**Supplementary Table 1.** Clinicopathologic characteristics of prostate cancer patients.

|  |  |
| --- | --- |
| **Characteristics** | **Number of cases** |
| Age(media=72) |  |
| <72 | 11 |
| ≥72 | 12 |
| Gleason Score |  |
| 1-4(highly differentiated) | 0 |
| 5-7(moderately differentiated) | 11 |
| 8-10(poorly differentiated) | 9 |
| unknow | 3 |
| Chemotherapy prior to blood sampling |  |
| Yes | 10 |
| No | 13 |

**Supplementary Table 2.** The sequences of ASOs, reporter constructs, primers, and probes.

|  |  |
| --- | --- |
| **Name** | **Sequences** |
| rsRNA-28S ASO | 5´-mAs mAs mUs mUs mCs As Gs Cs Gs Us Gs Gs Us Cs Gs Cs Cs As mCs mGs mUs mCs mUs-3´ |
| NC ASO | 5´-mGs mCs mGs mUs mAs dTs dTs dAs dTs dAs dGs dCs dCs dGs dAs mUs mUs mAs mAs mCs -3´ |
| pmirGLO-PTGIS 3′-UTR-WT | 5´-CTTGCGCAGGCTGCAACCCTGGTGTGCTGGGCGAA  AACCCTTATGACTCCCCCCTTCCAAATCAGGCTGGGTTGTCACTGAGACTAGATTCTCACCTGCCTTCAAAGAAGGGCCAATTCCCTTTAAAGGTCGCACCTCCTTGGAACCACAGTCATTAGTGAATTACACTCAAGGAAAAGATGTGCTCCCACCAGGCAGCTCCAGCTGTTACCTGAGATACTGAAGTGCAGCTC-3´ |
| pmirGLO-PTGIS 3′-UTR-MUT | 5’-CTTGCGCAGGCTGCAACCCTGGTGTGCTGGGCGAA  AACCCTTATGACTCCCCCCTTCCAAATCAGGCTGGGTTGTCACTGAGACTAGATTCTCACCTGCCGGACAATAAGGTAACATGACCTGTAACTTGATAACCTCCTTGGAACCACAGTCATTAGTGAATTACACTCAAGGAAAAGATGTGCTCCCACCAGGCAGCTCCAGCTGTTACCTGAGATACTGAAGTGCAGCTC-3’ |
| rsRNA-28S RT | 5´-GAAAGAAGGCGAGGAGCAGATCGAGGAAGAAGA  CGGAAGAATGTGCGTCTCGCCTTCTTTCAAATTCAG-3´ |
| U6-RT | 5´-CGCTTCACGAATTTGCGTGTCAT-3´ |
| U6 | Forward: 5´-GCTTCGGCAGCACATATACTAAAAT-3´  Reverse: 5´-CGCTTCACGAATTTGCGTGTCAT-3´ |
| rsRNA-28S | Forward: 5´-ACCTCAGATCAGACGTGGCG-3´  Reverse: 5´-GGAAGAAGACGGAAGAATGTGC-3´ |
| GAPDH | Forward: 5´-ACCTGACCTGCCGTCTAGAA-3´  Reverse: 5´-TCCACCACCCTGTTGCTGTA-3´ |
| PTGIS | Forward: 5´- CTGCCCCCAACCAGTATAGTA -3´  Reverse: 5´-GTTGGGGTATGCCTTGGACT-3´ |
| rsRNA-28S probe | 5′-DIG-ATTCAGCGCGGTGCCACGTCT-3′ |

**Note**: “m” refers to methyl-oxidation modification; “s” refers to phosphorothioate modification; “d” refers to DNA bases.

**Supplementary Table 3.** rsRNA-28S targets predicted by TargetRank

|  |  |  |
| --- | --- | --- |
| **Gene name** | **Function description** | **Score** |
| GPATCH1 | RNA binding activity; mRNA splicing. | 0.337 |
| ELMOD1 | Positive regulation of GTPase activity. | 0.281 |
| TRIM14 | Innate immune defense against viruses and bacteria. | 0.263 |
| PUS7L | Activating pseudouridine synthase activity. | 0.259 |
| TRIO | Reorganization of the actin cytoskeleton, cell migration and growth. | 0.257 |
| GLT6D1 | Multiple events of gain and loss in different mammal species. | 0.253 |
| H2AFJ | Core component of nucleosome; nucleosomes limit DNA accessibility to the cellular machineries which require DNA as a template. | 0.253 |
| KCNE1 | It encodes a transmembrane protein, which is related to the made of KVLQT1 gene and forms a delayed rectifier potassium channel. | 0.253 |
| PTGIS | It catalyzes the conversion of prostaglandin H2 into prostacyclin (prostaglandin I2), an effective vasodilator and platelet aggregation inhibitor. | 0.253 |
| TCF4 | It encodes protein recognizes an Ephrussi-box ('E-box') binding site ('CANNTG'); may play an important role in nervous system development. | 0.253 |
| GOLGA3 | Nuclear transport and Golgi apparatus localization. | 0.243 |
| OPCML | Binds opioids with the presence of acidic lipids; cell contact. | 0.238 |
| SP1 | Cell differentiation, cell growth, apoptosis, immune responses, response to DNA damage, and chromatin remodeling; can be an activator or a repressor. | 0.238 |
| GPR158 | Act upstream of or within G protein-coupled receptor signaling pathway and protein localization to plasma membrane. | 0.238 |
| LEMD3 | Can function as a specific repressor of TGF-beta, activin, and BMP signaling through its interaction with the R-SMAD proteins. | 0.237 |
| SPECC1L | Involved in cytokinesis and spindle organization. | 0.209 |
| OTUD3 | Deubiquitinating enzyme that hydrolyzes 'Lys-6'- and 'Lys-11'-linked polyubiquitin, also hydrolyzes heterotypic and homotypic chains. | 0.209 |
| GRAMD1C | Predicted to enable cholesterol binding activity and cholesterol transfer activity. | 0.209 |
| POP4 | Component of ribonuclease P, a ribonucleoprotein complex that generates. mature tRNA molecules by cleaving their 5'-ends. | 0.203 |
| ANKH | Regulates intra- and extracellular levels of inorganic pyrophosphate (PPi), probably functioning as PPi transporter. | 0.203 |
| TRIM33 | The protein encoded by this gene is thought to be a transcriptional corepressor. | 0.203 |
| KIAA0892  /MAU2 | Play an important role in the loading of the cohesin complex on to DNA. | 0.2 |

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**Supplementary Fig. 1: The secondary structure of rsRNA-28S in this study was predicted via RNAfold web server.**

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**Supplementary Fig. 2: the proliferative abilities of DU-145 and DU-145R cells were detected by CCK-8 assay.**

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**Supplementary Fig. 3: The rsRNA-28S levels in DU-145 and DU-145R cells were detected by qRT-PCR.**

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**Supplementary Fig. 4: rsRNA-28S knock down suppressed the proliferative abilities of DU-145 and DU-145R cells.**

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**Supplementary Fig. 5: PTGIS had no significant effect on the proliferative abilities of DU-145 and DU-145R cells.**

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**Supplementary Fig. 6: The rsRNA-28S levels in DU-145 and DU-145R cells transiently transfected with rsRNA-28S ASO were detected by qRT-PCR.**