

## Supplementary File S2: Modified QUADAS tool

### Domain 1: Patient selection

#### A. Risk of bias

Describe methods of patient selection:

- Was a consecutive or random sample of patients enrolled? Yes/No/Unclear

- Did the study avoid inappropriate exclusions? Yes/No/Unclear

Could the selection of patients have introduced bias? RISK: LOW/HIGH/UNCLEAR

#### B. Concerns regarding applicability

Describe criteria for genotyping

Is there concern that the included patients do not match the review question? CONCERN:  
LOW/HIGH/UNCLEAR

### Domain 2: DETERMINING GENOTYPE *(if more than 1 index test was used, please complete for each test)*

#### A. Risk of bias

Describe how genotype was identified

- Was genotype determined without knowledge of G6PD activity? Yes/No/Unclear

Could the conduct or interpretation of the index test have introduced bias? RISK: LOW/HIGH/UNCLEAR

### Domain 3: DETERMINING PHENOTYPE

#### A. Risk of bias

Describe the reference standard and how it was conducted and interpreted:

<ul style="list-style-type: none"> <li>Is the reference standard likely to correctly classify the target condition?</li> </ul>	Yes/No/Unclear
<ul style="list-style-type: none"> <li>Were the reference standard results interpreted without knowledge of the results of the index test?</li> </ul>	Yes/No/Unclear
Could the reference standard, its conduct, or its interpretation have introduced bias?	RISK: LOW/HIGH/UNCLEAR
<b>Domain 4: Flow and timing</b>	
<b>A. Risk of bias</b>	
<ul style="list-style-type: none"> <li>Was there an appropriate interval between sample collection and spectrophotometry (&lt;7 days at 4°C)?</li> </ul>	Yes/No/Unclear
<ul style="list-style-type: none"> <li>Did patients receive the same variant determination and spectrophotometry?</li> </ul>	Yes/No/Unclear
<ul style="list-style-type: none"> <li>Were all patients included in the analysis?</li> </ul>	Yes/No/Unclear
Could the patient flow have introduced bias?	RISK: LOW/HIGH/UNCLEAR