# miR-335 restrains the aggressive phenotypes of ovarian cancer cells by inhibiting 1 COL11A1 2

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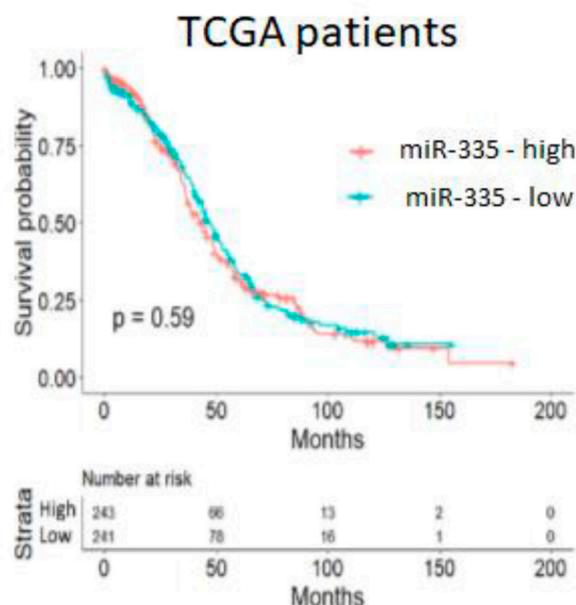
**Figure S1. Long-termoverall survivalsinthe TCGApatients (n= 8 483).**Kaplan–Meier curves stratified by the miR-335mRNA level and assessed by 9 log-rank testare illustrated.

**Table S1.**Complementary oligonucleotides used to construct 12 double-stranded, mutant miR-335-binding sites of COL11A1 3`-UTR or PDK1 13 3`-UTR.

| | Sequence |
|---|---|
| COL11A1 region 1 (Mut) F | GTAATTATTGGGTGTACAGTTCTATACT |
| COL11A1 region 1 (Mut) R | AGTATAGAACTGTACACCCAATAATTAC |
| COL11A1 region 2 (Mut) F | AAAATATTATGCAGGGTGATGCTTTATT |
| COL11A1 region 2 (Mut) R | AATAAAGCATCACCCTGCATAATATTTT |
| COL11A1 region 3 (Mut) F | GTTAGATTGGCTTATCAATCAAGTTCTT |
| COL11A1 region 3 (Mut) R | AAGAACTTGATTGATAAGCCAATCTAAC |
| PDK1 (Mut) F | TGGCTTGGTCATTGTAGGGCGTGGTTGT |
| PDK1 (Mut) R | ACAACCACGCCCTACAATGACCAAGCCA |

**Table S2.** MicroRNA target interactions of COL11A1 gene.

| COL11A1 | microRNA target interactions | miRNAs |
|---|---|---|

| | | |
|---|---|---|
| **3'UTR** | 596 | 162 |
| **5'UTR** | 1238 | 293 |
| **CDS** | 8874 | 1744 |

**Table S3.** Top 10 negative correlated microRNAs.

| TCGA_OV_Top10_neg_Cor | Spearman |
|---|---|
| hsa-miR-508-3p | -0.557299073 |
| hsa-miR-509-3p | -0.538068643 |
| hsa-miR-508-5p | -0.529931704 |
| hsa-miR-125b-1-3p | -0.510822844 |
| hsa-miR-106b-5p | -0.510332904 |
| hsa-miR-410-3p | -0.494012796 |
| hsa-miR-409-3p | -0.491745859 |
| hsa-miR-1228-5p | -0.449826617 |
| hsa-miR-101-3p | -0.446658052 |
| hsa-miR-616-3p | -0.425184671 |

**Table S4.** MicroRNAs with negative correlation and predicted microRNA target interactions.26 .

| miRNAs | MTIs | Correlation with COL11A1 (Spearman) |
|---|---|---|
| hsa-miR-509-3p | 4 | -0.538068643 |
| hsa-miR-30e-5p | 2 | -0.224647756 |
| hsa-miR-877-5p | 8 | -0.204469492 |

**Table S5.** Correlations between miR-335 and COL11A1 mRNA 28 levels.

| | | N | miR-335 mRNA level | *P* |
|---|---|---|---|---|
| Non-cancer | | 23 | 2306.63 ± 9604.63 | 0.002 |
| Cancerous | | 137 | 182.39 ± 1915.05 | |
| COL11A1 | low | 63 | 856.06 ± 4289.9 | <0.001 |
| | high | 74 | 3.90 ± 279.43 | |

Data was presented as median ±interquartile range(IQR); Data was analyzed by Mann-Whitney U test; COL11A1 level <1446.67 (low) and ≥1446.67(high).

**Table S6.** TCGA data.

| Characteristic | Number of patient |
|---|---|
| Stage | |
| I | 1 |
| II | 27 |
| III | 373 |

| | |
|---|---|
| IV | 80 |
| NA | 4 |
| Age | |
| ≧54 | 326 |
| <54 | 157 |
| Disease status | |
| Alive | 217 |
| Death | 268 |
| Debulking surgery | |
| Optimal surgery | 313 |
| Suboptimal surgery | 115 |

**Table S7.** TCGA miRNA data.

| | Mean | Early stage | Advanced stage | P adjust | Significant |
|---|---|---|---|---|---|
| **TCGA miR-335** | 197.005268 | 142.29 [66.91-196.38] | 106.62 [56.16-141.23] | 0.000336 | Downregulated in advance stage |

**Table S8.** TCGA miRNA data.

| | Mean | Advanced stage Optimal debulking surgery | Advanced stage suboptimal debulking surgery | P adjust | Significant |
|---|---|---|---|---|---|
| **TCGA miR-335** | 153.6643017 | 150.74 [52.06-158.26] | 161.25 [69.68-155.25] | 0.5150 | No significance |
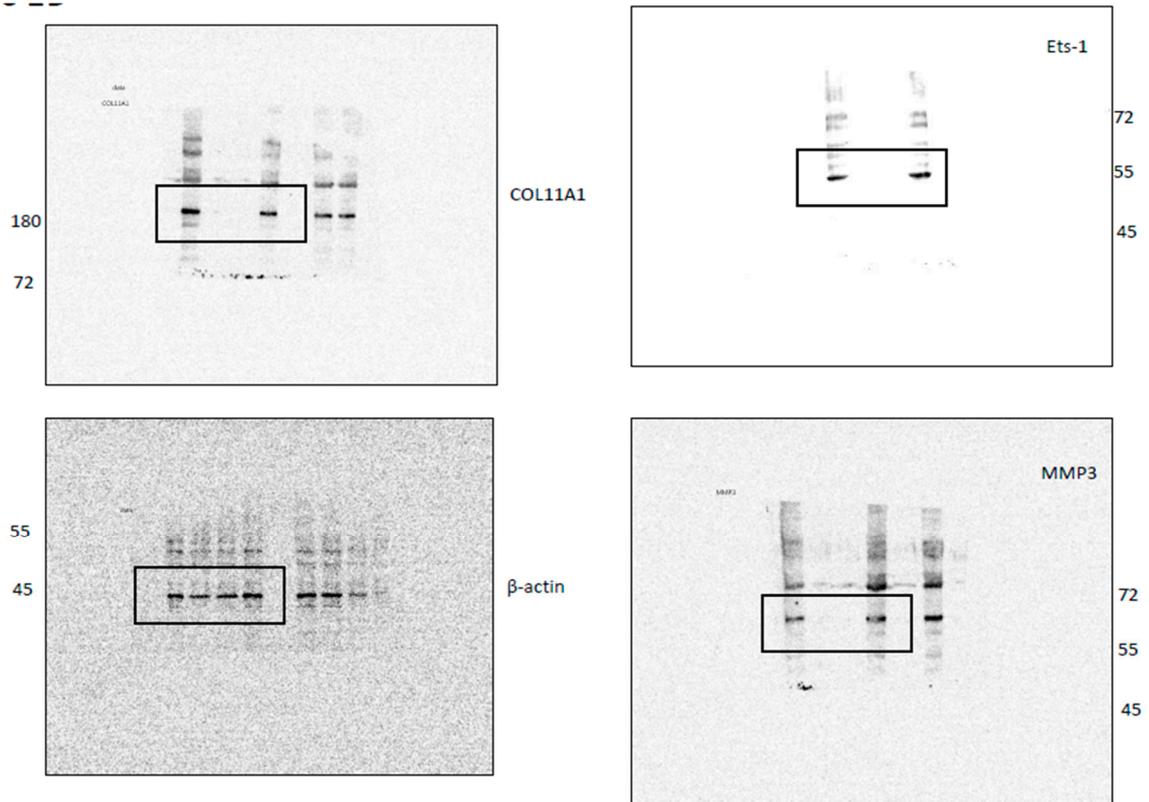
(**A**)
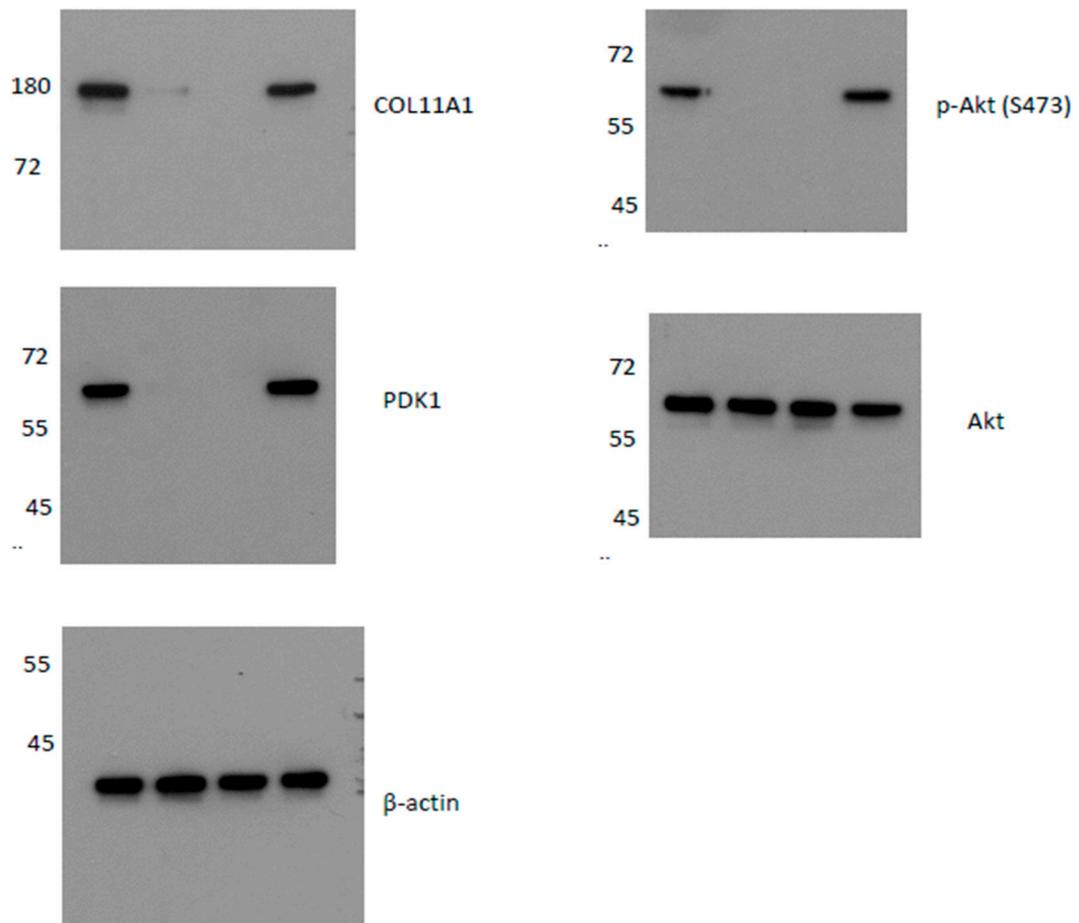


(**B**)
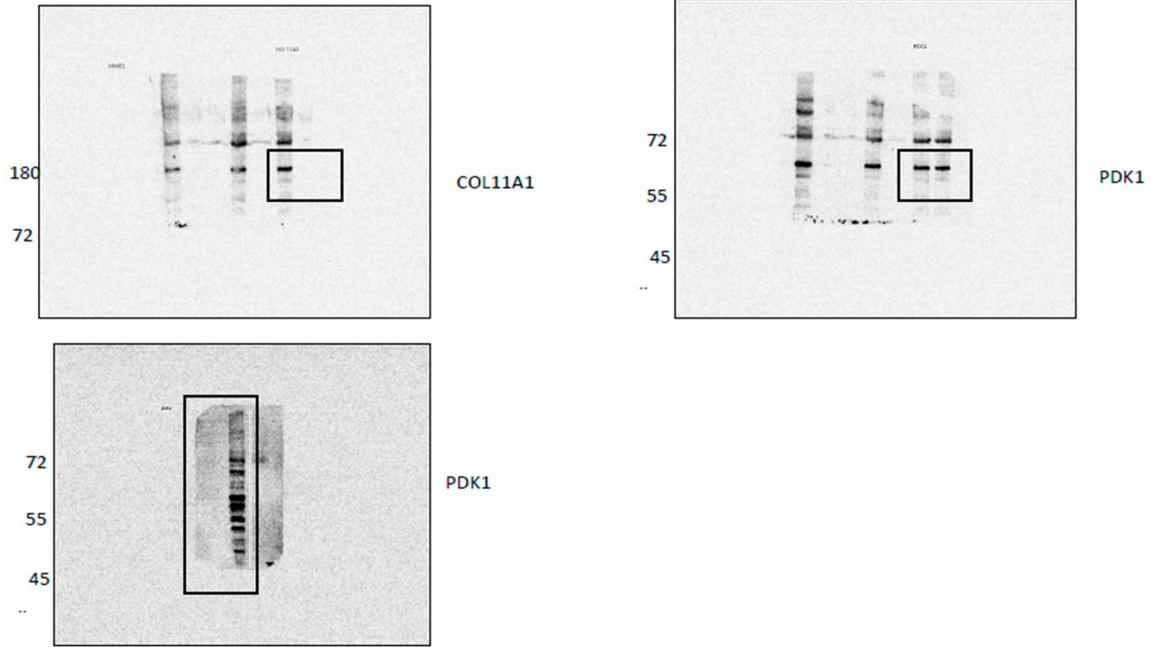
(**C**)

**Figure S2.** Western blot (**A**): reference to Figure 2E; (**B**): reference to Figure 3B; (**C**): reference to Figure 3D.