

**Table 1:** Cytogenetic, immunophenotyping and methylation pattern of cells from patients used for the characterization of the ALL mice model

SAMPLE	KARIOTYPE	IMMUNOPHENOTYPE	PERCENTAGE OF BLASTS IN PATIENTS' SAMPLE	METHYLATION PATTERN
ALL-T1	46, XX, del(1)(p32)?, del(6)(q23)?,t(11;14)(p13;q11)	CD3- CD7+CD2+CD5+CD4+/- (60%) CD3CITO+CD34-CD10-CD1A-TDTI+	>80%	325 hypermethylated genes 49 hypomethylated genes
ALL-B1	36,X,-Y,-2,-3,-4,-5,der(6q),-7,-9,-10,-14,-15,-16,-17,-18,-20,-22,+4 mar	CD45lo/verylo+ CD19+ CD34+(60%) CD38hi+ CD22+ CD10- CD20-(12%) TdT+(89%) CD3cito- CD7- CD2- CD5- CD1a- CD8- CD4- CD56- MPO- CD33- CD13- CD117- CD15lo+ CD11b- CD11c- CD14- GlicoforineA- CD61- CD41a- CD42b- CD36-	98.40%	879 hypermethylated genes 73 hypomethylated genes