



Two telomere-to-telomere pig genome assemblies and pan-genome analyses provide insights into genomic structural landscape and genetic adaptations

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Introduction



The complete human genome sequence

RESEARCH ARTICLE | EVOLUTION | 8



Evolutionary analysis of a complete chicken genome

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Edited by David W. Burt, University of Edinburgh Dick Vet Farm Animal Practice, Roslin, UK; received September 29, 2022; accepted January 18, 2023 by Editorial Board Member Scott V. Edwards

February 13, 2023 | 120 (8) e2216641120 | <https://doi.org/10.1073/pnas.2216641120> | IF: 9.4 | Q1

Article | Published: 08 January 2025

Telomere-to-telomere sheep genome assembly identifies variants associated with wool fineness

[Ling-Yun Luo](#), [Hui Wu](#), [Li-Ming Zhao](#), [Ya-Hui Zhang](#), [Jia-Hui Huang](#), [Qiu-Yue Liu](#), [Hai-Tao Wang](#), [Dong-Xin Mo](#), [He-Hua EEr](#), [Lian-Quan Zhang](#), [Hai-Liang Chen](#), [Shan-Gang Jia](#) , [Wei-Min Wang](#)  & [Meng-Hua Li](#) 

Article | [Open access](#) | Published: 20 November 2024

Telomere-to-telomere genome assembly of a male goat reveals variants associated with cashmere traits

[Hui Wu](#), [Ling-Yun Luo](#), [Ya-Hui Zhang](#), [Chong-Yan Zhang](#), [Jia-Hui Huang](#), [Dong-Xin Mo](#), [Li-Ming Zhao](#), [Zhi-Xin Wang](#), [Yi-Chuan Wang](#), [EEr He-Hua](#), [Wen-Lin Bai](#), [Di Han](#), [Xing-Tang Dou](#), [Yan-Ling Ren](#), [Renqing Dingkao](#), [Hai-Liang Chen](#), [Yong Ye](#), [Hai-Dong Du](#), [Zhan-Qiang Zhao](#), [Xi-Jun Wang](#), [Shan-Gang Jia](#) , [Zhi-Hong Liu](#)  & [Meng-Hua Li](#) 



Highlights

- ❑ Telomere-to-telomere assembly provided high-quality genomes for Min and Rongchang pigs
- ❑ Analysis of the telomere and centromere regions revealed chromosomal structural features
- ❑ The pig pan-genome and graph-based pan-genome were constructed based on the T2T framework
- ❑ Combining genomic, transcriptomic, and epigenomic data revealed candidate structural variations related to temperature adaptation in pigs
- ❑ Demonstrated the practicality of graph-based pan-genomes in enhancing the resolution of genome-wide association studies and improving the accuracy of genomic selection in animal breeding



Abstract

1. Two T2T native Chinese pig genomes



Min



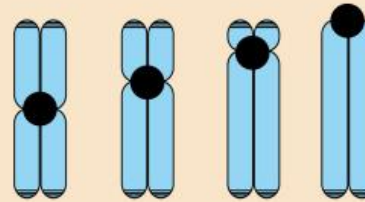
Rongchang

Genome assembly

Genome annotation

Genome assessment

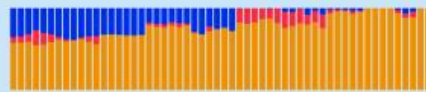
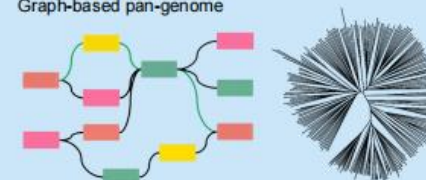
2. Telomeres and centromeres



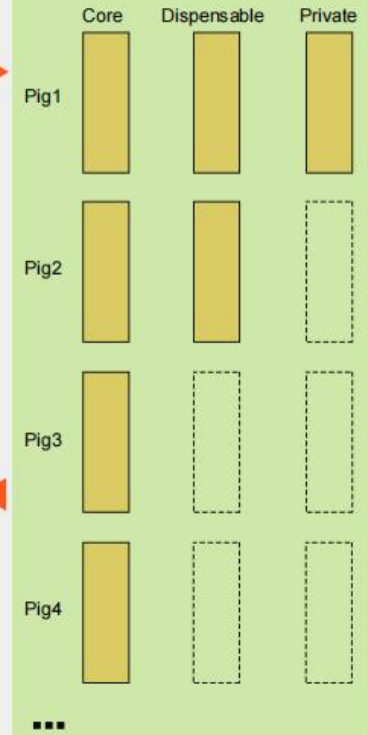
4. Structural variations



Graph-based pan-genome



3. Pan-genome



5. Cold and hot adaptation studies

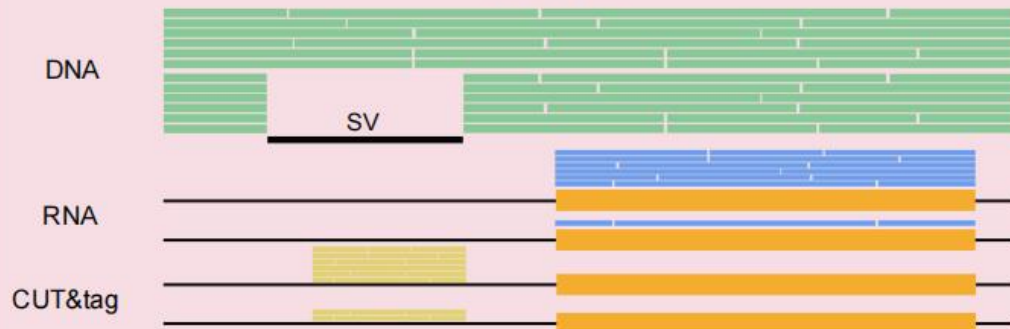


Cold stress

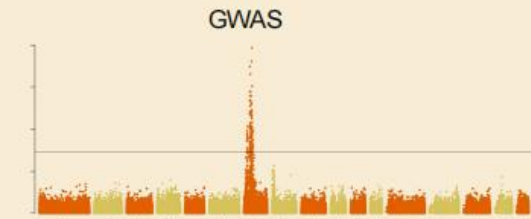


Hot stress

Multi-omics



6. Graph-based pan-genome in pig breeding



GS	
Panel	Prediction accuracy
SNP+SV	★★★★★
SNP	★★★
SV	★★★

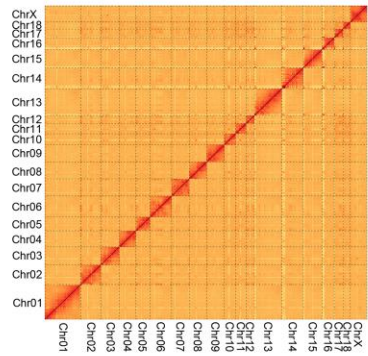


T2T genome assembly of Min and Rongchang pigs

A



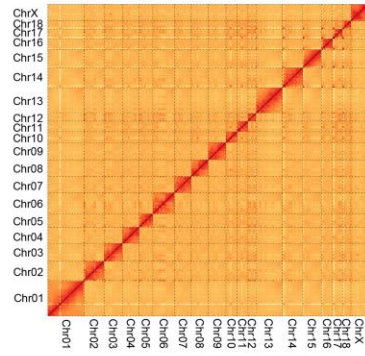
Min pig



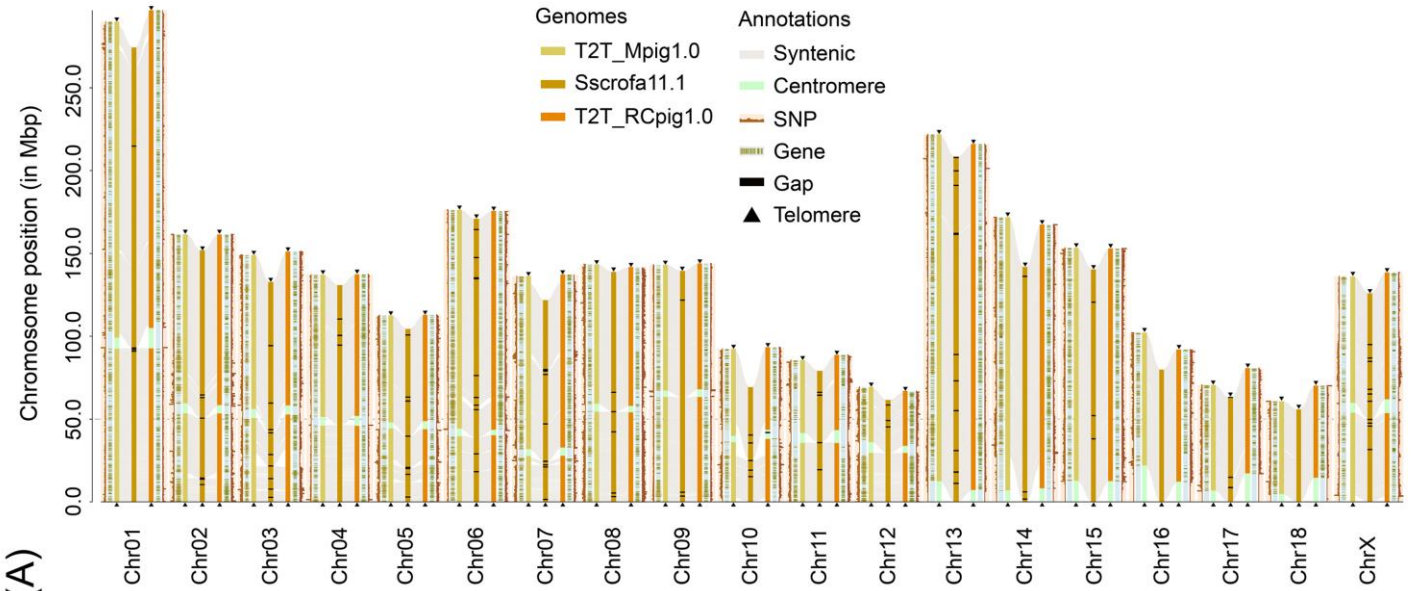
B



Rongchang pig



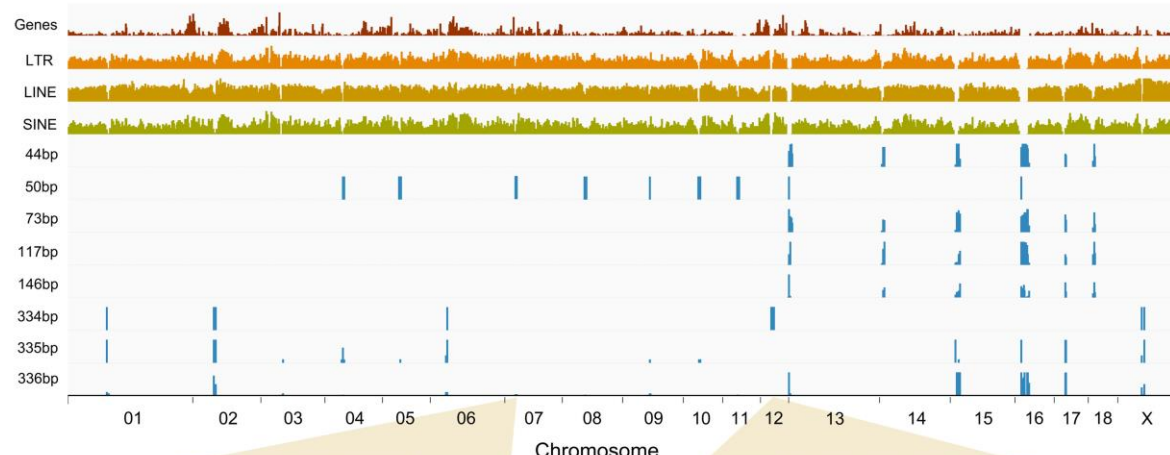
(A)





Centromere identification

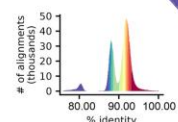
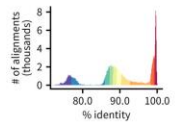
T2T_Mpig1.0



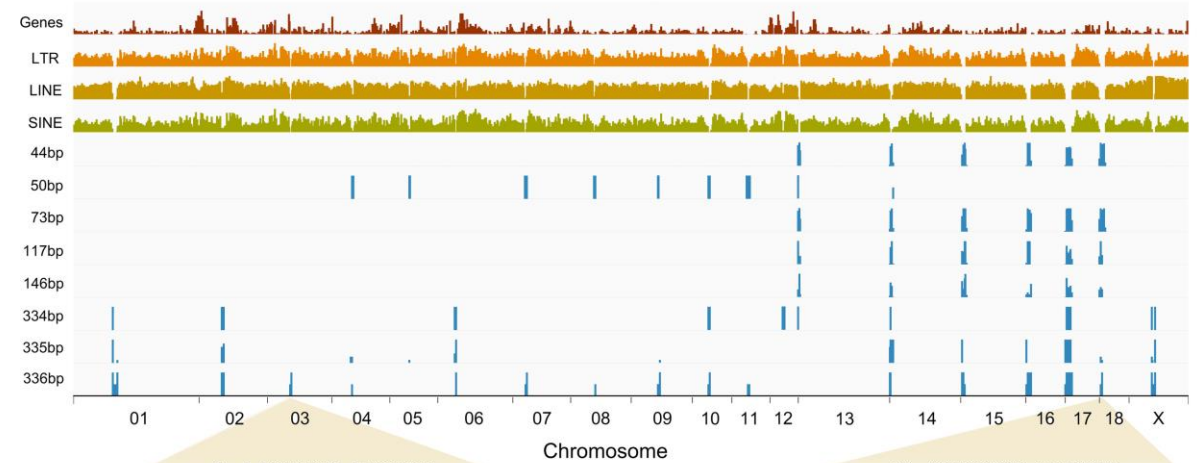
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Chr12:29964262-35868955



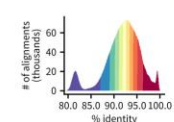
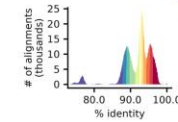
T2T_RCpig1.0



Chr3:53337267-57965290

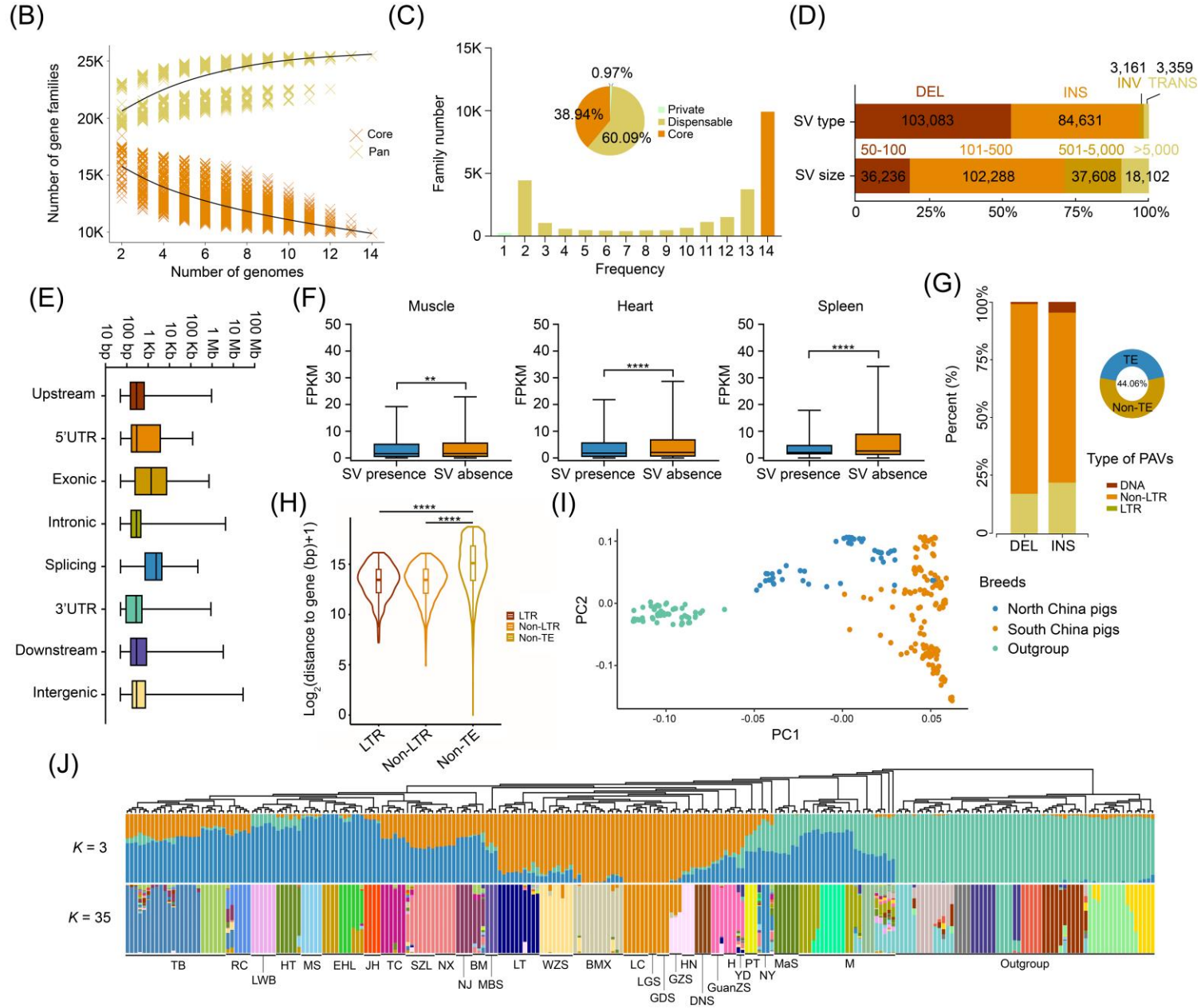


Chr18:2013830-14456208



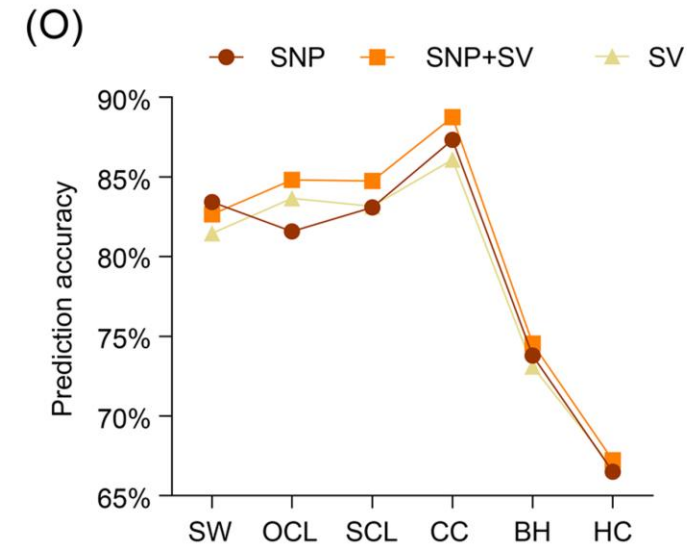
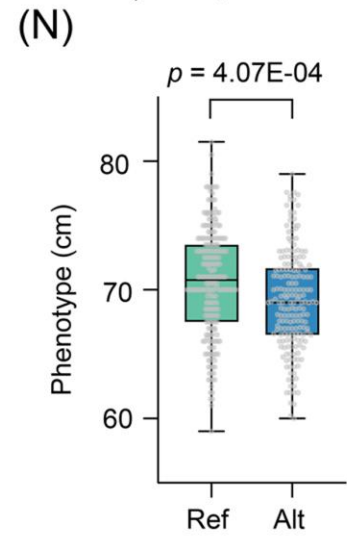
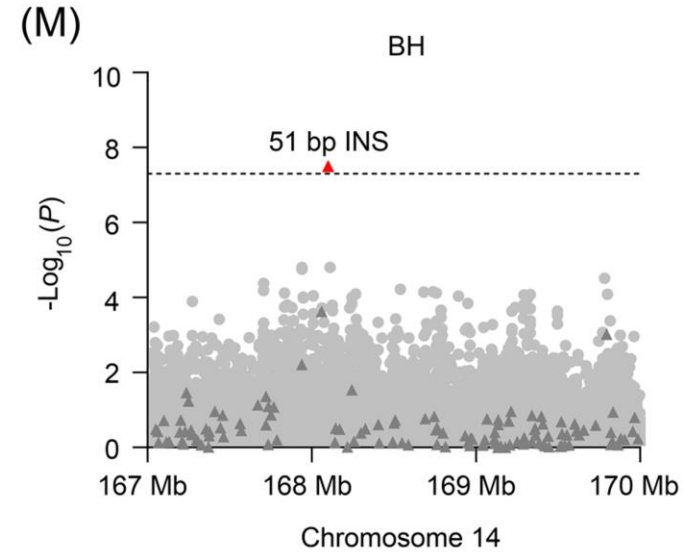
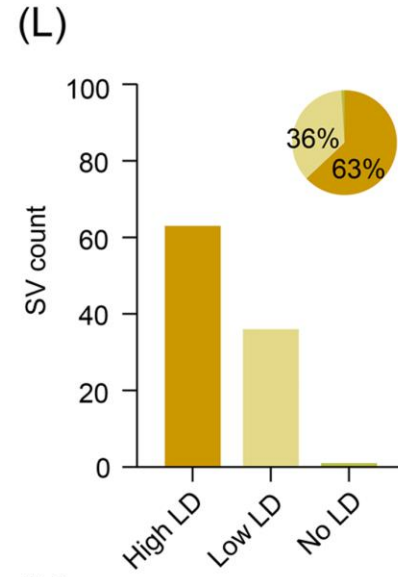
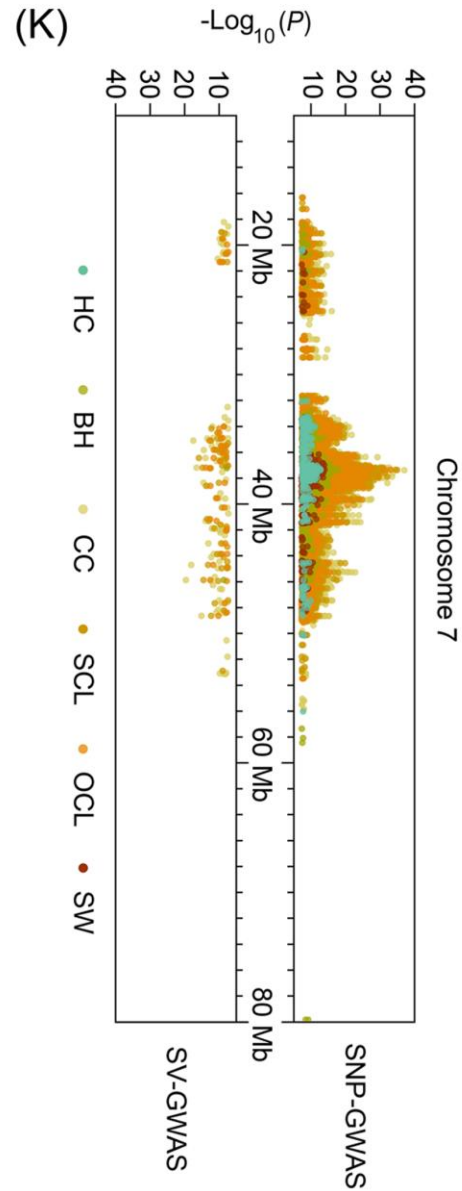
The centromeres on chromosomes 1 to 12 and X are metacentric/submetacentric, while the centromeres on chromosomes 13 to 18 are acrocentric/telocentric

Pangenome and Graph-based Pangenome Construction





A Graph-based pangenome approach in pig breeding





Summary

In this study, we utilized advanced sequencing technologies and assembly strategies to construct the T2T genomes of two native Chinese pig breeds — the Min pig and the Rongchang pig. These resources facilitated the analysis of complex genomic regions and structural variations, revealing the genetic adaptation characteristics of pigs and laying the foundation for advancing breeding and conservation strategies in pigs.



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<https://doi.org/10.1002/imt2.70013>



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