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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.

In this proof of concept study 47 donors were included. Previous eQTL studies have shown that this size is sufficient to detect eQTLs.

2. Data exclusions

Describe any data exclusions.

Two donors were included from downstream analysis as no genotype information was available to confidently assign the cells to these donors.

3. Replication

Describe whether the experimental findings were reliably reproduced.

77.7% (181/233) of the tested top cis-eQTLs (16/249 could not be tested as gene expression data was not available in the whole blood RNA-seq data) found in the total PBMCs were replicated (with 90.1% concordance) in whole blood RNA-seq data. The top co-expression QTLs found in CD4+ T cells remained after imputation and were replicated in whole blood RNA-seq data.

4. Randomization

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

The 47 donors were semi-randomly assigned to any of the 8 sample pools, taking into account that no relatives and approximately an equal number of male and females were included in each sample pool.

5. Blinding

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

All data was anonimyzed during data collection. During analysis, genotype information was used to assign each cell to its donor.

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.	CellRanger version 1.3, R package Seurat version 1.4, Demuxlet (http://www.biorxiv.org/content/early/2017/05/15/118778), eQTL pipeline version 1.2.4F (https://github.com/molgenis/systemsgenetics/tree/master/eqtl-mapping-pipeline). All custom-made code is made available via GitHub (https://github.com/molgenis/systemsgenetics/scRNA-seq).

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.	Processed (deanonimyzed) single-cell RNA-seq data, including a text file that links each cell barcode to its respective donor, has been deposited at the European Genome-phenome Archive (EGA), which is hosted by the EBI and the CRG, under accession number EGAS00001002560. Genotype data can be obtained and requested through our website (https://molgenis58.target.rug.nl/scrna-seq/) and will be made available through the Lifelines workspace.

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 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.	All research participants were enrolled in the general population (Northern part of the Netherlands) cohort Lifelines Deep (http://bmjopen.bmj.com/content/5/8/e006772.long).