

Supporting Information

Control of the two-dimensional crystallization of DNA origami with various loop arrangements[†]

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MATERIALS AND METHODS

Materials. Tris-HCl, EDTA, and MgCl₂ were purchased from Nacalai Tesque, Inc. (Kyoto, Japan). Single-stranded M13mp18 DNA was obtained from New England Biolabs, Inc. (Ipswich, MA, USA, catalog number: #N4040S). The staple strands for the origami tiles, loops, and connecting strands were received from Sigma Genosys (Hokkaido, Japan). The gel-filtration column and the sephacryl S-300 were purchased from Bio-Rad Laboratories, Inc. (Hercules, CA, USA) and GE Healthcare UK Ltd. (Buckinghamshire, UK), respectively. Water was deionized ($\geq 18.0 \text{ M}\Omega \text{ cm}$ specific resistance at 25°C) by a Milli-Q system (Millipore Corp., Bedford, MA, USA). The scaffolded DNA origami structures were designed by using the square lattice version of the caDNAno program (<http://cadnano.org>).

Design and preparation of the monomer origami tiles and 2D crystallization. We have designed the symmetric DNA origami structure for our self-assembly process. This structure was designed in such a way that four corners of this origami tile could exhibit strong π -stacking with the neighboring tiles. We believe that this is a better design when compared to the rectangular origami. Because, in case of rectangular origami design, the π -stacking with the neighboring tile is possible only at two corners. The other two corners are left out with phosphate backbone which will show repulsive force with the neighbor. However, in the present symmetric tile design, π -stacking is possible at all four corners. Thus, no repulsive interaction is possible with neighbor tiles.

Monomer origami tiles were prepared by annealing the solution of M13mp18 DNA (final concentration of 0.01 μM), main tile staple strands (4 equiv., 0.04 μM), loop sequences (4 equiv., 0.04 μM), Tris-HCl (20 mM, pH 7.6), EDTA (1 mM), and MgCl₂ (10 mM) from 85 to 15°C at a rate of -1.0°C/min. No connecting strands with sticky ends were used for the preparation of monomer. However, the connecting strands were replaced by the fully complementary sequences (with no sticky ends) that leave no base unpaired both in the M13mp18 and staple strands. The samples were purified using sephacryl S-300 gel-filtration column prior to the AFM imaging.

The one-pot 2D crystallization of the origami tile was carried out by mixing the solution of M13mp18 DNA (final concentration of 0.01 μM), main tile staples (4 equiv., 0.04 μM), loop sequences (4 equiv., 0.04 μM), connecting strands with sticky ends (10 equiv., 0.1 μM), Tris-HCl (20 mM, pH 7.6), EDTA (1 mM), and MgCl₂ (10 mM). The single-step annealing was performed from 85 to 15°C at a rate of -1.0°C/min.

AFM imaging. AFM images were recorded (except the image in Fig. 2E) using a fast-scanning AFM system (Nano Live Vision, RIBM Co. Ltd., Tsukuba, Japan) with a silicon nitride cantilever (resonant frequency 1.0-2.0 MHz, spring constant 0.1-0.3 N/m, EBDTip radius <15 nm, Olympus BL-AC10EGS-A2). 2 μL of the sample was adsorbed onto a freshly cleaved mica plate (ϕ 1.5 mm, RIBM Co. Ltd., Tsukuba, Japan) by incubating the solution on the mica surface for 5 min at room temperature. The mica surface was then washed several times using same buffer solution in which the origami was prepared. Scanning was performed in tapping mode under liquid environment by using same buffer solution.

For large scale imaging (as given in Fig. 2E), the image was recorded in tapping mode using a MultiModeTM microscope (Bruker) equipped with a Nanoscope V controller. A silicon nitride cantilever (Olympus BL-AC40TS-C2) was used for scanning.

Additional Discussion: The possible reasons for the lattice defects could be: (i) because the origami design adopts 10.67 bp per turn, the structure might not be perfectly planar, which may partially restrict the crystallization and lead to the defects; (ii) there is a possibility that the sticky ends may display nonspecific interactions that may affect lattice formation; (iii) experimental conditions may need to be optimized; (iv) because we performed the crystallization in solution and deposited it on a mica surface for AFM observation, there is a possibility of damage to the structure during surface immobilization; and (v) the structure may be damaged during the AFM scanning.

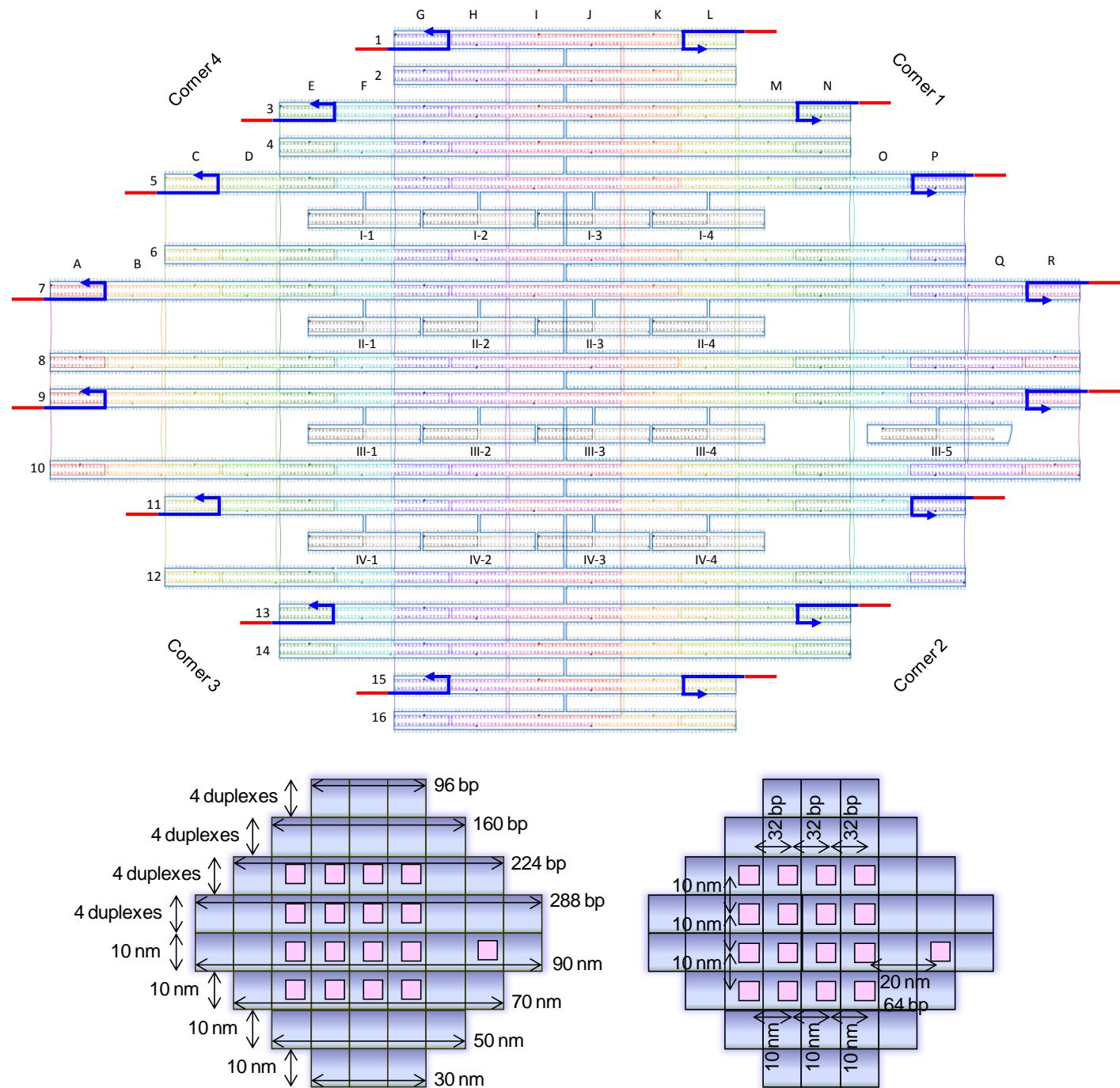


Fig. S1. Top: The caDNAo design of the symmetric tile with individual loops. M13mp18 DNA and staple strands are indicated by blue and color lines, respectively. The connecting strands at each corner are represented by blue color bold arrows. Red color region in the connecting strands represent the sticky ends. Bottom: Scheme of the symmetric tile represented as a matrix of blocks. One block represents four 32-mer duplexes. The main tile is given in lavender color and the individual loops are given in pink color. Note, the tile design for the single-stranded individual loops (no loops) is same as this except that the staple strands in the loops were not used. In both of these designs, 10.67 bp per turn were used.

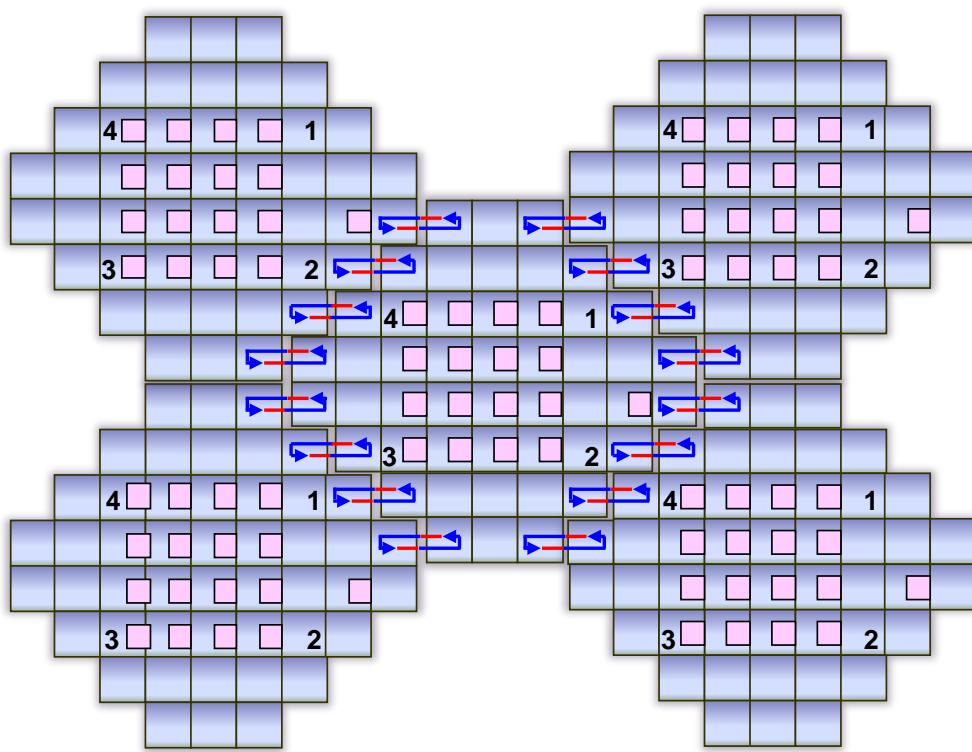


Fig. S2. The schematic of the self-assembly process which indicates the relative orientation of the tiles and their specific association though sticky ends with its neighbor. The individual duplex loops tiles are represented as a matrix of blocks. One block represents four 32-mer duplexes. The main tile is given in lavender color and the individual loops are given in pink color. The numbers represent the each corner of the tile. The sequences of the connecting strands and sticky ends are tabulated below.

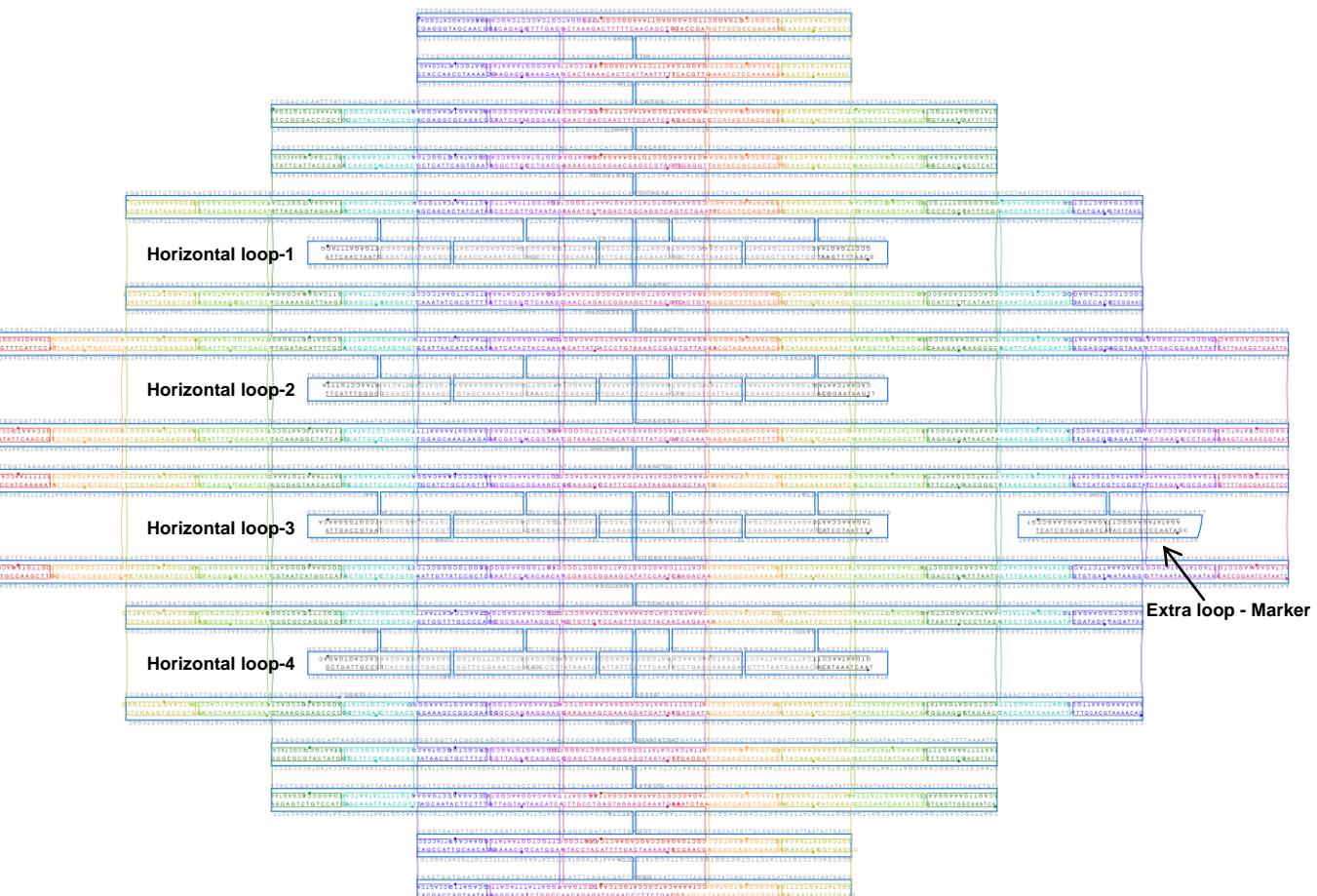


Fig. S3. The caDNAno design of the symmetric tile with horizontally connected loops. M13mp18 DNA and staple strands are indicated by blue and color lines, respectively. Note that only four short loops in a row were connected by loop staples to form a single long loop. Thus, totally four long horizontal loops were formed from 16 short loops, leaving one extra loop on the right side of the tile to function as a marker. In this design, 10.67 bp per turn were adopted.

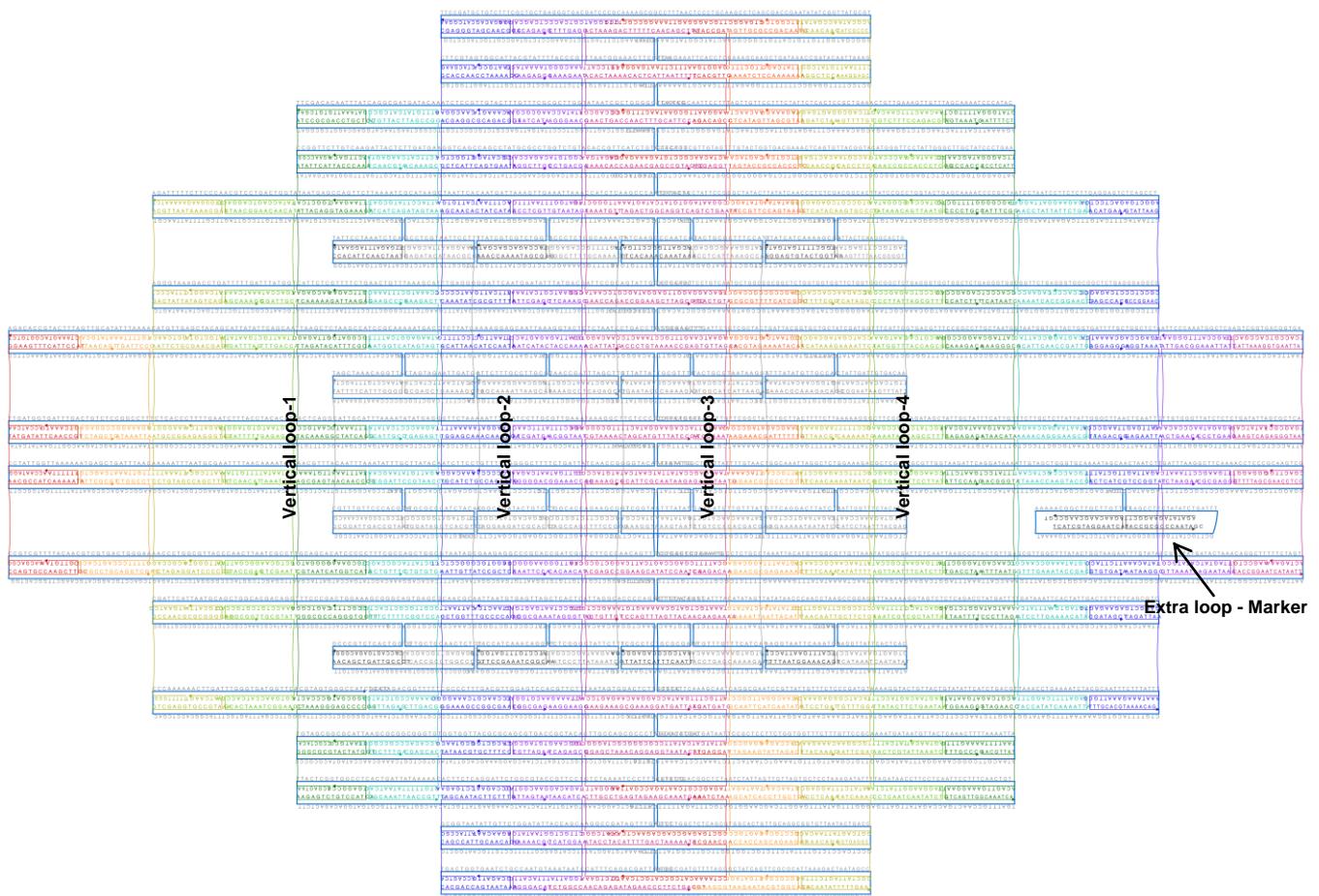


Fig. S4. The caDNAno design of the symmetric tile with vertically connected loops. M13mp18 DNA and staple strands are indicated by blue and color lines, respectively. Note that only four short loops in a column were connected by loop staples to form a single long loop. Thus, totally four long vertical loops were formed from 16 short loops, leaving one extra loop on the right side of the tile to function as a marker. 10.67 bp per turn were used in this design.

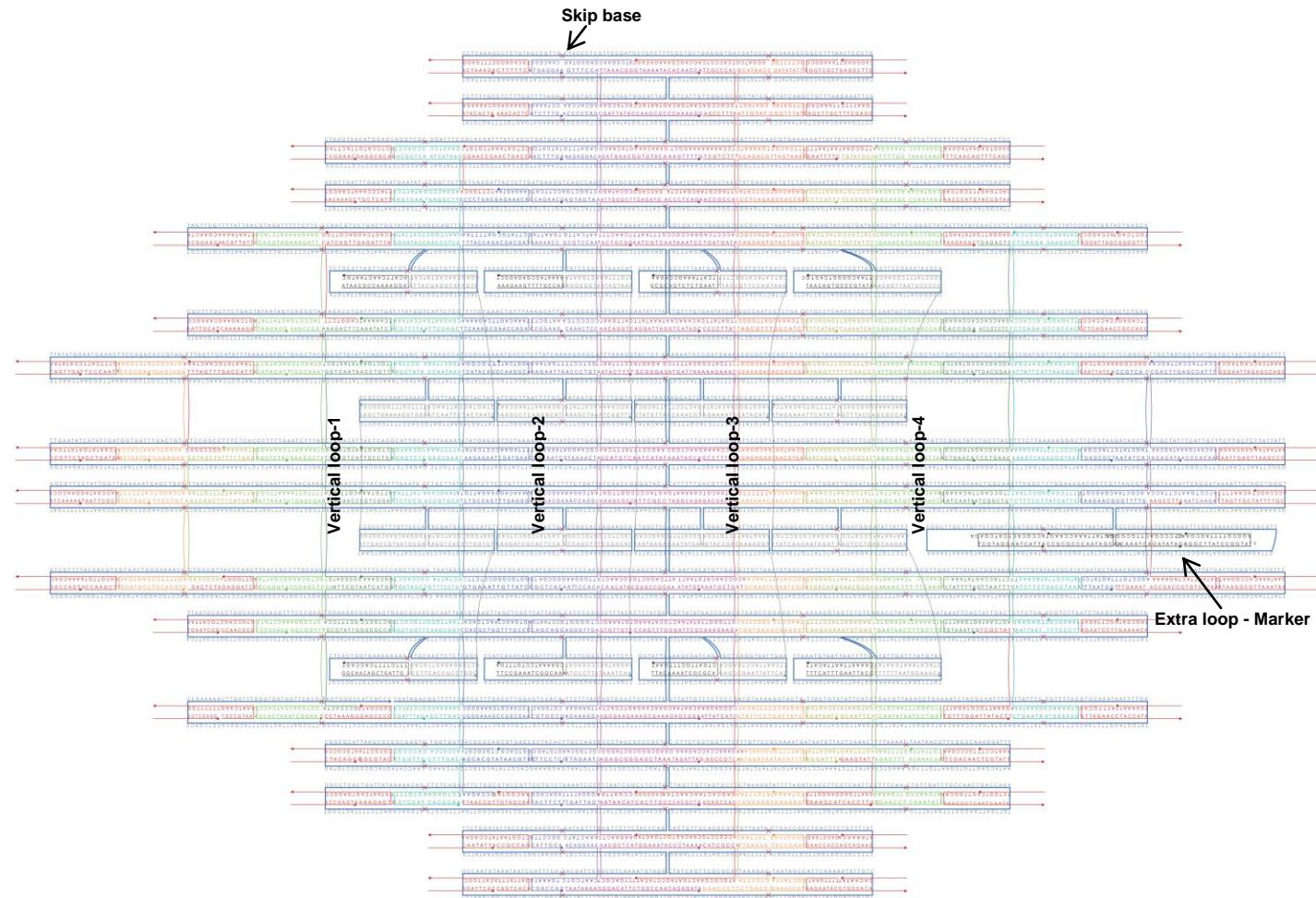


Fig. S5. The caDNAo design of the symmetric tile with vertically connected loops. In this design, we have adopted 10.5 bp per helical turn. M13mp18 DNA and staple strands are indicated by blue and color lines, respectively. The red color crosses represent the bases skipped. Note that only four short loops in a column were connected by loop staples to form a single long loop. Thus, totally four long vertical loops were formed from 16 short loops, leaving one extra loop on the right side of the tile to function as a marker.

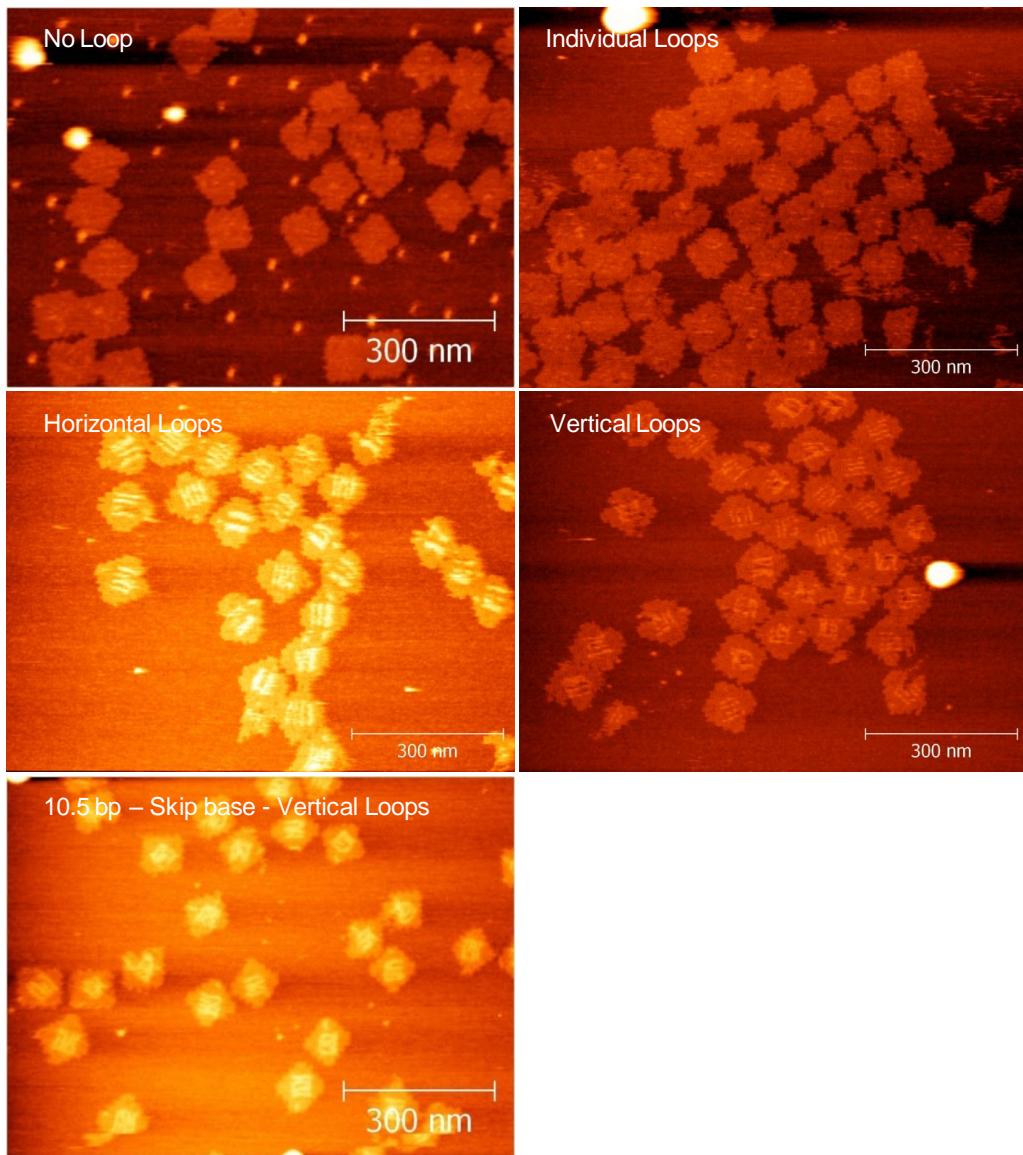


Fig. S6. Zoom-out images of the monomer tiles in each design.

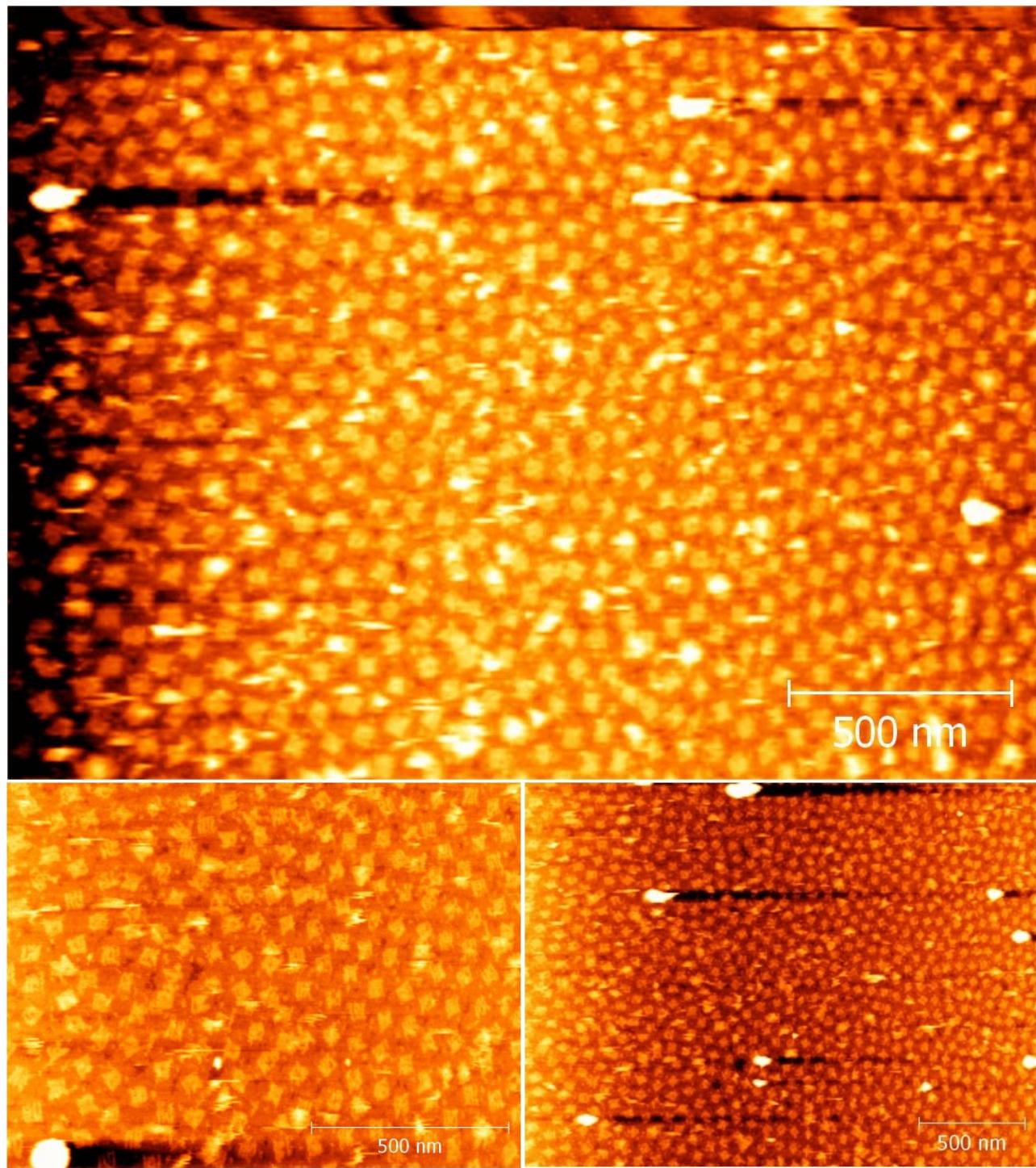


Fig. S7. Additional AFM images of the DNA origami 2D crystal prepared using the design with vertical loop connections as given in Fig. 1D and Fig. S4.

Staple strand sequences:

Name	Sequences (5' --- 3') - Main Tile Sequences (10.67 bp per turn)
1H	GCGGGATCGTCACCCTCAGCAGCGTACAGAGG
1I	TTTCCATTACTAAAGACTTTCAACAGCTTG
1J	CTGAGGCTTGCAGGGAGTTAAGGCCGCTTT
1K	TTGCTTCAGTTGCGCCGACAATGTCGGTCG
2H	CTTGAGGAAACGGTAAAATACGAAAGAGGC
2I	CCCAGCGAACACTAAAACACTCATTAATTTT
2J	ATACCGATGAGGTGAATTCTTAATGAGGAAG
2K	AACAACAAAAATCTCCAAAAAAATTATCAGC
3-4F	ATTGTATCATCGCCTATGTTACTTAGCCGGACCTTCATCAAGAGTAATCAACGTA
3G	CTGGCTGAACGAGGCGCAGACGGTACAAAGTA
3H	AAAAGAATTATACCAAGCGCGAACATCATA
3I	CAGATGAAGAACTGACCAACTTGCATTCCAC
3J	TCACGTTGAAGGAATTGCGAATAACTTGACC
3K	CAGTACAACTCATAGTTAGCGTAATAGAAAGG
3L	AAAGGAGCTTCAGCGGAGTGAGAACGATCTAA
3M	AACCCATGCGTCTTCAGACGTTAACAACTTCAACAGT
4G	CATTGTGAGCTCATTCACTGAATACGCATAGG
4H	AGGGAACCCGGTGTACAGACCAGGAGGCTTGC
4J	AGACAGCCACTACAACGCCGTAGAAAGAGGA
4K	GTATAGCCTAGTACCGCCACCCCTTCGTCAC
4L	AGTTTGTTACCGTAACACTGAGTAGAACCGC
4M	GCGGATAAGAACGCCACCCCTCAGCCAATAGG
5-6D	TATACCAGTCAGGACGCTAACGGAACAAACATTGACCATAATCAAAAGCAAAGC
5E	AAAGAGAAATTACAGGTAGAAAGATTAAGAAC
5-6F	ACAAAGCTATTACCTTATGCGATTTCATCAGATAGTAAGTCAAATGCTTAAACAGAACGGCG
5-6H	CCTGACGAAGATGGTTAATTCAACCTCGTTGTAATAGTCGAATCGTCATAATATTGAGC
5J	AGGAGGTTCGGAATAGGTGTATCAGTAAATTGGGCTTGGAAACACCAGAACGCCGTACTC
5-6L	CACCCCTCAGTGCCTCGAGAGGGTGTACAGTGCACCAACCACCAATTTCGG
5N	CCCTCATTAGCGGGTTTGCTCCCCCTGCC
5O	CAGAACCGAACCTATTATTCTGAAAGAGAAGGGATTAGGAT
6E	CTTAGAGCTAAAAAGATTAAGAGGTTCAGAA
6-5G	TCCTTTGCAAATATCGCTTTAATTCACTGAATCCCCAGCAACACTATCATAACTTAAAT
6J	TAGACTGGCAGGTCACTGAATTGACAGGAGGTTGAGGATAGCGTCAACTACTGAAATGTT
6-5K	GTAGCGACCGCGCTTTCATCGCGAGCCGCCAGCATTACCGTTCCAGTAAGCTGATATAA
6-5M	CAATGAAACCTTATTAGCGTTGCACCCCTCAGAGCCCTATAAACAGTTAATGCAGTACCAAG
6N	TATTCGGCCACCCCTCAGAGCCACCCATCTT
6O	ACCATTACAAAATCACCGAACCGACCC
7B	TGTTTAAATATGCAAATAACAGT
7C	AAAGGGTGAATTCTCGCAACGAGTATGCTGTA
7D	GGATTGCATTAATTGCTGAATATAAGATTAG

7E CAATGCCTTAGATACATTCGCA CGGGATGG
7-8F AAAGACTTATAAGAGGTCTTTAATGGTCAGTAGTATAGAACCTCATATTCAATTGCC
7-8H TTCAAAGCGGATTAGAGAGTACCTAATCATACTACCAAAAAGCCTTATTCAACGATCGATGA
7J AGACTGTAAGAACATCAAGTTGCCTAACTCCAACAGGTAGAACCAGACCGGAAGCTAGCGTC
7-8L TCATAGCCCCATCGATAGCAGCACACATAAAGAAAATTCAACCTTTAAGAAAAGTTAACGT
7N TCATAATCCATTAGCAAGGCCGGACAAAGACA
7O AGCAAGAACATTCAACCGATTGACCAGTAGC
7P ACCGGAACAGAGCCAGCAAAATCAGGGAGGG
8B TGATTCCCAGAAAGGCCGGAGACATCTAGCTG
8C TAAATTTATGCCGGAGAGGGTAGAAGATTCA
8D TTTGACCAGAGTAATGTGTAGGTACTATTTT
8E TTGTAAACTACAAAGGCTATCAGGTTAAATG
8-7G AACAGGATGGAGCAAACAAGAGACAAGGATAAAATTCGATTAACATCCAATATTCAATTGC
8J ACCCTGTAAAACCGAGTGTAGCACAAAGTACCGAGAAGGATACTTGCAGGAGAACATTATG
8-7K TTACAAAAAAGAAACGATTTTGTAAGCAGATAGCCGAAACGTAGAAAATACATCGTAATCA
8-7M AACGAGCGAAATAGCAGCCTTAAGCTATCTACCGAAGTATGGTTACAGCGCAACGTCAC
8N AAAGGGCGACAATGAAATAGCAATCAGAGAGA
8O GCTACAATAAAACAGGGAAGCGCAATAATAAG
8P AGGTAAATAATTGAGTTAACGCCATTAGACGG
8-7Q CCCTGAACAGAGATAACCCACAAGATTGACGGAAATTATTGAGCCATTGGGAATT
9B ATAAATTATTGTTAAATCAGCTCAATTGCGT
9C ACGCCAGGCCGTAGCCAGCTTCAATTGCGA
9D GAGAGATCGTTAATTTGTTAAATCAACAT
9E GGGGATGTAGCGAGTAACAACCCGTATTTAAA
9-10F TGAGAGTCAGATTGTATAAGCAAATCGGATCCGTAACCGCGCTATTACGCCAGCTGCTGTTTC
9-10H ACGGTAAATGGTTGATAATCAGAAAAGGGGACGGAAACCGCTGTTGGGAAGGGCGACAATTCCA
9J ATCCAAATTAAACAGCCATTATCAATCATATGTACCCCCGAAACTAGCATGTTATCCA
9-10L CAAAATGTCTTCCAGAGCCTAAATCAACAAAATAATCGTTAACACGCCAACATTCCA
9N ATAACATATTATCCTGAATCTAATTCCAAG
9-10P GAGAATTAAGATTAGTTGCTATTACTCATCGTCCGGTATTATACAAATTCTACCGTGTGATA
9Q CGCGAGGCTTGAAGCCTAAATCAACTGAACA
10B CTGGCCTTGTTCAGTCACGAATGCCCTGCAGGTCGAC
10D TAAATGTGCTGCAAGCGATTAAGTACCGAG
10E CAGTCGGCGTAATCATGGTCATAGCGAAAG
10-9G CATTAAATTGTTATCCGCTCATCGGTGGGGCTTTGCATCTGCCAGTTGAGCCCCAA
10J CCATTGCAATAAGAGAGCTAATGGCATTTCGAGCCAGTCATTAGGCTGCCAGCAAGCGAAAGCG
10-9K ACTATATGAGAACGCGAGAAAACCTGTAATTAGGCAGAGCAGAACGCGCTGTTTGTGCGAG
10-9M TTTTAACAGTTAATTCACTTCAATTGAGAACGCCATAGCTGTCTTCTTATCCCAACGCT
10N AACGGGTATCAACAGTAGGGCTTATGACCTAA
10-9O ATTATCAGTTGAAATACCGACCAGTATAAGCCAACGCTAAACCAAGTACCGCTGCACCCA
11D CTCGAATTAAACCTGCGTGCAGAGGCGGTT
11E GCCCACTAGGGCGCCAGGGTGGTCCCGCTTTC
11-12F CTGTGTGAGCGTTGCGCTACTGCTTCTTCGGTCCACGAAAAACCGTCTATCAATTAGAG
11-12H CACAACATGTGCTAATGAGTGAGAGCGAAATAGGGTGAATAGAACGTGGACTGGCGAGA

11J CAAGACAATAATGCTGATGCAAAAGTGTAAAGCCTGGACGAGCCGAAGCATATCCAATCG
11-12L TATATTTCCTCCGGCTTAGGTGTAACAATTGCTCTGTTACATCGGGAGAAACAATCCTGAT
11N ATTTAATGAAATCATAGGTCTGAGTTAATTT
12D TCGTATTCTGTGAACCACATACCCAGCACTAAATCGGAAC
12-11G GCGTAACCGGAAAGCCGGCGAACGTCCAACGTCAAAGGGCGCTGTTGCCAGCCTAACTCA
12J TCCAGTTAGTTACAACAAGAAAAATTGCTTGAATACCAGGAACAAGAGTCCACTAGTGTGT
12-11K GGAGCGGAGCAATTCAATATAATAACGGATTGCGCTGAAAATTAAATTACATTGTTATATA
12-11M TATCATTTTATACTCTGAATAACAGTAACAGTACCTTAAATCGCGCTATTAAAGACTACC
12-11O TACCATATCAAAATTATAGATTTCAGGTTAACCTTAAATCGCGCTATTAAAGACTACC
13F CTTGACGGACCACACCCGCCGCGCTGCTTGA
13G CCTGAGAATATAACGTGCTTCCTCACGCTGC
13H AAGGAAGGTGGCAAGTGTAGCGGTCGTTAGAA
13I AGGGATTTGGAGCTAACAGGAGGTAATACAT
13J AGATGATGATTATCATCATATTCCGCGGCGCTAGGGCGGAAGAAAGCGAAAGGATGATTATC
13K TAATAGATTAGAAGTATTAGACTCACCAGAA
13L TGTTGGATGCGGAACAAAGAAACTACAAAC
14F CGAGCACGGTGTITATAATCAGCGCAAATTAACCGTTG
14H TCAGAGCGTAGACAGGAACCGTACATTAGTAA
14I CTATCGGCCCTGCCTGAGTAGAAGCAAATGAA
14J TTGAGGATTAGAGCCGTCAATAGACCGATTAA
14K CAGTGCCAAGCATCACCTGCTGACTAACAC
14-13M CCTCAATCAATATCTGGAGGAAGGTTATCTAAAACCTGTATTAAATCCAGTAACAT
15H TAACATCACTTGCTGGTAATATCCAAAACGC
15I GTCTGAAAATACCTACATTGACTAAAATA
15J AAATCTAACGCTGAGAGCCAGCAGAACTCAA
15K CTGATAGCACCACCAGCAGAAGATGCGCTGCAA
16H TCATGGAATGGATTATTACATTGAGGGACAT
16I TCTGGCCAACAGAGATAGAACCCCTGACCT
16J CCGAACGACCTAAAACATGCCATGCTCAATC
16K GAAAGCGTAAGAATACGTGGCACATGCGCGAA

Name Sequences (5' --- 3') - Connecting Strands (10.67 bp per turn)

2D-1L CCAATAGG ACGCATAA CCGATATA ACAACAAAC
2D-9A CATGCCA AACGCCAT CAAAAATA TTTTTAA
2D-2L CTTAATT GTATCGGT AGGCTCCA
2D-8A TATGATAT TCAACCGT GTCAAATC ACCATCAA
2D-10A CCAGTGCC AAGCTTGC CGTTGTA AACGACGG
2D-3N ATGAATCG GTATGGGA TTTTGCTA AGTAAATG
2D-11C AATTTCT GCCAACGC GCAGGGAG CTGCATTA
2D-4N TTCAGGGA TAGCAAGC AGCCACCA
2D-10C TCTAGAGG ATCCCCGG GTTGGGTA
2D-12C GTCGAGGT GCCGTAAA AATCAAGT TTTTGGG
2D-5P CCGCTACA AGGCTGAG ACTCCTCA ACATGAAA

2D-13E	GTATTAAG GGGCGCGT ACTATGGT TTAATGCG
2D-6P	CGCCTCCC TCAGAGCC GAGCCACC
2D-12E	CTAAAGGG AGCCCCCG GGGCGATG
2D-14E	AAGAGTCT GTCCATCA TGAGGCCA CCGAGTAA
2D-7R	ATTACCGC TCACCGTC ACCGACTT CATTAAAG
2D-15G	GTGAATT A CAGCCATT GCAACAGG AGAACAT
2D-8R	TGAGCGCT AATATCAG AAAGTCAG AGGGTAAT
2D-14G	TAGCAATA CTTCTTG GCCAGAAT
2D-16G	CACGACCA GTAATAAA GCAGATT ACCAGTCA
2D-9R	GGGAGGTT GTTTAGC GAACCTCC CGAGGGTA
2D-1G	GCAACGGC AAAGACAG CATCGGAA CGACTTGC
2D-10R	ACTAGAAA AAGCCTGT CACCGGAA TCATAATT
2D-2G	CAACGGAG GCACCAAC CTAAAACG TAATGCCA CTACGAAG
2D-10Q	AATAAGGC GTTAAATA AGAATAAA TTAGTATC ATATGCGT TCTAAGAA
2D-11P	GTGTCGAA GACGCTGA GAAGAGTC CGATAGCT
2D-3E	TAGATTAA ATCCGCGA CCTGCTCC GATAAATT
2D-12P	AAATAAAG AAATTGCG TTTGCACG TAAAACAG
2D-4E	TGGCTCAT ATATTCA TACCCAAA TCTTGACA AGAACCGG
2D-12N	CCCTTAGA ACGTCAGA TGAATATA TGGAAGGG TTAGAACCC
2D-13N	AAAAATCT TAATTTA AAAGTTG TTTGCCCG
2D-5C	AACGTTAT ACGTTAAT AAAACGAA TTGGGAAG
2D-14N	ACAGTTGA AAGGAATT GTCAGTTG GCAAATCA
2D-6C	GCTCAACA GACTATTAGTCAGA ATCAGGTC TTTACCCT
2D-14L	AATTGAC AATATCT TAGGAGCA ACCTCAAA TATCAAAC
2D-15L	CGGTGTCT GGTCAGTA TTAACACC AAAACAGA
2D-7A	GGTGAGGC GGAAGTTT CATTCCAT CTAAAGTA
2D-16L	GGCTATTAGTC TTAACACC AAAACAGA

Name Sequences (5' --- 3') - Individual Loops (10.67 bp per turn)

I1-right	GAATTACGAGGCCAGATACTAAC
I2-right	TTGCCAGAGGGGAGGTTTGCAA
I3-right	GAAAGCGCAGTCTCCTCATTAAAG
I4-right	GCCTTGAGTAACTAAGTTTAACG
I1-left	ATTCAACTAATGTTGAGATTAGG
I2-left	CAAAATAGCGAGTACCAGACGACG
I3-left	CAAACAAATAAAACGATTGGCCTT
I4-left	GTGTACTGGTAATGGCTTGTATG
II1-right	CAATTCTACTAACGAGCTGAAAAA
II2-right	CTAAATCGGTTGAAAGCCTCAGA
II3-right	TATTACGCAGTACTGGCATGATTA
II4-right	CACAATCAATAGACGGAATAAGTT

II1-left	TTCATTGGGGCATAACCTGTTA
II2-left	AAAATTAAGCAAAGGCAAGGCAAA
II3-left	TACCCAAAAGAAGAACGCAATAA
II4-left	CGCAAAGACACCGTGGCAACATAT
III1-right	AGATGGGCGATGGGATAGGTAC
III2-right	CTTCTGGTGCGCAGCCAGCTTTC
III3-right	AACAACATGTTCCGTCCAGACGA
III4-right	TAGAAACCAATCCATCCTAATT
III5-right	AGATATAGAAGGCTTACCGGCCAATAGC
III1-left	ATTGACCGTAATTCCGTGGGAACA
III2-left	AAGATCGCACTCACGACAGTATCG
III3-left	GGTAAAGTAATTAATATAAAGTAC
III4-left	AAAATAATATCCTAGATAAGTCCT
III5-left	TCATCGTAGGAATCATAGAACAGCAAGCCGT
IV1-right	AGTTGCAGCAAGTCACCGCCTGGC
IV2-right	AATAGCCCAGAAATCCCTTATAA
IV3-right	TGAAACAAACATACCTGAGCAAAA
IV4-right	GTGAATAACCTTACATAATCAAT
IV1-left	GCTGATTGCCCTCACCAAGTGAGAC
IV2-left	CGAAATCGGCAAATCCTGTTGAT
IV3-left	TTCATTCAATTAATCGCCAGAG
IV4-left	AATGGAAACAGTTCATTTGAATT

Name	Sequences (5' --- 3') - Horizontally Connected Loops (10.67 bp per turn)
I4-RightL	GCCTTGAGTAACTAAGTTTAACG
I1-LeftE	ATTCAACTAATGTTGAGATTAGG
II4-RightL	CACAATCAATAGACGGAATAAGTT
II1-LeftE	TTCATTGGGGCATAACCTGTTA
III4-LeftE	TAGAAACCAATCCATCCTAATT
III5-RightQ	AGATATAGAAGGCTTACCGGCCAATAGC
III1-LeftE	ATTGACCGTAATTCCGTGGGAACA
III5-LeftO	TCATCGTAGGAATCATAGAACAGCAAGCCGT
IV4-RightL	GTGAATAACCTTACATAATCAAT
IV1-LeftE	GCTGATTGCCCTCACCAAGTGAGAC
I1-I2-G	TACGAGGCCAGATACATAACGCCCCAAACCAAAATAGCGAGTACCAAGACGACGATAAAAGGAAT
I2-I3-I	CAGAGGGGAGGCTTTGCAAAGATTACAAACAAATAACGATTGGCCTTGATAAGTTTG
I3-I4-K	GCGCAGTCTCCTCATTAAAGCCAGAGGAGTGTACTGGTAATGGCTTTGATGATACAATGAAA
II1-II2-G	TCTACTAAGCGAGCTGAAAGGTGTAGCAAATTAGCAAAGGCAAGGCAAAGAACATGCATCAAT
II2-II3-I	ATCGGTTGAAAGCCTCAGAGCATGGAATACCCAAAAGAACGAAACGCAATAACAAAGCTAA
II3-II4-K	ACGCAGTACTGGCATGATTAAGACGAAACGCAAAGACACCGTGGCAACATATAAAATCCTTATT
III1-III2-G	GGCGCATGGGATAGGTACGTTGCAGGAAGATCGCACTCACGACAGTATCGGCCTGTGTAGAT

III2-III3-I	TGGTGCCGCAGCCAGCTTCCGGAAAAGGTAAAGTAATTAATATAAAGTACCGACACCGCTTC
III3-III4-K	ACATGTTCCCTGTCCAGACGACGACAAGAAAAATAATCCTAGATAAGTCTGAACAATAAACAA
IV1-IV2-G	GCAGCAAGTCACCGCCTGGCCCTGGTTCCGAAATCGGCAAATCCTGTTGATGGTGAGAGAGTT
IV2-IV3-I	GCCCAGAGAAATCCCTATAAATCAATTATTCAATTCAATTACGCGCAGAGGCAGAAAGAATA
IV3-IV4-K	ACAAACATACCTGAGCAAAGAAGTTAATGGAAACAGTTCAATTGAATTACCTTATGATGAA

Name Sequences (5' --- 3') - Vertically Connected Loops (10.67 bp per turn)

Vertical-01	CCACATTCAACTAATGTTGAGATTAGGAATA
Vertical-02	AAACCAAAATAGCGAGTACCAGACGACGATAA
Vertical-03	TTCACAAACAAATAAAACGATTGGCCTTGATA
Vertical-04	AGGAGTGTACTGGTAATGGCTTTGATGATAC
Vertical-05	AACAGCTGATTGCCCTCACCACTGAGACGGGC
Vertical-06	GTTCCGAAATCGGCAAATCCTGTTGATGGTG
Vertical-07	ATTATTCAATTAAATCGCGCAGAGGCAG
Vertical-08	TTTTAATGGAAACAGTTCAATTGAATTACCTT
Vertical-09	AAAGGAATTACGAGGCCAGATAACGCCAGCATCAATTCTACTAACGAGCTGAAAAGGTG
Vertical-10	AGTTTGCCAGAGGGGAGGCTTGCAAAAGAAAAGCTAAATCGTTGTAAGCCTCAGAGCAT
Vertical-11	AATGGAAAGCGCAGTCTCCTCATTAAAGCCAGTCCTTATTACGCACTGGCATGATTAAGAC
Vertical-12	CAGTCCTTGAGTAACTAAGTTAACGGGTTGTCACAATCAATAGACGGAATAAGTTATT
Vertical-13	GTGTAGATGGCGCATGGATAAGTCACGTTGAGAGAGTTGCAGCAACTACCGCCTGGCCCTG
Vertical-14	ACCGCTTCTGGTGCCGCAGCCAGCTTCCGCAAAGAATAGCCGAGAAATCCCTATAATCA
Vertical-15	AATAAACACATGTTCTGTCCAGACGACATGATGAAACAAACATACTGAGCAAAGAAG
Vertical-16	CATGTAGAAACCAATCCATCTAATTACGAGGTGAGTGAATAACCTTACATAATCAATATAT
Vertical-17	GCGGATTGACCGTAATTCCGTGGAACAAACGTATTTCAATTGGGCATAACCTGTTAGCTA
Vertical-18	CAGGAAGATCGCACTCACGACAGTATCGCCTTAGCAAATTAAAGCAAAGGCAAGGAAAGAAT
Vertical-19	AAAAGGTAAAGTAATTAAATATAAAGTACCGACGGAATACCCAAAAGAAGAAACGCAATAATAAC
Vertical-20	AAGAAAAATAATATCCTAGATAAGTCTGAACGAAACGCAAAGACACCGTGGCAACATATAAAA
III5-RightQ	AGATATAGAAGGCTTATACCGCCCCAATAGC
III5-LeftO	TCATCGTAGGAATCATAGAACAAAGCAAGCCGT

Name Sequences (5' --- 3') - Main Tile Sequences (10.5 bp per turn) SKIP BASE

Skip-H1	ATCGGAACGAGGGTAGCAACGGCTGAGGAA
Skip-I1	ACTACGAATAAACGGTAAAATACACAACCAT
Skip-J1	GGGATCGTCACCCCTCAGCAGCGAAAGACAGC
Skip-K1	CGATAGTCATAACCGATATATTGCTTTGC
Skip-H2	GTTTCCATGGCACCAACCTAAAAATCTTG
Skip-I2	AGTACAACCGATTATACCAAGCGCCCAAAGG
Skip-J2	CGCCCACGTGCGCCGACAATGACAGTAATGCC
Skip-K2	TTGAAAATATTGTATCGGTTATCTTGATAC
Skip-F3	CGAAATCCGCGACCTACGGTCAATCATAAGAGAACCGGATATTACAGTGAA
Skip-H3	ACCCCCAGGGAGATTGTATCATCACTTGAA

Skip-I3	CGCATAGGGATGAACGGTGTACAAAGTTTG
Skip-J3	AGCCTTTACTCCAAAAAAAAGGCTGAAACAA
Skip-K3	CCTCATAGCCAGACGTTAGTAAATTTCACG
Skip-M3	ACTACAAATTTCGCTAACACAACGGAACAACAAAGGA
Skip-G4	GATTTAAGCCCTGACGAGAAACAAAGAGTAA
Skip-H4	AGAGGACACTGGCTGACCTTCATCCCAGAACG
Skip-I4	AACCGCCACACCCTCAGAACGCCGTTAATTCAACTTATTGGGCTTGAGATGACCCTCAG
Skip-J4	TCGTCTTTAGCGTAACGATCTAGACCAGG
Skip-K4	AGTACCGCCCTCAGAGCCACCACAGACAGC
Skip-L4	TGTATGGCGCCTGTAGCATTCCACCTCATTT
Skip-M4	GAATAGGTAGCAAGCCAATAGGCAGTACAA
Skip-D5	GAAGAAAAATCTACGACAGGTAGAAAGATTACCTGACTATTATTAAGAGG
Skip-F5	TAAGGCTTGAACTGGCTCATTATAGGAATACCAACCCCTCGCGAGAATGACCATAAAGCGTTTA
Skip-H5	AGTAGTAAAATCATTGTGAATTAAAAACCGCGTCAACCCCTCAAATGCTTCCGGAAG
Skip-I5	AATCGTCAATAAATCCTGATGATATGATATTCAAACAAATAATATTCAATTGAATTACTGCGG
Skip-L5	TCAGGGATGTATCACCGTACTCAGAATAAGTTATTATTCAAGGAGGTTGAGGCAGGTTICATAA
Skip-O5	GCCACCACTCAAGAGAAGGATTGATAAGTGCCGTCGA
Skip-E6	ATAATGCTAAAGACTCAAATATCTAAAAAT
Skip-G6	TTGCGGATTCAAAGCGAACAGATAAACAGTTCAGAAAATTACAGACGACGATCCTTATGC
Skip-I6	CCCCTTATTTCATCGCATTTCGAGAGTACCTTTAATTAAACAGGTAGGATTAGGTACAGC
Skip-K6	AGCGCGTTAGCGTTGCCATCTTCAGACGATTGGCCTCAGGAGTGTACTGGTGAGGTT
Skip-M6	AGAATCAACCGAACCAAGAGCCACGCCAGCATTGACTGAAACATGAAAGTATATAGCCG
Skip-N6	TGAGACTCGAACCAACCACAGAGGCCACCGGA
Skip-O6	CCATCGATCCTCAGAGCCGCACTCAGAGCC
Skip-B7	GTACGGTGTCTGAACTGCGAAC
Skip-D7	AAGCCCCGTAGCTAACATGTTGATACATT
Skip-E7	ATGTGTAGGGTCAATAACCTGTTGCTGAAT
Skip-F7	ATTAGCGGGCTTAGAGCTTAATAGCTATACCAATAAATTAAATGCAATGGAGTCTG
Skip-H7	CAAACCTCCGCTCCTTTGATAAGAAAGAATTAAACCTGTACGCAAGGATAAAATTGTAATCG
Skip-I7	GGGGGAGATGATAAAAAGAAACACCCAAAAGAACTGGCAAGCCTTATTCAAATACTTTT
Skip-L7	TCAAAATCAGTTGCCCTTAGCGTATAAGTTTCAACCGAGGAACCGAGGAAACAAACAGGG
Skip-N7	ACCGCCTCAGCAGCACCGTAATCAGTAAATAT
Skip-O7	TTAAGAAAATTATTCAAAAGGTCAATGAAA
Skip-Q7	ACCCACAAAACAATGAAATAGCAACCGACTTGAGCCATTCCATTACCAATTAGCAA
Skip-B8	GAGTAGAACAGTCAAATCACCAATTATGC
Skip-C8	TTTGTAAAGGTAGCTATTGAGGTGAGAAA
Skip-D8	TCGCAAATGTAAAGATTCAAAAGGAGATCTAC
Skip-E8	CGTTAATATCAGGT CATTGCCCTGACCTGAGTA
Skip-G8	AGATTGTAAAGAGAACATCGACTTAAACCCCTCATATTACAGGCAAGGCAGGTCAATT
Skip-I8	GCCTTACTTAACGTCAAAAATGAGTACCCGGTTGATAGCATGTCAATCATATAAATAGCA
Skip-K8	TTTTTGAGAGAGAATAACATAAGCAATAACCGGAATGCAAAGACACCACGGACAGACTGT
Skip-M8	TATTATTAGACGGGAGAATTAAACAAAGTTACCAAGAATTGAGGGAGGGAGGTAGCGAC
Skip-N8	TGACGGAAAGTAAGCAGATAGCCGACTGAACA
Skip-O8	GCCTAATTAAGTCAGAGGGTAATAGCCCTT

Skip-P8	ACCGTCATAGCTATCTTACCGATGAGCGCT
Skip-B9	CGGAGAGATCAGCTCATTTTTGTCTGGCC
Skip-C9	AACGCCAGGCCAGCTTCATCAAATTAAATT
Skip-D9	AAAGGCTATTTGTTAAAATTGCCATTAAAT
Skip-E9	GGGGGATGGTAACAACCGTCGGAATTGTAAA
Skip-F9	GAGCAAACTAAGCAAATATTTAATTCTCGACCGTGACGCTATTACGCCAGCATAGCTG
Skip-H9	TAAAACTAATCAGAAAAGCCCCAAGACGACGAAACCAGGCCTGTTGGGAAGGGCGACTCACAAT
Skip-I9	ATTCGCCTAGGCAGAGACGACGAACATGTAATTATTACAGGCTGCGCAAAAAGCGCC
Skip-L9	AAGCGCATTATCCAATCCAAATACAGCTAATTAATTACTAGGGCTTAATTGAGAGACAAAGA
Skip-N9	CCCTGAAC TGCCAGTTACAAATAATCAATA
Skip-P9	AATATCAACGCTAACGAGCGTCCAAGAACGGGTTTGAGCCTGTTAGTATCTTAATGGT
Skip-Q9	AATCAAGAACCTGAATCTTACCAAGAGAGATA
Skip-B10	TTCCTGTGGTTTCCCAGTCACGCATGCCTGCAGGTC
Skip-D10	GTGAGCGATGCTGCAAGGCATTACGGGTACC
Skip-E10	GCTTCCAATTCTGAATCATGGCTGGCGAAA
Skip-G10	AACTCACAGTGAAATTGTTATCCGTCGGTGGGCCCTTTCTGCCAGTTGAGGGAAACAGGA
Skip-I10	ATGCTGATGTTGGTTATATAACTGCATAAAGTGTAAAGCACATACGAGCCGGAAATATGTAA
Skip-K10	CGGCTTAGGCAAATCCAATCGCAAATGCCATATTTAACACAATAAACACATGTTAGAACAGGA
Skip-M10	CATAGGTCAAACCTTTCAAATAGCCAACGCTAACAGGAGCATGTAGAACACCAACAGCCA
Skip-N10	ATCGGCTGTTCTTACCAAGTATAAATATTAG
Skip-O10	TGAGAAGATCTTCTGACCTAAATATATGCGTTATACAAATCTTCCTTATCATTCTTCCAGA
Skip-D11	GAGCTCGAGTCGGGAAACCTGTCGGGGAGA
Skip-E11	GCCCACATGCGTATTGGCGGCCACACTGCC
Skip-F11	TTTCCTGTTAATTGCGTTGCGCTGGTGGTCAAGCGGTGAAAAACCGTCTATCACGATTAG
Skip-H11	TCCACACACTGGGTCCTAATGCAGCAGGAGGGTTGATTAAAGAACGTGGACCGTGGCG
Skip-I11	CCAGTTGGGATTGCAAAGAACGAGGGAGAACATAACGAACAAGAGTCCACTAGTGTGTT
Skip-L11	ACGCGAGATGAGAGACTACCTTTCAAGAAAATGTGAGTGTAGAATATAACAGTAAAGATGATG
Skip-N11	TTAATTTCAGTCAATAGTGAATTGTAAATCG
Skip-D12	GGCGGTTCGTAACCACCAACCGACTAAATCGGAA
Skip-G12	CTGCGCGTGGGAAAGCCGGCAATCCAACGTCAAAGGGCCACGCTGGTTGCCAGTGAGCT
Skip-I12	TTATCATCAAGAAACCACAGAAGGGAGCGGGCGTAGGAGGGAAAGAACGAAAGACGGAA
Skip-K12	CGGAAACAATATTCTGATTATCCAGTACCTTTACATTGATGAAACAAACATTAACCTC
Skip-M12	ATTTAATCAATATAATCTGATTCAGGTTAACGTCAAGATAACCTGCTTATCAAAT
Skip-O12	CTGAATAATGGAAGGGTAAAACAGAAATAAAATTAAATTCCCTTAAGACGC
Skip-F13	AGCTTGACAACCACACCCGCATGGITG
Skip-G13	GCCAGAAAGCACGTATAACGTGCCGGTCACG
Skip-H13	AGAAAGGAGCGCTGCCAAGTGTAGTTCTCG
Skip-I13	CCGATTAAAGAGCGGGAGCTAAATAGATTAG
Skip-K13	ATCTTAGATAGATAATACATTGATCATT
Skip-L13	GCAATTCAAAGTTGAGTAACATTAGGATT
Skip-F14	CTTGACGCCCTGAGAAGTGTGTTGTCCATCACGCAA
Skip-H14	TTAGAATCAGGGATTAGACAGGGTACTT
Skip-I14	AAGAACTCAATAACATCACTGCCACGCTG
Skip-J14	AGCCGTCAGAGCACTAACAACTAACAGGAGG

Skip-K14	TATTAACCAGCAAATGAAAAATCTCTAAAAT
Skip-M14	TGAACCTCAAATATCATCAACAGTTGAAAGAGACTTACAAACAACGTTATTA
Skip-H15	TGATTAGTAAACTATCGGCCTTGCATTGCA
Skip-I15	TTGACGCTAACGCTCATGGAAATACCCCTAAAA
Skip-J15	AGAGCCAGACCGCCTGCAACAGTGCTGAGTAG
Skip-K15	GTCTTATTAAAAATACCGAACCGGGTCAG
Skip-H16	ACAGGAAACAATCGTCTGAAATGCGACCAG
Skip-I16	TAATAAAAGGGACATTCTGCCAACAGAGATA
Skip-J16	CATCGCCAATGCGCGAACTGATAGCCTACATT
Skip-K16	GAACCCCTCTGACCTGAAAGCGTGGCTATTA

Name	Sequences (5' --- 3') - Connecting Strands (10.5 bp per turn) SKIP BASE
Skip-1L	TAAAGGCC CGGTCGCT GAGGCTTG ATCAAAAA
Skip-2L	TTAACACAG CAGCTTGC TTTCGAGG GGCCAGTG
Skip-3N	AATAGAAA TTTCAACA GTTTCAGC TGAATCGG
Skip-4N	TTCGTCAC AACCCATG TACCGTAA GGTGAGG
Skip-5P	ACCAGGCG AGGATTAG CGGGGTTT CTACAGGG
Skip-6P	CACCACCC CCTCAGAA CCGCCACC ACCGAGTA
Skip-7R	CAGTAGCA GGGATTAA GAGCCAGC CAATATTA
Skip-8R	GAGCAAGA GAATTGAG TTAAGCCC AGATTCAC
Skip-9R	ACAATTTT TTAGTTGC TATTTTGC ACTAAAGA
Skip-10R	ACCGGAAT ATAAGGCG TTAAATAA ATACACTA
Skip-11P	GCTTAGAT AGAACCT TGAAAACA CCGGAACG
Skip-12P	ATTTGCAC GTTAGAAC CTACCATA ACAAAAGC
Skip-13N	TGCCCCGAA TTCGACAA CTCGTATT ACGGAACA
Skip-14N	GTTGGCAA AAACCCTC AATCAATA GATTGCAT
Skip-15L	GAGGTGAG GAACCACC AGCAGAAG CAGTTGAT
Skip-16L	TTTTGAAT AAGAATAC GTGGCACA CCGTTCTA
Skip-9A	TAATTCGC AACCAATA GGAACGCC CAGGGAGT
Skip-10A	CCAAGCTT GACGTTGT AAAACGAC TGAATTTC
Skip-11C	CCAACCGCG GTGCCAGC TGCATTAA GGAGTGAG
Skip-12C	TGCCGTAA AAATCAAG TTTTTGG CACTGAGT
Skip-13E	CGCGTACT CGCGCTTA ATGCCCG TGCTCAGT
Skip-14E	AAAGAGTC TATAATCA GTGAGGCC CTCAGAGC
Skip-15G	CCGCCAGC CTGGTAAT ATCCAGAA AAAATCAC
Skip-16G	CAGTCACA GATTATT ACATTGGC AATAATAA
Skip-1G	CTTTTCA TACAGAGG CTTTGAGG ACCCAGCT
Skip-2G	AAACACTC CGAAAGAG GCAAAAGA GAATAAAC
Skip-3E	AGGCGCAG GCTCCATG TTACTTAG TAGCGATA
Skip-4E	TGCTCATT TTACCCAA ATCAACGT TCAAAATT
Skip-5C	ACATTATT TTAATAAA ACGAACTA AAATCCTT
Skip-6C	CAAAAAGA AGTCAGAA GCAAAGCG TCTGGTCA
Skip-7A	TCCCAATT GTTTCATT CCATATAA ATAAAACA
Skip-8A	GCTGATAA TCAATATG ATATTCAA GACAATAT

Skip-3L	ATTGCGAA TAATAATT GAATTTTC
Skip-5N	GAGGGTTG ATATAAGT TAAGAGGC
Skip-7P	GGCCGGA AACGTCAC GAATTATC
Skip-10Q	TTGAAAT ACCGACCG TGTGATAA CATAATTA CTAGAAAA AAGCCTTA
Skip-12N	TCGCTATT AGAAATTG CGTAGATT TGTTGGA TTATACTT
Skip-14L	GAAGTATT GAATTGAG GAAGGTTA TAAAGCAT CACCTTGC
Skip-14G	TTAACCGT TGTAGCAA AACGGTAC
Skip-12E	CCCTAAAG GGAGCCCC GGGCGATG
Skip-10C	GACTCTAG AGGATCCC AGTTGGGT
Skip-7C	GGCCGGAG TTTAGTTT GACCATTA TAAATATG CAACTAAA
Skip-5E	CAGGTCTT CATCAGTT GAGATTCA CCAGTCAG GACGTTGG
Skip-3G	TCTTGACA GGAACCGA ACTGACCA GCCTGATA AATTGTGT

Name Sequences (5' --- 3') - Vertical Loops (10.5 bp per turn) SKIP BASE

Skip-I1-L	ATAACGCC AAAAGGA ACATTCA ACTAATGC
Skip-I1-R	AGAGCAAC ACTATCAT ATTACGAG GCATAGTA GTAGTAGC ATTAACAT ATCAATTCTACTAATA
Skip-I2-L	AAAGAAGT TTTGCCAG AAAATAGC GAGAGGCT
Skip-I2-R	ATGTTTAG ACTGGATA AGGGGTA ATAGAAA TACCAAAA ACATTATG AAAGCTAA ATCGGTTG
Skip-I3-L	GCGCAGTC TCTGAAT TCATTAA AGCCAGAA
Skip-I3-R	CGTCATAC ATGGCTTT TTACCGTT CCAGTAAG AAGGTGGC AACATATA AGAAAATA CATACTA
Skip-I4-L	TAACAGTG CCCGTATA TTAACGGG GTCAGTGC
Skip-I4-R	TGCCTATT TCGGAACC AACAGTTA ATGCCCTT AGACAAAA GGGCGACA GGTTTACC AGCGCCAA
Skip-III1-L	ATTGACCG TAATGGGA TGGGAACA AACGGCGG GAGCTGAA AAGGTGGC TTTTCATT TGGGGCGC
Skip-III1-R	AGATGGGC GCATCGTA TAGGTCAC GTTGGTGT CCTGAGAG AGTTGCAG CCCTTCAC CGCCTGGC
Skip-III2-L	GAAGATCG CACTCCA CAGTATC GGCCTCAG AAAGCCTC AGAGCAT GCAAAAT TAAGCAAT
Skip-III2-R	CGCTTCTG GTGCCGGA GCCAGCTT TCCGGCAC AAGAATAG CCCGAGAT ATCCCTTA TAAATCAA
Skip-III3-L	TAATAAGA GAATATAA GGCATTT CGAGCCAG GTATGTTA GCAAACGT GACTCCTT ATTACGCA
Skip-III3-R	AAAGTAAT TCTGTCCA AGTACCGA CAAAAGGT TTCAATT CCTGAGCA GAGGCAGA TTATTCA
Skip-III4-L	TTATCAAC AATAGAT GCAGAAC GCGCCTGT ATAGAAAA TTCATAT ATTTTGT CACAATCA
Skip-III4-R	AAATAATA TCCCATCC AAGTCTG ACAAGAA GTACATAA ATCAATAT TTTTTAA TGGAAACA
Skip-III5-L1	CCGCACT CATCGAGA TCGTAGGA ATCATTA
Skip-III5-L2	CCGCGCCC AATAGCAA GGTATTAA ACCAAGTA
Skip-III5-R1	CTCCCGAC TTGCGGGA GCAAATCA GATATAGA
Skip-III5-R2	AGGCTTAT CCGGTATT AGGCGTT TAGCGAAC
Skip-IV1-L	GGCAACAG CTGATTG TTTCTTT TCACCAAGT
Skip-IV2-L	TTCCGAAA TCGGCAAA CGAAAATC CTGTTGAA
Skip-IV3-L	TTACAAAA TCGCGCA CTGATTG CTTTGAAT
Skip-IV4-L	TTTCATTT GAATTACC CAAAATTA ATTACATT