

Supplementary material

Figure captions

Fig S1. The standard curve plotting of Library. (a) Amplification curves of Library at 10 nM, 1 nM, 100 pM, 10 pM, 1 pM, 100 fM and 10 fM, respectively; (b) Linear fitting graph between C_q values and logarithmic values of concentration for Library.

Fig S2. The predicted secondary structure for the 12 sequence with the highest enrichment degree according to sequencing information. (M-Fold was executed with [Na⁺]=100 mM; [Mg²⁺]=2 mM; The temperature is 25°C; ΔG (kcal/mol)).

Fig S3. Sequence alignment of the top 12 sequences with the highest enrichment rankings obtained from sequencing.

Fig S4. TEM-EDS elemental mapping of PLL/BP: (A) TEM image; (B) P distribution; (C) C distribution; (D) N distribution; (E) O distribution.

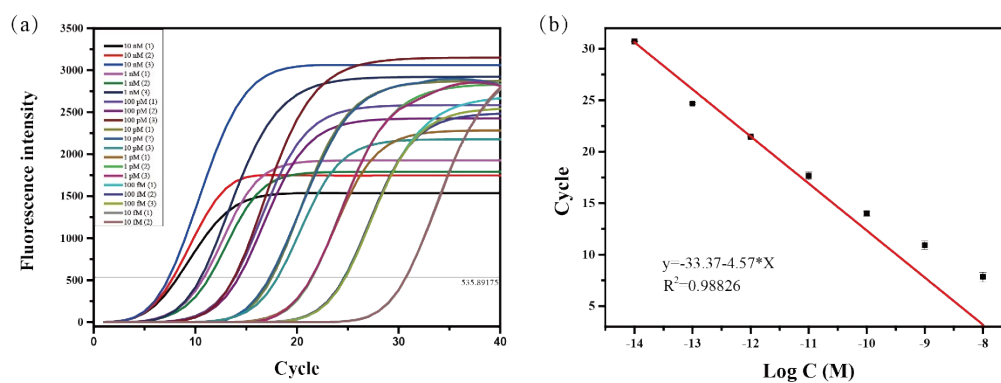


Fig S1. The standard curve plotting of Library. (a) Amplification curves of Library at 10 nM, 1 nM, 100 pM, 10 pM, 1 pM, 100 fM and 10 fM, respectively; (b) Linear fitting graph between C_q values and logarithmic values of concentration for Library.

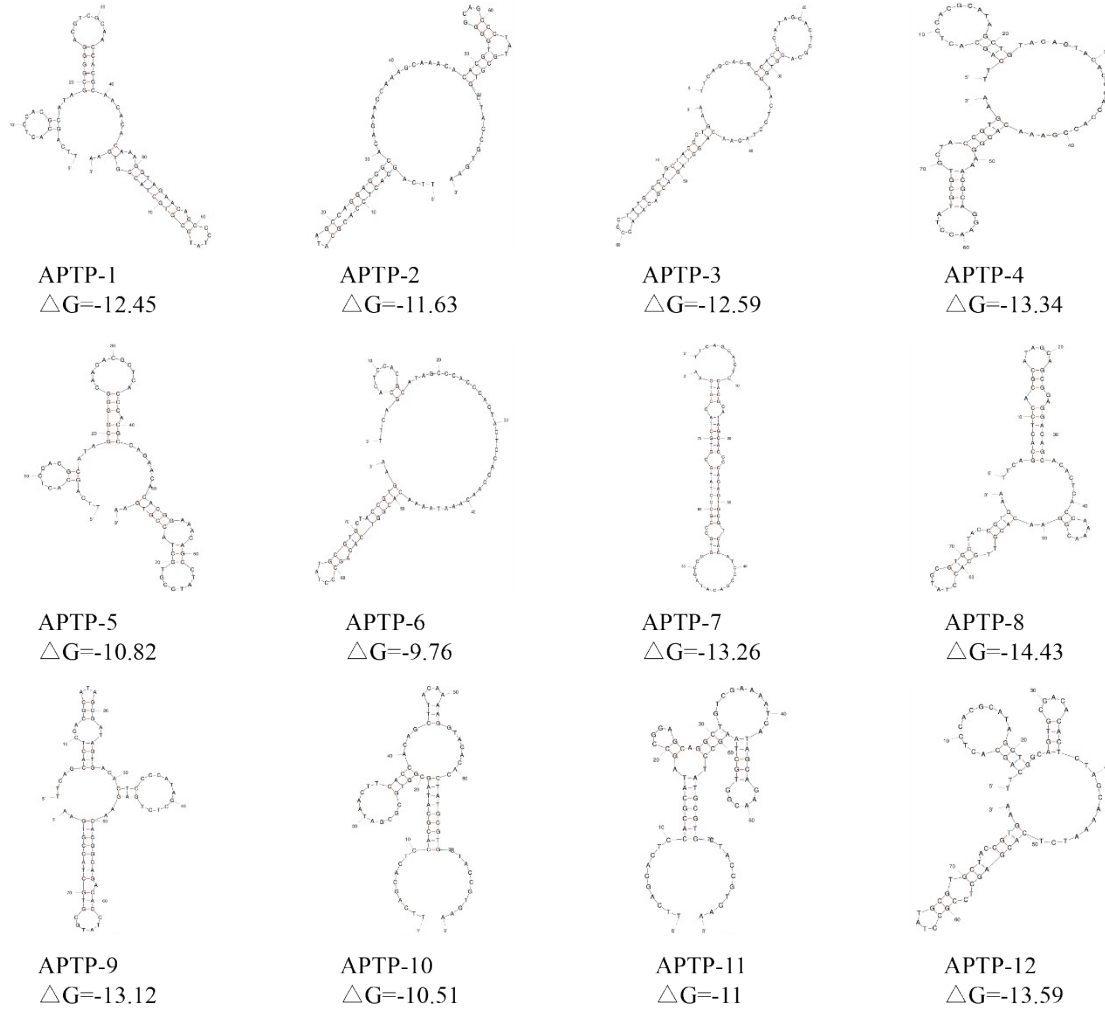


Fig S2. The predicted secondary structure for the 12 sequence with the highest enrichment degree according to sequencing information. (M-Fold was executed with $[Na^+]=100$ mM; $[Mg^{2+}]=2$ mM; The temperature is 25°C; ΔG (kcal/mol)).

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          *      20      *      40
Sequence_01 : ---GGGACGTCGCAACACGC---AACACACAAGGTAGAACAGC- : 40
Sequence_02 : ---CAGGAGGGCAGAGA-ACCA---AAGCAAACACACGTGGGGCAGC- : 40
Sequence_03 : --ACTCGACGTGGAACTCCTAC---AACAGGTAGACGACATAGC--- : 40
Sequence_04 : -----TGIACAGTACACCCACACCGAAACACGGAACGCAGGAA----- : 40
Sequence_05 : -----GGGCAACACGCTACCC---ACGCAGAACACACGGAACAG- : 40
Sequence_06 : -----CCACCACCTACTCCACCAACAAATAAACACGGTCACAGC : 40
Sequence_07 : ACCCCAGAGTGCGTCACATCCGACATAGCCGGTGCCCGC----- : 40
Sequence_08 : AGCGGAGGACAGCACACTCACCA---AACGGA-ACACGTTGCA----- : 40
Sequence_09 : -----GATAGTGACACTCCCATAGCTCTGAGAACACGCGCAGACA--- : 40
Sequence_10 : ---GGTCCGCGATAACTTCACCA---CAGCTTACAAAGTAGACA--- : 40
Sequence_11 : ---CGGAGCAGGCTGTGCGAAAATCATAGCAGAACGGTCTAAG----- : 40
Sequence_12 : -TGGCAGTGCAGACACACTCTAGC-AAATCTCACGAGCTCCG----- : 40
          G  C      CAC C CC      A C      A ACG

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Fig S3. Sequence alignment of the top 12 sequences with the highest enrichment rankings obtained from sequencing.

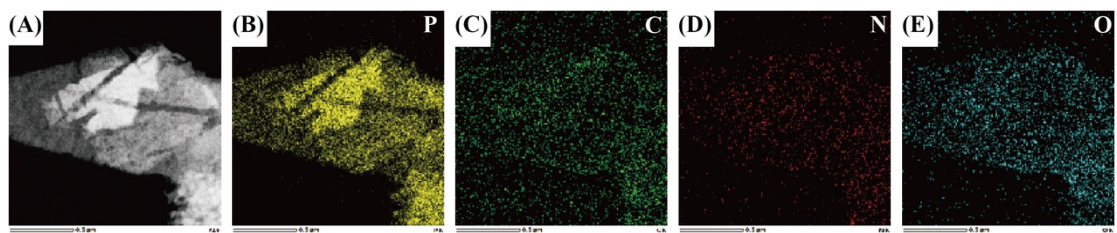


Fig 4. TEM-EDS elemental mapping of PLL/BP: (A) TEM image; (B) P distribution; (C) C distribution; (D) N distribution; (E) O distribution.

Table captions

Table S1 Synthesized sequence information.

Table S2 The twelve sequences with the highest enrichment scores.

Table S1 Synthesized sequence information.

Name	Sequence (5'-3')
Initial ssDNA Library	TTCAGCACTCCACGCATAGC-(N)40-
(Lib)	CCTATGCGTGCTACCGTGAA
Forward primer (P1)	TTCAGCACTCCACGCATAGC
Reverse primer (P2)	TTCACGGTAGCACGCATAGG
Lib-biotin	GCTATGCGTGGAGTGCTGAA-biotin
Lib-FAM	FAM-TTCAGCACTCCACGCATAGC
Lib-polyA	AAAAAAAAAAAAAAAAAAAAAAAAAA/iSp18/TTCACGGTAGCAC GCATAGG
AOTP-3-SH	HS-TTCAGCACTCCACGCATAGCACTCGCACGTGGAACCTCCTA CAACAGGTAGACGACATAGCCCTATGCGTGCTACCGTGAA

Table S2 The twelve sequences with the highest enrichment scores.

Name	Sequences information (5'-3')
APTP-1	TTCAGCACTCCACGCATAGCGGGGACGTCGCAACCACGCAACACAC AAAGGTAGAACAGCCCTATGCGTGCTACCGTGAA
APTP-2	TTCAGCACTCCACGCATAGCCAGGAGGGCACAGAACCAAAGCAAAC ACACGTGGGGCAGCCCTATGCGTGCTACCGTGAA
APTP-3	TTCAGCACTCCACGCATAGCACTCGCACGTGGAACCTCCTACAACAG GTAGACGACATAGCCCTATGCGTGCTACCGTGAA
APTP-4	TTCAGCACTCCACGCATAGCTGTACAGTACACCCACCACCGAAACA CGGAAACGCAGGAACCTATGCGTGCTACCGTGAA
APTP-5	TTCAGCACTCCACGCATAGCGGGGCAACACGCTCACCCACGCCAGA ACACACGGAAACAGCCTATGCGTGCTACCGTGAA
APTP-6	TTCAGCACTCCACGCATAGCCCACCCACTACTCCACCAACAAATAA AACACGGTCACAGCCCTATGCGTGCTACCGTGAA
APTP-7	TTCAGCACTCCACGCATAGCACCCCAGAGTGCGTCACATCCCGACAT AGCCGGTGCCCGCCCTATGCGTGCTACCGTGAA
APTP-8	TTCAGCACTCCACGCATAGCAGCGGAGGACAGCACACTCACCAAAA CGGAACACGTTGCACCTATGCGTGCTACCGTGAA
APTP-9	TTCAGCACTCCACGCATAGCGATAGTGACACTCCCCATAGCTCTGAG AACACGGCAGACACCTATGCGTGCTACCGTGAA
APTP-10	TTCAGCACTCCACGCATAGCGGTGCGCGATAACTTCACCACAGCTTA CAAAAGGTAGACACCTATGCGTGCTACCGTGAA
APTP-11	TTCAGCACTCCACGCATAGCCGGAGCAGGCTGTGCGAAAATCATAGC AGAACGGTGCTAAGCCTATGCGTGCTACCGTGAA
APTP-12	TTCAGCACTCCACGCATAGCTGGCAGTGCGACACACTCTAGCAAAA TCTCACGAGCTCCGCCTATGCGTGCTACCGTGAA

