

## **The Chicken Genotype-Tissue Expression (ChickenGTEx): a comprehensive atlas of genetic regulatory variants in chicken transcriptome**

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Although thousands of genetic variants have been reported to be associated with complex traits of economic value in livestock, the identification of causal variants and genes remains a huge challenge. Herewith, we developed the Farm Animal Genotype-Tissue Expression (FarmGTEx) project, aiming to decode the relationship of genetic variants, gene expression and phenotypic variations in farm animals. As a part of FarmGTEx, we here developed the pilot phase of ChickenGTEx by collecting a comprehensive dataset comprising of 9,230 publicly available RNA sequences (RNA-seq) from 8,015 unique samples across 79 tissues in chickens. The implementation of a uniform and stringent computational pipeline resulted in 6,930 clean samples that were used for calling single nucleotide polymorphism (SNP) and quantifying gene expression. To improve the coverage of SNPs across the chicken genome, we further built a multi-breed reference panel for genotype imputation (version 1) by collecting 2,884 whole genome sequences (WGS) in chickens, based on which we imputed the SNPs-derived from RNA-seq to sequence level. We then obtained a set of 1.5 million imputed SNPs, with an average imputation accuracy of ~97%, for associating imputed variants with gene expression across 30 major tissues with over 40 individuals. We identified a total of 13,283 (79.2% of all 16,779 annotated Ensembl genes) genes with at least one significant eQTL (eGene, FDR < 0.05) in at least one tissue. The number of eGenes increased with the increasing sample sizes across tissues, ranging from 45 in duodenum to 10,159 in liver. The number of independent eVariants ranged from 45 in duodenum to 23,188 in liver. Overall, this study will provide valuable sources not only for deciphering the genetic and biological basis of complex traits in chickens, but also for understanding the evolutionary and molecular mechanisms underlying gene regulation across vertebrates.