

Figure S1. Low ZNF180 expression is associated with higher risk scores and shorter OS. (A) Differential expression of the 15 genes in TCGA between tumor and normal tissues. P-values were calculated using paired Student's t-test. * $P<0.05$, *** $P<0.001$, **** $P<0.0001$. (B-a) mRNA expression levels of ZNF180 in CRC tissues and noncancerous tissues in TCGA dataset. P-values were calculated using paired Student's t-test, **** $P<0.0001$. (B-b) mRNA expression levels of ZNF180 in CRC tissues and noncancerous tissues in GSE39582 datasets. P-values were calculated using unpaired Student's t-test. * $P<0.05$. (C) KM analysis indicates that the downregulation of ZNF180 was significantly associated with poorer DFS in patients with CRC from the SYSU6 cohort ($n=220$). (D) KM analysis indicates that the downregulation of ZNF180 was significantly associated with poorer OS in patients with CRC. (E) Risk scores were negatively correlated with ZNF180 expression in TCGA and GSE39582 data sets. Protein expression levels of (F) ZNF180 and (G) METTL14 in 12 paired CRC tissues and adjacent normal tissues from the SYSU6 cohort were confirmed by western blotting. (H) Cell proliferation was determined by the MTS assay. P-values were calculated using one-way ANOVA and Scheffe test. CRC, colorectal cancer; DFS, disease-free survival; KM, Kaplan-Meier; METTL14, methyltransferase 14, N6-adenosine-methyltransferase non-catalytic subunit; N, normal; OD, optical density; OS, overall survival; SYSU6, The Sixth Affiliated Hospital of Sun Yat-sen University; T, tumor; TCGA, The Cancer Genome Atlas; ZNF180, zinc finger protein 180.

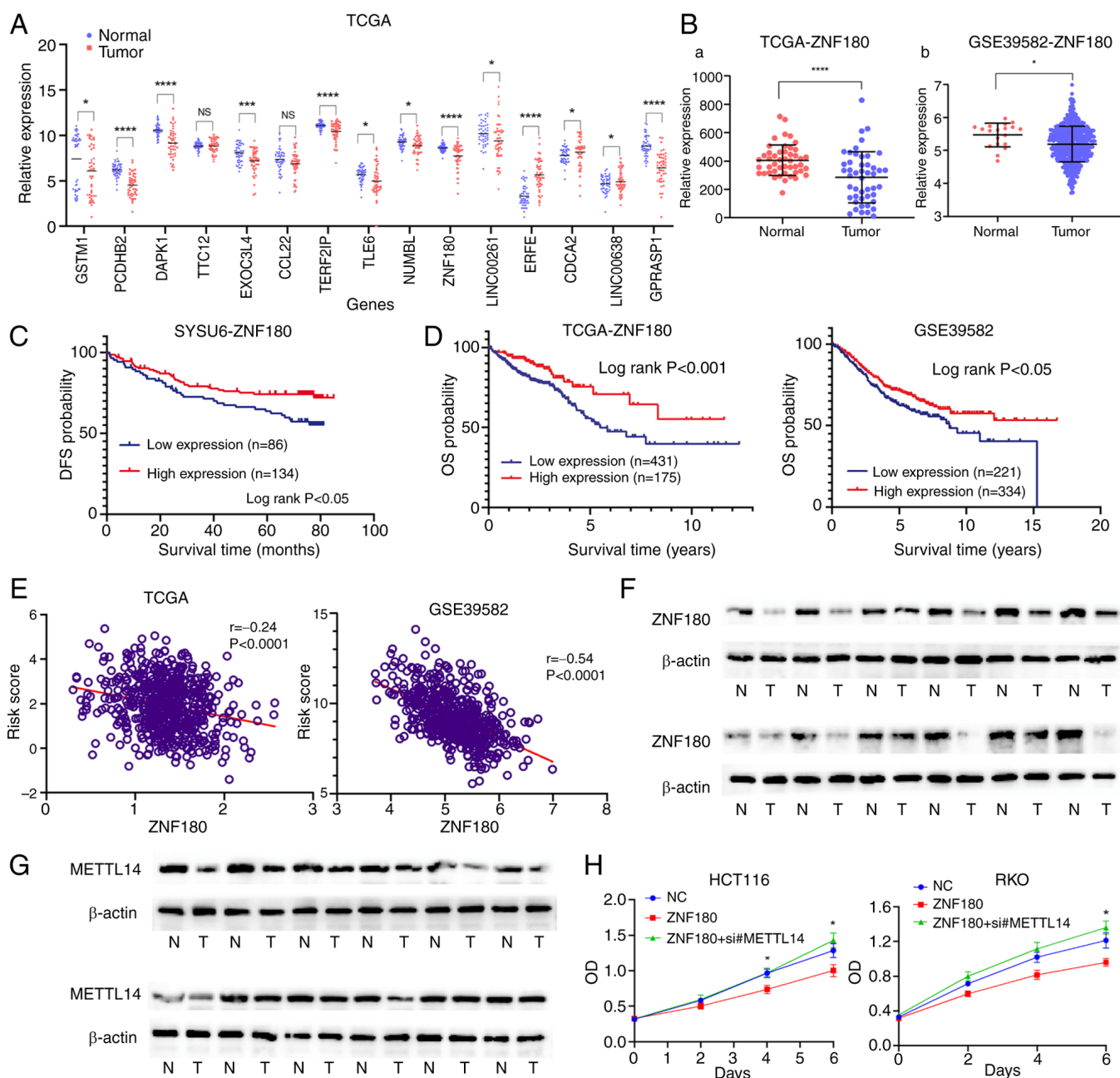


Figure S2. Association between ZNF180 and METTL14 expression. (A) mRNA expression levels of METTL14 in colorectal cancer tissues and noncancerous tissues in the GSE38211 cohort. P-values were calculated using unpaired Student's t-test. **** $P < 0.0001$. (B) ZNF180 expression was positively associated with METTL14 expression in tumor and normal tissues in TCGA dataset. P-values were calculated using paired Student's t-test. **** $P < 0.0001$. (C) Hoechst 33342 and EdU staining of HCT116 ZNF180-overexpressing cells. (D) Quantification of EdU staining. P-values were calculated using unpaired Student's t-test. * $P < 0.05$. (E) Quantification of Ki67 staining. * $P < 0.05$. Localization of Ki67 in ZNF180-overexpressing (F) RKO and (G) HCT116 cell lines detected by confocal immunofluorescence analysis. (H) Flow cytometric analysis of cell cycle distribution in ZNF180 overexpression and vector groups. (I) Migratory ability of ZNF180 overexpression and vector groups determined by Transwell assay. (J) Overexpression of ZNF180 had no effect on migration of the cells, as determined by a wound healing assay. (K) Localization of ZNF180 and METTL14 in RKO cells by confocal immunofluorescence analysis. EdU, 5-ethynyl-20-deoxyuridine; METTL14, methyltransferase 14, N6-adenosine-methyltransferase non-catalytic subunit; TCGA, The Cancer Genome Atlas; ZNF180, zinc finger protein 180.

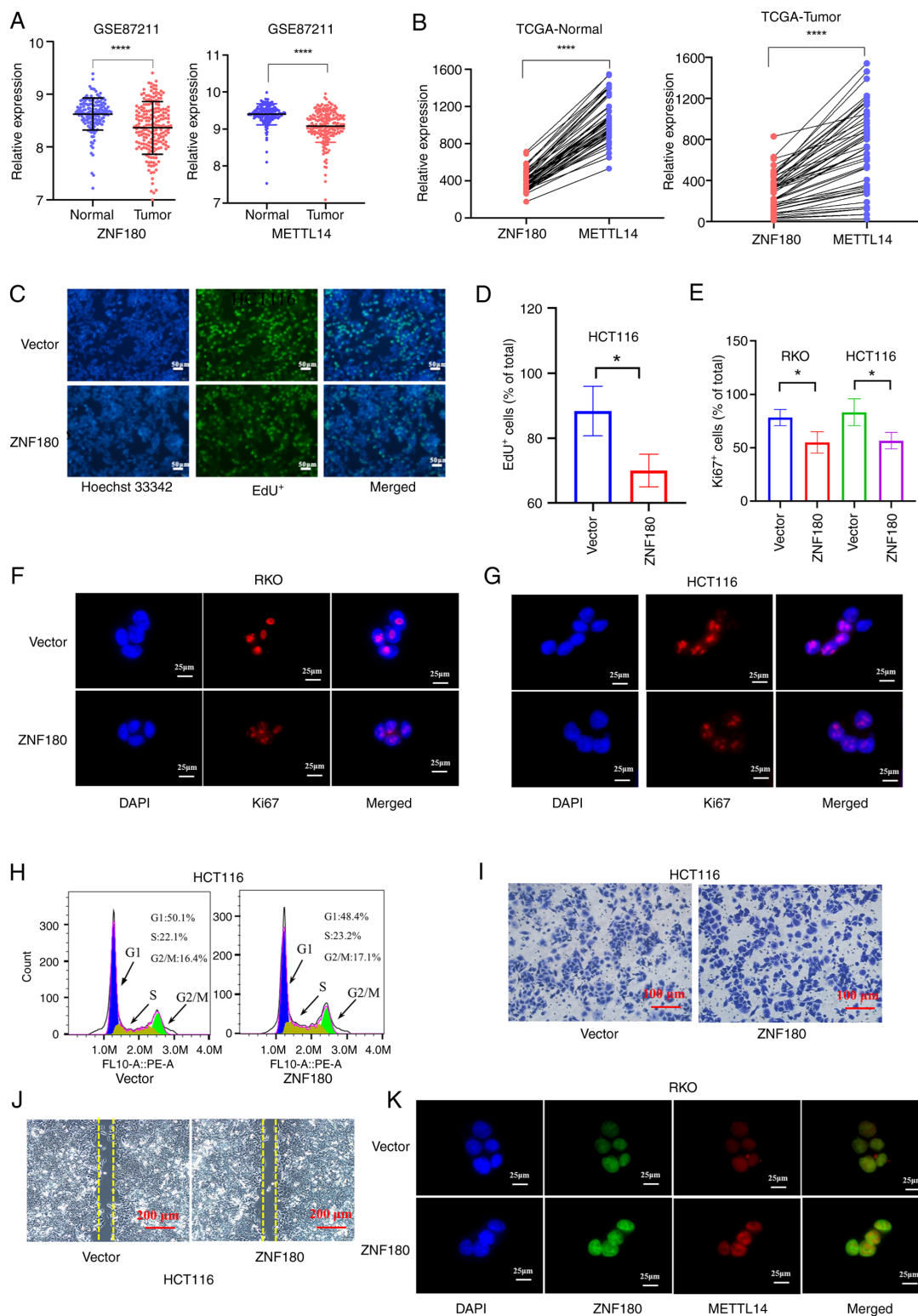


Figure S3. ZNF180 and METTL14 expression in CRC cell lines. mRNA expression levels of (A) ZNF180 and (B) METTL14 in numerous CRC cell lines obtained from DepMap portal.

