

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 (<i>n</i>) 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 <i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i>
☒	☐ 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. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted <i>Give P values as exact values whenever suitable.</i>
☒	☐ 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 <i>d</i> , Pearson's <i>r</i>), 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 commercial/custom code was used for data collection.
Data analysis	We used the following software in the analysis: R (v4.1.3), Plink (v 1.09), GenABEL(v1.8-0), Samtools (v1.9), Beagle (v4.1), Minimac (v2.0.1), BWA (v0.7.8), MTAG (v1.0.7), SnpEff (v4.3t), MatrixEQTL (v2.0.12), TopHat (v2.1.1), g:profile, All codes can be available upon reasonable request.

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 data presented in the study are deposited in the NCBI repository (<https://www.ncbi.nlm.nih.gov/>), accession number PRJNA721166, and DRYAD repository (<https://datadryad.org/stash/>), accession number 10.5061/dryad.4qc06.

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	No
Reporting on race, ethnicity, or other socially relevant groupings	No
Population characteristics	No
Recruitment	No
Ethics oversight	No

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	A total of 723 Huaxi cattle were originated from Ulgai, Inner Mongolia of China, and then moved to JinweifurenCo., Ltd for fattening. Blood and tissue samples from an adult male Huaxi cattle were used for genome sequencing and RNA sequencing.
Data exclusions	After genotype quality control, 685 individuals were used for subsequent analysis.
Replication	All GWAS results were provided in the supplementary Material and could be got the same results according the analysis of the data by the introduction of Methods part of the manuscript. The FASN gene function validation was conducted in three replicates.
Randomization	This study was to identify the significant SNPs of fatty acids in beef cattle by integrating genomic and transcriptomic dataset through multiple strategies, and validated the functional gene function. As the animal sample of resource population were random selected for fattening and slaughtering, in this way, the allocation for the samples is random.
Blinding	Because this study was to identify the functional gene associated with fatty acid traits and validated its function, blinding is not designed in our 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

Eukaryotic cell lines

Policy information about [cell lines and Sex and Gender in Research](#)

Cell line source(s)	Bovine primary preadipose was aseptically detached from newborn male Simmental calves.
Authentication	Cells were given by Jilin university. These cells have been published in previous study, which have been cited in our manuscript.
Mycoplasma contamination	None
Commonly misidentified lines (See ICLAC register)	None

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	Not applicable.
Wild animals	Not applicable.
Reporting on sex	All fattened beef cattle were male.
Field-collected samples	Whole blood and tissue samples were collected from Huaxi cattle at an average of 20 months in JinweifurenCo.,Ltd(Beijing) ,China.
Ethics oversight	All animals used in the study were treated following the guidelines for the experimental animals established by the Council of China Animal Welfare. Animal experiments were approved by the Science Research Department of the Institute of Animal Science, Chinese Academy of Agricultural Sciences (CAAS) (Beijing, China). Blood and meat samples were collected after obtaining the consent from the Jinweifuren Co., Ltd (Beijing).

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

Plants

Seed stocks	No
Novel plant genotypes	No
Authentication	NO