Fig. S1  

a  GC patients with high METTL3 expression had a shorter overall survival time in GSE66229 data set. 
b  After excluding the samples without clinical information, analysis of GSE66229 data set showed that METTL3 level was significantly higher in advanced-stage GC tissues. 

c-d METTL3 was more highly expressed in the diffuse-type GC tissues compared with the intestinal-type samples in both GSE66229 (excluding the samples without clinical information) and Cohort 1. 
e  The mRNA levels of METTL3 and EMT markers were evaluated by qRT-PCR in three GC cells, gastric epithelial cell line GES-1 was used as control. 
f  Confocal immunofluorescent analysis of the expression of EMT markers in indicated GC cell clones. *p<0.05.
Fig. S2  

a Gene ontology analysis of downregulated m6A peak-related gene sets in METTL3 knockdown cells.  
b Pathway analysis of downregulated m6A peak-related gene sets in METTL3 knockdown cells.  
c-d Anti-m6A antibody significantly enriched ZMYM1 mRNA level in GC cells. Bcl2 mRNA was used as a positive control.  
e Neither knocking down nor overexpressing METTL3 exerts significant effect on the protein expression of mutant ZMYM1 in GC cells.  
f The mRNA levels of ZMYM1 were decreased in both BGC823 and MKN-28 cells after treatment with 3-deazaadenosine (DAA).  
g-h Anti-HuR antibody significantly enriched ZMYM1 mRNA level in GC cells. SOX2 mRNA was used as a positive control. *p<0.05.