
Supplementary information

Meta-DNA structures

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Supplementary Information for

Meta-DNA Structures

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Materials and Methods

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Section 1. Materials and Methods

Reagents. DNA staple strands were purchased in 96-well plates from Integrated DNA Technologies (IL, US) or Jie Li Biology Co. Ltd (Shanghai, China). Staple strands were used directly without further purification. Scaffold single-stranded M13mp18 viral DNA was purchased from New England Biolabs (MA, US). N-trimethoxysilylpropyl-N, N, N trimethylammonium chloride (TMAPS) (50% in methanol), and tetraethyl orthosilicate (TEOS) were purchased from TCI, Japan. Copper grids were purchased from Ted Pella (CA, US).

Meta-DNA self-assembly and purification.

For the formation of simple structures, including single-stranded Meta-DNA, self-folded, self-linked Meta-DNA and M-SST based structures, a one-pot annealing process was conducted. M13mp18 scaffold (10 nM), core staple strands (50 nM), and M-bases DNA strands (50 nM) were mixed at a ratio of 1:5:5 in 1× TAE- Mg^{2+} buffer (40 mM Tris, 20 mM acetic acid, 2 mM EDTA and 12.5 mM magnesium acetate [pH 8.0]). The mixture was heated up to 90 °C and slowly cooled down from 90 °C to 4 °C using a PTC-200 Peltier Thermal Cycler, with the following program: from 90 °C to 86 °C at a rate of 4 °C per 5 min, from 85 °C to 70 °C at a rate of 1 °C per 5 min, from 70 °C to 40 °C at a rate of 1 °C per 15 min, from 40 °C to 25 °C at 1 °C per 10 min, then held at 4 °C at the end of the cycle.

For the assemblies of the high-ordered structures, including double-stranded Meta-DNA, M-junction and M-DX structures and 3D polyhedrons, a two-step annealing process was conducted. First, different types of M-DNAs with the corresponding M-bases were assembled at 10 nM (as described above). Then, they were mixed together in the appropriate ratios (the extra staple strands were not removed) and annealed from 55 °C to 20 °C at a rate of 1 °C per 5 min (total annealing time of 3 h), 1 °C per 30 min (18 h), 1 °C per 1 h (36 h), or 1 °C per 2 h (72 h), depending on different situations. Longer annealing process generally offers a higher assembly yield.

For the M-DNA based strand displacement reactions, the single-stranded M-DNA T1, T1-R, T2 were assembled at 20 nM concentration. M13mp18 scaffold (20 nM), core staple strands (100 nM), protruding staple strands (20 nM) were mixed at a ratio of 1:5:1 in 1× TAE- Mg^{2+} buffer. After annealing from 90 °C to 4 °C, the assembled M-DNAs were purified with 100K Amicon

centrifugal filters three times at a concentration speed of 3000 g. The double-stranded T1:T2 M-DNA was obtained by mixing T1 and T2 at an equal ratio and annealing from 55 °C to 20 °C at a rate of 1 °C per 5 min.

DOS (DNA origami silicification) protocol. In a typical experiment, 2% (v/v) TMAPS (50% in methanol) and 2% (v/v) TEOS were added slowly to a Tris-EDTA-Mg²⁺ buffer while vigorously stirring. The mixture was stirred for 30 min at 25 °C to ensure sufficient pre-hydrolysis occurred. Then, a certain amount (typically 100 µL) of this gel solution was transferred to a 1.5 mL centrifuge tube. Meanwhile, 10 µL of the DNA samples were adsorbed onto substrates for 5 min. Next, the substrates were placed face-down on the gel solution in the tube. After reacting under static conditions at 25 °C for several days, the surface with the DOS complex was washed with ethanol and deionized water to remove the unreacted reagents (DNA, TMAPS and TEOS).

Preparation of DNA functionalized AuNPs and immobilization on M-DNA.

20 nm AuNP (Ted Pella) and thiol modified oligonucleotides were mixed in PBS buffer (10 mM PB, 100 mM NaCl, pH 7.4) at a molar ratio of 1:1000. The mixture was incubated for 8 h, and then the concentration of NaCl was slowly increased to 300 mM over 24 h. After centrifugation to remove excess DNA, DNA-AuNP conjugates were added to the purified DNA origami with a molar ratio of 10:1. The mixture was stirred for 8 h at 25 °C to allow the AuNP binding to the DNA origami.

AFM imaging. AFM imaging was performed in the ‘ScanAsyst mode in fluid’ or ‘ScanAsyst mode in air’ with ScanAsyst-Fluid+ tips or ScanAsyst-air tips (Bruker). Samples were prepared for AFM imaging as described in the following. For fluid-scanning, 5 µL annealed sample was deposited onto a freshly cleaved mica surface (Ted Pella) and 1 µL NiCl₂ (25 mM) was added immediately to the samples. After waiting ~30 s for adsorption to the mica surface, an extra 40 µL of the same buffer was deposited on the AFM tip. For scanning in air, 5 µL sample was deposited onto freshly cleaved mica and left to adsorption for 3 min. The mica was then washed three times with Milli-Q water (Millipore) and then dried using compressed air.

TEM imaging. Philips CM12 transmission electron microscope operated at 80 kV in bright field mode was used for imaging. TEM samples were prepared by dropping 10 μ L of sample solution on an ultrathin 400-mesh carbon-coated grid (Ted Pella) that was previously glow discharged using an Emitech K100X instrument. After 5 minutes, the sample was wicked with filter paper. Then, the grid was stained with 3 μ L of 0.7 % uranyl formate solution for 30 seconds, and excess solution was wicked away with filter paper.

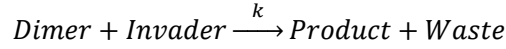
Agarose gel electrophoresis. Native gel electrophoresis was conducted on 1% agarose gel in $1\times$ TAE-Mg²⁺ buffer at 150 V sitting in an ice-water bath. 5 μ L sample at 10 nM concentration was loaded into the gel well. After running for 40 min, the gel was stained with SYBR Safe gel stain solution (Life Technologies) and visualized under ultraviolet light (Gel Doc XR+ system gel imager, Bio-Rad).

Persistence length measuring. Persistence length was measured using the open-source tool Easyworm ^[1]. Well-formed M-DNAs were selected manually from AFM images. To avoid the fitted splines jumping between strands in the helical designs, a 3-pixel gaussian filter was applied to the images. Persistence length was determined by using the contour length vs end-to-end distance method, which was previously used to estimate the persistence length of DNA 6-helix bundles in Kim's paper ^[2]. Standard deviation was calculated through a bootstrap method using the full dataset with 1000 iterations.

Fluorescence curve measurement. Fluorescence kinetics data were collected every 10 min using a Mx3005P quantitative polymerase chain reaction system (Agilent Technologies) over 24 h. In a typical experiment, 15 μ L 20 nM T1:T2 dsM-DNA were mixed with varying concentration of invader M-DNA T1-R 15 μ L in optical 8-tube stripes. Excitation and emission wavelengths were 494 nm and 522 nm for FAM. The rate constant of the reaction was obtained by fitting the data as described below.

Kinetic Model. M-SDR is an intermolecular reaction between a dsM-DNA and an invader M-DNA. Therefore, this reaction can be described using second order kinetics. The rate constant of

the forward reaction is defined as k . As the branch migration process is irreversible in M-SDR, the backward reaction can be effectively ignored. The M-SDR is as follows:



In our experimental protocol, the initial concentrations of the dsM-DNA (T1:T2) is $[D]_0$. The initial concentration of invader M-DNA is $[I]_0$, which is n -fold of $[D]_0$. The concentration of product is defined as $[P]$. The reaction rate can be described as follows:

$$\begin{aligned} r &= -\frac{d[D]}{dt} = \frac{d[P]}{dt} = k[D]_t[I]_t = k([D]_0 - [P])(n \cdot [D]_0 - [P]) \\ \frac{d[P]}{dt} &= k([D]_0 - [P])(n \cdot [D]_0 - [P]) \\ \int_0^t k dt &= \int_0^{[P]} \frac{d[P]}{([D]_0 - [P])(n \cdot [D]_0 - [P])} \end{aligned}$$

When n is not 1, the initial concentrations of the $[I]_0$ and $[D]_0$ are different. Then, definite integration can be applied to the above equation to obtain the following:

$$1/((n-1)[D]_0) \cdot [-\ln([D]_0 - [P]) + \ln([D]_0)] - \frac{1}{(n-1)[D]_0} \cdot [-\ln(n \cdot [D]_0 - [P]) + \ln(n \cdot [D]_0)] = kt$$

$$\begin{aligned} \ln \frac{[I]_t}{[D]_t} &= kt \cdot (n-1)[D]_0 + \ln(n) \\ \frac{(n-1)[D]_0}{[D]_t} &= \exp[kt \cdot (n-1)[D]_0 + \ln(n)] - 1 \end{aligned}$$

The next step is to correlate the above equation to the fluorescence kinetic curves. For each kinetic curve, at time 0, after time t , and at the end of the reaction (t goes to ∞), the normalized fluorescence intensities are I_0 , I_t , and I_∞ , respectively. Assuming the changes of fluorescence intensity are linearly correlated with the changes of reagent concentration, at any time t , $[D]_t/[D]_0$ equals to $(I_\infty - I_t)/(I_\infty - I_0)$. Therefore, the equation is transformed to:

$$I_t = I_\infty - (I_\infty - I_0) \frac{(n-1)}{\exp[kt \cdot (n-1)[D]_0 + \ln(n)] - 1}$$

The above equation is used to fit the normalized kinetic curve (I_t vs. t) to obtain the apparent rate constant: k .

Section 2. Coarse-grained Simulations of Meta-DNA

The oxDNA model and simulation setup

We use a coarse-grained model of DNA, oxDNA^[3-5], to study the properties of individual 6-helix bundles (6HB, i.e. individual M-DNAs) and the double-stranded Meta-DNA (dsM-DNA) structures. The oxDNA model has been parametrized to reproduce mechanical, structural and thermodynamic properties of double-stranded and single-stranded DNA. The model represents each nucleotide as a single rigid body in the simulation with multiple interaction sites. The model is schematically illustrated in Supplementary Fig. 27.

The oxDNA model has been applied to a wide variety of systems and where available, good agreement has been found with experimental data^[6]. The applications include studying of force-induced unzipping of a DNA origami^[7], origami folding^[8], conformational studies of DNA cages^[9], and ssDNA tetrahedron folding^[10]. The model has also recently been applied to the study of origin of chirality in liquid crystals created from helical origami bundles^[11].

We simulate the single-stranded M-DNA, as well as the dsM-DNAs. We consider for simulations only the designs for one helical turn (300° twist) and two helical turns (660° twist). For each case considered, we simulated the assembled duplex dsM-DNA for both left-handed and right-handed designs, as well as the individual single-stranded M-DNA.

We use the parametrization of the oxDNA model introduced in ref. 3 (oxDNA2) implemented on GPU^[12]. The simulations were carried out at 1M salt concentration (modeled using Debye-Huckel potential) at temperature 25 °C using an Andersen-like thermostat^[13], with individual step corresponding to approx. 0.01 ps. For each studied system, the simulation was run for a simulation time corresponding to at least approx. 6 μ s. We note that in a coarse-grained simulation, there is not a straightforward correspondence between the simulation time and the experimental time, as different processes can scale with different ratios between the model and the experiment. For instance, the model uses diffusion constant of 2.5, which corresponds to approximately 100x larger than the value measured for DNA duplex diffusion in vitro^[6]. Therefore, the simulated time interval is approximately 100 times larger than in a real experiment, as further discussed in ref. 5.

Double-strand meta-DNA simulation analysis

For each simulated 6HB (either a single 6HB or for two 6HBs bound in a duplex dsM-DNA), we measured its bent (B) and twist (Tw_{6HB}). We define Tw_{6HB} in the following way: We identify the

12 nucleotides that make up a slice of the 6HB, the n -th slice is defined as the six base pairs containing the scaffold nucleotides n positions away from the end of the scaffold. We then define the vector $\mathbf{e}_3(n)$ for n -th slice as the unit vector perpendicular to the best fit plane of the centers of mass of all nucleotides in the slice. In other words, we fit the plane position and orientation so that we minimize the distance from the plane of all centers of mass of the 12 nucleotides in the slice. We define vector $\mathbf{e}_1(n)$ as the unit vector (projected to the plane perpendicular to $\mathbf{e}_3(n)$) which points from the center of mass of the 12 nucleotides to the midpoint between the two base-paired nucleotides of the one of the selected DNA helices in the 6HB. We calculate the angle θ_n between n -th and $(n+1)$ -th slice as

$$\theta_n = \mathbf{r} \cdot (\mathbf{e}_1(n) \times \mathbf{P}(\mathbf{e}_1(n+1))) \cos^{-1} (\mathbf{e}_1(n) \cdot \mathbf{P}(\mathbf{e}_1(n+1)))$$

where $\mathbf{r}$ is a unit vector pointing from the first slice to the last slice in the bundle and $\mathbf{P}(\mathbf{e}_1(n+1))$ is a vector that is the projection of $\mathbf{e}_1(n+1)$ into the plane of n -th slice. The global twist of the bundle is then defined as $Tw_{6HB} = \sum_{n=1}^N \theta_n$ for N slices that represent the bundle. We leave out the first and last ten slices in order to remove end effects such as duplex fraying, and we also leave out from the list of slices those where cross-overs are located. We further define local twist (twist per slice) as Tw_{6HB}/N . Right-handed twist will hence be a positive number, and left-handed twist will be negative. We also represent the overall twisting as

$$Twe = \sum_{n=1}^N (\theta_n)^2 / N.$$

We note that slices that contain cross-over or are immediate neighbors of a slice that contains a cross-over are excluded from Twe calculation, as they are more flexible and could occasionally contribute significantly to the measured Twe for a particular configuration. However, typically the measured angle θ_n was only significantly different in the crossover position, and removing them resulted in θ_n being a smooth function of n .

Next, to characterize the bending of the bundle, we define bending per slice as

$$b(n) = 1 - \mathbf{e}_3(n) \cdot \mathbf{e}_3(n+1)$$

and characterize the overall bending of the bundle as $B_{6HB} = \sum_{n=1}^N b_n$. In a similar fashion as for twisting, the slices that contained cross-over were not included in bent measurements.

We define the global twist for the duplex dsM-DNAs structures in an analogous manner, treating individual 6HBs as “strands” and calculating the twist of the dsM-DNA. For each of the 6HBs that are bound in dsM-DNA, we make a list of corresponding n -th slices in the bundles as described previously. We define the center of mass of each slice $\mathbf{r}_{cm}^A(n)$ and $\mathbf{r}_{cm}^B(n)$ for the respective 6HBs

(denoted as A and B). We define dsM-DNA n-th slice midpoint as $\mathbf{m}(n) = (\mathbf{r}_{cm}^A(n) + \mathbf{r}_{cm}^B(n))/2$ and unit vector pointing from bundle A to bundle B in n-th slice as

$$\mathbf{v}_1(n) = (\mathbf{r}_{cm}^B(n) - \mathbf{r}_{cm}^A(n)) / |\mathbf{r}_{cm}^B(n) - \mathbf{r}_{cm}^A(n)|$$

The unit vector connecting the centers of mass of n-th and (n+1)-th meta-midpoint is

$$\mathbf{v}_3(n) = (\mathbf{m}(n+1) - \mathbf{m}(n)) / |\mathbf{m}(n+1) - \mathbf{m}(n)|$$

The twist angle between the respective n and n+1-th layers of the dsM-DNA is defined as

$$\sigma_n = R \cdot (\mathbf{P}^n(\mathbf{v}_1(n)) \times \mathbf{P}(\mathbf{v}_1(n+1))) \cdot \cos^{-1}(\mathbf{P}^n(\mathbf{v}_1(n)) \cdot \mathbf{P}^n(\mathbf{v}_1(n+1)))$$

where $\mathbf{P}^n$ is the projection operator to a plane perpendicular to vector $\mathbf{v}_3(n)$ and $\mathbf{R}$ is a unit vector pointing from first to the last layer of the dsM-DNA. We define twist of the dsM-DNA as $Tw(dsMDNA) = \sum_{n=1}^N \sigma_n$. Hence, positive $Tw(dsMDNA)$ corresponds to a right-handed dsM-DNA structure, and negative to a left-handed one.

We carry out all our simulations of dsM-DNA using pre-assembled dsM-DNA structures, which were obtained as follows. We export the designs of individual 6HB from Tiamat^[14] software into oxDNA representation, relax the structure using a Monte Carlo simulation with increased spring potential for mean bond-lengths on CPU and further using Molecular Dynamics with the oxDNA2 force field^[5] on GPU. We then bring the two bundles into the dsM-DNA structure by applying a spring potential to complementary patches and running the simulation on GPU until all patches are connected. We tried two different assembly protocols; in the first approach, potential is applied sequentially from the first to the last patch (adding new patches after all base pairs in the previous patches have formed), and the other approach where we apply the potential on patches at one end and then the other end (the first and then the last), and gradually move towards the center after the patches at both ends are well-formed. We found that these approaches lead to topologically distinct dsM-DNA structures, as discussed below. We note however that our approach to assemble the structure is not physical, as we explicitly impose a potential to force the assembly. However, once the structures are assembled, we remove the explicit potential that holds the staples together and sample respective configurations of the assembled dsM-DNA for at least 6.5 μs . As the topologically different structures observed in our different assembly protocols have counterparts observed on AFM, we believe they are representative of the actual assembly in experiment. Our method, however, does not allow us to estimate relative ratios of the occurrences of the respective structures. To obtain this information, we would need to obtain free-energy difference between the respective assemblies, and such a computationally intensive project is beyond the scope of our

current simulation study. Our model however allows for quantitative comparison of individual structures and possible rationalization of the handedness preference of different designs.

Results

We have measured the twist and bend for each individual 6HB, as well as for 6HB bound in dsM-DNA with 300 degrees and 660 degrees designs respectively. The results are summarized in Supplementary Table. 77-80. As previously noted, both in simulations and experimentally [5,8,15], DNA origami structures, such as the 6HBs presented here, are very sensitive to the positions of the cross-overs, which are designed based on the assumption of pitch 10.5 base pairs for the B-form DNA helix. However, as multiple studies have shown, the exact value of DNA pitch is sensitive to sequence and buffer conditions and can change with salt concentration and temperature [16, 17, 18, 19, 20]. While sequence-dependence averages out over large structures, buffer-dependent fluctuations become especially pronounced for large DNA structures and assemblies of larger structures out of multiple origamis. We have quantified the twist and bent of individual 6HBs for the 660° and 300° dsM-DNA designs respectively (Supplementary Fig. 26). We found the typical conformation of the individual 6HBs to be strained, which results both into bending and twisting of the individual bundle, as illustrated in Fig. 1F. The results for individual bundles are summarized in the Supplementary Table. 78, where the average values (and their standard deviations) of the measured twist, twisting and bending (as defined above) obtained from a sampling simulation of between 10^3 and 10^4 decorrelated configurations for each design are shown. We note that in order to calculate the relative contribution of the bending and twisting to the overall energy, we would also need to obtain torsional (C) and bending modulus (K) of the bundle^[21] and obtain the resulting energy of the particular configuration as

$$\beta E \sim K B_{6HB} + C T w e$$

(where $\beta = 1/KT$). However, to fully interpret the effects of the induced strain on the 6-HB, we would also need to include the higher order effects, such as twist-bend coupling [22] and also incorporate the defects introduced by the crossovers in the structure, which goes beyond first order approximations of bending and twisting effects. We hence focus on qualitative and semi-quantitative descriptions of M-DNAs and their dsM-DNA formation based on oxDNA simulations. We also note that even though oxDNA model has been parametrized to obtain the same structure shape as observed in 3D origami structural study^[15], it still does not possess enough

resolution to capture full details of cross-over geometry ^[23]. We observed that individual 6HB, as represented by the oxDNA model, are twisted (in a right-handed sense on average) and bent in their typical configuration, as illustrated in Supplementary Table. 77. This effect is a consequence of the helical pitch in the oxDNA model being 10.55 base pairs, which is not exactly commensurate with the crossover positioning in the M-DNA designs and results in the induced bending and twisting of the bundle in order to relax the stress in the structure. In fact, our measurements found the DNA duplexes in the M-DNAs to adopt pitch of approximately 10.41, which is undertwisted with respect to the equilibrium 10.55 pitch adopted by a DNA duplex in the oxDNA model.

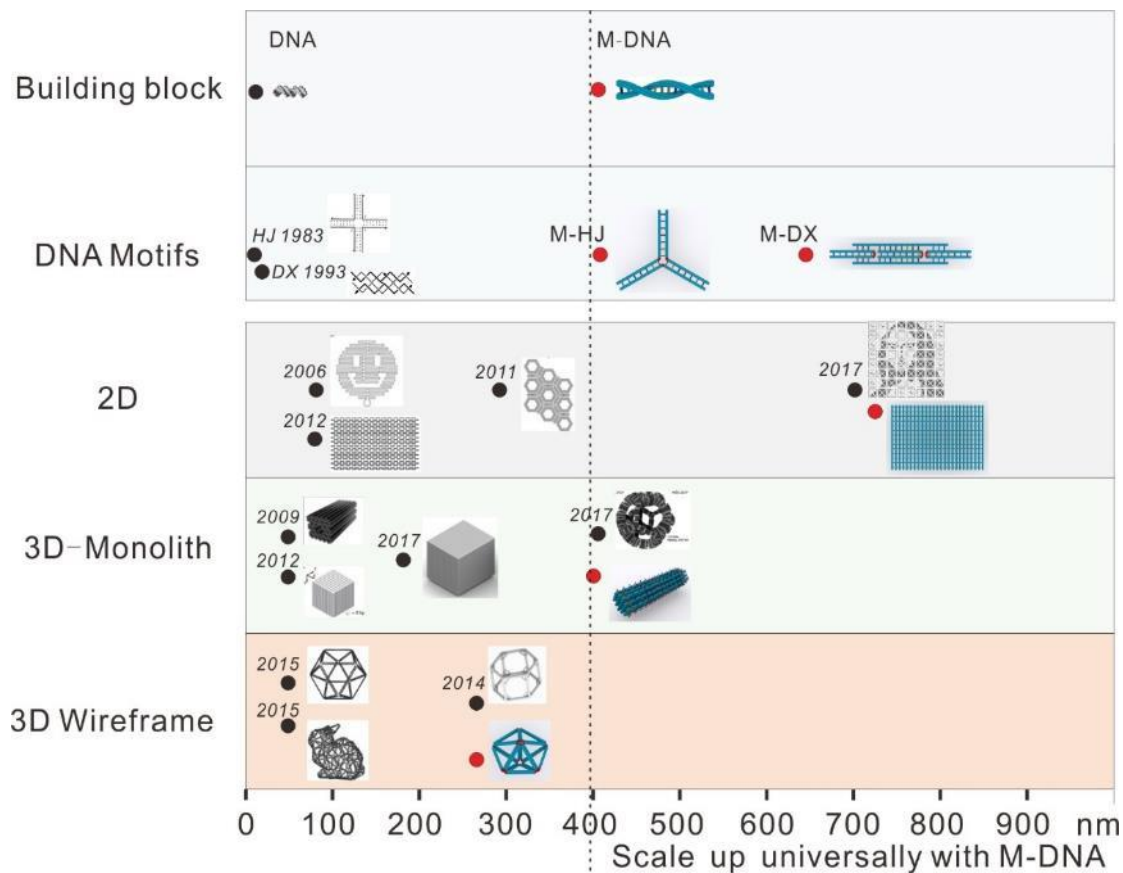
We have further simulated the formed dsM-DNA structures. Since sampling of the formation kinetics of the dsM-DNA is out of scope of this study, we only categorized structures obtained from the external force-free simulation performed after forced assembly, as described above. We cannot hence provide relative presence of the right-handed and left-handed dsM-DNA for the DNA model, but our sampling simulations have clearly revealed asymmetry between the left-handed and right-handed designs, both for 300° and 660° experimental design, which are likely at the origin of the asymmetry observed in the experiment. While repeating our assembly protocols where the individual staples are force-assembled in a specific order, we have identified multiple topologically distinct assemblies for the 300° and 660° left-handed and right-handed designs respectively, which are illustrated in Supplementary Fig. 29 and Movie S1 to S4. In particular, we identified cases where all the staple strands between two 6HB in dsM-DNA are formed, and yet they do not wrap around each other, effectively creating a structure that seems to be right-handed and then transitions to left-handed. Since AFM only provides 2D projection with limited resolution, it is not obvious to always identify from the projection if the dsM-DNA is correctly formed or corresponds to the non-wrapping alternative formation. Several candidates for each of the observed conformation, including the non-wrapping ones, have been identified for each of the structures and are shown in Supplementary Fig. 29.

The results of the twists and bending of the individual M-DNA when bound in dsM-DNA, along with the calculated overall twist of the dsM-DNA, are summarized in Supplementary Table. 78, showing that the twist of the individual bundles changes when they are bound in a dsM-DNA structure. This is further illustrated by the differences in bundle twist observed between the wrapped and unwrapped states as shown in Supplementary Table. 79-80. Kinetics of the assembly can also play a role. Most importantly, the observed twist and bending can be different between

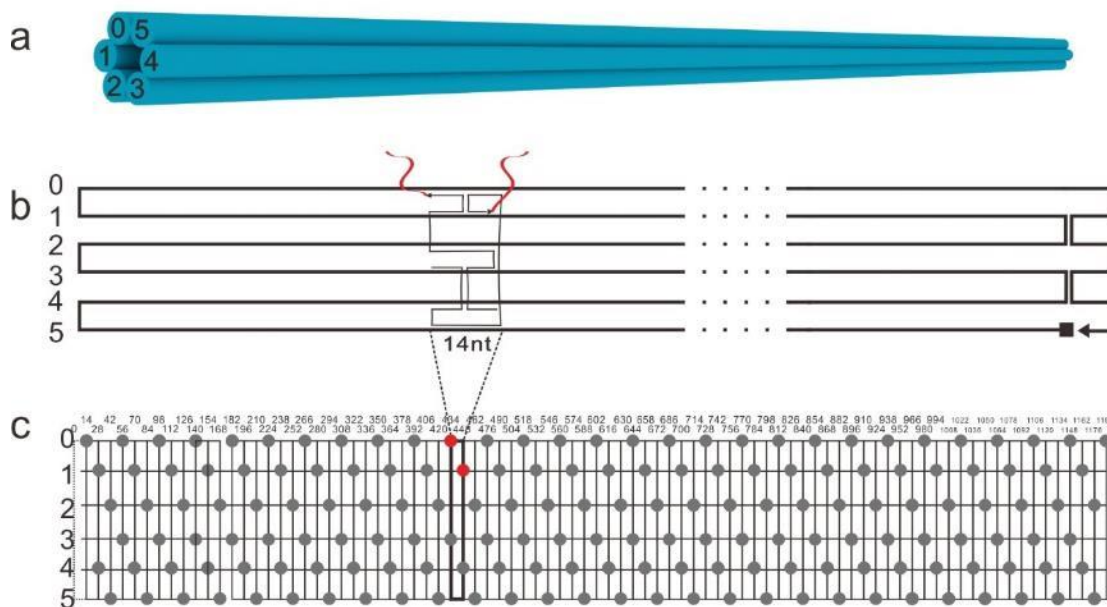
different observed dsM-DNA configurations. Experiments ^[24] and simulations ^[11] of cholesteric crystals studied formation of phases in a liquid crystal formation in an ensemble of M-DNAs and showed that M-DNA which were designed with right-handed twist preferred to wrap around in left-handed fashion due to the entropy maximization. While M-DNAs used in this experiment were held together by staple strands, it would be of interest in follow-up work to investigate the effects of the length of the patches and of alternative designs of M-DNA on the preference of relative yields of the dsM-DNA structures.

In summary, the complex mechanical properties of M-DNA, which are inherently bent and twisted, likely results in different observed yields of dsM-DNA. The structures are sensitive to the exact value of the DNA pitch, which is a likely reason for a build-up of an inherent twist in the M-DNA structures and resulting asymmetry of yields of different configurations in dsM-DNA formation.

Section 3. Basic design of Meta-DNA

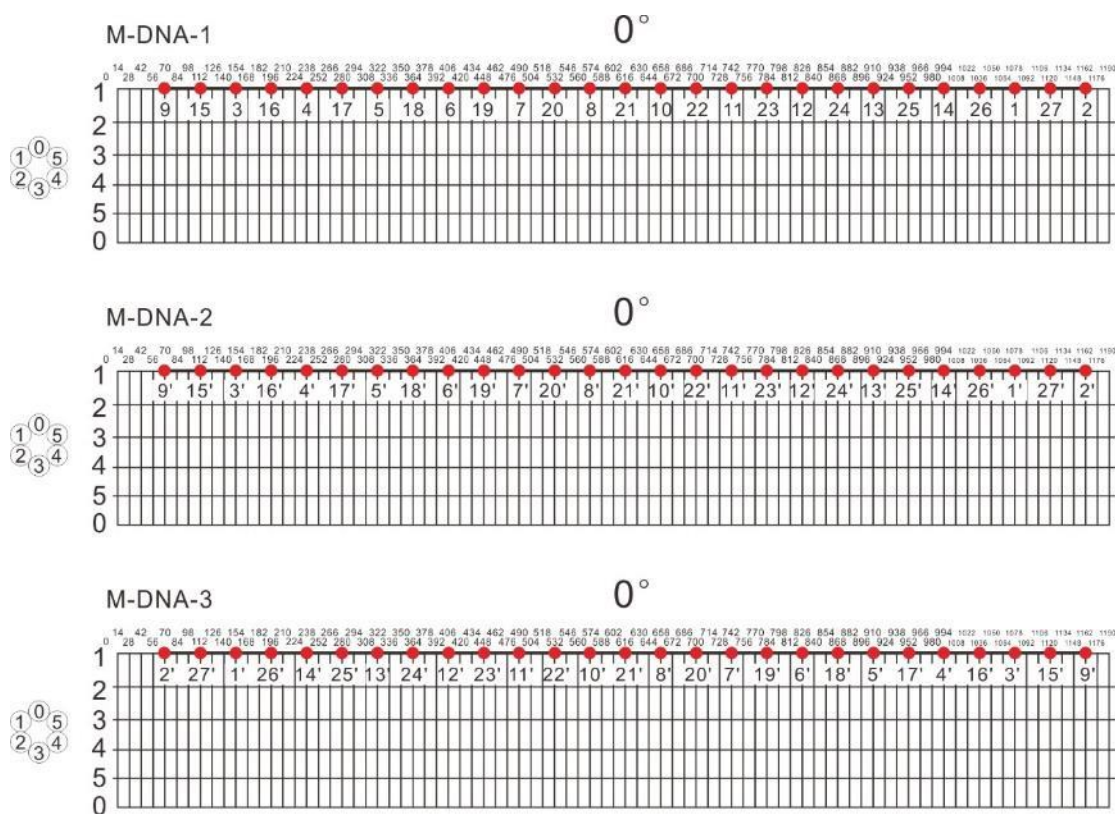


Supplementary Fig. 1. Overview of DNA nanostructures based on DNA and M-DNA. Each point in the plot corresponds to the size of a DNA nanostructure. HJ: holiday junction. DX: double crossover tile. M-DNA based strategy can construct various types of DNA nanostructures in a larger scale.

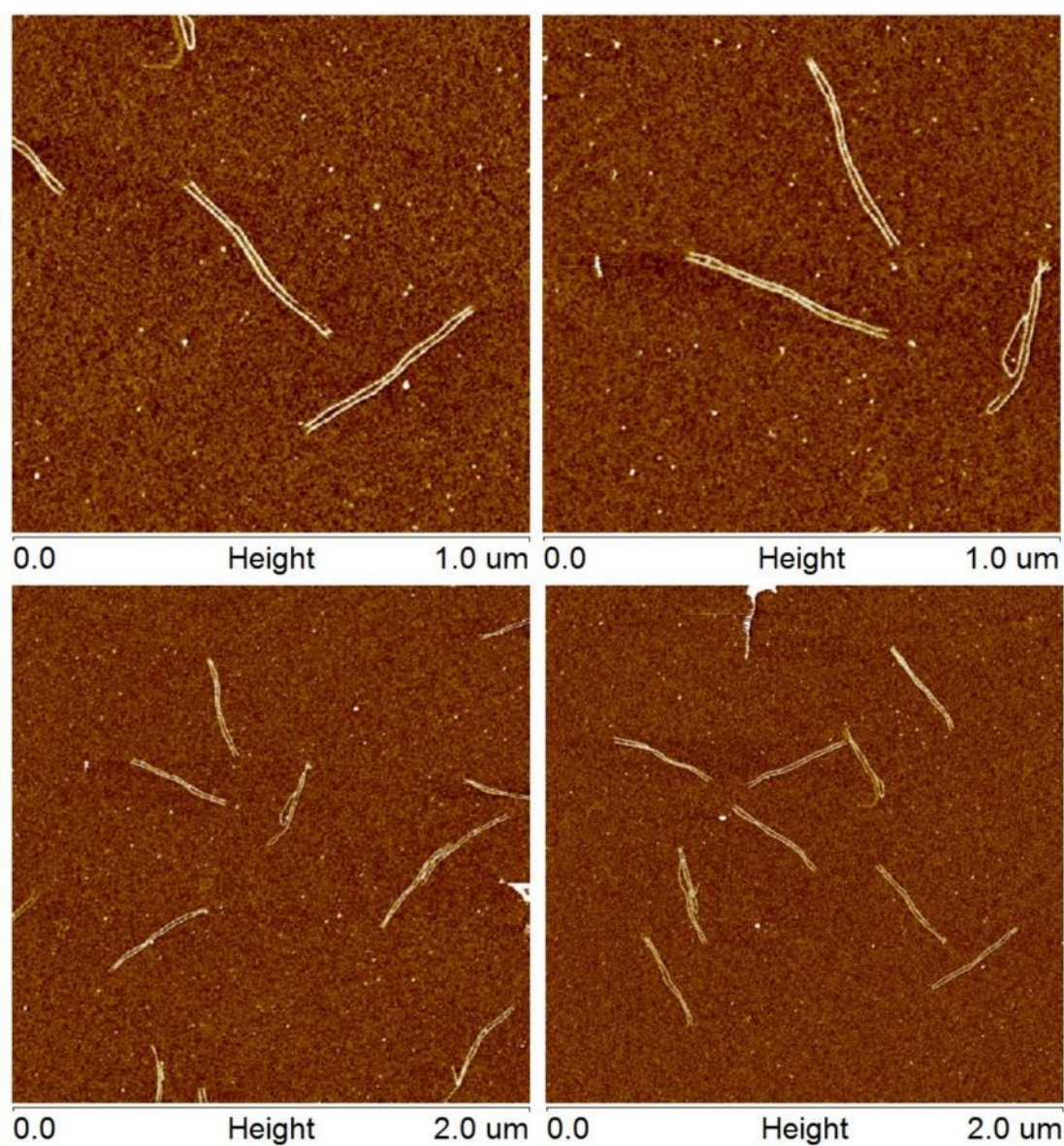


Supplementary Fig. 2. Design details of Meta-DNA. (a) Cylinder model of a 6HB origami as the M-DNA. (b) M13 scaffold and staple strands folding pathway. The red strands represent the protruding single-stranded nucleotides as the Meta-bases (typically a 10 nt random sequence extended from the surface of the origami with a 4T spacer). (c) A two-dimensional layout of the M-DNA. The M-DNA was composed of 6 double helices of DNA, which were labelled from 0 to 5. Each helix was about 400 nm long. The numbers on the top represent the nucleotide (nt) number of the scaffold in each helix. The circle spots represent possible protruding positions on the surface of the M-bases. The red spots represent the active positions, where the M-bases are located. The gray spots represent the inactive positions.

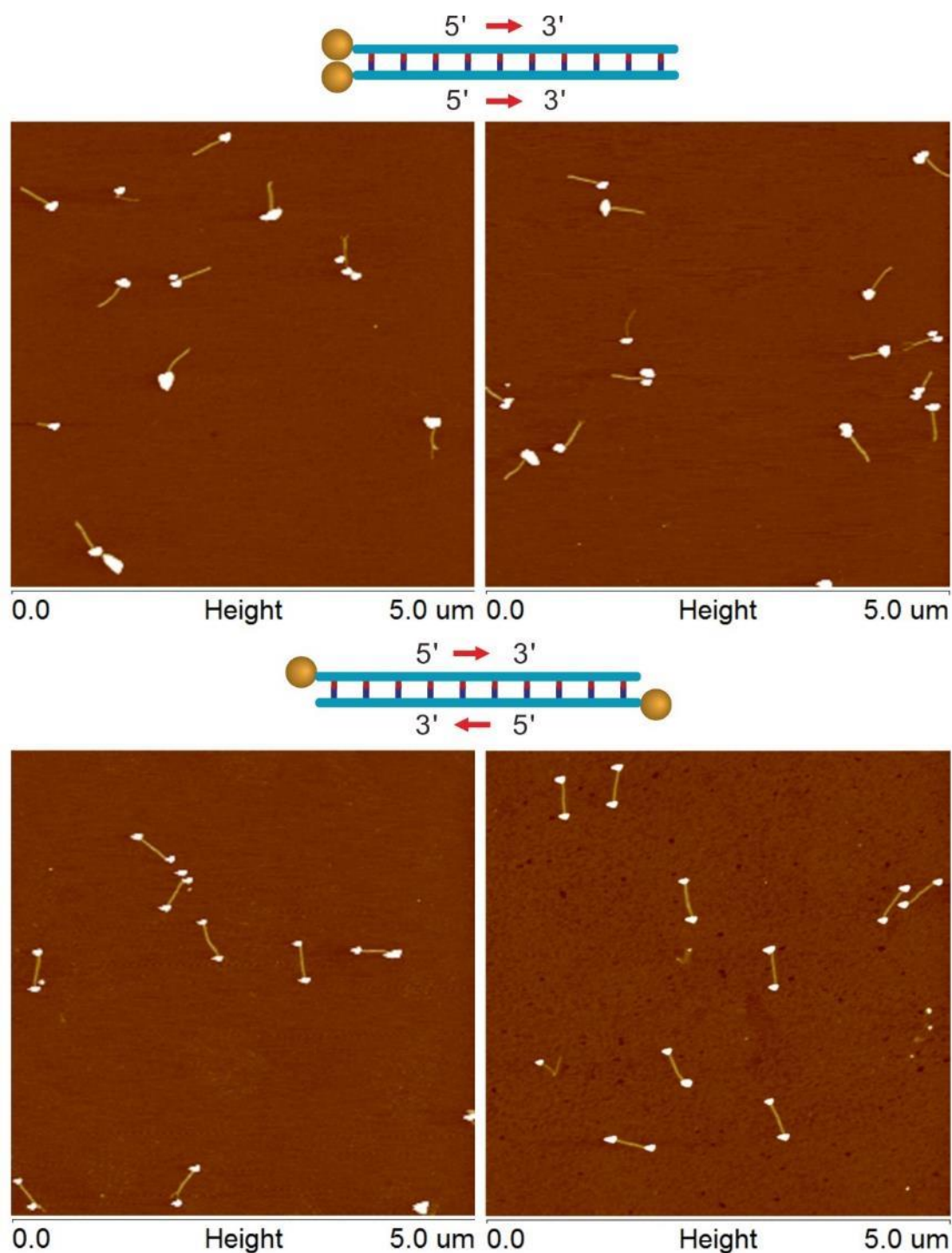
Section 4. Design and characterization of dsM-DNA



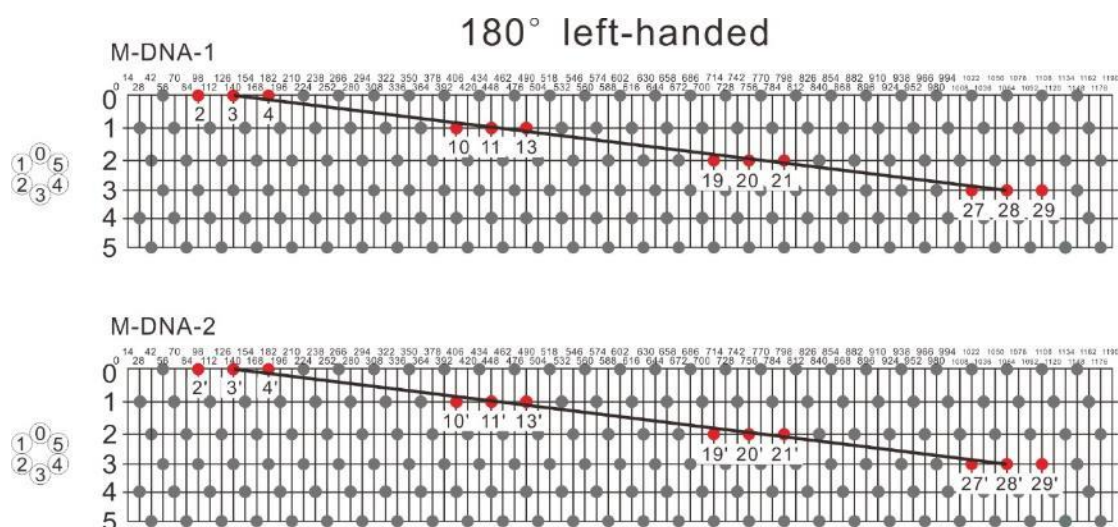
Supplementary Fig. 3. Scheme of design for formation of parallel and antiparallel double-stranded M-DNA. The numbers below the red spots (active positions) represent the M-base sequence number, the detailed sequences were listed in the supplementary Table. 72, where n and n' are complementary to each other that can form a M-base pair. Here the M-bases were located on the same helix (helix 1) of the 6HB. M-DNA-1 and M-DNA-2 hybridized to form parallel double-stranded M-DNA. M-DNA-1 and M-DNA-3 hybridized to form antiparallel double-stranded M-DNA. All the needed strands can be found in the Supplementary Table. 1-2.



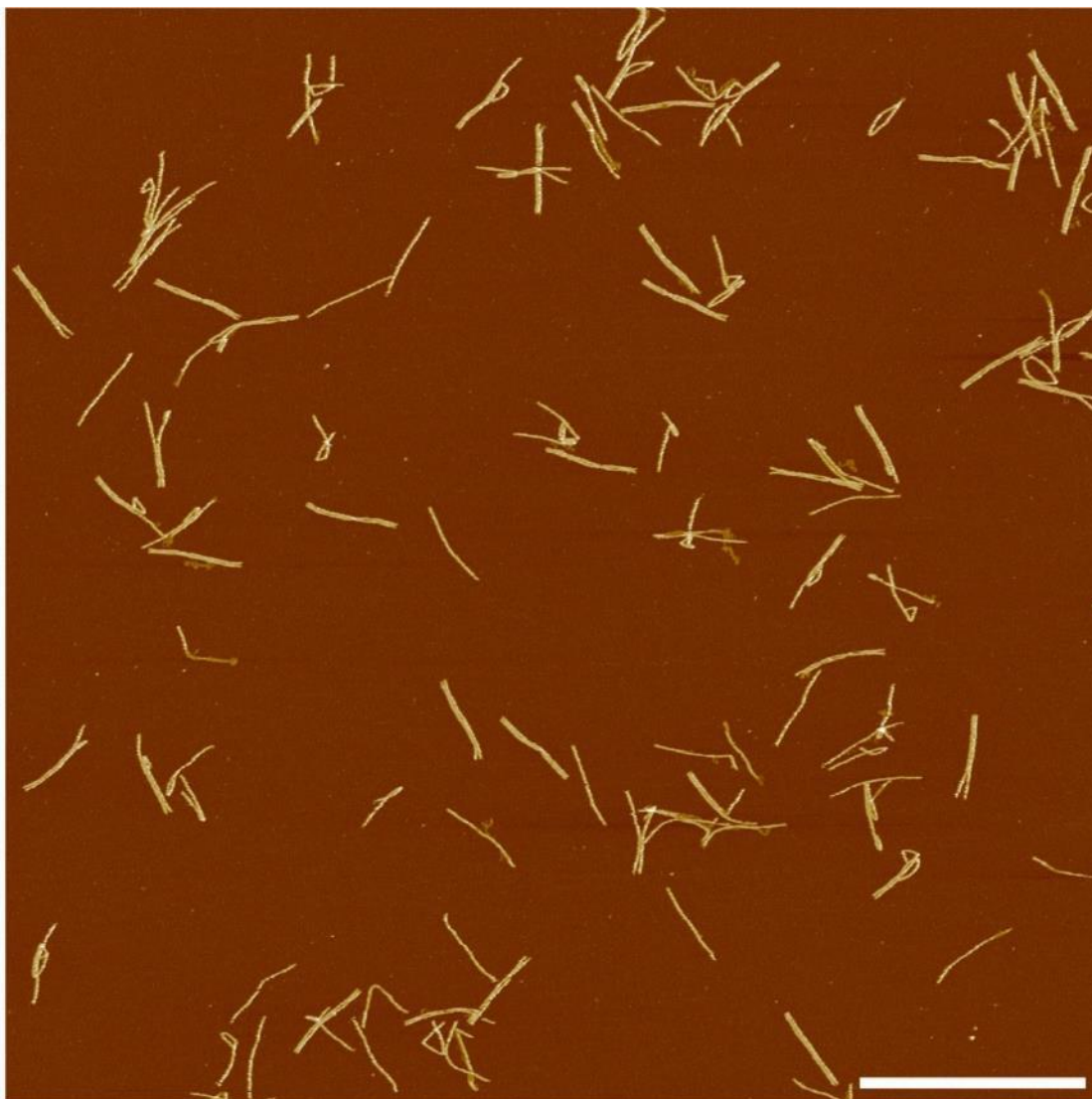
Supplementary Fig. 4. Additional AFM Images of double-stranded M-DNA at different magnifications.



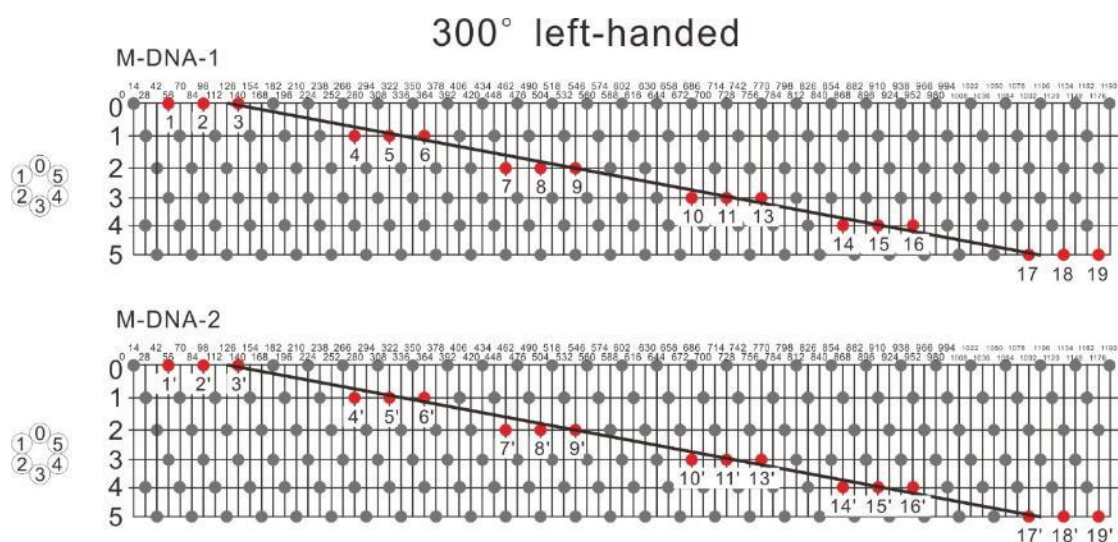
Supplementary Fig. 5. AFM images of double-stranded M-DNA with parallel and antiparallel hybridization directions. One gold nanoparticle was labelled at one end of the M-DNA to distinguish the different ends. The end of M-DNA with the gold nanoparticle was called “5 prime.” And the opposite end with no labelled gold nanoparticle was called the “3 prime.”



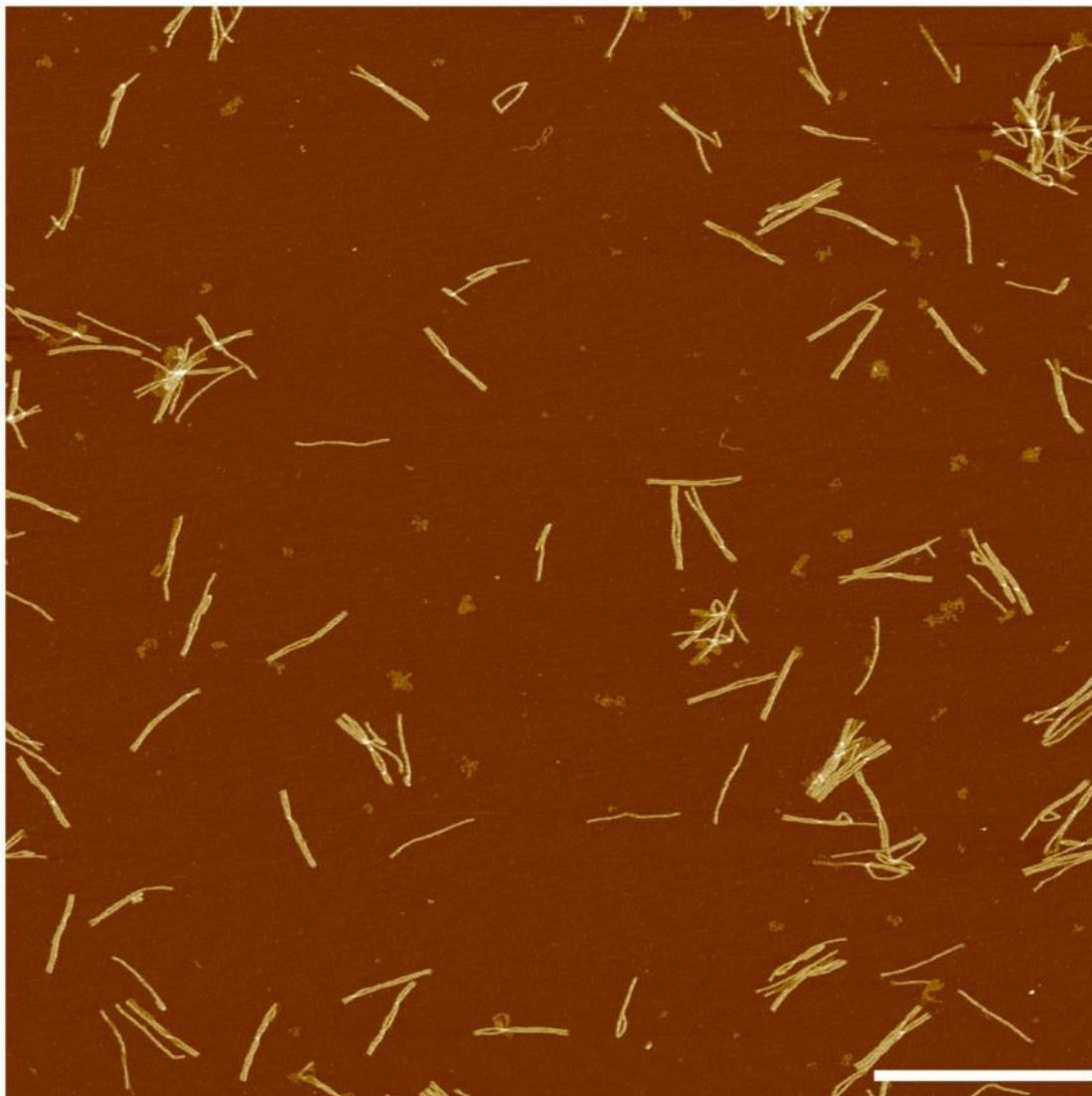
Supplementary Fig. 6. Schematic design for formation of left-handed double-stranded M-DNA with a twist angle of 180°. The numbers below the red spots represent the M-base sequence numbers. M-bases were located on helices 0, 1, 2, and 3 in a left-handed manner. All the needed strand sequences can be found in the Supplementary Table. 3-4.



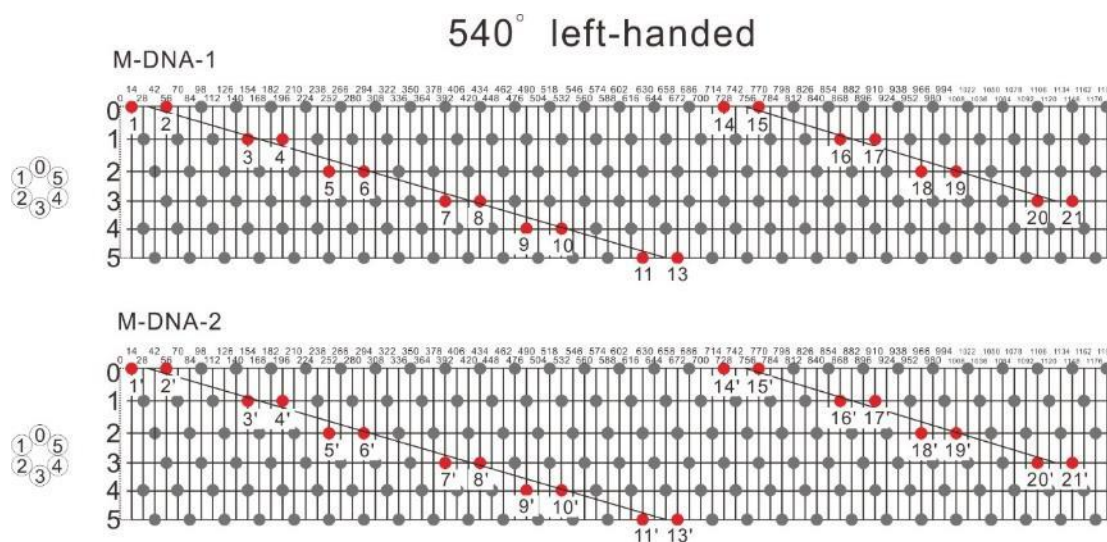
Supplementary Fig. 7. AFM image of left-handed double-stranded M-DNA with a twist angle of 180° . Scale bar $1\mu\text{m}$.



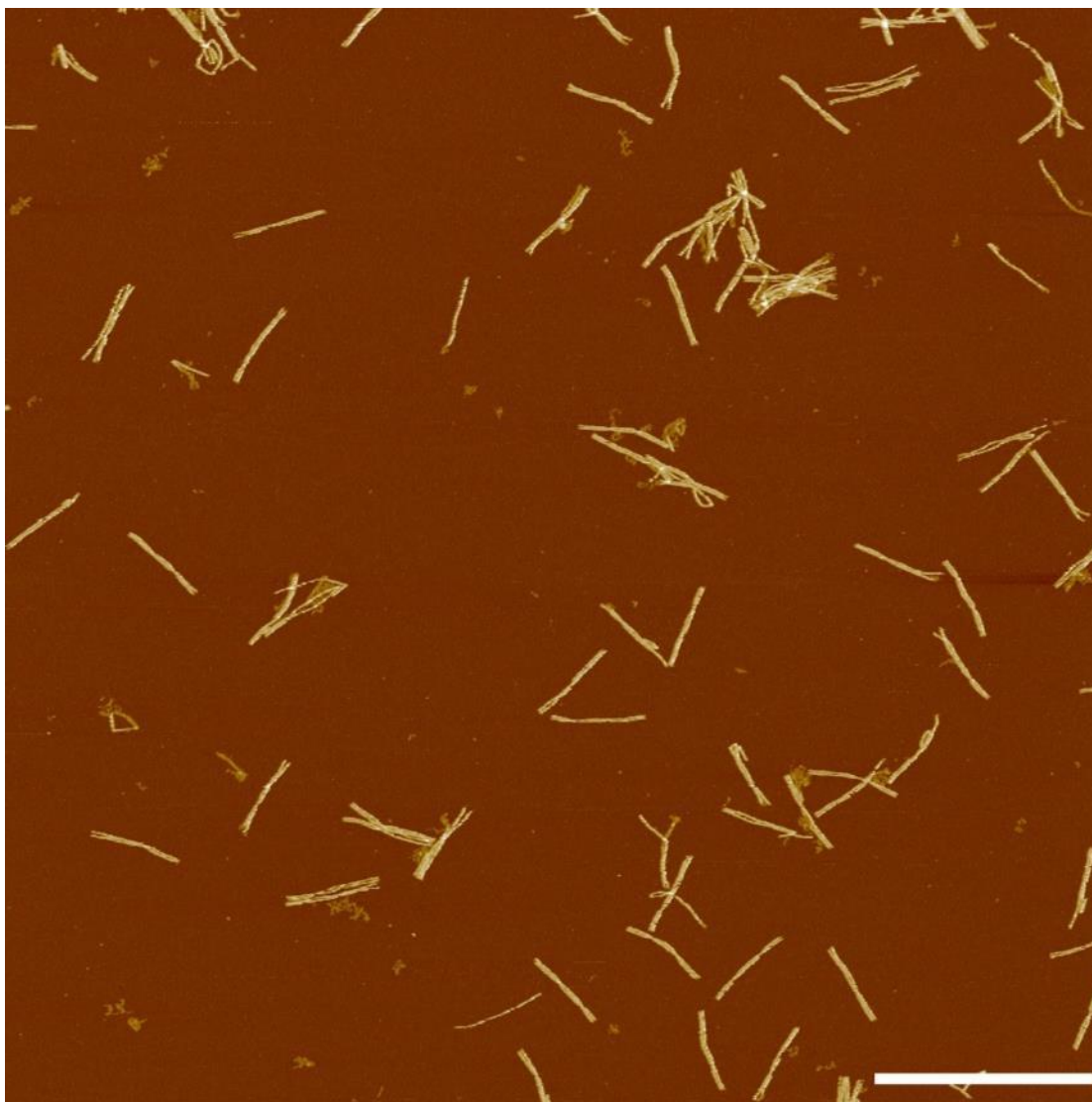
Supplementary Fig. 8. Schematic design for formation of left-handed double-stranded M-DNA with a twist angle of 300°. The number below the red spots represent the M-base sequence numbers. The M-bases were located on helices 0, 1, 2, 3, 4, and 5 in a left-handed manner. All the needed strand sequences can be found in the Supplementary Table. 5-6.



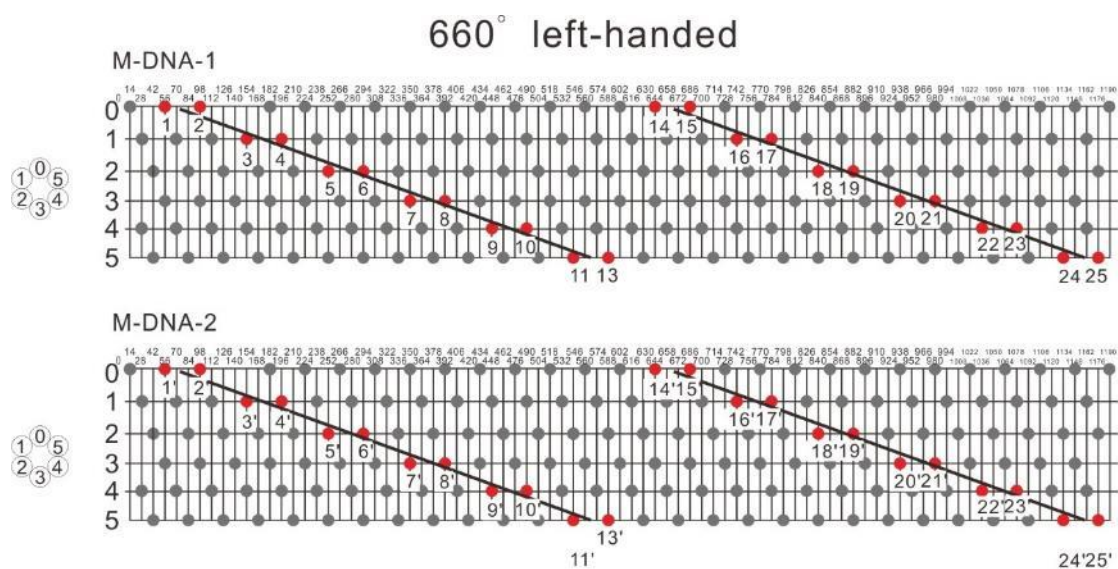
Supplementary Fig. 9. AFM image of left-handed double-stranded M-DNA with a twist angle of 300° . Scale bar $1\mu\text{m}$.



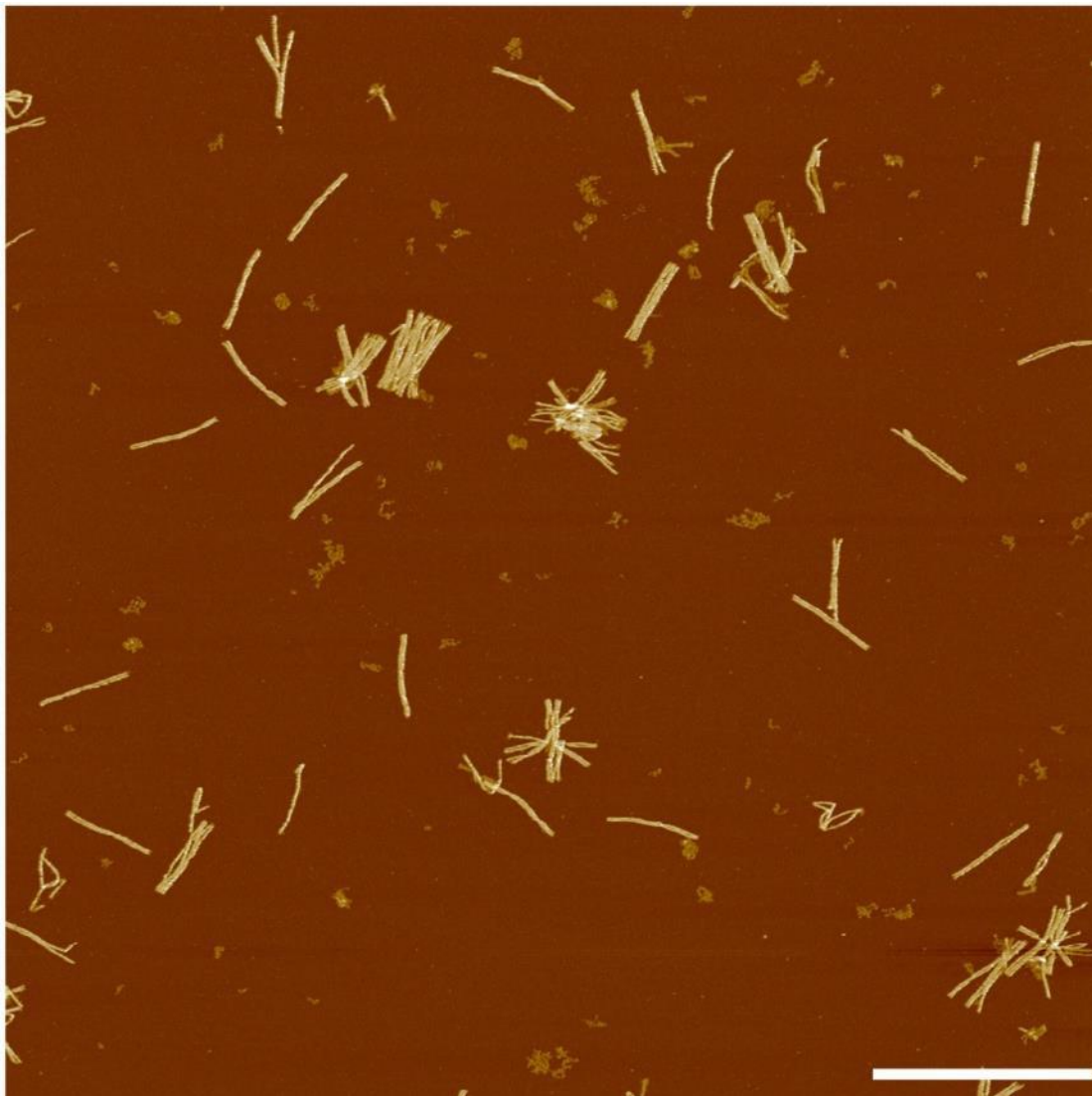
Supplementary Fig. 10. Schematic design for formation of left-handed double-stranded M-DNA with a twist angle of 540°. The number below the red spots represent the M-base sequence numbers. The M-bases were located on helices 0, 1, 2, 3, 4, 5, 0, 1, 2, and 3 in a left-handed manner. All the needed strand sequences can be found in the Supplementary Table. 7-8.



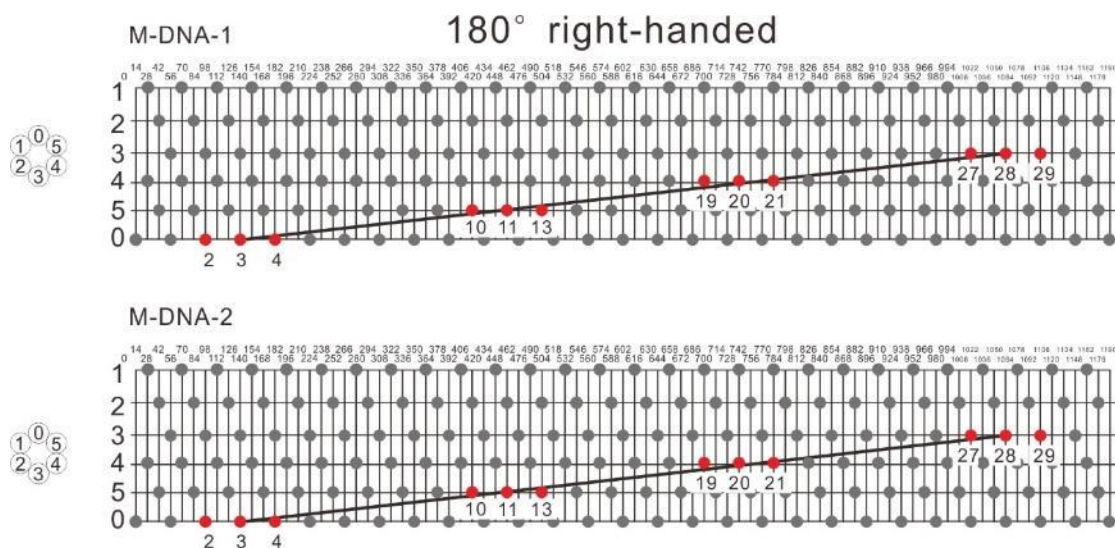
Supplementary Fig. 11. AFM image of left-handed double-stranded M-DNA with a twist angle of 540° . Scale bar $1\mu\text{m}$.



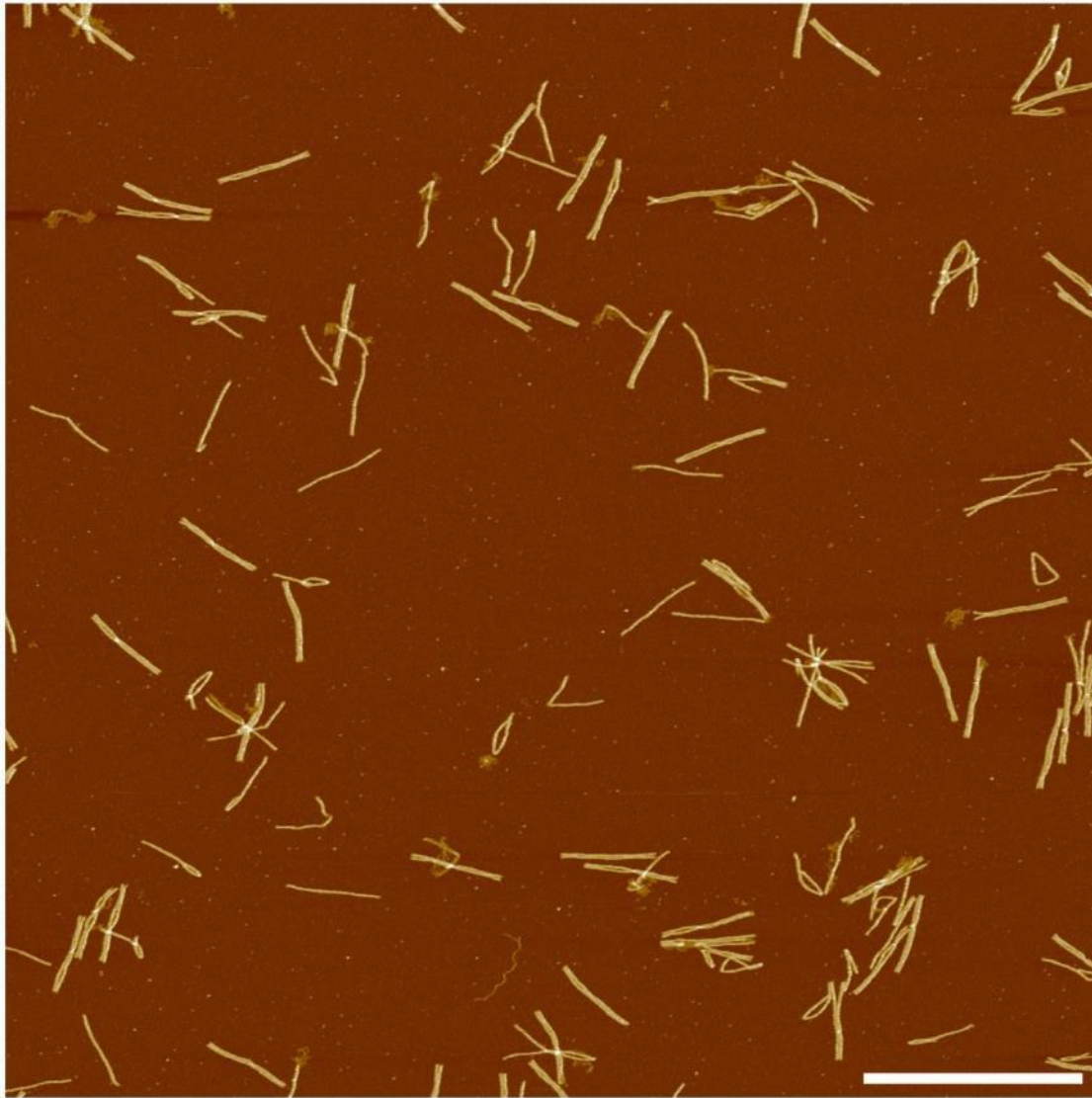
Supplementary Fig. 12. Schematic design for formation of left-handed double-stranded M-DNA with a twist angle of 660° . The number below the red spots represent the M-base sequence numbers. The M-bases were located on helices 0, 1, 2, 3, 4, 5, 0, 1, 2, 3, 4, and 5 in a left-handed manner. All the needed strand sequences can be found in the Supplementary Table. 9-10.



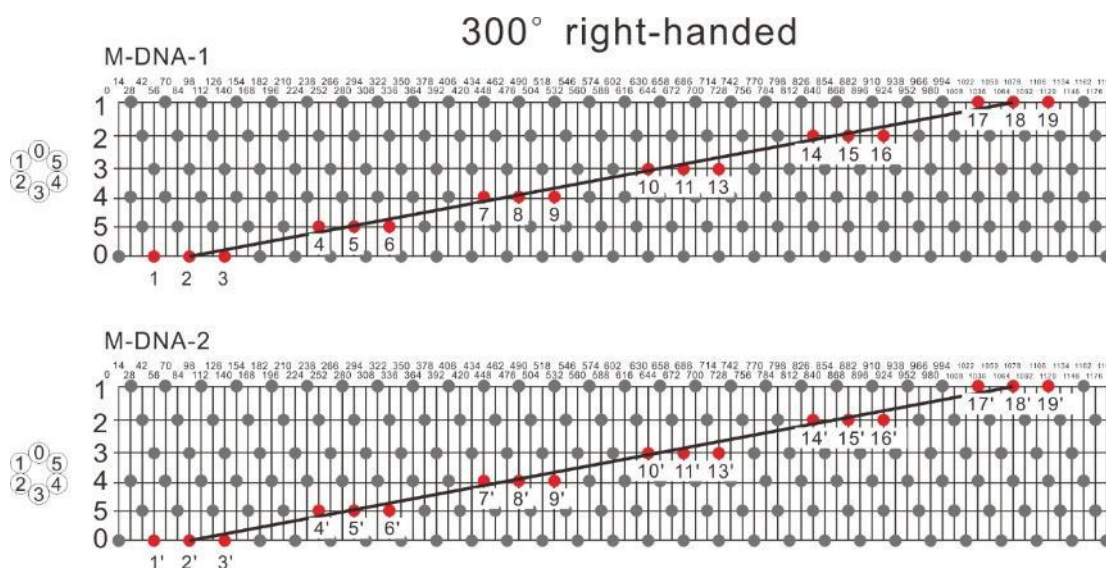
Supplementary Fig. 13. AFM image of left-handed double-stranded M-DNA with a twist angle of 660° . Scale bar $1\mu\text{m}$.



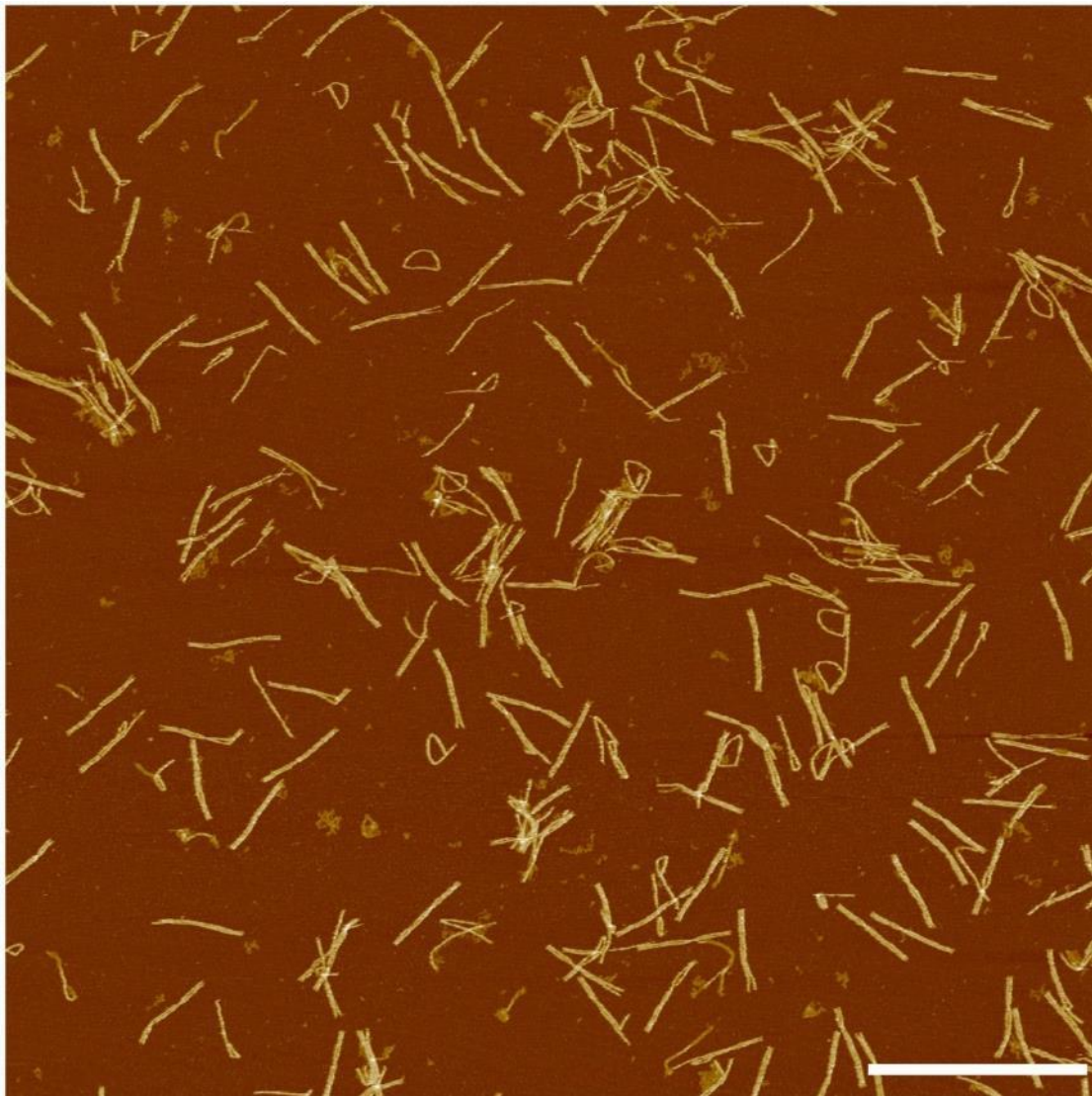
Supplementary Fig. 14. Schematic design for formation of right-handed double-stranded M-DNA with a twist angle of 180°. The numbers below the red spots represent the M-base sequence number. M-bases were located on helices 0, 5, 4, and 3 in a right-handed manner, which lead to formation of a right-handed double-stranded M-DNA from the two complementary M-DNA-1 and M-DNA-2. All the needed strand-sequences can be found in the Supplementary Table. 11-12.



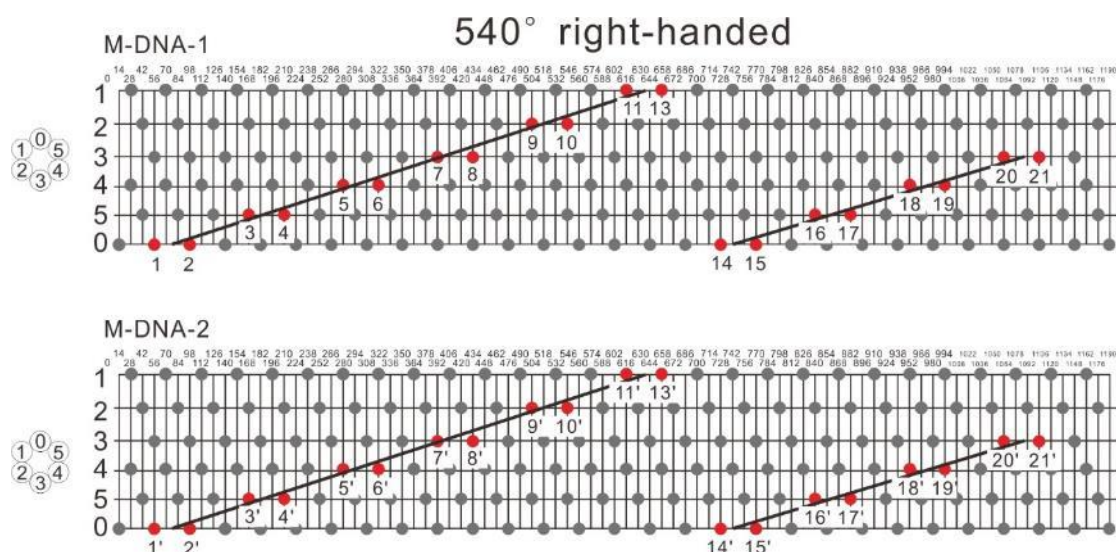
Supplementary Fig. 15. AFM image of right-handed double-stranded M-DNA with a twist angle of 180° . Scale bar $1\mu\text{m}$.



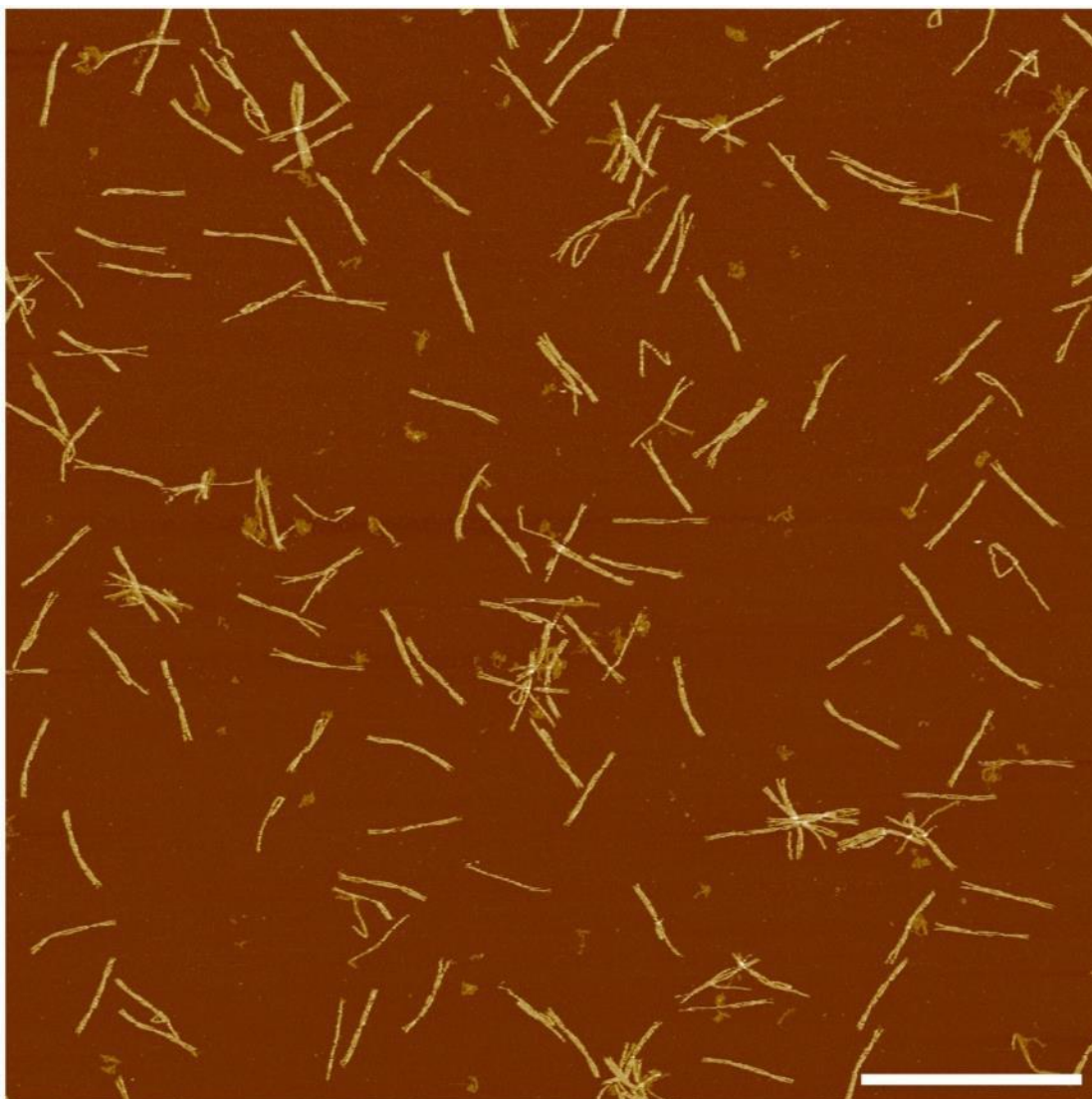
Supplementary Fig. 16. Schematic design for formation of right-handed double-stranded M-DNA with a twist angle of 300°. The number below the red spots represent the M-base sequence numbers. The M-bases were located on the helices 0, 5, 4, 3, 2, and 1 in a right-handed manner, which lead to formation of a right-handed double-stranded M-DNA from the two complementary M-DNA-1 and M-DNA-2. All the needed strand sequences can be found in the Supplementary Table. 13-14.



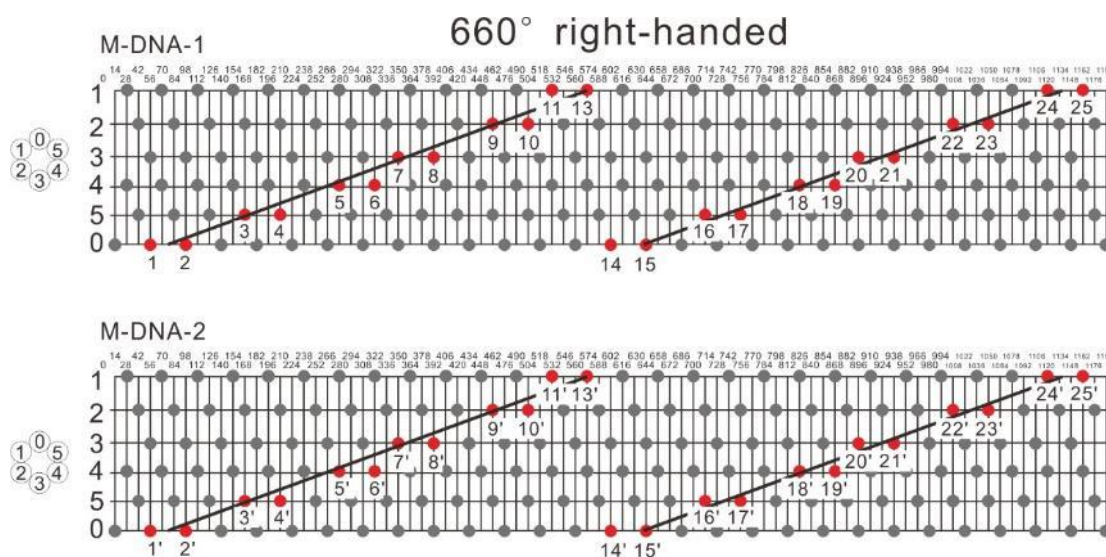
Supplementary Fig. 17. AFM image of right-handed double-stranded M-DNA with a twist angle of 300° . Scale bar $1\mu\text{m}$.



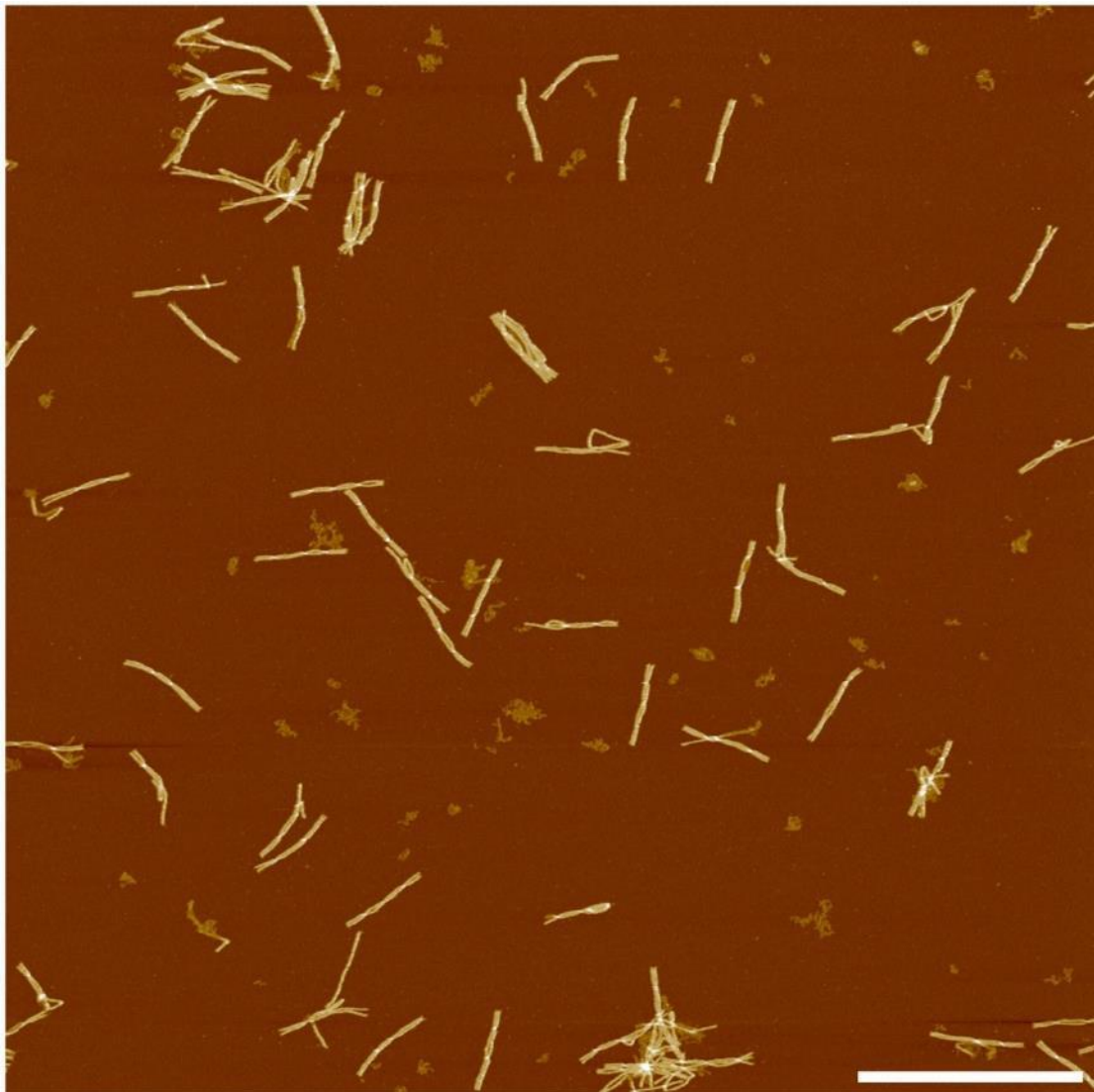
Supplementary Fig. 18. Schematic design for formation of right-handed double-stranded M-DNA with a twist angle of 540° (1.5 turn). The numbers below the red spots represent the M-base sequence numbers. M-bases were located on helices 0, 5, 4, 3, 2, 1, 0, 5, 4, and 3 in a right-handed manner, which lead to formation of right-handed double-stranded M-DNA. All the needed strand sequences can be found in the Supplementary Table. 15-16.



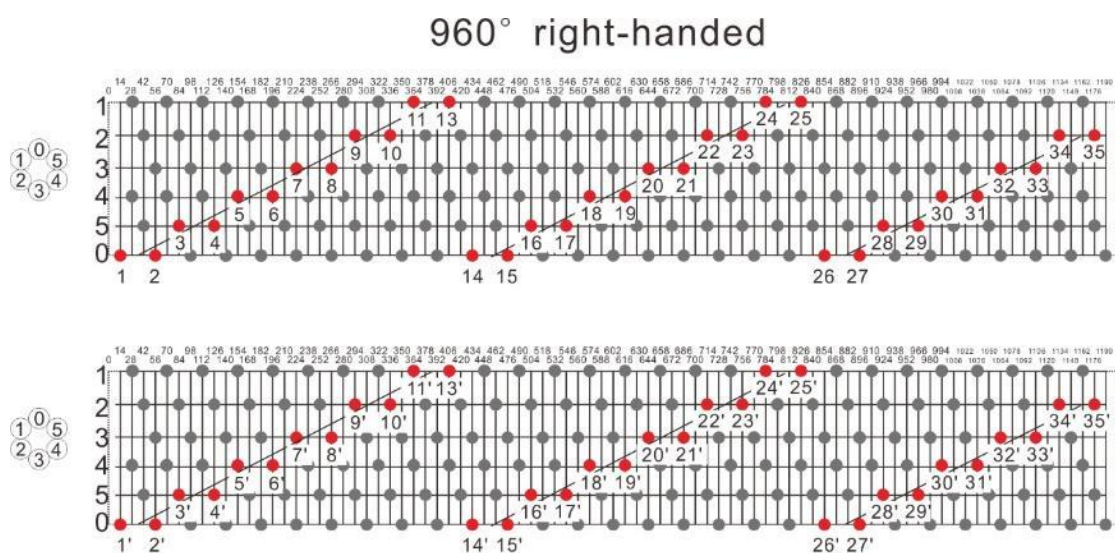
Supplementary Fig. 19. AFM image of right-handed double-stranded M-DNA with a twist angle of 540° . Scale bar $1\mu\text{m}$.



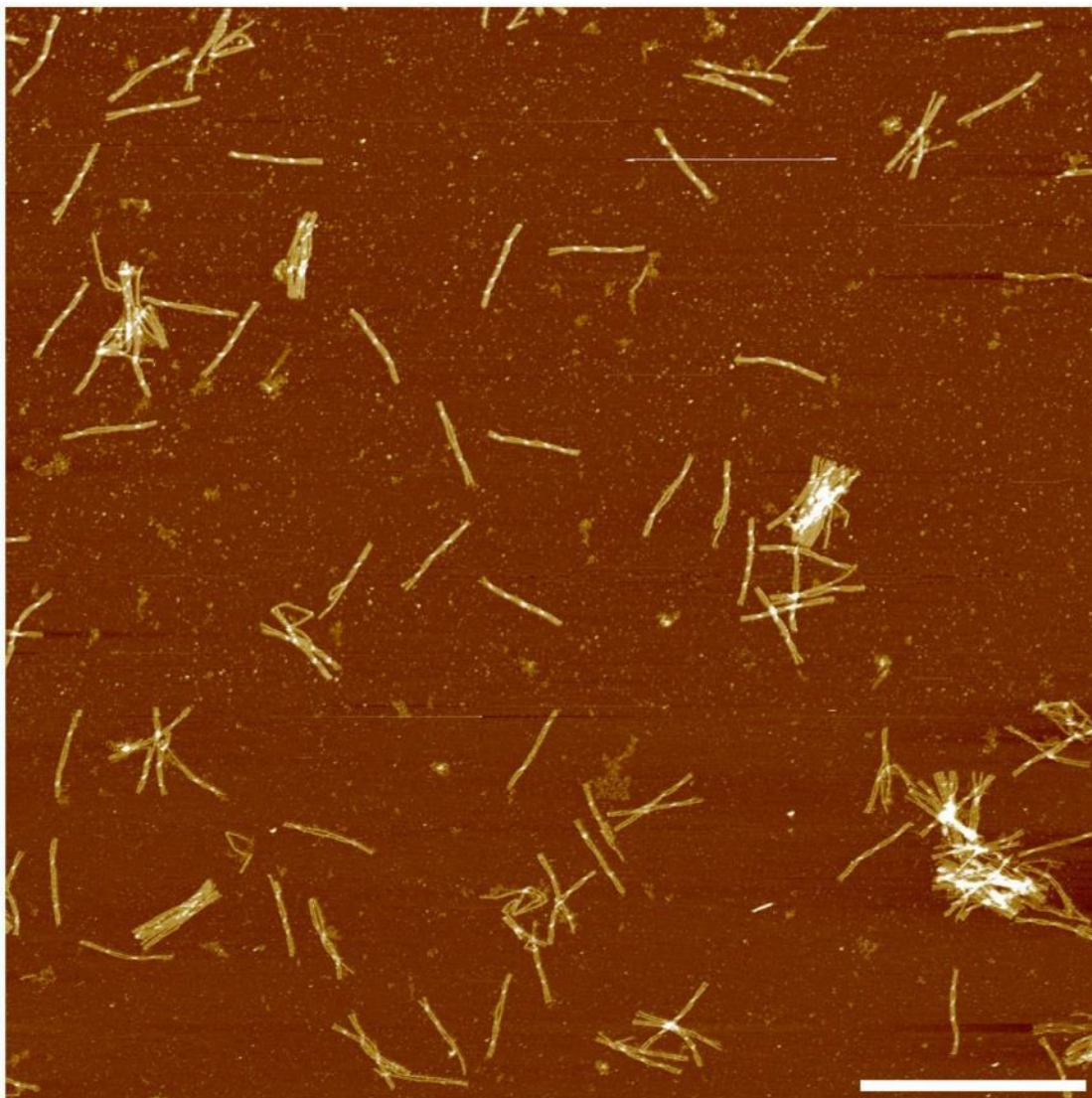
Supplementary Fig. 20. Schematic design for formation of right-handed double-stranded M-DNA with a twist angle of 660°. The numbers below the red spots represent the M-base sequence numbers. The M-bases were located on helices 0, 5, 4, 3, 2, 1, 0, 5, 4, 3, 2, and 1 in a right-handed manner, which lead to formation of right-handed double-stranded M-DNA with an almost two-turn twist. All the needed strand sequences can be found in the Supplementary Table. 17-18.



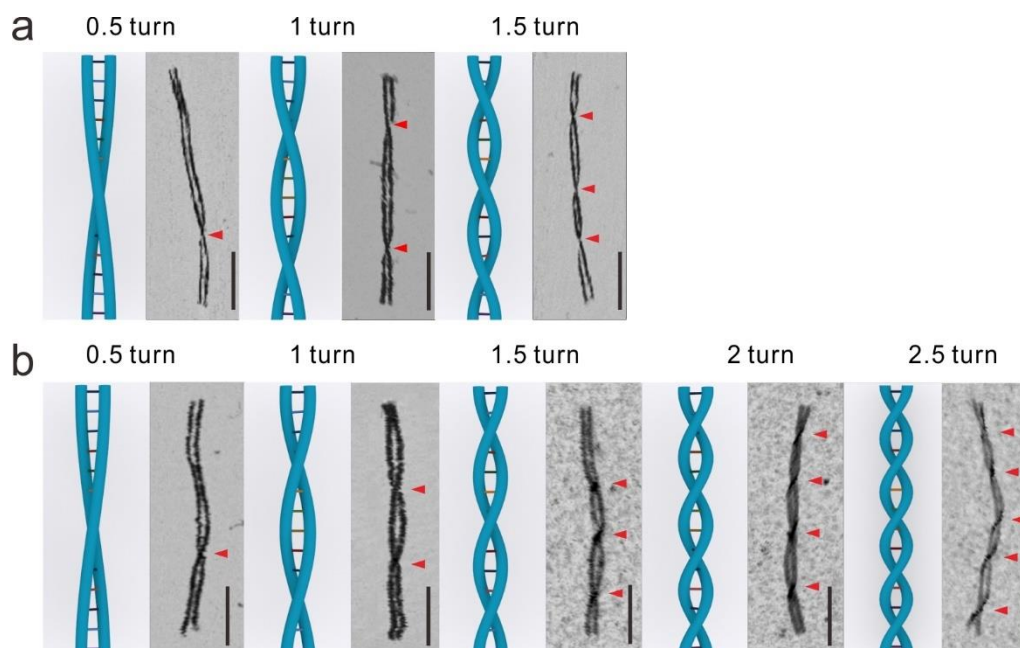
Supplementary Fig. 21. AFM images of right-handed double-stranded M-DNA with a twist angle of 660° . Scale bar $1\mu\text{m}$.



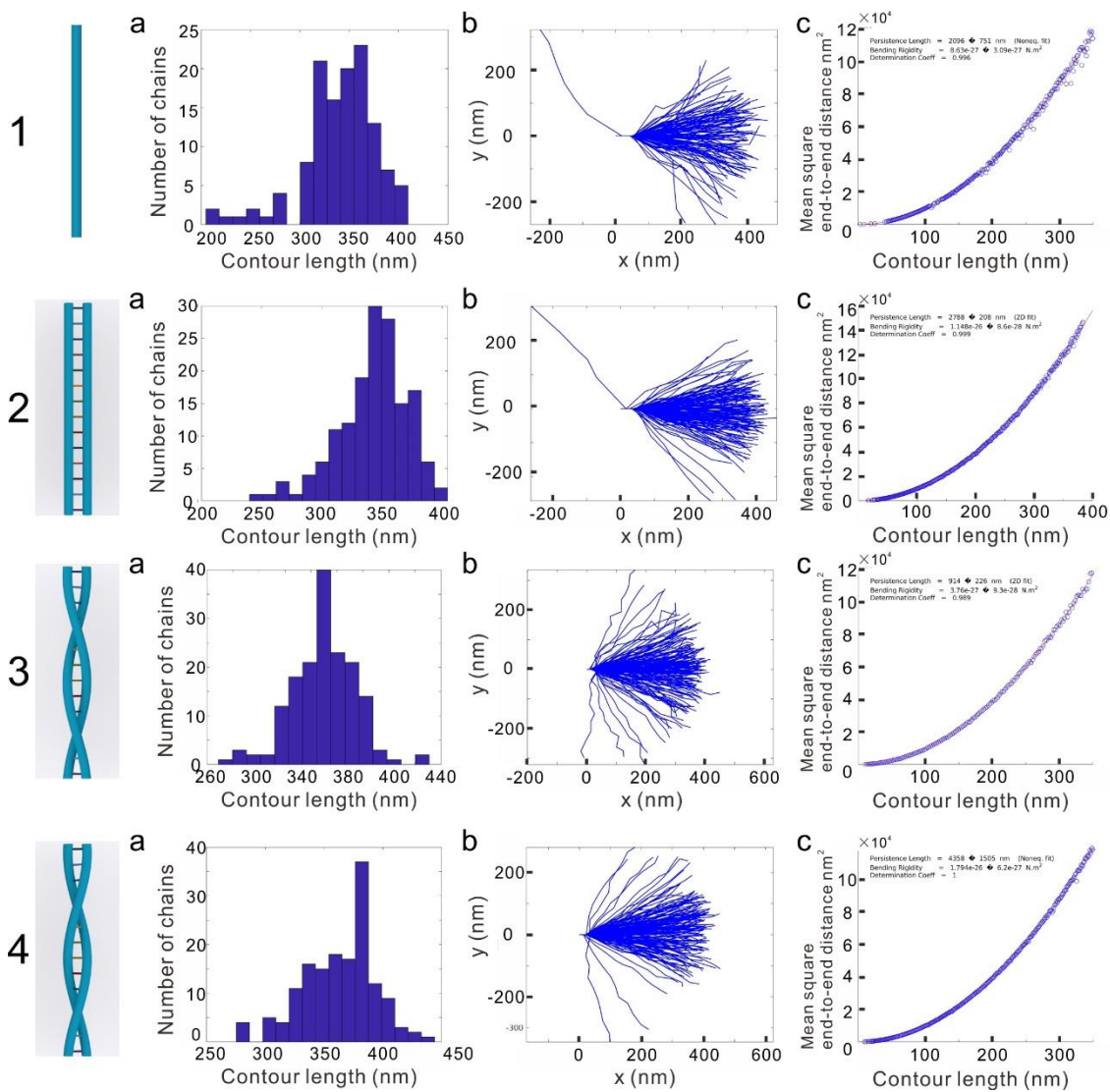
Supplementary Fig. 22. Schematic design for formation of right-handed double-stranded M-DNA with a twist angle of 960°. The numbers below the red spots represent the M-base sequence numbers. The M-bases were located on helices 0, 5, 4, 3, 2, 1, 0, 5, 4, 3, 2, 1, 0, 5, 4, 3, and 2 in a right-handed manner, which lead to formation of right-handed double-stranded M-DNA with an 2.5 turn twist. All the needed strand sequences can be found in the Supplementary Table 19-20.



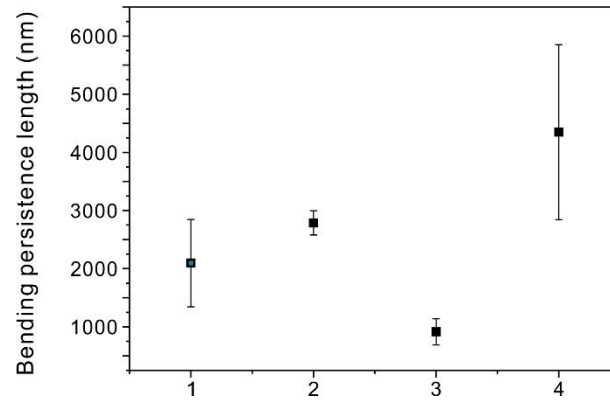
Supplementary Fig. 23. AFM images of right-handed double-stranded M-DNA with a twist angle of 960° . Scale bar $1\mu\text{m}$.



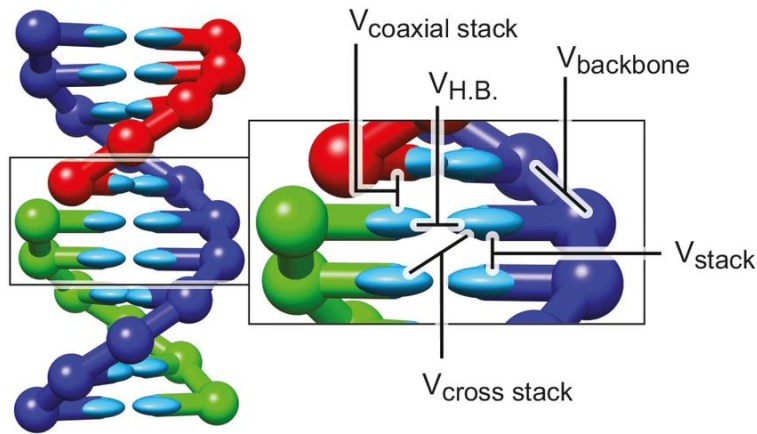
Supplementary Fig. 24. Scheme, (a) typical AFM image of left-handed dsM-DNA with turn numbers from 0.5 to 1.5 and (b) right-handed dsM-DNA with turn numbers from 0.5 to 2.5. Each blue cylinder represents one M-DNA. The red triangle indicates cross position. Scale bars: 100nm.



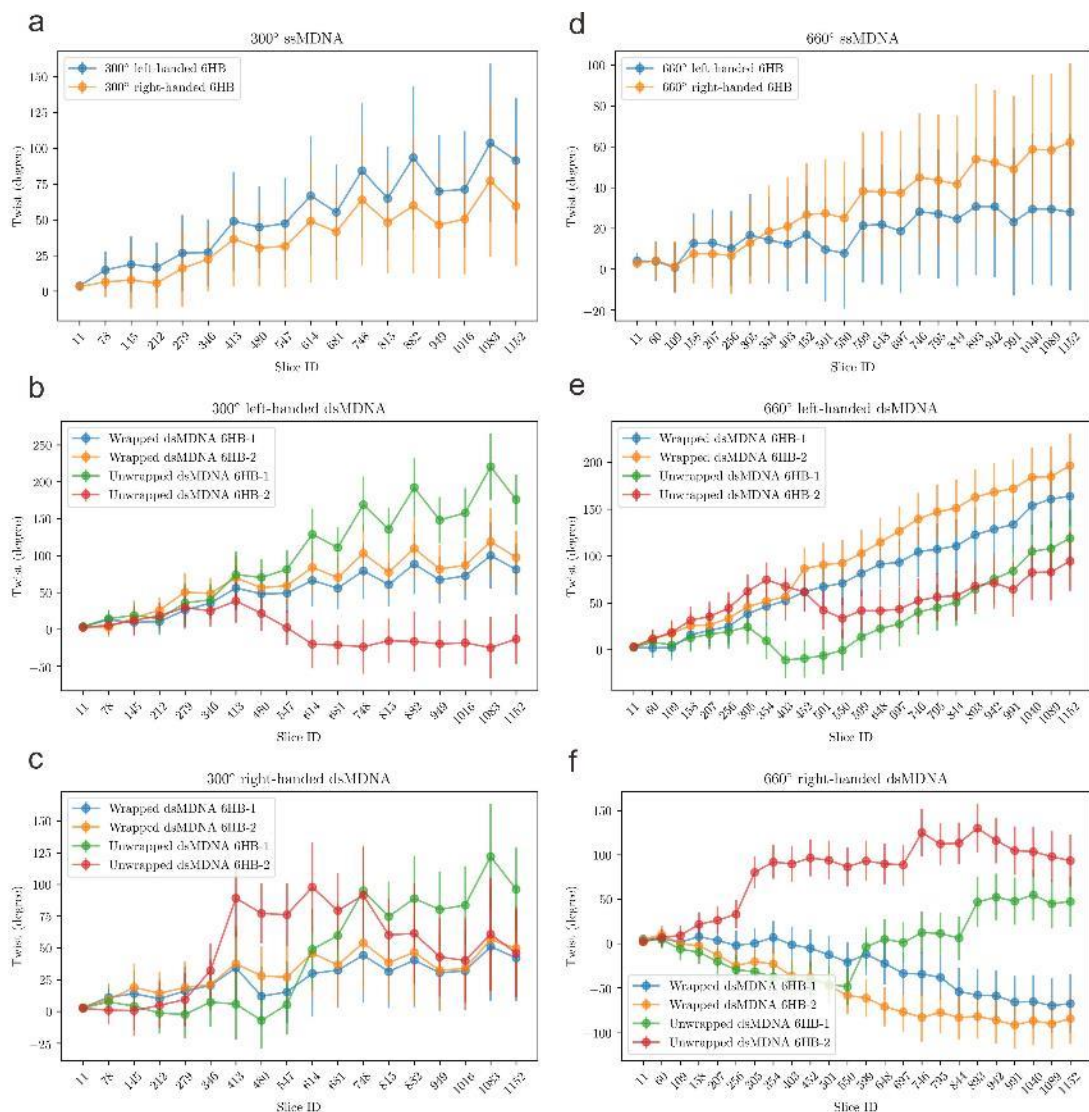
Supplementary Fig. 25. Sample scheme (number 1, 2, 3, 4), contour length distribution (a), aligned contour distribution (b), and calculation of the mean bending persistence length by fitting all measured data (c). Sample 1 is ssM-DNA. Sample 2 is parallel dsM-DNA. Sample 3 is left-handed dsM-DNA (1 turn). Sample 4 is right-handed dsM-DNA (1 turn).



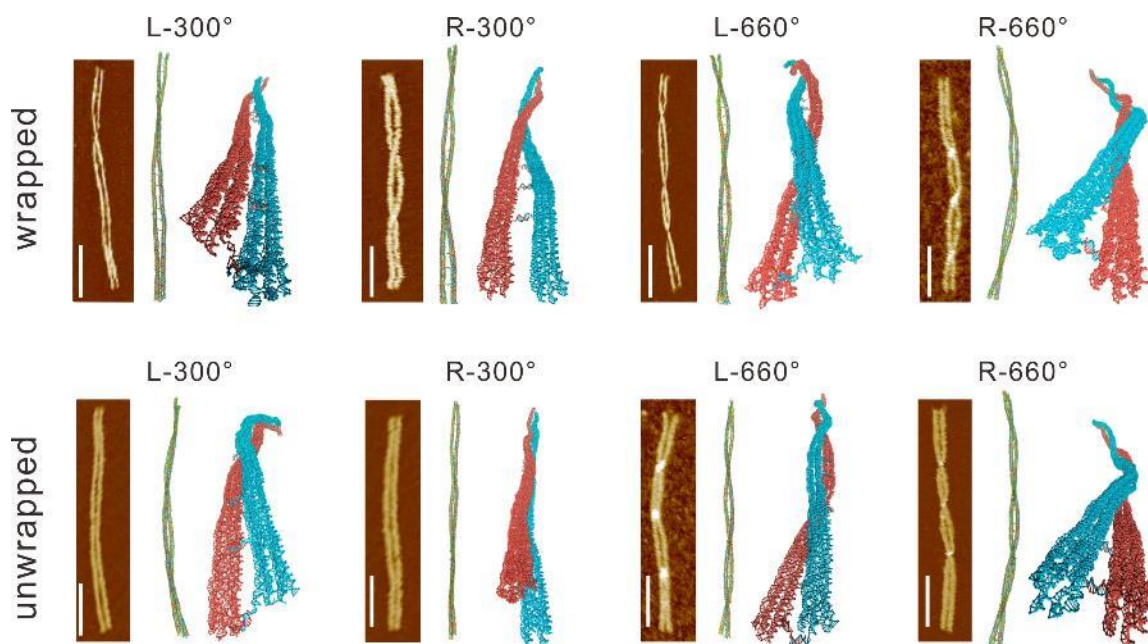
Supplementary Fig. 26. Measured bending persistence lengths of sample 1, sample 2, sample 3 and sample 4. Sample 1 is ssM-DNA. Sample 2 is parallel dsM-DNA. Sample 3 is left-handed dsM-DNA (1 turn). Sample 4 is right-handed dsM-DNA (1 turn).



Supplementary Fig. 27. A schematic illustration of the oxDNA model and the coarse-grained force field used for simulations of the dsM-DNA structures.

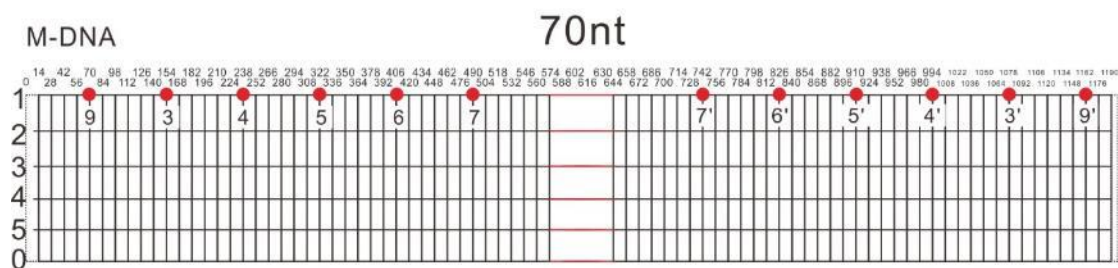
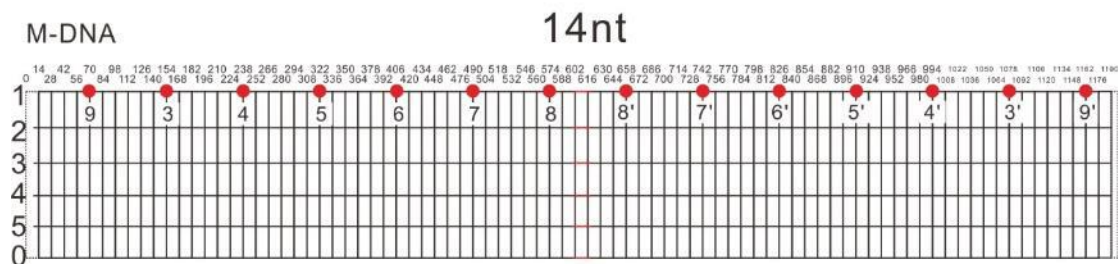
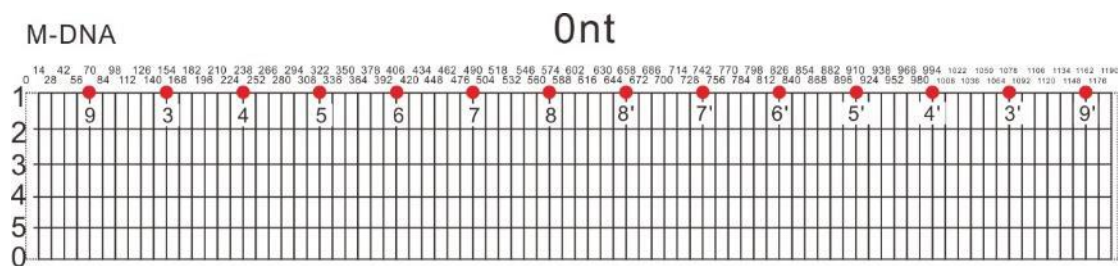


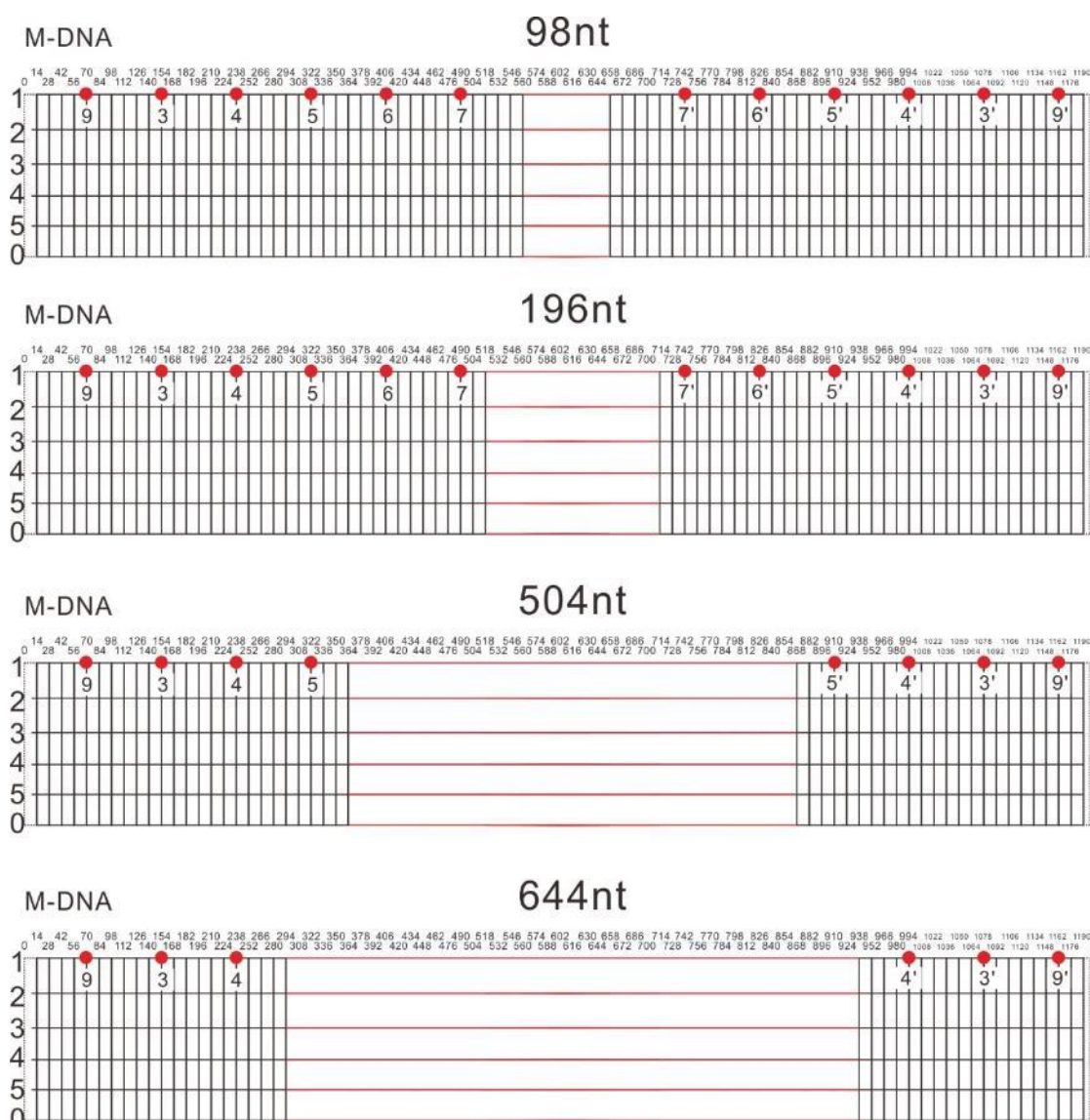
Supplementary Fig. 28. Mean twist change along the 6-helix bundles obtained from sampling simulations of different dsM-DNA assemblies, averaged over oxDNA simulation trajectories. (a-c) show the data for 300° designs, while (d-f) show the data for 660° designs. Often, the unwrapped topology has diverging twists in the two strands, while wrapped topologies have consistent twist between the two 6HBs. Furthermore, assembled designs almost always have higher twist than unassembled bundles, implying that the assembled state requires some degree of deviation from the most relaxed state.



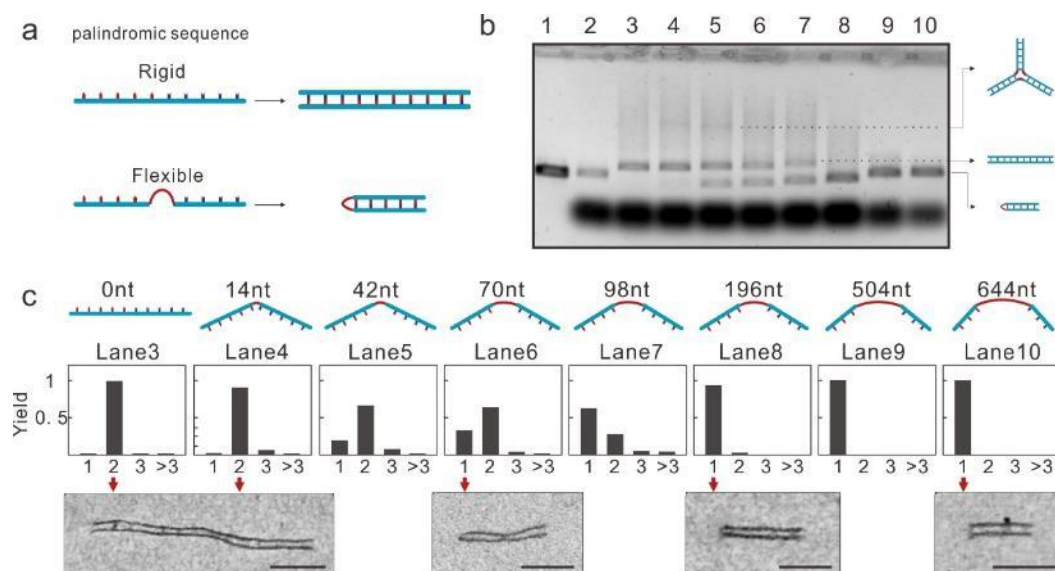
Supplementary Fig. 29. Illustrative examples from AFM imaging and simulation trajectories showing the wrapped and unwrapped isomers of the left-handed and right-handed dsM-DNA with designed twist degree of 300° and 660°. Scale bars: 100nm.

Section 5. M-Junctions and M-DX structures

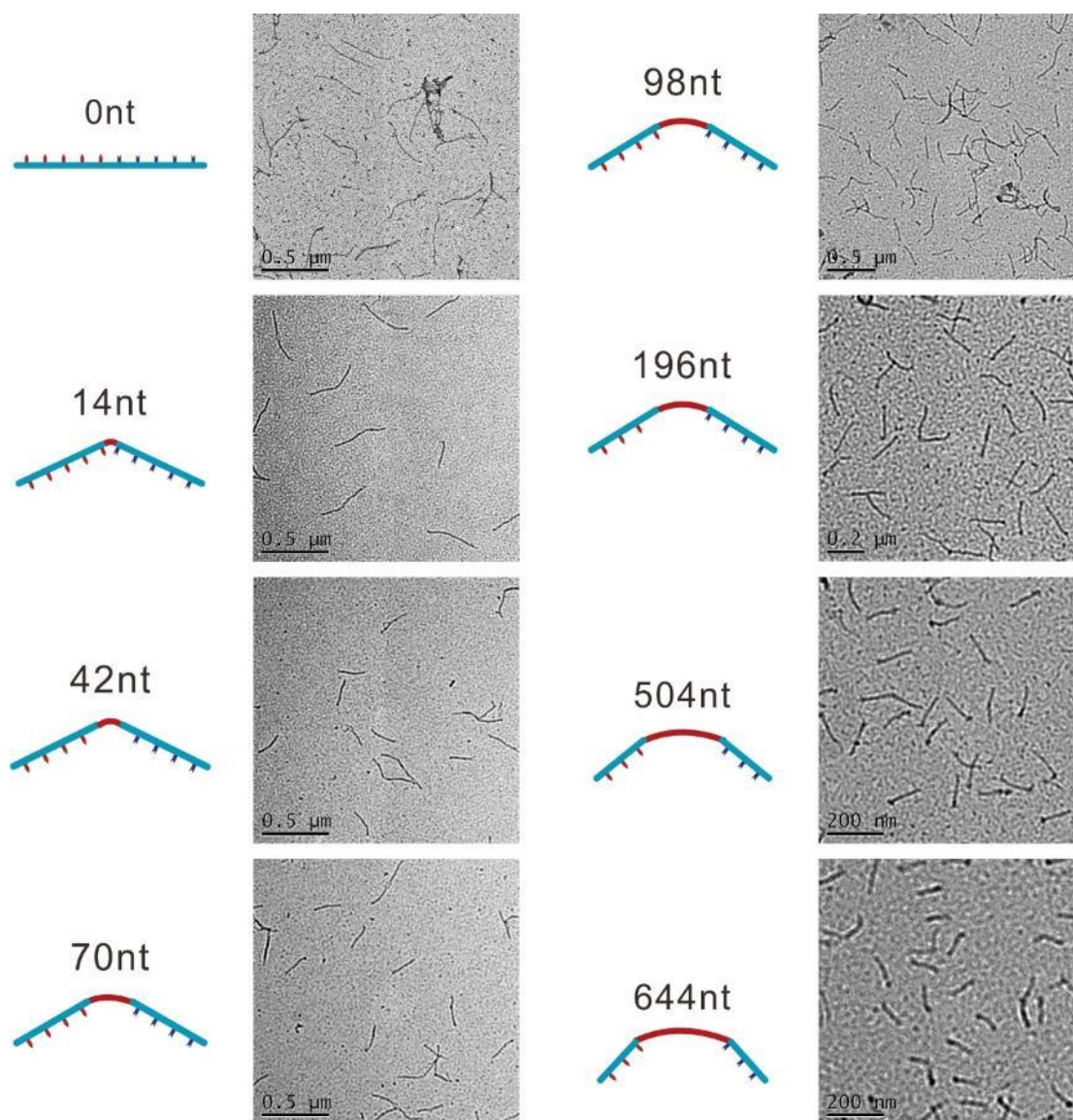




Supplementary Fig. 30. Schematic design for formation of self-folded M-DNA hair-pin structure. M-bases were all located on helix 1. The order of M-bases was in a palindromic sequence. The M-DNA will fold-back and self-hybridize when the middle part of the M-DNA was flexible. The red lines in the middle was the flexible region, which was formed by removing different numbers of staple strands of a total length of 0 nt to 644 nt in all of the helices. The structures were formed in a one-pot annealing process from 90°C to 25°C. All the needed strand sequences can be found in the Supplementary Table. 21-29.

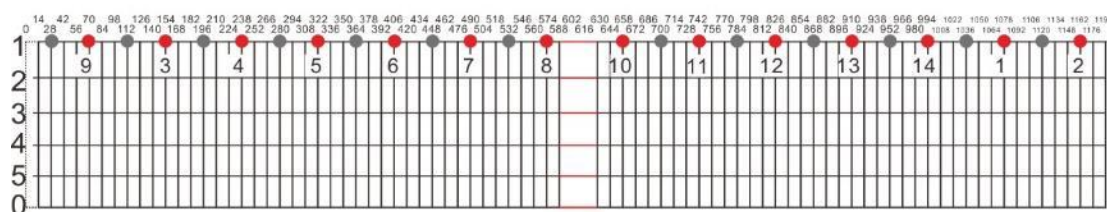


Supplementary Fig. 31. (a) Scheme showing the differences of a rigid and a flexible M-DNA with palindromic M-bases in self-assembly to either form an inter-molecular dimer or an intramolecular hairpin. (b) 1% agarose gel images of self-assembly behavior of M-DNA with different lengths of the flexible region. Lane 1 was M13 scaffold. Lane 2 was a single-stranded M-DNA with no M-bases. Lane 3 to Lane 10 were M-DNA with flexible region of 0 nt, 14 nt, 42 nt, 70 nt, 98 nt, 196 nt, 504 nt, and 644 nt respectively. (c) Statistical results of the yields of different products from (b). The numbers 1-3 or >3 represent the copies of the M-DNA in the product, 1 indicates a single M-DNA that was self-folded; 2 indicates hybridized two M-DNAs, 3 indicates hybridized three M-DNAs, like a Y-shaped junctions; >3 indicates aggregates with more than 3 M-DNAs. AFM images (or TEM images) of the typical self-hybridized double-stranded M-DNA and the self-folded M-DNA hairpins are shown below. Scale bars:100 nm. When the flexible region is long enough (like > 200 nt), the final structure is almost exclusively the self-folded hair-pin structure.

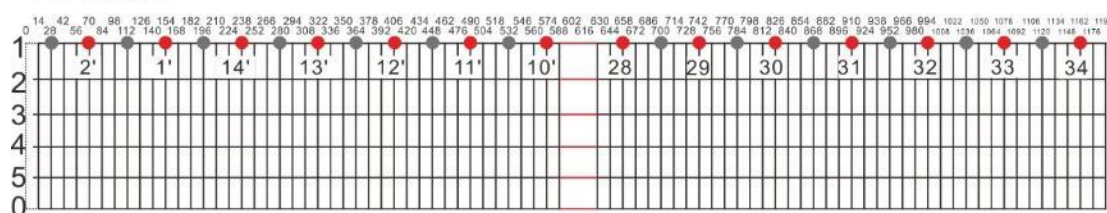


Supplementary Fig. 32. Typical negative-stained TEM Images of hybridized products of M-DNA with different flexible regions.

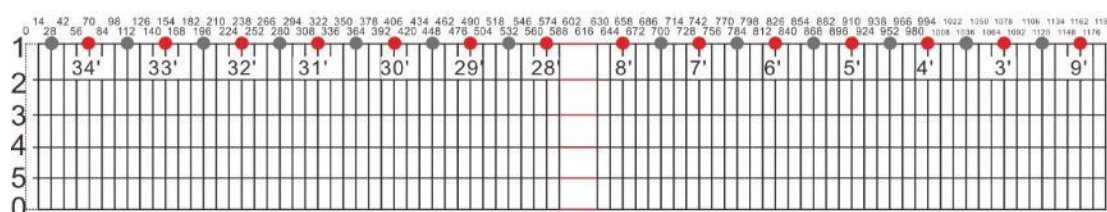
Y-M-DNA-1



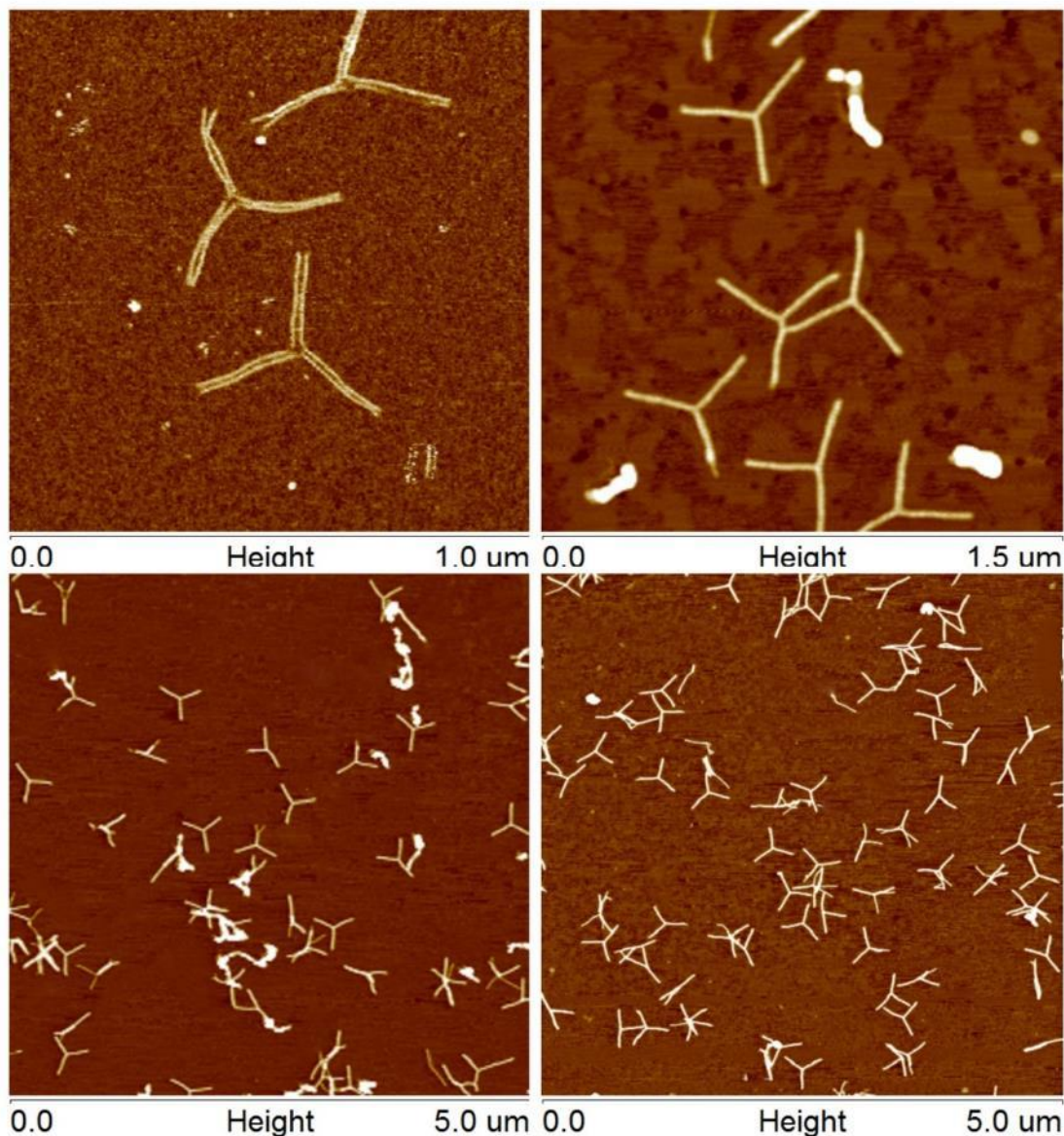
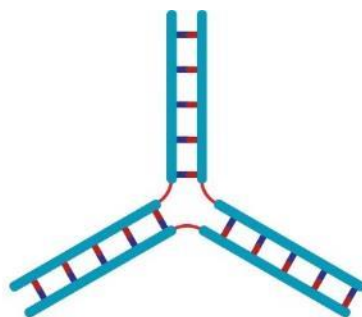
Y-M-DNA-2



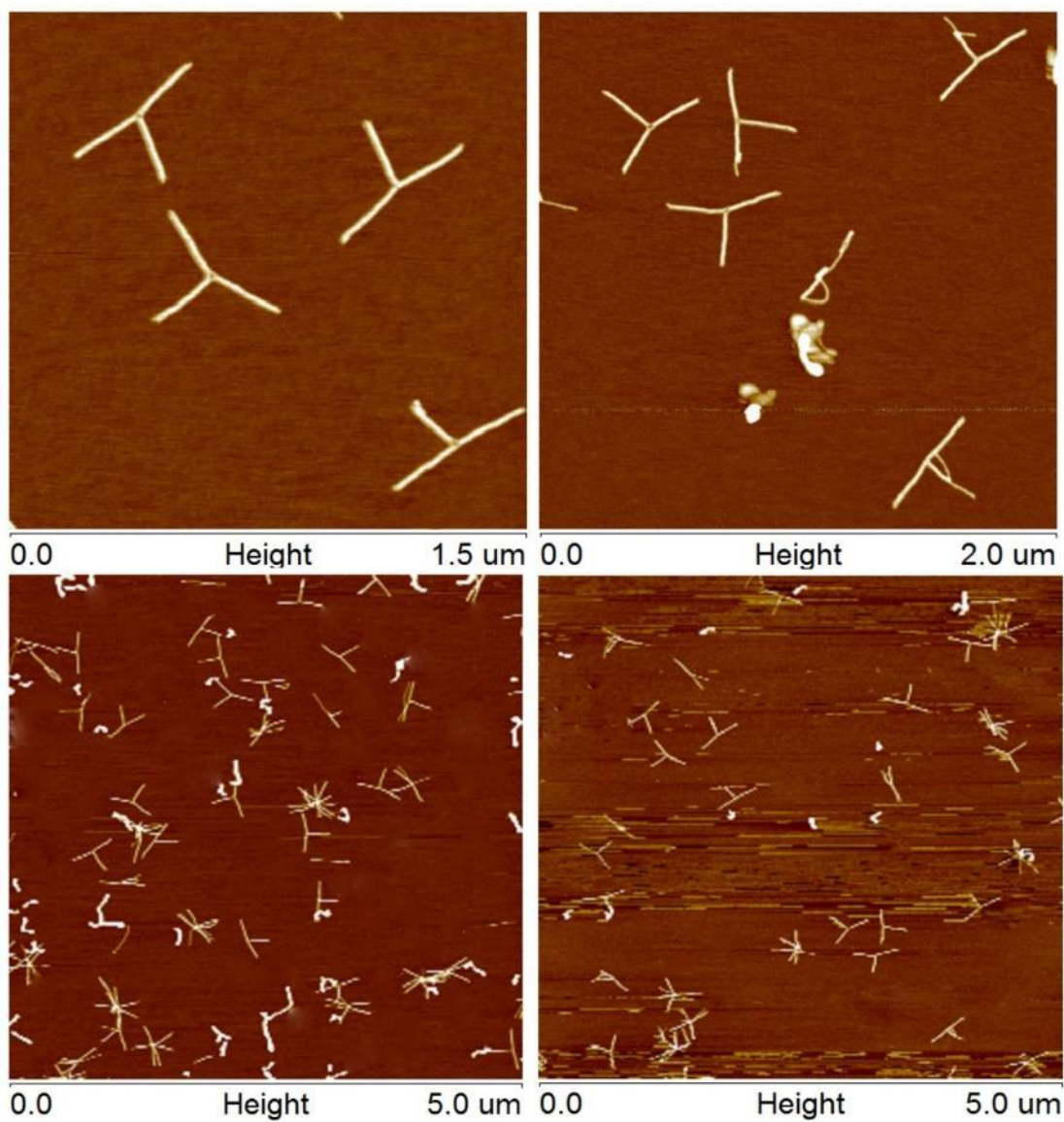
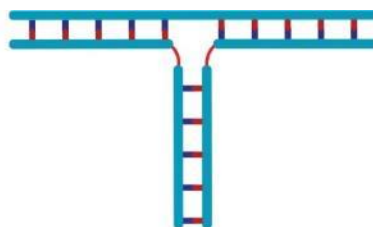
Y-M-DNA-3



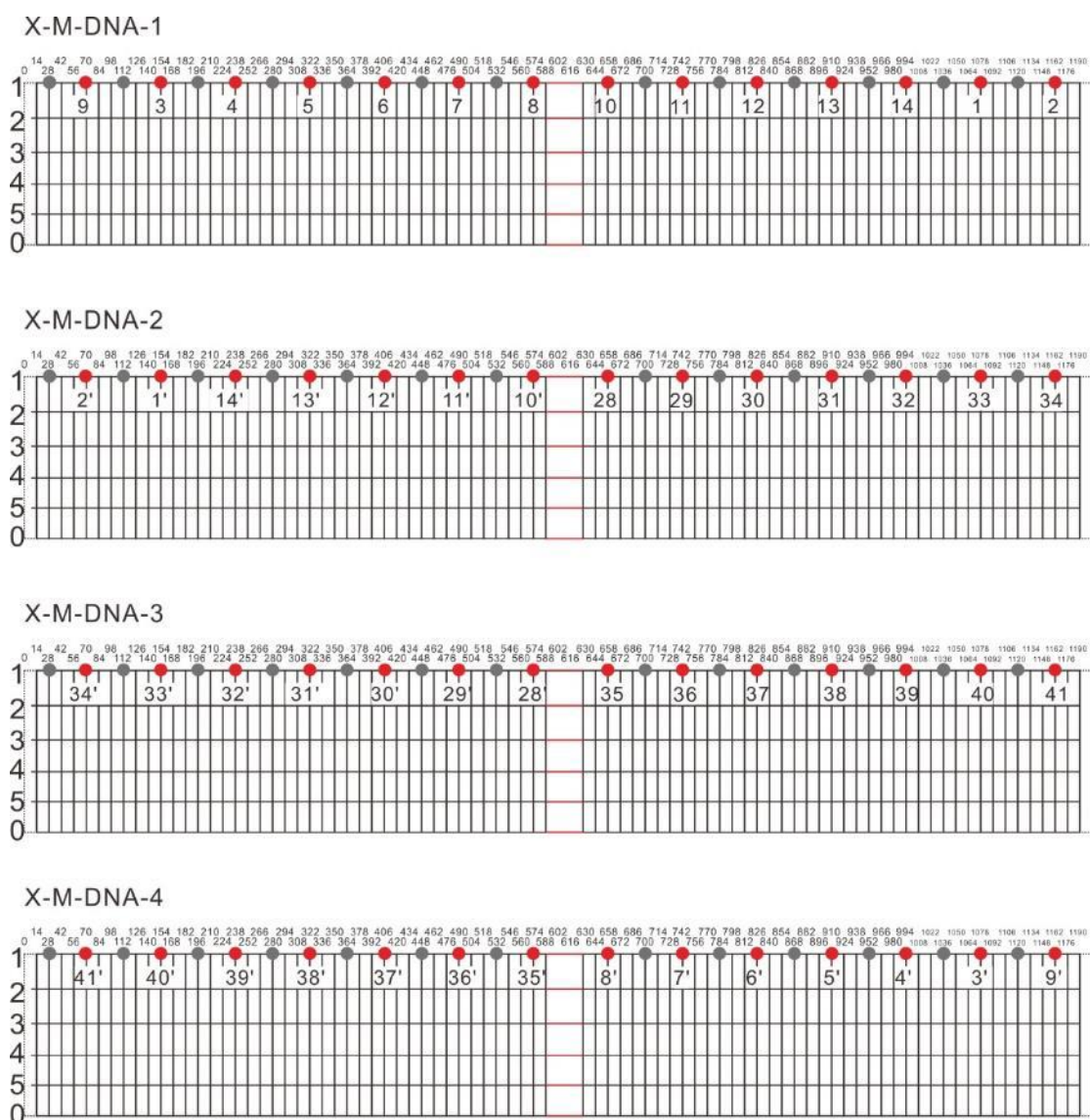
Supplementary Fig. 33. Schematic design for formation of Y-shaped junctions. M-bases were all located on helix 1. The flexible region was 42 nt long. The Y-shaped junction was formed by mixing Y-M-DNA-1, Y-M-DNA-2, and Y-M-DNA-3 and annealing from 55°C to 20°C at a rate of 1°C per 30 min. All the needed strand sequences can be found in the Supplementary Table. 30-31.



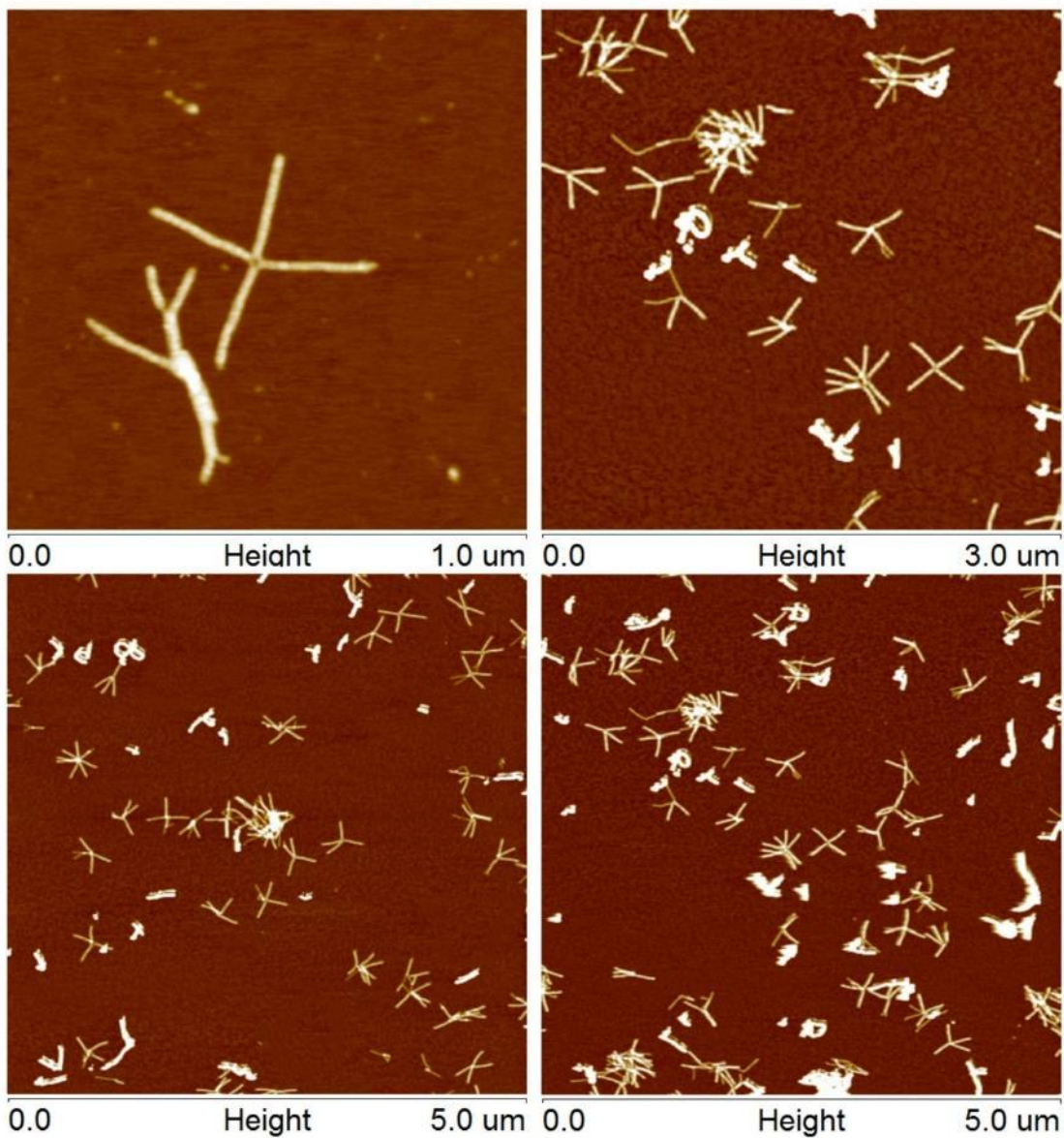
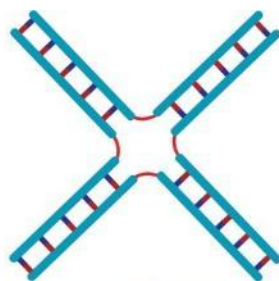
Supplementary Fig. 34. Additional AFM images of Y-shaped junction at different magnifications. The up-left micrograph was imaged in fluid, the others were imaged in air.



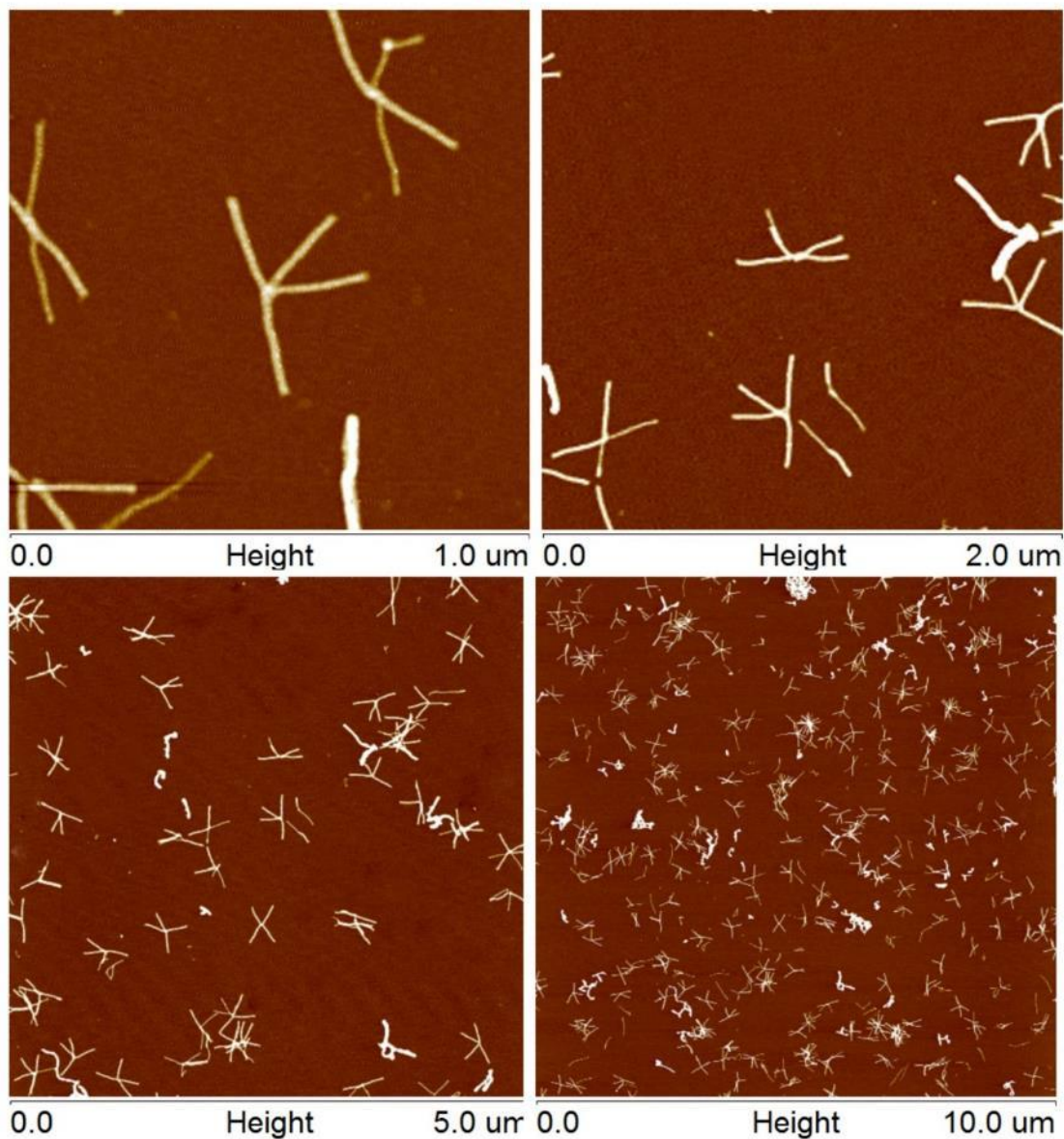
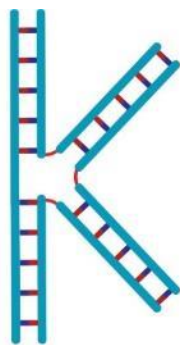
Supplementary Fig. 35. Additional AFM images of T-shaped junctions that is composed of one rigid M-DNA and two flexible M-DNAs at different magnifications.



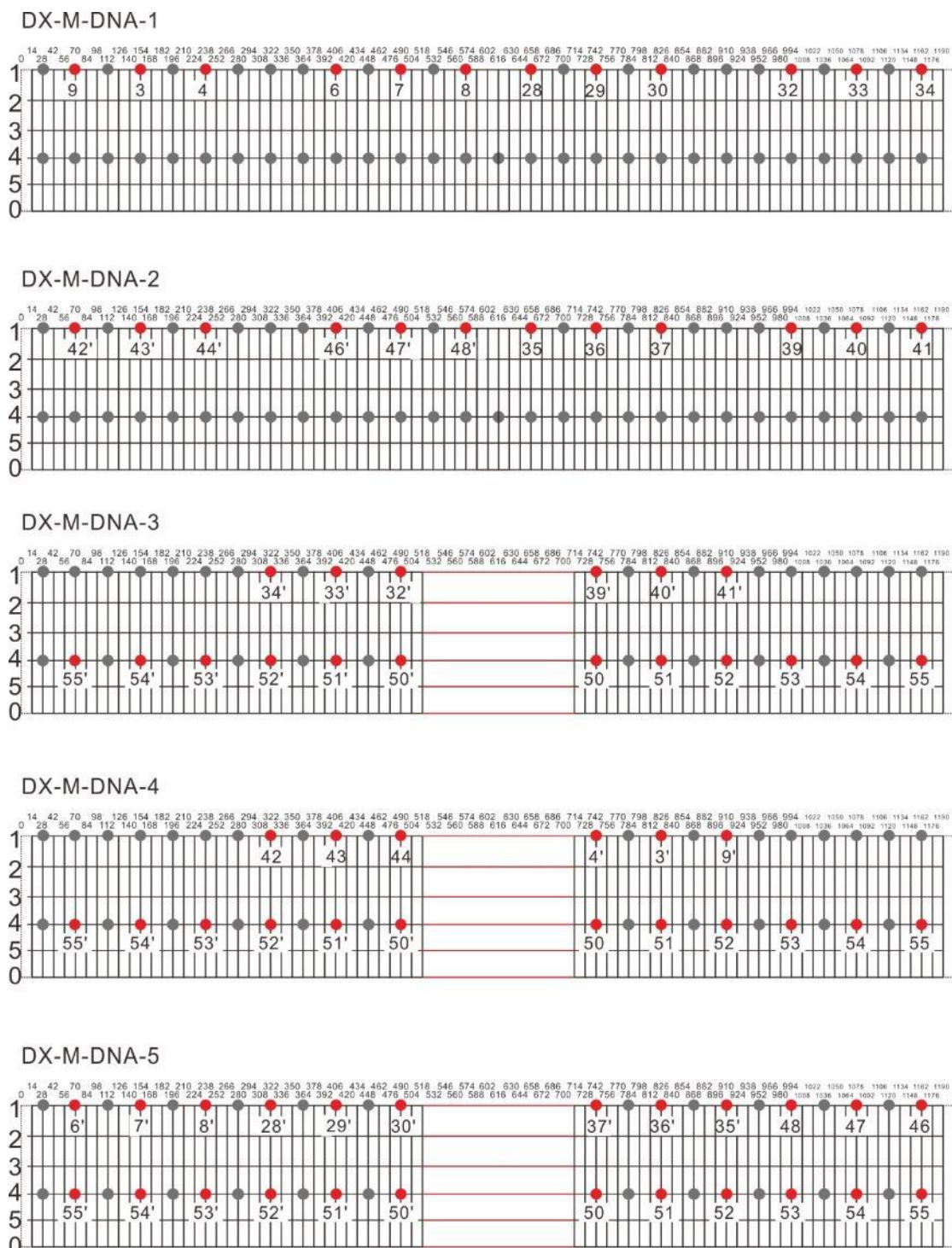
Supplementary Fig. 36. Schematic design for formation of X-shaped junctions. M-bases were all located on helix 1. The flexible region was 42 nt. The X-shaped junction was formed by mixing X-M-DNA-1, X-M-DNA-2, X-M-DNA-3, and X-M-DNA-4 and annealing from 55°C to 20°C at a rate of 1°C per 30min. All the needed strand sequences can be found in the Supplementary Table. 32-33.



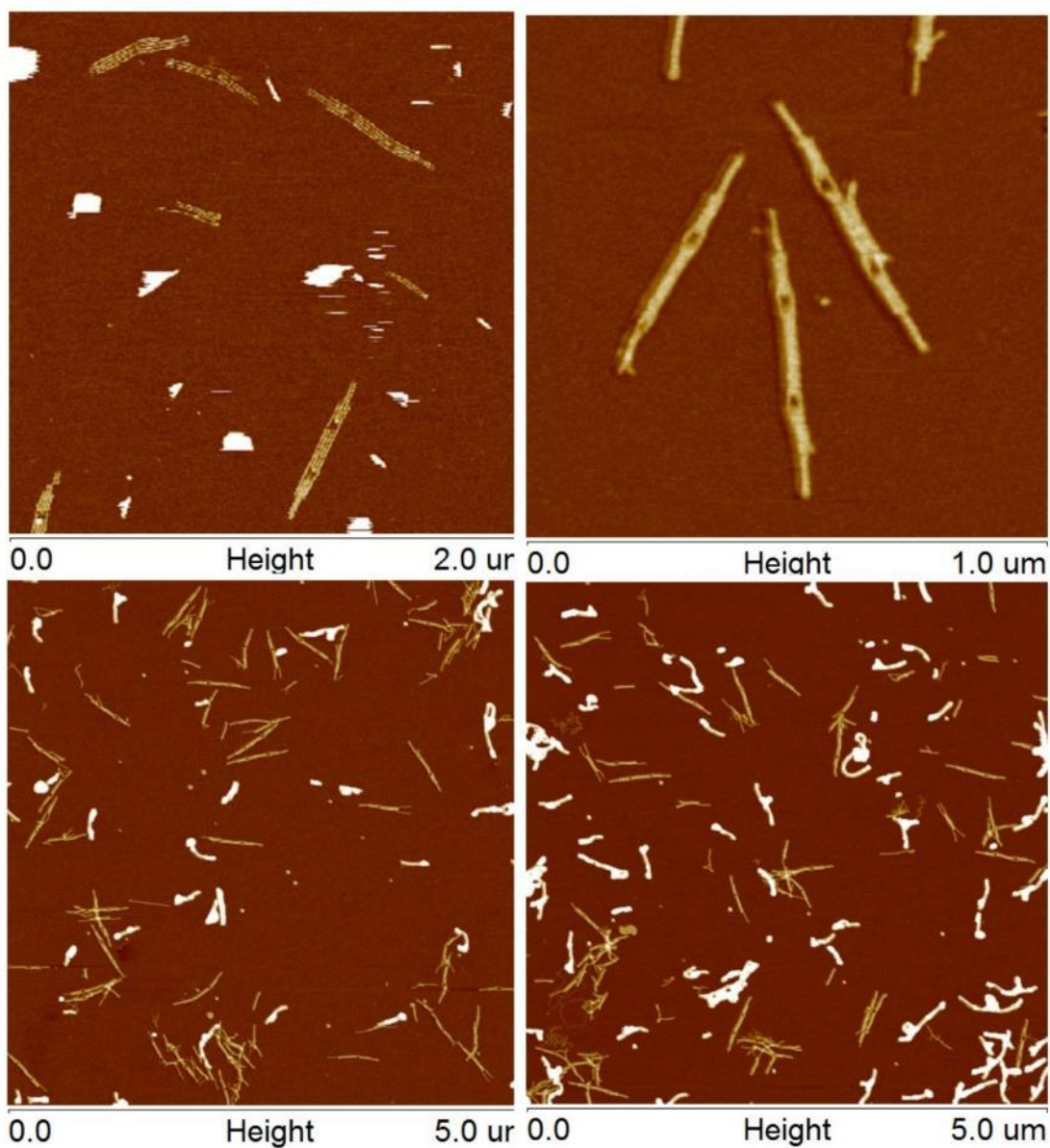
Supplementary Fig. 37. Additional AFM images of X-shaped junction at different magnifications.



Supplementary Fig. 38. Additional AFM images of K-shaped junction at different magnifications.

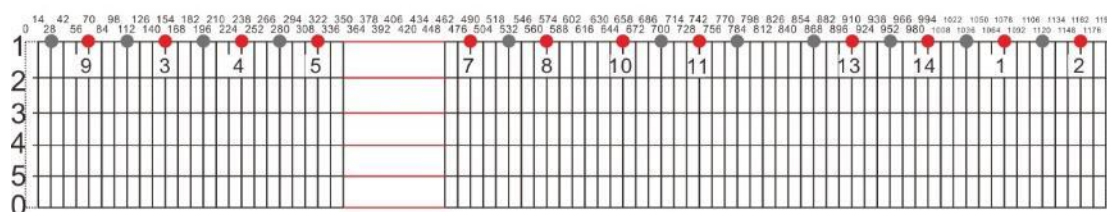


Supplementary Fig. 39. Schematic design for formation of DX tiles. The M-bases are located on helix 1 and helix 4, which are at opposite positions. DX-M-DNA-1 and DX-M-DNA-2 are rigid, while DX-M-DNA-3, DX-M-DNA-4, and DX-M-DNA-5 are flexible in the middle. The flexible region was 196 nt. The DX tile was formed by mixing these five M-DNA and annealing from 55°C to 20°C at a rate of 1°C per 30 min. All the needed strand sequences can be found in the Supplementary Table. 34-36.

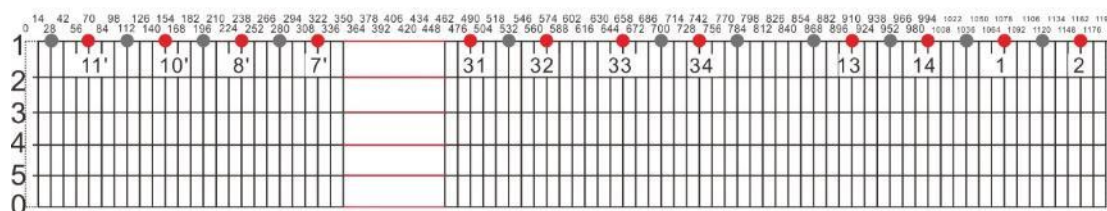


Supplementary Fig. 40. Additional AFM images of DX tile at different magnifications. The up-left micrograph was imaged in fluid, the others were imaged in air.

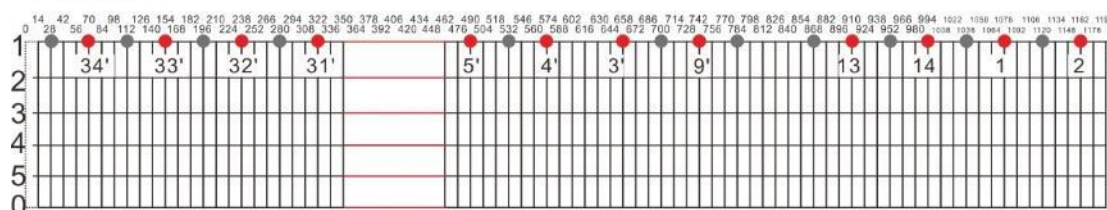
Y-e-M-DNA-1



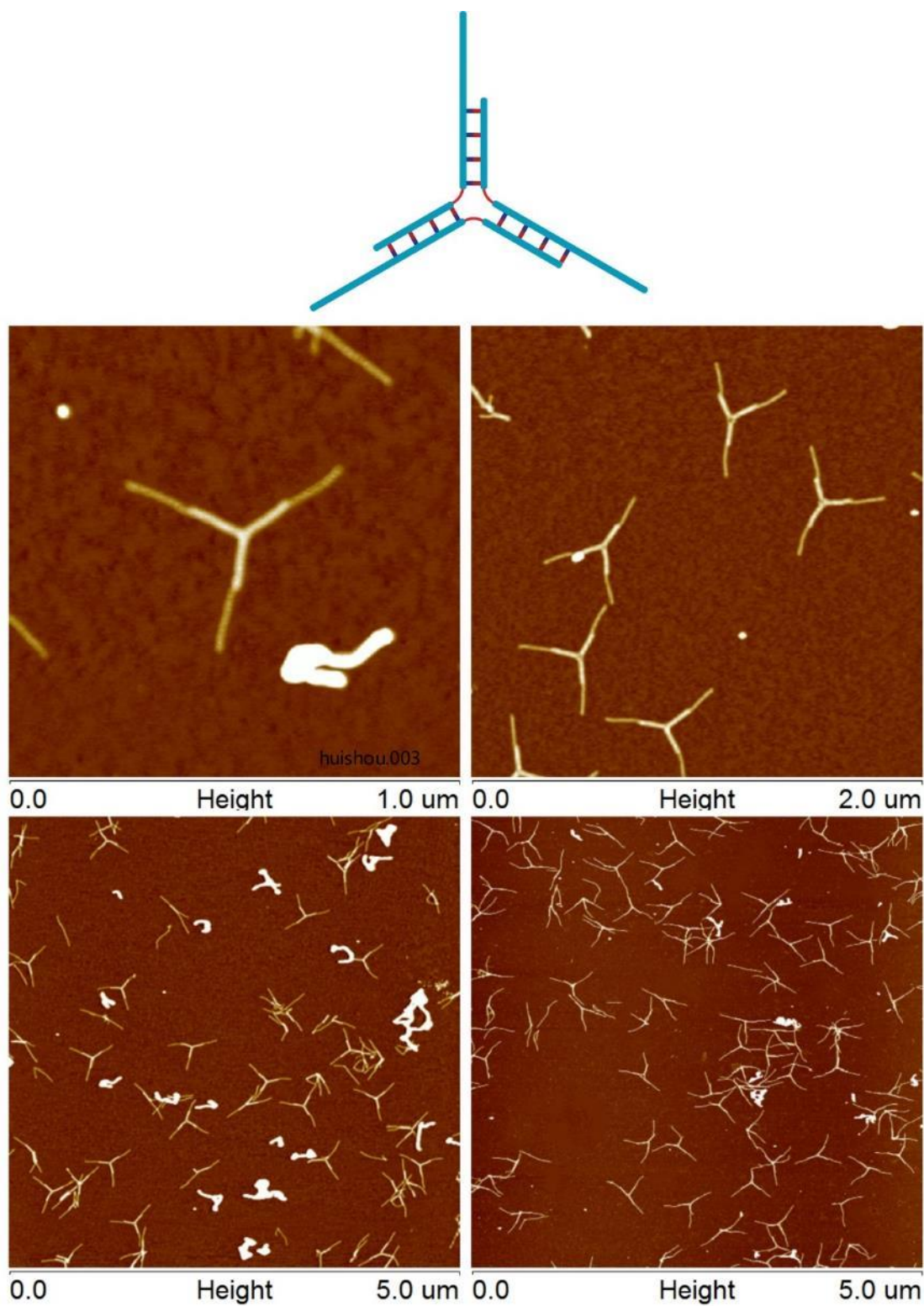
Y-e-M-DNA-2



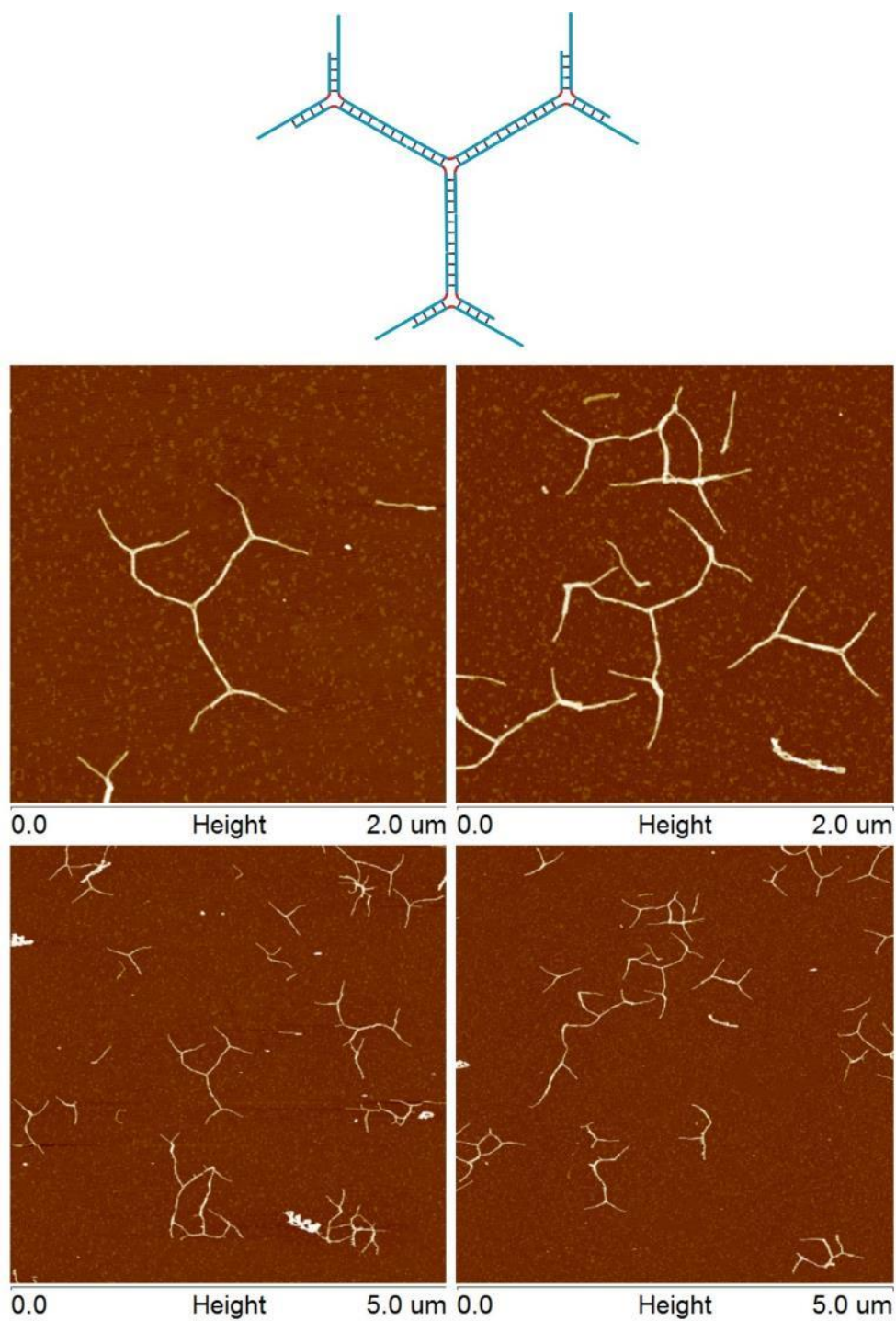
Y-e-M-DNA-3



Supplementary Fig. 41. Schematic design for formation of extensive Y-shaped (Y-e) junction. M-bases were all located on helix 1. The flexible region was 112 nt. The junction was formed by mixing three M-DNAs and annealing from 55°C to 20°C at a rate of 1°C per 30min. All the needed strand sequences can be found in the Supplementary Table. 37-38.

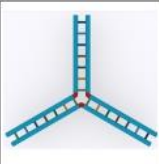
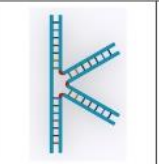
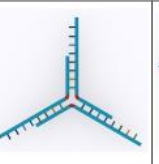
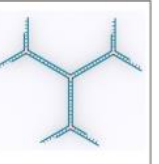


Supplementary Fig. 42. Additional AFM images of Y-e junction at different magnifications.



Supplementary Fig. 43. Additional AFM images of dendrimer Y structures that are assembled from four Y-e-junctions at different magnifications.

Summary and discussion for M-Junctions and M-DX structures.

						
81%	44%	35%	29%	38%	83%	4%

Supplementary Fig. 44. Estimated formation yields of M-Junction and M-tiles from AFM or TEM images. The yield of structure was estimated as $y=m/n$, where m is the total number of complete designed structures in images and n is the total number of complete designed structures, aggregates and ambiguous structures counted in images.

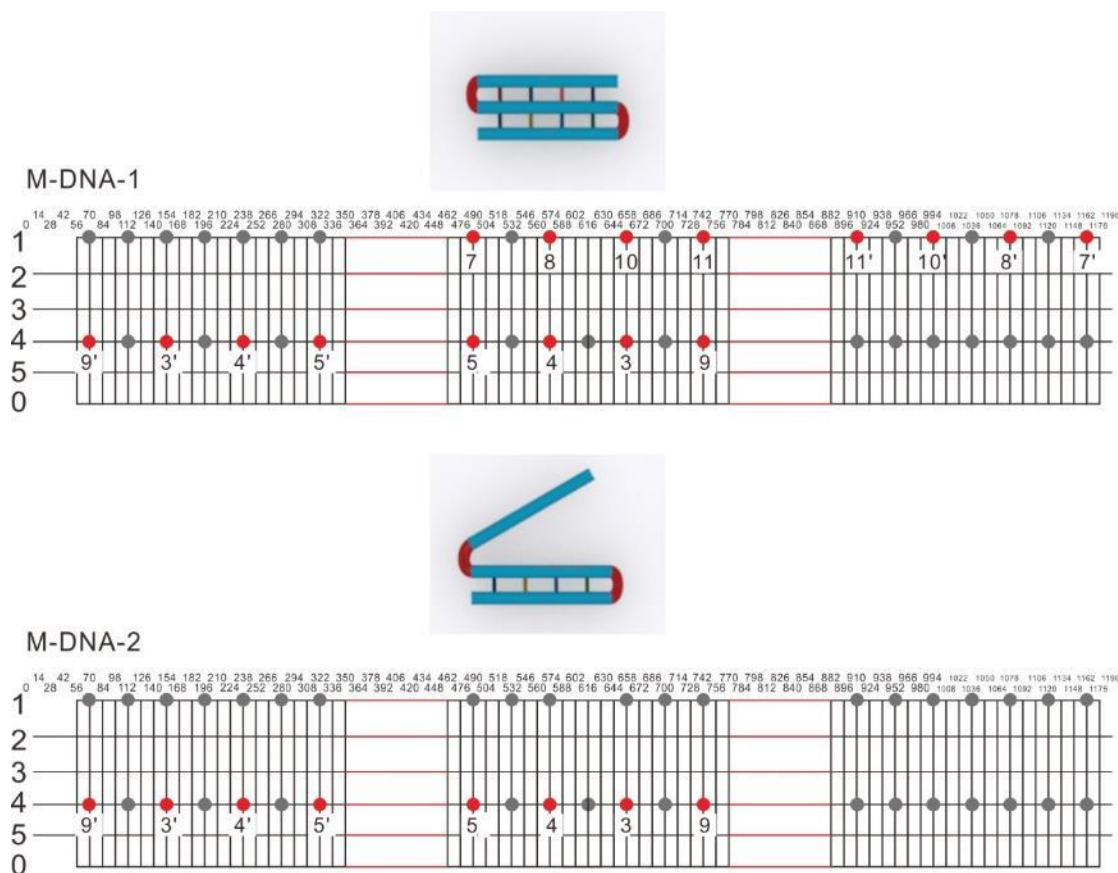
The key for designing these structures is introducing flexible loop regions in the middle of M-DNA to alter the stiffness of M-DNA, which is well studied in Supplementary Fig. 31.

The **assembly** yield is relatively high for simple M-Junctions, such as Y-shape (81%) and T-shape (44%) structures, which only consist of three ssM-DNAs. Y-shape has three flexible M-DNA while T-shape has two flexible M-DNA and one rigid M-DNA. This rigid M-DNA reduced the yield of T-shape due to its rigidity. For X-shape and K-shape structures, their yields are 35% and 29% respectively. We can see more aggregates from the AFM images of X-shape (Supplementary Fig. 37) and K-shape (Supplementary Fig. 38). The reason is that they are structurally more complicated than Y and T. Four ssM-DNAs are involved in their structures.

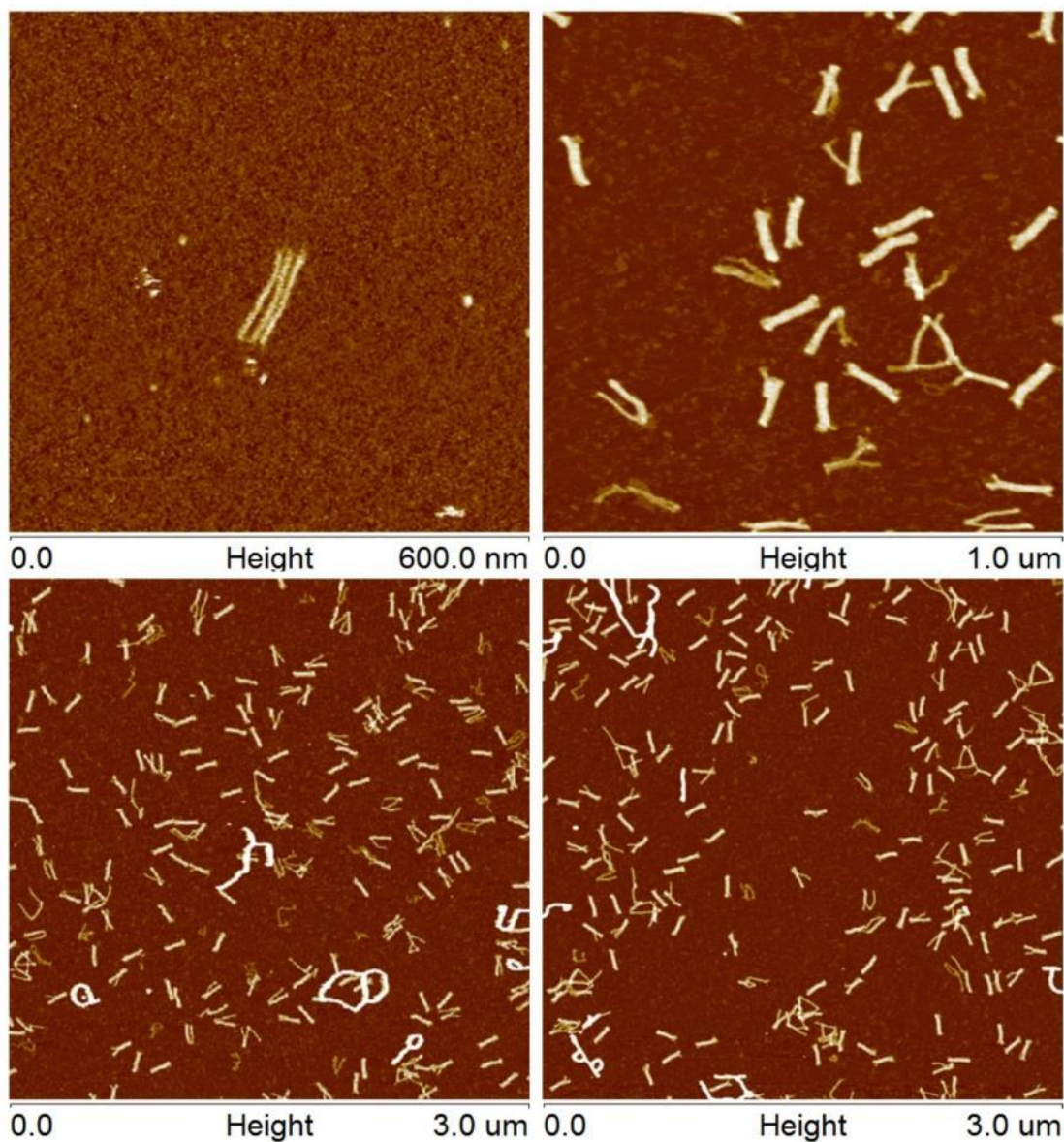
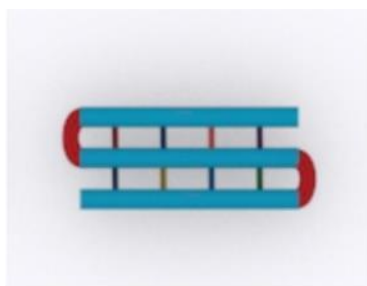
Although an individual M-Junction has a relatively decent yield, after sticky-end hybridization, perfect dendrimer structures are rarely observed (4% formation yield). The strong binding affinity of M-bases and the softness of Y-shape structures contribute to this low yield. AFM is not a perfect imaging tool for 3D objects because the soft dendrimer structures may collapse on the surface of mica and stack on top of one another which appears as incorrect formations.

In addition, all structures were assembled from unpurified M-DNAs. Removing extra staple strands can improve the yield of the structures. Further optimization of the annealing procedures, as well as the length and the sequence design of M-base, is another option to increase the yields of structures.

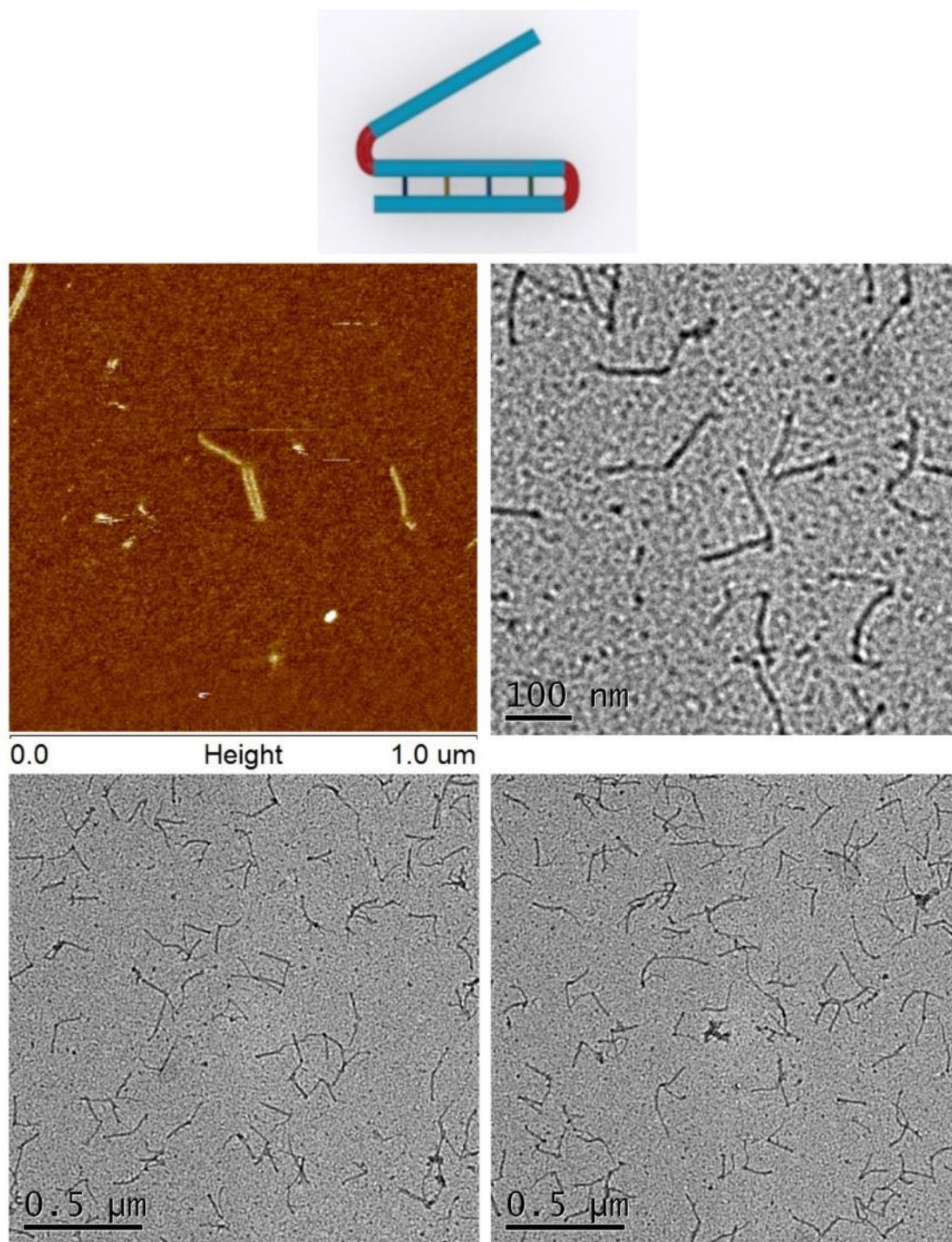
Section 6. Self-folded, self-linked M-DNA structures and self-assembled 3D polyhedra.



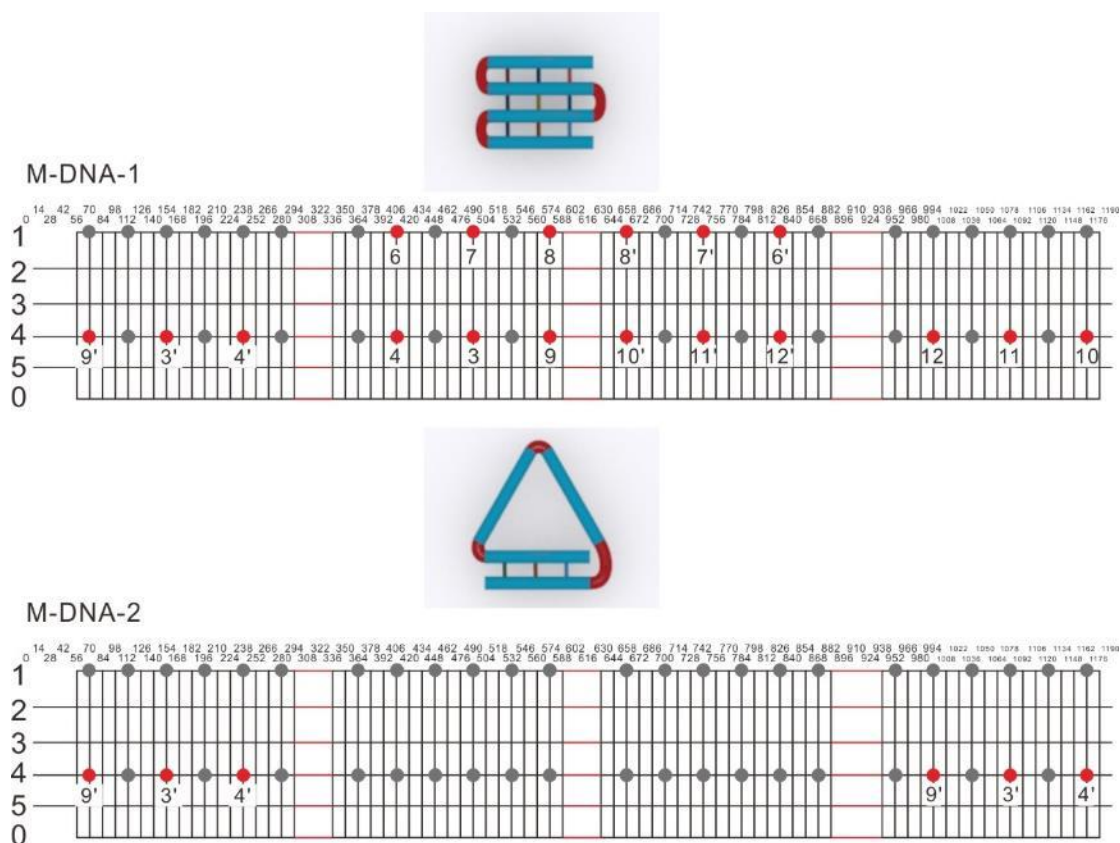
Supplementary Fig. 45. Schematic design for formation of self-folded fully-stacked and half-stacked M-DNA structure from a M-DNA with three rigid segments. M-bases were located on helix 1 and helix 4. Two of flexible regions, each 112 nt long, divided the M-DNA into three rigid segments. The self-folded structures were formed in a one-pot annealing process from 90°C to 25°C. All the needed strands can be found in the Supplementary Table. 39-40.



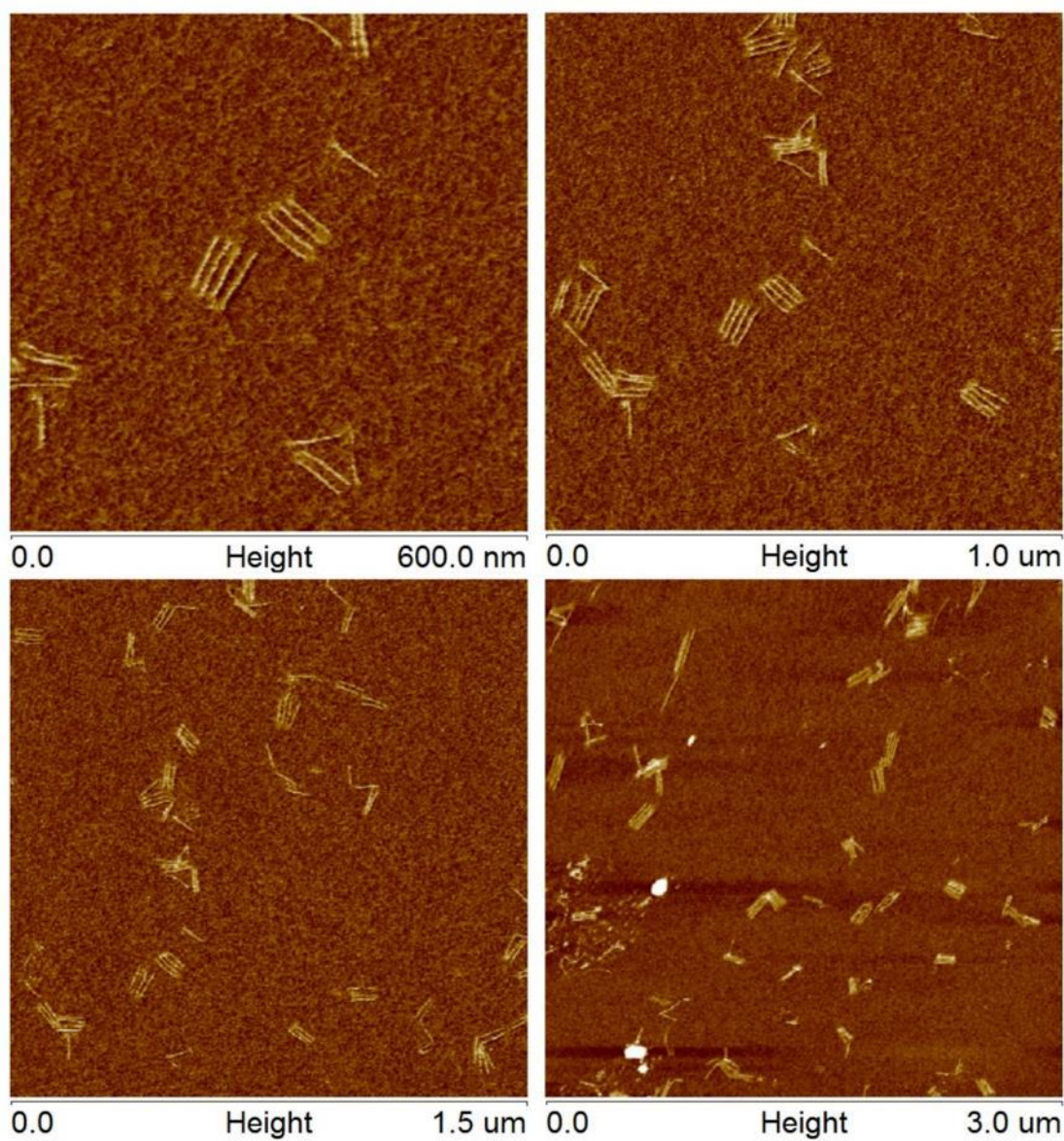
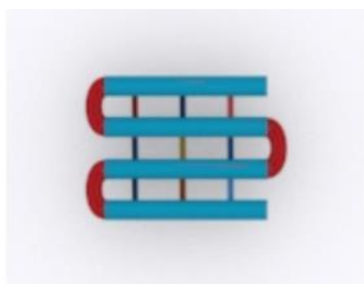
Supplementary Fig. 46. Additional AFM images of self-folded stacked three-segments at different magnifications.



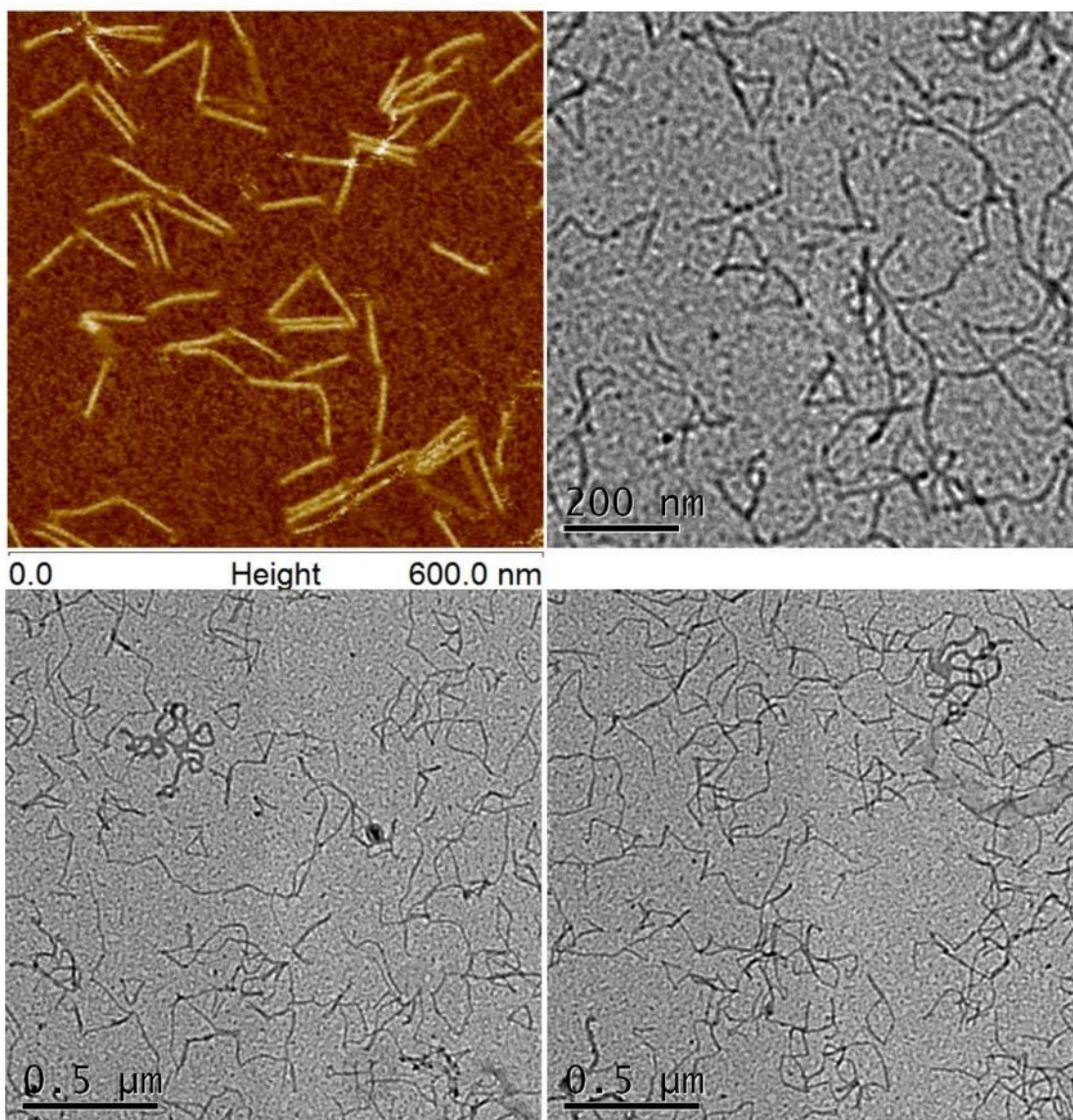
Supplementary Fig. 47. Additional AFM and negative-stained TEM images of self-folded half-stacked three-segments at different magnifications.



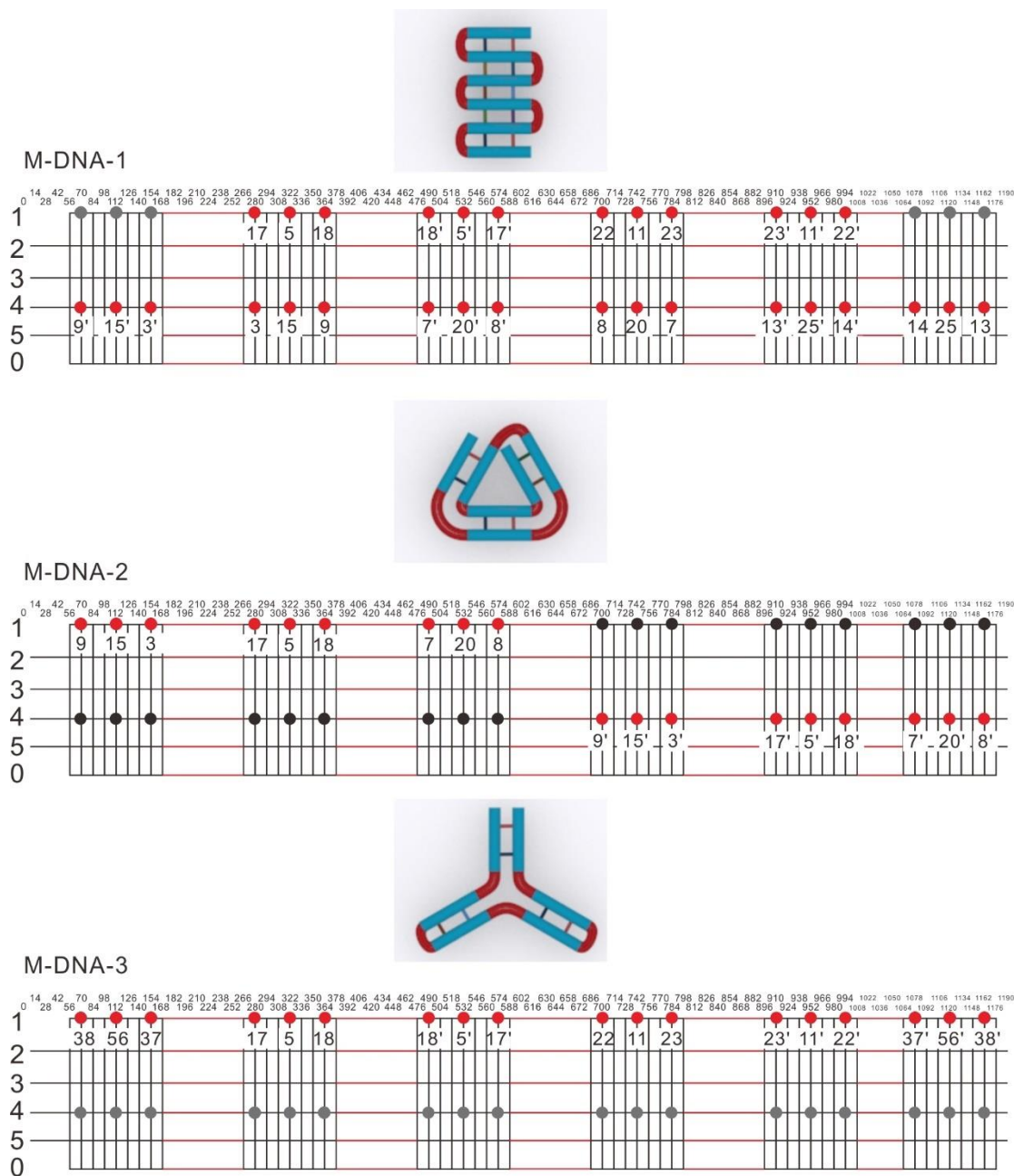
Supplementary Fig. 48. Schematic design for formation of self-folded stacked and triangular four-segments. The M-bases were located on helix 1 and helix 4. Three flexible regions divided M-DNA into four rigid segments. The flexible regions were all 42 nt. Four-segment structures were formed in a one-pot annealing process from 90°C to 25°C. All the needed strands can be found in the Supplementary Table, 41-42.



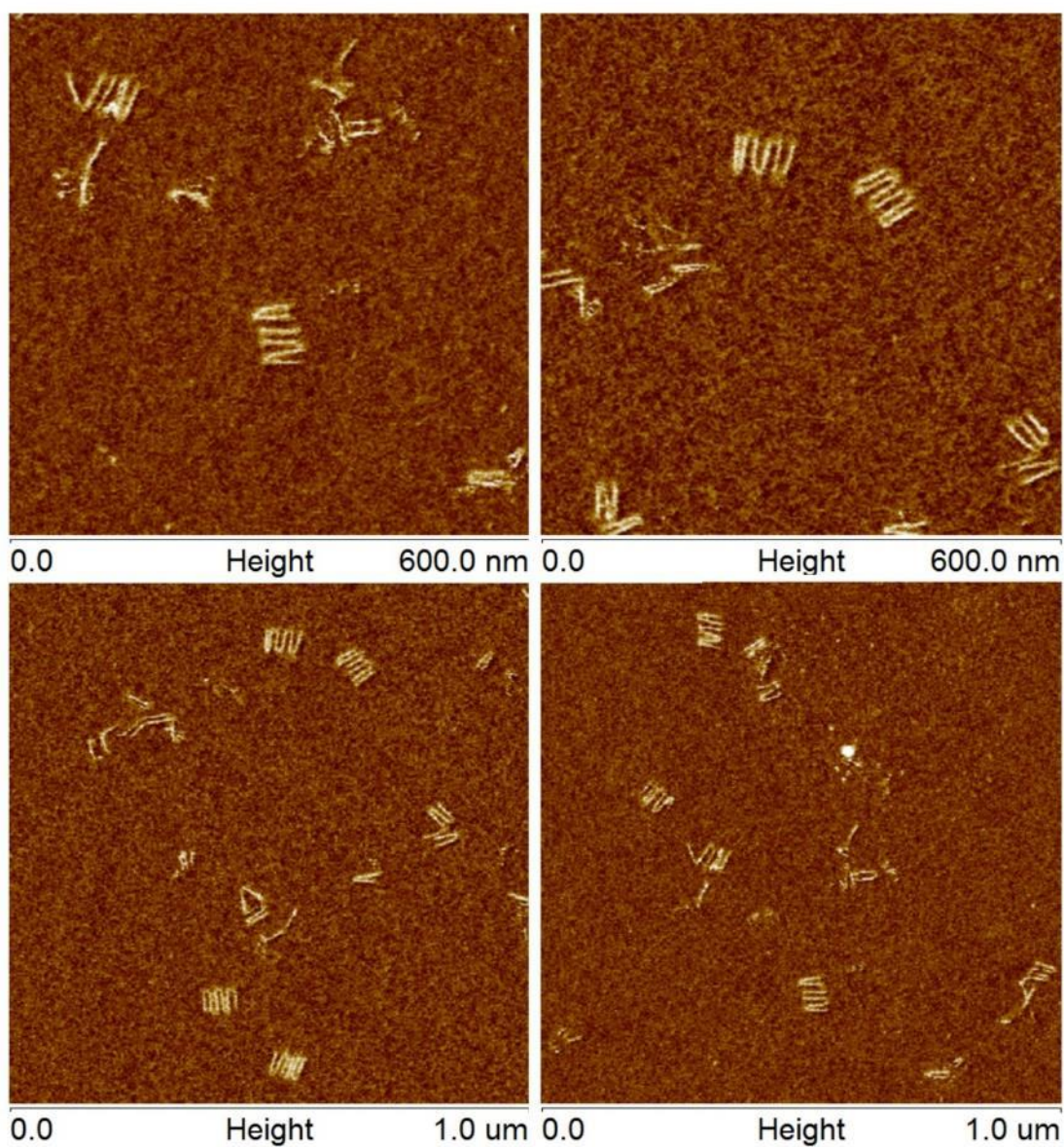
Supplementary Fig. 49. Additional AFM images of self-folded stacked four-segments at different magnifications.



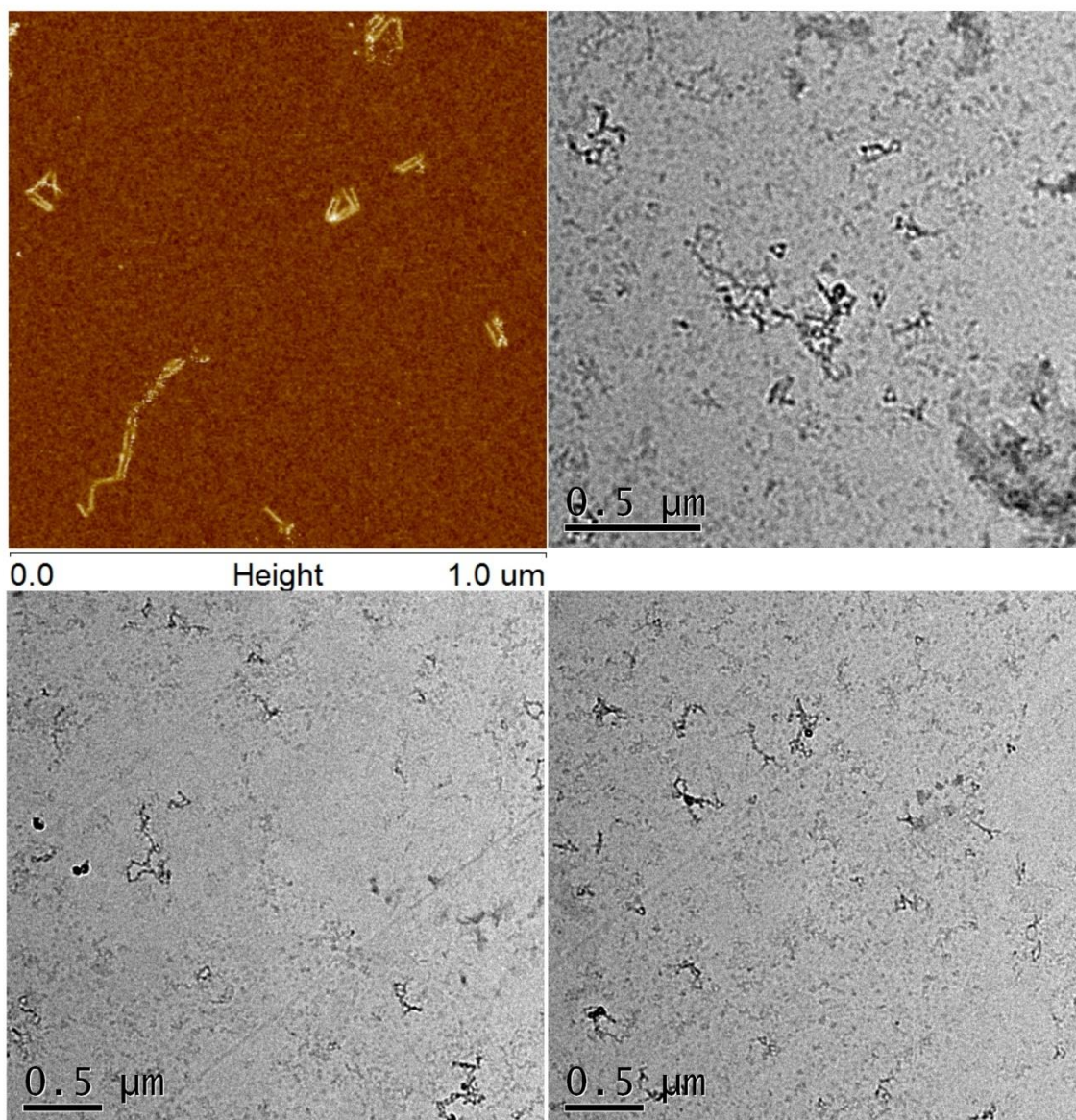
Supplementary Fig. 50. Additional AFM and negative-stained TEM Images of self-folded triangular four-segments at different magnifications. This low yield due to the complementary M-bases are too far away along the M-DNA that reduces their cooperativity.



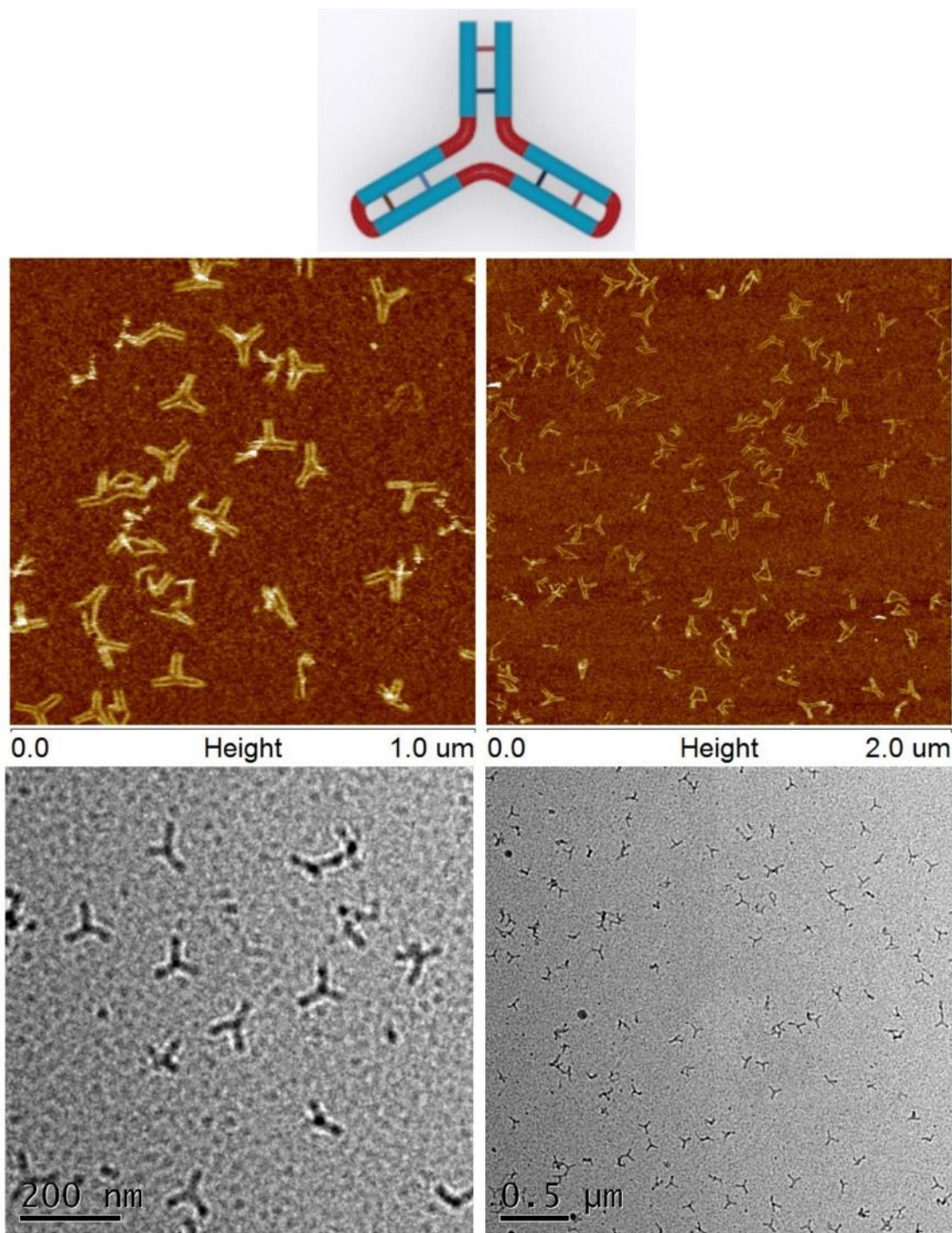
Supplementary Fig. 51. Schematic design for formation of self-folded stacked and Y-shaped six-segments. The M-bases were located on helix 1 and helix 4. Five flexible regions divided the M-DNA into six segments. The flexible regions were all 98 nt. Self-folded six-segment structures were formed in a one-pot annealing process from 90°C to 25°C. All the needed strands can be found in the Supplementary Table. 43-44.



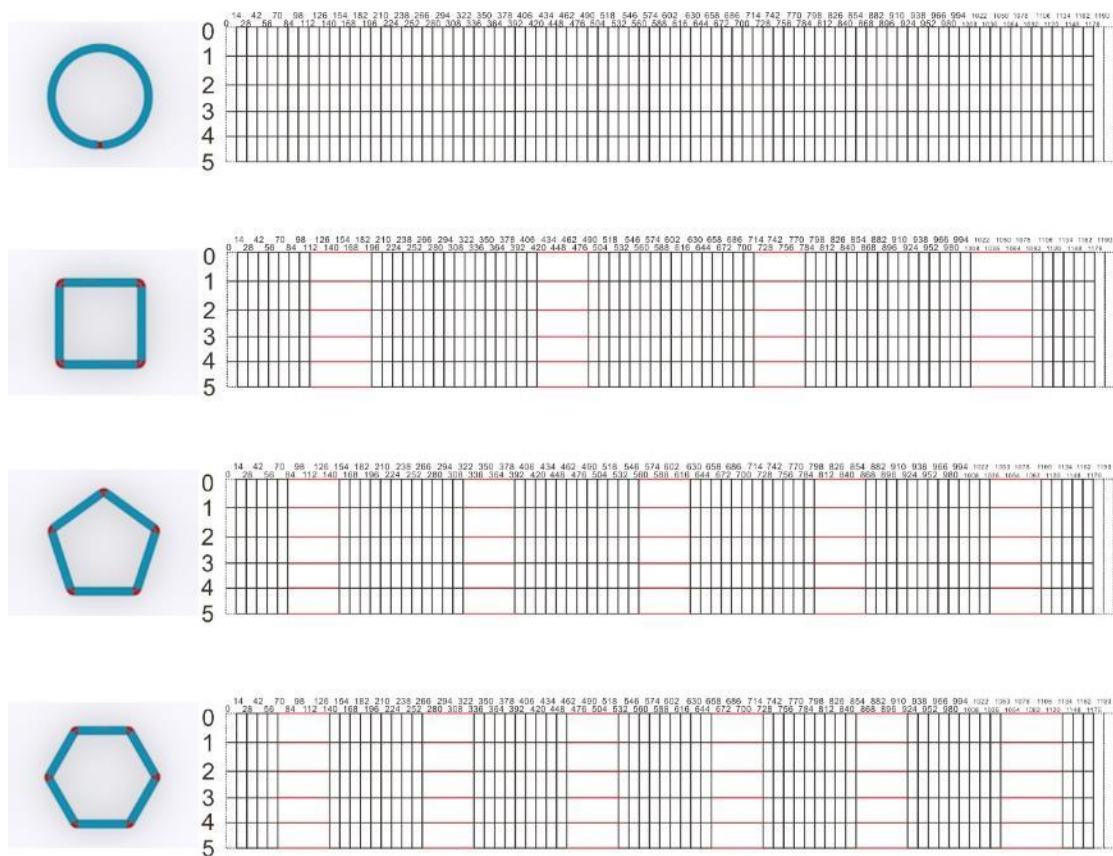
Supplementary Fig. 52. Additional AFM images of self-folded stacked six-segments at different magnifications.

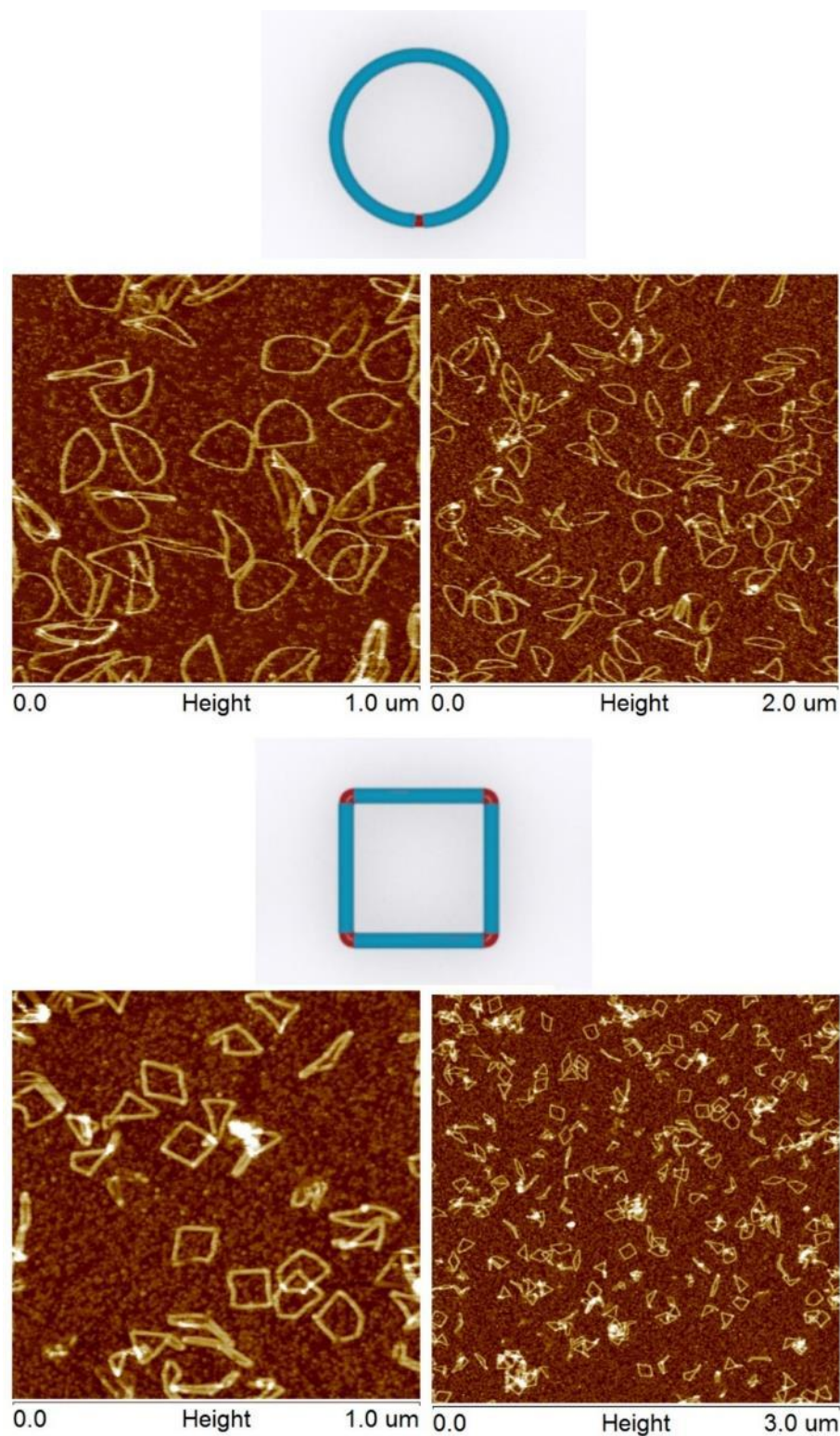


Supplementary Fig. 53. Additional AFM and negative-stained TEM images of self-folded triangular six-segments at different magnifications.

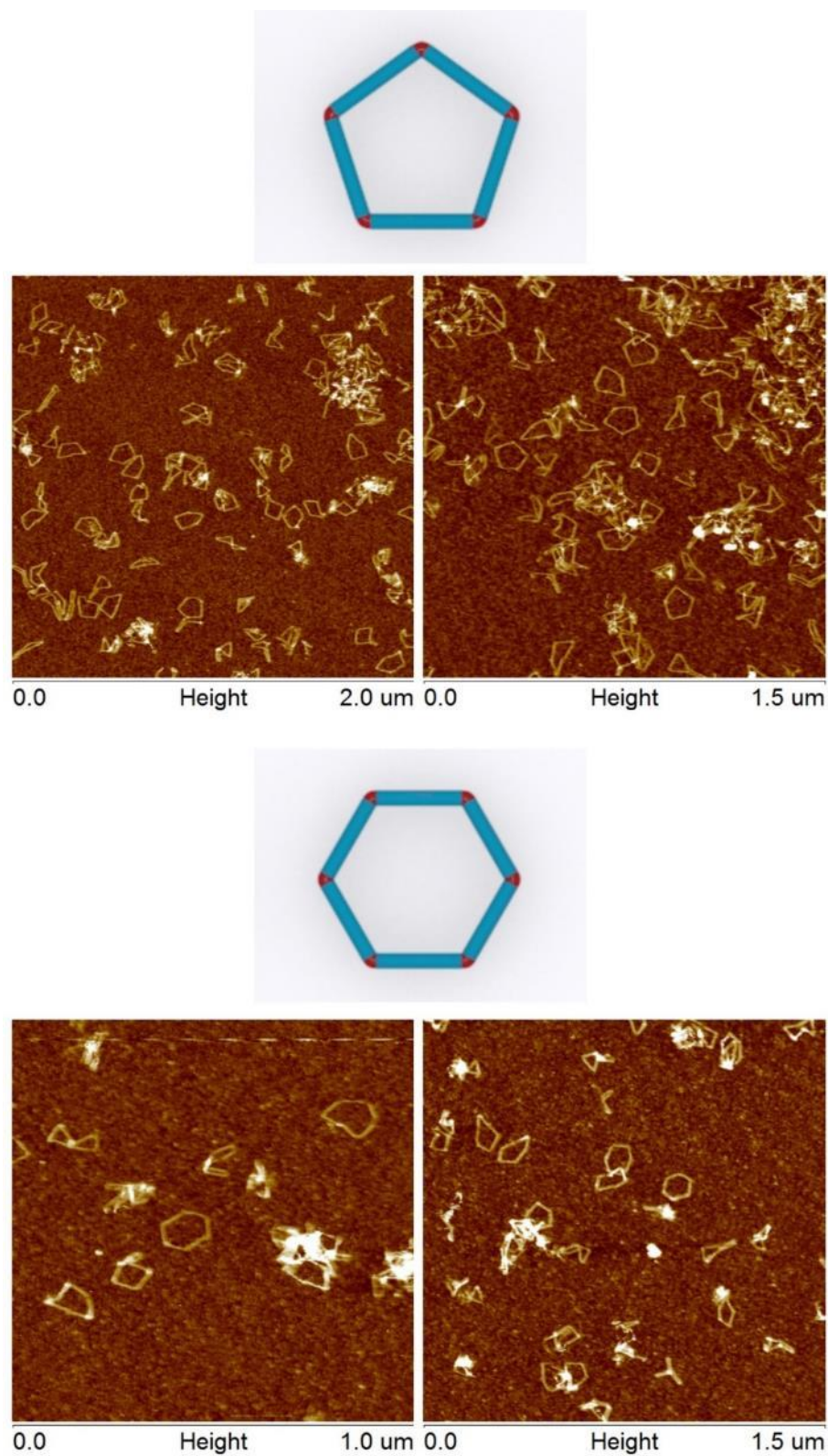


Supplementary Fig. 54. Additional AFM and negative-stained TEM images of self-folded Y-shaped six-segments at different magnifications.

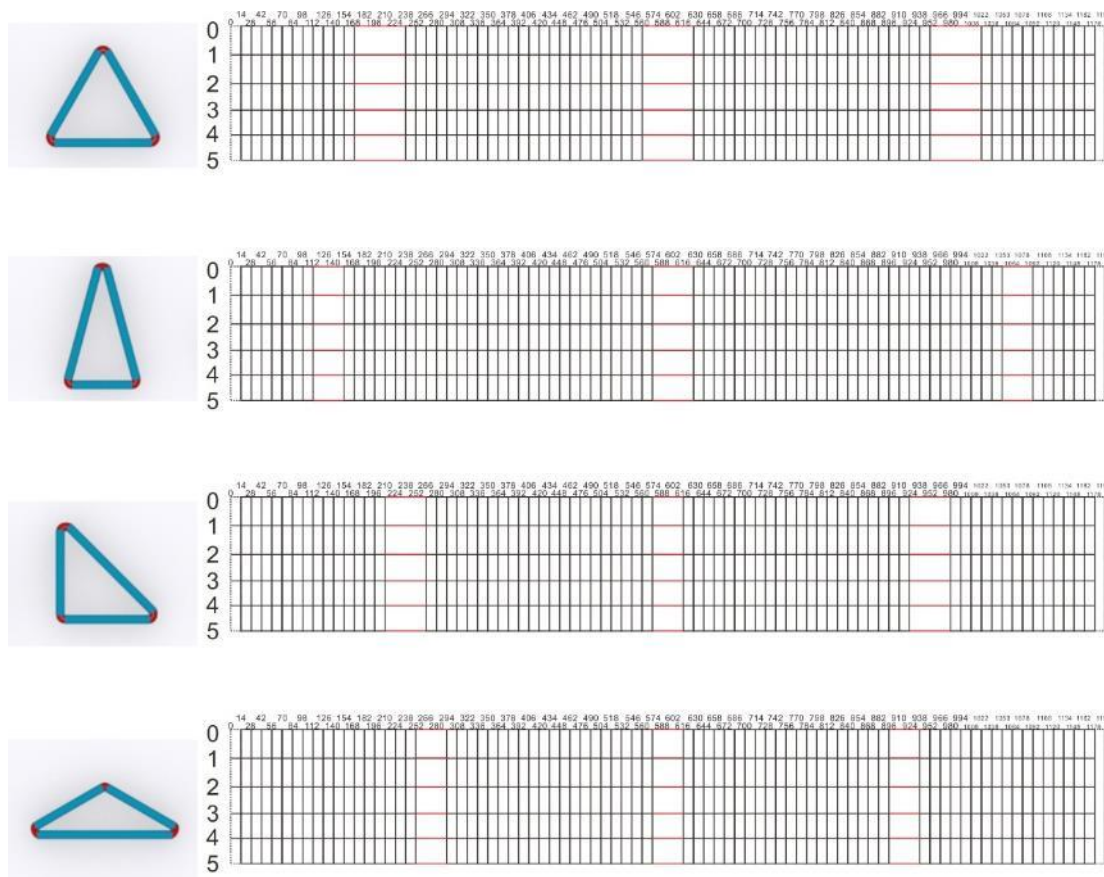




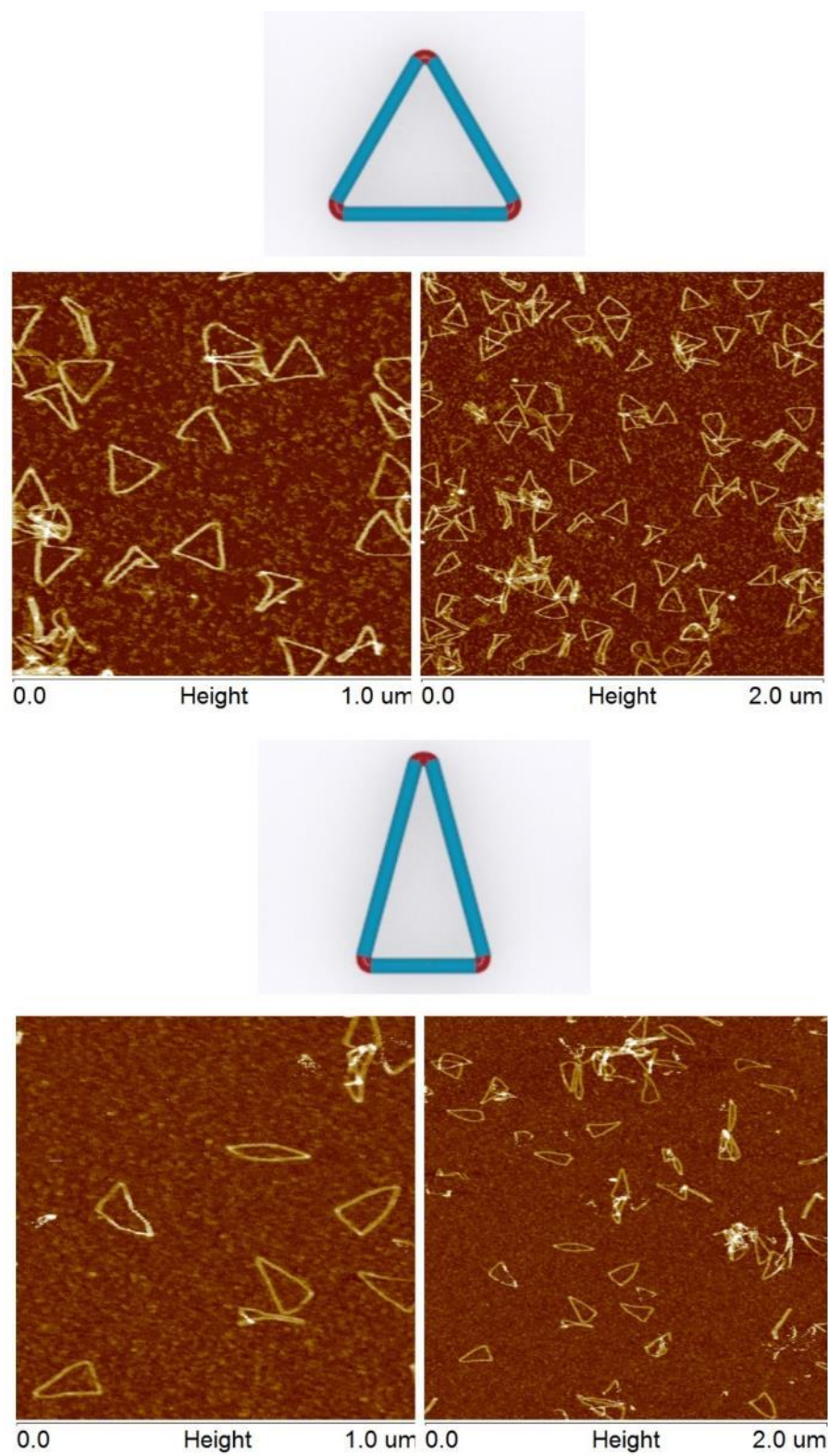
Supplementary Fig. 56. Additional AFM images of self-linked circle and square at different magnifications.



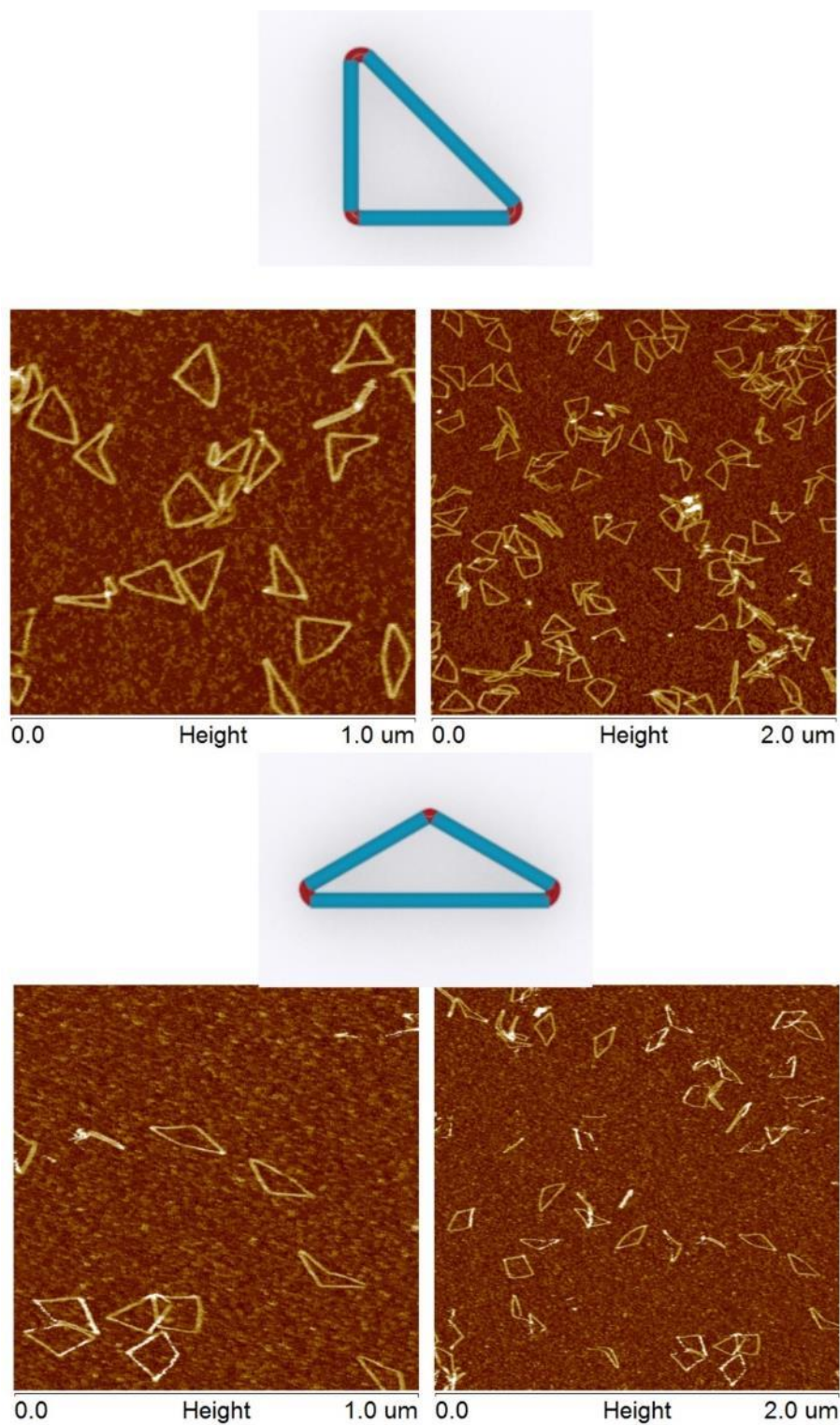
Supplementary Fig. 57. Additional AFM images of self-linked pentagon and hexagon at different magnifications.



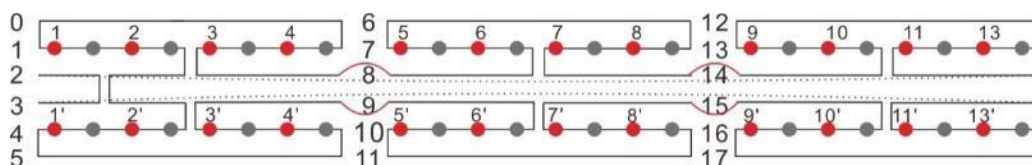
Supplementary Fig. 58. Schematic design for formation of self-linked triangles. M-DNA was linked from head to end through six staple strands of 6HB-link-56-1, 6HB-link-56-2, 6HB-link-56-3, 6HB-link-56-4, 6HB-link-56-5, and 6HB-link-56-6 (sequence information was in Supplementary Table. 69). Each triangle has three flexible regions, different positions of the flexible regions led to different shaped triangles with varying side lengths. For equilateral triangle, the side length was 322 nt. For isosceles acute triangle, the side length was 420 nt, 420 nt, and 224 nt. For right triangle, the side length was 308 nt, 308 nt, and 434 nt. For obtuse triangle, the side length was 280 nt, 280 nt, and 518 nt. The structures were formed in a one-pot annealing process from 90°C to 25°C. All the needed strands can be found in the Supplementary Table. 49-52.



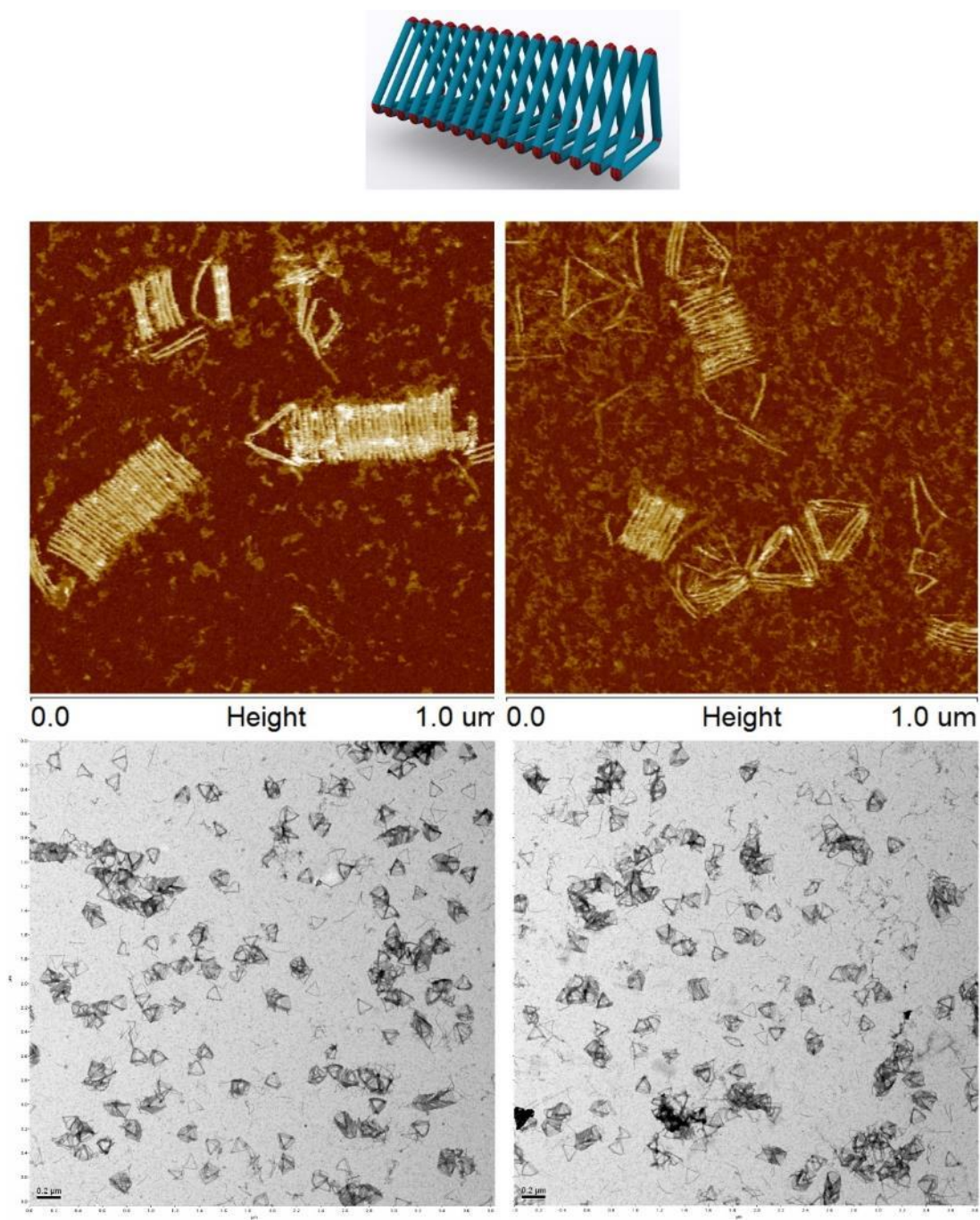
Supplementary Fig. 59. Additional AFM images of self-linked equilateral triangle and isosceles acute triangle.



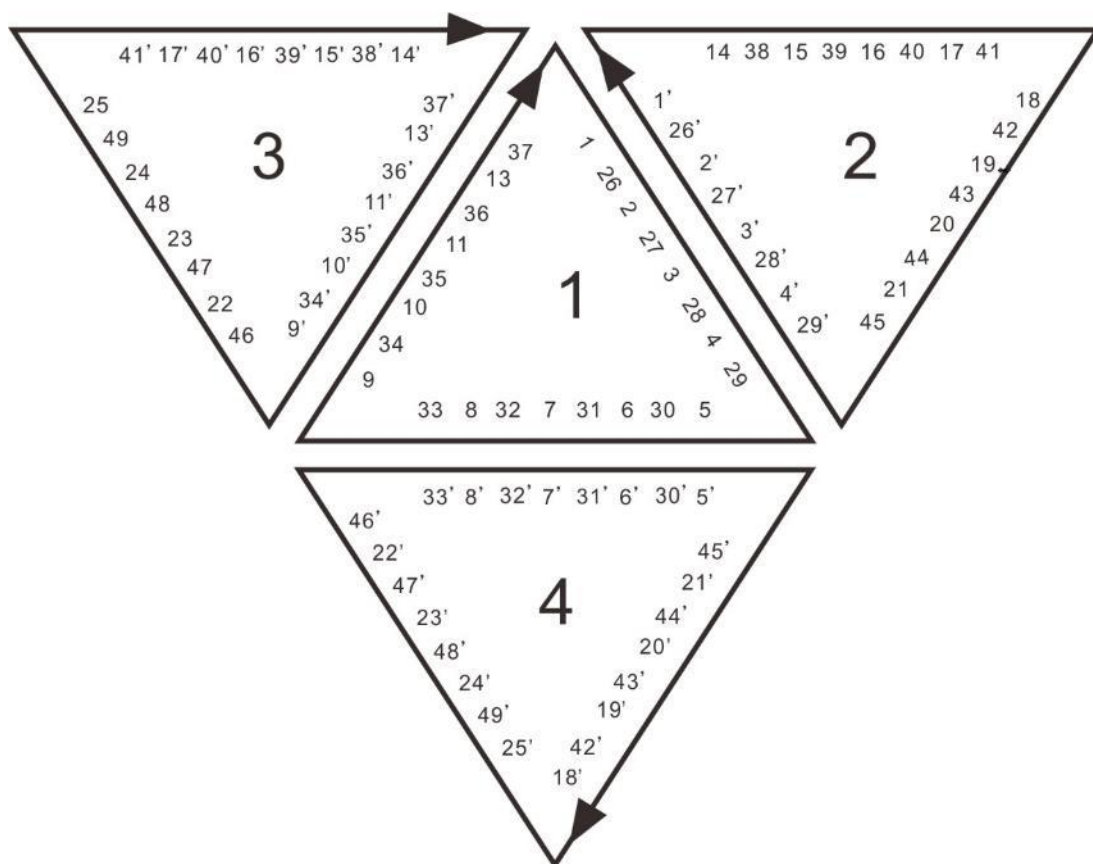
Supplementary Fig. 60. Additional AFM images of self-linked right triangle and obtuse triangle at different magnifications.



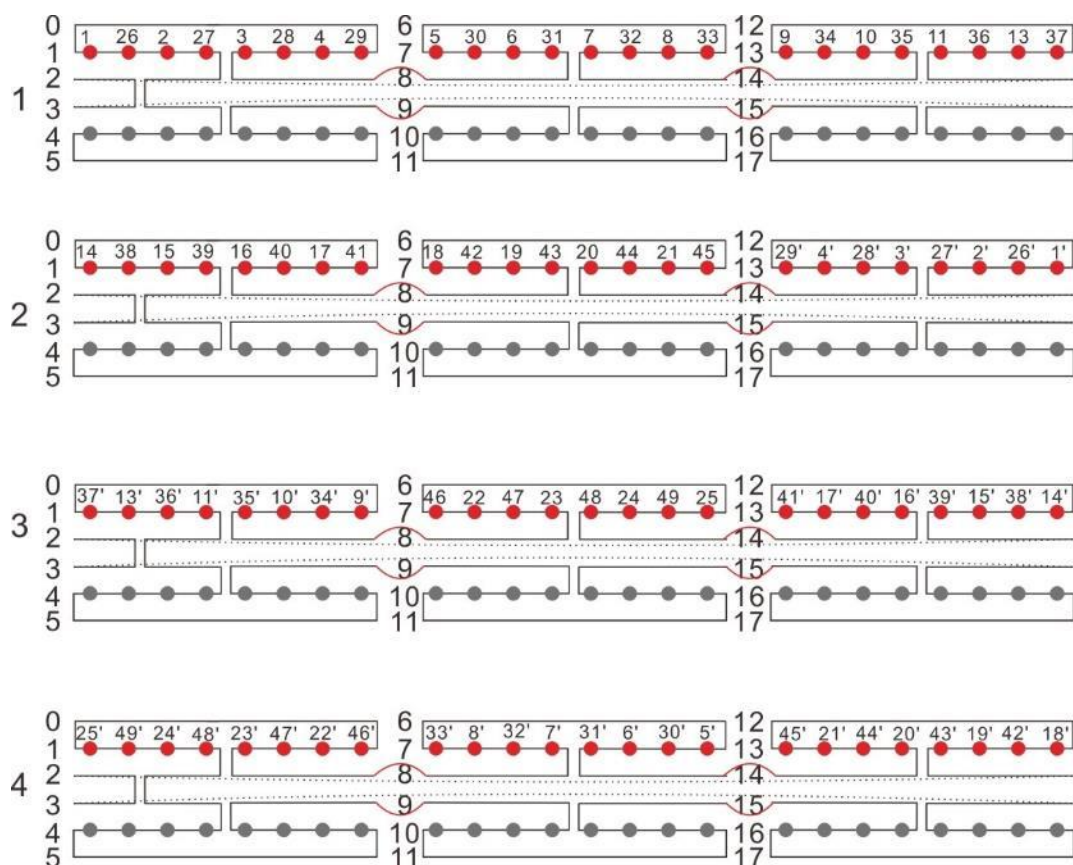
Supplementary Fig. 61. Schematic design for formation of stacked triangles. Gray line represents the scaffold folding pathway. Red spots represent the active positions, which means M-bases protruded from these positions. Gray spots represent the inactive positions. M-bases were located on helices 1, 7, 13, and helices 4, 10, and 16, which has opposite position with one another in the three rigid segments, which are linked by single-stranded scaffold regions. The stacked triangles were formed in a one-pot annealing process from 90°C to 25°C. The detailed basic staple strands of triangular M-DNA can be found in the Supplementary Table. 70. All the other needed strands can be found in the Supplementary Table. 53-54.



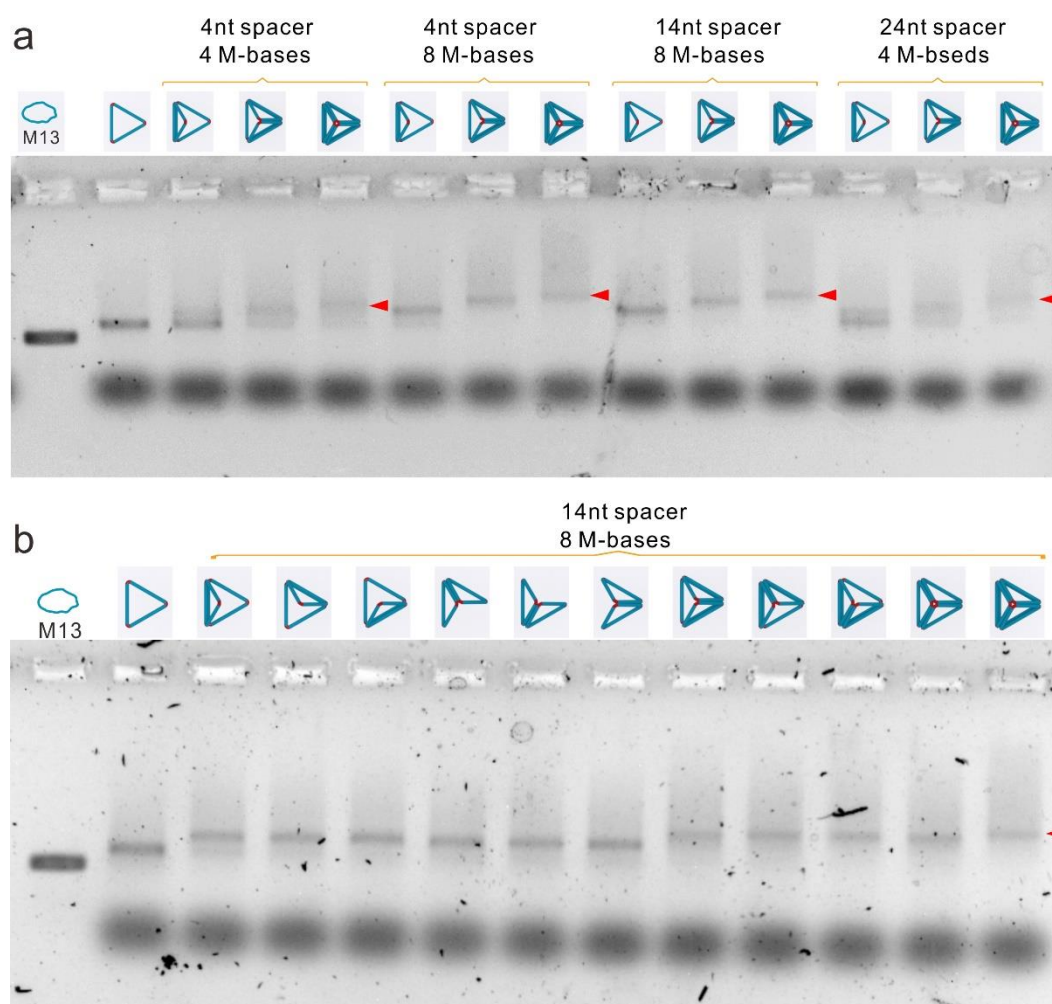
Supplementary Fig. 62. Additional AFM and negative-stained TEM images of stacked triangles at different magnifications.



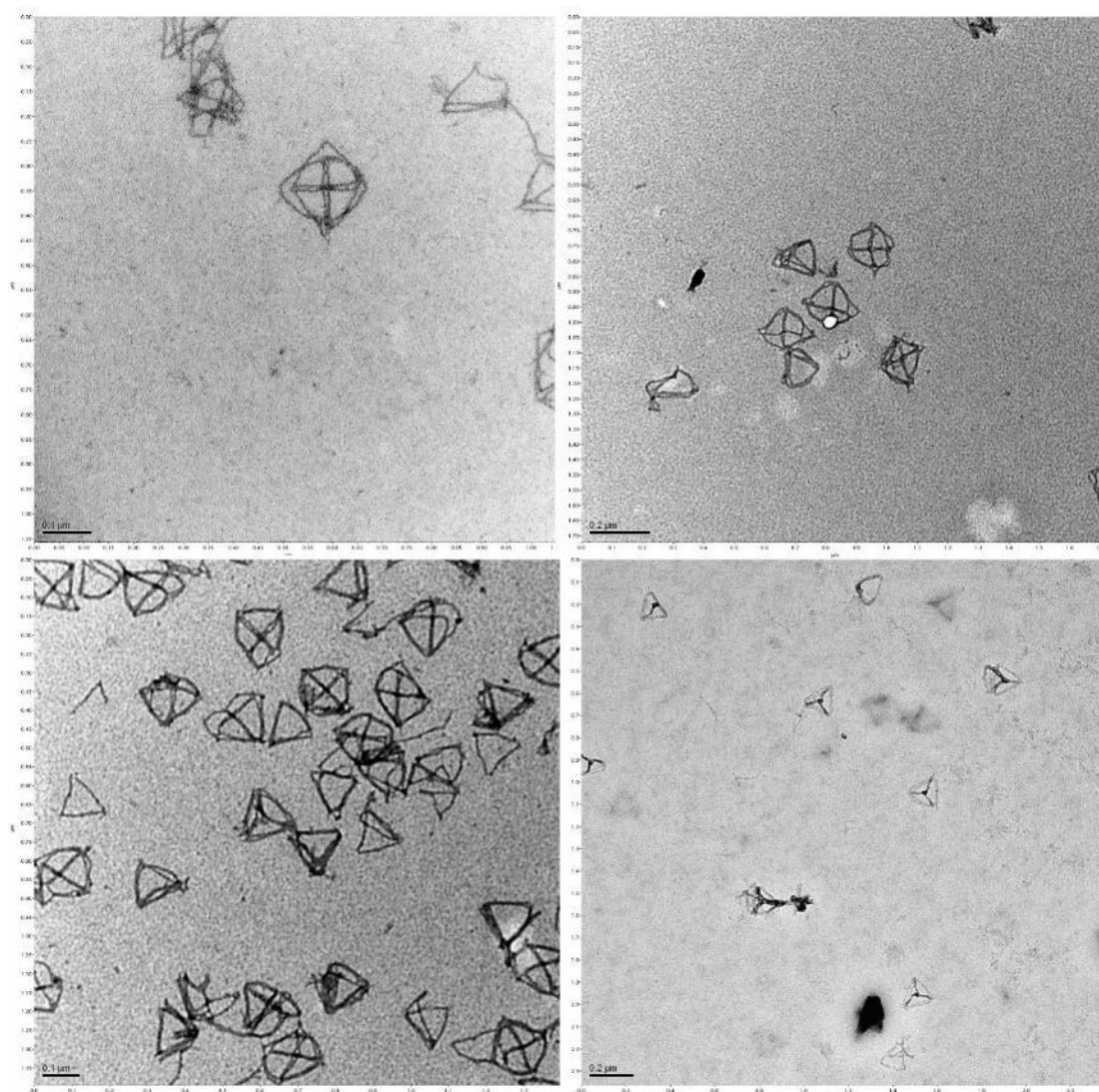
Supplementary Fig. 63. Net of tetrahedron. The numbers 1, 2, 3, and 4 represent four M-DNA triangles. The numbers on the sides represent M-bases that were used to link the triangles to form a tetrahedron. The arrow shows the direction of the M-DNA from 5 prime to 3 prime.



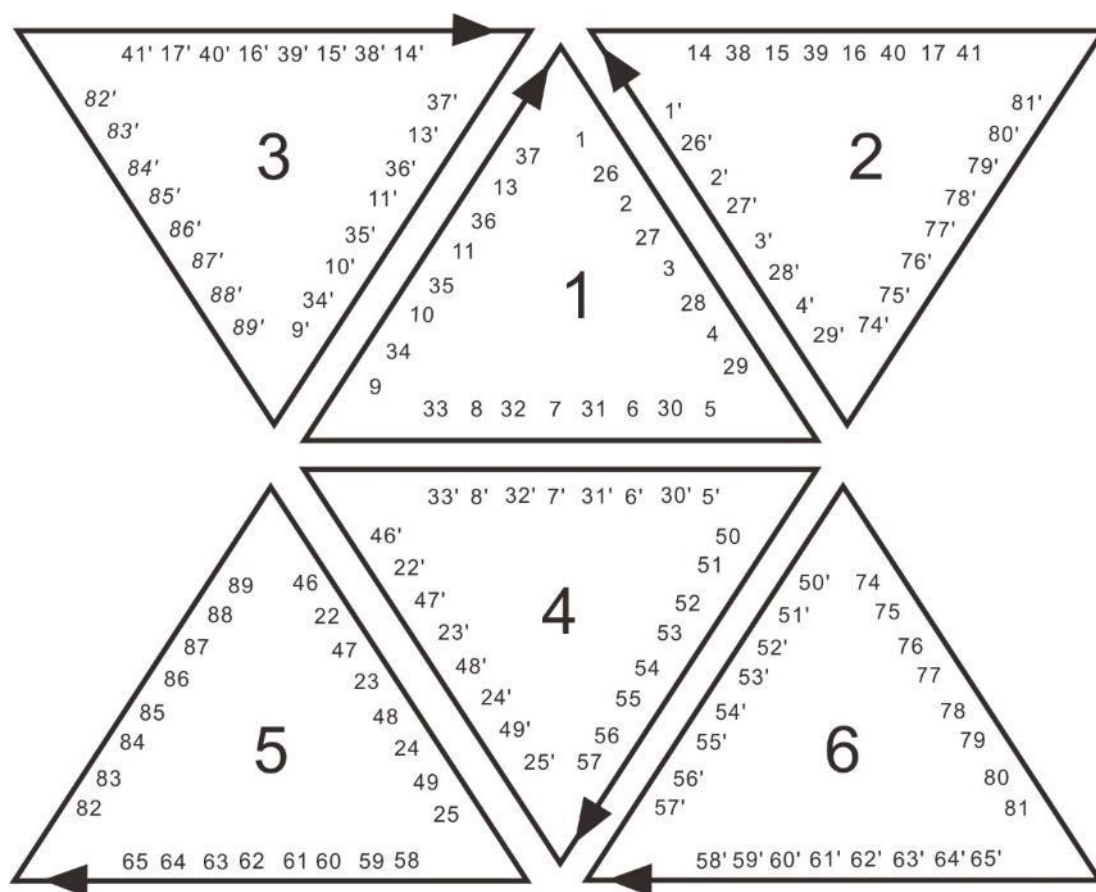
Supplementary Fig. 64. Schematic design for formation of tetrahedron. M-bases were located on helices 1, 7, and 13. Tetrahedron was formed by mixing the four triangular M-DNAs and annealing from 55°C to 20°C at 1°C per 30 min. All the needed strands can be found in the Supplementary Table. 55-56.



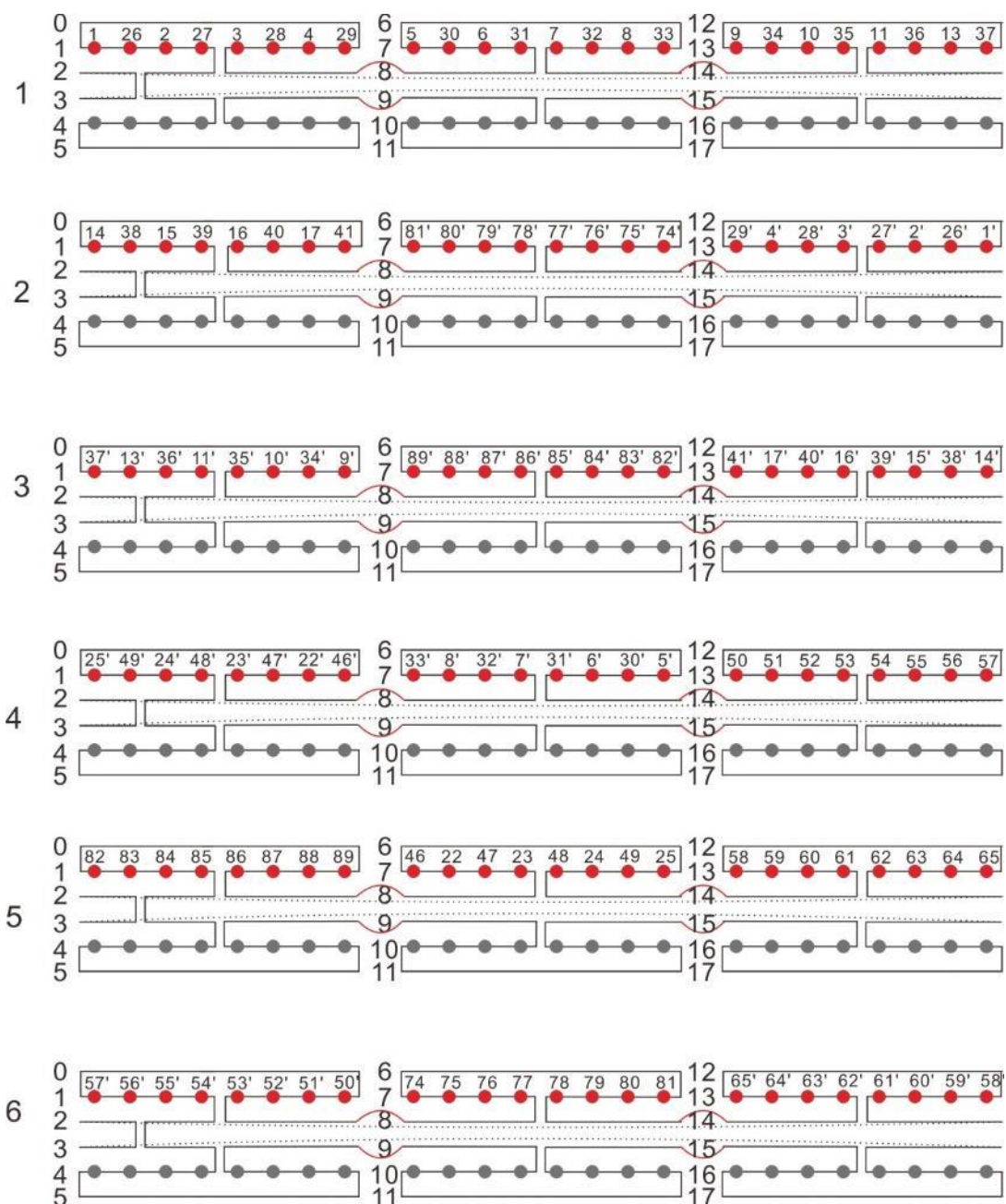
Supplementary Fig. 65. The effects of the number of M-bases and spacer length on tetrahedron formation. (a) 1% agarose gel image of formation of tetrahedron at different conditions. From left to right, M13 scaffold, single triangle, two, three, and four combined triangles with 4 M-bases and 4 nt spacer; 8 M-bases and 4 nt spacer; 8 M-bases and 14 nt spacer, and 4 M-bases and 24 nt spacer. Red arrows mark the tetrahedron band. From the gel data, we found that when each side of a triangle has 8 M-bases, and each M-base has 14 nt spacer (T_{14}) it gives the highest yield of tetrahedron. (b) Native 1% agarose gel images show the high-yield of M-DNA tetrahedrons that had been created. From left to right: M13 DNA, a single triangular M-DNA, six combinations of two triangles, four combinations of three triangles, and the final resulting product, which was a tetrahedron.



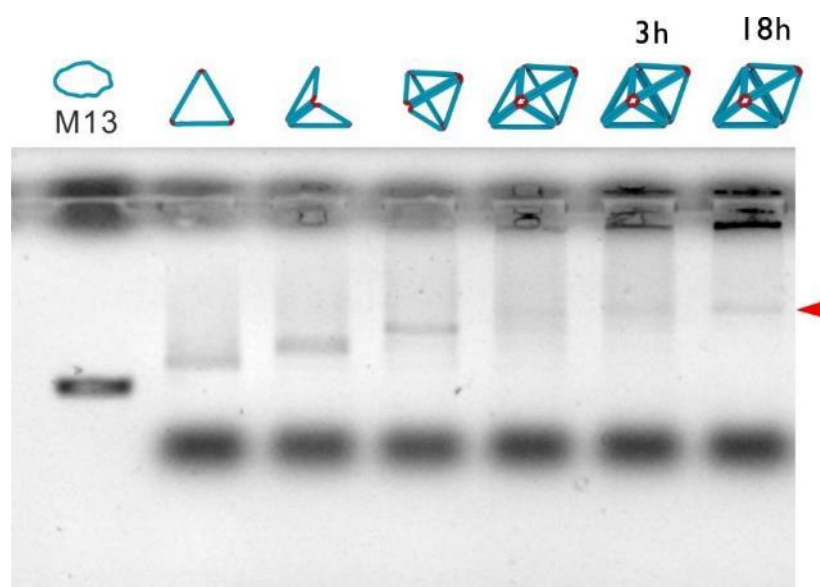
Supplementary Fig. 66. Additional TEM images of tetrahedron and DOS tetrahedron (bottom right) at different magnifications.



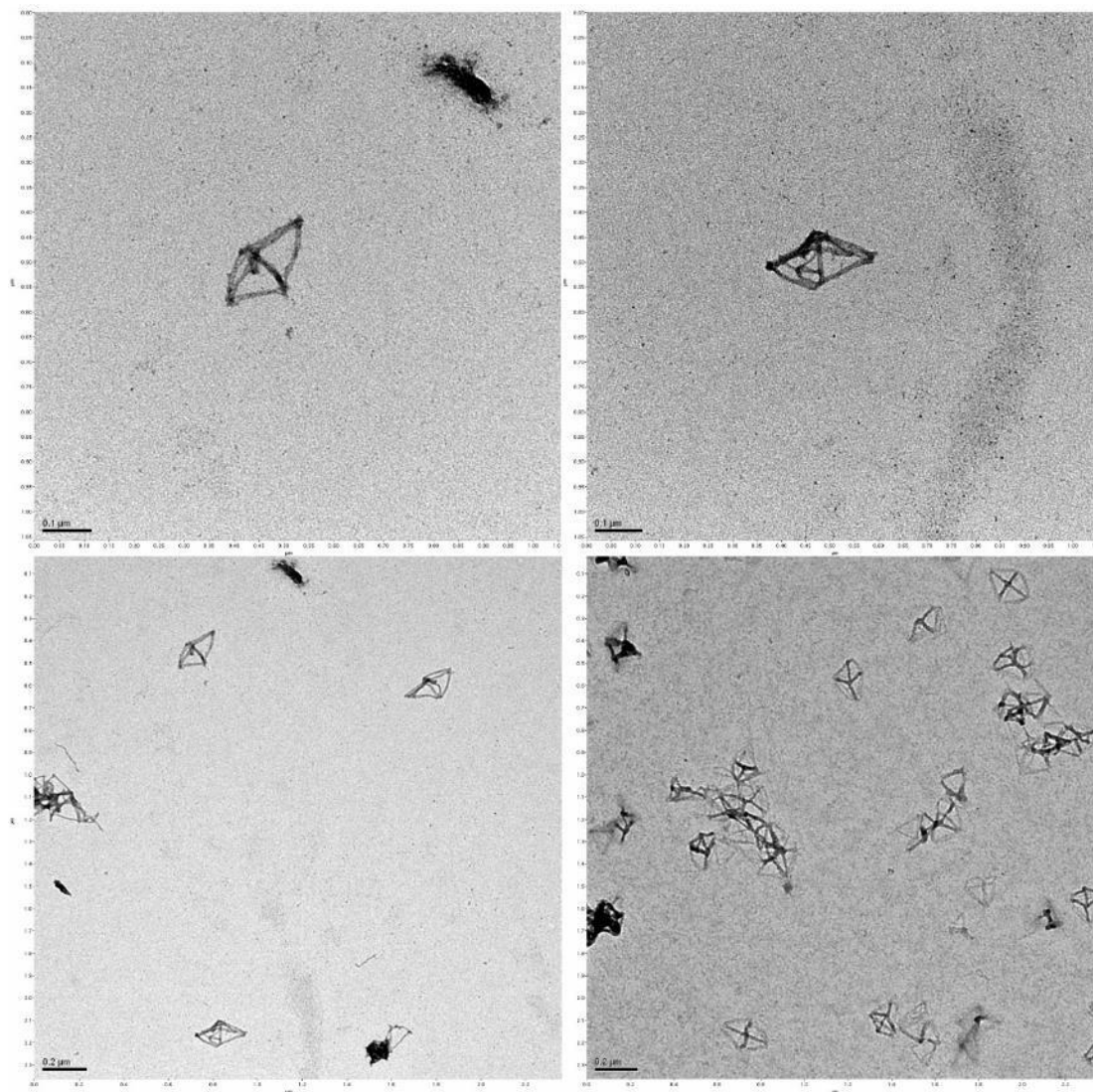
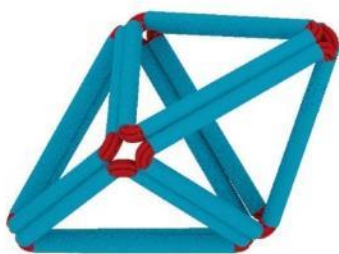
Supplementary Fig. 67. Net of triangular bipyramid. The numbers 1, 2, 3, 4, 5, and 6 in the middle represent six M-DNA triangles. The numbers on the sides represent M-bases that were used to link triangles to form the triangular bipyramid. The arrows show the direction of the triangular M-DNA.



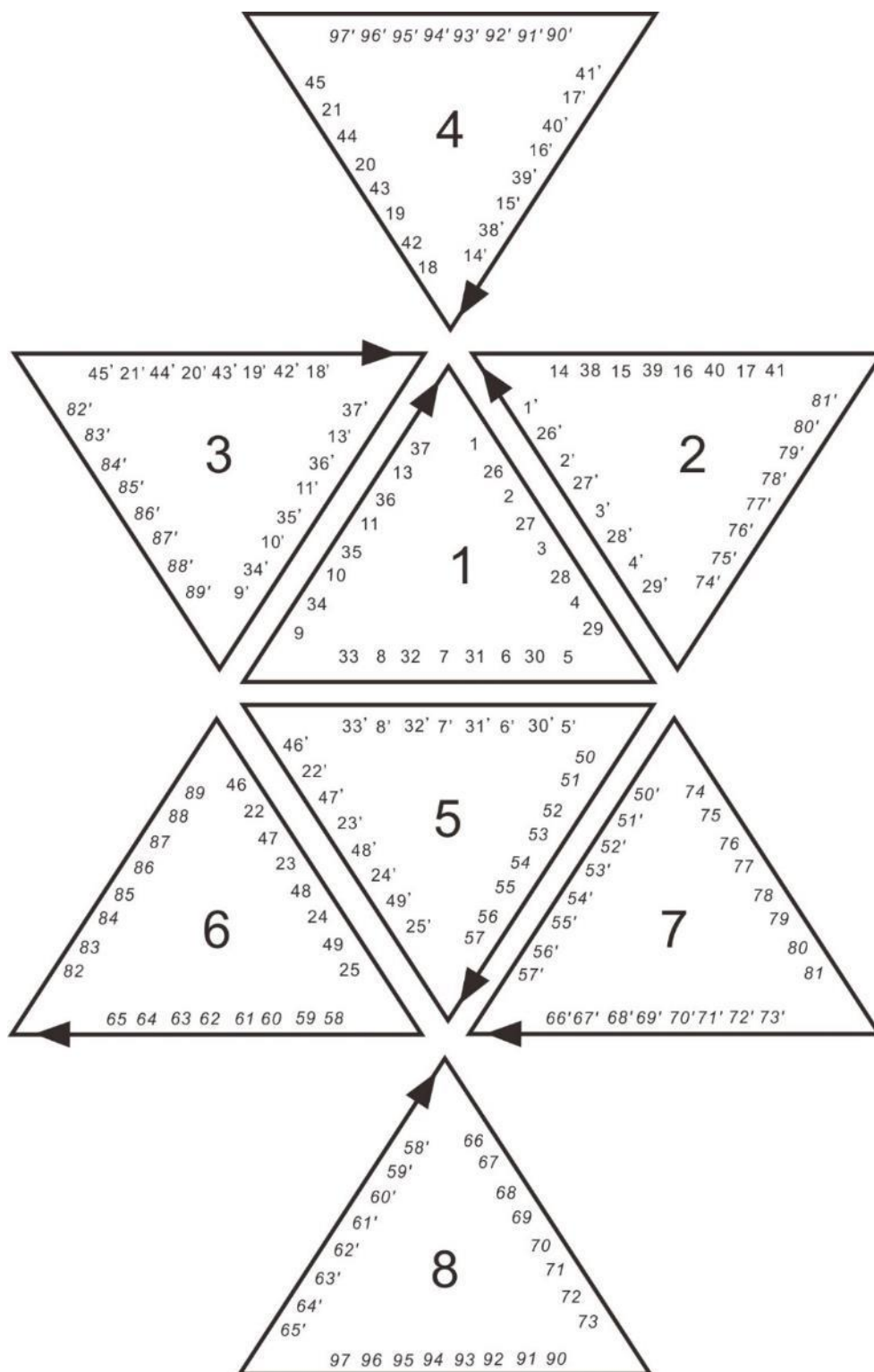
Supplementary Fig. 68. Schematic design for formation of triangular bipyramid. M-bases were located on helices 1, 7, and 13. Each side has 8 M-bases. Triangular bipyramid was formed by mixing six triangular M-DNAs and annealing from 55°C to 20°C at 1°C per 30 min. All the needed strands can be found in the Supplementary Table. 55-57.



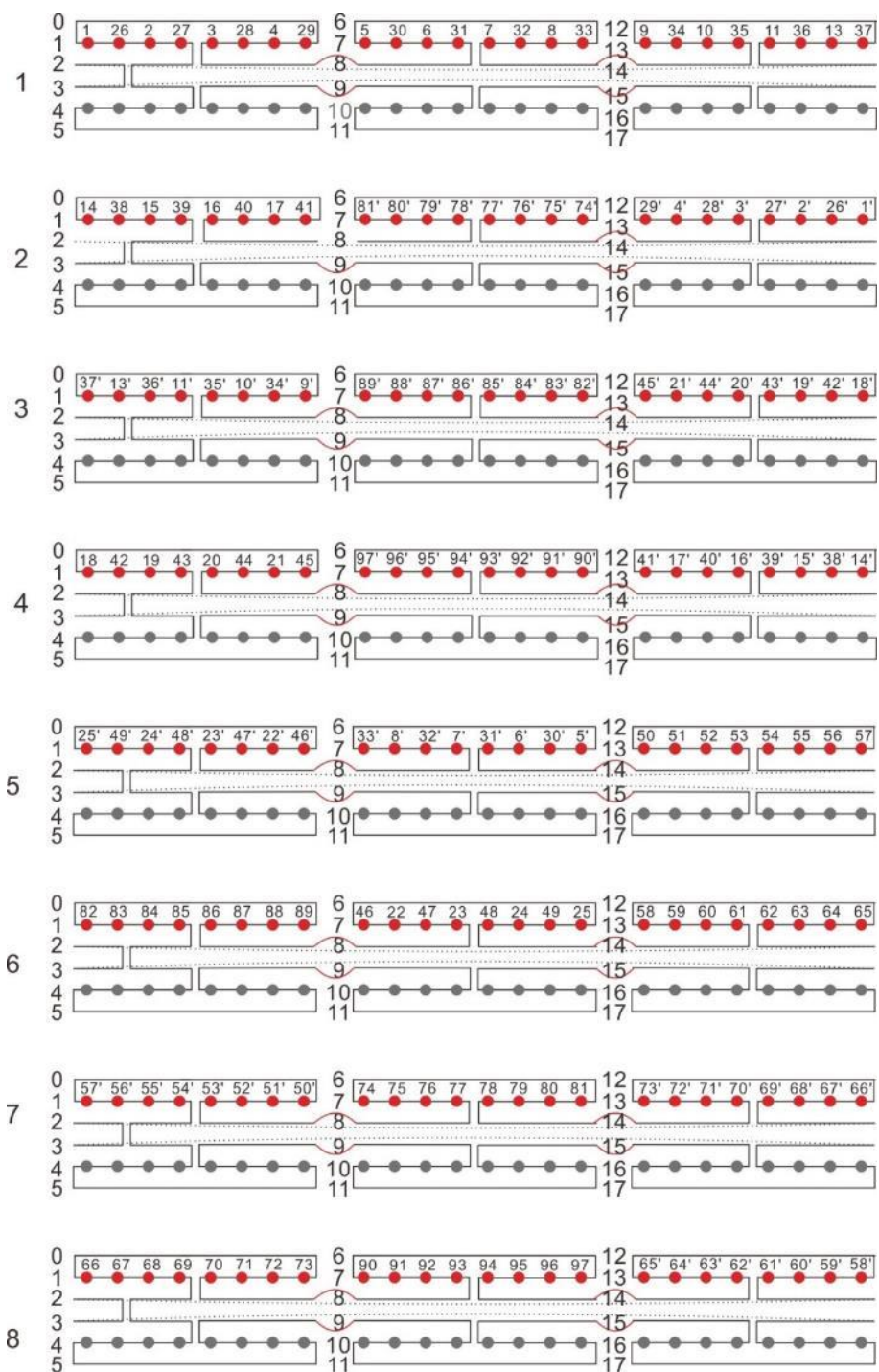
Supplementary Fig. 69. 1% agarose gel images of formation of triangular bipyramid. From left to right, M13 scaffold, single triangle, two, three, five, and six combined triangles. Red arrow shows the triangular bipyramid band. A slow (18 h) annealing process has a better yield than the quick annealing (3h).



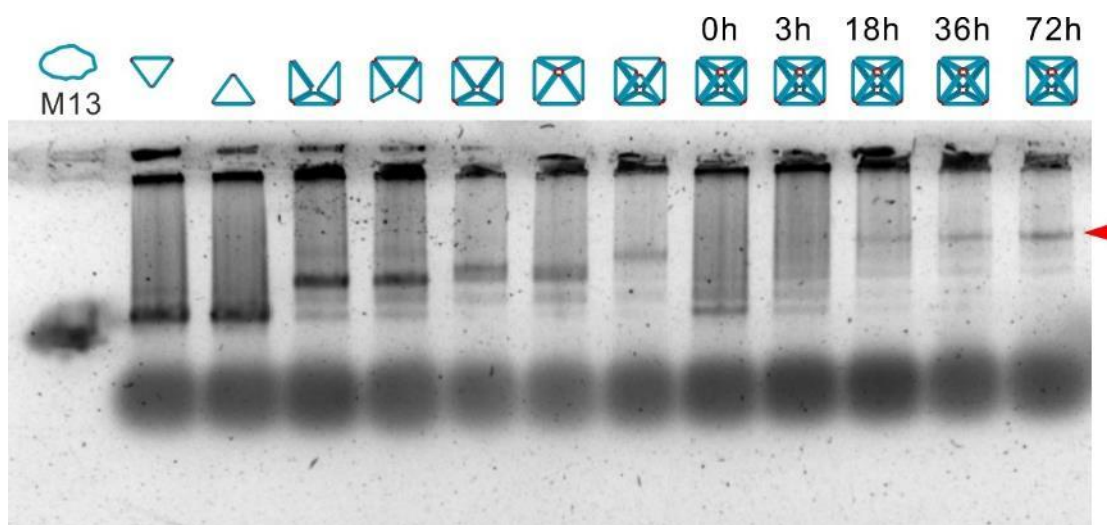
Supplementary Fig. 70. Additional TEM images of triangular bipyramid and DOS triangular bipyramid (bottom right) at different magnifications.



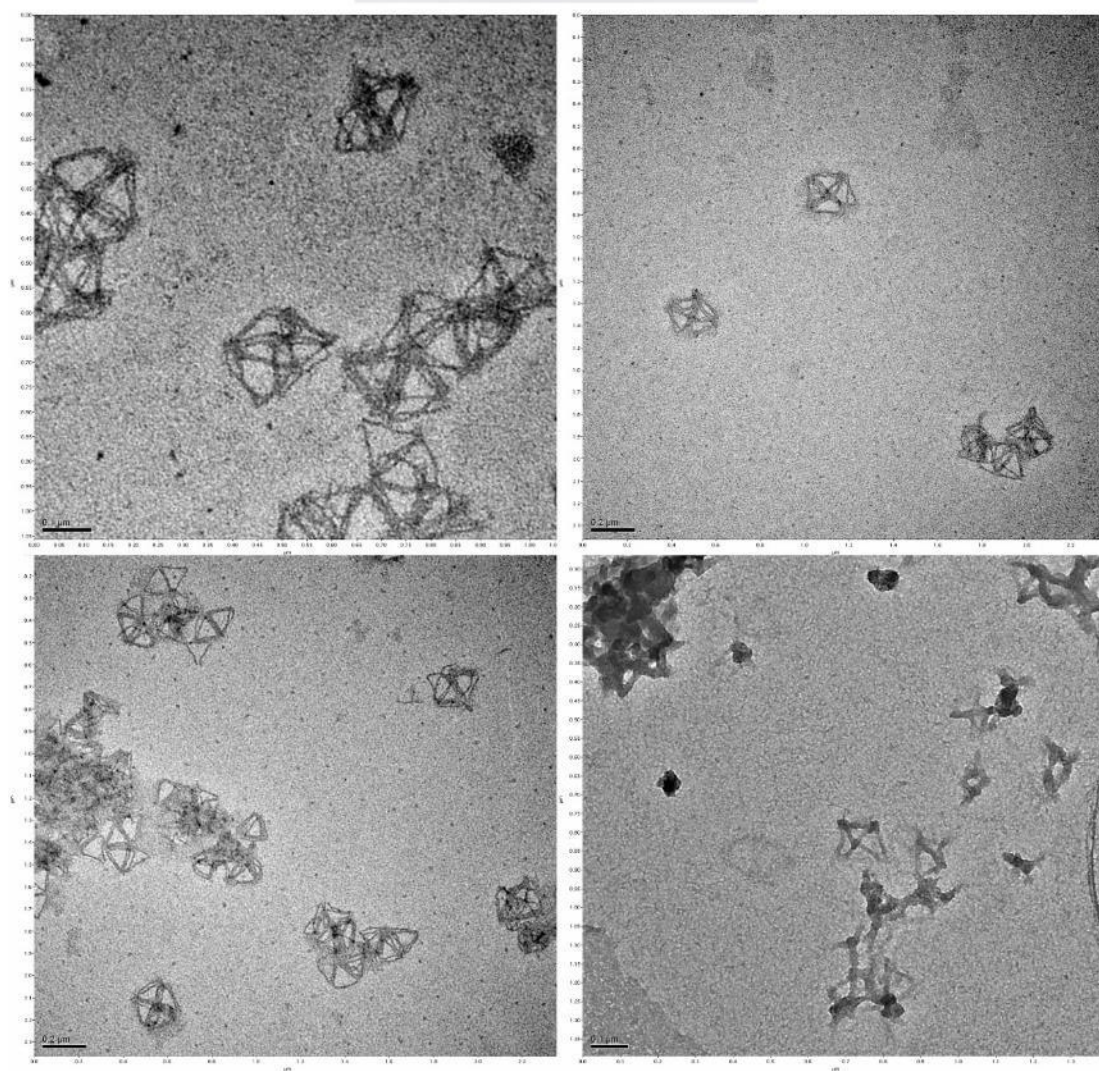
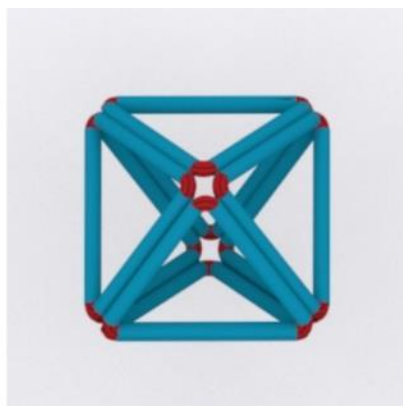
Supplementary Fig. 71. Net of octahedron. The numbers 1, 2, 3, 4, 5, 6, 7, and 8 in the middle represent eight M-DNA triangles. The numbers on the sides represent M-bases that were used to link the triangles to form an octahedron. The arrows show the direction of the triangular M-DNA.



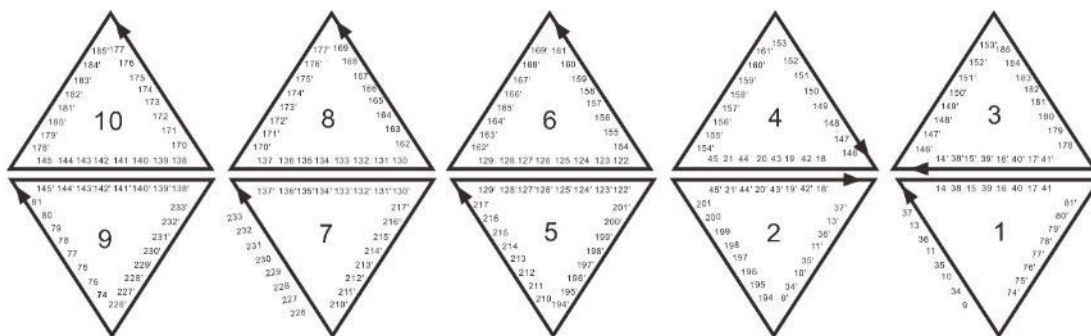
Supplementary Fig. 72. Schematic design for formation of octahedron. M-bases were located on helices 1, 7, and 13. Each side has 8 M-bases. Octahedron was formed by mixing eight triangular M-DNAs and annealing from 55°C to 20°C at 1°C per 2 h. All the needed strands can be found in the Supplementary Table. 55-58.



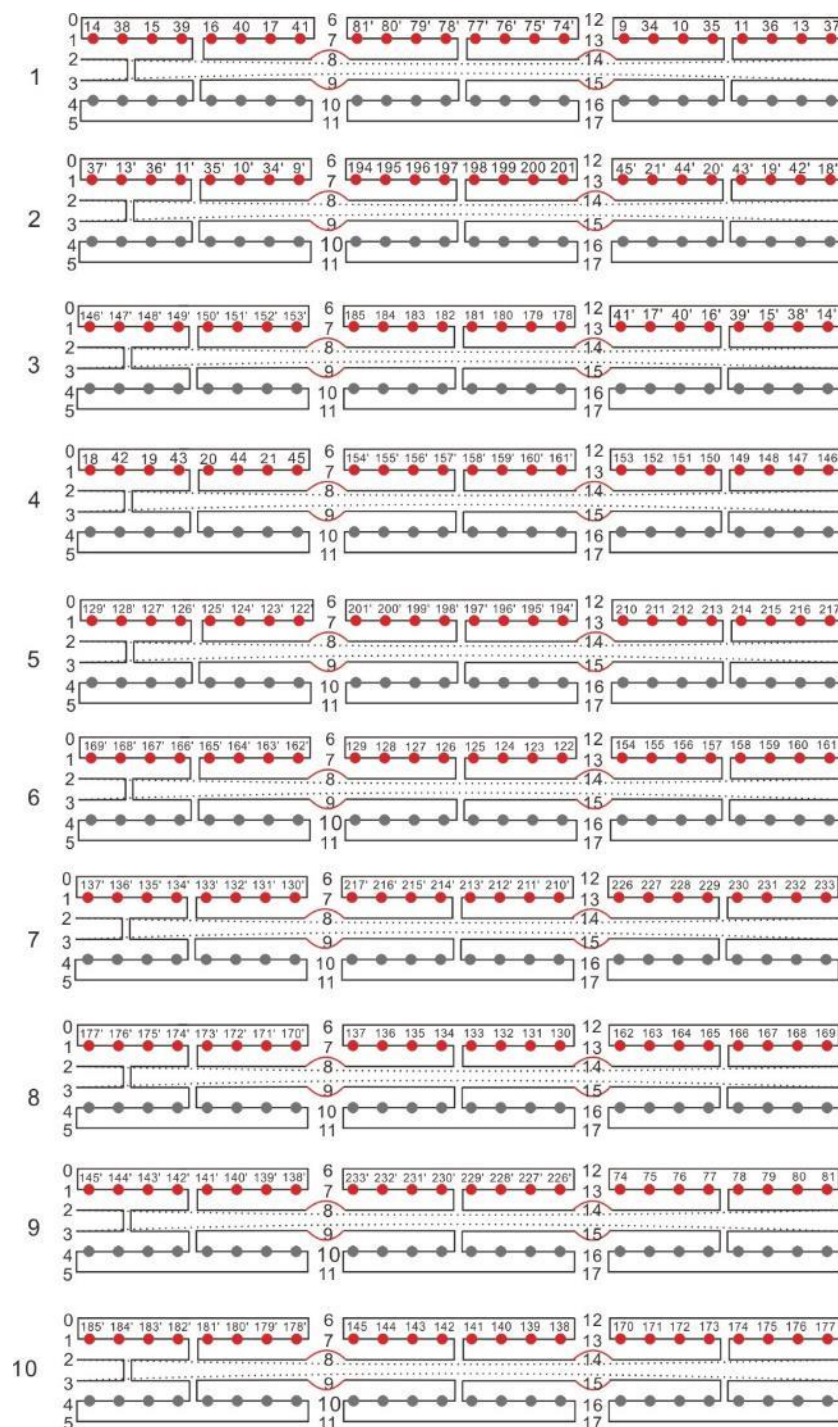
Supplementary Fig. 73. 1% agarose gel images of formation of octahedron at different annealing processes. From left to right, M13 scaffold, single triangle, single triangle, three, three, four, four, six, and eight combined triangles at different annealing conditions. The red arrow shows the octahedron band. Annealing with a 72h process has a better yield.



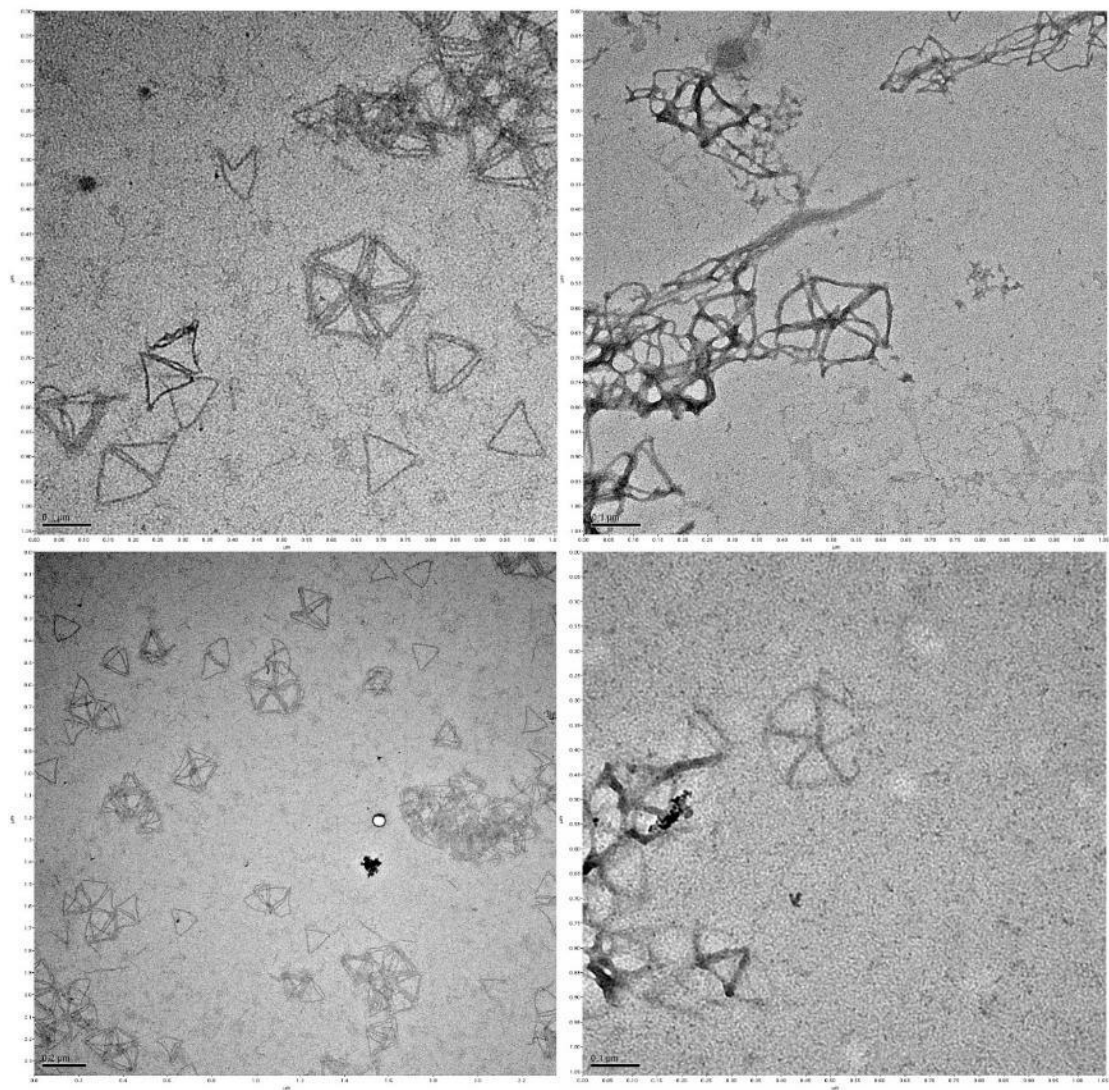
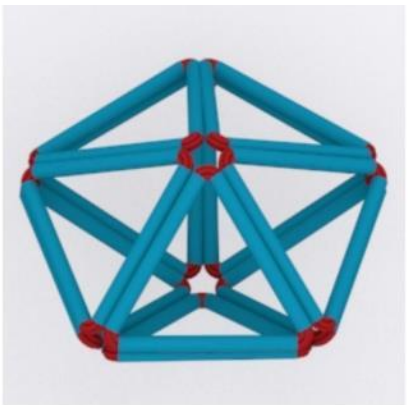
Supplementary Fig. 74. Additional TEM images of octahedron and DOS octahedron (bottom right) at different magnifications.



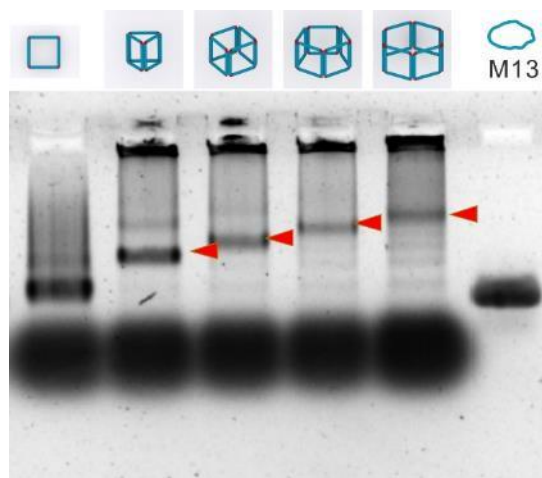
Supplementary Fig. 75. Net of pentagonal bipyramid. The numbers 1 to 10 in the middle represent ten triangles. The numbers on the sides represent M-bases that were used to link the triangles to form an octahedron. The arrows show the direction of the triangular M-DNA.



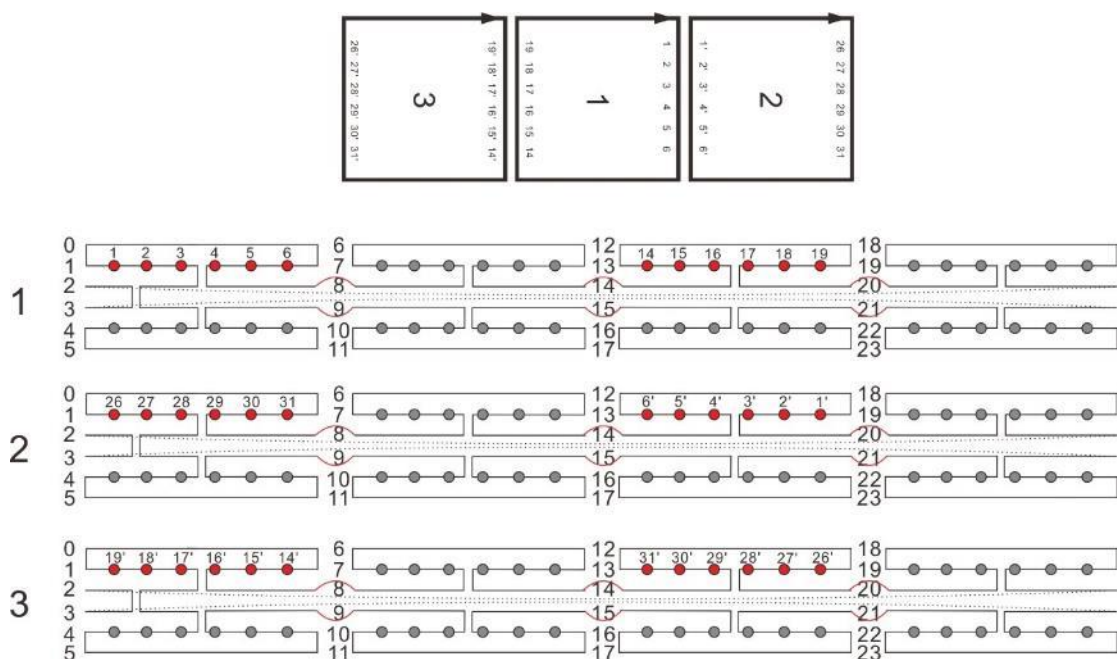
Supplementary Fig. 76. Schematic design for formation of octahedron. M-bases were located on helices 1, 7, and 13. Each side has 8 M-bases. Pentagonal bipyramid was formed by mixing ten triangular M-DNAs and annealing from 55°C to 20°C at 1°C per 2 h. All the needed strands can be found in the Supplementary Table. 55-59.



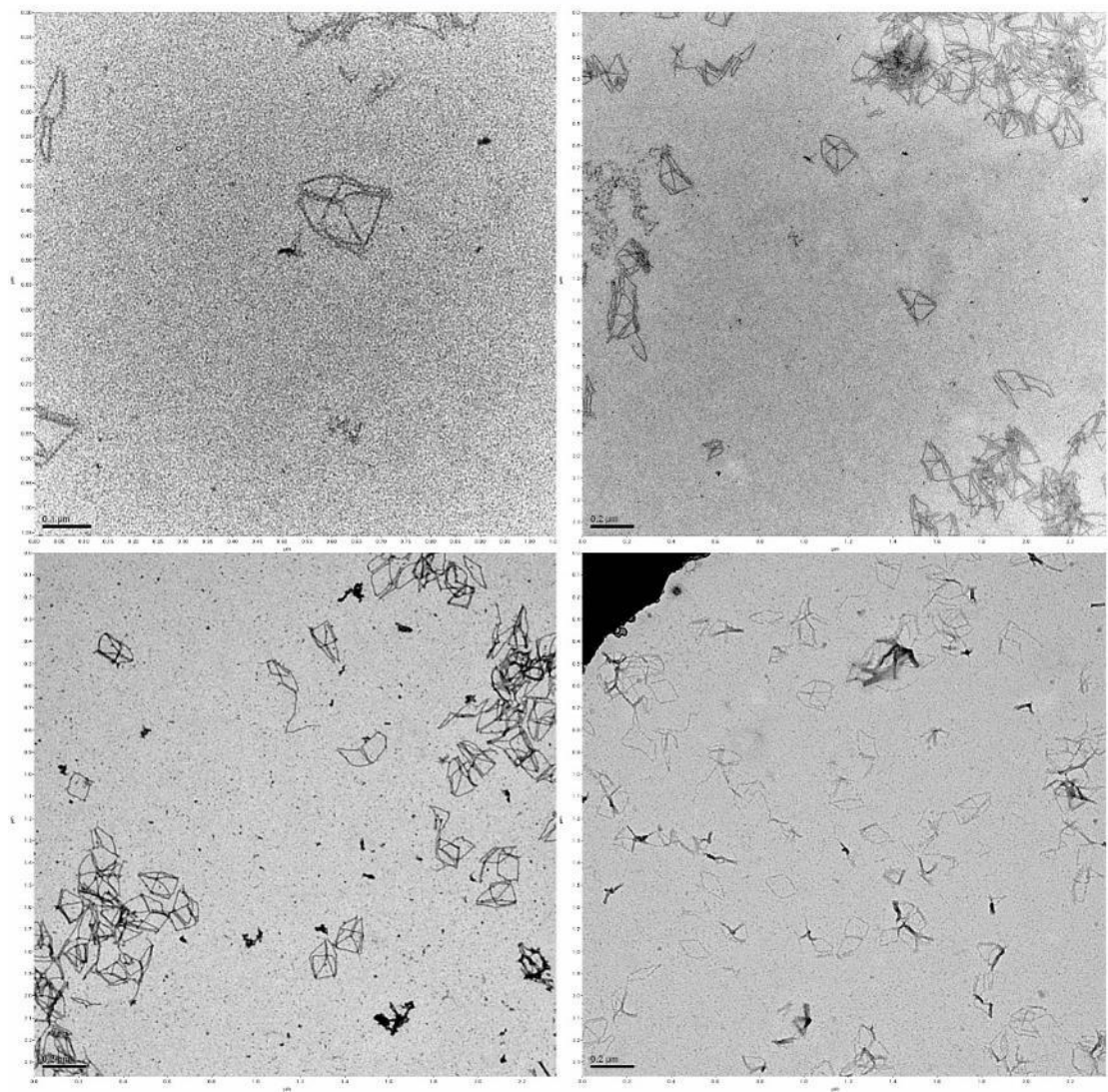
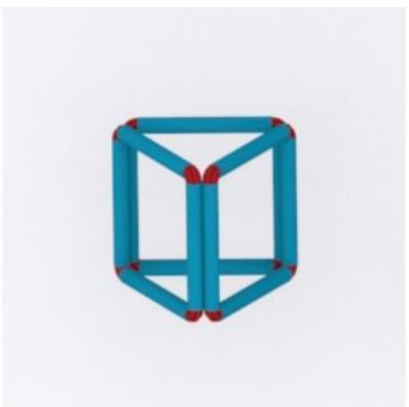
Supplementary Fig. 77. Additional TEM images of pentagonal bipyramid and DOS pentagonal bipyramid (bottom right) at different magnifications.



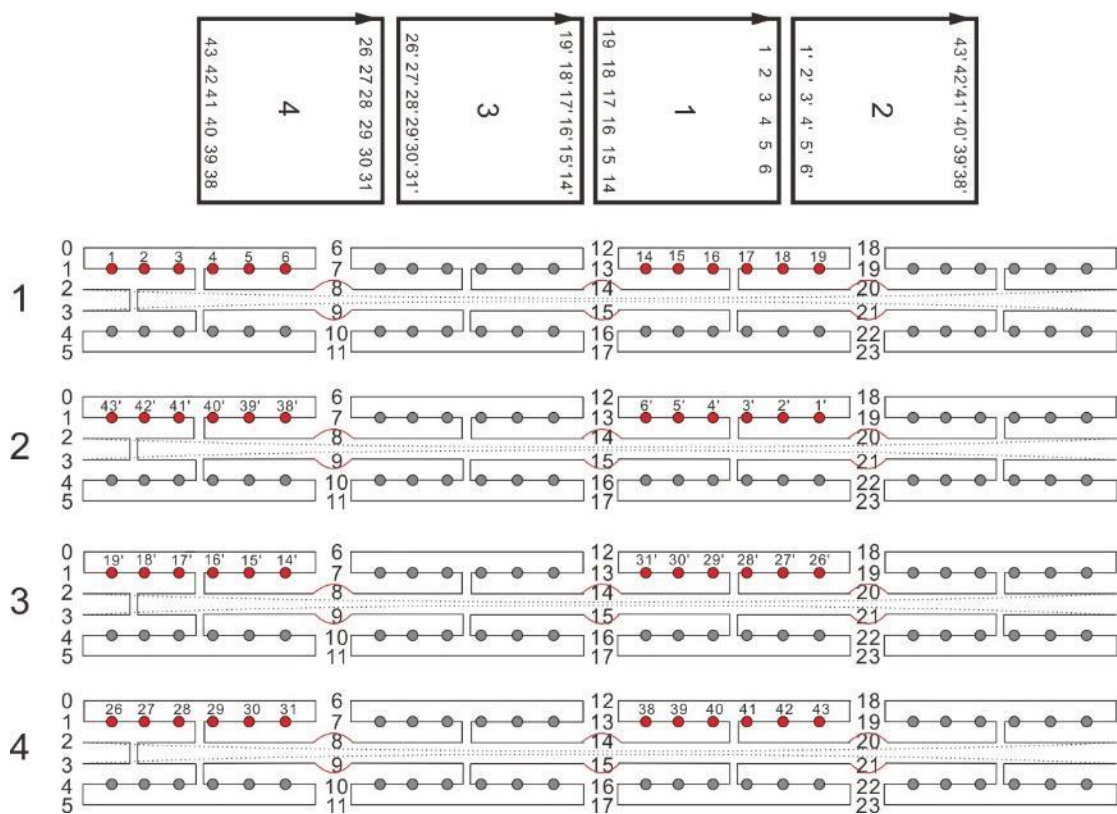
Supplementary Fig. 78. 1% agarose gel image confirming the formation of triangular prism, rectangular prism, pentagonal prism, and hexagonal prism. From left to right, basic rectangular M-DNA (squares), three, four, five, and six combined rectangular M-DNA and M13. Red arrows show the correctly formed prisms. The higher the number of squares in the prism, the slower the band runs in the gel.



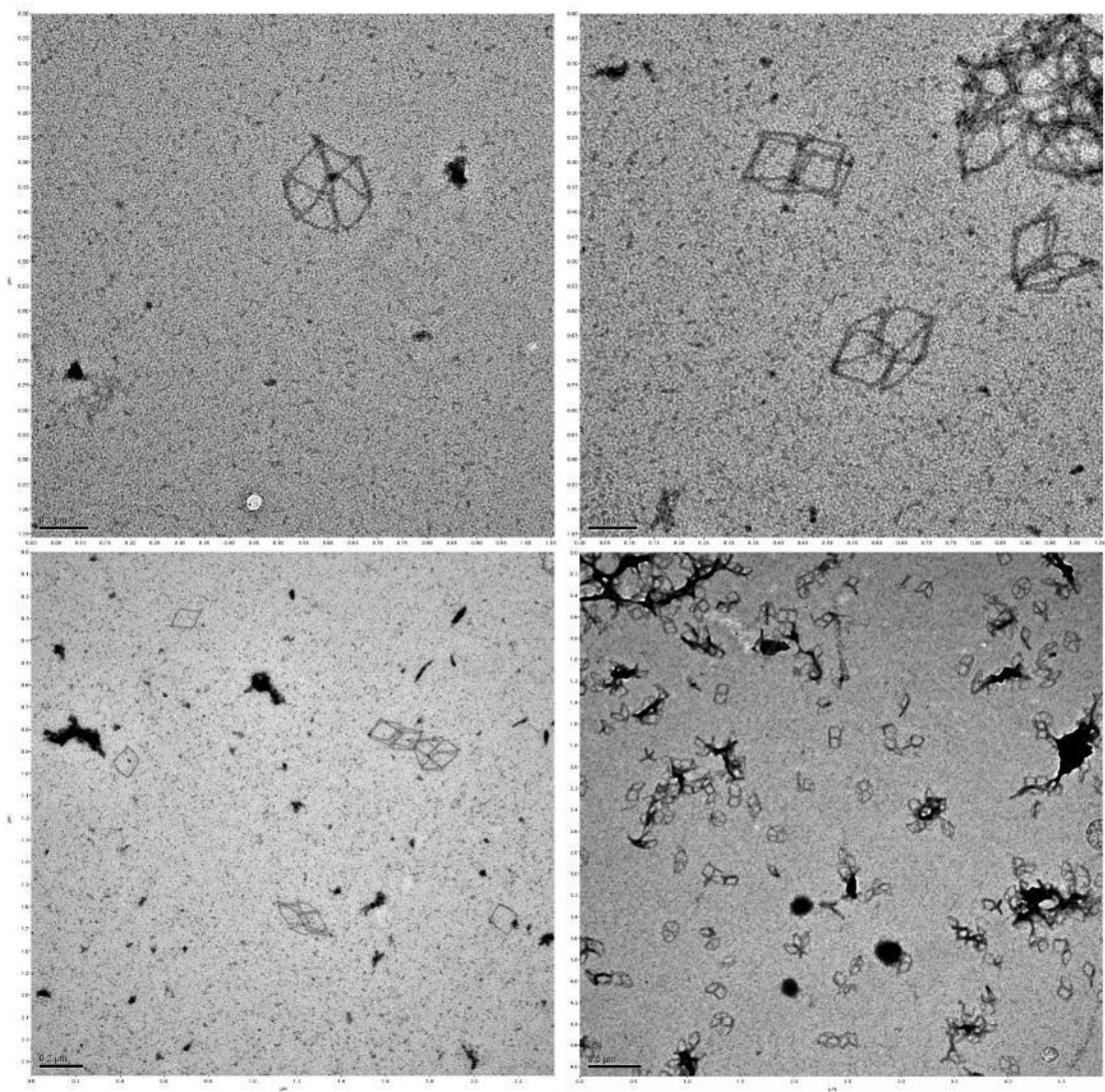
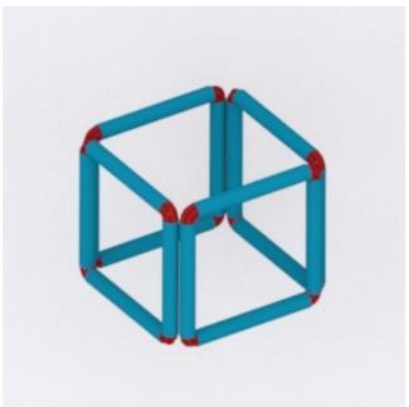
Supplementary Fig. 79. Net and schematic design for formation of triangular prism. M-bases were located on helix 1 and 13. Each side has 6 M-bases. This is the maximum number of M-bases that can be used in this length for a rectangular M-DNA. Triangular prism was formed by mixing three rectangular M-DNAs and annealing from 55° to 20° at 1°C per 2h. All the needed strands can be found in the Supplementary Table. 60-61.



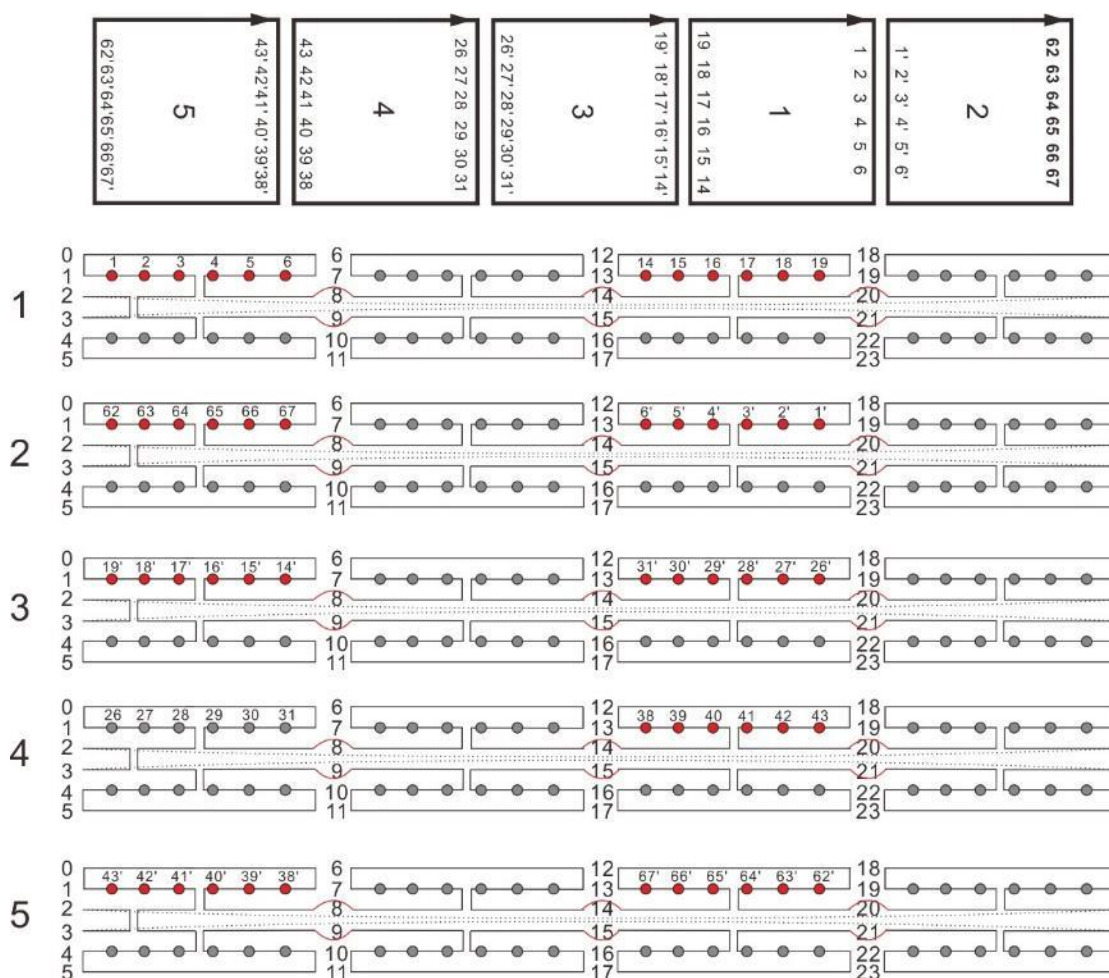
Supplementary Fig. 80. Additional TEM images of triangular prism and DOS triangular prism (bottom right) at different magnifications.



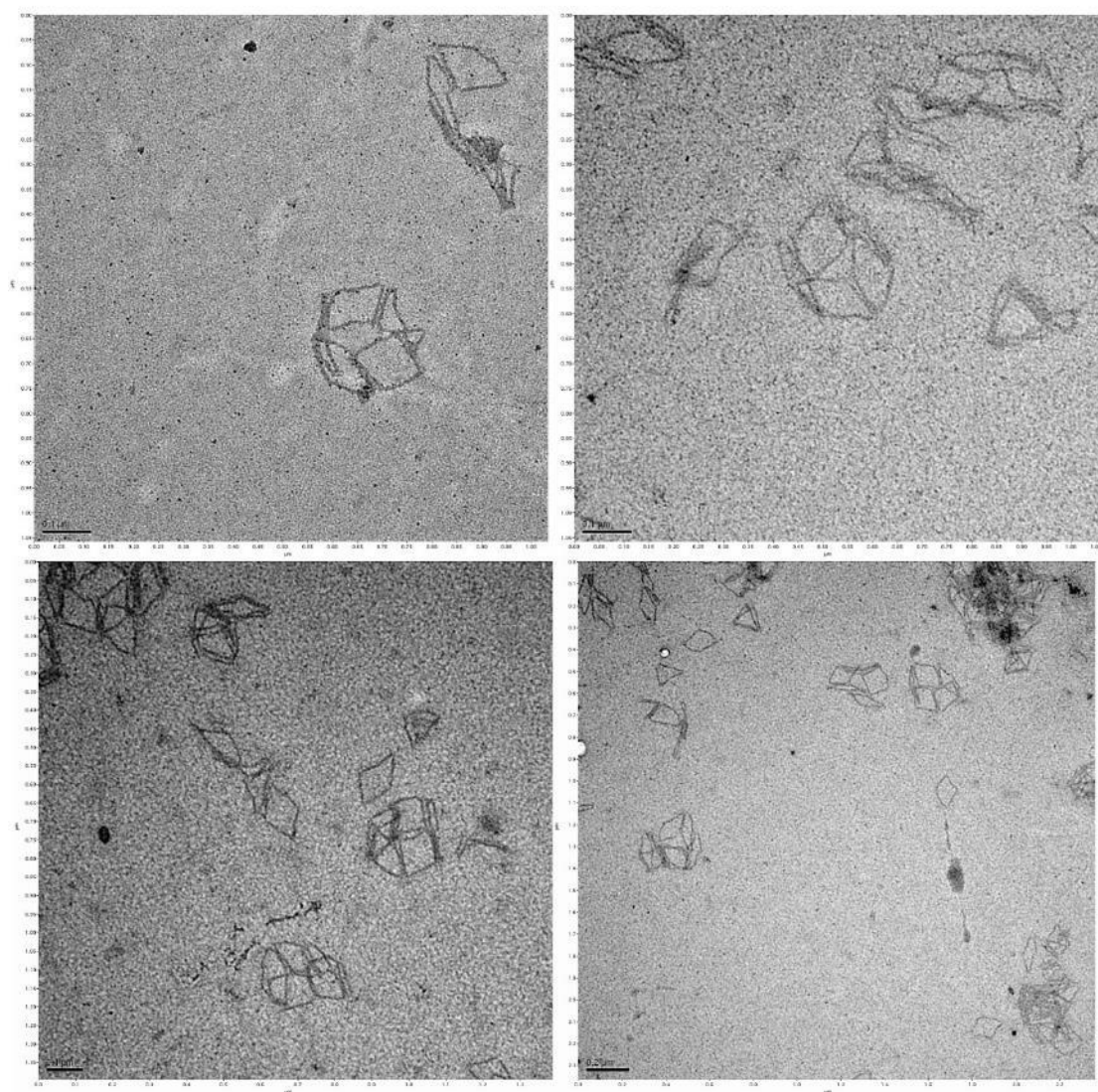
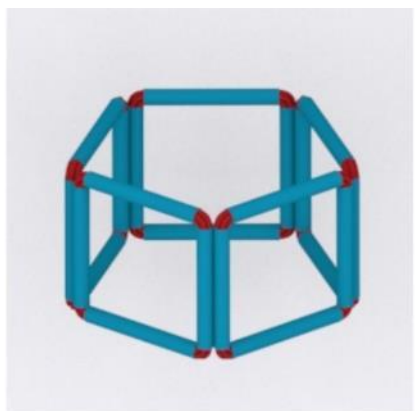
Supplementary Fig. 81. Net and schematic design for formation of rectangular prism. M-bases were located on helices 1 and 13. Each side has 6 M-bases. Rectangular prism was formed by mixing four rectangular M-DNAs and annealing from 55° to 20° at 1°C per 2h. All the needed strands can be found in the Supplementary Table. 60-62.



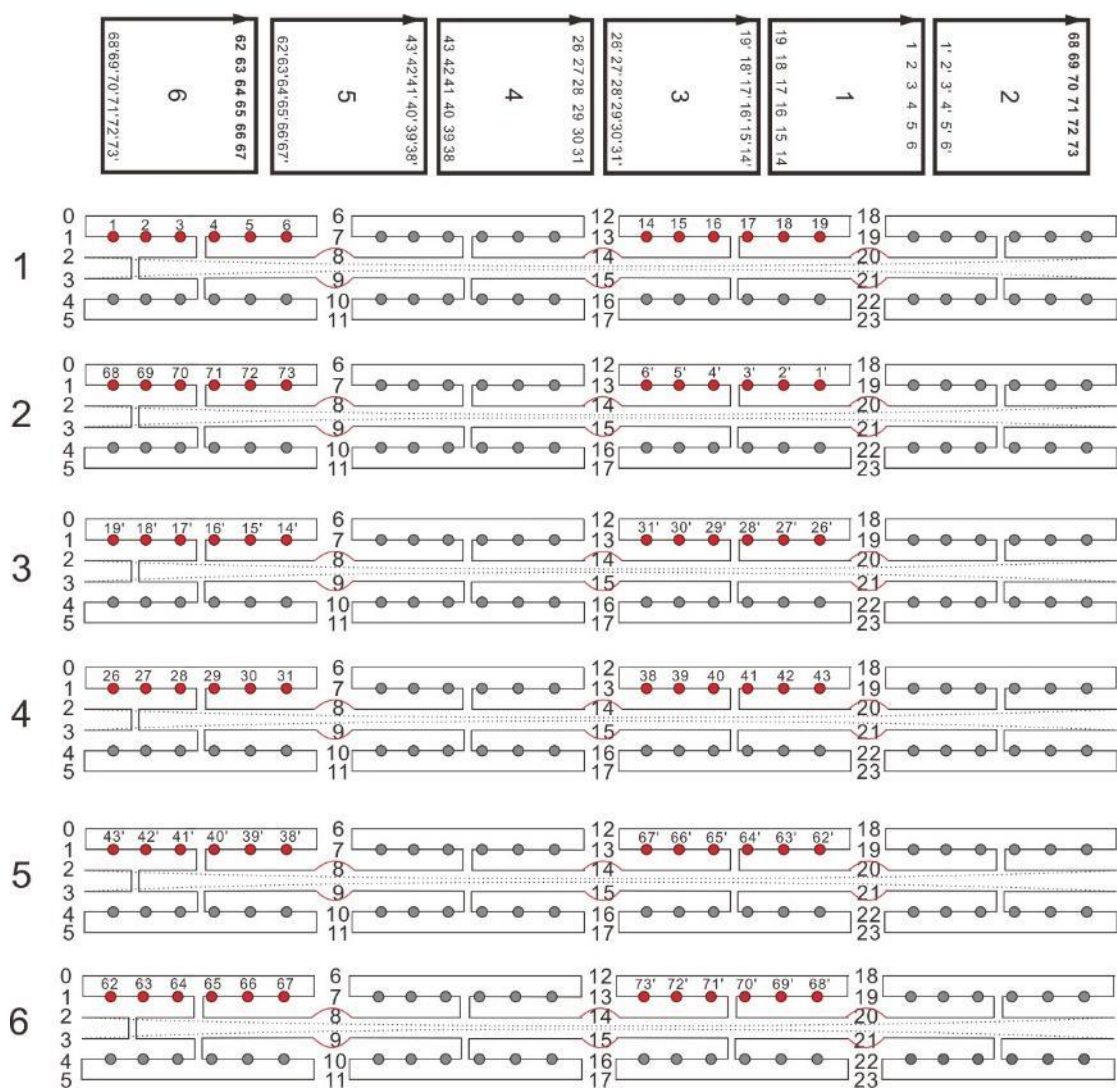
Supplementary Fig. 82. Additional TEM images of rectangular prism and DOS rectangular prism (bottom right) at different magnifications.



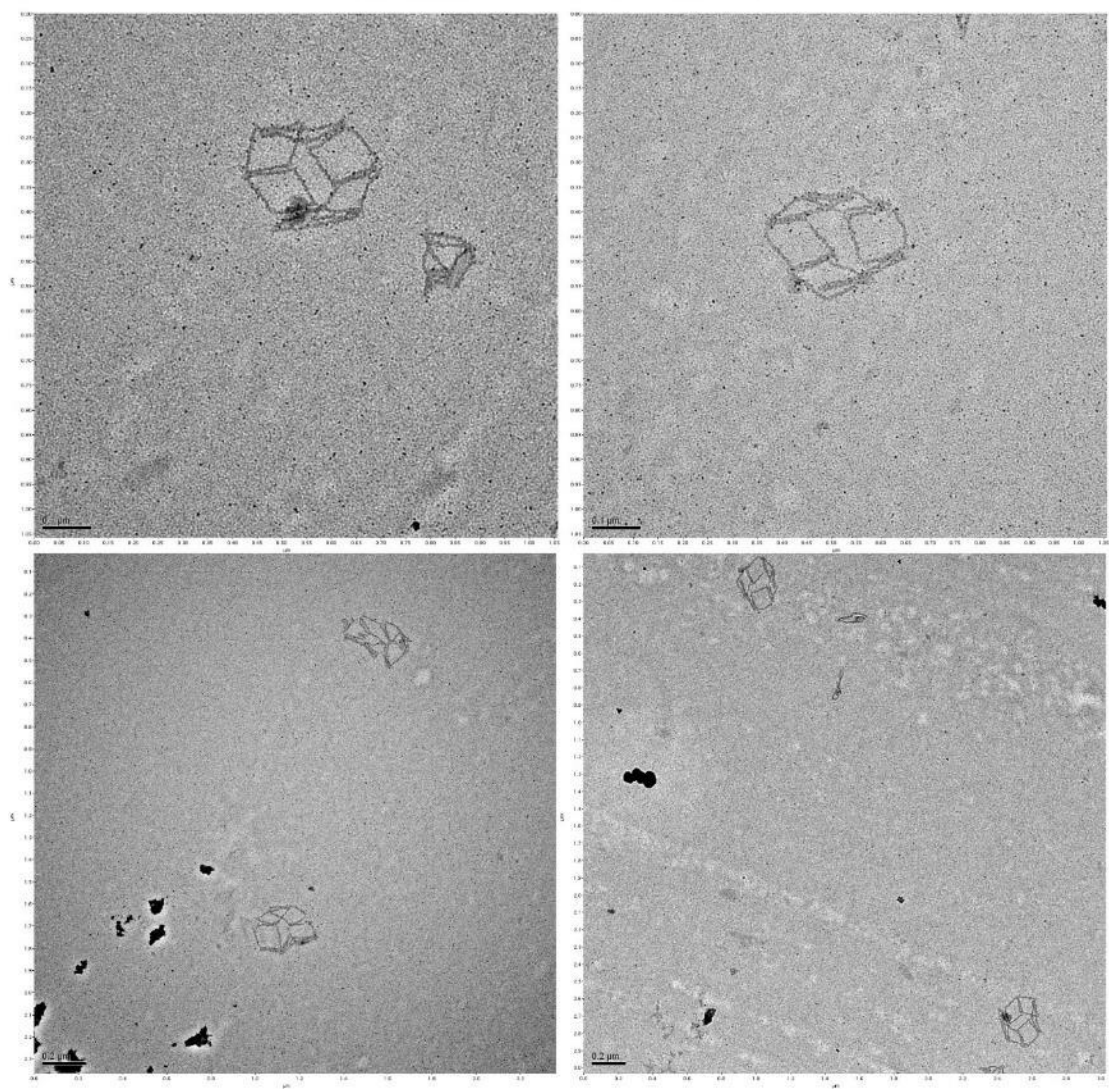
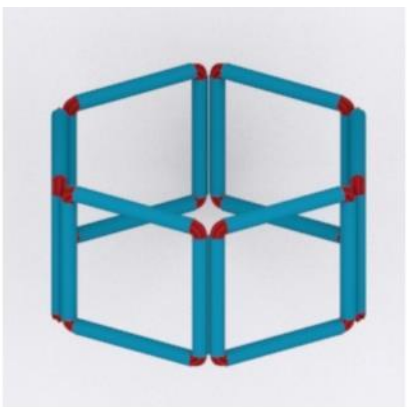
Supplementary Fig. 83. Net and schematic design for formation of pentagonal prism. M-bases were located on helices 1 and 13. Each side has 6 M-bases. Pentagonal prism was formed by mixing five rectangular M-DNAs and annealing from 55° to 20° at 1°C per 2h. All the needed strands can be found in the Supplementary Table. 60-63.



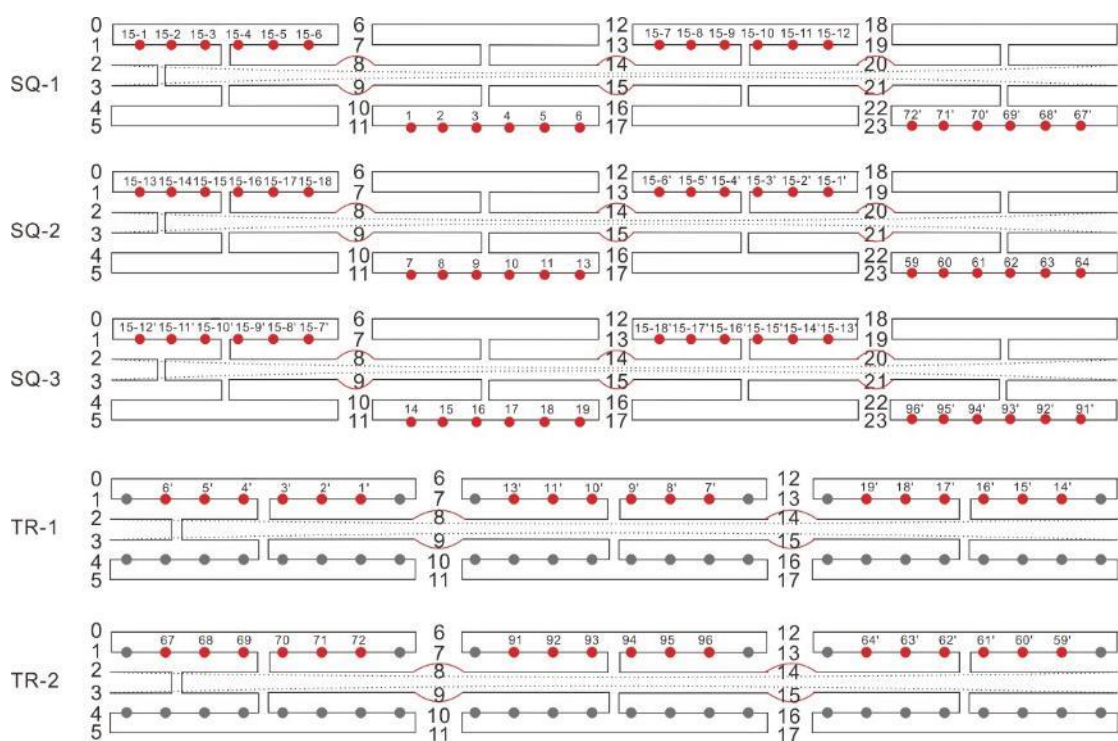
Supplementary Fig. 84. Additional negative-stained TEM images of pentagonal prism at different magnifications.



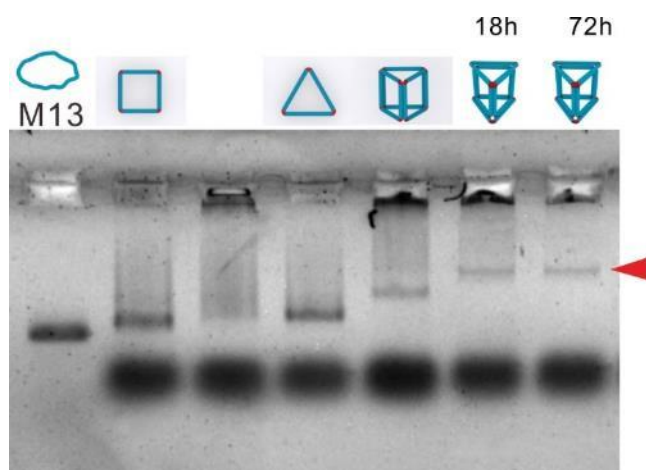
Supplementary Fig. 85. Net and schematic design for formation of hexagonal prism. M-bases were located on helices 1 and 13. Each side has 6 M-bases. Hexagonal prism was formed by mixing six rectangular M-DNAs and annealing from 55° to 20° at 1°C per 2h. All the needed strands can be found in the Supplementary Table. 60-64.



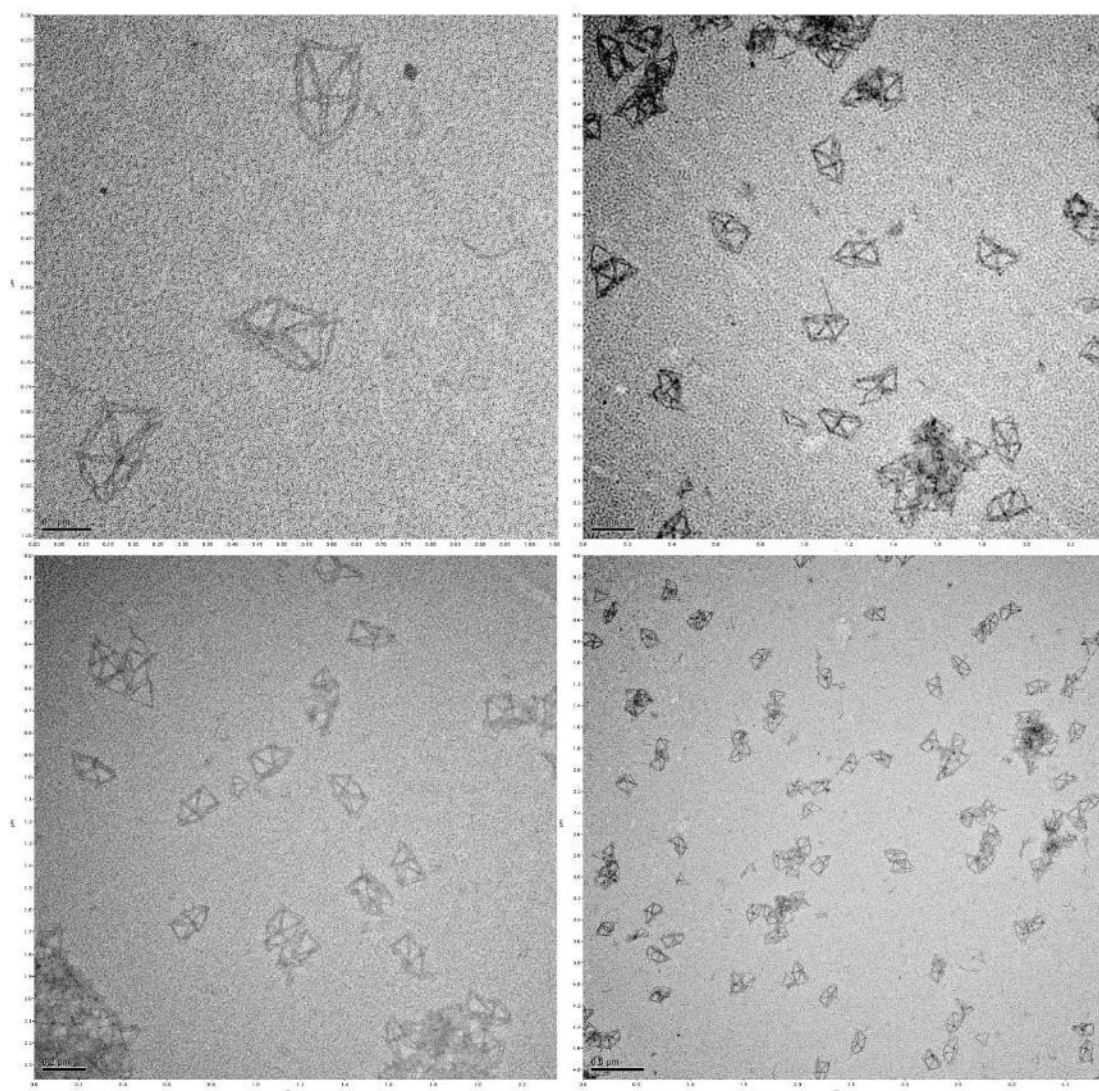
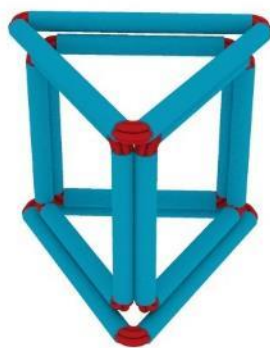
Supplementary Fig. 86. Additional negative-stained TEM images of hexagonal prism at different magnifications.



Supplementary Fig. 87. Schematic design for formation of blocked triangular prism. SQ-1, SQ-2, SQ-3, TR-1, and TR-2 were mixed together and annealed from 55° to 20°C. All the needed strands can be found in the Supplementary Table. 65-67. The 15 nt M-bases was labelled as 15-1 or 15-1' and so on. The sequences were listed on Supplementary Table. 73.

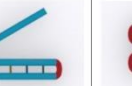
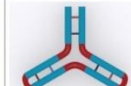


Supplementary Fig. 88. 1% agarose gel image confirming the formation of blocked triangular prism. From left to right, M13, basic square, basic triangle, triangular prism, and blocked triangular prism. Red arrow shows correct combined blocked triangular prism structure. Annealing with a 72h process has a higher yield.



Supplementary Fig. 89. Additional negative-stained TEM images of blocked triangular prism at different magnifications. Much higher yield of the designed structure is obtained with blocking the ends of the prism.

Summary and discussion for self-folded, self-linked structures and 3D polyhedron

							
95%	75%	72%	46%	8%	28%	4%	76%
							
86%	81%	71%	64%	55%	66%	42%	40%
							
83%	12%	28%	3%	41%	32%	29%	21%

Supplementary Fig. 90. Estimated formation yields of self-folded, self-linked structures, and 3D polyhedron. The yields of self-folded and self-linked structures were calculated from AFM images. They were estimated as $y=m/n$, where m is the total number of complete structures in images and n is the total number of complete designed structures, aggregates, and ambiguous structures counted in images. The yield of polyhedron was estimated by gel image analysis. The yield of individual structure was estimated by comparing the intensity of target band with the entire lane (not including staple strands lane below). The intensity was analyzed by image J.

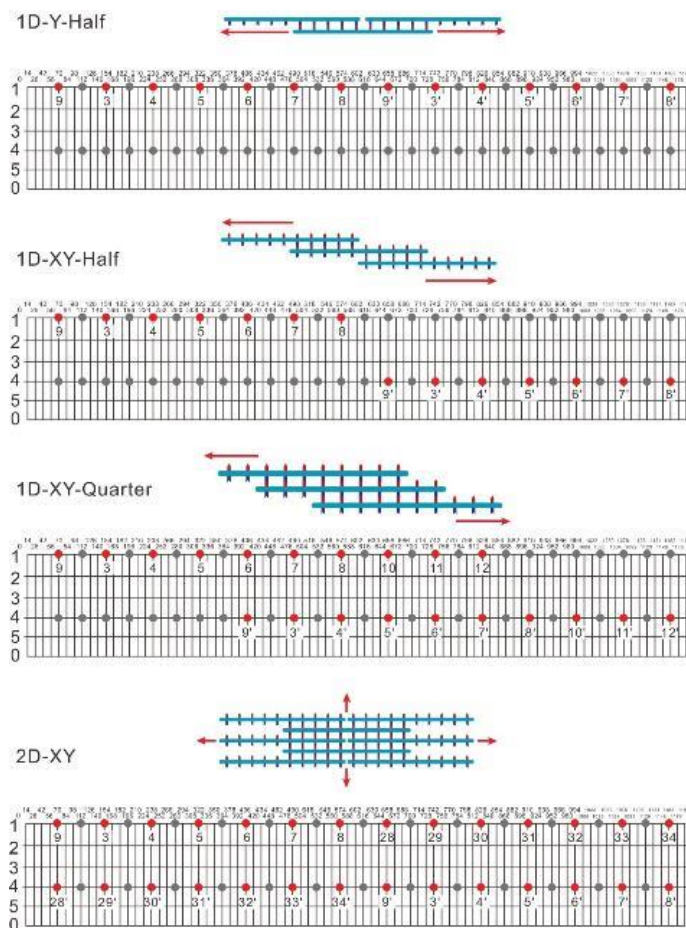
For the self-folded structures (first row in Supplementary Fig. 90), the formation yields of most structures are good (from 28% to 95%) except triangular four-segments (8%) and six-segments (4%) (Supplementary Fig. 50 and Supplementary Fig. 53). Triangular four-segments prefer to form linear arrays through intermolecular hybridization because the two ends with M-bases are relatively far away. Triangular six-segments prefer to fold into unclear aggregates. We believe the inherent structural design contributes most to the low yields of these two structures because both designs involve the long-range hybridizations between segments. Therefore, reducing concentration of the assembly monomers may increase the formation yield of the self-folded structure.

For the self-linked structures (second row in Supplementary Fig. 90), the yields are relatively high for these structures (40%-86%). The key is designing the appropriate linker staple strands, which should be longer than normal staple strands. It is an interesting result that the circular structure has

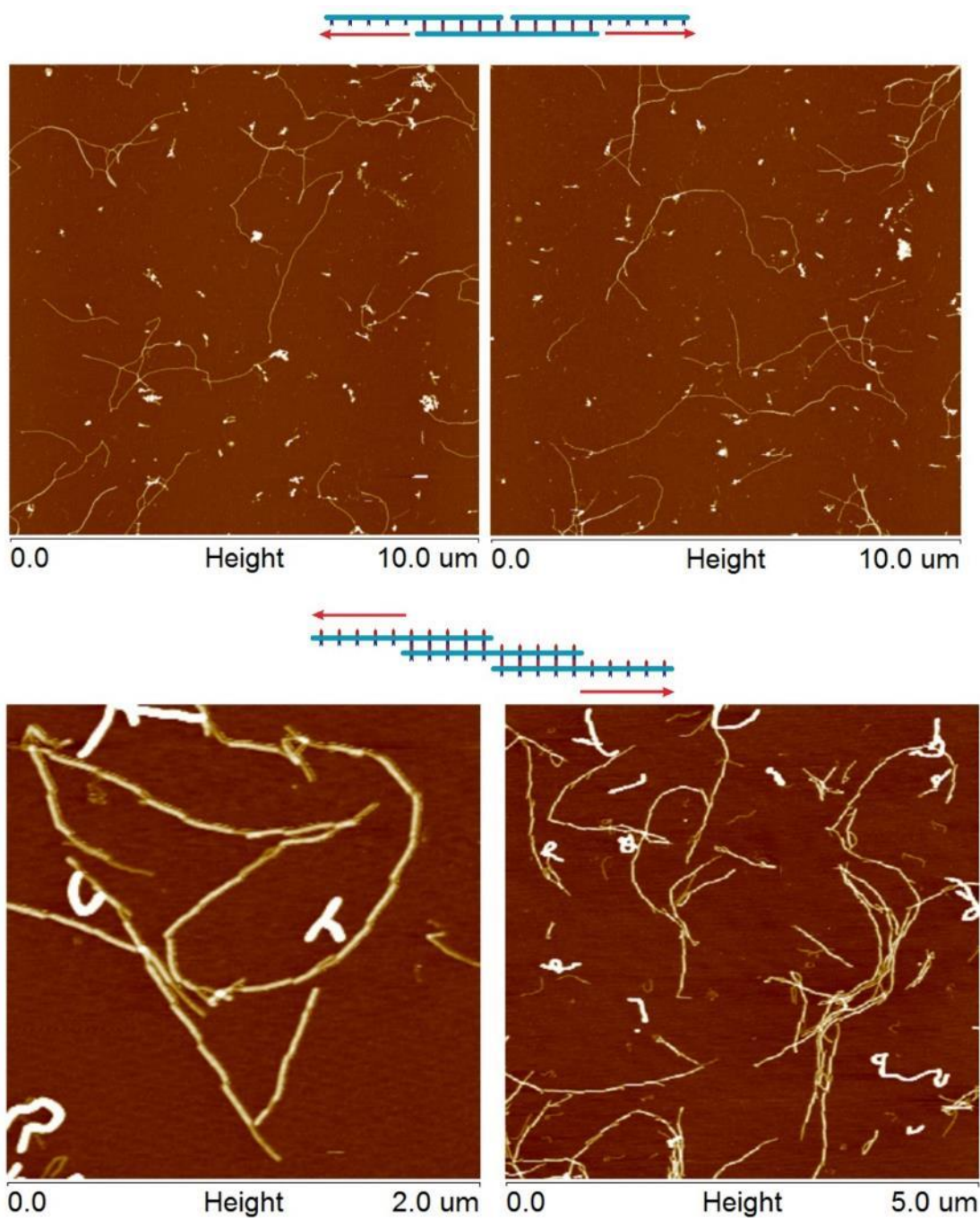
the highest yield (86%). Several staple strands may be deformed when bending the relatively rigid linear ssM-DNA to a circular configuration.

For the polyhedrons assembled from multiple M-DNA (third row in Supplementary Fig. 90), the more complicated the structure is, the lower the yield. The binding strength is important for the corrected formation of target assemblies. We tried 4 M-bases and 8 M-bases on each edge of triangular M-DNA (Supplementary Fig. 65) and found that 8 M-bases design has a much higher yield. Annealing procedure is also important. Longer annealing time is necessary for the formation of complicated polyhedrons.

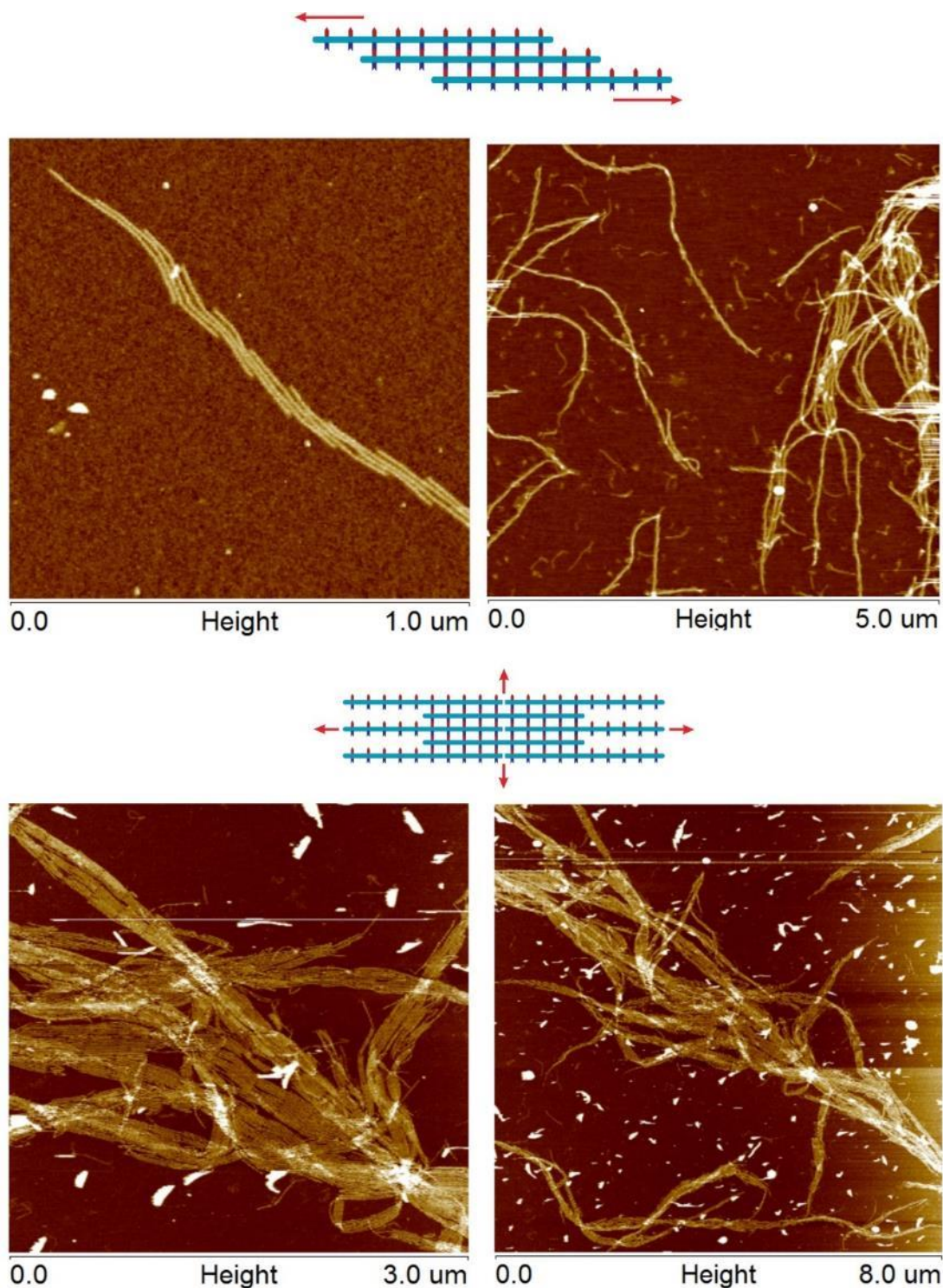
Section 7. Self-assembly of 1D, 2D, and 3D M-DNA structures based on M-SST.



Supplementary Fig. 91. Schematic design for formation of 1D and 2D array. For 1D-Y-Half structure, the M-bases were located on helix 1 in an order of 9, 3, 4, 5, 6, 7, 8, 9', 3', 4', 5', 6', 7', and 8'. Multiple copies of the same M-DNA hybridized one to another face to face, offset by half of its length, to form one-dimensional structure extending at the direction marked by the red arrows (y-direction). For 1D-XY-Half structure, the self-complementary M-bases were located on helix 1 and helix 4, which lead to a pseudo-1D structure extending at both x and y directions, with neighboring M-DNA offset by half of its length. For 1D-XY-Quarter structure, the complementary M-bases were located on helix 1 and helix 4, which is the same as that in the 1D-XY-Half structure. But the number and locations of the M-bases were different, which lead to different arrangements of M-DNA to form a pseudo-1D structure with the neighboring M-DNA offset by a quarter of its length. For 2D-XY structure, two sets of complementary M-bases were located on helix 1 and helix 4, which led to M-DNA extending in both x and y directions. Due to the large aspect ratio of the unit M-DNA, formation of long ribbons is expected. All structures were formed in one-pot assembly process from 90° to 25°C. All the needed strands can be found in the Supplementary Table. 68-69.

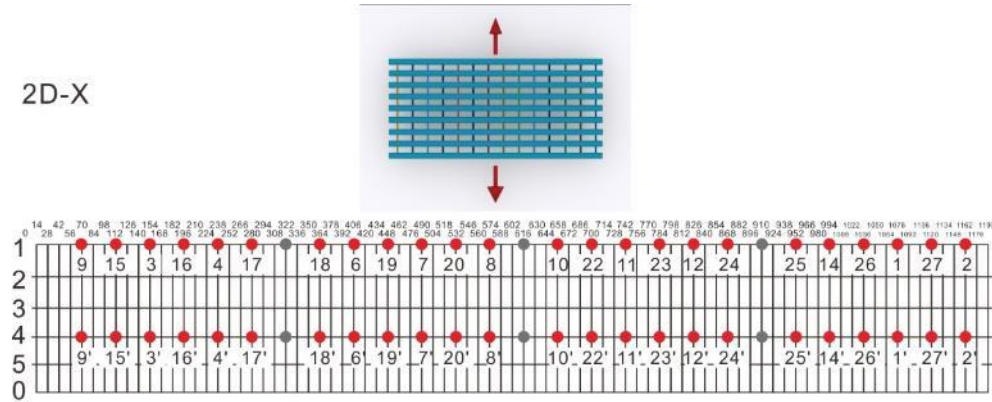


Supplementary Fig. 92. Additional AFM images of 1D-Y-Half and 1D-XY-Half structures at different magnifications.

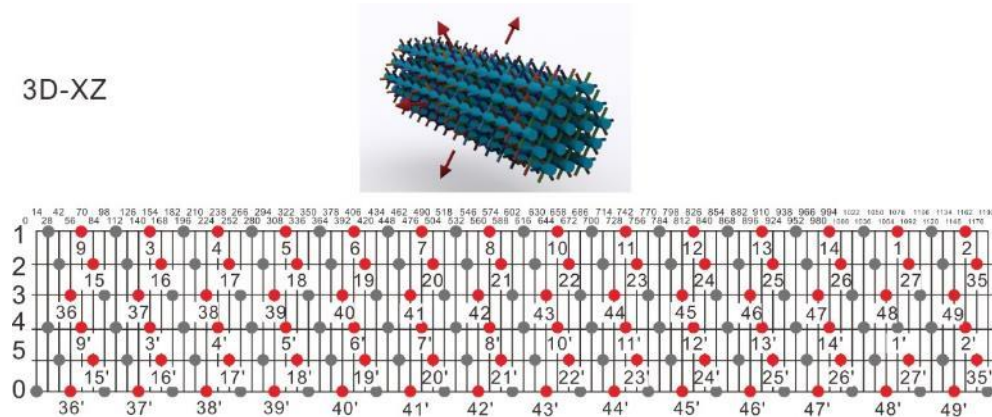


Supplementary Fig. 93. Additional AFM images of 1D-XY-Quarter and 2D-XY structures at different magnifications.

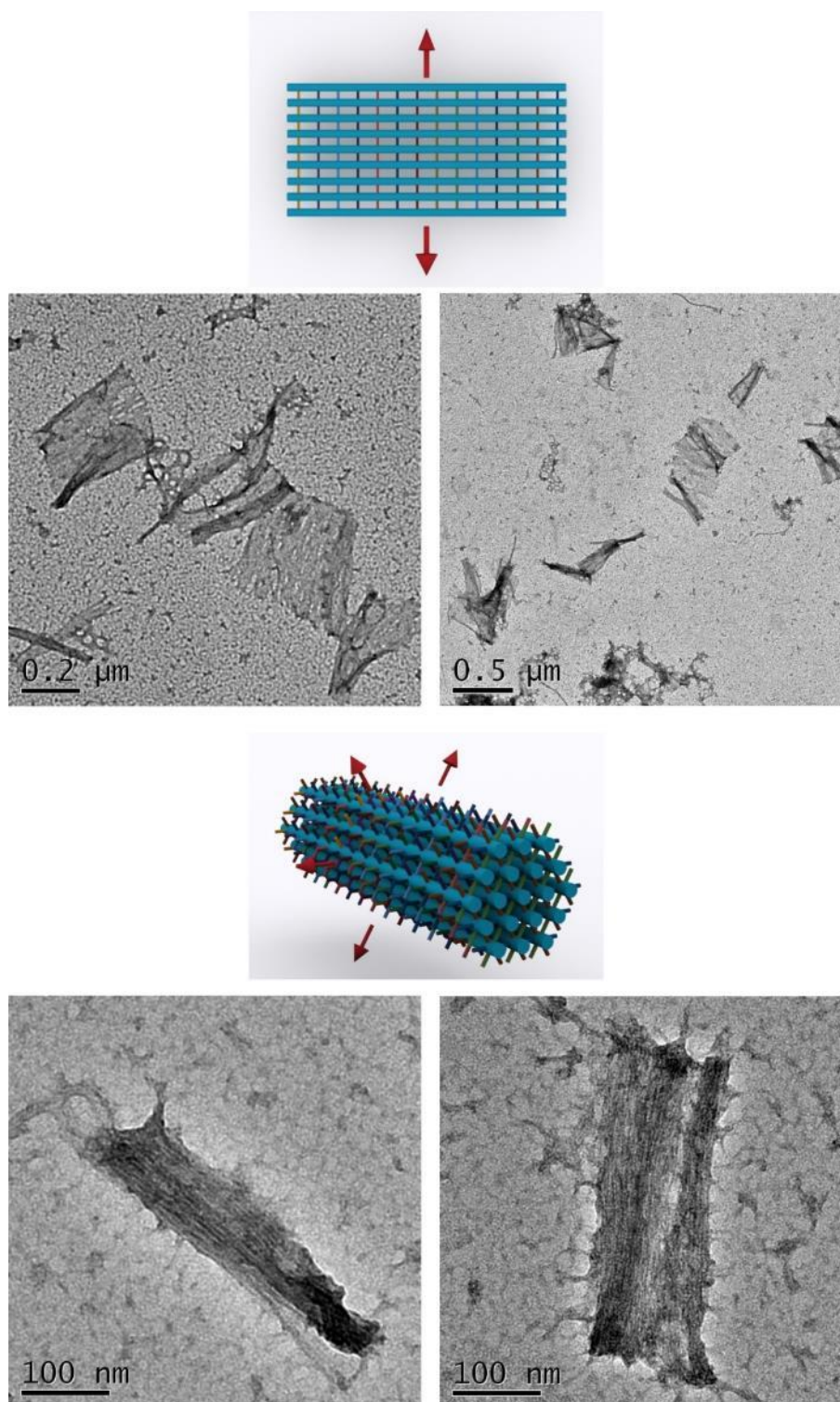
2D-X



3D-XZ



Supplementary Fig. 94. Schematic design for formation of 2D and 3D array. For the 2D-X structure, the M-bases were located on helix 1 and helix 4. The M-bases on helix 1 were complementary with the ones on helix 4, thus formed a 2D structure extending in x direction, with a fixed width of the length of the M-DNA. The strands can be found in the Supplementary Table. 70-71. For the 3D-XZ structure, M-bases were located on all of the six helices, which led to forming a three-dimensional structure extending in x and z directions, with a fixed length of the M-DNA. The strands can be found in the Supplementary Table. 72-73.



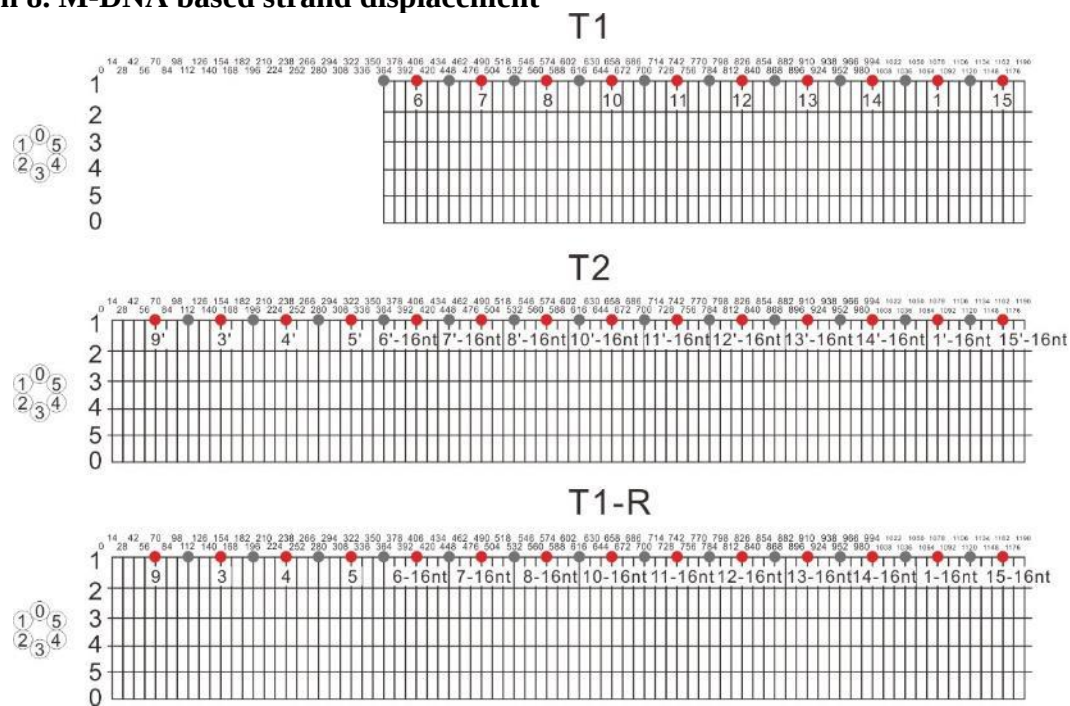
Supplementary Fig. 95. Additional negative-stained TEM images of 2D-X and 3D-XZ structures at different magnifications.

Summary and discussion for M-SST structures

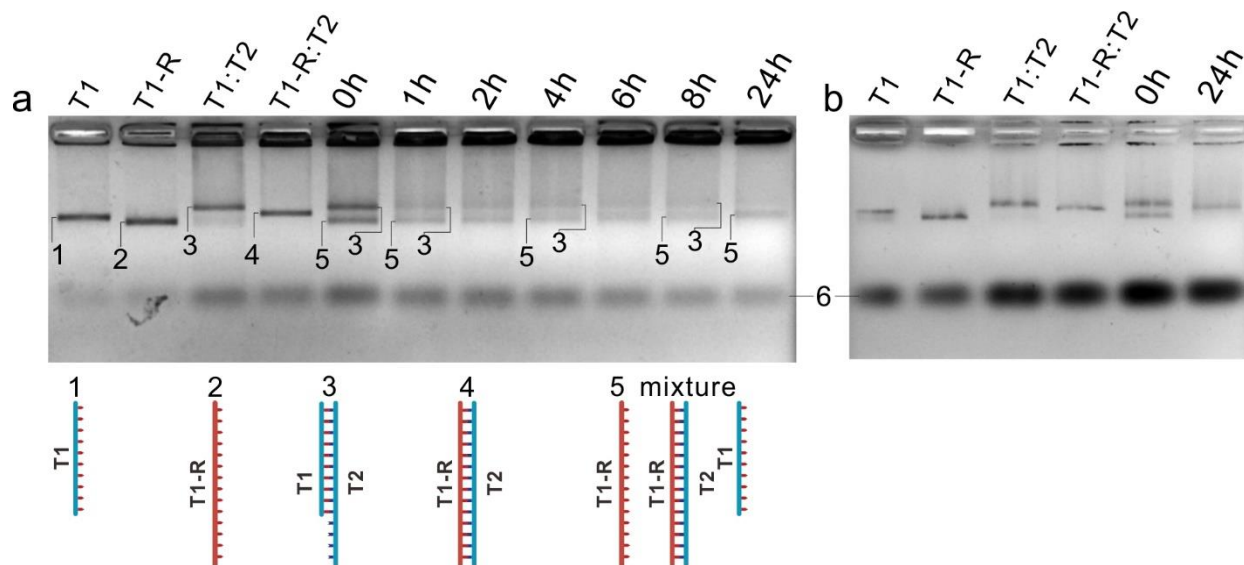
It's difficult to have a quantitative estimation of the yield of M-SST structures since the target structures are infinite arrays. Three types of products can be observed: unassembled monomers, well-ordered arrays (targets), and aggregates. For the 1D and 2D M-SST structures, there are few ssM-DNA observed in the AFM images or TEM images, indicating almost all the monomers were assembled into oligomers or multimers.

The yield of large 3D-XZ lattices is low. The main reason is that M-bases are relatively long and soft, which leads to a flexible connection and more possible mismatches between M-DNAs. Reducing the length of spacer or hybridization part of M-bases can be considered to construct better 3D structures. Other forces, like stacking force, can also be explored to assemble more rigid lattices.

Section 8. M-DNA based strand displacement



Supplementary Fig. 96. Schematic design for M-DNA strand displacement. All the M-bases were located on helix 1. T1 has a length of about 300nm, due to removal of one fourth of staple strands from M-DNA with normal length (420nm). T2 and T1-R have normal lengths. M-bases on T2 and T1-R are 16nt long, with a 6nt toehold on each M-base. The strand details can be found in the Supplementary Table74-76.

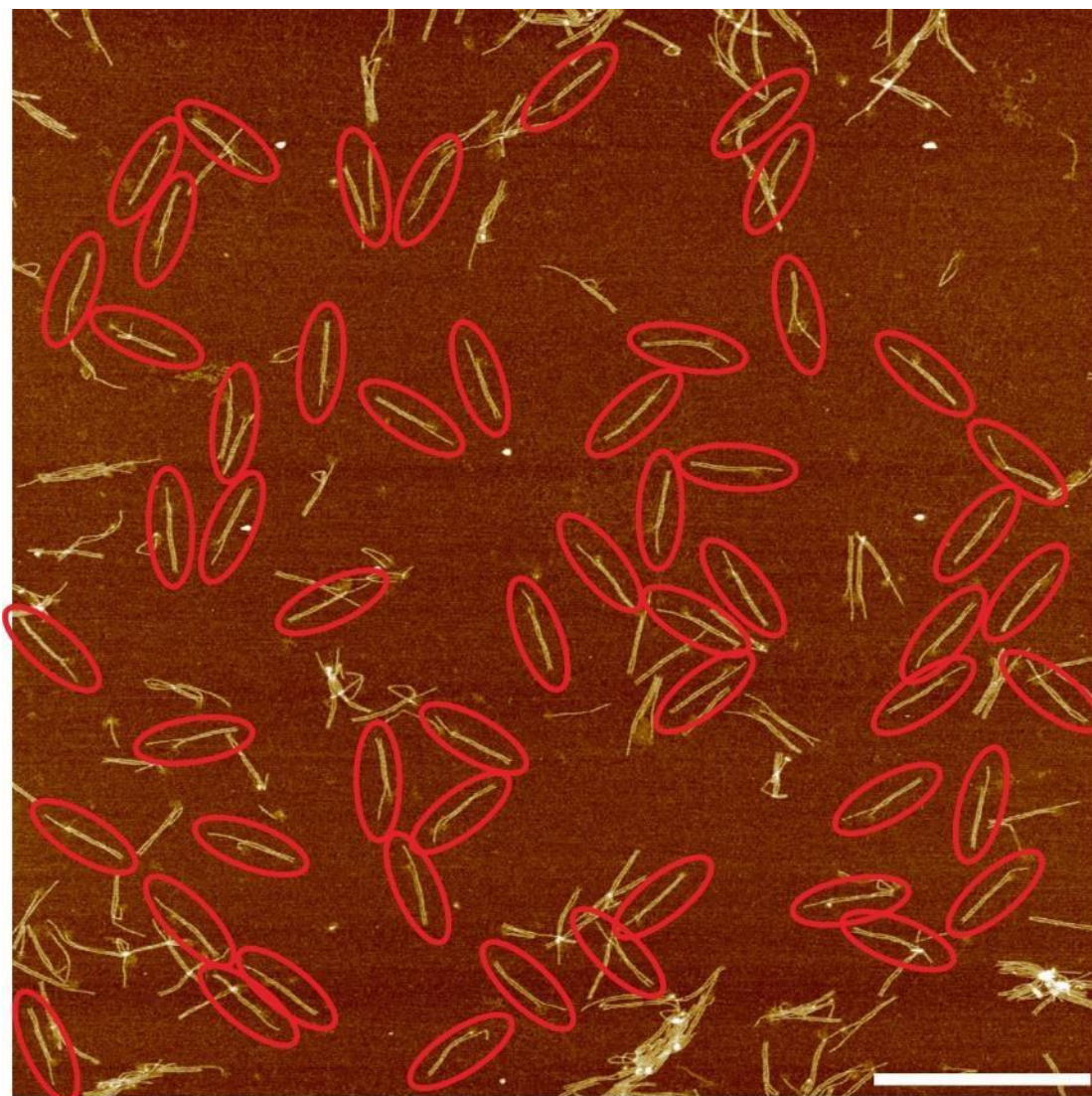


Supplementary Fig. 97. 1% agarose gel images of M-DNA strand displacement at different time points. (a) purified samples. (b) unpurified samples. The first four lanes from left to right: T1 ss-M-DNA, T1-R ss-M-DNA, T1:T2 ds-M-DNA, and T1-R:T2 ds-M-DNA. The left seven lanes in a are reaction samples (adding invader M-DNA T1-R to T1:T2 dsM-DNA) at 0 h, 1 h, 2 h, 4 h, 6 h, 8 h, and 24 h. The left two lanes in b are reaction samples at 0 h and 24 h.

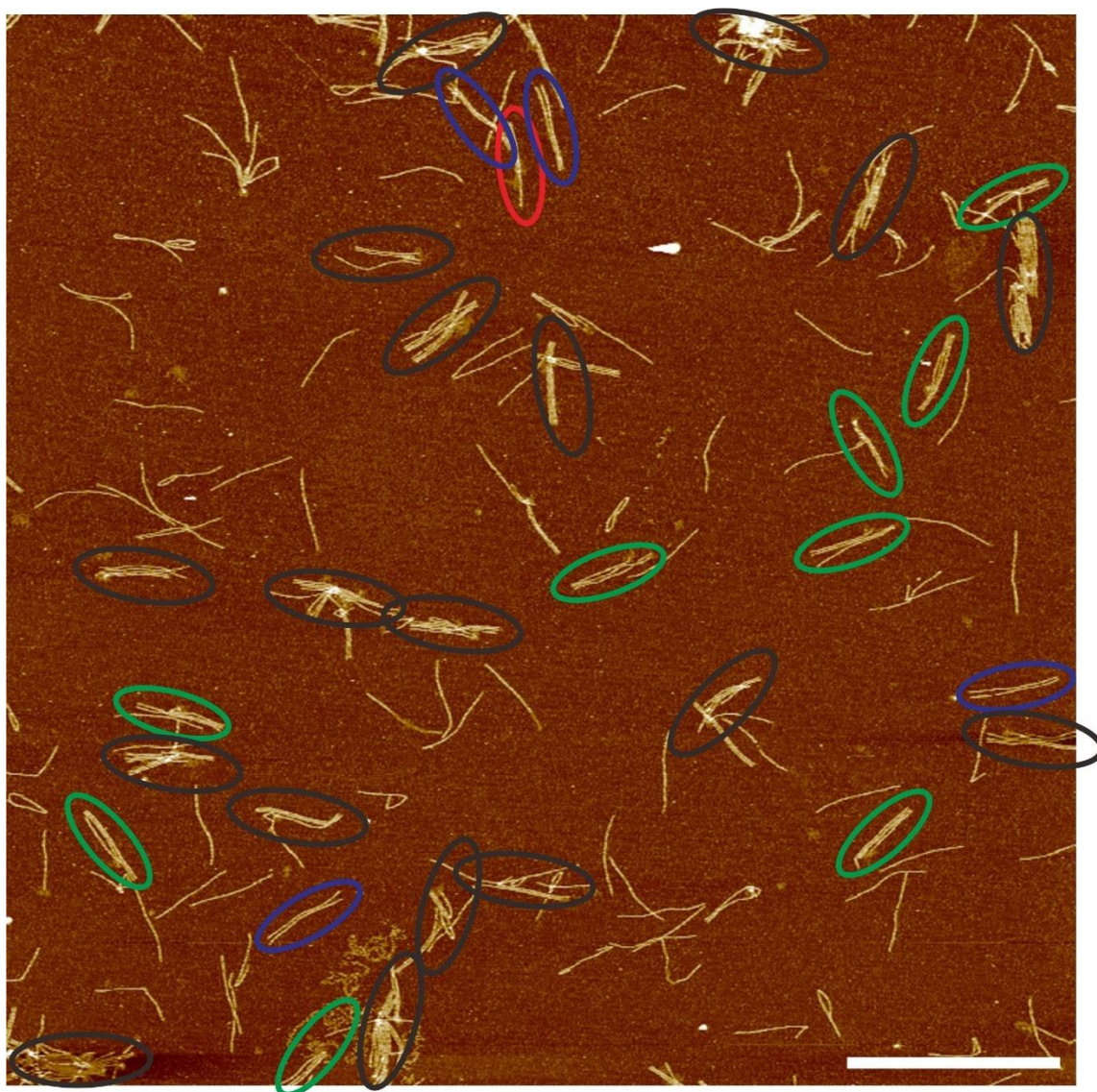
There are six major bands on the gel. Band 1 corresponds to T1 ss-M-DNA, Band 2 corresponds to T1-R ss-M-DNA. Band 3 corresponds to T1:T2 ds-M-DNA, Band 4 corresponds to T1-R:T2 ds-M-DNA. T1 migrates slower than T1-R and T1:T2 ds-M-DNA migrates slower than T1-R:T2 ds-M-DNA because of a large single-stranded loop region (the extra M13 scaffold strand) on structure T1 design,

Band 5 is a mixture band that contains T1-R, T1-R:T2, and T1. After adding invader M-DNA, band 5 migrates slower and slower as time goes by. At the starting time point (0h), almost all contents are T1-R. It runs at the same position as T1-R. At the 4h time point, the gel lane contains T1, T1-R and dsM-DNA T1-R:T2. After 24 hours, all the reagents including invader M-DNA and T1:T2 dsM-DNA are depleted. The band 3 disappears on Lane 24h. The band 5 is a mixture of T1-R:T2 and T1 products. It shows the same the migration rate with T1-R:T2 (band 4) or T1 (band 1).

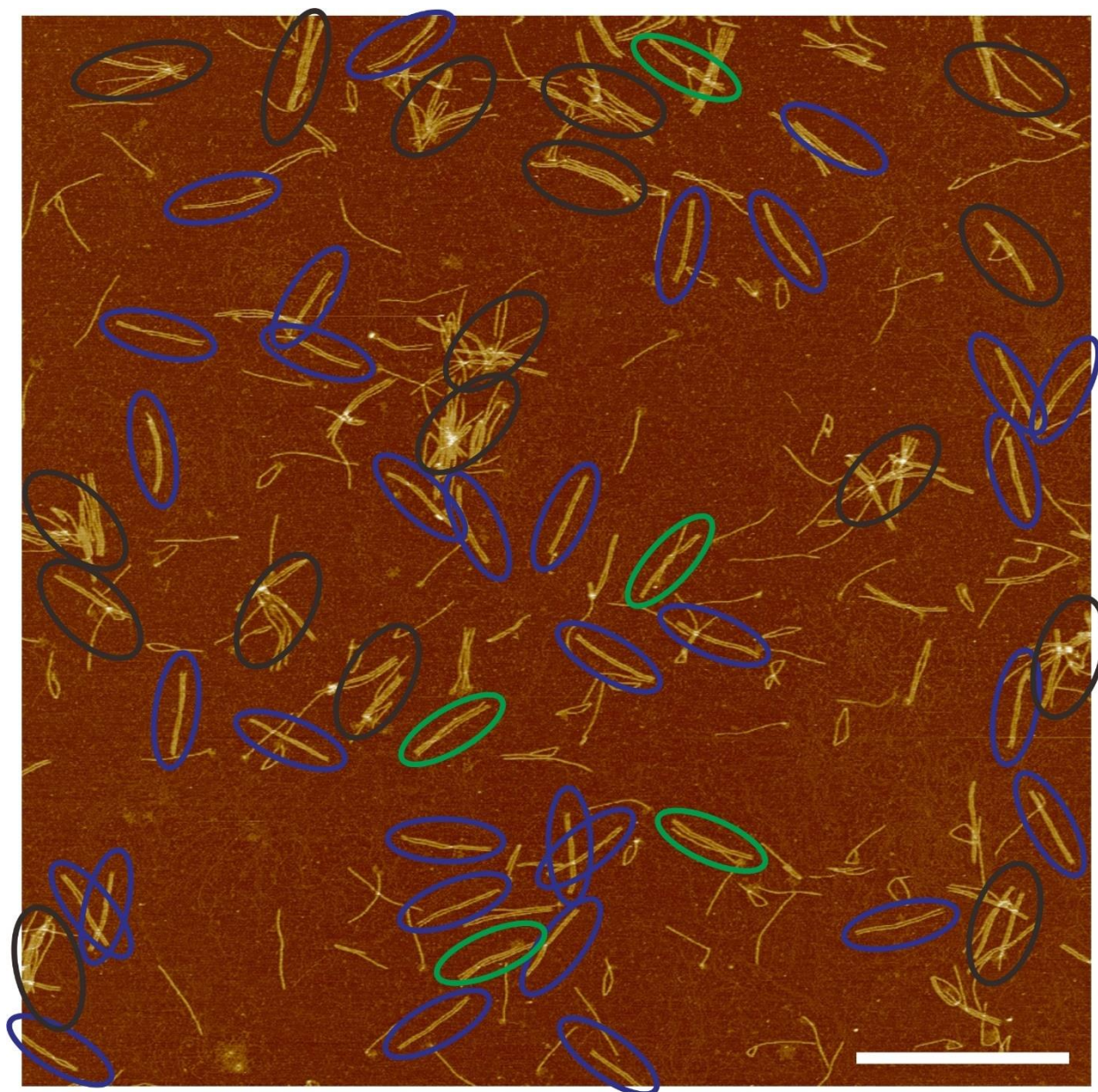
Band 6 corresponds to the staple strands. Compared with the band 6 in gel b, most of the staple strands were removed after purification. The small number of staple strands left in gel a don't have fluorophore label and they will not affect the kinetic study.



Supplementary Fig. 98. AFM images of initial-stated dsM-DNA T1:T2. Red circles indicate right formed T1:T2 double strand M-DNA. Scale bar: 1 μ m.



Supplementary Fig. 99. AFM images of M-SDR obtained at 1h after adding T1-R M-DNA strand. The red circle indicates the reagent T1:T2 dsM-DNA. Green circles indicate the intermediate-stated M-DNA. Blue circles indicate the M-DNA in final state (T1-R:T2). Ambiguous structures were counted as aggregates in black circles. The ssM-DNAs were not counted. The Yield of products (blue circle) is $13.7 \pm 2.4\%$ (91 as the total number). The yield of product was estimated as $y=m/n$, where m is the total number of products and n is the total number of reactants and products counted in each image. The standard error was calculated as $y\sqrt{1-y}/\sqrt{n}$, treating the yield as a Bernoulli probability ^[25]. Scale bar: 1 μm .



Supplementary Fig. 100. AFM images of M-SDR at 8h after adding T1-R M-DNA strand. Green circles indicate the intermediate-stated M-DNA. Blue circles indicate the M-DNA in final state (T1-R:T2). Ambiguous structures were counted as aggregates in black circles. The ssM-DNAs were not counted. The yield of products (blue circles) is $55 \pm 4.7\%$ (112 as the total number). The yield of product was estimated as $y=m/n$, where m is the total number of products and n is the total number of reactants and products counted in each image. The standard error was calculated as $y\sqrt{1-y}/\sqrt{n}$, treating the yield as a Bernoulli probability^[25]. Scale bar: 1 μm .

9. Supplementary Tables.

6HB-1	6HB-21	6HB-41	6HB-61	6HB-81	6HB-131	6HB-152	6HB-171
6HB-2	6HB-22	6HB-42	6HB-62	6HB-82	6HB-132	6HB-153	6HB-172
6HB-3	6HB-23	6HB-43	6HB-63	6HB-83	6HB-133	6HB-154	6HB-173
6HB-4	6HB-24	6HB-44	6HB-64	6HB-84	6HB-134	6HB-155	6HB-174
6HB-5	6HB-25	6HB-45	6HB-65	6HB-85	6HB-135	6HB-156	
6HB-6	6HB-26	6HB-46	6HB-66	6HB-86	6HB-136	6HB-157	
6HB-8	6HB-27	6HB-47	6HB-67	6HB-116	6HB-137	6HB-158	
6HB-9	6HB-28	6HB-48	6HB-68	6HB-117	6HB-139	6HB-159	
6HB-10	6HB-29	6HB-49	6HB-69	6HB-118	6HB-140	6HB-160	
6HB-11	6HB-30	6HB-50	6HB-70	6HB-119	6HB-141	6HB-161	
6HB-12	6HB-31	6HB-51	6HB-71	6HB-120	6HB-142	6HB-162	
6HB-13	6HB-32	6HB-52	6HB-73	6HB-122	6HB-143	6HB-163	
6HB-14	6HB-33	6HB-54	6HB-74	6HB-123	6HB-144	6HB-164	
6HB-15	6HB-34	6HB-55	6HB-75	6HB-124	6HB-145	6HB-165	
6HB-16	6HB-35	6HB-56	6HB-76	6HB-125	6HB-147	6HB-166	
6HB-17	6HB-36	6HB-57	6HB-77	6HB-127	6HB-148	6HB-167	
6HB-18	6HB-37	6HB-58	6HB-78	6HB-128	6HB-149	6HB-168	
6HB-19	6HB-38	6HB-59	6HB-79	6HB-129	6HB-150	6HB-169	
6HB-20	6HB-40	6HB-60	6HB-80	6HB-130	6HB-151	6HB-170	

Supplementary Table. 1. Core staple strands used for formation of parallel and antiparallel double-stranded M-DNA. Each name corresponds to one 42nt single strand DNA. Detailed sequence information can be found in Supplementary Sequence 1.

M-DNA-1	M-DNA-2	M-DNA-3
6HB-104-9	6HB-104-9'	6HB-104-2'
6HB-115-15	6HB-115-15'	6HB-115-27'
6HB-92-3	6HB-92-3'	6HB-92-1'
6HB-94-16	6HB-94-16'	6HB-94-26'
6HB-95-4	6HB-95-4'	6HB-95-14'
6HB-96-17	6HB-96-17'	6HB-96-25'
6HB-97-5	6HB-97-5'	6HB-97-13'
6HB-98-18	6HB-98-18'	6HB-98-24'
6HB-99-6	6HB-99-6'	6HB-99-12'
6HB-100-19	6HB-100-19'	6HB-100-23'
6HB-101-7	6HB-101-7'	6HB-101-11
6HB-102-20	6HB-102-20'	6HB-102-22'
6HB-103-8	6HB-103-8'	6HB-103-10'
6HB-105-21	6HB-105-21'	6HB-105-21'
6HB-106-10	6HB-106-10'	6HB-106-8'
6HB-107-22	6HB-107-22'	6HB-107-20'
6HB-108-11	6HB-108-11'	6HB-108-7'
6HB-109-23	6HB-109-23'	6HB-109-19'
6HB-110-12	6HB-110-12'	6HB-110-6'
6HB-111-24	6HB-111-24'	6HB-111-18'
6HB-112-13	6HB-112-13'	6HB-112-5'
6HB-113-25	6HB-113-25'	6HB-113-17'
6HB-114-14	6HB-114-14'	6HB-114-4'
6HB-87-26	6HB-87-26'	6HB-87-16'
6HB-88-1	6HB-88-1'	6HB-88-3'
6HB-89-27	6HB-89-27'	6HB-89-15'
6HB-90-2	6HB-90-2'	6HB-90-9'

Supplementary Table. 2. M-base DNA strands used for formation of parallel and antiparallel double-stranded M-DNA. Each of the protruding DNA has three parts. The first part is a 42-nt staple strand in the M-DNA, the second part is a 4T spacer to extend the M-base away from the M-DNA surface, and the third part is a 10-nt DNA, which acts as the M-base that hybridizes with a complementary single stranded DNA on another (or another part of the) M-DNA. The total length of the protruding DNA was 56 nt. For example, the sequence 6HB-104-9, the number 104 represents the numbering order of the staple strand, and the number 9 is the numbering of the M-bases. Detailed staple strands sequence information can be found in the Supplementary Sequence 1. Detailed 10nt M-base sequence information can be found in the Supplementary Sequence 5.

6HB-1	6HB-28	6HB-51	6HB-75	6HB-102	6HB-129	6HB-157
6HB-2	6HB-29	6HB-52	6HB-76	6HB-103	6HB-130	6HB-158
6HB-3	6HB-30	6HB-54	6HB-77	6HB-104	6HB-131	6HB-159
6HB-4	6HB-31	6HB-55	6HB-78	6HB-105	6HB-132	6HB-160
6HB-5	6HB-32	6HB-56	6HB-79	6HB-106	6HB-133	6HB-161
6HB-6	6HB-33	6HB-57	6HB-80	6HB-107	6HB-134	6HB-162
6HB-8	6HB-34	6HB-58	6HB-81	6HB-108	6HB-135	6HB-163
6HB-9	6HB-35	6HB-59	6HB-82	6HB-109	6HB-136	6HB-164
6HB-10	6HB-36	6HB-60	6HB-83	6HB-110	6HB-137	6HB-165
6HB-11	6HB-37	6HB-61	6HB-84	6HB-111	6HB-139	6HB-166
6HB-12	6HB-38	6HB-62	6HB-85	6HB-112	6HB-140	6HB-167
6HB-13	6HB-39	6HB-63	6HB-86	6HB-113	6HB-141	6HB-168
6HB-14	6HB-40	6HB-64	6HB-87	6HB-114	6HB-142	6HB-169
6HB-15	6HB-41	6HB-65	6HB-88	6HB-115	6HB-143	6HB-170
6HB-16	6HB-42	6HB-66	6HB-89	6HB-116	6HB-144	6HB-171
6HB-17	6HB-43	6HB-67	6HB-90	6HB-117	6HB-145	6HB-172
6HB-18	6HB-44	6HB-68	6HB-92	6HB-118	6HB-150	6HB-173
6HB-19	6HB-45	6HB-69	6HB-93	6HB-120	6HB-151	6HB-174
6HB-20	6HB-46	6HB-70	6HB-94	6HB-124	6HB-152	
6HB-21	6HB-47	6HB-71	6HB-95	6HB-125	6HB-153	
6HB-25	6HB-48	6HB-72	6HB-96	6HB-126	6HB-154	
6HB-26	6HB-49	6HB-73	6HB-97	6HB-127	6HB-155	
6HB-27	6HB-50	6HB-74	6HB-98	6HB-128	6HB-156	

Supplementary Table. 3. Core staple strands used for formation of left-handed double-stranded M-DNA with a twist angle of 180°. Detailed staple strands sequence information can be found in Supplementary Sequence 1.

M-DNA-1	M-DNA-2
6HB-119-2	6HB-119-2'
6HB-122-3	6HB-122-3'
6HB-123-4	6HB-123-4'
6HB-99-10	6HB-99-10'
6HB-100-11	6HB-100-11'
6HB-101-13	6HB-101-13'
6HB-22-19	6HB-22-19'
6HB-23-20	6HB-23-20'
6HB-24-21	6HB-24-21'
6HB-147-27	6HB-147-27'
6HB-148-28	6HB-148-28'
6HB-149-29	6HB-149-29'

Supplementary Table. 4. Protruding DNA strands used for formation of left-handed double-stranded M-DNA with a twist angle of 180°. Detailed staple strands sequence information can be found in Supplementary Sequence 1. Detailed 10nt M-base sequence information can be found in Supplementary Sequence 5.

6HB-1	6HB-28	6HB-55	6HB-78	6HB-108	6HB-134	6HB-160
6HB-2	6HB-29	6HB-56	6HB-79	6HB-109	6HB-135	6HB-161
6HB-3	6HB-30	6HB-57	6HB-80	6HB-110	6HB-136	6HB-162
6HB-4	6HB-33	6HB-58	6HB-81	6HB-111	6HB-139	6HB-163
6HB-5	6HB-35	6HB-59	6HB-82	6HB-112	6HB-140	6HB-164
6HB-6	6HB-36	6HB-60	6HB-83	6HB-113	6HB-141	6HB-165
6HB-8	6HB-37	6HB-61	6HB-87	6HB-114	6HB-142	6HB-169
6HB-9	6HB-38	6HB-62	6HB-88	6HB-115	6HB-143	6HB-170
6HB-10	6HB-39	6HB-63	6HB-89	6HB-116	6HB-144	6HB-171
6HB-11	6HB-40	6HB-64	6HB-90	6HB-117	6HB-145	6HB-172
6HB-12	6HB-41	6HB-65	6HB-92	6HB-118	6HB-147	6HB-173
6HB-13	6HB-42	6HB-66	6HB-93	6HB-120	6HB-148	6HB-174
6HB-14	6HB-43	6HB-67	6HB-94	6HB-123	6HB-149	
6HB-18	6HB-44	6HB-68	6HB-95	6HB-124	6HB-150	
6HB-19	6HB-45	6HB-69	6HB-99	6HB-125	6HB-151	
6HB-20	6HB-46	6HB-70	6HB-100	6HB-126	6HB-152	
6HB-21	6HB-47	6HB-71	6HB-101	6HB-127	6HB-153	
6HB-22	6HB-48	6HB-72	6HB-102	6HB-128	6HB-154	
6HB-23	6HB-49	6HB-73	6HB-103	6HB-129	6HB-155	
6HB-24	6HB-50	6HB-74	6HB-104	6HB-130	6HB-156	
6HB-25	6HB-51	6HB-75	6HB-105	6HB-131	6HB-157	
6HB-26	6HB-52	6HB-76	6HB-106	6HB-132	6HB-158	
6HB-27	6HB-54	6HB-77	6HB-107	6HB-133	6HB-159	

Supplementary Table. 5. Core staple strands used for formation of left-handed double-stranded M-DNA with a twist angle of 300°. Detailed staple strands sequence information can be found in Supplementary Sequence 1.

M-DNA-1	M-DNA-2
6HB-137-1	6HB-137-1'
6HB-119-2	6HB-119-2'
6HB-122-3	6HB-122-3'
6HB-96-4	6HB-96-4'
6HB-97-5	6HB-97-5'
6HB-98-6	6HB-98-6'
6HB-15-7	6HB-15-7'
6HB-16-8	6HB-16-8'
6HB-17-9	6HB-17-9'
6HB-166-10	6HB-166-10'
6HB-167-11	6HB-167-11'
6HB-168-13	6HB-168-13'
6HB-84-14	6HB-84-14'
6HB-85-15	6HB-85-15'
6HB-86-16	6HB-86-16'
6HB-31-17	6HB-31-17'
6HB-32-18	6HB-32-18'
6HB-34-19	6HB-34-19'

Supplementary Table. 6. Protruding DNA strands used for formation of left-handed double-stranded M-DNA with a twist angle of 300° . Detailed staple strands sequence information can be found in Supplementary Sequence 1. Detailed 10nt M-base sequence information can be found in Supplementary Sequence 5.

6HB-2	6HB-29	6HB-55	6HB-80	6HB-106	6HB-133	6HB-165
6HB-3	6HB-30	6HB-56	6HB-81	6HB-107	6HB-134	6HB-166
6HB-4	6HB-31	6HB-57	6HB-82	6HB-108	6HB-135	6HB-167
6HB-5	6HB-32	6HB-58	6HB-83	6HB-109	6HB-136	6HB-168
6HB-6	6HB-33	6HB-59	6HB-84	6HB-110	6HB-141	6HB-169
6HB-8	6HB-34	6HB-60	6HB-85	6HB-113	6HB-142	6HB-170
6HB-9	6HB-35	6HB-61	6HB-86	6HB-114	6HB-143	6HB-171
6HB-12	6HB-36	6HB-62	6HB-87	6HB-115	6HB-144	6HB-172
6HB-13	6HB-37	6HB-63	6HB-88	6HB-116	6HB-145	6HB-173
6HB-14	6HB-38	6HB-64	6HB-89	6HB-117	6HB-147	6HB-174
6HB-15	6HB-39	6HB-65	6HB-90	6HB-118	6HB-148	
6HB-16	6HB-40	6HB-66	6HB-93	6HB-119	6HB-151	
6HB-17	6HB-41	6HB-67	6HB-95	6HB-120	6HB-152	
6HB-18	6HB-42	6HB-68	6HB-96	6HB-122	6HB-153	
6HB-19	6HB-43	6HB-69	6HB-97	6HB-123	6HB-154	
6HB-20	6HB-44	6HB-70	6HB-98	6HB-124	6HB-155	
6HB-21	6HB-45	6HB-71	6HB-99	6HB-125	6HB-156	
6HB-22	6HB-46	6HB-72	6HB-100	6HB-127	6HB-157	
6HB-23	6HB-49	6HB-73	6HB-101	6HB-128	6HB-160	
6HB-24	6HB-50	6HB-76	6HB-102	6HB-129	6HB-161	
6HB-25	6HB-51	6HB-77	6HB-103	6HB-130	6HB-162	
6HB-26	6HB-52	6HB-78	6HB-104	6HB-131	6HB-163	
6HB-27	6HB-54	6HB-79	6HB-105	6HB-132	6HB-164	

Supplementary Table. 7. Core staple strands used for formation of left-handed double-stranded M-DNA with a twist angle of 540° . Detailed staple strands sequence information can be found in Supplementary Sequence 1.

M-DNA-1	M-DNA-2
6HB-126-1	6HB-126-1'
6HB-137-2	6HB-137-2'
6HB-92-3	6HB-92-3'
6HB-94-4	6HB-94-4'
6HB-10-5	6HB-10-5'
6HB-11-6	6HB-11-6'
6HB-158-7	6HB-158-7'
6HB-159-8	6HB-159-8'
6HB-74-9	6HB-74-9'
6HB-75-10	6HB-75-10'
6HB-47-11	6HB-47-11'
6HB-48-13	6HB-48-13'
6HB-139-14	6HB-139-14'
6HB-140-15	6HB-140-15'
6HB-111-16	6HB-111-16'
6HB-112-17	6HB-112-17'
6HB-28-18	6HB-28-18'
6HB-1-19	6HB-1-19'
6HB-149-20	6HB-149-20'
6HB-150-21	6HB-150-21'

Supplementary Table. 8. Protruding DNA strands used for formation of left-handed double-stranded M-DNA with a twist angle of 540° . Detailed staple strands sequence information can be found in Supplementary Sequence 1. Detailed 10nt M-base sequence information can be found in Supplementary Sequence 5.

6HB-1	6HB-27	6HB-52	6HB-78	6HB-102	6HB-127	6HB-153
6HB-2	6HB-28	6HB-54	6HB-79	6HB-103	6HB-128	6HB-154
6HB-3	6HB-29	6HB-55	6HB-80	6HB-104	6HB-129	6HB-155
6HB-4	6HB-30	6HB-56	6HB-81	6HB-105	6HB-130	6HB-156
6HB-5	6HB-31	6HB-57	6HB-82	6HB-106	6HB-131	6HB-159
6HB-6	6HB-33	6HB-58	6HB-83	6HB-107	6HB-132	6HB-160
6HB-8	6HB-35	6HB-59	6HB-84	6HB-110	6HB-133	6HB-161
6HB-9	6HB-36	6HB-62	6HB-85	6HB-111	6HB-134	6HB-162
6HB-12	6HB-37	6HB-63	6HB-86	6HB-112	6HB-139	6HB-163
6HB-13	6HB-38	6HB-64	6HB-87	6HB-113	6HB-140	6HB-164
6HB-14	6HB-39	6HB-65	6HB-88	6HB-114	6HB-141	6HB-165
6HB-15	6HB-40	6HB-66	6HB-89	6HB-115	6HB-142	6HB-166
6HB-16	6HB-41	6HB-67	6HB-90	6HB-116	6HB-143	6HB-167
6HB-17	6HB-42	6HB-68	6HB-93	6HB-117	6HB-144	6HB-168
6HB-18	6HB-43	6HB-69	6HB-95	6HB-118	6HB-145	6HB-169
6HB-19	6HB-44	6HB-70	6HB-96	6HB-120	6HB-147	6HB-170
6HB-20	6HB-47	6HB-71	6HB-97	6HB-122	6HB-148	6HB-171
6HB-21	6HB-48	6HB-72	6HB-98	6HB-123	6HB-149	6HB-172
6HB-22	6HB-49	6HB-75	6HB-99	6HB-124	6HB-150	
6HB-23	6HB-50	6HB-76	6HB-100	6HB-125	6HB-151	
6HB-24	6HB-51	6HB-77	6HB-101	6HB-126	6HB-152	

Supplementary Table. 9. Core staple strands used for formation of left-handed double-stranded M-DNA with a twist angle of 660° . Detailed staple strands sequence information can be found in Supplementary Sequence 1.

M-DNA-1	M-DNA-2
6HB-137-1	6HB-137-1'
6HB-119-2	6HB-119-2'
6HB-92-3	6HB-92-3'
6HB-94-4	6HB-94-4'
6HB-10-5	6HB-10-5'
6HB-11-6	6HB-11-6'
6HB-157-7	6HB-157-7'
6HB-158-8	6HB-158-8'
6HB-73-9	6HB-73-9'
6HB-74-10	6HB-74-10'
6HB-45-11	6HB-45-11'
6HB-46-13	6HB-46-13'
6HB-135-14	6HB-135-14'
6HB-136-15	6HB-136-15'
6HB-108-16	6HB-108-16'
6HB-109-17	6HB-109-17'
6HB-25-18	6HB-25-18'
6HB-26-19	6HB-26-19'
6HB-173-20	6HB-173-20'
6HB-174-21	6HB-174-21'
6HB-60-22	6HB-60-22'
6HB-61-23	6HB-61-23'
6HB-32-24	6HB-32-24'
6HB-34-25	6HB-34-25'

Supplementary Table. 10. Protruding DNA strands used for formation of left-handed double-stranded M-DNA with a twist angle of 660° . Detailed staple strands sequence information can be found in Supplementary Sequence 1. Detailed 10nt M-base sequence information can be found in Supplementary Sequence 5.

6HB-1	6HB-27	6HB-56	6HB-84	6HB-110	6HB-140	6HB-169
6HB-2	6HB-28	6HB-57	6HB-85	6HB-111	6HB-141	6HB-170
6HB-3	6HB-29	6HB-58	6HB-86	6HB-112	6HB-142	6HB-171
6HB-4	6HB-30	6HB-59	6HB-87	6HB-113	6HB-143	6HB-172
6HB-5	6HB-31	6HB-60	6HB-88	6HB-114	6HB-144	6HB-173
6HB-6	6HB-32	6HB-61	6HB-89	6HB-115	6HB-145	6HB-174
6HB-8	6HB-33	6HB-62	6HB-90	6HB-116	6HB-150	
6HB-9	6HB-34	6HB-63	6HB-92	6HB-117	6HB-151	
6HB-10	6HB-35	6HB-64	6HB-93	6HB-118	6HB-152	
6HB-11	6HB-36	6HB-65	6HB-94	6HB-120	6HB-153	
6HB-12	6HB-37	6HB-66	6HB-95	6HB-124	6HB-154	
6HB-13	6HB-38	6HB-67	6HB-96	6HB-125	6HB-155	
6HB-14	6HB-39	6HB-68	6HB-97	6HB-126	6HB-156	
6HB-15	6HB-40	6HB-69	6HB-98	6HB-127	6HB-157	
6HB-16	6HB-41	6HB-70	6HB-99	6HB-128	6HB-158	
6HB-17	6HB-45	6HB-71	6HB-100	6HB-129	6HB-159	
6HB-18	6HB-46	6HB-72	6HB-101	6HB-130	6HB-160	
6HB-19	6HB-47	6HB-73	6HB-102	6HB-131	6HB-161	
6HB-20	6HB-48	6HB-74	6HB-103	6HB-132	6HB-162	
6HB-21	6HB-49	6HB-75	6HB-104	6HB-133	6HB-163	
6HB-22	6HB-50	6HB-76	6HB-105	6HB-134	6HB-164	
6HB-23	6HB-51	6HB-77	6HB-106	6HB-135	6HB-165	
6HB-24	6HB-52	6HB-78	6HB-107	6HB-136	6HB-166	
6HB-25	6HB-54	6HB-82	6HB-108	6HB-137	6HB-167	
6HB-26	6HB-55	6HB-83	6HB-109	6HB-139	6HB-168	

Supplementary Table. 11. Core staple strands used for formation of right-handed double-stranded M-DNA with a twist angle of 180°. Detailed staple strands sequence information can be found in Supplementary Sequence 1.

M-DNA-1	M-DNA-2
6HB-119-2	6HB-119-2'
6HB-122-3	6HB-122-3'
6HB-123-4	6HB-123-4'
6HB-42-10	6HB-42-10'
6HB-43-11	6HB-43-11'
6HB-44-13	6HB-44-13'
6HB-79-19	6HB-79-19'
6HB-80-20	6HB-80-20'
6HB-81-21	6HB-81-21'
6HB-147-27	6HB-147-27'
6HB-148-28	6HB-148-28'
6HB-149-29	6HB-149-29'

Supplementary Table. 12. Protruding DNA strands used for formation of right-handed double-stranded M-DNA with a twist angle of 180° . Detailed staple strands sequence information can be found in the Supplementary Sequence 1. Detailed 10nt M-base sequence information can be found in the Supplementary Sequence 5.

6HB-1	6HB-28	6HB-55	6HB-81	6HB-108	6HB-134	6HB-160
6HB-2	6HB-29	6HB-56	6HB-82	6HB-109	6HB-135	6HB-161
6HB-3	6HB-30	6HB-57	6HB-83	6HB-110	6HB-136	6HB-162
6HB-4	6HB-31	6HB-58	6HB-84	6HB-111	6HB-139	6HB-163
6HB-5	6HB-32	6HB-59	6HB-85	6HB-112	6HB-140	6HB-164
6HB-6	6HB-33	6HB-60	6HB-86	6HB-113	6HB-141	6HB-168
6HB-8	6HB-34	6HB-61	6HB-90	6HB-114	6HB-142	6HB-169
6HB-9	6HB-35	6HB-62	6HB-92	6HB-115	6HB-143	6HB-170
6HB-10	6HB-36	6HB-63	6HB-93	6HB-116	6HB-144	6HB-171
6HB-11	6HB-39	6HB-64	6HB-94	6HB-117	6HB-145	6HB-172
6HB-12	6HB-41	6HB-65	6HB-95	6HB-118	6HB-147	6HB-173
6HB-13	6HB-42	6HB-66	6HB-96	6HB-120	6HB-148	6HB-174
6HB-14	6HB-43	6HB-67	6HB-97	6HB-123	6HB-149	
6HB-15	6HB-44	6HB-68	6HB-98	6HB-124	6HB-150	
6HB-16	6HB-45	6HB-69	6HB-99	6HB-125	6HB-151	
6HB-17	6HB-46	6HB-70	6HB-100	6HB-126	6HB-152	
6HB-18	6HB-47	6HB-71	6HB-101	6HB-127	6HB-153	
6HB-19	6HB-48	6HB-72	6HB-102	6HB-128	6HB-154	
6HB-20	6HB-49	6HB-76	6HB-103	6HB-129	6HB-155	
6HB-21	6HB-50	6HB-77	6HB-104	6HB-130	6HB-156	
6HB-22	6HB-51	6HB-78	6HB-105	6HB-131	6HB-157	
6HB-23	6HB-52	6HB-79	6HB-106	6HB-132	6HB-158	
6HB-24	6HB-54	6HB-80	6HB-107	6HB-133	6HB-159	

Supplementary Table. 13. Core staple strands used for formation of right-handed double-stranded M-DNA with a twist angle of 300°. Detailed staple strands sequence information can be found in Supplementary Sequence 1.

M-DNA-1	M-DNA-2
6HB-137-1	6HB-137-1'
6HB-119-2	6HB-119-2'
6HB-122-3	6HB-122-3'
6HB-37-4	6HB-37-4'
6HB-38-5	6HB-38-5'
6HB-40-6	6HB-40-6'
6HB-73-7	6HB-73-7'
6HB-74-8	6HB-74-8'
6HB-75-9	6HB-75-9'
6HB-165-10	6HB-165-10'
6HB-166-11	6HB-166-11'
6HB-167-13	6HB-167-13'
6HB-25-14	6HB-25-14'
6HB-26-15	6HB-26-15'
6HB-27-16	6HB-27-16'
6HB-87-17	6HB-87-17'
6HB-88-18	6HB-88-18'
6HB-89-19	6HB-89-19'

Supplementary Table. 14. Protruding DNA strands used for formation of right-handed double-stranded M-DNA with a twist angle of 300° . Detailed staple strands sequence information can be found in the Supplementary Sequence 1. Detailed 10nt M-base sequence information can be found in the Supplementary Sequence 5.

6HB-1	6HB-27	6HB-52	6HB-81	6HB-108	6HB-133	6HB-165
6HB-2	6HB-28	6HB-56	6HB-82	6HB-109	6HB-134	6HB-166
6HB-3	6HB-29	6HB-57	6HB-83	6HB-110	6HB-135	6HB-167
6HB-4	6HB-30	6HB-58	6HB-84	6HB-111	6HB-136	6HB-168
6HB-5	6HB-31	6HB-60	6HB-85	6HB-112	6HB-141	6HB-169
6HB-6	6HB-32	6HB-61	6HB-87	6HB-113	6HB-142	6HB-170
6HB-8	6HB-33	6HB-62	6HB-88	6HB-114	6HB-143	6HB-171
6HB-9	6HB-34	6HB-63	6HB-89	6HB-115	6HB-144	6HB-172
6HB-10	6HB-37	6HB-64	6HB-90	6HB-116	6HB-145	6HB-173
6HB-11	6HB-38	6HB-65	6HB-92	6HB-117	6HB-147	6HB-174
6HB-12	6HB-39	6HB-66	6HB-93	6HB-118	6HB-150	
6HB-13	6HB-40	6HB-67	6HB-94	6HB-120	6HB-151	
6HB-14	6HB-41	6HB-70	6HB-95	6HB-122	6HB-152	
6HB-15	6HB-42	6HB-71	6HB-96	6HB-123	6HB-153	
6HB-18	6HB-43	6HB-72	6HB-97	6HB-124	6HB-154	
6HB-19	6HB-44	6HB-73	6HB-98	6HB-125	6HB-155	
6HB-20	6HB-45	6HB-74	6HB-99	6HB-126	6HB-156	
6HB-21	6HB-46	6HB-75	6HB-100	6HB-127	6HB-157	
6HB-22	6HB-47	6HB-76	6HB-101	6HB-128	6HB-160	
6HB-23	6HB-48	6HB-77	6HB-102	6HB-129	6HB-161	
6HB-24	6HB-49	6HB-78	6HB-103	6HB-130	6HB-162	
6HB-25	6HB-50	6HB-79	6HB-104	6HB-131	6HB-163	
6HB-26	6HB-51	6HB-80	6HB-107	6HB-132	6HB-164	

Supplementary Table. 15. Core staple strands used for formation of right-handed double-stranded M-DNA with a twist angle of 540°. Detailed staple strands sequence information can be found in the Supplementary Sequence 1.

M-DNA-1	M-DNA-2
6HB-137-1	6HB-137-1'
6HB-119-2	6HB-119-2'
6HB-35-3	6HB-35-3'
6HB-36-4	6HB-36-4'
6HB-68-5	6HB-68-5'
6HB-69-6	6HB-69-6'
6HB-158-7	6HB-158-7'
6HB-159-8	6HB-159-8'
6HB-16-9	6HB-16-9'
6HB-17-10	6HB-17-10'
6HB-105-11	6HB-105-11'
6HB-106-13	6HB-106-13'
6HB-139-14	6HB-139-14'
6HB-140-15	6HB-140-15'
6HB-54-16	6HB-54-16'
6HB-55-17	6HB-55-17'
6HB-86-18	6HB-86-18'
6HB-59-19	6HB-59-19'
6HB-148-20	6HB-148-20'
6HB-149-21	6HB-149-21'

Supplementary Table. 16. Protruding DNA strands used for formation of right-handed double-stranded M-DNA with a twist angle of 540° . Detailed staple strands sequence information can be found in supplementary Sequence 1. Detailed 10nt M-base sequence information can be found in Supplementary Sequence 5.

6HB-3	6HB-29	6HB-57	6HB-83	6HB-112	6HB-141	6HB-167
6HB-4	6HB-30	6HB-58	6HB-85	6HB-113	6HB-142	6HB-168
6HB-5	6HB-31	6HB-59	6HB-86	6HB-114	6HB-143	6HB-169
6HB-6	6HB-32	6HB-60	6HB-87	6HB-115	6HB-144	6HB-170
6HB-8	6HB-33	6HB-61	6HB-88	6HB-116	6HB-145	6HB-171
6HB-9	6HB-34	6HB-62	6HB-92	6HB-117	6HB-147	6HB-174
6HB-10	6HB-37	6HB-63	6HB-93	6HB-118	6HB-148	
6HB-11	6HB-38	6HB-64	6HB-94	6HB-120	6HB-149	
6HB-12	6HB-39	6HB-65	6HB-95	6HB-122	6HB-150	
6HB-13	6HB-40	6HB-66	6HB-96	6HB-123	6HB-151	
6HB-14	6HB-41	6HB-67	6HB-97	6HB-124	6HB-152	
6HB-17	6HB-42	6HB-70	6HB-98	6HB-125	6HB-153	
6HB-18	6HB-43	6HB-71	6HB-99	6HB-126	6HB-154	
6HB-19	6HB-44	6HB-72	6HB-100	6HB-127	6HB-155	
6HB-20	6HB-45	6HB-73	6HB-101	6HB-128	6HB-156	
6HB-21	6HB-46	6HB-74	6HB-104	6HB-129	6HB-157	
6HB-22	6HB-47	6HB-75	6HB-105	6HB-130	6HB-160	
6HB-23	6HB-48	6HB-76	6HB-106	6HB-131	6HB-161	
6HB-24	6HB-50	6HB-77	6HB-107	6HB-132	6HB-162	
6HB-25	6HB-52	6HB-78	6HB-108	6HB-133	6HB-163	
6HB-26	6HB-54	6HB-79	6HB-109	6HB-136	6HB-164	
6HB-27	6HB-55	6HB-80	6HB-110	6HB-139	6HB-165	
6HB-28	6HB-56	6HB-81	6HB-111	6HB-140	6HB-166	

Supplementary Table. 17. Core staple strands used for formation of right-handed double-stranded M-DNA with a twist angle of 660° . Detailed staple strands sequence information can be found in Supplementary Sequence 1.

M-DNA-1	M-DNA-2
6HB-137-1	6HB-137-1'
6HB-119-2	6HB-119-2'
6HB-35-3	6HB-35-3'
6HB-36-4	6HB-36-4'
6HB-68-5	6HB-68-5'
6HB-69-6	6HB-69-6'
6HB-158-7	6HB-158-7'
6HB-159-8	6HB-159-8'
6HB-15-9	6HB-15-9'
6HB-16-10	6HB-16-10'
6HB-102-11	6HB-102-11'
6HB-103-13	6HB-103-13'
6HB-134-14	6HB-134-14'
6HB-135-15	6HB-135-15'
6HB-49-16	6HB-49-16'
6HB-51-17	6HB-51-17'
6HB-82-18	6HB-82-18'
6HB-84-19	6HB-84-19'
6HB-172-20	6HB-172-20'
6HB-173-21	6HB-173-21'
6HB-1-22	6HB-1-22'
6HB-2-23	6HB-2-23'
6HB-89-24	6HB-89-24'
6HB-90-25	6HB-90-25'

Supplementary Table. 18. Protruding DNA strands used for formation of right-handed double-stranded M-DNA with a twist angle of 660° . Detailed staple strands sequence information can be found in Supplementary Sequence 1. Detailed 10nt M-base sequence information can be found in Supplementary Sequence 5.

6HB-1	6HB-30	6HB-61	6HB-87	6HB-114	6HB-144	6HB-173
6HB-2	6HB-31	6HB-62	6HB-88	6HB-115	6HB-145	6HB-174
6HB-3	6HB-32	6HB-63	6HB-89	6HB-116	6HB-147	
6HB-6	6HB-34	6HB-64	6HB-90	6HB-117	6HB-150	
6HB-8	6HB-35	6HB-67	6HB-92	6HB-118	6HB-151	
6HB-9	6HB-36	6HB-68	6HB-93	6HB-119	6HB-152	
6HB-10	6HB-37	6HB-69	6HB-94	6HB-120	6HB-153	
6HB-13	6HB-38	6HB-70	6HB-95	6HB-122	6HB-156	
6HB-14	6HB-39	6HB-71	6HB-96	6HB-123	6HB-157	
6HB-15	6HB-40	6HB-72	6HB-97	6HB-124	6HB-158	
6HB-16	6HB-41	6HB-73	6HB-100	6HB-125	6HB-159	
6HB-17	6HB-42	6HB-74	6HB-101	6HB-127	6HB-160	
6HB-18	6HB-43	6HB-75	6HB-102	6HB-128	6HB-161	
6HB-19	6HB-46	6HB-78	6HB-103	6HB-129	6HB-162	
6HB-20	6HB-47	6HB-79	6HB-104	6HB-132	6HB-163	
6HB-21	6HB-48	6HB-80	6HB-105	6HB-133	6HB-164	
6HB-24	6HB-49	6HB-81	6HB-106	6HB-134	6HB-167	
6HB-25	6HB-51	6HB-82	6HB-107	6HB-135	6HB-168	
6HB-26	6HB-52	6HB-83	6HB-108	6HB-136	6HB-169	
6HB-27	6HB-54	6HB-84	6HB-111	6HB-139	6HB-170	
6HB-28	6HB-55	6HB-85	6HB-112	6HB-140	6HB-171	
6HB-29	6HB-58	6HB-86	6HB-113	6HB-141	6HB-172	

Supplementary Table. 19. Core staple strands used for formation of right-handed double-stranded M-DNA with a twist angle of 960° . Detailed staple strands sequence information can be found in Supplementary Sequence 1.

M-DNA-1	M-DNA-2
6HB-137-1	6HB-137-1'
6HB-126-2	6HB-126-2'
6HB-33-3	6HB-33-3'
6HB-50-4	6HB-50-4'
6HB-66-5	6HB-66-5'
6HB-65-6	6HB-65-6'
6HB-155-7	6HB-155-7'
6HB-154-8	6HB-154-8'
6HB-12-9	6HB-12-9'
6HB-11-10	6HB-11-10'
6HB-99-13	6HB-99-13'
6HB-98-14	6HB-98-14'
6HB-131-15	6HB-131-15'
6HB-130-16	6HB-130-16'
6HB-45-17	6HB-45-17'
6HB-44-18	6HB-44-18'
6HB-77-19	6HB-77-19'
6HB-76-20	6HB-76-20'
6HB-166-21	6HB-166-21'
6HB-165-22	6HB-165-22'
6HB-23-23	6HB-23-23'
6HB-22-24	6HB-22-24'
6HB-110-25	6HB-110-25'
6HB-109-26	6HB-109-26'
6HB-143-27	6HB-143-27'
6HB-142-28	6HB-142-28'
6HB-57-29	6HB-57-29'
6HB-56-30	6HB-56-30'
6HB-60-31	6HB-60-31'
6HB-59-32	6HB-59-32'
6HB-149-33	6HB-149-33'
6HB-148-34	6HB-148-34'
6HB-5-35	6HB-5-35'
6HB-4-36	6HB-4-36'

Supplementary Table. 20. Protruding DNA strands used for formation of right-handed double-stranded M-DNA with a twist angle of 960° . Detailed staple strands sequence information can be found in Supplementary Sequence 1. Detailed 10nt M-base sequence information can be found in Supplementary Sequence 5.

6HB-1	6HB-26	6HB-50	6HB-75	6HB-113	6HB-140	6HB-165
6HB-2	6HB-27	6HB-51	6HB-76	6HB-115	6HB-141	6HB-166
6HB-3	6HB-28	6HB-52	6HB-77	6HB-116	6HB-142	6HB-167
6HB-4	6HB-29	6HB-54	6HB-78	6HB-117	6HB-143	6HB-168
6HB-5	6HB-30	6HB-55	6HB-79	6HB-118	6HB-144	6HB-169
6HB-6	6HB-31	6HB-56	6HB-80	6HB-119	6HB-145	6HB-170
6HB-8	6HB-32	6HB-57	6HB-81	6HB-120	6HB-147	6HB-171
6HB-9	6HB-33	6HB-58	6HB-82	6HB-122	6HB-148	6HB-172
6HB-10	6HB-34	6HB-59	6HB-83	6HB-123	6HB-149	6HB-173
6HB-11	6HB-35	6HB-60	6HB-84	6HB-124	6HB-150	6HB-174
6HB-12	6HB-36	6HB-61	6HB-85	6HB-125	6HB-151	
6HB-13	6HB-37	6HB-62	6HB-86	6HB-126	6HB-152	
6HB-14	6HB-38	6HB-63	6HB-87	6HB-127	6HB-153	
6HB-15	6HB-39	6HB-64	6HB-89	6HB-128	6HB-154	
6HB-16	6HB-40	6HB-65	6HB-93	6HB-129	6HB-155	
6HB-17	6HB-41	6HB-66	6HB-94	6HB-130	6HB-156	
6HB-18	6HB-42	6HB-67	6HB-96	6HB-131	6HB-157	
6HB-19	6HB-43	6HB-68	6HB-98	6HB-132	6HB-158	
6HB-20	6HB-44	6HB-69	6HB-100	6HB-133	6HB-159	
6HB-21	6HB-45	6HB-70	6HB-102	6HB-134	6HB-160	
6HB-22	6HB-46	6HB-71	6HB-105	6HB-135	6HB-161	
6HB-23	6HB-47	6HB-72	6HB-107	6HB-136	6HB-162	
6HB-24	6HB-48	6HB-73	6HB-109	6HB-137	6HB-163	
6HB-25	6HB-49	6HB-74	6HB-111	6HB-139	6HB-164	

Supplementary Table. 21. Core staple strands used for formation of self-folded double-stranded M-DNA with 0nt flexible region. Detailed staple strands sequence information can be found in Supplementary Sequence 1.

6HB-1	6HB-26	6HB-50	6HB-75	6HB-115	6HB-142	6HB-167
6HB-2	6HB-27	6HB-51	6HB-76	6HB-116	6HB-143	6HB-168
6HB-3	6HB-28	6HB-52	6HB-77	6HB-117	6HB-144	6HB-169
6HB-4	6HB-29	6HB-54	6HB-78	6HB-118	6HB-145	6HB-170
6HB-5	6HB-30	6HB-55	6HB-79	6HB-119	6HB-147	6HB-171
6HB-6	6HB-31	6HB-56	6HB-80	6HB-120	6HB-148	6HB-172
6HB-8	6HB-32	6HB-57	6HB-81	6HB-122	6HB-149	6HB-173
6HB-9	6HB-33	6HB-58	6HB-82	6HB-123	6HB-150	6HB-174
6HB-10	6HB-34	6HB-59	6HB-83	6HB-124	6HB-151	
6HB-11	6HB-35	6HB-60	6HB-84	6HB-125	6HB-152	
6HB-12	6HB-36	6HB-61	6HB-85	6HB-126	6HB-153	
6HB-13	6HB-37	6HB-62	6HB-86	6HB-127	6HB-154	
6HB-14	6HB-38	6HB-63	6HB-87	6HB-128	6HB-155	
6HB-15	6HB-39	6HB-64	6HB-89	6HB-129	6HB-156	
6HB-16	6HB-40	6HB-65	6HB-93	6HB-130	6HB-157	
6HB-17	6HB-41	6HB-66	6HB-94	6HB-131	6HB-158	
6HB-18	6HB-42	6HB-67	6HB-96	6HB-132	6HB-159	
6HB-19	6HB-43	6HB-68	6HB-98	6HB-133	6HB-160	
6HB-20	6HB-44	6HB-69	6HB-100	6HB-135	6HB-161	
6HB-21	6HB-45	6HB-70	6HB-102	6HB-136	6HB-162	
6HB-22	6HB-46	6HB-71	6HB-107	6HB-137	6HB-163	
6HB-23	6HB-47	6HB-72	6HB-109	6HB-139	6HB-164	
6HB-24	6HB-48	6HB-73	6HB-111	6HB-140	6HB-165	
6HB-25	6HB-49	6HB-74	6HB-113	6HB-141	6HB-166	

Supplementary Table. 22. Core staple strands used for formation of self-folded double-stranded M-DNA with 14nt flexible region. Detailed staple strands sequence information can be found in Supplementary Sequence 1.

6HB-1	6HB-26	6HB-50	6HB-74	6HB-113	6HB-140	6HB-165
6HB-2	6HB-27	6HB-51	6HB-75	6HB-115	6HB-141	6HB-166
6HB-3	6HB-28	6HB-52	6HB-76	6HB-116	6HB-142	6HB-167
6HB-4	6HB-29	6HB-54	6HB-78	6HB-117	6HB-143	6HB-168
6HB-5	6HB-30	6HB-55	6HB-79	6HB-118	6HB-144	6HB-169
6HB-6	6HB-31	6HB-56	6HB-80	6HB-119	6HB-145	6HB-170
6HB-8	6HB-32	6HB-57	6HB-81	6HB-120	6HB-147	6HB-171
6HB-9	6HB-33	6HB-58	6HB-82	6HB-122	6HB-148	6HB-172
6HB-10	6HB-34	6HB-59	6HB-83	6HB-123	6HB-149	6HB-173
6HB-11	6HB-35	6HB-60	6HB-84	6HB-124	6HB-150	6HB-174
6HB-12	6HB-36	6HB-61	6HB-85	6HB-125	6HB-151	
6HB-13	6HB-37	6HB-62	6HB-86	6HB-126	6HB-152	
6HB-14	6HB-38	6HB-63	6HB-87	6HB-127	6HB-153	
6HB-15	6HB-39	6HB-64	6HB-89	6HB-128	6HB-154	
6HB-16	6HB-40	6HB-65	6HB-93	6HB-129	6HB-155	
6HB-17	6HB-41	6HB-66	6HB-94	6HB-130	6HB-156	
6HB-18	6HB-42	6HB-67	6HB-96	6HB-131	6HB-157	
6HB-20	6HB-43	6HB-68	6HB-98	6HB-132	6HB-158	
6HB-21	6HB-44	6HB-69	6HB-100	6HB-133	6HB-159	
6HB-22	6HB-45	6HB-70	6HB-102	6HB-135	6HB-160	
6HB-23	6HB-46	6HB-71	6HB-107	6HB-136	6HB-161	
6HB-24	6HB-48	6HB-72	6HB-109	6HB-137	6HB-162	
6HB-25	6HB-49	6HB-73	6HB-111	6HB-139	6HB-163	

Supplementary Table. 23. Core staple strands used for formation of self-folded double-stranded M-DNA with 42nt flexible region. Detailed staple strands sequence information can be found in Supplementary Sequence 1.

6HB-1	6HB-26	6HB-50	6HB-73	6HB-111	6HB-137	6HB-161
6HB-2	6HB-27	6HB-51	6HB-74	6HB-113	6HB-139	6HB-162
6HB-3	6HB-28	6HB-52	6HB-75	6HB-115	6HB-140	6HB-163
6HB-4	6HB-29	6HB-54	6HB-78	6HB-116	6HB-141	6HB-166
6HB-5	6HB-30	6HB-55	6HB-79	6HB-117	6HB-142	6HB-167
6HB-6	6HB-31	6HB-56	6HB-80	6HB-118	6HB-143	6HB-168
6HB-8	6HB-32	6HB-57	6HB-81	6HB-119	6HB-144	6HB-169
6HB-9	6HB-33	6HB-58	6HB-82	6HB-120	6HB-145	6HB-170
6HB-10	6HB-34	6HB-59	6HB-83	6HB-122	6HB-147	6HB-171
6HB-11	6HB-35	6HB-60	6HB-84	6HB-123	6HB-148	6HB-172
6HB-12	6HB-36	6HB-61	6HB-85	6HB-124	6HB-149	6HB-173
6HB-13	6HB-37	6HB-62	6HB-86	6HB-125	6HB-150	6HB-174
6HB-14	6HB-38	6HB-63	6HB-87	6HB-126	6HB-151	
6HB-15	6HB-39	6HB-64	6HB-89	6HB-127	6HB-152	
6HB-16	6HB-40	6HB-65	6HB-93	6HB-128	6HB-153	
6HB-17	6HB-41	6HB-66	6HB-94	6HB-129	6HB-154	
6HB-18	6HB-42	6HB-67	6HB-96	6HB-130	6HB-155	
6HB-21	6HB-43	6HB-68	6HB-98	6HB-131	6HB-156	
6HB-22	6HB-44	6HB-69	6HB-100	6HB-132	6HB-157	
6HB-23	6HB-45	6HB-70	6HB-102	6HB-133	6HB-158	
6HB-24	6HB-48	6HB-71	6HB-107	6HB-135	6HB-159	
6HB-25	6HB-49	6HB-72	6HB-109	6HB-136	6HB-160	

Supplementary Table. 24. Core staple strands used for formation of self-folded double-stranded M-DNA with 72nt flexible region. Detailed staple strands sequence information can be found in Supplementary Sequence 1.

6HB-1	6HB-26	6HB-50	6HB-73	6HB-111	6HB-140	6HB-163
6HB-2	6HB-27	6HB-51	6HB-74	6HB-113	6HB-141	6HB-166
6HB-3	6HB-28	6HB-52	6HB-75	6HB-115	6HB-142	6HB-167
6HB-4	6HB-29	6HB-54	6HB-78	6HB-116	6HB-143	6HB-168
6HB-5	6HB-30	6HB-55	6HB-79	6HB-117	6HB-144	6HB-169
6HB-6	6HB-31	6HB-56	6HB-80	6HB-118	6HB-145	6HB-170
6HB-8	6HB-32	6HB-57	6HB-81	6HB-119	6HB-147	6HB-171
6HB-9	6HB-33	6HB-58	6HB-82	6HB-120	6HB-148	6HB-172
6HB-10	6HB-34	6HB-59	6HB-83	6HB-122	6HB-149	6HB-173
6HB-11	6HB-35	6HB-60	6HB-84	6HB-123	6HB-150	6HB-174
6HB-12	6HB-36	6HB-61	6HB-85	6HB-124	6HB-151	
6HB-13	6HB-37	6HB-62	6HB-86	6HB-125	6HB-152	
6HB-14	6HB-38	6HB-63	6HB-87	6HB-126	6HB-153	
6HB-15	6HB-39	6HB-64	6HB-89	6HB-127	6HB-154	
6HB-16	6HB-40	6HB-65	6HB-93	6HB-128	6HB-155	
6HB-17	6HB-41	6HB-66	6HB-94	6HB-129	6HB-156	
6HB-18	6HB-42	6HB-67	6HB-96	6HB-130	6HB-157	
6HB-21	6HB-43	6HB-68	6HB-98	6HB-131	6HB-158	
6HB-22	6HB-44	6HB-69	6HB-100	6HB-132	6HB-159	
6HB-23	6HB-45	6HB-70	6HB-102	6HB-136	6HB-160	
6HB-24	6HB-48	6HB-71	6HB-107	6HB-137	6HB-161	
6HB-25	6HB-49	6HB-72	6HB-109	6HB-139	6HB-162	

Supplementary Table. 25. Core staple strands used for formation of self-folded double-stranded M-DNA with 98nt flexible region. Detailed staple strands sequence information can be found in Supplementary Sequence 1.

6HB-1	6HB-26	6HB-51	6HB-72	6HB-115	6HB-142	6HB-167
6HB-2	6HB-27	6HB-52	6HB-73	6HB-116	6HB-143	6HB-168
6HB-3	6HB-28	6HB-54	6HB-74	6HB-117	6HB-144	6HB-169
6HB-4	6HB-29	6HB-55	6HB-80	6HB-118	6HB-145	6HB-170
6HB-5	6HB-30	6HB-56	6HB-81	6HB-119	6HB-147	6HB-171
6HB-6	6HB-31	6HB-57	6HB-82	6HB-120	6HB-148	6HB-172
6HB-8	6HB-32	6HB-58	6HB-83	6HB-122	6HB-149	6HB-173
6HB-9	6HB-33	6HB-59	6HB-84	6HB-123	6HB-150	6HB-174
6HB-10	6HB-34	6HB-60	6HB-85	6HB-124	6HB-151	
6HB-11	6HB-35	6HB-61	6HB-86	6HB-125	6HB-152	
6HB-12	6HB-36	6HB-62	6HB-87	6HB-126	6HB-153	
6HB-13	6HB-37	6HB-63	6HB-89	6HB-127	6HB-154	
6HB-14	6HB-38	6HB-64	6HB-93	6HB-128	6HB-155	
6HB-15	6HB-39	6HB-65	6HB-94	6HB-129	6HB-156	
6HB-16	6HB-40	6HB-66	6HB-96	6HB-130	6HB-157	
6HB-18	6HB-41	6HB-67	6HB-98	6HB-131	6HB-158	
6HB-22	6HB-42	6HB-68	6HB-100	6HB-137	6HB-159	
6HB-23	6HB-43	6HB-69	6HB-109	6HB-139	6HB-160	
6HB-24	6HB-44	6HB-70	6HB-111	6HB-140	6HB-161	
6HB-25	6HB-50	6HB-71	6HB-113	6HB-141	6HB-162	

Supplementary Table. 26. Core staple strands used for formation of self-folded double-stranded M-DNA with 196nt flexible region. Detailed staple strands sequence information can be found in Supplementary Sequence 1.

6HB-1	6HB-28	6HB-55	6HB-69	6HB-116	6HB-144	6HB-171
6HB-2	6HB-29	6HB-56	6HB-72	6HB-117	6HB-145	6HB-172
6HB-3	6HB-30	6HB-57	6HB-83	6HB-118	6HB-147	6HB-173
6HB-4	6HB-31	6HB-58	6HB-84	6HB-119	6HB-148	6HB-174
6HB-5	6HB-32	6HB-59	6HB-85	6HB-120	6HB-149	
6HB-6	6HB-33	6HB-60	6HB-86	6HB-122	6HB-150	
6HB-8	6HB-34	6HB-61	6HB-87	6HB-123	6HB-151	
6HB-9	6HB-35	6HB-62	6HB-89	6HB-124	6HB-152	
6HB-10	6HB-36	6HB-63	6HB-93	6HB-125	6HB-153	
6HB-11	6HB-37	6HB-64	6HB-94	6HB-126	6HB-154	
6HB-12	6HB-38	6HB-65	6HB-96	6HB-127	6HB-155	
6HB-18	6HB-39	6HB-66	6HB-98	6HB-128	6HB-156	
6HB-26	6HB-40	6HB-67	6HB-113	6HB-137	6HB-157	
6HB-27	6HB-50	6HB-68	6HB-115	6HB-143	6HB-160	

Supplementary Table. 27. Core staple strands used for formation of self-folded double-stranded M-DNA with 504nt flexible region. Detailed staple strands sequence information can be found in Supplementary Sequence 1.

6HB-1	6HB-36	6HB-62	6HB-89	6HB-145
6HB-2	6HB-37	6HB-63	6HB-93	6HB-113
6HB-3	6HB-38	6HB-64	6HB-94	6HB-115
6HB-4	6HB-28	6HB-65	6HB-96	6HB-147
6HB-5	6HB-29	6HB-66	6HB-116	6HB-148
6HB-6	6HB-30	6HB-57	6HB-117	6HB-149
6HB-8	6HB-31	6HB-58	6HB-118	6HB-150
6HB-9	6HB-32	6HB-67	6HB-119	6HB-160
6HB-10	6HB-39	6HB-68	6HB-120	6HB-171
6HB-18	6HB-50	6HB-72	6HB-122	6HB-174
6HB-33	6HB-59	6HB-83	6HB-123	
6HB-34	6HB-60	6HB-86	6HB-124	
6HB-35	6HB-61	6HB-87	6HB-125	

Supplementary Table. 28. Core staple strands used for formation of self-folded double-stranded M-DNA with 644nt flexible region. Detailed staple strands sequence information can be found in Supplementary Sequence 1.

0nt, 14nt, 42nt	70nt, 98nt, 196nt	504nt	644nt
6HB-104-9	6HB-104-9	6HB-104-9	6HB-104-9
6HB-92-3	6HB-92-3	6HB-92-3	6HB-92-3
6HB-95-4	6HB-95-4	6HB-95-4	6HB-95-4
6HB-97-5	6HB-97-5	6HB-97-5	
6HB-99-6	6HB-99-6		
6HB-101-7	6HB-101-7		
6HB-103-8			
6HB-106-8'			
6HB-108-7'	6HB-108-7'		
6HB-110-6'	6HB-110-6'		
6HB-112-5'	6HB-112-5'	6HB-112-5'	
6HB-114-4'	6HB-114-4'	6HB-114-4'	6HB-114-4'
6HB-88-3'	6HB-88-3'	6HB-88-3'	6HB-88-3'
6HB-90-9'	6HB-90-9'	6HB-90-9'	6HB-90-9'

Supplementary Table. 29. Protruding DNA strands used for formation of self-folded double-stranded M-DNA. Detailed staple strands sequence information can be found in Supplementary Sequence 1. Detailed 10nt M-base sequence information can be found in Supplementary Sequence 5.

6HB-1	6HB-26	6HB-50	6HB-74	6HB-113	6HB-140	6HB-165
6HB-2	6HB-27	6HB-51	6HB-75	6HB-115	6HB-141	6HB-166
6HB-3	6HB-28	6HB-52	6HB-76	6HB-116	6HB-142	6HB-167
6HB-4	6HB-29	6HB-54	6HB-78	6HB-117	6HB-143	6HB-168
6HB-5	6HB-30	6HB-55	6HB-79	6HB-118	6HB-144	6HB-169
6HB-6	6HB-31	6HB-56	6HB-80	6HB-119	6HB-145	6HB-170
6HB-8	6HB-32	6HB-57	6HB-81	6HB-120	6HB-147	6HB-171
6HB-9	6HB-33	6HB-58	6HB-82	6HB-122	6HB-148	6HB-172
6HB-10	6HB-34	6HB-59	6HB-83	6HB-123	6HB-149	6HB-173
6HB-11	6HB-35	6HB-60	6HB-84	6HB-124	6HB-150	6HB-174
6HB-12	6HB-36	6HB-61	6HB-85	6HB-125	6HB-151	
6HB-13	6HB-37	6HB-62	6HB-86	6HB-126	6HB-152	
6HB-14	6HB-38	6HB-63	6HB-87	6HB-127	6HB-153	
6HB-15	6HB-39	6HB-64	6HB-89	6HB-128	6HB-154	
6HB-16	6HB-40	6HB-65	6HB-93	6HB-129	6HB-155	
6HB-17	6HB-41	6HB-66	6HB-94	6HB-130	6HB-156	
6HB-18	6HB-42	6HB-67	6HB-96	6HB-131	6HB-157	
6HB-20	6HB-43	6HB-68	6HB-98	6HB-132	6HB-158	
6HB-21	6HB-44	6HB-69	6HB-100	6HB-133	6HB-159	
6HB-22	6HB-45	6HB-70	6HB-102	6HB-135	6HB-160	
6HB-23	6HB-46	6HB-71	6HB-107	6HB-136	6HB-161	
6HB-24	6HB-48	6HB-72	6HB-109	6HB-137	6HB-162	
6HB-25	6HB-49	6HB-73	6HB-111	6HB-139	6HB-163	

Supplementary Table. 30. Core staple strands used for formation of Y-shaped junction. For T-shaped junction, six removed staple strands (6HB-19, 6HB-164, 6HB-105, 6HB-134, 6HB-47, 6HB-77) were added to one of the three M-DNA to form rigid M-DNA, which led to the formation of a T-shaped junction. Detailed staple strands sequence information can be found in Supplementary Sequence 1.

Y-M-DNA-1	Y-M-DNA-2	Y-M-DNA-3
6HB-104-9	6HB-104-2'	6HB-104-34'
6HB-92-3	6HB-92-1'	6HB-92-33'
6HB-95-4	6HB-95-14'	6HB-95-32'
6HB-97-5	6HB-97-13'	6HB-97-31'
6HB-99-6	6HB-99-12'	6HB-99-30'
6HB-101-7	6HB-101-11'	6HB-101-29'
6HB-103-8	6HB-103-10'	6HB-103-28'
6HB-106-10	6HB-106-28	6HB-106-8'
6HB-108-11	6HB-108-29	6HB-108-7'
6HB-110-12	6HB-110-30	6HB-110-6'
6HB-112-13	6HB-112-31	6HB-112-5'
6HB-114-14	6HB-114-32	6HB-114-4'
6HB-88-1	6HB-88-33	6HB-88-3'
6HB-90-2	6HB-90-34	6HB-90-9'

Supplementary Table. 31. Protruding DNA strands used for formation of Y-shaped junction structures. The protruding DNA strands for T-shaped junction were the same. Detailed staple strands sequence information can be found in Supplementary Sequence 1. Detailed 10nt M-base sequence information can be found in Supplementary Sequence 5.

6HB-1	6HB-26	6HB-50	6HB-74	6HB-113	6HB-140	6HB-165
6HB-2	6HB-27	6HB-51	6HB-75	6HB-115	6HB-141	6HB-166
6HB-3	6HB-28	6HB-52	6HB-76	6HB-116	6HB-142	6HB-167
6HB-4	6HB-29	6HB-54	6HB-78	6HB-117	6HB-143	6HB-168
6HB-5	6HB-30	6HB-55	6HB-79	6HB-118	6HB-144	6HB-169
6HB-6	6HB-31	6HB-56	6HB-80	6HB-119	6HB-145	6HB-170
6HB-8	6HB-32	6HB-57	6HB-81	6HB-120	6HB-147	6HB-171
6HB-9	6HB-33	6HB-58	6HB-82	6HB-122	6HB-148	6HB-172
6HB-10	6HB-34	6HB-59	6HB-83	6HB-123	6HB-149	6HB-173
6HB-11	6HB-35	6HB-60	6HB-84	6HB-124	6HB-150	6HB-174
6HB-12	6HB-36	6HB-61	6HB-85	6HB-125	6HB-151	
6HB-13	6HB-37	6HB-62	6HB-86	6HB-126	6HB-152	
6HB-14	6HB-38	6HB-63	6HB-87	6HB-127	6HB-153	
6HB-15	6HB-39	6HB-64	6HB-89	6HB-128	6HB-154	
6HB-16	6HB-40	6HB-65	6HB-93	6HB-129	6HB-155	
6HB-17	6HB-41	6HB-66	6HB-94	6HB-130	6HB-156	
6HB-18	6HB-42	6HB-67	6HB-96	6HB-131	6HB-157	
6HB-20	6HB-43	6HB-68	6HB-98	6HB-132	6HB-158	
6HB-21	6HB-44	6HB-69	6HB-100	6HB-133	6HB-159	
6HB-22	6HB-45	6HB-70	6HB-102	6HB-135	6HB-160	
6HB-23	6HB-46	6HB-71	6HB-107	6HB-136	6HB-161	
6HB-24	6HB-48	6HB-72	6HB-109	6HB-137	6HB-162	
6HB-25	6HB-49	6HB-73	6HB-111	6HB-139	6HB-163	

Supplementary Table. 32. Core staple strands used for formation of X-shaped junction. For K-shaped junction, six removed staple strands (6HB-19, 6HB-164, 6HB-105, 6HB-134, 6HB-47, 6HB-77) were added to one of the four M-DNA to form rigid M-DNA, which led to the formation of a K-shaped junction. Detailed staple strands sequence information can be found in Supplementary Sequence 1.

X-M-DNA-1	X-M-DNA-2	X-M-DNA-3	X-M-DNA-4
6HB-104-9	6HB-104-2'	6HB-104-34'	6HB-104-41'
6HB-92-3	6HB-92-1'	6HB-92-33'	6HB-92-40'
6HB-95-4	6HB-95-14'	6HB-95-32'	6HB-95-39'
6HB-97-5	6HB-97-13'	6HB-97-31'	6HB-97-38'
6HB-99-6	6HB-99-12'	6HB-99-30'	6HB-99-37'
6HB-101-7	6HB-101-11'	6HB-101-29'	6HB-101-36'
6HB-103-8	6HB-103-10'	6HB-103-28'	6HB-103-35'
6HB-106-10	6HB-106-28	6HB-106-35	6HB-106-8'
6HB-108-11	6HB-108-29	6HB-108-36	6HB-108-7'
6HB-110-12	6HB-110-30	6HB-110-37	6HB-110-6'
6HB-112-13	6HB-112-31	6HB-112-38	6HB-112-5'
6HB-114-14	6HB-114-32	6HB-114-39	6HB-114-4'
6HB-88-1	6HB-88-33	6HB-88-40	6HB-88-3'
6HB-90-2	6HB-90-34	6HB-90-41	6HB-90-9'

Supplementary Table. 33. Protruding DNA strands used for formation of X-shaped junction structures. The protruding DNA strands were the same for the K-shaped junction. Detailed staple strands sequence information can be found in Supplementary Sequence 1. Detailed 10nt M-base sequence information can be found in Supplementary Sequence 5.

6HB-1	6HB-26	6HB-50	6HB-75	6HB-111	6HB-137	6HB-163
6HB-2	6HB-27	6HB-51	6HB-76	6HB-112	6HB-139	6HB-164
6HB-3	6HB-28	6HB-52	6HB-77	6HB-113	6HB-140	6HB-165
6HB-4	6HB-29	6HB-54	6HB-78	6HB-115	6HB-141	6HB-166
6HB-5	6HB-30	6HB-55	6HB-79	6HB-116	6HB-142	6HB-167
6HB-6	6HB-31	6HB-56	6HB-80	6HB-117	6HB-143	6HB-168
6HB-8	6HB-32	6HB-57	6HB-81	6HB-118	6HB-144	6HB-169
6HB-9	6HB-33	6HB-58	6HB-82	6HB-119	6HB-145	6HB-170
6HB-10	6HB-34	6HB-59	6HB-83	6HB-120	6HB-147	6HB-171
6HB-11	6HB-35	6HB-60	6HB-84	6HB-122	6HB-148	6HB-172
6HB-12	6HB-36	6HB-61	6HB-85	6HB-123	6HB-149	6HB-173
6HB-13	6HB-37	6HB-62	6HB-86	6HB-124	6HB-150	6HB-174
6HB-14	6HB-38	6HB-63	6HB-87	6HB-125	6HB-151	
6HB-15	6HB-39	6HB-64	6HB-89	6HB-126	6HB-152	
6HB-16	6HB-40	6HB-65	6HB-93	6HB-127	6HB-153	
6HB-17	6HB-41	6HB-66	6HB-94	6HB-128	6HB-154	
6HB-18	6HB-42	6HB-67	6HB-96	6HB-129	6HB-155	
6HB-19	6HB-43	6HB-68	6HB-97	6HB-130	6HB-156	
6HB-20	6HB-44	6HB-69	6HB-98	6HB-131	6HB-157	
6HB-21	6HB-45	6HB-70	6HB-100	6HB-132	6HB-158	
6HB-22	6HB-46	6HB-71	6HB-102	6HB-133	6HB-159	
6HB-23	6HB-47	6HB-72	6HB-105	6HB-134	6HB-160	
6HB-24	6HB-48	6HB-73	6HB-107	6HB-135	6HB-161	
6HB-25	6HB-49	6HB-74	6HB-109	6HB-136	6HB-162	

Supplementary Table. 34. Core staple strands used for formation of DX-M-DNA-1 and DX-M-DNA-2.

Detailed staple strands sequence information can be found in Supplementary Sequence 1.

6HB-1	6HB-26	6HB-51	6HB-93	6HB-128	6HB-155
6HB-2	6HB-27	6HB-52	6HB-94	6HB-129	6HB-156
6HB-3	6HB-28	6HB-54	6HB-96	6HB-130	6HB-157
6HB-4	6HB-29	6HB-55	6HB-98	6HB-131	6HB-158
6HB-5	6HB-30	6HB-56	6HB-100	6HB-137	6HB-159
6HB-6	6HB-31	6HB-57	6HB-109	6HB-139	6HB-160
6HB-8	6HB-32	6HB-58	6HB-111	6HB-140	6HB-161
6HB-9	6HB-33	6HB-60	6HB-113	6HB-141	6HB-162
6HB-10	6HB-34	6HB-62	6HB-115	6HB-142	6HB-167
6HB-11	6HB-35	6HB-64	6HB-116	6HB-143	6HB-168
6HB-12	6HB-36	6HB-66	6HB-117	6HB-144	6HB-169
6HB-13	6HB-37	6HB-68	6HB-118	6HB-145	6HB-170
6HB-14	6HB-38	6HB-70	6HB-119	6HB-147	6HB-171
6HB-15	6HB-39	6HB-72	6HB-120	6HB-148	6HB-172
6HB-16	6HB-40	6HB-73	6HB-122	6HB-149	6HB-173
6HB-18	6HB-41	6HB-81	6HB-123	6HB-150	6HB-174
6HB-22	6HB-42	6HB-84	6HB-124	6HB-151	
6HB-23	6HB-43	6HB-86	6HB-125	6HB-152	
6HB-24	6HB-44	6HB-87	6HB-126	6HB-153	
6HB-25	6HB-50	6HB-89	6HB-127	6HB-154	

Supplementary Table. 35. Core staple strands used for formation of DX-M-DNA-3, DX-M-DNA-4 and DX-M-DNA-5. Detailed staple strands sequence information can be found in Supplementary Sequence 1.

DX-1	DX-2	DX-3	DX-4	DX-5
6HB-104-9	6HB-104-42'	6HB-104	6HB-104	6HB-104-6'
6HB-92-3	6HB-92-43'	6HB-92	6HB-92	6HB-92-7'
6HB-95-4	6HB-95-44'	6HB-95	6HB-95	6HB-95-8'
6HB-99-6	6HB-99-46'	6HB-97-34'	6HB-97-42	6HB-97-28'
6HB-101-7	6HB-101-47'	6HB-99-33'	6HB-99-43	6HB-99-29'
6HB-103-8	6HB-103-48'	6HB-101-32'	6HB-101-44	6HB-101-30'
6HB-106-28	6HB-106-35	6HB-108-39'	6HB-108-4'	6HB-108-37'
6HB-108-29	6HB-108-36	6HB-110-40'	6HB-110-3'	6HB-110-36'
6HB-110-30	6HB-110-37	6HB-112-41'	6HB-112-9'	6HB-112-35'
6HB-114-32	6HB-114-39	6HB-114	6HB-114	6HB-114-48
6HB-88-33	6HB-88-40	6HB-88	6HB-88	6HB-88-47
6HB-90-34	6HB-90-41	6HB-90	6HB-90	6HB-90-46
		6HB-83-55'	6HB-83-55'	6HB-83-55'
		6HB-65-54'	6HB-65-54'	6HB-65-54'
		6HB-67-53'	6HB-67-53'	6HB-67-53'
		6HB-69-52'	6HB-69-52'	6HB-69-52'
		6HB-71-51'	6HB-71-51'	6HB-71-51'
		6HB-74-50'	6HB-74-50'	6HB-74-50'
		6HB-76-49'	6HB-76-49'	6HB-76-49'
		6HB-78-49	6HB-78-49	6HB-78-49
		6HB-80-50	6HB-80-50	6HB-80-50
		6HB-82-51	6HB-82-51	6HB-82-51
		6HB-85-52	6HB-85-52	6HB-85-52
		6HB-59-53	6HB-59-53	6HB-59-53
		6HB-61-54	6HB-61-54	6HB-61-54
		6HB-63-55	6HB-63-55	6HB-63-55

Supplementary Table. 36. Protruding DNA strands used for formation of DX tile structures. Detailed staple strands sequence information can be found in Supplementary Sequence 1. Detailed 10nt M-base sequence information can be found in Supplementary Sequence 5.

6HB-1	6HB-26	6HB-51	6HB-77	6HB-115	6HB-142	6HB-167
6HB-2	6HB-27	6HB-52	6HB-78	6HB-116	6HB-143	6HB-168
6HB-3	6HB-28	6HB-54	6HB-79	6HB-117	6HB-144	6HB-169
6HB-4	6HB-29	6HB-55	6HB-80	6HB-118	6HB-145	6HB-170
6HB-5	6HB-30	6HB-56	6HB-81	6HB-119	6HB-147	6HB-171
6HB-6	6HB-31	6HB-57	6HB-82	6HB-120	6HB-148	6HB-172
6HB-8	6HB-32	6HB-58	6HB-83	6HB-122	6HB-149	6HB-173
6HB-9	6HB-33	6HB-59	6HB-84	6HB-123	6HB-150	6HB-174
6HB-10	6HB-34	6HB-60	6HB-85	6HB-124	6HB-151	
6HB-11	6HB-35	6HB-61	6HB-86	6HB-125	6HB-152	
6HB-12	6HB-36	6HB-62	6HB-87	6HB-126	6HB-153	
6HB-15	6HB-37	6HB-63	6HB-89	6HB-127	6HB-154	
6HB-16	6HB-38	6HB-64	6HB-93	6HB-131	6HB-155	
6HB-17	6HB-39	6HB-65	6HB-94	6HB-132	6HB-156	
6HB-18	6HB-40	6HB-66	6HB-96	6HB-133	6HB-157	
6HB-19	6HB-44	6HB-67	6HB-102	6HB-134	6HB-160	
6HB-20	6HB-45	6HB-68	6HB-105	6HB-135	6HB-161	
6HB-21	6HB-46	6HB-69	6HB-107	6HB-136	6HB-162	
6HB-22	6HB-47	6HB-72	6HB-109	6HB-137	6HB-163	
6HB-23	6HB-48	6HB-74	6HB-110	6HB-139	6HB-164	
6HB-24	6HB-49	6HB-75	6HB-111	6HB-140	6HB-165	
6HB-25	6HB-50	6HB-76	6HB-113	6HB-141	6HB-166	

Supplementary Table. 37. Core staple strands used for formation of Y-e-M-DNA-1, Y-e-M-DNA-2 and Y-e-M-DNA-3. Detailed staple strands sequence information can be found in Supplementary Sequence 1.

Y-G ₀ -1	Y-G ₀ -2	Y-G ₀ -3
6HB-104-9	6HB-104-11'	6HB-104-34'
6HB-92-3	6HB-92-10'	6HB-92-33'
6HB-95-4	6HB-95-8'	6HB-95-32'
6HB-97-5	6HB-97-7'	6HB-97-31'
6HB-101-7	6HB-101-31	6HB-101-5'
6HB-103-8	6HB-103-32	6HB-103-4'
6HB-106-10	6HB-106-33	6HB-106-3'
6HB-108-11	6HB-108-34	6HB-108-9'
6HB-112-13	6HB-112-13	6HB-112-13
6HB-114-14	6HB-114-14	6HB-114-14
6HB-88-1	6HB-88-1	6HB-88-1
6HB-90-2	6HB-90-2	6HB-90-2
Y-G ₁ -1	Y-G ₁ -2	Y-G ₁ -3
6HB-104-9	6HB-104-11'	6HB-104-34'
6HB-92-3	6HB-92-10'	6HB-92-33'
6HB-95-4	6HB-95-8'	6HB-95-32'
6HB-97-5	6HB-97-7'	6HB-97-31'
6HB-101-7	6HB-101-31	6HB-101-5'
6HB-103-8	6HB-103-32	6HB-103-4'
6HB-106-10	6HB-106-33	6HB-106-3'
6HB-108-11	6HB-108-34	6HB-108-9'
6HB-112-2'	6HB-112	6HB-112
6HB-114-1'	6HB-114	6HB-114
6HB-88-14'	6HB-88	6HB-88
6HB-90-13'	6HB-90	6HB-90

Supplementary Table. 38. Protruding DNA strands used for formation of extensive Y-shaped junctions. Y-G₀-1, Y-G₀-2, and Y-G₀-3 formed the Y-G₀ junction, Y-G₁-1, Y-G₁-2, and Y-G₁-3 formed the Y-G₁ junction, Mixing Y-G₀ and Y-G₁ formed dendrimer Y-structures. Detailed staple strands sequence information can be found in Supplementary Sequence 1. Detailed 10nt M-base sequence information can be found in Supplementary Sequence 5.

6HB-1	6HB-26	6HB-50	6HB-92	6HB-127	6HB-155
6HB-2	6HB-27	6HB-51	6HB-94	6HB-131	6HB-156
6HB-3	6HB-28	6HB-56	6HB-95	6HB-132	6HB-157
6HB-4	6HB-29	6HB-57	6HB-96	6HB-133	6HB-160
6HB-5	6HB-30	6HB-58	6HB-97	6HB-134	6HB-161
6HB-6	6HB-31	6HB-59	6HB-102	6HB-135	6HB-162
6HB-8	6HB-32	6HB-60	6HB-104	6HB-136	6HB-163
6HB-9	6HB-33	6HB-61	6HB-105	6HB-137	6HB-164
6HB-10	6HB-34	6HB-62	6HB-107	6HB-139	6HB-165
6HB-11	6HB-35	6HB-63	6HB-113	6HB-143	6HB-166
6HB-12	6HB-36	6HB-64	6HB-115	6HB-144	6HB-167
6HB-15	6HB-37	6HB-66	6HB-116	6HB-145	6HB-168
6HB-16	6HB-38	6HB-68	6HB-117	6HB-147	6HB-171
6HB-17	6HB-40	6HB-75	6HB-118	6HB-148	6HB-172
6HB-18	6HB-44	6HB-77	6HB-119	6HB-149	6HB-173
6HB-19	6HB-45	6HB-79	6HB-120	6HB-150	6HB-174
6HB-20	6HB-46	6HB-85	6HB-122	6HB-151	
6HB-21	6HB-47	6HB-86	6HB-123	6HB-152	
6HB-22	6HB-48	6HB-87	6HB-124	6HB-153	
6HB-23	6HB-49	6HB-89	6HB-125	6HB-154	

Supplementary Table. 39. Core staple strands used for formation of self-folded three-segments. Detailed staple strands sequence information can be found in Supplementary Sequence 1.

M-DNA-1	M-DNA-2
6HB-101-7	6HB-101
6HB-103-8	6HB-103
6HB-106-10	6HB-106
6HB-108-11	6HB-108
6HB-112-11'	6HB-112
6HB-114-10'	6HB-114
6HB-88-8'	6HB-88
6HB-90-7'	6HB-90
6HB-83-9'	6HB-83-9'
6HB-65-3'	6HB-65-3'
6HB-67-4'	6HB-67-4'
6HB-69-5'	6HB-69-5'
6HB-74-5	6HB-74-5
6HB-76-4	6HB-76-4
6HB-78-3	6HB-78-3
6HB-80-9	6HB-80-9

Supplementary Table. 40. Protruding DNA strands used for formation of self-folded stacked (M-DNA-1) and half-stacked (M-DNA-2) three-segments. Detailed staple strands sequence information can be found in Supplementary Sequence 1. Detailed 10nt M-base sequence information can be found in Supplementary Sequence 5.

6HB-1	6HB-28	6HB-54	6HB-102	6HB-136	6HB-162
6HB-2	6HB-29	6HB-55	6HB-107	6HB-137	6HB-163
6HB-3	6HB-30	6HB-57	6HB-109	6HB-139	6HB-165
6HB-4	6HB-31	6HB-58	6HB-111	6HB-140	6HB-166
6HB-5	6HB-32	6HB-60	6HB-113	6HB-141	6HB-167
6HB-6	6HB-33	6HB-62	6HB-115	6HB-142	6HB-168
6HB-8	6HB-34	6HB-64	6HB-116	6HB-144	6HB-169
6HB-9	6HB-35	6HB-66	6HB-117	6HB-145	6HB-170
6HB-10	6HB-36	6HB-68	6HB-118	6HB-147	6HB-171
6HB-12	6HB-37	6HB-70	6HB-119	6HB-148	6HB-174
6HB-13	6HB-38	6HB-73	6HB-120	6HB-149	
6HB-14	6HB-41	6HB-75	6HB-122	6HB-150	
6HB-15	6HB-42	6HB-79	6HB-123	6HB-151	
6HB-16	6HB-43	6HB-81	6HB-124	6HB-152	
6HB-17	6HB-44	6HB-84	6HB-125	6HB-153	
6HB-18	6HB-45	6HB-86	6HB-128	6HB-154	
6HB-20	6HB-46	6HB-87	6HB-129	6HB-155	
6HB-21	6HB-48	6HB-89	6HB-130	6HB-157	
6HB-22	6HB-49	6HB-94	6HB-131	6HB-158	
6HB-23	6HB-50	6HB-96	6HB-132	6HB-159	
6HB-24	6HB-51	6HB-98	6HB-133	6HB-160	
6HB-25	6HB-52	6HB-100	6HB-135	6HB-161	

Supplementary Table. 41. Core staple strands used for formation of self-folded four-segments. Detailed staple strands sequence information can be found in Supplementary Sequence 1.

M-DNA-1	M-DNA-2
6HB-104	6HB-104
6HB-92	6HB-92
6HB-95	6HB-95
6HB-99-6	6HB-99
6HB-101-7	6HB-101
6HB-103-8	6HB-103
6HB-106-8'	6HB-106
6HB-108-7'	6HB-108
6HB-110-6'	6HB-110
6HB-114	6HB-114
6HB-88	6HB-88
6HB-90	6HB-90
6HB-83-9'	6HB-83-9'
6HB-65-3'	6HB-65-3'
6HB-67-4'	6HB-67-4'
6HB-71-4	6HB-71-4
6HB-74-3	6HB-74-3
6HB-76-9	6HB-76-9
6HB-78-10'	6HB-78-10'
6HB-80-11'	6HB-80-11'
6HB-82-12'	6HB-82-12'
6HB-59-12	6HB-59-12
6HB-61-11	6HB-61-11
6HB-63-10	6HB-63-10

Supplementary Table. 42. Protruding DNA strands used for formation of self-folded stacked (M-DNA-1) and triangular (M-DNA-2) four-segments. Detailed staple strands sequence information can be found in Supplementary Sequence 1. Detailed 10nt M-base sequence information can be found in Supplementary Sequence 5.

6HB-3	6HB-27	6HB-40	6HB-56	6HB-127	6HB-143	6HB-163
6HB-4	6HB-28	6HB-41	6HB-57	6HB-128	6HB-144	6HB-167
6HB-6	6HB-29	6HB-44	6HB-58	6HB-131	6HB-145	6HB-168
6HB-11	6HB-31	6HB-45	6HB-117	6HB-132	6HB-149	6HB-171
6HB-12	6HB-32	6HB-46	6HB-118	6HB-133	6HB-150	6HB-173
6HB-16	6HB-33	6HB-49	6HB-119	6HB-136	6HB-152	6HB-174
6HB-17	6HB-34	6HB-50	6HB-120	6HB-137	6HB-156	
6HB-22	6HB-35	6HB-51	6HB-122	6HB-139	6HB-157	
6HB-23	6HB-38	6HB-52	6HB-125	6HB-140	6HB-162	

Supplementary Table. 43. Core staple strands used for formation of self-folded six-segments. Detailed staple strands sequence information can be found in Supplementary Sequence 1.

M-DNA-1		M-DNA-2		M-DNA-3	
6HB-104	6HB-83-9'	6HB-104-9	6HB-83	6HB-104-38	6HB-83
6HB-115	6HB-64-15'	6HB-115-15	6HB-64	6HB-115-56	6HB-64
6HB-92	6HB-65-3'	6HB-92-3	6HB-65	6HB-92-37	6HB-65
6HB-96-17	6HB-68-3	6HB-96-17	6HB-68	6HB-96-17	6HB-68
6HB-97-5	6HB-69-15	6HB-97-5	6HB-69	6HB-97-5	6HB-69
6HB-98-18	6HB-70-9	6HB-98-18	6HB-70	6HB-98-18	6HB-70
6HB-101-18'	6HB-74-7'	6HB-101-7	6HB-74	6HB-101-18'	6HB-74
6HB-102-5'	6HB-75-20'	6HB-102-20	6HB-75	6HB-102-5'	6HB-75
6HB-103-17'	6HB-76-8'	6HB-103-8	6HB-76	6HB-103-17'	6HB-76
6HB-107-22	6HB-79-8	6HB-107	6HB-79-9'	6HB-107-22	6HB-79
6HB-108-11	6HB-80-20	6HB-108	6HB-80-15'	6HB-108-11	6HB-80
6HB-109-23	6HB-81-7	6HB-109	6HB-81-3'	6HB-109-23	6HB-81
6HB-112-23'	6HB-85-13'	6HB-112	6HB-85-17'	6HB-112-23'	6HB-85
6HB-113-11'	6HB-86-25'	6HB-113	6HB-86-5'	6HB-113-11'	6HB-86
6HB-114-22'	6HB-59-14'	6HB-114	6HB-59-18'	6HB-114-22'	6HB-59
6HB-88	6HB-61-14	6HB-88	6HB-61-7'	6HB-88-37'	6HB-61
6HB-89	6HB-62-25	6HB-89	6HB-62-20'	6HB-89-56'	6HB-62
6HB-90	6HB-63-13	6HB-90	6HB-63-8'	6HB-90-38'	6HB-63

Supplementary Table. 44. Protruding DNA strands used for formation of self-folded stacked (M-DNA-1), triangular (M-DNA-2) and Y-shaped (M-DNA-3) six-segments. Detailed staple strands sequence information can be found in Supplementary Sequence 1. Detailed 10nt M-base sequence information can be found in Supplementary Sequence 5.

6HB-1	6HB-28	6HB-54	6HB-79	6HB-106	6HB-133	6HB-161
6HB-2	6HB-29	6HB-55	6HB-80	6HB-107	6HB-134	6HB-162
6HB-3	6HB-30	6HB-56	6HB-81	6HB-108	6HB-135	6HB-163
6HB-4	6HB-31	6HB-57	6HB-82	6HB-109	6HB-136	6HB-164
6HB-6	6HB-32	6HB-58	6HB-83	6HB-110	6HB-137	6HB-165
6HB-8	6HB-33	6HB-59	6HB-84	6HB-111	6HB-139	6HB-166
6HB-9	6HB-34	6HB-60	6HB-85	6HB-112	6HB-140	6HB-167
6HB-10	6HB-35	6HB-61	6HB-86	6HB-113	6HB-141	6HB-168
6HB-11	6HB-36	6HB-62	6HB-87	6HB-114	6HB-142	6HB-169
6HB-12	6HB-37	6HB-63	6HB-88	6HB-115	6HB-143	6HB-170
6HB-13	6HB-38	6HB-64	6HB-89	6HB-116	6HB-144	6HB-171
6HB-14	6HB-39	6HB-65	6HB-90	6HB-117	6HB-145	6HB-172
6HB-15	6HB-40	6HB-66	6HB-92	6HB-118	6HB-147	6HB-173
6HB-16	6HB-41	6HB-67	6HB-94	6HB-119	6HB-148	6HB-174
6HB-17	6HB-42	6HB-68	6HB-95	6HB-120	6HB-149	
6HB-18	6HB-43	6HB-69	6HB-96	6HB-122	6HB-150	
6HB-19	6HB-44	6HB-70	6HB-97	6HB-123	6HB-152	
6HB-20	6HB-45	6HB-71	6HB-98	6HB-124	6HB-153	
6HB-21	6HB-46	6HB-72	6HB-99	6HB-125	6HB-154	
6HB-22	6HB-47	6HB-73	6HB-100	6HB-127	6HB-155	
6HB-23	6HB-48	6HB-74	6HB-101	6HB-128	6HB-156	
6HB-24	6HB-49	6HB-75	6HB-102	6HB-129	6HB-157	
6HB-25	6HB-50	6HB-76	6HB-103	6HB-130	6HB-158	
6HB-26	6HB-51	6HB-77	6HB-104	6HB-131	6HB-159	
6HB-27	6HB-52	6HB-78	6HB-105	6HB-132	6HB-160	

Supplementary Table. 45. Core staple strands used for formation of self-linked Circle. Detailed staple strands sequence information can be found in Supplementary Sequence 1.

6HB-3	6HB-36	6HB-62	6HB-89	6HB-120	6HB-156
6HB-4	6HB-37	6HB-63	6HB-90	6HB-124	6HB-157
6HB-9	6HB-38	6HB-66	6HB-95	6HB-125	6HB-158
6HB-10	6HB-39	6HB-67	6HB-96	6HB-127	6HB-160
6HB-11	6HB-40	6HB-68	6HB-97	6HB-128	6HB-162
6HB-12	6HB-41	6HB-69	6HB-98	6HB-129	6HB-163
6HB-13	6HB-42	6HB-70	6HB-99	6HB-132	6HB-164
6HB-16	6HB-44	6HB-71	6HB-102	6HB-133	6HB-165
6HB-17	6HB-45	6HB-72	6HB-103	6HB-134	6HB-166
6HB-18	6HB-46	6HB-74	6HB-104	6HB-135	6HB-169
6HB-19	6HB-47	6HB-75	6HB-105	6HB-136	6HB-170
6HB-20	6HB-48	6HB-76	6HB-106	6HB-137	6HB-171
6HB-21	6HB-49	6HB-77	6HB-107	6HB-141	6HB-172
6HB-24	6HB-50	6HB-78	6HB-110	6HB-142	6HB-173
6HB-25	6HB-52	6HB-79	6HB-111	6HB-143	6HB-174
6HB-26	6HB-54	6HB-81	6HB-112	6HB-144	
6HB-27	6HB-55	6HB-82	6HB-113	6HB-145	
6HB-28	6HB-56	6HB-83	6HB-114	6HB-149	
6HB-29	6HB-57	6HB-84	6HB-115	6HB-150	
6HB-32	6HB-58	6HB-85	6HB-118	6HB-154	
6HB-34	6HB-59	6HB-86	6HB-119	6HB-155	

Supplementary Table. 46. Core staple strands used for formation of self-linked square. Detailed staple strands sequence information can be found in Supplementary Sequence 1.

6HB-1	6HB-34	6HB-59	6HB-86	6HB-114	6HB-145
6HB-4	6HB-35	6HB-62	6HB-87	6HB-116	6HB-147
6HB-8	6HB-36	6HB-63	6HB-89	6HB-118	6HB-150
6HB-9	6HB-37	6HB-65	6HB-90	6HB-120	6HB-153
6HB-10	6HB-38	6HB-66	6HB-94	6HB-123	6HB-154
6HB-11	6HB-39	6HB-67	6HB-95	6HB-124	6HB-155
6HB-14	6HB-42	6HB-68	6HB-96	6HB-125	6HB-156
6HB-15	6HB-43	6HB-71	6HB-97	6HB-127	6HB-159
6HB-16	6HB-44	6HB-72	6HB-99	6HB-129	6HB-160
6HB-17	6HB-45	6HB-73	6HB-100	6HB-130	6HB-161
6HB-18	6HB-48	6HB-74	6HB-101	6HB-131	6HB-162
6HB-20	6HB-49	6HB-75	6HB-102	6HB-132	6HB-163
6HB-21	6HB-50	6HB-78	6HB-104	6HB-135	6HB-165
6HB-22	6HB-51	6HB-79	6HB-106	6HB-136	6HB-166
6HB-23	6HB-52	6HB-80	6HB-107	6HB-137	6HB-167
6HB-26	6HB-55	6HB-81	6HB-108	6HB-139	6HB-168
6HB-27	6HB-56	6HB-83	6HB-109	6HB-140	6HB-172
6HB-28	6HB-57	6HB-84	6HB-112	6HB-143	6HB-173
6HB-32	6HB-58	6HB-85	6HB-113	6HB-144	6HB-174

Supplementary Table. 47. Core staple strands used for formation of self-linked pentagon. Detailed staple strands sequence information can be found in Supplementary Sequence 1.

6HB-1	6HB-34	6HB-63	6HB-94	6HB-124	6HB-157
6HB-4	6HB-35	6HB-65	6HB-95	6HB-128	6HB-158
6HB-8	6HB-36	6HB-66	6HB-98	6HB-129	6HB-159
6HB-9	6HB-37	6HB-67	6HB-99	6HB-130	6HB-160
6HB-10	6HB-39	6HB-70	6HB-100	6HB-133	6HB-163
6HB-12	6HB-41	6HB-71	6HB-103	6HB-134	6HB-164
6HB-13	6HB-42	6HB-72	6HB-104	6HB-135	6HB-165
6HB-14	6HB-43	6HB-73	6HB-105	6HB-137	6HB-168
6HB-17	6HB-45	6HB-75	6HB-106	6HB-139	6HB-169
6HB-18	6HB-46	6HB-76	6HB-108	6HB-140	6HB-170
6HB-19	6HB-47	6HB-77	6HB-109	6HB-141	6HB-173
6HB-20	6HB-51	6HB-80	6HB-110	6HB-144	6HB-174
6HB-23	6HB-52	6HB-81	6HB-113	6HB-145	
6HB-24	6HB-54	6HB-82	6HB-114	6HB-147	
6HB-25	6HB-57	6HB-86	6HB-116	6HB-150	
6HB-27	6HB-58	6HB-87	6HB-120	6HB-153	
6HB-28	6HB-59	6HB-90	6HB-122	6HB-154	
6HB-30	6HB-60	6HB-92	6HB-123	6HB-155	

Supplementary Table. 48. Core staple strands used for formation of self-linked hexagon. Detailed staple strands sequence information can be found in Supplementary Sequence 1.

6HB-2	6HB-29	6HB-54	6HB-81	6HB-109	6HB-137	6HB-166
6HB-3	6HB-30	6HB-55	6HB-82	6HB-110	6HB-139	6HB-167
6HB-4	6HB-31	6HB-56	6HB-83	6HB-111	6HB-140	6HB-168
6HB-6	6HB-32	6HB-60	6HB-84	6HB-112	6HB-141	6HB-169
6HB-10	6HB-33	6HB-61	6HB-85	6HB-113	6HB-142	6HB-170
6HB-11	6HB-34	6HB-62	6HB-87	6HB-115	6HB-143	6HB-171
6HB-12	6HB-35	6HB-63	6HB-88	6HB-116	6HB-144	6HB-172
6HB-13	6HB-37	6HB-64	6HB-89	6HB-117	6HB-148	6HB-173
6HB-14	6HB-38	6HB-65	6HB-90	6HB-118	6HB-149	
6HB-15	6HB-39	6HB-67	6HB-92	6HB-119	6HB-150	
6HB-16	6HB-40	6HB-68	6HB-96	6HB-120	6HB-152	
6HB-17	6HB-41	6HB-69	6HB-97	6HB-122	6HB-155	
6HB-18	6HB-42	6HB-70	6HB-98	6HB-125	6HB-156	
6HB-20	6HB-43	6HB-71	6HB-99	6HB-127	6HB-157	
6HB-21	6HB-44	6HB-72	6HB-100	6HB-128	6HB-158	
6HB-22	6HB-45	6HB-73	6HB-101	6HB-129	6HB-159	
6HB-23	6HB-48	6HB-74	6HB-102	6HB-130	6HB-160	
6HB-24	6HB-49	6HB-75	6HB-104	6HB-131	6HB-161	
6HB-25	6HB-50	6HB-78	6HB-106	6HB-132	6HB-162	
6HB-26	6HB-51	6HB-79	6HB-107	6HB-135	6HB-163	
6HB-27	6HB-52	6HB-80	6HB-108	6HB-136	6HB-165	

Supplementary Table. 49. Core staple strands used for self-linked equilateral triangles. Detailed staple strands sequence information can be found in Supplementary Sequence 1.

6HB-1	6HB-28	6HB-55	6HB-81	6HB-108	6HB-135	6HB-162
6HB-3	6HB-29	6HB-56	6HB-82	6HB-109	6HB-136	6HB-163
6HB-4	6HB-30	6HB-57	6HB-83	6HB-110	6HB-137	6HB-165
6HB-8	6HB-32	6HB-58	6HB-84	6HB-111	6HB-139	6HB-166
6HB-9	6HB-34	6HB-59	6HB-85	6HB-112	6HB-140	6HB-167
6HB-10	6HB-35	6HB-60	6HB-86	6HB-113	6HB-141	6HB-168
6HB-11	6HB-36	6HB-62	6HB-87	6HB-114	6HB-142	6HB-169
6HB-12	6HB-37	6HB-63	6HB-89	6HB-115	6HB-143	6HB-170
6HB-13	6HB-38	6HB-65	6HB-90	6HB-116	6HB-144	6HB-171
6HB-14	6HB-39	6HB-66	6HB-94	6HB-118	6HB-145	6HB-172
6HB-15	6HB-40	6HB-67	6HB-95	6HB-119	6HB-147	6HB-173
6HB-16	6HB-41	6HB-68	6HB-96	6HB-120	6HB-149	6HB-174
6HB-17	6HB-42	6HB-69	6HB-97	6HB-123	6HB-150	
6HB-18	6HB-43	6HB-70	6HB-98	6HB-124	6HB-153	
6HB-20	6HB-44	6HB-72	6HB-99	6HB-125	6HB-154	
6HB-21	6HB-45	6HB-73	6HB-100	6HB-127	6HB-155	
6HB-22	6HB-48	6HB-74	6HB-101	6HB-128	6HB-156	
6HB-23	6HB-49	6HB-75	6HB-102	6HB-129	6HB-157	
6HB-24	6HB-50	6HB-77	6HB-103	6HB-130	6HB-158	
6HB-25	6HB-51	6HB-78	6HB-104	6HB-131	6HB-159	
6HB-26	6HB-52	6HB-79	6HB-106	6HB-132	6HB-160	
6HB-27	6HB-54	6HB-80	6HB-107	6HB-133	6HB-161	

Supplementary Table. 50. Core staple strands used for self-linked isosceles acute triangle. Detailed staple strands sequence information can be found in Supplementary Sequence 1.

6HB-1	6HB-29	6HB-52	6HB-77	6HB-102	6HB-128	6HB-156
6HB-2	6HB-30	6HB-54	6HB-78	6HB-103	6HB-129	6HB-157
6HB-3	6HB-31	6HB-55	6HB-79	6HB-104	6HB-130	6HB-158
6HB-4	6HB-32	6HB-56	6HB-80	6HB-106	6HB-131	6HB-159
6HB-6	6HB-33	6HB-58	6HB-81	6HB-107	6HB-132	6HB-160
6HB-8	6HB-34	6HB-59	6HB-82	6HB-108	6HB-133	6HB-161
6HB-11	6HB-35	6HB-60	6HB-83	6HB-109	6HB-135	6HB-162
6HB-12	6HB-36	6HB-61	6HB-84	6HB-110	6HB-136	6HB-163
6HB-13	6HB-38	6HB-62	6HB-85	6HB-111	6HB-137	6HB-165
6HB-14	6HB-39	6HB-63	6HB-87	6HB-112	6HB-139	6HB-166
6HB-15	6HB-40	6HB-64	6HB-88	6HB-114	6HB-140	6HB-167
6HB-16	6HB-41	6HB-65	6HB-89	6HB-115	6HB-141	6HB-168
6HB-17	6HB-42	6HB-66	6HB-90	6HB-116	6HB-142	6HB-169
6HB-18	6HB-43	6HB-68	6HB-92	6HB-117	6HB-143	6HB-170
6HB-20	6HB-44	6HB-69	6HB-94	6HB-118	6HB-145	6HB-171
6HB-21	6HB-45	6HB-70	6HB-96	6HB-119	6HB-147	6HB-172
6HB-22	6HB-47	6HB-71	6HB-97	6HB-120	6HB-148	
6HB-23	6HB-48	6HB-72	6HB-98	6HB-122	6HB-149	
6HB-24	6HB-49	6HB-73	6HB-99	6HB-123	6HB-150	
6HB-25	6HB-50	6HB-74	6HB-100	6HB-125	6HB-152	
6HB-26	6HB-51	6HB-75	6HB-101	6HB-127	6HB-153	

Supplementary Table. 51. Core staple strands used for formation of self-linked right triangle. Detailed staple strands sequence information can be found in Supplementary Sequence 1.

6HB-1	6HB-26	6HB-50	6HB-74	6HB-100	6HB-124	6HB-152
6HB-2	6HB-28	6HB-51	6HB-75	6HB-101	6HB-127	6HB-153
6HB-3	6HB-29	6HB-52	6HB-77	6HB-102	6HB-128	6HB-154
6HB-4	6HB-30	6HB-54	6HB-78	6HB-103	6HB-129	6HB-156
6HB-6	6HB-31	6HB-55	6HB-79	6HB-104	6HB-130	6HB-157
6HB-8	6HB-32	6HB-57	6HB-80	6HB-106	6HB-131	6HB-158
6HB-9	6HB-33	6HB-58	6HB-81	6HB-107	6HB-132	6HB-159
6HB-11	6HB-34	6HB-59	6HB-82	6HB-108	6HB-133	6HB-160
6HB-12	6HB-35	6HB-60	6HB-83	6HB-109	6HB-135	6HB-161
6HB-13	6HB-36	6HB-61	6HB-84	6HB-110	6HB-136	6HB-162
6HB-14	6HB-37	6HB-62	6HB-86	6HB-111	6HB-137	6HB-163
6HB-15	6HB-39	6HB-63	6HB-87	6HB-113	6HB-139	6HB-165
6HB-16	6HB-40	6HB-64	6HB-88	6HB-114	6HB-140	6HB-166
6HB-17	6HB-41	6HB-65	6HB-89	6HB-115	6HB-141	6HB-167
6HB-18	6HB-42	6HB-66	6HB-90	6HB-116	6HB-142	6HB-168
6HB-20	6HB-43	6HB-67	6HB-92	6HB-117	6HB-144	6HB-169
6HB-21	6HB-44	6HB-69	6HB-94	6HB-118	6HB-145	6HB-170
6HB-22	6HB-45	6HB-70	6HB-95	6HB-119	6HB-147	6HB-171
6HB-23	6HB-47	6HB-71	6HB-97	6HB-120	6HB-148	6HB-172
6HB-24	6HB-48	6HB-72	6HB-98	6HB-122	6HB-149	6HB-174
6HB-25	6HB-49	6HB-73	6HB-99	6HB-123	6HB-150	

Supplementary Table. 52. Core staple strands used for formation of self-linked obtuse triangle. Detailed staple strands sequence information can be found in Supplementary Sequence 1.

TR-1	TR-28	TR-52	TR-76	TR-101	TR-125	TR-154
TR-2	TR-30	TR-53	TR-77	TR-102	TR-126	TR-155
TR-3	TR-31	TR-54	TR-78	TR-103	TR-128	TR-156
TR-4	TR-32	TR-55	TR-79	TR-104	TR-129	TR-158
TR-5	TR-33	TR-56	TR-80	TR-106	TR-130	TR-159
TR-6	TR-34	TR-57	TR-81	TR-107	TR-132	TR-160
TR-7	TR-35	TR-58	TR-82	TR-108	TR-133	TR-161
TR-8	TR-36	TR-59	TR-83	TR-109	TR-134	TR-162
TR-10	TR-37	TR-60	TR-84	TR-110	TR-135	TR-164
TR-11	TR-38	TR-61	TR-85	TR-111	TR-136	TR-165
TR-13	TR-39	TR-63	TR-86	TR-112	TR-137	TR-166
TR-14	TR-40	TR-64	TR-87	TR-113	TR-138	TR-167
TR-15	TR-41	TR-65	TR-88	TR-114	TR-141	
TR-16	TR-42	TR-66	TR-90	TR-115	TR-142	
TR-17	TR-43	TR-67	TR-91	TR-116	TR-143	
TR-18	TR-44	TR-69	TR-93	TR-118	TR-144	
TR-19	TR-46	TR-70	TR-94	TR-119	TR-145	
TR-22	TR-47	TR-71	TR-95	TR-120	TR-146	
TR-23	TR-48	TR-72	TR-96	TR-121	TR-150	
TR-25	TR-49	TR-73	TR-97	TR-122	TR-151	
TR-26	TR-50	TR-74	TR-99	TR-123	TR-152	
TR-27	TR-51	TR-75	TR-100	TR-124	TR-153	

Supplementary Table. 53. Core staple strands used for stacked triangles. Detailed staple strands sequence information can be found in Supplementary Sequence 3.

Stacked triangle
TR-92-1
TR-149-2
TR-45-3
TR-12-4
TR-68-5
TR-21-6
TR-163-7
TR-131-8
TR-29-9
TR-140-10
TR-62-11
TR-9-13
TR-98-1'
TR-105-2'
TR-117-3'
TR-148-4'
TR-89-5'
TR-127-6'
TR-157-7'
TR-24-8'
TR-139-9'
TR-168-10'
TR-147-11'
TR-20-13'

Supplementary Table. 54. Protruding DNA strands used for formation of stacked triangles. Detailed staple strands sequence information can be found in supplementary Sequence 3. Detailed 10nt M-base sequence information can be found in Supplementary Sequence 5.

TR-1	TR-30	TR-52	TR-76	TR-98	TR-122	TR-147
TR-2	TR-31	TR-53	TR-77	TR-99	TR-124	TR-148
TR-3	TR-32	TR-54	TR-78	TR-100	TR-125	TR-150
TR-5	TR-33	TR-55	TR-79	TR-101	TR-126	TR-151
TR-7	TR-34	TR-56	TR-80	TR-102	TR-127	TR-153
TR-8	TR-35	TR-57	TR-81	TR-105	TR-128	TR-154
TR-10	TR-36	TR-58	TR-82	TR-106	TR-129	TR-155
TR-11	TR-37	TR-59	TR-83	TR-107	TR-130	TR-156
TR-13	TR-38	TR-60	TR-84	TR-108	TR-132	TR-157
TR-15	TR-39	TR-61	TR-85	TR-109	TR-133	TR-158
TR-17	TR-40	TR-63	TR-86	TR-110	TR-134	TR-159
TR-18	TR-41	TR-64	TR-87	TR-111	TR-135	TR-160
TR-19	TR-42	TR-65	TR-88	TR-112	TR-136	TR-161
TR-20	TR-43	TR-66	TR-89	TR-114	TR-137	TR-162
TR-22	TR-44	TR-67	TR-90	TR-115	TR-138	TR-165
TR-23	TR-46	TR-69	TR-91	TR-116	TR-139	TR-166
TR-24	TR-47	TR-71	TR-93	TR-117	TR-141	TR-167
TR-25	TR-48	TR-72	TR-94	TR-118	TR-142	TR-168
TR-26	TR-49	TR-73	TR-95	TR-119	TR-143	
TR-27	TR-50	TR-74	TR-96	TR-120	TR-144	
TR-28	TR-51	TR-75	TR-97	TR-121	TR-145	

Supplementary Table. 55. Core staple strands used for tetrahedron. Detailed staple strands sequence information can be found in Supplementary Sequence 3. Detailed 10nt M-base sequence information can be found in Supplementary Sequence 5.

Tetra-1	Tetra-2	Tetra-3	Tetra-4
TR-92-1	TR-92-14	TR-4-13'	TR-92-25'
TR-149-2	TR-149-15	TR-6-11'	TR-149-24'
TR-45-3	TR-45-16	TR-146-10'	TR-45-23'
TR-12-4	TR-12-17	TR-152-9'	TR-12-22'
TR-68-5	TR-68-18	TR-14-22	TR-14-8'
TR-21-6	TR-21-19	TR-103-23	TR-103-7'
TR-163-7	TR-163-20	TR-164-24	TR-164-6'
TR-131-8	TR-131-21	TR-123-25	TR-123-5'
TR-29-9	TR-104-4'	TR-104-17'	TR-104-21'
TR-140-10	TR-16-3'	TR-16-16'	TR-16-20'
TR-62-11	TR-113-2'	TR-113-15'	TR-113-19'
TR-9-13	TR-70-1'	TR-70-14'	TR-70-18'
TR-4-26	TR-4-38	TR-92-37'	TR-4-49'
TR-6-27	TR-6-39	TR-149-36'	TR-6-48'
TR-146-28	TR-146-40	TR-45-35'	TR-146-47'
TR-152-29	TR-152-41	TR-12-34'	TR-152-46'
TR-14-30	TR-14-42	TR-68-46	TR-68-33'
TR-103-31	TR-103-43	TR-21-47	TR-21-32'
TR-164-32	TR-164-44	TR-163-48	TR-163-31'
TR-123-33	TR-123-45	TR-131-49	TR-131-30'
TR-104-34	TR-29-29'	TR-29-41'	TR-29-45'
TR-16-35	TR-140-28'	TR-140-40'	TR-140-44'
TR-113-36	TR-62-27'	TR-62-39'	TR-62-43'
TR-70-37	TR-9-26'	TR-9-38'	TR-9-42'

Supplementary Table. 56. Protruding DNA strands used for formation of tetrahedron. Detailed staple strands sequence information can be found in Supplementary Sequence 3. Detailed 10nt M-base sequence information can be found in Supplementary Sequence 5.

Bipyramid-1	Bipyramid-2	Bipyramid-3	Bipyramid-4	Bipyramid-5	Bipyramid-6
TR-92-1	TR-92-14	TR-92-37'	TR-92-25'	TR-92-82	TR-92-57'
TR-4-26	TR-4-38	TR-4-13'	TR-4-49'	TR-4-83	TR-4-56'
TR-149-2	TR-149-15	TR-149-36'	TR-149-24'	TR-149-84	TR-149-55'
TR-6-27	TR-6-39	TR-6-11'	TR-6-48'	TR-6-85	TR-6-54'
TR-45-3	TR-45-16	TR-45-35'	TR-45-23'	TR-45-86	TR-45-53'
TR-146-28	TR-146-40	TR-146-10'	TR-146-47'	TR-146-87	TR-146-52'
TR-12-4	TR-12-17	TR-12-34'	TR-12-22'	TR-12-88	TR-12-51'
TR-152-29	TR-152-41	TR-152-9'	TR-152-46'	TR-152-89	TR-152-50'
TR-68-5	TR-68-81'	TR-68-89'	TR-68-33'	TR-68-46	TR-68-74
TR-14-30	TR-14-80'	TR-14-88'	TR-14-8'	TR-14-22	TR-14-75
TR-21-6	TR-21-79'	TR-21-87'	TR-21-32'	TR-21-47	TR-21-76
TR-103-31	TR-103-78'	TR-103-86'	TR-103-7'	TR-103-23	TR-103-77
TR-163-7	TR-163-77'	TR-163-85'	TR-163-31'	TR-163-48	TR-163-78
TR-164-32	TR-164-76'	TR-164-84'	TR-164-6'	TR-164-24	TR-164-79
TR-131-8	TR-131-75'	TR-131-83'	TR-131-30'	TR-131-49	TR-131-80
TR-123-33	TR-123-74'	TR-123-82'	TR-123-5'	TR-123-25	TR-123-81
TR-29-9	TR-29-29'	TR-29-41'	TR-29-50	TR-29-58	TR-29-65'
TR-104-34	TR-104-4'	TR-104-17'	TR-104-51	TR-104-59	TR-104-64'
TR-140-10	TR-140-28'	TR-140-40'	TR-140-52	TR-140-60	TR-140-63'
TR-16-35	TR-16-3'	TR-16-16'	TR-16-53	TR-16-61	TR-16-62'
TR-62-11	TR-62-27'	TR-62-39'	TR-62-54	TR-62-62	TR-62-61'
TR-113-36	TR-113-2'	TR-113-15'	TR-113-55	TR-113-63	TR-113-60'
TR-9-13	TR-9-26'	TR-9-38'	TR-9-56	TR-9-64	TR-9-59'
TR-70-37	TR-70-1'	TR-70-14'	TR-70-57	TR-70-65	TR-70-58'

Supplementary Table. 57. Protruding DNA strands used for formation of triangular bipyramid. The core staple strands were the same with tetrahedron. Detailed staple strands sequence information can be found in Supplementary Sequence 3. Detailed 10nt M-base sequence information can be found in Supplementary Sequence 5.

Octa-1	Octa-2	Octa-3	Octa-4
TR-92-1	TR-92-14	TR-92-37'	TR-92-18
TR-4-26	TR-4-38	TR-4-13'	TR-4-42
TR-149-2	TR-149-15	TR-149-36'	TR-149-19
TR-6-27	TR-6-39	TR-6-11'	TR-6-43
TR-45-3	TR-45-16	TR-45-35'	TR-45-20
TR-146-28	TR-146-40	TR-146-10'	TR-146-44
TR-12-4	TR-12-17	TR-12-34'	TR-12-21
TR-152-29	TR-152-41	TR-152-9'	TR-152-45
TR-68-5	TR-68-81'	TR-68-89'	TR-68-97'
TR-14-30	TR-14-80'	TR-14-88'	TR-14-96'
TR-21-6	TR-21-79'	TR-21-87'	TR-21-95'
TR-103-31	TR-103-78'	TR-103-86'	TR-103-94'
TR-163-7	TR-163-77'	TR-163-85'	TR-163-93'
TR-164-32	TR-164-76'	TR-164-84'	TR-164-92'
TR-131-8	TR-131-75'	TR-131-83'	TR-131-91'
TR-123-33	TR-123-74'	TR-123-82'	TR-123-90'
TR-29-9	TR-29-29'	TR-29-45'	TR-29-41'
TR-104-34	TR-104-4'	TR-104-21'	TR-104-17'
TR-140-10	TR-140-28'	TR-140-44'	TR-140-40'
TR-16-35	TR-16-3'	TR-16-20'	TR-16-16'
TR-62-11	TR-62-27'	TR-62-43'	TR-62-39'
TR-113-36	TR-113-2'	TR-113-19'	TR-113-15'
TR-9-13	TR-9-26'	TR-9-42'	TR-9-38'
TR-70-37	TR-70-1'	TR-70-18'	TR-70-14'
Octa-5	Octa-6	Octa-7	Octa-8
TR-92-25'	TR-92-82	TR-92-57'	TR-92-66
TR-4-49'	TR-4-83	TR-4-56'	TR-4-67
TR-149-24'	TR-149-84	TR-149-55'	TR-149-68
TR-6-48'	TR-6-85	TR-6-54'	TR-6-69
TR-45-23'	TR-45-86	TR-45-53'	TR-45-70
TR-146-47'	TR-146-87	TR-146-52'	TR-146-71
TR-12-22'	TR-12-88	TR-12-51'	TR-12-72

TR-152-46'	TR-152-89	TR-152-50'	TR-152-73
TR-68-33'	TR-68-46	TR-68-74	TR-68-90
TR-14-8'	TR-14-22	TR-14-75	TR-14-91
TR-21-32'	TR-21-47	TR-21-76	TR-21-92
TR-103-7'	TR-103-23	TR-103-77	TR-103-93
TR-163-31'	TR-163-48	TR-163-78	TR-163-94
TR-164-6'	TR-164-24	TR-164-79	TR-164-95
TR-131-30'	TR-131-49	TR-131-80	TR-131-96
TR-123-5'	TR-123-25	TR-123-81	TR-123-97
TR-29-50	TR-29-58	TR-29-73'	TR-29-65'
TR-104-51	TR-104-59	TR-104-72'	TR-104-64'
TR-140-52	TR-140-60	TR-140-71'	TR-140-63'
TR-16-53	TR-16-61	TR-16-70'	TR-16-62'
TR-62-54	TR-62-62	TR-62-69'	TR-62-61'
TR-113-55	TR-113-63	TR-113-68'	TR-113-60'
TR-9-56	TR-9-64	TR-9-67'	TR-9-59'
TR-70-57	TR-70-65	TR-70-66'	TR-70-58'

Supplementary Table. 58. Protruding DNA strands used for formation of octahedron. The core staple strands were the same with tetrahedron. Detailed staple strands sequence information can be found in Supplementary Sequence 3. Detailed 10nt M-base sequence information can be found in Supplementary Sequence 5.

Penta-Bip-1	Penta-Bip-2	Penta-Bip-3	Penta-Bip-4	Penta-Bip-5
TR-92-14	TR-92-37'	TR-92-146'	TR-92-18	TR-92-129'
TR-4-38	TR-4-13'	TR-4-147'	TR-4-42	TR-4-128'
TR-149-15	TR-149-36'	TR-149-148'	TR-149-19	TR-149-127'
TR-6-39	TR-6-11'	TR-6-149'	TR-6-43	TR-6-126'
TR-45-16	TR-45-35'	TR-45-150'	TR-45-20	TR-45-125'
TR-146-40	TR-146-10'	TR-146-151'	TR-146-44	TR-146-124'
TR-12-17	TR-12-34'	TR-12-152'	TR-12-21	TR-12-123'
TR-152-41	TR-152-9'	TR-152-153'	TR-152-45	TR-152-122'
TR-68-81'	TR-68-194	TR-68-185	TR-68-154'	TR-68-201'
TR-14-80'	TR-14-195	TR-14-184	TR-14-155'	TR-14-200'
TR-21-79'	TR-21-196	TR-21-183	TR-21-156'	TR-21-199'
TR-103-78'	TR-103-197	TR-103-182	TR-103-157'	TR-103-198'
TR-163-77'	TR-163-198	TR-163-181	TR-163-158'	TR-163-197'
TR-164-76'	TR-164-199	TR-164-180	TR-164-159'	TR-164-196'
TR-131-75'	TR-131-200	TR-131-179	TR-131-160'	TR-131-195'
TR-123-74'	TR-123-201	TR-123-178	TR-123-161'	TR-123-194'
TR-29-9	TR-29-45'	TR-29-41'	TR-29-153	TR-29-210
TR-104-34	TR-104-21'	TR-104-17'	TR-104-152	TR-104-211
TR-140-10	TR-140-44'	TR-140-40'	TR-140-151	TR-140-212
TR-16-35	TR-16-20'	TR-16-16'	TR-16-150	TR-16-213
TR-62-11	TR-62-43'	TR-62-39'	TR-62-149	TR-62-214
TR-113-36	TR-113-19'	TR-113-15'	TR-113-148	TR-113-215
TR-9-13	TR-9-42'	TR-9-38'	TR-9-147	TR-9-216
TR-70-37	TR-70-18'	TR-70-14'	TR-70-146	TR-70-217
Penta-Bip-6	Penta-Bip-7	Penta-Bip-8	Penta-Bip-9	Penta-Bip-10
TR-92-169'	TR-92-137'	TR-92-177'	TR-92-145'	TR-92-185'
TR-4-168'	TR-4-136'	TR-4-176'	TR-4-144'	TR-4-184'
TR-149-167'	TR-149-135'	TR-149-175'	TR-149-143'	TR-149-183'
TR-6-166'	TR-6-134'	TR-6-174'	TR-6-142'	TR-6-182'
TR-45-165'	TR-45-133'	TR-45-173'	TR-45-141'	TR-45-181'
TR-146-164'	TR-146-132'	TR-146-172'	TR-146-140'	TR-146-180'
TR-12-163'	TR-12-131'	TR-12-171'	TR-12-139'	TR-12-179'

TR-152-162'	TR-152-130'	TR-152-170'	TR-152-138'	TR-152-178'
TR-68-129	TR-68-217'	TR-68-137	TR-68-233'	TR-68-145
TR-14-128	TR-14-216'	TR-14-136	TR-14-232'	TR-14-144
TR-21-127	TR-21-215'	TR-21-135	TR-21-231'	TR-21-143
TR-103-126	TR-103-214'	TR-103-134	TR-103-230'	TR-103-142
TR-163-125	TR-163-213'	TR-163-133	TR-163-229'	TR-163-141
TR-164-124	TR-164-212'	TR-164-132	TR-164-228'	TR-164-140
TR-131-123	TR-131-211'	TR-131-131	TR-131-227'	TR-131-139
TR-123-122	TR-123-210'	TR-123-130	TR-123-226'	TR-123-138
TR-29-154	TR-29-226	TR-29-162	TR-29-74	TR-29-170
TR-104-155	TR-104-227	TR-104-163	TR-104-75	TR-104-171
TR-140-156	TR-140-228	TR-140-164	TR-140-76	TR-140-172
TR-16-157	TR-16-229	TR-16-165	TR-16-77	TR-16-173
TR-62-158	TR-62-230	TR-62-166	TR-62-78	TR-62-174
TR-113-159	TR-113-231	TR-113-167	TR-113-79	TR-113-175
TR-9-160	TR-9-232	TR-9-168	TR-9-80	TR-9-176
TR-70-161	TR-70-233	TR-70-169	TR-70-81	TR-70-177

Supplementary Table. 59 Protruding DNA strands used for formation of pentagonal bipyrmaid. The core staple strands were the same with tetrahedron. Detailed staple strands sequence information can be found in Supplementary Sequence 3. Detailed 10nt M-base sequence information can be found in Supplementary Sequence 5.

SQ-1	SQ-32	SQ-57	SQ-82	SQ-107	SQ-138	SQ-163
SQ-2	SQ-33	SQ-58	SQ-83	SQ-108	SQ-139	SQ-164
SQ-3	SQ-34	SQ-59	SQ-84	SQ-109	SQ-140	SQ-165
SQ-4	SQ-35	SQ-60	SQ-85	SQ-110	SQ-141	SQ-166
SQ-5	SQ-36	SQ-61	SQ-86	SQ-111	SQ-142	SQ-167
SQ-6	SQ-37	SQ-62	SQ-87	SQ-118	SQ-143	SQ-168
SQ-7	SQ-38	SQ-63	SQ-88	SQ-119	SQ-144	SQ-169
SQ-8	SQ-39	SQ-64	SQ-89	SQ-120	SQ-145	SQ-170
SQ-9	SQ-40	SQ-65	SQ-90	SQ-121	SQ-146	SQ-171
SQ-10	SQ-41	SQ-66	SQ-91	SQ-122	SQ-147	SQ-172
SQ-11	SQ-42	SQ-67	SQ-92	SQ-123	SQ-148	SQ-173
SQ-12	SQ-43	SQ-68	SQ-93	SQ-124	SQ-149	SQ-174
SQ-13	SQ-44	SQ-69	SQ-94	SQ-125	SQ-150	SQ-175
SQ-14	SQ-45	SQ-70	SQ-95	SQ-126	SQ-151	SQ-176
SQ-15	SQ-46	SQ-71	SQ-96	SQ-127	SQ-152	
SQ-16	SQ-47	SQ-72	SQ-97	SQ-128	SQ-153	
SQ-17	SQ-48	SQ-73	SQ-98	SQ-129	SQ-154	
SQ-18	SQ-49	SQ-74	SQ-99	SQ-130	SQ-155	
SQ-19	SQ-50	SQ-75	SQ-100	SQ-131	SQ-156	
SQ-20	SQ-51	SQ-76	SQ-101	SQ-132	SQ-157	
SQ-21	SQ-52	SQ-77	SQ-102	SQ-133	SQ-158	
SQ-22	SQ-53	SQ-78	SQ-103	SQ-134	SQ-159	
SQ-23	SQ-54	SQ-79	SQ-104	SQ-135	SQ-160	
SQ-30	SQ-55	SQ-80	SQ-105	SQ-136	SQ-161	
SQ-31	SQ-56	SQ-81	SQ-106	SQ-137	SQ-162	

Supplementary Table. 60. The core staple strands used for formation of triangular prism. Detailed staple strands sequence information can be found in Supplementary Sequence 4. Detailed 10nt M-base sequence information can be found in Supplementary Sequence 5.

TP-1	TP-2	TP-3
SQ-24-1	SQ-24-26	SQ-24-19'
SQ-25-2	SQ-25-27	SQ-25-18'
SQ-26-3	SQ-26-28	SQ-26-17'
SQ-27-4	SQ-27-29	SQ-27-16'
SQ-28-5	SQ-28-30	SQ-28-15'
SQ-29-6	SQ-29-31	SQ-29-14'
SQ-112-14	SQ-112-6'	SQ-112-31'
SQ-113-15	SQ-113-5'	SQ-113-30'
SQ-114-16	SQ-114-4'	SQ-114-29'
SQ-115-17	SQ-115-3'	SQ-115-28'
SQ-116-18	SQ-116-2'	SQ-116-27'
SQ-117-19	SQ-117-1'	SQ-117-26'

Supplementary Table. 61. Protruding DNA strands used for formation of triangular prism. Detailed staple strands sequence information can be found in Supplementary Sequence 4. Detailed 10nt M-base sequence information can be found in Supplementary Sequence 5.

RP-1	RP-2	RP-3	RP-4
SQ-24-1	SQ-24-43'	SQ-24-19'	SQ-24-26
SQ-25-2	SQ-25-42'	SQ-25-18'	SQ-25-27
SQ-26-3	SQ-26-41'	SQ-26-17'	SQ-26-28
SQ-27-4	SQ-27-40'	SQ-27-16'	SQ-27-29
SQ-28-5	SQ-28-39'	SQ-28-15'	SQ-28-30
SQ-29-6	SQ-29-38'	SQ-29-14'	SQ-29-31
SQ-112-14	SQ-112-6'	SQ-112-31'	SQ-112-38
SQ-113-15	SQ-113-5'	SQ-113-30'	SQ-113-39
SQ-114-16	SQ-114-4'	SQ-114-29'	SQ-114-40
SQ-115-17	SQ-115-3'	SQ-115-28'	SQ-115-41
SQ-116-18	SQ-116-2'	SQ-116-27'	SQ-116-42
SQ-117-19	SQ-117-1'	SQ-117-26'	SQ-117-43

Supplementary Table. 62. Protruding DNA strands used for formation of rectangular prism. The core staple strands were the same with triangular prism. Detailed staple strands sequence information can be found in Supplementary Sequence 4. Detailed 10nt M-base sequence information can be found in Supplementary Sequence 5.

PP-1	PP-2	PP-3	PP-4	PP-5
SQ-24-1	SQ-24-62	SQ-24-19'	SQ-24-26	SQ-24-43'
SQ-25-2	SQ-25-63	SQ-25-18'	SQ-25-27	SQ-25-42'
SQ-26-3	SQ-26-64	SQ-26-17'	SQ-26-28	SQ-26-41'
SQ-27-4	SQ-27-65	SQ-27-16'	SQ-27-29	SQ-27-40'
SQ-28-5	SQ-28-66	SQ-28-15'	SQ-28-30	SQ-28-39'
SQ-29-6	SQ-29-67	SQ-29-14'	SQ-29-31	SQ-29-38'
SQ-112-14	SQ-112-6'	SQ-112-31'	SQ-112-38	SQ-112-67'
SQ-113-15	SQ-113-5'	SQ-113-30'	SQ-113-39	SQ-113-66'
SQ-114-16	SQ-114-4'	SQ-114-29'	SQ-114-40	SQ-114-65'
SQ-115-17	SQ-115-3'	SQ-115-28'	SQ-115-41	SQ-115-64'
SQ-116-18	SQ-116-2'	SQ-116-27'	SQ-116-42	SQ-116-63'
SQ-117-19	SQ-117-1'	SQ-117-26'	SQ-117-43	SQ-117-62'

Supplementary Table. 63. Protruding DNA strands used for formation of pentagonal prism. The core staple strands were the same with triangular prism. Detailed staple strands sequence information can be found in Supplementary Sequence 4. Detailed 10nt M-base sequence information can be found in Supplementary Sequence 5

HP-1	HP-2	HP-3	HP-4	HP-5	HP-6
SQ-24-1	SQ-24-68	SQ-24-19'	SQ-24-26	SQ-24-43'	SQ-24-62
SQ-25-2	SQ-25-69	SQ-25-18'	SQ-25-27	SQ-25-42'	SQ-25-63
SQ-26-3	SQ-26-70	SQ-26-17'	SQ-26-28	SQ-26-41'	SQ-26-64
SQ-27-4	SQ-27-71	SQ-27-16'	SQ-27-29	SQ-27-40'	SQ-27-65
SQ-28-5	SQ-28-72	SQ-28-15'	SQ-28-30	SQ-28-39'	SQ-28-66
SQ-29-6	SQ-29-73	SQ-29-14'	SQ-29-31	SQ-29-38'	SQ-29-67
SQ-112-14	SQ-112-6'	SQ-112-31'	SQ-112-38	SQ-112-67'	SQ-112-73'
SQ-113-15	SQ-113-5'	SQ-113-30'	SQ-113-39	SQ-113-66'	SQ-113-72'
SQ-114-16	SQ-114-4'	SQ-114-29'	SQ-114-40	SQ-114-65'	SQ-114-71'
SQ-115-17	SQ-115-3'	SQ-115-28'	SQ-115-41	SQ-115-64'	SQ-115-70'
SQ-116-18	SQ-116-2'	SQ-116-27'	SQ-116-42	SQ-116-63'	SQ-116-69'
SQ-117-19	SQ-117-1'	SQ-117-26'	SQ-117-43	SQ-117-62'	SQ-117-68'

Supplementary Table. 64. Protruding DNA strands used for formation of hexagonal prism. The core staple strands were the same with triangular prism. Detailed staple strands sequence information can be found in Supplementary Sequence 4. Detailed 10nt M-base sequence information can be found in Supplementary Sequence 5.

SQ-1	SQ-30	SQ-53	SQ-82	SQ-105	SQ-134	SQ-163
SQ-2	SQ-31	SQ-60	SQ-83	SQ-106	SQ-135	SQ-164
SQ-3	SQ-32	SQ-61	SQ-84	SQ-107	SQ-136	SQ-165
SQ-4	SQ-33	SQ-62	SQ-85	SQ-108	SQ-137	SQ-166
SQ-5	SQ-34	SQ-63	SQ-86	SQ-109	SQ-138	SQ-167
SQ-6	SQ-35	SQ-64	SQ-87	SQ-110	SQ-139	SQ-168
SQ-7	SQ-36	SQ-65	SQ-88	SQ-111	SQ-140	SQ-169
SQ-8	SQ-37	SQ-66	SQ-89	SQ-118	SQ-141	SQ-170
SQ-9	SQ-38	SQ-67	SQ-90	SQ-119	SQ-148	SQ-171
SQ-10	SQ-39	SQ-68	SQ-91	SQ-120	SQ-149	SQ-172
SQ-11	SQ-40	SQ-69	SQ-92	SQ-121	SQ-150	SQ-173
SQ-12	SQ-41	SQ-70	SQ-93	SQ-122	SQ-151	SQ-174
SQ-13	SQ-42	SQ-71	SQ-94	SQ-123	SQ-152	SQ-175
SQ-14	SQ-43	SQ-72	SQ-95	SQ-124	SQ-153	SQ-176
SQ-15	SQ-44	SQ-73	SQ-96	SQ-125	SQ-154	
SQ-16	SQ-45	SQ-74	SQ-97	SQ-126	SQ-155	
SQ-17	SQ-46	SQ-75	SQ-98	SQ-127	SQ-156	
SQ-18	SQ-47	SQ-76	SQ-99	SQ-128	SQ-157	
SQ-19	SQ-48	SQ-77	SQ-100	SQ-129	SQ-158	
SQ-20	SQ-49	SQ-78	SQ-101	SQ-130	SQ-159	
SQ-21	SQ-50	SQ-79	SQ-102	SQ-131	SQ-160	
SQ-22	SQ-51	SQ-80	SQ-103	SQ-132	SQ-161	
SQ-23	SQ-52	SQ-81	SQ-104	SQ-133	SQ-162	

Supplementary Table. 65. Core staple strands used for formation of rectangular M-DNA in blocked triangular prism. Detailed staple strands sequence information can be found in Supplementary Sequence 4.

TR-1	TR-28	TR-52	TR-76	TR-101	TR-125	TR-154
TR-2	TR-30	TR-53	TR-77	TR-102	TR-126	TR-155
TR-3	TR-31	TR-54	TR-78	TR-103	TR-128	TR-156
TR-4	TR-32	TR-55	TR-79	TR-104	TR-129	TR-158
TR-5	TR-33	TR-56	TR-80	TR-106	TR-130	TR-159
TR-6	TR-34	TR-57	TR-81	TR-107	TR-132	TR-160
TR-7	TR-35	TR-58	TR-82	TR-108	TR-133	TR-161
TR-8	TR-36	TR-59	TR-83	TR-109	TR-134	TR-162
TR-10	TR-37	TR-60	TR-84	TR-110	TR-135	TR-164
TR-11	TR-38	TR-61	TR-85	TR-111	TR-136	TR-165
TR-13	TR-39	TR-63	TR-86	TR-112	TR-137	TR-166
TR-14	TR-40	TR-64	TR-87	TR-113	TR-138	TR-167
TR-15	TR-41	TR-65	TR-88	TR-114	TR-141	
TR-16	TR-42	TR-66	TR-90	TR-115	TR-142	
TR-17	TR-43	TR-67	TR-91	TR-116	TR-143	
TR-18	TR-44	TR-69	TR-93	TR-118	TR-144	
TR-19	TR-46	TR-70	TR-94	TR-119	TR-145	
TR-22	TR-47	TR-71	TR-95	TR-120	TR-146	
TR-23	TR-48	TR-72	TR-96	TR-121	TR-150	
TR-25	TR-49	TR-73	TR-97	TR-122	TR-151	
TR-26	TR-50	TR-74	TR-99	TR-123	TR-152	
TR-27	TR-51	TR-75	TR-100	TR-124	TR-153	

Supplementary Table. 66. Core staple strands used for formation of triangular M-DNA in blocked triangular prism. Detailed staple strands sequence information can be found in Supplementary Sequence 3.

SQ-1	SQ-2	SQ-3	TR-1	TR-2
SQ-24-15-1	SQ-24-15-13	SQ-24-15-12'	TR-92	TR-92
SQ-25-15-2	SQ-25-15-14	SQ-25-15-11'	TR-4-6'	TR-4-67
SQ-26-15-3	SQ-26-15-15	SQ-26-15-10'	TR-149-5'	TR-149-68
SQ-27-15-4	SQ-27-15-16	SQ-27-15-9'	TR-6-4'	TR-6-69
SQ-28-15-5	SQ-28-15-17	SQ-28-15-8'	TR-45-3'	TR-45-70
SQ-29-15-6	SQ-29-15-18	SQ-29-15-7'	TR-146-2'	TR-146-71
SQ-54-1	SQ-54-7	SQ-54-14	TR-12-1'	TR-12-72
SQ-55-2	SQ-55-8	SQ-55-15	TR-152	TR-152
SQ-56-3	SQ-56-9	SQ-56-16	TR-68	TR-68
SQ-57-4	SQ-57-10	SQ-57-17	TR-14-13'	TR-14-91
SQ-58-5	SQ-58-11	SQ-58-18	TR-21-11'	TR-21-92
SQ-59-6	SQ-59-13	SQ-59-19	TR-103-10'	TR-103-93
SQ-112-15-7	SQ-112-15-6'	SQ-112-15-18'	TR-163-9'	TR-163-94
SQ-113-15-8	SQ-113-15-5'	SQ-113-15-17'	TR-164-8'	TR-164-95
SQ-114-15-9	SQ-114-15-4'	SQ-114-15-16'	TR-131-7'	TR-131-96
SQ-115-15-10	SQ-115-15-3'	SQ-115-15-15'	TR-123	TR-123
SQ-116-15-11	SQ-116-15-2'	SQ-116-15-14'	TR-29	TR-29
SQ-117-15-12	SQ-117-15-1'	SQ-117-15-13'	TR-104-19'	TR-104-64'
SQ-142-72'	SQ-142-59	SQ-142-96'	TR-140-18'	TR-140-63'
SQ-143-71'	SQ-143-60	SQ-143-95'	TR-16-17'	TR-16-62'
SQ-144-70'	SQ-144-61	SQ-144-94'	TR-62-16'	TR-62-61'
SQ-145-69'	SQ-145-62	SQ-145-93'	TR-113-15'	TR-113-60'
SQ-146-68'	SQ-146-63	SQ-146-92'	TR-9-14'	TR-9-59'
SQ-147-67'	SQ-147-64	SQ-147-91'	TR-70	TR-70

Supplementary Table. 67. Protruding DNA strands used for formation of blocked triangular prism. Detailed staple strands sequence information can be found in Supplementary Sequence 3 (triangular M-DNA) and Sequence 4 (rectangular M-DNA). Detailed 10nt M-base sequence information can be found in Supplementary Sequence 5. 15-1 to 15-18 were 15nt M-bases, detailed sequence information can be found in Supplementary Sequence 6.

6HB-1	6HB-26	6HB-50	6HB-93	6HB-129	6HB-155
6HB-2	6HB-27	6HB-51	6HB-94	6HB-130	6HB-156
6HB-3	6HB-28	6HB-52	6HB-96	6HB-131	6HB-157
6HB-4	6HB-29	6HB-54	6HB-98	6HB-132	6HB-158
6HB-5	6HB-30	6HB-55	6HB-100	6HB-133	6HB-159
6HB-6	6HB-31	6HB-56	6HB-102	6HB-134	6HB-160
6HB-8	6HB-32	6HB-57	6HB-105	6HB-135	6HB-161
6HB-9	6HB-33	6HB-58	6HB-107	6HB-136	6HB-162
6HB-10	6HB-34	6HB-60	6HB-109	6HB-137	6HB-163
6HB-11	6HB-35	6HB-62	6HB-111	6HB-139	6HB-164
6HB-12	6HB-36	6HB-64	6HB-113	6HB-140	6HB-165
6HB-13	6HB-37	6HB-66	6HB-115	6HB-141	6HB-166
6HB-14	6HB-38	6HB-68	6HB-116	6HB-142	6HB-167
6HB-15	6HB-39	6HB-70	6HB-117	6HB-143	6HB-168
6HB-16	6HB-40	6HB-72	6HB-118	6HB-144	6HB-169
6HB-17	6HB-41	6HB-73	6HB-119	6HB-145	6HB-170
6HB-18	6HB-42	6HB-75	6HB-120	6HB-147	6HB-171
6HB-19	6HB-43	6HB-77	6HB-122	6HB-148	6HB-172
6HB-20	6HB-44	6HB-79	6HB-123	6HB-149	6HB-173
6HB-21	6HB-45	6HB-81	6HB-124	6HB-150	6HB-174
6HB-22	6HB-46	6HB-84	6HB-125	6HB-151	
6HB-23	6HB-47	6HB-86	6HB-126	6HB-152	
6HB-24	6HB-48	6HB-87	6HB-127	6HB-153	
6HB-25	6HB-49	6HB-89	6HB-128	6HB-154	

Supplementary Table. 68. Core staple strands used for formation of 1D and 2D array. Detailed staple strands sequence information can be found in Supplementary Sequence 1.

1D-Y-Half	1D-XY-Half	1D-XY-Quarter	2D-XY
6HB-104-9	6HB-104-9	6HB-104-9	6HB-104-9
6HB-92-3	6HB-92-3	6HB-92-3	6HB-92-3
6HB-95-4	6HB-95-4	6HB-95-4	6HB-95-4
6HB-97-5	6HB-97-5	6HB-97-5	6HB-97-5
6HB-99-6	6HB-99-6	6HB-99-6	6HB-99-6
6HB-101-7	6HB-101-7	6HB-101-7	6HB-101-7
6HB-103-8	6HB-103-8	6HB-103-8	6HB-103-8
6HB-106-9'	6HB-106	6HB-106-10	6HB-106-28
6HB-108-3'	6HB-108	6HB-108-11	6HB-108-29
6HB-110-4'	6HB-110	6HB-110-12	6HB-110-30
6HB-112-5'	6HB-112	6HB-112	6HB-112-31
6HB-114-6'	6HB-114	6HB-114	6HB-114-32
6HB-88-7'	6HB-88	6HB-88	6HB-88-33
6HB-90-8'	6HB-90	6HB-90	6HB-90-34
6HB-83	6HB-83	6HB-83	6HB-83-28'
6HB-65	6HB-65	6HB-65	6HB-65-29'
6HB-67	6HB-67	6HB-67	6HB-67-30'
6HB-69	6HB-69	6HB-69	6HB-69-31'
6HB-71	6HB-71	6HB-71-9'	6HB-71-32'
6HB-74	6HB-74	6HB-74-3'	6HB-74-33'
6HB-76	6HB-76	6HB-76-4'	6HB-76-34'
6HB-78	6HB-78-9'	6HB-78-5'	6HB-78-9'
6HB-80	6HB-80-3'	6HB-80-6'	6HB-80-3'
6HB-82	6HB-82-4'	6HB-82-7'	6HB-82-4'
6HB-85	6HB-85-5'	6HB-85-8'	6HB-85-5'
6HB-59	6HB-59-6'	6HB-59-10'	6HB-59-6'
6HB-61	6HB-61-7'	6HB-61-11'	6HB-61-7'
6HB-63	6HB-63-8'	6HB-63-12'	6HB-63-8'

Supplementary Table. 69. Protruding DNA strands used for formation of 1D and 2D array. Detailed staple strands sequence information can be found in Supplementary Sequence 1. Detailed 10nt M-base sequence information can be found in Supplementary Sequence 5.

6HB-1	6HB-21	6HB-40	6HB-93	6HB-135	6HB-156
6HB-2	6HB-22	6HB-41	6HB-116	6HB-136	6HB-157
6HB-3	6HB-23	6HB-42	6HB-117	6HB-137	6HB-158
6HB-4	6HB-24	6HB-43	6HB-118	6HB-139	6HB-159
6HB-5	6HB-25	6HB-44	6HB-119	6HB-140	6HB-160
6HB-6	6HB-26	6HB-45	6HB-120	6HB-141	6HB-161
6HB-8	6HB-27	6HB-46	6HB-122	6HB-142	6HB-162
6HB-9	6HB-28	6HB-47	6HB-123	6HB-143	6HB-163
6HB-10	6HB-29	6HB-48	6HB-124	6HB-144	6HB-164
6HB-11	6HB-30	6HB-49	6HB-125	6HB-145	6HB-165
6HB-12	6HB-31	6HB-50	6HB-126	6HB-147	6HB-166
6HB-13	6HB-32	6HB-51	6HB-127	6HB-148	6HB-167
6HB-14	6HB-33	6HB-52	6HB-128	6HB-149	6HB-168
6HB-15	6HB-34	6HB-54	6HB-129	6HB-150	6HB-169
6HB-16	6HB-35	6HB-55	6HB-130	6HB-151	6HB-170
6HB-17	6HB-36	6HB-56	6HB-131	6HB-152	6HB-171
6HB-18	6HB-37	6HB-57	6HB-132	6HB-153	6HB-172
6HB-19	6HB-38	6HB-58	6HB-133	6HB-154	6HB-173
6HB-20	6HB-39	6HB-72	6HB-134	6HB-155	6HB-174

Supplementary Table. 70. Core staple strands used for formation of 2D-X array. Detailed staple strands sequence information can be found in Supplementary Sequence 1.

2D-X	
6HB-104-9	6HB-83-9'
6HB-115-15	6HB-64-15'
6HB-92-3	6HB-65-3'
6HB-94-16	6HB-66-16'
6HB-95-4	6HB-67-4'
6HB-96-17	6HB-68-17'
6HB-97	6HB-69
6HB-98-18	6HB-70-18'
6HB-99-6	6HB-71-6'
6HB-100-19	6HB-73-19'
6HB-101-7	6HB-74-7'
6HB-102-20	6HB-75-20'
6HB-103-8	6HB-76-8'
6HB-105	6HB-77
6HB-106-10	6HB-78-10'
6HB-107-22	6HB-79-22'
6HB-108-11	6HB-80-11'
6HB-109-23	6HB-81-23'
6HB-110-12	6HB-82-12'
6HB-111-24	6HB-84-24'
6HB-112	6HB-85
6HB-113-25	6HB-86-25'
6HB-114-14	6HB-59-14'
6HB-87-26	6HB-60-26'
6HB-88-1	6HB-61-1'
6HB-89-27	6HB-62-27'
6HB-90-2	6HB-63-2'

Supplementary Table. 71. Protruding DNA strands used for formation of 2D-X structure. Detailed staple strands sequence information can be found in Supplementary Sequence 1. Detailed 10nt M-base sequence information can be found in Supplementary Sequence 5.

6HB-2	6HB-26	6HB-49	6HB-75	6HB-100	6HB-125	6HB-151
6HB-4	6HB-28	6HB-52	6HB-77	6HB-102	6HB-126	6HB-153
6HB-6	6HB-30	6HB-55	6HB-79	6HB-105	6HB-128	6HB-155
6HB-9	6HB-32	6HB-57	6HB-81	6HB-107	6HB-130	6HB-157
6HB-11	6HB-33	6HB-60	6HB-84	6HB-109	6HB-132	6HB-159
6HB-13	6HB-36	6HB-62	6HB-86	6HB-111	6HB-134	6HB-162
6HB-15	6HB-38	6HB-64	6HB-87	6HB-113	6HB-136	6HB-164
6HB-17	6HB-39	6HB-66	6HB-89	6HB-115	6HB-140	6HB-166
6HB-18	6HB-41	6HB-68	6HB-93	6HB-116	6HB-142	6HB-168
6HB-20	6HB-43	6HB-70	6HB-94	6HB-118	6HB-144	6HB-170
6HB-22	6HB-45	6HB-72	6HB-96	6HB-119	6HB-147	6HB-171
6HB-24	6HB-47	6HB-73	6HB-98	6HB-123	6HB-149	6HB-173

Supplementary Table. 72. Core staple strands used for formation of 3D-XZ structure. Detailed staple strands sequence information can be found in Supplementary Sequence 1.

1	4	2	5	3	0
6HB-104-9	6HB-83-9'	6HB-29-15	6HB-50-15'	6HB-160-36	6HB-137-36'
6HB-92-3	6HB-65-3'	6HB-8-16	6HB-35-16'	6HB-152-37	6HB-122-37'
6HB-95-4	6HB-67-4'	6HB-10-17	6HB-37-17'	6HB-154-38	6HB-124-38'
6HB-97-5	6HB-69-5'	6HB-12-18	6HB-40-18'	6HB-156-39	6HB-127-39'
6HB-99-6	6HB-71-6'	6HB-14-19	6HB-42-19'	6HB-158-40	6HB-129-40'
6HB-101-7	6HB-74-7'	6HB-16-20	6HB-44-20'	6HB-161-41	6HB-131-41'
6HB-103-8	6HB-76-8'	6HB-19-21	6HB-46-21'	6HB-163-42	6HB-133-42'
6HB-106-10	6HB-78-10'	6HB-21-22	6HB-48-22'	6HB-165-43	6HB-135-43'
6HB-108-11	6HB-80-11'	6HB-23-23	6HB-51-23'	6HB-167-44	6HB-139-44'
6HB-110-12	6HB-82-12'	6HB-25-24	6HB-54-24'	6HB-169-45	6HB-141-45'
6HB-112-13	6HB-85-13'	6HB-27-25	6HB-56-25'	6HB-172-46	6HB-143-46'
6HB-114-14	6HB-59-14'	6HB-1-26	6HB-58-26'	6HB-174-47	6HB-145-47'
6HB-88-1	6HB-61-1'	6HB-3-27	6HB-31-27'	6HB-148-48	6HB-117-48'
6HB-90-2	6HB-63-2'	6HB-5-35	6HB-34-35'	6HB-150-49	6HB-120-49'

Supplementary Table. 73. Protruding DNA strands used for formation of 3D-XZ structure. Detailed staple strands sequence information can be found in Supplementary Sequence 1. Detailed 10nt M-base sequence information can be found in Supplementary Sequence 5.

6HB-1	6HB-31	6HB-61	6HB-102	6HB-142	6HB-172
6HB-2	6HB-32	6HB-62	6HB-105	6HB-143	6HB-173
6HB-3	6HB-34	6HB-63	6HB-107	6HB-144	6HB-174
6HB-4	6HB-41	6HB-70	6HB-109	6HB-145	
6HB-5	6HB-42	6HB-71	6HB-111	6HB-147	
6HB-13	6HB-43	6HB-73	6HB-113	6HB-148	
6HB-14	6HB-44	6HB-74	6HB-116	6HB-149	
6HB-15	6HB-45	6HB-75	6HB-117	6HB-150	
6HB-16	6HB-46	6HB-76	6HB-118	6HB-151	
6HB-17	6HB-47	6HB-77	6HB-120	6HB-158	
6HB-19	6HB-48	6HB-78	6HB-129	6HB-159	
6HB-20	6HB-49	6HB-79	6HB-130	6HB-161	
6HB-21	6HB-51	6HB-80	6HB-131	6HB-162	
6HB-22	6HB-52	6HB-81	6HB-132	6HB-163	
6HB-23	6HB-54	6HB-82	6HB-133	6HB-164	
6HB-24	6HB-55	6HB-84	6HB-134	6HB-165	
6HB-25	6HB-56	6HB-85	6HB-135	6HB-166	
6HB-26	6HB-57	6HB-86	6HB-136	6HB-167	
6HB-27	6HB-58	6HB-87	6HB-139	6HB-168	
6HB-28	6HB-59	6HB-89	6HB-140	6HB-169	
6HB-30	6HB-60	6HB-100	6HB-141	6HB-170	

Supplementary Table. 74. Core staple strands used for formation of T1 M-DNA. Each name corresponds to one 42nt single strand DNA. Detailed sequence information can be found in the Supplementary Sequence 1.

6HB-1	6HB-26	6HB-50	6HB-75	6HB-113	6HB-141	6HB-166
6HB-2	6HB-27	6HB-51	6HB-76	6HB-115	6HB-142	6HB-167
6HB-3	6HB-28	6HB-52	6HB-77	6HB-117	6HB-143	6HB-168
6HB-4	6HB-29	6HB-54	6HB-78	6HB-118	6HB-144	6HB-169
6HB-5	6HB-30	6HB-55	6HB-79	6HB-119	6HB-145	6HB-170
6HB-6	6HB-31	6HB-56	6HB-80	6HB-120	6HB-147	6HB-171
6HB-8	6HB-32	6HB-57	6HB-81	6HB-122	6HB-148	6HB-172
6HB-9	6HB-33	6HB-58	6HB-82	6HB-123	6HB-149	6HB-173
6HB-10	6HB-34	6HB-59	6HB-83	6HB-124	6HB-150	6HB-174
6HB-11	6HB-35	6HB-60	6HB-84	6HB-125	6HB-151	
6HB-12	6HB-36	6HB-61	6HB-85	6HB-126	6HB-152	
6HB-13	6HB-37	6HB-62	6HB-86	6HB-127	6HB-153	
6HB-14	6HB-38	6HB-63	6HB-87	6HB-128	6HB-154	
6HB-15	6HB-39	6HB-64	6HB-89	6HB-129	6HB-155	
6HB-16	6HB-40	6HB-65	6HB-93	6HB-130	6HB-156	
6HB-17	6HB-41	6HB-66	6HB-94	6HB-131	6HB-157	
6HB-18	6HB-42	6HB-67	6HB-96	6HB-132	6HB-158	
6HB-19	6HB-43	6HB-68	6HB-98	6HB-133	6HB-159	
6HB-20	6HB-44	6HB-69	6HB-100	6HB-134	6HB-150	
6HB-21	6HB-45	6HB-70	6HB-102	6HB-135	6HB-161	
6HB-22	6HB-46	6HB-71	6HB-105	6HB-136	6HB-162	
6HB-23	6HB-47	6HB-72	6HB-107	6HB-137	6HB-163	
6HB-24	6HB-48	6HB-73	6HB-109	6HB-139	6HB-164	
6HB-25	6HB-49	6HB-74	6HB-111	6HB-140	6HB-165	

Supplementary Table. 75. Core staple strands used for formation of T2 and T1-R M-DNA. Each name corresponds to one 42nt single strand DNA. Detailed sequence information can be found in the Supplementary Sequence 1

T1	T2	T1-R
	6HB-104-9'	6HB-104-9
	6HB-92-3'	6HB-92-3
	6HB-95-4'	6HB-95-4
	6HB-97-5'	6HB-97-5
6HB-99-6	6HB-99-AGAGGT-6'	6HB-99-6-ACCTCT
6HB-101-7	6HB-101-AGAGGT-7'	6HB-101-7-ACCTCT
6HB-103-8	6HB-103-AGAGGT-8'	6HB-103-8-ACCTCT
6HB-106-10	6HB-106-AGAGGT-10'	6HB-106-10-ACCTCT
6HB-108-11	6HB-108-AGAGGT-11'	6HB-108-11-ACCTCT
6HB-110-12-FAM	6HB-110-AGAGGT-TAMRA-12'	6HB-110-12-ACCTCT
6HB-112-13-FAM	6HB-112-AGAGGT-TAMRA-13'	6HB-112-13-ACCTCT
6HB-114-14-FAM	6HB-114-AGAGGT-TAMRA-14'	6HB-114-14-ACCTCT
6HB-88-1	6HB-88-AGAGGT-1'	6HB-88-1-ACCTCT
6HB-90-15	6HB-90-AGAGGT-15'	6HB-90-15-ACCTCT

Supplementary Table. 76. Protruding DNA strands used for formation of M-DNA in strand displacement. Detailed staple strands sequence information can be found in Supplementary Sequence 1. Detailed 10nt M-base sequence information can be found in Supplementary Sequence 5. 6-FAM fluorescent dye is on the 3' end of 6HB-110-12-FAM, 6HB-112-13-FAM, and 6HB-114-14-FAM while TAMRA quencher is in the middle of 6HB-110-AGAGGT-TAMRA-12', 6HB-112-AGAGGT-TAMRA-13', and 6HB-114-AGAGGT-TAMRA-14'.

6HB			Bend (B)	Overall twisting (Twe)	Twist (degree)	Pitch	Rise pbp (nm)
660° dsM-DNA	Left-handed	Mean	1.090E-04	8.300E-04	33.03	10.41	3.454E-01
		STD	4.000E-06	6.100E-05	39.14		8.053E-04
	Right-handed	Mean	1.076E-04	9.439E-04	63.75	10.41	3.459E-01
		STD	8.370E-06	9.420E-05	39.78		9.267E-04
300° dsM-DNA	Left-handed	Mean	1.140E-04	9.018E-04	90.57	10.42	3.461E-01
		STD	6.000E-06	7.690E-05	42.70		9.588E-04
	Right-handed	Mean	1.120E-04	8.624E-04	59.75	10.38	3.466E-01
		STD	5.000E-06	6.910E-05	40.82		8.232E-04

Supplementary Table. 77. Data summary of simulations of individual unbound 6-helix bundles used for different dsM-DNA designs, along with the measured average dsDNA properties in the bundle (pitch and rise per base pair).

Helical twist of dsM-DNA		300° Left-handed	300° Right-handed	660° Left-handed	660° Right-handed
Wrapped	Mean	-242.6°	328.0°	-492.6°	598.1°
	STD	30.0°	32.7°	27.9°	25.4°
Un-wrapped	Mean	-66.2°	-2.3°	-211.1°	30.0°
	STD	31.9°	36.9°	28.8°	27.8°

Supplementary Table. 78. Data summary of helical-twist for wrapped dsM-DNA and unwrapped dsM-DNA.

dsM-DNA Bundle 1				Bend (B)	Overall twisting (Twe)	Twist (degree)	Pitch	Rise pbp (nm)
660°	Left-handed	Wrapped	Mean	1.100E-04	8.640E-04	163.5	10.41	3.443E-01
			STD	5.000E-06	7.300E-05	31.07		7.410E-04
		Un-wrapped	Mean	1.110E-04	8.680E-04	118.6	10.41	3.450E-01
			STD	5.000E-06	7.200E-05	30.35		7.950E-04
	Right-handed	Wrapped	Mean	1.170E-04	1.026E-03	-56.81	10.45	3.450E-01
			STD	7.000E-06	9.400E-05	34.10		8.480E-04
		Un-wrapped	Mean	1.073E-04	9.847E-04	35.19	10.46	3.458E-01
			STD	1.480E-05	1.701E-04	29.81		9.868E-04
300°	Left-handed	Wrapped	Mean	1.130E-04	8.890E-04	80.74	10.42	3.447E-01
			STD	5.000E-06	7.600E-05	34.92		8.844E-04
		Un-wrapped	Mean	1.130E-04	9.050E-04	175.7	10.38	3.457E-01
			STD	5.000E-06	7.600E-05	33.70		1.124E-03
	Right-handed	Wrapped	Mean	1.120E-04	8.980E-04	42.06	10.42	3.453E-01
			STD	5.000E-06	8.000E-05	33.74		9.339E-04
		Un-wrapped	Mean	1.120E-04	9.180E-04	95.73	10.40	3.456E-01
			STD	5.000E-06	7.800E-05	32.54		8.449E-04

Supplementary Table. 79. Data summary for Bundle 1 of dsM-DNA.

dsM-DNA Bundle 2				Bend (B)	Overall twisting (Twe)	Twist (degree)	Pitch	Rise pbp (nm)
660°	Left-handed	Wrapped	Mean	1.110E-04	9.340E-04	196.4	10.40	3.446E-01
			STD	5.000E-06	7.600E-05	33.70		9.319E-04
		Un-wrapped	Mean	1.140E-04	9.200E-04	94.40	10.39	3.459E-01
			STD	5.000E-06	7.700E-05	30.55		8.724E-04
	Right-handed	Wrapped	Mean	1.150E-04	1.016E-03	-89.99	10.42	3.449E-01
			STD	7.000E-06	9.600E-05	28.98		7.757E-04
		Un-wrapped	Mean	1.140E-04	1.050E-03	94.55	10.45	3.456E-01
			STD	1.000E-05	1.010E-04	27.92		8.113E-04
300°	Left-handed	Wrapped	Mean	1.180E-04	9.140E-04	97.32	10.42	3.447E-01
			STD	6.000E-06	7.900E-05	35.78		8.513E-04
		Un-wrapped	Mean	1.170E-04	8.967E-04	-13.08	10.43	3.458E-01
			STD	6.000E-06	7.810E-05	33.41		8.908E-04
	Right-handed	Wrapped	Mean	1.120E-04	8.649E-04	49.85	10.42	3.451E-01
			STD	5.000E-06	7.460E-05	33.12		8.275E-04
		Un-wrapped	Mean	1.130E-04	8.770E-04	45.55	10.41	3.460E-01
			STD	6.432E-05	5.025E-04	17.32		1.002E-03

Supplementary Table. 80. Data summary for Bundle 2 of dsM-DNA.

Section 10. Supplementary sequence

Name	Start	End	Sequence
6HB-1	0[1021]	2[1008]	GCGCGTAGTCCACGATACCACATTCAACGGGAACCAGACGGG
6HB-2	0[1063]	2[1050]	GCGTAACGGTGTTACATTATTACAGGTTGTACAGAGCCTTT
6HB-3	0[1105]	2[1092]	GAGCGGGTAGCCCGTGCGGAAGAAAAATCTAATCTTATAAGAA
6HB-4	0[1147]	2[1134]	AGCCGGCAGTCCACTATGCGATTTTAAGAACAAAGCCAGTTA
6HB-5	0[1189]	2[1176]	GGAACCCAAAACCGTTGAGATGGTTTTAAAAACACCATCTTAC
6HB-6	0[139]	2[126]	ACATTATTAAGCAAGCAATGCCTGAGTACGAGAGGCCAGAAT
6HB-7	0[13]	4[7]	GAAGGGTATCAGGTTTTGAGA
6HB-8	0[181]	2[168]	AAATCCTTTCGCATACGCAAGGATAAAACGTACTCGATTGGC
6HB-9	0[223]	2[210]	TTAGAAGTAGGAACTTATGACCCTGTAACCTCAGAGAGCCGC
6HB-10	0[265]	2[252]	ACTAATAGCCAGCTAAAGCCTCAGAGCAGGATAGCTCAGAGC
6HB-11	0[307]	2[294]	AATTGAGTCGGATTAAATCATACAGGCATTTTCGTCGAACCGC
6HB-12	0[349]	2[336]	TCAATCAGATAGGTGTGGCATCAATTCTGACAGCCATCTTTT
6HB-13	0[391]	2[378]	AAATCTATCTGCCAACCTGTTTAGCTATCTTCCATCATCGG
6HB-14	0[433]	2[420]	CCGCCTGGATCGCAGATTTAGTTTGACCCTAAACAACAGAAT
6HB-15	0[475]	2[462]	CCAGCAGGAAACCATCATTCATATAACGAACAACCTCACCAA
6HB-16	0[517]	2[504]	GATAGCCGTTGGGAACATGTTTTAAATAAAATCTCAAATCAC
6HB-17	0[559]	2[546]	GACAATAAGCTGGCGATGGCTTAGAGCTTCGGTTTTACCGT
6HB-18	0[55]	2[42]	TCAATATATGAACGACCGTTCTAGCTGATGAAAGTTAAGTTT
6HB-19	0[601]	2[588]	ATAGAATAACGCCAGTACCTTTAATTGTTGATACGAAGGTA
6HB-20	0[643]	2[630]	GTCACACCCAGTGCCGAACCAGACCGGACACGCATGCGCCAA
6HB-21	0[685]	2[672]	TCAATCGCCCCGGGCCGAAAGACTTCAATTAAAGGTTTATTT
6HB-22	0[727]	2[714]	GCAACAGTTTCCTGTGAGAAGCAAAGCGGACAGCAGTGGCAA
6HB-23	0[769]	2[756]	GCCTTGCATACGAGGACCATAAATCAAAAGGACTATTACGCA
6HB-24	0[811]	2[798]	GTAATAATGAGTGAGAATCCCCCTCAAATAAAATATAACGGA
6HB-25	0[853]	2[840]	CCATCACGCTTTCCTGGATAGCGTCCAAAAGAGGCGCCGAAC
6HB-26	0[895]	2[882]	GTGTTTTATCGGCCAAAGAAGTTTTGCCAGCGATTAGCTATC
6HB-27	0[937]	2[924]	AAAGGGACAGGGTGACCAGACGACGATATATCATCGTTAAGC
6HB-28	0[979]	2[966]	TCCTCGTATTGCCCTTACGAGGCATAGTCATGTTATAATTGA
6HB-29	0[97]	2[84]	GAATTATCCGGTTGGAAAGGCCGGAGACGATTAGCGCGTCAT
6HB-30	1[1036]	5[1049]	ATTTTCAGAATAACGGACAGATGAACGGAGAAAGAAAATCCT
6HB-31	1[1078]	5[1091]	ATCAGATTTTGTTTACCTTCATCAAGAGTACGTTAATAAATC
6HB-32	1[1120]	5[1133]	CGTTTTAAACAGCCACCCAAATCAACGTAACGGCCAGTTTG
6HB-33	1[112]	5[125]	ATAACGGGCAGTCTCGGATAAGTGCCGTATGTGTAACAGGAA
6HB-34	1[1162]	5[1175]	TAAATCAAACGAGCCTTGCCCTGACGAGTTTCAACACGTCAA
6HB-35	1[154]	5[167]	TCGCGCATTCACAAAATAGGTGTATCACATTTTTAATATTTT
6HB-36	1[196]	5[209]	GAAGATGATTGACACTCAGAACCGCCACTACTTTTCATTTTT
6HB-37	1[238]	5[251]	TTTAACACTCAGAGACCCTCATTTTCAGTAAAGCTCTGGCCT

6HB-38	1[280]	5[293]	ACATAAAAGAGCCGACCGTAACACTGAGAGGCAAACGAGTAA
6HB-39	1[28]	5[41]	ACAGAAAGTCAGTGATTATTCTGAAACATAAAATTTAAACAAG
6HB-40	1[322]	5[335]	ATCGTCGAAAATCATGTAGCATTCACAACTAATAATTGACC
6HB-41	1[364]	5[377]	ATAGCGAGGTCATATAAAGTTTTGTCTGATTTTCAATCGTAA
6HB-42	1[406]	5[419]	GAATTTAGCCTTTATGTATGGGATTTTGATTAGATATCGGCC
6HB-43	1[448]	5[461]	CTCCGGCATCGATAGTGAGAAATAGAAAGAGTTGATCGCTTCT
6HB-44	1[490]	5[503]	TGCAAATACCATTATTTTTTCACGTTGATGCAACTCAGGCTG
6HB-45	1[532]	5[545]	CAAATATTTGAGCCAGCCTTTAATTGTATAATTGCTTCGCTA
6HB-46	1[574]	5[587]	TGGTTTGACGGAATAATTTCTTAAACAGCCTCCTTTGCGATTA
6HB-47	1[616]	5[629]	AGAATAAAGGGCGACAACAACCATCGCCAGCAAACCTTGTAAG
6HB-48	1[658]	5[671]	AGTATCAATCAATAAGGCTTGACAGGAGATATCGCCGACTCT
6HB-49	1[700]	5[713]	ACGCTCAAAGAAACCCTCAGCAGCGAAAGATTGCACATGGTC
6HB-50	1[70]	5[83]	GATGAATTTTGTATAAGAGAAGGATTAGAGTCAAACAATCAT
6HB-51	1[742]	5[755]	AACGCCAAGCAAACCTACAGAGGCTTTGAATCAGGCAATTCC
6HB-52	1[784]	5[797]	AATAAGAAAAGAACTTCCATTAAACGGGTGCTTTACCTGGGG
6HB-53	1[7]	3[13]	TCAAAATGCCCCGTACCCCTGC
6HB-54	1[826]	5[839]	GTCCAGACCAGAAGCCAACCTAAAACGATACTGCGTGCGCTC
6HB-55	1[868]	5[881]	ACGCGCCAGCCCTTCATCTTTGACCCCCAGAGGGGAGCTGCA
6HB-56	1[910]	5[923]	AATAATATAAGAGCACAACGGAGATTTGAAAACCATGCGTAT
6HB-57	1[952]	5[965]	AATAATCTATCAGATCCGCGACCTGCTCAAGAGCAACGGGCA
6HB-58	1[994]	5[1007]	AAACCAAACCTGAACACGGTCAATCATAATAATGCAAGTTGCA
6HB-59	2[1007]	4[994]	AGAATTAGTACCGCTGCTTTGACGAGCACTGAGAGGATACAT
6HB-60	2[1049]	4[1036]	ACAGAGATCGTAGGCCCCGCGCTTAACAGGCGATTTCATCA
6HB-61	2[1091]	4[1078]	ACGATTTATAGAAGGCGCTGGCAAGTGTATCCCTTATAAAAC
6HB-62	2[1133]	4[1120]	CAAAATAGCGAACC GCGAGAAAGGAAGGGTTGTCTCATTAT
6HB-63	2[1175]	4[1162]	CAACGCTAGATTAGAGCCCCCGATTTAGGACTCCATTTAATC
6HB-64	2[125]	4[112]	GGAAAGCATTCGCCCCGAACAAAGAAACCCCAAAAGGTAAAG
6HB-65	2[167]	4[154]	CTTGATAGAGGCGAAACGTTATTAATTTAACGTTAGAACCCT
6HB-66	2[209]	4[196]	CGCCAGCATGAAACCTTTACAAACAATTATCAGCTGCGGGAG
6HB-67	2[251]	4[238]	CACCACCATTTTCATGCCGTCAATAGATATTGCGGTAAATCGG
6HB-68	2[293]	4[280]	CTCCCTCTCAATATATCTAAAATATCTTATGTGAGGAATTAG
6HB-69	2[335]	4[322]	CATAATCCTATTAAGTCAGTTGGCAAATACGGCGGGTAGTAG
6HB-70	2[377]	4[364]	CATTTTCTAGCTTAACCTTGCTGAACCTTGGGCGCTTTGGGG
6HB-71	2[419]	4[406]	CAAGTTTTCAAATGCCACGCTGAGAGCCGACAGTACATTTTC
6HB-72	2[41]	4[28]	TAACGGGTAAAGAAATTGTTTGGATTATCTGGAGCATGCCGG
6HB-73	2[461]	4[448]	TGAAACCTTAGGTTAACAGAGGTGAGGCCCGGCACTCCCAAT
6HB-74	2[503]	4[490]	CAGTAGCCCAATCGATCGCCATTAAAAACGCCATTAAAGTAC
6HB-75	2[545]	4[532]	CACCGACATTTTAGATGGCTATTAGTCTGGGCTCTGAATAT
6HB-76	2[587]	4[574]	AATATTGAAATACCACCTGAAAGCGTAACTGCAAGTGATAAG

6HB-77	2[629]	4[616]	AGACAAAACACCGGAATAAAAGGGACATCACGACGTCCAACA
6HB-78	2[671]	4[658]	TGTCACATATGCGTTGGATTATTTACATTGCAGGTGTTTTAA
6HB-79	2[713]	4[700]	CATATAAACAGTAGGCTCATGGAAATACTCGTAATTCAAAAA
6HB-80	2[755]	4[742]	GTATGTTACATGTAATCCAGAACAATATCCGCTCATCTTTAC
6HB-81	2[797]	4[784]	ATACCCAGAATATATGCCTGAGTAGAAGTGTAAGAACAGTT
6HB-82	2[839]	4[826]	AAAGTTACGACGACAACCGTTGTAGCAAATTGCGTGAATCGT
6HB-83	2[83]	4[70]	ACATGGCATAACAGTTTCCTGATTATCAGAGCATGTTACCAT
6HB-84	2[881]	4[868]	TTACCGATGTTTATAGTGAGGCCACCGATCGTGCCGTAATAG
6HB-85	2[923]	4[910]	CCAATAATCCCATCCAGGAACGGTACGCGGCGGTTAAATAGC
6HB-86	2[965]	4[952]	GCGCTAAGGCTGTCAGAGCGGGAGCTAACAGTGAGACACTAT
6HB-87	3[1022]	1[1035]	CCAACTTTTTAGGACTGGTTTGCCCCAGTGCGCCGCGTTTTT
6HB-88	3[1064]	1[1077]	GCATAGGCGGAACACCGAAATCGGCAAAAGCGGTCCAAGCAA
6HB-89	3[1106]	1[1119]	ACCGGATAGGACGTAGATAGGGTTGAGTGAAGAAACGCGAGG
6HB-90	3[1148]	1[1161]	TTCAGTGATTACCTTATTAAGAACGTGAGCTTGAGAAGCCT
6HB-91	3[1190]	0[1190]	GTAGTAACAATTTTCAGCTACTAAATC
6HB-92	3[140]	1[153]	TAAGTATTTTAAATATATTTAAATTGTATAAAAGTTACAAAA
6HB-93	3[14]	1[27]	CTATTTACAGCTATTCATTGCCTGAGAGTACTTCTGACGTAAA
6HB-94	3[182]	1[195]	TTAGTACTATTTCATAAATTTTGTAAACGACAACAGCAAAA
6HB-95	3[224]	1[237]	CCCTCAGAAAAACAGCCATCAAAAATAAATACATTAATTACA
6HB-96	3[266]	1[279]	ATAGGAAAAGCAATTTTCATCAACATTAATAGGAGCAAACAGT
6HB-97	3[308]	1[321]	CAAACATAATCCAATCTCCGTGGGAACAACAACAGTTCTGTAA
6HB-98	3[350]	1[363]	TTAGCGTTGAAAAGCACGTTGGTGAGACAAATATTGAAAAC
6HB-99	3[392]	1[405]	GTAAATGGTCAATAGTTTGAGGGGACGACAGCAGCCAATAGT
6HB-100	3[434]	1[447]	ACAGTTTACGAGTACTCCAGCCAGCTTTGGTCAGTTTTTAAC
6HB-101	3[476]	1[489]	ATTGCGAGGAAGTTGGCAAAGCGCCATTTACCGAAATGCTGA
6HB-102	3[518]	1[531]	AAGGCTCTAGCTCAAGGGCGATCGGTGCTTAATGCACTTTTT
6HB-103	3[560]	1[573]	TGCTTTCTTTTTCGGAAAGGGGGATGTGGAATACGAATTTAA
6HB-104	3[56]	1[69]	GGCTGAGATATTACAGTAATCGTAAAACTATGATGGAACGTCA
6HB-105	3[602]	1[615]	TGCGCCGATTAGAGAGGGTTTTCCAGTTCTGGCCTTAAATA
6HB-106	3[644]	1[657]	ATATTCGTTCAAAGCAAGCTTGCATGCCTGGCAGACCTGTTT
6HB-107	3[686]	1[699]	TGCGGGAAGGAAGCTACCGAGCTCGAATCTACATTAAAGCCA
6HB-108	3[728]	1[741]	GAGGGTAATTATAGTGTGAAATTGTTATTACCGCCATTTAAC
6HB-109	3[770]	1[783]	TTTCATGCGAGAATCCGGAAGCATAAAGAACTCAAAGCCAGT
6HB-110	3[812]	1[825]	CCACTACATTCATTGCTAACTCACATTATACTTCTTAATTCT
6HB-111	3[854]	1[867]	TACACTATTTAGACAGTCGGGAAACCTGGTAAAAGATGCAGA
6HB-112	3[896]	1[909]	GCGCGAATTTTGCAAACGCGCGGGGAGACAGAATCCAAGAAA
6HB-113	3[938]	1[951]	AAATTGTCTCGTTTGTCTTTCTTTTCACACAGGAGACCAATC
6HB-114	3[980]	1[993]	GGAACGAAAAGGAATTCACCGCCTGGCCCGTATAAGGGTATT
6HB-115	3[98]	1[111]	TGCTCAGAGGGTGAATAATCAGAAAAGCCACCAGAAGAAACA

6HB-116	4[1035]	0[1022]	GTTGAGATGAAAGAATAAAAAACAGGGAAAGCAAGCCTACAGG
6HB-117	4[1077]	0[1064]	GAACAACTGGCTGAACGTCAAAAATGACCAATAGACGCTGC
6HB-118	4[1119]	0[1106]	ACCAGTCATTTCATTATATTATTTATCCCCTAAGAAGCGAAAG
6HB-119	4[111]	0[98]	ATTCAAATACCAGGCTGAATTTACCGTTCATCGGGAGGAGCG
6HB-120	4[1161]	0[1148]	ATTGTGAAATAAGGGTCTTTCCAGAGCCAGGTTTTTCGGGGAA
6HB-121	4[1196]	5[1196]	ATTGGGCTCTATCA
6HB-122	4[153]	0[140]	CATATATAGCCCGGACAAATAAATCCTCACCAAGTTTGAGTA
6HB-123	4[195]	0[182]	AAGCCTTCGCCACCGGAGGTTGAGGCAGTTACCTGTCGTATT
6HB-124	4[237]	0[224]	TTGTACCAGCCACCCCGCCACCAGAACCCAAAATTTGAGGAT
6HB-125	4[279]	0[266]	CAAAATTCCCATGTCCACCCTCAGAACCTTAATGGACTAACA
6HB-126	4[27]	0[14]	AGAGGGTGGAACCTCCTTGAGTAACAGTTATTTGCAATAATG
6HB-127	4[321]	0[308]	CATTAACCAACGCCCGGAACCAGAGCCCCTTGCTTGAAAGG
6HB-128	4[363]	0[350]	CGCGAGCAACGATCGCCCCCTTATTAGCGAATCCTCAAACCC
6HB-129	4[405]	0[392]	GCAAATGAATTTTCGCGTCAGACTGTAGGAAGAGTAAATGAA
6HB-130	4[447]	0[434]	TCTGCGACAGCGGAGCAGCACCGTAATCACTACCTATTAACA
6HB-131	4[489]	0[476]	GGTGTCTATAATAACCATTAGCAAGGCCTATGTAACGAACCA
6HB-132	4[531]	0[518]	AATGCTGCAAAAGGATTGGAATTAGACGAGAAAGCGAACT
6HB-133	4[573]	0[560]	AGGTCATGAGGTGATTATTCATTAAGGTGACCTATGGCACA
6HB-134	4[615]	0[602]	GGTCAGGACAATGACATTCAACCGATTGTAAGGCGAACAGAG
6HB-135	4[657]	0[644]	TTCGAGCGTCGCTGGAAAATTCATATGGGAAAAAGTTCACCA
6HB-136	4[699]	0[686]	GATTAAGTCGTCACGCAAAGACACCACGCCAGTATTTGACGC
6HB-137	4[69]	0[56]	CAATATGACTCCTCGATACAGGAGTGTACAGGTTTCAATTCA
6HB-138	4[6]	1[6]	GATCTACTTAATGCTAAACAGTACCATA
6HB-139	4[741]	0[728]	CCTGACTGCAACGGGTAGAAAATACATATCGCCATAGCCATT
6HB-140	4[783]	0[770]	CAGAAAAAGGAAGTTGGCATGATTAAGAATTTTCGACTATCG
6HB-141	4[825]	0[812]	CATAAATGAAGGCAGAAACCGAGGAAACGGTAAAGTTGATTA
6HB-142	4[867]	0[854]	TAAATGAAACACTTTTAAGAAAAGTAATCAGCTAAGTCTGT
6HB-143	4[909]	0[896]	GAGAGGCACAAAGTAAGAAACAATGAAATCCTGAACTGAGAA
6HB-144	4[951]	0[938]	CATAACCGTCGAAAGAGATAACCCACAATGTAGAAGCCGATT
6HB-145	4[993]	0[980]	AACGCCAGGCGCAGACCCTGAACAAAGTCAAGAACCGTGCTT
6HB-146	5[0]	0[0]	AAAGGCTTAGAACCC
6HB-147	5[1008]	3[1021]	GCAAGCGCTATGGTACTCATCGAGAACAGCGCATTGAACTGA
6HB-148	5[1050]	3[1063]	GTTTGATCACCACAAATCATTACCGCGCAAATAGCACCAGGC
6HB-149	5[1092]	3[1105]	AAAAGAACGCTAGGGCTTATCCGGTATTAATCCAAGACAAGA
6HB-150	5[1134]	3[1147]	GAACAAGGAACGTGTCCCAGCTTGC GGTAATTTGCTGCTCA
6HB-151	5[1176]	3[1189]	AGGGCGATAAAGGGTTGCTATTTTGACATCCTGAAGAACGA
6HB-152	5[126]	3[139]	GATTGTACATTTTGTGATTGCTTTGAATATTTAAAGGTTGATA
6HB-153	5[168]	3[181]	GTAAAAATTGCCCATTATTCATTTCAAGTCAGACAGGAGGT
6HB-154	5[210]	3[223]	TAACCAATATTAGAAAACATCAAGAAAAACCACCAACCGCCA

6HB-155	5[252]	3[265]	TCCTGTAGATTAGATTGAATTACCTTTTGCCACCCAAGCCCA
6HB-156	5[294]	3[307]	CAACCCGGAAGGTTATGTGAGTGAATAAACCCACCGACCAGTA
6HB-157	5[336]	3[349]	GTAATGGATATCTGTTAATTTCCCTTAGTTTGCCCTCATAG
6HB-158	5[378]	3[391]	CCGTGCAAAGCATCGATTAAAGACGCTGACGCGTTTGACGTTA
6HB-159	5[420]	3[433]	TCAGGAACAACAGTCATAGGTCTGAGAGAGTAGCGACTTTCA
6HB-160	5[42]	3[55]	AGAATCGAATCCTGATTGCGTAGATTTTCTGGTAAATTAAGA
6HB-161	5[462]	3[475]	GGTGCCGAAGATAAGGGTTATATAACTAGGAAACGTAAAGGA
6HB-162	5[504]	3[517]	CGCAACTCTAAACCAAGACAAAGAACGGCCAGCACAAAAA
6HB-163	5[546]	3[559]	TTACGCCTTTTTGATTAAATTCATCTTCTGAATTAATCAGCT
6HB-164	5[588]	3[601]	AGTTGGGCCTTCTGGACCGTGTGATAAAAGGGAGGCGATAGT
6HB-165	5[630]	3[643]	ACGACGGGACCAGTAATCATAATTACTATTTACCAAACCGAT
6HB-166	5[672]	3[685]	AGAGGATTCTGAAATATACAAATTCCTAGAATAAGCCGCTTT
6HB-167	5[714]	3[727]	ATAGCTGGAAAAACGGCTTAATTGAGAACATAAAGTCGGAAC
6HB-168	5[756]	3[769]	ACACAACCTGGTAATATTTAGGCAGAGGCCTCCTTAAAGACTT
6HB-169	5[798]	3[811]	TGCCTAACATCACTAAGTACCGACAAAAGCAATAACGTAATG
6HB-170	5[840]	3[853]	ACTGCCCACAAATTAATAAACACATGTGCAGATAAAAAGAA
6HB-171	5[84]	3[97]	ATGTACCCATCATAAACAGTACCTTTTACCAGTAAGGGGTTT
6HB-172	5[882]	3[895]	TTAATGATATAATCCAACAATAGATAAGTAGCAATATACCAA
6HB-173	5[924]	3[937]	TGGGCGCTTTTAGACTAATTTACGAGCAGAATTGAGCCTGAT
6HB-174	5[966]	3[979]	ACAGCTGTAGAATCTTTCCTTATCATTCCAGAGGGCTTAGCC

Supplementary Sequence 1. DNA sequences of linear M-DNA.

6HB-link-56-0	ACTTCTGAATAATGGAAGGGTTAGAACCTAAAGCACTAAATCGGAACCTAAAGGG
6HB- link -56-1	TTGCTATTTTGCACCCAGCTAGGTGCCGTACCATATCAAAATTATTTGCACGTAAA
6HB- link -56-2	CCTTGAGTAACAGTGCCCGTATAAACAGGGGTCGACAATTTTATCCTGAATCTTAC
6HB- link -56-3	AAACACCAGAACGAGTAGTAATTTTTTGTTAATGCCCCCTGCCTATTTGGAACCT
6HB- link -56-4	AGAGGGTAGCTATTTTGTAGAGATCTACAATCAAGATTGGGCTTGAGATGGTTTAA
6HB- link -56-5	AGGGCGAAAAACCGTCTATCATCACCCAAAAGGCTATCAGGTCATTGCCTGAGAGT

Supplementary Sequence 2. DNA sequences used to self-linking of M-DNA.

Name	Start	End	Sequence
TR-1	15[2]	14[2]	TTTTTATGAACGGTAATCGAAGGCGTTAAATAATTTTT
TR-2	0[244]	2[231]	GAAAGCGTTCCATTCTGGCTGACCTTCAAATAAGGCCATTAC
TR-3	10[300]	6[287]	AAATCGGTAAATTACGCTCAACAGTAGGCCTGAACTAGAAGG
TR-4	3[77]	1[90]	TGGTAATATTGCGACATCGCCACGCATTTATTCTGCCACCC
TR-5	16[342]	12[329]	GCTTCCGAACAAGCAGCAGAGAAGATAAAGACAACATCATAT
TR-6	3[161]	1[174]	TCTGACAGTAAATGAGCGAAAGACAGCATGGTAATCCATGTA
TR-7	7[259]	11[272]	CGCGCCTTTTAACATCACCATCAATATGCCTGTAATCTGCGA
TR-8	0[202]	2[189]	CATGGCTTTTGATGTTTCGTCATCGATAGGAAACCACCAGTAC
TR-9	15[287]	13[300]	ATAAATCAACGCGCCATGGTCATAGCTGCAATATAGAGGATT
TR-10	7[217]	11[230]	TCCAGACGCCAGTAGGTAAAGATTCAAAGATAAAAGGTGTCT
TR-11	17[273]	15[286]	CTCGAATGATTATACCGTCAATAGATAACCACGCTATCCCTT
TR-12	3[287]	1[300]	GGTTTAACCAACTTAAAACGAAAGAGGCTCAGACGATTAGCG
TR-13	0[76]	2[63]	GAAAGTACAACAACATAATAATTTTTTCACTATCGGCGTAAG
TR-14	9[77]	7[90]	ATTCAACCAGAAAAGACCGGAAGCAAACATCCAAACCACAAG
TR-15	12[202]	14[189]	TTGCGTAGATTTTCATAGGTCGCAAATCTCAGTTGTGAGAGA
TR-16	15[161]	13[174]	CATTTTTTTCATCAGCGATTAAGTTGGGATGAATAAATAGTG
TR-17	6[160]	8[147]	AACGCTAGATGGCTTTTAGACTGGATAGCTCGTTTAAGAACT
TR-18	5[147]	3[160]	TCGTCACTCAGTGCGATAGCAAGCCCAAGGATTATTCAATCG
TR-19	17[21]	15[34]	CAGCTTTAGAAAACCTGAATTACCTTTTTACCGTGTAGCATGT
TR-20	14[314]	16[301]	GTCAGTAATTAGACTGATGGCAATTCATTTTCTGTTAATGA
TR-21	9[119]	7[132]	GCATAGTCATAAATTTAATTGCTCCTTTAATTTGCATGAAAT
TR-22	12[76]	14[63]	TTATTCACGCCATTGTGTAGATGGGCGCGAAAAGCATCTTCT
TR-23	4[342]	0[329]	CTTAGCCAACCTGGCGGGAGGGAAGGTAACGGAACCAGCCGCC
TR-24	8[314]	10[301]	CAGTATACCCATCCCAATAGCAAGCAAAACATTTCTAAAGCT
TR-25	5[273]	3[286]	GAAGGCATCACAAAATTTTCGGTCATAGACCGACTTTGAGAT
TR-26	12[118]	14[105]	GATTGCTGGGCCTCGGAACAAACGGCGGAATTGTAAGAACGC
TR-27	7[133]	11[146]	AGCAATATTAAGACACACTATCATAACCCGTCCAAAGGTCAT
TR-28	1[91]	5[104]	TCAGAACACAGAGAACAATATTACCGCCTAGAAAGATATTCTG
TR-29	15[35]	13[48]	CAATCATGTTTGAGCGCTTCTGGTGCCGAAGATGAAACAGTA
TR-30	3[2]	2[2]	TTTTTAAAACCGTCTATCATAATGCGCGAACTGTTTTT
TR-31	10[174]	6[161]	GTAATAGAAAACCACAATAATAACGGAATTAAGAATCTTACC
TR-32	16[90]	12[77]	GATAGGTGATTGTAAATATATTTTAGTCTTGCTTAGGCGAA
TR-33	13[133]	17[146]	TAGCGATTGCTGATTTTCGCATTAAATTTTCGAGTAAGAAAGGG
TR-34	17[231]	15[244]	GCATGCCCAAAATTTCTAAATATCTTTCCTTGCTCAGGCGA
TR-35	13[301]	17[314]	TAGAAGTTTAACACTAGCCCGAGATAGGAGCTGCATGTGAAA
TR-36	13[259]	17[272]	CTAATAGAATGAAAGGTGGTCCGAAATTGCGTATTACCGAG
TR-37	1[2]	0[2]	TTTTTGGATAAGTGCCGTCGCTCAGTACCAGGCTTTTT
TR-38	4[48]	0[35]	CAAAAAATGCCTGAACAATATTTTGAAAAGTATAGATTAGG
TR-39	17[357]	15[370]	CATAAAGAGAAACCACGTTATTAATTTTTTCGCCATGACTCCA
TR-40	1[301]	5[314]	TTTGCCATAAAGGTTTTAATCATTGTGAATCATAATACACTA
TR-41	12[286]	14[273]	TTGTTTGTGTAATGGGGAGAGGCGGTTCCGCAAGAGAGCC
TR-42	0[160]	2[147]	AACGGGGCCTCAGCAATTTTCTGTATGGTTGACGCTTACATT

TR-43	16[389]	17[389]	TTTTTTGAGTGAGCTAACTCCTGGGGTGCCTAATTTTT
TR-44	11[2]	10[2]	TTTTTCAAAAAGATTAAGCAAAGCGGATTGCATTTTT
TR-45	3[203]	1[216]	TCAACGTACCGGATGGCTTTGAGGACTACAGTAAGGTAATCA
TR-46	2[272]	4[259]	TTTGGGACATCGGCCAAATAAATCCTCACGTAATGTGTACAG
TR-47	4[132]	0[119]	ACTTTCAGCTCATGTACACGACCAGTACCTCAGAAAACAGT
TR-48	11[147]	9[160]	TTTTGCGACGAGCGTACCGAAGCCCTTTTACCCAAACCAGAC
TR-49	4[216]	0[203]	GACAAGAAACAAAGGAAACGTCACCAATCAGCACCCGTCATA
TR-50	2[188]	4[175]	AAACTACACTGAGTATACAGGAGTGTACTCGGAACCTTTCCA
TR-51	11[231]	9[244]	GGAAGTTTGCGGGAATAAACACATGTTTTTAGGCGAAAGGC
TR-52	16[48]	12[35]	TCTGCCAATGTACCGGTTTGAAATACCGTAATGGATGAAACA
TR-53	0[370]	2[357]	ACCACCCACAACGGGTCGAAATCCGCGAAGGACGTGGGCGAC
TR-54	11[315]	9[328]	GTCAATACCGCGCCTAATTTACGAGCATATACAAATTTGAGA
TR-55	6[202]	8[189]	TGCTATTTTGCACCAAGTTACACAAAAGAGTACCGCAGAAGG
TR-56	13[175]	17[188]	AATTTATTTTAACCTAGGAACGCCATCACTGGCCTAGGGTTT
TR-57	10[90]	6[77]	AACAGTTTAATGCAATAAAGGTGGCAACAGATAACTAAGAAA
TR-58	11[63]	9[76]	TTCAAAGTTGTTTACGCTAATATCAGAGATATAAAATACCAC
TR-59	7[91]	11[104]	AATTGAGTACATACGATACATAACGCCACCTCAAAGGTCAGG
TR-60	6[286]	8[273]	CTTATCCGATTTAGAAAAACATTATGACATATTCATGAGAAAT
TR-61	14[272]	16[259]	AGCAGCAATTAGAGCTTCTGAATAATGGCCCCGGGTGGGCGC
TR-62	15[203]	13[216]	AGTTGCATTACCGTTGTAAAACGACGGCAGAAATGAAAGGA
TR-63	10[132]	6[119]	GAATCGTAAGAGCATCCTTATTACGCAGAGAAACACAGTTAC
TR-64	5[231]	3[244]	AGGAAGTCAGTCTCAAGTTTGCTTTAGAGTAGCACTTGCCC
TR-65	6[370]	8[357]	CTCATCGGTGGCATATCCAATAAATCATTGAGAGTTTACTAG
TR-66	1[259]	5[272]	GCGTTTTATTAGAGAGAACGAGTAGTAATGAACGGCCACTAC
TR-67	0[286]	2[273]	TTGATATCCAACCTTGAAAGAGGACAGAAATTGGGCTGAGCCA
TR-68	9[35]	7[48]	TACAGGTCCTGACTACTTCAAATATCGCAATAGCACAAAAGTC
TR-69	0[328]	2[315]	GCCAGCACATCTTTGGCGCAGACGGTCAATTACCTCGGAAAT
TR-70	15[329]	13[342]	CAGTTTGAGTCGGGCAATTCCACACAACAATTATCCGTATTA
TR-71	17[315]	15[328]	TTGTTATTATCAGATTTACAAACAATTCACAGAGGGTTGTTC
TR-72	10[258]	6[245]	GCGGGAGAGTCAAAACGCCAACATGTAACAGCTAACGAACCT
TR-73	6[34]	8[21]	CAGAGAGCCGAAAGATTATAGTCAGAAGCGGAACATCAATAG
TR-74	4[174]	0[161]	GACGTTAGACAGCCGTAGCATTTCCAAATTAGGAACAAGTTTT
TR-75	16[300]	12[287]	ATCGGCCAAAAGAACGCCTGCAACAGTGTACATTTATCCTGA
TR-76	10[342]	6[329]	GAATTAGAAAGGCTGTATCATATGCGTTGTAGAAACGTAGGA
TR-77	4[300]	0[287]	GAAGTATTTCAACGAATTATCACCGTCCCCCTTATTGGCC
TR-78	0[34]	2[21]	ATTAGCGATTTCTTCAAAGGAGCCTTTTTGATTATAGTCTT
TR-79	7[301]	11[314]	ATAATATAAGCCAAATGCCGAGAGGGTCAGAGCAGCAAATG
TR-80	7[343]	11[356]	ATAATCGCTGTTTAATCAGGTCATTGCCACAGGCACGCGAGC
TR-81	4[258]	0[245]	ACCAGGCAAACACCCAGCAAATCACCCTCAGACAGAATG
TR-82	13[217]	17[230]	ATTGAGGAAACCCTGTCCACGCTGGTTTACGGGCACAAGCTT
TR-83	13[2]	12[2]	TTTTTTTAAACAATTCATTAAAATTAATTACATTTTTT
TR-84	5[315]	3[328]	AAACACTTTGACAGATAATCAAAATCACATATTGATATGCCA
TR-85	8[272]	10[259]	CGCCATAGTTTATCTAAGAACGCGAGGCTCCCAATTACTTTT

TR-86	11[105]	9[118]	ATTAGAGACAGCCACAATAATAAGAGCATATGTTATTACGAG
TR-87	9[2]	8[2]	TTTTTATAAAACGAACTAAAAAATTCATATGGTTTTTT
TR-88	7[175]	11[188]	CAGATAGGGAAACGAAATAGCGAGAGGCTTTTGCCAATGCTG
TR-89	8[62]	10[49]	CAAAGACAATTGAGACGTCAAAAATGAAGTTTTAAAATCAGG
TR-90	12[389]	13[389]	TTTTTCATTATCATTTTTGCAAAAGTTTGAGTAATTTTT
TR-91	12[328]	14[315]	TCCTGATCCGCTCAAAACCTGTCGTGCCGTTGAGTTGAGGCG
TR-92	3[35]	1[48]	CATCCTAAGGCTCAAACAGCTTGATACAGAGAAGGCCCGGA
TR-93	5[2]	4[2]	TTTTTATCAGCTTGCTTTCAATTGTATCGGTTTTTTTT
TR-94	6[389]	7[389]	TTTTTAACCAAGTACCGCAAAGAACGGGTATTATTTTT
TR-95	14[104]	16[91]	GAGAAAAATATTAATCCAAGTTACAAAATGTTGGGAGTAATGG
TR-96	16[258]	12[245]	CAGGGTGGTTTGATAATCTAAAGCATCAAGGAGCAAGAACCT
TR-97	1[133]	5[146]	CCCTCATTACCAGGAAATACCTACATTGATTTTGTGCGGGA
TR-98	2[62]	4[49]	AATACGTTATCACCGCTGAGACTCCTCACGATAGTAAATCTC
TR-99	7[49]	11[62]	AGAGGGTACCACGGTTCATCAGTTGAGAAATCAAATTCGAGC
TR-100	1[175]	5[188]	CCGTAACAACGCCTCTCATAGTTAGCGTTTGTCTGAGGGTA
TR-101	10[48]	6[35]	TCTTTACAGAAAGAAATAAGTTTATTTTCCCTGAAGCCTTTA
TR-102	8[389]	9[389]	TTTTTGAATAAACACCGGAAAAACAAGAGAATCGTTTTT
TR-103	9[161]	7[174]	GACGATATAAAATGTAGAGCTTAATTGCTCCTGAAAAGTAAG
TR-104	15[77]	13[90]	ACAGGAACACGTTGCAGGCTGCGCAACTCGCGCAGCTGTAAA
TR-105	2[146]	4[133]	GGCAGATTTTCAGGCTTGAGTAACAGTGCCGCTTCTAAACA
TR-106	12[370]	14[357]	GGAACAATGTAAAGCACATTAATTGCGTGAACGTGTAAAAAT
TR-107	14[356]	16[343]	ACCGAACTGCCCGAACCAAGGAGCGGATACGAGACTGCCC
TR-108	10[216]	6[203]	GAACCCTATGTGTAATAAGAGAATATAAGTAAAGTGATTAGT
TR-109	7[2]	6[2]	TTTTTCGCATTAGACGGGATAAAAAACAGGGAAGTTTTT
TR-110	8[188]	10[175]	AAACCGACCGAACACAGCTACAATTTTATGAATATAGAGGGG
TR-111	0[389]	1[389]	TTTTTCCACCCTCAGAGCCCACCCTCAGAACCGTTTTT
TR-112	4[389]	5[389]	TTTTTGCTGATAAATTGTAGATTTGTATCATCTTTTT
TR-113	15[245]	13[258]	AAATCCTGTTTTTCCGACTCTAGAGGATAAGGGTTCTAACAA
TR-114	16[132]	12[119]	TCGGATTGTTAAAAGCAAATCCAATCGCAATCCTTTTCGCT
TR-115	6[328]	8[315]	ATCATTAACCTGTTAAGCAATAAAGCCTAGCTATTTTCTTAC
TR-116	1[343]	5[356]	CCACCGGCGATTGATCATTATACCAGTCCCTGCTCGCGCGAA
TR-117	2[230]	4[217]	CATTAGCCAGAATCTGAATTTACCGTTCAAGACTTTAATCTT
TR-118	4[90]	0[77]	TAAAGGAATCCAGATAGAACCCTTCTGATAGTACCGAAACAT
TR-119	16[216]	12[203]	ATTGCCCGCAAGCGCAATCAATATCTGGAACAGTTAAAGAAA
TR-120	6[76]	8[63]	CGATTTTCGAACCACGAGAATGACCATATTTAGGAAGAAACG
TR-121	10[389]	11[389]	TTTTTGTAGTAGCATTAAACCAATTCTACTAATATTTTT
TR-122	14[188]	16[175]	CTACCTTCAAAATCAGGTTTAACGTCAGTAACGCCTCCTGTA
TR-123	9[329]	7[342]	GATCTACCAAAATTTAGCTATATTTTCATTTTCATCCAATCA
TR-124	11[21]	9[34]	AGGAAGCAATAACAGAATTAAGTGAACAGTCACAAACATTAT
TR-125	5[21]	3[34]	GAGGTGAGGGTTTTGAGAGGGTTGATATTGGCTATGTAATAA
TR-126	11[357]	9[370]	TGAAAAGAGAACAAATTCCTTATCATTCATCATAACTGGAGC
TR-127	8[146]	10[133]	GGCATGAGCTATCTTCTTTCCAGAGCCTTGATAAGTACTGCG
TR-128	2[356]	4[343]	ATCAACAACCGCCCGCCACCAGAACCAATACCAACATGTTA

TR-129	2[389]	3[389]	TTTTTTTACCAGCGCCAAAAAAATCTACGTTATTTTT
TR-130	12[244]	14[231]	ACCATATTGCAGGTTTTTCACCAGTGAGGCCCCAGGAACCTC
TR-131	9[287]	7[300]	TAGCTGATTGTACCTTTGACCATTAGATTCAGATAAAGAAAA
TR-132	0[118]	2[105]	TAATGCCAGGCTTGCAGCGGAGTGAGAAAGCCATTGGACATT
TR-133	12[34]	14[21]	AACATCACCGGCACGGGACGACGACAGTTAAAACTGATAAAT
TR-134	14[389]	15[389]	TTTTTATAGCCCTAAAACAACGTCAAAGGGCGATTTTT
TR-135	13[49]	17[62]	CATAAATATTTAATCCGTTGATAATCAATCGTAAGGCAAAG
TR-136	1[217]	5[230]	GTAGCGAAAGGCCGCTGCTCATTCAAGTGCAAGAGTTTCATG
TR-137	11[189]	9[202]	TAGCTCAACATGTTTTTAAATAAAGAAGTTTTGCAGCAATGC
TR-138	13[91]	17[104]	TCGTGCGCTTTTCTAAGCAAATATTTAATTGACCAGGGCGA
TR-139	14[62]	16[49]	GACCTAACAATATATACCTGAGCAAAAGGAAACCACCGTGCA
TR-140	15[119]	13[132]	ATATTTTCTCCGTGTTCTGCTATTACGCCTAACGGAGAAAACA
TR-141	5[105]	3[118]	GTCGCTGCCCTGCCCTCAGAACCGCCACATAAAAGGCAACAG
TR-142	12[160]	14[147]	ACAGTACCTGCAAGACATTAAATGTGAGTTGTTAATAACTAT
TR-143	11[273]	9[286]	ACGAGTAGGTATTCAACAATAGATAAGTGCTTAATACCGTTC
TR-144	6[118]	8[105]	AAAATAAAGTACCTATTTCATTGAATCCCAAAGGAAGCAAACG
TR-145	2[104]	4[91]	CTGGCCACGCCACCTATTTTCGGAACCTAAACCGATGAACAAC
TR-146	3[245]	1[258]	TGACGAGGCATAGGAAACGGGTAAATATTAAAGCCTGTAGC
TR-147	14[230]	16[217]	AAATATCAAGGTAAATTTGCACGTAAAACCAAGTGCACAGCTG
TR-148	2[314]	4[301]	TATTCATTCTTTTCGAGGTTGAGGCAGGAAAAGAAGGGAACC
TR-149	3[119]	1[132]	GAAAAACACAGTTTCAGGGAGTTAAAGGCCCCGTATGCCACCA
TR-150	8[104]	10[91]	TAGAAAATTAAGCCTATTATTTATCCCATCCAACATGCTTTA
TR-151	17[2]	16[2]	TTTTTGATCGCACTCCAGCATCGGCCTCAGGAATTTTT
TR-152	3[329]	1[342]	TTTTAAGGGAACGAGACCCCCAGCGATTCCACCAGAGAGCCA
TR-153	6[244]	8[231]	CCCGACTTCATTTCCTATTTCAACGCAAGAGGGTGAAGAGGCA
TR-154	13[343]	17[356]	AATCCTTGAACCACAGTCCACTATTAAATGCGCTCCCGGAAG
TR-155	5[189]	3[202]	GCAACGGCTACAGAATTCATTTAAAGTTAACGATCACCCAAA
TR-156	8[356]	10[343]	AAAAAGCGCTGTCTGCAAGCCGTTTTTATTTGGGGAGGCAAA
TR-157	8[230]	10[217]	TTTTCGAGACGACAGGTTTTGAAGCCTTAAAGTACATTTTTA
TR-158	16[174]	12[161]	GCCAGCTTAACCAATCCGGCTTAGGTTGAAGAGTCTACAGTA
TR-159	5[357]	3[370]	ACAAAGTTCAGAGCTCCCTCAGAGCCGCGACAAAATGGGAAG
TR-160	17[63]	15[76]	CGCCATTTTTCAATTGTGAGTGAATAACTAATTTCCCCAAAA
TR-161	17[105]	15[118]	TCGGTGCTTGAATATAATTTCCCTTAGAAGACAAAACGTTA
TR-162	17[147]	15[160]	GGATGTGCTTTTACATTAAGACGCTGAGGGTTATAATCAGCT
TR-163	9[203]	7[216]	CTGAGTACATATATTTAAATATGCAACTAAATCAAAATTCTG
TR-164	9[245]	7[258]	CGGAGACAAGCCTTATATAACAGTTGATGTTTTAGTGCAGAA
TR-165	5[63]	3[76]	ACAATGATTAAGAGGTACTCAGGAGGTTCTGAAAGCCTTGC
TR-166	1[49]	5[62]	ATAGGTGGGCACAGGTAGAAGAACTCAAACGTTGATGCGCCG
TR-167	17[189]	15[202]	TCCCAGTCACGACGCCTGGCCTTCGCGTAAAATAACTGAGAG
TR-168	14[146]	16[133]	ATGTAAAAGCTTAGATCGGGAGAAACAAAGCTGGCCAACCCG

Supplementary Sequence 3. Basic DNA sequences used to form Triangle (triangular M-DNA).

Name	Start	End	Sequence
SQ-1	0[34]	2[21]	CCCGAAATCAGAGCTAAATCATACAGGCAACGCTCCTGTTTA
SQ-2	0[76]	2[63]	GTCAGAACCCTGTAGGTGGCATCAATTCCAACGCCACGACGA
SQ-3	0[118]	2[105]	TGACCATGGATAAAAAACCTGTTTAGCTATAATAAGAGAATAT
SQ-4	0[160]	2[147]	TGAATCCCCCTCAAAACATGTGAAAAATTTGGGAATTTAAAT
SQ-5	0[202]	2[189]	CTGGATACCGGAGACCCCCAAAAACAGGAAATCAGCATTTTAA
SQ-6	0[244]	2[231]	AAAAGAAGTAGCTGTAGCATGTCAATCAATTCGCGTGGTTTA
SQ-7	0[286]	2[273]	TACCAGAAGATCTATCTGGAGCAAACAAAATGTGACTGACGA
SQ-8	0[305]	1[305]	ttttTCATAACCCTCGTTTAAGAGCAACACTAtttt
SQ-9	1[2]	0[2]	ttttATTTCGAGCTTCAAAAATATCGCGTTTTAtttt
SQ-10	1[49]	5[62]	AGGTCAGCAACATGATCGCCATATTTAATACTAATCAAAAAC
SQ-11	1[91]	5[104]	GAGGTCACGACAAACATTTTCGAGCCAGTATTTTCTTATTTT
SQ-12	1[133]	5[146]	TAATGCTTAAAGTATTCTGCGAACGAGTCATTAGATTTTAAA
SQ-13	1[175]	5[188]	CGAACTACTCATTATTAAATTTTGTAAAGATTGTAAGGGTG
SQ-14	1[217]	5[230]	AGTTGAGCTTTAATCGCCATCAAAAATATATGTACGATATTC
SQ-15	1[259]	5[272]	TAACGCCCAGAACGTTTCATCAACATTAGAGAATCTAGCTAT
SQ-16	2[62]	4[49]	CAATAAAGATTAGAGGATTGCATCAAAAAGTTGTACAGTAGTA
SQ-17	2[104]	4[91]	AAAGTACTTTTGCAAATCAGGTCTTTAGAAGCCTATTTGGG
SQ-18	2[146]	4[133]	ATGCAACGTAGCTCATGCTTTAAACAGTTCATATATACATTT
SQ-19	2[188]	4[175]	GAAGTGGACGGAACATACTGCGGAATCGGATTCAAATAAGCA
SQ-20	2[230]	4[217]	ATTTCAAATTTAGGCAGAGGGGGTAATATCAATATCCCCGTT
SQ-21	2[272]	4[259]	GAAACACAAAAGGAAAAAACCAAAATAGGAGAGGGGATGAAC
SQ-22	2[305]	3[305]	tttttATTTCAGTGAATAAGACAACCCGTCGGATttttt
SQ-23	3[2]	2[2]	tttttACCAGTATAAAGCCTCAACAATAGATAAtttt
SQ-24	3[35]	1[48]	GGGCTTACATCCAAATAAAGCTAAATCGAGATTAACTCCAAC
SQ-25	3[77]	1[90]	AATTTAGCTGAAAAATACTTTTGCGGGACCCTGACTTGATAA
SQ-26	3[119]	1[132]	CAGTTGAGGTCAATAATTTTGTAGAACCTCAGAACTGAATA
SQ-27	3[161]	1[174]	TGTTAAAAAATTGTAATGTGTAGGTAAATCATAAAAAATAAAA
SQ-28	3[203]	1[216]	TTAACCAAGAAAAGCAGTCAAAATCACCAGTAAAATATTTCATC
SQ-29	3[245]	1[258]	TTCTGTGTAAACATAAATTAATGCCGCGAGAGGAGATACA
SQ-30	4[48]	0[35]	GCATTAAATTGAGATTGAGCTAATGCAGAAGCAAAGAGGAAG
SQ-31	4[90]	0[77]	GCGCGAGGCAGAGGAGGTAAAGTAATTCGCTCCTTTATTATA
SQ-32	4[132]	0[119]	CGCAAATTTCCCAACGGTGTCTGGAAGTTTAATTGACGAGAA
SQ-33	4[174]	0[161]	AATATTTATTCGCATACCAGTCAGGACGCTACGTTTATTCAT
SQ-34	4[216]	0[203]	GATAATCATAGGAACATTGTGAATTACCTAGAAAGGTTTAGA
SQ-35	4[258]	0[245]	GGTAATCAGCCAGCAGTAGTAAATTTGGGCTAATGCCTTTTGC
SQ-36	4[305]	5[305]	tttttTCATTGCCTGAGAGCAAAGGCTATCAGGttttt
SQ-37	5[2]	4[2]	tttttGCAAAATTAAGCAAAAGGCAAAGAATTAtttt
SQ-38	5[21]	3[34]	TAAAGCCGACTTCAGCGAACCAGACCGGAACGCGCAACAGTA
SQ-39	5[63]	3[76]	ATTATGAGCAAAGCGAGTACCTTTAATTTGTCCAGAACATGT
SQ-40	5[105]	3[118]	AACGCAAAAATCAAGGATGGCTTAGAGCTTCATTCCATATAA
SQ-41	5[147]	3[160]	TGCAATGCCTGAGTAAACGTTGTTTGACAGATTTAAATATTT
SQ-42	5[189]	3[202]	AGAAAGGGCGTCCAAACATTATTACAGGTTATGCGTCATTTT
SQ-43	5[231]	3[244]	AACCGTTGTTTGTCAATACCACATTCAACTTGAGATCTGGCC
SQ-44	5[273]	3[286]	TTTTGAGCGACGATATTACGAGGCATAGGCTTGCCGCGAGTA
SQ-45	6[34]	8[21]	ACCAACCGTTGTAAGCTGCAAGGCGATTAAACGGCGATCAACG

SQ-46	6[76]	8[63]	TTTCCATTTCGACTCCGGGCCTCTTCGCTATGGGCGATCAAGA
SQ-47	6[118]	8[105]	GCTACAGTCATGGTTTCGCCATTTCAGGCTACGACAGATGAACG
SQ-48	6[160]	8[147]	CCCTCAGCAGCGAAGACGGTCGGATTTTCTGTATGAATCATA
SQ-49	6[202]	8[189]	GAGGCTTGCCCTGGGCCTGAGAGAGTTGCAATCCCTTTTGTCTG
SQ-50	6[244]	8[231]	ACAACAATTGCGCTCCAGTGAGACGGGCTGTTGTTATTCCAC
SQ-51	6[286]	8[273]	AATTTCTCAGCTGCAGGCGGTTTTCGCTAGGACTCCACACTGA
SQ-52	6[305]	7[305]	tttttTTGCTTTTCGAGGTGATCGGTTTATCAGCttttt
SQ-53	7[2]	6[2]	tttttATACACTAAAACACAAAGAGGCAAAAGAttttt
SQ-54	7[49]	11[62]	AGCGCGATGACAAGTCACGTTGGTGTAGATTACGCTGCATGC
SQ-55	7[91]	11[104]	TAAATTGGACCAGGAGTTTGAGGGGACGGCGCAACGCTCGAA
SQ-56	7[133]	11[146]	CGGAACGCGAACTGACTCCAGCCAGCTTTGGTGCCATTGTTA
SQ-57	7[175]	11[188]	AACAGTTAGACGTTTCCGAAATCGGCAAAAGCAAGCGCATAAA
SQ-58	7[217]	11[230]	AATTGCGCCTCATAGAGATAGGGTTGAGAACAGCTTCACATT
SQ-59	7[259]	11[272]	AAAGGCTCACCAGTCTATTAAAGAACGTTTGGGCGGAAACCT
SQ-60	8[62]	10[49]	GTAATCTAACAAAGGTAATAACGTAATCCAAGCTCAGCTGG
SQ-61	8[104]	10[91]	GTGTACATGTCTGAAGAGGACTAAAGACTGTACCGATGTTGGG
SQ-62	8[146]	10[133]	AGGGAACAGGCGCAAGACAGCATCGGAAGTGTGAAGGAAACC
SQ-63	8[188]	10[175]	TCTTTCTCAGCGGGTTAAAGGCCGCTTGCCGGAAGGTCCAC
SQ-64	8[230]	10[217]	AGACAGCAATAATACCACGCATAACCGAAGCTAACGATTGCC
SQ-65	8[272]	10[259]	GTTTCGTCCAAAAGCTTGATACCGATAGCAGTCGGCCAGGGT
SQ-66	8[305]	9[305]	tttttAATAGGAACCCATGAAGGGCGAAAAACCttttt
SQ-67	9[2]	8[2]	tttttTCTCCGTGGGAACATAACAAAGCTGCTCttttt
SQ-68	9[35]	7[48]	CGTAATGGGGATGTAACGACGGCCAGTGGCCACTATATACCA
SQ-69	9[77]	7[90]	ACCGTGCATCGGTGTAGAGGATCCCCGGTTTTTCATCGCCTGA
SQ-70	9[119]	7[132]	CTCAGGAGCGCCATCATAGCTGTTTCCTCGAGGGTACTTAGC
SQ-71	9[161]	7[174]	TGTTTGATGCCCCACACACAACATACGATTGCGGGAACTTTC
SQ-72	9[203]	7[216]	CAAAAGAGCCTGGCGTGCCTAATGAGTGTATATTCCTAAAGG
SQ-73	9[245]	7[258]	GGAACAACCTTTTCACACTGCCCGCTTTCTTGCGCCCCAAAAA
SQ-74	10[48]	6[35]	CGAAAGGGGATAGGAACCGGATATTCATCAGCGATCGAAGGC
SQ-75	10[90]	6[77]	AAGGGCGATCTGCCCCGATAGGCTGGCTGTATCATGAGGAAG
SQ-76	10[132]	6[119]	AGGCAAAAGATCGCACCAACTTTGAAAGCCATGTTAGCAACG
SQ-77	10[174]	6[161]	GCTGGTTTGGTGGTAGTAAATGAATTTTGCTAAACATCGTCA
SQ-78	10[216]	6[203]	CTTCACCATAGCCCGTTAGCGTAACGATGGAACAAGGTCGCT
SQ-79	10[258]	6[245]	GGTTTTTGAGTCCAACAAACTACAACGCAAAATCTGACAATG
SQ-80	10[305]	11[305]	tttttCAACGCGCGGGGAGATTAATGAATCGGCttttt
SQ-81	11[2]	10[2]	tttttCAGGGTTTTCCCAGAAGTTGGGTAACGCttttt
SQ-82	11[21]	9[34]	TCACGACTAAAACGTCATCTTTGACCCCTACCCAAGATTGAC
SQ-83	11[63]	9[76]	CTGCAGGTAAACGGTACAACGGAGATTTGACCTTCCATCGTA
SQ-84	11[105]	9[118]	TTCGTAAAGGCTTTATCCGCGACCTGCTAGGACAGTATCGGC
SQ-85	11[147]	9[160]	TCCGCTCACAATTCGCAGGCGCCGCTTCTCCGGCAAAAATCC
SQ-86	11[189]	9[202]	GTGTAAAGCAGGGAAGTGAGAATAGAACTAAAGTTATAAAT
SQ-87	11[231]	9[244]	AATTGCGCCATCGCATTTTTTCACGTTGCTGTAGCCCAGTTT
SQ-88	11[273]	9[286]	GTCGTGCTAAACAGGAGCCTTTAATTGTTACCGTAAACGTCA
SQ-89	12[34]	14[21]	ACTGGTACTGGTAAAGTAATAACATCACCGCGTAAATTTTCA
SQ-90	12[76]	14[63]	TCCAGTAGGAAAAATCCATCACGCAAAATGGCGCGTACCGCCA
SQ-91	12[118]	14[105]	CATTAAAGTCTGAAAGTGTTTTTATAATTTCTCGTGTATCA

SQ-92	12[160]	14[147]	GGTCAGACGATTGGGCGGATAGTCACCACGGAAACAGTGCCG
SQ-93	12[202]	14[189]	CACCACCCCTTCTAAAATCTAAAGCATGAATTGAAAAATCA
SQ-94	12[244]	14[231]	CGCCACCATTTTTGACCGCCTGCAACAGAACTAATATCACCG
SQ-95	12[286]	14[273]	CACCACCCCTAAAAACCAGCAGAAGATATTTAGAAGGAAGGT
SQ-96	12[305]	13[305]	tttttACCGGAACCAGAGCTCATAATCAAAATCttttt
SQ-97	13[2]	12[2]	tttttGCCTTGAGTAACAGTTAACGGGGTCAGTttttt
SQ-98	13[49]	17[62]	CCTATTTAACCGCCATGCGCCGCTACAGTAACCGTCAGCCAT
SQ-99	13[91]	17[104]	AGGCTGACAGGAGGACGTATAACGTGCTCAGTGAGTTTGACG
SQ-100	13[133]	17[146]	TTGCTCAGGTTGATAACAGGAGGCCGATACAGGAAATTCACC
SQ-101	13[175]	17[188]	AGCAGCACACCATTTCAACAGTTGAAAGCACCTTGCAACAGA
SQ-102	13[217]	17[230]	AGCGTCACTTGAGCTTAGGAGCTAACTGCCACGGTGGCAC
SQ-103	13[259]	17[272]	AGCCCCCGACGGAAAATACATTTGAGGAAAACAGACGCGAAC
SQ-104	14[62]	16[49]	CCCTCAGCGGAACCTACATGGCTTTTGATTACCGCTGTAGCA
SQ-105	14[104]	16[91]	CCGTACTGACTCCTTGAAAGCGCAGTCCCTACATGCCACCG
SQ-106	14[146]	16[133]	TCGAGAGGTACCAGCCTTGATATTCACATTGGCAGCGGTACG
SQ-107	14[188]	16[175]	CCAGTAGCCGTAATCCGCCAGCATTGACTTCTGGCCTGAACC
SQ-108	14[230]	16[217]	TCACCGAGACTGTACCACCACCCTCAGAAGAATACCTGAGAG
SQ-109	14[272]	16[259]	AAATATTTTATTAGCCTCCCTCAGAGCCTTTAATGGGTGAGG
SQ-110	14[305]	15[305]	tttttACATTCAACCGATTACTTTACAAACAATttttt
SQ-111	15[2]	14[2]	tttttGTCTATCAACGCTGGGGATAGCAAGCCCttttt
SQ-112	15[35]	13[48]	ACCCGCCTTTGATTTATCCAGAACAATATGATACACCCCCTG
SQ-113	15[77]	13[90]	TTGCTTTGAGTCTGCGCTCATGGAAATATCTGAATTATTAAG
SQ-114	15[119]	13[132]	CAGAGCGCCTGAGAATGGATTATTTACAAACAAATCGGGGTT
SQ-115	15[161]	13[174]	GGTCAGTTCAAACCTAATAAAAGGGACAAGGAGGTATCGAT
SQ-116	15[203]	13[216]	TATCTAACAAATGAGACCTGAAAGCGTAGCCGCCATGCCTTT
SQ-117	15[245]	13[258]	AGCCGTCTATTAACAATGGCTATTAGTCGCCACCCCGGTCAT
SQ-118	16[48]	12[35]	ATACTTCGCGCTTAACCCTCAGAGCCACGTTAATGGGAGTGT
SQ-119	16[90]	12[77]	AGTAAAAGACGAGCTTTAGTACCGCCACATGAAAGTTACCGT
SQ-120	16[132]	12[119]	CCAGAATGGAGCTAATAAGTATAGCCCGGGATTAGAAATCCT
SQ-121	16[174]	12[161]	TCAAATATGGCAAACCATTAGCAAGGCATGAACTGAGGCA
SQ-122	16[216]	12[203]	CCAGCAGAATATCTCATTTGGGAATTAGTCAAGTTCCAGAAC
SQ-123	16[258]	12[245]	CGGTCAGAATAGATATTATTCATTAAAGGCATTTTTTCAGAAC
SQ-124	16[305]	17[305]	tttttATACCGAACGAACCCATCGCCATTAAAAttttt
SQ-125	17[2]	16[2]	tttttGAACTCAAACCTATCTTGCCCTGAGTAGAAAttttt
SQ-126	17[21]	15[34]	GGCCTTGATAAGTTTGCCCGTATAAACACACCCTCCCACCAC
SQ-127	17[63]	15[76]	TGCAACAAGCGTCATATTATTCTGAAACCCTCAGAACTATGG
SQ-128	17[105]	15[118]	CTCAATCGCCAGAACAAGAGAAGGATTAGAATAGGTTAGAAT
SQ-129	17[147]	15[160]	AGTCACACGACCAGCTCAATCATTTTTAGTAAAGGGAATATCT
SQ-130	17[189]	15[202]	GATAGAAAGAGCCGCGAGTAGCGACAGAAAGCCAGCGGAAGGT
SQ-131	17[231]	15[244]	AGACAATCTCAGAGGCGCGTTTTTCATCGGTGAATTAGATTAG
SQ-132	17[273]	15[286]	TGATAGCGGAACCGCGTTTGCCATCTTTGAGGGAGGTATTAG
SQ-133	18[34]	20[21]	AGAATTGGATTTCGAGATGAATATACAGTAAATCCAGCGCCA
SQ-134	18[76]	20[63]	TCAGAGGAGAGGCGAACAGAAATAAAGAAACATTAGTTTATT
SQ-135	18[118]	20[105]	AGCGCATGATGAAAGGAAGGGTTAGAACGGAATTAGGTGGCA
SQ-136	18[160]	20[147]	AAAATAGCAGCCTTACTCCTTATCGTAGTATTTTCATTACGC
SQ-137	18[202]	20[189]	CAATCCAATCAATAATGCAAATCCAATCATGGTTTAGTACCG
SQ-138	18[244]	20[231]	CTAATTTGCTATTACCTCCGGCTTAGGTAAGAATACGGCTGT

SQ-139	18[286]	20[273]	TATCCTGATAGCTTTGAATTTATCAAAATAGTATCATCCCAT
SQ-140	18[305]	19[305]	tttttCCCAGCTACAATTTGTTGCTATTTTGCAttttt
SQ-141	19[2]	18[2]	tttttCAAGAAACAATGAACCCAATAATAAGAGttttt
SQ-142	19[49]	23[62]	TTTTAAGAATCAATTTAAAAAGTTTGAGTAATTGCGTTACAAA
SQ-143	19[91]	23[104]	GGAAACCAAAGAAACCACCAGAAGGAGCCTACCATGAGCAAA
SQ-144	19[133]	23[146]	CTGGCATTAGCAAAGATGATGGCAATTCGATTGTTTAATTAC
SQ-145	19[175]	23[188]	CCCAATACGAGAACCTGACCTAAATTTAGCAAGACGAAACAG
SQ-146	19[217]	23[230]	TCTAAGATATCATTATAAGGCGTTAAATTGGGTATTCTGTGA
SQ-147	19[259]	23[272]	GAGGTTTTACGAGCAGAAAAAGCCTGTTTCATAGGTTGAAAA
SQ-148	20[62]	22[49]	TTGTCACAAAAGTAAGCGCTAATATCAGTACCAAGTAGATTT
SQ-149	20[104]	22[91]	ACATATAGAGGAAAGAGAATTAAC TGAAATTACCTATCAAAA
SQ-150	20[146]	22[133]	AGTATGTGATTAAGTACAGAGAGAATAAACAAAATTGGATTA
SQ-151	20[188]	22[175]	CACTCATGCAAGCAAACGATTTTTTTGTTTTTAATGAAAGAAC
SQ-152	20[230]	22[217]	CTTTCCTACGCGAGACAAAATAAACAGCACCTTGCTATAACT
SQ-153	20[272]	22[259]	CCTAATTTGAAGCCCCAACGCTAACGAGAGAATCCTCTGAGA
SQ-154	20[305]	21[305]	tttttGTCCTGAACAAGAATTATACAAATTCTTttttt
SQ-155	21[2]	20[2]	tttttTCGACAACCTCGTATAAGACAAAAGGGCGttttt
SQ-156	21[35]	19[48]	GAACGTTTAACGTCCTGATTGCTTTGAAAGAGATAAAGCCCT
SQ-157	21[77]	19[90]	GCGGAACCACGTAATAATTATTCATTTACACCCTGACCAGAA
SQ-158	21[119]	19[132]	ATTCCTGGAATAATCAAACATCAAGAAACATAAAAAAAGAA
SQ-159	21[161]	19[174]	GTAAATTAAC TTTTTTTGAATTACCTTTTAACGTCTACCGCG
SQ-160	21[203]	19[216]	CGACCGTAATGCTGTATGTGAGTGAATACATATTACCGGTAT
SQ-161	21[245]	19[258]	GAATCATTTTTTAAATTAATTTTCCCTTCGTCTTCTTGCGG
SQ-162	22[48]	18[35]	TCAGGTTATTAATTAGAAAATTCATATGCTTACCGACCCACA
SQ-163	22[90]	18[77]	TTATTTGAAAGAAACGCAAAGACACCACCAAAGTTAACAAAG
SQ-164	22[132]	18[119]	TACTTCTATTATCACGTAGAAAATACATAATACCCACAGGGA
SQ-165	22[174]	18[161]	GCGAGAATCATCTTAAGCAAGCCGTTTTGAATCATAAAAATG
SQ-166	22[216]	18[203]	ATATGTAGTGATAACCAAGAACGGGTATGGCTTATTTTATCC
SQ-167	22[258]	18[245]	GACTACCAATTACTATGTAGAAACCAATCTCCCGACCAGAGC
SQ-168	22[305]	23[305]	tttttAGAAGAGTCAATAGAGATTAAGACGCTGttttt
SQ-169	23[2]	22[2]	tttttACATCGGGAGAAACTAACAGTACCTTTTttttt
SQ-170	23[21]	21[34]	AATAACGAGTTAAGATAGCAATAGCTATGTTTACCTTTGCCC
SQ-171	23[63]	21[76]	ATCGCGCGTAATTGAGCAGATAGCCGAAGGAATAATCATTTT
SQ-172	23[105]	21[118]	AGAAGATTAGACGGCGCAATAATAACGGACATAAATCATCAT
SQ-173	23[147]	21[160]	ATTTAACAATTTTCATCAAATATAATCCTATCAATATATTTTA
SQ-174	23[189]	21[202]	TACATAAAATAAGAAATCAGATATAGAATAAACAGAAATAC
SQ-175	23[231]	21[244]	AATCGTCGCCAGTTGCGTTTTAGCGAACCAATAATAACACCG
SQ-176	23[273]	21[286]	CATAGCGAATCTTATTAAATCAAGATTAAAATAATATATGCG

Supplementary Sequence 4. Basic DNA sequences used to form square (rectangular M-DNA).

1	GTCGCTCTCT	1'	AGAGAGCGAC	41	CTAAGCGTCG	41'	CGACGCTTAG
2	CAAGTAGAAT	2'	ATTCTACTTG	42	GAACGTAATG	42'	CATTACG TTC
3	GAATGTCCGC	3'	GCGGACATTC	43	CATCGTGGAA	43'	TTCCACGATG
4	GTCAGTAGTC	4'	GACTACTGAC	44	ATCCGCTCGG	44'	CCGAGCGGAT
5	GCGAATGTCC	5'	GGACATTCGC	45	GGTTAAAGGC	45'	GCCTTTAACC
6	GCGTCAGTAG	6'	CTACTGACGC	46	ACCTCAGAAA	46'	TTTCTGAGGT
7	ATGGTGGGTG	7'	CACCCACCAT	47	CCGCGAACAT	47'	ATGTTGCGCG
8	AGAGGCAGTC	8'	GACTGCCTCT	48	TCGGAATAAC	48'	GTTATTCCGA
9	GCGACGACCT	9'	AGGTCGTCGC	49	TAGGACGGTT	49'	AACCGTCCTA
10	GACGACATAG	10'	CTATGTCGTC	50	GCAGGAGCTA	50'	TAGCTCCTGC
11	TTAGAGCATC	11'	GATGCTCTAA	51	GAACGTAAAC	51'	GTTACAGTTC
12	CAAGTCAATT	12'	AATTGACTTG	52	CGTTTATCCA	52'	TGGATAAACG
13	TCAGCGAATG	13'	CATTCGCTGA	53	CTCGTGTGCC	53'	GGCACACGAG
14	TCCGCGTAAG	14'	CTTACGCGGA	54	CTGTTGGATA	54'	TATCCAACAG
15	TTGCGTTCTT	15'	AAGAACGCAA	55	AGGTAGCTCT	55'	AGAGCTACCT
16	TAGCCTCAAT	16'	ATTGAGGCTA	56	GCCTGATTAT	56'	ATAATCAGGC
17	AGGCTGTTAG	17'	CTAACAGCCT	57	TAGTAGGCCA	57'	TGGCCTACTA
18	AAACCTAGCC	18'	GGCTAGGTTT	58	AACACGTAGG	58'	CCTACGTGTT
19	TACCAGTATC	19'	GATACTGGTA	59	GGAGGTTTAT	59'	ATGAACCTCC
20	ACACTTCGTG	20'	CACGAAGTGT	60	GTAACCTTTA	60'	TAAAGGTTAC
21	CTCCTCGCAC	21'	GTGCGAGGAG	61	CTTGATATTC	61'	GAATATCAAG
22	TCACTACACT	22'	AGTGTAGTGA	62	ACGGTATCTT	62'	AAGATACCGT
23	TTGCAGTGAG	23'	CTCACTGCAA	63	AGCCATGAGA	63'	TCTCATGGCT
24	TCATAGAGCG	24'	CGCTCTATGA	64	CTACACACCT	64'	AGGTGTGTAG
25	CCAGTCCGTA	25'	TACGGACTGG	65	GTTGACGAAAG	65'	CTTCGTCAAC
26	GGCTTAACCG	26'	CGGTTAAGCC	66	TAGTCACCTT	66'	AAGGTGACTA
27	CAGCAATGAA	27'	TTCATTGCTG	67	TGAACCACGT	67'	ACGTGGTTCA
28	GTCGTCACAA	28'	TTGTGACGAC	68	GGATTCTCAA	68'	TTGAGAATCC
29	AGGAAATTCG	29'	CGAATTTCTT	69	TGACACTGGT	69'	ACCAGTGTC
30	TGCCAAGCTC	30'	GAGCTTGGCA	70	GGTAACCGTG	70'	CACGGTTACC
31	GAGAAGAGTC	31'	GACTCTTCTC	71	CCTAGTATGT	71'	ACATACTAGG
32	GGCTGCGATA	32'	TATCGCAGCC	72	TCACGGCGGC	72'	GCCGCCGTGA
33	AAGTCGATGG	33'	CCATCGACTT	73	GACAGGCATA	73'	TATGCCTGTC
34	GGAACCTAGT	34'	ACTAAGTTCC	74	AACGTGAGCT	74'	AGCTCACGTT
35	GCTGGTTTGA	35'	TCAAACCAGC	75	CCATGTAAAG	75'	CTTTACATGG
36	TCATCTGTTC	36'	GAACAGATGA	76	CTCCATTGCA	76'	TGCAATGGAG
37	TACCTGCCGA	37'	TCGGCAGGTA	77	ACTTCCTCCT	77'	AGGAGGAAGT
38	CCAACATATC	38'	GATATGTTGG	78	TTCTGGACAT	78'	ATGTCCAGAA
39	GGTGTTCTCC	39'	GGAGAACACC	79	CCGCCTTGAC	79'	GTCAAGGCGG
40	ATGCAAATTC	40'	GAATTTGCAT	80	TTCAAAGCCA	80'	TGGCTTTGAA

81	TGCGTTAGAC	81'	GTCTAACGCA	121	AGTCATCACC	121'	GGTGATGACT
82	ACACAACCGG	82'	CCGGTTGTGT	122	ACTGGAACCT	122'	AGGTTCCAGT
83	TGGACTGTCT	83'	AGACAGTCCA	123	AACCTAACAC	123'	GTGTTAGGTT
84	CGTTCAAGAA	84'	TTCTTGAACG	124	CGCTTTCTTG	124'	CAAGAAAGCG
85	AGAAGCTGAA	85'	TTCAGCTTCT	125	GGTCGCGCAT	125'	ATGCGCGACC
86	CGGCTCACCA	86'	TGGTGAGCCG	126	CGCGTCTGAG	126'	CTCAGACGCG
87	GCTGTGCCAA	87'	TTGGCACAGC	127	TCTTTCGACT	127'	AGTCGAAAGA
88	TCGAAGTCGT	88'	ACGACTTCGA	128	CGTCAGGTCT	128'	AGACCTGACG
89	CGTTACTCAC	89'	GTGAGTAACG	129	GGCAGAGAAC	129'	GTTCTCTGCC
90	CCGATTCACA	90'	TGTGAATCGG	130	GTATTCGTAC	130'	GTACGAATAC
91	ACTGCATCAA	91'	TTGATGCAGT	131	CGCCGGATTT	131'	AAATCCGGCG
92	CTGCCGTTCT	92'	AGAACGGCAG	132	AACTAGCCTT	132'	AAGGCTAGTT
93	GTCTCGCAAC	93'	GTTGCGAGAC	133	CTGCATTAGG	133'	CCTAATGCAG
94	TCGCACATCG	94'	CGATGTGCGA	134	CGATCGGTAA	134'	TTACCGATCG
95	CGTGTCTAGC	95'	GCTAGACACG	135	GATCCTTTCC	135'	GGAAAGGATC
96	CACGCTTCAG	96'	CTGAAGCGTG	136	CTGGTCCTTC	136'	GAAGGACCAG
97	GTCGGAGAGG	97'	CCTCTCCGAC	137	AGTCTTGCGC	137'	GCGCAAGACT
98	GCGTTACCAC	98'	GTGGTAACGC	138	ATCTCCGCCA	138'	TGGCGGAGAT
99	CACCACAGTG	99'	CACTGTGGTG	139	ATTAGCACGA	139'	TCGTGCTAAT
100	AGCGCGCTTC	100'	GAAGCGCGCT	140	GTATGATGCG	140'	CGCATCATAC
101	AGCAACTCTT	101'	AAGAGTTGCT	141	TCCTACGCGA	141'	TCGCGTAGGA
102	CGTCTGGAAG	102'	CTCCAGACG	142	GCCACCAGCA	142'	TGCTGGTGGC
103	GCTTTAGCGG	103'	CCGCTAAAGC	143	GACGTATAAG	143'	CTTATACGTC
104	TTCCGTATAG	104'	CTATACGGAA	144	AGTGGAGGTG	144'	CACCTCCACT
105	GTTGGCGTGC	105'	GCACGCCAAC	145	AATCAGAGAG	145'	CTCTCTGATT
106	CGTGCGCCAT	106'	ATGGCGCACG	146	GAGGATGTTG	146'	CAACATCCTC
107	TTTGTTGGTC	107'	GACCAACAAA	147	CGGAGTCTGA	147'	TCAGACTCCG
108	GATAAGAACT	108'	AGTTCCTATC	148	CGGCAACTGT	148'	ACAGTTGCCG
109	TCCGGTCCAT	109'	ATGGACCGGA	149	TCGTTTAGTG	149'	CACTAAACGA
110	ACCGAAATCG	110'	CGATTTCGGT	150	CAAAGTGAGC	150'	GCTCACTTTG
111	AAGTGATAAA	111'	TTATCACTT	151	CCGAACAGGA	151'	TCCTGTTCGG
112	CCGTGAAACA	112'	TGTTTCACGG	152	CGCGAATTAA	152'	TTAATTCGCG
113	GAGATGGCTT	113'	AAGCCATCTC	153	TCCACATTAC	153'	GTAATGTGGA
114	TAGTGCGTAA	114'	TTACGCACTA	154	GGACTGCTAA	154'	TTAGCAGTCC
115	GGTCCGAACC	115'	GGTTCGGACC	155	CATGGCCGAG	155'	CTCGGCCATG
116	TCCGAGAAGC	116'	GCTTCTCGGA	156	GTGAATTGGT	156'	ACCAATTACAC
117	TCCTTCCGCC	117'	GGCGGAAGGA	157	GGTTGCCAGG	157'	CCTGGCAACC
118	CGGACCAAGG	118'	CCTTGGTCCG	158	GTGTATGAAC	158'	GTTCATACAC
119	GGCCGATATG	119'	CATATCGGCC	159	ATTGGAGGC	159'	GCCTCCAAAT
120	CCTGACTTAT	120'	ATAAGTCAGG	160	ATTGTGGAGC	160'	GCTCCACAAT

161	ACCGTTGATA	161'	TATCAACGGT	201	GTGTCGGCGA	201'	TCGCCGACAC
162	ATCGACGTGG	162'	CCACGTCGAT	202	ACTCCTGTAA	202'	TTACAGGAGT
163	TAGATCGAAC	163'	GTTCGATCTA	203	AGCAGCCACA	203'	TGTGGTGCT
164	AAACTCGTCC	164'	GGACGAGTTT	204	GTATCGTACA	204'	TGTACGATAC
165	CCGTCTTTGG	165'	CCAAAGACGG	205	GTGGATAGCA	205'	TGCTATCCAC
166	CACTTGCGAA	166'	TTCGCAAGTG	206	CTGCTTCCTG	206'	CAGGAAGCAG
167	CAATCACTCG	167'	CGAGTGATTG	207	CGCCTATACC	207'	GGTATAGGCG
168	GAGTTGTATG	168'	CATACAACTC	208	GACCTTTCAA	208'	TTGAAAGGTC
169	TGTGCTTACA	169'	TGTAAGCACA	209	ATTCGGCACT	209'	AGTGCCGAAT
170	TGGAGATGTT	170'	AACATCTCCA	210	GTTTCCACTC	210'	GAGTGGAAAC
171	ATAGCTGCTC	171'	GAGCAGCTAT	211	CTGACGGAAT	211'	ATTCCGTCAG
172	CAAACACCGA	172'	TCGGTGTTTG	212	GTAGCCAGGT	212'	ACCTGGCTAC
173	TTCACGAGCC	173'	GGCTCGTGAA	213	TCAGTGGTCA	213'	TGACCACTGA
174	TCAGGCGCGT	174'	ACGCGCCTGA	214	GCAAGTTTCG	214'	CGAAACTTGC
175	GTAAGACCTC	175'	GAGGTCTTAC	215	CGAGCCTACG	215'	CGTAGGCTCG
176	TATAAATCCT	176'	AGGATTTATA	216	TCCGTAGCAC	216'	GTGCTACGGA
177	GGTGCAGATA	177'	TATCTGCACC	217	CAAATGACCA	217'	TGGTCATTTG
178	TCAAGCCTTT	178'	AAAGGCTTGA	218	GGAAGTACGG	218'	CCGTACTTCC
179	CCAAGAGGCC	179'	GGCCTCTTGG	219	GAAGAGGACG	219'	CGTCCTCTTC
180	CAGGTACTAA	180'	TTAGTACCTG	220	TCTCGACTCC	220'	GGAGTCGAGA
181	GGTAGTGCCA	181'	TGGCACTACC	221	TATGAAGAGC	221'	GCTCTTCATA
182	TAGCGTGATC	182'	GATCACGCTA	222	ATATTAGACC	222'	GGTCTAATAT
183	GCGTATTACG	183'	CGTAATACGC	223	TCCAGCATAA	223'	TTATGCTGGA
184	GCGTGTAGCT	184'	AGCTACACGC	224	AAGCATCTCA	224'	TGAGATGCTT
185	ACCTATGTGC	185'	GCACATAGGT	225	AATCGGACTC	225'	GAGTCCGATT
186	CCAGAGTGTG	186'	CACACTCTGG	226	GTCACCGAGT	226'	ACTCGGTGAC
187	GCAATGCTTG	187'	CAAGCATTGC	227	GGCGTACGCT	227'	AGCGTACGCC
188	AATGCGTGCA	188'	TGCACGCATT	228	CCTCAAAGTC	228'	GACTTTGAGG
189	TATTCAGGCT	189'	AGCCTGAATA	229	AGCTGACAAG	229'	CTTGTCAGCT
190	TGCATTCTGC	190'	GCAGAATGCA	230	GCACTCAACG	230'	CGTTGAGTGC
191	AGATCCATTT	191'	AAATGGATCT	231	AACGAGGTAC	231'	GTACCTCGTT
192	TTATAGTCTT	192'	AAGACTATAA	232	GTCCTGGCCT	232'	AGGCCAGGAC
193	AACTTCAGAG	193'	CTCTGAAGTT	233	ACCACTAGAG	233'	CTCTAGTGGT
194	TGAAGATAGC	194'	GCTATCTTCA	234	TCTGCCATGT	234'	ACATGGCAGA
195	ATCGTTTCGT	195'	ACGAAACGAT	235	CAGGCAACGT	235'	ACGTTGCCTG
196	CCTTCACATA	196'	TATGTGAAGG	236	ACCGGATACA	236'	TGTATCCGGT
197	GCACCTTCCA	197'	TGGAAGGTGC	237	CGCCACCTTA	237'	TAAGGTGGCG
198	TCTGAGATAG	198'	CTATCTCAGA	238	ATGTGTCTTA	238'	TAAGACACAT
199	GAATCGCCTA	199'	TAGGCGATTG	239	ATGAGGTGTC	239'	GACACCTCAT
200	GAGTAAGCGC	200'	GCGCTTACTC	240	CTTCAGCCGT	240'	ACGGCTGAAG

Supplementary Sequence 5. Sequences of M-bases of 10nt. These sequences were generated to have fewer than five of the same continued nucleotides with scaffold M13 to avoid crosslinking of M-bases with DNA origami. These sequences also have less than five of the same continued nucleotides from each other to avoid crosslinking between uncomplimentary M-bases.

1	ATCGGAAACGCTGAG	1'	CTCAGCGTTTCCGAT
2	ACAAGAGTACAGGCA	2'	TGCCTGTACTCTTGT
3	AGGCAAAGAATTAGC	3'	GCTAATTCTTTGCCT
4	AGCTTGAGGTCAGTA	4'	TACTGACCTCAAGCT
5	CACCAGTCACACAGA	5'	TCTGTGTGACTGGTG
6	AATCGCAAGACAAAG	6'	CTTTGTCTTGCGATT
7	TTAGAATCGACCAGT	7'	ACTGGTCGATTCTAA
8	GATTAAAGTACCAAG	8'	CTTGGTACTTTAATC
9	GACGGTCAATCATAA	9'	TTATGATTGACCGTC
10	ATGCTGATGGACATT	10'	AATGTCCATCAGCAT
11	AACCCTTCGTTGGGT	11'	ACCCAACGAAGGGTT
12	GAAATCCGATGGTTG	12'	CAACCATCGGATTTTC
13	GGCTTAGTGACCTGA	13'	TCAGGTCACTAAGCC
14	CACAGTGAGAGACTA	14'	TAGTCTCTCACTGTG
15	AGGGTGAGCGCTTAA	15'	TTAAGCGCTCACCCCT
16	GAACCCTCATATATT	16'	AATATATGAGGGTTC
17	CATAGGTCACAATAT	17'	ATATTGTGACCTATG
18	ATAGTCAATAGTGAA	18'	TTCCTATTGACTAT

Supplementary Sequence 6. Sequences of M-bases of 15 nt.

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