



Figure S1 Validation of *CMTM4* overexpression and knockdown RT-qPCR. (A,B) Overexpression of *CMTM4* in AGS and SGC7901 cells determined by RT-qPCR. (C) Knockdown of *CMTM4* in AGS cells was determined by RT-qPCR. *, P<0.05; ***, P<0.001. RT-qPCR, real-time reverse transcription polymerase chain reaction.

Table S1 Demographic profiles of patients whose biopsies are included in this study

Patient characteristics	Chronic superficial gastritis	Gastric adenocarcinoma	P value
Age (years)	46±14.31	62±10.09	<0.01
Gender			0.359
Female	10 (43.5%)	7 (30.4%)	
Male	13 (56.5%)	16 (69.6%)	

The age data was presented as mean ± standard deviation and the gender data was presented as n (%).

Table S2 Differentially expressed proteins in AGS-CMTM4OE group compared with AGS-NC group

Protein	Description	log ₂ FC AGS-CMTM4OE. vs.AGS-NC	P value	AGS- CMTM4OE-1	AGS-CMTM4OE-2	AGS-CMTM4OE-3	AGS-NC-1	AGS-NC-2	AGS-NC-3
EmGFP-LacZ-E2F-TdTom	Beta-galactosidase (Fragment)	-1.357	0.022	2,358.2	2,619.4	3,086.6	5,568.4	8,514.2	6,572.6
B4DZ36	cDNA FLJ58441, highly similar to Attractin	-0.868	0.043	763	819.6	778.8	1,529.9	1,559.1	1,219.4
A8K5X7	cDNA FLJ76854	-0.644	0.015	73.2	76.4	78	121	117.5	117.1
TRAPPC2B	Trafficking protein particle complex subunit 2B	-0.572	0.011	340.2	261	227.5	381	403.4	447.2
NEDD8	NEDD8	-0.486	0.006	37.7	49.6	40.3	49.8	64.3	64.6
CARD4	Caspase recruitment domain family, member 4	-0.405	0.048	346.5	323.9	318.1	464.4	431.4	412.9
CDK13	Cyclin-dependent kinase 13 (Fragment)	-0.377	0.048	94.9	83.9	78.5	101.5	126.1	106.6
TF	Serotransferrin (Fragment)	-0.376	0.037	501.6	512	530.4	705.4	615.1	683.2
NPRL2	GATOR complex protein NPRL2	-0.348	0.025	101.6	91.3	74.1	114.1	110.1	115.7
HPS5	Hermansky-Pudlak syndrome 5 protein	-0.341	0.009	39.8	38	43	51.8	52.9	48.3
SLC39A9	Solute carrier family 39 (Zinc transporter), member 9, isoform CRA_b	-0.319	0.035	124.5	119.7	107.4	149.1	155.1	134.4
B2RBS8	cDNA, FLJ95666, highly similar to Homo sapiens albumin (ALB), mRNA	-0.305	0.001	2,964.3	2,616	2,809.4	3,705.8	3,490.2	3172.1
RPAP1	RNA polymerase II-associated protein 1	-0.299	0.000	27	27.8	27.2	34.7	32.8	33.4
XRCC3	Full-length cDNA clone CS0DC014YE11 of Neuroblastoma of Homo sapiens (human)	-0.291	0.045	75.9	78.3	67.9	86.8	96.9	88.1
B3KXB8	cDNA FLJ45106 fis, clone BRAWH3033293, highly similar to Synaptopodin	-0.291	0.022	86.8	80.9	77.5	109.1	98.5	92.4
B4DNA3	Adenylyl cyclase-associated protein	-0.288	0.024	96.7	94.2	101.8	111.1	121	125.3
PLEKHN1	Pleckstrin homology domain-containing family N member 1	-0.283	0.006	82	78.4	74.7	103.8	91.6	90.7
ALDH3A1	ALDH3A1 protein (Fragment)	0.264	0.004	8,026.9	8,154.5	8,633.1	6,070.3	7,233.3	7,367.1
NMI	N-myc-interactor	0.265	0.022	2,883.9	2,709.4	2,784.4	2,035	2,467.4	2,468.1
MAOB	Amine oxidase [flavin-containing] B	0.296	0.021	3,991.1	3,913.9	3,658.3	2,734.5	3,397.3	3,285.2
OLFM4	Olfactomedin 4, isoform CRA_a	0.297	0.030	1,297.2	1,217	1,180.1	1,142.5	941	922.7
ZNF703	Zinc finger protein 703	0.299	0.025	1,162.5	1,173.5	1,268.7	873.3	1,001	1,055.7
NDUFA4	Cytochrome c oxidase subunit NDUFA4	0.300	0.038	2,965.1	3,266.7	3,177.7	2,279.2	2,709.6	2,652.2
STAT1	Signal transducer and activator of transcription 1-alpha/beta	0.304	0.000	10,926.3	11,053.2	11,492.8	8,790	9,134.4	9,181.4
MX2	Interferon-induced GTP-binding protein Mx2	0.305	0.031	2,528.3	2,664.8	2,573.4	1,758.8	2,218.3	2,309.6
H2BC21	Histone H2B type 2-E	0.340	0.041	2,442.6	2,298.5	2,618.5	2,097.4	1,908.9	1,809.4
APOC3	Apolipoprotein C-III	0.349	0.011	286.6	236.6	237.7	183.3	218.5	195.4
TXNIP	Thioredoxin interacting protein (Fragment)	0.361	0.048	653.8	679.4	672.8	455.8	555.2	550.6
TFF1	Trefoil factor 1	0.414	0.023	211.3	203.7	190.8	126.9	166.5	161.3
HLA-A	MHC class I antigen (Fragment)	0.430	0.026	903.9	993.5	951.7	539.6	797.8	776.8
A8K4T9	cDNA FLJ77421, highly similar to Homo sapiens autoantigen p542 mRNA	0.437	0.049	432.8	379.5	384.9	250.3	335.9	298.4
BST2	Bone marrow stromal antigen 2	0.437	0.023	1,380.1	1,409.8	1241.9	768	1,133.8	1,076.5
CMTM4	CKLF-like MARVEL transmembrane domain-containing protein 4	1.127	0.049	1,318	1,263.6	951.2	529.2	556.6	532.1

NC, negative control.