

Supporting Information

Self-Assembly of Wireframe DNA Nanostructures from Junction Motifs

Kai Huang, Donglei Yang, Zhenyu Tan, Silian Chen, Ye Xiang, Yongli Mi, Chengde Mao, and Bryan Wei**

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S1 Methods

S1.1 Structure assembly

Component DNA strands were synthesized by Bioneer Corp.. To assemble expected nanostructures, these DNA strands were mixed to a roughly equal molar final concentration of 100 nM for 2D addressable structures, 1 μ M for extended structures and 500 nM for 3D polyhedral structures. A 20 μ L or 40 μ L DNA mixture was annealed in 0.5 \times TE buffer (5 mM Tris, pH=7.9, 1 mM EDTA) supplemented with 20 ~ 30 mM MgCl₂ under a ‘ramp’ annealing program cooling down from 90 to 25 $^{\circ}$ C (or 10 $^{\circ}$ C) over a period of 17-76 h or under an isothermal annealing program.

S1.2 Gel Electrophoresis and purification

The annealed samples were subjected to 1% or 2% native agarose gel electrophoresis in an ice-water bath, and the gel was prepared in 0.5 \times TBE buffer supplemented with 10 mM MgCl₂ and pre-stained with SYBR Safe (Thermo Scientific). Then the target gel bands were excised, carefully crushed using the flat end of a plastic pestle in a Freeze 'N Squeeze column (Bio-Rad), and then directly subjected to centrifugation at 106g for 2 min at 4 $^{\circ}$ C. Purified samples centrifuged through the column could be diluted before AFM.

S1.3 AFM imaging

AFM images were obtained using a SPM Multimode with Nanoscope V controller (Bruker Corp.). A 40 μ L drop of 0.5 \times TE buffer (10 mM MgCl₂) were applied to a freshly cleaved mica surface and then a 5 μ L droplet (2 to 10 nM) of purified sample (annealed sample without purification for the extended structures) and left for approximately 2 min. Supplementary 5 -10 μ L 10 mM NiCl₂ was added to increase the strength of DNA–mica binding and additional dilution of the sample was possibly performed to achieve the desired sample density. Samples were imaged under liquid ScanAsyst mode, with C-type triangular tips (resonant frequency, $f_0 = 40 - 75$ kHz; spring constant, $k = 0.24$ N m⁻¹) from the SNL-10 silicon nitride cantilever chip (Bruker Corp.).

S1.4 2D average of single particles from AFM micrographs

Full size AFM images are converted into gray-scale maps. Particles in the maps were semi-automatically or manually boxed by e2boxer.py program in EMAN2¹. 2D average images of particles were calculated using 2D classification in Relion1.4 or Relion2.0².

S1.5 Cryo-EM imaging

Freshly purified samples of DNA polyhedral nanostructures were pipetted onto lacey carbon grids (Ted Pella, No.01824) pre-treated with 0.1 M MgCl₂. The grids were blotted for approximate 4 to 7 s and were then frozen in liquid ethane using a cryo-plunger (Cryo Plunger 3, Gatan). Micrographs of DNA octahedron and icosahedron samples were collected using a FEI Tecnai Arctica operating at 200 kV

with a Falcon II camera (FEI) in movie mode.

S1.6 Single particle reconstruction

Raw images collected in movie mode were processed by MotionCor³ to reduce image blurring due to beam-induced motion. CTF parameters were calculated by Gctf⁴ and particles were semi-automatically or manually boxed by e2boxer.py program in EMAN2. 2D average images were calculated in Relion1.4 or Relion2.0 using 2D classification, and particles in blurry or unreasonable classes were rejected. Initial models were generated from clear and representative 2D average images by e2initialmodel.py program in EMAN2. Proper initial models were used as references and good particles were used as inputs to calculate the 3D maps by 3D auto refine in relion1.4 or relion2.0. 3D classification in Relion were also used to calculate different conformations and particles in the best or clearest conformations were used to calculate the final map by 3D auto refine in Relion. Final 3D maps were visualized using UCSF Chimera software⁵.

S2 Self-assembly of addressable 2D structures

Figures S1-S2 show schematic diagrams and gel results of addressable 2D honeycomb grid with Y-shaped (3-arm) motifs (Y_0) and diamond grid with X-shaped (4-arm) motifs (X_0).

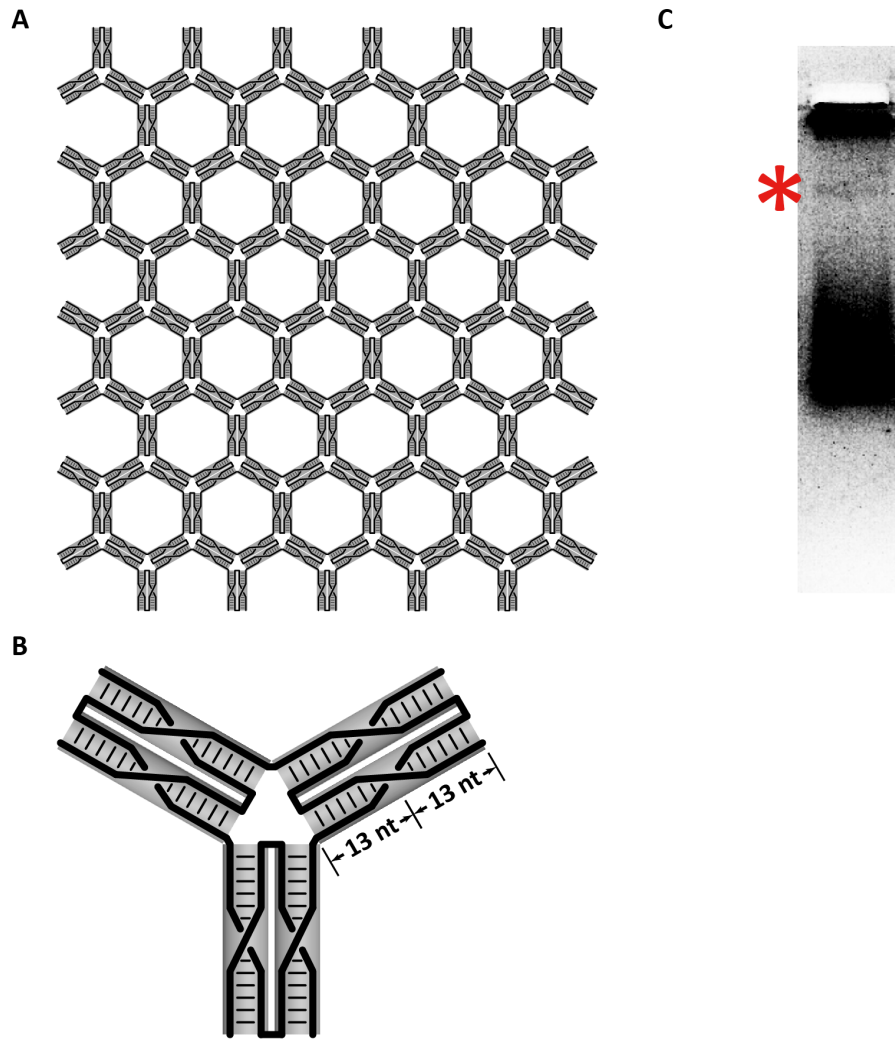


Figure S1. Addressable 2D honeycomb grid (Y_0). A. Schematic diagram of the addressable 2D honeycomb grid. B. Strand diagram with strand-level details of a typical Y-shaped (3-arm) motif. C. Native agarose gel electrophoresis result. The red asterisk points at the target band.

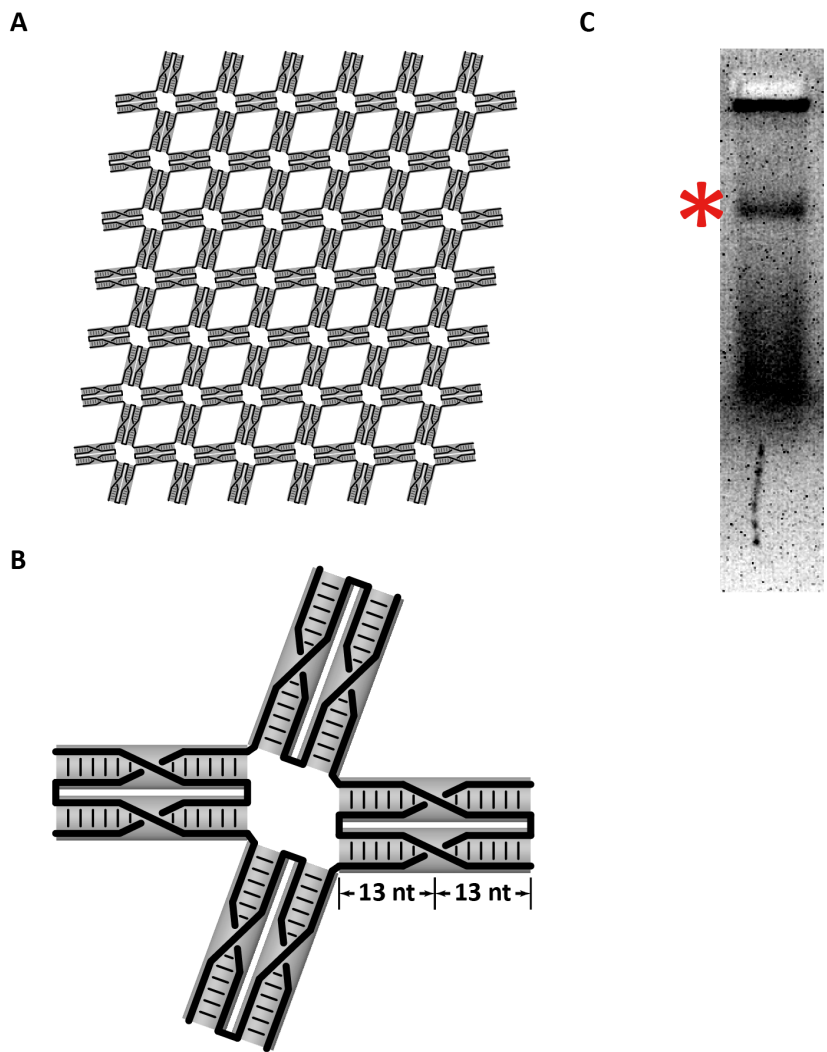


Figure S2. Addressable 2D diamond grid (X_0). A. Schematic diagram of the addressable 2D diamond grid. B. Strand diagram with strand-level details of a typical X-shaped (4-arm) motif. C. Native agarose gel electrophoresis result. The red asterisk points at the target band.

Single 'X'- and 'Y'-motifs (with and without T2 linkers) were subjected to 2% native agarose gel and the corresponding results are shown in Figure S3.

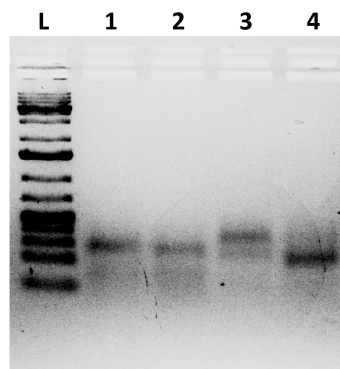


Figure S3. Native agarose gel electrophoresis results of single 'X'- and 'Y'-motifs.

Lane L: 1kb DNA ladder; lane 1: single 'X'-motif without T2 linkers; lane 2: single 'X'-motif with T2 linkers; lane 3: single 'Y'-motif without T2 linkers; lane 4: single 'Y'-motif with T2 linkers.

S3 Self-assembly of angle-controlled addressable 2D structures

Figures S4-S7 show schematic diagrams and gel results of addressable 2D addressable wireframe structures with angle control.

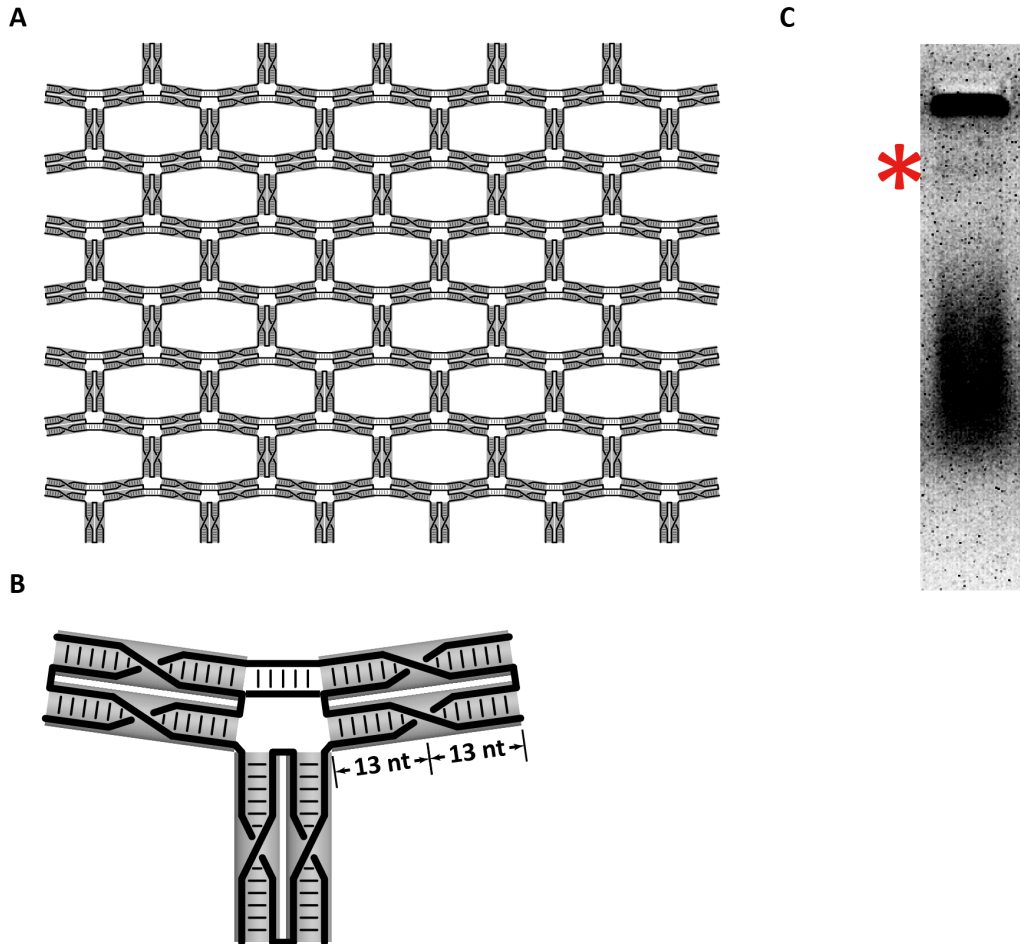


Figure S4. Addressable 2D honeycomb grid with angle control (Y_1). A. Schematic diagram of the addressable 2D honeycomb grid with angle control. B. Strand diagram with strand-level details of a typical T-shaped motif. C. Native agarose gel electrophoresis result. The red asterisk points at the target band.

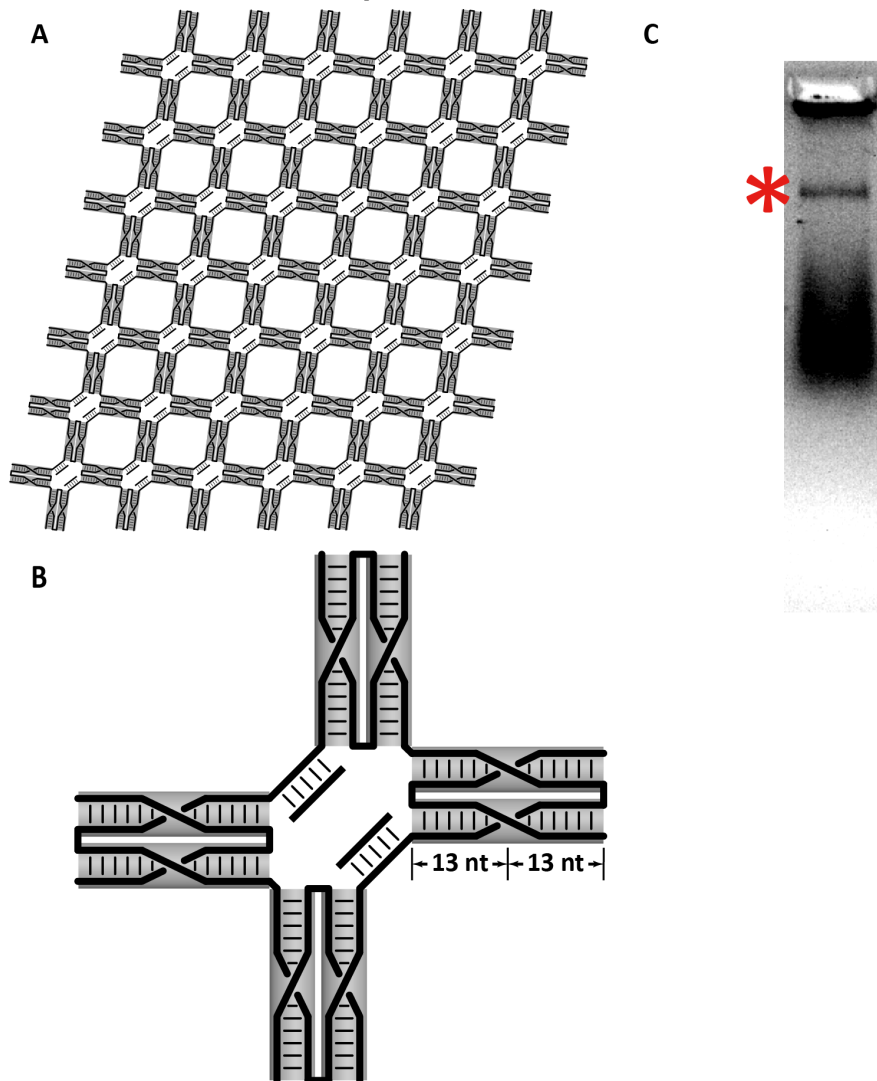


Figure S5. Addressable 2D tetragonal grid with angle control (X_1). A. Schematic diagram of the addressable 2D tetragonal grid with angle control. B. Strand diagram with strand-level details of a typical cross-shaped motif. C. Native agarose gel electrophoresis result. The red asterisk points at the target band.

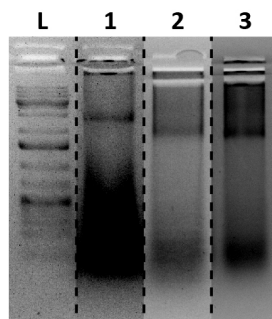


Figure S6. Native agarose gel results of 2D addressable grids constructed from 'X'- or 'Y'- motifs with different numbers of 10-nt single-stranded linkers. Lane L: 1kb DNA ladder; lane 1: 2D grid constructed from 'Y'-motif with single-stranded linker at one of the three crossover points of each vertex (Y_2 , see Figure 2C for design

details); lane 2: 2D grid constructed from ‘X’-motif with single-stranded linkers at two of the four crossover points of each vertex (X_2 , see Figure 2D for design details); lane 3: 2D grid constructed from ‘X’-motif with single-stranded linker at one of the four crossover points of each vertex (X_3 , see Figure 2E for design details).

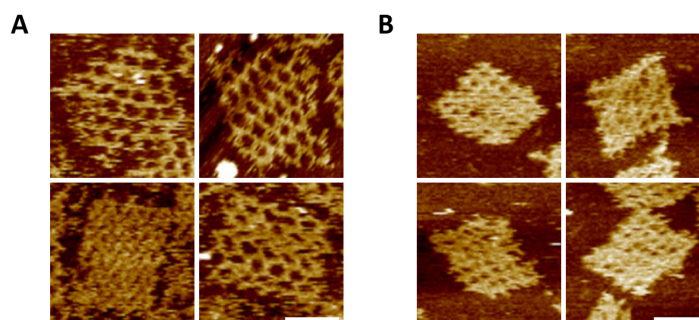


Figure S7. AFM results of 2D addressable grids constructed from ‘X’- or ‘Y’- motifs with 10-nt single-stranded linkers. A. Zoomed-in AFM images of structure Y_2 . B. Zoomed-in AFM images AFM of structure X_3 . Scale bars: 50 nm.

S4 Angle measurements based on 2D average of single particles

Structures	Y_0	Y_1	X_0	X_1	X_2
Measured angles ($^\circ$)	121 ± 7 (N = 24)	152 ± 3 (N = 13)	67 ± 4 (N = 18)	90 ± 3 (N = 17)	160 ± 3 (N = 13)

Table S1. Angle measurements for different 2D structures based on 2D average of single particles from AFM microscopies. N indicates the number of measured vertices of each corresponding averaged particle. As we can see the results of angle measurements in the table, the implementation strategy is effective. 2D averaged particles and the corresponding angle measurements are not available for structures Y_2 and X_3 .

S5 Self-assembly of extended 2D structures

Figures S8-S10 show full size AFM images of 1D extended ribbons and tube structures.

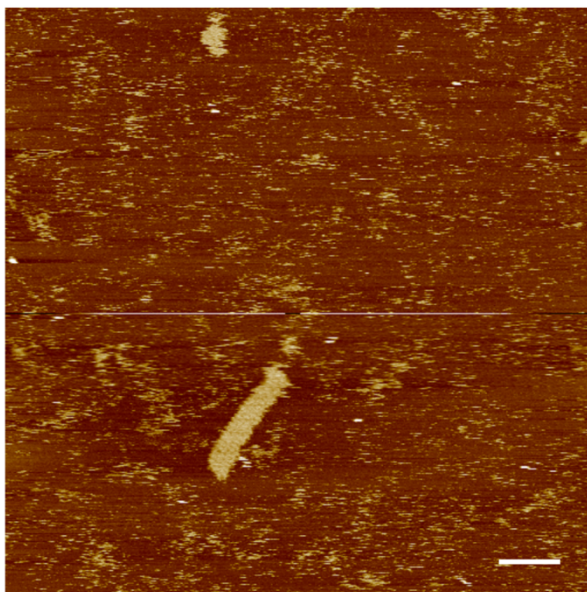


Figure S8. Full size AFM image of extended 1D ribbon from 'X'-motifs. Scale bar: 100 nm.

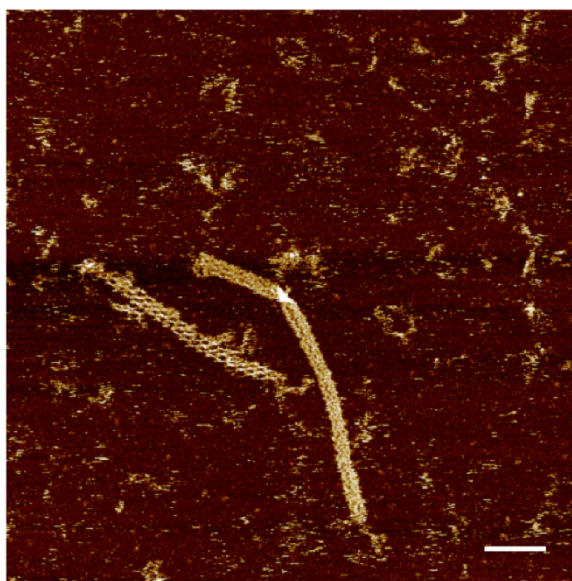


Figure S9. Full size AFM image of extended 1D ribbon from 'Y'-motifs. Scale bar: 100 nm.

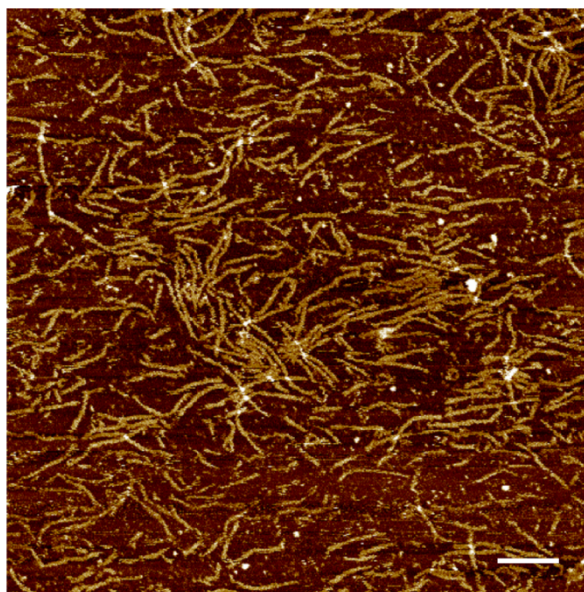


Figure S10. Full size AFM image of 1D extended tube structure from one continuous ‘Y’-motif. Scale bar: 100 nm.

We also designed similar ribbons from ‘X’-motifs or ‘Y’-motifs with less component motifs. Figure S11 shows a full size AFM image of tube structures composed of only two different component ‘Y’-motifs. Figure S12 shows full size AFM images of tube structures composed of two and four different component ‘X’-motifs respectively. As shown in the images, the overall structures tend to be circularized to form tubes.

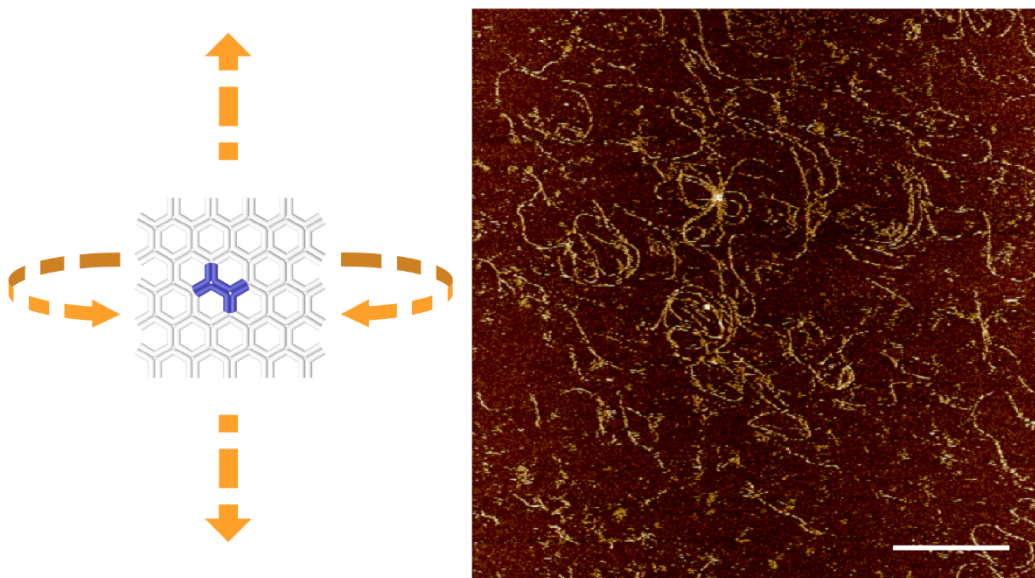


Figure S11. 1D extended tube structure with two different component ‘Y’-motifs. Each component strand in this tube structure is 32-nt long with four 8-nt domains. Left: schematic diagram (repetitive unit cells highlighted in blue); right: the corresponding AFM image (scale bar: 1 μ m).

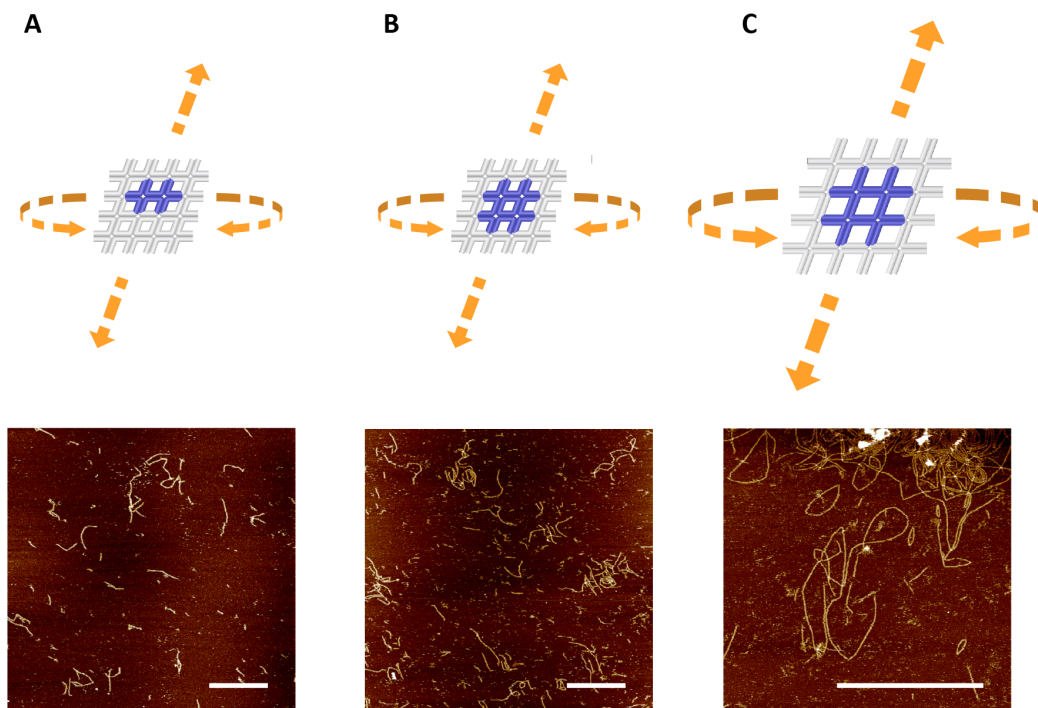


Figure S12. 1D extended tube structures with different component ‘X’-motifs. (A) Tube structure with two different component motifs. Each component strand is 32-nt long with four 8-nt domains. (B) Tube structure with four different component motifs. Each component strand is 32-nt long with four 8-nt domains. (C) Tube structure with four different component motifs. Each component strand is 52-nt long with four 13-nt domains. Top: schematic diagrams (repetitive unit cells highlighted in blue); bottom: the corresponding AFM images (scale bars: 100 nm).

Since the sizes of the extended structures of a specific design varied and their mobility in agarose gel were different, it was challenging to estimate the yield of desired structures from direct measurement. The fluorescent intensity of leftover strands was used to quantify the unsuccessful incorporation, and the self-assembly yield = $1 - (\text{the fluorescent intensity of leftover strands}) / (\text{the total fluorescent intensity of the entire gel lane})$. Yields of the two extended structures from repetitive units of different numbers of component strands were provided alongside the agarose gel electrophoresis results.

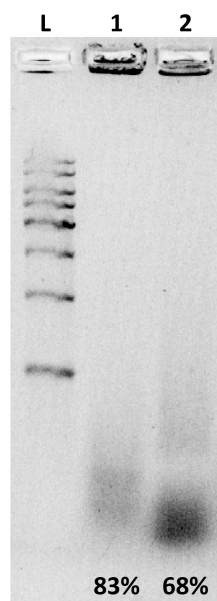


Figure S13. Native agarose gel electrophoresis results of extended structures from repetitive units of different sizes. Lane L: 1kb DNA ladder; lane 1: extended structures with two 'X'-motifs (eight component strands); lane 2: extended structures with four 'X'-motifs (sixteen component strands). Numbers at the bottom of the gel image denote the corresponding assembly yields.

S6 Self-assembly of 3D polyhedral structures

S6.1 Odd-edge vs. Even-edge

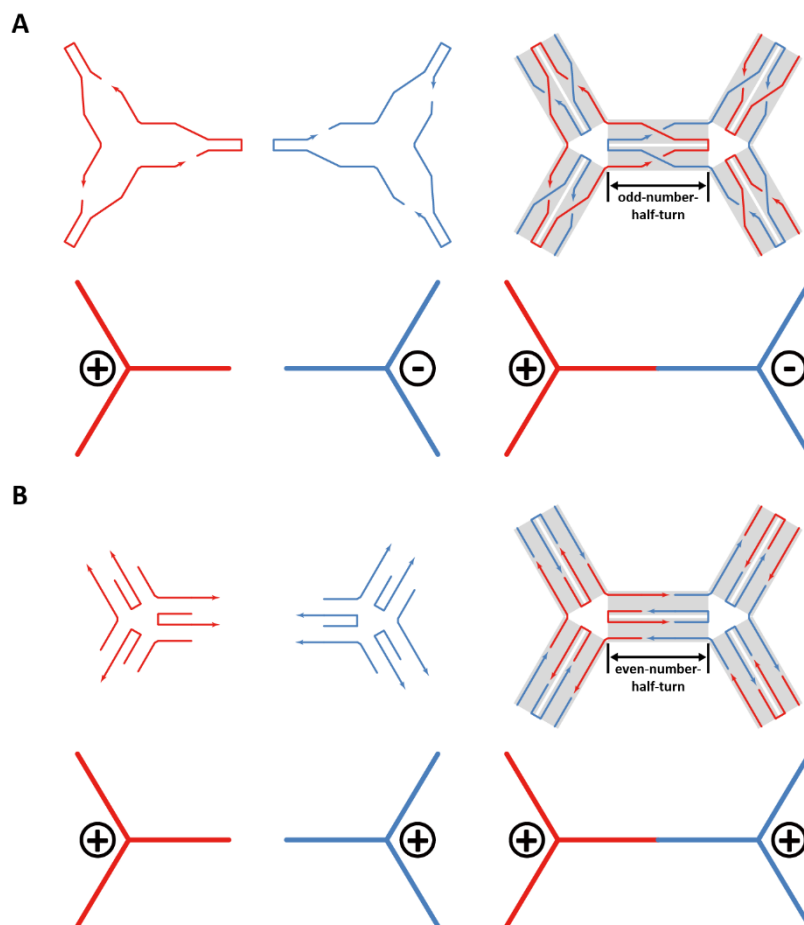


Figure S14. Schematic diagram of an odd-edge and an even-edge and corresponding assembly pattern. (A) Odd-edge and its corresponding “positive-negative” assembly pattern. (B) Even-edge and its corresponding “positive-positive” assembly pattern.

The odd-edge (shown in Figure S14A) formed between two motifs is an odd number of helical half-turns long (e.g., five half-turns is used to construct 2D addressable structures in our study). Each component DNA strand in one of these two motifs runs from 5' to 3' in a counterclockwise manner (colored in red shown in Figure S14A). On the contrary, each component DNA strand in another motif runs in a clockwise manner (colored in blue shown in Figure S14A). Red motif and blue motif can be defined as ‘positive’ motif and ‘negative’ motif, respectively. As a consequence of presence of odd-edge, neighboring motifs will form a kind of alternative ‘positive – negative’ assembly pattern.

However, the case in an even-edge (shown in Figure S14B) is quite different. All component DNA strands in every motif all run in a counterclockwise manner. Therefore, all motifs can be regarded as ‘positive’ motifs, resulting in another kind of assembly pattern called ‘positive – positive’ pattern shown in Figure S14B.

S6.2 Restriction of odd-edge in cyclization of odd numbers of units

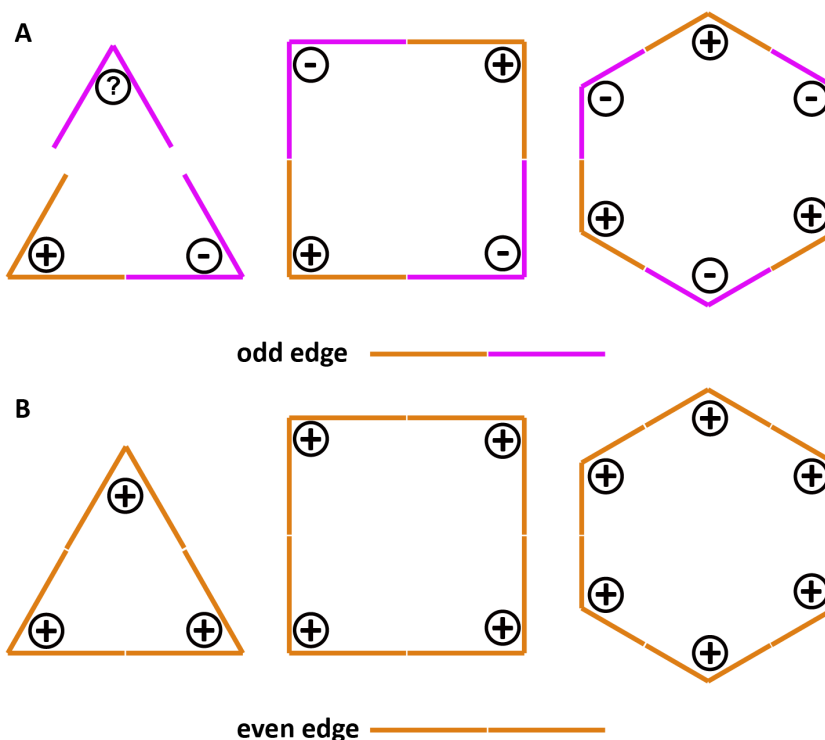


Figure S15. Schematic diagram demonstrating the restriction of odd-edge in cyclization of odd number of units. (A) The odd-edge prohibits the cyclization of odd number of units. (B) The even-edge has no such restriction.

For odd-edge, such an alternating assembly pattern leads to a conflict in tile arrangement when motifs try to cyclize into a triangle, a pentagon, or any other polygons with an odd number of units (shown in Figure S15A). The successful construction of both 2D honeycomb grid and 2D rhombic grid, each cavity of which results from cyclization of an even number of units, is a good example. As demonstrated in Figure S15B, the even-edge has no such restriction. The design of even-edge allows the cyclization of any arbitrary number of units in a polygonal face. Therefore, the design of even-edge is required to construct more complex 3D polyhedral nanostructures that are inaccessible from odd-edge.

S6.3 Detailed designs of edges and faces of 3D polyhedral structures

Figure S16 shows the detailed design of the face and an edge in a typical polyhedron (octahedron and icosahedron) with 32-bp edges. Besides typical 32-bp edges, we also constructed an octahedron with 42-bp edges. The detailed design diagram is shown in Figure S17.

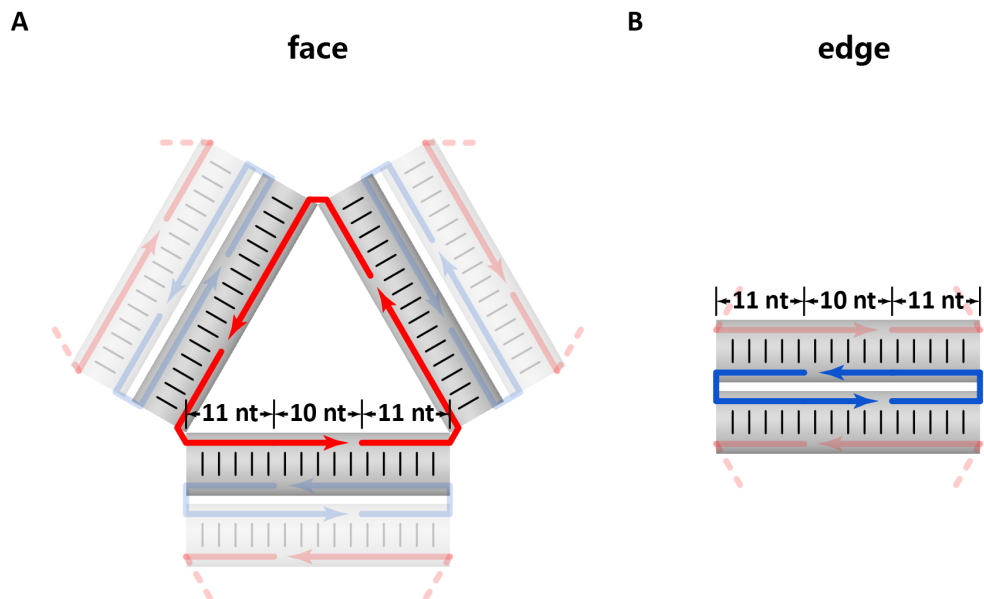


Figure S16. Detailed design of the face and an edge in a typical polyhedron with 32-bp edges. (A) The design of a face of a typical polyhedron. (B) The design of an edge of a typical polyhedron. Note that the strands in the same color (red or blue) correspond to distinct sequences.

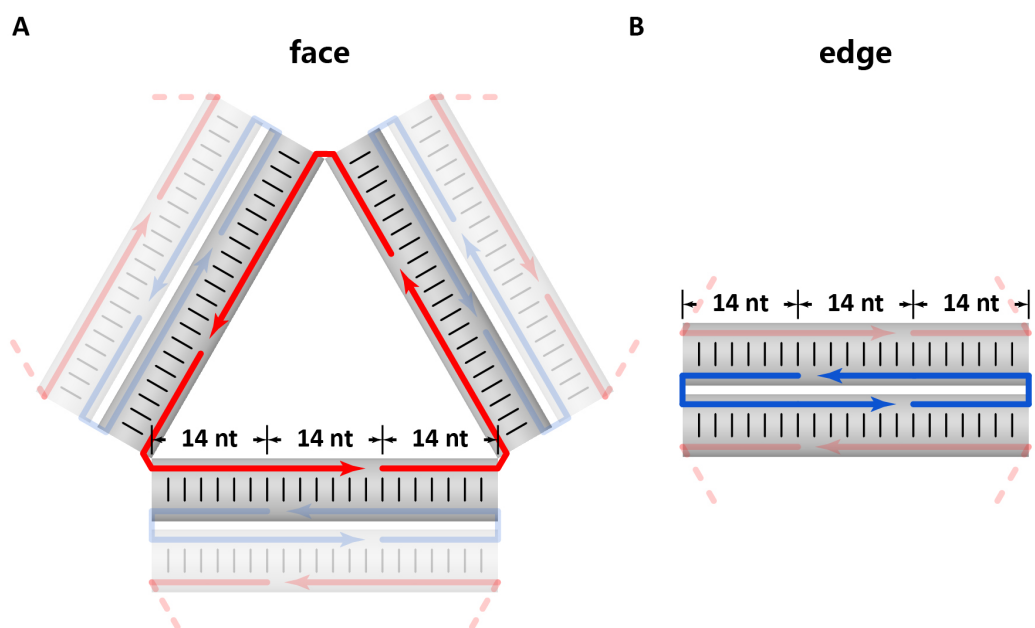


Figure S17. Detailed design of the face and an edge in an octahedron with 42-bp edges. (A) The design of a face of an octahedron with 42-bp edges. (B) The design of an edge of an octahedron with 42-bp edges.

S6.4 Agarose gel results and full size cryo-EM images

Figure S18 shows the agarose gel results of octahedra (32-bp edge length) with and without single-stranded T2 linkers.

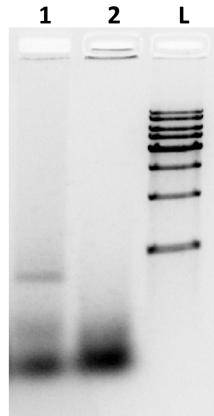
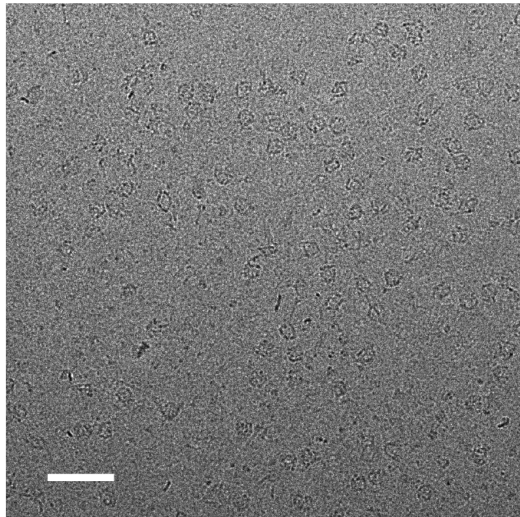


Figure S18. Native agarose gel results of octahedron (32-bp edge length) with and without T2 linkers. Lane 1: octahedron with single-stranded T2 linkers; lane 2: octahedron without any linkers; lane L: 1kb DNA ladder.

Figures S19-S21 show cryo-EM images of 3D polyhedral nanostructures.

A



B

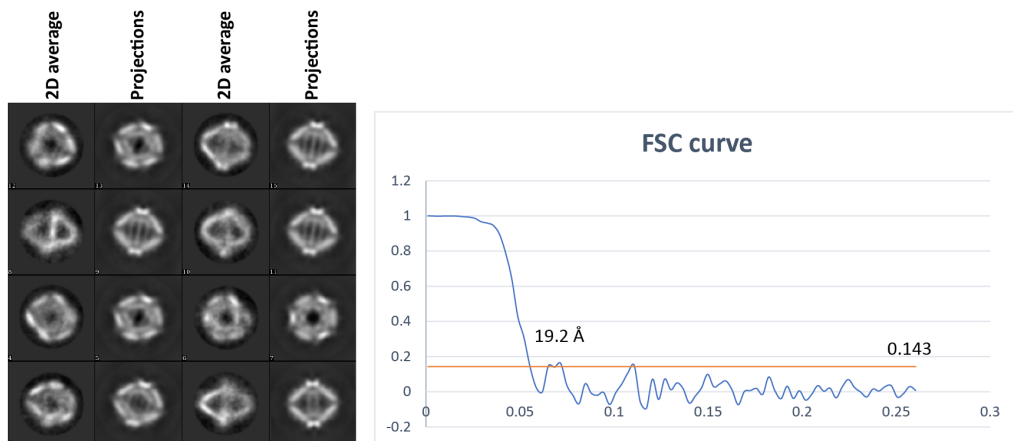


Figure S19. Cryo-EM image and 3D reconstruction of octahedron (32-bp edge length). (A) A representative raw image. Scale bar: 100 nm. (B) Left: Representative 2D averages and corresponding projections from 3D reconstruction.

Right: Gold-standard FSC plot of the 3D reconstruction.

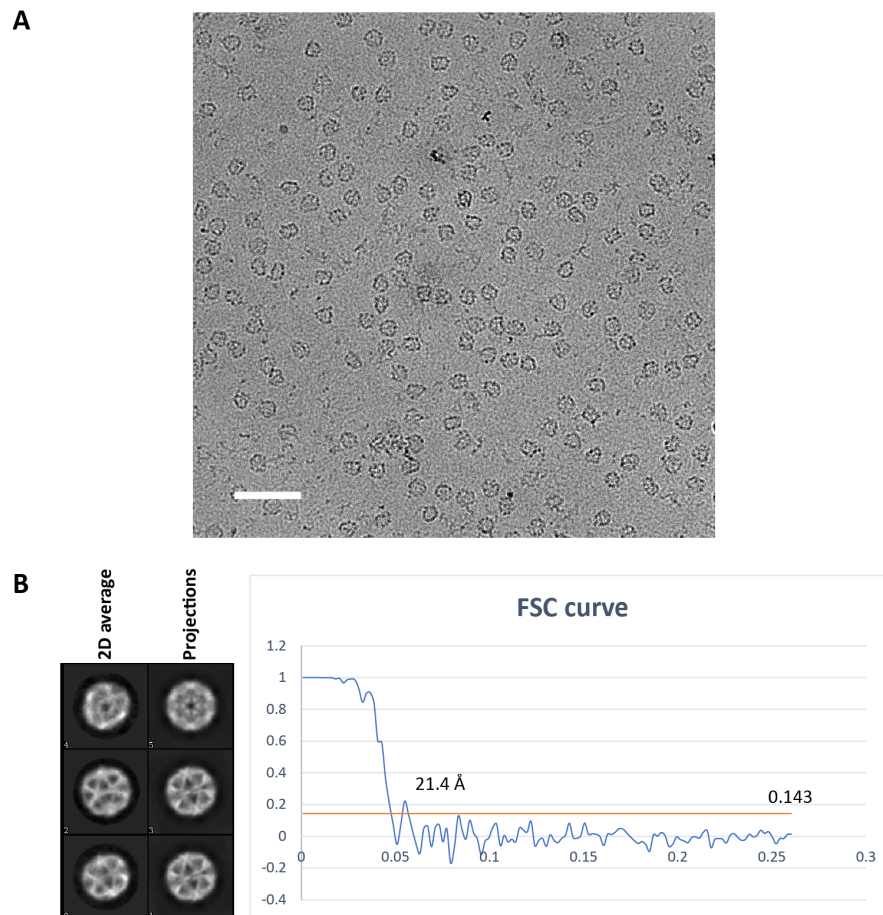


Figure S20. Cryo-EM image and 3D reconstruction of icosahedron. (A) A representative raw image. Scale bar: 100 nm. (B) Left: Representative 2D averages and corresponding projections from 3D reconstruction. Right: Gold-standard FSC plot of the 3D reconstruction.

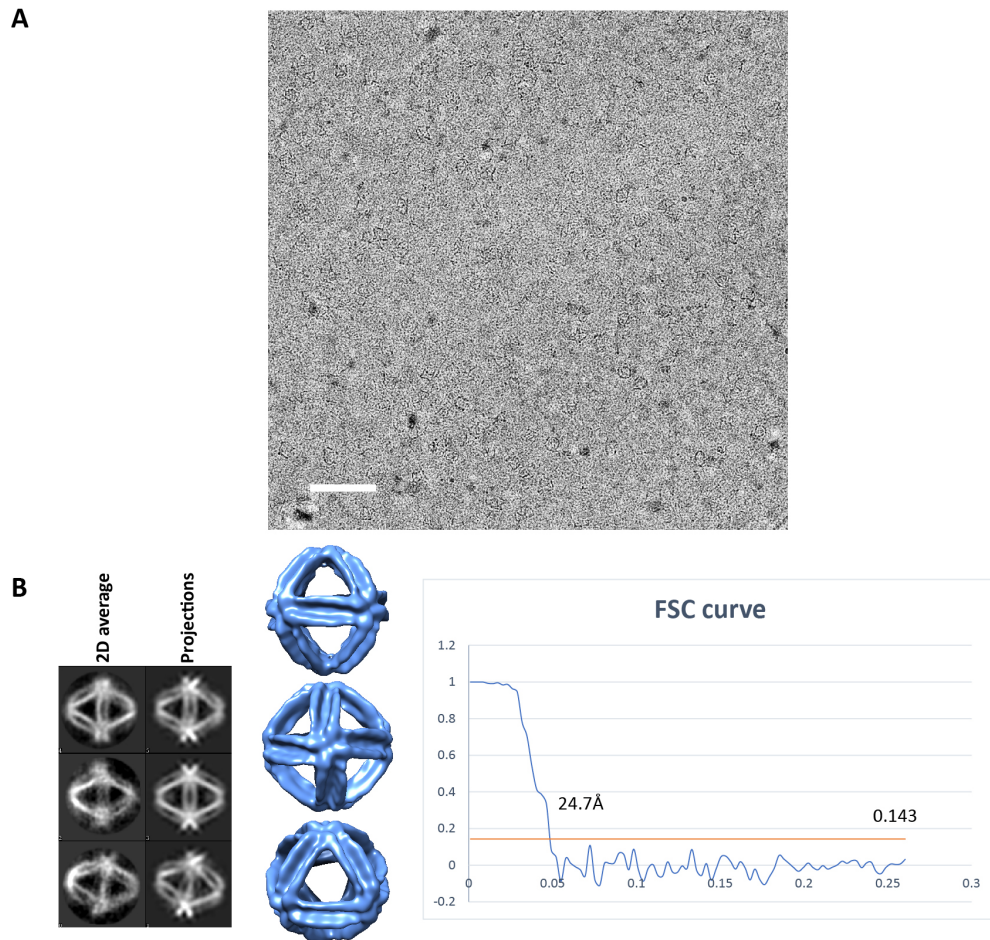


Figure S21. Cryo-EM image and 3D reconstruction of octahedron (42-bp edge length). (A) A representative raw image. Scale bar: 100 nm. (B) Left: Representative 2D averages and corresponding projections from 3D reconstruction. Middle: different views of 3D maps of octahedron (42-bp edge length) reconstructed from cryo-EM images. Right: Gold-standard FSC plot of the 3D reconstruction. An increase of edge lengths from 32 bp to 42 bp led to a resolution decay due to the elevated structural flexibility and particle heterogeneity.

S7 Yield quantification

Self-assembly yields of addressable structures in this study are summarized in Table S2.

Structure	Assembly yield
Y ₀	1.2%
Y ₁	1.7%
Y ₂	4.1%
X ₀	4.3%
X ₁	1.9%
X ₂	9.1%
X ₃	12.8%
Octahedron (32-bp edge length)	8.7%
Octahedron (42-bp edge length)	5.6%
Icosahedron	5.7%

Table S2. Self-assembly yields of addressable 2D structures and 3D polyhedral structures. The yields of similar DNA octahedron and icosahedron from repetitive motifs are more than 90%^{6, 7}. The yield gap is presumably due to the elevated complexity and limited optimization of self-assembly conditions.

References

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S8 DNA sequences

S8.1 DNA sequences for Y_0

Seq_ID	Sequences
1	GGGTGCAACGTATAAGGTTAGGTGGTAAGCACTTCCTATTCATCTCGATGAGG
2	GAGATAAGCCCTATGGGAACGCTCAGGCGGGAATCACATTGCAAAACTTGAGG
3	TTCGCCGAAACTGGATAAAGCAGCGGGCTAGGGTTAGGTTCCGATTACAGCAC
4	GCCTGGTCCCGGTTGTAAACAGCTCAAGAAAAGGCCCTCCTTCAAACAAATCCT
5	TGACTCACGCTGATAGTTTTCGCGCAACCTCAAGTTTTGCCCCTAACCCCTAGCC
6	CGCTGCTTTATCCTCTCGACTCGTAACGTGTATGGATAGAGGAAGCCCTTGAG
7	CCTTGAGGGATTGCAAACGTACTTACCGTTTTGTGGGAATTTCTATCCATACAC
8	GTTACGAGTCGAGCCGGGACCAGTGCCCTCAAGGGCTTCCTTCTCATATATAAA
9	TAAGGACTGTTCTCTTTCTTTTGTAAAGATGCACCCTCGATCAGTGACGTACGG
10	TTACGGCCGCGTTTAGTCCGCGATTAGGTATTAGTCCGTTTCGCATCCGGAACC
11	CTCTCCTTGGGCATAGAACAGTCCCTTATTTATATATGAGATCGAGGGTGCATC
12	TTACAAAAGAAAGTCGTTGGGAGGTTCCGAGCCTCTTTGTAAACGATCTAAT
13	CGATGCCAGAAGTTTGTGCAACCCTCCGTGCGGAGTTTGTACAAAGAGGCTCC
14	GAACCTCCCAACGAACGCGGCCGTAAATTAGATCGTTTATAACCCTTGCCCTAA
15	TCACTGAGGCTGTGACGTATATCTCTTCTCCGCGGTCTGCTTTGATCTTCTACT
16	TGAGGGTCCAGAATCGAGCGCTCGTCTATTCCGGCCAGGTCAAAAGAATAAG
17	TCAAGCAGCGGATACAGCCTCAGTGATTAGGCAAGGGTTGACGACCCGAGGA
18	AGAGATATACGTCTATGGCTCTCCGGAGATGTCGTGCAAGGCACTACCTGAAG
19	AGTGAATTCAACCCGTTTGACCTCGGAACGTACGACGCTTCTTGACGACATC
20	TCCGGAGAGCCATTTCTGGACCCCTCACTTCAGGTAGTGCTCACAAATCTCCGC
21	TCTACGGCTAATCCTAATGTTTCGGTCCAGATCCGTTGGGCTAGCTGGCTACACG
22	AATGTAGATACGTTAGGGTCCGAGGAGTTTCACCTAGCGGAGTGCGGGCACA
23	GGTCCAAGTCCCATGATTAGCCGTAGAGCGGAGATTTGTGGCCCAGGATCTGG
24	ACCGAAACATTAGTCAGCCACAGCGTCGAGTTAAAGTACTTGCAGTTAAACG
25	TCTTCTGGGATCACATTCAGCAACCCGTACTCGAGTGCCGTGACTTTAACTCG
26	ACGCTGTGGGCTGACGTATCTACATTCGTTTAACTGCAATGTTGCAATTTTCC
27	GTAGGGTGAGCACTCGATATTGATTTACCGTTATCTTGCTCGATTGTTCCATT
28	ACTGAGAAAAGGATCGTTAGCGCGGCATCCGAGGCACTCCACGATCGAAGAT
29	AGTGGATGGGCGCTGTGCTCACCCCTACGGAAAATTGCAACGCAAGATAACGGT
30	AAATCAATATCGATAAGACGACTAGCGCCTTGTCGTTCCGAATTTCACTCCTG
31	TTGGTCTCTTATGCAAGCACCCCTGGATCACGTACTCGTGTGCGAACGACAAGG
32	CGCTAGTCGTCTTTCCCTTTTCTCAGTCAGGAGTAAAATTTGGGCCACAGGCC
33	TTCTTGGCACATCAAGGACTTTTCTACCCCTATAGGTCTATTAGATTTTAGTCT
34	TTTTTTTTTGATGTGCCAAGAAGGGCCTGTGGCCCTAGACCTATAGGGTAGAAAAGTCCTTTTTTTTTT
35	TTTTTTTTTTAGGGCTTATCTCCCTCATCGAGATGATGTGATTCGCGCTGAGCGTTCCCATTTTTTTTTT
36	CCCTGAAAAGTGTATACGTTGCACCCGTGCTGAATCCGAATAGGAAGTGCTT
37	ACCACCTAACCTTTCTCTCATACCTCTGTAGCTACGCCATGCTACCTTATAG
38	GCGAGTTTTATATCAGATACGGTTGCGGACAACGGATTGACACAACATATCG
39	GGATTGATTGGTCACGCACCTCGTTAAGTGGAAGGAACCTCAATCCGTTGTCC
40	GCAACCGTATCTGACACTTTTCAGGGCGATATGTTGTGTTCCGCCAGCTGTACT

41	AATTCGTGGTGAAGAGCATGAATATGCACCTCTGGGACCTAAGCCGTAAAACC
42	CGAGCTCAAAAAGGTCAATCCCTCAAGGCCGTACGTCACCTGATTCCCACAAACG
43	GTAAGTACGTTTGTTCACCACGAATTAGTACAGCTGGCGGGTCCCAGAGTGC
44	ATATTCATGCTCTTCGGCCCTCAAAGTCCACGGCCACTTGGAGCAAACCCGCC
45	AAATACGCTAGGTCGTCACCAGGATTGTTGTACCTGTAGTCAAGTGGCCGTGG
46	ACTTTGAGGGCGGCCTTTTGAGCTCGGGCGGGTTTGCCTCCTTAAGAAGGTC
47	AATATAACTAGGAGTGATCTCCAATAATGCTTGGCCCGTTAAAATGCCGAGA
48	AACCGGTAGCTTATACTTCTGGCATCGAGTGAGAAGATCACAAACTCCGCACG
49	GAGGGTGCACAATTCCTAGTTATATTGACCTTCTTAAGGCGGGCCAAGCATT
50	ATTGGAGATACACTTCATGGTTCCAGCTGATTAGGTCGCGGAACACCGTTGTC
51	AATATGATTTTCATGCGCCTTGCATGCTAAATATAGAGTTTCGCGACCTAATCA
52	GCTGGAACCATGATAAGCTACCGGTTGACAACGGTGTTCCTCCGGACAGGGTC
53	GTGGGCACGTTCCGCAAGCCCACAACGACGTAGTGCAAATATAATGAGTAATT
54	CCAGACACGGTGATGGTTGAAATTCACCTCGTGTAGCCAGCTAGCGTCGTACGTT
55	CCGAGGTCAAACGTGGAACGTGCCACGACCCGTCCGGATTTGCACCTACGTC
56	GTTGTGGGCTTGCTAGGGCCGCTCAATTATACGACGTAACTTTAGGCACCGGG
57	CTTGATCGGGCCAATGAAGACCGCGATCCGATCGATATATGTTACGTCGTATA
58	ATTGAGCGGCCCTTCACCGTGTCTGGCCCGGTGCCAAAATTGCTATGGATACT
59	CGCCAAGGGTCCAATCGATCGAAACGTCCCAGGACTTATATGTATAACCTCG
60	AGCAGTCGTCTACTTGATCCCAGAAGAAATGGAACAATCGGGCAGCTCGAGTAC
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62	GTTTCGATCGATTTTAACCAAGCCATCAATTCGAGCAGCGGCTTGTTCCTCT
63	CTTGTCTGCGATGAACAGCCATTGGTTGAGCTTCGTTTTGCTGCTCGAATTG
64	ATGGGCTTGGTTAGTAGACGACTGCTAGAGGAACAAGCCTCAAGGTCACCACT
65	CCCGGTTACTCAACTCGAATACCACTCACGGATGGTTATTCCGTTTGTCTACA
66	TGCCCTGAACCGCTCATAAGAGACCAAAGACTAAAATCTACACGAGTACGTGA
67	TCCAGGGTGCTTGTTTGAGTAACCGGGAGTGGTGACCTTGATAACCATCCGTG
68	AGTGGTATTCGAGTTAAATCTGATGCTTCGCCGTGAGAGCCTAGAGTGTTTTC
69	TTTTTTTTTGCTCTCACGGCGAAGCATCAGATTTAGCGGTTTCAGGGCAGAAAACACTCTAGTTTTTTTT
70	TTTTTTTTTTAGGCGTAGCTACAGAGGTATGAGAGTAATAAAACTCGCCTATAAGGTAGCATTTTTTTTT
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72	CGCCATAGTTTCGAGCCTGCATAATGAAAGGCGCCGAGGTTAGCTCACGGGTT
73	ACATGAATTCCCTTGATATGTGCACAAAATGCGCGACGAGCTTCGTGGACCTGGC
74	AATAACCTACGCTGACCAATCAATCCGGTTTTACGGCTTAGTTCCTTCCACT
75	TAACGAGGTGCGTTAAGGAATTCATGTAACCCGTGAGCTAGCTCGTCGCGCAT
76	TTGTGCACATATCTTAGAAGCACCTGTAATATACGGGCCGATTCCCAGTTATG
77	TGAGCGTCCTTCCCTTTGGCCGGTATATCGGTCAGCGAATCGGCCCGTATATT
78	ACAGGTGCTTCTAGCGTAGGGTTATTCATAACTGGGAATTAACGCGGCGCAC
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81	AATCCTGGTGACGTTGTTCTCTAGGGTGTGCGCCGCGTTTTAGCTAGAGTTGG
82	TCGCTAGTTGCAATGTGCGTCTACTCGCATTCGATGTTGCCCTGTAACCTCTA
83	CCTAAAGAAGTGTGAACCCCTCGGGAAGCTATTGCAGGCTGCAACATCGAATG

84	CGAGTAGACGCACCACCGTCATTGGGTAGAAGTTACAGGTAGTGCGCGAAGCC
85	AAATACAGTGTCTGTGAGTTCTGATACGGCAAAGATCTTCTGCTTAGTCGATTT
86	AGGATAACTACTCTTGTAAAATCATATTAATTACTCATTATACTCTATATTTAG
87	CATGCAAGGCGCATCGACACTGTATTTGGCTTCGCGCACTGAAGATCTTTGCC
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109	TGCACAAATGGGCCAGCGAATTAATCAACGGCGGGCTTCTTTGGACTTATCGGA
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114	AAGCGAATCCACCTATCGTTGAACGACGGCTACTGCGAGAAACCAATAAGCTA
115	TAGGAGAAGCCAGAGAGAACGACCCTTCATAGATTTACGTTCTCGCAGTAGCC
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117	GGGTAACACGAATATGTGCCTCAGTCCATTGATAGCGTTTCGTGCAATCTGCC
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119	TCCCGAAGGGTTCTATTCGTGTTACCC TAGTCTACCC TGC AACGCTATCAATG
120	GACTGAGGCACATTTGTGCGAAAAGGGCGCCGGACTAGACTAATTGAGTTATGT
121	TTAAATAGTATCACAAC TCAATCAACAGCGTGCATGGTAGTCTAGTCCGGC
122	GCCCTTTTCGCACTGCCGTCCAAGGGACATAACTCAATTTGATCCGCTTTCCC
123	ACGCACGTTTCGTGATATGTAGGCTTGTGTACCC TGTG TATTCAGGCAGCGTA
124	CCTGAGTTC TAGGTTAAGAACTGGGCC TTGAACTGCGTATATTAGACCGCACC
125	GTTATTTTCGTCGTT CACGAACGTGCGTGGGAAAGCGGATCTACACAGGGTACA
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127	ACCACGCATCTGGTAAGTCGAAGCTCTACATTGGACCGATGTGAGTC TAGGGA
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130	ATGCTAATTATGCTTAGATATGGGCGGTTCTATAGTTTCATTAATGTAATAAT
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132	CCGATAGAGCGGTTCAATCCGCTAGCGAACAAAGCGAATAGTACGGTAGTGAA
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147	TACAACGACAACAGAGCGTATTTGTATAGGTCAAATCCCGTAGGTGCTTAAGTT
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152	ATGAGGCGTAATCTTGACATGTCGTGTTCTGCCAGGGCAGTCGCC TACGTACTG
153	TCATGGCAGCCTTGCAAGGCC TAAATTCAGACAATCTATCTACTGCCCTGGCAG
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155	TCGCTTACGTGGATCGACGTCAGTTTGAAACGAGGACCGTTCAAGGGACGATT
156	GCACATGTCTATGTTGATACTATTTAATACGCTGCC TGGACCATCGCACGCTG
157	TTGATGTGAGTTGTTCCACGTAAGCGATACCATGCTGACCCGGTCC TCGTTTC
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162	AGCAGCCAATATCTCCAGATGCGTGGTTGCAACGGGAGTGTGGTCCAATGTA
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164	TTTCCTTAAAGTCTTCGTGGGCCATCAGTCGTTGACTAGATTTGCATACAGGG
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166	TGATGGCCACGAGATATTGGCTGCTCCCTGTATGCAAATTACAGGGCGCAAG
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168	GAGCGTTGCGCATTGACGCGAGAGGAGCCACGCTTAGTGCC TTTAGGGTTCGC
169	TATTTATGGTCGTTGAATCTGGAACTCTTGCGCCCTGTATCATGAGTGAGAC

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177	GCTTTTAGCTTAATTTCTTGGTTGTAAACCTCTGTTCTCCCTAGTGCTGGTAT
178	TTAAAGCAAATCATACTTTATTTCTCGCAAGAGGTGAAGGCTCCTCGGGAGAAC
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180	GCGAGAAATAAGTGACACCCAAGGTGGTTCTCCCGAGGATTACCCATGCCCTC
181	GTGGGTGTCGATTTAGTCCGTCGTGACCCATCCGCTTATTAACTCGCGTTCCT
182	GGCCACCTGATTTTTGTTGTCGTTGTAGACGAAACTTGACCGGATTGACCT
183	ATACAATACGCTCTAATCGACACCCACGAGGGCATGGGTAATAAGCGGATGGG
184	TCAGACGGAGCTATAATTTCTCCCTTCCACACAGAACCGTCTGTACGAATCT
185	TGATGCATTAAGTGCAGATCAATCCCTAAAGAGATGCATACGGTCTGTGTG
186	GAAGGGAAGAAATTAATCAGGTGGCCAGATTTCGTGACAGTTTCATAGCAGACT
187	TGCAAGAACCCTGAACGCGCTACAGACCAACCCAGGCGTTGCACCATCAAGGT
188	GTCTTGAATCGATAAGGCTGCCATGAAATCGTCCCTTGAGATAGATTGTCCTG
189	AATTAGGCCCTTGCTCAGGGTCTTGCAAGTCTGCTATGAAACGCCCTGGGTTGG
190	TCTGTAGCGGTTTTTCATGCCAGGGAAGTTCGTTGAATCGTGCAGATTGACAG
191	TCGCTCCCGTTCAGGCACTGCAAGGCTATAAATCCCTCTTCGATTCAACGAAC
192	TTCCCTGGCATGATCGATTCCAGGACCTGTCAATCTGCATGCTCGATCTTTGT
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195	GCGCTGTCTGCGATGTGAACCATATGGACAAAGATCGAGCGACTGACAAGGTA
196	ACATTGTTTGAGATGGTGTGACTCTCATTTGCTCCATTTTAAAATCCATGAG
197	ACGCCTAGCTGGTGAGCGCATATCTCGTGTCTGCGTGACTAAATGGAGACAAT
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199	CAACCCACCGTGAAGGCACGAGCGTTAATATGCCACCATGTAGTTAAACAAG
200	ACTACTTAGGGTGTGAAGCTCGCGTACCGGGACTACAATTCAGCCCACGCAG
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208	GTCAAGTATATTGTATCCTATAGGCACCTGTAAACTCCCGGTCTACCCAGGAA
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213	CGAGAACAAGAAAGCCTAGCACAAATTGACTTAATTGTCTTAGGAATAAGTTTC
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216	AATTGTGCTAGGCTTAACTCCGCAATCATTGCCACGTGCAATAAGGAGTCAC
217	TACGGGATTCCTCACTGTTTCAGATCCCAGGTATACGATGTCGACGTGGCAATG
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219	CAGTCGAGCTTCTATCGCCTTTGTTCCGCATTGCTCCCATTGGGAGCCTAGGG
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230	TCTGGCAAATCAGATGGGTTTGGCACTCGCGAACAATCCTTGGAAAGTCCAATT
231	GCTTCATCACAAGCGGGCGGAAACCTTGGTCAATCAACTTAATAAAATCAGA
232	GATTTAGACTGCGTACCAGCTAGGCGTCTTGTTTAACTACGTCACGCAAGCAC
233	GAGATATGCGTCTCTTGTGATGAAGCAATTGGACTTCCAGTTGATTGACCAA
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239	TATACGGACGGCGTCACAAATCATCTTTTCAACACAAACATTAACATGGGCT
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241	CGCTAGTATTCCAATCCTTTTCAGTTTCGCCATGTGGATACGGGAGTACTGTCA
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256	TTTTTTTTTCGGTATACCCGGGAGACCGTTCTAACTGGTTGACTGTCTTATACAGGGTTAATTTTTTTTT
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S8.2 DNA sequences for X₀

Seq_ID	Sequences
1	CCCTTCTCACGGGTAAGACCTCAAACCTTTTCTGAATCGCTGTCTGCAGGGAGA
2	TTACCAACTCTTTTTGTAAGTCCAGTCCGCGAACGTGGTCCC GCCACATCC
3	CAGCTGATCATCTTGGTAGCCAGCGTTCATGGGAGGATCGCGGTGCTCC TGAC
4	AGTTGTATTTCGTCTCTAAACAGGTTCAATTTGGCAGCGGGCCCTACGCGTTAT
5	GACTTGCAGGAACTAACCTTCCCTTAGGCTACTTACTGTACCACGTTCCGCGG
6	ACTGGCAGTTACAAGATGATCAGCTGGGATGTGGCGGGATTGTCAATTAGGGCT
7	GACTCTGCCACAACGCCCGTGTAGTGC GCGATACCAC TTTTGTATCCTCGCGT
8	CAGTAGTAGGAGGTCACCTCACCTGAAAGTGACGCTGGTTGATTGGTTTCCCTC
9	TCAGGGTGAGTGATGAAAATTCGCGTGTCCCTCATGGGCCAAATTCACATCT
10	TTCAATCAAGCTCTCTGGCGTTCCCTTGAGGATGAGACAGTACTGCGTCCCGAA
11	GACTCGCGCTTCTAACGCGGAACATGCTCTGACTCTCCTACATCCAGAGC
12	GTA TACCCA ACTT CCTCTACTACTGACGCGAGGATACAACCAGCGTCACTT
13	TTTAGGGCCGGTTACAAAAGACGTGTGGATGCGGTGCTAGTACTGTCTCATCCT
14	CAAGGAACGCCAGGGAAGCGGAGTCTTCGGGACGCAGTTAACCGGTCCAAG
15	GTCGCTAGTCGAGTACCAAGATCCCTCTGCCATGCC TGGTTACTTCTCCGCC T
16	TGTAACAACGCGGTAGTGCTCGTTC CGTG GATAGACGGCTACATATCGAAGCG
17	GGAACGAGCACTATACGGCTCCTTTAGATAAACGGCGTCC TTTGTTAACATACA
18	AATGCTGAGGAGGTACAGTGTGTGGACATCGGGCTCCGAGTACAGTCCAAGTC
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21	GCTAAATGCTTGAGAGTAAGTATCCCTATTTTATCGTCTTCTCGGAGCCCGAT
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24	TAAACAGTGGGACTATTCTTGCCTGCGTGCCGTGCTTGTGTTAGCGCTATAGCC
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29	GCCAAACTGTTTCTTTGTGGCAGAGTCAGCCCTAATGACAAAGTGGTATCGCG
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35	TAACAACCCTAGACAGGAGAAGACCAAAACGGAGTGCAC TTCGATCAACCGGC
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37	TCGCTCCACGCTTTCTCGACTAGCGACCTTGGACCGAGTTCCAGGCATGGCAG
38	AGGGATCTTGGTATGCCGCTCAACGCCCAACATGAACCTCATAATCTACTTCT
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65	AGTGCCCTAGCCATAATCACATAGGAACGATGCTGTTCC TTAGTTCGTGCGCA
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67	CCAGTAAAAGGTCTCTAGGGTGAGATTGCACACAGCAGTGGCTTCTT CACAAT
68	CATTCTGCTCGAGTCTGAGGACTCTGGGATTGCTGTGTC CATCTCATTTCTTCG
69	GGCCGATGTGAAGGAAGGCTCGGTCACTCGACCTACGACTAATTAGCCAGGAT
70	CAGGAAAGTAATCGACCTTTTACTGGTGTATGTCTGACTTGCATACACGACGA
71	CTCTGAGAAGCCCCGCGACTGTGTCTGGGCTCCCTTACTGTGCGGAGGGACCAA
72	ATTACTCTTCGTGATAAAATCGTCCC GGGTGGTGGAGTCTCTACTGGCGAAGA
73	GGATTCTGCCCGGGTGACACGTGAAGTCAGACTAAACGATTGAGATAAACTAG
74	AAACTATTTAGACATCTCTGATCATATTAGACATTCGCTTATAAATTGACGTAC
75	TCTGTTCGAATACGACAAGTACCCGAGCCATGCCGCACGTTGTCGAGTGGCAG
76	TCTGTGGAATAAATAGGAACTGGATAGCTTTTATACTTGTAGCACAAGGGACT
77	TATCCAGTTCTTATTGATTTAGCCGAGCGGATTTAGGAGAATGACCTCTAA
78	AATACGATTATATTCCGACTAGACGACCGCAAGGCTATCAAGCCGGCTAAACG
79	AGTCGGAGTCCCATTTGTTTCGTGATGGGACTCATAACCCGTCGTCCCATTTCAA
80	GCATACCTCACGGTTTTATTTCCACAGACTGCCACTCGACACAAGTATAAAAAGC
81	GTAGCTCTGAGGAGTGCCTGAACATTTGATTTGAGAGAATATTGATAGCCTTGCG
82	GTCGTCTAGTCCGTGGGACTCCGACTCGTTTAGCCGGCTTGATTACTGTCCCA

83	GTGCAAGGGTAACTTACAGCCCTGGCTGGAATACAGGGTTGCTACGATAACGT
84	CAATCTACTGTTCCCTATCTTATGGGTACTAAAGTACGGATAGATACCAAGACT
85	ACCCATAAGATAGTCCATTTTAAAAACAGCTAGTCCATAGCGAAGCATAGTGA
86	CGAATCTAAGTCGTAGCCTTATACCCAGCGCTGAATGTTGTCTTACCCACAGA
87	TCATAGTCGGGTGTCTGGAAAAGATAATCGACGGGACAACCACTACAGGAGTTA
88	TTATAAGTGACAATGAACAGTAGATTGACGTTATCGTAGCTCCGTACTTTAGT
89	AATCTCACCCCTAGCTCGAGCAGAATGATTGTGAAGAAGCTCAACATTCAGCGC
90	TGGGTATAAGGCTCACCCGACTATGATCTGTGGGTAAGATATCCATGTTACTG
91	CCTATAGAACTCAATAAATGGACGTGTTAGGAGTCTCGCTCGGTATATGAAGC
92	ATGAGGAGTTAACAGAGGAACGCTCGGCGATACTCAAGATCACTGCTGTGTGC
93	CGAGCGTTCCCTCTTGGGCTTCTCAGAGTCGTCTGTATGCCAGTAAGGGAGCC
94	CAGACACAGTCGCTCCACATCTAGCAGCCCGGTTTCAAGCGTCAAATTAGGGC
95	TCCCACAATACAATCACTGACCTATTGGACTTGAGAATAATGTCAGTTGTGTG
96	TTCAGAGTTTGAATGTTAACTCCTCATGCTTCATATACCGTCTTGAGTATCGC
97	CGTAATTATACCGTGATTCGAACAGAGTACGTCAATTATCGTGCGGCATGGC
98	TCGGGTACTTGTCTCGGCATTCCGGCTACACGGCCCTAGTCGACTAATGCGCG
99	GGCCAGTCTGTTTTCTATCGAAGGCGATTTTTCTACACGATATTCACGACCACC
100	CGGAATACATTGTTCTCGACGATCTAGGATACAGCCCATCCGAAACTATCAAT
101	CCATCACGAAACACCGTGAGGTATGCTTGAATGGGACGATACTAGGGCCGTGT
102	AGCCGGAATGCCGAAACAGACTGGCCCCGCGCATTAGTCGTGGCGTCACGGATT
103	TATTCGACTGGTGCCACTTTTTCCGTTTCGGACATCACTTCGTACTGAAAAAG
104	TTTTGAATACTGATAAACACAACCTAACCCTAGGACCCATCGGGTTATGAGTC
105	TTAGTTGTGTTTATGTTACCCCTTGCACTGGGACAGTAATCACCCCTGTATTCCA
106	GCCAGGGCTGTAATAAGTGCCCCAAGGATTTGAACGTCGCTCCCCACATGGGC
107	AGTCACTGTAGACTCAGACGGTCCGGGCCAGCATACTTCGGGCTTAAGTTCGT
108	GAGTAGCCACATGTTTCAGTATTCAAAACTTTTCCAGTACGTGGGTCCTAGTGG
109	ATTATCTTTCCAGTTGTCACTTATAATAACTCCTGTAGTTACGACGTTCAAAT
110	CCTTGGGCCACTTGTCTACAGTACTGCCCATGTGGGAGTAGGACCTGTCCAA
111	TGAAGCTTGAGGCACTACAGCAACGTCGAGTATATCGAGTGATGTGTCCTAGC
112	CCTGGTAGTCCACTGCGGAAAATGTCCTAATGTCTATGATGGTTGTCCCGTCCG
113	GACAATTTCCGCATTGAGTTCTATAGGCAGTAACATGGATGCGAGACTCCTAA
114	CACGTCCATTTATTAGTCTGGTACTGTCTCCCTGAATTGTAAATCAAGCCCT
115	AACGACGATGCTCTATACTGCATTACCATGTAGGCCCTTCTATATCCCAGCT
116	ATTGGCATACTGGTGTGGACTACCAGGGCTAGGACACATCTCATAGACATTAG
117	CAATAGGTCAGTGTTCAAACTCTGAACACACAACCTGACATCAATTCAGGGAGG
118	ACAGTACCAGACTGAGCATCGTCGTTAGGGCTTGATTTATAAATCGGACTGCT
119	GCTCCGTGCGACGCGGTAATACTGAATTCCTGCCGATGGTACATGTGTTGCTT
120	AGGCAATTAACGGCTTACGTCTGGGCCGGTGGTGTGCGTTTATTCTCAAGTC
121	TTTTTTTTTCCGTTAATTGCCTAAGCAACACATGTCCGACACCACCGGCCACGACGTAAGTTTTTTTT
122	TCGCCTTCGATAGACAATGTATTCCGGGTGGTTCGTGAATTATCGTCCGGTAGG
123	CTTTTAATGTTACTAGTGGGTGCGTCTACATCGTGCAGATTAGCTATGGGAAA
124	TTGAGACCGTCTCGTCCGGTTGGGTGCGCTTAACTTGCCGTAGCAACGCCAGTC
125	GAGTATAGGTCCTTTGATTTTATAAAGACCATTCACTTCTATCGTGTAGAAAA

126	TTTATAAAATCAATCACCAGTCGAATAAAATCCGTGACGCCAGTGATGTCCGAA
127	ACGGAAAAGTGGGTGCGCCCTGGTTTGTGAAAAGCTGTAAGACTTCGGGAAATC
128	TCAGGACGTACGATTTCCCTCAACGCTGGTCTCTGAGACTTAGTATTCATAGTG
129	GAGGGTCATATTATAGGACCTATACTCGACTGGCGTTGCTGAAGTGAATGGTC
130	CCCGGACCGTCTGCATGTGGCTACTCACGAACTTAAGCCTCTTACAGCTTTTC
131	ACAAACCAGGGCGTCGTACGTCTGAGATTTCCCGAAGTTCGTACAACGGCTA
132	TTTGCGAGTATGGTCACAGTTAGCAATCCGACTATATAATCGCCAGCACCTAG
133	ACGTGCCGTCACTATCCAAAATTAGAACGCTTGGCCAGTCGAAGTATGCTGG
134	CTAATTTTGATATGCCTCAAGCTTCATTGGACAGGTCCCTCGATATACTCG
135	ACGTTGCTGTAGTTCTAATGTTTCGAGTCCCGGTGCCGCGACACTACTTGAATG
136	TGCTATAACGTGTTGACGCAATGGCACTACTAATCACACCGTACCTGTGGTCT
137	CCCTACGAGCCGCTGATGACGGCACGTCTAGGTGCTGGCGCTGGCCAAGCGTT
138	GGTAATGCAGTATCCAGTATGCCAATAGCTCGGGATATATTCGCGGCACCGGG
139	ACTCGAACATTAGACACGTTATAGCACATTCAGTAGTGTCGCGGGTCTGTGAT
140	CTCAAACGCCGGCCAAGACCGACCGTGCCGTTTGGGTCTTTTGATGATCGTG
141	AAGATGCTGCGACCCGAACTTTATAGCAATACAGCTGATTGAAGGGCTACAT
142	CTATAAAGTTTCGGTCTGCGCACGGAGCAGCAGTCCGATTTCCATCGGCAGGAA
143	TTCAGTATTACCGTCTGCGTTCCTAGCGAAAAGACCTGAGGTGACAGTGCCTAC
144	AAGGCTCTCTAGCTGGTGGCCGTACCACTGAGTTGTACTCAGAATCCGAAGGA
145	TGGGTCATCCACGTGTCGACGATCTTCACGATCAATCAAATCAGCTGTATTG
146	TTTTTTTTTCTCAGGTCTTTTCGCTAGGAACGCGGCTAGAGAGCCTTGTAGGCACTGTCAATTTTTTTTT
147	ACATTATCCCTCGTGAGACGGTCTCAATTTCCCATAGCTACGGCAAGTTAAGC
148	GCACCCAACCGACTCTGCGAATGGGTCTGCGCACGCCCTGCCTGGACTAAAC
149	TGAAATATACCTCTGCCTTGCCCTCCCGGTTTGCCCTATAGCCACGGGAGCAA
150	AGCCACCAAATTGTTCTTATCGGTGTTGTGTAATTTATTTTACGGGACTAAT
151	CAGCGTTGAGGAATAATATGACCCCTCCACTATGAATACTTAGGGCGTGCGCAG
152	GACCCATTCGACAGGATATATTTTCAGTTTAGTCCAGGCTTAAATTCCTGAG
153	CGAGTTTTATGATCTATAGCAGCTTCGTCAGATCCAACATCGTAATAGCGCAA
154	GAAATTACAAGTGCCTGCGGCCAGGATGTGCTAGGAAAGTAAGTCTCAGAGAC
155	TCCTGGCCCAGCTCCATACTCGCAAATAGCCGTTGTACGTTATATAGTCGGA
156	TTGCTAACTGTGATTGTGTTATATGCCGATAATAGTAGCCATAGGTACTTCAC
157	ACTAGGCGACGGGTTGAGGGCTGTGAATCAGGGCCTAGCACGGTATTAGCATT
158	ACTTAGTGGGTCTTCACTTGTAATTTCTTTCGCGCTATTACGCTTTCCTAGCACA
159	GTGCCATTGCGTCTGCGGCTCGTAGGGAGACCACAGGTACTGGCTACTATTATC
160	GGCATATAACACACCCGTCGCCTAGTGTGAAGTACCTATTCGCCATCGGAAG
161	GATCACTGACACCCGACGCTCTCTCTGATTAGCGTGCCTTCGAACACAGATCG
162	CTTTTACTCAAGGCATGGGACATCTTAGCCTATTATTAGTGGTGTGATTAGTA
163	AAGATGTCCCATGTGCCGGCTTTGAGATCACGACCGCGGAGACCCAAACGGC
164	ACGGTCGGTCTTGTGACCTAGGCGGGACCACCCCTCGCATATATCTTTCTTCAT
165	TCGGCATACTCAGTTAACGGTGACGGAACAGGGCGGTGACGTGTACAGCATAA
166	CCCTCGTCATCAGTCCCTGAGTAAAAGCGATCTGTGTTTCGCTAATAATAGGCT
167	TGGTACGGCCACCCGTGGATGACCCATCCTTCGGATTCTTTATGCGAGGGTGG
168	TCCCGCTAGGTCTGAGTATGCCGAATGAAGAAAGATATCAGAGCCGACCTC

169	ACCTCACTAGATTACGCCGTTACGGAAACGAGATTCTGATTCTGAAGTGGACT
170	GGGAGCATCTGGGTAACGGATTCAAAGATTCCTCGATGCTGAGTACAACCTCAG
171	TTTTTTTTTCCCAGATGCTCCCAGTCCACTTCAGAGCATCGAGGAATCTTTGAATCCGTTATTTTTTTTT
172	TTTTTTTTTATAGGGCAAACCGGGAAGGCAAGGCCAATTTGGTGGCTTTGCTCCCGTGGCTTTTTTTTT
173	TTTTTTTTTATCATAAACTCGCTCAGGGAATTTATGTTGGATCTGACGAAGCTGCTATAGTTTTTTTT
174	TTTTTTTTTGTAGGCCCTGATTACAGCCCTCAAGACCCACTAAGTAATGCTAATACCGTTTTTTTT
175	TTTTTTTTTGGTGTGTCAGTGATCCTTCCGATGGCAGACGCACGCTAATCAGAGAGAGCGTCGTTTTTTTT
176	TTTTTTTTTGTACCGCCCTGTTCCGTCACCGTTACTGATGACGAGGGTTATGCTGTACACTTTTTTTTT
177	TTTTTTTTTAATCTAGTGAGGTGAGGTCGGCTCTGTCAGAATCTCGTTTCCGTAACGGCTGTTTTTTTT
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179	TTTTTTTTTTTTTCCCTGCAAGTCGAGGAAACCAATCCAGTAAGTAGCCTAAGGGAAGGTTAGTTTTTTTT
180	TTTTTTTTTGGCCCATGAGGGACACGCAATTTTCGAGCTTGATTGAAAGATGTAGAATTTTTTTTTTTTT
181	TTTTTTTTTAACCGGCCCTAAACGCTTCGATATGTCTAGCACCCGCATCCACACGCTTTGTTTTTTTT
182	TTTTTTTTTGGACGCCGTTTATCTAAAGGAGCCGTCCTCCTCAGCATTTGTATGTTAAACAATTTTTTTTT
183	TTTTTTTTTCAAGCATTTAGCGGCTATAGCGCTAAGACGATAAAAATAGGGATACTTACTCTTTTTTTTT
184	TTTTTTTTTAAATAAATTACACAACACCGATAAGACGAGGGATAATGTATTAGTCCCGTCATTTTTTTTT
185	TTTTTTTTTGTAACATTAAGGCTACCCGACGATTCTGCACGATGTAGACGCACCCACTATTTTTTTTT
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187	TTTTTTTTTGTCTAAATAGTTTCTAGTTTATCTCAGACGAATGTCTAATATGATCAGAGATTTTTTTTT
188	TTTTTTTTTCGTCGGAAGCGACATCCCATGTCTGCCTTTGACTCAGGTTGACTGCGCTCGGTTTTTTTT
189	TTTTTTTTTGGACTTTTATGTGGTGCCTATCCGCATAGGTTACGGATAGGTAGATCGCGCTTTTTTTTT
190	TTTTTTTTTCCCGCTGCCAAATTGAACCTGTTTAGCCCGTGAGAAGGGATAACCGGTAGGGTTTTTTTT
191	TTTTTTTTTGTCCCACTGTTTATTCGCAGCTGGTACAACAAGCACGGCAGCGCAAGGAATTTTTTTTT
192	TTTTTTTTTCCACGAGCCTCCTCGCGCAGGCCTTGTCTTTAGTTTAGGTTACTGTAGCGTTTTTTTT
193	TTTTTTTTTCACGAAGAGTAATTTGGTCCCTCCGCGACTCCACGCACCCGGGACGATTTATTTTTTTTT
194	TTTTTTTTTGCTTGAAACCGGGCTGCTAGATGTGGTTGTATTGTGGGACGCCTAATTTGACTTTTTTTTT

S8.3 DNA sequences for Y_1

Seq_ID	Sequences
1	GGGTGCAACGTATAAGGTTAGGTGGTAAGCACTTCCTATTCATCTCGATGAGG
2	GAGATAAGCCCTATGGGAACGCTCAGGCGGGAATCACATTCCATCCGCAAACTTGAGG
3	TCGCCGCAAACCTGGATAAAGCAGCGGGCTAGGGTTAGGTTCCGATTTCAGCAC
4	GCACTGGTCCCGGTTGTAACAGCTCAAGAAAAGGCCTCCTTCAAACAAATCCT
5	TGACTCACGCTGATAGTTTGCGGCGAACCTCAAGTTTTGCCCTAACCTAGCC
6	CGCTGCTTTATCCTCCTCCATCCCTCGACTCGTAACGTGTATGGATAGAGGAAGCCCTGAG
7	CCTTGAGGGATTGCAAACGTACTTACCCTTTGTGGGAATTTCTATCCATACAC
8	GTTACGAGTCGAGCCGGGACCAGTGCCTCAAGGGCTTCCTCCTCCATCCTCTCATATATAA
9	TAAGGACTGTTCTCTTTCTTTTGTAAAGATGCACCCTCGATCAGTGACGTACGG
10	TTACGGCCGCGTTTAGTCCGCGATTAGGTATTAGTCCGTTCCGATCCGGAACC
11	CTCTCCTTGGGCATAGAACAGTCCTTATTTATATATGAGATCGAGGGTGCATC
12	TTACAAAAGAAAGTCCTCCATCCCGTTGGGAGGTTCCGGAGCCTCTTTGTTAAACGATCTAAT
13	CGATGCCAGAAGTTTGTGCAACCCCTCCGTGCGGAGTTTGTACAAAGAGGCTCC
14	GAACCTCCAACGAACGCGGCCGTAAATTAGATCGTTTATCCTCCATCCAACCTTGCCATA

15	TCACTGAGGCTGTGACGTATATCTCTTCCTCGGGTCGTCTTGATCTTCTCACT
16	TGAGGGTCCAGAATCGAGCGCCTCGTCTATTCCGGCCAGGTCAAAGAATAAG
17	TCAAGCAGCGGATACAGCCTCAGTGATTAGGCAAGGGTTGACGACCCGAGGA
18	AGAGATATACGTCTCCTCCATCCATGGCTCTCCGGAGATGTCTGCAAGGCACTACCTGAAG
19	AGTGAATTCAACCCGTTTGACCTCGGAACGTACGACGCTTCTTGCACGACATC
20	TCCGGAGAGCCATTTCTGGACCCTCACTTCAGGTAGTGCTCCTCCATCCCACAAATCTCCGC
21	TCTACGGCTAATCCTAATGTTTCGGTCCAGATCCTGGGCTAGCTGGCTACACG
22	AATGTAGATACGTTAGGGTCCGAGGAGTTTACCTAGCGCGAGTGCGGGCACA
23	GGTCCAAGTCCCATGATTAGCCGTAGAGCGGAGATTTGTGGCCAGGATCTGG
24	ACCGAAACATTAGTCTCCATCCCAGCCACAGCGTCGAGTTAAAGTACTTGCAGTTAAACG
25	TCTTCTGGGATCACATTCAGCAACCCGTACTCGAGTGCCTGTACTTTAACTCG
26	ACGCTGTGGGCTGACGTATCTACATTCGTTTAACTGCAATCCTCCATCCGTTGCAATTTTCC
27	GTAGGGTGAGCACTCGATATTGATTTACCGTTATCTTGCTCGATTGTTCCATT
28	ACTGAGAAAAGGATCGTTAGCGCGCGCATCCGAGGCACCTCCACGATCGAAGAT
29	AGTGGATGGGCGCTGTGCTCACCCACGAAAATTGCAACGCAAGATAACGGT
30	AAATCAATATCGATCCTCCATCCAAGACGACTAGCGCCTTGTCGTTGCAATTTCACTCCTG
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32	CGCTAGTCGTCTTTCTTTTCTCAGTCAGGAGTGAAATTTCTCCATCCGGGCCACAGGCC
33	TTCTTGGCACATCAAGGACTTTTCTACCCATAGGTCTATTAGATTTTAGTCT
34	TTTTTTTTTGATGTGCAAGAAGGGCCTGTGGCCCTAGACCTATAGGGTAGAAAAGTCCTTTTTTTTTT
35	TTTTTTTTTTAGGGCTTATCTCCCTCATCGAGATGATGTGATTCCCGCCTGAGCGTCCCATTTTTTTTT
36	CCCTGAAAAGTGTATACGTTGCACCCGTGCTGAATCCGAATAGGAAGTGCTT
37	ACCACCTAACCTTTCTCTCATACCTCTGTAGCTACGCCTATGCTACCTTATAG
38	GCGAGTTTTTATTATCCTCCATCCCAGATACGGTTGCGGACAACGGATTGACACAACATATCG
39	GGATTGATTGGTCACGCACCTCGTTAAGTGAAGGAACCTCAATCCGTTGTCC
40	GCAACCGTATCTGACACTTTTTCAGGGCGATATGTTGTGTTCTCCATCCCGCCAGCTGTACT
41	AATTCGTGGTGAAGAGCATGAATATGCACCTCTGGGACCTAAGCCGTAACCC
42	CGAGCTCAAAGGTCAATCCCTCAAGGCCGTACGTCACCTGATTCCCACAAACG
43	GTAAGTACGTTTGTTCACCACGAATTAGTACAGCTGGCGGGTCCCAGAGTGC
44	ATATTCATGCTCTTCTCCATCCCCGCCCTCAAAGTCCACGGCCACTTGGAGCAAACCCGCC
45	AAATACGCTAGGTCGTCACCAGGATTGTTGTACCTGTAGTCAAGTGGCCGTGG
46	ACTTTGAGGGCGGCCTTTTGGAGCTCGGGCGGGTTTGTCTCCTCCATCCCCTTAAGAAGGTC
47	AATATAACTAGGAGTGTATCTCCAATAATGCTTGGCCCGTTAAATGCCGAGA
48	AACCGGTAGCTTATACTTCTGGCATCGAGTGAGAAGATCACAACTCCGCACG
49	GAGGGTTGCACAATCCTAGTTATATTGACCTTCTTAAGGCGGGCCAAGCATT
50	ATTGGAGATACACTCCTCCATCCTCATGGTTCCAGCTGATTAGGTGCGGGAACACCGTTGTC
51	AATATGATTTTCATGCGCCTTGCATGCTAAATATAGAGTTCGCGACCTAATCA
52	GCTGGAACCATGATAAGCTACCGGTTGACAACGGTGTCTCCTCCATCCTCCGGACAGGGTC
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54	CCAGACACGGTGATGGTTGAATTCACCTCGTGTAGCCAGCTAGCGTCGTACGTT
55	CCGAGGTCAAACGTGGAACGTGCCACGACCCGTGTCGGATTTGCACTACGTC
56	GTTGTGGGCTTGCTCCTCCATCCAGGGCCGCTCAATTATACGACGTAACCTTTAGGCACCGGG
57	CTTGATCGGGCCAATGAAGACCGCGATCCGATCGATATATGTTACGTCGTATA

58	ATTGAGCGGCCCTTACACGTGTCTGGCCCGGTGCCTAAATCCTCCATCCTGCTATGGATACT
59	CGCCAAGGGTTCCAATCGATCGAAACGTCCCAGGACTTATATGTATAACCTCG
60	AGCAGTCGTCTACTTGATCCCAGAAGAAATGGAACAATCGGGCACTCGAGTAC
61	GGTTGCTGAATGTGGAACCTTGGCGAGTATCCATAGCATAAGTCTGGGAC
62	GTTTCGATCGATTTCTCCATCCTAACCAAGCCATCAATTCGAGCAGCGGCTTGTTCCTCT
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64	ATGGGCTTGGTTAGTAGACGACTGCTAGAGGAACAAGCCTCCTCCATCCCAAGGTCACCACT
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68	AGTGGTATTTCGAGTCTCCATCCTAAATCTGATGCTTCGCCGTGAGAGCCTAGAGTGTTC
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73	ACATGAATTCCTTGATATGTGCACAAATGCGCGACGAGCTTCGTGGACCTGGC
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75	TAACGAGGTGCGTTAAGGAATTCATGTAACCCGTGAGCTAGCTCGTCGCGCAT
76	TTGTGCACATATCTCCTCCATCCTAGAAGCACCTGTAATATACGGGCCGATTCCCAGTTATG
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87	CATGCAAGGCGCATCGACACTGTATTTGGCTTCGCGCACTGAAGATCTTTGCC
88	GTATCAGAACTCATCCTCCATCCCACACTCAACTATAACCAGGCAGGCGACAGTGGTCTTTGT
89	GGCCAGTTCCTAACGACGAAATAACGGTGCAGTCTAATTTTCGCTGCCTGGT
90	ATAGTTGAGTGTGGAGTAGTTATCCTACAAAGACCACTGTCTCCATCCCCTCGCGATATAG
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92	CTCCCTCACTATTTGGCCGATCAAGCGAGGTTATACATTATATCGATCGGA
93	TCGCGGCTTCATTGCATGACAATACACTATATCGCGAGGAGGGCATCGATTT
94	ATTGCCTCGAGGATCCTCCATCCCACGGAGTAAATGAGGATAGCGTACCCTCGGAGTAAGTC
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97	AGTTGGGTTGTAGAGTCTAGACATCGTCAAGATTGTTAGTTGAAACTATAGAA
98	TTTCAATCCAGATATCGCAGAACAAGTGTAGACAAACGGAAACGAAGCTCAA
99	CCAATGGCTGTTCTCTACAACCAACTACAGAGCGGTGCTCTAACAATCTTGA
100	CGATGTCTAGACTTCTCCATCCGGGCAGTTCTTGGCCGGCCGCCATTTTAGAGTGACGAGA

101	TAGCCACAGGTCTCGGCCATTACAGCCGGATTTAATGATTAATGGGCGGCCG
102	GCAAGAACTGCCCTCTGGATTGAAAATCTCGTCACTCTATCCTCCATCCGGGATGTACATGT
103	GACAGGGTTGCCAGGACTCCAGAGGCGGTTGCCATGTTATGCCATATCCCTGC
104	TTTTTTTTTTGGCAACCCTGTACATGTACATCCCTAACATGGCAACCCTCTGGAGTCCTTTTTTTT
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106	CTACACACCCGAGTGAATGTACGTTCCGACAGGTCACGAAGCGATATCGGTG
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109	TGCACAATGGGCCAGCGAATTAATCAACGGCGGGCTTCTTTGGACTTATCGGA
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115	TAGGAGAAGCCAGAGAGAACGACCCCTCATAGATTTACGTTCTCGCAGTAGCC
116	GTCGTTCAACGATGTGCGGTTAGAATTAGCTTATTGGTTTCTCCATCCGCAGGGTAGACTA
117	GGGTAACACGAATATGTGCTCAGTCCATTGATAGCGTTTCGTCGAATCTGCC
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125	GTTATTTTCGTCGTTACGAACGTGCGTGGGAAAGCGGATCTACACAGGGTACA
126	CAAGCCTACATATTCCTCCATCCAAGGCGGACTTGATCCCTAGACTCACCTAACTTTACCTC
127	ACCACGCATCTGGTAAGTCGAAGCTCTACATTGGACCGATGTGAGTCTAGGGA
128	TCAAGTCCGCCTTCTTAGAACTCAGGGAGGTAAAGTTAGTCCCTCCATCCACTAGGTGCGTCA
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135	GTGACAGGCAGTATAGGTTTATGCC'TTCGGTTCAGCTGGTGCACCTAAGCGTGG
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137	GCTGTAATGGCCGTTACTGCCGTGCTACTACGAGTCACGAGCCAGCTGAACCGA
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141	GTCATCACGGTTATTAAGCTAAAAGCAATGCTCCACCTCTTATGGATTGTCCC
142	GATGACGGACATGTCGTATACTTTTACCTTATGCATGAGTCTCCATCCGACGCCTTATGCT
143	GCACTACATGCTTGGTTCGAGTGCAGCTTCTCGTTCCTGCTATCGTTGGCT

144	TCGCCGTTACCCATGGCCATTGTGCAAATAACCCATATAAGAAGCCCGCCGT
145	TGATTAATTCGCTTAAGCATGTAGTGCAGCATAAGGCGTCGTGAACGAGAAGC
146	TGCACTCGGAACCTCCTCCATCCGACAGCAAGACAAACTTAAGCACCTAGATGCATAATAT
147	TACAACGACAACAGAGCGTATTGTATAGGTCAAATCCCGTAGGTGCTTAAGTT
148	TGTCTTGGTCTGCTGGGTAACGGCGAATATTATGCATCTTCTCCATCCCAATCCTCGACTT
149	GATGGGTCTCTGTGATTACGCCCATATACTTTATCATGTGTCAAGTTTCGTC
150	TGGCTCCCAGTCCCTCGGCTTCTCCTAGGCAGATTCGACGCGTAAATCTATGA
151	AGGGTCGTTCTCTTACAGAGACCCATCAAGTCGAGGATTGCATGATAAAGTAT
152	ATGAGGCGTAATCTCCTCCATCCTGCATGTCTGTTCTGCCAGGGCAGTCGCCTACGTACTG
153	TCATGGCAGCCTTGCAAGGCCAATTCAGACAATCTATCTACTGCCCTGGCAG
154	AACAGACATGTCAGGACTGGGAGCCACAGTACGTAGGCGTCTCCATCCGGTCAGCATGGTA
155	TCGCTTACGTGGATCGACGTCAGTTTGAACGAGGACCGTTCAAGGGACGATT
156	GCACATGTCTATGTTGATACTATTTAATACGCTGCCCTGGACCATCGCAGCCTG
157	TTGATGTGAGTTGTTCCACGTAAGCGATACCATGCTGACCCGGTCTCGTTTC
158	AAACTGACGTCGATCCTCCATCCCACGGACGACCAGAACCCGAGCGACCGTTACTGTTACA
159	TTTTACACATTCGTCGCAGACAGCGGTACGGTGCCTTTGGTCGCTCGGGTT
160	CTGGTCGTCGGTGCATAGACATGTGCTGTAACAGTAAACTCCTCCATCCGGCCACCTACTGC
161	AGATGGCCCTATTGACTTTAAGGAAACAATAATTTCAACTATGGACCCGGTAA
162	AGCAGCCAATATCTCCAGATGCGTGGTTGCAACGGGAGTGTGCGTCCAATGTA
163	GAGCTTCGACTTATAATAGGGCCATCTGCAGTAGGTGGCCGTTGAAATTATTG
164	TTTCCTTAAAGTCTCCTCCATCCTCGTGGGCCATCAGTCGTTGACTAGATTTGCATACAGGG
165	GTACGCGAGCTTCCCGCCGTTCTCGACTGCGTGGGCTGGTTCAGTCAACGAC
166	TGATGGCCACGAGATATTGGCTGCTCCCTGTATGCAAATCCTCCATCCTACAGGGCGCAAG
167	AGTTTCCAGATTCAGGGAGCACAAAAGTCTCACTCATGATAATTGTAGTCCCG
168	GAGCGTTGCGCATTGACGCGAGAGGAGCCACGCTTAGTGCCTTTAGGGTTTCGC
169	TATTTATGGTCGTTGAATCTGGAAACTCTTGCGCCCTGTATCATGAGTGAGAC
170	TTTTGTGCTCCCTTCCCTCCATCCCACATGGAGTGCCTTATAAAAATATCTCCGGCTTAGGTT
171	TGATGACGCTGACGTGGTGATCAACATCCCTCGCGCGGTGATATTTTATAGA
172	ACGACTCCATGTGATGCGCAACGCTCAACCTAAGCCGGATCCTCCATCCTGTGCGCTTTTCC
173	TGCGGACGACGGGCATTGGATCGGGCGATCTTAGCATTATGTTCAACTGTTAC
174	TTTTTTTTTCCCCTCGTCCGCAGGAAAAGGCGACATAATGCTAAGATCGCCCATCCAATGTTTTTTTT
175	TTTTTTTTTTCATGTCCGTCATCGGGACAATCCATACTCATGCATAAAGGTAAGTATACGATTTTTTTTT
176	CACCTTGGGTGCTTAAACCGTGATGACAGCCAACGATAGCGAGGTGGAGCATT
177	GCTTTTAGCTTAATTTCTTGGTTGTAAACCTCTGTTCTCCCTAGTGCTGGTAT
178	TTAAAGCAAATCATCCTCCATCCAATTTATTCTCGCAAGAGGTGAAGGCTCCTCGGGAGAAC
179	GTCGGCGACCGCATCGTCACCCCTGGTGATAACATGGGTTGCCTTCACCTCTT
180	GCGAGAATAAAGTGACACCCAAGGTGGTTCTCCCAGAGATCCTCCATCCTACCCATGCCCTC
181	GTGGTGTCGATTTAGCTCCGTCTGACCCATCCGTTATTAACCTCGCGTTTCT
182	GGCCACCTGATTTTTGTTGTGCTTGTAGACGAAACTTGACCGGGATTTGACCT
183	ATACAATACGCTCTAATCGACACCCACGAGGGCATGGGTAATAAGCGGATGGG
184	TCAGACGGAGCTATCCTCCATCCAATTTCTTCCCTTCCACACAGAACCGTCTGTCACGAATCT
185	TGATGCATTAACGTGCAGATCAATCCCTAAAGAGATGCATACGGTTCTGTGTG
186	GAAGGGAAGAATTAATCAGGTGGCCAGATTTCGTGACAGTCTCCATCCTTCATAGCAGACT

187	TGCAAGAACCCTGAACGCGCTACAGACCAACCAGGCGTTGCACCATCAAGGT
188	GTCCCTGGAATCGATAAGGCTGCCATGAAATCGTCCCTTGAGATAGATTGTCTG
189	AATTAGGCCTTGCTCAGGGTCTTGCAAGTCTGCTATGAAACGCCTGGGTGG
190	TCTGTAGCGCGTTTTCTCCATCCTCATGCCAGGGAAGTTTCGTTGAATCGTGCAGATTGACAG
191	TCGCTCCCGTTCAGGCACTGCAAGGCTATAAATCCCTCTTCGATTCAACGAAC
192	TTCCCTGGCATGATCGATTCCAGGACCTGTCAATCTGCATCCTCCATCCGCTCGATCTTGT
193	CCATATGGTTCACCTCTCAAACAATGTTACCTTGTGAGTCTTCGCTGGGCTGCA
194	TCAGTCGGATCTCTCGAATGTGTAATAATACCGGGTCCATAAACGCACCGTAC
195	GCGCTGTCTGCGATGTGAACCATATGGACAAAGATCGAGCGACTGACAAGGTA
196	ACATTGTTTGAGATCCTCCATCCGGTGTGACTCTCATTGTCTCCATTTTAAAAATCCATGAG
197	ACGCCTAGCTGGTGAGCGCATATCTCGTGTTCGCTGACTAAATGGAGACAAT
198	GAGAGTCAGCACCGAGATCCGACTGACTCATGGATTTTATCCTCCATCCGATTATATCCGGT
199	CAACCACCGTGAAGGCAGGAGCGTTAATATTGCCACCATGTAGTTAAACAAG
200	ACTACTTAGGGTGTGAAGCTCGCGTACCGGGACTACAATTCCAGCCCACGCAG
201	TCGAGAACGGCGGTTACGGTGGGTTGACCGGATATAATCTGGTGGCAATATT
202	AACGCTCGTGCCTTCTCCATCCGGATAGCCACCGCCTTTTGGTGGATGTGCAAAAGCTCGT
203	CAACTACTAAAAGCGCGTCCGTATAACCATGTATCCTGTATCCACCAAAG
204	GCGGTGGCTATCCCACCCTAAGTAGTACGAGCTTTTGCATCCTCCATCCTTAGTATCTCGCC
205	AACCACCTCCGCCAATATACTTGACCTTCGCGACCACACAATTCCGGAGGT
206	TCGGAGACGAGACTTCAGACGTCATCAGTAACAGTTGAACCCGCGGAGGGAT
207	GTTGATCACCACGTGGCGGAGGTGGTTGGCGAGATACTAAGTGGTCCGAAGG
208	GTCAAGTATATTGTCTCCATCCATCCTATAGGCACTTGTAACCTCCCGGTCTACCCAGGAA
209	TTTTTTTTTCGGGAGTTTACAAGTGCCTATAGGATGTCTCGTCTCCGATTCTGGGTAGACTTTTTTTTT
210	TTTTTTTTTGAGAACAGAGGTTTACAACCAAGAATGATTTGCTTTAAATACCAGCACTAGTTTTTTTT
211	CGAAGACTCAGGCACATTCGAGAGCGTGACTTCATCTGCTCACCCTGGAACCC
212	AAAATGTTTCGTCCAGATTTTATGGGACTGTACCGTCTGCTCCTCCATCCTTTACGTCCGTTT
213	CGAGAACAAGAAAGCCTAGCACAAATTGACTTAATTGTCTTAGGAATAAGTTTC
214	ACGTCCAAGTTTCTTGCGGTGCGCGACAGGAACGCGAGTTACCCATGTTATCA
215	CCAAGGTGACGATTTTCTTGTTCCTCGAAACGGACGTAAGACAATTAAGTC
216	AATTGTGCTAGGCTCCTCCATCCTAACTCCGGCAATCATTGCCACGTCGAATAAGGAGTCAC
217	TACGGGATCTCCACTGTTTCAGATCCCAGGTATACGATGTGACGCTGGCAATG
218	ATTGCCGGAGTTAGAACTTGGACGTGTGACTCCTTATTTCTCCATCCCGGTCTCTTGTAC
219	CAGTCGAGCTTCTATCGCCTTTGTTCCGCATTGCTCCATTGGGAGCCTAGGG
220	TAGTCTTCAAGCCTAGTTAATGCATCAACCTTGATGGTGTGCTGCATCTCTTTAG
221	GGATTGATCTGACTAGAAGCTCGACTGGTACAAGAGACCGTGGGAGCAATGCG
222	GAACAAAGGCGATTCTCCATCCGGCGGGCCTAGCCTCGTTGTGCGGCTCCACGTCGGCACG
223	GCCTTTTGACTCAC TACCAGCTCAACAGTCCAAAACATACGCCGACAACGA
224	GGCTAGGCCCGCCGGCTTGAAGACTACGTGCCGACGTGGTCTCCATCCGCTCAGAGACAAC
225	TATCACTTACCTAGTAACCTTGTTCATCGGATCCCGTCTATCAATTTATCGT
226	GTGCCAAACCCATTTGAACGGGAGCGATGCAGCCCAGCGAAGAGGGATTTATA
227	GCCTTGCAAGTGCCTAGGTAAGTGAATAGTTGTCTCTGAGCGACGGGATCCGAT
228	GAACAAGGTTACTTCTCCATCCCTGATTTGCCAGAGCTGTAGAGCGCCGGATTGTTTCGCGA
229	CTGCATTCATCGGGCCGCGTCTAGTAAGTAGCTTCACGTTGGCGCTCTACAGC

230	TCTGGCAAATCAGATGGGTTTGGCACTCGCGAACAAATCCTCCTCCATCCTGGAAGTCCAATT
231	GCTTCATCACAAGCGGGCGGAAACCTTGGTCAATCAACTTAATAAAATCAGA
232	GATTAGACTGCGTACCAGCTAGGCGTCTTGTTTAACTACGTCACGCAAGCAC
233	GAGATATGCGCTCTCTTGTGATGAAGCAATTGGACTTCCAGTTGATTGACCAA
234	GGTTTCCC GCCGTCTCCATCCGACATCGAAAAGGCACGCGGACACTTTGAACCGGCCTAA
235	AGTGAAATACCCAACCACGCCTCTGCATTGTGACATCTATAAGTGTCCGCGTG
236	CCTTTTCGATGTCCGCAGTCTAAATCTTAGGCCGGTTCATCCTCCATCCTGTTTGTGTTGAA
237	AAGATGATTTGTGCTTCTACCACGCAGCCCATGTTTAATTCATTGGCACAAA
238	TTCACGCAGAAATTTCTTTTAGTAGTTGACCTCCGAATTGTCAGGATACATGGT
239	TATACGGACGGCGTCACAAATCATCTTTTCAACACAAACATTAACATGGGCT
240	GCGTGGTAGAAAGTCTCCATCCGCAATCCGCTGTTTGACAGTACTCCCTGTCTGCATACA
241	CGCTAGTATTCCAATCCTTTCAGTTCGCCATGTGGATACGGGAGTACTGTCA
242	AACAGCGGAATGCAATTCTGCGTGAATGTATGCAGGACATCCTCCATCCAGCGAATAATACG
243	CCCGGTATACCGTTAACCTGTATAGGACAGTCAACCACCATACTCGCGTG
244	TTTTTTTTTGGACGAACATTTTGGGTTCCACGGTGGCAGACGGTACAGTCCATAAAATCTTTTTTTTT
245	TTTTTTTTTGCCTGAGTCTTCGAAACTTATTCCTGCAGATGAAGTCACGCTCTCGAATGTTTTTTTT
246	TTTTTTTTTGGAGAATCCCGTACCCTAGGCTCCCACATCGTATACCTGGGATCTGAACAGTTTTTTTT
247	TTTTTTTTTGAGTCAAAAGGGCAGATAAAATTGATTGTTTTGGACTGTTGAGCTGGGTAGTTTTTTTT
248	TTTTTTTTTCCGATGAATGCAGTCTGATTTTATTAACGTGAAGCTACTTACTAGACGCGCTTTTTTTTT
249	TTTTTTTTTGGGTATTTCACTTTTGTGCCAATGATAGATGTCACAATGCAGAGGCGTGGTTTTTTTT
250	TTTTTTTTTAGGAGGCCTTTTCTTGAGCTGTTACATCAGCGTGAGTCAAGGATTTGTTGATTTTTTTTT
251	TTTTTTTTTAACGGACTAATACCTAATCGCGGACTTGCCCAAGGAGAGGGTCCGGATGCGTTTTTTTT
252	TTTTTTTTTCTGGCCGGAATAGACGAGGCGCTCGTTCGCGCTGCTTGACTTATTCTTTTGATTTTTTTTT
253	TTTTTTTTTGCCTAGGTGAAACTCCTCGGACCCTTGGGACTTGGACCTGTGCCGCACTCTTTTTTTTT
254	TTTTTTTTTGAGTGCCTCGGATGCGCGCGCTAACGGCGCCATCCACTATCTTCGATCGTGTTTTTTTTT
255	TTTTTTTTTGGAAATACTAGCGCACGCGAGTATGGGTATCCACATGGCGAACTGAAAGGATTTTTTTTT
256	TTTTTTTTTCGGTATACCCGGGAGACCGTTCTAACTGGTTGACTGTCTATACAGGGTAAATTTTTTTTT
257	AGGGTTAGGG

Note: strand 257 pair with 77 DNA segments between two arms to form additional 10-bp duplex segments. Therefore, to form the addressable 2D honeycomb grid with angle control, strand 257 (final concentration: 7.7 μ M) and rest strands (final concentration: 100 nM) are mixed together and annealed.

S8.4 DNA sequences for Y_2

Seq_ID	Sequences
1	GGGTGCAACGTATAAGGTTAGGTGGTAAGCACTTCCTATTCATCTCGATGAGG
2	GAGATAAGCCCTATGGGAACGCTCAGGCGGGAATCACATTCTCCATCCGCAAAACTTGAGG
3	TTCGCCGCAAACGGATAAAGCAGCGGGCTAGGGTTAGGTTCCGATTACAGCAC
4	GCACTGGTCCCGTTGTAAACAGCTCAAGAAAAGGCCTCCTTCAAACAAATCCT
5	TGACTCACGCTGATAGTTTGC GGCAACCTCAAGTTTTGCCCTAACCTAGCC
6	CGCTGCTTTATCCTCCTCCATCCCTCGACTCGTAACGTGTATGGATAGAGGAAGCCCTGAG
7	CCTTGAGGGATTGCAAACGTACTTACCGTTTGTGGGAATTTCTATCCATACAC
8	GTTACGAGTCGAGCCGGGACCAGTGCCTCAAGGGCTTCCTCCTCCATCCTCTCATATATAAA

9	TAAGGACTGTTCTCTTTCTTTTGTAAAGATGCACCCCTCGATCAGTGACGTACGG
10	TTACGGCCGCGTTTAGTCCGCGATTAGGTATTAGTCCGTTTCGCATCCGGAACC
11	CTCTCCTTGGGCATAGAACAGTCCCTATTTATATATGAGATCGAGGGTGCATC
12	TTACAAAAGAAAGTCTCCATCCCCTGGGAGGTTTCGGAGCCTCTTTGTAAACGATCTAAT
13	CGATGCCAGAAGTTTGTGCAACCCCTCCGTGCGGAGTTTGTACAAAGAGGCTCC
14	GAACCTCCCAACGAACGCGGCCGTAAATTAGATCGTTTATCCTCCATCCAACCCCTGCCTAA
15	TCACTGAGGCTGTGACGTATATCTCTTCCCTCGGGTTCGTCTTGATCTTCTCACT
16	TGAGGGTCCAGAATCGAGCGCCTCGTCTATTCCGGCCAGGTCAAAGAATAAG
17	TCAAGCAGCGGATACAGCCTCAGTGATTAGGCAAGGGTTGACGACCCGAGGA
18	AGAGATATACGTCTCCTCCATCCATGGCTCTCCGGAGATGTTCGTGCAAGGCACTACCTGAAG
19	AGTGAATTCAACCCGTTTGACCTCGGAACGTACGACGCTTCTTGCACGACATC
20	TCCGGAGAGCCATTTCTGGACCCTCACTTCAGGTAGTGCTCCTCCATCCCACAAATCTCCGC
21	TCTACGGCTAATCCTAATGTTTTCGGTCCAGATCCTGGGCTAGCTGGCTACACG
22	AATGTAGATACGTTAGGGTCCGAGGAGTTTACCTAGCGCGAGTTCGGGACACA
23	GGTCCAAGTCCCATGATTAGCCGTAGAGCGGAGATTTGTGGCCAGGATCTGG
24	ACCGAAACATTAGTCTCCATCCCAGCCACAGCGTCGAGTTAAAGTACTTGCAGTTAAACG
25	TCTTCTGGGATCACATTCAGCAACCCGTACTCGAGTGCCTGTACTTTAACTCG
26	ACGCTGTGGGCTGACGTATCTACATTCGTTTAACTGCAATCCTCCATCCGTTGCAATTTTCC
27	GTAGGGTGAGCACTCGATATTGATTTACCGTTATCTTGTCTCGATTGTTCCATT
28	ACTGAGAAAAGGATCGTTAGCGCGCGCATCCGAGGCACCTCCACGATCGAAGAT
29	AGTGGATGGGCGCTGTGCTCACCCCTACGGAAAATTGCAACGCAAGATAACGGT
30	AAATCAATATCGATCCTCCATCCAAGACGACTAGCGCCTTGTCGTTTCGCAATTTCACTCCTG
31	TTGGTCTCTTATGCAAGCACCCCTGGATCACGTACTCGTGTGCGAACGACAAGG
32	CGCTAGTCGTCTTTCTTTTCTCAGTCAGGAGTGAAATTTCTCCATCCGGGCCACAGGCC
33	TTCTTGGCACATCAAGGACTTTTCTACCCATAGGTCTATTAGATTTTAGTCT
34	TTTTTTTTTGATGTGCCAAGAAGGGCCTGTGGCCCTAGACCTATAGGGTAGAAAAGTCCTTTTTTTTTT
35	TTTTTTTTTTAGGGCTTATCTCCCTCATCGAGATGATGTGATTCCCGCCTGAGCGTTCCTATTTTTTTT
36	CCCTGAAAAGTGTATACGTTGCACCCGTGCTGAATCCGAATAGGAAGTGCTT
37	ACCACCTAACCTTTCTCTCATACCTCTGTAGCTACGCCTATGTACCTTATAG
38	GCGAGTTTTTATTATCCTCCATCCCAGATACGGTTGCGGACAACGGATTGACACAACATATCG
39	GGATTGATTGGTCACGCACCTCGTTAAGTGAAGGAACCTCAATCCGTTGTCC
40	GCAACCGTATCTGACACTTTTTCAGGGCGATATGTTGTGTTCTCCATCCCCTTAAGAAGGTC
41	AATTCGTGGTGAAGAGCATGAATATGCACCTCTGGGACCTAAGCCGTAACCC
42	CGAGCTCAAAGGTCAATCCCTCAAGGCCGTACGTCACTGATTCCCACAAACG
43	GTAAGTACGTTTGTTCACCACGAATTAGTACAGCTGGCGGGTCCCAGAGTGC
44	ATATTCATGCTCTTCTCCATCCCCGCCCTCAAAGTCCACGGCCACTTGGAGCAAACCCGCC
45	AAATACGCTAGGTCGTCACCAGGATTGTTGTACCTGTAGTCAAGTGGCCGTGG
46	ACTTTGAGGGCGGCCTTTTGTAGCTCGGGCGGGTTGCTCTCCTCCATCCCCTTAAGAAGGTC
47	AATATAACTAGGAGTGTATCTCCAATAATGCTTGGCCCGTTAAATGCCGAGA
48	AACCGGTAGCTTATACCTTCTGGCATCGAGTGAGAAGATCACAACTCCGCACG
49	GAGGGTGCACAATTCCTAGTTATATTGACCTTCTTAAAGGCGGGCCAAGCATT
50	ATTGGAGATACACTCCTCCATCCTCATGGTTCCAGCTGATTAGGTTCGGGAACACCGTTGTC
51	AAATATGATTTTCATGCGCCTTGCATGCTAAATATAGAGTTCGCGACCTAATCA

52	GCTGGAACCATGATAAGCTACCGGTTGACAACGGTGTCTCTCCATCCTCCGGACAGGGTC
53	GTGGGCACGTTCCGCAAGCCCACAACGACGTAGTGCAAATATAATGAGTAATT
54	CCAGACACGGTGATGGTTGAATTCACTCGTGTAGCCAGCTAGCGTCGTACGTT
55	CCGAGGTCAAACGTGGAACGTGCCACGACCCTGTCCGGATTTGCACTACGTC
56	GTTGTGGGCTTGCTCCTCCATCCAGGGCCGCTCAATTATACGACGTAACCTTAGGCACCGGG
57	CTTGATCGGGCCAATGAAGACCGCGATCCGATCGATATATGTTACGTCGTATA
58	ATTGAGCGGCCCTTACACGTGTCTGGCCCGGTGCCTAAATCCTCCATCCTGCTATGGATACT
59	CGCCAAGGGTTCGAATCGATCGAAACGTCCCAGGACTTATATGTATAACCTCG
60	AGCAGTCGCTACTTGATCCCAGAAGAAATGGAACAATCGGGCACTCGAGTAC
61	GGTTGCTGAATGTGGAACCTTGGCGAGTATCCATAGCATAAGTCTGGGAC
62	GTTTCGATCGATTTCTCCATCCTAACCAAGCCCATCAATTGCGAGCAGCGGCTTGTTCCTCT
63	CTTGTCTGCGATGAACAGCCATTGGTTGAGCTTCGTTTTGCTGCTCGAATTG
64	ATGGGCTTGGTTAGTAGACGACTGCTAGAGGAACAAGCCTCCTCCATCCCAAGGTCACCACT
65	CCCGGTTACTCAACTCGAATACCACTCACGGATGGTTATTCGTTTTGTCTACA
66	TGCCCTGAACCGCTCATAAGAGACCAAAGACTAAAATCTACACGAGTACGTGA
67	TCCAGGGTGC'TTGT'TTGAGTAACCGGGAGTGGTGACCTTGATAACCATCCGTG
68	AGTGGTATTTCGAGTCTCCATCCTAAATCTGATGCTTCGCCGTGAGAGCCTAGAGTGT'TTTC
69	TTTTTTTTTGCTCTCACGGCGAAGCATCAGATTTAGCGGTTCCAGGGCAGAAAACACTCTAGTTTTTTTT
70	TTTTTTTTTTAGGCGTAGCTACAGAGGTATGAGAGTAATAAACTCGCCTATAAGGTAGCATTTTTTTTT
71	GAACGTACATTACCAATAAATGTCTGCACCGATATCGTTTCATCGACCCTACC
72	CGCCATAGTTTCGAGCCTGCATAATGAAAGGCGCCGAGGTCTCCATCCTAGCTCACGGGTT
73	ACATGAATTCCTTGATATGTGCACAAATGCGCGACGAGCTTCGTGGACCTGGC
74	AATAACCTACGCTGACCAATCAATCCGGTTTTACGGCTTAGTTCTTCCACT
75	TAACGAGGTGCGTTAAGGAATTCATGTAACCCGTGAGCTAGCTCGTCGCGCAT
76	TTGTGCACATATCTCCTCCATCCTAGAAGCACCTGTAATATACGGGCCGATTCCCAGTTATG
77	TGAGCGTCTTCCCTTTGGCCGGTATATCGGTCAGCGAATCGGCCCGTATATT
78	ACAGGTGCTTCTAGCGTAGGGTTATTATAACTGGGAATTCCTCCATCCAAACGCGGCGCAC
79	ACCCTAGAGAACATTGCAACTAGCGACCAACTCTAGCTATATGTAGTAGGTGA
80	CCAATGACGGTGTACCTAGCGTATTTTCTCGGCATTTTACTACAGGTACAAC
81	AATCCTGGTGACGTTGTTCTCTAGGGTGTGCGCCGCTTTTAGCTAGAGTTGG
82	TCGCTAGTTGCAATCCTCCATCCGTGCGTCTACTCGCATTCGATGTTGCCCTGTAACCTCTA
83	CCTAAAGAAGTGTGAACCTTCGGGAAGCTATTGCAGGCTGCAACATCGAATG
84	CGAGTAGACGCACCACCGTCATTGGGTAGAAGTTACAGGTCTCCATCCAGTGCAGCAAGCC
85	AAATACAGTGTGCTGAGTCTGATACGGCAAAGATCTTCTGCTTAGTCGATTT
86	AGGATAACTACTCTTGAAAATCATATTAATTACTCATTATACTCTATATTTAG
87	CATGCAAGGCGCATCGACACTGTATTTGGCTTCGCGCACTGAAGATCTTTGCC
88	GTATCAGAACTCATCCTCCATCCCACACTCAACTATAACCAGGCAGGCGACAGTGGTCTTTGT
89	GGCCAGTTC'TTAACGACGAAATAACGGTGC'GGT'CTAATTT'CGCCTGCCTGGT
90	ATAGTTGAGTGTGGAGTAGTTATCCTACAAAGACCACTGTCTCCATCCCCTCGCGATATAG
91	TGTATTGTCATGCTCCTCGAGGCAATAAATCGATGCCCTTATACGCAGTTCAA
92	CTTCCCTCACTATTTGGCCCGATCAAGCGAGGTTATACATTATATCGATCGGA
93	TCGCGGCTTTCATTGCATGACAATACACTATATCGCGAGGAGGGCATCGATTT
94	ATTGCCTCGAGGATCCTCCATCCCACGGAGTAAATGAGGATAGCGTACCCTCGGAGTAAGTC

95	CCGCCATATCTAACTAAGAATAGTTATTATTACATTAATGGTACGCTATCCT
96	CATTTACTCCGTGATAGTGAGGGAAGGACTTACTCCGAGTCTCCATCCAGCACCGCTCTGT
97	AGTTGGGTGTAGAGTCTAGACATCGTCAAGATTGTTAGTTGAAACTATAGAA
98	TTTTCAATCCAGATATCGCAGAACAAGTGTAGACAAACGAAACGAAGCTCAA
99	CCAATGGCTGTTCTCTACAACCCAACTACAGAGCGGTGCTCTAACAATCTTGA
100	CGATGTCTAGACTTCCCTCCATCCGGGCAGTTCTTGCCGGCCGCCATTTTAGAGTGACGAGA
101	TAGCCACAGGTCTCGGCCATTACAGCCGATTTAATGATTAATGGGCGGCCG
102	GCAAGAACTGCCCTCTGGATTGAAAATCTCGTCACTCTATCCTCCATCCGGGATGTACATGT
103	GACAGGGTTGCCAGGACTCCAGAGGCGGTTGCCATGTTATGCCATATCCCTGC
104	TTTTTTTTTTGGCAACCCTGTCACATGTACATCCCTAACATGGCAACCCTCTGGAGTCTTTTTTTTT
105	TTTTTTTTTCGAAACTATGGCGGGTAGGGTCGATGCCTCGGCGCCTTTCATTATGCAGGCTTTTTTTTT
106	CTACACACCCGAGTGTAAATGTACGTTCCGACAGTCCACGAAGCGATATCGGTG
107	CAGACATTTATTGTTCAACCCATTGCTCGAAATGGTGGCCTAGGCGTCTAG
108	GGTTGGGTTCTGTTCCCTCCATCCCAGACCTCGATGGTCCGATAAGTCCAGGCGTCGATGATA
109	TGCACAATGGGCCAGCGAATTAATCAACGGCGGGCTTCTTTGGACTTATCGGA
110	CCATCGAGGTCTGCTCGGGTGTGTAGTATCATCGACGCCTCCTCCATCCTAGAACCATACTG
111	AGCAGGAGTAGCAGGTGGATTTCGCTTACCAGCTGCTTTGTTATATGGGTTATT
112	ATTCTAACCGCACTGGAAGGACGCTCATCACCTACTACATTTTCGCTGACCGAT
113	ATACCGCCAAAGTTGCTACTCCTGCTCAGTATGGTTCACAAAGCAGCTGGT
114	AAGCGAATCCACCTCCTCCATCCATCGTTGAACGACGGCTACTGCGAGAAACCAATAAGCTA
115	TAGGAGAAGCCAGAGAGAACGACCCTTCATAGATTTACGTTCTCGCAGTAGCC
116	GTCGTTCAACGATGTGCGGTTAGAATTAGCTTATTGGTTTCTCCATCCGCAGGGTAGACTA
117	GGGTAAACGAATATGTGCCTCAGTCCATTGATAGCGTTTCGTCGAATCTGCC
118	CCCTTGGACGGCATAACACTTCTTTAGGAAATCGACTAAGCGCCTGCAATAGCT
119	TCCCGAAGGGTCTATTCGTGTTACCCTAGTCTACCCTGCAACGCTATCAATG
120	GACTGAGGCACATTCCTCCATCCGTGCGAAAAGGGCGCCGGACTAGACTAATTGAGTTATGT
121	TTAAATAGTATCACAACCTCACATCAACAGCGTGGATGGTAGTCTAGTCCGGC
122	GCCCTTTTCGCACTGCCGTCCAAGGGACATAACTCAATTTCTCCATCCGATCCGCTTTCCC
123	ACGCACGTTTCGTGATATGTAGGCTTGTGTACCCTGTGTATTCCAGGCAGCGTA
124	CCTGAGTTCAGGTTAAGAATGGGCCTTGAACGCGTATATTAGACCGCACC
125	GTTATTTTCGTCGTTACGAACGTGCGTGGGAAAGCGGATCTACACAGGGTACA
126	CAAGCCTACATATTCCTCCATCCAAGGCGGACTTGATCCCTAGACTCACCTAACTTTACCTC
127	ACCACGCATCTGGTAAGTCGAAGCTCTACATTGGACCGATGTGAGTCTAGGGA
128	TCAAGTCCGCCTTCTTAGAACTCAGGGAGGTAAAGTTAGTCTCCATCCACTAGGTGCGTCA
129	ACATTTTCGCATGACCGCTCTATCGGGCGCGCTCTCCAGTCACTCCCCTTGCA
130	ATGCTAATTATGCTTAGATATGGGCGGTTCTATAGTTTCATTAATGTAATAAT
131	AACTATTCCTAGTTCATGCGAAAATGTTGACGCACCTAGTCTGGAGAGCGCGC
132	CCGATAGAGCGGTTCCCTCCATCCCAATCCGCTAGCGAACAAGCGAATAGTACGGTAGTGAA
133	CTCCTCTCGCGTCACGACCATAAATAGCGAACCCCTAAAGTTATTCGCTTTGTT
134	CGCTAGCGGATTGGCATAATTAGCATTTCACTACCGTACTCCTCCATCCCTCGTACTCGTA
135	GTGACAGGCAGTATAGGTTTATGCCTTTCGGTTCAGCTGGTGCACCTAAGCGTGG
136	AGCCACACTGGTTTAGACCTGTGGCTAGCAGGGATATGGCATCATTAATCCG
137	GCTGTAATGGCCGTTACTGCCGTGCTACTACGAGTCACGAGCCAGCTGAACCGA

138	AGGCATAAACCTATCCTCCATCCGTCGAATTATGTTTGGCTAAGGTCAGTGACCGGCTGCAC
139	TTTTTTTTCTGACCTTAGCCAAACATAATTCGACAACCAGTGTGGCTGTGCAGCCGGTCATTTTTTTTT
140	TTTTTTTTGCCACCATTTTCGAGCAATAGGGTTGAACAGAACCCAACCTAGAACGCCTAGTTTTTTTT
141	GTCATCACGGTTATTAAGCTAAAAGCAATGCTCCACCTCTTATGGATTGTCCC
142	GATGACGGACATGTCGTATACTTTTACCTTATGCATGAGTCTCCATCCGACGCCTTATGCT
143	GCACTACATGCTTGGTCCGAGTGCAGCTTCTCGTTCACTGCTATCGTTGGCT
144	TCGCCGTTACCCATGGCCCATTTGTGCAAATAACCCATATAAGAAGCCCGCCGT
145	TGATTAATTCGCTTAAGCATGTAGTGCAGCATAAGGCGTCGTGAACGAGAAGC
146	TGCACTCGGAACCTCCTCCATCCGACAGCAAGACAAACTTAAGCACCTAGATGCATAATAT
147	TACAACGACAACAGAGCGTATTGTATAGGTCAAATCCCGTAGGTGCTTAAGTT
148	TGTCTTGGTCTGCTGGGTAACGGCGAATATTATGCATCTTCTCCATCCCAATCCTCGACTT
149	GATGGGTCTCTGTGATTACGCCTCATATACTTTATCATGTGTCAAGTTTCGTC
150	TGGTCCCAGTCCCTCGCTTCTCCTAGGCAGATTCGACCGTAAATCTATGA
151	AGGGTCGTTCTCTTACAGAGACCCATCAAGTCGAGGATTGCATGATAAAGTAT
152	ATGAGGCGTAATCTCCTCCATCCTGACATGTCTGTTCTGCCAGGGCAGTCGCCTACGTACTG
153	TCATGGCAGCCTTGCAAGGCCAATTCAGACAATCTATCTACTGCCCTGGCAG
154	AACAGACATGTCAGGACTGGGAGCCACAGTACGTAGGCGTCTCCATCCGGTCAGCATGGTA
155	TCGCTTACGTGGATCGACGTCAGTTTGAACGAGGACCGTTCAAGGGACGATT
156	GCACATGCTATGTTGATACTATTTAATACGCTGCCGTCGACCATCGCAGCGTG
157	TTGATGTGAGTTGTTCCACGTAAGCGATACCATGCTGACCCGGTCTCGTTTC
158	AAACTGACGTCGATCCTCCATCCCACGGACGACCAGAACCCGAGCGACCGTTTACTGTTACA
159	TTTACACATTCGTCGCAGACAGCGGTACGGTGCCTTTTGGTCGCTCGGGTT
160	CTGGTCCGTCGTCATAGACATGTGCTGTAACAGTAAACTCCTCCATCCGGCCACCTACTGC
161	AGATGGCCCTATTGACTTTAAGGAAACAATAATTTCAACTATGGACCCGGTAA
162	AGCAGCCAATATCTCCAGATGCGTGGTTGCAACGGGAGTGTCCGTTCAATGTA
163	GAGCTTCGACTTATAATAGGGCCATCTGCAGTAGGTGGCCGTTGAAATTATTG
164	TTTCCTTAAAGTCTCCTCCATCCTCGTGGGCCATCAGTCGTTGACTAGATTTGCATACAGGG
165	GTACGCGAGCTTCCCGCCGTTCTCGACTGCGTGGGCTGGTTCTAGTCAACGAC
166	TGATGGCCACGAGATATTGGCTGCTCCCTGTATGCAAATCCTCCATCCTACAGGGCGCAAG
167	AGTTCCAGATTCAGGGAGCACAAAAGTCTCACTCATGATAATTGTAGTCCCG
168	GAGCGTTGCGCATTGACGCGAGAGGAGCCACGCTTAGTGCCTTTAGGGTTCGC
169	TATTTATGGTCGTTGAATCTGGAAACTCTTGCGCCCTGTATCATGAGTGAGAC
170	TTTTGTGCTCCCTTCCATCCCACATGGAGTCGTTCTATAAAAATATCTCCGGCTTAGGTT
171	TGATGACGCTGACGTGGTGATCAACATCCCTCGCGCGGTGATATTTTATAGA
172	ACGACTCCATGTGATGCGCAACGCTCAACCTAAGCCGGATCCTCCATCCTGTGCGCTTTTCC
173	TGCGGACGACGGGCATTGGATCGGGCGATCTTAGCATTATGTTCAACTGTTAC
174	TTTTTTTTCCCGTCGTCGCGAGGAAAAGGCGACATAATGCTAAGATCGCCCGATCCAATGTTTTTTTT
175	TTTTTTTTCATGTCCGTCATCGGGACAATCCATACTCATGCATAAGGTAAAAGTATACGATTTTTTTTT
176	CACCTTGGGTGCTTAAACCGTGATGACAGCCAACGATAGCGAGGTGGAGCATT
177	GCTTTTAGCTTAATTTCTTGGTTGTAAACCTCTGTTCTCCCTAGTGTGGTAT
178	TTAAAGCAAATCATCCTCCATCCACTTTATTCTCGCAAGAGGTGAAGGCTCCTCGGGAGAAC
179	GTCGGCGACCGCATCGTCACCCCTGGTGATAACATGGGTTGCCTTACCTCTT
180	GCGAGAATAAAGTGACACCCAAGGTGGTTCTCCCGAGGATCCTCCATCCTACCCATGCCCTC

181	GTGGGTGTCGATTTAGCTCCGTCTGACCCATCCGCTTATTAACTCGCGTTCCT
182	GGCCACCTGATTTTTGTGTGTCGTTGTAGACGAACTTGACCGGGATTTGACCT
183	ATACAATACGCTCTAATCGACACCACGAGGGCATGGGTAATAAGCGGATGGG
184	TCAGACGGAGCTATCCTCCATCCAATTCTTCCCTTCCACACAGAACCGTCTGTCACGAATCT
185	TGATGCATTAACGTTCAGATCAATCCCTAAAGAGATGCATACGGTTCGTGTG
186	GAAGGGAAGAATTAATCAGGTGGCCAGATTTCGTGACAGTCCCTCCATCCTTCATAGCAGACT
187	TGCAAGAACCCTGAACGCGCTACAGACCAACCCAGGCGTTGCACCATCAAGGT
188	GTCCTGGAATCGATAAGGCTGCCATGAAATCGTCCCTTGAGATAGATTGTCTG
189	AATTAGGCCCTTGCTCAGGGTCTTGCAAGTCTGCTATGAAACGCCTGGGTTGG
190	TCTGTAGCGCGTTTTCTCCATCCTCATGCCAGGGAAGTTCGTTGAATCGTGCAGATTGACAG
191	TCGCTCCCCTCAGGCCTGCAAGGCTATAAATCCCTCTTCGATTC AACGAAC
192	TTCCCTGGCATGATCGATTCCAGGACCTGTCAATCTGCATCCTCCATCCGCTCGATCTTTGT
193	CCATATGGTTCACCTCTCAAACAATGTTACCTTGTCAGTCTTCGCTGGGCTGCA
194	TCAGTCGGATCTCTCGAATGTGTAATAATACCGGGTCCATAAACGCACCGTAC
195	GCGCTGTCTGCGATGTGAACCATATGGACAAAGATCGAGCGACTGACAAGGTA
196	ACATTGTTTGAGATCCTCCATCCGGTGTGACTCTCATTGTCTCCATTTTAAATCCATGAG
197	ACGCCCTAGCTGGTGAGCGCATATCTCGTGTTCGCTGACTAAATGGAGACAAT
198	GAGAGTCAGCACCGAGATCCGACTGACTCATGGATTTTATCCTCCATCCGATTATATCCGGT
199	CAACCACCGTGAAGGCAGAGCGTTAATATTGCCACCATGTAGTTAAACAAG
200	ACTACTTAGGGTGTGAAGCTCGCGTACCGGGACTACAATTCAGCCCACGCAG
201	TCGAGAACGGCGGTTACGGTGGGTTGACCGGATATAATCTGGTGGCAATATT
202	AACGCTCGTGCCTTCTCCATCCGGATAGCCACCGCCTTTTGGTGGATGTGCAAAAGCTCGT
203	CAACTACTAAAAGCGCGTCCGTATAACCATGTATCCTGTTCATCCACCAAAAG
204	GCGGTGGCTATCCCACCCTAAGTAGTACGAGCTTTTGCATCCTCCATCCTTAGTATCTCGCC
205	AACCACCTCCGCCAATATACTTGACCCTTCGCGACCCTACAATTCGGAGGT
206	TCGGAGACGAGACTTCAGACGTATCAGTAACAGTTGAACCCGCGGAGGGAT
207	GTTGATCACCACGTGGCGGAGGTGGTTGGCGAGATACTAAGTGGTTCGCGAAGG
208	GTCAAGTATATTGTCTCCATCCATCCTATAGGCACCTTGTAACCTCCCGGTCTACCCAGGAA
209	TTTTTTTTTCGGGAGTTTACAAGTGCCTATAGGATGTCTCGTCTCCGATTCTGGGTAGACTTTTTTTTT
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211	CGAAGACTCAGGCACATTCGAGAGCGTGACTTCATCTGCTCACCCTGGAACCC
212	AAAATGTTTCGTCCAGATTTTATGGGACTGTACCGTCTGCTCCTCCATCCTTTACGTCCGTTT
213	CGAGAACAAGAAAGCCTAGCACAATTGACTTAATTGTCTTAGGAATAAGTTTC
214	ACGTCCAAGTTTCTTGCGGTGCGCCGACAGGAACGCGAGTTACCCATGTTATCA
215	CCAAGGTGACGATTTTCTTGTTCCTCGAAACGGACGTAAAAGACAATTAAGTC
216	AATTGTGCTAGGCTCCTCCATCCTAACTCCGGCAATCATTGCCACGTGCAATAAGGAGTCAC
217	TACGGGATCTCCACTGTTTCAGATCCCAGGTATACGATGTCGACGTGGCAATG
218	ATTGCCGGAGTTAGAACTTGACGCTGTGACTCCTTATTTCTCCATCCCGGTCTCTTGTAC
219	CAGTCGAGCTTCTATCGCTTTGTTCCGCATTGCTCCATTGGGAGCCTAGGG
220	TAGTCTTCAAGCCTAGTTAATGCATCAACCTTGATGGTGTGCTGCATCTCTTTAG
221	GGATTGATCTGACTAGAAGCTCGACTGGTACAAGAGACCGTGGGAGCAATGCG
222	GAACAAAGGCGATTCTCCATCCGGCGGGCCTAGCCTCGTTGTGCGGCTCCACGTCCGGCAGC
223	GCCCTTTTGACTCACTACCCAGCTCAACAGTCCAAAACATACGCCGACAACGA

224	GGCTAGGCCCGCCGGCTTGAAGACTACGTGCCGACGTGGTCCCTCCATCCGCTCAGAGACAAC
225	TATTCACCTTACCTAGTAACCTTGTTCATCGGATCCCGTCTATCAATTTATCGT
226	GTGCCAAACCCATTTGAACGGGAGCGATGCAGCCCAGCGAAGAGGGATTTATA
227	GCCTTGCAGTGCCTAGGTAAGTGAATAGTTGTCTCTGAGCGACGGGATCCGAT
228	GAACAAGGTTACTTCCCTCCATCCCTGATTTGCCAGAGCTGTAGAGCGCCGGATTGTTTCGCGA
229	CTGCATTCATCGGGCCGCTCTAGTAAGTAGCTTCACGTTGGCGCTCTACAGC
230	TCTGGCAAATCAGATGGGTTTGGCACTCGCGAACAATCCTCCTCCATCCTGGAAGTCCAATT
231	GCTTCATCACAAGCGGGCGGAAACCTTGGTCAATCAACTTAATAAAATCAGA
232	GATTTAGACTGCGTACCAGCTAGGCGTCTTGTTTAACTACGTCACGCAAGCAC
233	GAGATATGCGCTCTCTTGTGATGAAGCAATTGGACTTCCAGTTGATTGACCAA
234	GGTTTCCC GCCGTCTCCATCCGACATCGAAAAGGCACGCGGACACTTTGAACCGGCCTAA
235	AGTGAAATACCCAACCACGCCCTCGCATTTGTGACATCTATAAGTGTCCGCGTG
236	CCTTTTCGATGTCCGAGTCTAAATCTTAGGCCGGTTCATCCTCCATCCTGTTTGTGTTGAA
237	AAGATGATTTGTGCTTCTACCACGCAGCCCATGTTTAATTCATTGGCACAAA
238	TTCACGCAGAAATTTCTTTTAGTAGTTGACCTCCGAATTGTCAGGATACATGGT
239	TATACGGACGGCGTCACAAATCATCTTTTCAACACAAACATTAACATGGGCT
240	GCGTGGTAGAAAGTCCCTCCATCCGCAATCCGCTGTTTGACAGTACTCCCTGTCTGCATACA
241	CGCTAGTATTCCAATCCTTTCAGTTCGCCATGTGGATACGGGAGTACTGTCA
242	AACAGCGGAATGCAATTCTGCGTGAATGTATGCAGGACATCCTCCATCCAGCGAATAATACG
243	CCCGGTATACCGTTAACCTGTATAGGACAGTCAACCACCATACTCGCGTG
244	TTTTTTTTTGGACGAACATTTTGGGTTCCACGGTGGCAGACGGTACAGTCCATAAAAATCTTTTTTTTT
245	TTTTTTTTTGCCTGAGTCTTCGAAACTTATCCTGCAGATGAAGTCACGCTCTCGAATGTTTTTTTT
246	TTTTTTTTTGGAGAATCCCGTACCCTAGGCTCCCACATCGTATACCTGGGATCTGAACAGTTTTTTTT
247	TTTTTTTTTGGAGTCAAAAGGGCAGGATAAAATGATTGTTTTGGACTGTTGAGCTGGGTAGTTTTTTTT
248	TTTTTTTTTCCGATGAATGCAGTCTGATTTTATTAACGTGAAGCTACTTACTAGACGCGGCTTTTTTTTT
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250	TTTTTTTTTAGGAGGCCTTTTCTTGAGCTGTTACATCAGCGTGAGTCAAGGATTTGTTGATTTTTTTTT
251	TTTTTTTTTAACGGACTAATACCTAATCGCGGACTTGCCCAAGGAGAGGGTCCGGATGCGTTTTTTTT
252	TTTTTTTTTCTGGCCGGAATAGACGAGGCGCTCGTCGCGCTGCTTGACTTATTCTTTTGATTTTTTTTT
253	TTTTTTTTTGGCTAGGTGAAACTCCTCGGACCTTGGGACTTGGACCTGTGCCGCACTCTTTTTTTTT
254	TTTTTTTTTGGAGTGCCTCGGATGCGCGGCTAACGGCGCCATCCACTATCTTCGATCGTGTTTTTTTTT
255	TTTTTTTTTGGAAATACTAGCGCACGCGAGTATGGGTATCCACATGGCGAACTGAAAGGATTTTTTTTT
256	TTTTTTTTTCCGTATACCCGGGAGACCGTTCTAACTGGTTGACTGTCTATACAGGGTTAATTTTTTTTT

S8.5 DNA sequences for X₁

Seq_ID	Sequences
1	CCCTTCTCAGGGCCCTAACCTAAGACCTCAAACCTTTTCTGAATCGCTGTCCGAGGGAGA
2	TTACCAACTCTTTTTGTAAGTCCAGTCCGCGAACGTGGTTCCCGCCACATCC
3	CAGCTGATCATCTCCCTAACCTGGTAGCCAGCGTTCATGGGAGGATCGCGGTGCTCCTGAC
4	AGTTGTATTCTGCTCTCTAAACAGGTTCAATTTGGCAGCGGGCCCTACGCGTTAT
5	GACTTGCAGGAACTAACCTTCCCTTAGGCTACTTACTGCCCTAACCTACCACGTTTCGCGG
6	ACTGGCAGTTACAAGATGATCAGCTGGGATGTGGCGGGATTGTCATTAGGGCT
7	GACTCTGCCACAACGCCCGTGTAGTGCAGGATACCACTTCCCTAACCTTGTATCCTCGCGT

8	CAGTAGTAGGAGGTCACTCACCCCTGAAAGTGACGCTGGTTGATTGGTTTCCTC
9	TCAGGGTGAGTGACCCTAACCCCTGAAAATTCGCGTGTCCCTCATGGGCCAAATTCACATCT
10	TTCAATCAAGCTCTCTGGCGTTCCTTGAGGATGAGACAGTACTGCGTCCCGAA
11	GACTCGCGCTTCCCCCTAACCCCTAACGCGGAACATGCTCTGACTCTCCTACATCCAGAGC
12	GTACTACCCAACTTCCCTCTACTACTGACGCGAGGATACAACCAGCGTCACTT
13	TTTAGGGCCGTTACAAAGACGTGTGGATGCGGTGCTAGCCCTAACCCCTACTGTCTCATCCT
14	CAAGGAACGCCAGGGAAGCGGAGTCTTCGGGACGCAGTTAACTCGGTCCAAG
15	GTCGCTAGTCGAGTACCAAGATCCCTCTGCCATGCCCTGGCCCTAACCCCTACTTCTCCGCCT
16	TGTAACAACGCGGTAGTGCTCGTTCGGTGGATAGACGGCTACATATCGAAGCG
17	GGAACGAGCACTACCCTAACCCCTACGCTCCTTTAGATAAACGGCGTCCTTGTAAACATAACA
18	AATGCTGAGGAGGTACAGTGTGTGGACATCGGGCTCCGAGTACAGTCCAAGTC
19	TTATGTCCGTCACCCCTAACCCCTTAGCTCAGGTACTAGAGGTAGAGGTTGCTAGTTCTGCAA
20	CAATAGACTCACGTCCGCGTTGTTACAAGGCGGAGAAGTAGCCGTCTATCCAC
21	GCTAAATGCTTGAGAGTAAGTATCCCTATTTTATCGTCTCCCTAACCCCTCTCGGAGCCCGAT
22	GTCCACACACTGTGTGACGGACATAAGACTTGGACTGTATGGAAGTAACGGCC
23	TAGGCACTTTGGGCAATGTGTTACAGCAAGTCAGTTTGCCCTAACCCCTACCAGCTGCGAA
24	TAAACAGTGGGACTATTCCCTTGCGCTGCCGTGCTTGTGTTAGCGCTATAGCC
25	AACGCTGGCTACCGACGAATAACAACGTGCAGGAGCACCGCCCTAACCCCTGCGGATAGGCACC
26	ACATAAAAGTCCAGCGGATCTACCTATCCGTAACCTATTGAAATAAAAGTGA
27	CTGAGTCTCTGTGCAGGCCGGCTTAGAGCTGGGCTGAATCCCTAACCCCTACAGAGTCATCAC
28	ATGTACTTCCTTTGAACAGTTTGGCGAATTAAGCGACTCGATCCTCCCATG
29	GCCAAACTGTTTCCCTAACCCCTTGTGGCAGAGTCAGCCCTAATGACAAAGTGGTATCGCG
30	CACTACACGGGCGTGTGAGTTACCCGGCAGTAAACTATAAGGGTCATTGCAG
31	CTCATCCAATTAACCCTAACCCCTGGGTGCCATCCTTTCCGGTCTCCTAATACTTGCTCGATCC
32	TACGTATCGACCATAAAGGAAGTACATGTGATGACTCTGTGTCGCTTTAATTC
33	TAGTTCGCGCGTTAGTTGGGTAGTACGCTCTGGATGTAGCCCTAACCCCTATAGTTTACTGC
34	CGGGTAACTCAACTTAATTGGATGAGCTGCAATGACCCTTACCGTGTAGGTCA
35	TAACAACCCTAGACAGGAGAAGACCAAAACGGAGTGCACCCCTAACCCCTTCGATCAACCGGC
36	TGTATAGCATGAGAAGCGTGGAGCGAGTACCGGTAGTTGTGAGAGTCAGAGCA
37	TCGCTCCACGCTTCCCTAACCCCTCTCGACTAGCGACCTTGGACCGAGTTCAGGCATGGCAG
38	AGGGATCTTGGTATGCCGCTCAACGCCCAACATGAACCTCATAATCTACTTCT
39	AACTTTCAGCCAGCCCTAACCCCTAAGATTTGCCATGCATAAACGTCACTACCCTTGTACTCC
40	TCCCTTGAGATAGTCTCATGCTATACAGCCGGTTGATCGACAACCTACCGGTAC
41	AGTACCTGAGCTACGTGAGTCTATTGTTGCAGAACTAGCCCTAACCCCTGAGGTTTCATGTTG
42	GGCGTTGAGCGGCCTGGCTGAAAGTTAGAAGTAGATTATTAGGAACAGCATCG
43	TTCTATGTGATTCCACCCTCGTCATGCGACGAACTCCCTAACCCCTAACATAGTAGCG
44	AGGCCACCCCTTAATCCCTATCATGATCAGGCTAGGCGGTAACCTCTACCTCT
45	TCATGATAGGGATCCCTAACCCCTCCCAAAGTGCTTAGGCCGTTACTTCCGCAAACCTGACTTG
46	CTGTAACACATTGTCAAGGCCTGCGCGAGGAGGCTCGTGGAACGCTACAGTAA
47	CCTAAACTAAAGACCCTAACCCCTTTCACATCGGCCCTTTCGCCAGTAGGTCGTAGGTCGAG
48	TGACCGAGCCTTCTTAAGGGTGGGCCTCGCTACTATGTTACCGCCTAGCCTGA
49	ACCTGAGTCAAAGCCCTAACCCCTCACAGAGACTCAGTCACTTTTATTTTCATTCAGCCCAGCT
50	CTAAGCCGGCCTGTCAACTGCTAACGGCATAATAGCGGTCCCGTCCCTGTAGGA

51	GGGCAATTCACGTCCCTAACCTCCGGGCAGAATCCAGTCCCTTGTGCTTCGTTTAGTCTGA
52	CTTCACGTGTCACTGCAGACATGGGATGTGCGTTCCGACGCCGAGCGCAGTCA
53	AAGGATGGACACCTGGTCGATACGTAGGATCGAGCAAGTCCCTAACCTGACCGCTATTATG
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55	TCGGCTAAATCAAATATAATCGTATTTTAGAGGTCATTCCCCTAACCTGCGACAATGTTAC
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57	CGCGCACCGTACACCCTAACCTTCTAGGGTTGTTATGACCTACACGGTGTGCACTCCGTTT
58	TGGTCTTCTCCTGTGAATAGGCGGCAAGACATCCGAGTATACCCTGATAACAT
59	CCAGCCCTCTGCTCCCTAACCTTCTCAGAGCTACAGTCTTGGTATCTTATTCTCTCAATC
60	AATGTTTACGCACTAGGATAAAAATTCGGTAACATTGTGCGCAGTGGGATCACGG
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62	TTGCCGCTATTTCAGCAGAGGGCTGGATGTTATCAGGGTCTATGGACTAGCG
63	TGTTTTAAAATGGCGACTTAGATTCGTCACTATGCTTCGCCCTAACCTTGGACAGACAATC
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67	CCAGTAAAAGGTCCCCTAACCTCTAGGGTGAGATTGCACACAGCAGTGGCTTCTTCACAAT
68	CATTCTGCTCGAGTCTGAGGACTCTGGGATTGTCTGTCCATCTCATTCCCTCG
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70	CAGGAAAGTAATCGACCTTTTACTGGTGTATGTCTGACTTGCATACACGACGA
71	CTCTGAGAAGCCCGCGACTGTGTCTGGGCTCCCTTACTGCCCTAACCTGCGGAGGGACCAA
72	ATTACTCTTCGTGATAAATCGTCCCGGGTGCCTGGAGTCTCTACTGGCGAAGA
73	GGATTCTGCCCGGGTGACACGTGAAGTCAGACTAAACGACCCCTAACCTTGGATAAACTAG
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75	TCTGTTTGAATACGACAAGTACCCGAGCCATGCCGCAGCCCTAACCTTGTGCGAGTGGCAG
76	TCTGTGGAATAAATAGGAAGTGGATAGCTTTTATACTTGTAGCACAAAGGGACT
77	TATCCAGTTCCTACCCTAACCTTTGATTTAGCCGAGCGGGATTTAGGAGAATGACCTCTAA
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83	GTGCAAGGGTAACTTACAGCCCTGGCTGGAATACAGGGTCCCTAACCTGCTACGATAACGT
84	CAATCTACTGTTCTATCTTATGGGTACTAAAGTACGGATAGATACCAAGACT
85	ACCCATAAGATAGCCCTAACCTCCATTTTAAAACACGCTAGTCCATAGCGAAGCATAGTGA
86	CGAATCTAAGTCGTAGCCTTATACCCAGCGCTGAATGTTGTCTTACCCACAGA
87	TCATAGTCGGGTGCCCTAACCTCTGAAAAGATAATCGACGGGACAACCACTACAGGAGTTA
88	TTATAAGTGACAATGAACAGTAGATTGACGTTATCGTAGCTCCGTACTTTAGT
89	AATCTCACCTAGCTCGAGCAGAATGATTGTGAAGAAGCCCTAACCTCAACATTCAGCGC
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91	CCTATAGAACTCAATAAATGGACGTGTTAGGAGTCTCGCCCTAACCTCGGTATATGAAGC
92	ATGAGGAGTTAACAGAGGAACGCTCGGGGATACTCAAGATCACTGCTGTGTGC
93	CGAGCGTTCCTCTCCCTAACCTGGGCTTCTCAGAGTCGTCGTGATGCCAGTAAGGGAGCC

94	CAGACACAGTCGCTCCACATCTAGCAGCCCGTTTCAAGCGTCAAATTAGGCG
95	TCCCACAATACAACCCTAACCCCTCACTGACCTATTGGACTTGAGAATAATGTCAGTTGTGTG
96	TTCAGAGTTTGAATGTTAACTCCTCATGCTTCATATAACCGTCTTGAGTATCGC
97	CGTAATTATAACCGCCCTAACCCCTGTATTCGAACAGAGTACGTCAATTATCGTGCGGCATGGC
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99	GGCAGTCTGTTCCCTAACCCCTCTATCGAAGCGATTTTCTACACGATATTCACGACCACC
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101	CCATCACGAAACACCGTGAGGTATGCTTGAATGGGACGACCCTAACCCCTACTAGGGCCGTGT
102	AGCCGGAATGCCGAAACAGACTGGCCCGCGCATTAGTCGTGGCGTCACGGATT
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106	GCCAGGGCTGTAATAAGTGGCCCAAGGATTTGAACGTCGTCTCCACATGGGC
107	AGTCACTGTAGACCCCTAACCCCTCAGACGGTCCGGGCCAGCATACTTCGGGCTTAAGTTTCGT
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130	CCCGGACCGTCTGCATGTGGCTACTCACGAACTTAAGCCCCCTAACCCCTTACAGCTTTTC
131	ACAAACCAGGGCGTCGTACGTCCTGAGATTTCCCGAAGTTCGTACAACGGCTA
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134	CTAATTTTGGATACCCTAACCCCTGCCTCAAGCTTCATTGGACAGGTCCTCTCGATATACTCG
135	ACGTTGCTGTAGTTCTAATGTTTCGAGTCCCGGTGCCGCGACACTACTTGAATG
136	TGCTATAACGTGTCCCTAACCCCTGACGCAATGGCACTACTAATCACACCGTACCTGTGGTCT

137	CCCTACGAGCCGCTGATGACGGCACGTCTAGGTGCTGGCGCTGGCCAAGCGTT
138	GGTAATGCAGTATCCAGTATGCCAATAGCTCGGGATATACCCTAACCCCTTCGCGGCACCGGG
139	ACTCGAACATTAGACACGTTATAGCACATTC AAGTAGTGTCCGCGGTTCGTGAT
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141	AAGATGCTGCGACCCGAACCTTTATAGCAATACAGCTGATTGAAGGGCTACAT
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148	GCACCCAACCGACTCTGCGAATGGGTCTGCGCACGCCCTGCCTGGACTAAAC
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158	ACTTAGTGGGTCTTCACTTGTAAATTTCTTTCGCTATTACGCTTTCCTAGCACA
159	GTGCCATTGCGTCGCGGCTCGTAGGGAGACCACAGGTACCCCTAACCCCTGGCTACTATTATC
160	GGCATATAACACACCCCGTCGCTAGTGTGAAGTACCTATTCTGCCATCGGAAG
161	GATCACTGACACCCGACGCTCTCTCTGATTAGCGTTCGCTCCCTAACCCCTCGAACACAGATCG
162	CTTTTACTCAAGGCATGGGACATCTTAGCCTATTATTAGTGGTGTGATTAGTA
163	AAGATGTCCCATGCCCTAACCCCTGCCGGCGTTTGAGATCACGACCGGGAGACCCAAACGGC
164	ACGGTCGGTCTTGTGACCTAGGCGGGACCACCCTCGCATATATCTTTCTTCAT
165	TCGGCATACTCAGCCCTAACCCCTAACGGTGACGGAACAGGGCGGTGACGTGTACAGCATAA
166	CCCTCGTCATCAGTCTTGTAGTAAAAGCGATCTGTGTTTCGCTAATAATAGGCT
167	TGGTACGGCCACCCGTGGATGACCCATCCTTCGGATTCTCCCTAACCCCTTATGCGAGGGTGG
168	TCCCGCCTAGGTCTGAGTATGCCGAATGAAGAAAGATATCAGAGCCGACCTC
169	ACCTCACTAGATTCAGCCGTTACGGAAACGAGATTCGACCCTAACCCCTTCTGAAGTGGACT
170	GGGAGCATCTGGGTAACGGATTCAAAGATTCCTCGATGCTGAGTACAACCTCAG
171	TTTTTTTTTCCAGATGCTCCAGTCCACTTCAGAGCATCGAGGAATCTTTGAATCCGTTATTTTTTTTT
172	TTTTTTTTTTATAGGGCAAACCGGGAAGGCAAGGCCAATTTGGTGGCTTTGCTCCCGTGGCTTTTTTTTT
173	TTTTTTTTTATCATAAACTCGCTCAGGGAATTTATGTTGGATCTGACGAAGCTGCTATAGTTTTTTTT
174	TTTTTTTTTTGCTAGGCCCTGATTCACAGCCCTCAAGACCCACTAAGTAATGCTAATACCGTTTTTTTT
175	TTTTTTTTTTGGTGTGATGATCCTTCCGATGGCAGACGCACGCTAATCAGAGAGAGCGTCTTTTTTTTT
176	TTTTTTTTTGTACCGCCCTGTTCCGTCACCGTTACTGATGACGAGGGTTATGCTGTACACTTTTTTTTT
177	TTTTTTTTTAATCTAGTGAGGTGAGGTGCGCTCTGTCAGAATCTCGTTTCCGTAACGGCTGTTTTTTTT
178	TTTTTTTTTTCGATTCAGAAAAGGTTTGAGGTCTTAAAGAGTTGGTAATCTCCCTGCGACATTTTTTTTT
179	TTTTTTTTTTTTCTGCAAGTCGAGGAAACCAATCCAGTAAGTAGCCTAAGGGAAGGTTAGTTTTTTTT

180	TTTTTTTTTGCCCATGAGGGACACGCGAATTTTCGAGCTTGATTGAAAGATGTAGAATTTTTTTTTTTT
181	TTTTTTTTTAACCGGCCCTAAACGCTTCGATATGTCTAGCACCGCATCCACACGTCTTTGTTTTTTTTTT
182	TTTTTTTTTGACGCCGTTTATCTAAAGGAGCCGTCCTCCTCAGCATTTGTATGTAAACAATTTTTTTTTT
183	TTTTTTTTTCAAGCATTTAGCGGCTATAGCGCTAAGACGATAAAATAGGGATACCTACTCTTTTTTTTTT
184	TTTTTTTTTAAATAAAATTACACAACACCGATAAGACGAGGGATAATGTATTAGTCCCGTCATTTTTTTTTT
185	TTTTTTTTTGTAACATTAAGCCTACCCGACGATCTGCACGATGTAGACGCACCCACTATTTTTTTTTT
186	TTTTTTTTTGATGGGCTGTATCCTAGATCGTCGAGCGGTATAATTACGATTGATAGTTTCGTTTTTTTTTT
187	TTTTTTTTTGTCTAAATAGTTTCTAGTTTATCTCAGACGAATGTCTAATATGATCAGAGATTTTTTTTTTT
188	TTTTTTTTTCGTCGGAAGCGACATCCCATGTCTGCCTTTGACTCAGGTTGACTGCGCTCGGTTTTTTTTTT
189	TTTTTTTTTGGACTTTTATGTGGTGCCTATCCGCATAGGTTACGGATAGGTAGATCGCGCTTTTTTTTTTT
190	TTTTTTTTTCCCGCTGCCAAATGAACCTGTTTAGCCCGTGAGAAGGGATAACGCGTAGGGTTTTTTTTTT
191	TTTTTTTTTGTCCACTGTTTATTCGCAGCTGGTACAACAAGCACGGCAGCGCAAGGAATATTTTTTTTTTT
192	TTTTTTTTTCCACGAGCCTCCTCGCGCAGGCCTTGTCTTTAGTTTAGGTTACTGTAGCGTTTTTTTTTTTT
193	TTTTTTTTTCACGAAGAGTAATTTGGTCCCTCCGCGACTCCACGCACCCGGGACGATTTATTTTTTTTTTT
194	TTTTTTTTTGCTTGAAACCGGGCTGCTAGATGTGGTTGTATTGTGGGACGCCTAATTTGACTTTTTTTTTTT
195	AGGGTTAGGG

Note: strand 195 pair with 84 DNA segments between two arms to form additional 10-bp duplex segments. Therefore, to form the addressable 2D tetragonal grid with angle control, strand 195 (final concentration: 8.4 μ M) and rest strands (final concentration: 100 nM) are mixed together and annealed.

S8.6 DNA sequences for X₂

Seq_ID	Sequences
1	CCCTTCTCACGGGCCCTAACCTAAGACCTCAAACCTTTTCTGAATCGCTGTCGCAGGGAGA
2	TTACCAACTCTTTTTGTAAGTCCAGTCCGCGAACGTGGTTCCCGCCACATCC
3	CAGCTGATCATCTCCCTAACCTGGTAGCCAGCGTTCATGGGAGGATCGCGGTGCTCCTGAC
4	AGTTGTATTTCGTCTCTAAACAGGTTCAATTTGGCAGCGGGCCCTACGCGTTAT
5	GACTTGCAGGAACTAACCTTCCCTTAGGCTACTTACTGCCCTAACCTACCACGTTTCGCGG
6	ACTGGCAGTTACAAGATGATCAGCTGGGATGTGGCGGGATTGTCATTAGGGCT
7	GACTCTGCCACAACGCCGTGTAGTGCAGGATACCCTTCCCTAACCTTGTATCCTCGCGT
8	CAGTAGTAGGAGGTCACTCACCTGAAAGTGACGCTGGTTGATTGGTTTCCCTC
9	TCAGGGTGAGTGACCCTAACCTGAAAATTCGCGTGTCCCTCATGGGCCAAATCTACATCT
10	TTCAATCAAGCTCTCTGGCGTTCCTTGAGGATGAGACAGTACTGCGTCCCGAA
11	GACTCGCGCTTCCCCCTAACCTAACGCGCAACTATGCTCTGACTCTCTACATCCAGAGC
12	GTACTACCAACTTCCCTCCTACTACTGACGCGAGGATACAACCAGCGTCACTT
13	TTTAGGGCCGTTACAAAGACGTGTGGATGCGGTGCTAGCCCTAACCTACTGTCTCATCCT
14	CAAGGAACGCCAGGGAAGCGGAGTCTTCGGGACGCAGTTAACTCGGTCCAAG
15	GTCGCTAGTCGAGTACCAAGATCCCTCTGCCATGCCCTGGCCCTAACCTTACTTCTCCGCCT
16	TGTAACAACGCGGTAGTGCTCGTTCGGTGGATAGACGGCTACATATCGAAGCG
17	GGAACGAGCACTACCCTAACCTACGCTCCTTTAGATAAACGGCGTCTTGTAAACATACA
18	AATGCTGAGGAGGTACAGTGTGTGGACATCGGGCTCCGAGTACAGTCCAAGTC
19	TTATGTCCGTCACCCCTAACCTTAGCTCAGGTACTAGAGGTAGAGGTTGCTAGTTCGCAA
20	CAATAGACTCACGTCCGCGTTGTTACAAGGCGGAGAAGTAGCCGTCTATCCAC

21	GCTAAATGCTTGAGAGTAAGTATCCCTATTTTATCGTCTCCCTAACCCCTCGGAGCCCGAT
22	GTCCACACACTGTGTGACGGACATAAGACTTGGACTGTATGGAAGTAACGGCC
23	TAGGCACTTTGGGCAATGTGTTACAGCAAGTCAGTTTGGCCCTAACCCCTACCAGCTGCGAA
24	TAAACAGTGGGACTATTCTTGCCTGCGCTGCCGTGCTTGTGTTAGCGCTATAGCC
25	AACGCTGGCTACCGACGAATACAACGTTCAGGAGCACCGCCCTAACCCCTGCGGATAGGCACC
26	ACATAAAAGTCCAGCGGATCTACCTATCCGTAACCTATTGAAATAAAAGTGA
27	CTGAGTCTCTGTGCAGGCCGGCTTAGAGCTGGGCTGAATCCCTAACCCCTACAGAGTCATCAC
28	ATGTACTTCCTTTGAAACAGTTTGGCGAATTAAGGCGACTCGATCCTCCCATG
29	GCCAAACTGTTTCCCTAACCCCTTGTGGCAGAGTCAGCCCTAATGACAAAGTGGTATCGCG
30	CACTACACGGGCGTGTGAGTTACCCGCGAGTAAACTATAAGGGTCATTGCAG
31	CTCATCCAATTAACCCTAACCCCTGGTGTCCATCCTTTCCGGTCTCCTAATACTTGCTCGATCC
32	TACGTATCGACCATAAAGGAAGTACATGTGATGACTCTGTGTCGCTTTAATTC
33	TAGTTCGCGCGTTAGTTGGGTAGTACGCTCTGGATGTAGCCCTAACCCCTATAGTTTACTGC
34	CGGGTAACTCAACTTAATTGGATGAGCTGCAATGACCCTTACCGTGTAGGTCA
35	TAACAACCCTAGACAGGAGAAGACCAAAACGGAGTGCACCCCTAACCCCTCGATCAACCGGC
36	TGTATAGCATGAGAAGCGTGGAGCGAGTACCGGTAGTTGTGAGAGTCAGAGCA
37	TCGCTCCACGCTTCCCTAACCCCTCTCGACTAGCGACCTTGGACCGAGTTCAGGCATGGCAG
38	AGGGATCTTGGTATGCCGCTCAACGCCCAACATGAACCTCATAATCTACTTCT
39	AACTTTCAGCCAGCCCTAACCCCTAAGATTTGCCATGCATAAACGTCCTACCCTTGACTCC
40	TCCCTTGAGATAGTCTCATGCTATACAGCCGGTTGATCGACAACCTACCGGTAC
41	AGTACCTGAGCTACGTGAGTCTATTGTTGCAGAACTAGCCCTAACCCCTGAGGTTTATGTTG
42	GGCGTTGAGCGGCCTGGCTGAAAGTTAGAAGTAGATTATTAGGAACAGCATCG
43	TTCCCTATGTGATTCCACCCTCGTTCATGCGACGAAACTCCCTAACCCCTAACATAGTAGCG
44	AGGCCACCCCTTAATCCCTATCATGATCAGGCTAGGCGGTAACCTCTACCTCT
45	TCATGATAGGGATCCCTAACCCCTCCCAAAGTGCCTAGGCCGTTACTTCCGCAAACCTGACTTG
46	CTGTAACACATTGTCAAGGCCTGCGCGAGGAGGCTCGTGGAACGCTACAGTAA
47	CCTAAACTAAAGACCCTAACCCCTCTTACATCGGCCCTTTCGCCAGTAGGTCGTAGGTCGAG
48	TGACCGAGCCTTCTTAAGGGTGGGCCTCGCTACTATGTTACCGCCTAGCCTGA
49	ACCTGAGTCAAAGCCCTAACCCCTCACAGAGACTCAGTCACTTTTATTTTATTTCAGCCAGCT
50	CTAAGCCGGCCTGTCAACTGCTAACGGCATAATAGCGGTCCCGTCTCTGTAGGA
51	GGGCAATTCACGTCCCTAACCCCTCCGGGCGAATCCAGTCCCTTGTGCTTCGTTTAGTCTGA
52	CTTCACGTGTCACTGCAGACATGGGATGTGCTTCCGACGCCGAGCGCAGTCA
53	AAGGATGGACACCTGGTCGATACGTAGGATCGAGCAAGTCCCTAACCCCTGACCGCTATTATG
54	CCGTTAGCAGTTGACGTGAATTGCCCTCCTACAGGACGGTTCCCTAAATCCCGC
55	TCGGCTAAATCAAATATAATCGTATTTTAGAGGTCATTCCCCTAACCCCTGCGACAATGTTAC
56	CGAATTTTATCCTTGTACGGTGCAGCGCCGTGATCCACTTATTAGGAGACCGA
57	CGCGCACCGTACACCCTAACCCCTCTAGGGTTGTTATGACCTACACGGTGTGCACTCCGTTT
58	TGGTCTTCTCCTGTGAATAGGCGGCAAGACATCCGAGTATACCCTGATAACAT
59	CCAGCCCTCTGCTCCCTAACCCCTCCTCAGAGCTACAGTCTTGGTATCTTATTCTCTCAATC
60	AATGTTACGCACTAGGATAAAATTCCGGTAACATTGTGCGAGTGGGATCACGG
61	CATGGCAAATCTTCTATCTCAAGGAGGAGTACAAGGTCCCTAACCCCTATACCTCGGATGTC
62	TTGCCGCTATTTCAGCAGAGGGCTGGATGTTATCAGGGTCTATGGACTAGCG
63	TGTTTTAAATGGCGACTTAGATTCGTCACTATGCTTCGCCCTAACCCCTGGACAGACAATC

64	CCAGAGTCCTCAGTGGCTAGGGCACTCGAAGGAATGAGATAGTGACGTTTATG
65	AGTGCCCTAGCCACCCTAACCCCTAATCACATAGGAACGATGCTGTTCCTGAGTTTCGTGCGCA
66	TGACGAGTGGTGGTGATTACTTTTCTGATCCTGGCTAATTAGTCAGACATACA
67	CCAGTAAAAGGTCCCCTAACCCCTTAGGGTGAGATTGCACACAGCAGTGGCTTCTTACAAT
68	CATTCTGCTCGAGTCTGAGGACTCTGGGATTGTCTGTCCATCTCATTCTCTCG
69	GGCCGATGTGAAGGAAGGCTCGGTCACTCGACCTACGACCCCTAACCCCTAATTAGCCAGGAT
70	CAGGAAAGTAATCGACCTTTTACTGGTGTATGTCTGACTTGCATACACGACGA
71	CTCTGAGAAGCCCAGGACTGTGTCTGGGCTCCCTTACTGCCCTAACCCCTGCGGAGGGACCAA
72	ATTACTCTTCGTGATAAATCGTCCCGGGTGCCTGGAGTCTCTACTGGCGAAGA
73	GGATTCTGCCCGGGTGACACGTGAAGTCAGACTAAACGACCCCTAACCCCTTGAGATAAACTAG
74	AAACTATTTAGACATCTCTGATCATATTAGACATTTCGTCTATAAATTGACGTAC
75	TCTGTTCGAATACGACAAGTACCCGAGCCATGCCGCAGCCCTAACCCCTTGTCGAGTGGCAG
76	TCTGTGGAATAAATAGGAAGTGGATAGCTTTTATACTTGTAGCACAAAGGGACT
77	TATCCAGTTCCTACCCTAACCCCTTGATTTAGCCGAGCGGGATTTAGGAGAATGACCTCTAA
78	AATACGATTATATTCGGACTAGACGACCGCAAGGCTATCAAGCCGGCTAAACG
79	AGTCGGAGTCCCACCCTAACCCCTGTTTCGTGATGGGACTCATAACCCGTCGTCCCATTCAA
80	GCATACCTCACGGTTTTTATTCCACAGACTGCCACTCGACACAAGTATAAAAAGC
81	GTAGCTCTGAGGAGTGCCTGAACATTGATTGAGAGAATACCCTAACCCCTTGATAGCCTTGCG
82	GTCGTCTAGTCCGTGGGACTCCGACTCGTTTAGCCGGCTTGATTACTGTCCCA
83	GTGCAAGGGTAACTTACAGCCCTGGCTGGAATACAGGGTCCCTAACCCCTGCTACGATAACGT
84	CAATCTACTGTTCTATCTTATGGGTACTAAAGTACGGATAGATACCAAGACT
85	ACCCATAAGATAGCCCTAACCCCTCCATTTTAAAACACGCTAGTCCATAGCGAAGCATAGTGA
86	CGAATCTAAGTCGTAGCCTTATACCCAGCGCTGAATGTTGTCTTACCCACAGA
87	TCATAGTCGGGTGCCCTAACCCCTCTGGAAAGATAATCGACGGGACAACCCTACAGGAGTTA
88	TTATAAGTGACAATGAACAGTAGATTGACGTTATCGTAGCTCCGTACTTTAGT
89	AATCTCACCCCTAGCTCGAGCAGAAATGATTGTGAAGAAGCCCTAACCCCTCAACATTCAGCGC
90	TGGGTATAAGGCTCACCCGACTATGATCTGTGGGTAAGATATCCATGTTACTG
91	CCTATAGAACTCAATAAATGGACGTGTTAGGAGTCTCGCCCTAACCCCTCGGTATATGAAGC
92	ATGAGGAGTTAACAGAGGAACGCTCGGCGATACTCAAGATCACTGCTGTGTGC
93	CGAGCGTTCCTCTCCCTAACCCCTGGGCTTCTCAGAGTCGTGATGCCAGTAAGGGAGCC
94	CAGACACAGTCGCTCCACATCTAGCAGCCCGGTTTCAAGCGTCAAATTAGGCG
95	TCCCACAATACAACCCTAACCCCTCACTGACCTATTGGACTTGAGAATAATGTCAGTTGTGTG
96	TTCAGAGTTTGAATGTTAACTCCTCATGCTTCATATAACCGTCTTGAGTATCGC
97	CGTAATTATACCGCCCTAACCCCTGTATTCGAACAGAGTACGTCAATTATCGTGCGGCATGGC
98	TCGGGTACTTGTCTCGGCATTCCGGCTACACGGCCCTAGTCGACTAATGCGCG
99	GGCCAGTCTGTTCCCTAACCCCTCTATCGAAGGCGATTTTCTACACGATATTCACGACCACC
100	CGGAATACATTGTTCTCGACGATCTAGGATACAGCCCATCCGAAACTATCAAT
101	CCATCACGAAACACCGTGAGGTATGCTTGAATGGGACGACCCCTAACCCCTACTAGGGCCGTGT
102	AGCCGGAATGCCGAAACAGACTGGCCCGCGCATTAGTCGTGGCGTCACGGATT
103	TATTCGACTGGTGCCCACTTTTCCGTTTCGGACATCACTCCCTAACCCCTCGTACTGGAAAAG
104	TTTTGAATACTGATAAACACAACCTAACCCCTAGGACCCATCGGGTTATGAGTC
105	TTAGTTGTGTTTACCCTAACCCCTGTTACCCTTGCCTGGGACAGTAATCACCCCTGTATTCCA
106	GCCAGGGCTGTAATAAGTGGCCCAAGGATTTGAACGTCGTCTCCACATGGGC

107	AGTCACTGTAGACCCCTAACCCCTCAGACGGTCCGGGCCAGCATACTTCGGGCTTAAGTTCGT
108	GAGTAGCCACATGTTTTCAGTATTCAAACTTTTCCAGTACGTGGGTCTTAGTGG
109	ATTATCTTCCAGTTGTCACTTATAATAACTCCTGTAGTCCCTAACCCCTACGACGTTCAAAT
110	CCTTGGGCCACTTGTCTACAGTACTGCCCATGTGGGAGTAGGACCTGTCCAA
111	TGAAGCTTGAGGCACTACAGCAACGTCGAGTATATCGAGCCCTAACCCCTGATGTGTCTTAGC
112	CCTGGTAGTCCACTGCGGAAATTGTCCTAATGTCTATGATGGTTGTCCCGTGC
113	GACAATTTCCGCACCCTAACCCCTTGAATTCTATAGGCAGTAACATGGATGCGAGACTCCTAA
114	CACGTCCATTTATTAGTCTGGTACTGTCTCCCTGAATTGTAAATCAAGCCCT
115	AACGACGATGCTCCCTAACCCCTATACTGCATTACCATGTAGGCCCTTCTATATCCCGAGCT
116	ATTGGCATACTGGTGTGGACTACCAGGGCTAGGACACATCTCATAGACATTAG
117	CAATAGGTCAGTGTTCAAACCTCTGAACACACAACCTGACACCCTAACCCCTCAATTCAGGGAGG
118	ACAGTACCAGACTGAGCATCGTCGTTAGGGCTTGATTTATAAATCGGACTGCT
119	GCTCCGTGCGACGCGTAATACTGAATTCCTGCCGATGGCCCTAACCCCTACATGTGTTGCTT
120	AGGCAATTAACGGCTTACGTCTGGGCCGGTGGTGTGCGTTTATTCTCAAGTC
121	TTTTTTTTTCCGTTAATTGCCTAAGCAACACATGTCCGACACCACGGCCACGACGTAAGTTTTTTTT
122	TCGCCTTCGATAGACAATGTATTCCGGGTGGTCTGTAATCCCTAACCCCTATCGTCCGGTAGG
123	CTTTTAATGTTACTAGTGGGTGCGTCTACATCGTGCAGATTAGCTATGGGAAA
124	TTGAGACCGTCTCGTCCGGTTGGGTGCGCTTAACTTGCCGCCCTAACCCCTAGCAACGCCAGTC
125	GAGTATAGGTCCTTTGATTTTATAAAGACCATTCACTTCTATCGTGTAGAAAA
126	TTTATAAAAATCAACCCTAACCCCTCACCAGTCAATAAATCCGTGACGCCAGTGATGTCCGAA
127	ACGGAAAAGTGGGTGCGCCCTGGTTTGTGAAAAGCTGTAAGACTTCGGGAAATC
128	TCAGGACGTACGACCCTAACCCCTTCCCTCAACGCTGGTCTCTGAGACTTAGTATTCATAGTG
129	GAGGGTCATATTATAGGACCTATACTCGACTGGCGTTGCTGAAGTGAATGGTC
130	CCCGGACCGTCTGCATGTGGCTACTCACGAACCTAAGCCCCCTAACCCCTTACAGCTTTTC
131	ACAAACCAGGGCGTCTGACGTCCTGAGATTTCCCGAAGTTCGTACAACGGCTA
132	TTTGCGAGTATGGTCACAGTTAGCAATCCGACTATATAACCCTAACCCCTCGCCAGCACCTAG
133	ACGTGCCGTCTATCTCAAAAATTAGAACGCTTGCCAGTCAAGTATGCTGG
134	CTAATTTTGATACCCTAACCCCTGCCTCAAGCTTCATTGGACAGGTCTCTCGATATACTCG
135	ACGTTGCTGTAGTTCTAATGTTTCGAGTCCCGGTGCCGCGACACTACTTGAATG
136	TGCTATAACGTGTCCCTAACCCCTGACGCAATGGCACTACTAATCACACCGTACCTGTGGTCT
137	CCCTACGAGCCGCTGATGACGGCACGTCTAGGTGCTGGCGCTGGCCAAGCGTT
138	GGTAATGCAGTATCCAGTATGCCAATAGCTCGGGATATACCCTAACCCCTTCGCGGCACCGGG
139	ACTCGAACATTAGACACGTTATAGCACATTCAAGTAGTGTCCGCGGTGCTGAT
140	CTCAAACGCCGGCCAAGACCGACCGTGCCGTTTGGGTCTCCCTAACCCCTTTGATTGATCGTG
141	AAGATGCTGCGACCCGAACCTTTATAGCAATACAGCTGATTGAAGGGCTACAT
142	CTATAAAGTTCGGCCCTAACCCCTCGTCGCACGGAGCAGCAGTCCGATTTCCATCGGCAGGAA
143	TTCAGTATTACCGTCGCGTTCTTAGCGAAAAGACCTGAGGTGACAGTGCCTAC
144	AAGGCTCTCTAGCCCTAACCCCTGGTGGCCGTACCACCTGAGTTGTACTCAGAATCCGAAGGA
145	TGGGTCACTCCACGTGTGCGAGCATCTTACGATCAATCAAATCAGCTGTATTG
146	TTTTTTTTTCTCAGGTCTTTTCGCTAGGAACGGCTAGAGAGCCTTGTAGGCACTGTCATTTTTTTTT
147	ACATTATCCCTCGCCCTAACCCCTGAGACGGTCTCAATTTCCCATAGCTACGGCAAGTTAAGC
148	GCACCCAACCGACTCTGCGAATGGGTCTGCGCACGCCCTGCCTGGACTAAAC
149	TGAAATATACCTCCCTAACCCCTGCCTTGCTTCCCGGTTTGGCCCTATAGCCACGGGAGCAA

150	AGCCACCAAATTGTTCTTATCGGTGTTGTGTAATTTATTTTGACGGGACTAAT
151	CAGCGTTGAGGAATAATATGACCCTCCACTATGAATACTCCCTAACCCCTAGGGCGTGCGCAG
152	GACCATTTCGAGGAGGTATATTTTCAGTTTAGTCCAGGCTTAAATTCCTGAG
153	CGAGTTTTATGATCTATAGCAGCTTCGTGATCCAAACACCCCTAACCCCTCGTAATAGCGCAA
154	GAAATTACAAGTGCGTCGGGCCAGGATGTGCTAGGAAAGTAAGTCTCAGAGAC
155	TCCTGGCCCGACGCCCTAACCCCTCCATACTCGCAAATAGCCGTTGTACGTTATATAGTCGGA
156	TTGCTAACTGTGATTGTGTTATATGCCGATAATAGTAGCCATAGGTACTTCAC
157	ACTAGGCGACGGGCCCTAACCCCTGAGGGCTGTGAATCAGGGCCTAGCACGGTATTAGCATT
158	ACTTAGTGGGTCTTCACTTGTAAATTTCTTTCGCTATTACGCTTTCCTAGCACA
159	GTGCCATTGCGTCGCGGCTCGTAGGGAGACCACAGGTACCCCTAACCCCTGGCTACTATTATC
160	GGCATATAACACACCCGTCGCTAGTGTGAAGTACCTATTCTGCCATCGGAAG
161	GATCACTGACACCCGACGCTCTCTGATTAGCGTCCCTAACCCCTCGAACACAGATCG
162	CTTTTACTCAAGGCATGGGACATCTTAGCCTATTATTAGTGGTGTGATTAGTA
163	AAGATGTCCCATGCCCTAACCCCTGCCGGCGTTTGAGATCACGACCGCGGAGACCCAAACGGC
164	ACGGTCGGTCTTGTGACCTAGGCGGGACCACCCCTCGCATATATCTTCTTCAT
165	TCGGCATACTCAGCCCTAACCCCTAACGGTACGGAACAGGGCGGTGACGTGTACAGCATAA
166	CCCTCGTCATCAGTCTTGAGTAAAAGCGATCTGTGTTTCGCTAATAATAGGCT
167	TGGTACGGCCACCCGTGGATGACCCATCCTTCGGATTCTCCCTAACCCCTATGCGAGGGTGG
168	TCCCGCCTAGGTCTGAGTATGCCGAATGAAGAAAGATATCAGAGCCGACCTC
169	ACCTCACTAGATTACGCCGTTACGGAAACGAGATTCTGACCCCTAACCCCTTCTGAAGTGGACT
170	GGGAGCATCTGGGTAACGGATTCAAAGATTCTCGATGCTGAGTACAACCTCAG
171	TTTTTTTTTCCCAGATGCTCCCAGTCCACTTCAGAGCATCGAGGAATCTTTGAATCCGTTATTTTTTTTT
172	TTTTTTTTTTATAGGGCAAACCGGGAAGGCAAGGCCAATTTGGTGGCTTTGCTCCCGTGGCTTTTTTTTT
173	TTTTTTTTTATCATAAACTCGCTCAGGGAATTTATGTTGGATCTGACGAAGCTGCTATAGTTTTTTTT
174	TTTTTTTTTGCTAGGCCCTGATTCACAGCCCTCAAGACCCACTAAGTAATGCTAATACCGTTTTTTTT
175	TTTTTTTTTGGTGTGATGATCCTTCCGATGGCAGACGCACGCTAATCAGAGAGAGCGTCTTTTTTTTT
176	TTTTTTTTTGTACCCGCCCTGTTCCGTCACCGTTACTGATGACGAGGGTTATGCTGTACACTTTTTTTTT
177	TTTTTTTTTAATCTAGTGAGGTGAGGTCGGCTCTGTCAGAATCTCGTTTCCGTAACGGCTGTTTTTTTT
178	TTTTTTTTTGCATTCAGAAAAGGTTTGAGGTCCTAAAGAGTTGGTAATCTCCCTGCGACATTTTTTTTT
179	TTTTTTTTTTTTTCTGCAAGTCGAGGAAACCAATCCAGTAAGTAGCCTAAGGGAAGGTTAGTTTTTTTT
180	TTTTTTTTTGCCCATGAGGGACACGCGAATTTTCGAGCTTGATTGAAAGATGTAGAATTTTTTTTT
181	TTTTTTTTTAACCGGCCCTAACCGTTCGATATGTCTAGCACCGCATCCACACGCTTTTGTTTTTTTTT
182	TTTTTTTTTGGACCCGTTTATCTAAAGGAGCCGTCCTCCTCAGCATTTGTATGTTAACAATTTTTTTTT
183	TTTTTTTTTCAAGCATTTAGCGGCTATAGCGCTAAGACGATAAAATAGGGATACTTACTTTTTTTTT
184	TTTTTTTTTAAATAAATACACAACACCGATAAGACGAGGGATAATGTATTAGTCCCGTCATTTTTTTTT
185	TTTTTTTTTGTAACATTAAGGCTACCCGACGATTCCTGCACGATGTAGACGCACCCACTATTTTTTTTT
186	TTTTTTTTTGATGGGCTGTATCCTAGATCGTCGAGCGGTATAATTACGATTGATAGTTTCGTTTTTTTT
187	TTTTTTTTTGTCTAAATAGTTTCTAGTTTATCTCAGACGAATGTCTAATATGATCAGAGATTTTTTTTT
188	TTTTTTTTTCGTCGGAAGCGACATCCCATGTCTGCCTTTGACTCAGGTTGACTGCGCTCGGTTTTTTTT
189	TTTTTTTTTGGACTTTTATGTGGTGCCATCCGCATAGGTTACGGATAGGTAGATCGCGCTTTTTTTTT
190	TTTTTTTTTCCCGCTGCCAAATTGAACCTGTTTAGCCCGTGAGAAGGATAACCGGTAGGGTTTTTTTT
191	TTTTTTTTTGTCCCACTGTTTATTCGACGCTGGTACAACAAGCACGGCAGCGCAAGGAATTTTTTTTT
192	TTTTTTTTTCCACGAGCCTCCTCGCGCAGGCCTTGCTTTTAGTTTAGGTTACTGTAGCGTTTTTTTT

193	TTTTTTTTTCACGAAGAGTAATTTGGTCCCTCCGCGACTCCACGCACCCGGGACGATTTATTTTTTTTT
194	TTTTTTTTTGCTTGAAACCGGGCTGCTAGATGTGGTTGTATTGTGGGACGCCTAATTTGACTTTTTTTTT

S8.7 DNA sequences for X₃

Seq_ID	Sequences
1	CCCTTCTCACGGGCCCTAACCCCTAAGACCTCAAACCTTTTCTGAATCGCTGTCGCAGGGAGA
2	TTACCAACTCTTTTTGTAAGTCCAGTCCGCGAACGTGGTTCGCCACATCC
3	CAGCTGATCATCTTGGTAGCCAGCGTTCATGGGAGGATCGCGGTGCTCCTGAC
4	AGTTGTATTTCGTCTCTAAACAGGTTCAATTTGGCAGCGGGCCCTACGCGTTAT
5	GACTTGCAGGAAACTAACCTTCCCTTAGGCTACTTACTGCCCTAACCCCTACCAGTTTCGCGG
6	ACTGGCAGTTACAAGATGATCAGCTGGGATGTGGCGGGATTGTCATTAGGGCT
7	GACTCTGCCACAACGCCCGTGTAGTGC GCGATAACCACTTTTGTATCCTCGCGT
8	CAGTAGTAGGAGGTCACCTCACCCCTGAAAAGTGACGCTGGTTGATTGGTTTCCTC
9	TCAGGGTGAGTGACCCCTAACCCCTGAAAATTCGCGTGTCCCTCATGGGCCAAATTCATCATCT
10	TTCAATCAAGCTCTCTGGCGTTCCTTGAGGATGAGACAGTACTGCGTCCCGAA
11	GACTCGCGCTTCCCTAACGCGCGAACTATGCTCTGACTCTCCTACATCCAGAGC
12	GTAATAACCAACTTCCCTCCTACTACTGACGCGAGGATACAACCAGCGTCACTT
13	TTTAGGGCCGGTTACAAAGACGTGTGGATGCGGTGCTAGCCCTAACCCCTACTGTCTCATCCT
14	CAAGGAACGCCAGGGAAGCGCGAGTCTTCGGGACGCAGTTAACTCGGTCCAAG
15	GTCGCTAGTCGAGTACCAAGATCCCTCTGCCATGCCTGGTTACTTCTCCGCT
16	TGTAACAACGCGGTAGTGCTCGTTCGCTGGATAGACGGCTACATATCGAAGCG
17	GGAACGAGCACTACCCTAACCCCTACGGCTCCTTTAGATAAACGGCGTCTTGTTAACATACA
18	AATGCTGAGGAGGTACAGTGTGTGGACATCGGGCTCCGAGTACAGTCCAAGTC
19	TTATGTCCGTCACCTTAGCTCAGGACTAGAGGTAGAGGTTGCTAGTTCTGCAA
20	CAATAGACTCACGTCCGCGTTGTTACAAGGCGGAGAAGTAGCCGTCTATCCAC
21	GCTAAATGCTTGAGAGTAAGTATCCCTATTTTATCGTCTCCCTAACCCCTCTCGGAGCCCGAT
22	GTCCACACACTGTGTGACGGACATAAGACTTGGACTGTATGGAAGTAACGGCC
23	TAGGCACTTTGGGCAATGTGTTACAGCAAGTCAGTTTGCTTACCAGCTGCGAA
24	TAAACAGTGGGACTATTCCCTTGCCTGCGCTGCCGTGCTTGTGTTAGCGCTATAGCC
25	AACGCTGGCTACCGACGAATAACAACGTGTCAGGAGCACCGCCCTAACCCCTGCGGATAGGCACC
26	ACATAAAAGTCCAGCGGATCTACCTATCCGTAACCTATTGAAATAAAAGTGA
27	CTGAGTCTCTGTGCAGGCCGGCTTAGAGCTGGGCTGAATTACAGAGTCATCAC
28	ATGTACTTCCCTTTGAAACAGTTTGGCGAATTAAGCGACTCGATCCTCCCATG
29	GCCAAACTGTTTCCCCTAACCCCTTGTGGCAGAGTCAGCCCTAATGACAAAGTGGTATCGCG
30	CCTACACGGGCGTGTGAGTTACCCGGCAGTAAACTATAAGGGTCATTGCAG
31	CTCATCCAATTAATGGTGTCCATCCTTTCGGTCTCCTAATACTTGTCTCGATCC
32	TACGTATCGACCATAAAGGAAGTACATGTGATGACTCTGTGTCGCTTTAATTC
33	TAGTTCGCGCGTTAGTTGGGTAGTACGCTCTGGATGTAGCCCTAACCCCTTATAGTTTACTGC
34	CGGGTAACTCAACTTAATTGGATGAGCTGCAATGACCCTTACCCTGTAGGTCA
35	TAACAACCCTAGACAGGAGAAGACCAAAACGGAGTGCACCTTCGATCAACCGGC
36	TGTATAGCATGAGAAGCGTGGAGCGAGTACCGGTAGTTGTGAGAGTCAGAGCA
37	TCGCTCCACGCTTCCCTAACCCCTCTCGACTAGCGACCTTGGACCGAGTTCAGGCATGGCAG
38	AGGGATCTTGGTATGCCGCTCAACGCCCAACATGAACCTCATAATCTACTTCT

39	AACTTTCAGCCAGTAAGATTTGCCATGCATAAACGTCACCTACCCTTGACTCC
40	TCCCTTGAGATAGTCTCATGCTATACAGCCGGTTGATCGACAACCTACCGGTAC
41	AGTACCTGAGCTACGTGAGTCTATTGTTGCAGAACTAGCCCCTAACCTGAGGTTTCATGTTG
42	GGCGTTGAGCGGCCTGGCTGAAAGTTAGAAGTAGATTATTAGGAACAGCATCG
43	TTCCTATGTGATTCCACCCTCGTCATGCGACGAAACTCTTAACATAGTAGCG
44	AGGCCACCCTTAATCCCTATCATGATCAGGCTAGGCGGTAACCTCTACCTCT
45	TCATGATAGGGATCCCTAACCTCCCAAAGTGCCCTAGGCGGTTACTTCCGCAAACCTGACTTG
46	CTGTAACACATTGTCAAGGCCTGCGCGAGGAGGCTCGTGGAACGCTACAGTAA
47	CCTAAACTAAAGATCTTCACATCGGCCTCTTCGCCAGTAGGTCGTAGGTCGAG
48	TGACCGAGCCTTCTTAAGGGTGGGCCTCGCTACTATGTTACCGCCTAGCCTGA
49	ACCTGAGTCAAAGCCCTAACCTCACAGAGACTCAGTCACTTTTATTTTCATTCAGCCCAGCT
50	CTAAGCCGGCCTGTCAACTGCTAACGGCATAATAGCGGTCCCCTCTGTAGGA
51	GGGCAATTCACGTTCCGGGCAGAATCCAGTCCCTTGTGCTTCGTTTAGTCTGA
52	CTTCACGTGTCACCTGCAGACATGGGATGTGCGTTCCGACGCCGAGCGCAGTCA
53	AAGGATGGACACCTGGTCGATACGTAGGATCGAGCAAGTCCCTAACCTGACCGCTATTATG
54	CCGTTAGCAGTTGACGTGAATTGCCCTCCTACAGGACGGTTCCTAAATCCCGC
55	TCGGCTAAATCAAATATAATCGTATTTTAGAGGTCATTCTGCGACAATGTTAC
56	CGAATTTTATCCTTGTACGGTGCAGCGCCGTGATCCCCTTATTAGGAGACCGA
57	CGCGCACCGTACACCCTAACCTTCTAGGGTTGTTATGACCTACACGGTGTGCACTCCGTTT
58	TGGTCTTCTCCTGTGAATAGGCGGCAAGACATCCGAGTATACCCTGATAACAT
59	CCAGCCCTCTGCTTTCCTCAGAGCTACAGTCTTGGTATCTTATTCTCTCAATC
60	AATGTTACGCACCTAGGATAAAAATTCGGTAACATTGTGCGCAGTGGGATCACGG
61	CATGGCAAATCTTCTATCTCAAGGGAGGAGTACAAGGGTCCCTAACCTTACTCGGATGTC
62	TTGCCGCCTATTCAGCAGAGGGCTGGATGTTATCAGGGTCTATGGACTAGCG
63	TGTTTTAAAATGGCGACTTAGATTCGTCACTATGCTTCGTTGGACAGACAATC
64	CCAGAGTCCCTCAGTGGCTAGGGCACTCGAAGGAATGAGATAGTGACGTTTATG
65	AGTGCCCTAGCCACCCTAACCTAATCACATAGGAACGATGCTGTTCTGAGTTTCGTGCA
66	TGACGAGTGGTGGTGATTACTTTCTGATCCTGGCTAATTAGTCAGACATACA
67	CCAGTAAAAGGTCTCTAGGGTGAGATTGCACACAGCAGTGGCTTCTTACAAT
68	CATTCTGCTCGAGTCTGAGGACTCTGGGATTGTCTGTCCATCTCATTCTCTCG
69	GGCCGATGTGAAGGAAGGCTCGGTCACTCGACCTACGACCCTAACCTAATTAGCCAGGAT
70	CAGGAAAGTAATCGACCTTTTACTGGTGTATGTCTGACTTGCATACACGACGA
71	CTCTGAGAAGCCCGGACTGTGTCTGGGCTCCCTTACTGTGCGGAGGGACCAA
72	ATTACTCTTCGTGATAAATCGTCCCGGGTGCCTGGAGTCTCTACTGGCGAAGA
73	GGATTCTGCCCAGGTGACACGTGAAGTCAGACTAAACGACCCTAACCTTGAGATAAACTAG
74	AAACTATTTAGACATCTCTGATCATATTAGACATTTCGTCTATAATTGACGTAC
75	TCTGTTTGAATACGACAAGTACCCGAGCCATGCCGCACGTTGTGAGTGGCAG
76	TCTGTGGAATAAATAGGAACGGATAGCTTTTATACTTGTAGCACAAGGGACT
77	TATCCAGTTCCTACCCTAACCTTTGATTTAGCCGAGCGGGATTTAGGAGAATGACCTCTAA
78	AATACGATTATATTCGGACTAGACGACCCTAAGGCTATCAAGCCGGCTAAACG
79	AGTCGGAGTCCCATTTGTTTCGTGATGGGACTCATAACCCGTGCTCCATTCAA
80	GCATACCTCACGGTTTTATTCCACAGACTGCCACTCGACACAAGTATAAAAAGC
81	GTAGCTCTGAGGAGTGGTGAACATTGATTGAGAGAATACCCTAACCTTGATAGCCTTGCG

82	GTCGTCTAGTCCGTGGGACTCCGACTCGTTTAGCCGGCTTGATTACTGTCCCA
83	GTGCAAGGGTAACTTACAGCCCTGGCTGGAATACAGGGTTGCTACGATAACGT
84	CAATCTACTGTTCCCTATCTTATGGGTACTAAAGTACGGATAGATACCAAGACT
85	ACCCATAAGATAGCCCTAACCCCTCCATTTTAAAAACACGCTAGTCCATAGCGAAGCATAGTGA
86	CGAATCTAAGTCGTAGCCTTATACCCAGCGCTGAATGTTGTCTTACCCACAGA
87	TCATAGTCGGGTGTCTGGAAAGATAATCGACGGGACAACCCTACAGGAGTTA
88	TTATAAGTGACAATGAACAGTAGATTGACGTTATCGTAGCTCCGTACTTTAGT
89	AATCTCACCCCTAGCTCGAGCAGAATGATTGTGAAGAAGCCCCCTAACCCCTCAACATTCAGCGC
90	TGGGTATAAGGCTCACCCGACTATGATCTGTGGGTAAGATATCCATGTTACTG
91	CCTATAGAACTCAATAAATGGACGTGTTAGGAGTCTCGCTCGGTATATGAAGC
92	ATGAGGAGTTAACAGAGGAACGCTCGGCGATACTCAAGATCACTGCTGTGTGC
93	CGAGCGTTCCCTCTCCCTAACCCCTGGGCTTCTCAGAGTCGTCGTGTATGCCAGTAAGGGAGCC
94	CAGACACAGTCGCTCCACATCTAGCAGCCCGGTTTTCAAGCGTCAAATTAGGCG
95	TCCCACAATACAATCACTGACCTATTGGACTTGAGAATAATGTCAGTTGTGTG
96	TTCAGAGTTTGAATGTTAACTCCTCATGCTTCATATACCGTCTTGAGTATCGC
97	CGTAATTATACCGCCCTAACCCCTGTATTGGAACAGAGTACGTCAATTATCGTGCGGCATGGC
98	TCGGGTACTTGTCTCGGCATTCCGGCTACACGGCCCTAGTCGACTAATGCGCG
99	GGCCAGTCTGTTTTCTATCGAAGGCGATTTTCTACACGATATTACAGACCACC
100	CGGAATACATTGTTCTCGACGATCTAGGATACAGCCATCCGAAACTATCAAT
101	CCATCACGAAACACCGTGAGGTATGCTTGAATGGGACGACCCTAACCCCTACTAGGGCCGTGT
102	AGCCGGAATGCCGAAACAGACTGGCCCGCGCATTAGTCGTGGCGTCACGGATT
103	TATTCGACTGGTGCCCACTTTTCCGTTTCGGACATCACTTCGTAAGTGGAAAAG
104	TTTTGAATACTGATAAACACAACCTAACCCCTAGGACCCATCGGGTTATGAGTC
105	TTAGTTGTGTTTACCCTAACCCCTGTACCCTTGCACTGGGACAGTAATCACCCGTATTCCA
106	GCCAGGGCTGTAATAAGTGGCCCAAGGATTTGAACGTCGTCTCCACATGGGC
107	AGTCACTGTAGACTCAGACGGTCCGGGCCAGCATACTTCGGGGCTTAAGTTCTGT
108	GAGTAGCCACATGTTTCAAGTATTCAAACCTTTTCCAGTACGTGGGTCTAGTGG
109	ATTATCTTTCCAGTTGTCACTTATAATAACTCCTGTAGTCCCTAACCCCTACGACGTTCAAAT
110	CCTTGGGCCACTTGTCTACAGTACTGCCCATGTGGGAGTAGGACCTGTCCAA
111	TGAAGCTTGAGGCACTACAGCAACGTCGAGTATATCGAGTGTGTCTTAGC
112	CCTGGTAGTCCACTGCGGAAATTGTCCTAATGTCTATGATGGTTGTCCCGTCCG
113	GACAATTTCCGCACCCTAACCCCTTGAGTTCTATAGGCAGTAACATGGATGCGAGACTCCTAA
114	CACGTCCATTTATTAGTCTGGTACTGTCCCTCCCTGAATTGTAAATCAAGCCCT
115	AACGACGATGCTCTATACTGCATTACCATGTAGGCCCTTCTATATCCCGAGCT
116	ATTGGCATACTGGTGTGGACTACCAGGGCTAGGACACATCTCATAGACATTAG
117	CAATAGGTCAGTGTTCAAACCTCTGAACACACAACCTGACACCCTAACCCCTCAATTCAGGGAGG
118	ACAGTACCAGACTGAGCATCGTCGTTAGGGCTTGATTTATAAATCGGACTGCT
119	GCTCCGTGCGACGCGTAATACTGAATTCCTGCCGATGGTACATGTGTTGCTT
120	AGGCAATTAACGGCTTACGTCGTGGGCCGGTGGTGTGCGTTTTATTCTCAAGTC
121	TTTTTTTTTCCGTTAATTGCCTAAGCAACACATGTCCGACACCACGGCCACGACGTAAGTTTTTTTT
122	TCGCCTTCGATAGACAATGTATTCCGGGTGGTTCGTGAATCCCTAACCCCTATCGTCGGGTAGG
123	CTTTTAATGTTACTAGTGGGTGCGTCTACATCGTGCAGATTAGCTATGGGAAA
124	TTGAGACCGTCTCGTCGGTTGGGTGCGCTTAACTTGCCGTAGCAACGCCAGTC

125	GAGTATAGGTCCTTTGATTTTATAAAGACCATTCACTTCTATCGTGTAGAAAA
126	TTTATAAAATCAACCCTAACCCCTCACCAGTCGAATAAATCCGTGACGCCAGTGATGTCCGAA
127	ACGGAAAAGTGGGTCGCCCTGGTTTGTGAAAAGCTGTAAGACTTCGGGAAATC
128	TCAGGACGTACGATTTCCCTCAACGCTGGTCTCTGAGACTTAGTATTATAGTGTG
129	GAGGGTCATATTATAGGACCTATACTCGACTGGCGTTGCTGAAGTGAATGGTC
130	CCCGGACCGTCTGCATGTGGCTACTCACGAACTTAAGCCCCCTAACCCCTTACAGCTTTTC
131	ACAAACCAGGGCGTCGTACGTCTGAGATTTCCCGAAGTTCGTACAACGGCTA
132	TTTGCGAGTATGGTCACAGTTAGCAATCCGACTATATAATCGCCAGCACCTAG
133	ACGTGCCGTCATCTATCCAAAATTAGAACGCTTGGCCAGTCGAAGTATGCTGG
134	CTAATTTTGGATACCCTAACCCCTGCCTCAAGCTTCATTGGACAGGTCCTCTCGATATACTCG
135	ACGTTGCTGTAGTTCTAATGTTTCGAGTCCCGGTGCCGCGACACTACTTGAATG
136	TGCTATAACGTGTTGACGCAATGGCACTACTAATCACACCGTACCTGTGGTCT
137	CCCTACGAGCCGCTGATGACGGCACGTCTAGGTGCTGGCGCTGGCCAAGCGTT
138	GGTAATGCAGTATCCAGTATGCCAATAGCTCGGGATATACCCTAACCCCTTCGCGGCACCGGG
139	ACTCGAACATTAGACACGTTATAGCACATTC AAGTAGTGTCCGCGGTGCTGAT
140	CTCAAACGCCGGCCAAGACCGACCGTGCCGTTTGGGTCTTTTGATTGATCGTG
141	AAGATGCTGCGACCCGAACTTTATAGCAATACAGCTGATTGAAGGGCTACAT
142	CTATAAAGTTTCGGCCCTAACCCCTCGTCGCACGGAGCAGCAGTCCGATTTCCATCGGCAGGAA
143	TTCAGTATTACCGTCGCGTTCCTAGCGAAAAGACCTGAGGTGACAGTGCCTAC
144	AAGGCTCTCTAGCTGGTGGCCGTACCCTGAGTTGTACTCAGAATCCGAAGGA
145	TGGGTCAATCCACGTGTCGCAGCATCTTCACGATCAATCAAATCAGCTGTATTG
146	TTTTTTTTCTCAGGTCTTTTCGCTAGGAACGCGGCTAGAGAGCCTGTAGGCACTGTCATTTTTTTT
147	ACATTATCCCTCGCCCTAACCCCTGAGACGGTCTCAATTTCCCATAGCTACGGCAAGTTAAGC
148	GCACCCAACCGACTCTGCGAATGGGTCTGCGCACGCCCTGCCTGGACTAAAC
149	TGAAATATACCTCTGCCTTGCTTCCCGGTTTGCCCTATAGCCACGGGAGCAA
150	AGCCACCAAATGTTCTTATCGGTGTTGTGTAATTTATTTTACGGGACTAAT
151	CAGCGTTGAGGAATAATATGACCCTCCACTATGAATACTCCCTAACCCCTAGGGCGTGCGCAG
152	GACCCATTCGCAGGAGGTATATTTTCAGTTTAGTCCAGGCTTAAATTCCCTGAG
153	CGAGTTTTATGATCTATAGCAGTTTCGTCAGATCCAACATCGTAATAGCGCAA
154	GAAATTACAAGTGCCTCGGGCCAGGATGTGCTAGGAAAGTAAGTCTCAGAGAC
155	TCCTGGCCCCGACGCCCTAACCCCTCCATACTCGCAAATAGCCGTTGTACGTTATATAGTCGGA
156	TTGCTAACTGTGATTGTGTTATATGCCGATAATAGTAGCCATAGGTACTTTCAC
157	ACTAGGCGACGGGTTGAGGGCTGTGAATCAGGGCCTAGCACGGTATTAGCATT
158	ACTTAGTGGGTCTTCACTTGTAAATTTCTTGGCTATTACGCTTTCCTAGCACA
159	GTGCCATTGCGTCGCGGCTCGTAGGGAGACCACAGGTACCCCTAACCCCTGGCTACTATTATC
160	GGCATATAACACACCCGTCGCTAGTGTGAAGTACCTATTCTGCCATCGGAAG
161	GATCACTGACACCCGACGCTCTCTCTGATTAGCGTGCCTTCGAACACAGATCG
162	CTTTTACTCAAGGCATGGGACATCTTAGCCTATTATTAGTGGTGTGATTAGTA
163	AAGATGTCCCATGCCCTAACCCCTGCCGGCGTTTGAGATCACGACCGCGGAGACCCAAACGGC
164	ACGGTCGGTCTTGTGACCTAGGCGGGACCACCCTCGCATATATCTTTCTTCAT
165	TCGGCATACTCAGTTAACGGTGACGGAACAGGGCGGTGACGTGTACAGCATAA
166	CCCTCGTCATCAGTCTTGTGATAAAGCGATCTGTGTTTCGCTAATAATAGGCT
167	TGGTACGGCCACCCGTGGATGACCCATCCTTCGGATTCTCCCTAACCCCTTATGCGAGGGTGG

168	TCCCGCCTAGGTCTCGAGTATGCCGAATGAAGAAAGATATCAGAGCCGACCTC
169	ACCTCACTAGATTACAGCCGTTACGGAAACGAGATTCTGATTCTGAAGTGGACT
170	GGGAGCATCTGGGTAACGGATTCAAAGATTCTCGATGCTGAGTACAACCTCAG
171	TTTTTTTTTCCAGATGCTCCAGTCCACTTCAGAGCATCGAGGAATCTTTGAATCCGTTATTTTTTTTT
172	TTTTTTTTTATAGGGCAAACCGGGAAGGCAAGGCCAATTTGGTGGCTTTGCTCCCGTGGCTTTTTTTTT
173	TTTTTTTTTATCATAAACTCGCTCAGGGAATTTATGTTGGATCTGACGAAGTCTATAGTTTTTTTT
174	TTTTTTTTTGCTAGGCCCTGATTACAGCCCTCAAGACCCACTAAGTAATGCTAATACCGTTTTTTTT
175	TTTTTTTTTGGTGTGAGTATCCTTCCGATGGCAGACGCACGCTAATCAGAGAGAGCGTCTTTTTTTTT
176	TTTTTTTTTGTACCGCCCTGTTCCGTCACCGTACTGATGACGAGGGTTATGCTGTACACTTTTTTTTT
177	TTTTTTTTTAATCTAGTGAGGTGAGGTCTGGCTCTGTCAGAATCTCGTTTCCGTAACGGCTGTTTTTTTT
178	TTTTTTTTTGCGATTACAGAAAAGTTTGGAGTCTTAAAGAGTTGGTAATCTCCCTGCGACATTTTTTTTT
179	TTTTTTTTTTTTTCTGCAAGTCGAGGAAACCAATCCAGTAAGTAGCCTAAGGGAAGTTAGTTTTTTTT
180	TTTTTTTTTGGCCCATGAGGGACACGCGAATTTTCGAGCTTGATTGAAAGATGTAGAATTTTTTTTT
181	TTTTTTTTTAACCGGCCCTAAACGCTTCGATATGCTTAGCACCCGCATCCACACGCTTTTGTTTTTTTTT
182	TTTTTTTTTGGACGCCGTTTATCTAAAGGAGCCGTCCTCCTCAGCATTTGTATGTTAAACAATTTTTTTTT
183	TTTTTTTTTCAAGCATTTAGCGGCTATAGCGCTAAGACGATAAAATAGGGATACCTACTTTTTTTTT
184	TTTTTTTTTAAATAAATTACACAACACCGATAAGACGAGGGATAATGTATTAGTCCCGTCATTTTTTTTT
185	TTTTTTTTTGTAACATTAAGCCTACCCGACGATTCGACGATGTAGACGCACCCACTATTTTTTTTT
186	TTTTTTTTTGATGGGCTGTATCCTAGATCGTCGAGCGGTATAATTACGATTGATAGTTTCGTTTTTTTT
187	TTTTTTTTTGTCTAAATAGTTTCTAGTTTATCTCAGACGAATGTCTAATATGATCAGAGATTTTTTTTT
188	TTTTTTTTTCGTCGGAAGCGACATCCCATGCTGCCTTTGACTCAGGTTGACTGCGCTCGGTTTTTTTT
189	TTTTTTTTTGGACTTTTATGTGGTGCCTATCCGCATAGGTTACGGATAGGTAGATCGCGCTTTTTTTTT
190	TTTTTTTTTCCCGCTGCCAAATTGAACCTGTTTAGCCCGTGAGAAGGGATAACGCGTAGGGTTTTTTTT
191	TTTTTTTTTGTCCACTGTTTATTCGAGCTGGTACAACAAGCACGGCAGCGCAAGGAATATTTTTTTTT
192	TTTTTTTTTCCACGAGCCTCCTCGCGCAGGCCTTGCTTTAGTTTAGGTTACTGTAGCGTTTTTTTT
193	TTTTTTTTTCACGAAGAGTAATTTGGTCCCTCCGCGACTCCACGCACCCGGGACGATTTATTTTTTTTT
194	TTTTTTTTTGCTTGAACCGGGCTGCTAGATGTGGTTGTATTGTGGGACGCCTAATTTGACTTTTTTTTT

S8.8 DNA sequences for extended 1D ribbon from 'X'-motifs

Seq_ID	Sequences
1	CAGCTGATCATCTTGGTAGCCAGCGTTCATGGGAGGATCGCGGTGCTCCTGAC
2	ACTGGCAGTTACAAGATGATCAGCTGGGATGTGGCGGGATTGTCATTAGGGCT
3	GACTCTGCCACAACGCCCGTGTAGTGCGGATAACCACTTTTGTATCCTCGCGT
4	GACTCGCGCTTCCCTAACGCGGAACTATGCTCTGACTCTCCTACATCCAGAGC
5	GTACTACCCAACCTCCTCCTACTACTGACGCGAGGATACAACCAGCGTCACTT
6	CAAGGAACGCCAGGGAAGCGGAGTCTTCGGGACGCAGTTAACTCGGTCCAAG
7	GTCGCTAGTCGAGTACCAAGATCCCTCTGCCATGCCTGGTTACTTCTCCGCT
8	CTGAGTCTCTGTGCAGGCCGGCTTAGAGCTGGGCTGAATTACAGAGTCATCAC
9	ATGTACTTCTTTGAAACAGTTTGGCGAATTAAGCGACTCGATCCTCCCATG
10	GCCAAACTGTTTCTTTGTGGCAGAGTCAGCCCTAATGACAAAGTGGTATCGCG
11	CACTACACGGGCGTGTGAGTTACCCGGCAGTAAACTATAAGGGTCATTGACG
12	CTCATCCAATTAATGGTGTCCATCCTTTCCGGTCTCCTAATACTTGCTCGATCC
13	TACGTATCGACCATAAAGGAAGTACATGTGATGACTCTGTGTCGCTTAAATTC

14	TAGTTCGCGCGTTAGTTGGGTAGTACGCTCTGGATGTAGTTATAGTTTACTGC
15	CGGGTAACTCAACTTAATTGGATGAGCTGCAATGACCCTTACCGTGTAGGTCA
16	TAACAACCCTAGACAGGAGAAGACCAAAACGGAGTGCACCTTCGATCAACCGGC
17	TGTATAGCATGAGAAGCGTGGAGCGAGTACCGGTAGTTGTGAGAGTCAGAGCA
18	TCGCTCCACGCTTTCTCGACTAGCGACCTTGGACCGAGTTCAGGCATGGCAG
19	AGGGATCTTGGTATGCCGCTCAACGCCCAACATGAACCTCATAATCTACTTCT
20	AACTTTCAGCCAGTAAGATTTGCCATGCATAAACGTCACCTACCCTTGTACTCC
21	TCCCTTGAGATAGTCTCATGCTATACAGCCGGTTGATCGACAACCTACCGGTAC
22	CTAAGCCGGCCTGTCAACTGCTAACGGCATAATAGCGGTCCCCTCTGTAGGA
23	GGGCAATTCACGTTCCGGGCAGAATCCAGTCCCTTGTGCTTCGTTTAGTCTGA
24	AAGGATGGACACCTGGTGCATACGTAGGATCGAGCAAGTTGACCGCTATTATG
25	CCGTTAGCAGTTGACGTGAATTGCCCTCCTACAGGACGGTTCCTAAATCCCGC
26	TCGGCTAAATCAAATATAATCGTATTTTAGAGGTCATTCTGCGACAATGTTAC
27	CGAATTTTATCCTTGTACGGTGCAGCGCCGTGATCCCCTTATTAGGAGACCGA
28	CGCGCACCGTACATTCTAGGGTTGTTATGACCTACACGGTGTGCACTCCGTTT
29	TGGTCTTCTCCTGTGAATAGGCGGCAAGACATCCGAGTATACCCGTATAACAT
30	CCAGCCCTCTGCTTTCCCTCAGAGCTACAGTCTTGGTATCTTATTCTCTCAATC
31	AATGTTACGCACTAGGATAAAAATTCGGTAAACATTGTGCGAGTGGGATCACGG
32	CATGGCAAATCTTCTATCTCAAGGGAGGAGTACAAGGGTTATACTCGGATGTC
33	TTGCCGCTATTTCAGCAGAGGGCTGGATGTTATCAGGGTTCATGGACTAGCG
34	TGTTTTAAATGGCGACTTAGATTCGTCATATGCTTCGTTGGACAGACAATC
35	CCAGAGTCCCTAGTGGCTAGGGCACTCGAAGGAATGAGATAGTGACGTTTATG
36	TCTGTTTCAATACGACAAGTACCCGAGCCATGCCGCACGTTGTCGAGTGGCAG
37	TCTGTGGAATAAATAGGAAGTGGATAGCTTTTATACTTGTAGCACAAAGGGACT
38	TATCCAGTTCCTATTTGATTTAGCCGAGCGGGATTTAGGAGAATGACCTCTAA
39	AATACGATTATATTCGGACTAGACGACCCGAAGGCTATCAAGCCGGCTAAACG
40	AGTCGGAGTCCCATTGTTTCGTGATGGGACTCATAACCCGTCGTCCCATTCAA
41	GCATACCTCACGGTTTTATTCCACAGACTGCCACTCGACACAAGTATAAAAGC
42	GTAGCTCTGAGGAGTGCCTGAACATTGATTGAGAGAATATTGATAGCCTTGCG
43	GTCGTCTAGTCCGTGGGACTCCGACTCGTTTAGCCGGCTTGATTACTGTCCCA
44	GTGCAAGGGTAACTTACAGCCCTGGCTGGAATACAGGGTTGCTACGATAACGT
45	CAATCTACTGTTCTATCTTATGGGTACTAAAAGTACGGATAGATACCAAGACT
46	ACCATAAGATAGTCCATTTTAAAACACGCTAGTCCATAGCGAAGCATAGTGA
47	CGAATCTAAGTCGTAGCCTTATACCCAGCGCTGAATGTTGTCTTACCCACAGA
48	TCATAGTCGGGTGTCTGGAAAGATAATCGACGGGACAACCACTACAGGAGTTA
49	TTATAAGTGACAATGAACAGTAGATTGACGTTATCGTAGCTCCGTACTTTAGT
50	GGAACGAGCACTATGTATTGAAACAGAGTACGTCAATTATCGTGCGGCATGGC
51	TCGGGTACTTGTCTTGTAACTGCCAGTCCGCGAACGTGGTTCCCCGCCACATCC
52	AGTTGTATTTCGTCTCCGCTTGTTACAAGGCGGAGAAGTAGCCGTCTATCCAC
53	CCATCACGAAACACCGTGAGGTATGCTTGAATGGGACGATACCACGTTTCGCGG
54	CAGTAGTAGGAGGTCACTCACCCCTGAAAAGTGACGCTGGTTCCGGTTATGAGTC
55	TCAGGGTGAGTGATGTTACCCTTGCACTGGGACAGTAATCACCCGTGATTCCA
56	GCCAGGGCTGTAATCTGGCGTTCCTTGAGGATGAGACAGTACTGCGTCCCGAA

57	ATTATCTTTCCAGTTGTCACCTTATAATAACTCCTGTAGTTACTGTCTCATCCT
58	TGTAACAACGCGGTAGTGCTCGTTCCGTGGATAGACGGCTGGTTGTCCCGTCG
59	AACGCTGGCTACCGACGAATACAACCTGTCAGGAGCACCGTGAGGTTTCATGTTG
60	GGCGTTGAGCGGCTGGCTGAAAGTTAGAAGTAGATTATTGAAATAAAAGTGA
61	AGTGCCCTAGCCATCACAGAGACTCAGTCACTTTTATTTTCATTCAGCCCAGCT
62	CTTCACGTGTCACTCTGAGGACTCTGGGATTGTCTGTCCATCTCATTCCTTCG
63	GGATTCTGCCCAGGTGACACGTGAAGTCAGACTAAACGATCAACATTCAGCGC
64	TGGGTATAAGGCTCACCCGACTATGATCTGTGGGTAAGATATAAATTGACGTAC
65	TTTTTTTTGTCTAAATAGTTTCTAGTTTATCTCAGACGAATGTCTAATATGATCAGAGATTTTTTTTT
66	TTTTTTTTCGTCGGAAGCGACATCCCATGTCTGCCTTTGACTCAGGTTGACTGCGCTCGGTTTTTTTT
67	TTTTTTTTGGACTTTTATGTGGTGCCTATCCGCATAGGTTACGGATAGGTAGATCGCGCTTTTTTTTT
68	TTTTTTTTCCCGCTGCCAAATTGAACCTGTTTAGCCCGTGAGAAGGGATAACGCGTAGGGTTTTTTTT
69	TTTTTTTTCAACATTCAGCGCTGGGTATAAGGCTCACCCGACTATGATCTGTGGGTAAGATTTTTTTTT
70	TTTTTTTTGAGGTTTCATGTTGGGCGTTGAGCGGCTGGCTGAAAGTTAGAAGTAGATTATTTTTTTTT
71	TTTTTTTTCTGAGGACTCTGGGATTGTCTGTCCATCTCATTCCTTCGAGTGCCTAGCCATTTTTTTTT
72	TTTTTTTTCCGCGTTGTTACAAGGCGGAGAAGTAGCCGCTATCCACGGAACGAGCACTATTTTTTTTT

S8.9 DNA sequences for extended 1D ribbon from 'Y'-motifs

Seq_ID	Sequences
1	ACACGGCCCTGGCATGAGACGTAAGAAATTGGCAATCTATGGGTTTCGCCTAG
2	ATCATCTATAACAAAAGTAACTCATATCATGCGTCCGGTCCCAGGCGCACAC
3	GCTGCAATACCCGCGAAATCCACTAAATGAGGATGGACAAGTCAGGGTGGAT
4	CCTTTGCGCCCATGCCAGGGCCGTGTCTGTAATTATAACTAGATTGCCAATT
5	GTGGCGCGATGCATGTTATAGATGATTGATACTGTCGCCACCGGACGCATGA
6	CCTCTCGATCATTCGGGTATTGCAGCTGTCGTTGGCTTTTGTCCATCCTCAT
7	GGCTGACTCTTAAGGAGGATTTACTGTTCTGTGGGAGATAATGGATCCTTCA
8	TAATGAAGTGGCCATGGGCGCAAAGGCATTGTTTGTAATACTGGGAATGTAG
9	CTGAATGTTTGAATGCATCGCGCCACGACTTTGCAAGGAGTATTTGAAAGTG
10	TCTTACGTCTCATACGAAACTCGAGCTGAAGGATCCATTTGGTATTAAACCA
11	TATGAGTTACTTTACGTAGCCTCTCACTACATTTCCAGTCTACCGCAAATCT
12	TTAGTGGATTTTGAATATCGGACCACCACTTTCAAATACGGTTGCATACAAA
13	GCTCGAGTTTTCGTAAGCTATCCTAGATGGTTTAAATACCAGTTATAATTACAG
14	TGAGAGGCTACGTCCATTACGTTGTGAGATTTGCGGTAGGGCGACAGTATCA
15	GTGGTCCGATATTCGCGCTCAGGAAATTTGTATGCAACCAAAGCCAACGACA
16	TCTAGGATAGCTTGGCCACTTCATTAGTGTGCGCCTGGGATTACAAACAATG
17	CACAACGTAATGGTTCAAACATTCAGATCCACCCTGACTTCCTTGCAAAGTC
18	TTTCTGAGCGCGCTTTACCTCGGTATCATCGTAAACGCACCTGCGGCGCT
19	TAAAGAGTCAGCCCTAGGCGAACCAATCTCCACAGAACAGTAAATCCTCC
20	CGTTTACGATGATACCGAGGTAAAGGAATGATCGAGAGGAGCGCCGAGGTG

S8.10 DNA sequences for tube structure from one continuous 'Y'-motif

Seq_ID	Sequences
1	TAACATACGTATGTTATTACCCTCGAGGGTAACTCTGTCCGGACAGAGGCCCTGTGCACAG

	GGCCTCCGAGATCTCGGAGTCGCGCTGCAGCGCGA
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S8.11 DNA sequences for extended 1D tube from ‘Y’-motifs (two species motifs with 16-nt arms)

Seq_ID	Sequences
1	CGCTTATGTTAAAGAGCCCTGAGGCCAGCCT
2	ACCTTAATTGTAAACTCACTGATAGGACGCAG
3	CGTTTGTTCCTAAGTGCAGTAGACCATGAAC
4	CTCTTTAAAACAAACGCTGCGTCCTCTACTGC
5	ACTTAGGAATTAAGGTAGGCTGGGTATCAGTG
6	AGTTTACACATAAGCGGTTTCATGGCCTCAGGG

S8.12 DNA sequences for extended 1D tube from ‘X’-motifs (two species motifs with 16-nt arms)

Seq_ID	Sequences
1	TCCGAGCGACTGCTCAAGCTGCACTTTAAACTA
2	ATGACCTCATAAAGCACCCTATCTAGAGATCG
3	ATGTTTGAACCTTCCTGCGGCGGATACCCACAT
4	TGCTAAATAACGCGAACAAGACGGTAGTGTACG
5	TTCGCGTTTCAAACATCGATCTCTTTCCGCCGC
6	AGGAAAGTGAGGTCATTAGTTTAATGATAGTGG
7	TGCTTTATCGCTCGGACGTACACTTGTGCAGCT
8	TGAGCAGTATTTAGCAATGTGGGTTCCGTCTTG

S8.13 DNA sequences for extended 1D tube from ‘X’-motifs (four species motifs with 16-nt arms)

Seq_ID	Sequences
1	TTTAGATGGGTTGACCACTATTTCTCTCCAGTT
2	GTTACTCGATTGCGGGTACCTGCATCACATAGC
3	TTCGTCTATATACTTGAGTCCGAATTCGCAGAA
4	GAAAGGCACTGCCGGGCATCCTGATCGGTTCCA
5	CTTAATTGTCAGAGACACTTTATGTAGAGGGCG
6	CCGTGCTCATGGCTCGGTGCGCTATAGAATATG
7	ACGCGAGGTTTGAATGACAGACCTTCAGCATT
8	CAGTACATGCAACGTAGAACTACTCAAAGCGG
9	CCCGGCAGCCTCGCGTCATATTCTTAGGTCTGT
10	CATTCAAACGAGTAACAACCTGGAGTTGCAGGTA
11	CCCGAATCAATTAAGCCGCTTTGTCATAAAGT
12	GTCTCTGATGCCTTTCTTCTGCGATTCAGGATG
13	TACGTTGCTAGACGAAGCTATGTGTTTCGGACT
14	CAAGTATAGAGCACGGCGCCCTCTTTAGCGCAC
15	CGAGCCATCATCTAAATGGAACCGTGAAATAGT
16	GGTCAACCATGTACTGTAATGCTGTGTAGTTTC

S8.14 DNA sequences for extended 1D tube from ‘X’-motifs (four species motifs with 26-nt arms)

Seq_ID	Sequences
1	CTTGTATATGACAGTTTGGCATCACGTTGAGCGAATATGTGTGCCAGAGGTCA
2	AGACGGATAGTTCACCCTGGCGGTACTGTAGAACCAGGCTTCTGCACGAGCAA
3	GGCCTCTCTGACGTAACGACGGGCTCCCTGCGACTCAGTTGGACTGCCACGAC
4	AACCCTTCACACCATTAAAGAACATGTGCATATCATACATTTTATGTAAGGAA
5	AATCCGACCCATTCTCTTGGTCAGGTATGTTAAGCCTCATATCGCACCGTGAC
6	CGGGCCACCCAGCGATCTCTCCGCGCACTAAAGCATCGTTCCGGGTGCTTGAG
7	TACTTTACTCGATAAAGGGCGGACTCTCACCTGTTTCATCTTTAGTTGGCGCGT
8	CACCGCTGCCCGCAAGATTTCACTAGCCCAGTTATTATCTAACACTTGATCGG
9	CATGTTCTTTAATTATCGAGTAAAGTACTCAAGCACCCGGGATGAACAGGTGA
10	GAGTCCGCCCTTTTGAAGTATCCGTCTTGACCTCTGGCACGCCTGGTTCTACA
11	GTACCGCCAGGGTTAATGGGTTCGGATTCCGATCAAGTGTTTGAGGCTTAACAT
12	ACCTGACCAAGAGTGGTGTGAAGGGTTGTCGTGGCAGTCCTGTATGATATGCA
13	CTAGTGAAATCTTTCGTCAGAGAGGCCTTGCTCGTGCAGAACTGAGTCGCAGG
14	GAGCCCGTCGTTATGCTGGGTGGCCCGTACGGTGCGATACGATGCTTTAGT
15	GCGCGGAGAGATCTTGTCATATACAAGTTCCTTACATAAACATATTGCTCAA
16	CGTGATGCCAAACTGCGGGCAGCGGTGACGCGCCAACCTAAGATAATAACTGGG

S8.15 DNA sequences for octahedron (32-bp edge length)

Seq_ID	Sequences
1	CGAGACTGCATTTCCGAAAGGCATCTCAGGATT
2	AACAAAGTAACCTCCTAAGACTCGACATCTTTTCG
3	GAGTTCCTTTATAACCGCTGCGGCCTAACTTGA
4	ATTGCAGGGCCTGCGGTGTTTACACTCCCGTAC
5	TTACCCTTTGCTTGAAAGTGATTGGGTCTGGTG
6	GTTGGTTCACCTCTGGTTTGATTTATGAATTTA
7	CTAGTATGGAATGGTGCGAAGGGATGGCGACCC
8	TCGAATGGAGCTAGCCAATAGCCTTATGGTCCA
9	CGTCGTATGAGTTTGAGCCTGTTGTGCGCCACG
10	TATCGACGGGCTGAGGGCGAACCCAGCATCAGT
11	ATTCCGGGAAGTTTGCGGGCCTCCCTCCAATTT
12	GCGCTACCGCTTCAGATTACTGGTTCGAACGCA
13	TCTAGCCCGGCTTGGGAACAGAATGCAAGCCGA
14	TGAGGTTTCTCTTCATTCACACTTGTCTAATAG
15	TTACAGAGTGCTGCGGCGTCTGTGGTAATGCCG
16	TTAATGATGTGTAATGTTAGCACGTTAAGCGGC
17	TACTGTACGAGTGTAAGTTCTTCATGGTGCAG
18	CACCGAAGTAGTATCTGCGCCAAACGGTCGTCC
19	AGGCGCGTGTCTAGGGACCCGCTATGTATCTCT
20	AAAGCCACACTCTTGCCCTAGCAGTGGTGTATT

21	TAGTTGTGCGGTTTCATCCAGGACTCCTCCTTGA
22	TAGGACACCCGTATCCACATTCCTGTAGTGAAA
23	CATCGCCGGTATCACATAATACGTGATCCATGC
24	GGAAGCGCCGTTTAGAATCCAAAGACAGGTTAG
25	GTAAACACCGCATGCAGTCTCGTCAAGTTAGG
26	CCCTTCGCACCGGTGAACCAACCACCAGACCC
27	TTTGGATTCTACTCATAACGACGTGGACCATAA
28	GGTTCGCCCTCTTCCATACTAGCGTGGCCGAC
29	TGCTAGGCAAGGCCCGTCGATATGCGTTCGAC
30	TTCTGTTCCCACGCGGTAGCGCAAATTTGGAGG
31	GTGCTAACATTTGCCGGGCTAGACGGCATTACC
32	AAGAACTTTACGTTACTTTGTAAATCCTGAGA
33	GGAATGTGGATTAAAGGAATCCGAAAGATGT
34	AGCGGGTCCCTGGCCCTGCAATTTAAATTCATA
35	CGTATTATGTGGCACTCTGTAACTATTAGACA
36	GTCCTGGATGACACATCATTAAGGACGACCGT
37	CCGCAGCGGTTGCAAAGGGTAAGTACGGGAGT
38	AATCACTTTCAGCTCCATTCGAGGGTCGCCAT
39	GGCTATTGGCTCGGGTGTCTACTAACCTGTC
40	AACAGGCTCAACTTCCCGGAATACTGATGCTG
41	CAGTAATCTGACCGCACAATAAATACACCAC
42	GAGGCCCGCAAGAGAAACCTCATCGGCTTGCA
43	ACAGACGCCGCTCGTACAGTAGCCGCTTAAC
44	TGCCTTTCGACTAGTTCGGTGCTGCACCATG
45	CGAGTCTTAGGTACCGGCGATGTTTCACTACA
46	AATCAAACCAGGTGTGGGCTTTAGAGATACAT
47	AGTGTGAATGAACGGCGCTTCCGCATGGATCA
48	TTGGCGCAGATGACACGCGCCTTCAAGGAGGA

S8.16 DNA sequences for octahedron (42-bp edge length)

Seq_ID	Sequences
1	CTATACGTTATTGGTTTTCCCTAGCAAAGGTAATACAGCCGTGTTTCG
2	CAGCTCGGCGGCTATTTTCCCTACATTCATCTTTGTCTCAAGCACA
3	TAATTGCAGATCGGTTTTAGGTACTCTGACCGGCGCTGTGTCAGGG
4	ACCGCTGGCGTGCTTTTTTGCCGAATCCCGCTAACTCTTTAACCTG
5	GATGTATGTTGGAGTTTTGAAGTACAATGAGAACATTGCCCTCGAT
6	GACGACGTAACCGTTTTTTCAGCGACGGGCGGTCGGACAGAAAGGA
7	CTCTCAGTTATACCTTTTCCATGTCCCGTTACTTAACTTGGTTTTCA
8	ACAGGGTCACGATATTTTCCGCATGGGCCGGAGACGGCCTAAACTG
9	TGAACCAGGATGCGTTTTATGGGTCCGTAGGTCGATCCCACAGGCT
10	CCTTAATTTCCGGGATTTTTCTTATCCTTATTATCTAAGGGAATACGA
11	CCCGGCTCACGCTTTTTTCTCCCATTACACCGCGTATCCGTGATTG
12	AATCATACCAATGCTTTTCCACTCTCGAAACAGCTTGTATCTTAAA

13	GGAAACTCCAGTAATTTTTTCACAAGGCTGACTTAGTCTTGTGCGCAA
14	CGGCGTTAATAGTGTTTTGTAAGCAAGTATGGCTCGTCCTTGGACC
15	ACCGAGGCTTTCAGTTTTGTCTGCACGTCAACTCGACATCAGTCG
16	TTCAGACAGCACGATTTTCATGTTACCCGTACCGGACTGCATCTCT
17	TACTACTGCTTCAATTTTAGCTAGTAGGAGTAATCAATTCACGTTC
18	GTGGGTACATATCGTTTATTAATGCGTCGAAGTGACAGTGCAAC
19	GTAGCGCAGTGTAGTTTTCCCGAGTGTAGTACGAGTCTGTACGCC
20	TGATCGCGGCCAAATTTTGTGCGTAATTTCCGGATGATGAGGATCAC
21	TAGAGCAACCGATGTTTCCAGTCACCGTGGAATGACCTCACACAC
22	GCGTAGTGTGGCTATTTTAATTTGGGCGTCCAGATTTCCCTAGTCATA
23	TTAGTTTGAGCTATTTTGTCTTCCGCTCGCTAGAATAAAGCGAAT
24	TTAGACCAGCAATCTTTTGAATATCAACGCAATACCTGTAGCATGA
25	TACTCCTACTAGCTTAGCCGCCGAGCTGCGAACACGGCTGTA
26	TTACCTTTGCTAGGCGATATGTACCCACGAACGTGAATTGAT
27	CTGGACGCCCAATTCGATCTGCAATTATGTGCTTGAGACAA
28	AGATGAATGTAGGGATAGCTCAAATAATATGACTAGGAAAT
29	TACTAACACTCGGGGACACGCCAGCGGTTCCTTTCTGTCCGA
30	CCGCCCGTCGCTGATTTGGCCGCGATCAGGCGTACAGACTCG
31	AGCGAGCGGAAGACCTGAAAGCCTCGGTGGTCCAAGGACGAG
32	CCATACTTGCTTACGATTGCTGGTCTAAATTCGCTTTATTCT
33	TCCACGGTGACTGGTCGTGCTGTCTGAAGTTGCACTGTCACT
34	TCGACGCATTTAATCTACACTGCGCTACGTGTGTGAGGTCAT
35	AGCGGGATTCCGGCACCAATAACGTATAGCCCTGACACAGCGC
36	CGGTCAGAGTACCTCTCCAACATACATCCAGGTTAAAGAGTT
37	GTAACGGGACATGGACGGTTACGTCGTCATCGAGGGCAATGT
38	TCTCATTGTACTTCTATCGTGACCCGTGTTGAAACCAAGTTAA
39	TTGCGTTGATATTCGCATCCTGGTTCACAGTTTAGGCCGTC
40	TCCGGCCCATGCGGTAGCCACACTACGTCATGCTACAGGTA
41	ATAATAAGGATAAGGGTATAACTGAGAGAGCCTGTGGGATCG
42	ACCTACGGACCATAAGCGTGAGCCGGGTCGTATTCCTTAG
43	CCGAAATTACGCACTCCCGAATTAAGGTTAAGATACAAGC
44	TGTTTCGAGAGTGGCATCGGTTGCTCTAGTGATCCTCATCAT
45	AGTCAGCCTTGTGAGCATTGGTATGATTCAATCACGGATACG
46	CGGTGTAATGGGAGCACTATTAACGCCGTTGCGACAAGACTA
47	GTACGGGTAACATGTTACTGGAGTTTCCCGACTGATGTGCGAG
48	TTGACGTGCAGGACTTGAAGCAGTAGTAAGAGATGCAGTCCG

S8.17 DNA sequences for icosahedron

Seq_ID	Sequences
1	ACGCCTAGAGTTTGATGCACTCAGGGCTCACTGG
2	AACGGGCTCCGTTGCTTGGCGTGGATAAAGATCT
3	TCTTGTTTAAAGTTACCAGCGTCGAGCCGGTCCGGT
4	TTCATGATTAGTTGCCAACCATACAACCTGCATC

5	CAGCACTACCATTGCGTTTCTACGATGCCAACTG
6	TCACGAGCAACTTATACGCCAGATCATGTACAGG
7	ATTTCTGTTCTTTTGATCGTGTATTGCAAAGACG
8	GGTCTGAACTATTTGTATGCAAACCTCCATAGTCT
9	GCTGTGGCGAGTTTAAAGGGCTGCCAATTTAGGC
10	GCTCTTATTCTTTCCTCGAGTGCTCAGAGAGGGT
11	GCAAGGGTGCCTTTATGTGAGAAAGGAACGAAGA
12	CCGAAGCCAAATTTGCGTACAACGGCTACTGCAT
13	ACCGCAGTAATTTTGGCACGGAAGGTCGGGTTTG
14	GAGCATGTGAATTCTCCAGTCGACGTACCTACGG
15	GGCCTCAAACCTTTATAAGATATTCTGATGGGTGG
16	TTCACTGAAGTTTTGAGTCCTACACGGCGTCGGG
17	GGGCGGACGAGTTCATGACACTTACCACCGTGC
18	ACCAAACGCCCTTCCCATTTCGTGTGAAGGCTCGC
19	TCTACTTAGGCTTACGAACCCACGCAGGTACCAT
20	CGTTGTGAGTATTACCCTCACCAAGGATGTACCC
21	GCAAGCCGAGATTCCAACACGTCATGTCGTGTTT
22	GTGGGAAGAGCTTTGTGACTGGGTTATATCTCCA
23	TATCTTGATTATTAAGTCCATTAGAGGTATTCTT
24	ATTCATTAGCATTCTGTAGCAGATCGTCTCCCAG
25	CAAGAGGTGGATTATTGGGCCGCGTATCCCTCTA
26	GTACGGTTAAGTTCTCTTGGAGTGCCTGTGTATC
27	TTCAATTCATCTTACCAGGTCGTCAACGCTCAC
28	AACAAAGTTCTTTGCACACACCTTGTCACTGTGG
29	CCTCTGCAATCTTCTACCGACTGTGCTGCAACGA
30	TAATACCGGTGTTTTAAGTTACGGCGGTCATGCT
31	TCAACCAATCTTTGTCAGCAATAACAACCAGTGG
32	TACGCACACGTTTATAGAGCTAGACCCGAAATAC
33	CTCTCCTCTTATTACAGCGGTGGCTAAACGGACG
34	GCCCTTCAGATTTGCATAAAGTTATCCCAATGCG
35	GCACGAGTTGTTTGTCTTTCAGGGTGTATCTA
36	ATTTATTAAGCTTCTCCGGCAATGCTGTAAGGCC
37	ATAGCAGTACTTTAAGGTACTCCGGGCTTTCAAT
38	GCCCAGCTATATTTACGGAATGAAAGGTGCCGGC
39	CACACATCCGATTAGGACACGAGAAGAAGAGGCT
40	ATGTTATGTTTTTAGGTGTTCCGGGCAACTTATTT
41	CGGAGTTGCGGTTGAAGTAATTCCGAATGTACGA
42	CCCGCGGAGACTTATCTTCTCGAAAGTAAACTC
43	TACGAATTTGGTTGCAGCTACGACGCACCATCCG
44	TAACGATAATGTTATCGCTCCGGTCTTGACCAGA
45	TCCTGAAATATTTACGTATGTATTCTGAAGCATA
46	CTTTACTGAGCTTGCCTATCAGCGCTATTCTCTC
47	GCTGCCTATGCTTTCAACCGTTTCACTAATCGTG

48	AACACTAGTCATTGCGTTCAGCAGTCCTGTGAGA
49	TGTAGGTGGCCTTCGGCCCTATGACAAACTTCTT
50	AAAGAGCCCAATTAGGTTGACAGCCTGATTGCT
51	AAGGGTAATACTTAAGGGCATAACTACTCCTTGT
52	AGAGGCAACACTTCGCGTGCGAGAAACAGGATTC
53	TGCCTGGTGGCTTGCTAACAGAGCGTGGTTATGA
54	AACCAAAGCGTTTGCCGAGGGTCTGGCACTTAGC
55	TGTGCTCTAAATTGGCGGTGATCGACATCAGTGT
56	AAATAGGATCCTTATACTTCTGAATCACTCTGGA
57	AAGGTGACACCTTACCCTAGTACGTTTATTCAAT
58	GTGTCTGCTTGTTGATTATGTAGTTCCGGACGGC
59	AGTGATCCCTTTTGTAACTAGAAGCGGCTCCAT
60	ACTAGATCGCCTTATAATTCTCCCGGTCAAACGA
61	CCACGCCAAGCACTCTAGGCGTTCGTACATTC
62	TCGACGCTGGTCGGAGCCCGTTGAGTTTACTT
63	GTATGGTTGGCCTTAAACAAGACGGATGGTGC
64	CGTAGAAACGCCTAATCATGAATCTGGTCAAG
65	CTGAGTGCATCTGGTAGTGCTGGTATGCTTCG
66	GAAACGGTTGACCGCAACTCCGAAACACGACA
67	TCATAGGGCCGGTCTCCGCGGGTGGAGATATA
68	GTTATGCCCTTCCAAATTCGTAAAGAATACCT
69	GCTCTGTTAGCCATTATCGTTACTGGGAGACG
70	CGATCACCGCCATATTTTCAGGATAGAGGGATA
71	ATCTGGCGTATTTTAGAGCACATAGATAAACA
72	ATACACGATCAGTTGCTCGTGAGGAGGAATAG
73	GTTTGCATACAGCATAGGCAGCGTGAGCGTTG
74	GCAGCCCTTTATAGTTCAGACCTCTCACAGGA
75	AGCACTCGAGGGGCCACCTACATCGTTGCAGC
76	TTTCTGACATAAGAATAAGAGCAGCGAATCAG
77	CGTTGTACGCAGTATTACCCTTCCACTGGTTG
78	CTTCCGTGCCATTTGGCTTCGGAATCCTGTT
79	GTGACTGGAGGCCACCAGGCACGTCCGTTTA
80	GAATATCTTATTTTACATGCTCGCTAAGTGCC
81	TTCAGAAGTATGCTCAGTAAAGGATACACACG
82	CGTACTAGGGTTGACTAGTGTTCCACAGTGAC
83	ACTACATAATCTTGGGCTCTTTAGCATGACCG
84	TTCTAGTTAACGTGTTGCCTCTGTATTTCGGG
85	GGGAGAATTATACGCTTTGGTTTCGCATTGGGA
86	AAGTGTGATGGGGATCCTATTTGGCCTTACAG
87	ACACGAATGGGGGTGTCACCTTATTGAAAGCC
88	CGTGGGTTTCGTCAAGCAGACACGCCGGCACCT
89	TTGGTGAGGGTAAGGGATCACTAGCCTCTTCT
90	TGTAGGACTCAGGCGATCTAGTAAATAAGTTG

91	GGAATTACTTCGCTCTTCCACAGATCTTTAT
92	TCGAGGAAGATTAATCAAGATAACCGACCGGC
93	GTCGTAGCTGCTGCTAATGAATGATGCAGGTT
94	ACCGGAGCGATTCCACCTCTTGCAGTTGGCAT
95	AATACATACGTTCTCGGCTTGCCCAGTGAGCC
96	TGACGTGTTGGAGAACAGAAATCACGATTAGT
97	ACCCAGTCACACTCGCCACAGCAAGAAGTTTG
98	CTAATGGACTTGGCACCTTGCACAAGGAGTA
99	ATCTGCTACAGATTACTGCGGTTTATAACCAC
100	CGCGGCCCAATAGTTTGGAGCCACACTGATGT
101	CCCTGAAGAACCTTAACCGTACCCTGTACATG
102	CGCTGATAGGCGATGAATTGAACGTCTTTGCA
103	ACGACCCGGTGAGAACTTTGTTAGACTATGGA
104	CTGCTGAACGCGATTGCAGAGGGCCTAAATTG
105	ACAGTCGGTAGCACCGGTATTAACCCTCTCTG
106	GCTGTCAACCTAGATTGGTTGATCTTCGTTCC
107	TTATTGCTGACACGTGTGCGTAATGCAGTAGC
108	TCTCGCACGCGTAAGAGGAGAGCAAACCCGAC
109	GCCACCGCTGTATCTGAAGGGCCCGTAGGTAC
110	AGACCCTCGGCACAACCTCGTGCCACCCATCA
111	CACTCCAAGAGACTTCAGTGAATCCAGAGTGA
112	AAGGTGTGTGCCTCGTCCGCCATTGAATAAA
113	CCGTAACCTAAGGGCGTTTGGTGCCCGTCCGA
114	TCTAGCTCTATGCCTAAGTAGAATGGAGCCGC
115	TAACCTTATGCTACTCACAACGTCGTTTGACC
116	CATTGCCGGAGAGTACTGCTATGCACGGTGGT
117	CGGAGTACCTTTATAGCTGGGCGCGAGCCTTC
118	TTCATTCTGATCGGATGTGTGATGGTACCTG
119	TCTCGTGTCTAAACATAACATGGGTACATCC
120	CCCGAACACCTGCTTAATAAATCCCGACGCCG