

Supplementary Materials: Opposing Regulation of Cancer Properties via KRT19-Mediated Differential Modulation of Wnt/ β -Catenin/Notch Signaling in Breast and Colon Cancers

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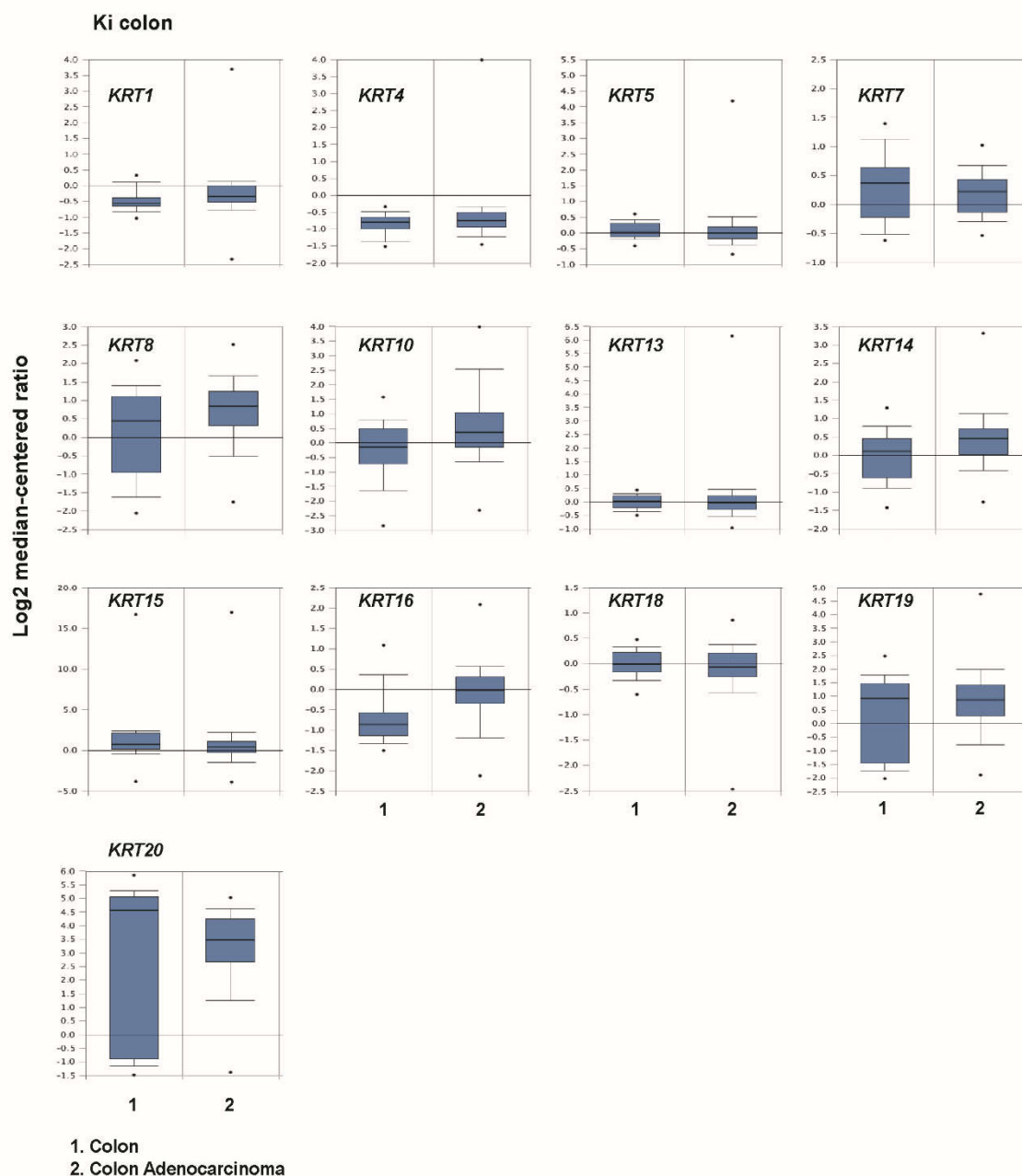


Figure S1. *KRTs* family genes expression analysis in colon cancer. Box plot comparing the expression of specific *KRTs* in normal (left plot) and cancer tissue (right plot) using data from the Oncomine database. Fold change in *KRTs* expression in colon cancer, shown as colon adenocarcinoma relative to normal colon tissue.

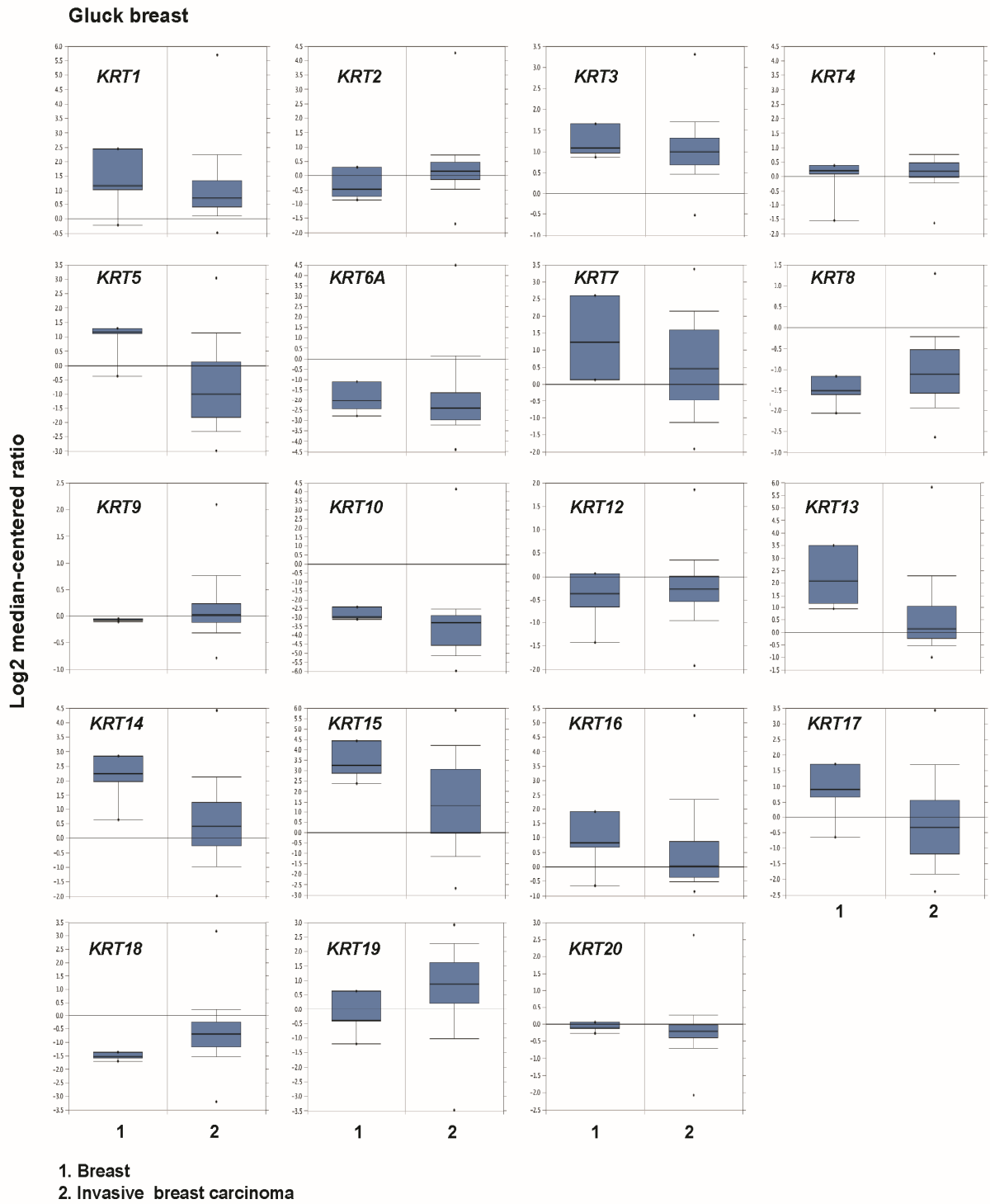


Figure S2. *KRTs* gene expression analysis in invasive breast carcinoma. Box plot comparing the expression of specific *KRTs* in normal (left plot) and cancer tissue (right plot) using data from the Oncomine database. Fold changes in *KRTs* expression in breast cancer, shown as invasive breast carcinoma relative to normal breast.

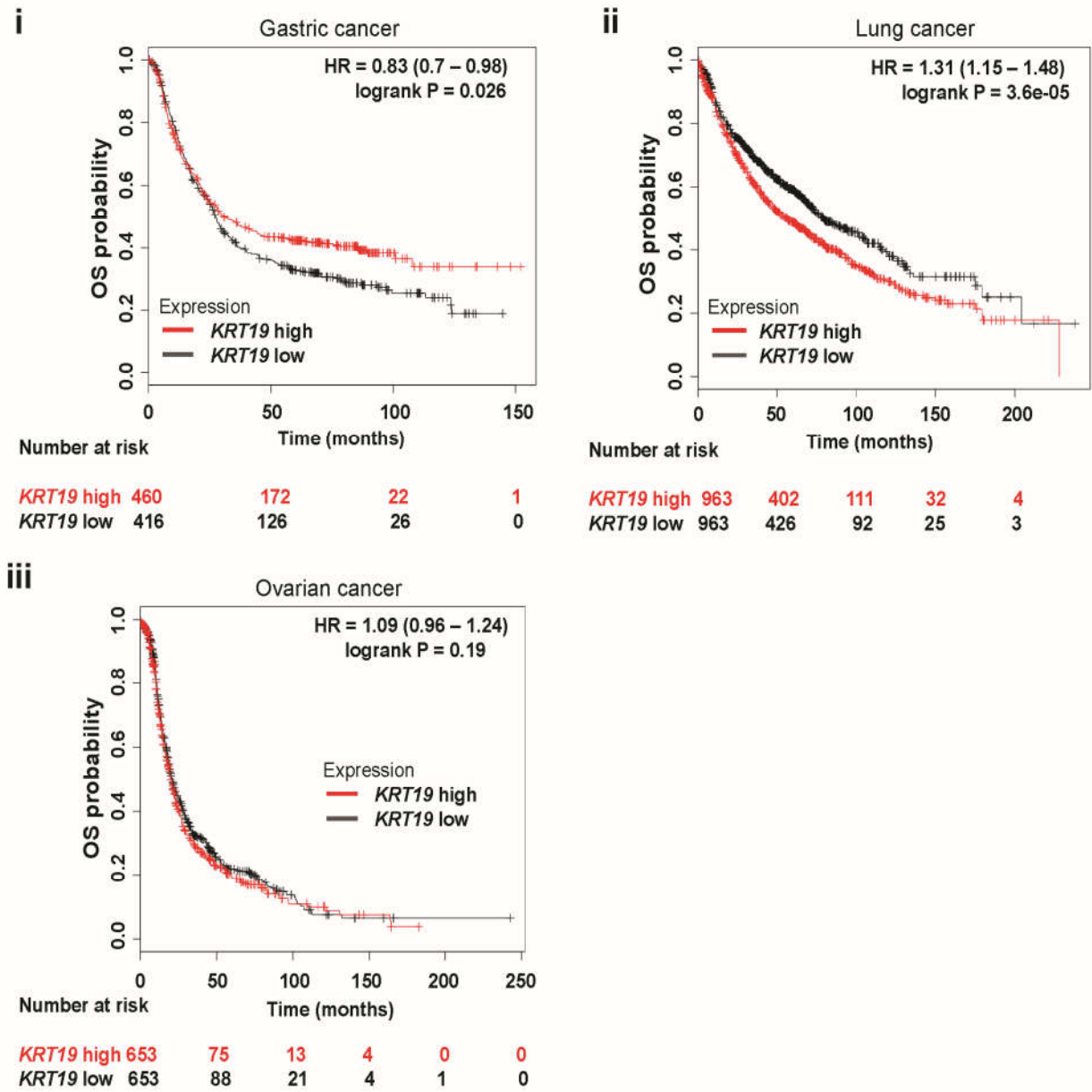


Figure S3. Kaplan-Meier curves for clinical outcomes of patients with (i) gastric cancer ($n = 876$), (ii) lung cancer ($n = 1926$), and (iii) ovarian cancer ($n = 1306$), using Kaplan-Meier Plotter database, with high (red) and low (black) expression levels of *KRT19*.

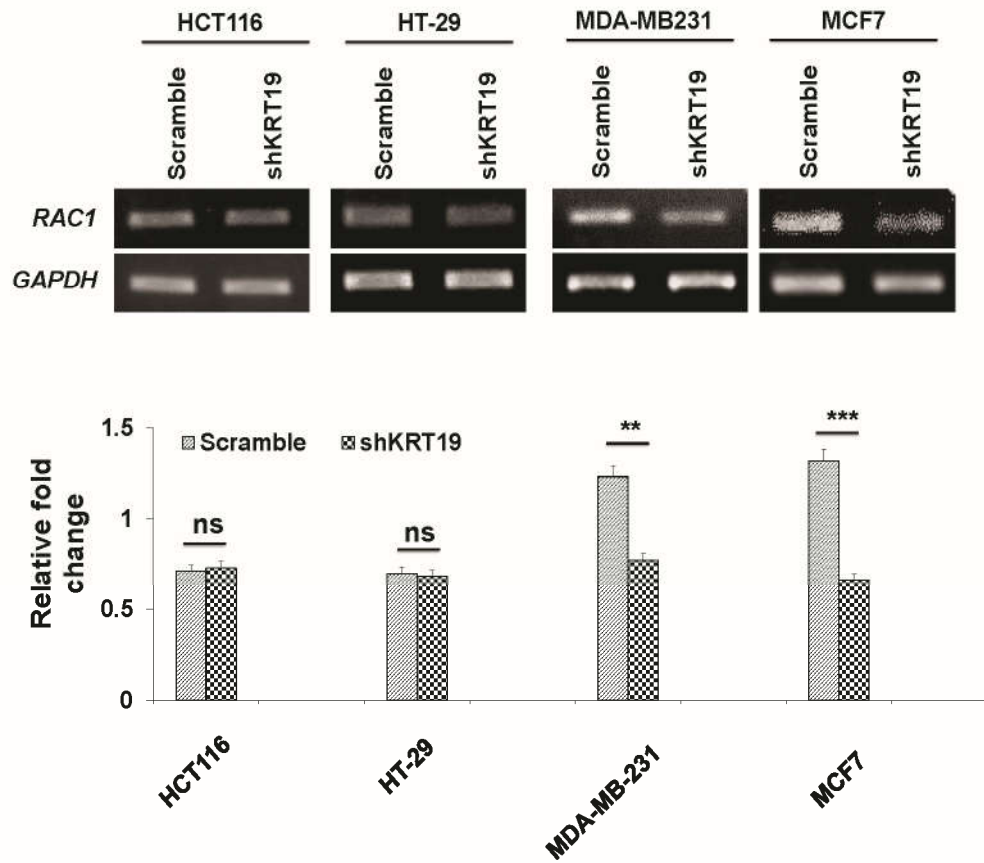


Figure S4. *RAC1* mRNA expression in scramble and shKRT19 cells analyzed by RT-PCR in the indicated cancer cell lines. *GAPDH* was used as a loading control. Bands were quantified by scanning densitometry and normalized to that of *GAPDH* (lower panel). Error bars represent \pm SDs of the means of three independent experiments (** $p < 0.01$, *** $p < 0.001$, ns = non-significant).

RAC1 mRNA sequence

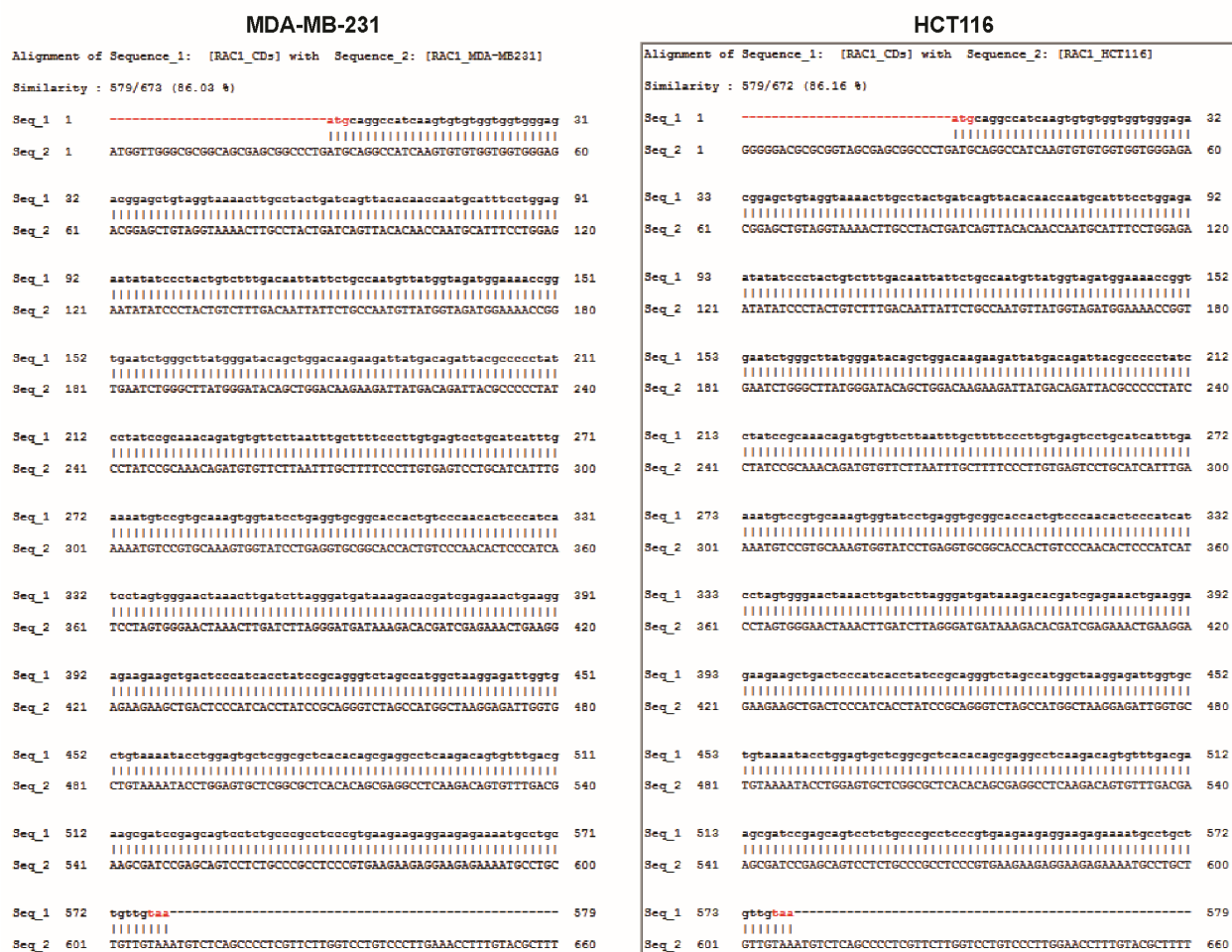


Figure S5. RAC1 cDNA sequencing performed using total RNA derived from MDA-MB231 and HCT116 cells.

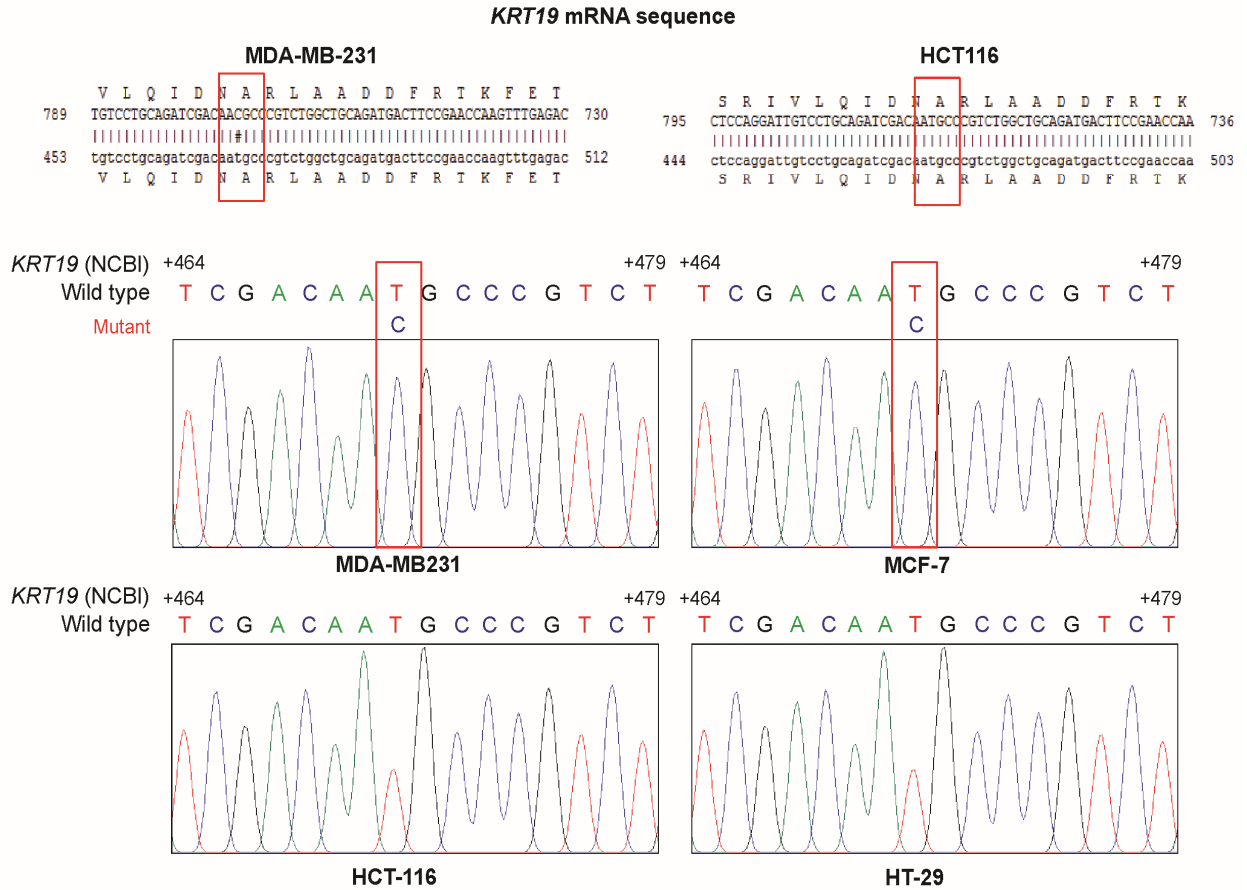


Figure S6. *KRT19* cDNA sequencing performed using total RNA derived from MDA-MB231, MCF7, HCT116, and HT29 cells. Chromatograms are shown for specific regions of sequences, and point mutations are indicated by red blocks.



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