Complex Genetic Architecture of the Chicken Genome
An Example of *Growth1* QTL Region

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ABSTRACT

Chicken body weight is an essential trait in both commercial and research, and it is known to be controlled by multiple effects. Virginia Chicken Lines were introduced with bi-directional selected lines (high-weight, HWS / low-weight, LWS) and as advanced intercrossed lines generated from the 41st generation of HWS and LWS. While accumulating recombination in each generation, extending generation to F18 provided a higher resolution for GWAS and variance-heterogeneity GWAS. This research discovered that haplotype and epistasis effects caused the complex genetic architecture in the *Growth1* QTL region. Two major peaks were detected from GWAS, and the haplotype-based association study carried out similar results while providing a more vital significance. Statistical epistasis results suggested that there is a local interaction network in which interaction effects play an essential role in this region.
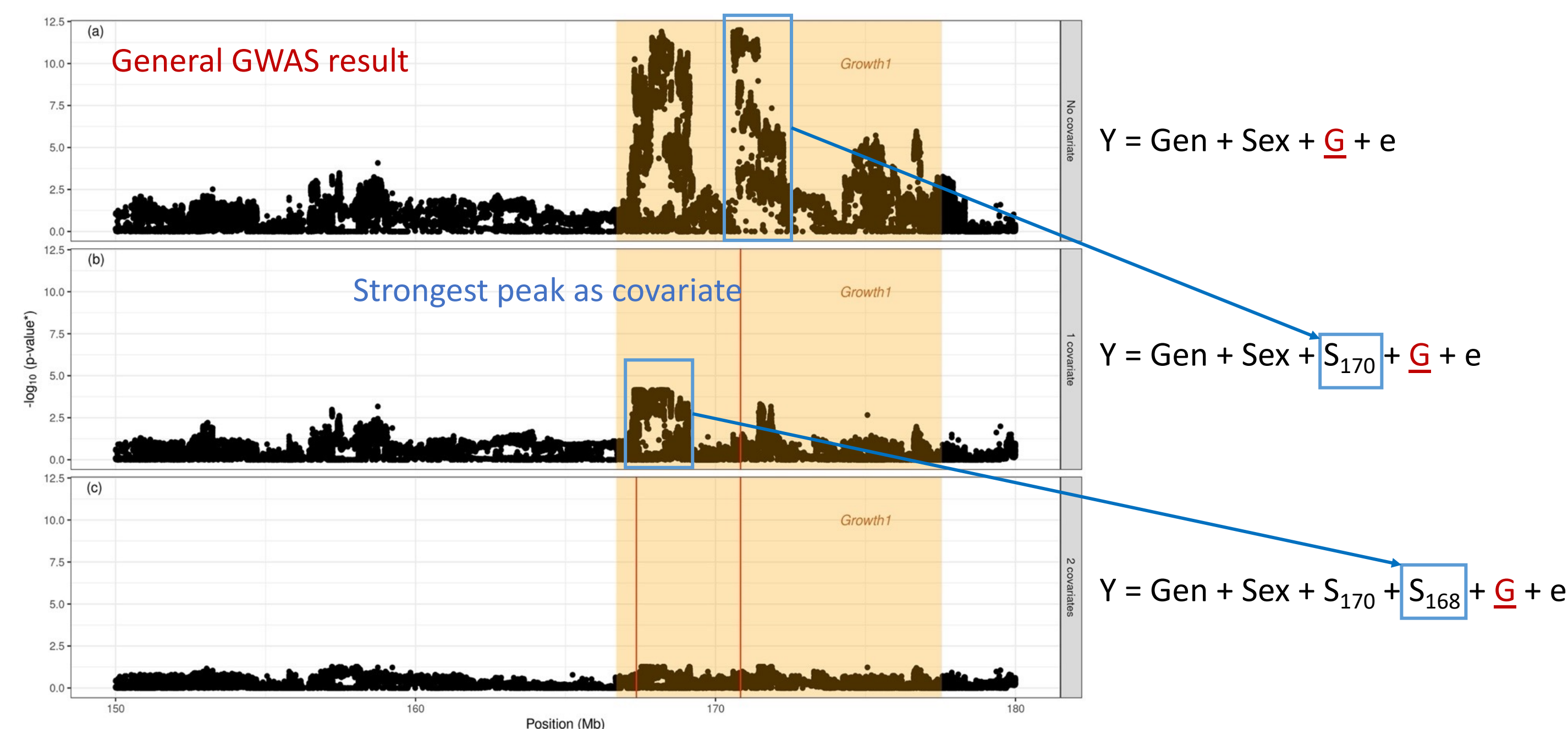
VIRGINIA CHICKEN LINES
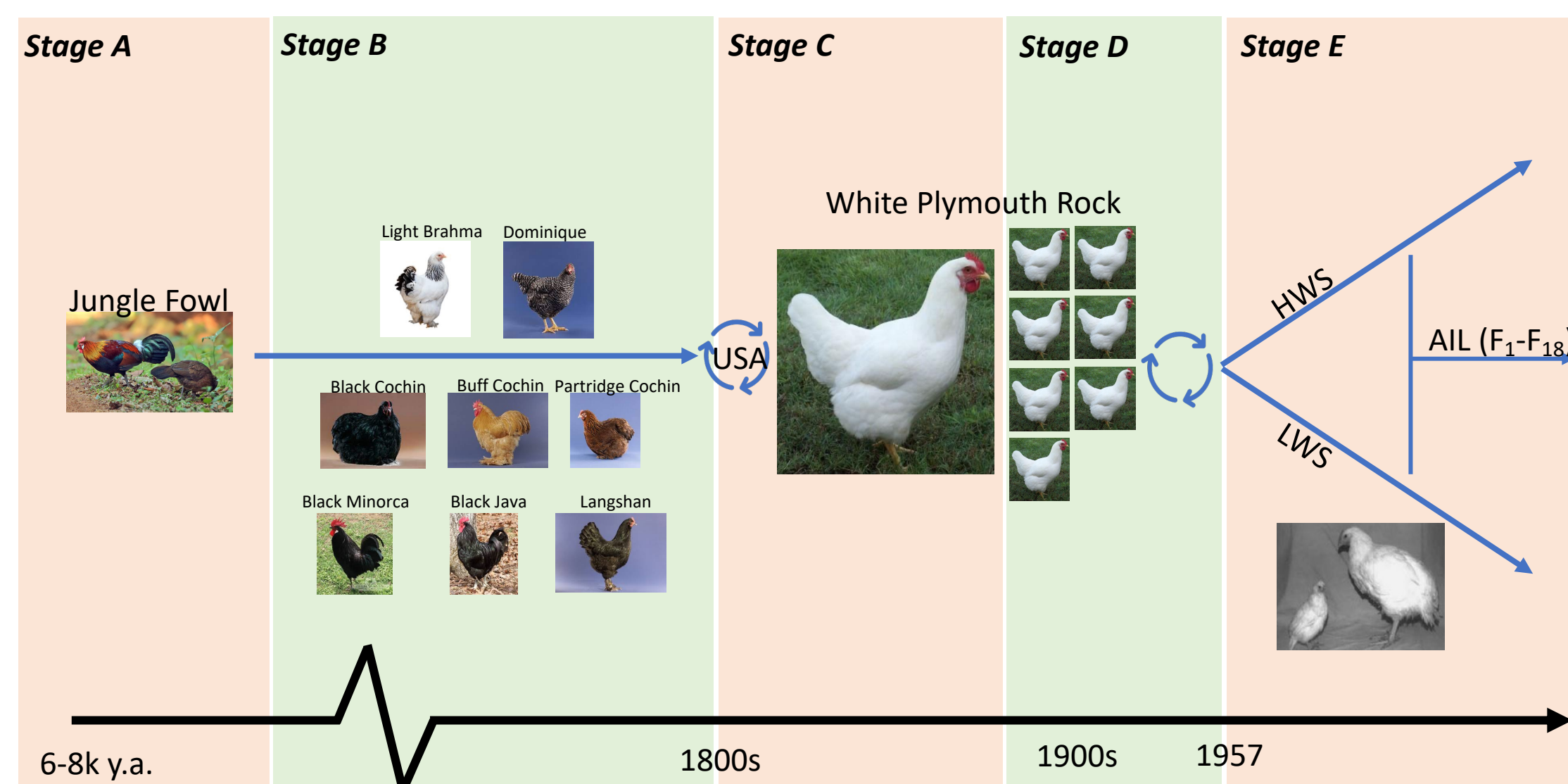
- **Stage A**: Chicken domestication from the wild ancestor, the Red Jungle Fowl.
- **Stage B**: Formation of endogenous and historical breeds independently in Europe and Asia.
- **Stage C**: Migration and admixture events started to create modern chicken breeds for meat and egg production in the USA.
- **Stage D**: The work at Virginia Polytechnic Institute starts to generate the experimental population with multiple inbred lines from the White Plymouth Rock breeds.
- **Stage E**: Siegel and his co-workers started the bidirectional single trait selection experiment 1957.

ASSOCIATION STUDIES (SNP & HAPLOTYPE)
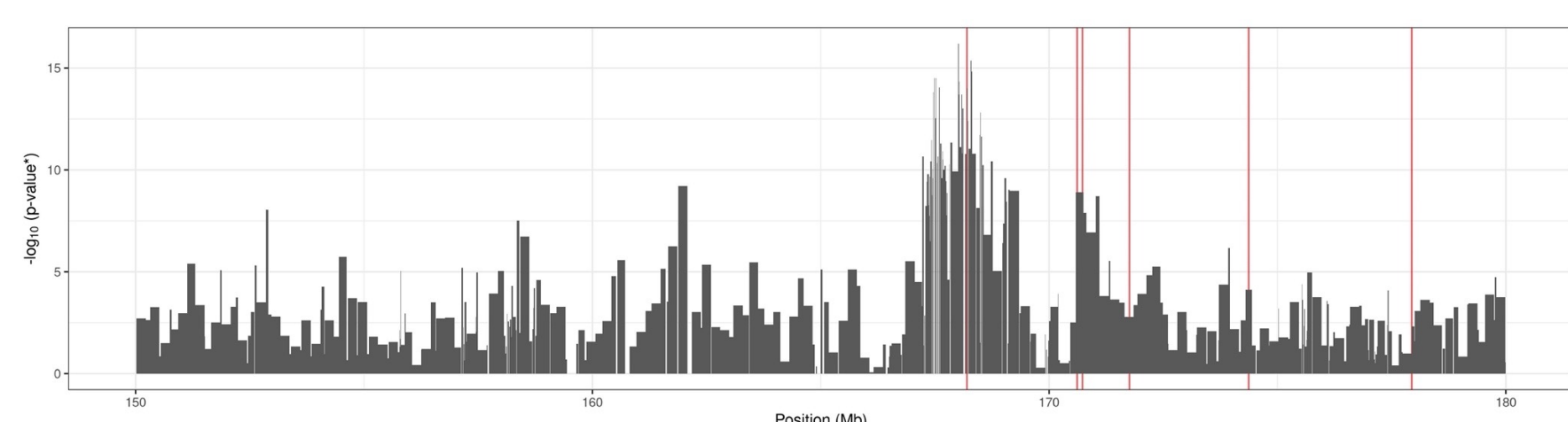
Genome-wide Association Study

$$y = 1\mu + S\beta_S + g\beta_g + A_j a_j + \varepsilon$$

- Single marker association study. Marker effect: a_j.
- Generation (β_g) and sex (β_S) are considered as fixed effects in the model.

Y = Gen + Sex + **G** + e

Y = Gen + Sex + S_{170} + **G** + e

Y = Gen + Sex + S_{170} + S_{168} + **G** + e

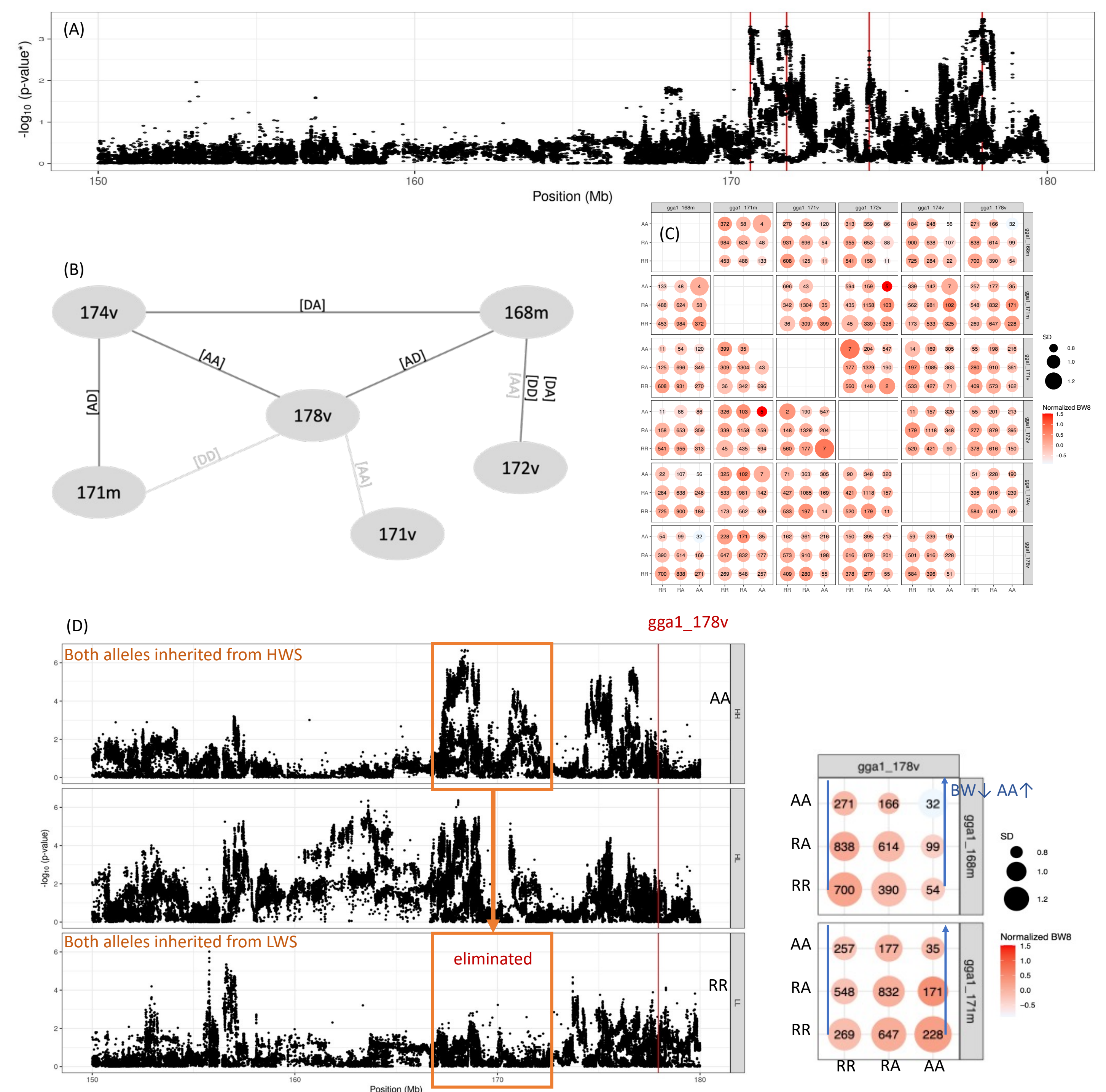### Haplotype-based association study

$$y = 1\mu + S\beta_S + g\beta_g + A_j a_j + \varepsilon$$
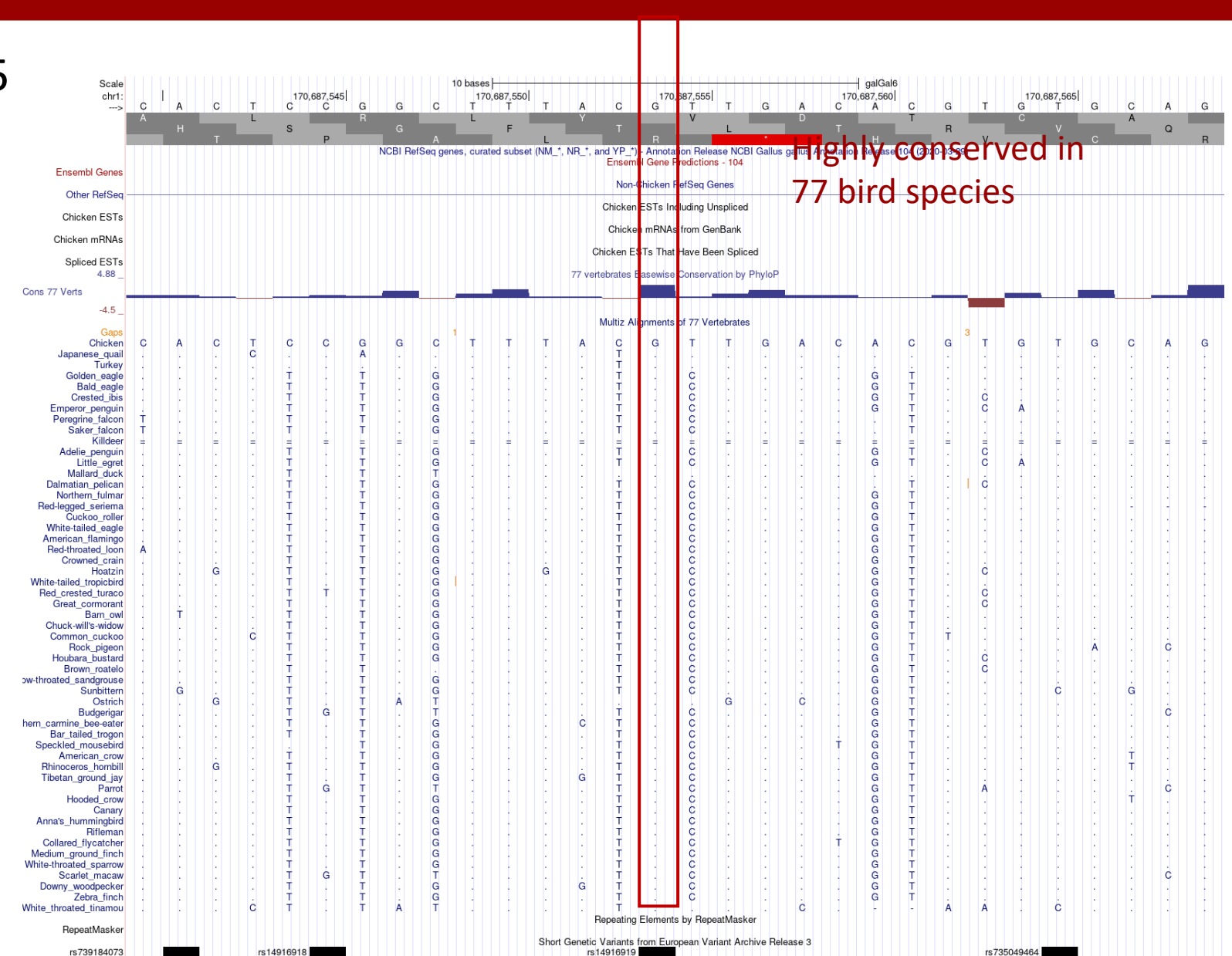

EPISTASIS

Variance-Heterogeneity GWAS (vGWAS)

- Interactions and haplotypes (Forsberg et at. 2015)
- Brown-Forsythe test: ANOVA based on the spread in each group. $y_{ij}^* = |y_{ij} - \tilde{y}_j|$

IDENTIFICATION OF CASUAL GENES

- Variants annotated by NCBI annotation release 105
- PhyloP scores was from

Highly conserved in 77 bird species

CONCLUSION

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- PhyloP scores was from

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