Supporting Information

A Nucleic Acid/Gold Nanorod-Based Nanoplatform for Targeted Gene Editing and Combined Tumor Therapy

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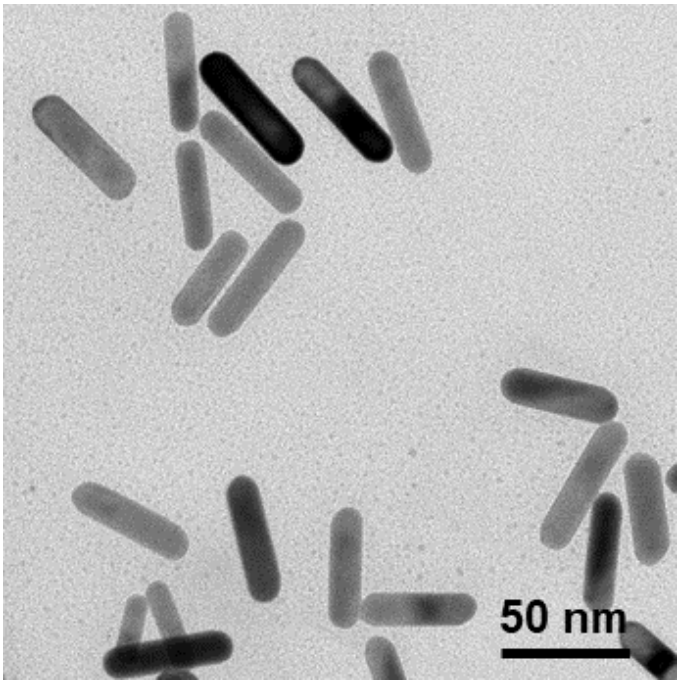

Figure S1. TEM image of GNRs, scale bar: 50 nm.

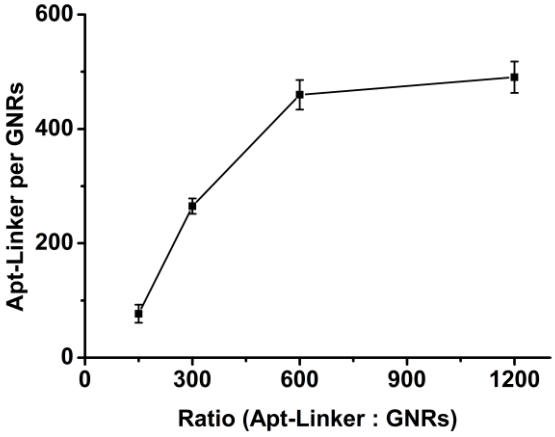

Figure S2. Linker-Apt loading efficiency at different molar ratio of Linker-Apt : GNRs.

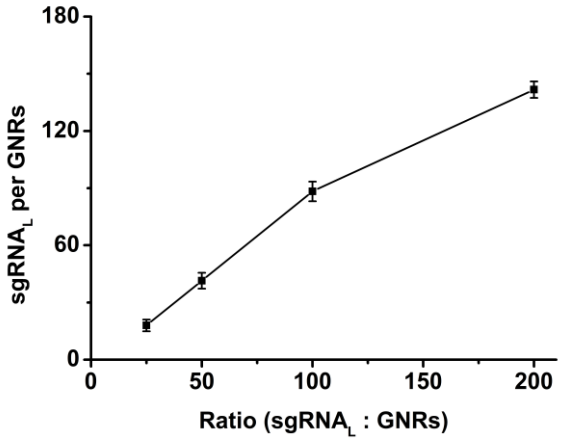

Figure S3. The $sgRNA_L$ loading efficiency at different molar ratio of $sgRNA_L$: GNRs.

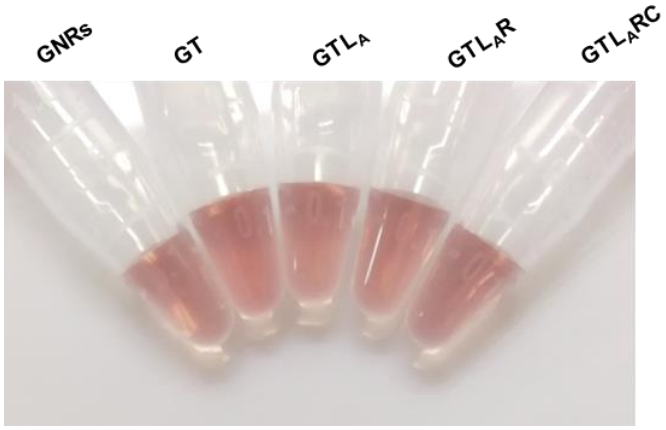

Figure S4. Photograph of GNRs solutions with indicated functionalizations step by step.

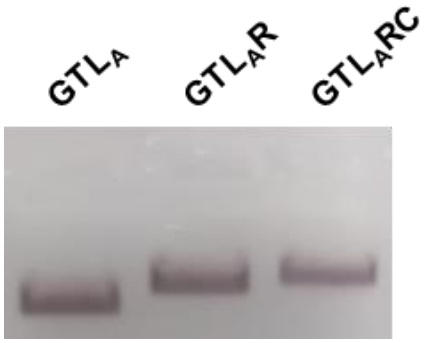

Figure S5. Gel electrophoresis of GNRs with indicated functionalizations step by step.

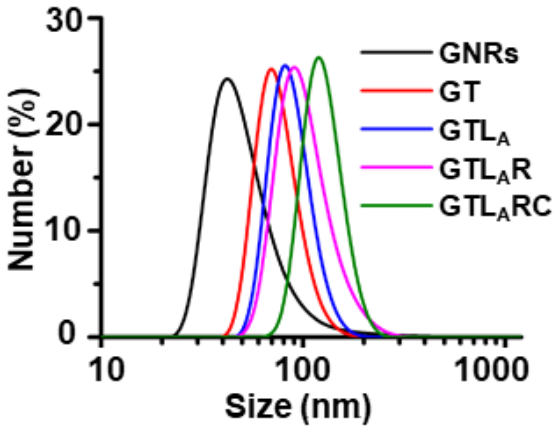

Figure S6. DLS analysis of GNRs with indicated functionalizations step by step.

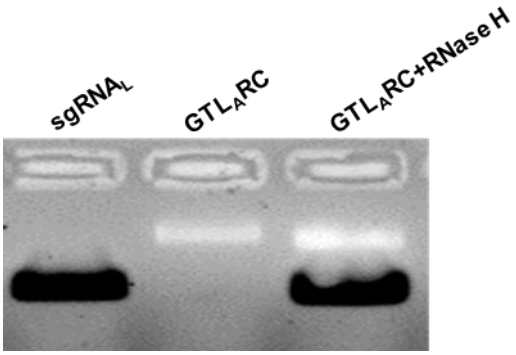

Figure S7. 1% agarose gel electrophoresis analysis of the controlled release of sgRNA from GTL_ARC based on the digestion of RNase H (stained by EB).

Figure S8. Photograph of GTL_ARC in various physiological solutions.

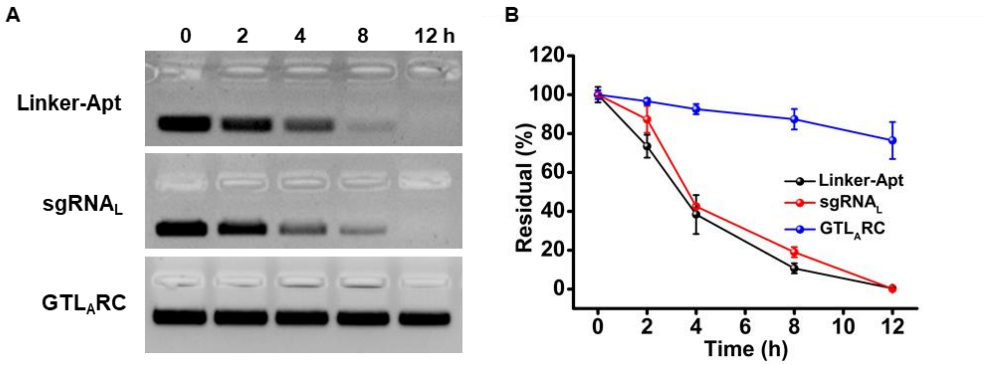

Figure S9. (A) 1% agarose gel electrophoresis analysis of the serum stability of Linker-Apt, $sgRNA_L$ and GTL_ARC (nucleic acids were released by GSH) with the incubation of 10% FBS at 37 ℃. (B) Statistic results of serum stability of Linker-Apt, $sgRNA_L$ and GTL_ARC by Image J analysis.

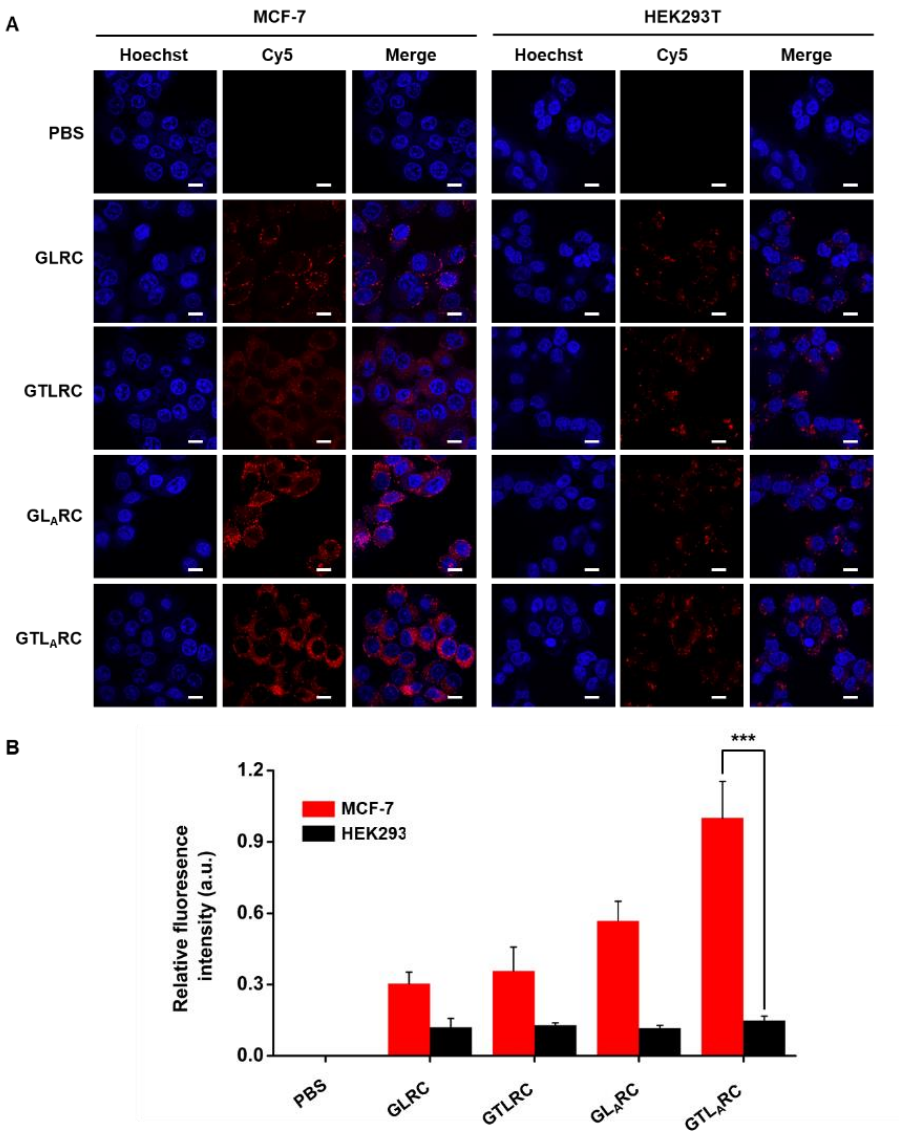

Figure S10. (A) Confocal images of MCF-7 and HEK293T cells after indicated treatments with or without aptamer or TAT functionalization. (Scale bars: 25 μm). (B) Statistic results of confocal images by Image J analysis.

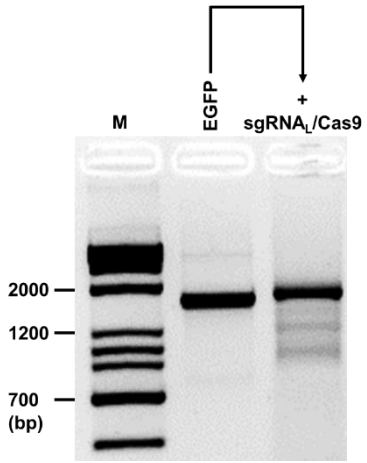

Figure S11. 2% agarose gel electrophoresis analysis of target EGFP gene editing based on sgRNA$_L$/Cas9 complex.

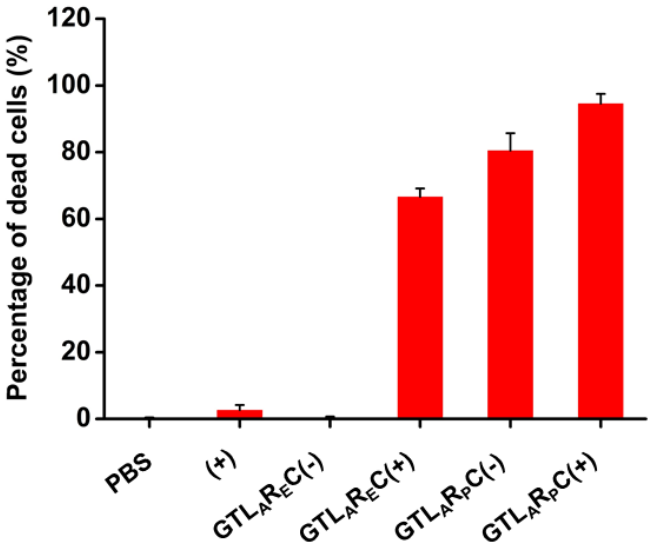

Figure S12. Statistic analysis of the percentage of dead cells by Image J analysis.

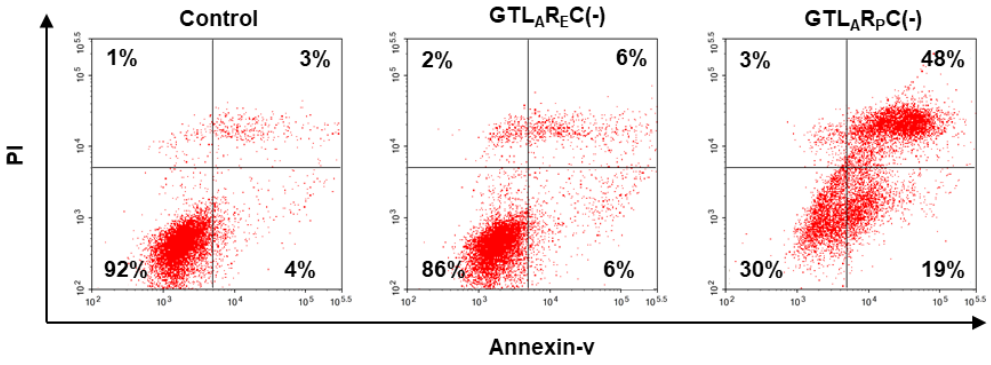

Figure S13. Flow cytometry assay of cell apoptosis of MCF-7 cells induced by PBS, $GTL_AR_EC(-)$, or $GTL_AR_PC(-)$.

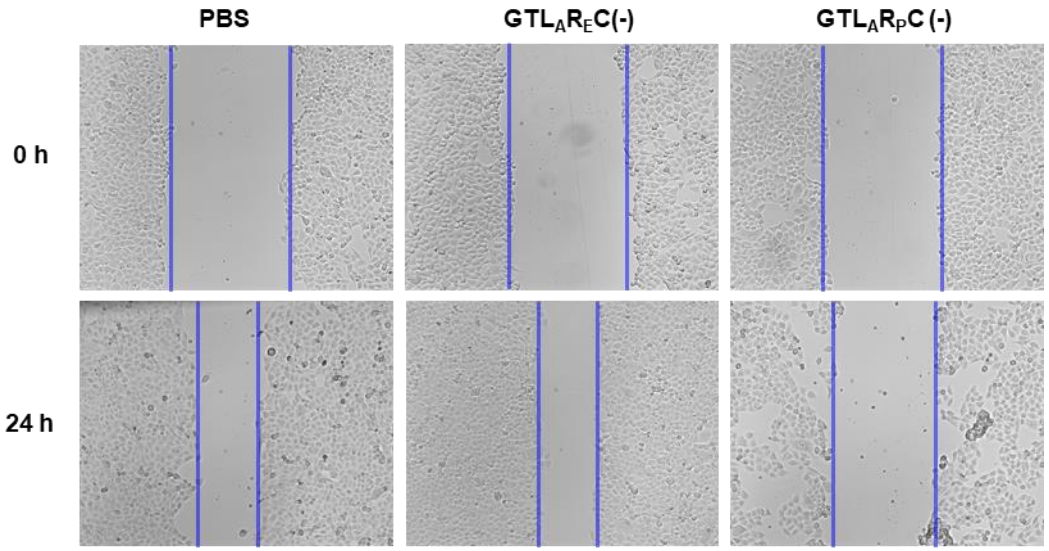

Figure S14. Images of the scratch wound-healing assay after the indicated treatments.

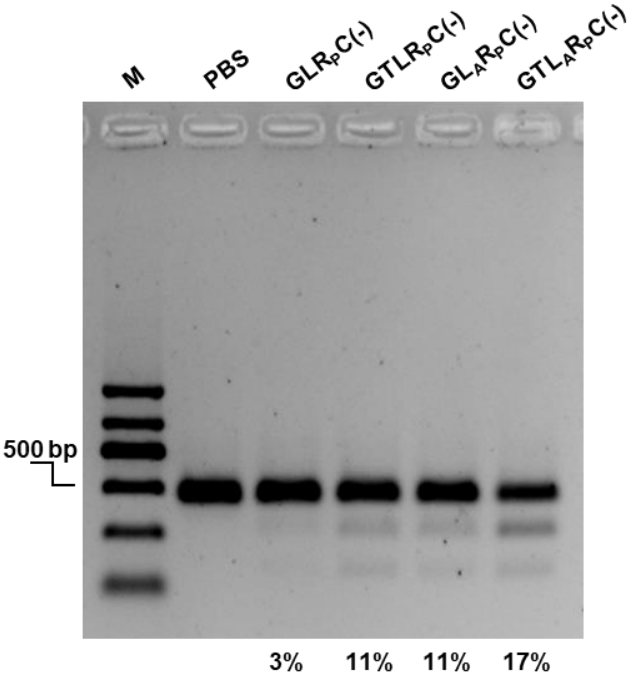

Figure S15. T7EI assay to detect genomic modification of PLK1 after the indicated treatments for 72 h.

Table S1. DNA sequences for construction of GTL_ARC.

Name	Sequence (5'-3')
Linker-Apt	HS-TTTTTGACCAGGATGGGCACCACCCTTTTTGCAGTTGATCCTTTGGATACCCTGG
Linker	HS-TTTTTGACCAGGATGGGCACCACCCTTTTT
Cy5 labeled Linker-Apt	HS-TTTTTGACCAGGATGGGCACCACCCTTTTTGCAGTTGATCCTTTGGATACCCTGG-**Cy5**
Cy5 labeled Linker	HS-TTTTTGACCAGGATGGGCACCACCCTTTTT-**Cy5**

Table S2. DNA sequences of sgRNA transcription template and primers.

Name	Sequence (5'-3')
S-sgRNA	GTTTAAGAGCTATGCTGGAAACAGCATAGCAAGTTTAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTTTT
AS-sgRNA	AAAAAAAGCACCGACTCGGTGCCACTTTTTCAAGTTGATAACGGACTAGCCTTATTTAAACTTGCTATGCTGTTTCCAGCATAGCTCTTAAAC
F-EGFP	**TAATACGACTCACTATA**GGGGGGCACGGGCAGCTTGCCGGGTTTAAGAGCTATGCTGGA
F-PLK1	**TAATACGACTCACTATA**GGGTACCTACGGCAAATTGTGCTGTTTAAGAGCTATGCTGGA
R-primer	GACCAGGATGGGCACCACCCAAAAAAAGCACCGACTCGGT

T7 promoter: **TAATACGACTCACTATA**

Table S3. DNA sequences of primers for qRT-PCR and T7EI assay.

Name	Sequence (5'-3')
PLK1-F	GGCAACCTTTTCCTGAATGA
PLK1-R	AATGGACCACACATCCACCT
β-actin-F	TCTGGCACCACACCTTCTACAATG
β-actin-R	GGATAGCACAGCCTGGATAGCAA
T7EI-F	GGTGCTGCGAATGGTTGTGG
T7EI-R	CAGCCTCCTCCAAATTCCAGC