Supplementary Information

Force-driven base recognition programs DNA origami-based supramolecular networks

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Experimental Section

Materials

All short ssDNA strands were purchased from Sangon Biotech Co., Ltd. (Shanghai, China). Streptavidin was purchased from Sangon Biotech Co., Ltd. (Shanghai, China). The M13mp18 phage scaffold strand was purchased from New England Biolabs Inc. Tris, acetic acid (CH_3COOH), magnesium acetate ($C_4H_6O_4Mg$), and ethylenediaminetetraacetic acid (EDTA, $C_{10}H_{16}N_2O_8$) were all purchased from Aladdin Biochemical Technology Co., Ltd. (Shanghai, China).

Fabrication of DNA Origami Structures

In this study, hexagonal DNA origami and twist-corrected rectangular DNA origami structures were employed. Hexagonal and twist-corrected rectangular origami structures were designed using caDNAno software (design diagram shown in Fig. S13 and Fig. S14). For preparation, staple strands (including internal and edge staples) were mixed with scaffold DNA at a 10:1 molar ratio in 1×TAE/Mg^{2+} buffer (40 mM Tris, 20 mM acetic acid, 2 mM EDTA, and 12.5 mM magnesium acetate, pH 7.5). The mixture was then heated to 95 °C for 3 min in a thermal cycler, followed by gradual cooling to 25 °C at a rate of 0.1 °C per 10 seconds. The synthesized DNA origami was obtained at a final concentration of 5 nM.

Atomic Force Microscopy (AFM) Imaging

Both rectangular DNA origami samples with 0/1 active edges and hexagonal DNA origami samples with 2 active edges were diluted to a final concentration of 0.25 nM. Streptavidin was then introduced and incubated with the sample for at least 30 minutes to ensure thorough recognition of biotin molecules on the origami structures. 3 μL of DNA origami sample was deposited onto freshly cleaved mica surfaces and allowed to adsorb for 5 min. For hexagonal DNA origami samples with 6 active edges, 30 μL of sample solution was applied to clean mica surfaces and maintained in a constant temperature and humidity environment for 34 hours, with the mica surface kept hydrated throughout the process. AFM imaging was conducted using a Multimode VIII AFM (Bruker Corporation) in liquid tapping mode with NP-S probes (Bruker Corporation) having a spring constant of 0.35 N/m. To identify biotin molecules on the origami, streptavidin was added to the samples and incubated for at least 30 minutes. In thermodynamic experiments, sample solutions were incubated at preset temperatures for 30 min and brought to target temperatures (25 °C, 35 °C, 45 °C, and 55 °C respectively) using the AFM external heating device prior to measurement to ensure the entire imaging process occurred at predetermined temperatures. Fast Fourier transform (FFT) analysis of AFM images was performed using Nanoscope Analysis 1.9 offline software.

UV Irradiation

The successfully prepared hexagonal or rectangular DNA origami samples were exposed to UVB irradiation (2.0 W/m^2) for 10 minutes at 25 °C, with the entire process conducted in an ice bath to prevent sample heating. Following UV treatment, the origami samples were incubated at predetermined temperatures for 30 min prior to AFM imaging.

Yield analysis.

The sample was deposited on mica for AFM imaging. The numbers of monomers and dimers in the AFM images were counted and marked as “M” and “D”, respectively (Fig. S1, S2, S9 and S10). The yield of the dimers was calculated as:

$$Y_{(dimer)} = \frac{2D}{M + 2D} \times 100\%$$

Count the numbers of monomers, dimers and trimers in AFM images marked as M, D and T respectively (Fig. S3, S11 and S12). The yield of the trimers was calculated as:

$$Y_{(timer)} = \frac{3T}{M + 2D + 3T} \times 100\%$$

For the large-scale assembled structures of DNA origami, we adopted the area ratio calculation method described in Fang's work[1]. The total area of the origami structures ($A_{origami}$) and the total imaging area (A_{total}) were calculated separately using imageJ software (Fig. 3 and 4). The relative area of the large-scale assembled structures were calculated as:

$$Y_{(origami)} = \frac{A_{origami}}{A_{total}} \times 100\%$$

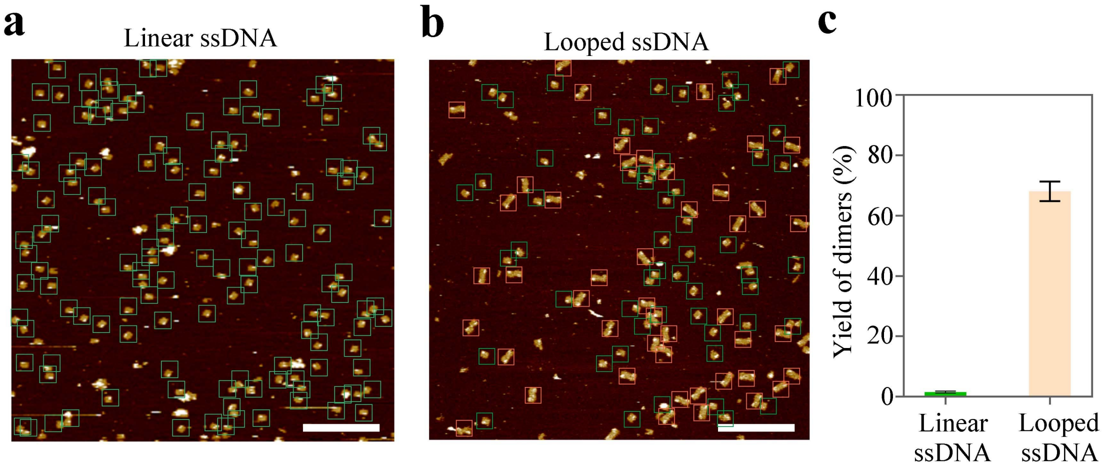
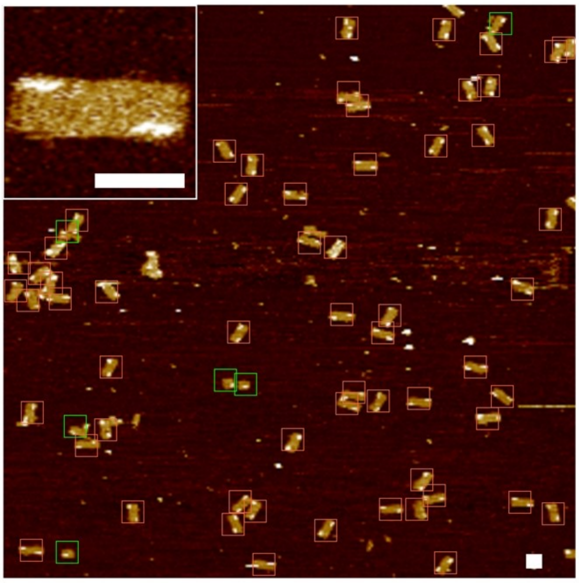
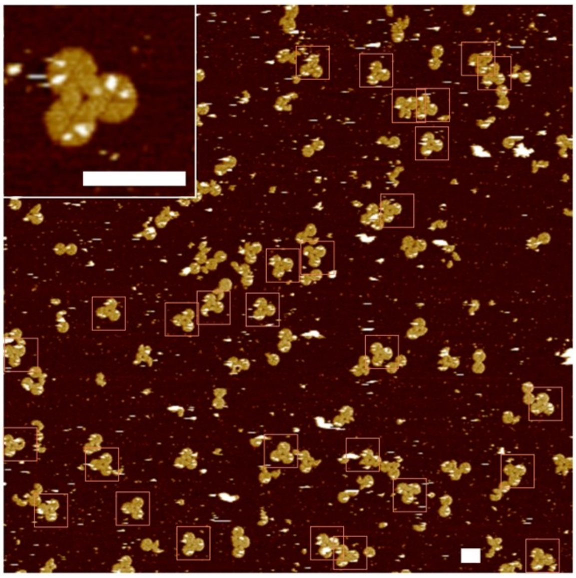


Fig. S1 (a) Representative AFM images of the DNA origami nanostructure with 4-nt polyA linear single-stranded DNA extending from the edge. Scale bars: 1 μm. (b) Representative AFM images of the DNA origami nanostructure with 4-nt polyA loop extending from the edge. Scale bars: 1 μm. (green boxes: monomers; orange boxes: dimers) (c) Histogram showing the yield of dimers mediated by linear ssDNA (*n*=202) and looped ssDNA (*n*=187).



Yield of dimers = 87.2 ± 2.6 %

Fig. S2 Representative AFM images of DNA origami dimers mediated by 4-nt polyG loop recognition. The corresponding dimers yields were analyzed from AFM images (*n*=197). Monomers: green boxes. Dimers: orange boxes. Scale bar: 100 nm.



Yield of trimers = 57.3 ± 3.8 %

Fig. S3 Representative AFM images of DNA origami trimers mediated by 4-nt polyG loop recognition at two adjacent active edges. The corresponding trimers yields were analyzed from AFM images (*n*=179). Trimers: orange boxes. Scale bar: 200 nm.

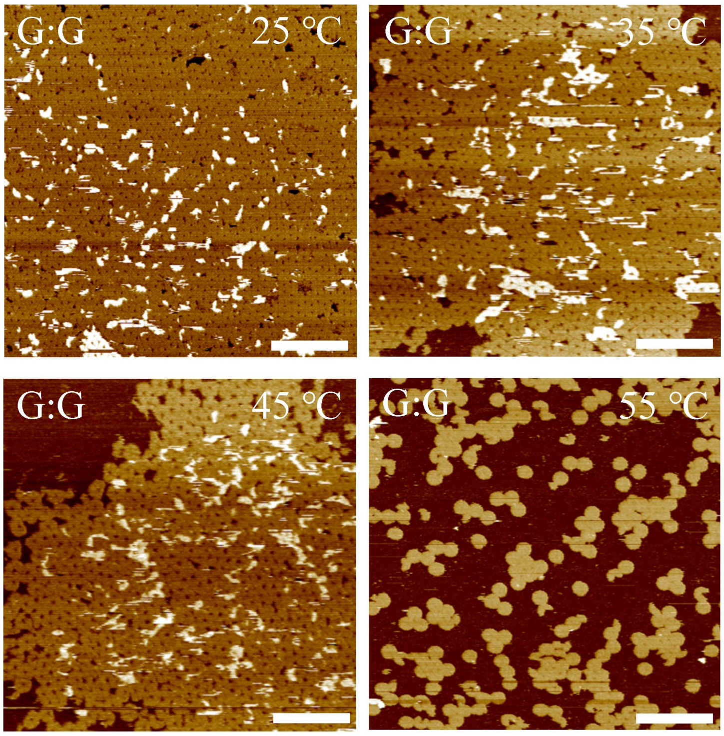


Fig. S4 Representative AFM images of G:G-mediated DNA origami assemblies after incubation at 25 °C, 35 °C, 45 °C, and 55 °C for 30 min. Scale bar: 600 nm.

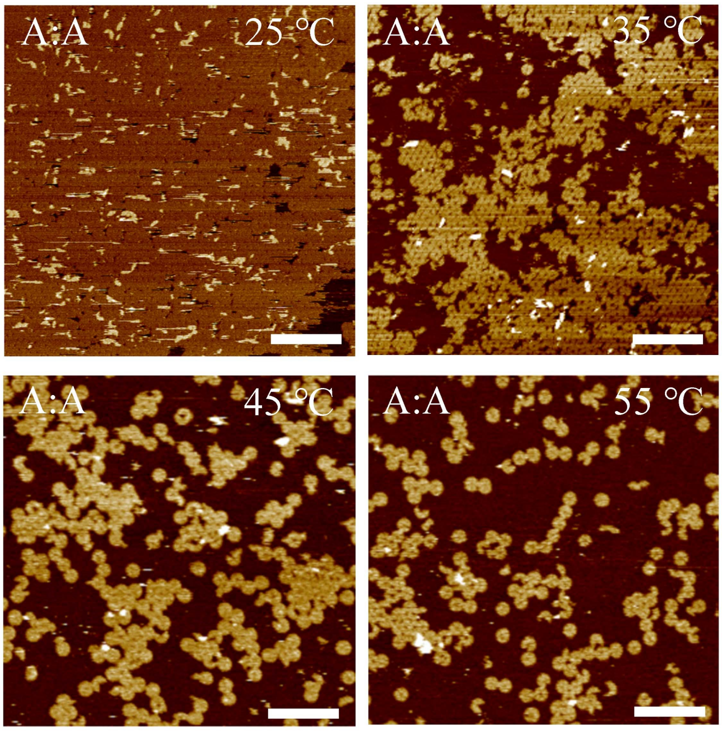


Fig. S5 Representative AFM images of A:A-mediated DNA origami assemblies after incubation at 25 °C, 35 °C, 45 °C, and 55 °C for 30 min. Scale bar: 600 nm.

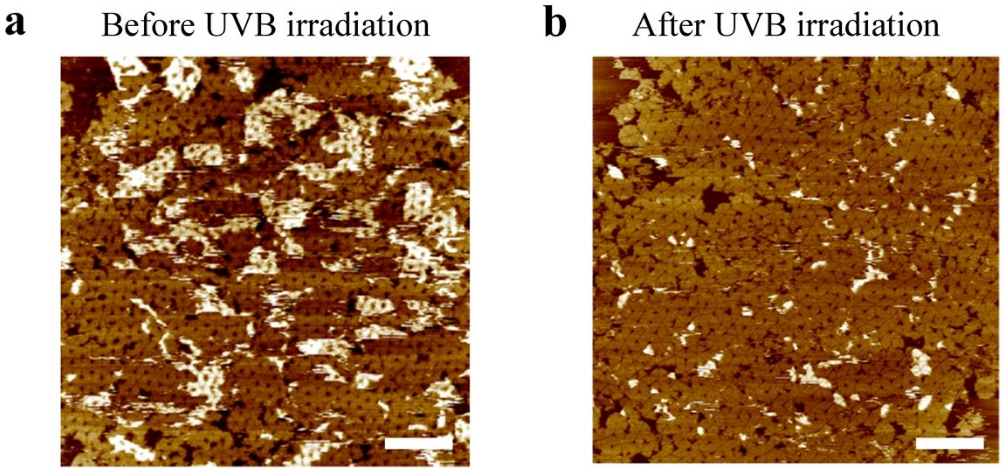


Fig. S6 (a) Representative AFM images of DNA origami large-scale assemblies by A:A recognition before UVB irradiation. (b) Representative AFM images of DNA origami large-scale assemblies by A:A recognition after UVB irradiation. Scale bar: 600 nm.

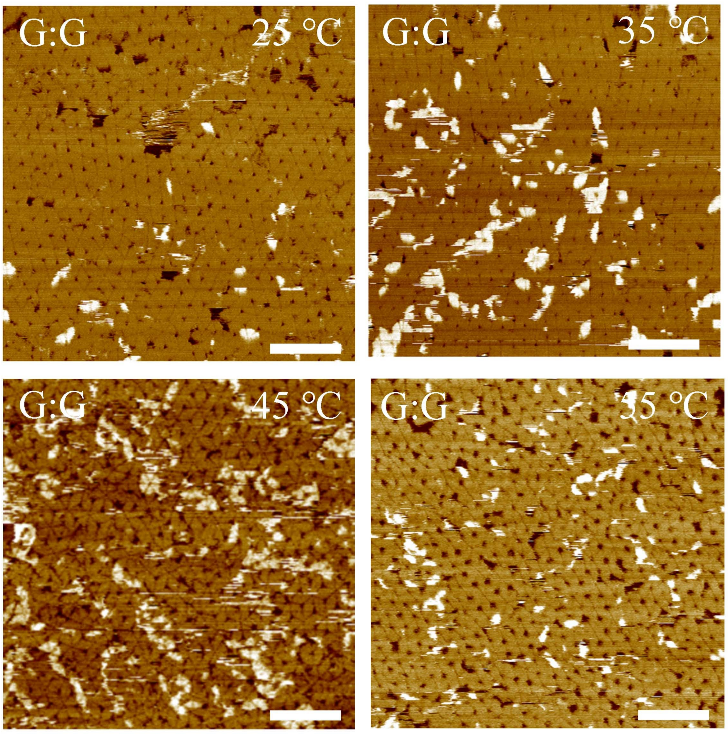


Fig. S7 Representative AFM images of DNA origami assemblies mediated by G:G recognition after UVB irradiation for 10 min and thermal incubation at 25 °C, 35 °C, 45 °C, and 55 °C for 30 min. Scale bar: 300 nm.

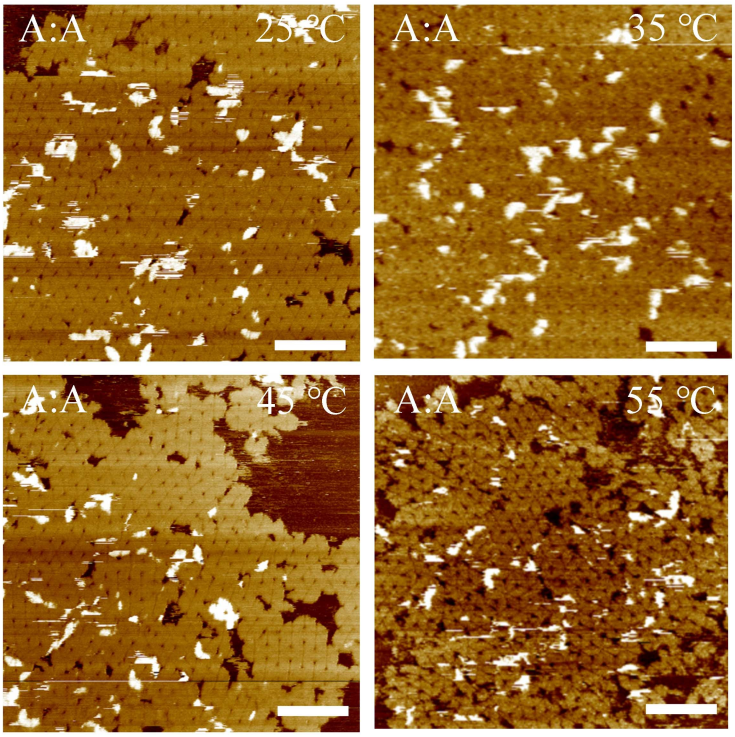


Fig. S8 Representative AFM images of DNA origami assemblies mediated by A:A recognition after UVB irradiation for 10 min and thermal incubation at 25 °C, 35 °C, 45 °C, and 55 °C for 30 min. Scale bar: 300 nm.

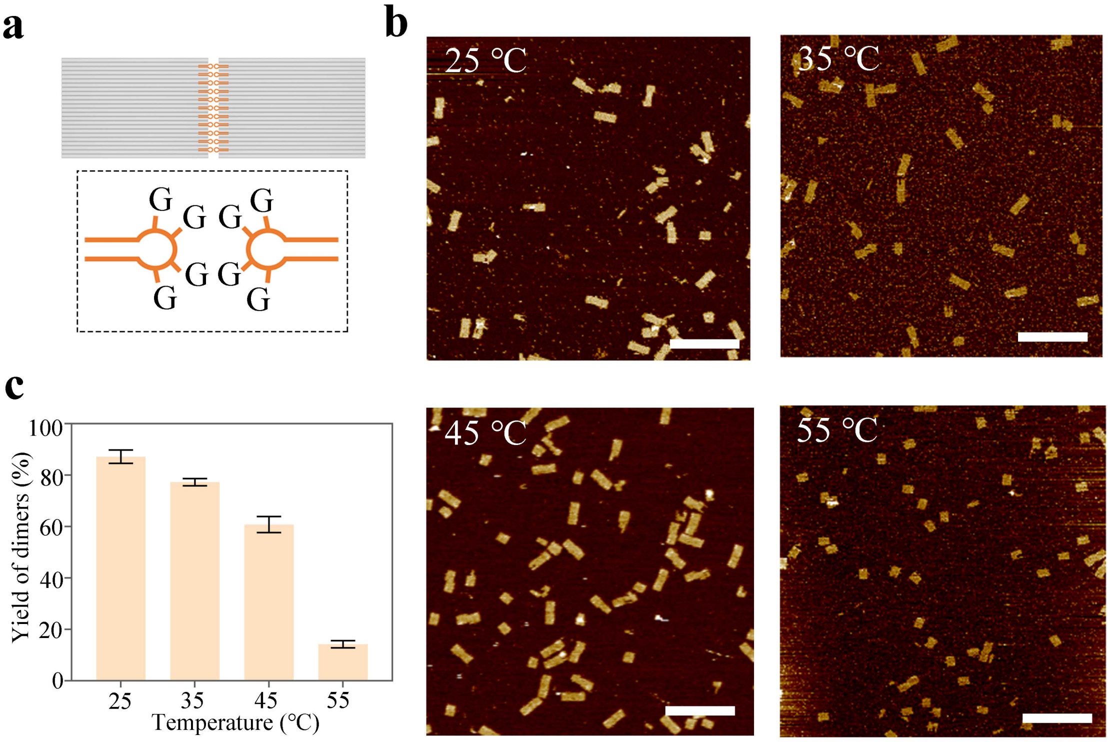


Fig. S9 (a) Schematic illustration of force-driven G:G base recognition-mediated origami dimerization. (b) Representative AFM images of origami dimers mediated by 4-nt polyG loop recognition at 25 °C, 35 °C, 45 °C and 55 °C, respectively. Scale bars: 500 nm. (c) Histogram showing the yield of rectangular origami dimers at 25 °C, 35°C, 45°C and 55°C analyzed from AFM images, respectively (*n*=197, 212, 179, 191).

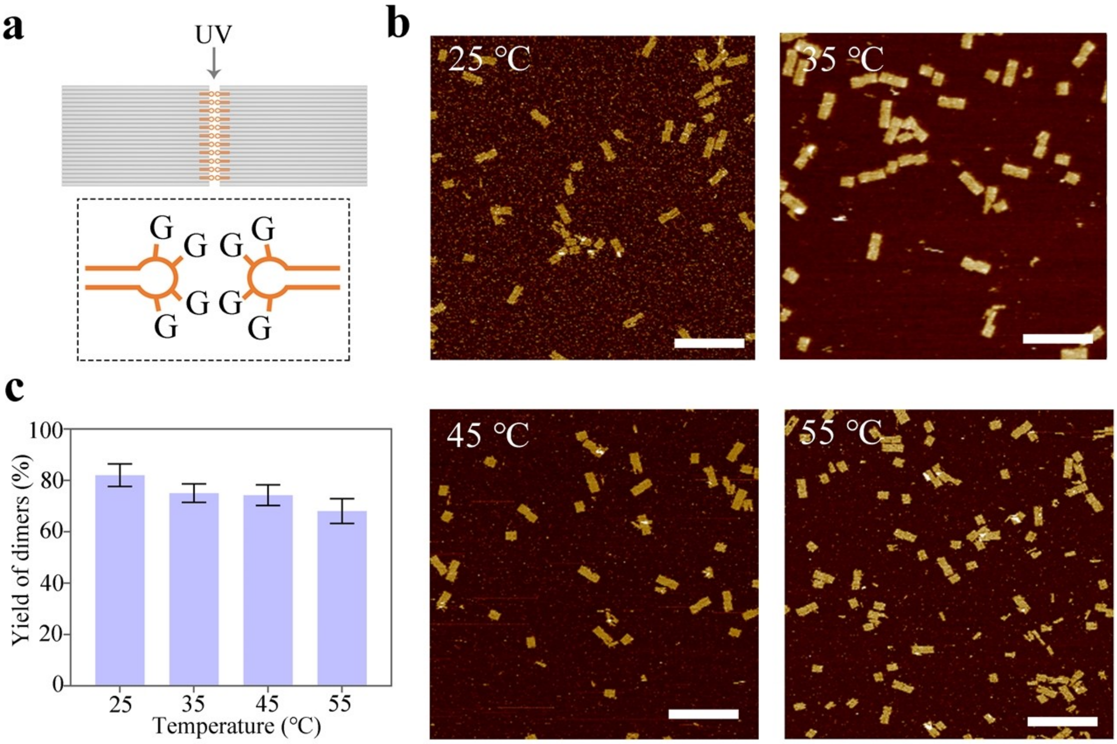


Fig. S10 (a) Schematic illustration of force-driven G:G base recognition-mediated origami dimerization after UVB pre-treatment. (b) Representative AFM images of origami dimers mediated by 4-nt loopG recogization. The samples were analysed after 10 min UVB irradiation followed by 30 min incubation at 25 °C, 35 °C, 45 °C, and 55 °C. Scale bars: 500 nm. (c) Histogram showing the yield of rectangular origami dimers at 25 ℃, 35 ℃, 45 ℃ and 55 ℃ after UVB pre-treatment analyzed from AFM images, respectively (*n*=177, 169, 182, 188).

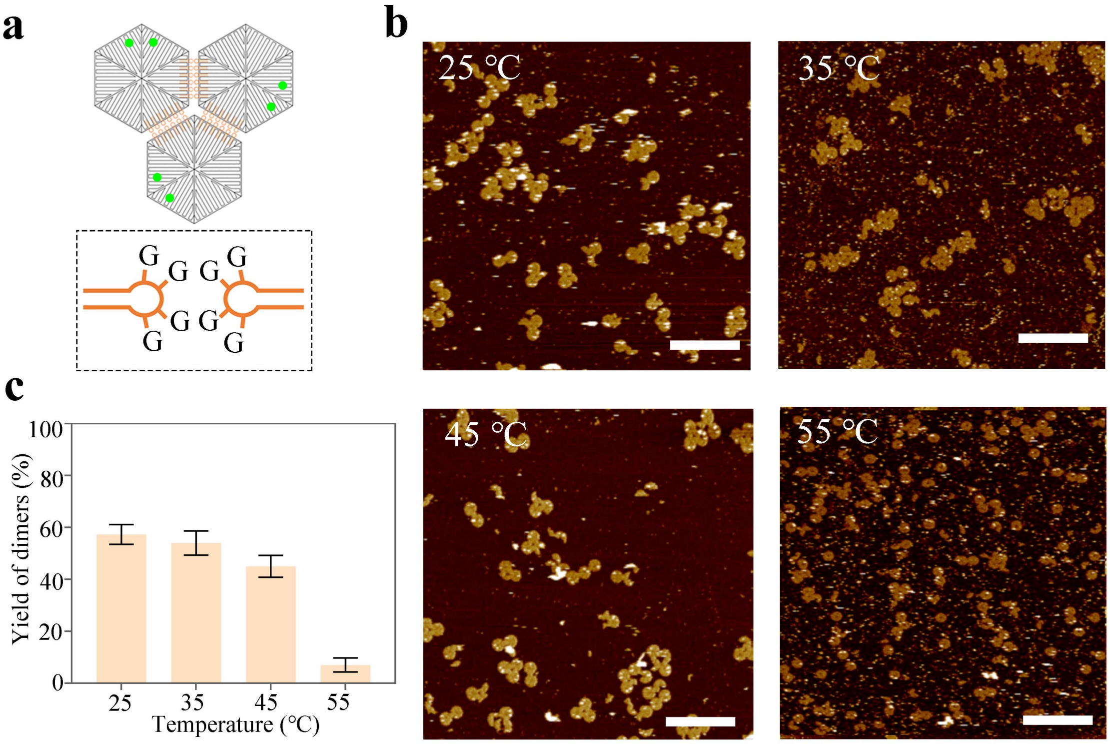


Fig. S11 (a) Schematic illustration of force-driven G:G base recognition-mediated origami trimerization. (b) Representative AFM images of origami trimers mediated by 4-nt polyG loop recognition at 25 °C, 35 °C, 45 °C and 55 °C, respectively. Scale bars: 600 nm. (c) Histogram showing the yield of rectangular origami trimers at 25 °C, 35 °C, 45 °C and 55 °C analyzed from AFM images, respectively (*n*= 179, 162, 169, 172, respectively).

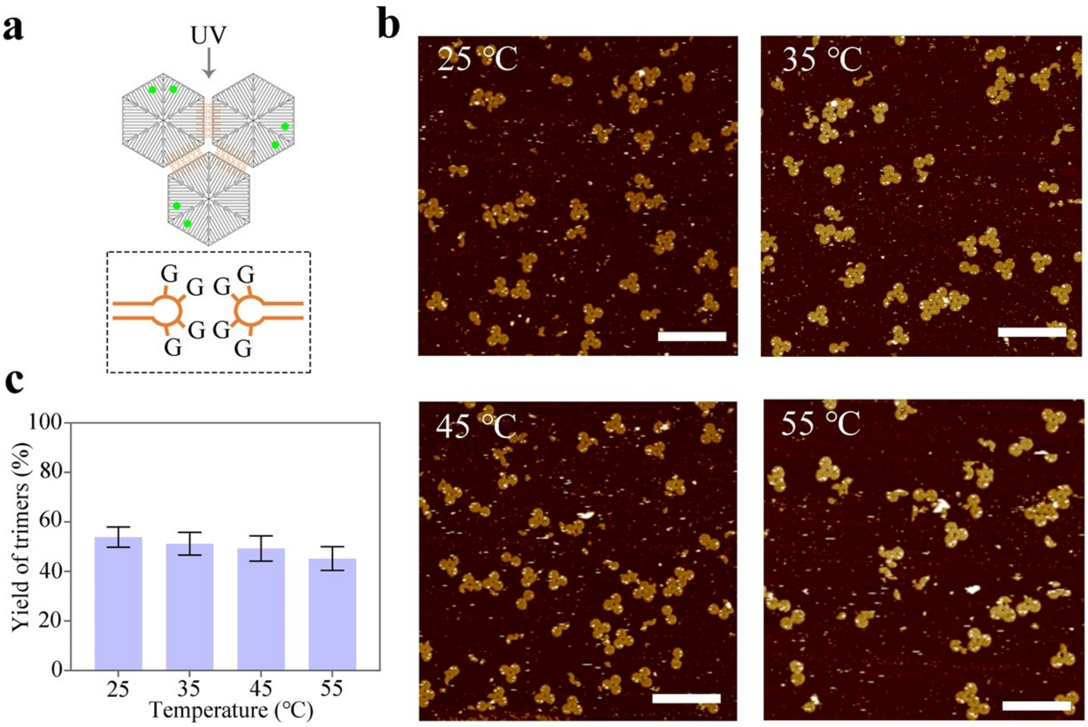


Fig. S12 (a) Schematic illustration of force-driven G:G base recognition-mediated origami trimerization after UVB pre-treatment. (b) Representative AFM images of the UVB irradiation effects on the thermostability of origami trimers mediated by 4-nt loopG. The samples were analysed after 10 min UVB irradiation followed by 30 min incubation at 25 °C, 35 °C, 45 °C, and 55 °C. Scale bars: 500 nm. (c) Histogram showing the yield of rectangular origami trimers at 25 °C, 35 °C, 45 °C and 55 °C after UVB pre-treatment analyzed from AFM images, respectively (*n*=179, 166, 172, 180, respectively).

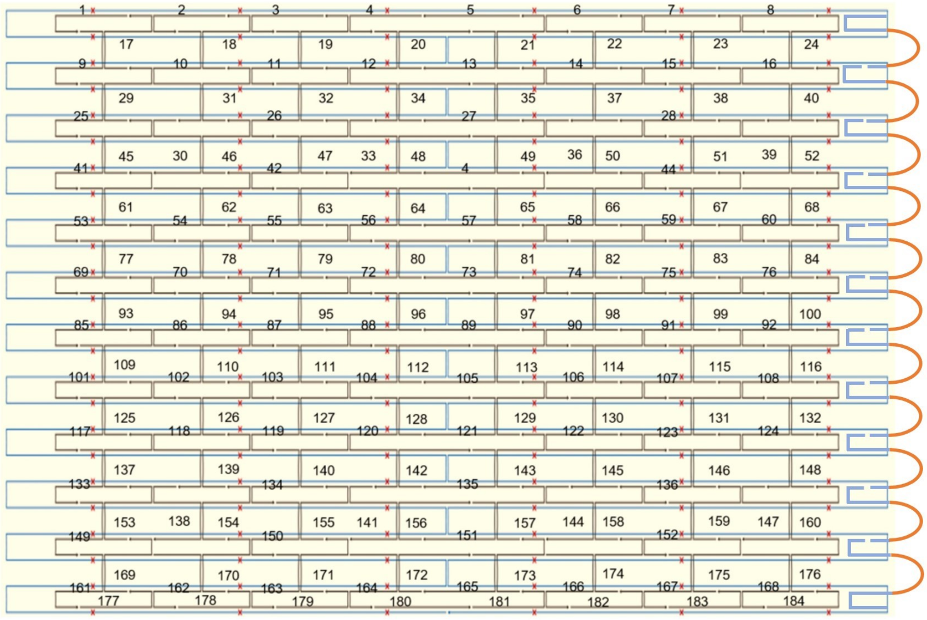


Fig. S13 Schematic representation of rectangular DNA origami with active edge staple designs.

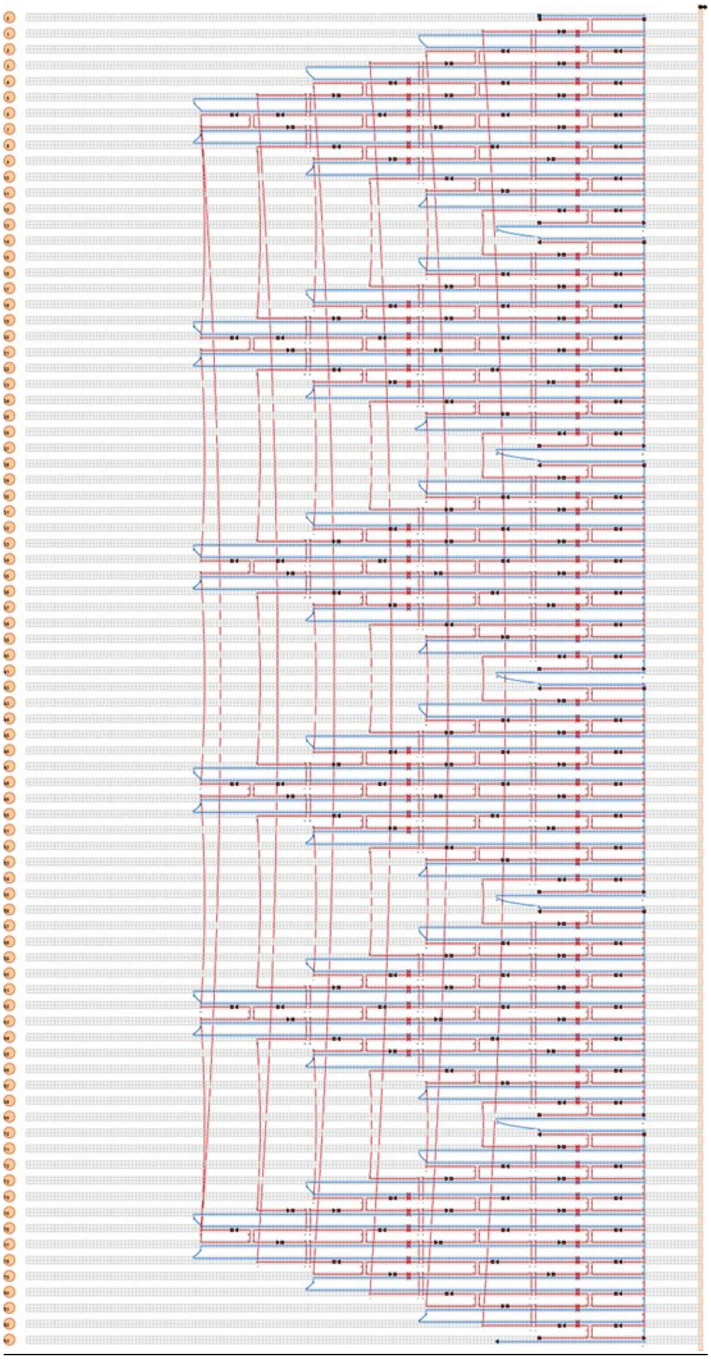


Fig. S14 Cadnano diagram of the hexagonal DNA origami nanostructure.

Supplementary DNA Sequences

DNA sequences of rectangular origami

Core staples

Seq name	Sequence 5’-3’
R01	AGAAAGGAACAACTAAAGGAATTCAAAAAAA
R02	ACAACTTTCAACAGTTTCAGCGGATGTATCGG
R03	TAAATGAATTTTCTGTATGGGATTAATTTCTT
R04	TCTAAAGTTTTGTCGTCTTTCCAGCCGACAA
R05	TCCACAGACAGCCCTCATAGTTAGCGTAACGA
R06	TCACCAGTACAAACTACAACGCCTAGTACCAG
R07	AGGAACCCATGTACCGTAACACTTGATATAA
R08	CCACCCTCATTTTCAGGGATAGCAACCGTACT
R09	AGGCTCCAGAGGCTTTGAGGACACGGGTAA
R10	TTTATCAGGACAGCATCGGAACGACACCAACCTAAAACGAGGTCAATC
R11	AAACAGCTTTTTGCGGGATCGTCAACACTAAA
R12	TGACAACTCGCTGAGGCTTGCATTATACCAAGCGCGATGATAAA
R13	TTAGGATTGGCTGAGACTCCTCAATAACCGAT
R14	GCGGATAACCTATTATTCTGAAACAGACGATTGGCCTTGAAGAGCCAC
R15	GTATAGCAAACAGTTAATGCCCAATCCTCA
R16	CAGGAGGTGGGGTCAGTGCCTTGAGTCTCTGAATTTACCGGGAACCAG
R17	ACGGCTACAAAAGGAGCCTTTAATGTGAGAAT
R18	CAGCGAAACTTGCTTTCGAGGTGTTGCTAA
R19	AAGGCCGCTGATACCGATAGTTGCGACGTTAG
R20	ATATTCGGAACCATCGCCCACGCAGAGAAGGA
R21	TATTAAGAAGCGGGGTTTTGCTCGTAGCAT
R22	TTTCGGAAGTGCCGTCGAGAGGGTGAGTTTCG
R23	GCCCGTATCCGGAATAGGTGTATCAGCCCAAT
R24	GTTTTAACTTAGTACCGCCACCCAGAGCCA
R25	AATACGTTTGAAAGAGGACAGACTGACCTT
R26	ACACTCATCCATGTTACTTAGCCGAAAGCTGC
R27	TTGACAGGCCACCACCAGAGCCGCGATTTGTA
R28	TTAAAGCCAGAGCCGCCACCCTCGACAGAA
R29	GACCAACTAATGCCACTACGAAGGGGGTAGCA
R30	ATAAGGGAACCGGATATTCATTACGTCAGGACGTTGGGAA
R31	GCGCAGACAAGAGGCAAAAGAATCCCTCAG
R32	GACCTGCTCTTTGACCCCCAGCGAGGGAGTTA
R33	TTGTGTCGTGACGAGAAACACCAAATTTCAACTTTAAT

R34	TCATCGCCAACAAAGTACAACGGACGCCAGCA
R35	CACCAGAAAGGTTGAGGCAGGTCATGAAAG
R36	CACCCTCAGAAACCATCGATAGCATTGAGCCATTTGGGAA
R37	CCACCCTCTATTCACAAACAAATACCTGCCTA
R38	GCCTCCCTCAGAATGGAAAGCGCAGTAACAGT
R39	AGCCACCACTGTAGCGCGTTTTCAAGGGAGGGAAGGTAAA
R40	AAATCACCTTCCAGTAAGCGTCAGTAATAA
R41	CATCAAGTAAAACGAACTAACGAGTTGAGA
R42	TCATTCAGATGCGATTTTAAGAACAGGCATAG
R43	GCAAGGCCTCACCAGTAGCACCATGGGCTTGA
R44	TCAAGTTTCATTAAAGGTGAATATAAAAGA
R45	TACGTTAAAGTAATCTTGACAAGAACCGAACT
R46	TTATACCACCAAATCAACGTAACGAACGAG
R47	ATTACCTTTGAATAAGGCTTGCCCAAATCCGC
R48	GATGGTTTGAACGAGTAGTAAATTTACCATTA
R49	CAGCAAAAGGAAACGTCACCAATGAGCCGC
R50	TCACCGACGCACCGTAATCAGTAGCAGAACCG
R51	GAAATTATTGCCTTTAGCGTCAGACCGGAACC
R52	ACCGATTGTCGGCATTTTCGGTCATAATCA
R53	TTTAGGACAAATGCTTTAAACAATCAGGTC
R54	ATGCAGATACATAACGGGAATCGTCATAAATAAAGCAAAG
R55	TAAGAGCAAATGTTTAGACTGGATAGGAAGCC
R56	CGTTTACCAGACGACAAAGAAGTTTTGCCATAATTCGA
R57	TTATTACGAAGAACTGGCATGATTGCGAGAGG
R58	CGTAGAAAATACATACCGAGGAAACGCAATAAGAAGCGCA
R59	AACGCAAAGATAGCCGAACAAACCCTGAAC
R60	GTTTATTTTGTCACAATCTTACCGAAGCCCTTTAATATCA
R61	ATCCCCCTATACCACATTCAACTAGAAAAATC
R62	AATACTGCCCAAAAGGAATTACGTGGCTCA
R63	AATAGTAAACACTATCATAACCCTCATTGTGA
R64	CTTTTGCAGATAAAAACCAAAATAAAGACTCC
R65	ATACCCAACAGTATGTTAGCAAATTAGAGC
R66	AAGGAAACATAAAGGTGGCAACATTATCACCG
R67	AAGTAAGCAGACACCACGGAATAATATTGACG
R68	AATAGCTATCAATAGAAAATTCAACATTCA
R69	TTTACCCCAACATGTTTTAAATTTCCATAT
R70	CGGATTGCAGAGCTTAATTGCTGAAACGAGTA
R71	CGAAAGACTTTGATAAGAGGTCATATTTCGCA
R72	GCTTCAATCAGGATTAGAGAGTTATTTTCA
R73	AGAGAGAAAAAAATGAAAATAGCAAGCAAACT
R74	TTAGACGGCCAAATAAGAAACGATAGAAGGCT
R75	AAAGTCACAAAATAAACAGCCAGCGTTTTA
R76	GAGAGATAGAGCGTCTTTCCAGAGGTTTTGAA

R77	CTGTAGCTTGACTATTATAGTCAGTTCATTGA
R78	GATGGCTTATCAAAAAGATTAAGAGCGTCC
R79	TTGCTCCTTTCAAATATCGCGTTTGAGGGGGT
R80	CCAACAGGAGCGAACCAGACCGGAGCCTTTAC
R81	TTAACGTCTAACATAAAAACAGGTAACGGA
R82	ATCCCAATGAGAATTAACTGAACAGTTACCAG
R83	GCCAGTTAGAGGGTAATTGAGCGCTTTAAGAA
R84	ACGCTAACACCCACAAGAATTGAAAATAGC
R85	AACAGTTTTGTACCAAAAACATTTTATTTC
R86	GATTTAGTCAATAAAGCCTCAGAGAACCCTCA
R87	AATGGTCAACAGGCAAGGCAAAGAGTAATGTG
R88	TTTGGGGATAGTAGTAGCATTAAAAGGCCG
R89	CCAATAGCTCATCGTAGGAATCATGGCATCAA
R90	TATCCGGTCTCATCGAGAACAAGCGACAAAAG
R91	GCGAACCTCCAAGAACGGGTATGACAATAA
R92	GCCTTAAACCAATCAATAATCGGCACGCGCCT
R93	TAAATCGGGATTCCCAATTCTGCGATATAATG
R94	AAATTAAGTTGACCATTAGATACTTTTGCG
R95	TAAATCATATAACCTGTTTAGCTAACCTTTAA
R96	TTCTACTACGCGAGCTGAAAAGGTTACCGCGC
R97	TTTTATTTAAGCAAATCAGATATTTTTTGT
R98	GTACCGCAATTCTAAGAACGCGAGTATTATTT
R99	CTTATCATTCCCGACTTGCGGGAGCCTAATTT
R100	TGTAGAAATCAAGATTAGTTGCTCTTACCA
R101	AACGCAAAATCGATGAACGGTACCGGTTGA
R102	TATATTTTGTCATTGCCTGAGAGTGGAAGATT
F103	TAGGTAAACTATTTTTGAGAGATCAAACGTTA
R104	GAGACAGCTAGCTGATAAATTAATTTTTGT
R105	GTAATAAGTTAGGCAGAGGCATTTATGATATT
R106	GTAAAGTAATCGCCATATTTAACAAAACTTTT
R107	ACAACATGCCAACGCTCAACAGTCTTCTGA
R108	GTTTATCAATATGCGTTATACAAACCGACCGT
R109	AACAAGAGGGATAAAAATTTTTAGCATAAAGC
R110	GCTATCAGAAATGCAATGCCTGAATTAGCA
R111	GAGGGTAGGATTCAAAAGGGTGAGACATCCAA
R112	CAACCGTTTCAAATCACCATCAATTCGAGCCA
R113	CATGTAATAGAATATAAAGTACCAAGCCGT
R114	AATTGAGAATTCTGTCCAGACGACTAAACCAA
R115	AGTATAAAGTTCAGCTAATGCAGATGTCTTTC
R116	TTAGTATCACAATAGATAAGTCCACGAGCA
R117	TAATCAGCGGATTGACCGTAATCGTAACCG
R118	GTATAAGCCAACCCGTCGGATTCTGACGACAGTATCGGCCGCAAGGCG

R119	ATATTTTGGCTTTCATCAACATTATCCAGCCA
R120	TAAATCAAAATAATTCGCGTCTCGGAAACCAGGCAAAGGGAAGG
R121	ATCGCAAGTATGTAAATGCTGATGATAGGAAC
R122	TCAAATATAACCTCCGGCTTAGGTAACAATTTCATTTGAAGGCGAATT
R123	CCTAAATCAAAATCATAGGTCTAAACAGTA
R124	GTGATAAAAAGACGCTGAGAAGAGATAACCTTGCTTCTGTTCGGGAGA
R125	ACAAACGGAAAAGCCCCAAAAACACTGGAGCA
R126	GCGAGTAAAAATATTTAAATTGTTACAAAG
R127	TGTAGCCATTAAAATTCGCATTAAATGCCGGA
R128	GCCATCAAGCTCATTTTTTAACCACAAATCCA
R129	TATAACTAACAAAGAACGCGAGAACGCCAA
R130	ACCTTTTTATTTTAGTTAATTTCATAGGGCTT
R131	GAATTTATTTAATGGTTTGAAATATTCTTACC
R132	CTTAGATTTAAGGCGTTAAATAAAGCCTGT
R133	TGCATCTTTCCCAGTCACGACGGCCTGCAG
R134	GCTTTCCGATTACGCCAGCTGGCGGCTGTTTC
R135	AGAAAACAAAGAAGATGATGAAACAGGCTGCG
R136	CATAAATCTTTGAATACCAAGTGTTAGAAC
R137	CCAGGGTTGCCAGTTTGAGGGGACCCGTGGGA
R138	ATTAAGTTTACCGAGCTCGAATTCGGGAAACCTGTCGTGC
R139	GATGTGCTTCAGGAAGATCGCACAATGTGA
R140	TCTTCGCTGCACCGCTTCTGGTGCGGCCTTCC
R141	GCGATCGGCAATTCCACACAACAGGTGCCTAATGAGTG
R142	CAACTGTTGCGCCATTCGCCATTCAAACATCA
R143	CTGAGCAAAAATTAATTACATTTTGGGTTA
R144	ATTCATTTTTGTTTGGATTATACTAAGAAACCACCAGAAG
R145	CGCGCAGATTACCTTTTTTAATGGGAGAGACT
R146	CCTGATTGCAATATATGTGAGTGATCAATAGT
R147	AACAATAACGTAAAACAGAAATAAAAATCCTTTGCCCGAA
R148	CTTTTACAAAATCGTCGCTATTAGCGATAG
R149	GTCGACTTCGGCCAACGCGCGGGGTTTTTC
R150	CTGTGTGATTGCGTTGCGCTCACTAGAGTTGC
R151	GCAATTCACATATTCCTGATTATCAAAGTGTA
R152	CTACCATAGTTTGAGTAACATTTAAAATAT
R153	TTAATGAACTAGAGGATCCCCGGGGGGTAACG
R154	TTCCAGTCGTAATCATGGTCATAAAAGGGG
R155	CACATTAAAATTGTTATCCGCTCATGCGGGCC
R156	AAGCCTGGTACGAGCCGGAAGCATAGATGATG
R157	ATTATCATTCAATATAATCCTGACAATTAC
R158	GCGGAACATCTGAATAATGGAAGGTACAAAAT

R159	ATTTTAAAATCAAAATTATTTGCACGGATTCG
R160	CTCGTATTAGAAATTGCGTAGATACAGTAC
R161	TTTTCACTCAAAGGGCGAAAAACCATCACC
R162	AGCTGATTGCCCTTCAGAGTCCACTATTAAAGGGTGCCGT
R163	AGCAAGCGTAGGGTTGAGTGTTGTAGGGAGCC
R164	CCCAGCAGGCGAAAAATCCCTTATAAATCAAGCCGGCG
R165	TCAATATCGAACCTCAAATATCAATTCCGAAA
R166	TCAACAGTTGAAAGGAGCAAATGAAAAATCTAGAGATAGA
R167	CTTTAGGGCCTGCAACAGTGCCAATACGTG
R168	AGATTAGAGCCGTCAAAAAACAGAGGTGAGGCCTATTAGT
R169	CTCCAACGCAGTGAGACGGGCAACCAGCTGCA
R170	TGGAACAACCGCCTGGCCCTGAGGCCCGCT
R171	GCCCGAGAGTCCACGCTGGTTTGCAGCTAACT
R172	TCGGCAAATCCTGTTTGATGGTGGACCCTCAA
R173	ACCTTGCTTGGTCAGTTGGCAAAGAGCGGA
R174	AGCCAGCAATTGAGGAAGGTTATCATCATTTT
R175	TTAACACCAGCACTAACAACTAATCGTTATTA
R176	CAGAAGATTAGATAATACATTTGTCGACAA
R177	CAAATCAAGTTTTTTGGGGTCGAAACGTGGA
R178	AAAGCACTAAATCGGAACCCTAATCCAGTT
R179	CCCGATTTAGAGCTTGACGGGGAAAAAGAATA
R180	AACGTGGCGAGAAAGGAAGGGAAACCAGTAA
R181	TAAAAGGGACATTCTGGCCAACAAAGCATC
R182	ACCCTTCTGACCTGAAAGCGTAAGACGCTGAG
R183	GCACAGACAATATTTTTGAATGGGGTCAGTA
R184	CTTTAATGCGCGAACTGATAGCCCCACCAG

Right edge staples (4-adenine-loop)

Seq name	Sequence 5’-3’
R185	CAGAACCGCCACCCTC TCAGAACC
R186-A	GCCACCCTAAAAATACAGGAGTGTACTGTACATGGC
R187-A	TTTTGATGAAAACGTTTGCCATCTTTTCATAGCCCC
R188-A	CTTATTAGAAAACAAAGACAAAAGGGCGTATGGTTT
R189-A	ACCAGCGCAAAAAGAGCAAGAAACAATGGTTAAGCC
R190-A	CAATAATAAAAACAATTTTATCCTGAATATTTTGCA
R191-A	CCCAGCTAAAAATATCCCATCCTAATTTGAACAAG
R192-A	AAAAATAAAAAACATAATTACTAGAAAAGAATAAAC
R193-A	ACCGGAATAAAAAATCCTTGAAAACATAATTAATTT
R194-A	TCCCTTAGAAAAAGATGAATATACAGTATTTCAGGT
R195-A	TTAACGTCAAAAAGACTTTACAAACAATAGGATTTA
R196-A	GAAGTATTAAAA AAAAATACCGAACGAACTAAAACATCGCCATT

Right edge staples (4-guanine-loop)

Seq name	Sequence 5’-3’
R185	CAGAACCGCCACCCTC TCAGAACC
R186-G	GCCACCCTGGGGATACAGGAGTGTACTG TACATGGC
R187-G	TTTTGATGGGGGCGTTTGCCATCTTTTC ATAGCCCC
R188-G	CTTATTAGGGGGCAAAGACAAAAGGGCG TATGGTTT
R189-G	ACCAGCGCGGGGAGAGCAAGAAACAATG GTTAAGCC
R190-G	CAATAATAGGGGCAATTTTATCCTGAAT ATTTTGCA
R191-G	CCCAGCTAGGGGTATCCCATCCTAATTT TGAACAAG
R192-G	AAAAATAAGGGGCATAATTACTAGAAAA GAATAAAC
R193-G	ACCGGAATGGGGAATCCTTGAAAACATA ATTAATTT
R194-G	TCCCTTAGGGGGAGATGAATATACAGTA TTTCAGGT
R195-G	TTAACGTCGGGGAGACTTTACAAACAAT AGGATTTA
R196-G	GAAGTATTGGGGAAAAATACCGAACGAA CTAAAACATCGCCATT

Biotinylated sequences

Seq name	Sequence 5’-3’
BioR30	ATAAGGGAACCGGATATTCATTACGTCAGGACGTTGGGAA-biotin
BioR33	TTGTGTCGTGACGAGAAACACCAAATTTCAACTTTAAT-biotin

DNA sequences of hexagonal origami

Core staples

Seq name	Sequence 5’-3’
HE01	CAGTACATAAGTAAATCGTCGCTATAAACTTTT
HE02	CCCTTAATTACCTTTTTTAATAGTTACAAAATCGCGCGTCAGATG
HE03	GACCAGGCTTACTTAGCCGGAACGTAAAACAC
HE04	ATACAAAGAACTGGCATGATTTTCCAACGCTCAACAGTAAGCCTGT
HE05	CTACAGAGAAGTACAACGGAGATTTTATCATAACCCTCGTTAGAAAACG
HE06	GCGAAACAGCTTTGAGGACTAAACCGATATATT
HE07	ATTCAGAGGCTTTTGCAAAAGCCACATTCAACTAATGAAATCTAC
HE08	GAGAGATGGAGAATTAACTGAATTTTCCCATCCTAATTTACGCGCCT
HE09	ATAGCTGTTTTTTAAACTATCGGCCTTGGGCTA
HE10	GTAATGTGTGTAATACTTTTGCGGGTAGCATT
HE11	GAATTTAAAAGAAACGCAAACGAGGAAACGCAATATAATATCA
HE12	AAATATCACGGTCAGTATTAACACGGGACATT
HE13	GATCGTCACCTTTTTATAGTCAGAAGCACTAAA
HE14	TCATACATAAGTTTTAACGGGG

HE15	TCATCTTTAGTTTCCATTAAACGGCGACAATG
HE16	GCCGCTTTAACTAAAGGAA
HE17	TTGCCAGAGGTCCAATACTGCGGAACCAGACCG
HE18	GACGATAAAAGGAATTACGAGGTTTAATTGTGTCGAAATCACCAAGC
HE19	ACAGTGCAAAGCATCACCTTGCTAGATAAT
HE20	CGTTAGACCGCTACAGGGCGCGTTTGGCAACAGCTGATTGGTTTGCG
HE21	ATATACCCGAAAGACTTCAATGCTTTAAACAGTTCTACCAGAC
HE22	ATTTTAGACATTATAATCAGTGAGGCAATCGTC
HE23	ACGAGTAGTAAATTGTTGTGAA
HE24	TTAATGCGATCAGAGCGGGAGCTATCTGTCCATCACGCAAAACGC
HE25	GAAGCAAAATTGCTCCTTTTGAGTTTAGCT
HE26	ACAAAGTTAAGCCCAATAATAAATAACATAAAAACAGATATTATT
HE27	TTGCGTGCTAAACAACTTTCTTTCATTAGCAAGGCCGGTGAGCCAT
HE28	AAGAAACAATTTTAAGAAAAGTAAGCAATAGAA
HE29	GCCACCCTGCCCAATAGGAACCCATTGTCGTCTTTCCAGAAAAAA
HE30	TTATTTTCAATCAATAATCGGCTGGACAATAA
HE31	AAGTTTGTACCGTAACACTGAACCGTACTCAGGAGGTAGCGGGGT
HE32	GCTCCATGGCATAGGCTGGCTGATTTGGACGTTGGGAAGAACAGATACA
HE33	TCGGCCAAATGAGTGAGCTAACTCACGACGGC
HE34	TTTATTTTATATTTTAAATGCACATCAATA
HE35	TCCAATCGCAAATAAGGCGTTAAATAAACGCCAAC
HE36	TGATATTAGGGTAGCTATTTTT
HE37	CATTTCGCATAAATCATACAGGCAAAAAACAT
HE38	ACCCAAAAGGCTTGCCCTGACG
HE39	AATCAAGATTAGTTGATCTTAC
HE40	TGGGATTTAATAATAATTTTTTCAGCTGAGGCTTGCAGGGAGCAACGG
HE41	CAGTAGCGAATCAAAATCACCGGAGCCACCAC
HE42	ATTAGACGAACCCACAAGAATTGAGTTACCAGAAGGAAACGACAC
HE43	CGCCTGGCAAATCAAAAGAATAGTTTGACGGGGAAAGCCGGCGCCGCGC
HE44	ATTATTCATTAACAATTTCATTTGAGAATCCTTGAAAACAGCAAA
HE45	CCAATAGGGAGCGAGTAACAACCCTTGAGGGGACGACGACCTC

	TT
HE46	ATCAGCTTACCGATAGTTGCGCGTAAAATA
HE47	GTAACAGTGCCCGTACCTATTA
HE48	TCAAATATTAATGGTTTGAAATCGAGCCAG
HE49	GGTGCCTACGCGCGGGGAGAGGCGCCCTTCAC
HE50	ACTCCAGCGCAACTGTTGGGAAGGATCCCCGGGTACCGAGCACAACAT
HE51	CATGAGGAGACCCCCAGCGATTATCGCGACCT
HE52	TCATGGAAATACAGAGATAGAACCCTTTAAAACAG
HE53	ATATTTTATTCTACTAATAGTAGAGAAGCC
HE54	AGGTAAATTTTATTTGTCACAATCAGATAGCCGA
HE55	ATCAACATAAATCAAAAATCTTTCATCGGAACGAGGGTAGTTAAAG
HE56	CCGAACGAATCAACAGTTGAAAGTTTCAAACATCAAGAAAATTAAGACG
HE57	CCAGAAGGATGATGGCAATTCA
HE58	ATACCCAATAAAGGTGGCAACATAATCACCGTCACCGACTAAACGTCA
HE59	ATAGCAACAGAACCGCCACCCTTTTACCGCCACCCTCAGAACCAGAG
HE60	AAATAAATCCGCCACCAGAACCACTTTGCCAT
HE61	AAGAGAACAGGAGGCCGATTAGCGTAACCACCACACCCGAACGTG
HE62	TAATAAGTTCTGTCCAGACGACTCTTTCCT
HE63	GTTTATCATCGCCATATTTAACAGAATAAACAC
HE64	TTAGGAGTCAATAGTGAATTTTTCTAAAACATC
HE65	ATTGAGAAACAATAGATAAGTCCTTTAGGGTAATTGAGCGCATAACGGA
HE66	CTGAGAAGTTGGGTTATATAACTATCATAATTACTAGAAAAGGGCTTA
HE67	GTTAATAATGCGATTTTAAGAACTTTTTGACAAGAACCGGAGGTGTACA
HE68	ATTACATTTTCAATTACCTGAGTTTTAAAATATCTTTAGGCTGGTCA
HE69	CTGGCCAACCTACATTTTGACGCTCCACCGAGTAA
HE70	TGTGATAAGACAAAGAACGCGAGATAATTAATTTT
HE71	TAGAAACCATCGTAGGAATCATTTTTACAAAATAAACAGCCGGAAGCGC
HE72	CATTTTTGCGAGCTTCAAAGCGAATCGTCATAAAT
HE73	ACAGGAAGTAAAACTAGCATGTCTTTAGACAGTCAAATCACATGCCTGA
HE74	AGAATGACAAAGATTAAGAGGAAGATGCTGTAGCTCAACAAATTCTGC

HE75	TTCTGAAAGTACCAGGCGGATAACGGAATAGGTGTATCGTTTC
HE76	TATGACCCTAGGTAAAGATTCAATTTTGATAATCAGAAAAGTTTTTTAA
HE77	GCCATGACAATATTTTTGAATCTGGTAAT
HE78	CCGCCGCGATTGGCCTTGATATAGTAAGCG
HE79	TAACGCCAAAAACCAAAATAGCGATTGAATCCCCCTCAAAATATC
HE80	CCACCACCACCATCGATAGCAGCCATTAAAGGT
HE81	TTAGTCTTTAGAGAGTTTACTACCTTTTATATG
HE82	CGGAATATGTAAATGCTGATTAGCGATAGCTTAGACAAAATTA
HE83	TTAGTATCTAACCTCCGGC
HE84	AAGGCTCCAAACATCGCCCACGCATAAGACTTTTT
HE85	CGGTCCGTTGAAAATCTCCACGTTAGTAAATGAATTTTCAGGG
HE86	TGATTGTTTGGATTACATATCA
HE87	GTCACCAGTAGCCCTCATAGTTAGCATCGGTTT
HE88	AGAGGGCGATCGGTGCGGGCAGTATCGGCCTCAGGATCAACAT
HE89	CCACGCTTGGTGGTTCCGAAATAACAAGAG
HE90	TTGGGAATGTAGAAAATAC
HE91	GCGAGAAAGGAACCCTAAAGGGATTTGTTGTTCCAGTTTGGCGGCAAAA
HE92	GCTGCCAGCTTTCCGGCACCTTTTAACAGTTGATTCCCTGTTTTAA
HE93	ACTAAATCGGAAGGGAAGAAAGCTAGCGGTCACGCTGCAAGGG
HE94	GCGTTTTAATTCGGATGGCTTAGAGCTATTAGATA
HE95	AATATACATGCACGTAAAACAGATTTCATTTTGCGGAACAAAAATCCTT
HE96	ACTACGTGAACCATCGTAAAGC
HE97	TATCATTCATCGAGAACAAGCAAGGCTTAT
HE98	CGCTATTACGCAGCTTGCATGCCTGCAAAGCCTGG
HE99	TGCCCGAAAGATTAGAGCCGTCAATGAACCTC
HE100	TAAATGTAACGCCATCAAAAATTTTTAAATCGGTTGTACCAGGCAAA
HE101	TTTGCTCACATGAAAGTATTAAGTTTTGAATTTACCGTTCCTCACAAAC
HE102	GAACGAGTAAAATTAAGCAATAATTTCTGTAGCCAGCTTTCAAGATCGC
HE103	TCCCTTATCCTGAGAGAGTTGCAGTTAATGAA
HE104	CGTTATACAATTTAGTATGTTAGCAAACTAGAG
HE105	CAGTGCCACAGCTGGCGAAAGGGGCCGTGCATCTG
HE106	CCAGTGTCGGATTCTCCGTGGTTGTTAAATCAGCTCACCCCAAAA
HE107	TGCGTTGGTCGTGCCAGCTGCACAAGCGGT
HE108	AGGTGAGGAACCCTCAATCAATATAGCACTAA

HE109	CAACGCTATCCAAATAAGAAACGAGCCTTTACAGAGAGAGAGC
HE110	TATTGGGCGAAGCATAAAGTGTAGGTCGACTCT
HE111	CTTTTCATACAGAATCAAGTTTGCGGGAGGGA
HE112	ACGAGCCGGCCAGGGTGGTTTTTTTGAGCACGTATAACGTAATACTTC
HE113	CGTAATGGGCAAAAGAATACACAGGCGCAG
HE114	CCAGCAAAATTTAGAATAGAAAGGAACTGCGG
HE115	AGCGTCATTGCAACAGGAAAATTAACCGTTGTAGCGCTTTCCT
HE116	GTACGGTGTCTTTCAGGCAAAGCGCCATTGGTC
HE117	AACATCCAAAATGGTCAATAACCTTAAGAGGT
HE118	ATATGCAAAAGCGGATTGC
HE119	CAACTAATCGTTATTAATTTTAATTTATTTTCAGGTTTAACAGAGGCGA
HE120	ATCCAGAAGTAATAACATCACTTTTTCCGCTCACAATTCCACTCGAATT
HE121	TCAGACTGCCCCCTTATTAGCGCACCAGAG
HE122	TCCACTAAAAAACCGTCTATCA
HE123	GGTAATCGATTGTATAAGCAAATATTCGCATTAAATTTGAACA
HE124	TTACCTTAAACGAACTAACGGAATGAGATTTAGGAATAAAGTT
HE125	AAGGCTATCAGGTCAGATGAAC
HE126	TGAAATGCGACCAGTAATAAAACGCCTGCA
HE127	TTTGATTACAATATTACCGCCAGCAAGAATACGTGGCACATAAAAATA
HE128	TATCCCAAACGAGCGTCTTTCCATTTCAAATCAGATATAGAAGCCGTTT
HE129	ACAACAACAGGAGCCTTTAATTGTGTAACGATCTA
HE130	CCTCAGAGCCTCATTAAAGCCAGTTTAGAAGGATTAGGATTTTAGTACC
HE131	AATTCATCATTCAACCGATTGACTTTAGCG
HE132	ATGTAATTTTCAGCTAATGCAGAACGAGCATG
HE133	AACGGCGGATATGGGCGCATCGTAAGATGTGCT
HE134	ACGGTCAAGAGGACAGATGAACTATTCATT
HE135	CGTAATCATCGCCATTCAG
HE136	GAATTAGCAGATTTAGTTTGACCTAATTGCTGA
HE137	CCAATGAAGGAACCGCCTCCCTCTTTAGCCACCACCCTCATTTTCTGTA
HE138	AAATTATTGTAACAGTACCTTTTTTGCTTTGAATACCAGGAAA
HE139	ACATTTGTCGACAACTCGTATTAGAAACCA
HE140	CCGGTATCGACTTGCGGGAGGT
HE141	GCAAGGCTCACGACGTTGTAAAACATTAAT
HE142	CACGGAATAAGATTGACGGAAATTATTACCGTAAT
HE143	GTTGGCAAACCACCAGCAGAAGACTGACCTGAA
HE144	ACAACATGTAGGCAGAGGCATTTACCGACCG

Edge staples (4-guanine-loop)

Seq name	Sequence 5’-3’
GHE145	CCAACGTCAAAGGGCGTTAAAGAACGTGGACTGGGGCGAAAATC
GHE146	CTGTTTGAGGTTTGCCCCAGCAGGGGGGTCCAGTCG
GHE147	GGAAACCTCGCTCACTGCCCGCTTGGGGGCCAGGGT
GHE148	TTTCCCAGGATTAAGTTGGGTAACGGGGGGTCACGT
GHE149	TGGTGTAGTGACCGTAATGGGATAGGGGTTAATATT
GHE150	TTGTTAAAATTTAAATTGTAAACGGGGGAGCAAACA
HE151	AGAGAATCTTGCCTGAGAGTCTGG

Edge staples (4-adenine-loop)

Seq name	Sequence 5’-3’
AHE145	CCAACGTCAAAGGGCGTTAAAGAACGTGGACTAAAACGAAAATC
AHE146	CTGTTTGAGGTTTGCCCCAGCAGGAAAATCCAGTCG
AHE147	GGAAACCTCGCTCACTGCCCGCTTAAAAGCCAGGGT
AHE148	TTTCCCAGGATTAAGTTGGGTAACAAAAGGTCACGT
AHE149	TGGTGTAGTGACCGTAATGGGATAAAAATTAATATT
AHE150	TTGTTAAAATTTAAATTGTAAACGAAAAAGCAAACA
HE151	AGAGAATCTTGCCTGAGAGTCTGG

Biotinylated sequences

BioHE143	GTTGGCAAACCACCAGCAGAAGACTGACCTGAA-biotin
BioHE12	AAATATCACGGTCAGTATTAACACGGGACATT-biotin
BioHE35	TCCAATCGCAAATAAGGCGTTAAATAAACGCCAAC-biotin

References:

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