SUPPLEMENTARY DATA

Fig. S1. Effects of CaA on the viability of liver and/or breast cells

A total of 2×10^3 cells were seeded in 96-well plates for 24 h. At the time of next day, they were treated by 0 or 20 μM of CaA for 24, 48, or 72 h, respectively. Then, such cells were incubated with 20.0 μl of CCK-8 solution (Dojindo Molecular Technologies, Inc, Kumamoto, Japan) for another 4 h. The absorbance at 450 nm was measured with a multi-well plate reader (Model 680, Bio-Rad, USA). The relative folds of cell viabilities were determined by comparing growth of cells not exposed to CaA. Our data showed that, CaA did not appreciably affect the viabilities of these cells at the concentration of 20 μM (Fig. S1). Annotation, MHCC97H (HCC cell line), MDA-MB-231 (TNBC cell line), L-02 (human liver epithelial cell line), and MCF-10A (human breast epithelial cell line).

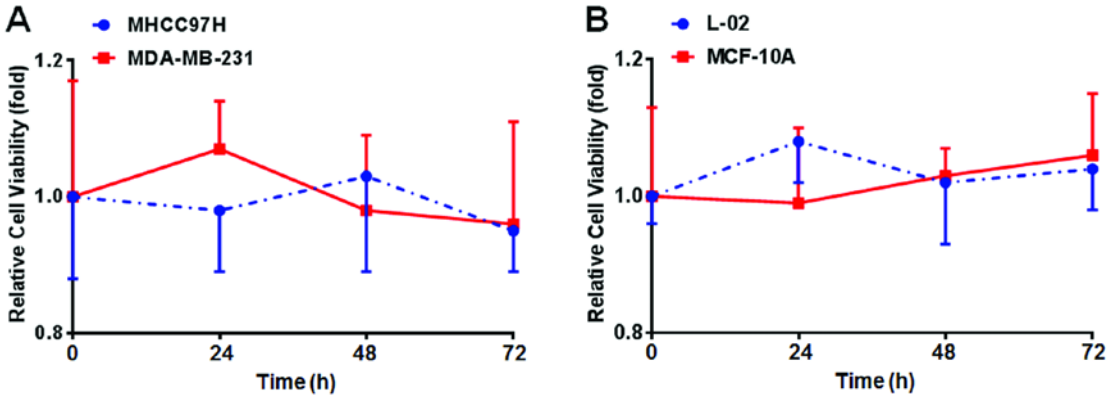

Fig. S2. The target sequences of miR-148a in the 3'-UTR of SMAD2

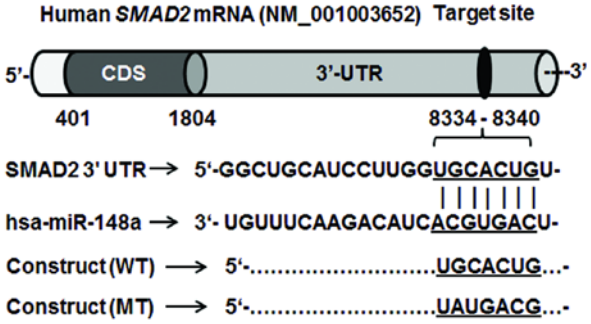

Fig. S3. CaA up-regulates the expression of miR-155 by demethylation

MHCC97H cells were treated by 0 or 20 μM CaA for 48 h, and the methylation status of miR-155 promoter regions were determined by qMSP. (A) Representative qMSP amplification curves for methylated (M) and unmethylated (U) miR-155. (B) Relative methylation ratio (mean ± SD, n = 3). **p <0.01 compared with medium control cells. (C) MHCC97H or MDA-MB-231 cells were treated by 0 or 20 μM CaA in the presence or absence of 100 μM SAM for 48 h, respectively. qRT-PCR analyses of miR-155 (mean ± SD, n = 3). *p <0.05 and **p <0.01 compared with medium control cells, and $^{\#\#}$p <0.01 compared with cells treated by 20 μM CaA alone. Annotation, the percentage of methylation in a sample was estimated using the following formula: methylation (%)= (M/M+U) ×100% = [1/(1+U/M)] ×100% = [1/(1+$2^{\Delta Ct}$)] ×100%.