

Part A: Core MR Methodology

Item	Question
A1	Is the exposure GWAS source clearly identified?
A2	Is the outcome GWAS source clearly identified?
A3	Are exposure GWAS sample sizes provided?
A4	Are outcome GWAS sample sizes provided?
A5	Is exposure GWAS ancestry composition reported?
A6	Is outcome GWAS ancestry composition reported?
A7	Is the significance threshold for instrument selection applied and justified?
A8	Is the LD method for instrument selection specified?
A9	Is the r^2 threshold for instrument selection reported?
A10	Is the distance parameter for instrument selection reported?
A11	Is the LD reference panel used for instrument selection named?
A12	Is the reference panel population used for instrument selection specified?
A13	Are numeric measures of instrument strength reported?
A14	Are instrument strength metrics adequate?

A15	Are IV assumptions explicitly stated?
A16	Is empirical assessment of IV assumptions performed?
A17	Are effect alleles harmonized between datasets?
A18	Are palindromic SNPs handled appropriately?
A19	Is sample overlap between exposure and outcome GWAS addressed?
A20	Are appropriate statistical methods used for overlapping samples?
A21	Are limitations of summary-level data for confounder control acknowledged?
A22	Is covariate adjustment appropriately described for individual-level data?
A23	Is systematic outlier detection applied?
A24	Is the outlier detection method adequately described?
A25	Are results presented before and after outlier removal?
A26	Is the impact of outlier removal discussed?
A27	Are sensitivity analyses performed to test pleiotropy/heterogeneity?
A28	Are sensitivity analysis results clearly reported?
A29	Are sensitivity analysis results interpreted?
A30	Are alternative MR estimators used beyond IVW?
A31	Are results consistent across multiple MR estimators?

A32	Is statistical power assessed or sample size justified?
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Part B: Cross-Ancestry Extensions to MR Methodology

Item	Question
B1	Is exposure GWAS ancestry clearly reported?
B2	Is outcome GWAS ancestry clearly reported?
B3	Is numeric breakdown provided for multi-ancestry GWAS?
B4	Is ancestry matching between exposure and outcome datasets assessed for instrument selection?
B5	Is an ancestry-appropriate LD reference panel used for single-ancestry GWAS?
B6	Is an appropriate LD reference panel used for instrument selection in multi-ancestry GWAS?
B7	Is the LD method for cross-ancestry instrument selection clearly stated?
B8	Is the r^2 threshold for cross-ancestry instrument selection stated?
B9	Is the distance parameter for cross-ancestry instrument selection stated?
B10	Is instrument strength assessed separately by ancestry?
B11	Are MAF thresholds for instrument selection stated per ancestry?
B12	Is the number of instruments excluded by ancestry due to MAF thresholds reported?
B13	Are allele frequency differences across ancestries considered in instrument selection?

B14	Is cross-ancestry instrument validity justified?
B15	Are binary trait definitions consistent across ancestries?
B16	Are continuous trait measurements consistent across ancestries?
B17	Are measurement units consistent or appropriately standardized?
B18	Are MR estimates reported separately by ancestry or tested for heterogeneity across ancestries?
B19	Are differences in MR estimates across ancestries interpreted?
B20	Is cross-ancestry colocalization assessed?
B21	Is pleiotropy assessed separately by ancestry?
B22	Are baseline risk differences across ancestries acknowledged when interpreting MR estimates?
B23	Is clinical relevance of MR estimates discussed by ancestry?
B24	Are generalizability limitations of MR estimates across ancestries addressed?