



# 两个端粒到端粒猪基因组组装和泛基因组分析提供了基因组结构特征和遗传适应性见解

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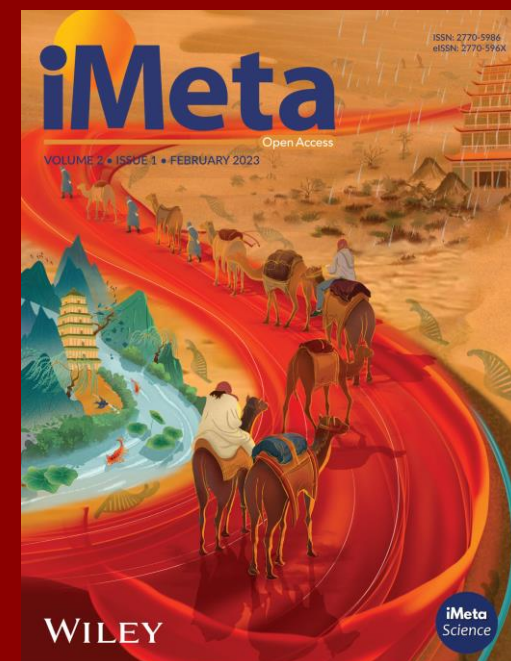
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# 简介



完整的人类基因组序列

RESEARCH ARTICLE | EVOLUTION | 8



## Evolutionary analysis of a complete chicken genome

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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](#)



# 亮点

- ▣ 端粒到端粒组装提供了高质量的民猪和荣昌猪基因组
- ▣ 对端粒和着丝粒区域的分析揭示了染色体结构特征
- ▣ 基于T2T框架构建了猪的泛基因组和图形泛基因组
- ▣ 结合基因组、转录组和表观基因组数据识别了与猪冷热适应有关的候选结构变异
- ▣ 展示了图形泛基因组在猪育种中可以提高全基因组关联研究的分辨率和基因组选择准确性



# 摘要

## 1. Two T2T native Chinese pig genomes



Min



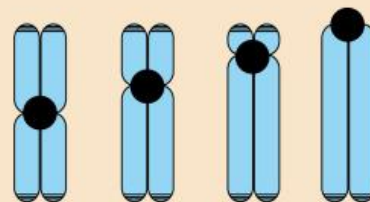
Rongchang

Genome assembly

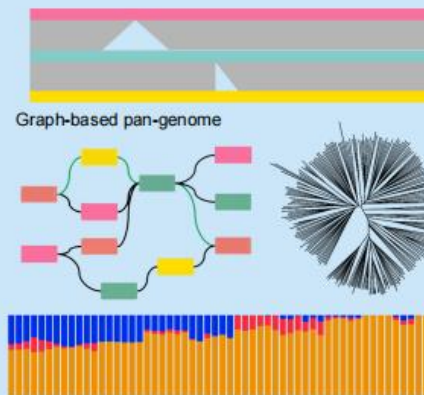
Genome annotation

Genome assessment

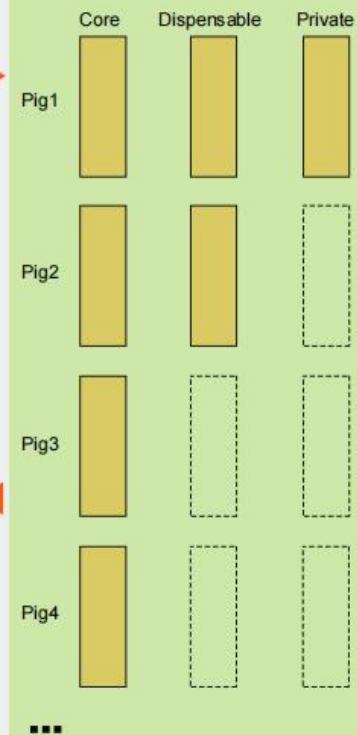
## 2. Telomeres and centromeres



## 4. Structural variations



## 3. Pan-genome



## 5. Cold and hot adaptation studies

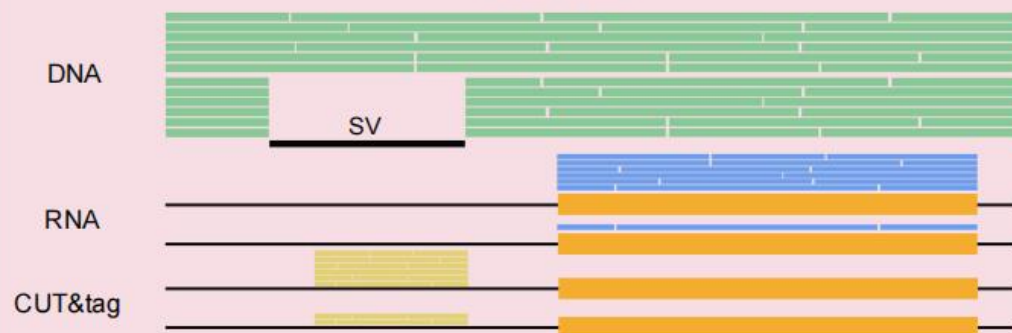


Cold stress

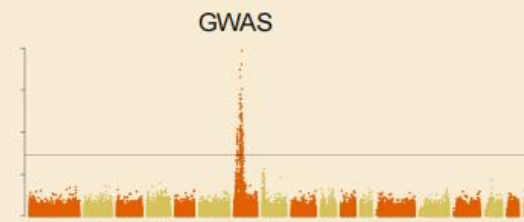


Hot stress

Multi-omics



## 6. Graph-based pan-genome in pig breeding



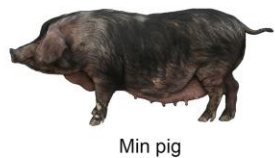
| GS     |                     |
|--------|---------------------|
| Panel  | Prediction accuracy |
| SNP+SV | ★★★★★               |
| SNP    | ★★★                 |
| SV     | ★★★                 |



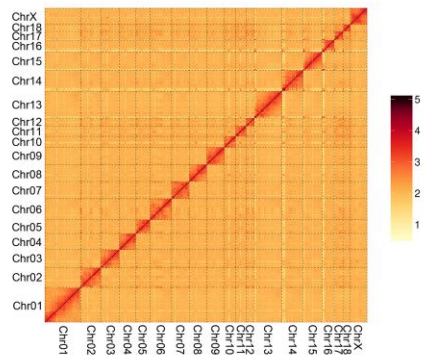


# 民猪和荣昌猪的T2T基因组组装

A



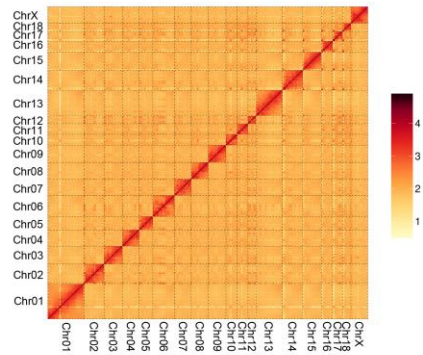
Min pig



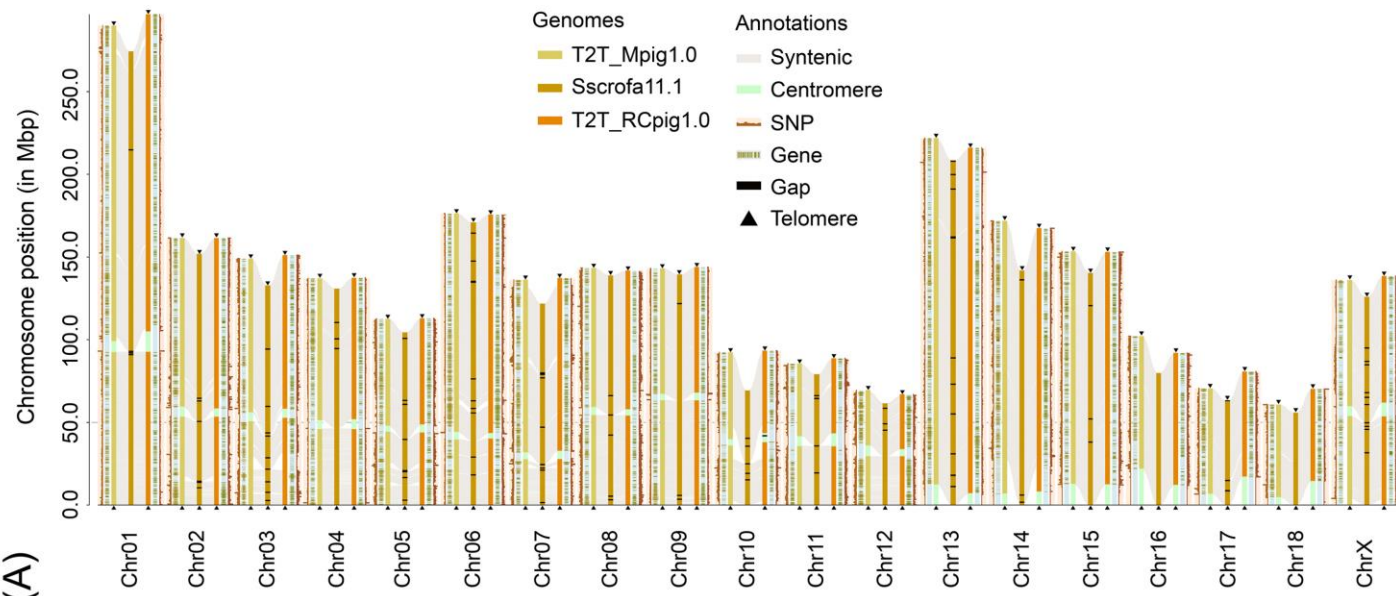
B



Rongchang pig



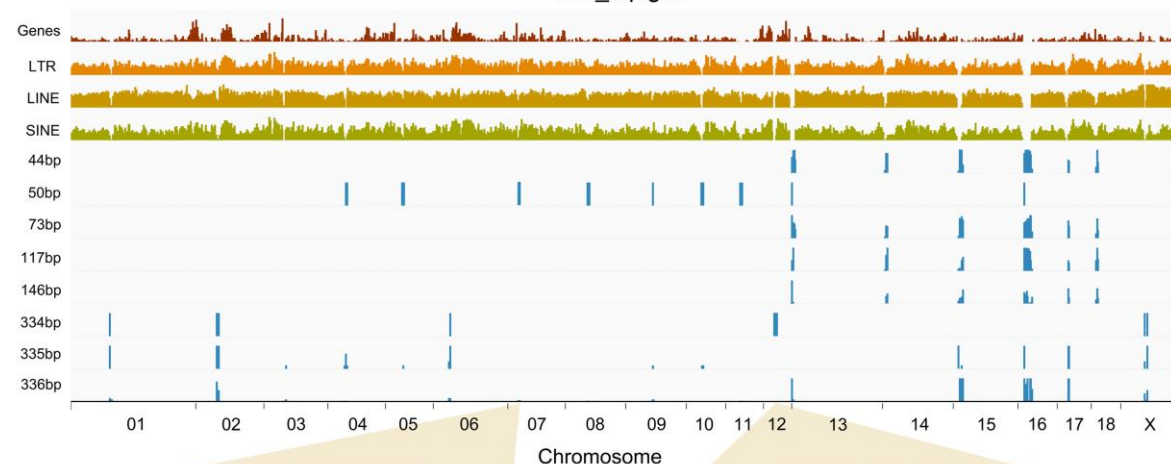
(A)





# 着丝粒鉴定

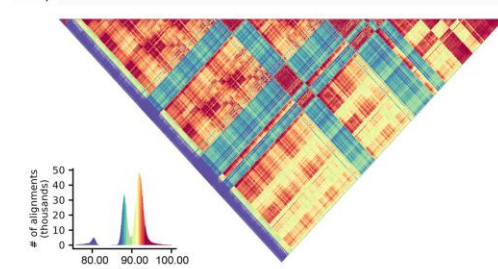
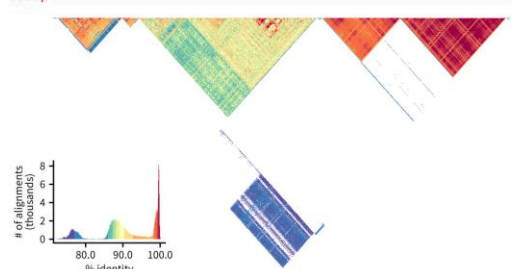
T2T\_Mpig1.0



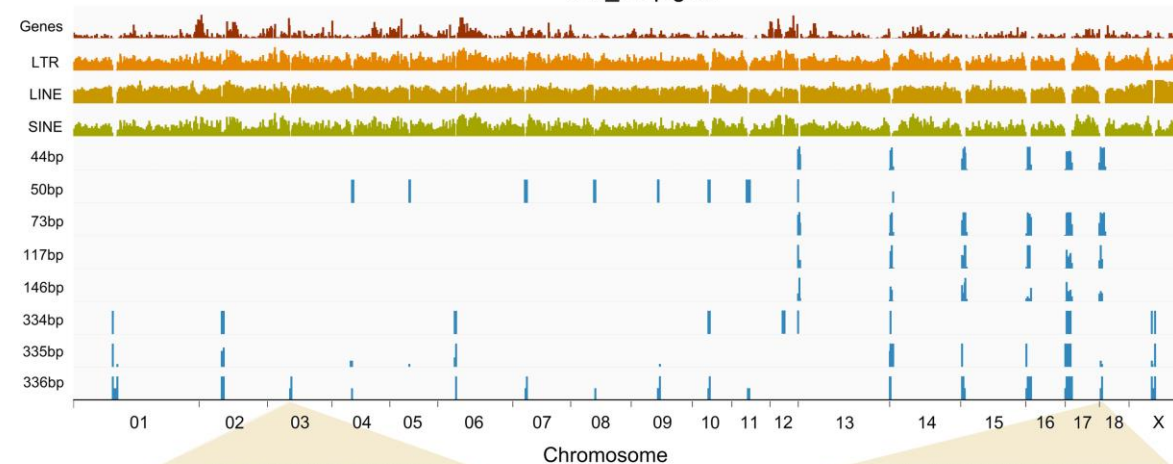
Chr7:28137327-31626397

Chromosome

Chr12:29964262-35868955

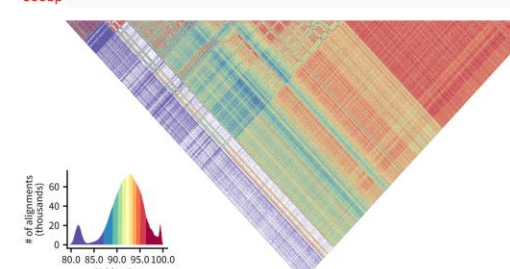
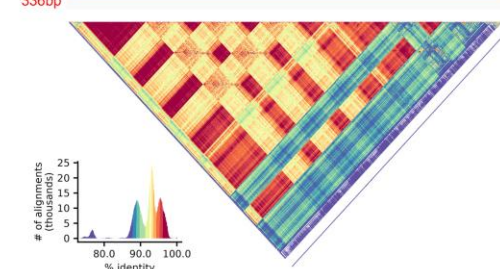


T2T\_RCPig1.0



Chr3:53337267-57965290

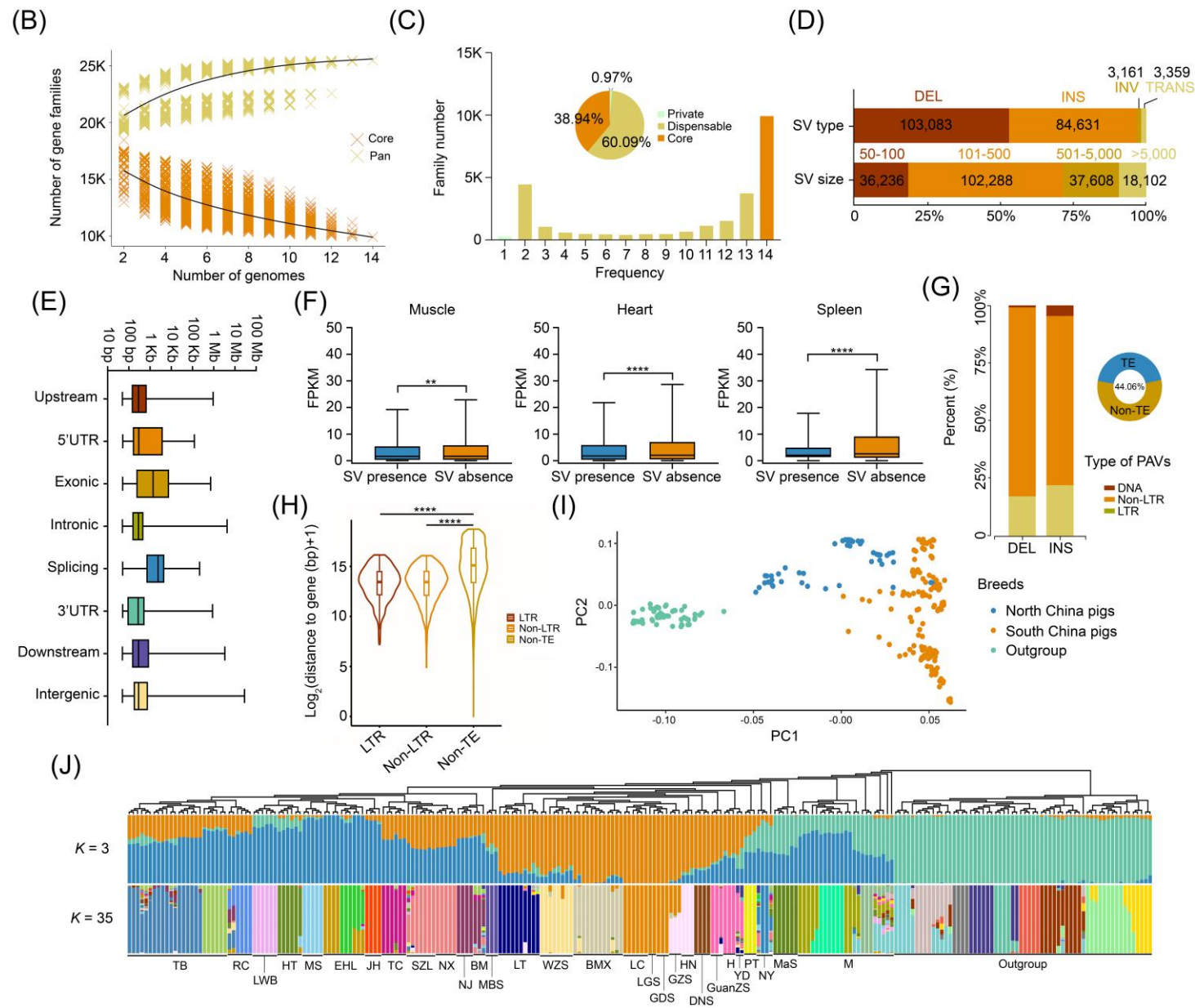
Chr18:2013830-14456208



1 至 12 号染色体和 X 染色体上的着丝粒为中/近中着丝粒，而 13 至 18 号染色体上为近端/端着丝粒



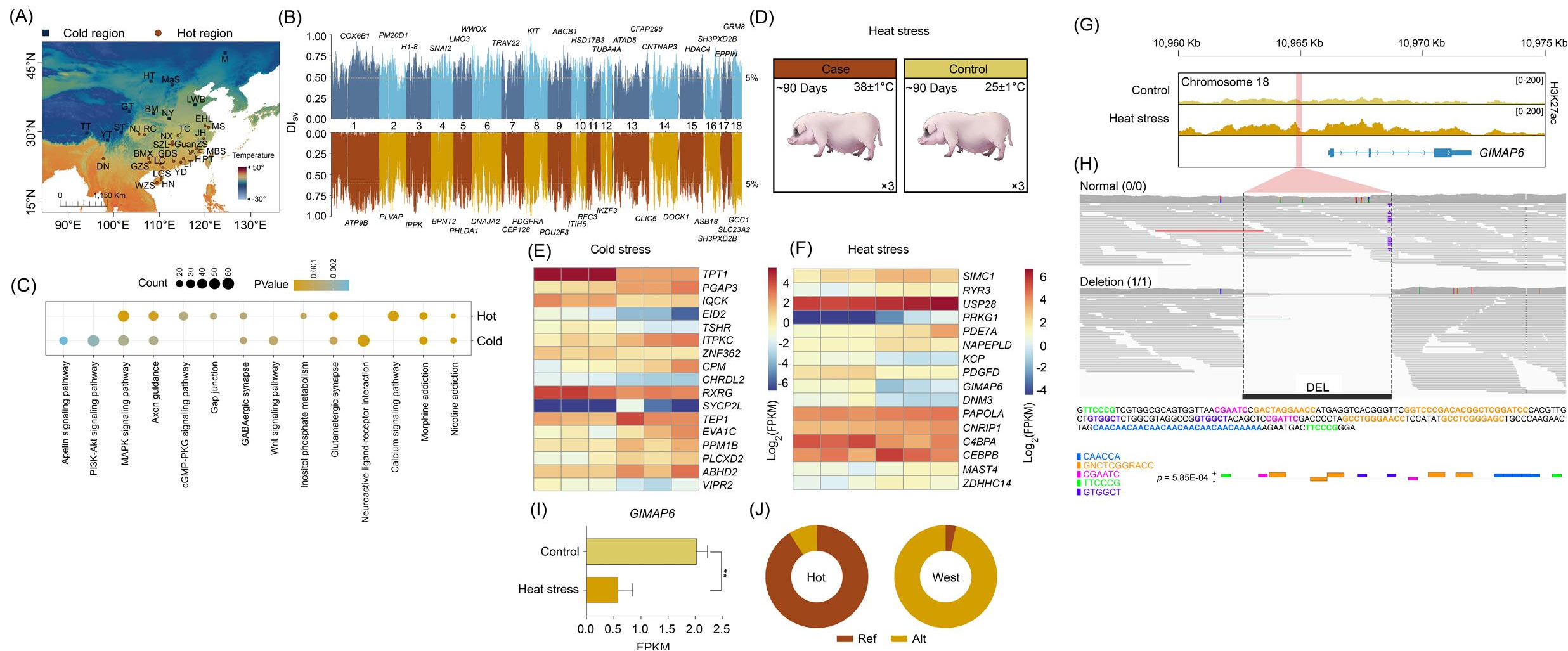
# 泛基因组和图形泛基因组构建







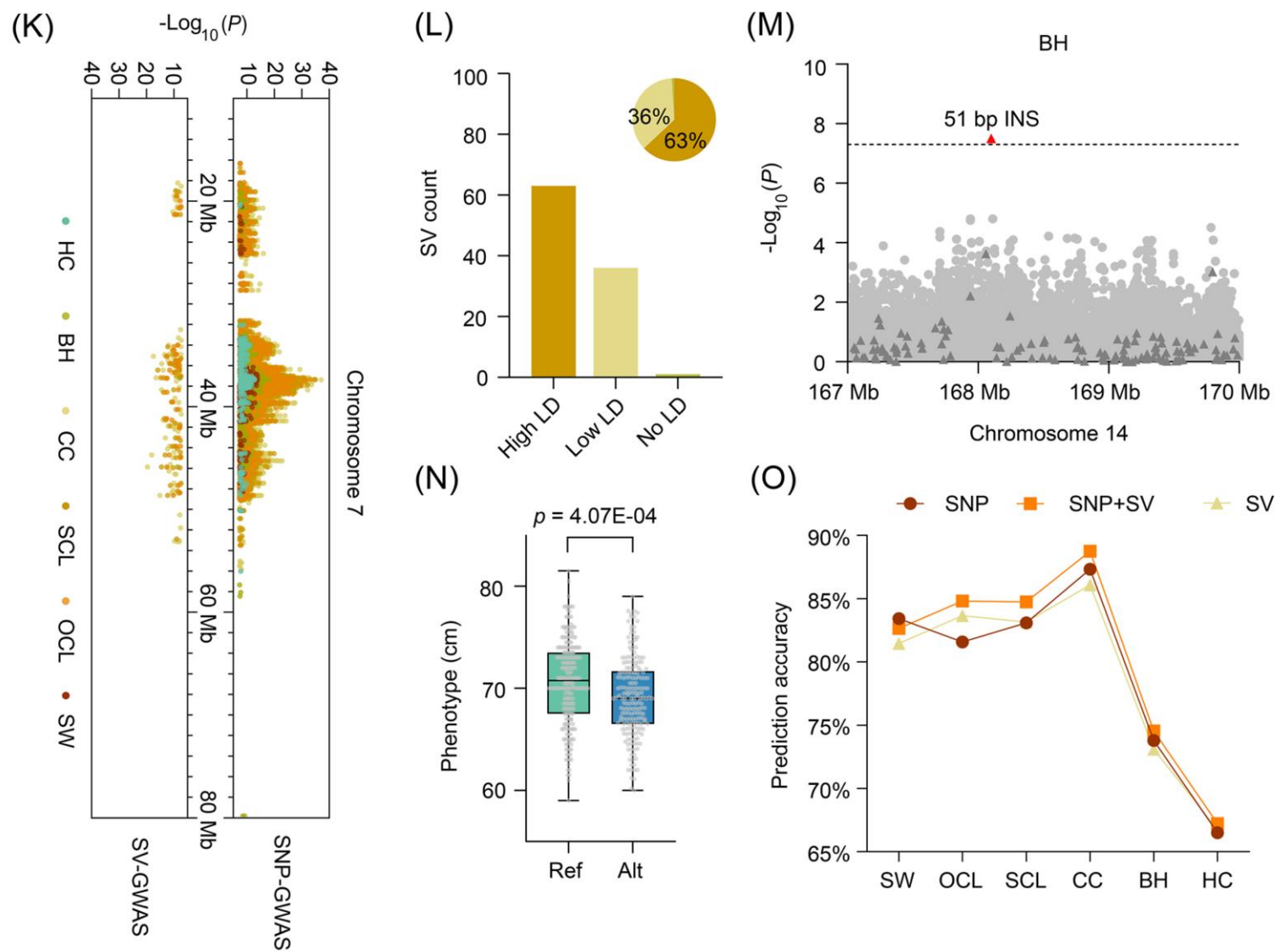
# 整合多组学对猪的冷热适应性分析







# 图形泛基因组在猪育种中的应用

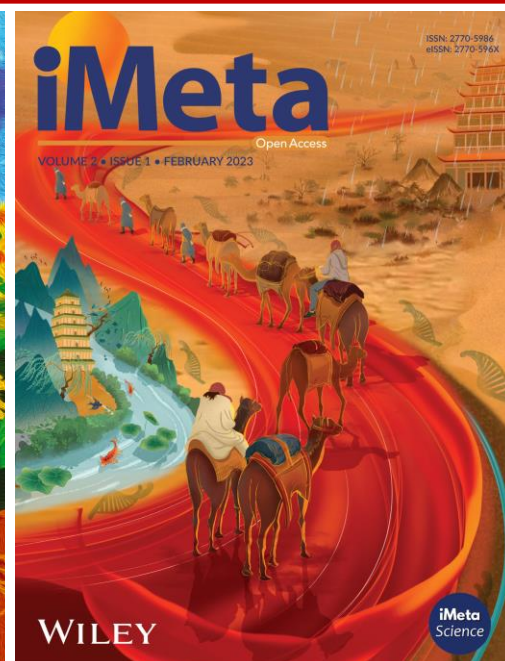
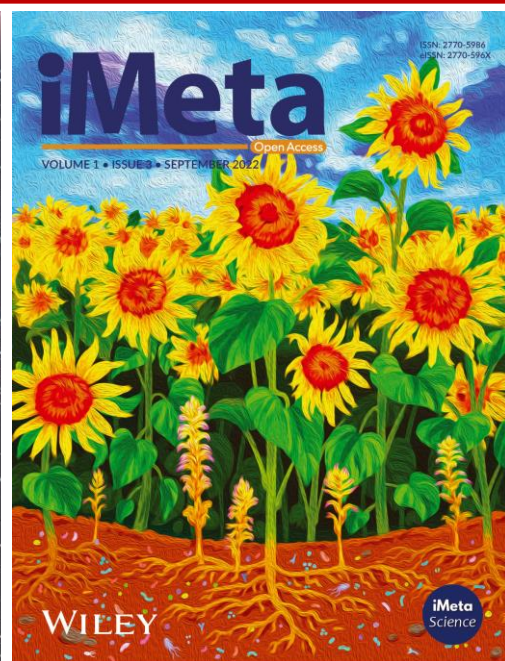




# 总结

在本研究中，我们利用先进的测序技术和组装策略构建了两个中国本土猪品种——民猪和荣昌猪的T2T基因组。这些资源促进了复杂基因组区域和结构变异的分析，揭示了猪的遗传适应性特征，为推进对猪的育种和保护策略奠定了基础。

Wencheng Zong<sup>1</sup>, Li Chen<sup>1,2</sup>, Dongjie Zhang<sup>3</sup>, Yuebo Zhang<sup>4,5</sup>, Jinbu Wang<sup>1</sup>, Xinhua Hou<sup>1</sup>, Jie Chai<sup>2</sup>, Yalong An<sup>6</sup>, Ming Tian<sup>3</sup>, Xinmiao He<sup>3</sup>, Chengyi Song<sup>7</sup>, Jun He<sup>4,5</sup>, Xin Liu<sup>1</sup>, Ligang Wang<sup>1</sup>, Enrico D'Alessandro<sup>8</sup>, Lixian Wang<sup>1</sup>, Yulong Yin<sup>4,5</sup>, Mingzhou Li<sup>9</sup>, Di Liu<sup>3</sup>, Jinyong Wang<sup>2</sup>, Longchao Zhang<sup>1</sup>. 2025. Two telomere-to-telomere pig genome assemblies and pan-genome analyses provide insights into genomic structural landscape and genetic adaptations. *iMeta* 4: e70013.  
<https://doi.org/10.1002/imt2.70013>



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