

Supplementary data

Table S1 Sample Information

orig.ident	group	Sample	pathological lesions
processed_NAG1.txt.gz	HP-	GSM3954946	Normal
processed_NAG2.txt.gz	HP-	GSM3954947	Normal
processed_NAG3.txt.gz	HP-	GSM3954948	Normal
processed_CAG1.txt.gz	HP-	GSM3954949	CAG
processed_CAG2.txt.gz	HP-	GSM3954950	CAG
processed_CAG3.txt.gz	HP-	GSM3954951	CAG
processed_IMS1.txt.gz	HP+	GSM3954952	IM
processed_IMS2.txt.gz	HP-	GSM3954953	IM
processed_IMS3.txt.gz	HP+	GSM3954954	IM
processed_IMS4.txt.gz	HP+	GSM3954955	IM
processed_IMW1.txt.gz	HP-	GSM3954956	IM
processed_IMW2.txt.gz	HP-	GSM3954957	IM
processed_EGC.txt.gz	HP-	GSM3954958	EGC

Table S2 The known markers for cell lineages in stomach.

Categories	Cell lineages	Marker genes
Gastric epithelial cells	PMC/GMC	<i>EPCAM, KRT19, MUC5AC, MUC6,</i>
Immune cells	chief cell	<i>PGA4,PGA3</i>
	T cell	<i>CD2, CD3D,CD3E,CD8A</i>
	B cell	<i>CD79A,CD19</i>
	Mast cells	<i>KIT, TPSAB1, CPA3, CST3</i>
	Macrophage	<i>CD14, CD163, CD68, CSF1R</i>
Stromal cells	Fibroblasts	<i>PDPN,COL1A2,DCN, COL3A1, COL6A1</i>
Malignant cells	Cancer cells	<i>CEACAM5, CEACAM6</i>
Intestinal cells	Enterocytes	<i>FABP1,CA1,VIL1</i>

Table S3 siRNA

Gene	Sequence (5' → 3')
si- <i>UPP1</i> #1	GUGCUCCAACGUCACUAUCAUTT
si- <i>UPP1</i> #2	GCUGAAAGUCACAAUGAUUTT
si- <i>P65</i> #1	UUAACGAUACUUCGUUUGGTT
si- <i>P65</i> #2	GATGAGATCTTCCTACTGT

Knockdown efficiency was above 70%

Table S4 Primer sequences

Gene	Sequence (5' → 3')
<i>UPP1</i>	F: ATGGGCATTCCTTCTATC R: GACAATCTGCTCAAACCTC
<i>P65</i>	F: TGCTGTGCGGCTCTGCTTCC R: AGGCTGGGGTCTGCGTAGGG
<i>GAPDH</i>	F: GAAGGTGAAGGTCGGAGTC R: GAAGATGGTGATGGGATTTC

Public data sets

Data set	Sample information
GSE134520	NAG (N=3), CAG (N=3), IM (N=6), EGC (N=1)
GSE118916	Tumor (N=15), NC (N=15)
GSE103236	Tumor (N=10), NC (N=10)
GSE2685	Tumor (N=8), NC (N=22)
GSE70394	HP ⁺ AGS (N=3), HP ⁻ AGS (N=3)
GSE108305	HP+AGS (N=2), HP-AGS (N=3)
GSE5081	HP+GC (N=8), HP-GC (N=8)
GSE78523	IM (N=30), NC (N=15)

Data set	Sample information
TCGA-STAD (2022.08)	Tumor (N=375), NC (N=32)

Data1 used by AlphaFold 3

The information of *UPP1* (NCBI)

UPP1 uridine phosphorylase 1 [*Homo sapiens* (human)]

Gene ID: 7378, updated on 23-Nov-2023

[Download Datasets](#)

Summary	
Official Symbol	UPP1 provided by HGNC
Official Full Name	uridine phosphorylase 1 provided by HGNC
Primary source	HGNC:HGNC:12576
See related	Ensembl:ENSG00000183696 MIM:191730 AllianceGenome:HGNC:12576
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Homo sapiens
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo
Also known as	UP; UPP; UPASE; UDRPASE
Summary	This gene encodes a uridine phosphorylase, an enzyme that catalyzes the reversible phosphorylation of uridine (or 2'- deoxyuridine) to uracil and ribose-1-phosphate (or deoxyribose-1-phosphate). The encoded enzyme functions in the degradation and salvage of pyrimidine ribonucleosides. [provided by RefSeq, Oct 2016]
Expression	Broad expression in bone marrow (RPKM 27.1), esophagus (RPKM 7.4) and 19 other tissues See more
Orthologs	mouse all

The gene contains multiple transcript, choose MANE project (transcript is specific clinical representative meaning, general important genes have the annotation) recommended the transcription, as below:



The 5'utr start site of this transcript was used as the right boundary of the promoter intercept. 2000bp forward was used as the left boundary of the promoter interception, and the specific sequence was as follows:

```
CCTACCAGCACCATGACAGTTTATAAATACCATGGCAACATTTAGAAGTTACCCTATATG
TTCTAAAAGGAAGAATTCCTAGAAAACATCATGAATAATCCACCCTTATTTAGTATATGAT
CAAGAAATAACCATAAAAATAGCCAACCAGCAGCCCTAGAGGCTGCCCTGCCCATGGA
ATTGCCATTCTTTTATTCCTTTACTTTCTCAATAAGCTTGCTTCTTTCACCTTACTCTGTG
GACTCACCCCTGGCCCCGAATTCCTTTCTTGACACAAGATCCAAGAACATTCTCTTGGGGTC
TGGATTGGGACCCCTTTTCCGGTAACAAACTAAACTAAGTTGTTAATCTACCTTCAGA
GAGAGAGAATAGCAACTTCCTAACCAGGCCAGTTTCAGTCTTCAGTCTGAGGCAGCAA
AATAGGGTCTGGAGGCAGGGAACATAAGGCCGATTCACACTTTAGCTATGACAGGAAA
TAGCCTCTGCGTAGGCCAAGTAAATGACTTTGTAACCTTTGCATCATCCCTTTCATTTACA
TAGTGTGTGCCCCAAGCGGAGGACATTGAAACTCCCCAAAATTCTGGAATGGGGCCTT
TGAGCCCCTACGCTCAGGCCCGCTCCACACTGTGGAGTGTACTTTCATTTACCTTTTTT
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TTTTTGAGATGGCGTCTCACTGTGTCAACCAAGGCTGGAATGCAGTGGCATGATCTCAG
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AGCTGGAATTACAGGCACCTGCCACTGTGACCGGCTAGGTTTTTTTTTTTGTTTTTTTTT
TTTTTTTACTTTTAGTAGAGACGGGGTTTCACCATCTTGGTTAGGCTGGTCTTGAAGTCC
TGACTTTGTAATCCACCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGTGTGAGCC
ACTGCGCCTGGCCGTACTTTTCATTTTCAATAAAACCCCTTAATTCCTTCCTTGATTGT
GTGTGTTTTCACTCTTGTCACCCAGTATGGAGTGCAATGGCGCGATCTCGGCTCACTGCA
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GCACGCGACACCACGTCCAGCTAATTTTTTGTATTTTGTAGTAGTGACGGGGTTTCACCA
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AGGAACTGGAGTTCCTTTAGGAAGCAAGTAACAGAGGTGCTGGGCTGCCCGGGCCT
CTAGGTTCGTCTTCTTTCCCAGGCTCTGTGCTCTCACCAGAGTGCGCGTTCGGGAAGCA
GGGAGAGGACCAGGAAAGACGCCTGAGACGGAGAGTGGGCACCGGCCGGGGGAG
GCAGGTCCGGCCCCCTGGGGGTGAGAGTGACGCGCCGGTTTGAGGCAGTTCGGCCACT
TAGCTGCGACTCGAAGTGAATGAGTCACTTCCCCTCCTCGGGCGAGCTCCTGGCTTTC
CCCCAGCAAGCGGGAAGT

***RELA* (P65)-human, Protein sequence**

Q04206-1

This isoform has been chosen as the **canonical** sequence. All positional information in this entry refers to it. This is also the sequence that appears in the downloadable versions of the entry.

Name 1

Synonyms p65

See also

sequence in UniParc or sequence clusters in UniRef

Tools

[Download](#)
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[Copy sequence](#)

Length 551

Mass (Da) 60,219

Last updated 2005-04-26 v2

Checksum¹ 8147A6AF9F2445C6

MDLFLPLIFP	AEPAQASQY	VEIIEQPKQR	GHRFRYKCEG	RSAGSIPGER	SDTTTKTHPT	IKINGYTGPG	TVRISLVTKD	PPHRPHPHL	VGKDCRDGFY	EAEPCDPRCI	HSFQNLGIQC	VKKRDLQEQI	SQRIQTNNIP
FQVPIEEQGR	DYDLNAVLRL	FQVTVRDPGG	RPLRLPPVL	HPIFDNRAPL	TAEKICIRVN	RNSGSCLGDD	ETFLLCDKVV	KEDIEVYFTG	PGWEARGSFY	QADVHRHQVAI	VFRTPPYPAD	SLQAPVVRSH	QLRRPSOREL
SEPMFEQYLP	DTDDRHRIEE	KKRKYETFK	SIMKKSFPFSG	PTDPRPPRRR	IAPVSRSAS	VKPAPAPQPV	FTSSLSTINY	DEFFTPMVFPS	GQISQASALA	PAPPQVLQPA	PAPAPAPAMV	SALAQAPAPV	PVLAPGPPQA
VAPPAPKPTQ	AGEGTLSLAL	LQLQFDEDDL	GALLGNSTDP	AVFTDASLV	NSEFQQLNQ	GIPVAPHTTE	PMILMEYPAI	TRLTVGAGRP	PDPAAPALGA	PGLNGLSLG	DEDFSSSIADP	DFSALLSQIS	S

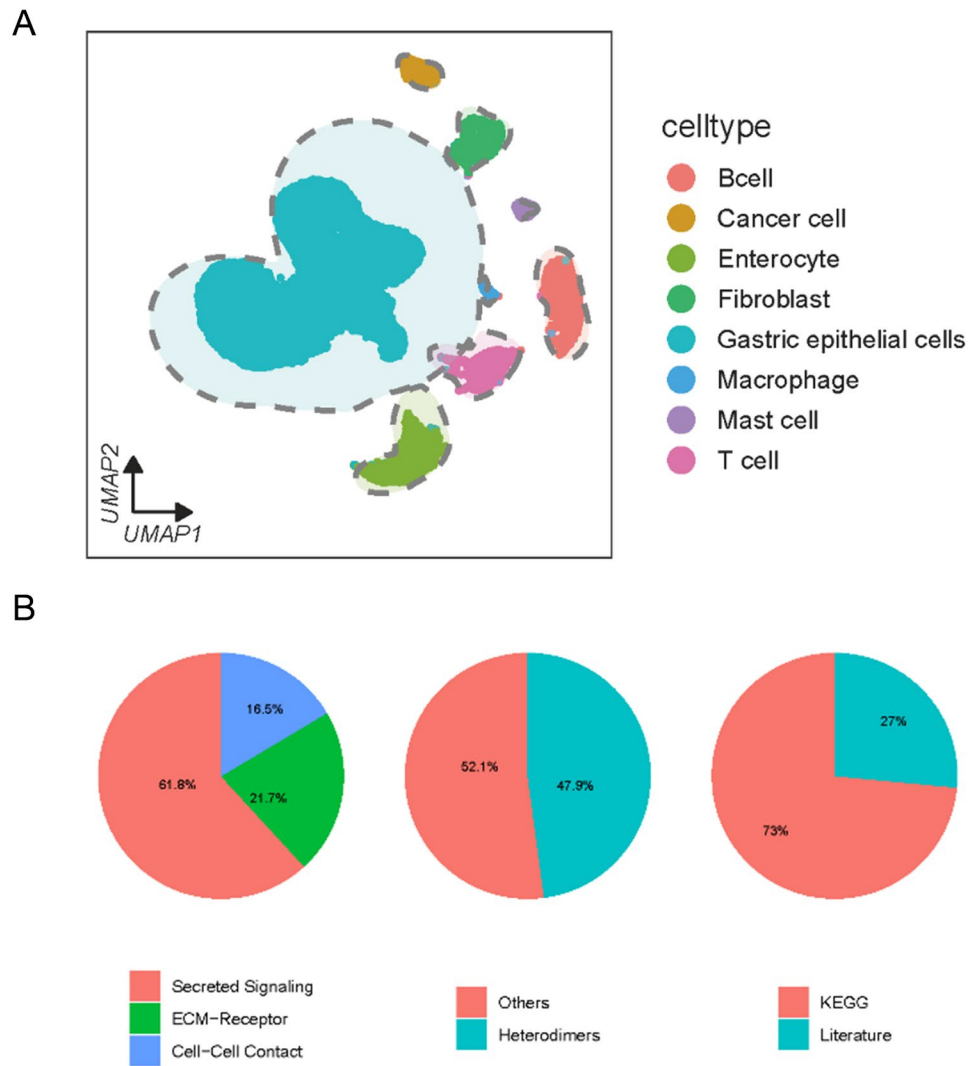


Figure S1 A variety of cell types in GEE135220 (A) and CellChatDB for cell communication analysis(B).

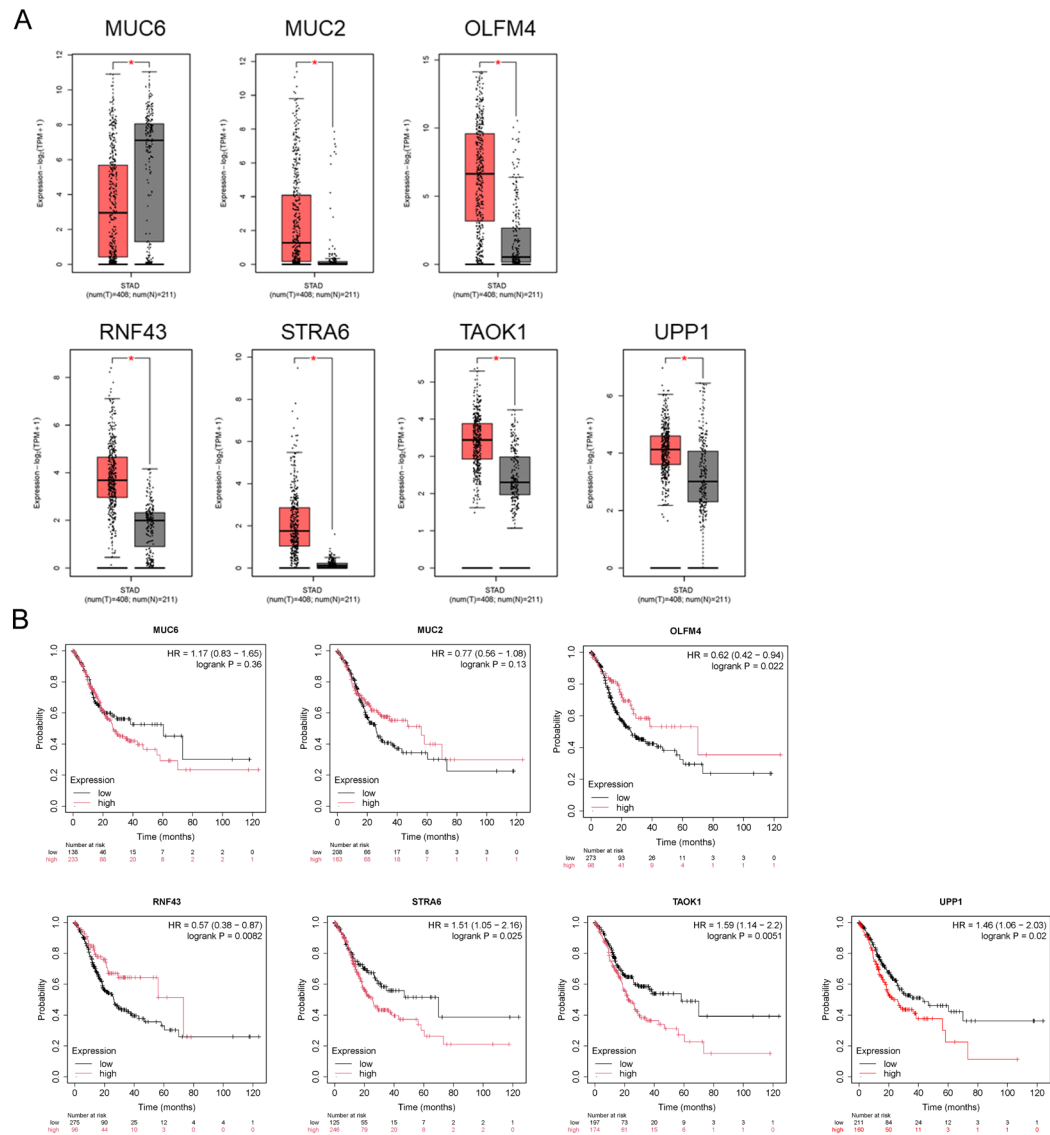
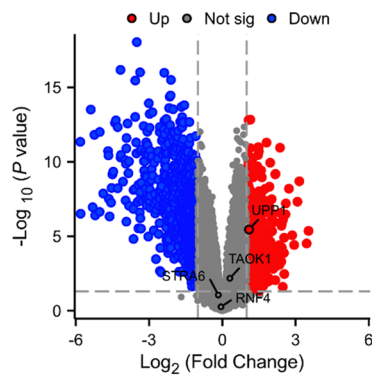
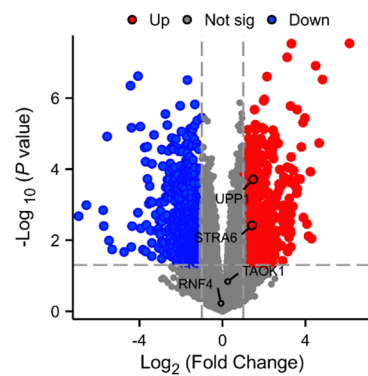


Figure S2 Expression level (A) and survival curves (B) of all key genes in gastric adenocarcinoma from the GEPIA and Kaplan-Meier Plotter databases. * $p < 0.05$; ** $p < 0.01$; * $p < 0.001$.**

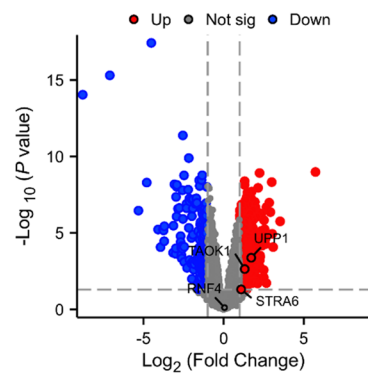
Normal VS GC



GSE118916
Samples (30):
15 gastric normal tissue
15 gastric cancer



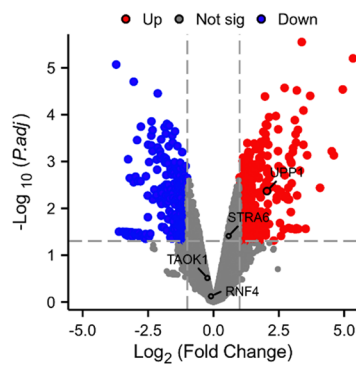
GSE103236
Samples (20):
10 gastric normal tissue
10 gastric cancer



GSE2685
Samples (30):
8 gastric normal tissue
22 gastric cancer

Figure S3 The datasets of gastric cancer and adjacent tissues included GSE118916, GSE103236 and GSE2685.

HP- VS HP+



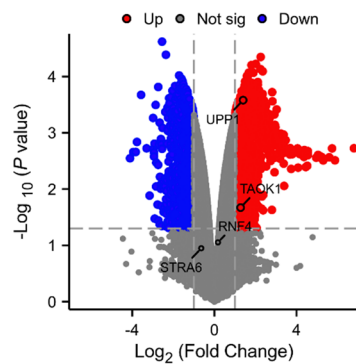
GSE108305

Samples (4):

2 Uninfected AGS cells

2 AGS cells infected with *H. pylori*

AGS cells were infected with *H. pylori* 26695 at 100 MOI for 4 h.



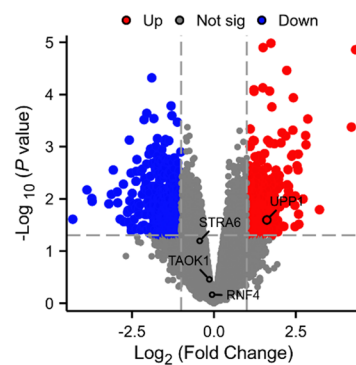
GSE70394

Samples (6):

3 Uninfected AGS cells

3 AGS cells infected with *H. pylori*

The human gastric carcinoma-derived cell line AGS was infected with *H. pylori* strain 60190 (ATCC 49503) for 24 hours.



GSE5081

Samples (16):

8 Gastric biopsy HP- ER-

8 Gastric biopsy HP+ ER+

Total RNA was extracted from frozen gastric biopsy specimens of patients with *Helicobacter pylori* positive (HP+) and *Helicobacter pylori* negative (HP-) antrum erosions (ER+)

Figure S4 The data sets of HP-positive and HP-negative gastric cancer included GSE108305, GSE70394 and GSE5081.

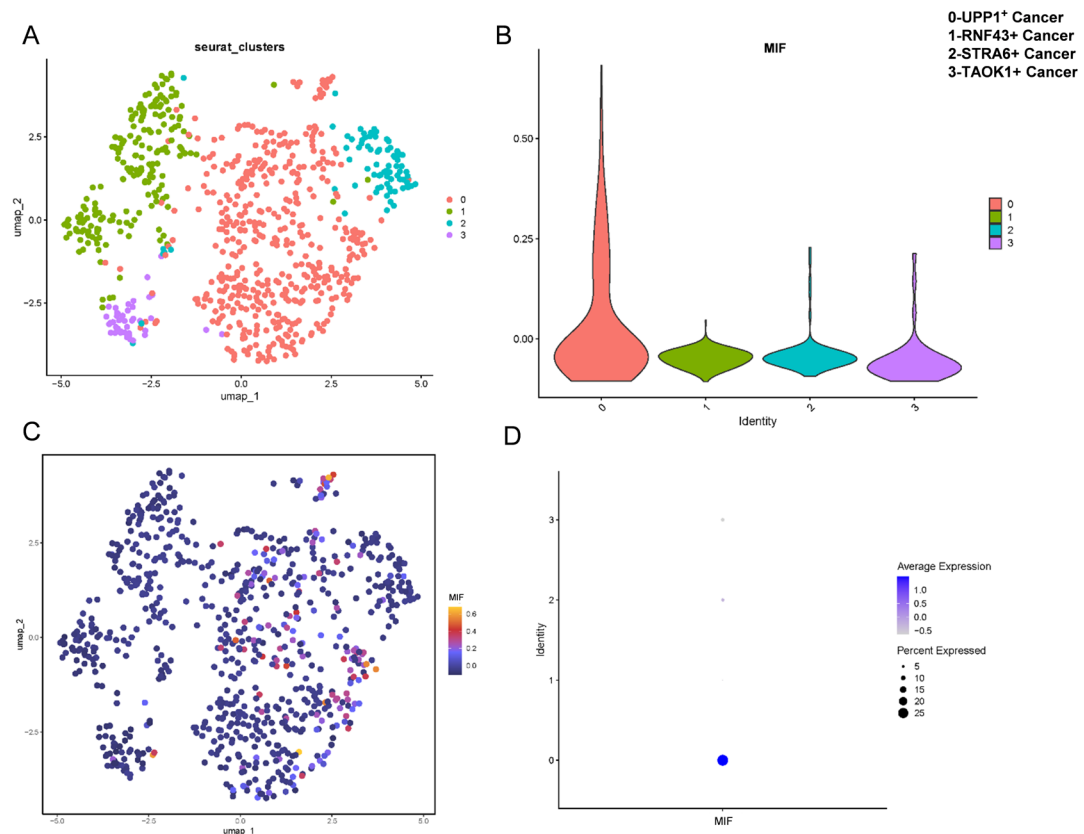


Figure S5 AddModuleScore is useful for the quantitative assessment of the MIF pathway in relation to UPP1 cancer clusters.

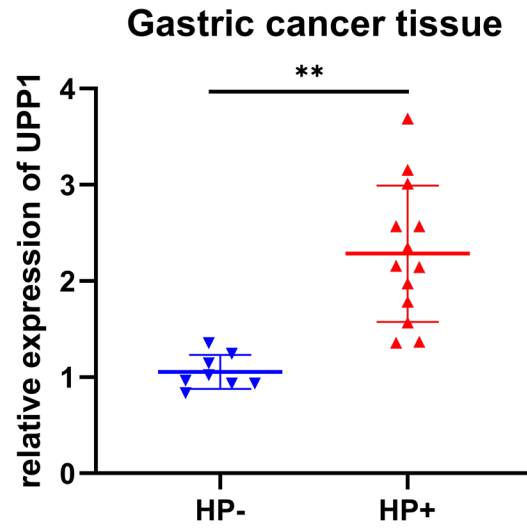


Figure S6 Compared with HP-negative gastric cancer tissues, the expression level of UPP1 in gastric cancer tissues infected with HP was significantly increased. * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$.