**Supplementary Figure Legends:**

Figure S1. Boxplots showing (A) mRNA in four METTLs (METTL2B, METTL3, METTL24, and METTL26), and (B) protein difference in three METTLs (METTL2B, METTL3, and METTL26) of CPTAC-LUAD tumor and NAT samples. Blue: normal adjacent tissues (NAT); red: LUAD tumor samples. Sample numbers are indicated.

Figure S2. Correlations between (A) DNA copy number and mRNA expression, as well as (B) mRNA expression and protein abundance in CPTAC-LUAD cohort.

Figure S3. Kaplan-Meier progression-free survival curve for METTL26 mRNA expression in LUAD patients.

Figure S4. Relative protein abundance of METTL7B and NTMT1 in more than 300 CCLE lines across 22 lineages.

Figure S5. Correlation between METTL1 and WDR4 protein abundance in CPTAC-LUAD cohort.

Figure S6. Druggability of SAM binding pockets of human METTL1 (PDB: 3CKK) was estimated by DoGSiteScorer tool of the ProteinsPlus server.

Figure S7: Sequence alignment of enzymatic domain of four proteins derived from genome sequences of the following: human METTL1, Yeast Trm8, *E. coli* TrmB, and *Bacillus subtilis* TrmB. The secondary structure of human METTL1 is shown above. Residues with 100% conservation are indicated in solid red boxes and those with identity of 70% or higher are depicted in light red color.