Supporting Information

Materials:

All chemical synthesized DNA strands were purchased from Integrated DNA Technologies, Inc. (www. Idtdna.com). The unmodified helper strands ordered in a 96-well plate format, suspended in ultrapure water without purification. All modified strands were ordered from IDT with HPLC purification. Colloidal solution of 10 nm AuNPs was purchased from Ted Pella Inc. Quantum dots Straptavidin conjugates were purchased from Invitrogen with the emission maximum near 585 nm. 100kDa MWCO centrifuge filters purchased from Pall, Inc.

Supplementary Figures:

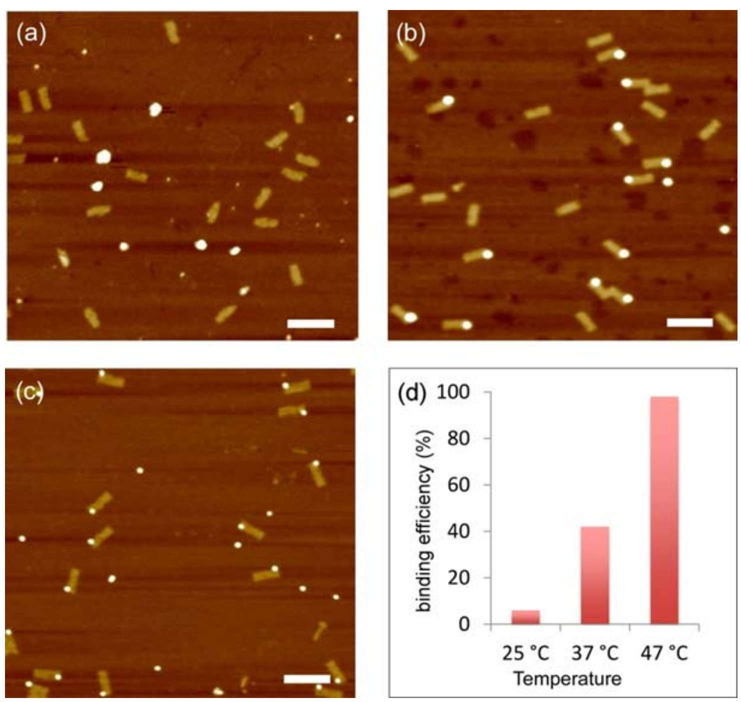

Figure S1. AFM images of the assembly of 10 nm AuNPs on DNA origami template as a function of annealing temperature. (a) The mixture of AuNPs and DNA origami was kept at room temperature (25 °C) over 18 hr. (b) Annealed from 37 °C to RT over 18 hr. (c) Annealed from 47 °C to RT over 18 hr. (d) Binding efficiency of AuNPs on the DNA origami template. The binding efficiency of room temperature is around 6% (N=341), ~42% at 37 °C (N= 467), and 98% at 47°C (N=352). The scale bar is 200 nm.

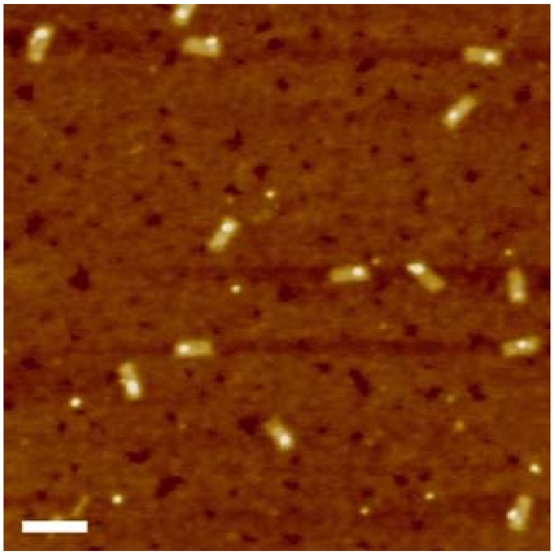

Figure S2. AFM image of the attachment of CdSe QDs on DNA origami scaffold after incubation at room temperature over 18 hr. The scale bar is 200 nm.

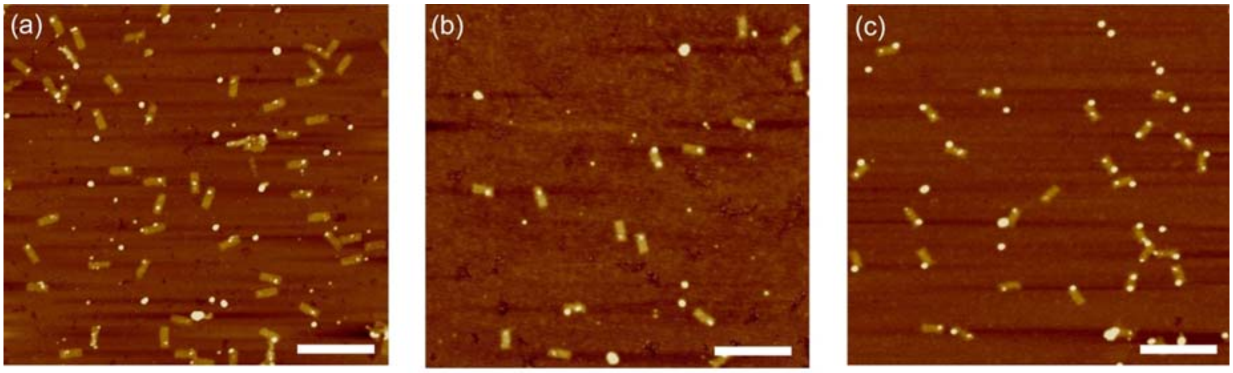

Figure S3. AFM images of the single-step assembly of AuNPs and QDs on DNA origami template as a function of annealing temperature. The mixture of DNA origami, AuNPs and QDs was annealed over 18 hr at (a) keeping at room temperature (25 °C). (b) Annealing from 37 °C to RT. (c) Annealing from 47 °C to RT. The scale bar is 400 nm.

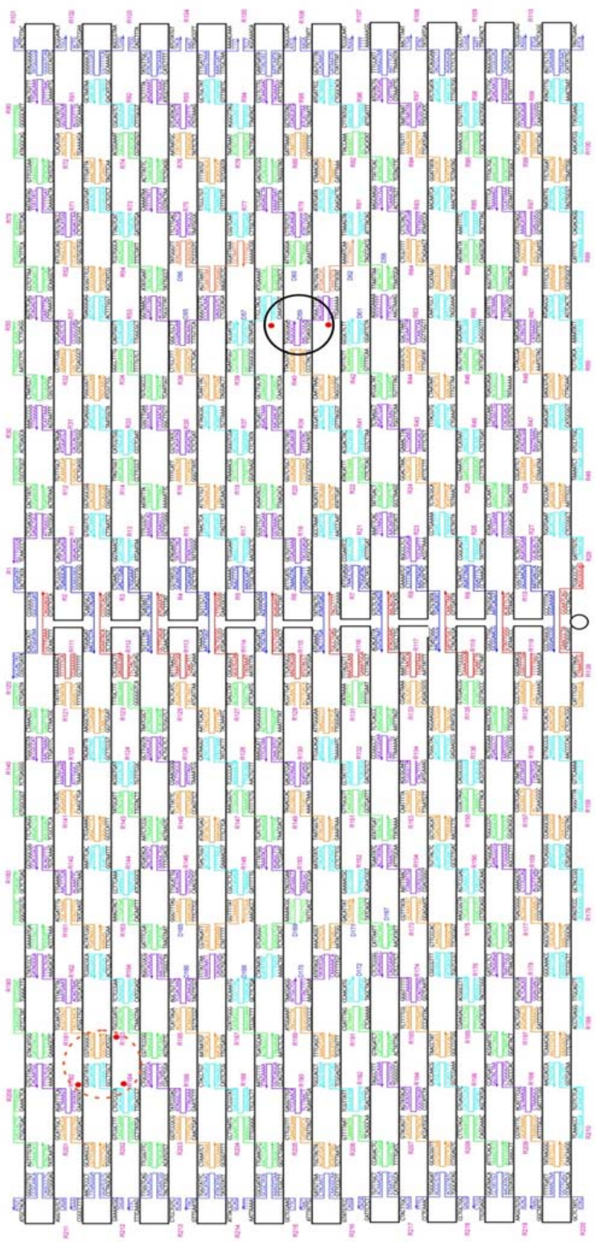

Figure S4. Schematic drawing of the rectangle DNA origami with labeled staple strands. The modified strands were marked with small red dots. The dotted red circle shows the anchor position of AuNPs, the solid black circle shows the anchor position of QDs in opposite direction of DNA origami scaffold.

Sequences of stable strands containing sticky-ends cohesion (from 5' to 3')

Bio57, 5'-Biotin- TGAGCT GTTTATCACGTAGGAATCATTACCACGCTAAC

Bio59, 5'-Biotin- TGAGCT AACTTTTTTAAAGCCAACGCTCAAACGCGCCT

Au182,
AAAAAAAAAAAAAAAGTTGCTTATATATTCTCTAAAGTTTTGTCGTCGTAACACGCAAC

Au183,
AAAAAAAAAAAAAAATTTTTACGGCTACTTACTTAGCCGGAACGTCATCAAG

Au184,
AAAAAAAAAAAAAAAAGTTGCTTACGGTCAAGACAGCATCGGAACGACATAACCGGCAAC

Sequences of unmodified stable strands

R1 TATAAGTATAGCCCGGAATAGGTGTATCACCG
R2 TGAGGCAGCCGCCGCCAGCATTGAATCTCCAA
R3 GACTTGAGTAAAGGTGAATTATCACTAAAACA
R4 GCAATAGCATAAGAGCAAGAAACATGGTTTAA
R5 AGGTTTTGTTAGCGAACCTCCCGAAATCGTCA
R6 TAAAGTACTTTCGAGCCAGTAATAAGTTTCAT
R7 TAACCTCCCATAGGTCTGAGAGACTAATGTGT
R8 CTTTTACACAGATGAATATACAGTGCCATCAA
R9 AGATTAGATCTTTAGGTGCACTAAGCAAGGCG
R10 GCCAACAGACCAGTAATAAAAGGGCGCCAGGG
R11 CACCAGAGGTCAGACGATTGGCCTCCGTCGAGAGGGTTGA
R12 ACAAACGACCTCAGAGCCGCCACCGCCAGCAA
R13 TTATTCATCCATTTGGGAATTAGAAGAACCAC
R14 AATCACCAAGGGAAGGTAAATATTTTTTTAAG
R15 GCCCAATATATCTTACCGAAGCCCGACGGAAA
R16 AAAAGTAAGATAACCCACAAGAATTTAGTTGC
R17 GAGGCGTTAAGCCTTAAATCAAGATGAGTTAA
R18 TATTTTGCGCTTATCCGGTATTCTAATTCTGT
R19 AGAGGCATCGACAAAAGGTAAAGTAAGAACGC
R20 CCAGACGAACAACGCCAACATGTATATAACTA
R21 ATCAAAATGGCTTAGGTTGGGTTAATTTAGGC
R22 TATGTAAACTGAGAAGAGTCAATACGGATTCG
R23 TTTAACGTTCGGGAGAAACAATAAGTGAATTT
R24 CCTGATTGAAAGAAATTGCGTAGAACATTTGA
R25 CTAAAATAGCCGTCAATAGATAATTTTTCAGG
R26 GGATTTAGTAGAAAGGAATTGAGGACCTGAAA
R27 GTCACACGAGATAGAACCCTTCTGAAGGTTAT
R28 GCGTAAGATTATTTACATTGGCAGTTAAAGGG
R29 CTAAACAGGAGGCCGAATTCACCA
R30 TGCTCAGTACCAGGCGGATAAGTGTGATATTC
R31 GCCACCACATGGATCTTCATTAAACGGGGTTT
R32 GGAAAGCGACCCTCAGAACCGCCATAGCAAGG
R33 ATTGAGGGGTAGCACCATTACCATCCCTCAGA
R34 CCGGAAACAGACAAAAGGGCGACAAGTTACCT
R35 ATCAGAGAGCAGATAGCCGAACAATTCAACCG
R36 GAAGGAAAGTCAGAGGGTAATTGAATCCTGAA
R37 TATAGAAGACCCACGTACAATTTTGCGCTAAT
R38 TCTTACCAGCGCCCAATAGCAAGCGTTCAGCT
R39 CATATTTACGACAATAAACAACATAAATCAGA
R40 AATGCAGACAGTAGGGCTTAATTGATCGCAAG
R41 TTAAGACGTGCTGATGCAAATCCAAGAATCGC
R42 ACAAAGAATTGAAAACATAGCGATACAAAATC
R43 ACAGAAATCTTTGAATACCAAGTTAGCTTAGA
R44 GCGCAGAGATATCAAAATTATTAGAAACAATT
R45 ATCAACACAAGTATTAGACTTTACCACGTAAA
R46 CGACAACTAATCAATATCTGGTCAATATTTTT
R47 GAAATGGAATACGTGGCACAGACAGTTGGCAA
R48 GAATGGCTCTACATTTTGACGCTCGAATCTTG
R49 ATTTTAGACAGGAACGGTACGCCAAATCGTCT
R50 CCTCAAGAGAAGGATTAGGATTAGGCCAGAAT
R51 GAGCCGCCCAGTCTCTGAATTTACCTGAGACT
R52 TAAGCGTCCCACCACCGGAACCGCTCGATAGC
R53 AGCGCCAAGTCACCAATGAAACCACTCCCTCA
R54 AGCACCGTAATAGAAAATTCATATATAACGGA
R55 GAGCGTCTGAACACCCTGAACAAACCGAGGAAACGCAATAGGTTTACC
R56 ATACCCAAGACGGGAGAATTAACTTTCCAGAGCCTAATTTCCGTTTTT

R57 GTTTATCACGTAGGAATCATTACCACGCTAAC
R60 ATTTTCATACAATAGATAAGTCCTCAAATTCT
R59 AACTTTTTTAAAGCCAACGCTCAAACGCGCCT
R62 TACCAGTACAAATATATTTTAGTT
R61 TAGAATCCCGCGAGAA
R58 CGTCGCTATTAATTAAAATTACCT
R63 AACCAACCGCGAATTATTCATTTCTTTTCCCT
R64 GAGCAAAAACTTCTGAATTATGGACCCGAACG
R65 AAACCCTCCGTATTAAATCCTTTGAGGAATTG
R66 TTATTAATTCACCAAGCTGAACCTCGAACTGA
R67 GGAAATACATTAGTCTTTAATGCGCAAATATC
R68 TAGCCCTACATTGCAACAGGAAAAGCCACCGA
R69 AGAAGTGTTTTTATAATCAGTGAGACGCTCAT
R70 CTGAAACATGAAAGTATTAAGAGGCGTTCCAG
R71 AACCAGAGATACATGGCTTTTGATCTATTATT
R72 AGTGTACTTCTTTTCATAATCAAAATCAAGTT
R73 TCACAATCAATCAGTAGCGACAGAATCACCGG
R74 TGCCTTTAACACCACGGAATAAGTAAGACTCC
R75 GCGCATTAAAGAACTGGCATGATTTTATTTTG
R76 TTATTACGAGAGAATAACATAAAAACAGCCAT
R77 CAAGCAAGGCCAGTTACAAAATAAACAGGGAA
R78 ATTATTTAACCAAGTACCGCACTCATCCCATC
R79 GCGTTATAGAACAAGAAAAATAATATCGAGAA
R80 CTAATTTAGAAAAAGCCTGTTTAGCTAAATTT
R81 CTGTAAATAATTTCATCTTCTGACTATCATAT
R82 AATGGTTTATATGTGAGTGAATAAACATCAAG
R83 TGGATTATGAAGATGATGAAACAACCTTGCTT
R84 AAAACAAATTCATCAATATAATCCACATTATC
R85 CTAAAGCATTTAAAAGTTTGAGTATGATTGTT
R86 ATTTTGCGGAGAGCCAGCAGCAAAAATACCGA
R87 CCGCCAGCAAACATCGCCATTAAATGAAAAAT
R88 ACGAACCACTGGTAATATCCAGAAAATTAACC
R89 GTAAAAGAGTCTGTCCATCACGCACAATATTA
R90 AATGCCCCCTGCCTATTTCGGAACGATACAGG
R91 GTTTGCCAGGTAATAAGTTTTAACAAACAGTT
R92 ACGCAAAGGCGTCAGACTGTAGCGTTATTAGC
R93 CTTTACAGCAGTATGTTAGCAAACTAAAAGAA
R94 GGTATTAATCCCAATCCAAATAAGATAGCAGC
R95 AATTACTACGAGCATGTAGAAACCCAAGAACG
R96 AAATCAATGAAATACCGACCGTGTGGAATCAT
R97 GATGGCAAATTAATTACATTTAACCAGTACAT
R98 GCCACGCTGAACAAAGAAACCACCTATCAGTA
R99 CGGCCTTGCCAGCAGAAGATAAAAGCAACAGT
R100 GTTGTAGCAATACTTCTTTGATTACAAACTAT
R101 CAGTGCCCGTATGGGGTCAGTGCC
R102 GTCATAGCCCCCCGTTTTCATCGG
R103 GGTGGCAACATAGTAGAAAATACA
R104 TCAAAAATGAAAAAACGATTTTTT
R105 TCCTTATCATTCAATCAATAATCG
R106 AGAATAAACACCGATAAATAAGGC
R107 TTTTAATGGAAAAATTTCATTTGA
R108 CATATTCCTGATAGAAGGAGCGGA
R109 TTAACACCGCCTCAGAGGTGAGGC
R110 AGTAGAAGAACTGTAATAACATCA
R111 AAAAAAGGTTTTTTCACGTTGAAACAGGAGGT
R112 CTCATCTTGAGGCGAAAGAATACACCGTCACC
R113 TTTCAACTTAAATTGGGCTTGAGAATGAAATA
R114 TAAATATTGCGTCCAATACTGCGGCTTGCGGG
R115 TCCATGTAAAGTACGGTGTCTGGAAGAGAATA
R116 AGGTAAAGAAATGCAATGCCTGAGTACCTTTT
R117 AAATAATTTTTAACCAATAGGAACAACAGTAC
R118 ATTAAGTTGAAAGGGGGATGTGCTCAACTAAT

R119	TGGTTTTTCGGTTTGCGTATTGGGACATTCTG
R120	TACTCAGGAGGTTTATGAATTGCG
R121	AATAATAACTCCAAAAGGAGCCTTCCAACCTA
R122	TCGGTTTAAAAGGAACAACTAAAGTACCGCCA
R123	AAACGAAATGACCCCCAGCGATTAACACCAGA
R124	GCGAAACATGCCACTACGAAGGCATAATTGTA
R125	ACGAGTAGTTAATCATTGTGAATTATGTTTAG
R126	CGATTTTAGCTTGCCCTGACGAGATACCAAGC
R127	ACTGGATACATTGAATCCCCCTCATTTAAATA
R128	AAACAGTTAGGGGGTAATAGTAAAACCTTATG
R129	TGCAACTAACAGTTGATTCCCAATAACCCTCA
R130	CGAGTAGACTGTAGCTCAACATGTAATGCTTT
R131	TATATTTTATTCAAAAGGGTGAGATTAAATCA
R132	AGACAGTCGGATAAAAATTTTTAGTCTGCGAA
R133	GCTCATTTCGCGTCTGGCCTTCCTTATTACGC
R134	CTTTCATCTCGCGTTAAATTTTTGAAGGCCGG
R135	CAGCTGGCGGGTAACGCCAGGGTTAACGCGCG
R136	CACGACGTGTGCGGGCCTCTTCGCGTAGCCAG
R137	GGGAGAGGCTTTTCACCAGTGAGAGAGGTGCCGTAAAGCA
R138	AGCTGATTCATTAATGAATCGGCCTTCCCAGT
R139	CTAAATCGGAACCCTAGGAATCAGAGCGGGAG
R140	CCCTCAGAACCGCCACCCTCAGAAAGCGGAGT
R141	GAGAATAGTCAGCTTGCTTTCGAGCGGGTAAA
R142	CTTAAACAAACTTTCAACAGTTTCCCGCCACC
R143	ATACGTAAAAGTACAACGGAGATTTCATTCAG
R144	CGCCTGATGGAAGTTTCCATTAAAGTGAATTT
R145	TGAATAAGAGAACTGGCTCATTATAAAGAAGT
R146	GGACGTTGAACGTAACAAAGCTGCTGTATCAT
R147	TTTGCCAGCAGAAAACGAGAACGAATTGCTGA
R148	CAAAAATCGCGAGAGGCTTTTGCAACCAGTCA
R149	ATCTGGTGTTTAGTTTGACCATTACTTTATTT
R150	TCGCAAATGATGGCTTAGAGCTTACCATAAAT
R151	CAACGCAAAAATCACCATCAATATAATATTTT
R152	ACCGTTCTCTTTTGCGGGAGAAGCGATACATT
R153	GTTAAAATAACATTAAATGTGAGCTTGGGAAG
R154	ACCCGTGGTTAAATTGTAAACGTTGATATTCA
R155	GGCGATCGTGTAAAACGACGGCCACCTGTCGT
R156	CTTGCATGTCAGGCTGCGCAACTGGAGTAACA
R157	GCCAGCTGGCCCTTCACCGCCTGGGAACCATC
R158	GAGTTGCACTTTCCAGTCGGGAAAGTGCCAAG
R159	ACCCAAATCAAGTTTTTTGGGGTCCGGGCAAT
R160	CTCAGAGCCACCACCCTCATTTTCTGGGATTT
R161	TGCTAAACGCTTGATACCGATAGTAAAGACTT
R162	CAATGACAAAATGAATTTTCTGTAAGGGATAG
R163	TTTCATGAAAATTGTGTCGAAATCATTCATTA
R164	GCTCCATGAGAGGCTTTGAGGACTTGCGCCGA
R165	CCCAAATCGGAAGAAAAATCTACGGATAAAAACCAAAATAAGGTCTTT
R166	CAGACGACTTAATAAAACGAACTATCGACAAGAACCGGATCGCGACCT
R169	ACCCTGACAGAGGTCATTTTTGCGGGTCAATA
R168	TTTTGATATATTATAGTCAGAAGCTCGTTTAC
R171	ACCTGTTTTTATGACCCTGTAATA
R170	CAAAAACAAGCTATATTTTCATTTATTGCTCC
R167	AGCTGATAAATTAATGTTGTATAA
R172	GGTAGCTAGGTTGTAC
R173	GCAAATATGATTCTCCGTGGGAACAAGCGCCA
R174	GATTGACCCCCAAAAACAGGAAGACCGGAGAG
R175	TTCGCCATCCTGCAGGTCGACTCTTTGCGCTC
R176	CCCGGGTATGCCGGAAACCAGGCAAAACGGCG
R177	ACTGCCCGGCAAGCGGTCCACGCTAAACCGTC
R178	CCAGCAGGACTCACATTAATTGCGAGAGGATC
R179	TATCAGGGCGATGGCCCACTACGTCCCTGAGA
R180	CAAGCCCAATAGGAACCCATGTACCTTTCCAG

R181	ACGTTAGTACAACCATCGCCCACGGGGTAGCA
R182	ATATATTCTCTAAAGTTTTGTCGTCGTAACAC
R183	ACGGCTACTTACTTAGCCGGAACGTCATCAAG
R184	ACGGTCAAGACAGCATCGGAACGACATAACCG
R185	AGTAATCTACGGAACAACATTATTAACACTAT
R186	AAAGATTCATAGGCTGGCTGACCTAGGCGCAG
R187	CATAACCCAAAGCGGATTGCATCATTAGAGAG
R188	AAGAGGAAGAGGCATAGTAAGAGCACAGGTAG
R189	TACCTTTAGGGGCGCGAGCTGAAAAGCATAAA
R190	TCAATTCTCTCCAACAGGTCAGGAAAAAGATT
R191	GCTAAATCTTTTTGAGAGATCTACTGATAATC
R192	TCAGGTCAAGCAATAAAGCCTCAGAGGTGGCA
R193	AGAAAAGCGTAATGGGATAGGTTACCGGCACC
R194	TAGATGGGTCATATGTACCCCGGTAAAGGCTA
R195	GCTTCTGGCCGAGCTCGAATTCGTCCTAATGA
R196	TCATAGCTCACTCCAGCCAGCTTTCGTTGGTG
R197	GTGAGCTACGAAAATCCTGTTTGAAAAGAACG
R198	CCGAAATCTGTAAAGCCTGGGGTGAATCATGG
R199	TGGACTCCAACGTCAAAGGGCGAAGGTTTGCC
R200	TGAGTTTCGTCACCAGTACAAACTATAGTTAG
R201	CGTAACGAGGTCGCTGAGGCTTGCACCCTCAG
R202	CAGCGAAATCATAAGGGAACCGAATGTACAGA
R203	CCAGGCGCATCAGTTGAGATTTAGCGCCAAAA
R204	GGAATTACGCCCGAAAGACTTCAACCAGACCG
R205	GAAGCAAAACTAATAGTAGTAGCAAGAATTAG
R206	CAAAATTATTGCCTGAGAGTCTGGAAAACTAG
R207	CATGTCAACGCATCGTAACCGTGCGGCCTCAG
R208	GAAGATCGGTTTCCTGTGTGAAATAGCCGGAA
R209	GCATAAAGGGCAAAATCCCTTATAGTTGTTCC
R210	AGTTTGGAACAAGAGTCCACTATTTGGTGGTT
R211	CAGACAGCCCTCACAACGCCTGTA
R212	TGCGGGATCGTCAGGGAGTTAAAG
R213	ACAGATGAACGGCTGACCAACTTT
R214	GCAGATACATAAGAATACCACATT
R215	CTTCAAAGCGAAATATCGCGTTTT
R216	CAGGCAAGGCAATTAACATCCAAT
R217	AACGGTAATCGTAGCAAACAAGAG
R218	GACGACCGTATCATCTGCCAGTTT
R219	ACACAACATACGTGTTATCCGCTC
R220	ATAGGGTTGAGTAATCAAAAGAAT

References:

(1) Rothemund, P. W. Nature 2006, 440, 297.

(2) Ding, B.; Deng, Z.; Yan, H.; Cabrini, S.; Zuckermann, R. N.; Bokor, J. Journal of the American Chemical Society 2010, 132, 3248.