Research

Cancer genome sequencing has revealed that many factors associated with epigenetic processes are mutated in cancers, and epigenetic processes have been targeted by specific drugs. The Cancer Epigenomics Laboratory examines epigenomic features of the cancer genome, such as chromatin interactions, transcription factors, histone modifications and long non-coding RNAs. This work is expected to have translational applications in terms of annotations for personal and clinical sequencing and development of clinical biomarkers. One of the mechanisms by which the non-coding "dark matter" of the human genome could be functional is by long-range chromatin interactions with target genes. Chromatin interactions are regions of the genome that are far apart in the linear genome sequence but come together in close 3-dimensional spatial proximity, may constitute common mechanisms for gene regulation. The lab currently focuses on using ChIP sequencing, RNA sequencing, as well as ChIA-PET for genome-wide elucidation of chromatin interactions, on cancer models to investigate detailed epigenomic profiles, allowing for new insights into possible cancer-associated biomarkers and cancer therapies. In addition, the lab is interested in continuing to develop and refine new genomic technologies to better understand chromatin and transcription. More details about the lab can be found at fullwoodlab.com.

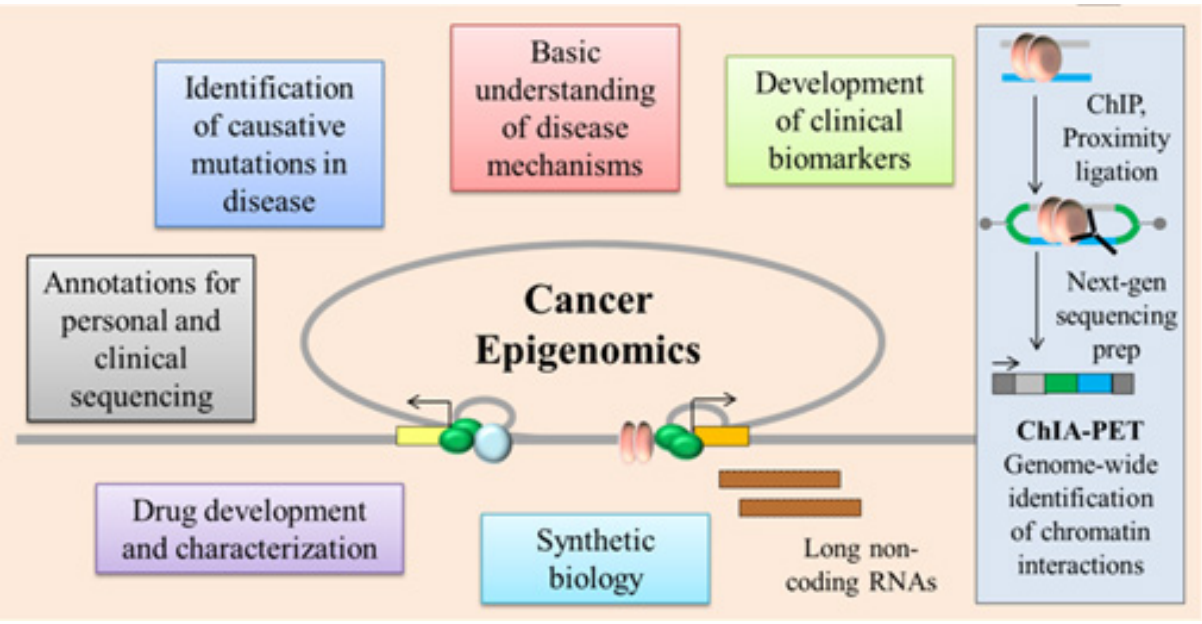

Figure Legend: Translational implications of cancer epigenomics. Inset: Chromatin Interaction Analysis with Paired-End Tag Sequencing (ChIA-PET), a genome-wide method for elucidating chromatin interactions.