

Supplementary Information

Programmable transformations of DNA origami made of small modular dynamic units

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Materials. The single-stranded DNA scaffold (p7560) was extracted from M13 bacteriophage. Chemically synthesized DNA short strands were purchased from IDT (www.idtdna.com) and were used without further purification. All other reagents were purchased from Sigma-Aldrich.

DNA origami design and folding. The DNA origami was designed with the software CaDNAno (<http://cadnano.org/>)¹. For DNA Origami folding, 10 nM scaffold together with a tenfold excess of each staple strand was mixed in 1×TE (10 mM Tris, 1 mM EDTA; pH 8.0) buffer with 10 mM MgCl₂. In the annealing process the folding mixture was heated at 80°C and slowly cooled down to 25°C at the rate of -1°C/3 min. Afterwards, the folded DNA origami was purified from excess staple strands by PEG precipitation. DNA origami samples were mixed with 15% PEG solution (15% PEG 8000, 1xTE, 505 mM NaCl, 10 mM MgCl₂) at 1:1 ratio, then the mixtures were centrifuged at 17,900 rcf for 25 min. The supernatant was removed and add 1×TE buffer with 10 mM MgCl₂ to resuspend the sample. The precipitation process can be repeated more rounds to remove excess staple strands.

Agarose gel electrophoresis. DNA origami samples were subjected to agarose gel electrophoresis at 70 V for 2-3 hours in an ice water bath. Gels were prepared with 0.5 ×TBE buffer containing 10 mM MgCl₂ and 0.005% (v/v) Ethidium Bromide.

AFM imaging. Take 2 µL samples and deposit onto freshly cleaved mica. Fill the sample area with 80 µL 1×TE buffer with 10 mM MgCl₂. The samples were imaged on a Multimode VIII system (Bruker) in liquid using commercial tips (SNL-10, Bruker).

Coarse-grained oxDNA simulations. The oxDNA topology and configuration files of all MEO structures were generated based on the MEO-36 caDNAno design file using an in-house MATLAB script. The protocol for relaxing each of these structures was adapted from our previous study;² briefly, this involved substituting the back-bone potential with linear springs, gradually increasing the spring constants, and then applying mutual traps between paired scaffold and staple bases to ensure proper hydrogen bonding during a $\sim 10^5$ timesteps-long molecular dynamics (MD) relaxation period. Then, a short MD simulation of 10^6 timesteps using the original oxDNA2 force field,³ but still enforcing mutual traps, followed by a longer equilibrium simulation with no mutual traps for 10^7 timesteps was conducted. The production step of the MD simulations where structural data was collected for analysis was then conducted for much longer 10^8 time steps. In these simulation stages, we used a timestep of 3.03 fs and the temperature was held constant at 30°C using an Anderson-like thermostat. To better match the experimental conditions of AFM imaging, we also carried out additional simulations for 10^7 timesteps implementing repulsion planes to apply external forces and constrain the structure in a confined quasi-2D configuration mimicking that of deposited and AFM-imaged structures. The stiffness constants of the repulsion planes were set to 0.0565 pN/nm. The output MD trajectories from these simulations with repulsion planes were used for calculating the mean configuration (by the singular value decomposition (SVD) algorithm⁴) and exported to UCSF Chimera⁵ to render images.

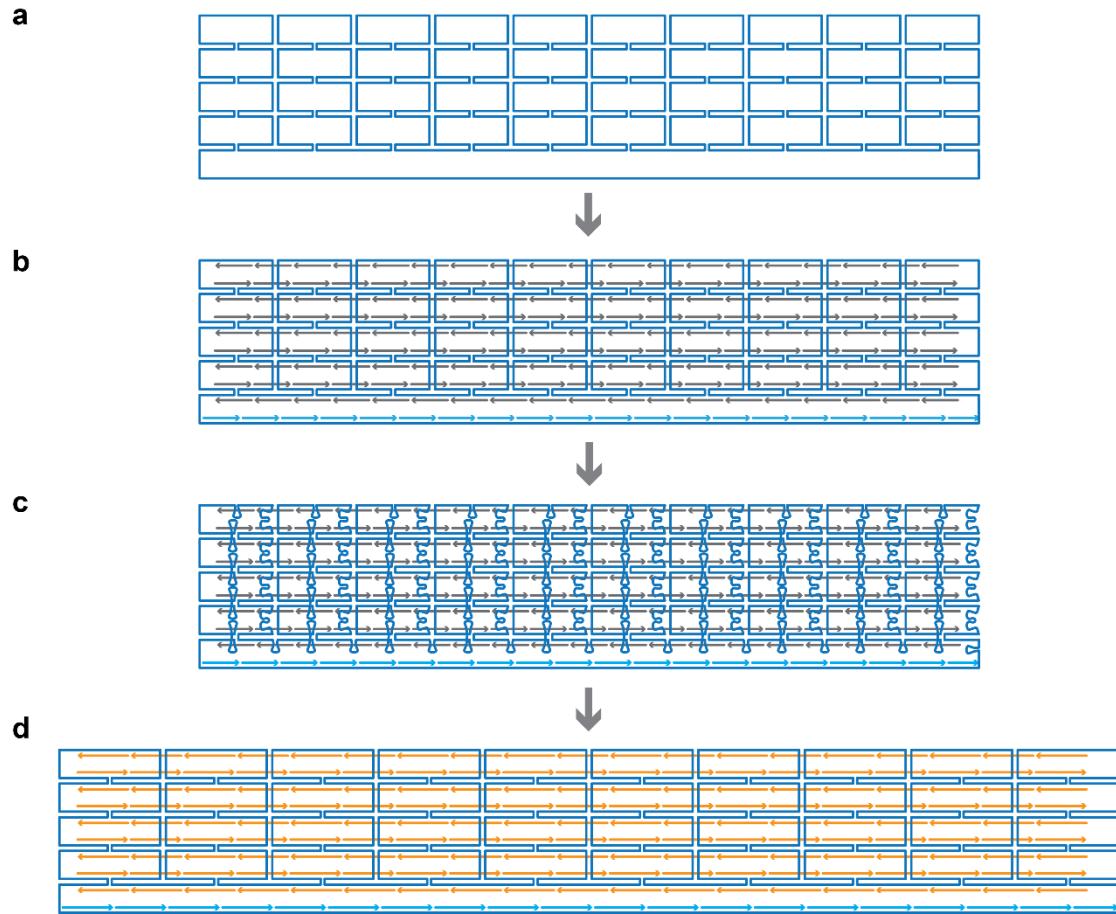


Figure S1. Design of 2D modular expandable DNA origami. a) Routing of DNA scaffold. All the crossovers are on the DNA scaffold. b) Adding DNA staples to the existing DNA scaffold. Each staple DNA is 26-nt long. c) Adding loops to the structure. Each loop is designed in the center of DNA unit. When the DNA unit contains crossover, a half crossover is converted into 20-nt loop to be shared by two neighboring DNA units. The DNA origami structure contains 19 columns and 9 rows of DNA units in total. d) DNA origami structure after fully expanded of each DNA unit. The half crossover becomes double crossover.

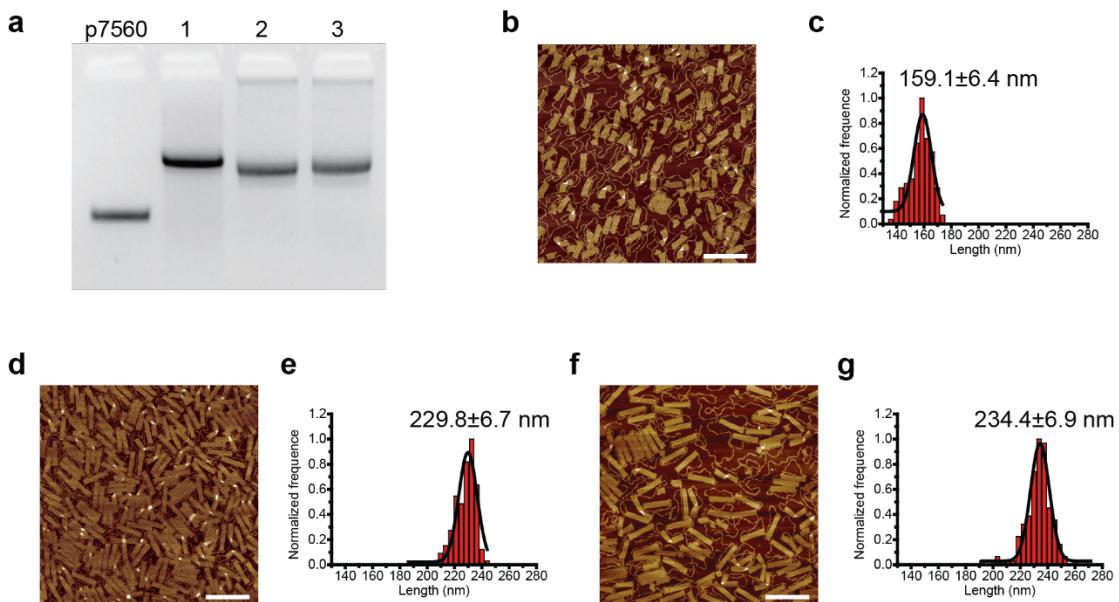


Figure S2. Characterization of one-pot assembled MEO-26 and MEO-36. a) 2% agarose gel electrophoresis analysis of MEO-26 and MEO-36. Lane 1: one-pot assembled MEO-26 using 26-base staple DNA. Lane 2: one-pot assembled MEO-36 using 36-base staple DNA. Lane 3: one-pot assembled MEO-36 using both 26-base and 36-base staple DNA. b), d) and f) were AFM imaging of three samples. Scale bar: 400 nm. c), e) and g) were length histogram of three samples and the corresponding Gaussian fitting. The mean length for three samples were 159.1 ± 6.4 nm (N=124), 229.8 ± 6.7 nm (N=139), and 234.4 ± 6.9 nm (N=152), respectively. The error is the standard deviation of Gaussian fits, and N presents the number of structures has been counted.

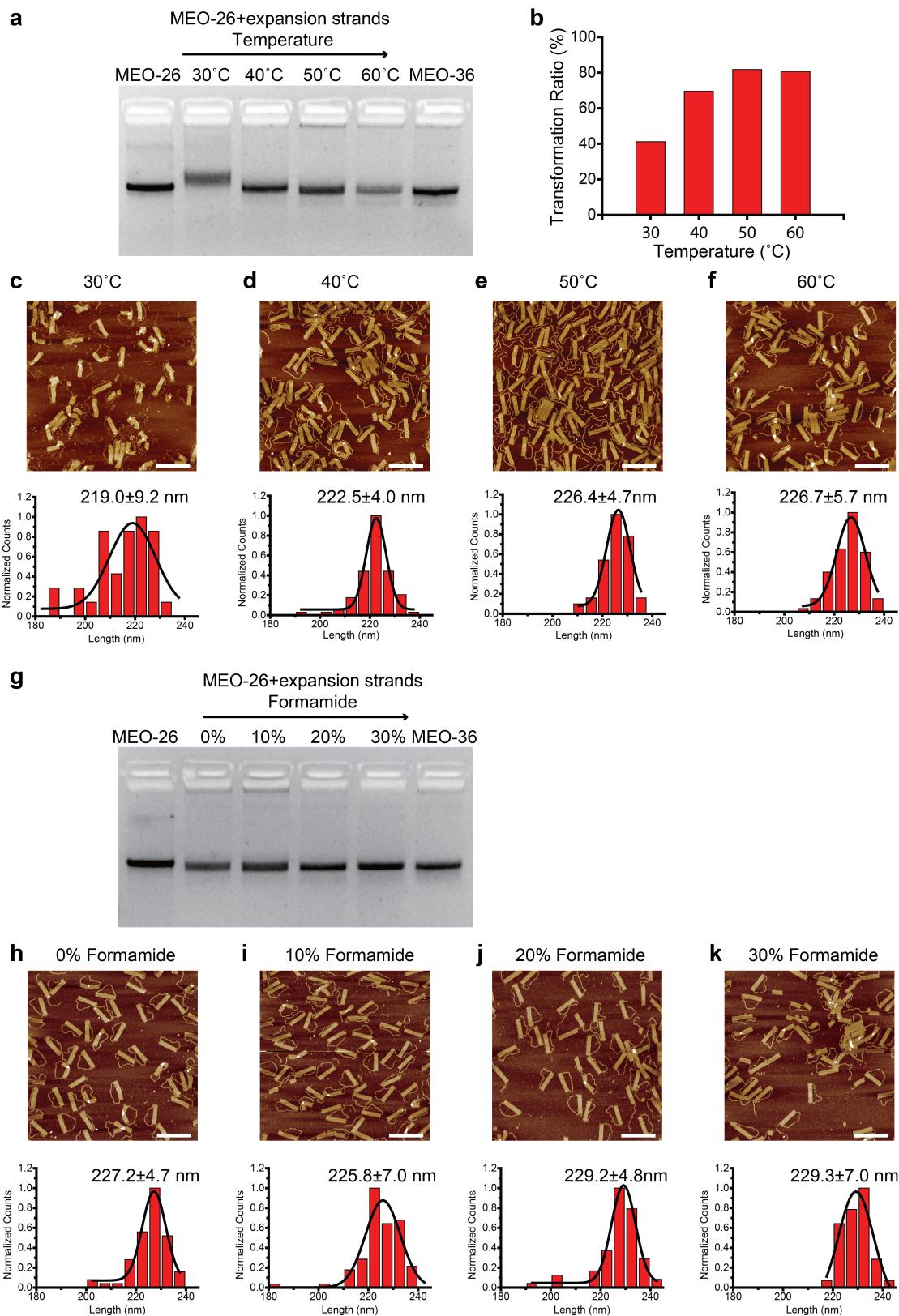


Figure S3. Optimization of expansion of MEO at different conditions. a) 2% native agarose gel electrophoresis of MEO after incubation with expansion strands at different temperatures. Unpurified MEO-26 was incubated with all the expansion strands with 30°C, 40°C, 50°C and 60°C overnight. b) The transformation yields of MEO at different temperatures. The structures with length over 220nm were counted as

successful transformation. The transformation ratio was 41.2% (N=34) for 30°C, 69.5% (N=82) for 40°C, 81.8% (N=137) for 50°C, and 80.7% (N=88) for 60°C. c), d), e) and f) Top: The AFM imaging results of products after expansion at the corresponding conditions. Scale bar: 400 nm. Below: the normalized length distribution of products at the corresponding conditions and the corresponding Gaussian fitting. The length for four samples were 219.0 ± 9.2 nm (N=34), 222.5 ± 4.0 nm (N=82), 226.4 ± 4.7 nm (N=137), and 226.7 ± 5.7 nm (N=88), respectively. g) 2% agarose gel electrophoresis of MEO after expansion at 50°C and different concentration of formamide. Unpurified MEO-26 was incubated with all the expansion strands with 0%, 10%, 20% and 30% of formamide at 50°C overnight. h), i), j) and k) Top: The AFM imaging of products after expansion at the corresponding conditions. Scale bar: 400 nm. Below: the normalized length distribution of products at the corresponding conditions and the corresponding Gaussian fitting. The length for four samples were 227.2 ± 4.7 nm (N=67), 225.8 ± 7.0 nm (N=86), 229.2 ± 4.8 nm (N=69), and 229.3 ± 7.0 nm (N=40), respectively. The error is the standard deviation of Gaussian fits, and N presents the number of structures that have been counted.

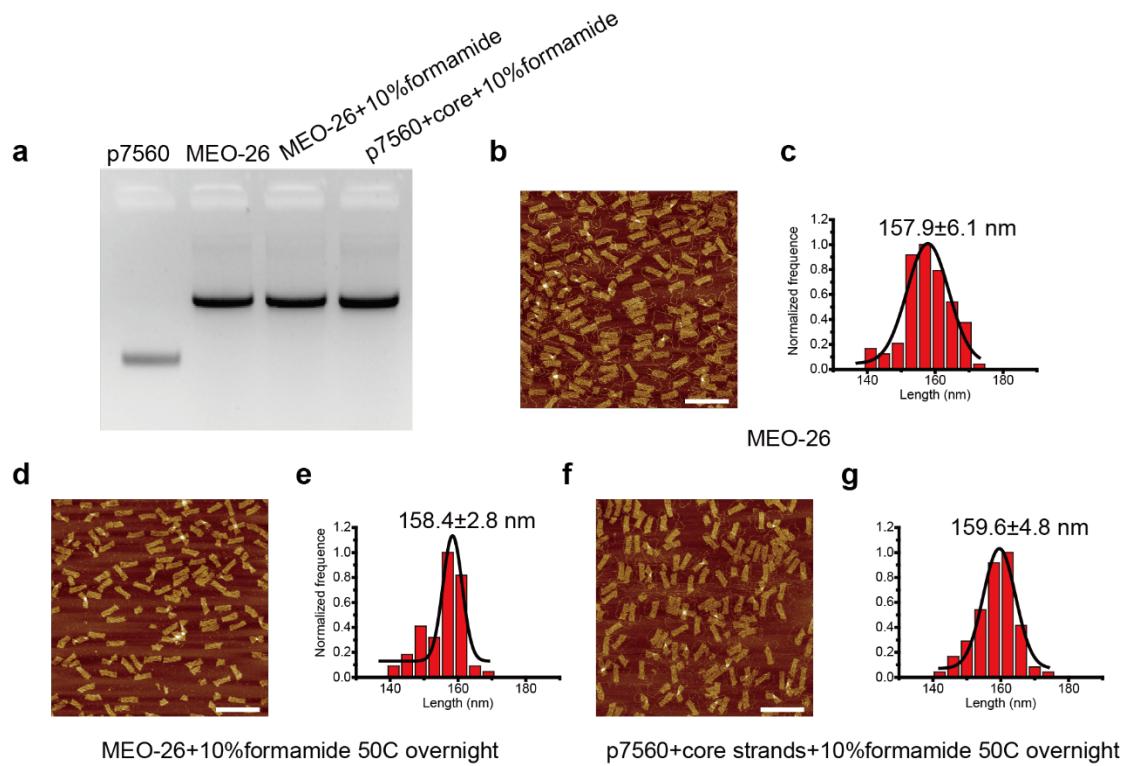


Figure S4. Stability test of MEO under 10% formamide and 50°C. a) 2% agarose gel electrophoresis of MEO-26 with 10% formamide and 50°C incubation overnight. A control was made with p7560 scaffold with 26-base staple DNA and 10% formamide incubated at 50°C overnight. b), d) and f) shows the AFM imaging of three samples. Scale bar: 400 nm. c), e), g) show the normalized frequency of length distribution of samples and the corresponding Gaussian fitting. The length for three samples were 157.9 ± 6.1 nm (N=100), 158.4 ± 2.8 nm (N=68), and 159.6 ± 4.8 nm (N=84), respectively. The error is the standard deviation of Gaussian fits, and N presents the number of structures that have been counted.

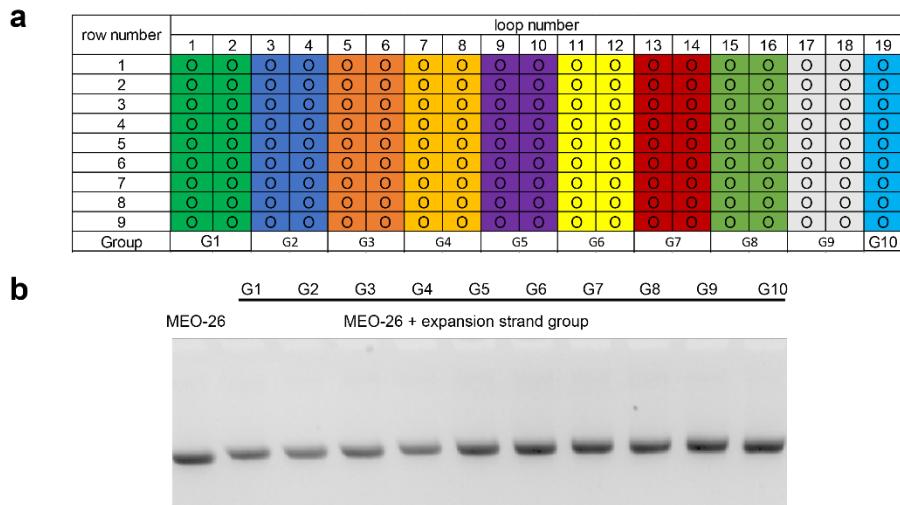


Figure S5. Strand displacement completeness test of MEO under 10% formamide and 50°C. The expansion strands were divided into 10 groups, from G1 to G10 (a), respectively. (b) Unpurified MEO-26 was incubated with each group under 50°C and 10% formamide overnight. MEO-26 and the products were analyzed by native agarose gel electrophoresis.

a

row number	number of expansion strands	loop number																		
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
MEO-L1	1	6	○	○	○	○	○	○	X	X	X	X	X	X	X	X	X	X	X	X
	2	6	○	○	○	○	○	○	X	X	X	X	X	X	X	X	X	X	X	X
	3	6	○	○	○	○	○	○	X	X	X	X	X	X	X	X	X	X	X	X
	4	6	○	○	○	○	○	○	X	X	X	X	X	X	X	X	X	X	X	X
	5	6	○	○	○	○	○	○	X	X	X	X	X	X	X	X	X	X	X	X
	6	6	○	○	○	○	○	○	X	X	X	X	X	X	X	X	X	X	X	X
	7	6	○	○	○	○	○	○	X	X	X	X	X	X	X	X	X	X	X	X
	8	6	○	○	○	○	○	○	X	X	X	X	X	X	X	X	X	X	X	X
	9	6	○	○	○	○	○	○	X	X	X	X	X	X	X	X	X	X	X	X

✗ 26-base staple DNA ○ 36-base staple DNA set E1

b

row number	number of expansion strands	loop number																		
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
MEO-L2	1	13	X	X	X	X	X	X	○	○	○	○	○	○	○	○	○	○	○	○
	2	13	X	X	X	X	X	X	○	○	○	○	○	○	○	○	○	○	○	○
	3	13	X	X	X	X	X	X	○	○	○	○	○	○	○	○	○	○	○	○
	4	13	X	X	X	X	X	X	○	○	○	○	○	○	○	○	○	○	○	○
	5	13	X	X	X	X	X	X	○	○	○	○	○	○	○	○	○	○	○	○
	6	13	X	X	X	X	X	X	○	○	○	○	○	○	○	○	○	○	○	○
	7	13	X	X	X	X	X	X	○	○	○	○	○	○	○	○	○	○	○	○
	8	13	X	X	X	X	X	X	○	○	○	○	○	○	○	○	○	○	○	○
	9	13	X	X	X	X	X	X	○	○	○	○	○	○	○	○	○	○	○	○

✗ 26-base staple DNA ○ 36-base staple DNA set E2

c

row number	number of expansion strands	loop number																		
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
MEO-36	1	19	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○
	2	19	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○
	3	19	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○
	4	19	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○
	5	19	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○
	6	19	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○
	7	19	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○
	8	19	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○
	9	19	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○

✗ 26-base staple DNA ○ 36-base staple DNA set E3

Figure S6. Illustration of distribution of expansion staples used for conformation MEO-L1 (a), MEO-L2 (b), and MEO-36 (c).

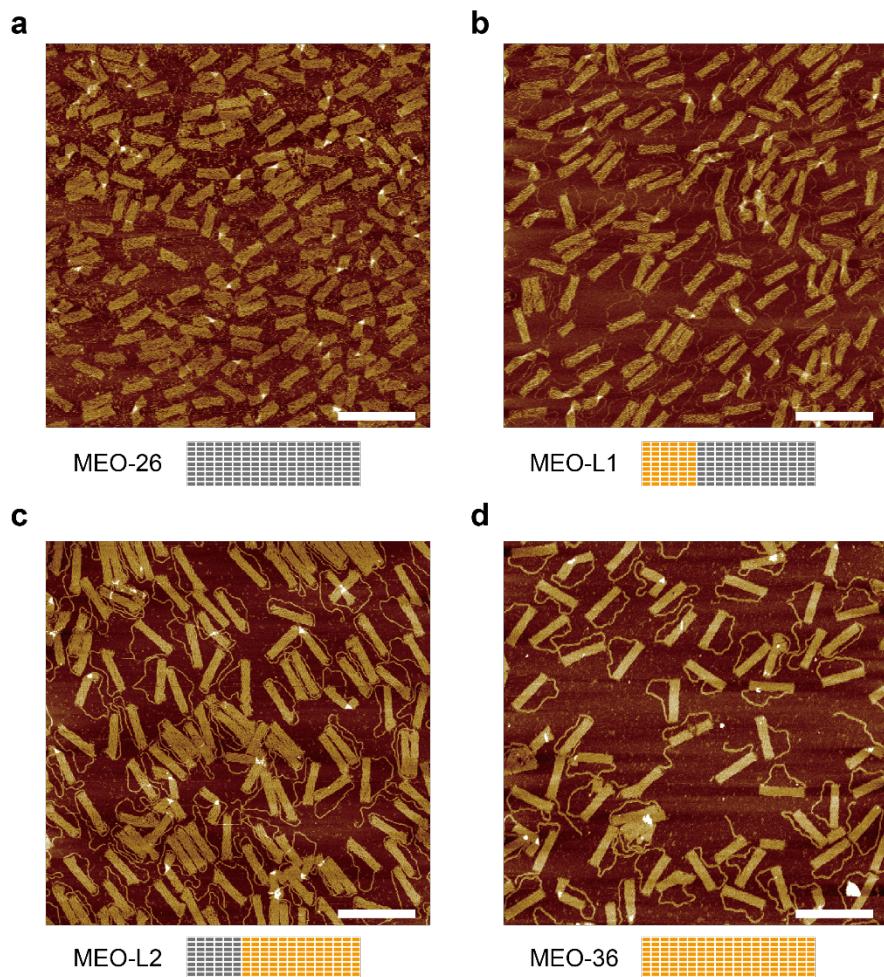


Figure S7. AFM imaging of one-step expansion of MEO-26 (a) into MEO-L1 (b), MEO-L2 (c) and MEO-36 (d) using expansion DNA set E1, E2 and E3, respectively. Scale bar: 400 nm.

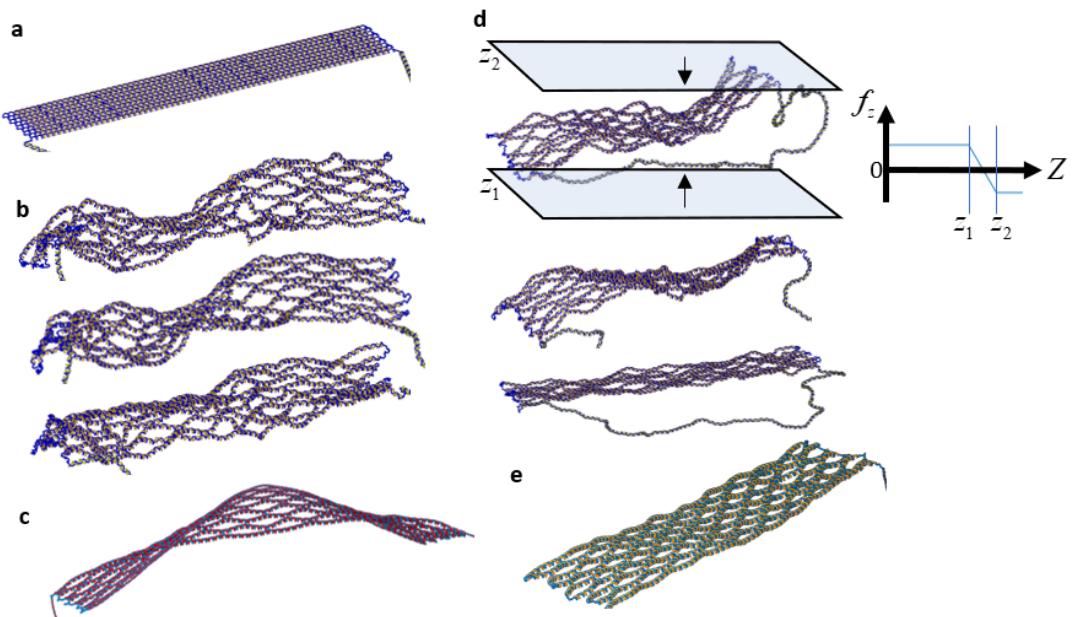


Figure S8. Schematic of the MD simulation protocol. a) Initial configuration from the caDNAno design file. b) Representative structures obtained from MD simulations in a 3D simulation box. c) Mean structure obtained from application of the SVD algorithm on all superimposed configurations obtained from an MD trajectory. d) In order to mimic the structure deposited on mica surface for AFM imaging, external forces using a set of repulsion planes separated by 8.5 nm were applied. The strength of the repulsion was chosen to flatten the structures but still allow some fluctuations along the Z direction. e) SVD-deduced mean configuration show good agreement with the AFM images, including this MEO-36 and other structures.

a

MEO-L1	row number	number of expansion strands	loop number																	
			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
	1	6	○	○	○	○	○	○	X	X	X	X	X	X	X	X	X	X	X	X
2	6		○	○	○	○	○	○	X	X	X	X	X	X	X	X	X	X	X	X
3	6		○	○	○	○	○	○	X	X	X	X	X	X	X	X	X	X	X	X
4	6		○	○	○	○	○	○	X	X	X	X	X	X	X	X	X	X	X	X
5	6		○	○	○	○	○	○	X	X	X	X	X	X	X	X	X	X	X	X
6	6		○	○	○	○	○	○	X	X	X	X	X	X	X	X	X	X	X	X
7	6		○	○	○	○	○	○	X	X	X	X	X	X	X	X	X	X	X	X
8	6		○	○	○	○	○	○	X	X	X	X	X	X	X	X	X	X	X	X
9	6		○	○	○	○	○	○	X	X	X	X	X	X	X	X	X	X	X	X

x 26-base staple DNA ○ 36-base staple DNA set E1

b

MEO-L3	row number	number of expansion strands	loop number																	
			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
	1	12	○	○	○	○	○	○	○	○	○	○	○	○	○	X	X	X	X	X
2	12		○	○	○	○	○	○	○	○	○	○	○	○	X	X	X	X	X	X
3	12		○	○	○	○	○	○	○	○	○	○	○	○	X	X	X	X	X	X
4	12		○	○	○	○	○	○	○	○	○	○	○	○	X	X	X	X	X	X
5	12		○	○	○	○	○	○	○	○	○	○	○	○	X	X	X	X	X	X
6	12		○	○	○	○	○	○	○	○	○	○	○	○	X	X	X	X	X	X
7	12		○	○	○	○	○	○	○	○	○	○	○	○	X	X	X	X	X	X
8	12		○	○	○	○	○	○	○	○	○	○	○	○	X	X	X	X	X	X
9	12		○	○	○	○	○	○	○	○	○	○	○	○	X	X	X	X	X	X

x 26-base staple DNA ○ 36-base staple DNA set E1 ○ 36-base staple DNA set E4

c

MEO-36	row number	number of expansion strands	loop number																	
			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
	1	19	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○
2	19		○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○
3	19		○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○
4	19		○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○
5	19		○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○
6	19		○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○
7	19		○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○
8	19		○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○
9	19		○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○

x 26-base staple DNA ○ 36-base staple DNA set E1 ○ 36-base staple DNA set E4

○ 36-base staple DNA set E5

Figure S9. Illustration of distribution of expansion staples used for conformation MEO-L1 (a), MEO-L3 (b), and MEO-36 (c).

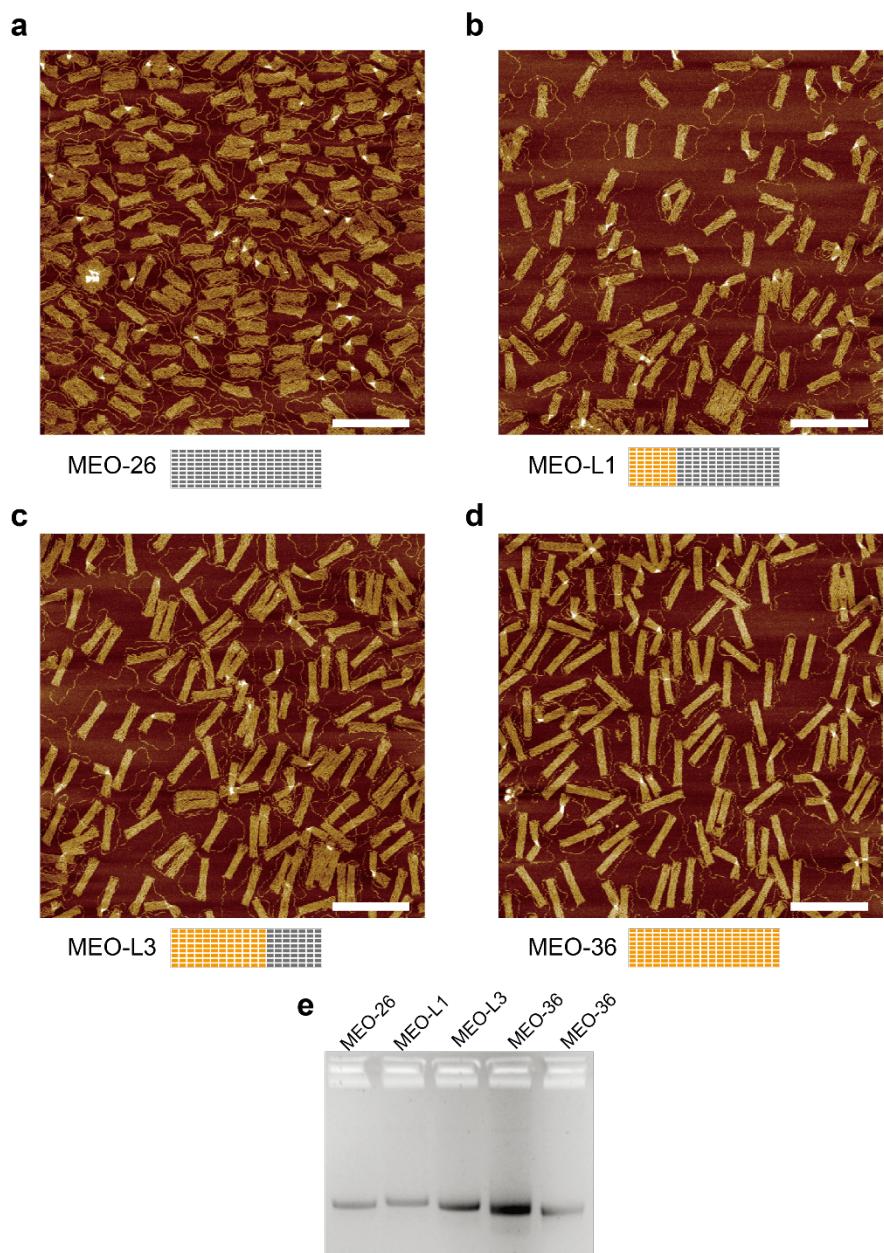


Figure S10. AFM imaging of multi-step expansion of MEO-26 (a) into MEO-L1 (b), MEO-L3 (c) and MEO-36 (d) using expansion set E1, E4 and E5, respectively. Scale bar: 400 nm. e) Agarose gel electrophoresis of MEO-26 and the expansion products MEO-L1, MEO-L3, MEO-36 and MEO-36 from one-pot assembly.

Curvature calculation of DNA origami structure. For a curved structure (in green) with a radian θ and inner radius r , there are mathematical relations as follow:

$$\sin\left(\frac{\theta}{2}\right) = \frac{d}{2} \div r,$$

$$L = r \cdot \theta,$$

then the θ is in relationship with L and d in the function:

$$\sin\left(\frac{\theta}{2}\right) \div \left(\frac{\theta}{2}\right) = \frac{d}{L},$$

where the arc length L and chord length d can be measured from AFM images. Monte Carlo simulation was employed to calculate θ . We set the value for θ from 0 to π with 1×10^{-7} increment. The error $e = |\sin\left(\frac{\theta}{2}\right) \div \left(\frac{\theta}{2}\right) - \frac{d}{L}|$ will reflect the closeness to the real value. The θ to get $e \ll 1 \times 10^{-7}$ would be accepted and convert into degree for the curvature of the structure.

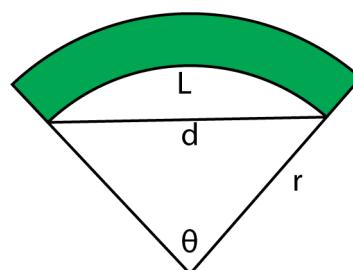


Figure S11. Schematic of curved structure with measured arch length and chord length to calculate the central angle.

a

row number	number of expansion strands	loop number																		
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
MEO-C1	12	X	O	O	X	O	O	X	O	O	X	O	O	X	O	O	X	O	O	X
	11	O	X	O	O	X	X	O	O	X	O	X	O	O	X	X	O	O	X	O
	10	O	X	O	X	O	X	O	X	O	X	O	X	O	X	O	X	O	X	O
	9	X	O	X	O	X	O	X	O	X	O	X	O	X	O	X	O	X	O	X
	4	X	X	X	O	X	X	X	O	X	X	X	X	O	X	X	X	O	X	X
	3	X	X	X	X	O	X	X	X	X	O	X	X	X	X	O	X	X	X	X
	2	X	X	X	X	X	O	X	X	X	O	X	X	X	O	X	X	X	X	X
	1	X	X	X	X	X	X	X	X	X	O	X	X	X	X	X	X	X	X	X
	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X

X 26-base staple DNA

O 36-base staple DNA set E6

b

row number	number of expansion strands	loop number																		
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
MEO-C2	19	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O
	18	O	O	O	O	O	O	O	O	O	X	O	O	O	O	O	O	O	O	O
	17	O	O	O	O	O	O	X	O	O	O	O	O	O	O	O	O	O	O	O
	16	O	O	X	O	O	O	O	O	O	O	O	O	O	O	O	O	O	X	O
	4	X	X	X	O	X	X	X	O	X	X	X	O	X	X	O	X	X	X	X
	3	X	X	X	X	O	X	X	X	X	O	X	X	X	X	O	X	X	X	X
	2	X	X	X	X	X	O	X	X	X	O	X	X	X	X	O	X	X	X	X
	1	X	X	X	X	X	X	X	X	X	O	X	X	X	X	X	X	X	X	X
	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X

X 26-base staple DNA

O 36-base staple DNA set E7

c

row number	number of expansion strands	loop number																		
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
MEO-C3	19	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O
	19	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O
	18	O	O	O	O	O	O	X	O	O	O	O	O	O	O	O	O	O	O	O
	17	O	O	X	O	O	O	O	O	O	O	O	O	O	O	O	O	O	X	O
	15	O	X	O	O	O	O	O	X	O	O	O	O	O	O	O	O	O	X	O
	13	X	O	O	X	O	O	O	X	O	O	O	X	O	O	O	X	O	O	X
	11	O	X	O	O	X	X	O	O	X	O	X	O	O	X	O	X	O	O	X
	9	X	O	X	O	X	O	X	O	X	O	X	O	X	O	X	O	X	O	X
	7	O	X	X	O	X	X	O	X	X	O	X	X	O	X	O	X	X	O	X

X 26-base staple DNA

O 36-base staple DNA set E8

Figure S12. Illustration of distribution of expansion staples used for one-step expansion to conformation MEO-C1, MEO-C2 and MEO-C3.

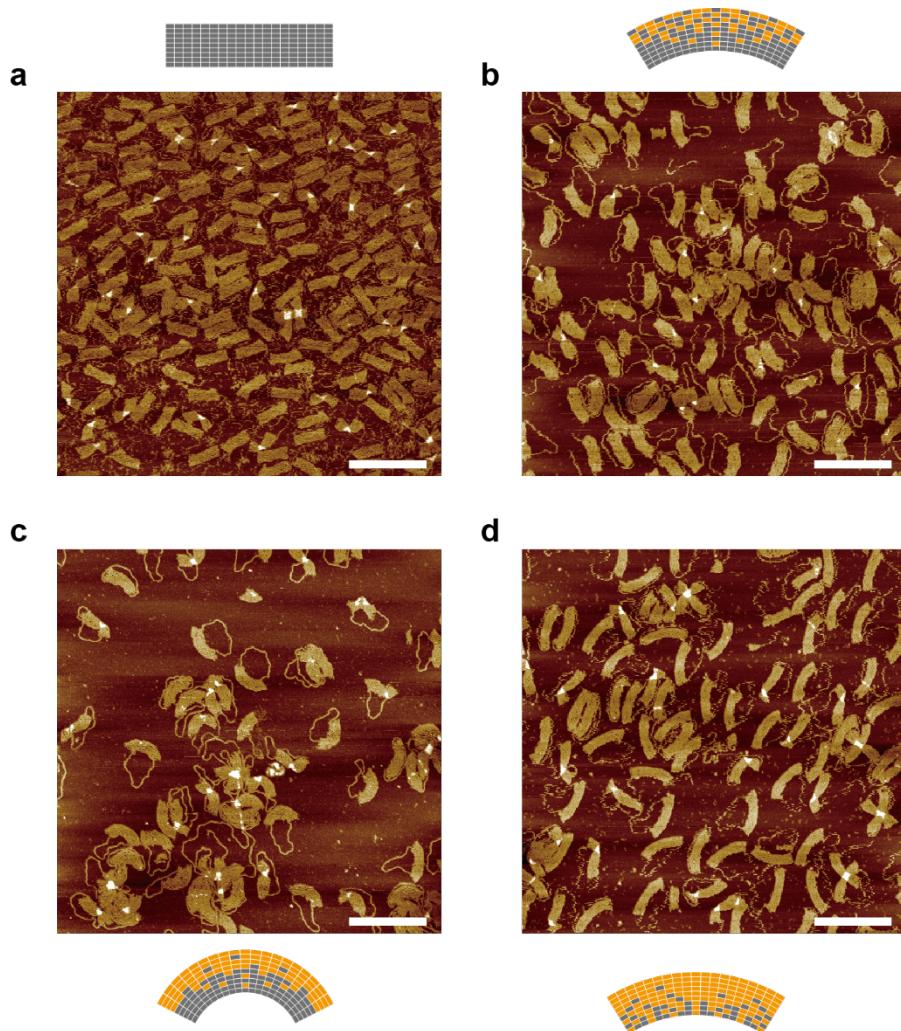


Figure S13. AFM imaging of one-step expansion of MEO-26 (a) into curved conformation MEO-C1 (b), MEO-C2 (c), MEO-C3 (d) using expansion set E6, E7 and E8, respectively. Scale bar: 400 nm.

a

MEO-C2	row number	number of expansion strands	loop number																	
			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
	1	19	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○
	2	18	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○
	3	17	○	○	○	○	○	○	X	○	○	○	○	○	○	X	○	○	○	○
	4	16	○	○	X	○	○	○	○	○	○	○	○	X	○	○	○	○	X	○
	5	4	X	X	X	○	X	X	X	○	X	X	X	○	X	X	X	○	X	X
	6	3	X	X	X	X	○	X	X	X	○	X	X	○	X	X	○	X	X	X
	7	2	X	X	X	X	X	X	○	X	X	X	X	○	X	X	X	X	X	X
	8	1	X	X	X	X	X	X	X	X	○	X	X	X	X	X	X	X	X	X
	9	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X

■ X 26-base staple DNA ■ ○ 36-base staple DNA set E6 ■ ○ 36-base staple DNA set E9

b

MEO-C3	row number	number of expansion strands	loop number																	
			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
	1	19	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○
	2	19	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○
	3	18	○	○	○	○	○	○	X	○	○	○	○	○	○	○	○	○	○	○
	4	17	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	X	○
	5	15	○	X	○	○	○	○	○	X	○	○	○	○	○	○	○	○	X	○
	6	13	X	○	○	X	○	○	○	○	X	○	○	○	○	X	○	○	○	X
	7	11	○	X	○	○	X	X	○	○	X	○	X	○	○	X	X	○	O	X
	8	9	X	○	X	○	X	X	○	X	○	X	○	X	○	X	O	X	○	X
	9	7	○	X	X	○	X	X	○	X	X	○	X	X	○	X	X	O	X	X

■ X 26-base staple DNA ■ ○ 36-base staple DNA set E6 ■ ○ 36-base staple DNA set E9

■ ○ 36-base staple DNA set E10

c

MEO-36	row number	number of expansion strands	loop number																	
			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
	1	19	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○
	2	19	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○
	3	19	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○
	4	19	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○
	5	19	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○
	6	19	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○
	7	19	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○
	8	19	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○
	9	19	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○

■ X 26-base staple DNA ■ ○ 36-base staple DNA set E6 ■ ○ 36-base staple DNA set E9

■ ○ 36-base staple DNA set E10 ■ ○ 36-base staple DNA set E11

Figure S14. Illustration of distribution of expansion staples used for conformation MEO-C2 (a), MEO-C3 (b) and MEO-36 (c).

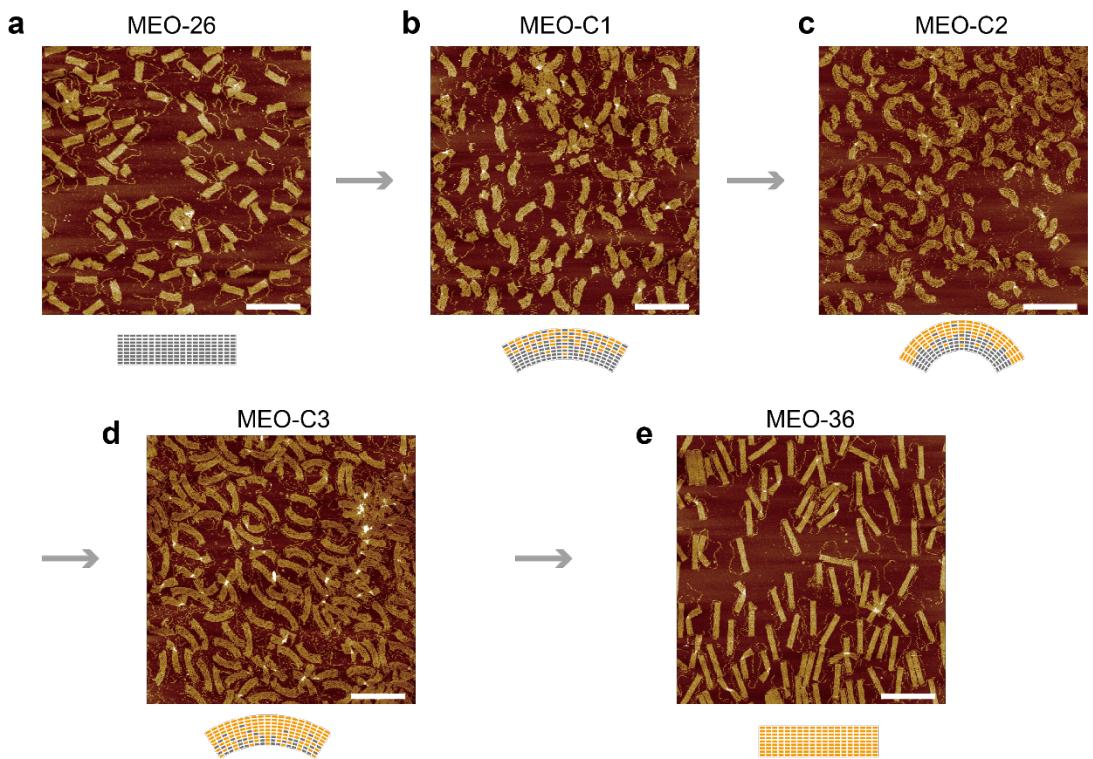


Figure S15. AFM imaging of multi-step expansion of MEO-26 (a) into MEO-C1 (b), MEO-C2 (c), MEO-C3 (d) and MEO-36 (e) by adding expansion set E6, E9, E10 and E11 continuously. Scale bar: 400 nm.

a

	row number	number of expansion strands for left part	loop number																			number of expansion strands for right part
			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	
MEO-C5	1	10	O	O	O	O	O	O	O	O	X	X	X	X	X	X	X	X	X	X	X	0
	2	9	O	O	O	O	X	O	O	O	X	X	X	X	X	X	X	X	X	X	X	0
	3	8	O	O	X	O	O	O	O	X	O	O	X	X	X	X	X	X	X	X	X	0
	4	7	O	X	O	O	X	O	O	O	X	O	O	X	X	X	X	X	X	X	X	0
	5	4	X	O	X	O	X	X	O	X	O	X	X	X	X	X	X	X	X	X	X	0
	6	3	O	X	X	X	X	O	X	X	X	O	X	X	X	X	X	X	X	X	X	0
	7	2	X	X	O	X	X	X	X	O	X	X	X	X	X	X	X	X	X	X	X	0
	8	1	X	X	X	X	O	X	X	X	X	X	X	X	X	X	X	X	X	X	X	0
	9	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	0

x 26-base staple DNA

o 36-base staple DNA set E12

b

	row number	number of expansion strands for left part	loop number																			number of expansion strands for right part
			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	
MEO-C6	1	10	O	O	O	O	O	O	O	O	X	X	X	X	X	X	X	X	X	X	X	0
	2	9	O	O	O	O	X	O	O	O	X	X	X	X	X	X	X	X	X	X	X	0
	3	8	O	O	X	O	O	O	O	X	O	O	X	X	X	X	O	X	X	X	X	1
	4	7	O	X	O	O	X	O	O	O	X	O	O	X	X	O	X	X	X	O	X	2
	5	4	X	O	X	O	X	X	O	X	O	O	O	X	X	O	X	X	X	O	O	3
	6	3	O	X	X	X	O	X	X	X	O	O	O	O	O	O	O	X	O	O	O	6
	7	2	X	X	O	X	X	X	X	O	X	X	O	O	O	O	X	O	X	O	O	7
	8	1	X	X	X	X	O	X	X	X	O	O	O	O	O	O	O	X	O	O	O	8
	9	0	X	X	X	X	X	X	X	X	O	O	O	O	O	O	O	O	O	O	O	9

x 26-base staple DNA

o 36-base staple DNA set E12

o 36-base staple DNA set E13

o 36-base staple DNA set E14

c

	row number	number of expansion strands for left part	loop number																			number of expansion strands for right part
			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	
MEO-C7	1	10	O	O	O	O	O	O	O	O	X	X	X	X	X	X	X	X	X	X	X	0
	2	10	O	O	O	O	O	O	O	O	X	X	X	X	X	X	X	X	X	X	X	0
	3	10	O	O	O	O	O	O	O	O	X	X	X	X	X	O	X	X	X	X	X	1
	4	10	O	O	O	O	O	O	O	O	X	X	O	X	X	O	X	X	O	X	X	2
	5	10	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	3
	6	10	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	X	O	X	O	6
	7	10	O	O	O	O	O	O	O	O	O	O	O	O	O	O	X	O	X	O	O	7
	8	10	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	8
	9	10	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	9

x 26-base staple DNA

o 36-base staple DNA set E12

o 36-base staple DNA set E13

o 36-base staple DNA set E14

d

	row number	number of expansion strands for left part	loop number																			number of expansion strands for right part
			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	
MEO-36	1	10	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	9
	2	10	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	9
	3	10	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	9
	4	10	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	9
	5	10	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	9
	6	10	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	9
	7	10	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	9
	8	10	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	9
	9	10	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	9

x 26-base staple DNA

o 36-base staple DNA set E12

o 36-base staple DNA set E13

o 36-base staple DNA set E14

Figure S16. Illustration of distribution of expansion staples used for conformation MEO-C5 (a), MEO-C6 (b), MEO-C7 (c) and MEO-36 (d).

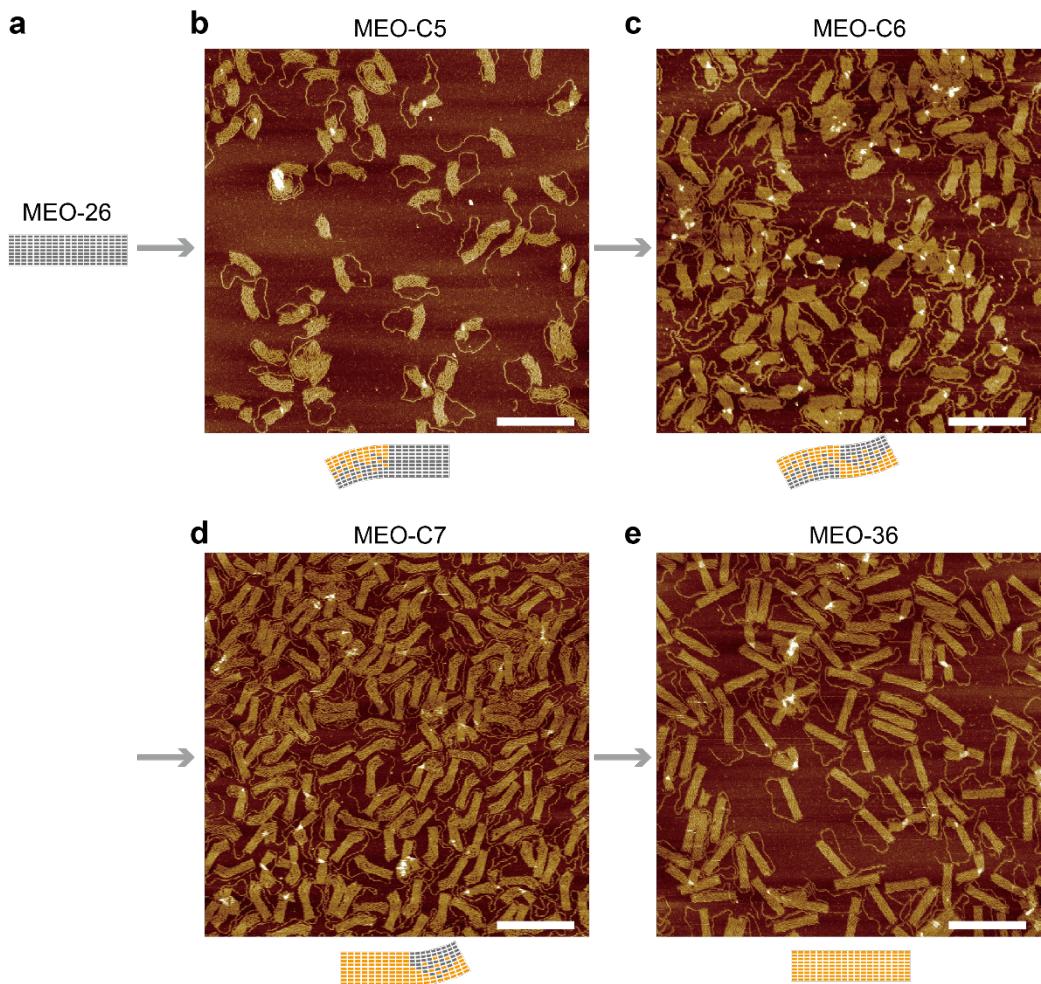


Figure S17. Modular expansion of MEO for curved conformation. MEO-26 (a) was modularly and step-wisely expanded into MEO-C5 (b), MEO-C6 (c), MEO-C7 (d) and MEO-36 (e) using expansion set E12, E13, E14 and E15, respectively. Scale bar: 400 nm.

a

row number	number of expansion strands for left part	loop number																			number of expansion strands for right part
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	
MEO-C4	10	○	○	○	○	○	○	○	○	○	X	X	X	X	X	X	X	X	X	0	
	9	○	○	○	○	○	○	○	○	X	○	X	X	X	X	X	X	X	X	0	
	9	○	○	○	○	○	X	○	○	○	X	X	X	X	X	X	X	X	X	0	
	9	○	○	X	○	○	○	○	○	○	X	X	X	X	X	X	X	X	X	0	
	2	X	X	X	○	X	X	X	○	X	X	X	X	X	X	X	X	X	X	0	
	2	X	X	X	X	○	X	X	X	○	X	X	X	X	X	X	X	X	X	0	
	1	X	X	X	X	X	○	X	X	X	X	X	X	X	X	X	X	X	X	0	
	1	X	X	X	X	X	X	X	X	○	X	X	X	X	X	X	X	X	X	0	
	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	0	

X 26-base staple DNA ○ 36-base staple DNA set E16

b

row number	number of expansion strands for left part	loop number																			number of expansion strands for right part
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	
MEO-C2	10	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	9	
	9	○	○	○	○	○	○	○	○	X	○	○	○	○	○	○	○	○	○	9	
	9	○	○	○	○	○	X	○	○	○	○	○	○	○	X	○	○	○	○	8	
	9	○	○	X	○	○	○	○	○	○	X	○	○	○	○	○	○	X	○	7	
	2	X	X	X	○	X	X	X	○	X	X	X	○	X	X	X	○	X	X	2	
	2	X	X	X	X	○	X	X	X	○	X	X	X	X	○	X	X	X	X	1	
	1	X	X	X	X	X	○	X	X	X	X	X	X	○	X	X	X	X	X	1	
	1	X	X	X	X	X	X	X	X	○	X	X	X	X	X	X	X	X	X	0	
	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	0	

X 26-base staple DNA ○ 36-base staple DNA set E16 ○ 36-base staple DNA set E17

Figure S18. Illustration of distribution of expansion staples used for conformation MEO-C4 (a), and MEO-C2 (b).

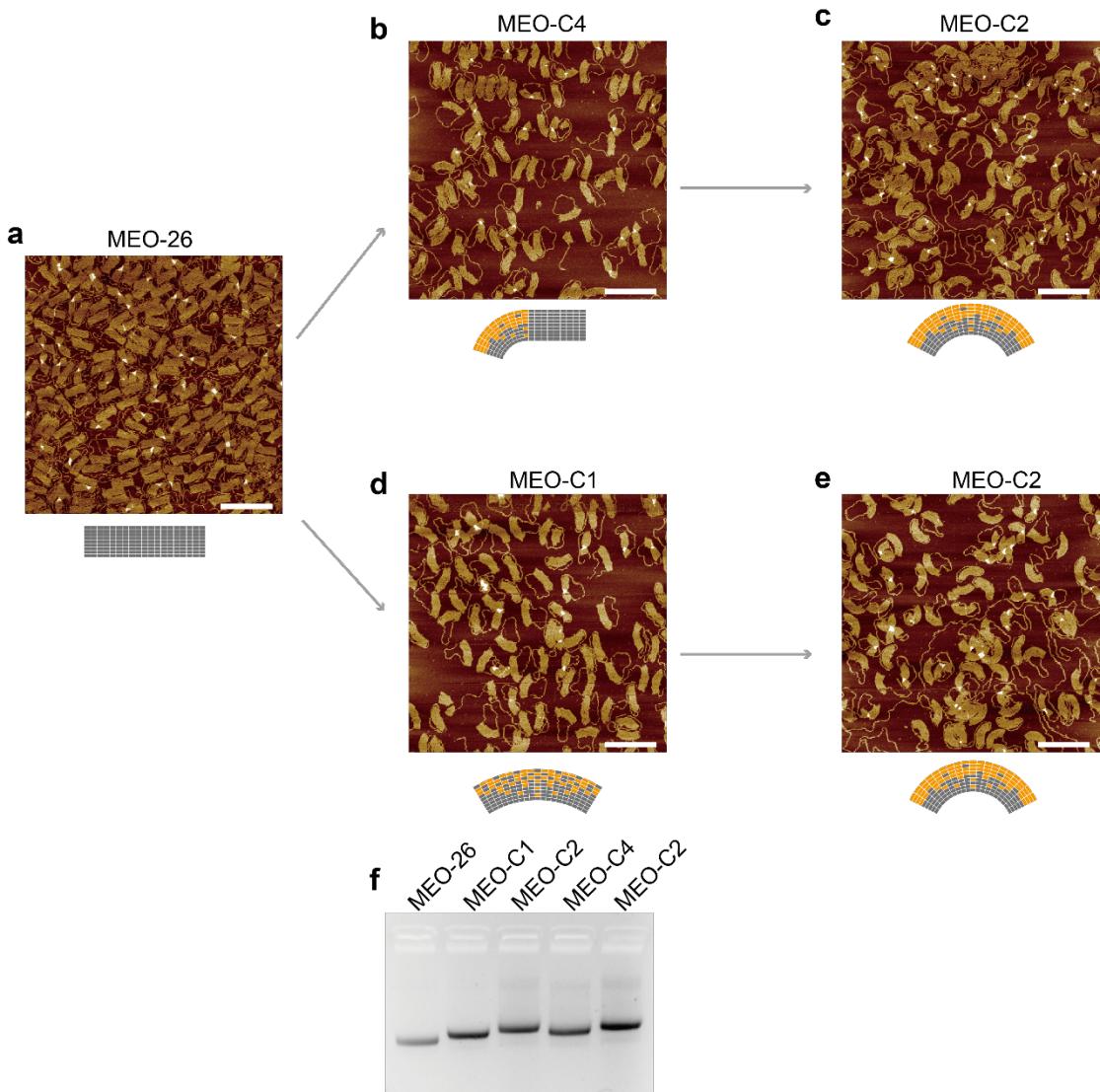


Figure S19. Alternative pathways for achieving curvature control of MEO-C2. Pathway 1: MEO-26 (a) was expanded into MEO-C4 (b) and MEO-C2 (c) by expansion set E16 and E17 continuously. Pathway 2: MEO-26 was expanded into MEO-C1 and MEO-C2 by expansion set E6 and E7 continuously. Scale bar: 400 nm. f) Agarose gel electrophoresis of MEO-26 and the expansion products MEO-C1, MEO-C2 and MEO-C4.

MEO-C8	row number	number of expansion strands	loop number																	
			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
	1	12	X	O	O	O	X	O	X	O	X	O	O	O	X	O	X	O	O	X
	2	11	O	X	O	O	O	X	O	O	X	X	O	X	O	X	X	O	O	X
	3	10	O	O	X	O	X	X	O	O	X	O	X	O	X	O	X	O	X	O
	4	9	X	O	O	X	O	X	O	X	O	X	O	X	O	X	X	O	O	X
	5	4	X	X	X	O	X	X	X	O	X	X	X	O	X	X	X	O	X	X
	6	3	X	X	X	X	O	X	X	X	O	X	X	X	X	O	X	X	X	X
	7	2	X	X	X	X	X	X	O	X	X	X	X	X	O	X	X	X	X	X
	8	1	X	X	X	X	X	X	X	X	O	X	X	X	X	X	X	X	X	X
	9	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X

X | 26-base staple DNA

O | 36-base staple DNA set E18

Figure S20. Illustration of distribution of expansion staples used for conformation MEO-C8.

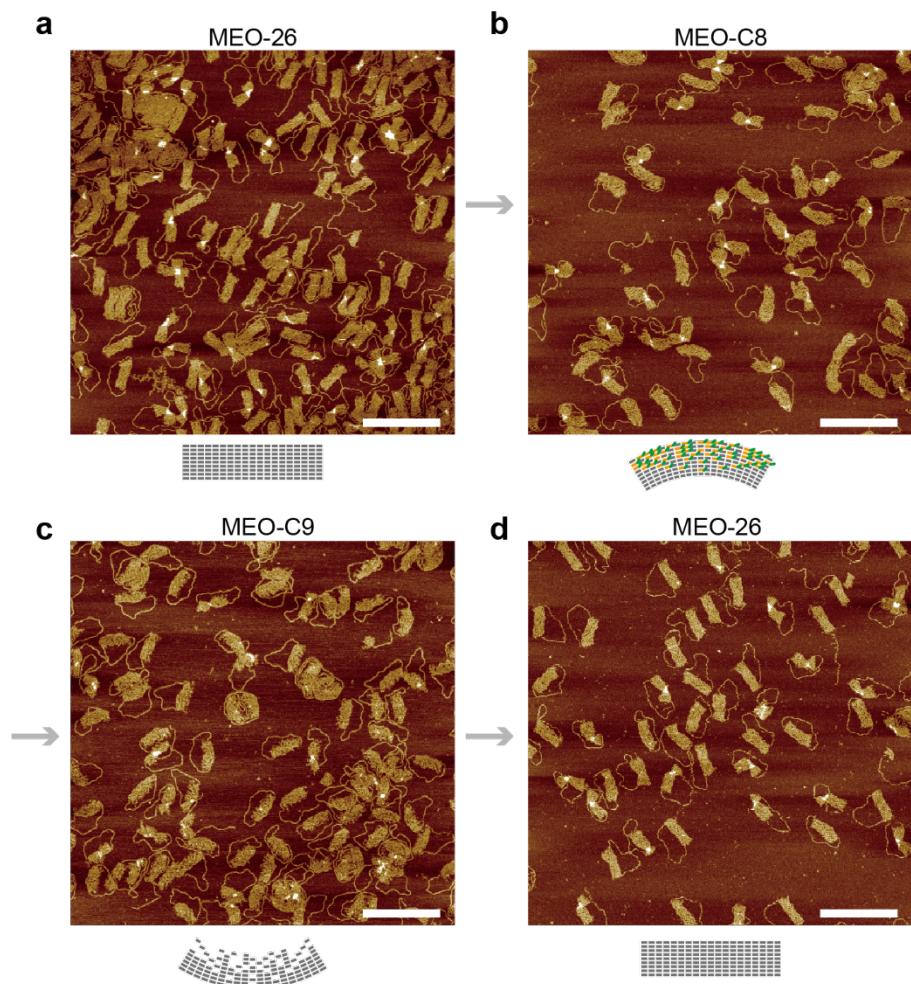
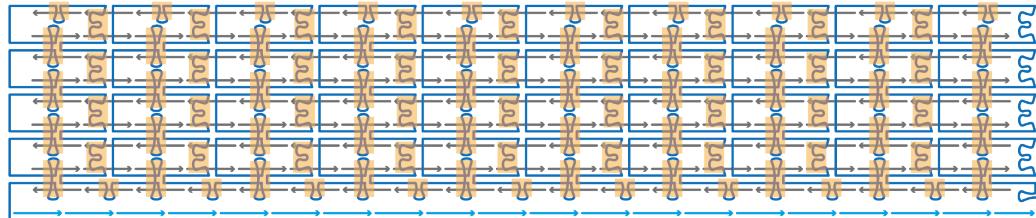


Figure S21. Reversible control for curved DNA structure by expansion. MEO-26 (a) was incubated expansion strand set E18 to generate curved conformation MEO-C8 (b). The expansion strand DNA was modified with 6-nt toehold. Then the expansion strand DNA was removed by the complementary DNA, resulting in MEO-C9 (c). After purification, the samples were incubated with 26-base staple DNA to recover the conformation MEO-26 (d). Scale bar: 400 nm.

a**b**

	row number	number of expansion strands	loop number																		
			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
MEO-C10	1	12	○	X	○	X	○	○	○	X	○	X	○	X	○	○	○	X	○	X	○
	2	11	○	X	○	X	○	○	○	X	○	X	○	X	○	○	○	X	○	X	○
	3	10	○	X	○	X	○	X	○	X	○	X	○	X	○	○	○	X	○	X	○
	4	9	X	X	○	X	○	X	○	X	○	X	○	X	○	○	○	X	○	X	○
	5	4	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	○
	6	3	X	X	X	X	○	X	X	X	X	X	X	X	X	○	○	X	X	X	X
	7	2	X	X	X	X	○	X	X	X	X	X	X	X	X	X	○	X	X	X	X
	8	1	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
	9	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X

X 26-base staple DNA

○ 36-base staple DNA set E1

c

	row number	number of expansion strands	loop number																		
			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
MEO-C11	1	12	X	○	○	○	X	○	X	○	○	X	○	X	○	○	○	X	○	X	○
	2	11	○	X	○	X	○	○	○	X	○	X	○	X	○	○	○	X	○	X	○
	3	10	X	○	X	○	X	○	X	○	X	○	X	○	○	○	X	○	X	○	X
	4	9	○	X	○	X	○	X	○	X	○	X	○	X	○	○	○	X	○	X	○
	5	4	X	X	X	○	X	X	X	○	X	X	X	○	X	X	○	X	X	X	X
	6	3	X	X	X	○	X	X	X	X	○	X	X	X	○	X	X	○	X	X	X
	7	2	X	X	X	X	X	X	X	○	X	X	X	X	○	X	X	X	X	X	X
	8	1	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
	9	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X

X 26-base staple DNA

○ 36-base staple DNA set E2

Figure S22. a) Illustration of DNA loop as flexible points in the DNA origami structure. Each 10-base or 20-base DNA loop represents a flexible point. Adding expansion strands will reduce the flexible points. Distribution of expansion staples used for conformation MEO-C10 (b) and MEO-C11 (c).

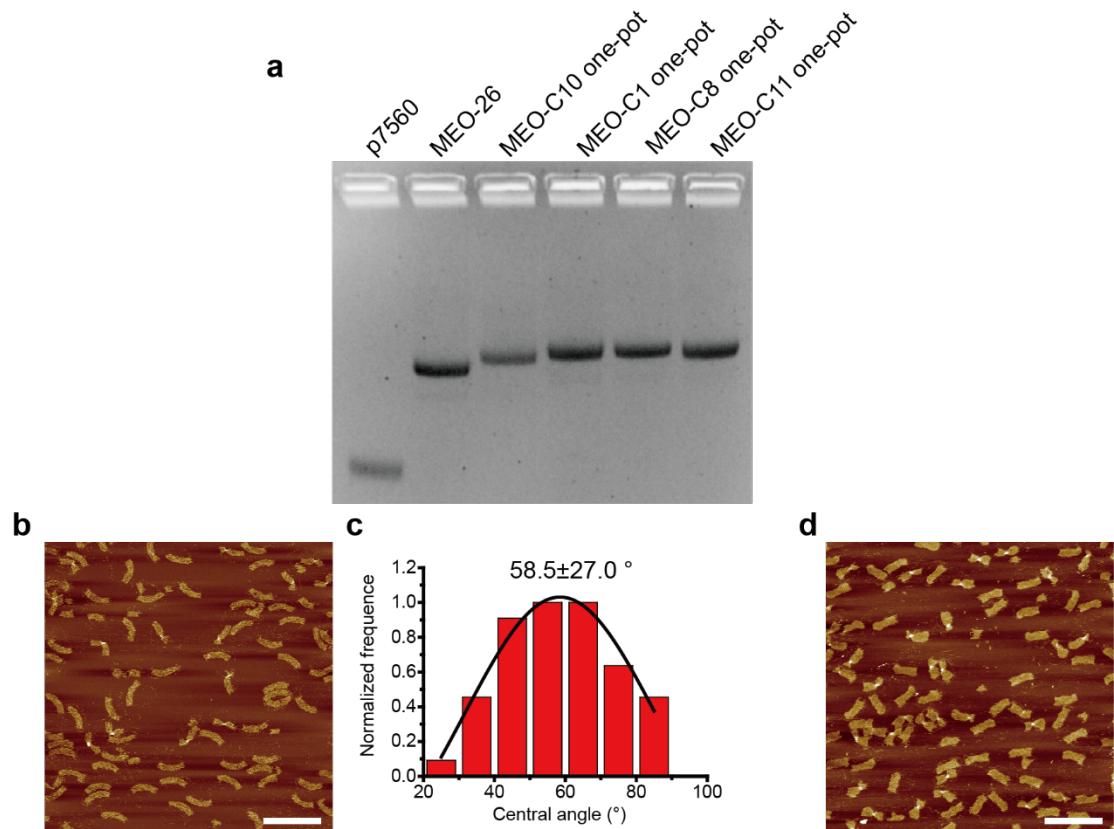


Figure S23. Effect of DNA loop number on the curvature of DNA origami structure. a) Agarose gel electrophoresis of MEO-26 and other conformations with same number of expansion strands but different distributions on the DNA origami array. AFM imaging of MEO-C10 (b) and MEO-C11 (d) and the histogram of curvature of MEO-C10 (c). Scale bar: 400nm.

a

row number	number of expansion strands	loop number																	
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
MEO-T1	19	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O
	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
	19	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O

x 26-base staple DNA

o 36-base staple DNA set E21

b

row number	number of expansion strands	loop number																	
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
MEO-T2	19	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O
	19	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O
	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
	19	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O
	19	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O

x 26-base staple DNA

o 36-base staple DNA set E22

c

row number	number of expansion strands	loop number																	
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
MEO-T3	19	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O
	19	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O
	19	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O
	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
	19	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O
	19	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O
	19	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O

x 26-base staple DNA

o 36-base staple DNA set E23

d

row number	number of expansion strands	loop number																	
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
MEO-T4	19	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O
	15	O	O	O	X	O	O	O	X	O	O	O	X	O	O	O	X	O	O
	10	O	X	O	X	O	X	O	X	O	X	O	X	O	X	O	X	O	X
	5	X	X	X	O	X	X	O	X	X	O	X	X	O	X	X	O	X	X
	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
	5	X	X	X	O	X	X	O	X	X	O	X	X	O	X	X	O	X	X
	10	O	X	O	X	O	X	O	X	O	X	O	X	O	X	O	X	O	X
	15	O	O	O	X	O	O	O	X	O	O	O	X	O	O	X	O	O	O
	19	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O

x 26-base staple DNA

o 36-base staple DNA set E24

Figure S24. Illustration of distribution of expansion staples used for conformation MEO-T1 (a), MEO-T2 (b), MEO-T3(c) and MEO-T4(d).

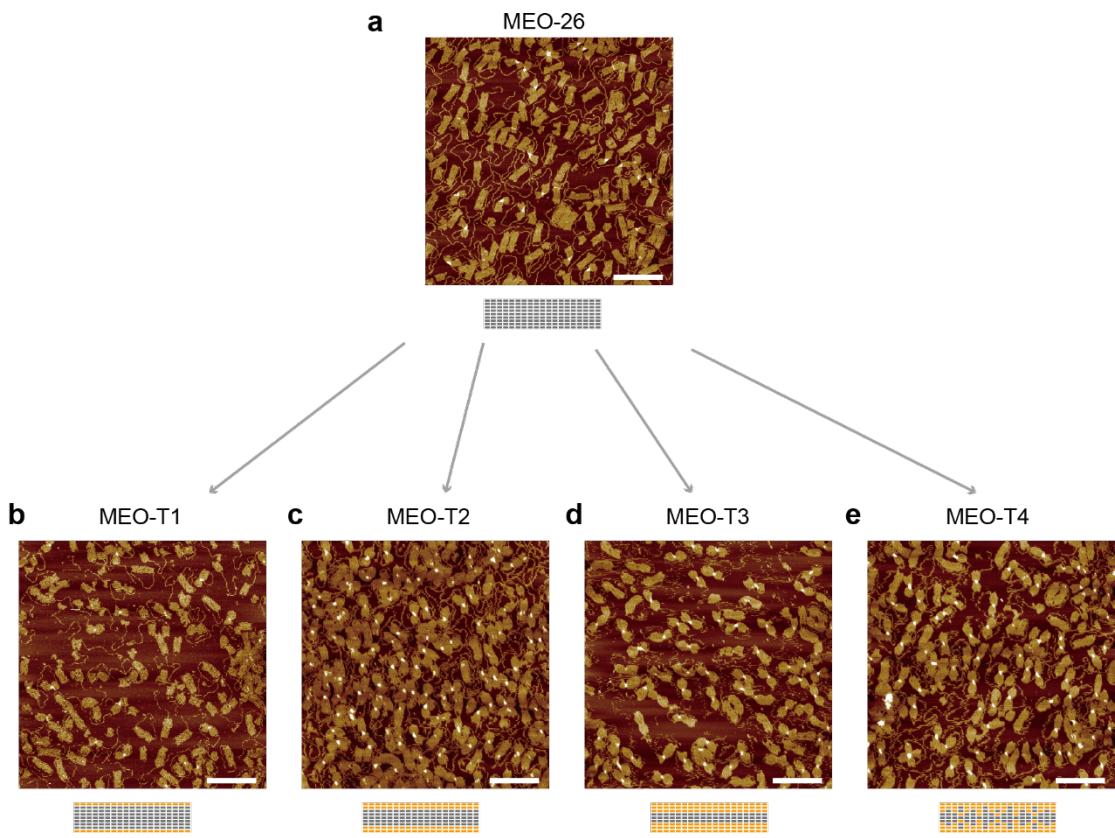


Figure S25. Twist control of MEO-26 by one-step expansion into conformation MEO-T1 (b), MEO-T2 (c), MEO-T3 (d) and MEO-T4 (e) using expansion set E21, E22, E23 and E24. Scale bar: 400 nm.

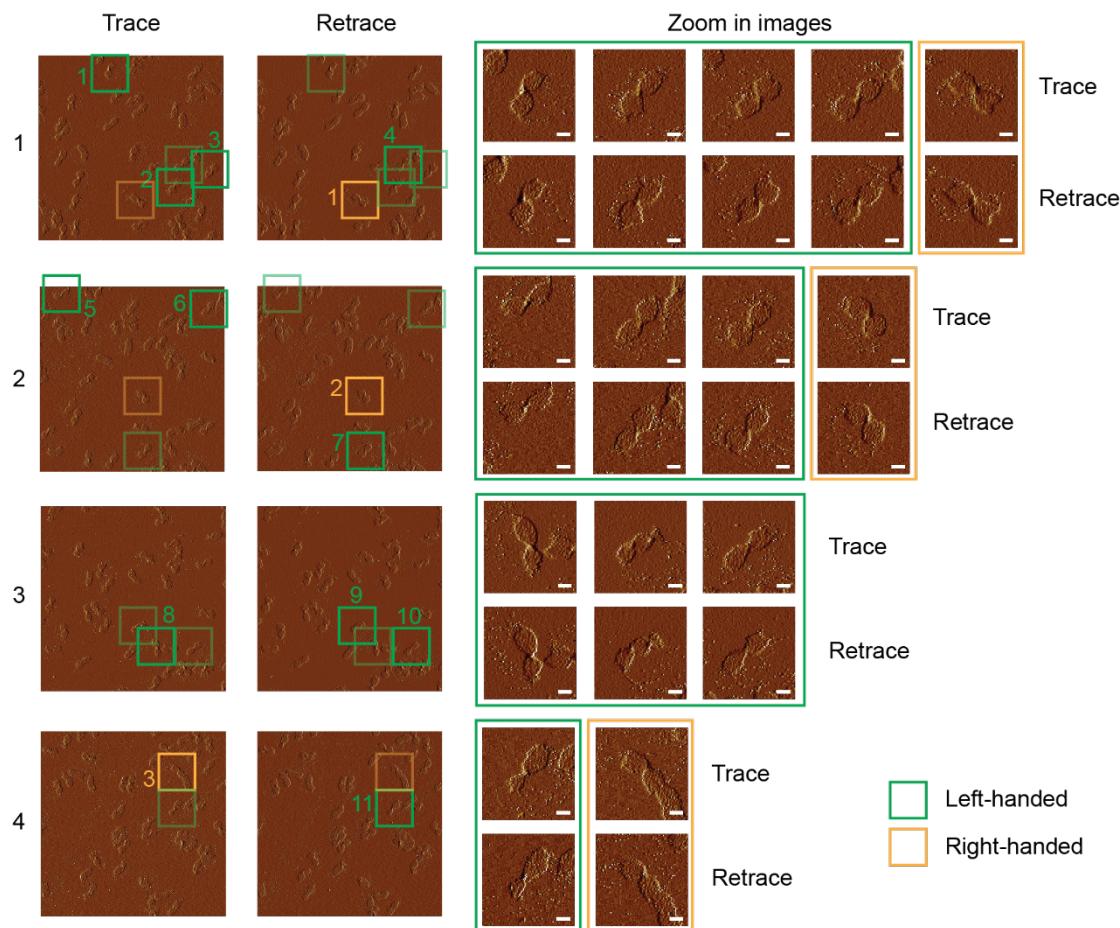


Figure S26. AFM amplitude imaging of sample MEO-T3 with the tip in trace and retrace direction to judge the chirality of the conformation. Scale bar: 50 nm.

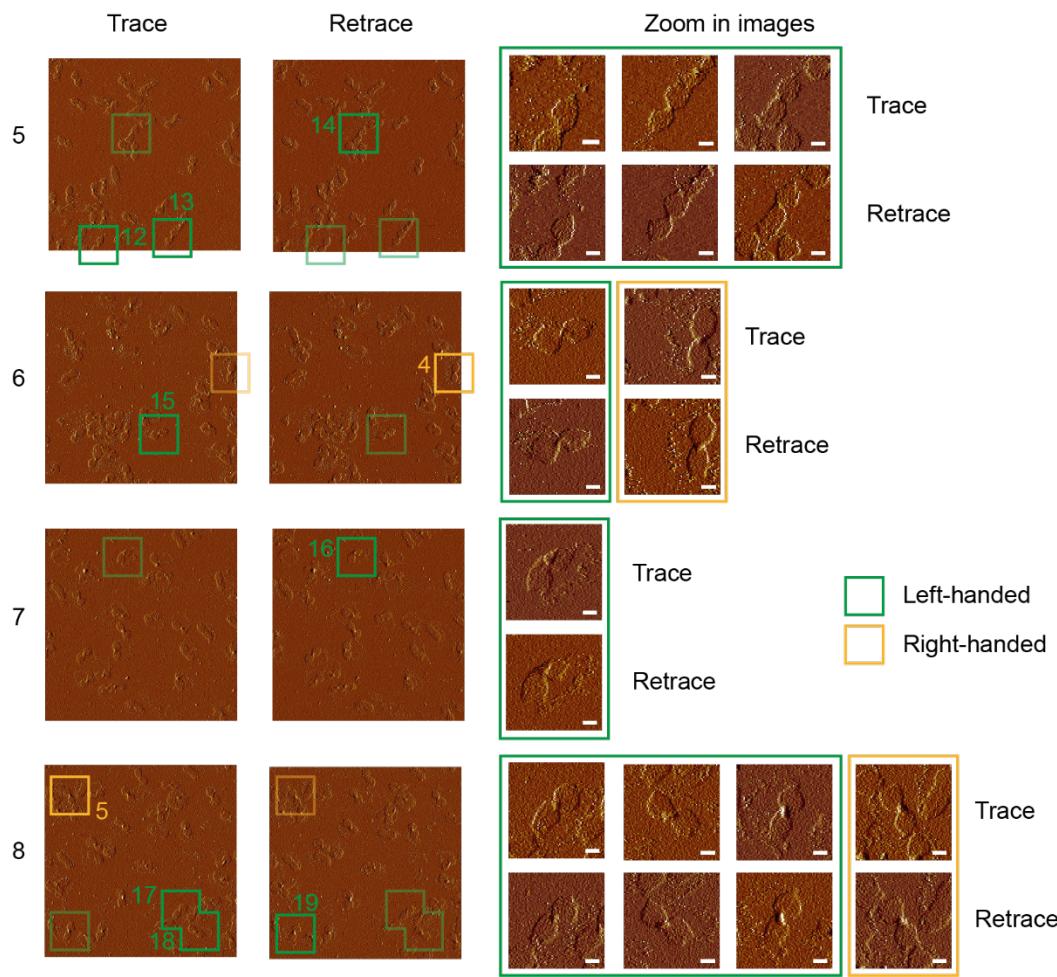


Figure S27. Additional AFM amplitude imaging of sample MEO-T3 with the tip in trace and retrace direction to judge the chirality of the conformation. Scale bar: 50 nm.

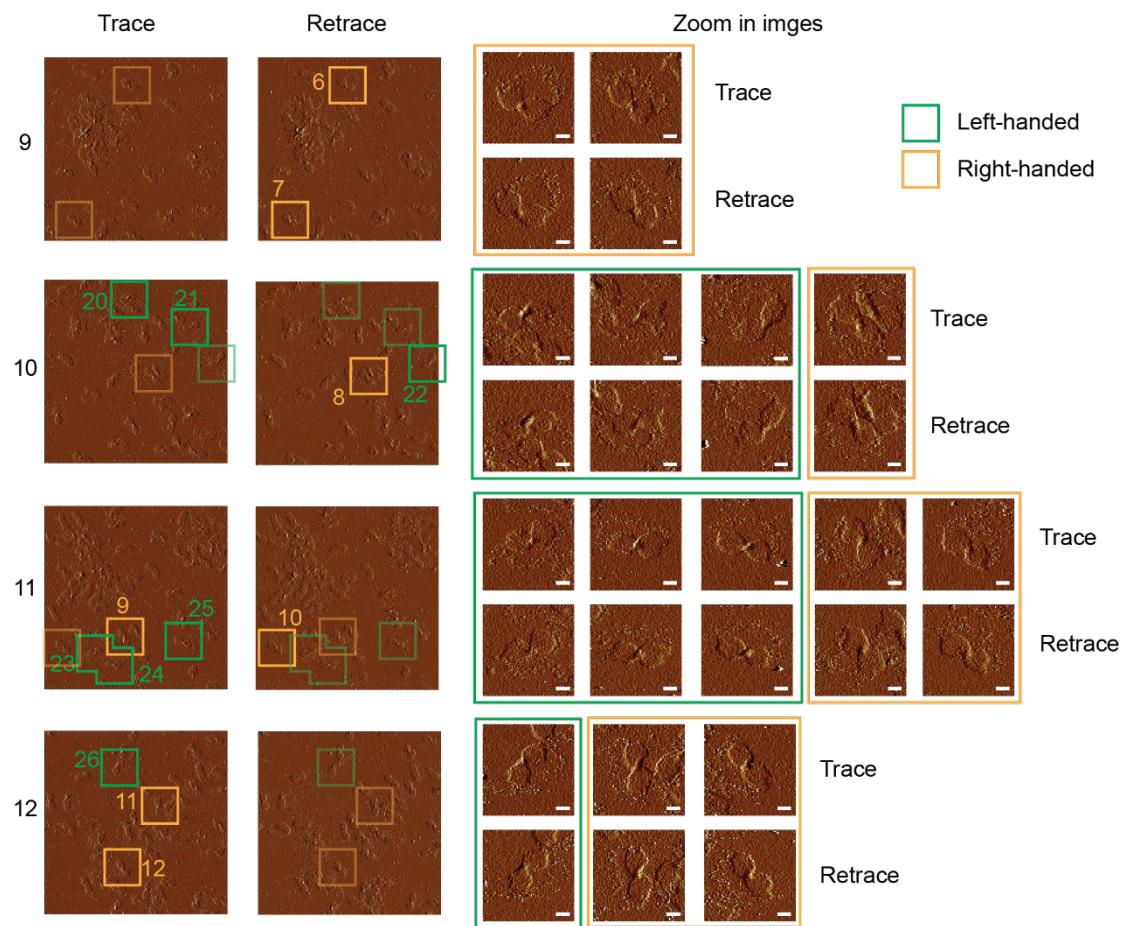


Figure S28. Additional AFM amplitude imaging of sample MEO-T3 with the tip in trace and retrace direction to judge the chirality of the conformation. Scale bar: 50 nm.

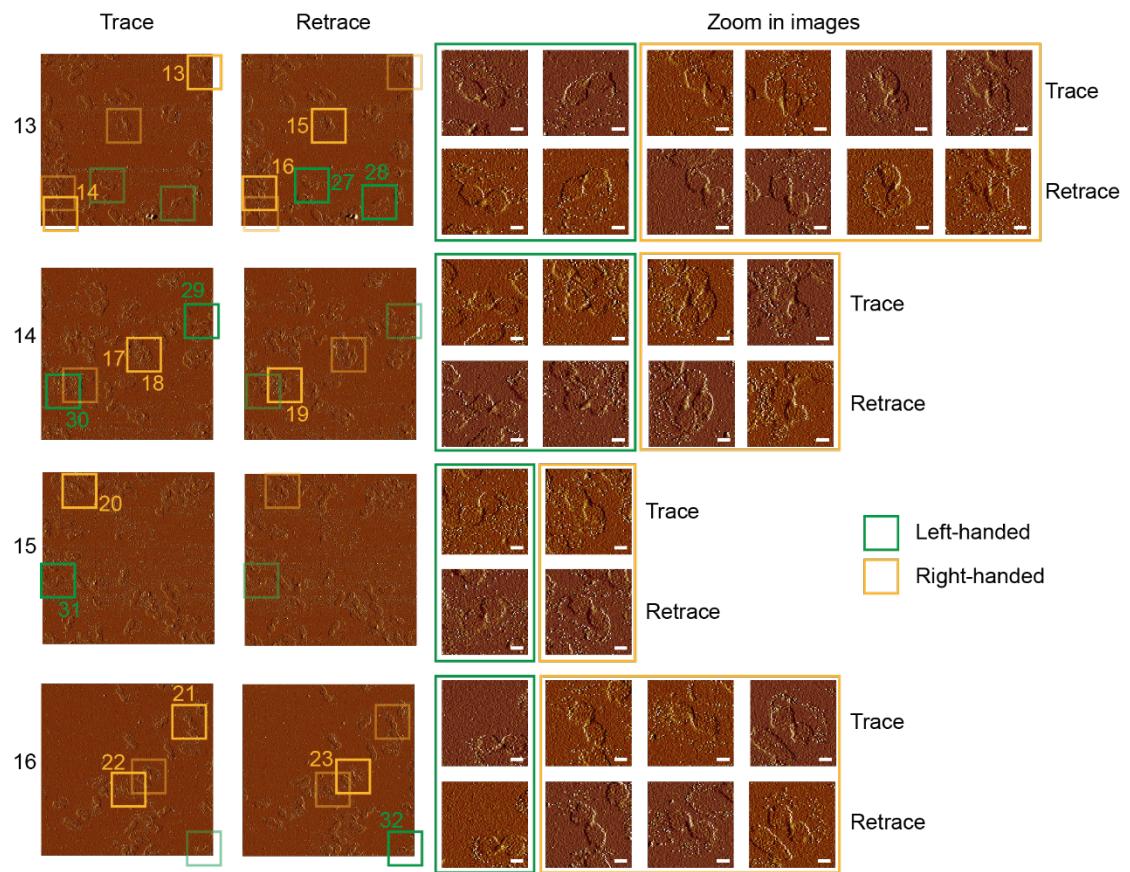


Figure S29. Additional AFM amplitude imaging of sample MEO-T3 with the tip in trace and retrace direction to judge the chirality of the conformation. Scale bar: 50 nm.

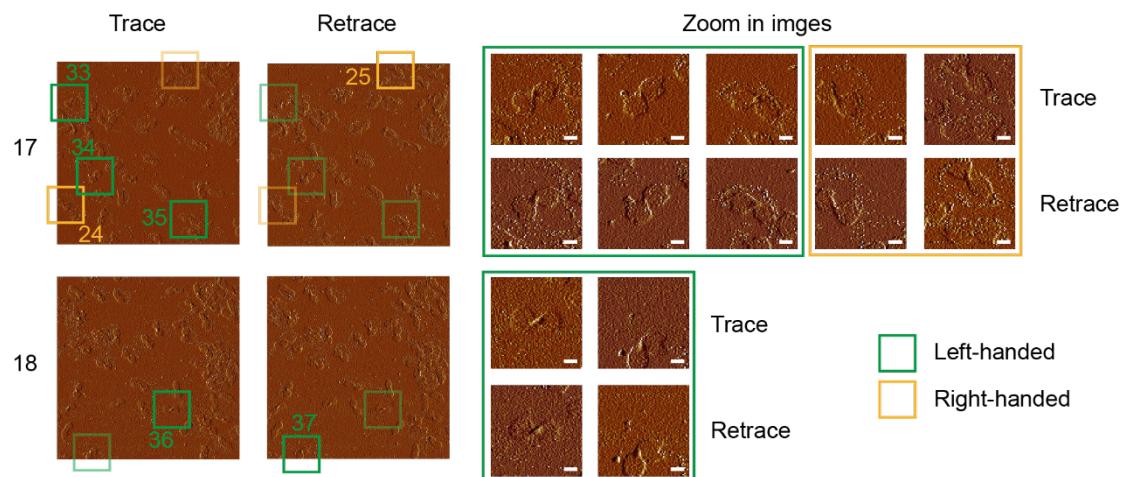


Figure S30. Additional AFM amplitude imaging of sample MEO-T3 with the tip in trace and retrace direction to judge the chirality of the conformation. Scale bar: 50 nm.

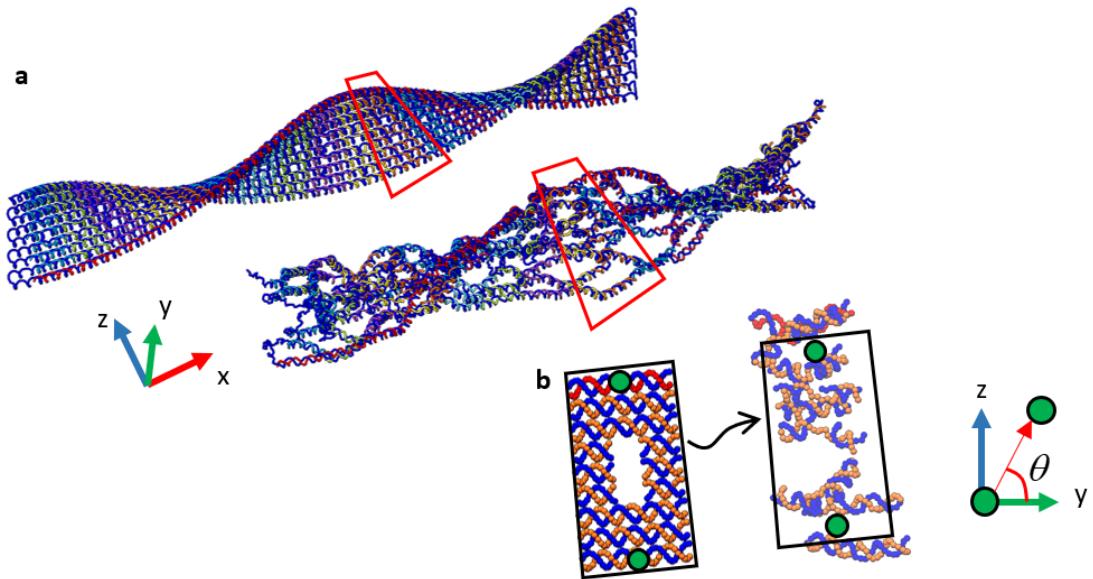


Figure S31. Schematic of procedure for calculating twist angles. a) To investigate the twist angle of MEO-T3, we created the initial configuration with different twist angles along the x direction. To calculate the twist angles, we divided the longitudinal length in each structure into 19 segments (each representing the array of 9 modules), as shown in different colors. b) After relaxation and equilibration, the twisted 3D conformation is coupled with other deformation modes, such as elongation and bending along the central axis. Therefore, to calculate the twist angle between adjacent segments, we used the SVD algorithm to transform (via a translation and rotation matrix $[T]$) each segment to the corresponding segment on the initial, idealized configuration, and then measure the relative twist angle between adjacent projected segments using select reference points on the structure (green circles).

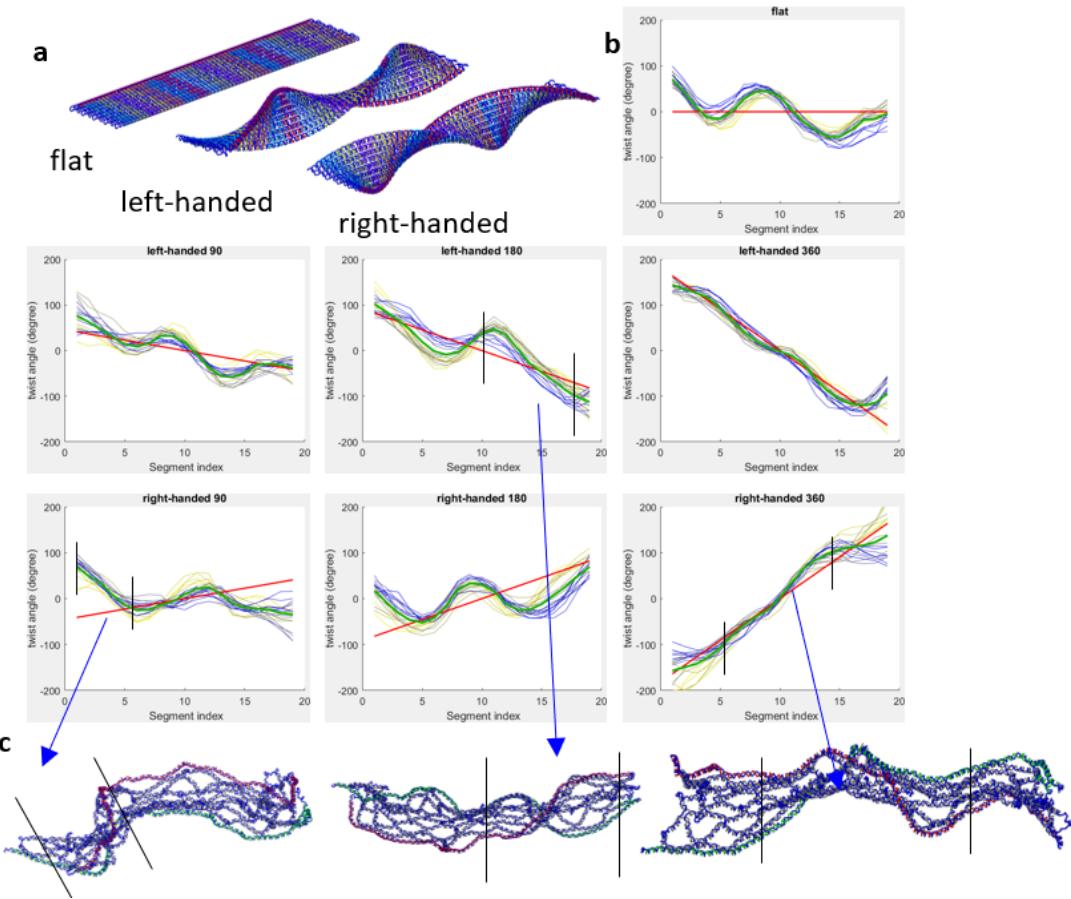


Figure S32. Quantitative estimation of the twist angle of MEO-T3. a) Initial configurations were created with the same topology, but with different levels of twist, such as flat, left-handed, or right-handed configurations. b) Simulation results of the twist angles. Initial configurations are specified in each plot and shown as red lines. After relaxation and equilibration, the MD trajectory yields a series of configurations in time, shown in yellow to blue. The green curve is the average curve across the entire trajectory, not the mean configuration. The simulations show that the possible twist angles in 3D solution are distributed across a wide range of left- and right-handed configurations. c) Visualization of the last configuration obtained from the MD trajectories initiated from right-handed-90, left-handed-180, and right-handed-180 configurations. The first and last row were rendered in red and green colors to better visualize the twist in each structure. Note that the twist angles are not uniformly distributed along the length of the structure but concentrate locally at certain regions. For example, the primary twist region are localized within the first one-quarter of the right-handed-90 structure, the last half of the left-handed-180 structure, and the middle portion of the right-handed-360 structure.

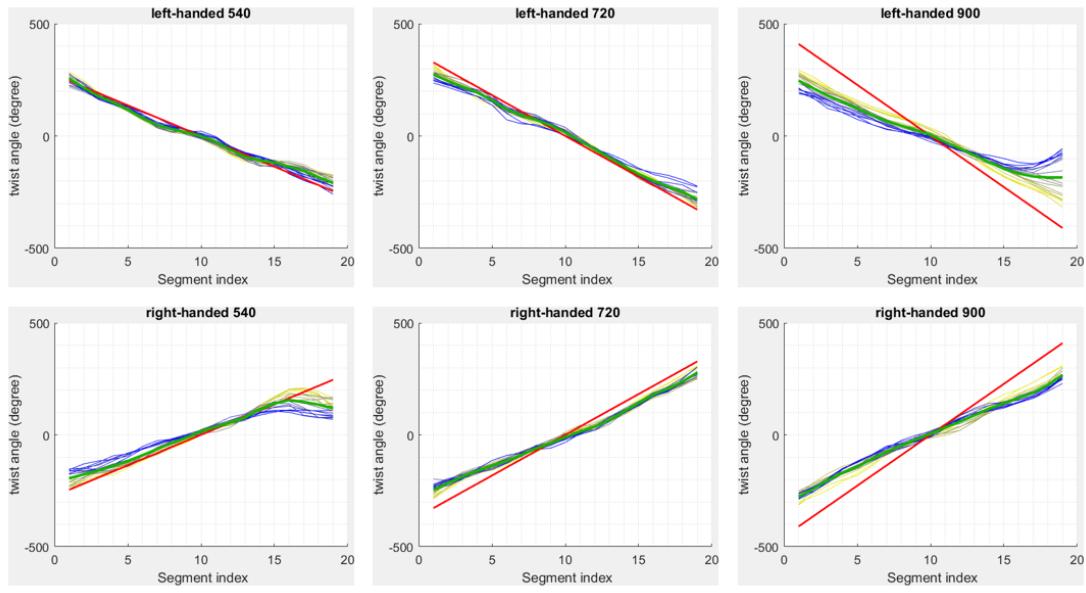


Figure S33. Exploring the upper and lower limits of twist angle. We created initial configurations with left- and right-handed twist of more than 1.5 turns, and the results shown here were obtained from simulation trajectories after relaxation and equilibrium steps. The data show that the simulations always relax the structures to roughly similar and smaller twist angles in both left- and right-handed systems, providing an estimate of the maximum possible left and right-handed twist MEO-T3 can accommodate. The results also illustrate the ability of the oxDNA model to correct intentionally over-twisted configurations.

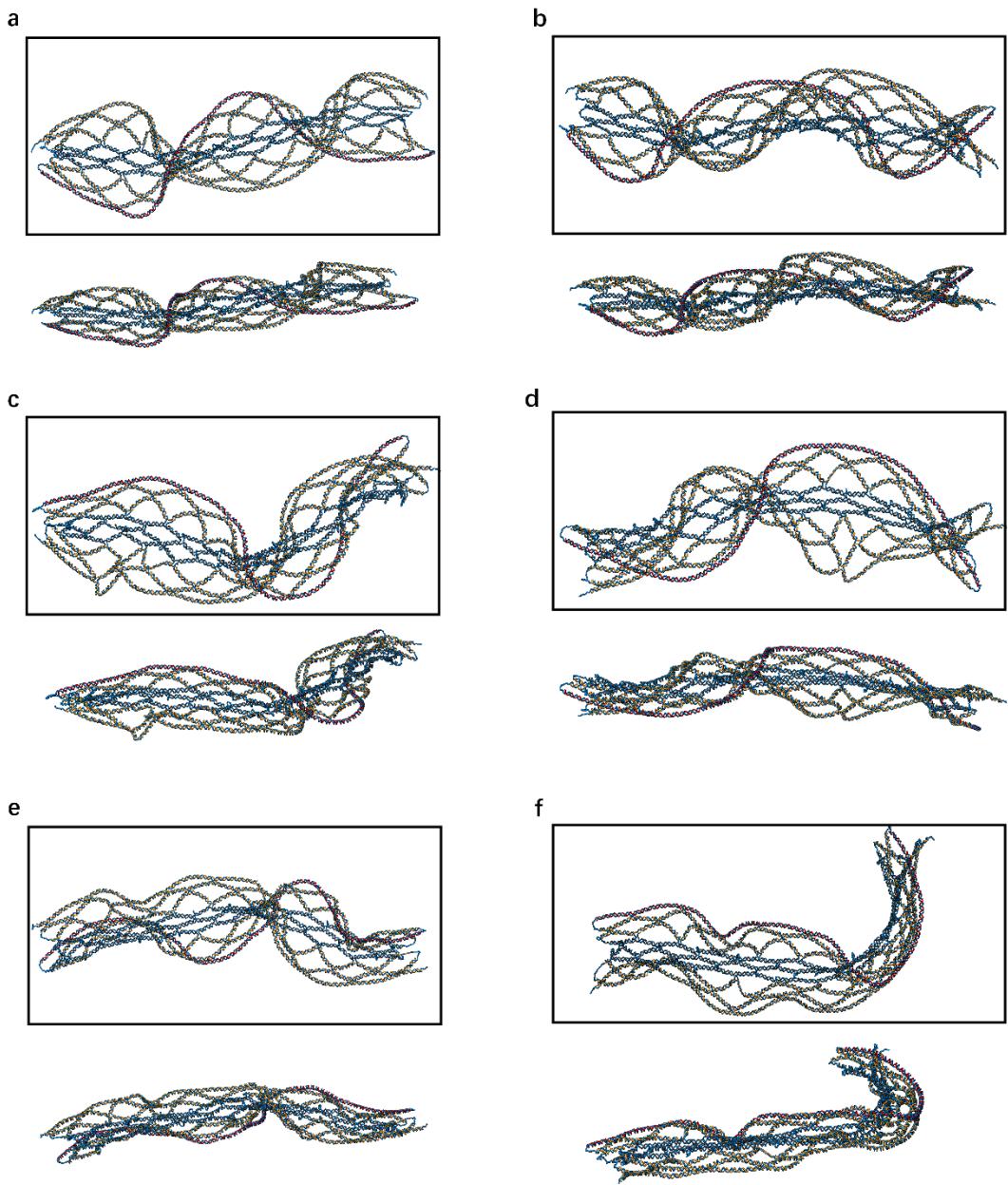


Figure S34. Mean configurations after applying clamping forces on MEO-T3. The staples on the first row of modules were rendered as red to distinguish differences in chirality. Here we only display the 19×9 modular units. The rest of the scaffold and staples were simulated in the system but not displayed for better visualization. a)-f) (Top) Images rendered from the view parallel to the normal vector of the repulsion planes. (Bottom) Tilted view from the top for distinguishing chirality.

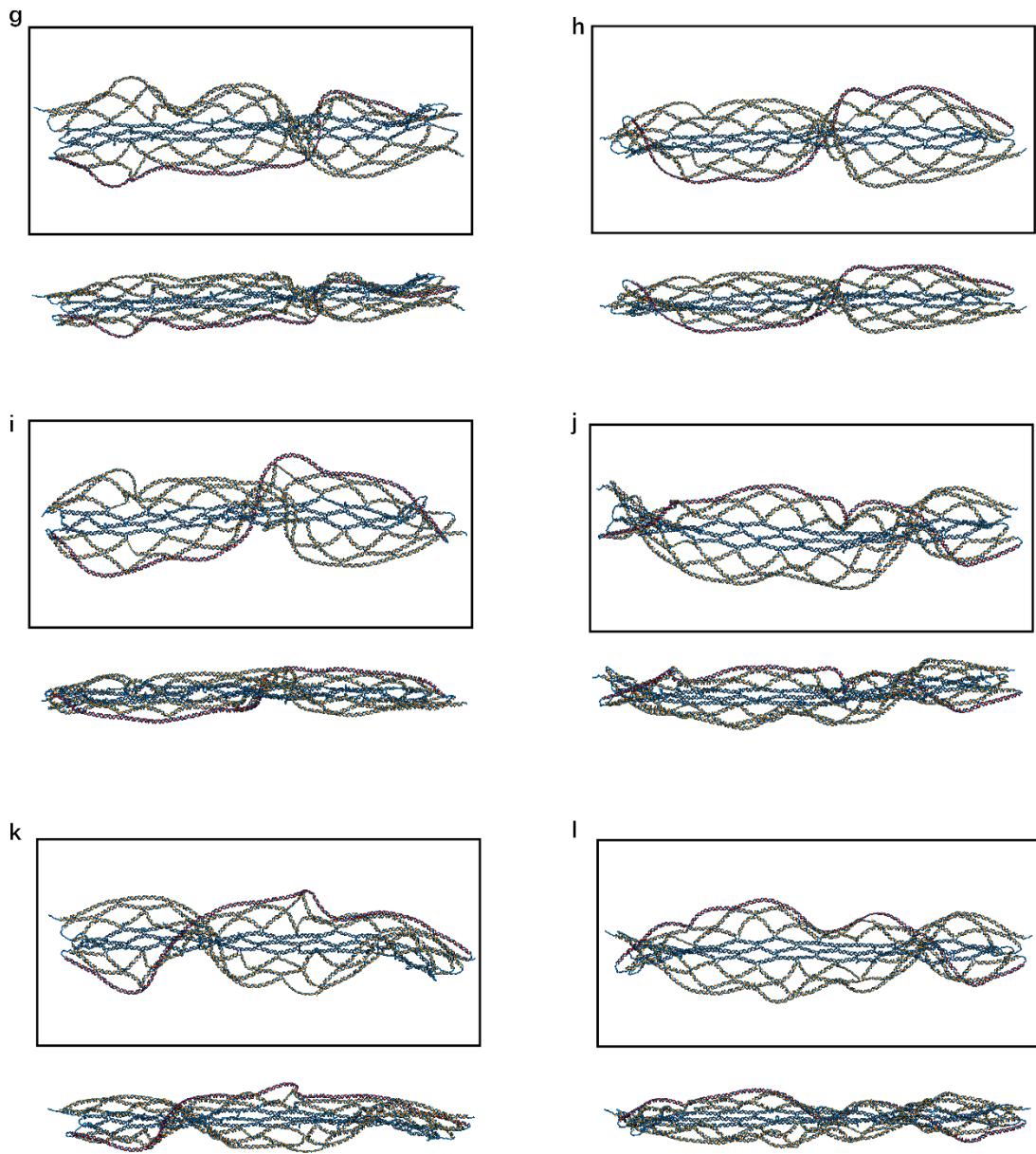


Figure S35. Additional mean configurations after applying clamping forces on MEO-T3. g)-l) (Top) Images rendered from the view parallel to the normal vector of the repulsion planes. (Bottom) Tilted view from the top for distinguishing chirality.

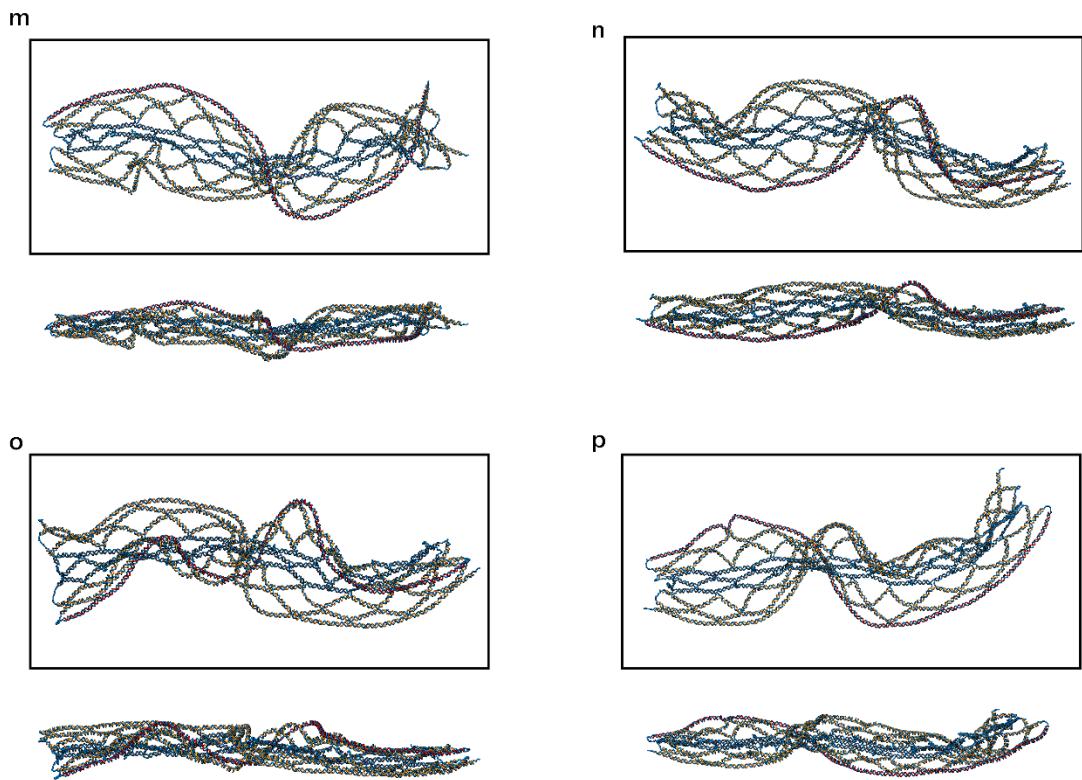


Figure S36. Additional mean configurations after applying clamping forces on MEO-T3. m)-p) (Top) Images rendered from the view parallel to the normal vector of the repulsion planes. (Bottom) Tilted view from the top for distinguishing chirality.

a

row number	number of expansion strands	loop number																		
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
MEO-T5	1	6	○	X	X	X	○	X	X	○	X	X	○	X	X	○	X	X	X	○
	2	6	○	X	X	X	○	X	X	○	X	X	○	X	X	○	X	X	X	○
	3	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
	4	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
	5	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
	6	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
	7	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
	8	6	○	X	X	X	○	X	X	○	X	X	X	○	X	X	○	X	X	○
	9	6	○	X	X	X	○	X	X	○	X	X	○	X	X	○	X	X	X	○

X 26-base staple DNA

○ 36-base staple DNA set E25

b

row number	number of expansion strands	loop number																		
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
MEO-T6	1	12	○	○	X	X	○	○	X	○	○	X	○	X	○	○	X	X	○	○
	2	12	○	○	X	X	○	○	X	○	○	X	○	X	○	○	X	X	○	○
	3	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
	4	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
	5	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
	6	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
	7	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
	8	12	○	○	X	X	○	○	X	○	○	X	○	X	○	○	X	X	○	○
	9	12	○	○	X	X	○	○	X	○	○	X	○	X	○	○	X	X	○	○

X 26-base staple DNA

○ 36-base staple DNA set E25

○ 36-base staple DNA set E26

c

row number	number of expansion strands	loop number																		
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
MEO-T2	1	19	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○
	2	19	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○
	3	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
	4	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
	5	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
	6	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
	7	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
	8	19	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○
	9	19	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○

X 26-base staple DNA

○ 36-base staple DNA set E25

○ 36-base staple DNA set E26

○ 36-base staple DNA set E27

Figure S37. Illustration of distribution of expansion staples used for conformation MEO-T5 (a), MEO-T6 (b) and MEO-T2 (c).

a

row number	number of expansion strands	loop number																		
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
MEO-T7	1	10	o	o	o	o	o	o	o	o	x	x	x	x	x	x	x	x	x	x
	2	10	o	o	o	o	o	o	o	o	x	x	x	x	x	x	x	x	x	x
	3	0	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x
	4	0	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x
	5	0	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x
	6	0	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x
	7	0	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x
	8	10	o	o	o	o	o	o	o	o	x	x	x	x	x	x	x	x	x	x
	9	10	o	o	o	o	o	o	o	o	x	x	x	x	x	x	x	x	x	x

x 26-base staple DNA o 36-base staple DNA set E28

b

row number	number of expansion strands	loop number																		
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
MEO-T2	1	19	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o
	2	19	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o
	3	0	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x
	4	0	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x
	5	0	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x
	6	0	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x
	7	0	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x
	8	19	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o
	9	19	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o

x 26-base staple DNA o 36-base staple DNA set E28 o 36-base staple DNA set E29

Figure S38. Illustration of distribution of expansion staples used for conformation MEO-T7 (a), MEO-T2 (b)).

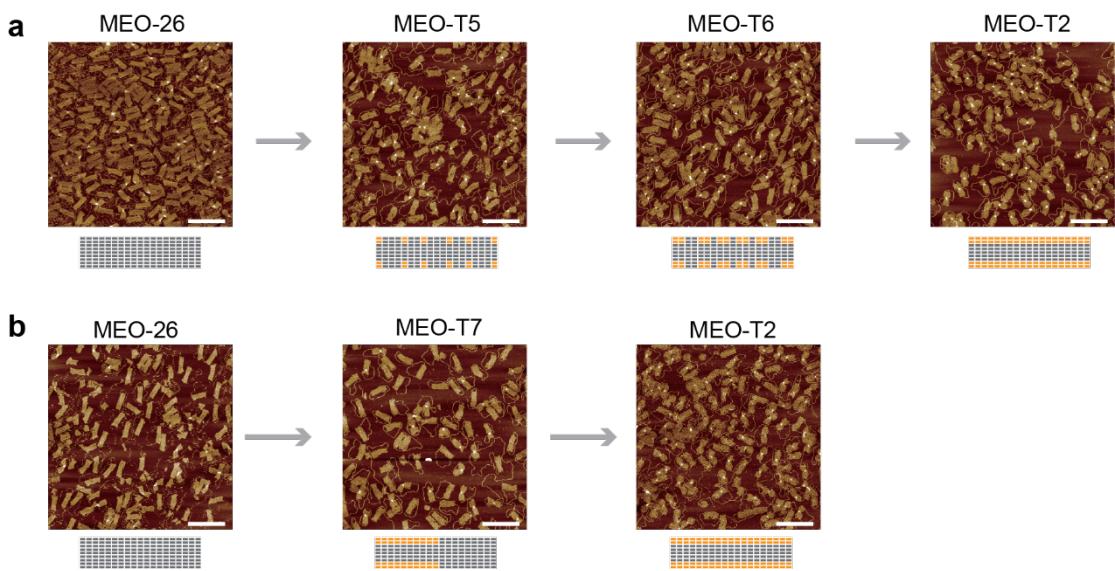


Figure S39. Multi-pathway and multi-step expansion of MEO for twist control. Two pathways were demonstrated to reach MEO-T2 from MEO-26: a) MEO-26 was incubated with expansion set E25, E26 and E27 to generate the conformation MEO-T5, MEO-T6 and MEO-T2, respectively. b) MEO-26 was incubated with expansion set E28 and E29 to generate the conformation MEO-T7 and MEO-T2, respectively. Scale bar: 400 nm.

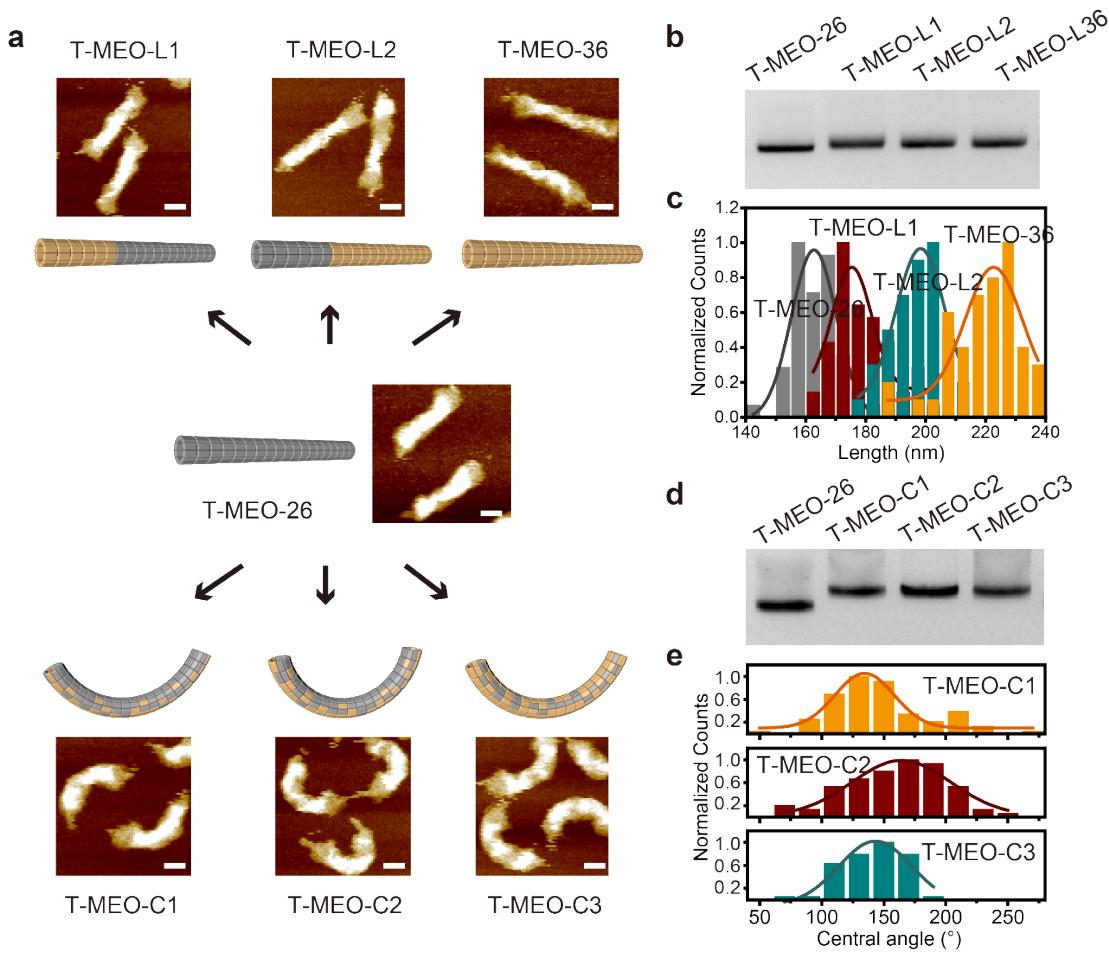


Figure S40. 3D tube MEO (T-MEO) for length and curvature transformation. (a) Top: one-step expansion of tube MEO-26 into TUBE MEO-L1, TUBE MEO-L2 and TUBE MEO-36. Bottom: one-step expansion of TUBE MEO-26 into TUBE MEO-C1, TUBE MEO-C2 and TUBE MEO-C3. Scale bar: 50 nm. (b) Agarose gel electrophoresis of the sample TUBE MEO-26, TUBE MEO-L1, TUBE MEO-L2 and TUBE MEO-36. (c) Normalized length histogram of TUBE MEO-26, TUBE MEO-L1, TUBE MEO-L2 and TUBE MEO-36 and the corresponding Gaussian fitting. The mean length is 162.7 ± 7.5 nm (N=50) for TUBE MEO-26, 175.4 ± 6.6 nm (N=52) for TUBE MEO-L1, 198.3 ± 8.1 nm (N=42) for TUBE MEO-L2, and 222.7 ± 9.6 nm (N=46) for TUBE MEO-36. (d) Agarose gel electrophoresis of the sample TUBE MEO-26, TUBE MEO-C1, TUBE MEO-C2 and TUBE MEO-C3. (e) Normalized curvature histogram of TUBE MEO-C1, TUBE MEO-C2 and TUBE MEO-C3 and the corresponding Gaussian fitting. The mean curvature is $134.5 \pm 23.7^\circ$ (N=93) for TUBE MEO-C1, $164.2 \pm 39.7^\circ$ (N=75) for TUBE MEO-C2, $143.2 \pm 29.3^\circ$ (N=64) for TUBE MEO-C3. The error is the standard deviation.

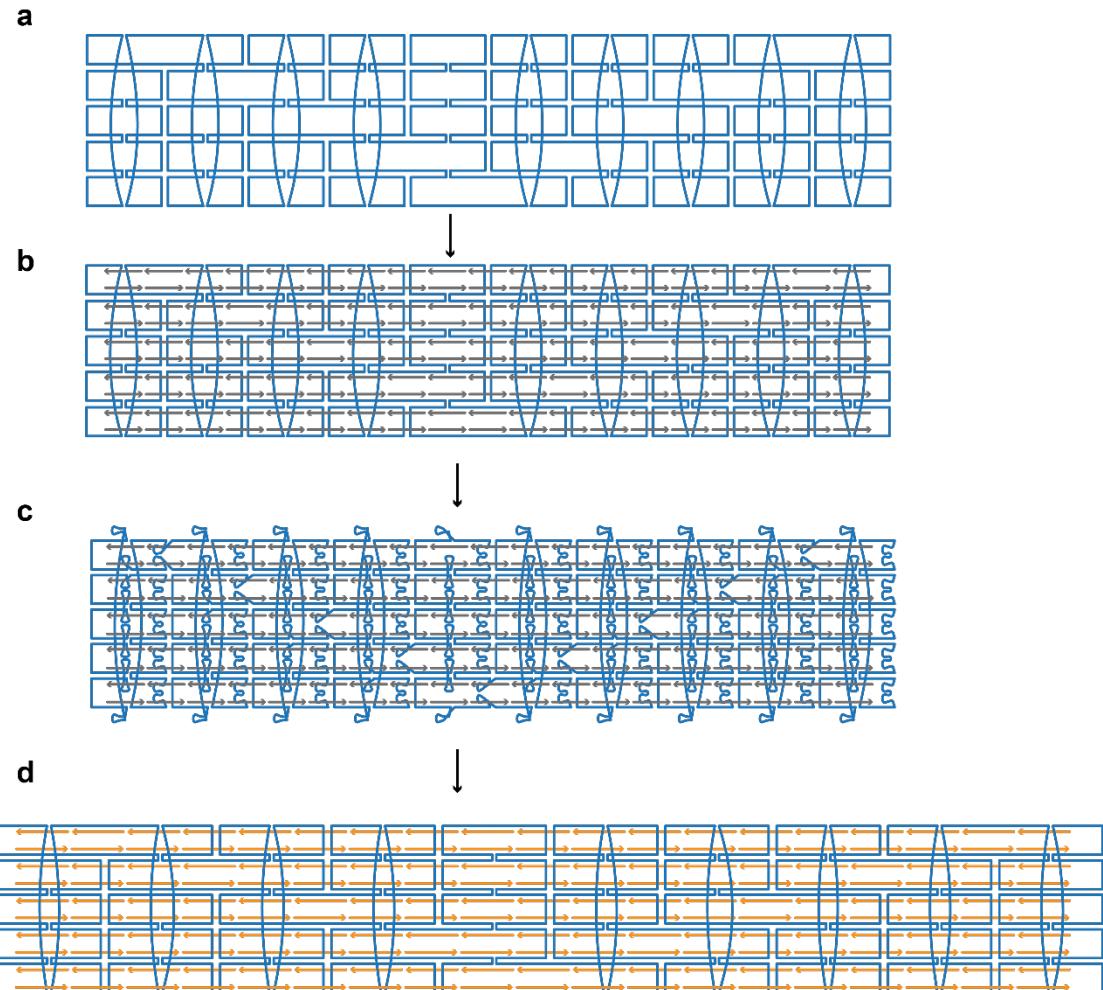


Figure S41. Design of tube modular expandable DNA origami. a) Routing of DNA scaffold. All the crossovers are on the DNA scaffold. b) Adding DNA staples to the existing DNA scaffold. Each staple DNA is 26-nt long. c) Adding loops to the structure. Each loop is designed in the center of DNA unit. When the DNA unit contains crossover, a half crossover is converted into 20-nt loop to be shared by two neighboring DNA units. The DNA origami structure contains 19 columns and 10 rows of DNA units in total. d) Tubular DNA origami structure after fully expanded of each DNA unit. The half crossover becomes double crossover.

a

	row number	number of expansion strands	loop number																		
			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
T-MEO-L1	1	6	○	○	○	○	○	○	X	X	X	X	X	X	X	X	X	X	X	X	X
	2	6	○	○	○	○	○	○	X	X	X	X	X	X	X	X	X	X	X	X	X
	3	6	○	○	○	○	○	○	X	X	X	X	X	X	X	X	X	X	X	X	X
	4	6	○	○	○	○	○	○	X	X	X	X	X	X	X	X	X	X	X	X	X
	5	6	○	○	○	○	○	○	X	X	X	X	X	X	X	X	X	X	X	X	X
	6	6	○	○	○	○	○	○	X	X	X	X	X	X	X	X	X	X	X	X	X
	7	6	○	○	○	○	○	○	X	X	X	X	X	X	X	X	X	X	X	X	X
	8	6	○	○	○	○	○	○	X	X	X	X	X	X	X	X	X	X	X	X	X
	9	6	○	○	○	○	○	○	X	X	X	X	X	X	X	X	X	X	X	X	X
	10	6	○	○	○	○	○	○	X	X	X	X	X	X	X	X	X	X	X	X	X
X 26-base staple DNA ○ 36-base staple DNA set TE1																					

b

	row number	number of expansion strands	loop number																		
			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
T-MEO-L2	1	13	X	X	X	X	X	X	○	○	○	○	○	○	○	○	○	○	○	○	○
	2	13	X	X	X	X	X	X	○	○	○	○	○	○	○	○	○	○	○	○	○
	3	13	X	X	X	X	X	X	○	○	○	○	○	○	○	○	○	○	○	○	○
	4	13	X	X	X	X	X	X	○	○	○	○	○	○	○	○	○	○	○	○	○
	5	13	X	X	X	X	X	X	○	○	○	○	○	○	○	○	○	○	○	○	○
	6	13	X	X	X	X	X	X	○	○	○	○	○	○	○	○	○	○	○	○	○
	7	13	X	X	X	X	X	X	○	○	○	○	○	○	○	○	○	○	○	○	○
	8	13	X	X	X	X	X	X	○	○	○	○	○	○	○	○	○	○	○	○	○
	9	13	X	X	X	X	X	X	○	○	○	○	○	○	○	○	○	○	○	○	○
	10	13	X	X	X	X	X	X	○	○	○	○	○	○	○	○	○	○	○	○	○
X 26-base staple DNA ○ 36-base staple DNA set TE2																					

c

	row number	number of expansion strands	loop number																		
			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
T-MEO-36	1	19	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○
	2	19	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○
	3	19	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○
	4	19	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○
	5	19	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○
	6	19	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○
	7	19	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○
	8	19	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○
	9	19	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○
	10	19	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○
X 26-base staple DNA ○ 36-base staple DNA set TE3																					

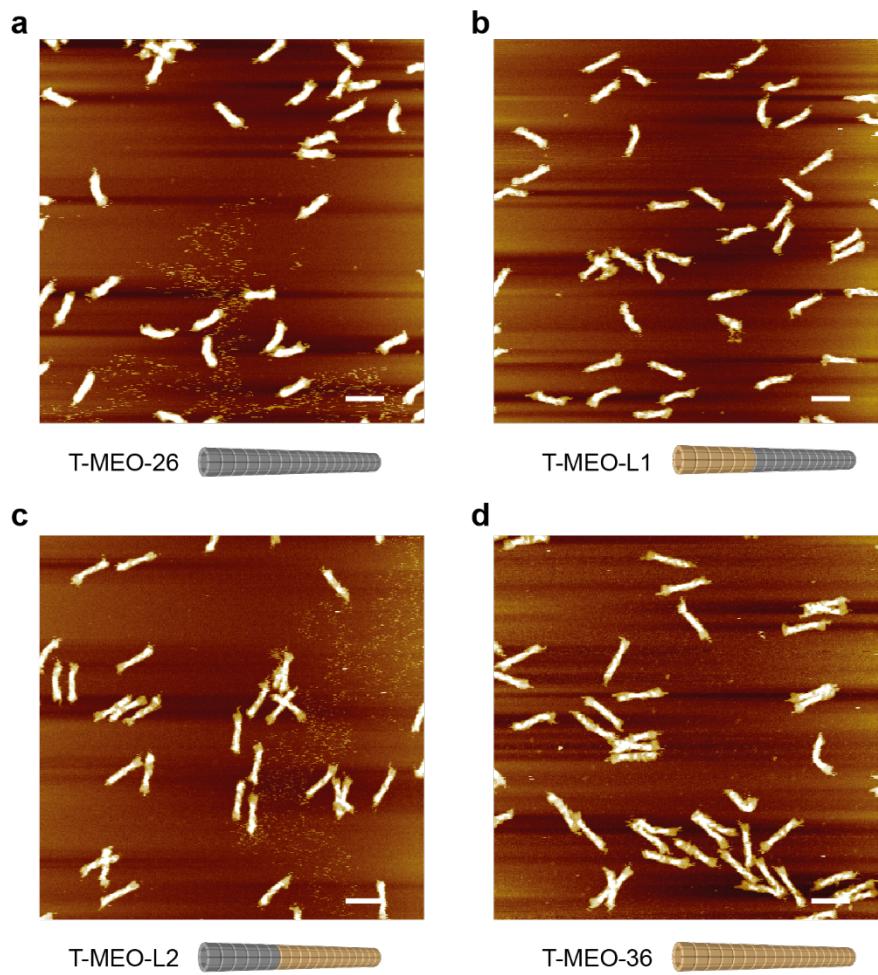


Figure S43. AFM imaging of one-step expansion of TUBE MEO-26 (a) into conformation TUBE MEO-L1 (b), TUBE MEO-L2 (c), TUBE MEO-36 (d) using expansion set TE1, TE2 and TE3, respectively. Scale bar: 200 nm.

a

row number	expansion strands	number of		loop number																	
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	
1	17	X	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X	
2	12	0	0	X	0	X	0	X	0	0	0	X	0	X	0	X	0	X	0	0	
3	5	X	X	0	X	X	X	0	X	X	0	X	X	0	X	X	0	X	X	X	
4	3	X	X	X	X	0	X	X	X	0	X	X	X	0	X	X	X	X	X	X	
5	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	
6	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	
7	3	X	X	X	X	0	X	X	X	0	X	X	X	0	X	X	X	X	X	X	
8	5	X	X	0	X	X	X	0	X	X	0	X	X	0	X	X	0	X	X	X	
9	12	0	0	X	0	X	0	X	0	0	0	0	0	0	0	0	0	0	0	0	
10	17	X	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X	

X 26-base staple DNA

O 36-base staple DNA set TE4

b

row number	expansion strands	number of		loop number																	
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	
1	19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2	14	0	X	0	0	X	0	0	0	0	X	0	0	0	X	0	X	0	0	0	
3	7	X	X	0	X	0	X	0	X	X	0	X	X	0	X	0	X	0	X	X	
4	5	X	0	X	X	0	X	X	X	0	X	X	X	0	X	0	X	0	0	X	
5	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	
6	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	
7	5	X	0	X	X	0	X	X	X	0	X	X	X	0	X	X	0	X	0	X	
8	7	X	X	0	X	0	X	0	X	X	0	X	X	0	X	0	X	0	0	X	
9	14	0	X	0	0	X	0	0	0	0	0	X	0	0	0	X	0	X	0	0	
10	19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

X 26-base staple DNA

O 36-base staple DNA set TE5

c

row number	expansion strands	number of		loop number																	
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	
1	19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2	19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3	12	0	X	0	X	0	X	0	0	X	0	0	0	0	X	0	X	0	X	0	
4	7	X	0	X	X	0	X	0	X	0	X	X	X	X	0	X	0	X	0		
5	3	X	X	X	X	0	X	X	X	0	X	X	0	X	X	X	X	X	X		
6	3	X	X	X	X	0	X	0	X	X	0	X	0	X	X	X	X	X	X		
7	7	X	0	X	X	0	X	0	X	0	X	X	X	X	0	X	0	X	0		
8	12	0	X	0	X	0	X	0	X	0	X	0	0	0	X	0	X	0	X		
9	19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
10	19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

X 26-base staple DNA

O 36-base staple DNA set TE6

Figure S44. Illustration of distribution of expansion staples used for conformation TUBE MEO-C1, TUBE MEO-C2 and TUBE MEO-C3.

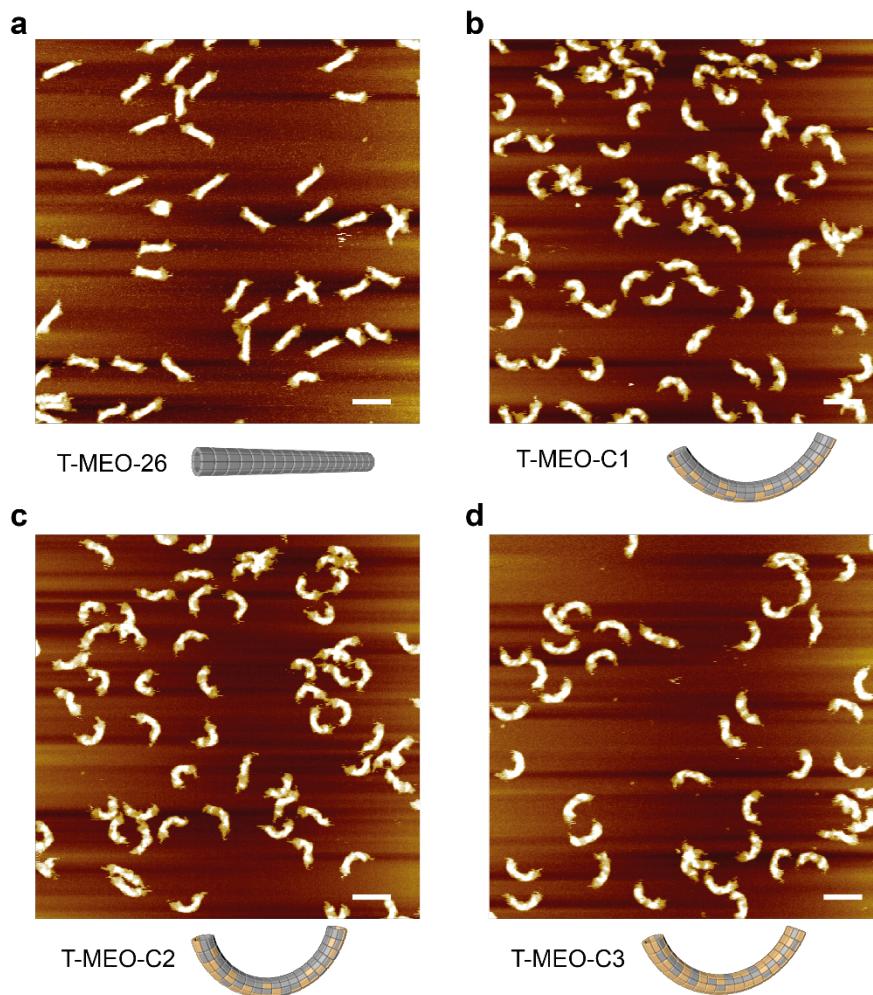


Figure S45. AFM imaging of one-step expansion of TUBE MEO-26 (a) into conformation TUBE MEO-C1 (b), TUBE MEO-C2 (c), TUBE MEO-C3 (d) using expansion set TE4, TE5 and TE6, respectively. Scale bar: 200 nm.

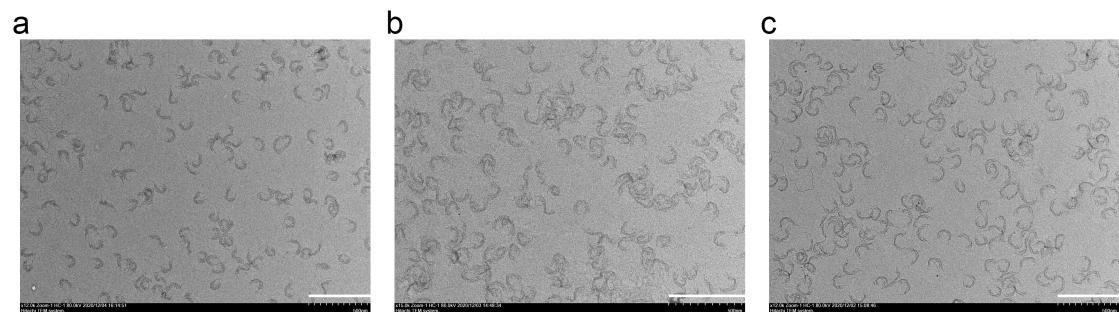


Figure S46. TEM imaging of one-step expansion of TUBE MEO-26 into conformation TUBE MEO-C1 (a), TUBE MEO-C2 (b) and TUBE MEO-C3. Scale bar: 500 nm.

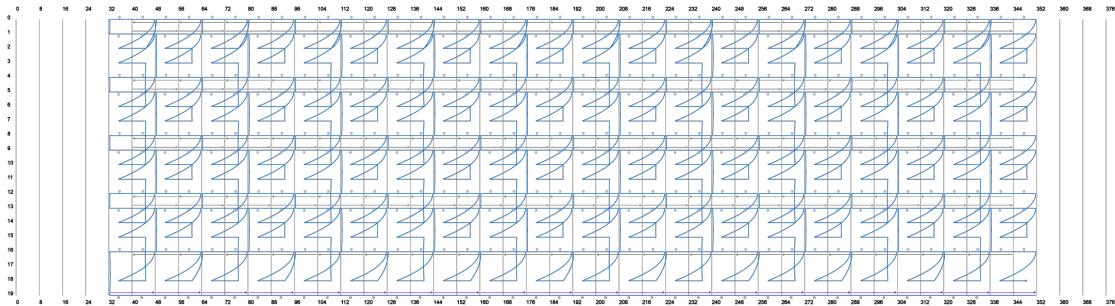


Figure S47. Diagram of 19×9 2D DNA origami array before expansion.

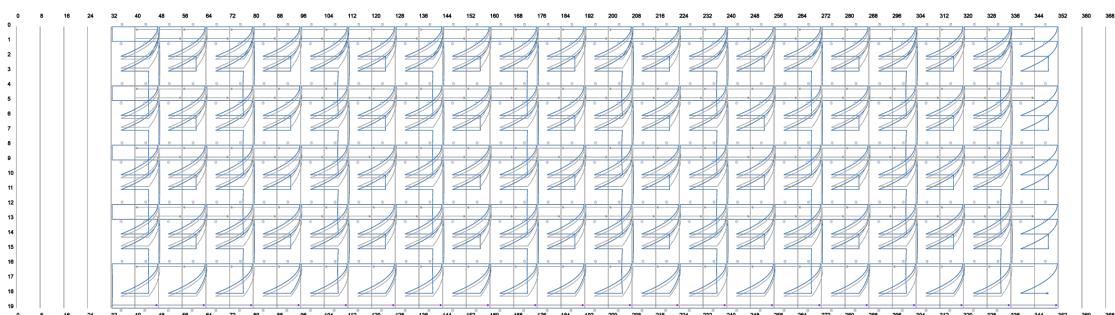


Figure S48. Diagram of 19×9 2D DNA origami array after fully expansion.

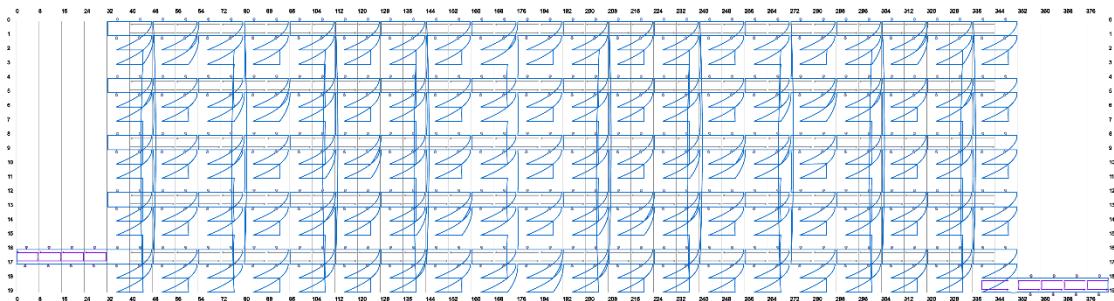


Figure S49. Diagram of 19×10 tube DNA origami array before expansion.

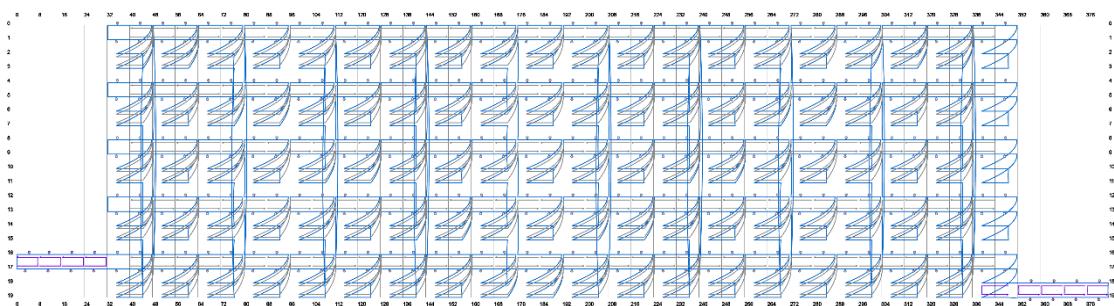


Figure S50. Diagram of 19×10 tube DNA origami array after fully expansion.

Table S1. Staple DNA sequence for 19×9 DNA origami array before expansion.

Start	End	Sequence	Length	note
0[55]	0[40]	CCGGTTGATAATCCAAAAACAGGAAG	26	core strand
0[71]	0[56]	TCAACATGTTTAAATCATATGTACC	26	core strand
0[87]	0[72]	GGCTTAGAGCTTAATAATGCTGTAGC	26	core strand
0[103]	0[88]	TTTAATCATTGTGCATTTGCGGAT	26	core strand
0[119]	0[104]	AGTAGTAAATTGGGTTAATTCAAC	26	core strand
0[135]	0[120]	TCTTAAACAGCTAACACCAAGAACG	26	core strand
0[151]	0[136]	TTGTATCGGTTATTCGAGGTGAATT	26	core strand
0[167]	0[152]	TGATACAGGAGTGAAGGAGCCTTAA	26	core strand
0[183]	0[168]	TTTACCGTTCCAGACATGGCTTTGA	26	core strand
0[199]	0[184]	GGCAACATATAAACGCAGTCCTGAA	26	core strand
0[215]	0[200]	TATGTTAGCAAACCACATACATAAAGGT	26	core strand
0[231]	0[216]	GCCGTTTTATTCCTTATTACGCAG	26	core strand
0[247]	0[232]	ATTAACCAAGTACGAGAACAGCAA	26	core strand
0[263]	0[248]	ATTAAGACGCTGATCCAAGAACGGGT	26	core strand
0[279]	0[264]	TCCCTTAGAATCCAGCGATAGCTTAG	26	core strand
0[295]	0[280]	ACAACATAATAGATTATTAATTAAATT	26	core strand
0[311]	0[296]	TGAGGAAGGTTATTTAGGAGCACTA	26	core strand
0[327]	0[312]	GGTACGCCAGAATAGTTGAAAGGAAT	26	core strand
0[343]	0[328]	AACAGGAGGCCGATTTAGACAGGAAC	26	core strand
1[40]	1[55]	AAACGTTAATATTAGCAAACAGAGA	26	core strand
1[56]	1[71]	ATCGATGAACGGAATATGCAACTAA	26	core strand
1[72]	1[87]	AGTACGGTGTCTGGGTCAAGGATTAGA	26	core strand
1[88]	1[103]	GAGTACCTTAATAATTACCTTATGC	26	core strand
1[104]	1[119]	GATTTAAGAACTACGTAACAAAGCT	26	core strand
1[120]	1[135]	GCTCATTCAGTGAGATAACGATAGTT	26	core strand
1[136]	1[151]	GCGCGACAATGAAATAATAATTTT	26	core strand
1[152]	1[167]	TCACGTTGAAAATTACTGGTAATAAG	26	core strand
1[168]	1[183]	TTTTAACGGGGCTGATATTACACAA	26	core strand
1[184]	1[199]	CAAATAATCCTCAGAACGCAAAGA	26	core strand
1[200]	1[215]	CACCAACGAAATAACGCAATAAAC	26	core strand
1[216]	1[231]	GGAATACCCAAAATCATCGTAGGAAT	26	core strand
1[232]	1[247]	CATTACCGCGCCCCGAGCATGTAGAA	26	core strand
1[248]	1[263]	ACCAATCAATAATGAAGAGTCATAG	26	core strand
1[264]	1[279]	TGAATTATCAAAAAATCAATATATG	26	core strand
1[280]	1[295]	TGAGTGAATAACCTAGAGCCGTCAAT	26	core strand
1[296]	1[311]	AGATAATACATTCAAATATCAAACC	26	core strand
1[312]	1[327]	CTCAATCAATATCCCTGAGAAGTGT	26	core strand
1[328]	1[343]	TTTATAATCAGTGTGGTTGCTTGAC	26	core strand
4[55]	4[40]	CCTGAGAGTCTGGTTTGTAAATC	26	core strand
4[71]	4[56]	TTCTGCGAACGAGTATCAGGTATTG	26	core strand
4[87]	4[72]	GCAAACTCCAACAAGTTGATTCCAA	26	core strand
4[103]	4[88]	AAATCTACGTTAAAACCAGACCGGAA	26	core strand

4[119]	4[104]	ATTACCCAAATCAACGTTGGGAAGAA	26	core strand
4[135]	4[120]	CGGTGCGCTGAGGCAGACCGGATATT	26	core strand
4[151]	4[136]	TAAAGGAATTGCGTAACCGATATATT	26	core strand
4[167]	4[152]	TAATGCCCTGCAGAAAGGAACAAC	26	core strand
4[183]	4[168]	AGACGATTGGCCTCCGTATAAACAGT	26	core strand
4[199]	4[184]	TGGTTTACCAGCGGTTGAGGCAGGTC	26	core strand
4[215]	4[200]	GGAAACCGAGGAATAGAAAATTCTATA	26	core strand
4[231]	4[216]	CGGTATTCTAAGAAAAGTTACAGAA	26	core strand
4[247]	4[232]	CCATCCTAATTATAGAAGGCTTATC	26	core strand
4[263]	4[248]	CGGCTTAGGTTGGAAAAATAATATC	26	core strand
4[279]	4[264]	GGAACAGTACATCCTTTAACCTC	26	core strand
4[295]	4[280]	TCGACAACTCGTATACTTTTAAT	26	core strand
4[311]	4[296]	CCTTGCTGAACCTCTTACAAACAAT	26	core strand
4[327]	4[312]	AAATTAACCGTTGATCTAAAGCATCA	26	core strand
4[343]	4[328]	AGGGCGCGTACTACTGTCCATCACGC	26	core strand
5[40]	5[55]	CCATCAAAATAAAATTAATGCCGGA	26	core strand
5[56]	5[71]	GAGGGTAGCTATTAGATTTAGTTG	26	core strand
5[72]	5[87]	ACCATTAGATACAGCCGAAAGACTT	26	core strand
5[88]	5[103]	CAAATATCGCGTTAAACGAACCAA	26	core strand
5[104]	5[119]	CGGAACAACATTACAGCGCATAGG	26	core strand
5[120]	5[135]	CTGGCTGACCTCTTGAGGGAGTTA	26	core strand
5[136]	5[151]	AAGGCCGCTTTGTGGGATTTGCTA	26	core strand
5[152]	5[167]	AACAACTTCAACCTATTCCGAAACC	26	core strand
5[168]	5[183]	TATTATTCTGAAACCGCCACCAGAAC	26	core strand
5[184]	5[199]	CACCACAGAGCCCCAAAGACAAAAG	26	core strand
5[200]	5[215]	GGCGACATTCAACTATCTAACCGAAG	26	core strand
5[216]	5[231]	CCCTTTTAAGAACCGCGAGCGTT	26	core strand
5[232]	5[247]	TAGCGAACCTCCAATGCAGAACGCG	26	core strand
5[248]	5[263]	CCTGTTTATCAACGTTATATAACTAT	26	core strand
5[264]	5[279]	ATGTAATGCTGAACATCAAGAAAAC	26	core strand
5[280]	5[295]	AAAATTAATTACATTAAATCCTTG	26	core strand
5[296]	5[311]	CCGAACGTTATTACACCGCCTGCAAC	26	core strand
5[312]	5[327]	AGTGCACGCGTATAGCAATACTCT	26	core strand
5[328]	5[343]	TTGATTAGTAATAAAGTGTAGCGGTC	26	core strand
8[55]	8[40]	GTTCTAGCTGATAAGCCAGCTTCAT	26	core strand
8[71]	8[56]	TTTCATTTGGGGATGATATTCAACC	26	core strand
8[87]	8[72]	AGATTAAGAGGAACGTGTTACCTATA	26	core strand
8[103]	8[88]	GGAATACACATTGATTGCATCAAAA	26	core strand
8[119]	8[104]	AACGGTGTACAGACAGTTGAGATTAA	26	core strand
8[135]	8[120]	TCGGAACGAGGGTAAGAGGACAGATG	26	core strand
8[151]	8[136]	TGAATTTCTGTAGCGAAAGACAGCA	26	core strand
8[167]	8[152]	AGAAGGATTAGGAAGACGTTAGTAAA	26	core strand
8[183]	8[168]	ACCACCCCTCAGAGGAGACTCCTCAAG	26	core strand
8[199]	8[184]	ATTATTCATTAACACCCCTCAGAGCC	26	core strand

8[215]	8[200]	AAATAGCAATAGCAATATTGACGGAA	26	core strand
8[231]	8[216]	ATTAGTTGCTATTGCAAGAACAAATG	26	core strand
8[247]	8[232]	AACATGTTCAGCTGCCTTAATCAAG	26	core strand
8[263]	8[248]	AAACTTTTCAAAGACGACAATAAAC	26	core strand
8[279]	8[264]	GATGATGAAACAAAAAGAACCGGAGA	26	core strand
8[295]	8[280]	GGAACAAAGAAACCTGAGCAAAAGAA	26	core strand
8[311]	8[296]	CGGTCAGTATTAAATTATCAGTTGC	26	core strand
8[327]	8[312]	TCCGCCCTTGCTGGAACAGAGGTGAGG	26	core strand
8[343]	8[328]	CTAGGGCGCTGGCAGAACTCAAACTA	26	core strand
9[40]	9[55]	CCC GT CGG ATT CT ATT CAA AAG GGT G	26	core strand
9[56]	9[71]	AGAAAGGCCGGAGCGCAGCTGAAAA	26	core strand
9[72]	9[87]	GGTGGCATCAATTCAAAATCAGGTC	26	core strand
9[88]	9[103]	TTTACCC TG ACT ACA ACT AAT GCAGA	26	core strand
9[104]	9[119]	TACATAACGCCAAGCGCAGACGGT	26	core strand
9[120]	9[135]	CAATCATAGGAAGCAACGCTACA	26	core strand
9[136]	9[151]	GAGGCTTGAGGACAGCCCTCATAGT	26	core strand
9[152]	9[167]	TAGCGTAACGATCTTAGCGGGTTTT	26	core strand
9[168]	9[183]	GCTCAGTACCAAGGCCACCACCGAAC	26	core strand
9[184]	9[199]	CGCCTCCCTCAGAGGTGAATTATCAC	26	core strand
9[200]	9[215]	CGTCACCGACTTGATCAGAGAGATAA	26	core strand
9[216]	9[231]	CCCACAAGAATTGTTGCACCCAGCTA	26	core strand
9[232]	9[247]	CAATTTTATCCTGAGAGAATATAAG	26	core strand
9[248]	9[263]	TACCGACAAAAGGTATATTTAGTTA	26	core strand
9[264]	9[279]	ATTCATCTCTGACCAAGTTACAAA	26	core strand
9[280]	9[295]	ATCGCGCAGAGGCCACCAGAAGGAGC	26	core strand
9[296]	9[311]	GGATTATCATCAAAACATGCCATT	26	core strand
9[312]	9[327]	AAAAATACCGAACTAATATCCAGAAC	26	core strand
9[328]	9[343]	AATATTACCGCCAACGGGAAAGCCG	26	core strand
12[55]	12[40]	TGTGTAGGTAAAGTTGACCGTAATGG	26	core strand
12[71]	12[56]	TCATACAGGCAAGAACGCTGAGTAA	26	core strand
12[87]	12[72]	AATGACCATAATAACATCCAATAAA	26	core strand
12[103]	12[88]	TCATAACCCCTCGTTCAGAAACGAG	26	core strand
12[119]	12[104]	CTTAGCCGGAACGAAGAGCAACACTA	26	core strand
12[135]	12[120]	ACGGGTTAAATACCTGCTCCATGTTA	26	core strand
12[151]	12[136]	AGCATTCCACAGAAAGTTCCATTAA	26	core strand
12[167]	12[152]	ATAGCCCCGAAACTACAACCCCTGT	26	core strand
12[183]	12[168]	ACCGGAACCAAGAGGGTTGATATAAGT	26	core strand
12[199]	12[184]	AGTAGCACCATTACATAATCAAACATC	26	core strand
12[215]	12[200]	ATTGAGCGCTAATCAGCAAAATCACC	26	core strand
12[231]	12[216]	GCCTAATTGCCAAAGTCAGAGGGTA	26	core strand
12[247]	12[232]	CGAGCCAGTAATAGCGTCTTCCAGA	26	core strand
12[263]	12[248]	TGATAAATAAGGCAGAGGCATT	26	core strand
12[279]	12[264]	GATTGCTTGAATAATACCGACCGTG	26	core strand
12[295]	12[280]	ATATAATCCTGATAACGGATTGCCT	26	core strand

12[311]	12[296]	ACTGATAGCCCTATGGCAATTCA	26	core strand
12[327]	12[312]	CCTACATTTGACCTTAATCGCGA	26	core strand
12[343]	12[328]	GATTTAGAGCTTGGCTCATGAAATA	26	core strand
13[40]	13[55]	GCATCGTAACCGTCAACGCAAGGATA	26	core strand
13[56]	13[71]	AAAATTTAGAAGCAAAGAATTAGC	26	core strand
13[72]	13[87]	AAAATTAAGCAATAATCGTCATAAAT	26	core strand
13[88]	13[103]	ATTCAATTGAATCCTTACCAAGACGACG	26	core strand
13[104]	13[119]	ATAAAAAACAAAACGGAGATTGTAT	26	core strand
13[120]	13[135]	CATCGCCTGATAAGTAATGCCACTAC	26	core strand
13[136]	13[151]	GAAGGCACCAACCATAAGGAACCCATG	26	core strand
13[152]	13[167]	TACCGTAACACTGGGTGTATCACCGT	26	core strand
13[168]	13[183]	ACTCAGGAGGTTTCGGCATTTCGG	26	core strand
13[184]	13[199]	TCATAGCCCCCTCCATTAGCAAGGC	26	core strand
13[200]	13[215]	CGGAAACGTCAACCACAGGGAAAGCGCA	26	core strand
13[216]	13[231]	TTAGACGGGAGAAGTTACAAAATAAA	26	core strand
13[232]	13[247]	CAGCCATATTATTCTTAATTGAGAAT	26	core strand
13[248]	13[263]	CGCCATATTAACGTTAAATAAGAAT	26	core strand
13[264]	13[279]	AAACACCGGAATCCAGATGAATATAC	26	core strand
13[280]	13[295]	AGTAACAGTACCTTGTTGGATTATA	26	core strand
13[296]	13[311]	CTTCTGAATAATGGCGTAAGAATACG	26	core strand
13[312]	13[327]	TGGCACAGACAATGCTCAATCGTCTG	26	core strand
13[328]	13[343]	AAATGGATTATTTAAGTTTTGGGG	26	core strand
16[55]	16[40]	GAAGCCTTATTTACGACGACAGTAT	26	core strand
16[71]	16[56]	CCAAAAACATTATTACTTTGGGGA	26	core strand
16[87]	16[72]	TCCAATACTGCGGTAAATCGGTTGTA	26	core strand
16[103]	16[88]	GAGGGGGTAATAGAGACTGGATAGCG	26	core strand
16[119]	16[104]	AAACAAAGTACAAAGAAGTTGCCA	26	core strand
16[135]	16[120]	ACTCATTTGACTATAACCAAGCGCG	26	core strand
16[151]	16[136]	GATAGCAAGCCAAATACACTAAAC	26	core strand
16[167]	16[152]	ACCGCCACCCCTCACCTCATTTCAGG	26	core strand
16[183]	16[168]	TAGCGCGTTTACACGCCACCTCAGA	26	core strand
16[199]	16[184]	AGCGACAGAACATAGCGTCAGACTG	26	core strand
16[215]	16[200]	GAATAACATAAAACACCGTAATCAGT	26	core strand
16[231]	16[216]	TAACGTCAAAATGCCTTACAGAGA	26	core strand
16[247]	16[232]	CTCAACAGTAGGGACGATTTTGTT	26	core strand
16[263]	16[248]	TGCGTTATACAAATATAAGCCAACG	26	core strand
16[279]	16[264]	TCAGGTTAACGTGTTAGTATCATA	26	core strand
16[295]	16[280]	GCACGTAAAACAGATTGCGTAGATT	26	core strand
16[311]	16[296]	TTCTGACCTGAAAATCAAAATTATT	26	core strand
16[327]	16[312]	ATAAAAGGGACATAGAGATAGAACCC	26	core strand
16[343]	16[328]	CATCACCCAAATCCACACGACCAGTA	26	core strand
19[32]	19[47]	ATCGCACTCCAGCCAGCTTCCGGCACCGCTCTGGTGCAGGAAACCAGGCAAAGC	56	loop strand
19[48]	19[63]	GCCATTGCCATTAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCAGGCTCT	56	loop strand
19[64]	19[79]	TCGCTATTACGCCAGCTGGCGAAAGGGGATGTGCTGCAAGGCATTAAGTGGGT	56	loop strand

19[80]	19[95]	AACGCCAGGGTTTCCCAGTCACGACGTTGAAAAACGACGCCAGTCCAAGCTT	56	loop strand
19[96]	19[111]	CTCAGGAGAACGCCAGGGTGGATGTTCTTCAAGTGTTGTGAATTGCGCACGA	56	loop strand
19[112]	19[127]	CTTAAGTGTCTTAGTGCTGAATTGTCAACCTTATGACAATGTCCGCCAAAATAA	56	loop strand
19[128]	19[143]	CCCCGCTCTAACTATTTACGCTCGCCCTGGAGTGACTCTATGATACCGACAGTG	56	loop strand
19[144]	19[159]	CGGCCCTGCCATCTGTAAGCAACTCGTCGGTGGCACGAATATAGGGCCTTGAAT	56	loop strand
19[160]	19[175]	CGGCTGACGCATTCACATAAAATCATTCCTCGAACCTGACCTCCCTGGTTGGGTGT	56	loop strand
19[176]	19[191]	AATGAGTAAACAGGGCTTAAGCTACGTGGTGGTTACCTCGATAAAAGACGGAGG	56	loop strand
19[192]	19[207]	ATCCCCGGGTACCGAGCTCGAATTGTAATCATGGTCATAGCTGTTCCCTGTGTGA	56	loop strand
19[208]	19[223]	AATTGTTATCCGCTACAATTCCACACACATACGAGCCGAAGCATAAAGTGTAA	56	loop strand
19[224]	19[239]	AGCCTGGGTGCTTAATGAGTGGCTAACCTCACATTAATTGCGTGGCTCACTGC	56	loop strand
19[240]	19[255]	CCGCTTCCAGTCGGAAACCTGTCGTGCCAGCTGCATTAATGAATGGCCAACGC	56	loop strand
19[256]	19[271]	GCGGGGAGAGGCCGGTTGCGTATTGGCGCCAGGGTGGTTTCTTTCACCAAGTG	56	loop strand
19[272]	19[287]	AGACGGGCAACAGCTGATTGCCCTTCACCGCCCTGGCCCTGAGAGAGTTGCAGCAAG	56	loop strand
19[288]	19[303]	CGGTCCACGCTGGTTGCCAGCAGCGAAATCCTGTTGATGGTGGTTCCGAA	56	loop strand
19[304]	19[319]	ATCGGCAAAATCCCTATAAATCAAAGAATAGCCCAGAGATAGGGTTGAGTGTGT	56	loop strand
19[320]	19[335]	TCCAGTTGAAACAAGAGTCCACTATTAAAGAACGTGGACTCCAACGTCAAAGGGC	56	loop strand
19[336]	19[351]	GAAAAACCGTCTATCA	16	loop strand

Table S2. Expansion DNA sequence for 19×9 DNA origami array.

Start	End	Sequence	Length	note
0[55]	0[40]	CCGGTTGATAATCAGAAAAGCCCCAAAAACAGGAAG	36	expansion strand
0[71]	0[56]	TCAACATGTTTACTAGCATGTCATATCATATGTACC	36	expansion strand
0[87]	0[72]	GGCTTAGAGCTTAATTGCTGAATATAATGCTGTAGC	36	expansion strand
0[103]	0[88]	TTTAATCATTGTGGATAAGAGGTCATTTGCGGAT	36	expansion strand
0[119]	0[104]	AGTAGTAAATTGGGCTTGAGATGGTTAATTCAAC	36	expansion strand
0[135]	0[120]	TCTTAAACAGCTCCCTGACGAGAACACCAAGAACG	36	expansion strand
0[151]	0[136]	TTGTATCGGTTTATCAGCTGCTTCGAGGTGAATT	36	expansion strand
0[167]	0[152]	TGATACAGGAGTGAAGGCTCCAAAAGGAGCCTTAA	36	expansion strand
0[183]	0[168]	TTTACCGTCCAGTAAGCGTCATACATGGCTTTGA	36	expansion strand
0[199]	0[184]	GGCAACATATAAAGAATGGAAGCGCAGTCCTGAA	36	expansion strand
0[215]	0[200]	TATGTTAGCAAACGTAGAAAATACATACATAAAGGT	36	expansion strand
0[231]	0[216]	GCCGTTTTATTGATTAAGACTCCTTATTACGCAG	36	expansion strand
0[247]	0[232]	ATTAACCAAGTACCGCACTCATCGAGAACAGCAA	36	expansion strand
0[263]	0[248]	ATTAAGACGCTGATCCTTATCATTCAAGAACGGGT	36	expansion strand
0[279]	0[264]	TCCCTTAGAACATCCTGAAAACATAGCGATAGCTTAG	36	expansion strand
0[295]	0[280]	ACAACATAAGATAAAATCGTCGCTATTAAATTAA	36	expansion strand
0[311]	0[296]	TGAGGAAGGTTATCTAAAATCTTTAGGAGCACTA	36	expansion strand
0[327]	0[312]	GGTACGCCAGAATGCAAATCACAGTTGAAAGGAAT	36	expansion strand
0[343]	0[328]	AACAGGAGGCCATTAAAGGGATTTAGACAGGAAC	36	expansion strand
1[40]	1[55]	AAACGTTAATTTGTTAAAATAGCAAACAGAGA	36	expansion strand
1[56]	1[71]	ATCGATGAACCGTAATCGTAAAAATATGCAACTAA	36	expansion strand
1[72]	1[87]	AGTACGGTGTGGAAAGTTTATGGTCAGGATTAGA	36	expansion strand
1[88]	1[103]	GAGTACCTTAATTGCTCCTTTAATTACCTTATGC	36	expansion strand
1[104]	1[119]	GATTTAAGAACACTGGCTCATTATACGTAACAAAGCT	36	expansion strand
1[120]	1[135]	GCTCATTCACTGAATAAGGCTGGATACCGATAGTT	36	expansion strand
1[136]	1[151]	GCGCGACAATGACAACAAACCATATAATAATT	36	expansion strand
1[152]	1[167]	TCACGTTGAAAATCTCCAAAAAATCTGGTAATAAG	36	expansion strand
1[168]	1[183]	TTTTAACGGGGTCAGTGCCTTGATGATATTCAACAA	36	expansion strand
1[184]	1[199]	CAAATAATCCTCATTAAAGCCAAGAACGCAAAGA	36	expansion strand
1[200]	1[215]	CACCAACGAAATAAGTTTATTTGACGCAATAAAC	36	expansion strand
1[216]	1[231]	GGAATACCCAAAAGAACACTGGCATTACCGTAGGAAT	36	expansion strand
1[232]	1[247]	CATTACCGCGCCAATAGCAAGCCGAGCATGTAGAA	36	expansion strand
1[248]	1[263]	ACCAATCAATAATCGGCTGTCTGAAAGAGTCATAG	36	expansion strand
1[264]	1[279]	TGAATTATCAAAATCATAGGTCAAATCAATATATG	36	expansion strand
1[280]	1[295]	TGAGTGAATAACCTTGCTTCTGTTAGAGCCGTCAT	36	expansion strand
1[296]	1[311]	AGATAATACATTGAGGATTAGCAAATATCAAACC	36	expansion strand
1[312]	1[327]	CTCAATCAATACTGGTCAGTGCCTGAGAAGTGT	36	expansion strand
1[328]	1[343]	TTTATAATCAGTGAGGCCACCGATGGTGCTTGAC	36	expansion strand
4[55]	4[40]	CCTGAGAGTCTGGTCGCATTAATTTGTTAAATC	36	expansion strand
4[71]	4[56]	TTCTCGGAACGAGCTAAAGGCTATCAGGTATTG	36	expansion strand
4[87]	4[72]	GCAAACTCCACATCCATATAACAGTTGATTCCAA	36	expansion strand
4[103]	4[88]	AAATCTACGTTAACTTCAAAGCGAACCGACCGGAA	36	expansion strand

4[119]	4[104]	ATTACCCAAATCAACCAGTCAGGACGTTGGGAAGAA	36	expansion strand
4[135]	4[120]	CGGTGCGCTGAGGCATCTTGACAAGAACCGGATATT	36	expansion strand
4[151]	4[136]	TAAAGGAATTGCGCGCCACCGATAACCGATATATT	36	expansion strand
4[167]	4[152]	TAATGCCCTGCGAGTGAGAATAGAAAGGAACAC	36	expansion strand
4[183]	4[168]	AGACGATTGGCCTGTAACAGTGCCTGTATAACAGT	36	expansion strand
4[199]	4[184]	TGGTTTACACAGCGTTGACAGGAGGTTGAGGCAGGTC	36	expansion strand
4[215]	4[200]	GGAAACCGAGGAATCACAAATCAATAGAAAAATTCTATA	36	expansion strand
4[231]	4[216]	CGGTATTCTAACAGAACAGAAAGTTACAGAA	36	expansion strand
4[247]	4[232]	CCATCCTAATTAAAATCAGATATAGAAGGCTTATC	36	expansion strand
4[263]	4[248]	CGGCTTAGGTTGGTCCTGAAACAAGAAAAATAATATC	36	expansion strand
4[279]	4[264]	GGAAACAGTACATTGAGAGACTACCTTTAACCTC	36	expansion strand
4[295]	4[280]	TCGACAACCTCGTATCATTTGAATTACCTTTTAAT	36	expansion strand
4[311]	4[296]	CCTTGCTAACCTAACAGTATTAGACTTTACAAACAA	36	expansion strand
4[327]	4[312]	AAATTAACCGTTGCAAATGAAAAATCTAAAGCATCA	36	expansion strand
4[343]	4[328]	AGGGCGCGTACTAGTAAAGAGTCTGTCCATCACGC	36	expansion strand
5[40]	5[55]	CCATCAAAATAATTGCGTCTGAAATTGCGGA	36	expansion strand
5[56]	5[71]	GAGGGTAGCTATTGGAGAGATTAGATTAGTTG	36	expansion strand
5[72]	5[87]	ACCATTAGATACTTCGCAAATGCCGAAAGACTT	36	expansion strand
5[88]	5[103]	CAAATATCGCGTTTAATTGAGTAAACGAACCAA	36	expansion strand
5[104]	5[119]	CGGAACAACATTATTACAGGTAGCCAGGCGATAGG	36	expansion strand
5[120]	5[135]	CTGGCTGACCTTCATCAAGAGTATTGCGAGGAGTTA	36	expansion strand
5[136]	5[151]	AAGGCCGCTTTGCGGGATCGTCTGGGATTTGCTA	36	expansion strand
5[152]	5[167]	AACAACTTTAACAGTTTCAGCGCTATTGCGAAC	36	expansion strand
5[168]	5[183]	TATTATTCTGAAACATGAAAGTACCGCCACCAGAAC	36	expansion strand
5[184]	5[199]	CACCAACAGGCCGCCAGCACCAAAGACAAAG	36	expansion strand
5[200]	5[215]	GGCGACATTCAACCGATTGAGGGTATCTTACCGAAG	36	expansion strand
5[216]	5[231]	CCCTTTTAAGAAAAGTAAGCAGACGCGAGCGTT	36	expansion strand
5[232]	5[247]	TAGCGAACCTCCGACTTGCAGGAATGCAGAACGCG	36	expansion strand
5[248]	5[263]	CCTGTTTACAAACATAGATAAGGTTATATAACTAT	36	expansion strand
5[264]	5[279]	ATGTAATGCTGATGCAAATCCAACATCAAGAAAAC	36	expansion strand
5[280]	5[295]	AAAATTAATTACATTAAACAATTGAAATCCCTTGC	36	expansion strand
5[296]	5[311]	CCGAACGTTATTAAATTAAAAGCACGCCGTGCAAC	36	expansion strand
5[312]	5[327]	AGTGCACGCGTAGAGGCCAGCAGTAGCAATACTCT	36	expansion strand
5[328]	5[343]	TTGATTAGTAATAACATCACTGAAAGTGTAGCGGTC	36	expansion strand
8[55]	8[40]	GTTCTAGCTGATAGCCTTCCTGTAGCCAGCTTCAT	36	expansion strand
8[71]	8[56]	TTTCATTTGGGCACCATCAATATGATATTCAACC	36	expansion strand
8[87]	8[72]	AGATTAAGAGGAAGGTCAATAACCTGTTAGCTATA	36	expansion strand
8[103]	8[88]	GGAATACACATTAAGCAAAGCGGATTGCAACAAA	36	expansion strand
8[119]	8[104]	AACGGTGTACAGAAAAGATTCATCAGTTGAGATT	36	expansion strand
8[135]	8[120]	TCGGAACGAGGGTCCAACCTTGAAAGAGGACAGATG	36	expansion strand
8[151]	8[136]	TGAATTTCCTGTAACCCCTCAGCAGCGAAAGACAGCA	36	expansion strand
8[167]	8[152]	AGAAGGATTAGGATCGTCTTCCAGACGTTAGTAAA	36	expansion strand
8[183]	8[168]	ACCACCCCTCAGAGTTAAGAGGCTGAGACTCCTCAAG	36	expansion strand
8[199]	8[184]	ATTATTCAATTAACTAGAACGCCACCCCTAGAGCC	36	expansion strand

8[215]	8[200]	AAATAGCAATAGCAGGGAGGTAAATATTGACGGAA	36	expansion strand
8[231]	8[216]	ATTAGTTGCTTAAATAAAGAGCAAGAACAAATG	36	expansion strand
8[247]	8[232]	AACATGTTAGCTAGGTTGAAGCCTAAATCAAG	36	expansion strand
8[263]	8[248]	AAACTTTTCAAACTGTCCAGACGACGACAATAAAC	36	expansion strand
8[279]	8[264]	GATGATGAAACAAATCGCAAGACAAAGAACCGGAGA	36	expansion strand
8[295]	8[280]	GGAACAAAGAAAATTTCATTACCTGAGCAGGAA	36	expansion strand
8[311]	8[296]	CGGTAGTATTAAATTGAGTAACATTATCATTTGC	36	expansion strand
8[327]	8[312]	TCCGCCCTTGCTGGCAGAAGATAAAACAGAGGTGAGG	36	expansion strand
8[343]	8[328]	CTAGGGCGCTGCCCTGAGTAGAAGAACTCAAACCA	36	expansion strand
9[40]	9[55]	CCCGTCGGATTCTCGTGGGAAACATTCAAAGGGTG	36	expansion strand
9[56]	9[71]	AGAAAGGCCGGAGACAGTCAAATCGCAGCTGAAAA	36	expansion strand
9[72]	9[87]	GGTGGCATCAATTCTACTAATAGCAAAATCAGGTC	36	expansion strand
9[88]	9[103]	TTTACCCCTGACTATTATAGTCAGCAACTATGCAGA	36	expansion strand
9[104]	9[119]	TACATAACGCCAAAGGAATTACAGGCGCAGACGGT	36	expansion strand
9[120]	9[135]	CAATCATAAGGAACCGAACTGAAGCAACGGCTACA	36	expansion strand
9[136]	9[151]	GAGGCTTGAGGACTAAAGACTTCAGCCCTCATAGT	36	expansion strand
9[152]	9[167]	TAGCGTAACGATCTAAAGTTGTTAGCGGGGTTT	36	expansion strand
9[168]	9[183]	GCTCAGTACCGCGGATAAGGCCACCACCGAAC	36	expansion strand
9[184]	9[199]	CGCCTCCCTCAGAGGCCACCCGGTAATTATCAC	36	expansion strand
9[200]	9[215]	CGTCACCGACTTGAGCCATTGGATCAGAGAGATAA	36	expansion strand
9[216]	9[231]	CCCACAAGAATTGAGTTAACGCCCTGCACCCAGCTA	36	expansion strand
9[232]	9[247]	CAATTTCATCCTGAATCTTACCAAGAGAATATAAG	36	expansion strand
9[248]	9[263]	TACCGACAAAAGGTAAAGTAATTATTTAGTTA	36	expansion strand
9[264]	9[279]	ATTTCATCTTCTGACCTAAATTACCAAGTTACAAA	36	expansion strand
9[280]	9[295]	ATCGCGCAGAGGCGAATTATTACACACCAGAGGAGC	36	expansion strand
9[296]	9[311]	GGAATTATCATCATATTCTGATAAACATGCCATT	36	expansion strand
9[312]	9[327]	AAAAATACCGAACGAACCACCAAGTAATATCCAGAAC	36	expansion strand
9[328]	9[343]	AATATTACCGCCAGCCATTGCAAACGGGAAAGCCG	36	expansion strand
12[55]	12[40]	TGTGTAGGTAAAGAACGGGGATTGACCGTAATGG	36	expansion strand
12[71]	12[56]	TCATACAGGAAGTTAAATGCAATGCCCTGAGTAA	36	expansion strand
12[87]	12[72]	AATGACCATAAATTAGTAGCATTAACATCCAATAAA	36	expansion strand
12[103]	12[88]	TCATAACCCCTCGTCTTAAACAGTTCAAGAACGAG	36	expansion strand
12[119]	12[104]	CTTAGCCGGAACGGAGGCATAGTAAGAGCAACACTA	36	expansion strand
12[135]	12[120]	ACGGGTAAAATACAATCCCGCACCTGCTCATGTTA	36	expansion strand
12[151]	12[136]	AGCATTCCACAGATTTCATGAGGAAGTTCCATTAA	36	expansion strand
12[167]	12[152]	ATAGCCCCGAATACCAAGTACAAACTACAACCCCTGT	36	expansion strand
12[183]	12[168]	ACCGGAACCAAGAGCGTCGAGAGGGTTGATATAAGT	36	expansion strand
12[199]	12[184]	AGTAGCACCATTAGCCATTTTCTATAATCAAACATC	36	expansion strand
12[215]	12[200]	ATTGAGCGCTAATGAATTAGAGCCAGCAAATCACC	36	expansion strand
12[231]	12[216]	GCCTAATTGCCAACCTGAAACAAAGTCAGAGGGTA	36	expansion strand
12[247]	12[232]	CGAGCCAGTAATAACGCTAACGAGCGTCTTCCAGA	36	expansion strand
12[263]	12[248]	TGATAAATAAGGCTGTAATTAGGCAGAGGGATT	36	expansion strand
12[279]	12[264]	GATTGCTTGAATAATGGTTGAAATACCGACCGTG	36	expansion strand
12[295]	12[280]	ATATAATCCTGATGAGAAACAATAACGGATTGCCT	36	expansion strand

12[311]	12[296]	ACTGATAGCCCTATATCAGATGATGGCAATTATCA	36	expansion strand
12[327]	12[312]	CCTACATTTGACGGCTATTAGTCTTAATCGCGCA	36	expansion strand
12[343]	12[328]	GATTTAGAGCTTGCAGGAAAAACGCTCATGGAAATA	36	expansion strand
13[40]	13[55]	GCATCGAACCGTCATCTGCCACAACGCAAGGATA	36	expansion strand
13[56]	13[71]	AAAATTTAGAACCTCATATAGCAAAGAATTAGC	36	expansion strand
13[72]	13[87]	AAAATTAAGCAATAAGCCTCAGAACGTCATAAAT	36	expansion strand
13[88]	13[103]	ATTCAATTGAATCCCCCTCAAATGTTACCAGACGACG	36	expansion strand
13[104]	13[119]	ATAAAAAACAAAATAGCGAGAGGCGGAGATTGTAT	36	expansion strand
13[120]	13[135]	CATCGCCTGATAAATTGTCAGTAATGCCACTAC	36	expansion strand
13[136]	13[151]	GAAGGCACCAACCTAAAACGAAAATAGGAACCCATG	36	expansion strand
13[152]	13[167]	TACCGTAACACTGAGTTTCGTCAGGTGTACCGT	36	expansion strand
13[168]	13[183]	ACTCAGGAGGTTAGTACCGCCATCGCATTTCGG	36	expansion strand
13[184]	13[199]	TCATAGCCCCCTTATTAGCGTTCCATTAGCAAGGC	36	expansion strand
13[200]	13[215]	CGGAAACGTCACCAATGAAACCAACAGGGAAAGCGCA	36	expansion strand
13[216]	13[231]	TTAGACGGGAGAATTAACACTGAACGTTACAAATAAA	36	expansion strand
13[232]	13[247]	CAGCCATATTATTATCCAACTCTTAATTGAGAAT	36	expansion strand
13[248]	13[263]	CGCCATATTAAACACGCCAACAGTTAAATAAGAAT	36	expansion strand
13[264]	13[279]	AAACACCGGAATCATAATTACTACAGATGAATATAC	36	expansion strand
13[280]	13[295]	AGTAACAGTACCTTTACATCGGTGTTGGATTATA	36	expansion strand
13[296]	13[311]	CTTCTGAATAATGGAAGGGTAGGCGTAAGAATACG	36	expansion strand
13[312]	13[327]	TGGCACAGACAATATTTGAATGCTCAATCGTCTG	36	expansion strand
13[328]	13[343]	AAATGGATTATTACATTGGCAGAAGTTTTGGGG	36	expansion strand
16[55]	16[40]	GAAGCCTTATTGTTGAGGGACGACGACAGTAT	36	expansion strand
16[71]	16[56]	CCAAAAACATTATGACCCGTAAATACTTTGCGGA	36	expansion strand
16[87]	16[72]	TCCAATACTGCGGAGCATAAAGCTAAATCGTTGTA	36	expansion strand
16[103]	16[88]	GAGGGGTAATAGTAAATGTTAGACTGGATAGCG	36	expansion strand
16[119]	16[104]	AAACAAAGTACAACCTTGCAAAAGAAGTTTGCCA	36	expansion strand
16[135]	16[120]	ACTCATTTGACCCCCAGCGATTACCAAGCGCG	36	expansion strand
16[151]	16[136]	GATAGCAAGCCCAGAGGCAAAAGAATACACTAAAC	36	expansion strand
16[167]	16[152]	ACCGCCACCCCTCAGAGCCACCCCTCATTTCAAG	36	expansion strand
16[183]	16[168]	TAGCGCTTTACCCCTCAGAACCGCCACCCCTCAGA	36	expansion strand
16[199]	16[184]	AGCGACAGAACATCAAGTTGCCTTACGCTCAGACTG	36	expansion strand
16[215]	16[200]	GAATAACATAAAATCGATAGCAGCACCGTAATCAGT	36	expansion strand
16[231]	16[216]	TAACGTCAAAATGAAAATAGCAGCCTTACAGAGA	36	expansion strand
16[247]	16[232]	CTCAACAGTAGGGCAAATAAGAAACGATTGTTGTT	36	expansion strand
16[263]	16[248]	TGCGTTATACAAATTCTTACCAAGTATAAGCCAACG	36	expansion strand
16[279]	16[264]	TCAGGTTAACGTGAAAAAGCTGTTAGTATCATA	36	expansion strand
16[295]	16[280]	GCACGTAAAACAGAAATAAGAAATTGCGTAGATT	36	expansion strand
16[311]	16[296]	TTCTGACCTGAAAAACCTACCATATCAAAATTATT	36	expansion strand
16[327]	16[312]	ATAAAAGGGACATTCTGGCAACAGAGATAGAACCC	36	expansion strand
16[343]	16[328]	CATCACCCAAATCATTCAACAGTCACACGACCAGTA	36	expansion strand

Table S3. Staple DNA sequence for 19×10 tube DNA origami array before expansion

Start	End	Sequence	Length	Note
0[55]	0[40]	GGGCCTGAAATCGAAGGAAGGAAGA	26	core strand
0[71]	0[56]	CATCTGTAAGCAAGGCACGAATATAG	26	core strand
0[87]	0[72]	AGATGGGCGCATCAGTGGGCCCTGC	26	core strand
0[103]	0[88]	TTAAATTGTTGTCACGTTGGTGT	26	core strand
0[119]	0[104]	AATGCAATGCCTGGTTAAAATTCGCA	26	core strand
0[135]	0[120]	ATAACAGTTGATTCTCATATATTTA	26	core strand
0[151]	0[136]	AAGCGAACAGACAGTTCATCCAT	26	core strand
0[167]	0[152]	TCAGGACGTTGGAATTGGAGCTTCA	26	core strand
0[183]	0[168]	CCTTATGCGATTCTCATTTACAG	26	core strand
0[199]	0[184]	GAAAAATCTAAAGTCATTGTGAATT	26	core strand
0[215]	0[200]	GCCACTACGAAGGCCAGCAGCAAAT	26	core strand
0[231]	0[216]	AAGAAATTGCGTATAAAACGTAAT	26	core strand
0[247]	0[232]	TTTCCAGACGTTATAAACAGAAATA	26	core strand
0[263]	0[248]	ATAACTATATGTAAGTTGTCGTC	26	core strand
0[279]	0[264]	GTAATAAGTTTATAGGTTGGTTAT	26	core strand
0[295]	0[280]	AACAAGAAAAATACAGGAGTGTACTG	26	core strand
0[311]	0[296]	AGCAAGGCCGGAATAGATAAGTCCTG	26	core strand
0[327]	0[312]	AGAGCCAGCAAAACACCATTACCAT	26	core strand
0[343]	0[328]	AGATATAGAAGGCCATTGGATT	26	core strand
1[40]	1[55]	CTGGCAAGTGTAGGCGCGTAACCACC	26	core strand
1[56]	1[71]	ACACCCCGCGCGCTACAGGCCGCG	26	core strand
1[72]	1[87]	TACTATGGTTGCTCGGATTCTCCGTG	26	core strand
1[88]	1[103]	GGAACAAACGGCGAAATCAGCTCATT	26	core strand
1[104]	1[119]	TTTTAACCAATAGCGGGAGAACCTT	26	core strand
1[120]	1[135]	TATTTCAACGCAACCCAATTCTGCGA	26	core strand
1[136]	1[151]	ACGAGTAGATTACAAAAAGATTAAG	26	core strand
1[152]	1[167]	AGGAAGCCGAAAAAGAAAAATCTAC	26	core strand
1[168]	1[183]	GTTAACAAACGAGAACGAGTAGTAA	26	core strand
1[184]	1[199]	ATTGGGCTTGAGACATCACCTTGCTG	26	core strand
1[200]	1[215]	AACCTCAAATATCTTGAGGACTAAA	26	core strand
1[216]	1[231]	GACTTTTCATGAGATTTCAAGTTT	26	core strand
1[232]	1[247]	AACGTCAGATGAACCTGTAGCATTCC	26	core strand
1[248]	1[263]	ACAGACAGCCCTCAATGCTGATGCAA	26	core strand
1[264]	1[279]	ATCCAATCGCAAGCTGAATTACCGT	26	core strand
1[280]	1[295]	TCCAGTAAGCGTCATATCCCATCCTA	26	core strand
1[296]	1[311]	ATTTACGAGCATGTCATAATCGGCT	26	core strand
1[312]	1[327]	GTCTTCCATTACCGGGTATTAAACC	26	core strand
1[328]	1[343]	AAGTACCGCACTCAGCAAGCCGTTT	26	core strand
4[55]	4[40]	TGCCCGCTTCCACTGTCGTGCCAGC	26	core strand
4[71]	4[56]	GAATCAGAGCGGGCGTTGCGCTCAC	26	core strand
4[87]	4[72]	AGTAACAAACCGTGTCTCGTTA	26	core strand
4[103]	4[88]	CCTGTAGCCAGCTTAAATGTGAGCG	26	core strand

4[119]	4[104]	TGTAATACTTTGCAGCTGGCCTT	26	core strand
4[135]	4[120]	ATAAACCTGTTAGAACATTATGACCC	26	core strand
4[151]	4[136]	AAGCGGATTGCATTGCAAATGGTCA	26	core strand
4[167]	4[152]	TTCATCAGTGAGATAGTCAGAAGCA	26	core strand
4[183]	4[168]	ACGAGAAACACCAACAGGTAGAAAGA	26	core strand
4[199]	4[184]	TCAACAGTGAAAAGGCTGCCCTG	26	core strand
4[215]	4[200]	CGGCTACAGAGGCCAGTTGGCAAA	26	core strand
4[231]	4[216]	ACAATAACGGATTACGAGGGTAGCAA	26	core strand
4[247]	4[232]	ACAAACTACAACGTACATCGGGAGAA	26	core strand
4[263]	4[248]	TTTAGTTAATTCTTCGTCACAGT	26	core strand
4[279]	4[264]	GAAAGCGCAGTCTTTCAAATATAT	26	core strand
4[295]	4[280]	TTCACACAAATTAAAGGCCAGAATG	26	core strand
4[311]	4[296]	AGGAGGTTGAGGCATTGCCCTTGATA	26	core strand
4[327]	4[312]	ATAATAACGGAATCGCCAGCATGAC	26	core strand
4[343]	4[328]	CGAACAAAGTTACCGAGGAAACGCA	26	core strand
5[40]	5[55]	GGGAGAGCGGTTGTGTAAAGCCTGG	26	core strand
5[56]	5[71]	GGTGCCTAATGAGAGCTAACAGGAG	26	core strand
5[72]	5[87]	GCGCATTAAAGGGGAACGGTACGCC	26	core strand
5[88]	5[103]	AGAATCCTGAGAAAATCAGTGAGGCC	26	core strand
5[104]	5[119]	ACCGAGTAAAGATAAGCAATAAACGC	26	core strand
5[120]	5[135]	CTCAGAGCATAAACTATATTTTCATT	26	core strand
5[136]	5[151]	TGGGGCGCGAGCTACGAGAATGACCA	26	core strand
5[152]	5[167]	TAAATCAAAATCATTAGGAATACC	26	core strand
5[168]	5[183]	ACATTCAACTAATTATTCACTACCCA	26	core strand
5[184]	5[199]	AATCAACGTAACAGGAATTGAGGAAG	26	core strand
5[200]	5[215]	GTTATCTAAAATACGCTTTGCCGGA	26	core strand
5[216]	5[231]	TCGTCACCCCTCAGCGCCTGATTGCTT	26	core strand
5[232]	5[247]	TGAATACCAAGTTTCAGGGATAGCAA	26	core strand
5[248]	5[263]	GCCCAATAGGAACATCTCTGACCTA	26	core strand
5[264]	5[279]	AATTTAATGGTTCCGTGTGATAAAT	26	core strand
5[280]	5[295]	AAGGCCTTAAACCGGAATCATAAT	26	core strand
5[296]	5[311]	TACTAGAAAAAGCGAGCCACCACCT	26	core strand
5[312]	5[327]	CAGAGCGCCACCACCCAAAAGAACT	26	core strand
5[328]	5[343]	GGCATGATTAAGACAATGAAATGCA	26	core strand
8[55]	8[40]	CCGGAAGCATAAGGTTTCTTTTC	26	core strand
8[71]	8[56]	AGTCACGAGCTTGACAAACATACGAG	26	core strand
8[87]	8[72]	CAAGGCCTTAAAGCCAGGTTTCCC	26	core strand
8[103]	8[88]	ATACTTCTTGATGGGGATGTGCTG	26	core strand
8[119]	8[104]	GAATTAGCAAAATAACCGTTGTAGCA	26	core strand
8[135]	8[120]	GCATTAACATCCACAGGCAAGGCAA	26	core strand
8[151]	8[136]	AACAGTTCAGAAAATAGTAGTA	26	core strand
8[167]	8[152]	ATAGTAAGAGCAACTCAAATGCTTA	26	core strand
8[183]	8[168]	GACAAGAACGGAGGAATTACGAGGC	26	core strand
8[199]	8[184]	CCGTCAATAGATAAGAGTAATCTT	26	core strand

8[215]	8[200]	GGGAGTTAAAGGCTAATAGATTAGAG	26	core strand
8[231]	8[216]	ATTACCTGAGCAAGCTGAGGCTTGCA	26	core strand
8[247]	8[232]	ACCACCCCTCATTATTATTTCATTTCA	26	core strand
8[263]	8[248]	AGAACCGCCACCCCACCCCTCAGAGCC	26	core strand
8[279]	8[264]	ATCACCGTACTCATACGCCACCCCTC	26	core strand
8[295]	8[280]	ACCAGTATAAAGCCCGGAATAGGTGT	26	core strand
8[311]	8[296]	ACCGCCACCCCTCATATACAAATTCTT	26	core strand
8[327]	8[312]	AAATACATACATACGCCACCCCTCAGA	26	core strand
8[343]	8[328]	TAAGAGCAAGAAAATAGCAAACGTAGA	26	core strand
9[40]	9[55]	GCCCTTCACCGCCGTATAGCTGTTT	26	core strand
9[56]	9[71]	CCTGTGTGAAATTAAAAGACGGCC	26	core strand
9[72]	9[87]	AGTGCCAAGCTTAGGGCGATCGGTG	26	core strand
9[88]	9[103]	CGGGCCTCTCGCTAGTAATAACATC	26	core strand
9[104]	9[119]	ACTTGCCTGAGTAAACTATCGGCCTT	26	core strand
9[120]	9[135]	GCTGGTAATATCCTACCGCCAGCCAT	26	core strand
9[136]	9[151]	TGCAACAGGAAAATAGCGTCCAATAC	26	core strand
9[152]	9[167]	TGCGGAATCGTCACACTATCATAACC	26	core strand
9[168]	9[183]	CTCGTTTACCAAGAGATGAACGGTGT	26	core strand
9[184]	9[199]	ACAGACCGAGGCGCATACATTGAGGA	26	core strand
9[200]	9[215]	TTTAGAAGTATTAGACAATGACAACA	26	core strand
9[216]	9[231]	ACCATGCCACGAAGAAGATGATGA	26	core strand
9[232]	9[247]	AACAAACATCAAGTAATTACATTAA	26	core strand
9[248]	9[263]	CAATTTCATTTGATTAATGGAAACAG	26	core strand
9[264]	9[279]	TACATAAAATCAATGTACCAGGCGGAT	26	core strand
9[280]	9[295]	AAGTGCCGTCGAGCAACGCTCAACAG	26	core strand
9[296]	9[311]	TAGGGCTTAATTGAAATCACCGGAAC	26	core strand
9[312]	9[327]	CAGAGGCCACCACCAAGGTGGCAACAT	26	core strand
9[328]	9[343]	ATAAAAGAAAACGCGGTAATTGAGCG	26	core strand
12[55]	12[40]	ATTCGTAATCATGCAAGCGGTCCACG	26	core strand
12[71]	12[56]	TGGTTGTGAAATTGTCACCGAGCTCGA	26	core strand
12[87]	12[72]	GCAACTGTTGGGAATGTTCTCTAAG	26	core strand
12[103]	12[88]	ACAAGAGAATCGACCATTCAAGCTGC	26	core strand
12[119]	12[104]	AAGGCTATCAGGTGAGTCTGGAGCAA	26	core strand
12[135]	12[120]	ATCGTCTGAAATGTGAGAGATCTACA	26	core strand
12[151]	12[136]	TGTTTAGACTGGAATTTGACGCTCA	26	core strand
12[167]	12[152]	GCAAAAGAAGTTGGTAATAGAAAAA	26	core strand
12[183]	12[168]	TTTGAAGAGGACGCGAGAGGCTTT	26	core strand
12[199]	12[184]	TCCTTTGCCCGAACGAACTGACCAAC	26	core strand
12[215]	12[200]	CGATAGTTGCGCCAACTCGTATTAAA	26	core strand
12[231]	12[216]	TTGCTTTCGAGGTAACAGCTTGATAC	26	core strand
12[247]	12[232]	TCCAAAAGGAGCCTCGGTTATCAGC	26	core strand
12[263]	12[248]	GTCGCTATTAATTCCAAAAAAAGGC	26	core strand
12[279]	12[264]	GGGGTTTGCTCAGCTCTGTAAATC	26	core strand
12[295]	12[280]	TTTAGGCAGAGGCGATTAGGATTAGC	26	core strand

12[311]	12[296]	CTTTTCATAATCACGCCAACATGTAA	26	core strand
12[327]	12[312]	ATCAATAGAAAATTAGCGTTGCCAT	26	core strand
12[343]	12[328]	GAACAAAGTCAGATTATTTGTCACA	26	core strand
13[40]	13[55]	CTGTTGATGGTGAAGCTACGTGGTG	26	core strand
13[56]	13[71]	CTTGTACCTCGAATGCGCACGACTT	26	core strand
13[72]	13[87]	AAGTGTCCCTAGTTCCGGCACCGCT	26	core strand
13[88]	13[103]	TCTGGTGC CGGAATGAACGGTAATCG	26	core strand
13[104]	13[119]	TAAAATAGCATGCAACC GTTCTAGC	26	core strand
13[120]	13[135]	TGATAAATTAAATGGATTATTTACATT	26	core strand
13[136]	13[151]	GGCAGATT CACCACAGTAATAAAGG	26	core strand
13[152]	13[167]	GACATTCTGGCAAACCCCTCTGACC	26	core strand
13[168]	13[183]	TGAAAGCGTAAGATGTTACTTAGCCG	26	core strand
13[184]	13[199]	GAACGAGGCAGCGTTATTAATTTT	26	core strand
13[200]	13[215]	AAAAGTTGAGTATTGCGGAACAAA	26	core strand
13[216]	13[231]	GAAACCAC CAGAATATCATCATATT	26	core strand
13[232]	13[247]	CTGATTATCAGATACA ACTAAAGGAA	26	core strand
13[248]	13[263]	TTGCGAATAATAAAATTCCCTTAG	26	core strand
13[264]	13[279]	AATCCCTGAAAACTTCTGAAACATGA	26	core strand
13[280]	13[295]	AAGTATTAAAGAGGATTTGAGCCAG	26	core strand
13[296]	13[311]	TAATAAGAGAATAGACTGTAGCGCGT	26	core strand
13[312]	13[327]	TTTCATCGCATTTCATATGGTTAC	26	core strand
13[328]	13[343]	CAGCGCAAAGACAGAGAGATAACA	26	core strand
16[55]	16[40]	GTAAACAGGGCTTCCTTATAATCAA	26	core strand
16[71]	16[56]	AAAATAACCCCGCGTTGGTGTAAATGA	26	core strand
16[87]	16[72]	ACTCCAGCCAGCTACAATGTCCC GCC	26	core strand
16[103]	16[88]	AGCCCCAAAAACATCAGGAAGATCGC	26	core strand
16[119]	16[104]	TCAATATGATATTGATAATCAGAAA	26	core strand
16[135]	16[120]	TGAATATAATGCTAGTCAAATCACCA	26	core strand
16[151]	16[136]	GAGGTATTTGAGAGCTTAATTGC	26	core strand
16[167]	16[152]	TTAGTCTTAATGCTCCTTTGATAA	26	core strand
16[183]	16[168]	GCGACCTGCTCCATTGAAATGGCTA	26	core strand
16[199]	16[184]	ATTTGTATCATCGTGTGTC GAAATCC	26	core strand
16[215]	16[200]	GCGATTATACCAAAAGTACAACGGAG	26	core strand
16[231]	16[216]	GGATTATACTTCTTCTTGACCCCCA	26	core strand
16[247]	16[232]	AGAATAGAAAGGAATCCTGATTGTT	26	core strand
16[263]	16[248]	GTCAATAGTGAATTTCAGCGGAGTG	26	core strand
16[279]	16[264]	TCGGAA CCTTATTAGACGCTGAGAAGA	26	core strand
16[295]	16[280]	CAGACGACGACAACCCCTGCCTATT	26	core strand
16[311]	16[296]	GCCTTTAGCGTCAAAGTAATTCTGTC	26	core strand
16[327]	16[312]	AGGTAAATATTGACAGAACATCAAGTT	26	core strand
16[343]	16[328]	TAGCAGCCTTACATTGAGGGAGGGA	26	core strand
17[40]	17[55]	GCTTGACGGGGAGCTGACG CATTTC	26	core strand
17[56]	17[71]	ACATAAATCATTTCTAATCTATT	26	core strand
17[72]	17[87]	ACGCTGCCCTGGTAACCGTGCATC	26	core strand

17[88]	17[103]	TGCCAGTTGAGGGGAAGATTGTATA	26	core strand
17[104]	17[119]	AGCAAATATTTAAAGTAATGTGAGG	26	core strand
17[120]	17[135]	TAAAGATTCAAAAGTAGCTAACATG	26	core strand
17[136]	17[151]	TTTTAAATATGCACCGAAGCAAAC	26	core strand
17[152]	17[167]	CAACAGGTCAAGACGCGAAGTGA	26	core strand
17[168]	17[183]	CCCTAAAACATCGTACCGAACGAA	26	core strand
17[184]	17[199]	ACCAGCAGAAGATTGAGGCCGTCAG	26	core strand
17[200]	17[215]	ATTAACACCGCCTACCAACCTAAA	26	core strand
17[216]	17[231]	CGAAAGAGGCAAAGAATAATGGAAG	26	core strand
17[232]	17[247]	GTTAGAACCTACCGTAAATGAATT	26	core strand
17[248]	17[263]	CTGTATGGGATTTTATCAAAATCAT	26	core strand
17[264]	17[279]	AGGTCTGAGAGACACGGGTCAGTGC	26	core strand
17[280]	17[295]	CTTGAGTAACAGTTAAACACATGTT	26	core strand
17[296]	17[311]	CAGCTAATGCAGAACGTCACCAATGA	26	core strand
17[312]	17[327]	AACCATCGATAGCCGAAATTATTCA	26	core strand
17[328]	17[343]	TTAAAGGTGAATTATTCGGTATT	26	core strand
18[348]	19[348]	TTGTTAACCGGTTTAGCG	20	loop strand
18[359]	19[359]	CAAATAAGAAACGATTTAACCTCCC	36	loop strand
18[367]	19[367]	ACAGCCATATTATTTATCCAATCAG	48	loop strand
18[375]	19[375]	CTTAATTGCCAGTTACAAAATAATT	48	loop strand
18[383]	19[383]	ACGCTAACGAGCGTCTTCCAGAGAC	48	loop strand
17[0]	16[0]	GGCGATGCCACTACGTGAACCAAGG	48	loop strand
17[8]	16[8]	ATCACCAAACTCAAGTTTGGAT	48	loop strand
17[16]	16[16]	GTCGAGGTGCCGTAAAGCACTAA	48	loop strand
17[24]	16[24]	TCGGAACCTAAAGGGAGGATAGG	36	loop strand

Table S4. Expansion strand sequence for 19X10 tube DNA origami array

Start	End	Sequence	Length	Note
0[55]	0[40]	GGGCCTTGAATCGCGTGGCAGAAAGGAAGGAAAGA	36	expansion strand
0[71]	0[56]	CATCTGTAAGCACTCGTCGGTGGCACGAATATAG	36	expansion strand
0[87]	0[72]	AGATGGCGCATCTGATACCGACAGTGC	36	expansion strand
0[103]	0[88]	TTAAATTGTTGTTAATGGGATAGGTCA	36	expansion strand
0[119]	0[104]	AATGCAATGCCGTAAATTTGTTAA	36	expansion strand
0[135]	0[120]	ATAACAGTTGATTTTAAACCTCATAT	36	expansion strand
0[151]	0[136]	AAGCGAACCAAGACGGTCTGGAA	36	expansion strand
0[167]	0[152]	TCAGGACGTTGGATCCGTTAATTGAGCT	36	expansion strand
0[183]	0[168]	CCTTATCGATTTAAAGACTGGCT	36	expansion strand
0[199]	0[184]	GAAAAATCTAAAGTCAC	36	expansion strand
0[215]	0[200]	GCCACTACGAAAGCACGCTGAGAGCC	36	expansion strand
0[231]	0[216]	AAGAAATTGCGTAATTAAACGGTAA	36	expansion strand
0[247]	0[232]	TTTCAGACGTTATTTGACGTAA	36	expansion strand
0[263]	0[248]	ATAACTATATGTATAACGATCTAAAG	36	expansion strand

0[279]	0[264]	GTAATAAGTTAACCTCCGGTTAGGTTGGTTAT	36	expansion strand
0[295]	0[280]	AACAAGAAAAATATTGATGATACAGGAGTGTACTG	36	expansion strand
0[311]	0[296]	AGCAAGGCCGAATTATCAACAATAGATAAGTCCTG	36	expansion strand
0[327]	0[312]	AGAGCCAGCAAATCACCAGTAGCACCATTAACATT	36	expansion strand
0[343]	0[328]	AGATATAGAAGGCCGACTTGAGCCATTGGGAATT	36	expansion strand
1[40]	1[55]	CTGGCAAGTGTAGCGGTACGCTGCGCTAACCAACC	36	expansion strand
1[56]	1[71]	ACACCCCGCGCTTAATGCGCCCTACAGGGCGC	36	expansion strand
1[72]	1[87]	TACTATGGTTGCTTGACGAGCACGGATTCTCGTG	36	expansion strand
1[88]	1[103]	GGAACAAACGGCGGATTGACCGTAAATCAGCTCATT	36	expansion strand
1[104]	1[119]	TTTTAACCAATAGGAACGCCATCCGGAGAACCTT	36	expansion strand
1[120]	1[135]	TATTTCACGCAGGATAAAAATCCAATTCTGCAGA	36	expansion strand
1[136]	1[151]	ACGAGTAGATTTAGTTGACCATCAAAAGATTAAG	36	expansion strand
1[152]	1[167]	AGGAAGCCGAAAGACTTCAAATAAGAAAAATCTAC	36	expansion strand
1[168]	1[183]	GTAAATAAAACGAACTAACGGAAGAACGAGTAGTAA	36	expansion strand
1[184]	1[199]	ATTGGGCTTGAGATGGTTAACATCACCTTGCTG	36	expansion strand
1[200]	1[215]	AACCTCAAATATCAAACCCCTCAATTGAGGACTAAA	36	expansion strand
1[216]	1[231]	GACTTTTCATGAGGAAGTTCCGATTTCAAGGTTT	36	expansion strand
1[232]	1[247]	AACGTCAGATGAATATACAGTAACCTGTAGCATTCC	36	expansion strand
1[248]	1[263]	ACAGACAGCCCTCATAGTTAGCGAATGCTGATGCAA	36	expansion strand
1[264]	1[279]	ATCCAATCGCAAGACAAAGAACGCTGAATTACCGT	36	expansion strand
1[280]	1[295]	TCCAGTAAGCGTCATACATGGCTATATCCCACCTA	36	expansion strand
1[296]	1[311]	ATTACCGAGCATGTAGAACCAATCAATACTGGCT	36	expansion strand
1[312]	1[327]	GTCTTCCTTATCATTCCAAGAACGGTATTAAACC	36	expansion strand
1[328]	1[343]	AAGTACCGCACTCATCGAGAACAGCAAGCCGTTT	36	expansion strand
4[55]	4[40]	TGCCCGTTCCAGTCGGAAACCTGTCGTGCCAGC	36	expansion strand
4[71]	4[56]	GAATCAGAGCGGGCACATTAATTGCGTTGCGCTCAC	36	expansion strand
4[87]	4[72]	AGTAACAAACCCCTCGTATAACGTGCTTCCTCGTTA	36	expansion strand
4[103]	4[88]	CCTGTAGCCAGCTTCATCAACATTAAATGTGAGCG	36	expansion strand
4[119]	4[104]	TGTAATACTTTGAAAAATAATTGCGCTCTGGCCTT	36	expansion strand
4[135]	4[120]	ATAACCTGTTAGTTGACCAAAACATTATGACCC	36	expansion strand
4[151]	4[136]	AAGCGGATTGCAATTAGACATTCGCAAATGGTCA	36	expansion strand
4[167]	4[152]	TTCATCAGTTGAGCCTGACTATTATAGTCAGAAC	36	expansion strand
4[183]	4[168]	ACGAGAAACACCACAAACATTATTACAGGTAGAAAGA	36	expansion strand
4[199]	4[184]	TCAACAGTTGAAATTCACTGAATAAGGCTTGCCTG	36	expansion strand
4[215]	4[200]	CGGCTACAGAGGCTCAATATCTGGTCAGTTGGCAA	36	expansion strand
4[231]	4[216]	ACAATAACGGATTCACTCGAACAGGGTAGCAA	36	expansion strand
4[247]	4[232]	ACAAACTACAACCGAGTACCTTTACATCGGGAGAA	36	expansion strand
4[263]	4[248]	TTTAGTTAACCTCAACACTGAGTTGCGTACCAAGT	36	expansion strand
4[279]	4[264]	GAAAGCCAGTCTCGAGAAAACCTTTCAAATATAT	36	expansion strand
4[295]	4[280]	TTCACAAACAAATAATCCTCATTAAGCCAGAATG	36	expansion strand
4[311]	4[296]	AGGAGGTTGAGGCAAGTCAGACGATTGGCCTTGATA	36	expansion strand

4[327]	4[312]	ATAATAACGGAATCCAGAGCCGCCAGCATTGAC	36	expansion strand
4[343]	4[328]	CGAACAAAGTTACCAGAAGGAAACCGAGGAAACGCA	36	expansion strand
5[40]	5[55]	GGGAGAGGCCTTGCCTATTGGGTGTAAGCCTGG	36	expansion strand
5[56]	5[71]	GGTGCTTAATGAGTGAAGTAACTAGCTAACAGGAG	36	expansion strand
5[72]	5[87]	GCCGATTAAAGGGATTAGACAGGAACGGTACGCC	36	expansion strand
5[88]	5[103]	AGAATCCTGAGAAGTGTAAAACTAGTGAGGCC	36	expansion strand
5[104]	5[119]	ACCGAGTAAAAGAGTCGTCCATTAAAGCAATAAAGC	36	expansion strand
5[120]	5[135]	CTCAGACATAAGCTAAATCGCTATATTTTATT	36	expansion strand
5[136]	5[151]	TGGGGCCGAGCTGAAAGGTGGACGAGAATGACCA	36	expansion strand
5[152]	5[167]	TAAATCAAAATCAGGTCTTACATTAGGAATACC	36	expansion strand
5[168]	5[183]	ACATTCAACTAATGCAGATACTTATTACCA	36	expansion strand
5[184]	5[199]	AATCAACGTAACAAAGCTGCTCAGGAATTGAGGAAG	36	expansion strand
5[200]	5[215]	GTTATCTAAAATATCTTAGGAGCGCTTTGCAGGA	36	expansion strand
5[216]	5[231]	TCGTCACCCCTCAGCAGCGAAAGACGCCTGATTGCTT	36	expansion strand
5[232]	5[247]	TGAATACCAAGTTACAAAATCGCTCAGGGATAGCAA	36	expansion strand
5[248]	5[263]	GCCCAATAGGAACCCATGTACCGATCTCTGACCTA	36	expansion strand
5[264]	5[279]	AATTAAATGGTTGAAATACCGACCGTGTGATAAAT	36	expansion strand
5[280]	5[295]	AAGGCCTTAAATAAGAATAAACACCGGAATCATAAT	36	expansion strand
5[296]	5[311]	TACTAGAAAAGCCTGTTAGTAGAGGCCACCCT	36	expansion strand
5[312]	5[327]	CAGAGCCGCCACCAGAACCAACCAACCAAAGAACT	36	expansion strand
5[328]	5[343]	GGCATGATTAAGACTCCTTATTACAATGAAATAGCA	36	expansion strand
8[55]	8[40]	CCGGAAGCATAAAGCGCAGGGTGGTTTCTTT	36	expansion strand
8[71]	8[56]	AGTCACGACGTTGCACAATTCCACACACATACGAG	36	expansion strand
8[87]	8[72]	CAAGGCCTTAAAGTTGGTAACGCCAGGGTTTCCC	36	expansion strand
8[103]	8[88]	ATACTTCTTGATGCTGGCAGGGGATGTGCTG	36	expansion strand
8[119]	8[104]	GAATTAGCAAATCACCGAAATTACCGTTGTAGCA	36	expansion strand
8[135]	8[120]	GCATTAACATCCAATAATCATACAGCGAAGGAAA	36	expansion strand
8[151]	8[136]	AACAGTTCAGAACATCAATTCTACTAATAGTAGTA	36	expansion strand
8[167]	8[152]	ATAGTAAGAGCAATTGAATCCCCCTCAATGCTTTA	36	expansion strand
8[183]	8[168]	GACAAGAACGGAAACGCCAAAGGAATTACGAGGC	36	expansion strand
8[199]	8[184]	CCGTCATAGATATGACCTTCATCAAGAGTAATCTT	36	expansion strand
8[215]	8[200]	GGGAGTTAAAGGCCACTAACAACTAATAGATTAGAG	36	expansion strand
8[231]	8[216]	ATTACCTGAGCAAATTGGTCGCTGAGGCTTGCA	36	expansion strand
8[247]	8[232]	ACCACCCCTCATTCAGAGGCCATTTCATTTCA	36	expansion strand
8[263]	8[248]	AGAACGCCACCCCTCAGAACGCCACCCCTCAGAGCC	36	expansion strand
8[279]	8[264]	ATCACCGTACTCAGGAGGTTAGTACGCCACCCCTC	36	expansion strand
8[295]	8[280]	ACCACTATAAGCTAAGTATAGCCCGAATTAGGTGT	36	expansion strand
8[311]	8[296]	ACCGCCACCCCTCATATGCCTTACAAATTCTT	36	expansion strand
8[327]	8[312]	AAATACATACATACCCCTCAGAGCCGCCACCCCTCAGA	36	expansion strand
8[343]	8[328]	TAAGAGCAAGAACGCAGTATGTTAGCAAACGTAGA	36	expansion strand
9[40]	9[55]	GCCCTTCACCGCCTGGCCCTGAGGTCAAGCTGTT	36	expansion strand

9[56]	9[71]	CCTGTGTGAAATTGTTATCCGTTAAAACGACGGCC	36	expansion strand
9[72]	9[87]	AGTGCCAAGCTTCTCAGGAGAAAGGGCGATCGGTG	36	expansion strand
9[88]	9[103]	CGGGCCTTCGCTATTACGCCATAGTAATAACATC	36	expansion strand
9[104]	9[119]	ACTTGCCCTGAGTAGAAGAACTCAAACATCGGCC	36	expansion strand
9[120]	9[135]	GCTGGTAATATCCAGAACAAATTACGCCAGCCAT	36	expansion strand
9[136]	9[151]	TGCAACAGGAAAACGCTCATGGTAGCGTCAATAC	36	expansion strand
9[152]	9[167]	TGCGGAATCGTCATAAAATTACACTATCATAACC	36	expansion strand
9[168]	9[183]	CTCGTTACCAGACGACGATAAAAGATGAACGGTGT	36	expansion strand
9[184]	9[199]	ACAGACCAGGCGCATAGGCTGGCATACATTGAGGA	36	expansion strand
9[200]	9[215]	TTTAGAAGTATTAGACTTACAAGACAATGACAACA	36	expansion strand
9[216]	9[231]	ACCATGCCCACGCATAACCGATAAGAAGATGATGA	36	expansion strand
9[232]	9[247]	AACAAACATCAAGAAAACAAAATTAAATTACATTAA	36	expansion strand
9[248]	9[263]	CAATTCATTGAAATTACCTTTTAATGGAAACAG	36	expansion strand
9[264]	9[279]	TACATAAATCAATATATGTGAGTGTACCGCGGAT	36	expansion strand
9[280]	9[295]	AAGTGCCGTCGAGAGGTTGATACAACGCTAACAG	36	expansion strand
9[296]	9[311]	TAGGGCTTAATTGAGAATGCCAAATCACCGGAAC	36	expansion strand
9[312]	9[327]	CAGAGCCACCACCGAACCGCTAAGGTGGCAACAT	36	expansion strand
9[328]	9[343]	ATAAAAGAAACGCAAAGACACCAGGGTAATTGAGCG	36	expansion strand
12[55]	12[40]	ATTCTGAAATCATGAGAGTTGCGAGCAAGCGGTACG	36	expansion strand
12[71]	12[56]	TGGTTGTGAATTGGATCCCCGGTACCGAGCTCGA	36	expansion strand
12[87]	12[72]	GCAACTGTTGGAGGCCAGGGTGGATGTTCTCTAAG	36	expansion strand
12[103]	12[88]	ACAAGAGAAATCGAGCGCATTGCCATTAGGCTGC	36	expansion strand
12[119]	12[104]	AAGGCTATCAGGTCAATTGCTGAGAGTCTGGAGCAA	36	expansion strand
12[135]	12[120]	ATCGTCTGAAATGTAGCTATTGAGAGATCTACA	36	expansion strand
12[151]	12[136]	TGTTTAGACTGAAAAATACCTACATTGACGCTCA	36	expansion strand
12[167]	12[152]	GCAAAAGAAGTTTGCCAGAGGGGTAATAGTAAA	36	expansion strand
12[183]	12[168]	TTTGAAAGAGGACAACCAAAATAGCGAGAGGTTT	36	expansion strand
12[199]	12[184]	TCCTTGCCTGAAATAAGGAACCGAACTGACCAAC	36	expansion strand
12[215]	12[200]	CGATAGTTGCGCCACAATTGACAACCTGTATTA	36	expansion strand
12[231]	12[216]	TTGCTTCGAGGTGAATTCTAACAGCCTTGATAC	36	expansion strand
12[247]	12[232]	TCCAAAAGGAGCCTTAATTGTATCGTTTATCAGC	36	expansion strand
12[263]	12[248]	GTCGCTATTAAATTGAAAATCTCCAAAAAAGGC	36	expansion strand
12[279]	12[264]	GGGGTTTGCTCAGAATAACCTGCTCTGTAAATC	36	expansion strand
12[295]	12[280]	TTTAGGCAGAGGCTCAAGAGAAGGATTAGGATTAGC	36	expansion strand
12[311]	12[296]	CTTTTCATAATCATATTAAACACGCCAACATGTAA	36	expansion strand
12[327]	12[312]	ATCAATGAAAATGCCCTTATTAGCCTTGCCAT	36	expansion strand
12[343]	12[328]	GAACAAAGTCAGACGGAATAAGTTATTGTCA	36	expansion strand
13[40]	13[55]	CTGTTGATGGTGGTCCGAAATAAGCTACGTGGTG	36	expansion strand
13[56]	13[71]	CTTGTACCTCGATAAGACGGAATGCGCACGACTT	36	expansion strand
13[72]	13[87]	AAGTGTCTTAGTGTGAAATTGTTCCGGCACCGCT	36	expansion strand
13[88]	13[103]	TCTGGTGCGGAAACCAGGCAAATGAACGGTAATCG	36	expansion strand

13[104]	13[119]	TAAAACATGCAATCATATCAACCGTTCTAGC	36	expansion strand
13[120]	13[135]	TGATAAAATTAAATGCCGGAGAGGGATTATTCACATT	36	expansion strand
13[136]	13[151]	GGCAGATTCAACCAGTCACACGACCAGTAATAAAAGG	36	expansion strand
13[152]	13[167]	GACATTCTGGCCAACAGAGATAGAACCTTCTGACC	36	expansion strand
13[168]	13[183]	TGAAAGCGTAAGAATACGTGGCATTTACTTAGCCG	36	expansion strand
13[184]	13[199]	GAACGAGGCAGACGGTCATCCGTTATTAATTT	36	expansion strand
13[200]	13[215]	AAAAGTTGAGTAACATTATCATTGCGGAACAAA	36	expansion strand
13[216]	13[231]	GAAACCACCAGAAGGAGCGGAATTATCATCATATT	36	expansion strand
13[232]	13[247]	CTGATTATCAGATGATGGCAATTACAACAAAGGAA	36	expansion strand
13[248]	13[263]	TTGCGAATAATAATTTCACGATTTCCCTTAG	36	expansion strand
13[264]	13[279]	AATCCTTGAAAACATAGCGATAGTCTGAAACATGA	36	expansion strand
13[280]	13[295]	AAGTATTAAAGAGGCTGAGACTCCATTGAGGCCAG	36	expansion strand
13[296]	13[311]	TAATAAGAGAATATAAAGTACCGGACTGTAGCGCGT	36	expansion strand
13[312]	13[327]	TTTCATCGGCATTTGGTCATATCATATGGTTAC	36	expansion strand
13[328]	13[343]	CAGCGCCAAAGACAAAAGGGCGAAGAGAGAAATAACA	36	expansion strand
16[55]	16[40]	GTAAACAGGGCTTCGGCAAAATCCCTATAAATCAA	36	expansion strand
16[71]	16[56]	AAAATAACCCCGCTGACCTCCTGGTTGGTGTAAATGA	36	expansion strand
16[87]	16[72]	ACTCCAGCCAGCTCACCTTATGACAATGTCCCGCC	36	expansion strand
16[103]	16[88]	AGCCCCAAAACAAGTATCGGCCTCAGGAAGATCGC	36	expansion strand
16[119]	16[104]	TCAATATGATATTGTACCCCGTTGATAATCAGAAA	36	expansion strand
16[135]	16[120]	TGAATATAATGCTGGCCGGAGACAGTCAAATCACCA	36	expansion strand
16[151]	16[136]	GAGGTCACTTTGCGGATGGCTTAGAGCTTAATTGC	36	expansion strand
16[167]	16[152]	TTAGTCTTAATGCCTTAATTGCTCCTTTGATAA	36	expansion strand
16[183]	16[168]	GCGACCTGCTCCACAGACAATTTTGAATGGCTA	36	expansion strand
16[199]	16[184]	ATTTGTATCATCGCCTGATAAATTGTCGAAATCC	36	expansion strand
16[215]	16[200]	GCGATTATACCAAGCGCGAACAAAGTACAACCGAG	36	expansion strand
16[231]	16[216]	GGATTATACCTCTAAAACACTCATCTTGACCCCCA	36	expansion strand
16[247]	16[232]	AGAATAGAAAGGACATCAATATAATCCTGATTGTT	36	expansion strand
16[263]	16[248]	GTCAATAGTGAATCTTCAACAGTTCAAGGGAGTG	36	expansion strand
16[279]	16[264]	TCGGAACCTATTACTTAGATTAAGACGCTGAGAAGA	36	expansion strand
16[295]	16[280]	CAGACGACGACAAACAGTTAATGCCCTGCCTATT	36	expansion strand
16[311]	16[296]	GCCTTTAGCGTCAACAAAAGGTAAGTAATTCTGTC	36	expansion strand
16[327]	16[312]	AGGTAATATTGATCACTAGCGACAGAACTCAAGTT	36	expansion strand
16[343]	16[328]	TAGCAGCCTTACCAATTCAACCGATTGAGGGAGGGA	36	expansion strand
17[40]	17[55]	GCTTGACGGGAAAGCCGGCAAGCTGACGCATTTC	36	expansion strand
17[56]	17[71]	ACATAAAATCTCCGAACCTCTAAATCTATT	36	expansion strand
17[72]	17[87]	ACGCTGCCCTGGAGTGACTCTAGTAACCGTGCATC	36	expansion strand
17[88]	17[103]	TGCCAGTTGAGGGACGACGAGAAAGTGTATA	36	expansion strand
17[104]	17[119]	AGCAAATTTAAATTGTAACCGAGTAATGTGTAGG	36	expansion strand
17[120]	17[135]	TAAAGATTCAAAAGGGTGAAGAAAGTAGCTAACATG	36	expansion strand
17[136]	17[151]	TTTTAAATATGCAACTAAAGTACCGGAAGCAAAC	36	expansion strand

17[152]	17[167]	CAACAGGTCAGGATTAGAGAGTACCGAACTGATAG	36	expansion strand
17[168]	17[183]	CCCTAAACATGCCATTAAAATACCGAACGAAACC	36	expansion strand
17[184]	17[199]	ACCAGCAGAAGATAAAACAGAGGTGAGGC GGTCAGT	36	expansion strand
17[200]	17[215]	ATTAACACCGCCTGCCAACAGTGCCACCAACCTAAAA	36	expansion strand
17[216]	17[231]	CGAAAGAGGCAAAGAATACTGAATAATGGAAGG	36	expansion strand
17[232]	17[247]	GTTAGAACCTACCATATCAAATGTAATGAATTT	36	expansion strand
17[248]	17[263]	CTGTATGGGATTTGCTAAACAATTATCAAATCAT	36	expansion strand
17[264]	17[279]	AGGTCTGAGAGACTACCTTTAACGGGTCAGTGC	36	expansion strand
17[280]	17[295]	CTTGAGTAACAGTGCCGTATAATAAACACATGTT	36	expansion strand
17[296]	17[311]	CAGCTAATGCAGAACGCGCCTGTACGTACCCAATGA	36	expansion strand
17[312]	17[327]	AACCATCGATAGCAGCACCGTAACGGAATTATTCA	36	expansion strand
17[328]	17[343]	TTAAAGGTGAATTATCACCGTCATTATCCGGTATT	36	expansion strand

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