Supplementary Material

Association analysis of transcriptome and quasi-targeted metabolomics reveals the regulation mechanism underlying broiler muscle tissue development at different levels of dietary guanidinoacetic acid

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# Supplementary Data

The raw data of transcriptome presented in the study are deposited in the Sequence Read Archive repository, accession number PRJNA1089708.

The raw result of quasi-targeted metabolomics analysis has been provided as supplementary materials in a zip file. Please download the file “Result-X101SC22030966-Z01-J001-B1-42 (quasi-targeted metabolomics).ZIP”.

# Supplementary Figures and Tables

## Supplementary Figures (1-10)



**Supplementary Figure 1.** KEGG enrichment pathway map of the expression regulation of core DEGs in vascular smooth muscle contraction pathway for Normal GAA group vs control group in RNA-seq analysis.



**Supplementary Figure 2.** KEGG enrichment pathway map of the expression regulation of core DEGs in TGF-β signaling pathway for High GAA group vs control group in RNA-seq analysis.



**Supplementary Figure 3.** KEGG enrichment pathway map of the expression regulation of core DEGs in intestinal immune network for IgA production pathway for High GAA group vs control group in RNA-seq analysis.



**Supplementary Figure 4.** KEGG enrichment pathway map of the expression regulation of core DEGs in TGF-β signaling pathway for High GAA group vs Normal GAA group in RNA-seq analysis.



**Supplementary Figure 5.** KEGG enrichment pathway map of the expression regulation of core DEGs in intestinal immune network for IgA production pathway for High GAA group vs Normal GAA group in RNA-seq analysis.



**Supplementary Figure 6.** KEGG enrichment pathway map of the expression regulation of core DEGs in vascular smooth muscle contraction pathway for High GAA group vs Normal GAA group in RNA-seq analysis.



**Supplementary Figure 7.** KEGG enrichment pathway map of the specific enrichment of core SDMs in nicotinate and nicotinamide metabolism pathway for Normal GAA group vs control group in metabolomics analysis.



**Supplementary Figure 8.** KEGG enrichment pathway map of the specific enrichment of core SDMs in inositol phosphate metabolism pathway for Normal GAA group vs control group in metabolomics analysis.



**Supplementary Figure 9.** KEGG enrichment pathway map of the specific enrichment of core SDMs in inositol phosphate metabolism pathway for High GAA group vs control group in metabolomics analysis.



**Supplementary Figure 10.** KEGG enrichment pathway map of the specific enrichment of core SDMs in nicotinate and nicotinamide metabolism pathway for High GAA group vs Normal GAA group in metabolomics analysis.