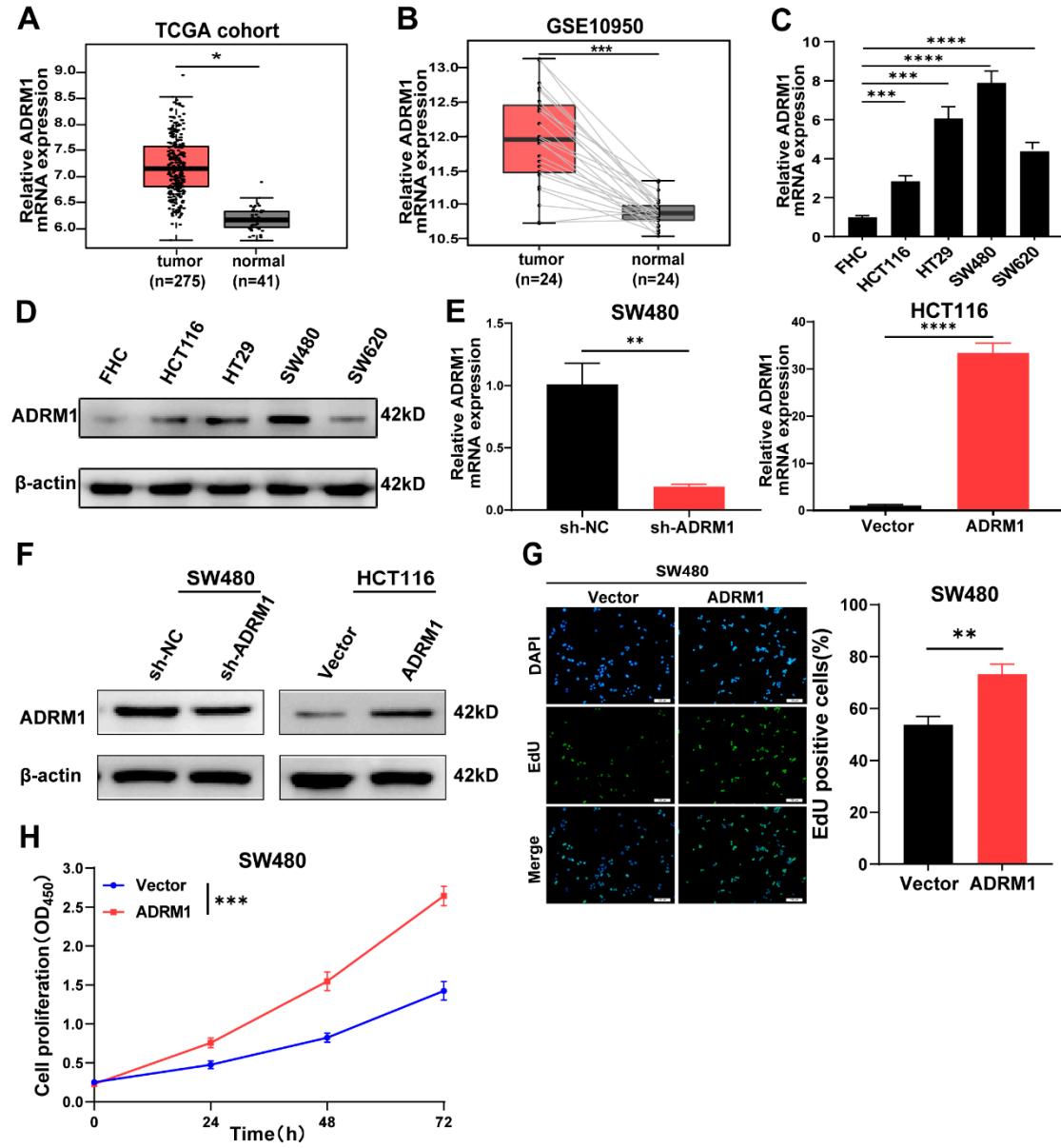


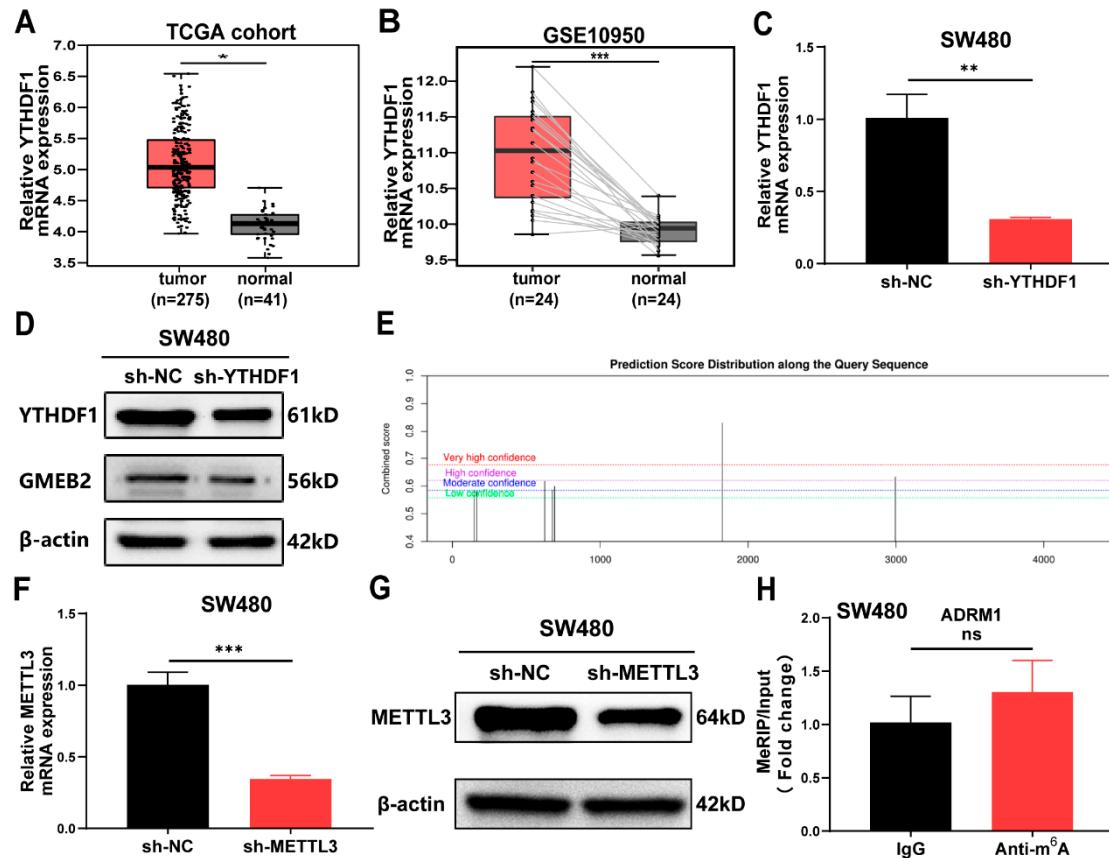
**Figure S1.** Knockdown of GMEB2 inhibits CRC cell proliferation. **(A)** GMEB1 and GMEB2 relative mRNA levels in FHC and CRC cell lines (HCT116, HT29, SW480 and SW620) (Student's t-test, \* $p < 0.05$ , \*\* $p < 0.01$ , \*\*\* $p < 0.001$ ). **(B)** Silencing efficiency of GMEB2 in HT29 cells measured by qRT-PCR (Student's t-test, \*\* $p < 0.01$ ). **(C)** Silencing or overexpression efficiencies of GMEB2 in SW480, HT29 and HCT116 cells measured by western blotting. **(D, F)** CCK-8 assay was used to detect the proliferation of SW480 and HT29 cells after overexpression or knockdown

GMEB2 (two-way ANOVA, \*\* $p < 0.01$ ). (E, G) EdU assay and the relative quantitative result of cell proliferation are shown in histogram form (Student's t-test, \*\*\* $p < 0.001$ ). (H) The colony formation assay and numbers of clones were counted (Student's t-test, \*\*\* $p < 0.001$ ). The results are presented as the mean  $\pm$  S.D. of three independent experiments.  $p < 0.05$ . (I) Annexin V-PI staining followed by cytometry analysis was performed to evaluate the cell apoptosis of shGMEB2 HT29 and SW480 cells and their corresponding NC cells. \*\* $p < 0.01$ , \*\*\* $p < 0.001$ . Scale bar, 100  $\mu$ m.



**Figure S2.** The mRNA and protein expression of ADRM1 in CRC cells. (A) ADRM1 mRNA level in the TCGA database (Student's t-test, \* $p < 0.05$ ). (B) ADRM1 mRNA level in GSE10950 of the GEO database (paired Student's t-test, \*\*\* $p < 0.001$ ). (C) ADRM1 mRNA levels in FHC and CRC cell lines (HCT116, HT29, SW480 and SW620) (Student's t-test, \*\*\* $p < 0.001$ , \*\*\*\* $p < 0.0001$ ). (D) ADRM1 protein levels in the FHC and CRC cell lines (HCT116, HT29, SW480 and SW620) measured by western blotting. (E) Silencing or overexpression efficiencies of ADRM1 in SW480 and HCT116 cells measured by qRT-PCR (Student's t-test, \*\* $p < 0.01$ , \*\*\* $p < 0.001$ ). (F) Silencing or overexpression efficiencies of ADRM1 in SW480 and HCT116 cells measured by western blotting. (G) EdU assay and the relative quantitative result of cell proliferation are shown in histogram form (Student's t-test, \*\*\* $p < 0.001$ ). (H) The colony formation assay and numbers of clones were counted (Student's t-test, \*\*\* $p < 0.001$ ). The results are presented as the mean  $\pm$  S.D. of three independent experiments.  $p < 0.05$ .

blotting. (G) EdU assay and the relative quantitative result of cell proliferation were shown in histogram form after overexpressing ADRM1 in SW480 cells (Student's t-test, \*\* $p < 0.01$ ). (H) A CCK-8 assay was used to detect the proliferation of ADRM1-overexpressed SW480 cells (two-way ANOVA, \*\*\* $p < 0.001$ ).



**Figure S3.** YTHDF1 can positively regulate GMEB2 expression. (A) YTHDF1 mRNA level in the TCGA database (Student's t-test, \* $p < 0.05$ ). (B) YTHDF1 mRNA level in GSE10950 of the GEO database (paired Student's t-test, \*\*\* $p < 0.001$ ). (C) Silencing efficiency of YTHDF1 in SW480 cells measured by qRT-PCR (Student's t-test, \*\* $p < 0.01$ ). (D) Silencing efficiency of YTHDF1 and subsequent GMEB2 expression in SW480 cells measured by western blotting. (E) The potential  $m^6A$  modification sites on GMEB2 mRNA were predicted by SRAMP. (F) Silencing efficiency of METTL3 in SW480 cells measured by qRT-PCR (Student's t-test, \*\*\* $p < 0.001$ ). (G) Silencing efficiency of METTL3 in SW480 cells measured by western blotting. (H) MeRIP-qPCR showed no ADRM1 mRNA enrichment precipitated by the  $m^6A$  antibody (Student's t-test, ns  $p > 0.05$ ).