Supplemental Table 1: circCRIM1 expression in normal ovarian and ovarian cancer tissues

Groups	N	circCRIM1 expression / β-actin	*P* value
Normal ovarian tissues	24	0.128±0.050	***0.001***
ovarian cancer tissues	130	0.914±0.223	

Bold and Italics means $P < 0.05$.

Supplemental Table 2: CRIM1 expression in normal ovarian and ovarian cancer tissues

Groups	N	CRIM1 expression / β-actin	*P* value
Normal ovarian tissues	24	0.238±0.063	***0.015***
Ovarian cancer tissues	130	0.992±0.299	

Bold and Italics means $P < 0.05$.

Supplemental Table 3: Correlation of circCRIM1 expression with different clinicopathological features of ovarian cancer

Clinicopathological features	N	circCRIM1 expression / β-actin	*P* value
The pathology types			0.254
Serous carcinoma	101	0.780±0.256	
The other pathology types	29	1.382 ±0.454	
Age			1.000
≤ 52	67	0.914 ±0.316	
> 52	63	0.915 ±0.319	
FIGO stages			0.067
I-II	44	0.471 ±0.172	
III-IV	85	1.155 ±0.328	
Pathology classification			0.464
Well+Mod	28	0.636±0.238	
Poor	99	0.898±0.266	

Bold and Italics means P < 0.05, one ovarian cancer patient lacks information on stage, and three lack information on differentiation.

Supplemental Table 4: Correlation of CRIM1 expression with different clinicopathological features of ovarian cancer

Clinicopathological features	N	CRIM1 expression / β-actin	*P* value
The pathology types			0.338
Serous carcinoma	101	0.839 ±0.342	
The other pathology types	29	1.526 ±0.621	
Age			0.914
≤ 52	67	1.023 ±0.461	
> 52	63	0.959 ±0.380	
FIGO stages			0.110
I-II	44	0.475 ±0.202	
III-IV	85	1.261 ±0.444	
Pathology classification			0.073
Well+Mod	28	0.348±0.102	
Poor	99	1.023±0.359	

Bold and Italics means $P < 0.05$, one ovarian cancer patient lacks information on stage, and three lack information on differentiation.

Supplemental Table 5: circCRIM1 expression plasmid construction (The bold area are circCRIM1 sequences)

GGGAATGGAGCTATATAGCAGAGCTCGTTTAGTGACCGTCAGATCGCCTGGAGACGCCATC
CACGCTGTTTTGACCTCCATAGAAGACACCGACTCTACTAGAGGATCTATTTCCGGTGAATT
CAAAGTGCTGAGATTACAGGCGTGAGCCACCACCCCCGGCCCACTTTTTGTAAAGGTACGT
ACTAATGACTTTTTTTTTATACTTCAG**ATGAGAACTGGACTGATGACCAACTGCTTGGTT**
TTAAACCATGCAATGAAAACCTTATTGCTGGCTGCAATATAATCAATGGGAAATGTGAA
TGTAACACCATTCGAACCTGCAGCAATCCCTTTGAGTTTCCAAGTCAGGATATGTGCC
TTTCAGCTTTAAAGAGAATTGAAGAAGAGAAGCCAGATTGCTCCAAGGCCCGCTGTG
AAGTCCAGTTCTCTCCACGTTGTCCTGAAGATTCTGTTCTGATCGAGGGTTATGCTCC
TCCTGGGGAGTGCTGTCCCTTACCCAGCCGCTGCGTGTGCAACCCCGCAGGCTGTCT
GCGCAAAGTCTGCCAGCCGGGAAACCTGAACATACTAGTGTCAAAAGCCTCAGGGAA
GCCGGGAGAGTGCTGTGACCTCTATGAGTGCAAACCAGTTTTCGGCGTGGACTGCAG
GACTGTGGAATGCCCTCCTGTTCAGCAGACCGCGTGTCCCCCGGACAGCTATGAAAC
TCAAGTCAGACTAACTGCAGATGGTTGCTGTACTTTGCCAACAAGGTAAGAAGCAAGG
AAAAGAATTAGGCTCGGCACGGTAGCTCACACCTGTAATCCCAGCAGGATCCATCGATACT
AGTAAGGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCCACAGTC
CCCGAGAAGTTGGGGGGAGGGGTCGGCAATTGAACGGGTGCCTAGAGAAGGTGGCGCGG
GGTAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTTCCCGAGGGGTGGGG

Supplemental Table 6: The sequences of shRNA targeting circCRIM1 (The bold area are the target sequences)

sh1-circCRIM1

Top strand:

GATCCG**TGCCAACAAGATGAGAACTGGAC**TTCAAGAGA**GTCCAGTTCTCATCTTGTTGGCA**TTTTTTC

Bottom strand:

AATTGAAAAAA**TGCCAACAAGATGAGAACTGGAC**TCTCTTGAA**GTCCAGTTCTCATCTTGTTGGCA**CG

sh2-circCRIM1

Top strand:

GATCCG**ACTTTGCCAACAAGATGAGAACTG**TTCAAGAGA**CAGTTCTCATCTTGTTGGCAAAGT**TTTTTTC

Bottom strand:

AATTGAAAAAA**ACTTTGCCAACAAGATGAGAACTG**TCTCTTGAA**CAGTTCTCATCTTGTTGGCAAAGT**CG

Supplemental Table 7: circCRIM1-FLAG expression plasmid construction (The bold area are 3×flag sequences)

AAAGTGCTGAGATTACAGGCGTGAGCCACCACCCCCGGCCCACTTTTTGTAAAGGTACGT
ACTAATGACTTTTTTTTTATACTTCAGATGAG**GACTACAAGGATGACGATGACAAGGAT**
TACAAAGACGACGATGATAAGGACTATAAGGATGATGACGACAAAAACTGGACTGAT
GACCAACTGCTTGGTTTTAAACCATGCAATGAAAACCTTATTGCTGGCTGCAATATAATCA
ATGGGAAATGTGAATGTAACACCATTCGAACCTGCAGCAATCCCTTTGAGTTTCCAAGTCA
GGATATGTGCCTTTCAGCTTTAAAGAGAATTGAAGAAGAGAAGCCAGATTGCTCCAAGGC
CCGCTGTGAAGTCCAGTTCTCTCCACGTTGTCCTGAAGATTCTGTTCTGATCGAGGGTTAT
GCTCCTCCTGGGGAGTGCTGTCCCTTACCCAGCCGCTGCGTGTGCAACCCCGCAGGCTGTC
TGCGCAAAGTCTGCCAGCCGGGAAACCTGAACATACTAGTGTCAAAAGCCTCAGGGAAGC
CGGGAGAGTGCTGTGACCTCTATGAGTGCAAACCAGTTTTCGGCGTGGACTGCAGGACTG
TGGAATGCCCTCCTGTTCAGCAGACCGCGTGTCCCCCGGACAGCTATGAAACTCAAGTCA
GACTAACTGCAGATGGTTGCTGTACTTTGCCAACAAGGTAAGAAGCAAGGAAAAGAATTA
GGCTCGGCACGGTAGCTCACACCTGTAATCCCAGCA

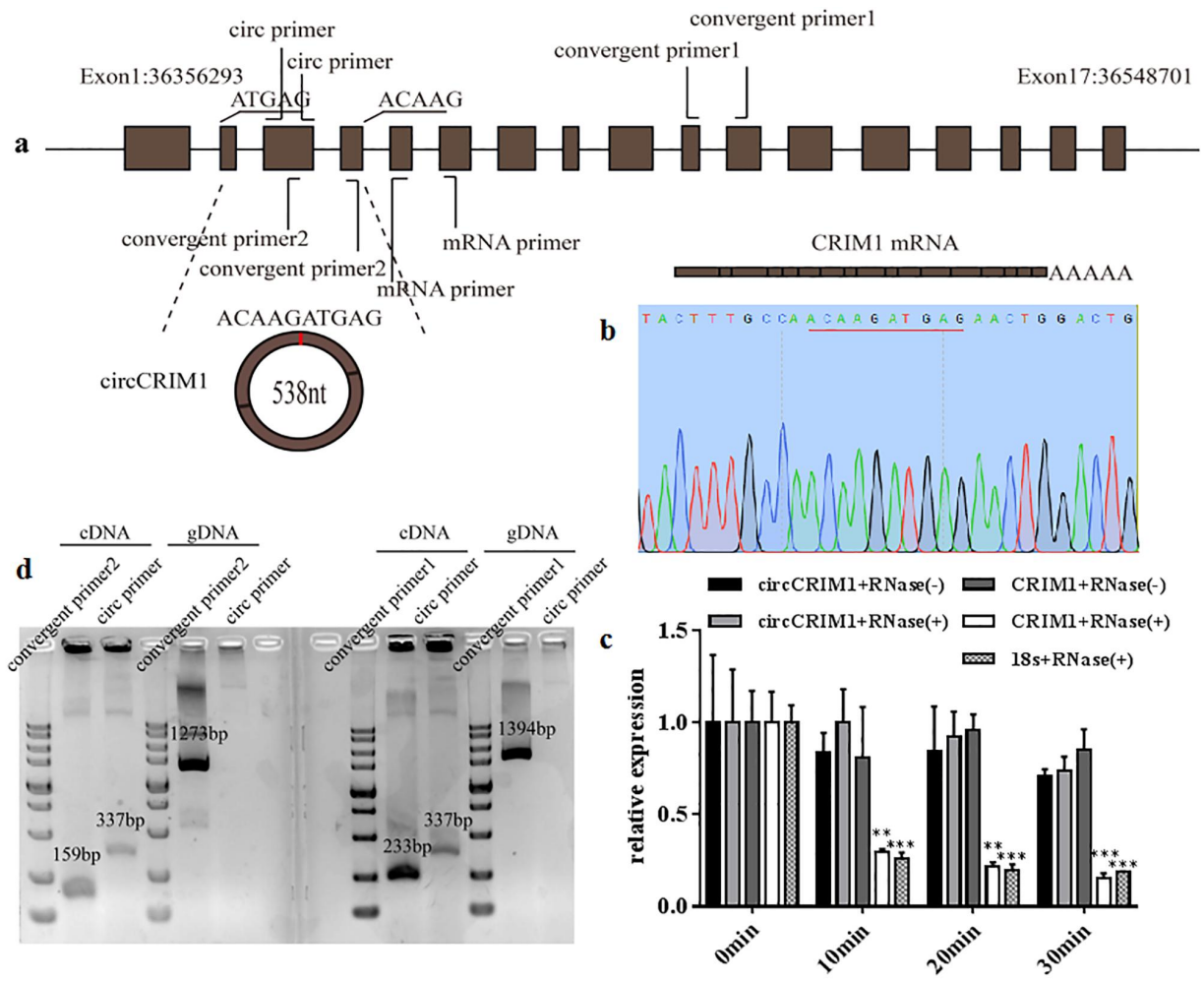
Supplemental Table 8: The introduced sequences of 188aa-flag plasmid (The bold area are 3×flag sequences)

ATGGTTGCTGTACTTTGCCAACAAGATGAGAACTGGACTGATGACCAACTGCTTGGTTTTAAACCATGCAAT
GAAAACCTTATTGCTGGCTGCAATATAATCAATGGGAAATGTGAATGTAACACCATTCGAACCTGCAGCAATC
CCTTTGAGTTTCCAAGTCAGGATATGTGCCTTTCAGCTTTAAAGAGAATTGAAGAAGAGAAGCCAGATTGCT
CCAAGGCCCGCTGTGAAGTCCAGTTCTCTCCACGTTGTCCTGAAGATTCTGTTCTGATCGAGGGTTATGCTCC
TCCTGGGGAGTGCTGTCCCTTACCCAGCCGCTGCGTGTGCAACCCCGCAGGCTGTCTGCGCAAAGTCTGCC
AGCCGGGAAACCTGAACATACTAGTGTCAAAAGCCTCAGGGAAGCCGGGAGAGTGCTGTGACCTCTATGA
GTGCAAACCAGTTTTCGGCGTGGACTGCAGGACTGTGGAATGCCCTCCTGTTCAGCAGACCGCGTGTCCCC
CGGACAGCTATGAAACTCAAGTCAGACTAACTGCAGATGGTTGCTGTACTTTGCCAACAAGA**GACTACA**
AGGATGACGATGACAAGGATTACAAAGACGACGATGATAAGGACTATAAGGATGAT
GACGACAAATGA

Supplemental Table 9: The detail of primer sequences

Names	Sequences
circ primer	L 5'-agtgctgtgacctctatga-3'
	R 5'-ctggcttctcttcttcaattc-3'
convergent primer1	L 5'-acatctgtcgctgtaagaa-3'
	R 5'-catttcccgtccattgaga-3'
convergent primer2	L 5'-gtgctgtcccttaccca-3'
	R 5'-cagtccacgccgaaa-3'
mRNA primer	L 5'-ctctggcttatgtggtttcc-3'
	R 5'-cgcaggctggctttgt-3'

Supplemental Figure 1: CircCRIM1 is derived from CRIM1 by back-splicing



CircCRIM1 was generated from exon2-4 of CRIM1 (a). Sanger sequencing verified the back-splicing junction of circCRIM1 (b). CircCRIM1 was more resistant to RNase R than CRIM1 and 18s (c). CircCRIM1 was only derived from RNA but not DNA (d). Three separate experiments were conducted; Data are shown as the mean ± SD. *P < 0.05, **P<0.01, ***P<0.001 and ****P<0.0001.