

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 1-3 | Title |
| | | (b) Provide in the abstract an informative and balanced summary of what was done and what was found. | Page 2/Line 31-49 | Abstract/Paragraph 2-4 |
| Introduction | | | | |
| Background rationale | 2 | Explain the scientific background and rationale for the investigation being reported. | Page 3-4/Line 52-172 | Introduction/Paragraph 1-6 |
| 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 4/Line 173-189 The study is a replication effort. | Introduction/Paragraph 7 |
| Methods | | | | |
| Study design | 4 | Present key elements of study design early in the paper. | Page 4/Line 191-205 | Method/Paragraph 1 |
| Setting | 5 | Describe the setting, locations and relevant dates, including periods of recruitment, exposure, follow-up, and data collection. | Page 4/Line 206-219 | Method/Paragraph 2 |
| 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> | Page 4/Line 220-240 | Method/Paragraph 2 |
| | | (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 This is a cross-sectional study. | N/A |
| Variables | 7 | (a) Clearly define all outcomes, exposures, predictors, potential confounders, and effect modifiers. Give diagnostic criteria, if applicable. | N/A There is no exposure in the study. | N/A |
| | | (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/Line 269-276 | Method/Paragraph 5 |

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| 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. | Page 4/Line 207-219 No comparability. | Method/Paragraph 2 |
| | | (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 5/Line 279-286 No comparability. | Method/Paragraph 5 |
| 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. | N/A No bias. | N/A |
| Study size | 10 | Explain how the study size was arrived at. | Page 5/Line 278-279 | Method/Paragraph 5 |
| 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> | Page 6/Line 290-298 | Method/Paragraph 6 |
| 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> | Page 6/Line 299-380 | Method/Paragraph 7-9 |
| | | (b) Describe any methods used to examine subgroups and interactions. | N/A No subgroup and interaction. | N/A |
| | | (c) Explain how missing data were addressed. | N/A No missing data. | N/A |
| | | (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. | Page 6/Line 290-298 | Method/Paragraph 6 |
| | | (e) Describe any sensitivity analyses. | N/A No sensitivity analysis. | N/A |
| | | (f) State whether Hardy-Weinberg equilibrium was considered and, if so, how. | Page 5/Line 269-276 | Method/Paragraph 5 |
| | | (g) Describe any methods used for inferring genotypes or haplotypes. | Page 5/Line 269-276 | Method/Paragraph 5 |
| | | (h) Describe any methods used to assess or address population stratification. | Page 5/Line 269-276 | Method/Paragraph 5 |
| | | (i) Describe any methods used to address multiple comparisons or to control risk of false positive findings. | Page 6/Line 346-353 | Method/Paragraph 8 |
| | | (j) Describe any methods used to address and correct for relatedness among subjects | N/A No relatedness among subjects. | N/A |

| 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 5/Line 269-279 | Method/Paragraph 5 |
| | | (b) Give reasons for non-participation at each stage. | N/A The participants participate at stage. | N/A |
| | | (c) Consider use of a flow diagram. | Page 5/Figure 1 | Method/Paragraph 5 |
| 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 7/Table 1 | Results/Paragraph 1 |
| | | (b) Indicate the number of participants with missing data for each variable of interest. | N/A No missing data. | N/A |
| | | (c) Cohort study – Summarize follow-up time (e.g., average and total amount). | N/A This is a cross-sectional study. | N/A |
| 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> | N/A This is a cross-sectional study. | N/A |
| | | Case-control study – Report numbers in each exposure category, or summary measures of exposure. <i>(Report numbers in each genotype category)</i> | N/A This is a cross-sectional study. | N/A |
| | | Cross-sectional study – Report numbers of outcome events or summary measures. <i>[Report outcomes (phenotypes) for each genotype category]</i> | Page 12-13/Line 505-521 | Results/Paragraph 5 |
| 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. | N/A No confounders. | N/A |
| | | (b) Report category boundaries when continuous variables were categorized. | N/A Continuous variables were not categorized. | N/A |
| | | (c) If relevant, consider translating estimates of relative risk into absolute risk for a meaningful time period. | N/A Not relevant. | N/A |
| | | (d) Report results of any adjustments for multiple comparisons. | Page 8-13/Line 423-521 | Results/Paragraph 4-5 |
| Other analyses | 17 | (a) Report other analyses done – e.g., analyses of subgroups and interactions, and sensitivity analyses. | Page 8-12/Line 423-504 | Results/Paragraph 4 |
| | | (b) If numerous genetic exposures (genetic variants) were examined, summarize results from all analyses undertaken. | Page 8-12/Line 423-504 | Results/Paragraph 4 |
| | | (c) If detailed results are available elsewhere, state how they can be accessed. | Page 7/Line 393-412 | Results/Paragraph 2 |
| Discussion | | | | |

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| Key results | 18 | Summarize key results with reference to study objectives. | Page 14/Line 549-625 | Discussion/Paragraph 3-7 |
| 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 14-15/Line 626-643 | Discussion/Paragraph 8 |
| Interpretation | 20 | Give a cautious overall interpretation of results considering objectives, limitations, multiplicity of analyses, results from similar studies, and other relevant evidence. | Page 14/Line 608-625 | Discussion/Paragraph 7 |
| Generalizability | 21 | Discuss the generalizability (external validity) of the study results. | Page 14/Line 608-625 | Discussion/Paragraph 7 |
| 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 15/Line 651-663 | Acknowledgments/Paragraph 1 |

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.