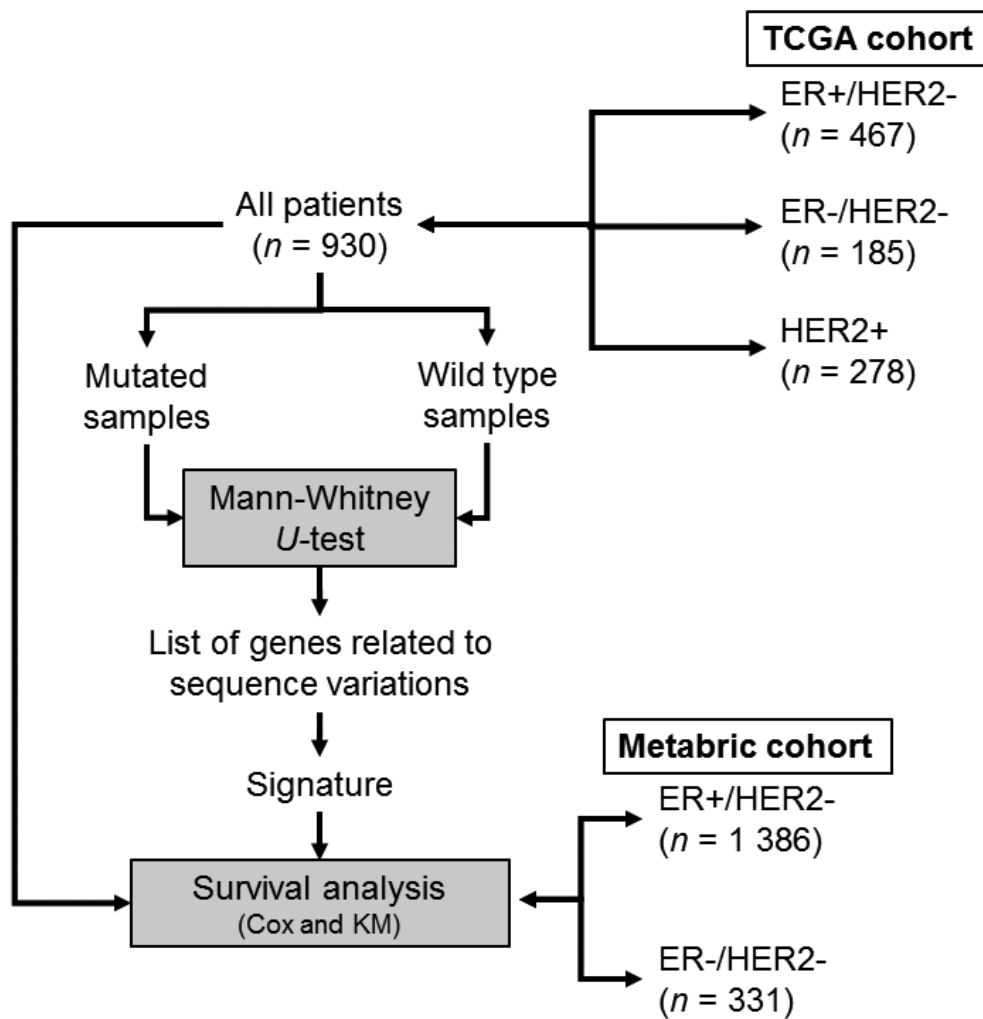
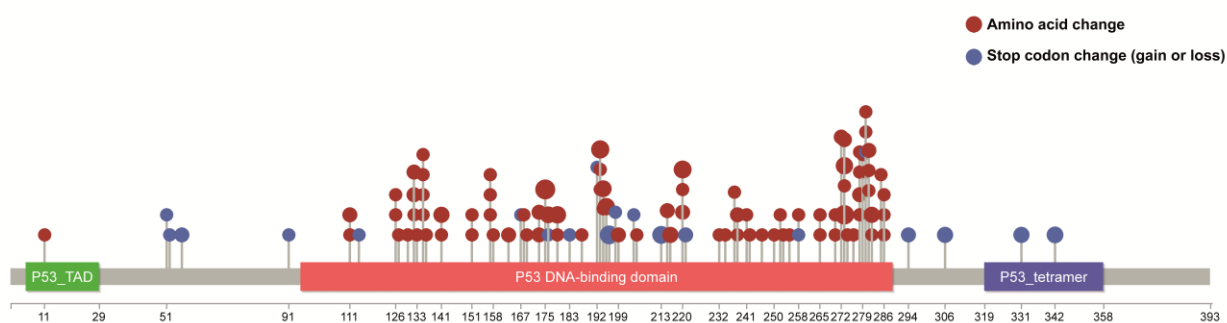
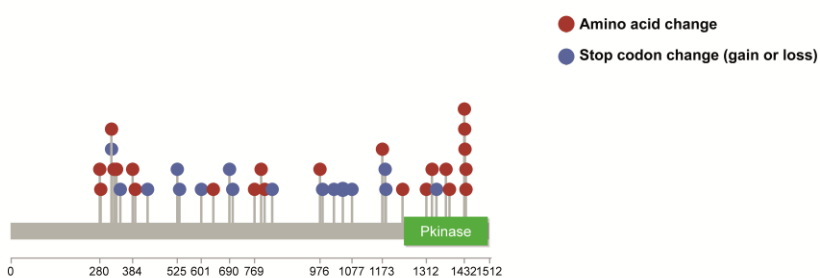
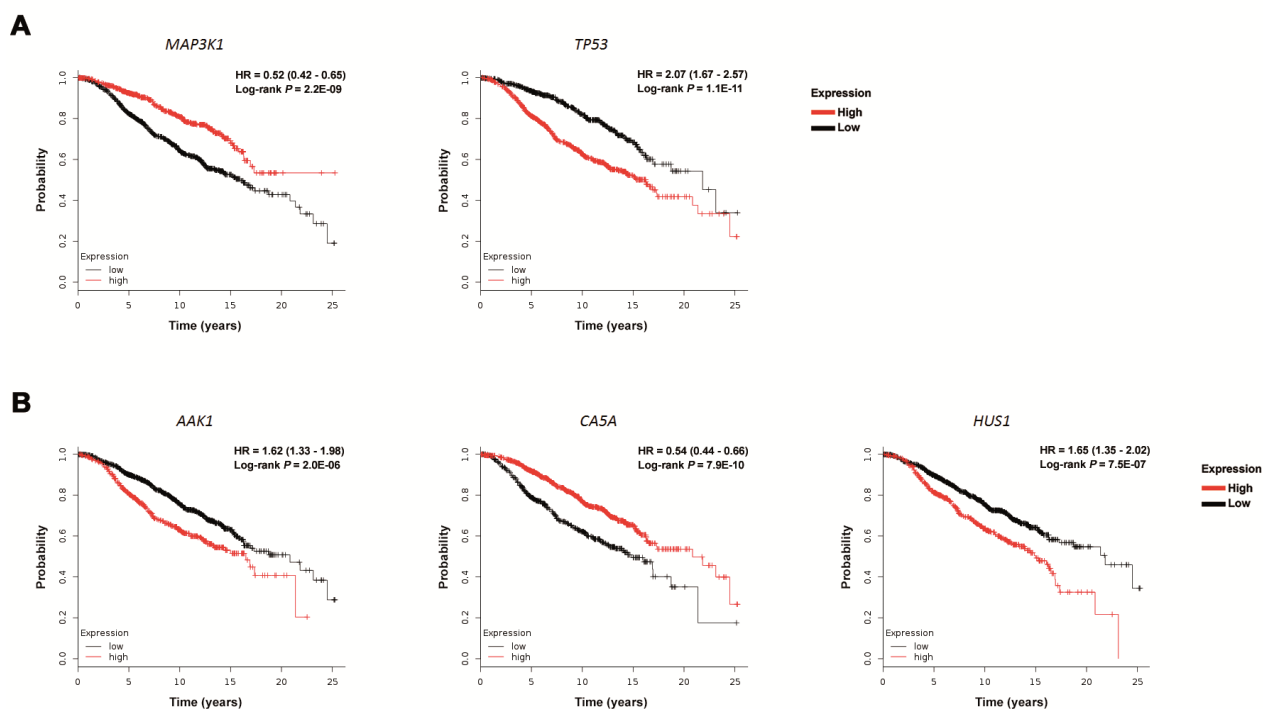




Supplementary Figure 1. Workflow of the study.

A**B**

Supplementary Figure 2. Coding mutations identified in TP53 and MAP3K1 genes. Needle plots depicting the type and distribution of mutations in *TP53* (A) and *MAP3K1* (B) genes. The length of each bar represents the number of mutations identified at each position. The horizontal axis represents the amino-acid sequence of genes.



Supplementary Figure 3. Prognostic value of expression signatures correlated with genetic variants in the validation cohort. (A) Kaplan-Meier analysis of overall survival for the signatures associated with mutations in the coding areas of *MAP3K1* and *TP53* genes in ER-positive/HER2-negative breast cancer. **(B)** Kaplan-Meier analysis of overall survival for the signatures associated with sequence variations in the non-coding regions of *AAK1*, *CA5A*, and *HUS1* genes in ER-positive/HER2-negative breast cancer.