

6. Exploring the Dynamic Nature of the Functional Regulatory Genome: Insights from Epigenomic States

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The functional regulatory genome refers to the part of the genome that is involved in regulating gene expression. One way that researchers study the functional regulatory genome is by using various epigenomic techniques, such as Reduced representation bisulphite sequencing (RRBS) to investigate DNA methylation, which allow them to identify and analyse changes in gene expression. However, few studies have attempted to integrate these various epigenomic data to provide a comprehensive global view of the epigenome. The aim of this study was to integrate many different omics data to identify epigenomic combinations which provide insight into the functional regulatory genome. This aim was obtained for a chicken cell line (SL-29), through combining gene expression (RNA-seq), DNA methylation (whole genome and RRBS), chromatin accessibility (ATAC-seq) and ChIP-seq of four histone marks (H3K4me1, H3K4me3, H3K27ac, H3K27me3) and an insulator (CTCF). We integrated this data by applying the ChromHMM algorithm which uses a hidden Markov model. We annotated 15 epigenomic states representing promoters, enhancers, transcribed regions, repressed regions, and quiescent regions. This integration of different omics data will be further applied to provide insight into the mechanisms which regulate gene expression during embryonic development in pig and chicken. In conclusion, this study established an integrative method to gain insight into the functional regulatory genome and the dynamic nature of gene regulation.