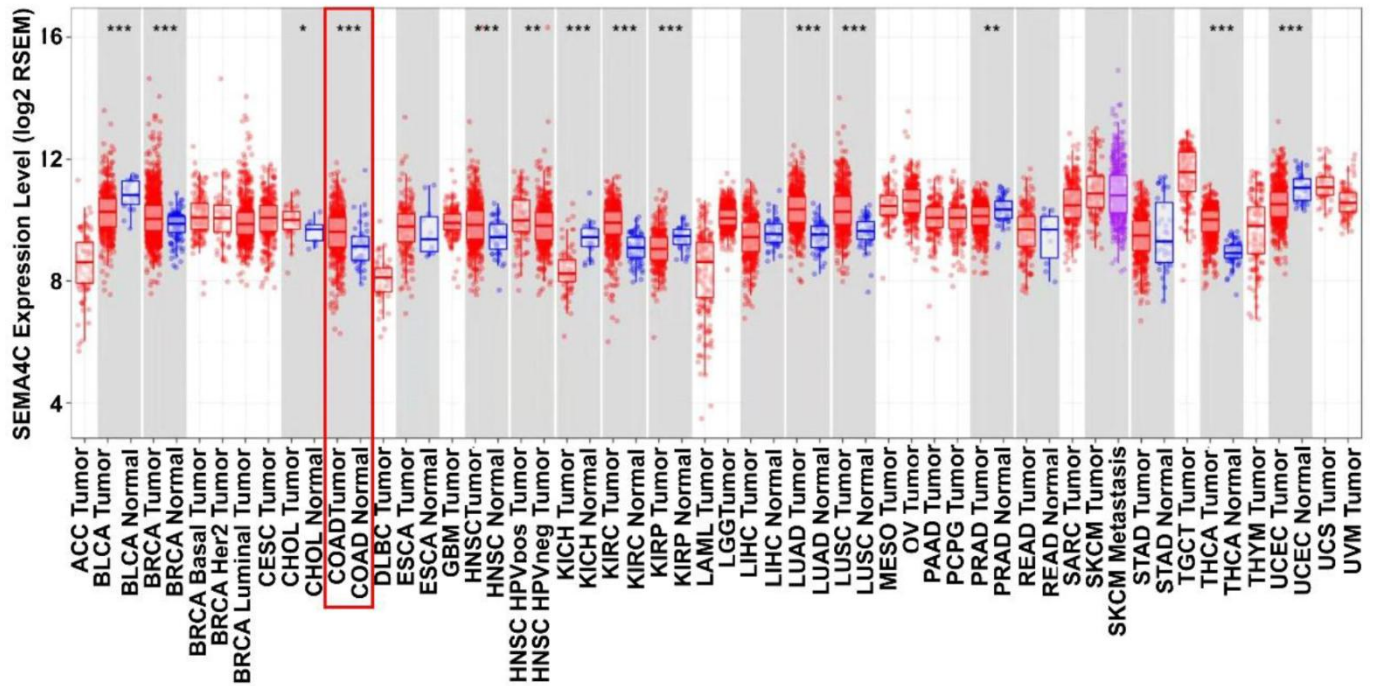
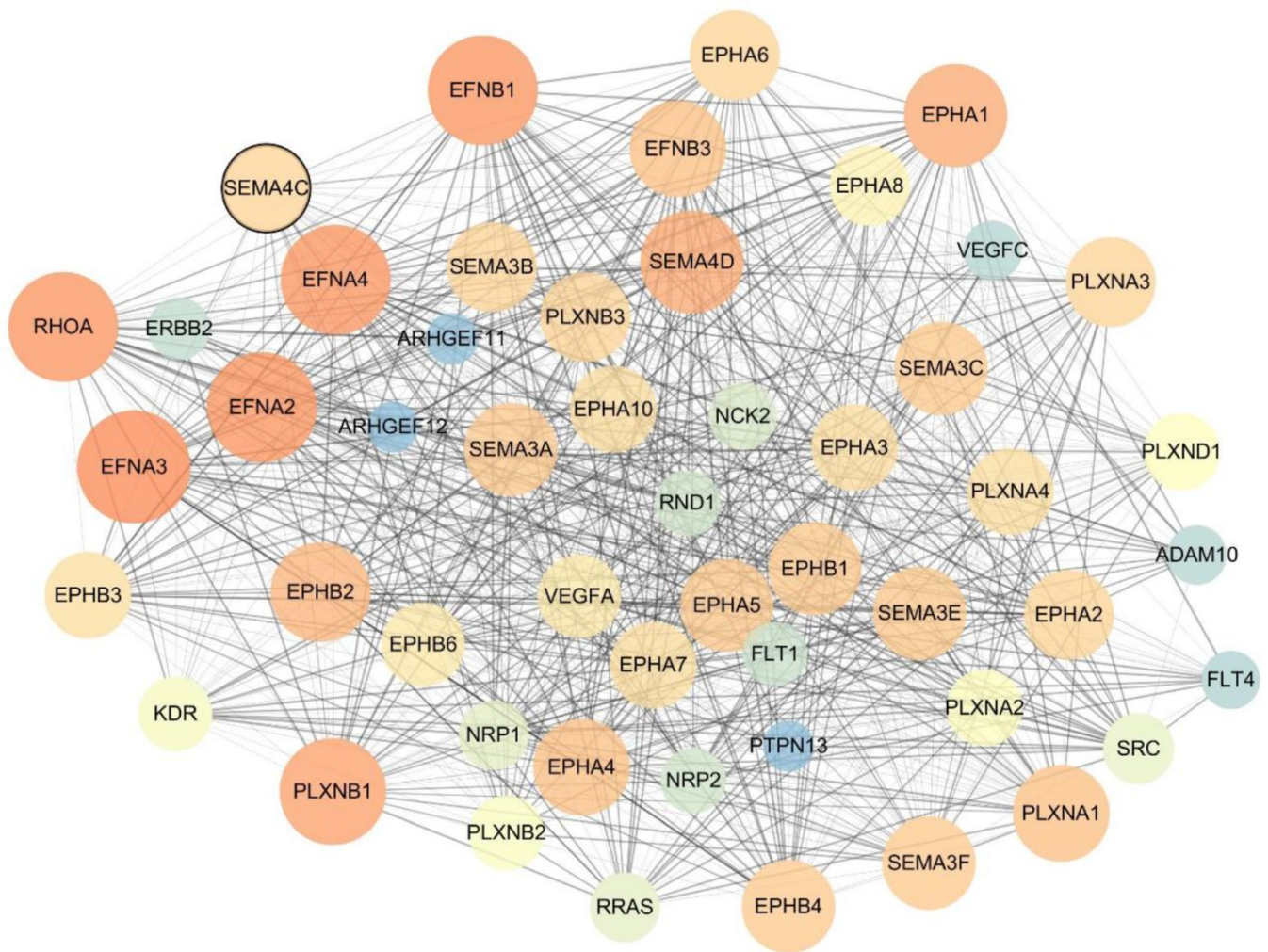


SUPPLEMENTARY FIGURES

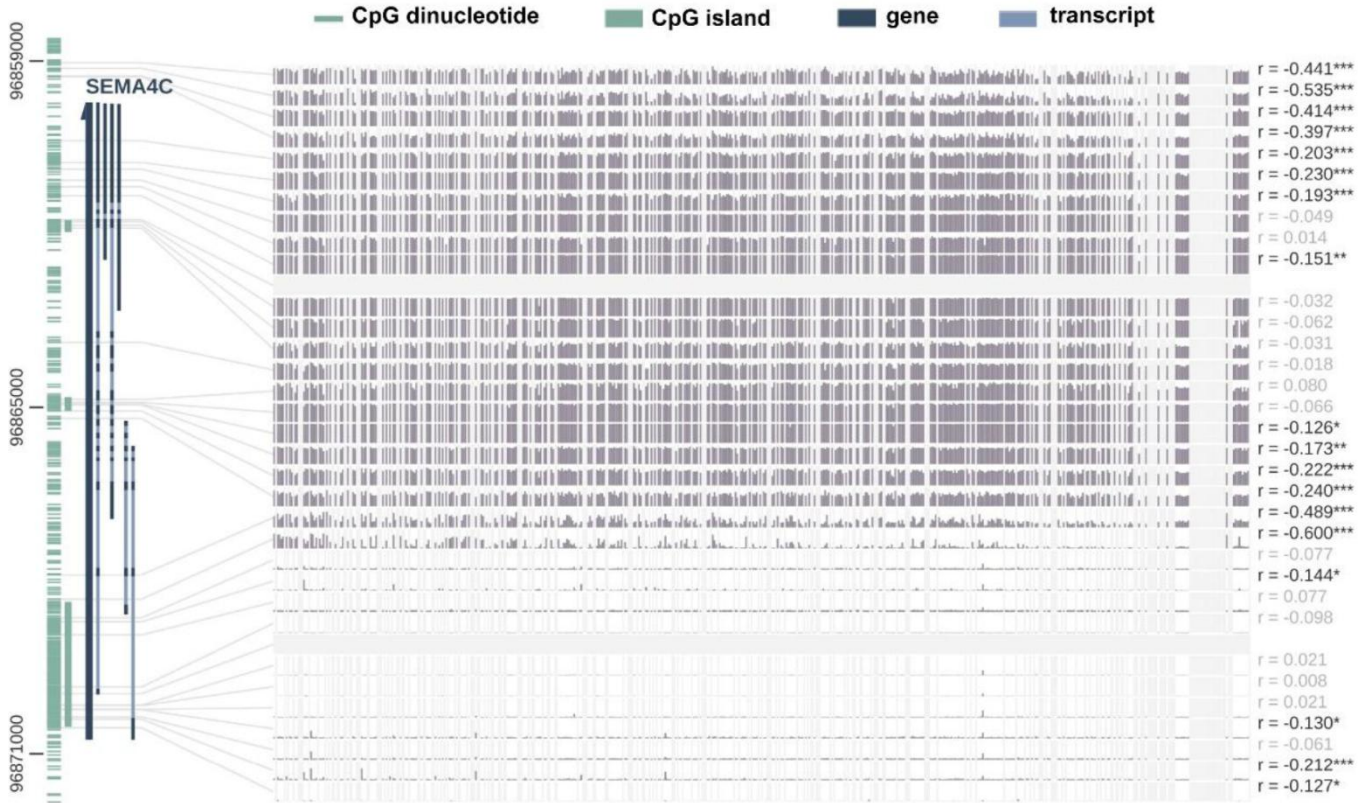


**Supplementary Figure 1. Pan-cancer expression profiling of SEMA4C mRNA levels in human cancers with the TIMER database.** The boxplots show the SEMA4C mRNA levels in the tumor (red) and normal (blue) tissue samples based on the TCGA data. SEMA4C was upregulated in 8 cancers (BRCA, CHOL, COAD, HNSC, KIRC, LUAD, LUSC, and THCA), and downregulated in 5 cancers (BLCA, KICH, KIRP, PRAD, and UCEC). Note: RSEM, RNA-Seq by expectation maximization; \*\*\*,  $P < 0.001$ ; \*\*,  $P < 0.01$ ; \*,  $P < 0.05$ ; BRCA: Breast invasive carcinoma; CHOL: Cholangio carcinoma; COAD: Colon adenocarcinoma; HNSC: Head and Neck squamous cell carcinoma; KIRC: Kidney renal clear cell carcinoma; LUAD: Lung adenocarcinoma; LUSC: Lung squamous cell carcinoma; THCA: Thyroid carcinoma; BLCA: Bladder Urothelial Carcinoma; KICH: Kidney Chromophobe; KIRP: Kidney renal papillary cell carcinoma; PRAD: Prostate adenocarcinoma; UCEC: Uterine Corpus Endometrial Carcinoma.



**Supplementary Figure 2. PPI network between SEMA4C and 50 SEMA4C-related genes.** The nodes denote proteins and the edges represent interactions between any two proteins in the PPI network.

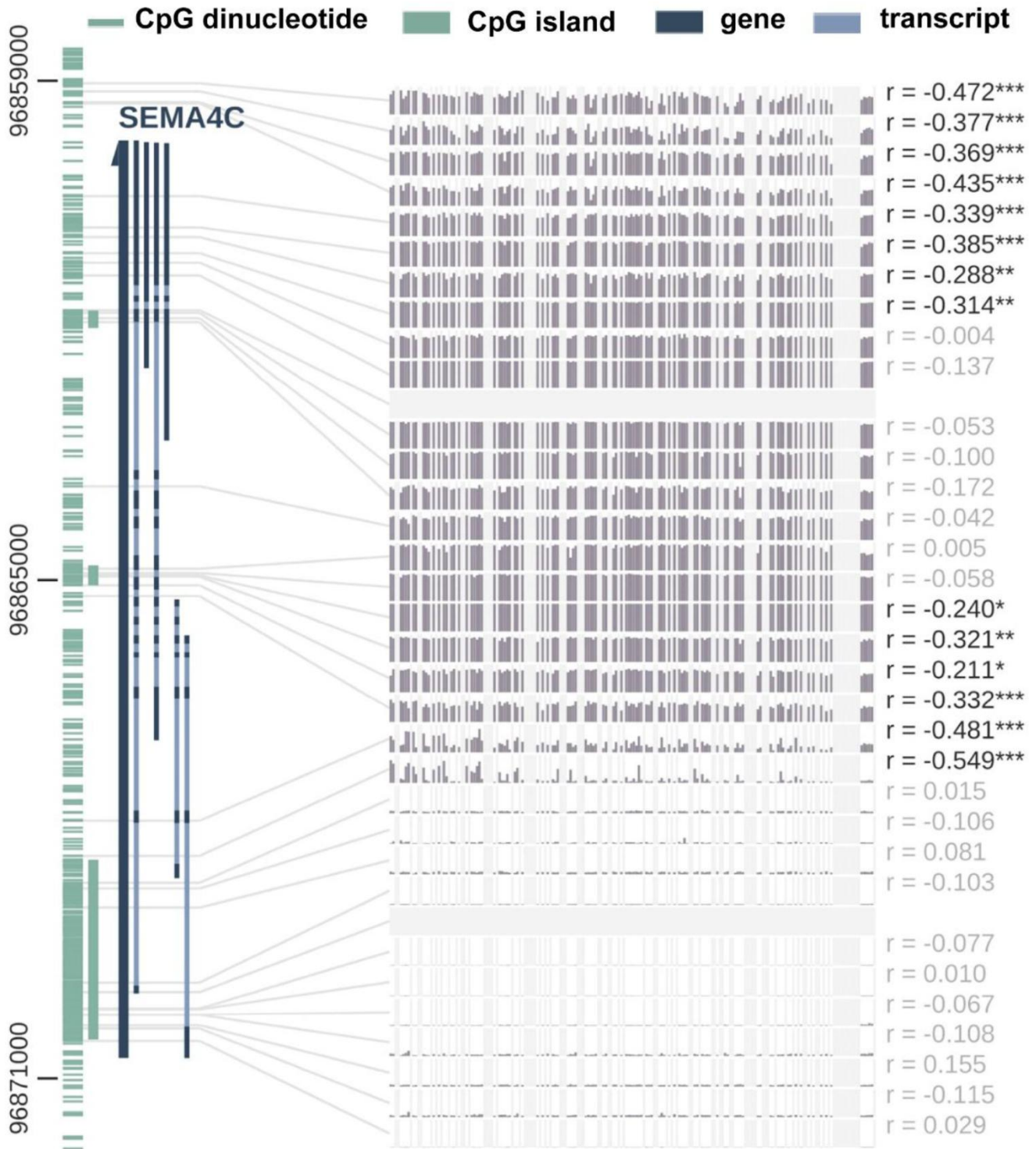
# TCGA-COAD



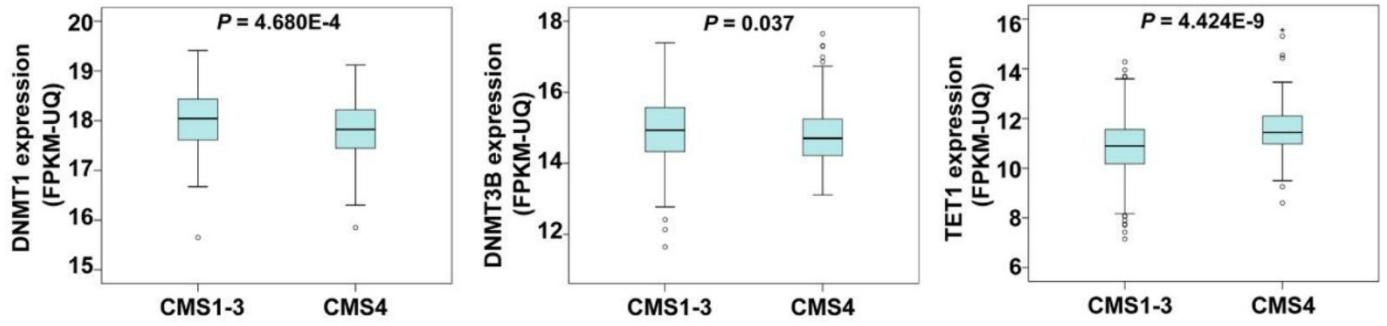
Supplementary Figure 3. Association between SEMA4C expression and DNA methylation in the TCGA-COAD cohort using the MEXPRESS tool. The correlation coefficients (r) are shown in the right panel; \*\*\*,  $P < 0.001$ ; \*\*,  $P < 0.01$ ; \*,  $P < 0.05$ .



# TCGA-READ



Supplementary Figure 4. Association between SEMA4C expression and DNA methylation in the TCGA-READ cohort using the MEXPRESS tool. The correlation coefficients (r) are indicated in the right panel; \*\*\*,  $P < 0.001$ ; \*\*,  $P < 0.01$ ; \*,  $P < 0.05$ .



Supplementary Figure 5. The mRNA levels of DNMT1, DNMT3B, or TET1 in the CMS1-3 and CMS4 molecular subtypes of the TCGA-CRC dataset.



Supplementary Figure 6. Analysis of SEMA4C gene alterations in the CRC samples using the cBioPortal. The plots show the (A) copy number alterations and (B) mutations in the SEMA4C gene in the CRC samples (n=526) in the cBioPortal. Each gray box along the x-axis represents a single CRC patient.