

Figure S1

Transcriptional level of TBCs and their prognostic analysis in AML patients.

(A) The transcriptional levels of TBCs in AML patients and normal subjects. Data were originated from TCGA-LAML and GTEx.

(B) The mRNA levels of *TBCB* in CB CD34⁺ cells and AML cell lines by RT-qPCR. Expression levels are normalized to 18S. CB, cord blood.

(C-F) No association between the mRNA levels of *TBCB* and the gender, age, cytogenetic risk and FAB classifications in AML patients.

(G-J) Kaplan–Meier survival curves of OS were drawn from AML patients grouped into high and low populations as per the median expression of *TBCC* (G), *TBCA* (H), *TBCD* (I) and *TBCE* (J). Data was originated from TCGA-LAML dataset.

(K-L) Kaplan–Meier survival curve of OS was delineated for AML patients grouped into high versus low expressed populations in line accordance with the median expression of *TBCB*. Data was originated from GSE71014 (K) and GSE12417 (L).

(M-P) Kaplan–Meier survival curve of OS was delineated for AML patients grouped by quartile boundaries of *TBCB* expression levels. Data was originated from TCGA-LAML (M), GSE37642 (N) GSE71014 (O) and GSE12417 (P).

One-way ANOVA was conducted with the results of RT-qPCR. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.

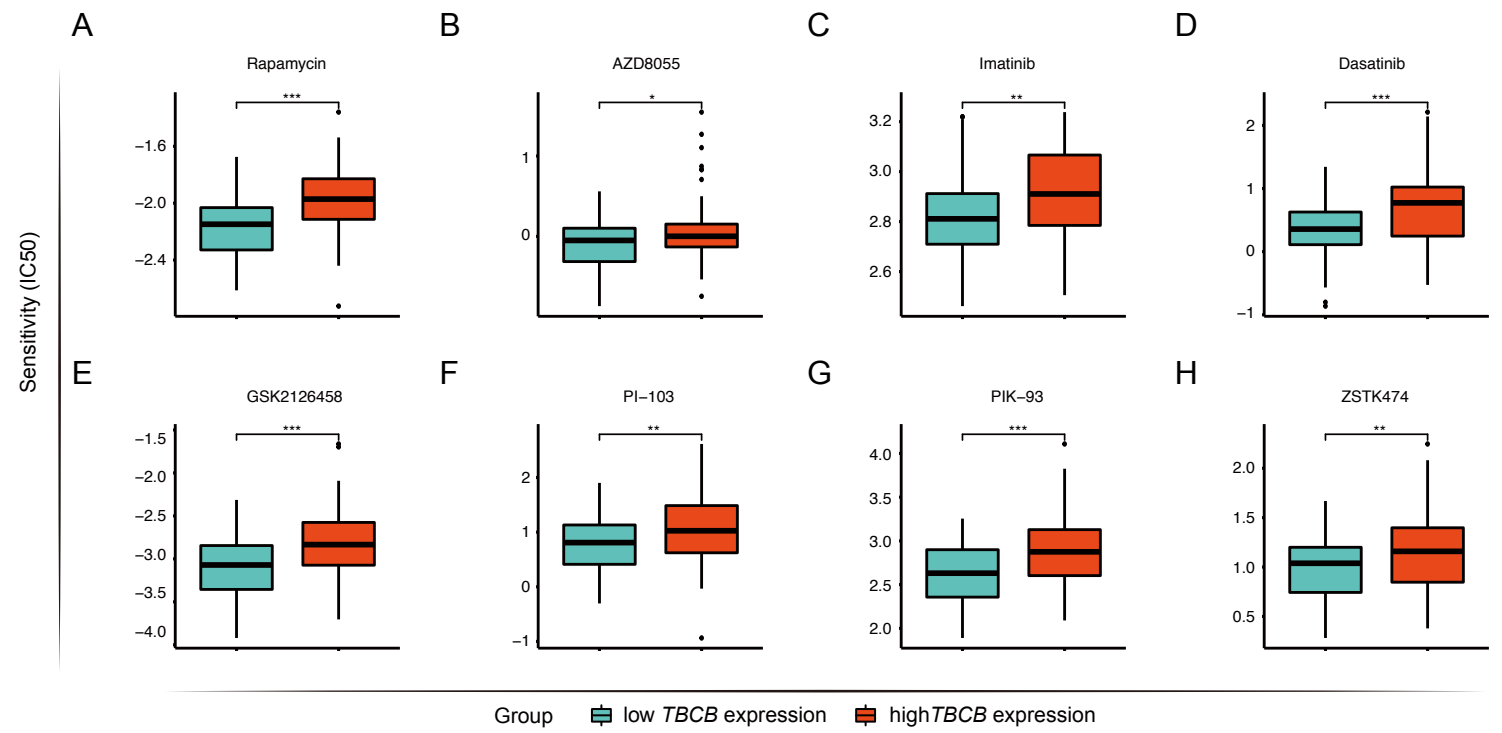


Figure S2

Prediction of drug resistance in high and low *TBCB* expression populations.

(A) Rapamycin. (B) AZD8055. (C) Imatinib. (D) Dasatinib. (E) GSK2126458. (F) PI-103. (G) PIK-93. (H) ZSTK474. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.