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E-mail: jzus_b@zju.edu.cn

Correspondence

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A novel A-to-G mutation in circBDP1 alters adipocyte proliferation and differentiation and affects bovine carcass traits

Enhui JIANG[1,2], Chiyuan ZHANG[1], Zhuoyuan HE[1], Yuli ZHANG[1], Yuta YANG[1], Chuanying PAN[1], Fugui JIANG[3], Enliang SONG[3], Sihuan ZHANG[1,2]✉, Xianyong LAN[1]✉

[1]*Key laboratory of Animal Genetics, Breeding and Reproduction of Shaanxi Province, College of Animal Science and Technology, Northwest A&F University, Yangling, Shaanxi 712100, China;*
[2]*College of Animal Science and Technology, Anhui Agricultural University, Hefei 230036, China;*
[3]*Institute of Animal Science and Veterinary, Shandong Academy of Agriculture Science, Jinan 250100, China.*

Fat deposition in cattle, influenced by factors such as genetics, age, sex, and nutrition, plays a crucial role in determining growth rates, beef yield and meat quality. Among these, genetics is the predominant factor (Kim et al., 2020; Xing et al., 2025). Research indicates a high heritability for visceral (36%) and subcutaneous (57%) fat (Fox et al., 2012). Gene mutations that affect adipocyte function are significant contributors to variations in fat deposition and meat quality (Mannen, 2011; Mwangi et al., 2019; Sun et al., 2023). Therefore, investigating genetic variations in fat-related genes is essential for enhancing cattle performance.

Genome-wide association studies (GWAS) have identified genetic variants in non-coding RNAs (ncRNAs), including miRNAs, lncRNAs and circRNAs, which have been primarily studied in humans (Ahmed et al., 2019; Liu et al., 2019; Hall et al., 2021). Meanwhile, there is a scarcity of research on connecting ncRNA variants to phenotypic traits in livestock (Jevsinek et al., 2013; Bruscadin et al., 2021; Shi and Sun, 2017; Li et al., 2018; Jin et al., 2019a). CircRNAs, which are formed through covalent binding of their 3' and 5' ends, can mediate transcription and post-transcriptional processes (Kelly et al., 2015). Certain circRNAs have been shown to influence adipocyte development, such as circFUT10 (Jiang et al., 2020), circFLT1 (Kang et al., 2020), and circINSR (Shen et al., 2021), by acting as sponges for miRNAs.

Given the pivotal role of circRNAs in adipose tissue development, identifying genetic variations within these molecules can facilitate the discovery of genetic markers in cattle breeding. Our previous study demonstrated that circBDP1 promotes bovine adipocyte proliferation and differentiation (Zhang et al., 2022). Recognizing that genetic variations in ncRNA can significantly impact their functional roles, this study aims to address the following questions: (1) Is there genetic variation in circBDP1? (2) Does genetic variation in circBDP1 influence bovine growth and carcass traits? (3) What are the functional implications of these genetic variations for circBDP1? The findings are expected to provide a foundation for advancing beef cattle breeding strategies.

By conducting circRNA sequencing and subsequent validation, we identified that bovine circBDP1, de-

✉ Sihuan ZHANG, sihuanzhang1990@163.com
Xianyong LAN, lanxianyong79@126.com
Sihuan ZHANG, https://orcid.org/0000-0003-2346-8987
Xianyong LAN, https://orcid.org/0000-0003-2254-5805

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rived from exons 14-16 of the BDP1 gene, promotes the proliferation and differentiation of preadipocytes (Zhang et al., 2022). Notably, we discovered an A>G mutation in exon 16 of BDP1 (circBDP1, ENSBTAT00000000474.6:c.2254A>G), as recorded in the Ensembl genome browser. Using primers designed to target exon 16 along with the adjacent intronic sequences, we successfully amplified and sequenced the resulting PCR product, and sequence alignment demonstrated the presence of this variant in both Qinchuan cattle and the SDBCGR population (Fig. 1).

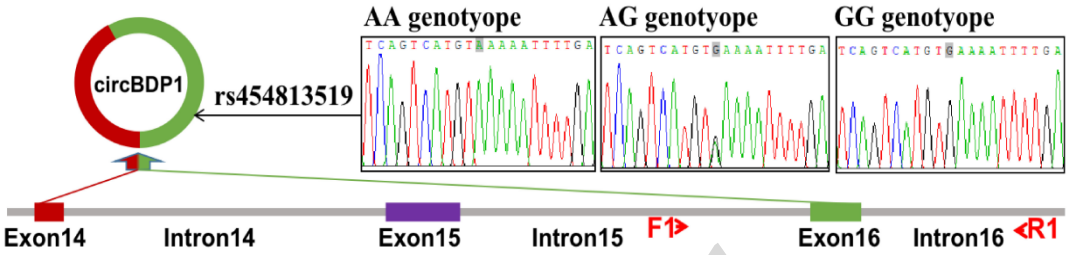

Fig. 1 The location and genotypes of circBDP1-SNP. The gray line represents the DNA sequence; the box with different color represents the different exons of the bovine *BDP1* gene; The black arrow indicates the location of rs454813519 on the circBDP1; the chromatograms showed different genotypes of rs454813519; F1 and R1 represents the primers.

The circBDP1-SNP genotypes in Qinchuan cattle and SDBCGR were identified through the sequencing of PCR products and the KASP method. PCR product sequencing was conducted in a total of 122 Qinchuan cattle and 231 SDBCGR individuals. Additionally, the KASP method was utilized to determine the circBDP1-SNP genotypes in 384 SDBCGR individuals (Fig. S1).

Three genotypes of circBDP1-SNP were identified in the Qinchuan and SDBCGR cattle populations: AA, AG, and GG. Notably, only one individual with the GG genotype was detected in both breeds, resulting in a genotypic frequency of less than 0.01. The predominant genotype was wild-type AA, with a frequency exceeding 85%, and the major allele was A, exhibiting a frequency greater than 90% (Fig. S2).

The analysis of genetic parameters revealed high homozygosity at this locus, indicating low polymorphism (PIC<0.25). This locus was found to be in Hardy-Weinberg equilibrium in both populations (P>0.05) (Table S2). Furthermore, the analysis of published global bovine genome sequences and data from the Bovine VariationDB (BGVD) indicated that the G allele may have originated from Indian indicine cattle (Chen et al., 2018; Chen et al., 2020; Zhou et al., 2022) (Fig. S3).

Association analysis revealed that the circBDP1-SNP genotypes were significantly associated with the yield of cupim, hanging tender, chuck short rib, and rectum in female SDBCGRs, as well as the gross weight of male SDBCGRs and body length of Qinchuan cattle (Figs. 2a and 2a; Table S3).

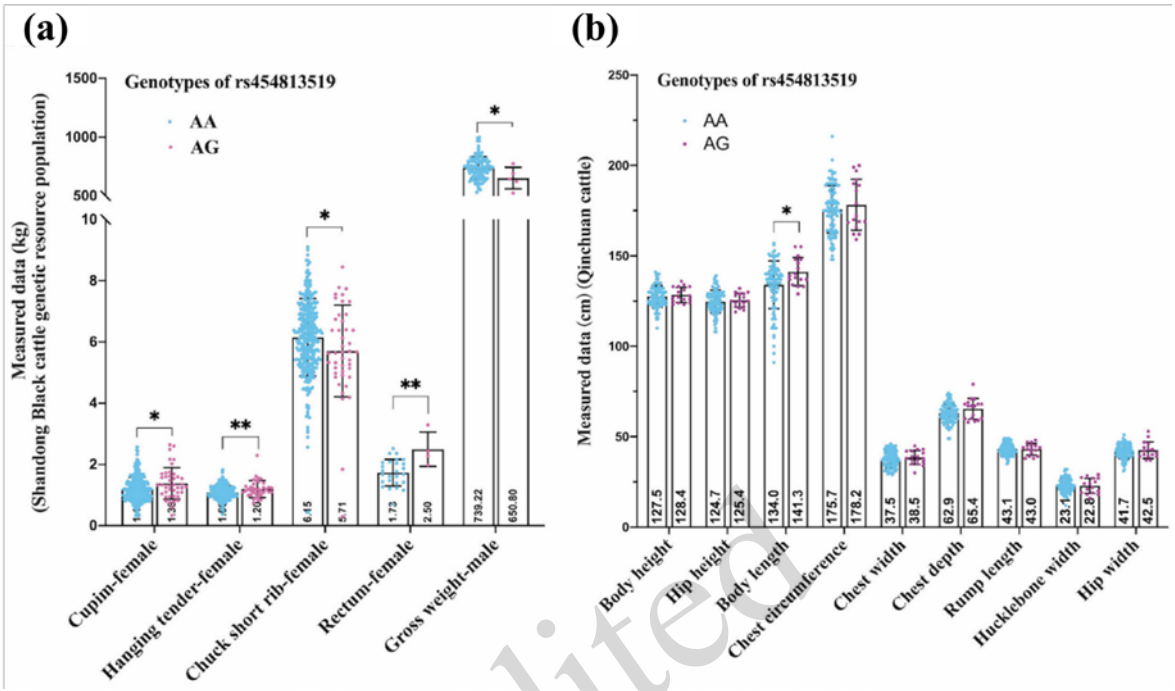

Fig. 2 Association between circBDP1-SNP genotypes and carcass traits of Shandong Black cattle genetic resource population (a) and body measurements of Qinchuan cattle (b).

Given that circBDP1-SNP is located within the circBDP1 gene and is significantly associated with various carcass traits in SDBCGR cattle and the body length of Qinchuan cattle, this study generated circBDP1 overexpression plasmids containing different circBDP1-SNP genotypes to investigate their regulatory effects on adipose tissue development. To assess the impact of these genotypes on preadipocyte proliferation, EdU labeling, quantitative reverse transcription polymerase chain reaction (qRT-PCR), and flow cytometry were performed.

The EdU assay results indicated that the proportion of proliferating cells in the circBDP1-A group (which contains the wild-type A allele of the circBDP1-SNP locus) was significantly higher than that in both the control group and the circBDP1-G group (containing the wild-type G allele) (Fig. 3a). Moreover, the qRT-PCR results demonstrated that circBDP1-A significantly enhanced the mRNA expression level of PCNA compared to both the circBDP1-G and control groups (Fig. 3b).

Flow cytometry analysis revealed no significant differences in cell division between the circBDP1-A and control groups; however, the circBDP1-G group exhibited a significantly lower number of cells in the division phase compared to both the control and circBDP1-A groups, while the number of cells in the G1 phase was significantly higher in the circBDP1-G group. These findings suggest that circBDP1-G inhibits cell cycle progression (Fig. 3c).

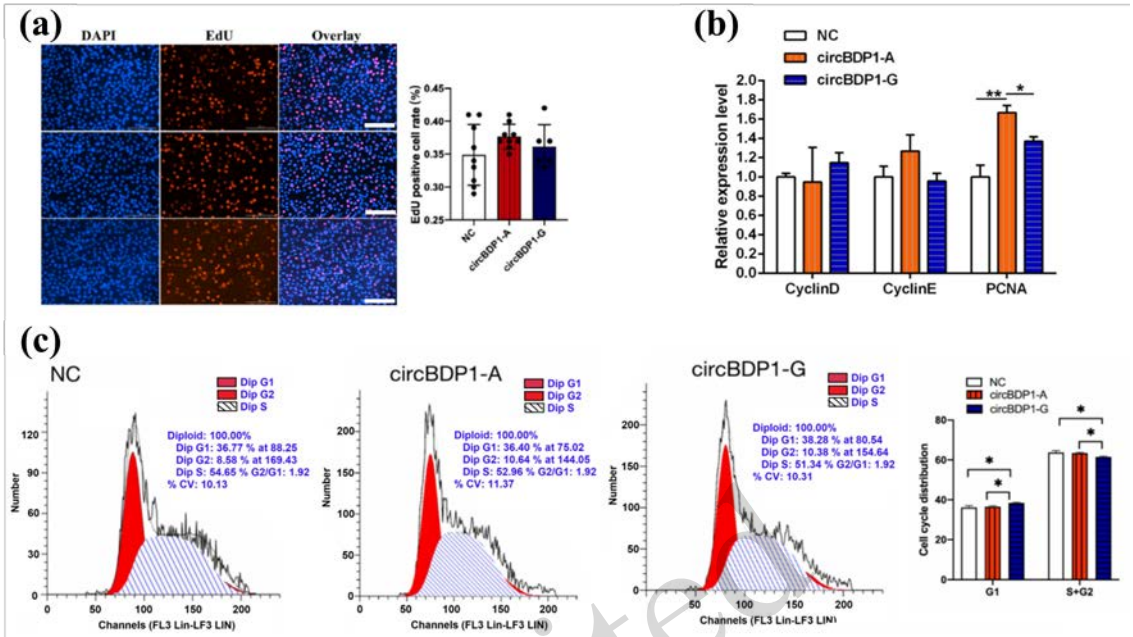

Fig. 3 The effect of circBDP1 with different genotypes of circBDP1-SNP on preadipocyte proliferation. (a) EdU (Bar=200 μm); (b) qRT-PCR; (c) Flow cytometry.

We further examined the impact of the mutation on preadipocyte apoptosis. The flow cytometry results demonstrated robust cell growth across all three groups, with approximately 90% of the total cell population classified as normal. The proportion of early apoptotic cells was significantly lower in both the circBDP1-A and circBDP1-G groups compared to the control group, and notably, it was significantly lower in the circBDP1-A group than the circBDP1-G group (Figs. S4a and S4b). Interestingly, the circBDP1-A group showed a higher number of late apoptotic cells compared to the other two groups.

Further analysis revealed no significant differences in the overall proportion of apoptotic cells (B2+B4) among the three groups, suggesting that while the mutation influenced the apoptotic process, its effect was not pronounced (Figs. S4a and S4b). The qRT-PCR results indicated that the mRNA expression level of the apoptosis-inhibiting gene Bcl-2 was significantly higher in the circBDP1-A group compared to both the control and circBDP1-G groups. This suggests that circBDP1-A may play a role in inhibiting cell apoptosis. Meanwhile, circBDP1-G did not demonstrate a significant effect on apoptosis (Fig. S4c).

Preadipocytes were induced to differentiate following the overexpression of circBDP1-A and circBDP1-G. To assess the mRNA and protein expression levels of differentiation marker genes, RNA samples were collected after 2 and 4 d of differentiation. The results indicated that the expression levels of adipocyte differentiation-related marker genes decreased with the A to G mutation, suggesting that adipocyte differentiation was impaired as a result of this mutation (Fig. S5). In conclusion, the mutation from circBDP1-A to circBDP1-G may influence phenotypic traits by modulating cell proliferation, apoptosis and differentiation levels.

In summary, the circBDP1-SNP variation within the circular RNA circBDP1 was significantly associated with carcass traits in a genetic resource population of Shandong black cattle. This variation diminished the stimulatory effect of circBDP1 on the proliferation and differentiation of preadipocytes, hence it holds potential as a DNA marker for molecular-assisted selection in beef cattle breeding.

Data availability statement

Data are available upon request from corresponding author.

Acknowledgements

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Authors' Contributions

Enhui Jiang: methodology, validation, data curation; Chiyuan Zhang: methodology, validation, data curation; Zhuoyuan He: validation; Yuli Zhang: validation; Yuta Yang: writing-review&editing, data curation; Chuanying Pan: writing-review&editing; Fugui Jiang: writing-review&editing; Enliang Song: writing-review&editing; Sihuan Zhang: project administration, funding acquisition; Xianyong Lan: project administration, funding acquisition;

Compliance with ethics guidelines

All animal experiments were maintained according to the Regulation for the Administration of Affairs Concerning Experimental Animals (State Council of China, 2017 Revision), and our study was approved by the Northwest A&F University Institutional Animal Care and Use Committee.

References

Ahmed, I., T. Karedath, F. M.Al-Dasim, and J. A. Malek. 2019. Identification of human genetic variants controlling circular RNA expression. *RNA*. 25(12):1765-1778. doi:10.1261/rna.071654.119.

Aljanabi, S. M, and I. Martinez. 1997. Universal and rapid salt-extraction of high quality genomic DNA for PCR-based techniques. *Nucleic Acids Res*. 25(22):4692-3. doi:10.1093/nar/25.22.4692.

Bruscadin, J. J., M. M. de Souza, K. S. de Oliveira, M. I. P. Rocha, J. Afonso, T. F. Cardoso, A. Zerlotini, L. L. Coutinho, S. C. M. Niciura, and L. C. de Almeida Regitano 2021. Muscle allele-specific expression QTLs may affect meat quality traits in Bos indicus. *Sci. Rep.* 11(1):7321. doi:10.1038/s41598-021-86782-2.

Cao, Y., H. Xu, R. Li, S. Gao, N. Chen, J. Luo, and Y. Jiang. 2019. Genetic basis of phenotypic differences between Chinese yunling black goats and nubian goats revealed by Allele-specific expression in their F1 hybrids. *Front. Genet.* 10:145. doi:10.3389/fgene.2019.00145.

Chen, N., Y. Cai, Q. Chen, R. Li, K. Wang, Y. Huang, S. Hu, S. Huang, H. Zhang, Z. Zheng, W. Song, Z. Ma, Y. Ma, R. Dang, Z. Zhang, L. Xu, Y. Jia, S. Liu, X. Yue, W. Deng, X. Zhang, Z. Sun, X. Lan, J. Han, H. Chen, D. G. Bradley, Y. Jiang, and C. Lei. 2018. Whole-genome resequencing reveals world-wide ancestry and adaptive introgression events of domesticated cattle in East Asia. *Nat. Commun.* 9(1):2337. doi:10.1038/s41467-018-04737-0.

Chen, N., W. Fu, J. Zhao, J. Shen, Q. Chen, Z. Zheng, H. Chen, T. S. Sonstegard, C. Lei, and Y. Jiang. 2020. BGVD: An integrated database for bovine sequencing variations and selective signatures. *Genomics Proteomics Bioinformatics.* 18(2):186-193. doi:10.1016/j.gpb.2019.03.007.

Colantoni, A., D. Capauto, V. Alfano, E. D'Ambra, S. D'Uva, G. G. Tartaglia, and M. Morlando. 2023. FUS alters circRNA metabolism in human motor neurons carrying the ALS-linked P525L mutation. Int J Mol Sci. 24(4):3181. doi:10.3390/ijms24043181.

Das, T., A. Deb, S. Parida, S. Mondal, S. Khatua, and Z. Ghosh. 2021. LncRBase V.2: an updated resource for multispecies lncRNAs and ClinicLSNP hosting genetic variants in lncRNAs for cancer patients. *RNA Biol.* 18(8):1136-1151. doi:10.1080/15476286.2020.1833529.

Deng, J., X. L. Xie, D. F. Wang, C. Zhao, F. H. Lv, X. Li, J. Yang, J. L. Yu, M. Shen, L. Gao, J. Q. Yang, M. J. Liu, W. R. Li, Y. T. Wang, F. Wang, J. Q. Li, E. Hehua, Y. G. Liu, Z. Q. Shen, Y. L. Ren, G. J. Liu, Z. H. Chen, N. A. Gorkhali, H. E. Rushdi, H. Salehian-Dehkordi, A. Esmailizadeh, M. Nosrati, S. R. Paiva, A. R. Caetano, O. Štěpánek, I. Olsaker, C. Weimann, G. Erhardt, I. Curik, J. Kantanen, J. M. Mwacharo, O. Hanotte, M. W. Bruford, E. Ciani, K. Periasamy, M. Amills, J. A. Lenstra, J. L. Han, H. P. Zhang. L. Li, and M. H. Li. 2020. Paternal origins and migratory episodes of domestic sheep. *Curr. Biol.* 30(20):4085-4095.e6. doi:10.1016/j.cub.2020.07.077.

Deniskova, T. E., A. V. Dotsev, M. I. Selionova, E. Kunz, I. Medugorac, H. Reyer, K. Wimmers, M. Barbato, A. A. Traspov, G. Brem, and N. A. Zinovieva. 2018. Population structure and genetic diversity of 25 Russian sheep breeds based on whole-genome genotyping. *Genet. Sel. Evol.* 50(1):29. doi:10.1186/s12711-018-0399-5.

Fox, C. S., Y. Liu, C. C. White, M. Feitosa, A. V. Smith, N. Heard-Costa, K. Lohman, A. D. Johnson, M. C. Foster, D. M. Greenawalt, P. Griffin, J. Ding, A. B. Newman, F. Tylavsky, I. Miljkovic, S. B. Kritchevsky, L. Launer, M. Garcia, G. Eiriksdottir, J. J. Carr, V. Gudnason, T. B. Harris, L. A. Cupples, and I. B. Borecki. 2012. Genome-wide association for abdominal subcutaneous and visceral adipose reveals a novel locus for visceral fat in women. *PLoS Genet.* 8(5):e1002695. doi:10.1371/journal.pgen.1002695.

Hall, I. F., M. Climent, C. Viviani Anselmi, L. Papa, V. Tragante, L. Lambroia, F. M. Farina, M. E. Kleber, W. März, C. Biguori, G. Condorelli, and L. Elia. 2021. rs41291957 controls miR-143 and miR-145 expression and impacts coronary artery disease risk. *EMBO. Mol. Med.* 13(10):e14060. doi:10.15252/emmm.202114060.

Jevsinek, Skok. D., I. Godnic, M. Zorc, S. Horvat, P. Dovc, M. Kovac, and T. Kunej. 2013. Genome-wide in silico screening for microRNA genetic variability in livestock species. *Anim. Genet.* 44(6):669-77. doi:10.1111/age.12072.

Jiang, R., H. Li, J. Yang, X. Shen, C. Song, Z. Yang, X. Wang, Y. Huang, X. Lan, C. Lei, and H. Chen. 2020. circRNA Profiling Reveals an abundant circFUT10 that promotes adipocyte proliferation and inhibits adipocyte differentiation via sponging let-7. *Mol. Ther. Nucleic Acids.* 20:491-501. doi:10.1016/j.omtn.2020.03.011.

Jin, Y., J. Wang, M. Zhang, S. Zhang, C. Lei, H. Chen, W. Guo, and X. Lan. 2019. Role of bta-miR-204 in the regulation of adipocyte proliferation, differentiation, and apoptosis. *J. Cell Physiol.* 234(7):11037-11046. doi:10.1002/jcp.27928.

Jin, Y., Q. Yang, J. Gao, Q. Tang, B. Duan, T. Yu, X. Qi, J. Liu, R. Wang, R. Dang, C. Lei, H. Chen, and X. Lan. 2018. Detection of Insertions/Deletions Within SIRT1, SIRT2 and SIRT3 genes and their associations with body measurement traits in cattle. *Biochem. Genet.* 56(6):663-676. doi:10.1007/s10528-018-9868-3.

Jin, Y., Q. Yang, M. Zhang, S. Zhang, H. Cai, R. Dang, C. Lei, H. Chen, and X. Lan. 2019. Identification of a novel polymorphism in bovine lncRNA ADNCR Gene and its association with growth traits. *Anim. Biotechnol.* 30(2):159-165. doi:10.1080/10495398.2018.1456446.

Kang, Z., S. Zhang, E. Jiang, X. Wang, Z. Wang, H. Chen, and X. Lan. 2020. circFLT1 and lncCCPG1 sponges miR-93 to regulate the proliferation and differentiation of adipocytes by promoting lncSLC30A9 expression. *Mol. Ther. Nucleic Acids.* 22:484-499. doi:10.1016/j.omtn.2020.09.011.

Kelly, S., C. Greenman. P. R. Cook, and A. Papantonis. 2015. Exon skipping is correlated with exon circularization. *J. Mol. Biol.* 427(15):2414-2417. doi:10.1016/j.jmb.2015.02.018.

Kim, M., T. Park. J. Y. Jeong, Y. Baek, and H. J. Lee. 2020. Association between rumen microbiota and marbling score in korean native beef cattle. *Animals (Basel).* 10(4):712. doi:10.3390/ani10040712.

Li, M., X. Sun, H. Cai, Y. Sun, M. Plath, C. Li, X. Lan, C. Lei, F. Lin, Y. Bai, and H. Chen. 2016. Long non-coding RNA ADNCR suppresses adipogenic differentiation by targeting miR-204. *Biochim. Biophys. Acta.* 1859(7):871-82. doi:10.1016/j.bbagrm.2016.05.003.

Li, N., Y. Zhang, H. P. Li, L. Han, X. M. Yan, H. B. Li, W. Du, J. S. Zhang, and Q. L. Yu. 2018. Differential expression of mRNA-miRNAs related to intramuscular fat content in the longissimus dorsi in Xinjiang brown cattle. *PLoS One.* 13(11):e0206757. doi:10.1371/journal.pone.0206757.

Li, X., E. Jiang, K. Zhang, S. Zhang, F. Jiang, E. Song, H. Chen, P. Guo, and X. Lan. 2022. Genetic variations within the bovine CRY2 gene are significantly associated with carcass traits. *Animals (Basel).* 12(13):1616. doi:10.3390/ani12131616.

Liu, Z., Y. Ran, C. Tao, S. Li, J. Chen, and E. Yang. 2019. Detection of circular RNA expression and related quantitative trait loci in the human dorsolateral prefrontal cortex. *Genome Biol.* 20(1):99. doi:10.1186/s13059-019-1701-8.

Mannen, H. 2011. Identification and utilization of genes associated with beef qualities. *Anim. Sci. J.* 82(1):1-7. doi:10.1111/j.1740-0929.2010.00845.x.

Mwangi, F, W., E. Charmley, C. P. Gardiner, B. S. Malau-Aduli, R. T. Kinobe, and A. E. O. Malau-Aduli. 2019. Diet and genetics influence beef cattle performance and meat quality characteristics. *Foods.* 8(12):648. doi:10.3390/foods8120648.

Rajcsanyi, L. S., I. Diebels, L. Pastoors, D. Kanber, T. Peters, A. L. Volckmar,Y. Zheng, M. Grosse, C. Dieterich, J. Hebebrand, F. J. Kaiser, B. Horsthemke, and A. Hinney. 2022. Evidence for correlations between BMI-associated SNPs and circRNAs. *Sci. Rep.* 12(1):12643. doi:10.1038/s41598-022-16495-7.

Rask-Andersen, M., T. Karlsson, W. E. Ek, and A. Johansson. 2019. Genome-wide association study of body fat distribution identifies adiposity loci and sex-specific genetic effects. *Nat. Commun.* 10(1):339. doi:10.1038/s41467-018-08000-4.

Roden, C., J. Gaillard, S. Kanoria, W. Rennie, S. Barish, J. Cheng, W. Pan, J. Liu, C. Cotsapas, Y. Ding, and J. Lu. 2017. Novel determinants of mammalian primary microRNA processing revealed by systematic evaluation of hairpin-containing transcripts and human genetic variation. *Genome Res.* 27(3):374-384. doi:10.1101/gr.208900.116.

Shen, X., J. Tang, W. Ru, X. Zhang, Y. Huang, C. Lei, H. Cao, X. Lan, and H. Chen, 2021. CircINSR Regulates Fetal Bovine Muscle and Fat Development. *Front. Cell Dev. Biol.* 8:615638. doi:10.3389/fcell.2020.615638.

Shi, J, and G. Sun. 2017. Effect of pre-miRNA-1658 gene polymorphism on chicken growth and carcass traits. *Asian-Australas J. Anim. Sci.* 30(4):455-461. doi:10.5713/ajas.16.0305.

Small, K. S., M. Todorčević, M. Civelek, J. S. El-Sayed Moustafa, X. Wang, M. M. Simon, J. Fernandez-Tajes, A. Mahajan, M. Horikoshi, A. Hugill, C. A. Glastonbury, L. Quaye, M. J. Neville, S. Sethi, M. Yon, C. Pan, N. Che, A. Vinuela, P. C. Tsai, A. Nag, A. Buil, G. Thorleifsson, A. Raghavan, Q. Ding, A. P. Morris, J. T. Bell, U. Thorsteinsdottir, K. Stefansson, M. Laakso, I. Dahlman, P. Arner, A. L. Gloyn, K. Musunuru, A. J. Lusis, R. D. Cox, F. Karpe, and M. I. McCarthy. 2018. Regulatory variants at KLF14 influence type 2 diabetes risk via a female-specific effect on adipocyte size and body composition. *Nat. Genet.* 50(9):1342. doi:10.1038/s41588-018-0180-2.

Song, C., J. Yang, R. Jiang, Z. Yang, H. Li, Y. Huang, X. Lan, C. Lei, Y. Ma, X. Qi, and H. Chen. 2019. MiR-148a-3p regulates proliferation and apoptosis of bovine muscle cells by targeting KLF6. *J. Cell Physiol.* 234(9):15742-15750. doi:10.1002/jcp.28232.

Sun Y., Zhang J, Hong J, Zhang Z, Lu P, Gao A, Ni M, Zhang Z, Yang H, Shen J, Lu J, Xue W, Lv Q, Bi Y, Zeng YA, Gu W, Ning

G, Wang W, Liu R, Wang J. 2023. Human RSPO1 mutation represses beige adipocyte thermogenesis and contributes to diet-induced adiposity. *Adv. Sci.* (Weinh). 10(12):e2207152. doi: 10.1002/advs.202207152.

Xing Y., Ma C., Guan H., Shen J., Shen Y., Li G., Sun G., Tian Y., Kang X., Liu X., Li H., Tian W. 2025. Multi-Omics insights into regulatory mechanisms underlying differential deposition of intramuscular and abdominal fat in chickens. biomolecules. 15(1):134. doi:10.3390/biom15010134.

Zhang, S., Z. Kang, H. Cai, E. Jiang, C. Pan, R. Dang, C. Lei, H. Chen, and X. Lan. 2021. Identification of novel alternative splicing of bovine lncRNA lncFAM200B and its effects on preadipocyte proliferation. *J. Cell Physiol.* 236(1):601-611. doi:10.1002/jcp.29887.

Zhang, S., Z. Kang, X. Sun, X. Cao, C. Pan, R. Dang, C. Lei, H. Chen, and X. Lan. 2019. Novel lncRNA lncFAM200B: molecular characteristics and effects of genetic variants on promoter activity and cattle body measurement traits. *Front. Genet. 10:968*. doi:10.3389/fgene.2019.00968.

Zhang, S., E. Jiang, Z. Kang, Y. Bi, H. Liu, H. Xu, Z. Wang, C. Lei, H. Chen, and X. Lan. 2022. CircRNA profiling reveals an abundant circBDP1 that regulates bovine fat development by sponging miR-181b/miR-204 targeting Sirt1/TRARG1. *J. Agric. Food Chem.* 70(44):14312-14328. doi:10.1021/acs.jafc.2c05939.

Zhou, Y., L.Yang, X. Han, J. Han, Y. Hu, F. Li, H. Xia, L. Peng, C. Boschiero, B. D. Rosen, D. M. Bickhart, S. Zhang, A. Guo, C. P. Van Tassell, T. P. L. Smith, L. Yang, and G. E. Liu. 2022. Assembly of a pangenome for global cattle reveals missing sequences and novel structural variations, providing new insights into their diversity and evolutionary history. *Genome Res.* 32(8):1585–601. doi:10.1101/gr.276550.122.

Supplementary information

Figs. S1-S5; Tables S1-S3; Materials and methods