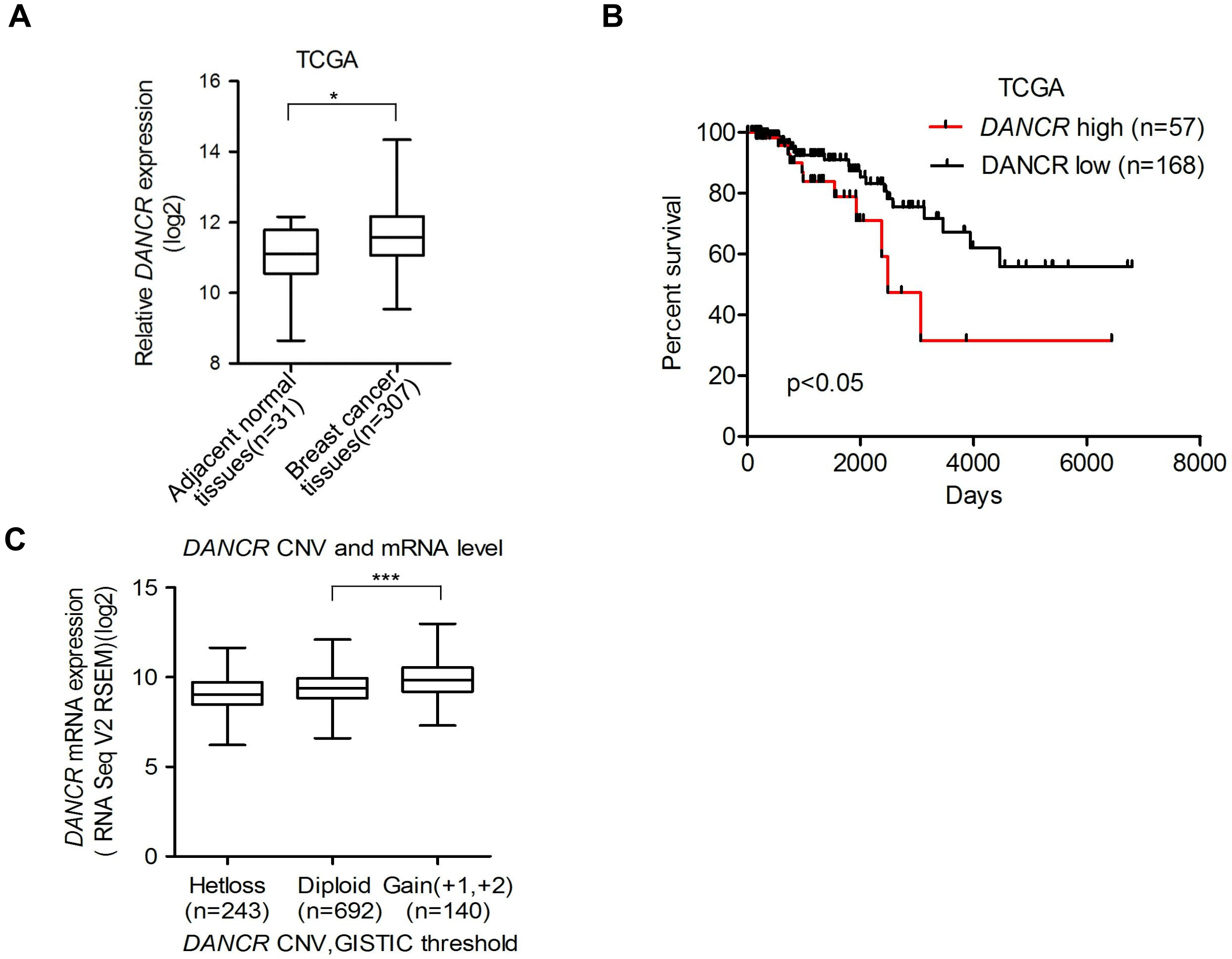

Supplementary Figure 1 Expression of *DANCR* in clinical breast cancer specimens
(A) *DANCR* mRNA expression levels are markedly higher in clinical breast cancer samples as compared to adjacent normal tissues. Data of *DANCR* mRNA expression were downloaded from the Cancer Genome Atlas (TCGA) microarray dataset. (B) Kaplan–Meier analysis of patients with high *DANCR* mRNA-expressing breast cancer versus low *DANCR* mRNA-expressing breast cancer from the TCGA microarray dataset. Statistical analysis was performed by log-rank test in a GraphPad Prism version 5.0 for Windows. (C) *DANCR* mRNA expression levels were markedly higher in samples with *DANCR* gained CNA compared with the samples without CNV in the TCGA dataset. Error bars ± SD. *, $P < 0.05$. *** $P<0.001$. Data are representative from two independent experiments.