Corresponding Author: Yukinori Okada, Yoichiro Kamatani

Date: Dec 8, 2017

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.

   The BioBank Japan Project was started in 2003 and has recruited approximately 200,000 participants. Clinical information were retrieved from medical records. DNA/serum samples were also collected. Most of them were genotyped by genome-wide SNP genotyping array. We selected as many subjects as possible if their genotype and phenotype (at least, one of the studied 58 quantitative traits) were both available.

2. Data exclusions

   Describe any data exclusions.

   We excluded samples and variants based on the standard quality control procedure in GWAS. Detailed information on quality controls were described in our manuscript.

3. Replication

   Describe whether the experimental findings were reliably reproduced.

   We searched for all of the identified loci in GWAS Catalog as well as previous literatures, and confirmed that around half of them robustly replicated the previous findings (51.7%). Because the BioBank Japan is the largest cohort in Japan and we simultaneously investigated more than 50 traits to illustrate a comprehensive landscape, to the best of our knowledge, there are no Japanese or east Asian replication cohort which covers all of the studied traits with enough sample sizes.

4. Randomization

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

   We applied quantitative genetics approach and treated the whole sample set as a single population, not allocated into groups.

5. Blinding

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

   Not applicable.

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.	We used publicly available softwares for the analyses. The used softwares were listed and described in the Method section in our manuscript.

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).	Not applicable.

10. Eukaryotic cell lines

a. State the source of each eukaryotic cell line used.	Not applicable.
b. Describe the method of cell line authentication used.	Not applicable.
c. Report whether the cell lines were tested for mycoplasma contamination.	Not applicable.
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.	Not applicable.

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.	Not applicable.

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 used 162,255 Japanese individuals from the BioBank Japan Project. For each of the studied 58 quantitative traits, GWAS was separately conducted using the subjects whose phenotype of the trait was available. We summarized detailed characteristics of the subjects for each trait in Supplementary Table 1.