



Integrative genomics and regulomics reveal the molecular architecture of complex traits in domestic chickens

Wei Han^{1,2,#,*}, Chenghao Zhou^{1,2,#}, Yuxin You^{3,#}, Guohui Li^{1,2}, Yunfen Zhu^{1,2}, Yijun Tang³, Tao Zeng⁴, Huiyong Zhang^{1,2}, Qian Xue^{1,2}, Jianmei Yin^{1,2}, Li Chen⁴, Xing Ju^{1,2}, Yixiu Jiang^{1,2}, Jiaqi Cai³, Lu Li⁵, Xiaofeng Zhang⁵, Zhaoyu Lin⁵, Jindong Ren⁴, Lizhi Lu^{4,*} and Dijun Chen^{3,6,*}



¹ Jiangsu Institute of Poultry Science, Yangzhou, China;

² Key Laboratory of Livestock and Poultry Resources (Poultry) Evaluation and Utilization, Ministry of Agriculture and Rural Affairs, Yangzhou, China;

³ State Key Laboratory of Pharmaceutical Biotechnology, Nanjing Drum Tower Hospital, School of Life Sciences, Nanjing University, Nanjing, China;

⁴ Institute of Animal Husbandry and Veterinary Science, Zhejiang Academy of Agricultural Sciences, Hangzhou, China;

⁵ National Resource Center for Mutant Mice of China; Ministry of Education Key Laboratory of Model Animal for Disease Study; Model Animal Research Center, Nanjing Drum Tower Hospital, School of Medicine, Nanjing University, Nanjing, China;

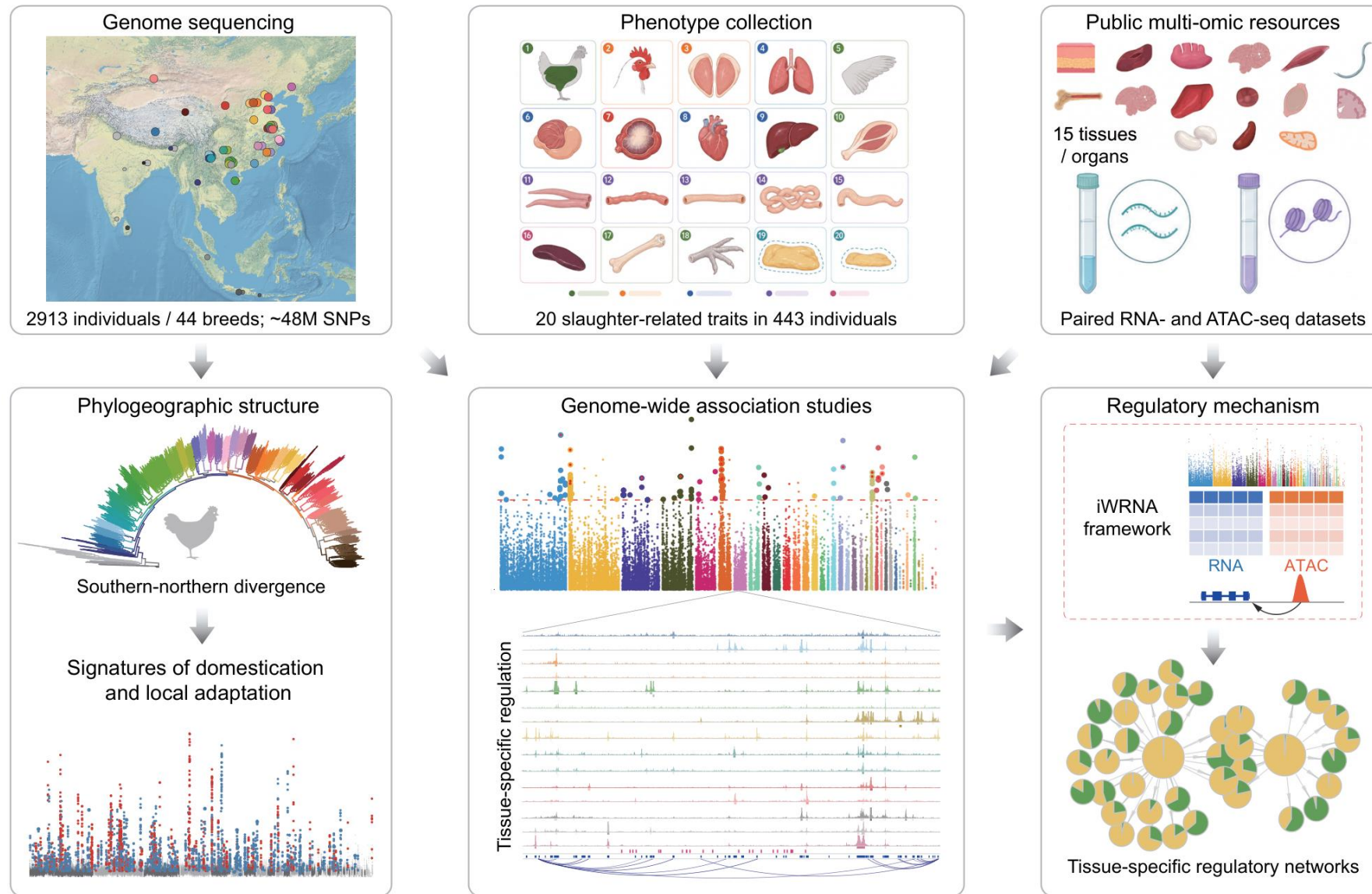
⁶ Chemistry and Biomedicine Innovation Center, Nanjing University, Nanjing, China

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Highlights



Graphical abstract. Integrative genomics and regulomics of complex traits in domestic chickens.

A large-scale genomic variation atlas of domestic chickens

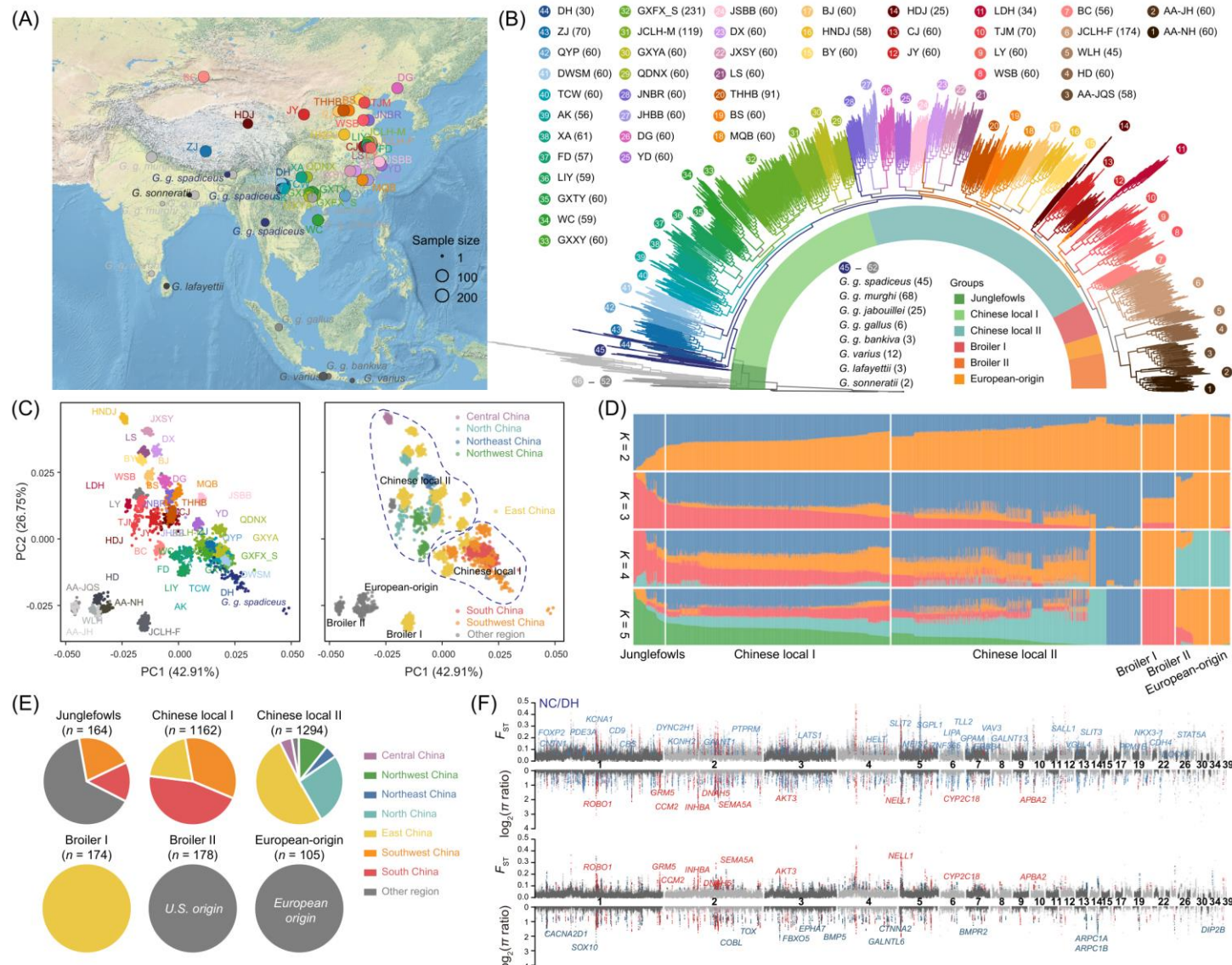


Figure 1. Genomic landscape and adaptive evolution in Chinese chickens.

Population structure

North–south genetic differentiation
in Chinese indigenous chickens

Candidate selection signals

Shared

AKT3 / NELL1 / INHBA...

Southern

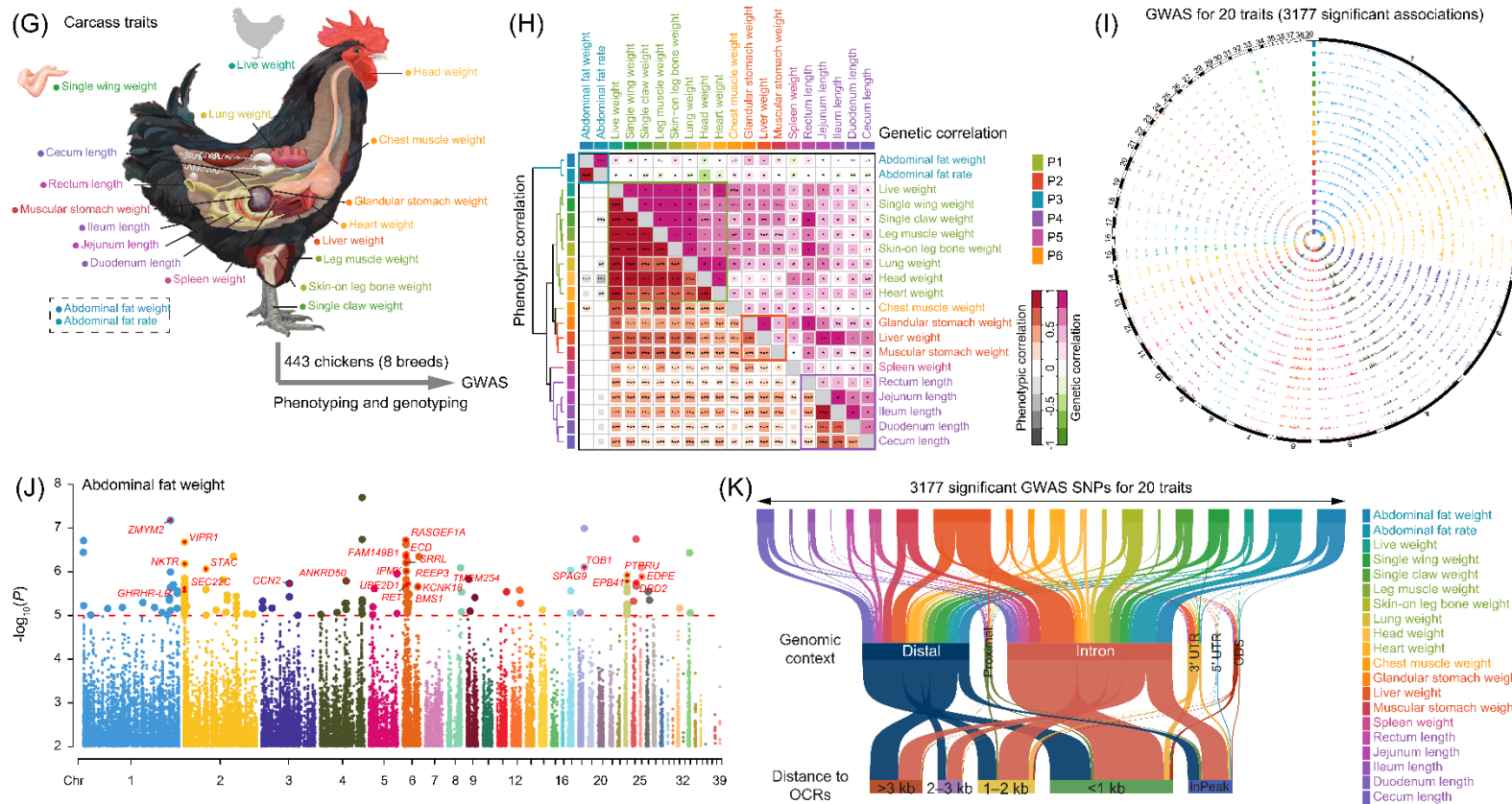
BMP2 / CTNNA2 / DIP2B...

Northern

SLIT2 / LIPA / FOXP2 / VAV3...



Genome-wide association analysis of 20 carcass traits



Slaughter-related trait:
3,177 trait–SNP associations

97.8% in noncoding regions
over half (55.3%) overlapped with
or were located near (<1 kb) open
chromatin regions (OCRs)

Figure 2. Genetic basis of complex traits in Chinese chickens.



iWRNA identifies trait-associated regulatory modules

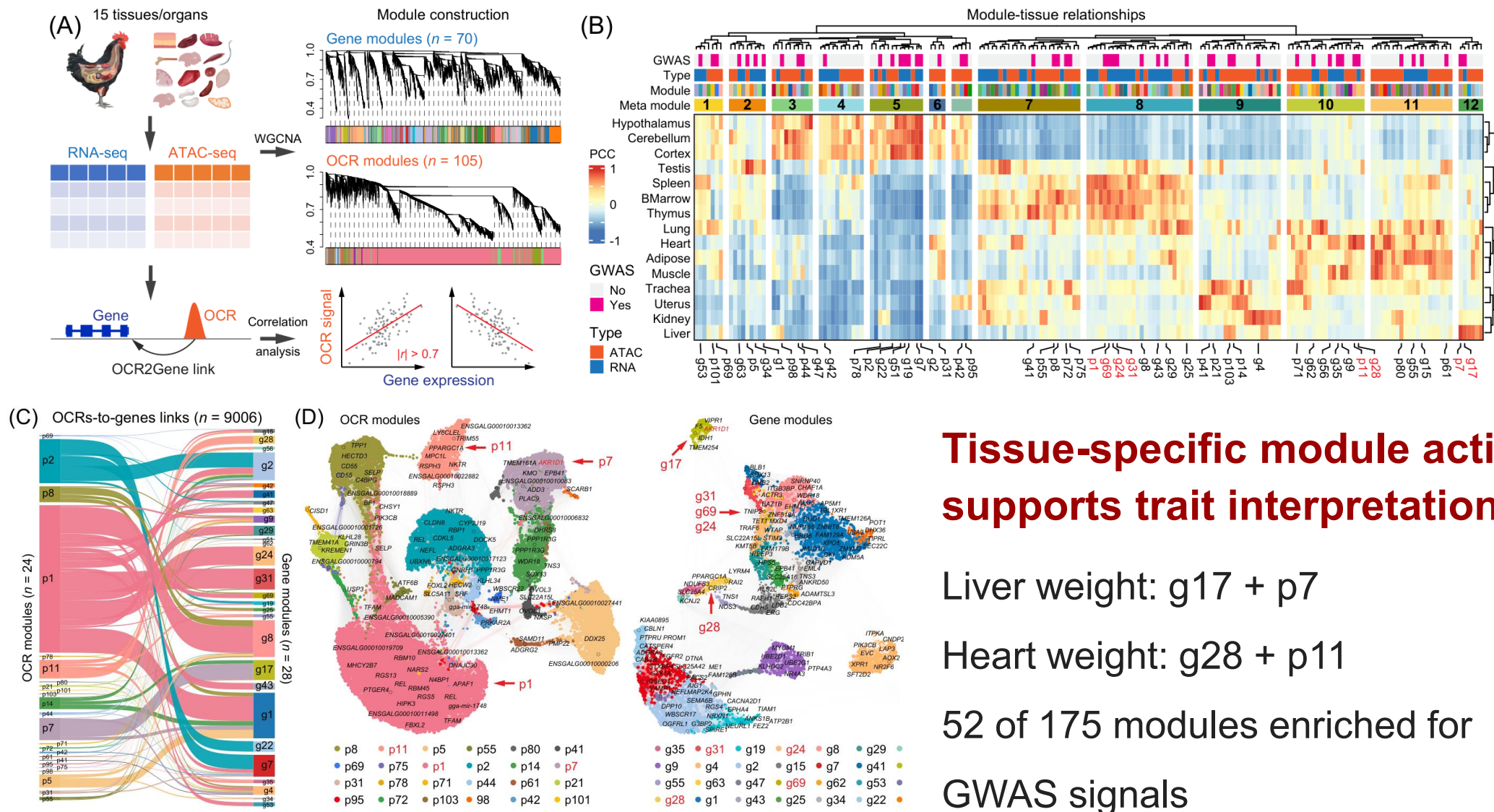
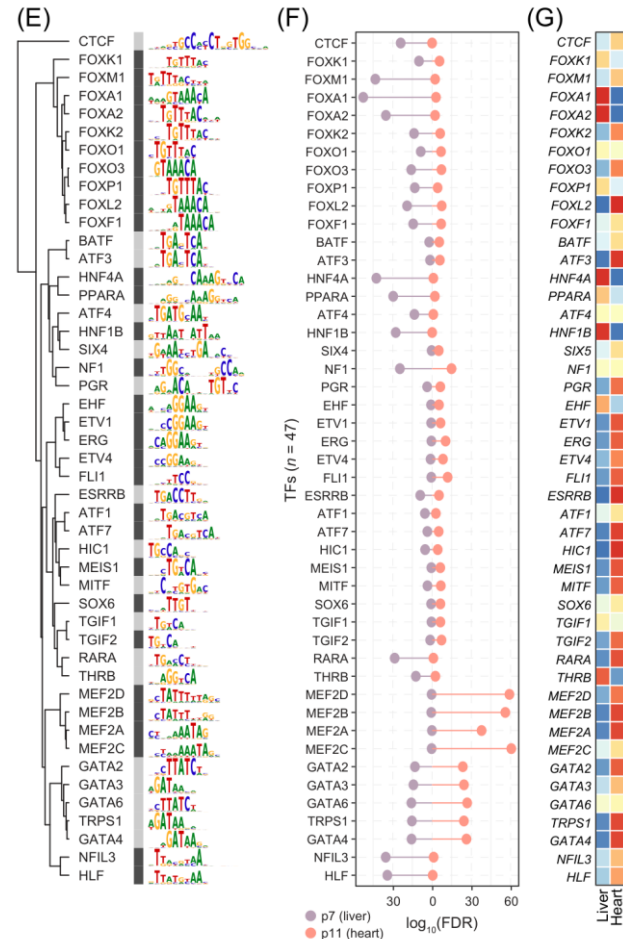


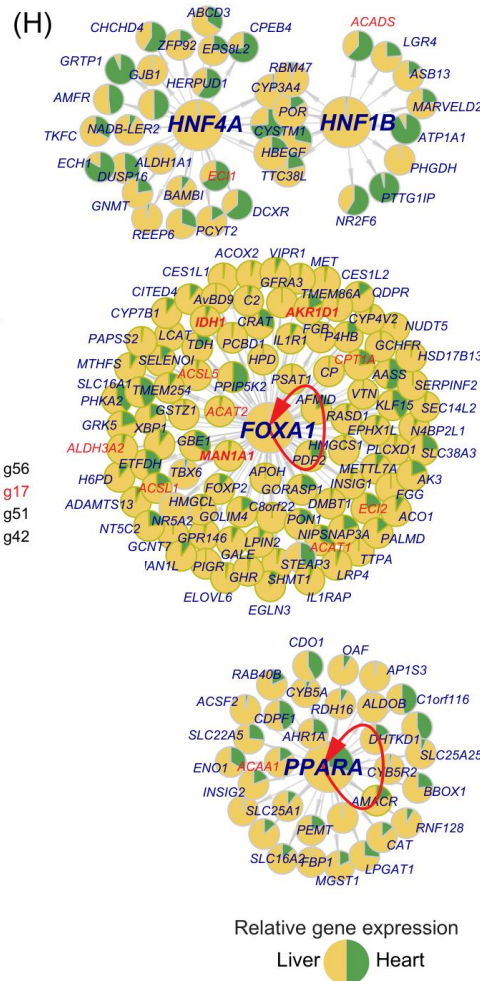
Figure 3. Identification of gene-regulatory modules underlying carcass traits

Tissue-specific transcriptional hierarchies associated with trait-related modules

motif and TF expression (E–G)



Liver-weight networks (H)



Functional and pathway analyses (I–K)

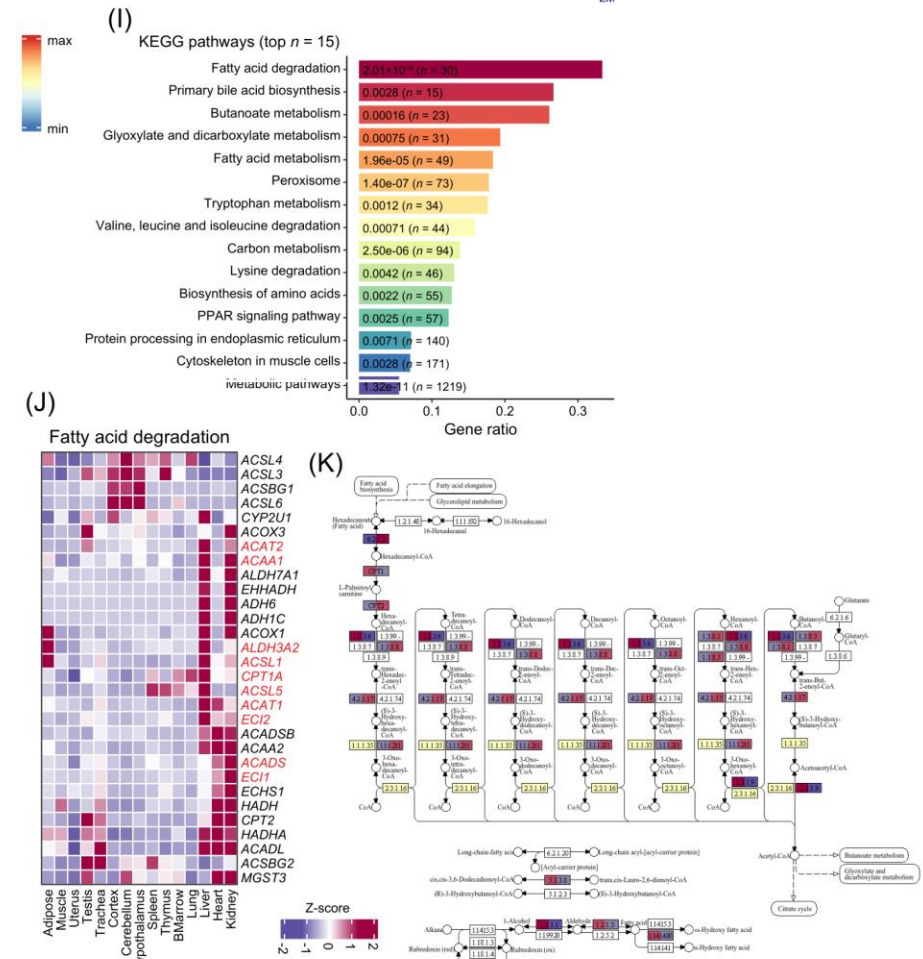


Figure 4. Motif enrichment and regulatory network construction of trait-associated modules.

Liver weight: *FOXA1* / *HNF4A* / *PPARA*...; Heart weight: *GATA4* / *MEF2* / *SOX6*...



Summary

- ❑ A high-depth genomic resource: 2913 chickens from 44 breeds/lines, integrated with 164 published junglefowl genome; GWAS prioritized variants
- ❑ North–south genetic differentiation in Chinese indigenous chickens, with shared and region-specific candidate signatures of selection.
- ❑ iWRNA integrates GWAS signals with multi-tissue transcriptomic and chromatin-accessibility data to nominate trait-associated regulatory modules.
- ❑ Website: <https://biobigdata.nju.edu.cn/chicken3k/>

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