

Figure. S1 The extent of the linkage disequilibrium in different populations.

Values are the mean LD r^2 values for all pairs of SNPs binned by distance. The plot illustrates the decay of linkage disequilibrium (LD), measured as r^2 , as a function of genomic distance (Kb) across six population: Horse (magenta), Yellow-feathered broiler chickens A (red), White-feathered broiler chicken (black), Yellow-feathered broiler chickens B (blue), Duroc pig (purple), and Maize (green).

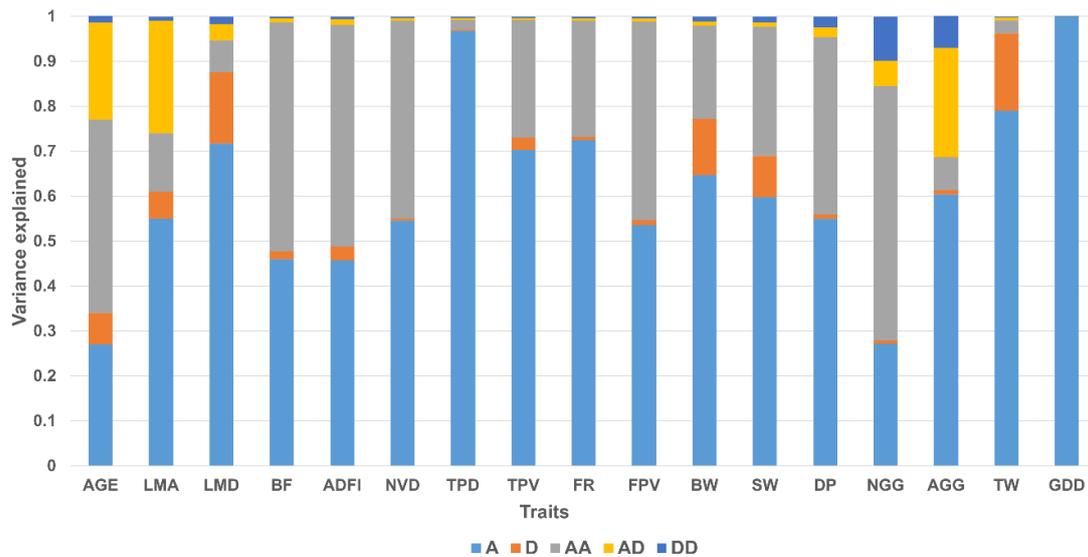


Figure. S2 Variance component partitioning of quantitative traits using a Rapid Mixed Model Algorithm.

This Fig. illustrates the partitioning of variance components for various quantitative traits using a rapid mixed model algorithm with a multi-genomic relationship matrix. The analysis decomposes the proportion of phenotypic variance explained by different random effects, excluding residual variance. The vertical axis represents the proportion of variance explained, while the horizontal axis lists the analyzed traits. The different colors represent specific genetic effects. A (blue): Additive effects. D (orange): Dominance effects. AA (gray): Additive × Additive epistatic effects. AD (yellow): Additive × Dominance epistatic effects. DD (dark black): Dominance × Dominance epistatic effects.

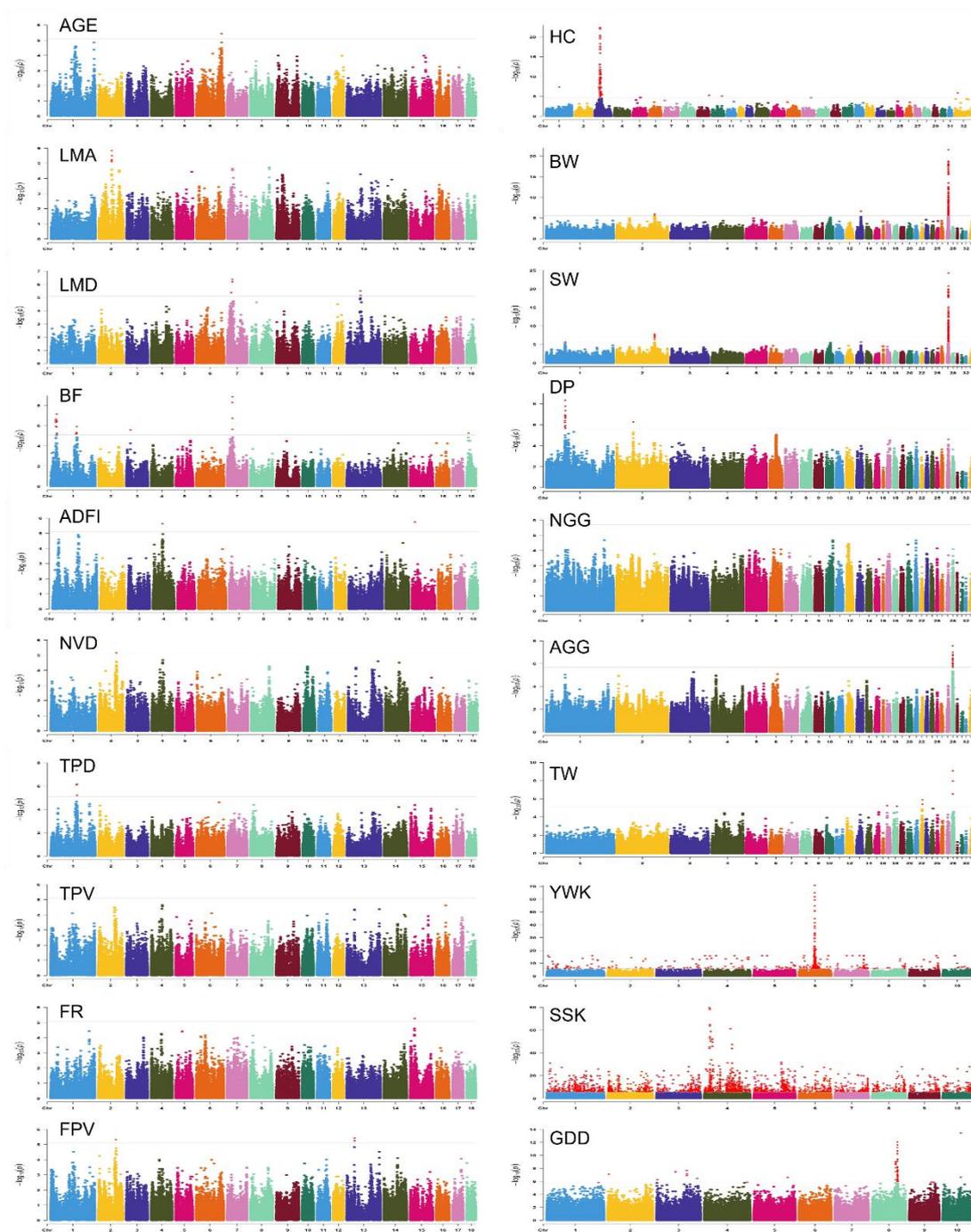


Figure. S3 The Manhattan plots of GWAS from 20 traits.

The GWAS results are displayed as $-\log_{10}(P)$ values against the chromosomal position on Manhattan plots.

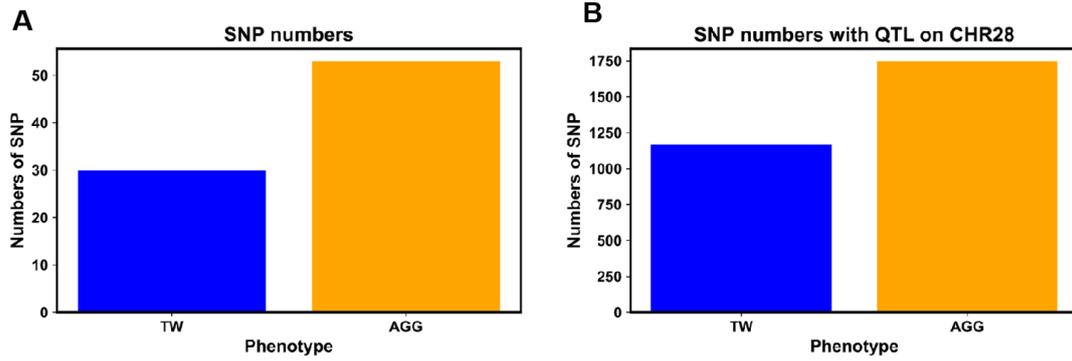


Figure. S4 SNP density within the region of Chr28:1.90-2.10 Mb.

(A) represents the original number of SNPs located within the QTL for TW and AGG phenotypes. (B) represents the number of SNPs located within the QTL for TW and AGG after being increased using sequencing technology. The resulting increase in marker density is approximately 40-fold compared to the original count.

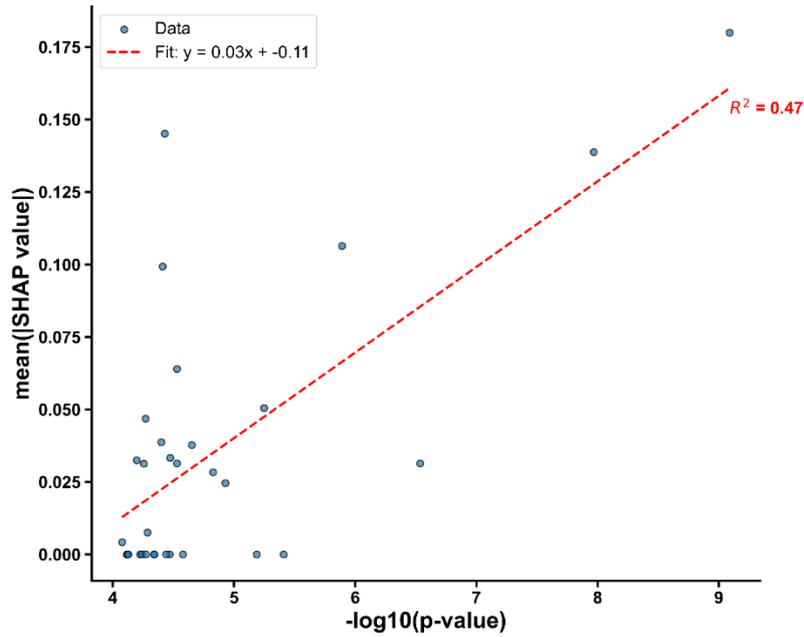


Figure. S5 Correlation between GWAS significant loci and mean SHAP value.

The scatter plot illustrates the relationship between GWAS significance and SHAP values. The x-axis represents significant loci identified based on the $-\log_{10}(\text{p-value})$ from GWAS, while the y-axis denotes the mean absolute SHAP value for each corresponding locus. The red dashed line represents a linear regression fit, showing a positive correlation between GWAS significance and SHAP importance scores. The equation of the regression line is provided.

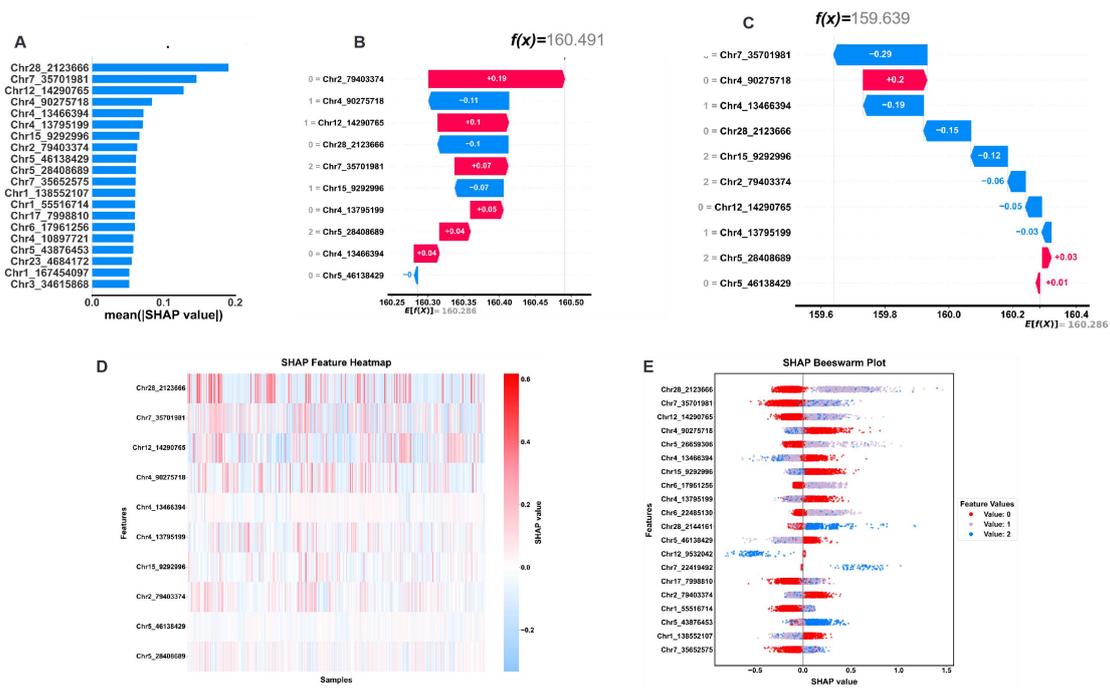


Figure. S6. SHAP Model Interpretation for the AGG Trait. (A) Importance-ranking plot of SNP features. (B) and (C) The single-sample feature waterfall plot illustrates the SHAP values on the X-axis, whereas the Y-axis delineates various feature values. Values 0, 1, and 2 correspond to the three genotypes AA, Aa, and aa, respectively. $E[f(x)]$ denotes the expected value across all the samples, whereas $f(x)$ represents the predicted value for a specific sample. (D) Heat map illustrating the distribution of features across clustered samples. The X-axis corresponds to the samples, whereas the y-axis denotes the features. (E) Characteristic attributes in SHAP are represented on a beeswarm plot, with each line corresponding to a specific SNP feature. Genotypes are represented by different colors: AA (0, red), Aa (1, gray), and aa (2, blue).

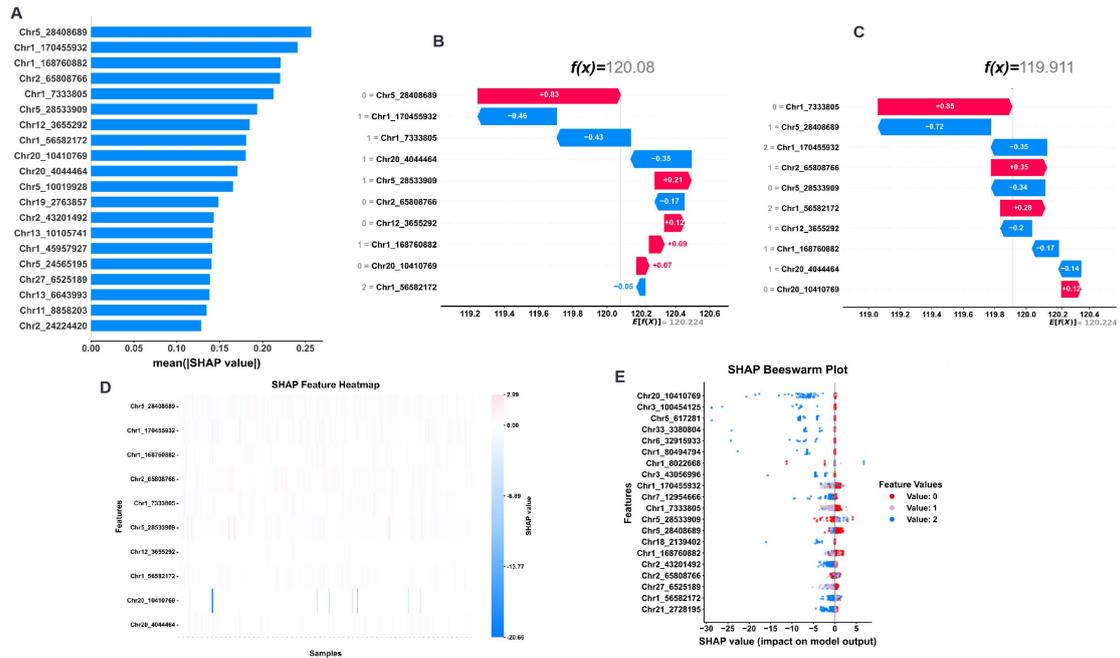


Figure. S7. SHAP Model Interpretation for the NGG Trait. (A) Importance-ranking plot of SNP features. (B) and (C) The single-sample feature waterfall plot illustrates the SHAP values on the X-axis, whereas the Y-axis delineates various feature values. Values 0, 1, and 2 correspond to the three genotypes AA, Aa, and aa, respectively. $E[f(x)]$ denotes the expected value across all the samples, whereas $f(x)$ represents the predicted value for a specific sample. (D) Heat map illustrating the distribution of features across clustered samples. The X-axis corresponds to the samples, whereas the y-axis denotes the features. (E) Characteristic attributes in SHAP are represented on a beeswarm plot, with each line corresponding to a specific SNP feature. Genotypes are represented by different colors: AA (0, red), Aa (1, gray), and aa (2, blue).

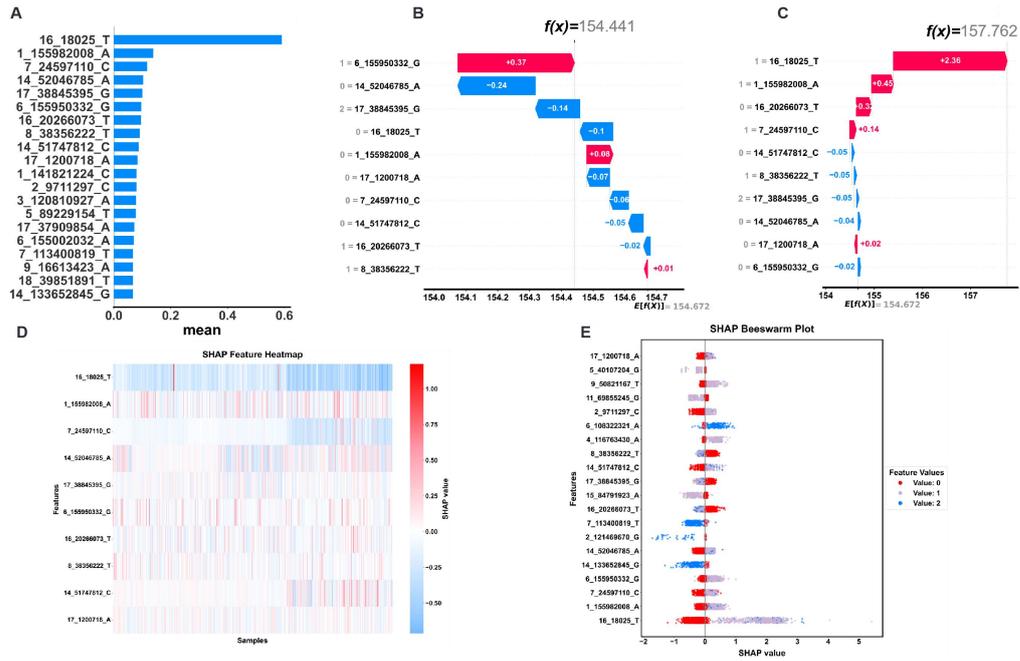


Figure. S8. SHAP Model Interpretation for the AGE Trait. (A) Importance-ranking plot of SNP features. (B) and (C) The single-sample feature waterfall plot illustrates the SHAP values on the X-axis, whereas the Y-axis delineates various feature values. Values 0, 1, and 2 correspond to the three genotypes AA, Aa, and aa, respectively. $E[f(x)]$ denotes the expected value across all the samples, whereas $f(x)$ represents the predicted value for a specific sample. (D) Heat map illustrating the distribution of features across clustered samples. The X-axis corresponds to the samples, whereas the y-axis denotes the features. (E) Characteristic attributes in SHAP are represented on a beeswarm plot, with each line corresponding to a specific SNP feature. Genotypes are represented by different colors: AA (0, red), Aa (1, gray), and aa (2, blue).