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Life Sciences Reporting Summary

Nature Research wishes to improve the reproducibility of the work we publish. This form is published with all life science papers and is intended to promote consistency and transparency in reporting. All life sciences submissions use this form; while some list items might not apply to an individual manuscript, 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.

   We aimed to include all available data-sets on allergic rhinitis worldwide. In this study we achieved a sample size that was several times larger than previous GWAS- studies, which was sufficent for providing genome-wide significant findings.

2. Data exclusions

   Describe any data exclusions.

   Other than the preliminary analyses/experimental optimization, no data were excluded.

3. Replication

   Describe whether the experimental findings were reliably reproduced.

   No experimental studies were performed.

4. Randomization

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

   No experimental studies were performed. Cases and controls for genome-wide association were analyzed based upon predefined criteria.

5. Blinding

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

   No blinding was performed and not considered relevant in this meta-Genome-wide association study.

   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 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 summary of the descriptive 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.	This is described in details in the methods section. In short, for AR, AS, and NAR, meta-analysis for the discovery phase was conducted using GWAMA, while meta-analysis of replication candidates from the AR discovery phase was carried out using R version 3.4.0, and the meta package version 4.8-2 with an inverse variance weighted fixed-effect model. Additional software include EasyQC (v9.2), STRING (v10), ChEMBL Database (v22), GGraph (v1.0.0), iGraph (v1.0.1), TidyVerse (v1.1.1), LDHUB platform (v1.3.1), GENCODE (v19 and v24, Genome-wide Complex Trait Analysis (GCTA) (v. 1.26.0), Plink (v1.90b3.42), PyMOL (v1.8.2.1), LDSC (v.1.0), LDHUB platform (v1.3.1), GTEx (V6p), UpSetR package (v1.3.2), GWAS Analysis of Regulatory or Functional Information Enrichment with LD correction (GARFIELD) method (v1), Python (v2.7.12), HIBAG (v1.2.3).

For all studies, we encourage code deposition in a community repository (e.g. GitHub). Authors must make computer code available to editors and reviewers upon request. The *Nature Methods* guidance for providing algorithms and software for publication may be useful for any submission.

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.	No unique materials were used.

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 eukaryotic cell lines were used.
b. Describe the method of cell line authentication used.	No eukaryotic cell lines were used.
c. Report whether the cell lines were tested for mycoplasma contamination.	No eukaryotic cell lines were used.
d. If any of the cell lines used in the paper are listed in the database of commonly misidentified cell lines maintained by ICLAC, provide a scientific rationale for their use.	No eukaryotic 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.	Relevant information on research participants in the individual studies is provided in the supplementary material.