

Supplementary Figure Legends

Fig. S1. Copy number (CN) distribution of normal samples. The plot shows the copy number distribution of the genome of peripheral blood mononuclear cells (PBMCs) (n=60). The copy number of 99.5% of the genome is between 1.7 and 2.3. This plot was used to establish the boundaries of what is called gained (CN > 2.3) and lost (CN < 1.7).

Fig. S2. Representative HIF1 α and HIF2 α staining of fresh frozen tumors classified as H1H2 and H2. Please note nuclear HIF α staining (arrows) in these samples.

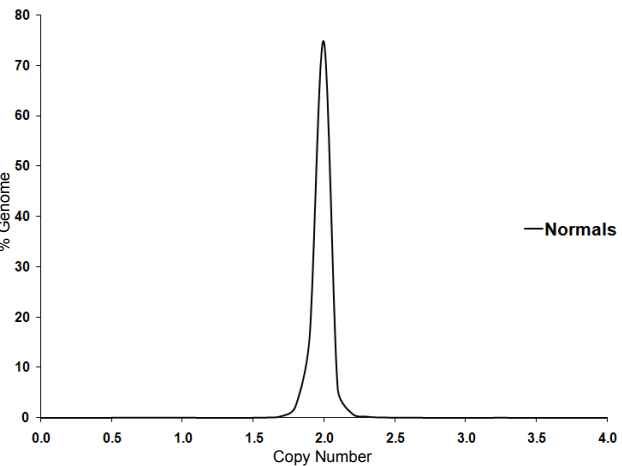
Fig. S3. Validation of *EZH2*, *STC2*, and *VCAN*. (A) Reduced cell numbers observed after silencing targets in RCC10 cells. (B) Increased cell death observed after silencing the targets in RCC10 cells. (C) Western blot analysis of targets of interest after silencing targets in 786-O and RCC10 cells. * represents P < 0.05.

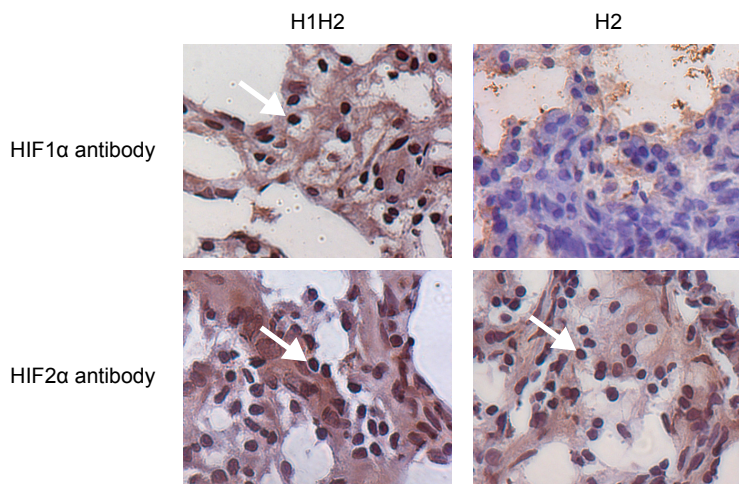
Fig. S4. Flow cytometry analysis in 786-O cells. (A) Representative plots of the BrdU incorporation studies. (B) Representative plots of the FITC-Annexin V and PI staining analysis.

Fig. S5. *STC2* and *VCAN* combination siRNA analysis in 786-O cells. (A) Verification of knockdown by qRT-PCR. (B) Relative cell numbers observed after silencing the targets. (C) Cell death observed after silencing the targets.

Fig. S6. TUNEL analysis. (A) Average percentage TUNEL positive nuclei. (B) Representative images of TUNEL stained sections (400X magnification).

Figure S1





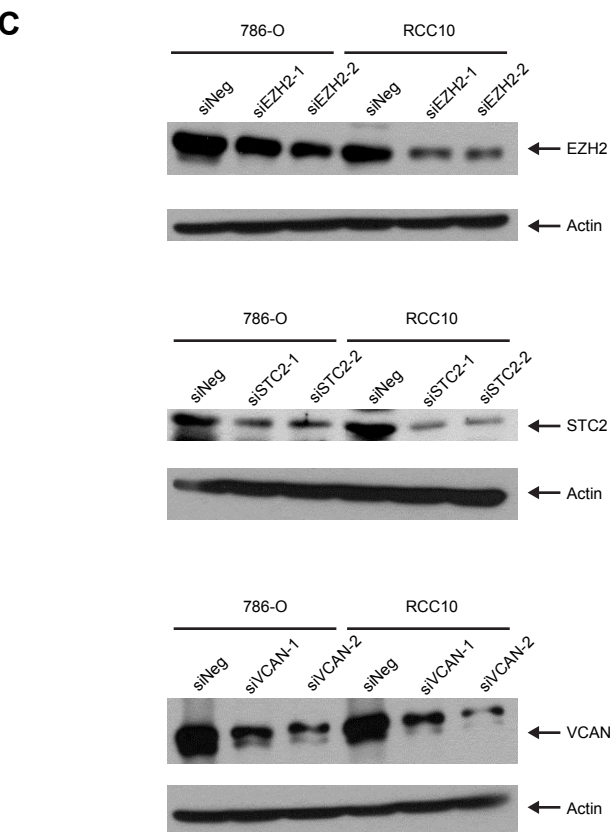
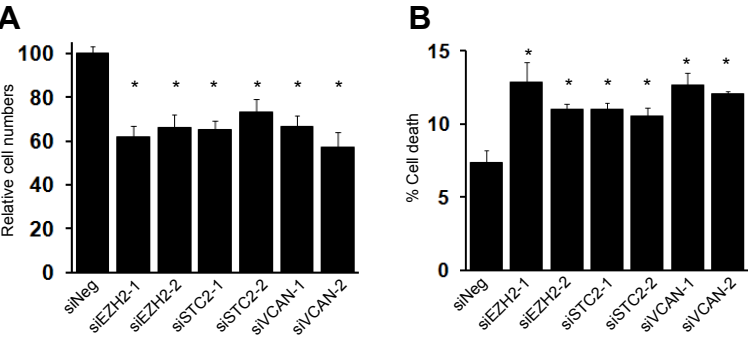


Figure S4

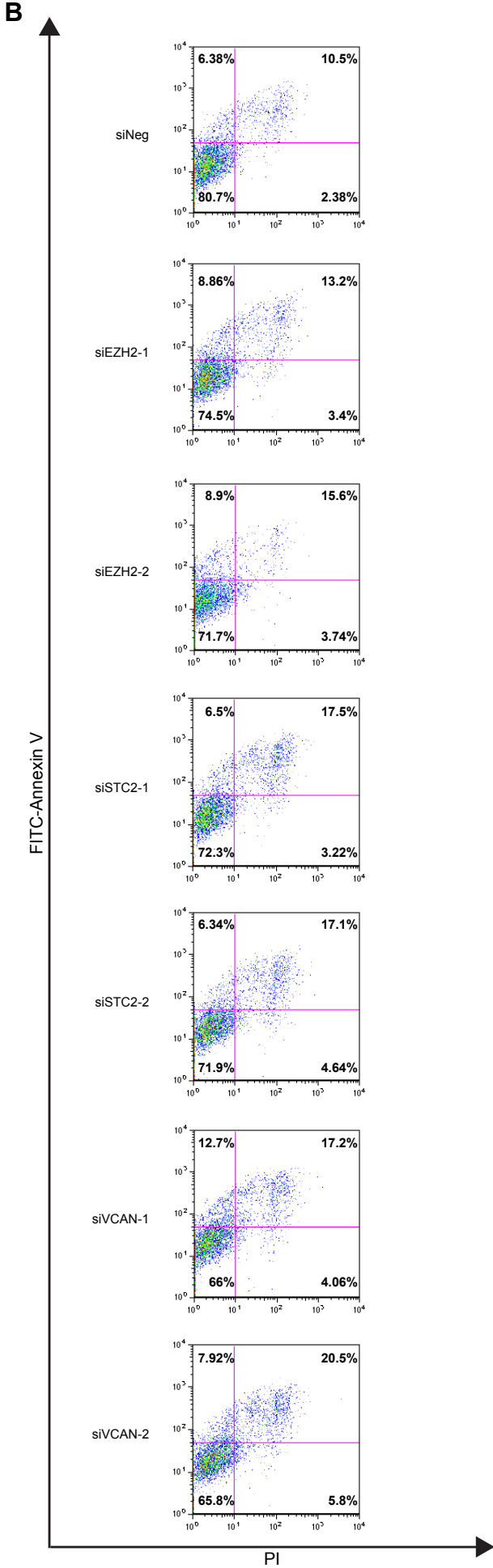
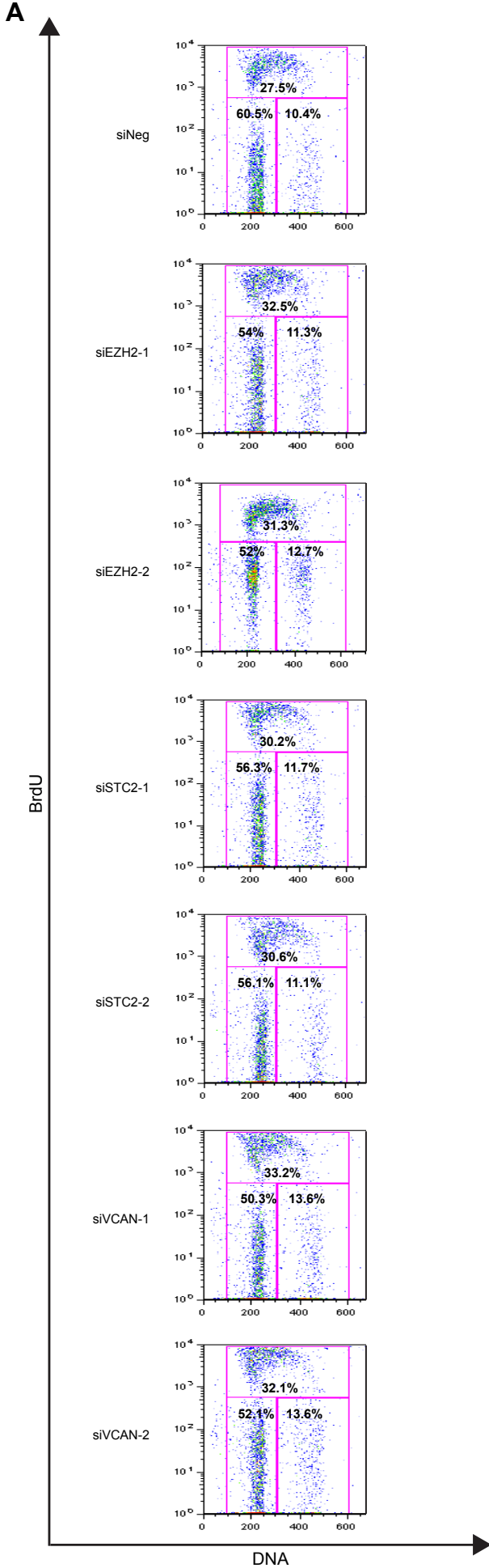


Figure S5

Dondeti et al. (2011)

