

Figure S1. Whole and protein coding transcriptome in paediatric ALL. **A** Number of common upregulated transcripts between the comparison T-ALL vs T naïve cells and B-ALL vs B naïve cells. Fisher's exact test scored the overlapping as significant with a p-value = $1.1e-56$. **B** Number of common upregulated protein coding RNAs between the comparison T-ALL vs T naïve cells and B-ALL vs B naïve cells. Fisher's exact test scored the overlapping as significant with a p-value = $5.4e-58$. **C** PCA of the whole transcriptome of all the samples. **D** PCA of the protein coding transcriptome of all the samples.

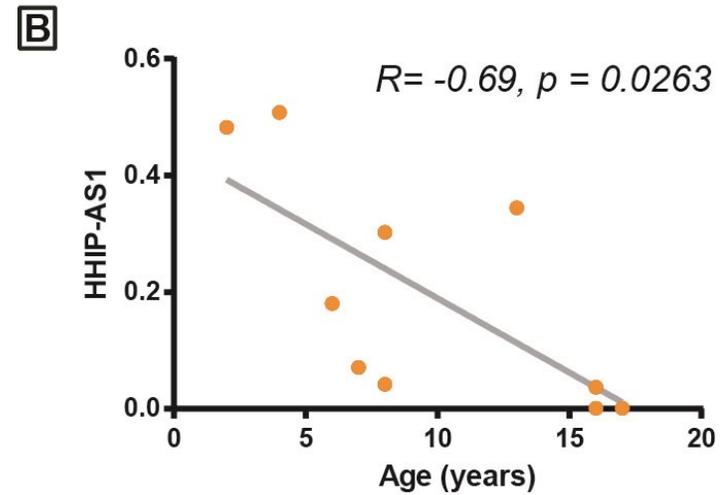
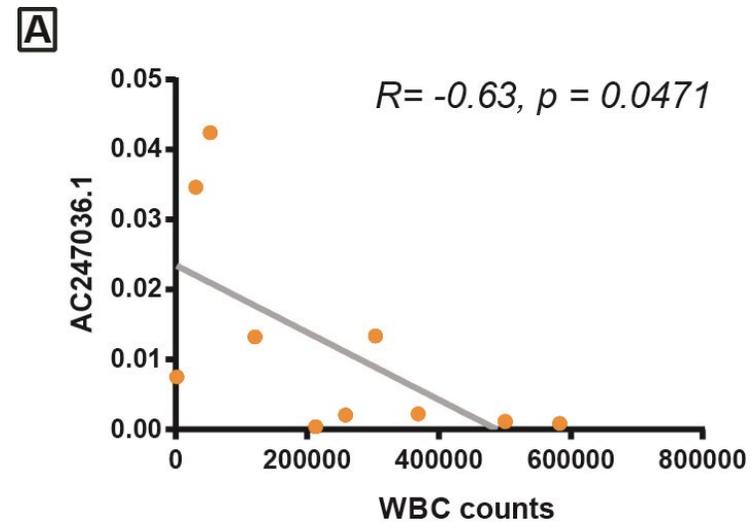


Figure S2. Correlation between lncRNA expression and clinical information. **A** Pearson correlation between AC247036.1 expression level in T-ALL patients from RT-PCR and WBC at diagnosis. **B** Pearson correlation between HHIP-AS1 expression level in T-ALL patients from RT-PCR and patients' age.

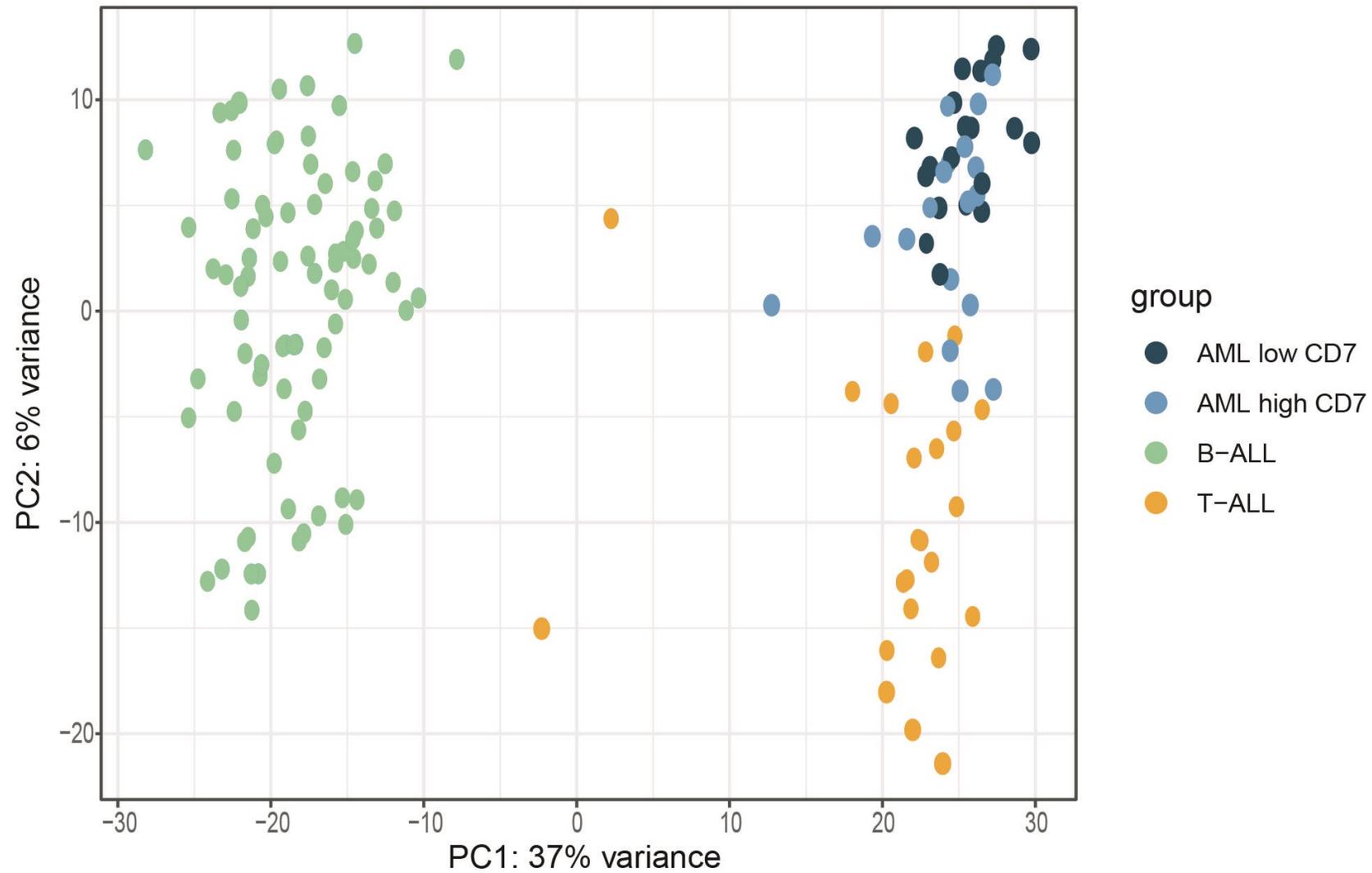


Figure S3. *lncRNA landscape in paediatric ALL and AML.* PCA of the lncRNA landscape of childhood B-ALL, T-ALL and AML RNA-seq samples from Paediatric Cancer Genome Project by Saint Jude Children's Research Hospital. Different shades of blue differentiate between low CD7-content-AML and high CD7-content-AML. The threshold to discriminate high-CD7-content AMLs and low-CD7-content AMLs was set based on the median of normalized RNA-seq counts of expression.