

1 **Supporting information**

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3 **Specimens**

4 Stored midstream urine samples, collected from women attending their first antenatal clinic visit at five  
5 health facilities in Madang Province (PNG) between 2018 and 2019 were de-identified and stored at -80 °C  
6 and transported to the University of Queensland Centre for Clinical Research (UQCCR, Brisbane,  
7 Australia) for analysis. We identified 69 *M. genitalium* positive samples (unpublished data) from this cross-  
8 sectional study and further analysed them as part of this study.

9 Urine samples were thawed at room temperature and nucleic acid extracted using the Qiagen DSP  
10 virus/pathogen midi kit on the QIAasymphony SP/AS platform (Qiagen, Australia), according to  
11 manufacturers' instructions with the Complex400-V3 DSP protocol.

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13 **TaqMan Probe-based PCR assays**

- 14 i) MgPa screening: *M. genitalium* primers and probe from a previous publication were used to detect  
15 *M. genitalium* within the clinical samples from this study.<sup>1</sup> In brief, reactions consisted of 12.5 µl  
16 Quantitect Probe mastermix (Qiagen), 10pmol of each primer, 0.2 µM probe, 5 µL of nucleic acid  
17 and PCR-grade water for a final volume of 25 µl. Samples were cycled using the Rotorgene 6000  
18 (QIAGEN, Australia) real-time PCR instrument using: initial denaturation at 95°C for 15mins,  
19 followed by 50 cycles of 95°C for 15 sec and 60 °C for 60 sec.
- 20 ii) Fluoroquinolone resistance assay: *M. genitalium*-positive samples were screened for the presence of  
21 *parC* fluoroquinolone susceptibility and resistance markers using a previously developed assay.<sup>2,3</sup>  
22 Reactions included 10 µl SensiFast Probe master mix, 0.5 µM of forward and reverse primers, 0.2  
23 µM of S83 wildtype (FAM-labelled) and S83I (G248T; HEX-labelled) probes and 3 µL of nucleic  
24 acid extract in a total reaction volume of 20 µL. Each reaction included 5 µl nucleic acid extract and

25 15µl of the prepared TaqMan mastermix and analysed using the Applied Biosystems 7500 Fast Dx  
26 Real-Time PCR instrument (Applied Biosystems®, Australia) using the following conditions: an  
27 initial hold at 95 °C for 5 minutes, followed by 50 cycles of 95 °C for 15s and 60 °C for 60s,  
28 acquiring data for both fluorescent probes on the annealing/ extension step.

### 29 **SpeedX ResistancePlus® MG PCR assay (Macrolide resistance)**

30 A commercial qualitative real-time PCR assay was used to identify *M. genitalium* and detect the five most  
31 common mutations in the 23S rRNA gene (A2058G, A2059G, A2058T, A2058C, and A2059C,  
32 *Escherichia coli* numbering) that are associated with resistance to azithromycin (a macrolide antibiotic).<sup>2</sup>  
33 <sup>4</sup> According to the manufacturer's instructions, each reaction constituted of 10 µl of Plex mastermix (2x),  
34 1 µL of 23S mix, 1 µL control mix, 5 µL of nucleic acid extract in a total reaction volume of 20 µL. The  
35 reaction was analysed using the Applied Biosystems 7500 Fast Dx Real-Time PCR instrument (Applied  
36 Biosystems®, Australia) using the following conditions: initial denaturation of 95°C for 2min, followed  
37 by a 10 cycle touch-down cycling (initial denaturation at 95 °C for 5 seconds (sec), then 61°C – 56.5°C (-  
38 0.5 °C per cycle) for 30 sec) followed by 40 cycles of 95 °C for 5 sec and 52 °C for 40 sec (data  
39 acquired). The selected channels for data acquisition included: FAM (*MgPa* gene), JOE (23S rRNA  
40 mutation) and TAMRA (Extraction control).

41 Controls for PCR assays:

42 Well-characterised *M. genitalium*-positive clinical samples harbouring macrolide and fluoroquinolone  
43 resistance markers served as controls in all PCR assays, and nuclease free water in place of nucleic acid  
44 served as negative controls for all assays.

### 45 **Reference**

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