Table S1. Estimated detection thresholds of nucleic acid amplication tests (NAAT) used in the study.

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| --- | --- | --- | --- | --- |
| **Pathogen** | **Laboratory methods** | **Type of sample** | **Target (antigen or gene)** | **Estimated detection threshold** |
| Malaria  | PCR & Sequencing | DNA extracted from 200 µl red blood cells | *Plasmodium cytochrome b* gene | 0.08 copy/µl |
| Leptospirosis | PCR & Sequencing | DNA extracted from 200 µl red blood cells | *16srRNA* gene | 16 copies/µl |
| Rickettsial disease | PCR & Sequencing | DNA extracted from 200 µl red blood cells | *ompB* gene | 200 copies/µl |
| PCR & Sequencing | DNA extracted from 200 µl red blood cells | *gltA* gene | 200 copies/µl |
| Scrub Typhus | PCR & Sequencing | DNA extracted from 200 µl red blood cells | *47kDa* gene | 1000 copies/µl |
| Dengue | RT-PCR | RNA extracted from 200 µl of plasma | PrM/E gene - Dengue virus 1-4 | 100 copies/ml  |
| Influenza | RT-PCR | RNA extracted from throatswab | *M* gene - Influenza A and B  | 4 copies/µl (IA) and 36 copies/µl (IB) |