

Zeta Potential Transition Correlates with Optimal DNA Origami Silicification Temperature

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1 Materials and Methods

Materials

All oligonucleotides were synthesized and supplied by Shanghai Sangong Biotech Co., Ltd. The M13 scaffold strands were obtained from BioRuler Co., Ltd. Magnesium chloride hexahydrate ($\geq 99\%$) were purchased from Adamas-Life. The Trichloromethane was purchased from Aladdin. Sodium hydroxide (NaOH), hydrochloric acid (HCl) and ethylenediaminetetraacetic acid disodium salt (EDTA-2Na, AR) were purchased from Sinopharm Group Chemical Reagent Co., Ltd. N-Trimethoxysilylpropyl-N,N,N-trimethylammonium chloride (TMAPS, 50% in methanol) and tetraethyl orthosilicate (TEOS) were purchased from TCI (Japan). SiO₂/Si wafers featuring a 285 nm thermally grown SiO₂ layer were obtained from commercial suppliers. All other chemicals were purchased from Sinopharm and Sigma-Aldrich. AFM probes were sourced from Bruker. Unless otherwise noted, all reagents and experimental consumables were used as received without further purification.

Preparation of DNA nanostructure

Square DNA origami (SDO) structures were designed using caDNAno software. For assembly, the scaffold strand was combined with 192 staple strands at a molar ratio of 1:10 in TE-Mg²⁺ buffer (5 mM Tris, 1 mM EDTA, and 12 mM magnesium chloride, pH 8.0). The mixture was subjected to thermal annealing in a PCR thermocycler (Eppendorf), consisting of an initial incubation at 65 °C for 25 min, followed by gradual cooling from 60 to 40 °C at a rate of -1 °C per 30 min. And subsequently from 40 °C to 25 °C at a rate of -1 °C per 20 min. Upon completion of the cooling steps, the sample was immediately held at 4 °C. Excess staple strands were removed via polyethylene glycol (PEG)-based purification. Briefly, the annealed solution was mixed with an equal volume of PEG buffer (5 mM Tris, 1 mM EDTA, 505 mM NaCl, and 15% (w/v) PEG 8000, pH 8.0), followed by centrifugation at $11,000 \times g$ for 17 min. The resulting DNA pellet was resuspended in $1 \times$ TE-Mg²⁺ buffer and incubated at 37 °C with gentle shaking (800 rpm) for 8 h to ensure complete dissolution. Subsequently, the DNA origami samples were purified by ultrafiltration using centrifugal filter units (MWCO 100 kDa). The samples were washed six times with $1 \times$ TE-Mg²⁺ buffer by centrifugation at $8,000 \times g$ for 5 min at 25 °C. After the sixth wash, a final inverted centrifugation step was performed at $5,000 \times g$ for 1.5 min at 25 °C to recover the concentrated DNA origami. The purified SDO was subsequently diluted to a final concentration of 20 nM in TE-Mg²⁺ buffer and quantified using a UV-2600i UV-vis spectrophotometer (Shimadzu). Triangular DNA origami (TDO), ring-shape DNA origami (RDO), and 14-helix bundle (14HB) DNA origami were also designed using caDNAno, with 208, 225, and 151 staple strands, respectively. All other assembly and purification procedures were identical to those described for SDO.

Agarose Gel Electrophoresis (AGE)

DNA samples were analyzed by agarose gel electrophoresis using a 1.0% agarose gel prepared in $1 \times$ TE-MgCl₂ buffer (12 mM MgCl₂) and stained with 0.01% GelRed. A 5 μ L aliquot of sample (10 nM in $1 \times$ TE-Mg buffer containing 12 mM MgCl₂) was mixed with 1 μ L of 6 \times loading buffer and loaded into the gel wells. Electrophoresis was carried out on ice at 100 V for 60 min using $1 \times$ TE-MgCl₂ buffer (12 mM MgCl₂) as the running buffer. The bands were visualized under ultraviolet illumination. Band intensities were quantified using ImageJ software. A 1kb marker (Takara) was used as the reference standard.

Silicification on surface

For surface silicification, the procedure was adapted from previously reported methods. Briefly, purified DNA origami structures were diluted to 2 nM and deposited onto plasma-treated mica or silicon wafer substrates. The precursor solution was prepared as follows: 1 mL of 1× TE-MgCl₂ buffer (containing 12 mM MgCl₂) was added to a 10 mL glass vial at room temperature. Subsequently, 20 μL of TMAPS (50% in methanol) was slowly introduced under vigorous stirring, and the mixture was allowed to react for 20 min. Then, 20 μL of TEOS (or an equivalent amount of other organoalkoxysilanes, OASs) was added dropwise while maintaining stirring, followed by an additional 20 min of stirring to yield the precursor solution. The resulting solution was transferred into a centrifuge tube until the substrate was completely immersed. The silicon wafer substrate bearing DNA origami was gently placed onto the liquid surface and kept undisturbed for a predetermined reaction period. After silicification, the sample was rinsed once with Milli-Q water, once with 80% ethanol, and once with Milli-Q water again, then dried under a stream of nitrogen and further air-dried under ambient conditions.

Zeta Potential Measurements

The concentration of the DNA liquid samples was diluted to 2 nM (total volume of 600 μL) and transferred into a disposable folded capillary cell (Malvern, DTS1070). The zeta potential of the samples was measured at different temperatures (4 °C, 15 °C, 25 °C, 32 °C, 37 °C, 45 °C, 55 °C, 65 °C, and 70 °C). Each measurement was performed after temperature equilibration to ensure stable conditions. The electrophoretic mobility obtained from the measurements was automatically converted to zeta potential values using the Smoluchowski model. All Zeta potential measurements were performed using a Zetasizer Ultra (Malvern Panalytical, Malvern, UK).

AFM experiments

AFM imaging was performed in ScanAsyst in Air mode using a MultiMode 8 atomic force microscope (Bruker). The measurements were carried out with a SCANASYST-AIR probe (Bruker; tip height ≈ 650 nm, cantilever length ≈ 115 μm, resonance frequency ≈ 70 kHz, spring constant ≈ 0.4 N m⁻¹). To minimize the influence of ambient humidity on height measurements, DNA/DNA-silica composites samples adsorbed on mica or silicon wafer were first dried under a nitrogen stream and subsequently kept at room temperature for 2 h prior to AFM characterization. Before imaging, the force curve of the probe was calibrated, after which the samples were scanned under ambient conditions.

Liquid-phase AFM imaging was performed using a fluid cell at room temperature (~25 °C). Freshly cleaved mica substrates were incubated with 2 nM DNA origami samples in buffer (10 μL, 5 mM Tris, 1 mM EDTA, 12 mM MgCl₂, pH 8.0) for 5 minutes to allow adsorption. The substrate was then gently rinsed and transferred to a liquid cell containing imaging buffer (45 μL, 1×TAE-Mg, 10 mM NiCl₂). AFM imaging was carried out in PeakForce mode. All AFM measurements in this study were performed at room temperature unless otherwise specified.

AFM image analysis

AFM image analysis was performed using NanoScope Analysis (Bruker). The Particle Analysis module was used to obtain the height (h), the sigma of height, projected area (A), and equivalent diameter (D) of individual particles. The uniformity of silicification was assessed using the thickness coefficient of variation (Thickness CV %, Equation 1). The sigma value of particle height obtained from Particle Analysis was used to calculate Thickness CV (%) as follows:

$$\text{Thickness CV (\%)} = \frac{\sigma_h}{\bar{h}} \times 100 \quad (1)$$

Where σ_h is the standard deviation of particle height and \bar{h} is the mean particle height. Lower Thickness CV values indicate more uniform silicification thickness among particles.

The structural fidelity after silicification was evaluated using area retention ($A_{retention}$, Equation 2) and diameter retention ($D_{retention}$, Equation 3), which reflect the preservation of the original particle geometry and overall dimensions relative to the corresponding unsilicified structures:

$$A_{retention} = \frac{A_{silicified}}{A_{pristine}} \quad (2)$$

$$D_{retention} = \frac{D_{silicified}}{D_{pristine}} \quad (3)$$

Root mean square roughness (R_q) quantifies nanoscale surface height fluctuations of individual DNA origami particles, reflecting local surface roughness arising from silica deposition morphology and growth kinetics. Surface roughness was analyzed using the Roughness function in NanoScope Analysis. A region of 201.03 nm \times 201.03 nm was selected for each measurement, and approximately 45 particles were included in the statistical analysis. Lower roughness values indicate a smoother and more homogeneous silicified surface.

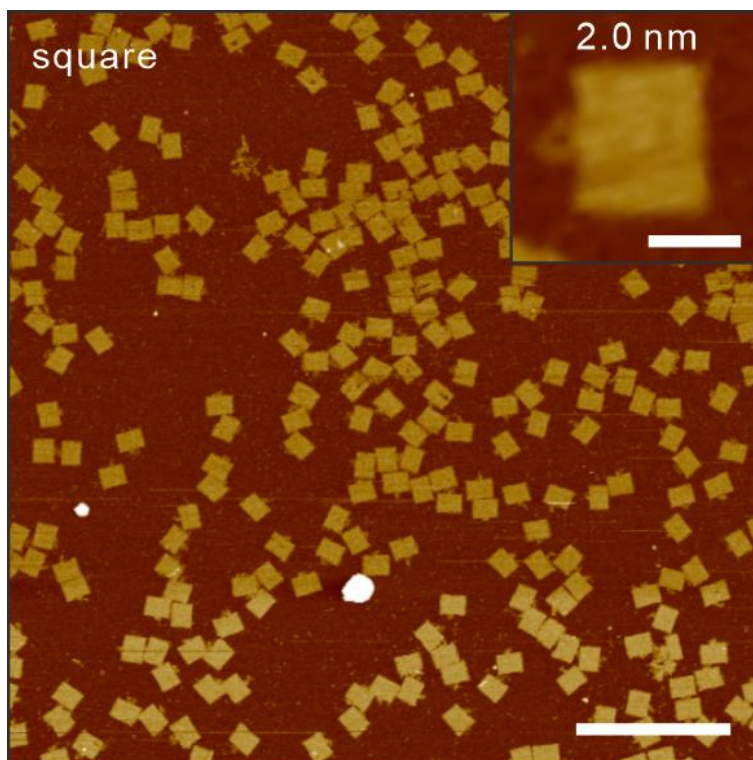
SEM Characterization

SEM imaging was performed using a Zeiss GeminiSEM 360 scanning electron microscope. For purified DNA samples, carbon-coated copper grids were treated in a PELCO easiGlow system (Ted Pella Inc.) for 60 s to increase surface hydrophilicity. Subsequently, 10 μ L of purified DNA (2 nM) was deposited onto the grids and incubated for 3 min to allow adsorption, followed by removal of excess solution using filter paper. Then, 5 μ L of 1% uranyl acetate was applied for 60 s as a negative stain, and the grids were then rinsed with 50 μ L of Milli-Q water and air-dried. For DNA-silica composites samples, the samples had been previously deposited onto silicon wafer and were directly imaged without further treatment. Imaging was conducted in STEM/InLens mode at an acceleration voltage of 15/2 kV. Due to aggregation of DSCs observed in SEM images, data variability was quantified using confidence intervals for error analysis.

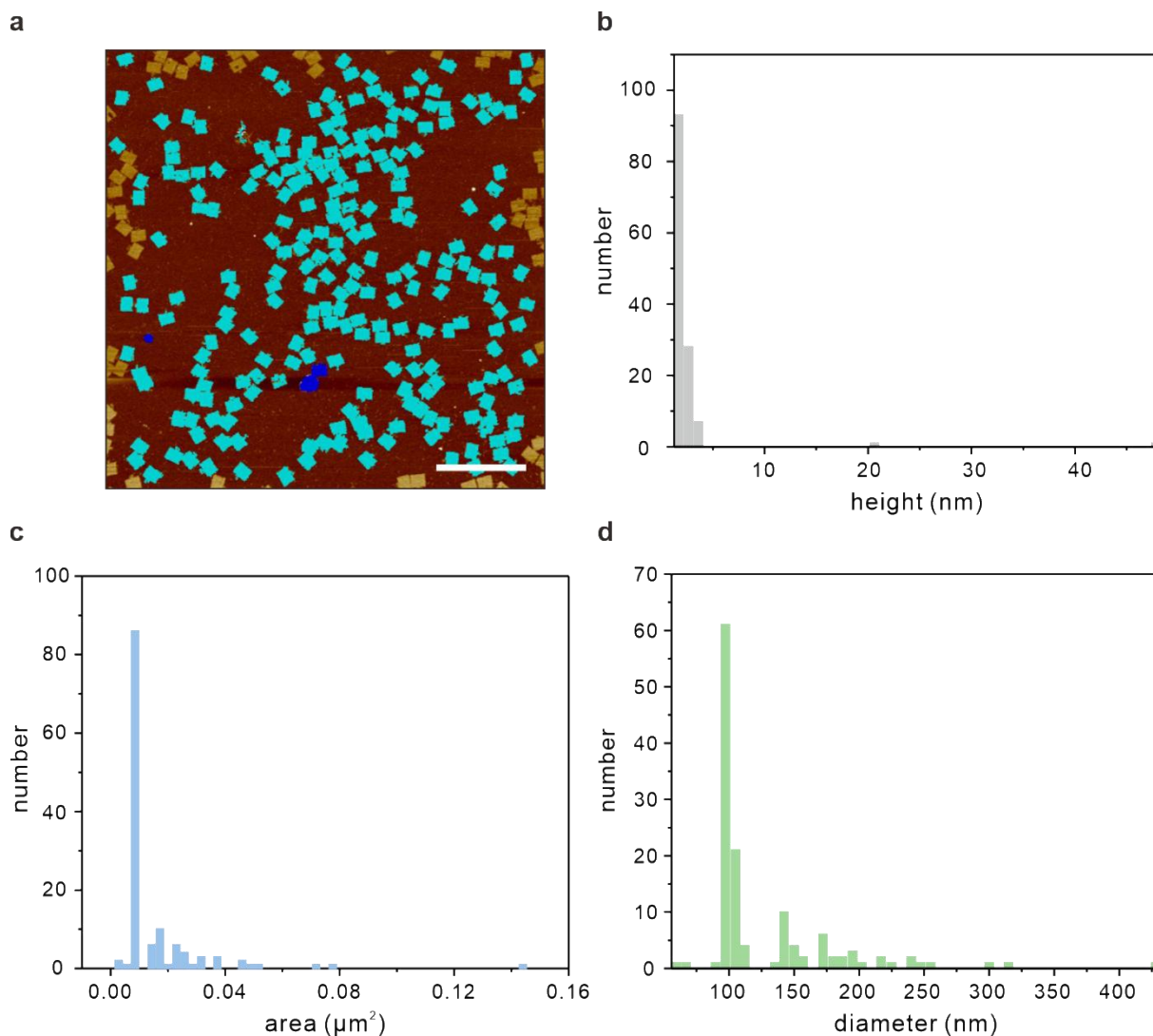
MD Simulations

We used a representative DNA origami fragment for MD simulations to investigate the effect of temperature on the interactions of silica precursors and DNA. All-atomistic MD simulations were performed with Amber14 package using ff14SB force field¹ and general Amber force field (GAFF)². Force field parameters for silicon were obtained from previous reports³. Simulation system was solvated to a cuboid box using transferable intermolecular potential three point (TIP3P) water model, followed by adding Mg²⁺ to a final concentration of 12.5 mM. Cl⁻ counterions were then added to neutralize overall charges. Two rounds of energy minimizations were then carried out, with all atoms of nucleotides restrained in the first round and without any constraints in the second round. Then, the system was heated from 0 K to the target temperature (277K, 298K, 318K, 328K, 338K, respectively) within 300 ps in a canonical ensemble (NVT), followed by a 700-ps equilibration run. For each temperature, 3 independent rounds of 250 ns MD simulations were performed with random velocities for each system under isothermal isobaric (NPT) condition. The particle mesh Ewald (PME) method⁴ was employed for long-range electrostatic interactions while a cutoff distance of 10 Å was applied for short-range electrostatic interactions as well as van der Waals interactions. Covalent bonds involving hydrogens were restricted using SHAKE methods. A time step of 2 fs was employed and the trajectory was stored every 100 ps. MD trajectories were analyzed using cpptraj package.

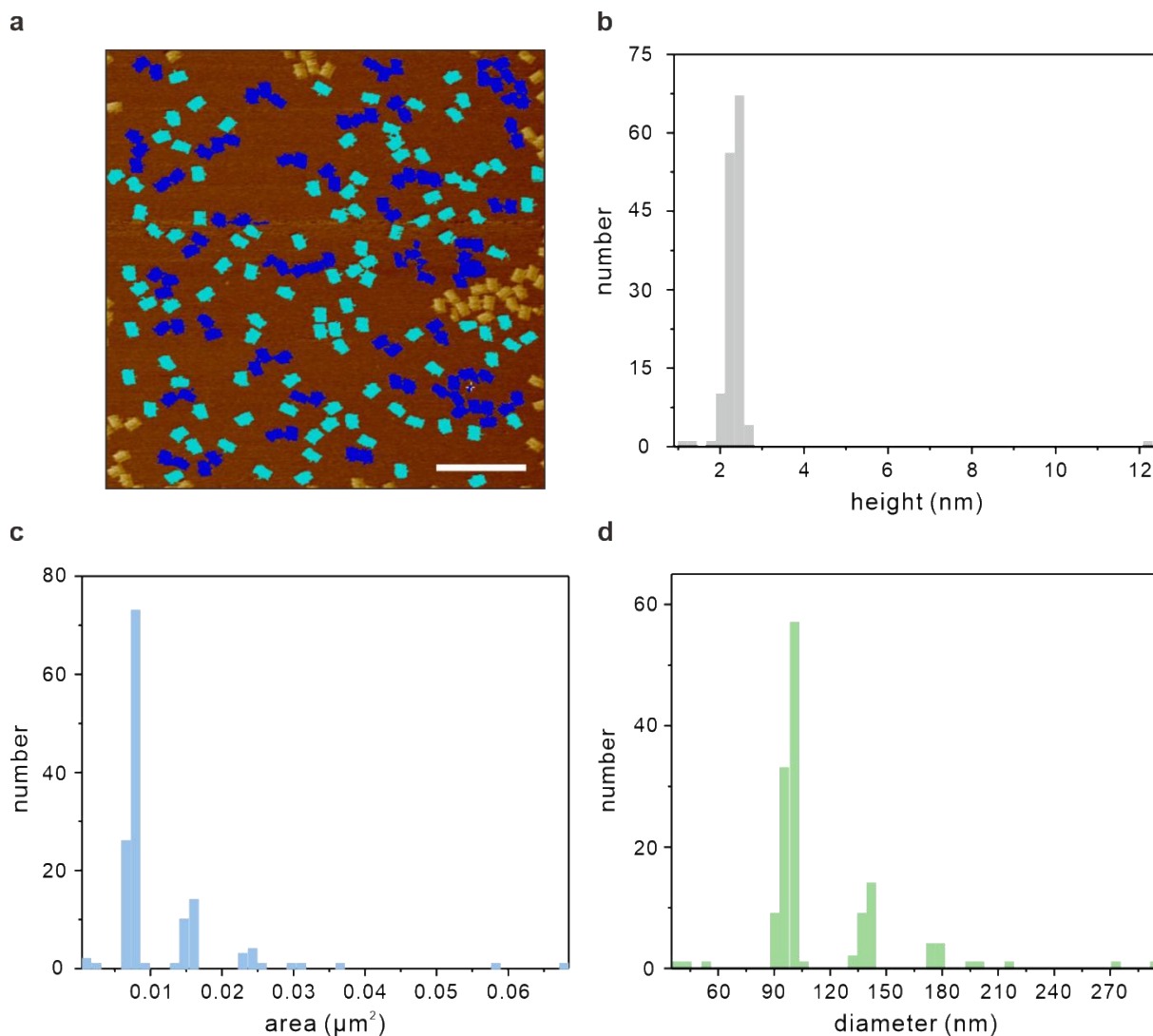
2 The height analysis of square DNA origami from AFM images



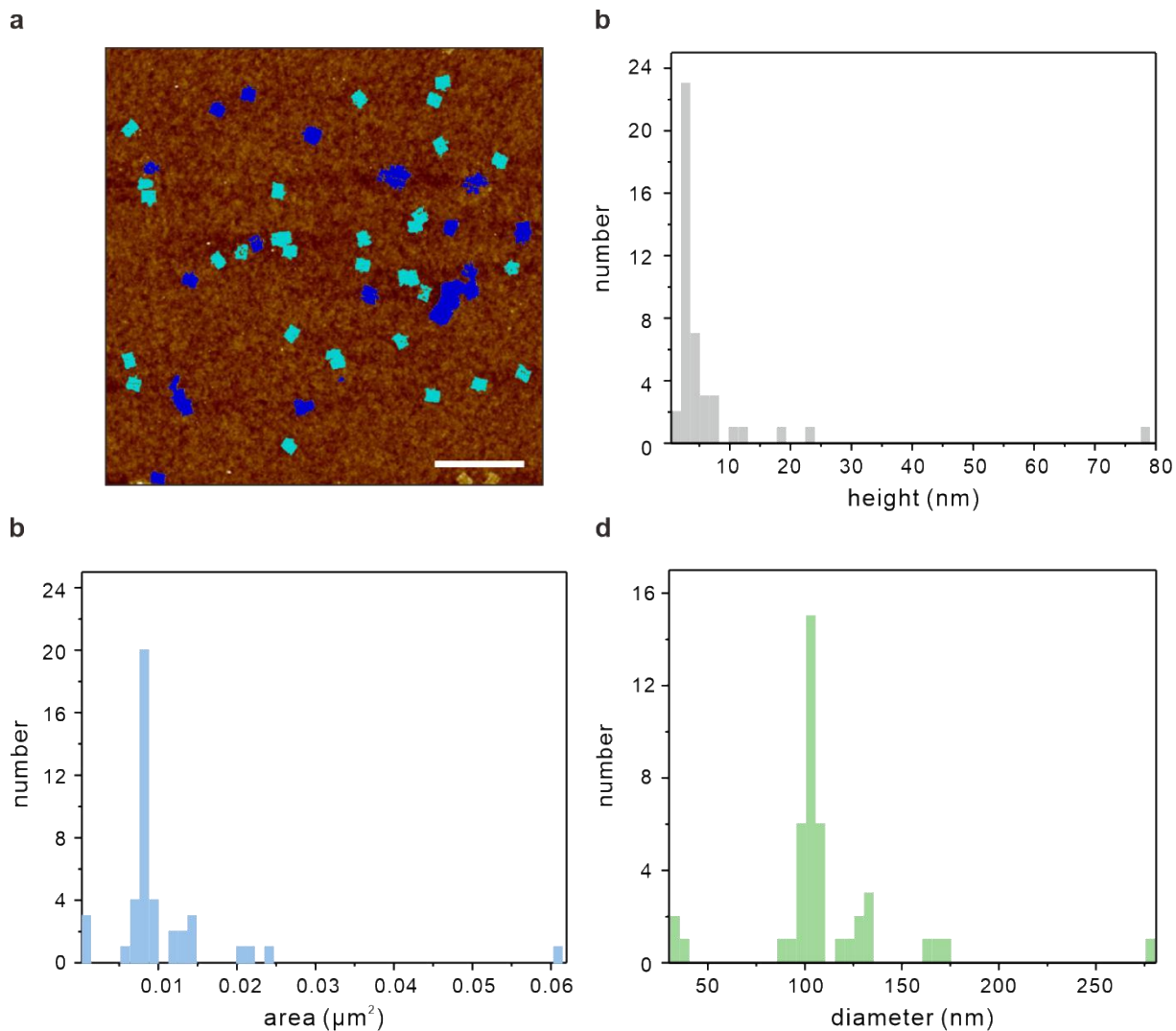
Supplementary Fig. 1. The morphology and height characteristics of pristine square DNA origami architectures in liquid-phase AFM. The AFM images of the square structures (scale bar, 600 nm), the inset shows a representative DNA origami with annotated average height (scale bar, 60 nm).



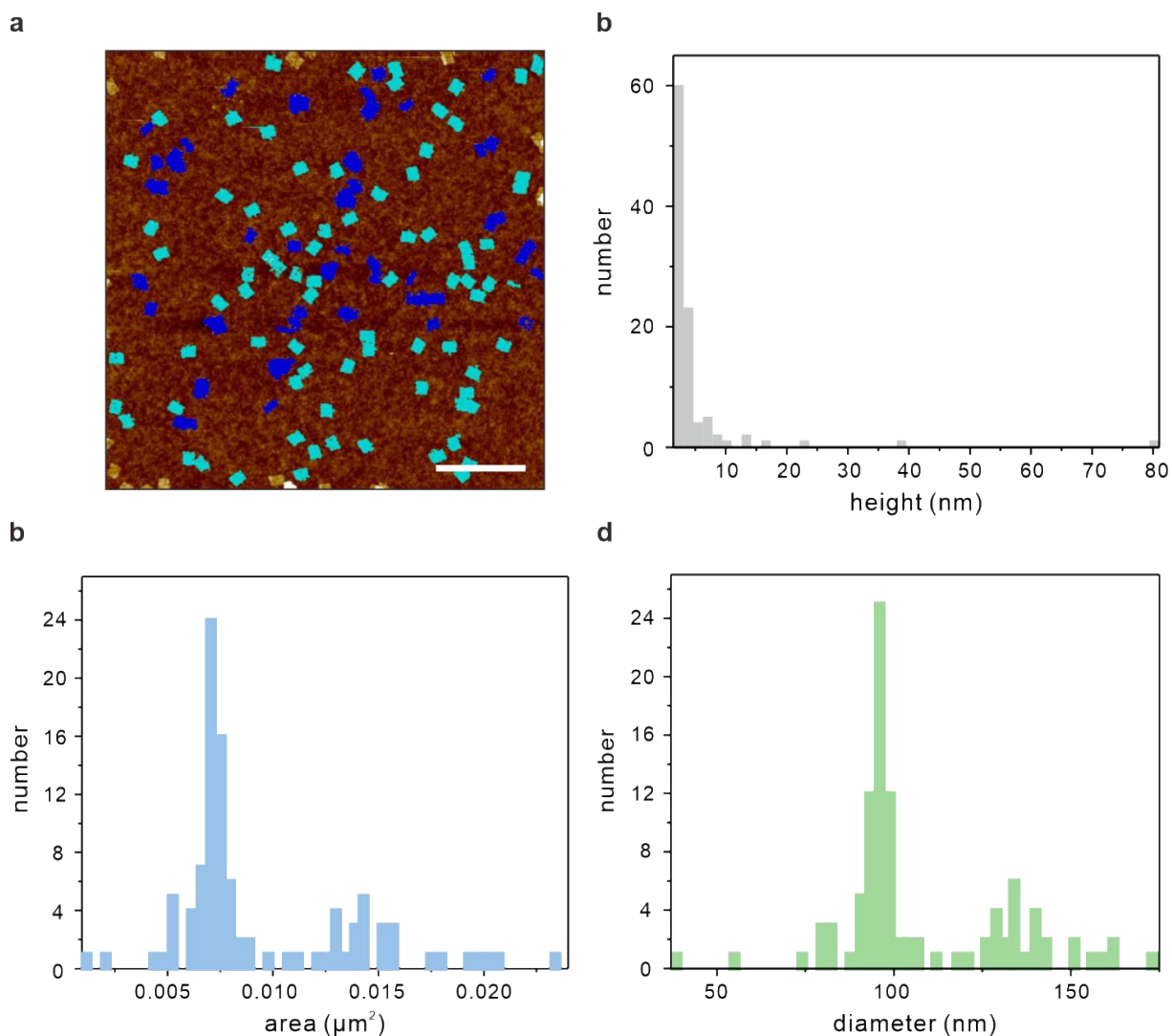
Supplementary Fig. 2. Measurement approach for the height and area of pristine square DNA origami (SDO) in liquid-phase AFM images. (a) Single particles in the AFM images were identified and screened using Nanoscope Analysis, with light blue particles included in the statistics, while dark blue particles were excluded due to stacking or structural deformation. Particle height statistics for individual particles are provided in the corresponding Figure S1 AFM images. (b) Pixel-by-pixel height distribution of the AFM images. (c) Histogram of average heights of all particles in the AFM image. (d) Histogram of average areas of all particles in the AFM image. All height measurements in this study were obtained using this method. Error bars in the height statistics represent standard deviations. Scale bar, 600 nm.



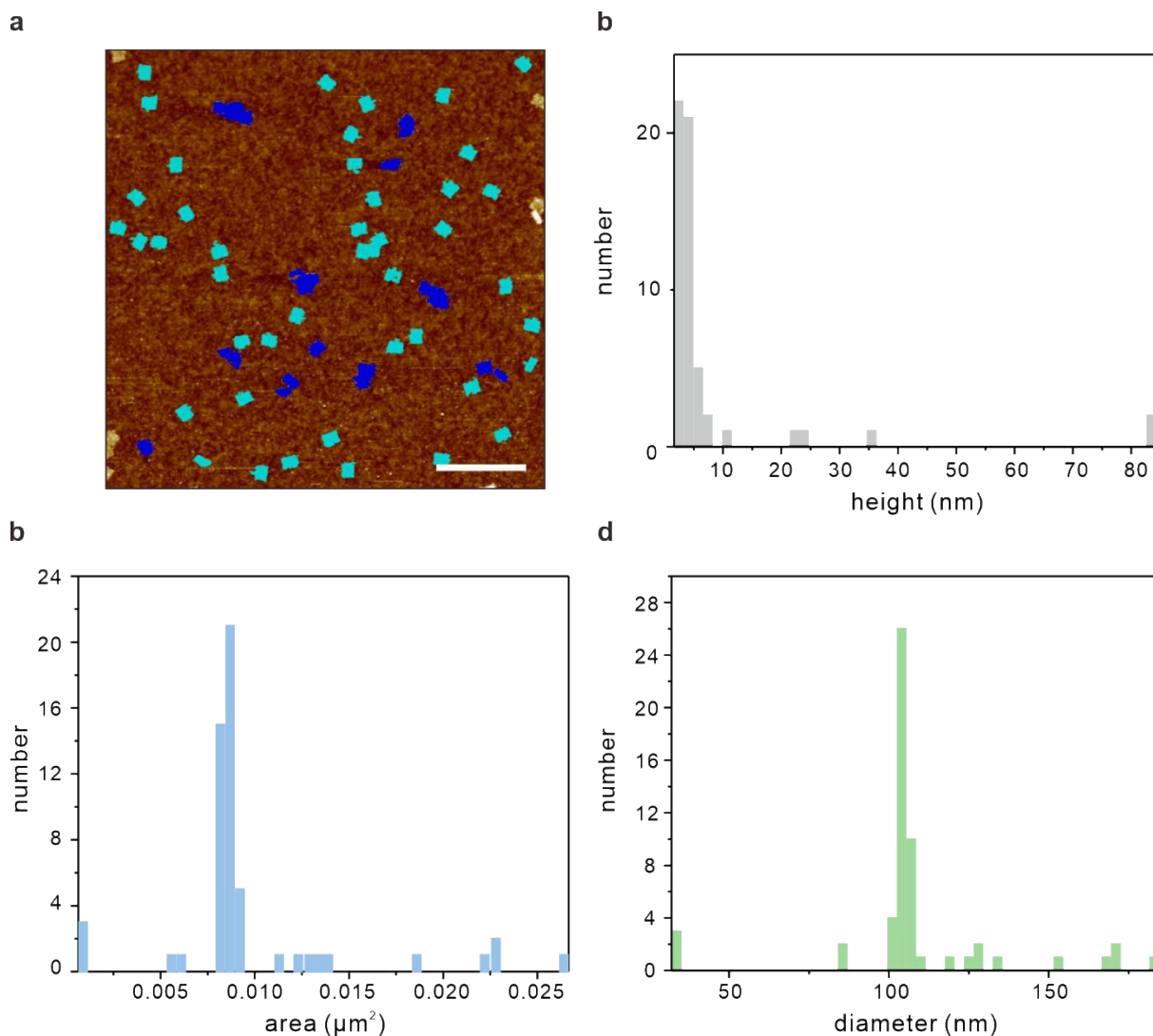
Supplementary Fig. 3. Measurement approach for the height and area of pristine square DNA origami (SDO) in air-phase AFM images. (a) Single particles in the AFM images were identified and screened using Nanoscope Analysis, with light blue particles included in the statistics, while dark blue particles were excluded due to stacking or structural deformation. Particle height statistics for individual particles are provided in the corresponding Figure 2b AFM images. (b) Pixel-by-pixel height distribution of the AFM images. (c) Histogram of average heights of all particles in the AFM image. (d) Histogram of average areas of all particles in the AFM image. All height measurements in this study were obtained using this method. Error bars in the height statistics represent standard deviations. Scale bar, 600 nm.



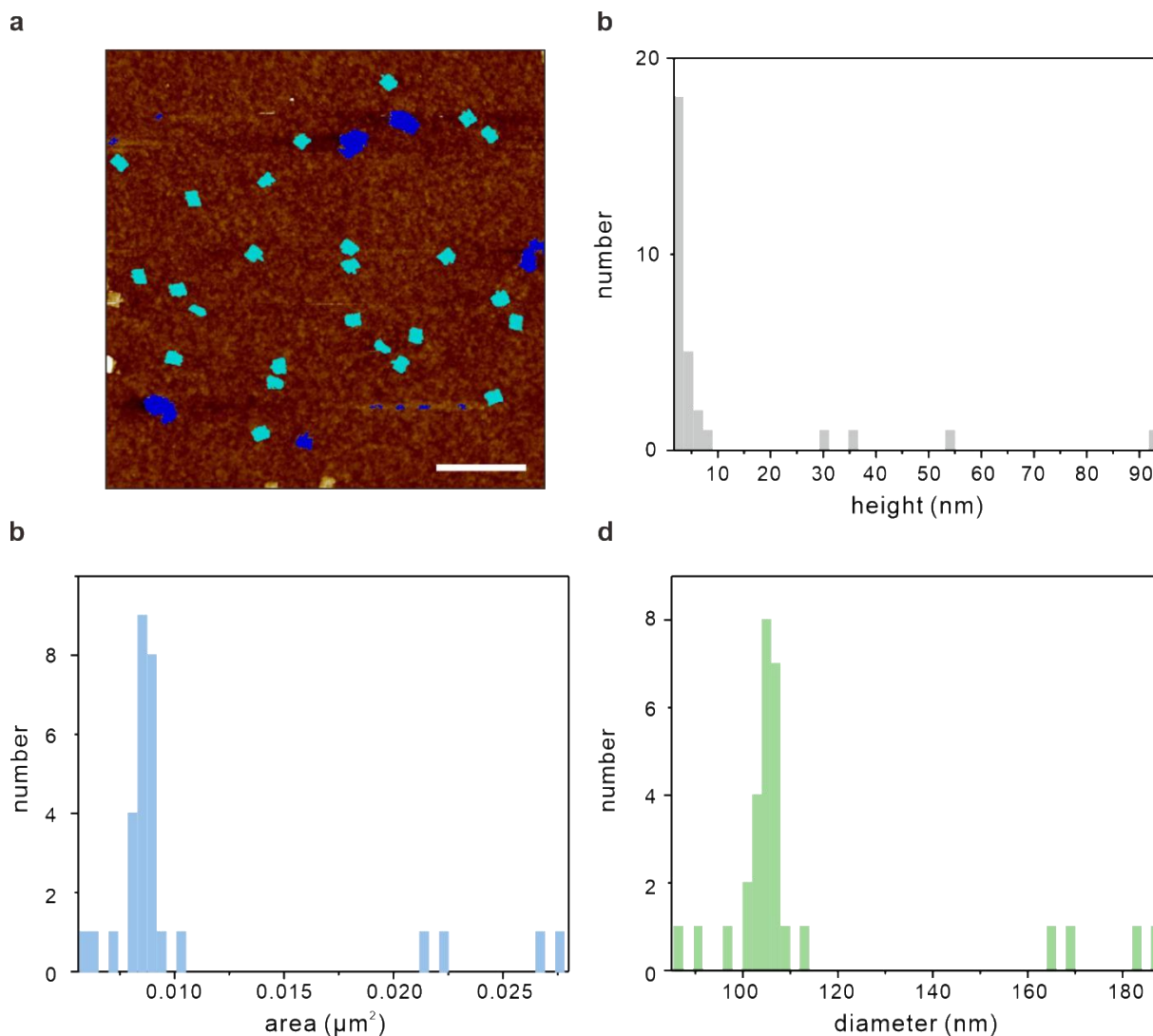
Supplementary Fig. 4. Measurement approach for the height and area of square DNA origami (SDO) after silicification at 4 °C in air-phase AFM images. (a) Single particles in the AFM images were identified and screened using Nanoscope Analysis, with light blue particles included in the statistics, while dark blue particles were excluded due to stacking or structural deformation. Particle height statistics for individual particles are provided in the corresponding Figure 2c AFM images. (b) Pixel-by-pixel height distribution of the AFM images. (c) Histogram of average heights of all particles in the AFM image. (d) Histogram of average areas of all particles in the AFM image. All height measurements in this study were obtained using this method. Error bars in the height statistics represent standard deviations. Scale bar, 600 nm.



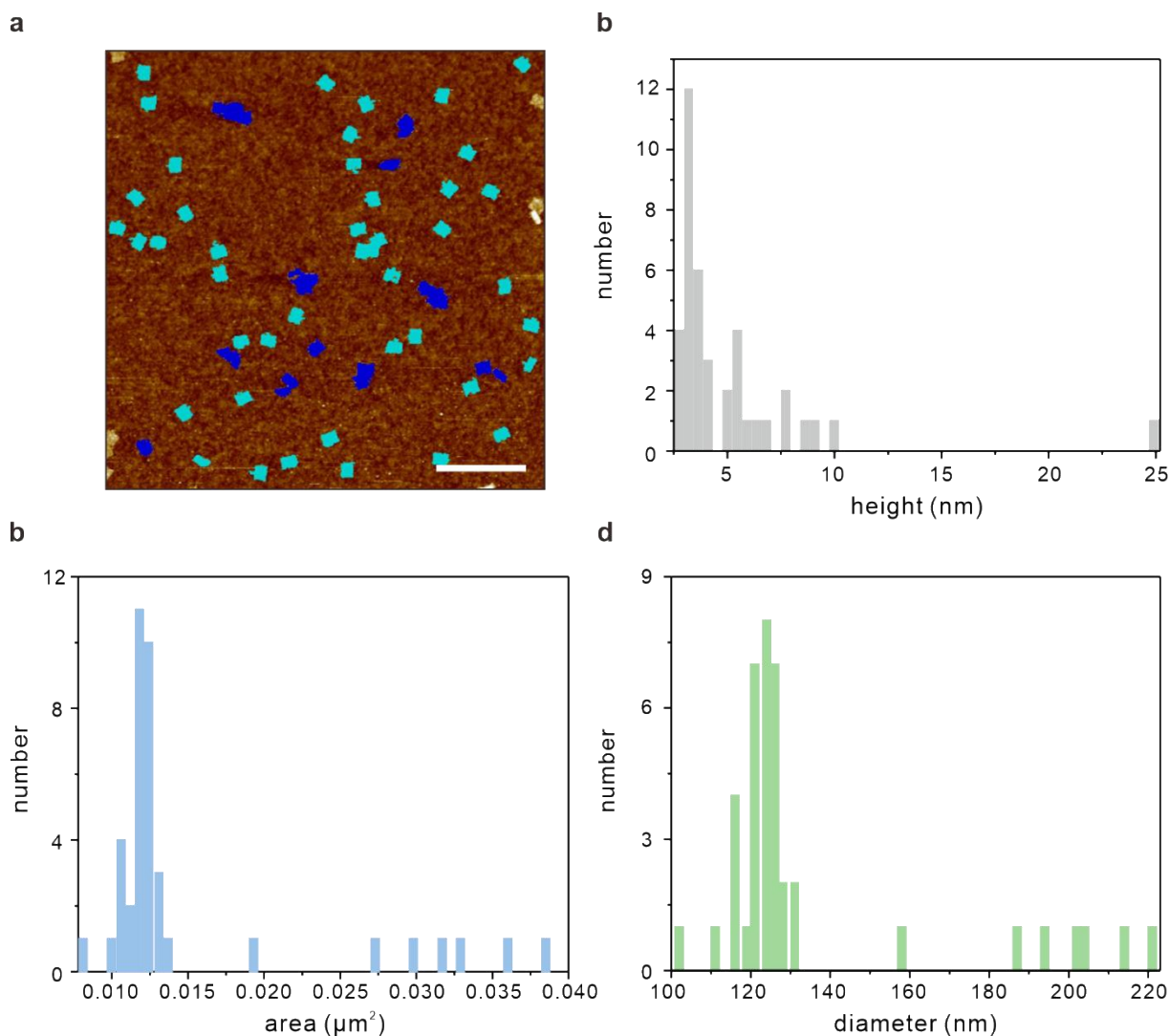
Supplementary Fig. 5. Measurement approach for the height and area of square DNA origami (SDO) after silicification at 15°C in air-phase AFM images. (a) Single particles in the AFM images were identified and screened using Nanoscope Analysis, with light blue particles included in the statistics, while dark blue particles were excluded due to stacking or structural deformation. Particle height statistics for individual particles are provided in the corresponding Figure 2d AFM images. (b) Pixel-by-pixel height distribution of the AFM images. (c) Histogram of average heights of all particles in the AFM image. (d) Histogram of average areas of all particles in the AFM image. All height measurements in this study were obtained using this method. Error bars in the height statistics represent standard deviations. Scale bar, 600 nm.



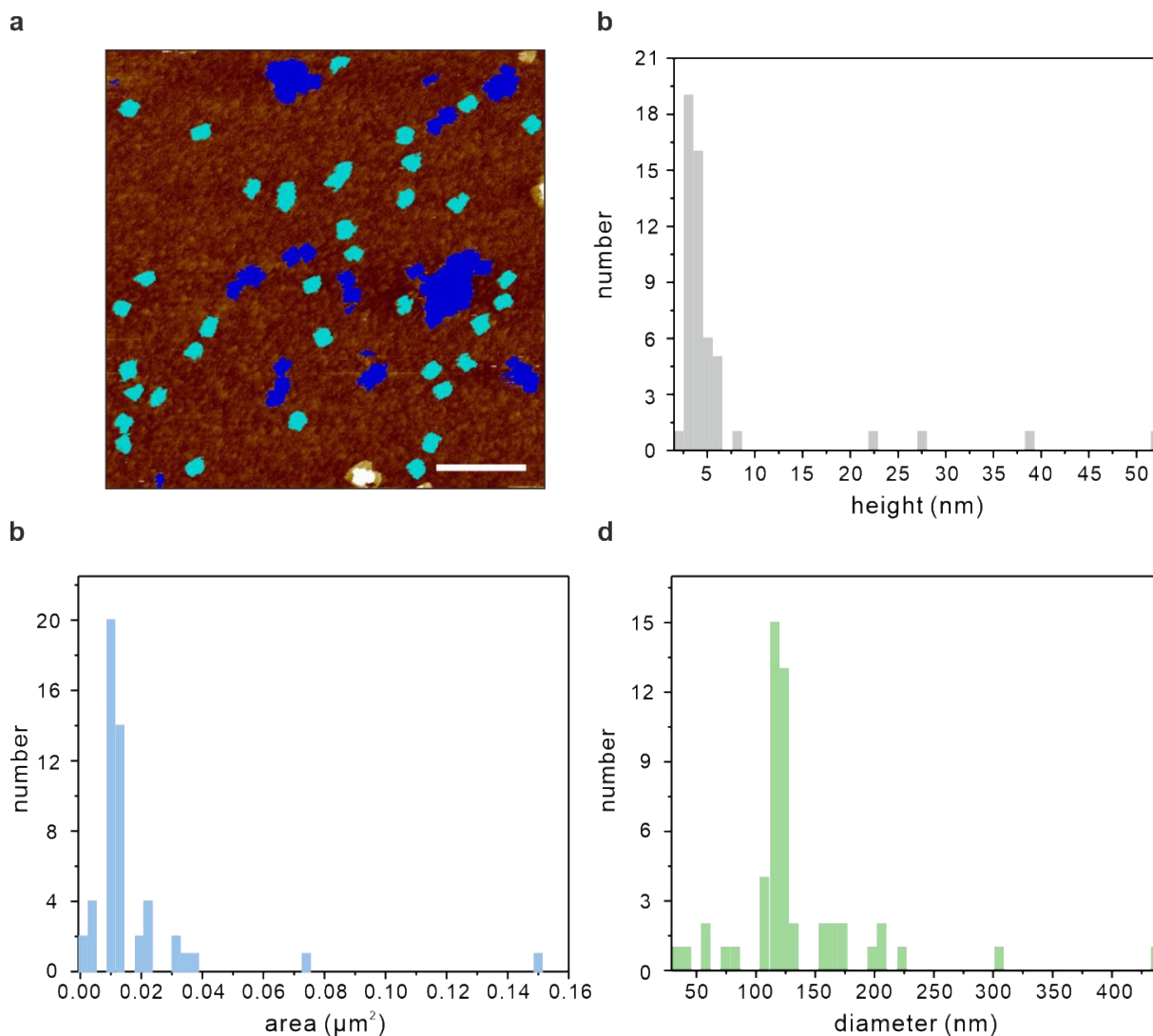
Supplementary Fig. 6. Measurement approach for the height and area of square DNA origami (SDO) after silicification at 25°C in air-phase AFM images. (a) Single particles in the AFM images were identified and screened using Nanoscope Analysis, with light blue particles included in the statistics, while dark blue particles were excluded due to stacking or structural deformation. Particle height statistics for individual particles are provided in the corresponding Figure 2e AFM images. (b) Pixel-by-pixel height distribution of the AFM images. (c) Histogram of average heights of all particles in the AFM image. (d) Histogram of average areas of all particles in the AFM image. All height measurements in this study were obtained using this method. Error bars in the height statistics represent standard deviations. Scale bar, 600 nm.



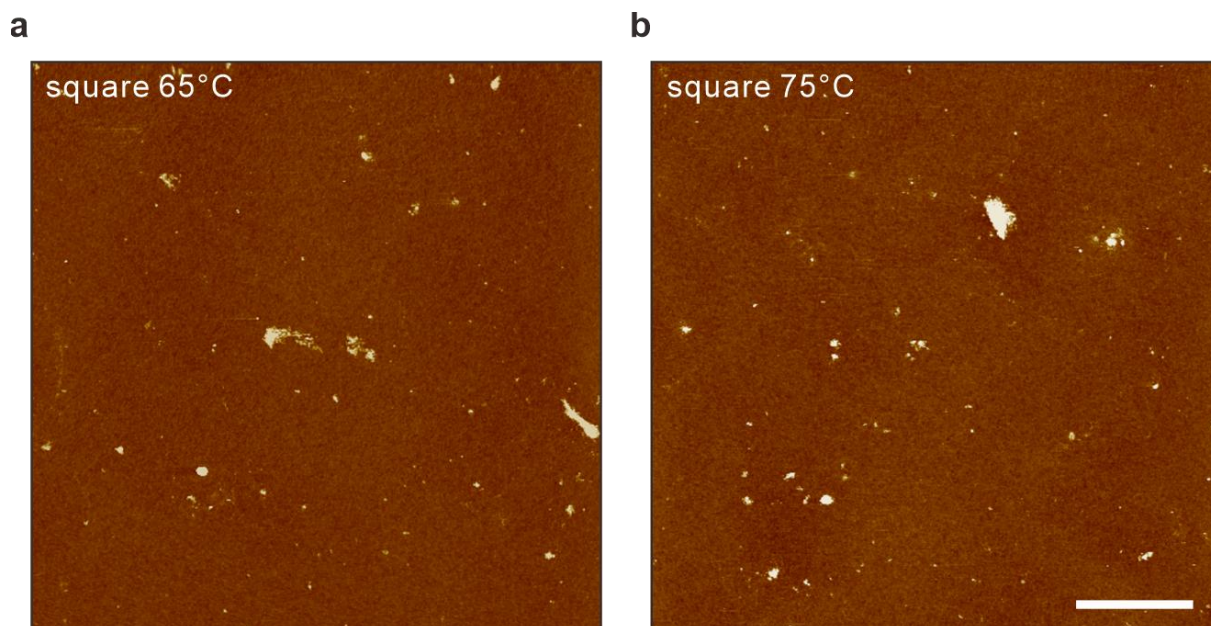
Supplementary Fig. 7. Measurement approach for the height and area of square DNA origami (SDO) after silicification at 37°C in air-phase AFM images. (a) Single particles in the AFM images were identified and screened using Nanoscope Analysis, with light blue particles included in the statistics, while dark blue particles were excluded due to stacking or structural deformation. Particle height statistics for individual particles are provided in the corresponding Figure 2f AFM images. (b) Pixel-by-pixel height distribution of the AFM images. (c) Histogram of average heights of all particles in the AFM image. (d) Histogram of average areas of all particles in the AFM image. All height measurements in this study were obtained using this method. Error bars in the height statistics represent standard deviations. Scale bar, 600 nm.



Supplementary Fig. 8. Measurement approach for the height and area of square DNA origami (SDO) after silicification at 45°C in air-phase AFM images. (a) Single particles in the AFM images were identified and screened using Nanoscope Analysis, with light blue particles included in the statistics, while dark blue particles were excluded due to stacking or structural deformation. Particle height statistics for individual particles are provided in the corresponding Figure 2g AFM images. (b) Pixel-by-pixel height distribution of the AFM images. (c) Histogram of average heights of all particles in the AFM image. (d) Histogram of average areas of all particles in the AFM image. All height measurements in this study were obtained using this method. Error bars in the height statistics represent standard deviations. Scale bar, 600 nm.

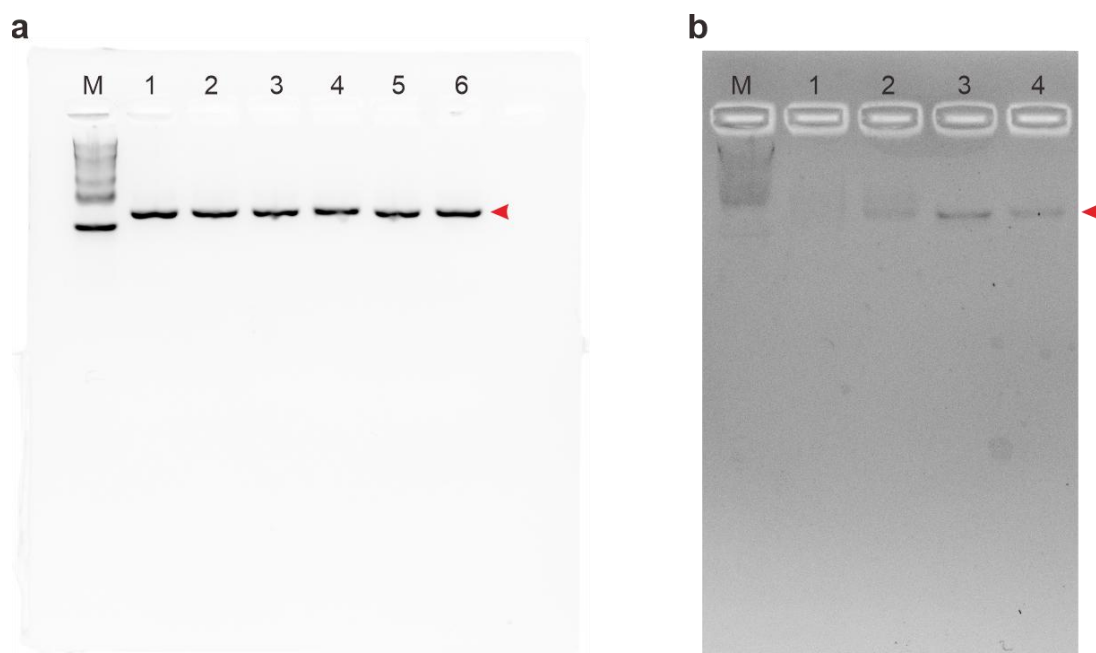


Supplementary Fig. 9. Measurement approach for the height and area of square DNA origami (SDO) after silicification at 55°C in air-phase AFM images. (a) Single particles in the AFM images were identified and screened using Nanoscope Analysis, with light blue particles included in the statistics, while dark blue particles were excluded due to stacking or structural deformation. Particle height statistics for individual particles are provided in the corresponding Figure 2h AFM images. (b) Pixel-by-pixel height distribution of the AFM images. (c) Histogram of average heights of all particles in the AFM image. (d) Histogram of average areas of all particles in the AFM image. All height measurements in this study were obtained using this method. Error bars in the height statistics represent standard deviations. Scale bar, 600 nm.



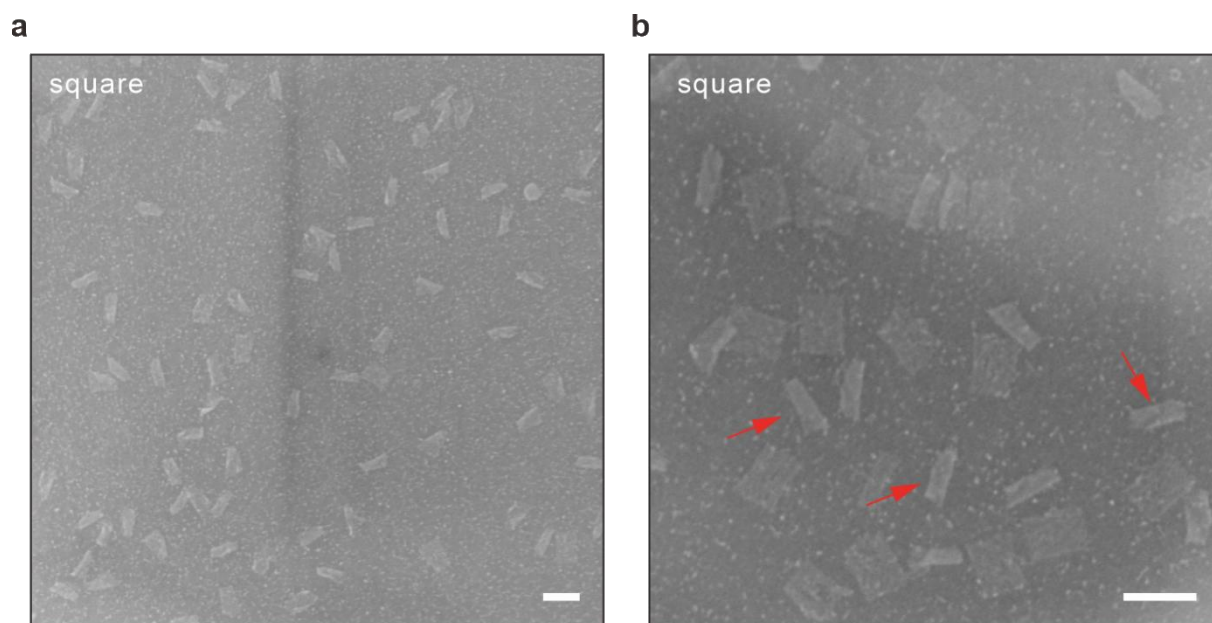
Supplementary Fig. 10. Representative AFM images of square DNA origami after silicification at elevated temperatures. Silicification at 65 °C (**a**) and 75 °C (**b**) led to structural deformation and collapse of the DNA origami, indicating that high temperatures compromise the integrity of the square DNA nanostructures. Scale bar, 2 μm .

3 Agarose gel electrophoresis characterization of square DNA origami (SDO)

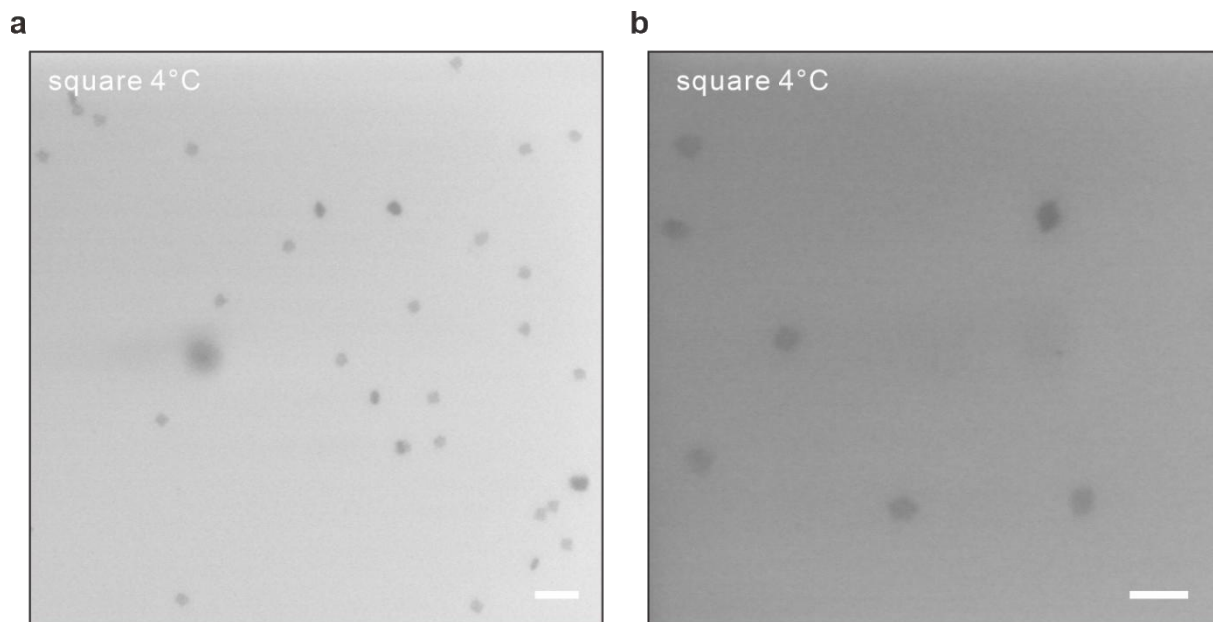


Supplementary Fig. 11. 1% Agarose gel electrophoresis analysis of square DNA origami (SDO). Representative agarose gel electrophoresis of purified square DNA origami after silicification at different silicification reaction temperatures. **a**, Lanes from left to right correspond to 1kb DNA ladder, pristine square DNA origami (10 nM) and square DNA origami (10 nM) silicification at 4, 15, 25, 37, and 45 °C, respectively, illustrating the effects of temperature on structural integrity. **b**, Lanes from left to right correspond to 1kb DNA ladder, square DNA origami (10 nM) silicification at 75, 65, 55 °C, respectively and pristine square DNA origami (10 nM), illustrating the effects of temperature on structural integrity. The red arrows indicated the corresponding electrophoretic band of the target products.

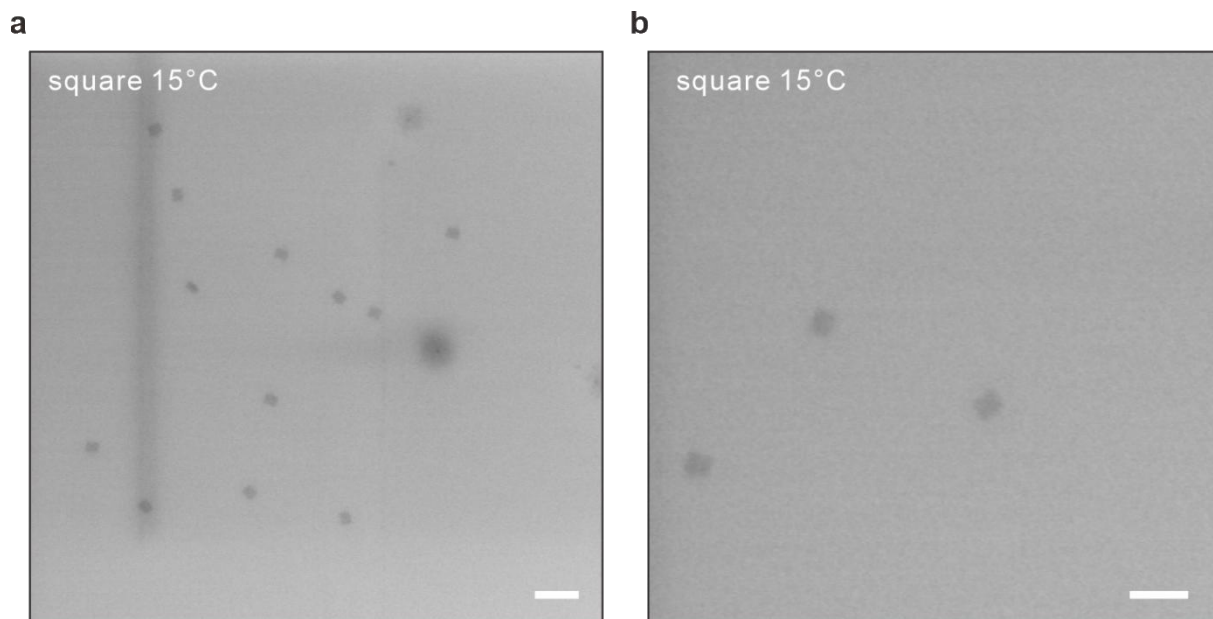
4 SEM images of SDO after silicification at different temperatures



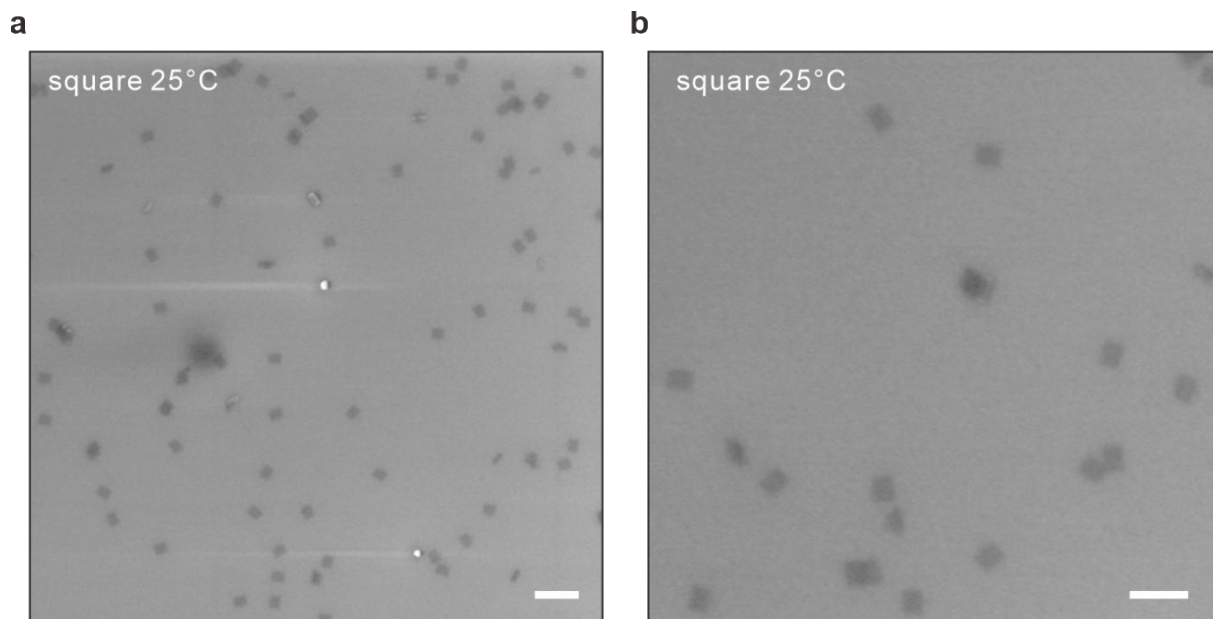
Supplementary Fig. 12. SEM images of pristine square DNA origami. (a, b) Images at different magnifications. Scale bar, 100 nm.



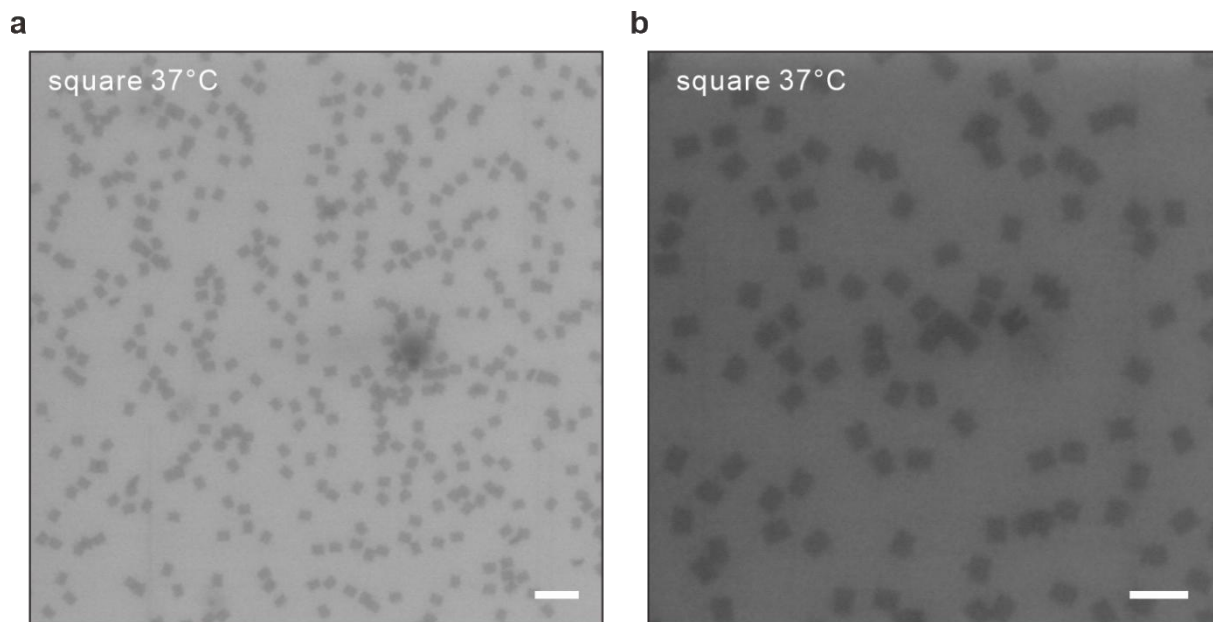
Supplementary Fig. 13. SEM images of square DNA origami after silicification at 4 °C. (a, b) Images at different magnifications. Scale bar, 300 nm and 200 nm.



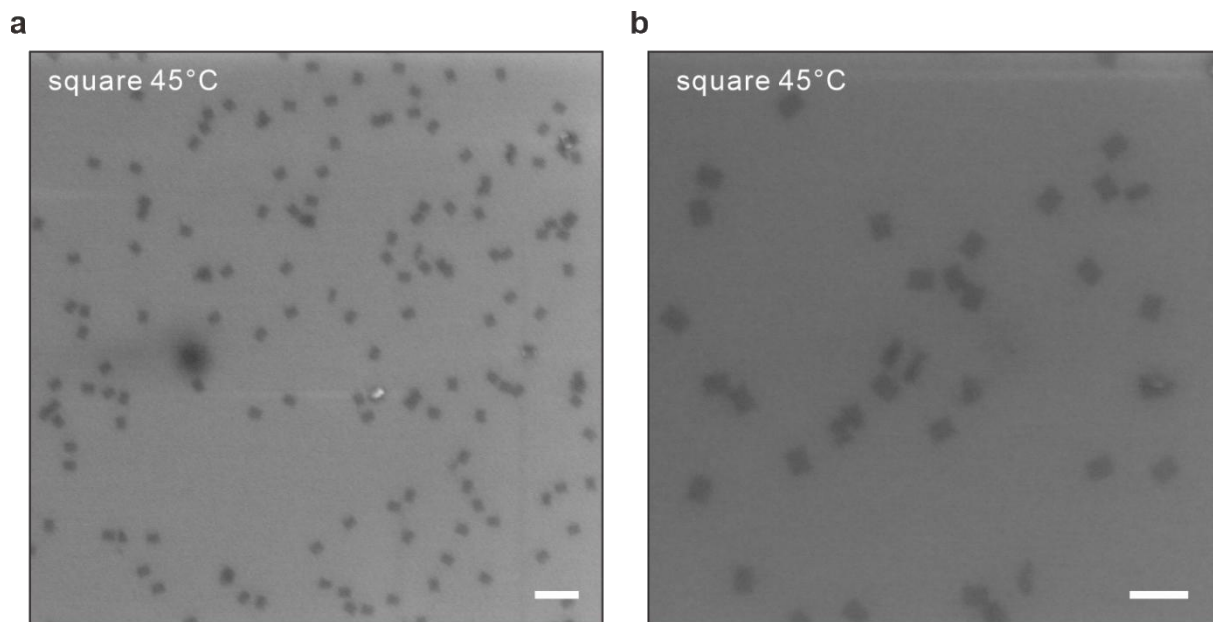
Supplementary Fig. 14. SEM images of square DNA origami after silicification at 15 °C. (a, b) Images at different magnifications. Scale bar, 300 nm and 200 nm.



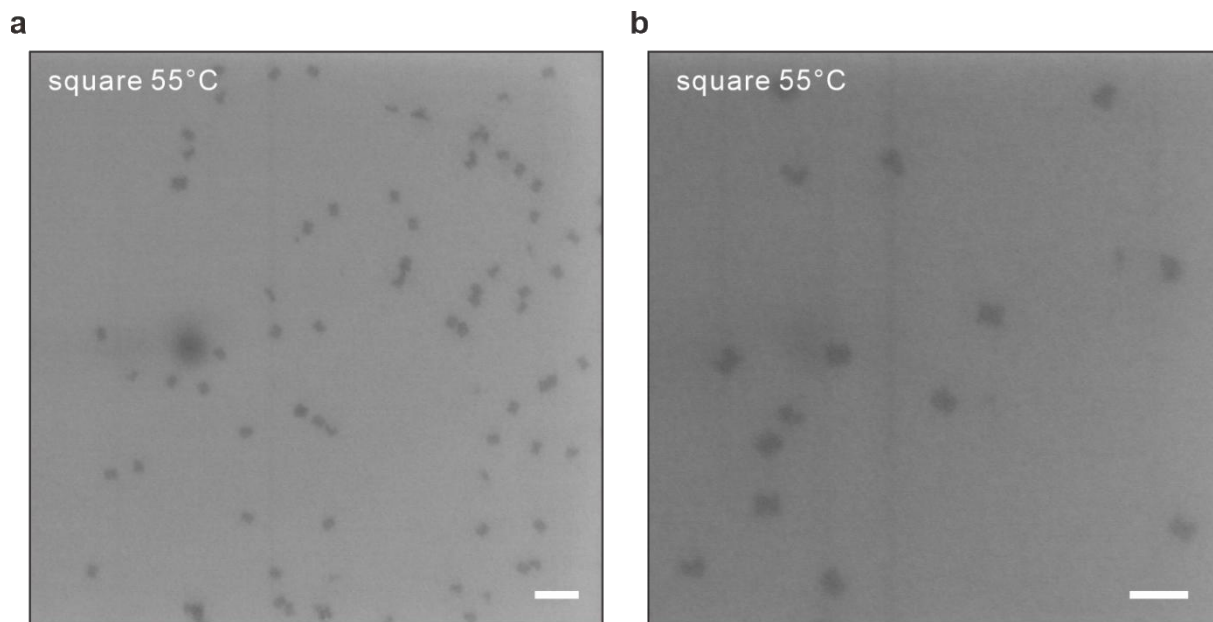
Supplementary Fig. 15. SEM images of square DNA origami after silicification at 25 °C. (a, b) Images at different magnifications. Scale bar, 300 nm and 200 nm.



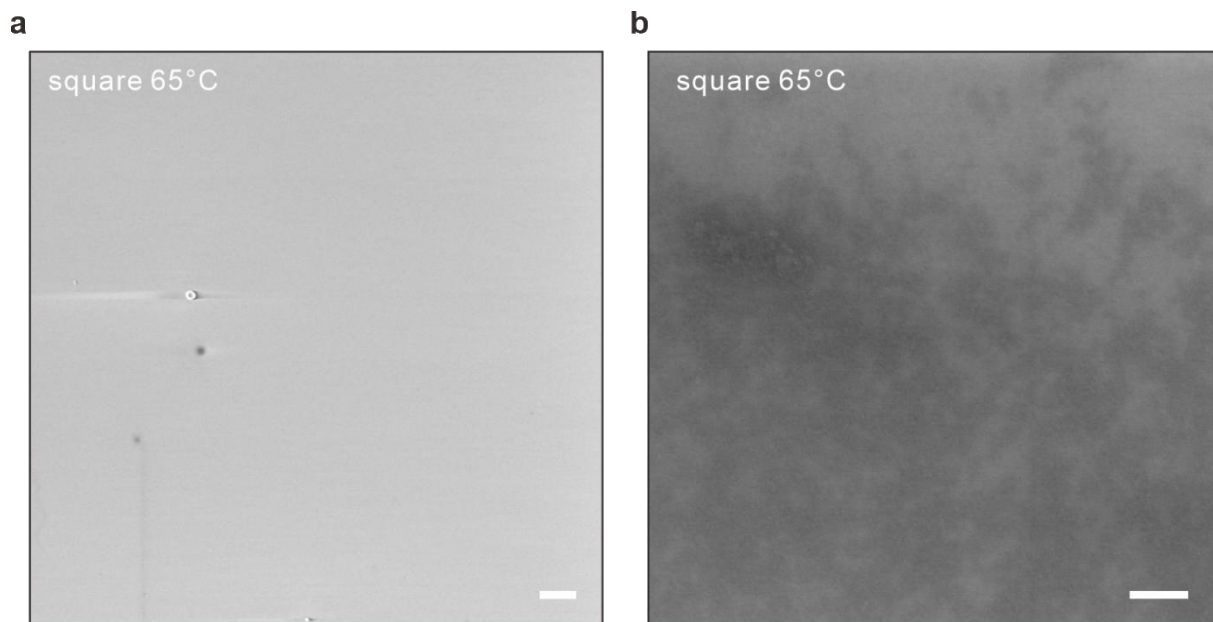
Supplementary Fig. 16. SEM images of square DNA origami after silicification at 37 °C. (a, b) Images at different magnifications. Scale bar, 300 nm and 200 nm.



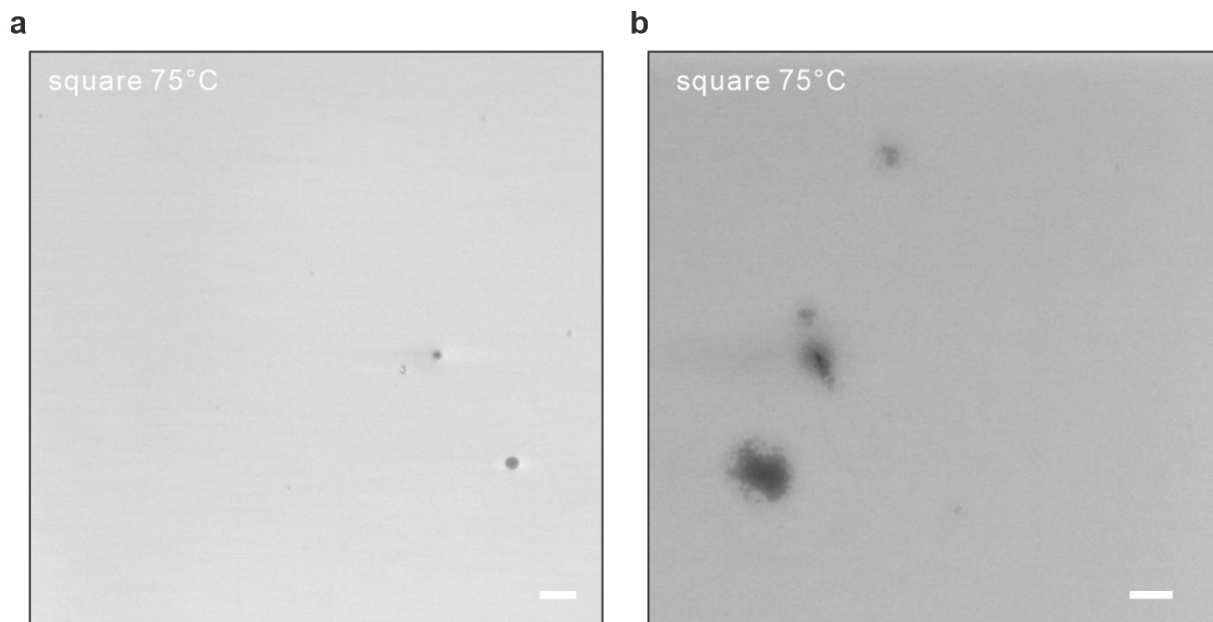
Supplementary Fig. 17. SEM images of square DNA origami after silicification at 45 °C. (a, b) Images at different magnifications. Scale bar, 300 nm and 200 nm.



Supplementary Fig. 18. SEM images of square DNA origami after silicification at 55 °C. (a, b) Images at different magnifications. Scale bar, 300 nm and 200 nm.

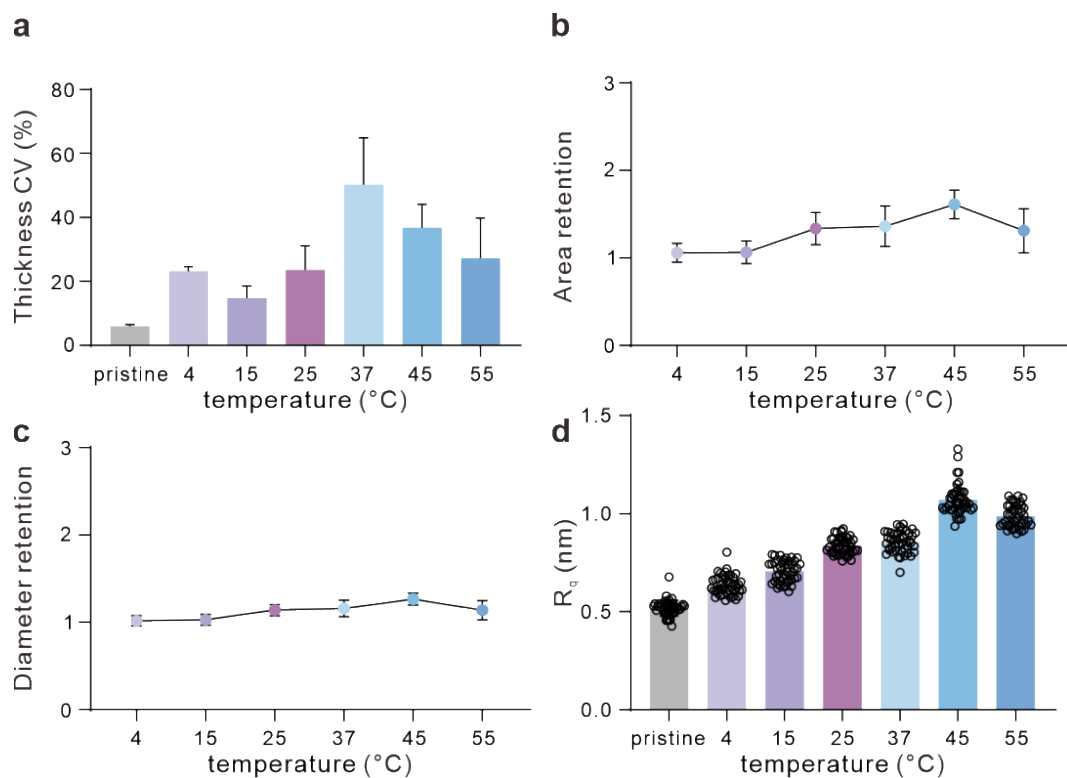


Supplementary Fig. 19. SEM images of square DNA origami after silicification at 65 °C. (a, b) Images at different magnifications. Scale bar, 1 μm and 200 nm.



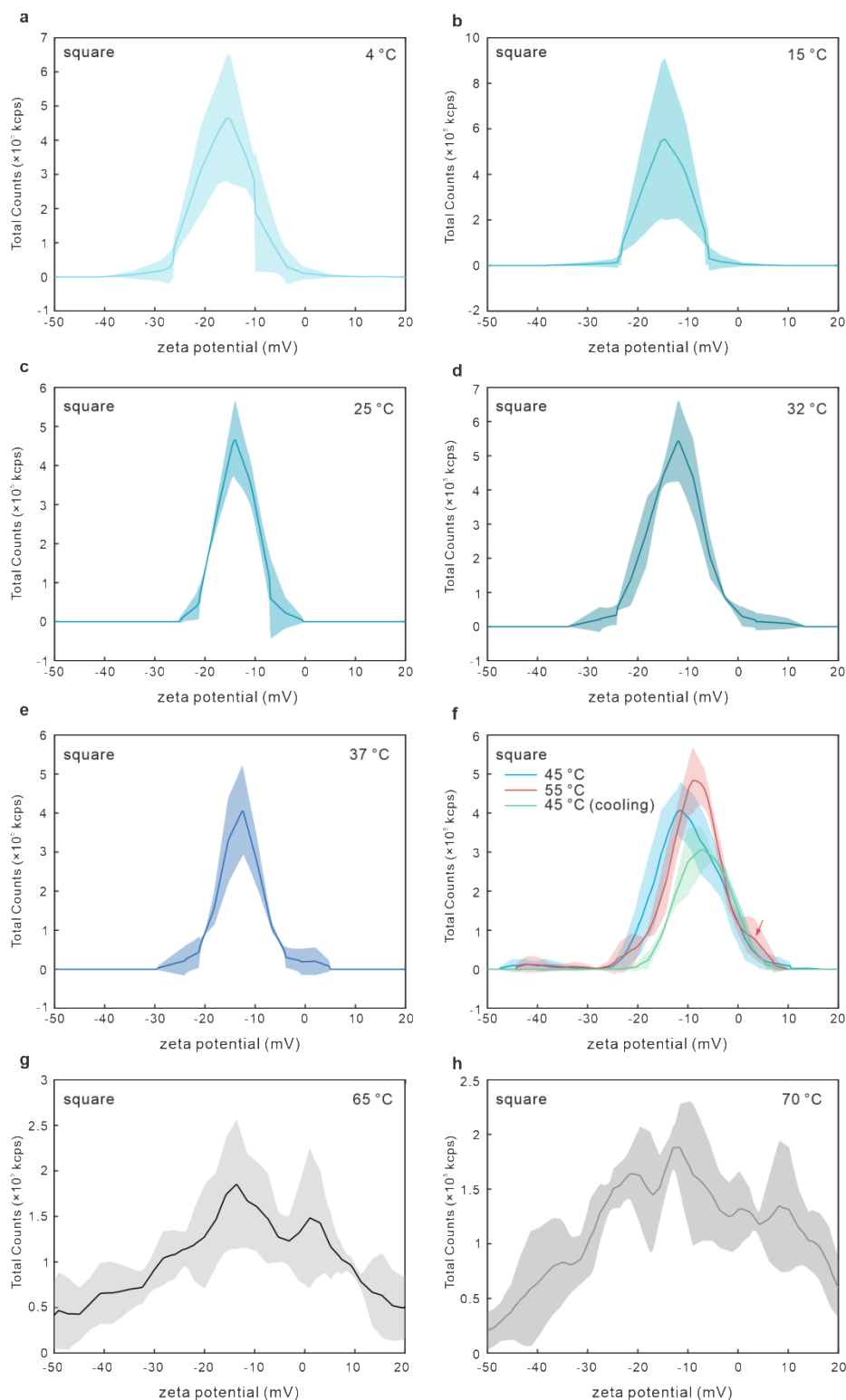
Supplementary Fig. 20. SEM images of square DNA origami after silicification at 75 °C. (a, b) Images at different magnifications. Scale bar, 1 μm and 300 nm.

5 The quantitative analysis of square DNA origami from air-AFM images



Supplementary Fig. 21. AFM-based quantitative analysis of pristine square DNA origami (SDO) and silicified structures at different temperatures. Thickness coefficient of variation (Thickness CV, %) (a), Area retention (b), Diameter retention (c) and Root mean square roughness (R_q) (d) of silicified SDO as a function of temperature. Data are presented as mean \pm standard deviation (mean \pm SD).

6 Temperature-dependent zeta-potential distributions of SDO



Supplementary Fig. 22. Zeta potential distributions of pristine square DNA origami measured at different temperatures. (a) 4 °C, (b) 15 °C, (c) 25 °C, (d) 32 °C, (e) 37 °C, (f) during a heating–cooling cycle (45 °C to 55 °C to 45 °C), (g) 65 °C, and (h) 70 °C. The line represents the mean distribution and the shaded area denotes the standard deviation from repeated three measurements.

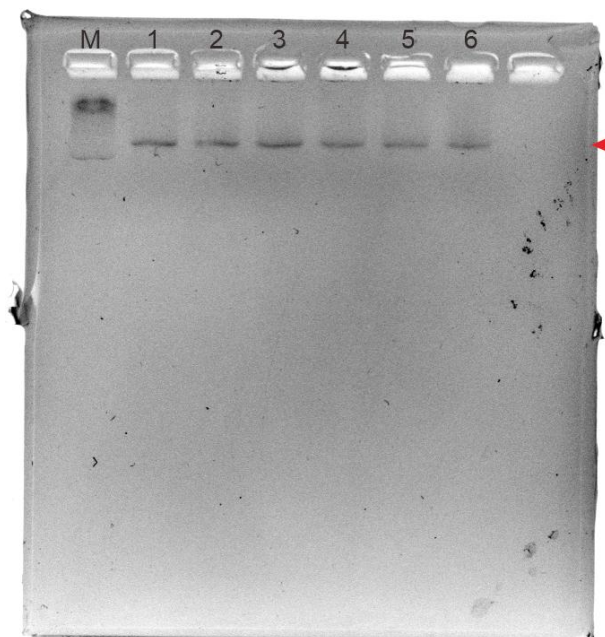
7 Agarose gel electrophoresis characterization of DNA origami nanostructures



Supplementary Fig. 23. 1% Agarose gel electrophoresis analysis of Triangular DNA origami (TDO). Representative agarose gel electrophoresis of purified Triangular DNA origami after silicification at different silicification reaction temperatures. Lanes from left to right correspond to 1kb DNA ladder, pristine Triangular DNA origami (10 nM) and Triangular DNA origami (10 nM) silicification at 4, 15, 25, 37, and 45 °C, respectively.

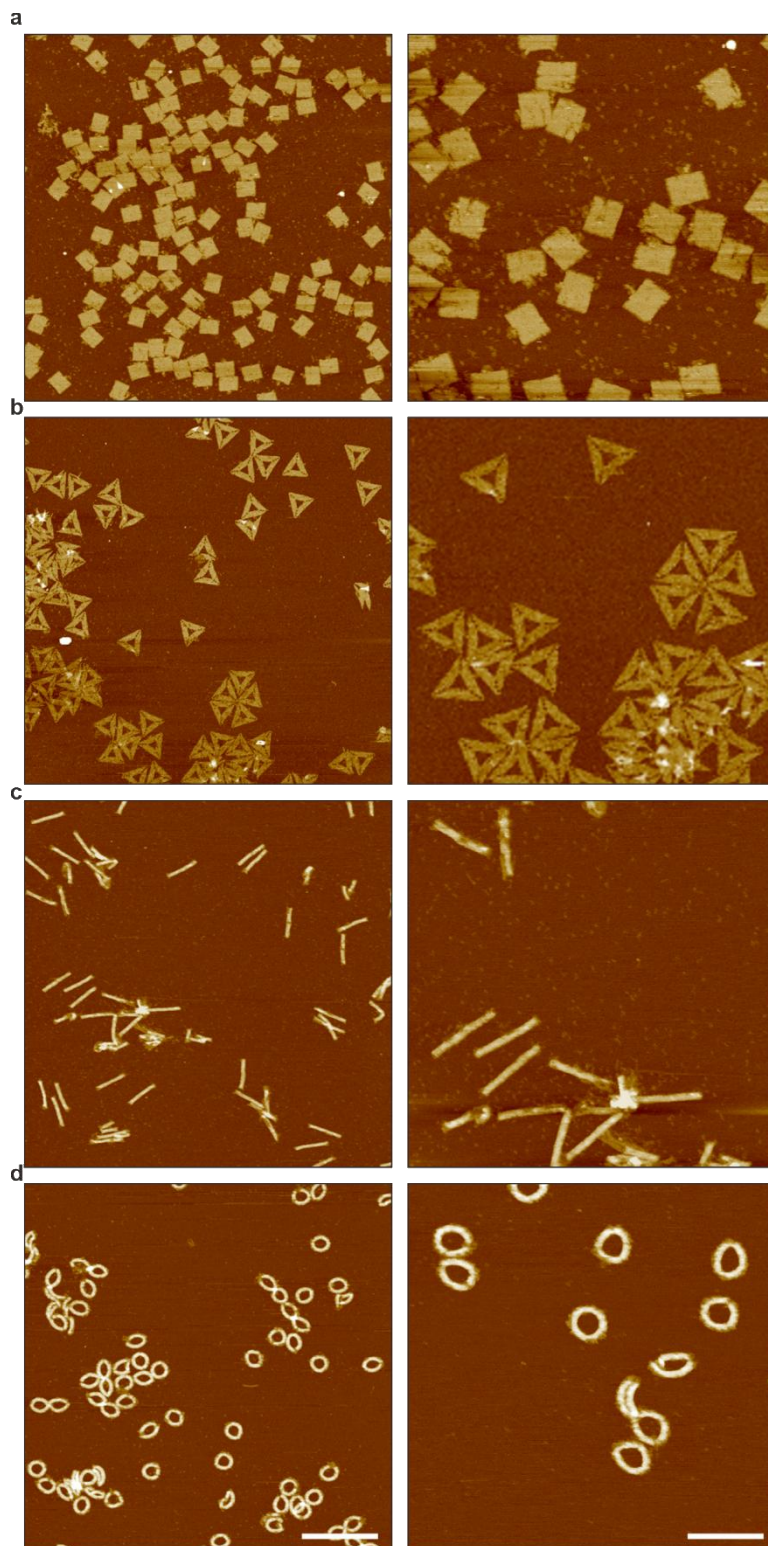


Supplementary Fig. 24. 1% Agarose gel electrophoresis analysis of ring-shaped DNA origami (RDO). Representative agarose gel electrophoresis of purified ring-shaped DNA origami after silicification at different silicification reaction temperatures. Lanes from left to right correspond to 1kb DNA ladder, pristine ring-shaped DNA origami (10 nM) and ring-shaped DNA origami (10 nM) silicification at 4, 15, 25, 37, and 45 °C, respectively.

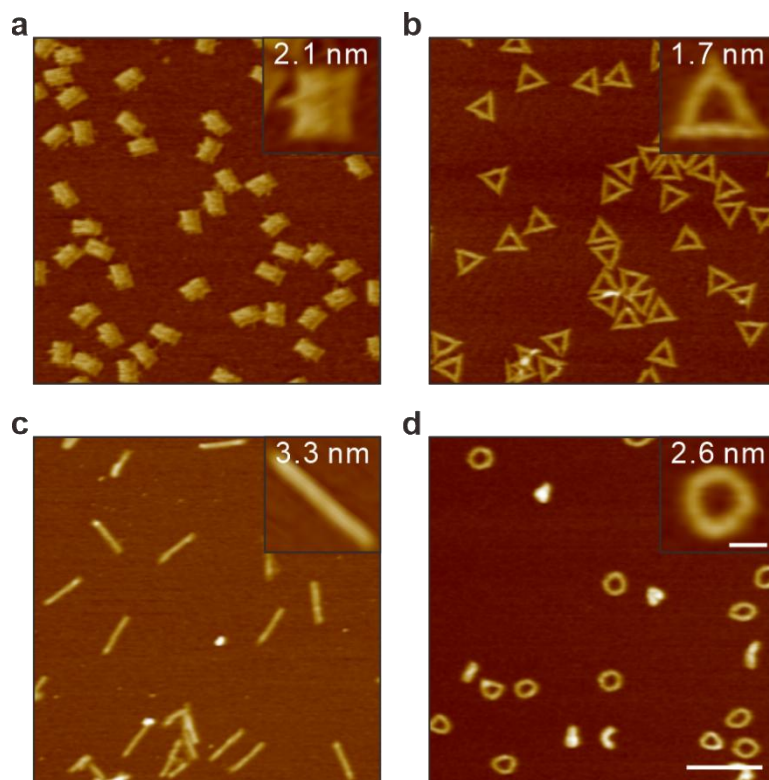


Supplementary Fig. 25. 1% Agarose gel electrophoresis analysis of 14-helix bundle DNA origami (14HB). Representative agarose gel electrophoresis of purified 14-helix bundle DNA origami after silicification at different silicification reaction temperatures. Lanes from left to right correspond to 1kb DNA ladder, pristine 14-helix bundle DNA origami (10 nM) and 14-helix bundle DNA origami (10 nM) silicification at 4, 15, 25, 37, and 45 °C, respectively. The red arrows indicated the corresponding electrophoretic band of the target products.

8 AFM imaging of DNA origami nanostructures under air- and liquid-phase conditions

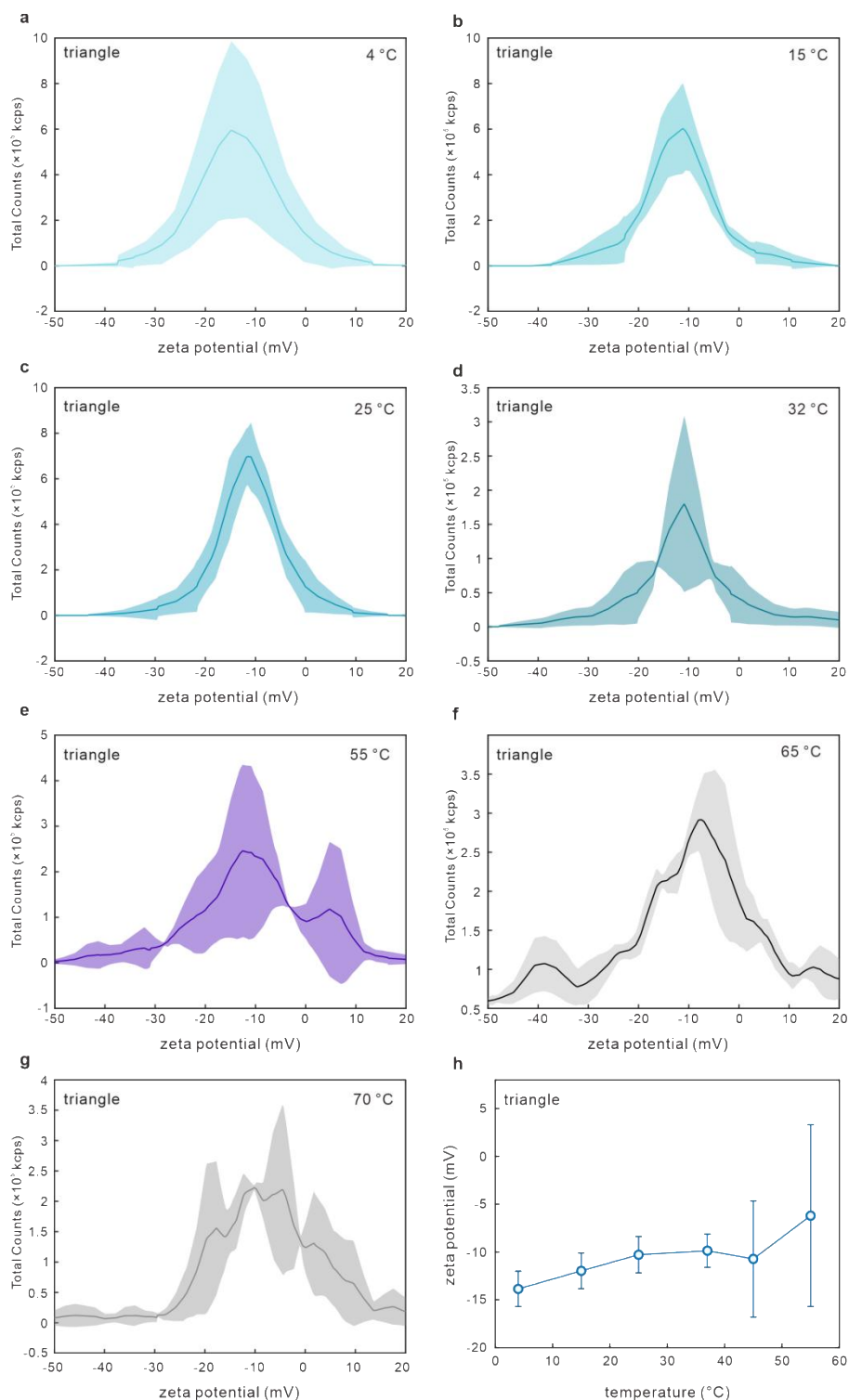


Supplementary Fig. 26. Liquid-phase AFM images of DNA origami nanostructures. Square (a), Triangular (b), 14-helix bundle (c), and ring (d) shapes. Left and Right panels show different magnifications with scale bars of 400 nm and 200 nm, respectively. All images were obtained under liquid conditions to preserve the native conformations of the DNA origamis.

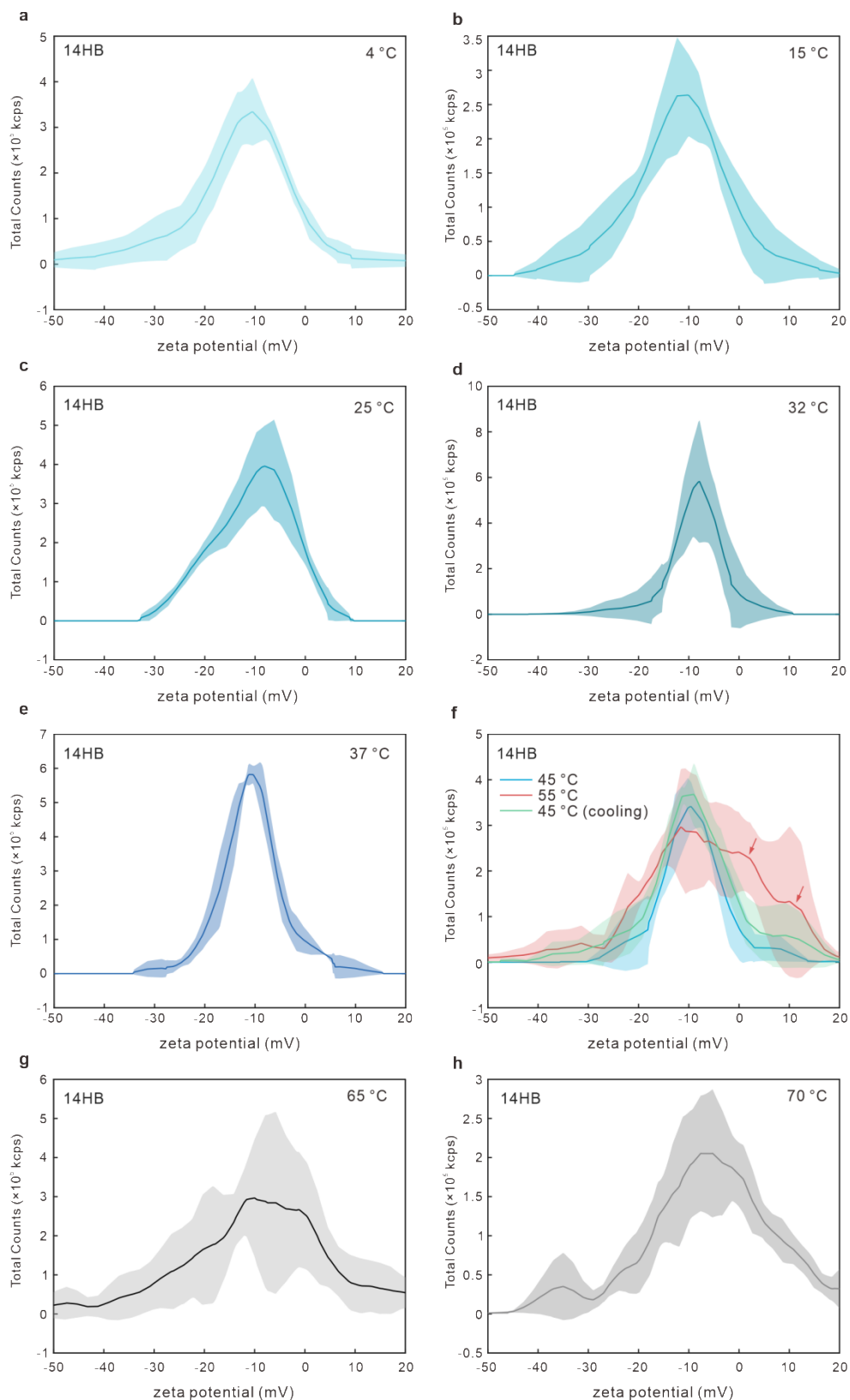


Supplementary Fig. 27. The morphology and height characteristics of different DNA origami architectures in air-phase AFM. Air-phase AFM images of the square (a), triangle (b), 14HB (c) and ring (d) structures (scale bar, 300 nm), the inset shows a representative DNA origami with annotated average height (scale bar, 50 nm).

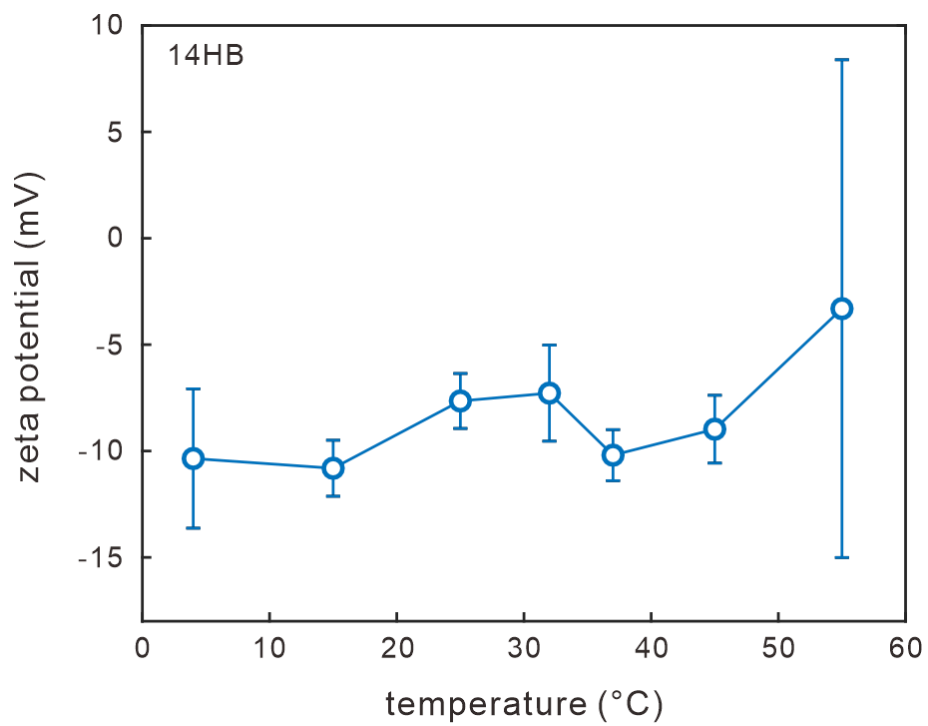
9 Temperature-dependent zeta-potential distributions of DNA origami nanostructures



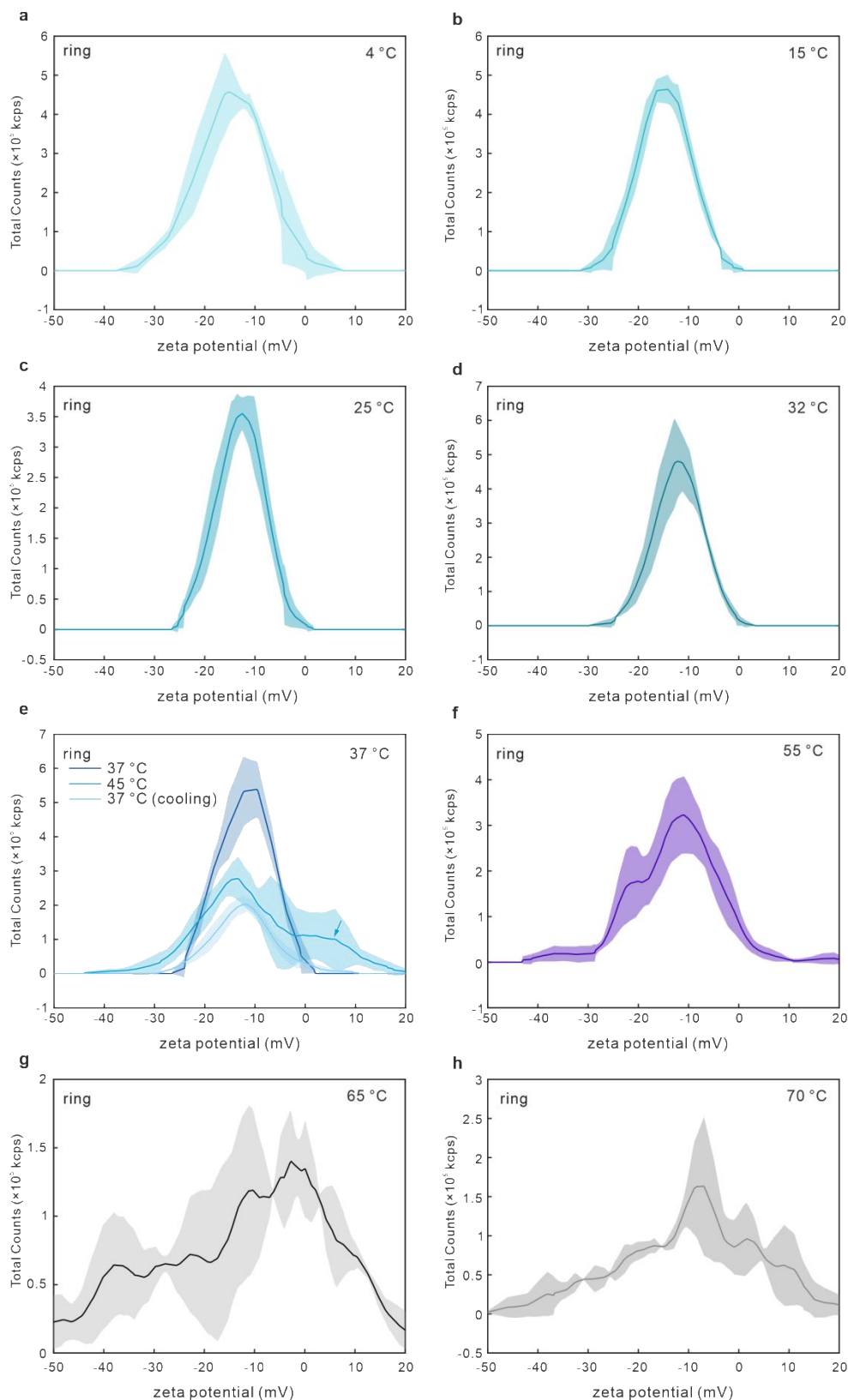
Supplementary Fig. 28. Zeta potential distributions of pristine triangular DNA origamis measured at different temperatures, and the temperature dependence of the peak zeta-potential. (a) 4 °C, (b) 15 °C, (c) 25 °C, (d) 32 °C, (e) 55 °C, (f) 65 °C, (g) 70 °C, and Peak zeta-potential of TDO increases with temperature from 4 °C to 55 °C (h). The line represents the mean distribution and the shaded area denotes the standard deviation from repeated three measurements.



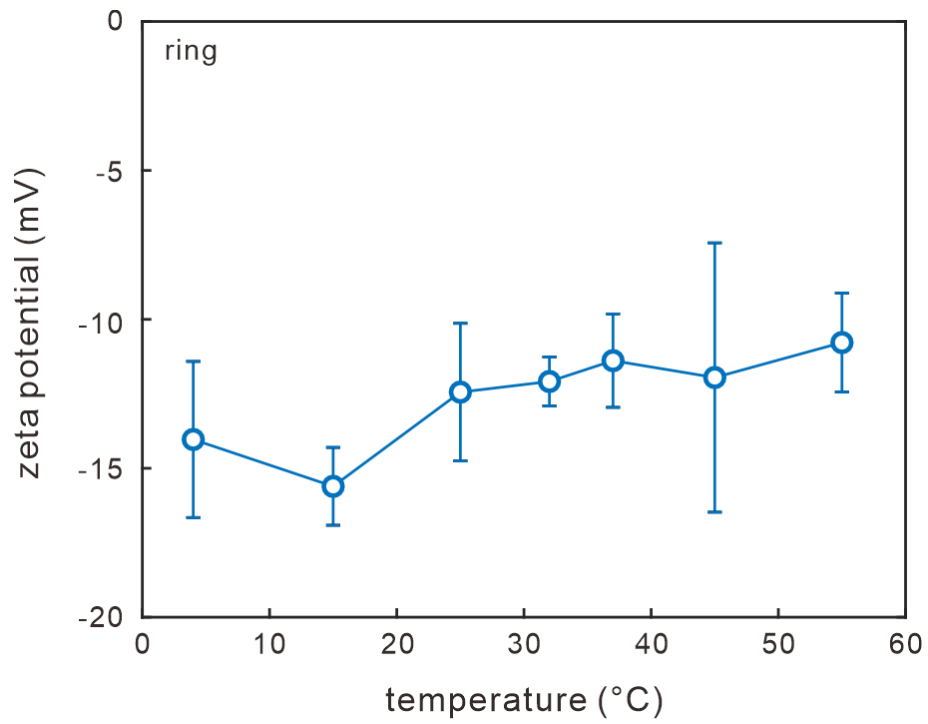
Supplementary Fig. 29. Zeta potential distributions of pristine 14-helix bundle DNA origami measured at different temperatures. (a) 4 °C, (b) 15 °C, (c) 25 °C, (d) 32 °C, (e) 37 °C, (f) during a heating–cooling cycle (45 °C to 55 °C to 45 °C), (g) 65 °C, and (h) 70 °C. The line represents the mean distribution and the shaded area denotes the standard deviation from repeated three measurements.



Supplementary Fig. 30. The temperature dependence of the peak zeta-potential. Peak zeta-potential of **pristine** 14HB increases with temperature from 4 °C to 55 °C.

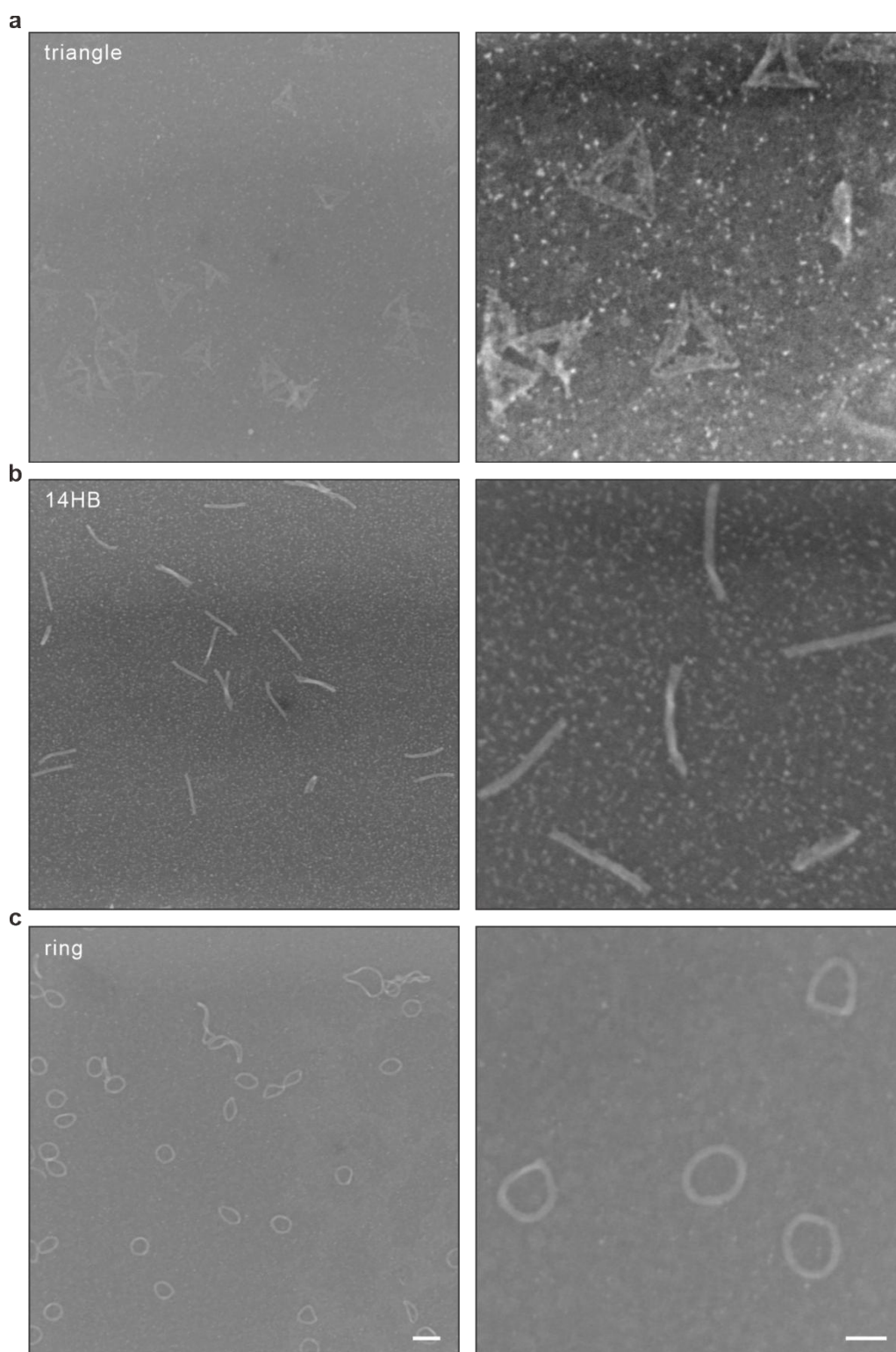


Supplementary Fig. 31. Zeta potential distributions of pristine ring-shaped DNA origami measured at different temperatures. (a) 4 °C, (b) 15 °C, (c) 25 °C, (d) 32 °C, (e) during a heating–cooling cycle (37 °C to 45 °C to 37 °C), (f) 55 °C, (g) 65 °C, and (h) 70 °C. The line represents the mean distribution and the shaded area denotes the standard deviation from repeated three measurements.

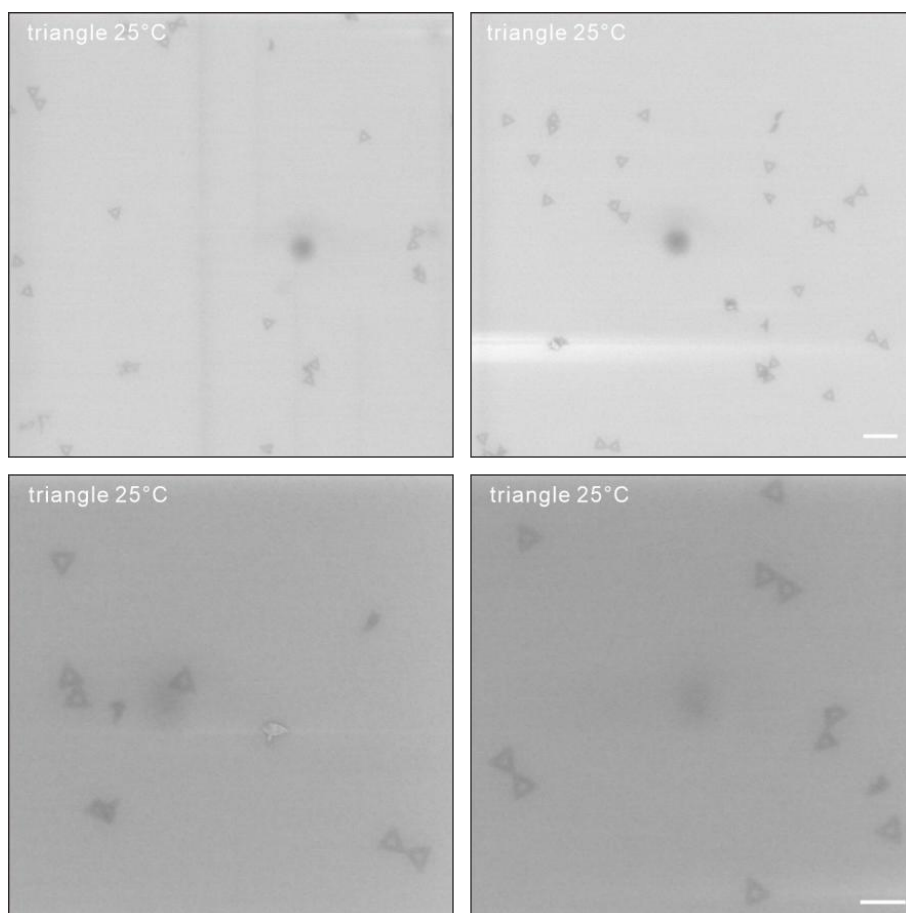


Supplementary Fig. 32. The temperature dependence of the peak zeta-potential. Peak zeta-potential of **pristine** RDO increases with temperature from 4 °C to 55 °C.

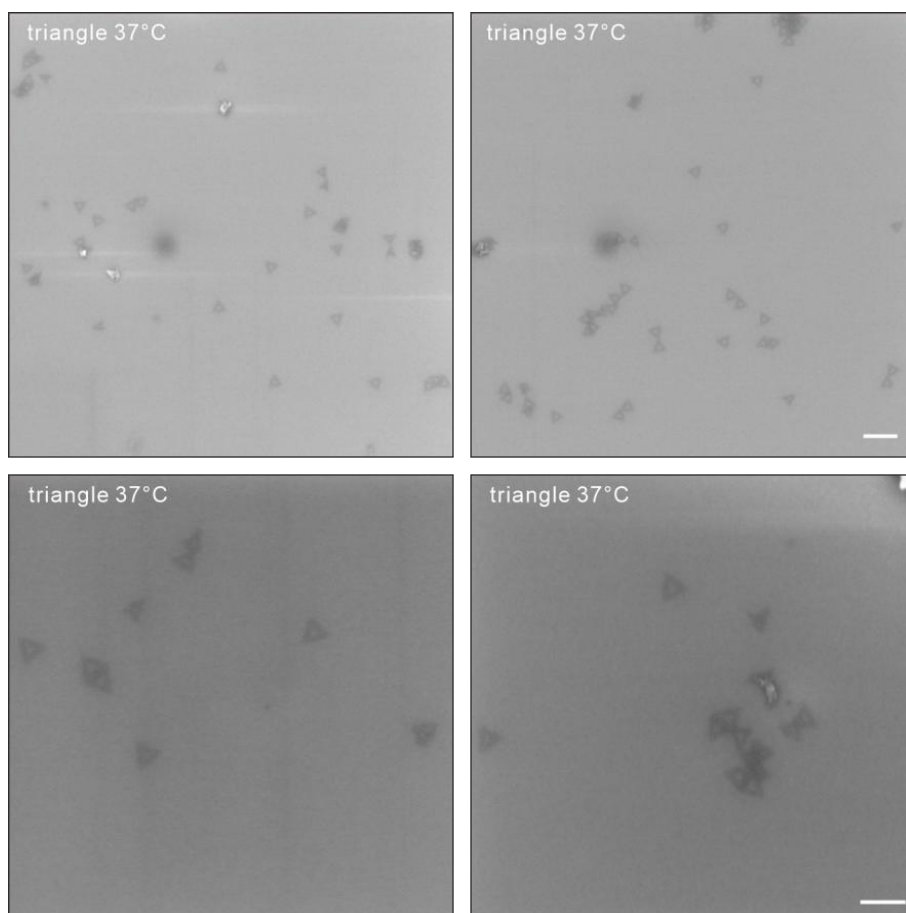
10 SEM images of pristine DNA origami and after silicification at different temperatures



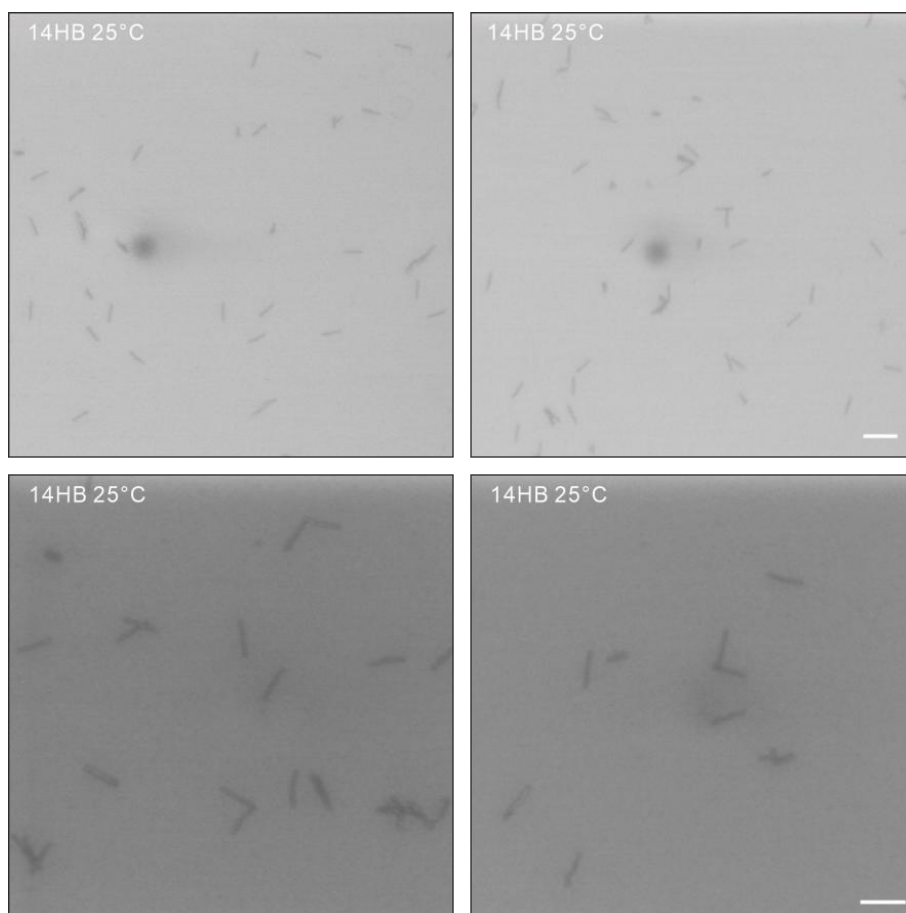
Supplementary Fig. 33. SEM images of pristine DNA origami nanostructures. Triangular (a), 14-helix bundle (b), and ring (c) shapes. Samples were stained with uranyl acetate prior to imaging to enhance contrast. Scale bars, 100 nm.



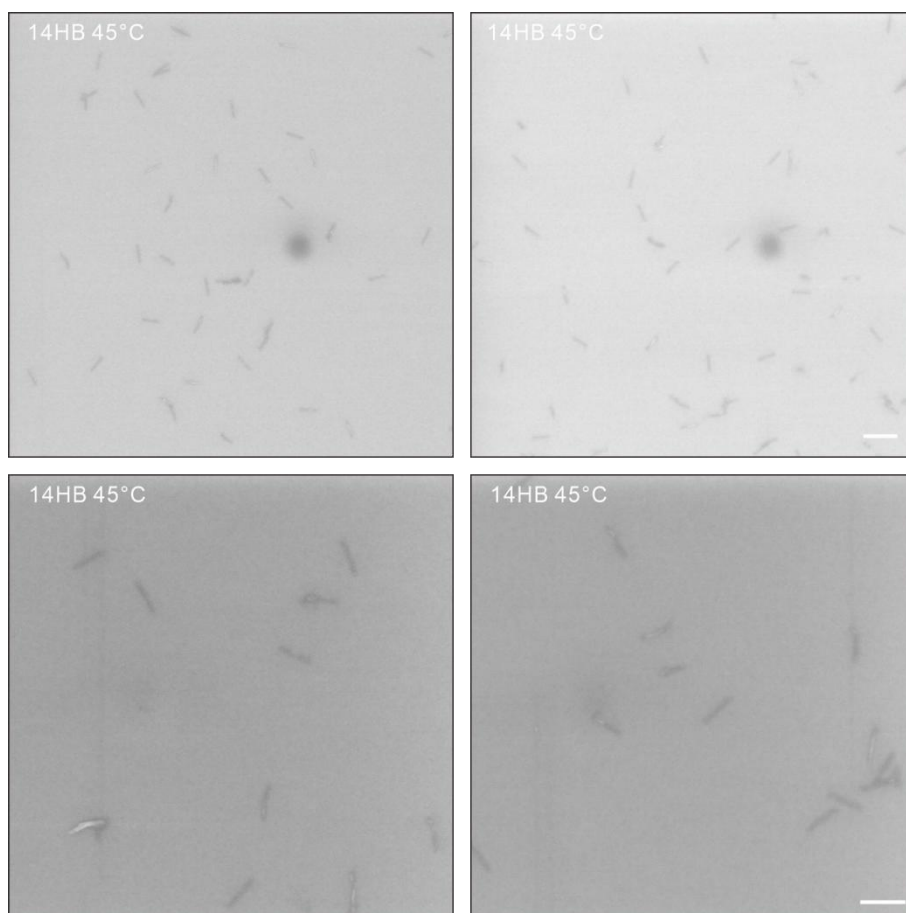
Supplementary Fig. 34. SEM image of Triangular DNA origami after silicification at 25 °C. The sample was silicified to form a conformal silica coating while preserving the original DNA origami structure. Scale bar, 300 nm and 200 nm.



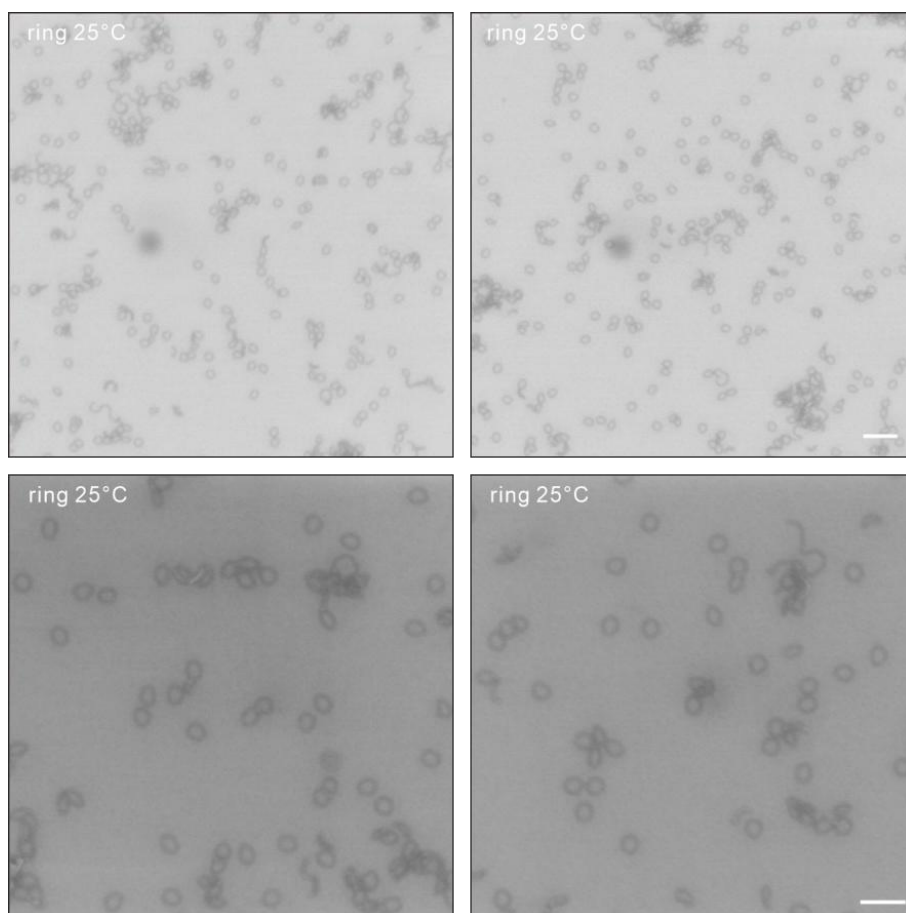
Supplementary Fig. 35. SEM image of Triangular DNA origami after silicification at 37 °C. The sample was silicified to form a conformal silica coating while preserving the original DNA origami structure. Scale bar, 300 nm and 200 nm.



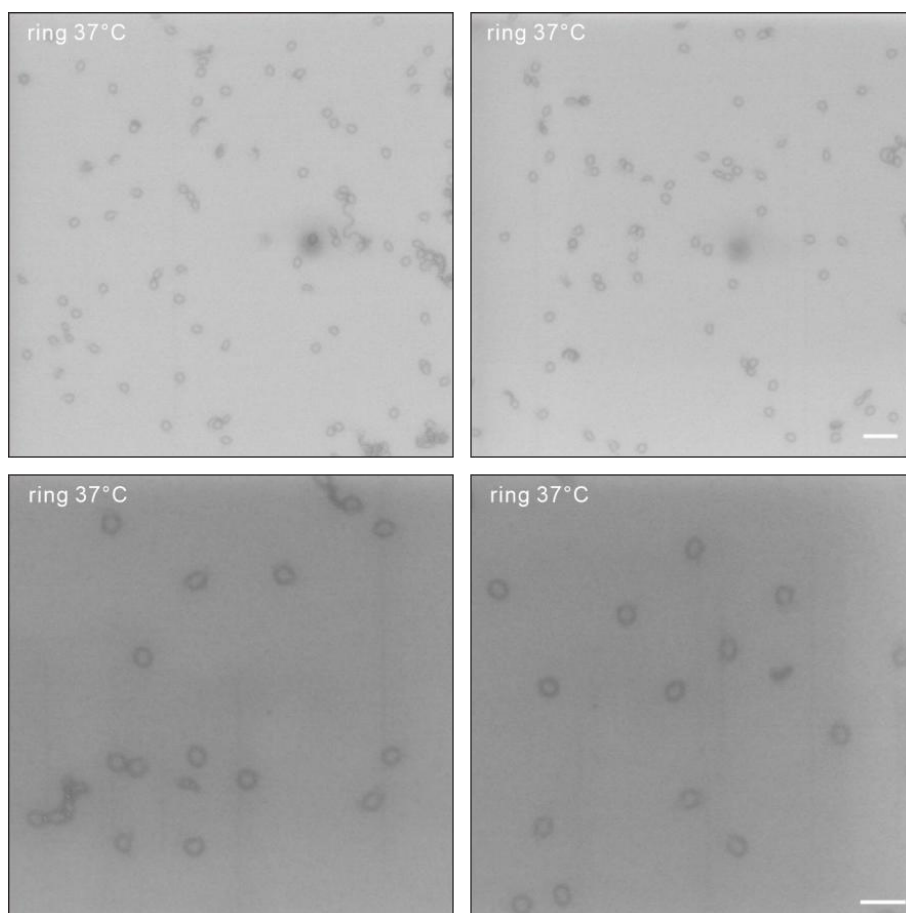
Supplementary Fig. 36. SEM image of 14 helix bundle DNA origami after silicification at 25 °C. The sample was silicified to form a conformal silica coating while preserving the original DNA origami structure. Scale bar, 300 nm and 200 nm.



Supplementary Fig. 37. SEM image of 14 helix bundle DNA origami after silicification at 45 °C. The sample was silicified to form a conformal silica coating while preserving the original DNA origami structure. Scale bar, 300 nm and 200 nm.

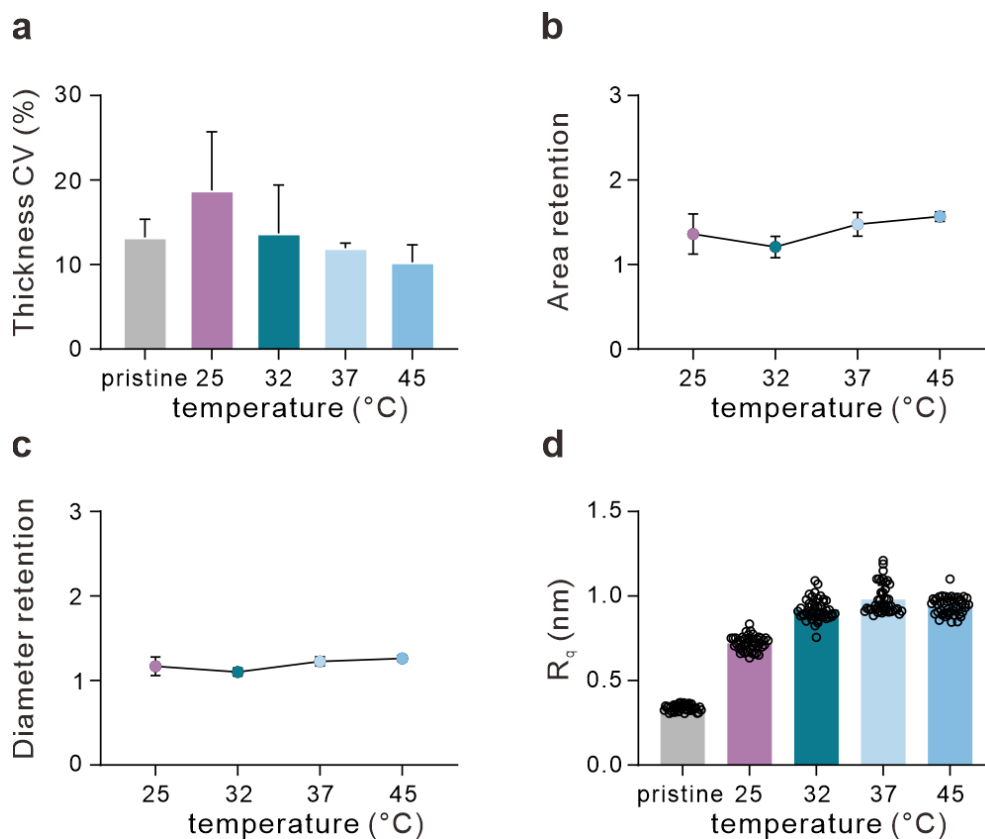


Supplementary Fig. 38. SEM image of ring-shaped DNA origami after silicification at 25 °C. The sample was silicified to form a conformal silica coating while preserving the original DNA origami structure. Scale bar, 300 nm and 200 nm.

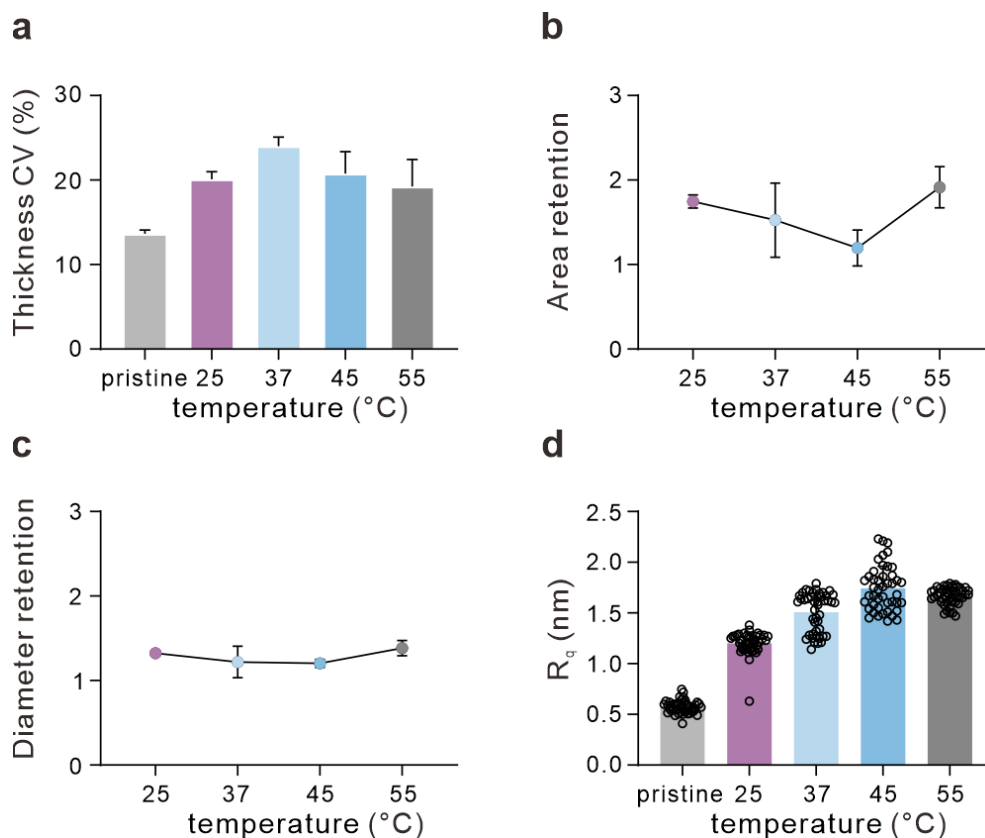


Supplementary Fig. 39. SEM image of ring-shaped DNA origami after silicification at 37 °C. The sample was silicified to form a conformal silica coating while preserving the original DNA origami structure. Scale bar, 300 nm and 200 nm.

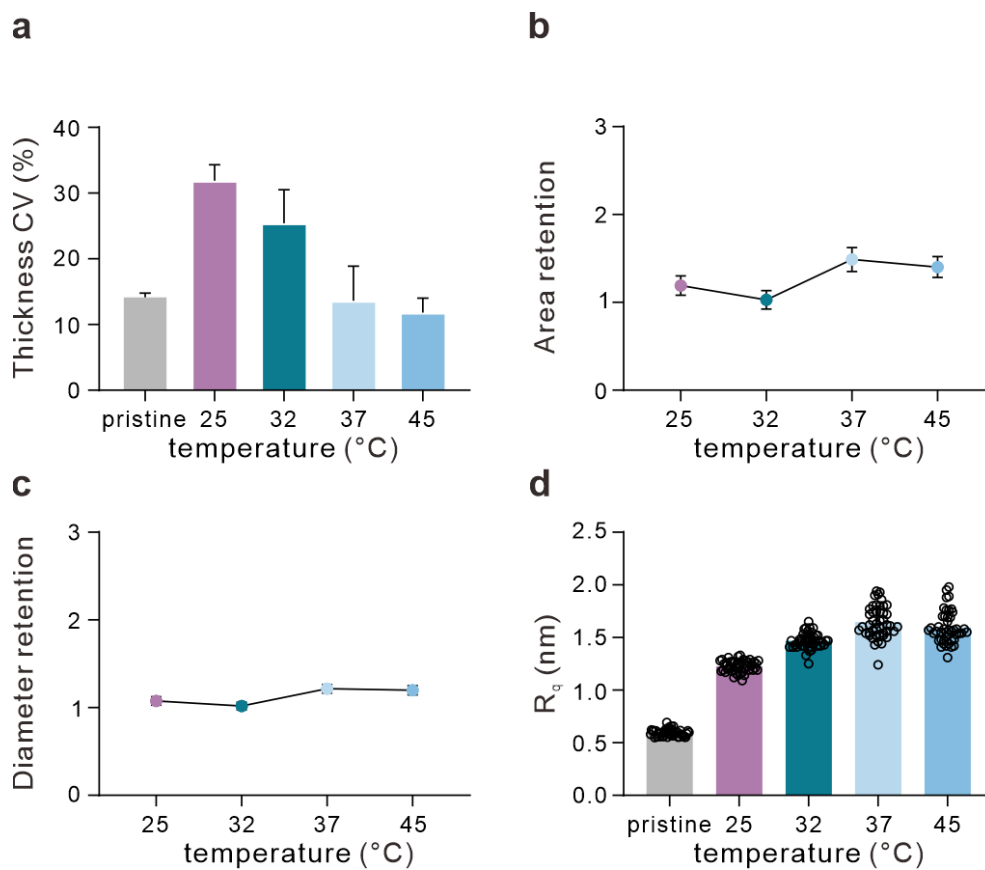
11 The quantitative analysis of DNA origami from AFM images



Supplementary Fig. 40. AFM-based quantitative analysis of pristine triangular DNA origami (TDO) and silicified structures at different temperatures. Thickness coefficient of variation (Thickness CV, %) (a), Area retention (b), Diameter retention (c) and Root mean square roughness (R_q) (d) of silicified TDO as a function of temperature. Data are presented as mean \pm standard deviation (mean \pm SD).

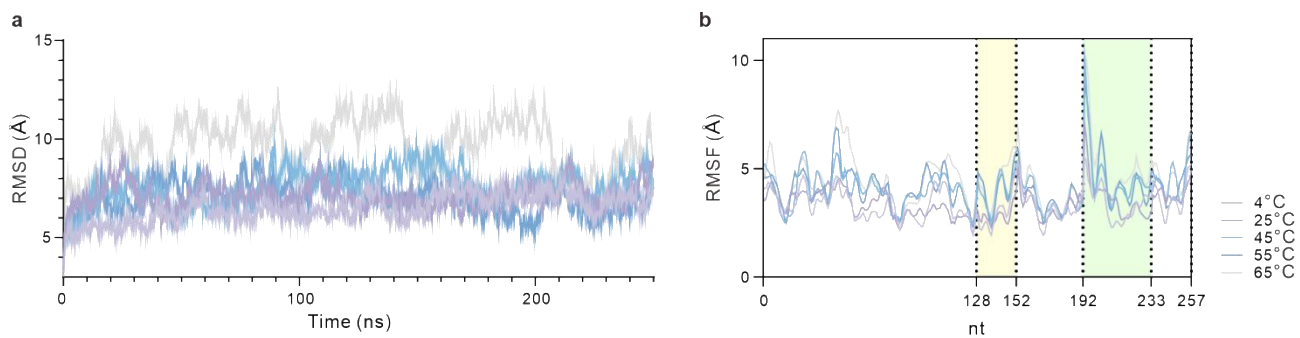


Supplementary Fig. 41. AFM-based quantitative analysis of pristine 14-helix bundle DNA origami (14HB) and silicified structures at different temperatures. Thickness coefficient of variation (Thickness CV, %) (a), Area retention (b), Diameter retention (c) and Root mean square roughness (R_q) (d) of silicified 14HB as a function of temperature. Data are presented as mean \pm standard deviation (mean \pm SD).

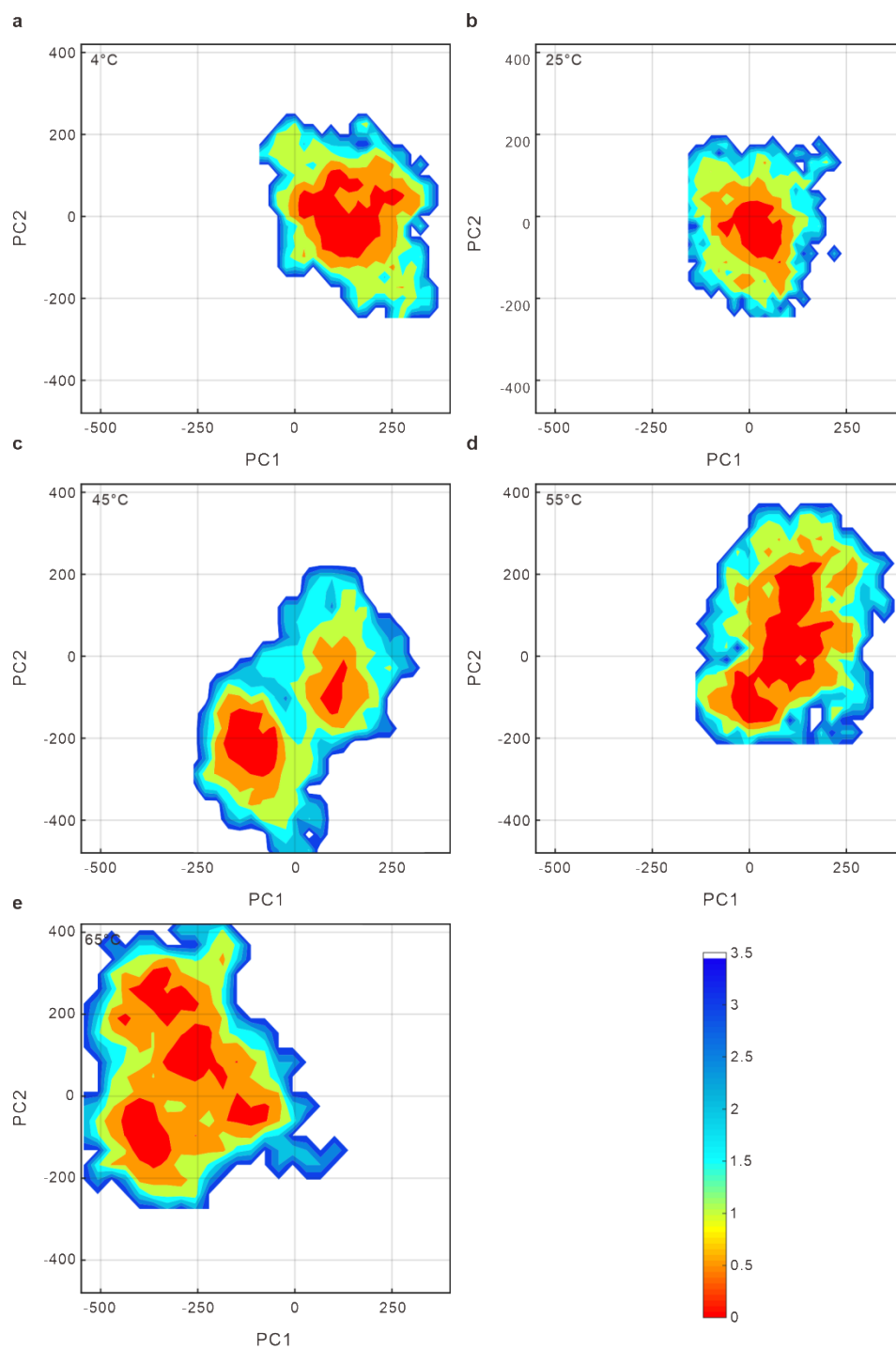


Supplementary Fig. 42. AFM-based quantitative analysis of pristine ring-shaped DNA origami (RDO) and silicified structures at different temperatures. Thickness coefficient of variation (Thickness CV, %) (a), Area retention (b), Diameter retention (c) and Root mean square roughness (R_q) (d) of silicified RDO as a function of temperature. Data are presented as mean \pm standard deviation (mean \pm SD).

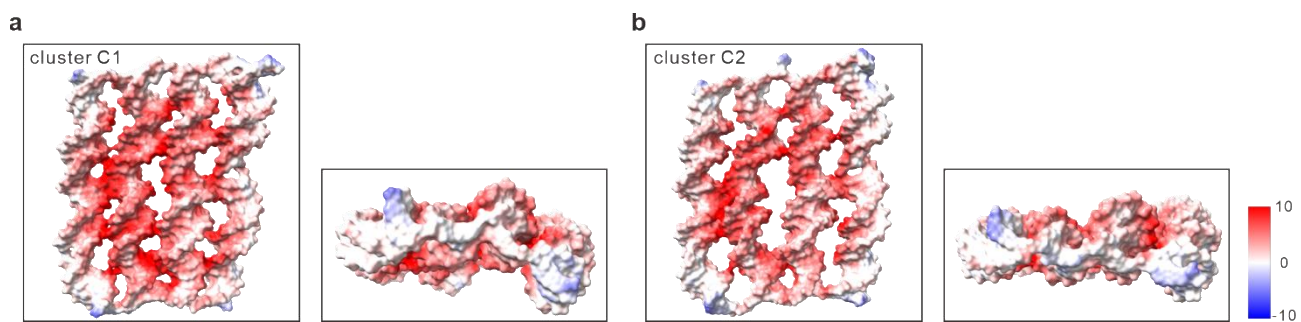
12 Molecular dynamics simulations of temperature-dependent silicification



Supplementary Fig. 43. Temperature-dependent structural dynamics of DNA origami fragment. Root-mean-square deviation (RMSD) (a) and root-mean-square fluctuation (RMSF) (b) of DNA origami fragment at different temperatures.



Supplementary Fig. 44. Temperature-dependent conformational distributions obtained from principal component analysis (PCA). The projections of the trajectories onto the first two principal components (PC1 and PC2) are shown for (a) 4 °C, (b) 25 °C, (c) 45 °C, (d) 55 °C, and (e) 65 °C. The contour color scale represents the probability density of sampled conformations, ranging from low density (blue) to high density (red).



Supplementary Fig. 45. Surface electrostatic potential analysis of the two representative conformational clusters. (a) cluster C1 and (b) cluster C2. For each cluster, the front view and the side view observed from the bottom of the front view are shown, with the electrostatic potential mapped onto the DNA origami surface. The electrostatic potential is color-coded from -10 (blue) to $+10$ (red).

13 Supplementary table

Table S1. Names, modifications, and sequences of DNA oligonucleotides used for the assembly of DNA origami. The header of the DNA sequence table is explained using 10[215] as an example. Here, 10 refers to the DNA double-helix index in the caDNAno design, and [215] indicates the starting position of the staple strand. Staple sequences of square DNA origami (SDO).

Start	End	Sequence	Length
10[215]	8[216]	TTTATTTTCGACTTGCGGGAGGTTTTTAACGT	32
10[119]	8[120]	AACGAGAAAAAATGTTTAGACTGGCTAACGGA	32
9[200]	11[199]	GAACCTCCCATCGTAGGAATCATTTCGACGACA	32
12[183]	10[184]	AGCCAGTAAGTAATTCTGTCCAGAACCGCGCC	32
15[296]	17[295]	AACATAGCAGTAACAGTACCTTTTCGTCAGAT	32
22[215]	20[216]	TTTTGACGCTGACCTGAAAGCGTAGCTGAGAG	32
13[264]	15[263]	GAATAAACATAGTGAATTTATCAAAATCGTCG	32
0[151]	1[135]	GTATAGCCCGGAATAGGTGTATCAAGTAAATG	32
14[23]	12[24]	AAAGGGTGTTTAGCTATATTTTCAAATGGTCA	32
10[55]	8[56]	GGATTGCAGACGATAAAAACCAAAACTAATG	32
17[136]	19[135]	TCCGTGGGTCACGTTGGTGTAGATGTTGGGTA	32
23[136]	23[167]	CAAAGGGCGAAAAACCGTCTATCAAGACAGGA	32
1[72]	3[71]	AGACAGCCAAAATCTCCAAAAAACAACAAC	32
4[23]	2[24]	AAAAGAATGAGGTGAATTTCTTAATTATCAGC	32
11[296]	13[295]	ATGTAGAATAGTATCATATGCGTTCTAGAAAA	32
9[136]	11[135]	CAATACTGTCAAATGCTTTAAACAGCGGATGG	32
9[40]	11[39]	TACCAGACTCAAAAAGATTAAGAGATTTCGAGC	32
17[104]	19[103]	TAAATGTGTGCATCTGCCAGTTTGGGCGAAAAG	32
15[200]	17[199]	TTAATGGTTCAATTACCTGAGCATATACTTC	32
19[296]	21[295]	TTAGACTTAAAAATACCGAACGAACTAAAACA	32
15[232]	17[231]	TGAGTGAAGTTACAAAATCGCGCAACCATATC	32
18[87]	16[88]	ACGACAGTCCTGTAGCCAGCTTCAGCCCCAA	32
11[104]	13[103]	TCCTTTTGGGAAGTTTCATTCCATAATCATAAC	32
5[136]	7[135]	TAGCCGGAGAACTGACCAACTTTGTAAAGAAC	32
6[119]	4[120]	CAGATGAAATCCGCGACCTGCTCCTACAGAGG	32
13[232]	15[231]	ACCGACCGGACTACCTTTTTAACCAATATATG	32
22[279]	20[280]	AATATCCAGCGCGAACTGATAGCCCCACCAGC	32
12[151]	10[152]	GCTCAACATTAATTGCTGAATATAATTCATTG	32
13[104]	15[103]	AGGCAAGGAGCCTTTATTTCAACGCTATTTTT	32
6[247]	4[248]	GAAACGCATATGGTTTACCAGCGGAGCCATT	32
22[55]	20[56]	CGGTCCACGTGCCTAATGAGTGAGGCTGTTTC	32
9[296]	11[295]	AACGAGCGACCAATCAATAATCGGTTACGAGC	32
18[55]	16[56]	CAGCCAGCAACGCCATCAAAAATATATTTAAA	32

20[23]	18[24]	CACAACATGCAAAGCGCCATTCGCTGGTGCCG	32
1[232]	3[231]	TGGCTTTTACCAGAACCACCACCAATTTTCGG	32
10[87]	8[88]	TTACCCTGCAAAGAAGTTTTGCTTCATCAG	32
20[119]	18[120]	AGGTGACGCTGCAAGGCGATTAAGGGCGCAT	32
1[296]	3[295]	AGTGCCCGCGCCTCCCTCAGAGCCGAGCCACC	32
9[264]	11[263]	GCTACAATTTCCAAGAACGGGTATCCTGAACA	32
15[40]	17[39]	ACCATCAAGTTAATATTTTTGTTAATTTTTTAA	32
6[87]	4[88]	CTGGCTGAATTTGTATCATCGCCTTGAGGAAG	32
6[183]	4[184]	TGTTAGCAATATAAAAAGAAACGAAACGTCAC	32
22[247]	20[248]	CAACAGGAACAATATTTTTGAATGGTCAGTAT	32
5[72]	7[71]	CAACGGAGCCTTCATCAAGAGTAATAGTAAAT	32
23[40]	22[56]	AATCCCTATAAATCAAAGAATAGCAGCAAG	32
16[119]	14[120]	TGTACCCCTACAAAGGCTATCAGGATACTTTT	32
23[16]	22[24]	TGATGGTGGTCCGAAAGGCGAAA	24
17[72]	19[71]	CTGGCCTTATCGGCCTCAGGAAGATCGGTGCG	32
23[72]	22[88]	TAGGGTTGAGTGTGTTCCAGTTTATTGCCCT	32
12[55]	10[56]	TTTGACCAGAACCAGACCGGAAGCAGCAAAGC	32
21[104]	23[103]	CAGTCGGGAGACGGGCAACAGCTGGGAACAAG	32
16[23]	14[24]	TTAAATTTAGAAAGGCCGAGACAAAGATTCA	32
6[279]	4[280]	TAGCCGAAACATTCAACCGATTGACATTAAAG	32
23[264]	22[280]	TTCTTTGATTAGTAATAACATCACTTGCTGGT	32
1[136]	3[135]	AATTTTCTTCAGCGAGTGAGAACCGCTTTT	32
5[168]	6[152]	GTGGCAACAACGTAGAAAATACATCAATCATA	32
3[200]	5[199]	AGACTGTACATTAGCAAGGCCGAAAGACACC	32
7[72]	9[71]	TGGGCTTGTAGGAATACCACATTCATAGCGAG	32
23[232]	22[248]	TCCATCACGCAAATTAACCGTTGTAGCCATTG	32
11[168]	13[167]	AAAGGTAAATAAGAGAATATAAAGGAACGCGA	32
14[215]	12[216]	AGGTTGGGGACCTAAATTTAATGGTTAACAAC	32
20[183]	18[184]	TTGCTGAATCAGTTGGCAAATCAATTATCATC	32
4[151]	2[152]	CATCGGAAGTCACCCTCAGCAGCGAACAACCTT	32
5[40]	7[39]	CCCAGCGAATATTCATTACCCAAAAGGCTTGC	32
9[232]	11[231]	TTAAATCACTCATCGAGAACAAGCAGAACGCG	32
4[279]	2[280]	GTGAATTAATAAATCACCGGAACCAGCCACCCT	32
19[168]	21[167]	ATATCTGGCCTCAAATATCAAACCACGACCAG	32
4[183]	2[184]	CAATGAAAAGAATCAAGTTTGCCCTCAGGTCAG	32
12[119]	10[120]	CGGTGTCTATAAGAGGTCATTTTTGTTTCAGAA	32
3[296]	5[295]	ACCGGAACATTGACGGAAATTATTGGGAGGGA	32
4[87]	2[88]	TTCCATTACGCATAACCGATATATAATTTTT	32
4[119]	2[120]	CTTTGAGGTGCAGGGAGTTAAAGGTAGAAAGG	32
19[200]	21[199]	AGGAATTGAAATGAAAAATCTAAACAGAGATA	32
22[87]	20[88]	TCACCGCCGCGTTGCGCTCACTGCGTACCGAG	32
23[200]	22[216]	TAATCAGTGAGGCCACCGAGTAAATACCTACA	32
13[296]	15[295]	AGCCTGTTGATAGCTTAGATTAAGTCCTTGAA	32

8[279]	6[280]	TTACAAAAACAATGAAATAGCAATTAAGCAGA	32
9[104]	11[103]	GTAATAGTTGACCATAAATCAAAATTAATTGC	32
5[264]	7[263]	AAAGGGCGCAAAGTTACCAGAAGGATAATAAG	32
17[264]	19[263]	AATTGCGTTTGCCCGAACGTTATTAGAGCCGT	32
10[151]	8[152]	AATCCCCCGGAATCGTCATAAATTTGGGAAG	32
23[168]	22[184]	ACGGTACGCCAGAATCCTGAGAAGGGATTATT	32
17[40]	19[39]	CCAATAGGTTTCCGGCACCGCTTCCATTTCAGG	32
1[168]	3[167]	TCCTCATTCCTTGATATTCACAAACGTAATCA	32
14[247]	12[248]	GTCTGAGATGTGATAAATAAGGCGCAACAGTA	32
7[264]	9[263]	AGCAAGAATAAACAGCCATATTATTGCACCCA	32
23[104]	22[120]	AGTCCACTATTAAGAACGTGGACTTTCTTTT	32
1[200]	3[199]	TCTGAATTTGACAGGAGGTTGAGGTTAGCGTC	32
6[151]	4[152]	AGGGAACCACGAGGCGCAGACGGTAAAGACAG	32
3[168]	5[167]	GTAGCGACCCATCGATAGCAGCACACATAAAG	32
12[23]	10[24]	ATAACCTGCAAATATCGCGTTTTAGAAGCCCG	32
9[72]	11[71]	AGGCTTTTACTATTATAGTCAGAAAACCTCCA	32
13[200]	15[199]	CATCTTCTTTATATAACTATATGTTTACCTTT	32
9[168]	11[167]	TCCGGTATAGCAAATCAGATATAGTACCGACA	32
18[279]	16[280]	TAAATCCTAGATTTTCAGGTTTAAACATCGGG	32
10[183]	8[184]	CAATAGCATCTAAGAACGCGAGGCCAGAGAGA	32
0[279]	1[263]	TATTTTCGGAACCTATTATTCTGAAACTGGTAA	32
22[23]	20[24]	ATCCTGTTACGAGCCGGAAGCATACAATTCCA	32
10[23]	8[24]	AAAGACTTAGCAACACTATCATAATACGAGGC	32
1[104]	3[103]	AGTTTTGTAAGGAATTGCGAATAATTTCGGTCG	32
19[136]	21[135]	ACGCCAGGCCAGTGCCAAGCTTGCCTGCATTA	32
0[119]	1[103]	AGGAGGTTTAGTACCGCCACCCTCCGATCTAA	32
8[247]	6[248]	ATCCAAATAATTGAGTTAAGCCCAAAACCGAG	32
13[72]	15[71]	TAGTAGTATAGAACCCTCATATATTCTAGCTG	32
3[104]	5[103]	CTGAGGCTACTAAAGACTTTTTTCAGATAAATT	32
0[87]	1[71]	CACCCTCAGAACCGCCACCCTCAGCATTCCAC	32
11[264]	13[263]	AGAAAAATGTATAAAGCCAACGCTTTAAATAA	32
17[232]	19[231]	AAAATTATGTAACATTATCATTTTTATATCTTT	32
14[279]	12[280]	AAGAGTCAACCGGAATCATAATTAATACAAAT	32
20[87]	18[88]	CTCGAATTCGCTATTACGCCAGCTAGGGGACG	32
0[247]	1[231]	GTATTAAGAGGCTGAGACTCCTCAGTCATACA	32
12[87]	10[88]	TGATTTCCGGATTAGAGAGTACCTATCAGGTC	32
16[87]	14[88]	AAACAGGAATGCCGAGAGGGTAGCAAGGATA	32
2[215]	0[216]	GCCAGCATTACCGTTCCAGTAAGCAGAGAAGG	32
7[232]	9[231]	CCCACAAGAAGAAACGATTTTTTTGTTGAAGCC	32
3[40]	5[39]	ATACCGATGCACCAACCTAAAACGCTTTGACC	32
16[183]	14[184]	TGATGAAAAACAATTTTCATTTGAAAAATGCTG	32
8[87]	6[88]	TTGAGATTAGATGGTTTAATTTTCACGCATAGG	32
21[200]	23[199]	GAACCCTTCTCAATCGTCTGAAATTGTTTTTA	32

7[136]	9[135]	TGGCTCATACGTTAATAAAAACGAAATAGCGTC	32
2[119]	0[120]	AACAACACTACGTCTTTCCAGACGTTCCGTA	32
21[72]	23[71]	CATTAATTTGGCCCTGAGAGAGTTGCCCGAGA	32
7[104]	9[103]	CATTGTGAATTACAGGTAGAAAAGACAGAGGGG	32
4[55]	2[56]	CTACGAAGAGTTGCGCCGACAATGAGGCTCCA	32
16[151]	15[167]	ACGGTAATTGGAGCAAACAAGAGAAAAATTAA	32
19[40]	21[39]	CTGCGCAAAATTGTTATCCGCTCAAAGTGTA	32
3[264]	5[263]	TCATAATCTCACCGTCACCGACTTCAAAGACA	32
14[87]	12[88]	AAAATTTTGCATTAACATCCAATAATAACAGT	32
8[215]	6[216]	CAAAAATGTGAGCGCTAATATCAGCAAAAGAA	32
2[151]	0[152]	TCAACAGTGTATGGGATTTTGCTATGATATA	32
15[168]	17[167]	TTACATTTCAAACATCAAGAAAACCAATTCAT	32
19[72]	21[71]	GGCCTCTTCGTAATCATGGTCATACTAACTCA	32
6[23]	4[24]	ACAAAGCTACACTAAAACACTCATAAAGAGGC	32
14[55]	12[56]	CAATGCCTAAAAGGTGGCATCAATAGATTTAG	32
10[247]	8[248]	GTACCGCAAGATTAGTTGCTATTTTTATCCCA	32
18[119]	16[120]	CGTAACCGAGCGAGTAACAACCCGCAATCATA	32
7[40]	9[39]	CCTGACGATAACGCCAAAAGGAATCCCTCGTT	32
0[215]	1[199]	ATTAGGATTAGCGGGTTTTGCTCGCGCAGTC	32
8[183]	6[184]	ATAACATAACTGAACACCCTGAACACGCAGTA	32
5[200]	7[199]	ACGGAATAATTAAGACTCCTTATTAAGTCAG	32
15[72]	17[71]	ATAAATTAAGATTGTATAAGCAAAATTCGCGT	32
18[23]	16[24]	GAAACCAGTTGTTAAATCAGCTCAAATTCGCA	32
12[279]	10[280]	TCTTACCAAATATCCCATCCTAATCTGTCTTT	32
15[136]	17[135]	TGAGAGTCCGTAAAACACTAGCATGTTCCGATTC	32
19[232]	21[231]	AGGAGCACCTGCAACAGTGCCACAGAATACG	32
20[151]	18[152]	AACGACGGGTTTTCCAGTCACGAACCGTAAT	32
22[119]	20[120]	CACCAGTGAAACCTGTGCGTGCCAGATGCCTGC	32
12[247]	10[248]	GGGCTTAATCAACAATAGATAAGTTAAACCAA	32
22[183]	20[184]	TACATTGGGGGACATTCTGGCCAAGCATCACC	32
0[303]	1[295]	TATAAACAGTTAATGCTGAGTAAC	24
1[40]	3[39]	CAGTACAACCTTTAATTGTATCGGTACAGCTTG	32
2[87]	0[88]	TCACGTTGCTCATAGTTAGCGTAAAGAACCGC	32
15[104]	17[103]	GAGAGATCGGTTGATAATCAGAAAATCAACAT	32
17[296]	19[295]	GAATATACTACAAACAATTCGACATAGAAGTA	32
8[23]	6[24]	ATAGTAAGGCTCATTAGTGAATATCAACGTA	32
10[279]	8[280]	CCTTATCATTATCCTGAATCTTATTTGCCAG	32
15[264]	17[263]	CTATTAATTAACGGATTCGCCTGAAATAAAGA	32
14[119]	12[120]	GCGGGAGACAAAGAATTAGCAAAACTAAAGTA	32
14[151]	12[152]	TACCAAAACAGAGCATAAAGCTAAATGCTGTA	32
14[183]	12[184]	ATGCAAATTTTCAAATATATTTTACATTTTCG	32
20[215]	18[216]	CCAGCAGCAGGAAGGTTATCTAAAGCGGAACA	32
22[151]	20[152]	TGCGTATTGCCAACGCGCGGGGAGCGTTGTAA	32

16[247]	14[248]	AATACCAATAACCTTGCTTCTGTAAATCATAG	32
18[215]	16[216]	AAGAAACCGGAAGGGTTAGAACCTGAGGCGAA	32
4[247]	2[248]	TGGGAATTCCTTATTAGCGTTTGCACCCTCA	32
18[151]	16[152]	GGGATAGGAACAAACGGCGGATTGATCGATGA	32
5[232]	7[231]	AAAATTCAATAATAACGGAATACCAGAGATAA	32
21[168]	22[152]	TAATAAAACAGATTCACCAGTCACAGGCGGTT	32
17[168]	19[167]	CAATATAAGATTATCAGATGATGGCTCAATCA	32
17[200]	19[199]	TGAATAATACCAGAAGGAGCGGAACAGTTGAA	32
21[232]	23[231]	TGGCACAGAAAACGCTCATGGAAAAGAGTCTG	32
8[119]	6[120]	ACAACATTATTACCTTATGCGATTAAAGAGGA	32
20[279]	18[280]	AGAAGATAAATACATTTGAGGATTACTCGTAT	32
11[136]	13[135]	CTTAGAGCTGTTTTAAATATGCAATTAAGCAA	32
21[264]	23[263]	TCTTAAATGAACAATATTACCGCCAGCAATAC	32
19[264]	21[263]	CAATAGATAAACAGAGGTGAGGCGGCTATTAG	32
6[55]	4[56]	AGAACCGTTATACCAAGCGCAATAATGCCA	32
7[296]	9[295]	TACCGAAGTCTTCCAGAGCCTAACCAACGCT	32
18[247]	16[248]	AAGTTTGATTGCACGTAAAACAGATTGCTTTG	32
8[55]	6[56]	CAGATACAGAAACACCAGAACGAGTCTTGACA	32
21[296]	23[303]	TCGCCATTACTCAAATATCGGCCTGCTGAGTAGAAGA	40
5[104]	7[103]	GTGTGCAACGGTGTACAGACCAGGACTTTAAT	32
1[264]	3[263]	TAAGTTTTCCACCCTCAGAGCCACCCATCTTT	32
2[55]	0[56]	AAAGGAGCACTACAACGCCTGTAGAGCCACCA	32
11[72]	13[71]	ACAGGTCAAATTCTGCGAACGAGTTCTACTAA	32
20[55]	18[56]	CTGTGTGACTGTTGGGAAGGGCGATCGCACTC	32
20[247]	18[248]	TAACACCGTAACAATAATAGATTAATTTAA	32
12[215]	10[216]	GCCAACATCATGTTTCAGCTAATGCAAGCCGTT	32
16[215]	14[216]	TTATTCATAAACAGTACATAAATCTCCGGCTT	32
21[136]	23[135]	ATGAATCGGGGCGCCAGGGTGGTTTCCAACGT	32
11[200]	13[199]	ATAAACAAGTAATTTAGGCAGAGGGTTAATTT	32
13[168]	14[152]	GAAAACCTCCAATCGCAAGACAAAATCGGTTG	32
11[40]	13[39]	TTCAAAGCTTAGATACATTTTCGCATTTGGGGC	32
6[215]	4[216]	CTGGCATGAGTTTATTTTGTACACCAGTAGC	32
19[104]	21[103]	GGGGATGTTCTAGAGGATCCCCGGCCGCTTTC	32
16[279]	14[280]	AGAAACAATAATTTCCCTTAGAAACGCTGAG	32
2[279]	0[280]	CAGAACCGAACGGGGTCAGTGCCTCCCCTGCC	32
3[232]	5[231]	TCATAGCCAGAGCCAGCAAAAATCAATCAATAG	32
4[215]	2[216]	ACCATTACGCGCGTTTTTCATCGGCGAGCCGCC	32
2[23]	0[16]	TGCTTTCTACCGTAACACTGAGTCCAATAGGAACCCATG	40
3[136]	5[135]	GCGGGATCCGAGGGTAGCAACGGCATGTTACT	32
13[136]	15[135]	TAAAGCCTACATTATGACCCTGTATCATTGCC	32
0[55]	1[39]	CCCTCATTTTCAGGGATAGCAAGCTTCGTAC	32
7[168]	9[167]	GAGAATTA AAAACAGGGAAGCGCAAAGGCTTA	32
2[183]	0[184]	ACGATTGGAAAGCCAGAATGGAAAAGTACCAG	32

3[72]	5[71]	CATCGCCCAAACGGGTAAAATACGACAAAGTA	32
8[151]	7[167]	AAAAATCTTATACCAGTCAGGACGTTAGACGG	32
16[55]	14[56]	TTGTAAACTATGATATCAACCGTTTTAAATG	32
2[247]	0[248]	GAGCCGCCGATGATACAGGAGTGTACATGAAA	32
18[183]	16[184]	ATATTCCTTCCTGATTGTTTGGATAAAGAAGA	32
7[200]	9[199]	AGGGTAATAAAAATAGCAGCCTTTAGTTTTAGC	32
11[232]	13[231]	CCTGTTTATTGAGAATCGCCATATTTTTGAAAT	32
5[296]	7[295]	AGGTAAATCCCTTTTTAAGAAAAGAGCTATCT	32
13[40]	15[39]	GCGAGCTGGAGTAATGTGTAGGTAGTCAAATC	32
0[183]	1[167]	GCGGATAAGTGCCGTCGAGAGGGTCAAATAAA	32
21[40]	23[39]	AGCCTGGGGCTGGTTTGCCCCAGCATCGGCAA	32

Table S2. Staple sequences of Triangular DNA origami (TDO).

Start	End	Sequence	Length
11[200]	12[184]	TATGATATCGGAGACAGTCAAATCTTTTGCTC	32
3[152]	1[159]	TTCATTTGAATACCAAGTTACAAAAGGTTAACGTCAGAT	40
5[296]	7[295]	GTTTTCATTTGAGGGAGGGAAGGTAAGAAACG	32
31[272]	29[279]	GGCAAGTGTAGCGGTCTATAATCAGTGAGGCCCTCATGGA	40
15[168]	17[167]	GTTGAAAAAATTGTATCGGTTTATAATACGTA	32
3[101]	5[103]	GAAGATGATGAGCGATAGCTTAGATTAACCTTTTT	35
15[104]	17[103]	CAGTTTCAGCGCCGACAATGACAAAACGGCTA	32
18[183]	17[199]	AGAGGCAAACGAAGGCACCAACCTTGAATCCC	32
27[280]	25[282]	GAAAAATCAGTTGGCAAATCAACATTTTAAAAGTT	35
29[136]	31[143]	GAGCCGGATGCCAGCTGCATTAATGGAACAAGAGTCCACT	40
7[56]	6[48]	ACAGTAGGATCATATGCGTTATAC	24
27[120]	25[119]	CAGCTTCTGACCGTAATGGGATATTTTGTTA	32
30[367]	31[378]	ATCAGAGCGGGAGCTAGCTTTGACGAGCACGTATAACGTGCTT	43
15[200]	16[184]	AGTACGGTAACATGTTTTAAATATTCCAAAAG	32
29[296]	31[303]	CGCTCAATTCCTGAGAAGTGTTTTACGCTGCGCGTAACCA	40
15[248]	13[247]	CTGCGAACATTAACATCCAATAAACTTTTGC	32
31[176]	30[184]	GAAAAACCGTCTATCATTAATTGC	24
19[144]	17[151]	AGGCTTGCCCTGACGAACTCATCTTTGACCCCTCCATTA	40
3[248]	1[255]	TTGAGGCAAATGGAAAGCGCAGTCAGTGCCCGTATAAACA	40
7[248]	5[247]	CAAACGTAATTATCACCGTCACCGGCACCGTA	32
5[200]	6[184]	AGCAAGGCATCACCAGTAGCACCAAATATAT	32
29[216]	27[215]	CCTTGCTGAGCCCTAAAACATCGCGATAAAAC	32
27[136]	29[135]	CTTCTGGTAAAGGGGGATGTGCTGCAACATAC	32
11[128]	13[135]	ATTCTGAAACATGAAAGTATAGCCCAGGAATAGCAGAACCG	40
15[120]	13[119]	AGAATAGACCCTCATAGTTAGCGTTCAGAACC	32
5[88]	4[80]	GAGAGACTAGACGCTGAGAAGAGT	24
8[367]	9[378]	AGAGGGTAATTGAGCGTTAGACGGGAGAATTAAGTGAACACCC	43
27[69]	29[71]	CAGTTTGAGGGGTAAAACGACGGCCAGCGAATTTCG	35

28[335]	29[327]	AAAAGGGACATTCTGGTTTACATT	24
7[296]	9[303]	CAAAGACAAGAGCAAGAAACAATGTTTAACGTCAAAAATG	40
31[304]	29[311]	CCACACCCGCCGCGCTGAACGGTACGCCAGAACGTCTGAA	40
17[280]	15[279]	GAAGCAAAAACCTTTAATTGCTCCTACCATTAG	32
29[152]	27[151]	GTGTAAAGATTACGCCAGCTGGCGGCCGAAA	32
7[72]	9[79]	GAGAATCGAATCGGCTGTCTTTCCAAGGCTTATCCGGTAT	40
17[200]	19[207]	CCTCAAATCGTCATAAATATTATAGATGGTTTAATTCA	40
19[176]	18[184]	TAGTAAATTGGGCTTGAAAACGAA	24
7[280]	5[279]	ACATATAAAAATATTGACGGAAATGCCTTTAG	32
9[5]	8[16]	GTTTTATTTTCATCGTAGGAATCATTACCGCACTCATCGAGA	43
16[47]	6[336]	GGGAGTTAAAGATGGTTTACCA	22
17[248]	15[247]	AAATCAGGTTTTGCGGATGGCTTATCCCAATT	32
19[208]	17[215]	ACTTAAATCATTGTGATCCAATACTGCGGAATGCTTTAAA	40
9[240]	7[247]	TAAACAGCCATATTATTTAAGAAAAGTAAGCATATGTTAG	40
23[200]	24[184]	TCCTGATTGATGATGGCAATTCATTGTACCCC	32
31[208]	29[215]	GAAAGCCGGCGAACGTACTTCTTTGATTAGTAACTATCGG	40
29[280]	27[279]	AATACCTACGTAAGAATACGTGGCCAGCAAAT	32
11[224]	13[231]	ATAAATTAATGCCGGATGTAGGTAAAGATTCAATTATGAC	40
15[296]	17[295]	GTCAATAAGTCAGGATTAGAGAGTGCGGATTG	32
27[248]	25[247]	CAACAGTGGAAGGTTATCTAAAATTCGTATTA	32
9[304]	7[311]	AAAATAGCAGCCTTTAGTTAAGCCCAATAATACCACGGAA	40
17[264]	19[271]	CTGACTATGAAGTTTTGCCAGAGGTATACCAGTCAGGACG	40
29[232]	31[239]	CAGAACAATAACCGTTGTAGCAATGGCGAGAAAGGAAGGG	40
15[88]	14[80]	GCTAAACAGTCGTCTTCCAGACG	24
17[152]	15[151]	ACGGGTAACAGCTTGCTTTCGAGGAATTGCGA	32
7[264]	9[271]	ATACATAAATTACCGAAGCCCTTTTTATCCCAATCCAAAT	40
16[335]	17[327]	AAGCGAACCAGACCGGCGAAAGAC	24
11[256]	13[263]	GAGAGATCTACAAAGGTCATATATTTAAATGCCTTTATT	40
14[79]	4[304]	TTAGTAAATGAGTCATAGCCCC	22
23[160]	25[167]	ACGGTAATCGTAAAACATCAGAAAAGCCCAATAATTCGC	40
9[48]	7[55]	AGCAAATCAGATATAGTTATCATTCCAAGAACAACGCTCA	40
9[144]	7[151]	AGATTAGTTGCTATTTTGTATCAACAATAGATAAAGTA	40
11[160]	13[167]	ACTCCTCAAGAGAAGGGCGGATAAGTGCCGTCTTTTCAGG	40
29[56]	28[48]	ACCGAGCTTGCCAAGCTTGCATGC	24
15[280]	13[282]	ATACATTTAAGGTGGCATCAATTCAGGATAAAAAT	35
17[232]	19[239]	AATGACCATTAGACTGGATAGCGATTACCTTATGCGATT	40
13[152]	11[159]	CACCCTCAGAGAGGGTTGATATAAGTATTAAGAGGCTGAG	40
31[336]	29[346]	GGCGCGTACTATGGTTAACAGGAGGCCGATTACACCAGTCACA	43
26[79]	14[304]	CGTGCATCTGCATATTTTCATT	22
13[120]	11[127]	GCCACCCTGTGTATCACCGTACTCTATTTTCGGAACCTATT	40
29[168]	31[175]	GCCTAATGCACTGCCCGCTTCCATCCAACGTCAAAGGGC	40
18[367]	19[378]	CAAAGGAATTACGAGTAGGAATACCACATTCAACTAATGCAG	43
27[88]	26[80]	CAGTATCGATGGGCGCATCGTAAC	24

13[264]	15[263]	TCAACGCATACTAATAGTAGTAGCGAGTAGAT	32
15[216]	13[215]	GTTTCATTAAGAATTAGCAAAAATTCGGTTGTA	32
19[304]	17[311]	CTAACGGAACAACATTTTTACCAGACGACGATAGATTAAG	40
31[5]	30[16]	AAGCGGTCCACGCTGGTTTTGCCCCAGCACCGCCTGGCCCTGAG	43
27[152]	25[151]	CCAGGCAACGTTCGGATTCTCCGTGGGAACGCC	32
8[183]	7[199]	TGTTTCAGCTCCAGACGACGACAATACGGAATA	32
31[240]	29[247]	AAGAAAGCGAAAGGAGTGTCCATCACGCAAATTATTACCG	40
19[336]	17[346]	TTCATCAGTTGAGATTGCATAGTAAGAGCAACTCGCGTTTTAA	43
27[104]	29[103]	AAGATCGCGGTAACGCCAGGGTTTGTGTGAAA	32
3[216]	1[223]	CCACCAGACAGTAAGCGTCATACATAAGTTTTAACGGGGT	40
17[296]	19[303]	CATCAAAAAAAAAACCAAAATAGCGACGTTAATAAAACGAA	40
3[264]	5[263]	GATTGGCCAATCACCGGAACCAGACGACAGAA	32
17[168]	19[175]	ATGCCACTAAGAATACACTAAAACGAAACACCAGAACGAG	40
23[128]	25[135]	TGAGAGTCTGGAGCAATAAGCAAATATTTAAACATTTTTT	40
24[183]	23[199]	GGTTGATATAGCATGTCAATCATACAATATAA	32
13[101]	15[103]	TACCGCCACCCAACGATCTAAAGTTTTACTTTCAA	35
17[136]	19[143]	AGGAAGTTCAGCGATTATACCAAGGCTCATTTCAGTGAATA	40
29[248]	27[247]	CCAGCCATAATGGCTATTAGTCTTACCGCCTG	32
3[120]	1[127]	TCAAGAAATTATTCATTTCAATTA AAAACAGAAATAAAGA	40
6[47]	28[336]	AAATTCCTACCCGACCAGTAAT	22
9[80]	7[87]	TCTAAGAACGCGAGGCGTAGAAACCAATCAATCCATATTT	40
5[136]	7[135]	ATGTAAATAAATACCGACCGTGTGCCAGTAAT	32
9[112]	7[119]	CGACTTGCGGGAGGTTAAAAATAATATCCCATCAGAGGCA	40
9[272]	7[279]	AAGAAACGATTTTTTGAATAGCAATAGCTATAGGTGGCA	40
29[72]	31[79]	TAATCATGGTGGTTTTTCTTTTCAATCGGCAAAATCCCTT	40
15[264]	17[263]	TTAGTTTGTGTTGATAAGAGGTCATTCTTTACC	32
30[183]	29[199]	GTTGCGCTAGTGAGCTAACTCACAGAGTAGAA	32
3[136]	5[135]	AATTACATATTAATTTCCCTTAGATAACTAT	32
5[120]	3[119]	TGGGTTATAATCCTTGAAAACATAAACAAACA	32
4[183]	3[199]	TGTGAGTGGGAAACAGTACATAAACCCCTCAGA	32
29[200]	31[207]	GAACTCAAATAACATCACTTGCCTTTTAGAGCTTGACGGG	40
29[37]	31[47]	CTCTAGAGGATCAGCTGATTGCCCTTCAGGCGAAAATCCTGTT	43
31[48]	29[55]	TGATGGTGGTTCGGAACCAGTGAGACGGGCAACCCCGGGT	40
17[72]	19[79]	AGACAGCAGTCGAAATCCGCGACCCCTTCATCAAGAGTAA	40
4[79]	26[304]	CAATAGTGAATTATCAAAACCCT	22
19[240]	17[247]	TTAAGAACTGGCTCATGGGTAATAGTAAAATGTAAATCAA	40
23[256]	25[263]	AAAATTATTTGCACGTATCATTTTGCGGAACAGCCCGAAC	40
9[208]	7[215]	TCTTTCCAGAGCCTAATACCAGAAGGAAACCGAACTGGCA	40
27[168]	29[167]	TCGCCATTTGCGGGCCTCTTCGCTCCTGGGGT	32
27[232]	29[231]	GTATTAATAATGCGCGAACTGATGTAATATC	32
27[296]	29[295]	CACCTTGCCCTTCTGACCTGAAAGCATTTTGA	32
1[160]	3[167]	GAATATACAGTAACAGTCGCCTGATTGCTTTGAATTACCT	40
3[200]	4[184]	GCCGCCACACCCTCAGAGCCACCATCAATATA	32

7[88]	5[87]	AACAACGCGAATCATAATTACTAGATAGGTCT	32
19[272]	17[279]	TTGGGAAGAAAAATCTAGAGGCTTTTGCAAAATATAGTCA	40
5[168]	7[167]	CAAAGAACATTTTCATCTTCTGACCAGGTAAAG	32
7[120]	5[119]	TTTTTCGAGATAAATAAGGCGTTAAGCTTAGGT	32
29[264]	31[271]	GAAAAACGACCGAGTAAAAGAGTCCGGGCGCTAGGGCGCT	40
5[232]	7[231]	CGATAGCAACTTGAGCCATTTGGGACTCCTTA	32
19[112]	17[119]	TCAACGTAACAAAGCTCGCGAAACAAAGTACATTGAGGAC	40
17[88]	15[87]	AGGGTAGCCAACCATCGCCACGCGGGATTTT	32
17[328]	19[335]	TTCAAATAACTATCATAACCCTCGATTACAGGTAGAAAGA	40
29[88]	27[87]	TGTTTCCTTCCCAGTCACGACGTTGACGACGA	32
1[224]	3[231]	CAGTGCCTTGAGTAACTCTGAATTTACCGTTCGCCGCCGC	40
14[183]	13[199]	AACACTGAGCCCAATAGGAACCCAGAGCATAA	32
27[216]	25[215]	AGAGGTGAACAACATAATAGATTAGGAAGTATT	32
3[232]	5[231]	CAGCATTGCCTCCCTCAGAGCCGCGAAACCAT	32
19[80]	17[87]	TCTTGACAAGAACCGGTGCGCTGATAAATTGTTTCGGAACG	40
31[80]	29[87]	ATAAATCAAAGAATACGTATTGGGCGCCAGGGTCATAGC	40
3[168]	5[167]	TTTTTAATAATAACCTTGCTTCTGTGCAAGA	32
15[152]	13[151]	ATAATAATAAACTACAACGCCTGTAGAGCCAC	32
16[183]	15[199]	GAGCCTTTTCTCCAAAAAAGGCGCAACTAA	32
30[15]	18[368]	AGAGTTGCAGCATAACATAACGC	22
13[168]	15[167]	GATAGCAAGTTTCGTACCAGTACTTTTTTCAC	32
17[37]	19[47]	GCCGCTTTTGCGCCGGAACGAGGCGCACGGTGTACAGACCAGG	43
24[111]	12[272]	TTTGTTAAAAATTTTAGAACCC	22
5[152]	3[151]	AAATCCAATAAATCGTCGCTATTATTAACAAT	32
25[120]	23[127]	AATCAGCTTTGTAAACGTTAATATCTATCAGGTCATTGCC	40
25[136]	27[135]	AACCAATAGGAACAAACGGCGGATCGGCACCG	32
15[69]	17[71]	ATTTTCTGTATATAACCGATATATTCGGCAGCGAA	35
7[104]	9[111]	AATTTAGGCCTAATTTACGAGCATGTTTTAGCGAACCTCC	40
8[15]	30[368]	ACAAGCAAGCCTCCTCGTTAGA	22
6[183]	5[199]	TTTAGTTAGCGAGAAAACTTTTTCTTACCATT	32
13[248]	11[255]	GGGAGAAGCAATGCCTGAGTAATGGAGGGTAGCTATTTTT	40
7[152]	5[151]	CCGACAAATAAATTTAATGGTTTGGCTGATGC	32
29[312]	27[314]	ATGGATTACCAACAGAGATAGAACTGAACCTCAA	35
6[335]	7[327]	GCGCCAAAGACAAAAGTTTTGTCA	24
7[216]	5[215]	TGATTAAGAATTAGAGCCAGCAAACGGAAACG	32
15[136]	17[135]	ACTAAAGGTGAATTTCTTAAACAGTTTTTCATG	32
13[200]	14[184]	AGCTAAATAAGCAATAAAGCCTCATGTACCGT	32
15[232]	17[231]	CAGTTGATGAGCTTAATTGCTGAAAAACGAG	32
19[5]	18[16]	GACCAACTTTGAAAGAGGACAGATGAAGACGGTCAATCATAAG	43
25[232]	27[231]	TCGACAACATCTTTAGGAGCACTAGGCGGTCA	32
29[104]	31[111]	TTGTTATCGGGGAGAGGCGGTTTGGCCCGAGATAGGGTTG	40
13[136]	15[135]	CCACCCTCAGCATTCCACAGACAGAAGGAACA	32
25[168]	27[167]	GTCTGGCCTGAGCGAGTAACAACCAGCGCCAT	32

1[200]	2[184]	ACTGGTAATGGCTTTTGATGATACAGAAACAA	32
9[336]	7[346]	AAAACAGGGAAGCGCACTAATATCAGAGAGATAGAAAATTCAT	43
7[328]	9[335]	CAATCAATAACCCACAAGAATTGACAGAGAGAATAACATA	40
17[120]	15[119]	TAAAGACTCTTGATACCGATAGTTGCGGAGTG	32
27[264]	29[263]	AGAGCCAGACAGACAATATTTTTGTGCAACAG	32
14[303]	15[295]	TGGGGCGCGAGCTGAACGCAAATG	24
25[248]	23[255]	AATCCTTTAAGAAACCACCAGAAGTAGAACCTACCATATC	40
5[248]	3[247]	ATCAGTAGGCCACCACCGGAACCGACAGGAGG	32
7[200]	9[207]	CCAAAAGAGGAAACGCAATAATACCAACGCTAACGAGCG	40
12[111]	2[272]	AGGAGGTTTAGAAACAAATAAA	22
5[104]	7[103]	AACCTCCGATAAGAATAAACACCGCAACATGT	32
13[216]	11[223]	CCAAAAACAAAGGGTGAGAAAGGCTCAACCGTTCTAGCTG	40
26[303]	27[295]	CAATCAATATCTGGTCTAAAGCAT	24
31[112]	29[119]	AGTGTGTCCAGTTTGAATCGGCCAACGCGCCGCTCACA	40
25[101]	27[103]	TCGCATTAATGGTCACGTTGGTGTAGGCCTCAGG	35
5[280]	3[282]	CGTCAGACATCTTTCATAATCAATTGATATTCAC	35
17[104]	19[111]	CAGAGGCTACGGAGATTTGTATCAATATTCATTACCCAAA	40
17[216]	15[215]	CAGTTCAGTATAATGCTGTAGCTCGTCTGGAA	32
25[264]	27[263]	GTTATTAAGTTGAAAGGAATTGAGCCACGCTG	32
28[47]	16[336]	CTGCAGGTCGATTCGAGCTTCA	22
7[37]	9[47]	AGTATAAAGCCGGGTATTAACCAAGTACCGCGCCAATAGCA	43
7[232]	9[239]	TTACGCAGGATAGCCGAACAAAGTTTTGCCAGTTACAAAA	40
23[224]	25[231]	TGAATAATGGAAGGGTGAGCGGAATTATCATCCAAACAAT	40
29[328]	31[335]	GGCAGATTAAGGGATTTTAGACAGTAATGCGCCGCTACAG	40
2[183]	1[199]	TAACGATTACCTTTTACATCGGGAGGAGTGT	32
19[48]	17[55]	CGCATAGGCTGGCTGATGCTCCATGTTACTTAGGGATCGT	40
7[312]	5[314]	TAAGTTTAGGCGACATCAACCGACGGCATTTCG	35
25[152]	23[159]	ATCAAAAAAACAGGAAGATTGTAACAAGAGAATCGATGA	40
1[256]	3[263]	GTTAATGCCCCCTGCCTCCTCATTAAGCCAGGGTCAGAC	40
17[56]	16[48]	CACCCTCAGTCGCTGAGGCTTGCA	24
25[216]	23[223]	AGACTTTAATATTCCTGATTATCAGTTTGGATTATACTTC	40
27[200]	28[184]	CAGCAGAACATTAAAAATACCGAATGGGAAGG	32
29[120]	27[119]	ATTCCACACAAGGCGATTAAGTTGACTCCAGC	32
4[303]	5[295]	CTTATTAGCGTTTGCCTGTAGCGC	24
9[176]	8[184]	TTATCCTGAATCTTAAAACAACA	24
5[69]	7[71]	TTATCAAAATCAAAAAGCCTGTTTAGTGCTTAATT	35
5[216]	3[215]	TCACCAATCACCTCAGAACCGCCAGAACCA	32
13[232]	15[231]	CCTGTAATTCATACAGGCAAGGCACCATATAA	32
26[183]	25[199]	ATTAATGTTCTGTAGCCAGCTTTACATTTG	32
5[264]	7[263]	TCAAGTTTTATTCATTAAGGTGAGAAAATAC	32
18[15]	8[368]	GGAACCGAACTTGAACAAAGTC	22
1[128]	3[135]	AATTGCGTAGATTTTCATCGCGCAGAGGCGAAACAAAATT	40
17[312]	15[314]	AGGAAGCCAAGCAAACCTCCAACAGCCTGTTTAGCT	35

31[144]	29[151]	ATTAAAGAACGTGGACGTCGGGAAACCTGTCGAGCATAAA	40
12[183]	11[199]	AGTACCAGATTAGGATTAGCGGGGACCATCAA	32
25[200]	26[184]	AGGATTTAAGCCGTC AATAGATAATCATCAAC	32
2[111]	24[272]	CCTGAGCAAAATGAGTAACATT	22
7[136]	9[143]	AAGAGAATATAAGTCCTGAACAAGTTGAAGCCTTAAATCA	40
7[168]	9[175]	TAATTCTGTAATGCAGAACGCGCCTGCACCCAGCTACAAT	40
28[183]	27[199]	GCGATCGGCAGGCTGCGCAACTGTCGAACCAC	32

Table S3. Staple sequences of 14-helix bundle DNA origami (14HB).

Start	End	Sequence	Length
2[464]	13[475]	GTAAAAATCACCGGAACACAGGAGCCGCGCT	31
7[294]	2[297]	AATCGTCCAGTAATATGCAGAAGAAACGAGACGGGGAAA	39
8[153]	0[147]	TGTACCACGGTAATTGTGAGCTGCTGCAGCCTAATCAAAAAGCGT CGAG	49
3[263]	0[252]	AGAACCGAGCTCGAATTCACGATGTTTCGGAA	31
13[245]	2[252]	CGTCTATCGTAATCCGAAGTACCAATTAGAAAAG	35
11[224]	8[217]	TTGCATGATTTTTAGTTTTGAATCGTCATAAATAGTTTAGCAATC ATA	49
0[62]	11[55]	AGAACCGCAACGCCGAAAGACAGCATCGCGAAGGCACGCGCGCA GGCAA	49
4[433]	7[440]	ATCAAGAAAACCAAATGAAAAGCAATTCATCAATAAACAATATGG GTTA	49
7[252]	8[238]	AAGGTGGTTAGACTGGATAGCGTCCAATGGGCGCGTAGTAGC	42
11[56]	8[49]	AGCGCCATCGTAACATTACAGTTTTAATTCGAGCTGCTTAGACAAT GCC	49
11[329]	8[322]	AATGGATAGGTTATTCCTGAAGCCAACATGTAATTAGAATCCAAA ACAA	49
13[392]	4[392]	AGGGAAGCACCGAGTAAGAGCTTTTATC	28
4[265]	11[265]	TAGCAGCGTCCAGAAGAAAATTCGCATTATCCCCGGGTACCG	42
7[336]	2[339]	CATAGCGTAACAACCAAGAAAGTTACAATAATTGAGCGA	39
2[317]	13[328]	GAAGGAAACGTCACCAATAATAAGATCGGAA	31
11[455]	8[448]	GAATGGCACAGTGCAGCAAGCATAAACACCGGAATATATGTATTT ACAT	49
2[251]	11[244]	GCTCCAAAAGGAGCAGGGAACATGGTCAGTCGACT	35
4[391]	7[398]	CTGAATCAATAATCAACCCTCAAGGAGCGGAATTAATAATCGTCA TAGG	49
8[237]	0[231]	ATTAACAAAATATTTTCAGCTCCCTGCAGTAGCTGTAAAGGGCACA TGAA	49
7[483]	2[486]	AAAGAACCGTGTGAAATCATTAGAACGCGAAACCGCTTA	39
11[287]	8[280]	ACGCTCATTAGAGCTCAGCTAAAGAGAATATAAAGACCTTGCTTT TTTA	49
13[350]	4[350]	TAGAGCTTAGCAATTATCAGAAGCCTAA	28
2[107]	13[118]	CAGTAAAGTTTTGTCGTGGTGTATATGGTGG	31

2[380]	13[391]	GAAGCCTTTAGCGTCAGTCTCTGAGAAAGGA	31
7[42]	2[45]	GCGGATGTCAAAGCAACGGAATGTGAATGCCACTAGAAC	39
13[476]	4[476]	TAATGCGAGCTAAACCAGAAGGAGGCGT	28
0[272]	3[262]	TGCCCCCAATTAGACCGTCACCGACTTGACAG	32
7[168]	2[171]	GTAGATTGAGAATGCCCTCGTCGGATATTAATTGTAGT	39
8[447]	0[441]	CGGGAGATAATCCTAGAGCCACAGACAAAGGAACGGTCACGCGG CCTTG	49
8[27]	0[21]	TTCAAAAATCAATAGACAGTATTCCGGCGGGCGCCCAACAGCCAG GGAT	49
13[308]	4[308]	CCGTAAATAGAAGAACTGAACTCCCAAT	28
0[398]	11[391]	AGCGCAGACTGTAGATTTTGTACAATCCCAATAATAAAGAATT CTGG	49
8[300]	0[294]	TCATTTGTGACAATAATAGATGGAAATCTATCGGTTGGGGTGAG TAAC	49
4[223]	7[230]	CAGGCGCCAAAAGAAACCAATAAGATTGTATAAGCTCCAATATAT ATTT	49
7[273]	2[276]	GTGAATATACCGACAATAAACGTCAAAAATAAAAAATTA	39
11[119]	8[112]	TATTACGTCCGTGGATAACGCCAGAAGCAAAGCGGTACGGTGCGG GAGA	49
2[485]	13[496]	TTAACCACCGGAACCGCCAGAGCAGGGCGC	31
8[174]	0[168]	AGAGCATGTCAATCCCAGCTTGGTAACGATAAAGTGGGTTGACAG TACC	49
13[266]	4[266]	ACGTGAACAATATTGAATAACATGAAAA	28
11[245]	4[245]	CTAGAGGAAATTTTAGTAAATGTTTCTCTCTTTGAAAGAGG	42
0[83]	11[76]	ACCCTCAGACAGCCGGGATCGTCACCCTAAAGAGGGCTGCATTTT AGGC	49
4[454]	7[461]	CGGGAGGGAGAACACACGCTGGATTGTTTGGATTAAGTACCTAAT GCTG	49
11[77]	8[70]	TGCGCAAACGTTGGCAGTTGACGAAAGACTTCAAATATAATGAAC CCTC	49
11[350]	8[343]	GATTCACACAGTTGTCCCATCAGAATCGCCATATTATAGCTTGATG ATG	49
13[413]	4[413]	GGGCGCTTGTTTTTTAGCAATCTATTTT	28
4[286]	7[293]	GTTTAAACAACATGTCGTCAATACTTTACAAACAATAATTACCTTCT GTA	49
7[357]	2[360]	GACGCTGTTAATTGCTAATTTTTTCCAGGAGATAAACCA	39
11[476]	8[469]	GCGCGAATCAGTATTCGTAGGTAAATAAGGCGTTATCCAATCGAA TATA	49
0[41]	11[34]	ACCACCCTTTCGTCGGTAGCAACGGCTAGTAAAATGCGTATTACC GCTT	49
2[275]	13[286]	TCAGCCAGCAAAATCACGTATAAACCAAATC	31
13[56]	4[56]	AGAGTTGTCGGCCAACCAACCTCAACTT	28

4[412]	7[419]	GCACCCAATCATTCCCTTGCTGATTCCCTGATTATCATTGCTTTTTTTT AA	49
8[258]	8[259]	AATTCTATAATATTTTGTGATTTAGAACAGTACATAAAATTC	42
11[308]	8[301]	TTTTGACGGAGCACTGTTTATAGGCATTTTCGAGCGCTATTAAACA ATT	49
13[371]	4[371]	GGCGAACCATCACGGAATTGACGCTAAC	28
2[128]	13[139]	ATAGACGTTAGTAAATGATATAAGAAATCCC	31
2[401]	13[412]	TTTCGCGTTTTTCATCGGAAGCCAGAAGGAGC	31
7[315]	2[318]	TTCCCTTAGGCAGCAACAATTTATTTAACCTGAGAGG	39
7[63]	2[66]	TGCTGAATATCGCGGTAGAAAATTTAAATTTAAACGCGAGC	39
11[161]	8[154]	TAAGTTGTCATCAAATCATAAACCATAAATCAAAAAATTCTGAAT CGGT	49
13[497]	4[497]	GTACTATCCTCGTTGCAATAATATCCGG	28
13[434]	4[434]	TGTAGCGGTACGCCAGCCCTTGCCTTAA	28
0[293]	11[286]	AGTGCCCCAGTAGCTTCATTAAGGTGACAGGGAAGGTAATAAGG AAAA	49
13[224]	4[224]	CAACGTCTCCTGTGACGGTCTACAGAC	28
0[104]	11[97]	CTCAGGAAACGATCGGAGTTAAAGGCCGAAAACACGTCGGGAGA AGGGC	49
7[84]	2[87]	TCAACATGGAAGCCGATTTAGAGTAAATATACACTCTTT	39
7[189]	2[192]	GATACATGCTTTAATAAAAACAAGAGTAACCTGCTTCTT	39
11[266]	7[272]	CCAGCCAACATTTGCGACGACAAAAGGTAAAGTAACACAATATAT GTGA	49
13[329]	4[329]	CCCTAAATAATAACCAGAGGGAATAAAC	28
0[419]	11[412]	CTCATTACATTTTCAAGACACCACGGAAAATGAAAATAATCAACC CTTC	49
8[48]	0[42]	TGAGTAATCTAGCTCTGCCAGCGGAAACGGGAGAGCGCCTGGCAG AGCC	49
7[21]	1[27]	TTTTGATGCAAACCTTCTACGTTAAGAATAAACGGCAGAGGCACC GTAA	49
8[321]	0[315]	AATTAATTTTGGCCATCTTTAGCTCAATGCCTGAGGCACTAATTTT AAC	49
4[244]	7[251]	ACAGATGGGGTAATTGTTAAATAAAATTGTAAACGTCTAATAGAGC TGAA	49
11[392]	8[385]	CCAACAGAATATCAGGCTGTCCTTACCAGTATAAAATCAAAACGC AGAG	49
13[455]	4[455]	AACCACCAAGGGATGCAGATACGACTTG	28
2[86]	13[97]	TGCCTCATAGTTAGCGTGGTTTAGAGCAGGC	31
0[314]	11[307]	GGGGTCACAAGGCCGGTAAATATTGACGAGAATTAACCTCAAAACC TACA	49
8[195]	0[189]	AAAATTATGATAATTCGCGTCGTCACGACACAACATGGAACATAG GATT	49
13[287]	4[287]	AAGTTTTCCCTTGCTGCGCATTATTTTTT	28

8[279]	0[273]	ATGGAAAGTATTAGAGATAATTTGCAACTCCAGAACCATCACCAG TTAA	49
4[475]	7[482]	TTAGCGATTTTCATAACACCGAATAATGGAAGGGTCAGATGCA AGAC	49
11[140]	8[133]	GGGGATGGAGTAACAGGCATACTTTACCCTGACTATCCATATTAT GACC	49
11[98]	8[91]	GATCGGTTTGACCGACATTCACAAAAAGATTAAGAGTTTTAACGC AAGG	49
2[191]	13[202]	AAAGTGAGAATAGAAAGGAAGGATAGAGTCC	31
4[307]	7[314]	CCAAATAACGCGCCTAACAACTCGTATTAATCCTACATTTATTA ATT	49
7[105]	2[108]	ACTAAAGATTGCATACTAATGACGAGAATGACCCCTTG	39
7[378]	2[381]	TGAATTTGCCAACGACCAATCTTACCAAGTTAAGCAATA	39
4[34]	7[41]	TGCGATTTAATAAAGGACGACTGATATCAACCGTTGTGTAGCATT TTT	49
0[335]	11[328]	GTACTGGTGAAACCTCAACCGATTGAGGACAAAGTATCACTTCGT CTGA	49
11[497]	8[490]	ACATCGCGATAAAACCAATAGTTTGAAATACCGACGCGAGAATTT TCAG	49
4[160]	7[167]	CCAAATCCAACACTCATTAAACGTAAACTAGCATAAAGCTACGA ACGA	49
13[77]	4[77]	CGCTGGTCGTGCCACAAAAGATGGGCTT	28
0[167]	11[160]	AGGCGGACTAAACAGCCGACAATGACAAGTATCATCTGGGGTAGG CGAT	49
0[482]	11[475]	AGCATTGCAGAGCCCGCAGTATGTTAGCAAAGTTACAGGAGGCTT TAAT	49
2[149]	13[160]	CATTGTATGGGATTTTGTAAGTGCAATAGCC	31
2[422]	13[433]	GCAGGTCATAGCCCCCTCAAACAATGGCAAG	31
8[111]	0[105]	AGCCTTTGTCATTGCGGCGGAGCGGGCCCTGCCCGCTGTTTGCACC GTA	49
8[384]	0[378]	GCGAATTCCACCAGAATCAATAAGGGACGTCTGTCGTGGCGAATT TACC	49
11[182]	8[175]	TTTCCCATGGCCTTACGACGAACAGTTCAGAAAACTAGTTTGAAG CCTC	49
0[125]	11[118]	CGGAATACTTTCCATTTCGGTCGCTGAGGCAGCGATGCGCTCATCTT CGC	49
7[210]	2[213]	ATAACCTTCATTGGCTTTTGATAGGCTCGGAACGAGCT	39
0[440]	11[433]	ATATTCATATTAGCGCAACATATAAAAAGTTACCGAAGAATCCAAG AATA	49
8[69]	0[63]	ATATATTGGAGAGGGGGCGCATTGCCATAATGAACAGCAAGCAC CCTC	49
8[342]	0[336]	AAACAAATTAAGTTGAGGATATTTACTGATTAGGGGAGCCCAG GAGT	49

13[182]	4[182]	TCCAGTTTACGAGCATCCGCGATCTTGA	28
11[413]	8[406]	TGACCTGGCATCACCAAGAACATCATATGCGTTATGACTACCGAA TACC	49
8[468]	0[462]	CAGTAACTACTTCTGCCTGCATATTAGTCCGATTAACACCCGGTTG AGG	49
7[441]	2[444]	TATAACTCATAATTACTCATCTTTTGAATTAAGAAAAG	39
4[97]	7[104]	AACGAGTGAATACCTAATGGGACAAAGGCTATCAGATTTCAAATA TGCA	49
2[338]	13[349]	CATATCGATAGCAGCACGATGATACCCGATT	31
13[140]	4[140]	TTATAAAGAGTGAGTACAACGCAAAGCT	28
4[496]	7[503]	TATTCTAACCGCGCCAGAGGTCTACCATATCAAAAAGCGTAGAAAC TTTT	49
0[230]	11[223]	AGTATTAATAATAATGTATCGGTTTATCAGGCGCAGTGAAATGCC AAGC	49
2[212]	13[223]	TGCTAAAGGAATTGCGAAGAGGCTTGGACTC	31
4[328]	7[335]	AGCCATAAGATAAGCTAAAATGAACGTTATTAATTCATCAAGTTG AAAA	49
7[126]	2[129]	GTTTCATTTATAGTCAAAAAGGCAGTGAAAAGCGCGACGAT	39
7[399]	2[402]	TCTGAGAACAAATTTTTCCCTTGCTACAAAAGAACTAAG	39
4[55]	7[62]	TAATCATCAACATTCGTGCATGATAAATTAATGCCTTAAATGGCTT AAT	49
0[356]	11[349]	GGCTTTTCGTAATCCCAAAGACAAAAGGGCGCTAAACTTCTTATTG GCA	49
2[44]	13[55]	GAGACCAGTACAAACTACCACCCTCCCTGAG	31
13[98]	4[98]	GAAAATCCTTTCCATCATCTTACACCAG	28
4[181]	7[188]	CAAGAACTTACCAGCCTGTAGATATGTACCCCGGTAGCAATAACC ATTA	49
0[188]	11[181]	AGCGGGGCAGCGGACAGCTTGATACCGATGTCGAACGGAAGCCC AGGGT	49
0[503]	11[496]	ACCACCACTCCCTCCATGATTAAGACTCAGGAAACAGAATCACCC TAAA	49
2[170]	13[181]	TGCACTTCAACAGTTTTTTTGTGCTGTGTGT	31
2[443]	13[454]	GTGGTTTGCCATCTTTTGACGATTTGCGCGT	31
8[132]	0[126]	CTGTAATGCAAACACGGATTCCCAGCTGACATTAAATCGGCATAT AGCC	49
8[405]	0[399]	AAGTTACTCATCATAACCTCAAGATAGAGTGAGGCAAAGCGAAAT GGAA	49
11[203]	8[196]	AAACGACCCATCAAGCGAGAGAATCCCCCTCAAATTTTCGCAAAAT TAGC	49
0[146]	11[139]	AGGGTTGAATTTTCCGCCACGCATAACAACAAAGCTAACTCGCG AAAG	49
7[231]	2[234]	TCATTTGACTGCGGCCAGAGGAACGGTGAATCATACTTT	39

11[35]	8[28]	CTGGTGCTTTGAGGACGAACTGAACCAGACCGGAAAAGAGGTGTA AAGA	49
0[461]	11[454]	CAGGTCACATAATCGAAAATACATACATAAAGTAATTTAGACTAT TTTT	49
8[90]	0[84]	ATAAAAAGAGATCTATAGGTCCTGTTGGAACCTGTTTGCCCCTACC GCC	49
8[216]	0[210]	CAGGCAAAAACAGGAGGAACGGGCCAGTTGTTATCAAGAACGGA GACTC	49
1[28]	4[35]	CACTGAGTCATTTTTGATTGCCCTCACGCGGTTTACGTAATTACC TTA	49
8[363]	0[357]	CCTGAGCTCATTTCAAATCACAGTCACACCGTTGTGACGGGCATA CAT	49
13[203]	4[203]	ACTATTACGCTCACACTTAGCGGCTGAC	28
8[426]	0[420]	CGCCTGAGATGATGATCTAAAAAGCGTTGAGAAGAGGGCGCATA AATC	49
11[434]	8[427]	CGTGGCAGCAGCAAGTACCGCACTAGAAAAAGCCTCTTAGGTACG GATT	49
1[504]	0[504]	AGAGCCGCCACCCTGAGCCGCCACCAGA	28
8[489]	0[483]	GTTTAACTTAGAACGAGGCGGCTGATAGGAGCGGGCCGCTACCGC CGCC	49
7[462]	2[465]	ATGCAAAAATAAGACGTTTTTAACTCCGCCGAACAAAC	39
4[118]	7[125]	TGCCCTGCAGATACGAACAAACCTGAGAGTCTGGAACTTTTGTCT GGAA	49
2[359]	13[370]	GCGAGTAGCGACAGAATTAAGCGTGAAAGCC	31
13[161]	4[161]	CGAGATAGTAAAGCCGCTGATCATTAC	28
0[251]	13[265]	CCTATTAATCTCCAAAACATTTGGGTGCCTATGCCCACT	42
4[370]	7[377]	GAGCGTCACGAGCACAGTTGGGCGGAACAAAGAAAATTCATTTCA ATAG	49
11[371]	8[364]	GTAATAAATCTGGTTGTAGAACTCAACAGTAGGGCAGAAGAGTCA ATTA	49
4[139]	7[146]	GCTCATTAAATTACGAACCCGTAGAGAATCGATGAAAAAACATAAC AGTT	49
2[233]	13[244]	AATTTTTTTCACGTTGATTCTGAAGAAAAAC	31
4[349]	7[356]	TTTGCCAAATAATAAAAGGAATTTGAGTAACATTA AAAAGAAAGA TTAA	49
7[147]	2[150]	GATTCCCATCAGGTGTAAGAGAACGTAAGAGATTTCAAC	39
7[420]	2[423]	CCTCCGGGTTTAGTGGGTATTTTAGTTGAGCTATCAAAC	39
4[76]	7[83]	GAGATGGGATTCATTGTAGATGTAGCTATTTTTGATTTTTAGCTGT AGC	49
0[377]	11[370]	GTCCAGCAAGTTAATTCATATGGTTTCCACAACAAATTAACGA CCA	49
2[65]	13[76]	AGCTGTAGCATTCCACAGAACCGCCGTCCA	31
13[119]	4[119]	TTCCGAATTGCGTTTATACCATAAGGCT	28

4[202]	7[209]	CTTCATCCAAAATAAAATAATCAGAAAAGCCCCAAGGCCAAAGATG GTCA	49
0[209]	11[202]	CTCAAGAGAACAACCTTCGAGGTGAATCCATGTTAATTCCACGTT GTA	49
2[296]	13[307]	TTAACCATTACCATTAGGTGCCTTCGAGGTG	31

Table S4. Staple sequences of ring-shaped DNA origami (RDO).

Start	End	Sequence	Length
11[399]	6[399]	GGGAGCCCCGGAGTCGAGAGCTCAGTAGAAGGATGTATTAAG	42
2[454]	11[461]	TTGAGCCGGTGAATTCACCGGCGGTACGCCAGA	33
6[167]	7[174]	TTCAGCTTCCGGCACTCGCCATTCAACGTTAATATT	38
9[84]	1[104]	CAGCAACCGCAACCAGAGCACAAACGTCAAGGATAG	35
1[21]	3[678]	GCCAACGCCAGGGTGGTTGTAAGAATACGTGGCCCCCTCTGA	41
7[175]	3[188]	TGTTAACTATCAGGTCGATGAAAAATTCA	29
0[300]	11[314]	CTCATTCTTTATGCGATTTCTTGACCGCCGCGCTTAAT	38
5[49]	6[42]	GTAAAGCCGCCAACATACGAGCCG	24
3[105]	5[90]	ATTTGCCAAAATCCCCTAACGGGGTCATTGCAGGGCGGAGGTGT	45
9[336]	1[356]	GGTCGCTGAGGCAACAGCTTGCCATCGCTTATCTA	35
11[525]	6[525]	CACGCATGCGGGAGGCGTTGCTTATCAATAGCAATCATCGTA	42
6[104]	4[119]	GCTGATTAGAAAAAGCCGCACAGGCGGCCTTTAGTGGGTGTACATC	46
6[503]	7[510]	CATGAAATAGCAATAGCAGATAGCCCCTGAATCTTACC	38
11[210]	0[203]	AAGGAACTGAAAAGGTGCATTTAAAATTCA	31
0[552]	11[566]	CTAATGATGACAATAACAAGTATATACTTCTTTGATT	38
7[427]	3[440]	GAGCCGTCAGACTGTCCCTTATTGGAGCC	29
11[84]	0[77]	TCACCCTGCTGGTCTGGACAAACATCCCTGC	31
11[483]	6[483]	TAATCACTGGCAAATAATATACCAGAAAAGTAAGCTATCTTA	42
9[630]	1[650]	TTTAGAAGTATTTCTAAAATAAGCCGTCTAGCCCT	35
6[251]	7[258]	TTTACGGTGTCTGGAAGCGAACGAGAAACGAGAATGAC	38
1[63]	3[48]	CTTTGCTCAGCAAATCGTTAATTGCGTTGCGCGTAGGAGCT	41
0[328]	0[301]	GCCACTACGAAGGCACCAGAACTGG	25
11[672]	0[665]	GAAAAAGAAATACCTACCATAAAAAAGTCTT	31
5[595]	6[588]	TGTAAATCTCTATATGTGAGTGAA	24
6[440]	4[455]	CCTTAGTGGAACCATCGATAGCAGCACCGTAATCGACATTAGCA	46
0[580]	0[553]	AGTGAATTTATCAAAATATGTTTCAG	25
5[259]	6[252]	ATTATAGTGATCAAAAATCAGGTC	24
11[420]	0[413]	CGATTAACCGCCTCCCTTATCATACAATGGA	31
9[546]	1[566]	AGTAGGGCTTAACTAGAAAAATCTTACCACCATAG	35
3[147]	5[132]	TAGATGGGACGACGACAGTAGGATAACCTCACCGGTGTGGAGCCG	45
6[188]	4[203]	CTACAAATTGTTCTAGCTGATAAATTAATGCCGGAGAACAAATCAC	46
3[21]	5[678]	TTTACCCCCTGGCCCTGAGACAGAGATAGAACCCTGCAAGGGACA	45
9[210]	1[230]	CAATTCTACTAAATTTTCGCAATTTGGGGTGGAAAGC	35
3[553]	2[539]	TAAAGTATATTGAGAATCGCCATATTTATGGCTGTCTTATCCC	43

9[294]	1[314]	ATTACCCAAATCGTGTACAGAGAGTAATTAACCT	35
1[189]	3[174]	AACCCTGTGTAGGTAAAGTTCGCGTCTGGCCTGAGCGCCAT	41
3[679]	8[672]	CCTGAAAGCGAGTCTGAAATGGA	23
5[175]	6[168]	AGCTCATTGGAATTCGCATTAAT	24
6[125]	7[132]	GAATGAAGGGTAAAGTTCGTTTTTCGTTGTAACCGA	38
6[524]	4[539]	GGAATCAACAAGTACCGCACTCATCGAGAACAAGCATCTTATCATT	46
2[496]	11[503]	AATTAACCAGGGAAAAAGAAGTGAGGCCACCG	33
9[126]	1[146]	TGGGTAACGCCAGATCGGTGCAGGGGGACCCGGAT	35
11[105]	6[105]	TGGGGTTTGTAGATCCTCACGCTGGCAAACGCGGTAAACGAT	42
3[511]	2[497]	TTATCCCCTACCCAGCTACAATTTTATGAGAGCGCTACGGGAG	43
11[504]	0[497]	AGTAAATTAATCAAGACCGCGCATAATAGC	31
6[272]	4[287]	ACCAGACCAAAAGGAATTACGAGGCATAGTAAGAGCCAATTCAAC T	46
1[399]	3[384]	GTTCCAAGGAGTGTACTGCGTCACCAGTACAACGCAGTAAC	41
7[217]	3[230]	CAGGCAAGTTGATTCATTAGATAAATAAG	29
0[342]	11[356]	AAAATAAAGGAAGTTTCCACCACGCGGTTGCTTTGACG	38
5[91]	6[84]	CCAGCATCGCCGCAACCAGCTTAC	24
9[378]	1[398]	TAGTACCGCCACATAAGTGCCATAGGTGTGTACC	35
6[461]	7[468]	CGAGTAGCGACAGAATTCATCGGCGTGGAACATATA	38
9[42]	1[62]	GGTCATAGCTGTGTTCTTCGCCGGTACTTGGTTT	35
0[594]	11[608]	AGAAGATAATAGCTTAGATAAAACAAAGAAGAACTCAAA	38
2[580]	11[587]	CTTAGGTGAGACTAGCGTTATAACATCACTGC	33
7[469]	3[482]	AAAGAATTTTTAAGAAGGAAACCAACAAA	29
11[441]	6[441]	CAGGAAAACAGATCTTTTCATAGCCAGCGGTTCAAGTTG	42
5[343]	6[336]	AACGAGGGAGCCCTCAGCAGCGAA	24
6[209]	7[216]	CAAGGGTAGCTATTTTGAGAGTCTGCCAATAAATCATA	38
9[672]	1[20]	TGACGCTCAATCTAGGGTTGAATTAAGAATCG	33
2[664]	11[671]	ACCACCATCGCCATACTAATACCATTGCAACAG	33
0[412]	0[385]	AAGCGCAGTCTCTGAATTAGCATTC	25
3[595]	2[581]	TTAGAATTTGAATTACCTTTTTTAATGAGCAAATCCACTCCGG	43
0[370]	0[343]	TCATAGTTAGCGTAACGAAACGGGT	25
1[147]	3[132]	TCTCCGGATAGGTCACGTACGTACAGCGCCATAGGTAAACA	41
3[133]	2[119]	ATCGGCGGCGGGTTTTCCAGTCACGATCGTTGGGCGAAACAG	43
5[637]	6[630]	AGTTTGAGTCTTTGCCGAACGTT	24
6[146]	4[161]	GTGCCGACTCGGCCTCAGGAAGATCGCACTCCAGCTTCTGCCAGT	46
6[545]	7[552]	TTAGCCGTTTTTATTGCAAATCAGAACAACGCCAACA	38
0[622]	0[595]	GCAATTCATCAATATAAAGACGCTG	25
9[588]	1[608]	ACAATTCATTTCAATATCAAGATATCCTG	35
11[126]	0[119]	AAGCACGCAAGGCGATTGTAGAGACATAGAC	31
1[357]	3[342]	AAGTTTTTCTGTATGGGAGACTTTTCATGATAGTGCTTT	41
3[525]	5[510]	ACCAATCCGGGTATTAACCAAAATAAACAGCCATATGCCTAATT	45
11[567]	6[567]	AGTAATACAAATGCCTGTTACCGGAAAAATAAGGATGGTTTG	42
6[335]	7[342]	AGATGTTACTTAGCCGGAAGTACCCGCTTTTGCGGGA	38

9[252]	1[272]	ATCCCCCTCAAAGGGGTAATACTGCGGATAAAAAA	35
0[426]	11[440]	AGCCAGATAAAACAAATAAAACCGGAAAGGGATTTTAGA	38
6[482]	4[497]	CCGAAGCACAAGCCCAATAATAAGAGCAAGAAACAAGACAGAGA GA	46
5[217]	6[210]	ATAAAGCCACAGGCAAAGAATTAG	24
6[293]	7[300]	ACAACACTATCATAACGCGAGAGGCATTTCAGTGAATAA	38
11[462]	0[455]	ATCCTGTTATTACGCAGAATATCACGGAAGG	31
2[538]	11[545]	ATCCTAACTGAACACCCGACTAATTAACCGTTG	33
6[230]	4[245]	CCATATATCCAACATGTTTTAAATATGCAACTAAAGTACTTAATTG	46
9[168]	1[188]	AAGATTGTATAAGTAATCGTATGATAATGCTTTAG	35
3[49]	2[35]	AACTCACCTTTCCTGTGTGAAATTGTTTACGGGCAACTTGCGT	43
1[105]	3[90]	CTCTCAAACCTAAATTCATCCGCCGGGCGCGCTCACGCTT	41
3[609]	5[594]	AATTATTTTTTCAGGTTAACGCTATTAATTAATTCGCTTGCTTC	45
7[259]	3[272]	CATAAACGATAAAAATTGCCAGTTAGATT	29
0[454]	0[427]	TAAATATTGACGAAATCTCATTA	25
5[133]	6[126]	CCACGGGAAAGTGCCAAGCTTCA	24
9[420]	1[440]	GCCGCCACCCTCGCGTTTGCCAGCCACCTCTATTC	35
1[315]	3[300]	AAAACGATCTTTGACCCCCATTGTGAATTACCAACCATTTC	41
3[175]	2[161]	CAAAAATCGGCAAAATTTAAATGTAAAGGTAACCGTTTGACC	43
3[441]	5[426]	AGCAAAAAACGTCACCAATACAGGAGGTTGAGGCGAGAGCCGCC	45
6[650]	4[665]	CCCTCAATAAGCAAATGAAAAATCTAAAGCATCACCAACTGCAACA	46
4[202]	9[209]	CATCAATGAGAAAGGCAAAACACATGTCAATGCAT	34
6[566]	4[581]	AAATACCAACAAATATATTTIAGTTAATTTTCATCTTACCAAGACAA	46
0[118]	0[91]	TTTCTCCGTGGTGAAGGCCGGGTCA	25
0[636]	11[650]	TATCAGTGAATTATCATCAAATAGAAGAACAATATTAC	38
7[301]	3[314]	GGCTTGTCATCATAAGATGAAATCAGCG	29
7[511]	3[524]	AACGCTACCGCGCCCCGGTATTAATAGAA	29
4[580]	9[587]	AGAACGCGCTGATGAATAAACTAGTATCATTTTA	34
5[385]	6[378]	CAAGCCCAGAGCCACCACCCTCAT	24
11[147]	6[147]	TAAAGGGGCGAAGGGCCTCAACTGTTAGCGCCATCGCTTCTG	42
2[118]	11[125]	CGGATCACGAAAAGCCGACCGAGGTGCCGTA	33
3[273]	5[258]	CATCAGTATACATAACGCCAGAAGCAAAGCGGATTAGCCCTGACT	45
11[546]	0[539]	TAGCAAAAGCCAACGCTCTAGAAAACAGAAC	31
11[588]	0[581]	CTGAGTAATTAATTACAATCCTTTTGTCAAT	31
4[622]	9[629]	GCGTAGATGCACGTAAATCGCGCAAAAGAAAGGA	34
6[356]	4[371]	CTCCAAATAGGAATTGCGAATAATAATTTTTTACGTCGGAGTGAG	46
4[496]	9[503]	TAACCCAGGTAATTACAAAGTACGGAATACTTAG	34
3[399]	5[384]	AAGTTTTTAAACAGTTAATGAGGAACCCATGTACCGCAGGGATAG	45
11[336]	0[329]	TACTATATAACCGATATGCCAAAAGCGTAAT	31
0[34]	0[679]	TGCCAGCTGCATTAATGTTGAATG	25
2[370]	11[377]	AATGAATTGTCGTCACAATGATATAACGTGCTT	33
5[679]	6[672]	TTCTGGCCAATGTCACACGACCAGTA	26
1[231]	3[216]	AAACTCTTGCTCCTTTTGAACATTATGACCCCAACAATCGG	41

0[664]	0[637]	TAATGCGCGAACTGATATTCCTGAT	25
2[34]	11[41]	ATTGGGCGCGCGGGACAAGAGCAAAGGGCGAAA	33
3[231]	5[216]	AGGTCATTAATGCTGTAGCTAGAGCATAAAGCTAAGTATTAAGCA	45
7[91]	3[104]	ATCCCACGTTCCGGCAGCCTCCCATGCTC	29
0[216]	11[230]	GCCTTTTGTGTAATACTTTCGCGAGGGGAAGAAAGCGA	38
3[63]	5[48]	GCATCAGCCCCTGCATCAGAGGGTGCCTAATGAGTCTCATAAAGT	45
4[412]	9[419]	GCCCCGTAACGGGGGGTTTTGGGTTGATACAGA	34
1[441]	3[426]	ATAAAAATTTGGGAATTAGCCTTGATATTCACGGTTAGGTC	41
11[273]	6[273]	CACGCTCCAATAGTAAAATAGAAGTTCCAAAATACCTCGTTT	42
2[286]	11[293]	AACATTATTAATAAATAGCGTGCAGGTAACCAC	33
6[41]	7[48]	GATTGCCCCAGCAGGCAAAATCCCTATCCGCTACAAT	38
0[468]	11[482]	AGGGAGCGAGGGCGACATTGACTCCAGAAGTGTTTTAA	38
7[343]	3[356]	TCGTCAGAGCCTTTAAATTTCTAAATTTT	29
4[76]	9[83]	CCGGTGCATGCCGGGGTTTCTAGCCTCCTCTCAG	34
4[664]	9[671]	GTGCCACCGGTCAGTTGAAAGGAGCACTAAATTT	34
11[21]	6[21]	CAACGTTCCACTGTGTTGTAAAGAATAAATCGGCGAAAATCC	42
3[189]	5[174]	AAAGGGTATGATATTC AACCTTAACCAATAGGAACATGTAAATC	45
6[587]	7[594]	TACTGACCTAAATTTACGTTAAATAGAAACAGTACATA	38
0[132]	11[146]	TGAGAGGCGTTTACCAGTCTGTGCTTAAATCGGAACCC	38
1[651]	3[636]	AAAACAGCAGAAGATAAAACCAGAAGGAGCGGAAAAGGAAC	41
4[328]	9[335]	TTTGTATCAAGCGCCTTTGAACATAGGCTGATTC	34
5[301]	6[294]	AGTAAATTGGCCCTGACGAGAAAC	24
11[168]	0[161]	TAGAGCAGCCCCAAAAACAACGGAATGTG	31
0[244]	0[217]	CAAAGCGAACCAGACCGCGGGAGAA	25
7[637]	3[650]	AAATCCAATATCTGGGGAAGGTCCACAGA	29
11[609]	6[609]	CTATCGACAAACTACCTGAGCAGAGGCTTTGAATGAAACAAT	42
5[511]	6[504]	TGCCAGTTTTAACGAGCGTCTTTC	24
6[377]	7[384]	TTTGAAAATCTCCAAGGTTATCACAGAACC GCCACC	38
1[567]	3[552]	GTCTGATGGGTTATATAATCTGTCCAGACGACAATTAAGG	41
0[496]	0[469]	AGCCTTTACAGAGAGAAACCGATTG	25
11[357]	6[357]	AGCACGCAACAAATACCGACGAGGTGATTGTATCAAAAAGG	42
0[48]	11[62]	GGAAACCGTCACTGCCCGCCGAGCTCTATCAGGGCGAT	38
9[462]	1[482]	TTAGCAAACGTAAGGAAACGCTGATTAACATAACA	35
2[160]	11[167]	GTAATGGTGGGAACGCCAGCTGAGCCCCGATT	33
3[357]	5[342]	GCTAAACAGGAACAACCTAAAGCAACGGCTACAGAGACAGCATCGG	45
4[244]	9[251]	CTGAATATTTTGC GGATTAGATAACCTGTTTGA	34
0[160]	0[133]	AGCGAGTAACAACCCGTGGAATTTG	25
0[678]	11[20]	GCTATTTACACAGACAATATTAACATGCGCTCGTGGACTC	40
7[553]	3[566]	TGTAATCCGTGTGATT CATAATATCTATA	29
2[622]	11[629]	AAGGGTTTGGATTATGATGAAGCCTTGCTGGTA	33
5[427]	6[420]	GCCAGCATCGCCACCAGAACCACC	24
3[343]	2[329]	GAGGACTTATTGCAGGGAGTTAAAGGCAAGAAACAAACTAA	43
3[637]	2[623]	AAAGAAATAAGACTTTACAAACAATTCCAAAACAGATAATGG	43

6[314]	4[329]	CGCAGACGGATTGTGTCGAAATCCGCGACCTGCTCCACAACGGAG A	46
11[294]	0[287]	CACACCAAGAACCGGATGGAACGAAATACCA	31
4[538]	9[545]	CCAAGAAAATAATCATAGAAGTTAGCGAACCAAC	34
6[62]	4[77]	CCAGAATTGCGATCCAGCGCAGTGTCACTGCGCGCCCTCAGCGGTG	46
0[76]	0[49]	GGCTGGTAATGGGTAAATCCAGTCG	25
2[412]	11[419]	ATGATACGTAAGCGAGTATAGTAAACAGGAGGC	33
11[42]	0[35]	AACCGTCGAATTCGTAAGAGAGAGGGCTGTCG	31
1[609]	3[594]	ATTGTTAGAACCTACCATTTGAAAACATAGCGACATTTCCC	41
3[469]	2[455]	GGTTTACCGGAAAATACATACATAAAGATTAGCACCAACCGAC	43
6[608]	4[623]	AACGGATGTCGTCAGATGAATATACAGTAACAGTACTAAAGAAATT	46
11[231]	6[231]	AAGGAGTTTTCAATGGTCATTTGACCCCAATTCTGTTTCATT	42
2[76]	11[83]	GGTGTGTTTCGTCATAGTTGAGCTACGTGAACCA	33
7[133]	3[146]	CGGCCAACCAGGCAAGGGAAGGAATGGTG	29
11[189]	6[189]	CCGGCGCCCGGTAAACTAGAGAGAATCATTGCCTTGAGAGAT	42
0[258]	11[272]	TAATTCTTAAGACTTCAAAAATCGTCCAAGTGTAGCGGT	38
3[301]	2[287]	AACTTTACGAACGTAACAAAGCTGCTCTTTAGGAATACGGAAC	43
11[630]	0[623]	ATATCCTAATACATTTGGATACTTCATGATG	31
4[454]	9[461]	AGGCCGGTACCAGTTTCGGTCATAATCAATATG	34
6[398]	4[413]	AGGCTGAATCCCCCTGCCTATTTTCGGAACCTATTATCAGTAACAGT	46
2[328]	11[335]	AACACTCAAAGAGGTGACCTTCTACAGGGCGCG	33
0[510]	11[524]	AATGAATAGATTTTTTGTGTAAGCCAGAGTCTGTCCAT	38
1[525]	3[510]	TAAGTCTTTACGAGCATGTCCAAATAAGAAACGAATATTAT	41
3[427]	2[413]	AGACGATTAAGAACCGCCACCCCTCAGACGTCAGTGCCTTTTTG	43
3[567]	5[552]	TGTAATGAGAAAACTTTTTATAAAGTACCGACACCGAGCCAGT	45
7[385]	3[398]	CTCAGACTCCTCAAGACCAGGCTTGTAAT	29
11[378]	0[371]	TCCTCGCTACTCAGGACGTTTCCACAGCCC	31
4[118]	9[125]	GACATAAGCCAGCAGTCTCGTTAACGGAACAAGT	34
8[671]	2[665]	TTATTTAGTATTAACAGAACGA	22
7[49]	3[62]	TCCACAGGCGGGCCGCGCGTGCATTAACG	29
0[174]	11[188]	ACATTACGTCCTGTAGCCACAGAAATTGACGGGGAAAG	38
3[259]	2[245]	AAAAAGAAGTGCTTTAAACAGTTCAGATAGATGGCTTAGAGTA	43
4[370]	9[377]	AATAGAAAACCTTTCTTGCTTTTAGTTGCGCGGTT	34
6[629]	7[636]	ATCTTTACATCGGGAACCAAGTTAGACAACCTCGTATT	38
0[286]	0[259]	GTCAGGACGTTGGGAAGTCGCGTTT	25
7[679]	3[20]	CACCAGGTGGTCCGAGCCCGATTCT	27
3[91]	2[77]	TCGCACTGGGAATGCCAACGGCAGCACGGTTACCTGTACACT	43
4[160]	9[167]	TTGAGGGGCGCATCGCTGCGCTTCGCTATTCAGG	34
2[244]	11[251]	CCTTTAACAACAGGAGCTATACGGGCGCTAGGG	33
5[553]	6[546]	AATAAGAGGATTAGGCAGAGGCAT	24
3[385]	2[371]	ACTGAGTGGCCTCAGAACCGCCACCCCTGCAACAGTTTTTAGTA	43
3[651]	5[636]	GGTGAGGGCTGAGAGCCAGCACATTATCATTTTGCTAATTTTAAA	45
11[315]	6[315]	GCGCCGCATCAACCAGGCGAGAGGACAGGGAACCGAACGAGG	42

4[34]	9[41]	TTCACCGAGTGAGATAAATCATCCAGTTTGTCAT	34
6[83]	7[90]	GGTGTGCACTCTGTGGGTCATACCGCGTCGGTGGTGCC	38
0[538]	0[511]	GCGCCTGTTTATCAACAACGTCAAA	25
0[384]	11[398]	CACAGAGAACTACAACGCCTATCACTTAGAATCAGAGC	38
2[202]	11[209]	GAGTAATCATATATTATGTACAACGTGGCGAGA	33
9[504]	1[524]	TTGCTATTTTGCAAGAACGCGAGGTTTTTAATAGA	35
11[63]	6[63]	GGCCAGATCCCGTCCGTGGCCAGCATTTCACGTGCTGCGG	42
0[90]	11[104]	CTGTTGCCGTTGCGGTATGGCGTGGAATCAAGTTTTT	38
1[273]	3[258]	TCTACGTTACAGGTAGAAAAGAGGAAGCCCGAAGAGGCATC	41
3[217]	2[203]	TTGTACCACTAGTAGTAGCATTAAACATGAGCCGAGAATGCCT	43
3[483]	5[468]	GTCAGAGCAAGAATTGAGTTAATCAATAGAAAATTACATAAGTTT	45
6[671]	7[678]	ATTTGCTGAACCTCAACAAATCAACACATTGGCAGATT	38
4[286]	9[293]	AATGCAGTGAGATTTTGCAAAGTTTAGACTATTC	34
0[202]	0[175]	ACGCAAGGATAAAAATTTTTCATCA	25
7[595]	3[608]	AATCAAGCCTGATTGCGAATTACCATCAA	29
5[469]	6[462]	ATTTTGTCCCACGCAAAGACACCA	24
6[20]	4[35]	TGTTTGAGAGTTGCAGCAAGCGGTCCACGCTGGTAGGATTGCCC	44
3[315]	5[300]	ATTATACCATCGCCTGATAAGCTTGAGATGGTTAACGAACGAGT	45
11[252]	0[245]	CGCTGGATAAATATTCATTTTCAGGAGAGCTT	31
11[651]	6[651]	CGCCAGGATTAGTCTTTAGGAATTGATCAGTTGGATATCAAA	42
6[419]	7[426]	ACTCTGAAACATGAAATAGGATTAGGCCACCACCCTCA	38
1[483]	3[468]	TAAAAATGAACACCCTGAGCGCCAAAGACAAATCTTCATAT	41

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