nature research

Corresponding author(s): Kaoru Ito

Last updated by author(s): Aug 12, 2020

Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Research policies, see our Editorial Policies and the Editorial Policy Checklist.

Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a	Confirmed	
☐	☒	The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement
☐	☒	A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☐	☒	The statistical test(s) used AND whether they are one- or two-sided *Only common tests should be described solely by name; describe more complex techniques in the Methods section.*
☐	☒	A description of all covariates tested
☐	☒	A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
☐	☒	A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
☐	☒	For null hypothesis testing, the test statistic (e.g. *F*, *t*, *r*) with confidence intervals, effect sizes, degrees of freedom and *P* value noted *Give P values as exact values whenever suitable.*
☒	☐	For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
☒	☐	For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
☐	☒	Estimates of effect sizes (e.g. Cohen's *d*, Pearson's *r*), indicating how they were calculated

Our web collection on statistics for biologists contains articles on many of the points above.

Software and code

Policy information about availability of computer code

Data collection	No software was used.

Data analysis	We used open source softwares for the analysis, as listed below. GATK(3.6), https://software.broadinstitute.org/gatk; BWA(0.7.5a), http://bio-bwa.sourceforge.net; picard(2.5.0), https://broadinstitute.github.io/picard; Minimac3(2.0.1), https://genome.sph.umich.edu/wiki/Minimac3; Eagle(2.4.1), https://data.broadinstitute.org/alkesgroup/Eagle; ANNOVAR(2017Jun01), http://annovar.openbioinformatics.org; PLINK(1.93,2.0), https://www.cog-genomics.org/plink/1.9; LDSC(1.0.1), https://github.com/bulik/ldsc; MANTRA(2.0), provided by the author; METASOFT(2.0), http://genetics.cs.ucla.edu/meta; R(3.5.1), https://www.r-project.org; LDpred(1.0.11), https://github.com/bvilhjal/ldpred; DEPICT(1, release 194), https://data.broadinstitute.org/mpg/depict; SAIGE(0.36.3), https://github.com/weizhouUMICH/SAIGE; Popcorn(0.9.9), https://github.com/brielin/Popcorn LocusZoom(1.4), http://locuszoom.sph.umich.edu Further details are described in the Method section.

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research guidelines for submitting code & software for further information.

Data

Policy information about availability of data

All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A list of figures that have associated raw data
- A description of any restrictions on data availability

We used publicly available data as listed below.

dbSNP, https://www.ncbi.nlm.nih.gov/snp; GWAS catalog, https://www.ebi.ac.uk/gwas; GTEx, https://gtexportal.org/home; 1000 Genomes Project, http://www.1000genomes.org; ClinVar, https://www.ncbi.nlm.nih.gov/clinvar; gnomAD, https://gnomad.broadinstitute.org; HapMap project, http://hapmap.ncbi.nlm.nih.gov; CARDIoGRAMplusC4D, http://www.cardiogramplusc4d.org; Opentargets, https://genetics.opentargets.org; Mouse Genome Informatics, http://www.informatics.jax.org; PubTator, https://www.ncbi.nlm.nih.gov/research/pubtator; Global Lipids Genetics Consortium Results, http://csg.sph.umich.edu/willer/public

Further details are described in the Method section.

The summary statistics of the Japanese GWAS, and polygenic risk score derived in this study are publicly available in the National Bioscience Database Center (research ID: hum0014, https://humandbs.biosciencedbc.jp/en/). The phenotype information can be provided by the Biobank Japan project upon a request (https://biobankjp.org/english/index.html).

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☒ Life sciences ☐ Behavioural & social sciences ☐ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see nature.com/documents/nr-reporting-summary-flat.pdf

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	Because we aimed to create the largest sample size in the Japanese population in order to gain the statistical power, we included as many case and control individuals as possible in our analysis.
Data exclusions	We excluded individuals according to the standard quality control procedure of GWAS. Further details are described in the Method section.
Replication	Our Japanese GWAS identified 48 genome-wide significant (GWS) loci, where 40 previously reported loci were replicated. We also evaluated the directional consistency of the GWS loci between the Japanese GWAS and previously reported GWAS, and found that all signals are concordant in terms of the effect on the disease development. Additionally, the seven out of eight novel loci were replicated in the previous European or the East Asian external data set. For the loci identified in our transethnic meta-analysis, the replication is not applicable because we used all the available data. Futhermore, since the current transethnic meta-analysis is the largest GWAS for coronary artery disease, replication in small cohorts is not feasible.

Randomization	Randomization is not applicable, because this is a population based case-control analysis.
Blinding	Blinding is not applicable, because this is a population based case-control analysis.

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involved in the study
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☒	☐ Animals and other organisms
☐	☒ Human research participants
☒	☐ Clinical data
☒	☐ Dual use research of concern

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Human research participants

Policy information about studies involving human research participants

Population characteristics	The number of male and female subjects, the mean and standard deviation of the age in the Japanese GWAS and the PRS performance-testing analysis are provided in Supplementary Table 18.
Recruitment	The Biobank Japan (BBJ) Project The BBJ project (https://biobankjp.org/english.) is a hospital-based biobank. Participants were recruited at 12 medical institutes throughout Japan. Detailed information is described in the following papers: Nagai A. et al. Overview of the BioBank Japan Project: Study design and profile. J Epidemiol 27, S2–S8 (2017), Hirata M. et al. Cross-sectional analysis of BioBank Japan clinical data: A large cohort of 200,000 patients with 47 common diseases. J Epidemiol 27, S9–S21 (2017). The Nagahama cohort study The Nagahama cohort study (http://zeroji-cohort.com/english.) is a population-based cohort in Nagahama City, Shiga prefecture in Japan. The Nagahama cohort study recruited almost 10,000 healthy individuals between the ages of 30 and 74 who were not currently suffering from major illnesses, and periodic health examinations were performed and disease morbidity information were collected every five years. The Japan Public Health Center-based Prospective (JPHC) Study The JPHC study (https://epi.ncc.go.jp/en/jphc/index.html) is a public health center (PHC) based population study. The JPHC study recruited 33,736 residents in 9 PHC areas. Detailed information was described in the following paper: Tsugane S. and Sawada N. The JPHC study: design and some findings on the typical Japanese diet. Jpn. J. Clin. Oncol. 44, 777–782 (2014). The Japan Multi-Institutional Collaborative Cohort (J-MICC) Study The J-MICC study (http://www.jmicc.com/en) is a multicenter population-based cohort recruiting community dwellers, health checkup examinees, or first-visit patients in a cancer hospital in 14 study areas thourghout Japan. Detailed information was described in the following paper: Hamajima N. and J-MICC Study Group. The Japan Multi-Institutional Collaborative Cohort Study (J-MICC Study) to detect gene-environment interactions for cancer. Asian Pac. J. Cancer Prev. 8, 317–323 (2007). Osaka Acute Coronary Insufficiency Study (OACIS) The OACIS is a prospective, multicenter observational study conducted by Osaka University and 24 collaborating hospitals in Japan. The OACIS study recruited patients with acute myocardial infarction (AMI) who were referred to the 25 cardiovascular care units involved in this study group during 1998-2014. AMI was diagnosed based on the combination of clinical presentation and examinations by cardiologists .
Ethics oversight	Our study was approved by the appropriate Institutional Review Board at each facility and the informed consent was obtained from all participants in each study. We obtained approval from ethics committees of (1) RIKEN Center for Integrative Medical Sciences, (2) the Institute of Medical Sciences, The University of Tokyo, (3) Kyoto University, (4) National Cancer Center Japan, (5) Nagoya University, (6) Aichi Cancer Center, (7) Osaka University

Note that full information on the approval of the study protocol must also be provided in the manuscript.