Supplementary Methods

Segment analysis. Due to the variability in aberration patterns from sample to sample, the genomic segmentation pattern is different for each sample. Therefore, from the segmentation data it is not possible to readily identify regions that are aberrant in at least 10% of samples. In order to be able to do this a novel algorithm called Most Parsimonious Segments (MPS) was developed (manuscript in preparation). The MPS algorithm takes the GLAD segmented data for all the samples as input and resegments the data to give the minimum number of segments needed such that all the samples have the same segmentation pattern and the copy number data is consistent with the original GLAD data. MPS is applied individually to each chromosome, from the start of the chromosome to the end. The algorithm examines the first segment in all samples for a given chromosome and identifies the shortest segment. The first segments of all samples then are resegmented to match the length of the shortest segment and this becomes the first segment of all the samples. The remainders of the longer segments become their own segments and are assigned the copy number of the parent segment from which they were derived. Then, the next segment is examined across all the samples and the process is repeated until the end of the given chromosome is reached. Then the process is repeated for all the chromosomes. Upon completion of the MPS, all the samples will have the same genomic segmentation pattern, and the copy number data is consistent with the original GLAD data, since the copy number of each segment is not altered in any way. MPS resulted in a total of 7,860 segments with an average length of 350 kilobases.

RNA extraction and qRT-PCR. Total RNA was extracted with TRIzol Reagent (Invitrogen) according to the manufacturer's protocol. cDNA was synthesized using the High Capacity RNA-to-cDNA Kit (Applied Biosystems). qRT-PCR analysis was done on an Applied Biosystems 7900HT instrument. mRNA levels were quantified using TaqMan assays for the targets of interest and values were normalized to 18S rRNA.

Western blot analysis. Cell lysis was performed using RIPA buffer. 20 µg of protein from each sample was run out on an 8% PAGE gel. Manufacturer's protocols were followed for the detection of *EZH2* (#5246 from Cell Signaling Technology), *STC2* (#AB63057 from Abcam), and *VCAN* (#16770002 from Novus Biologicals).

TUNEL staining. TUNEL staining was performed in accordance with the manufacturer's protocol (TumorTACS™ In Situ Apoptosis Detection Kit [4815-30-K] from Trevigen). After staining, the average percentage of TUNEL positive nuclei was calculated for each tumor from five independent fields of view.