Supporting Information

Organizing DNA Origami Tiles Into Larger Structures Using Pre-formed Scaffold Frames

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Experimental Materials and Methods

Materials: All DNA staple strands were purchased from Integrated Technologies, Inc. (www.IDTDNA.com) in the format of 96-well plates and desalted with concentrations normalized to 100 μM. Single stranded M13mp18 viral DNA and ΦX 174 DNA were purchased from New England Biolabs, Inc. (NEB, Catalog number: N4040S and N3023S). All DNA strands were used without further purification.

Assembly Procedure: 1) Each individual DNA origami staple tile was assembled by mixing M13mp18 DNA (10 nM) with the corresponding staple strands with a 1:5 molar ratio in 1×TAE-Mg^{2+} buffer (pH 8.0, 20mM Tris, 2 mM EDTA, 12.5 mM $Mg(OAc)_2$). The final volume of each reaction was 100 uL. The oligo mixtures were annealed in a PCR thermocycler, cooled from 90°C to 70°C at a rate of -0.5°C/min and subsequently cooled from 70°C to 4°C at a rate of -0.1°C/min. Following the anneal, the structures were purified with 100 kD MWCO Microcon centrifugal filter devices (Amicon, Catalog number: UFC510096).

2) Origami super-structures were assembled in a two-step annealing process. Individual origami staple tiles bearing unique single stranded probes along two edges at designed positions were annealed in separate tubes as described above and subsequently purified with 100 KD MWCO Microcon centrifugal filters to remove any excess staple strands. At the same PhiX174 scaffold strand (10 nM) and a complete set of bridges strands were mixed in a separate tube (molar ratio 1:10) and annealed from 90 °C to 4 °C over 10 h in 1×TAE-Mg^{2+} buffer. The two solutions were mixed together (molar ratio 1.5:1 or 2:1) and annealed from 45 °C to 4 °C at a rate of -2°C/h. The annealing cycle was repeated 10 times, and in each consecutive cycle the starting temperature was decreased by 0.5 °C from the prior cycle. The entire annealing program took approximately 100 hrs.

Agarose gel electrophoresis: The assembled products were loaded into agarose gels (0.3% agarose in 1×TAE-Mg^{2+} aqueous buffer, containing 0.5 μg/mL ethidium bromide) and subject to gel electrophoresis at 80V for one hour.

AFM imaging: The samples (2 μL) were deposited onto freshly cleaved mica (Ted Pella, Inc.) and left to adsorb for 3 min. Buffer (1×TAE-Mg^{2+}, 400 μL) was added on top of the sample and the sample was imaged in fluid tapping mode on a Pico-Plus AFM (Molecular Imaging, now Agilent Technologies) with SNL tips (Veeco Probes, Inc.).

Figure S1. Design of the triangular DNA origami staple tile. The red strand represents the M13 scaffold. The blue strands are the staple strands with arrows pointing to the 3' ends. The spacing between consecutive staple crossovers connecting neighboring parallel helices is 32 bps. The outermost helices are 384 bps or approximately 120 nm.

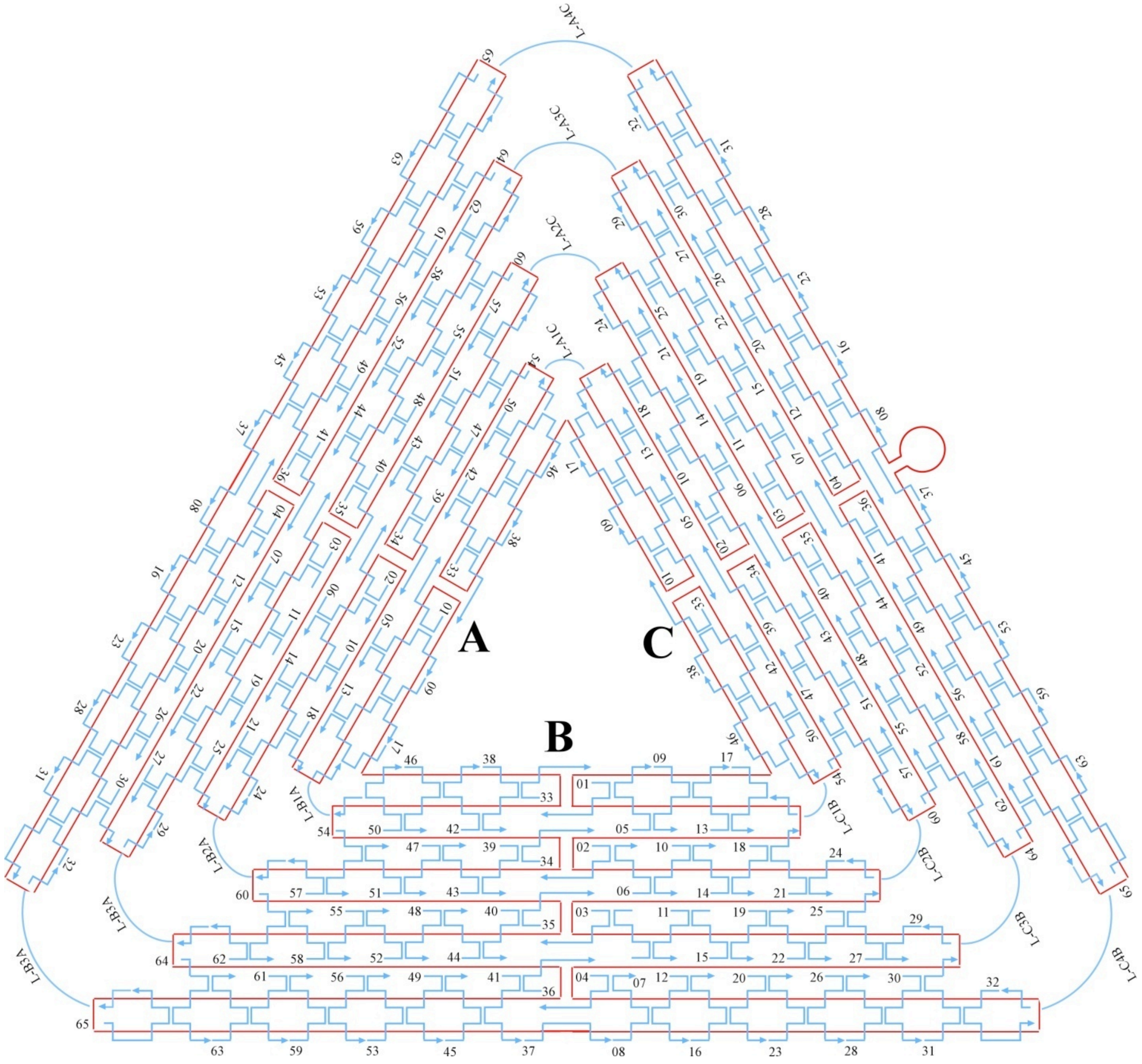


Figure S2. AFM image of the individual triangular shaped DNA Origami (the size of the image is 3.5 um × 3.5 um)

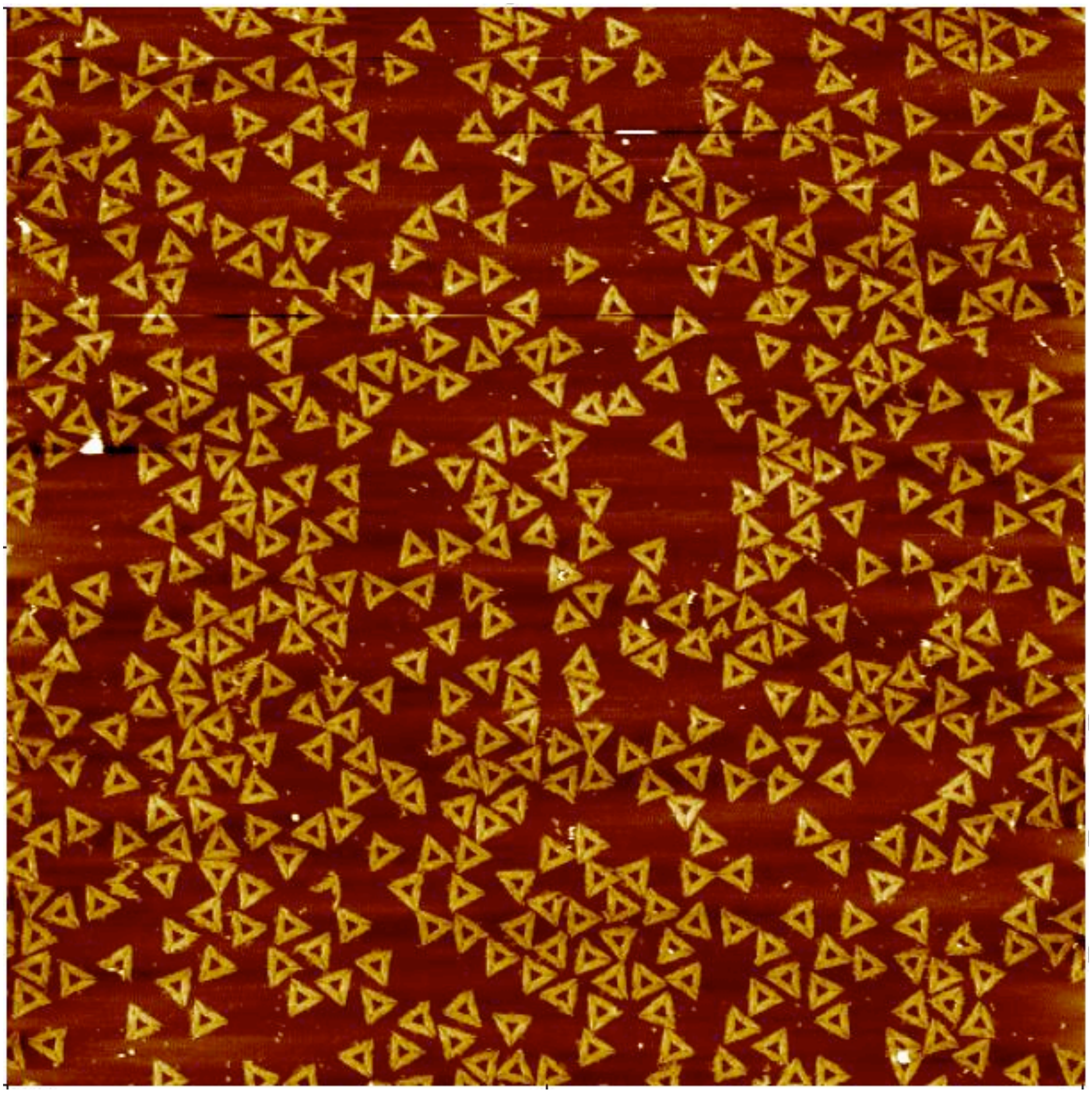


Figure S3. Agarose gel electrophoresis result for the triangular DNA Origami. (1.5% agarose gel)

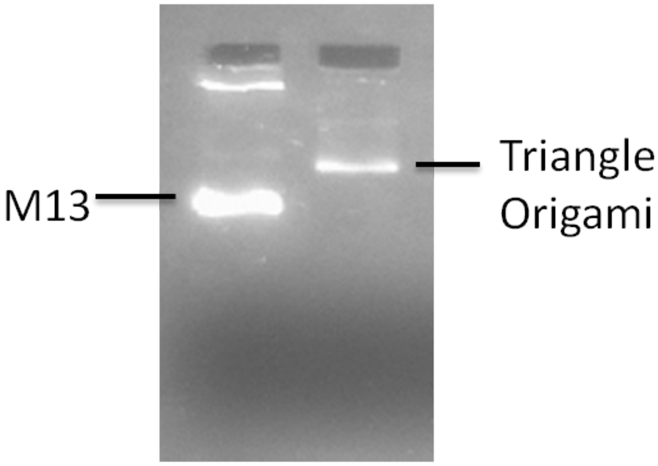
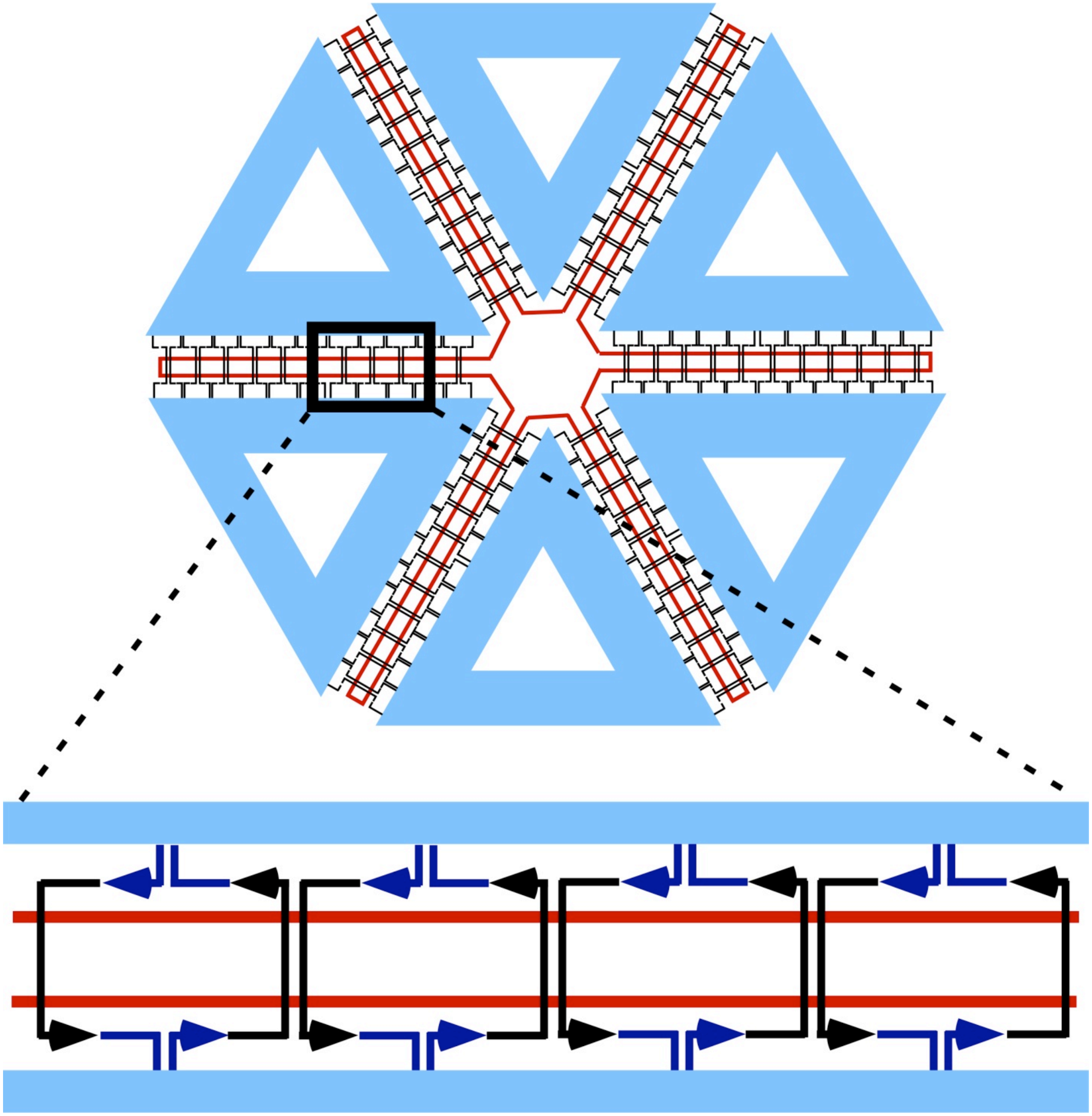
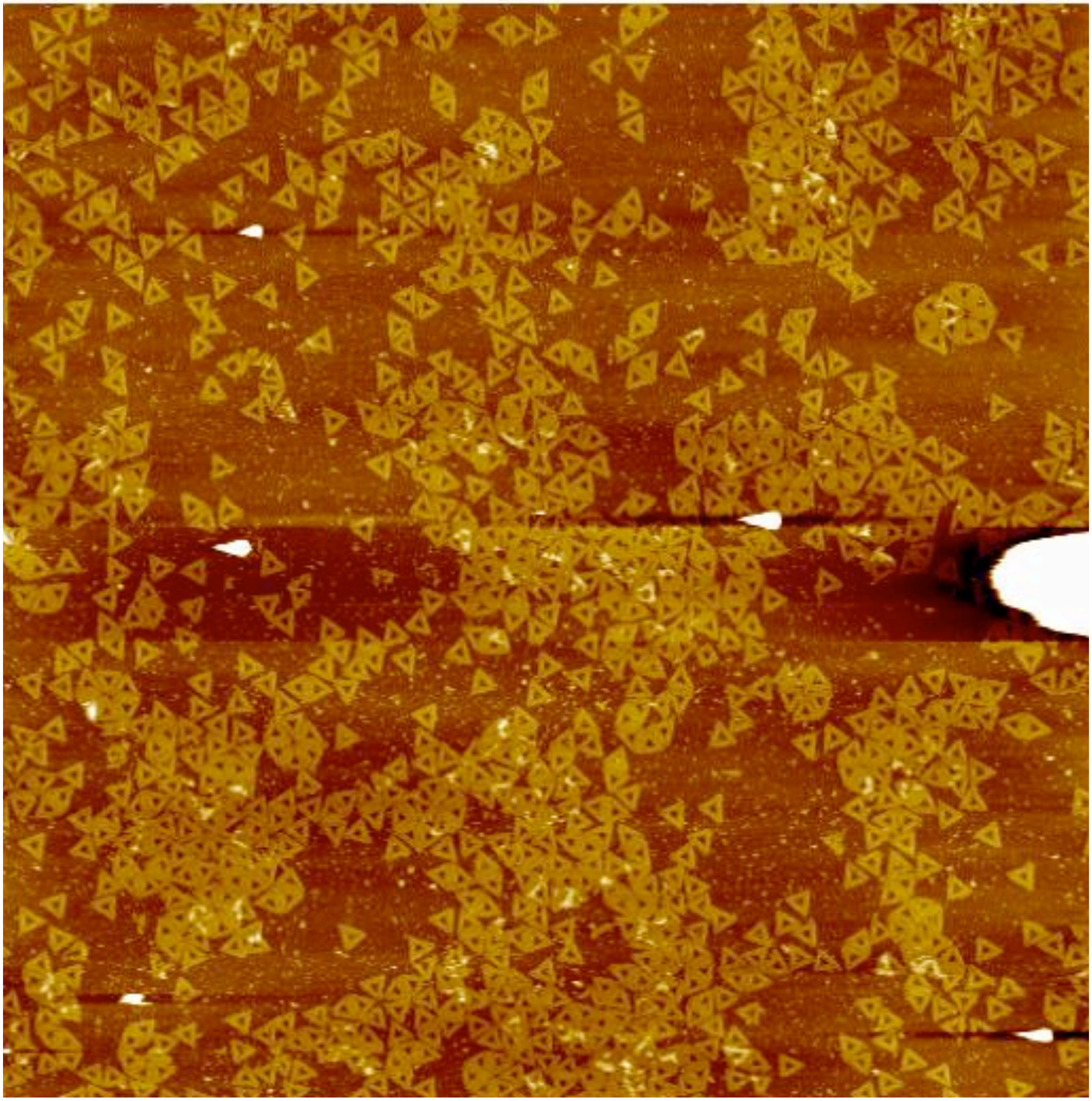
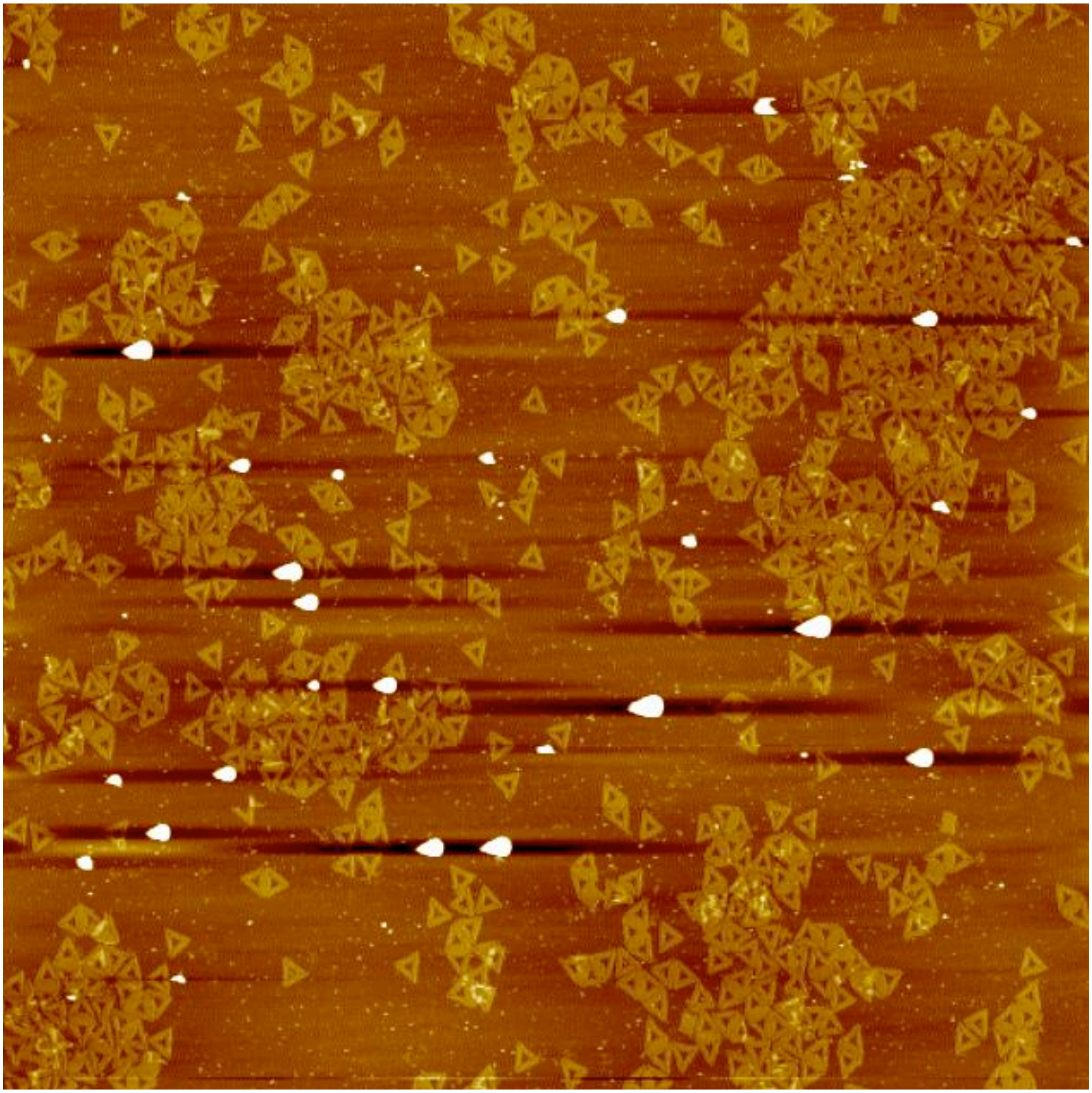


Figure S4. Design and AFM images of the triangular origami staple tile based super-structure using design 1 (the size of the AFM images are 5 um × 5 um)







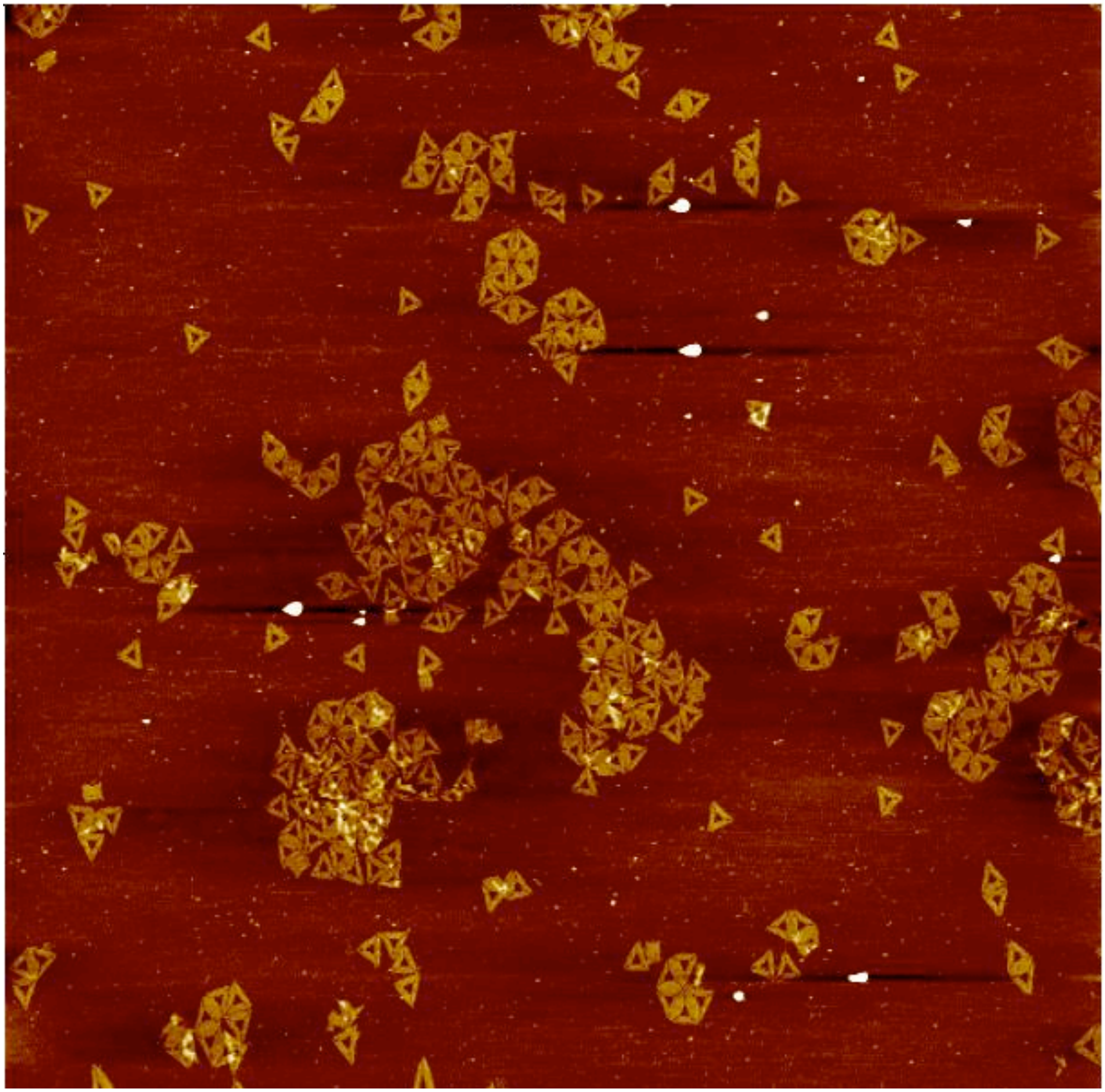
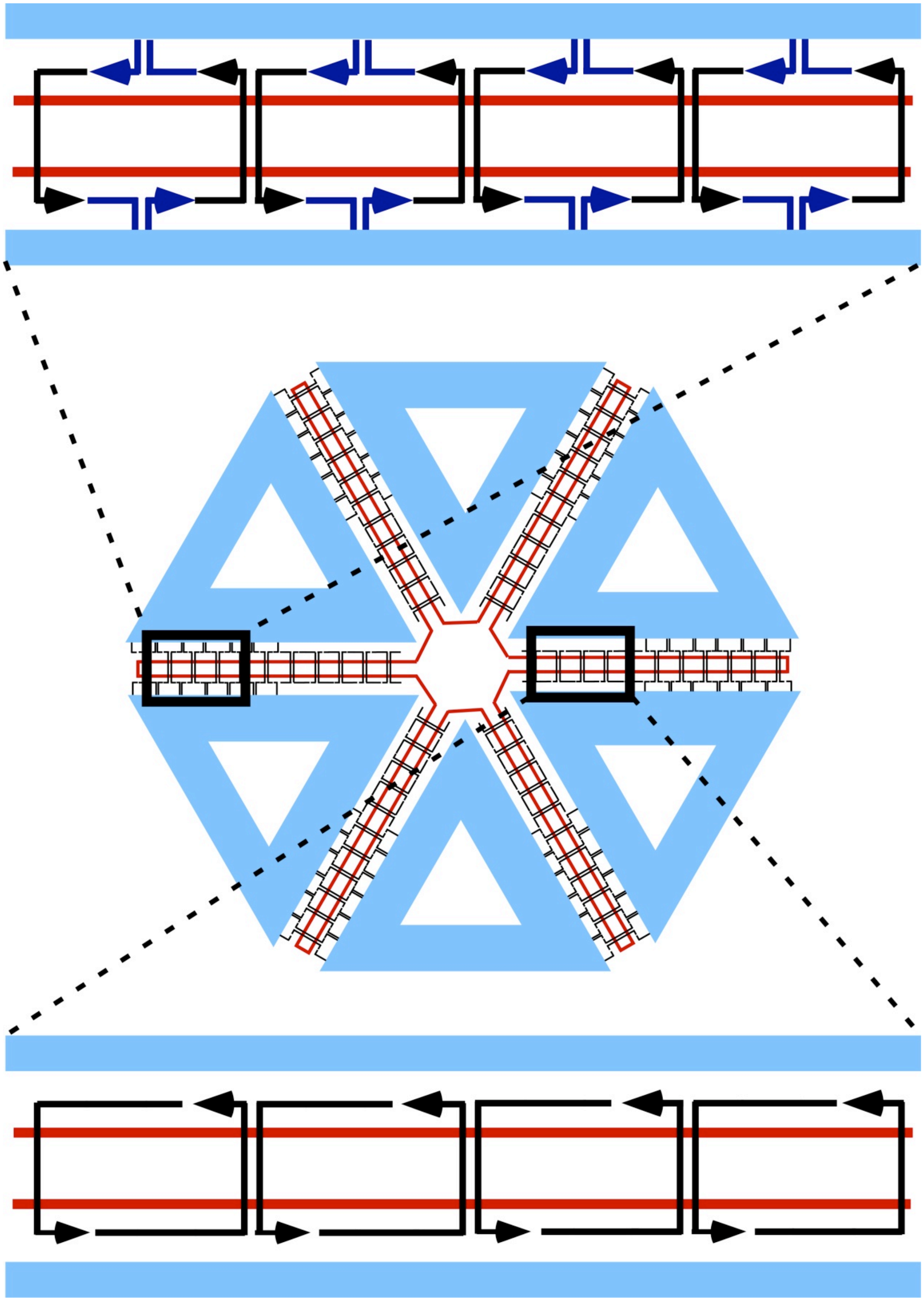
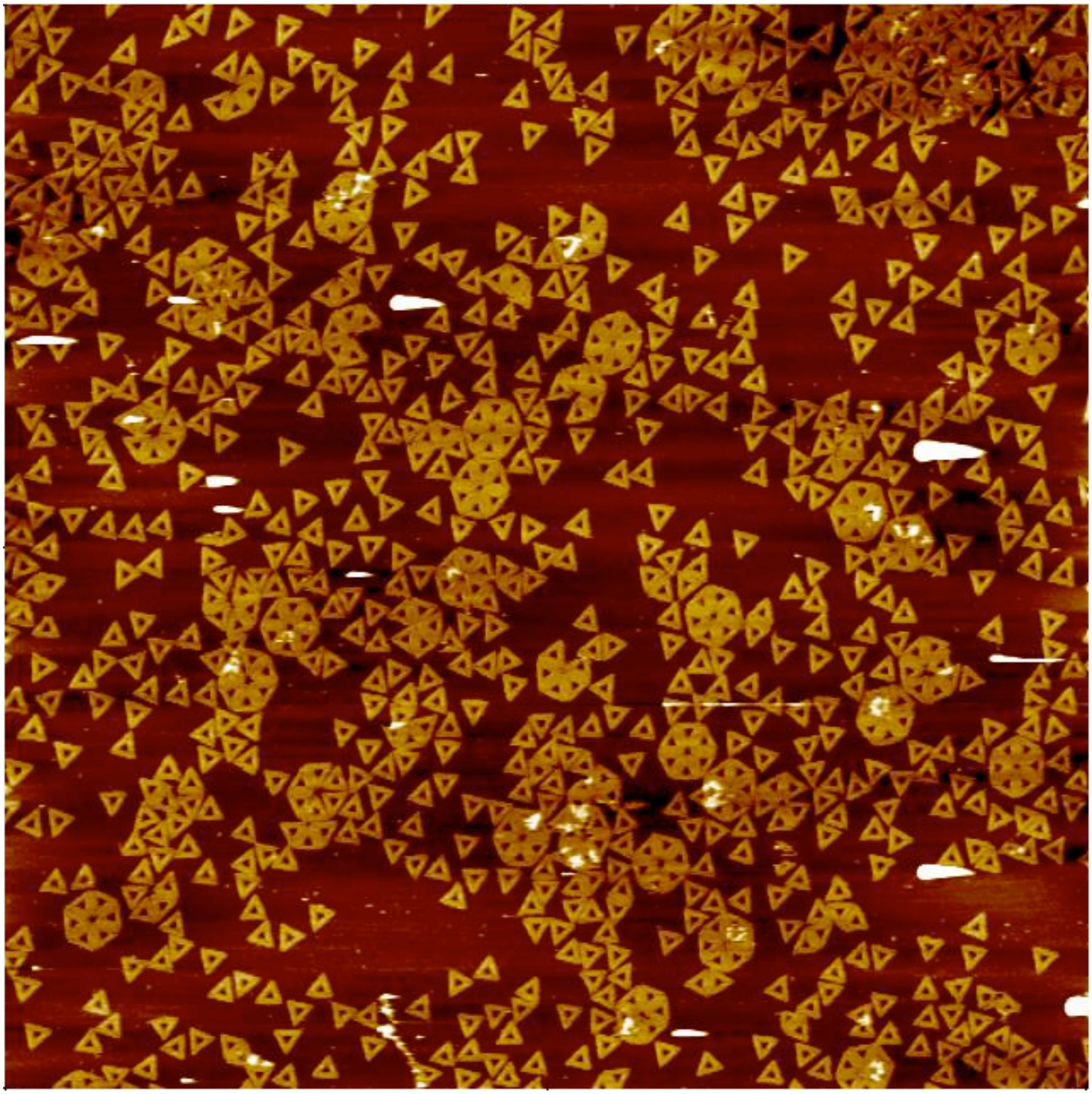
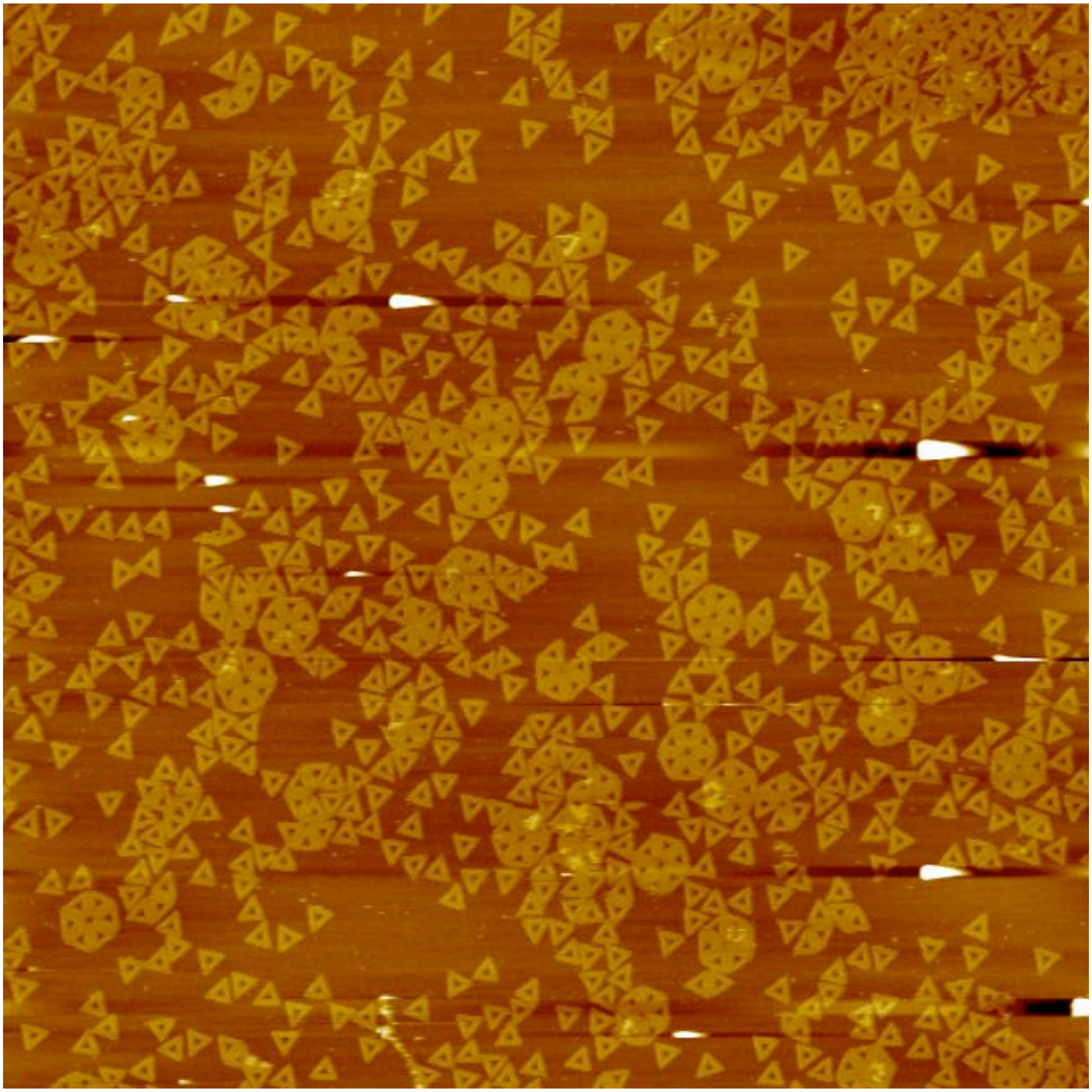


Figure S5. Design and AFM images of the triangular origami staple tile based super-structure using design 2 (the size of the AFM images are 5 um × 5 um)







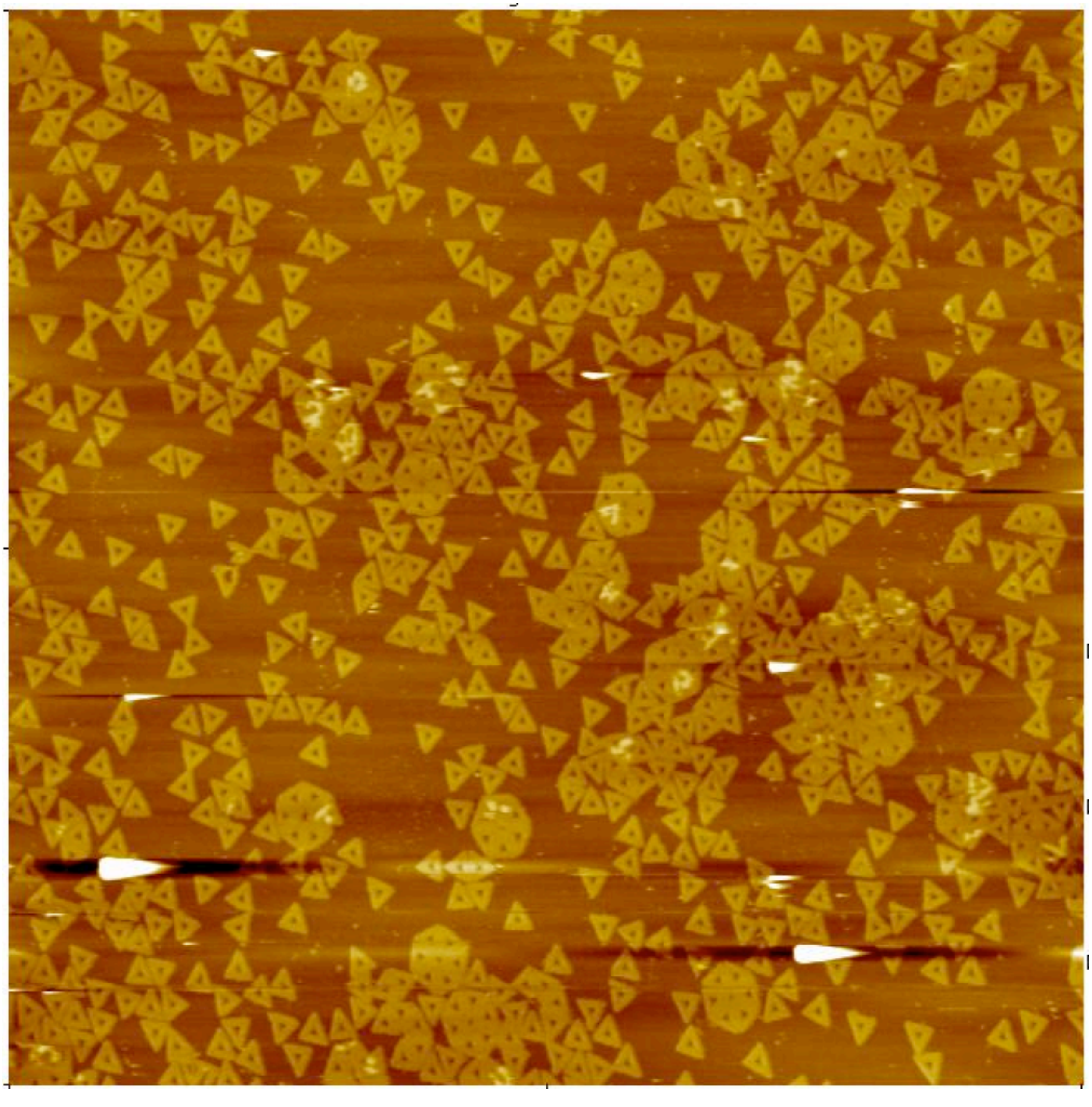
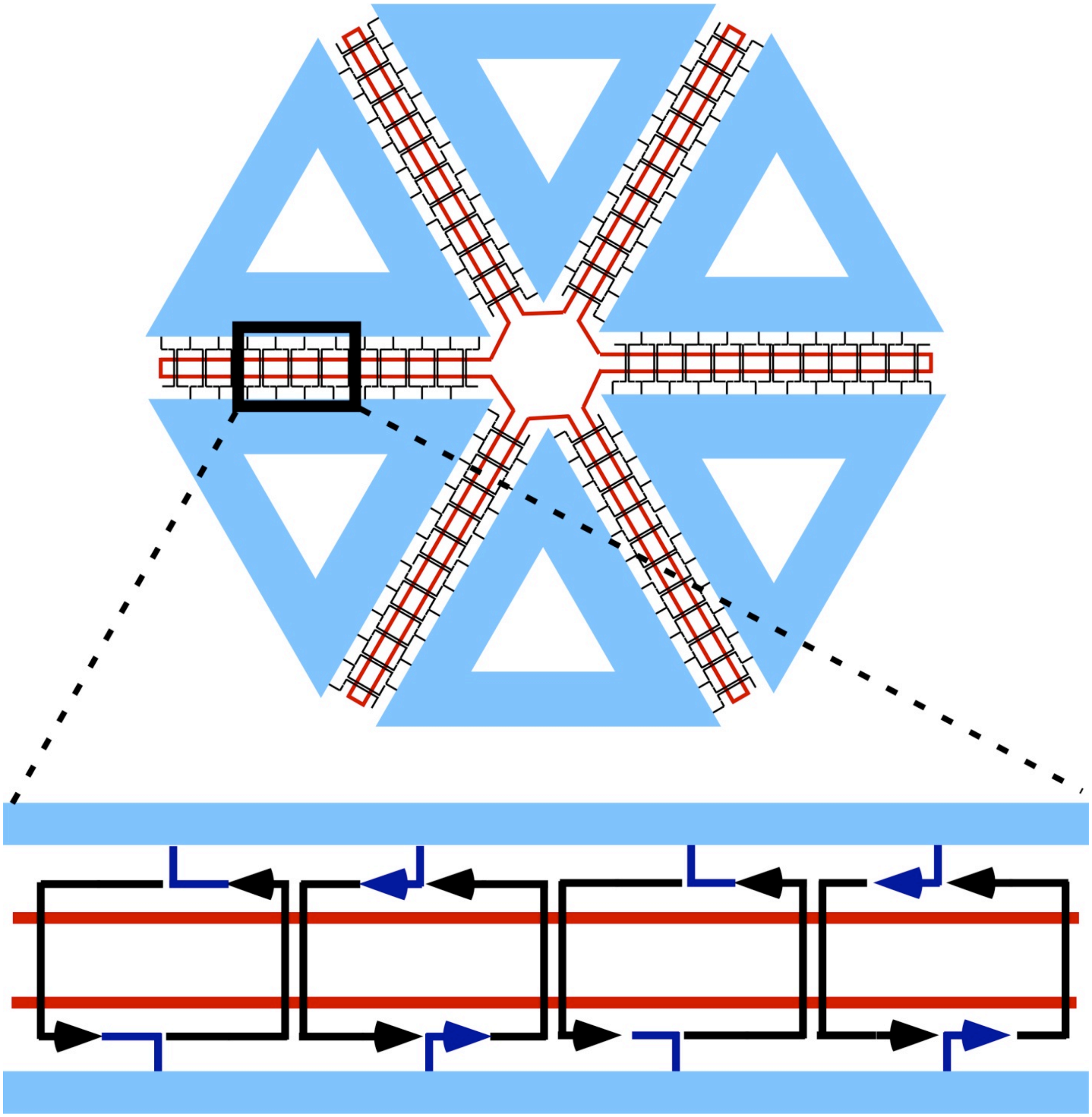
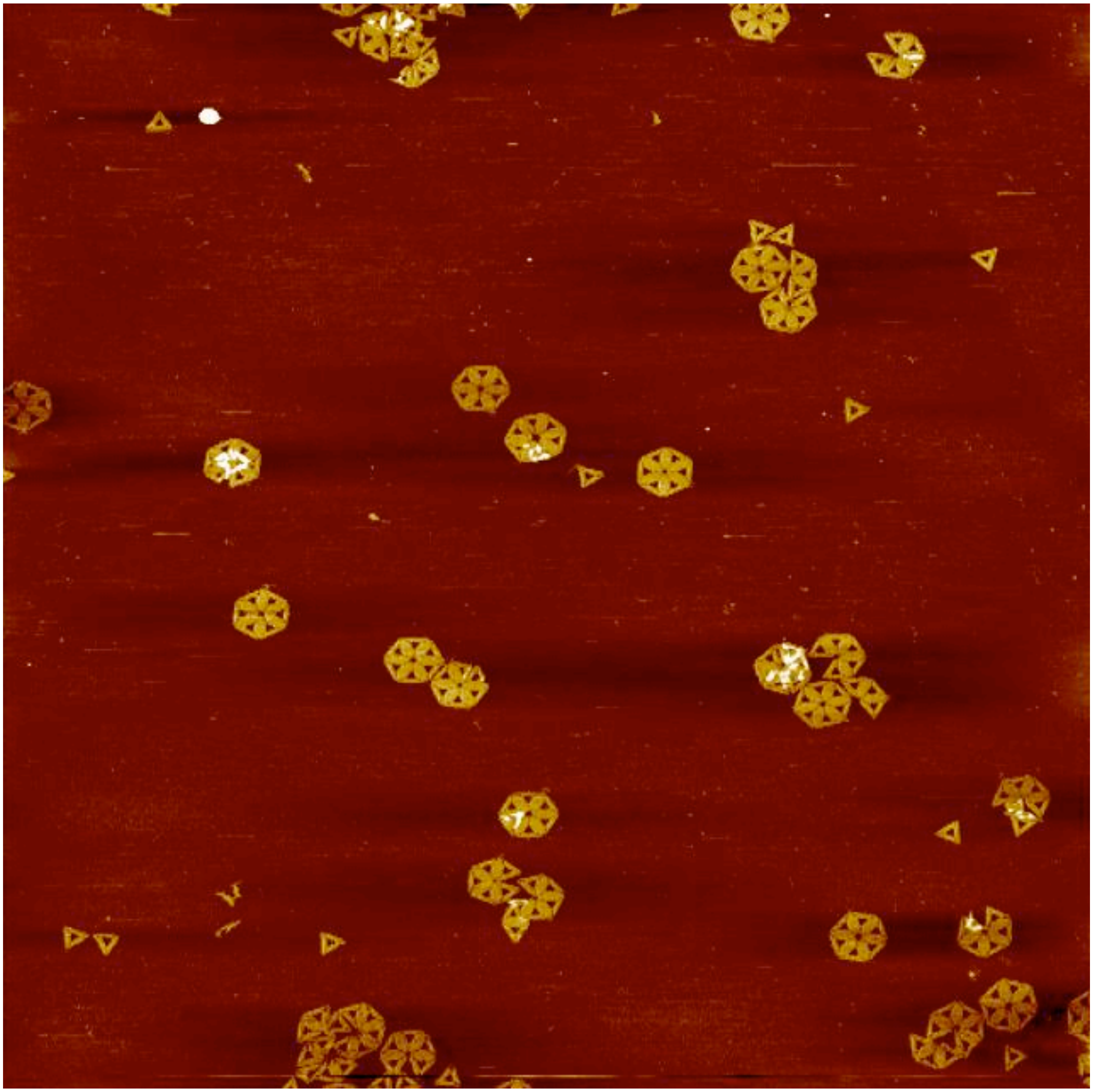
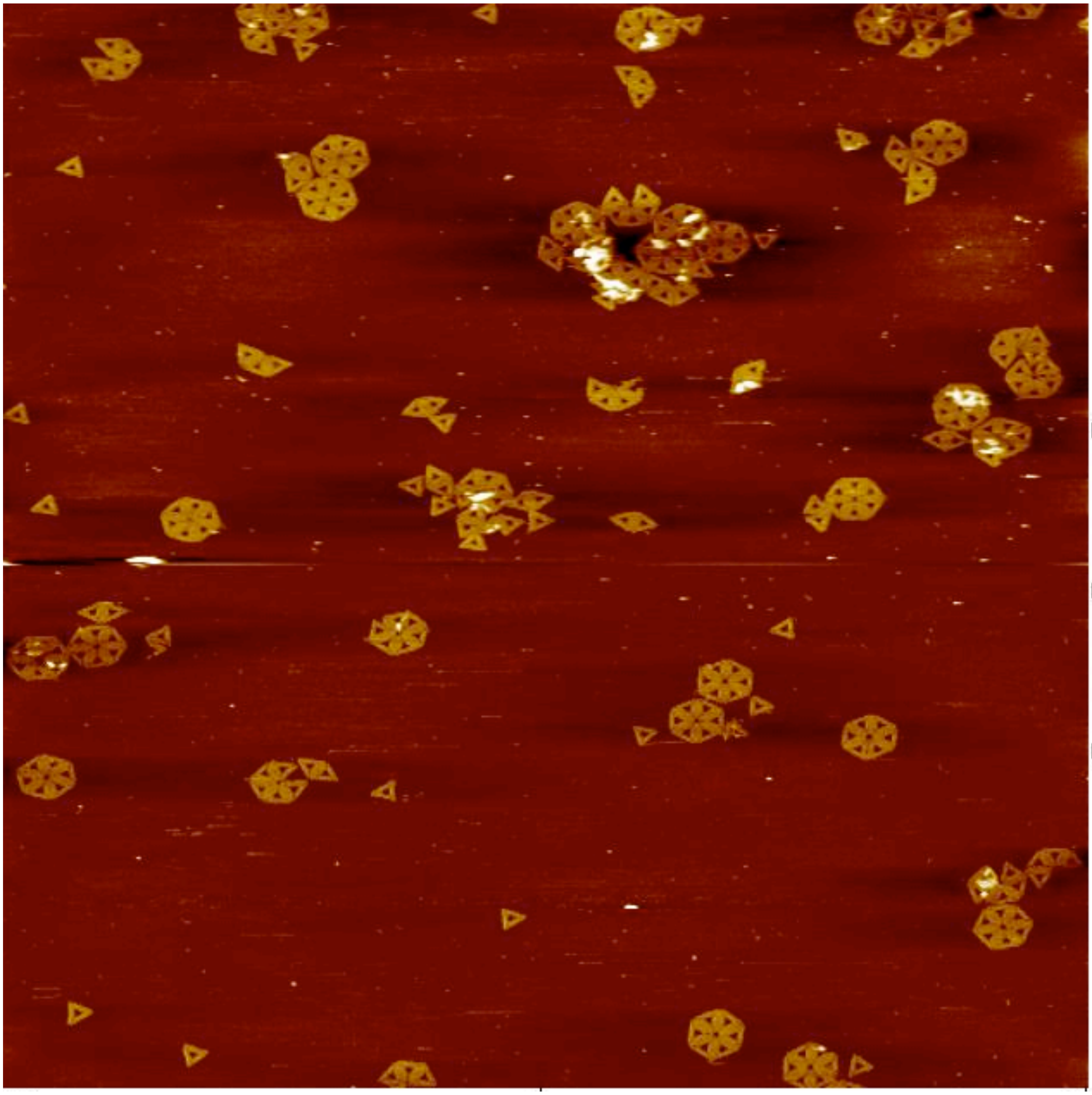
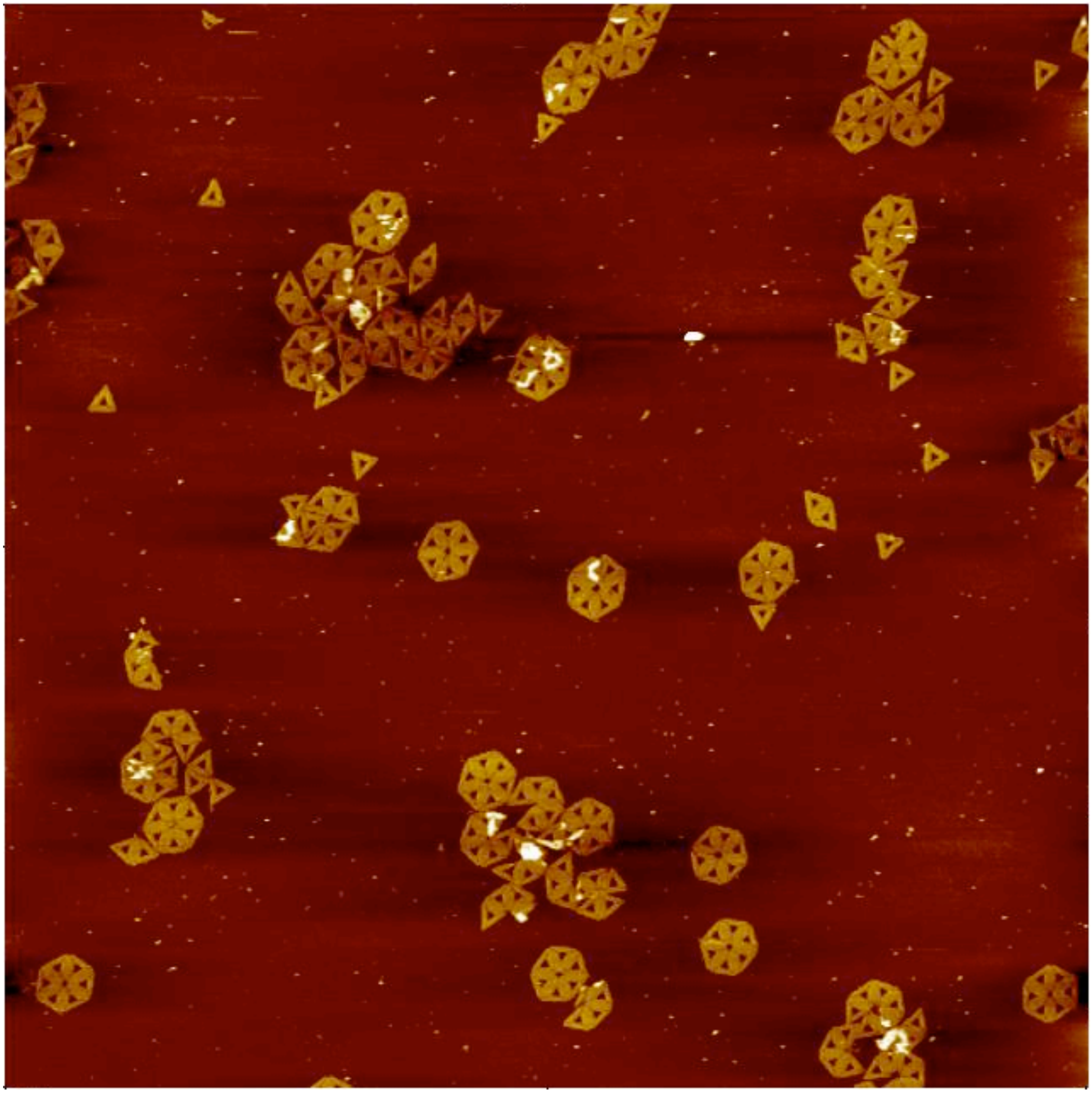


Figure S6. Design and AFM images (zoom out and zoom in) of the triangular origami staple tile based super-structure using design 3. The size of the AFM images are 5 um × 5 um. The size of the zoom out AFM images are 5 um × 5 um and the size of the zoom in images are 270 nm x 270 nm.









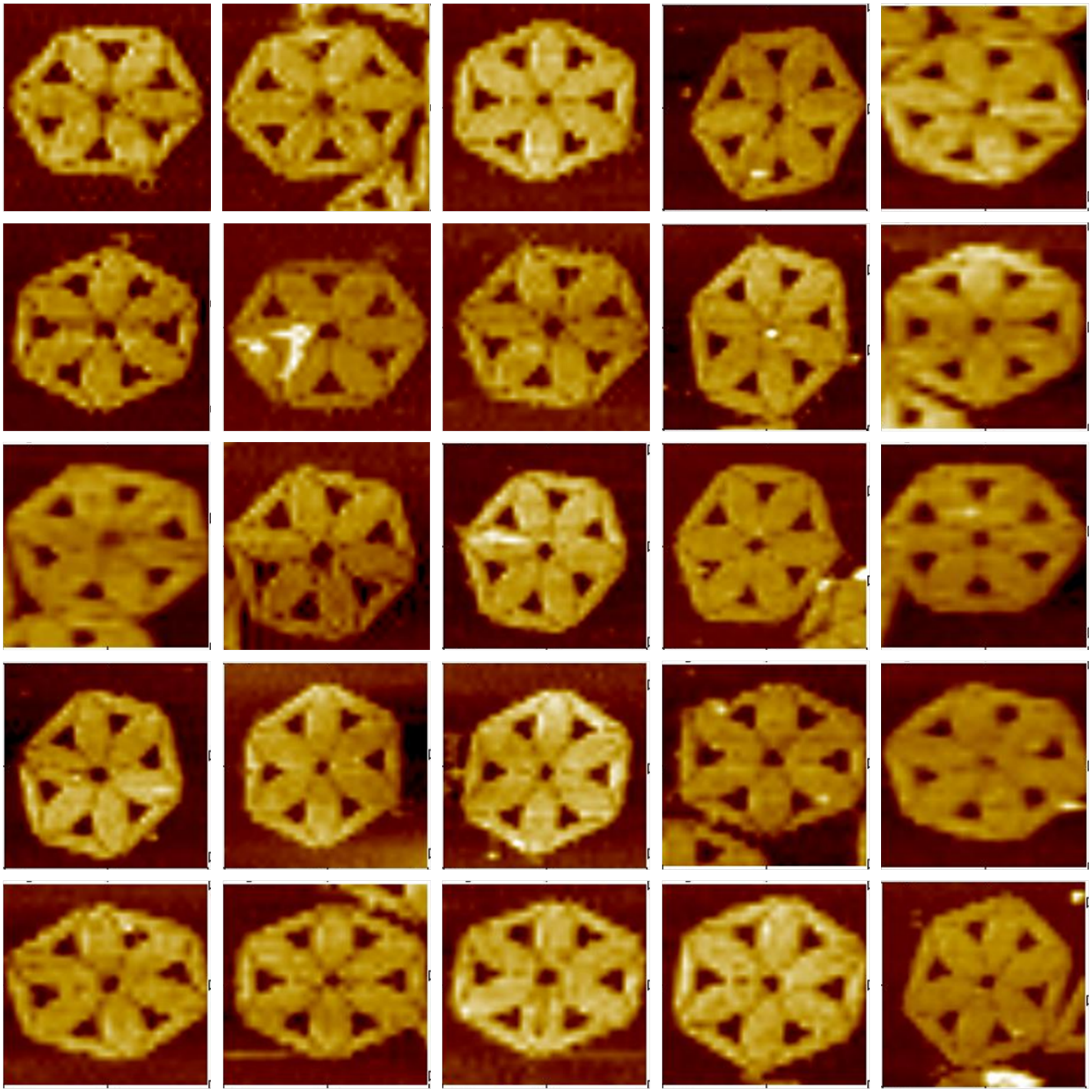


Figure S7. Design of the square DNA origami staple tile. The red strand represents the M13 scaffold. The black strands are the staple strands with arrows pointing to the 3' ends. The spacing between consecutive crossovers connecting neighboring parallel helices is 32 base-pairs. The outermost helices are 224 bps or approximately 21 full turns. To make 90 degree angles at each corner, each consecutive helix is 8 bps shorter (on both ends) than the outer, adjacent helix.

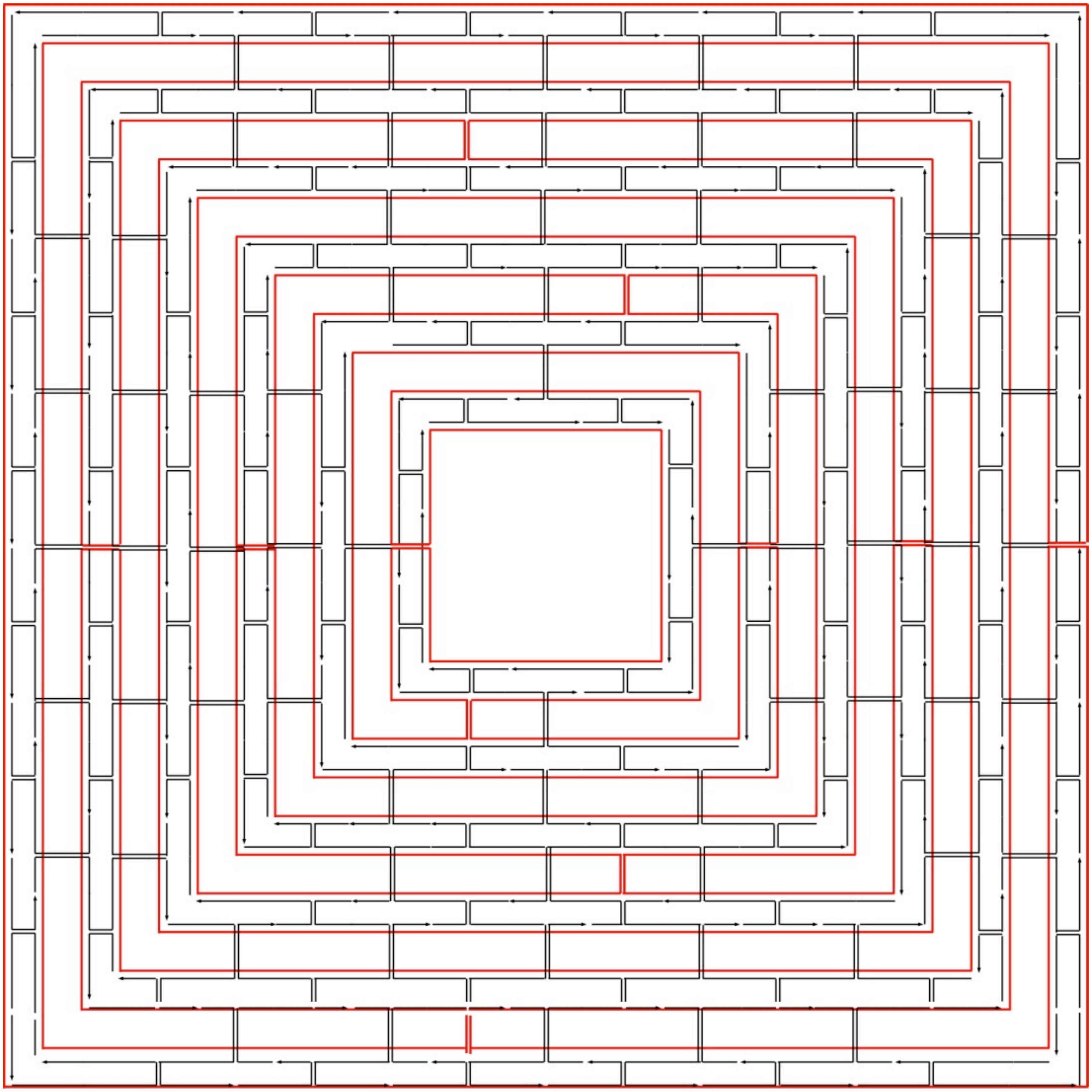


Figure S8. AFM image of the individual square shaped DNA origami staple tile. The size of the image is 2.5 um × 2.5 um.

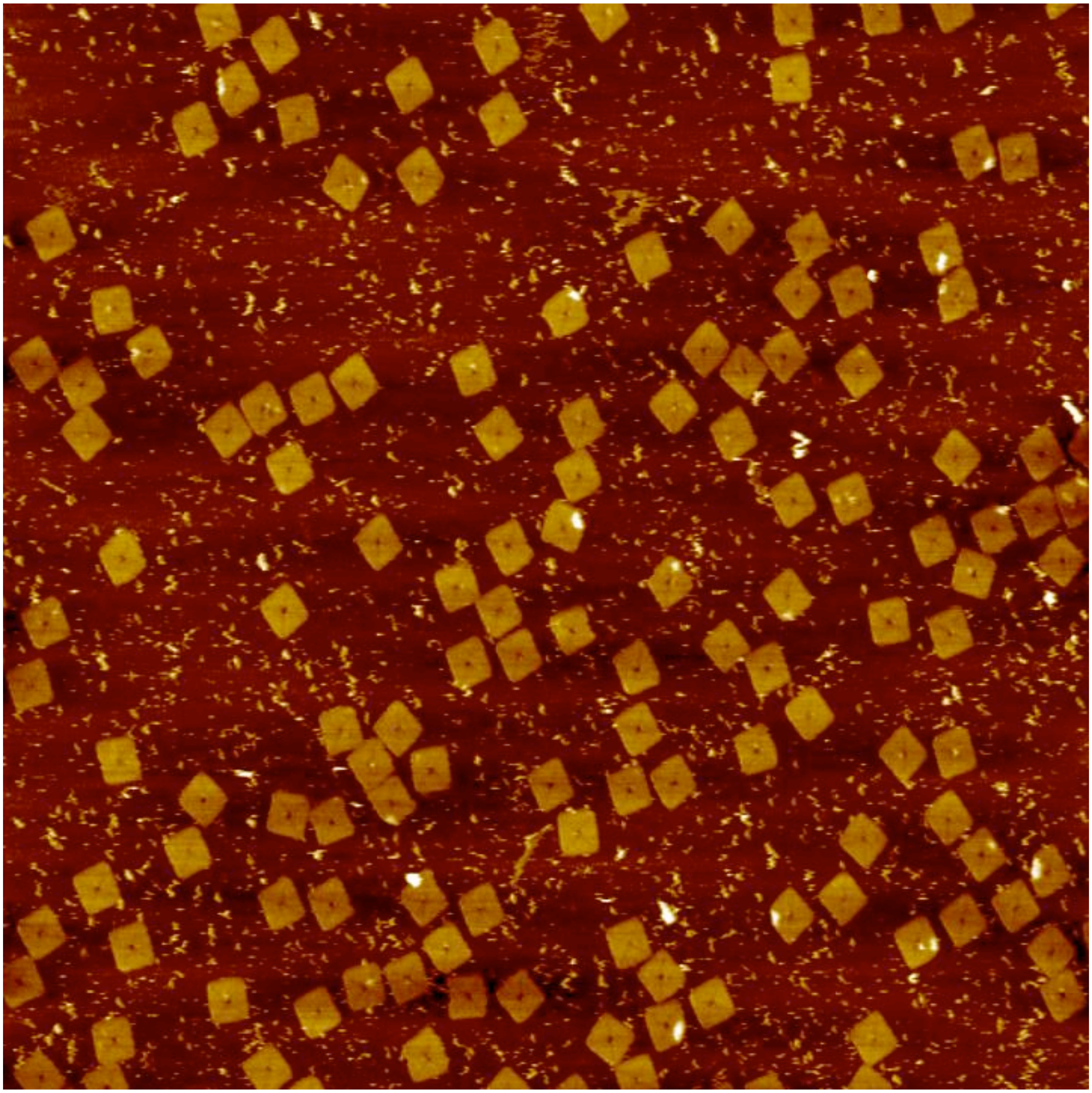


Figure S9. Agarose gel electrophoresis result for the square DNA origami. (1.5% agarose gel)

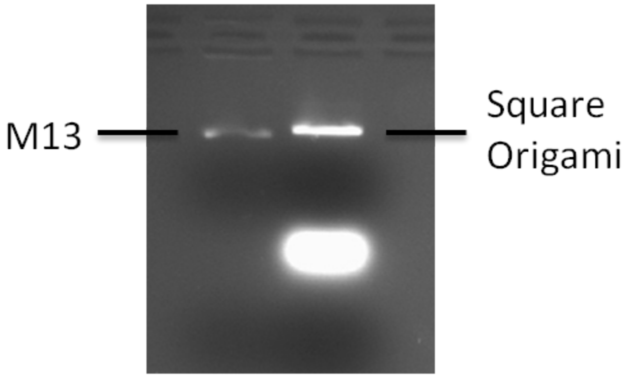
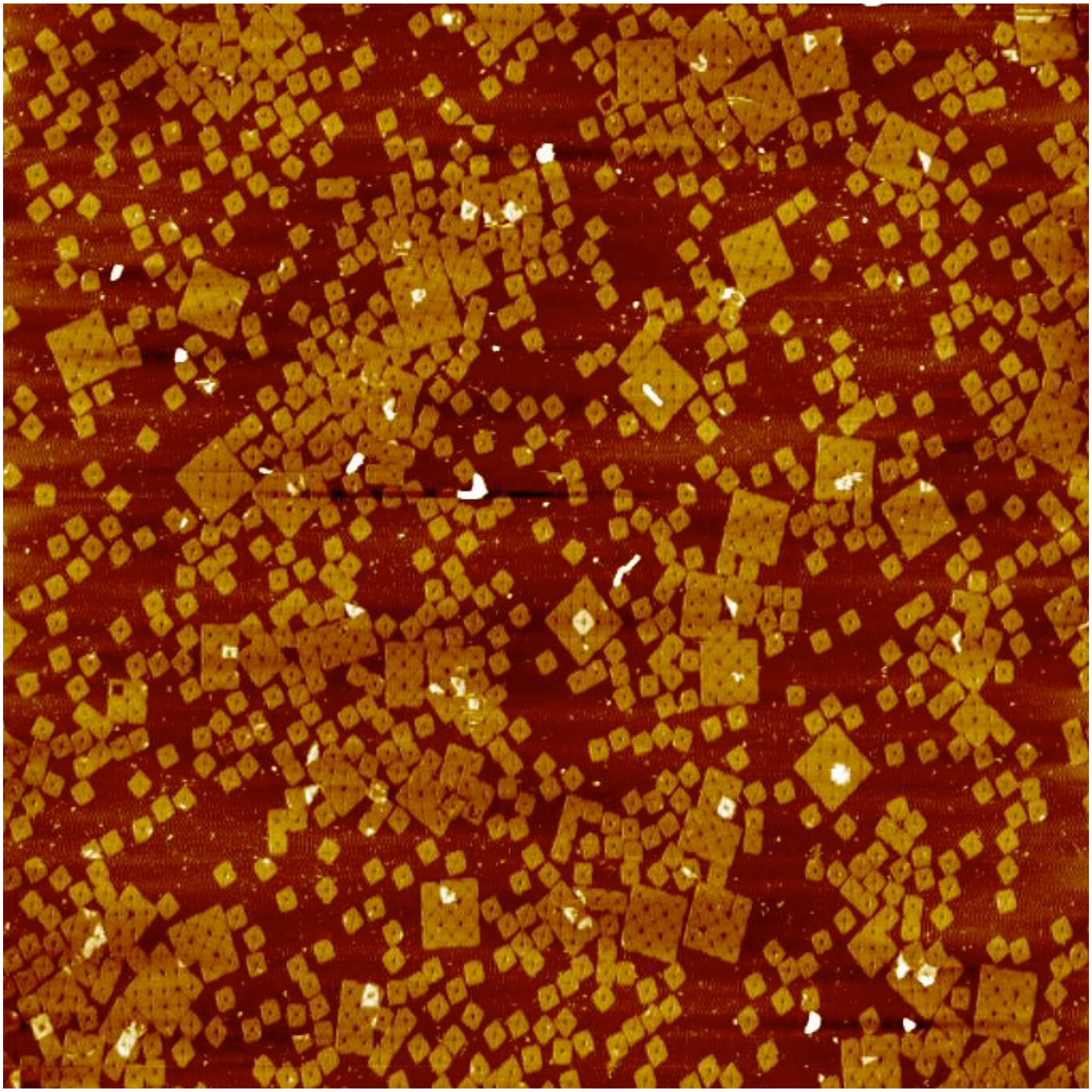
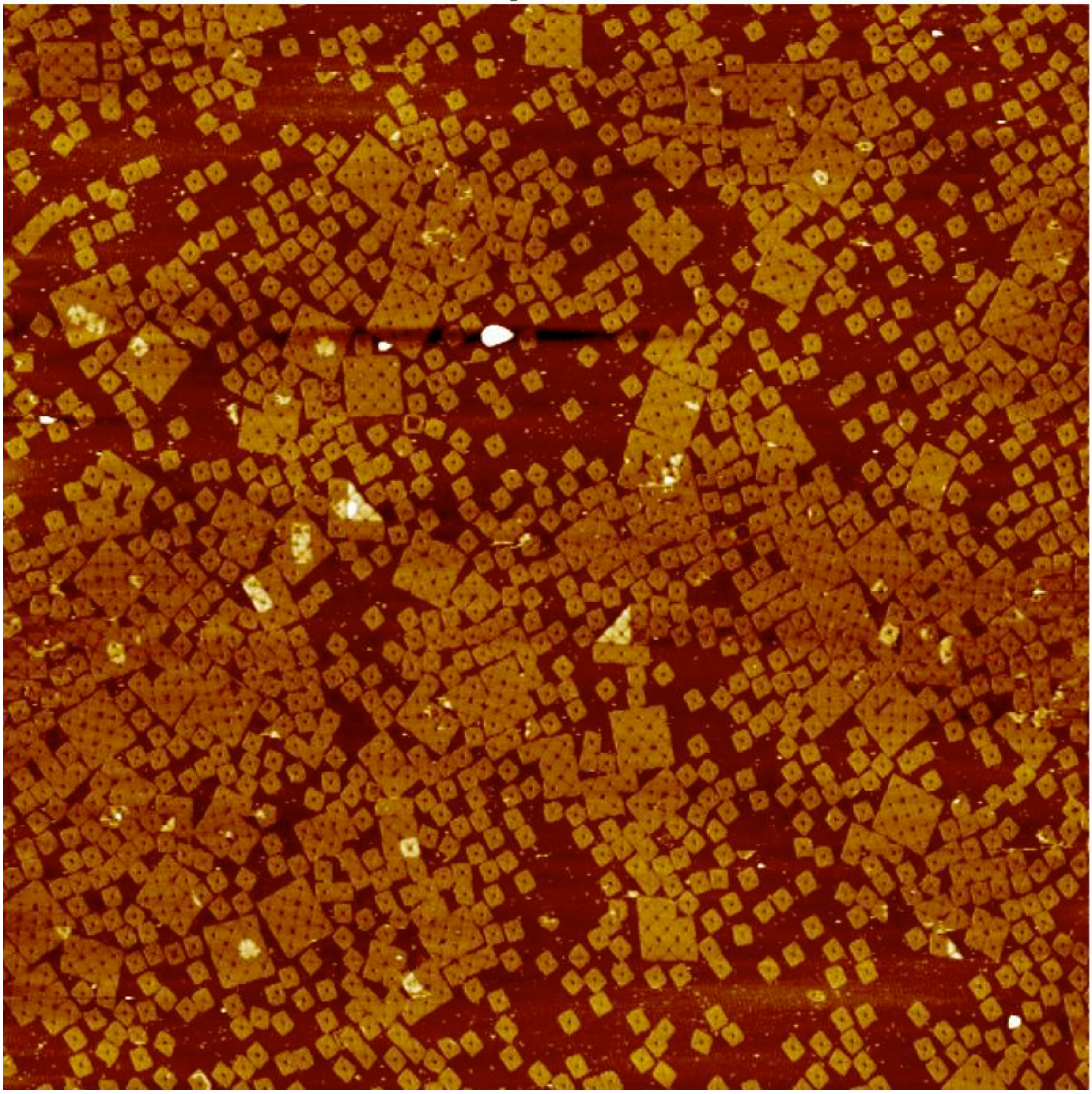
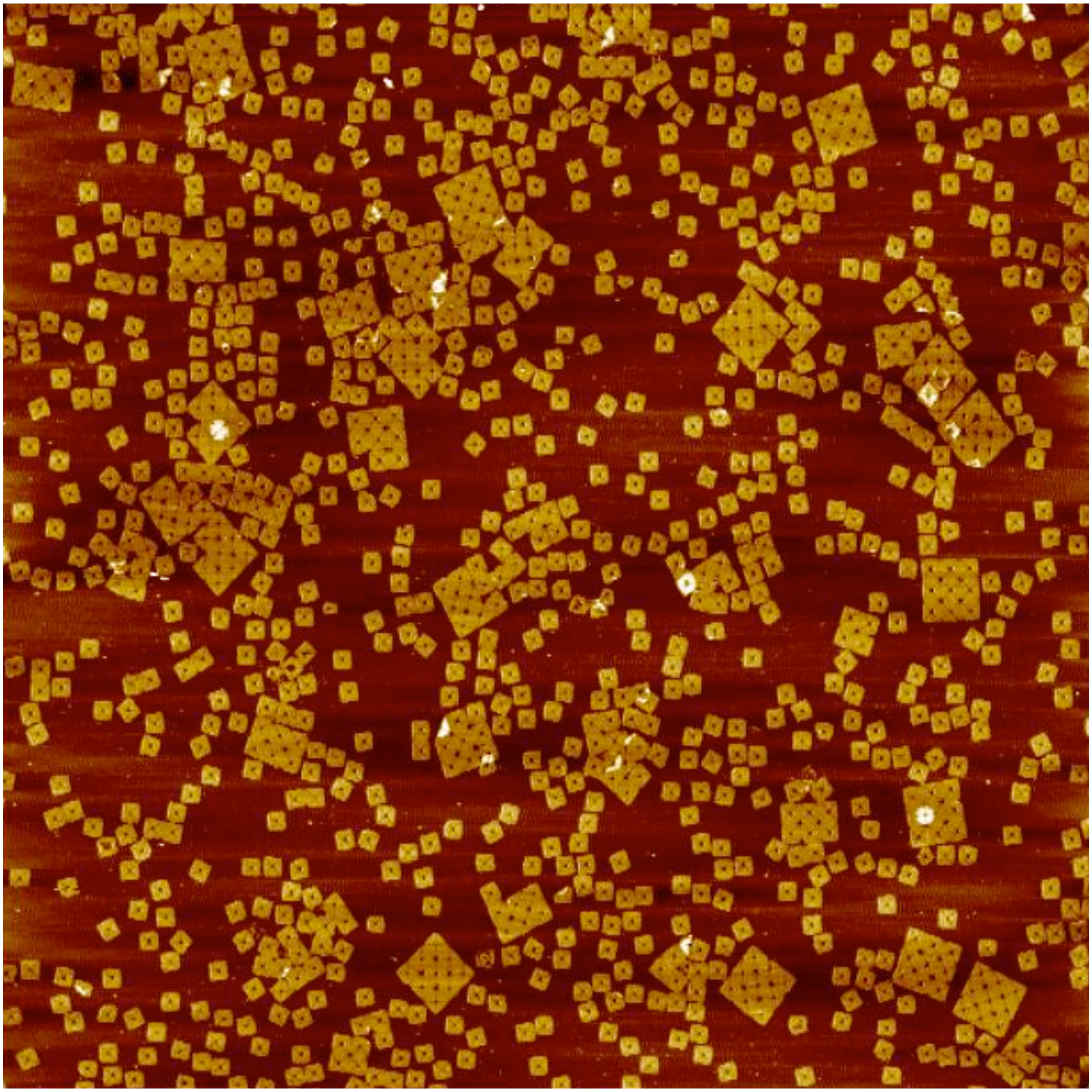


Figure S10. Zoom out and zoom in AFM images for 3 x 3 square staple tile based super-structures. The size of the zoom out images are 5 um × 5 um, and the size of the zoom in images are 340 nm x 340 nm.







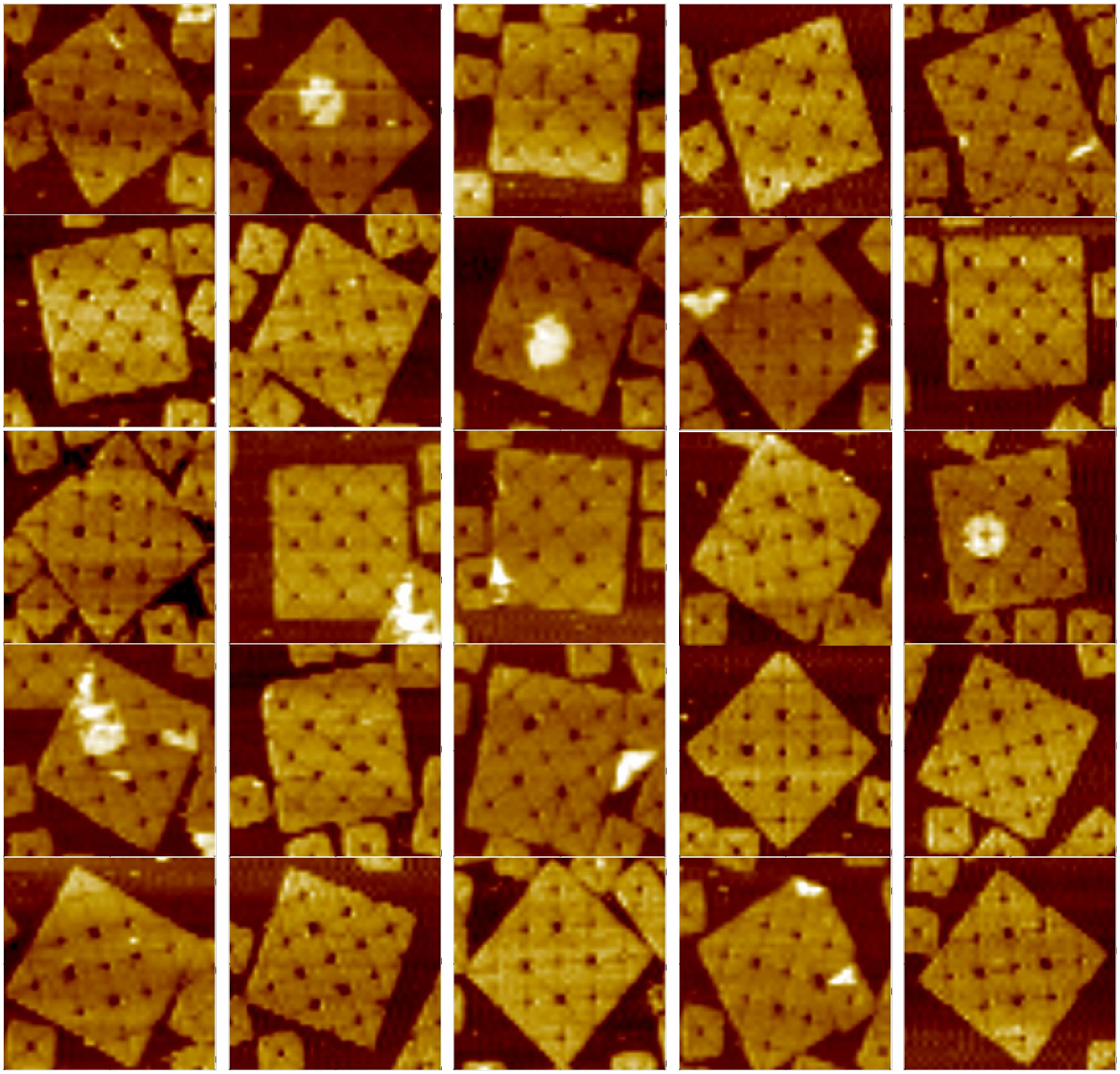


Figure S11. Design of the hexagonal DNA origami staple tile. The red strand represents the M13 scaffold. The black strands are the staple strands with arrows pointing to the 3’ ends. The design principle is the same as for the square origami. 9 parallel helices are arranged in a plane forming each side. The spacing between consecutive crossovers connecting neighboring parallel helixes is 32 bps. The outermost helices are 160 bps or approximately 15 full turns. To make 120 degree turns at each corner, each consecutive helix is 4 bps shorter (on both ends) than the outer, adjacent helix.

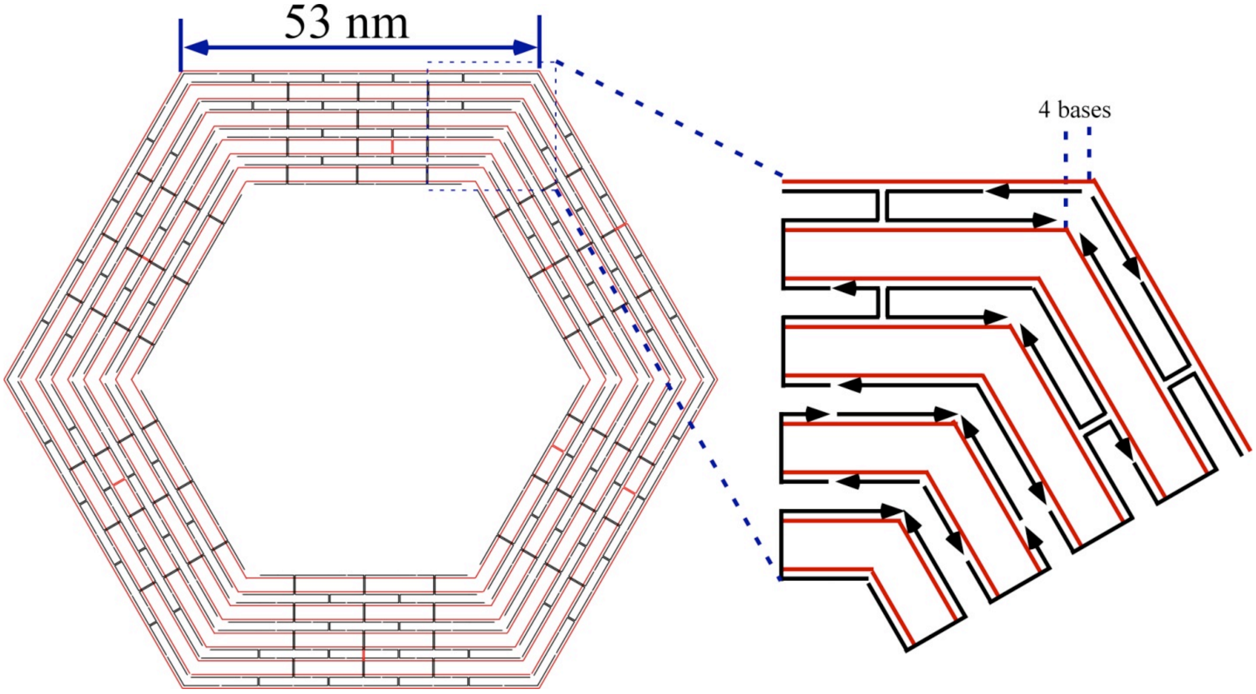


Figure S12. AFM image of individual hexagonal DNA origami staple tiles. The size of image is 5 um × 5 um.

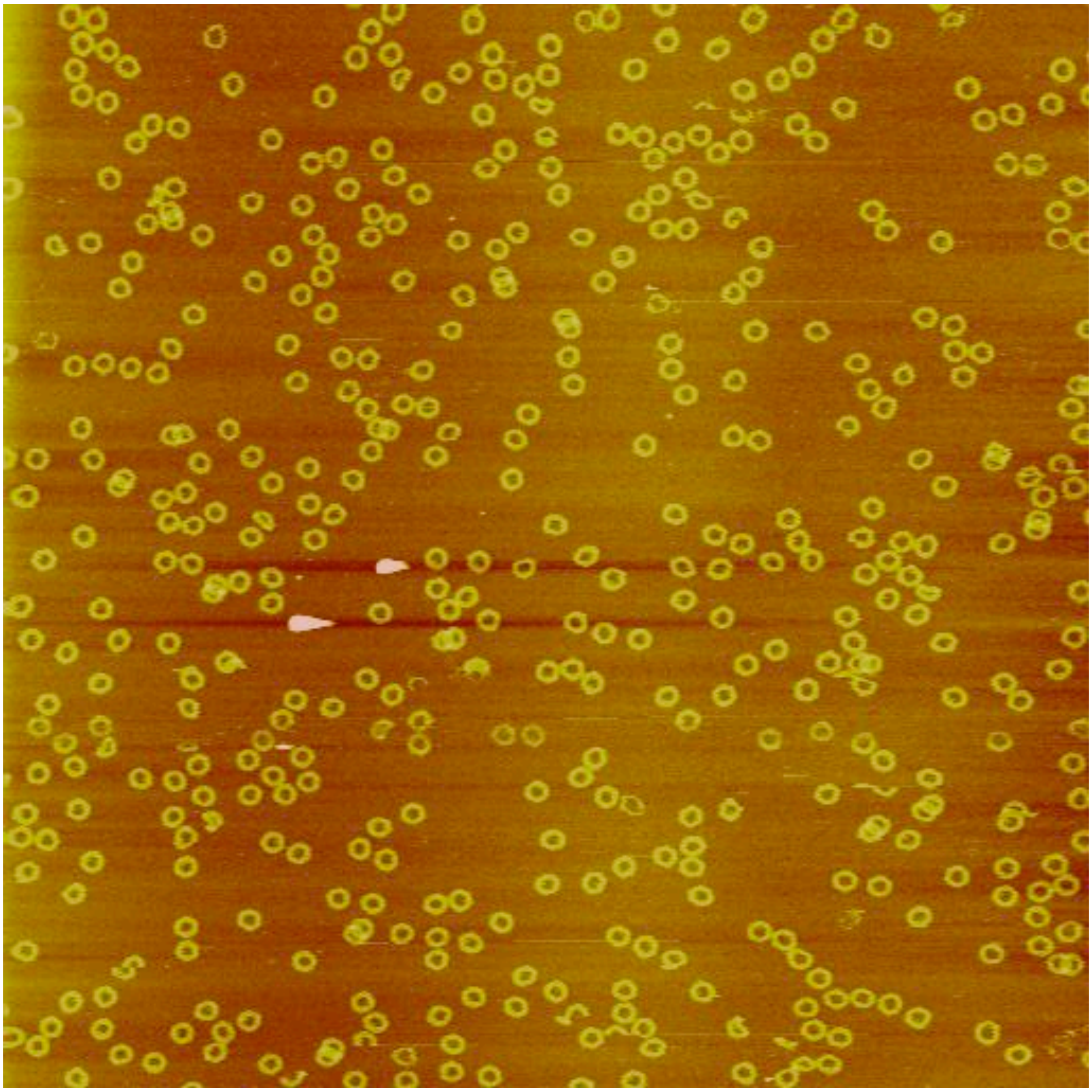


Figure S13. Agarose gel electrophoresis result for hexagonal shaped DNA Origami.

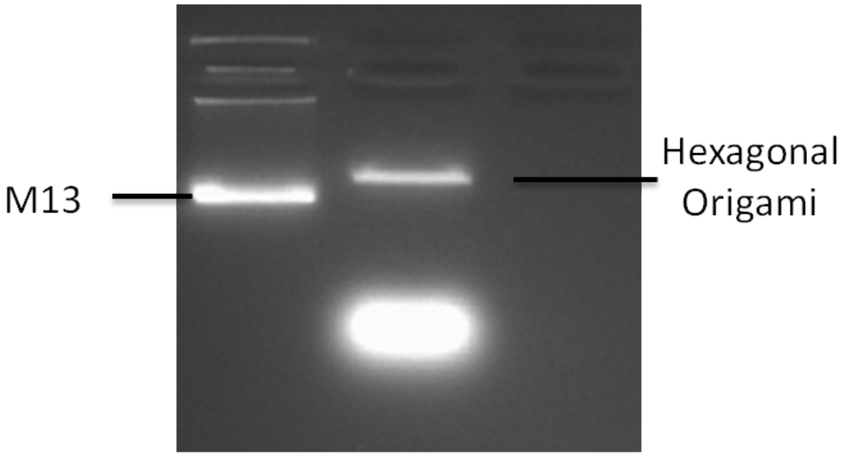
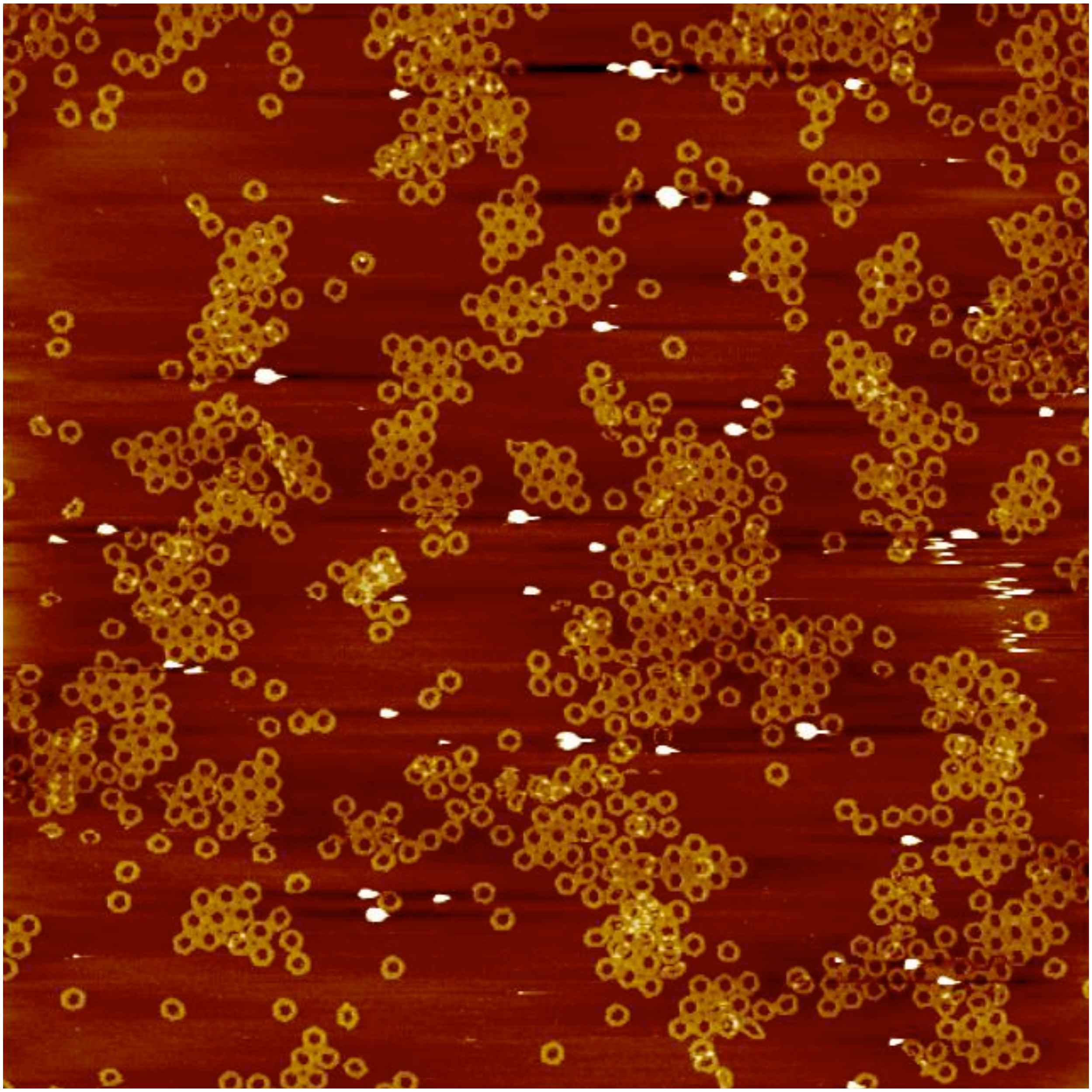
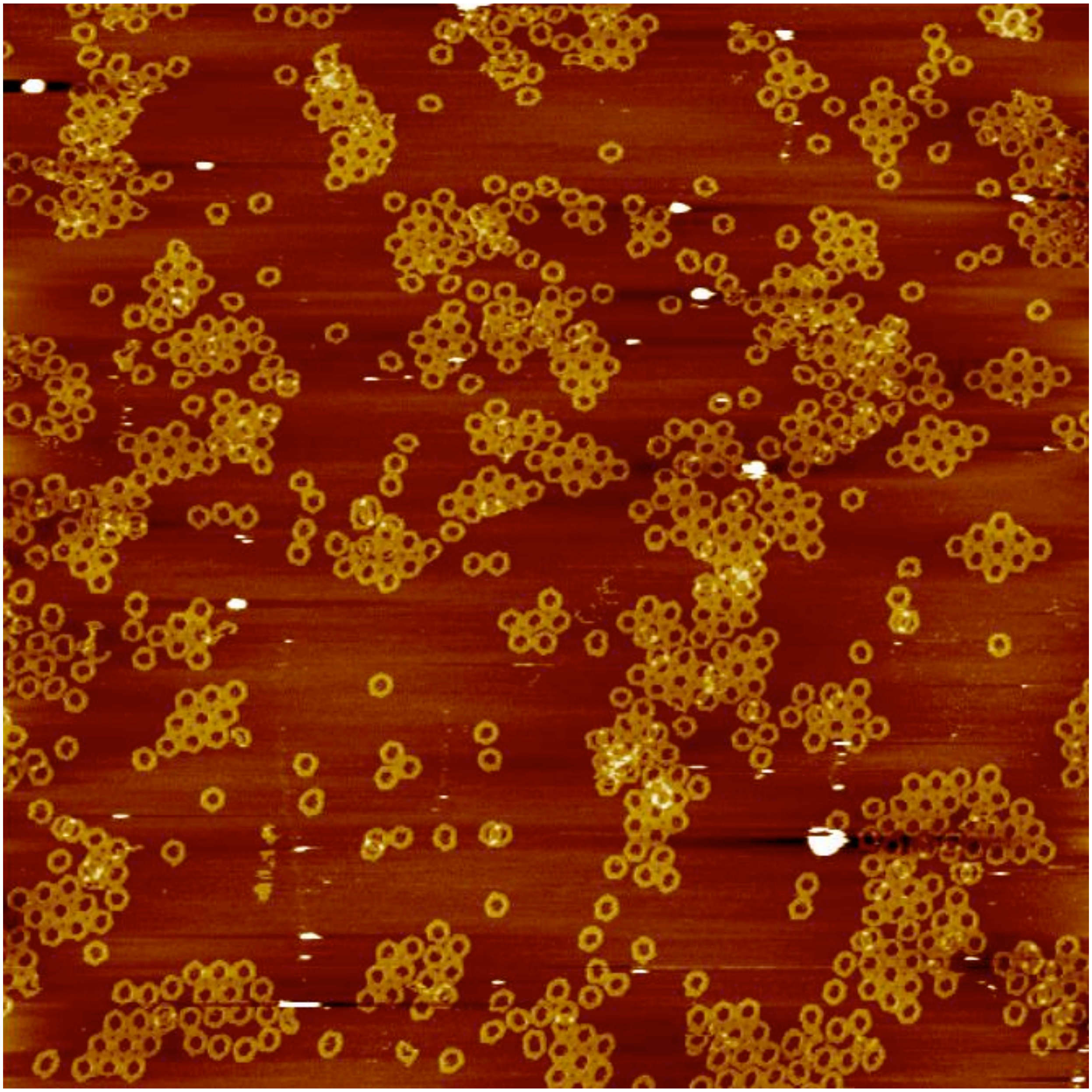
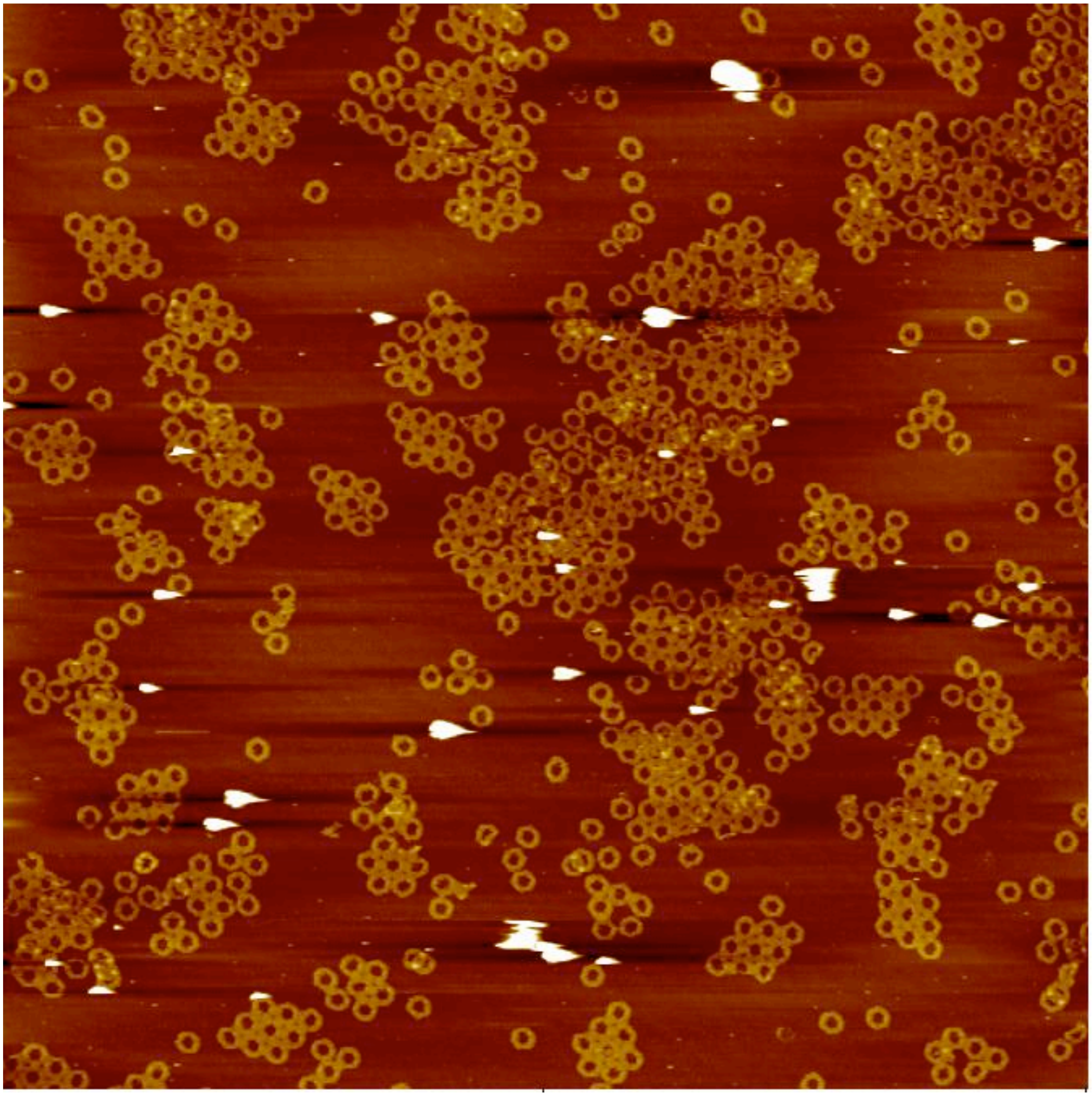


Figure S14. Zoom out and zoom in AFM images of 3 x 3 hexagonal staple tile based origami super-structures. The size of the zoom out images are 5 um × 5 um, and the size of the zoom in images are 470 nm x 470 nm.







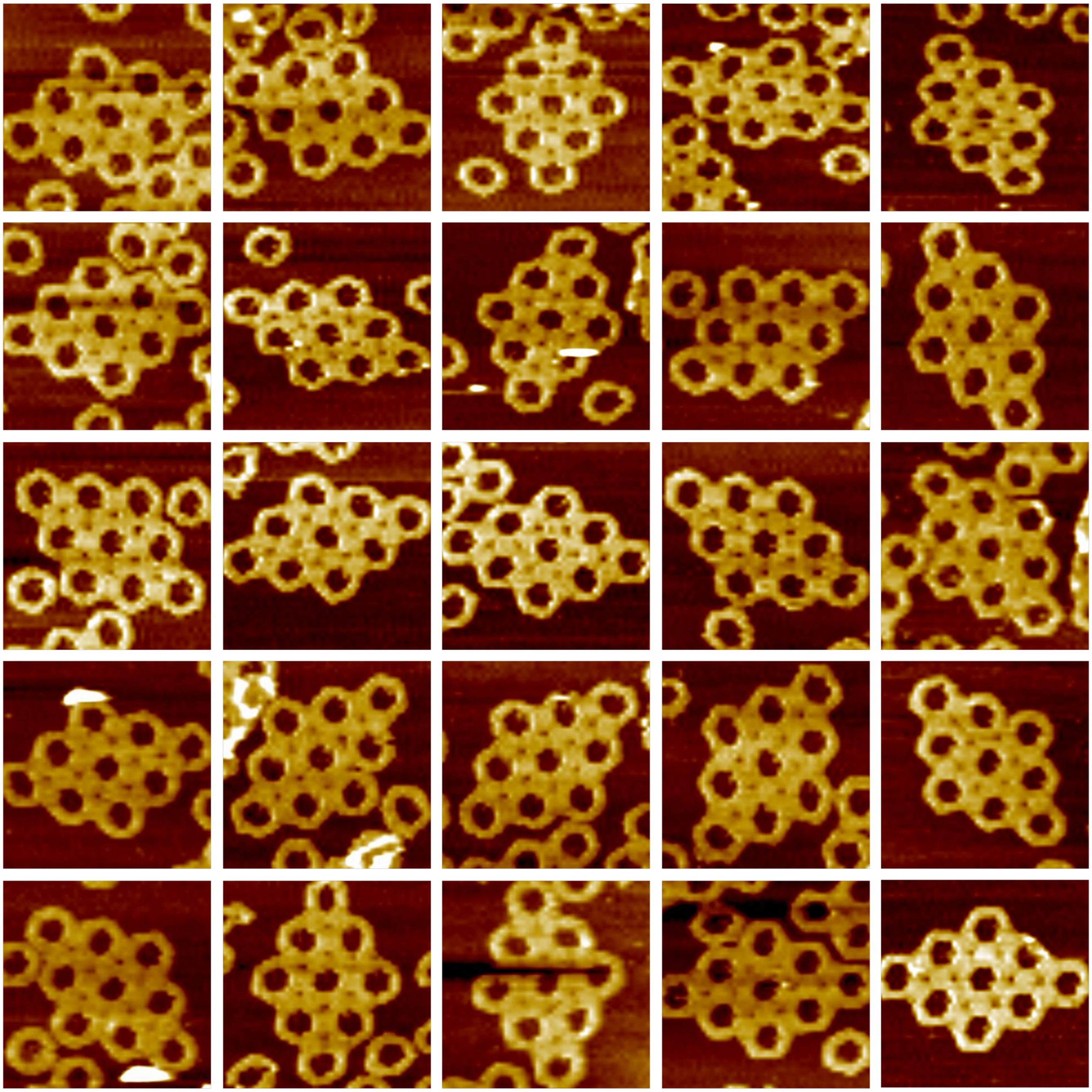


Figure S15. Design for the diamond shaped DNA origami staple tiles.

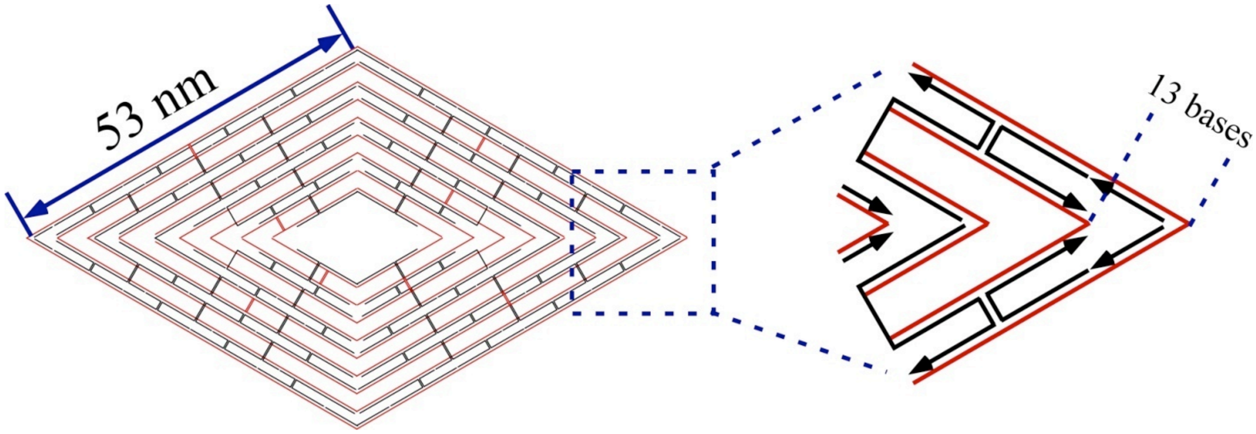


Figure S16. AFM image of the individual diamond shaped DNA origami staple tiles. The size of the image is 3 um × 3 um.

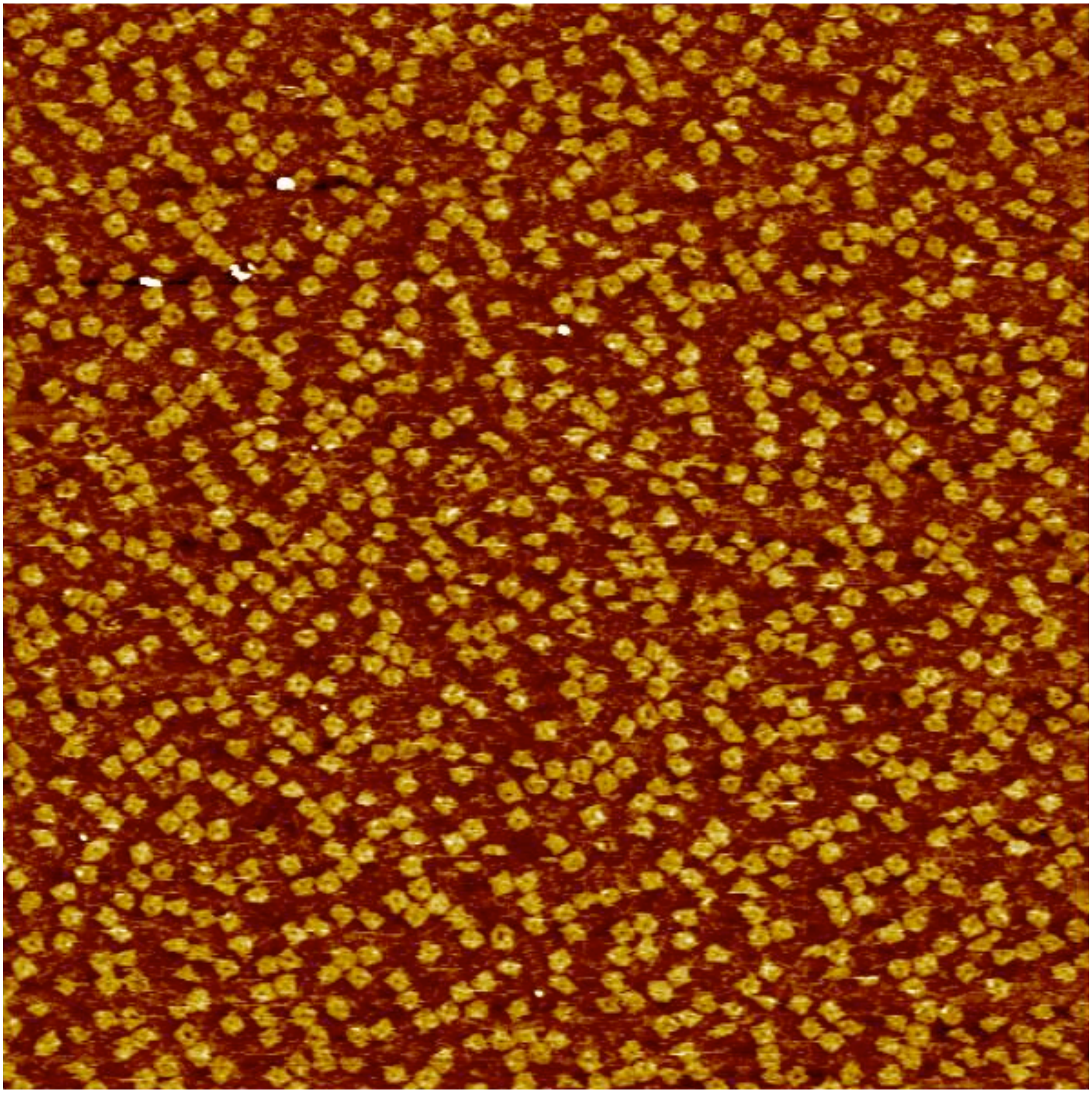


Figure S17. Agarose gel electrophoresis result for the diamond shaped DNA Origami.

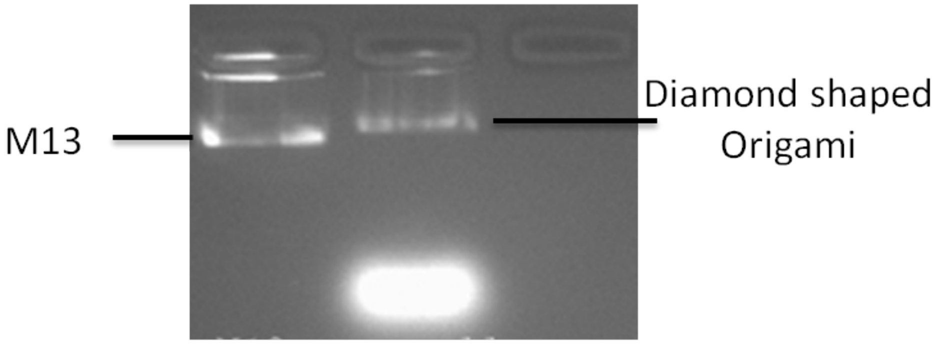
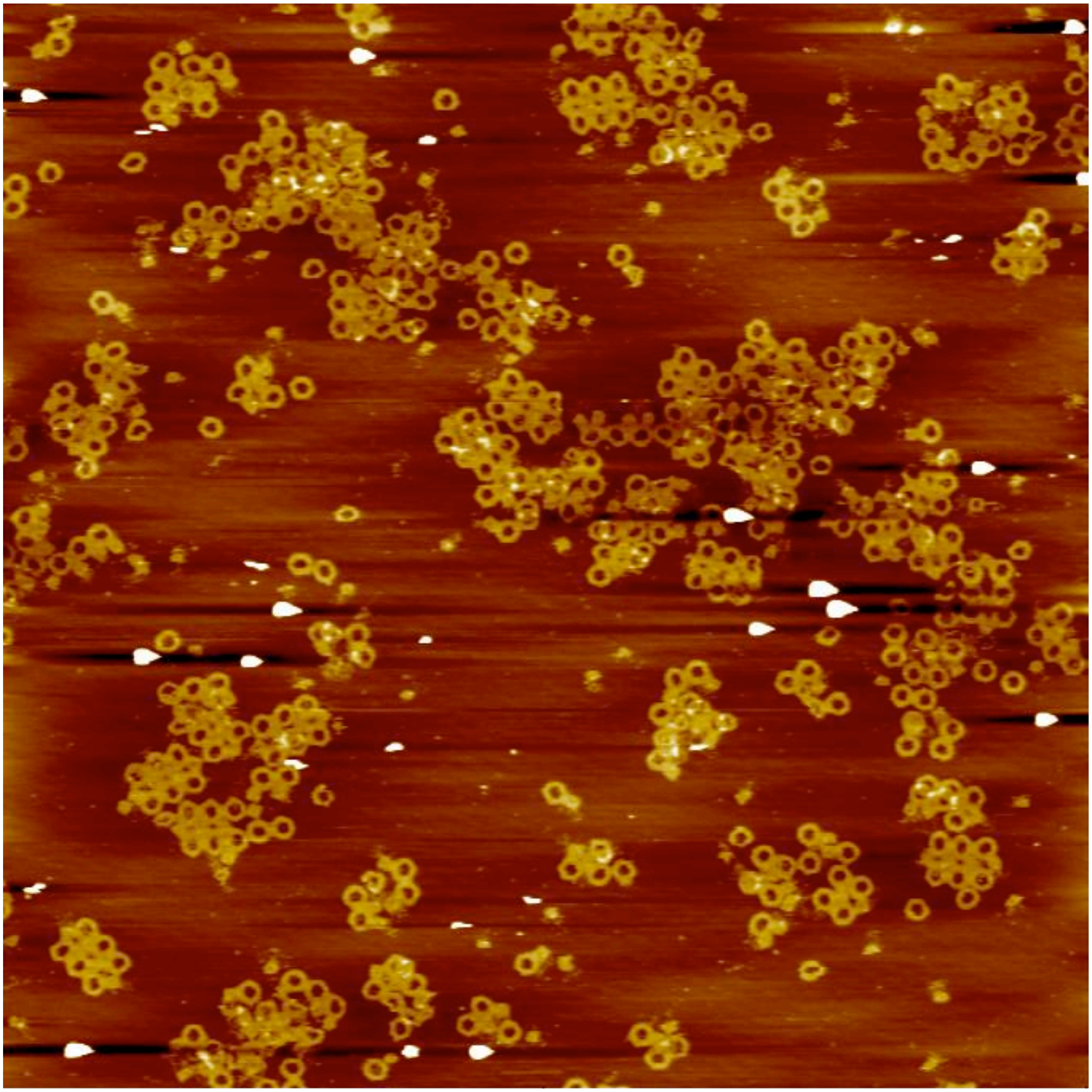
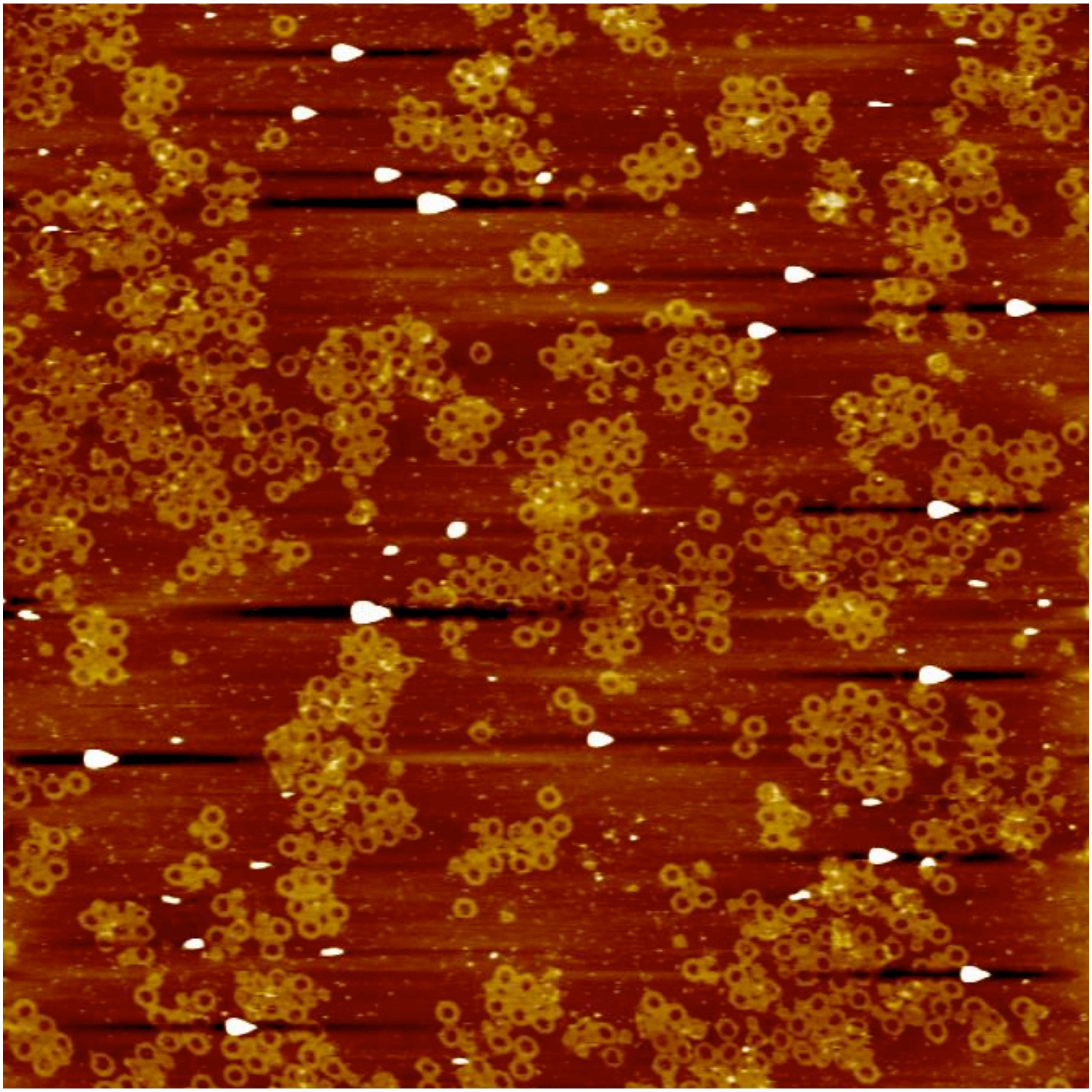
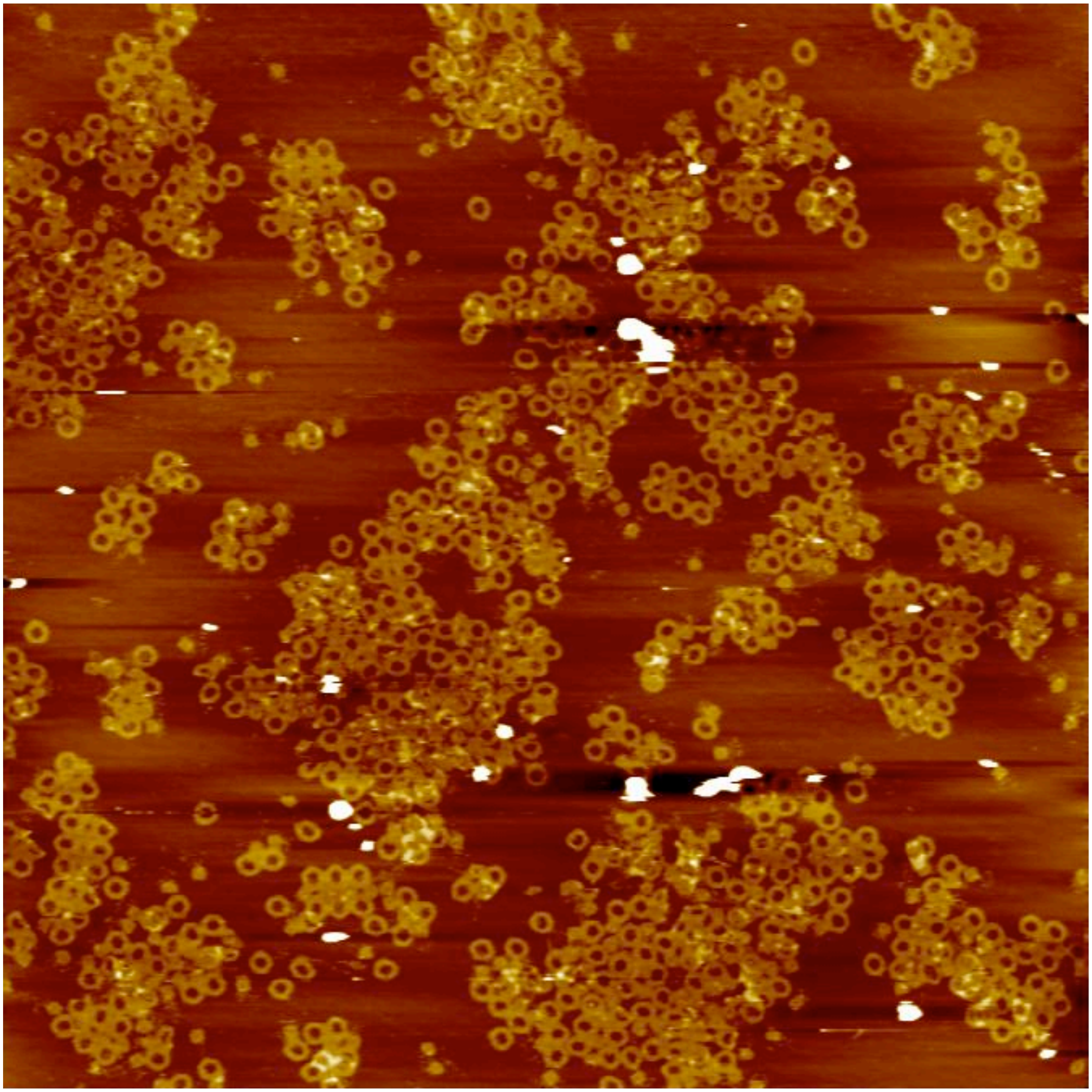


Figure S18. Zoom out and zoom in AFM images of the origami super-structures assembled from a mixture of hexagonal and diamond shaped origami into a 3 row closely packed pattern. The size of the zoom out images are 5 um × 5 um and the size of the zoom in images are 400 nm x 400 nm.







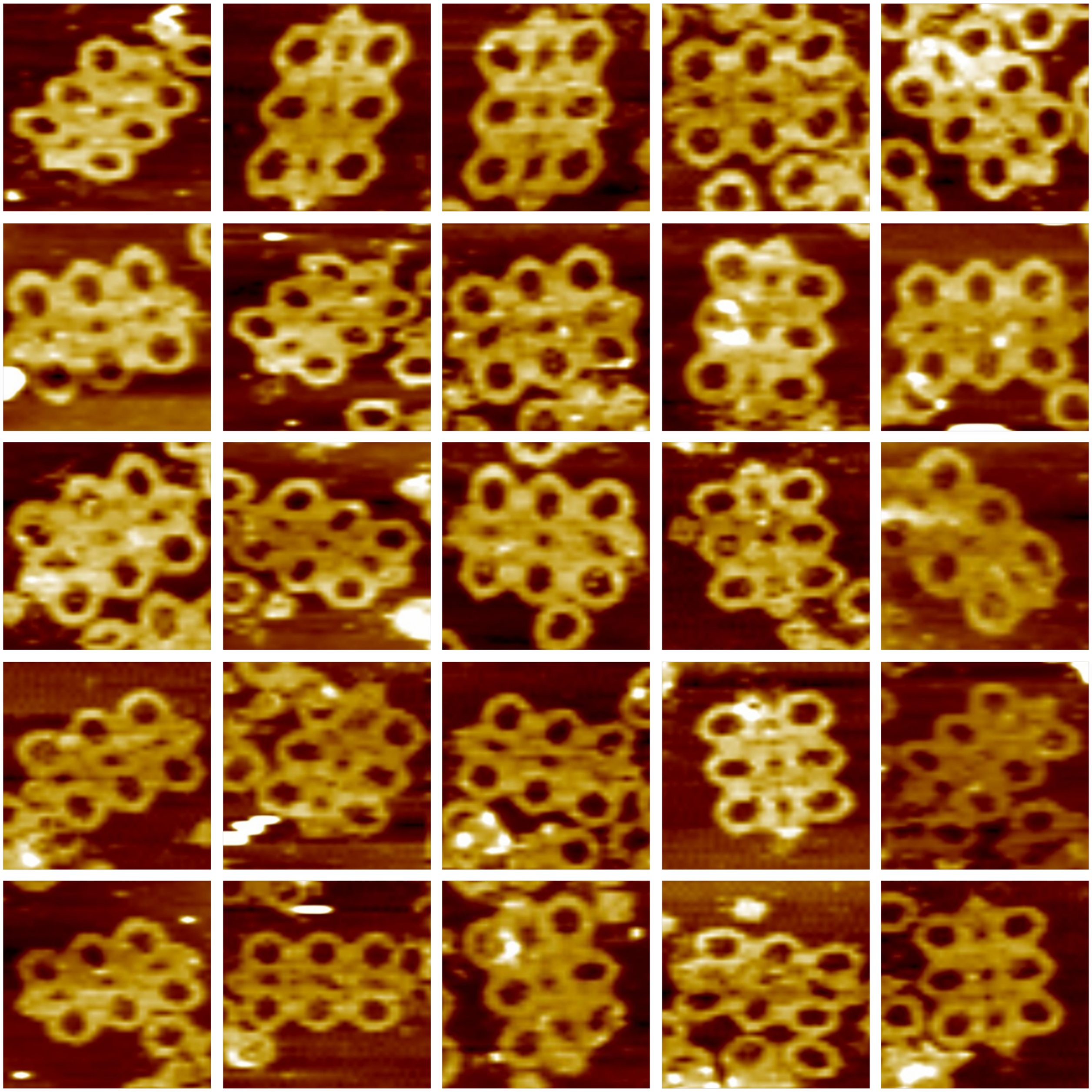
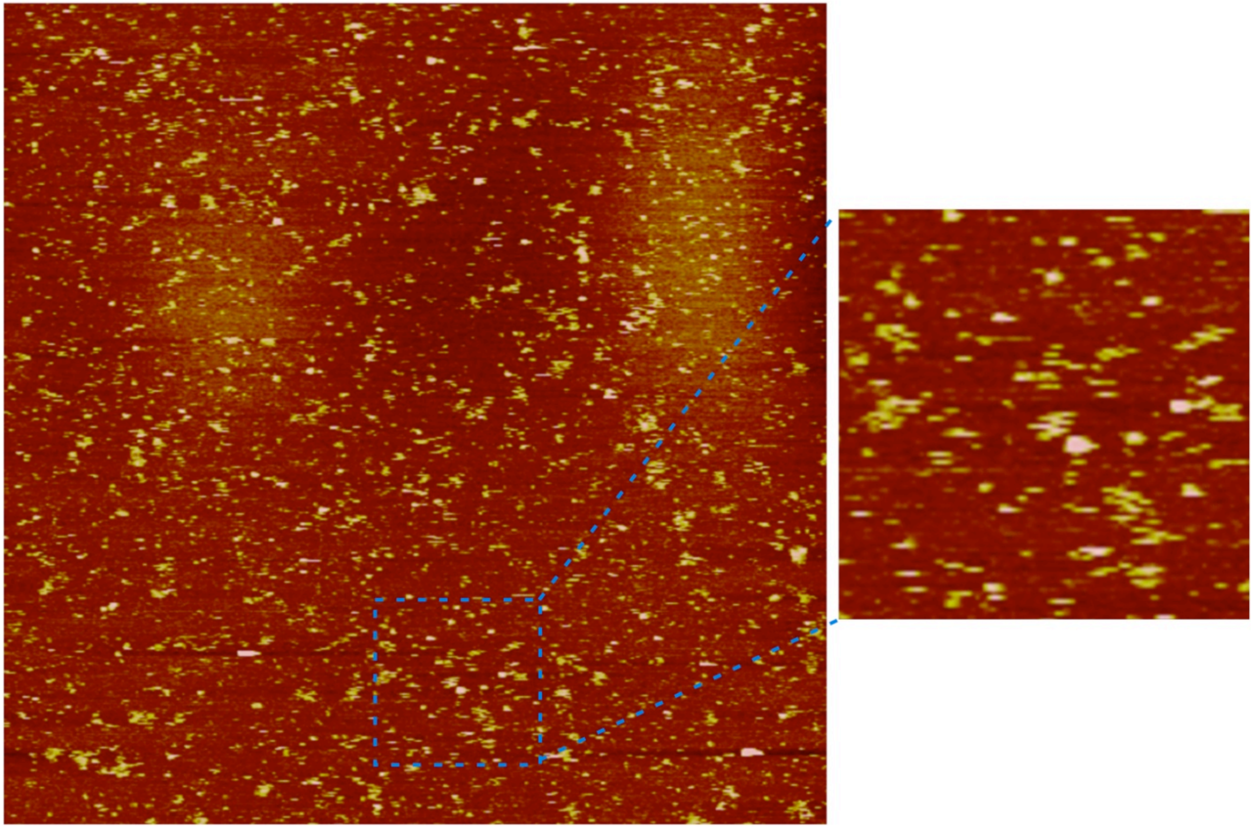
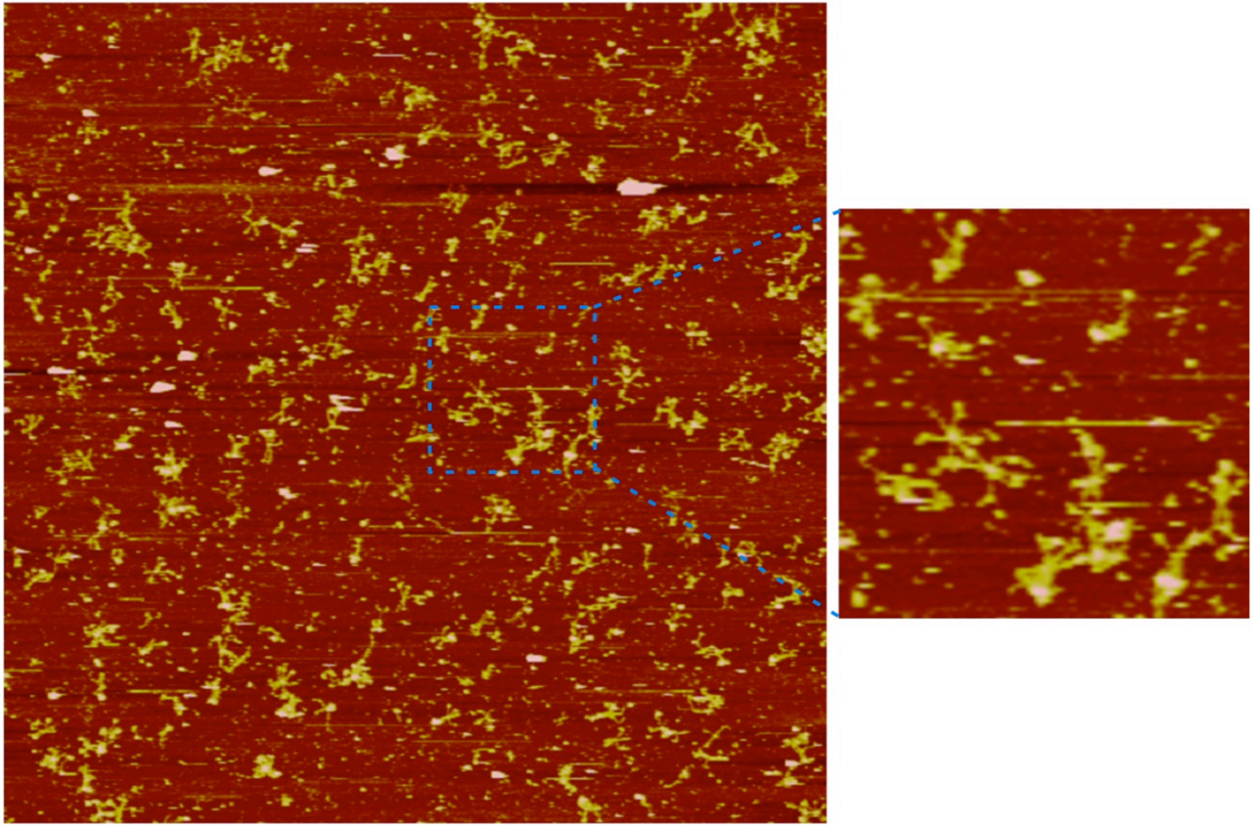


Figure S19. AFM images of the pre-formed scaffold frames used in Figure 2 of the main text. The size of each zoom-out AFM image is 5 um × 5 um. As these pre-formed scaffold frames are quite flexible, their structures do not appear to be well defined, although branching of the arms can sometimes be seen. Random deposition of these flexible structures onto mica surface and AFM cantilever perturbation of such highly loose structures made it difficult to see the details of these frames, but the branched morphologies suggest that the M13 strand is partially folded. It is possible that the flexible frame and the rigid origami unit tiles serve as scaffolds for each other to cooperatively and collectively assemble into the final super-origami structure.

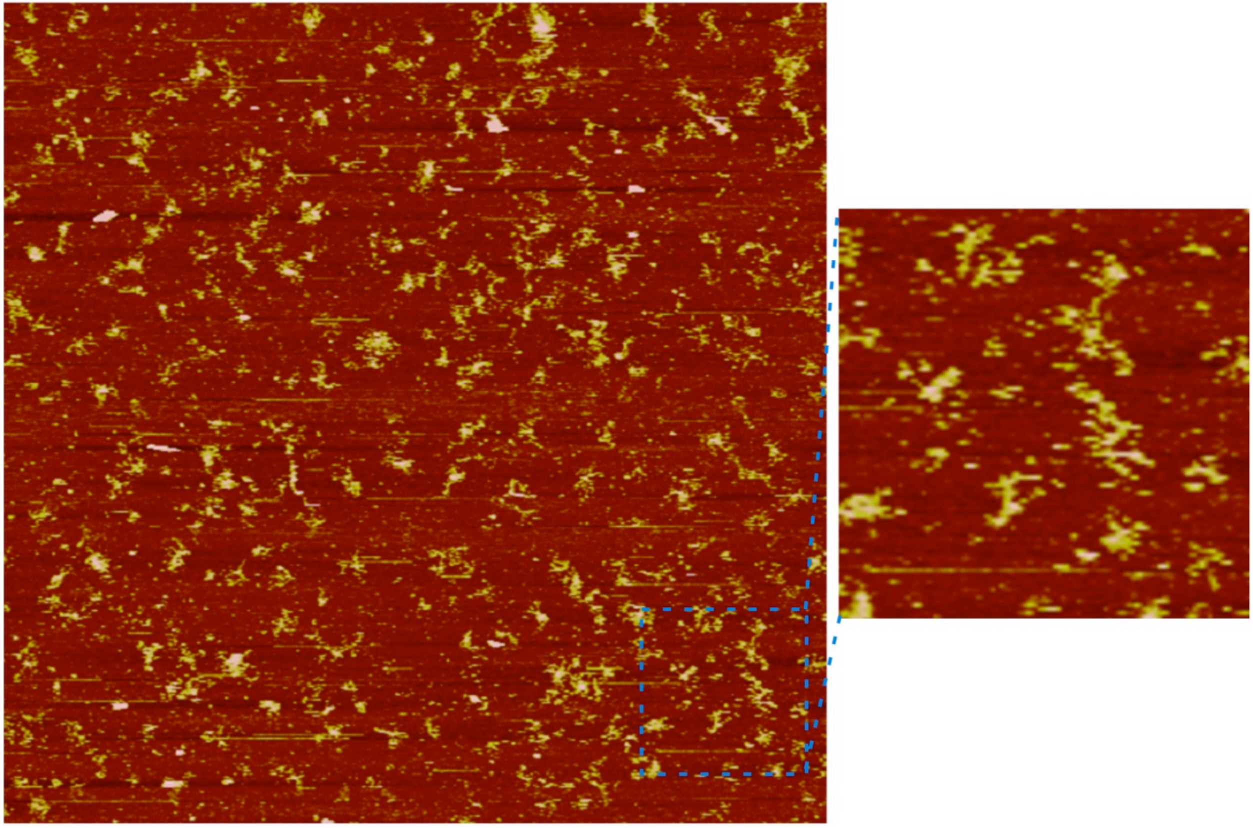


Strategy 1

Strategy 2



Strategy 3



DNA sequences:

Table S1. Unmodified triangle origami staples

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A02, AGCGTCATGTCTCTGAATTTACCGACTACCTT,
A03, TTCATAATCCCCTTATTAGCGTTTTTCTTACC,
A04, ATGGTTTATGTCACAATCAATAGATATTAAAC,
A05, TTTGATGATTAAGAGGCTGAGACTTGCTCAGTACCAGGCG,
A06, CCGGAACCCAGAATGGAAAGCGCAACATGGCT,
A07, AAAGACAACATTTTCGGTCATAGCCAAAATCA,
A08, GACGGGAGAATTAACTCGGAATAAGTTTATTTCCAGCGCC,
A09, GATAAGTGCCGTCGAGCTGAAACATGAAAGTATACAGGAG,
A10, TGTACTGGAAATCCTCATTAAAGCAGAGCCAC,
A11, CACCGGAAAGCGCGTTTTCATCGGAAGGGCGA,
A12, CATTCAACAAACGCAAAGACACCAGAACACCCTGAACAAA,
A13, TTTAACGGTTCGGAACCTATTATTAGGGTTGATATAAGTA,
A14, CTCAGAGCATATTCACAAACAAATTAATAAGT,
A15, GGAGGGAATTTAGCGTCAGACTGTCCGCCTCC,
A16, GTCAGAGGGTAATTGATGGCAACATATAAAAGCGATTGAG,
A17, TAGCCCGGAATAGGTGAATGCCCCCTGCCTATGGTCAGTG,
A18, CCTTGAGTCAGACGATTGGCCTTGCGCCACCC,
A19, TCAGAACCCAGAATCAAGTTTGCCGGTAAATA,
A20, TTGACGGAAATACATACATAAAGGGCGCTAATATCAGAGA,
A21, CAGAGCCAGGAGGTTGAGGCAGGTAACAGTGCCCG,
A22, ATTAAAGGCCGTAATCAGTAGCGAGCCACCCT,
A23, GATAACCCACAAGAATGTTAGCAAACGTAGAAAATTATTC,
A24, GCCGCCAGCATTGACACCACCCTC,
A25, AGAGCCGCACCATCGATAGCAGCATGAATTAT,
A26, CACCGTCACCTTATTACGCAGTATTGAGTTAAGCCCAATA,
A27, AGCCATTTAAACGTCACCAATGAACACCAGAACCA,
A28, ATAAGAGCAAGAAACATGGCATGATTAAGACTCCGACTTG,
A29, CCATTAGCAAGGCCGGGGGAATTA,
A30, GAGCCAGCGAATACCCAAAAGAACATGAAATAGCAATAGC,
A31, TATCTTACCGAAGCCCAAACGCAATAATAACGAAAATCACCAG,
A32, CAGAAGGAAACCGAGGTTTTTAAGAAAAGTAAGCAGATAGCCG,
A33, CCTTTTTTCATTTAACAATTTCATAGGATTAG,
A34, TTTAACCTATCATAGGTCTGAGAGTTCCAGTA,
A35, AGTATAAAATATGCGTTATACAAAGCCATCTT,
A36, CAAGTACCTCATTCCAAGAACGGGAAATTCAT,
A37, AGAGAATAACATAAAAACAGGGAAGCGCATTA,
A38, AAAACAAAATTAATTAAATGGAAACAGTACATTAGTGAAT,
A39, TTATCAAACCGGCTTAGGTTGGGTAAGCCTGT,
A40, TTAGTATCGCCAACGCTCAACAGTCGGCTGTC,
A41, TTTCCTTAGCACTCATCGAGAACAATAGCAGCCTTTACAG,
A42, AGAGTCAAAAATCAATATATGTGATGAAACAAACATCAAG,
A43, ACTAGAAATATATAACTATATGTACGCTGAGA,

A44, TCAATAATAGGGCTTAATTGAGAATCATAATT,
A45, AACGTCAAAAATGAAAAGCAAGCCGTTTTTATGAAACCAA,
A46, GAGCAAAAGAAGATGAGTGAATAACCTTGCTTATAGCTTA,
A47, GATTAAGAAATGCTGATGCAAATCAGAATAAA,
A48, CACCGGAATCGCCATATTTAACAAAATTTACG,
A49, AGCATGTATTTCATCGTAGGAATCAAACGATTTTTTGTTT,
A50, ACATAGCGCTGTAAATCGTCGCTATTCATTTCAATTACCT,
A51, GTTAAATACAATCGCAAGACAAAGCCTTGAAA,
A52, CCCATCCTCGCCAACATGTAATTTAATAAGGC,
A53, TCCCAATCCAAATAAGATTACCGCGCCCAATAAATAATAT,
A54, TCCCTTAGAATAACGCGAGAAAACTTTTACCGACC,
A55, GTGTGATAAGGCAGAGGCATTTTCAGTCCTGA,
A56, ACAAGAAAGCAAGCAAATCAGATAACAGCCATATTATTTA,
A57, GTTTGAAATTCAAATATATTTTAG,
A58, AATAGATAGAGCCAGTAATAAGAGATTTAATG,
A59, GCCAGTTACAAAATAATAGAAGGCTTATCCGGTTATCAAC,
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A61, GCGCCTGTTATTCTAAGAACGCGATTCCAGAGCCTAATTT,
A62, TCAGCTAAAAAAGGTAAAGTAATT,
A63, ACGCTAACGAGCGTCTGGCGTTTTAGCGAACCCAACATGT,
A64, ACGACAATAAATCCCGACTTGCGGGAGATCCTGAATCTTACCA,
A65, TGCTATTTTGCACCCAGCTACAATTTTGTTTTGAAGCCTTAAA,

B01, TCATATGTGTAATCGTAAAACTAGTCATTTTC,
B02, GTGAGAAAATGTGTAGGTAAAGATACAACTTT,
B03, GGCATCAAATTTGGGGCGCGAGCTAGTTAAAG,
B04, TTCGAGCTAAGACTTCAAATATCGGGAACGAG,
B05, ACAGTCAAAGAGAATCGATGAACGACCCCGGTTGATAATC,
B06, ATAGTAGTATGCAATGCCTGAGTAGGCCGGAG,
B07, AACCAGACGTTTAGCTATATTTTCTTCTACTA,
B08, GAATACCACATTCAACTTAAGAGGAAGCCCGATCAAAGCG,
B09, AGAAAAGCCCCAAAAAGAGTCTGGAGCAAACAATCACCAT,
B10, CAATATGACCCTCATATATTTTAAAGCATTAA,
B11, CATCCAATAAATGGTCAATAACCTCGGAAGCA,
B12, AACTCCAAGATTGCATCAAAAAGATAATGCAGATACATAA,
B13, CGTTCTAGTCAGGTCATTGCCTGACAGGAAGATTGTATAA,
B14, CAGGCAAGATAAAAATTTTTAGAATATTCAAC,
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B19, TTAGCAAATAGATTTAGTTTGACCAGTACCTT,
B20, TAATTGCTTTACCCTGACTATTATGAGGCATAGTAAGAGC,
B21, ATAAAGCCTTTGCGGGAGAAGCCTGGAGAGGGTAG,
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B23, AACACTATCATAACCCATCAAAAATCAGGTCTCCTTTTGA,
B24, ATGACCCTGTAATACTTCAGAGCA,
B25, TAAAGCTATATAACAGTTGATTCCCATTTTTG,
B26, CGGATGGCACGAGAATGACCATAATCGTTTACCAGACGAC,
B27, TAATTGCTTGGAAGTTTCATTCCAAATCGGTTGTA,
B28, GATAAAAACCAAAATATTAAACAGTTCAGAAATTAGAGCT,
B29, ACTAAAGTACGGTGTCGAATATAA,
B30, TGCTGTAGATCCCCCTCAAATGCTGCGAGAGGCTTTTGCA,
B31, AAAGAAGTTTTGCCAGCATAAATATTCATTGACTCAACATGTT,
B32, AATACTGCGGAATCGTAGGGGGTAATAGTAAAATGTTTAGACT,
B33, AGGGATAGCTCAGAGCCACCACCCCATGTCAA,
B34, CAACAGTTTATGGGATTTTGCTAATCAAAAGG,
B35, GCCGCTTTGCTGAGGCTTGCAGGGGAAAAGGT,
B36, GCGCAGACTCCATGTTACTTAGCCCGTTTTAA,
B37, ACAGGTAGAAAGATTCATCAGTTGAGATTTAG,
B38, CCTCAGAACCGCCACCCAAGCCCAATAGGAACGTAAATGA,
B39, ATTTTCTGTCAGCGGAGTGAGAATACCGATAT,
B40, ATTCGGTCTGCGGGATCGTCACCCGAAATCCG,
B41, CGACCTGCGGTCAATCATAAGGGAACGGAACAACATTATT,
B42, AGACGTTACCATGTACCGTAACACCCCTCAGAACCGCCAC,
B43, CACGCATAAGAAAGGAACAACTAAGTCTTTCC,
B44, ATTGTGTCTCAGCAGCGAAAGACACCATCGCC,
B45, TTAATAAAACGAACTAACCGAACTGACCAACTCCTGATAA,
B46, AGGTTTAGTACCGCCATGAGTTTCGTCACCAGGATCTAAA,
B47, GTTTTGTCAGGAATTGCGAATAATCCGACAAT,
B48, GACAACAAGCATCGGAACGAGGGTGAGATTTG,
B49, TATCATCGTTGAAAGAGGACAGATGGAAGAAAAATCTACG,
B50, AGCGTAACTACAAACTACAACGCCTATCACCGTACTCAGG,
B51, TAGTTGCGAATTTTTTCACGTTGATCATAGTT,
B52, GTACAACGAGCAACGGCTACAGAGGATACCGA,
B53, ACCAGTCAGGACGTTGGAACGGTGTACAGACCGAAACAAA,
B54, ACAGACAGCCCAAATCTCCAAAAAAAAATTTCTTA,
B55, AACAGCTTGCTTTGAGGACTAAAGCGATTATA,
B56, CCAAGCGCAGGCGCATAGGCTGGCAGAACTGGCTCATTAT,
B57, CGAGGTGAGGCTCCAAAAGGAGCC,
B58, ACCCCCAGACTTTTTCATGAGGAACTTGCTTT,
B59, ACCTTATGCGATTTTATGACCTTCATCAAGAGCATCTTTG,
B60, CGGTTTATCAGGTTTCCATTAAACGGGAATACACT,
B61, AAAACACTTAATCTTGACAAGAACTTAATCATTGTGAATT,
B62, GGCAAAAGTAAAATACGTAATGCC,
B63, TGGTTTAATTTCAACTCGGATATTCATTACCCACGAAAGA,
B64, ACCAACCTAAAAAATCAACGTAACAAATAAATTGGGCTTGAGA,
B65, CCTGACGAGAAACACCAGAACGAGTAGGCTGCTCATTCAGTGA,
Link-A1C, TTAATTAATTTTTTACCATATCAAA,
Link-A2C, TTAATTTCATCTTAGACTTTACAA,
Link-A3C, CTGTCCAGACGTATACCGAACGA,

Link-A4C, TCAAGATTAGTGTAGCAATACT,
Link-B1A, TGTAGCATTCCTTTTATAAACAGTT,
Link-B2A, TTTAATTGTATTTCCACCAGAGCC,
Link-B3A, ACTACGAAGGCTTAGCACCATTA,
Link-B4A, ATAAGGCTTGCAACAAAGTTAC,
Link-C1B, GTGGGAACAAATTTCTATTTTTGAG,
Link-C2B, CGGTGCGGGCCTTCCAAAAACATT,
Link-C3B, ATGAGTGAGCTTTTAAATATGCA,
Link-C4B, ACTATTAAAGAGGATAGCGTCC,
Loop, GCGCTTAATGCGCCGCTACAGGGC,

C01, TCGGGAGATATACAGTAACAGTACAAATAATT,
C02, CCTGATTAAAGGAGCGGAATTATCTCGGCCTC,
C03, GCAAATCACCTCAATCAATATCTGCAGGTCGA,
C04, CGACCAGTACATTGGCAGATTCACCTGATTGC,
C05, TGGCAATTTTTAACGTCAGATGAAAACAATAACGGATTCG,
C06, AAGGAATTACAAAGAAACCACCAGTCAGATGA,
C07, GGACATTCACCTCAAATATCAAACACAGTTGA,
C08, TTGACGAGCACGTATACTGAAATGGATTATTTAATAAAAG,
C09, CCTGATTGCTTTGAATTGCGTAGATTTTCAGGCATCAATA,
C10, TAATCCTGATTATCATTTTGCGGAGAGGAAGG,
C11, TTATCTAAAGCATCACCTTGCTGATGGCCAAC,
C12, AGAGATAGTTTGACGCTCAATCGTACGTGCTTTCCTCGTT,
C13, GATTATACACAGAAATAAAGAAATACCAAGTTACAAAATC,
C14, TAGGAGCATAAAAGTTTGAGTAACATTGTTTG,
C15, TGACCTGACAAATGAAAAATCTAAAATATCTT,
C16, AGAATCAGAGCGGGAGATGGAAATACCTACATAACCCTTC,
C17, GCGCAGAGGCGAATTAATTATTTGCACGTAAATTCTGAAT,
C18, AATGGAAGCGAACGTTATTAATTTCTAACAAC,
C19, TAATAGATCGCTGAGAGCCAGCAGAAGCGTAA,
C20, GAATACGTAACAGGAAAAACGCTCCTAAACAGGAGGCCGA,
C21, TCAATAGATATTAAATCCTTTGCCGGTTAGAACCT,
C22, CAATATTTGCCTGCAACAGTGCCATAGAGCCG,
C23, TTAAAGGGATTTTAGATACCGCCAGCCATTGCGGCACAGA,
C24, ACAATTCGACAACTCGTAATACAT,
C25, TTGAGGATGGTCAGTATTAACACCTTGAATGG,
C26, CTATTAGTATATCCAGAACAATATCAGGAACGGTACGCCA,
C27, CGCGAACTAAAACAGAGGTGAGGCTTAGAAGTATT,
C28, GAATCCTGAGAAGTGTATCGGCCTTGCTGGTACTTTAATG,
C29, ACCACCAGCAGAAGATGATAGCCC,
C30, TAAAACATTAGAAGAACTCAAACTTTTTATAATCAGTGAG,
C31, GCCACCGAGTAAAAGAACATCACTTGCCTGAGCGCCATTAAAA,
C32, TCTTTGATTAGTAATAGTCTGTCCATCACGCAAATTAACCGTT,
C33, CGCGTCTGATAGGAACGCCATCAACTTTTACA,

C34, AGGAAGATGGGGACGACGACAGTAATCATATT,
C35, CTCTAGAGCAAGCTTGCATGCCTGGTCAGTTG,
C36, CCTTCACCGTGAGACGGGCAACAGCAGTCACA,
C37, CGAGAAAGGAAGGGAAGCGTACTATGGTTGCT,
C38, GCTCATTTTTTAACCAGCCTTCCTGTAGCCAGGCATCTGC,
C39, CAGTTTGACGCACTCCAGCCAGCTAAACGACG,
C40, GCCAGTGCGATCCCCGGGTACCGAGTTTTTCT,
C41, TTTCACCAGCCTGGCCCTGAGAGAAAGCCGGCGAACGTGG,
C42, GTAACCGTCTTTCATCAACATTAAAATTTTTGTTAAATCA,
C43, ACGTTGTATTCCGGCACCGCTTCTGGCGCATC,
C44, CCAGGGTGGCTCGAATTCGTAATCCAGTCACG,
C45, TAGAGCTTGACGGGGAGTTGCAGCAAGCGGTCATTGGGCG,
C46, GTTAAAATTCGCATTAATGTGAGCGAGTAACACACGTTGG,
C47, TGTAGATGGGTGCCGGAAACCAGGAACGCCAG,
C48, GGTTTTCCATGGTCATAGCTGTTTGAGAGGCG,
C49, GTTTGCGTCACGCTGGTTTGCCCCAAGGGAGCCCCCGATT,
C50, GGATAGGTACCCGTCGGATTCTCCTAAACGTTAATATTTT,
C51, AGTTGGGTCAAAGCGCCATTCGCCCCGTAATG,
C52, CGCGCGGGCCTGTGTGAAATTGTTGGCGATTA,
C53, CTAAATCGGAACCCTAAGCAGGCGAAAATCCTTCGGCCAA,
C54, CGGCGGATTGAATTCAGGCTGCGCAACGGGGGATG,
C55, TGCTGCAAATCCGCTCACAATTCCCAGCTGCA,
C56, TTAATGAAGTTTGATGGTGGTTCCGAGGTGCCGTAAAGCA,
C57, TGGCGAAATGTTGGGAAGGGCGAT,
C58, TGTCGTGCACACAACATACGAGCCACGCCAGC,
C59, CAAGTTTTTTGGGGTCGAAATCGGCAAAATCCGGGAAACC,
C60, TCTTCGCTATTGGAAGCATAAAGTGTATGCCCGCT,
C61, TTCCAGTCCTTATAAATCAAAAGAGAACCATCACCCAAAT,
C62, GCGCTCACAAGCCTGGGGTGCCTA,
C63, CGATGGCCCACTACGTATAGCCCGAGATAGGGATTGCGTT,
C64, AACTCACATTATTGAGTGTTGTTCCAGAAACCGTCTATCAGGG,
C65, ACGTGGACTCCAACGTCAAAGGGCGAATTTGGAACAAGAGTCC,

Table S2. Triangle origami modified staples and bridges that hybridize with ΦX 174 scaffolds for design 1

Modified helpers for each triangle origami

6B Part
6B32;AATACTGCGGAATCGTAGGGGGTAATAGTAAACATGGTCA
6B31-1;TAACAGTCAAAGAAGTTTTGCCAGCATAAATA
6B30;TGCTGTAGATCCCCCTCAAATGCTGCGAGAGGCTTTTGCAGGGAGAGG
6B28-1;TCCTTCATGATAAAAACCAAAATATTAAACAG
6B26;CGGATGGCACGAGAATGACCATAATCGTTTACCAGACGACGAACTTAA
6B23-1;AACGTGACAACACTATCATAACCCATCAAAAA
6B20;TAATTGCTTTACCCTGACTATTATGAGGCATAGTAAGAGCGATGAGGG
6B16-1;TGTCTACACGCCAAAAGGAATTACAGTCAGAA
6B12;AACTCCAAGATTGCATCAAAAAGATAATGCAGATACATAAGTAGAGTC

6B08-1;CGCAATGGGAATACCACATTCAACTTAAGAGG
6B37;GTCCATCTACAGGTAGAAAGATTCATCAGTTGAGATTTAGAGAAAGAC
6B41;CGACCTGCGGTCAATCATAAGGGAACGGAACAACATTATTCGAAGGAG
6B45-1;GAGTAGTTTTAATAAAACGAACTAACCGAACT
6B49;TATCATCGTTGAAAGAGGACAGATGGAAGAAAAATCTACGGAAATGGT
6B53-1;TGACCAGCACCAGTCAGGACGTTGGAACGGTG
6B56;CCAAGCGCAGGCGCATAGGCTGGCAGAACTGGCTCATTATAAGGAAGC
6B59-1;ATGCGGCAACCTTATGCGATTTTATGACCTTC
6B61;AAAACACTTAATCTTGACAAGAACTTAATCATTGTGAATTTACGCTCG
6B63-1;TAGACATATGGTTTAATTTCAACTCGGATATT
6B64;ACCAACCTAAAAAATCAACGTAACAAATAAATTGGGCTTGAGAATTTATCC
6B65;AGCCCCTGACACCAGAACGAGTAGGCTGCTCATTCAGTGA

6A Part
6A32;CAGAAGGAAACCGAGGTTTTTAAGAAAAGTAAACCACCTA
6A31-1;GCCTTTACTATCTTACCGAAGCCCAAACGCAA
6A30;GAGCCAGCGAATACCCAAAAGAACATGAAATAGCAATAGCGCTTGCCT
6A28-1;GCTGCGGAATAAGAGCAAGAAACATGGCATGA
6A26;CACCGTCACCTTATTACGCAGTATTGAGTTAAGCCCAATACGACCAGG
6A23-1;TTTTTACCGATAACCCACAAGAATGTTAGCAA
6A20;TTGACGGAAATACATACATAAAGGGCGCTAATATCAGAGATTTAGACA
6A16-1;GCACGTAAGTCAGAGGGTAATTGATGGCAACA
6A12;CATTCAACAAACGCAAAGACACCAGAACACCCTGAACAAATTTTTGAC
6A08-1;GTCAGTAAGACGGGAGAATTAACTCGGAATAA
6A37;CACGCAAGAGAGAATAACATAAAAACAGGGAAGCGCATTAGAACGTCA
6A41;TTTCCTTAGCACTCATCGAGAACAATAGCAGCCTTTACAGGTAAACGC
6A45-1;TTAACCGGAACGTCAAAAATGAAAAGCAAGCC
6A49;AGCATGTATTTCATCGTAGGAATCAAACGATTTTTTGTTTACGCTCGA
6A53-1;TTCCGTAATCCCAATCCAAATAAGATTACCGC
6A56;ACAAGAAAGCAAGCAAATCAGATAACAGCCATATTATTTAATTCAGCG
6A59-1;AGGCCGTTGCCAGTTACAAAATAATAGAAGGC
6A61;GCGCCTGTTATTCTAAGAACGCGATTCCAGAGCCTAATTTTGAATGTT
6A63-1;TAAGCAATACGCTAACGAGCGTCTGGCGTTTT
6A64;ACGACAATAAATCCCGACTTGCGGGAGATCCTGAATCTTACCAGACGGCAG
6A65;AGCAGGAAACCCAGCTACAATTTTGTTTTGAAGCCTTAAA

5B Part
5B32;AATACTGCGGAATCGTAGGGGGTAATAGTAAAAGCGAGGG
5B31-1;GCGTACCAAAAGAAGTTTTGCCAGCATAAATA
5B30;TGCTGTAGATCCCCCTCAAATGCTGCGAGAGGCTTTTGCATAAACGCA
5B28-1;CGAGCACGGATAAAAACCAAAATATTAAACAG
5B26;CGGATGGCACGAGAATGACCATAATCGTTTACCAGACGACAGAGCGGT
5B23-1;TTTGTTACAACACTATCATAACCCATCAAAAA
5B20;TAATTGCTTTACCCTGACTATTATGAGGCATAGTAAGAGCTCGTCAGA
5B16-1;CGGTTAAACGCCAAAAGGAATTACAGTCAGAA
5B12;AACTCCAAGATTGCATCAAAAAGATAATGCAGATACATAATCCAAAAC

5B08-1;AGCTTAATGAATACCACATTCAACTTAAGAGG
5B37;TACGGATTACAGGTAGAAAGATTCATCAGTTGAGATTTAGAGAGGCCA
5B41;CGACCTGCGGTCAATCATAAGGGAACGGAACAACATTATTGTTCAGTA
5B45-1;CTTACCTATTAATAAAACGAACTAACCGAACT
5B49;TATCATCGTTGAAAGAGGACAGATGGAAGAAAAATCTACGTTAGTGGT
5B53-1;CAGATAGTACCAGTCAGGACGTTGGAACGGTG
5B56;CCAAGCGCAGGCGCATAGGCTGGCAGAACTGGCTCATTATAATCCACG
5B59-1;ACAAGAGAACCTTATGCGATTTTATGACCTTC
5B61;AAAACACTTAATCTTGACAAGAACTTAATCATTGTGAATTATCTCTAC
5B63-1;CTCATATCTGGTTTAATTTCAACTCGGATATT
5B64;ACCAACCTAAAAAATCAACGTAACAAATAAATTGGGCTTGAGATAAACCAG
5B65;CAAGCATAACACCAGAACGAGTAGGCTGCTCATTCAGTGA

5A Part
5A32;CAGAAGGAAACCGAGGTTTTTAAGAAAAGTAATCATCCAA
5A31-1;AGAATCGTTATCTTACCGAAGCCCAAACGCAA
5A30;GAGCCAGCGAATACCCAAAAGAACATGAAATAGCAATAGCTAGTTGAT
5A28-1;GTAAGAGCATAAGAGCAAGAAACATGGCATGA
5A26;CACCGTCACCTTATTACGCAGTATTGAGTTAAGCCCAATATTCTCGAG
5A23-1;CGAATTTTGATAACCCACAAGAATGTTAGCAA
5A20;TTGACGGAAATACATACATAAAGGGCGCTAATATCAGAGACTCATTTT
5A16-1;TCGATTTAGTCAGAGGGTAATTGATGGCAACA
5A12;CATTCAACAAACGCAAAGACACCAGAACACCCTGAACAAAATTCGTAA
5A08-1;CCTGCTTTGACGGGAGAATTAACTCGGAATAA
5A37;AGAAATATAGAGAATAACATAAAAACAGGGAAGCGCATTAATCAAGAT
5A41;TTTCCTTAGCACTCATCGAGAACAATAGCAGCCTTTACAGCCGAAAGT
5A45-1;TGGAAGCGAACGTCAAAAATGAAAAGCAAGCC
5A49;AGCATGTATTTCATCGTAGGAATCAAACGATTTTTTGTTTATAAAACT
5A53-1;CCAATCATTCCCAATCCAAATAAGATTACCGC
5A56;ACAAGAAAGCAAGCAAATCAGATAACAGCCATATTATTTATTTTATCG
5A59-1;GAGCAGATGCCAGTTACAAAATAATAGAAGGC
5A61;GCGCCTGTTATTCTAAGAACGCGATTCCAGAGCCTAATTTTTGTCGTC
5A63-1;AAACGTCGACGCTAACGAGCGTCTGGCGTTTT
5A64;ACGACAATAAATCCCGACTTGCGGGAGATCCTGAATCTTACCAGCTACAGT
5A65;AATCTCATACCCAGCTACAATTTTGTTTTGAAGCCTTAAA

4B Part
4B32;AATACTGCGGAATCGTAGGGGGTAATAGTAAACTCTCTTT
4B31-1;TATCTGGTAAAGAAGTTTTGCCAGCATAAATA
4B30;TGCTGTAGATCCCCCTCAAATGCTGCGAGAGGCTTTTGCATGAACGGC
4B28-1;GCTTGGTAGATAAAAACCAAAATATTAAACAG
4B26;CGGATGGCACGAGAATGACCATAATCGTTTACCAGACGACAGTTGGAT
4B23-1;AGATTTGTAACACTATCATAACCCATCAAAAA
4B20;TAATTGCTTTACCCTGACTATTATGAGGCATAGTAAGAGCCATTGTGA
4B16-1;GTTGCGGCCGCCAAAAGGAATTACAGTCAGAA
4B12;AACTCCAAGATTGCATCAAAAAGATAATGCAGATACATAATCATTCTG

4B08-1;TGGGAAGTGAATACCACATTCAACTTAAGAGG
4B37;TTGTTCCAACAGGTAGAAAGATTCATCAGTTGAGATTTAGAGCGACAG
4B41;CGACCTGCGGTCAATCATAAGGGAACGGAACAACATTATTTTCTTTAG
4B45-1;AGCAAGGTTTAATAAAACGAACTAACCGAACT
4B49;TATCATCGTTGAAAGAGGACAGATGGAAGAAAAATCTACGCCATATCT
4B53-1;ATTTAGCCACCAGTCAGGACGTTGGAACGGTG
4B56;CCAAGCGCAGGCGCATAGGCTGGCAGAACTGGCTCATTATACATAGAA
4B59-1;CTGGTAGCACCTTATGCGATTTTATGACCTTC
4B61;AAAACACTTAATCTTGACAAGAACTTAATCATTGTGAATTTTTAAGCG
4B63-1;AACAGGCCTGGTTTAATTTCAACTCGGATATT
4B64;ACCAACCTAAAAAATCAACGTAACAAATAAATTGGGCTTGAGAACAACCAA
4B65;CGTCCTGCACACCAGAACGAGTAGGCTGCTCATTCAGTGA

4A Part
4A32;CAGAAGGAAACCGAGGTTTTTAAGAAAAGTAAATGGGCAT
4A31-1;CACGTATTTATCTTACCGAAGCCCAAACGCAA
4A30;GAGCCAGCGAATACCCAAAAGAACATGAAATAGCAATAGCTTGCAAGC
4A28-1;ATTGCGTAATAAGAGCAAGAAACATGGCATGA
4A26;CACCGTCACCTTATTACGCAGTATTGAGTTAAGCCCAATACCCGACGA
4A23-1;CGCTACCTGATAACCCACAAGAATGTTAGCAA
4A20;TTGACGGAAATACATACATAAAGGGCGCTAATATCAGAGAGTAGGAAG
4A16-1;ACCGCATGGTCAGAGGGTAATTGATGGCAACA
4A12;CATTCAACAAACGCAAAGACACCAGAACACCCTGAACAAAGAAATGAA
4A08-1;ACCATACTGACGGGAGAATTAACTCGGAATAA
4A37;AGTCGGCGAGAGAATAACATAAAAACAGGGAAGCGCATTACAGGCACA
4A41;TTTCCTTAGCACTCATCGAGAACAATAGCAGCCTTTACAGTGTGAATC
4A45-1;TCGGCAGCAACGTCAAAAATGAAAAGCAAGCC
4A49;AGCATGTATTTCATCGTAGGAATCAAACGATTTTTTGTTTAAGAACCA
4A53-1;AAAATAGTTCCCAATCCAAATAAGATTACCGC
4A56;ACAAGAAAGCAAGCAAATCAGATAACAGCCATATTATTTACACGCAAA
4A59-1;AAAACGCCGCCAGTTACAAAATAATAGAAGGC
4A61;GCGCCTGTTATTCTAAGAACGCGATTCCAGAGCCTAATTTTCTAATCG
4A63-1;AGAGTGTCACGCTAACGAGCGTCTGGCGTTTT
4A64;ACGACAATAAATCCCGACTTGCGGGAGATCCTGAATCTTACCAAAAAACGA
4A65;ATGAGCCTACCCAGCTACAATTTTGTTTTGAAGCCTTAAA

3B Part
3B32;AATACTGCGGAATCGTAGGGGGTAATAGTAAAGTCGCATT
3B31-1;GAATAGCAAAAGAAGTTTTGCCAGCATAAATA
3B30;TGCTGTAGATCCCCCTCAAATGCTGCGAGAGGCTTTTGCAAAGCCTCT
3B28-1;GAGGCCTCGATAAAAACCAAAATATTAAACAG
3B26;CGGATGGCACGAGAATGACCATAATCGTTTACCAGACGACCAGCAATC
3B23-1;AATACCTTAACACTATCATAACCCATCAAAAA
3B20;TAATTGCTTTACCCTGACTATTATGAGGCATAGTAAGAGCTCTTTTTG
3B16-1;CGCGAATACGCCAAAAGGAATTACAGTCAGAA
3B12;AACTCCAAGATTGCATCAAAAAGATAATGCAGATACATAATCCTTAAG

3B08-1;AGCTTGCGGAATACCACATTCAACTTAAGAGG
3B37;GTTCTCTAACAGGTAGAAAGATTCATCAGTTGAGATTTAGGCAAAACT
3B41;CGACCTGCGGTCAATCATAAGGGAACGGAACAACATTATTAAAACCAT
3B45-1;GGCGGTGGTTAATAAAACGAACTAACCGAACT
3B49;TATCATCGTTGAAAGAGGACAGATGGAAGAAAAATCTACGTCTATAGT
3B53-1;TGGGGGAGACCAGTCAGGACGTTGGAACGGTG
3B56;CCAAGCGCAGGCGCATAGGCTGGCAGAACTGGCTCATTATCACATTGT
3B59-1;ATCCATTAACCTTATGCGATTTTATGACCTTC
3B61;AAAACACTTAATCTTGACAAGAACTTAATCATTGTGAATTACTTCTCA
3B63-1;CATCACGATGGTTTAATTTCAACTCGGATATT
3B64;ACCAACCTAAAAAATCAACGTAACAAATAAATTGGGCTTGAGAACGTCAGA
3B65;TCAACATAACACCAGAACGAGTAGGCTGCTCATTCAGTGA

3A Part
3A32;CAGAAGGAAACCGAGGTTTTTAAGAAAAGTAAGAACTCAA
3A31-1;AGACAGAATATCTTACCGAAGCCCAAACGCAA
3A30;GAGCCAGCGAATACCCAAAAGAACATGAAATAGCAATAGCTCTCTTCC
3A28-1;TATCCATCATAAGAGCAAGAAACATGGCATGA
3A26;CACCGTCACCTTATTACGCAGTATTGAGTTAAGCCCAATATGCTTATG
3A23-1;GATTGAGAGATAACCCACAAGAATGTTAGCAA
3A20;TTGACGGAAATACATACATAAAGGGCGCTAATATCAGAGAAAGAGTAG
3A16-1;AATAGCAGGTCAGAGGGTAATTGATGGCAACA
3A12;CATTCAACAAACGCAAAGACACCAGAACACCCTGAACAAAGTTTAAGA
3A08-1;AGTCAAAAGACGGGAGAATTAACTCGGAATAA
3A37;TAATAAGAAGAGAATAACATAAAAACAGGGAAGCGCATTATAATCAGC
3A41;TTTCCTTAGCACTCATCGAGAACAATAGCAGCCTTTACAGACGAACCA
3A45-1;ATTTGGAGAACGTCAAAAATGAAAAGCAAGCC
3A49;AGCATGTATTTCATCGTAGGAATCAAACGATTTTTTGTTTGCATGAAA
3A53-1;GTGTCAATTCCCAATCCAAATAAGATTACCGC
3A56;ACAAGAAAGCAAGCAAATCAGATAACAGCCATATTATTTACCTGACGG
3A59-1;TTAGAGCCGCCAGTTACAAAATAATAGAAGGC
3A61;GCGCCTGTTATTCTAAGAACGCGATTCCAGAGCCTAATTTAATACCAT
3A63-1;CCAGAAATACGCTAACGAGCGTCTGGCGTTTT
3A64;ACGACAATAAATCCCGACTTGCGGGAGATCCTGAATCTTACCATGTTCCAA
3A65;TATCAATAACCCAGCTACAATTTTGTTTTGAAGCCTTAAA

2B Part
2B32;AATACTGCGGAATCGTAGGGGGTAATAGTAAACCATGAAA
2B31-1;GAAGCAGCAAAGAAGTTTTGCCAGCATAAATA
2B30;TGCTGTAGATCCCCCTCAAATGCTGCGAGAGGCTTTTGCAATCAGTGA
2B28-1;CTTTGCAGGATAAAAACCAAAATATTAAACAG
2B26;CGGATGGCACGAGAATGACCATAATCGTTTACCAGACGACTAGCGCCA
2B23-1;ACCGCTGAAACACTATCATAACCCATCAAAAA
2B20;TAATTGCTTTACCCTGACTATTATGAGGCATAGTAAGAGCTTCTGCGT
2B16-1;TCAACCTCCGCCAAAAGGAATTACAGTCAGAA
2B12;AACTCCAAGATTGCATCAAAAAGATAATGCAGATACATAAAGCACTAA

2B08-1;TTTGATTTGAATACCACATTCAACTTAAGAGG
2B37;CCGTTTGAACAGGTAGAAAGATTCATCAGTTGAGATTTAGGGTCATTG
2B41;CGACCTGCGGTCAATCATAAGGGAACGGAACAACATTATTGCTTGAGT
2B45-1;ATCTCGGATTAATAAAACGAACTAACCGAACT
2B49;TATCATCGTTGAAAGAGGACAGATGGAAGAAAAATCTACGAACCTGCT
2B53-1;GGTGTTTTACCAGTCAGGACGTTGGAACGGTG
2B56;CCAAGCGCAGGCGCATAGGCTGGCAGAACTGGCTCATTATCCATAATA
2B59-1;TAGACTCCACCTTATGCGATTTTATGACCTTC
2B61;AAAACACTTAATCTTGACAAGAACTTAATCATTGTGAATTTTCTGTTG
2B63-1;TTTTGTGCTGGTTTAATTTCAACTCGGATATT
2B64;ACCAACCTAAAAAATCAACGTAACAAATAAATTGGGCTTGAGAATATACCT
2B65;GCGTGAAGACACCAGAACGAGTAGGCTGCTCATTCAGTGA

2A Part
2A32;CAGAAGGAAACCGAGGTTTTTAAGAAAAGTAACAGCAATC
2A31-1;TTTGCATCTATCTTACCGAAGCCCAAACGCAA
2A30;GAGCCAGCGAATACCCAAAAGAACATGAAATAGCAATAGCTCGGCAAT
2A28-1;AGTTGCATATAAGAGCAAGAAACATGGCATGA
2A26;CACCGTCACCTTATTACGCAGTATTGAGTTAAGCCCAATATTTAGTAA
2A23-1;AAATCCGGGATAACCCACAAGAATGTTAGCAA
2A20;TTGACGGAAATACATACATAAAGGGCGCTAATATCAGAGACGTCAACC
2A16-1;CATCAGCAGTCAGAGGGTAATTGATGGCAACA
2A12;CATTCAACAAACGCAAAGACACCAGAACACCCTGAACAAACCAGCACG
2A08-1;TCAGGAAAGACGGGAGAATTAACTCGGAATAA
2A37;ATCCTTTCAGAGAATAACATAAAAACAGGGAAGCGCATTATGCAGCAG
2A41;TTTCCTTAGCACTCATCGAGAACAATAGCAGCCTTTACAGCTTTATCA
2A45-1;CAAGTCCAAACGTCAAAAATGAAAAGCAAGCC
2A49;AGCATGTATTTCATCGTAGGAATCAAACGATTTTTTGTTTACCAAATC
2A53-1;ACGGCAGATCCCAATCCAAATAAGATTACCGC
2A56;ACAAGAAAGCAAGCAAATCAGATAACAGCCATATTATTTAAGTGCCAG
2A59-1;AAGAAGTCGCCAGTTACAAAATAATAGAAGGC
2A61;GCGCCTGTTATTCTAAGAACGCGATTCCAGAGCCTAATTTCTTTACCA
2A63-1;CAGAAACAACGCTAACGAGCGTCTGGCGTTTT
2A64;ACGACAATAAATCCCGACTTGCGGGAGATCCTGAATCTTACCAAAACTAGG
2A65;TTAGGAACACCCAGCTACAATTTTGTTTTGAAGCCTTAAA

1B Part
1B32;AATACTGCGGAATCGTAGGGGGTAATAGTAAAATTAGAGC
1B31-1;AATACCAGAAAGAAGTTTTGCCAGCATAAATA
1B30;TGCTGTAGATCCCCCTCAAATGCTGCGAGAGGCTTTTGCACATCACCC
1B28-1;TATCGGTAGATAAAAACCAAAATATTAAACAG
1B26;CGGATGGCACGAGAATGACCATAATCGTTTACCAGACGACGCAAGCAC
1B23-1;CCGGAGGCAACACTATCATAACCCATCAAAAA
1B20;TAATTGCTTTACCCTGACTATTATGAGGCATAGTAAGAGCGGCTTTTT
1B16-1;TTTAGACACGCCAAAAGGAATTACAGTCAGAA
1B12;AACTCCAAGATTGCATCAAAAAGATAATGCAGATACATAATGGCGCCA

1B08-1;CAATACCGGAATACCACATTCAACTTAAGAGG
1B37;CACCTCACACAGGTAGAAAGATTCATCAGTTGAGATTTAGCCAGCAAT
1B41;CGACCTGCGGTCAATCATAAGGGAACGGAACAACATTATTTTAAGTGG
1B45-1;TCTTTAATTTAATAAAACGAACTAACCGAACT
1B49;TATCATCGTTGAAAGAGGACAGATGGAAGAAAAATCTACGAACCTGAT
1B53-1;GCGGCATTACCAGTCAGGACGTTGGAACGGTG
1B56;CCAAGCGCAGGCGCATAGGCTGGCAGAACTGGCTCATTATTAGTAGCG
1B59-1;CCATGAAAACCTTATGCGATTTTATGACCTTC
1B61;AAAACACTTAATCTTGACAAGAACTTAATCATTGTGAATTCCAACATA
1B63-1;GTACGGGGTGGTTTAATTTCAACTCGGATATT
1B64;ACCAACCTAAAAAATCAACGTAACAAATAAATTGGGCTTGAGAAAGGACGT
1B65;CTTGACGGACACCAGAACGAGTAGGCTGCTCATTCAGTGA

1A Part
1A32;CAGAAGGAAACCGAGGTTTTTAAGAAAAGTAACATGGCGA
1A31-1;CATCATAGTATCTTACCGAAGCCCAAACGCAA
1A30;GAGCCAGCGAATACCCAAAAGAACATGAAATAGCAATAGCGCAGTCGG
1A28-1;GAAGAAGAATAAGAGCAAGAAACATGGCATGA
1A26;CACCGTCACCTTATTACGCAGTATTGAGTTAAGCCCAATACTCAAAGC
1A23-1;AAATTTAGGATAACCCACAAGAATGTTAGCAA
1A20;TTGACGGAAATACATACATAAAGGGCGCTAATATCAGAGAGGTCGGCA
1A16-1;CACCAACAGTCAGAGGGTAATTGATGGCAACA
1A12;CATTCAACAAACGCAAAGACACCAGAACACCCTGAACAAAGAAACAAC
1A08-1;ACAGATGTGACGGGAGAATTAACTCGGAATAA
1A37;ACCACCATAGAGAATAACATAAAAACAGGGAAGCGCATTAATCCATCT
1A41;TTTCCTTAGCACTCATCGAGAACAATAGCAGCCTTTACAGTACCAGCA
1A45-1;CAAAATATAACGTCAAAAATGAAAAGCAAGCC
1A49;AGCATGTATTTCATCGTAGGAATCAAACGATTTTTTGTTTAACGTTGA
1A53-1;GTCTGTAATCCCAATCCAAATAAGATTACCGC
1A56;ACAAGAAAGCAAGCAAATCAGATAACAGCCATATTATTTAAACAGGTG
1A59-1;AACAGAAGGCCAGTTACAAAATAATAGAAGGC
1A61;GCGCCTGTTATTCTAAGAACGCGATTCCAGAGCCTAATTTTGAGAACC
1A63-1;AGTTTGAAACGCTAACGAGCGTCTGGCGTTTT
1A64;ACGACAATAAATCCCGACTTGCGGGAGATCCTGAATCTTACCATTATGGCG
1A65;AACATGATACCCAGCTACAATTTTGTTTTGAAGCCTTAAA

Bridges
611;ATATAACCAAGTCTGA
612;AGAAATAAAGTAGTGT
621;AGTGGCATAGAAAAAA
622;AGCTTATCTAACACCA
631;TCCACTGTGCTGGAGT
632;CCGAAGAATCACCATA
641;ACATAAAACTTTAGGT
642;CGATGTAGAGTAAAAA
651;AATAGCAACAAACTAT

652;TTAACCGTGGCCACGA
661;GGAGAGCGTGAAGAAA
662;GAATGCAACCAACGGC

671;TCGCCAGCCGGCGTTG
672;CTGATTAGGATAACCG
681;AATAAGACAATATCAG
682;TCAAAAGCGACCAATC
691;CAAGATGGCAGGCAAA
692;GAACCAAAGAAAGGTC
6101;GCGCCAGTTCGGAACC
6102;GAGGGTAGTTGAATAT
6111;TCAAGTAAAGGATAAA
6112;CCATTCAAGGGGCCGA

5 Triangle Origami(65)
511;CATACCAAGAACGTGC
512;TCCTTGACAGACGAGC
521;TTAGTACCAAATGTGA
522;CATGAACATCGCAACG
531;GCGAGCGCAAATGTCA
532;CTCTTTTACAGAACGT
541;TTACATCAATCGGACT
542;TGAACAGCCTCCTTCC
551;GCACGTTTCATGATTT
552;ACTTGACTTCTTCTGC

561;GTGTTTCCTGGAAACG
562;AAGCGGTCTGCGCGTA
571;GAACAATTCCTGAATG
572;GGCAGAAGCAGCGGCT
581;CGCCATTAATCATCTT
582;AAATCGAAATAATGTT
591;CCTTCCATATCCAAAC
592;CAGTAGCAGATGAGAC
5101;GACGGGATCGCAGCGA
5102;AGCCTCAAGAACATAA
5111;CAATAAACAAAGTCCA
5112;TATCCCACTCAACAGG

4 Triangle Origami(54)
411;CGCGTCAGTGAAAAAG
412;CCAGAACGTTTTTGAC
421;GGCGAAAGTTAGCATC
422;GCTCACCTGTCGCAAA
431;CTGCGCAACCATATAA

432;ACCAACAGGGATAGGT
441;CCGCCAGCGTTAACGT
442;GACTTTTTAGTCCACT
451;ACAAGCAGCCTTTAGC
452;CTCCTAGATAGTAATT

461;AATTTTTCTTAGTGAG
462;CTTGGTTTGACTCATC
471;GTTAACTTCAGCTTCT
472;ATTCTGAACTGCGTCA
481;CTGCAGGTATCCCGAA
482;GCATTTTCTGGATACG
491;AAGCGCGCCCGTGGAC
492;TAAGCACTATAAATTT
4101;ACAGGTTGGTAACCCA
4102;GTCGCGTCCGCCGCCA
4111;AACTTTTCTGCTTCAA
4112;TTGCGTTCCCAGCCTC

3 Triangle Origami(43)
311;ACTGTAACTATGGCCG
312;AGCAGCCTCATAAGGC
321;TATTTAACTACAAACT
322;GTAACAGATGGCGGCG
331;CCAAAATTGCCAATTC
332;AGCATTGTAGGGTCAA
341;TGTCCGCATATCAAGT
342;GTTATTAATAAAGTGC
351;GACGGCCACCCTTCGG
352;TTTTCGTCTTAGCTGT

361;CAAAAATAGTCTTCTC
362;GCGTAACCCTGATAGC
371;ATTAGCCTCAGCAGCC
372;AGGGCGTTTGCGACCC
381;TACGACCAATACTCAT
382;GGGTAATTATATCACG
391;GCATTGGGTCATCCTT
392;TTGAACACATTATCAT
3101;GTCGTCAGTCATAGTG
3102;ACGCGATTCCAACGTG
3111;TAAACCAACAAACGCT
3112;GCATTCATCCATCAGC

2 Triangle Oriami(32)
211;CGCCCTGCGTATTCTG

212;GGTCTTTCATACGAAA
221;AAGAGCTTGCATCTCA
222;ATAAGCAAGATGCGGT
231;GAAGCCAAGCGAGCAG
232;GACGCAACGCATTGGG
241;AAATGCCAGAAAGATT
242;GTTGCTTGCAAGCCTC
251;GCCTCGATGGCGCATA
252;AAGCATTTACGCTCAA

261;GTGACATTCTGACCAG
262;GTAAAATACAGAAGGG
271;TAAAAAAGGTCATTTC
272;CCTTGCGACCTCCAAG
281;ACATACAAGAACTAAG
282;TTGCTGATTTGGGAGG
291;TTATTTCCAGAGCCAT
292;ATATGAGATAGACAAA
2101;CAGCTTTAGAAATATC
2102;CGACATTACCGTCTTT
2111;GTATCGGCCCACACCA
2112;AATATCAAAACAGCTT

1 Triangle Origami(21)
111;TCTTTTTGACACAGTC
112;CAATAGTCAGTCTCAT
121;CTCTTTCTTGCCCGGC
122;AACGTTATGATTGTCC
131;GCTCTTTTAGACCAAA
132;GTAAAGTTTGATTCTC
141;ATACCAGCACCAATCC
142;TCAGCGAAAGAGGAAG
151;CTCCCAAGAAATAATC
152;CTGGAGACCATTAAGC

161;CAAGATAAACATAAAT
162;AGCACCAATCACGAGT
171;GCGGCAGAAGCAGAAG
172;CCAGCAAGCTTGCCAC
181;AAGCAACTCCAAACAA
182;GACCGCCTTATCAGAA
191;CCTGCAACGAATGCCA
192;ATCACCTTGTACCTTC
1101;GCTTTAGCAGTATTGT
1102;ATGCCTACCATAGCAC
1111;GGCGGCCTGCAGATTT

1112;CTTGAATGCATCAGGG

Table S3. Triangle origami modified staples and bridges that hybridize with ΦX 174 scaffolds for design 2

Modified helpers for each triangle origami

6I1;CGAAGGAGTCGCCAGCCGGCGTTGACAGATGT
6I21;CACCAACAGAAACAACCTGATTAGGATAACCG
6T22;GAGTAGTTGAAATGGTAATAAGACAATATCAG
6I31;AAATTTAGGGTCGGCATCAAAAGCGACCAATC
6I32;TGACCAGCAAGGAAGCCAAGATGGCAGGCAAA
6I41;GAAGAAGACTCAAAGCGAACCAAAGAAAGGTC
6I42;ATGCGGCATACGCTCGGCGCCAGTTCGGAACC
6I51;CATCATAGGCAGTCGGGAGGGTAGTTGAATAT
6I52;TAGACATAATTTATCCTCAAGTAAAGGATAAA
6I6;CATGGCGACCATTCAAGGGGCCGAAGCCCCTG

5I1;GTTCAGTAACTTGACTTCTTCTGCGTCAGTAA
5I21;GCACGTAATTTTTGACGCACGTTTCATGATTT
5T22;CTTACCTATTAGTGGTTGAACAGCCTCCTTCC
5I31;TTTTTACCTTTAGACATTACATCAATCGGACT
5I32;CAGATAGTAATCCACGCTCTTTTACAGAACGT
5I41;GCTGCGGACGACCAGGGCGAGCGCAAATGTCA
5I42;ACAAGAGAATCTCTACCATGAACATCGCAACG
5I51;GCCTTTACGCTTGCCTTTAGTACCAAATGTGA
5I52;CTCATATCTAAACCAGTCCTTGACAGACGAGC
5I6;ACCACCTACATACCAAGAACGTGCCAAGCATA

4I1;TTCTTTAGCTCCTAGATAGTAATTCCTGCTTT
4I21;TCGATTTAATTCGTAAACAAGCAGCCTTTAGC
4T22;AGCAAGGTCCATATCTGACTTTTTAGTCCACT
4I31;CGAATTTTCTCATTTTCCGCCAGCGTTAACGT
4I32;ATTTAGCCACATAGAAACCAACAGGGATAGGT
4I41;GTAAGAGCTTCTCGAGCTGCGCAACCATATAA
4I42;CTGGTAGCTTTAAGCGGCTCACCTGTCGCAAA
4I51;AGAATCGTTAGTTGATGGCGAAAGTTAGCATC
4I52;AACAGGCCACAACCAACCAGAACGTTTTTGAC
4I6;TCATCCAACGCGTCAGTGAAAAAGCGTCCTGC

3I1;AAAACCATTTTTCGTCTTAGCTGTACCATACT
3I21;GGCGGTGGTCTATAGTGTTATTAATAAAGTGC
3I22;ACCGCATGGAAATGAAGACGGCCACCCTTCGG
3I31;TGGGGGAGCACATTGTAGCATTGTAGGGTCAA
3I32;CGCTACCTGTAGGAAGTGTCCGCATATCAAGT
3I41;ATCCATTAACTTCTCAGTAACAGATGGCGGCG
3I42;ATTGCGTACCCGACGACCAAAATTGCCAATTC
3I51;CATCACGAACGTCAGAAGCAGCCTCATAAGGC

3T52;CACGTATTTTGCAAGCTATTTAACTACAAACT
3I6;ATGGGCATACTGTAACTATGGCCGTCAACATA

2I1;GCTTGAGTAAGCATTTACGCTCAAAGTCAAAA
2I21;AATAGCAGGTTTAAGAGCCTCGATGGCGCATA
2T22;ATCTCGGAAACCTGCTGTTGCTTGCAAGCCTC
2I31;GATTGAGAAAGAGTAGAAATGCCAGAAAGATT
2I32;GGTGTTTTCCATAATAGACGCAACGCATTGGG
2I41;TATCCATCTGCTTATGGAAGCCAAGCGAGCAG
2I42;TAGACTCCTTCTGTTGATAAGCAAGATGCGGT
2I51;AGACAGAATCTCTTCCAAGAGCTTGCATCTCA
2I52;TTTTGTGCATATACCTGGTCTTTCATACGAAA
2I6;GAACTCAACGCCCTGCGTATTCTGGCGTGAAG

1I1;TTAAGTGGCTGGAGACCATTAAGCTCAGGAAA
1I21;CATCAGCACCAGCACGCTCCCAAGAAATAATC
1T22;TCTTTAATAACCTGATTCAGCGAAAGAGGAAG
1I31;AAATCCGGCGTCAACCATACCAGCACCAATCC
1I32;GCGGCATTTAGTAGCGGTAAAGTTTGATTCTC
1I41;AGTTGCATTTTAGTAAGCTCTTTTAGACCAAA
1I42;CCATGAAACCAACATAAACGTTATGATTGTCC
1I51;TTTGCATCTCGGCAATCTCTTTCTTGCCCGGC
1I52;GTACGGGGAAGGACGTCAATAGTCAGTCTCAT
1I6;CAGCAATCTCTTTTTGACACAGTCCTTGACGG

Table S4. Triangle origami modified staples and bridges that hybridize with ΦX 174 scaffolds for design 3

Modified helpers for each triangle origami

111;CATGGTCAATATAACCAAGTCTGA
112;AGAAATAAAGTAGTGTTAACAGTC
121;AGTGGCATAGAAAAAAAGTTTGAA
122;TGAGAACCAGCTTATCTAACACCA
131;GAACTTAATCCACTGTGCTGGAGT
132;CCGAAGAATCACCATAAACGTGAC
141;ACATAAAACTTTAGGTGTCTGTAA
142;AACGTTGACGATGTAGAGTAAAAA
151;GTAGAGTCAATAGCAACAAACTAT
152;TTAACCGTGGCCACGACGCAATGG
161;GGAGAGCGTGAAGAAAACCACCAT
162;ATCCATCTGAATGCAACCAACGGC
171;CGAAGGAGTCGCCAGCCGGCGTTG
172;CTGATTAGGATAACCGGAGTAGTT
181;AATAAGACAATATCAGCACCAACA
182;GGTCGGCATCAAAAGCGACCAATC
191;AAGGAAGCCAAGATGGCAGGCAAA
192;GAACCAAAGAAAGGTCATGCGGCA

1101;GCGCCAGTTCGGAACCGAAGAAGA
1102;GCAGTCGGGAGGGTAGTTGAATAT
1111;ATTTATCCTCAAGTAAAGGATAAA
1112;CCATTCAAGGGGCCGAAGCCCCTG
211;AGCGAGGGTATCCCACTCAACAGG
212;CAATAAACAAAGTCCAGCGTACCA
221;AGCCTCAAGAACATAATAAGCAAT
222;TGAATGTTGACGGGATCGCAGCGA
231;AGAGCGGTCAGTAGCAGATGAGAC
232;CCTTCCATATCCAAACTTTGTTAC
241;AAATCGAAATAATGTTTTCCGTAA
242;ACGCTCGACGCCATTAATCATCTT
251;TCCAAAACGGCAGAAGCAGCGGCT
252;GAACAATTCCTGAATGAGCTTAAT
261;AAGCGGTCTGCGCGTACACGCAAG
262;GAACGTCAGTGTTTCCTGGAAACG
271;GTTCAGTAACTTGACTTCTTCTGC
272;GCACGTTTCATGATTTCTTACCTA
281;TGAACAGCCTCCTTCCGCACGTAA
282;TTTAGACATTACATCAATCGGACT
291;AATCCACGCTCTTTTACAGAACGT
292;GCGAGCGCAAATGTCAACAAGAGA
2101;CATGAACATCGCAACGGCTGCGGA
2102;GCTTGCCTTTAGTACCAAATGTGA
2111;TAAACCAGTCCTTGACAGACGAGC
2112;CATACCAAGAACGTGCCAAGCATA
311;CTCTCTTTTTGCGTTCCCAGCCTC
312;AACTTTTCTGCTTCAATATCTGGT
321;GTCGCGTCCGCCGCCAAAACGTCG
322;TTGTCGTCACAGGTTGGTAACCCA
331;AGTTGGATTAAGCACTATAAATTT
332;AAGCGCGCCCGTGGACAGATTTGT
341;GCATTTTCTGGATACGCCAATCAT
342;ATAAAACTCTGCAGGTATCCCGAA
351;TCATTCTGATTCTGAACTGCGTCA
352;GTTAACTTCAGCTTCTTGGGAAGT
361;CTTGGTTTGACTCATCAGAAATAT
362;ATCAAGATAATTTTTCTTAGTGAG
371;TTCTTTAGCTCCTAGATAGTAATT
372;ACAAGCAGCCTTTAGCAGCAAGGT
381;GACTTTTTAGTCCACTTCGATTTA
382;CTCATTTTCCGCCAGCGTTAACGT
391;ACATAGAAACCAACAGGGATAGGT
392;CTGCGCAACCATATAACTGGTAGC
3101;GCTCACCTGTCGCAAAGTAAGAGC
3102;TAGTTGATGGCGAAAGTTAGCATC

3111;ACAACCAACCAGAACGTTTTTGAC
3112;CGCGTCAGTGAAAAAGCGTCCTGC
411;GTCGCATTGCATTCATCCATCAGC
412;TAAACCAACAAACGCTGAATAGCA
421;ACGCGATTCCAACGTGAGAGTGTC
422;TCTAATCGGTCGTCAGTCATAGTG
431;CAGCAATCTTGAACACATTATCAT
432;GCATTGGGTCATCCTTAATACCTT
441;GGGTAATTATATCACGAAAATAGT
442;AAGAACCATACGACCAATACTCAT
451;TCCTTAAGAGGGCGTTTGCGACCC
452;ATTAGCCTCAGCAGCCAGCTTGCG
461;GCGTAACCCTGATAGCAGTCGGCG
462;CAGGCACACAAAAATAGTCTTCTC
471;AAAACCATTTTTCGTCTTAGCTGT
472;GACGGCCACCCTTCGGGGCGGTGG
481;GTTATTAATAAAGTGCACCGCATG
482;GTAGGAAGTGTCCGCATATCAAGT
491;CACATTGTAGCATTGTAGGGTCAA
492;CCAAAATTGCCAATTCATCCATTA
4101;GTAACAGATGGCGGCGATTGCGTA
4102;TTGCAAGCTATTTAACTACAAACT
4111;ACGTCAGAAGCAGCCTCATAAGGC
4112;ACTGTAACTATGGCCGTCAACATA

511;CCATGAAAAATATCAAAACAGCTT
512;GTATCGGCCCACACCAGAAGCAGC
521;CGACATTACCGTCTTTCCAGAAAT
522;AATACCATCAGCTTTAGAAATATC
531;TAGCGCCAATATGAGATAGACAAA
532;TTATTTCCAGAGCCATACCGCTGA
541;TTGCTGATTTGGGAGGGTGTCAAT
542;GCATGAAAACATACAAGAACTAAG
551;AGCACTAACCTTGCGACCTCCAAG
552;TAAAAAAGGTCATTTCTTTGATTT
561;GTAAAATACAGAAGGGTAATAAGA
562;TAATCAGCGTGACATTCTGACCAG
571;GCTTGAGTAAGCATTTACGCTCAA
572;GCCTCGATGGCGCATAATCTCGGA
581;GTTGCTTGCAAGCCTCAATAGCAG
582;AAGAGTAGAAATGCCAGAAAGATT
591;CCATAATAGACGCAACGCATTGGG
592;GAAGCCAAGCGAGCAGTAGACTCC
5101;ATAAGCAAGATGCGGTTATCCATC
5102;TCTCTTCCAAGAGCTTGCATCTCA

5111;ATATACCTGGTCTTTCATACGAAA
5112;CGCCCTGCGTATTCTGGCGTGAAG
611;ATTAGAGCCTTGAATGCATCAGGG
612;GGCGGCCTGCAGATTTAATACCAG
621;ATGCCTACCATAGCACCAGAAACA
622;CTTTACCAGCTTTAGCAGTATTGT
631;GCAAGCACATCACCTTGTACCTTC
632;CCTGCAACGAATGCCACCGGAGGC
641;GACCGCCTTATCAGAAACGGCAGA
642;ACCAAATCAAGCAACTCCAAACAA
651;TGGCGCCACCAGCAAGCTTGCCAC
652;GCGGCAGAAGCAGAAGCAATACCG
661;AGCACCAATCACGAGTATCCTTTC
662;TGCAGCAGCAAGATAAACATAAAT
671;TTAAGTGGCTGGAGACCATTAAGC
672;CTCCCAAGAAATAATCTCTTTAAT
681;TCAGCGAAAGAGGAAGCATCAGCA
682;CGTCAACCATACCAGCACCAATCC
691;TAGTAGCGGTAAAGTTTGATTCTC
692;GCTCTTTTAGACCAAACCATGAAA
6101;AACGTTATGATTGTCCAGTTGCAT
6102;TCGGCAATCTCTTTCTTGCCCGGC
6111;AAGGACGTCAATAGTCAGTCTCAT
6112;TCTTTTTGACACAGTCCTTGACGG

Table S5. Unmodified square DNA origami staples

1	TTCAGGGATAGCAAG
2	GAACCGCCACCCTCAGCCCTTATT
3	TAGTACCGCCACCCTCAAAATCAC
4	CGGAATAGGTGTATCACGCCTCCC
5	GTGCCGTCGAGAGGGTCCACCCTC
6	TAGCGGGGTTTTGCTCACCAGAAC
7	AGGCTGAGACTCCTCATGACAGGAGGTTGAGGCAGGTC
8	CATGAAAGTATTAAG
9	ATCGGCATTTTCGGTCATAGCCAGCCACCACCCTCATT
10	AGTTTTGCCCATCTTTTCATAATCAGAACCGCCACCCTCA
11	AAACCAAAGAGCCACCACCGGAACCCGTACTCAGGAGGTT
12	TATCATAAGCCACCCTCAGAACCGTGATATAAGTATAGCC
13	AAAGGAATCACCCTCAGAGCCGCCAGTACCAGGCGGATAA
14	CCACATTCGAGCCGCCGCCAGCATAGAGAAGGATTAGGAT
15	AACCTATTATTCTGA
16	TATAAACAGTTAATGCCAAATAAA
17	AACGGGGTCAGTGCCTGCGCAGTC
18	GATGATACAGGAGTGTGTCATACAT
19	AAACGGGTAAAATACGAAAGAGGC

20	ACTAAAGACTTTTTCACTTTGACC
21	CGAGGGTAGCAACGGCACAAAGTACAACGGAGATTTGT
22	AAGACAGCATCGGAA
23	GATTGGCCTTGATATTCACAAACCCCTGCCTATTTCGG
24	AAAACGAAAAAGCCAGAATGGAAATGAGTAACAGTGCCCG
25	TCAGGACGTACCGTTCCAGTAAGCACTGGTAATAAGTTTT
26	ATGCGATTGCACCAACCTAAAACGTAATGCCACTACGAAG
27	TAATTTCAACACTAAAACACTCATTGAGGAAGTTTCCATT
28	AGAACGAGTTATACCAAGCGCGAATACAGAGGCTTTGAGG
29	GTCACCCTCAGCAGC
30	TGCAGGGAGTTAAAGGATCCGCGA
31	ACGCATAACCGATATAACGAGGCG
32	AGTTGCGCCGACAATGGAACTGAC
33	GAGGTGAATTTCTTAAAGTTTATT
34	CTTTAATTGTATCGGTTATGGTTT
35	AAAATCTCCAAAAAAAAACATTCAACCGATTGAGGGAGG
36	AATTTTTTCACGTTG
37	TCGCCTGATAAATTGTGTCGAACCGCTTTTGCGGGATC
38	TACCCAAAATGTTACTTAGCCGGATTCGGTCGCTGAGGCT
39	AAGAGTAACAATCATAAGGGAACCACAACAACCATCGCCC
40	AGACCAGGAAAGAGGACAGATGAAACAGCTTGATACCGAT
41	GAAACGCAATCAATAGAAAATTCATTATCAGCTTGCTTTC
42	AAATACATCAAAGACAAAAGGGCGAGGCTCCAAAAGGAGC
43	AAGGAATTGCGAATA
44	TTCAGCGGAGTGAGAACATTAAAG
45	GTATGGGATTTTGCTAGAGCCATT
46	CGTCTTTCCAGACGTTCCAGTAGC
47	CTCATAGTTAGCGTAAAACGTCAC
48	ACTACAACGCCTGTAGCGTAATCA
49	TACCGTAACACTGAGTTTAGCGTCAGACTGTAGCGCGT
50	CAATAGGAACCCATG
51	GTAAATATTGACGGAAATTATTTAGAAAGGAACAACTA
52	GGAATACCTCACCGTCACCGACTTAACAACTTTCAACAGT
53	CCAGAAGGAGAGCCAGCAAAATCAAGTAAATGAATTTTCT
54	AATCAAAACATTAGCAAGGCCGGACGATCTAAAGTTTTGT
55	TTTAAACACCATCGATAGCAGCACCATTCCACAGACAGCC
56	TCATAAATAGAATCAAGTTTGCCTTTCGTCACCAGTACAA
57	AGCGTTTGCAGAGGGGGTAATAGTATTCGAGC
58	CGGAACCAATAGCGAGAGGCTTTTAAACTCCAACAGGTCAATAAGAGG
59	TCAGAGCCCCCTCGTTTACCAGACTAAACCAAGTACCGCATTCCAAGA
60	AGAGCCACTACGAGGCATAGTAAGAAGCCGTTTTTATTTTACCAATCA
61	CACCACCAAACTAATGCAGATACAACCGCGCCCAATAGCAAATATCCC
62	TCCTCATTCTAACGGAACAACATTTCTAAGAA

63 TCTGAATTTTGGGAAGAAAAATCTCGACTTGCGGGAGGTTCATGTTCA
64 GGCTTTTTTAAGAACTGGCTCATAGATTAGTTGCTATTTAGTAATTC
65 AAAAGAATACTTTAATCATTGTGATTTATCCTGAATCTTATAGAACCC
66 CCCAGCGATAGTAAATTGGGCTTGTCTTTCCAGAGCCTAAAGCCTTTA
67 CCTGCTCCTCAACGTAACAAAGCTTTATCCCA
68 CAGACGGTTCTTGACAAGAACCGGTTTAACGTCAAAAATGCAGAGCAT
69 CAACTTTGCGCATAGGCTGGCTGACAGAGAGAATAACATACAAAGAAT
70 TTGTCACAAAGACACCACGGAATATTAGACGGGAGAATTAGCATTAAC
71 ACCAGCGCACATAAAGGTGGCAACAAAGTCAGAGGGTAATAAAAGGTG
72 GTGAATTACAAAAGAACTGGCATGAATTGAGT
73 TGGGAATTAAACCGAGGAAACGCAACAATGAAATAGCAATTTAGATAC
74 ACCATTACTAAGCAGATAGCCGAACCCTTTTTAAGAAAAGAATTCTGC
75 CAATGAAAGTTCAGAAAACGAGAAGACTATTATAGTCAGAGGAAGTTT
76 GTAGCGACATTCATTGAATCCCCCTCAAAAAGATTAAGAGTGTTTTAA
77 TTCATCAGTTGAGATTAAGGCT
78 AGGCTTGCCCTGACGATAAACA
79 ACGCAGTATGTTAGCAAGAGAT
80 ATAGCGTCCAATACTGCAAATA
81 GTTTTAAAAATGTTTAGACTGG
82 TTCAAAGCTTAATTGCTGAATAT
83 CGGTATATTACAGGTAGAAAGA
84 CGCGAGGCTCAACAATAGATAAG
85 TATTATGCTCATTCAGTGAATA
86 ATCCAAATACATTATGACCCTGT
87 CACAAGATTAAGACTCCTTATT
88 TAAGCCCATTTAGCTATATTTTC
89 CTTAGAGCGAACCAGACCGGAAGCGCAAAAGA
90 TCATTTTTACCGGAATCATAATTAATCAACAT
91 ACGGGTATTAGTATCATATGCGTTATTCGCGTCTGGCCTTTGGTGCCG
92 ATAATCGGGTATAAAGCCAACGCTTTTTTTAACCAATAGGTTATCATC
93 ATCCTAATTTGAGAATCGCCATATTTAACA
94 CTGAACAAGAAAAATAGCAAATCAGATATAGTAGGAATA
95 CCTGTTTAGTTTTAGCGAACCTCCACGTTAAT
96 GCTAATGCCATTTTCGAGCCAGTATATTTAAATTGTAAACTCCTGATT
97 TGTCCAGATACCGACAAAAGGTAAAGCCCCAAAAACAGGAGGAAGGGT
98 TCATATATAAGATTCAAAAGGGTGCAATCATATGTACCCCTTGCACGT
99 TTTCAACGGTCAAATCACCATCAATATGAT
100 TACTTTTGCGGGAGATTTGCCAGTTACAAAAGAAACACC
101 TACCAAAAAAGAAACGATTTTTTGATATTCAT
102 AAAGCTAAATGCCGGAGAGGGTAGTCATTGCCTGAGAGTCCGTCAGAT
103 TAGCAAAAGATAGCTTAGATTAAGTCCTTGAAAACATAGCACATCGGG
104 ATCCAATAATAGTGAATTTATCAAAATCGTCGCTATTAATTTGCTTTG
105 GCATCAATGACTACCTTTTTAACCTCCGGC

106 TTGGGGCGCGAGCTGTGAGCGCTAATATCAGAACGTAGA
107 ATAACCTGATAATAAGAGCAAGAAATAATAAC
108 ATTTCGCAAAATGCTGATGCAAATTTACCTTTTTAATGGTTCAATTA
109 GAACGAGTGAACGCGAGAAAACTTAAAATTAATTACATTTCAAACATC
110 CATTCCATGTTAATTTCATCTTCTACCGTAATGGGATAGGTGCATCTG
111 ATATGCAATTTGAAATACCGACCGTGTGAT
112 TGCTGTAGCTCAACAGAAGCCCGAAAGACTTCGGAATCG
113 AAGGCGTTAAATAAGAATAAACGCGGATGG
114 AGCCTGTTTTAATTGCTCCTTTTGGGATTAGAGAGTACCTGACGATAA
115 TCTTACCACTGTCTTTCCTTATCACTCATCGAGAACAAGCAGCAACAC
116 GGGCTTAATTACGAGCATGTAGAACATCGTAGGAATCATTTAACGCCA
117 CAACATGTAATTTAGGCAGAGGAGAACGCG
118 ATATAAAGCGACGACAATAAACAATTGAAGCCTTAAATCATATACCAG
119 TGTAGGTATTTAAATGCAATGCCTTGCACCCAGCTACAATATTACCTT
120 CGGAGACACAAGGATAAAAATTTTCCAACGCTAACGAGCGAGATGGTT
121 AACCGTTCTAGCTGATAAATTAATCGGTTG
122 GAGAGATCTTAAGCAATAAAGCCTAAAATAGCAGCCTTTACCTTCATC
123 AAGAGTCAAATCATACAGGCAAGGAAAACAGGGAAGCGCACGGTGTAC
124 GTCTGAGATCTACTAATAGTAGTAACTGAACACCCTGAACATATAAAA
125 GTTGGGTTATATAACTATATGTAATGGTCA
126 AAGACAAAAGATTTAGTTTGACCAAGCTATCTTACCGAAGCAAAGTTA
127 ATATTTTAATAACAGTTGATTCCCATCAGGTCTTTACCCTTGACCATA
128 TTTAATGGCTAAAGTACGGTGTCTAGCAAAGCGGATTGCATCAAATGC
129 TAAATGTGTCGCACTCCAGCCAGCCGCTATTACGCCAGC
130 AATTCGCATTAAATTTCAATTC
131 ATCGATGAACGGTAATAGATTT
132 AATATATGTGAGTGAAGAGGCG
133 TCGGATTCTCCGTGGGATCGGC
134 GGAAGAAGCGAGTAACAACCCG
135 GAAACCAGCTGTTGGGAAGGGCGATAACAACTAATAGATTAGGCGAAA
136 ATATTCCTACCAGAAGGAGCGGAAAATACATTTGAGGATTTAGAAG
137 GATGATGGTTGTTAAATCAGCTCACAACAGTA
138 ATATAAGTTAATATTTTGTTAA
139 GTTTGGATGTAACATTATCATTT
140 TAGAACCTTTGCCCGAACGTTATTACTCGTATTAAATCCTATTGCCCT
141 AAAACAGAACGAGCCGGAAGCATACTAACTCACATTAATTGCGTTG
142 AATTGCGTCGTAAAACTAGCATGTAGAAAGGC
143 GTTTAATGGAGCAAACAAGAGA
144 GAATATACAATTGTTATCCGCTC
145 AGAAACAACGTAATCATGGTCATAAAACCTGTCGTGCCAGAGGCGGTT
146 AATACCAATCTAGAGGATCCCCGGAAATGAAAAATCTAAAGCATCA
147 ATCGCGCATAACCTTGCTTCTGTAAATCATAG
148 ATTCATAAACAGTACATAAATC

149 CCTGAGCACCAGTGCCAAGCTTG
150 AAGAAAACGTTTTCCCAGTCACGACTCAATCAATATCTGGTCAGTAT
151 CCAGTTTGGCTGCAAGGCGATTAACAGTTGAAAGGAATTGAGGAAG
152 ACGACAGTAACAAACGGCGGATTGGACCTAAA
153 GGCCTCTTTTTCCGGCACCGCTTCCCTGTAGCCAGCTTTCCTAGAAAA
154 CTGCGCAAGCAAAGCGCCATTCGCAACGCCATCAAAAATAATACAAAT
155 CGGAACAAAGAAACCGATTATCA
156 AAGTTTGATATACTTCTGAATAATAGATTGTATAAGCAAAATAAGAGA
157 AGCCTGGGACCATATCAAAATTATGGTTGATAATCAGAAAGAGTAATG
158 AATTCCACACAACATAATAAAGA
159 CTGTGTGAAGTAACAGTACCTTTTTACAAAGGCTATCAGGCTATTTTT
160 CTCGAATTTAACGGATTCGCCTGATAATTTTCCCTTAGAAACGCTGAG
161 TGCCTGCAGGTCGACGTTACAAA
162 AACGACGGAAAGAAGATGATGAAAAACAATTTCATTTGAACCAATCGC
163 ACGCCAGGGGGCGCATCGTAACCGTCACGTTGGTGTAGATTTTCAAAT
164 GCGAAAGGGGGATGTAGGGGACG
165 TCTAAAATATCTTTAGGAGCACTCGGTGCG
166 AGACTTTACAAACAATTCGACAAATTTTAA
167 CACTGCCCGCTTTCCAGTCGGGGCTGTTTC
168 GCTGAACCTCAAATATCAAACCCGTTGTAA
169 ATCCTGTTGGAACAAGAGTCCACTATTAAAGA
170 GCAGCAAGCGGTCCACTCCAAC
171 TCACCGCCGAAAAACCGTCTATCAGCTATTAGTCTTTAATAGACGGGCA
172 ACAGCTGGTGCCTAATGAGTGAGAAGTGTAA
173 TTTCTTTTCACCAGTGGCGCGA
174 TGCGTATTCTAAAACATCGCCATTAAAAATAC
175 GCTGAGAGCCAGCAGCCCACCA
176 TAACACCGAAACAGAGGTGAGGCGGCCCGAGA
177 ATCGGCAAAATCCCTTAGTGTT
178 CAGTTTTGATGGTGGTTCCGAA
179 ACGTGGACGCTGGTTTGCCCCAGCAGAGCCGTCAATAGATCATTCAGG
180 AAGGGCTGGCCCTGAGAGAGTT
181 ATAGCCGGGCGCCAGGGTGGTT
182 CGAACGAAGCCAACGCGCGGGGAGCTGCATTAATGAATCGGTACCGAG
183 AAGATACCTGCAACAGTGCCAC
184 TAGGGTTGATAAATCAAAAGAATATCAGTTGGCAAATCAAGTTGGGTA

Table S6. Square origami modified staples and bridges that hybridize with ΦX 174 scaffolds to make 3 by 3 super-structures

Modified staples for each triangle origami

21101;ATCGGCATTTTCGGTCATAGCCAGCCACCACCCTCATTCTTCGGCG
21102;AATCTTTTGAACCGCCACCCTCAGCCCTTATT

21105;AAACCAAAGAGCCACCACCGGAACCCGTACTCAGGAGGTTGGCAGATT
21106;TTAAATTTCGGAATAGGTGTATCACGCCTCCC
21109;AAAGGAATCACCCTCAGAGCCGCCAGTACCAGGCGGATAAACTGGAAA
21110;GGTGGCGATAGCGGGGTTTTGCTCACCAGAAC

21201;GATTGGCCTTGATATTCACAAACCCCTGCCTATTTCGGGGGAAGCC
21202;GCAGGAGATATAAACAGTTAATGCCAAATAAA
21205;TCAGGACGTACCGTTCCAGTAAGCACTGGTAATAAGTTTTCCTCAGCA
21206;ACGAATCAGATGATACAGGAGTGTGTCATACAT
21209;TAATTTCAACACTAAAACACTCATTGAGGAAGTTTCCATTACGCGGCG
21210;AACAGGGTACTAAAGACTTTTTCACTTTGACC

21301;TCGCCTGATAAATTGTGTCGAACCGCTTTTGCGGGATCGAATCTCT
21302;GAAAACGATGCAGGGAGTTAAAGGATCCGCGA
21305;AAGAGTAACAATCATAAGGGAACCACAACAACCATCGCCCAGGAACAA
21306;ATGTTTATAGTTGCGCCGACAATGGAACTGAC
21309;GAAACGCAATCAATAGAAAATTCATTATCAGCTTGCTTTCAACGACGT
21310;ACATCATACTTTAATTGTATCGGTTATGGTTT

31101;ATCGGCATTTTCGGTCATAGCCAGCCACCACCCTCATTACGCTGCA
31102;TTGGTCAGGAACCGCCACCCTCAGCCCTTATT
31105;AAACCAAAGAGCCACCACCGGAACCCGTACTCAGGAGGTTATAATGTC
31106;GTCGTCATCGGAATAGGTGTATCACGCCTCCC
31109;AAAGGAATCACCCTCAGAGCCGCCAGTACCAGGCGGATAAGAGCAGTC
31110;GGCAGCAATAGCGGGGTTTTGCTCACCAGAAC

31201;GATTGGCCTTGATATTCACAAACCCCTGCCTATTTCGGTCGGTACG
31202;GCTTTAAATATAAACAGTTAATGCCAAATAAA
31205;TCAGGACGTACCGTTCCAGTAAGCACTGGTAATAAGTTTTACAAATGC
31206;TATCAGGGGATGATACAGGAGTGTGTCATACAT
31209;TAATTTCAACACTAAAACACTCATTGAGGAAGTTTCCATTATAACCAG
31210;GAGAGGAGACTAAAGACTTTTTCACTTTGACC

32401;GTAAATATTGACGGAAATTATTTAGAAAGGAACAACTATAGCAAGG
32402;AAAGACGGTTCAGCGGAGTGAGAACATTAAAG
32405;CCAGAAGGAGAGCCAGCAAAATCAAGTAAATGAATTTTCTGCCAGCGA
32406;AATGGTAACGTCTTTCCAGACGTTCCAGTAGC
32409;TTTAAACACCATCGATAGCAGCACCATTCCACAGACAGCCAGATGGGA
32410;CGCTCGGCACTACAACGCCTGTAGCGTAATCA

32101;ATCGGCATTTTCGGTCATAGCCAGCCACCACCCTCATTCCCCTGCA
32102;ACCTACATGAACCGCCACCCTCAGCCCTTATT
32105;AAACCAAAGAGCCACCACCGGAACCCGTACTCAGGAGGTTGTACCTCG
32106;CCAGGGCGCGGAATAGGTGTATCACGCCTCCC
32109;AAAGGAATCACCCTCAGAGCCGCCAGTACCAGGCGGATAACATCACTC
32110;TTGACGCATAGCGGGGTTTTGCTCACCAGAAC

32201;GATTGGCCTTGATATTCACAAACCCCTGCCTATTTCGGGCAAGGTA
32202;CGGCTTTATATAAACAGTTAATGCCAAATAAA
32205;TCAGGACGTACCGTTCCAGTAAGCACTGGTAATAAGTTTTCGTAAATT
32206;GAGACAGGGATGATACAGGAGTGTGTCATACAT
32209;TAATTTCAACACTAAAACACTCATTGAGGAAGTTTCCATTGCAATGAC
32210;ACAGGAGCACTAAAGACTTTTTCACTTTGACC

33401;GTAAATATTGACGGAAATTATTTAGAAAGGAACAACTAGTTACTCG
33402;ATCTTCGGTTCAGCGGAGTGAGAACATTAAAG
33405;CCAGAAGGAGAGCCAGCAAAATCAAGTAAATGAATTTTCTTTAATAGA
33406;AAACGTACCGTCTTTCCAGACGTTCCAGTAGC
33409;TTTAAACACCATCGATAGCAGCACCATTCCACAGACAGCCACCTATTA
33410;GGACTCAGACTACAACGCCTGTAGCGTAATCA

33101;ATCGGCATTTTCGGTCATAGCCAGCCACCACCCTCATTGAACAAAA
33102;ACCAGTCCGAACCGCCACCCTCAGCCCTTATT
33105;AAACCAAAGAGCCACCACCGGAACCCGTACTCAGGAGGTTCTCCTCAT
33106;TGACAGAACGGAATAGGTGTATCACGCCTCCC
33109;AAAGGAATCACCCTCAGAGCCGCCAGTACCAGGCGGATAAGAGCTTCT
33110;AGGTCGAATAGCGGGGTTTTGCTCACCAGAAC

23301;TCGCCTGATAAATTGTGTCGAACCGCTTTTGCGGGATCATATCCGA
23302;GTCATGGATGCAGGGAGTTAAAGGATCCGCGA
23305;AAGAGTAACAATCATAAGGGAACCACAACAACCATCGCCCTCATTTTT
23306;ATTTGAGCAGTTGCGCCGACAATGGAACTGAC
23309;GAAACGCAATCAATAGAAAATTCATTATCAGCTTGCTTTCGTCGGCTA
23310;CCTCAATCCTTTAATTGTATCGGTTATGGTTT

23401;GTAAATATTGACGGAAATTATTTAGAAAGGAACAACTACGTCGTAA
23402;GGATTAAGTTCAGCGGAGTGAGAACATTAAAG
23405;CCAGAAGGAGAGCCAGCAAAATCAAGTAAATGAATTTTCTTTTCATCC
23406;TCTGATTCCGTCTTTCCAGACGTTCCAGTAGC
23409;TTTAAACACCATCGATAGCAGCACCATTCCACAGACAGCCGTTTTTAG
23410;TTAGCTCCACTACAACGCCTGTAGCGTAATCA

23101;ATCGGCATTTTCGGTCATAGCCAGCCACCACCCTCATTAGCCACAT
23102;ATAACTGGGAACCGCCACCCTCAGCCCTTATT
23105;AAACCAAAGAGCCACCACCGGAACCCGTACTCAGGAGGTTGGCCACAA
23106;AAAGCGTCCGGAATAGGTGTATCACGCCTCCC
23109;AAAGGAATCACCCTCAGAGCCGCCAGTACCAGGCGGATAAAACCATAA
23110;AGCTATTTTAGCGGGGTTTTGCTCACCAGAAC

13301;TCGCCTGATAAATTGTGTCGAACCGCTTTTGCGGGATCCCATTAGC
13302;ACACAAAATGCAGGGAGTTAAAGGATCCGCGA
13305;AAGAGTAACAATCATAAGGGAACCACAACAACCATCGCCCCCTTGCGA

13306;CCATACGAAGTTGCGCCGACAATGGAACTGAC
13309;GAAACGCAATCAATAGAAAATTCATTATCAGCTTGCTTTCGGGATTAT
13310;TCGGTCGTCTTTAATTGTATCGGTTATGGTTT

13401;GTAAATATTGACGGAAATTATTTAGAAAGGAACAACTACCTGTCGC
13402;GCTGAATATTCAGCGGAGTGAGAACATTAAAG
13405;CCAGAAGGAGAGCCAGCAAAATCAAGTAAATGAATTTTCTCTCCAGCA
13406;CTTAATACCGTCTTTCCAGACGTTCCAGTAGC
13409;TTTAAACACCATCGATAGCAGCACCATTCCACAGACAGCCATATCCTT
13410;GCCAGCTTACTACAACGCCTGTAGCGTAATCA

12201;GATTGGCCTTGATATTCACAAACCCCTGCCTATTTCGGGAGCACAT
12202;TTCATCCATATAAACAGTTAATGCCAAATAAA
12205;TCAGGACGTACCGTTCCAGTAAGCACTGGTAATAAGTTTTCGAACGTC
12206;CCGTCAACGATGATACAGGAGTGTGTCATACAT
12209;TAATTTCAACACTAAAACACTCATTGAGGAAGTTTCCATTGCATACGA
12210;CCAAGAGCACTAAAGACTTTTTCACTTTGACC

12301;TCGCCTGATAAATTGTGTCGAACCGCTTTTGCGGGATCGAAAGAGT
12302;TCAATAGCTGCAGGGAGTTAAAGGATCCGCGA
12305;AAGAGTAACAATCATAAGGGAACCACAACAACCATCGCCCAATAATCA
12306;GGTAATAAAGTTGCGCCGACAATGGAACTGAC
12309;GAAACGCAATCAATAGAAAATTCATTATCAGCTTGCTTTCTCATCAGG
12310;CCTTGAATCTTTAATTGTATCGGTTATGGTTT

22101;ATCGGCATTTTCGGTCATAGCCAGCCACCACCCTCATTACTTGCCA
22102;CAAGCAACGAACCGCCACCCTCAGCCCTTATT
22105;AAACCAAAGAGCCACCACCGGAACCCGTACTCAGGAGGTTCGTACCTT
22106;AGCTTTAGCGGAATAGGTGTATCACGCCTCCC
22109;AAAGGAATCACCCTCAGAGCCGCCAGTACCAGGCGGATAAAGGCATGA
22110;GGGTGTCATAGCGGGGTTTTGCTCACCAGAAC

22201;GATTGGCCTTGATATTCACAAACCCCTGCCTATTTCGGTACCGTCT
22202;AAGTATCGTATAAACAGTTAATGCCAAATAAA
22205;TCAGGACGTACCGTTCCAGTAAGCACTGGTAATAAGTTTTAACCACAC
22206;GACGACATGATGATACAGGAGTGTGTCATACAT
22209;TAATTTCAACACTAAAACACTCATTGAGGAAGTTTCCATTGAAGAGCC
22210;GTTTGCTGACTAAAGACTTTTTCACTTTGACC

22301;TCGCCTGATAAATTGTGTCGAACCGCTTTTGCGGGATCTTGGTCAT
22302;AGCCGTTTTGCAGGGAGTTAAAGGATCCGCGA
22305;AAGAGTAACAATCATAAGGGAACCACAACAACCATCGCCCGAAACCTG
22306;TTGGTGTTAGTTGCGCCGACAATGGAACTGAC
22309;GAAACGCAATCAATAGAAAATTCATTATCAGCTTGCTTTCCCTTCTGT
22310;CATTTTGTCTTTAATTGTATCGGTTATGGTTT

22401;GTAAATATTGACGGAAATTATTTAGAAAGGAACAACTACCAGCAAT
22402;TTTTGCATTTCAGCGGAGTGAGAACATTAAAG
22405;CCAGAAGGAGAGCCAGCAAAATCAAGTAAATGAATTTTCTTTTTAGTA
22406;CAAATCCGCGTCTTTCCAGACGTTCCAGTAGC
22409;TTTAAACACCATCGATAGCAGCACCATTCCACAGACAGCCACCAGCAC
22410;CTCAGGAAACTACAACGCCTGTAGCGTAATCA

12401;GTAAATATTGACGGAAATTATTTAGAAAGGAACAACTAAGCAAGCA
12402;ACCGGAGGTTCAGCGGAGTGAGAACATTAAAG
12405;CCAGAAGGAGAGCCAGCAAAATCAAGTAAATGAATTTTCTATGGCGCC
12406;GCAATACCCGTCTTTCCAGACGTTCCAGTAGC
12409;TTTAAACACCATCGATAGCAGCACCATTCCACAGACAGCCCTTAAGTG
12410;CTCTTTAAACTACAACGCCTGTAGCGTAATCA

11201;GATTGGCCTTGATATTCACAAACCCCTGCCTATTTCGGGAAGGACG
11202;CCTTGACGTATAAACAGTTAATGCCAAATAAA
11205;TCAGGACGTACCGTTCCAGTAAGCACTGGTAATAAGTTTTAGGATAAA
11206;GAGGGTAGGATGATACAGGAGTGTGTCATACAT
11209;TAATTTCAACACTAAAACACTCATTGAGGAAGTTTCCATTCAGGCAAA
11210;TCAAAAGCACTAAAGACTTTTTCACTTTGACC

11301;TCGCCTGATAAATTGTGTCGAACCGCTTTTGCGGGATCATCCATCT
11302;ACCACCATTGCAGGGAGTTAAAGGATCCGCGA
11305;AAGAGTAACAATCATAAGGGAACCACAACAACCATCGCCCAACGTTGA
11306;GTCTGTAAAGTTGCGCCGACAATGGAACTGAC
11309;GAAACGCAATCAATAGAAAATTCATTATCAGCTTGCTTTCTGAGAACC
11310;AGTTTGAACTTTAATTGTATCGGTTATGGTTT

Bridges
2101;CCCCTCAGCGGCAAAAAAACCTACCGCGCTTC
2102;TAAGCAGAATTAAAATTTTTACCG
2103;TTATAACCAAGTCTGAAACATGATTAAACTCC
2104;TTATGGCGAGAAATAATCACACTC
2105;ATCACGAAGTCATGATAGAAAAAA
2106;AGCTTATCTGAATCGCGAGTGGTC
2107;GCGATAAAGCTGGAGTAACAGAAG
2108;AACAGGTGCCGAAGAACGGTCACA
2109;AACCTGACTATTCCACCTTTAGGT
2110;CGATGTAGTGCAACAACTGAACGG
2111;CACTGGTCCAAACTATCAAAATAT
2112;TACCAGCATTAACCGTATAATCAT
2113;ATAAGTACGCGTTCTTTGAAGAAA
2114;GAATGCAAGCAAATCACCAGAAGG

3101;TTCAAGAAATCACGAGTATCCTTT
3102;ATGCAGCAGCAAGATAGGTGATAA

3103;AACATACGAAGGCGCAGCATTAAG
3104;GCTCCCAATAACGATACCACTGAC
3105;ATCTTAAACAGAGGAAGCATCAGC
3106;GCGTCAACCATACCAGCTTCTTAG
3107;CCAGAACGGAAAACATTTGATTCT
3108;AGCTCTTTCCTTCATAGAAATTTC
3109;GCAAGTTGTGATTGTCCAGTTGCA
3110;CTCGGCAATCTCTTTCCCATACAA
3111;CGCCAGCAATATCGGTGAGTCTCA
3112;CTCTTTTTATAAGTCAAAGCACCT

4101;TTACCTCCAAATGAAGAGCGTCATAAGAGGTT
4102;CGGTTGTCAAATAACATCATGGTA
4103;TGAAGTAATTAGAGCGCATGACAAGTAAAGGA
4104;GCCAGATGCCCAGAGATCACGTTC
4105;TATGCAAATTAGCATATTCCATCA
4106;TTGGTCAGAGCAGCTTGCAGACCC
4107;AATAGATGACCAGAAAACTGGCCT
4108;AGGTCTGTTGAACACGTGGTAGAA
4109;TTGGCGAGAAAGCTCAGGCACAGA
4110;AGAAACGCGTCTCAGGAGGAAGCG
4111;CAAATGTTACATAGTGCCATGCTC
4112;ACAAGCGCAAGAGTAATTTGAGAT
4113;CGGAAACCATAACGAGAGTAGGCG
4114;TTAGTCGCCATCATCTTGATTAAG

5101;GTCAGGCAGACATAATTTATCCTC
5102;GCCAGTTTGAATATTATCCACGGC
5103;ATAGTTGTTATAGATAGCGGCATA
5104;AAGGTCATTTCAAATAACCCTGAA
5105;TTAGGGATACCAGCAAGGAAGCCA
5106;TAAGACGACCAATCTGTTTATTGG
5107;TTAATCGTGCCAAGAAGTAGTTGA
5108;TAACCGGAAAGCGGCATGGTCAAT
5109;TAGTGTTACCATCTCGAAGGAGTC
5110;AGAGCGCCAACGGCGTACAGTCGG
5111;TGGCATTAACACCATCCAATGGAG
5112;CCACGACGCTTCATGAACTTAATCCACTGTTC
5113;ACCATAAATCTACAGTAGAGTCAA
5114;ATAAAAAGTAAAAATGCGTGACGATGAGGGAC

4201;ATTAAAATTCGTATTCTGGCGTGA
4202;GCATATACCTGGTCTTTGTTGACC
4203;ACCAAAGACGAGCGCCAAGCATCT
4204;TGATAAGCTTTACGCTTGCCTTTA
4205;CAACGGCTACGCGAGCAGTAGACT

4206;TTCCATAATAGACGCAGCGGACGA
4207;AGCGCCAGAACGTTTTTGGAAAGA
4208;CTGTTGCTTTACCTTTAGACATTA
4209;CTTCCGCATTGGCGCATAATCTCG
4210;GAGCTTGAGTAAGCATCGTAATTT
4211;CGTTTTCTTCTGCGTCTACTGACC
4212;TGGTAAAAAGTAAGAACGTCAGTG

5201;AACGCGAATTTTAAAATGTCAACA
5202;ATAGTAATCCACGCTCCAATTCAG
5203;ACCGGACGCTCGACGCACAGCATC
5204;GTGGTTGACATTAATAATGTTTTC
5205;CAGCGCCTTGACTCATGATTTCTT
5206;GGATTGTTCAGTAACTTCCATGAT
5207;CCGTTTGAATGTTGACCGGTCTGG
5208;GGCCAAAGGGGATGAACATAATAA
5209;GGCAGCAAAGAAGCCTGAATGAGC
5210;TTAAATCCAAAACGGCTAAACTCA
5211;AGGAAAGCGAGGGTATTCGAAATC
5212;TCAGAAAACCCACAAAGTCCAGCGTACCATAA
5213;ACGCAAGCTAGCAATCCAAACTTT
5214;GCACGAGAGCGGTCAGCTCAACGCAGCGACGA

4301;TGTGACTCGTTCTGCTTCAATATC
4302;TCATCTCTCTTTTTGCATATCTAA
4303;TTGACGAACGTGCCAATTTCCCAG
4304;CAGTAACTGCATATTAAGCCACTT
4305;CCAACGCGGTTGCGCCGCCAAAAC
4306;AGATTTGTCGTCACAGTCAGTTTT
4307;TCGTTAGTTGATGGCGGCGCATAA
4308;ATCGAAGCAAAGGTCGCAAAGTAA
4309;CGAGCTGCAGGTTGGATACGCCAA
4310;AGCGATAAAACTCTGCGCAAGGAT
4311;TTTTCTCATTTTCCGCACTTCTGC
4312;AAGTGTTACAGCAGTCCACTTCGATTTAATTC
4313;GTAAACAATTTCGACTCATCAGAA
4314;CTTTATCAAGATAATTGCAGTAGTAATTCCTG

3201;TTCCAGAAAGGTCCATATCTGACT
3202;TAGACCTTTAGCAGCAATTGTTCC
3203;GCAACAGCTTTATCAATCCATTCT
3204;TGAGTTGTTACCATGAAAAATATC
3205;CAGAAGCAAAGTAGCGACAGCTTG
3206;TGAACAGCTTCTTGGGGCATCAGT
3207;TAGAAATATCCTTTGCCGGCTCAT
3208;CGAAGTTGAGTAGCGCCAATATGA

3209;ATACCGCTTTGTCATTGTGAGCAT
3210;CACTCCGTGGACAGATGATTCTGC
3211;ATGAACTAAGTCAACCGGTAAGTT
3112;CCCAGCTTTCAGCACTAACCTTGC

2301;AGAAACCAGTCAAAAACGATAAAC
2302;CAGCCAACGTGAGAGTACAGCCAT
2303;TAGCTTTAAGCGGCTCGCCTCTAA
2304;CATAAAACACCTTTAGCATCAACA
2305;CCAACCAGAGTCACGCAAAGCATT
2306;CCAATATCACGAAAATAACGTGAA
2307;CTGCGTGTAGCGAACTAGCAAGAA
2308;CCCTCGGCGCGATGGGCATACTGT
2309;GGCCACGTGCGTGTGAATCATTAG
2310;ATACTGATAGCAGTCGATTTTGCA
2311;AACTGGCGGCGATTGCACTCAGGC
2312;TGTACCATGTACCCGACGACCAAAATTAGGGT
2313;CAACGCTAATGGAAATGAAGACGG
2314;GCATAAAGTGCACCGCCCTGTAGGAAGTGTCC

1201;TGGTCTATAGTGTTATGTCCCCTTCGGGGCGG
1202;CATTTTTCTAATATCAAGTTGGGG
1203;TGTAGCATACCGTCTTCTCGTTCTCTAAAAAC
1204;GCGGCAAAACTGCGTATGTGCCAA
1205;TTAACTTCTCAGTAACGTTCAGCA
1206;AAGAGGGCAGATACAAACTCATCA
1207;AGAAGCAGATTATACTCATCGCGA
1208;CTTTCTTTTTGGGGTACCTTATGG
1209;ATACATATCACCATTACACTCATC
1210;ATCTTGAATCGAACTCAACGCCCT
1211;AAAGACAGATTTCATAGTGGAGGC
1212;GCAAAGCCTCTACGCGAATCTCTT
1213;TTGATGCGGTTATCCACATCAAAC
1214;ATTGCATTTCTGCTTATGGAAGCC

2207;GAACGAACCATAAAAATTCAGAAG
2208;GCGTGACAAGCCTCCAAGATTTGG
2209;AAACATACATACGCTCAAAGTCAA
2210;AGGTTTAAGAGCCTCGAATTGGGA
2211;ATCCTGACGGTTATTTCACAAGCC
2212;AGAAATGCCCTAGACAAATTAGAG

2201;CCAAGTCCGCATCACCCATGCCTA
2202;GGCAGATTTAATACCAAACCAAAT
2203;TTATCAGAAACGGCAGCATTAGAG
2204;GTTAGGAAAAGTGCCAGCCTGCAA

2205;CAAGAAGTAAAACTAGGGGCGGCC
2206;CCATAGCACCAGAAACCCTTTACC

1101;ACCAACATAAACGTTATAGACCAAACCATGAA
1102;GGTAAAGTTTGCCCGGCGTACGGG
1103;TCAATAGTAACCAATCCGCGGCATTTAGTAGC
1104;TAACCTGATTCAGCGACACACAGT
1105;GTATAATAACCACCATCAAATAAT
1106;GCTGGAGACATGGCGACCATTCAA
1107;CATCATAGAACATAAATCACCTCA
1108;GCCAGCAATAGCACCAGCAGTCGG
1109;TCGGAACCGAAGAAGAGAGCAGAA
1110;ACCAGCAACTCAAAGCGAACCAAA
1111;AAATTTAGTCCAAACAATTTAGAC
1112;CGGCTTTTTGACCGCCGGTCGGCA
1113;AATATCAGCACCAACATGAATGCC
1114;CATCACCTGAAACAACCTGATTAG

Table S7. Unmodified hexagonal DNA origami staples

1	TGATGATACAGGAGT
2	TTACCGTTCCAGTAAGCACCATTA
3	TAAAGCCAGAATGGAACCAATGAA
4	GCCTTGATATTCACAAAGTAGCGA
5	TTGACAGGAGGTTGAGCAGACTGT
6	GAGCCGCCGCCAGCA
7	AATTAGAGCCAGCAAAATCACCAGTAGCGTCATACATGGCTTT
8	ATCTTGACAAGGCCGGAAACGTCAAGCGCAGTCTCTGAAT
9	GCGCATAGTAGCAGCACCGTAATCACAAATAAATCCTCAT
10	GAAAGAGGAGTTTGCCTTTAGCGTGCAGGTCAGACGATTG
11	AAAGCTAAAATAAGAGAATATAAACCAACTTT
12	CACCAGAACCACCAC
13	GCCACCCTCAGAGCCAGCCATCTT
14	CCGCCTCCCTCAGAGCAGAGCCAC
15	CACGCATAACCGATATGCCGCTTT
16	TAGTTGCGCCGACAATGAAAGACA
17	ACAGCTTGATACCGA
18	TCGGTCATAGCCCCCTTATTAGCGTTTCCACCCTCAGAGCCGC
19	AATCCGCGCAAAATCACCGGAACCCGCCACCCTCAGAACC
20	GATTTGTATTGCAGGGAGTTAAAGATTCGGTCGCTGAGGC
21	ATTATACCCGTCACCCTCAGCAGCGACAACAACCATCGCC
22	CGAGGTGAATTTCTT
23	CCTTTAATTGTATCGGACTTTTTC
24	GAAAATCTCCAAAAAATCAAAAAT
25	AAAGGAATTGCGAATAAATAACAT

26 TTTCAGCGGAGTGAGAGGAGAATT
27 AACAACTTTCAACAG
28 CGGCTACAGAGGCTTTGAGGACTAAAGTTTATCAGCTTGCTTT
29 GTAATGCCGTTTCCATTAAACGGGAAGGCTCCAAAAGGAG
30 TAAGAAACCAGCCTTTACAGAGAGATAATTTTTTCACGTT
31 ATAAACAGGGAAGCGCATTAGACGATAGAAAGGAACAACT
32 TGTATGGGATTTTGC
33 TCGTCTTTCCAGACGTGAGAGATA
34 CCTCATAGTTAGCGTAAATAATAA
35 AACTACAACGCCTGTATAGCTATC
36 GTACCGTAACACTGAGGTAAGCAG
37 CCAATAGGAACCCAT
38 TCAGAGGGTAATTGAGCGCTAATATCATAGTAAATGAATTTTC
39 TTGCACCCGAATTGAGTTAAGCCCACGATCTAAAGTTTTG
40 GCAAAAGAAACAATGAAATAGCAAGCATTCCACAGACAGC
41 GACGATAAGCCCTTTTTAAGAAAATTTCGTCACCAGTACA
42 TTTCAGGGATAGCAA
43 AGAACCGCCACCCTCACGGAATAC
44 TTAGTACCGCCACCCTCTCCTTAT
45 CCGGAATAGGTGTATCAAAATACA
46 AGTGCCGTCGAGAGGGAGAAACGC
47 AGTACCAGGCGGATA
48 AAGGAAACCGAGGAAACGCAATAATAAGAGCCACCACCCTCAT
49 AACTAATGACTGGCATGATTAAGACAGAACCGCCACCCTC
50 TTCATCAGATGTTAGCAAACGTAGACCGTACTCAGGAGGT
51 CTAACGGAGGTGGCAACATATAAATTGATATAAGTATAGC
52 TTAGCGGGGTTTTGC
53 GAGGCTGAGACTCCTCATATGGTT
54 GAACCTATTATTCTGAGACATTCA
55 GTATAAACAGTTAATGTATTGACG
56 TAACGGGGTCAGTGCCATCACCGT
57 ACTGGTAATAAGTTT
58 TATTTTGTCACAATCAATAGAAAATTCAAGAGAAGGATTAGGA
59 ACCGATTGTAATTTCAACTTTAATAATAAGGCGTTAAATAGACGCTGA
60 ATTACCTTCCAAAGACAAAAGGGCAACATGAAAGTATTAA
61 AGATGGTTAGGGAGGGAAGGTAAACCCCCTGCCTATTTCG
62 GAAACACCTCATTAAAGGTGAATTTTGAGTAACAGTGCCC
63 CCATTAGCAAGAACCGGATATTCATCAACAGTAGGGCTTACAAGGATA
64 ACCATCGAGCTGGCTGACCTTCATTTTAACAACGCCAACAATACTTTT
65 CAGAATCAACAGATGAACGGTGTAGCATTTTCGAGCCAGTATCGGTTG
66 AGCGCGTTTTCATCGGCAT
67 CAATCATAAGGGAACCGAACTGAGTACCGACAAAAGGTAAAG
68 ACCAGTATAAAGCCAACGCTTACCCAAATCAACGTAACAAAGC

69 AAAATTTTTAGAACCCTCATATA
70 GCGGGAGATGAGAGTCTGGAGCAATAGCATGTCAATCATACGCTGAGA
71 TACCAAAAAATTCGACAACTCGTAATTAGACTTTACAAACAGCATCAC
72 TAAGCAATAAAGCCTCAGAGCAT
73 TAGCTATTTTTGAGAGATC
74 TACAAAGGATCAGAAAAGCCCCAAAAACAGG
75 TCATTGCCAGCCTTTATTTCAACGATTGAGAATCGCCATACAAGAGTA
76 ATCGATGAACATTATGACCCTGTATGTAATTTAGGCAGAGCAGACCAG
77 TTTGCCCGAACGTTATTAA
78 AATACATTTGAGGATTTAGAAGTTTAAATCC
79 GGCGGTCAGTATTAACACCGGGCGCCAGGGTGGT
80 GCCAGCAGGCCAACGCGCGGGGAGAGGCGGTT
81 CTTGCTGAAAACCTGTCGTGCCAGCTGCATTA
82 TGCGTATTGCCTGCAACAGTGCCATGTACCCCGGTTGATACTATCAGG
83 ATGAATCGCAAATGAAAAATCTAAACGGTAATCGTAAAACACAAGAGA
84 CGCTTTCCAGTCGGGACCTCAAATATCAAACCCT
85 TTCATAATACCTGCTCCATGTTACAATAAACAACATGTTCAATCATAC
86 CACCGGAATCATCGCCTGATAAATGCCTGTTTATCAACAATCTACTAA
87 TGCGGGATAAGCGCGAAACAAAGTAAGAAAAATAATATCCTTTGGGGC
88 GCATCGGAACGAGGGTAGC
89 ACACTAAAACACTCATCTTTGACCATGTAGAAACCAATCAAT
90 ATTCTGTCCAGACGACGACTTAGCCGGAACGAGGCGCAGACG
91 AGGCAAGGCAAAGAATTAGCAAA
92 TAGTAGTACACCAGAAGGAGCGGATTATCTAAAATATCTTAAGGAATT
93 GCGAGCTGTGATTATCAGATGATGACGCCAGGGTTTTCCCAAGCTTGC
94 TATTTTCACATCCTAATTTACGAGCCCCAGCG
95 ATGGTCAATAACCTGTTTAGCTA
96 TTAAAAGTTTGAGTAACAT
97 TATCATTTTAATAGATTAGAGCCGTCAATAG
98 AAAGAAACGCATTAACATCCAATAAGCTAATGCAGAACGCTGTGTCGA
99 CATATTCCAAAAGGTGGCATCAATTAGATAAGTCCTGAACACAACGGA
100 TCAATATAATCCTGATTGT
101 CTGCAAGGCGATTAAGTTGGGTAGCAATTCA
102 ATCAATATCTGGTCAGTTGGCGTTGCGCTCACTG
103 GAGGAAGGGTGCCTAATGAGTGAGCTAACTCA
104 ATGCCTGCACGAGCCGGAAGCATAAAGTGTAA
105 CATTAATTGCAAATCAACAGTTGATAGGAGCACTAACAACTGCGGAAC
106 AGCCTGGGAACGACGGCCAGTGCCAGTCACGACGTTGTAAATTATCAT
107 AATTCCACACAACATAGGTCGACTCTAGAGGATC
108 ATGAGGAAACTACGAAGGCACCAAATTCCAAGAACGGGTAAGATTTAG
109 GAAAATAGGATTTTTTGTTTAACGACTCATCGAGAACAAGATAACAGT
110 AAAAACAGCCATATTATTTATCCCTCATCGTAGGAATCATCTAAAGTA
111 AACTGAACACCCTGAACAA

112 TCTTTCCAGAGCCTAATTTGCCAAAGCAAATCAGATATAGAA
113 TCGGCTGTCTTTCCTTATCCCTAAAACGAAAGAGGCAAAAGA
114 TTTGACCATTAGATACATTTCGC
115 TGATTCCCCAAAATTATTTGCACGAAGGGCGATCGGTGCGTAGCAATA
116 CGGTGTCTAAATTGCGTAGATTTTCCATTCGCCATTCAGGCTTGCCTG
117 ATATGCAATACCGCGCCCAATAGCGTTACAAA
118 TGCTGTAGCTCAACATGTTTTAA
119 GGATTATACTTCTGAATAA
120 TGGAAGGGCGCCAGCTGGCGAAAGGGGGATG
121 TACCATATAATTCTGCGAACGAGTTTAAACCAAGTACCGCTAAAATAC
122 AAATAAAGGGAAGTTTCATTCCATCAAGCCGTTTTTATTTAATCCAAA
123 ACGTCAGATGAATATACAG
124 GGTGCCGGAAACCAGGCAAAGCGCAGGTTTA
125 CGGGTACCGAGCTCGAATTAATTGTTATCCGCTC
126 TGGTCATAGGCCTCTTCGCTATTATTAGAACC
127 CTTCTTTGCGCAAATTAACCGTTGGCTGTTTCCTGTGTGACGTAATCA
128 AGTAGAAGTGAGGCCACCGAGTAAAAGAGTCT
129 GTCCATCAATTAGTAATAACATCACTGCGCAACTGTTGGGTAAAACAG
130 TGTTTTTATAATCAGAACTCAAACTATCGGCCTT
131 ACCCACAAAGCTACAATTTTATCCACGCGAGGCGTTTTAGGCGGATGG
132 GAGCAAGACTTAAATCAAGATTAGCGGGAGGTTTTGAAGCTTAATTGC
133 TTACCGAAAAACCAAAATAGCGAGGTAATAGTAAAATGTTAAACTCCA
134 ATAGCCGAACAAAGTTACC
135 GCAACACTATCATAACCCTCGTTCAATACTGCGGAATCGTCA
136 CTTATCCGGTATTCTAAGATGAATCTTACCAACGCTAACGAG
137 CTTAGAGCTTAATTGCTGAATAT
138 TCCTTTTGATTGCTTTGAATACCAACGACAGTATCGGCCTGCAACAGG
139 ACAGGTCAAGAGGCGAATTATTCACGTAACCGTGCATCTGATTTTGAC
140 CCGGAAGCTAGACTGGATAGCGTCTACCAGAC
141 TTCGAGCTTCAAAGCGAACCAGA
142 ACAGTACCTTTTACATCGG
143 GAGAAACACAGCCAGCTTTCCGGCACCGCTT
144 TTCGCCTGATAAGAGGTCATTTTTCGAACCTCCCGACTTGTTGCTATT
145 AATCGCGCGGATTAGAGAGTACCTAGTTTTGCCAGAGGGGAGGCTTTT
146 ACCTGAGCAAAAGAAGATG
147 CACGTTGGTGTAGATGGGCGCATTTTCAATT
148 TGGTAATATCCAGAACAATGCCAGAATCCTGAGA
149 CAGCCATTCAGGAAGATCGCACTCATAACGGA
150 AAAAACGCGAAAAACCGTCTATCATAGACAGGAACGGTACATTACCGC
151 GCTCAATCATTAAAGAACGTGGACTCCAACGT
152 CAAAGGGCTCATGGAAATACCTACCCAGTTTGAGGGGACGAGTTACAA
153 GAACAAGAGTCCACTGTCTGAAATGGATTATTTA
154 CCAAAAGACAGATACATAACGCCATCAAATGCTTTAAACAGAAGCCCG

155	TACGCAGTTTGAGATTTAGGAATATGACCATAAATCAAAAAGCAAAGC
156	TACATAAAACAACATTATTACAGGTCCAATCGCAAGACAATAAATGCT
157	AAAGACACCACGGAATAAG
158	TGGGAAGAAAAATCTACGTTAATTTTTCAAATATATTTTAGT
159	AATATTCATTGAATCCCCCAAAGGAATTACGAGGCATAGTAA
160	AAAGACTTCAAATATCGCGTTTT
161	GGATTGCATCATTTGAATTACCTTACAACCCGTCGGATTCAGGGACAT
162	GATGCAAAACATAAATCAATATATCAGCTTTCATCAACATTCTGACCT
163	ACTATATGAGAACGCGAGAAAACTAAAACGAA
164	TCCGGCTTAGGTTGGGTTATATA
165	GAAACAAACATCAAGAAAA
166	CAAAATTAGCGGATTGACCGTAATGGGATAG
167	TAACAATTTCAAAAAGATTAAGAGGTTCAGAAAACGAGAACCACATTC
168	GAAACAGTGACTATTATAGTCAGAATCAGGTCTTTACCCTTAGAAAGA
169	ATAACCTTGCTTCTGTAAA
170	TTCGCGTCTGGCCTTCCTGTAGCGTGAGTGA
171	TTGGCAGATTCACCAGTCAAGTGTTGTTCCAGTT
172	TCTGGCCAATAAATCAAAAGAATAGCCCGAGA
173	GAAAGCGTTGATGGTGGTTCCGAAATCGGCAA
174	TAGGGTTGCACGACCAGTAATAAATCCGTGGGAACAAACGATTACATT
175	AATCCCTTACAGAGATAGAACCCTTAAATGTGAGCGAGTATTTTAATG
176	GGCGAAAATCCTGTTAAGAATACGTGGCACAGAC
177	TACCAGCGATGCGATTTTAAGAACATTTAATGGTTTGAAAAAATCATA
178	GAAATTATAGAACGAGTAGTAAATTCATAATTACTAGAAAAAGATTCA
179	CACCGACTTGAGCCATTTG
180	CTCATTCAGTGAATAAGGCTTGCATATGCGTTATACAAATTC
181	ATTTCATCTTCTGACCTAATGGCTCATTATACCAGTCAGGAC
182	GGTCTGAGAGACTACCTTTTTAA
183	GAAGAGTCCGATAGCTTAGATTAATTAAATTTTTGTTAAACTGATAGC
184	AAAGGGTGTATGATATTCAACCGTTTGTAAACGTTAATATCCGAACGA
185	TGTAGGTAAAGCCTGTTTAGTATCCCTGACGA
186	TTAAATGCAATGCCTGAGTAATG
187	GTCGCTATTAATTAATTTT
188	CCCTTAGACCAATAGGAACGCCATCAAAAAT
189	AAACATAGAATAGTGAATTTATCATACCGACCGTGTGATACATTGTGA
190	ACCATCAAAGAAAGGCCGGAGACAAGAATAAACACCGGAATGGGCTTG
191	ATAAATTAATGCCGGAGAG
192	GATTGTATAAGCAAATATTTAAATCTAGCTG
193	TATTTTTGAATGGCTATTAGCTGGTTTGCCCCAG
194	CCTAAAACTGGCCCTGAGAGAGTTGCAGCAAG
195	ACCACCAGAGACGGGCAACAGCTGATTGCCCT
196	CGGTCCACGTCTTTAATGCGCGAATCAGCTCATTTTTTAAATCCTTGA
197	TCACCGCCATCGCCATTAAAAATATTTGTTAAAATTCGCAGTCAAATC

198 TTCTTTTCACCAGTGCAGAAGATAAAACAGAGGT

S8. Modified staples and bridges for hexagonal origami staple based super-structures.

Modified staples

11302;CGGCTACAGAGGCTTTGAGGACTAAAGTTTATCAGCTTGCTTTGAACCAAA
11303;GGTCGGCACCTTTAATTGTATCGGACTTTTTC
11306;TAAGAAACCAGCCTTTACAGAGAGATAATTTTTTCACGTTCTGATTAG
11307;ATCCATCTAAAGGAATTGCGAATAAATAACAT
11310;AACAACTTTCAACAGTTAACCGT
11402;TCAGAGGGTAATTGAGCGCTAATATCATAGTAAATGAATTTTCATGTAGCT
11403;CAGGTGCCTCGTCTTTCCAGACGTGAGAGATA
11406;GCAAAAGAAACAATGAAATAGCAAGCATTCCACAGACAGCCTTATCAG
11407;ATGGCGAGAACTACAACGCCTGTATAGCTATC
11410;CCAATAGGAACCCATAGCAGAAA

12302;CGGCTACAGAGGCTTTGAGGACTAAAGTTTATCAGCTTGCTTTATAGTGTT
12303;GGGAGCACCCTTTAATTGTATCGGACTTTTTC
12306;TAAGAAACCAGCCTTTACAGAGAGATAATTTTTTCACGTTTCTCAGTA
12307;CACGAACGAAAGGAATTGCGAATAAATAACAT
12310;AACAACTTTCAACAGATCACCAT
12402;TCAGAGGGTAATTGAGCGCTAATATCATAGTAAATGAATTTTCAAAGACAG
12403;TTGATGCGTCGTCTTTCCAGACGTGAGAGATA
12406;GCAAAAGAAACAATGAAATAGCAAGCATTCCACAGACAGCCAGGGTTA
12407;GAATGGCAAACTACAACGCCTGTATAGCTATC
12410;CCAATAGGAACCCATATTGTTAT
12502;AAGGAAACCGAGGAAACGCAATAATAAGAGCCACCACCCTCATCCACCGGA
12503;CCTCCAAAAGAACCGCCACCCTCACGGAATAC
12506;TTCATCAGATGTTAGCAAACGTAGACCGTACTCAGGAGGTAAGCAATA
12507;CAAACATACCGGAATAGGTGTATCAAAATACA
12510;AGTACCAGGCGGATAATCTCTTT
12602;TATTTTGTCACAATCAATAGAAAATTCAAGAGAAGGATTAGGACGCGGCAT
12603;TAGACCAAGAGGCTGAGACTCCTCATATGGTT
12606;AGATGGTTAGGGAGGGAAGGTAAACCCCCTGCCTATTTCGCGTACGGG
12607;CACACAGTGTATAAACAGTTAATGTATTGACG
12610;ACTGGTAATAAGTTTCCATTCAA

13402;TCAGAGGGTAATTGAGCGCTAATATCATAGTAAATGAATTTTCGGTCAACG
13403;TCCGCATATCGTCTTTCCAGACGTGAGAGATA
13406;GCAAAAGAAACAATGAAATAGCAAGCATTCCACAGACAGCAGCTGTAC
13407;AAAATACTAACTACAACGCCTGTATAGCTATC
13410;CCAATAGGAACCCATCGACCCTC
13502;AAGGAAACCGAGGAAACGCAATAATAAGAGCCACCACCCTCATCACGAAAA
13503;TGGGATTAAGAACCGCCACCCTCACGGAATAC
13506;TTCATCAGATGTTAGCAAACGTAGACCGTACTCAGGAGGTCGTGAGAG
13507;CCAACCATCCGGAATAGGTGTATCAAAATACA
13510;AGTACCAGGCGGATACGCTGAAT

13602;TATTTTGTCACAATCAATAGAAAATTCAAGAGAAGGATTAGGATGGAGGCC
13603;ACTCATCCGAGGCTGAGACTCCTCATATGGTT
13606;AGATGGTTAGGGAGGGAAGGTAAACCCCCTGCCTATTTCGATCGCGAA
13607;TTCAGCAGGTATAAACAGTTAATGTATTGACG
13610;ACTGGTAATAAGTTTTCGTTCTC

21102;AATTAGAGCCAGCAAAATCACCAGTAGCGTCATACATGGCTTTCTTCGGCG
21103;AATCTTTTTTACCGTTCCAGTAAGCACCATTA
21106;GCGCATAGTAGCAGCACCGTAATCACAAATAAATCCTCATGGCAGATT
21107;TTAAATTTGCCTTGATATTCACAAAGTAGCGA
21110;GAGCCGCCGCCAGCAACTGGAAA
21202;TCGGTCATAGCCCCCTTATTAGCGTTTCCACCCTCAGAGCCGCAAGTACGC
21203;AGAAGGCGGCCACCCTCAGAGCCAGCCATCTT
21206;GATTTGTATTGCAGGGAGTTAAAGATTCGGTCGCTGAGGCTGATAAGC
21207;GGCGCATACACGCATAACCGATATGCCGCTTT
21210;ACAGCTTGATACCGATCTTAGAC
21302;CGGCTACAGAGGCTTTGAGGACTAAAGTTTATCAGCTTGCTTTCATAGAAA
21303;GTTGCCATCCTTTAATTGTATCGGACTTTTTC
21306;TAAGAAACCAGCCTTTACAGAGAGATAATTTTTTCACGTTGTCAAAGC
21307;TACTGAATAAAGGAATTGCGAATAAATAACAT
21310;AACAACTTTCAACAGGCGCAAGA
21402;TCAGAGGGTAATTGAGCGCTAATATCATAGTAAATGAATTTTCAAAGAAAC
21403;ATAGGTCTTCGTCTTTCCAGACGTGAGAGATA
21406;GCAAAAGAAACAATGAAATAGCAAGCATTCCACAGACAGCGTTTGGTC
21407;TAGCCAGAAACTACAACGCCTGTATAGCTATC
21410;CCAATAGGAACCCATGACGGTTG

22102;AATTAGAGCCAGCAAAATCACCAGTAGCGTCATACATGGCTTTCCTTCAAG
22103;TTAGCCATTTACCGTTCCAGTAAGCACCATTA
22106;GCGCATAGTAGCAGCACCGTAATCACAAATAAATCCTCATGGGATTGA
22107;CACAAGCCGCCTTGATATTCACAAAGTAGCGA
22110;GAGCCGCCGCCAGCAAAAGTCAA
22202;TCGGTCATAGCCCCCTTATTAGCGTTTCCACCCTCAGAGCCGCTAATAAGA
22203;CCTCCAAGGCCACCCTCAGAGCCAGCCATCTT
22206;GATTTGTATTGCAGGGAGTTAAAGATTCGGTCGCTGAGGCGTGTCAAT
22207;TAGACAAACACGCATAACCGATATGCCGCTTT
22210;ACAGCTTGATACCGACCAGAAAT
22302;CGGCTACAGAGGCTTTGAGGACTAAAGTTTATCAGCTTGCTTTTCAATACC
22303;ACACCAGACCTTTAATTGTATCGGACTTTTTC
22306;TAAGAAACCAGCCTTTACAGAGAGATAATTTTTTCACGTTTTGCAGTA
22307;AGCCATACAAAGGAATTGCGAATAAATAACAT
22310;AACAACTTTCAACAGAACCTCAG
22402;TCAGAGGGTAATTGAGCGCTAATATCATAGTAAATGAATTTTCATTTGGTC
22403;CCAGCCGTTCGTCTTTCCAGACGTGAGAGATA
22406;GCAAAAGAAACAATGAAATAGCAAGCATTCCACAGACAGCCGGAAACC

22407;GATTGGTGAACTACAACGCCTGTATAGCTATC
22410;CCAATAGGAACCCATCTCCTTCT
22502;AAGGAAACCGAGGAAACGCAATAATAAGAGCCACCACCCTCATGCATATAC
22503;TGGCGTGAAGAACCGCCACCCTCACGGAATAC
22506;TTCATCAGATGTTAGCAAACGTAGACCGTACTCAGGAGGTGAGTCTCA
22507;TCTCTTTCCCGGAATAGGTGTATCAAAATACA
22510;AGTACCAGGCGGATATTGATTCT
22602;TATTTTGTCACAATCAATAGAAAATTCAAGAGAAGGATTAGGAGAGGAAGC
22603;TCCCAAGCGAGGCTGAGACTCCTCATATGGTT
22606;AGATGGTTAGGGAGGGAAGGTAAACCCCCTGCCTATTTCGCACGAGTA
22607;CGGCAGACGTATAAACAGTTAATGTATTGACG
22610;ACTGGTAATAAGTTTATCAGAAA

23402;TCAGAGGGTAATTGAGCGCTAATATCATAGTAAATGAATTTTCATTTAATT
23403;TAATTCCTTCGTCTTTCCAGACGTGAGAGATA
23406;GCAAAAGAAACAATGAAATAGCAAGCATTCCACAGACAGCAATATCCG
23407;CGTCATGGAACTACAACGCCTGTATAGCTATC
23410;CCAATAGGAACCCATATCATTTT
23502;AAGGAAACCGAGGAAACGCAATAATAAGAGCCACCACCCTCATGATTTGTC
23503;CCAAAACGAGAACCGCCACCCTCACGGAATAC
23506;TTCATCAGATGTTAGCAAACGTAGACCGTACTCAGGAGGTCATCTCTC
23507;CAATATCTCCGGAATAGGTGTATCAAAATACA
23510;AGTACCAGGCGGATAGTAAGTTG
23602;TATTTTGTCACAATCAATAGAAAATTCAAGAGAAGGATTAGGATCATTGTG
23603;AGTTGCGGGAGGCTGAGACTCCTCATATGGTT
23606;AGATGGTTAGGGAGGGAAGGTAAACCCCCTGCCTATTTCGTAGCGACA
23607;GTTGTTCCGTATAAACAGTTAATGTATTGACG
23610;ACTGGTAATAAGTTTTCCATATC
23102;AATTAGAGCCAGCAAAATCACCAGTAGCGTCATACATGGCTTTCATAGAAA
23103;TGGTAGCTTTACCGTTCCAGTAAGCACCATTA
23106;GCGCATAGTAGCAGCACCGTAATCACAAATAAATCCTCATCAACCAAC
23107;GTCCTGCGGCCTTGATATTCACAAAGTAGCGA
23110;GAGCCGCCGCCAGCATAAGGCCA

31102;AATTAGAGCCAGCAAAATCACCAGTAGCGTCATACATGGCTTTCATGAAGT
31103;AGTATGCATTACCGTTCCAGTAAGCACCATTA
31106;GCGCATAGTAGCAGCACCGTAATCACAAATAAATCCTCATTCAATAGA
31107;ATTTGGCGGCCTTGATATTCACAAAGTAGCGA
31110;GAGCCGCCGCCAGCATCCAAATG
31202;TCGGTCATAGCCCCCTTATTAGCGTTTCCACCCTCAGAGCCGCATAACGAG
31203;CTCATTAGGCCACCCTCAGAGCCAGCCATCTT
31206;GATTTGTATTGCAGGGAGTTAAAGATTCGGTCGCTGAGGCGCTTTAAA
31207;TTCAAATACACGCATAACCGATATGCCGCTTT
31210;ACAGCTTGATACCGATATCAGGG
31302;CGGCTACAGAGGCTTTGAGGACTAAAGTTTATCAGCTTGCTTTGTCAATAT

31303;AGTCGGGACCTTTAATTGTATCGGACTTTTTC
31306;TAAGAAACCAGCCTTTACAGAGAGATAATTTTTTCACGTTTTAATCCA
31307;TGACGATGAAAGGAATTGCGAATAAATAACAT
31310;AACAACTTTCAACAGAGTCAATA

32602;TATTTTGTCACAATCAATAGAAAATTCAAGAGAAGGATTAGGACAACGGCG
32603;CGCCAGCGGAGGCTGAGACTCCTCATATGGTT
32606;AGATGGTTAGGGAGGGAAGGTAAACCCCCTGCCTATTTCGACCAATCT
32607;AAGATGGGGTATAAACAGTTAATGTATTGACG
32610;ACTGGTAATAAGTTTTGAATATT
32102;AATTAGAGCCAGCAAAATCACCAGTAGCGTCATACATGGCTTTGCCGAAGC
32103;GTTGACCATTACCGTTCCAGTAAGCACCATTA
32106;GCGCATAGTAGCAGCACCGTAATCACAAATAAATCCTCATGCCTTTAG
32107;CGGACGACGCCTTGATATTCACAAAGTAGCGA
32110;GAGCCGCCGCCAGCAGACATTAC
32202;TCGGTCATAGCCCCCTTATTAGCGTTTCCACCCTCAGAGCCGCACGCACGT
32203;AAGAACGTGCCACCCTCAGAGCCAGCCATCTT
32206;GATTTGTATTGCAGGGAGTTAAAGATTCGGTCGCTGAGGCGCGAACAA
32207;GGACGCTCCACGCATAACCGATATGCCGCTTT
32210;ACAGCTTGATACCGACGCCTTCC
32302;CGGCTACAGAGGCTTTGAGGACTAAAGTTTATCAGCTTGCTTTGACGGGAT
32303;GACGGCAGCCTTTAATTGTATCGGACTTTTTC
32306;TAAGAAACCAGCCTTTACAGAGAGATAATTTTTTCACGTTTATCCCAC
32307;TAAACGCAAAAGGAATTGCGAATAAATAACAT
32310;AACAACTTTCAACAGCAGTAGCA

33602;TATTTTGTCACAATCAATAGAAAATTCAAGAGAAGGATTAGGAGGCAGAAG
33603;AGAGGCCAGAGGCTGAGACTCCTCATATGGTT
33606;AGATGGTTAGGGAGGGAAGGTAAACCCCCTGCCTATTTCGACTTGACT
33607;TTAGTGGTGTATAAACAGTTAATGTATTGACG
33610;ACTGGTAATAAGTTTCTCTTTTA
33102;AATTAGAGCCAGCAAAATCACCAGTAGCGTCATACATGGCTTTTGAACAAA
33103;AACCAGTCTTACCGTTCCAGTAAGCACCATTA
33106;GCGCATAGTAGCAGCACCGTAATCACAAATAAATCCTCATTCTCCTCA
33107;TTGACAGAGCCTTGATATTCACAAAGTAGCGA
33110;GAGCCGCCGCCAGCAAGAGCTTC

Bridges
1101;CCCCTCAGCGGCAAAACGCTTCGCTTGGTCAA
1102;ACCTACCGATTAAAATTTTTACCG
1103;TTATAACCCATGATTAAACTCCTA
1104;AAATAAAAGTCTGAAATCACACTC
1105;ATCACGAAGTCATGATTTTGAATT
1106;AAAAAAAGTGAATCGCGAGTGGTC
1107;GCGATAAACAGAAGTGAGAACCAG
1108;GAAGAAGCTGGAGTAACGGTCACA

1109;AACCTGACTATTCCACCTGTAAAA
1110;TTAGGTGTTGCAACAACTGAACGG
1111;CACTGGTCAAATATAACGTTGACG

2201;AATAACCTAATCATGGTGGCGAAT
2202;GTTCTTGCTGGCTGGAGACAAATA
2203;AATCACCTCACTTAAGAAATCACC
2204;GTTCCTGAATGAATGGAATAGCAC
2205;CCGCCAGCGAAGCCTTCAAGAAGG
2206;AGGAGAAACCACCAGCAAGAGCAG
2207;CAATTTAGACATGGCGCATACGAA
2208;ACGATACCACTGACCCTTTGACCG
2209;GGCGGCTTTCAGCAATCTTAAACT
2210;GAATCACCCACATCACCTTGAATG

2301;CGGCAGAAAACGGAAAACATCCTT
2302;TTTCACGCCCAAATCAAGCAACTT
2303;TTGCCACCAAGTCCAAGGCGGCAA
2304;ACAAAACAGGGTCGCCTTTATCAG
2305;TCCTTTCCAGCAATATCGGTATAA
2306;ACCTTTAGGCAGCAGCAAGATAAT
2307;ATTAAGCTCAGGAAATCGTTAAGG
2308;CTCTTTAGTCGCAGTACAGCACGC
2309;ATCAGCACGGCGGAAAACGAACAA
2310;GTAAACATGTCAACCATACCAGCA

1201;TTTTTGAGTGCCATGCTCAGGAAC
1202;GCGGCACAGGAGGAAGCGGAGCAG
1203;AGAAAGCTCAGTCTCAGAATGTTT
1204;GTTGAACACGACCAGAAAGTCGTC
1205;TGTGGTAGAAACTGGCCTAACGAC
1206;AGTTCCATTTGCAGACCCATAATG
1207;AATTAGCATAAGCAGCCAACATCA
1208;TGCCCAGAGATTAGAGTCTTGGTC
1209;AATCACGTCGCATGACAAGTAAAG
1210;TCAGCGTCCATCATGGTAACGCTG
1211;CCAAATGAAGAAATAAATAAGAGGTTTTACCT

2401;CAAATCCGGGCAGCAACGGAAACC
2402;CATCATCTTTTTAGTAAGCTCTTT
2403;TGATTGTCCAGTTGCATGATTAAG
2404;GGTTAGCCTCGGTACGCTCGGCAA
2405;TTTTGCATGTCAGGCATCCACGGC
2406;ATAGTTGTCCAGCAATCTCTTTTT
2407;AGTCGCCGACTGAATGTATAGATA
2408;ACCCTGAAACAAATGCTCGTATTC

2409;CTGGTCTTTTAGGGATTTTATTGG
2410;TTAATCGTAAGCATCTCATTTTGT

2501;AGACATAACAAGAAAAGCGGCATG
2502;AACCAGTAACGCTCGGCGCCAGTT
2503;AAAGGTCATGCGGCATGTGTTAAC
2504;GAGGAGTGGCATTAACAGGAAGCC
2505;GACCAGCAACCATCCTTCATGAAC
2506;CTGTTCACAAATGGTAATAAGACG
2507;ATAACCGGAGTAGTTGCATAAACG
2508;AGGGACATAAAAAGTAGAAGGAGT
2509;TCCATCTCAAAATGTCTACAGTAG
2510;GCAAGGCCGAAAGACGGAGAGCGC

3201;GTTGATAATATCCTCAAGTAAGGG
3202;CCCTGCAACAACGCGAGCAGTAGA
3203;TTTTCCATAATAGACGTTAAAATT
3204;CCTACATACCAAAGACCTTGGAAA
3205;TGCTGTTGGAGCGCCTTTACGCTT
3206;TACCTCGCATTTGGCGCATAATCT
3207;TTGAGCTTGAGTAAGCAACGGCTG
3208;CAGGGCGAGCGCCAGAAATACTGA
3209;ATTGGTAAACGTTTTTTACCTTTA
3210;ATCACTCCGCGAGTCATTTCTTTG

4401;GATTAAGCCCGCACGTAATTTTTG
4402;TTTCTTCTGTCGTAACCCAGCTTG
4403;GGTTGAACGGCGTCGCGCGTCAGT
4404;CAGTGTTTCCTGCGCGTTCTGCTT
4405;TTTTTGCGTACACGCAAGGTAAAC
4406;TTCAGCGGTTCCCAGCCTCAATCT
4407;TCGGCTACAGTAACTTCTTTAACC
4408;GACGCCATTAATAATGTTGCGCCG
4409;GTCACAGGTTTTCCGTAAATTCAG
4410;ATGATGAGCGCATAAATTTGAGCA

4501;AAATGTCAAGGCCGTTTGAATGTT
4502;GAACATAACAGATAGTAATCCACG
4503;TGAACAGCATCGGACTTAAGCAAT
4504;CAATAAACTCAACAGGCTTACCTA
4505;CATGATTTAGCAGGAAAGCGAGGG
4506;AAAGTCCATACGGATTGTTCAGTA
4507;AAGCGGTCTGGAAACGGCGTACCA
4508;AGCCTCAACGCAGCGAAGCTTAAT
4509;CCTGAATGCGAGCACGAGAGCGGT
4510;ATCCAAACCGGTTAAATCCAAAAC

4511;AAATCGAAATCATCTTTTTGTTACTCGTCAGA

5201;TATCGAAGAAGAGAATCTCTACCA
5202;ATGTGACTCAGGTTGGATACGCCA
5203;AAGCGATAAAACTCTGCATATCTA
5204;CTTGACGAACGTGCCAAACTTCTG
5205;AAAGTGTTAGCATATTAAGCCACT
5206;TCCAACGCTTTTCGACTCATCAGA
5207;GCTTTATCAAGATAATGTCAGTTT
5208;ATCGTTAGTTGATGGCAGCAGTAG
5209;CGTAAACAGAAAGGTCGCAAAGTA
5210;TCGAGCTGCCAGCAGTCCACTTCG
5211;ATTTTCTCATTTTCCGCGCAAGGATAGGTCGA

4301;CACTAACCTCCGTGGACAGATTTG
4302;AGCATTTTGCTGATGAACTAAGTC
4303;CGCTGATTCTGCGTTTCATCCCGA
4304;CTCATTCTGATTCTGAATGAGAAG
4305;GCGCCAATACAGCTTCTTGGGAAG
4306;GCTTGGTTACATTAGAAATATCCT
4307;AGCAGCATCAGTGACGTTTAGTGA
4308;ATTCTTTAGCTCCTAGTATCAACC
4309;ATGAAAAAACCTTTAGCAGCAAGG
4310;TGACTTTTATCGGCAACAGCTTTA

5101;GGCAGCAATTAACGTATTTAGCCA
5102;CCAACAGCTGAATCATTAGCCTTG
5103;GATAGCAGTCGGCGTGCATATAAC
5104;TTAAGCGGCTCACCTTGGCACACA
5105;CATACTCATAGCATCAACAGGCCA
5106;CAGAACGTAATGAAGACGGCCATT
5107;AAGTGCACCGCATGGAGAAAAAGC
5108;TGTAGCGAACTGCGATAGGAAGTG
5109;CTACCTGTGGGCATACTGTAACCA
5110;CGTATTTTCGACGACCAAAATTAG
5111;GCGGCGATTGCGTACCGCAAGCTATTTAACTG

4201;TGTTCCAAACCATACGACCAATAT
4202;TAGTCACGCAGCTTTACCGTCTTT
4203;TTAGAGCCAATACCATCAAAGCAT
4204;TCATAAAACGCCTCTATTATTTCC
4205;CCTGACGGATCGGTCGTCAGCCAA
4206;TGTCAAAAACATACAATTGGGAGG
4207;ATTTGGAGGCATGAAAACGATAAA
4208;CAGCATGAGCCTGTCGTAAAAAAG
4209;ACGAACCACATTGCATTCATCAAA

4210;AGCAAAGCGTGACATTCAGAAGGG

4101;TATCGAACCTACGCGATTTCATAG
4102;TCCAGCAAGGCCGTCAACATACAT
4103;TCAGAAGCAGCCTTATTCTTGAAC
4104;TTAATACCTTTCTTTTAAACTCAT
4105;ACAGATACTGGGGTAATTATACTC
4106;TATCCTTAAATTCATCCATTAACT
4107;ATTGTAGCATTGTGCCAGAGGGCG
4108;CCAGCTTGCGGCAAAACAAGTTGG
4109;ATTAATATCTGCGTAACCGTCTTC
4110;TAAAAACCTTCGGGGCGGTGGTCT

3101;AATAATCAAACGCCCTGCATACGA
3102;AATCTCTTGAGCCTCGATACGCTC
3103;TCAATAGCAGGTTTAACCAAGAGC
3104;GTTATCCATCTGCTTAAGAAATGC
3105;GAAAGAGTTGGAAGCCAAGCATTG
3106;GGAACATTCTAGGGGCGGCCTCAT
3107;AGCACCAGAAACAAAAAGAGCCTT
3108;GATTTAATACCAGCATTACCAGCT
3109;AAGTCCTTCACCCATGCCTACAGT
3110;CGGTAGCAGCCAGCCTGCAACGTA

2101;CAAACTATTTCAGCGAAACCAATC
2102;TTAGTAGCACCACCATTACCAGCA
2103;GAATGCAATGAAGAAAGGTAAAGT
2104;ACCATGAAACCAACATACAGATGT
2105;CGGCGTTGAAACGTTATTGCCCGG
2106;GAAGGACGCACCAACAGAAACAAC
2107;TCAAAAGCAATATCAGTCAATAGT
2108;CCTTGACGGTATAATAAAATTTAG
2109;CAGGCAAAACCACCATCATGGCGA
2110;AGGATAAAGAAGAAGACTCAAAGC
2111;GAGGGTAGTCGGAACCCATCATAGGCAGTCGG

Table S9. Unmodified diamond shaped DNA origami staples

1 CCAATTCTGCGAACG
2 CTGGAAGTTTCATTCCTAAAATGT
3 CATGTTTTAAATATGCGCGGAATC
4 GCTTAATTGCTGAATACTCAAATG
5 TGATAAGAGGTCATTTATGACCATAAATCAAAAA
6 TTTAATTGCTCCTTT
7 AAGAAGTTTTGCCAGAGGGGGTAATAGATATAACAGTTGATTC
8 CACGTTGGGATAGCGTCCAATACTAACTAAAGTACGGTGT

9 ACAAACGGTATTCATTGAATCCCCTAATGCTGTAGCTCAA

10 ACATTAAATGTGAGCGAGTAAAGTTCAGAAAACGAGATTGCGGATGGCTTAGA

11 CAGGATTAGAGAGTA

12 GCGAACCAGACCGGAAGAAGCAAA

13 TTCAAATATCGCGTTTAGGAAGCC

14 AATATGATATTCAACCAGCTATTT

15 TGAGAAAGGCCGGAGAGGTCATTGCCTGAGAGTC

16 AAAGATTCAAAAGGG

17 AGGTCTTTACCCTGACTATTATAGTCAGCAAACTCCAACAGGT

18 GCCATCAACATCAAAAAGATTAAGTAATTCGAGCTTCAAA

19 TTAAATCATAATGCCGGAGAGGGTGTTCTAGCTGATAAAT

20 AATTGTAAACGTTAATATTTTCTACAAAGGCTATCACAGTCAAATCACCATC

21 CTGAGTAATGTGTAG

22 TTTAGAACCCTCATATAATCGTAA

23 GAAGCCTTTATTTCAAATACCAGT

24 AAACATTATGACCCTGCGTTAATA

25 CTCAGAGCATAAAGCTTTACAGGTAGAAAGATTC

26 ATTAAGCAATAAAGC

27 GAGCAAACAAGAGAATCGATGAACGGTATTTTAAATGCAATGC

28 ATAATCAGTGTCAATCATATGTACCGCAAGGATAAAAATT

29 TGCGATTTTGGGAAGAAAAATCTATAATACTTTTGCGGGA

30 CTTGAGATGGTTTAATTTCAATAACGGAACAACATTAAAATCGGTTGTACCAA

31 GGCAAAGAATTAGCA

3 TAGCATTAACATCCAAAACTAATG

2	
33	TGAAAAGGTGGCATCATACGAGGC
34	TGTTTAGCTATATTTTCCCTCGTT
35	CATTAGATACATTTCGATAGCGAGAGGCTTTTGC
36	TAGATTTAGTTTGAC
37	CAGTTGAGATTTAGGAATACCACATTCTAAATCATACAGGCAA
38	GAATAAGGTAACGCCAAAAGGAATATTCTACTAATAGTAG
39	CTTTCCGGAGCAACACTATCATAACATTTGGGGCGCGAGC
40	GGGACGACGACAGTATCGGCCGACGATAAAAACCAAACAAATGGTCAATAACC
41	TTAGACTGTGTAGATGGGCGCATCTGGGAAGGGCGATCGGAAAGGGGG
42	GTCATAAACGGATTGACCGTAATGCATTAAACGGGTAAAATTCATGAG
43	CTTTAAACCAACCCGTCGGATTCTGAAGGCACCAACCTAAAACGAAAG
44	ATTCAGGCTGCGCAACTGTGTAACCGTGCATCTGCCAGTTTG
45	ATGTGCTGAACCATCGCCCACGCAGGTTCCACAGCATTCAGAACGTGGA
46	GAAGTTTCTCGCTGAGGCTTGCAGTGCCCCAGCAGGCGAAGCGTA
47	ACAGAGGCTTTGAGGACTAAAGACTTTTACGTAATGCCACTACCCGTGGGA
48	ACAATGACAACCAAGGCGATTAAGTT
49	ATATTCGGATTACGCCAGCTGGCGTGCGGGCCTCTTCGCTGGATAGGT
50	GGAGTTAAAGGCCGC
51	GAGTCCACTATTAACGAAATCGGCAAAATCCC
52	CCTGTAGACAGCCCTCATAGTTAAATCCTGTTTGATGGTTAACCGAT
53	GCGGATTGAAATAATTCGCGTCTGCACTCATCTTTGACCCAAAGACAG
54	CGAAAGACGCTCATTTTTTAACCAGCGCGAAACAAAGTACTGAGTGAG
5	TTGAGAGAGTTAAAATTCGCATTAATCGCCTGATAAATTGTGTCGAAA

5
5
6 GCAAAAGAATACACTAAAAGCCTTCCTGTAGCCAGCTTTCAT
5
7 CATCGGAAGTCACCCTCAGCAGCGGTTGCGTCGTCAGTACAAACTACAA
5
8 CTAACTCACAGTCGGGAAACCTGTCTGATTGCCCTTCACCAAAT
5
9 ATAAAGTGTAAAGCCTGGGGTGCCTAAAACGGAGATTTGTATCAATTTTTG
6
0 TTTGCGGGATCCGAGGGTAGCAACGG
6
1 CCGCTTTCCATTAATTGCGTTGCGCCAGCGATTATACCAAATAGGAAC
6
2 CGTGCCAGCTGCATT
6
3 CGATCTAAAGTTTTAGCAAGCGGTCCACGCTG
6
4 TCGTCACCTTTCCAGACGTTAGTGCCTGGCCCTGAGAGACTCACTGC
6
5 AACTAGCAAAAAGCCCCAAAAACACTTAGCCGGAACGAGGCTCACAAT
6
6 CAGGACGTTAAGAACTGGCTCATTTAAGGGAACCGAACTGCATAGCTG
6
7 AAACGAACCTTTAATCATTGTGAAGACAGATGAACGGTGTACAGACCA
6
8 CGCGACCTGCTCCATGTTAGGAAGATTGTATAAGCAAATATT
6
9 TCCACACAAACGCGCGGGGAGAGGCTTTTATTTTTACCGTAACACTGAG
7
0 TTTCCTGTGAAAATCTCCAAAAAAATAATTTTTTCACGTTCAGTT
7
1 TACCGAGCTCGAATTCGTAATCATGGTACCAACTTTGAAAGAGTTACCTTA
7
2 ATGAATCGGCCACATACGAGCCGGAA
7
3 GTATTGGGGTGAAATTGTTATCCGCGCAGACGGTCAATCACCCGGTTG
7
4 AAGGCTCCAAAAGGA
7
5 ATTTTCTGTATGGGCACCAGTGAGACGGGCAA
7
6 GTCTATCAGCTAAACAACTTTCAACGCCAGGGTGGTTTTTCGGTTTGC
7
7 CAGATACACTTGCCCTGACGAGAATCATCAAGAGTAATCTATGCCTGC
7 ATAGTAAGACGTAACAAAGCTGCTTTCATTACCCAAATCACGTTGTAA

8
7
9 TACCAGACTCAGGAAGATCGCACTGGAAACCAGGCAAAGCGCCATTCG
8
0 CGCATAGGCTGGCTGACCTACACCAGAACGAGTAGTAAATTG
8
1 AGGTCGACATCGGTTTATCAGCTTAGGAATAGAACAAAGGGCGAAAAAC
8
2 AACGACGGTCTTAAACAGCTTGATTAAATCAAAAGAATAGGAAC
8
3 GTAACGCCAGGGTTTTCCCAGTCACGACACCGCTTCTGGTGCCCCAGCCAG
8
4 CCTTTAATTGTTCTAGAGGATCCCCG
8
5 GGTGAATTCCAGTGCCAAGCTTGCTGACAAGAACCGGATACATTCAGT
8
6 ACCGATAGTTGCGCC
8
7 CAGCGGAGTGAGAACAACTAAAGGAATTGCGA
8
8 CCAACGTGTGTTGTTCCAGTTTGCCCGAGATAGGGTTGAGCTTTCGA

Table S10. Modified staples and bridges for mixed super-structure
Modified staples for hexagonal DNA origami

31H
31H602;TATTTTGTCACAATCAATAGAAAATTCAAGAGAAGGATTAGGACTTCGGCG
31H603;AATCTTTTGAGGCTGAGACTCCTCATATGGTT
31H606;AGATGGTTAGGGAGGGAAGGTAAACCCCCTGCCTATTTCGGGCAGATT
31H607;TTAAATTTGTATAAACAGTTAATGTATTGACG
31H610;ACTGGTAATAAGTTTACTGGAAA

31H102;AATTAGAGCCAGCAAAATCACCAGTAGCGTCATACATGGCTTTAAGTACGC
31H103;AGAAGGCGTTACCGTTCCAGTAAGCACCATTA
31H106;GCGCATAGTAGCAGCACCGTAATCACAAATAAATCCTCATTGATAAGC
31H107;GGCGCATAGCCTTGATATTCACAAAGTAGCGA
31H110;GAGCCGCCGCCAGCATCTTAGAC

31H202;TCGGTCATAGCCCCCTTATTAGCGTTTCCACCCTCAGAGCCGCCATAGAAA
31H203;GTTGCCATGCCACCCTCAGAGCCAGCCATCTT
31H206;GATTTGTATTGCAGGGAGTTAAAGATTCGGTCGCTGAGGCGTCAAAGC
31H207;TACTGAATCACGCATAACCGATATGCCGCTTT
31H210;ACAGCTTGATACCGAGCGCAAGA

32
32H502;AAGGAAACCGAGGAAACGCAATAATAAGAGCCACCACCCTCATCTGTTGAA

32H503;GCCTAACGAGAACCGCCACCCTCACGGAATAC
32H506;TTCATCAGATGTTAGCAAACGTAGACCGTACTCAGGAGGTGATGCCCA
32H507;ACAAGTAACCGGAATAGGTGTATCAAAATACA
32H510;AGTACCAGGCGGATACTCCAAAT

32H602;TATTTTGTCACAATCAATAGAAAATTCAAGAGAAGGATTAGGACATGAAGT
32H603;AGTATGCAGAGGCTGAGACTCCTCATATGGTT
32H606;AGATGGTTAGGGAGGGAAGGTAAACCCCCTGCCTATTTCGTCAATAGA
32H607;ATTTGGCGGTATAAACAGTTAATGTATTGACG
32H610;ACTGGTAATAAGTTTTCCAAATG

32H102;AATTAGAGCCAGCAAAATCACCAGTAGCGTCATACATGGCTTTATAACGAG
32H103;CTCATTAGTTACCGTTCCAGTAAGCACCATTA
32H106;GCGCATAGTAGCAGCACCGTAATCACAAATAAATCCTCATGCTTTAAA
32H107;TTCAAATAGCCTTGATATTCACAAAGTAGCGA
32H110;GAGCCGCCGCCAGCATATCAGGG

32H202;TCGGTCATAGCCCCCTTATTAGCGTTTCCACCCTCAGAGCCGCGTCAATAT
32H203;AGTCGGGAGCCACCCTCAGAGCCAGCCATCTT
32H206;GATTTGTATTGCAGGGAGTTAAAGATTCGGTCGCTGAGGCTTAATCCA
32H207;TGACGATGCACGCATAACCGATATGCCGCTTT
32H210;ACAGCTTGATACCGAAGTCAATA

33
33H502;AAGGAAACCGAGGAAACGCAATAATAAGAGCCACCACCCTCATAGACGGA
G
33H503;ATCTCGAAAGAACCGCCACCCTCACGGAATAC
33H506;TTCATCAGATGTTAGCAAACGTAGACCGTACTCAGGAGGTTGGTAATA
33H507;CAGCAAGGCCGGAATAGGTGTATCAAAATACA
33H510;AGTACCAGGCGGATACTCGGCGC

33H602;TATTTTGTCACAATCAATAGAAAATTCAAGAGAAGGATTAGGACCTCAAGT
33H603;TGCAATTAGAGGCTGAGACTCCTCATATGGTT
33H606;AGATGGTTAGGGAGGGAAGGTAAACCCCCTGCCTATTTCGCGCCTTTA
33H607;CTCGCAACGTATAAACAGTTAATGTATTGACG
33H610;ACTGGTAATAAGTTTTTTTTTAC

33H102;AATTAGAGCCAGCAAAATCACCAGTAGCGTCATACATGGCTTTCACGTAAT
33H103;CTTCTGCGTTACCGTTCCAGTAAGCACCATTA
33H106;GCGCATAGTAGCAGCACCGTAATCACAAATAAATCCTCATACGCAAGG
33H107;AGCGGCTTGCCTTGATATTCACAAAGTAGCGA
33H110;GAGCCGCCGCCAGCATCCGTAAA

13H

13H302;CGGCTACAGAGGCTTTGAGGACTAAAGTTTATCAGCTTGCTTTCATAGAAA
13H303;TGGTAGCTCCTTTAATTGTATCGGACTTTTTC
13H306;TAAGAAACCAGCCTTTACAGAGAGATAATTTTTTCACGTTCAACCAAC
13H307;GTCCTGCGAAAGGAATTGCGAATAAATAACAT
13H310;AACAACTTTCAACAGTAAGGCCA

13H402;TCAGAGGGTAATTGAGCGCTAATATCATAGTAAATGAATTTTCGGCGATTG
13H403;AATTAGGGTCGTCTTTCCAGACGTGAGAGATA
13H406;GCAAAAGAAACAATGAAATAGCAAGCATTCCACAGACAGCGTGCACCG
13H407;GCCATTAGAACTACAACGCCTGTATAGCTATC
13H410;CCAATAGGAACCCATTAGCAGTC

13H502;AAGGAAACCGAGGAAACGCAATAATAAGAGCCACCACCCTCATCCTCGGCA
13H503;CAATATCAAGAACCGCCACCCTCACGGAATAC
13H506;TTCATCAGATGTTAGCAAACGTAGACCGTACTCAGGAGGTATAAAACG
13H507;AGCCAACGCCGGAATAGGTGTATCAAAATACA
13H510;AGTACCAGGCGGATAGCATGAGC

12H
12H202;TCGGTCATAGCCCCCTTATTAGCGTTTCCACCCTCAGAGCCGCTGGAGGCC
12H203;ACTCATCCGCCACCCTCAGAGCCAGCCATCTT
12H206;GATTTGTATTGCAGGGAGTTAAAGATTCGGTCGCTGAGGCATCGCGAA
12H207;TTCAGCAGCACGCATAACCGATATGCCGCTTT
12H210;ACAGCTTGATACCGATCGTTCTC

12H302;CGGCTACAGAGGCTTTGAGGACTAAAGTTTATCAGCTTGCTTTGGCGGTGG
12H303;TATCAAGTCCTTTAATTGTATCGGACTTTTTC
12H306;TAAGAAACCAGCCTTTACAGAGAGATAATTTTTTCACGTTATCCATTA
12H307;TACAAACTAAAGGAATTGCGAATAAATAACAT
12H310;AACAACTTTCAACAGTCAACATA

12H402;TCAGAGGGTAATTGAGCGCTAATATCATAGTAAATGAATTTTCCCTGCATA
12H403;CTTCCAAGTCGTCTTTCCAGACGTGAGAGATA
12H406;GCAAAAGAAACAATGAAATAGCAAGCATTCCACAGACAGCGCCAAGCA
12H407;AGTAGAAAAACTACAACGCCTGTATAGCTATC
12H410;CCAATAGGAACCCATTCGATACG

12H502;AAGGAAACCGAGGAAACGCAATAATAAGAGCCACCACCCTCATATTCAGAA
12H503;CCATAAAAAGAACCGCCACCCTCACGGAATAC
12H506;TTCATCAGATGTTAGCAAACGTAGACCGTACTCAGGAGGTCAATTGGG
12H507;CGGTTATTCCGGAATAGGTGTATCAAAATACA
12H510;AGTACCAGGCGGATATTACCGTC

11H

11H202;TCGGTCATAGCCCCCTTATTAGCGTTTCCACCCTCAGAGCCGCGGCAACAG
11H203;AAAAATATGCCACCCTCAGAGCCAGCCATCTT
11H206;GATTTGTATTGCAGGGAGTTAAAGATTCGGTCGCTGAGGCTTAGAAAT
11H207;CCAATATGCACGCATAACCGATATGCCGCTTT
11H210;ACAGCTTGATACCGAGATGAACT

11H302;CGGCTACAGAGGCTTTGAGGACTAAAGTTTATCAGCTTGCTTTAGTCATTT
11H303;GGTAAAATCCTTTAATTGTATCGGACTTTTTC
11H306;TAAGAAACCAGCCTTTACAGAGAGATAATTTTTTCACGTTTGGCGCAT
11H307;TGTTGCTTAAAGGAATTGCGAATAAATAACAT
11H310;AACAACTTTCAACAGCGCGAGCA

11H402;TCAGAGGGTAATTGAGCGCTAATATCATAGTAAATGAATTTTCCATCTCAT
11H403;GTCTTTCGTCGTCTTTCCAGACGTGAGAGATA
11H406;GCAAAAGAAACAATGAAATAGCAAGCATTCCACAGACAGCGCAATCTC
11H407;TGCATCTCAACTACAACGCCTGTATAGCTATC
11H410;CCAATAGGAACCCATTAGTAAGC

Modified staples for diamond shaped DNA origami
21P
21P302;GAGCAAACAAGAGAATCGATGAACGGTATTTTAAATGCAATGCAGCACGCT
21P303;AGGAAATGTTTAGAACCCTCATATAATCGTAA
21P306;TGCGATTTTGGGAAGAAAAATCTATAATACTTTTGCGGGATTATCAGC
21P307;AGTCCAACAAACATTATGACCCTGCGTTAATA
21P310;ATTAAGCAATAAAGCTGCCAGCC

21P402;CAGTTGAGATTTAGGAATACCACATTCTAAATCATACAGGCAAATGTAGCT
21P403;CAGGTGCCTAGCATTAACATCCAAAACTAATG
21P406;CTTTCCGGAGCAACACTATCATAACATTTGGGGCGCGAGCCTTATCAG
21P407;ATGGCGAGTGTTTAGCTATATTTTCCCTCGTT
21P410;TAGATTTAGTTTGACAGCAGAAA

22P
22P202;AGGTCTTTACCCTGACTATTATAGTCAGCAAACTCCAACAGGTAGCTTTAG
22P203;AAAACTAGGCGAACCAGACCGGAAGAAGCAAA
22P206;TTAAATCATAATGCCGGAGAGGGTGTTCTAGCTGATAAATCCTTGAAT
22P207;GCATCACCAATATGATATTCAACCAGCTATTT
22P210;AAAGATTCAAAAGGGCATCACCT

22P302;GAGCAAACAAGAGAATCGATGAACGGTATTTTAAATGCAATGCACCGCCTC
22P303;GGCGCCACTTTAGAACCCTCATATAATCGTAA
22P306;TGCGATTTTGGGAAGAAAAATCTATAATACTTTTGCGGGAGCACCAAA
22P307;TAAGTGGCAAACATTATGACCCTGCGTTAATA
22P310;ATTAAGCAATAAAGCCAGCGAAA

22P402;CAGTTGAGATTTAGGAATACCACATTCTAAATCATACAGGCAAACCAAACC
22P403;CGTTATTGTAGCATTAACATCCAAAACTAATG
22P406;CTTTCCGGAGCAACACTATCATAACATTTGGGGCGCGAGCACAGTCCT
22P407;ACCATCATTGTTTAGCTATATTTTCCCTCGTT
22P410;TAGATTTAGTTTGACGTCGGGAG

22P102;AAGAAGTTTTGCCAGAGGGGGTAATAGATATAACAGTTGATTCAGCGAACC
22P103;TAGGGTCGCTGGAAGTTTCATTCCTAAAATGT
22P106;ACAAACGGTATTCATTGAATCCCCTAATGCTGTAGCTCAAAACCTGAT
22P107;TGTATCCAGCTTAATTGCTGAATACTCAAATG
22P110;TTTAATTGCTCCTTTGCATTAAC

24P
24P102;AAGAAGTTTTGCCAGAGGGGGTAATAGATATAACAGTTGATTCAAGCAATG
24P103;CAACAGGACTGGAAGTTTCATTCCTAAAATGT
24P106;ACAAACGGTATTCATTGAATCCCCTAATGCTGTAGCTCAACGTACCAT
24P107;GCAGCGACGCTTAATTGCTGAATACTCAAATG
24P110;TTTAATTGCTCCTTTTTGTTACT

24P202;AGGTCTTTACCCTGACTATTATAGTCAGCAAACTCCAACAGGTGTTGGATT
24P203;GATTTGTCGCGAACCAGACCGGAAGAAGCAAA
24P206;TTAAATCATAATGCCGGAGAGGGTGTTCTAGCTGATAAATCATTCTGA
24P207;GGGAAGTAAATATGATATTCAACCAGCTATTT
24P210;AAAGATTCAAAAGGGTCTTTAGC

23P
23P402;CAGTTGAGATTTAGGAATACCACATTCTAAATCATACAGGCAAAATCCAAA
23P403;TGAGCTTATAGCATTAACATCCAAAACTAATG
23P406;CTTTCCGGAGCAACACTATCATAACATTTGGGGCGCGAGCTTGTTCAG
23P407;TTCTTACCTGTTTAGCTATATTTTCCCTCGTT
23P410;TAGATTTAGTTTGACGTAATCCA

23P102;AAGAAGTTTTGCCAGAGGGGGTAATAGATATAACAGTTGATTCATCTCTAC
23P103;CTCATATCCTGGAAGTTTCATTCCTAAAATGT
23P106;ACAAACGGTATTCATTGAATCCCCTAATGCTGTAGCTCAATTAAGCCA
23P107;GCGTCAGTGCTTAATTGCTGAATACTCAAATG
23P110;TTTAATTGCTCCTTTTCGCAAAG

23P202;AGGTCTTTACCCTGACTATTATAGTCAGCAAACTCCAACAGGTAATTTTCT
23P203;TCCACTTCGCGAACCAGACCGGAAGAAGCAAA
23P206;TTAAATCATAATGCCGGAGAGGGTGTTCTAGCTGATAAATTGCTTTAT
23P207;CTCATCAGAATATGATATTCAACCAGCTATTT
23P210;AAAGATTCAAAAGGGGAAGCGAT

23P302;GAGCAAACAAGAGAATCGATGAACGGTATTTTAAATGCAATGCTCATTTTT

23P303;ATTTGAGCTTTAGAACCCTCATATAATCGTAA
23P306;TGCGATTTTGGGAAGAAAAATCTATAATACTTTTGCGGGAGTCGGCTA
23P307;CCTCAATCAAACATTATGACCCTGCGTTAATA
23P310;ATTAAGCAATAAAGCTGGTTGAA
Bridges
3101;CCCCTCAGCGGCAAAACGCTTCGCTTGGTCAA
3102;ACCTACCGATTAAAATTTTTACCG
3103;TTATAACCCATGATTAAACTCCTA
3104;AAATAAAAGTCTGAAATCACACTC
3105;ATCACGAAGTCATGATTTTGAATT
3106;AAAAAAAGTGAATCGCGAGTGGTC
3107;GCGATAAACAGAAGTGAGAACCAG
3108;GAAGAAGCTGGAGTAACGGTCACA
3109;AACCTGACTATTCCACCTGTAAAA
3110;TTAGGTGTTGCAACAACTGAACGG
3111;CACTGGTCAAATATAACGTTGACG

3201;CGTCAAACAATCATGGTGGCGAAT
3202;GTTCTTGCAAAACCACCATTACCA
3203;TCTGAATGCAATGAAGAAATCACC
3204;GTTCCTGAATGAATGGTTGACAGA
3205;TAGCGGCGGAAGCCTTCAAGAAGG
3206;AGGAGAAACAGCACCAACAGAAAC
3207;GCATCAAAAGCAATATCATACGAA
3208;ACGATACCACTGACCCAAAAAATT
3209;AAACAGGCTCAGCAATCTTAAACT
3210;GAATCACCACCGAAGAAGACTCAA

4101;GAAGAAATAACGGAAAACATCCTT
4102;TTTCACGCTCATAAGAGGTTTTAC
4103;AGGACGGTTGTCAGCGGGCGGCAA
4104;ACAAAACAGGGTCGCCAGCGCATG
4105;GAGATTAGAGCAATATCGGTATAA
4106;ACCTTTAGATCAACATCATAGCCA
4107;ACGTTTGGTCAGTTCCCGTTAAGG
4108;CTCTTTAGTCGCAGTAGAAAACTG
4109;CACGACCAGGCGGAAAACGAACAA
4110;GTAAACATCAGAATGTTTATAGGT
4111;ACAAAGAAACGCGGCAAGTGCCATGCTCAGGA

3301;GGTAGTCGCATCATGGTAACGCTG
3302;AATCACGTATAAACATCATAGGCA
3303;GGCGACCATTCAAAGGTCTTGGTC
3304;AATTAGCATAAGCAGCTAATAACC
3305;TGACGGTATTGCAGACCCATAATG
3306;TGTGGTAGGGACGTCAATAGTCAC

3307;CCCGGCGTACGGGGAAAAGTCGTC
3308;AGAAAGCTCAGTCTCAAACATAAA
3309;ATGAAACCGGAGGAAGCGGAGCAG
3310;TTTTTGAGGTAGCGGTAAAGTTAG

3401;TAAGAGCTGGCAGCAACGGAAACC
3402;CATCATCTAGTTGATGGCGAAAGG
3403;TTTTGACAGAATCGTTTGATTAAG
3404;GGTTAGCCTCGGTACGCATCCAAC
3405;CTTCTCCTGTCAGGCATCCACGGC
3406;ATAGTTGTGAACGTGCCAAGCATA
3407;TAAACCAGTCCTTGACTATAGATA
3408;ACCCTGAAACAAATGCAAATGTGA
3409;CATGAACATTAGGGATTTTATTGG
3410;TTAATCGTAAATGTCAACAAGAGA

4201;CAGTTTGACAAGAAAAGCGGCATG
4202;AACCAGTAGGTCATGCGGCATACG
4203;AAGCCAAGATGGGAAAGTGTTAAC
4204;GAGGAGTGGCATTAACAATCTGAC
4205;AGACGACCACCATCCTTCATGAAC
4206;CTGTTCACACCGGAGTAGTTGAAA
4207;GGAGTCGCCAGCGATACATAAACG
4208;AGGGACATAAAAAGTACGGCGTCC
4209;AGCGCCAAAAAATGTCTACAGTAG
4210;GCAAGGCCACGACGCAATGGAGAA

3501;CGCTCTTTATTAGACATAATTTAT
3502;AAGGGGCCGCATCGGACTCAGATA
3503;TATTAGTGGTTGAACAGAAGCCCC
3504;AAATTGTTGACCACCTCTCATGAT
3505;TAACTTGAACATACCAAAGACGAG
3506;CGCTTGCCTCTGGAAACGTACGGA
3507;ATAGAGGCCAAAGCGGTTTAGTAC
3508;GGCTGCGGACGACCAGAGCCTGAA
3509;ACGGCAGAGGCGAGCGCCAGAACG
3510;CTTTAGACAAATCATCTTCGGTTA

3601;CGTCAGAATACATCACTCCTTCCG
3602;TTTTGACGAGTAGCAATCCAAACT
3603;GAGCACGAGAGCGGTCCACGTTTT
3604;TCAGTAAGAACGTCAGGCCTCAAC
3605;AAACGCAATGTTTCCTGCGCGTAC
3606;TAAACGCGATCCCACAAAGTCCAG
3607;GCAGGAAAGCGAGGGTAACAATTC
3608;TAACCGGACGCTCGACAATAAACT

3609;ACGGCAGCGCCATTAATAATGTTT
3610;TTCAGCGCACGGGATGAACATAAT
3611;GGCCGTTTGAATGTTGCTTCCATGATGAGACA

2401;CATATCACGCGCAAGGATAGGTCG
2402;CATTTTCCAGCAGCCTTATGGCCG
2403;CATCACGAACGTCAGAGCCAGCAG
2404;GATTTAATTCGTAAACGTAACAGA
2405;ACTTCTCAAAGCAGTAGTAATTCC
2406;CAAGATAAAGCATTGTGCCAATTC
2407;TGGGGGAGCACATTGTTTTTCGA
2408;AAATATCCGAAAGTGTGTTATTAA
2409;TCTATAGTTAACTTCTGCGTCATG
2410;AAAACTCTTTTTCGTCCCCTTCGG

2501;GGCGTGTGAGGTTGGATACGCCAA
2502;ATCGAAGCCACACAAAAATACTGA
2503;CTGTACCATACTCAGGGCGCATAA
2504;AGATTTGTCGTCACAGTGAAGACG
2505;CATGGAAAGTTGCGCCGCCAAAAC
2506;CAGTAACTGAAGTGTCCGCATAAA
2507;TCAACGCTACCTGTAGTTTCCCAG
2508;TCATCTCTCTTTTTGCACGACCAA
2509;CGTACCCGGTTCTGCTTCAATATC
2510;CGGCGTCGAAGCTATTTAACTGGC

2601;CGTATTTTTAACCCAGCTTGGTAA
2602;AAGCACTCGGGCATACTGTAACCA
2603;TGTAGCGAACTGCGATCGTGGACA
2604;ATTGTGAGCATTTTCAGAAAAAGC
2605;CAGAACGTTCCCGAAGTTGCGGCT
2606;TTCTGAACTAGCATCAACAGGCCA
2607;TTAAGCGGCTCACCTTAGCTTCTT
2608;GCGACAGCTTGGTTTTCATATAAC
2609;CCAACAGCTAGTGAGTTGTTCCAT
2610;TCCTAGACTTAACGTATTTAGCCA
2611;CATATCTGACTTTTTGCTTTAGCAGCAAGGTC

1201;TAAAAACCTCATTAGCCTTGCGAC
1202;GCAAGAACCTGCGTAACCGTCTTC
1203;CCAGCTTGCGGCAAAACATACGAC
1204;CGAAAATAGTCACGCAAGAGGGCG
1205;TATCCTTAAAGCATTGGGATTATC
1206;CCTCTAATTGGGGTAATTATACTC
1207;TTAATACCTTTCTTTTCGGTCGTC
1208;TGAGAGTGTCAAAAACTCTTGAAC

1209;TCCAGCAAGATAAACCAACCATCA
1210;CTGTCGCACTACGCGATTTCATAG
1211;CTGAATAGCAAAGCCTTTGCATTCATCAAACG

2301;CCAATCCGTTATCGAACTCAACGC
2302;CGAAAAGACTTTAATAACCTGATT
2303;TGGAGACAAATAATCTCAGAATCT
2304;AGCTTGATGCGGTTATACCTCACT
2305;CATAAATCCCATCTGCTTATGGAA
2306;TTGGGGATAATACCGCCAGCAATA
2307;CAGCAAGAGCAGAAGCTGAGAAAG
2308;TGCCACAAGCCTCAATTTAGACAT
2309;CAAACAATAGCAGGTTTAAGAGCC
2310;CTCAAAGTCGGAGGCGGCTTTTTG

1101;AAGTCAACAAATAATCAGCGTGAC
1102;GGGTAATATGATTCTGCGTTTGCT
1103;AGAAGAGCCATACCGCAGAACGAA
1104;AAGCCTCCAAGATTTGCAGTAGCG
1105;ATCCTTTGGAGGCATGAAAACATA
1106;AGGGTGTCAGCATCAGTGACGACA
1107;CAACCACACCAGAAGCAATCCTGA
1108;TCCTAGACAAATTAGAATACCATG
1109;CTTTATCAGCCAATACCATCAGCT
1110;TTTCCAGAAATTGTTCCAAGTATC

2201;TGAATGCCCAGCACTAACCTTGCG
2202;CTTTGATTTTATCGGTAGCAAGCA
2203;CATGCCTACAGTATTGTGGTCATT
2204;ACTGACCAGCCGTTTGTAATACCA
2205;GGCAGATTAGCTTGAGTAAGCATT
2206;AATCTCGGGTTAGGAACATTAGAG
2207;GGGCGGCCTCATCAGGAAACCTGC
2208;GGAAAGATTGGTGTTTCCAGAAAC
2209;CCATAGCATCCATAATAGACGCAA
2210;GTAGACTCCAAGAAGTCCTTTACC

2101;TGCAACGTTCTGTTGATAAGCAAG
2102;TTTGTGCATCAGAAACGGCAGAAG
2103;CAAATCAAGCAACTTATATACCTG
2104;TATTCTGGCGTGAAGTTGCCACCA
2105;GGCAGACTCGCCGACTGAATGCCA
2106;TTTTTGAGACGAGTATCCTTTCCT
2107;CAGCAGCAAGATAATCTCTCATTT
2108;GGCAATCTCTTTCTGATTAAGCTC
2109;CCCAAGCATTGTCCAGTTGCATTT

2110;TCTTTTTGAGGAAGCATCAGCACC
2111;TCAACCATACCAGCAGATTCTCAAATCCGGCG