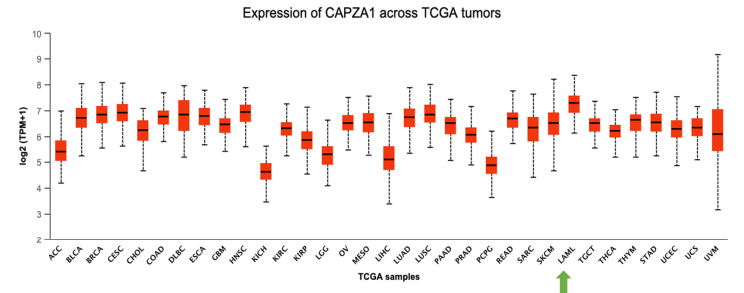
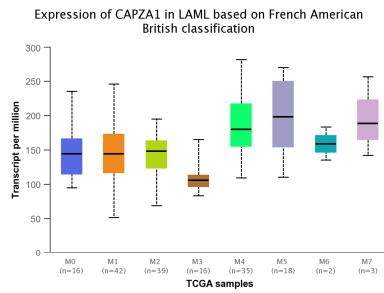
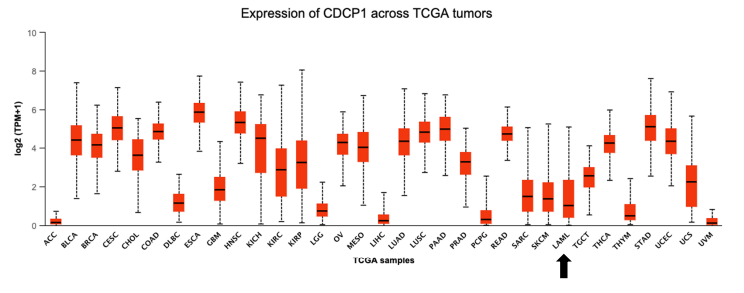
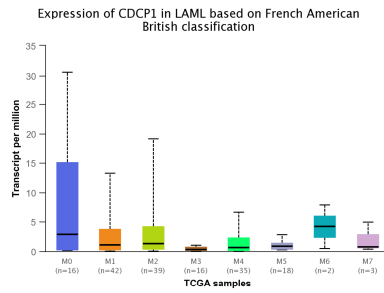
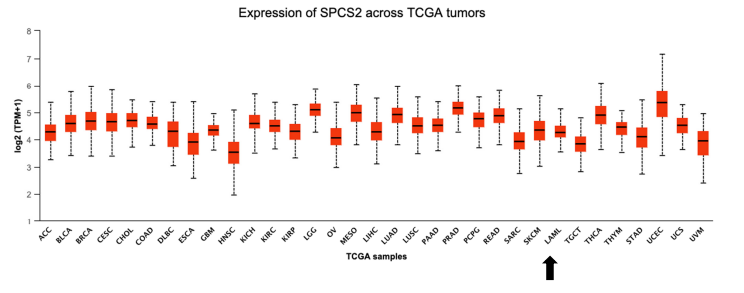
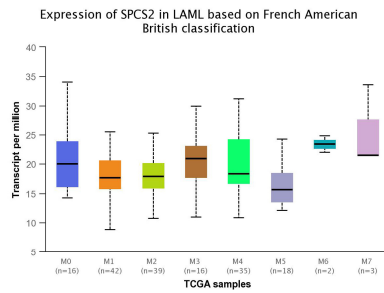
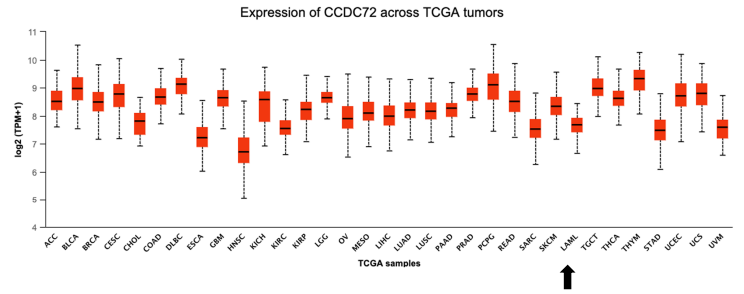
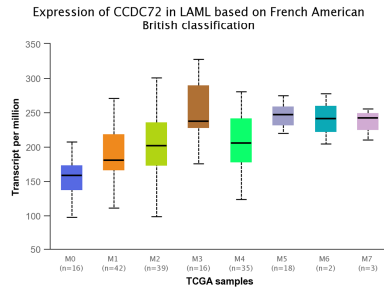
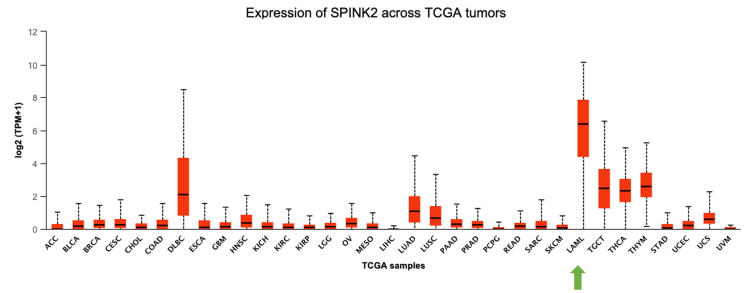
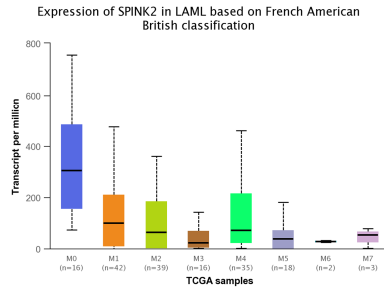


Figure S1. Workflow about samples selection and their distribution in AML 2002/01 trial-GSE75461 and TARGET program.



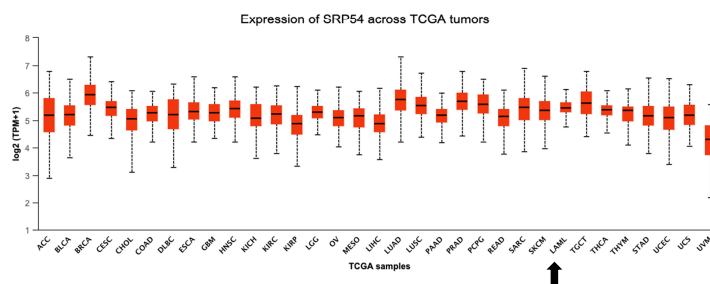
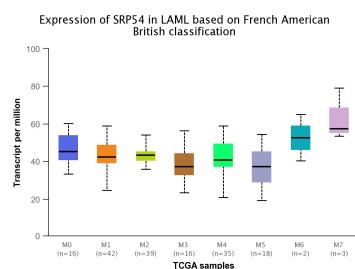
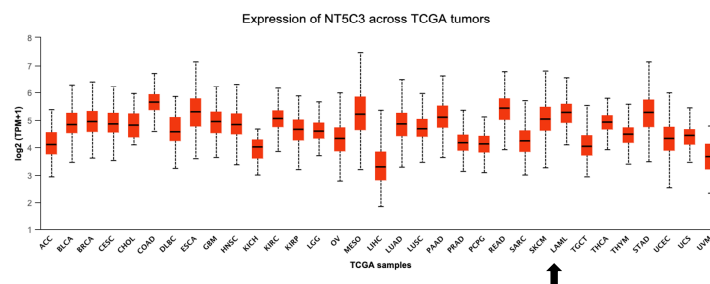
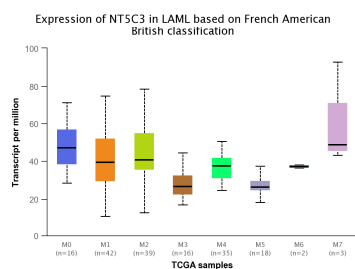
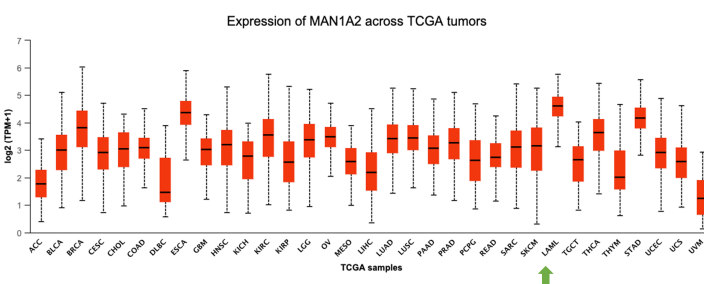
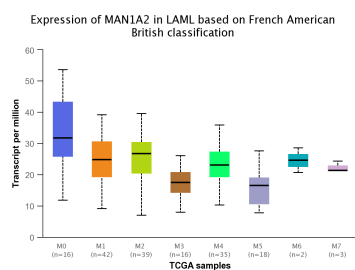
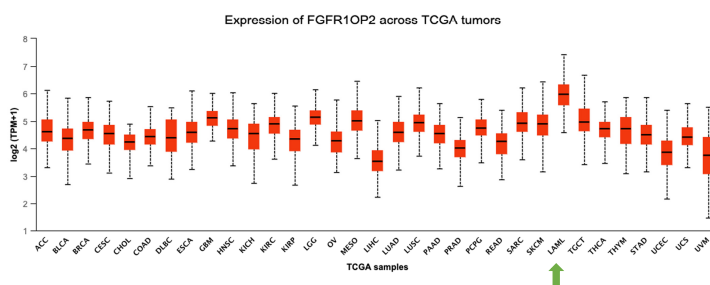
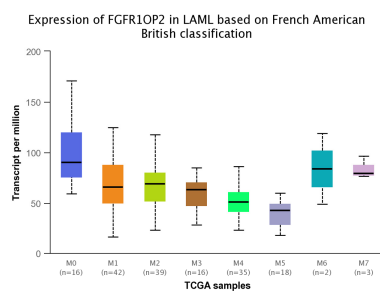


Figure S2. UALCAN analysis on SPINK2, CCDC72 (TMA7), SPCS2, CDCP1, CAPZA1, FGFR1OP2, MAN1A2, NT5C3A and SRP54 showing the expression levels in FAB subtypes and 33 different types of TCGA tumors. Arrows indicate AML hystotype; green arrows indicate higher expression in AML hystotype.

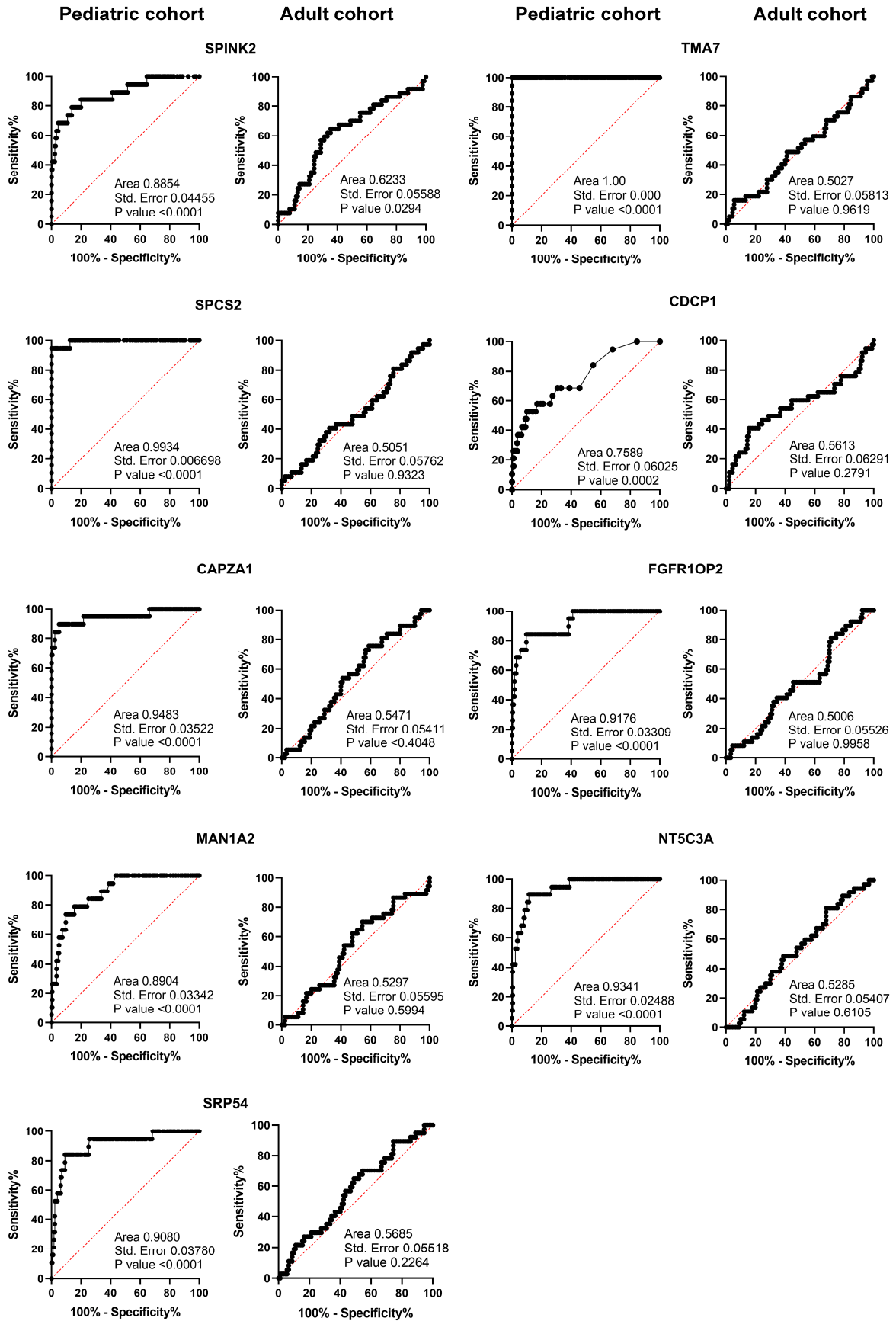


Figure S3. Roc Curve for SPINK2, TMA7, SPCS2, CDCP1, CAPZA1, FGFR10P2, MAN1A2, NT5C3A and SRP54 for pediatric and adult cohort.

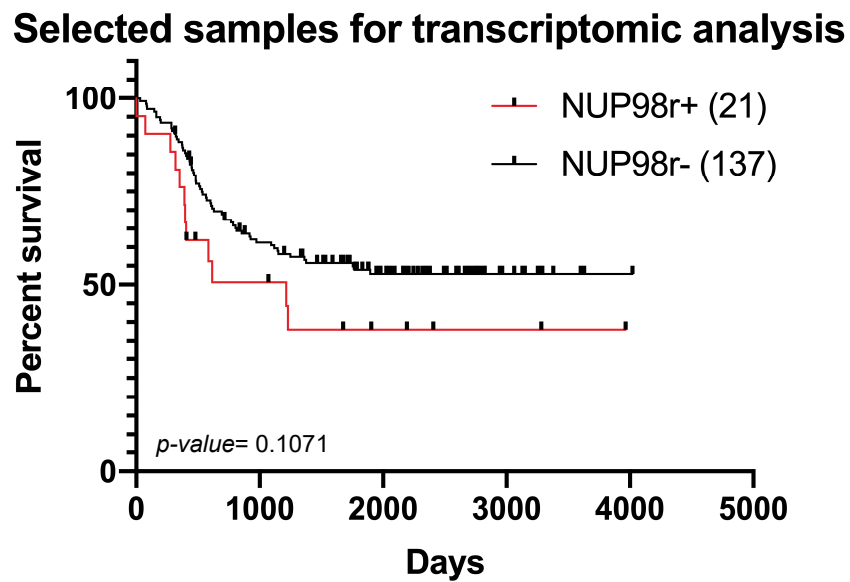
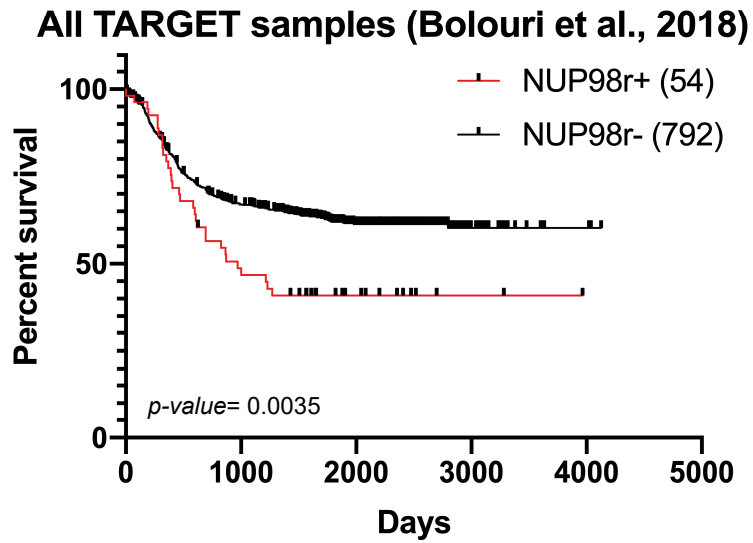


Figure S4. **Kaplan Meier curves showing the effect on Overall Survival of NUP98-rearrangements.** On the top, we show the effect of NUP98-rearrangements on overall survival in the entire cohort of TARGET program; on the bottom, the overall survival was calculated only in selected samples of TARGET program analyzed by transcriptome analysis.