

Supplementary Figure:

Figure S1. METTL3 and METTL14 expression in RCC. **a** METTL3 mRNA expression in RCC and matched normal tissues (n=47). **b** METTL3 expression in KIRC tissues from TCGA database(n=533). **c** METTL14 mRNA expression in TNM I/II group (n = 154) and TNM III/IV group (n = 56). **d** The correlation between METTL14 levels and TNM stages was analyzed on TCGA database. **e** Alluvial diagram showing the distribution of METTL14, TNM stage and tumor grade subtypes from TCGA dataset. **f, g** Kaplan–Meier analysis of METTL14 and OS or RFS of KIRC patients from TCGA database. **h** Time-dependent OS ROC analysis of METTL14 from TCGA database. Error bars represent the mean \pm SD. Student's t-test (**a, b**) and Wilcoxon t-test (**c**) were used. *P<0.05, **P<0.01, ***P<0.001.

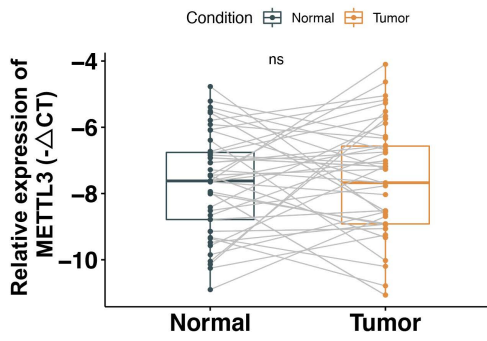
Figure S2. Effects of METTL3 on tumor growth and migration. **a** METTL3 mRNA levels in 769–P cell transfected with METTL3 siRNAs (si–METTL3–1, si–METTL3–2) or control(si–NC). **b, c** CCK–8 assay (**b**) and trans–well migration assay (**c**) of 769–P cell transfected with METTL3 siRNAs or control.

Figure S3. NEAT1_1 promotes growth and migration of RCC. **a** NEAT1_1 and NEAT1_2 expression levels in RCC cells. **b** NEAT1_2 expression in METTL14 interfering RCC cells. **c** NEAT1 levels in normal tissue and RCC tumor from TCGA database. **d** NEAT1_1 mRNA levels in 769-P and 786-O cells transfected with NEAT1_1 siRNAs or control. **e–h** Cell clone formation assays (**e**), CCK-8 assays (**f**) and trans-well migration assays (**g, h**) of 769-P and 786-O cells transfected with NEAT1_1 siRNAs or control. **i** METTL14 levels in 769-P and 786-O cells transfected with sh-METTL14 lentivirus or control. **j, k** Correlation analysis between m6A and METTL3 (**j**) and NEAT1 (**k**) in RCC samples (n=20). Error bars represent the mean \pm SD. Student's t-test were used. **P<0.01, ***P<0.001.

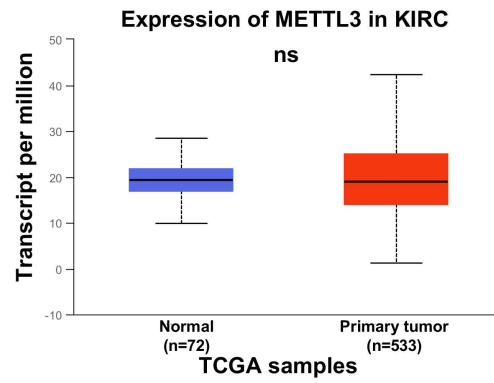
Figure S4. YTHDF2 is downregulated in RCC. **a** RNA pull-down assays in RCC cells showing negligible interaction between NEAT1_1 and other m6A readers. **b** IHC staining and relative histochemistry score for YTHDF2 protein expression in RCC tissue and paired normal kidney TMAs, Magnification, 100x, 400x. **c** YTHDF2 levels in normal tissue and RCC tumor from TCGA database. **d** Negative linear correlation between YTHDF2 and NEAT1 from TCGA database (n=533). **e, f** Kaplan–Meier analysis of correlation between YTHDF2 expression and OS/PFS from TCGA database. Error bars represent the mean \pm SD. Student's t-test were used. **P<0.01, ***P<0.001.

Supplementary Figure S1

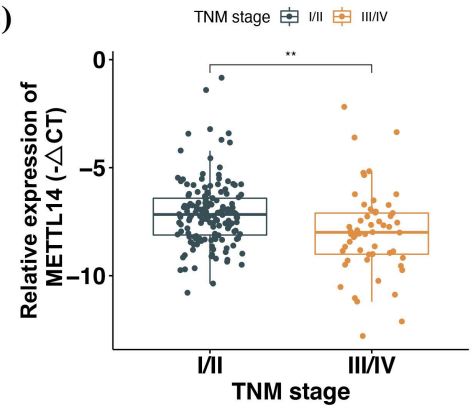
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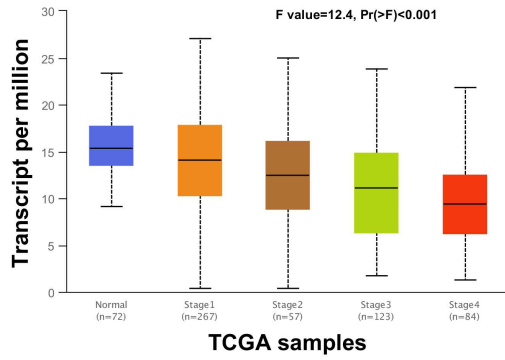
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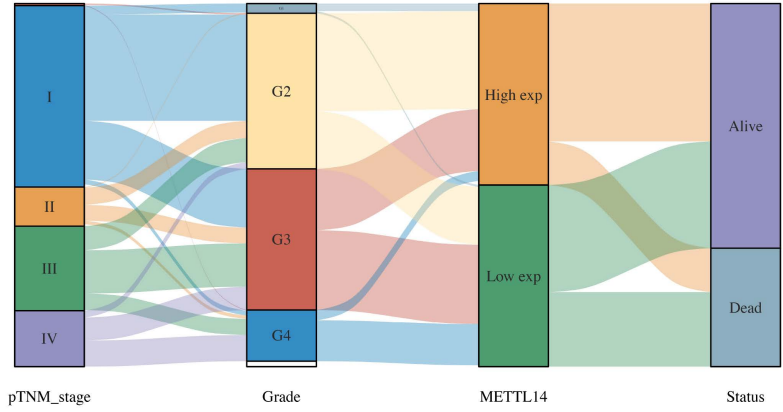
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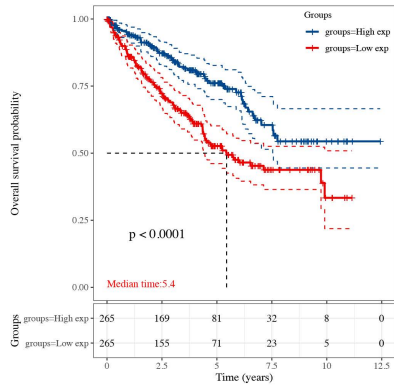
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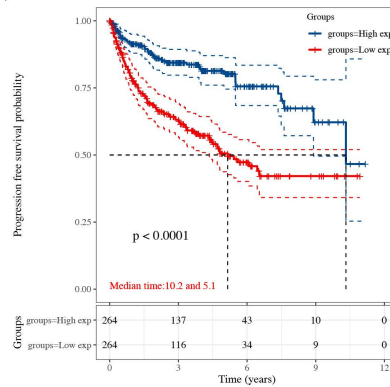
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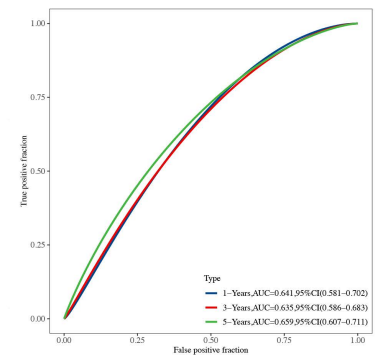
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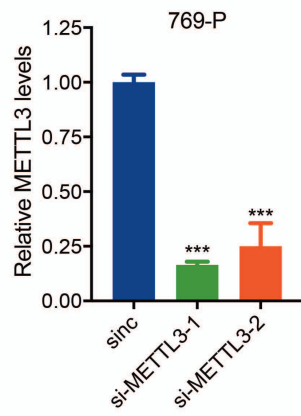
(G)



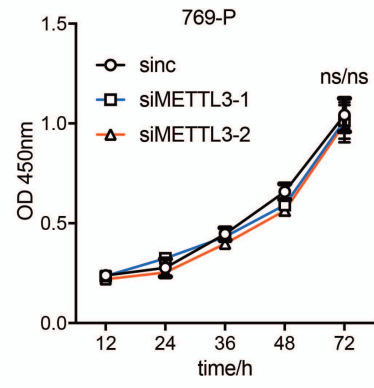
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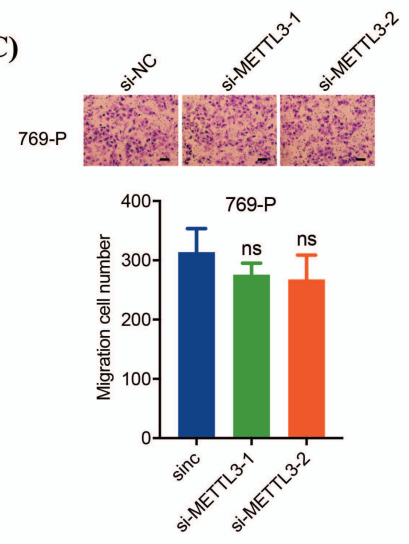
(A)

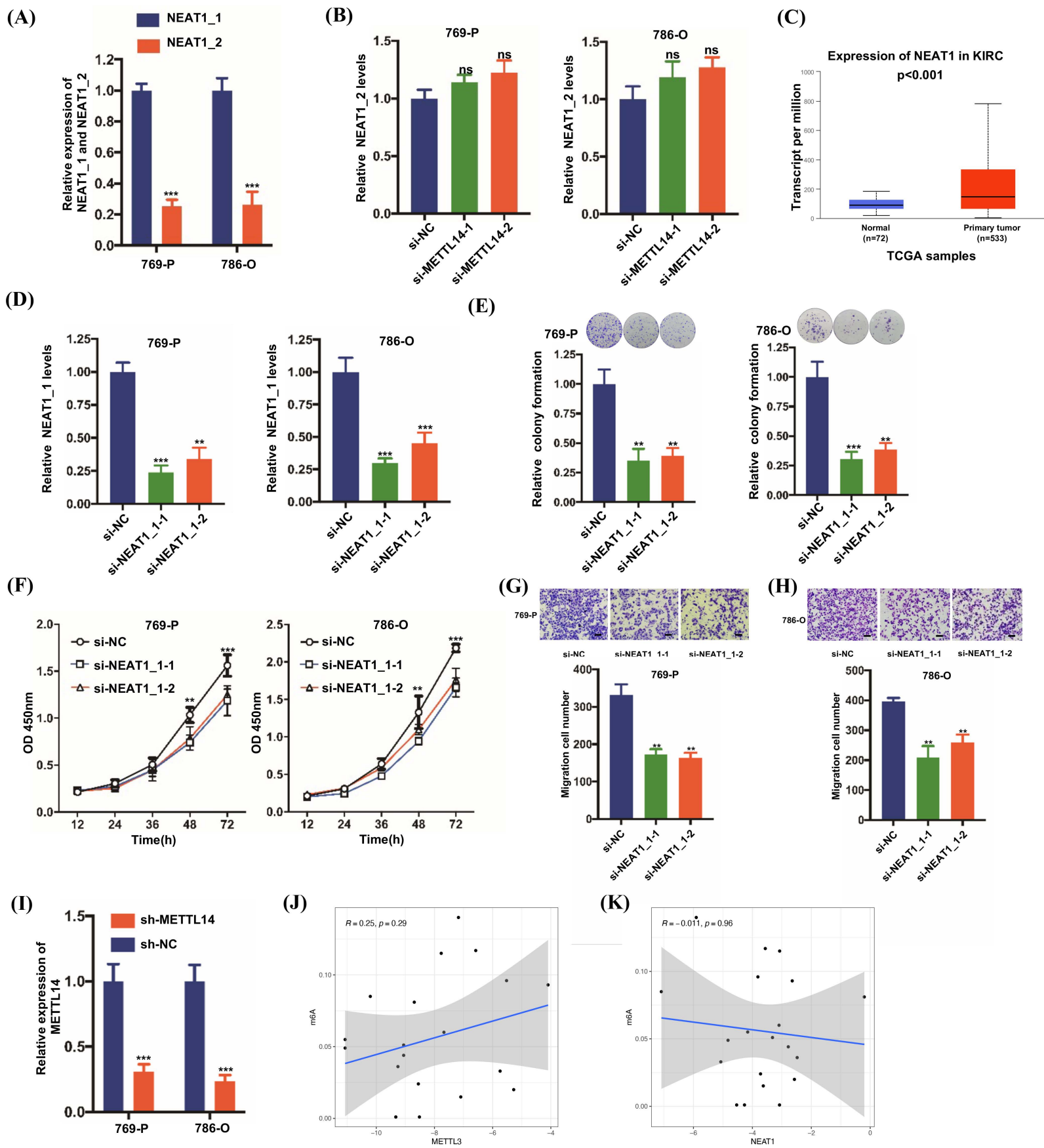


(B)



(C)





Supplementary Figure S4

