nature portfolio

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Reporting Summary

Nature Portfolio 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 Portfolio 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	ThermoFisher Scientific's Axiom Analysis Suite Software were used to generate genotype data
Data analysis	PLINK, SHAPEIT, IMPUTE2, PRSice2, R 3.6.2

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 Portfolio 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 description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our policy

Upon request, the authors will provide the de-identified genetic and clinical datasets that were used for analysis

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	We included as many study subjects with both clinical variables and genome-wide genotype data available from four study cohorts, which included 1581 liver recipients, and 1555 donors and 2062 kidney recipients and 533 donors. Power calculation was not performed in the beginning of the study. However, we were able to detect the association signals between our main variable of interest and the main outcome of interest.
Data exclusions	We followed the genotype data QC rules commonly used in the field to determine samples to exclude: 1. Samples with a genotype missing rate >3% were excluded; 2. Samples with very high heterozygosity and suspected contamination, as well as sex-mismatches, were removed from further analysis. 3. Samples with pairwise identity by descent >0.3 in genetically more heterogeneous US cohorts and >0.1 in majority European descent Leuven cohort were excluded from the study.
Replication	The replication effort has been incorporated into this study. The association between T2D-PRS and pre-transplant DM was consistently replicated between liver and kidney transplant cohorts. The association between recipient T2D-PRS and PTDM was also replicated among all four cohorts included in this study. The association between donor T2D-PRS and PTDM risk was consistent between two liver cohorts included in this report.
Randomization	Randomization is not relevant to this study since there is no intervention/treatment involved.
Blinding	Bliding is not relevant to this study because this is an observational study using existing clinical and genetic data.

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	This study included transplant recipients recruited in three transplant centers (UPenn, Baylor, and Leuven), as well as study participants in a multicenter clinical trial (DeKAF, NCT00270712). The relevant clinical characteristics and phenotypes of interest have been detailed in the Table 1 of the main manuscript text.
Recruitment	All patients who transplanted in the participating centers were recruited.
Ethics oversight	Study was approved by IRB in individual participating centers.

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

Clinical data

Policy information about clinical studies

All manuscripts should comply with the ICMJE guidelines for publication of clinical research and a completed CONSORT checklist must be included with all submissions.

Clinical trial registration	NCT00270712 (relevant only for the DeKAF stduy, which is one of the four cohorts)
Study protocol	https://clinicaltrials.gov/ct2/show/NCT00270712 (for the DeKAF study)
Data collection	For all cohorts: biological specimens are obtained at recruitment, where is clinical data is generated during before, and at predetermined intervals after transplantation.
Outcomes	outcomes for the reported study were not defined prior to the initiation of the trial, or the establishement of the different biorepositories.