

Figure S1. Overall THOR methylation levels. Box-and-whisker plot shows the distribution of overall (non allele-specific) THOR methylation level in the tumor types.

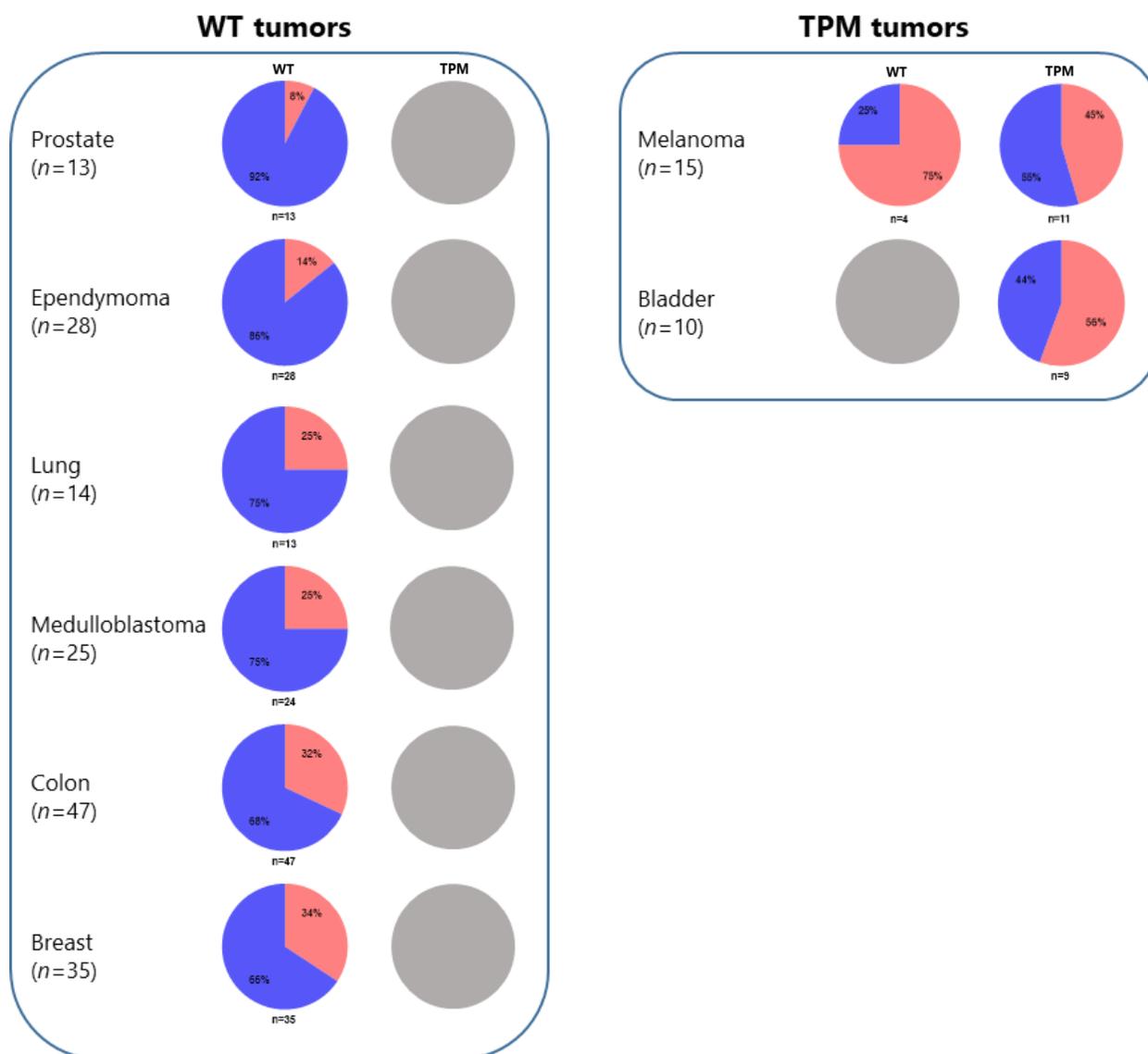


Figure S2. Prevalence of THOR-DAM in each cancer type. Each pie chart pair include the data for WT (left) and TPM (right) tumors. In all tumor types included in this figure, the tumors were almost entirely WT (under WT tumors) or TPM (under TPM tumors). Blue and red pies indicate presence and absence of THOR-DAM attribute, respectively. Grey pies indicate that one or no tumor sample was available ($n \leq 1$).

TPM gliomas ($n=15$)

WT gliomas ($n=4$)

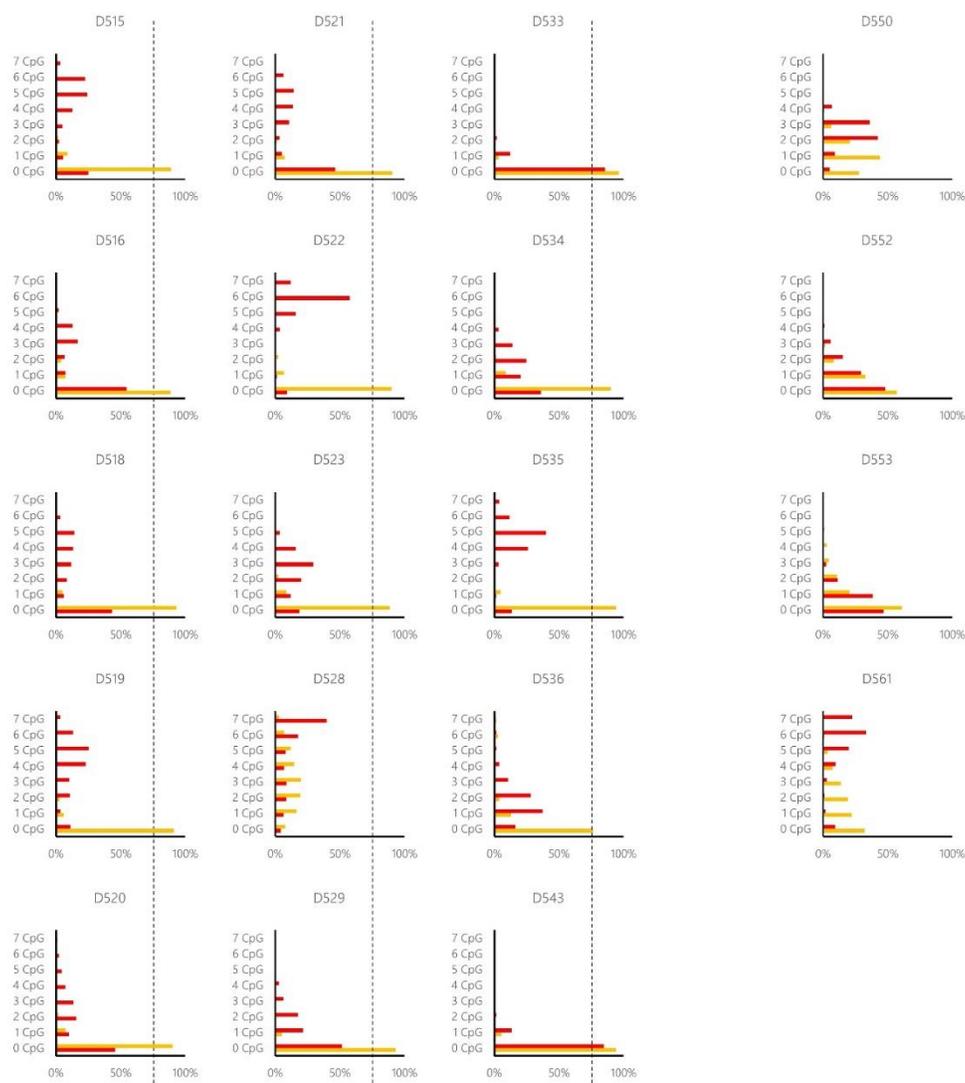


Figure S3. Proportion of allele-specific sequencing reads in glioma sub-cohort ($n=19$). Bar graphs indicate the proportion of sequencing reads separated based on the number of methylated CpG sites within each read. Red and yellow bars show data for low methylated and high methylated alleles respectively. (Dotted vertical line at 75% of sequencing reads to demonstrate the samples that exhibit high frequency of completely unmethylated sequencing reads).

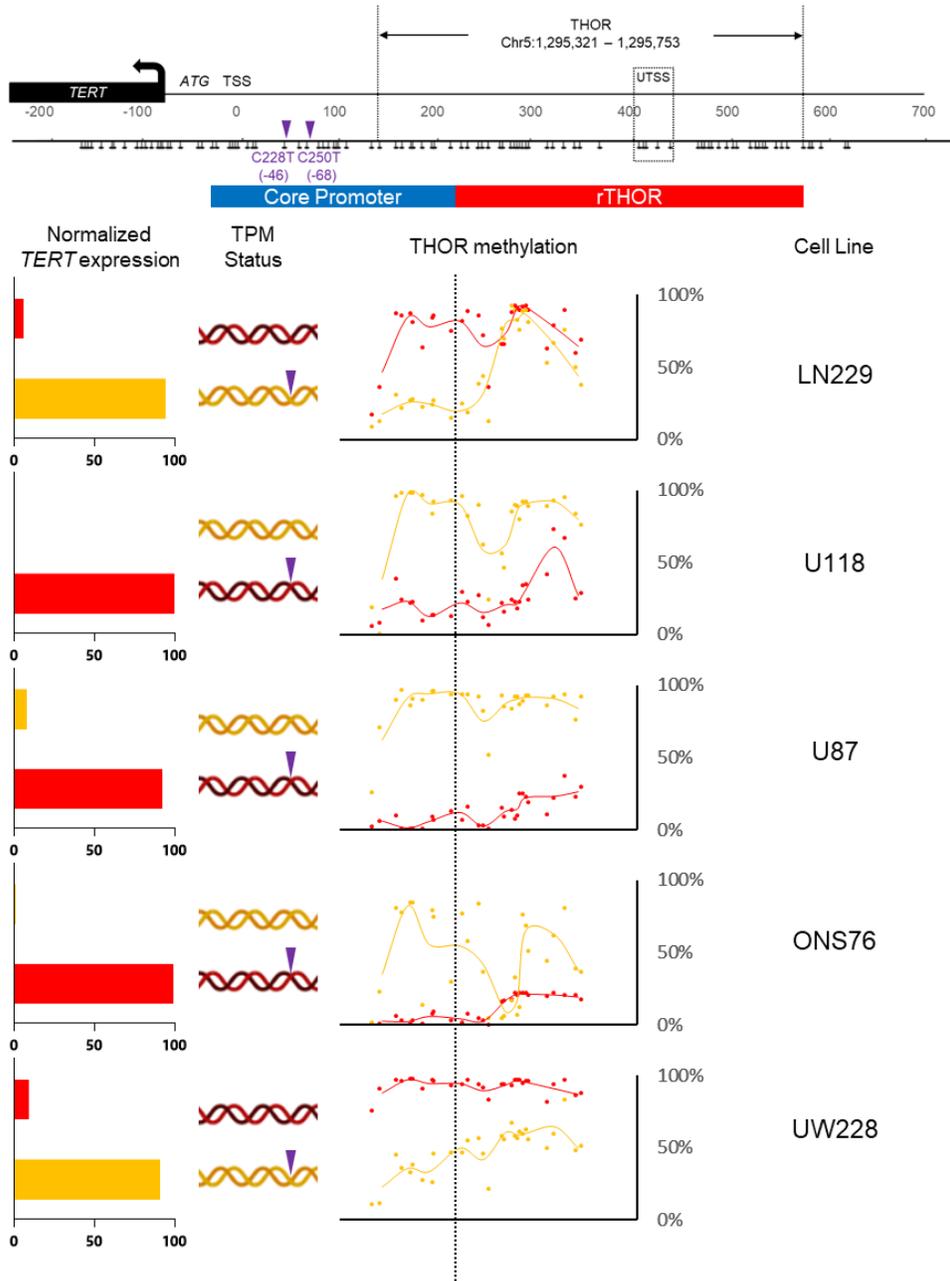


Figure S4. CpG methylation patterns of the *TERT* promoter in TPM cancer cell lines. Red and yellow colors indicate each of the alleles separated based on the promoter SNP and exon SNP. Line graphs with dots (raw values) indicate levels of CpG methylation in the *TERT* promoter. Position of purple triangle (TPM) shows which allele harbors TPM. Bar graphs show normalized allelic *TERT* expression.

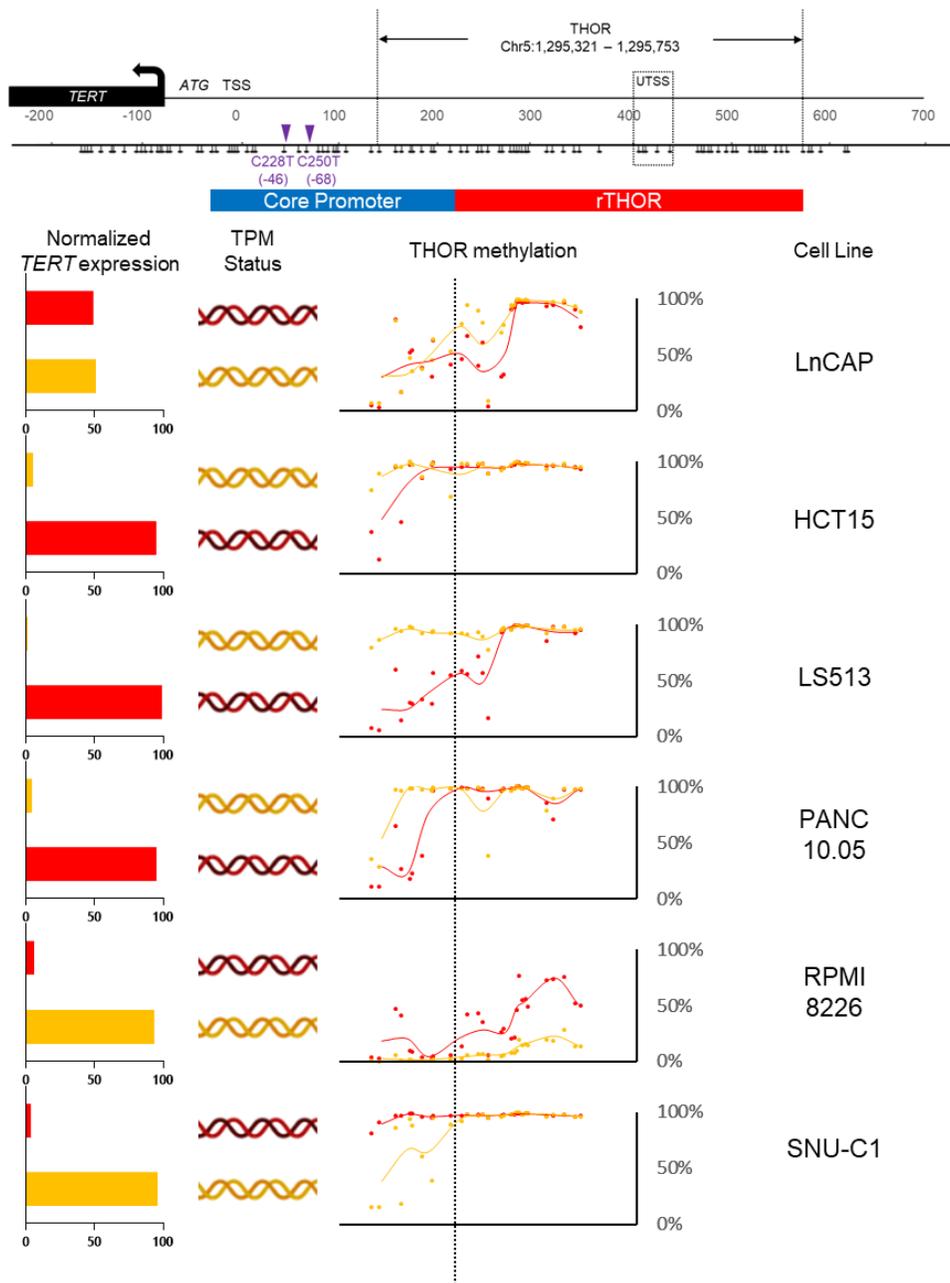


Figure S5. CpG methylation patterns of the *TERT* promoter in WT cancer cell lines. Red and yellow colors indicate each of the alleles separated based on the promoter SNP and exon SNP. Line graphs with dots (raw values) indicate levels of CpG methylation in the *TERT* promoter. Bar graphs show normalized allelic *TERT* expression.

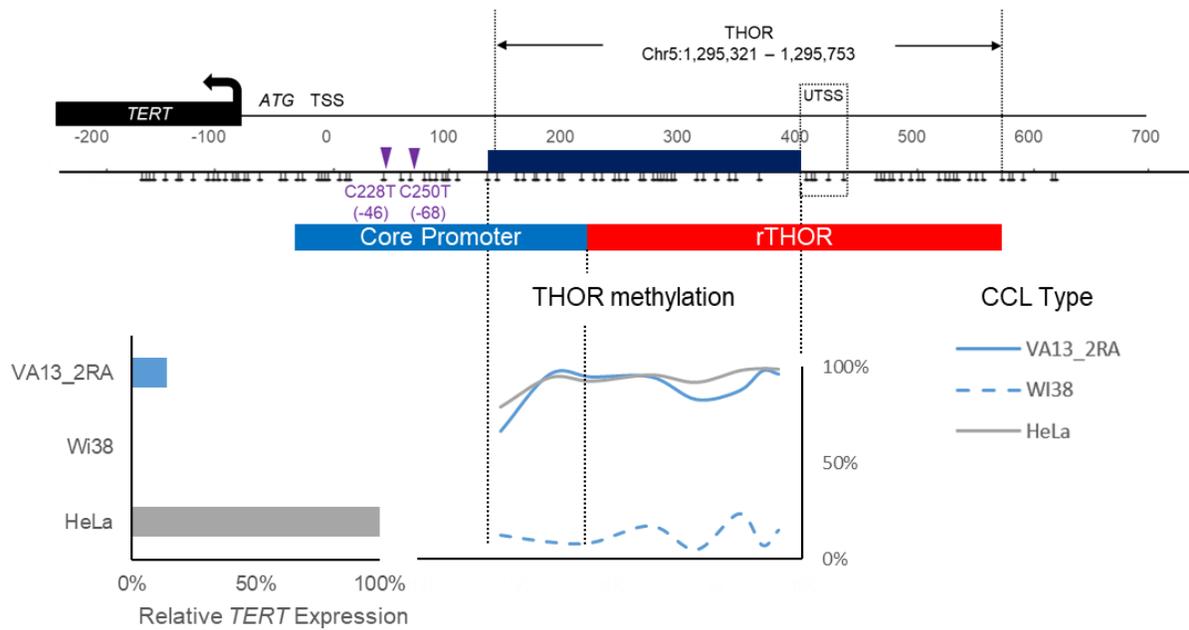


Figure S6. THOR methylation in an *in vitro* transformed human cell line. Line graphs show THOR methylation levels in a human fibroblast cell line WI38 and its corresponding immortalized cell line (VA13_2RA). Bar graphs show relative *TERT* expression (normalized to *TERT* expression in HeLa cells at 100%). HeLa cell data is included as a normalization control for *TERT* expression.

Table S1. List of primers used for ARMS-PCR

Name	Use	Primer Sequence (5' → 3')
TERT_pSNP_A	ARMS-PCR	TCGCGGGCACAGACGCCCAGGACCGGGCTT
TERT_pSNP_G	ARMS-PCR	TCGCGGGCACAGACGCCCAGGACCGGGCTC
TERT_exSNP_C	ARMS-PCR	CGTGGTGGCCGCGATGTGGATGGGGCGCCC
TERT_exSNP_T	ARMS-PCR	CGTGGTGGCCGCGATGTGGATGGGGCGCCC