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## Early risk assessment in pediatric and adult household contacts of confirmed tuberculosis cases by novel diagnostic tests (ERASE-TB): protocol for a prospective, non-interventional, longitudinal, multi-country cohort study

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5 6 7	2	tuberculosis cases by novel diagnostic tests (ERASE-TB): protocol for a
7 8 9	3	prospective, non-interventional, longitudinal, multi-country cohort study
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58 59 60	29	END TB strategy, ERASE-TB

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## 30 ABSTRACT

### 31 Introduction

The World Health Organization (WHO) End-TB Strategy calls for the development of novel diagnostics to detect tuberculosis earlier and more accurately. Better diagnostics, together with tools to predict disease progression are critical for achieving WHO END-TB targets. The Early Risk Assessment in TB contactS by new diagnostic tEsts (ERASE-TB) study aims to evaluate novel diagnostics and testing algorithms for early tuberculosis diagnosis and accurate prediction of disease progression among household contacts exposed to confirmed index cases in Mozambigue, Tanzania and Zimbabwe.

39

### 40 Methods and analysis

A total of 2,100 household contacts (HHCs) (aged ≥10 years) of adults with microbiologically-41 42 confirmed pulmonary tuberculosis will be recruited and followed up at 6-month intervals for 18 to 24 months. At each time-point a WHO symptom screen and digital chest-radiograph (dCXR) 43 will be performed, and blood and urine samples collected. Individuals screening positive (WHO 44 45 symptom screen or dCXR) will be requested to provide sputum for Xpert MTB/Rif Ultra. At baseline, HHCs will also be screened for HIV, diabetes (HbA1c), chronic lung disease 46 (spirometry), hypertension and anaemia. Study outcomes will be co-prevalent tuberculosis 47 (diagnosed at enrollment), incident tuberculosis (diagnosed during follow-up) or no 48 49 tuberculosis at completion of follow up. Novel diagnostics will be validated using fresh and 50 biobanked samples with a nested case control design. Cases are defined as HHCs diagnosed with tuberculosis (for early diagnosis) or with incident tuberculosis (for prediction of 51 progression) and will be matched by age, sex and country to HHCs who remain healthy 52 53 (controls). Statistical analyses will include assessment of diagnostic accuracy by constructing 54 receiver operating curves and calculation of sensitivity and specificity.

56 Ethics and dissemination

ERASE-TB has been approved by regulatory and ethical committees in each African country and by each partner organisation. Consent, with additional assent for participants <18 years, is voluntary. Attestation by impartial witnesses is sought in case of illiteracy. Confidentiality of participants is being maintained throughout. Study findings will be presented at scientific conferences and published in peer-reviewed international journals.

#### **Trial registration number**

NCT04781257

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2 3 4	65	Strengths and limitations of this study		
5 6	66	Strengths		
7 8 9 10	67	• Recruitment of highly infectious index cases aimed at maximising the number of		
	68	tuberculosis (TB) diagnoses in the household contact (HHCs) cohort.		
11 12	69	• Sequencing of <i>Mycobacterium tuberculosis</i> isolates from both index cases and HHCs		
13 14 15	70	allows confirmation of household transmission and thus determination of timing of the		
15 16 17	71	transmission event; resulting in more precise estimates of new test sensitivity		
18 19	72	compared to population-based cohorts with unknown timing of infection.		
20 21	73	• Large sample size across three southern African countries with high HIV prevalence;		
22 23	74	including adolescents will ensure study findings are generalisable to the clinically		
24 25	75	relevant population at high risk of TB compared to studies focused on adults only.		
26 27	76			
28 29	77	Limitations		
30 31	78	• Despite the large cohort of HHCs, the number of diagnosed TB cases will be small,		
32 33 34	79	limiting the power of the study and sub-group analyses such as by age and HIV status.		
35	80	• Geographically limited to sub-Saharan Africa, therefore results may not be		
37	81	generalisable to other populations, including those with lower HIV prevalence such as		
39 40	82	in South-East Asia or the Americas.		
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36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51	81	generalisable to other populations, including those with lower HIV prevalence such a		

## 83 INTRODUCTION

Tuberculosis (TB) remains a leading global public health problem, with an estimated 10 million new cases and 1.5 million deaths globally in 2020 [1]. In 2014, the World Health Assembly approved the World Health Organization (WHO) End-TB Strategy, aiming for a 90% reduction in TB incidence and 95% reduction in TB deaths by 2035 [2]. However, in 2019, three million TB cases ('the missing millions') remained undiagnosed and untreated globally, resulting in potentially avoidable morbidity, mortality and onward transmission. The Covid-19 pandemic has resulted in a large decrease in the number of people newly diagnosed with TB and reported. This has increased the diagnostic gap by a further 1.3 million, resulting in an estimated 4.2 million undiagnosed TB cases in 2020 [3]. Also, for the first time in a decade TB deaths have risen, from an estimated 1.4 million in 2019 to 1.5 million in 2020, as a result of reduced access to and provision of essential TB services including diagnostics during the Covid-19 pandemic.

97 Without an efficacious and safe vaccine, early detection and containment are the main tools 98 to interrupt transmission and successfully control TB. Similar to SARS-CoV2, asymptomatic 99 spreading of *M.tuberculosis* and subclinical but infectious disease states are a major concern 100 in the control of airborne infectious diseases [4]. Early and accurate identification of persons 101 with TB, combined with identification of those at risk of progression to TB and provision of 102 targeted preventive treatment are critical to reducing TB-associated morbidity and mortality, 103 and preventing onward transmission.

105 Currently available diagnostics such as sputum microscopy, mycobacterial culture and nucleic 106 acid amplification tests are based on direct pathogen detection, thus requiring a high 107 mycobacterial load; they therefore predominately target advanced TB when onward 108 transmission and significant lung damage has occurred [5,6]. Further, for many patients with 109 minimal or no symptoms, expectoration of high-quality sputum specimens remains

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challenging, limiting the accuracy of sputum-based tests. The same holds true for youngchildren and people living with HIV.

The Early **R**isk **A**ssessment in TB Contacts by new diagno**S**tic tEsts (ERASE-TB) study aims to fill this diagnostic gap by evaluating new sputum and non-sputum-based TB diagnostics for early TB detection (before onward transmission occurs), as well as tools for more accurate prediction of TB progression to allow for targeted preventive therapy.

- 3 117
- 118 METHODS AND ANALYSES

## 119 Study objectives

ERASE-TB's primary objectives are (I) to determine the sensitivity and specificity of novel diagnostics to detect TB, in particular asymptomatic or minimally symptomatic TB; (II) to evaluate novel diagnostics for detection of likely TB progression; and (III) to enhance the performance of novel diagnostics by simulating testing algorithms coupled with individual risk estimates from a mathematical model. The secondary objectives are (I) to determine the TB prevalence among household contacts (HHCs) of infectious TB index cases (ICs) at baseline and during a 18-24 months follow-up; (II) to establish a biorepository of cryopreserved specimens from HHCs for future development and validation of diagnostic tests; and (III) to assess the association of selected chronic disease conditions and TB among HHCs.

<sup>+3</sup> 129

## 130 Study endpoints

The study's primary endpoints are the presence or development of TB among HHCs with the
 following possible scenarios of (I) prevalent symptomatic TB at baseline, (II) incident TB during
 follow-up, and (III) remained healthy until study completion. An endpoint review committee will
 review the data and case classification before finalization.

56 135

Through the sequencing of *Mycobacterium tuberculosis* (*Mtb*) isolates, cases of co-prevalent
 or incident TB will be classified either as secondary, infected by the source case – the timepoint

of infection will be known; or as infected by another, unknown source of infection, with anunknown timepoint of infection.

## **Recruitment sites**

Recruitment of ICs and HHCs at selected primary healthcare facilities and communities has commenced in Harare, Zimbabwe in March 2021, Maputo, Mozambigue in August 2021, and Mbeya, Tanzania in September 2021. Partners of the ERASE-TB consortium are illustrated in Figure 1. All three countries have a high TB incidence ranging from 100 to 499/100,000 population [1] and HIV prevalence among adults aged 15 years and older of 5% to 20% [7]. The African research institutions have established collaborations with their respective National Tuberculosis Programs ensuring referral and approproate follow-up of TB patients. Figure 2 illustrates the geographic location of research institutions, healthcare facilities where recruitment is taking place, demographic characteristics of study populations, and estimates on TB incidence and HIV prevalence [8–15]. 

## 153 Study design

ERASE-TB is a non-interventional, longitudinal, prospective cohort study among HHCs aged ≥10 years exposed to highly infectious pulmonary TB ICs aged ≥18 years. Eligibility criteria are detailed in Figure 3 and the study design is shown in Figure 4. TB ICs are eligible if the bacterial load in their sputum is at least at the "medium" level according to Xpert MTB/RIF or Xpert MTB/RIF Ultra, and they have received less than seven daily doses of anti-TB treatment before enrollment. This maximises the likelihood of culturing and storing *Mtb* isolates. The total study duration will be 36 months. This includes 12-months enrollment of ICs and HHCs, and 18- to 24-months follow-ups of HHCs. Follow-up ends when a HHCs withdraws from the study, is lost to follow-up, dies, or is diagnosed with TB and referred for treatment. Scheduled or unscheduled unwell visits can be conducted physically and/or telephonically in case of abnormal finding e.g. by abnormal dCXR, or when a participant feels unwell inbetween scheduled follow-up visits.

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3 4	166	
5 6	167	Procedures
7 8	168	TB index cases
9 10	169	Following informed consent obtained, a questionnaire is administered to collect socio-
11 12	170	demographic information, TB risk factors, and the medical history of TB, HIV and other
13 14	171	diseases. Two spontaneous sputum samples are obtained, of which one is for mycobacterial
15 16	172	culturing and one for storage for performing retrospectively Molecular Bacterial Load Assay
17 18	173	(MBLA) to quantify viable Mtb by 16S rRNA [6]; an alternative means to quantify expectorated
19 20 21	174	bacterial load for an estimate of infectiousness. Both liquid and solid mycobacterial cultures
21 22 23	175	are performed on decontaminated sputum samples, with all Mtb isolates stored at -80 degrees
24 25	176	for future DNA extraction and whole genome sequencing. A questionnaire on symptom
26 27	177	duration and TB risk factors is also administered.
28 29	178	
30 31	179	Household key informant
32 33	180	At baseline, a household key informant (either the TB index case or one of the household
34 35	181	contacts) is identified and asked to answer questions of a household questionnaire that collects
36 37 38	182	socio-economic elements like structure of the house or flat, income and household assets, and
39 40	183	covariates possibly associated with risk of TB infection, e.g., windows/air exchange, presence
40 41 42	184	of comorbid conditions, and risk factors like the source of cooking energy, and properties of
43 44	185	the household kitchen.
45 46	186	
47 48	187	Household contacts
49 50	188	Informed consent is obtained from all eligible adult HHCs. For HHC <18 years of age, the
51 52	189	guardian is asked to provide informed consent, with assent also sought from children
53 54	190	dependent on local guidance. At baseline a questionnaire is administered collecting
55 56	191	information on socioeconomic and demographic characteristics, past medical history of TB,
57 58 59	192	HIV and other diseases, exposure risk factors, smoking and alcohol history. The physical
60	193	examination includes height, weight, mid-upper arm circumference and blood pressure

measurement. In addition, all HHCs are offered free HIV testing according to the National
Guidelines. All people with confirmed HIV infection will have CD4 counts performed and be
referred for TB preventive therapy. Those not yet on antiretroviral therapy (ART) and those
who interrupted ART are referred for ART at local services.

Point of care HbA1c (A1cCare, SD Biosensor, Gyeonggi-do, Republic of Korea) and haemoglobin (Hemocue 301+, Hemocue, Angelholm, Sweden) tests and spirometry (including pre- and post-bronchodilation with inhaled salbutamol) are performed at baseline or the sixmonth visit. HHCs who did not take up HIV testing or other screening at baseline are offered these tests at each study visit. Any HHCs with test results requiring treatment or further investigations are referred for respective services.

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HHCs are screened for TB using the WHO symptom questionnaire and a digital chestradiograph (dCXR), reviewed by a clinical officer. dCXRs are not performed in pregnant HHCs.
HHCs with a positive WHO symptom screening and abnormal dCXR are asked to provide
sputum samples for TB investigations i.e., for GeneXpert and mycobacterial culture. Those
with negative symptom screen and normal dCXR are asked to provide a spontaneous sputum
sample for storage (with sputum induction performed if required).

41 212

At baseline, urine, serum, plasma, whole blood (native, and with RNA preservation in PAXgene<sup>®</sup> tubes [BD Biosciences, NJ, USA]) are stored. A finger-prick sample is taken and investigated using the Xpert TB Host Response RUO Prototype cartridge (Cepheid, Sunnyvale, CA, USA). T-cell Activation Marker Tuberculosis (TAM-TB) assay and Interferon Gamma Release Assay (IGRA; STANDARDTM F TB-Feron FIA (IFN-gamma; SD Biosensor, Republic of Korea), are performed on fresh venous blood. In Tanzania and Mozambigue, storage of peripheral blood mononuclear cells for later characterization of the TB-specific immune response is also performed. 

Procedures for follow-up and unwell visits are similar to those at baseline. Measurement of HIV status, haemoglobin, HbA1c, spirometry, CD4 count and IGRA testing are not performed at follow-up visits, unless not done previously. At the last scheduled visit all HHCs not known to have HIV are re-offered HIV testing and a spontaneous or induced sputum sample is stored for all participants.

, 1 227

## 228 Household contacts screening positive for TB symptoms and/or with a DCXR 229 suggestive of TB

HHCs screening positive for symptoms and/or those with DCXRs suggestive of TB are asked for a sputum sample, which is investigated using Xpert MTB/RIF Ultra (Cepheid). If this sample is positive for *Mtb* (including a trace result), a minimum of two additional sputum samples are investigated, following decontamination, with Xpert MTB/RIF Ultra, solid and liquid culture. Isolates stored from these cultures will be sequenced for matching with the IC isolates in order to verify intra-household transmission. Sputum induction is performed for those unable to provide a spontaneous sputum sample. HHCs with microbiologically confirmed TB are referred for TB treatment to the National TB Programme.

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## 239 Patient and public involvement

The ERASE-TB study sites have established Community Advisory Boards, which are voices of communities, people affected, and study participants, providing a strategic link between the communities and the study team. Community Advisory Boards meet regularly and provide feedback on design, procedures and conduct of the study. They will also be closely involved in the dissemination of study results. In addition to the Community Advisory Boards, each study site conducts community engagement activities focused on young people with the aim to foster interst in science and research, specififcally in the field of respiratory diseases/illness. This includes close partnership with schools and universities. Furthermore, planned qualitative research will specifically aim to understand the perceptions of HHCs with regards to TB diagnostics and screening.

1 2		
- 3 4	250	
5 6	251	Sample size
7 8	252	An estimated 800 to 900 TB-confirmed ICs are required for the subsequent enrollment of an
9 10	253	anticipated 2,100 HHCs, i.e., 700 HHCs per country. Loss to follow-up of HHCs is estimated
11 12	254	to be 10%. A total of 64 HHCs (3%) are estimated to be diagnosed with TB during the study
13 14	255	period, based on previous active case finding studies among HHCs [16].
15 16	256	
17 18	257	Novel test candidates
<ol> <li>19</li> <li>20</li> <li>21</li> <li>22</li> <li>23</li> <li>24</li> <li>25</li> <li>26</li> <li>27</li> <li>28</li> <li>29</li> <li>30</li> <li>31</li> <li>32</li> <li>33</li> <li>34</li> <li>35</li> </ol>	258	A range of novel test candidates targeted at pathogen detection or identification of host
	259	responses to Mtb are being applied, either in real-time (for all participants) or retrospectively
	260	(in a case-control design). Whilst a number of novel test candidates have been pre-specified,
	261	the ERASE-TB biobanking processes allow for addition of further candidate tests to be
	262	evaluated on stored samples as they become available.
	263	
	264	DCXRs offer good sensitivity for diagnosis of pulmonary TB. However, high inter- and intra-
	265	investigator variability, and lack of trained interpreters present a barrier to implementation in
36 37	266	many high-TB burden settings. Computer-aided interpretation systems, such as CAD4TB
38 39	267	(Delft Imaging, Hertogenbosch, Netherlands) and qXR (Qure.ai, India) may increase image-
40 41 42	268	reading capacity, with good performance, and serve, therefore, as a systematic screening tool
43 44	269	to identify individuals in need of confirmatory TB tests [17,18].
45 46	270	
47 48	271	Xpert MTB/RIF Ultra is a nucleic acid amplification test for <i>Mtb</i> with a lower limit of detection
49 50	272	compared to the previous Xpert MTB/RIF generation, and, therefore, conferring higher
51 52	273	sensitivity in paucibacillary specimens. This, however, comes at the expense of specificity,
53 54	274	particularly in high TB incidence settings, resulting in 'false positives' [19]. WHO guidelines
55 56	275	recommend Xpert MTB/RIF Ultra for TB diagnosis among adults and children acknowledging
57 58	276	that further evaluation, particularly of the role of Xpert MTB/RIF Ultra for TB screening, is
59 60	277	needed [20,21].

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FLOW-TB is an advanced enzyme-linked immunosorbent assay for the detection of Mtb lipoarabinomannan (a mycobacterial cell wall component) in urinary specimens with results available within 65 minutes [22].

The T-cell activation marker-TB assay (TAM-TB) detects Mtb-specific CD4 T-cells through in-vitro antigen stimulation with Mtb-derived peptides, i.e., from ESAT-6 and CFP-10, followed by flow cytometry. TAM-TB discriminated latent Mtb infection from TB in freshly collected blood with 83% sensitivity and 96-98% specificity in previous studies. Further, TAM-TB may detect early TB disease progression up to 9 months prior to the identification of *Mtb* in sputum [23– 25].

Multiple transcriptomic signatures, capturing the host response to TB, have been described as promising candidate tests for earlier TB diagnosis (up to two years before microbiological diagnosis). An individual patient data meta-analysis suggested equivalent performance of eight signatures, with 25-40% sensitivity and 92-95% specificity 0-24 months before TB diagnosis. Diagnostic accuracy of each signature improved as the interval between testing and microbiological TB diagnosis shortened [26]. Several signatures have been developed into polymerase chain reaction (PCR)-based assays to facilitate real-time implementation: the recent CORTIS trial reported sensitivity of 48% and specificity of 75% for incipient TB for the RISK-11 signature [27]. Cepheid have developed a 3-transcript TB score into a fully automated in-cartridge PCR assay performed on finger-prick blood using the Xpert platform (Xpert TB Host Response RUO Prototype cartridge). This cartridge will be evaluated using freshly collected specimens in ERASE-TB; storage of RNA-stabilised blood samples also allows for retrospective evaluation of additional transcriptomic signatures in our cohort [28,29]

An alternative approach to capture the host response to TB is through protein-based biomarker signatures. Candidate tests in this category include a serum- or plasma-based multiplex assay assessing 13 protein biomarkers (CRP, procalcitonin[30], sTREM-1[31,32], angiopoietin2[33,34], interleukin-6[35], TRAIL[36] and IP-10[37]) that is being developed by the London
School of Hygiene and Tropical Medicine; in additon, a seven biomarker signauture is under
development as a point-of-care test for TB diagnosis, with 94% sensitivity and 73% specificity
detected in previous work [38].

14 311

## 312 Statistical analyses

Baseline characteristics and analytical data will be summarized using descriptive statistics inclusive of mean, median, range, standard deviation, and absolute as well as relative frequencies depending on the nature of data. A logistic regression model will be used to identify characteristics of TB among ICs, households and HHCs that are predictive of incident TB. From the study database, we will simulate algorithms of different tests to obtain the testing combination with the best accuracy. We will couple tests with a mathematical model that guantifies the risk of infection and/or disease to enhance predictive performance. The reporting of the development of the prediction model will follow the Transparent Reporting of a multivariable prediction model for Individual Prognosis Or Diagnosis (TRIPOD) Initiative [39].

The validation of novel diagnostic tests for detecting TB will be analysed as a 1:4 matched nested case-control study with HHCs diagnosed with TB at baseline and during follow-up serving as cases, and HHCs who do not develop TB during follow-up as controls; controls will be matched for site, age, sex, HIV status and other risk factors for developing TB. Sensitivity and specificity of novel tests will be determined using pre-existing positive/negative cut-offs where these exist; and receiver operating curves (ROC) constructed with area under the ROC curve calculated. For tests aiming to identify individuals at high risk of TB in the future, only HHCs who are diagnosed with TB during follow-up will serve as cases (i.e. those diagnosed with TB at baseline will be excluded). Stored samples from all timepoints will be retrieved and diagnostic accuracy (i.e. sensitivity and specificity) of the novel test determined at different 

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3 4 5 6 7 8 9 10 11 23 4 5 9 10 11 23 24 25 26 27 28 9 30 12 23 24 5 26 27 28 9 31 23 34 5 37 8 9 40 41 22 23 24 5 26 27 28 9 30 12 33 34 5 37 8 9 40 11 20 21 22 23 24 5 26 27 28 9 30 21 22 23 24 5 26 27 28 9 30 21 22 23 24 5 26 27 28 29 30 21 22 23 24 5 26 27 28 29 30 20 20 20 20 20 20 20 20 20 20 20 20 20	333	time-points before TB diagnosis. The decision of assigning the "active TB" endpoints to
	334	participants will be blinded from the new test results to avoid inclusion bias.
	335	
	336	Data management
	337	All source data will be kept confidential in secured locations with restricted access by
	338	authorized personnel only inclusive of monitors, auditors and reviewers of ethical and
	339	regulatory committees in line with applicable data privacy regulations. Each participant is
	340	asked to consent to this handling of the data, and is assigned a pseudonymous identification
	341	number that is used throughout the study on all source data.
	342	
	343	Accurate documentation of paper-based and electronic source data, e.g., original records and
	344	certified copies of original records, progress notes, screening logs, and recorded data from
	345	automated instruments, will be maintained. The pseudonymized clinical data captured on
	346	paper-based Case Report Forms will be entered at the sites into a database using the web-
	347	based Clinical Data Management System of OpenClinica (OpenClinica LLC, Waltham, MA,
	348	USA). The study specific database has been built, maintained and hosted by the LMU Klinikum
	349	on a centralized secure server. Data modifications and necessary corrections performed in the
	350	database also within the context of double data entry will be documented and tracked in audit
	351	trails. Data quality and plausibility are assured by a series of pre-programmed edit and range
43 44	352	checks in OpenClinica. Further validation checks are programmed in Stata (Statacorp, College
45 46 47 48 49 50 51 52 53 54 55 56	353	Station, TX, USA) with extracts of the database and electronically received data, e.g.,
	354	spirometry, dCXR and laboratory, will be integrated into analyses of datasets.
	355	
	356	Monitoring
	357	Assigned study monitors will visit the sites at regular intervals physically and/or virtually in
	358	addition to frequent day-to-day communication. Close follow-up on all study-related aspects
57 58 59	359	will be performed to ascertain compliance with standards of Good Clinical Practice, the
60	360	Declaration of Helsinki, and other local and national regulatory guidelines inclusive of

guidelines for infection prevention and control of airborne-transmitted diseases, e.g., social distancing in well-ventilated spaces, and wearing of personal protective equipment. In particular, monitors that support designated study personnel are responsible to verify (I) adequacy of the study personnels' qualifications and facilities, (II) accuracy of informed consent procedures and patient eligibility, (III) adherence to the study protocol, (IV) protection of rights and well-being of participants, (V) adherence to infection prevention and control measures (VI) accuracy and completeness of study documents and other study-related records, and (VII) maintenance of source documents.

370 Ethics and dissemination

The study protocol and informed consent/assent documents have been approved by regulatory and ethical committees of the participating institutions. This includes the Medical Research Council in Zimbabwe, the National Health Research Ethics Committee in Tanzania, the National Bioethics for Health Committee in Mozambique, and the ethical committees of London School of Hygiene & Tropical Medicine, United Kingdom, and the medical faculty of the Ludwig-Maximilians-Universität München, Germany.

37 377

 Adult ICs and HHCs are asked for written informed consent prior to their participation. Underage HHCs are asked for assent in addition to obtaining the consent of their legal guardians/parents; with ages for assent depending on local guidance. In case of illiteracy, the participant is asked to give its consent by fingerprint while an adult impartial, literate witness present during the entire consent procedure signs the consent on behalf. All participants have the right to withdraw from the study at any time. Findings derived from ERASE-TB will be presented at scientific conferences, and published in peer-reviewed international journals.

54 385

#### 386 Current study status

The recruitment of ICs and HHCs is in progress in Zimbabwe, Mozambique and Tanzania
 since March, August and September 2021, respectively. The follow-up of HHCs is anticipated

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3 4 5 6	389	to be completed in March, August and September 2023 in Zimbabwe, Mozambique and
	390	Tanzania, respectively; laboratory analyses are estimated to be performed by December 2024.
7 8	391	
9 10	392	Author contributions
11 12 13 14 15 16 17	393	The study proposal and protocol were written by NH, KK with scientific input from CK, TM, CG,
	394	JM. ETM, UP, DB, AM wrote the initial manuscript with scientific input on the database and
	395	data management section from FR, TA. NH, KK critically reviewed the initial draft of the
17 18 19	396	manuscript. KH, GK, CJC, ENN, TA, provided critical feedback on the manuscript. All authors
19         20         21         22         23         24         25         26         27         28         29         30         31         32         33         34         35         36         37         38         39         40         41         42         43         44	397	have read and approved the final version of the manuscript.
	398	
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	401	number RIA2018D-2508-ERASE-TB), the German Center for Infection Research (DZIF) grant
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	405	
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45 46	409	Mozambique, and the National Institute for Medical Research - Mbeya Medical Research
47 48 49 50 51 52 53 54	410	Centre, Tanzania for their exceptional efforts and contributions, which made this research
	411	possible.
	412	
	413	Consortium authorship
55 56	414	The following are members of the ERASE-TB consortium: Anna Shepherd <sup>a</sup> , Hazel M Dockrell <sup>a</sup> ,
57 58 59	415	Judith Bruchfeld <sup>b</sup> , Christopher Sundling <sup>b</sup> , Charles Sandy <sup>c</sup> , Mishelle Mugava <sup>c</sup> , Tsitsi
59 60	416	Bandason <sup>c</sup> , Martha Chipinduro <sup>c</sup> , Kuda Mutasa <sup>d</sup> , Sandra Rukobo <sup>d</sup> , Lwitiho Sudi <sup>e</sup> , Antelmo

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- 3 4	417	Haulee, Emmanuel Sichonee, Paschal Qwaraye, Bariki Mtafyae, Harrieth Mwambolae, Lilian
5 6 7 8 9 10 11 12 13 14	418	Minjae, Issa Sabie, Peter Edwine, Dogo Ngalisone, Stella Luswemae, Willyhelmina Olomie,
	419	Doreen Pamba <sup>e</sup> , Simeon Mwanyonga <sup>e</sup> , Celina Nhamuave <sup>f</sup> , António Machiana <sup>f</sup> , Carla Madeira <sup>f</sup> ,
	420	Emelva Manhiça <sup>f</sup> , Nádia Sitoe <sup>f</sup> , Jorge Ribeiro <sup>f</sup> , Christof Geldmacher <sup>g</sup> , Andrea Rachow <sup>g</sup> , Olena
	421	Ivanova <sup>9</sup> , Laura Olbrich <sup>9</sup> , Elmar Saathoff <sup>9</sup> , Michael Hoelscher <sup>9</sup> .
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24 25 26 27 28 29 30 31 32 33 34 35	427	<sup>d</sup> Zvitambo Research Institute, Harare, Zimbabwe
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2 3 4	575	Figure legend
5	576	Figure 1. The ERASE-TB consortium
7 8	577	Abbreviations: ERASE-TB=Early Risk Assessment in TB contactS by new diagnostic tEsts
9 10	578	
11 12	579	Figure 2. Location and characteristics of ERASE-TB study sites
13 14 15 16	580	Notes: The location of each study site is indicated by a red asterix. Source data used within
	581	this figure are taken from the references [7,8,41,42,9–15,40].
17 18	582	Abbreviations: ERASE=Early Risk Assessment in TB contactS by new diagnostic tEsts;
19 20 21	583	TB=tuberculosis; HIV=human immunodeficiency virus
21 22 23	584	
24 25	585	Figure 3. Eligibility criteria and schedules of events for index cases and household contacts
26 27	586	Notes: A=depending on the time point of study enrollment and consequently on the duration
28 29	587	available for follow-up, i.e. 18 or 24 months, the follow-up visit at 24 months $\pm 30$ days may be
30 31	588	conditional; <b>B</b> =the follow-up visit by phone may be conducted after the last scheduled follow-
32 33	589	up visit at 18 months $\pm 30$ days or 24 months $\pm 30$ days to assess whether symptoms suggestive
34 35	590	of TB have occurred, TB diagnosis has been made or anti-TB treatment has been initiated;
36 37	591	C=unwell visits by phone or on-site may be conducted between scheduled follow-up visits if a
38 39 40	592	participant presents at a recruitment healthcare facility with signs and symptoms suggestive of
40 41 42	593	TB; <b>D</b> =coached spontaneous or induced sputum collection for storage at scheduled follow-up
43 44	594	visit at 18 months $\pm$ 30 days or 24 months $\pm$ 30 days, and for repetition of HIV testing if tested
45 46	595	negative at baseline; E=coached spontaneous or induced sputum collection upon the decision
47 48	596	of the investigating team for testing by Xpert MTB/RIF Ultra if participant presents with signs
49 50	597	and symptoms suggestive of TB; F=coached spontaneous or induced sputum collection in
51 52	598	case of Xpert MTB/RIF Ultra positivity or strong clinical suspicion of TB for repetition of the
53 54	599	Xpert MTB/RIF Ultra; $G=$ in case of HIV positivity to be followed by the assessment of CD4
55 56 57	600	counts; H=CXR to be conducted at an unscheduled on-site unwell visit upon the decision of
57 58 59	601	the investigating team depending on the nature of symptoms reported, and the time elapsed
60	602	since the last CXR including its findings; I=not to be conducted among pregnant women;

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J=stored venous blood includes 6mL EDTA blood for whole blood and plasma, 4mL serum and 2.5mL PAXgene blood, all samples will be deep frozen for retrospective testing using new diagnostics as described in text; **K**=in case the evaluation of symptoms of a participant unable to present at a recruitment healthcare facility is required an unscheduled on-site or home visit will be arranged by phone, the resolution of symptoms can alternatively be addressed by phone; L=collection of PBMC at baseline and follow-up visit at 6 months ±30 days is optional, thus will not be performed at each participating site and for each participant; **M**=in case the evaluation of symptoms of a participant unable to present at a recruitment healthcare facility is required or doubtful if required an unscheduled unwell visit by phone will be arranged, the resolution of symptoms can alternatively be addressed by phone; N=spirometry and/or diabetes (HbA1c) will be performed at scheduled follow-up visits at 6 months ±30 days, 12 months ±30 days and 18 or 24 months ±30 days if required or not performed at baseline, anaemia (Hb) will be performed at baseline and scheduled follow-up visits at 6 months ±30 days, 12 months ±30 days and 18 or 24 months ±30 days if possible; **O**=blood pressure measurement will be performed at baseline and scheduled follow-up visits at 6 months ±30 days, 12 months ±30 days and 18 or 24 months ±30 days; P=WGS to be performed once Mtb infection is confirmed and an isolate could be recovered.

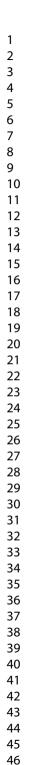
Abbreviations: TB=tuberculosis; WHO=World Health Organization; HIV=human immunodeficiency virus; WGS=whole genome sequencing; MBLA=molecular bacterial load assay; CXR=chest radiograph; IGRA=interferon gamma release assay; PBMC=peripheral blood mononuclear cell; TAM-TB=T- cell activation marker tuberculosis; MTB=Mycobacterium tuberculosis; RIF=rifampicin, Hb=haemoglobin; HbA1c=glycated hemoglobin; LAM=lioparabinomannan; CD4=cluster of differentiation 4

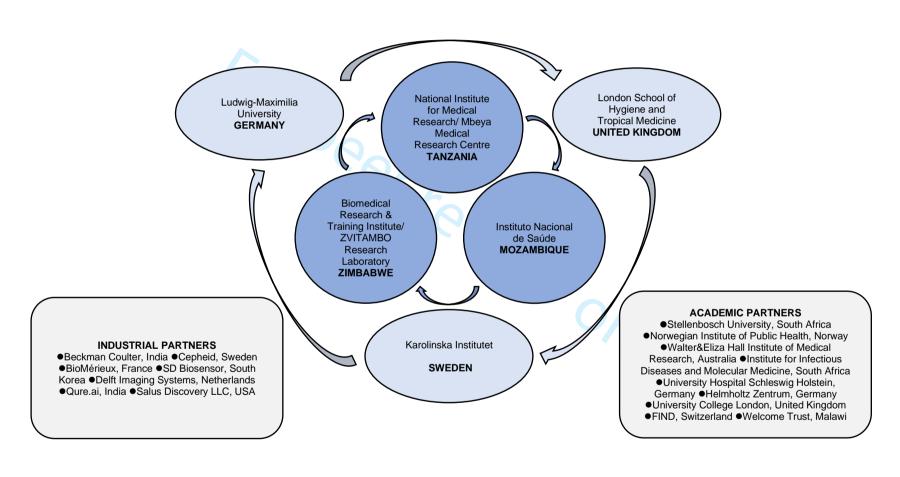
Figure 4. Study design

Abbreviations: HHC=household contact; TB=tuberculosis; IC=index case; WHO=World

Health Organization; CXR= chest radiograph; SS=symptom score; MTB=Mycobacterium

tuberculosis; RIF=rifampicin; pos=positive; CT=cpmputer tomography; FU=follow-up







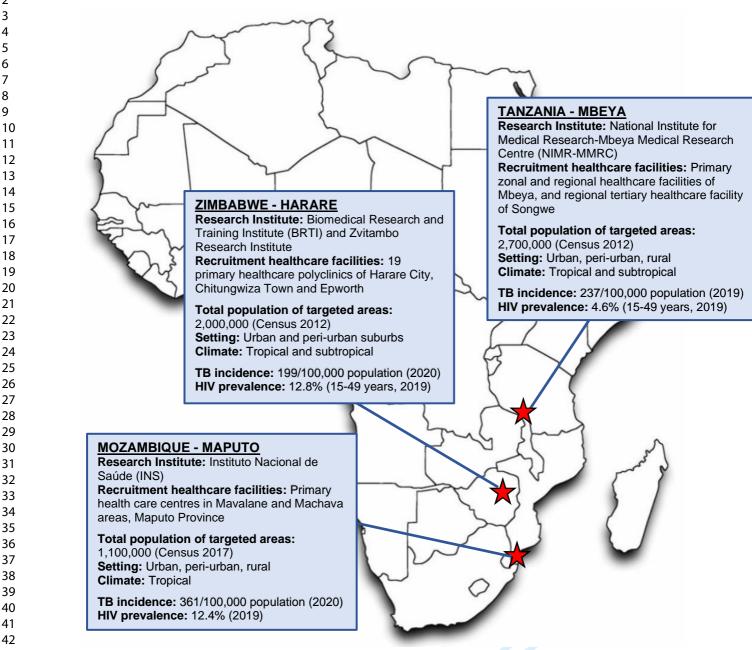
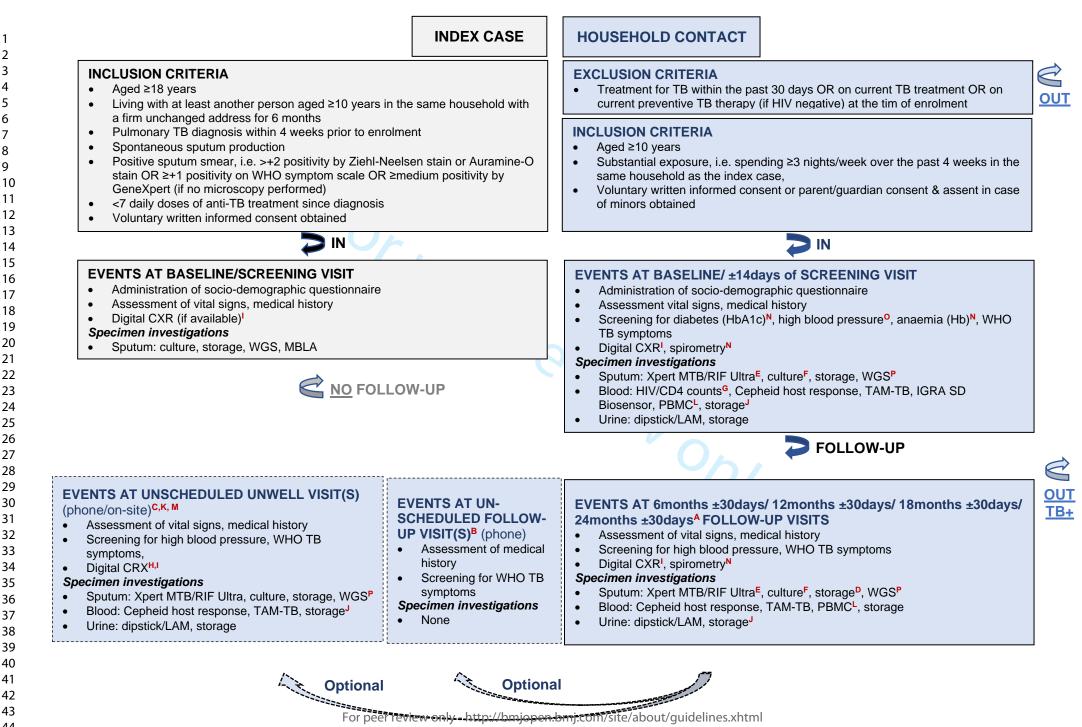


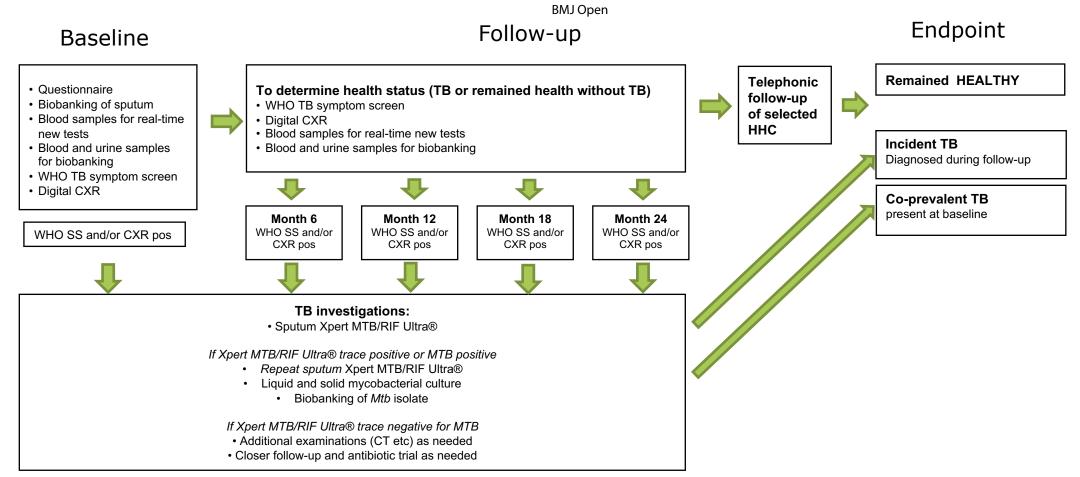
Figure 2. Location and characteristics of ERASE-TB study sites



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Figure 3. Eligibility criteria and schedules of events for index cases and household contacts

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## Early risk assessment in pediatric and adult household contacts of confirmed tuberculosis cases by novel diagnostic tests (ERASE-TB): protocol for a prospective, non-interventional, longitudinal, multi-country cohort study

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3 4	1	Early risk assessment in pediatric and adult household contacts of confirmed
5 6 7	2	tuberculosis cases by novel diagnostic tests (ERASE-TB): protocol for a
7 8 9	3	prospective, non-interventional, longitudinal, multi-country cohort study
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## 30 ABSTRACT

## 31 Introduction

The World Health Organization (WHO) End-TB Strategy calls for the development of novel diagnostics to detect tuberculosis earlier and more accurately. Better diagnostics, together with tools to predict disease progression are critical for achieving WHO END-TB targets. The Early Risk Assessment in TB contactS by new diagnostic tEsts (ERASE-TB) study aims to evaluate novel diagnostics and testing algorithms for early tuberculosis diagnosis and accurate prediction of disease progression among household contacts exposed to confirmed index cases in Mozambigue, Tanzania and Zimbabwe.

39

## 40 Methods and analysis

A total of 2,100 household contacts (HHCs) (aged ≥10 years) of adults with microbiologically-41 42 confirmed pulmonary tuberculosis will be recruited and followed up at 6-month intervals for 18 to 24 months. At each time-point a WHO symptom screen and digital chest-radiograph (dCXR) 43 will be performed, and blood and urine samples collected. Individuals screening positive (WHO 44 45 symptom screen or dCXR) will be requested to provide sputum for Xpert MTB/Rif Ultra. At baseline, HHCs will also be screened for HIV, diabetes (HbA1c), chronic lung disease 46 (spirometry), hypertension and anaemia. Study outcomes will be co-prevalent tuberculosis 47 (diagnosed at enrollment), incident tuberculosis (diagnosed during follow-up) or no 48 49 tuberculosis at completion of follow up. Novel diagnostics will be validated using fresh and 50 biobanked samples with a nested case control design. Cases are defined as HHCs diagnosed with tuberculosis (for early diagnosis) or with incident tuberculosis (for prediction of 51 progression) and will be matched by age, sex and country to HHCs who remain healthy 52 53 (controls). Statistical analyses will include assessment of diagnostic accuracy by constructing 54 receiver operating curves and calculation of sensitivity and specificity.

56 Ethics and dissemination

ERASE-TB has been approved by regulatory and ethical committees in each African country and by each partner organisation. Consent, with additional assent for participants <18 years, is voluntary. Attestation by impartial witnesses is sought in case of illiteracy. Confidentiality of <text> participants is being maintained throughout. Study findings will be presented at scientific conferences and published in peer-reviewed international journals.

#### Study registration number

NCT04781257 

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2 3 4	65	Strengths
5 6	66	• Recruitment of highly infectious index cases aimed at maximising the number of
7 8	67	tuberculosis (TB) diagnoses in the household contact (HHCs) cohort.
9 10	68	• Sequencing of Mycobacterium tuberculosis isolates from both index cases and HHCs
11 12	69	allows confirmation of household transmission and thus determination of timing of the
13 14	70	transmission event; resulting in more precise estimates of new test sensitivity
15 16 17	71	compared to population-based cohorts with unknown timing of infection.
17 18 19	72	• Large sample size across three southern African countries with high HIV prevalence;
20 21	73	including adolescents will ensure study findings are generalisable to the clinically
22 23	74	relevant population at high risk of TB compared to studies focused on adults only.
24 25	75	
26 27	76	Limitations
28 29	77	• Despite the large cohort of HHCs, the number of diagnosed TB cases will be small,
30 31	78	limiting the power of the study and sub-group analyses such as by age and HIV status.
32 33 34	79	• Geographically limited to sub-Saharan Africa, therefore results may not be
35 36	80	generalisable to other populations, including those with lower HIV prevalence such as
37 38	81	in South-East Asia or the Americas.
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### 82 INTRODUCTION

Tuberculosis (TB) remains a leading global public health problem, with an estimated 10 million new cases and 1.5 million deaths globally in 2020 [1]. In 2014, the World Health Assembly approved the World Health Organization (WHO) End-TB Strategy, aiming for a 90% reduction in TB incidence and 95% reduction in TB deaths by 2035 [2]. However, in 2019, three million TB cases ('the missing millions') remained undiagnosed and untreated globally, resulting in potentially avoidable morbidity, mortality and onward transmission. The Covid-19 pandemic has resulted in a large decrease in the number of people newly diagnosed with TB and reported. This has increased the diagnostic gap by a further 1.3 million, resulting in an estimated 4.2 million undiagnosed TB cases in 2020 [3]. Also, for the first time in a decade TB deaths have risen, from an estimated 1.4 million in 2019 to 1.5 million in 2020, as a result of reduced access to and provision of essential TB services including diagnostics during the Covid-19 pandemic.

Without an efficacious and safe vaccine, early detection and containment are the main tools to interrupt transmission and successfully control TB. Similar to SARS-CoV2, asymptomatic spreading of *M.tuberculosis* and subclinical but infectious disease states are a major concern in the control of airborne infectious diseases [4]. Early and accurate identification of persons with TB, combined with identification of those at risk of progression to TB and provision of targeted preventive treatment are critical to reducing TB-associated morbidity and mortality, and preventing onward transmission.

104 Currently available diagnostics such as sputum microscopy, mycobacterial culture and nucleic 105 acid amplification tests are based on direct pathogen detection, thus requiring a high 106 mycobacterial load; they therefore predominately target advanced TB when onward 107 transmission and significant lung damage has occurred [5,6]. Further, for many patients with 108 minimal or no symptoms, expectoration of high-quality sputum specimens remains

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challenging, limiting the accuracy of sputum-based tests. The same holds true for young children and people living with HIV.

The Early Risk Assessment in TB Contacts by new diagnoStic tEsts (ERASE-TB) study aims to fill this diagnostic gap by evaluating new sputum and non-sputum-based TB diagnostics for early TB detection (before onward transmission occurs), as well as tools for more accurate prediction of TB progression to allow for targeted preventive therapy. 

- METHODS AND ANALYSES

#### Study objectives

ERASE-TB's primary objectives are (I) to determine the sensitivity and specificity of novel diagnostics to detect TB, in particular asymptomatic or minimally symptomatic TB; (II) to evaluate novel diagnostics for detection of likely TB progression; and (III) to enhance the performance of novel diagnostics by simulating testing algorithms coupled with individual risk estimates from a mathematical model. The secondary objectives are (I) to determine the TB prevalence among household contacts (HHCs) of infectious TB index cases (ICs) at baseline and during a 18-24 months follow-up; (II) to establish a biorepository of cryopreserved specimens from HHCs for future development and validation of diagnostic tests; and (III) to assess the association of selected chronic disease conditions and TB among HHCs.

#### **Study endpoints**

The study's primary endpoints are the presence or development of TB among HHCs with the following possible scenarios of (I) prevalent symptomatic TB at baseline, (II) incident TB during follow-up, and (III) remained healthy until study completion. An endpoint review committee will review the data and case classification before finalization.

Through the sequencing of Mycobacterium tuberculosis (Mtb) isolates, cases of co-prevalent or incident TB will be classified either as secondary, infected by the source case - the timepoint 

of infection will be known; or as infected by another, unknown source of infection, with anunknown timepoint of infection.

### **Recruitment sites**

Recruitment of ICs and HHCs at selected primary healthcare facilities and communities has commenced in Harare, Zimbabwe in March 2021, Maputo, Mozambigue in August 2021, and Mbeya, Tanzania in September 2021. Partners of the ERASE-TB consortium are illustrated in Figure 1. All three countries have a high TB incidence ranging from 100 to 499/100,000 population [1] and HIV prevalence among adults aged 15 years and older of 5% to 20% [7]. The African research institutions have established collaborations with their respective National Tuberculosis Programs ensuring referral and approproate follow-up of TB patients. Figure 2 illustrates the geographic location of research institutions, healthcare facilities where recruitment is taking place, demographic characteristics of study populations, and estimates on TB incidence and HIV prevalence [8–15].

### 152 Study design

ERASE-TB is a non-interventional, longitudinal, prospective cohort study among HHCs aged ≥10 years exposed to highly infectious pulmonary TB ICs aged ≥18 years. Eligibility criteria are detailed in Figure 3 and the study design is shown in Figure 4. TB ICs are eligible if the bacterial load in their sputum is at least at the "medium" level according to Xpert MTB/RIF or Xpert MTB/RIF Ultra, and they have received less than seven daily doses of anti-TB treatment before enrollment. This maximises the likelihood of culturing and storing *Mtb* isolates. The total study duration will be 36 months. This includes 12-months enrollment of ICs and HHCs, and 18- to 24-months follow-ups of HHCs. Follow-up ends when a HHCs withdraws from the study, is lost to follow-up, dies, or is diagnosed with TB and referred for treatment. Scheduled or unscheduled unwell visits can be conducted physically and/or telephonically in case of abnormal finding e.g. by abnormal dCXR, or when a participant feels unwell inbetween scheduled follow-up visits.

2 3		
3 4 5	165	
6 7	166	Procedures
8 9	167	TB index cases
10 11	168	Following informed consent obtained, a questionnaire is administered to collect socio-
12 13 14	169	demographic information, TB risk factors, and the medical history of TB, HIV and other
	170	diseases. Two spontaneous sputum samples are obtained, of which one is for mycobacterial
15 16	171	culturing and one for storage for performing retrospectively Molecular Bacterial Load Assay
17 18	172	(MBLA) to quantify viable Mtb by 16S rRNA [6]; an alternative means to quantify expectorated
19 20	173	bacterial load for an estimate of infectiousness. Both liquid and solid mycobacterial cultures
21 22	174	are performed on decontaminated sputum samples, with all Mtb isolates stored at -80 degrees
23 24 25	175	for future DNA extraction and whole genome sequencing. A questionnaire on symptom
26 27	176	duration and TB risk factors is also administered.
28 29	177	
30 31	178	Household key informant
32 33	179	At baseline, a household key informant (either the TB index case or one of the household
34 35 36 37 38	180	contacts) is identified and asked to answer questions of a household questionnaire that collects
	181	socio-economic elements like structure of the house or flat, income and household assets, and
39 40	182	covariates possibly associated with risk of TB infection, e.g., windows/air exchange, presence
41 42	183	of comorbid conditions, and risk factors like the source of cooking energy, and properties of
43 44	184	the household kitchen.
45 46	185	
47 48	186	Household contacts
49 50	187	Informed consent is obtained from all eligible adult HHCs. For HHC <18 years of age, the
51 52	188	guardian is asked to provide informed consent, with assent also sought from children
53 54	189	dependent on local guidance. At baseline a questionnaire is administered collecting
55 56 57	190	information on socioeconomic and demographic characteristics, past medical history of TB,
57 58 59	191	HIV and other diseases, exposure risk factors, smoking and alcohol history. The physical
60	192	examination includes height, weight, mid-upper arm circumference and blood pressure

measurement. In addition, all HHCs are offered free HIV testing according to the National
Guidelines. All people with confirmed HIV infection will have CD4 counts performed and be
referred for TB preventive therapy. Those not yet on antiretroviral therapy (ART) and those
who interrupted ART are referred for ART at local services.

Point of care HbA1c (A1cCare, SD Biosensor, Gyeonggi-do, Republic of Korea) and haemoglobin (Hemocue 301+, Hemocue, Angelholm, Sweden) tests and spirometry (including pre- and post-bronchodilation with inhaled salbutamol) are performed at baseline or the sixmonth visit. HHCs who did not take up HIV testing or other screening at baseline are offered these tests at each study visit. Any HHCs with test results requiring treatment or further investigations are referred for respective services.

26 204

HHCs are screened for TB using the WHO symptom questionnaire and a digital chestradiograph (dCXR), reviewed by a clinical officer. dCXRs are not performed in pregnant HHCs.
HHCs with a positive WHO symptom screening and abnormal dCXR are asked to provide
sputum samples for TB investigations i.e., for GeneXpert and mycobacterial culture. Those
with negative symptom screen and normal dCXR are asked to provide a spontaneous sputum
sample for storage (with sputum induction performed if required).

41 211

At baseline, urine, serum, plasma, whole blood (native, and with RNA preservation in PAXgene<sup>®</sup> tubes [BD Biosciences, NJ, USA]) are stored. A finger-prick sample is taken and investigated using the Xpert TB Host Response RUO Prototype cartridge (Cepheid, Sunnyvale, CA, USA). T-cell Activation Marker Tuberculosis (TAM-TB) assay and Interferon Gamma Release Assay (IGRA; STANDARDTM F TB-Feron FIA (IFN-gamma; SD Biosensor, Republic of Korea), are performed on fresh venous blood. In Tanzania and Mozambigue, storage of peripheral blood mononuclear cells for later characterization of the TB-specific immune response is also performed. 

Procedures for follow-up and unwell visits are similar to those at baseline. Measurement of HIV status, haemoglobin, HbA1c, spirometry, CD4 count and IGRA testing are not performed at follow-up visits, unless not done previously. At the last scheduled visit all HHCs not known to have HIV are re-offered HIV testing and a spontaneous or induced sputum sample is stored for all participants.

#### Household contacts screening positive for TB symptoms and/or with a DCXR suggestive of TB

HHCs screening positive for symptoms and/or those with DCXRs suggestive of TB are asked for a sputum sample, which is investigated using Xpert MTB/RIF Ultra (Cepheid). If this sample is positive for *Mtb* (including a trace result), a minimum of two additional sputum samples are investigated, following decontamination, with Xpert MTB/RIF Ultra, solid and liquid culture. Isolates stored from these cultures will be sequenced for matching with the IC isolates in order to verify intra-household transmission. Sputum induction is performed for those unable to provide a spontaneous sputum sample. HHCs with microbiologically confirmed TB are referred for TB treatment to the National TB Programme.

#### Patient and public involvement

The ERASE-TB study sites have established Community Advisory Boards, which are voices of communities, people affected, and study participants, providing a strategic link between the communities and the study team. Community Advisory Boards meet regularly and provide feedback on design, procedures and conduct of the study. They will also be closely involved in the dissemination of study results. In addition to the Community Advisory Boards, each study site conducts community engagement activities focused on young people with the aim to foster interst in science and research, specififcally in the field of respiratory diseases/illness. This includes close partnership with schools and universities. Furthermore, planned qualitative research will specifically aim to understand the perceptions of HHCs with regards to TB diagnostics and screening.

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3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 9 0 21 22 23 24 25 26 27 28 29 30 31 32 33 43 5 36 37 38 9 40 41 42	249	
	250	Sample size
	251	An estimated 800 to 900 TB-confirmed ICs are required for the subsequent enrollment of an
	252	anticipated 2,100 HHCs, i.e., 700 HHCs per country. Loss to follow-up of HHCs is estimated
	253	to be 10%. A total of 64 HHCs (3%) are estimated to be diagnosed with TB during the study
	254	period, based on previous active case finding studies among HHCs [16]. Validation for
	255	subclinical and early TB will include incident (n=49) and co-prevalent TB cases (n=15).
	256	Validation for detection of incipient <i>M.tb</i> infection will include samples of participants with
	257	incident TB (n=49) matched 1:4 to samples of participants without TB (n=196). For tests
	258	diagnosing incipient <i>M.tb</i> infection sensitivities of 73% and 82% would be detected with a
	259	precision of 59-85% and 68-91% respectively. For specifcities of 92% and 94% the confidence
	260	intervals would be 87-95% and 90-97%.
	261	
	262	Novel test candidates
	263	A range of novel test candidates targeted at pathogen detection or identification of host
	264	responses to Mtb are being applied, either in real-time (for all participants) or retrospectively
	265	(in a case-control design). Whilst a number of novel test candidates have been pre-specified,
	266	the ERASE-TB biobanking processes allow for addition of further candidate tests to be
	267	evaluated on stored samples as they become available.
43 44	268	
45 46	269	DCXRs offer good sensitivity for diagnosis of pulmonary TB. However, high inter- and intra-
47 48	270	investigator variability, and lack of trained interpreters present a barrier to implementation in
49 50	271	many high-TB burden settings. Computer-aided interpretation systems, such as CAD4TB
51 52	272	(Delft Imaging, Hertogenbosch, Netherlands) and qXR (Qure.ai, India) may increase image-
53 54	273	reading capacity, with good performance, and serve, therefore, as a systematic screening tool
55 56 57	274	to identify individuals in need of confirmatory TB tests [17,18].
57 58 59 60	275	

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276 Xpert MTB/RIF Ultra is a nucleic acid amplification test for *Mtb* with a lower limit of detection 277 compared to the previous Xpert MTB/RIF generation, and, therefore, conferring higher 278 sensitivity in paucibacillary specimens. This, however, comes at the expense of specificity, 279 particularly in high TB incidence settings, resulting in 'false positives' [19]. WHO guidelines 280 recommend Xpert MTB/RIF Ultra for TB diagnosis among adults and children acknowledging 281 that further evaluation, particularly of the role of Xpert MTB/RIF Ultra for TB screening, is 282 needed [20,21].

FLOW-TB is an advanced enzyme-linked immunosorbent assay for the detection of *Mtb* lipoarabinomannan (a mycobacterial cell wall component) in urinary specimens with results available within 65 minutes [22].

The T-cell activation marker-TB assay (TAM-TB) detects Mtb-specific CD4 T-cells through *invitro* antigen stimulation with *Mtb*-derived peptides, i.e., from ESAT-6 and CFP-10, followed by flow cytometry. TAM-TB discriminated latent *Mtb* infection from TB in freshly collected blood with 83% sensitivity and 96-98% specificity in previous studies. Further, TAM-TB may detect early TB disease progression up to 9 months prior to the identification of *Mtb* in sputum [23– 25].

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Multiple transcriptomic signatures, capturing the host response to TB, have been described as promising candidate tests for earlier TB diagnosis (up to two years before microbiological diagnosis). An individual patient data meta-analysis suggested equivalent performance of eight signatures, with 25-40% sensitivity and 92-95% specificity 0-24 months before TB diagnosis. Diagnostic accuracy of each signature improved as the interval between testing and microbiological TB diagnosis shortened [26]. Several signatures have been developed into polymerase chain reaction (PCR)-based assays to facilitate real-time implementation: the recent CORTIS trial reported sensitivity of 48% and specificity of 75% for incipient TB for the RISK-11 signature [27]. Cepheid have developed a 3-transcript TB score into a fully automated

in-cartridge PCR assay performed on finger-prick blood using the Xpert platform (Xpert TB
 Host Response RUO Prototype cartridge). This cartridge will be evaluated using freshly
 collected specimens in ERASE-TB; storage of RNA-stabilised blood samples also allows for
 retrospective evaluation of additional transcriptomic signatures in our cohort [28,29]

An alternative approach to capture the host response to TB is through protein-based biomarker signatures. Candidate tests in this category include a serum- or plasma-based multiplex assay assessing 13 protein biomarkers (CRP, procalcitonin[30], sTREM-1[31,32], angiopoietin-2[33,34], interleukin-6[35], TRAIL[36] and IP-10[37]) that is being developed by the London School of Hygiene and Tropical Medicine; in additon, a seven biomarker signauture is under development as a point-of-care test for TB diagnosis, with 94% sensitivity and 73% specificity detected in previous work [38].

<sup>o</sup> 316

### 317 Statistical analyses

Baseline characteristics and analytical data will be summarized using descriptive statistics inclusive of mean, median, range, standard deviation, and absolute as well as relative frequencies depending on the nature of data. A logistic regression model will be used to identify characteristics of TB among ICs, households and HHCs that are predictive of incident TB. From the study database, we will simulate algorithms of different tests to obtain the testing combination with the best accuracy. We will couple tests with a mathematical model that quantifies the risk of infection and/or disease to enhance predictive performance. The reporting of the development of the prediction model will follow the Transparent Reporting of a multivariable prediction model for Individual Prognosis Or Diagnosis (TRIPOD) Initiative [39]. 

The validation of novel diagnostic tests for detecting TB will be analysed as a 1:4 matched nested case-control study with HHCs diagnosed with TB at baseline and during follow-up serving as cases, and HHCs who do not develop TB during follow-up as controls; controls will be matched for site, age, sex, HIV status and other risk factors for developing TB. Sensitivity Page 15 of 29

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and specificity of novel tests will be determined using pre-existing positive/negative cut-offs where these exist [40]; and receiver operating curves (ROC) constructed with area under the ROC curve calculated. For tests aiming to identify individuals at high risk of TB in the future, only HHCs who are diagnosed with TB during follow-up will serve as cases (i.e. those diagnosed with TB at baseline will be excluded). Stored samples from all timepoints will be retrieved and diagnostic accuracy (i.e. sensitivity and specificity) of the novel test determined at different time-points before TB diagnosis. The decision of assigning the "active TB" endpoints to participants will be blinded from the new test results to avoid inclusion bias.

#### Data management

All source data will be kept confidential in secured locations with restricted access by authorized personnel only inclusive of monitors, auditors and reviewers of ethical and regulatory committees in line with applicable data privacy regulations. Each participant is asked to consent to this handling of the data, and is assigned a pseudonymous identification number that is used throughout the study on all source data.

Accurate documentation of paper-based and electronic source data, e.g., original records and certified copies of original records, progress notes, screening logs, and recorded data from automated instruments, will be maintained. The pseudonymized clinical data captured on paper-based Case Report Forms will be entered at the sites into a database using the web-based Clinical Data Management System of OpenClinica (OpenClinica LLC, Waltham, MA, USA). The study specific database has been built, maintained and hosted by the LMU Klinikum on a centralized secure server. Data modifications and necessary corrections performed in the database also within the context of double data entry will be documented and tracked in audit trails. Data quality and plausibility are assured by a series of pre-programmed edit and range checks in OpenClinica. Further validation checks are programmed in Stata (Statacorp, College Station, TX, USA) with extracts of the database and electronically received data, e.g., spirometry, dCXR and laboratory, will be integrated into analyses of datasets.

1		
2 3 4	360	
5 6	361	Monitoring
7 8	362	Assigned study monitors will visit the sites at regular intervals physically and/or virtually in
9 10	363	addition to frequent day-to-day communication. Close follow-up on all study-related aspects
11 12	364	will be performed to ascertain compliance with standards of Good Clinical Practice, the
13 14	365	Declaration of Helsinki, and other local and national regulatory guidelines inclusive of
15 16	366	guidelines for infection prevention and control of airborne-transmitted diseases, e.g., social
17 18	367	distancing in well-ventilated spaces, and wearing of personal protective equipment. In
19 20	368	particular, monitors that support designated study personnel are responsible to verify (I)
21 22	369	adequacy of the study personnels' qualifications and facilities, (II) accuracy of informed
23 24 25	370	consent procedures and patient eligibility, (III) adherence to the study protocol, (IV) protection
26 27	371	of rights and well-being of participants, (V) adherence to infection prevention and control
28 29	372	measures (VI) accuracy and completeness of study documents and other study-related
30 31	373	records, and (VII) maintenance of source documents.
32 33	374	
34 35	375	Ethics and dissemination
36 37	376	The study protocol and informed consent/assent documents have been approved by regulatory
38 39	377	and ethical committees of the participating institutions [Medical Research Council in Zimbabwe
40 41	378	(MRCZ/A/2618), the National Health Research Ethics Committee in Tanzania (TMDA-
42 43	379	WEB0021/CTR/0004/03), the National Bioethics Committee for Health in Mozambique
44 45 46	380	(541/CNBS/21), and the ethical committees of London School of Hygiene & Tropical Medicine,
40 47 48	381	United Kingdom (22522-2), and the medical faculty of the Ludwig-Maximilians-Universität
48 49 50	382	München, Germany (20-0771)].
51	383	

53 Adult ICs and HHCs are asked for written informed consent prior to their participation. 384 54 55 Underage HHCs are asked for assent in addition to obtaining the consent of their legal 385 56 57 386 guardians/parents; with ages for assent depending on local guidance. In case of illiteracy, the 58 59 60 participant is asked to give its consent by fingerprint while an adult impartial, literate witness 387

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present during the entire consent procedure signs the consent on behalf. All participants have the right to withdraw from the study at any time. Findings derived from ERASE-TB will be presented at scientific conferences, and published in peer-reviewed international journals.

#### **Current study status**

The recruitment of ICs and HHCs is in progress in Zimbabwe, Mozambique and Tanzania since March, August and September 2021, respectively. The follow-up of HHCs is anticipated to be completed in March, August and September 2023 in Zimbabwe, Mozambigue and Tanzania, respectively; laboratory analyses are estimated to be performed by December 2024. 

#### **Author contributions**

The study proposal and protocol were written by NH, KK with scientific input from CK, TM, CG, JM. ETM, UP, DB, AM wrote the initial manuscript with scientific input on the database and data management section from FR, TA. NH, KK critically reviewed the initial draft of the manuscript. KH, GK, CJC, ENN, TA, provided critical feedback on the manuscript. All authors have read and approved the final version of the manuscript.

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5 6 7 8 9 10 11 12	417	possible.
	418	
	419	Consortium authorship
	420	The following are members of the ERASE-TB consortium: Anna Shepherd <sup>a</sup> , Hazel M Dockrell <sup>a</sup> ,
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15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39	422	Bandason <sup>c</sup> , Martha Chipinduro <sup>c</sup> , Kuda Mutasa <sup>d</sup> , Sandra Rukobo <sup>d</sup> , Lwitiho Sudi <sup>e</sup> , Antelmo
	423	Haule <sup>e</sup> , Emmanuel Sichone <sup>e</sup> , Paschal Qwaray <sup>e</sup> , Bariki Mtafya <sup>e</sup> , Harrieth Mwambola <sup>e</sup> , Lilian
	424	Minja <sup>e</sup> , Issa Sabi <sup>e</sup> , Peter Edwin <sup>e</sup> , Dogo Ngalison <sup>e</sup> , Stella Luswema <sup>e</sup> , Willyhelmina Olomi <sup>e</sup> ,
	425	Doreen Pamba <sup>e</sup> , Simeon Mwanyonga <sup>e</sup> , Celina Nhamuave <sup>f</sup> , António Machiana <sup>f</sup> , Carla Madeira <sup>f</sup> ,
	426	Emelva Manhiça <sup>f</sup> , Nádia Sitoe <sup>f</sup> , Jorge Ribeiro <sup>f</sup> , Christof Geldmacher <sup>g</sup> , Andrea Rachow <sup>g</sup> , Olena
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49 50	438	
51 52	439	Competing interests statement
53 54 55 56	440	None declaired.
	441	
57 58	442	Disclaimer
59 60	443	Not applicable.

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1 2		
2 3 4	584	Figure legend
5 6 7 8 9 10	585	Figure 1. The ERASE-TB consortium
	586	Abbreviations: ERASE-TB=Early Risk Assessment in TB contactS by new diagnostic tEsts
	587	
11 12	588	Figure 2. Location and characteristics of ERASE-TB study sites
13 14	589	Notes: The location of each study site is indicated by a red asterix. Source data used within
15 16	590	this figure are taken from the references [7,8,42,43,9–15,41].
17 18	591	Abbreviations: ERASE=Early Risk Assessment in TB contactS by new diagnostic tEsts;
19 20 21	592	TB=tuberculosis; HIV=human immunodeficiency virus
21 22 23	593	
24 25	594	Figure 3. Eligibility criteria and schedules of events for index cases and household contacts
26 27	595	Notes: A=depending on the time point of study enrollment and consequently on the duration
28 29	596	available for follow-up, i.e. 18 or 24 months, the follow-up visit at 24 months $\pm 30$ days may be
30 31 32 33	597	conditional; <b>B</b> =the follow-up visit by phone may be conducted after the last scheduled follow-
	598	up visit at 18 months $\pm 30$ days or 24 months $\pm 30$ days to assess whether symptoms suggestive
34 35	599	of TB have occurred, TB diagnosis has been made or anti-TB treatment has been initiated;
36 37	600	C=unwell visits by phone or on-site may be conducted between scheduled follow-up visits if a
38 39 40	601	participant presents at a recruitment healthcare facility with signs and symptoms suggestive of
41 42	602	TB; <b>D</b> =coached spontaneous or induced sputum collection for storage at scheduled follow-up
43 44	603	visit at 18 months $\pm$ 30 days or 24 months $\pm$ 30 days, and for repetition of HIV testing if tested
45 46	604	negative at baseline; E=coached spontaneous or induced sputum collection upon the decision
47 48	605	of the investigating team for testing by Xpert MTB/RIF Ultra if participant presents with signs
49 50	606	and symptoms suggestive of TB; F=coached spontaneous or induced sputum collection in
51 52	607	case of Xpert MTB/RIF Ultra positivity or strong clinical suspicion of TB for repetition of the
53 54	608	Xpert MTB/RIF Ultra; $G=$ in case of HIV positivity to be followed by the assessment of CD4
55 56 57	609	counts; H=CXR to be conducted at an unscheduled on-site unwell visit upon the decision of
58 59	610	the investigating team depending on the nature of symptoms reported, and the time elapsed
60	611	since the last CXR including its findings; I=not to be conducted among pregnant women;

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J=stored venous blood includes 6mL EDTA blood for whole blood and plasma, 4mL serum and 2.5mL PAXgene blood, all samples will be deep frozen for retrospective testing using new diagnostics as described in text; **K**=in case the evaluation of symptoms of a participant unable to present at a recruitment healthcare facility is required an unscheduled on-site or home visit will be arranged by phone, the resolution of symptoms can alternatively be addressed by phone; L=collection of PBMC at baseline and follow-up visit at 6 months ±30 days is optional, thus will not be performed at each participating site and for each participant; **M**=in case the evaluation of symptoms of a participant unable to present at a recruitment healthcare facility is required or doubtful if required an unscheduled unwell visit by phone will be arranged, the resolution of symptoms can alternatively be addressed by phone; N=spirometry and/or diabetes (HbA1c) will be performed at scheduled follow-up visits at 6 months ±30 days, 12 months ±30 days and 18 or 24 months ±30 days if required or not performed at baseline, anaemia (Hb) will be performed at baseline and scheduled follow-up visits at 6 months ±30 days, 12 months ±30 days and 18 or 24 months ±30 days if possible; **O**=blood pressure measurement will be performed at baseline and scheduled follow-up visits at 6 months ±30 days, 12 months ±30 days and 18 or 24 months ±30 days; P=WGS to be performed once Mtb infection is confirmed and an isolate could be recovered.

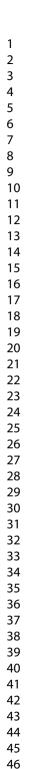
Abbreviations: TB=tuberculosis; WHO=World Health Organization; HIV=human immunodeficiency virus; WGS=whole genome sequencing; MBLA=molecular bacterial load assay; CXR=chest radiograph; IGRA=interferon gamma release assay; PBMC=peripheral blood mononuclear cell; TAM-TB=T- cell activation marker tuberculosis; MTB=Mycobacterium tuberculosis; RIF=rifampicin, Hb=haemoglobin; HbA1c=glycated hemoglobin; LAM=lioparabinomannan; CD4=cluster of differentiation 4

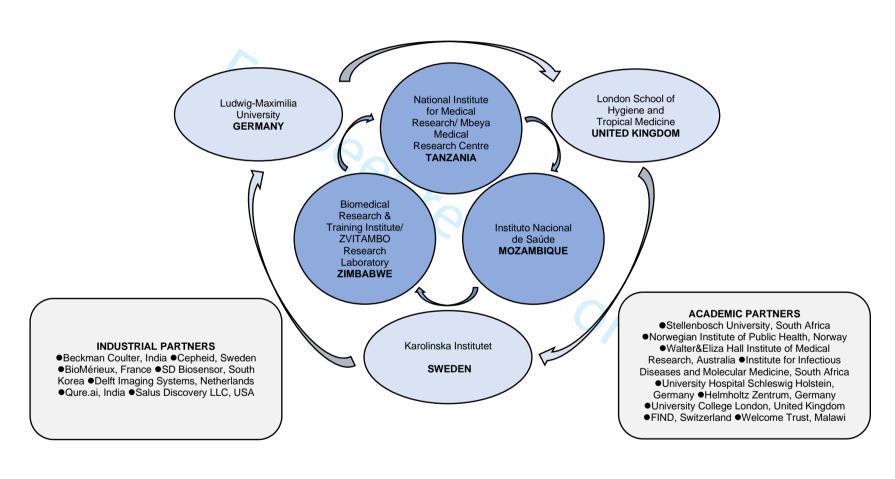
Figure 4. Study design

Abbreviations: HHC=household contact; TB=tuberculosis; IC=index case; WHO=World

Health Organization; CXR= chest radiograph; SS=symptom score; MTB=Mycobacterium

tuberculosis; RIF=rifampicin; pos=positive; CT=cpmputer tomography; FU=follow-up







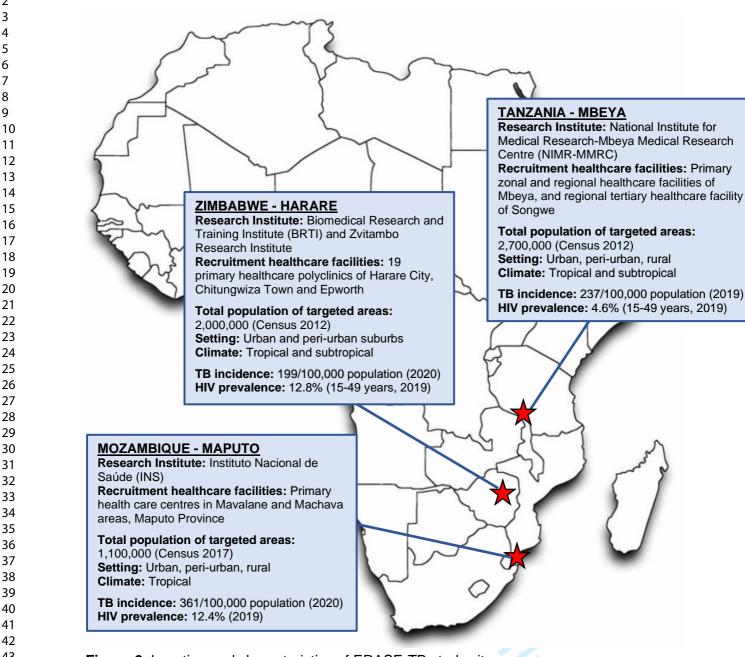
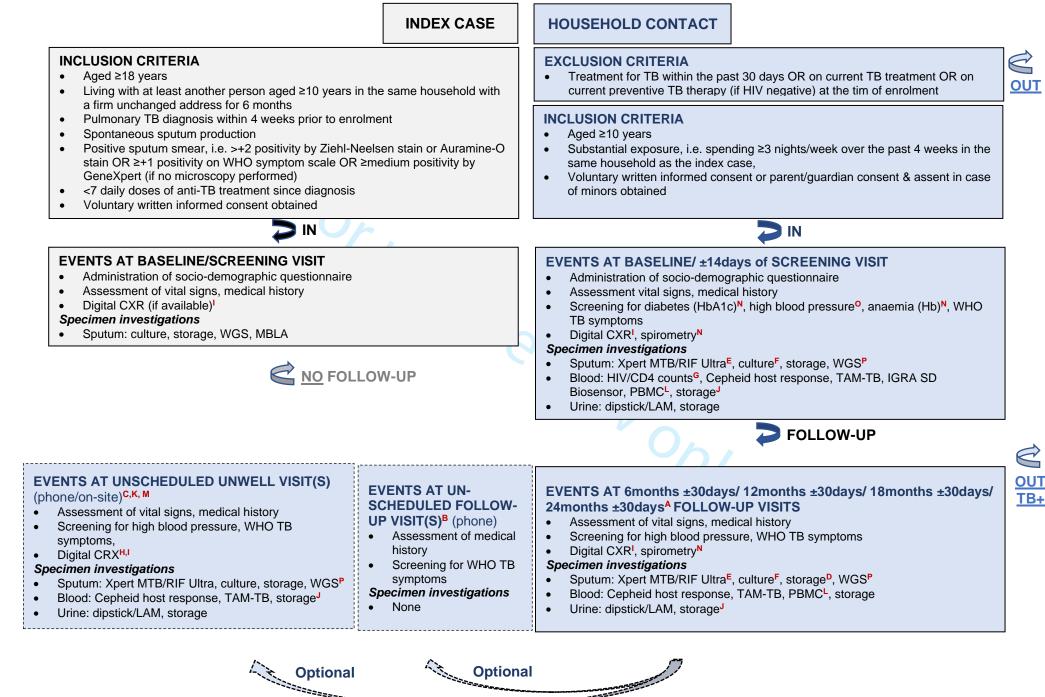


Figure 2. Location and characteristics of ERASE-TB study sites

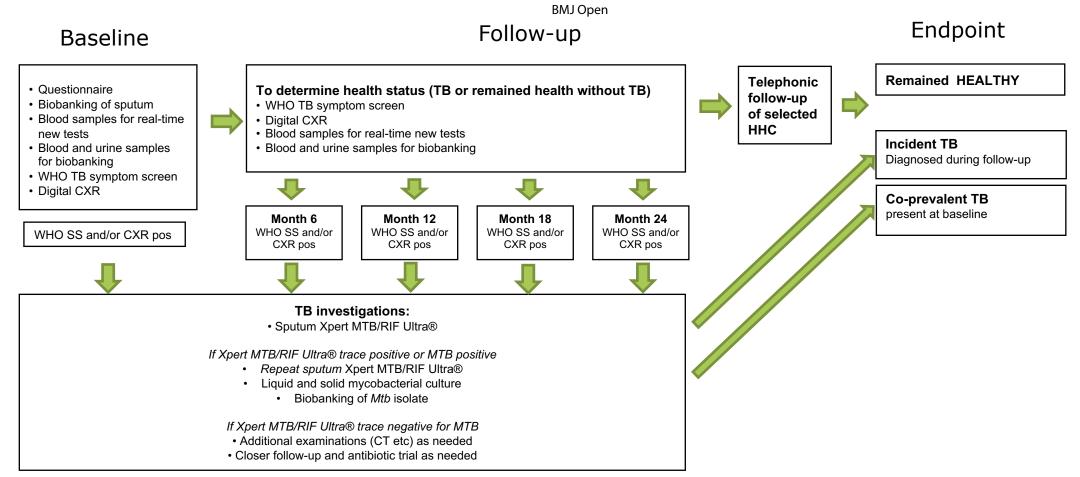


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Figure 3. Eligibility criteria and schedules of events for index cases and household contacts

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Section & Topic	No	Item	Reported on p #
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		(such as sensitivity, specificity, predictive values, or AUC)	
ABSTRACT			
	2	Structured summary of study design, methods, results, and conclusions	2-3
		(for specific guidance, see STARD for Abstracts)	
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	3	Scientific and clinical background, including the intended use and clinical role of the index test	5-6
	4	Study objectives and hypotheses	6
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	7	On what basis potentially eligible participants were identified	7 (Figure 3)
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	11	Rationale for choosing the reference standard (if alternatives exist)	8-10, 11-13
	12a	Definition of and rationale for test positivity cut-offs or result categories	13-14
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	12b	Definition of and rationale for test positivity cut-offs or result categories	13-14
		of the reference standard, distinguishing pre-specified from exploratory	
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		to the performers/readers of the index test	
	13b	Whether clinical information and index test results were available	13-14
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	15	How indeterminate index test or reference standard results were handled	13-14
	16	How missing data on the index test and reference standard were handled	14
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	18	Intended sample size and how it was determined	11
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	20	Baseline demographic and clinical characteristics of participants	8-10 (Figure 3)
	<b>2</b> 1a	Distribution of severity of disease in those with the target condition	
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	22	Time interval and any clinical interventions between index test and reference standard	
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	-	by the results of the reference standard	
	24	Estimates of diagnostic accuracy and their precision (such as 95% confidence intervals)	13-14
	25	Any adverse events from performing the index test or the reference standard	
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	26	Study limitations, including sources of potential bias, statistical uncertainty, and	3
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	27	Implications for practice, including the intended use and clinical role of the index test	5-6
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	20 29	Where the full study protocol can be accessed	
	30	Sources of funding and other support; role of funders	16
		For peer review only - http://bmjopen.bmj.com/site/about/guidelines.xhtml	



## STARD 2015

### AIM

STARD stands for "Standards for Reporting Diagnostic accuracy studies". This list of items was developed to contribute to the completeness and transparency of reporting of diagnostic accuracy studies. Authors can use the list to write informative study reports. Editors and peer-reviewers can use it to evaluate whether the information has been included in manuscripts submitted for publication.

### EXPLANATION

A **diagnostic accuracy study** evaluates the ability of one or more medical tests to correctly classify study participants as having a **target condition.** This can be a disease, a disease stage, response or benefit from therapy, or an event or condition in the future. A medical test can be an imaging procedure, a laboratory test, elements from history and physical examination, a combination of these, or any other method for collecting information about the current health status of a patient.

The test whose accuracy is evaluated is called **index test.** A study can evaluate the accuracy of one or more index tests. Evaluating the ability of a medical test to correctly classify patients is typically done by comparing the distribution of the index test results with those of the **reference standard**. The reference standard is the best available method for establishing the presence or absence of the target condition. An accuracy study can rely on one or more reference standards.

If test results are categorized as either positive or negative, the cross-tabulation of the index test results against those of the reference standard can be used to estimate the **sensitivity** of the index test (the proportion of participants *with* the target condition who have a positive index test), and its **specificity** (the proportion *without* the target condition who have a negative index test). From this cross-tabulation (sometimes referred to as the contingency or "2x2" table), several other accuracy statistics can be estimated, such as the positive and negative **predictive values** of the test. Confidence intervals around estimates of accuracy can then be calculated to quantify the statistical **precision** of the measurements.

If the index test results can take more than two values, categorization of test results as positive or negative requires a **test positivity cut-off**. When multiple such cut-offs can be defined, authors can report a receiver operating characteristic (ROC) curve which graphically represents the combination of sensitivity and specificity for each possible test positivity cut-off. The **area under the ROC curve** informs in a single numerical value about the overall diagnostic accuracy of the index test.

The **intended use** of a medical test can be diagnosis, screening, staging, monitoring, surveillance, prediction or prognosis. The **clinical role** of a test explains its position relative to existing tests in the clinical pathway. A replacement test, for example, replaces an existing test. A triage test is used before an existing test; an add-on test is used after an existing test.

Besides diagnostic accuracy, several other outcomes and statistics may be relevant in the evaluation of medical tests. Medical tests can also be used to classify patients for purposes other than diagnosis, such as staging or prognosis. The STARD list was not explicitly developed for these other outcomes, statistics, and study types, although most STARD items would still apply.

### DEVELOPMENT

This STARD list was released in 2015. The 30 items were identified by an international expert group of methodologists, researchers, and editors. The guiding principle in the development of STARD was to select items that, when reported, would help readers to judge the potential for bias in the study, to appraise the applicability of the study findings and the validity of conclusions and recommendations. The list represents an update of the first version, which was published in 2003.

More information can be found on <u>http://www.equator-network.org/reporting-guidelines/stard.</u>



# **BMJ Open**

### Early risk assessment in pediatric and adult household contacts of confirmed tuberculosis cases by novel diagnostic tests (ERASE-TB): protocol for a prospective, non-interventional, longitudinal, multi-country cohort study

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3 4	1	Early risk assessment in pediatric and adult household contacts of confirmed
5 6 7	2	tuberculosis cases by novel diagnostic tests (ERASE-TB): protocol for a
7 8 9	3	prospective, non-interventional, longitudinal, multi-country cohort study
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11 12 13 14 15 16 17	5	Edson Tawanda Marambire1*, Denise Banze2\$, Alfred Mfinanga3\$, Junior Mutsvangwa1, Theodora
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18	8	Heinrich <sup>6,7#</sup> , Katharina Kranzer <sup>1,5,6#</sup> , on behalf of the ERASE-TB Consortium
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44 45	22	
46 47	23	\$ Contributed equally
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50 51	25	
52 53	26	Word count: 3,668
54 55	27	
56 57	28	Keywords: Mycobacterium tuberculosis, diagnostics, cohort study, household contacts, WHO
58 59 60	29	END TB strategy, ERASE-TB

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#### 30 ABSTRACT

#### 31 Introduction

The World Health Organization (WHO) End-TB Strategy calls for the development of novel 32 33 diagnostics to detect tuberculosis earlier and more accurately. Better diagnostics, together with tools to predict disease progression are critical for achieving WHO END-TB targets. The Early 34 Risk Assessment in TB contactS by new diagnostic tEsts (ERASE-TB) study aims to evaluate 35 novel diagnostics and testing algorithms for early tuberculosis diagnosis and accurate 36 37 prediction of disease progression among household contacts exposed to confirmed index cases in Mozambigue, Tanzania and Zimbabwe. 38

39

#### Methods and analysis 40

A total of 2,100 household contacts (HHCs) (aged ≥10 years) of adults with microbiologically-41 42 confirmed pulmonary tuberculosis will be recruited and followed up at 6-month intervals for 18 to 24 months. At each time-point a WHO symptom screen and digital chest-radiograph (dCXR) 43 will be performed, and blood and urine samples collected. Individuals screening positive (WHO 44 45 symptom screen or dCXR) will be requested to provide sputum for Xpert MTB/Rif Ultra. At baseline, HHCs will also be screened for HIV, diabetes (HbA1c), chronic lung disease 46 (spirometry), hypertension and anaemia. Study outcomes will be co-prevalent tuberculosis 47 (diagnosed at enrollment), incident tuberculosis (diagnosed during follow-up) or no 48 49 tuberculosis at completion of follow up. Novel diagnostics will be validated using fresh and 50 biobanked samples with a nested case control design. Cases are defined as HHCs diagnosed with tuberculosis (for early diagnosis) or with incident tuberculosis (for prediction of 51 progression) and will be matched by age, sex and country to HHCs who remain healthy 52 53 (controls). Statistical analyses will include assessment of diagnostic accuracy by constructing 54 receiver operating curves and calculation of sensitivity and specificity.

55

#### Ethics and dissemination 56

ERASE-TB has been approved by regulatory and ethical committees in each African country and by each partner organisation. Consent, with additional assent for participants <18 years, is voluntary. Attestation by impartial witnesses is sought in case of illiteracy. Confidentiality of <text> participants is being maintained throughout. Study findings will be presented at scientific conferences and published in peer-reviewed international journals.

#### Study registration number

NCT04781257 

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1 ว		
2 3 4	65	Strengths and limitations of this study
5	66	• Recruitment of highly infectious index cases aimed at maximising the number of
7 8	67	tuberculosis (TB) diagnoses in the household contact (HHCs) cohort.
9 10	68	• Sequencing of Mycobacterium tuberculosis isolates from both index cases and HHCs
11 12	69	allows confirmation of household transmission and thus determination of timing of the
13 14	70	transmission event; resulting in more precise estimates of new test sensitivity
15 16 17	71	compared to population-based cohorts with unknown timing of infection.
17 18 19	72	• Large sample size across three southern African countries with high HIV prevalence;
20 21	73	including adolescents will ensure study findings are generalisable to the clinically
22 23	74	relevant population at high risk of TB compared to studies focused on adults only.
24 25	75	• Despite the large cohort of HHCs, the number of diagnosed TB cases will be small,
26 27	76	limiting the power of the study and sub-group analyses such as by age and HIV status.
28 29	77	Geographically limited to sub-Saharan Africa, therefore results may not be
30 31	78	generalisable to other populations, including those with lower HIV prevalence such as
32 33	79	in South-East Asia or the Americas.
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### 80 INTRODUCTION

Tuberculosis (TB) remains a leading global public health problem, with an estimated 10 million new cases and 1.5 million deaths globally in 2020 [1]. In 2014, the World Health Assembly approved the World Health Organization (WHO) End-TB Strategy, aiming for a 90% reduction in TB incidence and 95% reduction in TB deaths by 2035 [2]. However, in 2019, three million TB cases ('the missing millions') remained undiagnosed and untreated globally, resulting in potentially avoidable morbidity, mortality and onward transmission. The Covid-19 pandemic has resulted in a large decrease in the number of people newly diagnosed with TB and reported. This has increased the diagnostic gap by a further 1.3 million, resulting in an estimated 4.2 million undiagnosed TB cases in 2020 [3]. Also, for the first time in a decade TB deaths have risen, from an estimated 1.4 million in 2019 to 1.5 million in 2020, as a result of reduced access to and provision of essential TB services including diagnostics during the Covid-19 pandemic.

94 Without an efficacious and safe vaccine, early detection and containment are the main tools 95 to interrupt transmission and successfully control TB. Similar to SARS-CoV2, asymptomatic 96 spreading of *M.tuberculosis* and subclinical but infectious disease states are a major concern 97 in the control of airborne infectious diseases [4]. Early and accurate identification of persons 98 with TB, combined with identification of those at risk of progression to TB and provision of 99 targeted preventive treatment are critical to reducing TB-associated morbidity and mortality, 100 and preventing onward transmission.

102 Currently available diagnostics such as sputum microscopy, mycobacterial culture and nucleic 103 acid amplification tests are based on direct pathogen detection, thus requiring a high 104 mycobacterial load; they therefore predominately target advanced TB when onward 105 transmission and significant lung damage has occurred [5,6]. Further, for many patients with 106 minimal or no symptoms, expectoration of high-quality sputum specimens remains

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challenging, limiting the accuracy of sputum-based tests. The same holds true for young children and people living with HIV.

The Early Risk Assessment in TB Contacts by new diagnoStic tEsts (ERASE-TB) study aims to fill this diagnostic gap by evaluating new sputum and non-sputum-based TB diagnostics for early TB detection (before onward transmission occurs), as well as tools for more accurate prediction of TB progression to allow for targeted preventive therapy. 

- METHODS AND ANALYSES

#### Study objectives

ERASE-TB's primary objectives are (I) to determine the sensitivity and specificity of novel diagnostics to detect TB, in particular asymptomatic or minimally symptomatic TB; (II) to evaluate novel diagnostics for detection of likely TB progression; and (III) to enhance the performance of novel diagnostics by simulating testing algorithms coupled with individual risk estimates from a mathematical model. The secondary objectives are (I) to determine the TB prevalence among household contacts (HHCs) of infectious TB index cases (ICs) at baseline and during a 18-24 months follow-up; (II) to establish a biorepository of cryopreserved specimens from HHCs for future development and validation of diagnostic tests; and (III) to assess the association of selected chronic disease conditions and TB among HHCs.

#### **Study endpoints**

The study's primary endpoints are the presence or development of TB among HHCs with the following possible scenarios of (I) prevalent symptomatic TB at baseline, (II) incident TB during follow-up, and (III) remained healthy until study completion. An endpoint review committee will review the data and case classification before finalization.

Through the sequencing of Mycobacterium tuberculosis (Mtb) isolates, cases of co-prevalent or incident TB will be classified either as secondary, infected by the source case - the timepoint 

of infection will be known; or as infected by another, unknown source of infection, with anunknown timepoint of infection.

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### 138 Recruitment sites

Recruitment of ICs and HHCs at selected primary healthcare facilities and communities has commenced in Harare, Zimbabwe in March 2021, Maputo, Mozambigue in August 2021, and Mbeya, Tanzania in September 2021. Partners of the ERASE-TB consortium are illustrated in Figure 1. All three countries have a high TB incidence ranging from 100 to 499/100,000 population [1] and HIV prevalence among adults aged 15 years and older of 5% to 20% [7]. The African research institutions have established collaborations with their respective National Tuberculosis Programs ensuring referral and approproate follow-up of TB patients. Figure 2 illustrates the geographic location of research institutions, healthcare facilities where recruitment is taking place, demographic characteristics of study populations, and estimates on TB incidence and HIV prevalence [8–15]. 

### 150 Study design

ERASE-TB is a non-interventional, longitudinal, prospective cohort study among HHCs aged ≥10 years exposed to highly infectious pulmonary TB ICs aged ≥18 years. Eligibility criteria are detailed in Figure 3 and the study design is shown in Figure 4. TB ICs are eligible if the bacterial load in their sputum is at least at the "medium" level according to Xpert MTB/RIF or Xpert MTB/RIF Ultra, and they have received less than seven daily doses of anti-TB treatment before enrollment. This maximises the likelihood of culturing and storing *Mtb* isolates. The total study duration will be 36 months. This includes 12-months enrollment of ICs and HHCs, and 18- to 24-months follow-ups of HHCs. Follow-up ends when a HHCs withdraws from the study, is lost to follow-up, dies, or is diagnosed with TB and referred for treatment. Scheduled or unscheduled unwell visits can be conducted physically and/or telephonically in case of abnormal finding e.g. by abnormal dCXR, or when a participant feels unwell inbetween scheduled follow-up visits.

2		
3 4	163	
5 6	164	Procedures
7 8	165	TB index cases
9 10	166	Following informed consent obtained, a questionnaire is administered to collect socio-
11 12	167	demographic information, TB risk factors, and the medical history of TB, HIV and other
13 14	168	diseases. Two spontaneous sputum samples are obtained, of which one is for mycobacterial
15 16	169	culturing and one for storage for performing retrospectively Molecular Bacterial Load Assay
17 18	170	(MBLA) to quantify viable Mtb by 16S rRNA [6]; an alternative means to quantify expectorated
19 20	171	bacterial load for an estimate of infectiousness. Both liquid and solid mycobacterial cultures
21 22	172	are performed on decontaminated sputum samples, with all Mtb isolates stored at -80 degrees
23 24 25	173	for future DNA extraction and whole genome sequencing. A questionnaire on symptom
25 26 27	174	duration and TB risk factors is also administered.
28 29	175	
30 31	176	Household key informant
32 33	177	At baseline, a household key informant (either the TB index case or one of the household
34 35	178	contacts) is identified and asked to answer questions of a household questionnaire that collects
36 37	179	socio-economic elements like structure of the house or flat, income and household assets, and
38 39	180	covariates possibly associated with risk of TB infection, e.g., windows/air exchange, presence
40 41	181	of comorbid conditions, and risk factors like the source of cooking energy, and properties of
42 43 44	182	the household kitchen.
44 45 46	183	
40 47 48	184	Household contacts
49 50	185	Informed consent is obtained from all eligible adult HHCs. For HHC <18 years of age, the
51 52	186	guardian is asked to provide informed consent, with assent also sought from children
53 54	187	dependent on local guidance. At baseline a questionnaire is administered collecting
55 56	188	information on socioeconomic and demographic characteristics, past medical history of TB,
57 58	189	HIV and other diseases, exposure risk factors, smoking and alcohol history. The physical
59 60	190	examination includes height, weight, mid-upper arm circumference and blood pressure

measurement. In addition, all HHCs are offered free HIV testing according to the National
Guidelines. All people with confirmed HIV infection will have CD4 counts performed and be
referred for TB preventive therapy. Those not yet on antiretroviral therapy (ART) and those
who interrupted ART are referred for ART at local services.

Point of care HbA1c (A1cCare, SD Biosensor, Gyeonggi-do, Republic of Korea) and haemoglobin (Hemocue 301+, Hemocue, Angelholm, Sweden) tests and spirometry (including pre- and post-bronchodilation with inhaled salbutamol) are performed at baseline or the sixmonth visit. HHCs who did not take up HIV testing or other screening at baseline are offered these tests at each study visit. Any HHCs with test results requiring treatment or further investigations are referred for respective services.

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HHCs are screened for TB using the WHO symptom questionnaire and a digital chestradiograph (dCXR), reviewed by a clinical officer. dCXRs are not performed in pregnant HHCs.
HHCs with a positive WHO symptom screening and abnormal dCXR are asked to provide
sputum samples for TB investigations i.e., for GeneXpert and mycobacterial culture. Those
with negative symptom screen and normal dCXR are asked to provide a spontaneous sputum
sample for storage (with sputum induction performed if required).

41 209

At baseline, urine, serum, plasma, whole blood (native, and with RNA preservation in PAXgene<sup>®</sup> tubes [BD Biosciences, NJ, USA]) are stored. A finger-prick sample is taken and investigated using the Xpert TB Host Response RUO Prototype cartridge (Cepheid, Sunnyvale, CA, USA). T-cell Activation Marker Tuberculosis (TAM-TB) assay and Interferon Gamma Release Assay (IGRA; STANDARDTM F TB-Feron FIA (IFN-gamma; SD Biosensor, Republic of Korea), are performed on fresh venous blood. In Tanzania and Mozambigue, storage of peripheral blood mononuclear cells for later characterization of the TB-specific immune response is also performed. 

Procedures for follow-up and unwell visits are similar to those at baseline. Measurement of HIV status, haemoglobin, HbA1c, spirometry, CD4 count and IGRA testing are not performed at follow-up visits, unless not done previously. At the last scheduled visit all HHCs not known to have HIV are re-offered HIV testing and a spontaneous or induced sputum sample is stored for all participants.

### Household contacts screening positive for TB symptoms and/or with a DCXR suggestive of TB

HHCs screening positive for symptoms and/or those with DCXRs suggestive of TB are asked for a sputum sample, which is investigated using Xpert MTB/RIF Ultra (Cepheid). If this sample is positive for *Mtb* (including a trace result), a minimum of two additional sputum samples are investigated, following decontamination, with Xpert MTB/RIF Ultra, solid and liquid culture. Isolates stored from these cultures will be sequenced for matching with the IC isolates in order to verify intra-household transmission. Sputum induction is performed for those unable to provide a spontaneous sputum sample. HHCs with microbiologically confirmed TB are referred for TB treatment to the National TB Programme.

#### Patient and public involvement

The ERASE-TB study sites have established Community Advisory Boards, which are voices of communities, people affected, and study participants, providing a strategic link between the communities and the study team. Community Advisory Boards meet regularly and provide feedback on design, procedures and conduct of the study. They will also be closely involved in the dissemination of study results. In addition to the Community Advisory Boards, each study site conducts community engagement activities focused on young people with the aim to foster interst in science and research, specififcally in the field of respiratory diseases/illness. This includes close partnership with schools and universities. Furthermore, planned qualitative research will specifically aim to understand the perceptions of HHCs with regards to TB diagnostics and screening.

1 2		
2 3 4	247	
5 6	248	Sample size
7 8 9 10	249	An estimated 800 to 900 TB-confirmed ICs are required for the subsequent enrollment of an
	250	anticipated 2,100 HHCs, i.e., 700 HHCs per country. Loss to follow-up of HHCs is estimated
11 12	251	to be 10%. A total of 64 HHCs (3%) are estimated to be diagnosed with TB during the study
13 14	252	period, based on previous active case finding studies among HHCs [16]. Validation for
15 16	253	subclinical and early TB will include incident (n=49) and co-prevalent TB cases (n=15).
17 18	254	Validation for detection of incipient <i>M.tb</i> infection will include samples of participants with
19 20	255	incident TB (n=49) matched 1:4 to samples of participants without TB (n=196). For tests
21 22 23	256	diagnosing incipient <i>M.tb</i> infection sensitivities of 73% and 82% would be detected with a
23 24 25	257	precision of 59-85% and 68-91% respectively. For specifcities of 92% and 94% the confidence
26 27	258	intervals would be 87-95% and 90-97%.
28 29	259	
30 31	260	Novel test candidates
32 33	261	A range of novel test candidates targeted at pathogen detection or identification of host
34 35	262	responses to Mtb are being applied, either in real-time (for all participants) or retrospectively
36 37	263	(in a case-control design). Whilst a number of novel test candidates have been pre-specified,
38 39 40	264	the ERASE-TB biobanking processes allow for addition of further candidate tests to be
40 41 42	265	evaluated on stored samples as they become available.
43 44	266	
45 46	267	DCXRs offer good sensitivity for diagnosis of pulmonary TB. However, high inter- and intra-
47 48	268	investigator variability, and lack of trained interpreters present a barrier to implementation in
49 50	269	many high-TB burden settings. Computer-aided interpretation systems, such as CAD4TB
51 52	270	(Delft Imaging, Hertogenbosch, Netherlands) and qXR (Qure.ai, India) may increase image-
53 54	271	reading capacity, with good performance, and serve, therefore, as a systematic screening tool
55 56 57	272	to identify individuals in need of confirmatory TB tests [17,18].
57 58 59 60	273	

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274 Xpert MTB/RIF Ultra is a nucleic acid amplification test for *Mtb* with a lower limit of detection 275 compared to the previous Xpert MTB/RIF generation, and, therefore, conferring higher 276 sensitivity in paucibacillary specimens. This, however, comes at the expense of specificity, 277 particularly in high TB incidence settings, resulting in 'false positives' [19]. WHO guidelines 278 recommend Xpert MTB/RIF Ultra for TB diagnosis among adults and children acknowledging 279 that further evaluation, particularly of the role of Xpert MTB/RIF Ultra for TB screening, is 280 needed [20,21].

FLOW-TB is an advanced enzyme-linked immunosorbent assay for the detection of *Mtb* lipoarabinomannan (a mycobacterial cell wall component) in urinary specimens with results available within 65 minutes [22].

The T-cell activation marker-TB assay (TAM-TB) detects Mtb-specific CD4 T-cells through *invitro* antigen stimulation with *Mtb*-derived peptides, i.e., from ESAT-6 and CFP-10, followed by flow cytometry. TAM-TB discriminated latent *Mtb* infection from TB in freshly collected blood with 83% sensitivity and 96-98% specificity in previous studies. Further, TAM-TB may detect early TB disease progression up to 9 months prior to the identification of *Mtb* in sputum [23– 25].

Multiple transcriptomic signatures, capturing the host response to TB, have been described as promising candidate tests for earlier TB diagnosis (up to two years before microbiological diagnosis). An individual patient data meta-analysis suggested equivalent performance of eight signatures, with 25-40% sensitivity and 92-95% specificity 0-24 months before TB diagnosis. Diagnostic accuracy of each signature improved as the interval between testing and microbiological TB diagnosis shortened [26]. Several signatures have been developed into polymerase chain reaction (PCR)-based assays to facilitate real-time implementation: the recent CORTIS trial reported sensitivity of 48% and specificity of 75% for incipient TB for the RISK-11 signature [27]. Cepheid have developed a 3-transcript TB score into a fully automated

in-cartridge PCR assay performed on finger-prick blood using the Xpert platform (Xpert TB
 Host Response RUO Prototype cartridge). This cartridge will be evaluated using freshly
 collected specimens in ERASE-TB; storage of RNA-stabilised blood samples also allows for
 retrospective evaluation of additional transcriptomic signatures in our cohort [28,29]

An alternative approach to capture the host response to TB is through protein-based biomarker signatures. Candidate tests in this category include a serum- or plasma-based multiplex assay assessing 13 protein biomarkers (CRP, procalcitonin [30], sTREM-1 [31,32], angiopoietin-2 [33,34], interleukin-6 [35], TRAIL [36] and IP-10 [37]) that is being developed by the London School of Hygiene and Tropical Medicine; in additon, a seven biomarker signauture is under development as a point-of-care test for TB diagnosis, with 94% sensitivity and 73% specificity detected in previous work [38].

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## 315 Statistical analyses

Baseline characteristics and analytical data will be summarized using descriptive statistics inclusive of mean, median, range, standard deviation, and absolute as well as relative frequencies depending on the nature of data. A logistic regression model will be used to identify characteristics of TB among ICs, households and HHCs that are predictive of incident TB. From the study database, we will simulate algorithms of different tests to obtain the testing combination with the best accuracy. We will couple tests with a mathematical model that quantifies the risk of infection and/or disease to enhance predictive performance. The reporting of the development of the prediction model will follow the Transparent Reporting of a multivariable prediction model for Individual Prognosis Or Diagnosis (TRIPOD) Initiative [39]. 

The validation of novel diagnostic tests for detecting TB will be analysed as a 1:4 matched nested case-control study with HHCs diagnosed with TB at baseline and during follow-up serving as cases, and HHCs who do not develop TB during follow-up as controls; controls will be matched for site, age, sex, HIV status and other risk factors for developing TB. Sensitivity Page 15 of 29

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and specificity of novel tests will be determined using pre-existing positive/negative cut-offs where these exist [40]; and receiver operating curves (ROC) constructed with area under the ROC curve calculated. For tests aiming to identify individuals at high risk of TB in the future, only HHCs who are diagnosed with TB during follow-up will serve as cases (i.e. those diagnosed with TB at baseline will be excluded). Stored samples from all timepoints will be retrieved and diagnostic accuracy (i.e. sensitivity and specificity) of the novel test determined at different time-points before TB diagnosis. The decision of assigning the "active TB" endpoints to participants will be blinded from the new test results to avoid inclusion bias.

#### Data management

All source data will be kept confidential in secured locations with restricted access by authorized personnel only inclusive of monitors, auditors and reviewers of ethical and regulatory committees in line with applicable data privacy regulations. Each participant is asked to consent to this handling of the data, and is assigned a pseudonymous identification number that is used throughout the study on all source data.

Accurate documentation of paper-based and electronic source data, e.g., original records and certified copies of original records, progress notes, screening logs, and recorded data from automated instruments, will be maintained. The pseudonymized clinical data captured on paper-based Case Report Forms will be entered at the sites into a database using the web-based Clinical Data Management System of OpenClinica (OpenClinica LLC, Waltham, MA, USA). The study specific database has been built, maintained and hosted by the LMU Klinikum on a centralized secure server. Data modifications and necessary corrections performed in the database also within the context of double data entry will be documented and tracked in audit trails. Data quality and plausibility are assured by a series of pre-programmed edit and range checks in OpenClinica. Further validation checks are programmed in Stata (Statacorp, College Station, TX, USA) with extracts of the database and electronically received data, e.g., spirometry, dCXR and laboratory, will be integrated into analyses of datasets.

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3 4	358	
5 6	359	Monitoring
7 8	360	Assigned study monitors will visit the sites at regular intervals physically and/or virtually in
9 10	361	addition to frequent day-to-day communication. Close follow-up on all study-related aspects
11 12	362	will be performed to ascertain compliance with standards of Good Clinical Practice, the
13 14	363	Declaration of Helsinki, and other local and national regulatory guidelines inclusive of
15 16	364	guidelines for infection prevention and control of airborne-transmitted diseases, e.g., social
17 18	365	distancing in well-ventilated spaces, and wearing of personal protective equipment. In
19 20 21	366	particular, monitors that support designated study personnel are responsible to verify (I)
21 22 23	367	adequacy of the study personnels' qualifications and facilities, (II) accuracy of informed
24 25	368	consent procedures and patient eligibility, (III) adherence to the study protocol, (IV) protection
26 27	369	of rights and well-being of participants, (V) adherence to infection prevention and control
28 29	370	measures (VI) accuracy and completeness of study documents and other study-related
30 31	371	records, and (VII) maintenance of source documents.
32 33	372	
34 35	373	Ethics and dissemination
36 37	374	The study protocol and informed consent/assent documents have been approved by regulatory
38 39 40	375	and ethical committees of the participating institutions [Medical Research Council in Zimbabwe
40 41 42	376	(MRCZ/A/2618), the National Health Research Ethics Committee in Tanzania (TMDA-
43 44	377	WEB0021/CTR/0004/03), the National Bioethics Committee for Health in Mozambique
45 46	378	(541/CNBS/21), and the ethical committees of London School of Hygiene & Tropical Medicine,
47 48	379	United Kingdom (22522-2), and the medical faculty of the Ludwig-Maximilians-Universität
49 50	380	München, Germany (20-0771)].
51 52	381	

Adult ICs and HHCs are asked for written informed consent prior to their participation. Underage HHCs are asked for assent in addition to obtaining the consent of their legal guardians/parents; with ages for assent depending on local guidance. In case of illiteracy, the participant is asked to give its consent by fingerprint while an adult impartial, literate witness 

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present during the entire consent procedure signs the consent on behalf. All participants have the right to withdraw from the study at any time. Findings derived from ERASE-TB will be presented at scientific conferences, and published in peer-reviewed international journals. 

#### **Current study status**

The recruitment of ICs and HHCs is in progress in Zimbabwe, Mozambique and Tanzania since March, August and September 2021, respectively. The follow-up of HHCs is anticipated to be completed in March, August and September 2023 in Zimbabwe, Mozambigue and Tanzania, respectively; laboratory analyses are estimated to be performed by December 2024. 

#### **Author contributions**

The study proposal and protocol were written by NH, KK with scientific input from CK, TM, CG, JM. ETM, UP, DB, AM wrote the initial manuscript with scientific input on the database and data management section from FR, TA. NH, KK critically reviewed the initial draft of the manuscript. KH, GK, CJC, ENN, TA, provided critical feedback on the manuscript. All authors have read and approved the final version of the manuscript.

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	416	
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19 20 21	422	Minja <sup>e</sup> , Issa Sabi <sup>e</sup> , Peter Edwin <sup>e</sup> , Dogo Ngalison <sup>e</sup> , Stella Luswema <sup>e</sup> , Willyhelmina Olomi <sup>e</sup> ,
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38 39 40	431	<sup>d</sup> Zvitambo Research Institute, Harare, Zimbabwe
40 41 42	432	eNational Institute for Medical Research - Mbeya Medical Research Centre, Mbeya, Tanzania
43 44	433	fInstituto Nacional de Saúde, Marracuene, Mozambique
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47 48 49 50 51 52 53 54 55 56 57 58	435	Munich, Germany
	436	
	437	Competing interests statement
	438	None declaired.
	439	
	440	Disclaimer
59 60	441	Not applicable.

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3 4 5 6 7 8 9 10 11 12 13 14	582	Figure legend
	583	Figure 1. The ERASE-TB consortium
	584	Abbreviations: ERASE-TB=Early Risk Assessment in TB contactS by new diagnostic tEsts
	585	
	586	Figure 2. Location and characteristics of ERASE-TB study sites
	587	Notes: The location of each study site is indicated by a red asterix. Source data used within
15 16	588	this figure are taken from the references [7,8,41–43,9–15].
17 18	589	Abbreviations: ERASE=Early Risk Assessment in TB contactS by new diagnostic tEsts;
19 20 21	590	TB=tuberculosis; HIV=human immunodeficiency virus
22 23	591	
24 25	592	Figure 3. Eligibility criteria and schedules of events for index cases and household contacts
26 27	593	Notes: A=depending on the time point of study enrollment and consequently on the duration
28 29	594	available for follow-up, i.e. 18 or 24 months, the follow-up visit at 24 months $\pm 30$ days may be
30 31	595	conditional; <b>B</b> =the follow-up visit by phone may be conducted after the last scheduled follow-
32 33	596	up visit at 18 months $\pm$ 30 days or 24 months $\pm$ 30 days to assess whether symptoms suggestive
34 35	597	of TB have occurred, TB diagnosis has been made or anti-TB treatment has been initiated;
36 37	598	C=unwell visits by phone or on-site may be conducted between scheduled follow-up visits if a
38 39 40	599	participant presents at a recruitment healthcare facility with signs and symptoms suggestive of
40 41 42	600	TB; <b>D</b> =coached spontaneous or induced sputum collection for storage at scheduled follow-up
43 44	601	visit at 18 months $\pm$ 30 days or 24 months $\pm$ 30 days, and for repetition of HIV testing if tested
45 46	602	negative at baseline; E=coached spontaneous or induced sputum collection upon the decision
47 48	603	of the investigating team for testing by Xpert MTB/RIF Ultra if participant presents with signs
49 50	604	and symptoms suggestive of TB; F=coached spontaneous or induced sputum collection in
51 52	605	case of Xpert MTB/RIF Ultra positivity or strong clinical suspicion of TB for repetition of the
53 54	606	Xpert MTB/RIF Ultra; <b>G</b> =in case of HIV positivity to be followed by the assessment of CD4
55 56 57	607	counts; H=CXR to be conducted at an unscheduled on-site unwell visit upon the decision of
57 58 59	608	the investigating team depending on the nature of symptoms reported, and the time elapsed
60	609	since the last CXR including its findings; I=not to be conducted among pregnant women;

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J=stored venous blood includes 6mL EDTA blood for whole blood and plasma, 4mL serum and 2.5mL PAXgene blood, all samples will be deep frozen for retrospective testing using new diagnostics as described in text; **K**=in case the evaluation of symptoms of a participant unable to present at a recruitment healthcare facility is required an unscheduled on-site or home visit will be arranged by phone, the resolution of symptoms can alternatively be addressed by phone; L=collection of PBMC at baseline and follow-up visit at 6 months ±30 days is optional, thus will not be performed at each participating site and for each participant; **M**=in case the evaluation of symptoms of a participant unable to present at a recruitment healthcare facility is required or doubtful if required an unscheduled unwell visit by phone will be arranged, the resolution of symptoms can alternatively be addressed by phone; N=spirometry and/or diabetes (HbA1c) will be performed at scheduled follow-up visits at 6 months ±30 days, 12 months ±30 days and 18 or 24 months ±30 days if required or not performed at baseline, anaemia (Hb) will be performed at baseline and scheduled follow-up visits at 6 months ±30 days, 12 months ±30 days and 18 or 24 months ±30 days if possible; **O**=blood pressure measurement will be performed at baseline and scheduled follow-up visits at 6 months ±30 days, 12 months ±30 days and 18 or 24 months ±30 days; P=WGS to be performed once Mtb infection is confirmed and an isolate could be recovered.

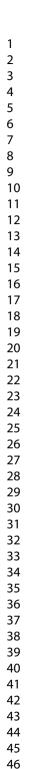
Abbreviations: TB=tuberculosis; WHO=World Health Organization; HIV=human immunodeficiency virus; WGS=whole genome sequencing; MBLA=molecular bacterial load assay; CXR=chest radiograph; IGRA=interferon gamma release assay; PBMC=peripheral blood mononuclear cell; TAM-TB=T- cell activation marker tuberculosis; MTB=Mycobacterium tuberculosis; RIF=rifampicin, Hb=haemoglobin; HbA1c=glycated hemoglobin; LAM=lioparabinomannan; CD4=cluster of differentiation 4

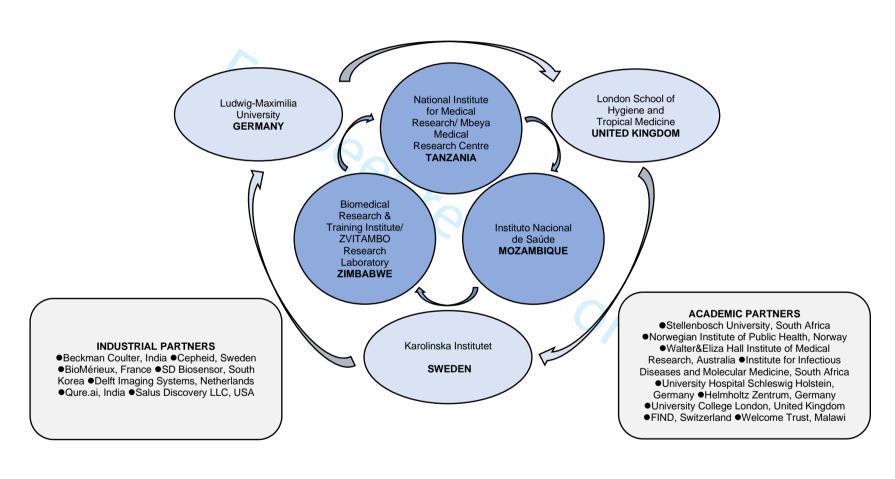
Figure 4. Study design

Abbreviations: HHC=household contact; TB=tuberculosis; IC=index case; WHO=World

Health Organization; CXR= chest radiograph; SS=symptom score; MTB=Mycobacterium

tuberculosis; RIF=rifampicin; pos=positive; CT=cpmputer tomography; FU=follow-up







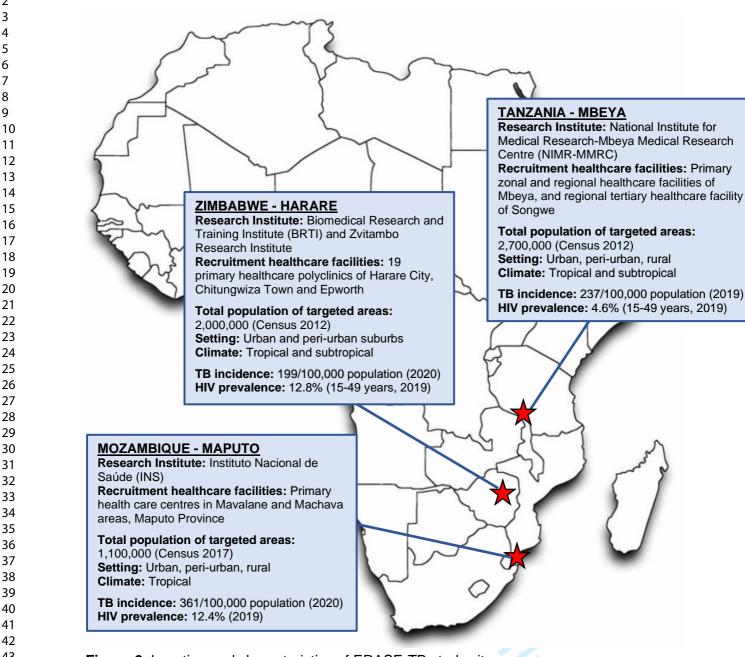
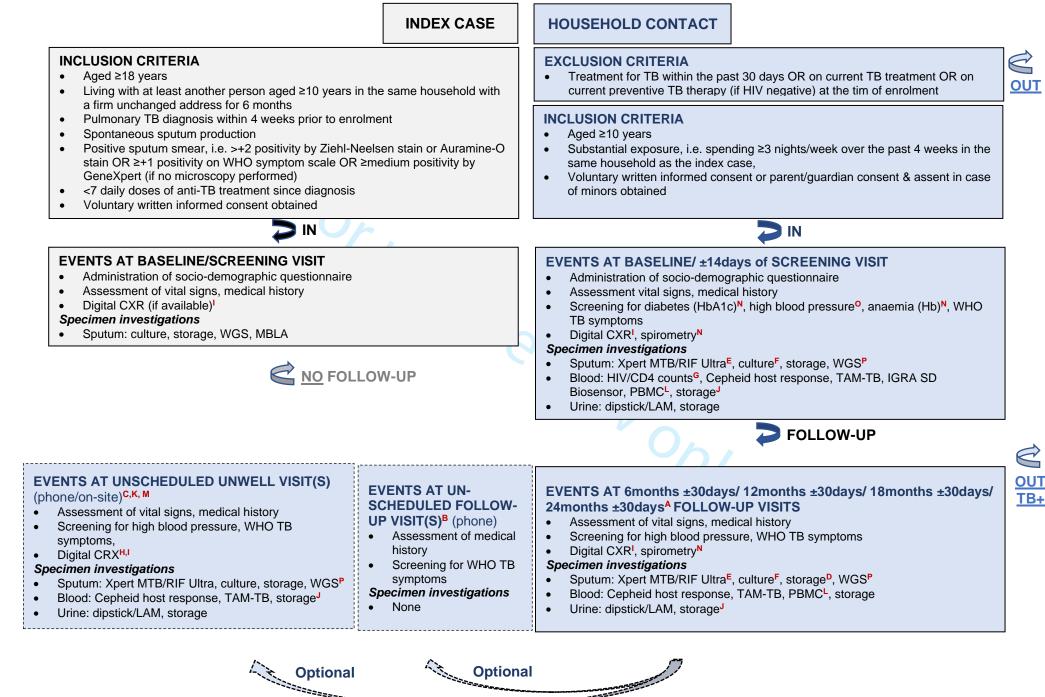


Figure 2. Location and characteristics of ERASE-TB study sites

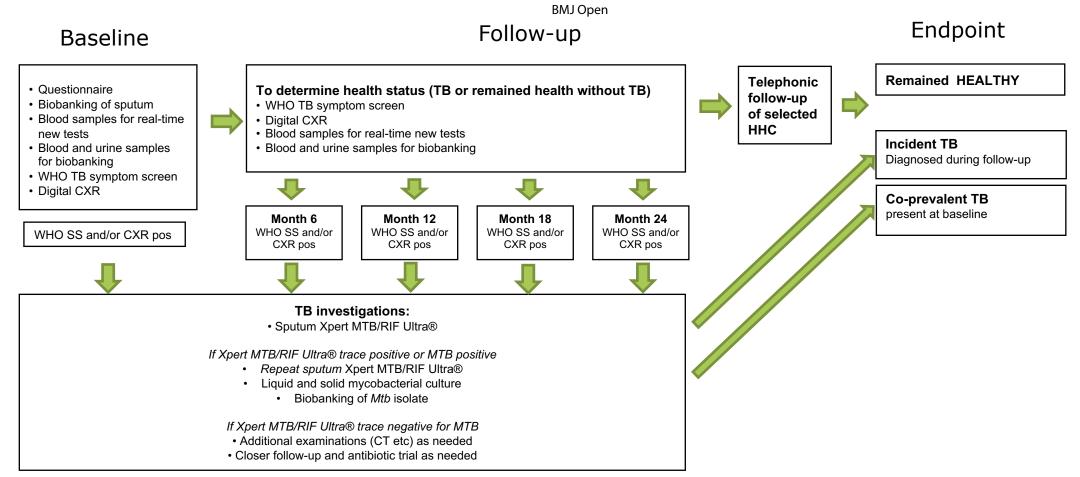


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Figure 3. Eligibility criteria and schedules of events for index cases and household contacts

. cases an.





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Section & Topic	No	Item	Reported on p #
TITLE OR ABSTRACT			
	1	Identification as a study of diagnostic accuracy using at least one measure of accuracy	2
		(such as sensitivity, specificity, predictive values, or AUC)	
ABSTRACT			
	2	Structured summary of study design, methods, results, and conclusions	2-3
		(for specific guidance, see STARD for Abstracts)	
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	3	Scientific and clinical background, including the intended use and clinical role of the index test	5-6
	4	Study objectives and hypotheses	6
METHODS			
Study design	5	Whether data collection was planned before the index test and reference standard	6-7
		were performed (prospective study) or after (retrospective study)	
Participants	6	Eligibility criteria	7 (Figure 3)
	7	On what basis potentially eligible participants were identified	7 (Figure 3)
		(such as symptoms, results from previous tests, inclusion in registry)	
	8	Where and when potentially eligible participants were identified (setting, location and dates)	7
	9	Whether participants formed a consecutive, random or convenience series	7, 11
Test methods	10a	Index test, in sufficient detail to allow replication	8-10, 11-13
	10b	Reference standard, in sufficient detail to allow replication	8-10, 11-13
	11	Rationale for choosing the reference standard (if alternatives exist)	8-10, 11-13
	12a	Definition of and rationale for test positivity cut-offs or result categories	13-14
		of the index test, distinguishing pre-specified from exploratory	
	12b	Definition of and rationale for test positivity cut-offs or result categories	13-14
		of the reference standard, distinguishing pre-specified from exploratory	
	13a	Whether clinical information and reference standard results were available	13-14
		to the performers/readers of the index test	
	13b	Whether clinical information and index test results were available	13-14
		to the assessors of the reference standard	
Analysis	14	Methods for estimating or comparing measures of diagnostic accuracy	13-14
	15	How indeterminate index test or reference standard results were handled	13-14
	16	How missing data on the index test and reference standard were handled	14
	17	Any analyses of variability in diagnostic accuracy, distinguishing pre-specified from exploratory	13-14
	18	Intended sample size and how it was determined	11
RESULTS			
Participants	19	Flow of participants, using a diagram	8-10 (Figure 3)
	20	Baseline demographic and clinical characteristics of participants	8-10 (Figure 3)
	21a	Distribution of severity of disease in those with the target condition	
	21b	Distribution of alternative diagnoses in those without the target condition	
	22	Time interval and any clinical interventions between index test and reference standard	
Test results	23	Cross-tabulation of the index test results (or their distribution)	
	-	by the results of the reference standard	
	24	Estimates of diagnostic accuracy and their precision (such as 95% confidence intervals)	13-14
	25	Any adverse events from performing the index test or the reference standard	
DISCUSSION	-		
	26	Study limitations, including sources of potential bias, statistical uncertainty, and	3
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OTHER			
INFORMATION			
	28	Registration number and name of registry	2
	29	Where the full study protocol can be accessed	
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		For peer review only - http://bmjopen.bmj.com/site/about/guidelines.xhtml	



# STARD 2015

## AIM

STARD stands for "Standards for Reporting Diagnostic accuracy studies". This list of items was developed to contribute to the completeness and transparency of reporting of diagnostic accuracy studies. Authors can use the list to write informative study reports. Editors and peer-reviewers can use it to evaluate whether the information has been included in manuscripts submitted for publication.

## EXPLANATION

A **diagnostic accuracy study** evaluates the ability of one or more medical tests to correctly classify study participants as having a **target condition.** This can be a disease, a disease stage, response or benefit from therapy, or an event or condition in the future. A medical test can be an imaging procedure, a laboratory test, elements from history and physical examination, a combination of these, or any other method for collecting information about the current health status of a patient.

The test whose accuracy is evaluated is called **index test.** A study can evaluate the accuracy of one or more index tests. Evaluating the ability of a medical test to correctly classify patients is typically done by comparing the distribution of the index test results with those of the **reference standard**. The reference standard is the best available method for establishing the presence or absence of the target condition. An accuracy study can rely on one or more reference standards.

If test results are categorized as either positive or negative, the cross-tabulation of the index test results against those of the reference standard can be used to estimate the **sensitivity** of the index test (the proportion of participants *with* the target condition who have a positive index test), and its **specificity** (the proportion *without* the target condition who have a negative index test). From this cross-tabulation (sometimes referred to as the contingency or "2x2" table), several other accuracy statistics can be estimated, such as the positive and negative **predictive values** of the test. Confidence intervals around estimates of accuracy can then be calculated to quantify the statistical **precision** of the measurements.

If the index test results can take more than two values, categorization of test results as positive or negative requires a **test positivity cut-off**. When multiple such cut-offs can be defined, authors can report a receiver operating characteristic (ROC) curve which graphically represents the combination of sensitivity and specificity for each possible test positivity cut-off. The **area under the ROC curve** informs in a single numerical value about the overall diagnostic accuracy of the index test.

The **intended use** of a medical test can be diagnosis, screening, staging, monitoring, surveillance, prediction or prognosis. The **clinical role** of a test explains its position relative to existing tests in the clinical pathway. A replacement test, for example, replaces an existing test. A triage test is used before an existing test; an add-on test is used after an existing test.

Besides diagnostic accuracy, several other outcomes and statistics may be relevant in the evaluation of medical tests. Medical tests can also be used to classify patients for purposes other than diagnosis, such as staging or prognosis. The STARD list was not explicitly developed for these other outcomes, statistics, and study types, although most STARD items would still apply.

### DEVELOPMENT

This STARD list was released in 2015. The 30 items were identified by an international expert group of methodologists, researchers, and editors. The guiding principle in the development of STARD was to select items that, when reported, would help readers to judge the potential for bias in the study, to appraise the applicability of the study findings and the validity of conclusions and recommendations. The list represents an update of the first version, which was published in 2003.

More information can be found on <u>http://www.equator-network.org/reporting-guidelines/stard.</u>

