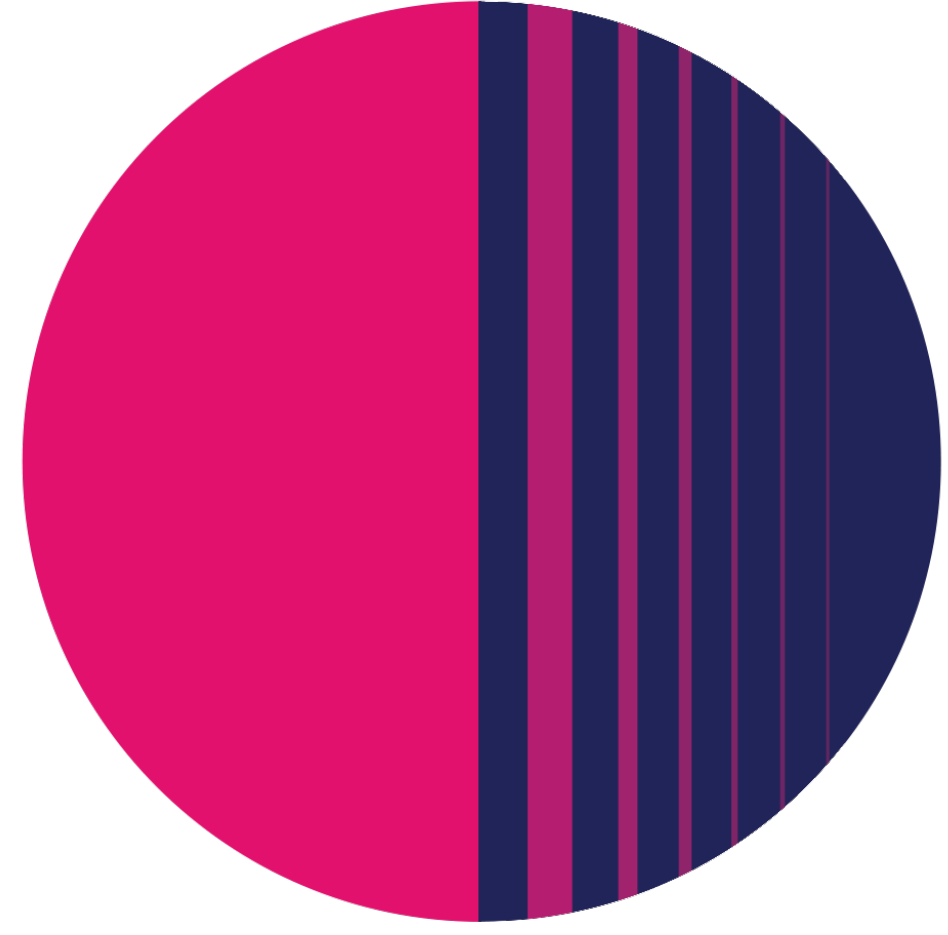
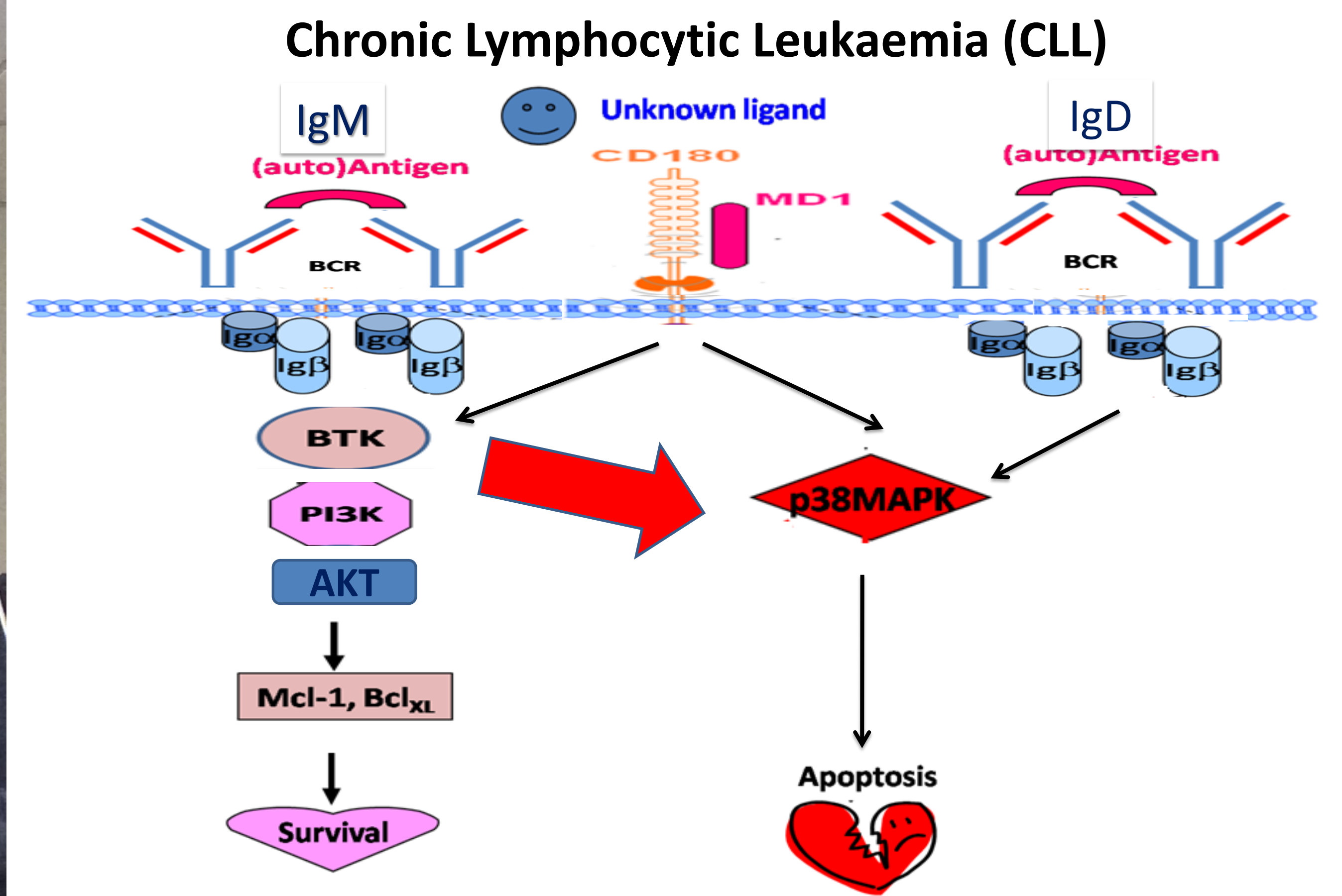


Modelling Leukaemia for Better Prognosis



STUDENTS AS CO-CREATORS

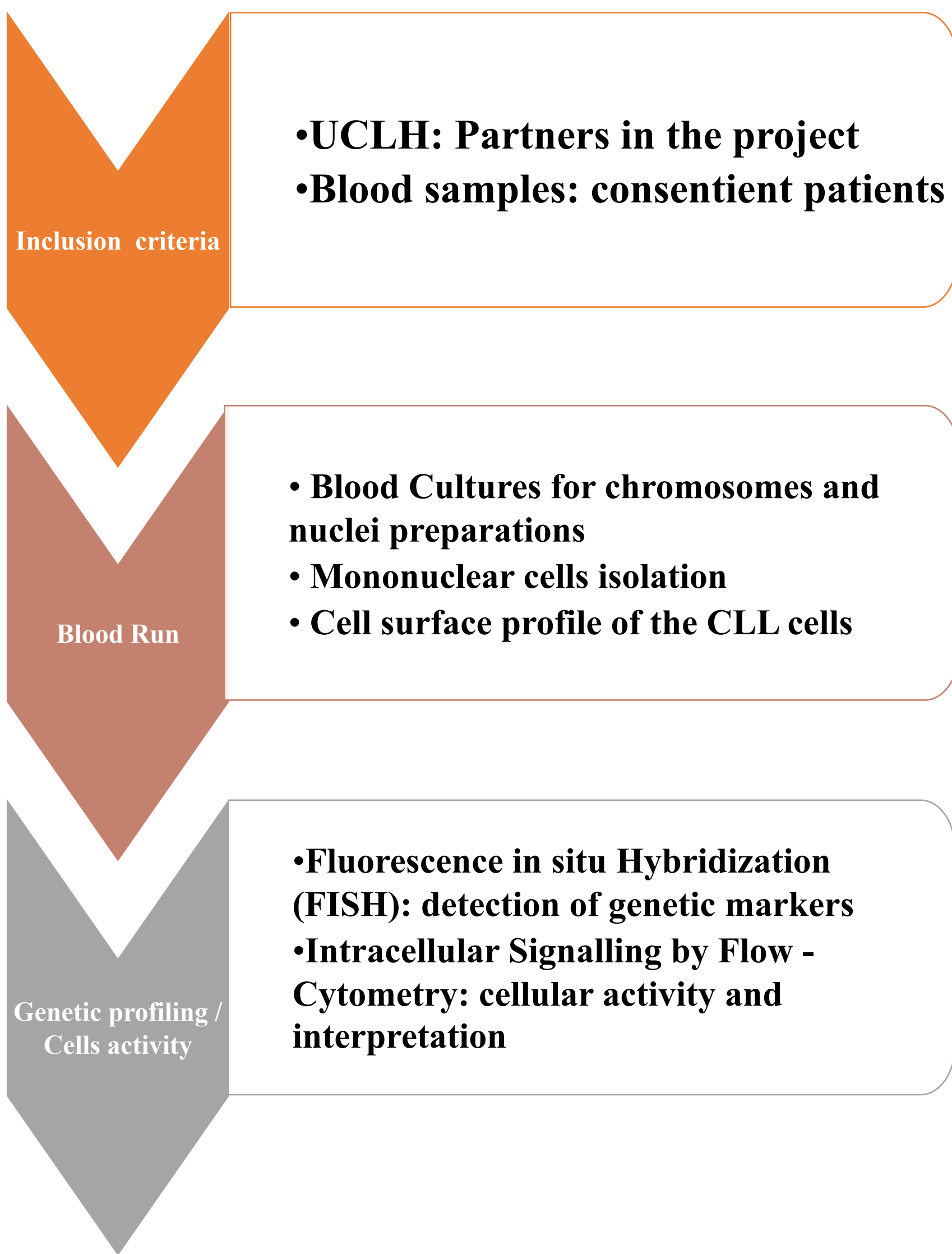
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The main objective of this proposal is to accumulate immunophenotypic, functional and genomic data to build a prototype of a computational model to improve prognosis of CLL

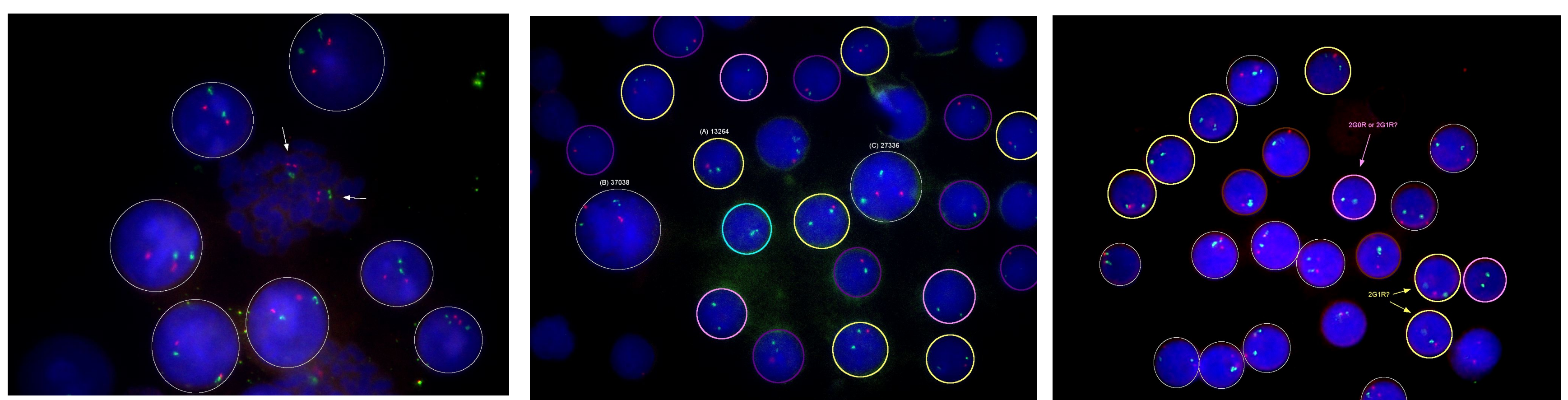
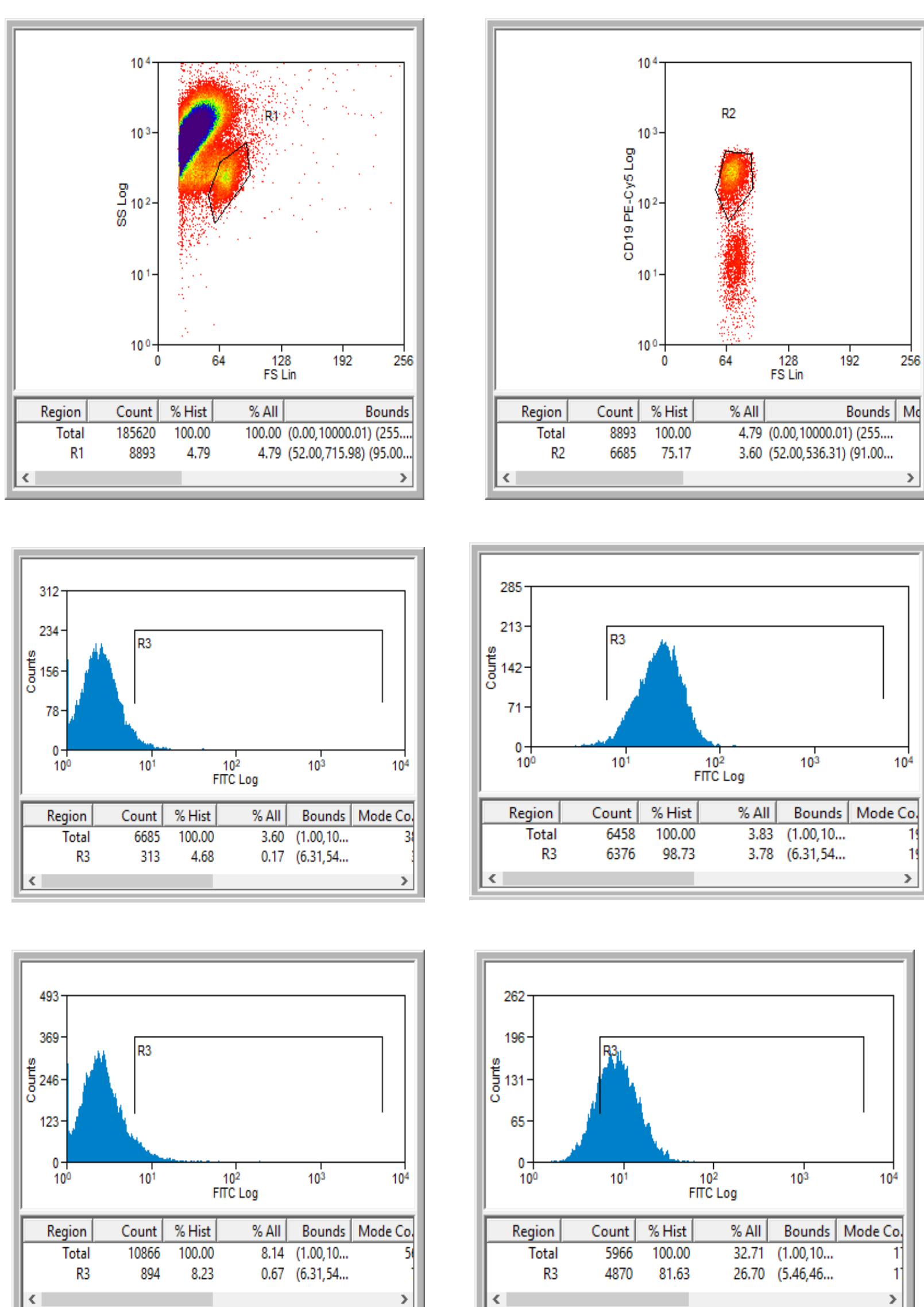
METHODS



RESULTS AND CONCLUSIONS

WHAT WAS KNOWN BEFORE THE PROJECT:
 Deletion of the *TP53* tumour suppressor gene in Chronic Lymphocytic Leukaemia (CLL) is associated with poor prognosis and is found in around **10% of all CLL cases**

WHAT WE HAVE DISCOVERED with our model:
TP53 gene deletion can be found in **66.7% of patients** with CLL cells co-expressing CD180 and IgM, thus indicating: (a) the **importance** of these two cell surface receptors in the aggressive course of the disease; (b) their potential **prognostic value**.



Examples of annotation on Fluorescence *in situ* Hybridization (FISH) images for the detection of *TP53* deletion. DNA in lymphocytes nuclei (blue) is simultaneously hybridised with a control probe (green) and a probe for the tumour suppressor gene *TP53* (red). On the left, cells from a patient with no *TP53* deletion and on the centre and right, cells from two different patients with the deletion and adverse prognosis. The nuclei showing the deletion of one copy of the gene are circled in yellow.

Patients	CD180%	IgM%	IgD%	CD38%	<i>P53</i> deletion - OUTCOME
UCLH001	High	High	Negative	Negative	YES
UCLH002	High	High	High	High	YES
UCLH003	Low	High	Negative	High	NO
UCLH004	High	High	High	High	YES
UCLH005	Low	Low	Low	High	NO
UCLH006	High	Negative	Negative	Negative	NO
UCLH007	High	High	High	Negative	YES
UCLH008	High	Negative	Negative	Negative	NO

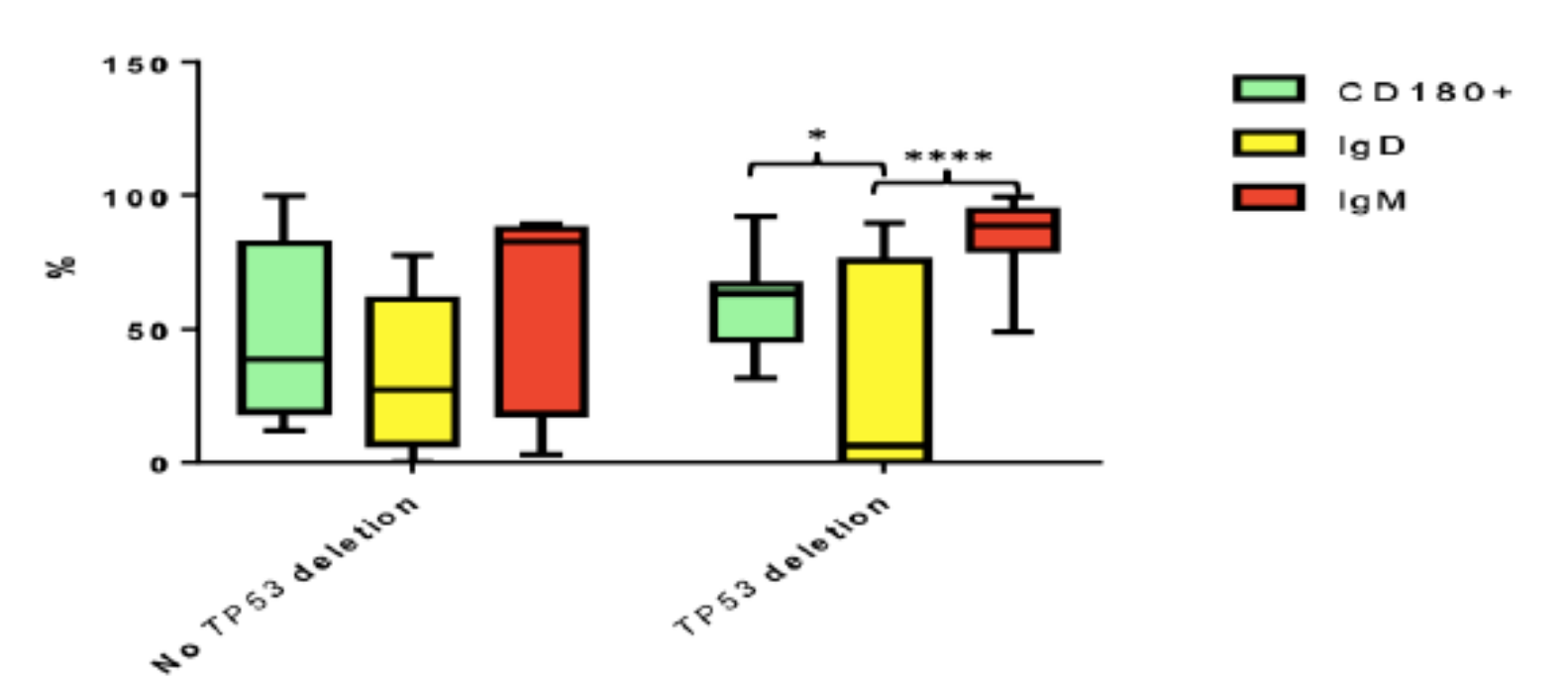


Figure 7. Comparison of association between receptors in patients with *TP53* deletion and patients with normal genotype. The data was divided into patients with deletion and without deletion and association between each receptor in each of the groups was analysed by performing Friedman test.