Non-Hodgkin lymphomas (NHLs) represent a diverse collection of cancers arising from cells of the immune system. Through the combination of copy number analysis, whole genome, exome, and RNA sequencing, numerous genes that are recurrently mutated or affected by somatic structural or copy number variation have been delineated. This has helped inform on the genetic underpinnings of the more common NHLs such as diffuse large B-cell lymphoma and follicular lymphoma. My presentation will highlight recent advances in the use of mutations in defining molecular subgroups within these cancers with an emphasis on the identification of novel cis-regulatory somatic mutations.