

Supplementary data

Colorimetric aptasensor for detecting *Bacillus carboniphilus* using aptamer isolated with a non-SELEX-based method

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Table S1. Sequences of the *B. carboniphilus*-specific aptamers isolated using the centrifugation-based partitioning method.

Aptamer	Sequences of the random region
BCA-01	TTG ATG TGA AGC TCG CAG CTT TCC GGG AGG CAT TGT TGA ACT TT
BCA-02	GCA TTC CGA GTG TTG GCT TAA GTT CCA TAC TCC TCG AAT GTG TAT
BCA-03	CCG CCT CTT GAT CGG CTG TTG CAT AGG TGC GTC AGC GGG CAT TCG
BCA-04	GCC ATC TCC CGG CTC AGG AGT AAC GCG CCC GCA TAC TTA GGG CAT
BCA-05	CGG ACG GCT CTC GGG TTC TGC GGG TGT AAC CGA GAA ATA TCT ACG
BCA-06	ATG GGA AAT CCC AAA TTC TCA ACC GTT GAA TGC AGC CTT TCT GGG
BCA-07	GGC CGT TCC CCT GCA TTG AAG GTG CGG TCT AGC GTT CAT CCT GAA
BCA-08	TCT TTT GGC TCC GGG GCC GAT GTT CTC CCA GTG CCC TTG CGC CAG A
BCA-09	AAA AGC TAA CCG GGA CGC TAT TTG TAA GCA GAT ATC CTG ACA CCT
BCA-10	AGA CTG GCA CGG TTG CGG GTG ACC TGC TAA CAA GCC CCA TTA TCT
BCA-11	CGT TAG GTG TCA ACC CTC GTC GGG TCT CGC AGC CAA GTA GTG TAC G
BCA-12	GGG CTG GTG AAG CCA AAC TGC TCC ATT GGT CCA GCT TCG TCC AGC
BCA-13	GCC GGA GTC CAC TGC TGT TCA CGA TCT TGT AAG GCC TTT CGC GAT
BCA-14	TGA TTT GGT TCC ACT GTT GCG GAG GGG TCT TAC TGC TAG TGG TTT
BCA-15	TGT GAT GGG GTG GGG GTT GTG AGG CCG GGT TGT TTG GTC TAC G
BCA-16	GTC TAC TTG GGG GTT TCC GCT TAT GTG TGT TAC GGG GGT TTT TGT
BCA-17	ACC GAG GGG GAG GCC ATC CGG GCA ATG TGT GGT GTT AGG GTC GGA
BCA-18	GGG TAC CTT CGT CAT GAC CAC AGG GTC TGC TAG TAC GGG TCT GTT
BCA-19	CGC CCA TTG GGG CTT GGT TAT TTT CAC CAA GTT GAG AAT TTT TGT
BCA-20	AGA AGG CTC GAA GTG CTC TAG AGA GTG GGC TAA TGT AAT TGC TCT
BCA-21	CAG CCA CGG TGT GGT TCA CCT TGG GTC CCT GGT TGG CGC CGC ATG
BCA-22	TCG GTT GTA AGT TCT TAC GTA TCC CGG GCG TTA CTC GTC TAT GGC
BCA-23	TTG TCG CAT CAA TTT TTT CAT CTG GTA GGC TCG CGA TTT C
BCA-24	TAA TAT AGT ATG GCT TTC AGC CGT TTA CCT GTG AGA TTA GGT TTT
BCA-25	TCC CTA AAT CAG CAC CGA AAT GGT GAG GAT TAA TCG ACT AAG AT

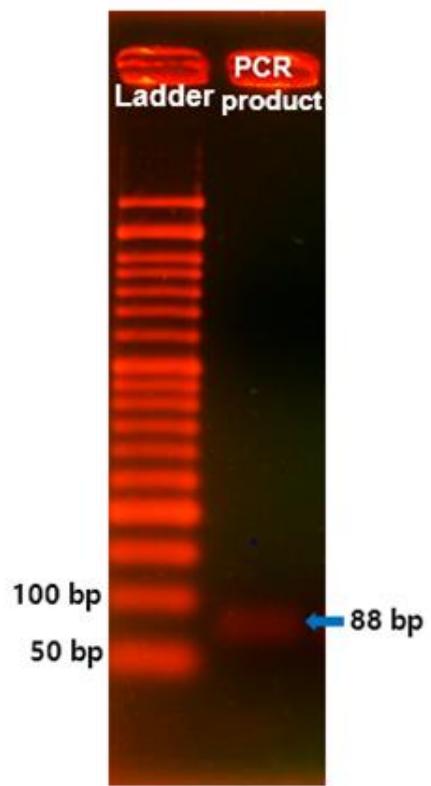


Figure S1. Agarose gel electrophoresis of the final PCR product. The band on lane 2 appeared between 50 and 100 base pairs(bp) is corresponding to the size, 88 bp of random DNA library used in aptamer selection

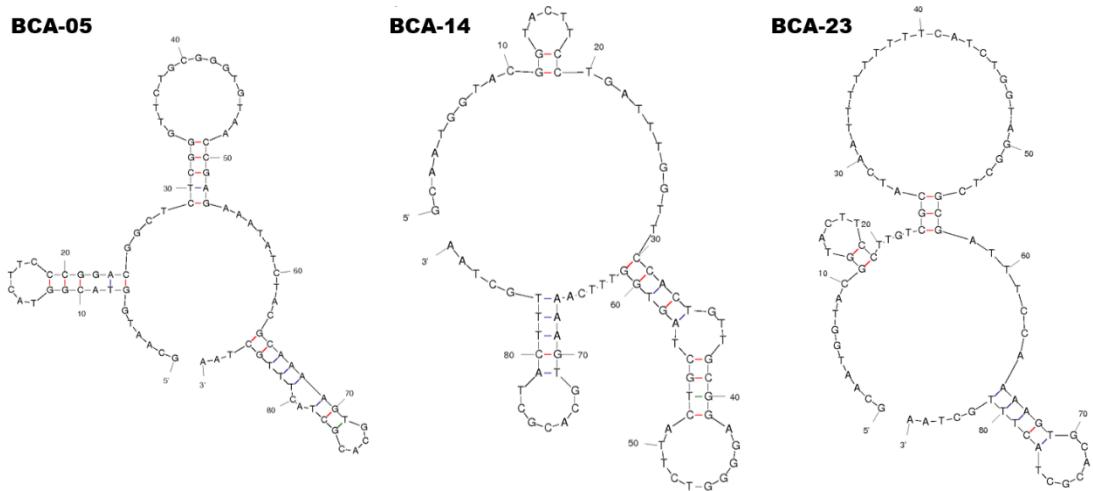


Figure S2. Secondary structures of isolated aptamers predicted by the Mfold algorithm.

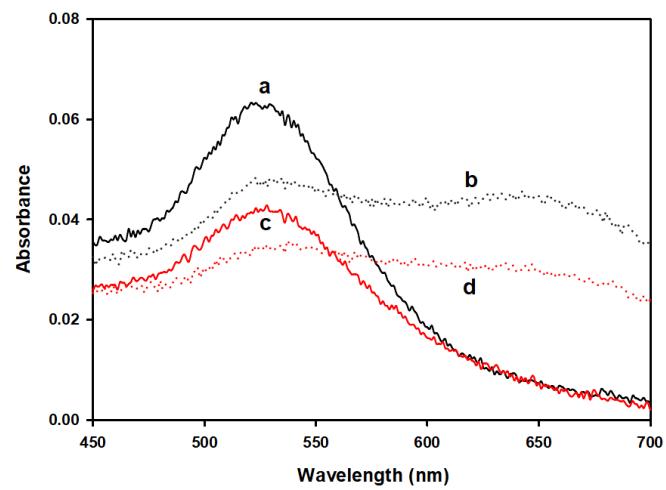


Figure S3. Ultraviolet-visible absorption spectra of AuNPs at each experimental condition: (a) AuNPs only (solid black line); (b) AuNPs without aptamer (black dot line); (c) AuNPs with the BCA-05 aptamer (solid red line); (d) AuNPs with the flow-through solution after BCA-05 binding to *B. carboniphilus* (red dot line). 0.6 M NaCl was added to b, c, and d.

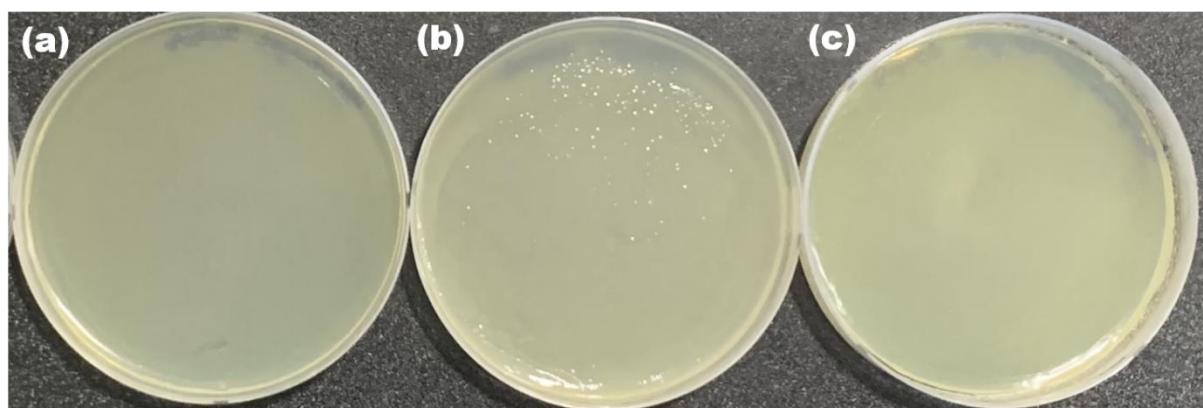


Figure S4. The formation of artificial biofilms on nutrient agar medium. (a) non-target bacterial mixture biofilm, (b) target bacterial biofilm, and (c) the target in bacterial mixture.