Supplementary Materials

Programming DNA Tube Circumference by Tile Offset Connection

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Materials and methods

Sample preparation: All the DNA strands were purchased from Integrated DNA Technologies, Inc. DNA nanostructures were designed using caDNAno.

To prepare DNA tubes, unpurified DNA strands were mixed together in an equal stoichiometric ratio in 1×TE buffer (containing 5 mM Tris and 1 mM EDTA) supplemented with 6 or 12.5 mM $MgCl_2$. Then, the DNA strands mixture was isothermally annealed at different temperatures in the PCR thermal cycler for a period of time. For 19 × 4 Tile array, 100 nM DNA concentration with 12.5 mM $MgCl_2$ and 72 hours annealing time were optimal annealing conditions. For 19 × 14 Tile model, 25 nM of DNA with 6 mM $MgCl_2$ and 72-85 hours annealing time were required for tube assembly.

Agarose gel electrophoresis for optimizing isothermal annealing protocol: To get the optimal isothermal temperature, we folded the core monomer structure of each model without x or y directional connector strands at different isothermal temperatures. Then, the obtained monomer samples were subjected to 1% agarose gel electrophoresis (gel was prepared in 0.5×TBE buffer supplemented with 10 mM $MgCl_2$, and 0.005% (v/v) EtBr for staining) at 60 V for 2 hours to compare the target band yields. Finally, the optimal temperatures of 49.4 °C for 19 × 4 Tile model and 46.5 °C for 19 × 14 Tile model were chosen for the subsequent isothermal annealing of DNA tubes.

AFM imaging: 5 μL of DNA sample was dropped onto the freshly-cleaved mica for absorption, and after 2 minutes incubation, 60 μL of 1×TE buffer containing 10 mM $MgCl_2$ were added onto the surface of mica for the imaging. Commercial silicon nitride cantilevers (Bruker, SNL-10) were used for scanning. All the samples were imaged using Bruker Multimode VIII atomic force microscopy in the ScanAsyst mode in liquid.

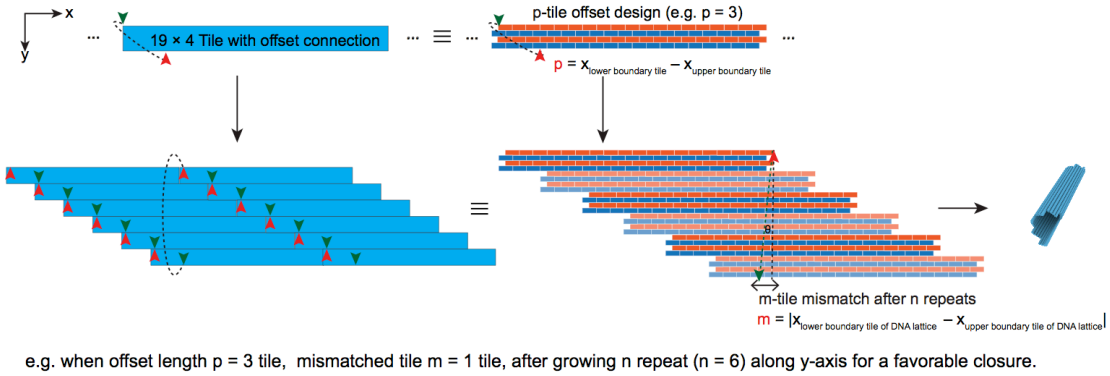

Figure S1. A schematic to illustrate the definition of the offset number (p), and the mismatch number (m) in a DNA nanotube using the offset design.

In a conventional SST tube, upper boundary tiles bind to lower boundary tiles with no offset, whereas in our offset-connection system, upper boundary tiles along the x-axis were designed to bind to the lower boundary tiles with p tile offset between the upper and lower boundaries. p=1, 2, … 9 for the 19 × 4 Tile array and the 19 × 14 Tile array.

For an arbitrary tube formed by X × Y tile arrays with p-tile offset, without considering mismatch, the formula for designing the circumference is: Tube circumference = 2nm × Y × n = 2nm × Y × (lcm{X, p}/p), where 2nm is the diameter of a DNA duplex, and n is the repeat number along y-axis.

However, in actual experiments, tubes can form with a degree of misalignment. This mismatch number is defined as m (tiles). When forming a tube with a X × Y array, if the tube closes with n repeats (n ≤ X) along the y-axis, we can calculate m as:

$$m = \min[\mathrm{mod}(p \times n, X), X - \mathrm{mod}(p \times n, X)]$$

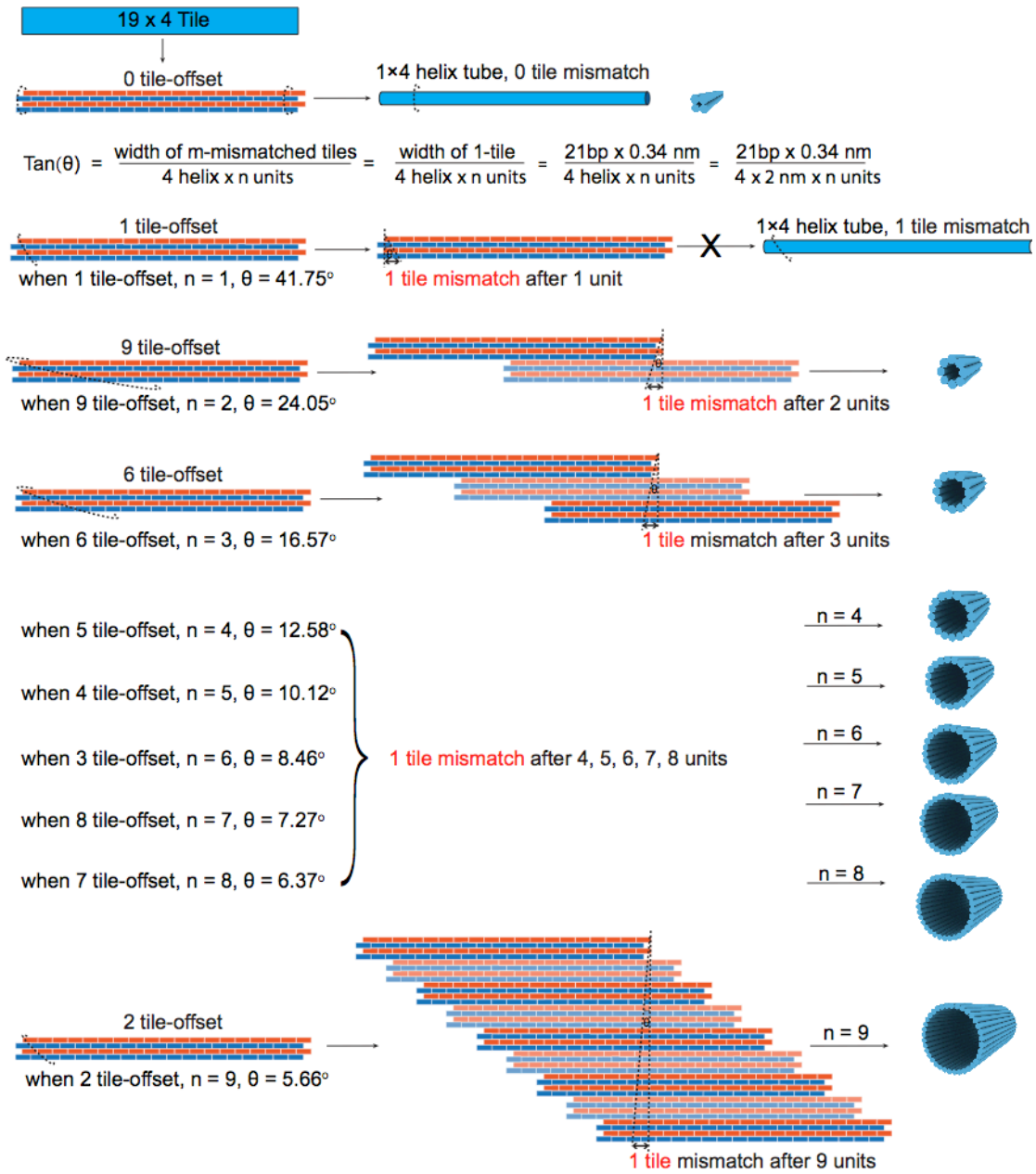

Figure S2. A schematic to illustrate the calculation of the possible twist angle (θ) after growing n repeats of 19 × 4 Tile array along y-axis to achieve a favorable connection with the minimal mismatched tile (m=1) for tube closure in each tile-offset-connection design.

As shown in Figure S2, the twist angle θ can be calculated by Tan (θ) = width of the mismatched tile / n × 4 helices. We take 1-tile offset as an example: m = 1, n = 1, the width of 1 tile-offset is about 7.14 nm since there are 21 bp in each tile unit, and the width of 4 helix is around 8 nm based on 2 nm per helix, and hence the angle θ is 41.75° by calculating the tan (θ) value from the formula.

Table S1. Summary of the calculated number (m) of mismatched tiles and twist angle (θ) after growing n repeats of 19 × 4 Tile array along y-axis perpendicular to the helix for each offset design. There are varied offset designs from 0 to 9 tile offset. Red labels the most favorable conditions anticipated and verified later in experiments.

Offset No. / Repeat No.	0-offset	1-offset	2-offset	3-offset	4-offset	5-offset	6-offset	7-offset	8-offset	9-offset
		X	Number of Mismatched tiles (twist angle θ)							
1×4-helix	0 (0°)	1 (41.75°)	2 (60.74°)	3 (69.45°)	4 (74.35°)	5 (77.37°)	6 (79.42°)	7 (80.91°)	8 (82.03°)	9 (82.9°)
2×4-helix		2(41.75°)	4 (60.74°)	6 (69.45°)	8 (74.35°)	9 (76.02°)	7 (72.25°)	5 (65.86°)	3 (53.24°)	1 (24.05°)
3×4-helix		3(41.75°)	6 (60.74°)	9 (69.45°)	7 (64.35°)	4(49.96°)	1 (16.57°)	2 (30.75°)	5 (56.1°)	8
4×4-helix		4(41.75°)	8 (60.74°)	7 (57.37°)	3 (33.8°)	1 (12.58°)	5	9 (63.53°)	6 (52.42°)	2
5×4-helix		5(41.75°)	9 (58.1°)	4 (35.53°)	1 (10.12°)	6	8	3 (28.17°)	2 (19.65°)	7
6×4-helix		6(41.75°)	7 (46.2°)	1 (8.46°)	5	8	2	4 (30.75°)	9 (53.24°)	3
7×4-helix		7(41.75°)	5 (32.52°)	2	9	3	4	8 (45.57°)	1 (7.27°)	6
8×4-helix		8(41.75°)	3 (18.5°)	5	6	2	9	1 (6.37°)	7	4
9×4-helix		9(41.75°)	1 (5.66°)	8	2	7	3	6	4	5
10×4-helix		9(38.77°)	1	8	2	7	3	6	7	5
11×4-helix		8(32.98°)	3	5	6	2	9	1	7	4
12×4-helix		7(27.5°)	5	2	9	3	4	8	1	6
13×4-helix		6(22.39°)	7	1	5	8	2	4	9	3
14×4-helix		5(17.68°)	9	4	1	6	8	3	2	7
15×4-helix		4(13.39°)	8	7	3	1	5	9	6	2
16×4-helix		3(9.5°)	6	9	7	4	1	2	5	8
17×4-helix		2(6°)	4	6	8	9	7	5	3	1
18×4-helix		1(2.84°)	2	3	4	5	6	7	8	9
19×4-helix		0	0	0	0	0	0	0	0	0

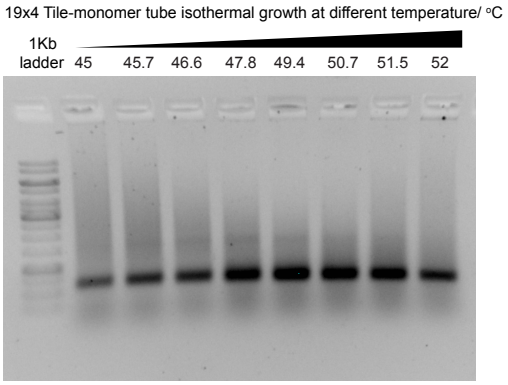

Figure S3. The agarose gel electrophoresis image of the annealed 19×4 tile monomer tube samples obtained from different isothermal temperatures from 48 °C to 52 °C.

To optimize the isothermal annealing temperature ranges for preparing tile-offset-connection tube, 19 × 4 Tile monomer tube with 0-tile offset y connector strands and without x connector strands was prepared by isothermal annealing at different temperatures ranges from 48 °C to 52 °C. We selected 49.4 °C as the optimized temperature for the subsequent growth of offset tubes, since at this temperature the target band presented the highest product yields in Figure S3.

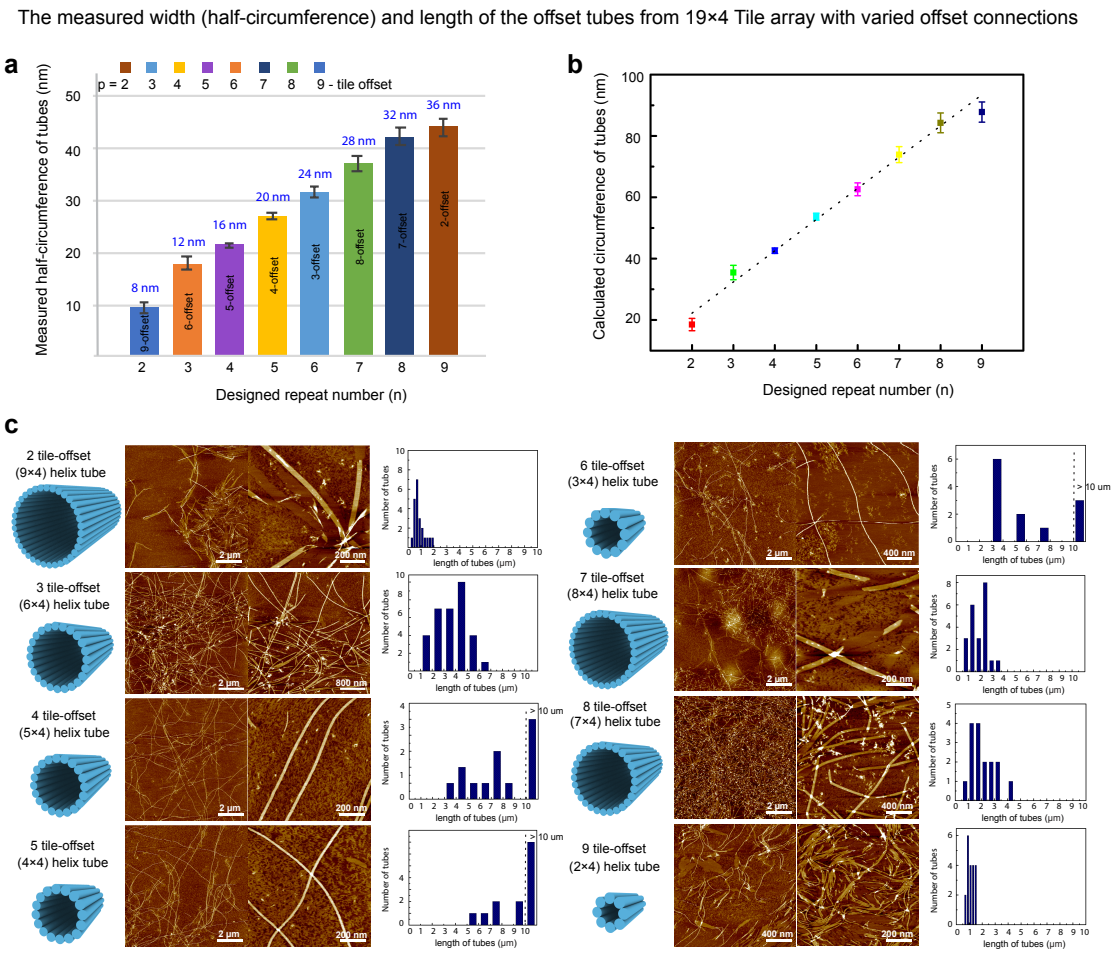

Figure S4. (a) The measured width of the offset tubes with varied tile-offset-connections from AFM images versus the repeating number n of 19 × 4 Tile growing along y-axis. Noted that the width of tube is approximately half of the circumference in theoretical under AFM. The calculated theoretical half-circumference values of the corresponding tubes were given in blue. (b) An approximately linear fitting plot shows the relationship between the circumference of tube and the repeating number n. (c) AFM images and the statistic length histogram of these tubes with 2 to 9-tile offset connections.

We carefully measured the width of these tubes from varied tile-offset connections, and calculated the corresponding circumference of the tubes, which presenting a proximately linear relationship with the predicted repeating number n for each corresponding offset design in Figure S4 a and b.

Table S2. The calculated number (m) of mismatched tiles and the twist angle (θ) after growing n repeats of 19 × 14 Tile array along the y-axis calculated based on 2 nm per helix width. Blue labels the conditions where the minimal mismatched tiles number (m) and twist angle (θ) could be achieved in theoretical. Red labels the favorable condition successfully verified later in experiments with increased flexibility due to the introduction of 2T spacer.

Offset No. / Repeat No.	0-offset	1-offset	2-offset	3-offset	4-offset	5-offset	6-offset	7-offset	8-offset	9-offset
	X Number of Mismatched tiles (twist angle θ)									
1×14-helix	0 (0°)	1 (14.3°)	2 (27.02°)	3 (37.42°)	4 (45.57°)	5 (51.89°)	6 (56.83°)	7 (60.74°)	8 (63.89°)	9 (66.46°)
2×14-helix		2	4 (27.02°)	6 (37.42°)	8 (45.57°)	9 (48.93°)	7 (41.75°)	5 (32.52°)	3 (20.93°)	1 (7.27°)
3×14-helix		3	6 (27.02°)	9 (37.42°)	7 (30.75°)	4 (18.78°)	1 (4.86°)	2 (9.65°)	5	8
4×14-helix		4	8 (27.02°)	7 (24.05°)	3 (10.83°)	1 (3.65°)	5	9	6	2
5×14-helix		5	9 (24.66°)	4 (11.53°)	1 (2.92°)	6	8	3	2	7
6×14-helix		6	7 (16.57°)	1 (2.43°)	5	8	2	4	9	3
7×14-helix		7	5 (10.02°)	2	9	3	4	8	1 (2.09°)	6
8×14-helix		8	3 (5.46°)	5	6	2	9	1 (1.83°)	7	4
9×14-helix		9	1 (1.62°)	8	2	7	3	6	4	5
10×14-helix		9	1	8	2	7	3	6	7	5
11×14-helix		8	3	5	6	2	9	1	7	4
12×14-helix		7	5	2	9	3	4	8	1	6
13×14-helix		6	7	1	5	8	2	4	9	3
14×14-helix		5	9	4	1	6	8	3	2	7
15×14-helix		4	8	7	3	1	5	9	6	2
16×14-helix		3	6	9	7	4	1	2	5	8
17×14-helix		2	4	6	8	9	7	5	3	1
18×14-helix		1	2	3	4	5	6	7	8	9
19×14-helix		0	0	0	0	0	0	0	0	0

In Table S2, we calculated the twist angles without considering the possible effects of 2T flexible spacer. The exact effect of 2T linkers on twist angles is not very clear, although twist angles would be probably reduced due to the slightly increased spacing arising from the length of 2T nucleotides (ca. 0.676 nm for each nucleotide) between the neighboring DNA helices.[1, 2] We calculated and speculated the possible decreases of all twist angles in a range of ca. 0.2 ~ 4° due to the introduction of 2T flexible spacer into tiles. However, for the twist angle which is approaching to the range for favorable tube closure, the decreases of the twist angle values after introducing 2T spacer are almost negligible. Therefore, we think the 2T spacer mainly contribute to the flexibility of tile connections for tube formation.

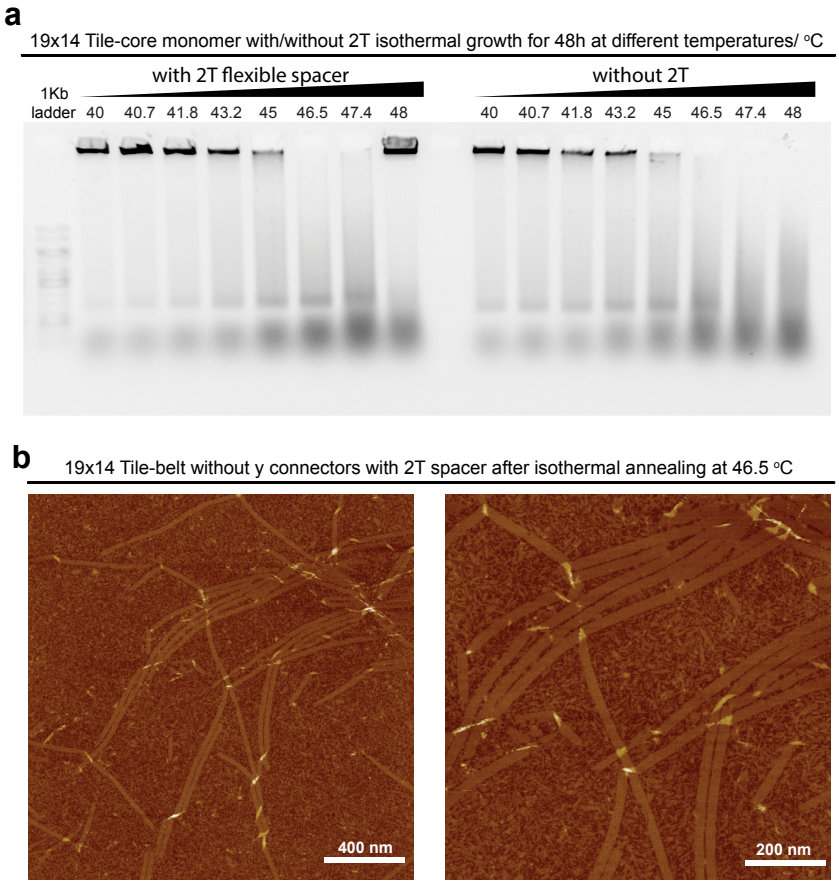

Figure S5. (a) The agarose gel electrophoresis image of the annealed 19×14 Tile monomer structures obtained from different isothermal temperatures from 40 °C to 48 °C. The temperature of 46.5 °C was chosen as the optimal isothermal temperature for both the structures with/without 2T flexible spacer. (b) the ribbon samples isothermal annealed from 19×14 Tile array with 2T spacer and without y connectors.

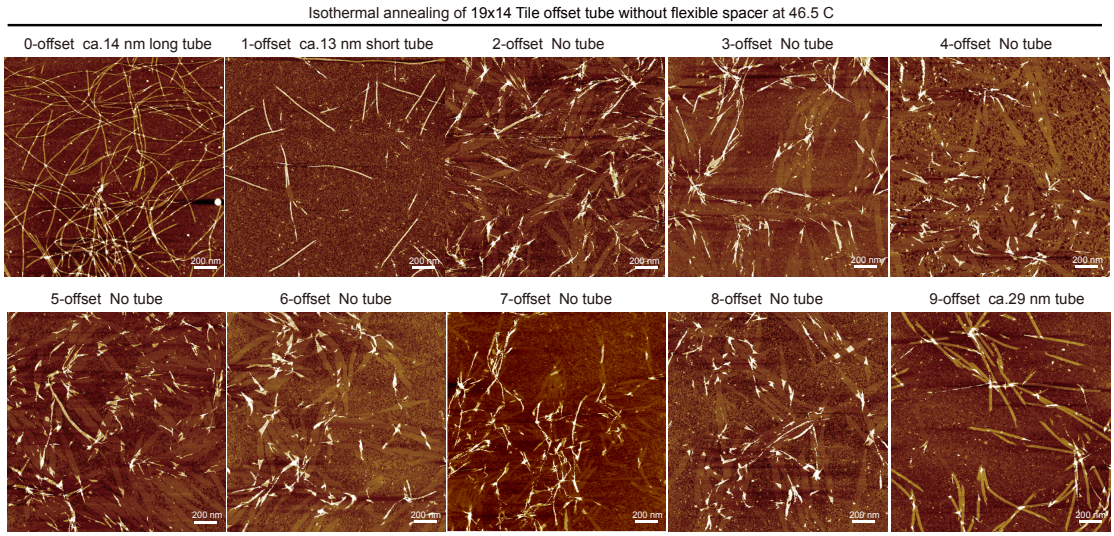

Figure S6. AFM images of samples after isothermal annealing at 46.5 °C based on 19×14 Tile array with varied tile-offset-connection designs from 0 to 9-tile offset.

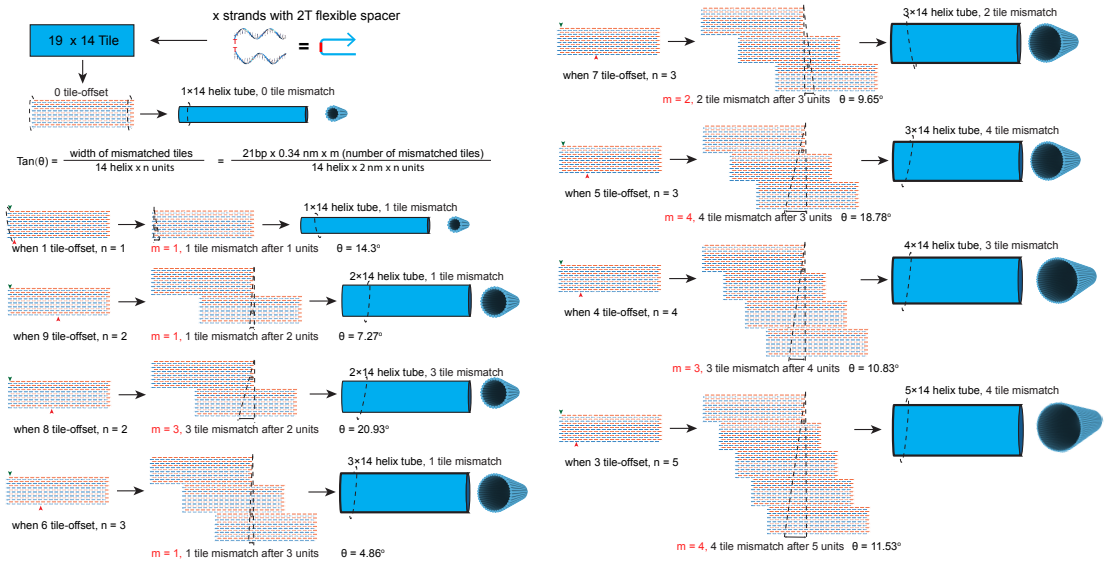

Figure S7. A Schematic to detail the calculation of twist angle (θ) after growing n repeats of 19 × 14 Tile array along y-axis to achieve a favorable connection of m-tile mismatch for tube closure in each offset design. The x strands used here all have a 2T flexible spacer in the middle half-crossover location.

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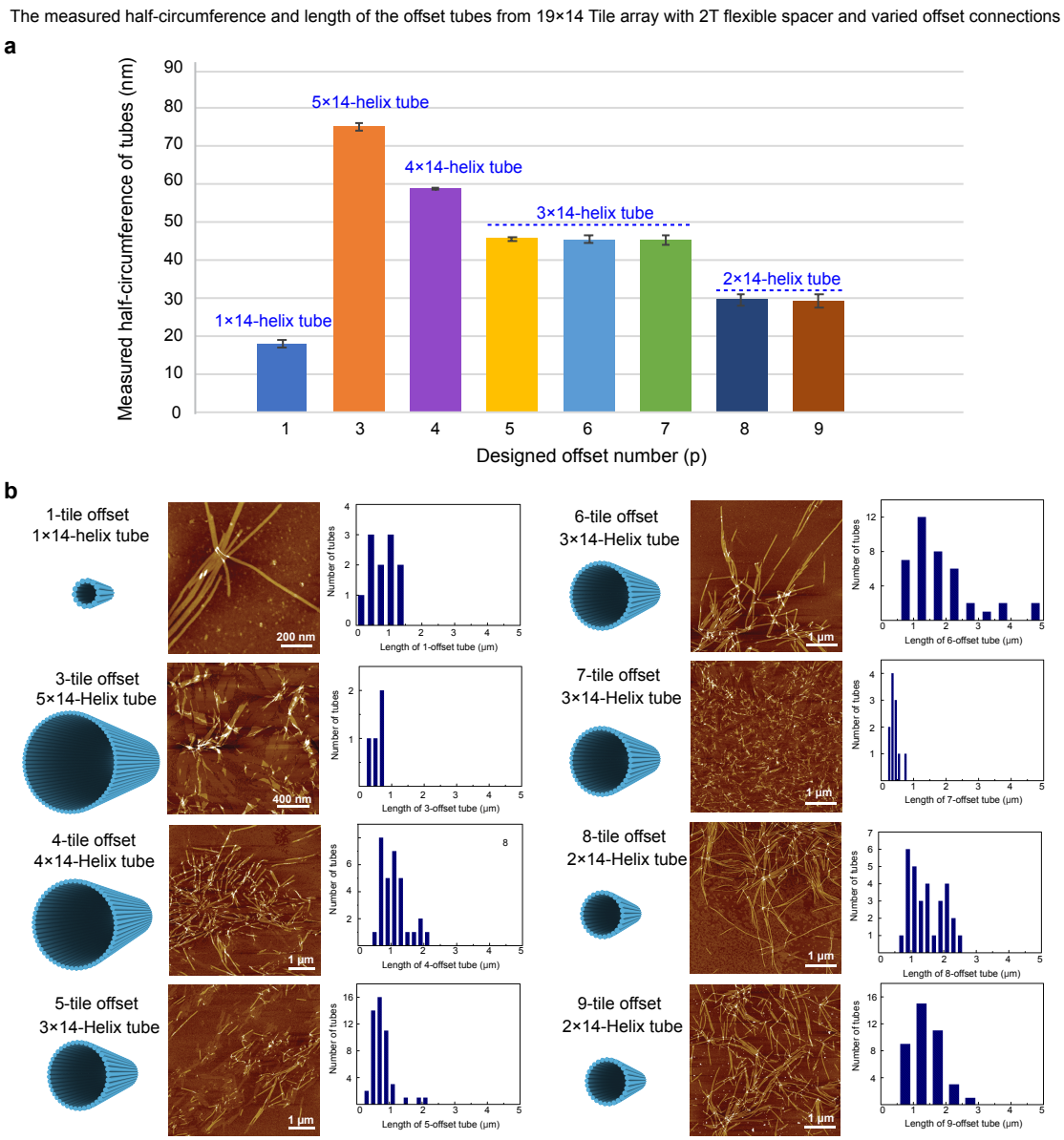
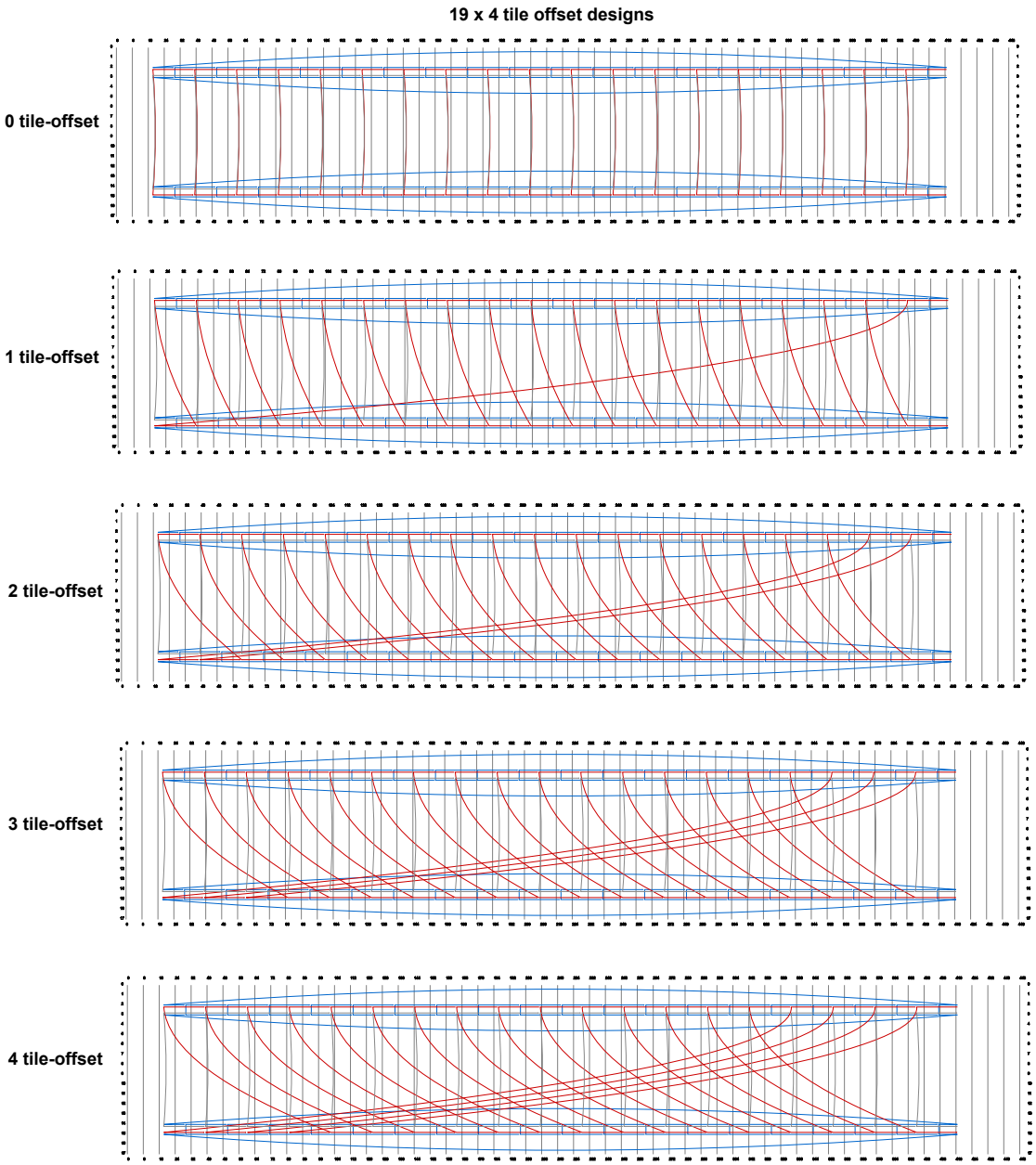


Figure S8. (a) The measured width (half-circumference) of the offset tubes with varied offset connections from AFM images based on 19 × 14 Tile model. (b) AFM images and the statistic length histogram of these offset tubes with 1, 3, 4, 5, 6, 7, 8 and 9 tile-offset connections.

Strand diagrams



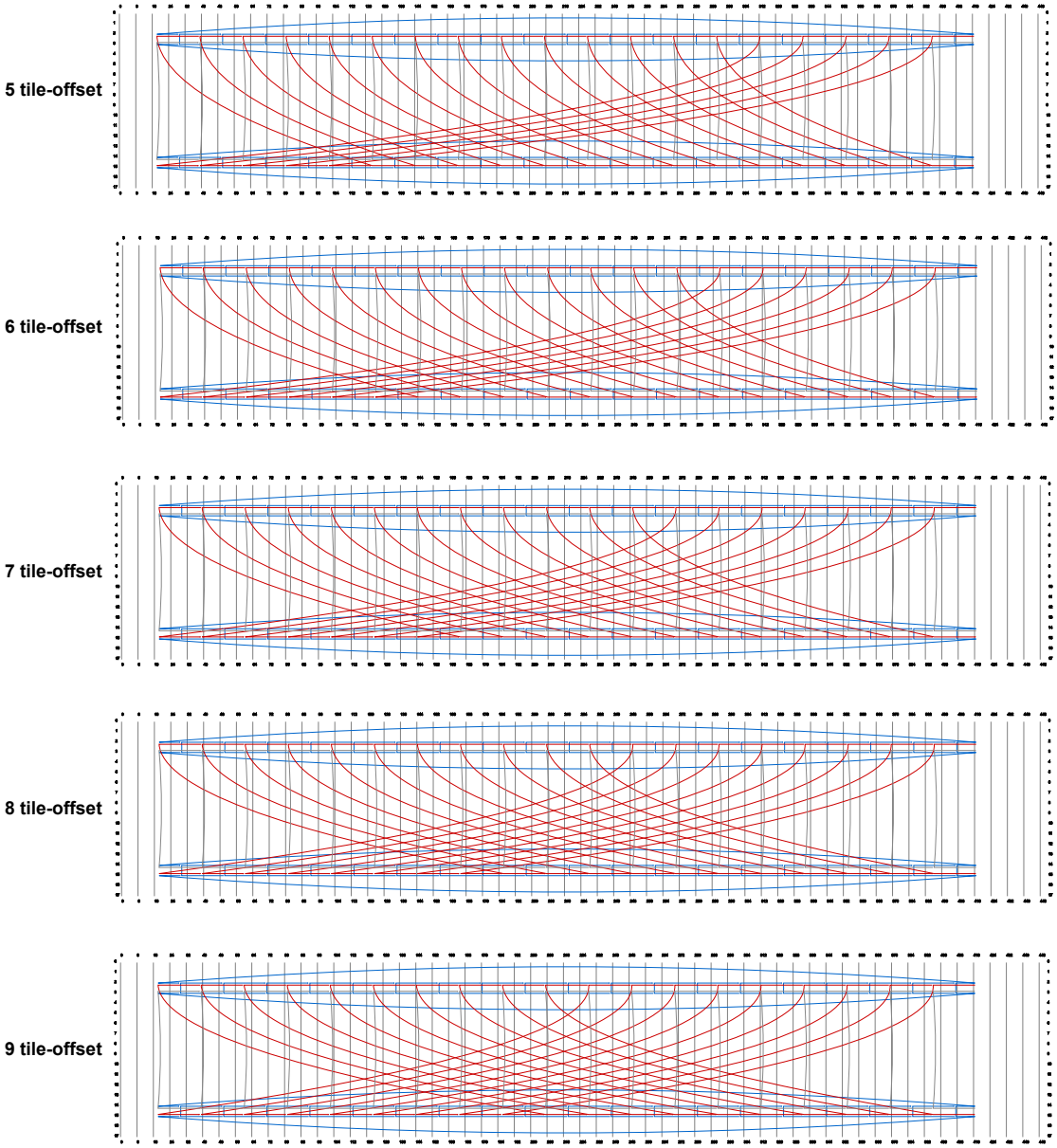
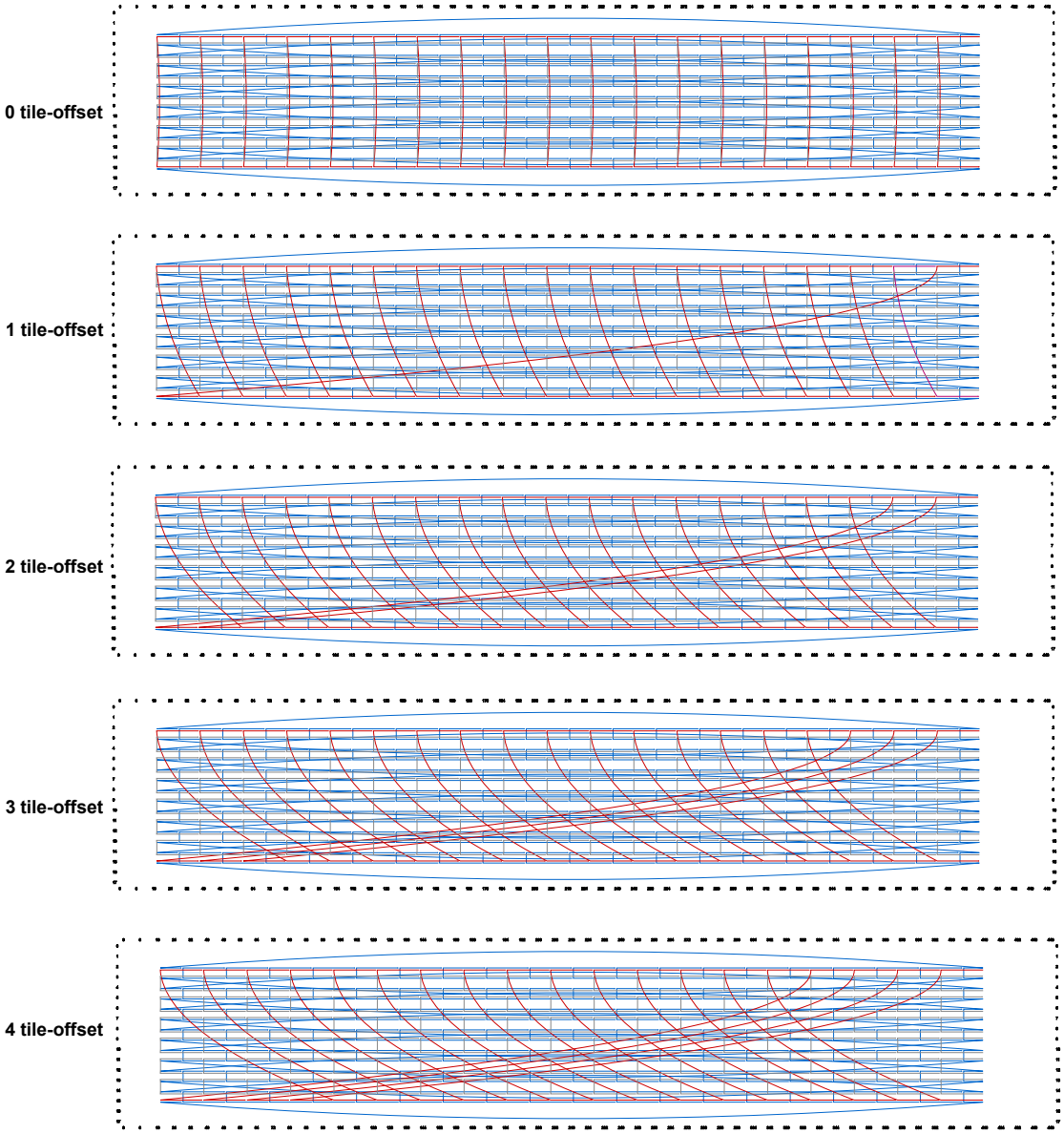


Figure S9. Strand diagram of 19×4 Tile model structure with varied offset connections from 0 to 9 offset. The offset strand is labeled by red. Zoom-in to see details.

Strand diagrams for 19 x14 tile with different offset design



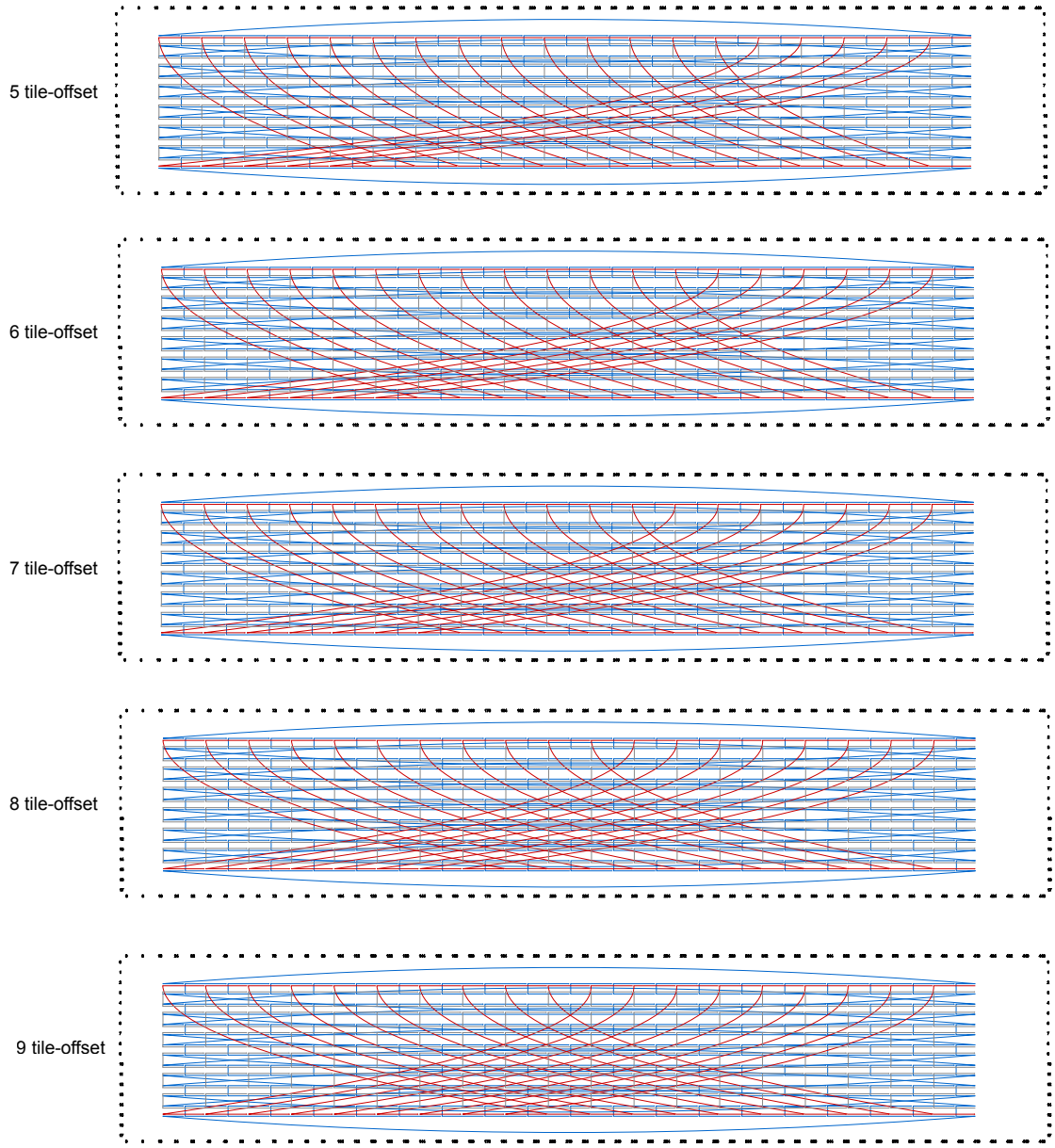


Figure S10. Strand diagram of 19×14 Tile model structure with varied offset connections from 0 to 9 offset. The offset strand is labeled by red. Zoom-in to see details.

Sequences of DNA strands.

Table S3. Sequences of the 19×4 Tile-core structure

Sequence of the 19×4 Tile-core structure: x and y strands	5' end
ACGTGTCGTGTCACTTACCACTAGGAGTTTATAACCCTTGAG	3,28
TGCGGGCCCATAGTATCAATGTTCCCCATTTTATCTCACTGA	3,49
CTTCGTGGGCGGGGGTCTGAGTGTAAGCCTGTTAGTGGGTCC	3,70
TAGGCGTAGAGGCGAACACATGAGCCATATGGTACCTTCGGT	3,91
CATAGTGTAACTAAACATCCGCATGGCCTCGTAGTTTGTACT	3,112
AGCCAATAGGCCGAGGCCAACCAAAAGAAATCTATTGCCGTA	3,133
CTTGATATTTGTCTACTTCCATGCCATTGAGAAAAGATCGGG	3,154
GCGAGTGCTCTGTTGCAATTGCAATGGGTATGTGAAAACGAA	3,175
CGGTCAAAGCCAGTCCATGCGCCAACGAAATCCTGCGGCGCC	3,196
CGCGCAGAAGGTCGCGCTCGTACGTGCACGCCCGTGGCCCAG	3,217
CCCTATATATGTAGGATGTTTGGAAAAAAGGGGTGTTCCAGA	3,238
ACAAATAAGTGGTTGGAATTAATGTTAGGCCATCTGCATCCA	3,259
TAAGCTTGGACACTAATGGTGCATTGTGCAATTCATGCGTCT	3,280
CCGCTATCGACAACCTGGTGATCATCTATGGATCATAGTGGA	3,301
GAGCTCGGGATTCAACCGTTACGTCTGAACTGATACGACTGC	3,322
CAGTGGGAAAAAGTAATCCAGCACAGTTCTACATCTAGAAGA	3,343
TTGTGACACAAAGTCTTGGTGACTATGAGTGCCACTACACAC	3,364
GCAACCGAAAATGATAAGTGGCCCTCAATCCCGAAGCGAACT	3,385
CACATTTAAGAAGATTTAGGAAGGTGGTCCAAGTGAGTCCCC	3,406
TATACGACGTCTTTTCTAAACACACGACACGTCATTGATACT	14,38
ATTAGTCCCATTATCCCGACCATGGGCCCGCACTCAGACCCC	14,59
TCATTGAGTTCAATTGTGACGCGCCCACGAAGATGTGTTCGC	14,80
CTGCAGTGAAGCGTCAATGAACTCTACGCCTACGGATGTTTA	14,101
CAGAACCGTCTAGCTTCCCGCGTTACACTATGGTTGGCCTCG	14,122
GTTATCTTGCCTTATTGGCAGGCCTATTGGCTTGGAAGTAGA	14,143
TACCAGTGAACACCGTCAGGCCAAATATCAAGCAATTGCAAC	14,164
CTGCGGTGTGGCCACACAGTGAGAGCACTCGCCGCATGGACT	14,185
CTTGAGGCGCACTGAGAGAACGGCTTTGACCGACGAGCGCGA	14,206
CGGCTCCTGATCGCTATGATACCTTCTGCGCGAAACATCCTA	14,227
GCCCTACGGGTGGGCATGCTCCATATATAGGGTAATTCCAAC	14,248

TGTTGCGTGACATCCAATCTGCACTTATTTGTCACCATTAGT	14,269
CCGACATAGGTTCCGTGACATGTCCAAGCTTATCACCAGGTT	14,290
ATACAGTTGTATTTCATAGGGGTCGATAGCGGTAACGGTTGA	14,311
CCCACAACGGGTGGGGGGGGAATCCCGAGCTCCTGGATTACT	14,332
CCGGAAGGAAATCATAAGATATTTTCCCACTGCACCAAGACT	14,353
ATGAGAGGGGTTTAGTCCCCTTTGTGTCACAACCACTTATCA	14,374
TCGGCATATCAAGTGAAGTGATTTTCGGTTGCTCCTAAATCT	14,395
GTCAATGTCCTCATCGGTTCATCTTAAATGTGGTGGTAAGTG	14,416
TACTTAAGTTAAGCCAACTGGGGACATTGACGTTTAGAAAAG	15,28
TTTTCCGCGTGTGCTGCAGGTACGTCGTATAGGTCGGGATAA	15,49
AGTCAACCTGAATACTGGGGATGGGACTAATCGTCACAATTG	15,70
TGTTACCTTGACCCATGCCGCAACTCAATGATTCATTGACGC	15,91
CGCAGGGTCGGCCTACCTAATTTCACTGCAGGCGGGAAGCTA	15,112
TAGATATGTTTTCTGGTAACAGACGGTTCTGCTGCCAATAAG	15,133
TTGGATATACGTAACGCGTCCGCAAGATAACGCCTGACGGTG	15,154
ACCGGTGGAGGTACACCTCCATTCACTGGTACACTGTGTGGC	15,175
GTAATTTCTAACGCTCCCATTCACACCGCAGGTTCTCTCAGT	15,196
TCTATTACGCGGCATGTAGCTGCGCCTCAAGTATCATAGCGA	15,217
TGAGGGTGGCCAGCATGACTTTCAGGAGCCGGAGCATGCCCA	15,238
GCTGTTTCTGCTTACTGACGCCCCGTAGGGCCAGATTGGATG	15,259
CAGCTACATGGTATACTTTGATCACGCAACAATGTCACGGAA	15,280
CTACGTATGAAACTCAGTAACCCTATGTCGGCCCTATGAAAT	15,301
TAGCGTTGGCAGCTATGAGTCACAACTGTATTCCCCCCCCAC	15,322
CTGGCTGCCAAAAACTAATGACCGTTGTGGGTATCTTATGAT	15,343
TTAGCCAAGGGGGCGAGAGGGTTCCTTCCGGAGGGGACTAAA	15,364
CTCACGTTCTGCGCACGAGCCCCCCTCTCATTCACTTCACTT	15,385
CAGTAGGTGGAACTATCGTTCGATATGCCGATGAACCGATGA	15,406

Table S4. Sequences of the 19×14 Tile-core structure: x strands and y strands

Sequence of 19×14 Tile- core- x strands	5' end
TGCGGGCCCATAGTATCAATGTTCCCCATTTTATCTCACTGA	3,49
CGCGTTCCGCTTCCGGTCTCTGTTTTCGGCCGCCGCTCTTTG	5,49
AGTCTCCCTTCACTCCTCTATGCTGGTCTACCAGAGACATCC	7,49
GCGTGTTCTAAAGAATAGAACGGCAGCACCTGGTCTCTGGAA	9,49
CCAAGAAGGAACTCGGAGTGGGATGCAACATCCACGGCCCGG	11,49

GTGAACCTCAGACCAAGGTTCGCACCTTACTACTAATGATGG	13,49
TTTTCCGCGTGTGCTGCAGGTACGTCGTATAGGTCGGGATAA	15,49
CTTCGTGGGCGGGGGTCTGAGTGTAAGCCTGTTAGTGGGTCC	3,70
ATCGAAAAAAAACCGAATGATAGTCGACAGGGAGGAGGACGT	5,70
AATACACGTATCCTTAAGGTACAGTGCTTCACGAGACTCATG	7,70
TACTGCACTAGAAGGAGCGGACTTGTCCGTCTAATGAAGGTG	9,70
ACTAGAGCAAAGGGGCGTCTAGCTTATGGTGCAGAGTGTGGA	11,70
ACACTCCATCAGATAAGATATGATTCCTACTCTTTCGCATTT	13,70
AGTCAACCTGAATACTGGGGATGGGACTAATCGTCACAATTG	15,70
TAGGCGTAGAGGCGAACACATGAGCCATATGGTACCTTCGGT	3,91
TATATATCGCCCGGAGCATTTAGGGTGCACACGCACGGCTTC	5,91
TCATCTCAGAAGCCGGCAATAAAGGAAAGGCCTCAAGGCCGG	7,91
AGCGTCCCCAGAAGCGAACAACGCACAGTTTGGTCAACTTAG	9,91
GGCATGCTTAGCTGAATATGGTACTCCACAAAGCATCATTTC	11,91
ATTAACTGCAGCCGACCCCCAAACCTCTCGAGGCTACCGTTC	13,91
TGTTACCTTGACCCATGCCGCAACTCAATGATTCATTGACGC	15,91
CATAGTGTAACTAAACATCCGCATGGCCTCGTAGTTTGTACT	3,112
ACACTATCGTCAGTGAGCCAAAGGATAGGATACATGTAGCCC	5,112
AAGGGCAAACTTTACGTTCTCAGGCAATGGTAAAAGCATAGA	7,112
CGGGCTCAAAGCACAGCTACACCATTTTAGTTGATAGTGGGC	9,112
ATCTGAAATTAATCAAAAGGTGGGACCACATTAGGGTGGTAA	11,112
CTCGGTCAAGGTATAGTATAGGCAGTGGGGAAAGGCCATCAG	13,112
CGCAGGGTCGGCCTACCTAATTTCACTGCAGGCGGGAAGCTA	15,112
AGCCAATAGGCCGAGGCCAACCAAAAGAAATCTATTGCCGTA	3,133
AGAGCCCGGTAAAATAAACCCTGCCTTTGTGGCCGGAGGGAG	5,133
CGGGAGGACAGAGGTCGTTCGGTCGGCGTAACTTCTAGTCCT	7,133
TTGCCGTGCACCATCCGCTGGAAACAGGTGTATTGTAGTTAC	9,133
CGTCGCAGTGTGCTGCCACGCCCGCTACCCTCAATCGATAAG	11,133
ATATTAAGGCTATTGTCGACAGGTTGGTGATCATTAAGGATC	13,133
TAGATATGTTTTCTGGTAACAGACGGTTCTGCTGCCAATAAG	15,133
CTTGATATTTGTCTACTTCCATGCCATTGAGAAAAGATCGGG	3,154
GGCCAAGCCATTATCCTTGTCGTCGCCTCCATGGACAAAAGG	5,154
AGATCACAGTATCATCGGAATTCGTTTTAGGTACAAAACTAA	7,154
TTCATGATGGGGATAGCATACTGGTGATCGGAATACTTTTAC	9,154
AGACCGGTCTTATGGGTCGTTGTAACAGATCTGATAGCATTG	11,154
CTGTCCATATGAGGATTATGGCCCCGTACATACCCATAAACT	13,154
TTGGATATACGTAACGCGTCCGCAAGATAACGCCTGACGGTG	15,154
GCGAGTGCTCTGTTGCAATTGCAATGGGTATGTGAAAACGAA	3,175
GGGACATGCGATGCCGGATTCTTGCACCAGCAGTCTCCGAGC	5,175

ACTACCTCTGAAGTGAATACCGTTTCAGAACTGATTAAGAGG	7,175
TGACATGGGTGGGCTGTTGGCACCGGGCGAGCATGCAGTGAA	9,175
GCTCAGTGTCACAGAGAAACGGACGCAATGCCCGATGTGAAT	11,175
TGAACAGCACTATTAAACCGCCGAGTCAATACCATATTACTC	13,175
ACCGGTGGAGGTACACCTCCATTCACTGGTACACTGTGTGGC	15,175
CGGTCAAAGCCAGTCCATGCGCCAACGAAATCCTGCGGCGCC	3,196
CCCGTTAGTCCGTCTCTCTTTCCTGCCAATCCGCCAACCAGC	5,196
CCACCTGTATGACCGTTCGCGGGTCAATTATGTGATACTTAA	7,196
CTATATTACCTACACCCCGTGCTCTAATGCGCCGATCCATCA	9,196
ACTTGTTCCAGTTAGGAAGTAACAGAAGGATCCATGCCTGGT	11,196
TCTCCTCATCATCTATTGCATGCGGCTAGAGTTGGAGGCCTA	13,196
GTAATTTCTAACGCTCCCATTCACACCGCAGGTTCTCTCAGT	15,196
CGCGCAGAAGGTCGCGCTCGTACGTGCACGCCCGTGGCCCAG	3,217
GGAAGTGTGCACTGGCTCACAAATTGACTCTAACGTGTCTGC	5,217
TCTCGACAAGCCTAAGATGTAAGCCCGTAGCTGCAGTCTCGT	7,217
GATAGTCGCTAAAAAGGTCCACCTTGAGTAGACGGCTGGGAG	9,217
TGGGCGATTGCGATCTGCGCAAGGAGTTCTTCTGCCGGGGTG	11,217
CCACTTCCTGACTGTAAGGAGCGCGTCCACCTGAGGGATACC	13,217
TCTATTACGCGGCATGTAGCTGCGCCTCAAGTATCATAGCGA	15,217
CCCTATATATGTAGGATGTTTGGAAAAAAGGGGTGTTCCAGA	3,238
AACCTGGCACTTTGCCTCCTTCAGAAATCGGCCGGGCAGCCC	5,238
TTCGTAGCGCCGGCGTTAACGAACCGTTTGTAGTAACTAACG	7,238
CGTATAAACGCTCGCGGGGCCGAAAACAATCTGCCATCTATG	9,238
CACATAATAGAATAAATCGGCCCTAGAATACCAGTTATTCAT	11,238
ATAGTAAAGTGATCTGTCAGTATGTATTGAAACGCATGCTGT	13,238
TGAGGGTGGCCAGCATGACTTTCAGGAGCCGGAGCATGCCCA	15,238
ACAAATAAGTGGTTGGAATTAATGTTAGGCCATCTGCATCCA	3,259
TAACAGCTCTACCACATTTAACGGACTTAGAAGTCTGGGCGG	5,259
ATATCATATCGATCACTACGTGCGCGTTCTAATTAAATACCC	7,259
TGACTTTTTCGGTCATCCCATTCACACAGAGCGAGTTCACTA	9,259
CTCCGAACCACTAGGATATTGACGCGGTTGGATACACTCAAT	11,259
TATATAACGTAATCGCGGAATAGTCATCAGGCCTATCATGGG	13,259
GCTGTTTCTGCTTACTGACGCCCCGTAGGGCCAGATTGGATG	15,259
TAAGCTTGGACACTAATGGTGCATTGTGCAATTCATGCGTCT	3,280
GAAGGATCGCGTGTCTACTGTGTCAGGCGTGCAATGAATAGT	5,280
TATGATTAATAGGACCCCCGGTGTAGGCGCCTGCGCTGGCTG	7,280
AGTGACACCTGTCAGTTGCATCGAAGCTTTCGATGCACGTTT	9,280
CCTGCTCTACCGCATACTTGCGGATCTCTGGTTCAGCTGGGT	11,280
GTGGCGTATGATTAGGCTGCCCATTCAAATGCGGGACTAACA	13,280

CAGCTACATGGTATACTTTGATCACGCAACAATGTCACGGAA	15,280
CCGCTATCGACAACCTGGTGATCATCTATGGATCATAGTGGA	3,301
GAGTCCATTAGCGTGAGCACGTAAGTCCCTCTCATACTCTTG	5,301
GGGTGCTAGCTATTGCTATAACTGCCGCTGTTAGTTACTTCG	7,301
CTAATAGCCGAGACGTTGATTTCGCTCAACCTTAGTATAGAC	9,301
TGTTCCGCTGCCGCCGTGGGGACAAATTCAATGTCCGCATGA	11,301
GGTGCCGGGGATGGGTGTAATGTTAAAGGTTGGACTTCCGAA	13,301
CTACGTATGAAACTCAGTAACCCTATGTCGGCCCTATGAAAT	15,301
GAGCTCGGGATTCAACCGTTACGTCTGAACTGATACGACTGC	3,322
CTATCAGTTGAGTGTGGTTAGTCGTGTGCCTCGGGTATGGCT	5,322
AATTCGAGGATCGCCTCTTGTTAATGACGTCCTTCATCTACC	7,322
CCATAGCCTGCGGCCCCCTCGCCTCCCCACCCATGACAGGAT	9,322
TACTATATTTATTAAGTCGCTCGATCGACCTTCGAAAACCAT	11,322
ACCGCGGTAGCCAGATCTTCACCCACGGAACTAAACTCCTAT	13,322
TAGCGTTGGCAGCTATGAGTCACAACTGTATTCCCCCCCCAC	15,322
CAGTGGGAAAAAGTAATCCAGCACAGTTCTACATCTAGAAGA	3,343
GTTGGATCATTGTGGATACCATCTACGTCTTCGGATATAAAT	5,343
CGTTAGGTAGGGGCTATAAGGTTGTATGAACATCGGATGTAC	7,343
ACCTTAGGGAACTCTGCTCCTTAATGCGAGTCCCTAGCTCAC	9,343
TTATGTTAATTTGTCATTGGTAATACGTACCCAGACAACTGT	11,343
GCGTCTCTTGGAAAGCTGGATGCGCGGAATGGTGGACTCTCC	13,343
CTGGCTGCCAAAAACTAATGACCGTTGTGGGTATCTTATGAT	15,343
TTGTGACACAAAGTCTTGGTGACTATGAGTGCCACTACACAC	3,364
GGGGTCACATACTTGCAGTTATCTCCCTTTAAGAGGCCGCGC	5,364
AACATCCGCGAGTCCAGTAGGCGGGTAAGGTGGTGGTTTGAC	7,364
CCGTCTTTATATTGAAACGGAGGATAAAGTAAGACTTATCAG	9,364
GAAGATCACGAGGACTTTCACGTAAATGGTATAGGAGCGTTT	11,364
TGCGATTTGATGATCAGCAGCGAGTTAACTCTAGCCACGCCC	13,364
TTAGCCAAGGGGGCGAGAGGGTTCCTTCCGGAGGGGACTAAA	15,364
GCAACCGAAAATGATAAGTGGCCCTCAATCCCGAAGCGAACT	3,385
TCTAATTAAAGTATGTGTTCTTAATCGTAGAGCTTACATGAC	5,385
CGGGCGGGACTGATAAAACTGTGAGCCTATCTAGGTTCACGT	7,385
CCTAGCAAGAGGAGGTGTGAACCAATAATAATTGCATATTCG	9,385
CTCAGAAGGAGATATGGGAACCAGTCAGGCTTACCTCTCGTG	11,385
TCTAAGTGTATCGGGACTAAGCACTCTCTATAAATAAACGCA	13,385
CTCACGTTCTGCGCACGAGCCCCCCTCTCATTCACTTCACTT	15,385
CACATTTAAGAAGATTTAGGAAGGTGGTCCAAGTGAGTCCCC	3,406
GGATGCACAACCGGGCCTCACGACGGGCTACACTTAGGCCGA	5,406
AGCGCCTTTAATAAAAGCACCCGTGTTTCACAGATCGATTCG	7,406

TAAACCCATCGATCGGAAATAGAGCGATTAGGAGAAGCTCTA	9,406
GCGGATAGAAGCTGTAGTCTCAATCATAAAAGTGCCCAGCCA	11,406
CGTGACCCGTGCCGTAACTTTGTGCGCGGGTATATAGTTTCA	13,406
CAGTAGGTGGAACTATCGTTCGATATGCCGATGAACCGATGA	15,406

Sequence of 19×14 Tile- core- y strands	5' end
GGCCGAAAACCGTCCGCCCCAACACGACACGTCATTGATACT	4,38
CCTGTCGACTCAAAGAGCGGCATGGGCCCGCACTCAGACCCC	4,59
TGTGCACCCTACGTCCTCCTCCGCCCACGAAGATGTGTTCGC	4,80
ATCCTATCCTGAAGCCGTGCGCTCTACGCCTACGGATGTTTA	4,101
CACAAAGGCAGGGCTACATGTGTTACACTATGGTTGGCCTCG	4,122
TGGAGGCGACCTCCCTCCGGCGCCTATTGGCTTGGAAGTAGA	4,143
GCTGGTGCAACCTTTTGTCCACAAATATCAAGCAATTGCAAC	4,164
GATTGGCAGGGCTCGGAGACTAGAGCACTCGCCGCATGGACT	4,185
AGAGTCAATTGCTGGTTGGCGGGCTTTGACCGACGAGCGCGA	4,206
CCGATTTCTGGCAGACACGTTCCTTCTGCGCGAAACATCCTA	4,227
TCTAAGTCCGGGGCTGCCCGGCATATATAGGGTAATTCCAAC	4,248
CACGCCTGACCCGCCCAGACTCACTTATTTGTCACCATTAGT	4,269
GAGGGACTTAACTATTCATTGGTCCAAGCTTATCACCAGGTT	4,290
AGGCACACGACAAGAGTATGAGTCGATAGCGGTAACGGTTGA	4,311
AAGACGTAGAAGCCATACCCGATCCCGAGCTCCTGGATTACT	4,332
TAAAGGGAGAATTTATATCCGTTTTCCCACTGCACCAAGACT	4,353
TCTACGATTAGCGCGGCCTCTTTGTGTCACAACCACTTATCA	4,374
GTAGCCCGTCGTCATGTAAGCTTTTCGGTTGCTCCTAAATCT	4,395
GCAGAACTAATCGGCCTAAGTTCTTAAATGTGGTGGTAAGTG	4,416
GTAGACCAGCTAGGCAGTGACTCATTGCAGGGAGAGACCGGA	6,38
TGAAGCACTGGGATGTCTCTGAGCGGAACGCGATCATTCGGT	6,59
GCCTTTCCTTCATGAGTCTCGTTTTTTTCGATAAATGCTCCG	6,80
ACCATTGCCTCCGGCCTTGAGGGCGATATATATTGGCTCACT	6,101
TTACGCCGACTCTATGCTTTTGACGATAGTGTGGGTTTATTT	6,122
CCTAAAACGAAGGACTAGAAGTACCGGGCTCTGACAAGGATA	6,143
GTTCTGAAACTTAGTTTTGTAATGGCTTGGCCGAATCCGGCA	6,164
ATAATTGACCCCTCTTAATCATCGCATGTCCCAAAGAGAGAC	6,185
GCTACGGGCTTTAAGTATCACGGACTAACGGGTGTGAGCCAG	6,206
ACAAACGGTTACGAGACTGCATGCACACTTCCAAGGAGGCAA	6,227
TAGAACGCGCCGTTAGTTACTAGTGCCAGGTTTTAAATGTGG	6,248
GGCGCCTACAGGGTATTTAATTAGAGCTGTTAACAGTAGACA	6,269

ACAGCGGCAGCAGCCAGCGCACGCGATCCTTCCGTGCTCACG	6,290
GACGTCATTACGAAGTAACTACTAATGGACTCCTAACCACAC	6,311
GTTCATACAAGGTAGATGAAGTCAACTGATAGTGGTATCCAC	6,332
ACCTTACCCGGTACATCCGATAATGATCCAACTAACTGCAAG	6,353
GATAGGCTCAGTCAAACCACCTATGTGACCCCAGAACACATA	6,374
GTGAAACACGACGTGAACCTACTTTAATTAGAGTGAGGCCCG	6,395
CGAATAGTATCGAATCGATCTGTTGTGCATCCTCAGATCAAC	6,416
AGGTGCTGCCAGGAACTAGCAACTCCTCAGTCATAGAGGAGT	8,38
GACGGACAAGTTCCAGAGACCGAAGGGAGACTTACCTTAAGG	8,59
AAACTGTGCGCACCTTCATTAATACGTGTATTTATTGCCGGC	8,80
ACTAAAATGGCTAAGTTGACCTTCTGAGATGAGAGAACGTAA	8,101
ACACCTGTTTGCCCACTATCAAGTTTGCCCTTCGAACGACCT	8,122
CCGATCACCAGTAACTACAATCTGTCCTCCCGATTCCGATGA	8,143
CTCGCCCGGTGTAAAAGTATTTACTGTGATCTGGTATTCACT	8,164
CGCATTAGAGTTCACTGCATGTCAGAGGTAGTCGCGAACGGT	8,185
CTACTCAAGGTGATGGATCGGCATACAGGTGGTACATCTTAG	8,206
GATTGTTTTCCTCCCAGCCGTGCTTGTCGAGACGTTAACGCC	8,227
CTCTGTGTGACATAGATGGCAGGCGCTACGAAACGTAGTGAT	8,248
GAAAGCTTCGTAGTGAACTCGCGATATGATATCCGGGGGTCC	8,269
GGTTGAGCGAAAACGTGCATCTATTAATCATATTATAGCAAT	8,290
GGTGGGGAGGGTCTATACTAAAGCTAGCACCCACAAGAGGCG	8,311
ACTCGCATTAATCCTGTCATGATCCTCGAATTCCTTATAGCC	8,332
TACTTTATCCGTGAGCTAGGGCCTACCTAACGCCTACTGGAC	8,353
TTATTATTGGCTGATAAGTCTTCGCGGATGTTCAGTTTTATC	8,374
CTAATCGCTCCGAATATGCAAAGTCCCGCCCGGGTGCTTTTA	8,395
TGAACCCGACTAGAGCTTCTCTTAAAGGCGCTAGGCTACGAA	8,416
ATGTTGCATCCCCCTTTCAACCTCGTGGCGAGGTTCTATTCT	10,38
CACCATAAGCCCGGGCCGTGGTTAGAACACGCTCCGCTCCTT	10,59
TTGTGGAGTATCCACACTCTGCTAGTGCAGTATTGTTCGCTT	10,80
ATGTGGTCCCGAAATGATGCTCTGGGGACGCTTGTAGCTGTG	10,101
AGGGTAGCGGTTACCACCCTACTTTGAGCCCGCCAGCGGATG	10,122
GATCTGTTACCTTATCGATTGGTGCACGGCAAGTATGCTATC	10,143
GCATTGCGTCCAATGCTATCACCCATCATGAAGCCAACAGCC	10,164
ATCCTTCTGTATTCACATCGGCACCCATGTCACACGGGGTGT	10,185
AAGAACTCCTACCAGGCATGGAGGTAATATAGTGGACCTTTT	10,206
GTATTCTAGGCACCCCGGCAGTAGCGACTATCGGCCCCGCGA	10,227
CCAACCGCGTATGAATAACTGGCGTTTATACGATGGGATGAC	10,248
CCAGAGATCCATTGAGTGTATCGAAAAAGTCAATGCAACTGA	10,269
TTGAATTTGTACCCAGCTGAACAGGTGTCACTAATCAACGTC	10,290

AGGTCGATCGTCATGCGGACATCGGCTATTAGCGAGGGGGCC	10,311
GGTACGTATTATGGTTTTCGAGCAGGCTATGGAGGAGCAGAG	10,332
TACCATTTACACAGTTGTCTGTTCCCTAAGGTTCCGTTTCAA	10,353
AGCCTGACTGAAACGCTCCTATATAAAGACGGTTCACACCTC	10,374
TTTTATGATTCACGAGAGGTACTCTTGCTAGGTATTTCCGAT	10,395
CACACAACCCTGGCTGGGCACCGATGGGTTTAGGCGGGTCAC	10,416
AGTAAGGTGCTAACACCCCCTAGAATAATTCGCCACTCCGAG	12,38
AGTAGGAATCCCATCATTAGTTTCCTTCTTGGTAGACGCCCC	12,59
TCGAGAGGTTAAATGCGAAAGTTTGCTCTAGTCCATATTCAG	12,80
TCCCCACTGCGAACGGTAGCCCTAAGCATGCCACCTTTTGAT	12,101
ATCACCAACCCTGATGGCCTTTAATTTCAGATGCGTGGCAGC	12,122
ATGTACGGGGGATCCTTAATGACACTGCGACGAACGACCCAT	12,143
TATTGACTCGAGTTTATGGGTAAGACCGGTCTCGTTTCTCTG	12,164
CTCTAGCCGCGAGTAATATGGTGACACTGAGCTACTTCCTAA	12,185
GGTGGACGCGTAGGCCTCCAACTGGAACAAGTTGCGCAGATC	12,206
TTCAATACATGGTATCCCTCAGCAATCGCCCAGCCGATTTAT	12,227
CCTGATGACTACAGCATGCGTTCTATTATGTGCAATATCCTA	12,248
CATTTGAATGCCCATGATAGGGTGGTTCGGAGGCAAGTATGC	12,269
AACCTTTAACTGTTAGTCCCGGGTAGAGCAGGCCCCACGGCG	12,290
GTTCCGTGGGTTCGGAAGTCCGCAGCGGAACAAGCGACTTAA	12,311
CATTCCGCGCATAGGAGTTTATAAATATAGTAACCAATGACA	12,332
GAGTTAACTCGGAGAGTCCACAATTAACATAAGTGAAAGTCC	12,353
ATAGAGAGTGGGGCGTGGCTATCGTGATCTTCGTTCCCATAT	12,374
ACCCGCGCACTGCGTTTATTTCTCCTTCTGAGGAGACTACAG	12,395
AACCCGATCGTGAAACTATATCTTCTATCCGCACAAAAAACG	12,416
TATACGACGTCTTTTCTAAACATCGACTCCTCGAACCTTGGT	14,38
ATTAGTCCCATTATCCCGACCCTGAGGTTCACATATCTTATC	14,59
TCATTGAGTTCAATTGTGACGTGATGGAGTGTTGGGGGTCGG	14,80
CTGCAGTGAAGCGTCAATGAACTGCAGTTAATCTATACTATA	14,101
CAGAACCGTCTAGCTTCCCGCCCTTGACCGAGTGTCGACAAT	14,122
GTTATCTTGCCTTATTGGCAGAGCCTTAATATCCATAATCCT	14,143
TACCAGTGAACACCGTCAGGCCATATGGACAGGCGGTTTAAT	14,164
CTGCGGTGTGGCCACACAGTGAGTGCTGTTCAATGCAATAGA	14,185
CTTGAGGCGCACTGAGAGAACTGATGAGGAGACTCCTTACAG	14,206
CGGCTCCTGATCGCTATGATATCAGGAAGTGGACTGACAGAT	14,227
GCCCTACGGGTGGGCATGCTCCACTTTACTATATTCCGCGAT	14,248
TGTTGCGTGACATCCAATCTGTACGTTATATAGGCAGCCTAA	14,269
CCGACATAGGTTCCGTGACATTCATACGCCACATTACACCCA	14,290
ATACAGTTGTATTTCATAGGGTCCCCGGCACCTGAAGATCTG	14,311

CCCACAACGGGTGGGGGGGGAGCTACCGCGGTATCCAGCTTT	14,332
CCGGAAGGAAATCATAAGATACCAAGAGACGCGCTGCTGATC	14,353
ATGAGAGGGGTTTAGTCCCCTATCAAATCGCACTTAGTCCCG	14,374
TCGGCATATCAAGTGAAGTGAATACACTTAGAAAAGTTACGG	14,395
GTCAATGTCCTCATCGGTTCACACGGGTCACGGCAACTGTAG	14,416

Table S5. Sequences of the 19×4 Tile - x strands with 2T flexible spacer

Sequence of 19×14 Tile-x strands with 2T spacer	5' end
ACGTGTCGTGTCACTTACCACTTTAGGAGTTTATAACCCTTGAG	3,28
CTTCGTGGGCGGGGGTCTGAGTTTGTAAGCCTGTTAGTGGGTCC	3,70
TAGGCGTAGAGGCGAACACATTTGAGCCATATGGTACCTTCGGT	3,91
CATAGTGTAACTAAACATCCGTTCATGGCCTCGTAGTTTGTACT	3,112
AGCCAATAGGCCGAGGCCAACTTCAAAAGAAATCTATTGCCGTA	3,133
CTTGATATTTGTCTACTTCCATTTGCCATTGAGAAAAGATCGGG	3,154
GCGAGTGCTCTGTTGCAATTGTTCAATGGGTATGTGAAAACGAA	3,175
CGGTCAAAGCCAGTCCATGCGTTCCAACGAAATCCTGCGGCGCC	3,196
CGCGCAGAAGGTCGCGCTCGTTTACGTGCACGCCCGTGGCCCAG	3,217
CCCTATATATGTAGGATGTTTTTGGAAAAAAGGGGTGTTCCAGA	3,238
ACAAATAAGTGGTTGGAATTATTATGTTAGGCCATCTGCATCCA	3,259
TAAGCTTGGACACTAATGGTGTTCATTGTGCAATTCATGCGTCT	3,280
CCGCTATCGACAACCTGGTGATTTCATCTATGGATCATAGTGGA	3,301
GAGCTCGGGATTCAACCGTTATTCGTCTGAACTGATACGACTGC	3,322
CAGTGGGAAAAAGTAATCCAGTTCACAGTTCTACATCTAGAAGA	3,343
TTGTGACACAAAGTCTTGGTGTTACTATGAGTGCCACTACACAC	3,364
GCAACCGAAAATGATAAGTGGTTCCCTCAATCCCGAAGCGAACT	3,385
CACATTTAAGAAGATTTAGGATTAGGTGGTCCAAGTGAGTCCCC	3,406
CCCTGCAATGAGTTGATCTGATTTTAGTTCTGCTGGGGCGGACG	5,28
ATCGAAAAAAAACCGAATGATTTAGTCGACAGGGAGGAGGACGT	5,70
TATATATCGCCCGGAGCATTTTTAGGGTGCACACGCACGGCTTC	5,91
ACACTATCGTCAGTGAGCCAATTAGGATAGGATACATGTAGCCC	5,112
AGAGCCCGGTAAAATAAACCCTTTGCCTTTGTGGCCGGAGGGAG	5,133
GGCCAAGCCATTATCCTTGTCTTGTCGCCTCCATGGACAAAAGG	5,154
GGGACATGCGATGCCGGATTCTTTTGCACCAGCAGTCTCCGAGC	5,175
CCCGTTAGTCCGTCTCTCTTTTTCCTGCCAATCCGCCAACCAGC	5,196
GGAAGTGTGCACTGGCTCACATTAATTGACTCTAACGTGTCTGC	5,217
AACCTGGCACTTTGCCTCCTTTTCAGAAATCGGCCGGGCAGCCC	5,238

TAACAGCTCTACCACATTTAATTCGGACTTAGAAGTCTGGGCGG	5,259
GAAGGATCGCGTGTCTACTGTTTGTCAGGCGTGCAATGAATAGT	5,280
GAGTCCATTAGCGTGAGCACGTTTAAGTCCCTCTCATACTCTTG	5,301
CTATCAGTTGAGTGTGGTTAGTTTCGTGTGCCTCGGGTATGGCT	5,322
GTTGGATCATTGTGGATACCATTTCTACGTCTTCGGATATAAAT	5,343
GGGGTCACATACTTGCAGTTATTTCTCCCTTTAAGAGGCCGCGC	5,364
TCTAATTAAAGTATGTGTTCTTTTAATCGTAGAGCTTACATGAC	5,385
GGATGCACAACCGGGCCTCACTTGACGGGCTACACTTAGGCCGA	5,406
GACTGAGGAGTTTCGTAGCCTTTATACTATTCGGTCACTGCCTA	7,28
AATACACGTATCCTTAAGGTATTCAGTGCTTCACGAGACTCATG	7,70
TCATCTCAGAAGCCGGCAATATTAAGGAAAGGCCTCAAGGCCGG	7,91
AAGGGCAAACTTTACGTTCTCTTAGGCAATGGTAAAAGCATAGA	7,112
CGGGAGGACAGAGGTCGTTCGTTGTCGGCGTAACTTCTAGTCCT	7,133
AGATCACAGTATCATCGGAATTTTCGTTTTAGGTACAAAACTAA	7,154
ACTACCTCTGAAGTGAATACCTTGTTTCAGAACTGATTAAGAGG	7,175
CCACCTGTATGACCGTTCGCGTTGGTCAATTATGTGATACTTAA	7,196
TCTCGACAAGCCTAAGATGTATTAGCCCGTAGCTGCAGTCTCGT	7,217
TTCGTAGCGCCGGCGTTAACGTTAACCGTTTGTAGTAACTAACG	7,238
ATATCATATCGATCACTACGTTTGCGCGTTCTAATTAAATACCC	7,259
TATGATTAATAGGACCCCCGGTTTGTAGGCGCCTGCGCTGGCTG	7,280
GGGTGCTAGCTATTGCTATAATTCTGCCGCTGTTAGTTACTTCG	7,301
AATTCGAGGATCGCCTCTTGTTTTAATGACGTCCTTCATCTACC	7,322
CGTTAGGTAGGGGCTATAAGGTTTTGTATGAACATCGGATGTAC	7,343
AACATCCGCGAGTCCAGTAGGTTCGGGTAAGGTGGTGGTTTGAC	7,364
CGGGCGGGACTGATAAAACTGTTTGAGCCTATCTAGGTTCACGT	7,385
AGCGCCTTTAATAAAAGCACCTTCGTGTTTCACAGATCGATTCG	7,406
CTCGCCACGAGGTGACCCGCCTTGTCGGGTTCATGCTAGTTCCT	9,28
TACTGCACTAGAAGGAGCGGATTCTTGTCCGTCTAATGAAGGTG	9,70
AGCGTCCCCAGAAGCGAACAATTCGCACAGTTTGGTCAACTTAG	9,91
CGGGCTCAAAGCACAGCTACATTCCATTTTAGTTGATAGTGGGC	9,112
TTGCCGTGCACCATCCGCTGGTTAAACAGGTGTATTGTAGTTAC	9,133
TTCATGATGGGGATAGCATACTTTGGTGATCGGAATACTTTTAC	9,154
TGACATGGGTGGGCTGTTGGCTTACCGGGCGAGCATGCAGTGAA	9,175
CTATATTACCTACACCCCGTGTTCTCTAATGCGCCGATCCATCA	9,196
GATAGTCGCTAAAAAGGTCCATTCCTTGAGTAGACGGCTGGGAG	9,217
CGTATAAACGCTCGCGGGGCCTTGAAAACAATCTGCCATCTATG	9,238
TGACTTTTTCGGTCATCCCATTTTCACACAGAGCGAGTTCACTA	9,259
AGTGACACCTGTCAGTTGCATTTCGAAGCTTTCGATGCACGTTT	9,280
CTAATAGCCGAGACGTTGATTTTTCGCTCAACCTTAGTATAGAC	9,301

CCATAGCCTGCGGCCCCCTCGTTCCTCCCCACCCATGACAGGAT	9,322
ACCTTAGGGAACTCTGCTCCTTTTAATGCGAGTCCCTAGCTCAC	9,343
CCGTCTTTATATTGAAACGGATTGGATAAAGTAAGACTTATCAG	9,364
CCTAGCAAGAGGAGGTGTGAATTCCAATAATAATTGCATATTCG	9,385
TAAACCCATCGATCGGAAATATTGAGCGATTAGGAGAAGCTCTA	9,406
CGAATTATTCTCGTTTTTTGTTTGGGTTGTGTGGTTGAAAGGGG	11,28
ACTAGAGCAAAGGGGCGTCTATTGCTTATGGTGCAGAGTGTGGA	11,70
GGCATGCTTAGCTGAATATGGTTTACTCCACAAAGCATCATTTC	11,91
ATCTGAAATTAATCAAAAGGTTTGGGACCACATTAGGGTGGTAA	11,112
CGTCGCAGTGTGCTGCCACGCTTCCGCTACCCTCAATCGATAAG	11,133
AGACCGGTCTTATGGGTCGTTTTGTAACAGATCTGATAGCATTG	11,154
GCTCAGTGTCACAGAGAAACGTTGACGCAATGCCCGATGTGAAT	11,175
ACTTGTTCCAGTTAGGAAGTATTACAGAAGGATCCATGCCTGGT	11,196
TGGGCGATTGCGATCTGCGCATTAGGAGTTCTTCTGCCGGGGTG	11,217
CACATAATAGAATAAATCGGCTTCCTAGAATACCAGTTATTCAT	11,238
CTCCGAACCACTAGGATATTGTTACGCGGTTGGATACACTCAAT	11,259
CCTGCTCTACCGCATACTTGCTTGGATCTCTGGTTCAGCTGGGT	11,280
TGTTCCGCTGCCGCCGTGGGGTTACAAATTCAATGTCCGCATGA	11,301
TACTATATTTATTAAGTCGCTTTCGATCGACCTTCGAAAACCAT	11,322
TTATGTTAATTTGTCATTGGTTTAATACGTACCCAGACAACTGT	11,343
GAAGATCACGAGGACTTTCACTTGTAAATGGTATAGGAGCGTTT	11,364
CTCAGAAGGAGATATGGGAACTTCAGTCAGGCTTACCTCTCGTG	11,385
GCGGATAGAAGCTGTAGTCTCTTAATCATAAAAGTGCCCAGCCA	11,406
GAGGAGTCGATCTACAGTTGCTTCGATCGGGTTAGGGGGTGTTA	13,28
ACACTCCATCAGATAAGATATTTGATTCCTACTCTTTCGCATTT	13,70
ATTAACTGCAGCCGACCCCCATTAACCTCTCGAGGCTACCGTTC	13,91
CTCGGTCAAGGTATAGTATAGTTGCAGTGGGGAAAGGCCATCAG	13,112
ATATTAAGGCTATTGTCGACATTGGTTGGTGATCATTAAGGATC	13,133
CTGTCCATATGAGGATTATGGTTCCCCGTACATACCCATAAACT	13,154
TGAACAGCACTATTAAACCGCTTCGAGTCAATACCATATTACTC	13,175
TCTCCTCATCATCTATTGCATTTGCGGCTAGAGTTGGAGGCCTA	13,196
CCACTTCCTGACTGTAAGGAGTTCGCGTCCACCTGAGGGATACC	13,217
ATAGTAAAGTGATCTGTCAGTTTATGTATTGAAACGCATGCTGT	13,238
TATATAACGTAATCGCGGAATTTAGTCATCAGGCCTATCATGGG	13,259
GTGGCGTATGATTAGGCTGCCTTCATTCAAATGCGGGACTAACA	13,280
GGTGCCGGGGATGGGTGTAATTTGTTAAAGGTTGGACTTCCGAA	13,301
ACCGCGGTAGCCAGATCTTCATTCCCACGGAACTAAACTCCTAT	13,322
GCGTCTCTTGGAAAGCTGGATTTGCGCGGAATGGTGGACTCTCC	13,343
TGCGATTTGATGATCAGCAGCTTGAGTTAACTCTAGCCACGCCC	13,364

TCTAAGTGTATCGGGACTAAGTTCACTCTCTATAAATAAACGCA	13,385
CGTGACCCGTGCCGTAACTTTTTGTGCGCGGGTATATAGTTTCA	13,406
TACTTAAGTTAAGCCAACTGGTTGGACATTGACGTTTAGAAAAG	15,28
AGTCAACCTGAATACTGGGGATTTGGGACTAATCGTCACAATTG	15,70
TGTTACCTTGACCCATGCCGCTTAACTCAATGATTCATTGACGC	15,91
CGCAGGGTCGGCCTACCTAATTTTTCACTGCAGGCGGGAAGCTA	15,112
TAGATATGTTTTCTGGTAACATTGACGGTTCTGCTGCCAATAAG	15,133
TTGGATATACGTAACGCGTCCTTGCAAGATAACGCCTGACGGTG	15,154
ACCGGTGGAGGTACACCTCCATTTTCACTGGTACACTGTGTGGC	15,175
GTAATTTCTAACGCTCCCATTTTCACACCGCAGGTTCTCTCAGT	15,196
TCTATTACGCGGCATGTAGCTTTGCGCCTCAAGTATCATAGCGA	15,217
TGAGGGTGGCCAGCATGACTTTTTCAGGAGCCGGAGCATGCCCA	15,238
GCTGTTTCTGCTTACTGACGCTTCCCGTAGGGCCAGATTGGATG	15,259
CAGCTACATGGTATACTTTGATTTCACGCAACAATGTCACGGAA	15,280
CTACGTATGAAACTCAGTAACTTCCTATGTCGGCCCTATGAAAT	15,301
TAGCGTTGGCAGCTATGAGTCTTACAACTGTATTCCCCCCCCAC	15,322
CTGGCTGCCAAAAACTAATGATTCCGTTGTGGGTATCTTATGAT	15,343
TTAGCCAAGGGGGCGAGAGGGTTTTCCTTCCGGAGGGGACTAAA	15,364
CTCACGTTCTGCGCACGAGCCTTCCCCTCTCATTCACTTCACTT	15,385
CAGTAGGTGGAACTATCGTTCTTGATATGCCGATGAACCGATGA	15,406

Table S6. Sequences of the varied 0-9 tile offset y-connectors used in both of 19×4 Tile and 19×14 Tile models.

Sequences of 0-tile offset, y connectors	5' end	3' end
AAATGGGGAACTCAAGGGTTATAACTTAAGTAACCTGCAGCA	2,38	15,38
CAGGCTTACATCAGTGAGATACACGCGGAAAATCCCCAGTAT	2,59	15,59
CATATGGCTCGGACCCACTAATCAGGTTGACTGCGGCATGGG	2,80	15,80
CGAGGCCATGACCGAAGGTACTCAAGGTAACAATTAGGTAGG	2,101	15,101
ATTTCTTTTGAGTACAAACTACCGACCCTGCGTGTTACCAGA	2,122	15,122
CTCAATGGCATACGGCAATAGAAACATATCTAGGACGCGTTA	2,143	15,143
ATACCCATTGCCCGATCTTTTCGTATATCCAATGGAGGTGTA	2,164	15,164
ATTTCGTTGGTTCGTTTTCACCCTCCACCGGTAATGGGAGCG	2,185	15,185
GCGTGCACGTGGCGCCGCAGGTTAGAAATTACAGCTACATGC	2,206	15,206
CCTTTTTTCCCTGGGCCACGGCGCGTAATAGAAAGTCATGCT	2,227	15,227
GGCCTAACATTCTGGAACACCGGCCACCCTCAGCGTCAGTAA	2,248	15,248

TTGCACAATGTGGATGCAGATGCAGAAACAGCTCAAAGTATA	2,269	15,269
CCATAGATGAAGACGCATGAACCATGTAGCTGGTTACTGAGT	2,290	15,290
AGTTCAGACGTCCACTATGATTTCATACGTAGGACTCATAGC	2,311	15,311
TAGAACTGTGGCAGTCGTATCTGCCAACGCTATCATTAGTTT	2,332	15,332
CACTCATAGTTCTTCTAGATGTTGGCAGCCAGCCCTCTCGCC	2,353	15,353
GGATTGAGGGGTGTGTAGTGGCCCTTGGCTAAGGCTCGTGCG	2,374	15,374
TGGACCACCTAGTTCGCTTCGCAGAACGTGAGGAACGATAGT	2,395	15,395
TAAACTCCTAGGGGACTCACTTCCACCTACTGCCAGTTGGCT	2,416	15,416

Sequences of 1-tile offset, y connectors	5' end	3' end
AAATGGGGAACTCAAGGGTTACACGCGGAAAATCCCCAGTAT	2,38	15,59
CAGGCTTACATCAGTGAGATATCAGGTTGACTGCGGCATGGG	2,59	15,80
CATATGGCTCGGACCCACTAATCAAGGTAACAATTAGGTAGG	2,80	15,101
CGAGGCCATGACCGAAGGTACCCGACCCTGCGTGTTACCAGA	2,101	15,122
ATTTCTTTTGAGTACAAACTAAAACATATCTAGGACGCGTTA	2,122	15,143
CTCAATGGCATACGGCAATAGCGTATATCCAATGGAGGTGTA	2,143	15,164
ATACCCATTGCCCGATCTTTTCCTCCACCGGTAATGGGAGCG	2,164	15,185
ATTTCGTTGGTTCGTTTTCACTTAGAAATTACAGCTACATGC	2,185	15,206
GCGTGCACGTGGCGCCGCAGGCGCGTAATAGAAAGTCATGCT	2,206	15,227
CCTTTTTTCCCTGGGCCACGGGGCCACCCTCAGCGTCAGTAA	2,227	15,248
GGCCTAACATTCTGGAACACCGCAGAAACAGCTCAAAGTATA	2,248	15,269
TTGCACAATGTGGATGCAGATCCATGTAGCTGGTTACTGAGT	2,269	15,290
CCATAGATGAAGACGCATGAATTCATACGTAGGACTCATAGC	2,290	15,311
AGTTCAGACGTCCACTATGATTGCCAACGCTATCATTAGTTT	2,311	15,332
TAGAACTGTGGCAGTCGTATCTTGGCAGCCAGCCCTCTCGCC	2,332	15,353
CACTCATAGTTCTTCTAGATGCCCTTGGCTAAGGCTCGTGCG	2,353	15,374
GGATTGAGGGGTGTGTAGTGGCAGAACGTGAGGAACGATAGT	2,374	15,395
TGGACCACCTAGTTCGCTTCGTCCACCTACTGCCAGTTGGCT	2,395	15,416
TAAACTCCTAGGGGACTCACTTAACTTAAGTAACCTGCAGCA	2,416	15,38

Sequences of 2-tile offset, y connectors	5' end	3' end
AAATGGGGAACTCAAGGGTTATCAGGTTGACTGCGGCATGGG	2,38	15,80
CAGGCTTACATCAGTGAGATATCAAGGTAACAATTAGGTAGG	2,59	15,101
CATATGGCTCGGACCCACTAACCGACCCTGCGTGTTACCAGA	2,80	15,122
CGAGGCCATGACCGAAGGTACAAACATATCTAGGACGCGTTA	2,101	15,143
ATTTCTTTTGAGTACAAACTACGTATATCCAATGGAGGTGTA	2,122	15,164
CTCAATGGCATACGGCAATAGCCTCCACCGGTAATGGGAGCG	2,143	15,185

ATACCCATTGCCCGATCTTTTTTAGAAATTACAGCTACATGC	2,164	15,206
ATTTCGTTGGTTCGTTTTCACCGCGTAATAGAAAGTCATGCT	2,185	15,227
GCGTGCACGTGGCGCCGCAGGGGCCACCCTCAGCGTCAGTAA	2,206	15,248
CCTTTTTTCCCTGGGCCACGGGCAGAAACAGCTCAAAGTATA	2,227	15,269
GGCCTAACATTCTGGAACACCCCATGTAGCTGGTTACTGAGT	2,248	15,290
TTGCACAATGTGGATGCAGATTTCATACGTAGGACTCATAGC	2,269	15,311
CCATAGATGAAGACGCATGAATGCCAACGCTATCATTAGTTT	2,290	15,332
AGTTCAGACGTCCACTATGATTTGGCAGCCAGCCCTCTCGCC	2,311	15,353
TAGAACTGTGGCAGTCGTATCCCCTTGGCTAAGGCTCGTGCG	2,332	15,374
CACTCATAGTTCTTCTAGATGCAGAACGTGAGGAACGATAGT	2,353	15,395
GGATTGAGGGGTGTGTAGTGGTCCACCTACTGCCAGTTGGCT	2,374	15,416
TGGACCACCTAGTTCGCTTCGTAACTTAAGTAACCTGCAGCA	2,395	15,38
TAAACTCCTAGGGGACTCACTCACGCGGAAAATCCCCAGTAT	2,416	15,59

Sequences of 3-tile offset, y connectors	5' end	3' end
AAATGGGGAACTCAAGGGTTATCAAGGTAACAATTAGGTAGG	2,38	15,101
CAGGCTTACATCAGTGAGATACCGACCCTGCGTGTTACCAGA	2,59	15,122
CATATGGCTCGGACCCACTAAAAACATATCTAGGACGCGTTA	2,80	15,143
CGAGGCCATGACCGAAGGTACCGTATATCCAATGGAGGTGTA	2,101	15,164
ATTTCTTTTGAGTACAAACTACCTCCACCGGTAATGGGAGCG	2,122	15,185
CTCAATGGCATACGGCAATAGTTAGAAATTACAGCTACATGC	2,143	15,206
ATACCCATTGCCCGATCTTTTCGCGTAATAGAAAGTCATGCT	2,164	15,227
ATTTCGTTGGTTCGTTTTCACGGCCACCCTCAGCGTCAGTAA	2,185	15,248
GCGTGCACGTGGCGCCGCAGGGCAGAAACAGCTCAAAGTATA	2,206	15,269
CCTTTTTTCCCTGGGCCACGGCCATGTAGCTGGTTACTGAGT	2,227	15,290
GGCCTAACATTCTGGAACACCTTCATACGTAGGACTCATAGC	2,248	15,311
TTGCACAATGTGGATGCAGATTGCCAACGCTATCATTAGTTT	2,269	15,332
CCATAGATGAAGACGCATGAATTGGCAGCCAGCCCTCTCGCC	2,290	15,353
AGTTCAGACGTCCACTATGATCCCTTGGCTAAGGCTCGTGCG	2,311	15,374
TAGAACTGTGGCAGTCGTATCCAGAACGTGAGGAACGATAGT	2,332	15,395
CACTCATAGTTCTTCTAGATGTCCACCTACTGCCAGTTGGCT	2,353	15,416
GGATTGAGGGGTGTGTAGTGGTAACTTAAGTAACCTGCAGCA	2,374	15,38
TGGACCACCTAGTTCGCTTCGCACGCGGAAAATCCCCAGTAT	2,395	15,59
TAAACTCCTAGGGGACTCACTTCAGGTTGACTGCGGCATGGG	2,416	15,80

Sequences of 4-tile offset, y connectors	5' end	3' end
AAATGGGGAACTCAAGGGTTACCGACCCTGCGTGTTACCAGA	2,38	15,122

CAGGCTTACATCAGTGAGATAAAACATATCTAGGACGCGTTA	2,59	15,143
CATATGGCTCGGACCCACTAACGTATATCCAATGGAGGTGTA	2,80	15,164
CGAGGCCATGACCGAAGGTACCCTCCACCGGTAATGGGAGCG	2,101	15,185
ATTTCTTTTGAGTACAAACTATTAGAAATTACAGCTACATGC	2,122	15,206
CTCAATGGCATACGGCAATAGCGCGTAATAGAAAGTCATGCT	2,143	15,227
ATACCCATTGCCCGATCTTTTGGCCACCCTCAGCGTCAGTAA	2,164	15,248
ATTTCGTTGGTTCGTTTTCACGCAGAAACAGCTCAAAGTATA	2,185	15,269
GCGTGCACGTGGCGCCGCAGGCCATGTAGCTGGTTACTGAGT	2,206	15,290
CCTTTTTTCCCTGGGCCACGGTTCATACGTAGGACTCATAGC	2,227	15,311
GGCCTAACATTCTGGAACACCTGCCAACGCTATCATTAGTTT	2,248	15,332
TTGCACAATGTGGATGCAGATTTGGCAGCCAGCCCTCTCGCC	2,269	15,353
CCATAGATGAAGACGCATGAACCCTTGGCTAAGGCTCGTGCG	2,290	15,374
AGTTCAGACGTCCACTATGATCAGAACGTGAGGAACGATAGT	2,311	15,395
TAGAACTGTGGCAGTCGTATCTCCACCTACTGCCAGTTGGCT	2,332	15,416
CACTCATAGTTCTTCTAGATGTAACTTAAGTAACCTGCAGCA	2,353	15,38
GGATTGAGGGGTGTGTAGTGGCACGCGGAAAATCCCCAGTAT	2,374	15,59
TGGACCACCTAGTTCGCTTCGTCAGGTTGACTGCGGCATGGG	2,395	15,80
TAAACTCCTAGGGGACTCACTTCAAGGTAACAATTAGGTAGG	2,416	15,101

Sequences of 5-tile offset, y connectors	5' end	3' end
AAATGGGGAACTCAAGGGTTAAAACATATCTAGGACGCGTTA	2,38	15,143
CAGGCTTACATCAGTGAGATACGTATATCCAATGGAGGTGTA	2,59	15,164
CATATGGCTCGGACCCACTAACCTCCACCGGTAATGGGAGCG	2,80	15,185
CGAGGCCATGACCGAAGGTACTTAGAAATTACAGCTACATGC	2,101	15,206
ATTTCTTTTGAGTACAAACTACGCGTAATAGAAAGTCATGCT	2,122	15,227
CTCAATGGCATACGGCAATAGGGCCACCCTCAGCGTCAGTAA	2,143	15,248
ATACCCATTGCCCGATCTTTTGCAGAAACAGCTCAAAGTATA	2,164	15,269
ATTTCGTTGGTTCGTTTTCACCCATGTAGCTGGTTACTGAGT	2,185	15,290
GCGTGCACGTGGCGCCGCAGGTTCATACGTAGGACTCATAGC	2,206	15,311
CCTTTTTTCCCTGGGCCACGGTGCCAACGCTATCATTAGTTT	2,227	15,332
GGCCTAACATTCTGGAACACCTTGGCAGCCAGCCCTCTCGCC	2,248	15,353
TTGCACAATGTGGATGCAGATCCCTTGGCTAAGGCTCGTGCG	2,269	15,374
CCATAGATGAAGACGCATGAACAGAACGTGAGGAACGATAGT	2,290	15,395
AGTTCAGACGTCCACTATGATTCCACCTACTGCCAGTTGGCT	2,311	15,416

TAGAACTGTGGCAGTCGTATCTAACTTAAGTAACCTGCAGCA	2,332	15,38
CACTCATAGTTCTTCTAGATGCACGCGGAAAATCCCCAGTAT	2,353	15,59
GGATTGAGGGGTGTGTAGTGGTCAGGTTGACTGCGGCATGGG	2,374	15,80
TGGACCACCTAGTTCGCTTCGTCAAGGTAACAATTAGGTAGG	2,395	15,101
TAAACTCCTAGGGGACTCACTCCGACCCTGCGTGTTACCAGA	2,416	15,122

Sequences of 6-tile offset, y connectors	5' end	3' end
AAATGGGGAACTCAAGGGTTACGTATATCCAATGGAGGTGTA	2,38	15,164
CAGGCTTACATCAGTGAGATACCTCCACCGGTAATGGGAGCG	2,59	15,185
CATATGGCTCGGACCCACTAATTAGAAATTACAGCTACATGC	2,80	15,206
CGAGGCCATGACCGAAGGTACCGCGTAATAGAAAGTCATGCT	2,101	15,227
ATTTCTTTTGAGTACAAACTAGGCCACCCTCAGCGTCAGTAA	2,122	15,248
CTCAATGGCATACGGCAATAGGCAGAAACAGCTCAAAGTATA	2,143	15,269
ATACCCATTGCCCGATCTTTTCCATGTAGCTGGTTACTGAGT	2,164	15,290
ATTTCGTTGGTTCGTTTTCACTTCATACGTAGGACTCATAGC	2,185	15,311
GCGTGCACGTGGCGCCGCAGGTGCCAACGCTATCATTAGTTT	2,206	15,332
CCTTTTTTCCCTGGGCCACGGTTGGCAGCCAGCCCTCTCGCC	2,227	15,353
GGCCTAACATTCTGGAACACCCCCTTGGCTAAGGCTCGTGCG	2,248	15,374
TTGCACAATGTGGATGCAGATCAGAACGTGAGGAACGATAGT	2,269	15,395
CCATAGATGAAGACGCATGAATCCACCTACTGCCAGTTGGCT	2,290	15,416
AGTTCAGACGTCCACTATGATTAACTTAAGTAACCTGCAGCA	2,311	15,38
TAGAACTGTGGCAGTCGTATCCACGCGGAAAATCCCCAGTAT	2,332	15,59
CACTCATAGTTCTTCTAGATGTCAGGTTGACTGCGGCATGGG	2,353	15,80
GGATTGAGGGGTGTGTAGTGGTCAAGGTAACAATTAGGTAGG	2,374	15,101
TGGACCACCTAGTTCGCTTCGCCGACCCTGCGTGTTACCAGA	2,395	15,122
TAAACTCCTAGGGGACTCACTAAACATATCTAGGACGCGTTA	2,416	15,143

Sequences of 7-tile offset, y connectors	5' end	3' end
AAATGGGGAACTCAAGGGTTACCTCCACCGGTAATGGGAGCG	2,38	15,185
CAGGCTTACATCAGTGAGATATTAGAAATTACAGCTACATGC	2,59	15,206
CATATGGCTCGGACCCACTAACGCGTAATAGAAAGTCATGCT	2,80	15,227
CGAGGCCATGACCGAAGGTACGGCCACCCTCAGCGTCAGTAA	2,101	15,248
ATTTCTTTTGAGTACAAACTAGCAGAAACAGCTCAAAGTATA	2,122	15,269
CTCAATGGCATACGGCAATAGCCATGTAGCTGGTTACTGAGT	2,143	15,290
ATACCCATTGCCCGATCTTTTTTCATACGTAGGACTCATAGC	2,164	15,311
ATTTCGTTGGTTCGTTTTCACTGCCAACGCTATCATTAGTTT	2,185	15,332

GCGTGCACGTGGCGCCGCAGGTTGGCAGCCAGCCCTCTCGCC	2,206	15,353
CCTTTTTTCCCTGGGCCACGGCCCTTGGCTAAGGCTCGTGCG	2,227	15,374
GGCCTAACATTCTGGAACACCCAGAACGTGAGGAACGATAGT	2,248	15,395
TTGCACAATGTGGATGCAGATTCCACCTACTGCCAGTTGGCT	2,269	15,416
CCATAGATGAAGACGCATGAATAACTTAAGTAACCTGCAGCA	2,290	15,38
AGTTCAGACGTCCACTATGATCACGCGGAAAATCCCCAGTAT	2,311	15,59
TAGAACTGTGGCAGTCGTATCTCAGGTTGACTGCGGCATGGG	2,332	15,80
CACTCATAGTTCTTCTAGATGTCAAGGTAACAATTAGGTAGG	2,353	15,101
GGATTGAGGGGTGTGTAGTGGCCGACCCTGCGTGTTACCAGA	2,374	15,122
TGGACCACCTAGTTCGCTTCGAAACATATCTAGGACGCGTTA	2,395	15,143
TAAACTCCTAGGGGACTCACTCGTATATCCAATGGAGGTGTA	2,416	15,164

Sequences of 8-tile offset, y connectors	5' end	3' end
AAATGGGGAACTCAAGGGTTATTAGAAATTACAGCTACATGC	2,38	15,206
CAGGCTTACATCAGTGAGATACGCGTAATAGAAAGTCATGCT	2,59	15,227
CATATGGCTCGGACCCACTAAGGCCACCCTCAGCGTCAGTAA	2,80	15,248
CGAGGCCATGACCGAAGGTACGCAGAAACAGCTCAAAGTATA	2,101	15,269
ATTTCTTTTGAGTACAAACTACCATGTAGCTGGTTACTGAGT	2,122	15,290
CTCAATGGCATACGGCAATAGTTCATACGTAGGACTCATAGC	2,143	15,311
ATACCCATTGCCCGATCTTTTTGCCAACGCTATCATTAGTTT	2,164	15,332
ATTTCGTTGGTTCGTTTTCACTTGGCAGCCAGCCCTCTCGCC	2,185	15,353
GCGTGCACGTGGCGCCGCAGGCCCTTGGCTAAGGCTCGTGCG	2,206	15,374
CCTTTTTTCCCTGGGCCACGGCAGAACGTGAGGAACGATAGT	2,227	15,395
GGCCTAACATTCTGGAACACCTCCACCTACTGCCAGTTGGCT	2,248	15,416
TTGCACAATGTGGATGCAGATTAACTTAAGTAACCTGCAGCA	2,269	15,38
CCATAGATGAAGACGCATGAACACGCGGAAAATCCCCAGTAT	2,290	15,59
AGTTCAGACGTCCACTATGATTCAGGTTGACTGCGGCATGGG	2,311	15,80
TAGAACTGTGGCAGTCGTATCTCAAGGTAACAATTAGGTAGG	2,332	15,101
CACTCATAGTTCTTCTAGATGCCGACCCTGCGTGTTACCAGA	2,353	15,122
GGATTGAGGGGTGTGTAGTGGAAACATATCTAGGACGCGTTA	2,374	15,143
TGGACCACCTAGTTCGCTTCGCGTATATCCAATGGAGGTGTA	2,395	15,164
TAAACTCCTAGGGGACTCACTCCTCCACCGGTAATGGGAGCG	2,416	15,185

Sequences of 9-tile offset, y connectors	5' end	3' end
AAATGGGGAACTCAAGGGTTACGCGTAATAGAAAGTCATGCT	2,38	15,227

CAGGCTTACATCAGTGAGATAGGCCACCCTCAGCGTCAGTAA	2,59	15,248
CATATGGCTCGGACCCACTAAGCAGAAACAGCTCAAAGTATA	2,80	15,269
CGAGGCCATGACCGAAGGTACCCATGTAGCTGGTTACTGAGT	2,101	15,290
ATTTCTTTTGAGTACAAACTATTCATACGTAGGACTCATAGC	2,122	15,311
CTCAATGGCATACGGCAATAGTGCCAACGCTATCATTAGTTT	2,143	15,332
ATACCCATTGCCCGATCTTTTTTGGCAGCCAGCCCTCTCGCC	2,164	15,353
ATTTCGTTGGTTCGTTTTCACCCCTTGGCTAAGGCTCGTGCG	2,185	15,374
GCGTGCACGTGGCGCCGCAGGCAGAACGTGAGGAACGATAGT	2,206	15,395
CCTTTTTTCCCTGGGCCACGGTCCACCTACTGCCAGTTGGCT	2,227	15,416
GGCCTAACATTCTGGAACACCTAACTTAAGTAACCTGCAGCA	2,248	15,38
TTGCACAATGTGGATGCAGATCACGCGGAAAATCCCCAGTAT	2,269	15,59
CCATAGATGAAGACGCATGAATCAGGTTGACTGCGGCATGGG	2,290	15,80
AGTTCAGACGTCCACTATGATTCAAGGTAACAATTAGGTAGG	2,311	15,101
TAGAACTGTGGCAGTCGTATCCCGACCCTGCGTGTTACCAGA	2,332	15,122
CACTCATAGTTCTTCTAGATGAAACATATCTAGGACGCGTTA	2,353	15,143
GGATTGAGGGGTGTGTAGTGGCGTATATCCAATGGAGGTGTA	2,374	15,164
TGGACCACCTAGTTCGCTTCGCCTCCACCGGTAATGGGAGCG	2,395	15,185
TAAACTCCTAGGGGACTCACTTTAGAAATTACAGCTACATGC	2,416	15,206

Sequences of x-connectors used in 19×14 Tile model	5' end
ACGTGTCGTGTCACTTACCACTAGGAGTTTATAACCCTTGAG	3,28
CCCTGCAATGAGTTGATCTGATTAGTTCTGCTGGGGCGGACG	5,28
GACTGAGGAGTTTCGTAGCCTATACTATTCGGTCACTGCCTA	7,28
CTCGCCACGAGGTGACCCGCCGTCGGGTTCATGCTAGTTCCT	9,28
CGAATTATTCTCGTTTTTTGTGGGTTGTGTGGTTGAAAGGGG	11,28
GAGGAGTCGATCTACAGTTGCCGATCGGGTTAGGGGGTGTTA	13,28
TACTTAAGTTAAGCCAACTGGGGACATTGACGTTTAGAAAAG	15,28

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