Supporting Information

Framework Nucleic Acid-programmed Aptamer–paclitaxel Conjugates as Targeted Therapeutics for Triple-negative Breast Cancer

Lin Li, ‡a Pengyao Wei, ‡a Tong Kong, a Bo Yuan, a Pan Fu, a Yong Li, b,c Yuhui Wang, *a,d Jianping Zheng, *a,d Kaizhe Wang *a,d

[a]. Ningbo Key Laboratory of Biomedical Imaging Probe Materials and Technology, Ningbo Cixi Institute of Biomedical Engineering, Ningbo Institute of Materials Technology and Engineering of Chinese Academy of Sciences, Ningbo 315300, P. R. China. E-mail: wangkaizhe@nimte.ac.cn; wangyuhui@nimte.ac.cn; zhengjianping@nimte.ac.cn

[b]. Cancer Care Centre, St George Hospital, Kogarah, NSW 2217 Australia.

[c]. St George and Sutherland Clinical Campuses, School of Medicine and Health, UNSW.

[d]. University of Chinese Academy of Sciences, Beijing 100049, P. R. China

[‡]. Lin Li and Pengyao Wei contribute equally to this work.

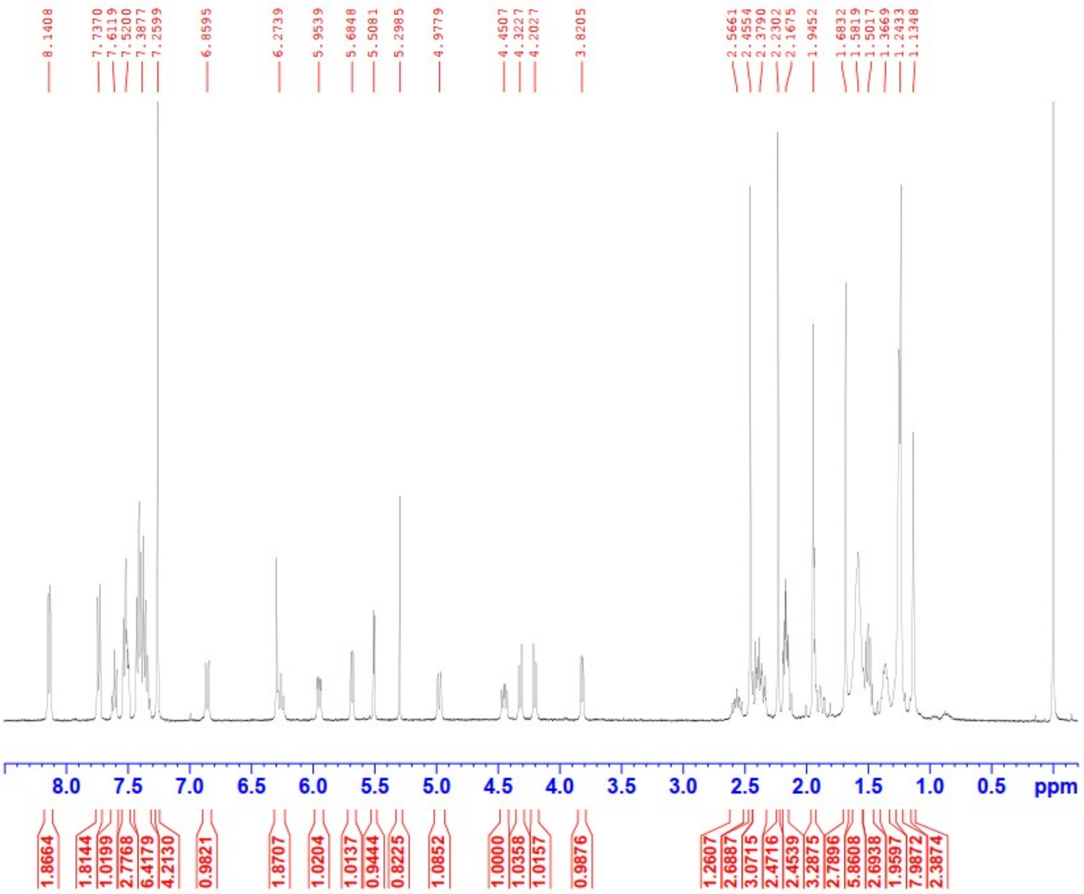

Figure S1. ^{1}HNMR analysis of PTX prodrug in D_2O.

This was purified by reverse-phase chromatography eluting with methanol and ethyl acetate to give a white solid in 93% yield. ^{1}H NMR (400 MHz, $CDCl_3$): δ (ppm) 1.13 (s, 2H), 1.24 (d, J = 5.71 Hz, 8H), 1.37 (m, 2H), 1.50 (m, 3H), 1.58 (m, 6H), 1.68 (s, 3H), 1.95 (m, 3H), 2.17 (m, 2H), 2.23 (s, 2H), 2.38 (m, 3H), 2.46 (s, 3H), 2.57 (m, 1H), 3.82 (d, J = 6.90 Hz, 1H), 4.20 (d, J = 8.49 Hz, 1h), 4.32 (d, J = 8.48 Hz, 1H), 4.45 (m, 1H), 4.98 (m, 1H), 5.30 (s, 1H), 5.51 (d, J = 3.23 Hz, 1H), 5.68 (d, J = 7.08 Hz, 1H), 5.95 (dd, J_1 = 3.15 Hz, J_2 = 6.10 Hz, 1H), 6.27 (m, 2H), 6.86 (d, J = 9.17 Hz, 1H), 7.26 (s, 4H), 7.38 (m, 6H), 7.52 (m, 3H), 7.61 (m, 1H), 7.74 (m, 2H), 8.14 (m, 2H). HRMS (ESI): m/z $[C_{58}H_{67}NO_{15}]^+$ calcd for 1017.4551, found: 1018.4723.

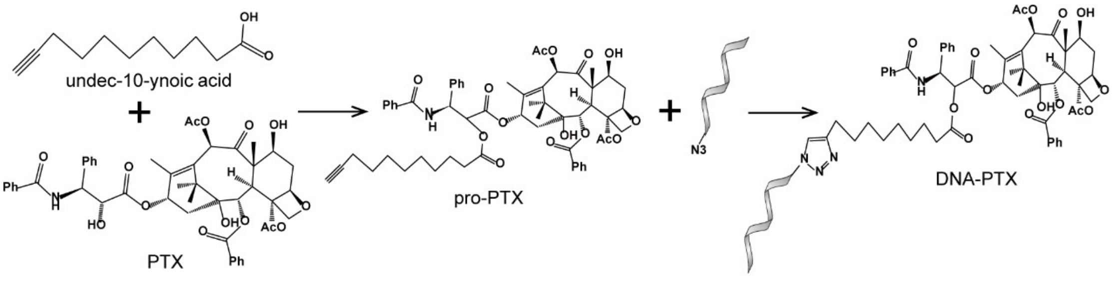

Figure S2. The synthetic route of the paclitaxel anchored ss-DNA strand (DNA-PTX).

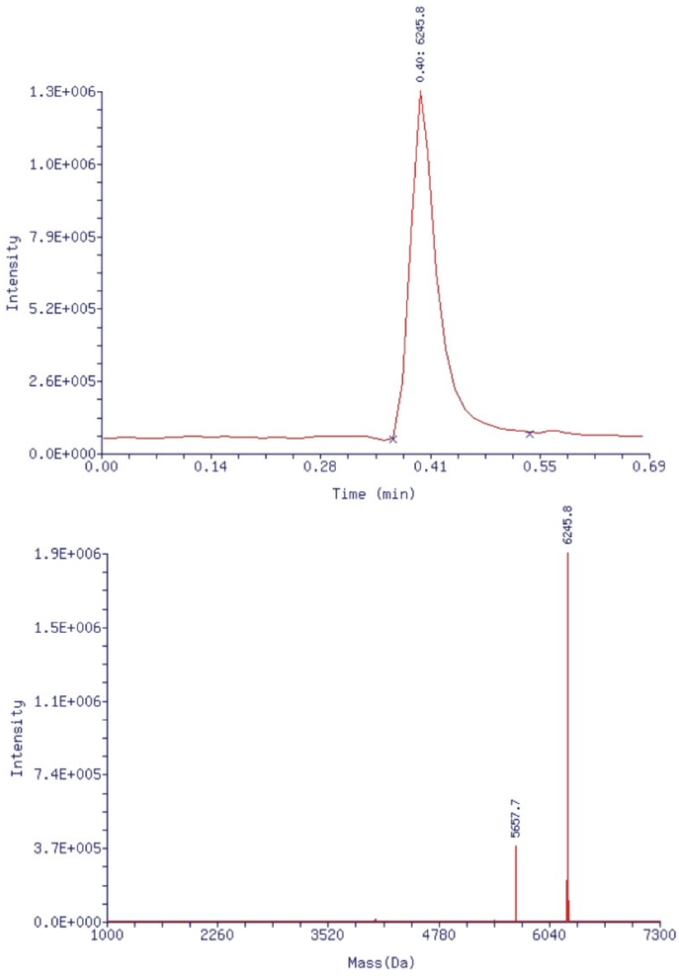

Figure S3. LC-MS profile of paclitaxel anchored ss-DNA strand (DNA-PTX) in water solution. The retention time of DNA-PTX was 0.40 min. High purity of DNA-PTX was showed in the LC profiles.

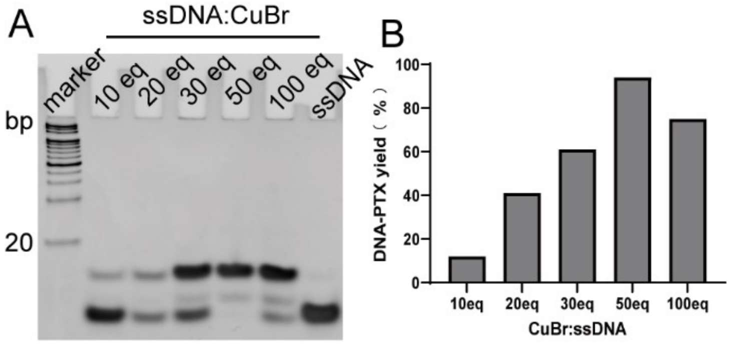

Figure S4. The conjugation yields of PTX-DNA. (A) DNA-PTX bands by 17% nondenaturing polyacrylamide gel electrophoresis (PAGE) under different CuBr:ssDNA molar ratio reaction conditions. (B) Conjugation yields corresponding to gray values of DNA-PTX target bands (A) under different CuBr:DNA molar ratios.

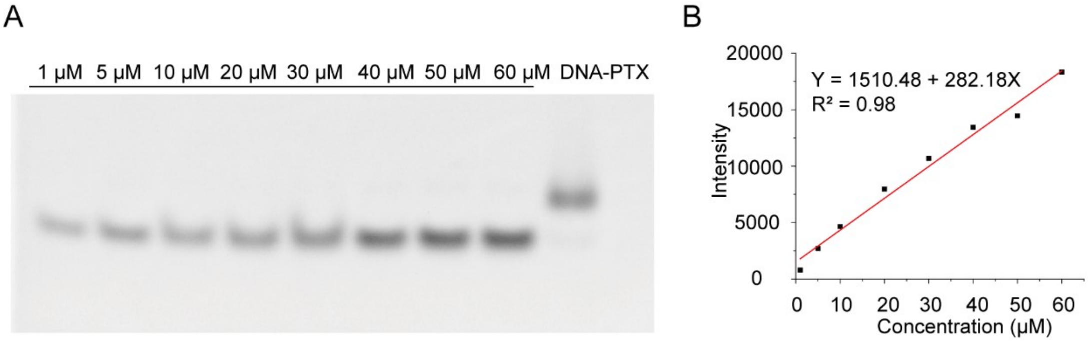

Figure S5. (A)17% non-denaturing polyacrylamide gel electrophoresis (PAGE) of the PTX anchored DNA strand at different concertation. (B) Establishment of the concentration of DNA-PTX.

Image J was used to quantify the gray value of each ss-DNA band in the image, and the fitting curve was obtained $y = 1510.48 + 282.18x$. y represents the gray value of bands, and x is the ss-DNA concentration. The concentration of DNA-PTX was quantified based on the gray values of DNA-PTX bands.

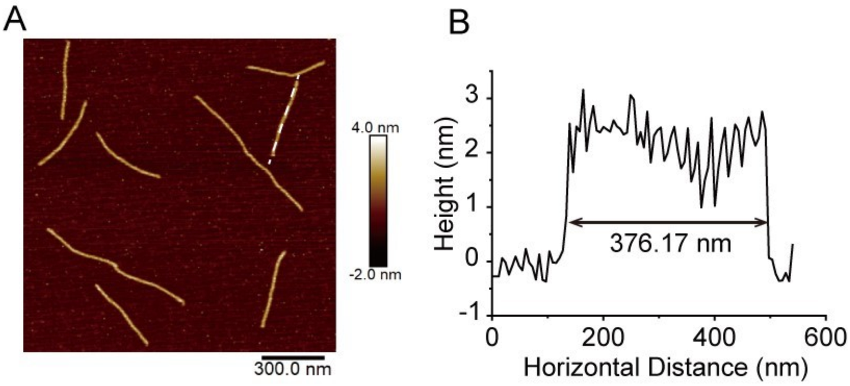

Figure S6. The characterization of 6-HB DONs nanostructures. (A) Representative AFM images of 6-HB DONs nanostructures. (B)The length value is obtained from the dashed white line.

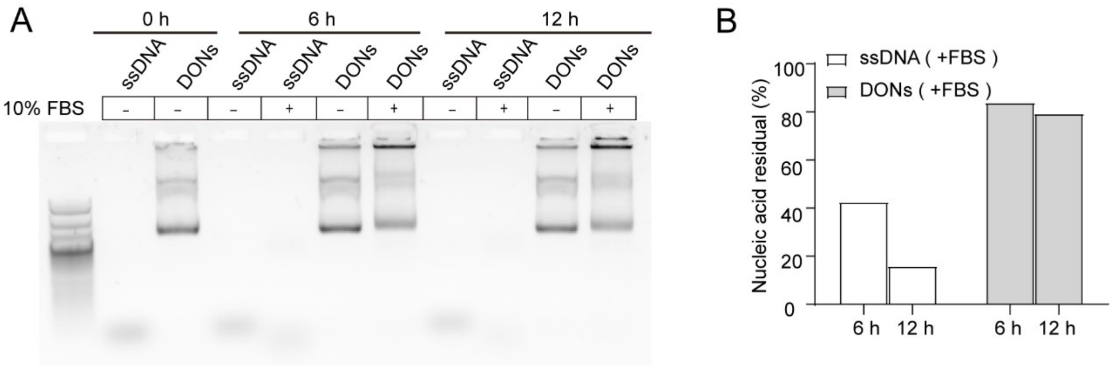

Figure S7. (A) Electrophoresis analysis of the stability of the DONs-AS1411-PTX nanostructures.

The DNA-PTX and DONs-AS1411-PTX nanostructures were incubated in 10% FBS at 37 °C for 0–12 h and then examined by agarose gel electrophoresis. (B) Image J measured the gray value of gel bands after DNA-PTX and DONs-AS1411-PTX was incubated with or without 10%FBS for 6h and 12h.

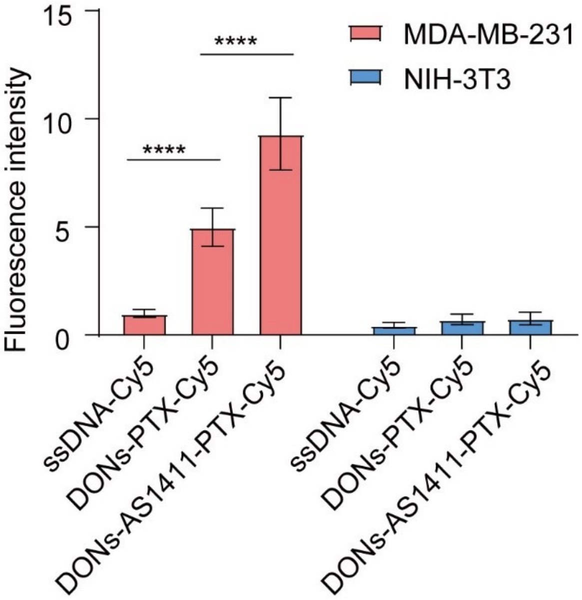

Figure S8. Corresponding average fluorescence intensity of cells in confocal microscopy images.

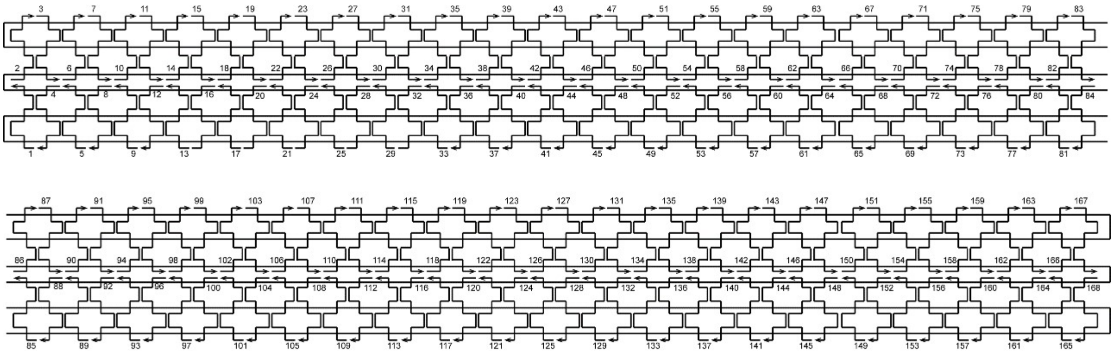

Figure S9. Schematic illustration of the design of 6-HB DONs.

Table S1. Sequences of unmodified helper strands used to assemble the 6HB-DON.

Name	Sequence (5'-3')
1	TGTGTAGGTAAAGAATAGTAGTAGCATTCCTCAGAACCGCCA
2	CATCAATTCTACTATTCAAAAGGGTGAGATAGATTAGAGCCG
3	AACCAGAGCCACCAACCCTCAGAGCCGCAGCTGAAAAGGTGG
4	CCCTCAGAGCCACCCCGGAACCGCCTCCAAGTATTAGACTTT
5	TCAATAGATAATACATTTGAGGATTTAGCTCAGAGCCGCCAC
6	ACAAACAATTCGACAGCACTAACAACTAAAAGGCCGGAGACA
7	CCTTATTAGCGTTTAGCATTGACAGGAGATGGTCAATAACCT
8	AAAATATCTTTAGGAACTCGTATTAAATATCAAAATCACCGG

9	TTATTAATTTTAAAAGTTGAAAGGAATTCCGTTCTAGCTGAT
10	GTCAAATCACCATCTCATTTGGGGCGCGCACCAGAACCACCA
11	CCAGAGCCGCCGCCGCCATCTTTTCATACCTTTGCCCGAACG
12	GTTTAGCTATATTTAATATGATATTCAAGAGGAAGGTTATCT
13	CACCGTAATCAGTAAGCGCAGTCTCTGATCTGGAAGTTTCAT
14	GTTGGCAAATCAACAGTTTGAGTAACATTTCGGTCATAGCCC
15	TGATTATCAGATGAAGCAAATGAAAAATTGGAGCAAACAAGA
16	AAATTAATGCCGGAGATACATTTCGCAAGTTGAGGCAGGTCA
17	AAGCCAGAATGGAAGCGACAGAATCAAGTATCATCATATTCC
18	GACGATTGGCCTTGTTTTCATCGGCATTTATCATTTTGCGGA
19	ACAAAGAAACCACCTATCAAACCCTCAATTGAGAGATCTACA
20	TGCTGAACCTCAAAAGAAGGAGCGGAATTTTGCCTTTAGCGT
21	AAGGCTATCAGGTCGATTCCCAATTCTGATAAATCCTCATTA
22	CAGACTGTAGCGCGATATTCACAAACAACGAACGAGTAGATT
23	TAGTTTGACCATTAGAGGGTAGCTATTTTCAATATCTGGTCA
24	TCCATATAACAGTTATTGCCTGAGAGTCCTAAAGCATCACCT
25	GGGAATTAGAGCCAGGGGTCAGTGCCTTCATTTTTGCGGATG
26	CAACCGATTGAGGGAGTATTAAGAGGCTAGCTTCAAAGCGAA
27	CGCTGAGAGCCAGCTGGCAATTCATCAAACCATCGATAGCAG
28	GTACCTTTTACATCACGTGGCACAGACATCAGCTCATTTTTT
29	GAATCGATGAACGGACTAAAGTACGGTGATTTACCGTTCCAG
30	TTCTGAAACATGAAAGGGAAGGTAAATAAATATACAGTAACA
31	TAAGCGTCATACATACGTCACCAATGAATATAATCCTGATTG
32	TTTGGATTATACTTAGTATTAACACCGCGCATGTCAATCATA
33	GAGGTGAGGCGGTCCTGAATAATGGAAGAGCACCATTACCAT
34	TAATAAGTTTTAACGCAAAATCACCAGTGGTTAGAACCTACC
35	ATATCAAAATTATTGAACGAACCACCAGCCAAAAACAGGAAG
36	CCATTAAAAATACCTGCACGTAAAACAGGACTTGAGCCATTT
37	GTATAAACAGTTAATTATCACCGTCACCAAATAAAGAAATTG
38	CGTAGATTTTCAGGTGCGCGAACTGATAACGTTAATATTTTG
39	CTATTAGTCTTTAATTTAACGTCAGATGTTGACGGAAATTAT
40	CTATTAGTCTTTAATTTAACGTCAGATGTTGACGGAAATTAT
41	TCATTAAAGGTGAATGCCCCCTGCCTATAGGATTAGAGAGTA
42	ATTGTATAAGCAAATTTTGATAAGAGGTGAGTAACAGTGCCC
43	TGTACCCCGGTTGATGCTGAATATAATGCAGGAGTGTACTGG
44	GCTTAGAGCTTAATTAATCAGAAAAGCCCAGAAGATAAAACA
45	GTTTTAAATATGCATAATCGTAAAACTACTGCAACAGTGCCA
46	TAGCAAGGCCGGAAGGCTTTTGATGATACTGTAGCTCAACAT
47	CCTTTAATTGCTCCTATTTAAATTGTAAGCCCTAAAACATCG
48	CCAGACCGGAAGCAAAATTTTTGTTAAAATATTTTTGAATGG
49	GAAAGCGTAAGAATGGGAGAAACAATAAAAAAGGGCGACATT
50	TAACCCACAAGAATCCAGACGTTAGTAACCAAAAGGAATTAC
51	AACCAATAGGAACGCGCGTTTTAATTCGGAGACTCCTCAAGA

52	GTTTTGTCGTCTTTTGAGTTAAGCCCAATTATCAAAATCATA
53	GCAACTGTTGGGAAGCAACACTATCATACGTAACGATCTAAA
54	AAGACTTCAAATATCCATCAAAAATAATAACCCTTCTGACCT
55	GGTCTGAGAGACTAATCCTGAGAAGTGTGGCCTCTTCGCTAT
56	GAGGCATAGTAAGAGGGCGATCGGTGCGTTTTATAATCAGTG
57	GAGGCATAGTAAGAGGGCGATCGGTGCGTTTTATAATCAGTG
58	AAGACGCTGAGAAGAAGAGTCTGTCCATGCCATTCAGGCTGC
59	GACGACGATAAAAAGCAAAGCGCCATTCCACGCAAATTAACC
60	GTTGTAGCAATACTCCTTGAAAACATAGCGAAGCCCTTTTTA
61	TTTTCCCTTAGAATTCTTTGATTAGTAACGGCACCGCTTCTG
62	AAGTTTTGCCAGAGTCCAGCCAGCTTTCTAACATCACTTGCC
63	TGAGTAGAAGAACTGCTTCTGTAAATCGTTACCAGAAGGAAA
64	GAGTGAATAACCTTCAAACTATCGGCCTGACAGTATCGGCCT
65	TAGCGTCCAATACTTTTGAGGGGACGACTGCTGGTAATATCC
66	AGAACAATATTACCTGGAAACAGTACATCCAAAAGAACTGGC
67	ATTACCTTTTTAAGCCAGCCATTGCAAGGGCGCATCGTAAC
68	CCCCCTCAAATGCTACGTTGGTGTAGATCAGGAAAAACGCTC
69	ATGGAAATACCTACATTAATTACATTTAGTTAGCAAACGTAG
70	ATCAAGAAAACAAAATTTTGACGCTCAACGGCGGATTGACCG
71	ATAAATCAAAAATCTCCGTGGGAACAAATCGTCTGAAATGGA
72	TTATTTACATTGGCCTGAGCAAAAGAAGTAAAAGAAACGCAA
73	TTCATTTCAATTACAGATTCACCAGTCATGTGAGCGAGTAAC
74	AAGCAAAGCGGATTTCATCAACATTAAACACGACCAGTAATA
75	AAAGGGACATTCTGAGTTACAAAATCGCACAATCAATAGAAA
76	TGCTTTGAATACCAGCCAACAGAGATAGTCGCGTCTGGCCTT
77	CCTGTAGCCAGCTTGCATCAAAAAGATTCAGTACCAGGCGGA
78	AACCCGTCGGATTCAGGTCTTTACCCTGTATAGCCCGGAATA
79	TAATGGGATAGGTCTTAAACAGTTCAGATACCGCCACCCTCA
80	CGTGCATCTGCCAGGCGGAATCGTCATACAGAGCCACCACCC
81	CAGGAAGATCGCACGGGGTAATAGTAAAGAACCCATGTACCG
82	GTGCCGGAAACCAGCCAAAATAGCGAGACTACAACGCCTGTA
83	AACAATGAAATAGCGCCCTCATAGTTAGACCCTCGTTTACCA
84	GCATTCCACAGACAAATAGCTATCTTACCGATAGCTTAGATT
85	AGAAAAGTAAGCAGGTCACCAGTACAAAGGCTTTTGCAAAAG
86	TAACACTGAGTTTCATAGCCGAACAAAGTCGCTATTAATTAA
87	CCGAGGAAACGCAAAGCAAGCCCAATAGATGTTTAGACTGGA
88	TCATTTTCAGGGATTAATAACGGAATACAAATCAATATATGT
89	ATGATTAAGACTCCAGAACCGCCACCCTAATATTCATTGAAT
90	GAACCGCCACCCTCTTATTACGCAGTATACAATTTCATTTGA
91	AAAATACATACATACTCAGGAGGTTTAGAAACGAGAATGACC
92	GGTGTATCACCGTAAAGGTGGCAACATAATGATGAAACAAAC
93	AGACACCACGGAATAGGGTTGATATAAGACTATTATAGTCAG
94	TAAGTGCCGTCGAGAAGTTTATTTTGTCGCAGAGGCGAATTA

95	ATTCATATGGTTTAAGCGGGGTTTTGCTAAGAGGAAGCCCGA
96	GAAGGATTAGGATTCCAGCGCCAAAGACCGGATTCGCCTGAT
97	AACGGTACGCCAGACCTTTTTAACCTCCTAATATCAGAGAGA
98	GAACGCGAGGCGTTGCATCGGAACGAGGAGGCTGGCTGACCT
99	TACGCCAGCTGGCGGCAGATACATAACGATGAATTTTCTGTA
100	AGCAGCGAAAGACATTAGCGAACCTCCCCCAACATGTAATTT
101	CTGCCCGCTTTCCACTTGACAAGAACCGGGATCGTCACCCTC
102	CACATTCAACTAATAAGGGGGATGTGCGGATTTTAGACAGG
103	AGGCAGAGGCATTTCCATCACCCAAATCCGTGCCAGCTGCAT
104	TCATCAAGAGTAATGTCGGGAAACCTGTAAGTTTTTTGGGGT
105	CGAGGTGCCGTAAACATATTTAACAACGGACTTGCGGGAGGT
106	TAATTGAGAATCGCGCACTAAATCGGAATTGCGTTGCGCTCA
107	AAATCAACGTAACACTAACTCACATTAACCCTAAAGGGAGCC
108	CCCGATTTAGAGCTTATAAAGCCAACGCTATTTTGCACCCAG
109	CAAATTCTTACCAGTGACGGGGAAAGCCGTAAAGCCTGGGGT
110	CCCTGACGAGAAACCGGAAGCATAAAGTGGCGAACGTGGCGA
111	GAAAGGAAGGGAAGAAGCCTGTTTAGTAGCTAACGAGCGTCT
112	ATAATTACTAGAAAAAAGCGAAAGGAGCCGCTCACAATTCCA
113	GATGGTTTAATTTCGTGAAATTGTTATCGGGCGCTAGGGCGC
114	TGGCAAGTGTAGCGGCGTTAAATAAGAAATAAACAGCCATAT
115	GTGTGATAAATAAGGTCACGCTGCGCGTCGTAATCATGGTCA
116	CGATTTTAAGAACTACCGAGCTCGAATTAACCACCACACCCG
117	CCGCGCTTAATGCGCTAAATTTAATGGTTTTTTGTTTAACG
118	TTTCATCTTCTGACCCGCTACAGGGCGCGCAGGTCGACTCTA
119	AAGAAAAATCTACGAAGCTTGCATGCCTGTACTATGGTTGCT
120	TTGACGAGCACGTAAAAACTTTTTCAAAAGAGAATAACATAA
121	ACAAAGAACGCGAGTAACGTGCTTTCCTACGACGTTGTAAAA
122	TATTACAGGTAGAAGGGTTTTCCCAGTCCGTTAGAATCAGAG
123	CGGGAGCTAAACAGTAAATGCTGATGCATTAACTGAACACCC
124	TATATAACTATATGGAGGCCGATTAAAGTGCAAGGCGATTAA
125	GTTGGGTAACGCCAAGATTCATCAGTTGTTTCAGCGGAGTGA
126	CGACGGCCAGTGCCTTAATAAAACGAACCGAATAATAATTTT
127	GAGGATCCCCGGGTGGCTCATTATACCACTCCAAAAGGAGCC
128	TAGCTGTTTCCTGTAACTTTAATCATTGTTCGAGGTGAATTT
129	CACAACATACGAGCACCAGAACGAGTAGCCGACAATGACAAC
130	GCCTAATGAGTGAGAAGCTGCTCATTCATCGGTCGCTGAGGC
131	TTTGAAGCCTTAAAAGGCCGCTTTTGCGGATATTCATTACCC
132	TTGCAGGGAGTTAATCAAGATTAGTTGCTCAACAGTAGGGCT
133	CTACAATTTTATCCCATAACCGATATATGTGAATAAGGCTTG
134	AACCATCGCCCACGTGAATCTTACCAACTCATATGCGTTATA
135	TTCCAGAGCCTAATTACCGATAGTTGCGTAAATTGGGCTTGA
136	CTTAAACAGCTTGATTGCCAGTTACAAATAAACACCGGAATC
137	TATTTATCCCAATCTTTATCAGCTTGCTTGAATTACCTTATG

138	TTTAATTGTATCGGCAAATAAGAAACGATTGAAATACCGACC
139	TCAAAAATGAAAATCTCCAAAAAAAAGGGTCAGGACGTTGGG
140	TTCACGTTGAAAATAGCAGCCTTTACAGTATATTTTAGTTAA
141	AAACAGGGAAGCGCAACTAAAGGAATTGTAACGGAACAACAT
142	GAATAGAAAGGAACATTAGACGGGAGAAAATCCAATCGCAAG
143	TGAACAAAGTCAGAACAACTTTCAACAGAGATTTAGGAATAC
144	TGGGATTTTGCTAAGGGTAATTGAGCGCGGCTTAGGTTGGGT
145	GCCCACTACGTGAATCGAGCCAGTAATAATCCGGTATTCTAA
146	TAATGAATCGGCCACAGACCAGGCGCATGTAGCAACGGCTAC
147	AGATGAACGGTGTAACGCGCGGGGAGAGCTATCAGGGCGATG
148	TTTACGAGCATGTATTTGATGGTGGTTCAGGCGAAAATCCTG
149	CGGAGATTTGTATCTGGTTTGCCCCAGCCGAAATCGGCAAAA
150	TCCCTTATAAATCAGAACAAGAAAAATACTTATCATTCCAAG
151	AATAGATAAGTCCTAAAGAATAGCCCGATGAGAGAGTTGCAG
152	CGACCTGCTCCATGTCACCGCCTGGCCCGATAGGGTTGAGTG
153	TTGTTCCAGTTTGGCTAATGCAGAACGCATCGAGAACAAGCA
154	AACAACATGTTCAGAACAAGAGTCCACTAGTGAGACGGGCAA
155	TCAATCATAAGGGATTTTTCTTTTCACCATTAAAGAACGTGG
156	ACTCCAACGTCAAAAAGTAATTCTGTCCATTACCGCGCCCAA
157	ACCGACAAAAGGTAGGGCGAAAAACCGTGCGGTTTGCGTATT
158	GGGCGCCAGGGTGGACCGAACTGACCAAATGAGGAAGTTTCC
159	CAGCTGATTGCCCTTTACTTAGCCGGAATACGAAGGCACCAA
160	CAAGCGGTCCACGCATCGCCTGATAAATCTAAAACACTCATC
161	GAAACCAATCAATAATTATACCAAGCGCGAAACAAAGTACAA
162	TTTGACCCCCAGCGATCGGCTGTCTTTCATATCCCATCCTAA
163	AACGGGTATTAAACGGCAAAAGAATACATGTGTCGAAATCCG
164	CCTAAAACGAAAGACAAGTACCGCACTCGCCTGTTTATCAAC
165	AGCCGTTTTTATTTATACGTAATGCCACCGAGGCGCAGACGG
166	ATTAAACGGGTAAATCATCGTAGGAATCAGACGACGACAATA
167	TAGCAAGCAAATCACTAAAGACTTTTTCCTTTGAAAGAGGAC
168	AGAGGCTTTGAGGAGATATAGAAGGCTTAGAGAATATAAAGT

Table S2. Sequences of helper strands functionalized with the single-stranded DNA capture probe. Strand names refer to unmodified helper strands listed in Table S1. The 17 bases region complementary to the Cy5-DNA conjugate is highlighted in red.

Name	**Sequence (5'-3')**
4	CCCTCAGAGCCACCCCGGAACCGCCTCCAAGTATTAGACTTT CGTTGTTGAGTCAACGGCCT
8	AAAATATCTTTAGGAACTCGTATTAAATATCAAAATCACCGG CGTTGTTGAGTCAACGGCCT
12	GTTTAGCTATATTTAATATGATATTCAAGAGGAAGGTTATCT

	CGTTGTTGAGTCAACGGCCT
16	AAATTAATGCCGGAGATACATTTCGCAAGTTGAGGCAGGTCACGTTGTTGAGTCAACGGCCT
20	TGCTGAACCTCAAAAGAAGGAGCGGAATTTTGCCTTTAGCGTCGTTGTTGAGTCAACGGCCT
24	TCCATATAACAGTTATTGCCTGAGAGTCCTAAAGCATCACCTCGTTGTTGAGTCAACGGCCT
28	GTACCTTTTACATCACGTGGCACAGACATCAGCTCATTTTTCGTTGTTGAGTCAACGGCCT
32	TTTGGATTATACTTAGTATTAACACCGCGCATGTCAATCATACGTTGTTGAGTCAACGGCCT

Cy5 labelled single strand：AGGCCGTTGACTCAACG-Cy5

Table S3. Sequences of helper strands functionalized with the single-stranded DNA capture probe. Strand names refer to unmodified helper strands listed in Table S1. The 18 bases region complementary to the DNA-AS1411 conjugate is highlighted in red.

Name	**Sequence (5'-3')**
22	CAGACTGTAGCGCGATATTCACAAACAACGAACGAGTAGATTATACGAGTTGAGAATACGAGTTGAAGTTGAGA
38	CGTAGATTTTCAGGTGCGCGAACTGATAACGTTAATATTTTGATACGAGTTGAGAATACGAGTTGAAGTTGAGA
54	AAGACTTCAAATATCCATCAAAAATAATAACCCTTCTGACCTATACGAGTTGAGAATACGAGTTGAAGTTGAGA
58	AAGACGCTGAGAAGAAGAGTCTGTCCATGCCATTCAGGCTGCATACGAGTTGAGAATACGAGTTGAAGTTGAGA
70	ATCAAGAAAACAAAATTTTGACGCTCAACGGCGGATTGACCGATACGAGTTGAGAATACGAGTTGAAGTTGAGA
82	GTGCCGGAAACCAGCCAAAATAGCGAGACTACAACGCCTGTAATACGAGTTGAGAATACGAGTTGAAGTTGAGA
86	TAACACTGAGTTTCATAGCCGAACAAAGTCGCTATTAATTAAATACGAGTTGAGAATACGAGTTGAAGTTGAGA
94	TAAGTGCCGTCGAGAAGTTTATTTTGTCGCAGAGGCGAATTAATACGAGTTGAGAATACGAGTTGAAGTTGAGA
102	CACATTCAACTAATAAAGGGGGATGTGCGGATTTTAGACAGGATACGAGTTGAGAATACGAGTTGAAGTTGAGA
106	TAATTGAGAATCGCGCACTAAATCGGAATTGCGTTGCGCTCAATACGAGTTGAGAATACGAGTTGAAGTTGAGA
110	CCCTGACGAGAAACCGGAAGCATAAAGTGGCGAACGTGGCGAATACGAGTTGAGAATACGAGTTGAAGTTGAGA
118	TTTCATCTTCTGACCCGCTACAGGGCGCGCAGGTCGACTCTAATACGAGTTGAGAATACGAGTTGAAGTTGAGA

126	CGACGGCCAGTGCCTTAATAAAACGAACCGAATAATAATTTTATACGAGTTGAGAATACGAGTTGAAGTTGAGA
130	GCCTAATGAGTGAGAAGCTGCTCATTCATCGGTCGCTGAGGCATACGAGTTGAGAATACGAGTTGAAGTTGAGA
134	AACCATCGCCCACGTGAATCTTACCAACTCATATGCGTTATAATACGAGTTGAGAATACGAGTTGAAGTTGAGA
138	TTTAATTGTATCGGCAAATAAGAAACGATTGAAATACCGACCATACGAGTTGAGAATACGAGTTGAAGTTGAGA
142	GAATAGAAAGGAACATTAGACGGGAGAAAATCCAATCGCAAGATACGAGTTGAGAATACGAGTTGAAGTTGAGA
146	TAATGAATCGGCCACAGACCAGGCGCATGTAGCAACGGCTACATACGAGTTGAGAATACGAGTTGAAGTTGAGA
150	TCCCTTATAAATCAGAACAAGAAAAATACTTATCATTCCAAGATACGAGTTGAGAATACGAGTTGAAGTTGAGA
154	AACAACATGTTCAGAACAAGAGTCCACTAGTGAGACGGGCAAATACGAGTTGAGAATACGAGTTGAAGTTGAGA
158	GGGCGCCAGGGTGGACCGAACTGACCAAATGAGGAAGTTTCCATACGAGTTGAGAATACGAGTTGAAGTTGAGA
162	TTTGACCCCCAGCGATCGGCTGTCTTTCATATCCCATCCTAAATACGAGTTGAGAATACGAGTTGAAGTTGAGA
166	ATTAAACGGGTAAATCATCGTAGGAATCAGACGACGACAATAATACGAGTTGAGAATACGAGTTGAAGTTGAGA

DNA-AS1411 aptamer：
GGTGGTGGTGGTTGTGGTGGTGGTGGTCTCAACTTCAACTCGTATTCTCAACTCGTAT

Table S3. Sequences of helper strands functionalized with the single-stranded DNA capture probe. Strand names refer to unmodified helper strands listed in Table S1. The 18 bases region complementary to the PTX-DNA conjugate is highlighted in red.

Name	Sequence (5’-3’)
1	TGTGTAGGTAAAGAATAGTAGTAGCATTCCTCAGAACCGCCATTCCACGATCAATGATCT
2	CATCAATTCTACTATTCAAAAGGGTGAGATAGATTAGAGCCGTTCCACGATCAATGATCT
3	AACCAGAGCCACCAACCCTCAGAGCCGCAGCTGAAAAGGTGGTTCCACGATCAATGATCT
6	ACAAACAATTCGACAGCACTAACAACTAAAAGGCCGGAGACATTCCACGATCAATGATCT
7	CCTTATTAGCGTTTAGCATTGACAGGAGATGGTCAATAACCTTTCCACGATCAATGATCT
9	TTATTAATTTTAAAAGTTGAAAGGAATTCCGTTCTAGCTGATTTCCACGATCAATGATCT
11	CCAGAGCCGCCGCCGCCATCTTTTCATACCTTTGCCCGAACGTTCCACGATC

	AATGATCT
15	TGATTATCAGATGAAGCAAATGAAAAATTGGAGCAAACAAGATTCCACGATCAATGATCT
17	AAGCCAGAATGGAAGCGACAGAATCAAGTATCATCATATTCCTTCCACGATCAATGATCT
18	GACGATTGGCCTTGTTTTCATCGGCATTTATCATTTTGCGGATTCCACGATCAATGATCT
19	ACAAAGAAACCACCTATCAAACCCTCAATTGAGAGATCTACATTCCACGATCAATGATCT
23	TAGTTTGACCATTAGAGGGTAGCTATTTTCAATATCTGGTCATTCCACGATCAATGATCT
24	TCCATATAACAGTTATTGCCTGAGAGTCCTAAAGCATCACCTTTCCACGATCAATGATCT
25	GGGAATTAGAGCCAGGGGTCAGTGCCTTCATTTTTGCGGATGTTCCACGATCAATGATCT
27	CGCTGAGAGCCAGCTGGCAATTCATCAAACCATCGATAGCAGTTCCACGATCAATGATCT
31	TAAGCGTCATACATACGTCACCAATGAATATAATCCTGATTGTTCCACGATCAATGATCT
33	GAGGTGAGGCGGTCCTGAATAATGGAAGAGCACCATTACCATTTCCACGATCAATGATCT
35	ATATCAAAATTATTGAACGAACCACCAGCCAAAAACAGGAAGTTCCACGATCAATGATCT
39	CTATTAGTCTTTAATTTAACGTCAGATGTTGACGGAAATTATTTCCACGATCAATGATCT
41	TCATTAAAGGTGAATGCCCCCTGCCTATAGGATTAGAGAGTATTCCACGATCAATGATCT
43	TGTACCCCGGTTGATGCTGAATATAATGCAGGAGTGTACTGGTTCCACGATCAATGATCT
44	GCTTAGAGCTTAATTAATCAGAAAAGCCCAGAAGATAAAACATTCCACGATCAATGATCT
47	CCTTTAATTGCTCCTATTTAAATTGTAAGCCCTAAAACATCGTTCCACGATCAATGATCT
48	CCAGACCGGAAGCAAAATTTTTGTTAAAATATTTTTGAATGGTTCCACGATCAATGATCT
49	GAAAGCGTAAGAATGGGAGAAACAATAAAAAAGGGCGACATTTTCCACGATCAATGATCT
51	AACCAATAGGAACGCGCGTTTTAATTCGGAGACTCCTCAAGATTCCACGATCAATGATCT
52	GTTTTGTCGTCTTTTGAGTTAAGCCCAATTATCAAAATCATATTCCACGATCAATGATCT
55	GGTCTGAGAGACTAATCCTGAGAAGTGTGGCCTCTTCGCTATTTCCACGATCAATGATCT

56	GAGGCATAGTAAGAGGGCGATCGGTGCGTTTTATAATCAGTGTTCCACGATCAATGATCT
57	GAGGCATAGTAAGAGGGCGATCGGTGCGTTTTATAATCAGTGTTCCACGATCAATGATCT
59	GACGACGATAAAAAGCAAAGCGCCATTCCACGCAAATTAACCTTCCACGATCAATGATCT
60	GTTGTAGCAATACTCCTTGAAAACATAGCGAAGCCCTTTTTATTCCACGATCAATGATCT
63	TGAGTAGAAGAACTGCTTCTGTAAATCGTTACCAGAAGGAAATTCCACGATCAATGATCT
64	GAGTGAATAACCTTCAAACTATCGGCCTGACAGTATCGGCCTTTCCACGATCAATGATCT
65	TAGCGTCCAATACTTTTGAGGGGACGACTGCTGGTAATATCCTTCCACGATCAATGATCT
67	ATTACCTTTTTAAGCCAGCCATTGCAAGGGCGCATCGTAACTTCCACGATCAATGATCT
68	CCCCCTCAAATGCTACGTTGGTGTAGATCAGGAAAAACGCTCTTCCACGATCAATGATCT
71	ATAAATCAAAAATCTCCGTGGGAACAAATCGTCTGAAATGGATTCCACGATCAATGATCT
72	TTATTTACATTGGCCTGAGCAAAAGAAGTAAAAGAAACGCAATTCCACGATCAATGATCT
73	TTCATTTCAATTACAGATTCACCAGTCATGTGAGCGAGTAACTTCCACGATCAATGATCT
75	AAAGGGACATTCTGAGTTACAAAATCGCACAATCAATAGAAATTCCACGATCAATGATCT
76	TGCTTTGAATACCAGCCAACAGAGATAGTCGCGTCTGGCCTTTTCCACGATCAATGATCT
79	TAATGGGATAGGTCTTAAACAGTTCAGATACCGCCACCCTCATTCCACGATCAATGATCT
80	CGTGCATCTGCCAGGCGGAATCGTCATACAGAGCCACCACCCTTCCACGATCAATGATCT
81	CAGGAAGATCGCACGGGGTAATAGTAAAGAACCCATGTACCGTTCCACGATCAATGATCT
83	AACAATGAAATAGCGCCCTCATAGTTAGACCCTCGTTTACCATTCCACGATCAATGATCT
84	GCATTCCACAGACAAATAGCTATCTTACCGATAGCTTAGATTTTCCACGATCAATGATCT
85	AGAAAAGTAAGCAGGTCACCAGTACAAAGGCTTTTGCAAAAGTTCCACGATCAATGATCT
87	CCGAGGAAACGCAAAGCAAGCCCAATAGATGTTTAGACTGGATTCCACGATCAATGATCT
88	TCATTTTCAGGGATTAATAACGGAATACAAATCAATATATGTTTCCACGATCAATGATCT

91	AAAATACATACATACTCAGGAGGTTTAGAAACGAGAATGACCTTCCACGATCAATGATCT
92	GGTGTATCACCGTAAAGGTGGCAACATAATGATGAAACAAACTTCCACGATCAATGATCT
93	AGACACCACGGAATAGGGTTGATATAAGACTATTATAGTCAGTTCCACGATCAATGATCT
95	ATTCATATGGTTTAAGCGGGGTTTTGCTAAGAGGAAGCCCGATTCCACGATCAATGATCT
96	GAAGGATTAGGATTCCAGCGCCAAAGACCGGATTCGCCTGATTTCCACGATCAATGATCT
99	TACGCCAGCTGGCGGCAGATACATAACGATGAATTTTCTGTATTCCACGATCAATGATCT
100	AGCAGCGAAAGACATTAGCGAACCTCCCCCAACATGTAATTTTTCCACGATCAATGATCT
101	CTGCCCGCTTTCCACTTGACAAGAACCGGGATCGTCACCCTCTTCCACGATCAATGATCT
103	AGGCAGAGGCATTTCCATCACCCAAATCCGTGCCAGCTGCATTTCCACGATCAATGATCT
104	TCATCAAGAGTAATGTCGGGAAACCTGTAAGTTTTTTGGGGTTTCCACGATCAATGATCT
107	AAATCAACGTAACACTAACTCACATTAACCCTAAAGGGAGCCTTCCACGATCAATGATCT
108	CCCGATTTAGAGCTTATAAAGCCAACGCTATTTTGCACCCAGTTCCACGATCAATGATCT
109	CAAATTCTTACCAGTGACGGGGAAAGCCGTAAAGCCTGGGGTTTCCACGATCAATGATCT
111	GAAAGGAAGGGAAGAAGCCTGTTTAGTAGCTAACGAGCGTCTTTCCACGATCAATGATCT
112	ATAATTACTAGAAAAAAGCGAAAGGAGCCGCTCACAATTCCATTCCACGATCAATGATCT
115	GTGTGATAAATAAGGTCACGCTGCGCGTCGTAATCATGGTCATTCCACGATCAATGATCT
116	CGATTTTAAGAACTACCGAGCTCGAATTAACCACCACACCCGTTCCACGATCAATGATCT
120	TTGACGAGCACGTAAAAACTTTTTCAAAAGAGAATAACATAATTCCACGATCAATGATCT
123	CGGGAGCTAAACAGTAAATGCTGATGCATTAACTGAACACCCTTCCACGATCAATGATCT
124	TATATAACTATATGGAGGCCGATTAAAGTGCAAGGCGATTAATTCCACGATCAATGATCT
125	GTTGGGTAACGCCAAGATTCATCAGTTGTTTCAGCGGAGTGATTCCACGATCAATGATCT
127	GAGGATCCCCGGGTGGCTCATTATACCACTCCAAAAGGAGCCTTCCACGATCAATGATCT

128	TAGCTGTTTCCTGTAACTTTAATCATTGTTCGAGGTGAATTTTTCCACGATCAATGATCT
131	TTTGAAGCCTTAAAAGGCCGCTTTTGCGGATATTCATTACCCTTCCACGATCAATGATCT
132	TTGCAGGGAGTTAATCAAGATTAGTTGCTCAACAGTAGGGCTTTCCACGATCAATGATCT
133	CTACAATTTTATCCCATAACCGATATATGTGAATAAGGCTTGTTCCACGATCAATGATCT
135	TTCCAGAGCCTAATTACCGATAGTTGCGTAAATTGGGCTTGATTCCACGATCAATGATCT
136	CTTAAACAGCTTGATTGCCAGTTACAAATAAACACCGGAATCTTCCACGATCAATGATCT
139	TCAAAAATGAAAATCTCCAAAAAAAAGGGTCAGGACGTTGGGTTCCACGATCAATGATCT
140	TTCACGTTGAAAATAGCAGCCTTTACAGTATATTTTAGTTAATTCCACGATCAATGATCT
141	AAACAGGGAAGCGCAACTAAAGGAATTGTAACGGAACAACATTTCCACGATCAATGATCT
143	TGAACAAAGTCAGAACAACTTTCAACAGAGATTTAGGAATACTTCCACGATCAATGATCT
144	TGGGATTTTGCTAAGGGTAATTGAGCGCGGCTTAGGTTGGGTTTCCACGATCAATGATCT
147	AGATGAACGGTGTAACGCGCGGGGAGAGCTATCAGGGCGATGTTCCACGATCAATGATCT
148	TTTACGAGCATGTATTTGATGGTGGTTCAGGCGAAAATCCTGTTCCACGATCAATGATCT
149	CGGAGATTTGTATCTGGTTTGCCCCAGCCGAAATCGGCAAAATTCCACGATCAATGATCT
151	AATAGATAAGTCCTAAAGAATAGCCCGATGAGAGAGTTGCAGTTCCACGATCAATGATCT
152	CGACCTGCTCCATGTCACCGCCTGGCCCGATAGGGTTGAGTGTTCCACGATCAATGATCT
155	TCAATCATAAGGGATTTTTCTTTTCACCATTAAAGAACGTGGTTCCACGATCAATGATCT
156	ACTCCAACGTCAAAAAGTAATTCTGTCCATTACCGCGCCCAATTCCACGATCAATGATCT
157	ACCGACAAAAGGTAGGGCGAAAAACCGTGCGGTTTGCGTATTTTCCACGATCAATGATCT
159	CAGCTGATTGCCCTTTACTTAGCCGGAATACGAAGGCACCAATTCCACGATCAATGATCT
160	CAAGCGGTCCACGCATCGCCTGATAAATCTAAAACACTCATCTTCCACGATCAATGATCT
163	AACGGGTATTAAACGGCAAAAGAATACATGTGTCGAAATCCGTTCCACGATCAATGATCT

164	CCTAAAACGAAAGACAAGTACCGCACTCGCCTGTTTATCAACTTCCACGATCAATGATCT
165	AGCCGTTTTTATTTATACGTAATGCCACCGAGGCGCAGACGGTTCCACGATCAATGATCT
167	TAGCAAGCAAATCACTAAAGACTTTTTCCTTTGAAAGAGGACTTCCACGATCAATGATCT
168	AGAGGCTTTGAGGAGATATAGAAGGCTTAGAGAATATAAAGTTTCCACGATCAATGATCT

DNA-PTX：PTX-AGATCATTGATCGTGG