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.	1-92	Title and Abstrac
		(b) Provide in the abstract an informative and balanced summary of what was done and what was found.	86-92	Title and Abstrac
Introduction				
Background rationale	2	Explain the scientific background and rationale for the investigation being reported.	100-147	Introduction
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.)*	100-147	Introduction
Methods				
Study design	4	Present key elements of study design early in the paper.	149-199	Methods
Setting	5	Describe the setting, locations and relevant dates, including periods of recruitment, exposure, follow-up, and data collection.	149-199	Methods
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.)*	Not involved	Not involved
		(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.	Not involved	Not involved
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).	149-199	Methods

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.	149-199	Methods
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.	Not involved	Not involved
Study size	10	Explain how the study size was arrived at.	149-156	Method
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.)*	Not involved	Not involved
Statistical methods	12	(a) Describe all statistical methods, including those used to control for confounding. *[State software version used and options (or settings) chosen.]*	194-199	Methods
		(b) Describe any methods used to examine subgroups and interactions.	Not involved	Not involved
		(c) Explain how missing data were addressed.	Not involved	Not involved
		(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.	Not involved	Not involved
		(e) Describe any sensitivity analyses.	Not involved	Not involved
		(f) State whether Hardy-Weinberg equilibrium was considered and, if so, how.	Not involved	Not involved
		(g) Describe any methods used for inferring genotypes or haplotypes.	Not involved	Not involved
		(h) Describe any methods used to assess or address population stratification.	Not involved	Not involved
		(i) Describe any methods used to address multiple comparisons or to control risk of false positive findings.	Not involved	Not involved
		(j) Describe any methods used to address and correct for relatedness among subjects	194-199	Methods

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).*	201-208	Results
		(b) Give reasons for non-participation at each stage.	Not involved	Not involved
		(c) Consider use of a flow diagram.	Not involved	Not involved
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.)*	201-208	Results
		(b) Indicate the number of participants with missing data for each variable of interest.	Not involved	Not involved
		(c) **Cohort study** – Summarize follow-up time (e.g., average and total amount).	Not involved	Not involved
Outcome data	15*	**Cohort study** – Report numbers of outcome events or summary measures over time. *[Report outcomes (phenotypes) for each genotype category over time]*	Not involved	Not involved
		Case-control study – Report numbers in each exposure category, or summary measures of exposure. *(Report numbers in each genotype category)*	Not involved	Not involved
		Cross-sectional study – Report numbers of outcome events or summary measures. *[Report outcomes (phenotypes) for each genotype category]*	Not involved	Not involved
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.	210-291	Results
		(b) Report category boundaries when continuous variables were categorized.	210-291	Results
		(c) If relevant, consider translating estimates of relative risk into absolute risk for a meaningful time period.	210-291	Results
		(d) Report results of any adjustments for multiple comparisons.	210-291	Results
Other analyses	17	(a) Report other analyses done – e.g., analyses of subgroups and interactions, and sensitivity analyses.	210-291	Results
		(b) If numerous genetic exposures (genetic variants) were examined, summarize results from all analyses undertaken.	210-291	Results
		(c) If detailed results are available elsewhere, state how they can be accessed.	210-291	Results
Discussion				
Key results	18	Summarize key results with reference to study objectives.	293-417	Discussion

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.	418-428	Discussion
Interpretation	20	Give a cautious overall interpretation of results considering objectives, limitations, multiplicity of analyses, results from similar studies, and other relevant evidence.	430-441	Discussion
Generalizability	21	Discuss the generalizability (external validity) of the study results.	Not involved	Not involved
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.	Not involved	Not involved

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.

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*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.