both assessed with LDA their performance was comparable. This probably reflects the nature of the derivation cohorts on which the score values were derived, with Anderson *et al.*<sup>36</sup> deriving the signature from a paediatric cohort.<sup>36</sup>

However, as there is currently no test for rapidly ruling in the highly probable TB group, it is still possible that a whole-blood transcriptomic signature test may be useful for assessment of TB in those cases where a negative microbiological test result is obtained. The prevalence of highly probable TB within the culture-unconfirmed cohort from the IDEA study was found to be 17.5%. Thus, we are able to assess the predictive performance of transcriptomic tests for highly probable TB in those with a negative culture test for TB.

The best-performing, previously identified signature was the Sweeney *et al.*<sup>39</sup> signature, which gave an AUC of 0.80 (95% CI 0.74 to 0.85) for detecting highly probable TB cases when assessed using LDA on the full cohort, with a sensitivity of 82.1% and specificity of 73.8% when a balanced cut-off point was selected. The scenario in which such a test would be useful is in a TB suspect for whom the culture (or other microbiological test, e.g. Xpert® MTB/RIF Ultra) is negative or not available. The prevalence of highly probable TB in the culture-unconfirmed TB suspects recruited into the IDEA study was 17.5%.

Using this prevalence value, the Sweeney *et al.*<sup>39</sup> gene signature for highly probable TB would provide a poor PPV of 0.4, but a very high NPV of 0.95. Therefore, it could be that such a transcriptomic signature, if developed into a simple and cheap rapid blood test and validated in new cohorts, could provide a sufficiently high NPV to be considered as a useful rule-out test in the microbiologically unconfirmed population. Furthermore, in settings with higher prevalence rates of highly probable TB, the PPV of these tests would be higher.

A rapid test with high diagnostic accuracy would be particularly helpful in the context of patients who are smear negative on initial assessment for TB, as culture takes a long time to give a definitive result. We present data on the performance of the score signatures<sup>20,36,39</sup> in this subcohort of patients; both the Sweeney *et al.*<sup>39</sup> and the Kaforou *et al.*<sup>20</sup> signatures provided reasonably high NPV (89–90%). If this result is validated in other studies, this may provide clinicians with sufficient reason to withhold treatment (or at least delay it until culture results are available) in smear-negative TB patients who test negative with these signatures.

The performance of all signatures was very poor within the HIV+ population in this cohort. This suggests that HIV co-infection masks the transcriptomic signal that differentiates TB from OD in the wider population. However, as the number of HIV+ participants in our cohort was small, this study was likely to be underpowered to validate performance within this population. Nevertheless, it is intriguing that others have shown that their identified signatures can perform with comparable test accuracy for detecting TB from OD in HIV+ and HIV– populations.<sup>20,39</sup>

Our data suggest that the performance of signatures for distinguishing TB from OD was compromised by sarcoidosis, as well as by HIV co-infection. If sarcoidosis could be excluded early in the diagnostic work-up of active TB, then the performance of transcriptomic signatures would improve and may potentially be of use in specific patient subgroups.

Our transcriptomic validation substudy has some limitations. We used microarray to determine the transcriptional profile of the whole-blood samples used in this cohort, and this technology has now more or less been replaced by RNA sequencing. Nevertheless, as the previously published signatures were all generated by microarray, this was the appropriate platform to use. It is generally accepted that clinical diagnostic scores overdiagnose TB in children, but to what extent this occurs in adult TB is unknown.<sup>44</sup> It is possible that the presence of patients without TB in the highly probable group negatively affects the transcriptomic signatures' performance. Thus, these signatures could still be clinically useful for paucibacillary (i.e. smear negative and Xpert negative) if these cases are removed from the analysis. In future studies, we aim to use this novel data set to derive and test new signatures, with a particular focus on identifying signatures with high diagnostic performance for smear-negative, culture-negative and EPTB cases of TB.

The suboptimal performance of the published signatures and the newly derived signatures highlights the unmet need in TB diagnosis, which is a rapid, accurate and generalisable test of the full spectrum of TB, including culture-negative TB. Although a similar cohort has been used to derive signatures of paediatric TB,<sup>36</sup> our study is the first one to address it in a large clinical adult TB cohort.





# Chapter 4 Proteomics

## Introduction

Serum protein biomarkers have the potential to be rapid, cheap and easy-to-use tests to rule in or rule out active TB disease. The 'proteomic signatures' measure the changes in individual proteins found in the serum as a result of the host's response to disease. Many of the changes observed are not unique to one condition, as they reflect overlapping strategies to combat or adapt to disease processes. However, certain proteins, when used in combination, can provide a high level of diagnostic accuracy when applied in the correct clinical situation. Therefore, the cohort used for selection and testing of proteomic signatures needs to be appropriate to the clinical question and condition for which it is being developed.

### *Proteomic biomarkers: current methodologies*

Proteins in sera are present in a dynamic range that spans at least four orders of magnitude, and the accurate detection of all proteins and their isoforms has not yet been achieved by any technology. In order to overcome this limitation, many proteomic signatures have been generated after immune depletion of the most abundant proteins. This assumes that depleted proteins are not useful biomarkers and serum albumin and immunoglobulin G, which account for > 90% of the total protein mass, will often be removed. Depletion allows accurate quantification of less abundant proteins, but it can alter the abundance of proteins that interact with the proteins being depleted. SELDI-TOF provides a quick, reproducible and cheap profiling technology for intact proteins, but is limited by dynamic range and does not provide identification of the protein signatures. LC-MS is a newer technology and provides both accurate quantification and protein identification, but is slow and costly compared with SELDI-TOF and ELISA. ELISA is fast and cheap, and highly suitable for the development of a point-of-care test for TB. It is, however, limited to the quantification of only a few proteins, in which distinct antibody pairs have been developed and tested. In ELISA, the identity of the signature is required prior to beginning the investigation and, thus, it requires the identification of any signature developed by another technology to be known.

To investigate the utility of the serum proteomic signatures to diagnose TB, we reviewed the most important and relevant studies carried out previously.

### *Previously published signatures*

We selected 12 published studies reporting a proteomic signature for the detection of TB cases and summarised the key study characteristics (*Table 7*).

In 2014, when the VANDET study proposal was funded, the majority of signatures generated were based on SELDI-TOF analysis. Of note, a large prospective cohort study by Agranoff *et al.*<sup>45</sup> in 2006 identified a signature with a sensitivity of 93.5% and a specificity of 94.9% (AUC of 0.96). This signature was validated in a cohort of mainly PTB patients and gave a reduced sensitivity of 88.9% and specificity of 77.2%. Ratzinger *et al.*<sup>46</sup> also validated this signature externally in a UK cohort that was diverse in the presentation of the site of TB disease, including more EPTB. In this report the accuracy reduced to 54% (95% CI 47% to 61%). Although the latter reported that the accuracy of the protein markers could be improved using additional clinical data, the poor performance of the protein signature as a test meant that it will not be considered an important test to assess within the VANDET study.

Recently, two published SELDI-TOF profiles were identified for active TB compared with healthy or mainly HC cohorts, making them not useful for clinical validation.<sup>48,50</sup> Sandhu *et al.*<sup>49</sup> published a novel 54 mass-to-charge ratio ( $m/z$ ) cluster using SELDI-TOF that performed with high accuracy (84% sensitivity, 90% specificity, AUC = 0.93). This signature remains unvalidated, but it was generated using a prospective cohort of mainly patients with PTB and other non-TB diseases and, therefore, warrants assessment within the VANDET study.

**TABLE 7** Summary of publications presenting proteomic signatures for detecting of active TB cases

Study	Cohort (in validation if done)	Classification accuracy	Technology	Suitable for validation, why
Agranoff <i>et al.</i> 2006 <sup>45</sup>	TB, <i>n</i> = 179; 86–87% smear positive; OD, <i>n</i> = 170	AUC = 0.96	SELDI-TOF	No, failed validation
Ratzinger <i>et al.</i> 2012 <sup>46</sup>	N/A	AUC = 54%	SELDI-TOF	No, low performance
Liu <i>et al.</i> 2010 <sup>47</sup>	ATB, <i>n</i> = 87; HC, <i>n</i> = 55; OD, <i>n</i> = 13	Accuracy = 88.09–93.55%	SELDI-TOF	No, HCs
Zhang <i>et al.</i> 2012 <sup>48</sup>	TB, <i>n</i> = 129; HC, <i>n</i> = 60; OD, <i>n</i> = 69	Sensitivity of 96.9% and a specificity of 97.8%	SELDI-TOF	No, HCs
Sandhu <i>et al.</i> 2012 <sup>49</sup>	TB, <i>n</i> = 151; OD, <i>n</i> = 110	Sensitivity of 84%, specificity of 90% and AUC = 0.93	SELDI-TOF	Yes, no validation done
Hamilton and Levin (unpublished)	TB, <i>n</i> = 300; OD, <i>n</i> = 300	AUC = 84.7, 95% CI 0.7 to 0.9 or AUC = 81.9 <sup>a</sup>	SELDI-TOF/ELISA	Yes, no validation done, ELISA signature available
Liu <i>et al.</i> 2013 <sup>50</sup>	TB, <i>n</i> = 180; HC, <i>n</i> = 90; OD, <i>n</i> = 121	Accuracy of 80.1% (75.0% sensitivity, 83.5% specificity)	SELDI-TOF	No, low performance and HCs in the control group
Song <i>et al.</i> 2014 <sup>51</sup>	TB, <i>n</i> = 26; OD, <i>n</i> = 31	AUC = 0.947 (95% CI 0.8 to 1)	LC–MS/ELISA (AUC)	Yes
Xu <i>et al.</i> 2015 <sup>52</sup>	PTB, <i>n</i> = 40, pneumonia, <i>n</i> = 40; lung cancer, <i>n</i> = 40; HC, <i>n</i> = 40	TB vs. pneumonia AUC = 0.955 vs. lung cancer AUC = 0.954	LC–MS/ELISA (AUC)	Yes
Li <i>et al.</i> 2015 <sup>53</sup>	TB, <i>n</i> = 125; pneumonia, <i>n</i> = 15; HC, <i>n</i> = 32	AUC = 0.904	LC–MS/ELISA (AUC)	No, HCs in validation
Achkar <i>et al.</i> 2015 <sup>21</sup>	TB, <i>n</i> = 28; OD, <i>n</i> = 45	HIV– AUC 0.96; HIV+ AUC 0.95	LC–MS (AUC)	Yes
Chegou <i>et al.</i> 2016 <sup>54</sup>	TB, <i>n</i> = 214; OD, <i>n</i> = 487	Sensitivity of 81.3% (95% CI 69.2% to 89.5%) and specificity of 79.5% (95% CI 71.8% to 85.5%)	ELISA	No
De Groote <i>et al.</i> 2017 <sup>19</sup>	TB, <i>n</i> = 92; OD, <i>n</i> = 123	AUC = 0.87 (95% CI 0.81 to 0.91)	SOMAscan® (Somalogic Inc., Boulder, CO, USA)	No, technology not available

ATB, active tuberculosis; N/A, not applicable.  
 a An unpublished communication.

In a larger cohort (*n* = 600), our collaborators (SH, LC and ML) have identified a four-peak protein signature with excellent performance in paediatric TB (AUC = 84.7, CI 0.7 to 0.9 or AUC = 81.9), depending on whether or not the data were analysed using a DRS forward selection method. Hamilton and Levin (unpublished) have also successfully identified all four proteins in the cohort and are currently developing and validating this as an ELISA for point-of-care testing.

Liquid chromatography–mass spectrometry has become the method of choice for biomarker discovery, and we identified four studies each identifying a signature for active TB using this method. Song *et al.*<sup>51</sup> identified serpin family A member 1 (SERPINA1), also known as alpha-1-antitrypsin, as a single and highly accurate marker of TB (AUC = 0.947, 95% CI 0.8 to 1.0). The authors performed no validation and their choice of disease controls, diseased patients who do not exhibit symptoms of active TB, is highly suspect.

More promisingly, Xu *et al.*<sup>52</sup> pooled immunodepleted serum and used LC–MS to detect a three-protein signature [calcium-binding protein A9 (S100A9), superoxide dismutase 3 (SOD3) and matrix metalloproteinase 9 (MMP9)] that could discriminate active TB from controls. They validated these proteins using ELISA in the case–control cohort but included diseases that often confound diagnosis of active TB (PTB,  $n = 40$ ; pneumonia,  $n = 40$ ; lung cancer,  $n = 40$ ; and HC,  $n = 40$ ). This signature could resolve PTB and pneumonia (AUC = 0.955) and discriminate between PTB and lung cancer (AUC = 0.954) with high accuracy. However, it was limited in terms of the spectrum of disease subtypes included in the active TB group (all culture-confirmed PTB) and other non-TB disease (limited to two disease types).

The findings from the IDEA study demonstrate that the differential diagnoses for active TB are numerous and varied (> 200 final diagnoses were reported in the OD group), reflecting the heterogeneous nature of different types of TB disease and the various clinical presentations that are associated with them.<sup>12</sup> Achkar *et al.*<sup>21</sup> took LC–MS a step closer to a real-life road test when they recruited patients from four different hospitals, including both culture-negative and HIV+ patients, and a verification cohort of TB cases and patients with ODs with TB-like symptoms. The signature differed depending on HIV infection status and gave excellent classification of active TB from other non-TB-like diseases (HIV– AUC = 0.96 and HIV+ AUC = 0.95). The progression shown by this work demonstrates the potential of a proteomic signature detected by LC–MS in active TB diagnosis.

In the last year a new technology has been utilised to generate a signature for active TB: SOMAScan. This technology relies on aptamers and combines the benefits of both LC–MS and ELISA into one assay that is potentially customisable into a point-of-care test.<sup>19</sup> However, the commercial availability is limited and not available to be investigated in the VANTDET study. De Groote *et al.*<sup>19</sup> discovered a novel six-protein signature [SYWC (*WARS*), kallistatin (*SERPINA4*), C9 (*C9*), gelsolin (*GSM*), testican-2 (*SPOCK2*) and aldolase C (*ALDOC*)] that provides a high classification accuracy (AUC = 0.87, 95% CI 0.81 to 0.91) in culture-confirmed TB.<sup>19</sup> The cohort tested did not include culture-negative TB but did include TB and other related diseases with similar symptoms and HIV co-infection.

## Aim

Our aim was to assess the clinical utility of proteomic signatures for the diagnosis of active TB. We chose five signatures for validation: two identified by SELDI-TOF [i.e. Sandhu *et al.*<sup>49</sup> and Hamilton *et al.* (unpublished)] and three by LC–MS (i.e. Song *et al.*,<sup>51</sup> Xu *et al.*<sup>52</sup> and Achkar *et al.*<sup>21</sup>). All five were chosen because the signatures were developed in a cohort of prospectively recruited patients with ODs.

## Objectives

- Assess the utility of the SELDI-TOF four-protein signature in the IDEA study cohort.
- Bridge signatures derived by SELDI-TOF with LC–MS technology.
- Assess the utility of all signatures using LC–MS.

## Methods

### Cohort selection

A cohort of 171 samples was selected randomly from the HIV– patients of eligible individuals within the full IDEA study cohort. The sera were processed in blocks of nine patients and a pooled serum sample was created by mixing equal volumes of patient sera. The internal control was included in each batch processed by LC–MS. SELDI-TOF mass spectrometry was performed in one batch on a total of 90 serum samples, as this was the maximum number achievable given the limited number of chips available (see *Chapter 2, Issues and problems*). The 90 patients used were a direct subset of the 171 individuals eligible for analysis, allowing for a bridging assessment between technologies. During experimentation and analysis, samples were excluded if consent was withdrawn, if the patient was found to have not been followed up by clinical assessment, or if errors occurred in experimental processing. The final cohorts consisted of 86 individuals in the SELDI-TOF arm and 166 individuals in the LC–MS arm.

### Serum samples

In the IDEA study, blood for serum collection was collected into a BD serum tube (Becton, Dickinson and Company, Franklin Lakes, NJ, USA) and allowed to clot for 60 minutes before centrifuging at 1000 g for 10 minutes at room temperature to remove cell debris and clots. Serum supernatant was aliquoted into sterile 2-ml tubes and kept at  $-80^{\circ}\text{C}$  until use.

### SELDI-TOF

Protein profiling of serum by SELDI-TOF mass spectrometry was achieved by placing serum samples on anionic (Q10), cationic (CM10) and immobilised metal affinity chromatography (IMAC) ProteinChip arrays (Bio-Rad Laboratories, CA, USA). The arrays were primed twice with binding buffers for Q10 (50 mM Tris, 0.1% Triton X-100, pH 7.5 and 9.5), CM10 (50 mM ammonium acetate, 0.01% Triton X-100, pH 4.0 and 6.0) and IMAC  $\text{Cu}^{2+}$  (0.1 mM sodium phosphate, 0.5 mM sodium chloride, pH 7.0), and incubated at room temperature with shaking for 5 minutes. A 1 : 10 dilution of serum in binding buffer was then applied to the Q10 and CM10 arrays and a 1 : 5 dilution of serum in binding buffer was applied to the IMAC  $\text{Cu}^{2+}$  array and incubated at room temperature with shaking for 1 hour. The arrays were washed twice with binding buffer and deionised water and dried at room temperature for 15 minutes. Saturated sinapinic acid (0.7  $\mu\text{l}$ ) was applied twice to each spot on the CM10 and IMAC arrays and 50% saturated sinapinic acid was applied to the Q10 array, allowing the matrix to air dry between each application. Time-of-flight spectra were generated using a PCS-4000 mass spectrometer (Bio-Rad Laboratories, CA, USA). Low-range spectra ( $m/z$  0–20,000) were obtained at a laser energy of 2800–3400 nJ with a focus mass of 6000 nJ and the matrix attenuated to 1000 nJ. High-range spectra ( $m/z$  0–200,000) were obtained at a laser energy of 3800–4200 nJ with a focus mass of 30,000 nJ and the matrix attenuated to 10,000 nJ. Ten shots were obtained per position and mass accuracy was calibrated externally using All-in-One Peptide or protein molecular mass standards (Bio-Rad Laboratories, CA, USA).

### Liquid chromatography–mass spectrometry

An internal standard was made by pooling equal amounts of serum from the first 100 patients. For each batch an equal amount of serum from nine patients and the internal standard were solubilised in 1% sodium deoxycholate, and 100 mM ammonium bicarbonate. Ten  $\mu\text{g}$  of protein was reduced with 10 mM dithiothreitol for 15 minutes at  $60^{\circ}\text{C}$ , followed by alkylation with 20 mM iodoacetamide for 15 minutes at room temperature in the dark. Trypsin (Promega, Madison, WI, USA) was added at a 1 : 50 (enzyme–protein) ratio and digestion was carried out at  $37^{\circ}\text{C}$  overnight. Peptide digests were purified using the  $\text{C}_{18}$  STop And Go Extraction (STAGE) tips and eluted peptides were dried and labelled with nine labels from the TMT10plex Mass Tag Labelling Kit (Thermo Fisher Scientific, Waltham, MA, USA), as described in the instructions with minor modifications.<sup>55</sup> Peptides were dissolved in 25  $\mu\text{l}$  of 100 mM triethylammonium bicarbonate (TEAB) and 10  $\mu\text{l}$  of each label in acetonitrile, and incubated for 60 minutes at room temperature before it was quenched with 2.5  $\mu\text{l}$  of 50% [volume/volume (v/v)] TEAB and combined. Samples were diluted to a final acetonitrile concentration of 3% (v/v) acetonitrile, acidified to 0.1% (v/v) trifluoroacetic acid and purified, again, by the  $\text{C}_{18}$  STAGE tips. Each fraction was dried completely and dissolved in 2% (weight/volume) acetonitrile–0.1% (v/v) formic acid prior to LC–MS.

Mass spectrometry analysis was performed as described in Reuschl *et al.*,<sup>56</sup> except that the resolution of MS2 scans was 35 K, MS2 charge targets were limited to  $1\text{E}^5$  and isolation window set to 1.5  $m/z$ .

### Data processing

Surface-enhanced laser desorption ionisation time-of-flight spectra were analysed using ProteinChip data manager (version 4.1.0, Bio-Rad Laboratories, CA, USA) and normalised using total ion current. Peak clusters were auto-detected using a peak threshold of 20% and a mass window of 0.3% and the raw data converted for subsequent analysis using R software.

Raw LC–MS spectra were identified and quantified using MaxQuant 1.5.15 (Max Planck Institute of Biochemistry, Planegg, Germany), using a 1% peptide and protein false discovery rate (FDR) as described by Cox and Mann and using the UniProt SwissProt database (UniProt, European Bioinformatics Institute,

Cambridgeshire, UK), downloaded on 5 June 2014, with additional common contaminant proteins and TMT-10 plex quantitation mode enabled. Reporter ion intensities for tandem mass spectrometry scans were filtered to ensure < 75% precursor isolation purity, summed and assigned to proteins based on unique matches and parsimony as described previously. For every patient, each protein was quantitated using the sum of all peptide intensities. This number was divided by the same measure for the pooled internal control to give a block normalised ratio (accounting for batch processing). This value was pre-processed by  $\log_2$  transformation and checked for normality and batch effects.

### Statistical analysis

To assess the performance of the four-protein signature evaluated using the SELDI-TOF platform, the four proteins were identified using their mass values. The DRS method<sup>20,57</sup> was used to calculate a score from the abundance data of the four proteins, as described previously.

To identify differentially expressed proteins, analysis of variance and Welch's *t*-test were calculated between all disease groups, and *p*-values were adjusted for the effect of multiple hypothesis testing using the FDR (< 0.1) method.

The performance of published signatures using the depleted LC-MS data set was assessed using abundance data (for the Song *et al.*<sup>51</sup> signature containing one protein) or LDA, for signatures incorporating multiple proteins, on the full cohort.

To assess for diagnostic performance, the abundance, DRS or probability values generated for each signature (depending on whether a raw abundance, DRS or LDA approach was taken for analysis, respectively) were used to generate ROC curves and determine diagnostic accuracy data (sensitivity, specificity, etc.).

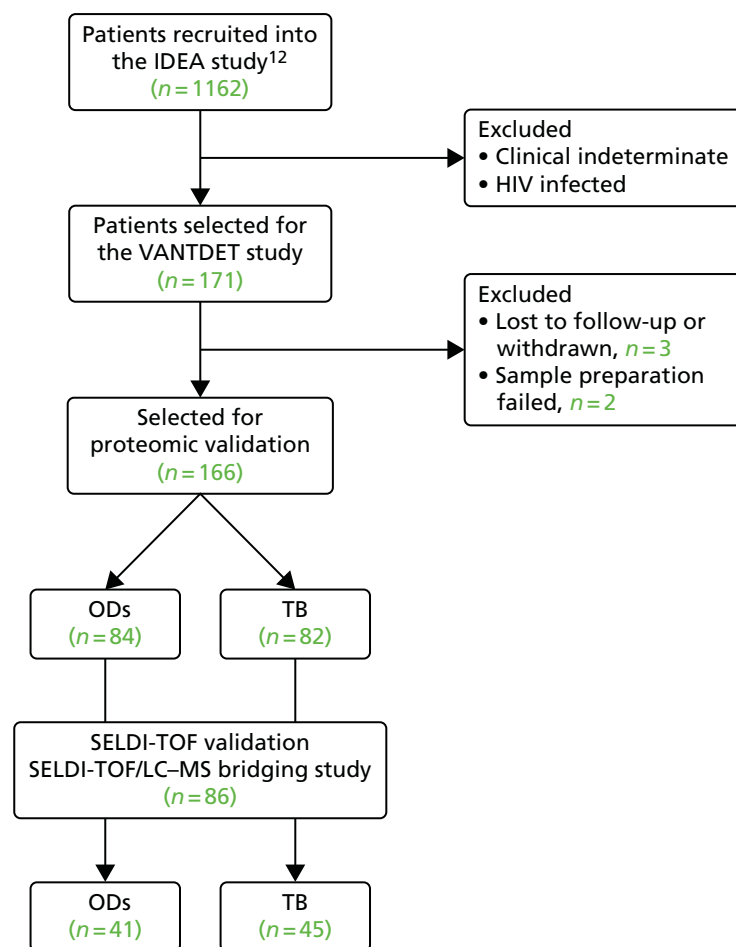
## Results

A cohort of 171 samples was selected randomly from the eligible HIV- individuals within the full IDEA study cohort. SELDI-TOF mass spectrometry was performed on a total of 90 serum samples. This was the maximum number achievable given the limited number of SELDI-TOF chips available (see *Chapter 2, Issues and problems*). LC-MS analysis was performed on the full cohort of 171 samples; the 90 samples used in SELDI-TOF were a direct subset of the 171 individuals eligible for analysis, allowing for a bridging assessment between the two technologies (*Figure 4*). During experimentation and analysis, samples were excluded if consent was withdrawn, if the patient was found to have not been followed up by clinical assessment, or if errors occurred in experimental processing. The final cohorts with complete SELDI-TOF and LC-MS data were  $n = 86$  for SELDI-TOF, and  $n = 86$  and  $n = 166$  for LC-MS (see *Figure 4*).

We also performed an additional LC-MS experiment on a larger number of samples ( $n = 279$ ) using crude sera, which included samples from HIV+ patients. This experiment was sent to an external contractor (FingerPrints Proteomics, URL: <http://proteomics.lifesci.dundee.ac.uk/>). This data set was restricted to 218 proteins and we were unable to consistently identify and quantitate the protein signatures found in the studies reviewed (see *Table 36* in *Appendix 6*), apart from SERPINA1. This data set was therefore not utilised in biomarker validation results presented below.

### Cohort characteristics

The demographic characteristics of the proteomic validation cohorts are given in *Tables 8* and *9* (for LC-MS and SELDI-TOF, respectively). Statistical analysis of the patient demographics in the LC-MS cohort ( $n = 166$ ) identified differences ( $p < 0.05$ ) between the two major diagnostic groups under investigation, with patient age, weight and BMI all lower in patients with a final diagnosis of active TB (Dosanjh categories 1 and 2) than in those classified as having ODs (Dosanjh category 4). A similar trend was observed for these characteristics in the SELDI-TOF subset, with a statically significant difference in age and weight (see *Table 9*).



**FIGURE 4** Flow diagram for the proteomics validation substudy.

No HIV-infected individuals were included, because at the time of the initial experimentation there was not a validated procedure for ensuring that samples were not infectious for steps required for proteomic sample processing. It was considered that the validity of a test could be adequately assessed in a HIV- cohort.

### **Performance of previously published signatures using SELDI-TOF**

We selected two SELDI-TOF signatures for validation using this technology in the SELDI-TOF VANTDET study cohort: those described by Sandhu *et al.*<sup>49</sup> and Hamilton and Levin (unpublished) (see *Table 33* in *Appendix 6*). To allow interstudy comparisons to be made, all SELDI-TOF profiles were acquired for the surfaces utilised in these studies.

The Sandhu *et al.*<sup>49</sup> signature consisted of two sets of  $m/z$  SELDI-TOF peaks, one set ( $n = 98$ ) derived from crude sera on the CM10 and the second set from 54  $m/z$  peaks from fractionated sera. We acquired SELDI-TOF data on the CM10 surface at pH 4.0 and pH 6.0 in line with these signatures; however, we found that only 2 out of 54 and 2 out of 98 peaks matched between the profiles of Sandhu *et al.*<sup>49</sup> and our spectra. Based on this, we were unable to validate the Sandhu *et al.*<sup>49</sup> signatures for diagnosis of TB in our cohort.

The signature proposed by Hamilton and Levin (unpublished) is based on the signature of four to six  $m/z$  peaks, corresponding to four unique proteins, and working closely with Hamilton and Levin (unpublished) we could detect the same peaks in our SELDI-TOF profiles (see *Table 33*). With these data we assessed the classification accuracy in the VANTDET study cohort ( $n = 86$ ) using the DRS methodology they propose (see *Methods*). This resulted in an AUC = 0.66 (95% CI 0.54 to 0.77) in the full cohort when comparing all TB (Dosanjh categories 1 and 2,  $n = 45$ ) to OD (Dosanjh category 4,  $n = 41$ ). The AUC improved if only

**TABLE 8** Demographic and clinical characteristics of the LC–MS proteomic signature validation cohort

Demographic and clinical characteristic	Culture-confirmed TB (Dosanjh category 1) (N = 60)	Highly probable TB (Dosanjh category 2) (N = 22)	ODs (Dosanjh category 4) (N = 84)	p-value overall <sup>a</sup>
Clinical setting, n (%)				0.59
Inpatient	22 (36.7)	7 (31.8)	24 (28.6)	
Outpatient	38 (63.3)	15 (68.2)	60 (71.4)	
Age (years), median (range)	30.5 (17.0–72.0)	31.0 (18.0–54.0)	47.0 (21.0–85.0)	< 0.001
Male, n (%)	37 (61.7)	10 (45.5)	47 (56.0)	0.416
Ethnic origin, n (%)				0.598
Asian	3 (5.00)	0 (0.00)	4 (4.76)	
Black	9 (15.0)	3 (13.6)	15 (17.9)	
Indian subcontinent	41 (68.3)	17 (77.3)	43 (51.2)	
Middle Eastern	1 (1.67)	0 (0.00)	1 (1.19)	
Mixed	1 (1.67)	0 (0.00)	3 (3.57)	
Unable/unwilling to respond	0 (0.00)	0 (0.00)	1 (1.19)	
White	5 (8.33)	2 (9.09)	17 (20.20)	
Height (m), median (range)	1.69 (1.50–1.88)	1.63 (1.48–1.85)	1.70 (1.51–1.93)	0.475
Height missing, n (%)	26 (43.3)	7 (31.8)	31 (36.9)	0.578
Weight (kg), median (range)	60.0 (38.5–127.0)	61.4 (44.6–77.0)	68.2 (41.5–124.0)	0.001
Weight missing, n (%)	2 (3.33)	2 (9.09)	5 (5.95)	0.508
BMI (kg/m <sup>2</sup> ), median (range)	21.6 (15.7–40.1)	21.0 (16.0–34.6)	24.5 (17.3–36.7)	0.039
BMI missing, n (%)	26 (43.3)	9 (40.9)	33 (39.3)	0.888
BCG vaccinated yes, n (%)	39 (65.0)	9 (40.9)	54 (64.3)	0.104
BCG scar visible, n (%)				0.125
Missing	15 (25.0)	2 (9.09)	11 (13.1)	
No	2 (3.33)	1 (4.55)	5 (5.95)	
Unsure	3 (5.0)	4 (18.2)	15 (17.9)	
Yes	40 (66.7)	15 (68.2)	53 (63.1)	
HIV+, n (%)	0 (0)	0 (0)	0 (0)	
TB contact no, n (%)	45 (75.0)	19 (86.4)	68 (81.0)	0.491

<sup>a</sup> Where the data were categorical, a chi-squared test was used to compare characteristics between groups; where the data were continuous, the groups were compared using a Kruskal–Wallis test.



**TABLE 9** Demographic and clinical characteristics of the 86 participants used for validation of the four-protein SELDI-TOF signature

Demographic and clinical characteristic	Culture-confirmed TB (Dosanjh category 1) (n = 33)	Highly probable TB (Dosanjh category 2) (n = 12)	ODs (Dosanjh category 4) (n = 41)	p-value overall <sup>a</sup>
Clinical setting, n (%)				0.454
Inpatient	14 (42.4)	5 (41.7)	12 (29.3)	
Outpatient	19 (57.6)	7 (58.3)	29 (70.7)	
Age (years), median (range)	29.0 (17.0–72.0)	29.5 (18.0–54.0)	46.0 (22.0–85.0)	< 0.001
Male, n (%)	20 (60.6)	6 (50.0)	21 (51.2)	0.68
Ethnic origin, n (%)				0.389
Asian	3 (9.09)	0 (0.00)	2 (4.88)	
Black	6 (18.20)	1 (8.33)	9 (22.00)	
Indian subcontinent	21 (63.6)	10 (83.3)	18 (43.9)	
Mixed	0 (0.00)	0 (0.00)	1 (2.44)	
Unable/unwilling to respond	0 (0.00)	0 (0.00)	1 (2.44)	
White	3 (9.09)	1 (8.33)	10 (24.40)	
Height (m), median (range)	1.70 (1.50–1.88)	1.63 (1.48–1.85)	1.68 (1.52–1.85)	0.806
Height missing, n (%)	12 (36.4)	5 (41.7)	16 (39.0)	0.955
Weight (kg), median (range)	62.0 (38.5–127.0)	58.0 (44.6–77.0)	69.5 (41.5–96.0)	0.04
Weight missing, n (%)	2 (6.06)	0 (0.00)	3 (7.32)	1
BMI (kg/m <sup>2</sup> ), median (range)	21.4 (15.7–40.1)	20.8 (16.0–34.6)	24.6 (17.3–32.6)	0.147
BM missing, n (%)	12 (36.4)	5 (41.7)	17 (41.5)	0.912
BCG vaccinated yes, n (%)	19 (57.6)	5 (41.7)	22 (53.7)	0.639
BCG scar visible, n (%)				0.322
Missing	10 (30.3)	0 (0.0)	8 (19.5)	
No	1 (3.03)	1 (8.33)	2 (4.88)	
Unsure	2 (6.06)	1 (8.33)	5 (12.20)	
Yes	20 (60.6)	10 (83.3)	26 (63.4)	
HIV+, n (%)	33 (100)	12 (100)	41 (100)	.
TB contact no, n (%)	24 (72.7)	10 (83.3)	34 (82.9)	0.55

a Where the data were categorical, a chi-squared test was used to compare characteristics between groups; where the data were continuous the groups were compared using a Kruskal–Wallis test.

culture-confirmed TB (Dosanjh category 1,  $n = 33$ ) was included in the TB disease group, providing an AUC = 0.74 (95% CI 0.63 to 0.86), whereas no classification was observed for detection of highly probable TB (Dosanjh category 2,  $n = 12$ ) from OD patients (AUC = 0.58, 95% CI 0.4 to 0.76) (Figure 5).

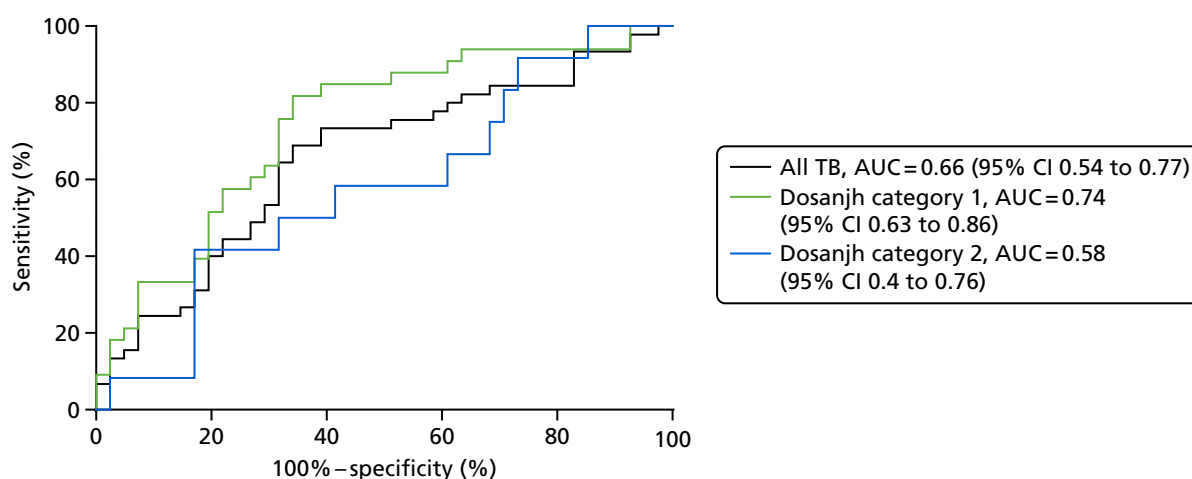
### Bridging study

Our study was designed to bridge the two technologies, LC–MS and SELDI-TOF, by analysing the same 86 samples. This aimed to answer the question ‘can signatures identified in SELDI-TOF be reproduced by LC–MS?’ in the affirmative enabling the transfer of signature testing to LC–MS for larger cohorts, which is limited in SELDI-TOF owing to the discontinuation of consumables. To do this we took three out of the four protein identifications provided from the Hamilton and Levin (unpublished) SELDI-TOF signature (patent pending), extracted the quantitative data for these proteins in the LC–MS data set and analysed them using correlation (see Table 34). Correlation between the methods was low; only protein 1 achieved statistical significance ( $p < 0.05$ ) (see Figure 20a). We also compared the proteins for significant difference between the different categories in diagnosis of active TB and found no proteins significant in the SELDI-TOF data and one protein (protein 2) significant when measured by LC–MS.

### Performance of previously published signatures using liquid chromatography–mass spectrometry

Next, we asked if any of the key published and unpublished signatures [i.e. the signatures identified by Hamilton and Levin (unpublished), Song *et al.*,<sup>51</sup> Xu *et al.*,<sup>52</sup> Achkar *et al.*<sup>21</sup> and De Groote *et al.*<sup>19</sup>] could provide accurate disease classification for active TB using the LC–MS platform. To do this, we utilised the quantitative LC–MS data set generated on immunodepleted sera from 166 individuals, extracting specific quantitative data for the protein signatures within each signature. The data set consisted of spectra collected from immunodepleted sera digested with trypsin and labelled by TMT-10 plex labelling (see Methods). Samples were fractionated by strong anion exchange chromatography into six fractions and each fraction was analysed by LC–MS.

Using the software MaxQuant we identified 8773 peptide identifications mapping to 720 proteins, each with a quantitative value in at least one patient, and 380 proteins with a quantitative value for all patients. Imputation was required for 18% of the proteins used for the discovery of novel signatures (42/228). Overall, the imputation rate for OD samples ( $n = 84$ ) was 0.3% of all of the reported protein abundances. Similarly, for TB samples ( $n = 82$ ) the proportion of imputed values was 0.1%.



**FIGURE 5** Performance of the four-protein signature (Hamilton and Levin, unpublished) on SELDI-TOF, for the classification of TB in the VANTDET SELDI-TOF substudy cohort ( $n = 86$ ). The DRS for the four target proteins was calculated and assessed to diagnostic performance using ROC curve analysis. The performance for classifying all TB (Dosanjh categories 1 and 2 combined,  $n = 45$ , black line), culture-confirmed TB (Dosanjh category 1,  $n = 33$ , green line) and highly probable TB (Dosanjh category 2,  $n = 12$ , blue line) against all OD patients ( $n = 41$ ) is displayed.

### Detection of key proteins from published signatures

All proteins from the four key publications [Hamilton and Levin (unpublished), Song *et al.*,<sup>51</sup> Xu *et al.*,<sup>52</sup> Achkar *et al.*<sup>21</sup>] were detected in our depleted LC–MS data set and could therefore be validated within our cohort of 166 patients. Unfortunately, we could not validate the De Groote *et al.*<sup>19</sup> signature within this data set, as only four of the six proteins could be detected, and two of these had > 50% missing values. For those signatures we could validate, we first assessed the abundance of the proteins in the key patient groups. The average of the relative abundance ( $\log_2$  ratio) and statistical analysis of the proteins is shown in *Table 35* in *Appendix 6* for the key patient groups. When comparing all TB cases with ODs, the majority of proteins (10/18) were found to be significantly different between these groups, this number fell to 5 out of 18 if only highly probable TB (Dosanjh category 2) cases were considered [P08294 from the Xu *et al.*<sup>52</sup> signature, Levin 1 and Levin 2 from the Hamilton and Levin (unpublished) signature, and P02654 and P49908 from the Achkar *et al.*<sup>21</sup> signature] (see *Table 35*).

### Validation of diagnostic performance of serum protein signatures using liquid chromatography–mass spectrometry

To assess whether or not these protein signatures could be used to classify all TB cases from OD, we used LDA (*Figure 6*) to test the performance of the signatures in separate diagnostic groups, with the exception of the Song *et al.*<sup>51</sup> signature, for which only one protein (P01009 or SERPINA1) is used<sup>51</sup> and the raw abundance data can be used for validation purposes (see *Figure 21*).

All four signatures performed similarly, providing an AUC = 0.62–0.67 for detection of all TB cases within the cohort. The AUC values, as well as the sensitivity and specificity scores, can be found in *Appendix 6* (see *Table 37*) and *Appendix 7* (see *Table 38*). We further assessed their performance for the classification of either culture-confirmed or highly probable active TB (i.e. Dosanjh categories 1 and 2, respectively) against all OD for culture-confirmed TB; the best classification accuracy was achieved with the Xu *et al.*<sup>52</sup> and Achkar *et al.*<sup>21</sup> signatures, providing AUCs = 0.70 (see *Table 39*). All of the signatures gave a poor performance for detecting highly probable TB, with no significant discriminatory ability (AUC = 0.53–0.59). The performance of all signatures for diagnosing PTB was greater than that for EPTB, for which no discriminatory ability was achieved by any of the published signatures (see *Table 37* in *Appendix 6* and *Table 39* in *Appendix 7*). Thus, the subgroup in which all signatures performed optimally in VANTDET was the culture-confirmed TB group.

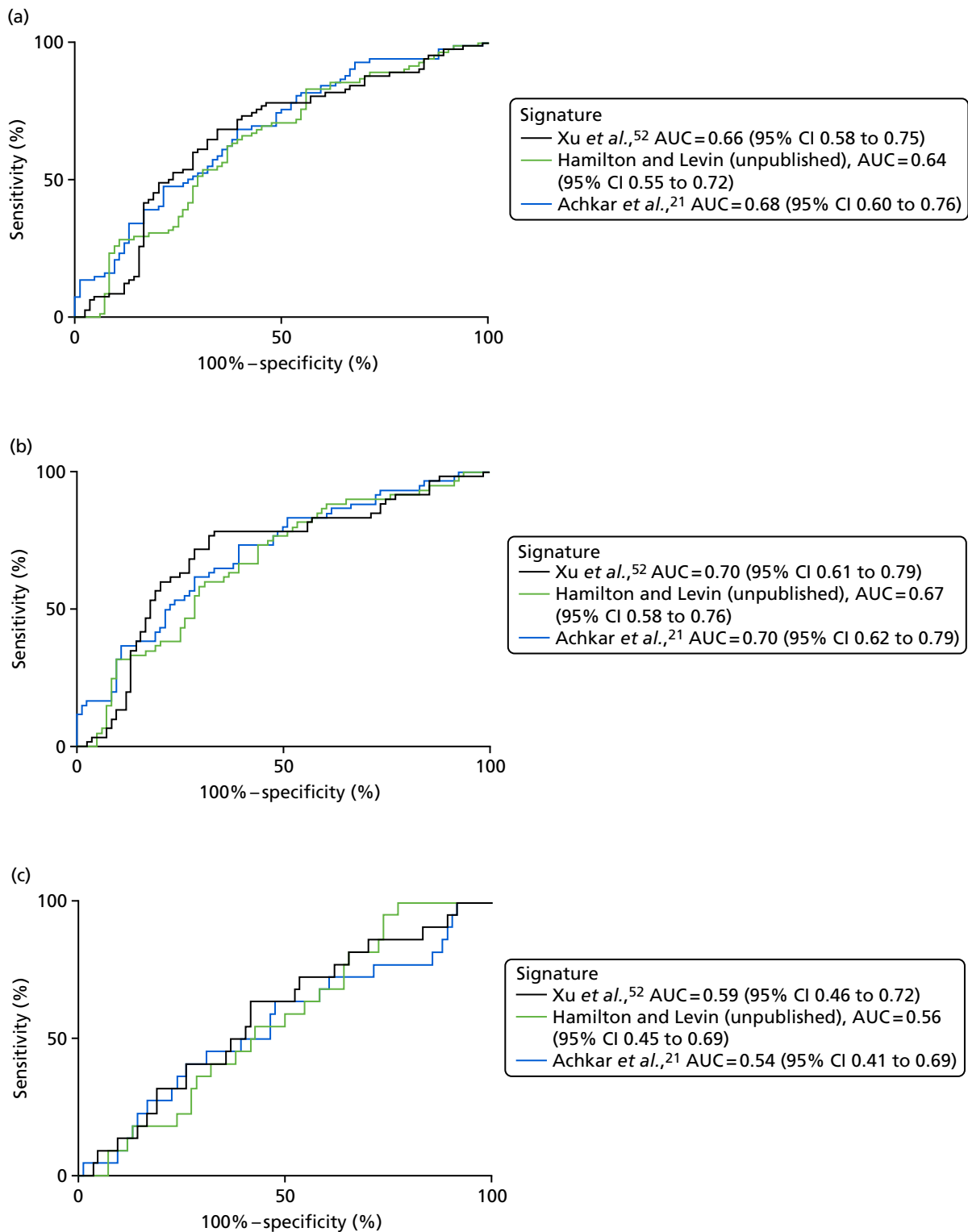
### Removal of sarcoidosis from other disease

It is known from our own studies, and those by others, that the serum proteomic profiles of patients with sarcoidosis are very similar to those of patients with active TB. We therefore carried out a LDA on the detection of all TB, as well as stratifying by Dosanjh category, when patients with sarcoidosis were removed from the OD cohort. The results from these analyses are shown in *Appendix 8* (see *Tables 40* and *41*). For the detection of all TB, the performance of all of the published signatures improved slightly. However, when the performance in key subgroups was assessed, the performances of the signatures changed very little, or even reduced in diagnostic accuracy.

## Discussion

The focus of this substudy of VANTDET was to test the diagnostic accuracy of previously identified protein signatures that occur in the serum of patients with active TB. To do this we reviewed and tested previously published proteomic signatures using the two major technological platforms, SELDI-TOF and LC–MS.

Our results indicate that diagnosis of TB cases in UK hospitals is not possible using currently identified proteomic signatures in SELDI-TOF or LC–MS technology. We used ROC curve analysis to indicate diagnostic accuracy for the binary classification of TB or OD. Applying this, none of the signatures tested met the GO/NO-GO threshold (AUC > 0.85) outlined in the management plan for this proteomics substudy of the VANTDET study. The best-performing signature was described by Achkar *et al.*<sup>21</sup> and resulted in an AUC = 0.68 when measured by LC–MS and analysed by LDA. Using SELDI-TOF, the Hamilton and Levin (unpublished)



**FIGURE 6** The diagnostic performance of the Xu *et al.*,<sup>52</sup> Hamilton and Levin (unpublished) and Achkar *et al.*,<sup>21</sup> protein signatures on the LC-MS depleted data set ( $n = 166$ ) using LDA. The diagnostic performance is presented for discrimination of TB vs. OD, discrimination of Dosanjh category 1 vs. OD (Dosanjh category 4) and discrimination of Dosanjh category 2 vs. OD (Dosanjh category 4).

signature performed with an AUC = 0.66 when analysed by calculating the DRS. The classification accuracy was reduced compared with that reported by our collaborators in their cohort of TB and OD patients (AUC = 0.85). The other SELDI-TOF signature developed by Sandhu *et al.*<sup>49</sup> was not measurable because of poor interlaboratory reproducibility. All signatures improved their classification accuracy if only culture-confirmed active TB cases were considered for diagnosis. Herein, the Hamilton and Levin (unpublished) SELDI-TOF signature gave an AUC = 0.74, which was the optimal diagnostic performance we identified using any proteomic technique; the Xu *et al.*<sup>52</sup> and Achkar *et al.*<sup>21</sup> signatures gave a test accuracy performance of AUC = 0.70 using LC-MS as assessed using LDA.

We utilised the Dosanjh categorisation of active TB as our reference standard, in which TB diagnosis is based on both (1) gold standard microbiological culture and (2) clinical diagnosis of culture-negative TB. Approximately 28% of all TB cases recruited were culture negative, and this was driven by the relatively high prevalence of EPTB and other forms of paucibacillary TB cases among the UK cohort. Here, the development of new diagnostics is vital, as standard methods, such as culture or polymerase chain reaction (PCR), perform poorly. Our data show that the host response signatures found in the serum proteome for TB also perform poorly in culture-unconfirmed TB. The markers tested here perform better in culture-confirmed (mainly pulmonary) TB potentially as a result of the robust acute-phase response in this type of disease that tracks with increased symptoms and more extensive immunopathology or necrotic disease. A limitation of the previous signatures for TB is their development in cohorts with a high prevalence of pulmonary TB, in which severity of disease at presentation is probably greater. The signature in the Achkar *et al.*<sup>21</sup> study was the only signature developed from patients in different hospitals, including both culture-negative TB and OD with TB-like symptoms, very similar to the IDEA study cohort utilised in the VANTDET study. The IDEA study<sup>12</sup> also recruited prospectively, resulting in a cohort of diverse OD diagnoses (> 100), all classified as one group (Dosanjh category 4). The high diversity among this group, and similarity of symptoms reported by patients from all groups, reflects the real clinical problem, but it hampers any biomarker that is driven by a generalised mechanism in the host response to disease. For example, in diseases consisting of both neutrophil-driven necrotic disease and macrophage recruitment it is likely that the same proteins that are altered will be the same as found in active TB (e.g. S100A8/A9, MMP9). In developing their signatures, both Xu *et al.*<sup>52</sup> and Song *et al.*<sup>51</sup> limit selection of control groups to specific diseases, and controls often did not have similar symptoms in the Song *et al.*<sup>51</sup> study. This artificial selection leads to the development of tests that work well between diseases that are specifically different in the host response orchestrated, but also leads to the selection of markers that reflect only the difference between healthy and sick people. In utilising the IDEA study cohort, the VANTDET study improved on this by creating a design that tested the utility of such markers in a complex environment in which symptomatic people present on a case-by-case basis.

Our study was limited by technological problems in the platforms utilised and the cross-platform compatibility available for protein detection and quantitation. The discontinuation of SELDI-TOF limited the numbers of samples that could be analysed and the poor interlaboratory reproducibility limited us to validating only the four-protein signature developed in-house [developed by Hamilton and Levin (unpublished)]. The transfer of these biomarkers to new methods, LC-MS and ELISA, is troublesome. First, the identification of the proteins was not made until late 2017 and remains unpublished. Second, markers detected by SELDI-TOF do not always correlate accurately to antigenic regions raised during *in vivo* immune responses, making the development of ELISA difficult. LC-MS detects tryptic peptides for proteins and, therefore, can also not fully recapitulate what is observed in SELDI-TOF, which may be large fragments of proteins. Our goal was to analyse 200 samples from the IDEA study cohort, but this was limited to 90 by SELDI-TOF and 171 by LC-MS, as a result of low levels of consumables left in the UK and limited access to LC-MS equipment internally. Furthermore, the larger data set of crude sera resulted in poor protein coverage and an inability to detect the published signatures. To combat the limited power of our initial investigations, we analysed only HIV- samples. HIV status is known to affect proteomic profile in the serum of people with TB; however, as our cohort consisted of limited numbers of HIV+ (15%) co-infected patients, we decided to test signatures in HIV- patients initially and expand into HIV+ individuals if we achieved an AUC > 0.85. This AUC was never achieved using our approach by LC-MS or SELDI-TOF.

Liquid chromatography–mass spectrometry and SELDI-TOF failed to achieve the minimum requirements set in the VANTDET study for a clinically useful signature. Both technologies are limited by the depth of proteomic coverage and the ease of cross-platform development to a point-of-care test; and this was apparent in our study. Recently, a new technology termed SOMAscan offers an attractive method able to overcome these limitations. De Groote *et al.*<sup>19</sup> used this technology to discover and test a novel eight-protein signature for TB in the serum of people with PTB compared with other related non-TB diseases. This study was multicentre and prospective, but was limited to culture-confirmed PTB, for which it gave an AUC = 0.87 (95% CI 0.81 to 0.91). Testing of this signature in the VANTDET study using SOMAscan was not possible owing to the limited accessibility to this technology in the public domain at the time of project conception. Furthermore, the proteins comprising this signature were not all detected in either of our LC–MS data sets.

To address our secondary objective of using these proteomic data sets to derive novel signatures that may offer improved accuracy for diagnosing either all TB cases or specific subgroups of TB, we will be applying variable selection methods to identify the proteins providing the best classification accuracy (in both crude and depleted sera samples). We intend to train a prediction model on 60% of the cohort and test the accuracy of the model on the remaining 40% (test set). This work was not within the scope of this report, but will be the logical next step in utilising this novel proteomic data set to derive a clinically useful proteomic signature with potential to be used in the diagnostic work-up of TB.

Our study provided two important conclusions. The previously reported proteomic signatures for detecting TB were not found to be clinically useful in this cohort, probably because of the differences in the complexity of TB/OD patients in the respective cohorts. Therefore, our data from the IDEA study cohort, which does reflect real-life clinical practice, provide a springboard for future studies and an opportunity to derive new signatures that are robust and can pave the way for future validation in similar cohorts.



# Chapter 5 Cellular immune signatures

## Introduction

The IGRA tests measure the presence of circulating memory T lymphocytes producing IFN $\gamma$  in response to the *Mtb* region of difference 1 (RD1) antigens. In addition to being the gold standard test for LTBI, they are able to detect between 55% and 87% of all active TB cases, depending on the population and test used.<sup>12</sup> However, as IGRAs cannot discriminate between these two states of infection, they lack the specificity to be used as a rule-in test for active TB. To improve on the specificity of such an immune-based test, various groups have explored the *Mtb*-specific T-cell response with greater complexity than simply measuring production of IFN $\gamma$ , and have found that, by using flow cytometry to measure phenotypic and functional markers of *Mtb*-specific T cells, cellular immune signatures have the potential to be used as immune-based tests to discriminate between active and LTBI.

The first group to identify a signature that differed between disease states sufficiently to allow discrimination between active TB and LTBI was Harari *et al.*,<sup>24</sup> who, in 2011, showed that the functionality of CD4-positive T cells could discriminate between active and LTBI. Specifically, the proportion of *Mtb*-specific T cells with a polyfunctional profile [IFN $\gamma$  positive, interleukin 2 (IL-2), positive, tumour necrosis factor alpha (TNF- $\alpha$ ) positive] was higher in those with LTBI, whereas the proportion secreting TNF- $\alpha$  only (IFN $\gamma$  negative, IL-2 negative, TNF- $\alpha$  positive) was higher in those with active TB and could discriminate between the two groups with high accuracy in a training and test cohort.<sup>24</sup>

Work from our laboratory exploited the potential diagnostic value of TNF $\alpha$ -only-secreting *Mtb*-specific T cells while simultaneously improving diagnostic accuracy by combining measurement of T-cell memory/differentiation phenotype (based on cell surface markers) in parallel. Indeed, Pollock *et al.*<sup>25</sup> demonstrated that measurement of the proportion of TNF- $\alpha$ -only-secreting purified protein derivative (PPD)-specific cluster of differentiation 3 (CD3)- and CD4-positive cells that were CD45RA-CCR7-CD127- (i.e. highly differentiated late-effector T cells) was highly discriminatory between active TB and LTBI (see *Table 42* in *Appendix 9*). The signature had 100% sensitivity and 93% specificity in a test cohort of 34 patients ( $n = 13$ , active TB;  $n = 21$ , LTBI), of whom 50% were HIV+.<sup>25</sup> Since then, additional cellular immune signatures have been identified that also show promise in their ability to discriminate between active TB and LTBI, including one that combined the proportion of TNF- $\alpha$ -only population (among all cytokine responders as in Harari *et al.*<sup>24</sup>) with the presence of a detectable cluster of differentiation 8 (CD8)- and IFN $\gamma$ -positive T-cell response into a SCORE value.<sup>58</sup>

However, in recent years, the research focus has returned to the CD4-positive IFN $\gamma$ -producing *Mtb*-specific population, and several groups have reported using the memory marker CD27 to differentiate TB from LTBI patients. Different approaches to incorporating this marker into a cellular immune signature have been taken (i.e. by measuring the levels of CD27 as a ratio in relation to the parent population<sup>27</sup> or measuring the presence/absence of expression in combination with the memory marker CD45RA).<sup>28</sup> The discrimination between groups was high in these studies, with a specificity of > 90% for active TB for the CD27-CD45RA- signature.<sup>28</sup> More recently, the incorporation of activation markers, such as human leucocyte antigen – antigen D related (HLA-DR), in cellular immune signatures has been shown in several studies to provide improved discrimination between these two disease states;<sup>26</sup> a finding that has been validated by external groups, including those with/without co-infection with HIV.<sup>59,60</sup> For reference throughout this chapter, the signatures are referred to using either the numerical value or short description, as follows: (1) %TNF- $\alpha$  only,<sup>24</sup> (2) % differentiated T effector cells ( $T_{EFF}$ ),<sup>25</sup> (3) SCORE,<sup>58</sup> (4) CD27 MFI (median fluorescence intensity) ratio,<sup>27</sup> (5) %CD27-/+CD45RA-<sup>28</sup> and (6) %HLA-DR.<sup>26</sup>



Flow cytometry is already established in many NHS diagnostic laboratories throughout the UK and is suitable for routine diagnostic use.<sup>61</sup> These signatures therefore warrant prospective validation in a large-scale independent cohort in routine practice. As yet, none of the studies have tested the performance of such signatures in key patient groups that reflect those to present in a clinical setting, such as those with ODs and LTBI, and TB patients with hard-to-diagnose forms of the disease (i.e. culture-unconfirmed TB and/or EPTB). Indeed, patients were not recruited as part of routine clinical practice in any of the previous studies that have been conducted.

### **Aim**

By combining the markers required to measure all of the signatures that have shown promise into one panel of antibodies, we sought to validate the performance of these signatures on a cohort of individuals with suspected TB recruited as part of routine clinical practice (i.e. using the IDEA study cohort).

### **Objectives**

- To validate the performance of the six (see *Introduction*) previously reported cellular immune signatures in diagnosing active TB.
- To perform substudy analyses where specific clinical groups are included/excluded in the classification analysis (i.e. culture-confirmed TB/highly probable TB, PTB/EPTB, etc.).

## **Methods**

### **Cohort selection**

As the cellular immune signatures to be validated are dependent on a detectable T-cell response to *Mtb* antigens, and have thus been proposed as a test to allow for discrimination between active and LTBI, only those with a positive IGRA can be assessed. We therefore identified those individuals eligible for the final IDEA study analysis who had sufficient PBMCs available in the biobank and had a positive IGRA test (with a positive QFT-GIT and/or T-SPOT.*TB* being sufficient to be classified as IGRA positive). To balance the two groups, we carried out a nested control approach and randomly selected patients from the active TB group to generate our final cohort, with the exception that all eligible HIV-infected samples were included in the final cohort. Using this approach, all of the individuals selected from Dosanjh category 4 had a positive IGRA result and can therefore be classified as having both ODs and LTBI; we therefore refer to this group in the chapter as 'OD/LTBI'.

### **Experimental design**

#### **Blinding of patient status**

The patients were selected for this study by the data manager (AB) and the statistician (YT), using the criteria detailed in *Cohort selection*. The laboratory researchers (research associates and technicians: AH, MTW and TM) involved in the sampling handling, experiments and analysis, had access to only the patient IDs and locations. The demographic and clinical data related to each patient were not revealed to the researchers until the final analysis was complete and locked (i.e. the cellular immunology data could not be changed).

#### **Batching**

Each experiment took place over 2 days. Between five and nine samples were defrosted in each experiment and between one and three vials of PBMCs were required, depending on recovery. The details of viability, cell counting, plate layouts, antibody quantities and timings, etc., were entered on to a standards experimental log sheet. Records of antibody volumes/concentrations used, antigen batches and other details were also taken and stored for each experiment.

### Cell culture and antigen stimulations

Thawed PBMCs were initially resuspended in RPMI-1640 (Sigma, St Louis, MO, USA) and supplemented with 10% heat-inactivated fetal bovine serum (referred to as R-10 from here on). The cells were then washed, resuspended in RPMI-1640 and counted using trypan blue and an automated cell counter (Countess II FL Automated Cell Counter, Invitrogen, CA, USA). PBMCs were then resuspended in R-10 to give a final concentration of  $15 \times 10^6$  cells/ml. The cells were distributed in three to six wells of a 48-well plate (CELLSTAR™, Greiner Bio-One Kremsmünster, Austria) (in a volume of 100–250  $\mu$ l) and rested for precisely 6 hours [at 37 °C in 5% carbon dioxide (CO<sub>2</sub>)]. After resting, the cells were stimulated with phorbol 12-myristate 13-acetate (PMA)/ionomycin-positive control (PMA concentration of 5 ng/ml and ionomycin concentration of 500 ng/ml), tuberculin PPD RT50 (AJ Vaccines, Copenhagen, Denmark/Statens Serum Institut, Copenhagen, Denmark) (16.7  $\mu$ g/ml final concentration) and a combination of four RD1-related peptides shown previously to have a powerful discriminatory power (including ECRR, final concentration of 5  $\mu$ g/ml per peptide). Unstimulated cells were used as a negative control. After stimulation, the cells were incubated for a further 2 hours and 2  $\mu$ l of a monensin–brefeldin A mix (BioLegend, San Diego, CA, USA) (both at a 1 $\times$  concentration according to manufacturer's instructions) was added and the plate was incubated for a further 16 hours (total stimulation time = 18 hours).

### Multicolour staining

Following stimulation, cells were incubated on ice for 10 minutes followed by scraping and washing with phosphate-buffered saline (PBS). Cells were then stained with a dead cell marker (LIVE/DEAD™ Fixable Near-IR, Life Cell Technologies, Auckland, New Zealand) at 1 $\times$  in PBS for 10 minutes on ice, protected from light. After washing in fluorescence-activated cell sorting (FACS) buffer (PBS containing 2 mM ethylenediaminetetraacetic acid, 0.5% bovine serum albumin), all cells were placed in Block buffer (10% human serum in FACS buffer) containing a mixture of pre-titrated fluorochrome-conjugated antibodies for detection of surface markers (see *Table 43*). After washing with FACS buffer (PBS, 2 mM ethylenediaminetetraacetic acid, 0.5% bovine serum albumin), the cells were fixed and permeabilised using Cytotfix/Cytoperm™ buffer (fixation/permeabilisation kit; Becton Dickinson and Company) for 20 minutes on ice protected from light. The cells were washed with BD Perm/Wash™ buffer (Becton Dickinson and Company) from the same kit and then stained with pre-titrated fluorochrome-conjugated antibodies diluted in Perm/Wash for the detection of intracellular cytokines (see *Table 1*). The cells were washed twice with FACS buffer before acquiring samples on a BD LSRFortessa™ cell analyser (Becton Dickinson and Company), containing five lasers [ultraviolet (UV) 355 nm, violet 405 nm, blue 488 nm, yellow–green 561 nm and red 633 nm]. Antibody concentrations were optimised during titration experiments using the MFI staining index calculation approach.

### Interexperimental controls

Various controls were included in each experiment, including the use of 8-Peak Rainbow Beads (BioLegend), which allowed for fine-tuning of the voltage settings to allow for comparable detection of fluorescence peaks across experiments. Single-stained controls for each antibody/viability dye cells or mouse/rat beads (selected to allow to detection of maximum possible brightness for each marker) were used to allow for calculation on the compensation matrix. Finally, PBMCs from a PPD-responsive anonymous leucocyte cone donor were used as a fully stained control in each experiment, as well as for fluorescence minus one control for each target antibody. All the controls ensured the standardisation and calibration of the BD LSRFortessa cell analyser across experiments.

### Acquisition on flow cytometer

The samples and controls were acquired straight after the last experimental step using the BD LSRFortessa cell analyser, coupled with a computer and FACS Diva v8.01 software (Becton Dickinson and Company). A maximum of  $2 \times 10^6$  events (set at live singlet lymphocytes) were collected for each condition of each sample. Flow cytometry standard files were exported later that day to be further analysed using FlowJo version 10.4.2 (Treestar; Becton Dickinson and Company).

### **Use of purified protein derivative-responsive control**

Leucocyte cones obtained from an anonymous donor were purchased from NHS Blood and Transplant. On receipt, cells were washed in RPMI-1640, counted and stored in cryovials containing approximately 20,000,000 live cells per vial. Cells from these samples were screened for responsiveness to PPD using flow cytometry. One PPD cytokine responder was used as an internal responsive control in each experiment.

### **Analysis and gating**

The data were analysed using FlowJo version 10. Before analysis was applied to each experiment, the compensation matrix (derived from the FACS Diva software and compensation controls) was checked and adjusted accordingly so that over/under-compensation did not affect gating. For images showing the gating strategies used for the full analysis of all signatures, see *Appendix 9* and *Figures 22–24*.

### **Selection of viable T cells**

Gates were set on lymphocytes followed by single cells using forward and side scatter properties. Live lymphocytes were selected using LIVE/DEAD Fixable Near-IR versus forward scatter. Samples were checked against time in case an abnormality occurred while acquiring. CD3-positive T cells were selected within the live lymphocytes population gated against the CD4-positive T cells; this gate allowed for detection of highly activated CD3- and CD4-positive T cells on which surface expression of surface CD3 positive can be downregulated.<sup>62</sup> To visualise these gates see *Figure 22*.

### **Selection of cytokine-specific T cells**

Within the CD3 population, CD4- and CD8-positive T-cell populations were further selected. The IFN $\gamma$ -positive gate (after removal of artefacts as described in *Appendix 9*) was selected on either CD4-positive versus IFN $\gamma$  or CD8 versus IFN $\gamma$ , depending on the parent T-cell population of interest. IL-2 and TNF- $\alpha$  were plotted against each other and gated on this plot for either CD4 positive or CD8 positive.

Phenotypic gates (i.e. for CD45RA/CCR7, CCR7/CD127, CD127 positive/negative CD27/CD45RA and HLA-DR positive) were first gated on the CD4-positive population and were then transferred to cytokine-specific populations as required for each published signature (see *Figures 23* and *24*).

### **Determining the inclusion criteria for antigen responsiveness**

For the purpose of this study, we defined a set of inclusion criteria to ensure that only those samples with a definite response to *Mtb* antigens, and with sufficient cells to allow for accurate calculation of phenotype, were included. Therefore, to identify samples with a sufficient antigen-specific cytokine response (whether CD4 positive–IFN $\gamma$  positive or CD4 positive–TNF- $\alpha$  only), only those with at least twice the levels of cytokine above background were included (i.e. per cent of cells > 2 $\times$  unstimulated). In addition, if phenotypic analysis of cytokine-specific cells was required for signature calculation, only those with  $\geq 10$  analysable events were included. These criteria are similar, although not identical, to those used in the publications where the signatures were first proposed.

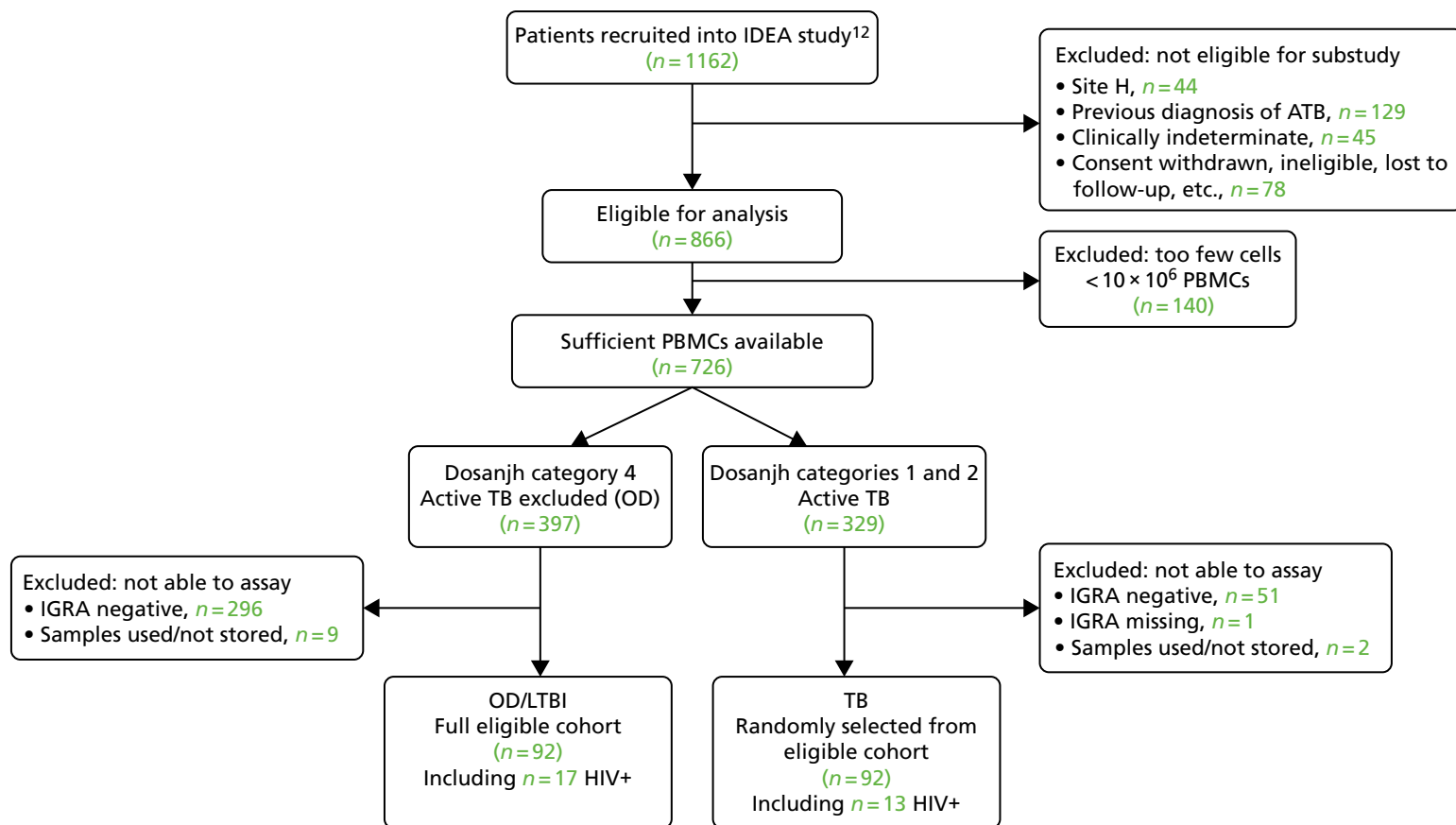
### **Statistical analysis**

All statistics were performed using Prism software. Differences in signature measurements between groups was determined using either a Mann–Whitney *U*-test or a Kruskal–Wallis test (depending on the number of groups). Diagnostic accuracy for discriminating between groups was calculated using ROC curve analysis.

## **Results**

### **Cohort selection**

The nested case–control approach was used to select the final cohort for validation of cellular immune signatures, resulting in a cohort of 184 participants samples being defrosted for the stimulation and flow cytometry staining (*Figure 7*), with equal numbers of TB and OD/LTBI participants ( $n = 92$ ).



**FIGURE 7** Study flow chart of patients included in the validation of cellular immune signatures substudy. A nested case–control approach was used to select the patients from the full cohort of IGRA-positive participants who were eligible for analysis in the IDEA study, resulting in a total of 92 patients per group (with the TB patients being randomly selected and all the HIV+ and IGRA-positive patients being selected). Note: this cohort was larger than originally anticipated (i.e.  $n = 164$ ), as additional IGRA-positive patients were identified since the October 2016 protocol was written. ATB, active tuberculosis.

**Cohort characteristics**

The main demographic characteristics of the final analysed cohort are present in *Table 10*. As with the other VANTDET substudy and main IDEA study cohorts, there was a significant difference in age between the groups, with the OD group being older than the TB groups. Unlike in the IDEA study and transcriptomic substudy cohort, we do not observe a significant difference in ethnicity in this substudy cohort. This is probably because of the smaller cohort size. There were no significant differences in the key clinical characteristics (*Table 11*).

**TABLE 10** Demographic characteristics of final cohort for validation of cellular immune signatures substudy ( $n = 184$ )

Characteristic	Dosanjh category			<i>p</i> -value
	1: culture-confirmed TB	2: highly probable TB	4: OD/LTBI	
Total, <i>n</i>	60	32	92	
Age (years), median (range)	33 (16–72)	36.5 (21–76)	40.5 (17–80)	0.0027
Female, <i>n</i> (%)	18 (30.0)	13 (40.6)	34 (37.0)	0.5365
Ethnic origin, <i>n</i> (%)				0.2136
Asian	3 (5.0)	3 (9.4)	7 (7.6)	
Black	18 (30.0)	6 (18.8)	29 (31.5)	
Hispanic	1 (1.7)	1 (3.1)	1 (1.1)	
Indian subcontinent	32 (53.3)	20 (62.5)	34 (37.0)	
Middle Eastern	0 (0.0)	0 (0.0)	5 (5.4)	
Mixed	0 (0.0)	1 (3.1)	1 (1.1)	
White	6 (10.0)	1 (3.1)	14 (15.2)	
Unknown	0 (0.0)	0 (0.0)	1 (1.1)	

**TABLE 11** Clinical characteristics of the validation of cellular immune signature substudy cohort ( $n = 184$ )

Characteristic	Dosanjh category			<i>p</i> -value
	1: culture-confirmed TB	2: highly probable TB	4: OD/LTBI	
Total, <i>n</i>	60	32	92	
Height (m)				
Median (range)	1.68 (1.50–1.89)	1.71 (1.50–1.80)	1.7 (1.50–1.96)	0.823
Missing, <i>n</i> (%)	24 (40.0)	13 (40.6)	26 (28.3)	
Weight (kg)				
Median (range)	60.2 (41.3–97.0)	64 (44.7–116.0)	70.5 (42.0–132.0)	
Missing, <i>n</i> (%)	0 (0)	1 (3.1)	4 (4.3)	
BMI (kg/m <sup>2</sup> )				
Median (range)	21.7 (15.7–32.0)	23.7 (16.1–42.2)	24.3 (14.9–47.2)	
Missing, <i>n</i> (%)	24 (40.0)	14 (43.8)	27 (29.3)	
BCG positive, <i>n</i> (%)	46 (76.7)	25 (78.1)	64 (69.6)	0.500
HIV+, <i>n</i> (%)	6 (10.0)	6 (18.75)	13 (14.1)	0.495

The groups were compared for each characteristic, using either a Mann–Whitney *U*-test or chi-squared test.

The distribution of disease in the TB groups is presented in *Table 44* and the list of main diagnoses in the OD group is presented in *Table 45* (see *Appendix 10*). Individuals with PTB and EPTB were presented in both the culture-confirmed (Dosanjh category 1) and the highly probable (Dosanjh category 2) TB groups.

### Recovery and detection of antigen-specific responses

Of the 184 samples in which PBMCs were defrosted, 181 (98%) were used for the full 2-day experiment (three were not plated or used for the full experiment owing to the recovery of no/too few live cells; two were TB; and one was OD/LTBI). Of the 181 samples that were assayed (i.e. stimulated, stained with full antibody panel and analysed), all were stimulated with PPD, all had a negative control (unstimulated), 179 (99%) were stimulated with PMA/ionomycin and 107 (59%) were stimulated with the RD1 antigens (ECRR). The *Mtb* antigen condition was included in each assay only when there were sufficient cells to have four conditions ( $> 7 \times 10^6$ ). The PMA/ionomycin stimulation condition was excluded in two cases as a result of low numbers of cells. For details of the recovery rate of PBMC from storage, viability before plating and at acquisition, viability after stimulation and overall cytokine responses to all antigens, see *Appendix 11*, *Tables 46–49* and *Figure 25*. In summary, all of those samples stimulated with PMA/ionomycin responded by producing cytokines, whereas responses to PPD and *Mtb* antigens were less frequent (with 87% and 93% of those stimulated responding with a detectable IFN $\gamma$  response, respectively). Those individuals who did not meet the criteria for antigen responsiveness were excluded from diagnostic accuracy analysis.

### Diagnostic performance of signatures in full cohort

Here we present the diagnostic performance of six previously identified cellular immune signatures for the detection of TB from OD/LTBI in the IGRA-positive population of TB suspects.

### Distribution of signature values in tuberculosis and other disease/latent tuberculosis infection groups

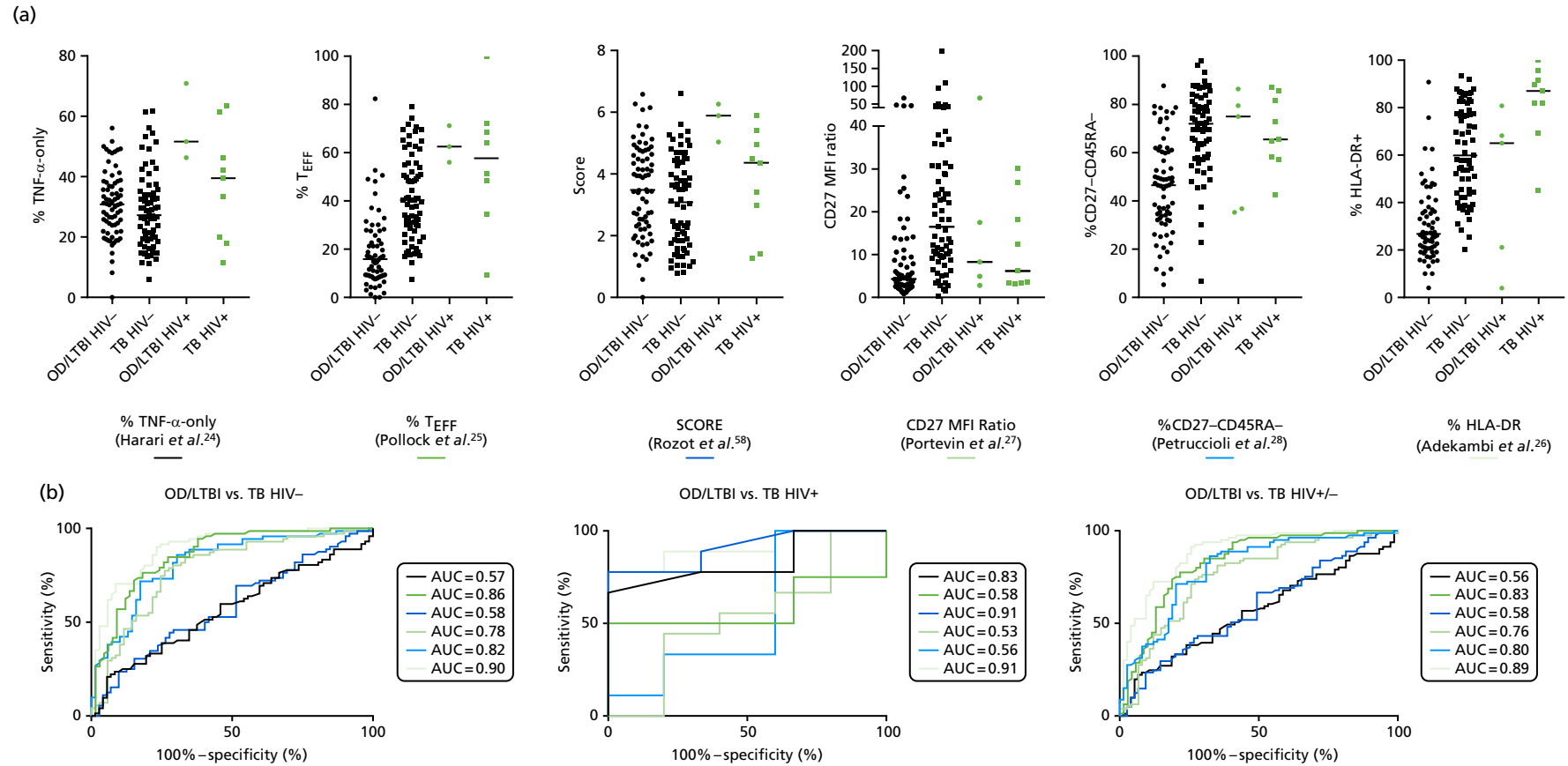
The distribution of signature measurements in the TB and OD/LTBI groups after stimulation with PPD is displayed in *Figure 8a* and the values after RD1 antigen stimulation are displayed in *Appendix 12*. There was significant and strong correlation in four of the six signature scores between PPD and RD1 stimulations in those individuals who had both stimulations (see *Figure 27*; shown only for %HLA-DR).

### Performance characteristics

The performance of each of the signatures for discriminating all TB from those with OD/LTBI is presented in *Figure 8* and *Table 12* for the PPD stimulation, stratified by HIV infection status.

The diagnostic accuracy of the discriminatory signatures was optimal for the culture-confirmed TB group (with the %HLA-DR signature achieving the highest AUC of 0.92, 95% CI 0.88 to 0.97), although the performance for the culture-unconfirmed group (Dosanjh category 2) was still reasonable for this hard-to-diagnose group of patients (*Table 13*). To evaluate if the Dosanjh category 4 subcategory influences the diagnostic accuracy of the signatures, we evaluated the performance of detecting all TB using only the Dosanjh subcategories 4B or 4C patients in the TB-excluded (OD/LTBI) group. Interestingly, the performance of the cellular immune signatures was comparable, suggesting that likelihood and risk of LTBI in the OD/LTBI group does not influence test accuracy of cellular immune signatures (see *Table 52* in *Appendix 13*).

The next best-performing signatures in the HIV– and HIV–/+ combined subgroups were, in order of decreasing accuracy, the %T<sub>EFF</sub> (of CD4-positive TNF- $\alpha$ -only cells) proposed by Pollock *et al.*<sup>25</sup> (AUC = 0.86 in HIV–, 95% CI 0.79 to 0.92), %CD27–CD45RA– proposed by Petruccioli *et al.*<sup>28</sup> (AUC = 0.82 in HIV–, 95% CI 0.75 to 0.89) and CD27 MFI ratio proposed by Portevin *et al.*<sup>27</sup> (AUC = 0.78, 95% CI 0.70 to 0.86), all of which showed highly significant discrimination between TB and OD/LTBI above the level of AUC = 0.5 ( $p < 0.0001$ ). However, none of these signatures performed well in the HIV+ population, with AUCs  $\leq 0.58$  in all cases (see *Table 12*). No statistical analysis to compare diagnostic accuracy between the signatures was performed.



**FIGURE 8** Performance of published signatures in full cohort, stratified by HIV infection status. (a) Dot plots scoring the signature values after PPD stimulation in TB suspects, stratified by diagnosis (TB or OD) and HIV infection status (positive or negative); and (b) ROC curves demonstrating diagnostic performance of signatures in the detection of active TB cases within the combined HIV+/- population, HIV+ alone and HIV- alone.

**TABLE 12** Performance of published cellular immune signature in diagnosing all TB, stratified by HIV infection status

Signature, reference	HIV	TB, n	OD/LTBI, n	AUC, % (95% CI)	Cut-off point	Sensitivity, % (95% CI)	Specificity, % (95% CI)	PPV	NPV
%TNF- $\alpha$ -only <sup>24</sup>	-	72	72	0.57 (0.47 to 0.66)	< 29.3 <sup>a</sup>	54.2 (42 to 66)	54.2 (42 to 66)	0.80	0.26
					< 18.7 <sup>b</sup>	23.6 (14.4 to 35.1)	90.3 (81 to 96)	0.89	0.26
	+	9	3	0.83 (0.59 to 1.07)	< 49.0 <sup>a</sup>	77.8 (40 to 97.2)	66.7 (9.4 to 99.2)	0.64	0.80
					< 44.2 <sup>b</sup>	66.7 (29.9 to 92.5)	100 (29.4 to 100)	1.0	0.80
	-/+	81	75	0.56 (0.47 to 0.65)	< 29.8 <sup>a</sup>	55.6 (44.1 to 66.6)	56 (44.1 to 67.5)	0.81	0.28
					< 18.7 <sup>b</sup>	23.46 (14.8 to 34.2)	90.7 (81.7 to 96.2)	0.89	0.26
%T <sub>EFF</sub> <sup>25</sup>	-	72	66	0.86 (0.79 to 0.92)	> 27.6 <sup>a</sup>	76.4 (64.9 to 85.6)	77.3 (65.3 to 86.7)	0.92	0.50
					> 37.2 <sup>b</sup>	56.9 (44.73 to 68.6)	90.9 (81.3 to 96.6)	0.95	0.39
	+	8	3	0.58 (0.25 to 0.92)	< 59.3 <sup>a</sup>	50 (15.7 to 84.3)	66.7 (9.4 to 99.2)	0.54	0.63
					< 53.7 <sup>b</sup>	50 (15.7 to 84.3)	100 (29.4 to 100)	1.0	0.72
	-/+	80	69	0.83 (0.76 to 0.90)	> 28.1 <sup>a</sup>	77.5 (66.8 to 86.1)	76.8 (65.1 to 86.1)	0.92	0.51
					> 49.4 <sup>b</sup>	36.3 (25.8 to 47.8)	91.3 (82.0 to 96.7)	0.93	0.30
SCORE <sup>58</sup>	-	72	72	0.58 (0.49 to 0.68)	< 3.43 <sup>a</sup>	52.8 (40.7 to 64.7)	52.8 (40.7 to 64.7)	0.79	0.25
					< 1.7 <sup>b</sup>	23.6 (14.4 to 35.1)	90.3 (81 to 96)	0.89	0.26
	+	9	3	0.91 (0.73 to 1.1)	< 5.2 <sup>a</sup>	77.8 (40 to 97.2)	66.7 (9.4 to 99.2)	0.64	0.85
					< 5.0 <sup>b</sup>	77.8 (40 to 97.2)	100 (29.2 to 100)	1.0	0.85
	-/+	81	75	0.58 (0.49 to 0.67)	< 3.5 <sup>a</sup>	51.9 (40.5 to 63.1)	52 (40.2 to 63.7)	0.78	0.25
					< 1.7 <sup>b</sup>	23.5 (14.8 to 34.2)	90.7 (81.7 to 96.2)	0.89	0.26
CD27 MFI ratio <sup>27</sup>	-	71	69	0.78 (0.70 to 0.86)	> 9.5 <sup>a</sup>	74.7 (62.9 to 84.2)	75.4 (63.5 to 85)	0.91	0.47
					> 25 <sup>b</sup>	32.4 (21.8 to 44.6)	91.3 (82 to 96.7)	0.92	0.29
	+	9	5	0.53 (0.19 to 0.88)	< 7.2 <sup>a</sup>	55.6 (21.2 to 86.3)	60 (14.7 to 94.7)	0.52	0.64
					< 4.3 <sup>b</sup>	44.4 (13.7 to 78.9)	80 (28.4 to 99.5)	0.63	0.65
	-/+	80	74	0.76 (0.68 to 0.84)	> 9.3 <sup>a</sup>	72.5 (61.4 to 81.9)	73 (61.4 to 82.7)	0.90	0.45
					> 25.0 <sup>b</sup>	31.3 (21.4 to 42.6)	90.5 (81.5 to 96.1)	0.92	0.29

continued



**TABLE 12** Performance of published cellular immune signature in diagnosing all TB, stratified by HIV infection status (*continued*)

Signature, reference	HIV	TB, n	OD/LTBI, n	AUC, % (95% CI)	Cut-off point	Sensitivity, % (95% CI)	Specificity, % (95% CI)	PPV	NPV
%CD27– CD45RA <sup>28</sup>	–	71	69	0.82 (0.75 to 0.89)	> 60.1 <sup>a</sup>	73.2 (61.4 to 83.1)	72.5 (60.4 to 82.5)	0.90	0.45
					> 76.5 <sup>b</sup>	39.4 (28 to 51.8)	91.3 (82 to 96.7)	0.94	0.31
	+	9	5	0.56 (0.19 to 0.92)	> 69.1 <sup>a</sup>	44.4 (13.7 to 78.8)	40 (5.3 to 85.3)	0.36	0.48
					> 86.8 <sup>b</sup>	11.1 (0.28 to 48.3)	100 (47.8 to 100)	1.0	0.59
	–/+	80	74	0.80 (0.73 to 0.87)	> 60.7 <sup>a</sup>	72.5 (61.4 to 81.9)	73 (61.4 to 82.7)	0.90	0.45
					> 76.6 <sup>b</sup>	38.8 (28.1 to 50.3)	90.5 (81.5 to 96.1)	0.93	0.31
%HLA-DR <sup>26</sup>	–	71	69	0.90 (0.84 to 0.95)	> 41.5 <sup>a</sup>	80.3 (69.1 to 88.8)	81.2 (70 to 89.6)	0.93	0.56
					> 49.6 <sup>b</sup>	70.4 (58.4 to 80.7)	91.3 (82 to 96.7)	0.96	0.48
	+	9	5	0.91 (0.76 to 1.1)	> 75.0 <sup>a</sup>	77.8 (40 to 97.2)	80 (28.4 to 99.5)	0.75	0.82
					> 81.3 <sup>b</sup>	77.8 (40 to 97.2)	100 (47.8 to 100)	1.0	0.85
	–/+	80	74	0.89 (0.84 to 0.94)	> 42.2 <sup>a</sup>	80.3 (69.9 to 88.3)	79.2 (68.5 to 87.6)	0.93	0.55
					> 54.3 <sup>b</sup>	64.2 (52.8 to 74.6)	90.9 (82.2 to 96.3)	0.96	0.44

–, negative; –/+, negative and positive; +, positive.

a Point at which sensitivity = specificity.

b Setting specificity to > 90%.

**Note**

For calculation of PPV and NPV, the following prevalence values were used: for the HIV– and +/– populations, the prevalence of TB in the T-SPOT.TB-positive population was 76.7%; for the HIV+ population, the prevalence of TB in the T-SPOT.TB-positive population was 43.6%.

**TABLE 13** Performance of cellular immune signatures in detecting TB, stratified by Dosanjh criteria

Comparison	Signature	TB, n	OD/LTBI, n	AUC, % (95% CI)	Cut-off point	Sensitivity, % (95% CI)	Specificity, % (95% CI)	PPV	NPV
Dosanjh category 1 vs. Dosanjh category 4	%TNF- $\alpha$ -only <sup>24</sup>	47	72	0.58 (0.47 to 0.68)	< 28.90 <sup>a</sup>	55.3 (40.1 to 69.8)	55.6 (43.4 to 67.3)	0.62	0.48
					< 18.70 <sup>b</sup>	23.4 (12.3 to 38.0)	90.3 (81.0 to 96.0)	0.76	0.47
	%T <sub>EFF</sub> <sup>25</sup>	48	66	0.88 (0.82 to 0.94)	> 29.30 <sup>a</sup>	81.3 (67.4 to 91.1)	81.8 (70.4 to 90.2)	0.86	0.77
					> 42.20 <sup>b</sup>	47.9 (33.3 to 62.8)	90.9 (81.3 to 96.6)	0.88	0.57
SCORE <sup>58</sup>	47	72	0.58 (0.48 to 0.69)	< 3.46 <sup>a</sup>	51.1 (36.1 to 65.9)	51.4 (39.3 to 63.4)	0.58	0.44	
				< 1.70 <sup>b</sup>	23.4 (12.3 to 38.0)	90.3 (81.0 to 96.0)	0.76	0.47	

**TABLE 13** Performance of cellular immune signatures in detecting TB, stratified by Dosanjh criteria (*continued*)

Comparison	Signature	TB, n	OD/LTBI, n	AUC, % (95% CI)	Cut-off point	Sensitivity, % (95% CI)	Specificity, % (95% CI)	PPV	NPV
Dosanjh category 2 vs. Dosanjh category 4	CD27 MFI ratio <sup>27</sup>	46	69	0.81 (0.73 to 0.89)	> 10.4 <sup>a</sup>	73.9 (58.9 to 85.7)	75.4 (63.5 to 85.0)	0.80	0.68
					> 25.0 <sup>b</sup>	39.1 (25.1 to 54.6)	91.3 (82.0 to 96.7)	0.86	0.53
	%CD27–CD45RA <sup>–28</sup>	46	69	0.84 (0.77 to 0.92)	> 61.3 <sup>a</sup>	78.3 (63.6 to 89.1)	78.3 (66.7 to 87.3)	0.83	0.73
					> 76.5 <sup>b</sup>	47.8 (32.9 to 63.1)	91.3 (82.0 to 96.7)	0.88	0.57
	%HLA-DR <sup>26</sup>	46	69	0.92 (0.88 to 0.97)	> 44.2 <sup>a</sup>	82.6 (68.6 to 92.2)	82.6 (71.6 to 90.7)	0.86	0.78
					> 49.6 <sup>b</sup>	78.3 (63.6 to 89.1)	91.3 (82.0 to 96.7)	0.92	0.76
	%TNF- $\alpha$ -only <sup>24</sup>	25	72	0.55 (0.41 to 0.69)	< 30.3 <sup>a</sup>	52.0 (31.3 to 72.2)	52.8 (40.7 to 64.7)	0.21	0.82
					< 18.7 <sup>b</sup>	24.0 (9.4 to 45.1)	90.3 (81.0 to 96.0)	0.38	0.83
	%T <sub>EFF</sub> <sup>25</sup>	24	66	0.81 (0.71 to 0.90)	> 23.0 <sup>a</sup>	70.8 (48.9 to 87.4)	72.7 (60.4 to 83.0)	0.39	0.91
					> 37.2 <sup>b</sup>	45.8 (25.6 to 67.2)	90.9 (81.3 to 96.6)	0.55	0.87
	SCORE <sup>58</sup>	25	72	0.58 (0.45 to 0.72)	< 3.3 <sup>a</sup>	56.0 (34.9 to 75.6)	56.9 (44.7 to 68.6)	0.24	0.84
					< 1.6 <sup>b</sup>	24.0 (9.4 to 45.1)	90.3 (81.0 to 96.0)	0.38	0.83
	CD27 MFI ratio <sup>27</sup>	25	69	0.73 (0.62 to 0.84)	> 7.5 <sup>a</sup>	68.0 (46.5 to 85.1)	68.1 (55.8 to 78.8)	0.34	0.90
					> 25.1 <sup>b</sup>	20.0 (6.8 to 40.7)	91.3 (82.0 to 96.7)	0.36	0.82
%CD27–CD45RA <sup>–28</sup>	25	69	0.77 (0.67 to 0.87)	> 57.4 <sup>a</sup>	72.0 (50.6 to 87.9)	71.0 (58.8 to 81.3)	0.37	0.91	
				> 76.5 <sup>b</sup>	24.0 (9.4 to 45.1)	91.3 (82.0 to 86.7)	0.40	0.83	
%HLA-DR <sup>26</sup>	25	69	0.84 (0.76 to 0.93)	> 38.1 <sup>a</sup>	76.0 (54.9 to 90.6)	76.8 (65.1 to 86.1)	0.44	0.93	
				> 49.6 <sup>b</sup>	56.0 (34.9 to 75.6)	91.3 (82.0 to 96.7)	0.61	0.89	

a Point at which sensitivity = specificity.

b Setting specificity to > 90%.

**Note**

For calculating PPV and NPV, the prevalence of Dosanjh 1 was 57.1%, and the prevalence of Dosanjh 2 was 19.6%.

The two signatures that measured proportions of functional *Mtb*-specific subsets only, and not phenotype of *Mtb*-specific cells, were the %TNF- $\alpha$ -only (of CD4-positive and cytokine-positive) signature proposed by Harari *et al.*<sup>24</sup> and the SCORE signature proposed by Rozot *et al.*<sup>58</sup> These did not provide significant discrimination between TB groups in the HIV– or HIV+/- populations, with AUCs of  $\leq 0.57$  that were not significant ( $p > 0.05$ ). Owing to the small numbers of responders in the HIV– cohort, this population was excluded from subsequent subcohort analyses.

### Diagnostic performance in key subgroups of tuberculosis

Next, we sought to evaluate the performance of the cellular immune signatures in detecting important subsets of TB. First, we assessed the diagnostic accuracy for identifying either the culture-confirmed TB cases (Dosanjh category 1) or culture-unconfirmed TB cases (Dosanjh category 2). We were also able to evaluate the influence of the Dosanjh category 4 subcategories (B, C and D, which correspond to decreasing risk/likelihood of having LTBI) on the signature performance. The signature values in each of the Dosanjh categories are presented in *Figure 28* in *Appendix 13*.

As with the full cohort analysis, the signatures measuring functionality only (cytokine responses), that is the TNF- $\alpha$ -only<sup>24</sup> signature and the SCORE<sup>58</sup> signatures, showed no differences between Dosanjh categories in the HIV- cohort. However, the four signatures measuring phenotype (%T<sub>EFF</sub><sup>25</sup> CD27-MFI ratio,<sup>27</sup> %CD27-CD45RA<sup>-28</sup> and %HLA-DR<sup>26</sup>) showed significantly higher values in both Dosanjh categories 1 and 2 TB groups than in the OD/LTBI Dosanjh category 4 subcategories. Interestingly, no differences were observed in the signature values between the Dosanjh category 4 subcategories (only 4B and 4C could be used for statistical comparisons as there were too few participants in the 4D group).

### The performance of signatures in the smear-negative interferon gamma release assay-positive cohort of tuberculosis suspects

Smear microscopy results are available on the same day that the patient presents to secondary care and IGRA results are usually available by the next day. The flow cytometry signature aims to distinguish active TB from LTBI in those who are IGRA positive, when it is unclear whether the *Mtb* infection is latent or active. In this subanalysis, we therefore assessed the performance of the two best-flow signatures (the %HLA-DR<sup>26</sup> and %T<sub>EFF</sub><sup>25</sup>), within the IGRA-positive smear-negative population within this cohort (*Table 14*).

The pre-test probability of a TB suspect having TB after presenting with both a negative smear and a positive IGRA test is 79% (note, 59% and 20% for culture-positive and culture-negative TB subgroups, respectively), which is high, but not high enough to be confident that commencing TB treatment is the correct treatment course. The findings from this subanalysis show that, by using either the %HLA-DR<sup>26</sup> or %T<sub>EFF</sub><sup>25</sup> signature tests, a high PPV for all TB (0.94) and culture-confirmed TB alone (0.87) can be achieved.

The HIV- cohort was further stratified by disease type, with the TB group split into either PTB or EPTB and the OD/LTBI group split into groups based on most frequent final diagnoses (see *Figure 29* and *Table 53*). Again, only the signatures measuring phenotype showed differences between groups. Although no differences between other diagnoses in the OD/LTBI were observed, both PTB and EPTB showed elevated signature levels compared with the OD/LTBI groups.

Diagnostic accuracy was highest for detection of PTB cases from the overall OD/LTBI group (maximum AUC of 0.93, 95% CI 0.87 to 0.98) compared with EPTB in which performance was reduced (maximum AUC of 0.88, 95% CI 0.82 to 0.94), as achieved using the %HLA-DR<sup>26</sup> signature that achieved the highest test accuracy. The diagnostic performance characteristics, including AUCs, sensitivity and specificity, for detecting either PTB or EPTB are presented in *Table 53*.

## Discussion

Here we present the first validation of previously identified cellular immune signatures for the detection of active TB cases in a cohort of TB suspects recruited as part of routine clinical practice. The immunological nature of these assays, with the signatures being measurable only when a detectable *Mtb*-specific CD4-positive response can be characterised, confines the eligible patient population to those who respond to *Mtb* antigens (i.e. the IGRA-positive individuals) and, therefore, the challenge for these assays is to discriminate between active TB and OD/LTBI. We found that, of the six signatures validated in this cohort,

**TABLE 14** The performance of the %HLA-DR<sup>26</sup> and %T<sub>EFF</sub><sup>25</sup> signatures in detecting subgroups of TB patients among smear-negative patients in the IGRA-positive cohort used in the validation of flow cytometric signatures substudy

Diagnostic performance characteristic	%HLA-DR <sup>26</sup>	%T <sub>EFF</sub> <sup>25</sup>
<i>Performance in detecting smear-negative TB (Dosanjh categories 1 and 2)</i>		
<i>Prevalence of TB in all smear-negative T-SPOT.TB-positive TB suspects = 79% (from overall IDEA study population)</i>		
TB/OD (n/n)	49/45	50/43
AUC, % (95% CI)	0.91 (0.84 to 0.97)	0.90 (0.83 to 0.96)
Cut-off point <sup>a</sup>	> 41.2	> 24.6
Sensitivity, % (95% CI)	81.6 (68.0 to 91.2)	80 (66.3 to 90.0)
Specificity, % (95% CI)	80 (65.4 to 90.4)	81.4 (66.6 to 91.6)
PPV/NPV	0.94/0.54	0.94/0.52
<i>Performance in detecting smear-negative culture-positive (Dosanjh category 1) TB</i>		
<i>Prevalence of culture-positive TB in all smear-negative T-SPOT.TB-positive TB suspects = 59%</i>		
TB/OD (n/n)	29/45	31/43
AUC, % (95% CI)	0.91 (0.83 to 0.98)	0.92 (0.86 to 0.98)
Cut-off point <sup>a</sup>	> 43.1	> 28.2
Sensitivity, % (95% CI)	82.8 (64.2 to 94.2)	83.9 (66.3 to 94.6)
Specificity, % (95% CI)	82.2 (68.0 to 92)	86.1 (72.1 to 94.7)
PPV/NPV	0.87/0.73	0.90/0.78
<i>Performance in detecting smear-negative and culture-negative (Dosanjh category 2) TB</i>		
<i>Prevalence of culture-unconfirmed TB in smear-negative TB suspects = 20%</i>		
TB/OD (n/n)	20/45	19/43
AUC, % (95% CI)	0.90 (0.82 to 0.98)	0.86 (0.76 to 0.96)
Cut-off point <sup>a</sup>	> 39.1	> 22.5
Sensitivity, % (95% CI)	80 (56.3 to 94.3)	79 (54.4 to 94.0)
Specificity, % (95% CI)	77.8 (62.9 to 88.8)	79.1 (64.0 to 90.0)
PPV/NPV	0.47/0.94	0.49/0.94

<sup>a</sup> For this analysis, the cut-off points for the signatures were determined by finding the value where sensitivity = specificity.

only those that measured incorporated phenotypic markers in the flow cytometry signature (i.e. %T<sub>EFF</sub>, CD27 expression or %HLA-DR<sup>25–27</sup>) showed discriminatory ability, whereas the signatures measuring functionality did not differentiate between TB and OD/LTBI.

The best-performing signature was found to be the %HLA-DR signature,<sup>26</sup> which has recently been validated in several cohorts and shown to have high test accuracy for differentiating TB from healthy LTBI.<sup>26,59,60</sup> This is the first study to demonstrate its diagnostic performance in a cohort in which the LTBI group also had OD and in which all patients were recruited with suspected TB. The performance we present here (AUC = 0.90) is not as high as previously found (AUCs 0.92–1.0). However, when only culture-confirmed TB among HIV– patients was considered, the diagnostic accuracy of this signature was comparable to that reported by Riou *et al.*<sup>60</sup> (also AUC = 0.92). Therefore, the overall lower performance we present here for detection of all TB using previously described cellular immune signatures probably reflects the inclusion of paucibacillary and hard-to-diagnose TB patients, particularly those with culture-unconfirmed TB.

The %T<sub>EFF</sub><sup>25</sup> signature also performed with reasonably high accuracy for detection of all TB, providing an AUC of 0.86 for detecting all TB in the HIV– population. Unlike in the original paper, in which performance was high in a mixed cohort of HIV+ and HIV– patients, in this study the signature could not discriminate between TB and OD/LTBI in the HIV+ population.

Both the %HLA-DR<sup>26</sup> and %T<sub>EFF</sub><sup>25</sup> signatures could be useful in the setting of IGRA-positive TB suspects, as, in this scenario, they are able to provide a high PPV for all TB (0.95 and 0.95, respectively) and for culture-confirmed TB (0.92 and 0.88, respectively). Therefore, on initial screening of an IGRA-positive suspect, a positive result in these tests could provide clinicians with sufficient evidence (i.e. ≈90% probability) to start treatment immediately, without any need to wait for culture confirmation. This is the testing algorithm in which these assays could be useful. In future studies, we wish to determine these signatures in the smear-negative group of TB patients. Importantly, we also assessed the performance of these two signatures in the smear-negative subgroup within the cohort. These signatures were found to provide very high PPVs for all TB and culture-confirmed TB within the T-SPOT.*TB*-positive smear-negative population of TB suspects. These patients usually require several more investigations to inform treatment decision, or else treatment will be started without confidence in the correct diagnosis having been made. For culture-confirmed TB, the prevalence of which in the smear-negative T-SPOT.*TB*-positive population was 59%, the PPVs of 0.87 and 0.88 raised the pre-test probability of TB by 28–29% (i.e. from 59% pre-test probability to 87–88% post-test probability). The increase in the pre-test probability for all TB cases in this specific population was 13% (from 79% to a PPV of 94%), demonstrating that a positive test result with either of these assays would provide a rapid rule-in test, facilitating an accelerated decision to treat. A positive result in this setting would thus provide strong support for a diagnosis of TB and a decision to treat.

We found in this study that the signatures measuring polyfunctional profiles (%TNF- $\alpha$ -only<sup>24</sup> and SCORE<sup>58</sup>) do not appear to be able to discriminate between TB and OD/LTBI groups. Several research groups have measured similar profiles, and it appears that these signatures are not reproducible across different studies. Day *et al.*<sup>63</sup> found that there were differences between LTBI and smear-negative and smear-positive TB, not with TNF- $\alpha$ -only CD4-positive responses, but with IFN $\gamma$ +TNF- $\alpha$ +IL-2– and IL-2 responses.

Incorporating measurement of CD27 showed reasonable test accuracy in our cohort, but only in the HIV– population, and to a lesser extent than the %HLA-DR<sup>26</sup> and %T<sub>EFF</sub><sup>25</sup> signatures (although statistical analyses to compare tests were not performed).

There are some limitations. Some of the PBMC stimulations did not result in detectable cytokine responses, meaning that they were excluded from the diagnostic performance analysis. Therefore, the performance may not be fully reflected in the analysis we present and, in practice, these tests may result in a number of failed or indeterminate results.

This is the largest validation of cellular immune signatures in a cohort of TB and LTBI patients and the first to test their performance in a cohort of TB suspects. We have demonstrated that cellular immune signatures can provide high test accuracy and may be useful for a rapid blood-based test for TB in the IGRA-positive population.

# Chapter 6 Candidate rule-out tests

## Introduction

Interferon gamma release assays are the recommended immunological assays to detect *Mtb* infection. There are two commercially available IGRAs, both of which measure IFN $\gamma$  production in response to RD1 antigens (the T-SPOT.*TB*, which uses the T-SPOT.*TB* platform, and the QFT-GIT, which uses ELISA). IGRAs are unable to discriminate between active disease and LTBI and, as such, are unsuitable as tests to rule in active TB (because of poor specificity). Their sensitivity for detecting active TB cases is reasonably high, leading to the possibility that these tests could be used as a rule-out test for active TB. Ideally, such a test would provide > 95% sensitivity for all TB cases for it to be clinically useful. The IDEA study demonstrated that the T-SPOT.*TB* tests provided optimal accuracy (as compared with QFT-GIT), but that neither test in their current format provides sufficient sensitivity (between 67.3% and 82.3%) for detecting all TB<sup>12</sup> for this important clinical utility.<sup>11,12</sup> In this substudy we explored two candidate approaches to improve on the sensitivity of immunological tests for active TB.

### Additional *Mycobacterium tuberculosis* antigens

A strategy for improving diagnostic sensitivity of immune based tests is to include additional *Mtb* antigens. Use of *Mtb*-specific antigens for stimulation ensures that, although different secreted immune mediators are being measured than in IGRA (i.e. chemokines instead of IFN $\gamma$ ), diagnostic specificity is not compromised. Various studies have taken this approach in an attempt to stratify different types of TB infection and/or improve sensitivity.<sup>22,64</sup> Indeed, the new updated version of the QuantiFERON test (QuantiFERON TB Gold-Plus, QIAGEN, Hilden, Germany) contains an additional antigen tube containing peptides that are proposed to stimulate *Mtb* CD8-positive T cells and drive improved test sensitivity for TB. However, very few studies have been performed to validate this new test and one recent study found its sensitivity and specificity for active TB were similar to those of the QFT-GIT.<sup>65</sup>

The recently completed IDEA study identified that four *Mtb* RD1-related antigens were able to provide good sensitivity for active TB when used in a next-generation T-SPOT.*TB* assay: ESAT-6, CFP-10, Rv3615c [Esx-1 substrate protein C (EspC)] and Rv3798c.<sup>12</sup> Use of all four of these antigens in a stimulation assay together is therefore likely to maximise detection of *Mtb* infection. Indeed, in the next-generation T-SPOT.*TB* assay, combinations of these four antigens could provide an improved performance, with a sensitivity of 89.9% for all TB and of 94.4% for culture-confirmed TB.<sup>12</sup>

### Detection of additional or alternative analytes

A further powerful and pragmatic approach to enhance test sensitivity is to include measurement of alternative or additional immune mediators. We and others<sup>66–68</sup> have proposed to improve on the sensitivity provided by detection of IFN $\gamma$  by measuring immune mediators in which secretion is promoted by IFN $\gamma$ , thereby providing an amplified signal. Two such chemokines are chemokine (C-X-C motif) ligand 9 [CXCL9, also known as MIG (monokine induced by gamma interferon)] and chemokine (C-X-C motif) ligand 10 (CXCL10, also known as interferon gamma-induced protein-10), both of which are produced by monocytes, neutrophils and other cells in response to IFN $\gamma$  production by antigen-specific T cells and have been found to provide increased sensitivity for TB cases in some studies.<sup>68,69</sup> Others have proposed to detect alternative cytokines, such as IL-2, TNF- $\alpha$  or Th2-type cytokines,<sup>68,70</sup> although the evidence for these cytokines providing improved sensitivity for TB (over that of IFN $\gamma$ ) is limited.

### Alternative assay platforms

We and others have previously developed a highly sensitive whole-blood molecular test with high potential to reliably rule out the diagnosis of TB based on measurement of IFN $\gamma$ -dependent chemokine release in response to *Mtb*-specific antigens.<sup>23</sup> The assay involves overnight stimulation of blood with ESAT-6 and CFP-10, and

the subsequent measurement of *CXCL9* and *CXCL10* expression by qRT-PCR. To further improve sensitivity, we incorporated a third highly immunodominant and *Mtb*-specific antigen, EspC (Rv3615c), an immunogenic RD1-dependent antigen.<sup>22</sup> In preliminary studies using a case–control approach, the assay was found to be 100% sensitive for active TB ( $n = 39$ ), when combining pairs of antigens and regardless of the pairing (i.e. any two of ESAT-6, CFP-10 and EspC) (Connell D, Reuschl AK, Lalvani A, *et al.*, Imperial College London, unpublished data, 2012). Specificity was also high (94%), with only 1 of 16 IGRA-negative BCG-vaccinated HCs scoring positive in the assay. These compelling data suggest potential for a stimulated chemokine qRT-PCR test with sufficiently high diagnostic sensitivity to be used to rule out TB infection (and, therefore, active TB disease) at first presentation. The promising results with this assay to date now merit validation in a large-scale prospective cohort study of patients undergoing routine diagnostic work-up for suspected active TB.

As an alternative to the ELISA platform for detecting proteins as used in the current QFT-GIT, we further propose that the detection of target analytes from plasma of stimulated blood could be improved on this platform using Meso Scale Discovery (MSD) technology, which provides a broader dynamic range and greater sensitivity for low-abundance proteins than ELISA ([www.mesoscale.com/](http://www.mesoscale.com/)).

### Rationale for candidate rule-out assays

#### Assay platforms

Given the promising performance of qRT-PCR detection of *Mtb* antigen-specific *CXCL9* and *CXCL10* production in stimulated PBMC samples in our unpublished case–control cohort, coupled with data from Kasproicz *et al.*<sup>23</sup> showing that performance appeared to be better than that of T-SPOT.TB, we decided to use this assay approach for the detection of our target genes. An additional IFN $\gamma$ -related gene was selected for inclusion in the candidate molecular rule-out test. Basic leucine zipper atf-like transcription factor 2 (*BATF2*), which was significantly overexpressed in whole blood collected from TB patients (Long Hoang, National Heart and Lung Institute, Imperial College London, 2017), encodes a transcription factor and is expressed in macrophages stimulated by IFN $\gamma$ .<sup>71</sup>

Additionally, within the IDEA study biobank, we were also able to use the surplus supernatants from the QFT-GIT tests performed to evaluate whether or not the use of selected analytes could improve on the sensitivity compared with measuring IFN $\gamma$  alone. Analytes were assessed either singly or in combination. Therefore, as an additional substudy, to further test the proof of concept that detection of alternative analytes can improve on test accuracy when compared with IFN $\gamma$ , we chose to measure target chemokines in the QFT-GIT supernatants using MSD.

#### Aim

The aim of this substudy was to evaluate the diagnostic accuracy of two candidate immune-based tests to measure previously identified chemokine and cytokines for their use in ruling out active TB cases.

#### Primary objective

- To determine whether or not the detection of molecules downstream of IFN $\gamma$ , namely *CXCL9*, *CXCL10* and *BATF2*, by qRT-PCR from RD1-stimulated PBMCs, can provide a greater sensitivity for active TB than in currently available tests (i.e. a molecular rule-out test).

#### Secondary objectives

- To determine whether or not detection of *CXCL10* or IFN $\gamma$  in the GFT-GIT supernatants by MSD can provide improved diagnostic accuracy for detecting TB cases than in the ELISA platform.
- To determine the performance of the above tests for discriminating between active TB and OD in the IGRA-positive population of TB suspects.

## Methods

### Cohort selection

As the existing data on this candidate molecular rule-out test are limited when compared with the other tests, we decided (at the SMG meetings and ISAB meetings) that for this technology we would take a two-stage approach to validation. First, we planned to assess the performance of the test in an artificial cohort, selected from within the IDEA study cohort, to act as a proof of principle that the candidate tests can provide greater sensitivity for active TB than the current immunological tests: the T-SPOT.*TB* and QFT-GIT. Therefore, we designed a 'GO/NO-GO' cohort for the first stage of validation. If high sensitivity for active TB was achieved in the cohort (i.e. greater than T-SPOT.*TB*), then the test would be rolled out on the full cohort of eligible patients for whom a PBMC sample was available (note that the cellular immune test was prioritised within the VANTDET study, but for most participants more than one PBMC vial was available so inclusion in both substudies was achievable in many cases).

For overall eligibility, the same inclusion criteria were used for assessment of the T-SPOT.*TB* and QFT-GIT tests within the IDEA study (i.e. diagnosis of either TB or OD, no history/evidence of previous TB), with the exception that individuals from site H were included in this cohort and only those with an available PBMC sample were included. HIV+ individuals were included.

### GO/NO-GO cohort

For the GO/NO-GO cohort, 25 individuals with available PBMC samples were picked randomly from each of the four different groups: (1) active TB T-SPOT.*TB* positive, (2) active TB T-SPOT.*TB* negative, (3) OD T-SPOT.*TB* positive and (4) OD T-SPOT.*TB* negative. Previous studies exploring novel immune tests for active TB lack the active-TB IGRA-negative group, which we have enriched for in this cohort. Should any of the analytes we detect in these candidate assays provide > 95% sensitivity for active TB, with an acceptable level of specificity (> 65%), then the GO/NO-GO criteria from the first study would have been met, and the assays would have been performed on the full IDEA study cohort, in which PBMCs were available. For detection of *CXCL10* and *IFN $\gamma$* , by MSD using QFT-GIT supernatants, we used a similar cohort of TB and OD patients.

### Full cohort

In the event that 95% sensitivity and > 65% specificity for all active TB cases is achieved (i.e. GO criteria met), the assay will be performed on all available eligible individuals with available PBMCs.

### Experimental set-up for molecular rule-out test

All 100 samples were placed into blocks of five or six samples for each experiment, selected randomly.

### Stimulation

After thawing the frozen PBMCs and counting them with a Countess II FL Automated Cell Counter, the samples were spun down and resuspended in R10, and plated at  $1 \times 10^6$  PBMCs per well in a 48-well plate (CELLSTAR); at least three wells were required for each sample. Cells were immediately stimulated with one of the following antigen formulations (200  $\mu$ l total volume): pooled 15-mer overlapping peptides from the *Mtb* antigens ECRR in R10 (final peptide concentration of 10  $\mu$ g/ml); IFN $\gamma$  (10  $\mu$ g/ml) in R10, to act as the positive control; and R10 containing dimethyl sulfoxide (final concentration 1.48% to match that of ECRR), to act as a negative control. Stimulated PBMCs were incubated at 37 °C in 5% CO<sub>2</sub> for 16 hours.

### Ribonucleic acid extraction and quality control

After 16 hours' stimulation, the cells were lysed with Buffer RLT (QIAGEN, Hilden, Germany) with 1%  $\beta$ -mercaptoethanol. Total RNA from the stimulated cells was extracted using the QIAGEN RNeasy Micro kit as per the manufacturer's instructions (QIAGEN, Hilden, Germany). Total RNA was eluted in 14  $\mu$ l of RNase-free water and stored at -80 °C until further used. Quantification of the concentration and quality of the RNA were measured using a NanoDrop 8000 spectrophotometer and an Agilent 2100 Bioanalyzer, respectively.



### Two-step quantitative reverse transcription-polymerase chain reaction

Extracted messenger RNA was reverse transcribed to cDNA using First Strand cDNA Synthesis (Thermo Fisher Scientific). PCR was performed using a TC-512 Thermal Cycler (Techne, Staffordshire, UK), with RNase inhibitor (Thermo Fisher Scientific) and random hexamers (Thermo Fisher Scientific). The amplification and detection was performed using Applied Biosciences™ 7500 Fast Real-Time PCR System (Thermo Fisher Scientific), using the default settings suitable for Quantitation-Comparative Ct (threshold cycle) to perform the analysis  $2^{-\Delta\Delta Ct}$ . The probes and primers (Life Technologies, CA, USA) assay ID for the internal reference *HPRT1* (Hs02800695\_m1) and target genes *CXCL10* (Hs01124251\_g1), *CXCL9* (Hs00171065\_m1), *IFN $\gamma$*  (Hs00989291\_m1) and *BATF2* (Hs00912737\_m1) were used. The relative fold change was calculated as the ratio between the mean Ct values of the target gene and reference gene (*GAPDH*) in each stimulated sample in relation to the unstimulated sample.

### Detection of candidate biomarkers from QuantiFERON supernatants

During the IDEA study, the excess supernatants from the QFT-GIT test were harvested and stored at  $-80^{\circ}\text{C}$ . An additional project was to test the performance of promising candidate immune mediators IFN $\gamma$ , IL-2, CXCL10, monocyte chemoattractant protein 1 (MCP-1), monocyte chemoattractant protein 3 (MCP-3), macrophage inflammatory protein 1 $\beta$  (MIP-1 $\beta$ ) and TNF- $\alpha$ . Using the MSD U-PLEX platform to detect all of these chemokines and cytokines as per manufacturer's instructions with some variation with longer stimulation time; plates were read using a MESO QuickPlex SQ 120 instrument (Meso Scale Discovery, Rockville, MD, USA). Concentration was calculated by normalising the stimulated supernatant from the nil sample.

### Statistical analysis

All statistics were performed using Prism software. Differences between groups (in normalised fold change gene expression or analyte concentration) were determined using a Kruskal–Wallis test with Dunn's post hoc test for multiple comparisons. Diagnostic accuracy for discriminating between groups was calculated using ROC curve analysis.

## Results

### Cohort characteristics

The details of the cohort eligible for analysis and the stratification between the full eligible cohort and GO/NO-GO cohort are given in *Figure 9*.

From the 100 individuals selected to be part of the GO/NO-GO cohort, three were not found in the biobank and an additional three samples were found, subsequently, to be ineligible (having a previous history of TB), leaving a total of 94 in the full cohort of assay individuals.

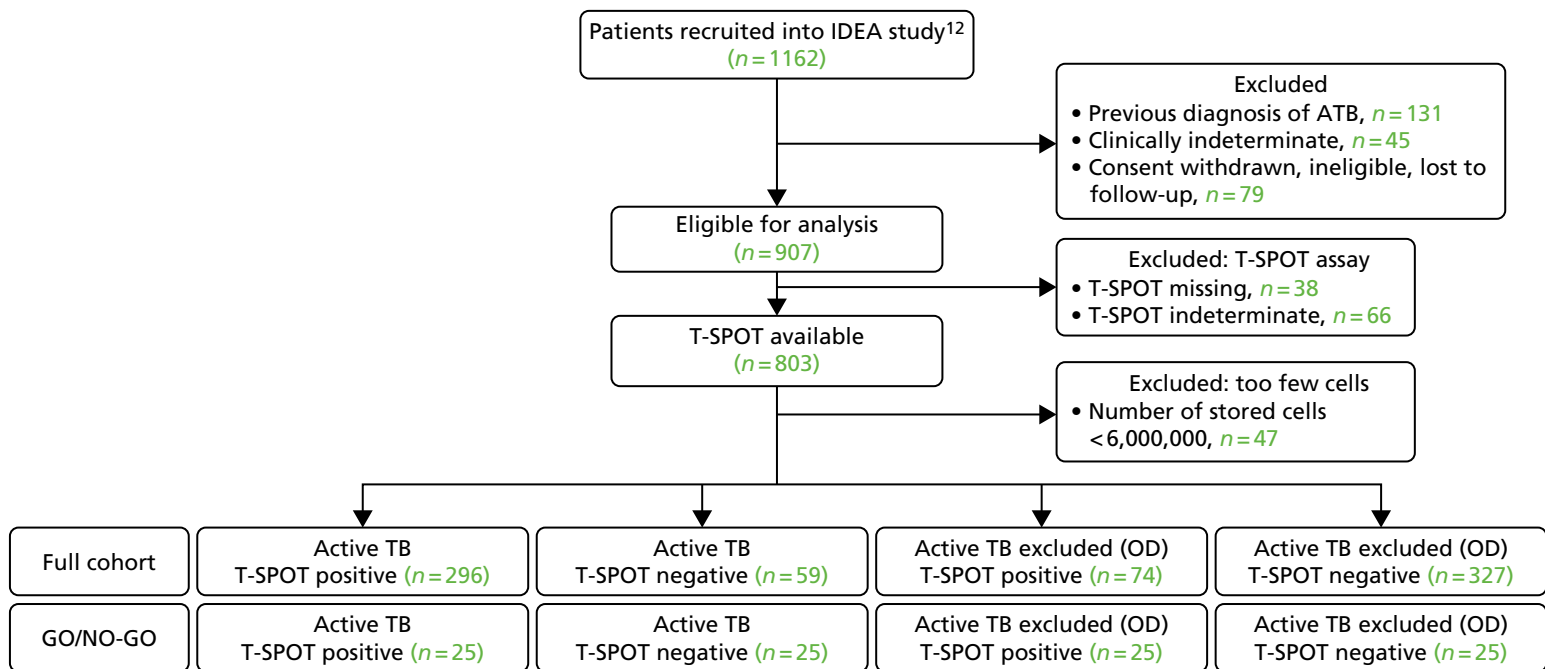
The demographic and clinical characteristics of the final cohort are shown in *Table 15*. Further details on the severity and type of TB disease, or OD, within the full cohort are given in *Appendix 14* (see *Tables 54* and *55*).

### Validation of molecular rule-out tests

To measure gene expression of all analytes (*CXCL10*, *CXCL9*, *BATF2* and *IFN $\gamma$* ) using qRT-PCR, a minimum of 50 ng of total RNA was needed. Of the 94 samples that were assayed, 13 samples yielded low amounts of RNA (around  $\approx 40$  ng); therefore, not all analytes could be measured. In these cases, *BATF2* expression was not measured.

### Gene expression of target analytes in response to the positive control

As all of the target genes (*CXCL9*, *CXCL10* and *BATF2*) are known to be up-regulated in response to IFN $\gamma$ , this was used as the positive control in the assay. Previously, phytohaemagglutinin (PHA) was used in our laboratory for these assays (as is used in T-SPOT.TB and QFT-GIT). However, preliminary optimisation experiments in the VANTDET study revealed that the levels of the target genes were not reliably increased using PHA. This is probably a result of the reduced viability of PBMCs following PHA stimulation, which we



**FIGURE 9** Study flow diagram for the validation of the candidate rule-out tests. ATB, active tuberculosis.

**TABLE 15** Demographic and clinical characteristics for the GO/NO-GO cohort for the assessment of a candidate molecular rule-out test for active TB

Demographic/ clinical characteristic	Active TB		OD		p-value
	T-SPOT.TB positive (N = 24)	T-SPOT.TB negative (N = 22)	T-SPOT.TB positive (N = 22)	T-SPOT.TB negative (N = 26)	
Age (years), median (range)	33 (19–57)	48.5 (27–81)	43.95 (19–74)	49.19 (21–84)	0.0011
Female, n (%)	12 (50)	7 (31.8)	8 (36)	10 (38)	
Ethnic origin, n (%)					N/A
Asian	2 (8.3)	2 (9.1)	1 (4.5)	2 (7.7)	
Black	4 (16.6)	0 (0)	3 (13.6)	7 (26.9)	
Indian subcontinent	17 (70.8)	13 (59.1)	10 (45.5)	9 (34.6)	
Mixed	0 (0)	2 (9.1)	0 (0)	0 (0)	
White	1 (4.2)	5 (22.7)	8 (36.4)	8 (30.1)	
HIV+, n (%)	1 (4.2)	2 (9.1)	6 (27.3)	1 (3.8)	0.032
TST, n (%)					< 0.0001
Positive	5 (20.8)	9 (40.9)	0 (0)	1 (3.8)	
Negative	0 (0)	0 (0)	1 (4.5)	8 (30.1)	
Not tested	19 (79.2)	13 (59.1)	21 (95.5)	19 (73.1)	
BCG, n (%)					
Yes	18 (75)	17 (77.3)	19 (86.4)	22 (84.6)	
No	6 (25)	5 (22.7)	3 (13.6)	4 (15.4)	
Height (m), median (range)	1.69 (1.52–1.85)	1.69 (1.61–1.8)	1.65 (1.55–1.88)	1.68 (1.52–1.86)	0.3981
Height missing, n (%)	4	10 (45.5)	2	7	
Weight (kg), median (range)	61 (42–123.5)	61.5 (47.4–96)	64.5 (45–82.6)	72.3 (48.3–140)	0.2815
Weight missing, n (%)	1	0	0	4	
BMI (kg/m <sup>2</sup> ), median (range)	23.1 (17.6–36.9)	22.6 (18.9–31.1)	22.4	24.4 (15.9–43.2)	0.6108
BMI missing, n (%)	4	10	2	8	

N/A, not applicable.

**Note**

Characteristics were compared across groups using either a Kruskal–Wallis test or a chi-squared test.

confirmed by flow cytometry (data not shown). By plotting the normalised relative expression of target genes in response to ECRR or IFN $\gamma$ , we were able to select a cut-off point for an acceptable response in the positive control condition. The cut-off points selected were as follows: > 100 for *CXCL10*, > 100 for *CXCL9* and > 10 for *BATF2* (as shown in *Figure 31* in *Appendix 15*).

**Gene expression in response to *Mycobacterium tuberculosis* antigens**

The results of the PCR detection of target genes in response to the antigen conditions (normalised to unstimulated) are shown in *Table 16*.

**TABLE 16** Quantitative reverse transcription-polymerase chain reaction detection of *CXCL10*, *CXCL9* and *BATF2* in response to *Mtb* antigens or positive control in the GO/NO-GO cohort of patients selected for validation of candidate molecular rule-out tests

Analyte/measurement	Active TB		OD	
	T-SPOT. <i>TB</i> positive (N = 24)	T-SPOT. <i>TB</i> negative (N = 22)	T-SPOT. <i>TB</i> positive (N = 22)	T-SPOT. <i>TB</i> negative (N = 26)
<b>CXCL10</b>				
Total for analysis, n (%)	19 (75)	19 (87)	12 (55)	21 (81)
Total failed, n (%)	5 (25)	3 (13)	10 (45)	5 (19)
PCR indeterminate	0	1	0	1
<i>HPRT1</i> fail	3	2	6	5
Low levels in positive control	2	1	4	0
Fold change ECRR/unstimulated, mean (range)	23,604.50 (116.68–14,0596.57)	9362.95 (8.11–46,681.24)	115,353 (1.45–56,513.26)	1408.53 (1.5–18,053.68)
IFN $\gamma$ /unstimulated, mean (range)	50,483.2 (224.9–325,447.0)	126,019.7 (829.6–432,419.1)	104,350.1 (156.8–384,828.4)	55,180.4 (361.6–381,780.3)
<b>CXCL9</b>				
Total for analysis, n (%)	18 (76)	18 (83)	13 (59)	21 (81)
Total failed, n (%)	6 (24)	4 (17)	9 (40.9)	5 (19)
PCR indeterminate	0	1	1	1
<i>HPRT1</i> fail	3	2	6	5
Low levels in positive control	3	2	2	0
Fold change ECRR/unstimulated, mean (range)	33,280.75 (350.84–120,140.97)	15,049.99 (0.99–74,914.48)	1030.38 (0.19–5146.35)	788.49 (0.23–7952.44)
IFN $\gamma$ /unstimulated, mean (range)	97,456.2 (301.1–605,633.7)	245,973.5 (1025.6–804,235.3)	171,387.5 (220.2–792,079.3)	123,803.4 (1033.6–795,414.8)
<b>BATF2</b>				
Total for analysis, n (%)	19 (80)	14 (66.7)	10 (45.5)	18 (69.2)
Total failed, n (%)	5 (20)	8 (33.3)	12 (54.5)	8 (30.8)
Low RNA concentration	1	4	4	4
PCR indeterminate	0	1	1	0
<i>HPRT1</i> fail	3	2	6	4
Low levels in positive control	1	1	1	0
Fold change ECRR/unstimulated, mean (range)	33,280.75 (350.84–120,140.97)	15,049.99 (0.99–74,914.48)	42,919.01 (0.19–545,582.52)	788.49 (0.23–7952.44)
IFN $\gamma$ /unstimulated, mean (range)	97,456.2 (301.1–605,633.7)	245,973.5 (1025.6–804,235.3)	171,387.5 (220.2–792,079.3)	123,803.4 (1033.6–795,414.8)

Of note, a high proportion (15–27%) of the assays resulted in a 'fail' result, as a result of a number of factors. The most prevalent reason for assay failure was unreliable detection of the housekeeping gene *HPRT1*. Individuals with HIV co-infection were responsible for many of the assay failures, particularly for detection of *Mtb*-specific *CXCL10*. We also, for comparison, measured the levels of IFN $\gamma$  in response to the antigens using the same approach. The findings are shown in *Table 56* in *Appendix 15*. The gene expression data for individuals within each group who passed test inclusion criteria for passing the assay are presented in *Figure 30* in *Appendix 15*.

The T-SPOT.*TB*-positive TB group displayed the highest *Mtb*-specific expression of all target genes when compared with other groups, with the exception of *CXCL10*, for which levels were also very high in the T-SPOT.*TB*-positive OD (i.e. OD/LTBI) group.

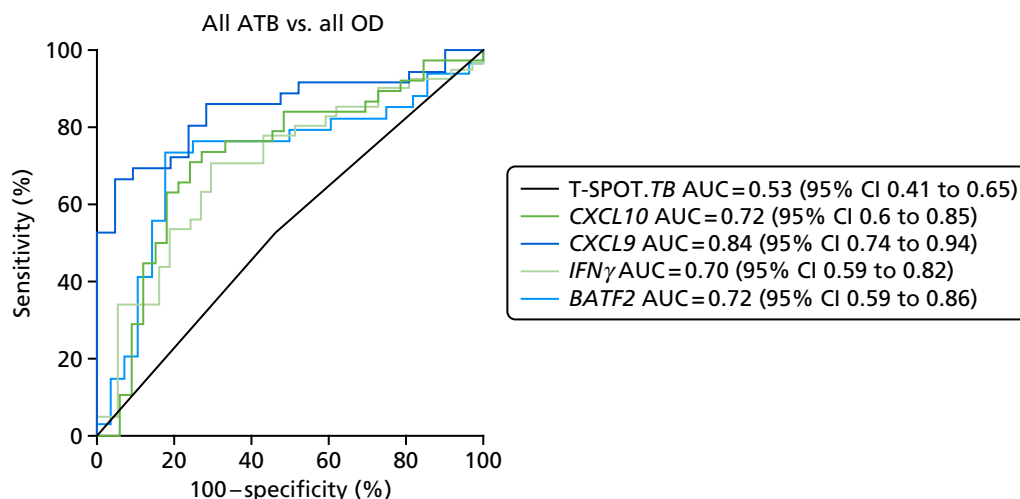
### Diagnostic performance for detection of active tuberculosis

The diagnostic performance of the target genes for detecting all TB cases compared with all OD is presented in *Figure 10*. Although obtaining > 95% sensitivity for all active TB is achievable when the cut-off point for fold/change over unstimulated is set at around 10 for *CXCL9* and *CXCL10*, this was coupled with very low specificity ( $\approx 5\%$ ). For *BATF2* and *IFN $\gamma$* , the cut-off point corresponding to > 95% sensitivity was < 1, suggesting that it is not achievable to use these analytes to detect this proportion of all TB cases.

When compared with the T-SPOT.*TB* test within the same cohort, which showed no diagnostic accuracy in this setting owing to the artificial way the participants were selected (AUC of 0.53), all of the analytes showed improved diagnostic accuracy. This suggests that this method of qRT-PCR measurement of cytokines may provide greater sensitivity than the T-SPOT.*TB* platform, as even *IFN $\gamma$*  detection by qRT-PCR performed better than the T-SPOT.*TB* in detecting active TB patients. However, these ROC curve analyses do not include those individuals for whom the qRT-PCR assay failed.

The best-performing gene for detection of all active TB was *CXCL9*, which provided an AUC of 0.84 (95% CI 0.74 to 0.94) for detecting all TB cases in this cohort. However, none of the new assays was able to provide 95% sensitivity with an acceptable corresponding specificity (i.e. > 65%) (see *Appendix 15, Table 57*). In fact, in all cases, the specificity for either TB group, or indeed LTBI, was unexpectedly low, with a wide range of gene expression values in all groups.

As the proportion of T-SPOT.*TB*-positive OD patients within this artificial cohort was inflated, the true specificity of these tests is likely to be greater in a cohort that better reflects the levels of T-SPOT.*TB* positivity in the TB and OD groups. To test this, we compared the diagnostic performance of the tests for detecting all TB cases (T-SPOT.*TB* positive/negative) with their performance for detecting T-SPOT.*TB*-negative OD cases only (see *Figure 32* in *Appendix 15*). In this setting, the performance of target genes was more like that seen in the T-SPOT.*TB* test (AUC = 0.76), with *CXCL9* again providing the best test accuracy (AUC = 0.86).



**FIGURE 10** Diagnostic performance of candidate qRT-PCR detection of *CXCL10*, *CXCL9*, *BATF2* or *IFN $\gamma$*  in the candidate molecular rule out, as assessed in the GO/NO-GO cohort. The classification of all TB from all OD (either T-SPOT.*TB* positive/negative for both) using these readouts is shown ( $n = 2-48$  per group depending on the test). The performance of the T-SPOT.*TB* assay in this cohort is also shown. ATB, active tuberculosis.

We also compared the performance of target genes when only T-SPOT.*TB*-positive TB and T-SPOT.*TB*-negative OD were considered. In this setting, none of the tests provided 100% accuracy and, therefore, performed suboptimally to the T-SPOT.*TB* (see *Figure 33* in *Appendix 15*). The full performance data for these calculations, including sensitivity and specificity values, are shown in *Appendix 15*.

### Discriminating active tuberculosis from latent tuberculosis infection/other disease

To address our secondary objective of assessing the performance of our target genes in discriminating between active TB and LTBI in our cohort, we assessed their performance using ROC analysis comparing TB (T-SPOT.*TB* positive) and OD (T-SPOT.*TB* positive) (see *Figure 34*). In this setting, the T-SPOT.*TB* provides no discrimination (as results used are either 'positive' or 'negative' rather than numerical). All of the target genes, including *IFN $\gamma$* , provided some discrimination between active TB and OD/LTBI in this subcohort of patients, with *CXCL9* providing the highest AUC of 0.97 (95% CI 0.91 to 1.0).

### Performance of *CXCL10* and *IFN $\gamma$* in QuantiFERON® GOLD In-Tube supernatants using Meso Scale Discovery

Of the 95 samples from IDEA study participants selected for QFT-GIT supernatant experiments using the MSD platform, 75 overlapped with samples from the candidate molecular rule-out test cohort, and two of the analytes measured (*CXCL10* and *IFN $\gamma$* ) could therefore be compared across the two approaches (data shown in *Figure 35*). The diagnostic performance of both *IFN $\gamma$*  and *CXCL10* for detecting TB cases was similar using both platforms. The detection of differences between patient groups based on either T-SPOT.*TB* assay (for qRT-PCR) or QFT-GIT (for MSD assays) was good, but greater discrimination was seen between QFT-GIT-positive/negative groups in the MSD assay platform, probably reflecting the fact that the analytes were measured from the same stimulated samples (whereas a new stimulation was performed for the molecular rule-out assay).

## Discussion

In this substudy we have evaluated two candidate approaches for improving the sensitivity of immune-based tests for active TB: (1) the molecular rule-out test for measuring chemokines from stimulated PBMCs using qRT-PCR; and (2) the measurement of *IFN $\gamma$*  and *CXCL10* in QFT-GIT supernatants using MSD. Unlike other studies that used a case-control approach and in which patients were often pre-selected for immune assay responsiveness, in this study we have designed a cohort that is deliberately enriched for patients in whom current immune-based tests fail (i.e. those in the TB group who are IGRA negative and those in the OD group who are IGRA positive). This artificial cohort selection approach was used to provide a GO/NO-GO point for the validation of these candidate tests.

We found that *CXCL9*, *CXCL10* and *BATF-2* gene expression was upregulated in response to RD1 antigens (ECRR) in TB patients, including in T-SPOT.*TB*-negative TB patients. We confirmed previous findings<sup>23,67</sup> that the levels of *CXCL9* and *CXCL10* produced by stimulated blood cells are detected at amplified levels compared with those of *IFN $\gamma$* . However, these genes were also upregulated in a large proportion of OD patients in our cohort, which compromised diagnostic performance. This phenomenon was also observed by others, where IGRA-negative controls also displayed production of *CXCL10* in response to *Mtb* antigens,<sup>23,67</sup> suggesting potential non-specific production of this chemokine in some tests. Although reasonably high diagnostic accuracy was found (AUC = 0.84 for *CXCL9*) for all TB in our GO/NO-GO cohort, this did not correspond to a test which could provide > 95% sensitivity and 65% specificity at a given threshold. Therefore, this approach is unlikely to be clinically useful as a rule-out test for all TB. Of all the analytes measured in the molecular rule-out assay approach, *CXCL9* provided best diagnostic accuracy for detection of all TB cases from all OD, and for discrimination of TB from OD/LTBI in T-SPOT.*TB*-positive patients. To our knowledge, this is the first study to test the performance of these chemokines in discriminating between TB and LTBI in a cohort in which the LTBI patients had OD and were suspected of active TB at the point of recruitment. It appears that *CXCL9* may be a useful marker for differentiating between these groups. However, it should be noted that statistical analyses to compare diagnostic accuracy (i.e. AUC, sensitivity or specificity values) between analytes were not performed.

We reported a high proportion of assay failures for the candidate molecular rule-out test assay, which were probably a result of poor recovery of some PBMC samples from cryopreservation and into culture. Using either fresh blood or fresh isolated PBMCs for this candidate assay would have been optimal, but we did not have this material available within the VANTDET study. Kasprowicz *et al.*<sup>23</sup> have already demonstrated that detection of *Mtb*-specific *CXCL9* and *CXCL10* using a similar qRT-PCR approach at as little as 50 µl of fresh blood per condition is achievable. Their findings now warrant validation in a cohort of TB suspects, similar to the IDEA study cohort, but using fresh blood samples. We anticipate that fresh samples would result in fewer assays failures and a better performance for detecting all TB cases.

Using supernatants stored from the QFT-GIT tests conducted as part of the IDEA study, we were able to assess the use of the sensitive MSD platform for detection of target analytes and compare the performance of *CXCL10* and IFN $\gamma$  between the two candidate platforms. This way, we could compare the performance (although somewhat indirectly) in detection of these analytes by using either qRT-PCR (for the detection of the transcribed genes) or ELISA (for detection of the proteins). We found comparable performance for detection of the analytes and very similar diagnostic accuracy for detecting TB. However, neither approach was able to provide the required diagnostic accuracy to be used as a rule-out test for all TB and, furthermore, not all IGRA-positive individuals were detected using the new assays. Nevertheless, we were able to demonstrate that MSD is able to detect analytes, such as *CXCL10* in plasma, including a wide range of concentrations. Although this is not required for a simple positive/negative immune test, a test for discriminating between disease states, in which differences in quantity of analytes may provide discriminatory power, may benefit from using a MSD platform for quantitation. We plan to investigate this in our future experiments using MSD.

Both of the candidate rule-out test experimental approaches we have evaluated are complex, with multiple steps required (which can introduce significant variability), and requiring technical expertise as well as expensive equipment to perform. This is not in keeping with the WHO's target product profile for a triage test for TB, which stipulates that such a triage test should take between 5 and 30 minutes to get a result, cost  $\approx$ US\$1–2 and be achievable using a single device that requires no calibration.<sup>16</sup> However, we propose that in high-income settings, where TB incidence is generally low, an immune-based test providing > 95% sensitivity for all active TB would be clinically useful if available at low cost. Further work is needed to determine the price at which such an assay would be cost-effective.

# Chapter 7 Health economic analysis

## Introduction

We present methods for assessment of the cost-effectiveness of several novel tests as rule-out and rule-in tests for active TB. That is, in the case of a rule-out test, we consider using novel tests as an initial test, with a negative result indicating that a patient does not have TB, thus accelerating diagnosis of the actual cause of disease in such patients. In the case of a rule-in test, we consider using novel tests as an initial test, with a positive result indicating that a patient does have TB, averting the need for other tests for TB. The use of several tests was compared against current practice, as determined by analysis of patient records. We considered which diagnostic tests were performed, their costs and the time taken between decision points involving each test. The time taken to diagnose, rule in or rule out, TB is a key consideration. Our report adheres to the Consolidated Health Economic Evaluation Reporting Standards (CHEERS) statement.<sup>72</sup>

## Methods

### Decision tree model

We developed a decision tree model to calculate the incremental costs and incremental QALYs of changing from current practice to using a novel test as an initial rule-in or rule-out test. Current practice was determined by analysis of patient records. Adding a rule-out test to the diagnostic pathway introduces additional delays in the diagnosis of active TB in those patients who have the disease, as it introduces an additional step in the pathway. Patients who were not initially diagnosed with active TB have a follow-up consultation after approximately 2 months; those who had a false-negative rule-out test result (i.e. they had TB incorrectly ruled out) can have TB identified at this point. The final diagnostic outcomes were the four categories described in Dosanjh *et al.*,<sup>11</sup> herein referred to as 'Dosanjh categories'.

The health economic analysis was undertaken from an NHS perspective. No discounting was required as the diagnostic process occurs over a relatively short time period. The time horizon was up to final diagnosis of TB, which was assumed to be < 1 year.

The model contained two levels of uncertainty:

1. individual-level uncertainty – patient records revealed variation in the number and type of tests used for TB diagnosis and time to diagnosis
2. parameter uncertainty – uncertainty in the costs of tests and procedures, and the sensitivity and specificity of the novel tests.

Uncertainty distributions for each are estimated for either uniform or gamma distributions, depending on the form of the data available.

A (balanced) bootstrap sample of TB and non-TB patients was created for each simulation of the decision tree, which retained the TB and non-TB subsample sizes. Individual patient costs and time to diagnosis were jointly sampled to preserve the dependency between them. We sampled across the model parameter distributions to obtain a set of realisations. This was then repeated in a Monte Carlo framework to obtain a sample of 10,000 model runs, which encapsulated the first-order (patient variability) and second-order (parameter) uncertainty in the model outputs. *Table 17* summarises the key model parameters.



TABLE 17 Key model parameters

Parameter	Symbol	Main model value
Follow-up time for those not diagnosed with TB (days)	$T_{followup}$	Direct estimate from clinical data set
Cohort ATB prevalence	$n_+/n$	Direct estimate from clinical data set, also stratified by HIV status
Active TB QALY loss	$q$	Gamma(5.427,0.0154) <sup>73</sup>
Hepatotoxicity as a result of treatment QALY loss	$q_h$	Gamma(65.753,7e-5) <sup>73</sup>
Nausea as a result of treatment QALY loss	$q_n$	Gamma(109.67,3e-6) <sup>73</sup>
Current time to diagnosis by TB status	$\bar{t}_+, \bar{t}_-$	Direct estimate from clinical data set
Current combined cost of diagnosis by TB status	$\bar{c}_+, \bar{c}_-$	Direct estimate from clinical data set

ATB, active tuberculosis.

The model was implemented in the statistical programming language R. The key model parameters are presented in *Table 17*.

An example decision tree representation is given in *Figure 11*. Equivalent figures for alternative scenarios are given in *Appendix 16, Figures 36 and 37*.

### Estimation of costs and health impact used in the model

The costs and distributions used in the probabilistic sensitivity analyses are summarised in *Tables 63–65* in *Appendix 16*, using 2014/15 prices. When necessary, costs were inflated from previous years using the Hospital and Community Health Service pay and price index.<sup>74</sup>

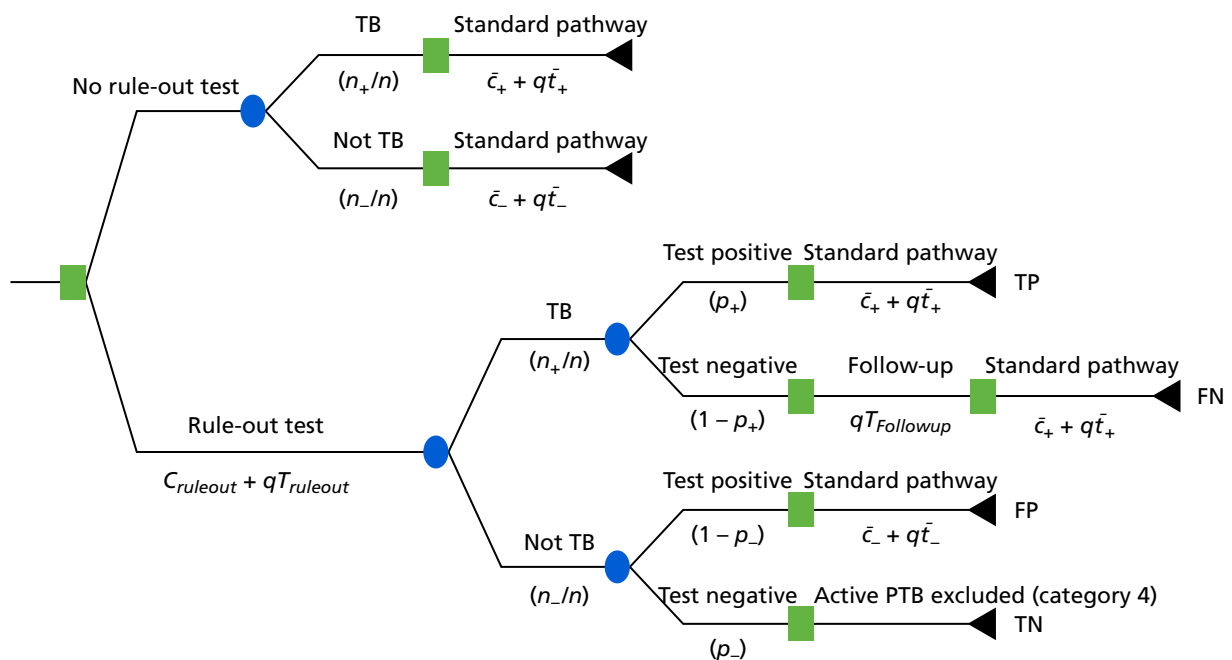


FIGURE 11 Decision tree comparing current practice ('no rule-out test') with a diagnostic pathway incorporating an initial rule-out test ('rule-out test'). The 'standard pathway' branch represents the range of variation observed in the patient cohort. Probabilities are shown below branches following a circular chance node and costs are below branches following a square decision node. FN, false negative; FP, false positive; TN, true negative; TP, true positive.

If uncertainty bounds were not available in the recent sources used, uncertainty ranges were informed by previous studies. Uniform distributions were used when upper and lower limits were available and gamma distributions were used when the standard error of the average cost was available.

When modifying costs, the uncertainty around the central value was transformed maintaining the proportions from the original value rather than an absolute difference. For example, a lower bound of half and an upper bound of twice the point estimate values were used.<sup>10,17,75</sup> Skewed distributions were represented using a gamma distribution.

As the end point of the diagnosis is diagnosis of TB or ruling out TB, treatment costs after final diagnosis are out of scope. However, when a patient was started on TB treatment and then a lack of response to that treatment informed a decision that the patient did not in fact have TB, the cost of this treatment was included, as it is part of the cost of ruling out TB in those patients.

The treatment costs are given in *Table 66*. Following the NICE guidelines for active TB management,<sup>8</sup> it was assumed that such patients are on treatment until their 2-month follow-up appointment, when they are reassessed for response to treatment. The regimen in this period is daily treatment with rifampicin, isoniazid, pyrazinamide (Rifater, sanofi) and ethambutol. From the NICE *British National Formulary*,<sup>76</sup> adult dosages are fixed except for ethambutol, which is determined by patient weight. The mean weight at time of first presentation, of 67.98 kg, was used in the model.

### Selection of tests to evaluate in health economic analysis

In the VANTDET study, we have evaluated several signatures using each new technology, but we wished to evaluate the health economics in only the most promising signatures. As none of the proteomic signatures performed with high enough test accuracy to be clinically useful, these signatures were not used in these analyses. For the transcriptomic signature, the test accuracy data for the Sweeney *et al.*<sup>39</sup> four-gene signatures, calculated using the TBS method, were used. For the flow cytometry data, the test accuracy for the %HLA-DR signature<sup>26</sup> in the HIV– cohort was used. For the molecular rule-out test, the performance of the CXCL9 qRT-PCR in *Mtb* antigen-stimulated PBMC was used. *Table 18* gives the test sensitivity and specificity values used for the probabilistic sensitivity analyses.

The QALY loss as a result of TB treatment is given in *Table 17*. The sum total was used in the analysis:

$$q_{Tx} = q_h + q_n. \quad (1)$$

**TABLE 18** Diagnostic test performance and distributions for different tests

Patient stratum	Test	Rule			
		In		Out	
		Sensitivity	Specificity	Sensitivity	Specificity
All	Transcriptomic	Uniform (0.865,0.932)	Uniform (0.493,0.609)	Uniform (0.245,0.346)	Uniform (0.919,0.972)
All	Molecular	–	–	Uniform (0.85,1.0)	Uniform (0.057,0.44)
HIV–	Cellular immune flow cytometry	Uniform (0.548,0.771)	Uniform (0.836,0.971)	–	–

### Cost-effectiveness outcomes

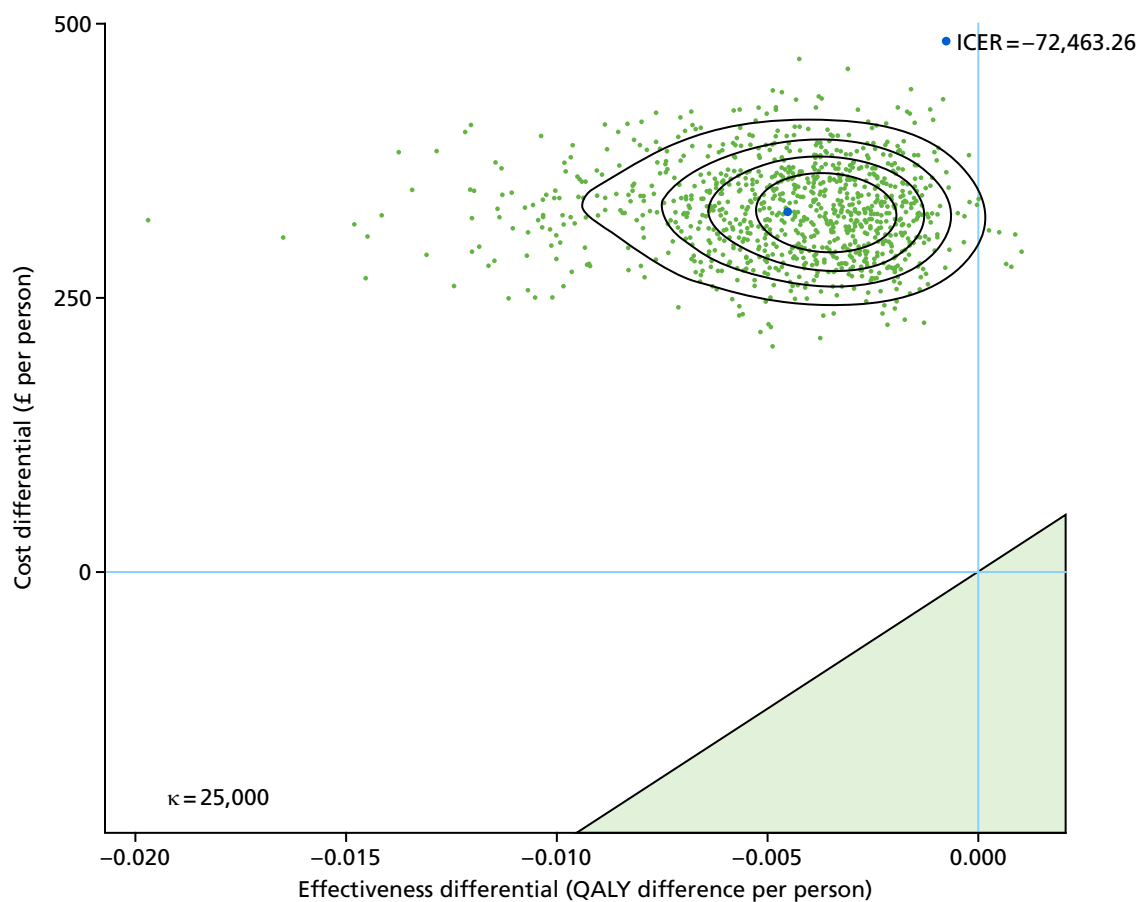
The current ('status quo') cost and QALY loss are the weighted sums of the TB and non-TB pathways observed in the clinical data:

$$C_{\text{status-quo}} = (n_-/n)\bar{c}_- + (n_+/n)\bar{c}_+ \quad (2)$$

$$E_{\text{status-quo}} = (n_-/n)q\bar{t}_- + (n_+/n)q\bar{t}_+ \quad (3)$$

## Results

For decision tree diagrams, please see *Appendix 16*. The results of the cost-effectiveness analysis for the Sweeney *et al.*<sup>39</sup> transcriptomic signatures used as a rule-out test are given in *Figure 12* and *Table 19*, and the transcriptomic signatures used as a rule-in test are given in *Figure 13* and *Table 20*.

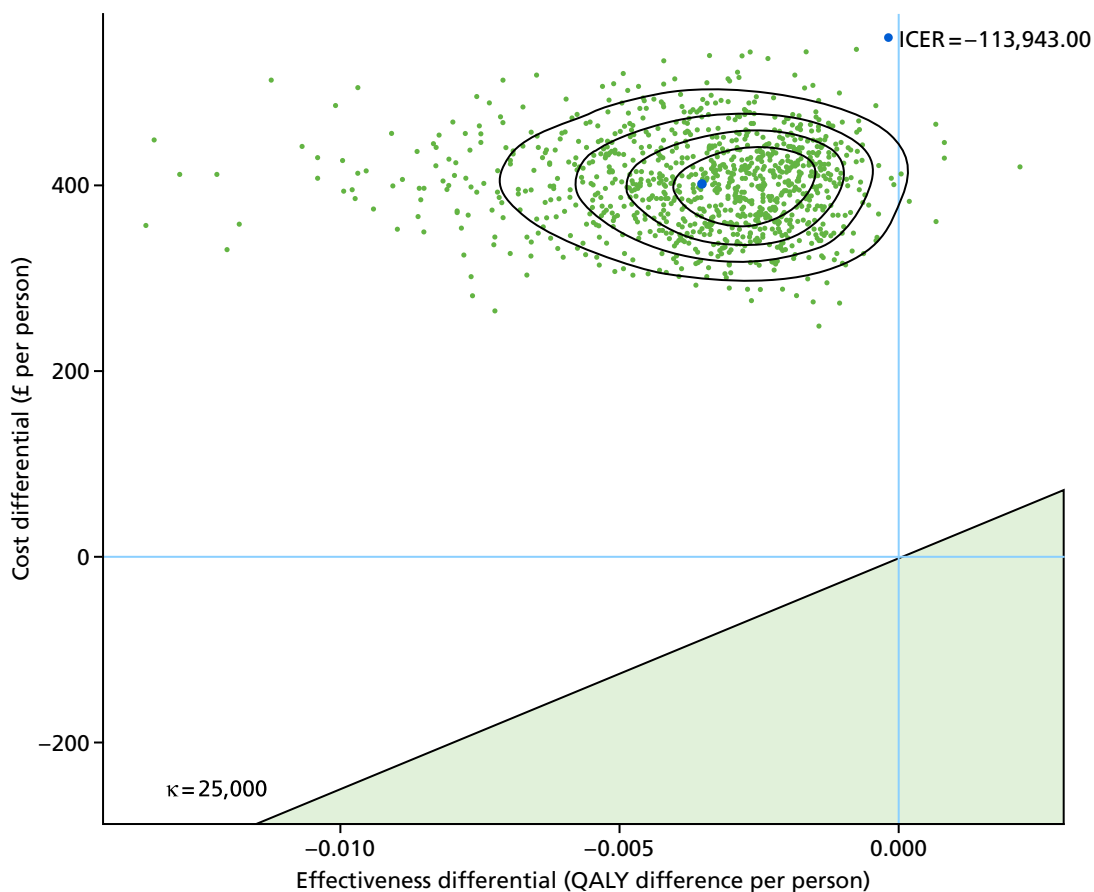


**FIGURE 12** Cost-effectiveness planes for status quo against transcriptomic rule-out test scenario, with contour lines.

**TABLE 19** Cost-effectiveness statistics for transcriptomic rule-out scenarios

Scenario	Incremental		Probability cost-effective	
	QALY gain	Cost incurred (£)	WTP £20,000/QALY	WTP £30,000/QALY
HIV-	-0.0045	329	0	0

WTP, willingness to pay.



**FIGURE 13** Cost-effectiveness planes for status quo against transcriptomic rule-in test scenario, with contour lines.

**TABLE 20** Cost-effectiveness statistics for transcriptomic rule-in scenarios

Scenario	Incremental		Probability cost-effective	
	QALY gain	Cost incurred (£)	WTP £20,000/QALY	WTP £30,000/QALY
Total	-0.0035	402	0	0

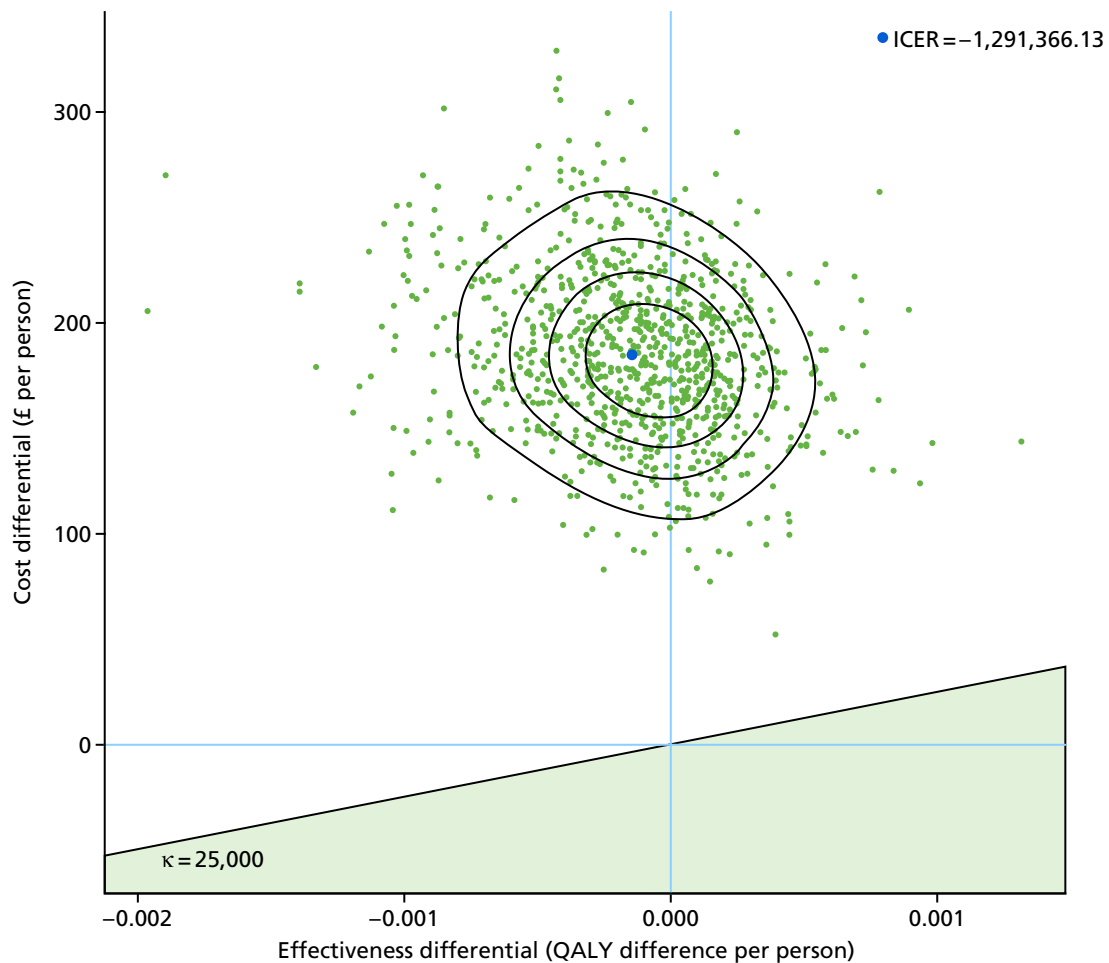
WTP, willingness to pay.

### Flow cytometry rule-in test

The results of the cost-effectiveness analysis for the %HLA-DR flow cytometry signatures<sup>26</sup> to be used as a rule-in test are presented in *Figure 14* and *Table 21*.

### Molecular rule-out test

The results of the cost-effectiveness analysis for the molecular rule-out test are presented in *Figure 15* and *Table 22*.



**FIGURE 14** Cost-effectiveness planes for status quo against flow cytometry %HLA-DR rule-in test scenario, with contour lines.

**TABLE 21** Cost-effectiveness statistics for flow cytometry rule-in scenario

Scenario	Incremental		Probability cost-effective	
	QALY gain	Cost incurred (£)	WTP £20,000/QALY	WTP £30,000/QALY
Total	-0.00014	185	0	0

WTP, willingness to pay.

## Discussion

This health economic analysis has demonstrated that the use of those tests that performed best in classifying all TB cases in our VANTDET substudies (i.e. the Sweeney *et al.*<sup>39</sup> four-gene transcriptomic signature, the %HLA-DR cellular immune signature<sup>26</sup> and the CXCL9 qRT-PCR test for ruling out active TB) cannot be considered cost-effective, given the assumption of the modelling. This is due in part to the significant cost of these tests, which, in their current proposed format, are very expensive. Furthermore, the sensitivity and specificity provided by these tests were suboptimal, meaning that they did not improve effectiveness when introduced into the current diagnostic pathway. All tests incurred extra costs and there was a minor reduction in QALYs, probably because of the increased delay in diagnosis resulting from the introduction of new tests into the standard pathway. This was the case even when tests were considered as either rule-in or rule-out tests.

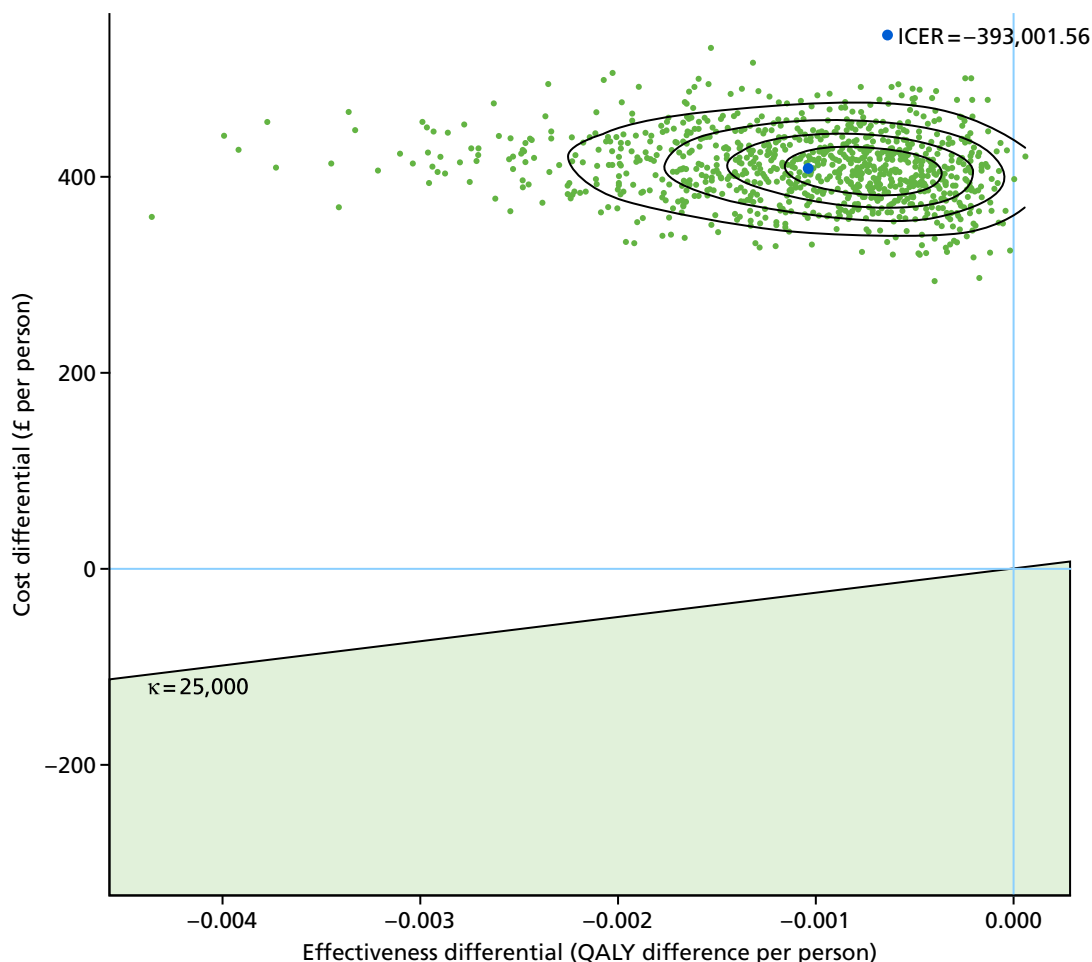


FIGURE 15 Cost-effectiveness planes for status quo against molecular rule-out test scenario, with contour lines.

TABLE 22 Cost-effectiveness statistics for molecular rule-out scenarios

Scenario	Incremental		Probability cost-effective	
	QALY gain	Cost incurred (£)	WTP £20,000/QALY	WTP £30,000/QALY
Total	-0.0010	408	0	0

WTP, willingness to pay.

It should be noted that, as all of the technologies and signatures are being investigated in research laboratory settings, and have not begun to be commercialised in any way, the cost estimates had a high degree of uncertainty, which affected the cost-effectiveness analysis. The effectiveness for the %HLA-DR cellular immune assay, for which we propose using in the context of IGRA-positive TB suspects only, the cost-effectiveness plane demonstrated reasonable effectiveness, but with a very high cost differential. If the test accuracy of this signature could improve slightly, alongside a significant reduction in cost, it might be that this approach could be cost-effective for diagnosing TB in the IGRA-positive population. It is feasible that the cost of some of these technologies will become more economical in the coming years. Furthermore, it is likely that the costs of a commercial assay using simpler but comparable technologies (i.e. a simple flow cytometry method rather than complex multicolour analysis) would be lower.

This health economic analysis has some limitations. Given the lack of accurate data on novel test costs, we have relied on estimates based on current laboratory research costs and timings, which may not reflect the likely costs of these tests after they have been developed commercially. Therefore, there is a high level of uncertainty in our analyses. The uncertainty about the test sensitivities and specificities is represented as marginal distributions when there is a correlation between the two values that may be represented in a joint distribution if the appropriate information is available. Furthermore, we highlight that one of the main assumptions of the analysis is that we consider a relatively short time frame up to TB diagnosis and, therefore, cannot extend the conclusions beyond this.

### **Recommendations**

In these analyses, we have considered the introduction of new tests into the pathway of a wide range of TB suspects, that is in complex populations with a diverse mix of TB and OD patients, with wide-ranging symptoms, disease severities and clinical suspicion of TB. It is likely that a blood-based test for a specific subset of TB, which could be used to assist in diagnosis against a specific subset of OD patients, would be a more cost-effective approach for these blood-based novel tests. In addition, such a test may have improved performance when used in combination with other tests. We have not yet evaluated such scenarios in this study, but it is a direction for future research on novel tests for diagnosing TB.

For rule-out tests, a test with a combination of high sensitivity and specificity, low cost and rapid speed of result is required to be clinically effective or cost-effective as a screening tool, or as a test to be used at the beginning of a diagnostic pathway for a TB suspect.<sup>16</sup>

Future research on the cost-effectiveness of tests would benefit from looking at long-term impacts beyond initial diagnosis and ideally would consider the infectious nature of the condition.

## Chapter 8 General discussion

### Principal findings

In this large study to validate new technologies for the diagnostic evaluation of active TB, we successfully evaluated four promising approaches for the diagnosis of active TB, all of which used blood samples: transcriptomics, proteomics, flow cytometry and immunological rule-out tests. In each substudy, we were able to evaluate multiple previously identified signatures and assess their diagnostic performance.

For the transcriptomic signature substudy, we report that diagnostic performances range from 0.81 to 0.84 for all previously reported gene expression signatures, for the detection of active TB in the full cohort (using LDA). The performance for all TB and for culture-confirmed TB was not found to be clinically useful. Although performance for either culture-confirmed TB or for PTB was highest, the scenario in which a transcriptomic test is likely to be useful is where current tests fail. For this reason, despite a maximum AUC of 0.80 for identifying highly probable TB, the Sweeney *et al.*<sup>39</sup> four-gene signature may be a useful clinical test for patients who test negative with microbiological tests. For culture-negative TB, this signature could provide a high NPV (0.95), which may be clinically useful.

None of the previously identified proteomic signatures was able to provide high diagnostic accuracy for detecting active TB cases, with the maximum test accuracy being for the Hamilton and Levin (unpublished) four-protein signature, detected by SELDI-TOF, which provided an AUC of 0.74 for culture-confirmed TB, using the DRS method. We were able to compare this signature across two proteomic technology platforms, SELDI-TOF and LC-MS, and found relatively poor corroboration between the two platforms. We were able to assess the performance of four published signatures<sup>19,21,51,52</sup> using LC-MS, none of which performed well for detecting TB (not culture-confirmed or PTB groups).

Of the six previously identified cellular immune signatures for active TB, the %HLA-DR signature<sup>26</sup> was found to perform the best, providing an AUC of 0.90 for all TB in the HIV- population. The %HLA-DR and %T<sub>EFF</sub> tests<sup>25,26</sup> provide high PPV for all TB and for culture-confirmed TB in IGRA-positive TB suspects and, therefore, may be clinically useful. Only the signatures that measured the phenotype (either memory/differentiation phenotype, or activation status) provided discriminatory ability. Those signatures measuring function alone did not perform well.

We tested two novel approaches for the development of a rule-out test. We found that the detection of CXCL9 by qRT-PCR of stimulated PBMCs provided a sensitive assay that could detect a high proportion of TB cases. However, the assay has a high failure rate and was also hampered by poor specificity. The use of CXCL9 for discriminating between TB and OD/LTBI in immune assays should be considered.

None of the signatures validated was found to be cost-effective when evaluated for use to rule in or rule out active TB, relative to the current standard diagnostic pathway in the UK. The signature that performed best was the %HLA-DR flow cytometry signature<sup>26</sup> for the ruling in of all TB in the IGRA-positive population. However, this signature resulted in significant cost incurred and a slight reduction in QALY.

### Strengths and limitations

In the IDEA study, we consecutively recruited a unique, large, multicentre, prospective cohort of individuals who were suspected of having active TB, as part of routine clinical practice. The cohorts we used in these validation studies (with the exception of the rule-out test, for which an artificial cohort was selected)



represent the full spectrum of clinical disease reflecting heterogeneity of all clinical phenotypes and other differential diagnoses. The study participants, patients with suspected TB symptoms but unknown diagnosis at point of enrolment, represent the uncertainty faced by clinicians. The high-resource setting provides a high-quality diagnostic facility and reliable and accurate diagnosis for culture-unconfirmed, highly probable TB.

Ultimately, our study provided a real-life road test for the published signatures and evaluated their clinical utility, a crucial test before they enter the next phases of biomarker development. We present the performance of the previously published signatures in our hands. The previously proposed thresholds for each signature were not reported here, as, overall, these thresholds provided suboptimal performance in our cohort. In our experience with diagnostic tests in which the outcome is a continuous, the threshold for optimal diagnostic performance does change between laboratories and cohorts, for a number of reasons, particularly when these tests are yet to be standardised and when the cohorts are so variable. We therefore took several approaches to define optimal thresholds and their associated performance characteristics. Our findings suggest that the performance of all signatures and technologies in detecting TB in the HIV+ population was very poor, much worse than in the HIV- population. This is not in line with other studies, in which performance of signatures in the HIV+ population has either been comparable to that in the HIV- population, or marginally worse.<sup>20,39,60</sup> We were likely under powered to fully assess diagnostic performance in the HIV+ population, owing to the small number of these patients in the parent IDEA study cohort. As such, further validation is required in this population, in particular for the proteomic and cellular immune signature validations. Within the IDEA study cohort, there is a small number of patients who are classified as 'clinically indeterminate' (Dosanjh category 3), who were not included within this study, as assessing the performance of new tests within this population would give no known assessment of performance against gold standard/current practice. Nevertheless, they represent a subset of TB suspects who present in real-life clinical practice. We did, however, include this population when all calculations of pre-test probability for TB subsets were made.

In addition to providing detailed statistics on the diagnostic accuracy of the previously published signatures, we herein present complex health economic analyses, in which the most promising signatures were evaluated for cost-effectiveness for either the rule-in or rule-out of active TB. However, we did not present health economic analysis for all subgroups (i.e. culture-confirmed TB alone or PTB alone), and it is likely that effectiveness in these scenarios will improve as the cohort of patients becomes smaller and the clinical question narrower.

We are lacking some analyses. In particular, we do not compare different signatures with each other using a formal statistical comparison. Furthermore, there is a need for further subgroup analyses using these data, for example to perform health economic analysis in particular clinical scenarios (i.e. within the smear-negative groups), as a conclusion of this study is that these new tests are likely to be useful in specific types of TB suspects.

## Recommendations for clinical practice

Given the poor performance of each of the new technologies for detecting the full spectrum of active TB cases in this study, and their lack of cost-effectiveness for this purpose, it is unlikely that the findings of this project will immediately have implications for changing current practice when it comes to the diagnostic pathways for TB suspects in the UK. None of the tests evaluated had sufficiently high diagnostic accuracy to provide a clinically useful rule-in or rule-out function over and above the clinical utility of the currently available diagnostic tests. However, diagnostic assessment of certain key groups of patients could potentially be improved by the flow cytometric and the transcriptomic tests. Smear microscopy results are available on the same day that the patient presents to secondary care and IGRA results are usually available by the next day. The role of new tests need to be considered in the context of patients with suspected TB for whom both these test results are known. In patients with suspected TB who are IGRA

positive and smear negative, there is commonly a high index of suspicion for TB but a definitive diagnosis is not possible until culture results become available, typically after 2–3 weeks. A test that could rule in or rule out TB in these patients is thus an important unmet clinical need.

The %HLA-DR and %T<sub>EFF</sub> flow-cytometry tests<sup>25,26</sup> gave 94% PPV in the smear-negative IGRA-positive group, providing what is, effectively, a rule-in test and facilitating a decision to start treatment for presumptive TB. The test could thus form part of the diagnostic assessment pathway, forming part of an algorithm alongside smear microscopy and IGRA. Interestingly, two transcriptomic signatures provided high NPVs of 89–90% for culture-positive TB in the smear-negative population (unstratified by IGRA result). These NPVs may thus provide clinicians with sufficient basis for withholding treatment (or at least delaying it until culture results are available) in smear-negative TB suspects who test negative with these signatures.

## Recommendations for future research

Smear still remains a quick, cheap and specific method for quickly ruling in TB in cases with high bacterial load. Therefore, a new test is not required for this subpopulation. However, it remains the case that most research into new TB diagnostics includes only individuals with ‘typical’ TB with high bacterial load, who are positive with either culture or smear tests, or both. The clinical need is in fact in the smear-negative patients, for whom there is currently not a quick test available for either rule-in or rule-out of active TB. This is particularly the case in low-prevalence settings, such as in the UK, where a high proportion of those diagnosed with TB are paucibacillary and/or have EPTB.

We have demonstrated that the transcriptomic test is able to provide a reasonably high NPV in those TB suspects who have a negative smear result. These tests are likely to be cheap and rapid if developed commercially and, if found to be reproducible using a rapid qRT-PCR approach, could potentially be developed into near-patient or point-of-care tests. For the reasons already discussed, we propose that future research into the use of these tests focuses on the smear-negative TB suspects and includes those with clinically diagnosed (i.e. culture-negative) TB. The high accuracy for diagnosing TB using the Adekambi *et al.*<sup>26</sup> and Pollock *et al.*<sup>25</sup> flow cytometry assays reported in *Chapter 5* suggests a clinically useful role for these tests to help rule in a diagnosis of TB in smear-negative IGRA-positive patients, for whom this is currently a clear unmet clinical need. Accordingly, further development, standardisation and simplification of these assays should be prioritised in order to deliver an in vitro diagnostic for routine clinical use. An automated flow cytometry set-up that allows for simple assay preparation and automated gating and analysis would help to make the tests suitable for routine diagnostic laboratories. It is unlikely that these tests would be applicable to low-income high-burden settings, given their complexity and costs. We also propose that the tests are further validated within the specific subpopulations for which they would be useful (i.e. smear-negative TB suspects).

An overall conclusion from this study is that blood-based tests for TB can perform best when specific subtypes of TB are considered and when specific subsets of OD can be excluded. As such, we recommend that future studies exploring these technologies focus on specific subtypes of TB, most usefully those groups where a diagnostic test is most needed (i.e. EPTB, culture/smear-negative TB).

It appears that, although the ‘omic’ technologies are hampered by specific differential diagnoses (e.g. sarcoidosis) for the cellular immune signatures, for which immune cells are stimulated with *Mtb* antigens before the test is performed, there is no subgroup within the OD population which hampered diagnostic performance. As such, we conclude that immune-based tests are more useful when all TB is considered (with the exception, perhaps, of those infected with HIV).

## Conclusion

In conclusion, in this report we presented the validation of new technologies for the diagnostic evaluation of TB and have fully evaluated their use in a real-life clinical setting. Overall, the diagnostic performance of all previously identified 'signatures' of TB was lower than previously reported. This probably reflects the nature of the cohort we used, which includes the harder-to-diagnose groups, such as those with culture-unconfirmed TB and EPTB, which were under-represented in previous cohorts.

We have addressed all of our primary objectives. Some analyses are outstanding; importantly, we are yet to fully address our secondary objective of deriving novel signatures for active TB using the data we generated in the substudies. This is an area of ongoing investigation by our group and was beyond the scope of this report. This study provided a real-life road test for these technologies and highlights the need for new diagnostic tests and signatures for TB to be derived and evaluated in cohorts that included the full spectrum of TB cases, and where the hard-to-diagnose subgroups of TB are considered.

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## Contributions of authors

**Alice Halliday** (Research Associate) led the cellular immune signature validation substudy, oversaw the candidate rule-out validation studies, managed the overall VANTDET project co-ordination, co-ordinated the write up of the report and contributed to writing all sections.

**Pooja Jain** (Bioinformatician) led the statistical analysis for the transcriptomics and proteomics substudies, conducted the main statistical analyses for these two chapters (see *Chapters 3* and *4*, respectively), and supported the writing of methods, results and discussion sections in these chapters (see *Chapters 3* and *4*).

**Long Hoang** (Research Associate) led the validation of transcriptomic signature substudies, oversaw the validation of the molecular rule-out test, conducted statistical analysis and supported the write up of *Chapters 3* and *6*.

**Robert Parker** (Research Associate) led the validation of proteomic signatures substudy and led the writing of *Chapter 4*.

**Mica Tolosa-Wright** (Research Technician), with the support of **Alice Halliday** and **Long Hoang**, led the validation of the molecular rule-out test substudy and led the writing of *Chapter 6*.

**Tereza Masonou** (MSc student and Research Technician) supported the validation of cellular immune signature experimental work and analysis and interpretation of the data. She also supported the report write up by writing the methodology section for *Chapter 5* and production of results tables.

**Nathan Green** (Health Economics Statistician) led the health economic analysis for the project and led the write up of the chapter (see *Chapter 7*).

**Aime Boakye** (IDEA study administrator) managed and co-ordinated the clinical database for the IDEA study patients and co-ordinated the cohort selection for the separate substudies within the VANTDET study. She ensured that the research staff remained blind to clinical data throughout the study period, until analysis phase. She also supported and led many of the public engagement and involvement activities.

**Yemisi Takwoingi** (Senior Research Fellow in Biostatistics) provided statistical analysis oversight, support and advice on study design throughout the project.

**Shea Hamilton** (Research Associate) performed the experimental work for the validation of the four-protein signature by SELDI-TOF technology.

**Vinay Mandagere** (Medical Student) designed and conducted the QuantiFERON supernatant project in *Chapter 6*.

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**Lachlan Coin** (Associate Professor) analysed the SELDI-TOF signature validation data.

**Jon Deeks** (Professor of Biostatistics) was a co-investigator on the project, contributed to the study design and support of statistical analysis approaches.

**Peter J White** (Reader in Public Health Modelling) was a co-investigator on the project, contributed to the study design and led the statistical analysis of diagnostic pathways and the economic analysis.

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## Data-sharing statement

All data requests should be submitted to the corresponding author for consideration. Please note exclusive use will be retained until the publication of major outputs. Access to anonymised data may be granted following review.

## Patient data

This work uses data provided by patients and collected by the NHS as part of their care and support. Using patient data is vital to improve health and care for everyone. There is huge potential to make better use of information from people's patient records, to understand more about disease, develop new treatments, monitor safety, and plan NHS services. Patient data should be kept safe and secure, to protect everyone's privacy, and it's important that there are safeguards to make sure that it is stored and used responsibly. Everyone should be able to find out about how patient data are used. #datasaveslives You can find out more about the background to this citation here: <https://understandingpatientdata.org.uk/data-citation>.



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## Appendix 1 Prevalence data from the IDEA study

**TABLE 23** Calculated prevalence data for TB populations, using the IDEA study data

Target population	<i>n</i>	Parent population	<i>n</i>	Prevalence (%)
All TB	363	Full cohort	845	43.0
All TB (HIV-)	338	Full cohort (HIV-)	710	47.6
All TB (HIV+)	32	Full cohort (HIV+)	201	15.9
Culture-confirmed TB	261	Full cohort	845	30.9
Highly probable TB	102	Full cohort	845	12.1
Culture-confirmed TB (HIV-)	248	Full cohort (HIV-)	710	34.9
Highly probable TB (HIV-)	90	Full cohort (HIV-)	710	12.7
Highly probable TB	102	Culture-negative TB suspects (full)	584	17.5
Highly probable TB (HIV-)	90	Culture-negative TB suspects (HIV-)	462	19.5
Highly probable TB (HIV+)	14	Culture-negative TB suspects (HIV+)	183	7.7
All TB (T-SPOT. <i>TB</i> positive, full)	270	T-SPOT. <i>TB</i> positive (full)	352	76.7
Dosanjh category 1 (T-SPOT. <i>TB</i> positive)	201	T-SPOT. <i>TB</i> positive (full)	352	57.1
Dosanjh category 2 (T-SPOT. <i>TB</i> positive/negative)	69	T-SPOT. <i>TB</i> positive (full)	352	19.6
All TB (T-SPOT. <i>TB</i> positive and HIV+)	17	T-SPOT. <i>TB</i> positive (HIV+)	39	43.6

These estimates include the 'clinically indeterminate' patients within the parent populations.



## Appendix 2 Distribution of disease types in the transcriptomic validation cohort

**TABLE 24** Distribution of severity and disease in the TB group

Type of TB disease	TB group, <i>n</i> (%)		Total, <i>n</i> (%)
	Culture-confirmed	Highly probable	
All TB	212 (70.4)	89 (29.6)	301 (100)
Culture negative	0 (0)	76 (25.2)	76 (25.2)
Smear-positive TB	48 (22.6)	2 (2.2)	50 (16.6)
Smear-negative	139 (65.6)	59 (66.3)	198 (65.8)
Smear not tested	25 (8.3)	28 (9.3)	53 (17.6)
PTB	85 (40.1)	16 (18.0)	101 (33.6)
EPTB	100 (47.2)	64 (71.9)	164 (54.5)
PTB + EPTB	27 (12.7)	9 (10.1)	36 (12.0)
Site of infection <sup>a</sup>			
Abdomen	6 (2.8)	2 (2.2)	8 (2.7)
Bones	5 (2.4)	1 (1.1)	6 (2.0)
Brains	1 (0.5)	4 (4.5)	5 (1.7)
Chest	1 (0.5)	1 (1.1)	2 (0.7)
Lungs	112 (52.8)	24 (27.0)	136 (45.2)
Lymph node	87 (41.0)	44 (49.4)	131 (43.5)
Miliary TB (disseminated)	11 (5.2)	0 (0)	11 (3.7)
Pericardium	3 (1.4)	2 (2.2)	5 (1.7)
Pleura	13 (6.1)	10 (11.2)	23 (7.6)
Spine	10 (4.7)	6 (6.7)	16 (5.3)
Other	12 (5.7)	10 (11.2)	22 (7.3)

<sup>a</sup> Some patients had TB disease in more than one of the sites.

**TABLE 25** Distribution of alternative diagnoses in the OD group

Diagnosis	<i>n</i> (%)
LRTI	79 (24.2)
Pneumonia	66 (20.2)
Non-pneumonia LRTI	13 (4.0)
Sarcoidosis	34 (10.4)
Cancer	26 (8.0)
Self-resolved illness	17 (5.2)
Chest infection	11 (3.4)
URTI	10 (3.1)
Other <sup>a</sup>	169 (51.7)

LRTI, lower respiratory tract infection; URTI, upper respiratory tract infection.

<sup>a</sup> Fewer than five patients per diagnosis.

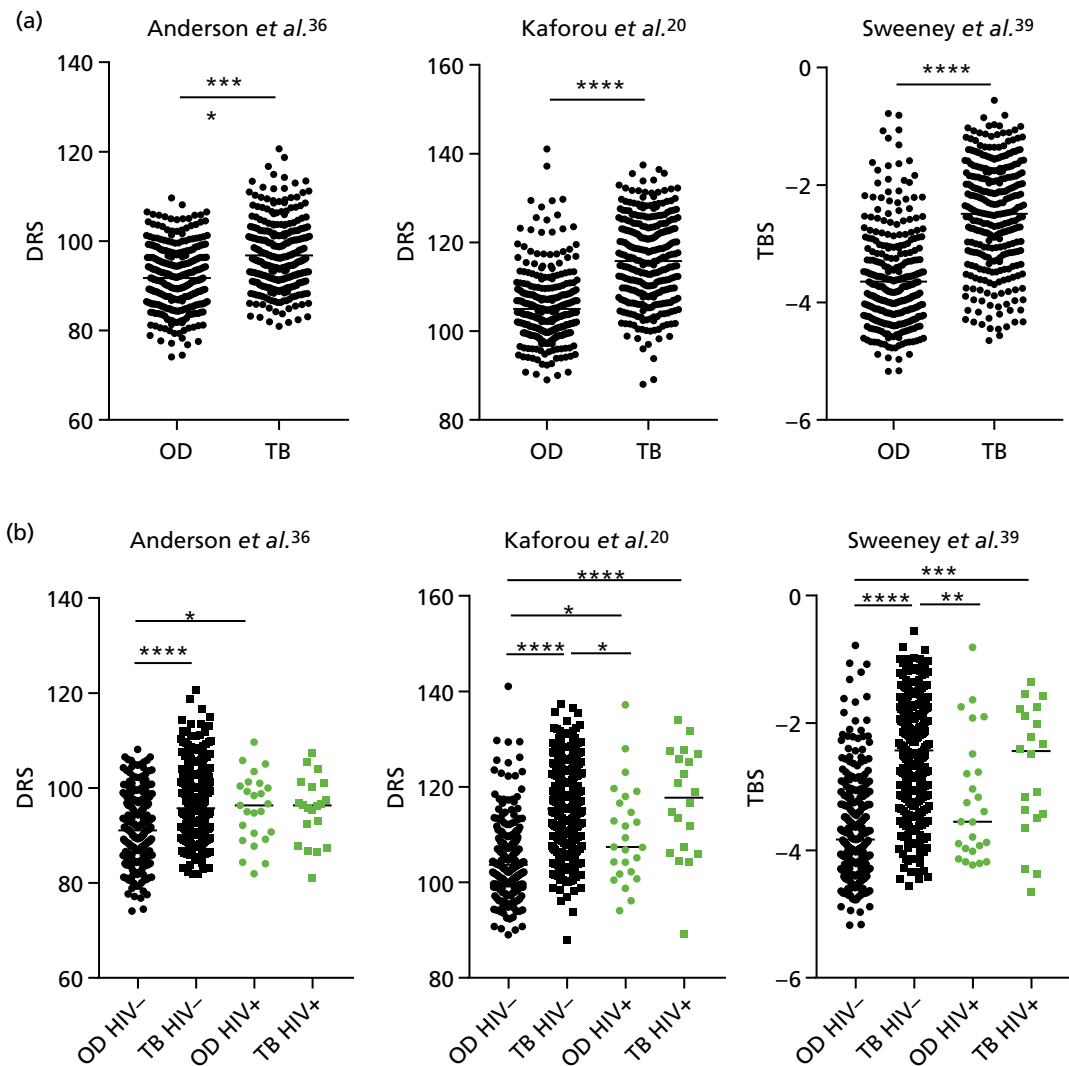




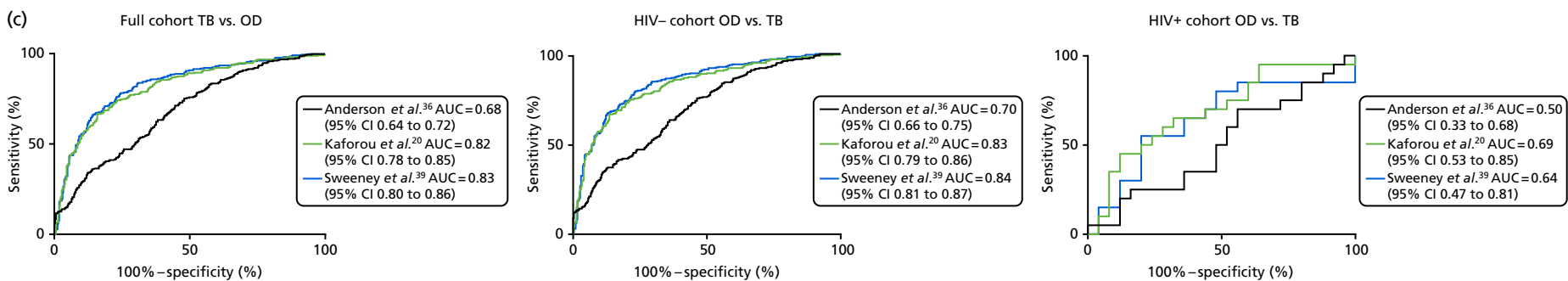
## Appendix 3 Additional analyses for validation of transcriptomic 'score' signatures

**TABLE 26** Cross-tabulation of previously published transcriptomic score signature results by the reference standard

Signature	All TB ( <i>n</i> = 301) (Dosanjh categories 1 and 2)	Culture-confirmed TB ( <i>n</i> = 212) (Dosanjh category 1)	Highly probable TB ( <i>n</i> = 89) (Dosanjh category 2)	OD ( <i>n</i> = 327) (Dosanjh category 4)
<i>Anderson et al.</i> <sup>36</sup>				
Median (range)	95.77 (80.95–120.6)	96.12 (80.95–120.6)	95.38 (81.83–118.7)	91.21 (74.06–109.7)
Missing, <i>n</i>	0	0	0	0
<i>Kaforou et al.</i> <sup>20</sup>				
Median (range)	115.5 (88.01–137.5)	117.5 (88.01–136.4)	111.7 (89.07–137.5)	103.8 (89.02–141.1)
Missing, <i>n</i>	0	0	0	0
<i>Sweeney et al.</i> <sup>39</sup>				
Median (range)	–2.431 (–4.648 to –0.556)	–2.181 (–4.412 to –0.556)	–2.813 (–4.648 to –1.139)	–3.817 (–5.175 to –0.780)
Missing, <i>n</i>	0	0	0	0



**FIGURE 16** Performance of published 'score'-based signatures in the full cohort, stratified by HIV infection status. (a) Dot plot displaying the score values using each signature in the full cohort stratified by OD group (Dosanjh category 4) ( $n = 327$ ) or the TB groups (Dosanjh categories 1 and 2) ( $n = 301$ ); (b) groups further stratified by HIV status; and (c) ROC curves displaying diagnostic performance of scores in the full cohort, HIV- or HIV+ cohorts. Statistical differences between score values between groups were determined using either the Mann-Whitney  $U$ -test (when only two groups are compared) or Kruskal-Wallis with Dunn's post hoc test (for multiple comparisons) for three or more groups. \* $p < 0.05$ ; \*\* $p < 0.005$ ; \*\*\* $p < 0.0005$ ; \*\*\*\* $p < 0.0001$ . (continued)

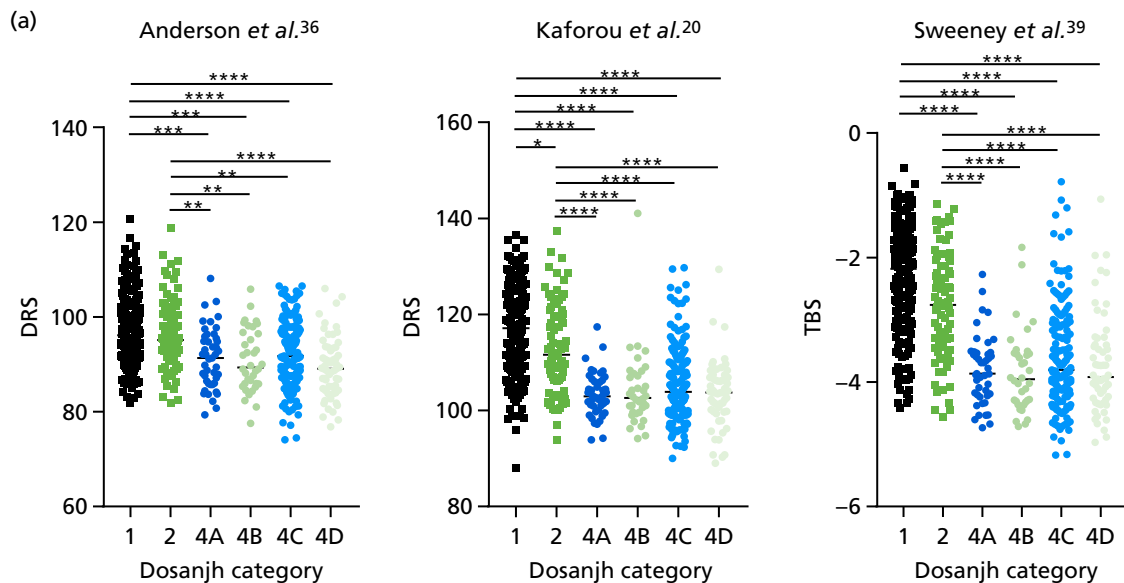


**FIGURE 16** Performance of published 'score'-based signatures in the full cohort, stratified by HIV infection status. (a) Dot plot displaying the score values using each signature in the full cohort stratified by OD group (Dosanjh category 4) ( $n = 327$ ) or the TB groups (Dosanjh categories 1 and 2) ( $n = 301$ ); (b) groups further stratified by HIV status; and (c) ROC curves displaying diagnostic performance of scores in the full cohort, HIV- or HIV+ cohorts. Statistical differences between score values between groups were determined using either the Mann-Whitney  $U$ -test (when only two groups are compared) or Kruskal-Wallis with Dunn's post hoc test (for multiple comparisons) for three or more groups. \* $p < 0.05$ ; \*\* $p < 0.005$ ; \*\*\* $p < 0.0005$ ; \*\*\*\* $p < 0.0001$ .

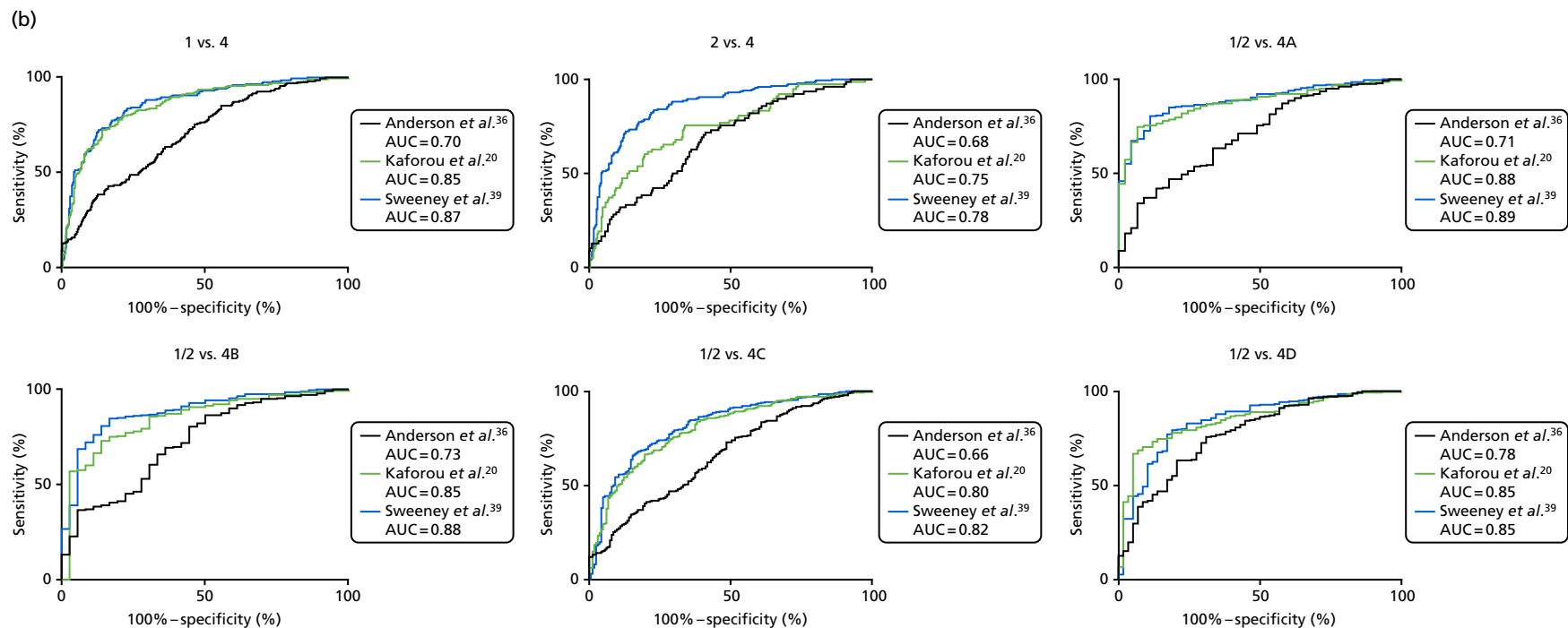
**TABLE 27** Performance of score signatures based on Dosanjh category in the full cohort

Comparison <sup>a</sup>	Signature	Patients, <i>n</i>	Controls, <i>n</i>	AUC, % (95% CI)
1 vs. 4	Anderson <i>et al.</i> <sup>36</sup>	212	327	0.69 (0.65 to 0.74)
	Kaforou <i>et al.</i> <sup>20</sup>	212	327	0.85 (0.81 to 0.88)
	Sweeney <i>et al.</i> <sup>39</sup>	212	327	0.86 (0.83 to 0.89)
2 vs. 4	Anderson <i>et al.</i> <sup>36</sup>	89	327	0.66 (0.60 to 0.72)
	Kaforou <i>et al.</i> <sup>20</sup>	89	327	0.74 (0.68 to 0.80)
	Sweeney <i>et al.</i> <sup>39</sup>	89	327	0.75 (0.70 to 0.81)
1/2 vs. 4A	Anderson <i>et al.</i> <sup>36</sup>	301	46	0.71 (0.63 to 0.78)
	Kaforou <i>et al.</i> <sup>20</sup>	301	46	0.86 (0.82 to 0.91)
	Sweeney <i>et al.</i> <sup>39</sup>	301	46	0.88 (0.84 to 0.92)
1/2 vs. 4B	Anderson <i>et al.</i> <sup>36</sup>	301	36	0.72 (0.63 to 0.81)
	Kaforou <i>et al.</i> <sup>20</sup>	301	36	0.85 (0.78 to 0.91)
	Sweeney <i>et al.</i> <sup>39</sup>	301	36	0.88 (0.82 to 0.93)
1/2 vs. 4C	Anderson <i>et al.</i> <sup>36</sup>	301	175	0.65 (0.60 to 0.70)
	Kaforou <i>et al.</i> <sup>20</sup>	301	175	0.78 (0.74 to 0.83)
	Sweeney <i>et al.</i> <sup>39</sup>	301	175	0.80 (0.76 to 0.84)
1/2 vs. 4D	Anderson <i>et al.</i> <sup>36</sup>	301	70	0.73 (0.66 to 0.79)
	Kaforou <i>et al.</i> <sup>20</sup>	301	70	0.85 (0.79 to 0.89)
	Sweeney <i>et al.</i> <sup>39</sup>	301	70	0.84 (0.79 to 0.89)

a See Table 2 for description of risk categories.



**FIGURE 17** Performance of published SCORE signatures by Dosanjh category in the HIV- population [1, culture-confirmed TB; 2, highly probable TB; 4A, active TB excluded (inactive TB); 4B, active TB excluded (one or more risk factors for TB exposure, TST positive); 4C, active TB excluded (one or more risk factors for TB exposure, TST negative); 4D, active TB excluded (no risk factors for TB exposure, TST negative)]. (a) Dot plots showing the individual score values within each category; and (b) ROC curves displaying the diagnostic performance of each signature for discriminating between groups. Diagnostic groups were compared using a Kruskal-Wallis test with Dunn's post hoc test for multiple comparisons. (*continued*)

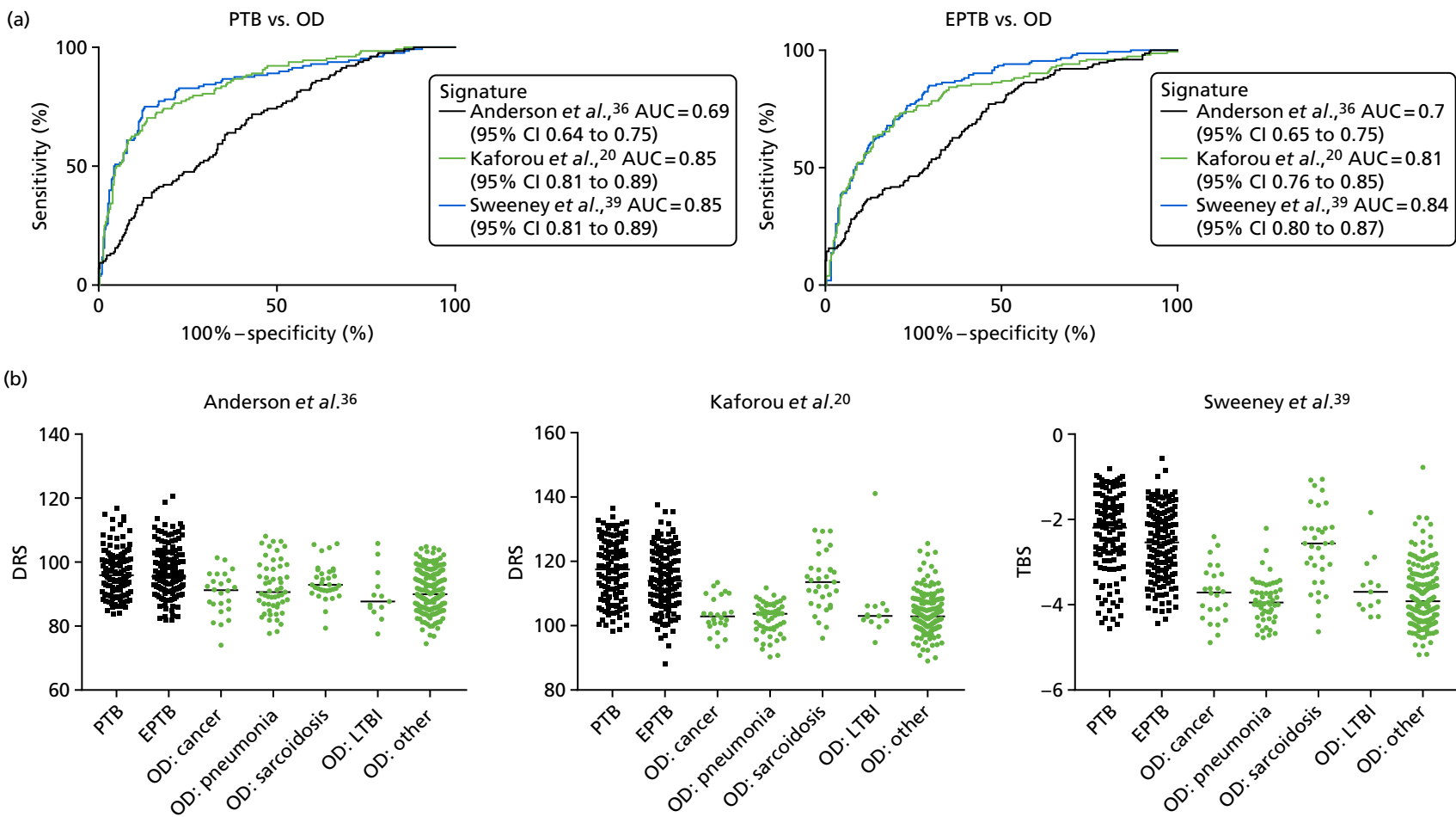


**FIGURE 17** Performance of published SCORE signatures by Dosanjh category in the HIV- population [1, culture-confirmed TB; 2, highly probable TB; 4A, active TB excluded (inactive TB); 4B, active TB excluded (one or more risk factors for TB exposure, TST positive); 4C, active TB excluded (one or more risk factors for TB exposure, TST negative); 4D, active TB excluded (no risk factors for TB exposure, TST negative)]. (a) Dot plots showing the individual score values within each category; and (b) ROC curves displaying the diagnostic performance of each signature for discriminating between groups. Diagnostic groups were compared using a Kruskal-Wallis test with Dunn's post hoc test for multiple comparisons.

**TABLE 28** Performance of score signatures based on Dosanjh category, HIV- cohort only

Comparison <sup>a</sup>	Signature	Patients (n)	Controls (n)	AUC
1 vs. 4	Anderson <i>et al.</i> <sup>36</sup>	203	302	0.70
	Kaforou <i>et al.</i> <sup>20</sup>	203	275	0.85
	Sweeney <i>et al.</i> <sup>39</sup>	203	302	0.87
2 vs. 4	Anderson <i>et al.</i> <sup>36</sup>	78	302	0.68
	Kaforou <i>et al.</i> <sup>20</sup>	78	275	0.75
	Sweeney <i>et al.</i> <sup>39</sup>	78	302	0.78
1/2 vs. 4A	Anderson <i>et al.</i> <sup>36</sup>	281	45	0.71
	Kaforou <i>et al.</i> <sup>20</sup>	281	45	0.88
	Sweeney <i>et al.</i> <sup>39</sup>	281	45	0.89
1/2 vs. 4B	Anderson <i>et al.</i> <sup>36</sup>	281	36	0.73
	Kaforou <i>et al.</i> <sup>20</sup>	281	36	0.85
	Sweeney <i>et al.</i> <sup>39</sup>	281	26	0.88
1/2 vs. 4C	Anderson <i>et al.</i> <sup>36</sup>	281	163	0.66
	Kaforou <i>et al.</i> <sup>20</sup>	281	163	0.80
	Sweeney <i>et al.</i> <sup>39</sup>	281	163	0.82
1/2 vs. 4D	Anderson <i>et al.</i> <sup>36</sup>	281	58	0.78
	Kaforou <i>et al.</i> <sup>20</sup>	281	58	0.85
	Sweeney <i>et al.</i> <sup>39</sup>	281	58	0.85

a See *Table 2* for description of risk categories.



**FIGURE 18** Performance of score signatures in PTB and EPTB, and in OD stratified by disease types. (a) The diagnostic accuracy for the score signatures for detecting either PTB or EPTB was performed for each signatures; (b) the score values by disease subtype within the TB and OD groups is shown in the dot plots; and (c) scores were compared between groups using a Kruskal–Wallis test and the results of the Dunn’s multiple comparison post hoc tests are shown. Statistical differences between score values between groups were determined using the Kruskal–Wallis test with Dunn’s post hoc test for multiple comparisons. ns, not significant. \* $p < 0.05$ ; \*\* $p < 0.005$ ; \*\*\* $p < 0.0005$ ; \*\*\*\* $p < 0.0001$ . (continued)



(c)

Signature	Anderson <i>et al.</i> <sup>36</sup>	Kaforou <i>et al.</i> <sup>20</sup>	Sweeney <i>et al.</i> <sup>39</sup>
OD: LTBI vs. OD: other	ns	ns	ns
OD: sarcoidosis vs. OD: other	ns	****	****
OD: sarcoidosis vs. OD: LTBI	ns	*	ns
OD: pneumonia vs. OD: other	ns	ns	ns
OD: pneumonia vs. OD: LTBI	ns	ns	ns
OD: cancer vs. OD: other	ns	ns	ns
OD: cancer vs. OD: LTBI	ns	ns	ns
OD: cancer vs. OD: sarcoidosis	ns	**	**
OD: cancer vs. OD: pneumonia	ns	ns	ns
EPTB vs. OD: cancer	****	****	****
EPTB vs. OD: other	****	****	****
EPTB vs. OD: LTBI	*	**	*
EPTB vs. OD: sarcoidosis	ns	ns	ns
EPTB vs. OD: pneumonia	**	****	****
EPTB vs. OD: cancer	**	****	****
PTB vs. OD: other	****	****	****
PTB vs. OD: LTBI	*	***	**
PTB vs. OD: sarcoidosis	ns	ns	ns
PTB vs. OD: pneumonia	**	****	****
PTB vs. OD: cancer	**	****	****
PTB vs. EPTB	ns	ns	ns

**FIGURE 18** Performance of score signatures in PTB and EPTB, and in OD stratified by disease types. (a) The diagnostic accuracy for the score signatures for detecting either PTB or EPTB was performed for each signatures; (b) the score values by disease subtype within the TB and OD groups is shown in the dot plots; and (c) scores were compared between groups using a Kruskal–Wallis test and the results of the Dunn’s multiple comparison post hoc tests are shown. Statistical differences between score values between groups were determined using the Kruskal–Wallis test with Dunn’s post hoc test for multiple comparisons. ns, not significant. \* $p < 0.05$ ; \*\* $p < 0.005$ ; \*\*\* $p < 0.0005$ ; \*\*\*\* $p < 0.0001$ .

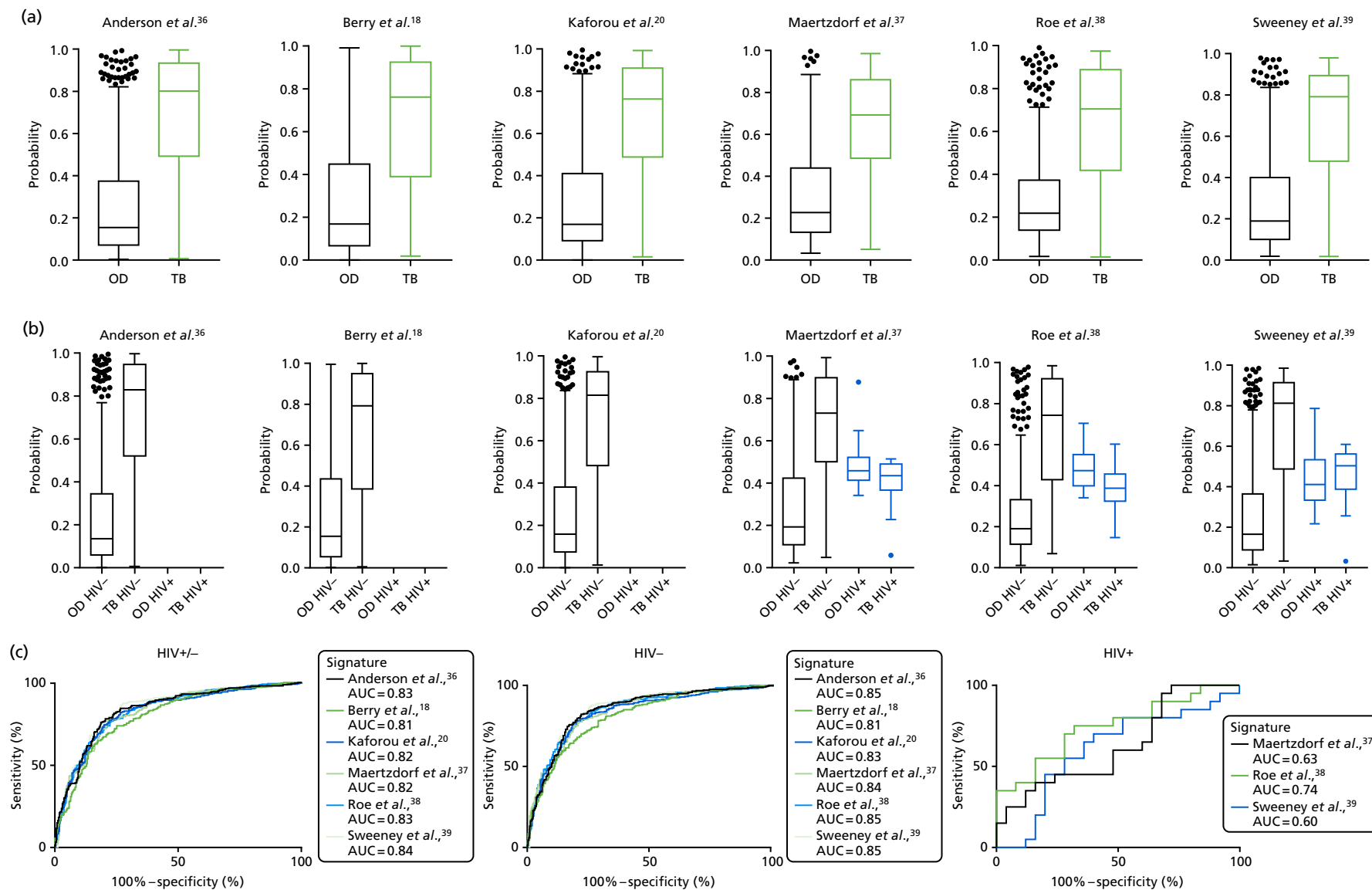
## Appendix 4 Additional information on transcriptomic signatures used for validation studies

**TABLE 29** Summary of previously identified signatures, including cohort characteristics and measures of diagnostic performance

Characteristic/measure of diagnostic performance	Signature							
	Berry <i>et al.</i> <sup>18</sup>		Kaforou <i>et al.</i> <sup>20</sup>		Anderson <i>et al.</i> <sup>36</sup>	Maertzdorf <i>et al.</i> <sup>37</sup>	Roe <i>et al.</i> <sup>38</sup>	Sweeney <i>et al.</i> <sup>39</sup>
Study design	Case-control study (training/test and validation)		Case-control study (training/test and validation)		Children with suspected TB (training/test and validation)	Case-control study (training/test and qRT-PCR validation)	Case-control study	Meta-analysis
Statistical methods	LDA		Elastic net		Elastic net	Random forest	SVML	DerSimonian and Laird, Fisher's sum of logs
Location	UK/South Africa		South Africa/Malawi		South Africa/Malawi/Kenya	India/The Gambia/Uganda	UK	Multiple/meta-analysis
Case type training/test cohort (n)	Training PTB positive (54)	Test PTB positive (33)	Training PTB positive (194)	Test	ATB positive/negative (42/27)	PTB positive (113)	ATB positive (46)	ATB positive/negative (296)
Non-TB group training/test cohort (n)	LTBI (69)/healthy (24)	Other inflammatory diseases (172)	LTBI (167)	OD (175)	Discovery cohort: n = 57 LTBI and n = 175 OD; validation cohort: n = 14 LTBI and n = 64 OD	HCs (including latent) (76)	Other: fever (70)	Various cohorts including OD and LTBI
Number of genes	393	86	27	44	51	4	4	3
Validated AUC	N/A	0.83	0.98	0.95	0.89	0.98	0.95	0.84
Sensitivity/specificity	94.1/96.7	90/83	95/90	93/91	82.9/82.8	88/75	7	81/74
Routine clinical practice	No	No	No	No	Yes	No	No	No
Immunocompromised included?	No	No	HIV+/-	HIV+/-	HIV+/-	No	No	HIV+/-
EPTB included?	No	No	Unknown	No	Yes	No	Yes	Yes
Culture negative included?	No	No	No	No	Yes	No	No	Some

+/-, culture positive/negative; ATB, active tuberculosis; N/A, not applicable.

## Appendix 5 Additional analyses for validation of transcriptomic signatures using linear discriminant analysis



**FIGURE 19** Validation of published transcriptomic signatures. (a) Using LDA in full cohort; (b) stratified by HIV infection status; and (c) ROC curve analyses in the full cohort, HIV- and HIV+ populations.

TABLE 30 Performance of all previously published transcriptomic signatures in full cohort using LDA

LDA signature, reference	HIV	TB, n	OD, n	AUC, % (95% CI)	Cut-off point	Sensitivity, % (95% CI)	Specificity, % (95% CI)	PPV	NPV
Anderson <i>et al.</i> <sup>36</sup>	-	281	302	0.85 (0.82 to 0.88)	> 0.09 <sup>a</sup>	95.0 (91.8 to 97.3)	39.1 (33.5 to 44.8)	0.59	0.90
					> 0.82 <sup>b</sup>	52.0 (45.9 to 57.9)	90.0 (86.1 to 93.2)	0.83	0.67
					> 0.40 <sup>c</sup>	82.2 (77.2 to 86.5)	78.2 (73.1 to 82.7)	0.77	0.83
	+	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
	-/+	301	327	0.83 (0.80 to 0.87)	> 0.09 <sup>a</sup>	95.0 (91.8 to 97.3)	33.6 (28.5 to 39.0)	0.52	0.90
					> 0.82 <sup>b</sup>	47.8 (42.1 to 53.7)	90.2 (86.5 to 93.2)	0.79	0.70
> 0.36 <sup>c</sup>					84.4 (79.8 to 88.3)	73.4 (68.3 to 78.1)	0.71	0.86	
Berry <i>et al.</i> <sup>18</sup>	-	281	302	0.81 (0.78 to 0.85)	> 0.08 <sup>a</sup>	95.0 (91.8 to 97.3)	35.4 (30.0 to 41.1)	0.57	0.89
					> 0.81 <sup>b</sup>	47.7 (41.7 to 53.7)	90.0 (86.1 to 93.2)	0.81	0.65
					> 0.37 <sup>c</sup>	78.3 (73.0 to 83.0)	71.2 (65.7 to 76.2)	0.71	0.8
	+	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
	-/+	301	327	0.80 (0.77 to 0.84)	> 0.10 <sup>a</sup>	95.0 (91.8 to 97.3)	35.5 (30.3 to 40.9)	0.52	0.90
					> 0.83 <sup>b</sup>	42.9 (37.2 to 48.6)	90.2 (86.5 to 93.2)	0.77	0.68
> 0.43 <sup>c</sup>					73.8 (68.4 to 79.5)	74.9 (69.9 to 79.5)	0.69	0.79	
Kaforou <i>et al.</i> <sup>20</sup>	-	281	302	0.83 (0.80 to 0.87)	> 0.09 <sup>a</sup>	95.0 (91.8 to 97.3)	29.5 (24.4 to 35.0)	0.55	0.87
					> 0.80 <sup>b</sup>	52.3 (46.3 to 58.3)	90.0 (86.1 to 93.2)	0.80	0.71
					> 0.43 <sup>c</sup>	78.3 (73.0 to 83.0)	80.0 (64.8 to 84.2)	0.83	0.68
	+	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
	-/+	301	327	0.82 (0.79 to 0.86)	> 0.11 <sup>a</sup>	95.0 (91.8 to 97.3)	30 (25.1 to 35.3)	0.51	0.89
					> 0.87 <sup>b</sup>	48.8 (43.0 to 54.6)	90.2 (86.5 to 93.2)	0.79	0.70
> 0.38 <sup>c</sup>					82.0 (77.3 to 86.2)	73.0 (67.9 to 77.8)	0.70	0.84	

continued

TABLE 30 Performance of all previously published transcriptomic signatures in full cohort using LDA (continued)

LDA signature, reference	HIV	TB, n	OD, n	AUC, % (95% CI)	Cut-off point	Sensitivity, % (95% CI)	Specificity, % (95% CI)	PPV	NPV
Maertsdorf <i>et al.</i> <sup>37</sup>	-	281	302	0.84 (0.81 to 0.88)	> 0.18 <sup>a</sup>	95.0 (91.8 to 97.3)	46.4 (40.6 to 52.2)	0.62	0.91
					> 0.73 <sup>b</sup>	49.8 (43.8 to 55.8)	90.0 (86.1 to 93.2)	0.79	0.70
					> 0.44 <sup>c</sup>	79.0 (73.8 to 83.6)	77.8 (72.7 to 82.3)	0.82	0.66
	+	20	25	0.63 (0.46 to 0.9)	< 0.50 <sup>a</sup>	95.0 (75.1 to 99.9)	32.0 (15.0 to 53.5)	0.21	0.97
					< 0.38 <sup>b</sup>	25.0 (8.7 to 49.1)	92.0 (74.0 to 99.0)	0.37	0.87
					> 0.52 <sup>c</sup>	100 (83.2 to 100)	28.0 (12.1 to 49.4)	0.21	1.0
	-/+	301	327	0.82 (0.79 to 0.86)	> 0.18 <sup>a</sup>	95.0 (91.8 to 97.3)	37.6 (32.3 to 43.1)	0.53	0.91
					> 0.72 <sup>b</sup>	46.1 (40.8 to 52.3)	90.2 (86.5 to 93.2)	0.78	0.69
					> 0.46 <sup>c</sup>	77.1 (71.9 to 81.7)	78.2 (73.4 to 82.3)	0.73	0.82
Roe <i>et al.</i> <sup>38</sup>	-	281	302	0.85 (0.82 to 0.88)	> 0.16 <sup>a</sup>	95.0 (91.8 to 97.3)	40.4 (34.8 to 46.2)	0.59	0.90
					> 0.68 <sup>b</sup>	55.5 (49.5 to 61.4)	90.0 (86.1 to 93.2)	0.84	0.69
					> 0.31 <sup>c</sup>	84.0 (79.2 to 88.1)	73.5 (68.2 to 78.4)	0.74	0.84
	+	20	25	0.74 (0.60 to 0.89)	< 0.57 <sup>a</sup>	95.0 (75.1 to 99.9)	20.0 (6.8 to 40.7)	0.18	0.95
					< 0.40 <sup>b</sup>	40.0 (19.1 to 64.0)	92.0 (74.0 to 99.0)	0.49	0.89
					> 0.45 <sup>c</sup>	75.0 (50.9 to 91.3)	68.0 (46.5 to 85.1)	0.31	0.94
	-/+	301	327	0.83 (0.80 to 0.86)	> 0.18 <sup>a</sup>	95.0 (91.9 to 97.3)	39.1 (33.8 to 44.7)	0.54	0.91
					> 0.70 <sup>b</sup>	50.5 (44.7 to 56.3)	90.2 (86.5 to 93.2)	0.80	0.71
					> 0.40 <sup>c</sup>	76.7 (71.6 to 81.4)	77.0 (72.1 to 81.5)	0.72	0.81

**TABLE 30** Performance of all previously published transcriptomic signatures in full cohort using LDA (*continued*)

LDA signature, reference	HIV	TB, n	OD, n	AUC, % (95% CI)	Cut-off point	Sensitivity, % (95% CI)	Specificity, % (95% CI)	PPV	NPV
Sweeney <i>et al.</i> <sup>39</sup>	–	302	281	0.85 (0.82 to 0.89)	> 0.15 <sup>a</sup>	95.0 (91.9 to 97.3)	47.0 (41.3 to 52.8)	0.62	0.91
					> 0.78 <sup>b</sup>	52.7 (46.7 to 58.6)	90.0 (86.1 to 93.2)	0.83	0.68
					> 0.32 <sup>c</sup>	87.9 (83.5 to 91.5)	73.8 (68.5 to 78.7)	0.75	0.87
	+	20	25	0.60 (0.43 to 0.78)	> 0.26 <sup>a</sup>	95.0 (75.1 to 99.9)	8.0 (0.99 to 26.0)	0.16	0.89
					> 0.71 <sup>b</sup>	0.00 (0.0 to 16.8)	92.0 (74.0 to 99.0)	0.00	0.83
					> 0.43 <sup>c</sup>	70.0 (45.7 to 88.1)	60.0 (38.7 to 78.9)	0.25	0.92
	–/+	301	327	0.84 (0.81 to 0.87)	> 0.15 <sup>a</sup>	95.0 (91.9 to 97.2)	43.1 (37.7 to 48.7)	0.56	0.92
					> 0.78 <sup>b</sup>	50.8 (40.0 to 56.6)	90.2 (86.5 to 93.2)	0.80	0.71
					> 0.33 <sup>c</sup>	87.4 (83.1 to 90.9)	72.5 (67.3 to 77.3)	0.71	0.89

–, negative; +, positive; N/A, not applicable.

<sup>a</sup> To provide sensitivity > 95%.<sup>b</sup> To provide specificity > 90%.<sup>c</sup> To provide the optimal Youden index.**TABLE 31** Performance of all transcriptomic signatures in detecting either culture-confirmed TB (Dosanjh category 1) or culture-unconfirmed TB (Dosanjh category 2), using LDA according to Dosanjh criteria

Comparison	Signature	Patients, n	Controls, n	AUC, % (95% CI)
Dosanjh category 1 vs. Dosanjh category 4	Anderson <i>et al.</i> <sup>36</sup>	203	302	0.86 (0.83 to 0.90)
	Berry <i>et al.</i> <sup>18</sup>	203	302	0.84 (0.81 to 0.88)
	Kaforou <i>et al.</i> <sup>20</sup>	203	302	0.86 (0.82 to 0.89)
	Maertsdorf <sup>37</sup>	203	302	0.86 (0.83 to 0.89)
	Roe <i>et al.</i> <sup>38</sup>	203	302	0.87 (0.84 to 0.90)
	Sweeney <i>et al.</i> <sup>39</sup>	203	302	0.87 (0.84 to 0.91)
Dosanjh category 2 vs. Dosanjh category 4	Anderson <i>et al.</i> <sup>36</sup>	78	302	0.78 (0.73 to 0.84)
	Berry <i>et al.</i> <sup>18</sup>	78	302	0.68 (0.61 to 0.75)
	Kaforou <i>et al.</i> <sup>20</sup>	78	302	0.73 (0.66 to 0.80)
	Maertsdorf <sup>37</sup>	78	302	0.79 (0.74 to 0.85)
	Roe <i>et al.</i> <sup>38</sup>	78	302	0.79 (0.74 to 0.85)
	Sweeney <i>et al.</i> <sup>39</sup>	78	302	0.80 (0.74 to 0.85)



**TABLE 32** Diagnostic performance of previously published signatures for detection of PTB or EPTB, by LDA

Comparison	Signature	Patients, <i>n</i>	Controls, <i>n</i>	AUC, % (95% CI)
PTB vs. OD	Anderson <i>et al.</i> <sup>36</sup>	128	302	0.84 (0.80 to 0.89)
	Berry <i>et al.</i> <sup>18</sup>	128	302	0.83 (0.79 to 0.87)
	Kaforou <i>et al.</i> <sup>20</sup>	128	302	0.84 (0.80 to 0.89)
	Maertsdorf <sup>37</sup>	128	302	0.85 (0.81 to 0.89)
	Roe <i>et al.</i> <sup>38</sup>	128	302	0.86 (0.82 to 0.90)
	Sweeney <i>et al.</i> <sup>39</sup>	128	302	0.86 (0.82 to 0.90)
EPTB vs. OD	Anderson <i>et al.</i> <sup>36</sup>	153	302	0.84 (0.80 to 0.87)
	Berry <i>et al.</i> <sup>18</sup>	153	302	0.78 (0.73 to 0.82)
	Kaforou <i>et al.</i> <sup>20</sup>	153	302	0.82 (0.78 to 0.86)
	Maertsdorf <sup>37</sup>	153	302	0.83 (0.79 to 0.87)
	Roe <i>et al.</i> <sup>38</sup>	153	302	0.84 (0.80 to 0.87)
	Sweeney <i>et al.</i> <sup>39</sup>	153	302	0.85 (0.81 to 0.89)

## Appendix 6 Supporting data for proteomic signature validation

**TABLE 33** Details of proteins within the SELDI-TOF signature discovered by Hamilton and Levin (unpublished)

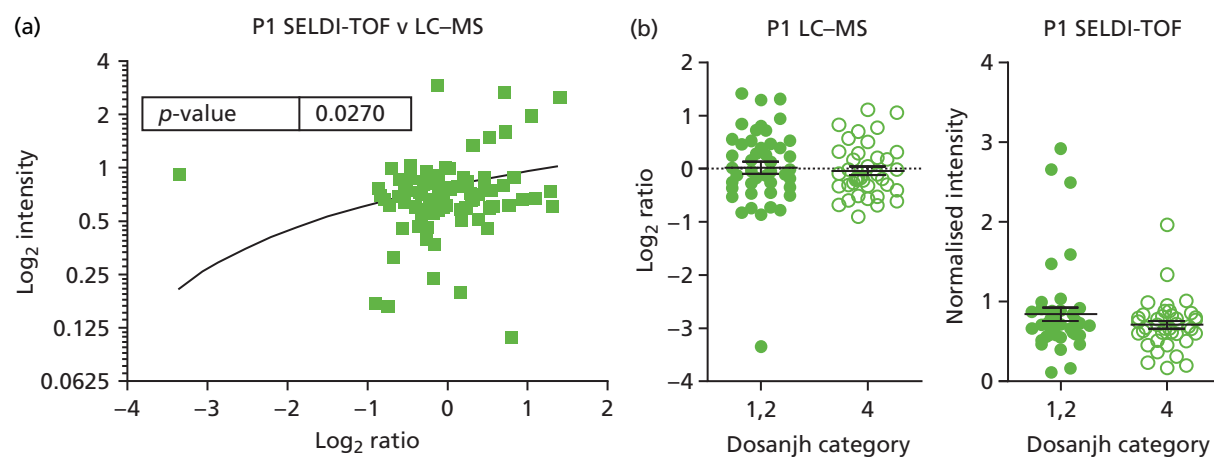
Surface	MW (Da)	Protein ID
Q10 pH 9.5 low	4357 and 4468	Patent pending
CM10 pH 6.0 low	8613	Patent pending
IMAC	5099/5092	Patent pending
CM10 pH 6.0	13,762 and 13,801	Patent pending

### Analysis for bridging study

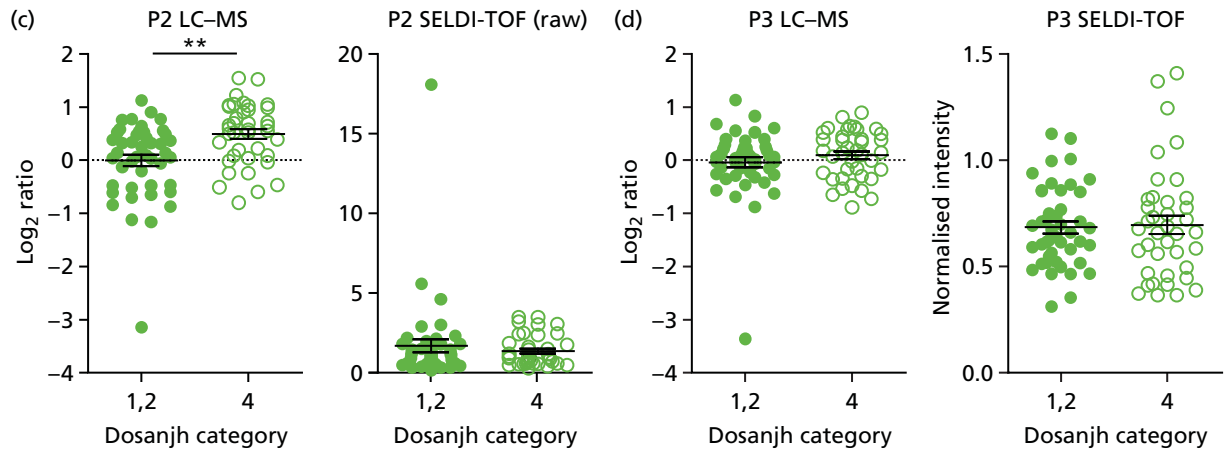
**TABLE 34** Correlation matrix showing  $r$  and  $p$ -value (Pearson's) for SELDI-TOF normalised intensity and LC-MS normalised ratio for proteins 1–3 in the Hamilton and Levin (unpublished) signature

Protein	P1 (LC-MS), $r$ ( $p$ -value)	P2 (LC-MS), $r$ ( $p$ -value)	P3 (LC-MS), $r$ ( $p$ -value)
P1 (SELDI-TOF)	0.17 (0.027)	-0.215 (0.00060)	-0.14 (0.12)
P2 (SELDI-TOF)	0.15 (0.085)	-0.15 (0.16)	0.02 (0.68)
P3 (SELDI-TOF)	0.12 (0.30)	-0.13 (0.83)	0.07 (0.17)

P1, protein 1; P2, protein 2; P3, protein 3.



**FIGURE 20** Comparison of three proteins from the Hamilton and Levin (unpublished) signature with LC-MS data. (a) Correlation of protein 1 SELDI-TOF intensity for protein 1 with LC-MS ratio; and (b–d) dot plots for proteins 1–3 in LC-MS and SELDI-TOF data. Abundance was compared between groups using a Mann-Whitney  $U$ -test. P1, protein 1; P2, protein 2; P3, protein 3.  $**p < 0.005$ . (continued)



**FIGURE 20** Comparison of three proteins from the Hamilton and Levin (unpublished) signature with LC-MS data. (a) Correlation of protein 1 SELDI-TOF intensity for protein 1 with LC-MS ratio; and (b-d) dot plots for proteins 1-3 in LC-MS and SELDI-TOF data. Abundance was compared between groups using a Mann-Whitney *U*-test. P1, protein 1; P2, protein 2; P3, protein 3. \*\* $p < 0.005$ .

## Abundance of signature proteins

**TABLE 35** Abundance of signature proteins in full cohort and comparisons between key patient groups (log<sub>2</sub> ratio of total intensity, normalised to internal control)

Signature (protein ID)	TB (Dosanjh categories 1 and 2) vs. OD (Dosanjh category 4) (minimum, maximum)			Culture-confirmed TB (Dosanjh category 1) vs. OD (Dosanjh category 4) (minimum, maximum)			Highly probable TB (Dosanjh category 2) vs. OD (Dosanjh category 4) (minimum, maximum)		
	ATB (n = 82)	OD (n = 84)	p-value overall	ATB (n = 60)	OD (n = 84)	p-value overall	ATB (n = 22)	OD (n = 84)	p-value overall
Song <i>et al.</i> <sup>51</sup> (P01009)	-0.10 (-0.98, 4.63)	-0.27 (-2.08, 4.36)	0.007	-0.07 (-0.98, 4.63)	-0.27 (-2.08, 4.36)	0.001	-0.24 (-0.58, 0.20)	-0.27 (-2.08, 4.36)	0.668
Xu <i>et al.</i> <sup>52</sup> (P14780_MMP9)	-0.19 (-1.29, 4.10)	-0.20 (-2.97, 4.30)	0.612	-0.16 (-1.29, 4.10)	-0.20 (-2.97, 4.30)	0.335	-0.20 (-0.56, 0.00)	-0.20 (-2.97, 4.30)	0.503
Xu <i>et al.</i> <sup>52</sup> (P06702_S100A9)	-0.21 (-0.96, 4.21)	-0.30 (-2.40, 3.85)	0.036	-0.16 (-0.96, 4.21)	-0.30 (-2.40, 3.85)	0.008	-0.27 (-0.58, 0.00)	-0.30 (-2.40, 3.85)	0.858
Xu <i>et al.</i> <sup>52</sup> (P08294_SOD)	-0.28 (-1.53, 4.26)	-0.17 (-0.72, 4.56)	< 0.001	-0.28 (-1.53, 4.26)	-0.17 (-0.72, 4.56)	< 0.001	-0.30 (-0.55, 0.49)	-0.17 (-0.72, 4.56)	0.019
Hamilton and Levin (unpublished) (Levin 1)	-0.23 (-1.06, 4.36)	-0.11 (-2.23, 4.56)	< 0.001	-0.23 (-1.06, 4.36)	-0.11 (-2.23, 4.56)	< 0.001	-0.20 (-0.47, -0.05)	-0.11 (-2.23, 4.56)	0.015
Hamilton and Levin (unpublished) (Levin 2)	-0.20 (-0.94, 4.42)	-0.19 (-2.21, 4.44)	0.233	-0.20 (-0.94, 4.42)	-0.19 (-2.21, 4.44)	0.795	-0.23 (-0.44, -0.09)	-0.19 (-2.21, 4.44)	0.018
Hamilton and Levin (unpublished) (Levin 3)	-0.21 (-0.97, 4.51)	-0.23 (-1.89, 4.48)	0.679	-0.17 (-0.97, 4.51)	-0.23 (-1.89, 4.48)	0.206	-0.26 (-0.46, -0.02)	-0.23 (-1.89, 4.48)	0.152
Hamilton and Levin (unpublished) (Levin 4)	-0.21 (-1.30, 4.22)	-0.21 (-2.80, 4.63)	0.475	-0.20 (-1.30, 4.22)	-0.21 (-2.80, 4.63)	0.59	-0.23 (-0.91, 0.34)	-0.21 (-2.80, 4.63)	0.493
Achkar <i>et al.</i> <sup>21</sup> (O00391)	-0.20 (-1.29, 4.31)	-0.17 (-2.89, 4.39)	0.086	-0.19 (-1.29, 4.31)	-0.17 (-2.89, 4.39)	0.12	-0.21 (-0.43, 0.00)	-0.17 (-2.89, 4.39)	0.252

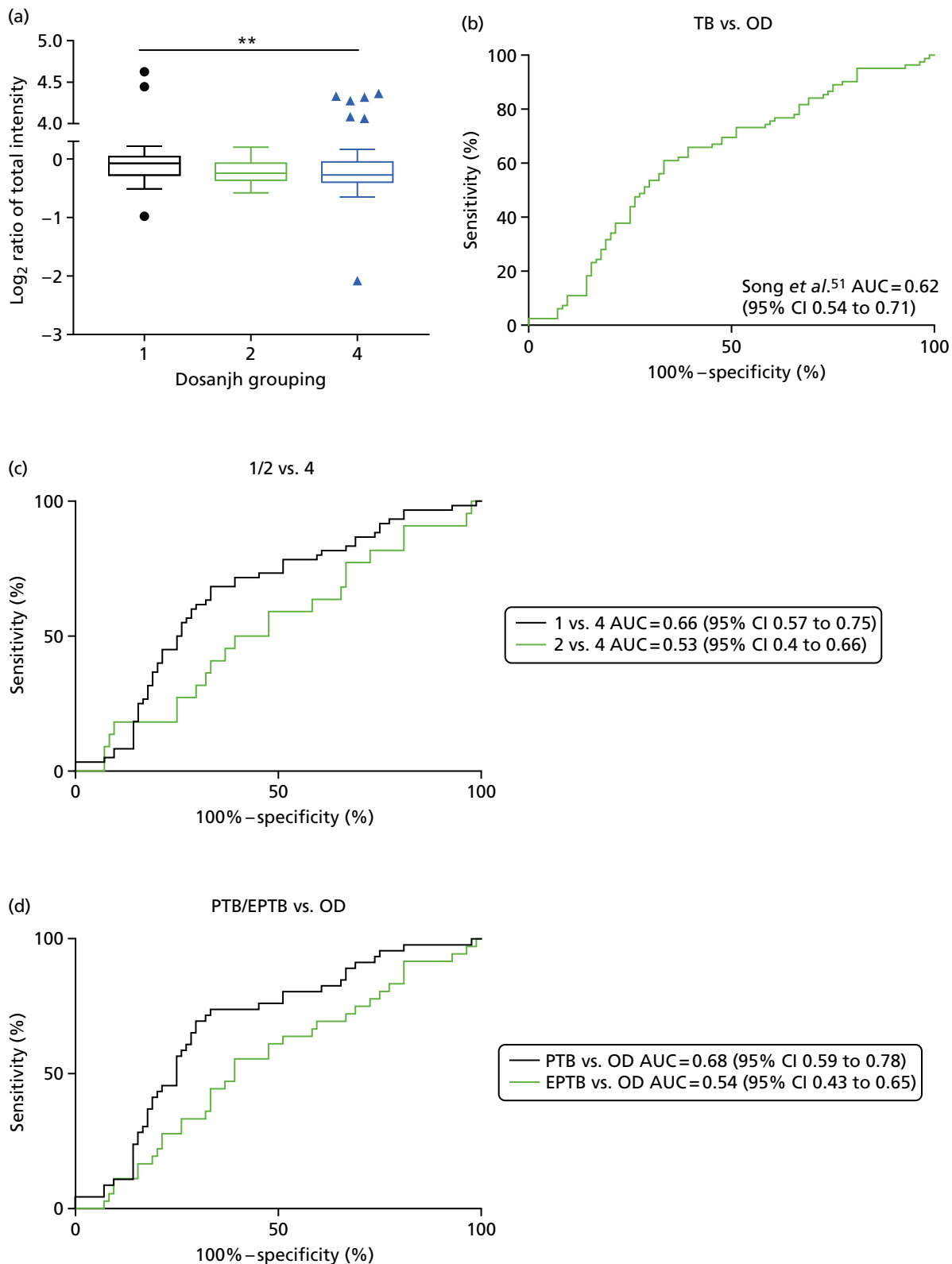
**TABLE 35** Abundance of signature proteins in full cohort and comparisons between key patient groups (log<sub>2</sub> ratio of total intensity, normalised to internal control) (continued)

Signature (protein ID)	TB (Dosanjh categories 1 and 2) vs. OD (Dosanjh category 4) (minimum, maximum)			Culture-confirmed TB (Dosanjh category 1) vs. OD (Dosanjh category 4) (minimum, maximum)			Highly probable TB (Dosanjh category 2) vs. OD (Dosanjh category 4) (minimum, maximum)		
	ATB (n = 82)	OD (n = 84)	p-value overall	ATB (n = 60)	OD (n = 84)	p-value overall	ATB (n = 22)	OD (n = 84)	p-value overall
Achkar <i>et al.</i> <sup>21</sup> (P02654)	-0.23 (-1.08, 4.32)	-0.10 (-2.49, 4.68)	< 0.001	-0.25 (-1.08, 4.32)	-0.10 (-2.49, 4.68)	< 0.001	-0.19 (-0.44, 0.01)	-0.10 (-2.49, 4.68)	0.04
Achkar <i>et al.</i> <sup>21</sup> (P07359)	-0.19 (-1.22, 4.34)	-0.18 (-2.48, 4.47)	0.361	-0.19 (-1.22, 4.34)	-0.18 (-2.48, 4.47)	0.404	-0.18 (-0.45, -0.04)	-0.18 (-2.48, 4.47)	0.549
Achkar <i>et al.</i> <sup>21</sup> (P08571)	-0.19 (-1.31, 4.49)	-0.19 (-2.73, 4.47)	0.804	-0.19 (-1.31, 4.49)	-0.19 (-2.73, 4.47)	0.644	-0.20 (-0.50, 0.01)	-0.19 (-2.73, 4.47)	0.773
Achkar <i>et al.</i> <sup>21</sup> (P12955)	-0.22 (-1.33, 3.74)	-0.18 (-2.63, 3.99)	< 0.001	-0.23 (-1.33, 3.74)	-0.18 (-2.63, 3.99)	< 0.001	-0.22 (-0.41, 0.01)	-0.18 (-2.63, 3.99)	0.029
Achkar <i>et al.</i> <sup>21</sup> (P14151)	-0.18 (-1.14, 4.39)	-0.19 (-2.49, 4.53)	0.608	-0.17 (-1.14, 4.39)	-0.19 (-2.49, 4.53)	0.399	-0.19 (-0.42, 0.02)	-0.19 (-2.49, 4.53)	0.703
Achkar <i>et al.</i> <sup>21</sup> (P22105)	-0.21 (-1.23, 4.33)	-0.15 (-2.56, 4.52)	0.023	-0.22 (-1.23, 4.33)	-0.15 (-2.56, 4.52)	0.009	-0.19 (-0.44, 0.01)	-0.15 (-2.56, 4.52)	0.657
Achkar <i>et al.</i> <sup>21</sup> (P49747)	-0.24 (-1.17, 4.31)	-0.12 (-2.56, 4.59)	< 0.001	-0.24 (-1.17, 4.31)	-0.13 (-2.56, 4.59)	0.001	-0.25 (-0.45, -0.03)	-0.15 (-2.56, 4.59)	0.051
Achkar <i>et al.</i> <sup>21</sup> (P49908)	-0.23 (-1.17, 4.40)	-0.14 (-2.54, 4.52)	0.001	-0.23 (-1.17, 4.40)	-0.14 (-2.54, 4.52)	0.002	-0.22 (-0.45, 0.03)	-0.14 (-2.54, 4.52)	0.038
Achkar <i>et al.</i> <sup>21</sup> (P51884)	-0.24 (-1.07, 4.39)	-0.12 (-2.16, 4.53)	< 0.001	-0.26 (-1.07, 4.39)	-0.12 (-2.16, 4.53)	< 0.001	-0.19 (0.49, 0.01)	-0.12 (2.16, 4.53)	-0.074

ATB, active tuberculosis; ID, identification.

#### Notes

p-values showing significant differences between protein abundance were calculated using the analysis of variance and Welch's *t*-test and were adjusted for the effect of multiple hypothesis testing using the FDR (< 0.1) method.



**FIGURE 21** Abundance of SERPINA1 (alpha-1-antitrypsin or P01009). (a) Box plot depicts the median values and distribution of data in Dosanjh categories 1, 2 and 4; (b) ROC curves present the ability of the levels of SERPINA1 protein to discriminate between all TB vs. OD; (c) either culture-confirmed TB (Dosanjh category 1) or highly probable TB (Dosanjh category 2) (1/2) vs. OD (Dosanjh category 4); and (d) PTB vs. OD or EPTB vs. OD. Medians were compared between groups using the Kruskal–Wallis test. \*\* $p < 0.005$ .

## Missing and imputed data

Spreadsheets detailing the missing data for each signature are available on request.

**TABLE 36** Performance of LC–MS technology in detecting proteins from key previously published signatures, including the proportion of missing data in the cohorts

Study	Published signature	Depleted LC–MS missing values, %	Crude Dundee LC–MS missing values, %
Song <i>et al.</i> <sup>51</sup>	P01009	0	0
Xu <i>et al.</i> <sup>52</sup>	P06702	21.43	61.65
Xu <i>et al.</i> <sup>52</sup>	P08294	0.6	Not Measured
Xu <i>et al.</i> <sup>52</sup>	P14780	10.71	Not measured
Hamilton and Levin (unpublished)	Levin 1	0	0
Hamilton and Levin (unpublished)	Levin 2	0	0
Hamilton and Levin (unpublished)	Levin 3	0	11.11
Hamilton and Levin (unpublished)	Levin 4	0	65.59
Achkar <i>et al.</i> <sup>21</sup>	O00391	0	Not measured
Achkar <i>et al.</i> <sup>21</sup>	P02654	0	0
Achkar <i>et al.</i> <sup>21</sup>	P07359	0	Not measured
Achkar <i>et al.</i> <sup>21</sup>	P08571	0	96.77
Achkar <i>et al.</i> <sup>21</sup>	P12955	21.43	Not measured
Achkar <i>et al.</i> <sup>21</sup>	P14151	0	Not measured
Achkar <i>et al.</i> <sup>21</sup>	P22105	0	Not measured
Achkar <i>et al.</i> <sup>21</sup>	P49747	0	Not measured
Achkar <i>et al.</i> <sup>21</sup>	P49908	0	Not measured
Achkar <i>et al.</i> <sup>21</sup>	P51884	0	0

### Notes

The coverage of proteins using either the depleted data set ( $n = 168$ ) or crude data set ( $n = 267$ ) is presented.

**TABLE 37** Diagnostic performance of the Song *et al.*<sup>51</sup> signature in the validation of TB in the full LC–MS validation cohort ( $n = 168$ ) and in key subgroups of TB

Characteristic	TB vs. OD	1 vs. 4	2 vs. 4	PTB vs. OD	EPTB vs. OD
Patients, $n$	82	60	22	46	36
Control, $n$	84	84	84	84	84
AUC, % (95% CI)	0.62 (0.54 to 0.71)	0.66 (0.57 to 0.75)	0.53 (0.4 to 0.66)	0.68 (0.59 to 0.78)	0.54 (0.43 to 0.65)
Cut-off point	–0.44* –0.11 <sup>§</sup>	–0.42* –0.11 <sup>§</sup>	–0.53* –0.11 <sup>§</sup>	–0.4* –0.11 <sup>§</sup>	–0.53* –0.11 <sup>§</sup>
Sensitivity, % (95% CI)	95 (88 to 99)* 11 (5.1 to 20) <sup>§</sup>	95 (86 to 99)* 8.3 (2.8 to 18) <sup>§</sup>	95 (77 to 100)* 18 (5.2 to 40) <sup>§</sup>	96 (85 to 99)* 11 (3.6 to 24) <sup>§</sup>	97 (85 to 100)* 11 (3.1 to 26) <sup>§</sup>
Specificity, % (95% CI)	19 (11 to 29)* 90 (82 to 96) <sup>§</sup>	19 (11 to 29)* 90 (82 to 96) <sup>§</sup>	3.6 (0.74 to 10)* 90 (82 to 96) <sup>§</sup>	25 (16 to 36)* 90 (82 to 96) <sup>§</sup>	3.6 (0.74 to 10)* 90 (82 to 96) <sup>§</sup>

### Notes

Different cut-off points were selected, either to provide sensitivity of > 95% (\*) or specificity of > 90% (°).

## Appendix 7 Additional analyses for diagnostic evaluation of serum protein signatures for detection of active tuberculosis using linear discriminant analysis

**TABLE 38** Diagnostic performance of serum proteomic signatures in full cohort ( $n = 166$ )

Signature, reference	TB, $n$	OD/LTBI, $n$	AUC, % (95% CI)	Cut-off point	Sensitivity, % (95% CI)	Specificity, % (95% CI)
Xu <i>et al.</i> <sup>52</sup>	82	84	0.66 (0.58 to 0.75)	> 0.29 <sup>a</sup>	95.1 (88 to 98.7)	14.3 (7.6 to 23.6)
				> 0.65 <sup>b</sup>	8.5 (3.5 to 16.8)	90.5 (82.1 to 95.8)
Hamilton and Levin (unpublished)	82	84	0.64 (0.55 to 0.72)	> 0.34 <sup>a</sup>	95 (88 to 98.6)	14.1 (7.5 to 23.3)
				> 0.63 <sup>b</sup>	25.6 (16.6 to 36.4)	90.5 (82.1 to 95.8)
Achkar <i>et al.</i> <sup>21</sup>	82	84	0.68 (0.60 to 0.76)	> 0.18 <sup>a</sup>	95.1 (88 to 98.7)	11.9 (5.9 to 20.8)
				> 0.77 <sup>b</sup>	20.7 (12.6 to 31.1)	90.5 (82.1 to 95.8)

a Cut-off point to provide sensitivity > 95%.

b Cut-off point to provide sensitivity > 90%.

**TABLE 39** Diagnostic performance of Xu *et al.*<sup>52</sup>, Hamilton and Levin (unpublished) and Achkar *et al.*<sup>21</sup> serum proteomic signatures in key patient subgroups in full cohort, using LDA

Comparison	Signature	Patients, $n$	Controls, $n$	AUC, % (95% CI)
1 vs. 4	Xu <i>et al.</i> <sup>52</sup>	60	84	0.70 (0.61 to 0.79)
	Hamilton and Levin (unpublished)	60	84	0.67 (0.58 to 0.76)
	Achkar <i>et al.</i> <sup>21</sup>	60	84	0.70 (0.62 to 0.79)
2 vs. 4	Xu <i>et al.</i> <sup>52</sup>	22	84	0.59 (0.46 to 0.72)
	Hamilton and Levin (unpublished)	22	84	0.57 (0.45 to 0.69)
	Achkar <i>et al.</i> <sup>21</sup>	22	84	0.55 (0.41 to 0.69)
EPTB vs. OD	Xu <i>et al.</i> <sup>52</sup>	36	84	0.61 (0.50 to 0.71)
	Hamilton and Levin (unpublished)	36	84	0.51 (0.40 to 0.62)
	Achkar <i>et al.</i> <sup>21</sup>	36	84	0.60 (0.49 to 0.70)
PTB vs. OD	Xu <i>et al.</i> <sup>52</sup>	46	84	0.67 (0.57 to 0.78)
	Hamilton and Levin (unpublished)	46	84	0.69 (0.59 to 0.78)
	Achkar <i>et al.</i> <sup>21</sup>	46	84	0.70 (0.60 to 0.79)

### Notes

We also performed LDA for the Song *et al.*<sup>51</sup> signature using this approach, but it should be noted that, as this signature comprises only one protein, this statistical approach is not recommended.





## Appendix 8 Validation of published proteomic signatures using liquid chromatography–mass spectrometry by linear discriminant analysis (with the removal of sarcoidosis)

**TABLE 40** Performance of Xu *et al.*,<sup>52</sup> Hamilton and Levin (unpublished) and Achkar *et al.*<sup>21</sup> signatures for detecting all TB, using LDA, with patients with sarcoidosis removed

Signature, reference	TB, n	OD, n	AUC, % (95% CI)	Cut-off point	Sensitivity, % (95% CI)	Specificity, % (95% CI)
Xu <i>et al.</i> <sup>52</sup>	82	79	0.68 (0.60 to 0.76)	> 0.30	95.1 (88 to 98.7)	13.9 (7.16 to 23.6)
				> 0.65	11 (5.1 to 19.8)	91.1 (82.6 to 96.4)
Hamilton and Levin (unpublished)	82	79	0.65 (0.56 to 0.73)	> 0.35	95.1 (88 to 98.7)	19 (11 to 29.4)
				> 0.69	19.5 (11.6 to 29.7)	91.1 (82.6 to 96.4)
Achkar <i>et al.</i> <sup>21</sup>	82	79	0.69 (0.60 to 0.76)	> 0.21	95.1 (88 to 98.7)	13.9 (7.2 to 23.6)
				> 0.76	24.4 (15.6 to 35.1)	91.1 (82.6 to 96.4)

**TABLE 41** Performance of Xu *et al.*,<sup>52</sup> Hamilton and Levin (unpublished) and Achkar *et al.*<sup>21</sup> signatures for detecting key subgroups of TB, using LDA, with sarcoidosis removed

Comparison	Signature	TB, n	OD, n	AUC, % (95% CI)
1 vs. 4	Xu <i>et al.</i> <sup>52</sup>	60	79	0.72 (0.63 to 0.81)
	Hamilton and Levin (unpublished)	60	79	0.68 (0.59 to 0.77)
	Achkar <i>et al.</i> <sup>21</sup>	60	79	0.71 (0.63 to 0.80)
2 vs. 4	Xu <i>et al.</i> <sup>52</sup>	22	79	0.60 (0.47 to 0.73)
	Hamilton and Levin (unpublished)	22	79	0.55 (0.43 to 0.67)
	Achkar <i>et al.</i> <sup>21</sup>	22	79	0.53 (0.39 to 0.67)
EPTB vs. OD	Xu <i>et al.</i> <sup>52</sup>	36	79	0.63 (0.53 to 0.74)
	Hamilton and Levin (unpublished)	36	79	0.53 (0.42 to 0.64)
	Achkar <i>et al.</i> <sup>21</sup>	36	79	0.60 (0.49 to 0.70)
PTB vs. OD	Xu <i>et al.</i> <sup>52</sup>	46	79	0.69 (0.59 to 0.79)
	Hamilton and Levin (unpublished)	46	79	0.70 (0.61 to 0.80)
	Achkar <i>et al.</i> <sup>21</sup>	46	79	0.70 (0.61 to 0.80)



## Appendix 9 Additional information for flow cytometry introduction and methods

The BV421 fluorochrome on the IFN $\gamma$ -specific antibody invariably showed a false-positive signal in unstimulated samples. This increased background manifested as an aggregate population on the CD3-positive population, an observation that has been noted for the BV421 fluorochrome and specific IFN $\gamma$  antibodies elsewhere.<sup>77</sup> The false positive could easily be differentiated from a true-positive signal based on the fluorescence in other channels; the 'streak' was not positive for AF700 or APC and showed an increasing fluorescence in the BV510 channel. The BV421 aggregate was therefore removed from each file before the final cytokine gates were applied, by selecting the 'streak' of artefact staining on the IFN $\gamma$ -positive TNF- $\alpha$ -positive plot within the CD3-positive population (*Tables 42 and 43, Figures 22–24*).

**TABLE 42** Summary of cellular immune signatures to be validated, with reference to the original publication and the study design and characteristics of the discovery cohorts

Summary	Harari <i>et al.</i> <sup>24</sup>	Pollock <i>et al.</i> <sup>25</sup>	Rozot <i>et al.</i> <sup>58</sup>	Portevin <i>et al.</i> <sup>27</sup>	Petruccioli <i>et al.</i> <sup>28</sup>	Adekambi <i>et al.</i> <sup>26</sup>
Signature	%TNF- $\alpha$ -only	%T <sub>EFF</sub>	SCORE (combination of %TNF- $\alpha$ -only and presence of IFN $\gamma$ response)	CD27 MFI ratio	%CD27-CD45RA	%HLA-DR positive
Parent population	CD4 positive, cytokine positive (IFN $\gamma$ /IL-2/TNF- $\alpha$ )	CD4 positive, TNF- $\alpha$ only	CD4 positive, cytokine positive and CD8 positive	CD4 positive, IFN $\gamma$ positive	CD4 positive, IFN $\gamma$ positive	CD4 positive, IFN $\gamma$ positive
TB type, <i>n</i> <sup>a</sup>	Culture-positive PTB/EPTB, 16	Culture-positive PTB, 13	C+/- PTB/EPTB, 53	Children C+/- PTB, 6	Culture-positive PTB, 13	Culture-positive PTB, 26
LTBI type, <i>n</i> <sup>a</sup>	Healthy, 77	Healthy (HIV+/-), 21	Healthy, 141	Healthy children, 30	Healthy, 30	Healthy, 25
HIV included?	No	Yes	No	No	No	No (in validation)
AUC <sup>a</sup>	0.99	0.99	0.89	–	0.85 (%CD45RA-CD27-); 0.91 (%CD45RA-CD27+)	1.0
Sensitivity, % <sup>a</sup>	100	100	81.1	83.3	69.2 (%CD45RA-CD27-); 76.9 (%CD45RA-CD27+)	100
Specificity, % <sup>a</sup>	96	92.9	86.5	95.6–100	87% (%CD45RA-CD27-); 90% (%CD45RA-CD27+)	96
Internal validation	Yes (AUC 0.82) and includes C+/- and EPTB	No	No	Yes	No	Yes
External validation	Wilkinson <i>et al.</i> <sup>59</sup> (did not work)	Halliday <i>et al.</i> <sup>78</sup> (AUC vs. remote 0.99)	No	Petruccioli <i>et al.</i> <sup>28</sup> (AUC)	–	Wilkinson <i>et al.</i> <sup>59</sup> HIV+/- (AUC = 0.98); Riou <i>et al.</i> <sup>60</sup> HIV+/- (AUC 0.92/0.99)

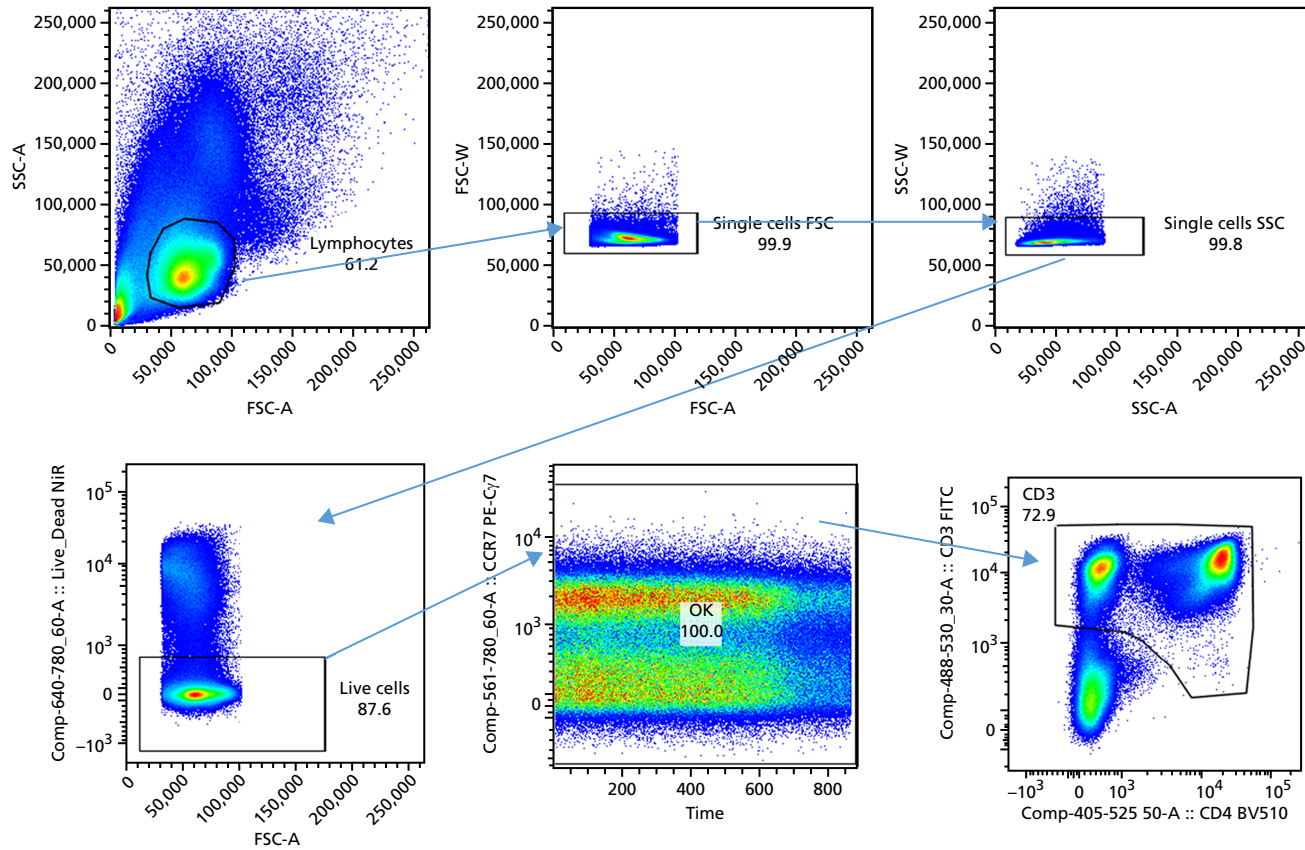
C+/-, culture positive/negative.

**Note**<sup>a</sup> Where two cohorts (discovery and validation) were described, the TB type and test accuracy values are given for the validation cohort.

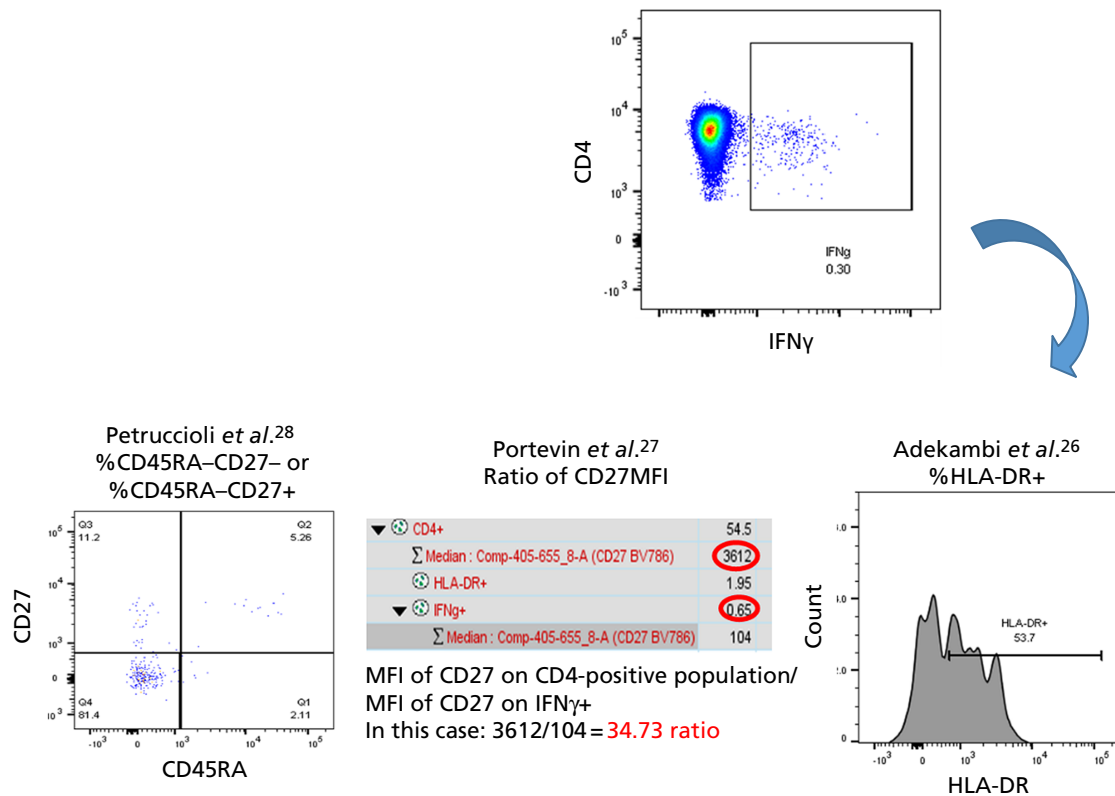
**TABLE 43** Details of antibodies used and their final dilutions during staining

Target	Surface/ intracellular	Species, isotype, clone	Fluorochrome	Bandpass Filter Fortessa A	Dilution	Company supplied
CD45RA	Surface	Mouse IgG <sub>1</sub> , κ, HI30 RUO	BUV395	355–450/50	1 in 100	Becton Dickinson and Company
CD3	Surface	Mouse IgG <sub>2a</sub> , κ, HIT3a	FITC	488–530/30	1 in 30	BioLegend
CD4	Surface	Mouse IgG2b, κ, OKT4	BV510	405–425/50	1 in 30	BioLegend
CD8	Surface	Mouse (BALB/c) IgG1, κ, SK1	BV605	405–560/520	1 in 30	BioLegend
CCR7	Surface	Rat IgG2a, κ, 3D12	PE-Cy7	561–780/60	1 in 15	Becton Dickinson and Company
CD127	Surface	Mouse IgG <sub>1</sub> , κ, HIL-7R-M21	PE	561–582/15	1 in 40	Becton Dickinson and Company
CD27	Surface	Mouse IgG <sub>1</sub> , κ, O323	BV785	405–655/8	1 in 40	BioLegend
HLA-DR	Surface	Mouse IgG2a, κ, L243	PerCP-Cy5.5	488–710/50	1 in 40	BioLegend
IFN $\gamma$	IC	Mouse IgG1, κ, 4S.B3	BV421	405–450/50	1 in 30	BioLegend
TNF- $\alpha$	IC	Mouse IgG <sub>1</sub> , κ, MAb11	APC	640–670/14	1 in 50	BioLegend
IL-2	IC	Rat IgG2a, κ, MQ1-17H12	AF700	640–720/40	1 in 50	BioLegend

APC, allophycocyanin; FITC, fluorescein isothiocyanate; IC, intracellular; IgG, immunoglobulin G; PE, phycoerythrin.

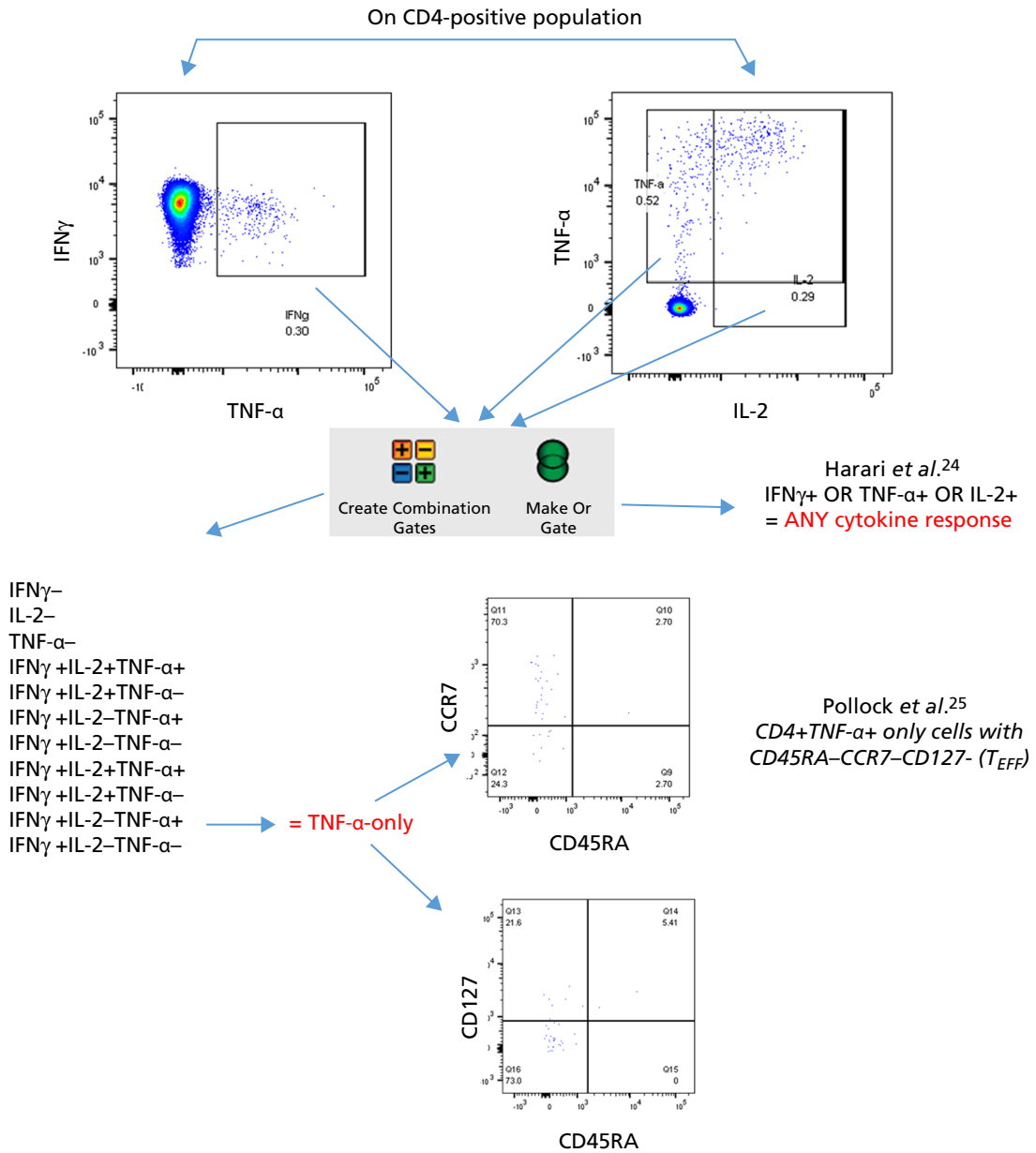


**FIGURE 22** Initial basic gating strategies for the cellular immunological signatures as set on FlowJo version 10. Gates were set on the lymphocyte populations, live cells and on single cells, and further gated on the CD3-positive population. FITC, fluorescein isothiocyanate; FSC, forward scatter; SSC, side scatter.



**FIGURE 23** Gating strategies for the validating signatures exploring IFN $\gamma$ -positive cytokine responses within the CD4-positive population. Petruccioli *et al.*<sup>28</sup> measures memory cells lost in differentiation, Portevin *et al.*<sup>27</sup> incorporates a MFI ratio for measuring differentiation and Adekambi *et al.*<sup>26</sup> measures the %HLA-DR activation marker.





**FIGURE 24** Gating strategy for validating Pollock *et al.*<sup>25</sup> and Harari *et al.*<sup>24</sup> signatures. Pollock *et al.* investigates the effector phenotype within the CD4-positive TNF- $\alpha$ -only population (IFN $\gamma$  negative, IL-2 negative, TNF- $\gamma$  positive) and Harari *et al.*<sup>24</sup> investigates %TNF- $\alpha$  positive within any cytokine producers in the CD4-positive population.

## Appendix 10 Additional cohort characteristics of the validation of cellular immune signatures sub-study

**TABLE 44** Distribution of severity and disease in TB group of cellular immune signature validation cohort

Type of TB	Culture-confirmed TB (Dosanjh category 1)	Highly probable TB (Dosanjh category 2)	All TB (total)
All TB, <i>n</i>	60	32	92
Culture, <i>n</i> (%)			
Positive	60 (100)	0 (0)	60 (65.2)
Negative	0 (0)	27 (84.4)	27 (29.4)
Not tested/failed	0 (0)	5 (15.6)	5 (5.4)
Smear, <i>n</i> (%)			
Positive	18 (30)	2 (6.3)	20 (21.8)
Negative	34 (56.7)	25 (78.1)	59 (64.1)
Not tested/failed	8 (13.3)	5 (15.6)	13 (14.1)
PTB, <i>n</i> (%)	30 (50)	4 (12.5)	34 (37)
EPTB, <i>n</i> (%)	19 (31.7)	27 (84.4)	46 (50)
PTB + EPTB, <i>n</i> (%) <sup>a</sup>	11 (18.3)	1 (3.1)	12 (13)
Site of infection, <i>n</i> (%) <sup>b</sup>			
Abdomen	1 (1.7)	1 (3.1)	2 (2.2)
Brains	1 (1.7)	2 (6.2)	3 (3.3)
Chest	1 (1.7)	1 (3.1)	2 (2.2)
Lungs	41 (68.3)	5 (15.6)	46 (50)
Lymph node	22 (36.7)	16 (50)	38 (41.3)
Miliary TB	3 (5)	0 (0)	3 (3.3)
Pericardium	2 (3.3)	1 (3.1)	3 (3.3)
Pleura	3 (5)	2 (6.2)	5 (5.4)
Spine	2 (3.3)	2 (6.2)	4 (4.3)
Other (skin, eye, liver, bowel, CNS, intestine, neck, peritoneum)	3 (5)	4 (12.5)	7 (7.6)

CNS, central nervous system.

a In this table, those diagnosed with TB pulmonary and extrapulmonary involvement were classified as 'PTB + EPTB'; however, in the main analysis, the PTB + EPTB existed as a subset of the overall PTB group.

b Individuals can be allocated more than one site of infection.

### Note

For site of infection, some individuals will have TB in more than one of these sites, therefore the numbers do not equal the total amount in parent columns.

**TABLE 45** Distribution of alternative diagnoses in OD group ( $n = 92$ ) in the validation cohort for cellular immune signatures

Diagnosis	<i>n</i> (%)
Cancer	8 (8.7)
Pneumonia	11 (11.9)
Sarcoidosis (including sarcoidosis and other)	3 (3.3)
LRTI/chest infection	9 (9.8)
URTI	4 (4.3)
Self-resolving illness	9 (9.8)
Other	48 (52.2)

LRTI, lower respiratory tract infection; URTI, upper respiratory tract infection.

# Appendix 11 Viability, cell recovery and cytokine responses to antigens

## Recovery and viability

Vials of PBMCs from baseline blood samples of TB suspects were collected into the IDEA study biobank between 2011 and 2013. The vials used in this substudy were kept in cryogenic conditions for a median of 60 months (range 38–70 months), before being defrosted and used in experiments. After defrosting of cells and washing, cells were counted and compared with the total number of stored cells when cryopreserved. The mean recovery of live cells from cryopreserved PBMC vials for the full cohort was 48.1% (range 0–116.7%, median 48.4%), with a mean viability of 81% (range 0–100%, median 85%). The recovery rate from the HIV+ participants was lower than from the HIV– participants (median of 48.96% in HIV– participants vs. 33.33% in HIV+ participants;  $p = 0.01$ ), when compared using a Mann–Whitney  $U$ -test. No differences were observed between TB and OD groups (whether or not HIV status was used to further stratify these groups).

## Responses to antigen stimulations

### Positive control antigen

Ionomycin/PMA was used as a positive control stimulation to ensure that the assay was successfully able to detect a definite response to stimulation, in the form of cytokine production. All of the samples stimulated with PMA/ionomycin produced the three cytokines to a level that was at least twice above background, displaying wide ranges of responses, from < 1% to > 90% of cells producing cytokines (Table 46).

**TABLE 46** Responses to PMA/ionomycin in full cohort

Measurement	All TB ( $N = 90$ )	Dosanjh category		
		1 ( $N = 58$ )	2 ( $N = 32$ )	OD/LTBI: 4 ( $N = 91$ )
Stimulated, $n$	90	58	32	88
Cytokine responses, $n$ with response over background (%), % range				
CD4-positive IFN $\gamma$ response	90 (100), 0.28–46.9	58 (100), 0.28–46.9	32 (100), 1.89–46.2	88 (100), 3.7–53.4
CD4-positive IL-2 response	90 (100), 0.26–55	58 (100), 0.26–47.4	32 (100), 8.23–55	88 (100), 20.9–63.5
CD4-positive TNF- $\alpha$ response	90 (100), 0.46–81.4	58 (100), 0.46–81.4	32 (100), 16.5–75.9	88 (100)
CD4-positive TNF- $\alpha$ -only response	90 (100), 0.12–30.5	58 (100), 0.12–30.5	32 (100), 5.79–29.6	87 (99)
CD4-positive any cytokine response	90 (100), 0.46–84.6	58 (100), 0.46–84.6	32 (100), 20.3–79.3	87 (99)
CD8-positive IFN $\gamma$ response	90 (100), 1.82–89.8	58 (100), 1.82–89.8	32 (100), 11.2–79.2	88 (100)
CD8-positive IL-2 response	90 (100), 0.68–54.2	58 (100), 0.68–54.2	32 (100), 0.94–50.5	88 (100)
CD8-positive TNF- $\alpha$ -positive response	90 (100), 5.99–95.3	58 (100), 5.99–95.3	32 (100), 16.4–91.9	88 (100)

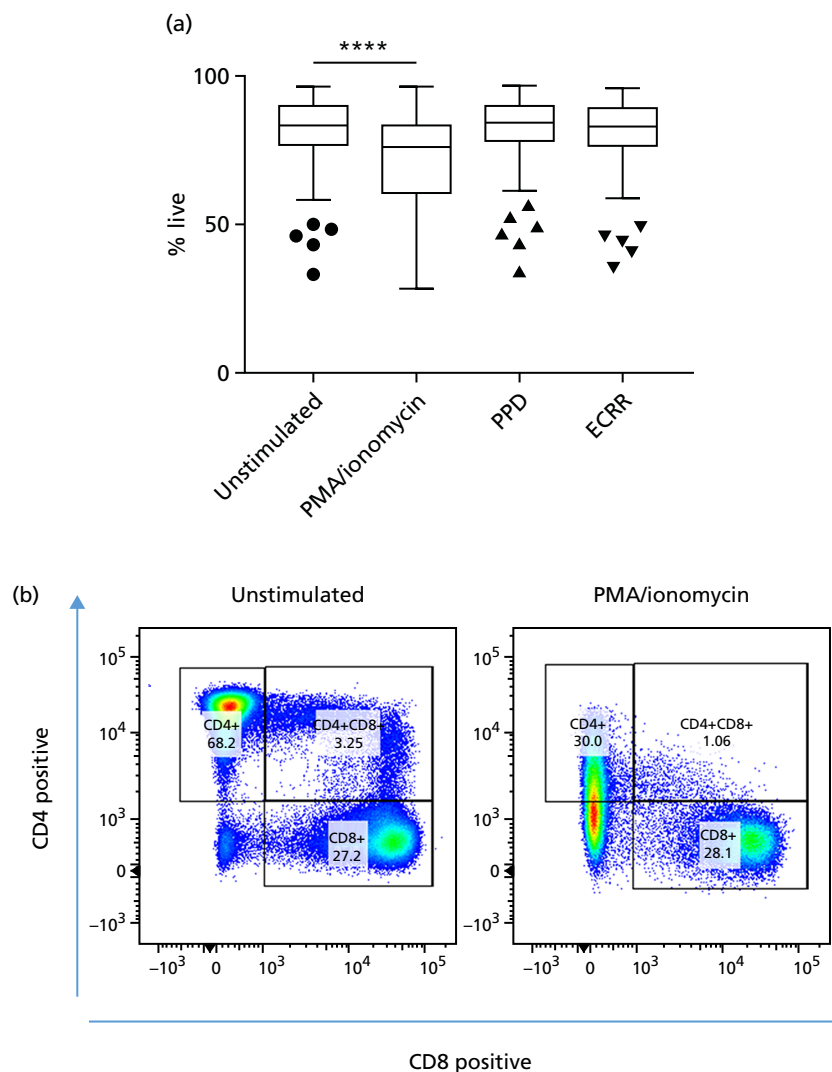
It was noted that the PMA/ionomycin condition reduced the viability of the lymphocyte population compared with the other conditions. Furthermore, this stimulation resulted in a massive reduction in the surface expression of CD4, such that the proportion of CD4-positive cells, as measured by flow cytometry staining, was dramatically reduced (*Figure 25*).

### Purified peptide derivative

All of the 181 samples that were plated were stimulated with PPD; the cytokine responses to this antigen are summarised in *Tables 47* and *48*.

### Mycobacterium tuberculosis antigens

Fifty-seven per cent of the samples ( $n = 107$ ) were also stimulated with a cocktail of RD1-related *Mtb* antigens. The responses to this stimulation are summarised in *Tables 49* and *50*.



**FIGURE 25** The effect of PMA/ionomycin on (a) viability of lymphocytes; and (b) CD4-positive surface expression. \*\*\*\* $p < 0.0001$ .

**TABLE 47** Responses to PPD, stratified by Dosanjh criteria

Measurement	All TB (N = 90)	Dosanjh category		
		1 (N = 58)	2 (N = 32)	OD/LTBI: 4 (N = 91)
Stimulated, n	90	58	32	91
CD4-positive IFN $\gamma$ response, n (%), % range	81 (90)	51 (88)	30 (94)	77 (85), 0.005–8.3
CD4-positive IL-2 response, n (%)	78 (87)	50	28	75
CD4-positive TNF- $\alpha$ response, n	84	54	30	81
CD4-positive TNF- $\alpha$ -only response, n	85	54	31	79
CD4-positive any cytokine response, n	82	52	30	78
CD8-positive IFN $\gamma$ response, n (%)	33	21 (66)	12	42
CD8-positive IL-2 response, n	36	23	13	40
CD8-positive TNF- $\alpha$ -positive response, n	43	28	15	41

**TABLE 48** Responses to PPD, stratified by patient group and HIV infection status

Measurement	Patient group and HIV infection status, n			
	TB HIV- (N = 78)	TB HIV+ (N = 12)	OD/LTBI HIV- (N = 78)	OD/LTBI (N = 13)
CD4-positive IFN $\gamma$ response	71	10	70	7
CD4-positive TNF- $\alpha$ -only response	74	11	72	7
CD4-positive any cytokine response	72	10	75	5

**TABLE 49** Details of samples with positive CD4 and CD8 T-cell cytokine responses to *Mtb* antigens

Measurement	All TB (N = 56)	Dosanjh category		
		1 (N = 37)	2 (N = 19)	OD/LTBI: 4 (N = 51)
Stimulated, n	56	37	19	51
CD4-positive IFN $\gamma$ response, n	54	36	18	45
CD4-positive IL-2 response, n	53	35	18	36
CD4-positive TNF- $\alpha$ response, n	55	36	19	38
CD4-positive TNF- $\alpha$ -only response, n	53	36	17	35
CD4-positive any cytokine response, n	53	35	18	39
CD8-positive IFN $\gamma$ response, n (%)	30	21	9	22
CD8-positive IL-2 response, n	31	23	8	24
CD8-positive TNF- $\alpha$ -positive response, n	30	19	11	17

**Notes**

One hundred and seven samples (59% of those assayed) were stimulated with the pooled RD1-related *Mtb* antigens.

**TABLE 50** Responses to *Mtb* antigens, stratified by patient group and HIV infection status

Measurement	Patient group and HIV infection status, <i>n</i>			
	TB HIV- (N = 47)	TB HIV+ (N = 9)	OD/LTBI HIV- (N = 31)	OD/LTBI (N = 7)
CD4-positive IFN $\gamma$ response	46	8	26	6
CD4-positive TNF- $\alpha$ -only response	45	8	21	3
CD4-positive any cytokine response	46	7	22	3

## Appendix 12 Performance of signatures after *Mycobacterium tuberculosis* region of difference 1-related antigen stimulation

### Performance of cellular immune signatures using *Mycobacterium tuberculosis*-specific region of difference 1-related antigens

Here we present the performance of the signatures when four *Mtb* RD1-related antigens were used to stimulate the PBMCs, which was done in a large subset of the overall cohort, where PBMC numbers permitted. The four antigens used were ESAT-6, CFP-10, Rv3615c and Rv3879c (ECRR) (Figure 26).

Overall, the performance of the signatures using the *Mtb* RD1-related antigen stimulus was comparable to that using PPD, and, as with PPD, the %HLA-DR signature performed the best.<sup>26</sup> The number of individuals within the HIV+ cohort was small and, therefore, little can be concluded about the performance of the signatures in this important subpopulation of TB suspects.

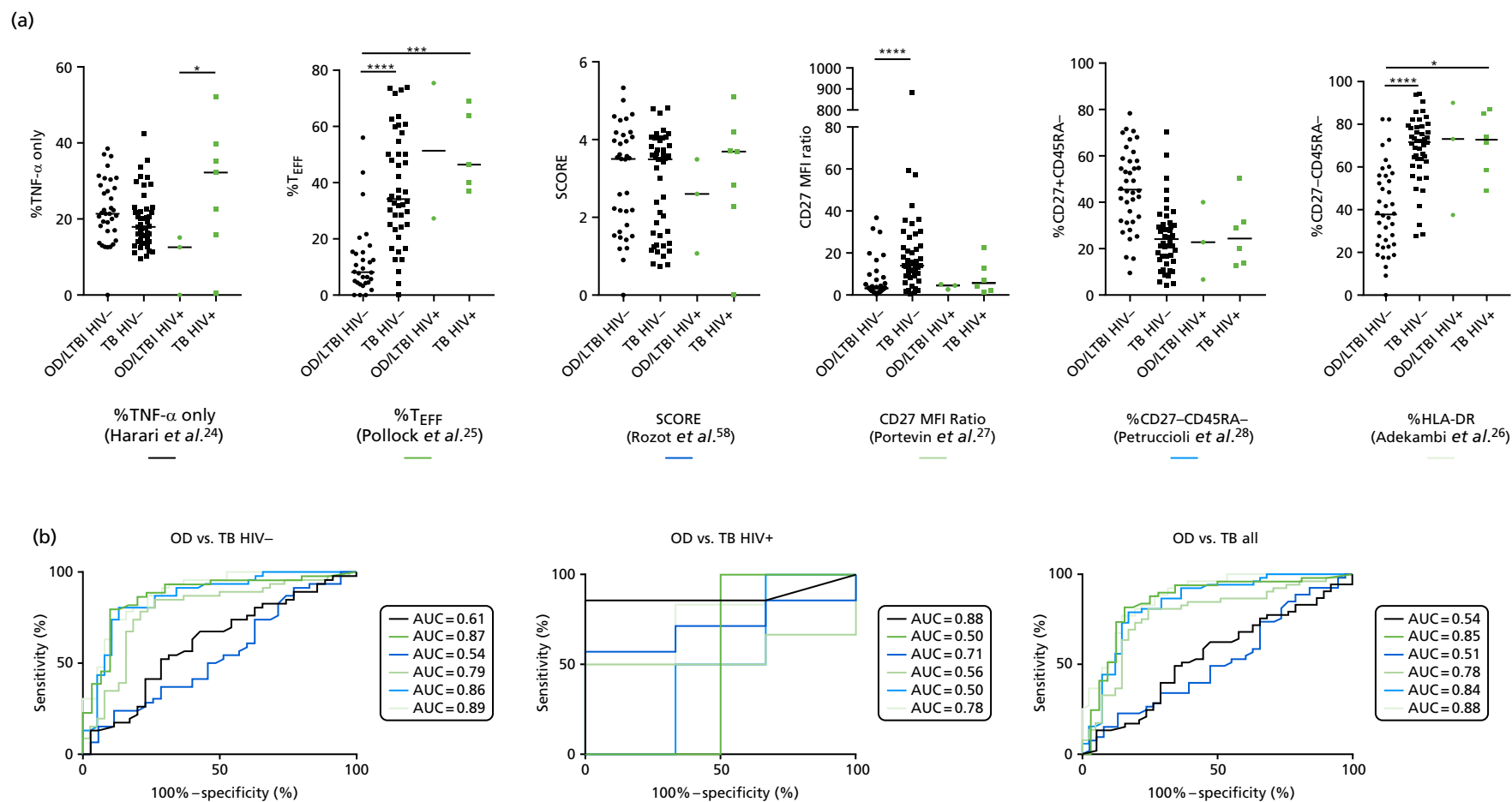
### Correlation between *Mycobacterium tuberculosis* region of difference 1-related and purified protein derivative antigen responses

In order to check whether or not the PPD and *Mtb* RD1-related stimuli elicited a comparable response within the same individuals, we did a direct comparison within the individuals in which both stimuli were used (Figure 27).

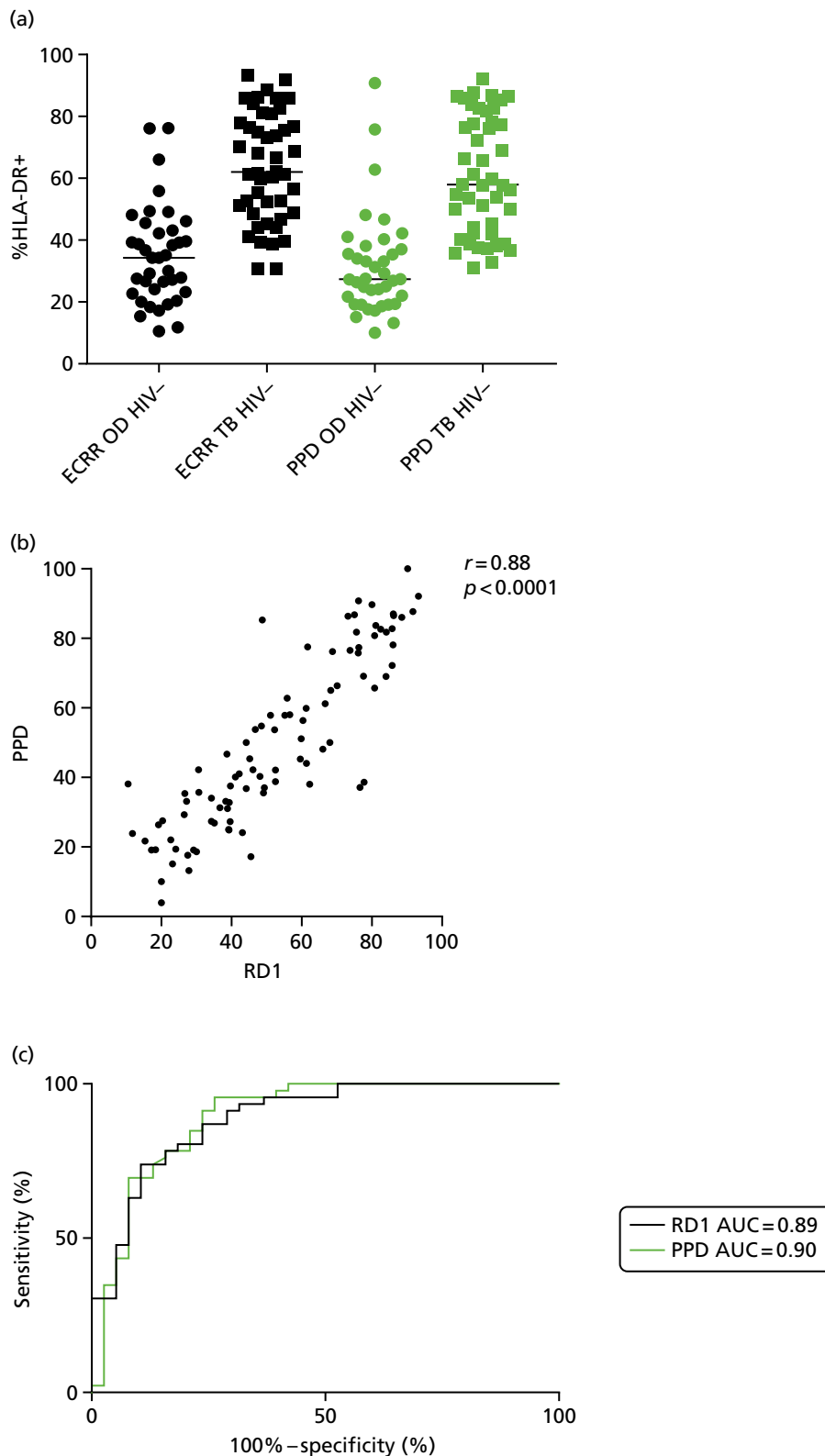
### Performance of signatures after ECRR stimulation

The diagnostic performance of the signatures after stimulation with *Mtb* antigens is summarised in Table 51.





**FIGURE 26** Performance of published signatures after stimulation with *Mtb* antigens. (a) Dot plots indicating signature values in individuals in each of the groups; and (b) ROC curves for each signatures, within the HIV- overall population, the HIV+ population and the entire cohort.



**FIGURE 27** Correlation of %HLA-DR signature<sup>26</sup> using PPD and RD1 (ECRR) antigens. Agreement between %HLA-DR signature using the two conditions was shown, as demonstrated by (a) similar group distributions, averages and variability; (b) high correlation (statistics for Pearson's correlation shown); and (c) comparable diagnostic accuracy for detection active TB.

**TABLE 51** Performance of published cellular immune signatures in the diagnosis of all active TB after *Mtb* peptide stimulation, stratified by HIV infection status

Signature, reference	HIV	TB, n	OD/LTBI, n	AUC, % (95% CI)	Cut-off point	Sensitivity, % (95% CI)	Specificity, % (95% CI)	PPV	NPV
%TNF- $\alpha$ -only <sup>24</sup>	-	46	35	0.61 (0.49 to 0.74)	< 20.3 <sup>a</sup>	60.9 (45.4 to 75.9)	60.0 (42.1 to 76.2)	0.83	0.32
					< 12.7 <sup>b</sup>	13.0 (4.9 to 26.3)	94.3 (80.8 to 99.3)	0.88	0.25
	+	7	3	0.88 (0.65 to 1.11)	> 13.9 <sup>a</sup>	85.7 (42.1 to 99.6)	66.7 (9.4 to 99.2)	0.67	0.86
					> 15.5 <sup>b</sup>	85.7 (42.1 to 99.6)	100 (29.2 to 100)	1.0	0.90
	-/+	53	38	0.54 (0.42 to 0.66)	< 20.3 <sup>a</sup>	56.6 (42.3 to 70.2)	55.3 (38.3 to 71.4)	0.49	0.63
					< 12.5 <sup>b</sup>	13.2 (0.5 to 25.3)	94.7 (82.3 to 99.4)	0.89	0.25
%TEFF <sup>25</sup>	-	44	30	0.87 (0.79 to 0.96)	> 17.2 <sup>a</sup>	81.8 (67.3 to 91.8)	80.0 (61.4 to 92.3)	0.93	0.57
					> 22.6 <sup>b</sup>	80.0 (64.7 to 90.2)	90.0 (73.5 to 97.9)	0.96	0.57
	+	5	2	0.5 (-0.19 to 1.19)	> 43.2 <sup>a</sup>	60.0 (14.6 to 94.7)	50.0 (1.3 to 98.7)	0.48	0.62
					> 55.2 <sup>a</sup>	40.0 (05.3 to 85.3)	50.0 (01.3 to 98.7)	0.38	0.52
	-/+	49	32	0.85 (0.76 to 0.95)	> 21.1 <sup>a</sup>	81.6 (68.0 to 91.2)	81.3 (63.6 to 92.8)	0.93	0.57
					> 36.4 <sup>b</sup>	51.0 (36.3 to 65.6)	90.6 (75.0 to 98.0)	0.95	0.36
SCORE <sup>58</sup>	-	46	35	0.54 (0.42 to 0.67)	< 3.5 <sup>a</sup>	50.0 (34.9 to 65.1)	51.4 (34.0 to 68.6)	0.77	0.24
					< 1.2 <sup>b</sup>	15.2 (6.3 to 28.9)	91.4 (76.9 to 98.2)	0.85	0.25
	+	7	3	0.71 (0.39 to 1.0)	> 2.7 <sup>a</sup>	71.4 (29.0 to 96.3)	66.7 (9.4 to 99.2)	0.62	0.75
					> 3.6 <sup>b</sup>	57.1 (18.4 to 90.1)	100 (29.2 to 100)	1.0	0.75
	-/+	53	38	0.51 (0.39 to 0.64)	< 03.5 <sup>a</sup>	49.1 (35.1 to 63.2)	47.4 (31.0 to 64.2)	0.75	0.22
					< 1.18 <sup>b</sup>	15.1 (6.7 to 27.6)	92.1 (78.6 to 98.3)	0.86	0.25

**TABLE 51** Performance of published cellular immune signatures in the diagnosis of all active TB after *Mtb* peptide stimulation, stratified by HIV infection status (*continued*)

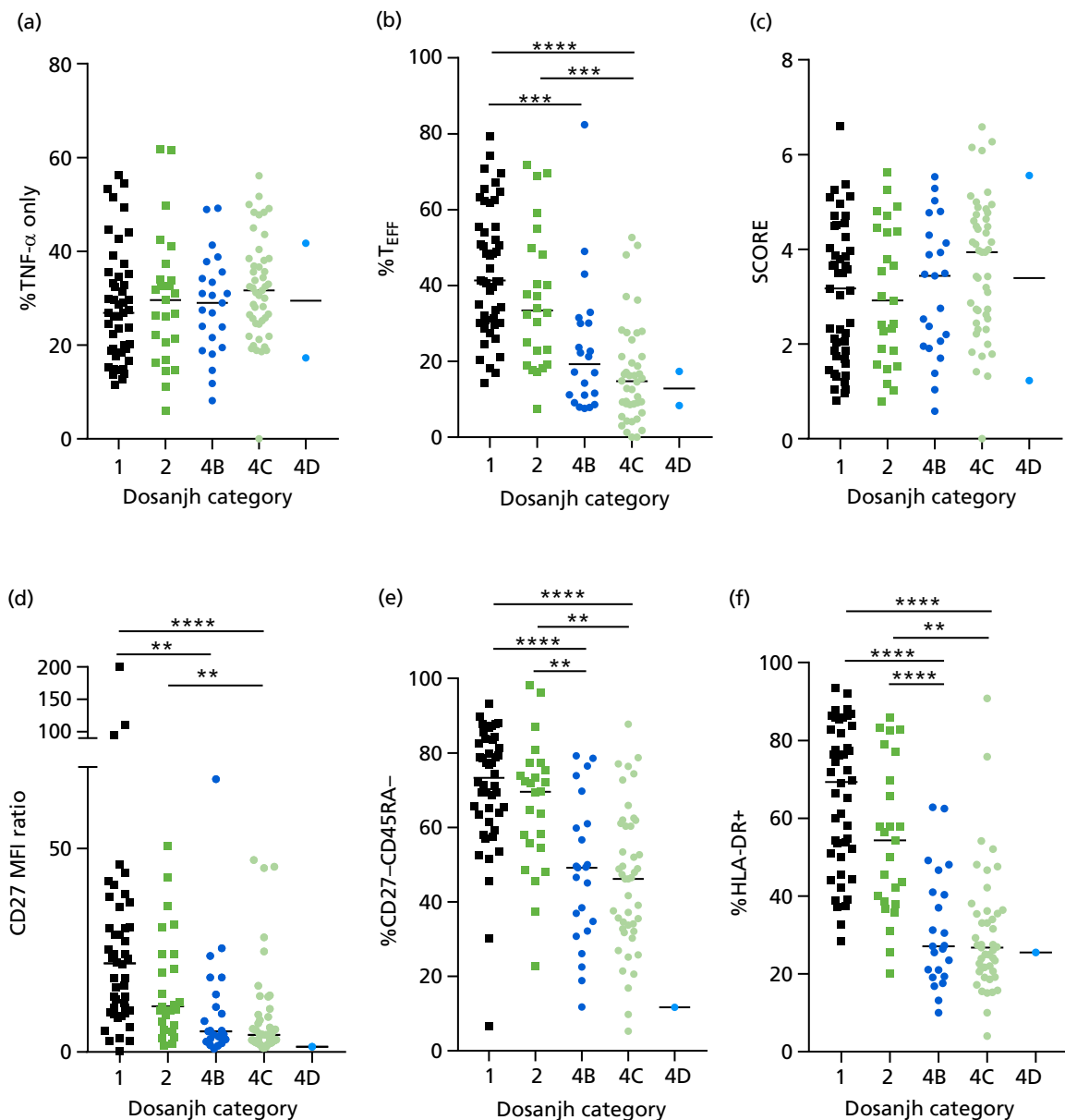
Signature, reference	HIV	TB, n	OD/LTBI, n	AUC, % (95% CI)	Cut-off point	Sensitivity, % (95% CI)	Specificity, % (95% CI)	PPV	NPV
CD27 MFI ratio <sup>27</sup>	–	46	38	0.79 (0.69 to 0.89)	> 08.8 <sup>a</sup>	78.3 (63.6 to 89.1)	76.0 (62.7 to 90.5)	0.92	0.52
					> 20.1 <sup>b</sup>	34.8 (21.4 to 50.3)	92.1 (78.6 to 98.3)	0.96	0.30
	+	6	3	0.56 (0.17 to 0.94)	> 4.8 <sup>a</sup>	50.0 (11.8 to 88.2)	66.7 (9.4 to 99.2)	0.54	0.63
					> 6.1 <sup>b</sup>	50.0 (11.8 to 88.2)	100 (29.2 to 100)	1.0	0.72
	–/+	52	41	0.78 (0.68 to 0.88)	> 07.1 <sup>a</sup>	75.0 (61.1 to 86.0)	75.6 (60.0 to 87.6)	0.91	0.80
					> 19.5 <sup>b</sup>	32.7 (20.3 to 47.1)	90.2 (76.9 to 97.3)	0.92	0.29
%CD27–CD45RA <sup>28</sup>	–	46	38	0.86 (0.78 to 0.95)	> 58.3 <sup>a</sup>	80.4 (66.1 to 90.6)	81.6 (65.7 to 92.3)	0.93	0.56
					> 70.7 <sup>b</sup>	54.4 (39.0 to 69.1)	92.1 (78.6 to 98.3)	0.96	0.38
	+	6	3	0.5 (0.01 to 0.99)	> 73.7 <sup>a</sup>	50.0 (11.8 to 88.2)	66.7 (9.4 to 99.2)	0.54	0.63
					> 73.7 <sup>b</sup>	50.0 (11.8 to 88.2)	66.7 (9.4 to 99.2)	0.54	0.63
	–/+	52	41	0.84 (0.75 to 0.93)	> 59.0 <sup>a</sup>	78.9 (65.3 to 88.9)	78.1 (62.4 to 89.4)	0.92	0.53
					> 72.9 <sup>b</sup>	44.2 (30.5 to 58.7)	90.2 (76.9 to 97.3)	0.94	0.33
%HLA-DR <sup>26</sup>	–	46	38	0.89 (0.82 to 0.96)	> 46.5 <sup>a</sup>	80.4 (66.1 to 90.6)	81.6 (65.7 to 92.3)	0.93	0.56
					> 56.3 <sup>b</sup>	63.0 (47.6 to 76.8)	92.1 (78.6 to 98.3)	0.96	0.43
	+	6	3	0.78 (0.45 to 1.1)	> 78.8 <sup>a</sup>	66.7 (22.3 to 95.7)	66.7 (09.4 to 99.2)	0.61	0.72
					> 82.5 <sup>b</sup>	50.0 (11.8 to 88.2)	100 (29.2 to 100)	1.0	0.72
	–/+	52	41	0.88 (0.81 to 0.95)	> 48.3 <sup>a</sup>	80.8 (67.5 to 90.4)	80.5 (65.1 to 91.2)	0.93	0.56
					> 66.4 <sup>b</sup>	51.9 (37.6 to 66)	90.2 (76.9 to 97.3)	0.95	0.36

a Point at which sensitivity = specificity.

b Setting specificity to &gt; 90%.



## Appendix 13 Additional analyses for the validation of cellular immune signatures for the diagnostic evaluation of active tuberculosis



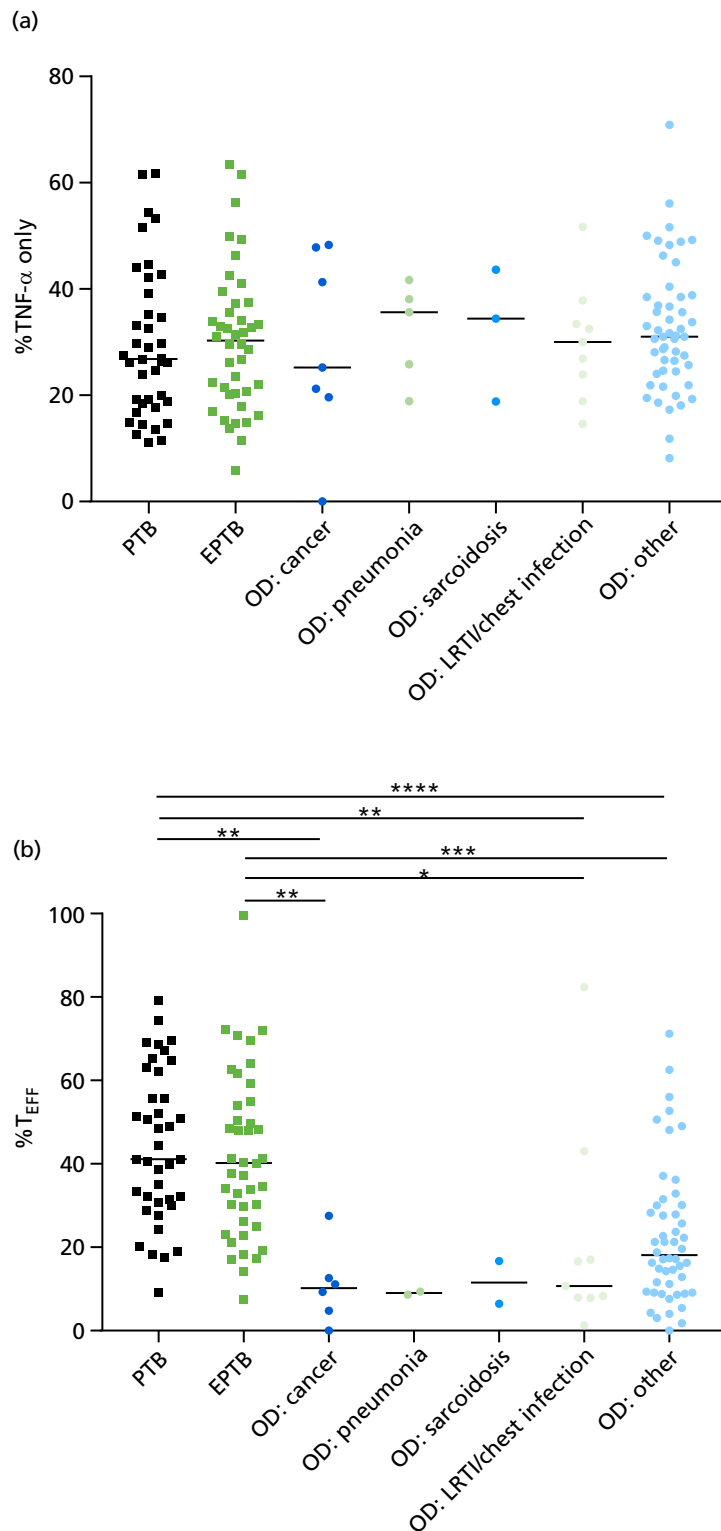
**FIGURE 28** Performance of published cellular immune signatures according to Dosanjh classification (HIV- patients only). (a) Harari *et al.*<sup>24</sup> (%TNF- $\alpha$  only); (b) Pollock *et al.*<sup>25</sup> (%T<sub>EFF</sub>); (c) Rozot *et al.*<sup>58</sup> (SCORE); (d) Portevin *et al.*<sup>27</sup> (CD27 MFI ratio); (e) Petruccioli *et al.*<sup>28</sup> (%CD27-CD45RA-); and (f) Adekambi *et al.*<sup>26</sup> (%HLA-DR). Statistical differences between groups were determined using Kruskal-Wallis with Dunn's post hoc test for multiple comparisons. \* $p < 0.05$ ; \*\* $p < 0.005$ ; \*\*\* $p < 0.0005$ ; \*\*\*\* $p < 0.0001$ .

**TABLE 52** Performance of cellular immune signatures for the detection of TB vs. OD, when Dosanjh category 4 is further stratified by risk of LTBI

Comparison (Dosanjh category)	Signature	TB, n	OD/LTBI, n	AUC, % (95% CI)	Cut-off point	Sensitivity, % (95% CI)	Specificity, % (95% CI)	PPV	NPV
1/2 vs. 4B	Harari <i>et al.</i> <sup>24</sup> (%TNF- $\alpha$ only)	72	23	0.51 (0.38 to 0.64)	< 28.8 <sup>a</sup>	52.8 (40.7 to 64.7)	52.2 (30.6 to 73.2)	0.50	0.55
					< 14.5 <sup>b</sup>	9.7 (4.0 to 19.0)	91.3 (72.0 to 98.9)	0.50	0.53
	Pollock <i>et al.</i> <sup>25</sup> (%T <sub>EFF</sub> )	72	22	0.80 (0.69 to 0.92)	> 30.1 <sup>a</sup>	73.6 (61.9 to 83.3)	72.7 (49.8 to 89.3)	0.71	0.75
					> 43.7 <sup>b</sup>	41.7 (30.2 to 53.9)	90.9 (70.8 to 98.9)	0.81	0.63
	Rozot <i>et al.</i> <sup>58</sup> (SCORE)	72	23	0.52 (0.39 to 0.66)	< 3.3 <sup>a</sup>	52.8 (40.7 to 64.7)	52.2 (30.6 to 73.2)	0.50	0.55
					< 1.4 <sup>b</sup>	15.3 (7.9 to 25.7)	91.3 (72.0 to 98.9)	0.61	0.54
Portevin <i>et al.</i> <sup>27</sup> (CD27 MFI ratio)	71	23	0.75 (0.63 to 0.87)	> 10.2 <sup>a</sup>	69.0 (56.9 to 79.5)	69.6 (47.1 to 86.8)	0.67	0.71	
				> 23.8 <sup>b</sup>	38.0 (26.8 to 50.3)	91.3 (72.0 to 98.9)	0.80	0.62	
Petruccioli <i>et al.</i> <sup>28</sup> (%CD27-CD45RA-)	71	23	0.80 (0.69 to 0.90)	> 60.4 <sup>a</sup>	73.2 (61.4 to 83.1)	73.9 (51.6 to 89.8)	0.72	0.75	
				> 76.6 <sup>b</sup>	39.4 (28.0 to 51.8)	91.3 (72.0 to 98.9)	0.80	0.62	
Adekambi <i>et al.</i> <sup>26</sup> (%HLA-DR)	71	23	0.88 (0.81 to 0.96)	> 42.2 <sup>a</sup>	78.9 (67.6 to 87.7)	78.3 (56.3 to 92.6)	0.77	0.80	
				> 49.6 <sup>b</sup>	70.4 (58.4 to 80.7)	91.3 (72.0 to 98.9)	0.88	0.77	
1/2 vs. 4C	Harari <i>et al.</i> <sup>24</sup> (%TNF- $\alpha$ only)	72	47	0.59 (0.49 to 0.70)	< 29.7 <sup>a</sup>	56.9 (44.7 to 68.6)	57.5 (42.2 to 71.7)	0.55	0.60
					< 19.1 <sup>b</sup>	25.0 (15.5 to 36.6)	91.5 (79.6 to 97.6)	0.73	0.57
	Pollock <i>et al.</i> <sup>25</sup> (%T <sub>EFF</sub> )	72	42	0.88 (0.82 to 0.95)	> 25.9 <sup>a</sup>	79.2 (68.0 to 87.8)	78.6 (63.2 to 89.7)	0.77	0.81
					> 36.7 <sup>b</sup>	56.9 (44.7 to 68.6)	90.5 (77.4 to 97.3)	0.84	0.70
	Rozot <i>et al.</i> <sup>58</sup> (SCORE)	72	47	0.62 (0.51 to 0.72)	< 3.5 <sup>a</sup>	52.8 (40.7 to 64.7)	53.2 (38.1 to 67.9)	0.51	0.55
					< 1.8 <sup>b</sup>	25.0 (15.6 to 36.6)	91.5 (79.6 to 97.6)	0.73	0.57
Portevin <i>et al.</i> <sup>27</sup> (CD27 MFI ratio)	71	45	0.79 (0.70 to 0.88)	> 9.2 <sup>a</sup>	77.5 (66.0 to 86.5)	77.8 (62.9 to 88.8)	0.76	0.79	
				> 25.0 <sup>b</sup>	32.4 (21.8 to 44.6)	91.1 (78.8 to 97.5)	0.77	0.60	
Petruccioli <i>et al.</i> <sup>28</sup> (%CD27-CD45RA-)	71	45	0.83 (0.75 to 0.90)	> 59.8 <sup>a</sup>	73.2 (61.4 to 83.1)	71.1 (55.7 to 83.6)	0.70	0.75	
				> 74.5 <sup>b</sup>	42.3 (30.6 to 54.6)	91.1 (78.8 to 97.5)	0.81	0.63	
Adekambi <i>et al.</i> <sup>26</sup> (%HLA-DR)	71	45	0.90 (0.84 to 0.96)	> 39.7 <sup>a</sup>	81.7 (70.7 to 89.9)	82.2 (68.0 to 92.0)	0.81	0.83	
				> 49.1 <sup>b</sup>	70.4 (58.4 to 80.7)	91.1 (78.8 to 97.5)	0.88	0.77	

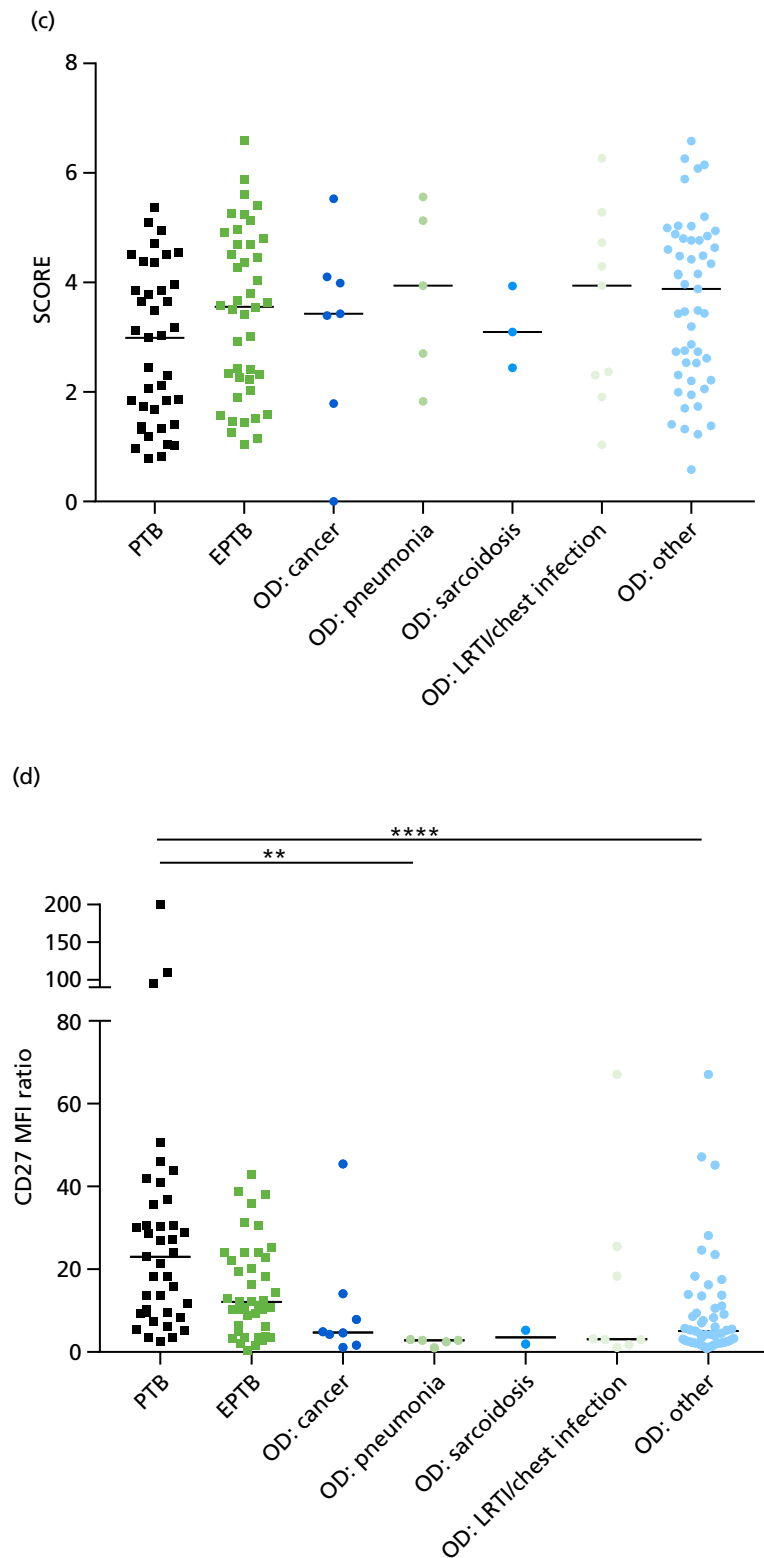
a Point at which sensitivity = specificity.

b Setting specificity to > 90%.

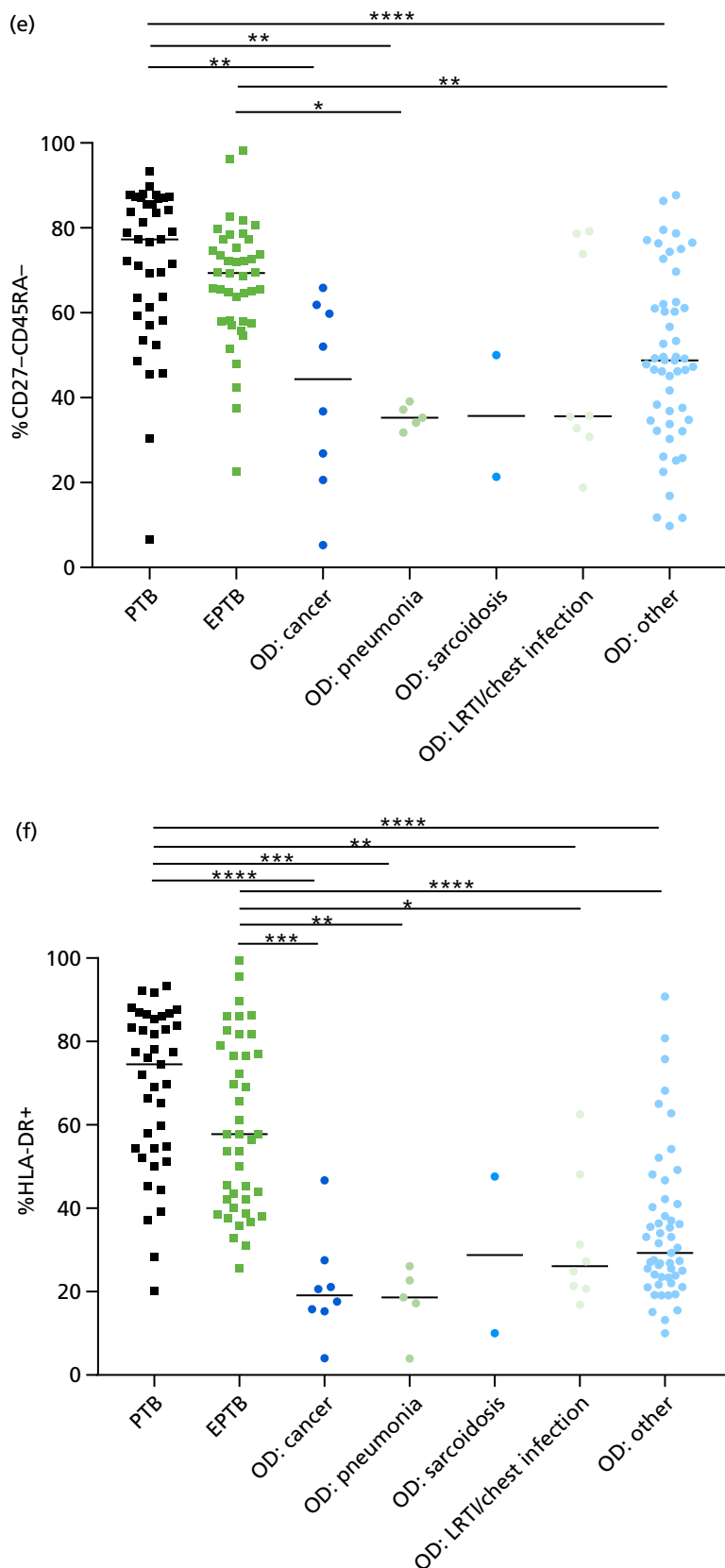


**FIGURE 29** Performance of cellular immune signatures in different TB and OD/LTBI disease types. (a) Harari *et al.*<sup>24</sup> (%TNF- $\alpha$  only); (b) Pollock *et al.*<sup>25</sup> (%T<sub>EFF</sub>); (c) Rozot *et al.*<sup>58</sup> (SCORE); (d) Portevin *et al.*<sup>27</sup> (CD27 MFI ratio); (e) Petruccioli *et al.*<sup>28</sup> (%CD27-CD45RA-); and (f) Adekambi *et al.*<sup>26</sup> (%HLA-DR). Statistical differences between groups were determined using Kruskal–Wallis with Dunn’s post hoc test for multiple comparisons. LRTI, lower respiratory tract infection. \* $p < 0.05$ ; \*\* $p < 0.005$ ; \*\*\* $p < 0.0005$ ; \*\*\*\* $p < 0.0001$ . (continued)





**FIGURE 29** Performance of cellular immune signatures in different TB and OD/LTBI disease types. (a) Harari *et al.*<sup>24</sup> (%TNF- $\alpha$  only); (b) Pollock *et al.*<sup>25</sup> (%T<sub>EFF</sub>); (c) Rozot *et al.*<sup>58</sup> (SCORE); (d) Portevin *et al.*<sup>27</sup> (CD27 MFI ratio); (e) Petruccioli *et al.*<sup>28</sup> (%CD27-CD45RA-); and (f) Adekambi *et al.*<sup>26</sup> (%HLA-DR). Statistical differences between groups were determined using Kruskal-Wallis with Dunn's post hoc test for multiple comparisons. LRTI, lower respiratory tract infection. \* $p < 0.05$ ; \*\* $p < 0.005$ ; \*\*\* $p < 0.0005$ ; \*\*\*\* $p < 0.0001$ . (continued)



**FIGURE 29** Performance of cellular immune signatures in different TB and OD/LTBI disease types. (a) Harari *et al.*<sup>24</sup> (%TNF- $\alpha$  only); (b) Pollock *et al.*<sup>25</sup> (%T<sub>EFF</sub>); (c) Rozot *et al.*<sup>58</sup> (SCORE); (d) Portevin *et al.*<sup>27</sup> (CD27 MFI ratio); (e) Petruccioli *et al.*<sup>28</sup> (%CD27-CD45RA-); and (f) Adekambi *et al.*<sup>26</sup> (%HLA-DR). Statistical differences between groups were determined using Kruskal-Wallis with Dunn's post hoc test for multiple comparisons. LRTI, lower respiratory tract infection. \* $p < 0.05$ ; \*\* $p < 0.005$ ; \*\*\* $p < 0.0005$ ; \*\*\*\* $p < 0.0001$ .

TABLE 53 Performance of cellular immune signatures for diagnosing either PTB or EPTB

Comparison	Signature	TB, n	OD/LTBI, n	AUC, % (95% CI)	Cut-off point	Sensitivity, % (95% CI)	Specificity, % (95% CI)
PTB vs. OD/LTBI	Harari <i>et al.</i> <sup>24</sup> (%TNF- $\alpha$ only)	39	72	0.57 (0.45 to 0.69)	< 28.5 <sup>a</sup>	56.4 (39.6 to 72.2)	56.9 (44.7 to 68.6)
					< 18.7 <sup>b</sup>	25.6 (13.0 to 90.3)	90.3 (81.0 to 96.0)
	Pollock <i>et al.</i> <sup>25</sup> (%T <sub>EFF</sub> )	39	66	0.88 (0.81 to 0.94)	> 28.55 <sup>a</sup>	82.05 (66.5 to 92.5)	81.8 (70.4 to 90.2)
					> 37.9 <sup>b</sup>	61.5 (44.6 to 76.6)	90.9 (81.3 to 96.6)
	Rozot <i>et al.</i> <sup>58</sup> (SCORE)	39	72	0.63 (0.52 to 0.74)	< 3.2 <sup>a</sup>	59.0 (42.1 to 74.4)	58.3 (46.1 to 69.9)
					< 1.7 <sup>b</sup>	28.2 (15.0 to 44.9)	90.3 (91 to 96)
	Portevin <i>et al.</i> <sup>27</sup> (CD27 MFI ratio)	39	69	0.83 (0.75 to 0.90)	> 60.7 <sup>a</sup>	74.4 (57.9 to 87)	75.4 (63.5 to 85.0)
> 25.1 <sup>b</sup>					46.2 (30.1 to 62.8)	91.3 (82.0 to 96.7)	
Petruccioli <i>et al.</i> <sup>28</sup> (%CD27-CD45RA-)	39	69	0.83 (0.75 to 0.92)	> 60.7 <sup>a</sup>	74.4 (57.9 to 87.0)	75.4 (63.5 to 85.0)	
				> 76.5 <sup>b</sup>	53.9 (37.2 to 69.9)	91.3 (82.0 to 96.7)	
Adekambi <i>et al.</i> <sup>26</sup> (%HLA-DR)	39	69	0.93 (0.87 to 0.98)	> 47.2 <sup>a</sup>	84.6 (69.5 to 94.1)	85.5 (75.0 to 92.8)	
				> 49.6 <sup>b</sup>	84.6 (69.5 to 94.1)	91.3 (82.0 to 96.7)	
EPTB vs. OD/LTBI	Harari <i>et al.</i> <sup>24</sup> (%TNF- $\alpha$ only)	25	72	0.53 (0.42 to 0.64)	< 30.8 <sup>a</sup>	50.0 (34.2 to 65.8)	50.0 (78.0 to 62.0)
					< 18.7 <sup>b</sup>	21.4 (10.3 to 36.8)	90.3 (81.0 to 96.0)
	Pollock <i>et al.</i> <sup>25</sup> (%T <sub>EFF</sub> )	24	66	0.84 (0.77 to 0.92)	> 25.9 <sup>a</sup>	75.6 (59.7 to 87.6)	75.8 (63.6 to 85.5)
					> 37.2 <sup>b</sup>	56.1 (39.8 to 71.5)	90.9 (81.3 to 96.6)
	Rozot <i>et al.</i> <sup>58</sup> (SCORE)	25	72	0.51 (0.40 to 0.62)	< 03.5 <sup>a</sup>	47.6 (32.0 to 63.6)	48.6 (36.7 to 60.7)
					< 01.6 <sup>b</sup>	19.1 (8.6 to 34.1)	90.3 (81.0 to 96.0)
	Portevin <i>et al.</i> <sup>27</sup> (CD27 MFI ratio)	25	69	0.71 (0.61 to 0.81)	> 08.2 <sup>a</sup>	70.7 (54.5 to 83.9)	71.0 (58.9 to 81.3)
> 25.0 <sup>b</sup>					17.1 (07.2 to 32.1)	91.3 (82.0 to 96.7)	
Petruccioli <i>et al.</i> <sup>28</sup> (%CD27-CD45RA-)	25	69	0.80 (0.72 to 0.89)	> 59.1 <sup>a</sup>	70.7 (54.5 to 83.9)	71.0 (58.9 to 81.3)	
				> 76.5 <sup>b</sup>	24.4 (12.4 to 40.3)	91.3 (82.0 to 96.7)	
Adekambi <i>et al.</i> <sup>26</sup> (%HLA-DR)	25	69	0.88 (0.82 to 0.94)	> 39.5 <sup>a</sup>	78.1 (62.4 to 89.4)	78.3 (66.7 to 87.3)	
				> 49.6 <sup>b</sup>	61.0 (44.5 to 75.8)	91.3 (82.0 to 96.7)	

a Point at which sensitivity = specificity.

b Setting specificity to &gt; 90%.

## Appendix 14 Additional cohort characteristics for the molecular rule-out test assessment

**TABLE 54** Distribution of disease types and severity within the TB patients in the GO/NO-GO cohort for the validation of the molecular rule-out tests

Characteristic	Active TB		Total (N = 46)
	T-SPOT.TB positive (N = 24)	T-SPOT.TB negative (N = 22)	
<b>Dosanjh category, n</b>			
Culture-confirmed TB (category 1)	21	16	37
Highly probable TB (category 2)	4	6	10
Smear positive, n	3	5	8
Smear not tested, n	4	3	7
PTB, n	5	12	17
EPTB, n	17	8	25
PTB and EPTB, n	2	2	4
<b>Site of infection, n</b>			
Lung only	5	12	17
Lymph node only	14	5	1
Lung and lymph node	1	1	2
Lung and other	1	1	2
Lymph node and other	1	1	2
Pleura	1	1	2

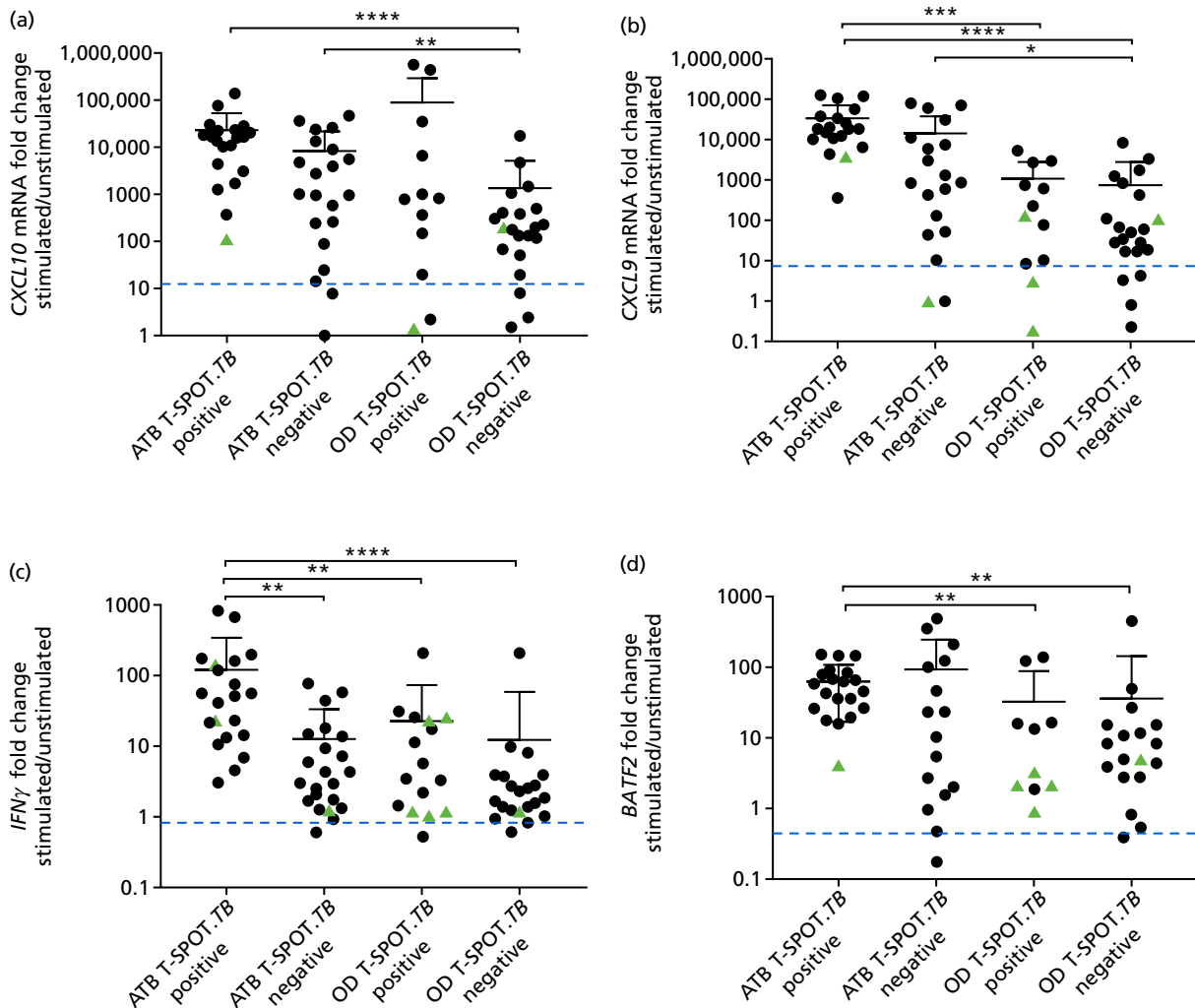
**TABLE 55** Distribution of ODs in the OD patients within the TB patients in the GO/NO-GO cohort for the validation of the molecular rule-out test

Final diagnosis	OD		Total (N = 48)
	T-SPOT.TB positive (N = 22)	T-SPOT.TB negative (N = 26)	
Cancer	1	3	4
Sarcoidosis	0	2	2
Chest infection	1	2	3
Pneumonia	6	6	12
URTI	1	1	2
LRTI	0	1	1
LTBI	1		2
Other	12	11	23

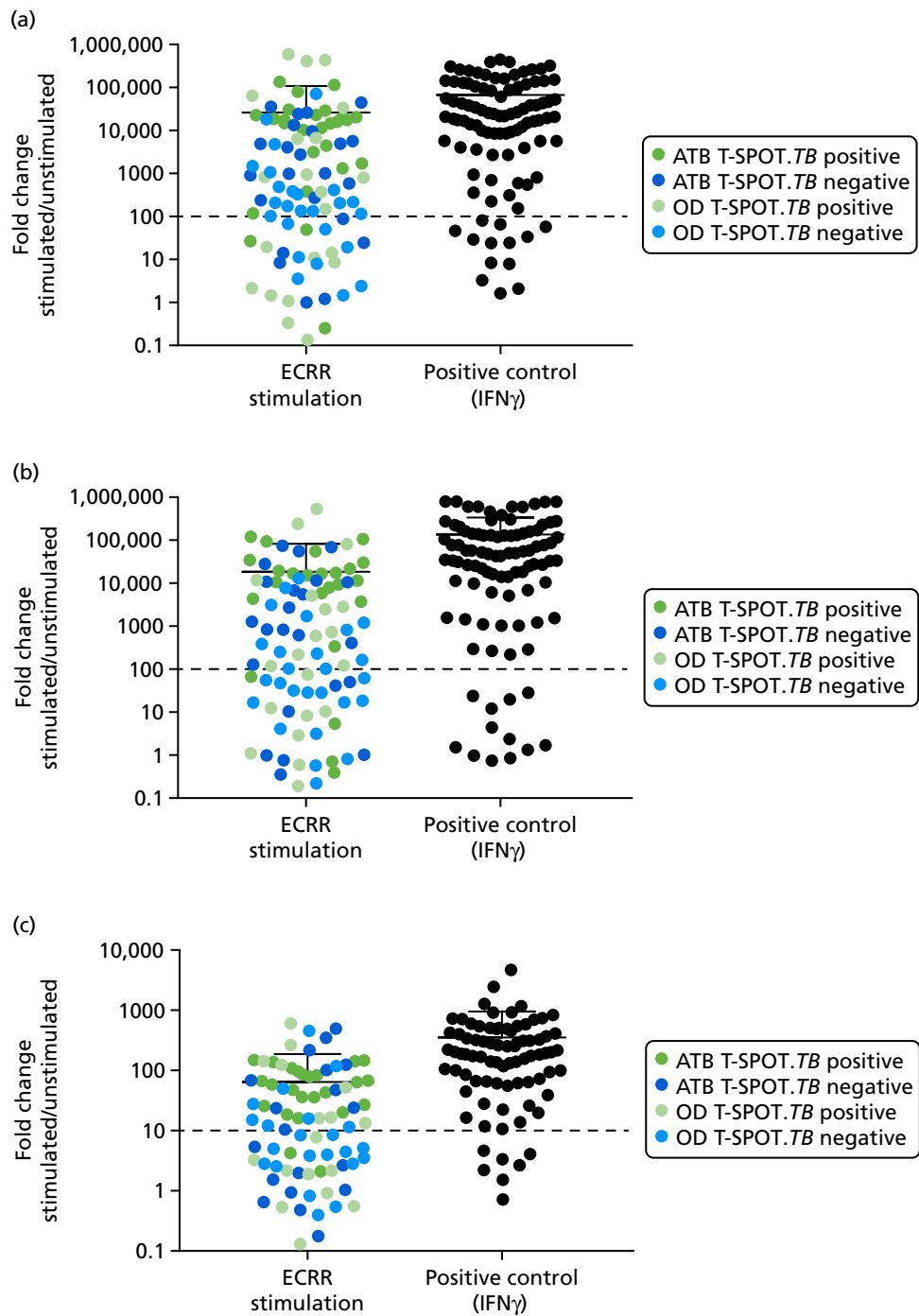
LRTI, lower respiratory tract infection; URTI, upper respiratory tract infection.



## Appendix 15 Additional data for the validation of candidate rule-out tests



**FIGURE 30** Relative abundance of (a) CXCL10, (b) CXCL9, (c) IFN $\gamma$  and (d) BATF2 in key patient groups within the GO/NO-GO cohort for assessment of the candidate molecular rule-out test. The cut-off points shown are the level of expression required for the test to provide > 95% sensitivity for all active TB cases. HIV+ individuals are shown in green triangles. The gene expression cut-off values for achieving 95% sensitivity for all TB cases are displayed. Statistical differences between groups were determined using Kruskal–Wallis with Dunn’s post hoc test for multiple comparisons. ATB, active tuberculosis; mRNA, messenger ribonucleic acid. \* $p < 0.05$ ; \*\* $p < 0.005$ ; \*\*\* $p < 0.0005$ ; \*\*\*\* $p < 0.0001$ .



**FIGURE 31** Selection of cut-off point for target genes (a) *CXCL10*; (b) *CXCL9*; and (c) *BATF2* in response to IFN $\gamma$ -positive control condition. ATB, active tuberculosis.

**TABLE 56** Measurement of *IFN $\gamma$*  transcripts in stimulated PBMC samples using qRT-PCR

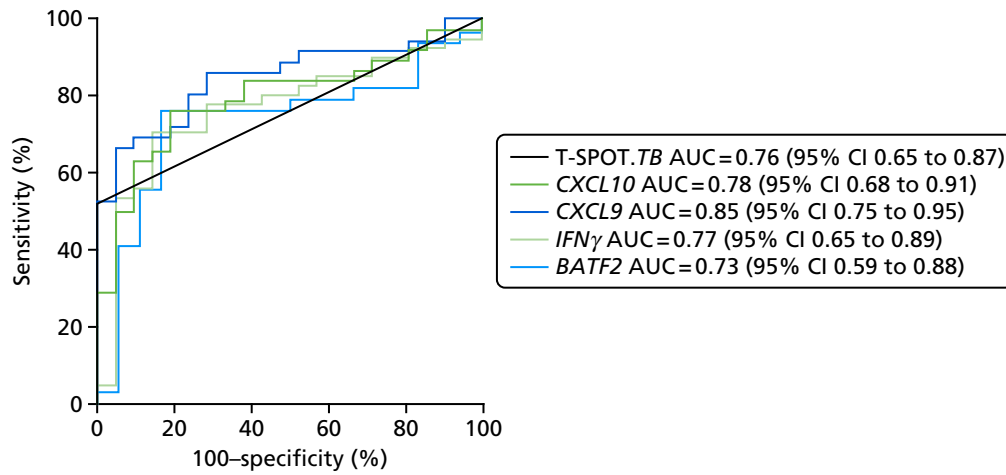
Measurement	Active TB		OD	
	T-SPOT. <i>TB</i> positive	T-SPOT. <i>TB</i> negative	T-SPOT. <i>TB</i> positive	T-SPOT. <i>TB</i> negative
<i>n</i>	24	22	22	26
Total for analysis, <i>n</i>	21	20	16	21
QC failed total, <i>n</i>	3	2	6	5
<i>HPRT1</i> , <i>n</i>	3	2	6	5
Indeterminate, <i>n</i>	0	0	0	0
ECRR/unstimulated fold change	122.09 (0.03 to 787.82)	12.99 (0.90 to 70.02)	21.73 (0.51 to 207.58)	12.01 (0.61 to 200)
IFN $\gamma$ /unstimulated	21, 72.82 (0.06 to 344.81)	21, 49.76 (0.60 to 425.01)	18, 26.79 (0.72 to 179.44)	21, 25.52 (0.40 to 449.46)



**TABLE 57** Diagnostic accuracy data for candidate molecular rule-out test: all TB vs. all OD

Test/analyte	ATB T-SPOT. <i>TB</i> test positive, <i>n</i>	ATB T-SPOT. <i>TB</i> test negative, <i>n</i>	OD T-SPOT. <i>TB</i> test positive, <i>n</i>	OD T-SPOT. <i>TB</i> test negative, <i>n</i>	AUC, % (95% CI)	Cut-off point	Sensitivity, % (95% CI)	Specificity, % (95% CI)
T-SPOT. <i>TB</i>	24	22	22	26	0.53 (0.41 to 0.65)		52 (37 to 67)	54 (39 to 69)
<i>CXCL10</i>	19	19	12	21	0.72 (0.62 to 0.86)	11	95 (82 to 99)	15 (5.1 to 32)
<i>CXCL9</i>	18	18	12	21	0.84 (0.74 to 0.94)	1	97 (85 to 99)	9.1 (1.9 to 24)
<i>IFN<math>\gamma</math></i>	21	20	16	21	0.70 (0.59 to 0.82)	0.85	95 (83 to 99)	8.1 (1.7 to 22)
<i>BATF2</i>	19	15	10	18	0.72 (0.59 to 0.80)	0.44	97 (85 to 100)	3.6 (0.09 to 18)

ATB, active tuberculosis.



**FIGURE 32** Diagnostic performance of *CXCL10*, *CXCL9*, *IFN $\gamma$*  and *BATF2Mtb*-specific gene expression in all TB vs. T-SPOT.TB test-negative OD.

**TABLE 58** Diagnostic accuracy data for candidate molecular rule-out test: all TB vs. T-SPOT.*TB* test-negative OD

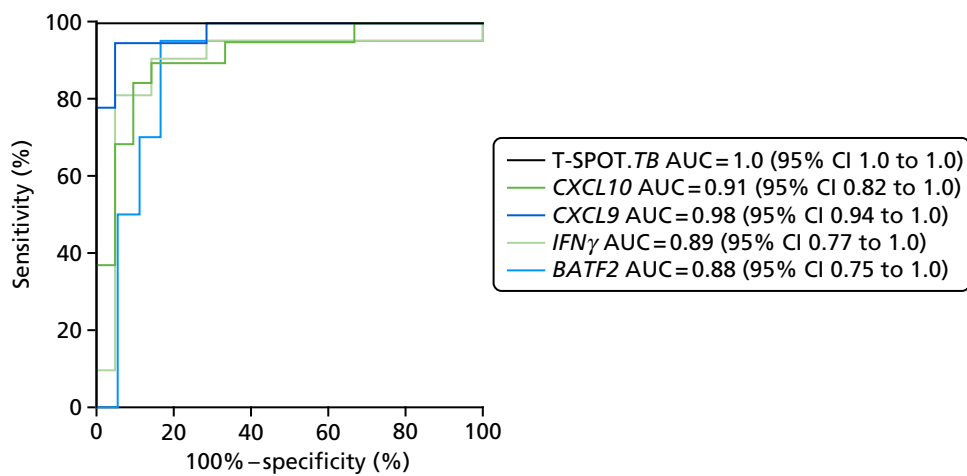
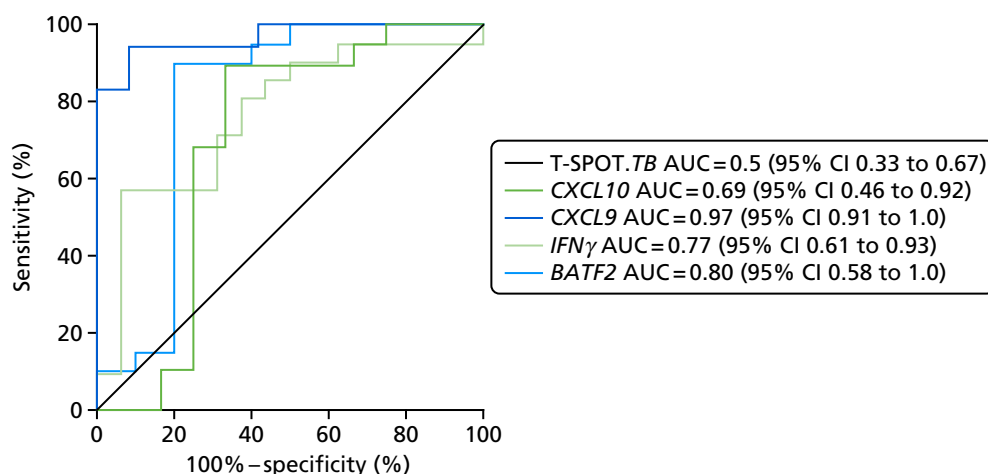
Test/analyte	ATB T-SPOT. <i>TB</i> test positive, <i>n</i>	ATB T-SPOT. <i>TB</i> test negative, <i>n</i>	OD T-SPOT. <i>TB</i> test negative, <i>n</i>	AUC, % (95% CI)	Cut-off point	Sensitivity, % (95% CI)	Specificity, % (95% CI)
T-SPOT. <i>TB</i>	24	22	26	0.76 (0.65 to 0.87)		52 (37 to 67)	100 (87 to 100)
<i>CXCL10</i>	19	19	21	0.78 (0.65 to 0.91)	11	95 (82 to 99)	14 (3 to 36)
<i>CXCL9</i>	18	18	21	0.85 (0.75 to 0.95)	1	97 (85 to 100)	9.5 (1.2 to 30)
<i>IFN<math>\gamma</math></i>	21	20	21	0.77 (0.65 to 0.89)	0.85	95 (85 to 99)	9.5 (1.2 to 30)
<i>BATF2</i>	19	14	18	0.74 (0.59 to 0.88)	0.44	97 (85 to 100)	5.6 (0.14 to 27)

ATB, active tuberculosis.

**TABLE 59** Diagnostic accuracy data for candidate molecular rule-out test: T-SPOT.*TB* test-positive TB vs. T-SPOT.*TB* test-negative OD

Test/analyte	ATB T-SPOT. <i>TB</i> test positive, <i>n</i>	OD T-SPOT. <i>TB</i> test negative, <i>n</i>	AUC, % (95% CI)	Cut-off point	Sensitivity, % (95% CI)	Specificity, % (95% CI)
T-SPOT. <i>TB</i>	24	26	1.0 (1.0 to 1.0)		100 (86.28 to 100)	100 (86.77 to 100)
<i>CXCL10</i>	19	21	0.91 (0.81 to 1.0)	340	95 (86.8 to 100)	67 (43 to 85)
<i>CXCL9</i>	18	21	0.98 (0.94 to 1.0)	229	100 (81 to 100)	71 (48 to 100)
<i>IFN<math>\gamma</math></i>	21	21	0.89 (0.77 to 1.0)	2.9	95 (76 to 100)	71 (48 to 89)
<i>BATF2</i>	19	18	0.88 (0.75 to 1.0)	16	95 (75 to 100)	83 (59 to 96)

ATB, active tuberculosis.

**FIGURE 33** Diagnostic performance of *CXCL10*, *CXCL9*, *IFN $\gamma$*  and *BATF2* *Mtb*-specific gene expression in T-SPOT.*TB* test-positive TB vs. T-SPOT.*TB* test-negative OD.**FIGURE 34** The performance of qRT-PCR detection of *CXCL10*, *CXCL9*, *IFN $\gamma$* , *BATF2* and T-SPOT for discriminating between T-SPOT.*TB*-positive TB cases (*n* = 19–24) and T-SPOT.*TB*-positive OD/LTBI cases (*n* = 10–22).

**TABLE 60** Diagnostic accuracy data for candidate molecular rule-out test: T-SPOT.TB test-positive ATB vs. T-SPOT.TB test-positive

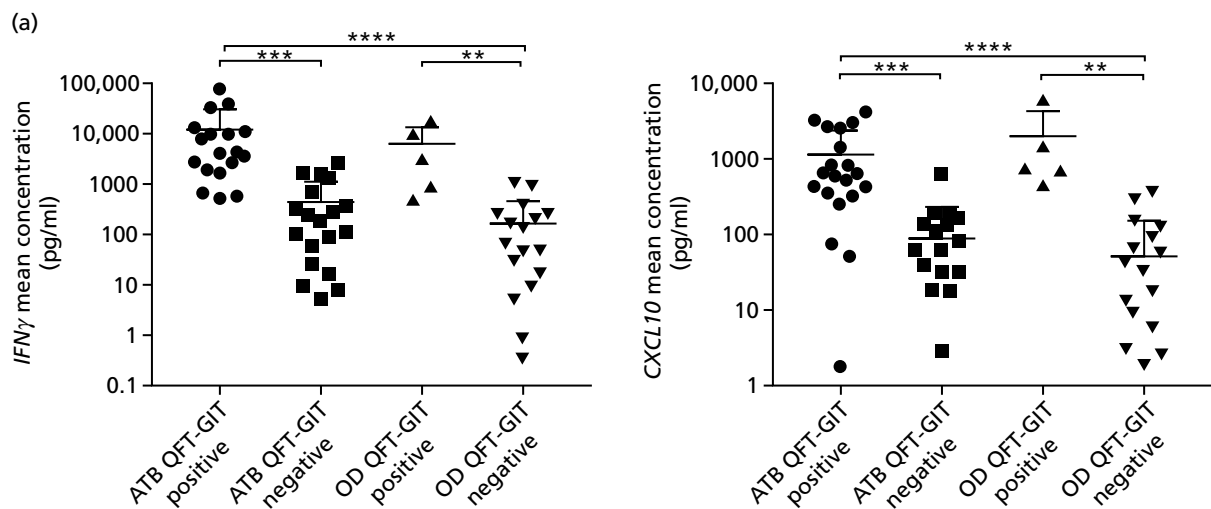
Test/analyte	ATB T-SPOT.TB test positive, <i>n</i>	OD T-SPOT.TB test positive, <i>n</i>	AUC, % (95% CI)	Cut-off point	Sensitivity, % (95% CI)	Specificity, % (95% CI)
T-SPOT.TB	24	22	0.50 (0.35 to 0.67)		0 (86.28 to 100)	100 (85 to 100)
CXCL10	19	12	0.69 (0.46 to 0.92)	260	95 (74 to 100)	33 (9.9 to 65)
CXCL9	18	12	0.97 (0.91 to 1.0)	286	100 (81 to 100)	71 (48 to 89)
IFN $\gamma$	21	16	0.77 (0.61 to 0.93)	2.9	95 (76 to 100)	71 (48 to 89)
BATF2	19	10	0.8 (0.58 to 1.0)	16	95 (75 to 100)	60 (59 to 96)

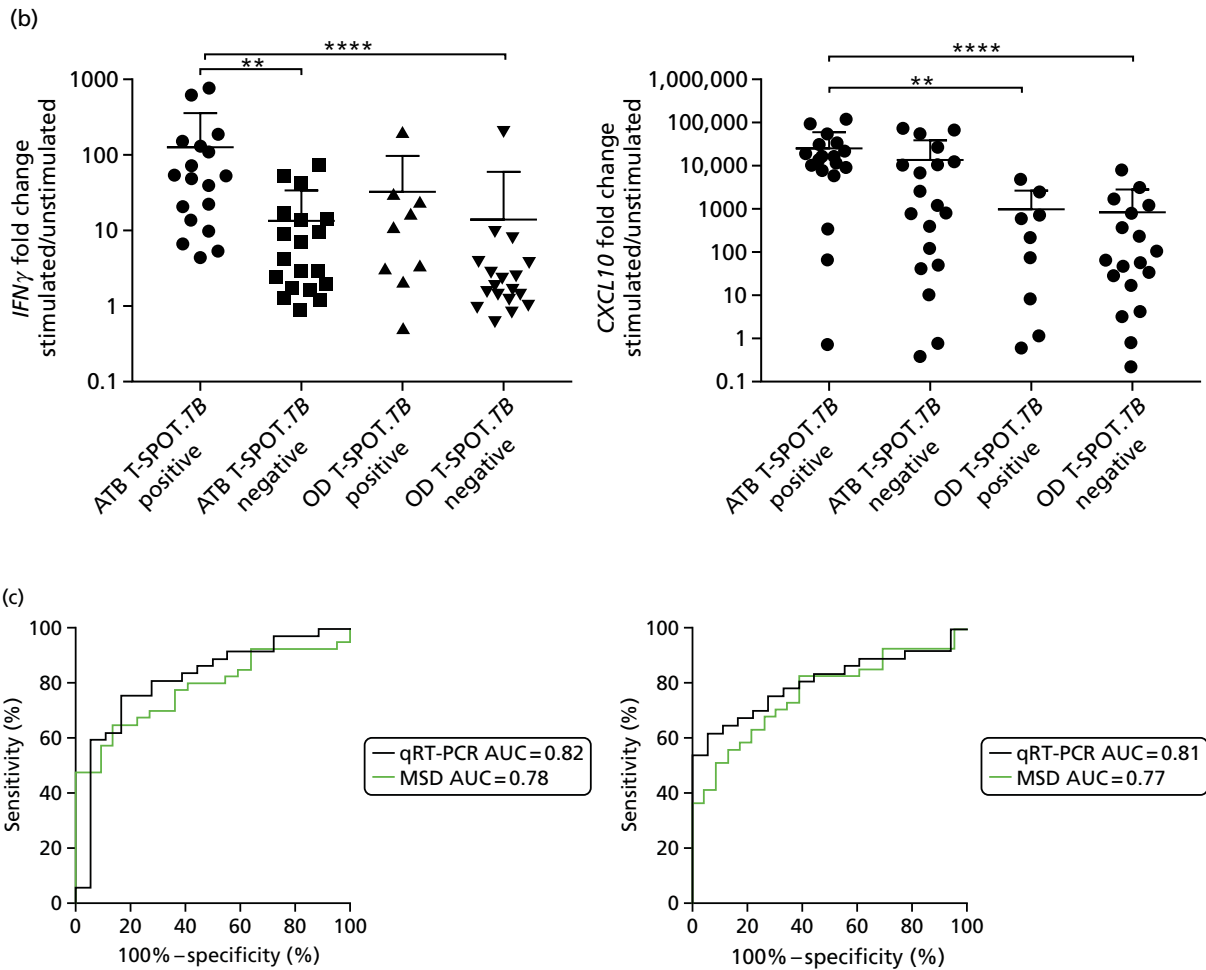
ATB, active tuberculosis.

**TABLE 61** Performance of IFN $\gamma$  and CXCL10 analytes from QuantiFERON supernatants detected by MSD for the detection of all TB in the GO/NO-GO cohort

Test/analyte	ATB QFT-GIT positive, <i>n</i>	ATB QFT-GIT negative, <i>n</i>	OD QFT-GIT positive, <i>n</i>	OD QFT-GIT negative, <i>n</i>	AUC, % (95% CI)	Cut-off point	Sensitivity, % (95% CI)	Specificity, % (95% CI)
QFT	20	21	5	23	0.7 (0.5 to 0.8)		49 (33 to 65)	63 (63 to 94)
CXCL10	20	21	5	23	0.66 (0.53 to 0.79)	-19	95 (83 to 99)	3.6 (0.09 to 18)
IFN $\gamma$	19	21	5	22	0.69 (0.57 to 0.82)	-18	95 (83 to 99)	3.7 (0.09 to 19)

ATB, active tuberculosis.

**FIGURE 35** Comparison of detection of IFN $\gamma$  or CXCL10 in *Mtb* antigen-stimulated samples. (a) Using either MSD from QFT-GIT supernatants of qRT-PCR from stimulated PBMCs; (b) comparing between patient groups in the overlapping cohort (*n* = 75), where both tests were performed; and (c) the diagnostic accuracy of using either IFN $\gamma$  or CXCL10 using either platform, for detection all TB cases, was assessed by ROC curve analysis. Protein levels and fold changes in gene expression were compared between groups using Kruskal–Wallis with Dunn’s post hoc test for multiple comparisons. ATB, active tuberculosis. \**p* < 0.05; \*\**p* < 0.005; \*\*\**p* < 0.0005; \*\*\*\**p* < 0.0001. (continued)



**FIGURE 35** Comparison of detection of *IFN $\gamma$*  or *CXCL10* in *Mtb* antigen-stimulated samples. (a) Using either MSD from QFT-GIT supernatants or qRT-PCR from stimulated PBMCs; (b) comparing between patient groups in the overlapping cohort ( $n = 75$ ), where both tests were performed; and (c) the diagnostic accuracy of using either *IFN $\gamma$*  or *CXCL10* using either platform, for detection all TB cases, was assessed by ROC curve analysis. Protein levels and fold changes in gene expression were compared between groups using Kruskal–Wallis with Dunn’s post hoc test for multiple comparisons. ATB, active tuberculosis. \* $p < 0.05$ ; \*\* $p < 0.005$ ; \*\*\* $p < 0.0005$ ; \*\*\*\* $p < 0.0001$ .



## Appendix 16 Additional tables for health economic analysis: methodology

**TABLE 62** Health impact of adverse event as a result of TB treatment

Adverse event	Symbol	Cost of treatment (£)	QALY loss
Hepatotoxicity	$q_h$	Gamma(6.679,87.889)	Gamma(65.753,7 × 10 <sup>5</sup> )
Nausea and vomiting	$q_n$	63	Gamma(109.67,3 × 10 <sup>6</sup> )

**Note**  
All values from White P and Jit.<sup>73</sup>

**TABLE 63** Time to obtain a result and cost of new tests

Test	Cost, £		Time for a result (days)
	Unit	Total staff <sup>a</sup>	
Transcriptomic PCR test	16.5	Uniform(145.2,193.6)	Uniform(1,1.5)
Cellular immune flow cytometry	150	Uniform(145.2,193.6)	Uniform(2,7)
Molecular rule-out qRT-PCR test	Uniform(27,35)	Uniform(145.2,193.6)	Uniform(2,5)

**a** Assuming £24.20 per hour staff cost for research associate or equivalent and Uniform(6,8) hours staff time.

**Note**  
Estimate staff costs using available knowledge/prediction of equivalent staff time, from VANTDET study team.

**TABLE 64** Health-care professional consultation visit monetary costs incurred

Consultation type	Cost, £ (SE)	Distribution	Source
First visit: respiratory medicine, multiprofessional	241	Gamma(53.3,4.52)	National tariff 2014–15, Annex 5A <sup>79</sup> Hughes <i>et al.</i> <sup>80</sup>
	167 (33)		
Follow-up visit: respiratory medicine, multiprofessional	143	Gamma(18.78,7.62)	National tariff 2014–15, Annex 5A <sup>79</sup> Hughes <i>et al.</i> <sup>80</sup>
	167 (33)		

SE, standard error.



**TABLE 65** Test and sampling procedure costs for cost-effectiveness calculations

Test	Unit cost, £ (SE) (SA range)	Distribution	Sources
Culture	22.29 (2.23)	Gamma(100,0.22)	Drobniewski <i>et al.</i> <sup>81</sup>
Sputum smear microscopy	7	Gamma(106,0.07)	NICE guidance <sup>8</sup>
	1.56 (0.68)		Hughes <i>et al.</i> <sup>80</sup>
TST	17.48		Auguste <i>et al.</i> <sup>82</sup>
	16–8 (32)	Uniform(8,36)	NICE guidance <sup>75</sup>
T-SPOT.TB	59.57		Auguste <i>et al.</i> <sup>82</sup>
	55–45 (99)	Uniform(50,106)	NICE guidance <sup>8</sup>
QFT-GIT	58–29 (87)	Uniform(29,87)	Pareek <i>et al.</i> <sup>17</sup>
Chest X-ray	35		NICE guidance <sup>8</sup>
	28–19 (34)	Uniform(23,43)	NICE guidance <sup>75</sup>
Bronchoalveolar lavage	23.24	N/A	St Mary's R&D office (St Mary's Hospital, R&D Office, Imperial College Healthcare NHS Trust, London, 2017, personal communication)
	–11.62 (46.48)	Uniform(11.62,46.48)	Proportions from NICE clinical guidelines (2006); Pareek <i>et al.</i> ; <sup>17</sup> NICE guidance <sup>10</sup>
Endobronchial ultrasound	2634	N/A	St Mary's R&D office
Bronchoscopy procedure	612	N/A	St Mary's R&D office
	–306 (1224)	Uniform(306,1224)	Proportions from NICE clinical guidelines (2006); Pareek <i>et al.</i> ; <sup>17</sup> NICE guidance <sup>10</sup>
Histology from biopsy	25	N/A	St Mary's R&D office
	–12.5 (50)	Uniform(12.5,50)	Proportions from NICE clinical guidelines (2006); Pareek <i>et al.</i> ; <sup>17</sup> NICE guidance <sup>10</sup>
Needle aspirate	90.21	N/A	St Mary's R&D office
	–45.1 (180.42)	Uniform(45.1,180.42)	Proportions from NICE clinical guidelines (2006); Pareek <i>et al.</i> ; <sup>17</sup> NICE guidance <sup>10</sup>
PCR	202.45	N/A	St Mary's R&D office
	–101.2 (404.9)	Uniform(101.2,404.9)	Proportions from NICE clinical guidelines (2006); Pareek <i>et al.</i> ; <sup>17</sup> NICE guidance <sup>10</sup>

N/A, not applicable; SA, sensitivity analysis; SE, standard error.

**TABLE 66** Active TB treatment costs for the first 60 days

Drug	Dosage (mg/day) <sup>a</sup>	Dosage by patient weight (mg/kg/day) <sup>a</sup>	Batch cost <sup>b</sup> (£)	Quantity per batch (capsule or tablet) <sup>b</sup>	Dosage per capsule or tablet <sup>b</sup>	60-day total cost (£)
Rifampicin	600	–	48.00	100	300	57.60
Isoniazid	300	–	19.24	56	50	123.69
Pyrazinamide	2000	–	38.34	30	500	306.72
Ethambutol	–	15	42.74	56	400	116.74

<sup>a</sup> British National Formulary.<sup>76</sup>

<sup>b</sup> NICE guidance NG33.<sup>9</sup>

Final cost is the sum of all listed 60-day total drug costs.

## Distributional formulation of individual level/sample uncertainty

The number of individuals who enter the diagnostic pathway was defined as  $n$ . Of these, we defined  $n_+$  as active TB cases and the remainder as non-active TB. We defined the probability of a given patient being an active TB case as  $n_+/n$  (and so the probability of non-active TB is  $1 - (n_+/n)$ ). This can therefore be considered as a draw from a Bernoulli distribution and so for the total sample, the binomial distribution gives the number of active TB and non-active TB cases in a sample population, denoted with subscript TB and  $\sim$ TB, respectively, as:

$$X_{TB} \sim \text{Bin}(n_+/n, n) \quad (4)$$

$$X_{\sim TB} = n - X_{TB} \quad (5)$$

that is,

$$p(X_{TB} | n_+/n) = \binom{n}{X_{TB}} (n_+/n)^{X_{TB}} (1 - n_+/n)^{(n - X_{TB})}. \quad (6)$$

By the same principle, patients are then randomly split between those who test positive and those who test negative:

$$X_+^{TB} \sim \text{Bin}(p_+, X_{TB}) \quad (7)$$

$$X_-^{TB} = X_{TB} - X_+^{TB} \quad (8)$$

$$X_+^{\sim TB} \sim \text{Bin}(1 - p_+, X_{\sim TB}) \quad (9)$$

$$X_-^{\sim TB} = X_{\sim TB} - X_+^{\sim TB} \quad (10)$$

This process results in a final random subdivision of the sample population into one of the four end states.

## Use as rule-out test

Each of the terminal nodes (outcomes) of the decision tree has an associated cost and health utility (measured in QALYs). For the patient cohort these were defined as:

$$C_{\text{novel}} = C_{\text{ruleout}} + (n_+/n)\bar{c}_+ + (n_-/n)(1 - p_-)\bar{c}_- \quad (11)$$

$$E_{\text{novel}} = qT_{\text{ruleout}} + (n_+/n)q(\bar{t}_+ + (1 - p_+)T_{\text{followup}}) + (n_-/n)q(1 - p_-)\bar{t}_- \quad (12)$$

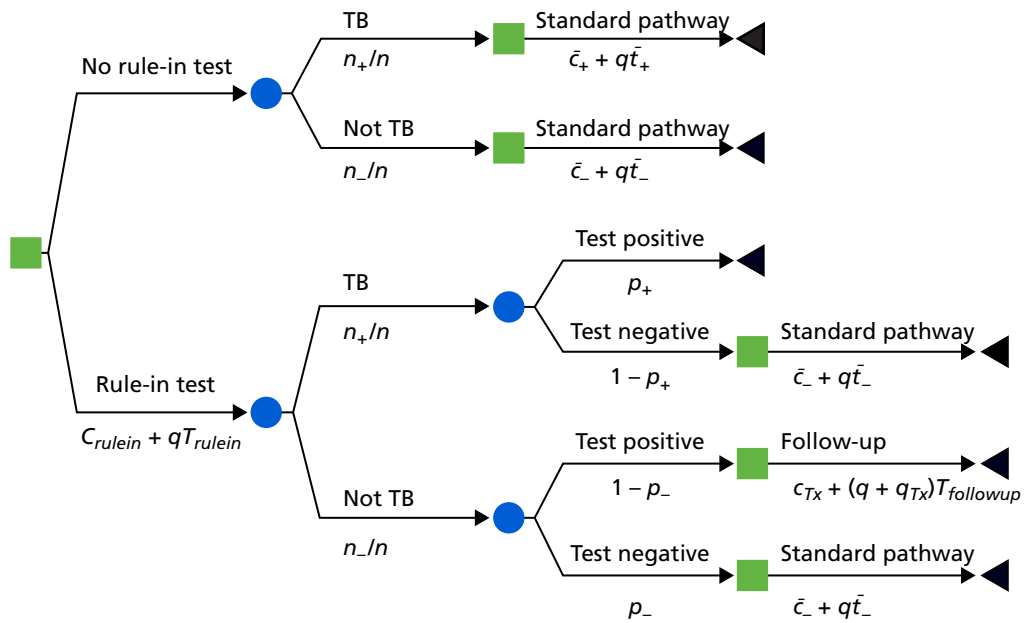
### Use as rule-in test

#### Cost-effectiveness outcomes

For the patient cohort the cost and health detriment were defined as:

$$C_{novel} = C_{rulein} + (n_+/n)(1 - p_+)\bar{c}_+ + (n_-/n)((1 - p_-)C_{Tx} + p_-\bar{c}_-) \quad (13)$$

$$E_{novel} = qT_{rulein} + (n_+/n)(1 - p_+)q\bar{t}_- + (n_-/n)(p_-q\bar{t}_- + (1 - p_-)(q + q_{Tx})T_{followup}) \quad (14)$$



**FIGURE 36** Decision tree comparing current practice ('no rule-in test') with a diagnostic pathway incorporating an initial rule-in test. The 'standard pathway' branch represents the range of variation observed in the patient cohort. Probabilities are shown below branches following a circular chance node and costs are below branches following a square decision node.

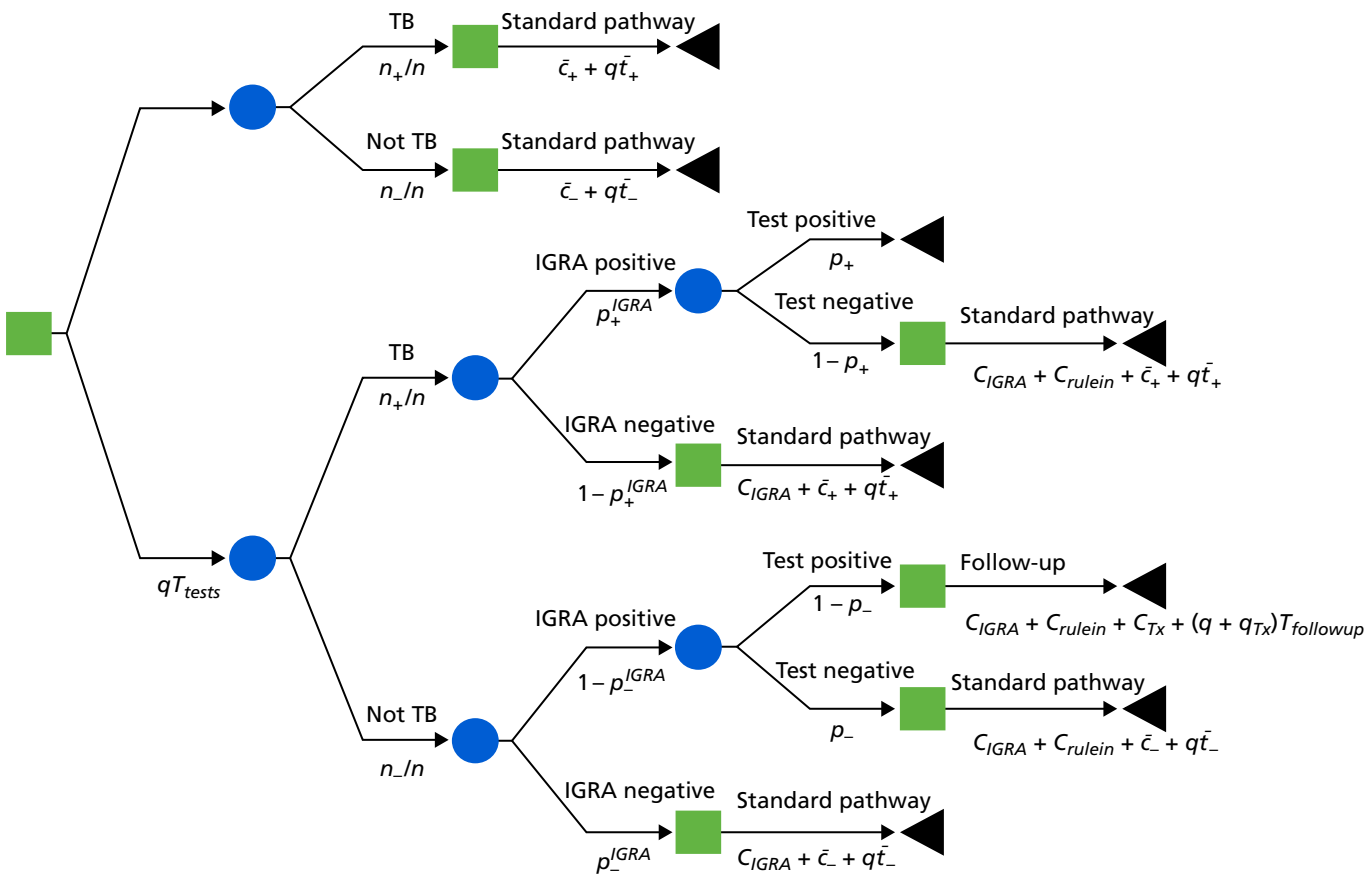
### Use of dual testing as rule-in test

#### Cost-effectiveness outcomes

For the patient cohort the cost and health detriment were defined as:

$$C_{novel} = C_{rulein} + (n_+/n)(C_{IGRA} + \bar{c}_+)(p_+^{IGRA}(1 - p_+) + (1 - p_+^{IGRA})) + (n_-/n)((1 - p_-^{IGRA})(1 - p_-)(C_{IGRA} + C_{Tx}) + (C_{IGRA} + \bar{c}_-)((1 - p_-^{IGRA})p_- + p_-^{IGRA})) \quad (15)$$

$$E_{novel} = qT_{rulein} + (n_+/n)q\bar{t}_-(p_+^{IGRA}(1 - p_+) + (1 - p_+^{IGRA})) + (n_-/n)(q\bar{t}_-((1 - p_-^{IGRA})p_- + p_-^{IGRA}) + (1 - p_-^{IGRA})(1 - p_-)(q + q_{Tx})T_{followup}) \quad (16)$$



**FIGURE 37** Decision tree comparing current practice ('no rule-in test') with a diagnostic pathway incorporating an initial dual rule-in test. The 'standard pathway' branch represents the range of variation observed in the patient cohort. Probabilities are shown below branches following a circular chance node and costs are below branches following a square decision node.



## Appendix 17 Inclusion criteria of cellular immune signatures from previous publications

The publications proposing the cellular immune signatures each used different inclusion criteria and/or definitions of 'responders' in their studies (*Table 67*). To ensure a fair comparison of all signatures within this study, we applied universal inclusion criteria for the main analysis. However, we have also validated each signature according to the inclusion criteria reported in each of the reported publications that have shown promising diagnostic performance.

**TABLE 67** Inclusion criteria for 'responders' and diagnostic performance analysis from previous publications

Parent population	Signature	Study	Inclusion criteria			
			Viability (%)	Frequency of parent (%)	Above background	Number of cells in parent
CD4 positive, IFN $\gamma$ /IL-2/TNF- $\alpha$ positive	%TNF- $\alpha$ only	Harari <i>et al.</i> <sup>24</sup>	–	> 0.05	–	> $\times 2$
CD4 positive, TNF- $\alpha$ only	%T <sub>EFF</sub>	Pollock <i>et al.</i> <sup>25</sup> (%T <sub>EFF</sub> )	–	> 0.001	> $\times 2$	> $\times 2$
CD4 positive and CD4 positive, IFN $\gamma$ positive	CD27 MFI ratio	Portevin <i>et al.</i> <sup>27</sup>	–	> 0.05	> $\times 2$	$\geq 5$
CD4 positive, IFN $\gamma$ positive	%CD27–CD45RA–	Petruccioli <i>et al.</i> <sup>28</sup>	–	> 0.003	Antigen – unstimulated > 0.003	$\geq 30$
CD4 positive, IFN $\gamma$ positive	%HLA-DR	Adekambi <i>et al.</i> <sup>26</sup>	75–95	$\geq 0.05$	–	–
All	All phenotype signatures	VANTDET	Any	Any	> $\times 2$	$\geq 10$







**EME**  
**HS&DR**  
**HTA**  
**PGfAR**  
**PHR**

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