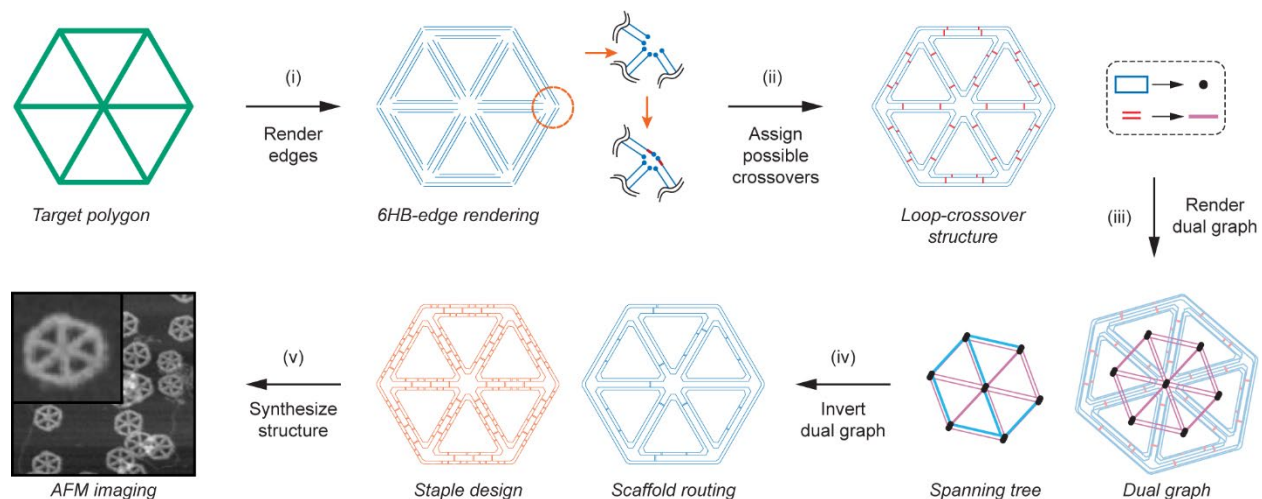


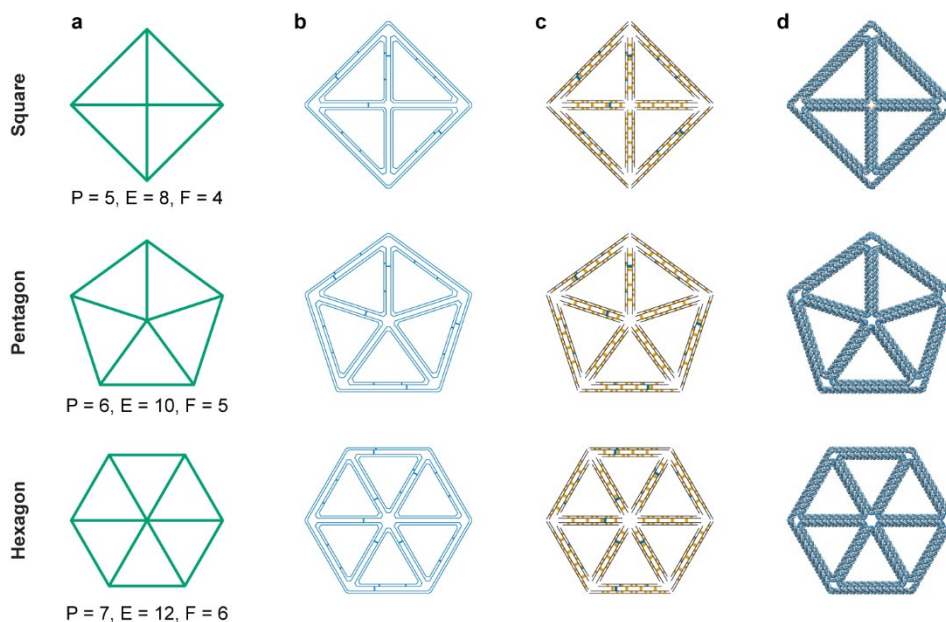
**Supplementary Information**

**Automated Sequence Design of 2D Wireframe DNA origami with Honeycomb Edges**

*Jun et al.*



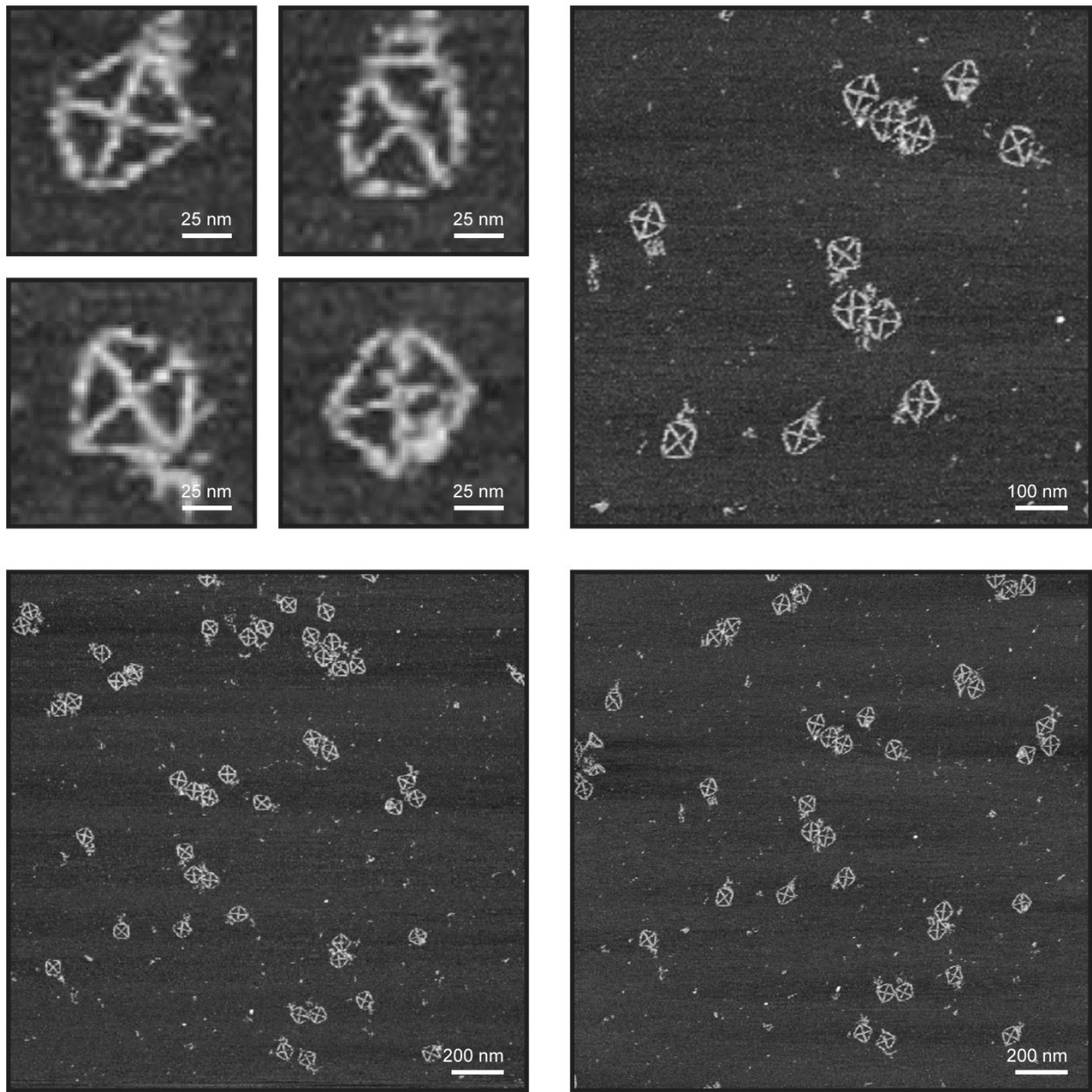
**Supplementary Figure 1** Schematic illustrating design algorithm for the 6HB-based hexagonal DNA origami. The arbitrary target geometry is based on a polygon mesh, with discretized line segments (step i) to represent six DNA duplexes per wireframe edge with the endpoints joined (step ii) to form closed loops with geometrically allowable scaffold double crossovers between them. The dual graph of the loop-crossover structure is obtained (step iii) by converting each closed scaffold loop to a node and each possible scaffold double crossover connecting them to an edge. The minimum spanning tree of the dual graph was then determined and inverted (step iv), defining the DNA scaffold routing. Staple sequences generated (step v) by the algorithm were used with the input scaffold to synthesize the 2D DNA origami in one-pot thermal annealing.



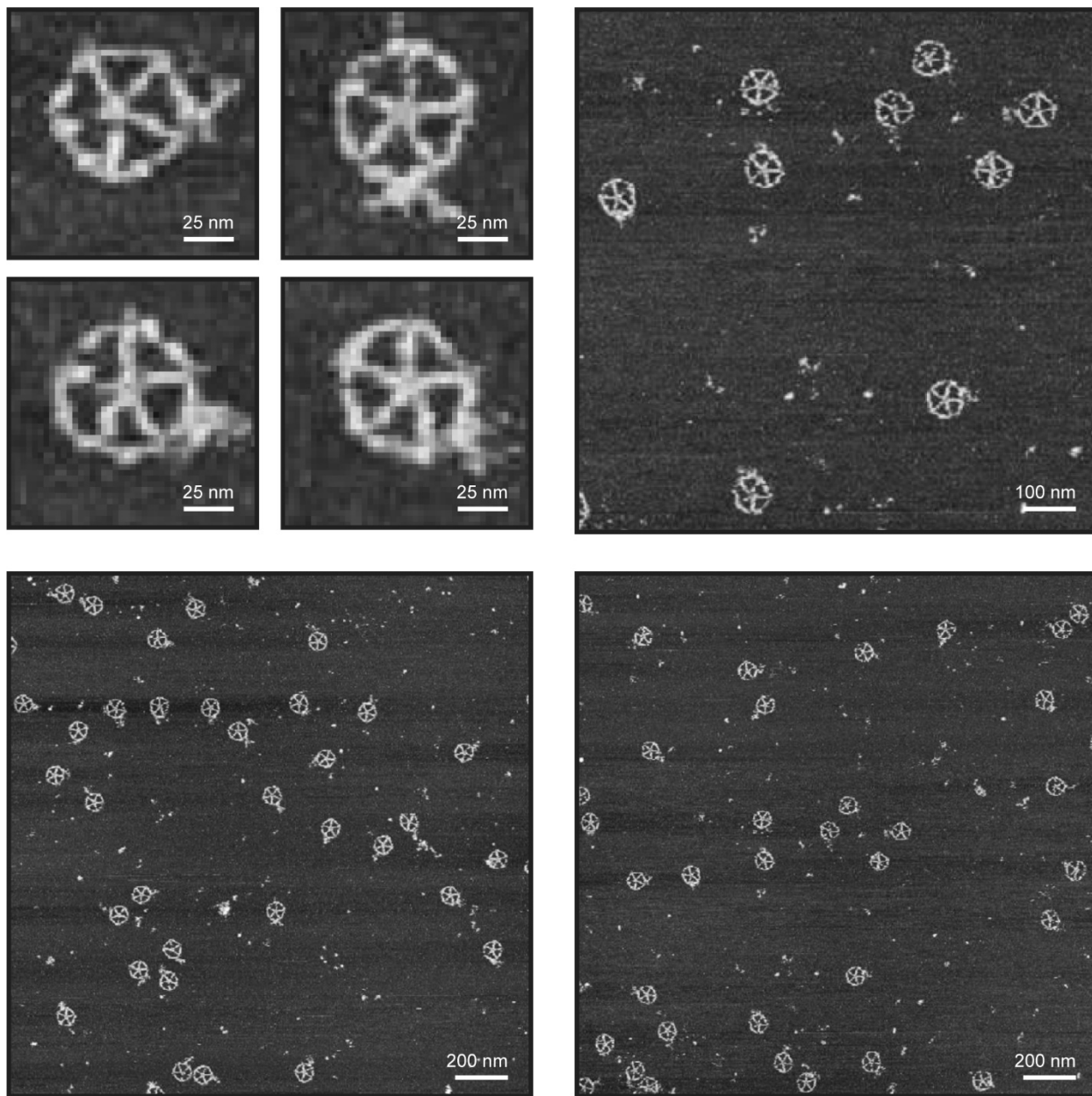
**Supplementary Figure 2** Target geometries, scaffold routing paths, crossover models, and atomic models for polygons. **a** The target geometries. The letters, P, E, and F denote the number of points, edges, and faces, respectively. **b** Scaffold routing path. The continuous blue loop is the single-stranded DNA scaffold that routes throughout the entire origami object of arbitrary shape. **c** Scaffold double crossovers (blue) determined by the spanning tree algorithm and staple double crossovers (orange). **d** Atomic model.

**Supplementary Table 1** Design parameters for polygons with the DX and 6HB edges. # indicates the type of scaffolds in **Supplementary Table 4**.

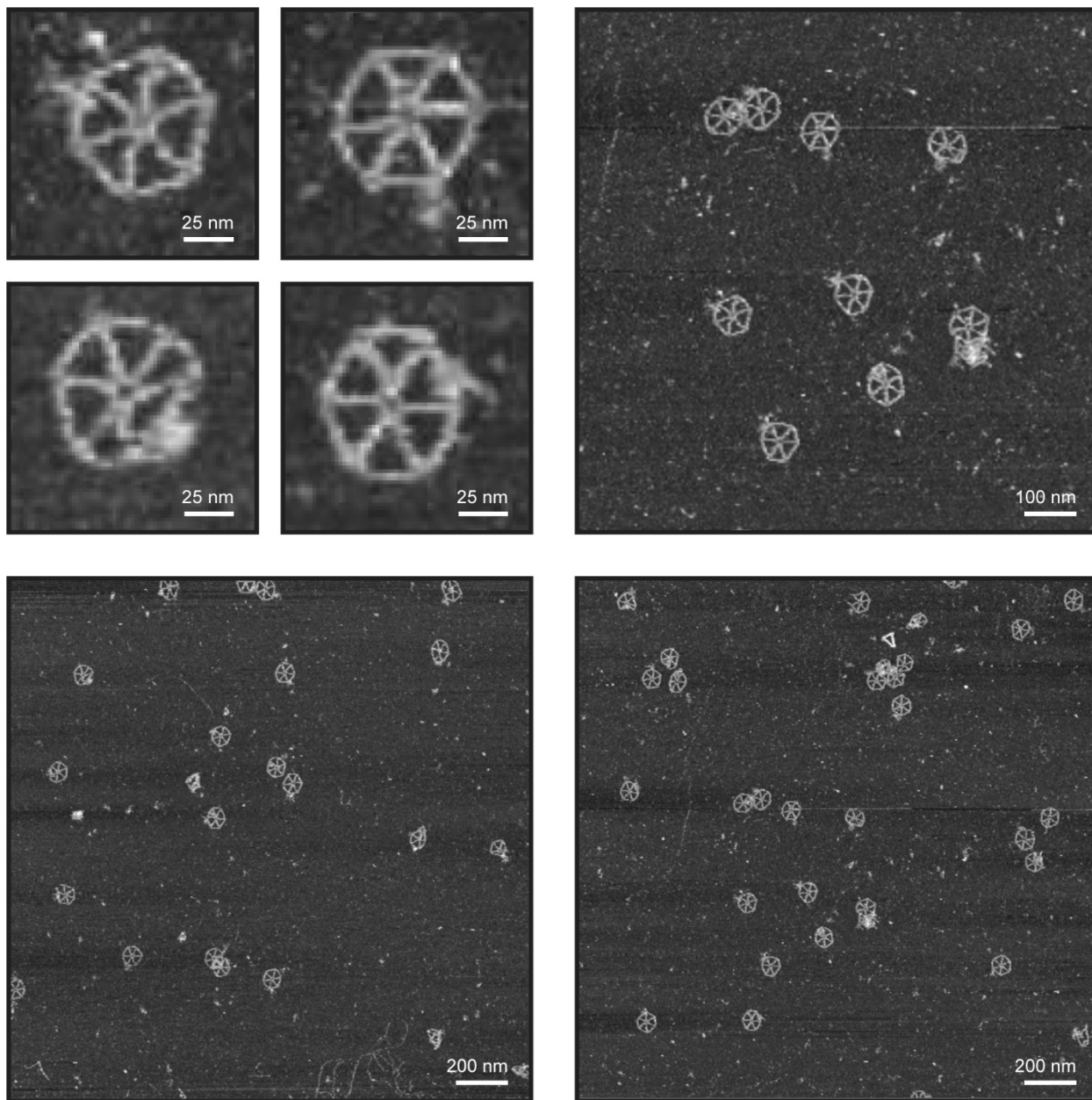
Edge type	Target geometry	Edge length	Scaffold			Staples		
			Required length	# of double crossovers	# of unpaired nucleotides	# of staples	# of double crossovers	# of unpaired nucleotides
<b>DX</b>	Square	84-bp	1,756-nt (#2)	4	20	42	32	92
	Pentagon	84-bp	1,986-nt (#2)	5	46	48	35	120
	Hexagon	84-bp	2,185-nt (#2)	6	43	51	42	120
<b>6HB</b>	Square	84-bp	5,902-nt (#1)	14	190	133	214	244
	Pentagon	84-bp	6,475-nt (#1)	17	125	154	233	352
	Hexagon	84-bp	7,157-nt (#1)	20	95	168	262	382
	Hexagon	63-bp	5,645-nt (#1)	20	95	123	190	382



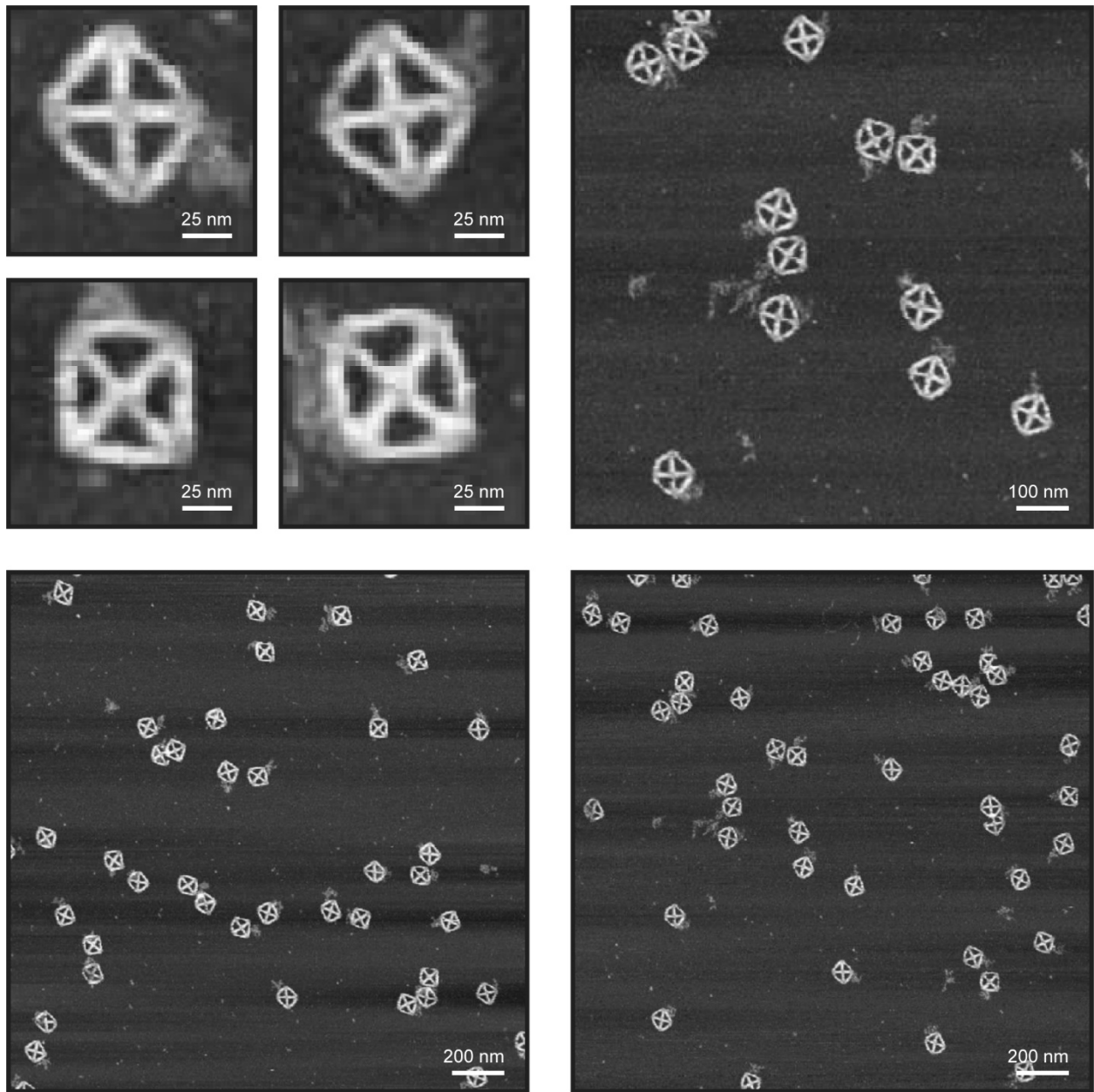
**Supplementary Figure 3** AFM imaging of DX-based square DNA origami of 84-bp edge-length.



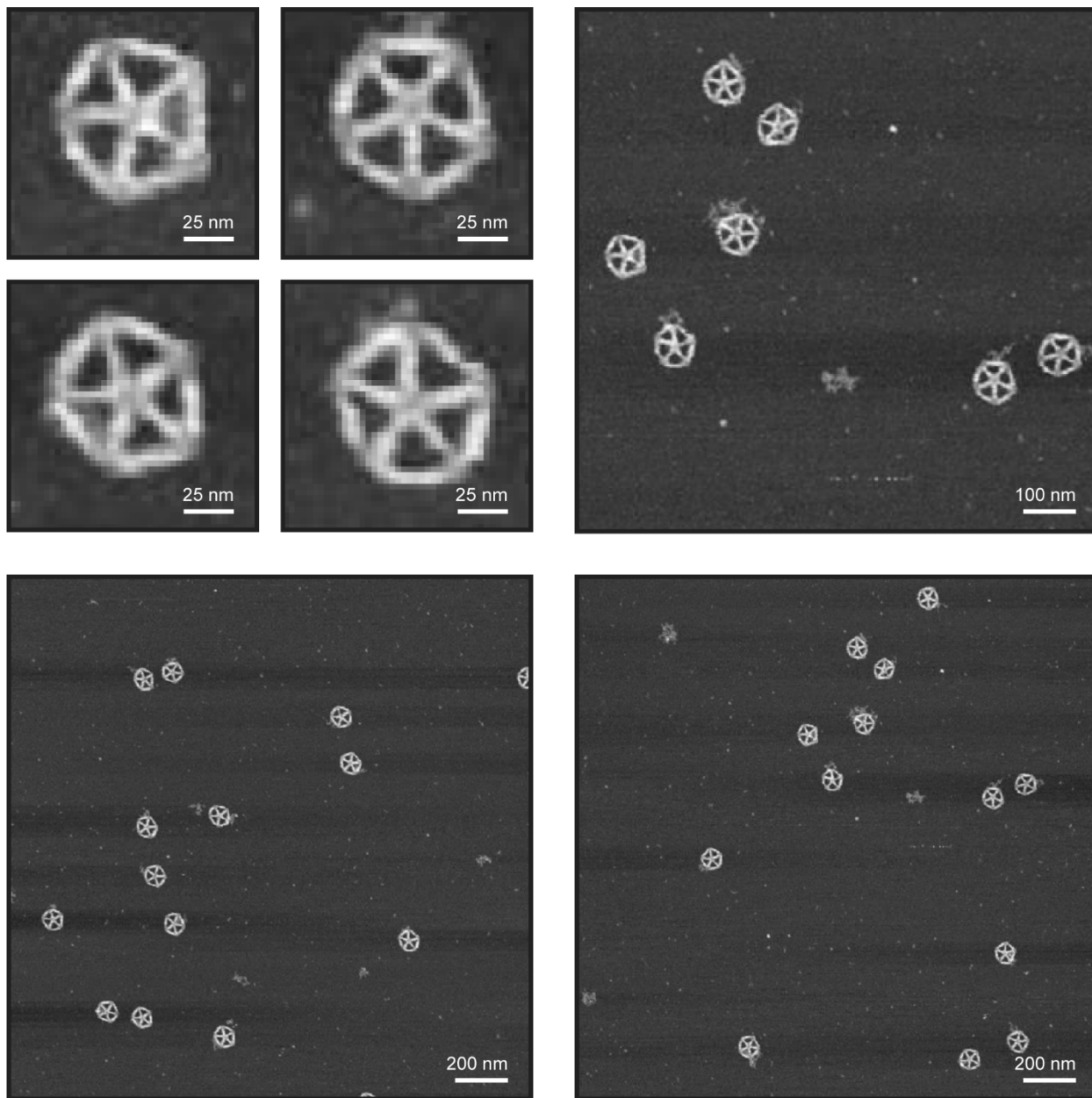
**Supplementary Figure 4** AFM imaging of DX-based pentagonal DNA origami of 84-bp edge-length.



**Supplementary Figure 5** AFM imaging of DX-based hexagonal DNA origami of 84-edge-length.

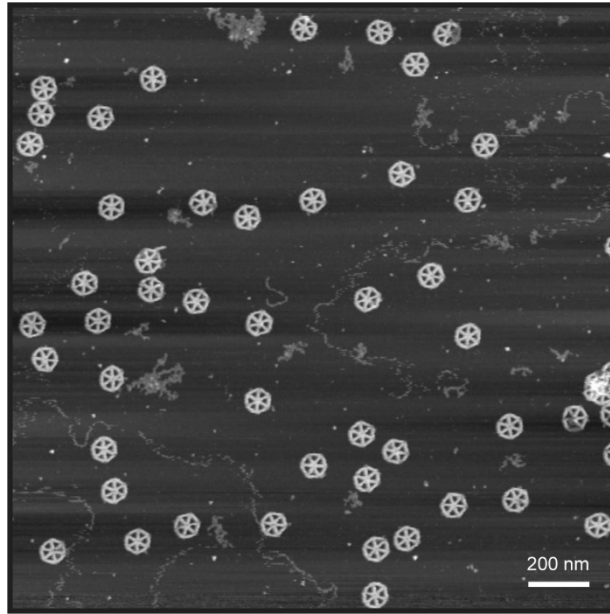


**Supplementary Figure 6** AFM imaging of 6HB-based square DNA origami of 84-bp edge-length.

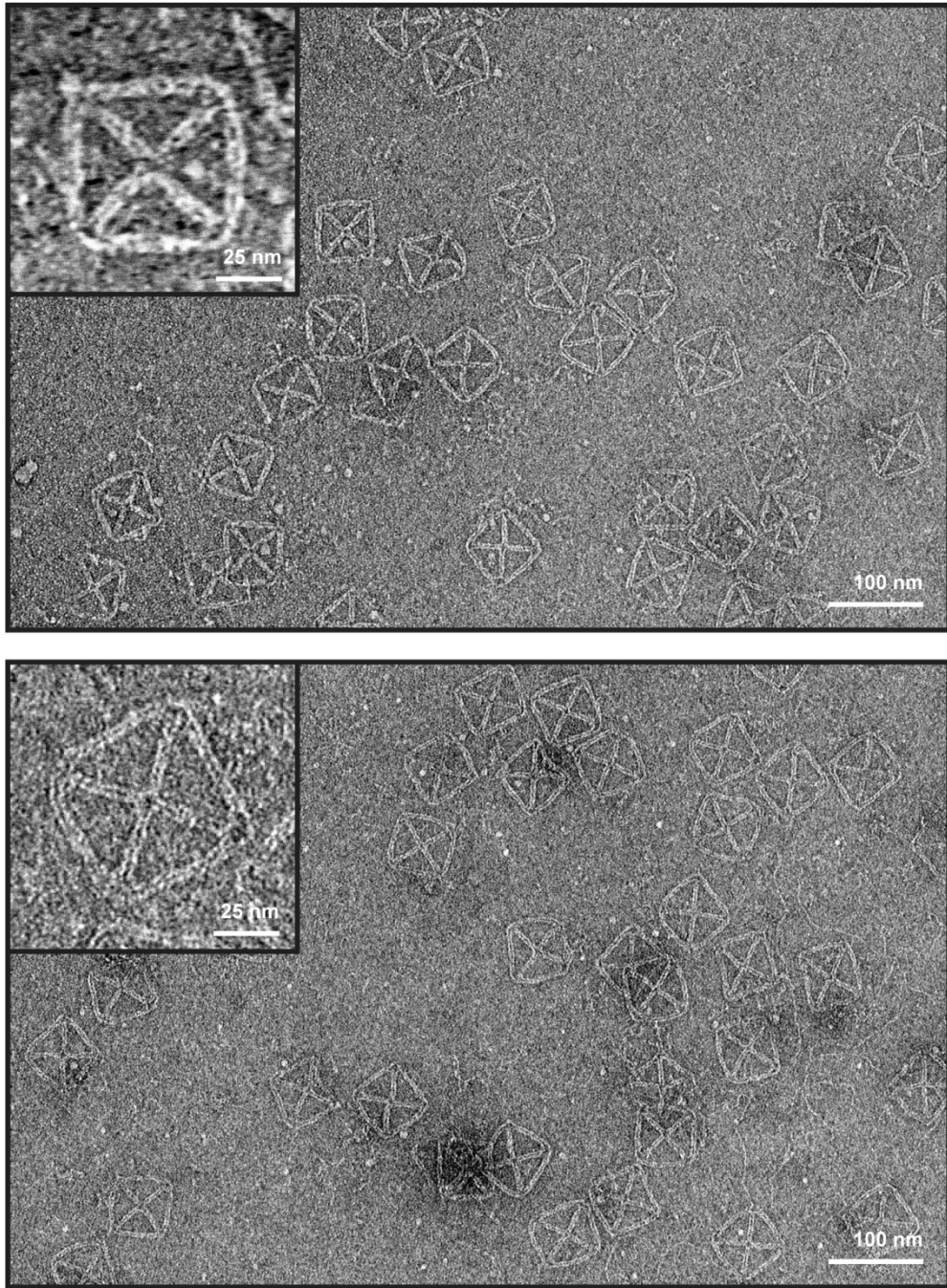


**Supplementary Figure 7** AFM imaging of 6HB-based pentagonal DNA origami of 84-bp edge-length.

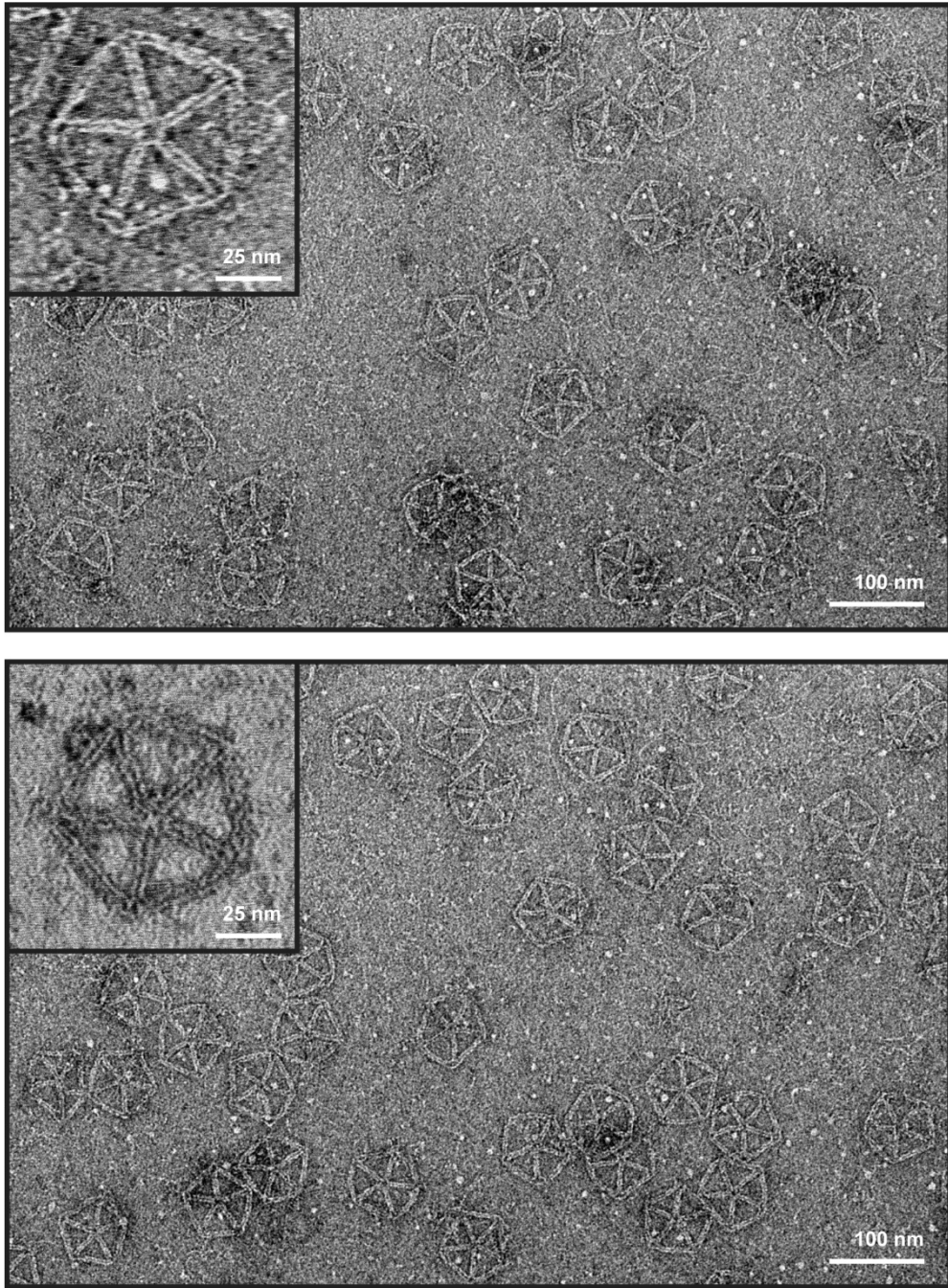




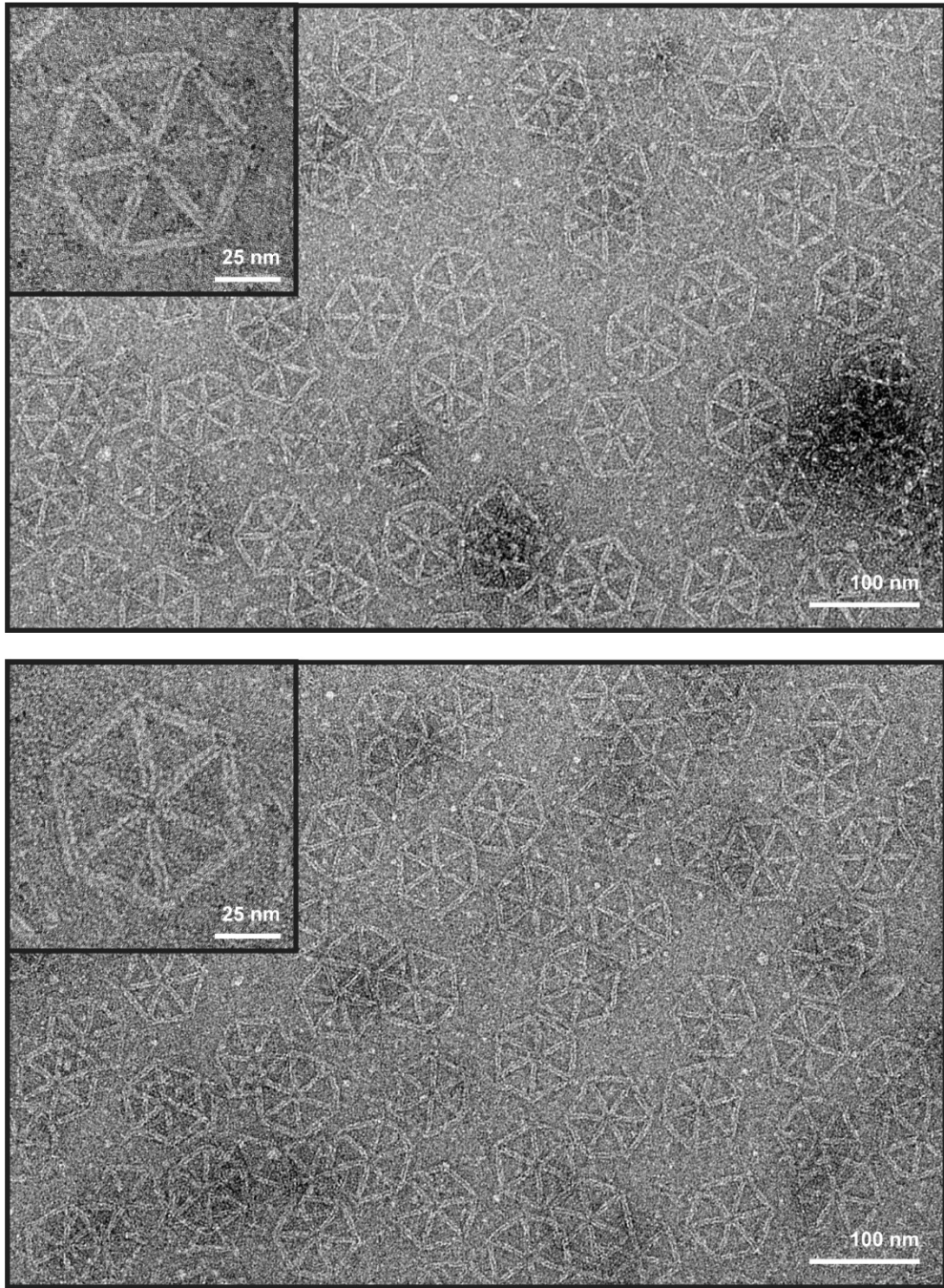
**Supplementary Figure 8** AFM imaging of 6HB-based hexagonal DNA origami of 84-edge-length.



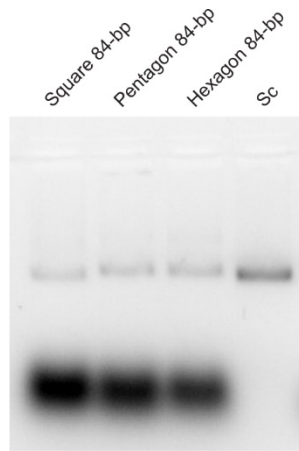
**Supplementary Figure 9** TEM imaging of 6HB-based square DNA origami of 84-bp edge-length.



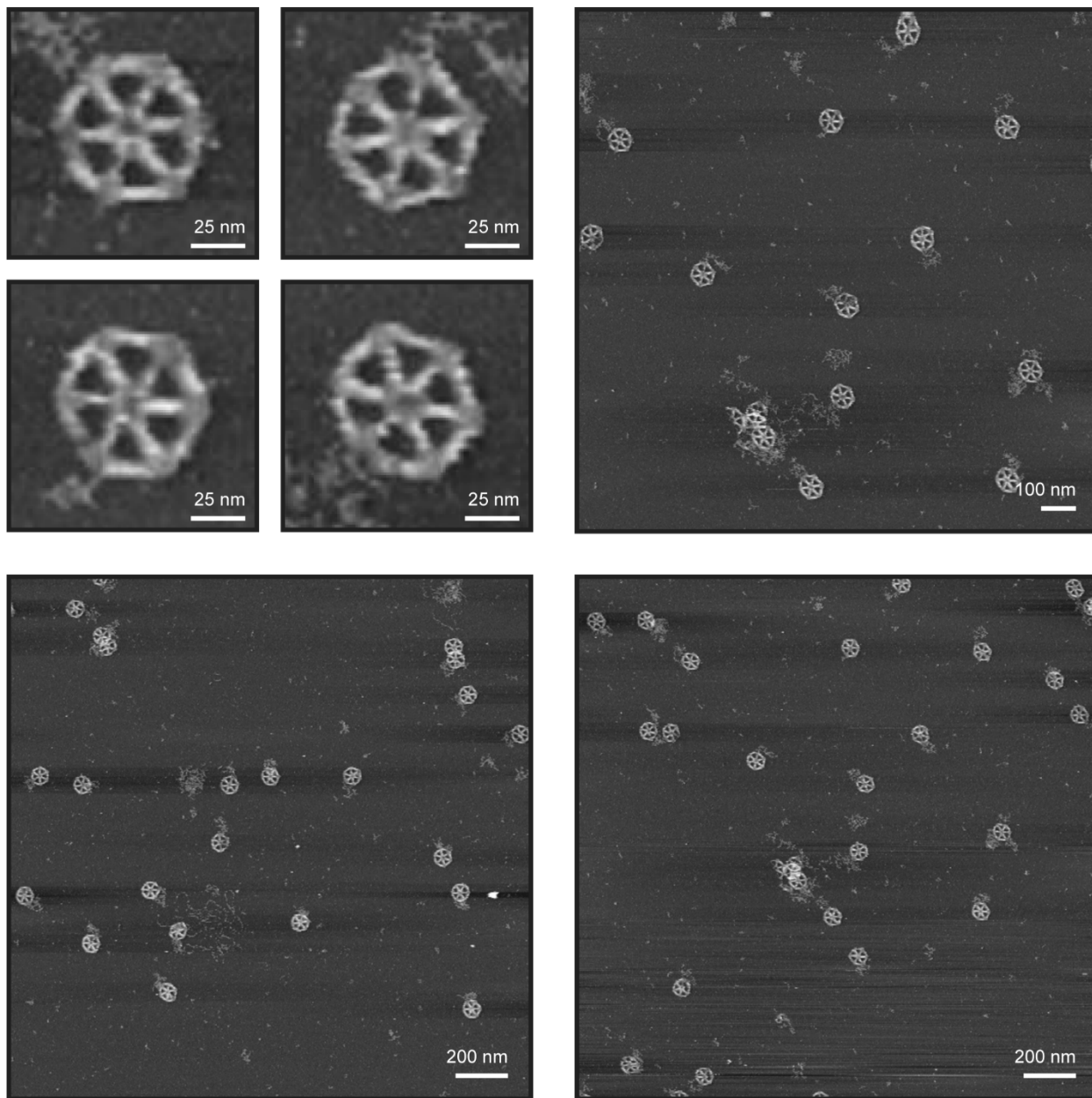
**Supplementary Figure 10** TEM imaging of 6HB-based pentagonal DNA origami object of 84-bp edge-length.



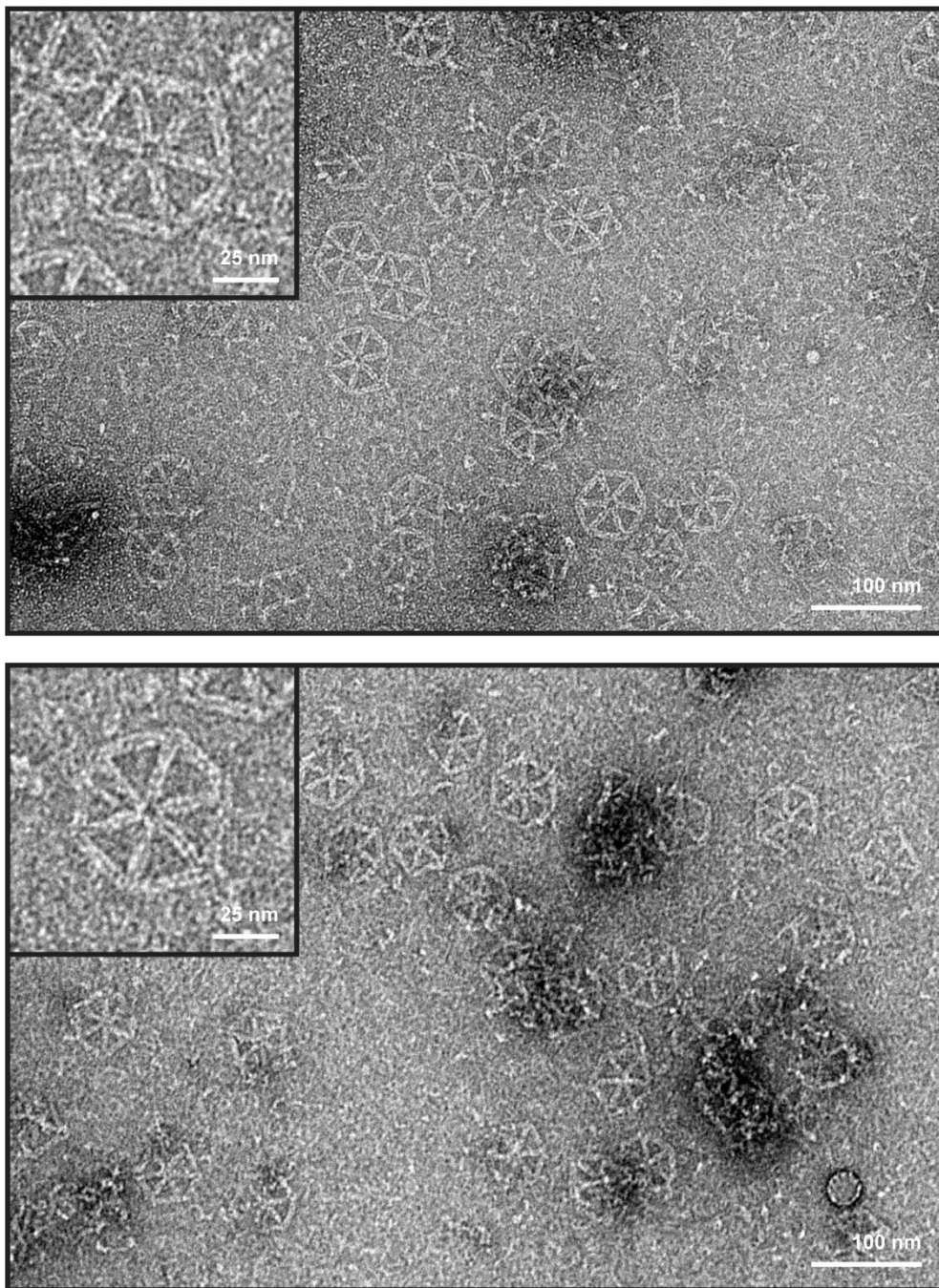
**Supplementary Figure 11** TEM imaging of 6HB-based hexagonal DNA origami object of 84-bp edge-length.



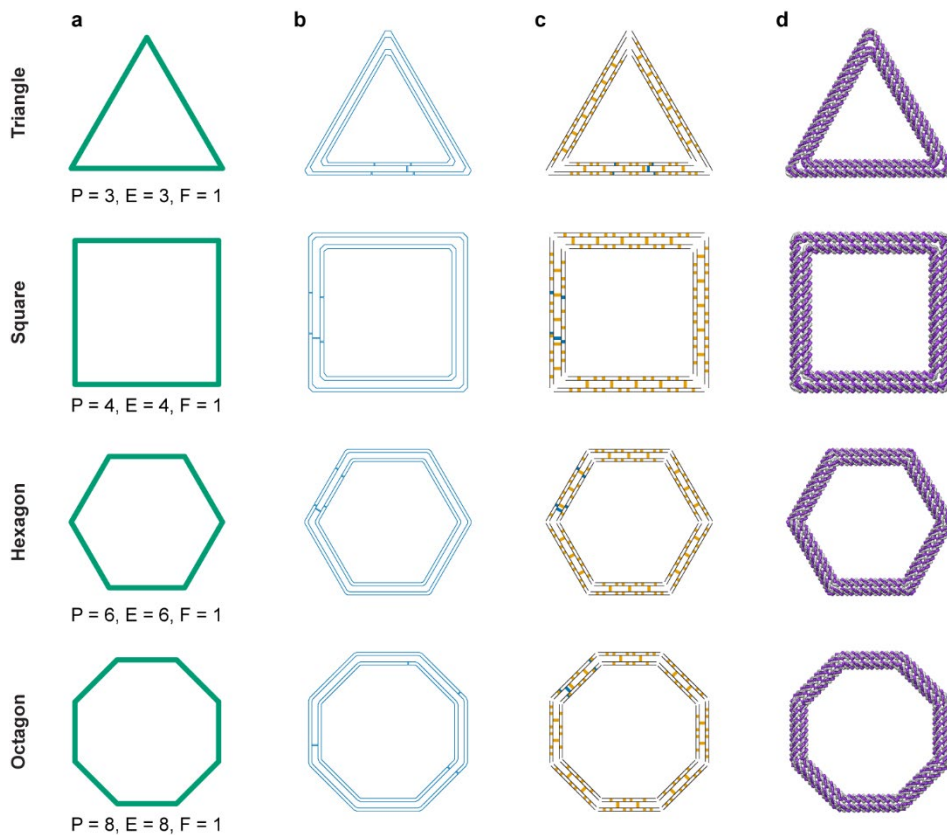
**Supplementary Figure 12** Agarose gel electrophoresis for 6HB-based square, pentagonal, and hexagonal DNA origami objects.



**Supplementary Figure 13** AFM imaging of 6HB-based hexagonal DNA origami of 63-bp edge-length.



**Supplementary Figure 14** TEM imaging the 6HB-based hexagonal DNA origami of 63-bp edge-length.

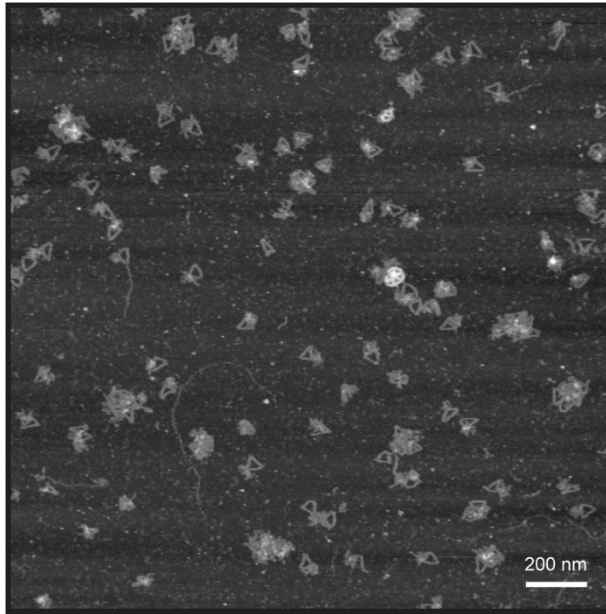


**Supplementary Figure 15** Target geometries, scaffold routing paths, crossover models, and atomic models for the triangle, square, hexagon, and octagon without internal mesh. **a** The target geometries. The letters, P, E, and F denote the number of points, edges, and faces, respectively. **b** Scaffold routing path. The continuous blue loop is the single-stranded DNA scaffold that routes throughout the entire origami object of arbitrary shape. **c** Scaffold double crossovers (blue) determined by the spanning tree algorithm and staple double crossovers (orange). **d** Atomic model.

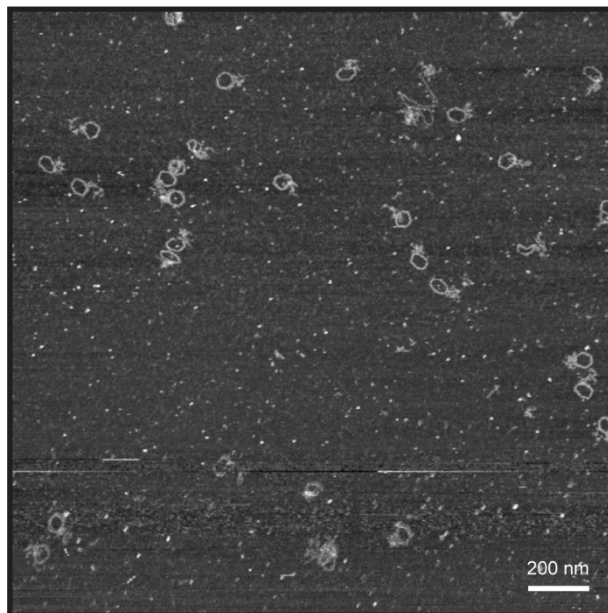


**Supplementary Table 2** Design parameters for the triangle, square, hexagon, and octagon without internal mesh. # indicates the type of scaffolds in **Supplementary Table 4**.

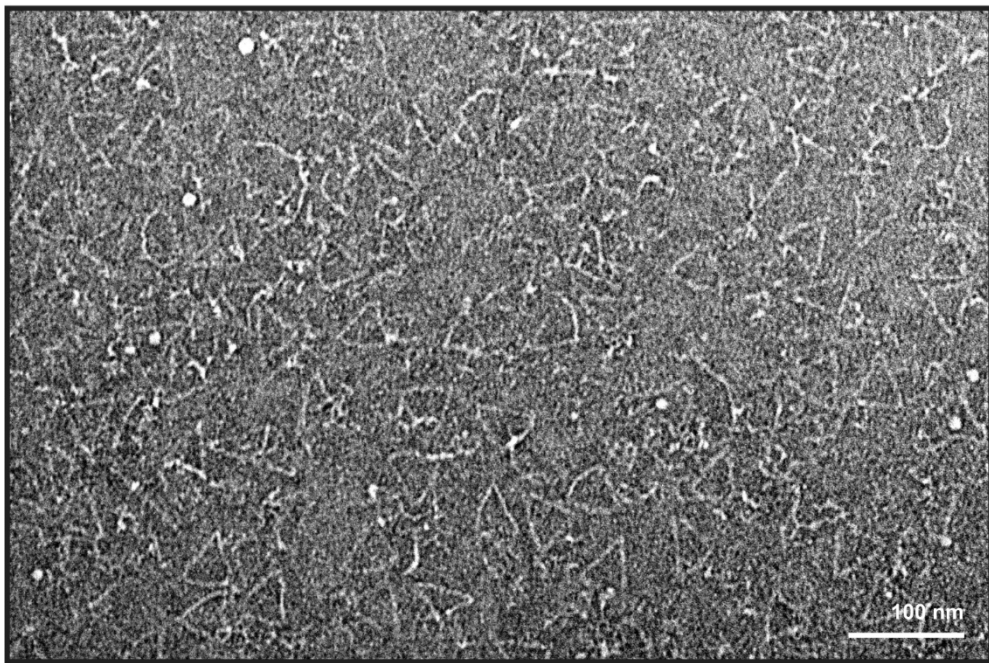
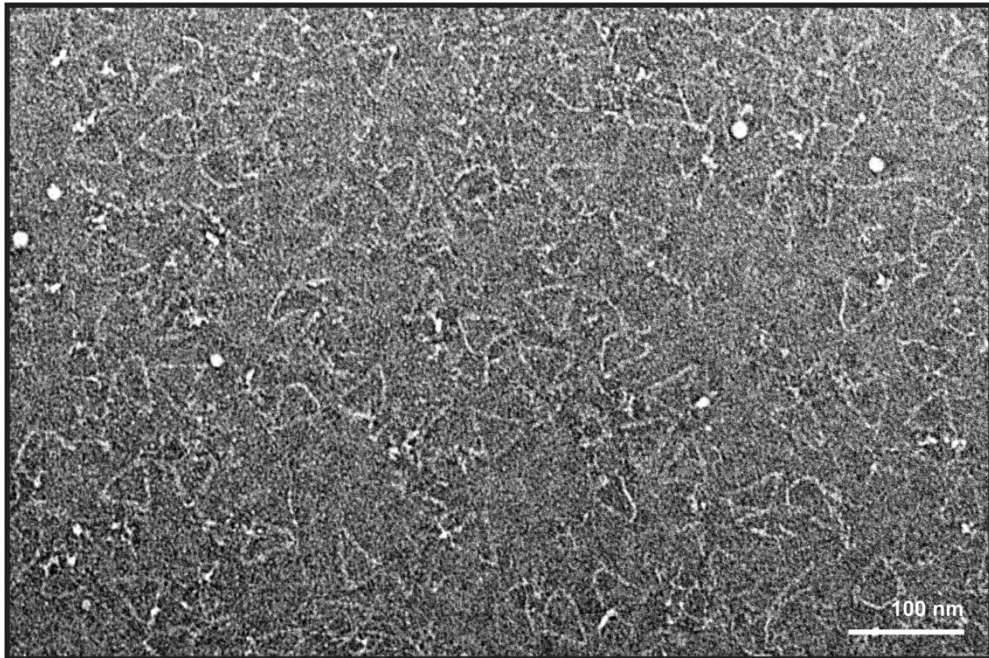
Edge type	Target geometry	Edge length	Scaffold			Staples		
			Required length	# of double crossovers	# of unpaired nucleotides	# of staples	# of double crossovers	# of unpaired nucleotides
<b>DX</b>	Triangle	128-bp	855-nt (#2)	1	24	18	17	30
	Hexagon	74-bp	954-nt (#2)	1	24	18	17	42
<b>6HB</b>	Triangle	128-bp	2,772-nt (#2)	5	69	64	106	87
	Square	105-bp	2,908-nt (#1)	5	96	68	115	100
	Hexagon	74-bp	3,042-nt (#1)	5	120	69	115	66
	Octagon	57-bp	3,072-nt (#1)	5	136	69	109	120



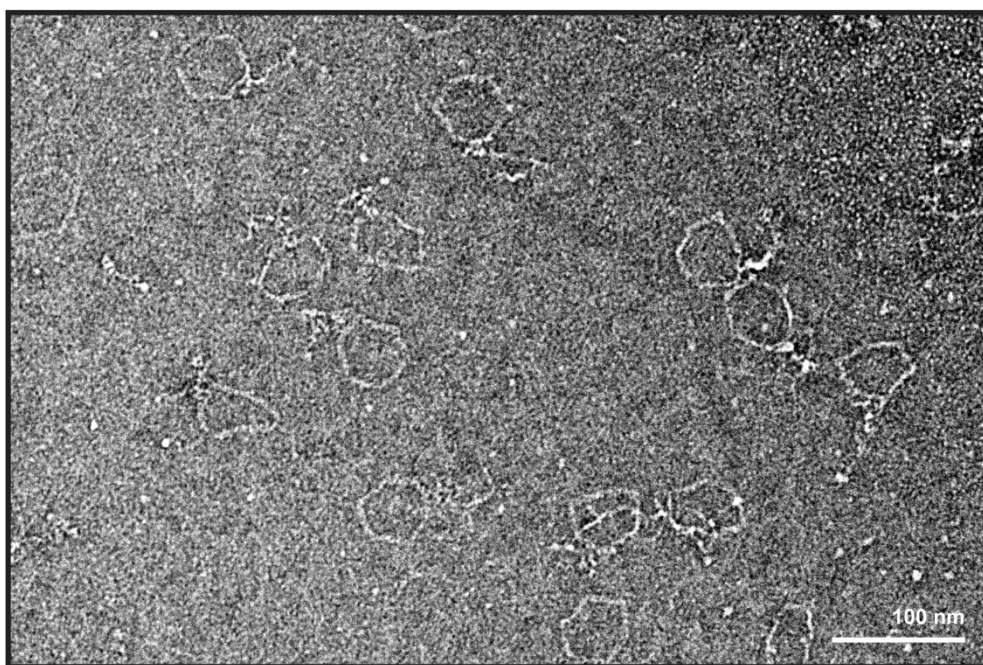
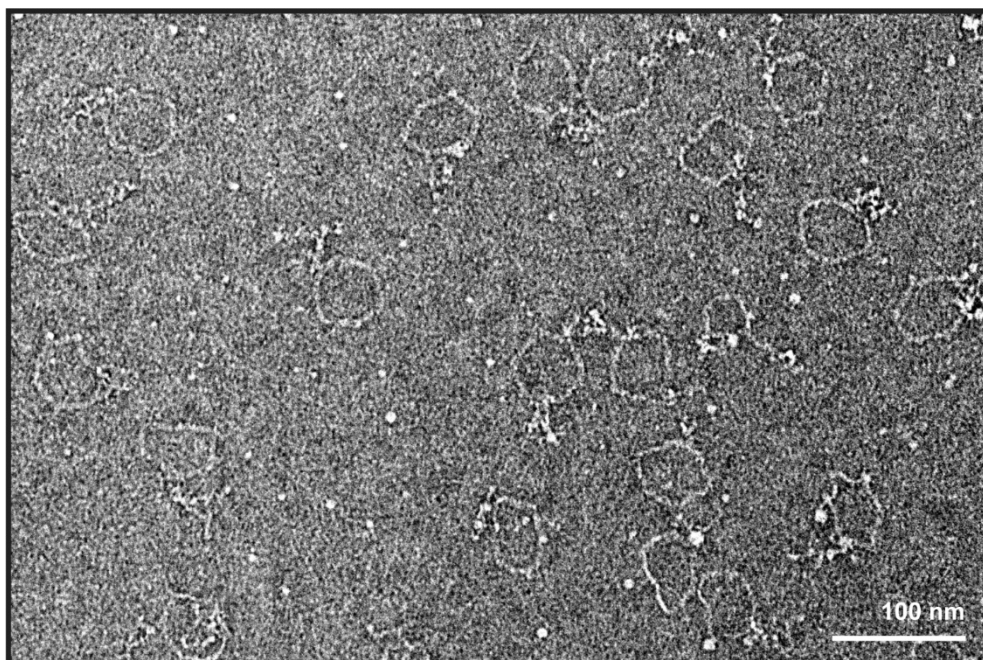
**Supplementary Figure 16** AFM imaging of DX-based triangular DNA origami of 128-bp edge-length without internal mesh.



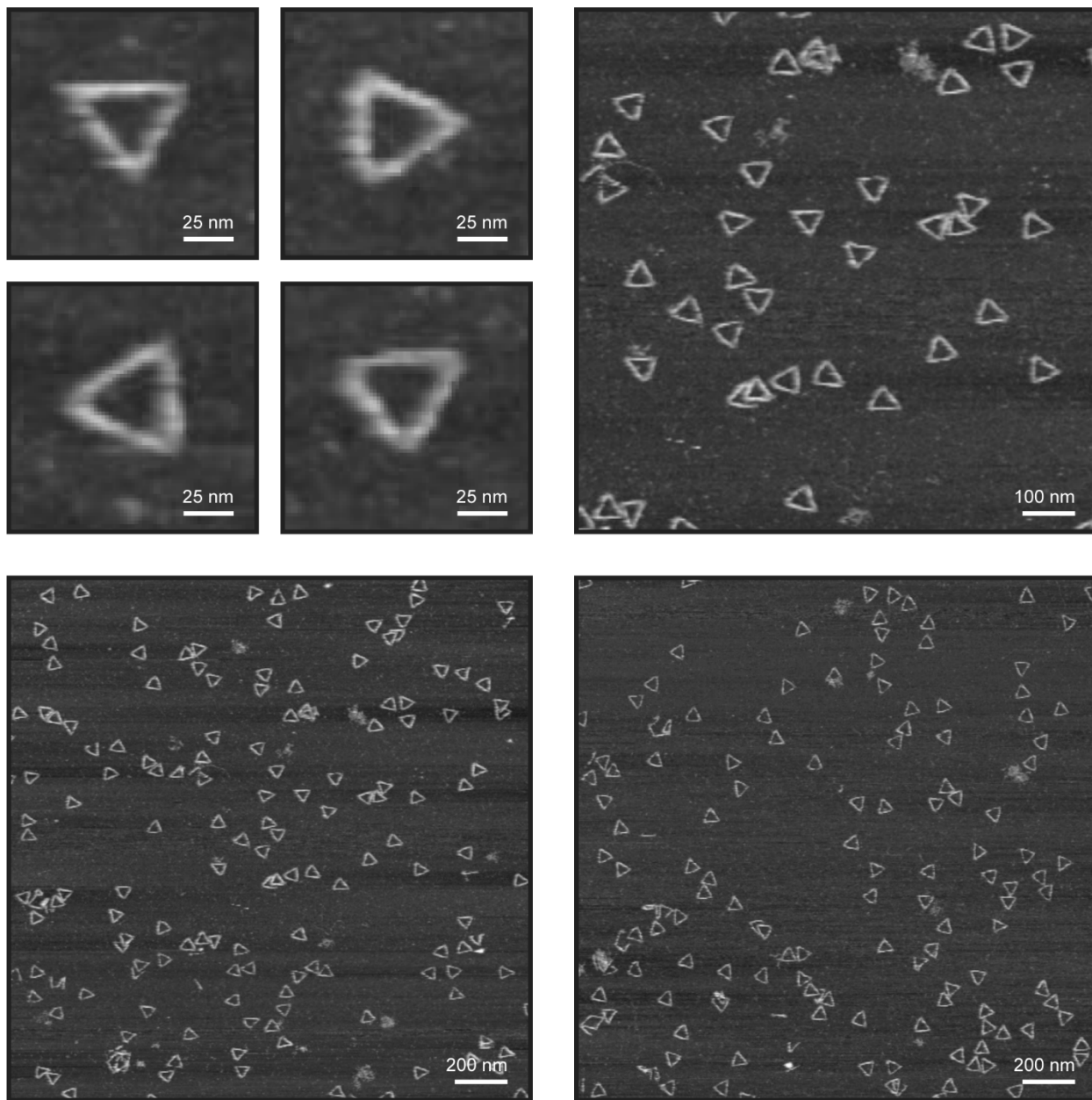
**Supplementary Figure 17** AFM imaging of DX-based hexagonal DNA origami of 74-bp edge-length without internal mesh.



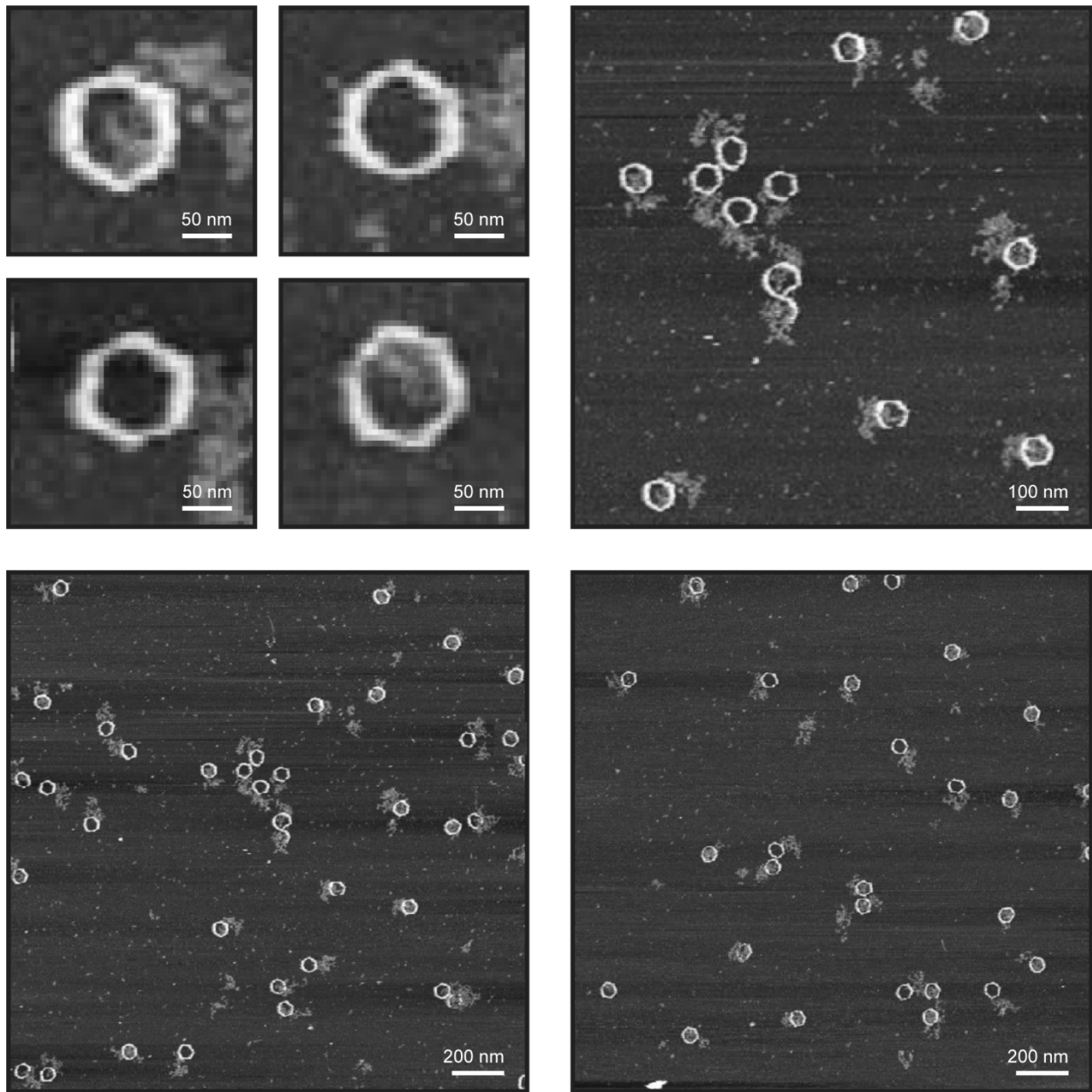
**Supplementary Figure 18** TEM imaging of DX-based triangular DNA origami of 128-bp edge-length without internal mesh.



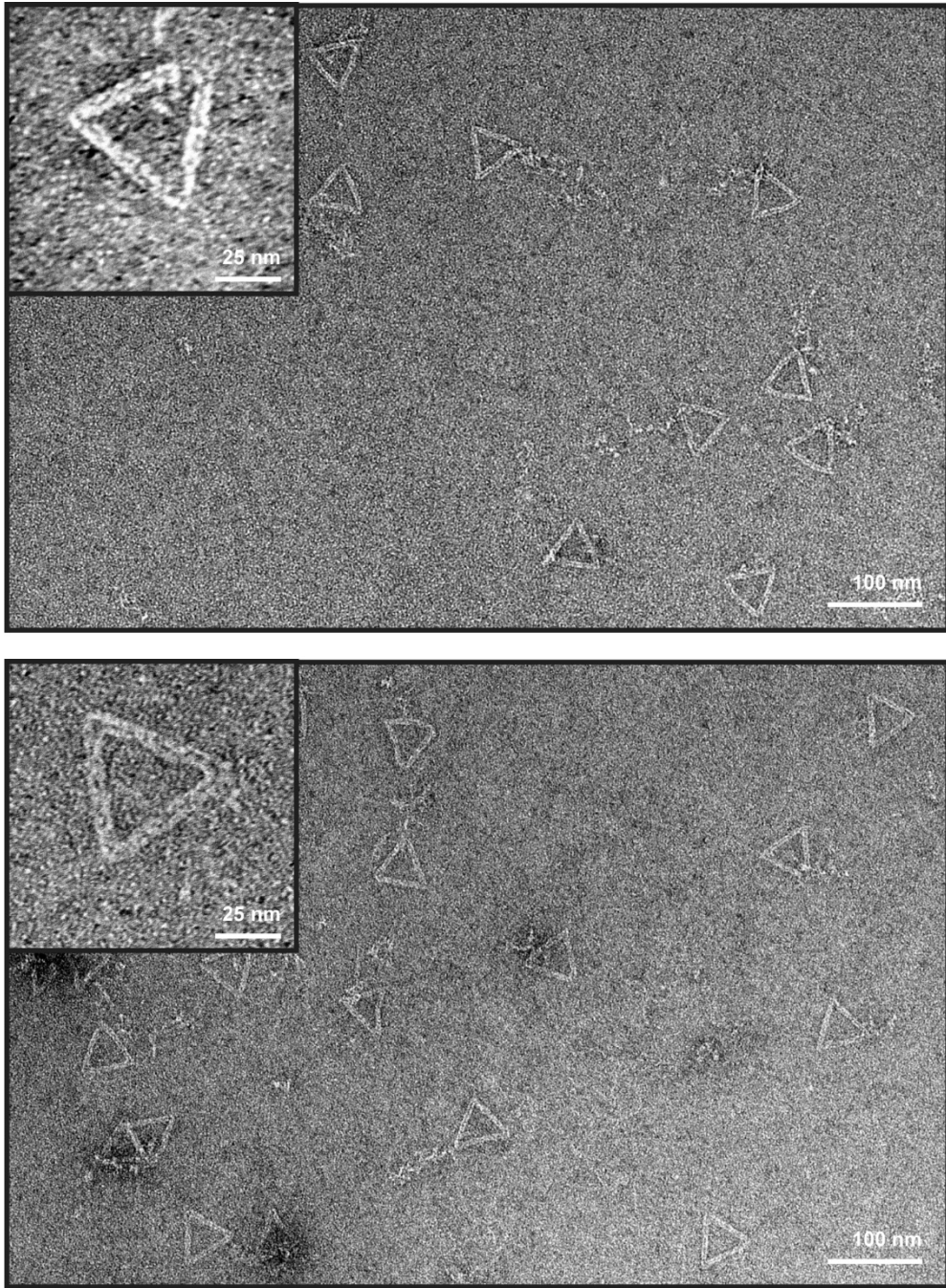
**Supplementary Figure 19** TEM imaging of DX-based hexagonal DNA origami of 74-bp edge-length without internal mesh.



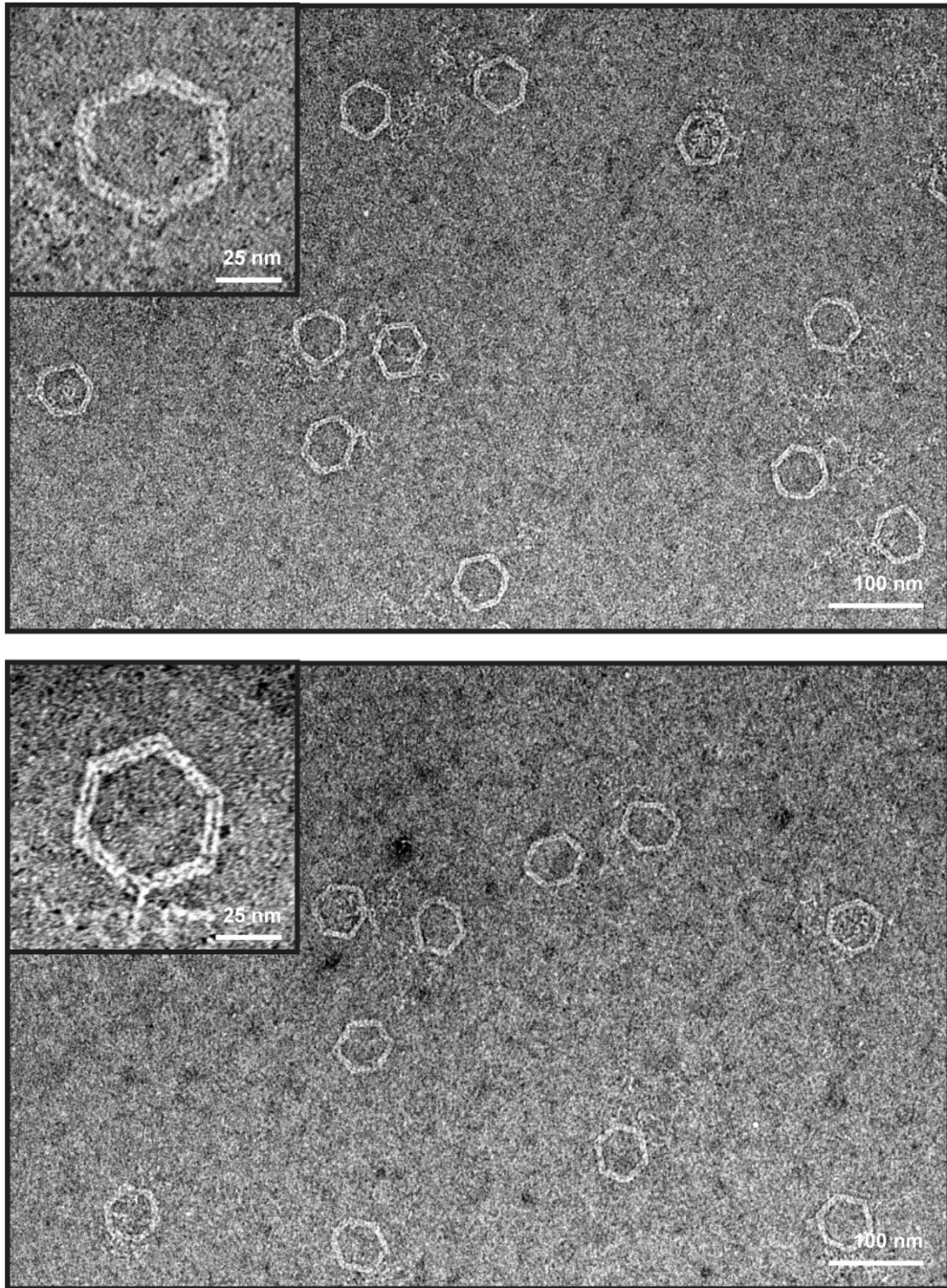
**Supplementary Figure 20** AFM imaging of 6HB-based triangular DNA origami of 128-bp edge-length without internal mesh.



**Supplementary Figure 21** AFM imaging of 6HB-based hexagonal DNA origami of 74-bp edge-length without internal mesh.

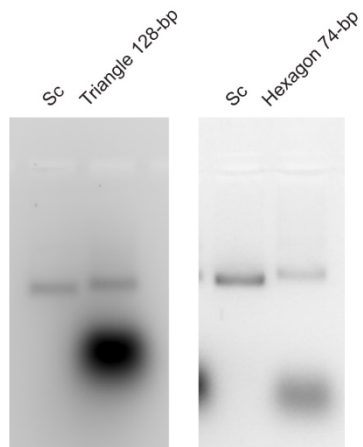


**Supplementary Figure 22** TEM imaging of 6HB-based triangular DNA origami of 128-bp edge-length without internal mesh.

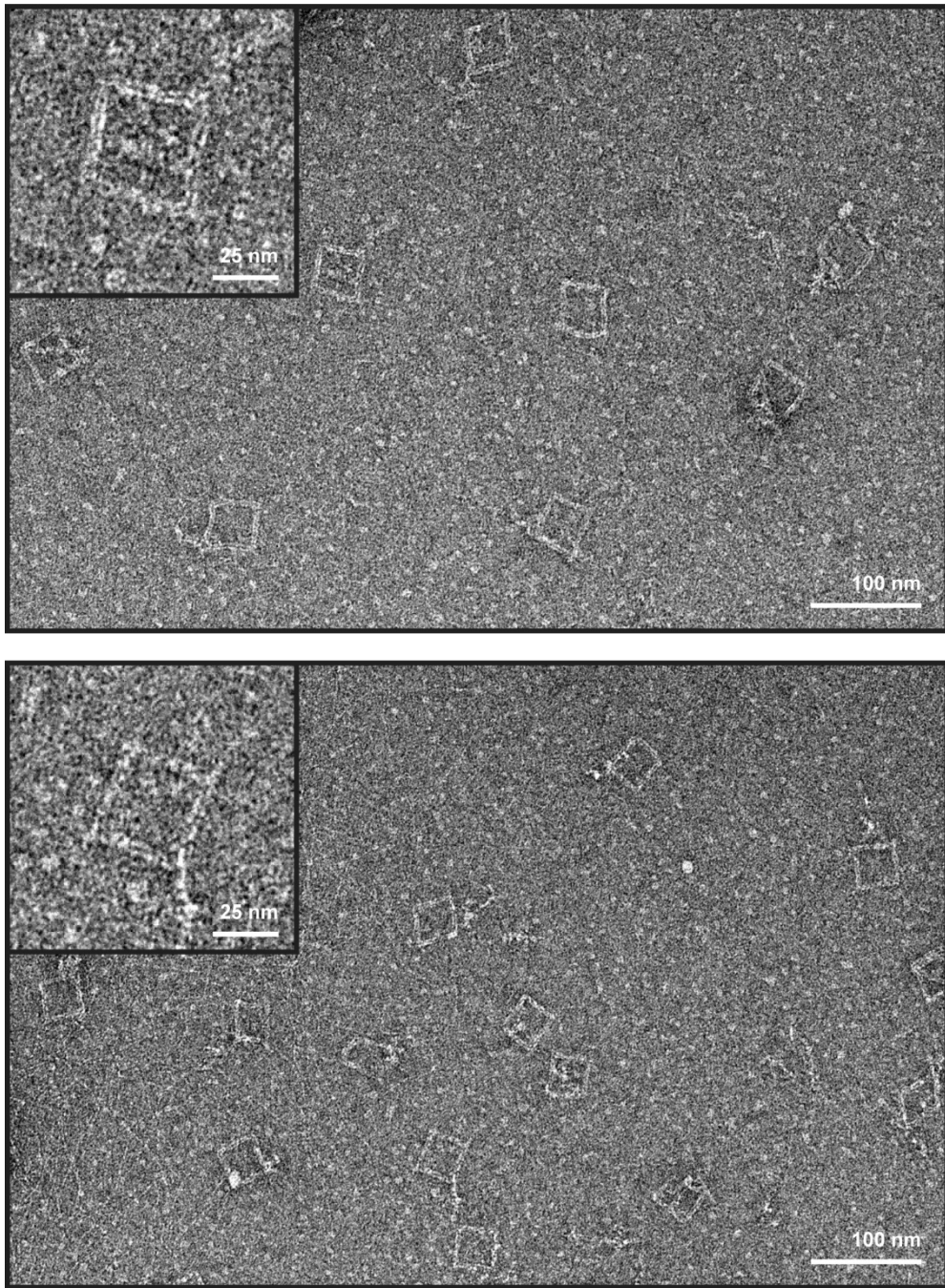


**Supplementary Figure 23** TEM imaging of 6HB-based hexagonal DNA origami of 74-bp edge-length without internal mesh.



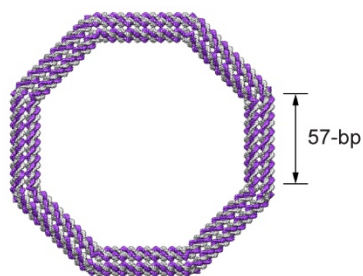


**Supplementary Figure 24** Agarose gel electrophoresis for 6HB-based triangular and hexagonal DNA origami objects without internal mesh.



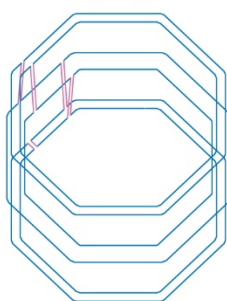
**Supplementary Figure 25** TEM imaging of 6HB-based square DNA origami of 105-bp edge-length without internal mesh.

6HB-based octagonal DNA origami



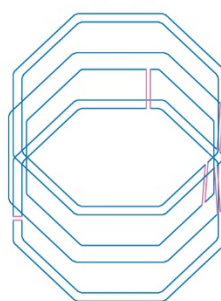
Atomic model

Design Type 1

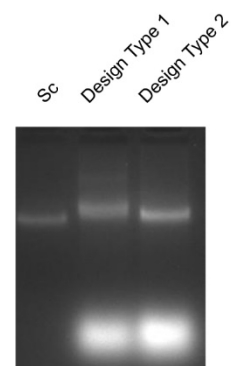


Scaffold routing

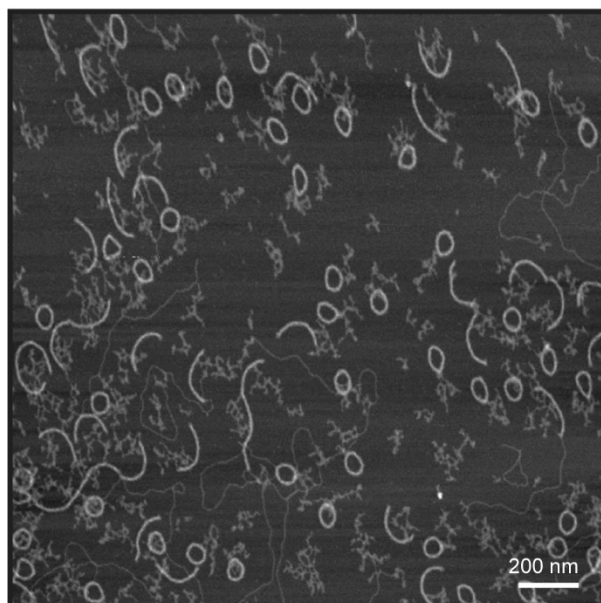
Design Type 2



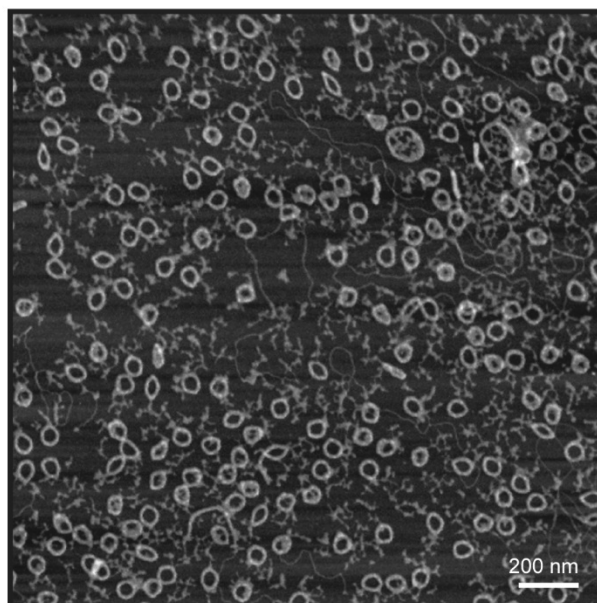
Scaffold routing



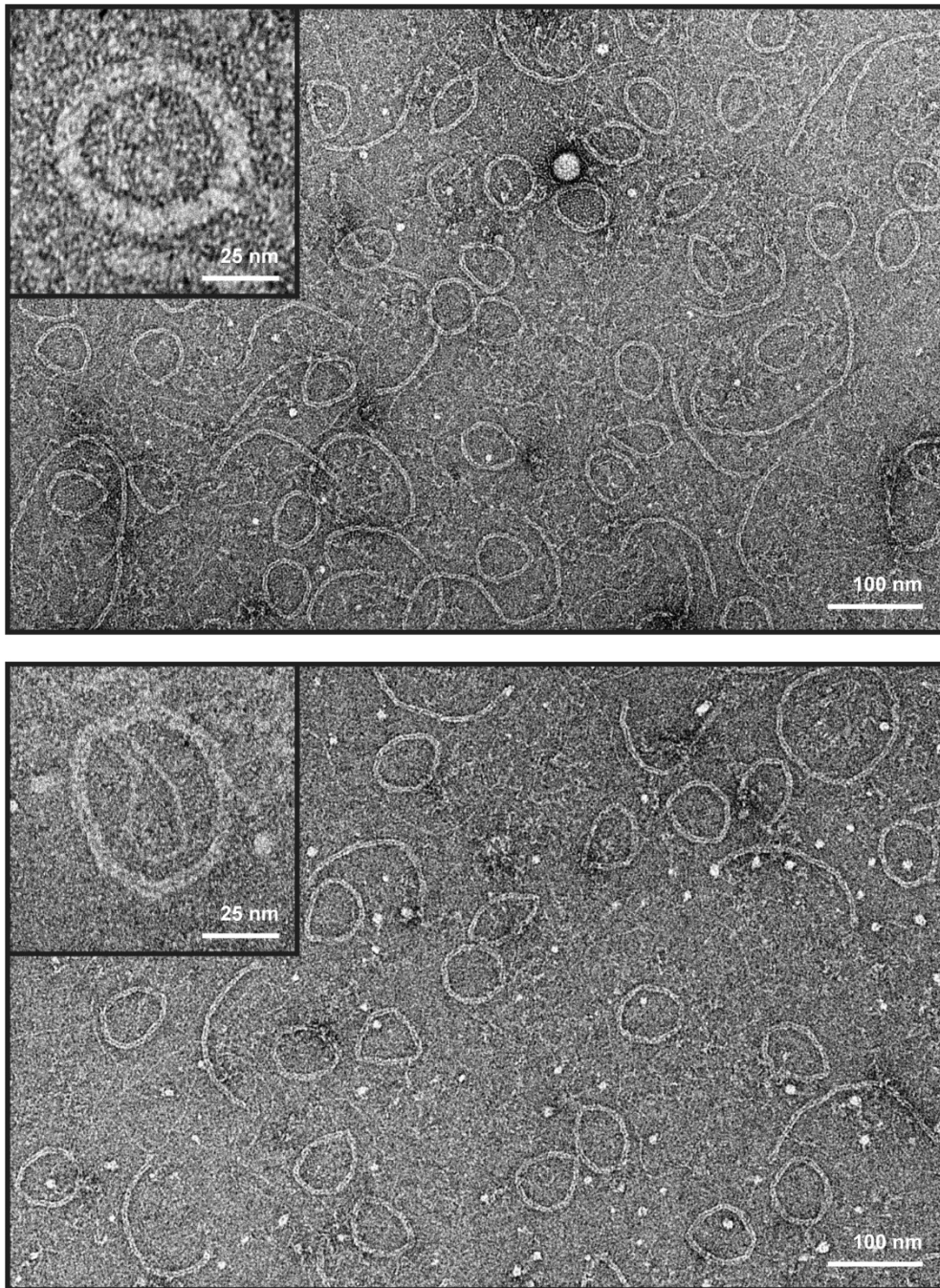
Design Type 1



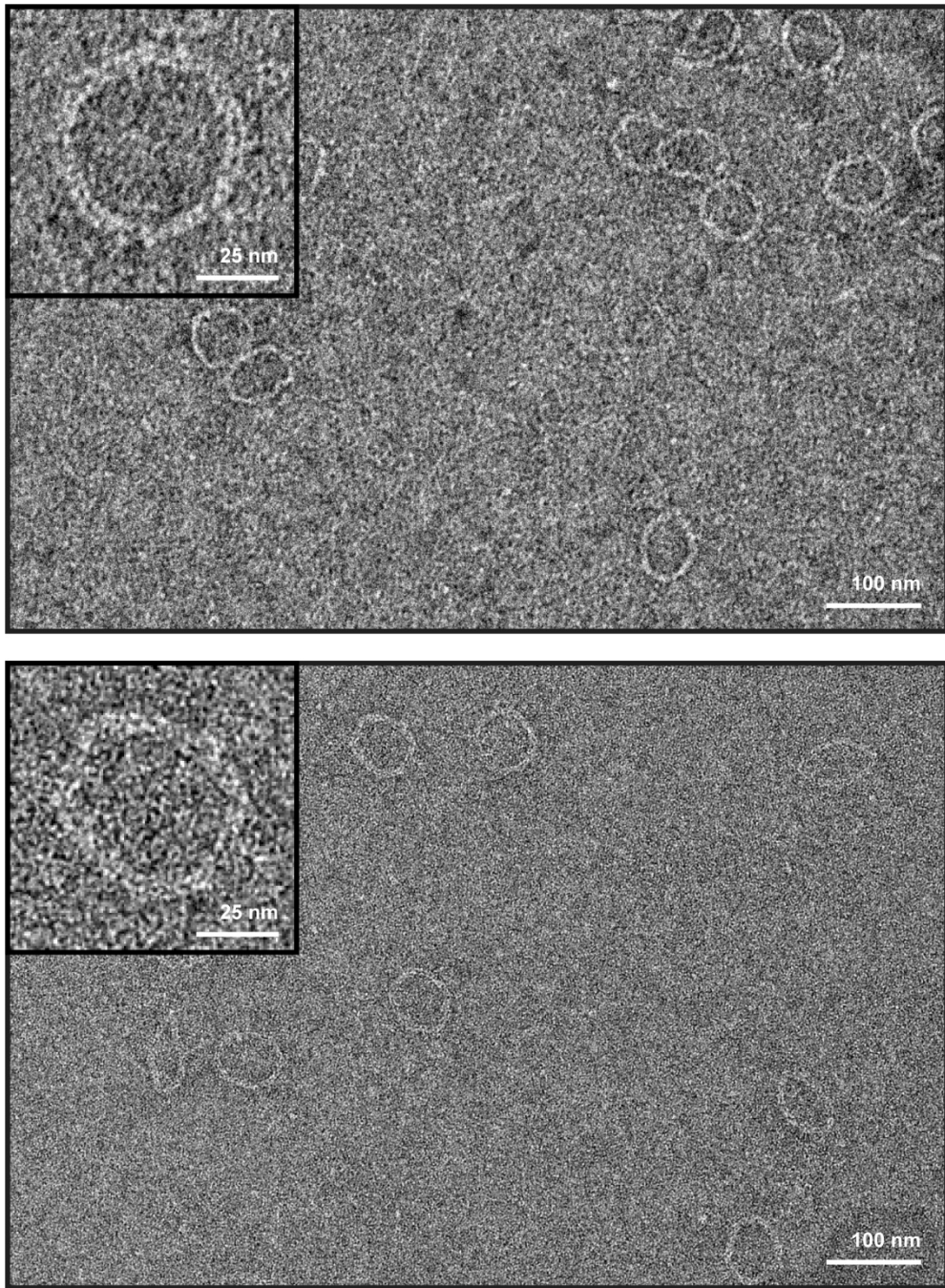
Design Type 2



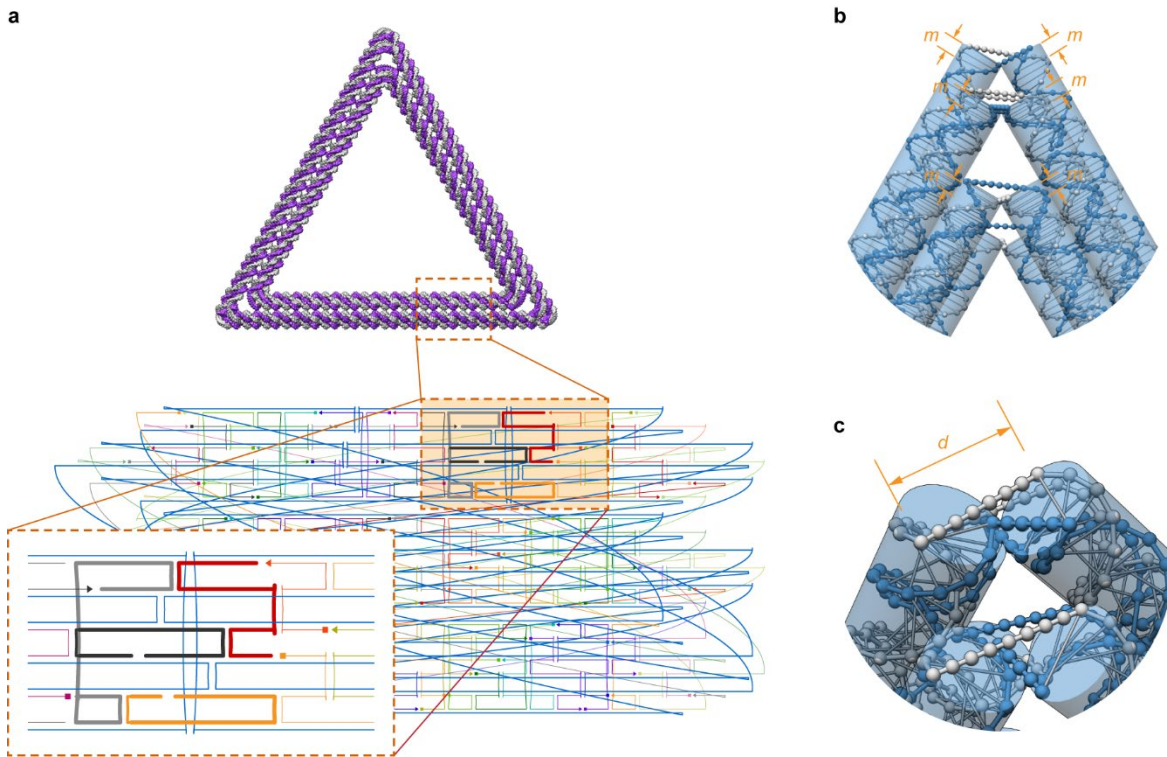
**Supplementary Figure 26** Two designs, agarose gel electrophoresis, and AFM imaging of 6HB-based octagonal DNA origami of 57-bp edge-length without internal mesh. All scaffold double-crossovers are located on the same edge in Design Type 1 versus distributed to different edges in Design Type 2.



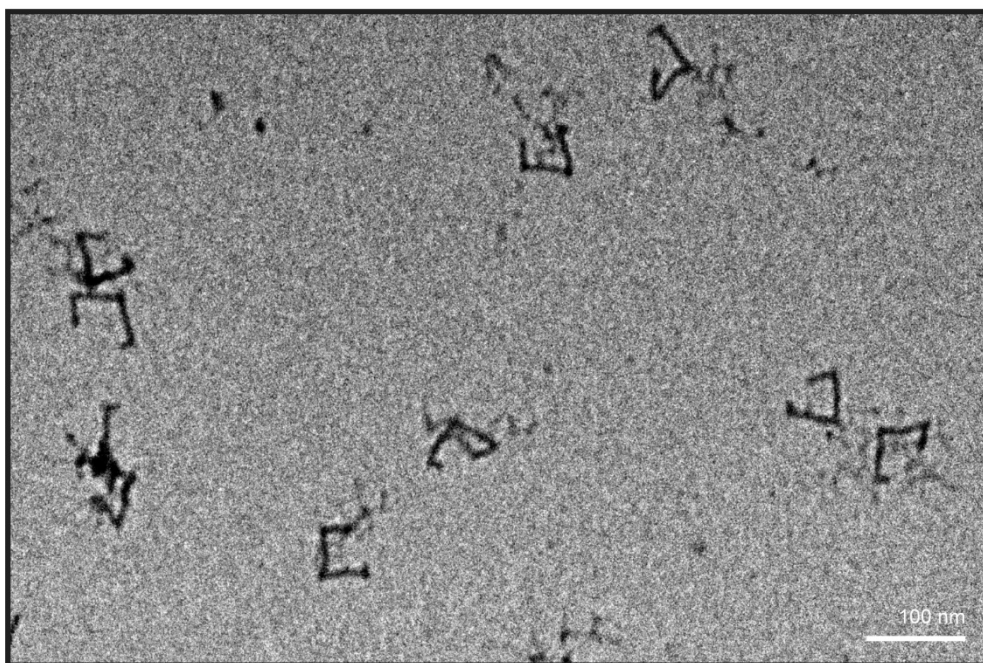
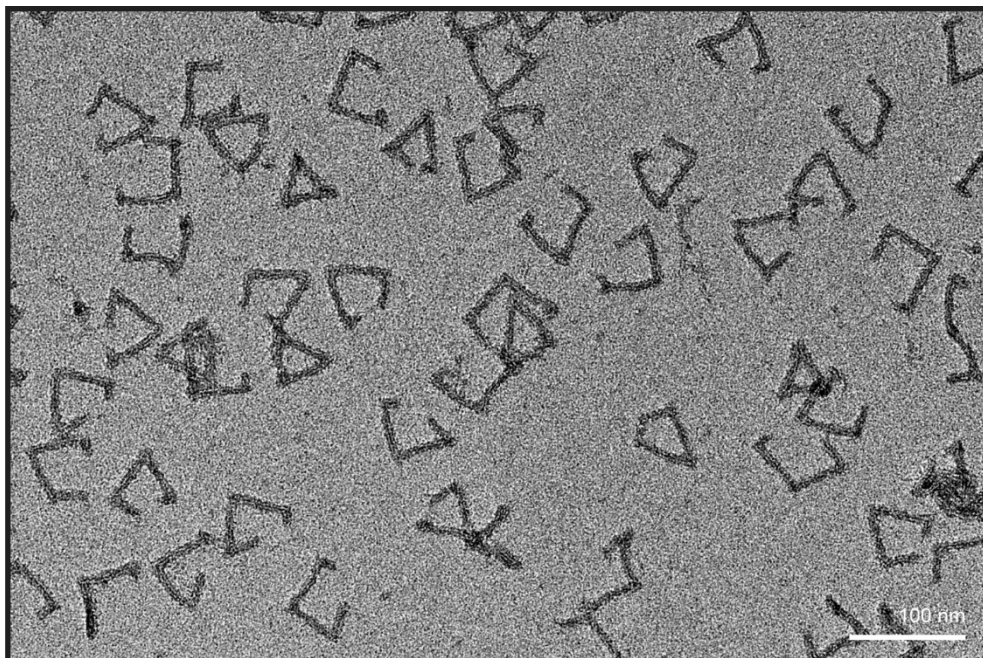
**Supplementary Figure 27** TEM imaging of 6HB-based octagonal DNA origami of 57-bp edge-length without internal mesh when using the Design Type 1 shown in **Supplementary Fig. 26**.



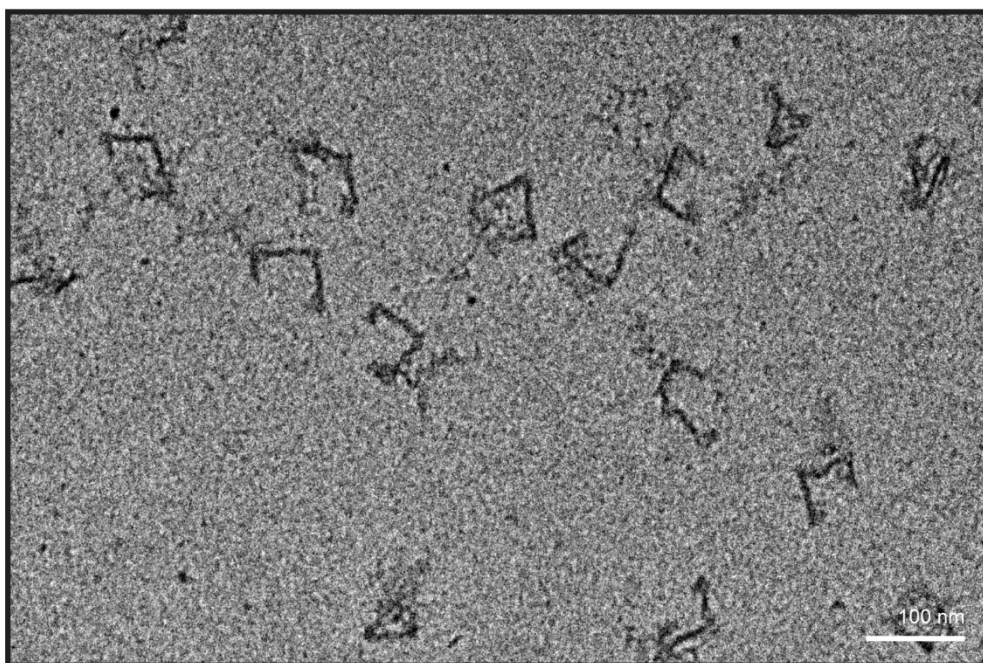
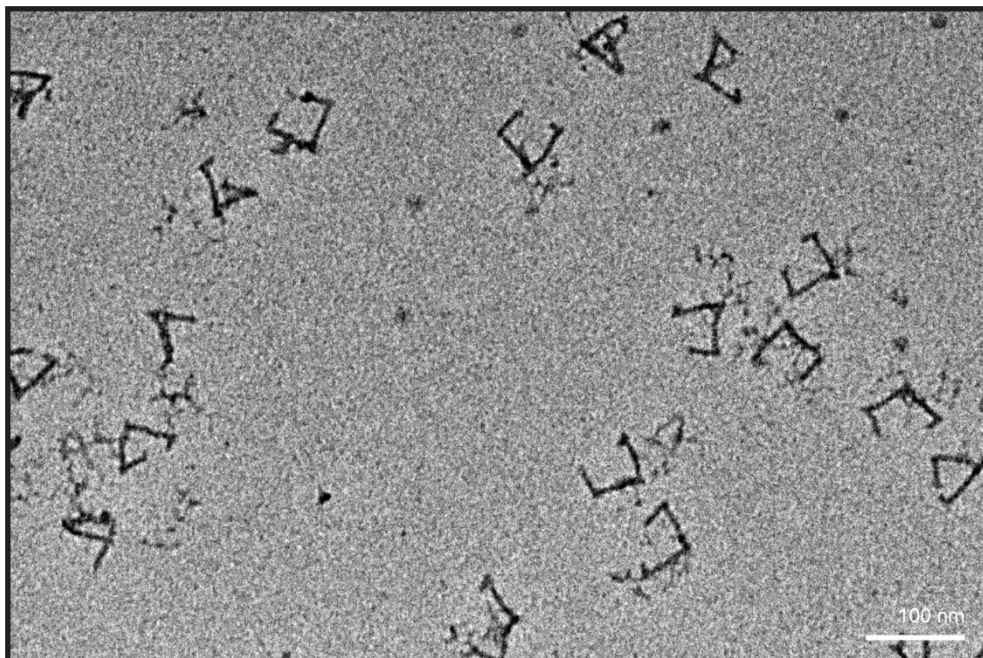
**Supplementary Figure 28** TEM imaging of 6HB-based octagonal DNA origami of 57-bp edge-length without internal mesh when using Design Type 2 shown in **Supplementary Fig. 26**.



**Supplementary Figure 29** 6HB-based open triangular DNA origami. **a** Four staples (gray, red, black and orange thick lines in the caDNAo map) on one edge of the triangle where three scaffold double-crossovers exists were removed. The stability of programmed internal vertex angles was evaluated by **b** reducing the mitered edge length ( $m$ ) by 2-bp and **c** changing the parameter to determine axial rise per nucleotide in both the scaffold and staple loop (the axial rise is calculated by dividing the distance ( $d$ ) by the design parameter).

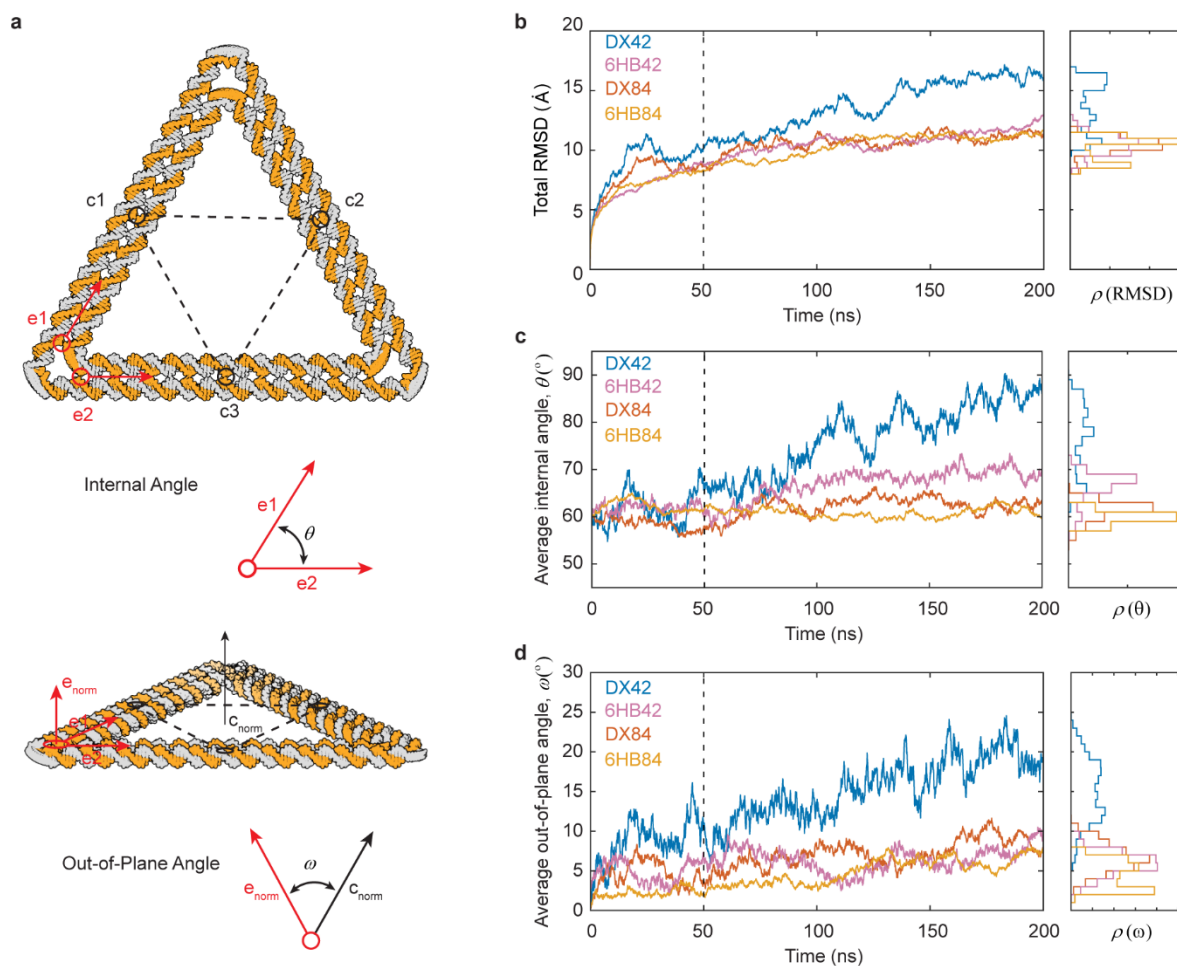


**Supplementary Figure 30** TEM imaging of the DNA open triangular object (Top) and with reducing the mitered edge length  $m$  (**Supplementary Fig. 26b**) as 2-bp (Bottom).

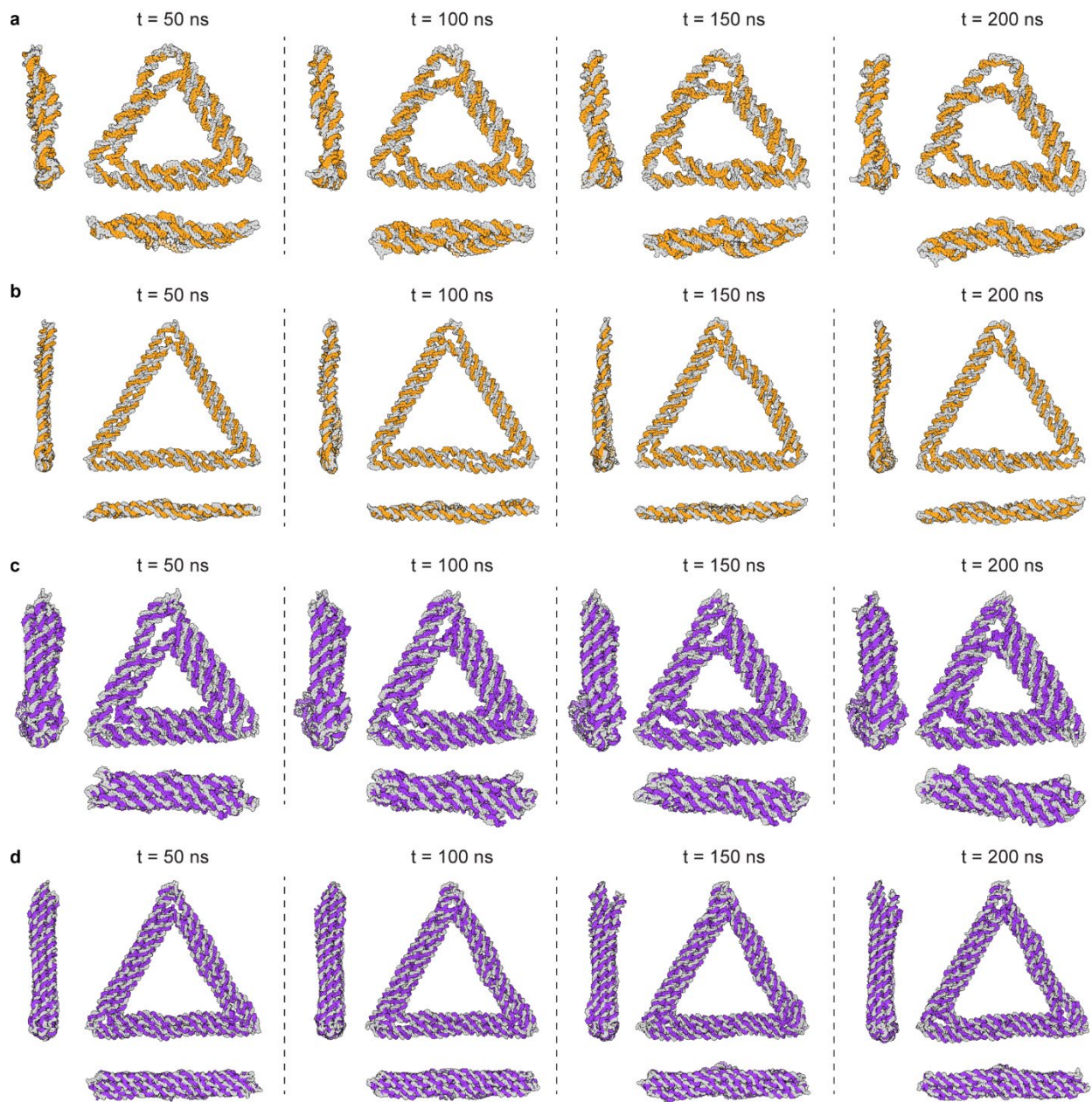


**Supplementary Figure 31** TEM imaging of DNA open triangles with the different number of unpaired nucleotides crossing the vertex. The number of unpaired nucleotides is calculated by dividing the distance  $d$  (**Supplementary Fig. 26c**) with the parameter 0.34 (top) and 0.55 (bottom).





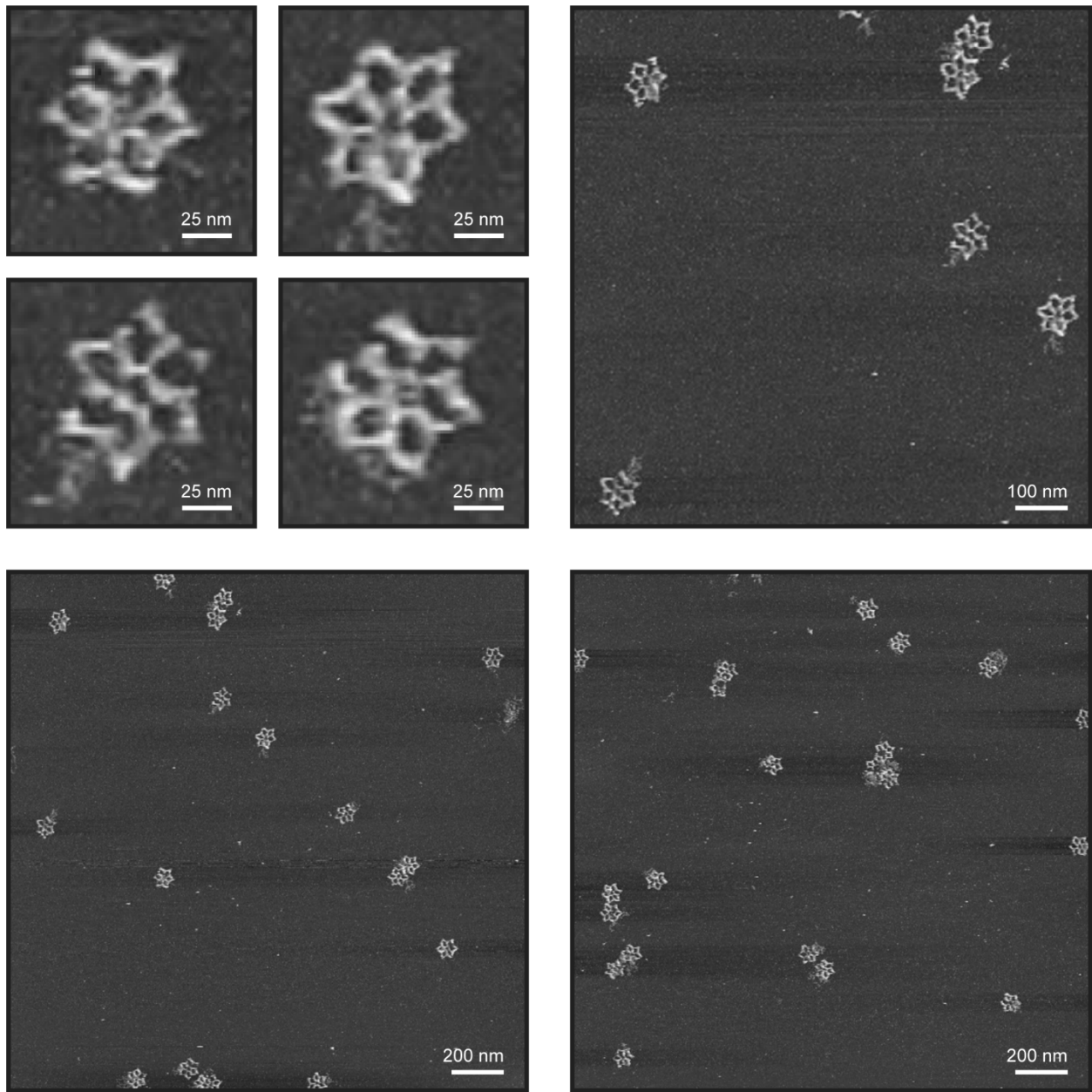
**Supplementary Figure 32** Molecular dynamics trajectory data. **a** Schematic illustrating the calculation of the (top) internal angles,  $\theta$ , and (bottom) out-of-plane angles,  $\omega$ , of a wireframe DNA origami object. **b** The total RMSD of each triangular wireframe object over 200 ns MD simulation (left), and a histogram of the total RMSD values after  $t = 50$  ns equilibration time. **c** The average internal angle,  $\theta$ , of each triangular wireframe object over 200 ns MD simulation time (left), and a histogram of the internal angles after  $t = 50$  ns equilibration time. **d** The average out-of-plane angle,  $\omega$ , of each triangular wireframe object over 200 ns MD simulation time (left), and a histogram of the internal angles after  $t = 50$  ns equilibration time.



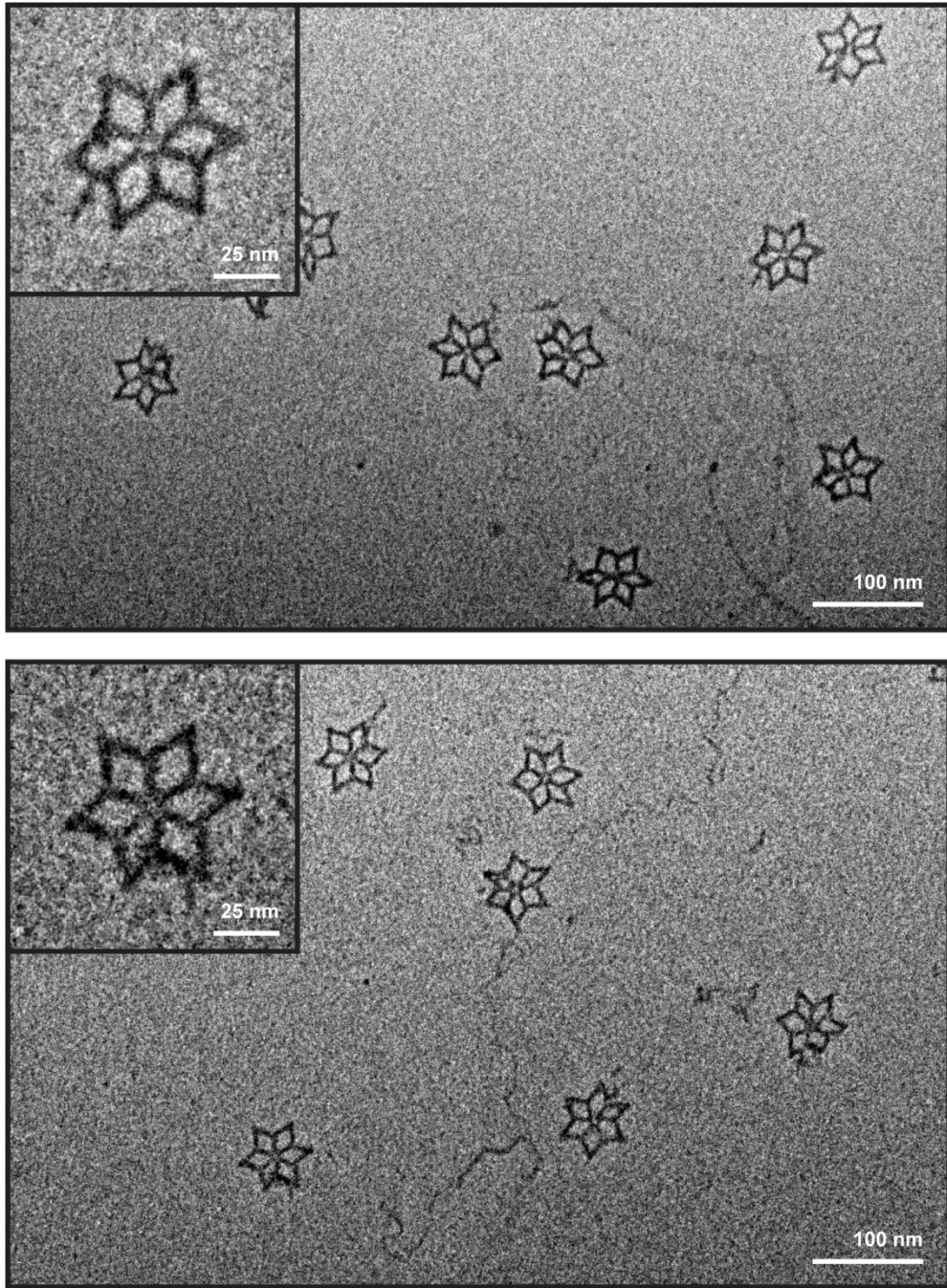
**Supplementary Figure 33** Instantaneous configurations of the triangular origami objects from MD simulations. **a** DX-based DNA triangular origami with 42-bp edge-length **b** DX-based DNA triangular origami with 84-bp edge-length **c** 6HB-based DNA triangular origami with 42-bp edge-length **d** 6HB-based DNA triangular origami with 84-bp edge-length.

**Supplementary Table 3** Design parameters for the 6HB-based star and curved beam DNA origami objects. # indicates the type of scaffolds in **Supplementary Table 4**.

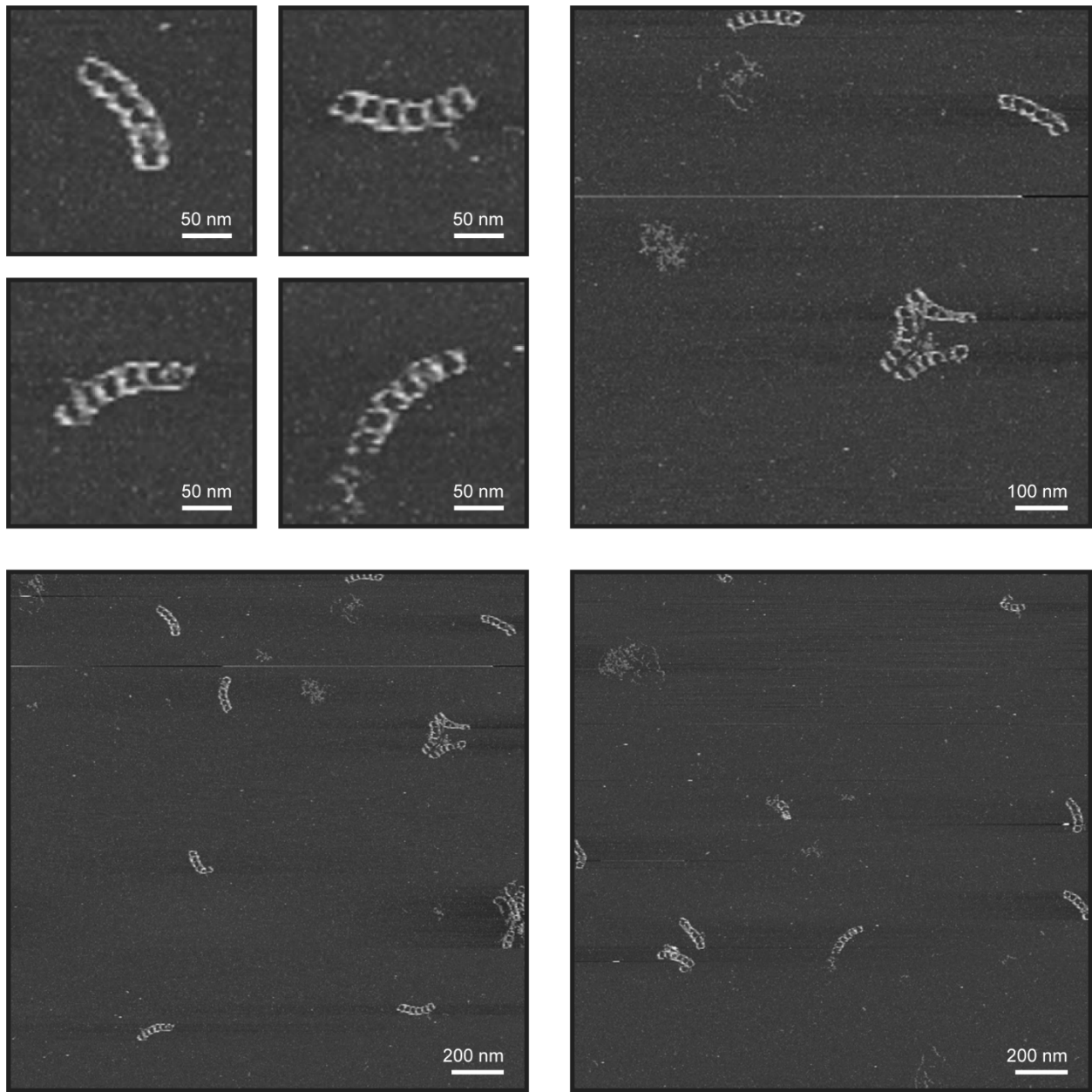
Target geometry	Edge length	Scaffold			Staples		
		Required length	# of double crossovers	# of unpaired nucleotides	# of staples	# of double crossovers	# of unpaired nucleotides
<b>Star</b>	42-bp	5,869-nt (#1)	20	295	128	184	374
<b>Curved beam</b>	42-bp	6,869-nt (#1)	20	331	154	211	392
<b>Hexagon with a hole</b>	42-bp	12,096-nt	59	198	282	361	1,128
<b>Circle</b>	42-bp	16,029-nt	74	863	364	427	1,258
<b>Quarter circle</b>	42-bp	11,354-nt	26	393	264	402	496
<b>Annulus</b>	42-bp	12,013-nt	35	573	265	376	767
<b>A-shape</b>	42-bp	13,831-nt	35	551	311	471	605
<b>G-shape</b>	42-bp	16,662-nt	41	690	375	561	791



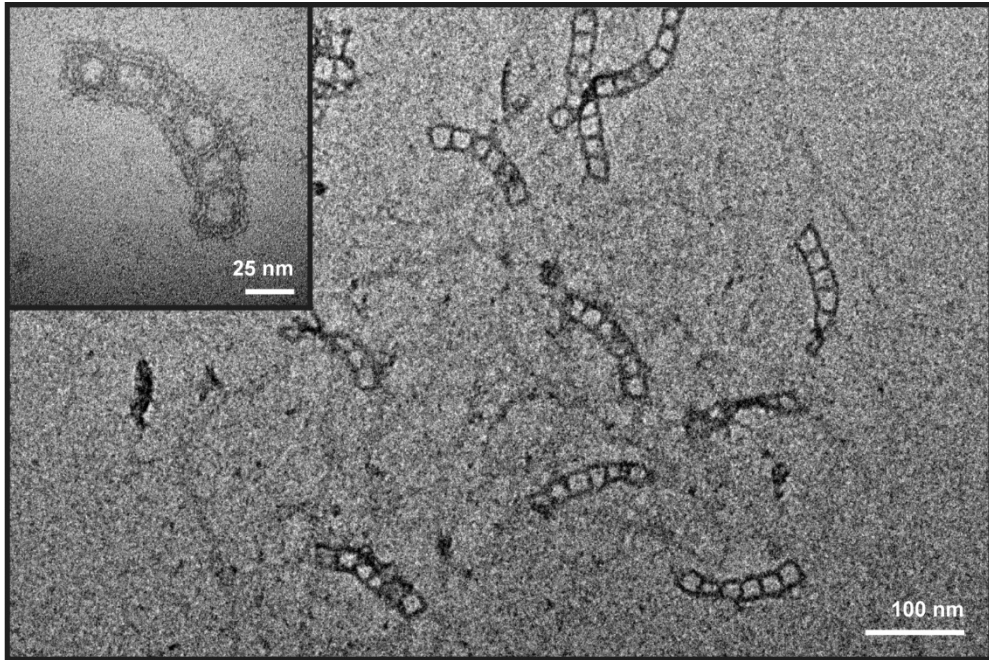
**Supplementary Figure 34** AFM imaging of 6HB-based star DNA origami of 42-bp edge-length.



**Supplementary Figure 35** TEM imaging of 6HB-based star DNA origami of 42-bp edge-length.



**Supplementary Figure 36** AFM imaging of 6HB-based curved beam DNA origami of 42-bp edge-length.



**Supplementary Figure 37** TEM imaging of 6HB-based curved beam DNA origami of 42-bp edge-length.

**Supplementary Table 4** Sequences for the 7,249-nt (#1) and 2,775-nt (#2) length scaffolds used.

No	Scaffold sequence
#1	<p>AATGCTACTACTATTAGTAGAATTGATGCCACCTTTTCAGCTCGCGCCCAATGAAAATATAGCTAAACAGGTTATTGACC  ATTTGCGAAATGTATCTAATGGTCAAACCTAACTACTCGTTCGAGCAATTGGGAATCAACTGTTATATGGAATGAAACTTC  CAGACACCGTACTTTAGTTGCATATTTAAAACATGTTGAGCTACAGCATTATTCAGCAATTAAGCTCTAAGCCATCCGCA  AAAATGACCTCTTATCAAAGGAGCAATTAAGGTTACTCTCTAATCTGACCTGTTGGAGTTTGCTTCCGGTCTGGTTCGCT  TTGAAGCTCGAATTAACGCGATATTTGAAGTCTTTCCGGCTTCTCTTAATCTTTTTGATGCAATCCGCTTTGCTTCTGA  CTATAATAGTCAGGGTAAAGACCTGATTTTGGATTATGGTCATTCTCGTTTTCTGAACTGTTAAAGCATTGAGGGGGAT  TCAATGAATATTTATGACGATTCGCGAGTATTGGACGCTATCCAGTCTAAACATTTTACTATTACCCCTCTGGCAAACTT  CTTTTGCAAAAGCCTCTCGCTATTTGGTTTTATCGTCTGCTGGTAAACGAGGGTTATGATAGTGTGCTTCTACTATGCC  TCGTAATTCCTTTGGCGTTATGTATCTGCATTAGTTGAATGTGGTATTCTAAATCTCAACTGATGAATCTTTTACCTGT  AATAATGTTGTTCCGTTAGTTCGTTTTATTAACGTAGATTTTCTCCCAACGTCCTGACTGGTATAATGAGCCAGTCTTA  AAATCGCATAAGGTAATCACAATGATTAAGTTGAAATTAACCATCTCAAGCCCAATTTACTACTCGTCTGGTGTCTTCT  CGTCAGGGCAAGCCTTATTCAGTGAATGAGCAGCTTTGTTACGTTGATTTGGGTAATGAATATCCGGTTCTTGTCAAGATTA  CTCTTGATGAAGGTGAGCCAGCCTATGCGCCTGGTCTGTACACCGTTCATCTGTCTCTTTCAAAGTTGGTCAGTTCGGTTC  CCTTATGATTGACCGTCTGCGCCTGTTCCGGCTAAGTAACATGGAGCAGGTCGCGGATTTGACACAATTTATCAGGCGAT  GATACAATCTCCGTTGACTTTGTTTCCGCTGGTATAATCGTGGGGTCAAAGATGAGTGTGTTAGTGTATTCTTTTG  CCTCTTTGTTTTAGGTTGGTGCCTTCGTAGTGGCATTACGTATTTACCCGTTAATGGAACTTCTCATGAAAAAGTCT  TTAGTCTCAAAGCCTCTGTAGCCGTTGCTACCCTCGTCCGATGCTGTCTTTGCTGCTGAGGGTGACGATCCCGCAAAAG  CGGCCTTAACTCCCTGCAAGCCTCAGCGACCGAATATATCGGTTATGCGTGGGCGATGGTGTGTTGTCATTGTCGGCGCAAC  TATCGGTATCAAGCTGTTAAGAAATTCACCTCGAAAGCAAGCTGATAAACCAGTACAATTAAGGCTCCTTTTGGAGCCTT  TTTTTGGAGATTTTCAACGTGAAAAAATTTATTTCGCAATTCCTTTAGTTGTTCCCTTTCTATTCTCACTCCGCTGAAACT  GTTGAAAGTTGTTAGCAAAATCCCATACAGAAAATTCATTTACTAACGCTTGAAAGACGACAAAACCTTAGATCGTTACG  CTAACTATGAGGGCTGTCTGTGGAATGCTACAGGCGTTGAGTTGTTACTGGTGACGAAACTCAGTGTACGGTACATGGGT  TCCTATTGGGCTTGCTATCCCTGAAAATGAGGGTGGTGGCTGAGGGTGGCGGTTCTGAGGGTGGCGGTTCTGAGGGTGGC  GGTACTAAACCTCCTGAGTACGGTGATACACCTATTCCGGCTATACTTATATCAACCTCTCGACGGCACTTATCCGCTG  GTACTGAGCAAAACCCGCTAATCCTAATCCTTCTCTTGAGGAGTCTCAGCCTTAAATACTTTTATGTTTTCAGAAATAG  GTTCCGAAATAGGCGAGGGGCTAATGTTTATACGGGCACTGTTACTCAAGGCACTGACCCCGTTAAACTTATTACCAG  TACTCTCTGTATCATCAAAGCCATGTATGACGTTACTGGAACGGTAAATTCAGAGACTGCGCTTCCATTCTGGCTTTA  ATGAGGATTTATTTGTTTGTGAATATCAAGGCCAATCGTCTGACCTGCCCTCAACCTCTGTCAATGCTGCGGCGGCTCTGG  TGGTGGTTCTGGTGGCGGCTCTGAGGGTGGTGGCTCTGAGGGTGGCGGTTCTGAGGGTGGCGGCTCTGAGGGAGGCGGTTCC  GGTGGTGGCTCTGTTCCGGTGATTTTATTATGAAAAGATGGCAAACGCTAATAAGGGGGCTATGACCAGAAATGCCGATG  AAAACGCGCTACAGTCTGACGCTAAAGGCAAACTTGATTCGTGCTACTGATTACGGTGTCTGATCGATGGTTTATTGG  TGACGTTTCCGGCCTTGCTAATGTTAATGGTGTACTGGTATTTTCTGGCTCTAATTCCTCAATGGCTCAAGTCCGTGAC  GGTATAATTCACCTTAAATGAATAATTTCCGTCATATTTACCTTCCCTCCCTCAATCGGTTGAATGTGCGCCTTTTGTCT  TTGGCGCTGGTAAACCATATGAATTTTCTATTGATTGTGACAAAATAAACTATTCCGTGGTGTCTTTGCGTTTCTTTATA  GTATTCCGTTATTATTGCGTTTCCCTCGTTTCTTCTGTAACCTTTGTTGAACTTTGTTGCGGCTATCTGCTTACTTTTCTTAA  AAAAAGGGCTT  CGGTAAGATAGCTATTGCTATTTTATTGTTTCTTCTCTTATTATTGGGCTTAACTCAATTCCTGTGGGTTATCTCTCTGAT  ATTAGCGCTCAATTACCCTCTGACTTTGTTAGGGTGTTCAGTTAATTCCTCCGCTCAATGCGCTTCCCTGTTTTTATGTTA  TTCTCTCTGTAAGGCTGCTATTTTCTTTTACGTTAAACAAAAATCGTTTCTTATTGGATTGGGATAAATAATATGG  CTGTTTATTTTGAACCTGCAAAATAGGCTCTGGAAAGACGCTCGTTAGCGTTGGTAAGATTACAGGATAAAATGTAGCTGG  GTGCAAAATAGCAACTAATCTTGATTTAAGGCTTCAAACCTCCCGCAAGTGGGAGGTTTCGCTAAAACGCTTCCGCTTCT  AGAATACCGGATAAGCCTTCTATATCTGATTTGCTTGCTATTGGGCGCGGTAATGATTCCTACGATGAAAATAAAACGGCT  TGCTGTTTCTCGATGAGTGGGCTACTTGGTTTAAACCCGTTCTTGGAAATGATAAGGAAAGACAGCCGATTATTGATTGGTT  TCTACATGCTCGTAAATAGGATGGGATATTATTTTCTGTTTCTGGAACTTATCTATTGTTGATAAACAGGCGGCTTCTGCA  TTAGCTGAACATGTTGTTTATTGCTGCTGCTGGACAGAATTACTTTACCTTTTGTGCGTACTTTATATTCTCTTATTACTG  GCTCGAAAATGCCTCTGCCTAAATTACATGTTGGCGTTGTTAAATATGGCGATTCTCAATTAAGCCCTACTGTTGAGCGTTG  GCTTTTACTGGTAAGAATTTGTATAACGCATATGATACTAAACAGGCTTTTTCTAGTAATTATGATTCGGGTGTTTATTCT  TATTTAACGCTTATTTATCACAGGTCGGTATTTCAAACATTAATTTAGGTGAGAAGATGAAATTAACATAAAATATATT  TGAAAAAGTTTTCTCGCTTCTTTGCTTTCGCGATTGGATTGTCATCAGCATTACATATAGTTATAAACCCAACCTAAGCC  GGAGGTTAAAAAGGTAGTCTCTCAGACCTATGATTTTGTATAAATTAATGACTTCTCTCAGCGTCTAATCTAAGCTAT  CGTATGTTTTCAAGGATTTAAGGGAAAATTAATTAATAGCGACGATTTACAGAAGCAAGGTTATTCACTCACATATTTG</p>





<p>TTTAAGGTCACATCGCATGTAATTTACTTATTCTCTGTTGTTGAGCCACCCGGGCGCCAGATTTTGTAAAGCTTTGTCTC  TTAGTTTGTATAGACAGATTTCAGAGTGCAAGGTTTCGTTTCGCTCGTACCTGGTTTTCCCTGGTCTTCACAGATAGGATTTG  ACTTTCTACAACCTTATGCGGCTTCTACCCGTTTGAAGGCCGATACAGGTGCTGCGCAAAATGCGGGCGAACATAGAGTA  TCAAAACAACGCCTTCTAATCTAGGAATATAGGGAAGATACGTATTTGCTACCATGCTTTCTGGGGTCATTAACGACCAACC  TCTTTTCTTTAAAGTAGGATTGCAACAATGAATGAATACACGTGGTCCGATAACTGACCAAGTAACATGGTTATCACTCGAT  GTCCGCCAGACGTGTGCAAACCAACCCGGGAGTTACGTCATAATCCTTCGCTACGTCGTGAAGATATTTACTTGTGAATAT  CGAGGGTAATAAGATAATAGACTGTGACTAGTATTGCCAGACTGTCGCTACCTGCAACACATAACTATCCTGAGGTTACTGC  ATAGTACTGATTACCCCGAGTCAAATTTCTAACCTTCTAACATGTACCTAGTAACAGCTCAATAATTATGTCAGAATATA  GCTCTGGGAACCTCGGACAATTATGATACACGGTATTAATATCTTGCTTGCCTTAGCCACTTCTCATCTTTGGATACCGAT  TCTATTTTGCATAGCAGTTCCTTTACACATATAAGAATTCGCCATAGGTATGACCTACCCAGATCGTCGATTATCTGCT  GGAAAATTTATTAACACTATGTTTCTCTCCAGATGTGAGTATACACGATAAATAATACCTGGTACCGTTGGTGTATTA  CCTTGTCTTAAGTGCTTAATCGCGCTTAGTGATAAGGTTGACTAGTCGACGCGTGGCCGCAATTATCTTGTGCATAAT  TTGACTTTGTTCTATATGACTATGATCTCTGTCATCTCACCTATTGATGCCACCTTTTCAGCCTGCAG</p>
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**Supplementary Table 5** Staple sequence for the DX-based square DNA origami of 84-bp edge-length. The sequence is represented by colors; unpaired nucleotides with blue, crossovers with orange, and the 14-nt seed dsDNA domain with green.

Staple ID	Length (bp)	Staple sequences
1	58	ATAACCATGAGTGTGGCTGGTTTATTGCTGCTCGGCCCTTCGGGCATAACACTGCGGC
2	58	ATACATTCAAATAGCGGTATTATCCCGTAAGTTCGCTATGTGGCTGTATCCGCTCAT
3	58	GGTTGAGTACTCATTAGATTGATTTAAATTTACTCATATATACTCCAGTCACAGAAA
4	54	CGCGGTTTTTTTTCCCCTATTTGTGATAAATGCTTTTTTTTAATAATATTGAA
5	53	TAAACGAATAGCCTCTCCATTTCCAAGAGTTTGAGGGGACGACGCGAAATGTG
6	53	ATCAGGGCGATGGCCACTTTTCGTGAACCATCACCTAATCAAGTTAATAG
7	53	GCTCATTTTTTAACCAATATTTGCCGAAATCGGCAAAATCCCTTATAAGATAG
8	53	AGAAAGCGAAAGGAGCGGGTTTGTAGGGCGCTGGCAAGTGTAGCGGTGTGAA
9	53	ACTGGTTTTTTTGAGGCGGATACGTGGGTCTCGTTTTTTTGGTATCATTGCA
10	53	GTGCCTTTTTTCTGATTAAGCATCTAGGTGAATTTTTTTATCCTTTTTGAT
11	53	AGTAATTTTTTATGCTGAAGAGAGCTGAATGATTTTTTTGCCATACCAAAC
12	52	GATCGGTTTTTAGGACCGAAGTTTCGCCCGTTTTAAGAAGGTTTCGGTCT
13	51	GCCGCTTTTTATACACTATTTGGCATGACAGTTTTTAAGAGAATTAACAAC
14	47	GTTTCTTAGACGTATACGCCTATTTTTATAGGTTAATGTTTCAGACCC
15	42	AACATTTCCGTGCGTTGCGCTCAGAATAAGTAATGAGTATTC
16	42	TTCCCTTTTTTGCTACAGGGCGCACATTAATTGTCGCCCTTA
17	42	GCCTTCTGTACCCGCGCGCTTAATGCGCGCGGCATTTT
18	42	CAGAAACGCTGCACGCTGCGCTAACCACTTTGCTCACC
19	42	CTTTTTTGCAACAGCGGTAAGATCCTTGAGAGGAGCTAACCG
20	42	ATCATGTAACTTACATCGAAGTGGATCTCAAAACATGGGGG
21	42	GTTGGGAACCGTCAGTTGGGTGCACGAGTGGGCGCCTTGATC
22	42	CCTGTAGCAAATGACGGGAAAGCCGGCGAACACCACGATG
23	42	TTGCGCAAACAGGGAGCCCCGATTTAGAGCGGCAACAACG
24	42	GAACTACTTACAGCACTAAATCGGAACCTAAATTAAGTGGC
25	42	CGGCAACAATTTTGGGGTCGAGGTGCCGTAATCTAGCTTCC
26	42	GCAAGAGCAAATCCAATGATGAGCACTTTTAATTGACGCCGG
27	42	GAGCCGGTGAAGAGTTGCAGGACCACTTCTGCGATAAATCTG
28	42	CCCTCCCGTATAAAGAAGCTGGACTCCAACGTAGATGGTAAG
29	42	TACACGACGGTGGAAACAAGAGTCCACTATTCGTAGTTATC
30	42	ACTATGGATGAAGGGTTGAGTGTGTTCCAGTAGTCAGGCA

31	42	CAGATCGCTG <b>AAT</b> CAAAAGA <b>ATAGACCGAGAT</b> ACGAAATAGA
32	42	AATTTAAAAG <b>GATTGGTAACTGTCAGACCAAGC</b> TTCATTTTT
33	42	TAACGTGAGT <b>TTGTACCCCGTTGTAATTCGCC</b> AAAATCCCT
34	42	TTTTCGGGGA <b>AATTCGACGAAAGGGCTCGTGC</b> AGGTGGCAC
35	37	CAATCAT <b>ATTCGTTCCACTGAGCG</b> CATGATAATAATG
36	31	AAAGGAAGAG <b>TAATTACATGCGATGTGACCT</b>
37	31	GACGAGCGTG <b>ACGTGGCGAGAAAGGAAGGGA</b>
38	31	GCACTGGGGC <b>CCAAAGGGCGAAAAACCGTCT</b>
39	31	AATCTCATGA <b>CGTTAAATTTTTGTTAAATCA</b>
40	26	CAACTTACTTCT <b>GAT</b> GCAGTGC <b>TGCC</b>
41	26	AGCATCTTACGG <b>ACT</b> CAGAATGACTT
42	26	GAGACAATAAC <b>CTT</b> TATTTTTCTAA

**Supplementary Table 6** Staple sequence for the 6HB-based square DNA origami of 84-bp edge-length. The sequence is represented by colors; unpaired nucleotides with blue, crossovers with orange, the 14-nt seed dsDNA domain with green, and the 4-nt dsDNA domain with red.

Staple ID	Length (bp)	Staple sequences
1	59	TGTTGTTCC <b>AAGT</b> TAATGCC <b>CCCTATGGCT</b> TTTTGATGATAC <b>AGGAT</b> ATAAA <b>CGTT</b> TGGA
2	59	ATCGTCACC <b>CAAAGGCT</b> CAAA <b>AGGTA</b> AATATTGAC <b>CGAAATTAC</b> CAAAA <b>AT</b> CAGCAG
3	59	TCAATAACC <b>TACTCAGGAGGTTTACACCACCCTCAGAGCCGCCACT</b> CACCG <b>TGTT</b> TAGC
4	59	<b>CTTA</b> TTTTTTGAAAACATAG <b>A</b> CATTATC <b>TTTTTTTT</b> TGCGGA <b>CTTA</b> ATT <b>TT</b> CACCAG
5	59	GACAG <b>AACGATCTGA</b> ATACACTAAA <b>AACTCATCTCATAGTTAGCGTAA</b> TCAAGTTTGC
6	58	TAGCGAGAGGCTTT <b>TTTAAGAAGTTTTGCCAGAGA</b> TACATAACG <b>TTTTTTTT</b> CAAAAG
7	58	ATTCTAAGAA <b>TTTT</b> GCGTTT <b>CCCCCTTTTT</b> TAA <b>CGATTATT</b> TTTGGCAGATT <b>CC</b>
8	58	ATTTAACAATTT <b>TTTTATTACGTTTTTTAATGGA</b> TCAATATA <b>TTTTTTTT</b> CCTGAT
9	57	GGGTAATTG <b>TTTT</b> TAATATCAGAG <b>AA</b> TAAAGAGCAAGA <b>TTTTTTT</b> ATGAAATAGCAAT
10	56	ACTTTA <b>CAC</b> ATT <b>GGG</b> AGGCCGATT <b>TTTT</b> TAGGGATTT <b>AGT</b> GAAAT <b>GAG</b> TT <b>CAG</b>
11	56	AATAGAT <b>GACCAGGT</b> AATAAAACGA <b>TTTTT</b> TAAACGGAACA <b>AA</b> TGAA <b>TAG</b> CGAAC
12	55	CTCAA <b>CC</b> CAGTACAA <b>ACTACG</b> GCATT <b>CCCTCGTTACCAGAGAGCAAC</b> AAAGTA
13	55	GATAAA <b>AGCCAGCAGCAAATA</b> AGGTG <b>GGAGGGTTGATATAAC</b> GCCAG <b>CA</b> TAA <b>CAT</b>
14	55	CGCTGC <b>GC</b> AGGCG <b>ATAGCGGGTTTTGC</b> TTGAT <b>ACCCTAAAACATCGCG</b> TCAGT
15	55	TTTGT <b>TGGGAAGCGCATTAGA</b> ACGGC <b>TAATTGCGAATAATAC</b> CGTCA <b>CT</b> CCTTAT
16	55	AGTAGG <b>GG</b> AAGTT <b>TAACAGTTTCAGCGGT</b> CACCA <b>GAATAAACAGCCAT</b> AAAATA
17	55	ACGAGT <b>AA</b> AGTTT <b>CAGCC</b> AATAG <b>GA</b> ACTT <b>CATAATTCAAAGCGAACCA</b> CTTTTG
18	55	TAGGTT <b>GT</b> GAGAA <b>GAGCAAATCAGATA</b> TAGAACG <b>CAATATATTTTAGT</b> CCCGAA
19	55	CTCCTT <b>ATA</b> AGCA <b>GAACAGAAATAAAGAC</b> GCGCA <b>GGTCA</b> CAAT <b>CAATAG</b> AGTTGC
20	54	TGACCT <b>TTTT</b> AATGGT <b>TGG</b> ACAGAT <b>TTT</b> GTGTAC <b>AT</b> AGAGCC <b>TTT</b> AGATAATA <b>AA</b>
21	53	GGGAAGAAA <b>TTTTTT</b> AGGAGCGGGCGCTAGGGCGCTGG <b>CGGTGGT</b> TCCTCAAG
22	53	AATGCAGGGGGTA <b>ACC</b> CAGCTACA <b>ATTTTATCCTGAATTTTTT</b> CAACGCTAA
23	53	AGTAA <b>ACC</b> GCCA <b>GAAGCAAAGCGGATTGCATCAAAA</b> TTTTTTAAGAGGAAG
24	53	TAGTATCAT <b>TTTTTTTT</b> TACAA <b>ATTTACCAGTATAAAA</b> ATAC <b>GG</b> GATTTT
25	53	AACAAAGCT <b>TTTTTTTT</b> CAGTGAATA <b>AGGCTTGCCCTGATT</b> GATT <b>CC</b> CTCAT
26	53	CCCAAT <b>AG</b> ATAAC <b>CA</b> TATCC <b>ATCCTTTTTTTT</b> AATTTACG <b>GA</b> AAGTCAGA
27	52	AGGTGT <b>AC</b> AGAAC <b>CGAAGA</b> ACTCAA <b>ACTATCGGCCTTGCTTTTT</b> TATCCAGAA
28	51	CAGACGT <b>TA</b> ACCTAAAACGA <b>TTTT</b> GCAAAA <b>AAAGTTTTGTTTT</b> GTCTTTC
29	51	CCTCAGA <b>ATT</b> AGTTT <b>GACCTTTT</b> ATACAT <b>CACCCTCAGTTTTT</b> CCGCCAC
30	51	TCAAACCCT <b>TTTTATATCTGGT</b> CAGTT <b>GGCAAATCAATACCA</b> ACTTATGC
31	51	AAACATGA <b>ATAAAT</b> CAAAAG <b>TTTT</b> CCCGA <b>GT</b> CGGAACCT <b>TTTTT</b> TATCTG

32	51	AGCTTGCTAGGCTTGCAGGGTTTTAAGGCCTAATTGTATTTTTGTTTATC
33	50	CGTTATTTATATAA CTTTTT CGCCTGTTTATCAACAATAGCAAGTCAAT
34	50	AAAATCTTTCATTAGTATTAACCAAGTACCGCACTCATTTTTACAAGCA
35	50	CATAGTAACGACGAAGCGCGTTTTTCATCAACGCCCAAGCGCGACTGTAG
36	50	GCAGCCTAATTGAGAGTTACAATAGCACCATTACCAA ACTTTCCATTAA
37	50	ATTAACTAACCACCCTGATA GTTCACAAACAATATTAGGATAAATCCT
38	50	ATAAGAAAATTGGGCTTCGAGCTCAAATCACCGGAGATAGCAATCCAT
39	50	GAGCCGCGTATAGCGGGCGGAGCTGAAGAAAAATTTGATTAGGCAGAA
40	50	ATTATCAATTTTTTGGAAACGAGGGTAGCACGGGAGTCGGCTGTCCGATTT
41	50	GCCGACACGCAGTATTTATTTTAGGCGAATTATTCACACGTAAATAGCCG
42	49	TGATTGCTTAACGTCAGTTTTTTTGAATATACAGTAACAGTCAGTTAAG
43	48	CCGCCACCCTCAGTTTTCCACCCTCAGAGCGTACCCTTCGCAAATGG
44	48	TCTGAATTTACCGTTTTGTAAGCGTCATA CGCCTATATAGGGTTGAG
45	48	AGGGCGACATTCATTTTTTGTAGGGAGGGAAGAGCCTTGCTTTTGCGGG
46	48	AGAATAACATGACTAAATAGAAAGGAACAATGGGAATTCCEAATCCA
47	48	TGCGGATGGCCA ACTAACCGTAACACTGAGTCTTATTAAAGCAA ACTCC
48	48	AACAGTGCCAATAGTAGCAGGCGGATAAGTGGAGGCAGAATACCGAAC
49	47	GGCGAAATCAAGTGATGATGGCAATTCAAACAGTCTGAAAGCGTA
50	47	CAACGGAATTATACGTAGCATTCCACAGAGACTGTTAAAAACCAAAA
51	47	AACGTCATCCACTAAGTAACAGTGCCCGGTGTACTAAATTAATTAC
52	46	GCTCCATGTTATAGAAAAGGCATTTTTCGAGCCTTTTGCATAGTAAA
53	46	CCATCACCCAAGTGGCGATGGTTGCTTTGACGCTTCTGAACATAAA
54	46	AGCTATCTTACCACGATAGCTTGATACCGATAAAATTCCAAGTT
55	45	ACAAGAGAAGGGCGTGGATTATACTTCTAGAAAA CGTAATAAGT
56	45	GCTTTCCTGGCCATGAATAACCTTGCTGGAATTAAAGCACTAA
57	45	CAATATTAGAGTCTGTCCTTTTTTTTTTCACGCAAACTCTCAAATA
58	45	CTTTAGCGTCA CAGCCCTTTGACCCCAAGCGGATTTGTTACGAGG
59	44	ACCATCGCCGAAGCCTAGATTTTCAGGTTTTGAATAATATGGT
60	44	GAATTTCCAATGAAACCATCGATAGCAGCACTTTT CAGTAGC
61	42	ATTCCTGATGTGAGACAGAGATAGAACCAGCACGTGAAAGCC
62	42	GAACAAGGTAGGA AATCATAGGTACCTTTTACATTTTTTAT
63	42	AACGTCACGTGATGTAATGCCACTACGAAGGCACCAAGTAAAT
64	42	CGGAACCGCCACCACCAATTCTGCGAACGAGTAGACCGCCAC
65	42	TCAATATATTATCATTTTTTGGGGTCGAGTGACGGGATAACGT
66	42	CCAGAA TTGAGACTCCGAAATCGGCAAAATCCCTTAAGTATT
67	42	TCACACGCTAAACAGGATTTAGCTAAAGGGAGC CAATCAGA
68	42	AACGGAAAGGTGGCAGTCAGTGCCTTGTAAAGAACAATAAT
69	42	TTACCAGCTTAAACAACCGATATATTCGGTCGCTGTTTCGAGG
70	42	TTTCATCAAAAATACACAAGAATATCGCAAGACA AAGTCCT
71	42	GGGAACCAATAAGGAAAGGTAAGTAACTTTGCGGCGTCATA
72	42	CGCGCCCAATAGATAGAACGCGAGAAAATATATGTTCCGGCT
73	42	TGAGGAATGACAAAGGCTCATTATACCAAGCAGGTCATGGA
74	42	AGAAACGATACATAATACCCAAAAGAACTTACCAAGTCAAAA
75	42	AACAAAGTGGCATGAACGTAGAAAATA CCAAAGACTACCTGA
76	42	CGAAAGACTGAA CCAATGTAGAAACCAAGAACGGAAGGTGA
77	42	CATTCCATCAATAAAATTA ACTGAACA CAGCATCCACGTTG
78	42	CTTTGAGAAAAACATAACGTCAAAAATGTTATTTATAGAGCC
79	42	GCTAAACTTAGCA AAGCCTAATTTGCCAATCGCCAGCTCAAC
80	42	ACGGGT AAGCCAACTATTTAACAACGCCTTTCCAGGCGCGGA
81	42	CGAGCGTCAACATGTAA TTTTTTTTTTAGGCAGAACCTGTT
82	42	GGACATTTGTTAGCCGATTTAGAGCTGTGCCGTTATCAT
83	42	CTCCCGATCTGTC CCGACCGTGTGATAGAACTGAA CAGGTA
84	42	GAAAGATGCGGAA TGAGGTTTTGAAGCACCGACACGTTAAA
85	42	ATAAAGTTAAATCTAGCGTCCAATACTTCATCAGATCATAA

86	42	TAAGAA <b>TACGGT</b> <b>CATTGAGATT</b> <b>AGGAAG</b> ACTGG <b>AA</b> AGATTA
87	42	ATGTTT <b>AT</b> ACCAC <b>AGGAACGAGGCGCAGAA</b> ACAC <b>CA</b> GAGAAT
88	42	GTTGCT <b>AA</b> GTAAT <b>AGGAATCATAATT</b> <b>ACCTTAGCCT</b> TCAACT
89	42	TTATTT <b>GTTT</b> CAAT <b>TACCACGGAATAAGT</b> GTTAGC <b>AA</b> TTAAGA
90	42	GAATATAATGA <b>AC</b> ACTATCATGGATTAGAGAG <b>TT</b> TAATTGCT
91	42	AAATAT <b>GTT</b> AGAG <b>CACCTTTAATTGCT</b> <b>CGACCGGAG</b> CGTTTG
92	42	TTTCAG <b>GACC</b> AGAG <b>GATATCGCGTTTTAATT</b> GAGAT <b>TC</b> ACCAGA
93	42	ATAAC <b>AGC</b> GAGAA <b>AGGTTTAATTTCAACA</b> CTTCA <b>ACC</b> ACCAC
94	42	CCCGAAA <b>GTT</b> AATCAT <b>TTTTTTTT</b> GTGAATTA <b>CA</b> TCAACGT
95	42	AGAAAA <b>AGA</b> ATGA <b>CGACGCTCAATCGT</b> <b>CACAGGAA</b> ACAAC
96	42	AAAAC <b>GAT</b> CTACG <b>TCGCATAGGCTGGCT</b> GAGCAC <b>TC</b> GGTACG
97	42	CCAGAA <b>TAC</b> ATTT <b>TCATAAATCAAAAAT</b> T <b>CAGGACAT</b> CAAGA
98	42	AATAC <b>CTC</b> TGAG <b>ATAAAATATCTTTAGG</b> ACCTT <b>CG</b> TTGGGA
99	42	GTAAT <b>CTG</b> TTAT <b>CAGT</b> TTTTT <b>ATAATAAA</b> AC <b>CT</b> TACCCT
100	42	GATTTT <b>AAT</b> AGT <b>CACCATTGCAACAGGAC</b> AGTGA <b>GA</b> AGGAAT
101	42	GACTAT <b>TAGA</b> ACT <b>GAACCGGATATT</b> <b>CATCAGTTGAG</b> CCACCG
102	42	TATATTT <b>GCTGA</b> <b>ATAACCGTTGTAGCACT</b> GAGT <b>AA</b> CCACCA
103	42	CACTT <b>GCA</b> TACTT <b>CCTAAAGCATCACCTT</b> CATTT <b>GC</b> CGGAAT
104	42	TCTACT <b>ACG</b> CTGA <b>GACAGAGGTGAGGCGC</b> ATTAA <b>AG</b> TCAGAC
105	42	AGAAG <b>GAA</b> ATCCT <b>CCTTTAATGC</b> <b>CGGAAC</b> ACCC <b>CG</b> CGGTCA
106	42	GTTTG <b>ATA</b> AGTGT <b>ACGCGCTTAATGCGCT</b> ATTAGT <b>AT</b> TAAAG
107	42	TGAATGG <b>CCG</b> CTACAGG <b>TTTTTTTT</b> CGCGTACT <b>AG</b> AAAGGAA
108	42	GCGGG <b>GAC</b> CCAGT <b>AATCGTCGCTATTAAA</b> AGAA <b>AG</b> TATTAG
109	41	<b>CAATTTTT</b> <b>ACTCGTATTAAATCCTTT</b> <b>GTAATTTCT</b> GTTCAG
110	41	AATATT <b>CC</b> ATTAT <b>TCCA</b> ACTTT <b>GAAAGAT</b> GAAAT <b>AA</b> GACGA
111	40	CTAAT <b>GCA</b> GAAAG <b>GCTTAGATTAAGACGCGG</b> TAAATTTAAA
112	40	ACAAAA <b>TA</b> ATTG <b>CGCTTTTTAAGAAAAGT</b> TAATGACAACA
113	40	TGCAAATCCAT <b>GTGAGAGACTACCTTT</b> TATCA <b>AT</b> CATTAC
114	40	GAGGAAACGCG <b>TGGAAGGGTTAGAAC</b> AGATG <b>AA</b> TATAAA
115	39	AATAAGAAAT <b>TCGACTTGAGCCAT</b> <b>TCTAAAGGA</b> CAGAGG
116	39	AACAGGTCAA <b>ATCGGT</b> CATAG <b>CCCTTC</b> GTCA <b>AT</b> GT
117	39	GAACCACCAT <b>AATTGACAGGAGGT</b> <b>TCCGTCGAC</b> ATCAAT
118	39	AGCAAAA <b>AGT</b> GAG <b>AGACTTTTT</b> CAT <b>GAGCTTTT</b> ACAGAG
119	39	CCATCT <b>TC</b> CATGT <b>AAGTACGGTGTCTGGG</b> TGGTCATTTT
120	39	GATTGG <b>CT</b> CAGT <b>CTAGCATTGCC</b> <b>CAGCG</b> ACC <b>GCCTGC</b>
121	39	<b>GAAATATCATCGCCTGATAAATTTTT</b> AAATCCGCGACCT
122	39	ATCGGAACCA <b>ACCACCAGAAGGAGCT</b> CTGTAA <b>ATAAA</b> AG
123	39	<b>TGTTAAAAACCGTCTATCAGGGTTTT</b> CCCACTACGTGAA
124	39	TTTAACGGGA <b>CTGAAACAACATCAGA</b> AATA <b>ATG</b> ACTCC
125	33	AGCC <b>GCGGG</b> GAGAAACA <b>TTTTTTTT</b> GGATT <b>CGCC</b>
126	27	AGAATACGTGGC <b>TTTTTT</b> CAATATTTT
127	26	CGACA <b>TTTTTT</b> TAAACA <b>CAAT</b> CTTC
128	25	AGTTTGAG <b>TC</b> GATAG <b>CTT</b> TATCCGGT
129	23	GCAAAA <b>GCT</b> ACCA <b>TA</b> AGGAAACC
130	23	AGTGA <b>ATTTT</b> AAC <b>CA</b> ATGCTGA
131	20	CCTCAG <b>AGC</b> CTCCCTCAGAG
132	20	AAGAG <b>GCG</b> GAAAGCGCAGTC
133	20	TGAAT <b>TC</b> GCCAAAGACAAA

**Supplementary Table 7** Staple sequence for the DX-based pentagonal DNA origami of 84-bp edge-length. The sequence is represented by colors; unpaired nucleotides with blue, crossovers with orange, and the 14-nt seed dsDNA domain with green.

Staple ID	Length (bp)	Staple sequences
1	58	GAAGATCAGTTGGT <b>TGCGCTCGGCCCTTCGTTGCAGGACCACTTC</b> GTGCACGAGTGGG
2	58	TATTCCTTTTT <b>CATTGGTAACTGTCA</b> GTGCCTCACTGATTAAGGCCGCATTTTGCC
3	58	AGACAAAGCTTAA <b>ATAACCCTGATAAAATGATCCGCTCATGAGACA</b> AAACAAAATCTGGC
4	58	ATCCTTTTTGATA <b>TGTGAAGAACCAGGGAAAAGTCAAATCCTATC</b> ATCTCATGACCAA
5	58	GCCCCGAAGAACG <b>GGGGGATCATGTA</b> ACTTTTT <b>TGACAACAT</b> TTTTTCCAATGATG
6	54	CAACAG <b>TTTTTT</b> CGGTAAGAT <b>CT</b> TCTGCTATGT <b>TTTTTT</b> GGCGCGGTA <b>TGA</b> ACC
7	54	TGCAC <b>TTTTTTTT</b> TGAATCTGT <b>CA</b> ACAACAGAGA <b>TTTTTT</b> AGTAAATTACATG
8	53	AACTA <b>TTTTTT</b> ATGAACGAA <b>AT</b> TTAGATTGAT <b>TTTTTT</b> AAAACCTCATTTT
9	53	TACT <b>TTTTTT</b> ACAACGATC <b>GG</b> AGCTGAATGA <b>TTTTTT</b> CCATACCAAACGA
10	53	TCCCG <b>TTTTTT</b> ACAATTAAT <b>AT</b> AAATCTGGAG <b>TTTTTT</b> GGTGAGCGTGGGT
11	53	TACGC <b>TTTTTT</b> TTTTATAG <b>GT</b> GGTTGAGTAC <b>TTTTTT</b> ACCAGTCACAGAA
12	53	ATGAG <b>TTTTTT</b> ATTCAACAT <b>TT</b> CACCCAGAAA <b>TTTTTT</b> CGCTGGTGA <b>AG</b> ATCT
13	50	<b>CGCCCGC</b> ATTT <b>TGCGCAGTTTT</b> TGAT <b>CGGCCTTCAAACGGGT</b> AG <b>AC</b> CT
14	50	<b>TAGGGCGCTGGCAAGTGT</b> TTTT <b>GTCACGCTGCGCGTA</b> ACCACC <b>ACC</b> GTGA
15	50	<b>CGTCAGACCCCAATCAT</b> TTTT <b>CCCCGTTGTAATTCGCGTTAAAC</b> AGGC
16	50	<b>GGGTTGAGTGT</b> TGTTCCATTT <b>GGAACAAGAGTCCACTATTA</b> AG <b>TA</b> AGCT
17	50	<b>TTTTGGGGT</b> CGAGGTGC <b>TTTT</b> AGCACTAAAT <b>CGGAACCTAAAGC</b> AACT
18	42	GCCTCTCCAC <b>CGCGTTGCGCTCTAGA</b> AGGCG <b>TT</b> AAACGAATA
19	42	AGGGGACGAC <b>GGCTACAGGGCGCACATTA</b> AT <b>TC</b> AAGAGTTTG
20	42	CGAAAGGGCC <b>TACCCGCCGCGCTTAATGCGC</b> ACGAATT <b>TCGA</b>
21	42	TGACGCCGGG <b>CCTTTTCGGGGAAATGTGCGCGT</b> ATCCCGTAT
22	42	CGGTCGCCGC <b>ATTTCTTAGACGTCAGGTGGCA</b> AGAGCAACT
23	42	TCAGAATGAC <b>TTTAATGTCATGATAATAATG</b> GTACACTATTC
24	42	ACAGTAAGAG <b>ATGGCGAGAAAGGAAGGAAGAG</b> GATGGCATG
25	42	GCTGCCATAA <b>CGACGGGGAAAGCCGGCGAACG</b> ATTATGCAGT
26	42	AACACTGCGG <b>CGGAGCCCCGATTTAGAGCTT</b> CATGAGTGAT
27	42	GTTGGGAACC <b>GGAGGACCGAAGGAGCTAACCGC</b> GCCTTGATC
28	42	TGTAGCAATG <b>GGGCGATGGCCACTACGTGA</b> ACCACGATGCC
29	42	GCGCAAATA <b>TGGGCGAAAACCGTCTATCAGC</b> AACAACGTT
30	42	ACTACTTACT <b>CAACGTGGACTCCAACGTCAA</b> ATAACTGGCGA
31	42	TTTATTGCTG <b>AGACTGGATGGAGGCGGATAA</b> AGGCTGGCTGG
32	42	CGAGCGAACG <b>AGAAGCCGCATAAGTGTGTAGA</b> AACCAGGTA
33	42	TGGGGCCAGA <b>TCGGCAAAATCCCTTATAAATC</b> ATTGCAGCAC
34	42	CCCGTATCGT <b>ATTTTAACCAATAGGCCGAAATG</b> GTAAGCCCT
35	42	CGACGGGGAG <b>TTTTTTGTTAAATCAGCTCATTG</b> TATCTACA
36	42	ATTGAAAAG <b>GTCTAAATACATTCAAATATGT</b> CTTCAATAAT
37	42	CTCATATATA <b>CTAGACAGATCGTGAGATAG</b> ACCAAGTTTA
38	30	CGATGTGACC <b>TTGTTTTGATACTCTATGTT</b>
39	30	AAGCATCTTA <b>CAAGCGAAAGGAGCGGGCGC</b>
40	30	CGAGCGTGAC <b>ACCATCACCTAATCAAGTT</b>
41	30	CTCGCGGTAT <b>CAAAAGAATAGACCGAGATA</b>
42	30	TAATTTAAAA <b>GGAGTTTTCGTTC</b> ACTGAG
43	27	CCTATT <b>TTTT</b> TGTTTATTT <b>TA</b> AGAGT
44	26	AGCACTTTTAAA <b>GCTT</b> GAGAGTTTT <b>C</b>
45	26	TTACATCGAACT <b>GAGT</b> AAAAGATGCT
46	26	TTCTGTTTTG <b>CTCCG</b> TGTCGCCCT
47	26	AATCCCTAACG <b>TG</b> ATCTAGGTGAAG

**Supplementary Table 8** Staple sequence for the 6HB-based pentagonal DNA origami of 84-bp edge-length. The sequence is represented by colors; unpaired nucleotides with blue, crossovers with orange, the 14-nt seed dsDNA domain with green, and the 4-nt dsDNA domain with red.

Staple ID	Length (bp)	Staple sequences
1	59	GCTAATGACCACC <b>CGCCG</b> CAGCATTGACAGGAG <b>GCCACCCTCAGAGCC</b> AGAACGCGC
2	59	TCAGAAAATACATATCATTACCCAAATCATATAAGAACGATCTAAAGTTTTTTTTTGTGTC
3	59	AAATCAAGCCAGCTGTATAACGTGCTTTCAGTGAAGAAATACCACATTTTTTTAACTAA
4	57	GATTTTAAAGCTAACTTTCCAGTCGGTTTTTAAACCTGTCGTAAGAATAGTCTTTA
5	55	ATGCTGAAAATCA <b>TTTCTTATCATTCTTTCGGTGAAGCGTCATACAA</b> TCATA
6	55	TGCAT <b>GTTGCGTTGCGCTCA</b> CAAGAGTGAGGCGGT <b>CAGTATTAACC</b> GTAAAGG
7	55	AGTTGCAGCAAGTTTTTCCACGCTGGTTT <b>CGT</b> GGTTTTTCTTTTTTTCACC
8	55	ACAGTTGTAAAGCA <b>CAATTTCA</b> TTTGAGTTAA <b>CAGATAATACATTGG</b> TTTTT
9	55	TAGTAAAATGTTTTTTACTGGATAGCGT <b>CCAC</b> CAGACGACGTTTTTTTAAAAAC
10	55	CGGATGGCAAAC <b>TGCCTAATTTGCCA</b> GATCAAT <b>ACAGTTGATTCCCAA</b> AGAAC
11	55	TTTAATGCGCGATTTTTGATAGCCCTAAAACA <b>AA</b> ACTATCGGTTTTTTTGTGCTG
12	55	CCAAAAAAAAGGTTTTCAAAGGAGCCTTT <b>AC</b> GGAGTGAGATTTTTTTAGAAAG
13	55	GAAGGCATTTGAGGTCTAAGAACCGGAGGCCA <b>GGATTTGTATCATCGA</b> TTTTTC
14	55	GAAAGC <b>CGGGTCGAA</b> CGGGGAGAA <b>TAA</b> CAATAAT <b>ATAGCATTGCTTCTGT</b> TGTTA
15	54	AAACAGTACATTTTTTATCAATAT <b>ACA</b> ATGACAA <b>TTTTTCCATCGCCCTGAC</b>
16	53	TCTGACCTA <b>TTTTT</b> AATGGTT <b>ATA</b> AAGAATA <b>TTTTTTT</b> AACACCGGAATC
17	52	GGCGTT <b>AGAA</b> TACA <b>CA</b> AATAACGG <b>TTTTTTT</b> TCGCTGATT <b>GT</b> TTCATCT
18	52	AGAACCGC <b>TTTTTTT</b> CACC <b>CTCAGAGCCACCACCCTCC</b> CTGAT <b>AC</b> CATTTG
19	52	AAAGAAAC <b>TTTTTTT</b> CACCAGAA <b>GGAGCGGAATTATCT</b> GGCTT <b>GT</b> TTTTCA
20	52	ATCATGGT <b>TTTTTTT</b> CATAGCT <b>GTTTCTGTGTGAAAGT</b> GCC <b>GA</b> ACCGAG
21	52	ATTTCAATTACC <b>TTTT</b> GCAAAAGAA <b>GC</b> ACGACCAGT <b>TTTTTTT</b> AATAAAAG
22	52	CGCCAG <b>GCC</b> CAGC <b>ACC</b> CGAAAGACTTCAAATATCG <b>CTTTTTTT</b> GTTTAAT
23	52	TAATCATT <b>TTTTTTT</b> GTGAATTACCTTATGCGATTT <b>TTT</b> CTGCG <b>TT</b> TATTT
24	50	AGGGATAACCTAAA <b>ACA</b> ACGG <b>ACAAAATCACCAGTAC</b> CGGTATACTAAAG
25	50	TTAGACT <b>TTTTTT</b> ACAACA <b>ATT</b> AAGTGCCG <b>TTTTTT</b> AGAGGGTTGA <b>ACG</b>
26	50	GCCAACAACCACCA <b>CG</b> AAAA <b>AGTTGACGCTCAATCGC</b> TGGCCA <b>AT</b> GTTC
27	50	ATAATCAGGAATTG <b>AC</b> GTCA <b>ATGT</b> CAGATGAAT <b>ATAAC</b> ATTT <b>AT</b> CACCTT
28	50	TGGCTCTAGAGCTT <b>AC</b> ATATA <b>AG</b> AAA <b>ATTCATATGGT</b> TCCAG <b>ACC</b> AACAG
29	50	TTCTGCAAATCCA <b>AC</b> GTTCC <b>AC</b> ATAG <b>CCCCCTTATG</b> CTGTCT <b>AG</b> GTCTG
30	50	TCCGCTCGAACGTG <b>GAT</b> AGTA <b>GAC</b> GGAA <b>TACCCAAAG</b> CATTAG <b>GGT</b> GCCG
31	48	GGACAT <b>TT</b> CTGAAATG <b>TTTTTTT</b> TATTT <b>ACATTGGCAGTCT</b> AAATAA
32	48	CATAA <b>TTTTTT</b> AAAAATCAG <b>GGCCCG</b> AGAT <b>TTTTTT</b> GTTGAGTGTC <b>GCC</b>
33	48	GATGGCAA <b>TG</b> AGTCA <b>AGGTATTA</b> AA <b>CCAAGGT</b> AGCG <b>CT</b> GATGATACAG
34	48	CACAACAT <b>AT</b> CACC <b>ACTGA</b> ACAA <b>AGTCA</b> AGAAGG <b>AAA</b> ACCAGGCAA
35	48	TCAGGACG <b>TT</b> CAAAG <b>CATA</b> AA <b>CAGCCATATGA</b> ATA <b>GA</b> ACGAGTAGAT
36	48	ATAGGAAC <b>CG</b> GTAG <b>CAAGCGA</b> ACT <b>CCCGA</b> ACTTGA <b>GA</b> ATTGTGT <b>CGA</b>
37	48	TAACA <b>TTTTTT</b> CTGCTCAT <b>TCT</b> CGTTAG <b>TTTTTT</b> CAGAGCGGG <b>ACA</b>
38	48	GCAA <b>ATTA</b> ACA <b>CTGTTCCAGTTTGGACT</b> GCCC <b>GC</b> AGGAGGCC <b>CAAGCT</b>
39	47	GCTAG <b>GGT</b> CATTT <b>GACG</b> CAGT <b>ATGTTAGATAGCA</b> GTGGCCCTGAGAG
40	47	TATATT <b>TCT</b> CAT <b>TATCACCGGA</b> AC <b>CAGCC</b> AT <b>CCG</b> GCGAATTATC
41	46	ATCAGAA <b>CAA</b> TTTT <b>AG</b> CCGTT <b>TT</b> CAGTAGCGACAT <b>TTT</b> CAAGTT
42	46	GTTTTGAAGCC <b>TTTTT</b> AATCAAG <b>TA</b> CGGAAAT <b>TATTTT</b> AAAGGT

43	46	AATCAAATAA <b>TTTT</b> ACGATTT <b>TT</b> AAAGGTGGCAA <b>TTTT</b> TAAAAG
44	46	GAGCGTAATA <b>TTTT</b> GAGAGATA <b>ACT</b> TTTTTAAGAAA <b>TTT</b> AGCAGA
45	46	CTGTTTATCAA <b>TTTT</b> TAGATAAG <b>TC</b> CTCAGAGCCGC <b>TTT</b> CTCAGA
46	46	TGCAA <b>TTTT</b> <b>GTGCCACGCTGAG</b> AAGAGTCTGTC <b>TTTT</b> CATCAC
47	46	GGTACC <b>GAC</b> GCCA <b>GGAGTAGA</b> AGAACT <b>CT</b> CGCCA <b>TA</b> ACCGTCTATC
48	46	<b>ACCGT</b> TGAGGC <b>TTTT</b> <b>TCAGACGATTGGC</b> TTGAT <b>TTCA</b> CCGGAA
49	46	AACATT <b>AAGAGGC</b> <b>TTTCAACAGTTTCAG</b> ATTGTAT <b>GT</b> AAAACATAGC
50	46	<b>TGCCG</b> TAATAA <b>TTTTTTA</b> ACGGGG <b>TCAGTGCCTTGAGTT</b> AGCAGC
51	46	<b>GAATC</b> TGCTCC <b>TTTTTT</b> ACTTAGCC <b>GGAACGAGGCGCAG</b> AAGGTA
52	46	<b>AAACC</b> ATTAGAT <b>TTTT</b> ATTT <b>CGCAAATGGTCAATAACCTA</b> GAAAAT
53	46	<b>TAGCG</b> CCATTC <b>TTTT</b> <b>CTGCGCAACTGTTGGGAAGGGCGA</b> TCTTAC
54	46	GGAAC <b>TTTTTT</b> <b>TACGCCAGAATCCTGAGAAGT</b> AGGATT <b>TG</b> CGTAGA
55	46	ACCCTC <b>AAT</b> AGGC <b>TATAACCCTCGTTTAA</b> TACTG <b>CC</b> GTCAACCTCA
56	45	AGGCAGAGG <b>CT</b> TCTGT <b>CCCTGAAAGCGTAAGG</b> AAAA <b>CT</b> ATACAA
57	45	ACCGTA <b>ATATTTT</b> CATCGTAGGA <b>ATCAT</b> CCATCG <b>AA</b> ACAGTGCC
58	45	AATATT <b>GTAGTTGCTATTTTGCACCCA</b> GAGGGAG <b>GG</b> ACGGTCAAT
59	45	CGAAGC <b>CCCCA</b> AGAATTGAGTT <b>AAGCA</b> ATAGC <b>TA</b> TCGGTGC
60	45	CTAACT <b>CACGTGGACAGCAGAAGATAAA</b> ACTTTGT <b>GT</b> TAAAACGAC
61	45	GAAAGTATT <b>AT</b> CATTT <b>TTGTTTGGATTATACA</b> ATCCT <b>TC</b> GGTTTA
62	45	GACCAGGCG <b>CGA</b> ACCG <b>CTTTCGTCA</b> CCAGTAGCGGG <b>ATG</b> GAATCG
63	45	CACCCGCCG <b>CT</b> TTAAT <b>TTAATAAAACGAA</b> TCGAGGAA <b>GG</b> GCGAAA
64	45	AAGTTGGGT <b>AG</b> GCTCG <b>AGTAAAGCCTGGGGT</b> GGCGAA <b>AT</b> AAAAAT
65	45	ATAATTACT <b>AC</b> AGAGC <b>CTCAGAGCCGCCACCA</b> AA <b>CA</b> ACAGAGA
66	44	GTATAACAT <b>GCGTCA</b> CCAAT <b>GAAAT</b> ACCGC <b>GC</b> GTTGAAAATCT
67	44	CATAAGGGAA <b>TCATTCA</b> ACCGATT <b>GCT</b> TACAAT <b>TC</b> AGAGGGGGTAA
68	44	GCCTCTTCGG <b>CAACAATGAAATAG</b> CCCAATA <b>AT</b> GGCTATTAGTC
69	42	CCC <b>GAT</b> CTAAAT <b>CAAAAACAGGG</b> AAG <b>CAGA</b> ACT <b>GC</b> ATCAAT
70	42	TTTT <b>CA</b> TGTAGAA <b>ATAACCTCCG</b> AAATCGCGCAG <b>AT</b> AATTTA
71	42	ACAAT <b>TT</b> ACCGC <b>CA</b> AGCCAACCTATTACGCC <b>GA</b> TCCAGA
72	42	AGCAAG <b>GA</b> ATCAG <b>AA</b> AGTTTCCAATAATTTTT <b>TC</b> ACCCAATA
73	42	TAGGGC <b>TC</b> CAGT <b>ATAGC</b> ATT <b>GCAACAGA</b> ATACG <b>TA</b> AAAGGT
74	42	AGACAA <b>AT</b> ACCA <b>CG</b> TACCTTTAAAGAAGTTT <b>GT</b> TTATCC
75	42	TAAGACT <b>ATA</b> ACA <b>TG</b> GAACCTACCCTTCACCGC <b>CC</b> CTTAC
76	42	AAAGT <b>AA</b> TTTT <b>CGGAATCG</b> CATATTT <b>AT</b> GC <b>GT</b> CTCATG
77	42	TTTACAT <b>AT</b> CAAG <b>AAT</b> CAAACCCATTACCAGT <b>CA</b> ATGATGA
78	42	CCGCCT <b>CC</b> T <b>GAA</b> CAAGAAAA <b>TAATA</b> TAGCCAC <b>CA</b> CAAA <b>CA</b>
79	42	ACATAC <b>ATGTTT</b> AACGT <b>CAAAAATGAAAC</b> AAACG <b>TG</b> TTTAGC
80	42	AACAA <b>CC</b> GGGAG <b>AC</b> GACCGTGTAGCACTA <b>AA</b> CA <b>CA</b> GTACCT
81	42	AGCGGG <b>GT</b> TTGCC <b>CC</b> CATAT <b>CAAAATTAC</b> TTGCT <b>TT</b> GATACC
82	42	CAAGAA <b>CG</b> GTGT <b>ATG</b> ACAGCCCT <b>CATAGT</b> ATT <b>CG</b> GAACAGT
83	42	GCTTT <b>GA</b> ACGAGA <b>AG</b> ATTCATCAGTT <b>GAT</b> ATTAT <b>ACC</b> TTAT
84	42	ATTCTT <b>ATA</b> ATT <b>GAA</b> GCCAGTAATAAGAGA <b>ATAG</b> ATCAACAG
85	42	AATAAA <b>TT</b> AGTT <b>AACTTT</b> GAA <b>TACCAAGTTACAGCT</b> TTCAAA
86	42	CGAGCA <b>TA</b> ATCAA <b>AAA</b> AGCCAGAAT <b>GG</b> AAAA <b>CTTT</b> TAGGTT
87	42	GGGTT <b>TA</b> CCCTTT <b>TCCAATCAATAATCGT</b> AGCGT <b>TG</b> TCTCTG
88	42	AGAGACT <b>ATA</b> ACT <b>AA</b> CAAGA <b>ACCGGA</b> AGCGC <b>AT</b> GCCATC
89	42	TAAAGC <b>AT</b> AGAGC <b>TG</b> GAAGGG <b>AAGAAA</b> GAAGGT <b>GG</b> CATGAT
90	42	ACAAT <b>TTTT</b> T <b>GA</b> AT <b>AAGAGCAATAA</b> AGTACCGA <b>CG</b> GCACAG
91	42	AGAGAG <b>AC</b> CTTAT <b>TGGGCG</b> AGC <b>TGA</b> ACGAAAG <b>GG</b> GGAGCC
92	42	TAAATC <b>CT</b> TTTT <b>GTGTT</b> AGTAA <b>TGAATA</b> ACAGC <b>TC</b> TGTAAA
93	42	AGGGTT <b>AT</b> ATTA <b>TAGGTGA</b> ATTTCTT <b>ATTT</b> CTG <b>TT</b> AGGATT
94	42	TCGTCG <b>CG</b> AACCT <b>AGA</b> ACGTT <b>ATTAATTGA</b> AGGA <b>TA</b> TGGGAT
95	42	TTTGCT <b>AG</b> CTTT <b>CGTA</b> ATTT <b>CCCTTAGT</b> TCTGA <b>AT</b> TTGAGT
96	42	TCAGCT <b>TA</b> CAAC <b>TG</b> AGACT <b>CC</b> CAAG <b>AT</b> TAAA <b>GT</b> AATGGA



97	42	ATTGCGAATAT <b>T</b> ACTCATCTTGTTAATGCCCC <b>A</b> CTAAAGGA
98	42	GCAAGC <b>A</b> CCGGAA <b>A</b> ACCC <b>C</b> AGCGATT <b>A</b> CTAAAA <b>C</b> AACGGG
99	42	TAAAT <b>A</b> CATGAG <b>G</b> TATAGAAGG <b>T</b> TATGCACCA <b>T</b> CGCGAAA
100	42	ACTTTT <b>T</b> CGTAAT <b>G</b> GG <b>C</b> AAAAGAA <b>T</b> ACATACCA <b>A</b> GTACCATT
101	42	TAAAG <b>A</b> ACATTA <b>A</b> CT <b>G</b> CAG <b>G</b> TC <b>G</b> ACT <b>C</b> GACGT <b>T</b> AGTAAT
102	42	CGGAAT <b>A</b> CGGATA <b>T</b> AC <b>G</b> CCAAAAGGA <b>T</b> ATGCTTT <b>T</b> CGCTGA
103	42	TGTAGC <b>A</b> AGGGAG <b>T</b> TGAAT <b>C</b> CCC <b>T</b> CAATACGAG <b>G</b> A <b>T</b> CCTTGA
104	42	GGCTT <b>G</b> CTCCAC <b>A</b> CC <b>G</b> TACT <b>C</b> AG <b>G</b> AAAGAG <b>T</b> ACATAGTA
105	42	AGAGCA <b>A</b> TATTCAT <b>T</b> AAAGG <b>C</b> CGCTTT <b>T</b> CAA <b>A</b> CT <b>A</b> TACCGCC
106	42	TCATA <b>A</b> CACTAT <b>C</b> GG <b>T</b> GAC <b>T</b> TCAT <b>C</b> GGTTT <b>A</b> GC <b>A</b> ACGCC
107	42	AACAT <b>C</b> AG <b>A</b> ACCA <b>C</b> CT <b>C</b> CA <b>A</b> CG <b>T</b> CA <b>A</b> AG <b>C</b> CTAA <b>T</b> ATCCCG
108	42	GCTTTT <b>G</b> CAAA <b>T</b> ATGTTTT <b>A</b> ACCG <b>A</b> ACTGAC <b>T</b> AGCGAGAG
109	42	TGAAT <b>C</b> TAGGG <b>C</b> AA <b>T</b> G <b>C</b> AA <b>C</b> TAAAG <b>T</b> AGCTCA <b>A</b> CTGCTCCT
110	42	TTTGAT <b>A</b> TAGAG <b>A</b> G <b>T</b> A <b>A</b> CGAG <b>C</b> G <b>T</b> CTTTTACC <b>A</b> TGGAAGT
111	42	GTCAG <b>G</b> AAGAG <b>G</b> T <b>C</b> AATATA <b>A</b> T <b>G</b> CT <b>G</b> T <b>A</b> C <b>G</b> GT <b>G</b> T <b>C</b> GCGCAA
112	42	ATTAAT <b>T</b> CAGTA <b>A</b> CT <b>A</b> ATAGATTAGAG <b>C</b> GGAAG <b>G</b> TCAA <b>T</b> CA
113	42	ACCGAA <b>C</b> CTTG <b>C</b> T <b>G</b> GTTTTCC <b>A</b> GT <b>C</b> ACTAGAG <b>G</b> AGTGAG
114	42	CCCTGA <b>C</b> GATTT <b>A</b> G <b>T</b> AAG <b>G</b> CT <b>T</b> GC <b>C</b> CT <b>G</b> C <b>G</b> AGCA <b>C</b> G <b>C</b> ATTAA
115	42	TGAAT <b>C</b> GG <b>C</b> AAAA <b>T</b> G <b>T</b> CAG <b>A</b> AG <b>C</b> AAAG <b>C</b> G <b>T</b> AGAA <b>A</b> ACCAG
116	42	ATTACAG <b>G</b> GATT <b>G</b> CT <b>G</b> GT <b>T</b> CC <b>G</b> AAAT <b>C</b> GG <b>C</b> CAAC <b>G</b> TATGGTT
117	42	AACGAG <b>T</b> CGCGTA <b>C</b> CG <b>C</b> GGG <b>G</b> AGAG <b>G</b> CG <b>T</b> TGAT <b>G</b> GA <b>T</b> CAAAA
118	42	ATCCT <b>G</b> TGTTTT <b>G</b> CG <b>C</b> CG <b>C</b> TACAG <b>G</b> AG <b>T</b> AA <b>T</b> CAACATT
119	42	AGATTA <b>A</b> ACGG <b>A</b> AT <b>G</b> GG <b>C</b> T <b>T</b> GAGAT <b>G</b> GG <b>C</b> TAA <b>T</b> ATTGGG
120	42	TATATT <b>T</b> CGCT <b>G</b> CG <b>A</b> CGGG <b>C</b> AACAG <b>C</b> T <b>G</b> ATT <b>G</b> AA <b>A</b> GCGGGC
121	41	GATAGT <b>T</b> TCCAG <b>A</b> CC <b>A</b> GTACCAG <b>G</b> CG <b>G</b> ATCGACA <b>A</b> GT <b>A</b> AAA
122	40	TATCTTTAGGG <b>A</b> AT <b>C</b> AAT <b>A</b> TCTGG <b>T</b> CTCAA <b>T</b> AACAAA
123	40	TCGGC <b>A</b> TAGA <b>A</b> CG <b>T</b> AG <b>T</b> GAATTTAT <b>C</b> ATGATTATCAGAT
124	40	GTCT <b>T</b> GCGCC <b>G</b> AT <b>G</b> TGAGTGAATA <b>A</b> CTTTGC <b>A</b> CC <b>T</b> CGTAT
125	40	TTTT <b>C</b> AGATTAC <b>T</b> G <b>C</b> AAAT <b>G</b> AAAA <b>T</b> CAAAG <b>T</b> GAGGCCA
126	40	GGAATT <b>A</b> GC <b>G</b> TTT <b>T</b> AC <b>G</b> GT <b>A</b> CAGAG <b>G</b> CCAGCAAGCCCA
127	40	TGCAG <b>A</b> CGAGAA <b>A</b> CG <b>C</b> ATA <b>A</b> CCGAT <b>A</b> TAGCG <b>T</b> ATAGCC
128	40	TGTCAC <b>A</b> TACAA <b>A</b> GA <b>A</b> CCAG <b>A</b> CC <b>G</b> GA <b>A</b> CTATTATACCAG
129	40	GAAAC <b>G</b> TGAACA <b>C</b> AAT <b>C</b> AAGTTTTTT <b>G</b> GGCACAATTCCA
130	39	GAAAT <b>C</b> CTTCT <b>G</b> ACAG <b>A</b> CGAC <b>G</b> ACA <b>A</b> TAGATGTAATTT
131	39	CTGAGA <b>A</b> TATCAAT <b>A</b> T <b>T</b> TTTT <b>T</b> AATCCTGAT <b>G</b> CGGAAC
132	39	GAAC <b>A</b> T <b>G</b> CTATTT <b>C</b> G <b>A</b> AC <b>T</b> TTTT <b>T</b> ATTCTGAAACAT
133	39	GAACG <b>A</b> GCATGTACCG <b>T</b> TTTT <b>T</b> AACACTG <b>A</b> GCACC <b>T</b> C
134	39	CAAAA <b>A</b> ACTTT <b>G</b> AAAGAG <b>G</b> AC <b>A</b> TTTT <b>T</b> GAACGGTGTACA
135	39	TCGAG <b>C</b> TTGGGAAGA <b>A</b> T <b>T</b> TTTT <b>T</b> AATCTAC <b>G</b> TTCA <b>A</b> CTT
136	39	AGTG <b>A</b> AG <b>T</b> G <b>T</b> AG <b>C</b> GG <b>T</b> C <b>A</b> CG <b>T</b> TTTT <b>T</b> GCGTAAC <b>C</b> ACCA
137	39	TGAACC <b>A</b> CGAGCCGG <b>A</b> T <b>T</b> TTTT <b>T</b> GCATAAAG <b>T</b> ATTCGTA
138	39	GGCCAGTGCG <b>A</b> T <b>T</b> G <b>T</b> AG <b>C</b> A <b>A</b> T <b>A</b> CT <b>T</b> ACAGAG <b>G</b> TCCACTA
139	39	GTAAT <b>C</b> T <b>G</b> GG <b>C</b> AAAGGGG <b>G</b> AT <b>G</b> TTTT <b>T</b> TGCAAGGCGATT
140	34	GAGTGTACT <b>G</b> TTAG <b>C</b> GT <b>C</b> AG <b>A</b> CTTACC <b>G</b> CACTC
141	34	AATCCGCG <b>A</b> CT <b>A</b> T <b>C</b> ACCG <b>T</b> CAC <b>C</b> GT <b>T</b> GCGGGAG
142	34	TTAGTTTGA <b>C</b> G <b>C</b> AAAG <b>A</b> CAC <b>C</b> AG <b>T</b> ATTTATCCC
143	34	AGCGCCATT <b>C</b> G <b>A</b> CA <b>A</b> AG <b>T</b> T <b>A</b> CC <b>G</b> AGGGTAATT
144	34	TAGAAC <b>C</b> TACAT <b>T</b> C <b>T</b> G <b>T</b> T <b>T</b> AG <b>T</b> AT <b>C</b> AAACAAC
145	28	CAGAAA <b>T</b> TTTT <b>T</b> AAAGAA <b>T</b> TA <b>G</b> AAGTA
146	27	GATAGCTTAGA <b>T</b> TTTT <b>T</b> TTTT <b>T</b> TAAGACG
147	27	GCAGCGAAAG <b>A</b> T <b>T</b> TTTT <b>T</b> T <b>C</b> AGCATCG
148	27	AGGGCGATGGC <b>T</b> TTTT <b>T</b> TT <b>C</b> CACTACG
149	26	CCGAGTAA <b>A</b> GC <b>C</b> AG <b>C</b> ATTTTT <b>A</b> TGG

150	23	GCTGAACCAGTTGGTATCTAAAA
151	21	AATTTACTCGCAAGTATGTAA
152	21	CAAAGTACGAAAGACCACTAC
153	21	TTCATTATTGCTGATTTTTG
154	21	TCTACTACGAGAAATGACGGG

**Supplementary Table 9** Staple sequence for the DX-based hexagonal DNA origami of 84-bp edge-length. The sequence is represented by colors; unpaired nucleotides with blue, crossovers with orange, the 14-nt seed dsDNA domain with green, and the 4-nt dsDNA domain with red.

Staple ID	Length (bp)	Staple sequences
1	58	GATTTAAACTTCGTGTATTCATTCATTGTCAGTTATCGGACCACATTTTTAATTTAA
2	58	TAGCAAATACGTATGGGAACCGGAGCTGAACTCGCCTTGATCGTCTCCCTATATT
3	58	TATTGACGCCGGGTGAGTATTCAACATTTTGAAAAAGGAAGAGTACAAGAGCAACTCG
4	58	GTCACAGAAAAGCGCCTATTTTTATAGGAAAGGGCCTCGTGATAATCTTACGGATGG
5	58	ACGTTGCGCAAACGCTGAGATAGGTGCCTACGAAATAGACAGATCTATTAAGTGGCGA
6	58	ACACTGCGGCCAAACCTTGCCTCTGAATGGTACGAGCGAACGAACTTACTTCTGACA
7	56	CTCCCGGTTTGACACCGTCTGGCGGACATCGAAGAGGTTGGTTTTTTTTGTTAAT
8	55	CTCATTTTTTTATAGGCCGAAATCGGC AAAATGTGGGTTACATTTTTTTGAACTG
9	55	GGCAAGTGTATCACGCTGCGCGTAACCACTGTAGAAAGTCTTTTTTAATCCT
10	55	AGAACGTGGATACGTCAAAGGGCGAAAAACCGTCCGCTCATGATTTTTTACAATA
11	55	TGATAATCTCTCAAATCCCTTAACGTGAGTTTCGTAGTTATCTTTTTTACACGA
12	55	CTAAATCGGATAAAGGGAGCCCGGATTTAGACTCTCCACCCTTTTTATAGGTT
13	54	GTTCTGTTTTTCTATGTGGCGCTATTCTCAGATTTTTTATGACTTGGTGAATT
14	54	ATGCAGTTTTTGTGCTGCCATACGAAGGAGCTATTTTTCCGCTTTTTTAGCGTG
15	54	ACACCTTTTTTTCGATGCCTGTCTCCCGGCATTTTTACAATTAATATTAAA
16	43	GATCTTTATTGCTGATTTTTTAAATCTGGAGTGTAAATCAG
17	43	ACCTTTTTCGCGCATTTTTTTTTCCTTCCCTTCCACTATTAA
18	43	ATCTCAAAGCTTTAATTTTTTCAAATCTGGGCTAGGGCGCT
19	43	CGGGTGTAGACCAATTTTTTTTACTCATAAAGATCCTTTT
20	43	TGAGTTTCTTAGACGTTTTTTTCAGGTGGCAGCCGTAAGCA
21	42	TTTTGCGCAGCGCGTTGCGCTCAGCGAAGGATTCGCCGCA
22	42	GCCTTCAAACGGCTACAGGGCGCACATTAATACCTGTATCG
23	42	CGCATAAGTGTACCCGCGCGCTTAATGCGCGGTAGGAAGC
24	42	GACCGCGTGTGTTTTGTTTTTATACTCTATGTAGTGACGTAA
25	42	AAACTAAGAGAGTGAAGAACCAGGGAAAACCACTGTCTATAC
26	42	GCTCAACAACAAAGAAAGCGAAAGGAGCGGGCCGCCGGGTG
27	42	AAATTACATGCAACGTGGCGAGAAAGGAAGGGGAGAATAAGT
28	42	TAAACGAATAGGCTTGACGGGGAAAGCCGGCGGATGTGACCT
29	42	GATAATAATGGGGACGACGCAATTCGACGTTAATGTCAT
30	42	AATGTGCGCGCAAGTTTTTTGGGGTCCGAGGTTTTTCGGGGA
31	42	TGTTTTATTTTTACGTGAACCATCACCTAATAACCCCTATT
32	42	TCAAATATGTATCTATCAGGGCGATGGCCACCTAAATACAT
33	42	CTTATCCCTTGATAAATGCTTCAATAATATCCGTGTCGCC
34	42	ACCCAGAAACGTGTTCCAGTTTGGAAACAAGAGGTTTTTGCTC
35	42	TAAAAGATGCTGACCGAGATAGGGTTGAGTGTCTGGTGAAAG
36	42	TGGGTGCACGACCTTATAAATCAAAGAATAGAAGATCAGT
37	42	AGGCGGATAAAGTTTTCCAATGATGAGCACTTGACTGGATGG
38	42	CACTTCTGCGCAGAGTTTTTCGCCCGAAGAACGTTGCAGGAC

39	42	CGGCTGGCTG <b>GT</b> CAACAGCGGTAAGAT <b>C</b> TT <b>GT</b> CGGCCCTTC
40	42	TGGGTCTCGC <b>GT</b> TGTAATTCGC <b>TTAAATTTT</b> CCGGTGAGCG
41	42	AGCACTGGGG <b>CCCCAATCATATGTACCCCGG</b> TATCATTGC
42	42	GCCCTCCCGT <b>AT</b> TCGTTCCACTGAGCGT <b>CAGAC</b> AGATGGTAA
43	42	ACCAAACGAC <b>GG</b> CACAACATGGGGGAT <b>CATGTA</b> TGAAGCCAT
44	42	GCATTGGTAA <b>CGAGT</b> CAGGCAACTATGGAT <b>GAC</b> ACTGATTAA
45	42	CTTTAAAAGA <b>AAGT</b> GATAACCAT <b>GTTACTTGGT</b> GCAATCCTA
46	26	ACGATCGGAGGA <b>CA</b> CCATGAGTGATA
47	26	CATGACAGTAAG <b>AT</b> GAGTACTACCA
48	26	GTCGCCGCATAC <b>AC</b> GGTATTATCCCG
49	26	ACTACTTACTCT <b>AAG</b> CAATGGCAACA
50	26	AAGGATCTAGGT <b>GT</b> TATACTTTAGATT
51	26	CCTAGATTAGAA <b>GC</b> CAGAAAGCATGG

**Supplementary Table 10** Staple sequence for the 6HB-based hexagonal DNA origami object of 84-bp edge-length. The sequence is represented by colors; unpaired nucleotides with blue, crossovers with orange, and the 14-nt seed dsDNA domain with green.

Staple ID	Length (bp)	Staple sequences
1	59	AGTATAGCCA <b>GA</b> CAGGTAGAAAGATT <b>AACGGA</b> AGCGCGAAACA <b>TTTTTT</b> AGTACAACG
2	59	TGGTAATA <b>ACT</b> TTCC <b>AT</b> GACCAACTTT <b>GAAAGAGGACA</b> <b>TTTTTT</b> GATGAACGGT <b>A</b> AATAA
3	58	GCCAGCTTTG <b>CACGACGGCCAGT</b> GCTCATT <b>TTGTT</b> CAGGTT <b>AA</b> CGTGAGGAT <b>AT</b> TGTG
4	58	CTACGA <b>TTTTTT</b> GGCACCA <b>CT</b> TCGAGGTGA <b>ATTTCTTTTTTT</b> TAACAGCT <b>CG</b> GAA
5	58	GGAATACCCA <b>CGCGACAGAATCAAG</b> CTATTAT <b>GAGAGACTACCTT</b> AAACAAT <b>AAT</b> GAT
6	58	CCAGCAGGCG <b>CCCACCACACCCGC</b> AGTACG <b>GCAATTACCTGAGC</b> ACTCAAT <b>CT</b> GATG
7	58	GCAGATTCAC <b>GCAGCTACAATTT</b> AGGTCAG <b>GATAACCTTGCTTCTC</b> CGCACT <b>CC</b> AGT
8	57	CTCAGAA <b>AA</b> CCGC <b>CA</b> ACAATGAAATA <b>TTTTTT</b> CAATAGCTAT <b>CACCACG</b> GGTACAGA
9	57	TTCTGAATA <b>AT</b> GAGTAACATTATCATT <b>TTAA</b> CAAAGAA <b>ACCACAT</b> CAAT <b>AG</b> ATAAAA
10	57	AAATAAGGC <b>GG</b> AATCGCCAT <b>TTTAA</b> CAAACAT <b>GTAATTTAGATTTAA</b> TATAGTAA
11	57	CCTTGAT <b>AG</b> GGTTG <b>AG</b> CGCCAGGGTGG <b>TTTTTT</b> TTTTCTTT <b>CAAGTCCA</b> CTGATAGC
12	57	GTCTCT <b>GC</b> ATTAA <b>AA</b> ACGTTAATAT <b>TTTTTT</b> TGTTAA <b>ATCCGCAT</b> CGACGTCAA
13	57	TATATGTAA <b>ACA</b> ACAT <b>GTT</b> CAGCTAAT <b>GCCGCGCCTGTTTATCT</b> TAAC <b>TG</b> GTCTTT
14	57	CACCAG <b>ACC</b> CTCAG <b>G</b> TAAATCCAGAT <b>TTTTTT</b> CAATATTACC <b>GA</b> ATGG <b>TT</b> CAATAG
15	57	AGAATCCTT <b>GT</b> TCCTTATCATT <b>CCAAGAATATTA</b> AA <b>CCAAGTAG</b> TAAAT <b>CAG</b> CAAAC
16	57	CAAAATTA <b>ATCT</b> AAAGCATCAC <b>TTGCTGTCAAATATCAAAC</b> CAAAGAA <b>GAA</b> ATATG
17	57	ATCGGGAGA <b>AA</b> ACTAATAGATTAG <b>AGCCGTAGATAATACATT</b> CAGATG <b>AG</b> TTTAGC
18	56	GAGATTTA <b>TCGTTGGGAAGAAA</b> AGACTG <b>GATCTTCTGACCTAAG</b> CAGAGGGATAA
19	55	ATTAAG <b>TA</b> AGGGC <b>GA</b> ATC <b>TTTGCCCGAT</b> ATCAA <b>ATAGCATT</b> CATTAT <b>GG</b> AGAAT
20	55	AACTAA <b>AAATTTTCT</b> CAATCATAAGGG <b>AG</b> CAAAA <b>GGTATCGGTTTATCAT</b> TTTGA
21	55	GGGAGG <b>TAT</b> CAGAT <b>CATTACCGCGCCCA</b> ATTAC <b>CTTTT</b> GCGGAT <b>GGCT</b> CACCGA
22	55	ATTAC <b>TC</b> GAGAA <b>AAGGTA</b> AGTAATT <b>CA</b> AGACA <b>ATCCCCCTCAA</b> T <b>GCT</b> CACCC
23	55	GCGGGC <b>GCC</b> GATT <b>TGGA</b> AGGTTAT <b>CTAAT</b> GCTTT <b>GTGCGAACGAGTAGA</b> AACTC
24	55	GGAAAC <b>GCG</b> ACTT <b>GCGAGCATGTAGAA</b> TTAAGA <b>CGCCGAAAGACTTCC</b> ATTAG
25	55	GATAA <b>ATAAG</b> CAAA <b>ATTTA</b> AGTATC <b>GCACAGACAGCCCTCG</b> AGTAA <b>CA</b> AGCGCA
26	54	CAATC <b>TTTTTT</b> ATATGTAC <b>CGCTATCAGGT</b> CATT <b>GTTTTTTT</b> CCTGAGAGTCTG
27	54	GTTTA <b>TTTTTT</b> TTTGT <b>CACA</b> AA <b>TTAGTCTTTTTTTTT</b> ATGCGCGAA <b>CT</b> ATTA
28	54	AAGAA <b>TTTTTT</b> GTGGACT <b>CCAT</b> AACCGTGCA <b>TTTTTTT</b> CTGCCAGT <b>TG</b> CGTA
29	54	CCGTT <b>TTTTTT</b> GTAGCAAT <b>ACCAGAATCTGAGAA</b> <b>TTTTTTT</b> GTGTTTTTATAA
30	54	CGCCA <b>TTTTTT</b> CATTGACAG <b>GA</b> TTCA <b>AAACTTTTTTT</b> AATAAA <b>TCC</b> T <b>A</b> ATTT

31	54	TTCCATTTTTGTTCGGGAAACATAAAGTGAAAGCTTTTTCTGGGGTGCCTA
32	54	CCAGATTTTTCCACCACCGCCGCCACCCTTTTTAGAGCCACCAGCCGC
33	54	AGTCATTTTTGAGGGTAAAGCCTTACAGAGAGATTTTTATAACATAAAAA
34	53	GCATCGGAAAGTGAATACGACGACAATAAATGCTGATAGTTCAGAAAACGAGA
35	51	GAAACCGTATGTTATTCATTACCCAATCAACGTAATTTTCAAAGCTG
36	51	AAGTGCCTCCGCACTAGGGCTTAATTGATTAAATAGAGGGCTTTGCAAAA
37	51	AGGGAGTTTTTTAAAGGCCGCTTTTGGGGATCGTTTAAACGCAAATC
38	50	ACATTAAGGGCGCTGCCAATTCAATACCAAGTTACAGAAATTGAAGAGCTT
39	50	TGATACAATTGCGAATTTAATTAATACACTAAAACACAGACGGTGTATGG
40	50	TCAGCATGCGATTTTCATTGAAGAACCGGAGAAAACGACAAACACCAGA
41	50	CGATGAGGTAACGCATAGTAGATTATTTGCACGTACGTATTAACTCGGTG
42	50	ACGGGAACCAATGAAGAGGAAGCTGAGAAGAGTCATAATTTAAGCCATT
43	50	GTAAAATGAAGCCTTAGGTCATTTTTTAATGGAAATAGGAATATAGAAG
44	49	GTGGTTTTTTTTCCGAAATCGGCAAAGTCCACGCTTTTTGTTTGCC
45	49	TAAGATTTTTCTCCTTATTACGCAGAGGAAACGCATTTTTAATAAC
46	49	AGCGATTTTTGTAACAACCCGTCGGCGTCTGGCTTTTTTCCTGTA
47	49	AATAATTTTTAAGGGACATTCTGGCAATGGATTATTTTTTACATTG
48	48	CCAATTTTTAGGAACCCATGTACCAATGAAAGTTTTTTAAGA
49	48	ACCGTTTTTCCAGTAAGCGTCATACATGGCGCTTGCCTAAAAC
50	48	ACGATTTTTCTAAAGTTTGTCTGTTTTAACGGTTTTGTCTAGT
51	48	AGTTGTTTTAGATTTAGGAATACCACATTCAAATAGCGAGAATAA
52	48	GCCTTATAGTTAGAGGGGACGACGCAATTGTAGCCAGAATGCTAGCT
53	47	ATTGTTTTTCGAAATCCGATCACCCTACTTTTTTCAGGAGG
54	46	ATACGAGGATCCCATCAAAAATAATTCACTTCTCCAAGTTTTTTG
55	46	AGAGATCAAAGGCCCTATTATTCTGAAGTAACACTCTGGTGCCGG
56	46	AAATGAATCCAGAGGCTCAATCGTCTGACAACAGAGGGAGGGAAGG
57	46	ACAGGAATGGTTGCGAGTTGCAGCAAGCATCCCTGTGTGAGGCGGT
58	45	GGCCAAAGGCCCAACCGTAATGGGATAAGCTCAATCATGGTC
59	45	CCTGAGTACGAACAGATAGGGTTGAGTGATTGCGCTTTCCTCG
60	45	AGCGCGTTTTTCGCTGAAGAGGCTTTGAGGACCGGATAGCAAACG
61	45	CAGGGAAGCGAATATCAGCGATAGCTTAGACCAATCAATTATCA
62	45	CGAGCGTCTAATAGCATGAGCGCTAATATCCGATTAGATAGAA
63	45	GCGCGTACTACGGTACGCTTCTTTGATTAGTAACAGATAAATC
64	45	CAAGAAAGACAAAAGAGCGTAAGAATACACGCTCATAAACAGCCA
65	45	ATGAGTGAGCTTAGTTTCGGATTGCGCTGATAATATCTCTAAAG
66	45	GACTCTAGAGCCGGAAGCCTGTGCGTCCAGCCCCAAATGTGGGAA
67	45	GAGCAAACAACCCTGTGTTAGAACCCTACCAACGTTATGCGCAAC
68	45	AAAGGGTGAATACAAAGCCGGTTGATAATCACACCGCTTGAGTTT
69	45	ACAGGAAGCACTCACTACAACGCTGTGAGTTAAATATGATAT
70	43	TCAGTGAGGCTAGAGCTAACAAATTTCAATTTGATCCAGCAGCAA
71	42	ATGACCATAAAAAATCACCGCTTAGTTTTGGTTATATAAC
72	42	TTCAAAGCGAGACCGGAGTCGCTATTTTTAATTTCCCTT
73	42	TGCTGTAGCTATGTTTTATGATGAAATTTTCATCAAGAAAA
74	42	TTCCGAAATGATAACCTATATACAGTTTTGTACCTTTTAC
75	42	AAGCCTTTATACGCAAGTAATCCTGATTTTTTTGGATTATAC
76	42	GAAAGTTTTGCGGGGGTAGGTTTGAAATTTTACCGTGTGAT
77	42	TTTTAGTTAATAAGGGGCTTGAGGTATCATCGCCTCATTTC
78	42	AAAATCAAGAAAAGGCAAAATCAAAAGAACTGGCGATAAGT
79	42	ATATATGAGCCGCTAAGAACGCCAGTACACGACATCGAG
80	42	CGAATTATGGCAAAGCGAACGTGGAAAATCCTGTTAATATCT
81	42	AAATTGCTTTACAATACGCCACATCAACATTAATAGAAGT
82	42	CCAGCGATTACTTAACTTTCAACCGGAATAGGTGTCGACCTG
83	42	CCAACGCAATCATAACGATAAAAACCAACTAATGGGCGGAT

84	42	AAAATT <b>C</b> AGCAAG <b>A</b> TCCCTCAGATCCCAATCCAA <b>AA</b> GCCCAA
85	42	ACACCG <b>G</b> TCAACA <b>G</b> CT <b>C</b> AGA <b>A</b> CC <b>G</b> CC <b>A</b> AGTACC <b>AC</b> AGATAC
86	42	CCTAAA <b>A</b> CTTGCT <b>G</b> AGCCGCCACGAGCGGGAGCT <b>AC</b> TCAAAC
87	42	AGGGCG <b>A</b> GTATT <b>G</b> GGCAGGTCATCCTGTGTGAA <b>AG</b> AGAGGC
88	42	ACTAT <b>C</b> AGTATCATATCCTGATTAT <b>C</b> ATATATTTAGCAAC
89	42	CTCCAT <b>G</b> TATAC <b>CA</b> CAACATTACCAAAAAA <b>AG</b> GTGACCC
90	42	TTTGCC <b>CA</b> AAT <b>G</b> CA <b>T</b> TA <b>AA</b> CGGGT <b>AA</b> ACATAGG <b>CA</b> GAAACG
91	42	CGGGCC <b>T</b> TGTGCT <b>G</b> T <b>CC</b> AGT <b>C</b> AC <b>G</b> AC <b>G</b> AAGGT <b>G</b> AATAAAG
92	42	AAGGAT <b>T</b> GAGCCA <b>CC</b> GTTATACAA <b>AT</b> CCCTGTT <b>TA</b> TAACCC
93	42	ACCCT <b>AA</b> GGATT <b>AA</b> ATT <b>AC</b> GAGGCATAG <b>TA</b> AG <b>AT</b> CAAGAG
94	42	TCGTTT <b>AC</b> AAAAG <b>GG</b> CGGGGTTT <b>G</b> CT <b>CC</b> CCT <b>CA</b> GTATAAAG
95	42	ATAAC <b>G</b> CCAGAC <b>G</b> ATT <b>ACT</b> AGAAAA <b>AG</b> TACC <b>GA</b> ACCGCC
96	42	GAGCCA <b>G</b> TAATTT <b>CA</b> TAGCGT <b>CCA</b> AT <b>AC</b> GT <b>C</b> AGG <b>AG</b> GTTTAA
97	42	TTTCAA <b>CG</b> TAAAT <b>T</b> AGAATATA <b>AA</b> GT <b>AC</b> CTTTTT <b>CT</b> CGTCAT
98	42	ACGAGT <b>AT</b> TTAAT <b>CG</b> GCT <b>C</b> ATTAT <b>AC</b> CATGCGGA <b>AA</b> AATATA
99	42	TGTTGG <b>G</b> T <b>AC</b> GGT <b>AA</b> TCGT <b>AAA</b> CT <b>AG</b> T <b>C</b> AGGC <b>TT</b> AATTTT
100	42	AGGGGG <b>ACT</b> TCGC <b>T</b> CA <b>AT</b> TC <b>G</b> ACA <b>ACT</b> AA <b>AC</b> AG <b>AC</b> ATCAAT
101	42	CCAGGC <b>G</b> ATACGT <b>AG</b> ATAGTT <b>G</b> CG <b>CC</b> GATCTTTT <b>CA</b> GCCCTT
102	42	TTTAAG <b>AA</b> TATA <b>AA</b> AT <b>GG</b> CT <b>G</b> AC <b>CT</b> TCATAGTTT <b>CA</b> ACAACC
103	42	ATGAGG <b>CA</b> AAGAG <b>T</b> ATA <b>AA</b> GGT <b>GG</b> CAA <b>CA</b> AAGTA <b>AA</b> TTAGCG
104	42	ATCGCC <b>CCCC</b> CT <b>TG</b> CAGATAG <b>CC</b> GA <b>CT</b> ACATA <b>CA</b> ATCTTG
105	42	TAGAAAA <b>AA</b> AGTT <b>AA</b> TTTT <b>CG</b> GT <b>C</b> ATAG <b>CG</b> CAT <b>AC</b> TTTTTC
106	42	ACAAGA <b>ACT</b> AAAG <b>AA</b> CCGATAT <b>AT</b> TC <b>GG</b> CATCGG <b>CC</b> CAGAAG
107	42	CCTGA <b>ACT</b> AGGTC <b>TAG</b> T <b>C</b> AGA <b>AG</b> CAA <b>AG</b> ATCAGT <b>AC</b> AGTAGC
108	42	ACCATT <b>AT</b> AGAG <b>C</b> ATA <b>AT</b> AT <b>CC</b> CAT <b>C</b> ATAGT <b>AC</b> AT <b>CA</b> AAA
109	42	TGGGA <b>AT</b> CCATT <b>G</b> ATAG <b>C</b> AG <b>C</b> CGT <b>AC</b> GGATT <b>GA</b> TTTATC
110	42	CGAGGC <b>G</b> TCAT <b>CT</b> CC <b>AAA</b> AG <b>GG</b> AG <b>CT</b> AATA <b>TA</b> AGGAAC
111	42	CCGT <b>CA</b> CT <b>GA</b> AT <b>TA</b> ACT <b>GA</b> AC <b>ACC</b> CT <b>GA</b> AGGT <b>GA</b> TAATCG
112	42	TGCCTATAGTACA <b>AA</b> GC <b>C</b> AG <b>CT</b> TT <b>CC</b> GG <b>AAA</b> AG <b>CA</b> TTTTTG
113	42	TAATA <b>AGA</b> TATGG <b>T</b> AG <b>ACA</b> ATATTTTT <b>G</b> CAGCC <b>AC</b> GCCACC
114	42	CGCCAA <b>AT</b> GAGTT <b>ATA</b> AGAA <b>AC</b> GATTTTT <b>AC</b> AAA <b>AT</b> GGAAAT
115	42	ACCTAC <b>AG</b> AC <b>CT</b> G <b>AG</b> GG <b>G</b> CAG <b>ATT</b> CA <b>AC</b> AGAGAG <b>AA</b> CGTCAA
116	42	CCCTT <b>CT</b> TTTT <b>GA</b> CC <b>TA</b> ATTT <b>G</b> CCAGTT <b>GT</b> TT <b>AT</b> AACCCA
117	42	AACAAG <b>CT</b> GAGT <b>GA</b> ATTAGAGAGT <b>AC</b> CTT <b>GC</b> AC <b>CA</b> GGCGTT
118	42	TTAGCG <b>AC</b> GGTATTTTT <b>AT</b> TTT <b>C</b> AT <b>GC</b> AGT <b>AC</b> AC <b>TC</b> CTTT
119	42	GCTTAT <b>CA</b> CT <b>CC</b> CGATTAGTT <b>G</b> CTATTT <b>TA</b> ATT <b>GT</b> AAATCA
120	42	CATCAC <b>GA</b> AC <b>C</b> ACGCTGAGAGAG <b>CA</b> AG <b>CA</b> ATTGAGTCTGTC
121	42	CGTCAC <b>CT</b> CG <b>AA</b> AG <b>G</b> AGACAGT <b>CA</b> AA <b>T</b> GGT <b>AG</b> CT <b>CC</b> AAAA
122	42	TATCGG <b>CC</b> ATCG <b>CC</b> AGTT <b>GG</b> AA <b>CA</b> AG <b>CC</b> AGT <b>AG</b> AACCAC
123	42	GAAGAT <b>CG</b> ATTGT <b>AT</b> TAAT <b>G</b> CC <b>GG</b> AGAG <b>CA</b> CCAT <b>CT</b> GCCCC
124	42	ATACCG <b>AA</b> GAAG <b>AA</b> ACAGGAG <b>GC</b> GATATA <b>AC</b> GT <b>CT</b> TCACC
125	42	GCCTGG <b>CT</b> AG <b>CC</b> G <b>AC</b> CAGCAG <b>AA</b> GATA <b>AA</b> ATA <b>AC</b> AA <b>TT</b> TTAG
126	42	AAAAG <b>AA</b> CTGAG <b>AT</b> TT <b>G</b> AC <b>G</b> AG <b>C</b> AG <b>TT</b> AAAG <b>GT</b> CACTTG
127	42	GGTCAGTTT <b>C</b> ATT <b>TT</b> GT <b>CT</b> G <b>GA</b> AGTTT <b>CC</b> GC <b>TA</b> AGAGAAAG
128	42	GAAGGG <b>AA</b> AG <b>CC</b> GT <b>CA</b> ACAGTT <b>G</b> AAA <b>GA</b> AATCG <b>CA</b> TAACAG
129	42	GACGGG <b>GA</b> AAAG <b>CT</b> AG <b>CG</b> GT <b>C</b> AG <b>CT</b> GATT <b>CC</b> AG <b>AG</b> AGG
130	42	GGAG <b>CC</b> CT <b>ATT</b> G <b>CG</b> TT <b>G</b> CG <b>CT</b> CA <b>CT</b> G <b>CT</b> CG <b>AA</b> CTTAGGAG
131	42	GGTTT <b>G</b> CA <b>AA</b> ACC <b>GT</b> T <b>GG</b> T <b>G</b> TAGAT <b>GG</b> GG <b>C</b> ATTA <b>AC</b> GATTGG
132	42	GGGCG <b>AT</b> GCGCG <b>G</b> GT <b>G</b> TTAT <b>CC</b> G <b>CT</b> CA <b>AA</b> ATT <b>CG</b> TTTTTAA
133	42	CCAAT <b>AG</b> CGGATT <b>GT</b> AC <b>T</b> G <b>AA</b> CCAT <b>C</b> ATGCATT <b>AA</b> CA <b>CA</b> AC
134	42	CAAAC <b>G</b> GAAC <b>GC</b> CG <b>GT</b> AC <b>CG</b> AG <b>CT</b> G <b>CA</b> AAT <b>CC</b> ATGAATC
135	42	ATTAG <b>AC</b> GTAGAT <b>T</b> GG <b>GC</b> G <b>G</b> AG <b>CT</b> G <b>AA</b> TT <b>G</b> TAA <b>AT</b> GGCGAA
136	41	CAAAG <b>ACT</b> TACC <b>G</b> AA <b>TA</b> AT <b>CA</b> AAAT <b>CA</b> CTGAT <b>AC</b> CA <b>T</b> GCCA
137	40	ATCATCATATT <b>GC</b> ACC <b>CT</b> CATTT <b>CA</b> AG <b>ACT</b> CA <b>AT</b> GCAA

138	40	TGCCTG <b>AGA</b> ACCCT <b>TGATGATGGCAATTCC</b> AGAAG <b>GCA</b> AAGC
139	40	TTGAAAATCTTT <b>TTTTCAGCGGAGTGACT</b> TAAAC <b>AGCCGGAA</b>
140	40	CAATCG <b>CTGTCCAGAAGGCTTGCCTGAT</b> AGCGAAAGACA
141	40	GAAAG <b>AGACCGAACGACGTTAGTAAATGGG</b> AGGAGTGTAC
142	39	AATGTT <b>TATCTACGTTATTTTTTTT</b> TAAAAC <b>GAACTCATC</b>
143	39	CTCATT <b>CCGAGGGTAGCTTTTTTT</b> AACGGCT <b>ACGGCTTGC</b>
144	39	TATTATTTAG <b>CTTGCAACAGGAAAAGTGGCACT</b> TACCAG
145	39	TTAGAATCAC <b>AGACGGGCAACAGCTG</b> TTGTT <b>CATTA</b> AAA
146	39	ATAGCTGTTG <b>AATTTTTGTTAAATCG</b> GCAC <b>GTCTATCA</b>
147	39	TCAACCGTTG <b>AAGTGCCCGTATAAAA</b> GCATT <b>CGCCTCAG</b>
148	38	TAAATATTGAC <b>TTTTTTTGGAAATTATT</b> CATT <b>AAACAA</b>
149	38	CAGTATTAACA <b>TTTTTTTCCGCCTGCAACAGTGA</b> TTAA
150	38	GGGTCGAGGTG <b>TTTTTTTCCGTAAAGCACTAAAC</b> CGCT
151	38	AAACCAGGCAA <b>TTTTTTTAGCGCCATT</b> CGCC <b>ATCATGT</b>
152	36	ACCCTG <b>ATT</b> TGCCTTT <b>TTTTTTT</b> GCGTCAGACTGT
153	36	TCCAAC <b>ATCCTGAATCTTTTTTTT</b> TACCAACGCTAA
154	36	CAACTA <b>AGCGCTTAATGTTTTTTT</b> CGCCGCTACAGG
155	36	TATATT <b>CAAGCTTGCATTTTTTT</b> TGCCTGCAGGTC
156	36	ATTTTT <b>AGTAATGTGTATTTTTTT</b> GGTAAAGATTCA
157	32	ATGAAAA <b>TTACATTTAATTGCTGAATATAA</b>
158	30	GCTGTC <b>TAAAACATGCGTTTTAATTCGAGC</b>
159	30	CACTAA <b>ACAATAATGACCATTAGATACAT</b>
160	30	AAAAGT <b>TTGGAAGGAATACTTTTGCGGGAG</b>
161	29	TTTAGT <b>AGTCGAGAGGGTTTTTT</b> TGATATA
162	23	GATTTT <b>GGAATAGATTTTTTCACG</b>
163	21	AAATAT <b>TAAGAACTATT</b> TGTGA
164	21	AAGATT <b>AACCATCGCA</b> AGGCC
165	21	TGATA <b>AGAAATCAAG</b> ACTTGC
166	21	TTGATT <b>CGCAAGTGGAA</b> AGGA
167	21	TCTACT <b>AAGGGTTCA</b> AGGCG
168	21	GGCT <b>GGGGATAGAGCGGA</b> ATT

**Supplementary Table 11** Staple sequence for the 6HB-based hexagonal DNA origami of 63-bp edge-length. The sequence is represented by colors; unpaired nucleotides with blue, crossovers with orange, the 14-nt seed dsDNA domain with green, and the 4-nt dsDNA domain with red.

Staple ID	Length (bp)	Staple sequences
1	60	TTTTGC <b>TAAGAGA</b> <b>AAGTTTATTTTGTCAA</b> ACAGC <b>CACTCCAACAGGTCAGG</b> GATAAGTGC
2	60	TTTCAG <b>GACAGAAAGTATAAAGCCAACGC</b> GCGCC <b>CTGACCATTAGATACA</b> ATGAATATAC
3	60	AATGC <b>AGAGATTTACATGATTAAGACTCAG</b> GCGCA <b>TGAAGCAAAGCGGATG</b> CAAAAAGGAAT
4	60	AGTTTT <b>CAGGACTAATGGTTAATTTT</b> CATGACAA <b>GCTAAAACACTCATC</b> AGAAATACGTA
5	60	AAATCA <b>CAGCCATACGGAAATTATTCAA</b> AATCA <b>ATAGCTCAACATGTTTT</b> TACCATTAG
6	60	TTTTT <b>GAGTAAGAAGAGAATATAAAGTAA</b> ATCGG <b>CTAGCATTGCCCCGAG</b> CTTTAATGC
7	59	GTCAGATATCTGGT <b>CTCAAAA</b> <b>TGTAGGGCTTAATTGT</b> TTCAT <b>CAAATGGTCAATAACCT</b>
8	59	AACGCCAGACGGT <b>CAGGTAGAACGCAGTATGTTAGCA</b> GAATA <b>AAAAAGATTAAGAGGAA</b>
9	59	ATTAGTGAGGCCGAT <b>TGAACCC</b> <b>TAAGGTAAAGTAAT</b> TAGCATG <b>TGCTTGACGGGGAAAGC</b>
10	59	CAGGCCAACC <b>CGCTCATTAAAGTAGAAAATTCATATT</b> AATTT <b>GAGAGTACCTTTAATTG</b>
11	58	ATCATAGGTG <b>ACCAATGAAACCATCT</b> AGAGCT <b>TCAGCTACAATTTTAC</b> CGATT <b>GCTTTT</b>
12	58	TGAGTAGAAC <b>AAAACATCGCCATTAA</b> AGGT <b>GGAAACGGGTATTAAG</b> GCAGAT <b>CGGC</b>

13	58	GGAACGAGGCTGCATCACATAAAAAACAGGGACTTATTAAAGATTCATCAGTTGATACAT
14	58	CGTATTAATGCATCGGGAGAAACACCAATTAGAAGGCTTATCCGATCATATACGTT
15	58	ATCCTCATTTTAAAGTATAGCCCGGGCTTCAATAAGAAACGATTAAAAGAAGAAAG
16	58	GTAACAATTTTTAGCTGCTCATTAGTGCAGCAACACTATCATACAGGTCTCACCTG
17	57	CCATCGGAATAATGACTGGATAAGCGGGCGTAGGGCTTTTTTGTCTGGCAAGTGT
18	57	CTTTACAGAGA AACGTAGAAAATACATACAGGTGGCAACATATTTTGTGTGCGTTTT
19	57	TTCCAGAGCCGGTTTACCAGCGCAAAGAAGGGCGACATTCAATCCTGAATTTTTCG
20	57	CCTCCCGACTCACCGGAATCATAATTACTAAAGCCTGTTTAGTGTATTCTATAACAG
21	57	CCGTTTTTATAGAATCGCCATATTTAACACAACATGTAATTTACCAAGTAGGGCGCG
22	57	TCGTGAAAGACAGCTTTTTTATCGGAACGAGGGTAAATGAATTTTTTTTGTATG
23	57	GATAACCCACCGAACAAGTTACCAGAAACCGAGGAAACGCATCAGAGGCATAAAT
24	56	GCCCAATATTTTTTGAACCCATGTACCGTATAATTAATTTTCTTTTTTTAGAA
25	56	AGTTTTCGTTTTTTTACCAGTACAACTACCCTAACAATAATTTTTTGTATTAG
26	56	CGGGTAACGTTAGTAGCAACGGTATTGTGAATTACCTTATGCGTTTTTTATTTTA
27	56	ACAACTTTTTAAAGGAATTGCCACGCAACGCGCCTGCAATAGCTATCTACAACAA
28	56	GTAGCATTTTTTTTTACAGACAGCCCTCACGAGGCCACCGAGTTTTTTTAAAGAG
29	55	AAACTAGCATTTTCGAGCCAATTCCAACATCAATTCTACTAAGCCCTAGACAATA
30	55	AGCTTGGAGTAGTAAATTGGTACCCAACGAAAGAGGCAAAAGAAGGCATGAGGA
31	55	GCTTGCCGAATACCCAAAAACTGAATTACCCTGACTATTAGTAAGATTCAACT
32	55	AGAATGACGCAAGACACCAATCCAAGCGAACAGACCGGTTGATAAAGCGGGG
33	55	GACTACAGGGAGGGAAGGTATTGACCTAATTGCTGAATATAACGTACAGCCAGCA
34	55	GCCCGAGCGTTATACAAATTCAGATATTGCGAACGAGTAGACCTTTTACGTAGAT
35	54	AGAAAATAAGTTTTTTTTTTACGGGGTCAGGAACGCGAGATTTTTTTAACTTT
36	54	TTCAATCATCATATTTTTTTCTGATTATCTACATTTTGATTTTTTTGCTCAA
37	54	AAGGGTTTTTAAACCGAATCCGCGACCTGCTCCATTTTTTTTGTACTTAGCC
38	53	TACGAGGCAATAGTATAGACGGGAGAATTGAACGGGAATACCAATAAG
39	53	CGTCGAGAGGGAAGCAATATTTATTTTCCCGGAATAGGATTAGGAAAAGCC
40	53	CAAGGCCGGAATGCTGGATTAGTTGCTATTAATATTGTGGGAATTACTGAGA
41	53	AGTAACAGTATTTAGTAAATAGCAAGCAATCTTACCATAAAGAAATTCCTTT
42	53	GCGAACTGATATAGTAGTGTCTTTTCTTATCGTAATAATACGTGGCAGAATC
43	53	ATGCCACTACGAATACAACCCGGATATTATGCTTGAGAAGACTTTTTTTATC
44	52	TTCAGGGATAGAACCACCCTTTTTGAGCCGCCGCTACTGGTCTGGCTC
45	52	GTATCGGTCCCAACCTAAAACCAAAATAGCGAGTTTTTTTAGGCTTTTGCAA
46	51	AGACTTTAACATGTTTTGAAATACCGACGTTGATTTTTTTTAAATAAG
47	51	TATCTTCATCAATAAAAAAGCTCATGGCCATCACCCGCTGCAAACGCCT
48	51	TCAGAGCGTGCCCGCAAATCCAATCGCAGAAAACACGCGTTTTTCATAGCAA
49	51	AAGCCTTTAAAGGTGAATAAGAATAAATGCGGGATGCAACTAAAGTACGG
50	51	ATAACATGTTACGCTAAAGTCCTAAGGGAAGAAAGCGAAAGGGCTATCAAC
51	51	AAGAGTCGTTATATGCTATTTTCGAACTATTATTTTTTTCTGAAACA
52	51	ATCAAAATTTTTTTTACCAGAACAGAGCCACCACCGGATTAGCCAGTTA
53	51	TTGATTACAATATATACTTCTGAATAATGGAAGGGTTTTTTTTTAGAACC
54	51	ATTACATTTTTTTTAAACAATTTCAATTTGAATTACCTTAAATAGTTTTTG
55	51	AATAGATATGCAGATAACCGATATTTTTTTTATTCGGTCGCTGAGGAAGGA
56	51	TGCTGAACTTTTTTTCTCAAATATCAAACCTCAATCATTTTCGCTAGGAA
57	51	GAGGTTTTTTTTGAATTTCTTAAACAAGTCCAAAAGGATTTTTCTTTAATT
58	51	TCCTCGTTTTTTTTAGAATCAGAGCGGGAGCTAAACAATTTAGAAAGAAACC
59	51	TTTTATATTACATGGGATCGTCACCCTTTGCTAATTAATGCGCTAGTTAG
60	51	AAATCGTAATTTCAACCACCAGAAGGAGTCAATAGTTCATTTCAAACACTG
61	51	CGTAACGATTTTTTTTCTAAAGTTTTGTCGCTTTTCTTTGACCATCAAGA
62	51	GAATAGACTTGCAAGCCAGTAATAAAAGGGACATTCTTTTTTTGGCCAAC
63	49	CTTGCTTTTTTTGGTAATATCCAGAAGTAATAACATTTTTTACTTGCC
64	49	ATTAATTTTTTTTAAAAGTTTGAGACAAACAATTTTTTGACAAC
65	49	TAACCTTTTTTTTCCGGCTTAGGTTGGATAGTGAATTTTTTATCAAA
66	49	ATTATACCTTTTTAAAGCGCAAACAGAGCCACCTTTTTTTCCCTCATT

67	49	CCACCC <b>T</b> CAAAG <b>T</b> AGCGCATAGGCTG <b>T</b> TTTT <b>T</b> CTGACCT <b>T</b> CCCAGCG
68	49	CGCAG <b>T</b> TTTT <b>T</b> TCT <b>T</b> GA <b>T</b> T <b>T</b> ACCG <b>A</b> TATTCACAA <b>T</b> TTTT <b>T</b> CAAATAA
69	47	CAAAA <b>T</b> ACCCTCGTTTT <b>T</b> TTTT <b>T</b> CCAG <b>A</b> CGACG <b>A</b> TAAA <b>A</b> ATCAAC
70	46	AACAA <b>G</b> ATAATA <b>A</b> CTGACGAG <b>A</b> TTTT <b>T</b> TTACACCAGAA <b>C</b> TTTT <b>C</b>
71	46	AATTGT <b>G</b> TACC <b>G</b> CG <b>A</b> CG <b>A</b> T <b>T</b> GGC <b>T</b> T <b>G</b> TCCAG <b>T</b> CGTTAATAAAA
72	45	GGAGGTTTA <b>G</b> TCGAA <b>T</b> GA <b>C</b> CA <b>A</b> CTTT <b>G</b> AAAA <b>A</b> ATCT <b>A</b> AAGCGTC
73	45	GCGACAGAA <b>T</b> CCAT <b>C</b> TA <b>G</b> A <b>A</b> CC <b>G</b> CC <b>A</b> CC <b>T</b> GCCCC <b>T</b> A <b>A</b> CTATA
74	45	TTGCGC <b>C</b> GAAA <b>T</b> CGGG <b>G</b> T <b>A</b> T <b>A</b> GT <b>A</b> AAA <b>A</b> ATCG <b>T</b> CG <b>C</b> AAGAAACA
75	45	TTGAATACC <b>A</b> GAAAA <b>C</b> AT <b>A</b> T <b>G</b> T <b>G</b> AG <b>T</b> GA <b>A</b> TTTT <b>A</b> AT <b>G</b> ATCATT <b>T</b>
76	45	CAGAAGATA <b>A</b> CTAA <b>G</b> CGAA <b>A</b> GG <b>A</b> ATT <b>G</b> AG <b>G</b> TGGAT <b>T</b> ACCGCCA
77	45	AGCGGTCAC <b>G</b> GTATA <b>A</b> AC <b>G</b> GT <b>A</b> CG <b>C</b> AG <b>A</b> T <b>C</b> ACAC <b>G</b> GGAG <b>T</b> TA
78	45	AAGAAGTTT <b>T</b> A <b>T</b> CCC <b>C</b> G <b>A</b> GT <b>A</b> AG <b>C</b> CA <b>A</b> TT <b>T</b> AAG <b>A</b> ACCGAT <b>A</b> G
79	42	<b>G</b> CC <b>G</b> AA <b>A</b> AGAAA <b>A</b> T <b>A</b> CA <b>C</b> GTCAA <b>A</b> TTTT <b>T</b> AAA <b>A</b> ATAGCAG <b>C</b>
80	42	<b>C</b> T <b>C</b> TTTT <b>G</b> AAG <b>G</b> T <b>C</b> ATT <b>C</b> T <b>A</b> CCA <b>A</b> TTTT <b>T</b> AACGAGCG <b>T</b> C <b>T</b>
81	42	<b>T</b> G <b>T</b> CT <b>G</b> GA <b>A</b> GT <b>T</b> CC <b>A</b> T <b>A</b> GAAC <b>G</b> CG <b>T</b> TTTT <b>T</b> GTTTTAGCG <b>A</b> A
82	42	<b>G</b> TT <b>T</b> AG <b>C</b> T <b>A</b> T <b>T</b> C <b>A</b> TT <b>T</b> G <b>C</b> CG <b>A</b> CT <b>A</b> TTTT <b>T</b> GAACAAG <b>C</b> AAG
83	42	<b>C</b> GG <b>C</b> GA <b>A</b> CG <b>T</b> AG <b>A</b> AG <b>G</b> GA <b>A</b> CA <b>A</b> GA <b>A</b> TTTT <b>T</b> AATATCC <b>C</b> AT <b>C</b>
84	42	<b>A</b> GT <b>T</b> C <b>A</b> GA <b>A</b> GA <b>A</b> T <b>G</b> A <b>C</b> G <b>T</b> A <b>A</b> T <b>T</b> G <b>A</b> GTTTT <b>T</b> AATATCAG <b>A</b> GA
85	42	TCACGT <b>T</b> G <b>A</b> CA <b>A</b> T <b>G</b> T <b>A</b> CC <b>G</b> A <b>A</b> GC <b>C</b> TT <b>T</b> A <b>A</b> T <b>A</b> AG <b>A</b> A <b>A</b> ATA
86	42	TTCATT <b>G</b> CC <b>A</b> G <b>A</b> GT <b>C</b> CA <b>A</b> AAAA <b>A</b> AG <b>C</b> CT <b>T</b> G <b>A</b> T <b>A</b> A <b>G</b> TA <b>A</b> G
87	42	TCACC <b>A</b> G <b>A</b> T <b>C</b> CT <b>G</b> A <b>T</b> G <b>C</b> TT <b>T</b> G <b>A</b> C <b>G</b> A <b>G</b> A <b>C</b> T <b>G</b> CG <b>C</b> GG <b>A</b> G <b>A</b> T <b>G</b> A
88	42	GGT <b>G</b> T <b>A</b> CC <b>A</b> G <b>T</b> CA <b>G</b> A <b>T</b> G <b>A</b> T <b>A</b> C <b>A</b> GG <b>A</b> G <b>T</b> G <b>A</b> GC <b>A</b> T <b>T</b> GA <b>A</b> AC <b>C</b> G
89	42	ATTATA <b>C</b> A <b>G</b> AC <b>C</b> A <b>G</b> CA <b>A</b> CG <b>G</b> A <b>G</b> A <b>T</b> TT <b>G</b> T <b>C</b> ACC <b>C</b> T <b>C</b> A <b>C</b> AG <b>G</b> A <b>G</b>
90	42	GTT <b>G</b> AG <b>G</b> G <b>C</b> TTTT <b>G</b> G <b>A</b> CG <b>T</b> GG <b>G</b> A <b>A</b> GA <b>A</b> AG <b>A</b> GG <b>A</b> C <b>A</b> CT <b>G</b> ATA
91	42	ATACAT <b>G</b> C <b>A</b> GG <b>T</b> CA <b>A</b> CC <b>T</b> C <b>A</b> GA <b>A</b> CC <b>G</b> CA <b>T</b> CA <b>T</b> CG <b>A</b> T <b>G</b> A <b>A</b> C
92	42	AAGCC <b>G</b> TT <b>T</b> C <b>A</b> G <b>C</b> T <b>A</b> ACC <b>A</b> CC <b>A</b> CC <b>C</b> CT <b>A</b> TGG <b>T</b> G <b>A</b> AG <b>T</b> G <b>T</b>
93	42	TTCCGG <b>T</b> CA <b>C</b> T <b>G</b> T <b>A</b> G <b>T</b> AG <b>C</b> G <b>A</b> T <b>A</b> G <b>C</b> T <b>T</b> AG <b>G</b> CT <b>G</b> A <b>T</b> GT <b>A</b> TA <b>A</b> C
94	42	TGTA <b>A</b> AT <b>A</b> T <b>T</b> A <b>A</b> G <b>A</b> GC <b>T</b> TT <b>A</b> GC <b>G</b> T <b>C</b> A <b>G</b> A <b>T</b> AG <b>C</b> CA <b>C</b> CC <b>C</b>
95	42	AGTT <b>A</b> AT <b>C</b> A <b>G</b> A <b>G</b> CC <b>T</b> T <b>A</b> T <b>T</b> AG <b>C</b> G <b>T</b> TT <b>C</b> A <b>A</b> G <b>T</b> TC <b>G</b> CT <b>G</b> A <b>G</b>
96	42	CACCG <b>A</b> CT <b>T</b> G <b>C</b> AG <b>T</b> A <b>G</b> C <b>A</b> CC <b>A</b> TTTT <b>T</b> A <b>A</b> T <b>G</b> G <b>A</b> T <b>A</b> T <b>C</b> ACC <b>G</b> T
97	42	GCA <b>A</b> AG <b>C</b> GA <b>A</b> TT <b>A</b> TA <b>A</b> T <b>A</b> C <b>A</b> TT <b>T</b> G <b>A</b> G <b>C</b> AA <b>A</b> GA <b>A</b> T <b>C</b> T <b>T</b> CT <b>G</b>
98	42	TGCG <b>G</b> A <b>A</b> GA <b>T</b> TT <b>A</b> GA <b>A</b> T <b>C</b> GC <b>G</b> C <b>A</b> G <b>A</b> GA <b>A</b> GA <b>T</b> GA <b>C</b> TT <b>C</b> T <b>G</b> T
99	42	ACCT <b>A</b> AA <b>A</b> AC <b>T</b> T <b>G</b> T <b>A</b> AA <b>C</b> AA <b>C</b> AT <b>C</b> A <b>A</b> GT <b>T</b> AC <b>A</b> AG <b>T</b> ATT
100	42	G <b>C</b> GC <b>G</b> T <b>A</b> GC <b>C</b> GC <b>G</b> CA <b>C</b> A <b>A</b> CT <b>T</b> CA <b>A</b> C <b>A</b> GC <b>T</b> TT <b>T</b> G <b>C</b> G <b>C</b> A <b>G</b> A <b>T</b>
101	42	CGCT <b>G</b> A <b>G</b> ATT <b>A</b> AC <b>A</b> G <b>C</b> AA <b>A</b> TT <b>A</b> AC <b>G</b> TT <b>C</b> A <b>A</b> C <b>A</b> G <b>A</b> TA <b>A</b> T <b>C</b> C
102	42	GCC <b>A</b> TT <b>G</b> T <b>A</b> G <b>C</b> A <b>A</b> G <b>T</b> G <b>A</b> GG <b>C</b> G <b>T</b> C <b>A</b> G <b>T</b> AG <b>C</b> C <b>A</b> G <b>C</b> T <b>A</b> AAA <b>A</b>
103	42	TG <b>A</b> TT <b>G</b> T <b>A</b> AG <b>G</b> TT <b>A</b> AG <b>C</b> AA <b>T</b> G <b>A</b> AAAA <b>A</b> T <b>A</b> C <b>A</b> G <b>A</b> G <b>T</b> ACT <b>T</b> C <b>T</b>
104	40	TC <b>C</b> T <b>T</b> AG <b>A</b> CA <b>A</b> AT <b>G</b> C <b>C</b> TT <b>G</b> A <b>G</b> T <b>A</b> AC <b>A</b> C <b>A</b> CC <b>C</b> CG <b>C</b> ATT
105	40	AG <b>C</b> CG <b>C</b> GA <b>A</b> T <b>T</b> A <b>A</b> T <b>A</b> T <b>A</b> TTTT <b>T</b> AG <b>T</b> TC <b>G</b> CT <b>A</b> TT <b>A</b> CT <b>T</b> GA
106	40	T <b>C</b> T <b>G</b> T <b>A</b> A <b>A</b> T <b>A</b> CC <b>A</b> G <b>A</b> T <b>A</b> G <b>T</b> GG <b>C</b> A <b>A</b> T <b>T</b> AG <b>G</b> A <b>G</b> CA <b>A</b> G <b>T</b> CCA
107	40	GG <b>A</b> T <b>T</b> C <b>A</b> G <b>C</b> AG <b>C</b> T <b>G</b> AA <b>A</b> T <b>G</b> G <b>A</b> T <b>T</b> A <b>T</b> TC <b>A</b> G <b>T</b> G <b>C</b> T <b>A</b> C <b>A</b> G <b>G</b>
108	39	AT <b>G</b> AA <b>A</b> T <b>A</b> GT <b>T</b> G <b>T</b> CCA <b>A</b> ACT <b>G</b> CG <b>G</b> A <b>T</b> GT <b>T</b> TA <b>A</b> TTTT <b>T</b>
109	39	T <b>G</b> AA <b>A</b> GT <b>C</b> CT <b>C</b> A <b>G</b> AG <b>C</b> TTTT <b>T</b> T <b>G</b> CC <b>A</b> CC <b>C</b> T <b>T</b> TC <b>A</b> T <b>A</b>
110	39	G <b>C</b> G <b>T</b> TA <b>A</b> AA <b>C</b> AG <b>T</b> A <b>C</b> A <b>T</b> TTTT <b>T</b> T <b>A</b> AA <b>T</b> CA <b>A</b> TA <b>A</b> A <b>T</b> TA
111	39	T <b>A</b> CC <b>A</b> T <b>A</b> AG <b>T</b> T <b>G</b> G <b>C</b> AAA <b>T</b> TTTT <b>T</b> T <b>C</b> A <b>A</b> C <b>A</b> GT <b>A</b> T <b>C</b> AC <b>C</b> T
112	39	AG <b>A</b> G <b>A</b> T <b>A</b> TA <b>A</b> AG <b>G</b> G <b>A</b> T <b>T</b> TTTT <b>T</b> TT <b>A</b> G <b>A</b> C <b>A</b> G <b>C</b> GT <b>G</b> CT <b>T</b>
113	38	CG <b>A</b> ACT <b>A</b> AC <b>G</b> G <b>T</b> TTTT <b>T</b> TT <b>A</b> CA <b>A</b> C <b>A</b> T <b>T</b> AT <b>T</b> CA <b>A</b> T <b>C</b> A <b>T</b>
114	36	A <b>A</b> TT <b>C</b> GA <b>A</b> AT <b>A</b> GG <b>T</b> G <b>T</b> A <b>T</b> TTTT <b>T</b> TT <b>C</b> AC <b>C</b> G <b>T</b> A <b>C</b> T <b>C</b> A
115	36	G <b>A</b> T <b>G</b> G <b>C</b> T <b>G</b> A <b>T</b> A <b>G</b> C <b>A</b> G <b>C</b> A <b>T</b> TTTT <b>T</b> TT <b>C</b> C <b>G</b> T <b>A</b> AT <b>C</b> A <b>G</b> T <b>A</b>
116	36	TT <b>G</b> ATT <b>C</b> A <b>T</b> A <b>C</b> G <b>G</b> ATT <b>T</b> TTTT <b>T</b> TT <b>C</b> G <b>C</b> CT <b>G</b> ATT <b>G</b> CT
117	36	AG <b>C</b> T <b>G</b> AA <b>A</b> AA <b>T</b> AC <b>C</b> GA <b>T</b> TTTT <b>T</b> TT <b>A</b> C <b>G</b> A <b>A</b> CC <b>A</b> CC <b>A</b> G
118	34	CA <b>A</b> AA <b>T</b> CA <b>A</b> T <b>C</b> A <b>A</b> GG <b>T</b> G <b>A</b> G <b>A</b> CT <b>C</b> CT <b>C</b> AG <b>T</b> A <b>C</b>
119	34	TC <b>A</b> TT <b>A</b> CC <b>T</b> CA <b>A</b> C <b>A</b> T <b>A</b> TT <b>T</b> G <b>C</b> A <b>C</b> G <b>T</b> AA <b>A</b> TT <b>A</b> A <b>C</b>



120	34	AATCAATCCGACAATCTGACCTGAAAGCATGGCT
121	34	GTAATCTACTTTAACTACAGAGGCTTTGATTAAA
122	30	CAGATAGAAGAATTCTCAAATGCTTTAAAC
123	27	CTAATTTACGCTGTCCAGACGACGACA

**Supplementary Table 12** Staple sequence for the DX-based triangular DNA origami of 128-bp edge-length without internal mesh. The sequence is represented by colors; unpaired nucleotides with blue, crossovers with orange, and the 14-nt seed dsDNA domain with green.

Staple ID	Length (bp)	Staple sequences
1	77	CAAAGGGCGAA <del>TTTCTATCAGGGCGATGGCCACTG</del> CTCATTTTTT <del>TTTTTTT</del> ACCAATAGGC C <del>GG</del> ACTCCAACGT
2	77	GAGAAAGGAAG <del>TTTAGCGAAAGGAGCGGGCGT</del> AGACTAGGTGAA <del>TTTTTTT</del> ATCCTTTTTG A <del>TGG</del> CGAACGTGGC
3	77	CAGGACCACTT <del>TTTCGGCCCTTCCGGCTGGCTGGT</del> ACTATGGATGA <del>TTTTTTT</del> CGAAATAGAC A <del>GCG</del> GATAAAGTTG
4	58	GACCGAGATAGGG <del>GGGGCCAGATGGTAA</del> GGTATCATTG <del>CAGCACT</del> TTGAGTGTTGTC
5	42	TAGGTGCCTC <del>AGCGTTGCGCTCTGGATGGAGGA</del> TCGCTGAGA
6	42	ATTGGTAACT <del>GGCTACAGGGCGCACATTAATTC</del> TGATTAAGC
7	42	TTTACTCATA <del>TACCCGCCGCGCTTAATGCGCT</del> CAGACCAAG
8	42	TTGATTTAAA <del>ACACGCTGCGCGTAACCACCACA</del> TACTTTAGA
9	42	AATTTAAAAG <del>GGGCGCTGGCAAGTGTAGCGGT</del> CATTTTT
10	42	CCAAAATCCCT <del>TAGAGCTTGACGGGGAAAGC</del> CAATCTCATGA
11	42	TTTCGTTCCA <del>CCCTAAAGGGAGCCCCGATT</del> AACGTGAGT
12	42	ACCCCAATCA <del>TCCGTAAAGCACTAAATCGGAAT</del> GAGCGTCAG
13	42	GTTGTAATTC <del>GAAAGTTTTTGGGGTCGAGGT</del> GATGTACCCCG
14	42	TTGTTAAATC <del>AACGTGAACCATCACCTAATCC</del> GTTAAATTT
15	42	AATCCCTTAT <del>AGAGTCCACTATTAAGAACGTA</del> AATCGGCAA
16	42	TCGTAGTTAT <del>CCCGGTGAGCGTGGGTCTCGCGC</del> CCTCCGTA
17	42	GGAGTCAGGC <del>ATTATTGCTGATAAATCTGGAGT</del> ACACGACGG
18	26	CAGTTTGAACA <del>AAATCAAAGAATA</del>

**Supplementary Table 13** Staple sequence for the 6HB-based triangular DNA origami of 128-bp edge-length without internal mesh. The sequence is represented by colors; unpaired nucleotides with blue, crossovers with orange, and the 14-nt seed dsDNA domain with green.

Staple ID	Length (bp)	Staple sequences
1	58	GAGTAT <del>GGACCGAATGATAATCTCATGA</del> AGAAAGGAAGGG <del>TTTTTT</del> AGAAAGCGAAAG
2	58	TGAGAG <del>TTGACGC</del> CACCGAGATAGGG <del>TTT</del> CTATCAGGGCG <del>TTTTTT</del> TGGCCACTACG
3	58	TTTATA <del>GCGGCAA</del> CCACGACGGGGAGT <del>CAA</del> AAGGTGGCAT <del>TTTTTT</del> AATAGGTGAGAT
4	57	GGTAAGCCCTCC <del>TTT</del> AGTTATCT <del>AAATTAATAGACTGGAT</del> TTTTCGGATAAAGTTGC
5	57	GCAAAATCCCTTA <del>TTTAAAGAATA</del> GGGGCAAGAGCAACT <del>TTTT</del> CGCATACACTATT
6	57	TTTAAAAGGATCT <del>TTT</del> GATCCTTT <del>TGGAGCTAACCGCTTTTTTT</del> CAACATGGGGGAT
7	52	AGCTTC <del>CGTTAAT</del> GGACCCAGAAAAG <del>TTTTTT</del> TGGTAGCAAATACGCACTA
8	52	ATCGGAGAGTATT <del>CT</del> TAGTGACGTAA <del>TTTTTT</del> TCCGGGTGGTTGGATCT

9	51	GTAATC <b>TTTTTT</b> GTACTATGCAGTAACTTGTCCGAGG <b>TTTTTTT</b> TCCAG
10	48	CTAAGAGACAAATTAC <b>ATTCGCCGCATTTT</b> GGAAG <b>CGT</b> GGAAGAACC
11	48	AATCGA <b>CCACACGTT</b> CATGAGACAATA <b>ACTTTGAT</b> CACTTCATTTTTAA
12	48	ATCATA <b>ACTCAGGAGTGCACGAGTGGGTT</b> GGTTG <b>AT</b> AGGCCGAAATCG
13	45	GACAGGAGAT <b>T</b> TGCAG <b>CGCCCTCCGGCTGGA</b> AGAGT <b>TC</b> CTATAT
14	45	GAGCGGGCG <b>CATTTAA</b> AGTTGGGAACCGG <b>AGT</b> ATCCG <b>CT</b> TGGCGG
15	45	TGAACCATC <b>AT</b> AACCA <b>AGTACTCACCAGT</b> CACAGTT <b>G</b> TAGTTAT
16	44	GCGGCCAC <b>G</b> TAGAA <b>GTAGCCTCTCACCCCT</b> TGGTT <b>TG</b> TCTCGC
17	43	CATGTA <b>ACTCGCCCTGATAAATGCTTCAATTTT</b> AAAAAGGAA
18	43	CTCAGAATGAC <b>TTACATCGAACTGGATCTCATT</b> TAAAGATCCT
19	43	AGGACCACT <b>TCGAATTCGACGAAAGGGCCTT</b> ACGCCTATT
20	42	TCAAC <b>AACCTGTATCACTAGGTACATGT</b> GAGCACTTGGTGGC
21	42	CTGGCGCCCGT <b>TC</b> CACTATTACAGGTACGAGC <b>GA</b> AACAAAAT
22	42	CACATT <b>AATAGACA</b> AACTATTA <b>ACTGGCG</b> TTTCT <b>TG</b> AAAAGA
23	42	TAACCA <b>CGGTAAC</b> TGTGACACCACGAT <b>GGGAACC</b> CCGGACCA
24	42	TTGACG <b>GTTTCGT</b> TC <b>ACTGCGGCCAACT</b> GCCCTT <b>AT</b> CTTCAC
25	42	AGCACT <b>AGTTGTA</b> AAGTAAGAGAATTAT <b>G</b> CTCAC <b>CA</b> CAGTCT
26	42	TCCTAG <b>ACGT</b> CGA <b>CATATAGAACA</b> AGTAGCGT <b>GGA</b> TTGCTG
27	42	ATGACAAAGTCAAAT <b>TCTCTGAATCTGTGAGCCGGT</b> GCAAATT
28	42	GGTTGG <b>TGAAACA</b> AT <b>GCGCTCCAGGCT</b> GAGGCAA <b>CT</b> TACTCT
29	42	AATAAT <b>GGA</b> ACTA <b>CTATGGATGAACGAA</b> ATTGCGT <b>TG</b> GTAATA
30	42	ACACCA <b>ATTTAAA</b> AAGAC <b>GT</b> CAGGT <b>GGCT</b> TGCGC <b>AG</b> ATCGCT
31	42	AACAAC <b>GACTTTT</b> CTTGTGCAATC <b>TACCC</b> GGTA <b>CC</b> AGGGCG
32	42	GAGAT <b>AGCCGCTACC</b> AGGTATTTATTT <b>AT</b> CATT <b>CA</b> GGGAAA
33	42	CGTGTAT <b>TCGTGTAGCCGCGTTAATGCGT</b> GCCT <b>CCA</b> ATGGC
34	42	TGTGCG <b>CCCTGTA</b> GACTGATTAAGCATT <b>CACACC</b> CTACTCAC
35	42	ATCTGG <b>ACAGTTATCTATTTGTTTATTTG</b> ACGAG <b>CG</b> TCAGAC
36	42	ACCAAA <b>CTTCTAA</b> ACCATGTTACT <b>TTGGT</b> GAGAAA <b>CC</b> TGCGCG
37	42	CAAGTT <b>TGGT</b> CAC <b>GATAGTGT</b> TAAATAAGTGATA <b>AT</b> ACATTC
38	42	ACATCG <b>AA</b> TTTT <b>CCTGGCAAGTGTAGCA</b> CTCAT <b>AA</b> AGCCAT
39	42	AAATAT <b>GCTGAATGTATACTTTAGATTGT</b> AGGGC <b>GAG</b> CAGAT
40	42	ATAAGT <b>AAAGCTTAA</b> CGAA <b>ACCTTGCACT</b> AT <b>TG</b> CATAAG
41	42	GACGT <b>AGCG</b> AAA <b>T</b> CGGCGAAC <b>GTGGCG</b> CAAAA <b>TG</b> ACAACG
42	42	CCGTGT <b>CTACTTCTCCCTTAACGTGAGT</b> GGAAG <b>CT</b> TTATA
43	42	TGTGTA <b>AGTAAATATTCCTTTTTTTGCGGT</b> GATA <b>ACC</b> ACTGA
44	42	ACCAT <b>AGC</b> ATTT <b>TCTCGATATTCACAAA</b> AGGAA <b>CT</b> TAGAGC
45	42	GCGTCAG <b>CCCCGATTGCTATGCAAAA</b> ATATTAC <b>CG</b> CCTCC
46	42	ATTATC <b>TGAATCG</b> ACCCTAAAGGGAG <b>CACCCCA</b> ATGCCATA
47	42	TGTTTT <b>TGCAGTGCTCATATGTACCCCGAAT</b> CGG <b>AT</b> ATCCAA
48	42	AGATGAG <b>ACTAGTCCAGAA</b> ACGCTGGT <b>GG</b> CATG <b>ACT</b> TCGCGT
49	42	ACGGAT <b>GAAAGTAAGACAGTCTGGCAA</b> TAAGTGG <b>CG</b> CCGTAA
50	42	TAAATTT <b>TCGAGTTAACGCAAGCAAG</b> AGGTAG <b>CA</b> AGATGC
51	42	GTGTTG <b>CT</b> ATTA <b>ATCAAGTTTTTTGGG</b> TTGTTA <b>AG</b> CATCTT
52	42	TGAAGA <b>TCAGAAA</b> AATCAGCTC <b>ATTTTT</b> CCCTAA <b>TA</b> CCGTGT
53	42	TGCTAT <b>GCCAATGATTAGAAGTTAGAAA</b> ATTCTG <b>AA</b> GGGCGA
54	42	GGTAT <b>ACATAGTCTAGTACAACCTTATTATCTT</b> CTGAGGGG
55	41	AAAAC <b>GGAGTGTGTATTATCCCGTATTT</b> TCGC <b>CT</b> CGGGT
56	41	AGCTA <b>TTTTTGA</b> CCGAAGAAC <b>GTTTTT</b> GGCGC <b>GG</b> TTCCAG
57	40	ATAAAT <b>CA</b> AACGA <b>AGCGTTGTTTTGAT</b> AGAAGAATAATTG
58	40	TGAGCTGGTT <b>GGAACGTGGACTCCACA</b> AGAG <b>TA</b> AAGTTC
59	39	GGGGT <b>TTTTTTT</b> GGTCATACCTAT <b>GCGAAGGAA</b> ACATTT
60	39	AGCGC <b>TTTTTTT</b> GATTAAGCACT <b>ACGTTAATT</b> CATGAT
61	39	AGGGAAAACA <b>ACCTTCAAACGGGTAG</b> CGCAG <b>CA</b> CAGAGA

62	39	TGTTGTACTCTATGTGCGATGTGACCTTGCTATACAAA
63	27	ACGACGAGCGCTCGACTGGGGCCAGAT
64	23	TTTGGAACGTCAACATAATTAT

**Supplementary Table 14** Staple sequence for the DX-based hexagonal DNA origami of 74-bp edge-length without internal mesh. The sequence is represented by colors; unpaired nucleotides with blue, crossovers with orange, and the 14-nt seed dsDNA domain with green.

Staple ID	Length (bp)	Staple sequences
1	78	AGCAATGGCAACTTTTTTGCGCAAACCTATTGAGGCGGATAATTTAGTTGCAGGACCACTTCTGCGCCACGATGCCTGT
2	78	TCAAGTTTTTTGTTTCGAGGTGCCGTAAAGCATTGGTATTTACTGTGACACCAAGTTTACTCACCATCACCTAA
3	78	AACCACCACACCTTTTGCGCTTAATGCGCAGCCGGTGAGCTTTGTGGGTCTCGCGGTATCATTGTACGCTGCGCGT
4	78	ACTATTAAGAAATTTGACTCCAACGTCAAAGGATCTAGTTTTGAAGATCCTTTTTGATAATCGGAACAAGAGTCC
5	78	AGGCCGAAATCGTTTAATCCCTTATAAATCGTCAGACCCCTTAATCATATGTACCCCGGTTGTTTTTTAACCAAT
6	78	CGGCGAACGTGGTTTAAAGGAAGGGAAGATCTACACGACGTTGGGAGTCAGGCAACTATGGATTGACGGGGAAAGC
7	47	AATAGACTGGATGAAGTGGCGAACTACTTACTCTAGCTTTTGTTAA
8	42	CCGGCTGGCTGGCGTTGCGCTCGAGCGTGACACTCGGCCCTT
9	42	GATAAATCTGGCTACAGGGCGCACATTAATTGTTTATTGCT
10	42	GCCAGATGGTAGGGCGCTGGCAAGTGTAGCGGCAGCACTGGG
11	42	TATCGTAGTTAAAGCGAAAGGAGCGGGCGCTAAGCCCTCCCG
12	42	GACAGATCGCTGGGAGCCCCGATTTAGAGCTGAACGAAATA
13	42	CCTCACTGATTGCACTAAATCGGAACCTAAAGAGATAGGTG
14	42	TAGATTGATTGGGGCGATGGCCACTACGTGAATATATACTT
15	42	TTTTAATTTAAAGGGCGAAAAACCGTCTATCAAAAACCTTCAT
16	42	AATCCCTTAAAGGTTGAGTGTGTTCCAGTTTCATGACCAA
17	42	GTTCCACTGACAAAAGAATAGACCGAGATAGGTGAGTTTTC
18	37	TCAGCTCAAATTCGCGTTAAATTTCCCGCAACAATT

**Supplementary Table 15** Staple sequence for the 6HB-based hexagonal DNA origami object of 74-bp edge-length without internal mesh. The sequence is represented by colors; unpaired nucleotides with blue, crossovers with orange, and the 14-nt seed dsDNA domain with green.

Staple ID	Length (bp)	Staple sequences
1	55	CATTCCATAAAACGAACTAGAGCCACCATAACAACGCTGAGACTCCTCAAGTCGAG
2	50	GTAAATACGTAAATTTTCATCGGCATTTTCGGTTAGCCCCCTTATTGCC
3	49	ACCAGAATGAGAAAGTGTACTGGTAATAAGTTAACGGGTGTCAGATAAA
4	49	ACGGTCAGCCACGACCACAGAGCCCGCTTATTGACAGGAGAGGTG
5	48	CGCTCCCTTGGCCACCCTCATTAGCAAGTTTGGCGAAATGCAA
6	48	GGATGAGTACCGGCACCAACTTTTAAACGAAAGAAGGAGTTTCAAACGG

7	48	ATAGCCCGGACACCCTCTTTCAGGGATAGCAAGTTTCGATTAGGATTA
8	48	ATTACAGAAAGATTTGGGAAGATTTTCTACGTTAACAGACAGCATA
9	48	AGCCAGAATTTAGCGAGTCTCGCGCAAAGATTTCAAAGGGAATTC
10	48	TATTATTCTTCATGAAAGTATCTGGCATGATTTTAAGACTCAGGAA
11	46	TCATTAAGTTGAGGCTTGATACCGATAGAAAGAGGAATGCTTTAAA
12	46	GTTAGCGTAAACAGGACGCATCAGTTGAGATTTACCAGACTTATTA
13	46	TTTACCATGAATTCGTTGAAAATCTCAAATCAATTTTGCCAGAG
14	46	TTTCAGCGGAGCAGTAGCATAACCCTCGTTAAGAGCACACCACG
15	46	ATCAAGTTAGCGTTGACTTTTTTCATGAGGCAAAAACAACAGGTCA
16	46	AAAGGAGCCTTATCTTGATGTTTAGACTGGATTGGCATCCGACATT
17	46	GCAACATTTGCCTTGATGGGATTTTGCTAATTTCAAACGAGGCATAG
18	46	GCAGCGAAAGAGTACAAACCGAAAGACTTCAAATTAATACGTCACC
19	46	CAACAACCATCATCATAAGAATGACCATAAATTAGTTTGACCGACT
20	46	CCATTAACAGAACAGGCCGCTTTTGCGAAATTGTTGCATCAAAAA
21	45	TAAGACACTATAAATTGGGTTTTAGATGGTTTAAACAACCTTCAG
22	45	GGGGAGTAAAACAAGAACCGTTTTTCATTACCAAAAAAAAACCA
23	45	CAGTAAAACGAGGGAACCGATTTTACCAACTTTGTGCGCCGTGA
24	45	GATTGGAAGCCGAGATTTGTTTTATCGCCTGATGGATCGTCTCA
25	43	ACAAAGTTAGGAATCTCATTATACCAGTGATCTAATCGGAACC
26	43	ATCTTACAGGAATCTTTAATCATTGTGTTTCTGTAGTAACA
27	43	GAAAAGGAGCGTCCTTCATCAAGAGTATAATTGTCATTAA
28	43	GTCAATAACCCCTCAACAGATGAACGGTGTAAACAACAGGTCA
29	43	ACATGTTATCGCGAAGCGCAAAACAACAGCATCACCGGAAC
30	43	GGATGGCTGCAAACTAATACACTAAAAAGACTAAATGCCATC
31	42	ACCGCTAGGAACCCTGCCACTACGAATTTAATTGCTTTAGT
32	42	CCACAAGAATAGCGTGAATAAGGCTTGAAAGGAACATGGCT
33	42	GATTCCCGACTATTCATGTTACTTAGCCTCGGTCCGTCAGAG
34	42	ACTCAGGAGGTCTGTAGCGCGTGTCTCAGTACCATATCACCGT
35	42	CTTTGAGCTCATCTGAACCAGACCGGAATAGAGCTCGACAGA
36	42	CGCAGTAGCCATTAGTTTTGTCTCTTGAAGTGAACCAT
37	42	ATTTAATCCAGACAGTTAATGCCCTTGTAGCTAGCCGA
38	42	TCAACTAAAGCAGAAAACGTAGAAAATATAAAACGTTAGTA
39	42	GTGCCCGCATACATTTTTTAAAGAAAAGTATGCAGATTATGCG
40	42	AATGAATAATTACCTACATAACGCCAAGAAGCCCAAAGGTG
41	42	GAACCGCATAGGTGGGCGGATAAGTGCAGAGAAGGTCAACCAG
42	42	GAATAAGATACAGGAGAAAGGAACAACCTCCTGACGACGATA
43	42	TTTGATGTTTATTTTAAAGCCCAATAACCAGACGAGAAAC
44	42	AAAACCAATTGAGTGTCAATCAATACGTCATATTGCGAA
45	42	AAGCTGCTTTTTCAACCGTTCAGTAAGGAAAATAGATAAC
46	42	TAATAATTCATTACAGAGAGGCTTTTGCAATCAGAGCATATGG
47	42	CAACCGAATAAATCATCGGTTTATCAGCGGCTGACAATACTG
48	42	ATAGGCTTTGCTTTATATTACAAACAATTGAGGGGCGAGCT
49	42	CGGAATCTTGGGGCAGGGAAGGTAATAGGCCTTGCAGGTG
50	42	GACGATTTGACGGAGCTATATTTTCATGTCATAACAGGCGC
51	42	AATTTCTTACAGACATATTCATTGAATCCCTGTTAAATTAT
52	42	TGAGCCACAGAACCCATAACCGATATATGGAACGACAGGTCT
53	42	CCGCCACTTTGGGACGAACGAGTAGATTCAAAAATGGCGCAG
54	42	TTACCCATATTCTGATTAGAGCCAGCAACACCACCTTGAGGC
55	42	TCCGCGAGAGTTAAGCCACCCTCAGAGCAATCACCAACAGTT
56	42	TTGCAGGCTGCTCATAGTCAGAAGCAATCCATATAGTAGCA
57	42	AATGAAAGCCACCGGAACGAGGGTAGCTTATACCTTTTAAT
58	42	CCAGCGAACGGCTATCACCGGAACCGCATCGATAGCTCA
59	42	TCGAGCTAATGCTGTAGCAGCACCGTAAATCAAACAGAGG

60	42	TTTTCA <b>TT</b> CAGTA <b>GT</b> AATT <b>GT</b> GGAAT <b>ATT</b> CAAAG <b>CT</b> TGACCC
61	40	ACCGA <b>TT</b> ACGCAATAA <b>TA</b> ACGGAA <b>TC</b> AACGGAACACATT
62	39	GCGGGGTTTT <b>GT</b> ACCG <b>TA</b> ACACT <b>G</b> AGCCCA <b>AA</b> CCCTCA
63	39	TACTA <b>TTT</b> AGTAGCATT <b>G</b> CGCTAA <b>TA</b> AAGA <b>AG</b> CGTAACA
64	39	CTAA <b>ATT</b> GGT <b>GT</b> CTGGAAG <b>TT</b> CA <b>TA</b> GCGGAT <b>GT</b> CGAAA
65	39	TACAAA <b>CC</b> CTCA <b>TA</b> GA <b>ACC</b> GGCC <b>ACC</b> CTACGATATAAGT
66	38	AGAA <b>ATT</b> TCGCAAAG <b>AA</b> GAAACAAT <b>GT</b> TAGCAATAGCT
67	38	AATT <b>TTTT</b> TCACCGT <b>CA</b> CCATTAGAT <b>TTTT</b> TCGCAAATG
68	38	TTTAG <b>TTTT</b> CGTCAG <b>AC</b> CTTTTGATA <b>ATT</b> TCATTTTTGC
69	29	AGGGTTCCAAAAG <b>AA</b> TAAGAG <b>GC</b> CTGTAG

**Supplementary Table 16** Staple sequence for the 6HB-based square DNA origami of 105-bp edge-length without internal mesh. The sequence is represented by colors; unpaired nucleotides with blue, crossovers with orange, and the 14-nt seed dsDNA domain with green.

Staple ID	Length (bp)	Staple sequences
1	57	GTTTCC <b>AA</b> CAGCAT <b>TC</b> ATCTTT <b>TTTT</b> TCAA <b>AA</b> ATCACC <b>GG</b> TCAGACTG <b>TTTT</b> AGCGCG
2	55	TAACAC <b>TG</b> CGATTTT <b>TA</b> AGACCCTCAG <b>AA</b> GA <b>ACC</b> AGCTGAGACTCCT <b>CA</b> CGTCGA
3	53	GCTGT <b>AG</b> T <b>C</b> ATT <b>GA</b> CA <b>AC</b> GGAG <b>ATT</b> GT <b>TT</b> TGATA <b>CA</b> ACCACCT <b>TTTT</b> GCCGCCG
4	53	ACATTT <b>CT</b> CGTTT <b>AC</b> GGT <b>GT</b> ACAG <b>ACC</b> AGGAACA <b>ACT</b> GAAT <b>TTTT</b> TCCAGTA
5	53	CAATA <b>TC</b> GGAA <b>CA</b> AGA <b>AC</b> CGAG <b>TAG</b> TA <b>AC</b> AGACA <b>GT</b> GCCCC <b>TTTT</b> TTTCGGA
6	52	ATCAAG <b>AG</b> TCAGCGGAGT <b>GT</b> <b>TTTT</b> ATAGAA <b>AG</b> GCGCATAG <b>TTT</b> GACCTTC
7	52	GAAATCC <b>GC</b> GAGGTGAATTT <b>TTTT</b> AAACAG <b>CA</b> TCATCGCCT <b>TTTT</b> TGTGTC
8	52	CCACTAC <b>GT</b> CGTCACCCTCA <b>TTTT</b> TGCGAA <b>GT</b> TAAACGGG <b>TTTT</b> CGTAATG
9	52	TCAACT <b>TT</b> CTACAACGCCTG <b>TTTT</b> CATTCC <b>AA</b> TTGGGCTT <b>TTTT</b> TTAATT
10	49	TAGTAAGAG <b>TTTT</b> CA <b>CT</b> ATCATA <b>ACC</b> CGCAAAT <b>TTTT</b> AACTGTTA
11	49	CGGATTGCA <b>TTTT</b> AAAAG <b>ATT</b> AAGAG <b>GA</b> GACCG <b>TTTT</b> ACTCCAACAG
12	49	CAATACTGC <b>TTTT</b> ATCGTCATA <b>AA</b> TAT <b>CT</b> CAACA <b>TTTT</b> AAATATGCAA
13	49	AAATCTACG <b>TTTT</b> ATA <b>AA</b> ACGA <b>ACT</b> AAACGGAA <b>TTTT</b> AAAGA <b>ACT</b> GG
14	45	TATAGCCCG <b>GT</b> ACCGC <b>CC</b> CTCAGAG <b>CC</b> ACC <b>CC</b> CT <b>CT</b> CTCAGGA
15	44	CCAG <b>CA</b> TCACCAGT <b>TTTT</b> GCACCATTAC <b>CC</b> ACCAG <b>GC</b> GATAGT
16	44	TATACCAG <b>TG</b> ACTCC <b>TAC</b> ATACATA <b>AA</b> GG <b>TT</b> TATTC <b>TG</b> TCACCA
17	44	CATGATTA <b>AC</b> AGGAC <b>GG</b> TGA <b>ATT</b> AC <b>TT</b> AT <b>GT</b> AGTTT <b>CG</b> AAACAT
18	44	ACCT <b>AG</b> GCAACATAT <b>TTTT</b> AAAAGAAACG <b>CC</b> AGTTA <b>ACC</b> CTCAT
19	44	GCTATATT <b>TA</b> AAGGA <b>AG</b> ACA <b>AGA</b> ACCG <b>GA</b> TTGCTAA <b>AG</b> GCTTTT
20	44	CTAAAGTA <b>CT</b> TAGAC <b>CT</b> CCAT <b>GT</b> TACT <b>TA</b> ATCGGT <b>TG</b> GAGGTT
21	44	AGCG <b>TT</b> TCAACCGAT <b>TTTT</b> TGAGGGAGGG <b>AG</b> CAGT <b>CT</b> TAAAGG
22	44	GTCAGGAT <b>TT</b> ATAGT <b>CCA</b> AC <b>CT</b> AAA <b>AC</b> GA <b>ATT</b> TAAAG <b>GA</b> GCCACC
23	42	TAGCGGGGTTA <b>TT</b> ACAGAGGCATTTT <b>CA</b> GGG <b>TG</b> ATTAGGAT
24	42	TTATTA <b>GA</b> TCGGC <b>ACT</b> CA <b>AG</b> CGA <b>AC</b> CAAGCCC <b>GT</b> GAGGAA
25	42	AGTAC <b>CG</b> TATCACCGTTTTA <b>ATT</b> TCGA <b>GT</b> TTTTCGGTCTTGCTC
26	42	TCTACT <b>ATT</b> TAGG <b>ACT</b> GT <b>CT</b> ATT <b>CAG</b> TGGTCTTT <b>CG</b> GGGTCA
27	42	TCCCA <b>ATT</b> TTGCA <b>ATA</b> AGGG <b>AA</b> CCGA <b>CA</b> AAAT <b>TA</b> CAAATA
28	42	TCATTT <b>TAG</b> AAT <b>GA</b> A <b>AT</b> CTTT <b>GAC</b> CCCC <b>AC</b> ACGCAT <b>AA</b> CCGCC
29	42	GGTTTA <b>GA</b> ATAGG <b>TAG</b> GCGG <b>TA</b> AG <b>TG</b> CA <b>GAG</b> AA <b>GA</b> GCAAGC
30	42	TGACGA <b>GG</b> TAA <b>CG</b> AA <b>GT</b> G <b>CC</b> GT <b>ATA</b> AAA <b>AA</b> GAC <b>AG</b> GAAACG

31	42	AGTTAGCAAACACCAACATTATTACAGGTA AACCGACCACGGA
32	42	ATAAGTTGAGTAACTCTAAAGTTTTGTCAATAAGGTTTCATCA
33	42	GTGCCTTTATTTTGTAGCATT CAGAAGGAGAAAGACTTGCCC
34	42	GTTGAGAATAGTAGT CACAATCAATAGATTTTAAACCAGACGT
35	42	TCAACGTTGAATTGTACTGGTAATAAGA AATTCACATCAAT
36	42	TAGTAAAAACAAA GATACCACATTCAACAAGGTGGTATGGTT
37	42	TACCAGCCAGGAGTTCTGTATGGGATTTATTCATTGATACAT
38	42	GATGATAGCCAAA GGGCGCGAGCTGAATAATGCAACCCAAA
39	42	AACGCCATCATTGACAAAAGGGCGACACATACATCAACTTT
40	42	AGAGGACAATAATACCAGAATGGAAAGCAGGTAAATTAGAT
41	42	AATTGCAGATGAACCAGACGACGATAATTTGACCTATTGAC
42	42	GGAAATATTAAA GATTTTTTTCACGTTGTGACCAAAATAGCG
43	42	AATCCTCATTCATTACGAGTAGATTTAGA AACCAACTTTGAA
44	42	AGAGGCTTCTGCGAAAAGGTGAATTATCTTCACAACCAAAA
45	42	CAGACGGCCAAAAGGATTGGCCTTGATAACCGTCAAGTTGAT
46	42	AAAGGCTTCAATCAAGAAGTTTTGCCAATATAACCCGACTT
47	42	GAGCCATGTCAGACGAGCCTTTAATTGTGCCGGAATAATAGT
48	42	GAGGCA GTTGGGAAGGAAGTTTCATTCCGAGGGGGCAGGGCG
49	42	AAAATGTGGTGTCTTTAGAGCCAGCAAAATTGACATATCAGC
50	42	CGCGAAACAATGACACCTCAGAGCCGATTAGCAATATAAT
51	42	TGCGCCGCAAAGTAATCCCCCTCAAATGTTGCTGAAGGCCGG
52	42	AAACGT CGAGCCAACAACAACCATCGCCGCGATTACAGTTCA
53	42	ACCCTCAACCAATGGGCTTAGAGCTTAAC TTTAAATACCAAG
54	42	GAAAACGTGCGGATAAACCATCGATAGCCCTCAGAACCGAT
55	42	ACACTAAGTCGCTGCCTCAGAGCCGCCAAGCACC GTAAGAGG
56	42	ATATTCGAACACTCCATAAATCAAAAAC TTTTGATAATCAG
57	42	TAGCGAACCGCCTCAGGCTTGCAGGGAGAGAGGCATTTACCC
58	42	ACCGGAAGAATCAACCTTTAATTGCTCTCAGGTCAAGAAT
59	42	TGACTATAGAGAGTAGTTTGCCTTTAGCGAACCAAGCCGCTTT
60	42	TTTTCCGTTTGCCGGAACGAGGGTAGTTTTTCAAAGACTTC
61	40	GAAAGTAAGAAAA TTTACGCAGTATGCAACTGGCTCAT
62	40	AAATATCGCGTATGAGGACTAAAGCCAACGGCAGCCCCC
63	39	CCAATA GCCGCCACACCTCAGAACC GCTTTGATATAAG
64	29	GAGGGTAGCAAACGTTAAGAGTGTACCG
65	24	CAACAGTTAATCTTTACGAGGCA
66	24	TTGCTTTCGACCTGGGATAGCGTC
67	24	TGCGGGAAAGGCAGAAGCAAAG
68	24	GTACAAAATCATTTGGGAAGAA

**Supplementary Table 17** Staple sequence for the 6HB-based octagonal DNA origami of 57-bp edge-length without internal mesh when using Design Type 1 shown in **Supplementary Fig. 26**. The sequence is represented by colors; unpaired nucleotides with blue, crossovers with orange, and the 14-nt seed dsDNA domain with green.

Staple ID	Length (bp)	Staple sequences
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1	58	CGTCATTTCTCAGCAGGAGTTAGGCCGTTTTGTGTATCACCGTTAAACAGTTATTAC
2	56	TCATAGCCCCTTTTTAGCGTTTGGCGCCAAAGATTTTAAGGGCGACATTATTGCT
3	56	CCACCGGAACTTTTCCCTCAGAGAAGACACCACTTTTATAAGTTTATTTGCTGT
4	56	GGTCAGACGATTTTCCTTGATATGAAACGCAATTTTTAACGGAATACCCGCAAAT
5	56	CTCAGAGCCGTTTTCAGAACCACAGTATGTTAGTTTTACGTAGAAAATATATAAC
6	56	GTA CTGGTAATTTTTTTAAACGGGACTTGAGTTATTTTCCAATAATAAGAAATATCA
7	56	GCGCAGTCTCTTTTTTTACC GTTCGAAGCCCTTTTBTAGAAAAGTAAGCTCAATT
8	56	AGCGACAGAATTTTGTTTGCCTTAAATTATTCATTTTAAGGTGAATTATAGCTTC
9	52	CATTAGTTTTGCCGGAACGCCAGCAAATTTTTCAGTAGCACCAACGGATT
10	51	AAGAATTTGGATATTACCCATACCGTAACACTGAGTTAGTAATCTATACCA
11	51	CATGTTTTCTTAGCCTCTGTAGGATTTTGCTAAACAACGCGACCGCCAAAA
12	51	CCTAATTTTCGAAAGATTTAATTATCGGTTTATCAGTCTCGAAGGCTAGACTG
13	49	GAGAGATTTTTCAAGA AATGAAAGTACAGTACCAGGCGACGAGTAGA
14	48	CGTCGAGAGGGTACCGCCCTTGAGTAACAGTTTCGGAAGCTGAGACTC
15	46	CGCCACCCTAAAGGCTTTGAGATGGTTAATAGCGCTAGCAAGAA
16	46	TTGACGGAAGCGTCAATGATACCGATAGTGAGGAAGTCAATTGAATCC
17	46	ACAACAACCATGCTTTGATAAACAGTTCAGAATAATTCGCACCCTC
18	46	TAGCGTAACGACCAACTTTACAGGTAGAAAGAACATTTCAAAGAA
19	46	AAACGCACCGCCAAGAAAGGAACAACCTAACGGAGAACCCTCGTTT
20	46	ATAATAATTTATTATACAAAACCAAATAGAAATATAATGTCACA
21	46	AACCGACACAAACTAGCATTCCACAGAGGTGTACAACGAACTAAC
22	45	GTAATTGTCAACTCTCATTGAGTGAATGAGCCAATACAGGAGT
23	45	CTGAAAACGTTGGGTGACCTTCATCAAGTCGTACAGAATGGAAA
24	45	ATTAGATTTTCATCAGGGAACCGAACTGATCTAAAAGGTTGAGGCA
25	45	GAAGTTTCGAGGCAATTGTGTGAAATCCTTTCAAAGCCACCACC
26	45	ATTGCTGCGAGAGGTTTGACCCCGAGCTTACGTAACAGAGCCA
27	45	AGAGAGTTCCAATAACGTAATGCCACTATGCTTTGCGATTTTCGG
28	45	CGCGTTAACGAGACAACGGGTACAGAGCGCCCAACCGTAATCAGT
29	42	AGGTTTAGTTGATAAGCGGGGTTTTGCTTTAAGAGCCTATTA
30	42	TAAATCAAAGACTTTTTGGGAATTAGAGTACCAAGCTGAGG
31	42	GGCAACATTATGAAAGAGGATTTGATGAAACAGCCCATAGT
32	42	ACGACGACGATCAAGCGCGAATTTAAAGTACAAGGATGCGA
33	42	CCCAAATGCTTGACTAAAGATTTTTTTTCAATGCGCCCAATG
34	42	CCCGGAATAGGCCAGAAGCAAAGGATTAGGATTTAAGTATAG
35	42	CTACTAATTTTAGTAGCATTACACCCTGTTACCTTCAAATCA
36	42	GGTCAATTTTTGTTTAGCTATATTTTCTAATAAAGACCAG
37	42	AGTTGATTTTTAATTCTGCGAACGAGTAATACCAAGCGCAG
38	42	AGCTCAAATTTTTTTTAAATATGCAACTACTATCATATTTGTA
39	42	CCTTTGTTTTGAGGTCATTTTTGCGGAGTTTTGCGAATACA
40	42	AAAGCGATTTTGACCGGAAGCAAACCTCTAAATATTTCCAT
41	42	GCATCAAATTTATTAAGAGGAAGCCCGAAAATCAAACAGCAT
42	42	ACAATGATTTGATGCACCCTCATTTTCAAAGCTGTTAATCA
43	42	ACGTAAACGGGATAGCGTCATACATGGCTAATAGCATCAGAGG
44	42	TTGTGAAACAAGATAGCTATCTTACCCAGTAAGCAAGCCC
45	42	GTCAGGAGGTGGCAAGATAGCCGAACAATAAGCCAGTACA
46	42	GCGCATAACGCCTGAAATAAATCCTCATAGTTACCGCGCGAG
47	42	AACTACAGGCTGGCAAGAAAATCTACGATTTGGGAGAAGGA

48	42	CTGGCATGACAGGATTTTGTGCTTTTCATCATAAGTTGAGA
49	42	ACGGTCACAGACGTCGCGCCAGCATTGATTAAGTTTGACC
50	42	TTTAGGAGATTTAGACTCCTTATTACGCCACCAGAGTAGTAAA
51	42	GGAATTACATTCCACATACATAAAGGTGCCCTCAGCAGTTTC
52	42	TCATCGCTGAGAACTCTCAGAACCAGCAACATGTGTCTG
53	42	AGCGGAGCTGATAATAGTAAGAGCAACAAGTACGATAAAAAG
54	42	ATCAATACACCGGATGAAAATCTCCAAAACATCCTTTTGC
55	42	CTAAAACAAAAAGGTTTATAATCAAAATGAAAATTGAGCTTA
56	42	AAAAGAATGGCTTACATATGGTTTACCACATCTTCTCCAAA
57	42	GATAGCGACCTTTACAACCGATTGAGGGTTCATCGGAGGTGA
58	42	TAAACGGAACAGCGACTGTAGCGGTTAGGGAAGCAGGATT
59	42	ATTTCTGTAAAACTGCGGAATCGTCAACAGGTGTAAATA
60	42	ACCGACTGCAGCAGCATAACCGATATAAGGGTAGATGACCA
61	42	CGGAACGTTCCGGTCTGAAACCATCGATATGAGCCACAAATAT
62	41	AATAGGACATTACATGCGATTTTAAGTGGCTCATTGAC
63	41	TGAATTGGAACGAATCAACTAATGCATACATAACTGCTC
64	41	AGGAGCCGGCAAAACAGAGGGGGTAATTTAAATGTTACCAA
65	41	CTTGCAAGCGAAAAGGCTTTTACCCTGTATTATAGTGGGAT
66	39	ATTGGGCTGCCCTGACGATTTAACACCACACCCAGAAC
67	39	CTCAAGAGAAAGTGCCCTGCTATGCCCGTAACTCAGG
68	39	TTCTGAAGTCAGTGCACCCTCAGAACCAGGAGATAAGTGC

**Supplementary Table 18** Staple sequence for the 6HB-based octagonal DNA origami of 57-bp edge-length without internal mesh when using Design Type 2 shown in **Supplementary Fig. 26**. The sequence is represented by colors; unpaired nucleotides with blue, crossovers with orange, and the 14-nt seed dsDNA domain with green.

Staple ID	Length (bp)	Staple sequences
1	58	TAGTATTTAGCAACATAACGAAAAGGAATTAAATACCAAGCGCGCCACCAGCAACAAA
2	56	ATACATAAAGTTTTCAACATATAAGAAGCCCTTTTTTTAGAAAAGTAAGCTCAATT
3	56	ACCGACTTGATTTTTTGGGAATTTGGCTTTTGATTTTTACAGGAGTGTATAAGTA
4	56	GATTGAGGGATTTTAGGTAAATATAAACAGTGCCTTTTATAACAGTTAAGATTAG
5	53	GCTACAAGCTTTGAAGCGACAGAATCAAGTTTGTTTTAGCGTCAGACTGACA
6	53	ATGCCACCTGCTCCTCATAGCCCCCTTATTAGCGTTTTCCATCTTTTCCCTCA
7	53	TAAAGGCTAATCTTTACCATTAGCAAGGCCGGATTTTTTCACCAATGACATTA
8	52	AGAACTTTTTTGATTAAGAAGAAACGCAATTTTTAACGGAATACCAGCAAAT
9	51	AGCTTTTTTTCGAAGGGCTTGATGGTTTAATTTCAATATCGGTGTAGCAT
10	51	CTAAAATTTCTTTTTCTCATAAGAACCGAAGTACCAAGGCTTTTCGCGTT
11	49	CTACTAATTTTAGTAGCATTACACCCTGACAACCTTCAACTGCCAGAGG
12	47	GGAGGTTTTAGGCAGGTCAGATGCTGTAGCTCAATTTTTTTTAAATA
13	47	GAGCCTTTTACCCTCAGAGCCTATAACAGTTGATTTTTAATTCTGCG
14	47	AAGCCTTTTATGGAAAGCGCAATTGCTCTTTTGTGTTGAGGTCATT
15	46	TCAGGACGTTGATTGCGATTAGTAAATGAATTAGCGCTAGCAAGAA



16	46	ATTCAGTGAAATGACAAGCAAGCCAATAGGGTTGATACTGGTAA
17	46	AAATCCGCGACTACGAAATTATAGTCAGAAAGCATTCCAGCCACCA
18	46	TCATACAAGAGCCAAACCAAATCAACGTACCGATACCACCACCCTC
19	46	TTCATCAAGAAGCCTTTTGTAGTACCTTGAACCGCCACCAGGGAGT
20	46	GAAAGATTCAATTAGCGAAGAAAATGTTTAGACTGGTGGCAAGATAGC
21	46	AAATCCTAACCATCCAGACCAGGCGCATCAGCGAAAACCTCCAACA
22	46	TTCTGAAGTTTACCATTTTAAGAACTGGGAAAATCAAAGTTTTGTC
23	45	CTCCTCAAAGAGCCCGGAGCCTTTAATTGCTTTTAAACATTCAACC
24	45	CTGAAAAGGATAGCGATAAAAACCAAACAGTTGATAGAAAATAC
25	45	TCGCTGAATTCATTGCAAAAATCACCAGTCGTTCCATTTAGTACCG
26	45	CGGAACCCGCCACCTTTGACCATTAGATGTTTCAGATCTTTGACCC
27	45	CGAGAGGAACCAATTAGTTGCGCCGACAAAGGCTTATCACCGTC
28	44	TAAAGGAGGAAGAATTTATTTTGTCACAATCAATTTTTAATTCA
29	43	AACGAGTAATAATCAAGAATACACTAAAGGAGATTAATCAC
30	43	TGCAACTAGATTAAAGATTTCCATTAACGAACGAGCGTTTTTC
31	43	TTTGCAGGACGGAAGCAGACAGCATCGGAACGGTGTAGATAGCA
32	42	GAACAACTTAGTTTCAGCGGAGTGAGAAAACGAGCAAAGA
33	42	GTTTCCAGACGATAATAATTTTTCACGTTCTCATTACCAG
34	42	ACCGGATGGCTTGCTCAGAACCGCCACCCAGGAGGGTAAGCG
35	42	CTACCCTGACTGCACCAACCTTTAACGAAAATAAATTGTCG
36	42	GGAGGATTAGAGCGGGATCGTTTCCCTCAGAGGCTGTGACC
37	42	ATTAGGGATACAACCATCGCTTTACGCATAAACAAATGCTC
38	42	GAGAGATTTTTCAAGAAATGAAAGTAACGATCTTCCAAAA
39	42	GGTCAATTTTTGTTTAGCTATATTTTCAATCGTCAACCCTC
40	42	TAGCCCGTTTTAGGTGTATCACCGTACTCTCAGAGTATTCGG
41	42	GATTAGCTTTTTGCTCAGTACCAGGATTTTCGTCTTAAA
42	42	TCCACAGAGAGAAAGTCCCCCTGCCTATAAGGGCGATTGTG
43	42	AAAAGGCTTATGCGAGCGCCAAAGACAATTCGGAAGCTGAGA
44	42	AATTACTCCAAAATCATAGTTAGCGTATTAAGAAGCTATTA
45	42	AACACTGCGGATAAGTCAGTGCCTTGAGTGACGGAACGAGTA
46	42	ACAATGAGAAATAAGAAATCTACGTTAATTAGAAAAGTGGGATT
47	42	CACCACGAATAGCATCAGAGGGTAATTGTCTGTAGAACAAC
48	42	TTGCTAAACAAAATAGCTATCTTACCAAGAAAACACTAACG
49	42	CGAACAAGCAAACGGATTTAGGAATACCAAGACGAGTCCAAT
50	42	GTTTACCACATTACATACGCAGTATGTTAAGTTACCGCGCAG
51	42	ACTGCGGATTTGGGAGAAGGAAACCGAGTCTTTACTAATG
52	42	TAAGTTGGTGAAAGTCCCTGACGAGAAAATACCGAGTACCGT
53	42	TCAGAGCAGAGCCAAACAAAGTACAACAACACTCAAACGAG
54	42	AATGACCGATTTAGCTCAGAACCGCCACATAATCATGTATCA
55	42	GAACCACTTTTCGATGTTACTTAGCCGGGGTAAAGATTGCA
56	42	ATCGGCACACCAGAGTGTCTGGAAGTTCAAAGCATACGTA
57	42	TCAAAAAGTACGGCCGCCGACGATTGTAGCGGCAGACA
58	42	TTAATTCAATATAACGATTGGCCTTGATAATCAGTAGAGGAC
59	42	GCACCGTATTCACAGAGCTTAATTGCTGGAGCTTCAAGCAACG
60	42	AGATGAACGAGGGTAAAGCGAACCAGACTGGCTTAAACAAAT
61	42	CAGCTTGCACCAGAAATTATTCATTAATTAACGGGGTGCCGT
62	41	CAGATACCTATCATATAAATATTCATTATCCCCCTCAGGCA

63	41	CGGTCA <sup>AA</sup> TGAGG <sup>AA</sup> GGAAGCCGAAACTTCAAAT <sup>AG</sup> AGGA
64	41	GTAAT <sup>TG</sup> TGAAT <sup>TT</sup> CACCAGTACAAAACAACGC <sup>TT</sup> TATC
65	39	GTAATAG <sup>TA</sup> GGCTTTTGC <sup>TTT</sup> AAGAAG <sup>TA</sup> TATTAGGTA
66	39	CCAGCGATT <sup>C</sup> GAAATGCTTTAAACAACATTT <sup>CG</sup> CCTCCC
67	39	CCACCCTCAT <sup>AG</sup> TCTCTGAATTTA <sup>CA</sup> GCACC <sup>AG</sup> ACAAGA
68	36	<sup>TAT</sup> GA <sup>CT</sup> TGAGTTA <sup>TTTT</sup> CCAATAATAAG <sup>AA</sup> TATCA
69	25	TCGCCT <sup>GG</sup> AGGCA <sup>AAAA</sup> AATCAGGT

**Supplementary Table 19** Staple sequence for the 6HB-based star DNA origami of 42-bp edge-length. The sequence is represented by colors; unpaired nucleotides with blue, crossovers with orange, and the 14-nt seed dsDNA domain with green.

Staple ID	Length (bp)	Staple sequences
1	58	CATACAGCGTTTGC <sup>CG</sup> CCACC <sup>AT</sup> CAGAGCCACC <sup>ACC</sup> CGGAAC <sup>CG</sup> CATTTTCGTTATT C
2	58	CTAATGCAGC <sup>TAT</sup> CAAAAATCAGGTGCGACC <sup>TATATCTGGT</sup> CAGTTAGGCGGTAAAA G
3	58	GAAGG <sup>TTTT</sup> TAAATATTGACGGAAAG <sup>TC</sup> CATAATCAAGGGATAGCAAG <sup>TT</sup> ATAGGAACC C
4	57	CAAAGT <sup>TT</sup> AAGAA <sup>AC</sup> AAAAGAAGTTTTGCCAGAGGG <sup>TTTTTT</sup> GGTAATAGT <sup>AC</sup> TTTA
5	57	GGAATT <sup>AG</sup> GCGAC <sup>AG</sup> AGTTTCGT <sup>TAATCTTGACA</sup> AGAATTTTTTTCCGGATATTCAT
6	56	AACAC <sup>CT</sup> CAAGA <sup>AG</sup> ATTTTGCTAAAC <sup>AG</sup> AGGTTTAGT <sup>TTTTTTTT</sup> ACCGCCACCCTC
7	56	TGACC <sup>CA</sup> ACT <sup>CG</sup> ATGCCACTACGA <sup>GA</sup> ACAGGTCAG <sup>TTTTTTT</sup> GATTAGAGAGTA
8	56	AGGCA <sup>TTTT</sup> GTCAGACGAT <sup>TG</sup> ATACA <sup>GT</sup> AATTACTAGAAAAAGAAG <sup>AA</sup> CAGTTT
9	56	AATCA <sup>TTTT</sup> GTTTTTTGGG <sup>GA</sup> GCGAA <sup>AGGC</sup> ATTTTCGAG <sup>CG</sup> GTTTAA <sup>AC</sup> GAGGTG
10	56	CTCAAT <sup>TTTT</sup> CTATCGGCCT <sup>TA</sup> ACCA <sup>TT</sup> GAACAAGAAAA <sup>TA</sup> TATTCA <sup>AA</sup> CCCTCA
11	56	CGCCATTT <sup>GCC</sup> ATTGCAACAGGA <sup>AT</sup> TCGAACCTCCTAATTGCTGAAT <sup>TT</sup> ATGCTGTA
12	56	ATTAT <sup>TTTT</sup> TATCCCAAT <sup>CCT</sup> GAACTAAGAATACGTGG <sup>CT</sup> AGACT <sup>TC</sup> CCTAAAA
13	56	GAACC <sup>TTT</sup> CTAAAGGGAGCCCCG <sup>AG</sup> TTAGACAGTAGATACATTT <sup>TT</sup> AATGGTCA
14	56	AGCGC <sup>TTTT</sup> AAAGACAAA <sup>GG</sup> AGCCA <sup>GG</sup> CAAGACAAGA <sup>ACT</sup> ATTAAT <sup>TC</sup> CAGTAC
15	56	TAATT <sup>TAC</sup> AGTA <sup>AA</sup> TCGGTTTATCAG <sup>CC</sup> GCGAGCTGA <sup>TTTTTTT</sup> AAAGGTGGCATC
16	56	GTCAA <sup>TTT</sup> AAATGAAAATAGCAG <sup>CA</sup> TAACGCAATAAATATCGCGT <sup>TT</sup> ATTTCGAGC
17	56	GAGGT <sup>GG</sup> GCAA <sup>TT</sup> TGTGTGCAAA <sup>TC</sup> CTTTACCCTG <sup>TTTTTTT</sup> ACTATTATAGTC
18	56	AATAG <sup>AA</sup> TCAAT <sup>AG</sup> GCCGCTTTTGC <sup>GG</sup> ACGGTGTCTG <sup>TTTTTTT</sup> GAAGTTTCATTC
19	55	CACCT <sup>TTT</sup> GCTGAACC <sup>TA</sup> CGAGGCGCAG <sup>TT</sup> TCAAT <sup>CC</sup> AGTGA <sup>TT</sup> GGCTTGCCCT
20	55	ATTAA <sup>AC</sup> CCCTGCCTATT <sup>TCT</sup> CAGAG <sup>GT</sup> CACCGGAACCAGA <sup>AT</sup> TCTTT <sup>TC</sup> ATAGCC
21	55	AACCGT <sup>TTTT</sup> TATCAGGGCG <sup>AT</sup> AACCA <sup>CT</sup> ACCAGTATAAAG <sup>CA</sup> ATCGC <sup>GA</sup> TAATAA
22	54	CTACC <sup>TAG</sup> GCCGGAACGT <sup>CT</sup> CAATA <sup>GCA</sup> AAGTGCTCATTATAAGG <sup>GA</sup> AGCAT
23	54	TATGCGTTA <sup>TT</sup> AATTC <sup>TC</sup> ACACCTGCGCT <sup>TCT</sup> GAA <sup>TT</sup> CGTTCAGTAA <sup>ATA</sup> AAA
24	54	AATGGCTAT <sup>TT</sup> CTTTAA <sup>AG</sup> ACGATAAAA <sup>CA</sup> ATAACT <sup>TT</sup> AAACAGGGAA <sup>GT</sup> TAAAC
25	54	AAAGTACCG <sup>TT</sup> AAGGT <sup>ACC</sup> GCAC <sup>TC</sup> GAGA <sup>AA</sup> CGGGG <sup>TT</sup> CCGGCGAACG <sup>TA</sup> ATCG
26	54	AAATATATT <sup>TT</sup> TAAT <sup>TG</sup> TATAAT <sup>TT</sup> AAT <sup>GG</sup> GTGAAT <sup>TT</sup> CACCGTCACC <sup>GG</sup> GAGG
27	54	GTTCAG <sup>AGA</sup> ATCC <sup>CC</sup> AGTGCCACG <sup>TC</sup> GAGAG <sup>TT</sup> AGCAA <sup>AA</sup> AACCATT <sup>TT</sup> AGCAG
28	53	TCCTC <sup>TTT</sup> ATTAAAGCCAGAATGG <sup>TG</sup> ATAAGTGC <sup>CG</sup> T <sup>CG</sup> ATAAAT <sup>CG</sup> GAAA
29	52	TGAAATG <sup>TT</sup> ATTTA <sup>CA</sup> AGAAT <sup>TT</sup> TAAAG <sup>CA</sup> AATACT <sup>TT</sup> ATTTTGACGCT <sup>TA</sup> TTAC

30	52	AGAATCAA	GAAACGA	ACGAGTAG	ATGTTAGCAA	ACGTATTTTTTT	GAAAATA	
31	51	CACCGA	ATAAGTTT	ATTTTTTT	GTCACA	AACCAATGT	GAAAAATCGAGAGA	
32	51	GCGGGG	TCTCCTC	ATACTATGG	TGCTTTGACGAG	CTTTTTTT	ACGTATAA	
33	51	ATTCTA	AATCAGATA	ATGAAATAG	CAATAGCTATCT	TTTTTTTT	TACCGAAG	
34	51	TAAACA	GTCTCGT	CATCGTAG	GAATCATTACCG	CGTTTTTT	CCCAATAG	
35	51	ACAAAC	AGGAATC	AGAGTGTACT	GTTTTTTT	GTAATAAG	TTTTAACGGTTG	
36	51	AATTCG	AGAAAGC	GCCCTGAACA	ATTTTTTT	AGTCAGAG	GGTAATTGCCAT	
37	51	CAAGATTA	TTTTTTT	GTTGCTATTTT	GCCAGAAGGA	AAAAGAA	CCTACGTT	
38	51	GCAATT	CTAAGT	CCCAATAAT	CGGTTTTTTT	CTGTCTTT	CCTATCAAGAA	
39	51	CCCTTA	GTCCAAT	CCAAAATCACC	TTTTTTT	AGTAGCACC	ATTACCTTACC	
40	51	TTTATAAT	TTTTTTT	CAGTGAGGCC	CACCACGCGAGG	CTTGAAG	CTCCTGAA	
41	51	TGAATA	TAGGCAG	AGGAGCGGG	CGTTTTTTT	CTAGGGCG	GTGGCAAA	CCCCA
42	51	GTTGTTCC	TTTTTTT	AGTTTGG	AACAAGGGCCGATT	ATCCTGA	GCATCACG	
43	51	CGCTCC	TTTTTTT	T	CAGAGCCGCCACTG	CTCAGTAAG	ATAGGCGTGGAC	
44	50	GCGGAATCG	TTAAAT	ATTCATTA	ATACCTTATTT	GCGATTTT	AATTTT	
45	50	AGATAA	TTTAC	TTTGA	AATACTAATT	CTCATCAG	AGGATCGAAAG	
46	50	GAAGGA	TTT	GCGAATT	ACATCGGAACG	ATTAGCA	CTTTTGTGGCTTA	
47	50	CAGAAATTT	AAAGAAA	CTTGAT	ACCGATTTG	CGCAGTAG	TAGTTG	
48	50	TGAATA	TTT	ACCTTGCT	TGTAGCATTCCA	TT	CAGCCGAGCCATCCTCAT	
49	49	ACGGAGATTT	GTAT	TGATAA	ACAACAGTTGAAAG	TTGGAAG	GTTATCTA	
50	49	AGTTTCC	ATTAAT	ATACGT	ATATTAAT	CCTTTT	TCGTTATTAATTT	
51	49	CGGTCG	CTGAGGC	TAGTTAA	ATAATCCT	GATTGTT	TATACTTCTGAATA	
52	49	AAAGGCT	CCAAAA	TAATTG	TCAGTACCTTTT	ACTTTGAA	ACAATAACGG	
53	49	GACGTTAG	TAAAT	TGTATG	GAACAAAATTA	TTTACA	ATTTTCAATTTG	
54	49	AACGGTGT	ACAGAT	ATAGGC	TGAAAACATAG	CGATTGATTA	AAGACGCTG	
55	49	GAATT	TTTTTTT	ACGAGGC	ATAGTAAGT	AGGAATACC	TTTTTTCATTCAA	
56	49	GCTCAACAT	GAAGACA	GT	CATCATATTCCT	GAATATCC	CATCCATCGTC	
57	48	GCGTC	TTTTTTT	AGACTGT	AGCGGTTT	ATAAAGGT	TTTTTCAACAT	
58	48	ATAAAC	AGAGCGC	TACGACC	AGTAATAAA	ACATTAT	TTTTTTCATGAGGA	
59	48	GACAGG	AGGGTC	AATGG	TTGAAATACT	AATGGAT	GTCGCTTTCCA	
60	48	TGAGTA	GATTCCA	AGACA	ATAAACAAC	AGAACCT	ATAACCGATATATT	
61	48	TGAGAT	TAGCAAC	AAACAT	CGCCATTAAG	AGCAC	TGAAACAAAGTACA	
62	47	ACCATG	ATAGCA	ACTTCT	TTTTTGATTAGTA	ACCAAGT	AAAGTAAT	
63	47	TTTCAA	ACCGCC	ACCAGAA	TTT	CACCACCAGAG	AGTGCCCTCATCTT	
64	47	ACTTCA	AA	CGAACAACAT	TTT	ATTACAGGTAG	GGTTTACCTGCGCGA	
65	47	GAGCT	GACGAG	CGTCTTT	TTT	CAGAGCCTAA	TAACCCACATTGGCA	
66	45	AGAAGCAA	GCAAGCG	CAACA	CTAATAGAT	GCCCTAAC	TATCAT	
67	45	CCTTTA	AATTGT	AAAGA	CTCATTTT	GCGGAACC	AGTCA	CAATATCA
68	45	TTCAAAG	CGAG	GCAAAG	GATTTAG	AGTATACAGAC	AGACGGGA	
69	45	CATATA	ACAGCC	ACGCACCAT	ATCAAATTAAG	ACGACGA	CGAACGGG	
70	45	AATTCT	ACTAAC	GTTGAAT	ACCAAGTTACA	ACAACG	TGGTCACG	
71	45	ATAACCT	GTTAA	ACAAG	TGCGTAGATTTT	CAAGTAAT	AAAGGAAG	
72	45	AGAACC	GCCAA	AGTTAAC	AGTACATAAATA	AAATTT	AGTGCCTT	
73	45	AGGAAC	TTAAAGG	AATCGGC	TCCCTTAG	AGGGTT	TATAAGTATA	
74	45	AGCATGT	AGCTGGT	ATATG	CAACTAAAGT	GATCGT	CGATGATG	
75	45	TACCCAA	ATCACTTT	GATTAT	CAAAATCAT	AGGCTT	AAACCGAA	
76	44	CTTGAG	AA	CACCA	GCAAGAC	ACCACGGT	AATCAGTCCAATACT	
77	44	AAACTA	CTAACAC	TTTCA	ACCGATTG	AGACTT	GAACTTTTTT	
78	44	CAGCGG	ATAGGT	GATAT	TTCACAACA	AGCGTCA	TTTAGTATCA	

79	44	CGAAAGAAACCAGACAACGATTTTTTGTGCATTAAATTTTTTG
80	44	AATTTCTTAGCTATGCCGTAAGCACTAGGCGAGAGAGAATAT
81	43	GCCCCGAAGTGAGAAAATTACCTGAGCAAAGCCTGTACATGGC
82	43	GACGAGAATGGTTTAAAGAACTGGCTCATTGATAGCGTAGCGAC
83	43	ATGTACCGAACGCCCTGTAAATCGTCGCGGAGAACCATTTG
84	42	CAAACCCTCTGCAACTCAAATGATACATAACGCCCAGTATT
85	42	CGCTACATCAAAGGAAAAGAAATAGCCGCCAGGCAGGATTA
86	42	AATAAAAGCTTTTGAAGTAAGCAGCTTTACAGAGAGCAAAATA
87	42	TCTTACCAAGAAAATAGAAAGGCAAACGCTCATGGCCAATAA
88	42	CAAATTATTATTTTATAAATCAGATTTAGAGCTTGCAAGCAA
89	42	TCCAACGGGGCGCAGAGAGAAGGAAAAGCGCAGTCTAATGCGC
90	42	CTGACCACAATATATAGCGTAACGATCTCCCTCAGCAGCATT
91	42	ACTGATATAGAGCCCCAGCGATTATACCGGATTGCATCAGT
92	42	AACACCGTCAATCAGCTCCATGTTACTTACCATAATTAAACA
93	42	GATTCAAAAGAAAGAGGCTTTGAGGACCTCCTTTTACAAA
94	42	GAATTAATAATAAGCGGAAGCAAACCTCCGCACCAATACAAAC
95	42	GCGAGAGCGAACTATAACGGAATACCCAACCGAGGAGCCGAA
96	42	TTTTGATGGCCTTGATCACCGTACTCAGACTTTCATGATGAA
97	42	TCTGTCCTTTGCAACAACAACCATCGCTTGATTCACTTGCC
98	42	TAAGAGCAACGCTAACTTGCGGGAGGTTGTTTTAGATCCGGT
99	42	CTGACCAAACGTAATAAATTCATATGGTATTAGCATTTTAAC
100	42	TTTTTTATAGTAGCTACGTGAACCATCGTGTAGCCAACAGT
101	42	GGAAGAATCGAGGTATTTTTCATTTGGGGTTGCTTTCGTGAGA
102	42	GCCGTTTACC GTT GACGGTACGCCAGAAAAGGGATCGGGAGC
103	41	TGCAAATAATCCTTGGCTGACCTTCATCAAGAGCATAAATTTT
104	41	AACTTTTATTGTGAATACGAGAATGAGCCGGACAAATAT
105	41	AACCCTCAAAGATTCATCAAAAAGATTATTTGACCGTCAAT
106	41	GAGAGATTTGCCAGTGATAAGAGGTCATGGCTACACCACCA
107	41	TATTAATAAACATCCCAATTCTGCGAACGACAATGGTAAAA
108	41	CTGCGCGTGGCCATAGCATTTCGAAATTGCGACAGAGG
109	41	GAGTAAACCGCCGCAACCGCCACCCTCATCATAGTTGTGAG
110	40	AAATATCTTTAGAAATACCGAACGAACCACCTATAAAACA
111	40	AAAAGTTTGAGTAAGGGACATTCTGGCCAACCTAACCCCTC
112	40	ATGGAAGGGTTATGTTTCAGCTAATGCAGAACTTTATCAAC
113	40	ATTCGCCTGATTAATTGAGAATCGCCATATTTCCAACATG
114	40	AATTACCTTTTCGACCGTGTGATAAATAAGTTAAGAATA
115	40	AGAAGAGTCAATTTAGGTTGGGTTATATAACTAATGCTGA
116	40	ATAAAAGTTTGCAAATGTTTAGACTGATACCAGATTGGG
117	39	CCCTTTTACACCCAGCTTTTTTTACAATTTTACTTAAAT
118	39	GCAGCGATTTTAAATATCCAGAACAATCATAATTTACG
119	39	CAAGCAAGAGAGTAAAAATTTTTTGGAGTCTGTCAAGTGTT
120	39	CGTGCTTGAAGTCCACTTTTTTTATTAAGAAGTTGAGT
121	39	GCTGAGATTCCTCAGAAATTTTTTCCGCCACCCCGGAAC
122	36	TTAAGACTTTTTTTCCTTATTACGCAGTTATCAGGA
123	30	CGTTGGTTTTTTAAGAAAAATGGCATGA
124	27	AGGGCTTGCTTTGAAATCTCCAAAAA
125	27	CTCCGGCAGTGAATAAGAGGACAGATG
126	26	AACATGAAAGTTTTTTTATTAAGAG
127	25	CCCTTATTCATCGTATTATTCTGA

**Supplementary Table 20** Staple sequence for the 6HB-based curved beam DNA origami of 42-bp edge-length. The sequence is represented by colors; unpaired nucleotides with blue, and crossovers with orange, the 14-nt seed dsDNA domain with green, and the 4-nt dsDNA domain with red.

Staple ID	Length (bp)	Staple sequences
1	60	CTAACTCACG <b>GT</b> <b>AAAACGAACTAA</b> <b>CA</b> TACCA <b>GAGCTGCATTAATGA</b> AGCACTGCCCGC TT
2	59	ATGAATT <b>TTTT</b> <b>TGTATGGGATTTT</b> <b>GC</b> AGAACCGCCAT <b>TTTT</b> CTCAGAGCCAC <b>CG</b> TTAGTA A
3	59	AGGGAGCCCC <b>TTTTT</b> TTAGAG <b>CC</b> ACCAACCTAAT <b>TTTAAAGAGGCAAAGAAT</b> <b>AAA</b> ATA T
4	58	GTTTTCCAG <b>TTTTT</b> CGACGTTGTA <b>AAAGGGATGTGC</b> <b>TTTTTT</b> TGCAAGGC <b>GC</b> ACACG
5	58	AATCA <b>GT</b> <b>TATCAAATCAT</b> <b>TT</b> CTGAGAGACTAC <b>CA</b> ATGGAA <b>ACTTTTT</b> CATAAATCA
6	58	GATTAT <b>CGAGCCGGAAGCAT</b> <b>TT</b> GTGTAAAGCCT <b>GC</b> AGGAAGAT <b>TTTTT</b> CTCCAGCCA
7	58	GGCTAC <b>AA</b> TAGAG <b>GG</b> GAACCG <b>TTTT</b> CTCAGAGCCGC <b>CT</b> TTTT <b>CATTTTTT</b> CAAAATC
8	58	AATCG <b>CAACGTTATTAATTTT</b> AAGTTTGAGTAA <b>CG</b> GAATTGAG <b>TTTTT</b> GTTATCTAA
9	57	CAGGAAAA <b>CT</b> GAAAGCGTAAGAT <b>ACGTGGCACAGACAAT</b> <b>TTT</b> AATAT <b>CA</b> CTTTCA
10	56	<b>ACGT</b> TACCAGCG <b>CC</b> GAGCA <b>CT</b> TGAGG <b>CTTGCAGGA</b> AGTT <b>TT</b> CCAAATCAAATAGC
11	55	GTTGCGCTTATCGGCC <b>TGGTGCCTCATTATTACAGGTAG</b> ATTT <b>AA</b> ACGCGCGGG
12	55	AGTCAAT <b>TG</b> AGTGA <b>AA</b> TATGC <b>GT</b> TATACAA <b>ATTCTTTA</b> ACCAAT <b>TG</b> AACGCCATCA
13	55	CGCGAGGCGT <b>TTTT</b> CGAACCTCCCG <b>ATT</b> TACGCCAAC <b>TTTT</b> ATGTAATT <b>CT</b> TAAAT
14	55	TCATT <b>CG</b> TTTAT <b>CAGCCTAATTTGCCAGTTAC</b> GAAGATTG <b>TT</b> AGCAAATATTT
15	55	GATTGTTTGG <b>TTTT</b> ACTTCTGAATA <b>ATT</b> TGAGAGCC <b>TTTT</b> AGCAGCAA <b>ATTA</b> ACA
16	55	TTCCAC <b>AG</b> CACCG <b>CAATACCGAACGAACCACC</b> ACCGTGCAT <b>CT</b> CAGTTTGAGGG
17	55	AAATCC <b>TT</b> AGGAG <b>CCAGTACCTTTTACATCGGGACA</b> ACCCG <b>TT</b> ATTCTCCGTGG
18	55	TATCT <b>TAGTGTACTGGTAATG</b> AGTTA <b>ATATGGTTGCTTTGAC</b> AAAGA <b>CG</b> AAAATT
19	55	ATATATTTTAT <b>TTTTTTT</b> CATCTTCT <b>GGT</b> CGAATTAT <b>TTTTT</b> CATTTCA <b>AA</b> TACCA
20	54	AAGAG <b>TG</b> CAAAAGAAGTT <b>TTTGCCAGAGGGGTAATAGTAG</b> ACCAG <b>GT</b> CCCTTA
21	54	CCCTG <b>AG</b> GCATAGTAAGAG <b>TCAACACTATCATAACCCTCGA</b> CAAAG <b>CT</b> GCAGCA
22	54	TTATG <b>CG</b> AAAAGATTCATCAT <b>GTTGAGATTTAGGAATACC</b> ATTAATT <b>TG</b> CCAGGG
23	54	CGCGTTT <b>TTTTT</b> TCGAG <b>CTTCAAAGCA</b> CGAAG <b>GTTGACGGGGAAAGCT</b> TTAGTT
24	54	TCGCC <b>TT</b> CTTTACCCTGACT <b>TATTATAGTCAGAAGCAAAGG</b> CGAAA <b>CA</b> ATCAAG
25	54	GGGAA <b>CT</b> AAATATTCATTG <b>TAATCCCCCTCAAATGCTTTAG</b> CCGGAA <b>GA</b> ACGT
26	54	AAGGTGAATAATTCTACT <b>TTAGTAGTAGCATTGTAAA</b> ACT <b>GT</b> TCTAT <b>CT</b> GTGTGC
27	52	GTCAGACGAT <b>TTTTT</b> C <b>TTGATATTCACAAGGAA</b> ACCGAGGA <b>ATT</b> CAATAAT
28	52	CGCAGTATGT <b>TTTTT</b> CAAACGTAGAAA <b>TGGTATTA</b> AA <b>CCAAGTT</b> CGCACTC
29	51	ACACTGA <b>TTTTTTT</b> G <b>TTTCGT</b> CACCAGTAAATCTACGTTA <b>AT</b> AACGCCAGG
30	51	AACGG <b>AT</b> TGAGCGCT <b>TTTTT</b> TCAGAGAGATA <b>ACC</b> CA <b>CT</b> ACCAG <b>AA</b> ACAAAT
31	51	GGAT <b>AA</b> AGTATT <b>TTTTT</b> TACAAACAAT <b>TG</b> ATTAGAGC <b>TTTTTT</b> CAATAGAT
32	51	CCACC <b>AC</b> GCGTTTT <b>TTTTT</b> G <b>CATTTTCGGT</b> CATAG <b>CA</b> GAGCC <b>AA</b> CCGGAA
33	51	AGAG <b>GG</b> AAAACA <b>TTTT</b> ATAGCTTAGAT <b>TT</b> AAATCGT <b>TTTTT</b> TATTAATTA
34	51	ACAG <b>GA</b> CCGAAG <b>TTTT</b> TTAAGAAAAG <b>TA</b> ATAAGAGC <b>TTTTT</b> GAAACAATG

35	51	ATCGAGCAACATGTTTTTTTAATGCAGAACGCGCTAAGAACGACATACA
36	51	TAAACCATGTAGTTTTAATCAATAATCGCTGAACAATTTTTAAAATAATA
37	50	AGTTTTCAAAAATGTTTTAAAATAGCAAATAAGAAACGATTTTTGTTTA
38	50	CCGTATCATTACCATTTTTTAGCAAGGTAGAGCCAGCAATTTTCCAGTA
39	49	AGAGCTAGTAAGCGTGCAGCGAACACCCGCCGCGCTTAATTTGCCGCTA
40	49	CAGGCAACCGATTTTTGGAGGGAAGGTAATATTGTGGGAATCCGGAAA
41	48	CCCCTACGTTGAACCATCACCCAAAAGTACAACGGAGTTTTGTATCA
42	48	TTGGAACAAGTAGTCCACTATTAACGAGGCGCAGACGGTTAATCATAA
43	48	TGGTGGTTCCTGAAATCGGCAAAACGCATAGGCTGGCTTTCCTTCATC
44	48	TCACCGCCTGTGCCCTGAGAGAGTTGCTCATTCAAGTATTAAGGCTTG
45	48	GAGAGGCGGTTTTGCATTGTTGGGCCAACTTTAATCATTTTGAATTACC
46	47	AGTCTTTCAAACGTGAGAAATAGAAAGGAACCTAAAGGAAGAATA
47	47	GACGACGACATCGGCAGAACTGGCTCATTGGAACAATAGAGTGAG
48	47	GTGTACAAATGTTAGGAATCATTACCGCGCCTTTTAGCAAGCA
49	47	CAACGTATTTACCATAAATAATGTAATGCTTTTTTGCAAATCC
50	47	AGATGGTCATTCAACCAGAAGGAGCGGAATTATTTTTATATTCCT
51	46	TTCTGGCCAACTTGACGCGCGTAACGATCTAAAAGCCCACAGTGCC
52	46	AGGAGCGGGTTTTGGGCGCTGGCAAGTGAAGTTTTTCCATATAA
53	45	TCCAGAACCCTCAGCAGGTCGACTCTAGGATCCCCGGGGAAG
54	45	CGAAAGGCGACGGCATAGGAACCCATGTATAGTTATCAATCGTCT
55	45	CAATAAAACAAGCCTGCGGAATCGTACGAACGTGTTGTTCCAGT
56	45	TATATTGGGTGACGACGATTATACCAAGCCGGATTGGTTGAGGCAG
57	45	AGGGTAAATACCCAAATCAAAAATCAGGGATAAATAGGGCGATGG
58	45	CAGTTGATTCAAGGGAAGTTTCCATTAACGCCAACAGGAACCGC
59	45	ATGTACCAACGTCACGCCATGTTACTTAAACAGTTCCTCTATTA
60	45	ACTGTAACCAGAGCGCCCGAAAGACTTCCACTAAAGGAACCCTAA
61	45	TGCTTTCCTTTTTAGAAATCAGAGCATCCTGATTTTACCAACGCTA
62	45	CGTCACCCATTAAATAGCCGAACAAAGTAAGAATTTATTATTATA
63	45	CTTTTTTTTTTAAAGCGAGAGGCTTTTAATCTTGTCTGTTTGA
64	45	ACAGGAACGTTTCGCCAGAATCCTCGGAATTTTTTACTAGAAA
65	45	GTTGAAATTATCAAAAAGGAATTACGACGAGAAATGATTGCCCT
66	45	AAAGAGTCTTTTCATCACGCAAAATAGATTTTTTTTTAACGTCA
67	45	CATCACTTGTTGAGTAGAAGAAATGCGCTTTTGATAGCCCTA
68	44	AAGACTTTTTTACGTACCTTTAATTTTTCTTTGGAGGCTTTGTA
69	44	AATTGACCAGGCAATTTTTCGCCATTTCGCCATGGTCAAGTTTA
70	44	TGAGGCGCATTAAATTTCTGGTGCCGGAATTATCCGTATAATCCT
71	44	ACTGTTGTACCGAGAGAACCGCCACCCTCTAAACACAGAACAAT
72	44	CCTGATTACAGTAACTAACAACATAACGACAACTTTTTTCAA
73	44	AAATTGTAATTGAGTGACCAACTTTGAAAGTCCAATAAGCCGT
74	44	ACGAGCGTCCAATCCAGCCTTTACAGAGAGGGCAACATTCCTTA
75	44	GATAAGTGCTGTCTATAAAAAGAAACGCAAAGATTTTCGGAATA
76	44	AAAATAATTGCGAAAACAAGAACCAGGATACCAAAATCCTCCGG
77	44	AAGCCTGTAGTAGGGAGGCAGAGGCATTTCCGGTATGAGAAG
78	44	GCTCAACTAGTATCTAACCTTGCTTCTGAGACGCTCTAAGAA
79	44	GAACAAACGCAACAGCCACCAGAACGAGTAAACGCCTTTTGCG
80	44	GATGAATATGCTTTGATTACCTGAGCAAAAGAGAAAATCGTATT
81	44	GCCCAATAAGCAGAGCCAGAATGGAAAGCGCAGTTTTGAATTTA
82	44	AAACATCGCGTCAGTATGAAAAATCTAAAGTCATCACTCACAA
83	44	TTGCCATACCCTAGTCAGGATTAGAGATGAGGAAGAAAGCGAA

84	43	CATATGGAATTTTGTAAACGGGGTCAGTGCTCGGTCGGTATAACG
85	43	AAAATTATGGAAGGATAAGTATAGCCCGTTGCGAAAGTAATAA
86	43	AATATCTTTTGCCCGAAGACAAAGAACGCGAAGATGGGATTCTG
87	43	TGACCATTTATACATTTTCGCAAATGGTCACTAAATCACTCA
88	43	CGACCGTACCTAAATTAGGATTAGCGGCCTTTAAACCGAGTA
89	43	TGAGAATTTTATATTTAACAAGTTGCTATTTAAAGGTAGTTGC
90	43	AGTTACTTTTCGCGCAGAGGGATAAATAATGAGGCCTTGATC
91	43	CCGCCTTTTTAGTGCCACGCTGCACGTAATTTGATTTAATAAT
92	43	ATCAAGACTTGCGGTCCGAACCTATTATATACCGAGATTTTAG
93	43	ATATATGTAGTGAAATATATAGAAGGCTTATCGAGCCAGCCAAC
94	43	GCTTCCGCAACATACAGATGATGGCAATCATCACACAGAGG
95	42	ACAGTTCACCTCCTCGAATTCGTAATTCAGGGCTATT
96	42	GCCGACAGCCTATGAGGTTTTGCTAATTTACGAGAGTTAAT
97	42	TCGAGAAGCCTTGAATGTAGCAATACTTCAACAGAACCATATC
98	42	GGTTATGAGAAGGTTAATGGTCTTAGAATCCTCTGAGAC
99	42	TTTTTCAGGTTGATGTTAGAACCTTGAGGATTTAGAGTGCCG
100	42	GTACCGCCAGCGGAATCGGCCTTGCTGGTTTGAATCTGCGCA
101	42	TGGGAAGAAACAGATTCACCAACCTGTCGTGCCTCAGGACGT
102	42	GAGCTGATTTTTGGTGGCATCTATCACCGTCACCATCGATA
103	42	AGAAAAGTTTTCAAAAACAGAAAATAAACAGCTAAAACAG
104	42	TTGTTAATTTTTAGCTCATTTTACCAGTATAAAGTAATAAG
105	42	CATTAAATTTTTGAGCGAGTAAGAAACAATAACATGAAACAA
106	42	GTAGATGTTTTGCATCGTAAGCAGAAGATAAATTGCTGAAC
107	42	AAGCTTGATTACGCGAACCTTCTGACCGCTCATGTCGTCTT
108	42	TTTTTTGTCAATTTGACAGAATCAAGTTACAGGAGCATCAA
109	42	TCTTTGAAAGAGGAACGCCGCCAGCATTGGCCTTTAGTTTAGC
110	42	AAGATTACCCCAAGGTGCCGTAAGCAATAACCTGCGTCAG
111	42	CACCTCCCCCTTATGCGAACGAGTAGACGGCGAATACGTAA
112	42	GCAAACGGTAAAACGTGGCGAGAAAGGCCAATTCTTAGCGT
113	42	TTGCGGAACGAGGGGTCACGCTGCGGTATGCAACTGCTGTA
114	42	GCTCAAACCTAATTGCTGAATATAGAGCCACCACCGTCATTT
115	42	GGATAGCAGTTTTGGAAATACCTACATTAGAGATACAGCTGG
116	42	GGACTCCCGGTTGATTAACGTAACACCAATTAAGACAGAAAA
117	42	AAATCCGGACCATAAAAGAAGTGGCATGCTGTAACACAATCAT
118	42	CGAGAACTGACCTGAAGGGCGAAAAACCAAGCATGTAAGTCAG
119	42	AAATCCATATGAAACGACTTGAGCCATTACGGAAAGAGTTAA
120	42	TAAATCATCGCATTAGGTAAGTAATTCTTCATCTAGACTG
121	42	TTTTATTTGTCCAGTATTTTGTAAAAAAGAAATGAACG
122	42	GATAGCGAGGACAGAGCCCGAGATAGGGACGTTAAACGACGA
123	42	TAAAGTAATAACACATATTATTTATCCTTTCCAGAACAATA
124	42	GCCCCATGACAAAAACAGGAGGCGGATTTGACCGCCTTAA
125	42	AGCGGTCCAGCTTTTACATTTAACAATTGGGTTAGACGACG
126	42	CTTAGGTTTCATTGCGCTTCCCTGTAGCCACGCTGCCAAAT
127	42	ATAAAAATTCATTAGTTTGCCCGCAGCGCGTCTGAATTAC
128	42	TCCTCAACAGCTTGGTTTTATAATCAGGCGGTTAGAAATAC
129	42	TGGTTTAGGTCAACAATATCTGGTCAGGAAACCCTAATGC
130	42	GAACAAATGGCAAGACCGTAATGGGATTCTTTTGGGCTTG
131	42	AGATACAGTAAATACCAGTGAGACGGGGCGGATATCAACA
132	41	GGCGATTTTTGTGCGGGCCTTTCGTCATGCCTTTTTCAG

133	40	GCACGTTTTAAATAACCACCAAGACAGCATCGGATGGCTT
134	39	TTGCGGGATTCACCCTCACATACATGGCTTTTGATGAT
135	39	CCCACGCATCCGATATATCTTGAGTAACTTTGCCCGTA
136	39	TGAATTTCTAACAGCTTGTCTGAAACATTTTAGTATTA
137	39	AAAAAAGGCTCAAAAGGAGGGTTTTGCTCTTTACCAGGC
138	39	ACCGGAACCAATAAAGTACGGTGTCTGTAGCGTAGCAAC
139	39	AAATAGCTAAAAAGGGCGACATTCGCGTACAGGCCGCTT
140	39	TCCCATCAACCAGCTACAATTTGGGAGCTCAACCATCG
141	39	ATTTTCCTAATAAGAATAAACAGAGAAGCTTTTCGAGG
142	39	AATACATTATAAAGAAATTGCGTAACCGTAATCTCCAA
143	38	GGTGTTTTACCGTACTCAGGATAGCTGTTTTGTGTGA
144	38	CGCCTGTAGTTTTTTTCCACAGACAGCCCTCACCGTA
145	38	GAAATGGATTTTTTTTTATTACATTGGCAAACACTACAA
146	37	TGCCACTGAACCAGCCACCCTCAGAGCCTTACCAGAA
147	32	TCCAGTCGGGAAGTATTAAGTTGATTAATTGC
148	27	GCAGCACCTTTTTCAGTAGCGGGGCGC
149	27	GGAAGCGCTTTTGACGGGAGATAATC
150	27	AGAATATATTTTACCGACAAAATAATT
151	27	ACATCAAGTTTTCAAATTAACATCAA
152	27	CTCAAATATTTTACCCTCAATGTTGGT
153	22	ATTACCGCCTTTCCATTGCAA
154	21	ACCAGTATTTTTAAAGGGACA