

Supplementary Table 1. Primers, shRNAs, and sgRNAs used in this study

Name	Sequence
YTHDF1(human) forward	5'-CAAGCACACAACCTCCATCTTCG-3'
Reverse	5'-GTAAGAAACTGGTTCGCCCTCAT-3'
GAPDH (human) forward	5'-AGAAGGCTGGGGCTCATTG-3'
Reverse	5'-GAGGGGCCATCCACAGTCTTC-3'
shYTHDF1-1 target sequence	GGATACAGTTCATGACAATGA
shYTHDF1-2 target sequence	GGCGTGTGTTTCATCATCAAGA
shNC target sequence	GTTCTCCGAACGTGTCACG
sgYTHDF1-1 sequence	CACCGAAGCATGTCGGCCACCAGCG
sgYTHDF1-2 sequence	CACCGTAGGTAGTGAGATACGGGAT
sgNC sequence	CACCGCGAGGTATTCGGCTCCGCG

Supplementary Table 2. Antibodies used in this study

Antibodies	Supplier	Reference
YTHDF1	Proteintech	17479-1-AP
YTHDF1	Abcam	ab220162
IFNGR1	Proteintech	10808-1-AP
JAK1	Cell Signaling	3344
JAK2	Cell Signaling	3230
STAT1	Cell Signaling	14994
β -Actin	Cell Signaling	4970
TruStain FcX™ PLUS (anti-mouse CD16/32)	Biolegend	155603
CD45	Biolegend	103138
CD3 ϵ	Biolegend	100308
CD4	Biolegend	100422
CD8a	Biolegend	100706
Gr-1	Biolegend	108408
CD11b	Biolegend	101206
F4/80	Biolegend	123114
CD11c	Biolegend	117307
MHC II	Biolegend	107631

Supplementary Table 3. Univariate and multivariate Cox regression analysis of YTHDF1 mRNA and clinicopathological parameters in predicting the survival of patients with gastric cancer in our cohort 1

Variable	Univariate COX regression		Multivariate COX regression	
	OR (95% CI)	P-value	OR (95% CI)	P-value
Age	1.025(0.995-1.055)	0.106	1.026(0.991-1.062)	0.149
Gender				
Female				
Male	0.613(0.316-1.191)	0.149	0.471(0.214-1.036)	0.061
H. pylori infection				
no				
yes	0.879(0.396-1.951)	0.751	0.645(0.248-1.675)	0.368
Anatomic subdivision				
Cardia/proximal				
Fundus/body	0.648(0.271-1.549)	0.330	0.868(0.275-2.741)	0.810
Antrum/distal	0.681(0.281-1.649)	0.394	1.045(0.335-3.259)	0.939
Histological grade				
Moderately differentiated				
Poorly differentiated	1.377(0.516-3.672)	0.523	1.540(0.528-4.488)	0.429
Lauren classification				
Intestinal type				
Mixed type	0.805(0.287-2.263)	0.681	1.216(0.370-3.998)	0.748
Diffuse type	0.993(0.466-2.116)	0.986	1.064(0.421-2.691)	0.895
Pathology primary tumor				
T1				
T2	1.472(0.201-10.773)	0.703	0.871(0.084-9.087)	0.908
T3	5.988(1.318-27.214)	0.020	4.602(0.223-95.043)	0.323
T4	12.418(2.766-55.752)	0.001	5.752(0.251-131.842)	0.274
Spread to lymph nodes				
N0				
N1	2.785(0.660-11.758)	0.163	1.620(0.330-7.965)	0.552
N2	7.937(2.143-29.395)	0.002	9.030(0.509-160.254)	0.134
N3	10.558(3.072-36.285)	<0.001	9.897(0.526-186.076)	0.126
Pathologic stage				
I				
II	9.072(1.134-72.558)	0.038	8,185(1.019-65.761)	0.048
III	26.278(3.483-198.235)	0.002	23,129(3.041-175.891)	0.002
YTHDF1 mRNA expression	1.344(1.155-1.565)	<0.001	1.274(1.092-1.485)	0.002