

Figure S1 ROR2 promoted gastric cancer cell migration and invasion *in vitro*. (A,B) AGS and GTL16 cells stably expressing ROR2 WT and Con as well as MGC803 cells stably expressing shROR2 and NC were subjected to transwell migration (A, AGS-Con *vs.* AGS-ROR2 WT P=0.022736, GTL16-Con *vs.* GTL6-ROR2 WT P=0.000899, MGC803-Con *vs.* MGC803-ROR2 WT P=0.000868) and invasion assays (B, AGS-Con *vs.* AGS-ROR2 WT P=0.000305, GTL16-Con *vs.* GTL6-ROR2 WT P=0.003627, MGC803-Con *vs.* MGC803-ROR2 WT P=0.000487). Representative images at 200× magnification and quantitative analysis of transwell assays after crystal violet staining are presented. Columns are the mean of 3 independent experiments, and bars = SD. *P<0.05; **P<0.01; ***P<0.001; SD, standard deviation; ROR2 WT and Con, ROR2-overexpressing (WT) and the empty vector plasmids (Con); shROR2 and NC, short hairpin (shRNA) targeting *ROR2* (shROR2) and the empty vector plasmids (NC).



Figure S2 Screening for the ROR2-modulating gene. Representative qRT-PCR images of 15 genes closely related to tumor proliferation and migration were examined at the mRNA level according to signaling explorer antibody microarray. qRT-PCR was conducted using AGS-ROR2 WT, GTL16-ROR2 WT, SNU216-ROR2 WT, SNU601-ROR2, SGC7901-shROR2, MGC803-shROR2, and their respective control cells. Relative mRNA expressions are presented in groups. qRT-PCR, quantitative real-time polymerase chain reaction; ROR2 WT and Con, ROR2-overexpressing (WT) and the empty vector plasmids (Con); shROR2 and NC, short hairpin (shRNA) targeting *ROR2* (shROR2) and the empty vector plasmids (NC).

Table S1 Sequence of qRT-PCR primers

Primer	Sequence	
ROR2 forward	TCCGAACGACCCTTTAGGAC	
ROR2 reverse	TTTAGCCACCGCACGTTAGG	
B2M forward	GAGGCTATCCAGCGTACTCCA	
B2M reverse	CGGCAGGCATACTCATCTTT	
SVOP forward	AAGACTGAATTTTTGCCCACGA	
SVOP reverse	GCCAAGCCAATGATGAGCA	
NKX2-6 forward	GTACCTGAGAATGGACGCAGA	
NKX2-6 reverse	GCTCCGAACCATCCAGCTTT	
RAB20 forward	AAGCCCGACAGCAAGATCG	
RAB20 reverse	GGTGATTCACATCATAGGTGAGG	
STAT3 forward	CAGCAGCTTGACACACGGTA	
STAT3 reverse	AAACACCAAAGTGGCATGTGA	
AARSD1 forward	CTGGCTCATGTGGAACATTATGC	
AARSD1 reverse	GCAGGTGGAGGTCTCTTGG	
STMN4 forward	CTGGCCGATCCCCTGAATAAG	
STMN4 reverse	TCCAGTCAGCACTGTCTTTCC	
Claudin11 forward	CGGTGTGGCTAAGTACAGGC	
Claudin11 reverse	CGCAGTGTAGTAGAAACGGTTTT	
AKT2 forward	ACCACAGTCATCGAGAGGACC	
AKT2 reverse	GGAGCCACACTTGTAGTCCA	
SLC25A21 forward	CCAAGCCTGAAGTCAGCTTAG	
SLC25A21 reverse	TGCACATCTCTGAATCTGAAACC	
Calcyclin forward	GGGAGGGTGACAAGCACAC	
Calcyclin reverse	AGCTTCGAGCCAATGGTGAG	
SLC39A7 forward	GGACACGCTCACAGTCATACA	
SLC39A7 reverse	CTCCTCGCCTCTTCTGAACC	
LAMA1 forward	GTGATGGCAACAGCGCAAA	
LAMA1 reverse	GACCCAGTGATATTCTCTCCCA	
CDH9 forward	TTCCATACAGTTGACACCATCCT	
CDH9 reverse	TCAGACCCGCTATCTTTTGC	
TIMP1 forward	CTTCTGCAATTCCGACCTCGT	
TIMP1 reverse	ACGCTGGTATAAGGTGGTCTG	
Androgen receptor forward	CCAGGGACCATGTTTTGCC	
Androgen receptor reverse	CGAAGACGACAAGATGGACAA	

Table S1	(continued)
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Table S1 (continued)

Primer	Sequence
FOXA2 forward	GGAGCAGCTACTATGCAGAGC
FOXA2 reverse	CGTGTTCATGCCGTTCATCC
MMP3 forward	CTGGACTCCGACACTCTGGA
MMP3 reverse	CAGGAAAGGTTCTGAAGTGACC
PIAS1 forward	ACAGTGCGGAACTAAAGCAAA
PIAS1 reverse	GGACTTGAATGTACGTTGGGG
<i>HIF1</i> α forward	ATGTAATGCTCCCCTCACCC
$HIF1\alpha$ reverse	CCTGAATCTGGGGCATGGTA
EPAS1 forward	CGGAGGTGTTCTATGAGCTGG
EPAS1 reverse	AGCTTGTGTGTTCGCAGGAA
ANGPTL4 forward	GGGTCTGGAGAAGGTGCATA
ANGPTL4 reverse	GTGGAGAAGGGTACGGAGAG
VEGFA forward	CTGTCTTGGGTGCATTGGAG
VEGFA reverse	ACCAGGGTCTCGATTGGATG
MMP3-region 1-forward	AGCTATGTATGTACACTTTCCACT
MMP3-region 1-reverse	AGAGAAGAAGTAGGTTGACTTGGT
MMP3-region 2-forward	TGTGTTGCCTTGCAAAATTGG
MMP3-region 2-reverse	TTCATCCAAATGGCAGCAGG
MMP3-region 3-forward	TGGAATGTTTGGAAATGGTCCTG
MMP3-region 3-reverse	GCGCAGCTTTTAAAGAGTGACA

qRT-PCR, quantitative real-time polymerase chain reaction.

Table S2 Sequence of shRNAs

shRNA	Sequence
shROR2#1	ACAAGCTGAACGTGAAGAT
shROR2#2	ACAGCCCAAATCATAACTT

 Table S3 Predicted c-JUN binding sites in MMP3 promoter region

Predicted site	Initial position	Terminal position	Sequence
CBS-1	-468	-455	CTTACATCTTTTA
CBS-2	-203	-190	GTTGTATCATCCT
CBS-3	-137	-124	AGGATGAGTCAAG