

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/paragraph 1
		(b) Provide in the abstract an informative and balanced summary of what was done and what was found.	Page 2-3/Line 35-69	Abstract/paragraph 1
Introduction				
Background rationale	2	Explain the scientific background and rationale for the investigation being reported.	Page 3-5/Line 74-150	Introduction/paragraph 1-4
Objectives	3	State specific objectives, including any pre-specified hypotheses. <i>(State if the study is the first report of a genetic association, a replication effort, or both.)</i>	Page 5/Line 150-157	Introduction/paragraph 1
Methods				
Study design	4	Present key elements of study design early in the paper.	Page 5-6/Line 162-181	Methods/paragraph 1
Setting	5	Describe the setting, locations and relevant dates, including periods of recruitment, exposure, follow-up, and data collection.	Page 5-6/Line 162-181	Methods/paragraph 1
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. <i>(Give information on the criteria and methods for selection of subsets of participants from a larger study, when relevant.)</i>	Not applicable , is not involved.	Not applicable , is 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 applicable , is not involved.	Not applicable , is 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).	Not applicable , is not involved.	Not applicable , is not involved.

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 6-9/Line 183-252	All 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 applicable , is not involved.	Not applicable , is not involved.
Study size	10	Explain how the study size was arrived at.	Page 5-6/Line 163-165	Methods/paragraph 1
Quantitative variables	11	Explain how quantitative variables were handled in the analyses. If applicable, describe which groupings were chosen, and why. <i>(If applicable, describe how effects of treatment were dealt with.)</i>	Not applicable , is not involved.	Not applicable , is not involved.
Statistical methods	12	(a) Describe all statistical methods, including those used to control for confounding. <i>[State software version used and options (or settings) chosen.]</i>	Not applicable , is not involved.	Not applicable , is not involved.
		(b) Describe any methods used to examine subgroups and interactions.	Not applicable , is not involved.	Not applicable , is not involved.
		(c) Explain how missing data were addressed.	Not applicable , is not involved.	Not applicable , is 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 applicable , is not involved.	Not applicable , is not involved.
		(e) Describe any sensitivity analyses.	Not applicable , is not involved.	Not applicable , is not involved.
		(f) State whether Hardy-Weinberg equilibrium was considered and, if so, how.	Not applicable , is not involved.	Not applicable , is not involved.
		(g) Describe any methods used for inferring genotypes or haplotypes.	Page 6-7/Line 183-228	All methods
		(h) Describe any methods used to assess or address population stratification.	Page 5-6/Line 163-165	Methods/paragraph 1
		(i) Describe any methods used to address multiple comparisons or to control risk of false positive findings.	Page 5-8/Line 162-251	All methods
		(j) Describe any methods used to address and correct for relatedness among subjects	Not applicable , is not involved.	Not applicable , is not involved.

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. <i>(Report numbers of individuals in whom genotyping was attempted and numbers of individuals in whom genotyping was successful).</i>	Page 8/Line 255-266	Results/paragraph 1
		(b) Give reasons for non-participation at each stage.	Not applicable , is not involved.	Not applicable , is not involved.
		(c) Consider use of a flow diagram.	Not applicable , is not involved.	Not applicable , is not involved.
Descriptive data	14*	(a) Give characteristics of study participants (e.g., demographic, clinical, social) and information on exposures and potential confounders. <i>(Consider giving information by genotype.)</i>	Page 8/Line 255-266	Results/paragraph 1
		(b) Indicate the number of participants with missing data for each variable of interest.	Not applicable , is not involved.	Not applicable , is not involved.
		(c) Cohort study – Summarize follow-up time (e.g., average and total amount).	Not applicable , is not involved.	Not applicable , is not involved.
Outcome data	15*	Cohort study – Report numbers of outcome events or summary measures over time. <i>[Report outcomes (phenotypes) for each genotype category over time]</i>	is not involved.	is not involved.
		Case-control study – Report numbers in each exposure category, or summary measures of exposure. <i>(Report numbers in each genotype category)</i>	Not applicable , is not involved.	Not applicable , is not involved.
		Cross-sectional study – Report numbers of outcome events or summary measures. <i>[Report outcomes (phenotypes) for each genotype category]</i>	Not applicable , is not involved.	Not applicable , is 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.	Page 9-12/Line 268-374	All Results
		(b) Report category boundaries when continuous variables were categorized.	Not applicable , is not involved.	Not applicable , is not involved.
		(c) If relevant, consider translating estimates of relative risk into absolute risk for a meaningful time period.	Not applicable , is not involved.	Not applicable , is not involved.
		(d) Report results of any adjustments for multiple comparisons.	Not applicable , is not involved.	Not applicable , is not involved.
Other analyses	17	(a) Report other analyses done – e.g., analyses of subgroups and interactions, and sensitivity analyses.	Not applicable , is not involved.	Not applicable , is not involved.
		(b) If numerous genetic exposures (genetic variants) were examined, summarize results from all analyses undertaken.	Page 9-12/Line 268-374	All Results
		(c) If detailed results are available elsewhere, state how they can be accessed.	Not applicable , is not involved.	Not applicable , is not involved.
Discussion				
Key results	18	Summarize key results with reference to study objectives.	Page 12-20/Line 376-619	All 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.	Page 20/Line 620-633	Discussion/last paragraph
Interpretation	20	Give a cautious overall interpretation of results considering objectives, limitations, multiplicity of analyses, results from similar studies, and other relevant evidence.	Page 12/Line 377-386	Discussion/Paragraph 1
Generalizability	21	Discuss the generalizability (external validity) of the study results.	Page 12-20/Line 376-619	All Discussion
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 20/Line 636-639	Funding/Paragraph 2

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.