

## **Supplementary Materials and Methods:**

Supplemental Bioinformatics and Biostatistics Methods (Figure 3)

Raw RNA sequencing data in BAM format and clinical data for TCGA-BRCA [1,2] project were downloaded from Genomic Data Commons (GDC)[3] using R (v3.4.4)[4] and extension package TCGAbiolinks (v2.6.12)[5]. Aligned reads were assembled into transcripts and quantified using Stringtie (v1.3.0)[6]. The annotation file was obtained from the GDC portal (<https://gdc.cancer.gov/about-data/data-harmonization-and-generation/gdc-reference-files>). The read count matrices were normalized and transformed using edgeR (v3.20.9)[7] and limma (v3.34.9)[8]. For the isoform p53 $\beta$ , its normalized counts were dichotomized into high and low levels by splitting the values at the cutoff selected by conditional [9] method from the R package partykit (v1.2-0)[10], and a Cox model was used to regress overall survival outcome on p53 $\beta$  levels in the patients with stage III/IV breast tumors. The asymptotic P-value presented has not been adjusted for multiple testing or for measurement errors in the isoform quantification from the sequencing reads

## **Supplementary References:**

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