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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	All DNA samples were collected from blood samples of 158 healthy Large White pigs. Qualified DNA libraries that passed quality control were sequenced on the DNBSEQ-T7 platform to generate 150 bp paired-end reads. Finally, after removing samples with identity-by-state (IBS) values below 90%, and all female individuals, a total of 134 RNA samples were retained for subsequent analysis. All RNA samples were isolated from peripheral blood mononuclear cells (PBMC) and neutrophils (Neu) obtained from 157 healthy Large White pigs. A total of 307 qualified RNA samples (PBMC=157, Neu=150) meeting the quality control thresholds (total RNA >200 ng and RNA Integrity Number >7.0) were selected for subsequent library construction. Sequencing libraries were prepared using the NEBNext® Ultra™ II RNA Library Prep Kit for Illumina® (NEB #E7775L) following the manufacturer's instructions, and were ultimately sequenced on the Illumina NovaSeq X Plus platform with a 150 bp paired-end (PE150) configuration. Finally, after removing samples with low mapping rates, identity-by-state (IBS) values below 90%, and all female individuals, a total of 259 RNA samples were retained for subsequent analysis.
Data analysis	All the computational scripts and codes (with software version) for RNA-Seq, WGS analyses, as well as the respective quality control, molecular phenotype normalization, genotype imputation, molQTL mapping, functional enrichment, colocalization are available at the FarmGTEx GitHub website (https://github.com/FarmGTEx/PigGTEx-Pipeline-v0). For RNA-Seq data analysis, we used fastp (v0.19.4), STAR (v2.5.3a), Subread (v2.0.6) and StringTie (v2.2.1), LeafCutter (v0.2.9) for quality control, mapping, gene expression quantification, alternative splicing, respectively. We use PCA for sample clustering. We use PCA to determine the optimal PC value for molQTL mapping. We used WGCNA (v1.69) for co-expression analysis. For gene functional enrichment analysis, we utilized the KEGG and GO functions implemented in the online tool KOBAS 3.0 (http://bioinfo.org/kobas/). We used Fisher's exact test to determine the enrichment multiples of molGene genes related to immune traits. For WGS analysis, we used fastp (v0.19.4), BWA (v0.7.17), Picard (v2.25.7), GATK (v4.1.4.1) for quality control, mapping, marked duplicated reads, variants calling, respectively. We removed SNPs with MAF < 0.05 and/or missing rate > 0.9 using bcftools (v1.9). For QTL mapping, we used TensorQTL (v1.0.3), aFC (v0.3), MashR (v0.2-6) for cis-QTL mapping, effect size estimation, tissue-sharing pattern

estimation, respectively. We used SnpEff (v5.1.2) to annotate the genomic regulatory regions of all molQTL.
Statistical analysis was performed using R v3.6.3.

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

The raw sequence data reported in this paper have been deposited in the Genome Sequence Archive (RNA-seq: CRA032459, CRA032460, https://ngdc.cncb.ac.cn/gsa) and Genome Variation Map (WGS: GVM001201, GVM001202, https://ngdc.cncb.ac.cn/gvm/) at the National Genomics Data Center (NGDC), part of the China National Center for Bioinformation / Beijing Institute of Genomics, Chinese Academy of Sciences.

Research involving human participants, their data, or biological material

Policy information about studies with human participants or human data. See also policy information about sex, gender (identity/presentation), and sexual orientation and race, ethnicity and racism.

Reporting on sex and gender	134 females and 24 males
Reporting on race, ethnicity, or other socially relevant groupings	NA
Population characteristics	NA
Recruitment	NA
Ethics oversight	NA

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

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	In summary, we analyzed 134 WGS datasets (10× sequencing depth), along with RNA-seq data from 134 PBMCs and 125 neutrophil samples. Following quality control filtering of lower-quality samples (see below), all remaining samples were included in subsequent analyses.
Data exclusions	We filtered out RNA-seq samples with a unique mapping rate below 65%, resulting in 134 PBMCs samples and 125 neutrophil samples. In total, 134 WGS samples and 259 RNA-seq samples were ultimately used for molQTL mapping.
Replication	To validate the cis-acting expression quantitative trait loci (cis-eQTLs), this study employed an integrated strategy combining linear mixed models (LMM) with external validation. First, we observed a strong correlation (Pearson's r = 0.75) between the summary statistics of cis-eQTLs derived from TensorQTL's linear regression model and those from the linear mixed model. Second, utilizing publicly available molQTL data from 11 immune tissues in the PigGTEx database for cross-tissue analysis, the results demonstrated that functionally or anatomically related tissues preferentially shared molQTLs: Specifically, 52.3% of eQTLs and sQTLs in PBMCs and 35% in neutrophils were shared with functionally/anatomically related tissues, with even higher sharing rates observed in functionally related tissues.
Randomization	The study is descriptive, sample were grouped by cell group, thus the randomization was not done.
Blinding	In this study, we analyzed all RNA-seq data and WGS data using a unified pipeline, and then conducted co-localization analysis of GWAS data. The blinded research design may not be applicable to this study. In cell culture experiments, researchers were aware of group allocation during data collection and analysis. Blinded analysis could not be implemented as the experiments required execution by a limited number of highly skilled personnel.

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
☒	☐ Clinical data
☒	☐ Dual use research of concern
☒	☐ Plants

Methods

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

Animals and other research organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research, and Sex and Gender in Research

Laboratory animals	The samples were randomly collected from 134 healthy Yorkshire pigs between 68 and 75 days old (average 70 days old)
Wild animals	NA
Reporting on sex	NA
Field-collected samples	NA
Ethics oversight	All the following procedures involving animals were approved by the Animal Welfare Committee of China Agricultural University in Beijing, China. Animal experiments were also conducted in strict accordance with regulations and guidelines established by this committee (permit number: DK996).

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

Plants

Seed stocks	NA
Novel plant genotypes	NA
Authentication	NA