STROBE-MR checklist of recommended items to address in reports of Mendelian randomization studies[1 2]

Item No.	Section	Checklist item	Page No.	Relevant text from manuscript
1	**TITLE and ABSTRACT**	Indicate Mendelian randomization (MR) as the study's design in the title and/or the abstract if that is a main purpose of the study	1	**Title:** "A Mendelian randomization study..." **Abstract:** "**Methods**:...two-sample MR analysis..."
	INTRODUCTION			
2	**Background**	Explain the scientific background and rationale for the reported study. What is the exposure? Is a potential causal relationship between exposure and outcome plausible? Justify why MR is a helpful method to address the study question	2-3	"Sleep is a key mediator..." to "...the causal relationship between daytime napping and IBD are still questioned."
3	**Objectives**	State specific objectives clearly, including pre-specified causal hypotheses (if any). State that MR is a method that, under specific assumptions, intends to estimate causal effects	3	"In this study, we aimed to comprehensively illuminate the causal relationship between daytime napping and IBD by conducting two-sample Mendelian randomization analyses..."
	METHODS			
4	**Study design and data sources**	Present key elements of the study design early in the article. Consider including a table listing sources of data for all phases of the study. For each data source contributing to the analysis, describe the following:	3-4	"**2.1 Study Design and Data Sources**" entire section; **Table 1**. Details of the GWAS data.
	a)	Setting: Describe the study design and the underlying population, if possible. Describe the setting, locations, and relevant dates, including periods of recruitment, exposure, follow-up, and data collection, when available.	3-4, Table 1	"We sourced Genome Wide Association Study (GWAS) data... from distinct databases..." & **Table 1** (Source, Ancestry, Year).
	b)	Participants: Give the eligibility criteria, and the sources and methods of selection of participants. Report the sample size, and whether any power or sample size calculations were carried out prior to the main analysis	Table 1	**Table 1** (Sample size).
	c)	Describe measurement, quality control and selection of genetic variants	4	"2.2 Selection of the Instrumental Variables" entire section.
	d)	For each exposure, outcome, and other relevant variables, describe methods of assessment and diagnostic criteria for diseases	Table 1	**Table 1** (Trait, Dataset, Year indicates source GWAS).
	e)	Provide details of ethics committee approval and participant informed consent, if relevant	/	Not applicable.
5	**Assumptions**	Explicitly state the three core IV assumptions for the main analysis (relevance, independence and exclusion restriction) as well assumptions for any additional or sensitivity analysis	4–5, 7	"**2.2 Selection of the Instrumental Variables**" (relevance, independence), "**2.3 Statistic Analysis**" and "**3.2 Sensitivity**

					analysis" (exclusion restriction, pleiotropy tests).
6	**Statistical methods: main analysis**		Describe statistical methods and statistics used	4-5	"**2.3 Statistic Analysis**" entire section.
		a)	Describe how quantitative variables were handled in the analyses (i.e., scale, units, model)	4-5	"Inverse Variance Weighted (IVW) test was performed as the primary method… Weighted Median and Maximum Likelihood MR methods were used as supplementary analysis."
		b)	Describe how genetic variants were handled in the analyses and, if applicable, how their weights were selected	4	"SNPs were selected as instrumental variables… F-statistics were used to evaluate the strength and validity."
		c)	Describe the MR estimator (e.g. two-stage least squares, Wald ratio) and related statistics. Detail the included covariates and, in case of two-sample MR, whether the same covariate set was used for adjustment in the two samples	4-5	"IVW, Weighted Median, Maximum Likelihood… Association with $P < 0.05$ were considered significant."
		d)	Explain how missing data were addressed	4	SNPs with inconsistent alleles (i.e., A/G vs. A/C) and palindromic SNPs (i.e., A/T or G/C) were excluded
		e)	If applicable, indicate how multiple testing was addressed	5	"Associations with $P < 0.05$ assessed by the above methods were considered signifcant."
7	**Assessment of assumptions**		Describe any methods or prior knowledge used to assess the assumptions or justify their validity	4-5, 7	" Cochran's Q test,Egger intercept test, MR-PRESSO, Leave-one-out analysis" in 2.3 and 3.2.
8	**Sensitivity analyses and additional analyses**		Describe any sensitivity analyses or additional analyses performed (e.g. comparison of effect estimates from different approaches, independent replication, bias analytic techniques, validation of instruments, simulations)	4-5, 7	"**2.3 Statistic Analysis**" and "**3.2 Sensitivity analysis**".
9	**Software and pre-registration**				
		a)	Name statistical software and package(s), including version and settings used	5	"R (version 4.4.1) package TwoSampleMR (version 0.6.4) and MR-PRESSO (version 1.0)."
		b)	State whether the study protocol and details were pre-registered (as well as when and where)	/	Not mentioned.
	RESULTS				

10	**Descriptive data**			
	a)	Report the numbers of individuals at each stage of included studies and reasons for exclusion. Consider use of a flow diagram	5-6; Supplementary Tables S1–S2	"After careful screening, we obtained 22 eligible candidate SNPs…" and Supplementary Table S1/S2.
	b)	Report summary statistics for phenotypic exposure(s), outcome(s), and other relevant variables (e.g. means, SDs, proportions)	3-4, 6-7	**Table 1** (sample sizes), **Figure 2** (OR, 95% CI, P-values).
	c)	If the data sources include meta-analyses of previous studies, provide the assessments of heterogeneity across these studies	/	Not applicable.
	d)	For two-sample MR: i. Provide justification of the similarity of the genetic variant-exposure associations between the exposure and outcome samples ii. Provide information on the number of individuals who overlap between the exposure and outcome studies	3	"We sourced Genome Wide Association Study (GWAS) data on daytime napping and IBD from distinct databases to conduct initial MR analysis, effectively eliminating the potential population overlap."
11	**Main results**			
	a)	Report the associations between genetic variant and exposure, and between genetic variant and outcome, preferably on an interpretable scale	6-7	Figure 2 (OR and CI for each outcome).
	b)	Report MR estimates of the relationship between exposure and outcome, and the measures of uncertainty from the MR analysis, on an interpretable scale, such as odds ratio or relative risk per SD difference	6	"IVW (OR = 0.327, 95%CI = 0.147–0.703, P = 0.006)…"
	c)	If relevant, consider translating estimates of relative risk into absolute risk for a meaningful time period	/	Not applicable.
	d)	Consider plots to visualize results (e.g. forest plot, scatterplot of associations between genetic variants and outcome versus between genetic variants and exposure)	6-7	Figure 2 (forest plots), Figure 3 (leave-one-out plot).
12	**Assessment of assumptions**			
	a)	Report the assessment of the validity of the assumptions	1	"No significant evidence of heterogeneity and horizontal pleiotropy were identified…"
	b)	Report any additional statistics (e.g., assessments of heterogeneity across genetic variants, such as I^2, Q statistic or E-value)	7	**Table 2** (Cochran's Q, Egger intercept, MR-PRESSO global test).
13	**Sensitivity analyses and**			

	additional analyses				
		a)	Report any sensitivity analyses to assess the robustness of the main results to violations of the assumptions	7	"**3.2 Sensitivity analysis**" entire section.
		b)	Report results from other sensitivity analyses or additional analyses	7	**Table 2** and Figure 3.
		c)	Report any assessment of direction of causal relationship (e.g., bidirectional MR)	/	Not performed.
		d)	When relevant, report and compare with estimates from non-MR analyses	8	"contrary to a previous MR analysis… a recent cohort study found a positive association…"
		e)	Consider additional plots to visualize results (e.g., leave-one-out analyses)	7	Figure 3 (leave-one-out analysis).
	DISCUSSION				
14	**Key results**		Summarize key results with reference to study objectives	7	"The daytime napping was identified the protective factor for IBD and UC, but no relation with CD"
15	**Limitations**		Discuss limitations of the study, taking into account the validity of the IV assumptions, other sources of potential bias, and imprecision. Discuss both direction and magnitude of any potential bias and any efforts to address them	9	"due to data limitations, we failed to analyze the causal relationship between napping and IBD unclassified… MR analysis relies on indirect evidence…"
16	**Interpretation**				
		a)	Meaning: Give a cautious overall interpretation of results in the context of their limitations and in comparison with other studies	9	"Our findings provide valuable insights… additional research is necessary to validate these findings…"
		b)	Mechanism: Discuss underlying biological mechanisms that could drive a potential causal relationship between the investigated exposure and the outcome, and whether the gene-environment equivalence assumption is reasonable. Use causal language carefully, clarifying that IV estimates may provide causal effects only under certain assumptions	9-10	"daytime napping to facilitate the restoration of intestinal immune function, mitigate inflammatory responses…"
		c)	Clinical relevance: Discuss whether the results have clinical or public policy relevance, and to what extent they inform effect sizes of possible interventions	9	"Given the important role of lifestyle in the occurrence and development of chronic diseases, people should also be encouraged to pay attention to and improve their rest habits to promote intestinal health"
17	**Generalizability**		Discuss the generalizability of the study results (a) to other populations, (b) across other exposure periods/timings, and (c) across other levels of exposure	8	"systematically assess… in a European population… more integrated and personalized strategies may be needed…"

	OTHER INFORMATION			
18	**Funding**	Describe sources of funding and the role of funders in the present study and, if applicable, sources of funding for the databases and original study or studies on which the present study is based	12	"Funding Declaration: This work was supported by Heilongjiang Province Traditional Chinese Medicine Scientific Research Project, ZHY2025-158."
19	**Data and data sharing**	Provide the data used to perform all analyses or report where and how the data can be accessed, and reference these sources in the article. Provide the statistical code needed to reproduce the results in the article, or report whether the code is publicly accessible and if so, where	3-4	"FinnGen data… from consortium's website… UK Biobank data was provided by IEU OpenGWAS Project database…"
20	**Conflicts of Interest**	All authors should declare all potential conflicts of interest	13	The authors declare that they have no competing interests.

1. Skrivankova VW, Richmond RC, Woolf BAR, Yarmolinsky J, Davies NM, Swanson SA, et al. Strengthening the Reporting of Observational Studies in Epidemiology using Mendelian Randomization (STROBE-MR) Statement. JAMA. 2021;under review.

2. Skrivankova VW, Richmond RC, Woolf BAR, Davies NM, Swanson SA, VanderWeele TJ, et al. Strengthening the Reporting of Observational Studies in Epidemiology using Mendelian Randomisation (STROBE-MR): Explanation and Elaboration. BMJ. 2021;375:n2233.