Supplemental Figures

Fig. S1. Sample clustering based on varied numbers of the most variable differentially expressed genes (DEGs) in TCGA CN-AMLs. These numbers were tested: 100 **(A)**, 200 **(B)**, 250 **(C)**, 300 (Fig. 3B), and 400 **(D)**. Heat map representing the expression (DESeq2 normalized counts). We obtained the best classification from n=300.

Fig. S1

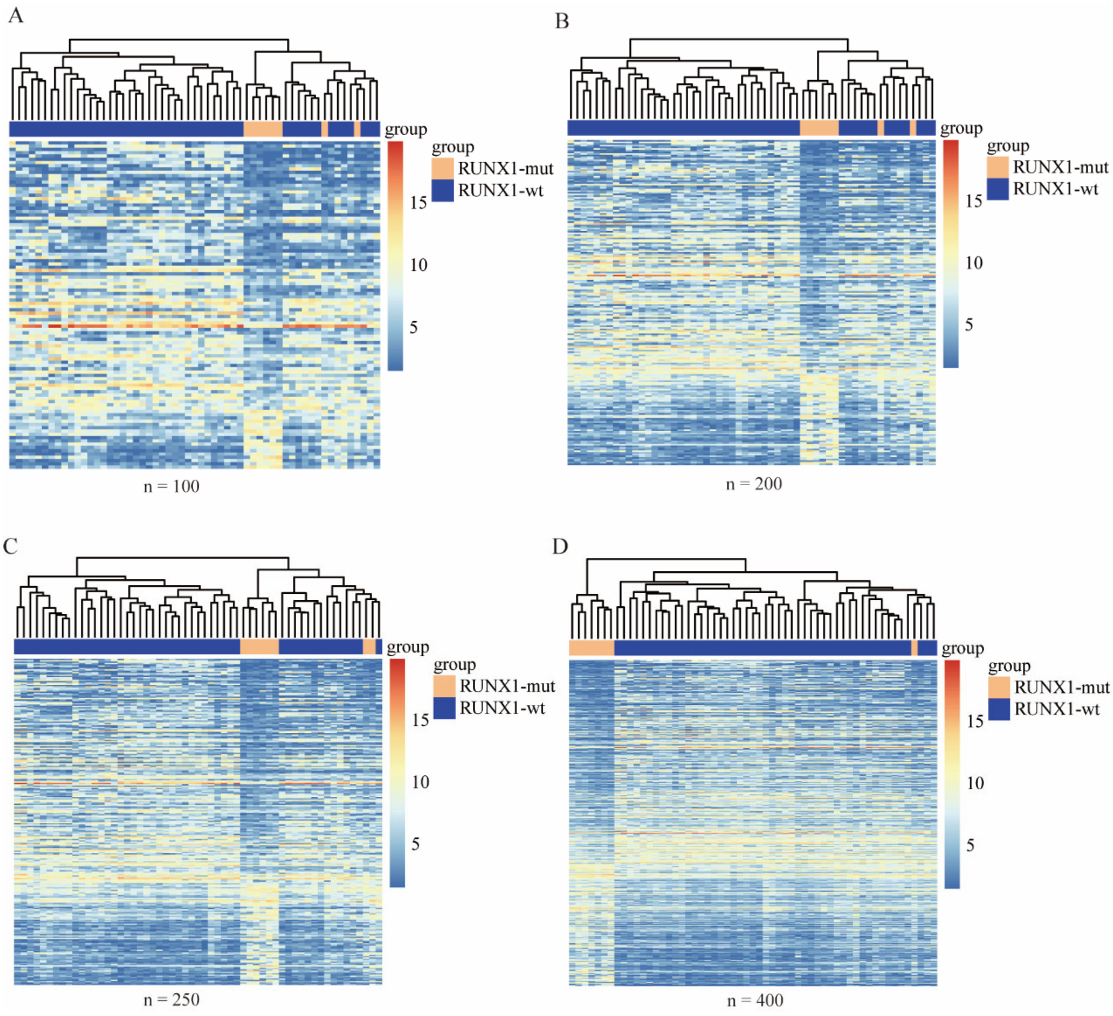

Fig. S2: The Kaplan-Meier plots of the overall survival of the TCGA patients with AML grouped by the expression levels of CD96 and LTK.