Appendix Table F3. Assessment of risk of bias in the study of genetic test–based selection of patients

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Author**  **Year**  **Country**  **PMID**  **Study name (if available)** | **Q1** | **Q2** | **Q3** | **Q4** | **Q5** | **Q6** | **Q7** | **Q8** | **Q9** | **Q10** | **Q11** | **Q12** | **Q13** | **Q14** | **Q15** | **Q16** | **Q17** |
| Mega  2011  USA  22088980  ELEVATE-TIMI 56 | Unclear | Low | Low (4% excluded after randomization) | Low | Low (enrollment in trial was stratified by baseline genotype status) | Low | Low | High (4 periods of 14 d) | Low | Low | Low (central; reports randomization system) | Low (central; interactive voice-response system) | Low | Low | Low | Low | Low |

**Quality items**

Q1: Consecutive sample of patients enrolled

Q2: Case-control design avoided

Q3: Study avoided inappropriate exclusions and post-hoc exclusions were <5%

Q4: Index test results interpreted without knowledge of outcomes?

Q5: If a test threshold was used, was it prespecified?

Q6: Reference standard likely to correctly classify the target condition (low if at least one clinical outcome assessed)?

Q7: Reference standard results interpreted without knowledge of index test results?

Q8: Appropriate interval between index test and reference standard (at least 12 mo of followup)?

Q9: All patients received a reference standard (outcome data for >90% of patients)?

Q10: All patients received the same reference standard?

Q11: Random sequence generation

Q12: Allocation concealment

Q13: Blinding of participants and personnel

Q14: Blinding of outcome assessment

Q15: Incomplete outcome data (do they report enough data to estimate uncertainty for the primary outcome)

Q16: Selective reporting bias (do they report numerical results on the primary and secondary outcome; and are these identified in the methods)

Q17: Other bias (e.g., extreme numerical errors and inconsistencies)