

# Helen Bian

Investigating the functional classification of known and novel single nucleotide polymorphisms (SNPs) associated with Chronic Lymphocytic Leukemia predisposition

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Chronic lymphocytic leukemia (CLL) is a B-cell malignancy that is the most common form of leukemia affecting adults in western countries. Although there are known risk factors for CLL (e.g. old age), the cause of CLL is still unknown. Data suggest that genetics play a role in the disease etiology of CLL. Genome-wide association studies (GWAS) have identified over thirty single nucleotide polymorphisms (SNPs) associated with CLL. My research for my thesis seeks to investigate the genetic component of CLL, with a focus on GWAS-identified SNPs. The goal of my research is to identify causal SNPs that contribute to the CLL disease phenotype in order to better comprehend genetic variation. The broad objective of identifying causal SNPs is to better understand how genetic variation in noncoding regions contributes to development of diseases such as CLL, as well as how non-coding SNPs alter gene regulation in disease states.