Table S1. STrengthening the REporting of Genetic Association studies (STREGA) reporting recommendations, extended from STROBE Statement.

Item	Item no	STROBE Guideline	Extension for Genetic Association Studies (STREGA)	Section, paragraph
Title and Abstract	1	(a) Indicate the study's design with a commonly used term in the title or the abstract.		Abstract, 2
		(b) Provide in the abstract an informative and balanced summary of what was done and what was found.		Abstract, 2
Introduction				
Background rationale	2	Explain the scientific background and rationale for the investigation being reported.		Abstract, 2 and Introduction, 3, 4 and 4.
Objectives	3	State specific objectives, including any pre-specified hypotheses		Abstract, 2 and Introduction, and 4.
Methods				
Study design	4	Present key elements of study design early in the paper.		Materials and methods, 7-8
Setting	5	Describe the setting, locations, and relevant dates, including periods of recruitment, exposure, follow-up and data collection.		Materials and methods, 6
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.	***The information is given in: Study subjects for the* Case–control study**	Materials and methods,6-8. Case–control study

		Cross-sectional study – Give the eligibility criteria, and the sources and methods of selection of participants.		
		(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.		
Variables	7	(a) Clearly define all outcomes, exposures, predictors, potential confounders, and effect modifiers. Give diagnostic criteria, if applicable.		Materials and methods,6-8
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. Specify whether genotypes were assigned using all of the data from the study simultaneously or in smaller batches.***	Materials and methods,6-8
Bias	9	(a) Describe any efforts to address potential sources of bias.	***(b) 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.***	
Study size	10	Explain how the study size was arrived at.		Materials and methods, 7
Quantitative variables	11	Explain how quantitative variables were handled in the analyses. If applicable,	***If applicable, describe how effects of treatment were dealt with.***	

		describe which groupings were chosen, and why.		
Statistical methods	12	(a) Describe all statistical methods, including those used to control for confounding.	***State software version used and options (or settings) chosen.***	Materials and methods 10
		(b) Describe any methods used to examine subgroups and interactions.		Materials and methods 10
		(c) Explain how missing data were addressed.		
		(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.		
		(e) Describe any sensitivity analyses.		
			(f) State whether Hardy-Weinberg equilibrium was considered and, if so, how.	NA
			(g) Describe any methods used for inferring genotypes or haplotypes.	NA
			(h) Describe any methods used to assess or address population stratification.	NA
			(i) Describe any methods used to address multiple comparisons or to control risk of false positive findings.	Materials and methods 9
			(j) Describe any methods used to address and	NA

			correct for relatedness among subjects.	
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.***	Results, 11, Table 1
		(b) Give reasons for non-participation at each stage.		
		(c) Consider use of a flow diagram.		
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.***	Results, 11,
		(b) Indicate the number of participants with missing data for each variable of interest.		
		(c) **Cohort study –** Summarize follow-up time, e.g. average and total amount.		
Outcome data	15*	**Cohort study –** Report numbers of outcome events or summary measures over time.	***Report outcomes (phenotypes) for each genotype category over time***	Results, 11, Table 2 - 4
		Case–control study – Report numbers in each exposure category, or summary measures of exposure.	***Report numbers in each genotype category***	
		Cross-sectional study – Report numbers of outcome events or summary measures.	***Report outcomes (phenotypes) for each genotype category***	
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		Results, 12-14

		were adjusted for and why they were included.	Table 2 and, 3
		(b) Report category boundaries when continuous variables were categorized.	
		(c) If relevant, consider translating estimates of relative risk into absolute risk for a meaningful time period.	
		(d) Report results of any adjustments for multiple comparisons.	N.A
Other analyses	17	(a) Report other analyses done – e.g. analyses of subgroups and interactions, and sensitivity analyses.	Results, 12 Table 3 and Results, 14
		(b) If numerous genetic exposures (genetic variants) were examined, summarize results from all analyses undertaken.	
		(c) If detailed results are available elsewhere, state how they can be accessed.	NA
Discussion			
Key results	18	Summarize key results with reference to study objectives.	Discussion, 18-
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.	Discussion, 23
Interpretation	20	Give a cautious overall interpretation of results considering objectives, limitations, multiplicity of analyses, results from similar studies, and other relevant evidence.	Discussion 18-20
Generalizability	21	Discuss the generalizability (external validity) of the study results.	Discussion, 17-22

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.	Funding 23-24

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*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.