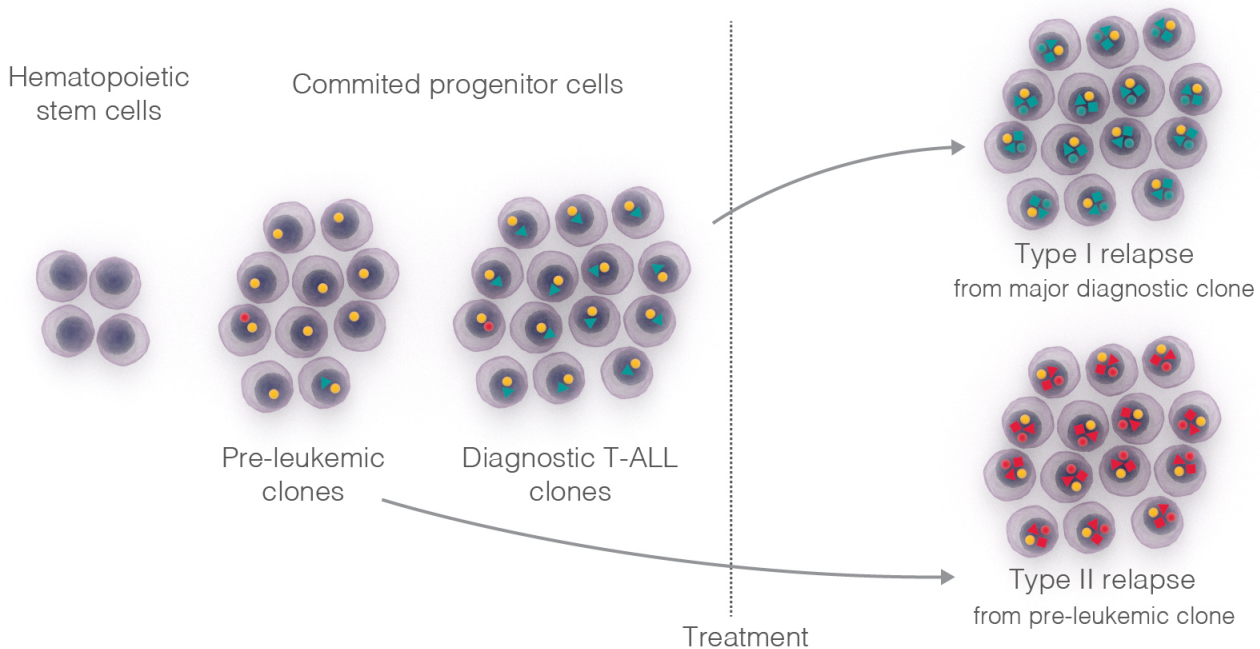


Complete genomic characterization of 13 patients at first diagnosis, remission and relapse identifies two types of relapse in T-cell acute lymphoblastic leukemia



Relapse is characterized by selection of subclones and acquisition of relapse-specific changes

- ➡ mutations of epigenetic modulators (mutations in SUZ12, WHSC1 or SMARCA4)
- ➡ activation of the nucleotidase NT5C2 (chemotherapy resistance)