B and T cell lymphomas are common cancers of the immune system. Although diverse, these cancers characteristically harbor mutations and genomic aberrations that are solely found in malignant cells. The identification and characterization of these genomic aberrations is a major challenge for designing novel targeted therapies against cancers.

Typically cells of the immune system develop via a process that causes intentional breaks in DNA – double strand breaks (DSBs). Under normal circumstances these DSBs are tightly regulated, but in the case of B and T cell lymphomas, this process is misregulated resulting in tumors that have many genomic alterations. We have developed novel mouse models that readily develop B- and T-cell lymphomas due to defects in DNA DSB regulation. Our preliminary analysis revealed that these lymphomas carry numerous genomic aberrations reminiscent of human malignancies.

In this project, the overarching goals are i) to identify the unique gene signatures and genomic aberrations that are associated with B- and T-cell lymphomas using high throughput RNA and DNA genome sequencing technologies, and ii) to validate some of the oncogenic candidate genes using lymphoma cell lines and molecular and cell biology techniques.