

# Whole-genome resequencing data reveal the genetic diversity of local chickens in southern Zhejiang and surrounding areas in China

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The authors are fully responsible for both the content and the formal aspects of the electronic supplementary material. No editorial adjustments were made.

## Electronic Supplementary Material (ESM)

Figure S1. Appearance of the Wenzhou Red Chicken

Figure S2. Distribution of SNPs on chromosomes

Figure S3. Plot of the first and the third principal component from the principal component analysis (PCA) of the chicken populations analysed in this study

Figure S4. Plot of the second and the third principal component from the principal component analysis (PCA) of the chicken populations analysed in this study

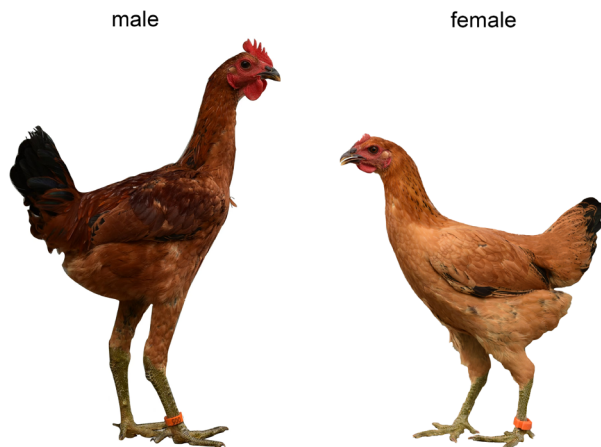
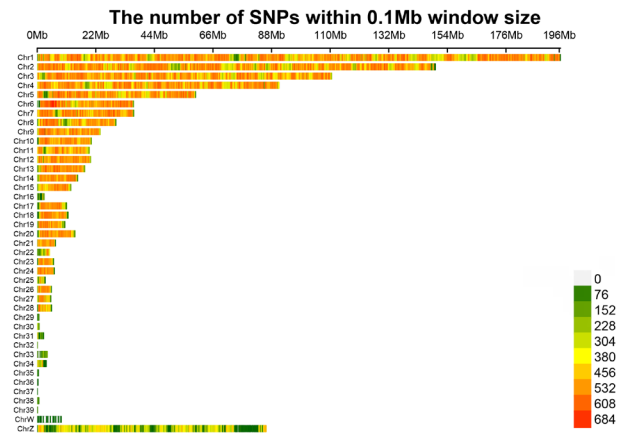
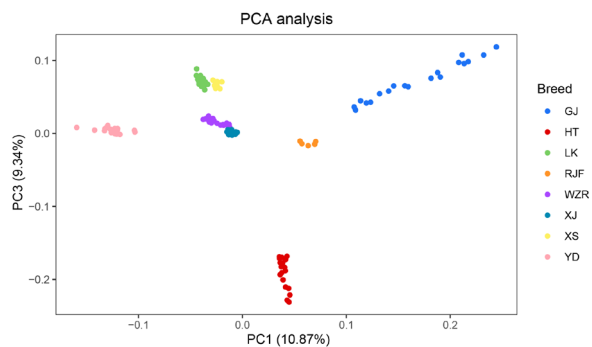
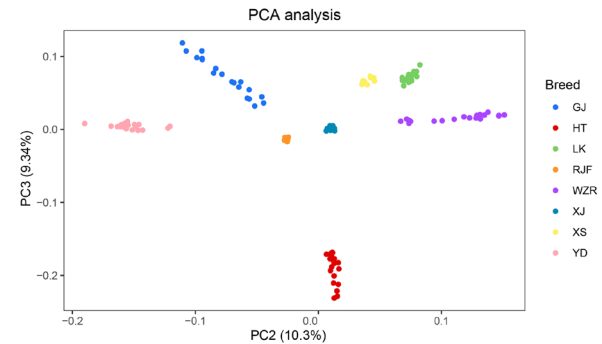


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Figure S2. Distribution of SNPs on chromosomes  
SNP = single nucleotide polymorphismFigure S3. Plot of the first and the third principal component from the principal component analysis (PCA) of the chicken populations analysed in this study  
GJ = Gaojiao chicken; HT = Hetao chicken; LK = Ling-kun chicken; RJF = Red Jungle Fowl; WZR = Wenzhou Red chicken; XJ = Xianju chicken; XS = Xiaoshan chicken; YD = Yandang Partridge chickenFigure S4. Plot of the second and the third principal component from the principal component analysis (PCA) of the chicken populations analysed in this study  
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