

Adapted Newcastle–Ottawa Risk-of-Bias Tool

Domains, signalling questions, and scoring guide

#	Domain	Signalling questions (answer Yes / Partial / No)	Scoring rule
1	Case selection / Sampling frame	<p>1. Was the source population clearly enumerated (birth-cohort, census list, HDSS)?</p> <p>2. Were all eligible cases recruited consecutively or randomly?</p>	<p>Low = “Yes” to both.</p> <p>Moderate = “Yes” to Q1 but “Partial”/“No” to Q2.</p> <p>High = “No” to Q1 (e.g., convenience or special-subgroup enrolment).</p>
2	Control representativeness	<p>1. Were controls drawn from the same geographic catchment as cases?</p> <p>2. For susceptibility outcomes, were controls parasite-negative?</p> <p>3. For severity outcomes, were controls community-based rather than hospital out-patients?</p>	<p>Low = “Yes” to all applicable questions.</p> <p>Moderate = “Yes” to Q1 but at least one “Partial”.</p> <p>High = “No” to Q1 or controls are hospitalised with malaria.</p>
3	Exposure ascertainment (genotyping)	<p>1. Was genotyping done by validated PCR (or sequencing) methods?</p> <p>2. Were $\geq 5\%$ of samples duplicated with $\geq 99\%$ concordance?</p> <p>3. Were $< 2\%$ genotypes missing?</p>	<p>Low = “Yes” to all three.</p> <p>Moderate = One “Partial”.</p> <p>High = Any “No”.</p>
4	Confounding control	<p>1. Did analyses adjust for age and sex?</p> <p>2. Did they adjust for bed-net use or socio-economic status?</p> <p>3. Did they adjust for at least one other RBC polymorphism (e.g., α-thalassaemia)?</p>	<p>Low = “Yes” to all three.</p> <p>Moderate = “Yes” to Q1 but “Partial/No” to Q2 or Q3.</p> <p>High = “No” to Q1 or unadjusted analyses.</p>

5	Precision	<p>1. Were ≥ 30 individuals carrying the dual-variant combination?</p> <p>2. Was the 95 % CI width $< \pm 30$ % of the point estimate?</p>	<p>Low = “Yes” to either Q1 or Q2.</p> <p>Moderate = 10–29 dual carriers <i>and</i> CI width 30–60 %.</p> <p>High = < 10 dual carriers <i>or</i> CI width > 60 % or infinite OR.</p>
6	Outcome measurement	<p>1. Were WHO malaria criteria used?</p> <p>2. Were laboratory indices measured with accredited equipment?</p> <p>3. Was follow-up ≥ 90 % complete (for cohort studies)?</p>	<p>Low = “Yes” to all applicable questions.</p> <p>Moderate = One “Partial”.</p> <p>High = Any “No”.</p>
7	Missing data / Exclusions	<p>1. Were < 5 % of participants excluded after enrolment?</p> <p>2. Were exclusions balanced across genotype groups?</p> <p>3. Were reasons for exclusion stated?</p>	<p>Low = “Yes” to all.</p> <p>Moderate = 5–10 % missing <i>or</i> unclear balance.</p> <p>High = > 10 % missing <i>or</i> selective exclusions.</p>

How to use the tool

1. Answer each signalling question for a study with *Yes*, *Partial* (some but not all criteria met), or *No*.
2. Assign a domain rating using the rule in the right-hand column.
3. Overall study risk
 - Serious (high) = ≥ 2 domains rated High or one High plus a High Precision judgement.
 - Moderate = one High or three Moderate domains.
 - Low = all domains Low or one Moderate.
4. GRADE downgrades: –1 level for overall Moderate risk; –2 levels for overall Serious risk.