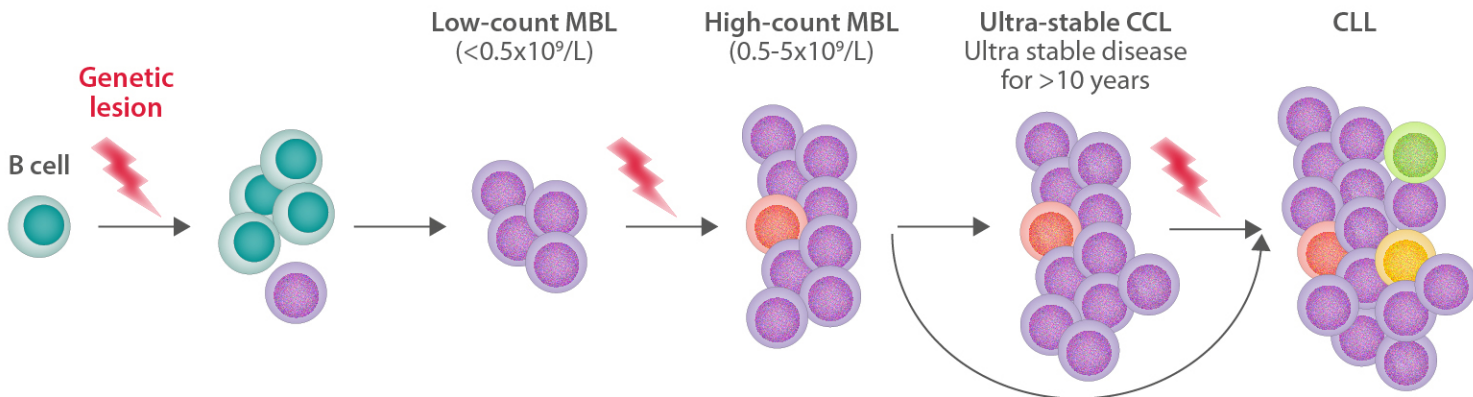# Insight into the genetic lesions involved in the transformation from MBL to CLL, analyzing for the first time low-count MBL cases, using whole-genome sequencing and targeted re-sequencing

Model for progression from Monoclonal B-cell Lymphocytosis (MBL) to Chronic Lymphocytic Leukemia (CLL)

	Somatic variants (tot: 37,033)	Analogous mutation rates	Non-synonymous exonic variants	Missense variants
Low-count MBL	2,040 (range: 298-2871)	0.63 mutations per Mb	8.9 (range: 1-16)	47/53 (88.7%)
High-count MBL	2,558 (range: 1428-3483)	0.79 mutations per Mb	14.8 (range: 9-27)	61/73 (83.7%)
Ultra-stable CLL	2,400 (range: 1650-3176)	0.74 mutations per Mb	11.6 (range: 7-19)	50/59 (84.7%)