

STROBE Statement—checklist of items that should be included in reports of observational studies
with STREGA reporting guidelines, extended from STROBE Statement

	Item	Recommendation	Extension for Genetic Association Studies	Page
Title and abstract	1	(a) Indicate the study’s design with a commonly used term in the title or the abstract		1, 2
		(b) Provide in the abstract an informative and balanced summary of what was done and what was found		1, 2
Introduction				
Background/ rationale	2	Explain the scientific background and rationale for the investigation being reported		2
Objectives	3	State specific objectives, including any prespecified hypotheses	State if the study is the first report of a genetic association, a replication effort, or both	2
Methods				
Study design	4	Present key elements of study design early in the paper		2, 3
Setting	5	Describe the setting, locations, and relevant dates, including periods of recruitment, exposure, follow-up, and data collection		2, 3
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	3
		(b) Cohort study—For matched studies, give matching criteria and number of exposed and unexposed Case-control study—For matched studies, give matching		3

		criteria and the number of controls per case		
Variables	7	Clearly define all outcomes, exposures, predictors, potential confounders, and effect modifiers. Give diagnostic criteria, if applicable	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)	3, 4, 5
Data sources/ measurement	8*	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	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/center 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	3, 4, 5
Bias	9	Describe any efforts to address potential sources of bias	For 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	5
Study size	10	Explain how the study size was arrived at		5
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	5

Statistical methods	12	(a) Describe all statistical methods, including those used to control for confounding	State software version used and options (or settings) chosen	5
		(b) Describe any methods used to examine subgroups and interactions		5
		(c) Explain how missing data were addressed		5
		(d) Cohort study—If applicable, explain how loss to follow-up was addressed		3, 4, 5
		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		
		(e) Describe any sensitivity analyses		—
		(f) State whether Hardy–Weinberg equilibrium was considered and, if so, how	—	
		(g) Describe any methods used for inferring genotypes or haplotypes	—	
		(h) Describe any methods used to assess or address population stratification	—	
	(i) Describe any methods used to address multiple comparisons or to control risk of false-positive findings	—		
	(j) Describe any methods used to address and correct for relatedness among subjects	—		
Results				
Participants	13*	(a) Report numbers of individuals at each stage of study—eg 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	3

		(b) Give reasons for non-participation at each stage		3
		(c) Consider use of a flow diagram		3
Descriptive data	14*	(a) Give characteristics of study participants (eg demographic, clinical, social) and information on exposures and potential confounders	Consider giving information by genotype	6, 7
		(b) Indicate number of participants with missing data for each variable of interest		6, 7
		(c) <i>Cohort study</i> —Summarise follow-up time (eg, average and total amount)		6, 7
Outcome data	15*	<i>Cohort study</i> —Report numbers of outcome events or summary measures over time	Report outcomes (phenotypes) for each genotype category over time	6, 7
		<i>Case-control study</i> —Report numbers in each exposure category, or summary measures of exposure	Report numbers in each genotype category	6, 7
		<i>Cross-sectional study</i> —Report numbers of outcome events or summary measures	Report outcomes (phenotypes) for each genotype category	6, 7
Main results	16	(a) Give unadjusted estimates and, if applicable, confounder-adjusted estimates and their precision (eg 95% confidence interval). Make clear which confounders were adjusted for and why they were included		6, 7
		(b) Report category boundaries when continuous variables were categorized		6, 7
		(c) If relevant, consider translating estimates of relative risk into absolute risk for a meaningful time period		6, 7
		(d) Report results of any adjustments for multiple comparisons		6, 7
Other analyses	17	Report other analyses done—eg analyses of subgroups and interactions, and sensitivity analyses		6, 7
		(b) If numerous genetic exposures (genetic variants) were examined, summarize results from all analyses undertaken		6, 7
		(c) If detailed results are available elsewhere, state how they		6, 7

can be accessed

Discussion			
Key results	18	Summarise key results with reference to study objectives	9
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	8, 9
Interpretation	20	Give a cautious overall interpretation of results considering objectives, limitations, multiplicity of analyses, results from similar studies, and other relevant evidence	8, 9
Generalisability	21	Discuss the generalisability (external validity) of the study results	9
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	9

*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.

Note: An Explanation and Elaboration article discusses each checklist item and gives methodological background and published examples of transparent reporting. The STROBE checklist is best used in conjunction with this article (freely available on the Web sites of PLoS Medicine at <http://www.plosmedicine.org/>, Annals of Internal Medicine at <http://www.annals.org/>, and Epidemiology at <http://www.epidem.com/>). Information on the STROBE Initiative is available at www.strobe-statement.org.