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Biology of Richter's Transformation

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Hematology

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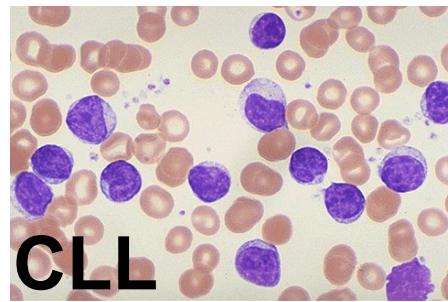
IOR - Institute of Oncology Research

USI – Universita' della Svizzera Italiana

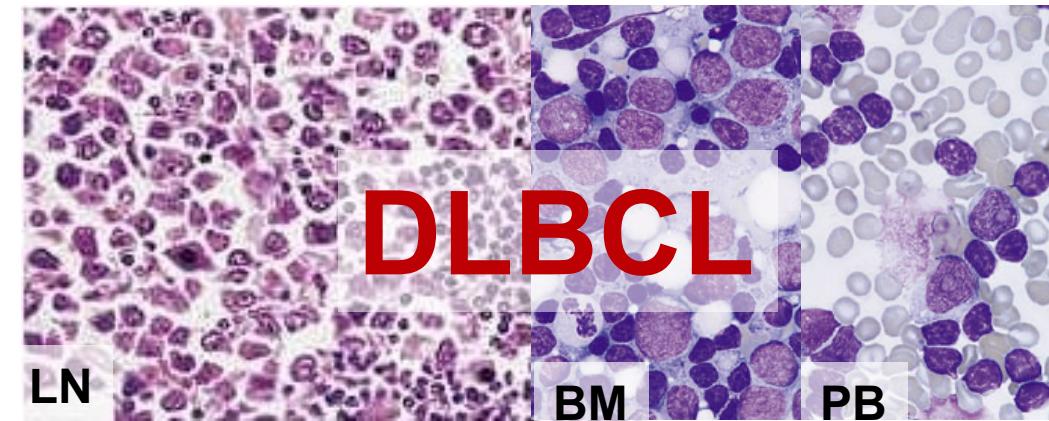
Bellinzona - Switzerland

Genetics of LBCL-variant of RT

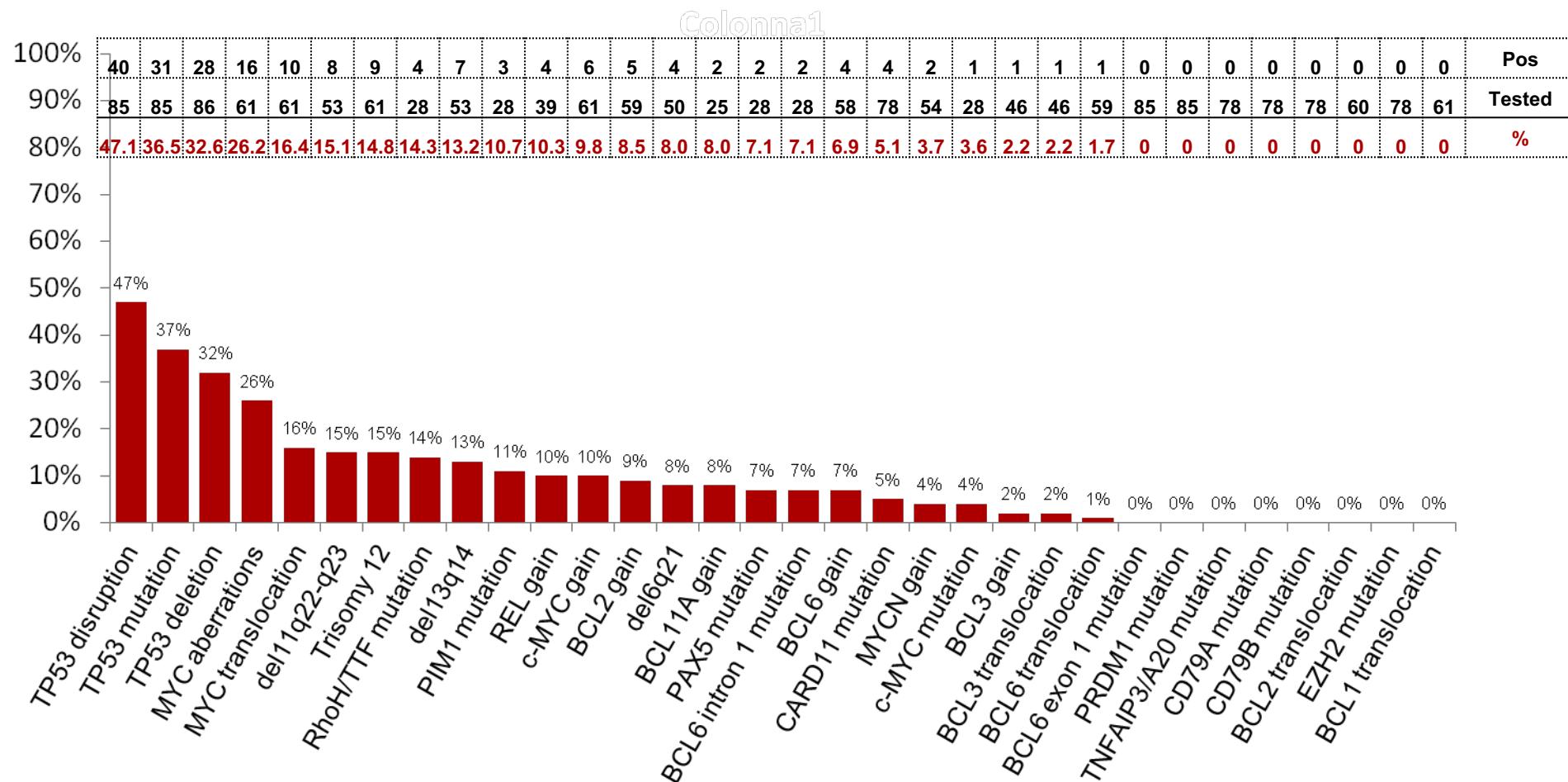
Pathologic variants of RT



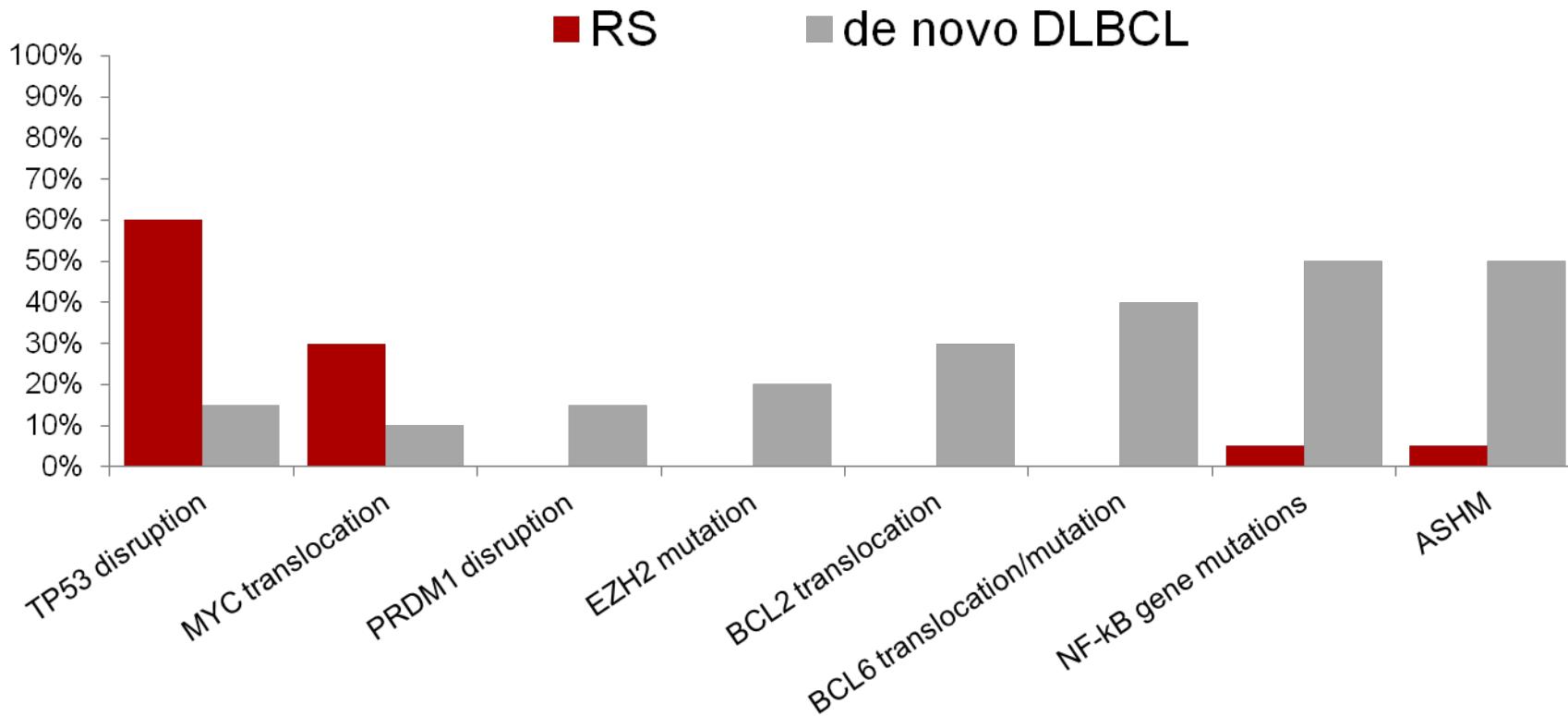
95-99%



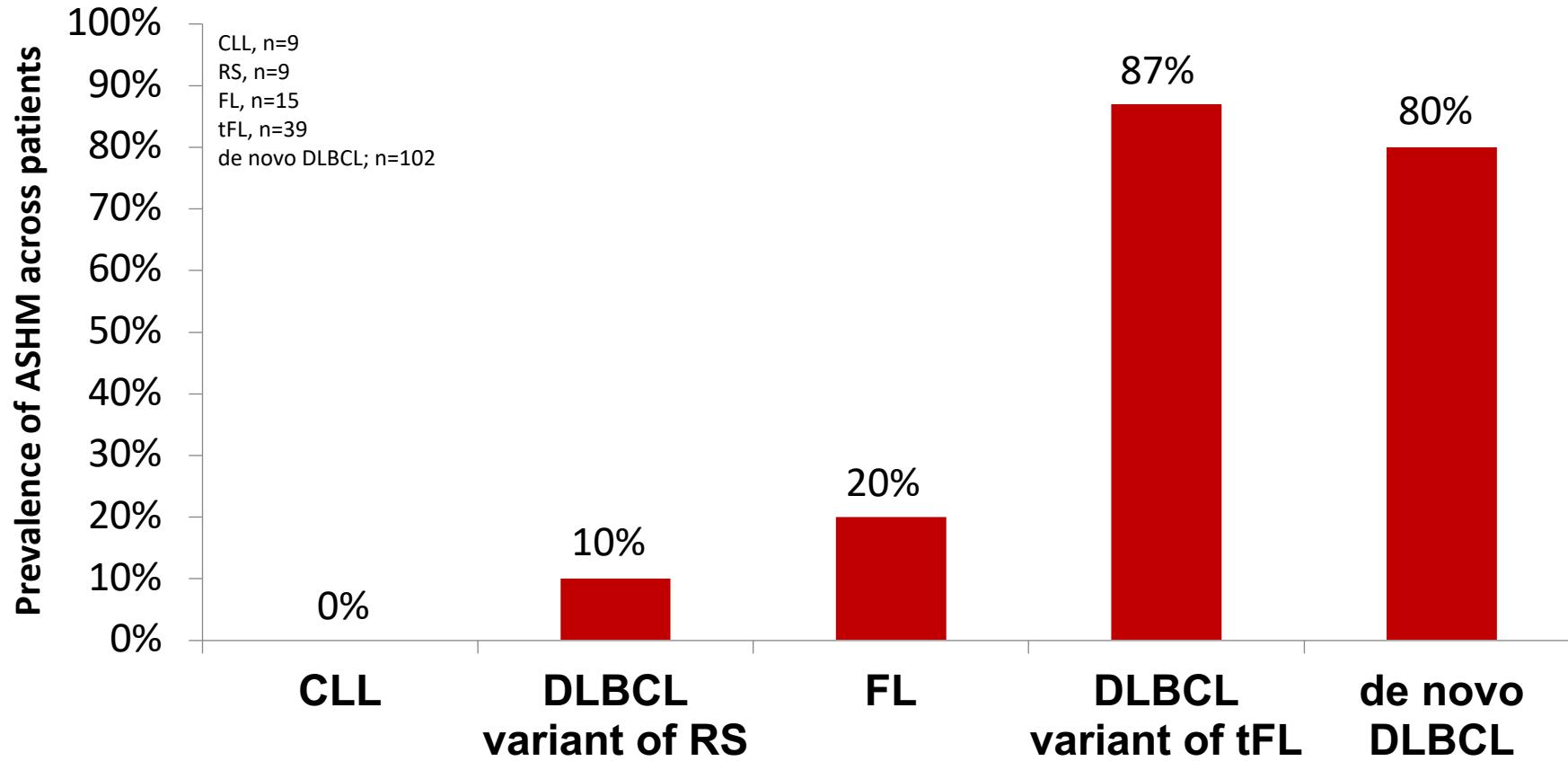
“Driver” genetic lesions of RT in 2013



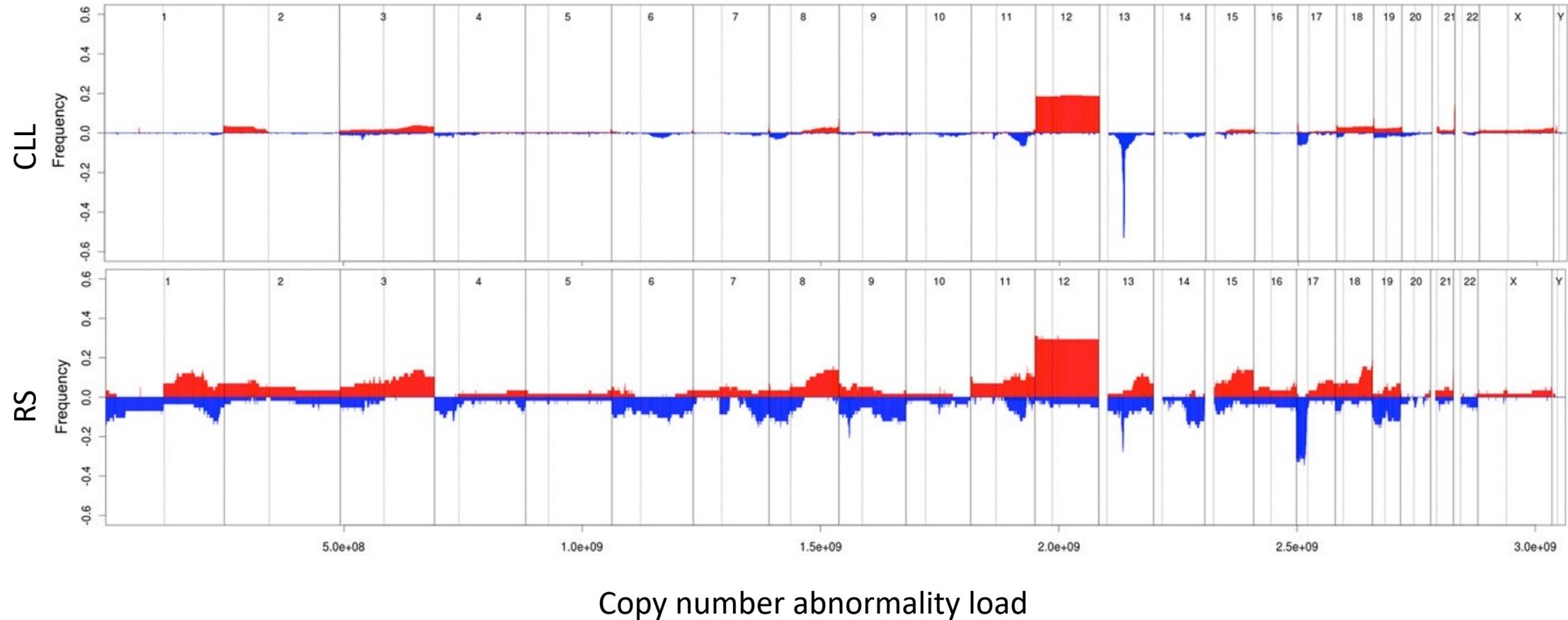
The genetic profile of clonally related RT vs DLBCL



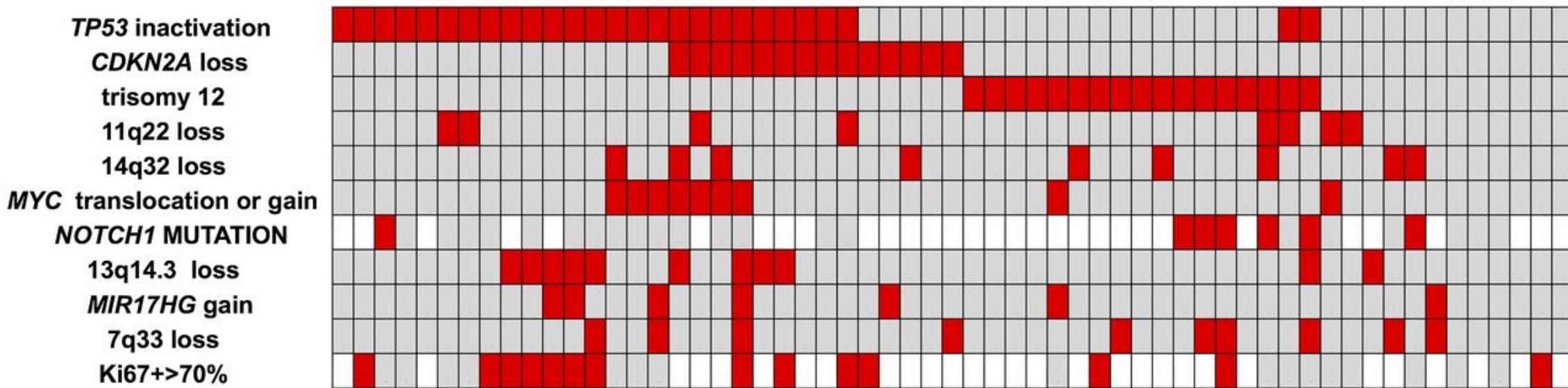
Aberrant somatic hypermutation is not a mechanism of genetic instability of RT



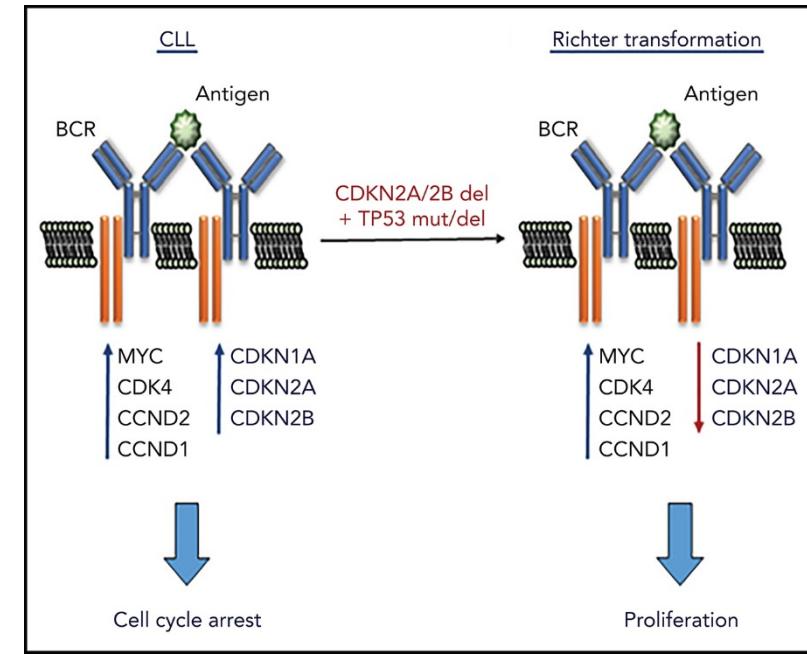
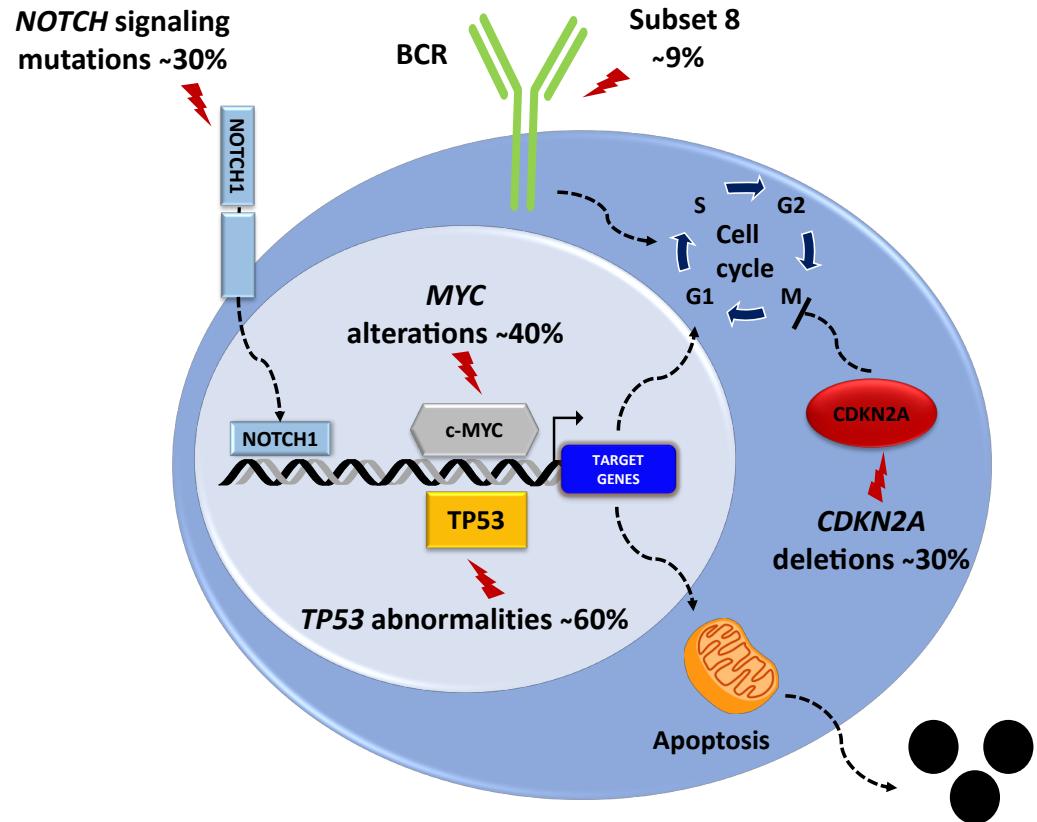
Genomic complexity of RT



TP53 and *CNKN2A* disruption and *MYC* activation



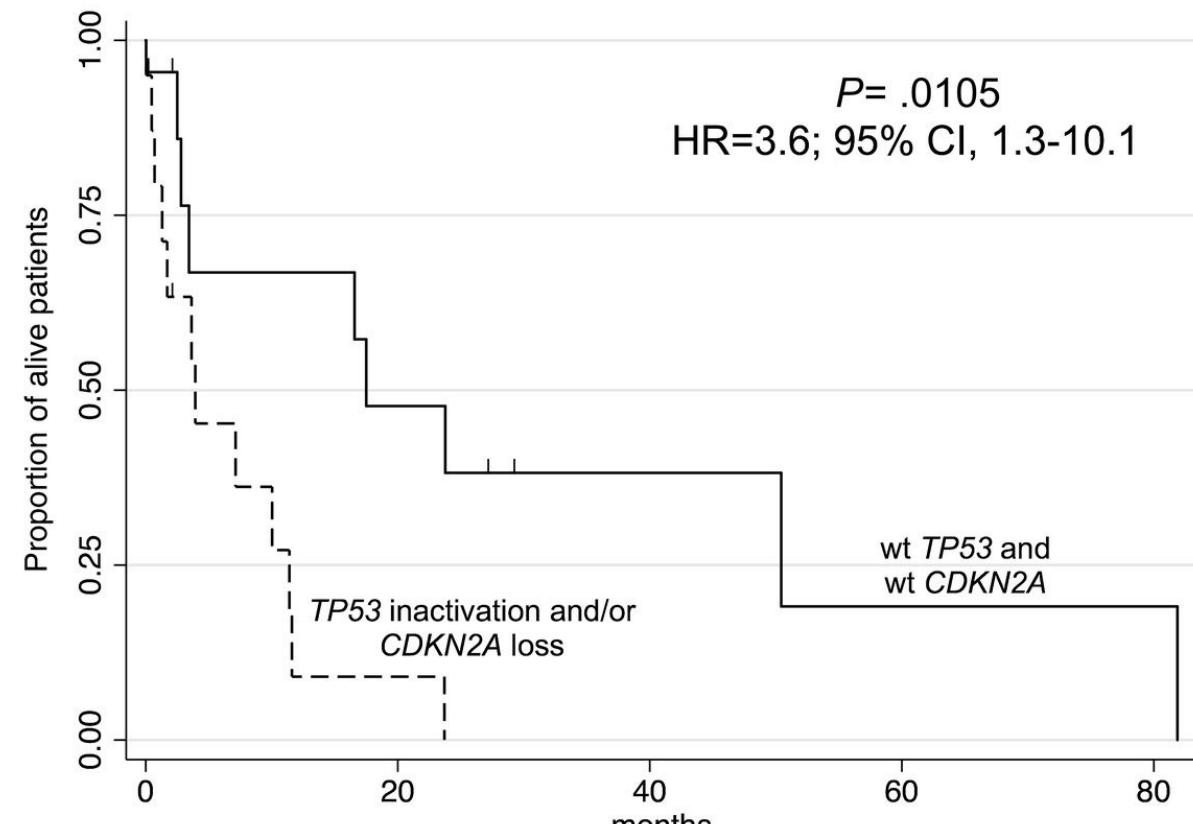
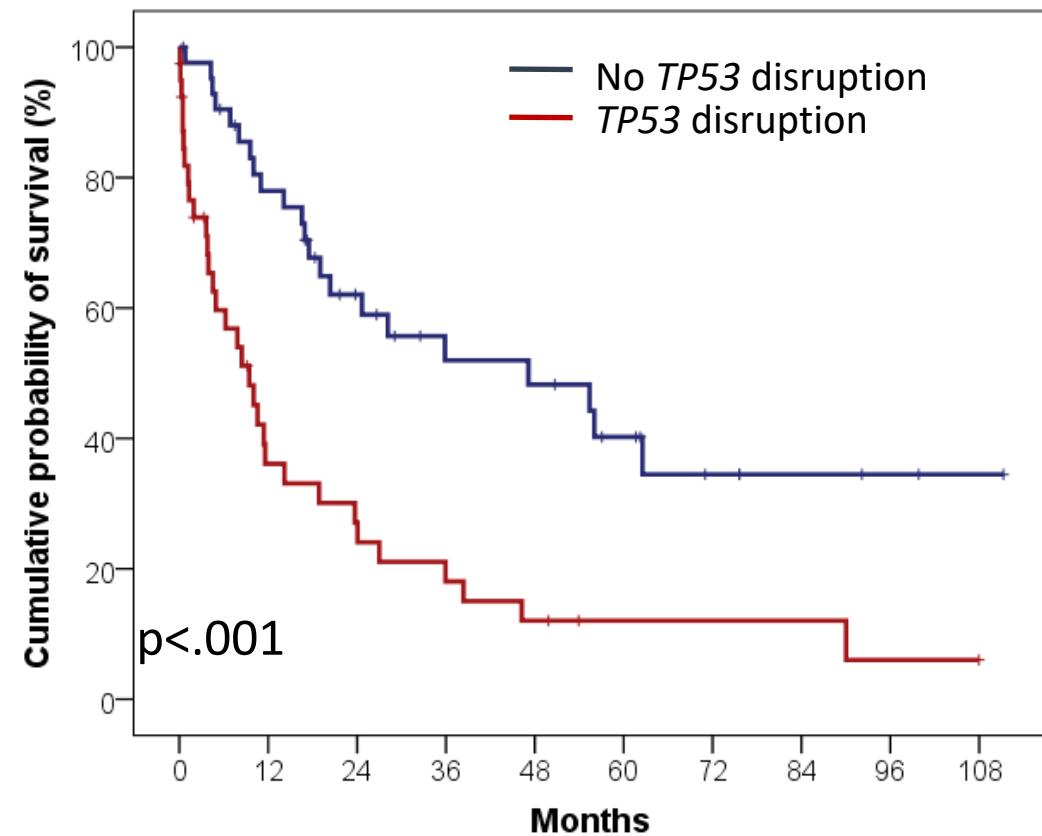
Proliferation and apoptosis are the master cellular programs deregulated in RT



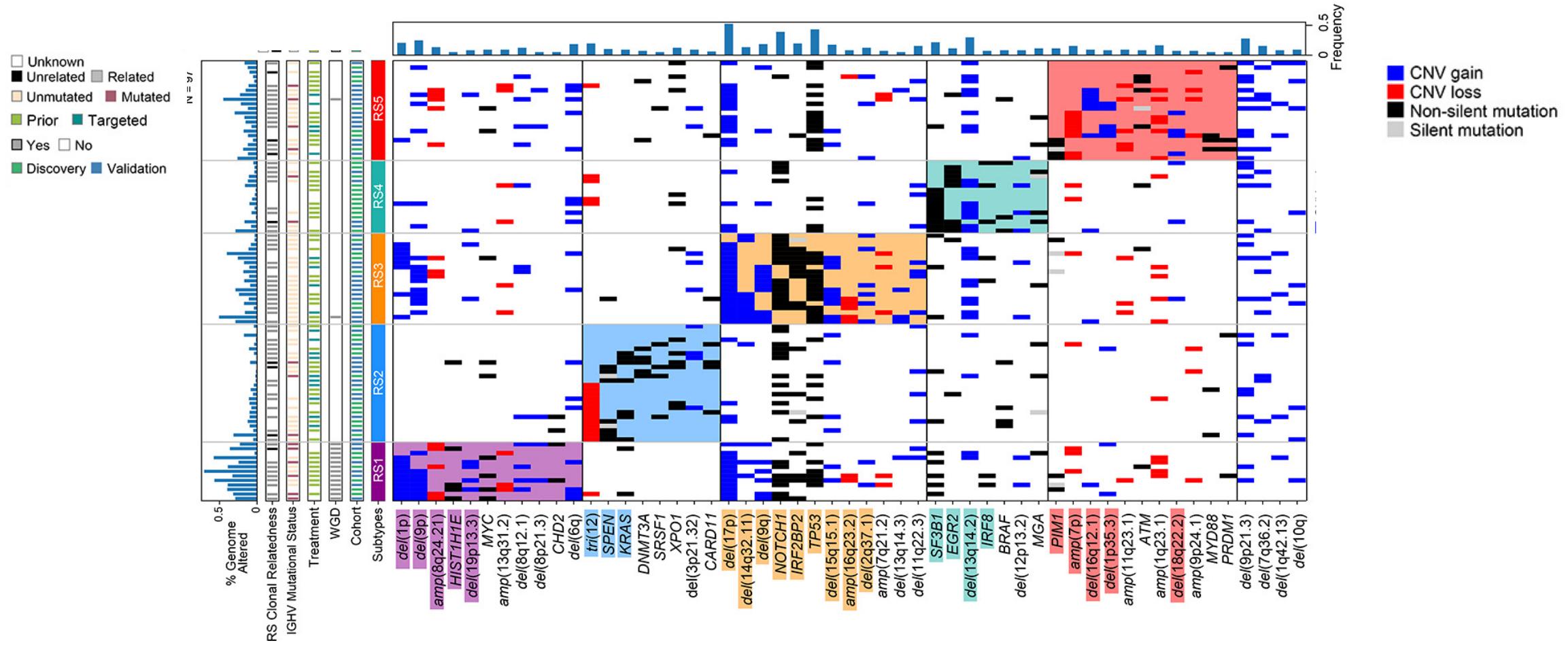
Chakraborty S, Blood. 2021

Rapidly progressive kinetics
Chemorefractoriness

TP53 and *CDKN2A* disruption prognosticate survival of RT

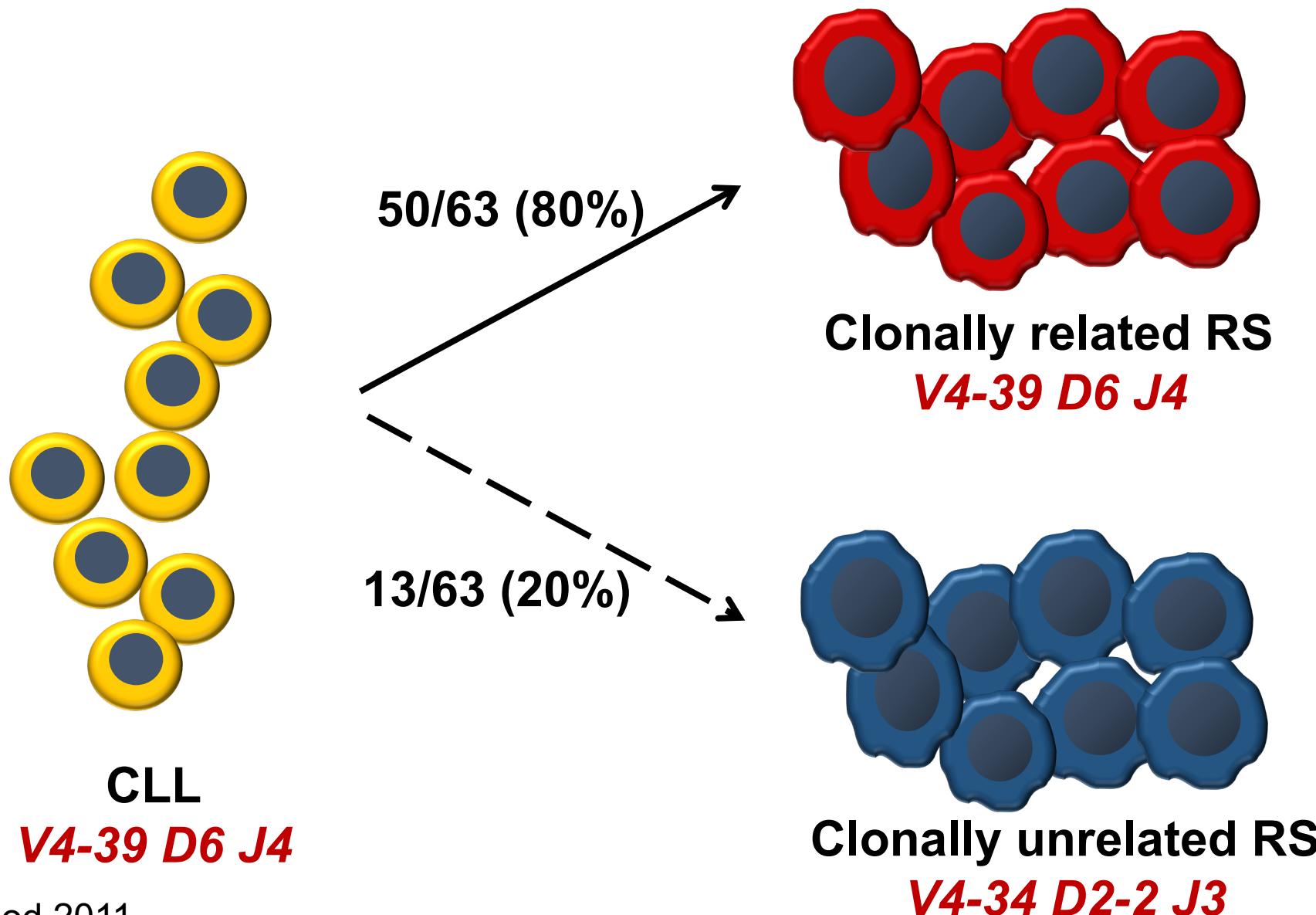


Genetics of RT in 2023

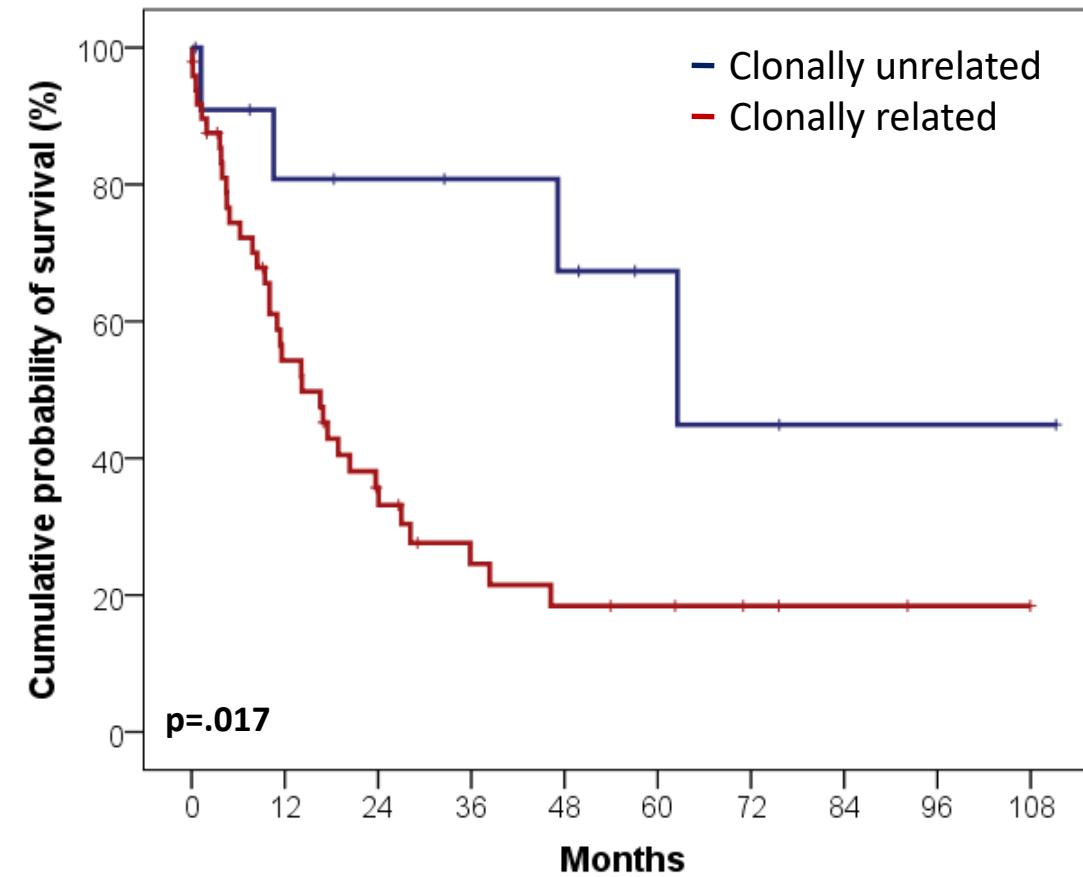
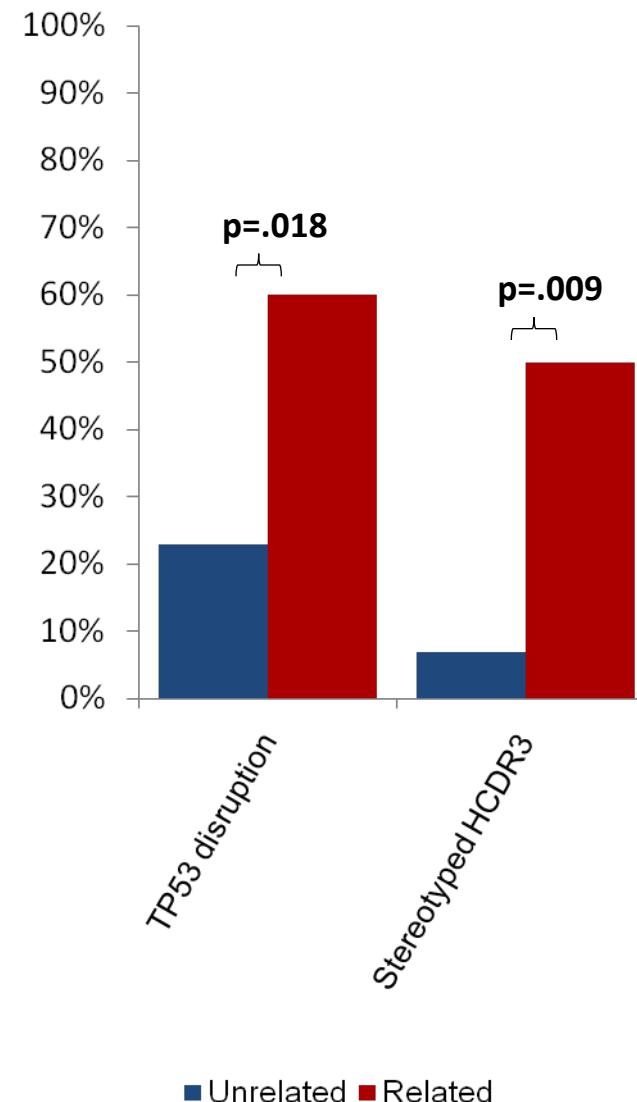


Genetics of de novo LBCL in CLL

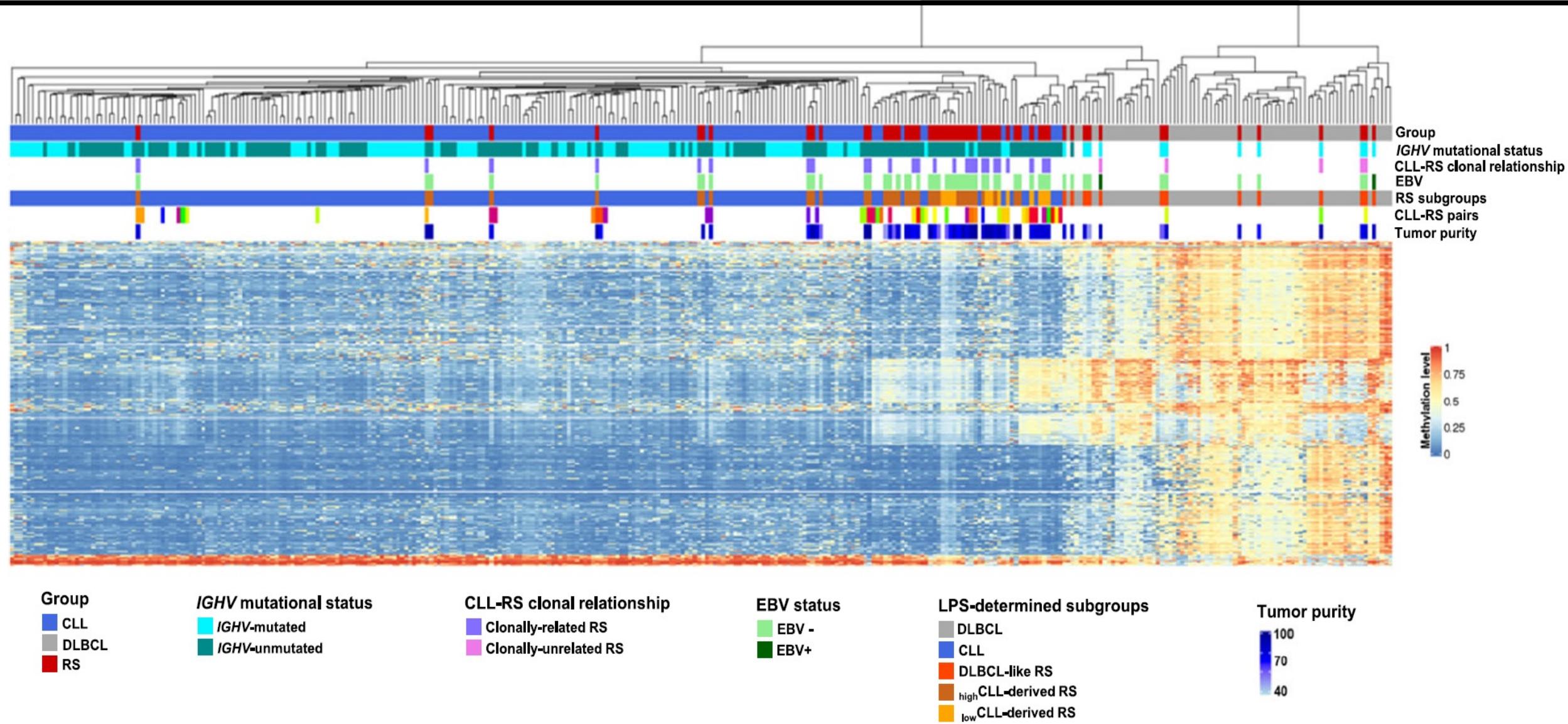
Clonally related vs unrelated variants of RT



Clonally related and unrelated Richter's syndrome

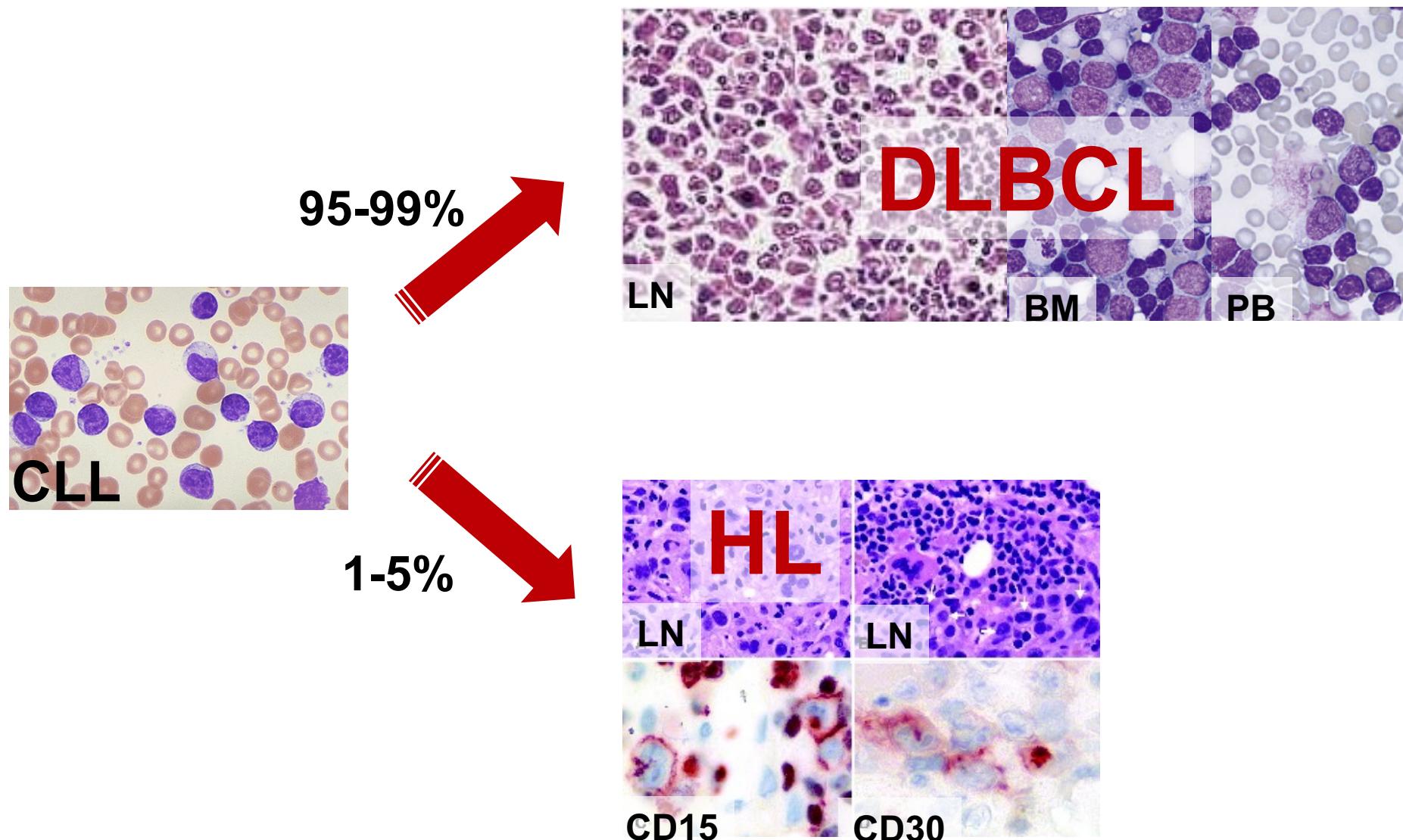


Epigenetically, de novo LBCL arising in patients with CLL cluster apart from RT

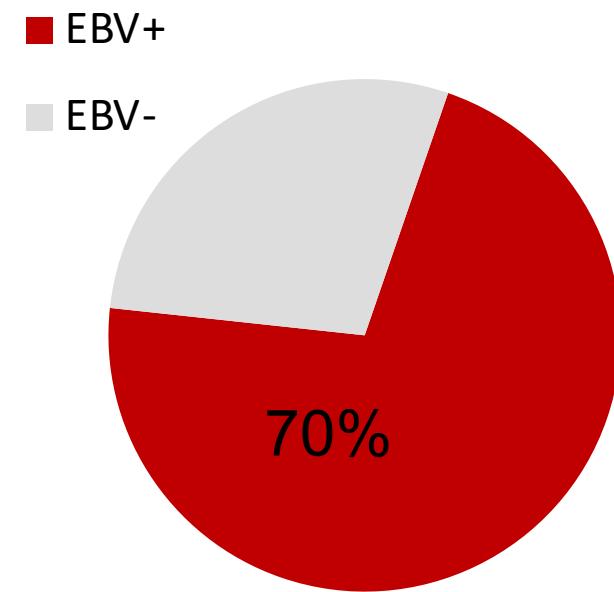
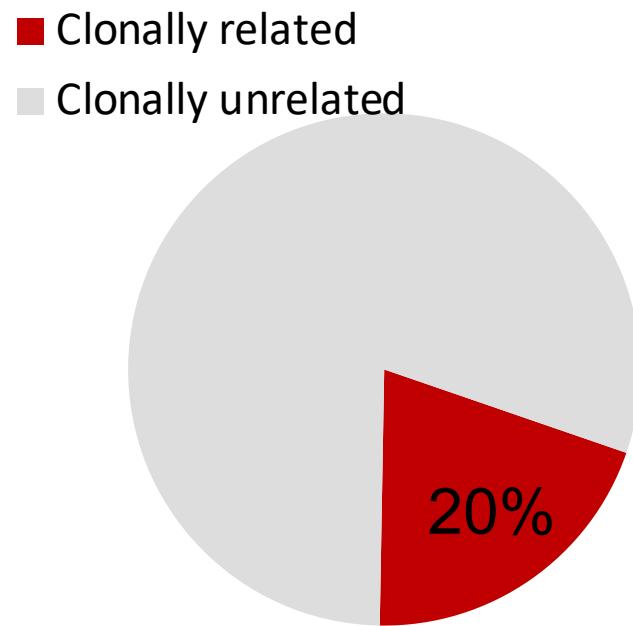


Genetics of cHL variant of RT

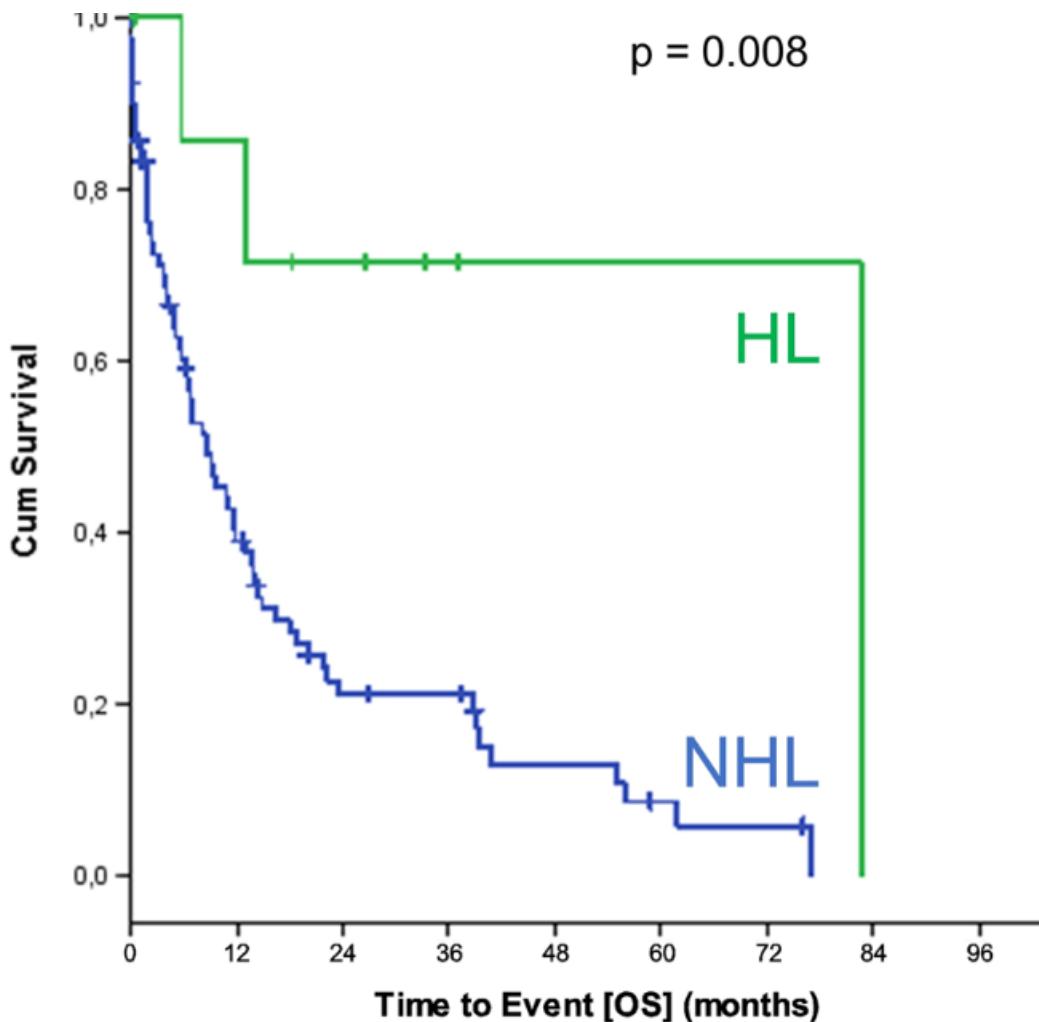
Pathologic variants of RT



Classic Hodgkin lymphoma variant of RT

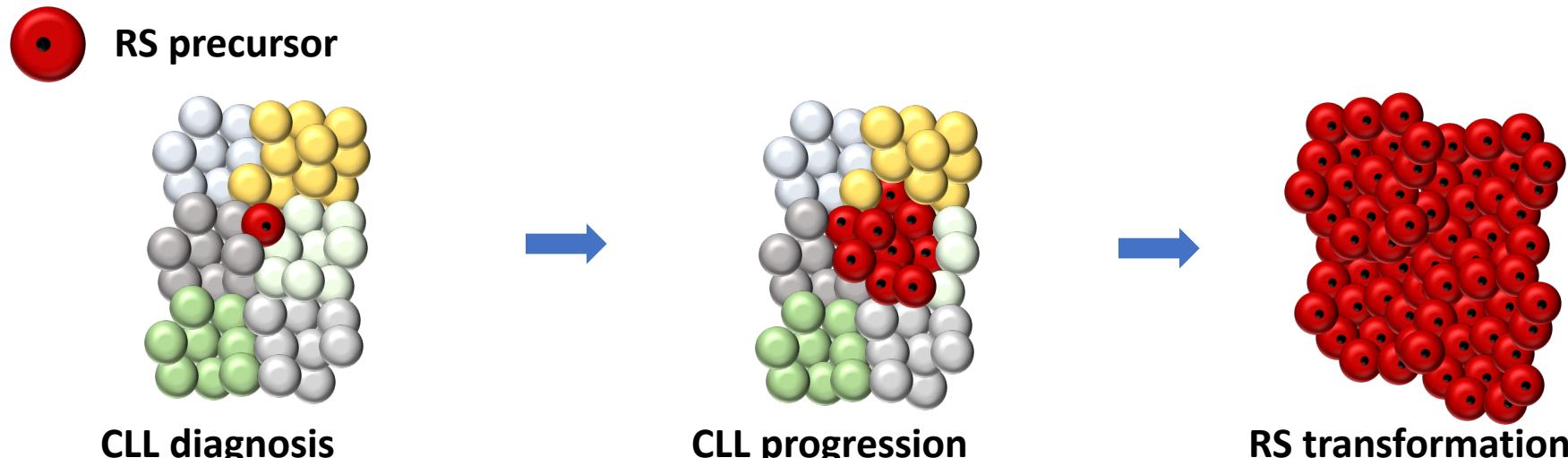
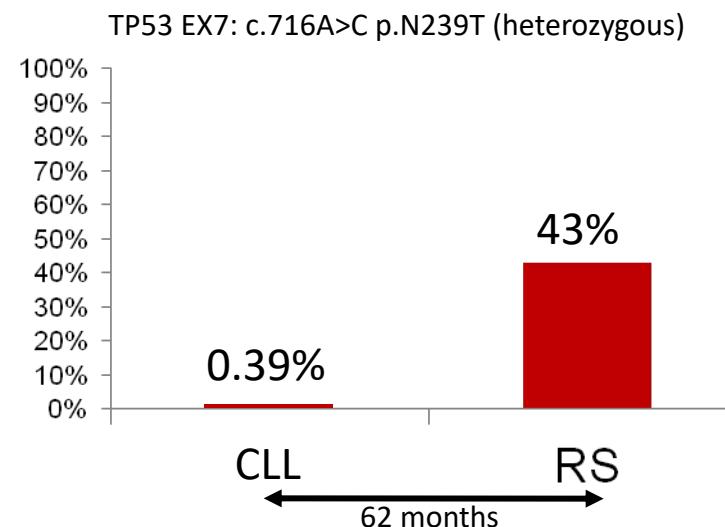
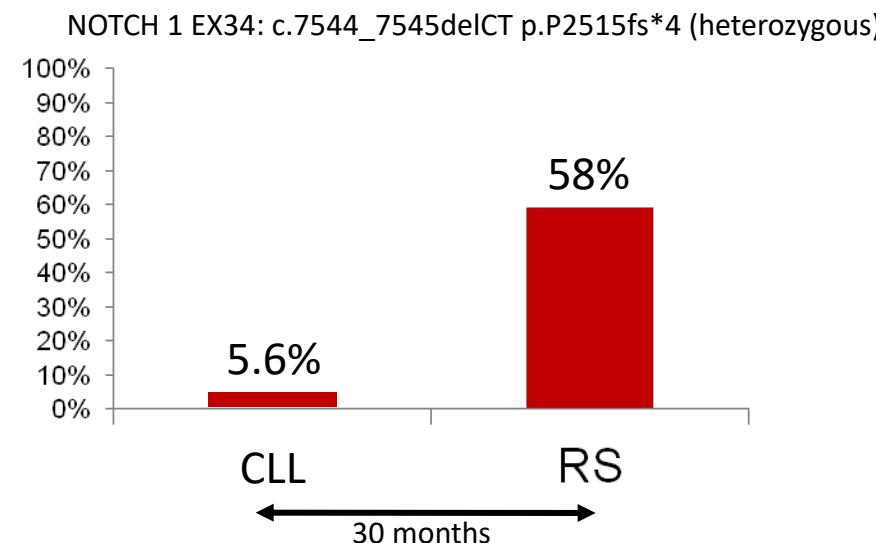


Post-transformation survival of cHL arising in patients with CLL

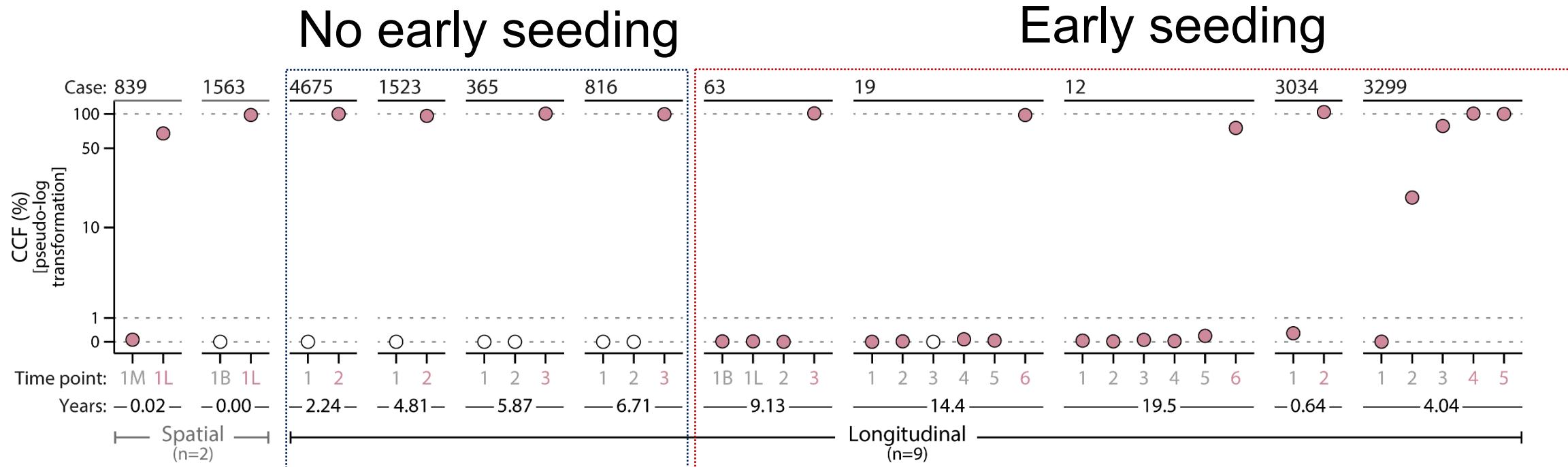


Early seeding of transformed clones

Early seeding of the RT clones



Early seeding of the RT clone is frequent (ca. 50%)

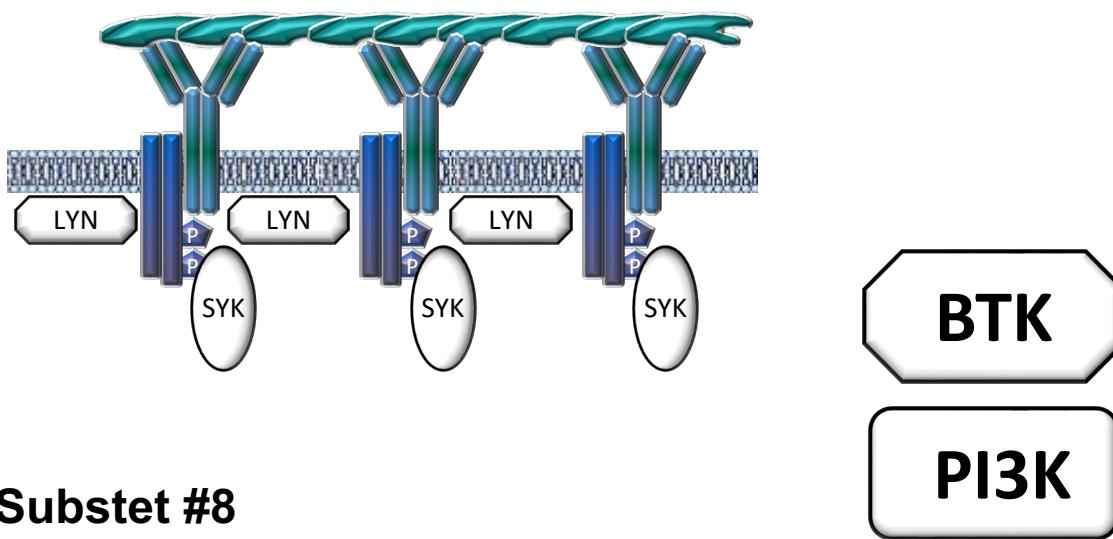


BCR signaling

Usage of subset 8 configuration of the BCR is biased in RT

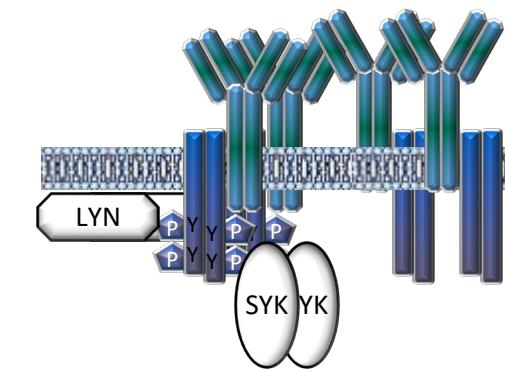
External antigens

Autoantigens exposed on apoptotic cells



Cell autonomous BCR signal

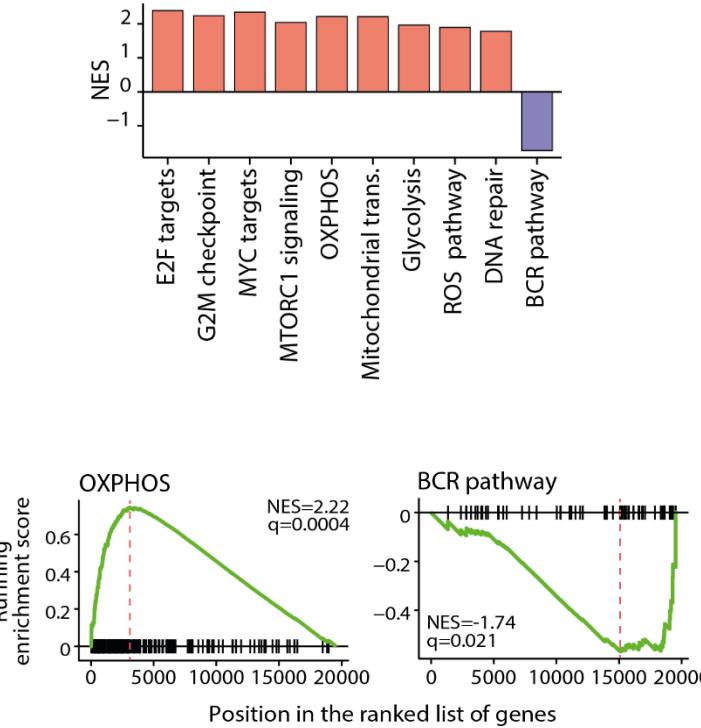
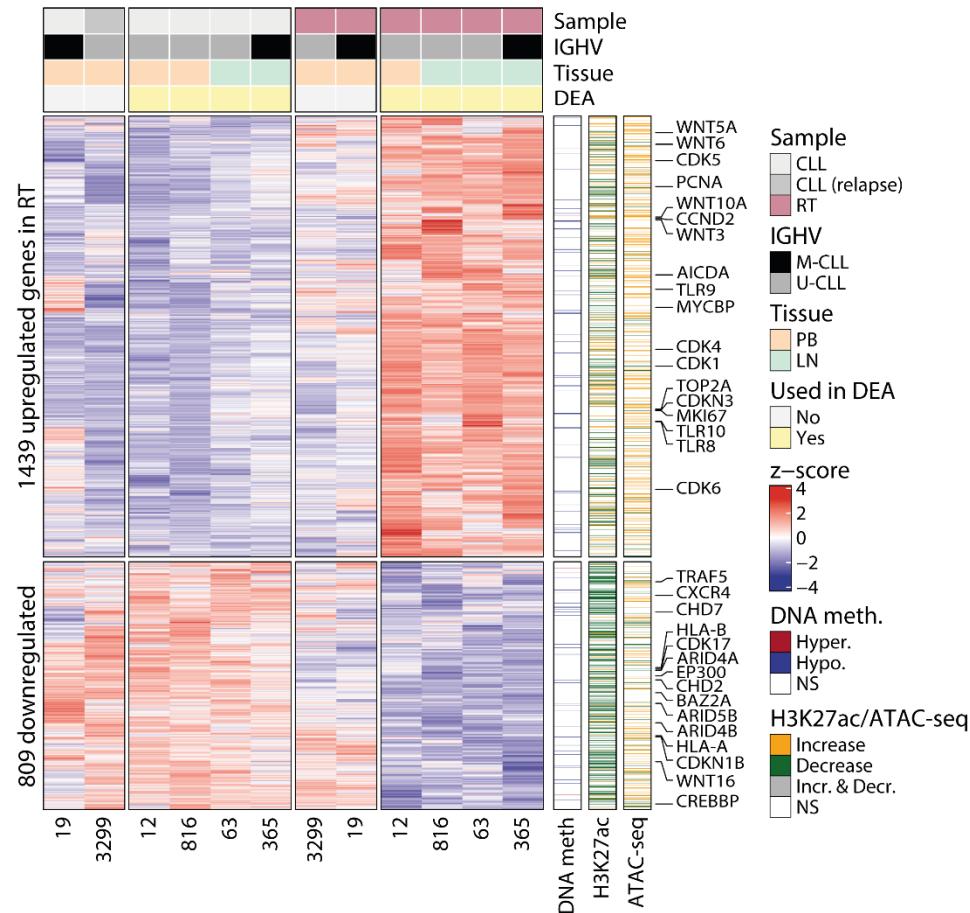
Interaction between of one BCR with another BCR that functions as an autoantigen



Subset #8

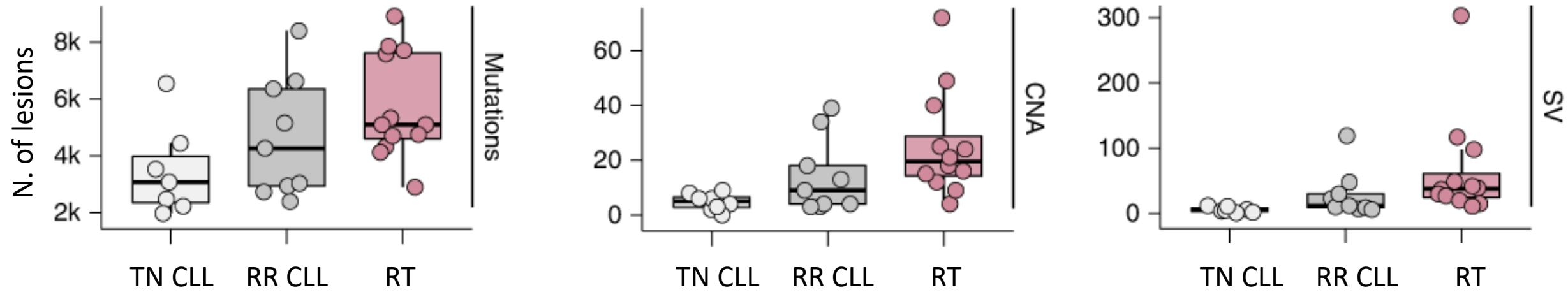
- 0.5% of CLL
- 10% of Richter syndrome
- IGHV unmutated
- Low affinity homotypic interactions
- Extreme antigen polyreactivity
- Strong phosphorylation of PLC γ 2 and ERK1/2

The OXPHOS^{high}-BCR^{low} transcriptional axis of RT

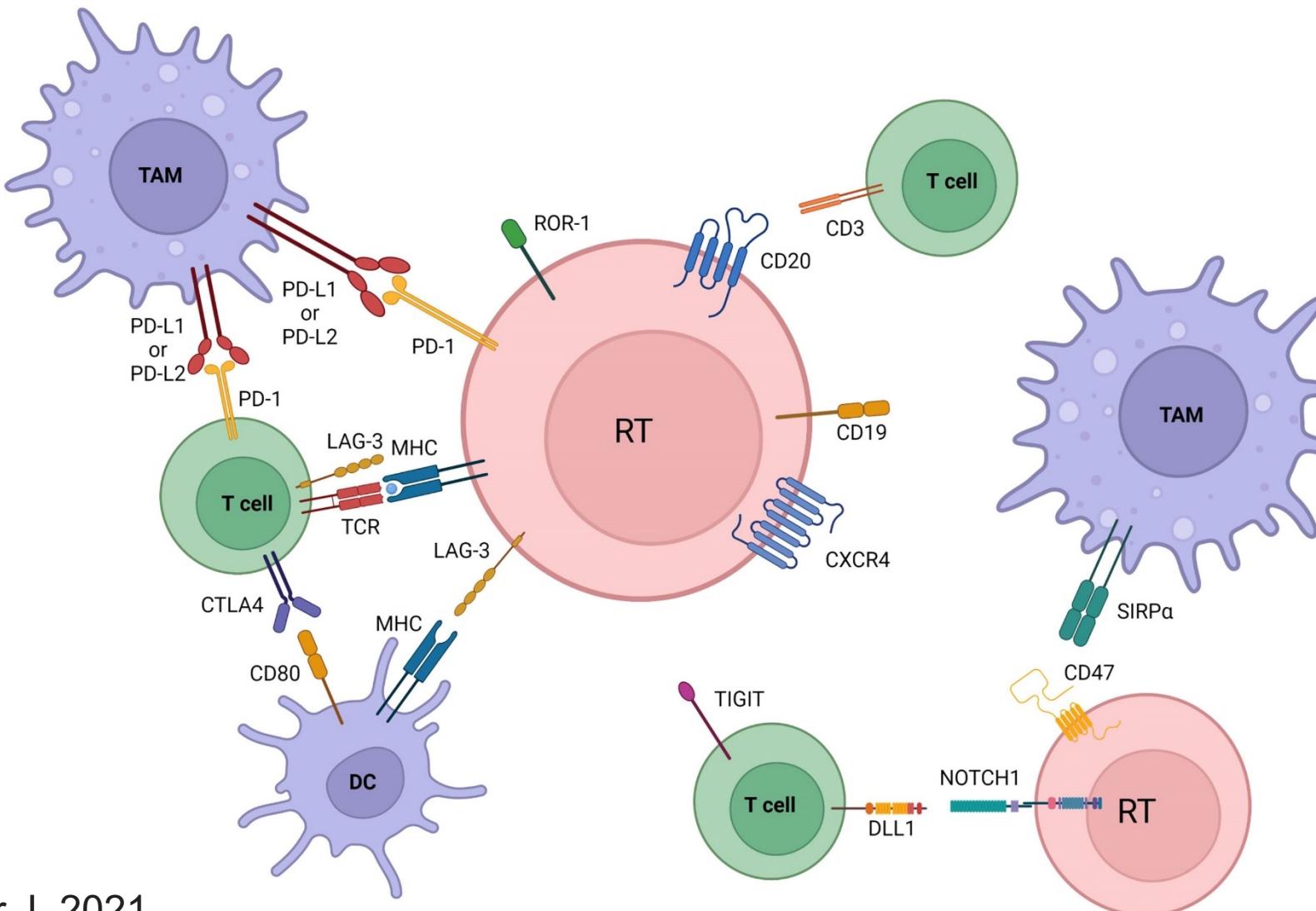


Immune escape

Genomic complexity of RT (implication for neoantigens?)



RT has an immune suppressive microenvironment



Implications for management

- RT should be carefully differentiated from de novo LBCL and de novo cHL and other lymphomas
- Treatment of RT should include agents that circumvents the block of DNA damage response (e.g. venetoclax)
- Treatment of RT should leverage on immunotherapy
- Early seeding of RT clones prompts the development of diagnostic tests for their detection during the CLL phase