Supporting Information

A covalently conjugated branched DNA aptamer cluster-based

nanoplatform for efficiently targeted drug delivery[†]

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Table of contents

Additional figures

Figure S1	<u>S2</u>
Figure S2	<u>S3</u>
Figure S3	S4
Figure S4	<u>S5</u>
Figure S5	<u>S6</u>
Figure S6	<u></u>
Figure S7	<u>S8</u>
Figure S8	<u></u>
Figure S9	<u>S10</u>
Figure S10	<u>S11</u>
Figure S11	<u>S12</u>
Figure S12	<u></u>
Unprocessed gels	<u></u>
Additional tables	
Table S1	<u>S15</u>
Table S2	<u>S15</u>

Additional figures



Fig. S1 6% native PAGE analysis of step-by-step construction of capture strand-modified tetrahedron (Capture-TET).



Fig. S2 AFM images of TET and TET+5Apt, scale bars: 50 nm.



Fig. S3 0.7% agarose gel electrophoresis analysis of DOX, TET+5Apt, and TET+5Apt-DOX.



Fig. S4 Cumulative DOX release efficiency of TET+5Apt-DOX in DNase I.



Fig. S5 Confocal images of MCF-7 cells treated with TET, TET with one aptamer at one vertex (TET+1Apt), TET with one aptamer at each vertex (TET+4V-1Apt), TET with four aptamers at one vertex (TET+4Apt), TET with five aptamers at one vertex (TET+5Apt), or TET with five aptamers at each vertex (TET+4V-5Apt) for 8 h (nuclei were labeled with Hoechst, blue; TETs were labeled with Cy5, red; scale bars: 40 μ m).



Fig. S6 (a) Flow cytometry analysis of MCF-7 cells treated with TET, TET with one aptamer at one vertex (TET+1Apt), TET with one aptamer at each vertex (TET+4V-1Apt), TET with four aptamers at one vertex (TET+4Apt), TET with five aptamers at one vertex (TET+5Apt), or TET with five aptamers at each vertex (TET+4V-5Apt) for 8 h. (b) Quantification of the relative mean fluorescence intensity (MFI). The error bars represent the SD values of three independent experiments.



Fig. S7 Confocal images of MCF-7 cells treated with DOX-loaded TET (TET-DOX), DOX-loaded TET with one aptamer at one vertex (TET+1Apt-DOX), or DOX-loaded TET with five aptamers at one vertex (TET+5Apt-DOX) for 8 h, scale bars: 40 µm.



Fig. S8 (a) Flow cytometry analysis of MCF-7 cells treated with DOX-loaded TET (TET-DOX), DOX-loaded TET with one aptamer at one vertex (TET+1Apt-DOX), or DOX-loaded TET with five aptamers at one vertex (TET+5Apt-DOX) for 8 h (b) Quantification of the relative mean fluorescence intensity (MFI). The error bars represent the SD values of three independent experiments. (t test: ***P < 0.001).



Fig. S9 Cell viability of MCF-7 cells treated by different concentrations of DOX. The error bars represent the SD values of three independent experiments.



Fig. S10 Cell viability of MCF-7 cells with the indicated treatments of TET, TET+1Apt, or TET+5Apt, respectively. The error bars represent the SD values of three independent experiments.



Fig. S11 Statistic analysis of the percentage of dead cells by Image J analysis. The error bars represent the SD values of three independent experiments. (t test: **P < 0.01).



Fig. S12 Cell apoptosis analysis of L929 cells treated with DOX-loaded TET (TET-DOX), DOX-loaded TET with one aptamer at one vertex (TET+1Apt-DOX), or DOX-loaded TET with five aptamers at one vertex (TET+5Apt-DOX). (DOX: 2.0μ M).

Unprocessed gels



Raw gel for Fig. 2(b)

1



Raw gel for Fig. 3(a)



Raw gel for Fig. S1



Raw gel for Fig. S3

Additional tables

Name	Sequence (5'-3')
Aptamer	GCAGTTGATCCTTTGGATACCCTGGTTTTT-NH ₂
Linker	NH ₂ -CTCTCTCTCTCTCTCTCTC

Table S1 DNA sequences of the aptamer and linker

Table S2 DNA sequences for assembly of DNA tetrahedron

Name	Sequence (5'-3')
S1	TATCACCAGGCAGTTGACAGTGTAGCAAGCTGTAATAGATGC GAGGGTCCAATAC
S2	TCAACTGCCTGGTGATAAAACGACACTACGTGGGAATCTACT ATGGCGGCTCTTC
83	TTCAGACTTAGGAATGTGCTTCCCACGTAGTGTCGTTTGTATT GGACCCTCGCAT
S4	ACATTCCTAAGTCTGAAACATTACAGCTTGCTACACGAGAAG AGCCGCCATAGTA
Capture-S1	TATCACCAGGCAGTTGACAGTGTAGCAAGCTGTAATAGATGCG AGGGTCCAATACTTTT <mark>GAGAGGAGAGAGAGAGAGAGAG</mark>
Capture-S2	TCAACTGCCTGGTGATAAAACGACACTACGTGGGAATCTACT ATGGCGGCTCTTCTTTTGAGAGGAGAG
Capture-S3	TTCAGACTTAGGAATGTGCTTCCCACGTAGTGTCGTTTGTATT GGACCCTCGCATTTTT <mark>GAGAGAGAGAGAGAGAGAG</mark>
Capture-S4	ACATTCCTAAGTCTGAAACATTACAGCTTGCTACACGAGAAG AGCCGCCATAGTATTTT <mark>GAGAGAGAGAGAGAGAGAGAG</mark>
Cy5-S3	Cy5-TTCAGACTTAGGAATGTGCTTCCCACGTAGTGTCGTTTGT ATTGGACCCTCGCAT
Cy5-Capture-S3	Cy5-TTCAGACTTAGGAATGTGCTTCCCACGTAGTGTCGTTTGT ATTGGACCCTCGCATTTTTTGAGAGGAGAG