



**SUPPLEMENTARY FIG. S3.** Thyroid cancer cell lines show TSS methylation level correlated with *TERT* promoter mutation status. Read-level methylation plots using IGV for heterozygous *TERT* mutant thyroid cancer cell lines (A) BCPAP and (B) FTC-238, homozygous mutant (C) FTC-133, and homozygous wild type (D) WRO at the promoter and gene body for *TERT*. Depth of coverage at the *TERT* gene is shown in the top graph where the coverage at each base is shown by the gray line plot with the minimum and maximum CpG coverage stated. Each horizontal line in the mutant and wild-type allele depiction is a single nCATS read sorted based on the *TERT* promoter mutation as mutant or wild type, where red denotes a methylated CpG and blue denotes an unmethylated CpG. The *TERT* chromosomal coordinates are shown at the bottom to designate position. IGV, integrative genome viewer; TSS, transcription start site.