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☐ Initial submission ☐ Revised version ☒ Final submission

Life Sciences Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form is intended for publication with all accepted life science papers and provides structure for consistency and transparency in reporting. Every life science submission will use this form; some list items might not apply to an individual manuscript, but all fields must be completed for clarity.

For further information on the points included in this form, see Reporting Life Sciences Research. For further information on Nature Research policies, including our data availability policy, see Authors & Referees and the Editorial Policy Checklist.

Experimental design

1. Sample size

Describe how sample size was determined.

Studies were invited to participate in the meta-analysis if: (1) genome-wide genotype data were available for >2,000 individuals (prior to final phenotype exclusions); and (2): information was available on asthma, hay fever and eczema status.

2. Data exclusions

Describe any data exclusions.

Pre-defined exclusion criteria were applied at the study-level as part of standard GWAS quality control procedures. These included, for example, excluding samples and SNPs with high levels of missing data.

3. Replication

Describe whether the experimental findings were reliably reproduced.

No replication phase was included in this study.

4. Randomization

Describe how samples/organisms/participants were allocated into experimental groups.

Participants were allocated to the case or control groups based on available information for asthma, hay fever and eczema. Specifically, participants suffering from one or more allergic condition were considered as cases. Participants who had never suffered from any allergic condition were considered as controls.

5. Blinding

Describe whether the investigators were blinded to group allocation during data collection and/or analysis.

For most studies, investigators involved in blood collection and DNA genotyping were blinded to case-control status.

Note: all studies involving animals and/or human research participants must disclose whether blinding and randomization were used.

6. Statistical parameters

For all figures and tables that use statistical methods, confirm that the following items are present in relevant figure legends (or in the Methods section if additional space is needed).

n/a	Confirmed
☐	☒ The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement (animals, litters, cultures, etc.)
☐	☒ A description of how samples were collected, noting whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☒	☐ A statement indicating how many times each experiment was replicated
☐	☒ The statistical test(s) used and whether they are one- or two-sided (note: only common tests should be described solely by name; more complex techniques should be described in the Methods section)
☐	☒ A description of any assumptions or corrections, such as an adjustment for multiple comparisons
☐	☒ The test results (e.g. *P* values) given as exact values whenever possible and with confidence intervals noted
☐	☒ A clear description of statistics including central tendency (e.g. median, mean) and variation (e.g. standard deviation, interquartile range)
☒	☐ Clearly defined error bars

See the web collection on statistics for biologists for further resources and guidance.

Software

Policy information about availability of computer code

7. Software

Describe the software used to analyze the data in this study.	R, PLINK, METAL, SNPTEST, BOLT-LMM, RAREMETALWORKER, GCTA, MACH2DAT, EPACTS, EIGENSTRAT

For manuscripts utilizing custom algorithms or software that are central to the paper but not yet described in the published literature, software must be made available to editors and reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). *Nature Methods* guidance for providing algorithms and software for publication provides further information on this topic.

Materials and reagents

Policy information about availability of materials

8. Materials availability

Indicate whether there are restrictions on availability of unique materials or if these materials are only available for distribution by a for-profit company.	Summary statistics of the meta-analysis without the 23andMe study will be made publicly available at the time of publication. The full GWAS summary statistics for the 23andMe discovery data set will be made available through 23andMe to qualified researchers under an agreement with 23andMe that protects the privacy of the 23andMe participants. Please contact David Hinds (dhinds@23andme.com) for more information and to apply to access the 23andMe data.

9. Antibodies

Describe the antibodies used and how they were validated for use in the system under study (i.e. assay and species).	No antibodies were used

10. Eukaryotic cell lines

a. State the source of each eukaryotic cell line used.	No cell lines were used
b. Describe the method of cell line authentication used.	No cell lines were used
c. Report whether the cell lines were tested for mycoplasma contamination.	No cell lines were used
d. If any of the cell lines used are listed in the database of commonly misidentified cell lines maintained by ICLAC, provide a scientific rationale for their use.	No cell lines were used

Animals and human research participants

Policy information about studies involving animals; when reporting animal research, follow the ARRIVE guidelines

11. Description of research animals

Provide details on animals and/or animal-derived materials used in the study.	No animals were used

Policy information about studies involving human research participants

12. Description of human research participants

Describe the covariate-relevant population characteristics of the human research participants.	We studied 180,129 participants who reported having suffered from asthma and/or hay fever and/or eczema, and 180,709 participants who reported not suffering from any of these diseases. Mean age within each contributing study varied between 4 and 62, with females representing 39% to 68% of the sample size.