Bioinformatic characterization of the normal thyroid reference epigenome

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ABSTRACT

The thyroid, necessary for normal growth and development, is essential for the regulation of metabolism in every cell of the human body. Its function -- to produce and secrete appropriate levels of thyroid hormone -- is simple; however, the incidence of thyroid abnormalities is increasing and accurate assessment of abnormal thyroids for different individuals is challenging. A fundamental understanding of the normal thyroid is therefore needed. One way to characterize the normal thyroid is to study its epigenome and matched transcriptome. In this study we are analyzing grossly uninvolved tumour-adjacent thyroids from four human individuals using ChIP-seq, RNA-seq, and bisulfite-seq. We examine 4 activating (H3K4me1, H3K4me3, H3K27ac, H3K36me3) and 2 repressing (H3K9me3, H3K27me3) histone post-translational modifications, identify chromatin states using a hidden Markov model, establish maps of regulatory elements, and compare DNA methylation and RNA expression profiles between samples. The goals of this study are (1) to understand and characterize regions of regulation which are consistent and regions of regulation which are variable between the thyroids of different individuals and (2) to produce an available reference thyroid epigenome as a resource and reference of human epigenomic data for comparison and integration of future studies.