

A high-quality assembly revealing the *PMEL* gene for the unique plumage phenotype in Liancheng ducks

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Brief introduction

Plumage coloration is a distinctive trait in ducks, and the Liancheng duck, characterized by its white plumage and black beak and webbed feet, serves as an excellent subject for such studies. However, academic comprehension of the genetic mechanisms underlying duck plumage coloration remains limited. The aim was to identify the genetic mechanism of white plumage in Liancheng ducks.

Methods and Results

In this study, the Liancheng duck genome (GCA_039998735.1) was hereby de novo assembled using HiFi reads, and F2 segregating populations were generated from Liancheng and Pekin ducks. Inheritance of F2 population traits conforming to the law of independent assortment. Beyond the epistatic effect of the *MITF* gene, genome-wide association study analysis pinpointed a 0.8-Mb genomic region encompassing the *PMEL* gene. Additionally, linkage disequilibrium analysis revealed 2 candidate SNPs (Chr33: 5,303,994A>G; 5,303,997A>G) that might alter *PMEL* transcription, potentially influencing plumage coloration in Liancheng ducks.

Conclusion

Our study has assembled a high-quality genome for the Liancheng duck and has presented compelling evidence that the white plumage characteristic of this breed is attributable to the *PMEL* gene. Overall, these findings offer significant insights and direction for future studies and breeding programs aimed at understanding and manipulating avian plumage coloration.

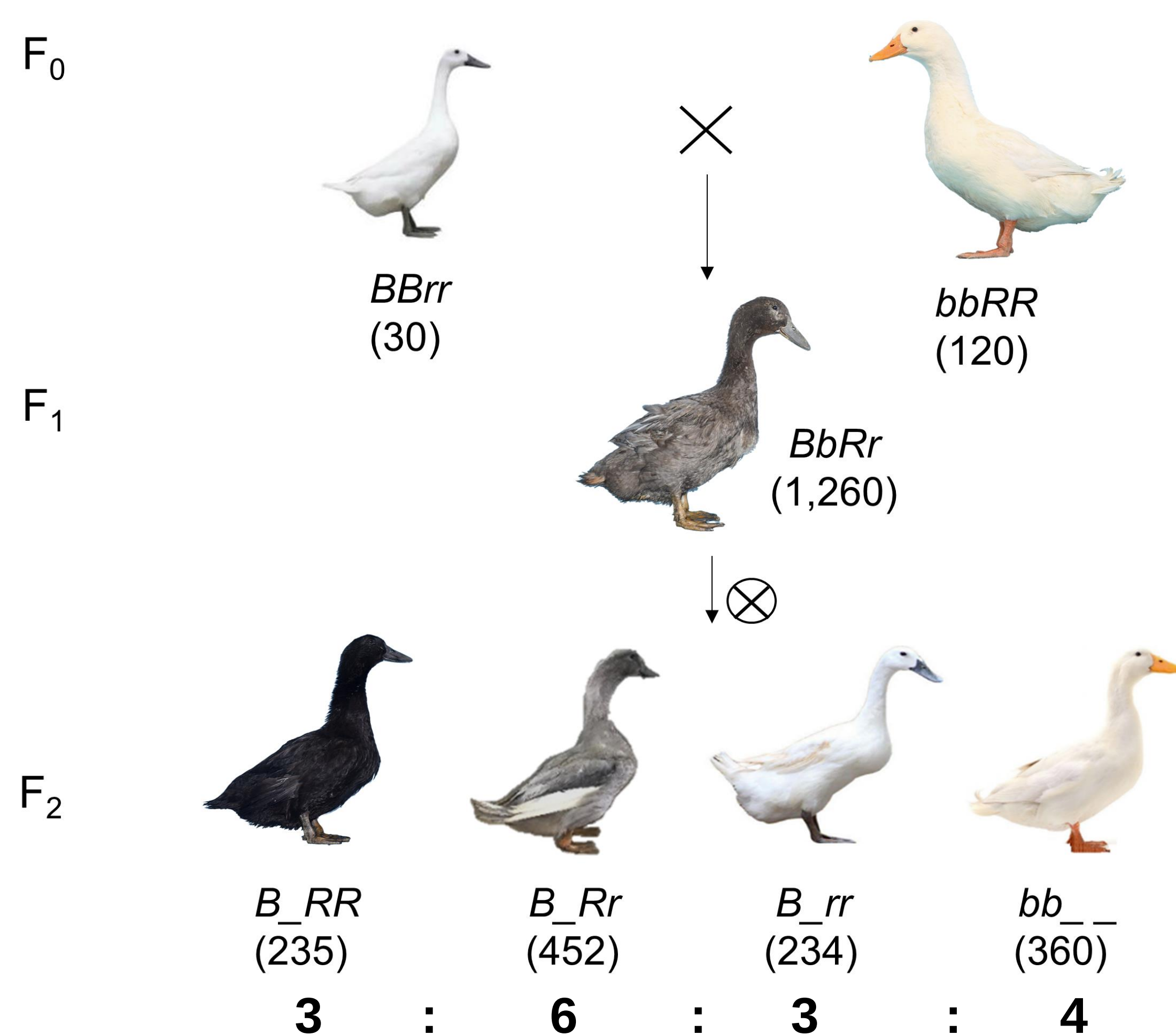


Fig. 1. The show of plumage colors in the F2 population

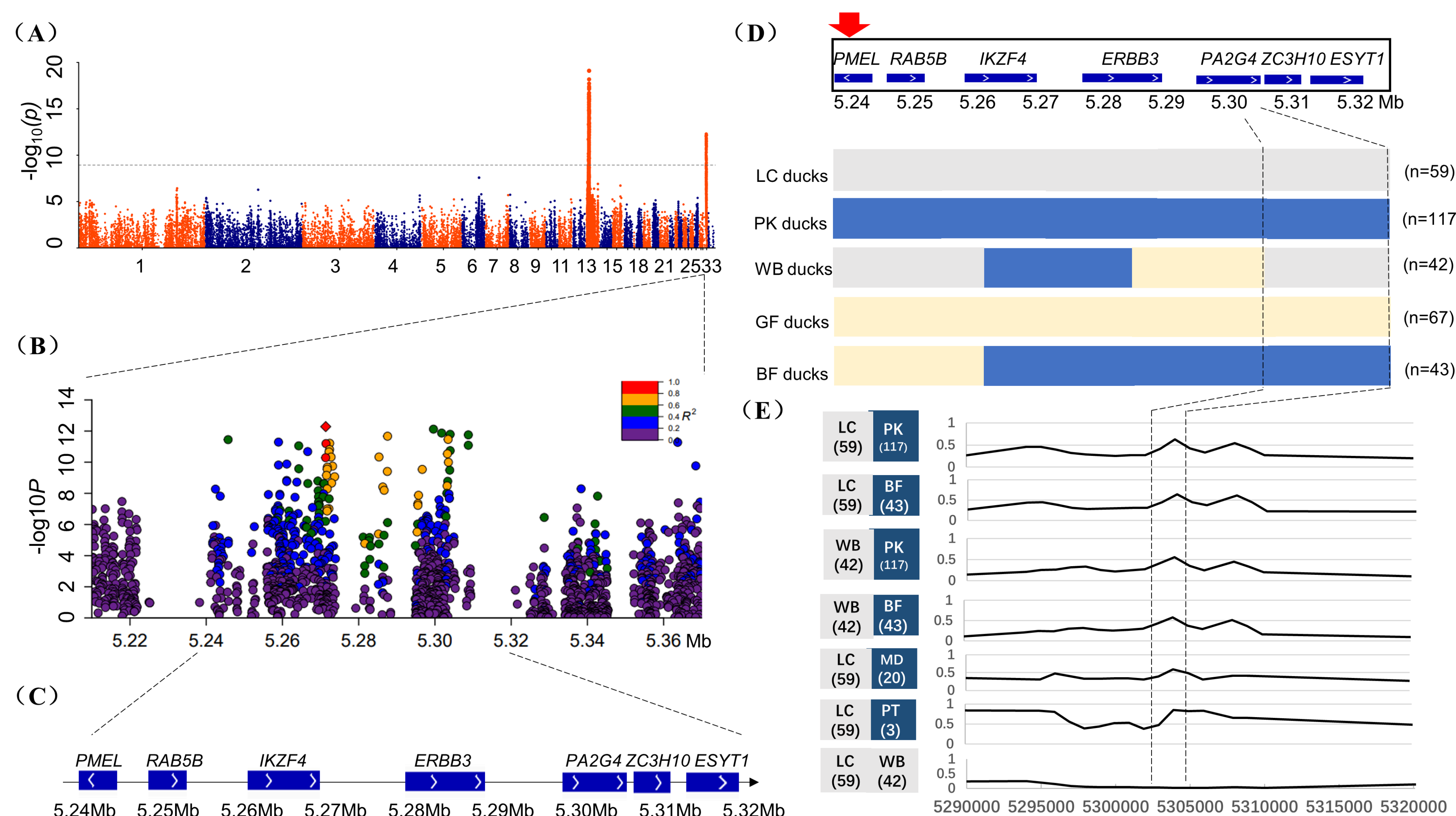


Fig. 2. Screening for the candidate region associated with Liancheng ducks

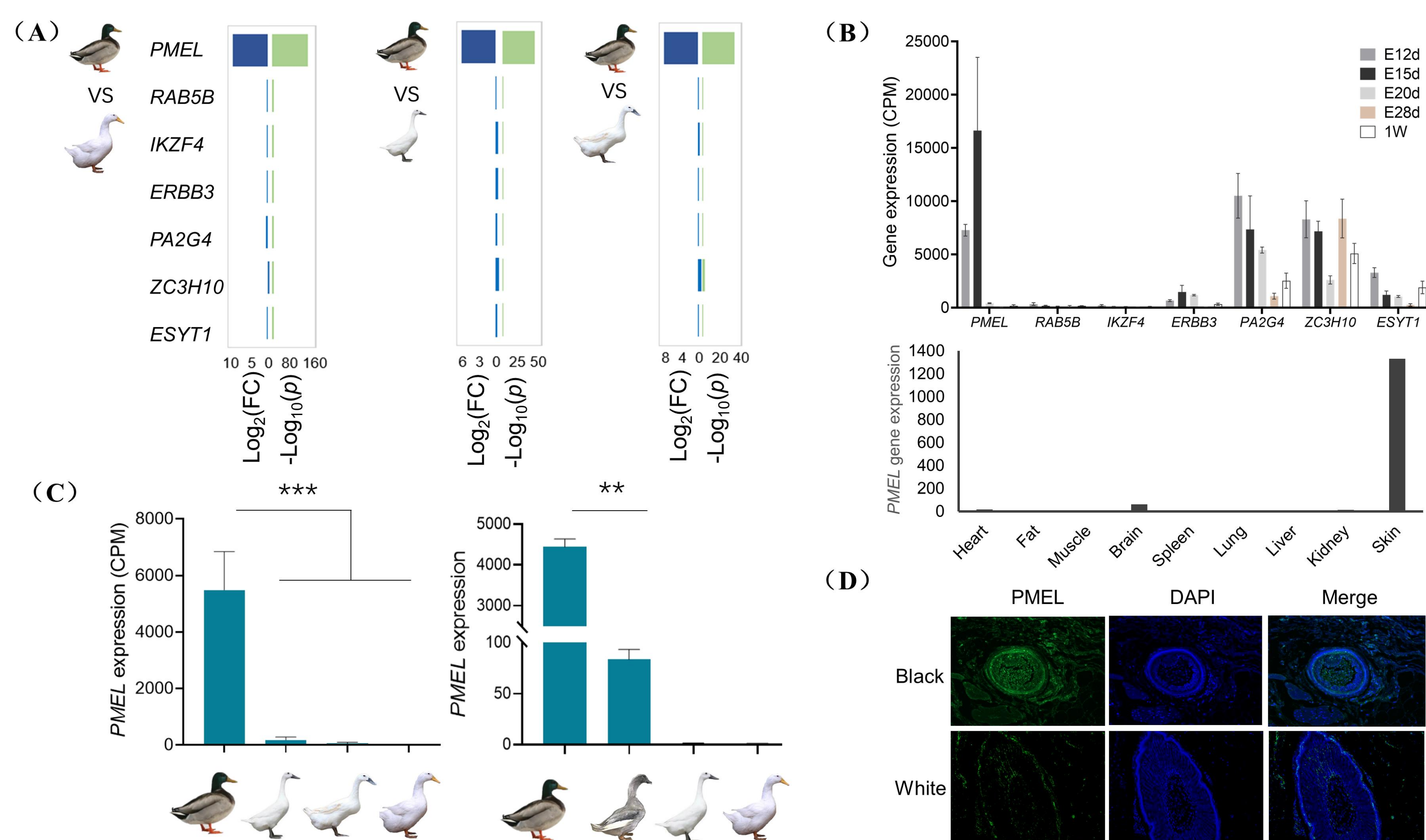


Fig. 3. Identification of the candidate gene for white plumage in Liancheng ducks.

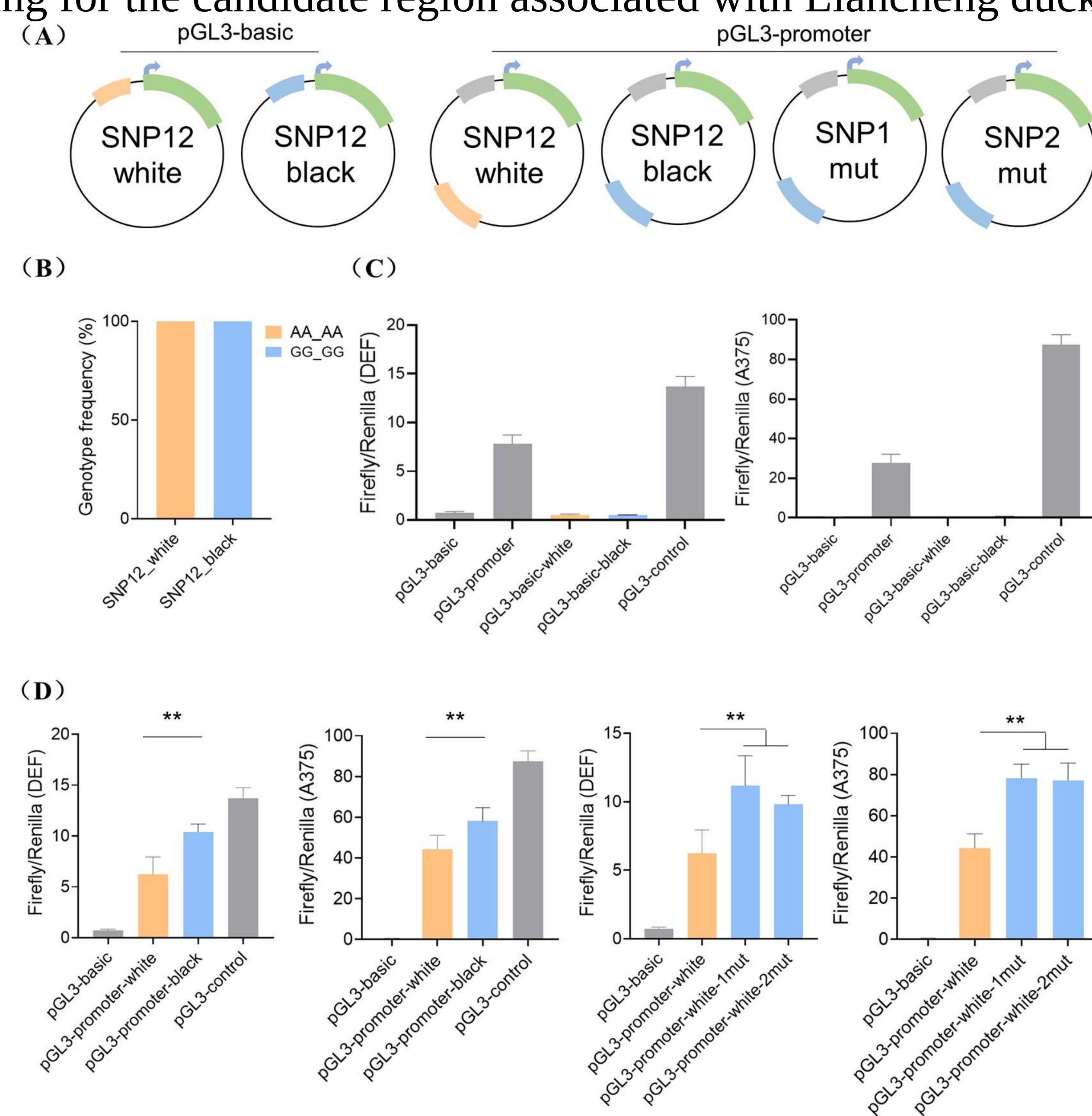


Fig.4. Functional analysis results

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