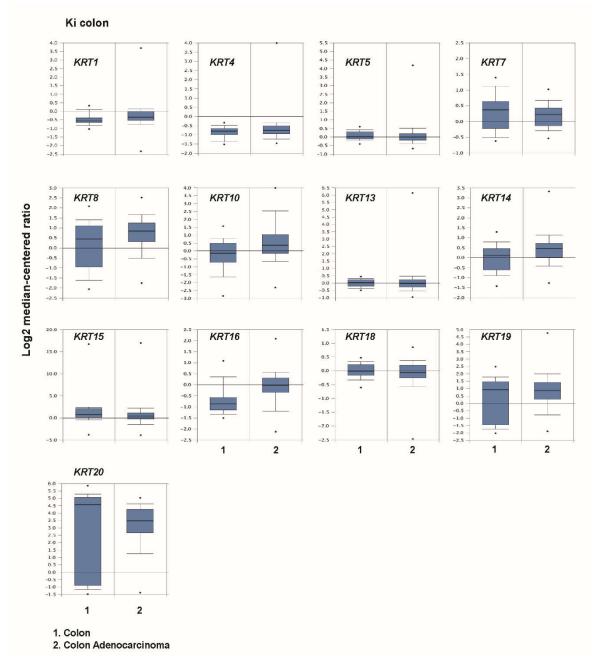




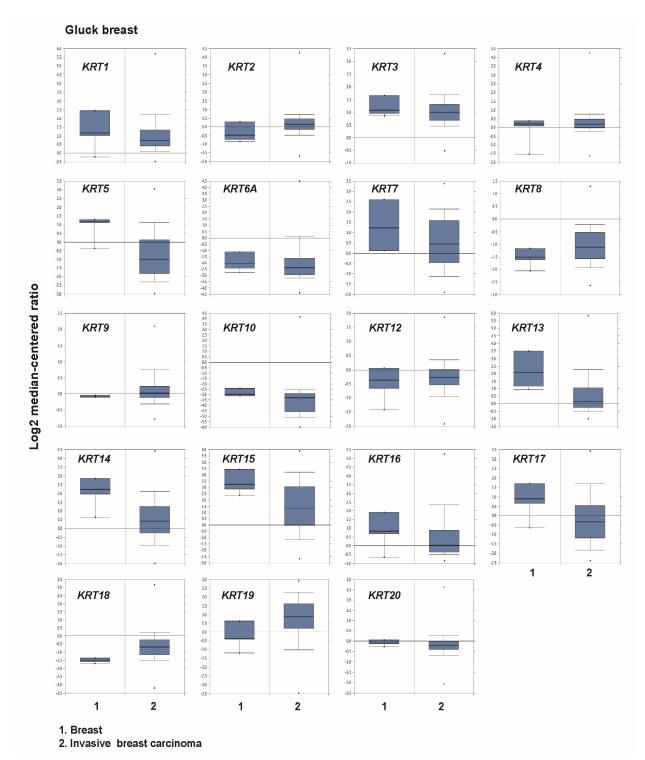
## Supplementary Materials: Opposing Regulation of Cancer Properties via KRT19-Mediated Differential Modulation of Wnt/β-Catenin/Notch Signaling in Breast and Colon Cancers

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



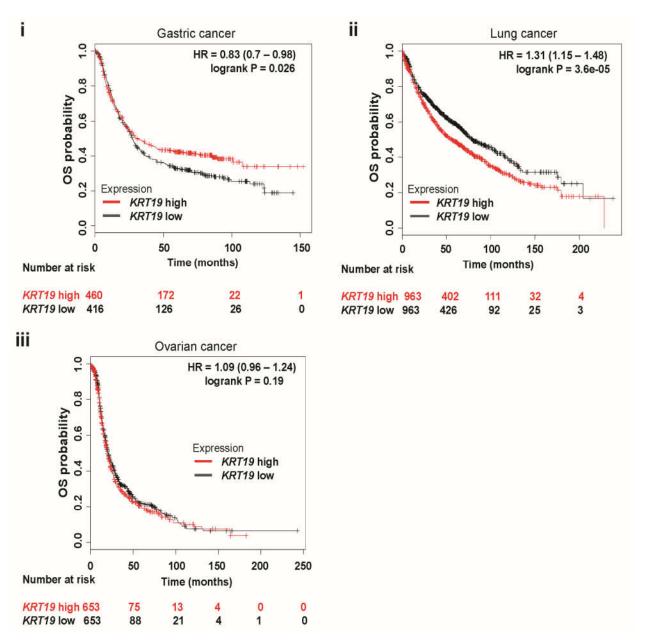
**Figure S1.** *KRTs* family genes expression analysis in colon cancer. Box plot comparing the expression of specific *KRTs* in normal (left plot) and cancer tissue (right plot) using data from the Oncomine database. Fold change in *KRTs* expression in colon cancer, shown as colon adenocarcinoma relative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

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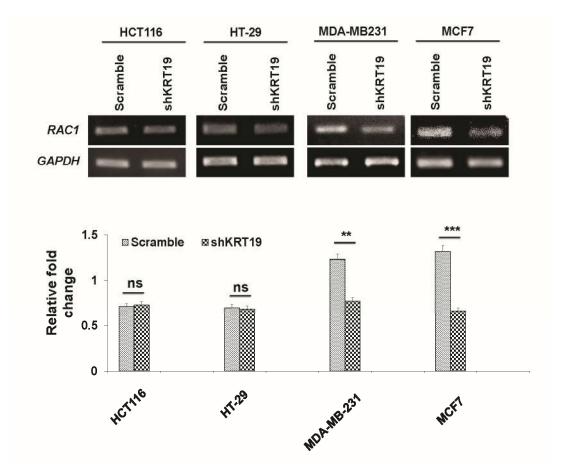
**Figure S2.** *KRTs* gene expression analysis in invasive breast carcinoma. Box plot comparing the expression of specific *KRTs* in normal (left plot) and cancer tissue (right plot) using data from the Oncomine database. Fold changes in *KRTs* expression in breast cancer, shown as invasive breast carcinoma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

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**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*.

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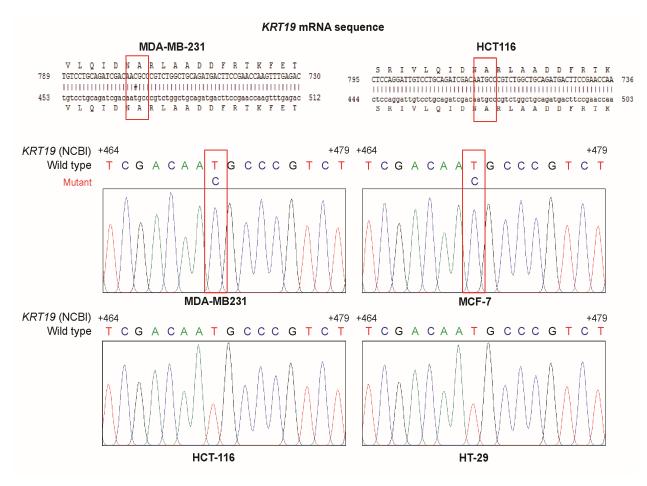
**Figure S4.** *RAC1* mRNA expression in scramble and shKRT19 cells analyzed by RT-PCR in the indicated cancer cell lines. *GAPDH* was used as a loading control. Bands were quantified by scanning densitometry and normalized to that of *GAPDH* (lower panel). Error bars represent  $\pm$  SDs of the means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

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## RAC1 mRNA sequence MDA-MB-231 **HCT116** Alignment of Sequence\_1: [RAC1\_CDs] with Sequence\_2: [RAC1\_HCT116] Alignment of Sequence\_1: [RAC1\_CDs] with Sequence\_2: [RAC1\_MDA-MB231] Similarity : 579/672 (86.16 %) Similarity : 579/673 (86.03 %) Seq\_1 1 atgcaggccatcaagtgtgtggtggtggtggaga Seq\_2 1 Seq\_2 1 GGGGGACGCGCGGTAGCGAGCGGCCCTGATGCAG Seq 1 33 cggagctgtaggtaaaacttgcctactgatcagttacacaaccaatgcatttcctggaga 92 Seq\_1 32 acggagctgtaggtaaaacttgcctactgatcagttacacaaccaatgcatttcctggag 91 Seq\_2 61 ACGGAGCTGTAGGTAAAACTTGCCTACTGATCAGTTACACAACCAATGCATTTCCTGGAG Seq\_2 61 CGGAGCTGTAGGTAAAACTTGCCTACTGATCAGTTACACAACCAATGCATTTCCTGGAGA Seq\_1 92 aatatatccctactgtctttgacaattattctgccaatgttatggtagatggaaaccgg 151 Seq\_1 93 Seg 2 121 Seq 2 121 Seq\_1 152 Seq\_1 153 gaatctgggcttatgggatacagctggacaagaagattatgacagattacgcccctatc 212 Seq\_2 181 Seq\_2 181 cctatccgcaacagatgtgttcttaatttgcttttcccttgtgagtcctgcatcatttg 271 Seq\_1 212 Seq\_1 213 ctatecgcaaacagatgtgttettaatttgetttteeettgtgagteetgcateatttga 272 Seq\_2 241 Seq\_2 241 CTATCCGCAAACAGATGTGTTCTTAATTTGCTTTTCCCTTGTGAGTCCTGCATCATTTGA aaabgboogbgcaaagbggbaboobgaggbgoggcaccacbgbcccaacacbcccabcab 332 Seq\_1 273 Seq 1 272 aaaatgtccgtgcaaagtggtatcctgaggtgcggcaccactgtcccaacactcccatca 331 Seq\_2 301 Seq\_2 301 Seq\_1 332 Seq\_1 333 Seq\_2 361 Seq\_2 361 gaagaagctgactcccatcacctatccgcagggtctagccatggctaaggagattggtgc 452 Seq\_1 392 agaagaagetgactcccatcacctatccgcagggtctagccatggctaaggagattggtg 451 Seq\_1 393 AGAAGAAGCTGACTCCCATCACCTATCCGCAGGGTCTAGCCATGGCTAAGGAGATTGGTC Seq\_2 421 Seq\_2 421 Seq 1 452 ctgtaaaatacctggagtgctcggcgctcacacagcgaggcctcaagacagtgtttgacg 511 Seq\_1 453 tgtaaaatacctggagtgctcggcgctcacacagcgaggcctcaagacagtgttttgacga 512 Seq\_2 481 CTGTAAAATACCTGGAGTGCTCGGCGCTCACACAGCGAGGCCTCAAGACAGTGTTTGACG Seq\_2 481 TGTAAAATACCTGGAGTGCTCGGCGCTCACACAGCGAGGCCTCAAGACAGTGTTTGACGA Seq\_1 512 Seq\_1 513 Seq\_2 541 Seq 2 541 Seq\_1 572 ----- 579 Seq\_1 573 --- 579 TTGTAAATGTCTCAGCCCCTCGTTCTTGGTCCTGTCCCTTGAAACCTTTGTACGCTTT 660 Seq\_2 601 GTTGTAAATGTCTCAGCCCCTCGTTCTTGGTCCTGTCCCTTGGAACCTTTGTACGCTTTT 660

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

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**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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