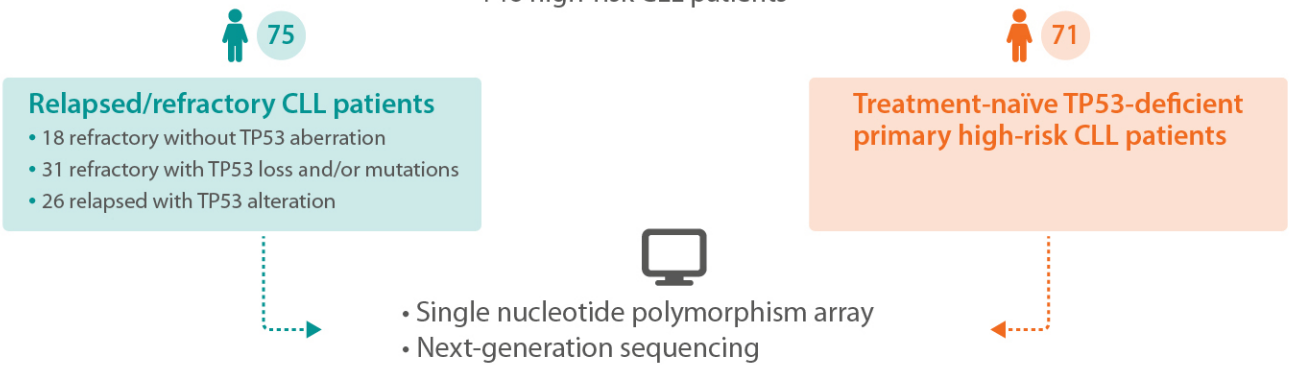
Genomic alterations contributing to the pathogenesis of high-risk chronic lymphocytic leukemia (CLL)

Prospective clinical trials of the French/German CLL study groups (FCLLSG / GCLLSG)

146 high-risk CLL patients



Landscape of genomic copy number alterations (CNAs)		
Median CNA numbers	38	39
Significantly enriched CNAs (GISTIC2.0 analysis)		
• gain(8)(q24.21)	< 0.0001	< 0.0001
• del(9)(p21.3)	0.0076	not significant
NOTCH1 mutations	24%	21%
SF3B1 mutations	24%	23%

Characterization of genomic alterations		
del(9)(p21.3) covering the *CDKN2A/B* loci	11%	7%
gain(8) covering the *MYC* locus	17%	15%
Alterations associated with NOTCH1 signaling: ***RBPJ*** in 8.2%; ***SPEN*** in 3.7%; ***SNW1*** in 7.5%		

Edelmann *et al.*, Haematologica, 2020