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

Subbroto Kumar Saha, Yingfu Yin, Hee Sung Chae and Ssang-Goo Cho*

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 ± SDs of the means of three independent experiments (**p < 0.01, ***p < 0.001, ns = non-significant).
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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