

Supporting Information

A Study of DNA Design Dependency of Segmented DNA-Induced Gold Nanoparticle Aggregation towards Versatile Bioassay Development

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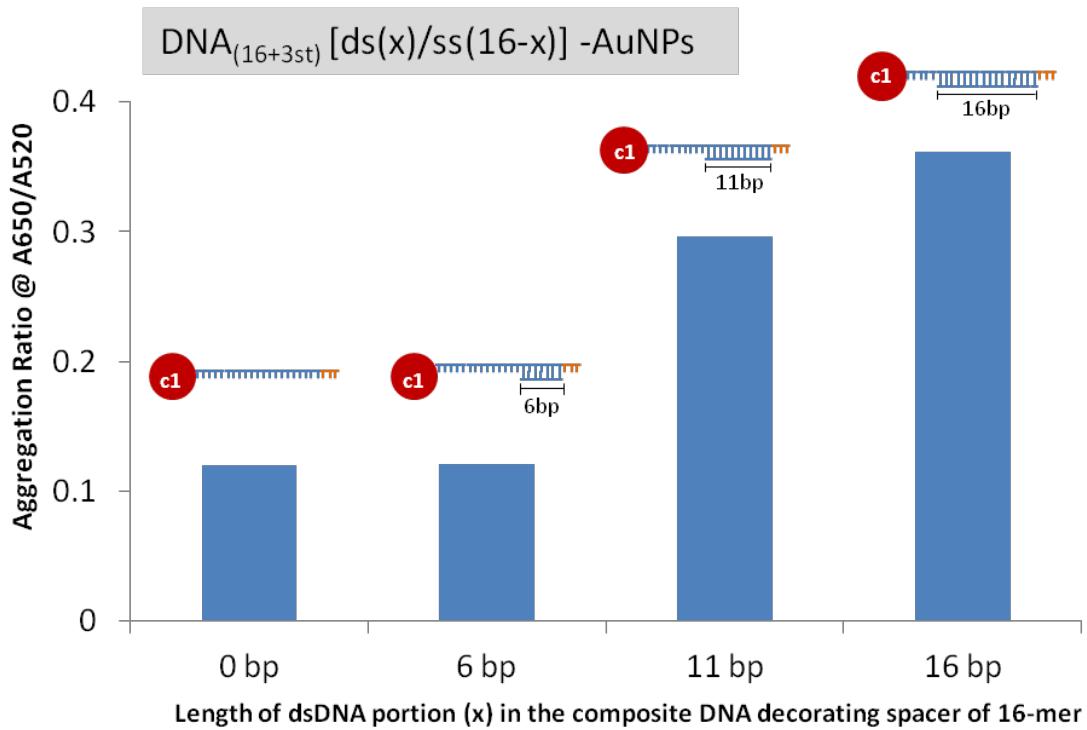


Figure S1. Aggregation degree measured by ratio $R = A_{650}/A_{520}$ as a function of rigid dsDNA length in a designer set of 16-mer composite DNA decorating spacer. 11bp is determined to be the minimum requirement as an effective partial-rigid spacer.

Table S1. DNA Sequences Used in This Study

DNA Spacer	Sticky-ends	DNA Sequences (from 5' to 3')
45-mer ERE (dsDNA)	-	5'-AAA AAG TCC AAA GTC AGTCA CAG <u>TGACC</u> GAT CAA AGT ATT TTT -3' 5'- AAA AAT ACT TTG ATC A <u>GGTCA</u> CTG <u>TGACC</u> GAC TTT GGA CTT TTT -3'
c1 [ds(21)]	3-st	5'-(SH) AAA AAG TCC AAA GTC AGG TCA CAG -3' 5'- TGA CCT GAC TTT GGA CTT TTT -3'
c2[ds(21)]	3-st	5'-(SH) AAA AAT ACT TTG ATC AGG TCA CTG -3' 5'- TGA CCT GAT CAA AGT ATT TTT -3'
c1[ds(16)/ss(5)]	3-st	5'-(SH) AAA AAG TCC AAA GTC AGG TCA CAG -3' 5'- TGA CCT GAC TTT GGA C-3'
c2[ds(16)/ss(5)]	3-st	5'-(SH) AAA AAT ACT TTG ATC AGG TCA CTG -3' 5'- TGA CCT GAT CAA AGT A -3'
c1[ds(11)/ss(10)]	3-st	5'-(SH) AAA AAG TCC AAA GTC AGG TCA CAG -3' 5'- TGA CCT GAC TT-3'
c2[ds(11)/ss(10)]	3-st	5'-(SH) AAA AAT ACT TTG ATC AGG TCA CTG -3' 5'- TGA CCT GAT CA -3'
c1[ds(16)]	3-st	5'-(SH)GTC CAA AGT CAG GTC ACA G -3' 5'- TGA CCT GAC TTT GGA C -3'
c2[ds(16)]	3-st	5'-(SH)AACT TTG ATC AGG TCA CTG -3' 5'- TGA CCT GAT CAA AGT T -3'
c1 [ds(11)/ss(5)]	3-st	5'-(SH)GTC CAA AGT CAG GTC ACA G -3' 5'- TGA CCT GAC TT-3'
c2 [ds(11)/ss(5)]	3-st	5'-(SH)AACT TTG ATC AGG TCA CTG -3' 5'- TGA CCT GAT CA -3'
c1 [ds(6)/ss(10)]	3-st	5'-(SH)GTC CAA AGT CAG GTC ACA G -3' 5'- TGA CCT -3'
c2 [ds(6)/ss(10)]	3-st	5'-(SH)AACT TTG ATC AGG TCA CTG -3' 5'- TGA CCT -3'
c1 [ds(11)]	3-st	5'-(SH)A GTC AGG TCA CAG -3' 5'- TGA CCT GAC T-3'
c2[ds(11)]	3-st	5'-(SH)G ATC AGG TCA CTG -3' 5'- TGA CCT GAT C-3'
c1 [ds(6)]	3-st	5'-(SH)AGG TCA CAG -3' 5'- CCT GAC-3'
c2[ds(6)]	3-st	5'-(SH) AGG TCA CTG -3' 5'- TGA CCT-3'
c1[ds(16)]	3-st	5'-(SH)GTC CAA AGT CAG GTC ACA G -3' 5'- A CCT GAC TTT GGA C -3'
c2[ds(16)]	3-st	5'-(SH)AACT TTG ATC AGG TCA CTG -3' 5'- A CCT GAT CAA AGT T -3'
c1[ds(16)]	8-st	5'-(SH)GTC CAA AGT CAG GTC ACA G -3' 5'- T GAC TTT GGA C -3'
c2[ds(16)]	8-st	5'-(SH)AACT TTG ATC AGG TCA CTG -3' 5'- T GAT CAA AGT T -3'

c1[ds(16)]	1-st	5'- (SH)GTC CAA AGT CAG GTC ACA G -3' 5'- TG TGA CCT GAC TTT GGA C -3'
c2[ds(16)]	1-st	5'- (SH)AACT TTG ATC AGG TCA CTG -3' 5'- AG TGA CCT GAT CAA AGT T -3'
mtERE	-	5'- GTC CAA AGT CA <u>GTTCA</u> CAG <u>TGATC</u> TGA TCA AAG T -3' 5'- ACT TTG ATC A <u>GATCA</u> CTG <u>TGAAC</u> TGAC TTT GGA C -3'
wtERE	-	5'- GTC CAA AGT CA <u>GGTCA</u> CAG <u>TGACC</u> TGA TCA AAG T -3' 5'- ACT TTG ATC A <u>GGTCA</u> CTG <u>TGACC</u> T GAC TTT GGA C -3'

Note: Underlined sequences indicate the estrogen responsive element (ERE). Nucleotides in red indicate mutated nucleotides.