Multiomics analysis reveals signatures of selection and loci associated with complex traits in pigs

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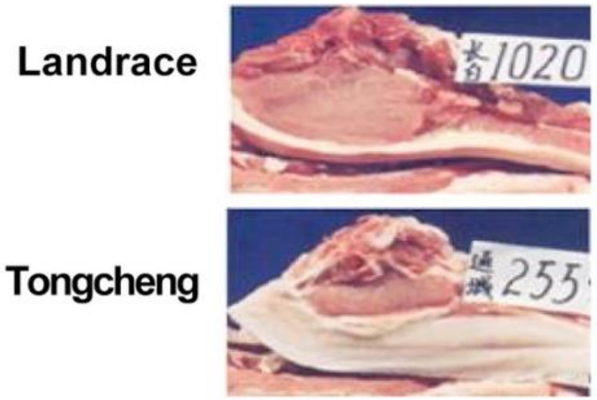
Introduction

Western pigs
Lean pigs

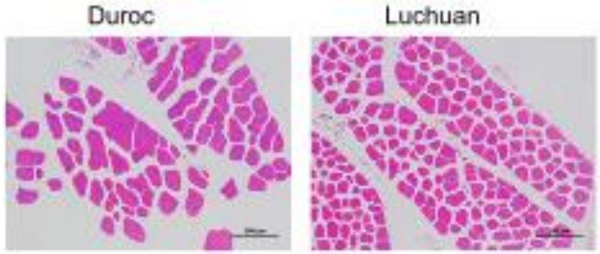
- Fast growth rate
- Low fat content
- Weak disease resistance
- …



(Yang *et al.*, 2021)

Eastern pigs
Fatty pigs

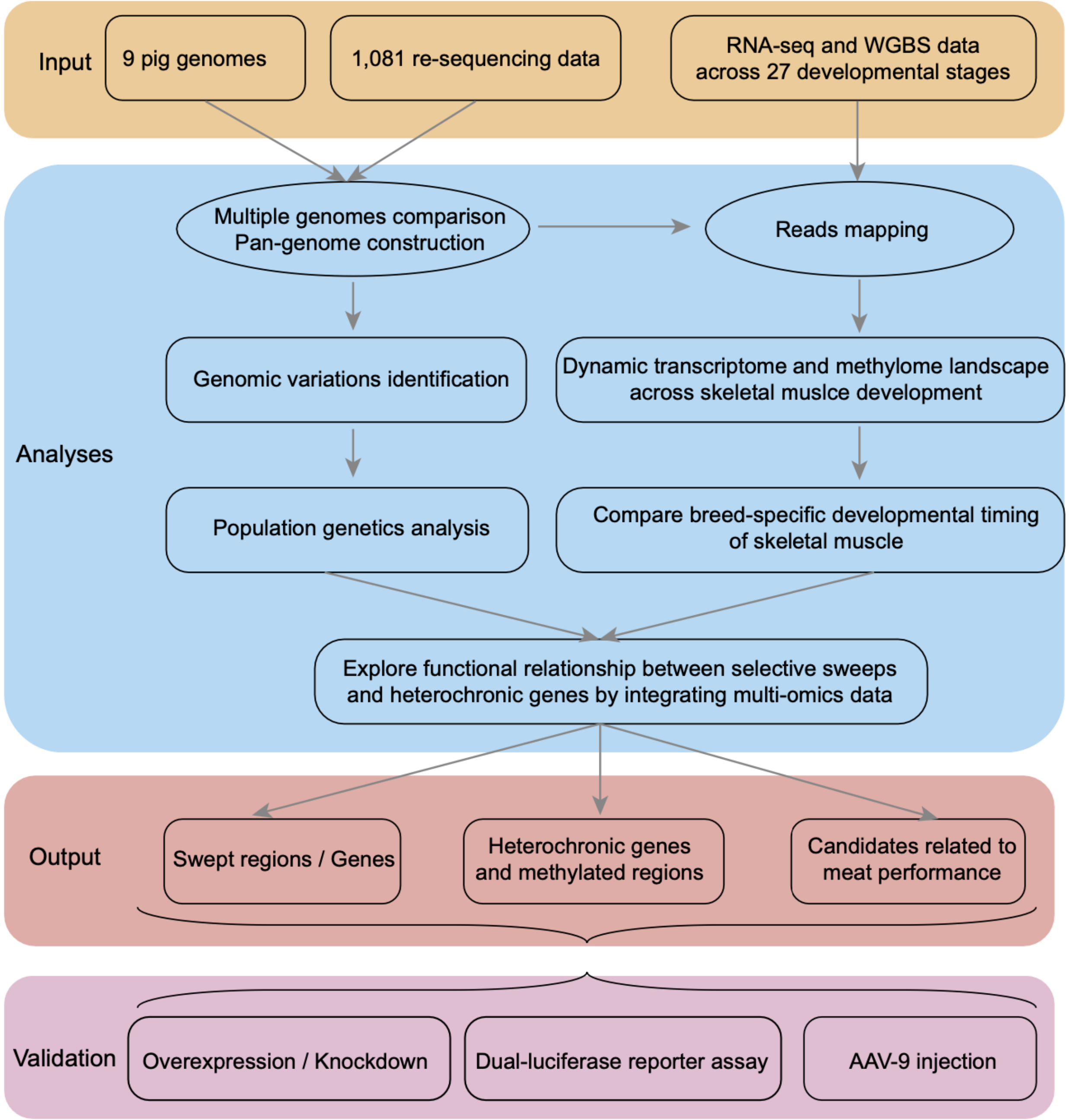
- Slow growth rate
- High fat content
- Strong disease resistance
- Tolerant to roughage
- …



Fiber density
(Liu *et al.*, 2022)

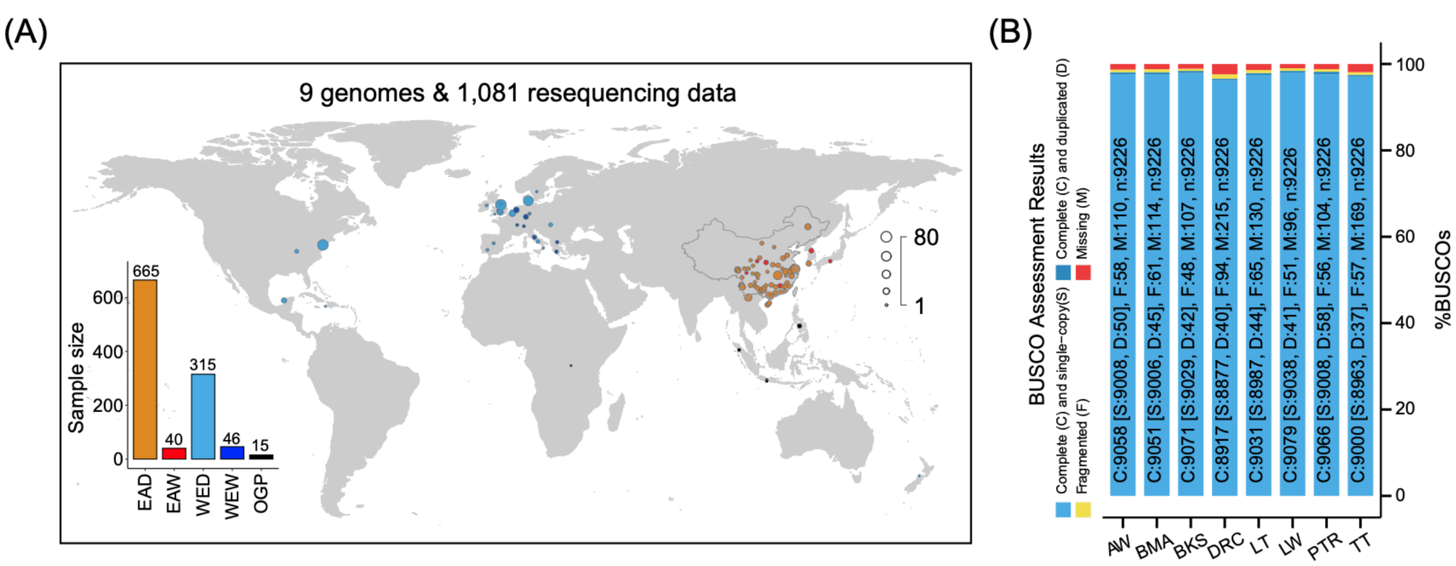
➢ Obvious differences in the phenotypes of Eastern pigs (fatty pigs) and Western pigs (lean pigs)

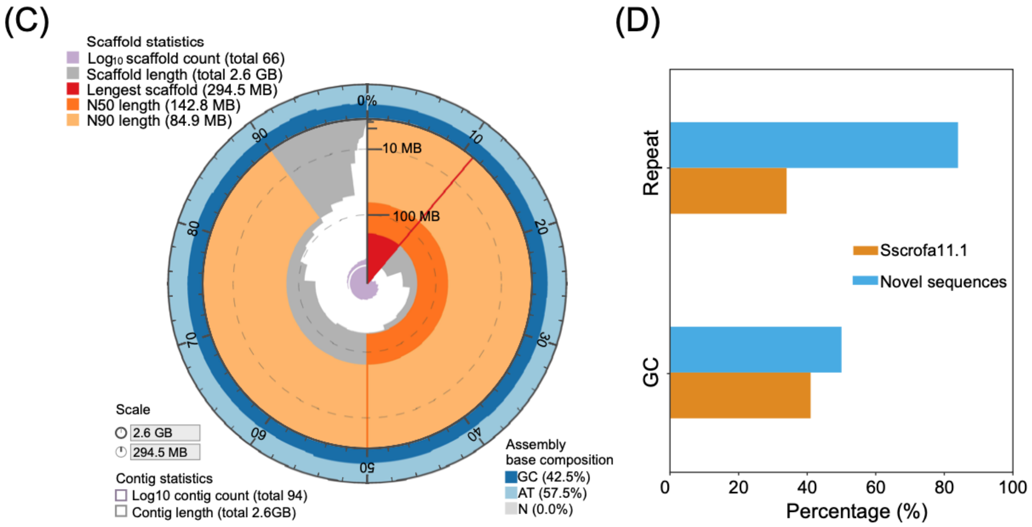
Research Technical Roadmap

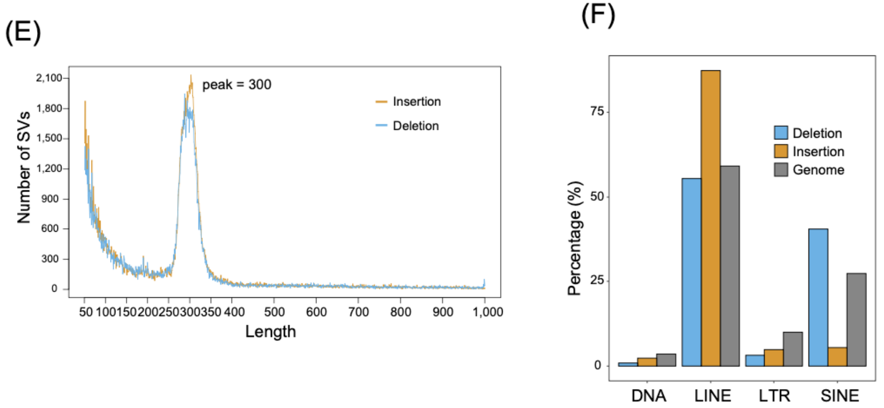


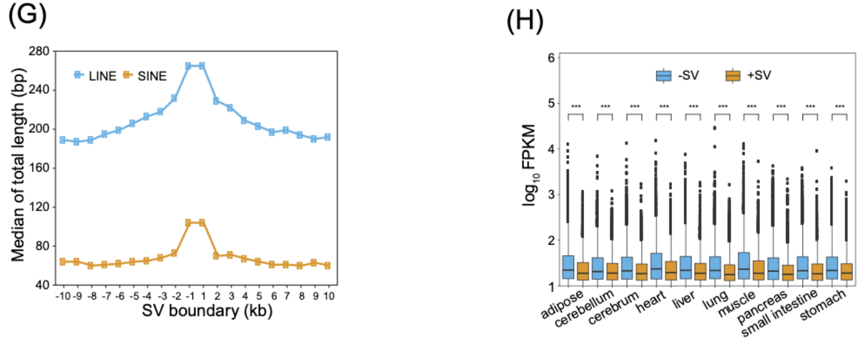
- Seven newly generated high-quality de novo assembled genomes
- Pan-genome construction and structural variation analysis
- Analysis of population structure, genetic variation and selection signals
- Analysis of differential regulatory mechanisms of skeletal muscle growth and development between Eastern and Western pigs
- Functional experimental verification

A pan-genome sequence and genetic variation dataset in pigs



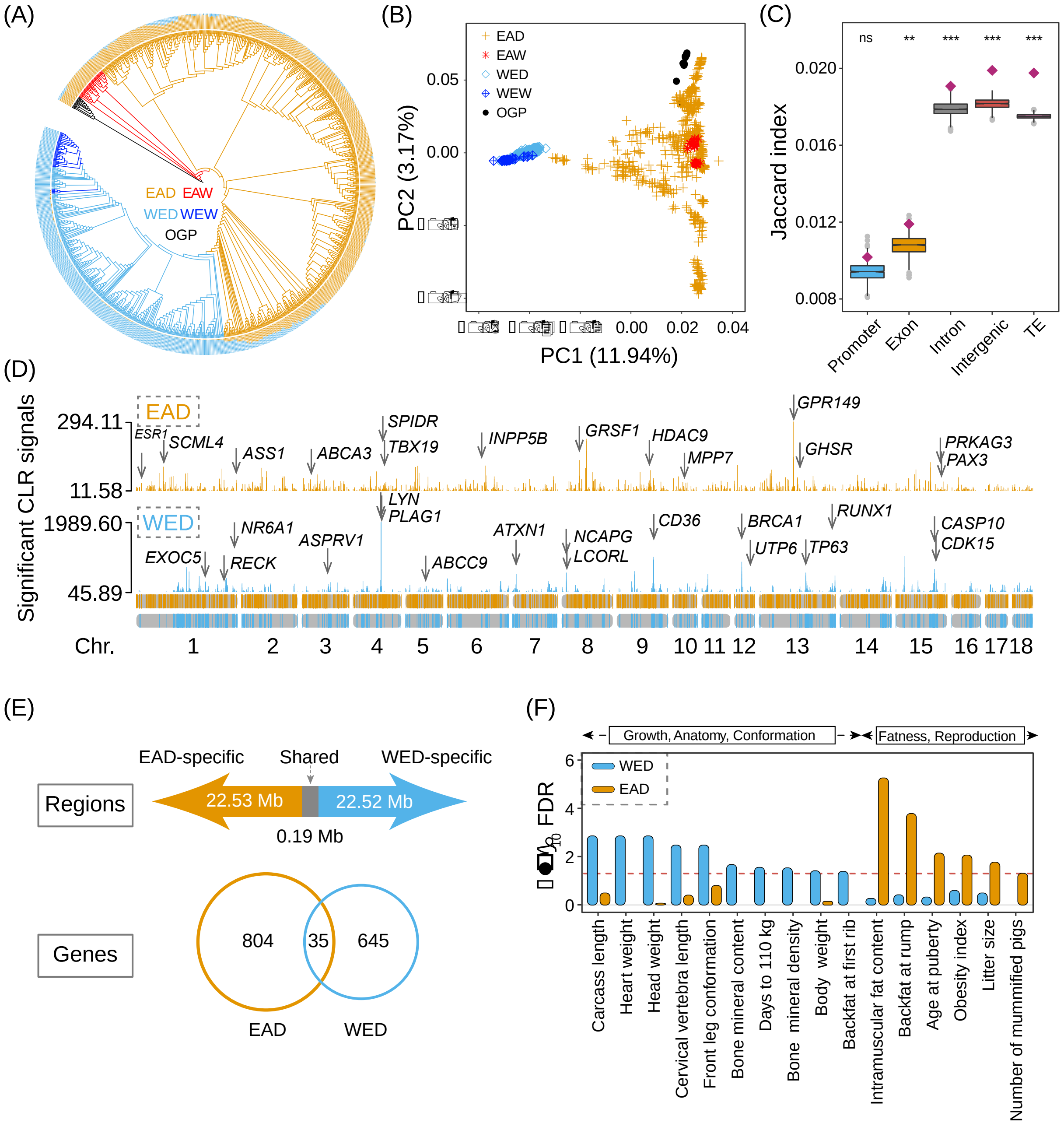






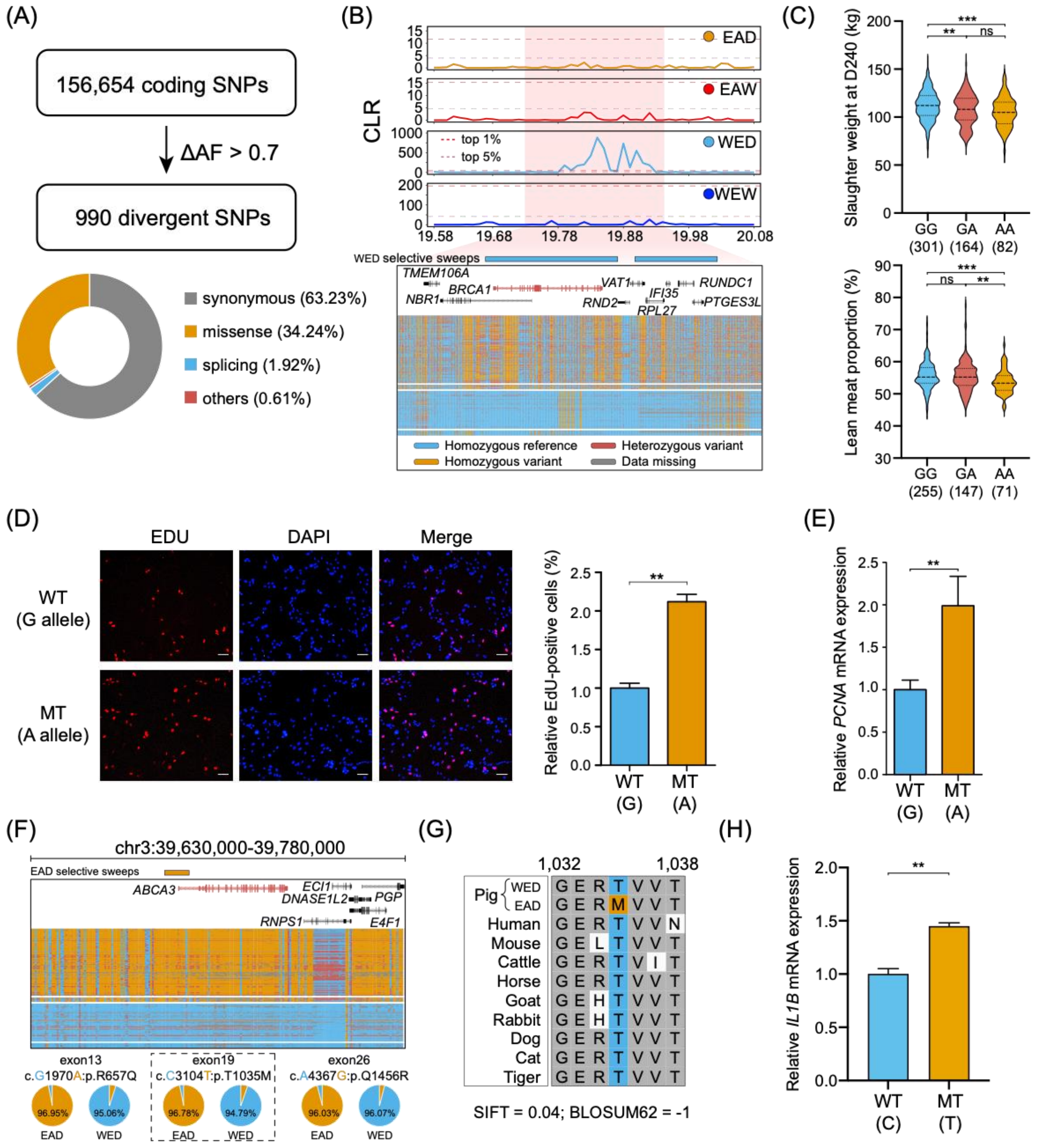
- **Genome assembly:**
  - ➢ An Asian wild boar, three Chinese breeds (Bama, Tibetan and Lantang) and three European breeds (Large White, Berkshire and Pietrain)
- **Pan-genome:**
  - ➢ 134.24 Mb of non-redundant non-reference sequence, 187,927 structural variants, 1,099 novel protein-coding genes

Population structure and potential selection signatures



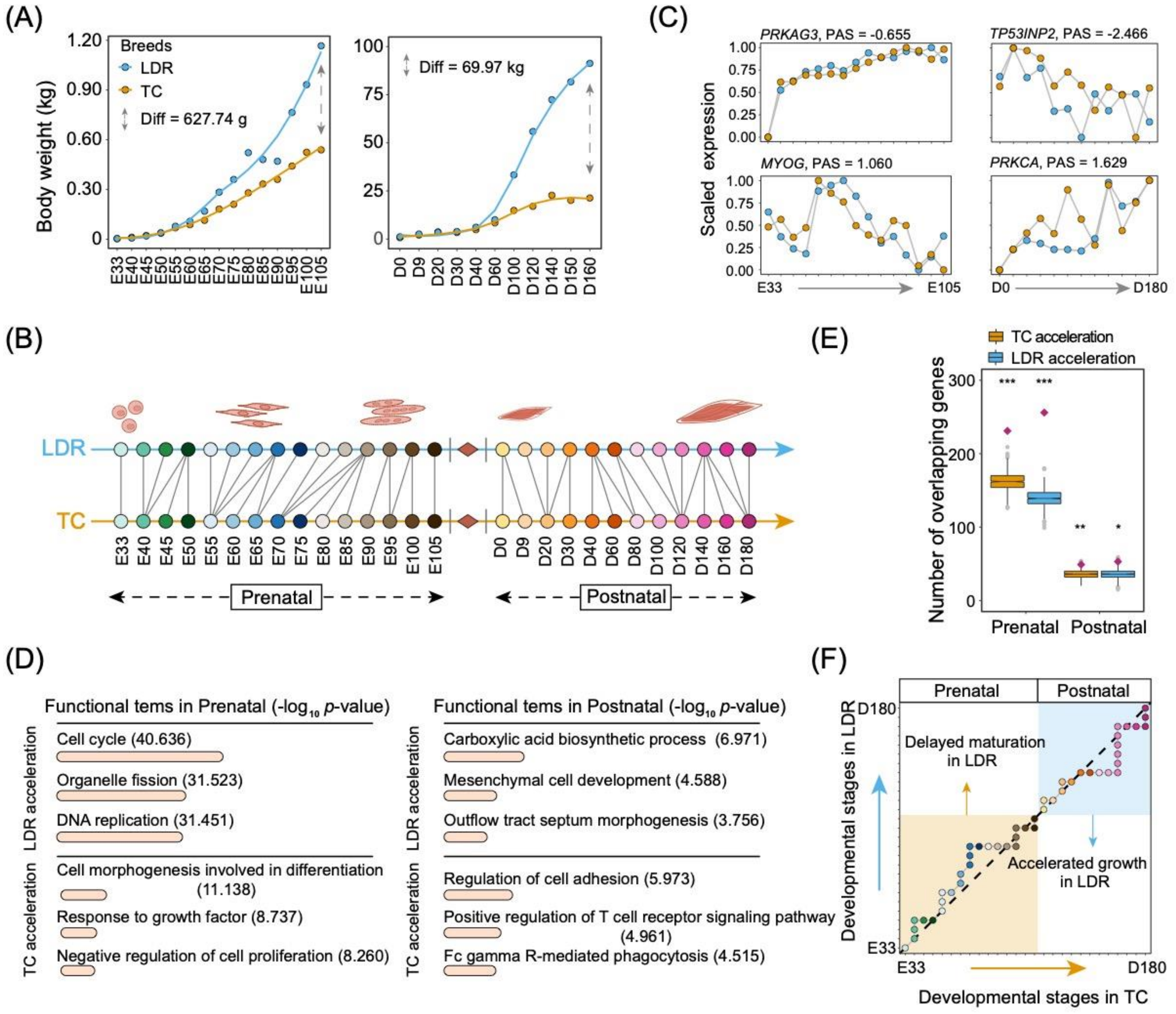
- The 1,081 individuals were mainly distributed in Europe and Asia
- Five groups: Eastern domestic pig, Eastern wild pig, Western domestic pig, Western wild pig and an outgroup
- EAD swept genes drive traits associated with fatness type and reproductive class
- WED swept genes are mainly involved in the growth, anatomy and conformation categories

Functional implication of coding variants linked to selective sweeps



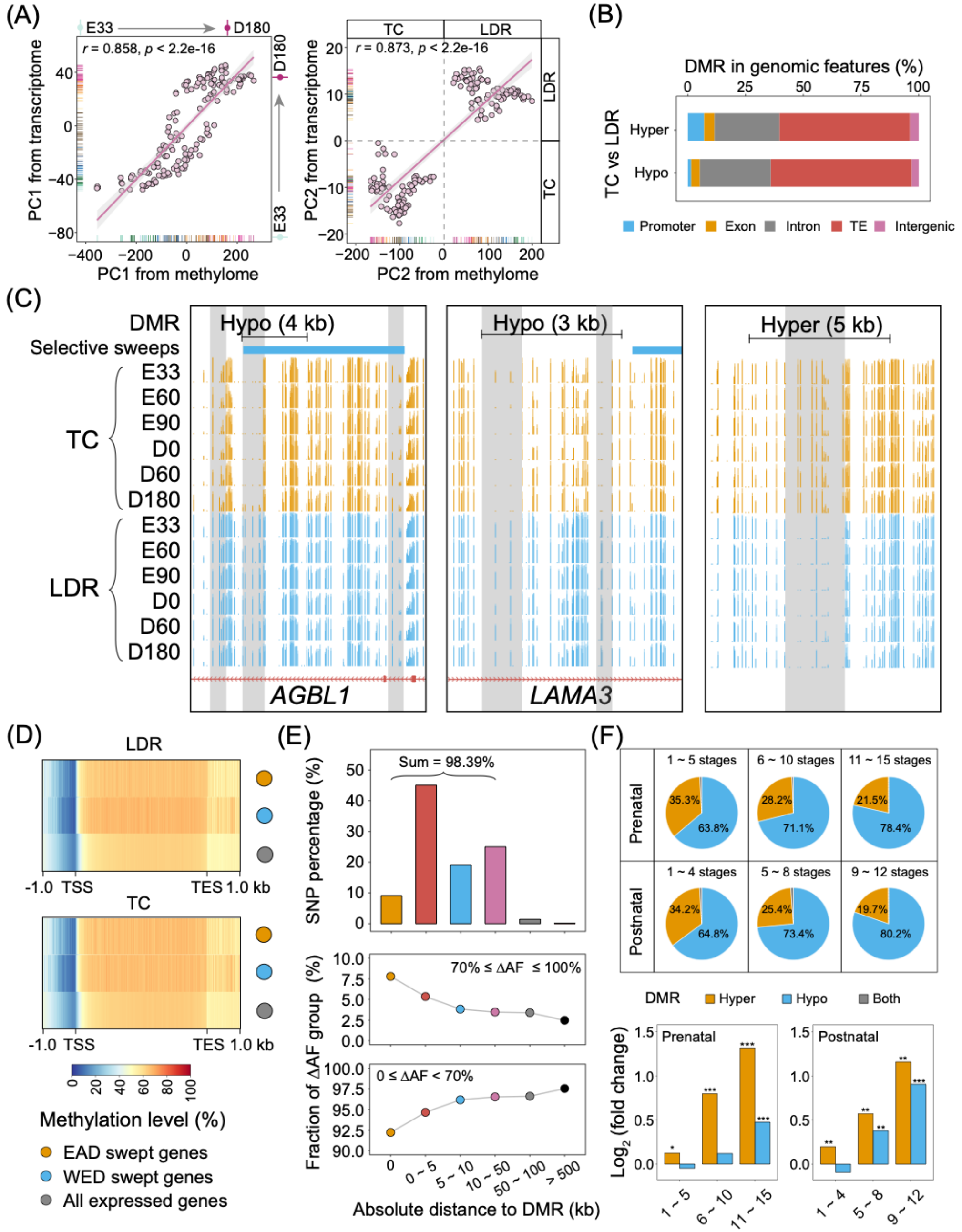
- 990 nearly fixed coding variants were screened
- c.G965A *BRCA1* expression showed enhanced adipocyte growth and development ability
- The C allele in *ABCA3* is nearly fixed in WED
- The wild-type C allele is associated with lower levels of *IL1B* gene expression
- C allele in *ABCA3* reduces immune responses and lung damage

Swept genes regulate developmental heterochrony of skeletal muscle between EAD and WED pigs



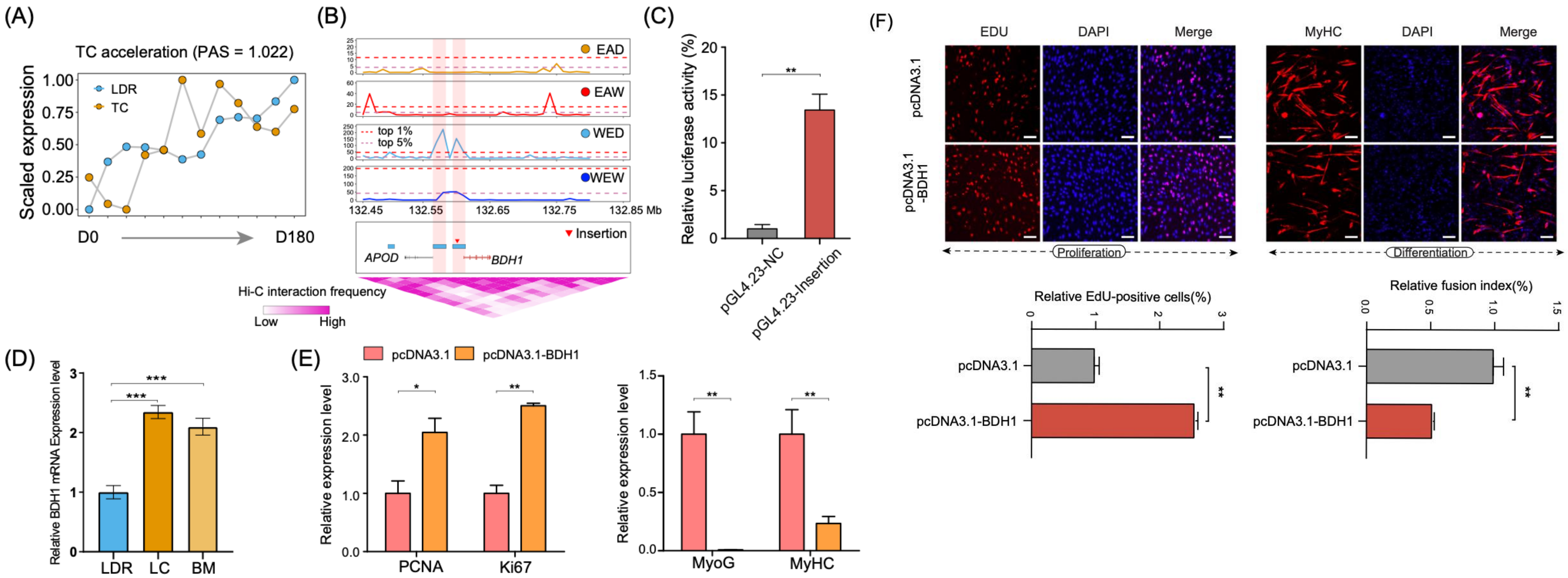
- Skeletal muscle growth and development are asynchronous in Landrace and Tongcheng pigs
- LDR-accelerated genes in the prenatal stage are significantly overexpressed in cell cycle and DNA replication. In contrast, TC-accelerated genes mainly promote cell differentiation and maturation
- In the postnatal period, genes with more advanced LDR progression continue to be enriched in cell development and biosynthesis processes, while TC-accelerated genes are related to immune response

Selective sweeps regulated gene expression by reshaping DNA methylation pattern



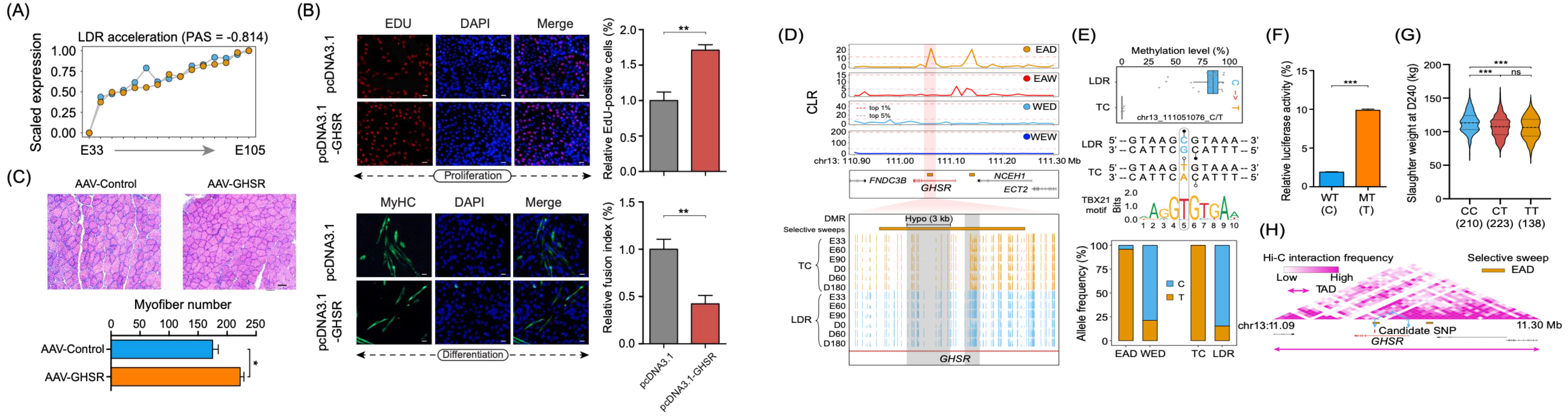
- Whole-genome bisulfite sequencing was performed on skeletal muscle samples from 27 developmental stages
- Tongcheng pigs had higher overall CpG methylation levels
- DNA methylation changes have a reshaping effect on gene expression patterns
- DNA methylation has a potential association with genetic selection
- Dynamic DMRs face selective elimination, highlighting DNA methylation in pig domestication

Genetic basis of candidate genes in skeletal muscle development and meat performance



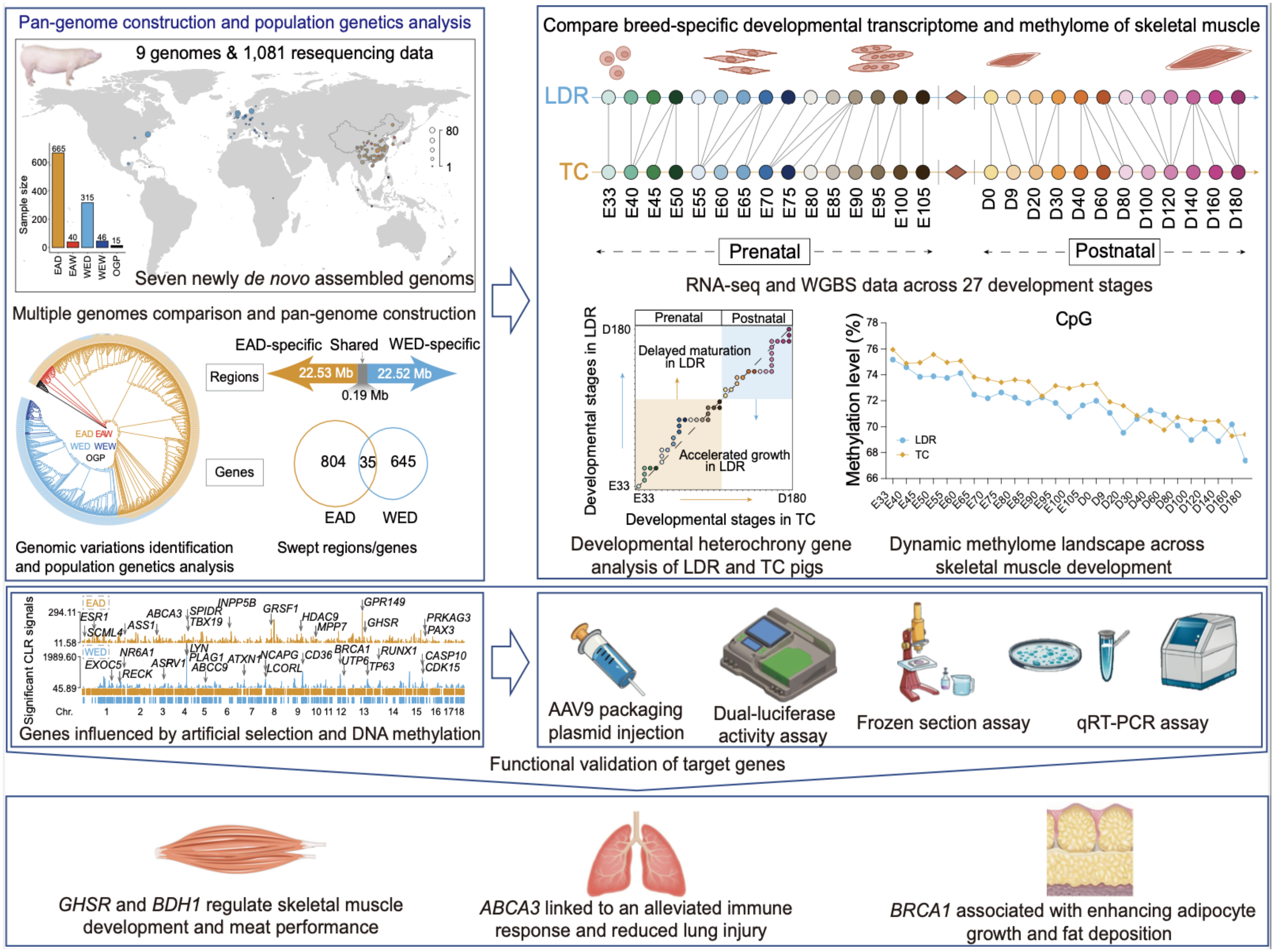
- ➢ The *BDH1* gene showed a faster expression pattern in TC skeletal muscle in the postnatal stage than in LDR
- ➢ Insertion upstream of this gene enhanced its enhancer, exerting a positive regulatory effect on the *BDH1* gene
- ➢ The *BDH1* expression level of Chinese local pig breeds was higher than that of LDR breeds
- ➢ *BDH1* promotes the growth of skeletal muscle in EAD pigs after birth

Genetic basis of candidate genes in skeletal muscle development and meat performance



- *GHSR* is a key factor in accelerating myoblast proliferation
- *GHSR* can promote myoblast proliferation but inhibit its differentiation and fusion in vivo and in vitro
- The CpG-SNP of the mutant allele was almost completely fixed in the EAD population and TC breed
- The methylation status in TC was completely lost due to the transition from C to T allele
- This SNP reduces D240 slaughter weight by 4.22 kg, with T allele carriers showing lower weights

Conclusion



- Constructed a comprehensive pig pan-genome and genetic variation dataset, enabling the analysis of complex traits;
- Revealed epigenetic and heterochronic gene regulation mechanisms in skeletal muscle growth across 27 developmental stages;
- Identified Highlighted the impact of artificial selection on DNA methylation and gene regulation linked to muscle growth and meat quality differences;
- Identified key genetic markers related to fat deposition, muscle growth, and immunity for breeding programs.

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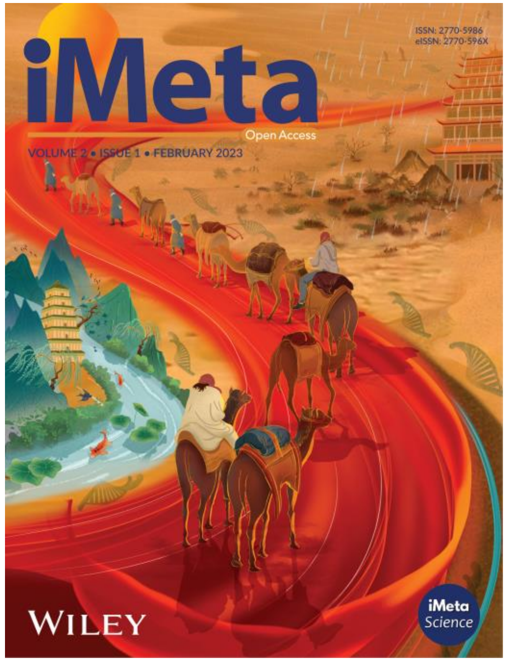

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