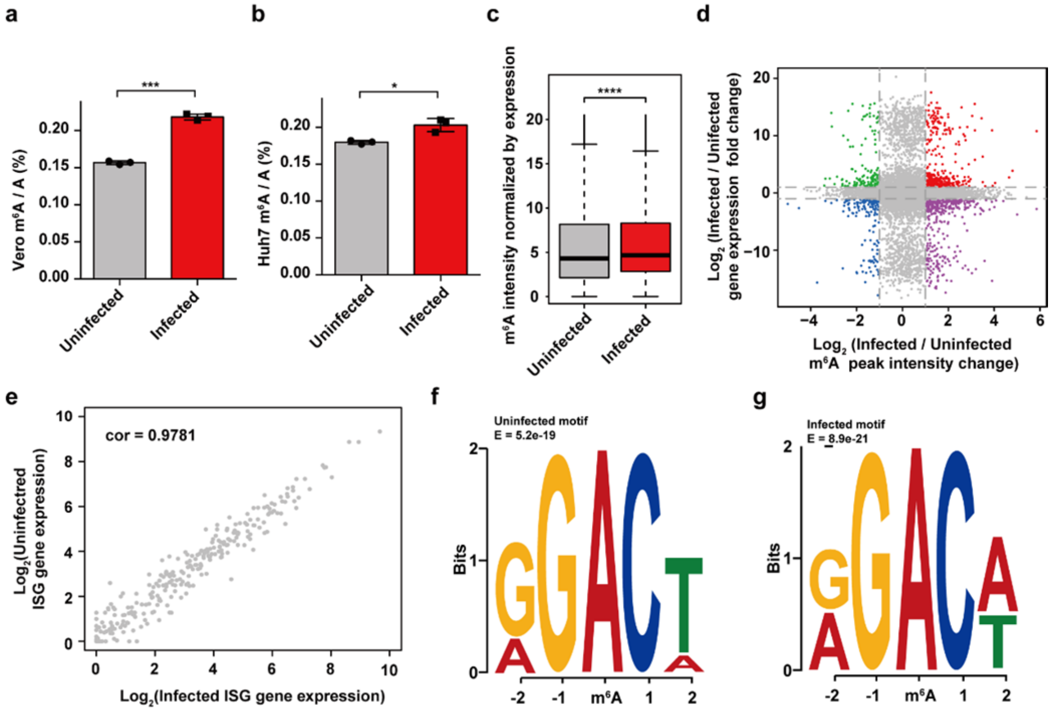

Fig S6. The influences of SARS-CoV-2 infection on m^{6}A methylome of Huh7 cell transcripts.

(**a and b**) m^{6}A abundance quantification in uninfected and SARS-CoV-2-infected Vero (**a**) and Huh7 cells (**b**) by the liquid chromatography-tandem mass spectrometry (LC-MS/MS). All data are the mean ± SD of the indicated number of replicates (N = 3). Statistical significance of the difference was determined by unpaired Student's t-test. ****P* < 0.001; **P* < 0.05.

(**c**) m^{6}A intensity analysis in uninfected and SARS-CoV-2-infected Huh7 cells. Statistical significance of the difference was determined by unpaired two-sided Mann-Whitney U-test. *****P* < 0.0001.

(**d**) Correlation between changes in gene expression and m^{6}A modification between uninfected and SARS-CoV-2-infected Huh7 cells. Red dots showing transcripts with increased gene expression level and upregulated m^{6}A signals; pink dots showing transcripts with decreased gene expression level and upregulated m^{6}A signals; green dots showing transcripts with increased gene expression level and downregulated m^{6}A signals; blue dots showing transcripts with decreased gene expression level and downregulated m^{6}A signals; grey dots showing transcripts with either unchanged gene expression level or unchanged m^{6}A signals.

(**e**) Correlation analysis of expression level of interferon-stimulated genes between uninfected and SARS-CoV-2-infected Huh7 cells.

(**f and g**) Transcriptome-wide motif analysis revealed consensus m^{6}A peaks in uninfected (**f**) and SARS-CoV-2-infected Huh7 cells (**g**), respectively.