Materials Design Analysis Reporting (MDAR) Checklist for Authors

The MDAR framework establishes a minimum set of requirements in transparent reporting applicable to studies in the life sciences (see Statement of Task: doi:10.31222/osf.io/9sm4x.). The MDAR checklist is a tool for authors, editors and others seeking to adopt the MDAR framework for transparent reporting in manuscripts and other outputs. Please refer to the MDAR Elaboration Document for additional context for the MDAR framework.

Materials

Antibodies	Yes (indicate where provided: section/paragraph)	n/a
For commercial reagents, provide supplier name, catalogue number and RRID, if available.	Material/##Western blot and image analyses paragraph	

Cell materials	Yes (indicate where provided: section/paragraph)	n/a
Cell lines: Provide species information, strain. Provide accession number in repository **OR** supplier name, catalog number, clone number, **OR** RRID	Material/##Dataset paragraph	
Primary cultures: Provide species, strain, sex of origin, genetic modification status.	Material/##Dataset paragraph	

Experimental animals	Yes (indicate where provided: section/paragraph)	n/a
Laboratory animals: Provide species, strain, sex, age, genetic modification status. Provide accession number in repository **OR** supplier name, catalog number, clone number, **OR** RRID		n/a
Animal observed in or captured from the field: Provide species, sex and age where possible		n/a
Model organisms: Provide Accession number in repository (where relevant) **OR** RRID		n/a

Plants and microbes	Yes (indicate where provided: section/paragraph)	n/a
Plants: provide species and strain, unique accession number if available, and source (including location for collected wild specimens)		n/a
Microbes: provide species and strain, unique accession number if available, and source		n/a

Human research participants	Yes (indicate where provided: section/paragraph)	n/a
Identify authority granting ethics approval (IRB or equivalent committee(s), provide reference number for approval.	Material/## This study was approved by the Ethics Committee of Zhujiang Hospital of Southern Medical University (No. 2017-gdek-004)	
Provide statement confirming informed consent obtained from study participants.		n/a
Report on age and sex for all study participants.		n/a

Design

Study protocol	Yes (indicate where provided: section/paragraph)	n/a
For clinical trials, provide the trial registration number **OR** cite DOI in manuscript.		n/a

Laboratory protocol	Yes (indicate where provided: section/paragraph)	n/a
Provide DOI or other citation details if detailed step-by-step protocols are available.		n/a

Experimental study design (statistics details)	Yes (indicate where provided: section/paragraph)	n/a
State whether and how the following have been done**, or** if they were not carried out.		
Sample size determination	Material/##Real-time reverse transcription polymerase chain reaction analysis, ##Western blot and image chain reaction analysis, ##Western blot and image	
Randomisation	Material/##Real-time reverse transcription polymerase chain reaction analysis, ##Western blot and image	
Blinding	Material/##Real-time reverse transcription polymerase chain reaction analysis, ##Western blot and image	
Inclusion/exclusion criteria	Material/##Real-time reverse transcription polymerase chain reaction analysis, ##Western blot and image	

Sample definition and in-laboratory replication	Yes (indicate where provided: section/paragraph)	n/a
State number of times the experiment was replicated in laboratory		n/a
Define whether data describe technical or biological replicates		n/a

Ethics	Yes (indicate where provided: section/paragraph)	n/a
Studies involving human participants: State details of authority granting ethics approval (IRB or equivalent committee(s), provide reference number for approval.	Material/##Dataset paragraph	
Studies involving experimental animals: State details of authority granting ethics approval (IRB or equivalent committee(s), provide reference number for approval.		n/a
Studies involving specimen and field samples: State if relevant permits obtained, provide details of authority approving study; if none were required, explain why.	Material/##Dataset paragraph	

Dual Use Research of Concern (DURC)	Yes (indicate where provided: section/paragraph)	n/a
If study is subject to dual use research of concern, state the authority granting approval and reference number for the regulatory approval		n/a

Analysis

Attrition	Yes (indicate where provided: section/paragraph)	n/a
State if sample or data point from the analysis is excluded, and whether the criteria for exclusion were determined and specified in advance.		n/a

Statistics	Yes (indicate where provided: section/paragraph)	n/a
Describe statistical tests used and justify choice of tests.	Material/##Statistical analysis	

Data Availability	Yes (indicate where provided: section/paragraph)	n/a
State whether newly created datasets are available, including protocols for access or restriction on access.	Footnote/Data Availability Statement	
If data are publicly available, provide accession number in repository or DOI or URL.	Footnote/Data Availability Statement	
If publicly available data are reused, provide accession number in repository or DOI or URL, where possible.	Footnote/Data Availability Statement	

Code Availability	Yes (indicate where provided: section/paragraph)	n/a
For all newly generated code and software essential for replicating the main findings of the study:		
State whether the code or software is available.	The datasets used in this study are openly available in the TCGA database at https://www.cancer.gov/about-	
If code is publicly available, provide accession number in repository, or DOI or URL.	The datasets used in this study are openly available in the TCGA database at https://www.cancer.gov/about-nci/organization/ccg/research/structural-genomics/tcga and the ProteomeXchange database at http://dx.doi.org/10.6019/PXD002171. Some of the images were obtained from the GEPIA database at http://gepia.cancer-pku.cn/ and the HPA database at https://www.proteinatlas.org/.	

Reporting

Adherence to community standards	Yes (indicate where provided: section/paragraph)	n/a
MDAR framework recommends adoption of discipline-specific guidelines, established and endorsed through community initiatives. Journals have their own policy about requiring specific guidelines and recommendations to complement MDAR.		
State if relevant guidelines (eg., ICMJE, MIBBI, ARRIVE) have been followed, and whether a checklist (eg., CONSORT, PRISMA, ARRIVE) is provided with the manuscript.	ICMJE guidelines were followed as the journal follows ICMJE guidelines for publication.	

Article information: https://dx.doi.org/10.21037/jgo-23-247

STREGA Reporting Recommendations, Extended from STROBE Statement

Item	Item No	Description	Reported on Page Number/Line Number	Reported on Section/Paragraph
Title and Abstract	1	(a) Indicate the study's design with a commonly used term in the title or the abstract.	Page 1/line 3-4	title/1 Paragraph
		(b) Provide in the abstract an informative and balanced summary of what was done and what was found.	Page 2/line 40-53	Abstract/1-4 Paragraph
Introduction				
Background rationale	2	Explain the scientific background and rationale for the investigation being reported.	Page 2-3/line 959-81	introduction/1-3Paragraph
Objectives	3	State specific objectives, including any pre-specified hypotheses. *(State if the study is the first report of a genetic association, a replication effort, or both.)*	Page 3-4/line 82-92	introduction/4Paragraph
Methods				
Study design	4	Present key elements of study design early in the paper.	Page 4/line 96-112	Methods/1Paragraph
Setting	5	Describe the setting, locations and relevant dates, including periods of recruitment, exposure, follow-up, and data collection.	Page 4/line 96-112	Methods/1Paragraph
Participants	6	(a) **Cohort study** – Give the eligibility criteria, and the sources and methods of selection of participants. Describe methods of follow-up. **Case-control study** – Give the eligibility criteria, and the sources and methods of case ascertainment and control selection. Give the rationale for the choice of cases and controls. **Cross-sectional study** – Give the eligibility criteria, and the sources and methods of selection of participants. (*Give information on the criteria and methods for selection of subsets of participants from a larger study, when relevant.)*	N/A	N/A
		(b) **Cohort study** – For matched studies, give matching criteria and number of exposed and unexposed. **Case-control study** – For matched studies, give matching criteria and the number of controls per case.	N/A	N/A
Variables	7	(a) Clearly define all outcomes, exposures, predictors, potential confounders, and effect modifiers. Give diagnostic criteria, if applicable. (b) Clearly define genetic exposures (genetic variants) using a widely-used nomenclature system. Identify variables likely to be associated with population stratification (confounding by ethnic origin).	Page 5-7/line 130-191	Methods/4-8Paragraph

Data sources/ measurement	8*	(a) For each variable of interest, give sources of data and details of methods of assessment (measurement). Describe comparability of assessment methods if there is more than one group. (b) Describe laboratory methods, including source and storage of DNA, genotyping methods and platforms (including the allele calling algorithm used, and its version), error rates and call rates. State the laboratory/centre where genotyping was done. Describe comparability of laboratory methods if there is more than one group. Specify whether genotypes were assigned using all of the data from the study simultaneously or in smaller batches.	Page 4-5/line 65-129	Methods/1-3Paragraph
Bias	9	(a) Describe any efforts to address potential sources of bias. (b) or quantitative outcome variables, specify if any investigation of potential bias resulting from pharmacotherapy was undertaken. If relevant, describe the nature and magnitude of the potential bias, and explain what approach was used to deal with this.	Page 4-5/line 965-129	Methods/1-3Paragrap
Study size	10	Explain how the study size was arrived at.	Page 4/line 96-112	Methods/1 Paragraph
Quantitative variables	11	Explain how quantitative variables were handled in the analyses. If applicable, describe which groupings were chosen, and why. *(If applicable, describe how effects of treatment were dealt with.)*	Page 5-7/line 130-191	Methods/4-8Paragraph
Statistical methods	12	(a) Describe all statistical methods, including those used to control for confounding. *[State software version used and options (or settings) chosen.]*	Page 7/line 193-194	Methods/9Paragraph
		(b) Describe any methods used to examine subgroups and interactions.	Page 7/line 193-194	Methods/9Paragraph
		(c) Explain how missing data were addressed.	Page 7/line 193-194	Methods/9Paragraph
		(d) **Cohort study** – If applicable, explain how loss to follow-up was addressed. **Case-control study** – If applicable, explain how matching of cases and controls was addressed. **Cross-sectional study** – If applicable, describe analytical methods taking account of sampling strategy.	N/A	N/A
		(e) Describe any sensitivity analyses.	Page 7/line 193-194	Methods/9Paragraph
		(f) State whether Hardy-Weinberg equilibrium was considered and, if so, how.	Page 7/line 193-194	Methods/9Paragraph
		(g) Describe any methods used for inferring genotypes or haplotypes.	Page 7/line 193-194	Methods/9Paragraph
		(h) Describe any methods used to assess or address population stratification.	Page 7/line 193-194	Methods/9Paragraph
		(i) Describe any methods used to address multiple comparisons or to control risk of false positive findings.	Page 7/line 193-194	Methods/9Paragraph
		(j) Describe any methods used to address and correct for relatedness among subjects	Page 7/line 193-194	Methods/9Paragraph

Results				
Participants	13*	(a) Report the numbers of individuals at each stage of the study – e.g., numbers potentially eligible, examined for eligibility, confirmed eligible, included in the study, completing follow-up, and analysed. *(Report numbers of individuals in whom genotyping was attempted and numbers of individuals in whom genotyping was successful).*	Page 7-8/line 198-208	Result/1 Paragraph
		(b) Give reasons for non-participation at each stage.	Page 7-8/line 198-208	Result/1 Paragraph
		(c) Consider use of a flow diagram.	Page 7-8/line 198-208	Result/1 Paragraph
Descriptive data	14*	(a) Give characteristics of study participants (e.g., demographic, clinical, social) and information on exposures and potential confounders. *(Consider giving information by genotype.)*	Page 7-10/line 198-283	Result/1-5Paragraph
		(b) Indicate the number of participants with missing data for each variable of interest.	Page 7-10/line 198-283	Result/1-5Paragraph
		(c) **Cohort study** – Summarize follow-up time (e.g., average and total amount).	n/a	n/a
Outcome data	15*	**Cohort study** – Report numbers of outcome events or summary measures over time. *[Report outcomes (phenotypes) for each genotype category over time]*	n/a	n/a
		Case-control study – Report numbers in each exposure category, or summary measures of exposure. *(Report numbers in each genotype category)*	n/a	n/a
		Cross-sectional study – Report numbers of outcome events or summary measures. *[Report outcomes (phenotypes) for each genotype category]*	n/a	n/a
Main results	16	(a) Give unadjusted estimates and, if applicable, confounder-adjusted estimates and their precision (e.g., 95% confidence intervals). Make clear which confounders were adjusted for and why they were included.	Page 7-10/line 198-283	Result/1-5Paragraph
		(b) Report category boundaries when continuous variables were categorized.	Page 7-10/line 198-283	Result/1-5Paragraph
		(c) If relevant, consider translating estimates of relative risk into absolute risk for a meaningful time period.	Page 7-10/line 198-283	Result/1-5Paragraph
		(d) Report results of any adjustments for multiple comparisons.	Page 7-10/line 198-283	Result/1-5Paragraph
Other analyses	17	(a) Report other analyses done – e.g., analyses of subgroups and interactions, and sensitivity analyses.	n/a	n/a
		(b) If numerous genetic exposures (genetic variants) were examined, summarize results from all analyses undertaken.	n/a	n/a
		(c) If detailed results are available elsewhere, state how they can be accessed.	n/a	n/a
Discussion				
Key results	18	Summarize key results with reference to study objectives.	Page 10-11/line 286-300	Discussion/1-2Paragraph

Limitations	19	Discuss limitations of the study, taking into account sources of potential bias or imprecision. Discuss both direction and magnitude of any potential bias.	Page 13/line 358-367	Discussion/9-10Paragraph
Interpretation	20	Give a cautious overall interpretation of results considering objectives, limitations, multiplicity of analyses, results from similar studies, and other relevant evidence.	Page 10-13/line 286-366	Discussion/1-10Paragraph
Generalizability	21	Discuss the generalizability (external validity) of the study results.	Page 13/line 368-371	Discussion/11Paragraph
Other Information				
Funding	22	Give the source of funding and the role of the funders for the present study and, if applicable, for the original study on which the present article is based.	Page 13-14/line 374-380	Funding

From: Little J, Higgins JPT, Ioannidis JPA, Moher D, Gagnon F, et al. (2009) STrengthening the REporting of Genetic Association Studies (STREGA)—An extension of the STROBE Statement. PLoS Med 6(2): e1000022. doi:10.1371/journal.pmed.1000022

* Give information separately for cases and controls in case-control studies and, if applicable, for exposed and unexposed groups in cohort and cross-sectional studies.

Article information: https://dx.doi.org/10.21037/jgo-23-247
*As the checklist was provided upon initial submission, the page number/line number reported may be changed due to copyediting and may not be referable in the published version. In this case, the section/paragraph may be used as an alternative reference.