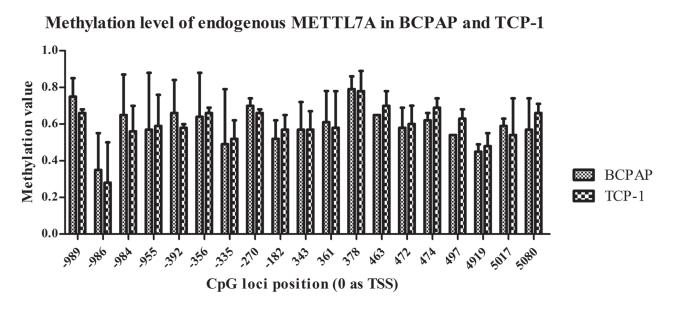
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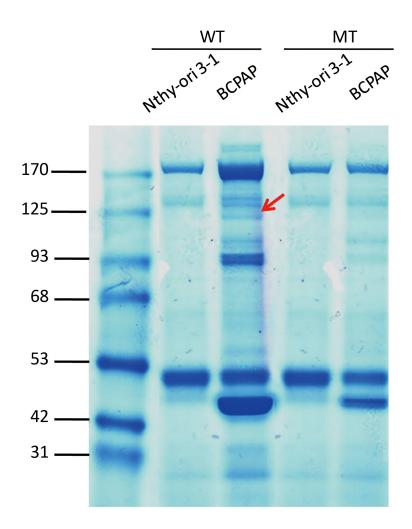
DNA methylation of METTL7A gene body regulates its transcriptional level in thyroid cancer

SUPPLEMENTARY FIGURES



Supplementary Figure 1: Methylation level of endogenous genomic METTL7A in BCPAP and TPC-1 cell lines. The data of METTL7A in two cell lines is normalized by methylation level of LINE-1, which is thought as a stable methylated region and can represent the overall methylation level of genomic DNA.

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Supplementary Figure 2: The blue staining of the protein patterns of wild type and mutant METTL7A template in Nthy-ori 3-1 and BCPAP cells.