

Supplementary Information for

**RGS3 acts as a tumor promoter by facilitating the activation of the
TGF- β signaling pathway and promoting EMT in ovarian cancer**

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Figure S1

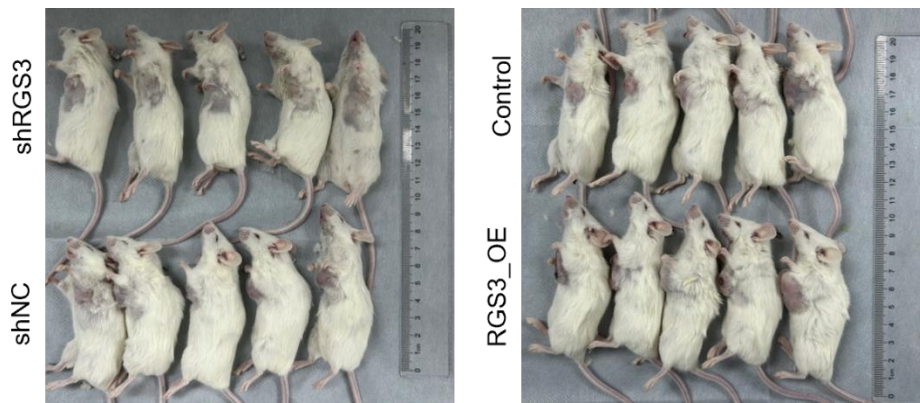


Figure S1. Xenograft tumor growth and size comparison between RGS3 knockdown and overexpression groups.

Figure S2

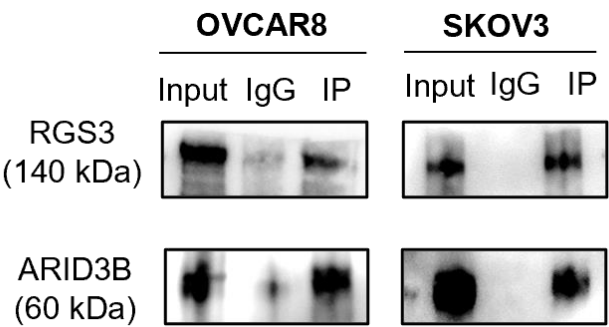


Figure S2. Co-immunoprecipitation of ARID3B and RGS3 in SKOV3 and OVCAR8 cells.

Figure S3

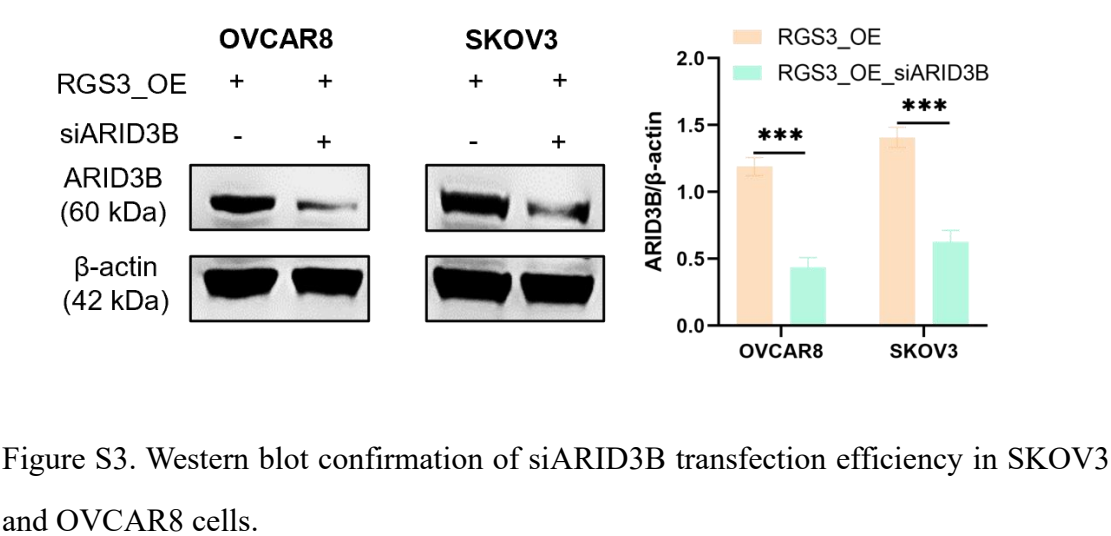


Table S1. Relationship between RGS3 expression level and clinical characteristic parameters of patients

Clinical parameters	Cases (n)	RGS3 expression (%)		p-value
		Low	High	
Age (years)				
≥ 50	27	10	17	0.553
< 50	4	1	3	
FIGO staging				
I	1	1	0	0.3703
II	2	1	1	
III	4	2	2	
IV	6	1	5	
T stage				
T1	1	1	0	0.2956
T2	4	2	2	
T3	8	2	6	
N stage				
N1	9	4	5	>0.99
N0	4	1	3	
M stage				
M1	8	4	4	0.5649
M0	5	1	4	
Pathology diagnosis				
Normal ovarian tissue	5	5	0	0.0002
Ovarian serous carcinoma	13	6	7	
Metastasis serous carcinoma from ovary	13	0	13	

Table S2. Pairing residues of RGS3-ARID3B interaction interface

Receptor-ligand interface residue pair(s)	residue spacing (Å)
105A-518A	3.968
109A-443A	2.805
110A-443A	4.208
110A-447A	4.5
111A-440A	4.455
111A-443A	3.323
111A-444A	4.627
111A-447A	3.063
112A-443A	2.798
112A-446A	3.518
112A-447A	4.08
112A-450A	3.504
113A-447A	2.989
113A-450A	2.378
114A-450A	4.152
114A-454A	4.835
115A-450A	3.001
115A-454A	3.436
116A-454A	3.278
117A-511A	4.396
117A-513A	3.094
118A-510A	3.854
119A-453A	4.918
119A-454A	3.065
119A-457A	3.324
119A-458A	3.991
121A-501A	4.887
122A-457A	2.792
122A-466A	2.898
122A-497A	4.851
122A-499A	2.819
122A-501A	3.415
123A-457A	3.529
123A-460A	3.991
123A-464A	3.055
123A-466A	4.842
123A-501A	4.629
125A-460A	4.774
129A-123A	3.365
131A-120A	3.418

131A-123A	3.137
132A-335A	4.852
132A-336A	4.551
133A-116A	3.365
133A-119A	4.782
133A-120A	4.598
134A-120A	2.212
136A-116A	4.399
136A-335A	4.544
165A-438A	4.096
165A-442A	3.38
165A-446A	3.639
166A-435A	3.599
166A-438A	4.764
166A-439A	2.45
167A-434A	4.178
167A-435A	1.543
167A-438A	4.261
168A-435A	2.806
169A-435A	4.348
182A-513A	3.221
184A-518A	2.787
226A-435A	4.583
228A-433A	4.877
228A-435A	4.522
229A-436A	3.953
231A-436A	4.324
231A-439A	3.863
234A-446A	4.299
257A-335A	4.919
261A-446A	2.705
262A-446A	3.655
262A-449A	2.76
262A-450A	3.346
262A-453A	4.948
273A-338A	2.775
274A-331A	4.493
274A-334A	2.585
274A-335A	2.957
274A-338A	3.493
275A-338A	2.631

Docking Score: -260.56 kcal/mol

Confidence Score: 0.9013

Ligand rmsd (Å): 80.94

Docking Score: The docking scores are calculated by ITScorePP or ITScorePR. A more negative docking score means a more possible binding model.

Confidence Score: to indicate the binding likeliness of two molecules as follows. Roughly, when the confidence score is above 0.7, the two molecules would be very likely to bind.

- $$\text{Confidence_score} = 1.0 / [1.0 + e^{0.02 * (\text{Docking_Score} + 150)}]$$

Ligand rmsd: The ligand RMSDs are calculated by comparing the ligands in the docking models with the input or modeled structures.

Interface redidues: The interface information for each model includes all the residue pairs within 5.0 Å between the receptor and the ligand for the corresponding model.

Users can click to check/download the files for different models.

RGS3 short hairpin RNA (shRNA) Sequence

ATGGAGTGGCTAAGCCCTGATATCGCTCTGCCCAGAAGAGATGAGTGGACT
CAAACCTTCTCCAGCCAGGAAGAGGATCACGCATGCCAAAGTCCAGGGTGC
AGGTCAGCTGAGGCTGTCCATTGATGCCCAGGACCGGGTTCTGCTGCTTCA
CATTATAGAAGGTAAAGGCCTGATCAGCAAACAGCCTGGCACCTGTGATCC
GTATGTGAAGATTTCTTTGATCCCTGAAGATAGTAGACTACGCCACCAGAA
GACGCAGACCGTTCCAGACTGCAGAGACCCGGCTTCCACGAGCACTTCT
TCTTTCCTGTCCAAGAGGAGGATGATCAGAAGCGTCTCTTGGTTACTGTGT
GGAACAGGGCCAGCCAGTCCAGACAGAGTGGACTCATTGGCTGCATGAGC
TTTGGGGTGAAGTCTCTCCTGACTCCAGACAAGGAGATCAGTGGTTGGTAC
TACCTCCTAGGGGAGCACCTGGGCCGGACCAAGCACTTGAAGGTGGCCAG
GCGGCGACTGCGGCCGCTGAGAGACCCGCTGCTGAGAATGCCAGGAGGTG
GGGACACTGAGAATGGGAAGAACTAAAGATCACCATCCCGAGGGGAAA
GGACGGCTTTGGCTTCACCATCTGCTGCGACTCTCCAGTTCGAGTCCAGGC
CGTGGATTCCGGGGGTCCGGCGGAACGGGCAGGGCTGCAGCAGCTGGAC
ACGGTGCTGCAGCTGAATGAGAGGCCTGTGGAGCACTGGAAATGTGTGGA
GCTGGCCCACGAGATCCGGAGCTGCCCCAGTGAGATCATCCTACTCGTGTG
GCGCATGGTCCCCCAGGTCAAGCCAGGACCAGATGGCGGGGTCTGCGGC
GGGCCTCCTGCAAGTCGACACATGACCTCCAGTCACCCCCCAACAAACGG
GAGAAGAAGTGCACCCATGGGGTCCAGGCACGGCCTGAGCAGCGCCACA
GCTGCCACCTGGTATGTGACAGCTCTGATGGGCTGCTGCTCGGCGGCTGGG
AGCGCTACACCGAGGTGGCCAAGCGCGGGGGCCAGCACACCCTGCCTGCA
CTGTCCCGTGCCACTGCCCCACCGACCCCAACTACATCATCCTGGCCCCG
CTGAATCCTGGGAGCCAGCTGCTCCG**GCCTGTGTACCAGGAGGATAC**CATC
CCCGAAGAATCAGGGAGTCCCAGTAAAGGGAAGTCCTACACAGGCCTGGG
GAAGAAGTCCCGGCTGATGAAGACAGTGCAGACCATGAAGGGCCACGGG
AACTACCAAACTGCCCCGGTTGTGAGGCCGCATGCCACGCACTCAAGCTAT
GGCACCTACGTACCCCTGGCCCCCAAAGTCCTGGTGTTCCTGTCTTTGTT
CAGCCTCTAGATCTCTGTAATCCTGCCCCGACCCTCCTGCTGTCAGAGGAG
CTGCTGCTGTATGAAGGGAGGAACAAGGCTGCCGAGGTGACACTGTTTGC
CTATTCGGACCTGCTGCTCTTCACCAAGGAGGACGAGCCTGGCCGCTGCGA
CGTCCTGAGGAACCCCCCTCTACCTCCAGAGTGTGAAGCTGCAGGAAGGTT
CTTCAGAAGACCTGAAATTCTGCGTGCTCTATCTAGCAGAGAAG**GCAGAGT**
GCTTATTCACCTTGGAAGCGCACTCGCAGGAGCAGAAGAAGAGAGTGTGC
TGGTGCCTGTCTCGGAGAACATCGCCAAGCAGCAACAGCTGGCAGCATCACC
CCCGGACAGCAAGATGTTTGAGACGGAGGCAGATGAGAAGAGGGAGATG
GCCTTGAGGAAGGGAAGGGGCCTGGTGCCGAGGATTCCCCACCCAGCAA
GGAGCCCTCTCCTGGCCAGGAGCTTCCTCCAGGACAAGACCTTCCACCCA
ACAAGGACTCCCCTTCTGGGCAGGAACCCGCTCCCAGCCAAGAACCACTG
TCCAGCAAAGACTCAGCTACCTCTGAAGGATCCCCCTCCAGGCCCAGATGCT
CCGCCCAGCAAGGATGTGCCACCATGCCAGGAACCCCTCCAGCCCAAGA
CCTCTCACCTGCCAGGACCTACCTGCTGGTCAAGAACCCCTGCCTCACCA
GGACCCTCTACTACCAAAGACCTCCCTGCCATCCAGGAATCCCCACCCG

GGACCTTCCACCCTGTCAAGATCTGCCTCCTAGCCAGGTCTCCCTGCCAGC
 CAAGGCCCTTACTGAGGACACCATGAGCTCCGGGGACCTACTAGCAGCTAC
 TGGGGACCCACCTGCGGCCCCCAGGCCAGCCTTCGTGATCCCTGAGGTCC
 GGCTGGATAGCACCTACAGCCAGAAGGCAGGGGCAGAGCAGGGCTGCTCG
 GGAGATGAGGAGGATGCAGAAGAGGCCGAGGAGGTGGAGGAGGGGGAG
 GAAGGGGAGGAGGACGAGGATGAGGACACCAGCGATGACAACCTACGGAG
 AGCGCAGTGAGGCCAAGCGCAGCAGCATGATCGAGACGGGGCCAGGGGGC
 TGAGGGTGGCCTCTCACTGCGTGTGCAGAACTCGCTGCGGGCGCCGGACGC
 ACAGCGAGGGCAGCCTGCTGCAGGAGCCCCGAGGGCCCTGCTTTGCCTCC
 GACACCACCTTGCCTGCTCAGACGGTGAGGGCGCCGCCTCCACCTGGGG
 CATGCCTTCGCCCAGCACCCCTCAAGAAAGAGCTGGGCGCAATGGTGGCT
 CCATGCACCACCTTTCCCTCTTCTTCACAGGACACAGGAAGATGAGCGGGG
 CTGACACCGTTGGGGATGATGACGAAGCCTCCCGGAAGAGAAAGAGCAA
 AAACCTAGCCAAGGACATGAAGAACAAGCTGGGGATCTTCAGACGGCGGA
 ATGAGTCCCCTGGAGCCCCCTCCCGCGGGCAAGGCAGACAAAATGATGAAG
 TCATTCAAGCCCACCTCAGAGGAAGCCCTCAAGTGGGGCGAGTCCTTGA
 GAAGCTGCTGGTTCACAAATACGGGTTAGCAGTGTTCCAAGCCTTCCTTCG
 CACTGAGTTCAGTGAGGAGAATCTGGAGTTCTGGTTGGCTTGTGAGGACTT
 CAAGAAGGTCAAGTCACAGTCCAAGATGGCATCCAAGGCCAAGAAGATCT
 TTGCTGAATACATCGCGATCCAGGCATGCAAGGAGGTCAACCTGGACTCCT
 ACACGCGGGAGCACACCAAGGACAACCTGCAGAGCGTCACGCGGGGCTG
 CTTCGACCTGGCACAGAAGCGCATCTTCGGGCTCATGGAAAAGGACTCGT
 ACCCTCGCTTTCTCCGTTCTGACCTCTACCTGGACCTTATTAACCAGAAGAA
 GATGAGTCCCCCGCTTTAG

RGS3 overexpression Sequence (RGS3-3Flag)

GGATCCGCAGAGTGCTTATTCACCTTTGTTCAAGAGACAAAGTGAATAAGCA
 CTCTGCTTTTTTTGAATTTCGAATTCGCCACCATGGAGTGGCTAAGCCCTGATA
 TCGCTCTGCCCAGAAGAGATGAGTGGACTCAAACCTTCTCCAGCCAGGAAG
 AGGATCACGCATGCCAAAGTCCAGGGTGCAGGTCAGCTGAGGCTGTCCAT
 TGATGCCCAGGACCGGGTTCTGCTGCTTCACATTATAGAAGGTAAAGGCCT
 GATCAGCAAACAGCCTGGCACCTGTGATCCGTATGTGAAGATTTCTTTGATC
 CCTGAAGATAGTAGACTACGCCACCAGAAGACGCAGACCGTTCCAGACTG
 CAGAGACCCGGCTTTCCACGAGCACTTCTTCTTTCTGTCCAAGAGGAGG
 ATGATCAGAAGCGTCTCTTGGTTACTGTGTGGAACAGGGGCCAGCCAGTCCA
 GACAGAGTGGACTCATTGGCTGCATGAGCTTTGGGGTGAAGTCTCTCCTGA
 CTCCAGACAAGGAGATCAGTGGTTGGTACTACCTCCTAGGGGAGCACCTG
 GGCCGGACCAAGCACTTGAAGGTGGCCAGGCGGCGACTGCGGCCGCTGA
 GAGACCCGCTGCTGAGAATGCCAGGAGGTGGGGACACTGAGAATGGGAA
 GAACTAAAGATCACCATCCCGAGGGGAAAGGACGGCTTTGGCTTCACCA
 TCTGCTGCGACTCTCCAGTTCGAGTCCAGGCCGTGGATTCCGGGGGTCCGG
 CGGAACGGGCAGGGCTGCAGCAGCTGGACACGGTGCTGCAGCTGAATGA
 GAGGCCTGTGGAGCACTGGAAATGTGTGGAGCTGGCCCACGAGATCCGGA
 GCTGCCCCAGTGAGATCATCCTACTCGTGTGGCGCATGGTCCCCCAGGTCA

AGCCAGGACCAGATGGCGGGGTCCTGCGGCGGGCCTCCTGCAAGTCGACA
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GGTCCAGGCACGGCCTGAGCAGCGCCACAGCTGCCACCTGGTATGTGACA
GCTCTGATGGGCTGCTGCTCGGCGGCTGGGAGCGCTACACCGAGGTGGCC
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TCTGAAGGATCCCCTCCAGGCCCAGATGCTCCGCCCAGCAAGGATGTGCCA
CCATGCCAGGAACCCCTCCAGCCCAAGACCTCTCACCCCTGCCAGGACCTA
CCTGCTGGTCAAGAACCCCTGCCTCACCAGGACCCTCTACTCACCAAAGA
CCTCCCTGCCATCCAGGAATCCCCCACCCGGGACCTTCCACCCTGTCAAGA
TCTGCCTCCTAGCCAGGTCTCCCTGCCAGCCAAGGCCCTTACTGAGGACAC
CATGAGCTCCGGGGACCTACTAGCAGCTACTGGGGACCCACCTGCGGCCCC
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GAAGGCAGGGGCAGAGCAGGGCTGCTCGGGAGATGAGGAGGATGCAGAA
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GAGGACACCAGCGATGACAACTACGGAGAGCGCAGTGAGGCCAAGCGCA
GCAGCATGATCGAGACGGGCCAGGGGGCTGAGGGTGGCCTCTCACTGCGT
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GACGGTGAGGGCGCCGCTCCACCTGGGGCATGCCTTCGCCCAGCACCCCT
CAAGAAAGAGCTGGGCCGCAATGGTGGCTCCATGCACCACCTTTCCCTCTT
CTTCACAGGACACAGGAAGATGAGCGGGGCTGACACCGTTGGGGATGATG
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GAACAAGCTGGGGATCTTCAGACGGCGGAATGAGTCCCCTGGAGCCCCCTC
CCGCGGGCAAGGCAGACAAAATGATGAAGTCATTCAAGCCCACCTCAGAG
GAAGCCCTCAAGTGGGGCGAGTCCTTGGAGAAGCTGCTGGTTCACAAATA
CGGGTTAGCAGTGTTCCAAGCCTTCCTTCGCACTGAGTTCAGTGAGGAGA
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TCCAAGATGGCATCCAAGGCCAAGAAGATCTTTGCTGAATACATCGCGATC
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ACAAGGATGACGACGATAAGGACTATAAGGACGATGATGACAAGGACTAC
AAAGATGATGACGATAAATAGGGATCC

Lentiviral vectors containing RGS3 short hairpin RNA (shRNA) and RGS3 overexpression constructs synthesized by General Biosystems (Anhui, China) are shown above. Control groups were infected with an empty vector.