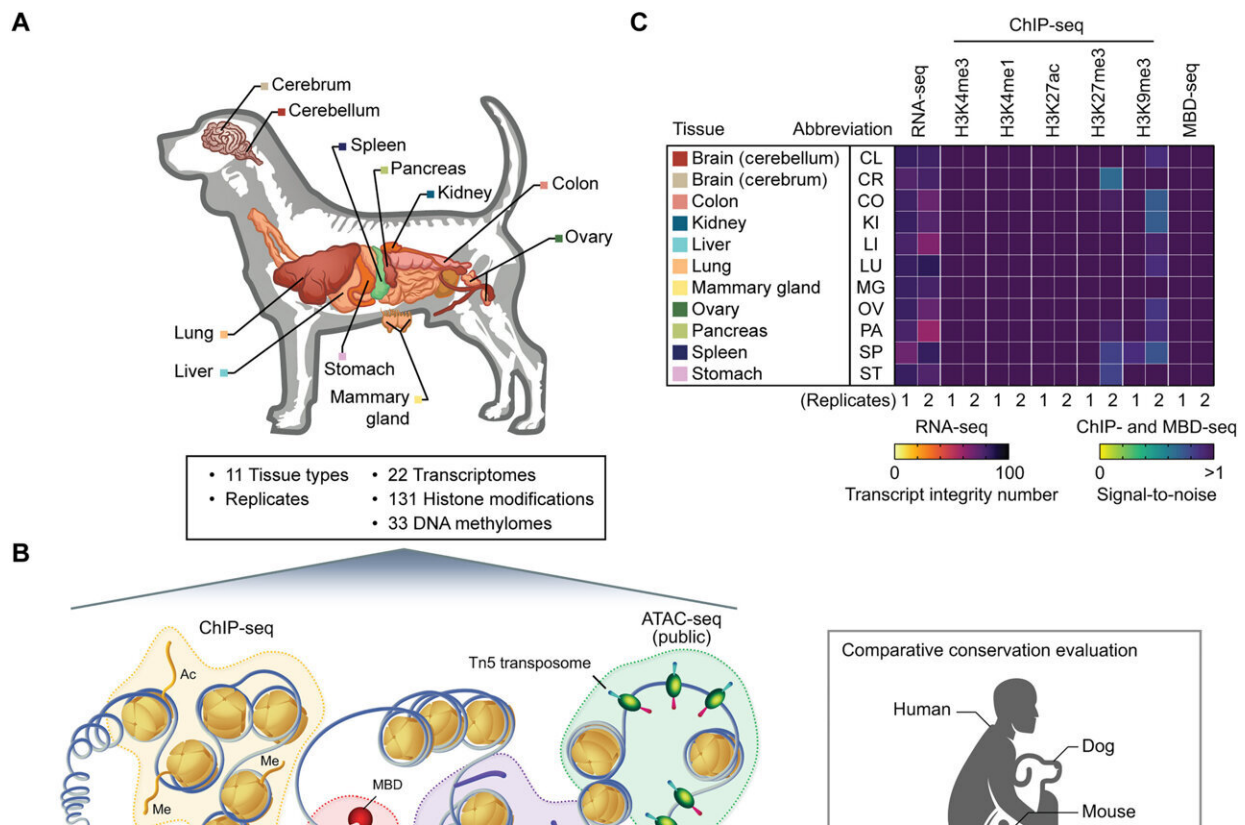# Researchers create EpiC Dog, a reference tool for canine epigenetics

July 17 2023, by Justin Jackson

Overview of the integrative mapping approach to generate a dog reference epigenome. (A) Diagram of 11 primary tissue types from beagle dogs sampled for the study. (B) Synopsis of next-generation sequencing (NGS) methods, data integration approaches, and analyses performed for the integrative profiling the dog epigenome. See also Methods. (C) Matrix of in-house generated NGS dataset quality from 11 primary tissue types, including information on RNA expression, defined epigenomic modifications, and DNA methylation. Normalized data integrity measures for each NGS sample profile [transcript

integrity number for whole-transcriptome RNA-seq and relative strand cross-correlation coefficient (RSC) quality score for histone ChIP-seq and MBD-seq] are displayed. Two replicates per sampled tissue were profiled. Indicated tissue abbreviations were used all throughout the manuscript. Credit: *Science Advances* (2023). DOI: 10.1126/sciadv.ade3399

Researchers at the College of Veterinary Medicine, Seoul National University, Korea, have created a browsable epigenetic atlas for dogs called EpiC Dog (Epigenome Catalog of the Dog) to assist with future research efforts.

The paper, "Integrative mapping of the dog epigenome: Reference annotation for comparative intertissue and cross-species studies," published in *Science Advances*, details the methods used to build a comprehensive understanding of canine epigenetic factors.

Epigenetics are changes in gene expression that can occur without alterations to the underlying DNA sequence. These changes can be influenced by various factors, such as diet, environmental conditions, lifestyle choices, and psychological stress and can be passed on to future generations.

Canis familiaris, aka the [domestic dog](#), are a fascinating species to investigate epigenetically as they share most environmental conditions with humans. There are several hundred breeds artificially produced through human trait selection.

There was no time in history when large numbers of wild beagles chased bison across the open plains or a snarling pug pack kept [saber-toothed cats](#) away from a fresh caribou kill. That was left to the common ancestor of all domestic dogs, the gray wolf.

While domestication began more than 20,000 years ago, most dog breeds we recognize today were engineered around 150 years ago in Great Britain. During the Victorian era, unique dog breeds became highly fashionable, and cross-breeding intensified in what is called the "Victorian Explosion" of dogs.

The rapid diversification of phenotypic traits, from morphology to behavior, are all present in the dog genome, with many lessons that can be learned about evolution and epigenetic effects.

The researchers performed genome-wide segmentation and functional annotation to generate a reference dog epigenome. Two dataset replicates were made of RNA sequencing, chromatin immunoprecipitation with sequencing of five major histone marks, and binding domain sequencing from 11 tissue types collected from three adult beagles.

Beagles were chosen as they are an integral part of human cancer research. Guided by licensed veterinarians, the research team collected biopsies from the cerebrum, cerebellum, colon, kidney, liver, lung, mammary gland, ovary, pancreas, spleen and stomach. Selection for these tissue types was primarily based on tumor development risk and prevalence to prioritize utility for comparative oncology studies.

Sequence data from the tissue samples were combined with a computational data integration at the transcript level for genome-wide functional annotation, chromatin state discovery, and downstream epigenome analyses.

With a robust definition of the dog epigenome, analyses using the human and mouse ENCODE data allowed the team to connect observations in dogs to existing knowledge on human and mouse epigenome activity.

Clustering and analysis of gene expression patterns across species showed both tissue-specific and species-specific clusters, providing insights into the conservation and divergence of gene expression across humans, mice and dogs.

The EpiC Dog reference (currently on GitHub) provides an epigenomic catalog of the dog that can be used for comparative biology in human medical research when using dogs as a model and in veterinary medical research on canine diseases.

  More information: Keun Hong Son et al, Integrative mapping of the dog epigenome: Reference annotation for comparative intertissue and cross-species studies, *Science Advances* (2023). DOI: 10.1126/sciadv.ade3399

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