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	Short reads WGS sequencing data of 16 samples were collected via illumina platforms. Long reads WGS sequencing data of 6 samples were collected via ONT PromethION platform. RNA-seq sequencing data of 12 samples were collected via illumina platforms. Genomic methylation sequencing data of 12 samples were collected via MGI T7 sequencing platform. Cut&Tag sequencing data of 50 samples were collected via Illumina platform. Hi-C sequencing data of 5 samples were collected via Illumina HiSeq instruments. Iso-seq sequencing data of 11 samples were PacBio sequencing platform.
Data analysis	Short reads and long reads WGS data processing and phasing analysis:Fastp v0.23.2; BWA v0.7.17; SAMTools v1.9; Minimap2 v2.17; GATK v4.1.4.1; Whatshap v1.4; IGV v2.6.1; KMC v3.2.1; KMC_tools v3.2.1 RNA-seq data processing: HISAT2 v2.2.0; StringTie v2.2.1; edgeR v3.36.0 GM-seq data processing: sambamba v0.8.2; Astair v3.3.2; MethylDackel (latest version); Metilene (latest version) Cut-Tag data processing: Picard v2.20; MACS2 v2.1.1; Diffbind v3.12.0 Hi-C data processing: juicer v1.6; juicer_tools v1.22.01; Mustache v1.0.1; Homer v4.11; HiCexplorer v3.7.2; TADcompare (latest version). Iso-Seq data processing: IsoSeq3 v3.1.0; Cupcake v29.0.0; kallisto v0.48.0;

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 in National Genomics Data Center , China National Center for Bioinformation / Beijing Institute of Genomics, Chinese Academy of Sciences (GSA: CRA026879) that are publicly accessible at https://ngdc.cncb.ac.cn/gsa/browse/CRA026879.

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	*Use the terms sex (biological attribute) and gender (shaped by social and cultural circumstances) carefully in order to avoid confusing both terms. Indicate if findings apply to only one sex or gender; describe whether sex and gender were considered in study design; whether sex and/or gender was determined based on self-reporting or assigned and methods used. Provide in the source data disaggregated sex and gender data, where this information has been collected, and if consent has been obtained for sharing of individual-level data; provide overall numbers in this Reporting Summary. Please state if this information has not been collected. Report sex- and gender-based analyses where performed, justify reasons for lack of sex- and gender-based analysis.*
Reporting on race, ethnicity, or other socially relevant groupings	*Please specify the socially constructed or socially relevant categorization variable(s) used in your manuscript and explain why they were used. Please note that such variables should not be used as proxies for other socially constructed/relevant variables (for example, race or ethnicity should not be used as a proxy for socioeconomic status). Provide clear definitions of the relevant terms used, how they were provided (by the participants/respondents, the researchers, or third parties), and the method(s) used to classify people into the different categories (e.g. self-report, census or administrative data, social media data, etc.) Please provide details about how you controlled for confounding variables in your analyses.*
Population characteristics	*Describe the covariate-relevant population characteristics of the human research participants (e.g. age, genotypic information, past and current diagnosis and treatment categories). If you filled out the behavioural & social sciences study design questions and have nothing to add here, write "See above."*
Recruitment	*Describe how participants were recruited. Outline any potential self-selection bias or other biases that may be present and how these are likely to impact results.*
Ethics oversight	*Identify the organization(s) that approved the study protocol.*

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	To construct a comprehensive phased multi omics data analysis atlas, samples of two tissues, dorsal longest muscle and adipose, were collected from six Eurasian crossbred pigs.
Data exclusions	Full details of pedigree verification can be found in Methods. To identify potential sample misidentification, we performed pedigree-based checks and called variants from RNA-Seq, DNA methylation, and histone modification data. We then clustered samples based on these variant profiles. Tissues from the same individuals formed tight clusters, followed by samples from littermates for the same cross.
Replication	All key experimental findings were independently replicated with consistent results. Replicates were performed across different biological samples and experimental batches to confirm reproducibility. No findings were found to be irreproducible.
Randomization	Randomization was not relevant to this study.

Blinding	Blinding was not necessary for the development of this study.

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

Antibodies

Antibodies used	H3K4me1:CST5326T; H3K4me3:CST9751T; H3K27me3:CST9733T; H3K27ac:CST8173T; CTCF:#15410210; IgG:ab172730
Validation	Full details of validation can be found in Methods.

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	We collected 16 pigs composed of 6 trio families pigs,2 families from Large White × Erhualian, 2 families from Berkshire × Ganxi and 2 families from Duroc × Liangguang. Each family has 2 offspring.
Wild animals	No wild animals involved.
Reporting on sex	The 16 pigs contained 7 males and 9 females. As for a data resource, the samples are from different sex, no sex-based analysis was required.
Field-collected samples	All experimental pigs were sampled under standard procedures within 30 min after slaughter at room temperature.
Ethics oversight	All animal procedures were performed in accordance with the guidelines for the care and use of laboratory animals issued by the Ministry of Agriculture and Rural Affairs of China. The study protocol was approved by the Animal Welfare and Ethics Committee of Jiangxi Agricultural University (Approval No. JXAU2020023, approved on December 17, 2021).

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

Plants

Seed stocks	*Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.*
Novel plant genotypes	*Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.*
Authentication	*Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosiacism, off-target gene editing) were examined.*

ChIP-seq

Data deposition

☐ Confirm that both raw and final processed data have been deposited in a public database such as GEO.

☒ Confirm that you have deposited or provided access to graph files (e.g. BED files) for the called peaks.

Data access links
May remain private before publication.

The raw sequence data reported in this paper have been deposited in the Genome Sequence Archive in National Genomics Data Center , China National Center for Bioinformation / Beijing Institute of Genomics, Chinese Academy of Sciences (GSA: CRA026879) that are publicly accessible at https://ngdc.cncb.ac.cn/gsa/browse/CRA026879.

Files in database submission

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Genome browser session
(e.g. UCSC)

No longer applicable

Methodology

Replicates	Full details can be found in Methods, Supplementary File and Supplementary Data.
Sequencing depth	Full details can be found in Supplementary Data.
Antibodies	H3K4me1:CST5326T; H3K4me3:CST9751T; H3K27me3:CST9733T; H3K27ac:CST8173T; CTCF:#15410210; IgG:ab172730
Peak calling parameters	macs2: "-f BAMPE -q 0.05 --nomodel --shift -0 --keep-dup all"
Data quality	Full details can be found in Methods.
Software	fastp v0.23.2; BWA v0.7.17; Picard v2.20; SAMtools v1.9; MACS2 v2.1.1; Diffbind v3.12.0; Whatshap v1.4