

Supplementary figure

Title: Genetic architecture and candidate genes detected for chicken internal organ weight with a 600 K single nucleotide polymorphism array

Author information

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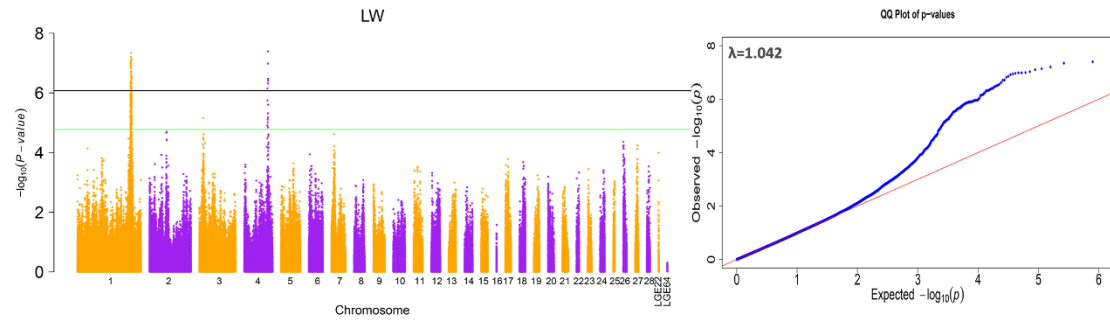
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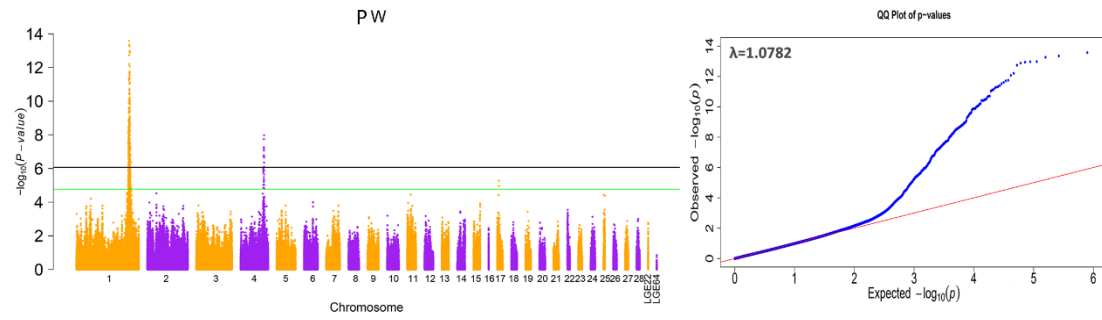
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Supplementary Figure S1. Manhattan plot and QQ-plot of genome-wide association analysis for LW (liver weight). The left plot is the Manhattan plot, which shows the $-\log_{10}$ (observed p values) for association of single nucleotide polymorphisms (y-axis) plotted against their chromosomal positions on each chromosome (x-axis). The right plot is the QQ test for population structure, the x-axis indicates the expected $-\log_{10}$ -transformed p values, and the y-axis shows the observed $-\log_{10}$ -transformed p values.



Supplementary Figure S2. Manhattan plot and QQ-plot of genome-wide association analysis for PW (proventriculus weight). The left plot is the Manhattan plot, which shows the $-\log_{10}$ (observed p values) for association of single nucleotide polymorphisms (y-axis) plotted against their chromosomal positions on each chromosome (x-axis). The right plot is the QQ test for population structure, the x-axis indicates the expected $-\log_{10}$ -transformed p values, and the y-axis shows the observed $-\log_{10}$ -transformed p values.



Supplementary Figure S3. Manhattan plot and QQ-plot of genome-wide association analysis for GW (gizzard weight). The left plot is the Manhattan plot, which shows the $-\log_{10}$ (observed p values) for association of single nucleotide polymorphisms (y-axis) plotted against their chromosomal positions on each chromosome (x-axis). The right plot is the QQ test for population structure, the x-axis indicates the expected $-\log_{10}$ -transformed p values, and the y-axis shows the observed $-\log_{10}$ -transformed p values.

