SUPPLEMENTAL FIGURES

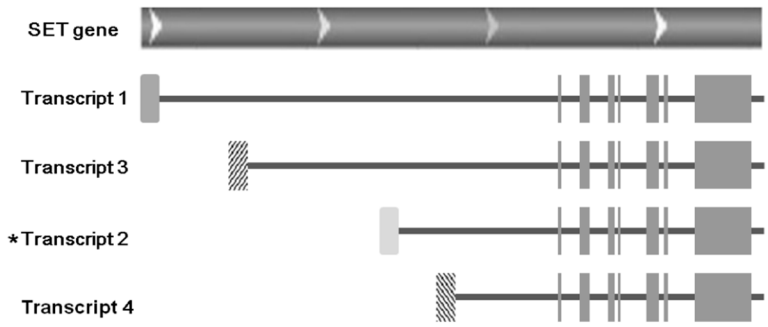

Figure S1. SET transcript variants produced by alternative promoters. SET gene is 19,742 bp long and located at human chromosome 9q34. It generates four transcription variants with transcript 1 and 2 being the two major transcripts. Gray boxes represent exons. Each SET variant is consists of 8 exons. Note the divergent exon 1 among the transcript variants. *, the transcript which we focused on in this study.

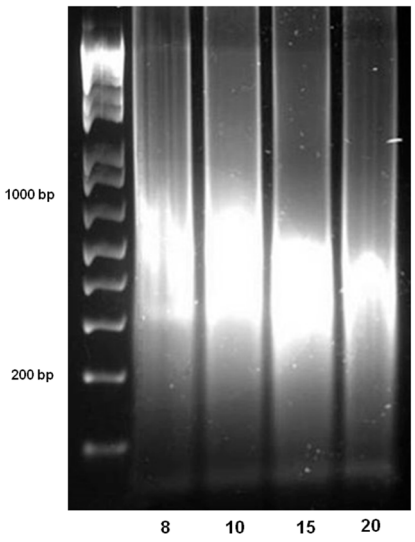

Figure S2. Optimization of sonication. Increasing number of bursts, ranging from 8 to 20, was applied. Following sonication, DNA was freed from chromatin, isolated, and resolved in agarose gel (2 %) electrophoresis. Numbers at the bottom shows the sonication times. 15 times of 15 s sonication bursts with 15 s intervals is optimal for achieving 200-1000 bp lengths of DNA fragments, an ideal length range for ChIP assay.

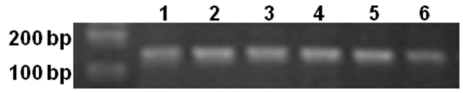

Figure S3. High specificity of real-time PCR. To determine the specificity of real-time PCR used for the measurement of ZFX expression level. Final real-time PCR products (35 cycles) were resolved by electrophoresis using 1.5% agarose gel. Left lane is the DNA markers. Lanes 1-3: Real-time PCR products of triplicate controls transfected with pEF1-vector; Lanes 4-6: Real-time PCR products of the triplicate ZFX overexpression group transfected with pEF1-ZFX. The clear, single DNA band with predicted size of 133 bp indicated a high PCR specificity has been achieved, and the CT values accurately measured the ZFX transcript levels.

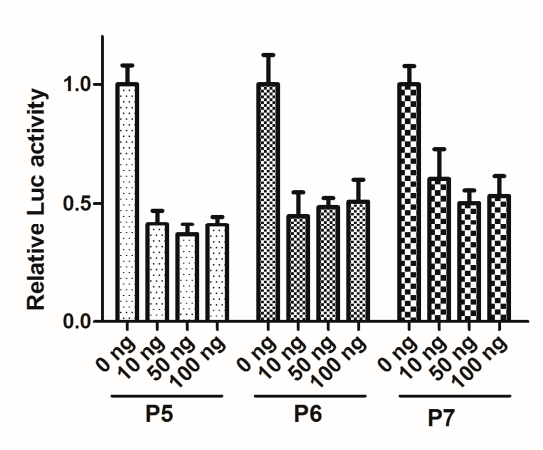

Figure S4. E2F3a displayed similar inhibition activity in P5, P6 and P7 promoters. HeLa cells were co-transfected with different amounts of pCMV-E2F3a (0-100 ng, pCMV-vector was used as "stuffer" to keep a constant DNA amount) and 100 ng of P5, P6 or P7 reporter plasmids. Luciferase activity was measured at 24 h post-transfection. A uniform inhibition was observed in all the three promoter constructs tested, suggesting either a non-specific nature of the effect or the presence of an negative element(s) further downstream of the deleted region. Quantitative data is presented as means±SD from three independent experiments. (*, $p<0.05$).