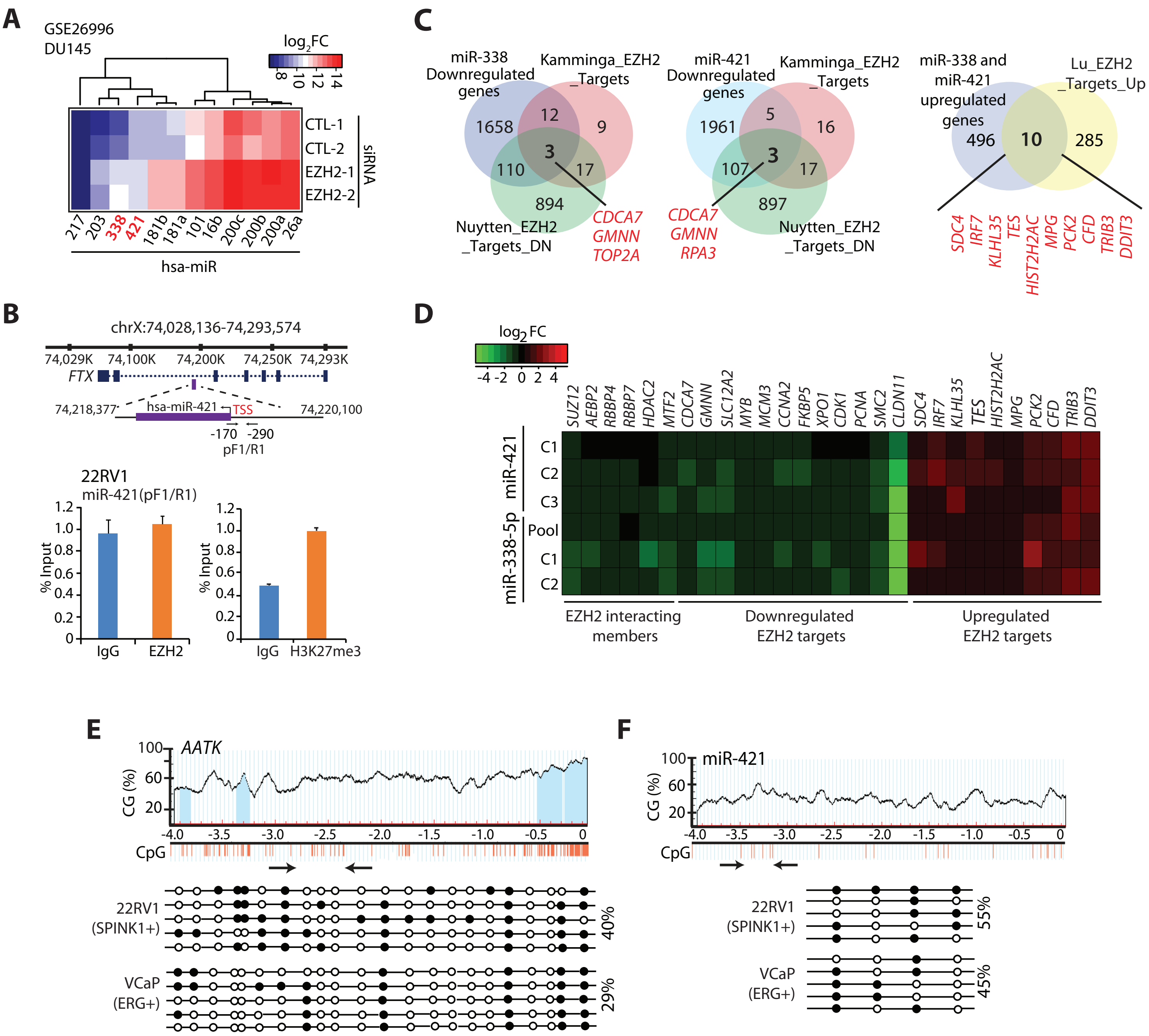
Supplementary Figure S7



Supplementary Figure 7. MiR-338-5p and miR-421 are epigenetically silenced by EZH2 in SPINK1-positive prostate cancer. **A.** Heatmap showing EZH2-regulated miRNAs, including miR-338-5p and miR-421 in DU145 cells (GSE26996). Shades of red and blue represents $\log_2$ fold-change in miRNA expression. **B.** Schematic of EZH2 binding sites in a region upstream of miR-421 (top panel). ChIP assay showing occupancy of EZH2 on the miR-421 promoter. **C.** Venn diagram showing the overlap of genes downregulated and upregulated genes in 22RV1-338-5p and 22RV1-miR-421 cells with Kamminga_EZH2 targets; Nuytten_EZH2_targets_DN and Lu_EZH2_targets_UP respectively. **D.** Heatmap depicts the change in expression of PRC2 complex members and their target genes in 22RV1-miR-338-5p and 22RV1-miR-421 cells. **E.** Schematic represents the presence of CpG methylation marks on the promoter region of AATK (top panel). Bisulfite–DNA sequencing of the promoter region of *AATK* in 22RV1 (SPINK1+) and VCaP (ERG+) cells. **F.** Same as in (E), except bisulfite sequencing of miR-421. Data represents DNA sequences obtained from five independent clones. Hollow circles represent non-methylated CpG dinucleotides, whereas black solid circles show methylated CpG sites. Bar plot data represent mean ± SEM. $*P \leq 0.05$ and $**P \leq 0.001$ using two-tailed unpaired Student's *t* test.