

## Supporting Information

### **Self-Assembly of Wireframe DNA Nanostructures from Junction Motifs**

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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  $\mu$ M for extended structures and 500 nM for 3D polyhedral structures. A 20  $\mu$ L or 40  $\mu$ 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 MgCl<sub>2</sub> 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 MgCl<sub>2</sub> 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  $\mu$ L drop of 0.5 $\times$ TE buffer (10 mM MgCl<sub>2</sub>) were applied to a freshly cleaved mica surface and then a 5  $\mu$ 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  $\mu$ L 10 mM NiCl<sub>2</sub> 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<sup>-1</sup>) 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 EMAN2<sup>1</sup>. 2D average images of particles were calculated using 2D classification in Relion1.4 or Relion2.0<sup>2</sup>.

### **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 MgCl<sub>2</sub>. 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 MotionCor<sup>3</sup> to reduce image blurring due to beam-induced motion. CTF parameters were calculated by Gctf<sup>4</sup> 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 software<sup>5</sup>.

### **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 ( $X_0$ ).

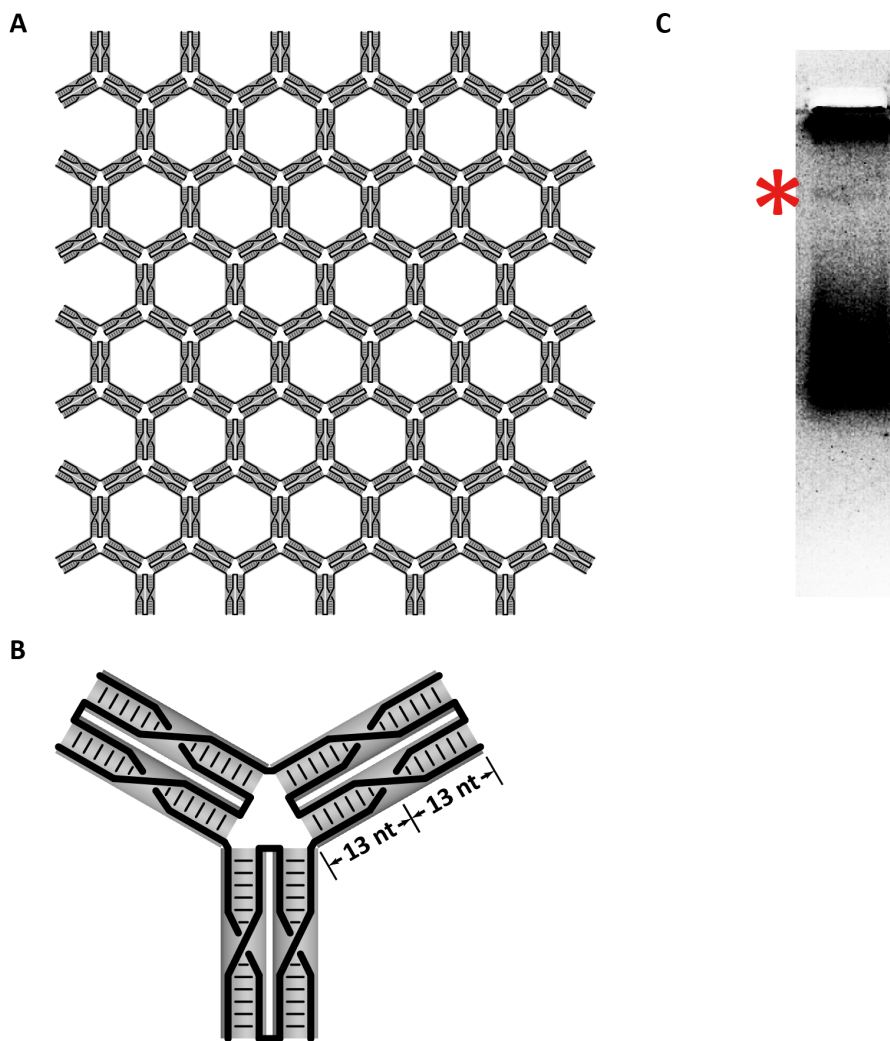


Figure S1. Addressable 2D honeycomb grid ( $Y_0$ ). A. Schematic diagram of the addressable 2D honeycomb grid. B. Strand diagram with strand-level details of a typical Y-shaped (3-arm) motif. C. Native agarose gel electrophoresis result. The red asterisk points at the target band.

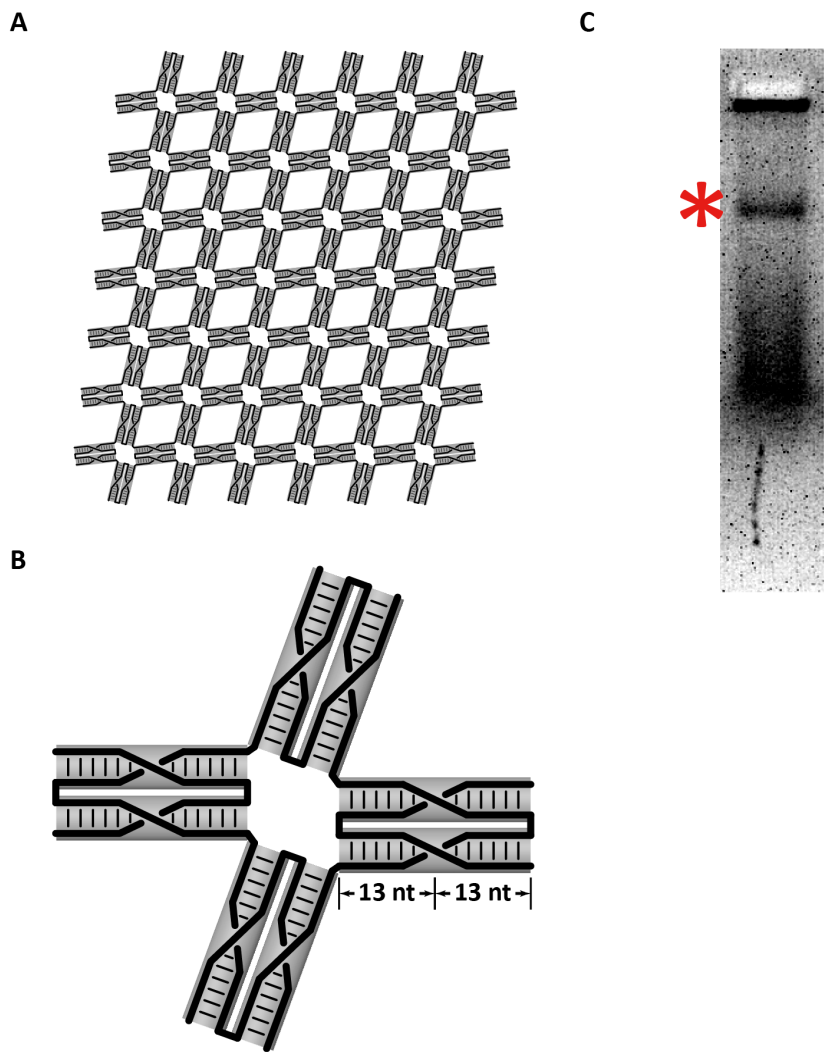


Figure S2. Addressable 2D diamond grid ( $X_0$ ). A. Schematic diagram of the addressable 2D diamond grid. B. Strand diagram with strand-level details of a typical X-shaped (4-arm) motif. C. Native agarose gel electrophoresis result. The red asterisk points at the target band.

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.

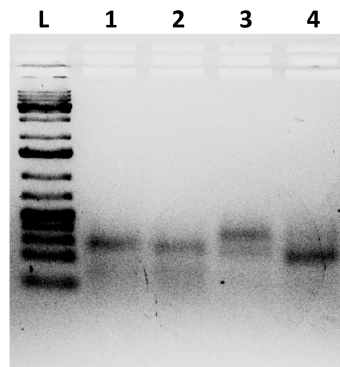


Figure S3. Native agarose gel electrophoresis results of single 'X'- and 'Y'-motifs.

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.

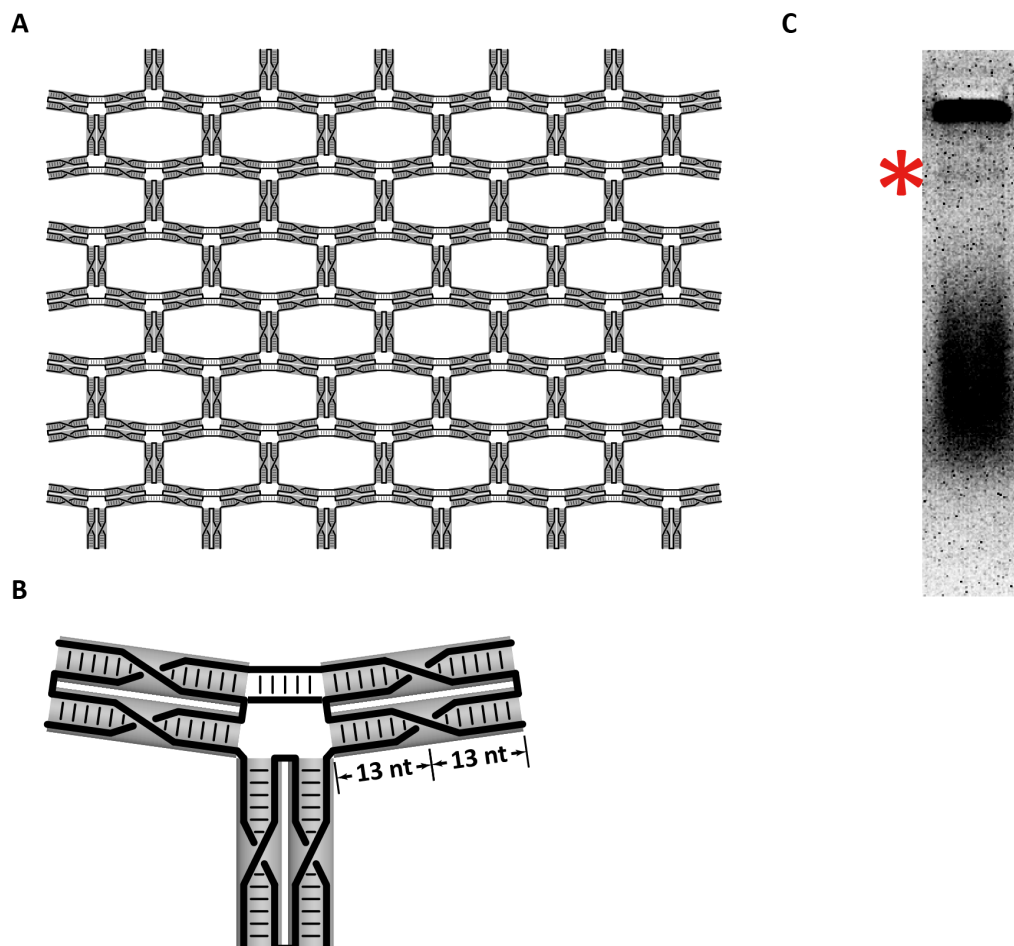


Figure S4. Addressable 2D honeycomb grid with angle control ( $Y_1$ ). A. Schematic diagram of the addressable 2D honeycomb grid with angle control. B. Strand diagram with strand-level details of a typical T-shaped motif. C. Native agarose gel electrophoresis result. The red asterisk points at the target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

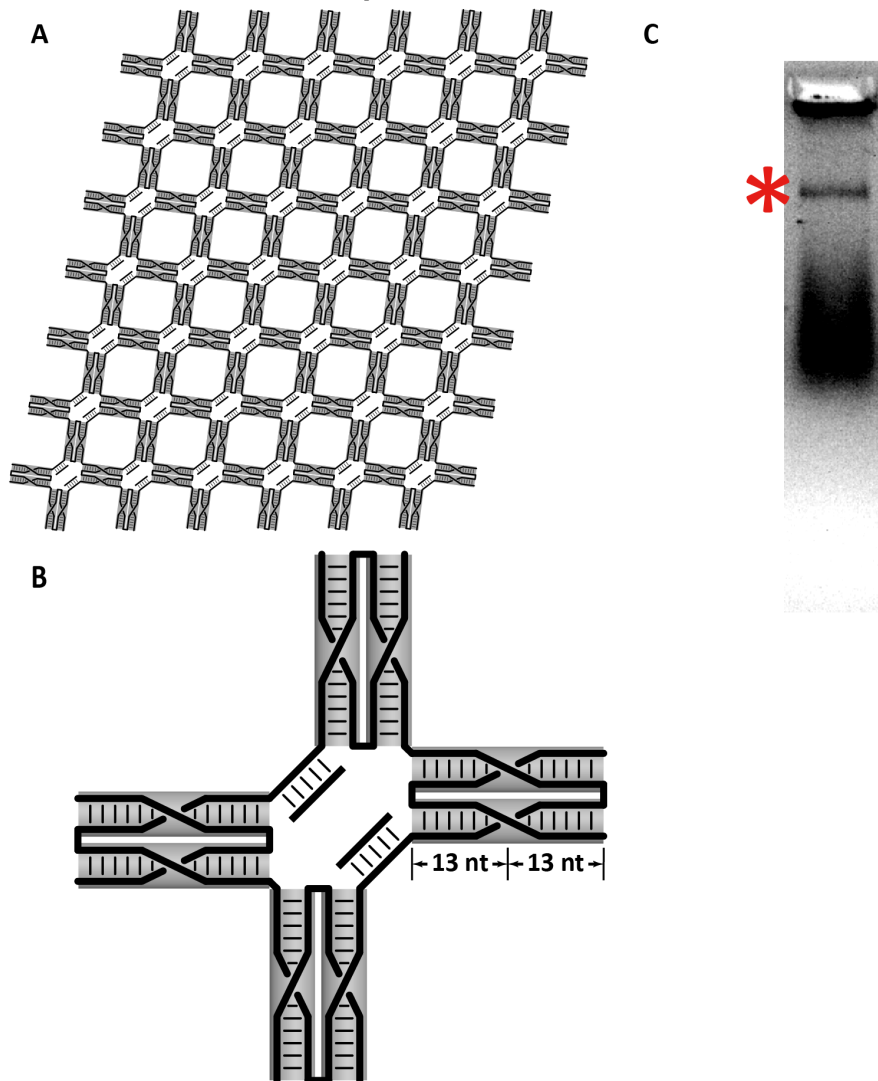


Figure S5. Addressable 2D tetragonal grid with angle control ( $X_1$ ). A. Schematic diagram of the addressable 2D tetragonal grid with angle control. B. Strand diagram with strand-level details of a typical cross-shaped motif. C. Native agarose gel electrophoresis result. The red asterisk points at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

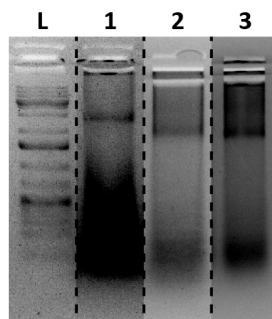


Figure S6. Native agarose gel results of 2D addressable grids constructed from 'X'- or 'Y'- motifs with different numbers of 10-nt single-stranded linkers. Lane L: 1kb DNA ladder; lane 1: 2D grid constructed from 'Y'-motif with single-stranded linker at one of the three crossover points of each vertex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

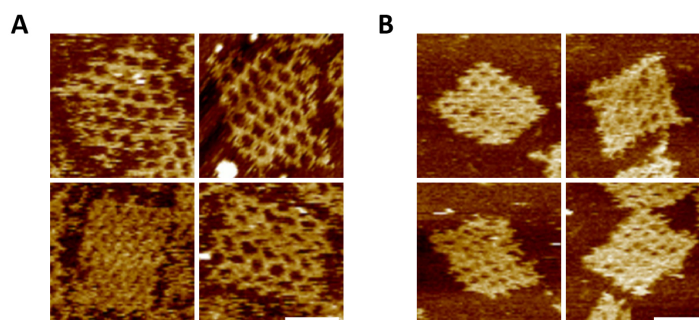


Figure S7. AFM results of 2D addressable grids constructed from ‘X’- or ‘Y’- motifs with 10-nt single-stranded linkers. A. Zoomed-in AFM images of structure  $Y_2$ . B. Zoomed-in AFM images AFM of structure  $X_3$ . Scale bars: 50 nm.

#### S4 Angle measurements based on 2D average of single particles

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

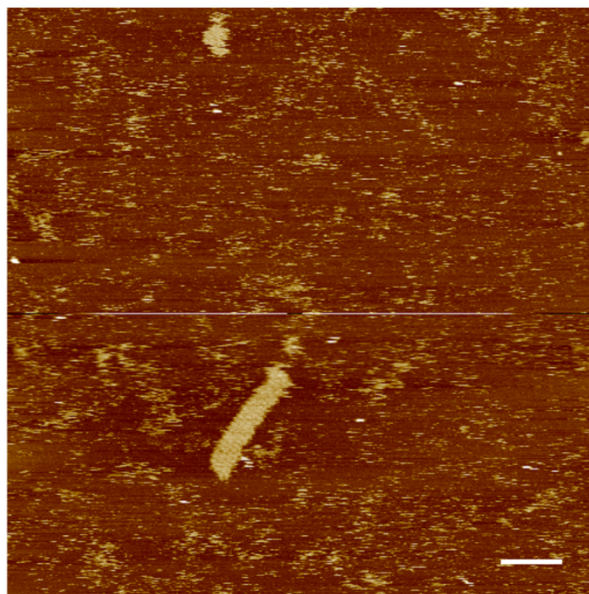


Figure S8. Full size AFM image of extended 1D ribbon from 'X'-motifs. Scale bar: 100 nm.

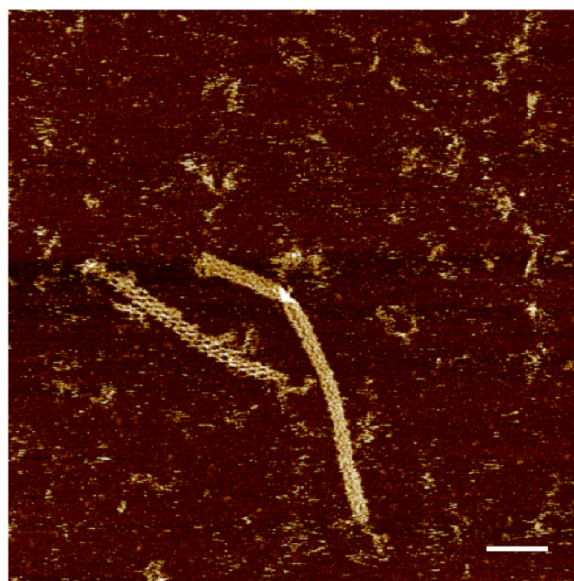


Figure S9. Full size AFM image of extended 1D ribbon from 'Y'-motifs. Scale bar: 100 nm.

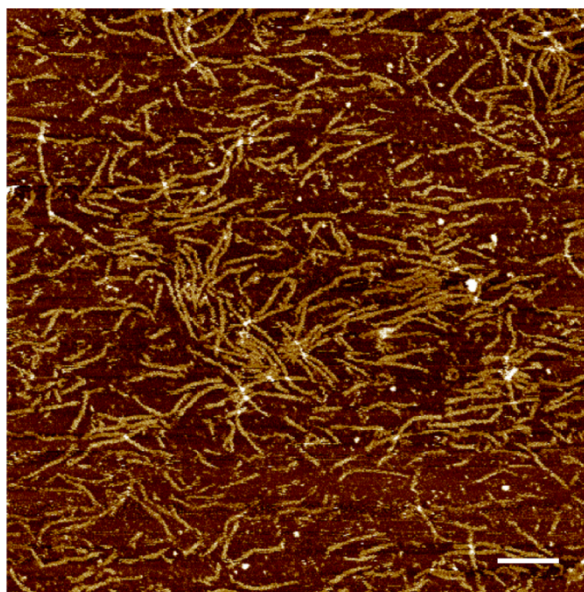


Figure S10. Full size AFM image of 1D extended tube structure from one continuous ‘Y’-motif. Scale bar: 100 nm.

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.

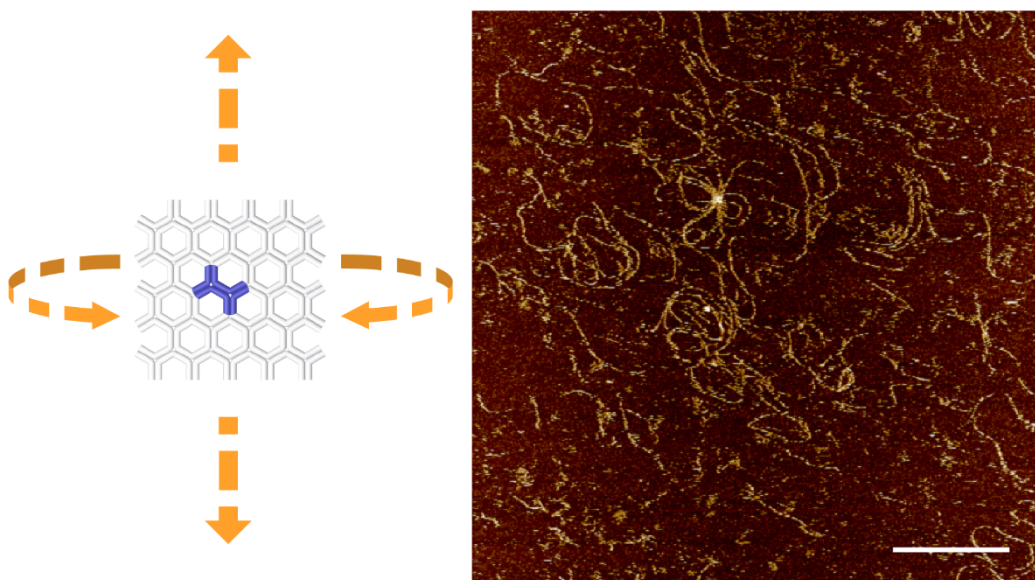


Figure S11. 1D extended tube structure with two different component ‘Y’-motifs. Each component strand in this tube structure is 32-nt long with four 8-nt domains. Left: schematic diagram (repetitive unit cells highlighted in blue); right: the corresponding AFM image (scale bar: 1  $\mu$ m).

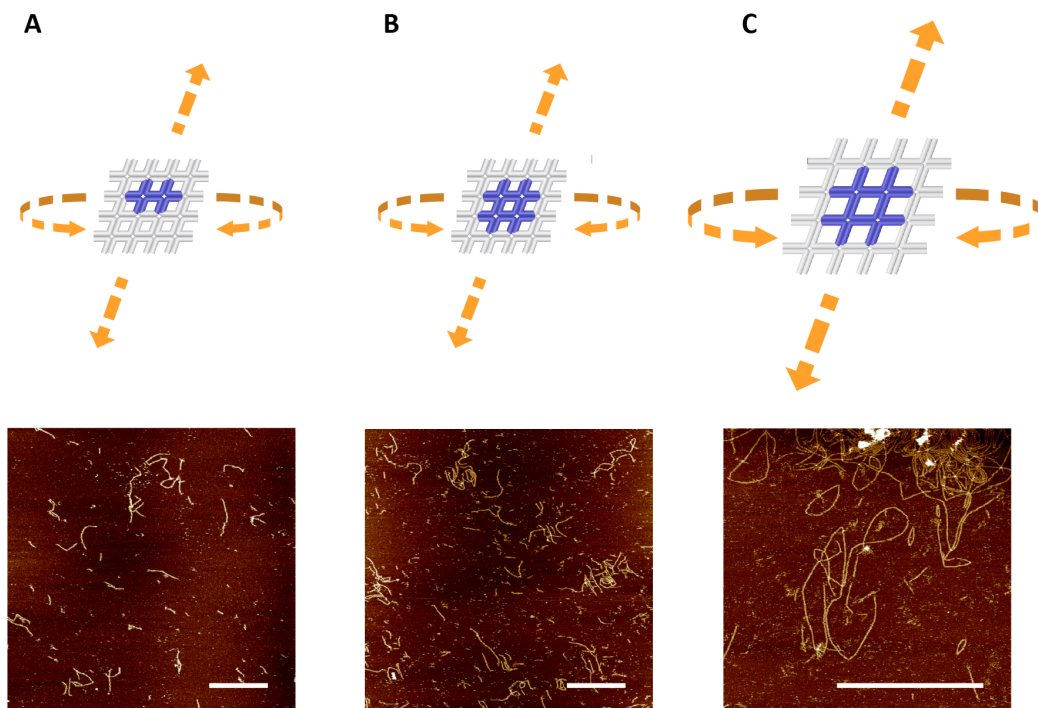


Figure S12. 1D extended tube structures with different component ‘X’-motifs. (A) Tube structure with two different component motifs. Each component strand is 32-nt long with four 8-nt domains. (B) Tube structure with four different component motifs. Each component strand is 32-nt long with four 8-nt 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.

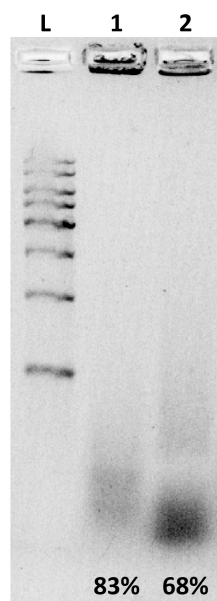


Figure S13. Native agarose gel electrophoresis results of extended structures from repetitive units of different sizes. Lane L: 1kb DNA ladder; lane 1: extended structures with two 'X'-motifs (eight component strands); lane 2: extended structures with four 'X'-motifs (sixteen component strands). Numbers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

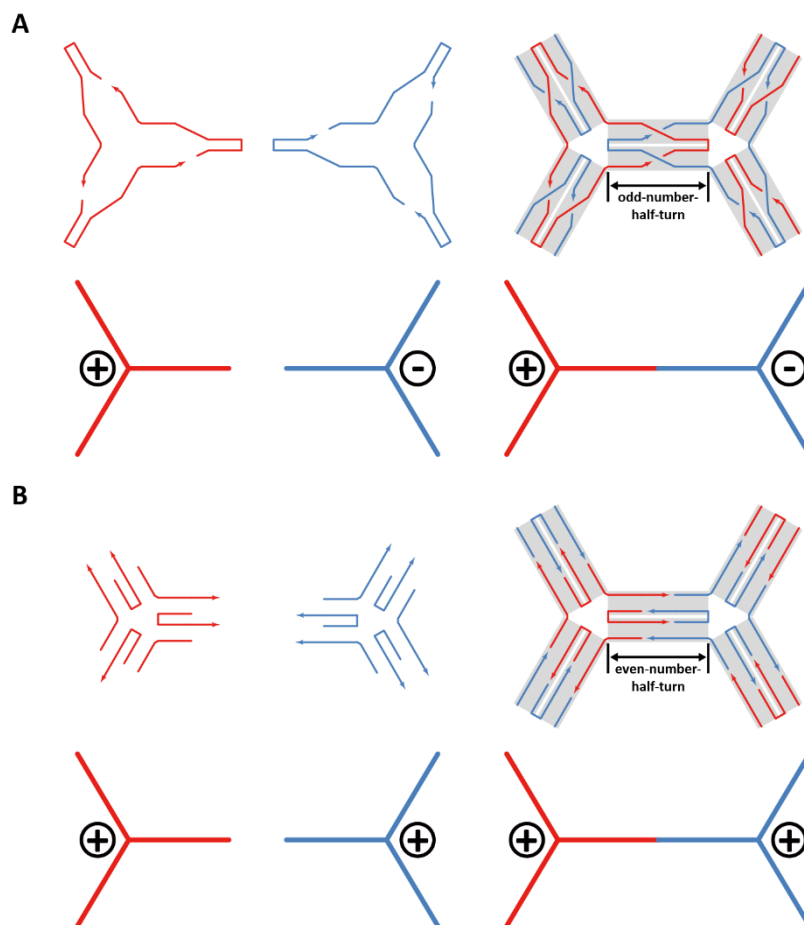


Figure S14. Schematic diagram of an odd-edge and an even-edge and corresponding assembly pattern. (A) Odd-edge and its corresponding “positive-negative” assembly pattern. (B) Even-edge and its corresponding “positive-positive” assembly pattern.

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

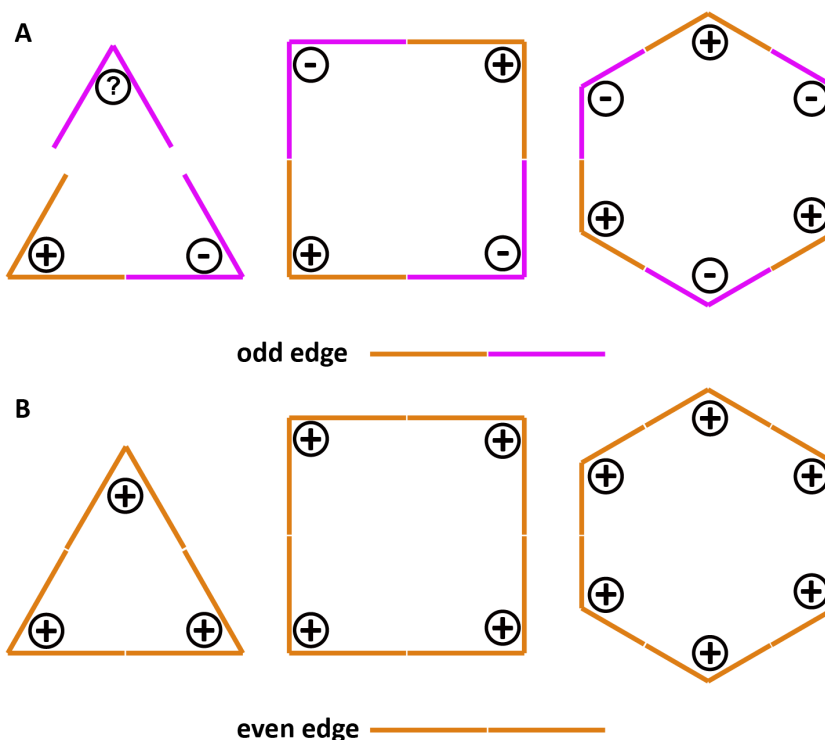


Figure S15. Schematic diagram demonstrating the restriction of odd-edge in cyclization of odd number of units. (A) The odd-edge prohibits the cyclization of odd number of units. (B) The even-edge has no such restriction.

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.

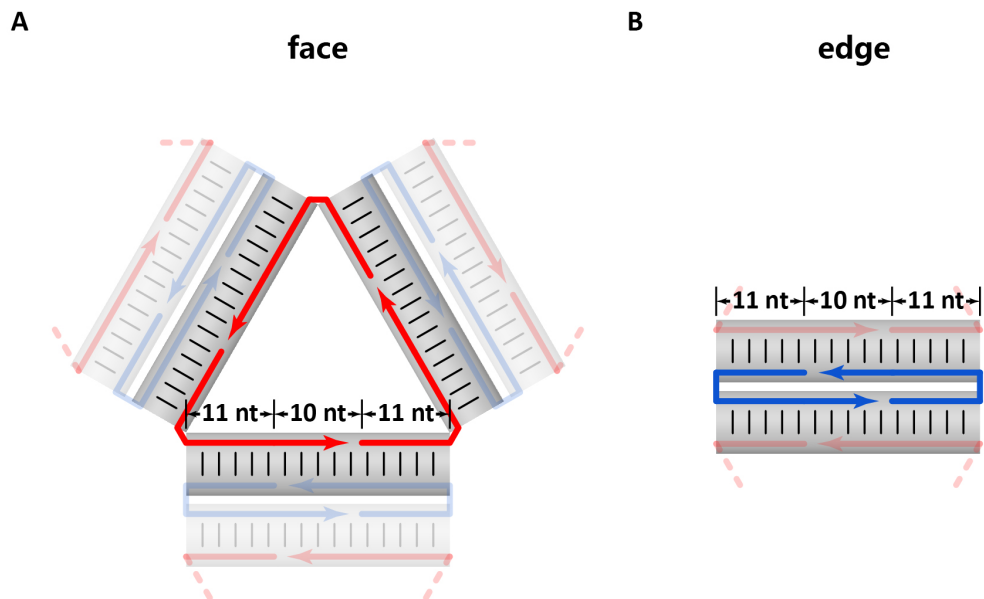


Figure S16. Detailed design of the face and an edge in a typical polyhedron with 32-bp edges. (A) The design of a face of a typical polyhedron. (B) The design of an edge of a typical polyhedron. Note that the strands in the same color (red or blue) correspond to distinct sequences.

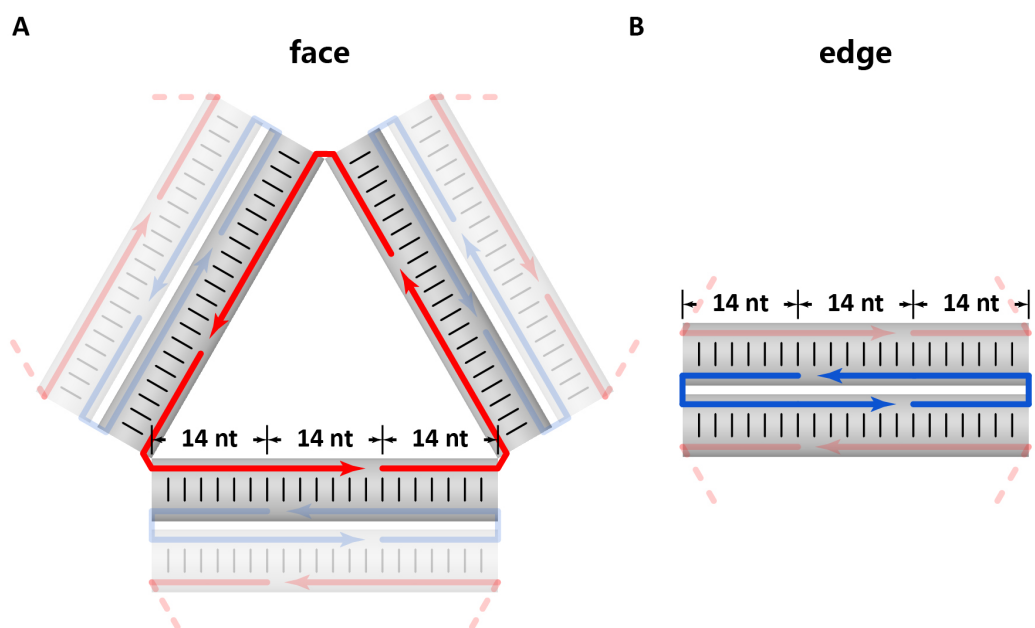


Figure S17. Detailed design of the face and an edge in an octahedron with 42-bp edges. (A) The design of a face of an octahedron with 42-bp edges. (B) The design of an edge of an octahedron with 42-bp edges.

#### 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.



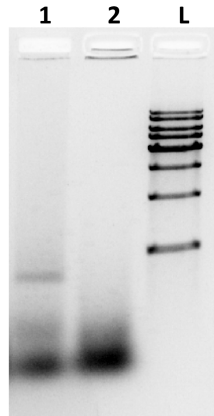
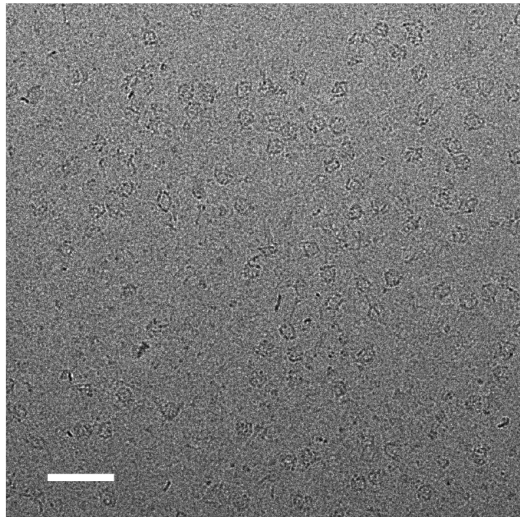


Figure S18. Native agarose gel results of octahedron (32-bp edge length) with and without T2 linkers. Lane 1: octahedron with single-stranded T2 linkers; lane 2: octahedron without any linkers; lane L: 1kb DNA ladder.

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

**A**



**B**

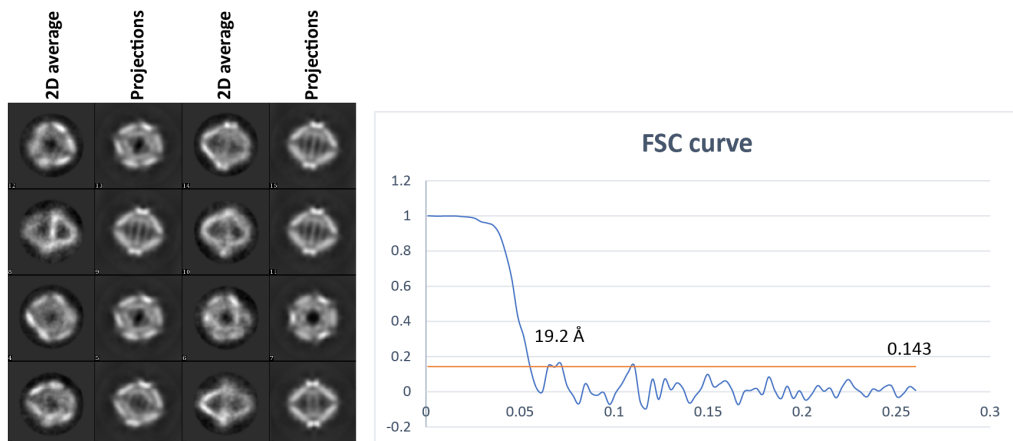


Figure S19. Cryo-EM image and 3D reconstruction of octahedron (32-bp edge length). (A) A representative raw image. Scale bar: 100 nm. (B) Left: Representative 2D averages and corresponding projections from 3D reconstruction.

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

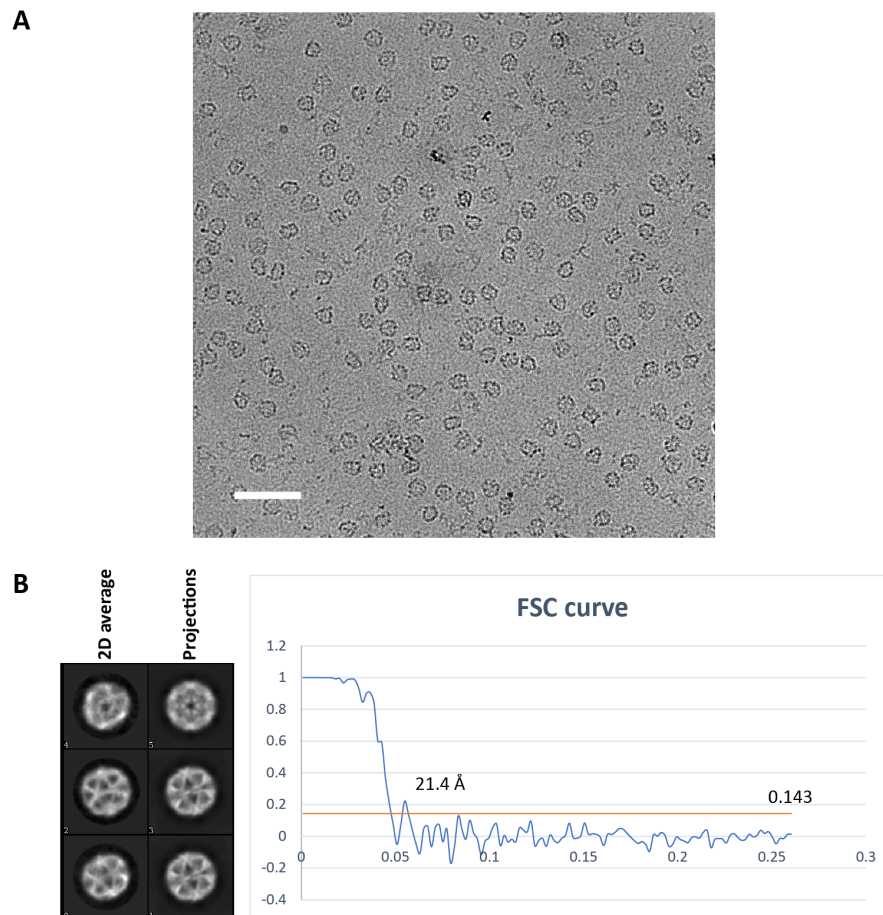


Figure S20. Cryo-EM image and 3D reconstruction of icosahedron. (A) A representative raw image. Scale bar: 100 nm. (B) Left: Representative 2D averages and corresponding projections from 3D reconstruction. Right: Gold-standard FSC plot of the 3D reconstruction.

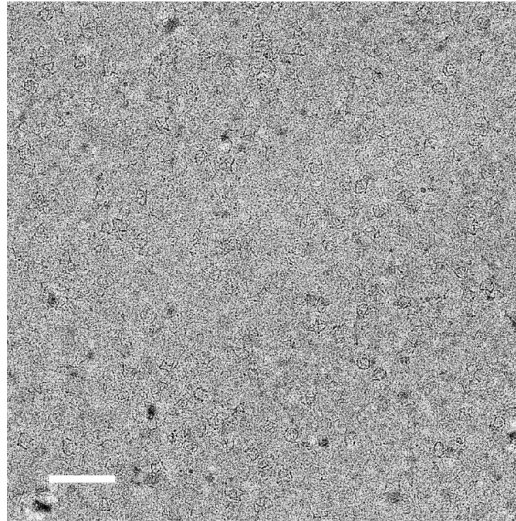
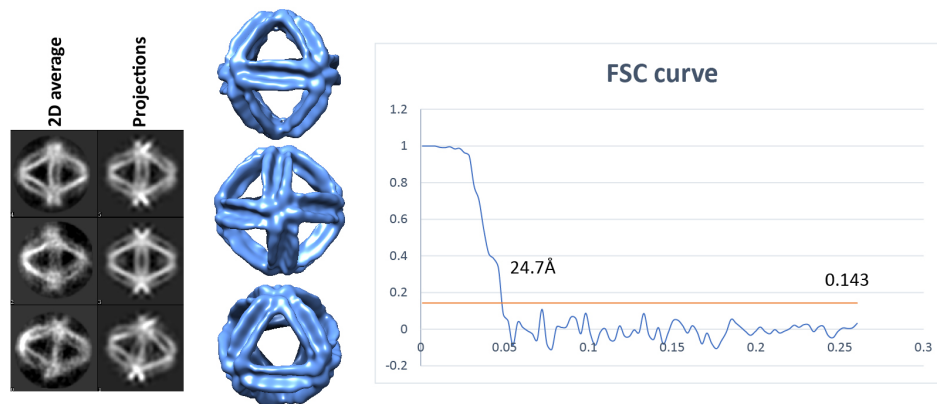
**A****B**

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 <sub>0</sub>	1.2%
Y <sub>1</sub>	1.7%
Y <sub>2</sub>	4.1%
X <sub>0</sub>	4.3%
X <sub>1</sub>	1.9%
X <sub>2</sub>	9.1%
X <sub>3</sub>	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%<sup>6, 7</sup>. 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	TGACTCACGCTGATAGTTTTCGCGGCAACCTCAAGTTTTGCCCCTAACCCCTAGCC
6	CGCTGCTTTATCCTCTCGACTCGTAACGTGTATGGATAGAGGAAGCCCTTGAG
7	CCTTGAGGGATTGCAAACGTACTTACCGTTTTGTGGGAATTTCTATCCATACAC
8	GTTACGAGTCGAGCCGGGACCAGTGCCCTCAAGGGCTTCCTTCTCATATATAAA
9	TAAGGACTGTTCTCTTTCTTTTGTAAAGATGCACCCTCGATCAGTGACGTACGG
10	TTACGGCCGCGTTTAGTCCGCGATTAGGTATTAGTCCGTTTCGCATCCGGAACC
11	CTCTCCTTGGGCATAGAACAGTCCTTATTTATATATGAGATCGAGGGTGCATC
12	TTACAAAAGAAAGTCGTTGGGAGGTTTCGGAGCCTCTTTGTAAACGATCTAAT
13	CGATGCCAGAAGTTTGTGCAACCCCTCCGTGCGGAGTTTGTACAAAGAGGCTCC
14	GAACCTCCCAACGAACGCGGCCGTAAATTAGATCGTTTATAACCCCTTGCCATA
15	TCACTGAGGCTGTGACGTATATCTCTTCTCCGCGGTCTGCTTTGATCTTCTACT
16	TGAGGGTCCAGAATCGAGCGCTCGTCTATTCCGGCCAGGTCAAAAGAATAAG
17	TCAAGCAGCGGATACAGCCTCAGTGATTAGGCAAGGGTTGACGACCCGAGGA
18	AGAGATATACGCTATAGGCTCTCCGGAGATGTCGTGCAAGGCACTACCTGAAG
19	AGTGAATTCAACCCGTTTACCTCGGAACGTACGACGCTTCTTGCACGACATC
20	TCCGGAGAGCCATTTCTGGACCCCTCACTTCAGGTAGTGCTCACAAATCTCCGC
21	TCTACGGCTAATCCTAATGTTTCGGTCCAGATCCCTGGGCTAGCTGGCTACACG
22	AATGTAGATACGTTAGGGTCCGAGGAGTTTACCTAGCGGAGTGCGGGCACA
23	GGTCCAAGTCCCATGATTAGCCGTAGAGCGGAGATTTGTGGCCCAGGATCTGG
24	ACCGAAACATTAGTCAGCCACAGCGTCGAGTTAAAGTACTTGCAGTTAAACG
25	TCTTCTGGGATCACATTCAGCAACCCGTACTCGAGTGCCGTGACTTTAACTCG
26	ACGCTGTGGGCTGACGTATCTACATTCGTTTAACTGCAATGTTGCAATTTTCC
27	GTAGGGTGAGCACTCGATATTGATTTACCGTTATCTTGCCTCGATTGTTCCATT
28	ACTGAGAAAAGGATCGTTAGCGCGGCATCCGAGGCACTCCACGATCGAAGAT
29	AGTGGATGGGCGCTGTGCTCACCCCTACGGAAAATTGCAACGCAAGATAACGGT
30	AAATCAATATCGATAAGACGACTAGCGCCTTGTCGTTTCGCAATTTCACTCCTG
31	TTGGTCTCTTATGCAAGCACCCCTGGATCACGTACTCGTGTGCGAACGACAAGG
32	CGCTAGTCGTCTTTCCCTTTTCTCAGTCAGGAGTCAAATTTGGGCCACAGGCC
33	TTCTTGGCACATCAAGGACTTTTCTACCCCTATAGGCTCTATTAGATTTTAGTCT
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	CCGAGGTCAAACGTGGAACGTGCCACGACCCGTCCGGATTTGCCTACGTC
56	GTTGTGGGCTTGCTAGGGCCGCTCAATTATACGACGTAACTTTAGGCACCGGG
57	CTTGATCGGGCCAATGAAGACCGCGATCCGATCGATATATGTTACGTCGTATA
58	ATTGAGCGGCCCTTACCGTGTCTGGCCCGGTGCCAAAATTGCTATGGATACT
59	CGCCAAGGGTCCAATCGATCGAAACGTCCCAGGACTTATATGTATAACCTCG
60	AGCAGTCGTCTACTTGATCCCAGAAGAAATGGAACAATCGGGCCTCGAGTAC
61	GGGTGCTGAATGTGGAACCCTTGGCGAGTATCCATAGCATAAGTCCCTGGGAC
62	GTTTCGATCGATTTTAACCAAGCCCATCAATTCGAGCAGCGGCTTGTTCCTCT
63	CTTGTCTGCGATGAACAGCCATTGGTTGAGCTTCGTTTTGCTGCTCGAATTG
64	ATGGGCTTGGTTAGTAGACGACTGCTAGAGGAACAAGCCTCAAGGTCACCACT
65	CCCGGTTACTCAACTCGAATACCACTCACGGATGGTTATTCCGTTTGTCTACA
66	TGCCCTGAACCGCTCATAAGAGACCAAAGACTAAAATCTACACGAGTACGTGA
67	TCCAGGGTGCTTGTTTGAGTAACCGGGAGTGGTGACCTTGATAACCATCCGTG
68	AGTGGTATTCGAGTTAAATCTGATGCTTCGCCGTGAGAGCCTAGAGTGTTTTC
69	TTTTTTTTTGCTCTCACGGCGAAGCATCAGATTTAGCGGTTTCAGGGCAGAAAACACTCTAGTTTTTTTT
70	TTTTTTTTTTAGGCGTAGCTACAGAGGTATGAGAGTAATAAAACTCGCCTATAAGGTAGCATTTTTTTTT
71	GAACGTACATTACCAATAAATGTCTGCACCGATATCGCTTCATCGACCCTACC
72	CGCCATAGTTTCGAGCCTGCATAATGAAAGGCGCCGAGGTTAGCTCACGGGTT
73	ACATGAATTCCTTGATATGTGCACAAATGCGCGACGAGCTTCGTGGACCTGGC
74	AATAACCTACGCTGACCAATCAATCCGGTTTTACGGCTTAGTTCCTTCCACT
75	TAACGAGGTGCGTTAAGGAATTCATGTAACCCGTGAGCTAGCTCGTCGCGCAT
76	TTGTGCACATATCTTAGAAGCACCTGTAATATACGGGCCGATTCCCAGTTATG
77	TGAGCGTCCTTCCCTTTGGCCGGTATATCGGTCAGCGAATCGGCCCGTATATT
78	ACAGGTGCTTCTAGCGTAGGGTTATTCATAACTGGGAATTAACGCGGCGCAC
79	ACCCTAGAGAACATTGCAACTAGCGACCAACTCTAGCTATATGTAGTAGGTGA
80	CCCAATGACGGTGTACCTAGCGTATTTTCTCGGCATTTTACTACAGGTACAAC
81	AATCCTGGTGACGTTGTTCTCTAGGGTGTGCGCCGCTTTTAGCTAGAGTTGG
82	TCGCTAGTTGCAATGTGCGTCTACTCGCATTCGATGTTGCCCTGTAACCTCTA
83	CCTAAAGAAGTGTGAACCCTTCCGGGAAGCTATTGCAGGCTGCAACATCGAATG

84	CGAGTAGACGCACCACCGTCATTGGGTAGAAGTTACAGGTAGTGCGCGAAGCC
85	AAATACAGTGTCGTGAGTTCTGATACGGCAAAGATCTTCTGCTTAGTCGATTT
86	AGGATAACTACTCTTGA AAAATCATATTAATTACTCATTATACTCTATATTTAG
87	CATGCAAGGCGCATCGACACTGTATTTGGCTTCGCGCACTGAAGATCTTTGCC
88	GTATCAGAACTCATCACACTCAACTATACCAGGCAGGCGACAGTGGTCTTTGT
89	GGCCAGTCTTAACGACGAAATAACGGTGC GGTC TAATTTCCCTGCCTGGT
90	ATAGTTGAGTGTGGAGTAGTTATCCTACAAAGACCAC TGCTTCGCGATATAG
91	TGTATTGTCATGCTCCTCGAGGCAATAAATCGATGCCCTTATACGCAGTTCAA
92	CTTCCCTCACTATTTGGCCGATCAAGCGAGGTTATACATTATATCGATCGGA
93	TCGCGGTCTTCATTGCATGACAATACACTATATCGCGAGGAGGGCATCGATTT
94	ATTGCCCTCGAGGATCACGGAGTAAATGAGGATAGCGTACCCTCGGAGTAAGTC
95	CCGCCATATCTAACTAAGAA TAGTTATTATTACATTAATGGTACGCTATCCT
96	CATTTACTCCGTGATAGTGAGGGAAGGACTTACTCCGAGTAGCACCGCTCTGT
97	AGTTGGGTTGTAGAGTCTAGACATCGTCAAGATTGTTAGTTGAAACTATAGAA
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99	CCAATGGCTGTTCTCTACAACCCAAC TACAGAGCGGTGCTCTAACAATCTTGA
100	CGATGTCTAGACTTGGGCGAGTTCCTTGCCGGCCGCCATTTTAGAGTGACGAGA
101	TAGCCACAGGCTCGGCCATTACAGCCGGATTTAATGATTAATGGGCGGCCG
102	GCAAGAACTGCCCTCTGGATTGAAAATCTCGTCACTCTATGGGATGTACATGT
103	GACAGGGTTGCCAGGACTCCAGAGGCGGTTGCCATGTTATGCCATATCCCTGC
104	TTTTTTTTTTGGCAACCCTGTACATGTACATCCCTAACATGGCAACCGCTCTGGAGTCTTTTTTTTT
105	TTTTTTTTTCGAAACTATGGCGGGTAGGGTCGATGCCTCGGCGCCTTTCATTATGCAGGCTTTTTTTTT
106	CTACACACCCGAGTGTAATGTACGTTTCGCCAGGTCCACGAAGCGATATCGGTG
107	CAGACATTTATTGTTCAACCC TATTGCTCGAAATGGTGGCCTAGGCGTTCTAG
108	GGTTGGGTTCTGTT CAGACCTCGATGGTCCGATAAGTCCAGGCGTCGATGATA
109	TGCACAAATGGGCCAGCGAATTAATCAACGGCGGGCTTCTTTGGACTTATCGGA
110	CCATCGAGGTC TGCTCGGGTGTGTAGTATCATCGACGCCTTAGAACCATACTG
111	AGCAGGAGTAGCAGGTGGATTCGCTTACCAGCTGCTTTGTTATATGGGTATT
112	ATTCTAACCGCACTGGAAGGACGCTCATCACCTACTACATTTTCGCTGACCGAT
113	ATACCGGCCAAAAGTTGCTACTCCTGCTCAGTATGGTCTACAAAGCAGCTGGT
114	AAGCGAATCCACCTATCGTTGAACGACGGCTACTGCGAGAAACCAATAAGCTA
115	TAGGAGAAGCCAGAGAGAACGACCCTTCATAGATTTACGTTCTCGCAGTAGCC
116	GTCGTTCAACGATGTGCGGTTAGAATTAGCTTATTGGTTTGCAGGGTAGACTA
117	GGGTAACACGAATATGTGCCTCAGTCCATTGATAGCGTTTCGTCGAATCTGCC
118	CCCTTGACGGCATACTTCTTTAGGAAATCGACTAAGCGCCTGCAATAGCT
119	TCCCGAAGGGTTCTATTCGTGTTACCC TAGTCTACCC TGAACGCTATCAATG
120	GACTGAGGCACATTTGTGCGAAAAGGGCGCCGGACTAGACTAATTGAGTTATGT
121	TTAAATAGTATCACAAC TCAATCAACAGCGTGCGATGGTAGTCTAGTCCGGC
122	GCCCTTTTCGCACTGCCGTCCAAGGGACATAACTCAATTTGATCCGCTTTCCC
123	ACGCACGTTTCGTGATATGTAGGCTTGTGTACCC TGTGTATTCCAGGCAGCGTA
124	CCTGAGTTC TAGGTTAAGAACTGGGCC TTGAACTGCGTATATTAGACCGCACC
125	GTTATTTTCGTCGTT CACGAACGTGCGTGGGAAAGCGGATCTACACAGGGTACA
126	CAAGCCTACATATTAAGGCGGACTTGATCCCTAGACTCACCTAACTTTACCTC

127	ACCACGCATCTGGTAAGTCGAAGCTCTACATTGGACCGATGTGAGTC TAGGGA
128	TCAAGTCCGCCCTCCTAGAACTCAGGGAGGTAAAGTTAGTACTAGGTGCGTCA
129	ACATTTTCGCATGACCGCTCTATCGGGCGCGCTCTCCAGTCAC TCCCGTTGCA
130	ATGCTAATTATGCTTAGATATGGGCGGTTCTATAGTTTCATTAATGTAATAAT
131	AACTATTCTTAGTTTCATGCGAAAAATGTTGACGCACCTAGTCTGGAGAGCGCGC
132	CCGATAGAGCGGTTCAATCCGCTAGCGAACAAAGCGAATAGTACGGTAGTGAA
133	CTCCTCTCGCGTCACGACCATAAAATAGCGAACCC TAAAGTTATTCGCTTTGTT
134	CGCTAGCGGATTGGCATAAATTAGCATTTCACTACCGTACTCTCGTGACTCGTA
135	GTGACAGGCAGTATAGGTTTATGCC TTCGGTTCAGCTGGTGCAC TAAGCGTGG
136	AGCCACACTGGTTTAGACCTGTGGCTAGCAGGGATATGGCATCAT TAAATCCG
137	GCTGTAATGGCCGTTACTGCCGTGCTACTACGAGTCACGAGCCAGCTGAACCGA
138	AGGCATAAACCTATGTGCAATTATGTTTGGCTAAGGTCAGTGACCGGCTGCAC
139	TTTTTTTTTCTGACCTTAGCCAAACATAAATTCGACAACCAGTGTGGCTGTGCAGCCGGTCATTTTTTTTT
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141	GTCATCACGGTTATTAAGCTAAAAGCAATGCTCCACCTCTTATGGATTGTCCC
142	GATGACGGACATGTCGTATAC TTTTACCTTATGCATGAGTGACGCC TTTATGCT
143	GCACTACATGCTTGGTTCGGAGTGCAGCTTCTCGTTCACTGCTATCGTTGGCT
144	TCGCCGTTACCCATGGCCATTTGTGCAAATAACCCATATAAGAAGCCCGCCGT
145	TGATTAATTCGCTTAAGCATGTAGTGCAGCATAAGGCGTCGTGAACGAGAAGC
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147	TACAACGACAACAGAGCGTATTTGTATAGGTCAAATCCCGTAGGTGCTTAAGTT
148	TGTCTTGGTCTGCTGGGTAACGGCGAATATTATGCATCTTCAATCCTCGACTT
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150	TGGCTCCAGTCCCTCGGCTTCTCCTAGGCAGATTCGACGCGTAAATCTATGA
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152	ATGAGGCGTAATCTTGACATGTCGT TCTGCCAGGGCAGTCGCC TACGTACTG
153	TCATGGCAGCCTTGCAAGGCC TAAATTCAGACAATCTATCTACTGCCCTGGCAG
154	AACAGACATGTCAGGACTGGGAGCCACAGTACGTAGGCGTGGTCAGCATGGTA
155	TCGCTTACGTGGATCGACGTCAGTTTGAAACGAGGACCGTTCAAGGGACGATT
156	GCACATGTCTATGTTGATACTATTTAATACGCTGCC TGGACCATCGCACGCTG
157	TTGATGTGAGTTGTTCCACGTAAGCGATACCATGCTGACCCGGTCC TCGTTTC
158	AAACTGACGTCGATCACGGACGACCAGAACCCGAGCGACCGTTTACTGTTACA
159	TTTTACACATTCGTCGCAGACAGCGCGTACGGTGC GTTTTGGTGCCTCGGGTT
160	CTGGTCGTCCGTGCATAGACATGTGCTGTAACAGTAAACTGGCCACCTACTGC
161	AGATGGCCCTATTGACTTTAAGGAAACAATAATTTCAACTATGGACCCGGTAA
162	AGCAGCCAATATCTCCAGATGCGTGGTTGCAACGGGAGTGTGGTCCAATGTA
163	GAGCTTCGACTTATAATAGGGCCATCTGCAGTAGGTGGCCGTTGAAATTATTG
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165	GTACGCGAGCTTCCC GCCGTTCTCGACTGCGTGGGCTGGTTCTAGTCAACGAC
166	TGATGGCCCACGAGATATTGGCTGCTCCCTGTATGCAAATTACAGGGCGCAAG
167	AGTTTCCAGATTCAGGGAGCACAAAAGTCTCACTCATGATAATTGTAGTCCCG
168	GAGCGTTGCGCATTGACGCGAGAGGAGCCACGCTTAGTGCC TTTAGGGTTCGC
169	TATTTATGGTCGTTGAATCTGGAACTCTTGCGCCCTGTATCATGAGTGAGAC



170	TTTTGTGCTCCCTTCACATGGAGTCGTTCTATAAAAATATCTCCGGCTTAGGTT
171	TGATGACGTCTGACGTGGTGATCAACATCCCTCGCGCGGTGATATTTTATAGA
172	ACGACTCCATGTGATGCGCAACGCTCAACCTAAGCCGGATTGTCGCCTTTTCC
173	TGCGGACGACGGGCATTGGATCGGGCGATCTTAGCATTATGTTCAACTGTTAC
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177	GCTTTTAGCTTAATTTCTTGGTTGTAAACCTCTGTTCTCCCTAGTGCTGGTAT
178	TTAAAGCAAATCATACTTTATTTCTCGCAAGAGGTGAAGGCTCCTCGGGAGAAC
179	GTCGGCGACCGCATCGTCACCCTTGGTGATAACATGGGTGTCCTCACCTCTT
180	GCGAGAAATAAGTGACACCCAAGGTGGTTCCTCCGAGGATTACCCATGCCCTC
181	GTGGGTGTCGATTTAGTCCGTCGTGACCCATCCGCTTATTAACTCGCGTTCCT
182	GGCCACCTGATTTTTGTTGTCGTTGTAGACGAAACTTGACCGGATTGACCT
183	ATACAATACGCTCTAATCGACACCCACGAGGGCATGGGTAATAAGCGGATGGG
184	TCAGACGGAGCTATAATTTCTCCCTTCCACACAGAACCGTCTGTCACGAATCT
185	TGATGCATTAAGTGTGATCAATCCCTAAAGAGATGCATACGGTTCGTGTG
186	GAAGGGAAGAAATTAATCAGGTGGCCAGATTTCGTGACAGTTTCATAGCAGACT
187	TGCAAGAACCCTGAACGCGCTACAGACCAACCCAGGCGTTGCACCATCAAGGT
188	GTCTTGAATCGATAAGGCTGCCATGAAATCGTCCCTTGAGATAGATTGTCCTG
189	AATTAGGCCCTTGCTCAGGGTCTTGCAAGTCTGCTATGAAACGCCCTGGGTTGG
190	TCTGTAGCGGTTTTTCATGCCAGGGAAGTTCGTTGAATCGTGCAGATTGACAG
191	TCGCTCCCGTTCAGGCACTGCAAGGCTATAAATCCCTCTTCGATTCAACGAAC
192	TTCCCTGGCATGATCGATTCCAGGACCTGTCAATCTGCATGCTCGATCTTTGT
193	CCATATGGTTCACCTCTCAAACAATGTTACCTTGTGAGTCTTCGCTGGGCTGCA
194	TCAGTCGGATCTCTCGAATGTGTAATAATACCGGGTCCATAAACGCACCCTAC
195	GCGCTGTCTGCGATGTGAACCATATGGACAAAGATCGAGCGACTGACAAGGTA
196	ACATTGTTTGAGATGGTGTGACTCTCATTTGCTCCATTTTAAAATCCATGAG
197	ACGCCTAGCTGGTGAGCGCATATCTCGTGTTCGCTGACTAAATGGAGACAAT
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199	CAACCCACCGTGAAGGCACGAGCGTTAATATGCCACCATGTAGTTAAACAAG
200	ACTACTTAGGGTGTGAAGCTCGCGTACCGGGACTACAATTCAGCCCACGCAG
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202	AACGCTCGTGCCTTGGATAGCCACCGCCTTTTGGTGGATGTGCAAAAGCTCGT
203	CAACTACTAAAAGCGCCGTCCGTATAACCATGTATCCTGTCATCCACCAAAAG
204	GCGGTGGCTATCCCACCCTAAGTAGTACGAGCTTTTGCATTTAGTATCTCGCC
205	AACCACCTCCGCCAATATACTTGACCCCTTCGCGACCCTACAATTCGGAGGT
206	TCGGAGACGAGACTTCAGACGTCATCAGTAACAGTTGAACCCGCGGAGGGAT
207	GTTGATCACCACGTGGCGGAGGTGGTTGGCGAGATACTAAGTGGTTCGGAAGG
208	GTCAAGTATATTTGATCCTATAGGCACCTGTAAACTCCCGGTCTACCCAGGAA
209	TTTTTTTTTCGGGAGTTTACAAGTGCCTATAGGATGTCTCGTCTCCGATTCTGGGTAGACTTTTTTTTT
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211	CGAAGACTCAGGCACATTCGAGAGCGTGACTTCATCTGCTCACCGTGAACCC
212	AAAATGTTTCGTCCAGATTTTATGGGACTGTACCGTCTGCTTTTACGTCCGTTT

213	CGAGAACAAGAAAGCCTAGCACAAATTGACTTAATTGTCTTAGGAATAAGTTTC
214	ACGTCCAAGTTTCTTGCGGTCGCCGACAGGAACGCGAGTTACCCATGTTATCA
215	CCAAGGGTGACGATTTTCTTGTCTCGAAACGGACGTAAAAGACAATTAAGTC
216	AATTGTGCTAGGCTTAACTCCGGCAATCATTGCCACGTGGAATAAGGAGTCAC
217	TACGGGATTTCTCCACTGTTTCAGATCCCAGGTATACGATGTCGACGTGGCAATG
218	ATTGCCGGAGTTAGAACTTGGACGTGTGACTCCTTATTTTCGGTCTCTTGTAC
219	CAGTCGAGCTTCTATCGCCTTTGTTCCGCATTGCTCCCATTGGGAGCCTAGGG
220	TAGTCTTCAAGCCTAGTTAATGCATCAACCTTGATGGTGTGCATCTCTTTAG
221	GGATTGATCTGACTAGAAGCTCGACTGGTACAAGAGACCGTGGGAGCAATGCC
222	GAACAAAGGCGATTGGCGGGCCTAGCCTCGTTGTGCGCGTCCACGTCCGCACG
223	GCCCTTTTGACTCACTACCCAGCTCAACAGTCCAAAACATACGCCGACAACGA
224	GGCTAGGCCCGCCGGCTTGAAGACTACGTGCCGACGTGGTGTCTCAGAGACAAC
225	TATTCACCTACCTAGTAACCTTGTTCATCGGATCCCGTCTATCAATTTATCGT
226	GTGCCAAACCCATTTGAACGGGAGCGATGCAGCCCAGCGAAGAGGGATTTATA
227	GCCTTGCAGTGCTTAGGTAAGTGAATAGTTGTCTCTGAGCGACGGGATCCGAT
228	GAACAAGGTTACTTCTGATTTGCCAGAGCTGTAGAGCGCCGGATTGTTTCGCGA
229	CTGCATTCATCGGGCCGCTTAGTAAGTAGCTTCACGTTGGCGCTCTACAGC
230	TCTGGCAAATCAGATGGGTTTGGCACTCGCGAACAATCCTTGGAAAGTCCAATT
231	GCTTCATCACAAGCGGGCGGAAACCTTGGTCAATCAACTTAATAAAATCAGA
232	GATTTAGACTGCGTACCAGCTAGGCGTCTTGTTTAACTACGTCACGCAAGCAC
233	GAGATATGCGTCTCTTGTGATGAAGCAATTGGACTTCCAGTTGATTGACCAA
234	GGTTTCCCGCCCGTGACATCGAAAAGGCACGCGGACACTTTGAACCGGCCTAA
235	AGTGAAAATACCCAACCACGCCCTGTCATTGTGACATCTATAAGTGTCCGCGTG
236	CCTTTTCGATGTCCGCAGTCTAAATCTTAGGCCGGTTCATTGTTTGTGTTGAA
237	AAGATGATTTGTGCTTCTACCACGCAGCCATGTTTAATTCATTGGCACAAA
238	TTCACGCAGAAATTTCTTTTAGTAGTTGACCTCCGAATTGTCAGGATACATGGT
239	TATACGGACGGCGTCACAAATCATCTTTTCAACACAAACATTAACATGGGCT
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241	CGCTAGTATTCCAATCCTTTTCAGTTTCGCCATGTGGATACGGGAGTACTGTCA
242	AACAGCGGAATGCAATTCTGCGTGAATGTATGCAGGACAGTTAGAACGGTCT
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245	TTTTTTTTTGCCTGAGTCTTCGGAACTTATTCCTGCAGATGAAGTCACGCTCTCGAATGTTTTTTTTT
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256	TTTTTTTTTCGGTATACCCGGGAGACCGTTCTAACTGGTTGACTGTCTTATACAGGGTTAATTTTTTTTT
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### S8.2 DNA sequences for $X_0$

Seq_ID	Sequences
1	CCCTTCTCACGGGTAAGACCTCAAACCTTTTCTGAATCGCTGTCTGCAGGGAGA
2	TTACCAACTCTTTTTGTAAGTCCAGTCCGCGAACGTGGTTCCCGCCACATCC
3	CAGCTGATCATCTTGGTAGCCAGCGTTCATGGGAGGATCGCGGTGCTCCTGAC
4	AGTTGTATTCGTCTCTAAACAGGTTCAATTTGGCAGCGGGCCCTACGCGTTAT
5	GACTTGCAGGAACTAACCTTCCCTTAGGCTACTTACTGTACCACGTTCCGCGG
6	ACTGGCAGTTACAAGATGATCAGCTGGGATGTGGCGGGATTGTCAATTAGGGCT
7	GACTCTGCCACAACGCCCGTGTAGTGCAGGATACCACCTTTTGTATCCTCGCGT
8	CAGTAGTAGGAGGTCACCTCACCTGAAAGTGACGCTGGTTGATTGGTTTCCCTC
9	TCAGGGTGAGTGATGAAAATTCGCGTGTCCCTCATGGGCCAAATTCACATCT
10	TTCAATCAAGCTCTCTGGCGTTCCCTTGAGGATGAGACAGTACTGCGTCCCGAA
11	GACTCGCGCTTCTAACGCGGAATATGCTCTGACTCTCCTACATCCAGAGC
12	GTAACCAACTTCCCTCTACTACTGACGCGAGGATACAACCAGCGTCACTT
13	TTTAGGGCCGGTTACAAAAGACGTGTGGATGCGGTGCTAGTACTGTCTCATCCT
14	CAAGGAACGCCAGGGAAGCGGAGTCTTCGGGACGCAGTTAACCGGTCCAAG
15	GTCGCTAGTCGAGTACCAAGATCCCTCTGCCATGCCCTGGTTACTTCTCCGCT
16	TGTAACAACCGCGGTAGTGTCTCGTTCCGTGGATAGACGGCTACATATCGAAGCG
17	GGAACGAGCACTATACGGCTCCTTTAGATAAACGGCGTCTTGTAAACATACA
18	AATGCTGAGGAGGTACAGTGTGTGGACATCGGGCTCCGAGTACAGTCCAAGTC
19	TTATGTCCGTCACTTAGCTCAGGTAAGTACTAGAGGTAGAGTTGCTAGTTCTGCAA
20	CAATAGACTCACGTCCGCGTGTGTTACAAGCGGAGAAGTAGCCGCTATCCAC
21	GCTAAATGCTTGAGAGTAAGTATCCCTATTTTATCGTCTTCTCGGAGCCCGAT
22	GTCCACACACTGTGTGACGGACATAAGACTTGGACTGTATGGAAGTAACGGCC
23	TAGGCACTTTGGGCAATGTGTTACAGCAAGTCAGTTTGCCTACCAGCTGCGAA
24	TAAACAGTGGGACTATTCTTGCCTGCGTGCCGTGCTTGTGTTAGCGCTATAGCC
25	AACGCTGGCTACCGACGAATACAACGTTCAGGAGCACCGTGGGATAGGCACC
26	ACATAAAAGTCCAGCGCATCTACCTATCCGTAACCTATTGAAATAAAAGTGA
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28	ATGTACTTCCCTTTGAAAACAGTTTGGCGAATTAAAGCGACTCGATCCTCCCATG
29	GCCAAACTGTTTCTTTGTGGCAGAGTCAGCCCTAATGACAAAGTGGTATCGCG
30	CACTACACGGGCGTGTGAGTTACCCGGCAGTAAACTATAAGGGTCATTGCAG
31	CTCATCCAATTAATGGTGTCCATCCTTTCGGTCTCCTAATACTTGTCTCGATCC
32	TACGTATCGACCATAAAGGAAGTACATGTGATGACTCTGTGTCGCTTTAATTC
33	TAGTTCGCGCGTTAGTTGGGTAGTACGCTCTGGATGTAGTTATAGTTTACTGC
34	CGGGTAACTCAACTTAATTGGATGAGCTGCAATGACCTTACCCTGTAGGTCA
35	TAACAACCCTAGACAGGAGAAGACCAAAACGGAGTGCACCTTCGATCAACCGGC
36	TGTATAGCATGAGAAGCGTGGAGCGAGTACCGGTAGTTGTGAGAGTCAGAGCA
37	TCGCTCCACGCTTCTCAGACTAGCGACCTTGGACCGAGTTCCAGGCATGGCAG
38	AGGGATCTTGGTATGCCGCTCAACGCCCAACATGAACCTCATAATCTACTTCT
39	AACTTTCAGCCAGTAAGATTTGCCATGCATAAACGTCACCTACCCTTGTACTCC

40	TCCCTTGAGATAGTCTCATGCTATACAGCCGGTTGATCGACAAC TACCGGTAC
41	AGTACCTGAGCTACGTGAGTCTATTGTTGCAGAACTAGCTGAGGTT CATGTTG
42	GGCGTTGAGCGCCTGGCTGAAAGTTAGAAGTAGATTATTAGGAACAGCATCG
43	TTCTTATGTGATTCCACCACCTCGTCATGCGACGAAACTCTTAAACATAGTAGCG
44	AGGCCACCCCTTAATCCCTATCATGATCAGGCTAGGCCGTAACCTCTACCTCT
45	TCATGATAGGGATTCCCAAAGTGCCTAGGCCGTTACTTCCGCAAAC TGACTTG
46	CTGTAACACATTGTCAAGGCCTGCGCGAGGAGGCTCGTGGAACGCTACAGTAA
47	CCTAAACTAAAAGATCTTCACATCGGCCCTCTTCGCCAGTAGGTCGTAGGTCGAG
48	TGACCGAGCCTTCTTAAGGGTGGGCCCTCGCTACTATGTTACCGCCTAGCCTGA
49	ACCTGAGTCAAAGTCACAGAGACTCAGTCAC TTTTATTTTCA TTCAGCCAGCT
50	CTAAGCCGGCCTGTCAACTGCTAACGGCATAATAGCGGTCCC GTCTGTAGGA
51	GGGCAATTCACGTTCCGGGCAGAATCCAGTCCC TTGTGCTTCGTTTAGTCTGA
52	CTTCACGTGTCACTGCAGACATGGGATGTCGCTTCCGACGCCGAGCGCAGTCA
53	AAGGATGGACACCTGGTCGATACGTAGGATCGAGCAAGTTGACCGCTATTATG
54	CCGTTAGCAGTTGACGTGAATTGCCCTCTACAGGACGGTTCC TAAATCCCGC
55	TCGGCTAAATCAAATATAATCGTATTTTAGAGGTCATTC TCGACAATGTTAC
56	CGAATTTTATCCTTTGTACGGTGCGCGCCGTGATCCC ACTTATTAGGAGACCGA
57	CGCGCACCGTACATTTCTAGGGTTGTTATGACCTACACGGTGTGC ACTCCGTTT
58	TGGTCTTCTCCTGTGAATAGGCGCAAGACATCCGAGTATAC CCTGATAACAT
59	CCAGCCCTCTGCTTTCTCAGAGCTACAGTCTTGGTATCTT ATTTCTCTCAATC
60	AATGTTACGCAC TAGGATAAAAATTCGGTAACATTTGTCGCAGTGGGATCACGG
61	CATGGCAAATCTTCTATCTCAAGGAGGAGTACAAGGTTATACTCGGATGTC
62	TTGCCGCCTATT CAGCAGAGGGCTGGATGTTATCAGGGTTCTATGGACTAGCG
63	TGTTTTAAAATGGCGACTTAGATTCGTCACTATGCTTCGTTGGACAGACAATC
64	CCAGAGTCTCAGTGGCTAGGGCACTCGAAGGAATGAGATAGTGACGTTTATG
65	AGTGCCCTAGCCATAATCACATAGGAACGATGCTGTTCC TTAGTTCGTGCGCA
66	TGACGAGTGGTGGTGATTACTTTCTGATCCTGGCTAATTAGTCAGACATAACA
67	CCAGTAAAAGGTCTCTAGGGTGAGATTGCACACAGCAGTGGCTTCTT CACAAT
68	CATTCTGCTCGAGTCTGAGGACTCTGGGATTGTCTGTCCATCTCATTTCTTCG
69	GGCCGATGTGAAGGAAGGCTCGGTCACTCGACCTACGACTAATTAGCCAGGAT
70	CAGGAAAGTAATCGACCTTTTACTGGTGTATGTCTGACTTGCATACACGACGA
71	CTCTGAGAAGCCCCGCGACTGTGTCTGGGCTCCCTTACTGTGCGGAGGGACCAA
72	ATTACTCTTCGTGATAAAATCGTCCC GGGTGGTGGAGTCTCTACTGGCGAAGA
73	GGATTCTGCCCGGGTGACACGTGAAGTCAGACTAAACGATTGAGATAAACTAG
74	AAACTATTTAGACATCTCTGATCATATTAGACATTCGCTTATAATTGACGTAC
75	TCTGTTCGAATACGACAAGTACCCGAGCCATGCCGCACGTTGTCGAGTGGCAG
76	TCTGTGGAATAAATAGGAACTGGATAGCTTTTATACTTGTAGCACAAAGGACT
77	TATCCAGTTCCTATTTGATTTAGCCGAGCGGATTTAGGAGAATGACCTCTAA
78	AATACGATTATATTCGGACTAGACGACCGCAAGGCTATCAAGCCGGCTAAACG
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	AGCCGGAATGCCGAAACAGACTGGCCCCGCGCATTAGTCTGTGGCGTCACGGATT
103	TATTCGACTGGTGCCACTTTTCCGTTTCGGACATCACTTCGTACTGGA AAAAG
104	TTTTGAATACTGATAAACACA ACTAACC ACTAGGACCATCGGGTTATGAGTC
105	TTAGTTGTGTTTATGTTACCCCTTGCACTGGGACAGTAATCACCCCTGTATTCCA
106	GCCAGGGCTGTAATAAGTGCCCAAGGATTTGAACGTCGCTCCACATGGGC
107	AGTCACTGTAGACTCAGACGGTCCGGGCCAGCATACTTCGGGCTTAAGTTCGT
108	GAGTAGCCACATGTTTCAGTATTCAAA ACTTTTCCAGTACGTGGGTCCTAGTGG
109	ATTATCTTTCCAGTTGTC ACTTATAATAACTCCCTGTAGTTACGACGTTCAAAT
110	CCTTGGGCCACTTGTCTACAGT GACTGCCCATGTGGGAGTAGGACCTGTCCAA
111	TGAAGCTTGAGGCACTACAGCAACGTCGAGTATATCGAGTGATGTGTCCTAGC
112	CCTGGTAGTCCACTGCGGAAAATGTCC TAATGTCTATGATGGTTGTCCCGTCCG
113	GACAATTTCCGCATTGAGTTCTATAGGCAGTAACATGGATGCGAGACTCCTAA
114	CACGTCCATTTATTAGTCTGGTACTGTCC TCCCTGAATTGTAAATCAAGCCCT
115	AACGACGATGCTCTATACTGCATTACCATGTAGGCCCTTCTATATCCCAGCT
116	ATTGGCATACTGGTGTGGACTACCAGGGCTAGGACACATCTCATAGACATTAG
117	CAATAGGTCAGTGTTCAA ACTCTGAACACACA ACTGACATCAATTCAGGGAGG
118	ACAGTACCAGACTGAGCATCGTCGTTAGGGCTTGATTTATAAATCGGACTGCT
119	GCTCCGTGCGACGCGGTAATACTGAATTCCTGCCGATGGTACATGTGTTGCTT
120	AGGCAATTAACGGCTTACGTCTGGGCCGGTGGTGTGCGTTTATTCTCAAGTC
121	TTTTTTTTTCCGTTAATTGCCTAAGCAACACATGTCCGACACCACCGGCCACGACGTAAGTTTTTTTTT
122	TCGCCTTCGATAGACAATGTATTCGGGTGGTTCGTGAATTATCGTCCGGTAGG
123	CTTTTAATGTTACTAGTGGGTGCGTCTACATCGTGCAGATTAGCTATGGGAAA
124	TTGAGACCGTCTCGTCCGGTTGGGTGCGCTTAACTTGCCGTAGCAACGCCAGTC
125	GAGTATAGGTCCTTTGATTTTATAAAGACCATTCACTTCTATCGTGTAGAAAA

126	TTTATAAAATCAATCACCAGTCGAATAAATCCGTGACGCCAGTGATGTCCGAA
127	ACGGAAAAGTGGGTGCGCCTGGTTTGTGAAAAGCTGTAAGACTTCGGGAAATC
128	TCAGGACGTACGATTTCTCAACGCTGGTCTCTGAGACTTAGTATTCATAGTG
129	GAGGGTCATATTATAGGACCTATACTCGACTGGCGTTGCTGAAGTGAATGGTC
130	CCCGGACCGTCTGCATGTGGCTACTCACGAACTTAAGCCTCTTACAGCTTTTC
131	ACAAACCAGGGCGTCGTACGTCTGAGATTTCCCGAAGTTCGTACAACGGCTA
132	TTTGCGAGTATGGTCACAGTTAGCAATCCGACTATATAATCGCCAGCACCTAG
133	ACGTGCCGTCACTATCCAAAATTAGAACGCTTGGCCAGTCGAAGTATGCTGG
134	CTAATTTTGATATGCCTCAAGCTTCATTGGACAGGTCCCTCGATATACTCG
135	ACGTTGCTGTAGTTCTAATGTTTCGAGTCCCGGTGCCGCGACACTACTTGAATG
136	TGCTATAACGTGTTGACGCAATGGCACTACTAATCACACCGTACCTGTGGTCT
137	CCCTACGAGCCGCTGATGACGGCACGTCTAGGTGCTGGCGTGGCCAAGCGTT
138	GGTAATGCAGTATCCAGTATGCCAATAGCTCGGGATATATTCGCGGCACCGGG
139	ACTCGAACATTAGACACGTTATAGCACATTCAAGTAGTGTCGCGGGTCTGTGAT
140	CTCAAACGCCGGCCAAGACCGACCGTGCCGTTTGGGTCTTTTGATGATCGTG
141	AAGATGCTGCGACCCGAACTTTATAGCAATACAGCTGATTGAAGGGCTACAT
142	CTATAAAGTTTCGGTCTGCGCACGGAGCAGCAGTCCGATTTCCATCGGCAGGAA
143	TTCAGTATTACCGTCTGCGTTCCTAGCGAAAAGACCTGAGGTGACAGTGCCTAC
144	AAGGCTCTCTAGCTGGTGGCCGTACCACTGAGTTGTACTCAGAATCCGAAGGA
145	TGGGTCATCCACGTGTCGACGATCTTCACGATCAATCAAATCAGCTGTATTG
146	TTTTTTTTCTCAGGTCTTTTCGCTAGGAACGCGGCTAGAGAGCCTTGTAGGCACTGTCAATTTTTTTTT
147	ACATTATCCCTCGTGAGACGGTCTCAATTTCCCATAGCTACGGCAAGTTAAGC
148	GCACCCAACCGACTCTGCGAATGGGTCTGCGCACGCCCTGCCTGGACTAAAC
149	TGAAATATACCTCTGCCTTGCCCTCCCGGTTTGCCCTATAGCCACGGGAGCAA
150	AGCCACCAAATTGTTCTTATCGGTGTTGTGTAATTTATTTTACGGGACTAAT
151	CAGCGTTGAGGAATAATATGACCCTCCACTATGAATACTTAGGGCGTGCGCAG
152	GACCCATTGCGAGGAGGTATATTTTCAGTTTAGTCCAGGCTTAAATTCCTGAG
153	CGAGTTTTATGATCTATAGCAGCTTCGTCAGATCCAACATCGTAATAGCGCAA
154	GAAATTACAAGTGCCTCGGGCCAGGATGTGCTAGGAAAGTAAGTCTCAGAGAC
155	TCCTGGCCCCGACGTCCATACTCGCAAATAGCCGTTGTACGTTATATAGTCGGA
156	TTGCTAACTGTGATTGTGTTATATGCCGATAATAGTAGCCATAGGTACTTCAC
157	ACTAGGCGACGGGTTGAGGGCTGTGAATCAGGGCCTAGCACGGTATTAGCATT
158	ACTTAGTGGGTCTTCACTTGTAATTTCTTTCGCGCTATTACGCTTTCCTAGCACA
159	GTGCCATTGCGTCTGCGGCTCGTAGGGAGACCACAGGTACTGGCTACTATTATC
160	GGCATATAACACACCCGTCGCTAGTGTGAAGTACCTATTCGCCATCGGAAG
161	GATCACTGACACCCGACGCTCTCTCTGATTAGCGTGCCTTCGAACACAGATCG
162	CTTTTACTCAAGGCATGGGACATCTTAGCCTATTATTAGTGGTGTGATTAGTA
163	AAGATGTCCCATGTGCCGGCTTTGAGATCACGACCGCGGAGACCCAAACGGC
164	ACGGTCGGTCTTGTGACCTAGGCGGGACCACCCCTCGCATATATCTTTCTTCAT
165	TCGGCATACTCAGTTAACGGTGACGGAACAGGGCGGTGACGTGTACAGCATAA
166	CCCTCGTCATCAGTCCCTGAGTAAAAGCGATCTGTGTTTCGCTAATAATAGGCT
167	TGGTACGGCCACCCGTGGATGACCCATCCTTCGGATTCTTTATGCGAGGGTGG
168	TCCCGCTAGGTCTGAGTATGCCGAATGAAGAAAGATATCAGAGCCGACCTC

169	ACCTCACTAGATTCAGCCGTTACGGAAACGAGATTCTGATTCTGAAGTGGACT
170	GGGAGCATCTGGGTAACGGATTCAAAGATTCCTCGATGCTGAGTACAACCTCAG
171	TTTTTTTTTCCCAGATGCTCCCAGTCCACTTCAGAGCATCGAGGAATCTTTGAATCCGTTATTTTTTTTT
172	TTTTTTTTTATAGGGCAAACCGGGAAGGCAAGGCCAATTTGGTGGCTTTGCTCCCGTGGCTTTTTTTTT
173	TTTTTTTTTATCATAAACTCGCTCAGGGAATTTATGTTGGATCTGACGAAGCTGCTATAGTTTTTTTT
174	TTTTTTTTTGCTAGGCCCTGATTACAGCCCTCAAGACCCACTAAGTAATGCTAATACCGTTTTTTTT
175	TTTTTTTTTGGTGTGTCAGTGATCCTTCCGATGGCAGACGCACGCTAATCAGAGAGAGCGTCGTTTTTTTT
176	TTTTTTTTTGTCACCGCCCTGTTCCGTACCGTTACTGATGACGAGGGTTATGCTGTACACTTTTTTTTT
177	TTTTTTTTTAATCTAGTGAGGTGAGGTCGGCTCTGTCAGAATCTCGTTTCCGTAACGGCTGTTTTTTTT
178	TTTTTTTTTGCGATTTCAGAAAAGGTTTGAGGTCTTAAAGAGTTGGTAATCTCCCTGCGACATTTTTTTTT
179	TTTTTTTTTTTTCTGCAAGTCGAGGAAACCAATCCAGTAAGTAGCCTAAGGGAAGGTTAGTTTTTTTT
180	TTTTTTTTTGGCCCATGAGGGACACGCAATTTTCGAGCTTGATTGAAAGATGTAGAATTTTTTTTTTTTT
181	TTTTTTTTTAACCGGCCCTAAACGCTTCGATATGTCTAGCACCCGCATCCACACGCTTTGTTTTTTTT
182	TTTTTTTTTGGACGCCGTTTATCTAAAGGAGCCGCTCCTCCTCAGCATTTGTATGTTAAACAATTTTTTTTT
183	TTTTTTTTTCAAGCATTTAGCGGCTATAGCGCTAAGACGATAAAAATAGGGATACTTACTCTTTTTTTTT
184	TTTTTTTTTAAATAAATTACACAACACCGATAAGACGAGGGATAATGTATTAGTCCCCTCATTTTTTTTT
185	TTTTTTTTTGTAACATTAAGCCTACCCGACGATTCTGCACGATGTAGACGCACCCACTATTTTTTTTT
186	TTTTTTTTTGATGGGCTGTATCCTAGATCGTCGAGCGGTATAATTACGATTGATAGTTTCGTTTTTTTT
187	TTTTTTTTTGTCTAAATAGTTTCTAGTTTATCTCAGACGAATGTCTAATATGATCAGAGATTTTTTTTT
188	TTTTTTTTTCGTGCGAAGCGACATCCCATGTCTGCCTTTGACTCAGGTTGACTGCGCTCGGTTTTTTTT
189	TTTTTTTTTGGACTTTTATGTGGTGCCTATCCGCATAGGTTACGGATAGGTAGATCGCGCTTTTTTTTT
190	TTTTTTTTTCCCGCTGCCAAATTGAACCTGTTTAGCCCGTGAGAAGGGATAACCGCTAGGGTTTTTTTT
191	TTTTTTTTTGTCCCACTGTTTATTCGCAGCTGGTACAACAAGCACGGCAGCGCAAGGAATATTTTTTTTT
192	TTTTTTTTTCCACGAGCCTCCTCGCGCAGGCCTTGTCTTTAGTTTAGGTTACTGTAGCGTTTTTTTTTTTT
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	GTTACGAGTCGAGCCGGGACCAGTGCCTCAAGGGCTTCCTCCTCCATCCTCTCATATATAAA
9	TAAGGACTGTTCTCTTTCTTTTGTAAAGATGCACCCTCGATCAGTGACGTACGG
10	TTACGGCCGCGTTTAGTCCGCGATTAGGTATTAGTCCGTTCCGATCCGGAACC
11	CTCTCCTTGGGCATAGAACAGTCCTTATTTATATATGAGATCGAGGGTGCATC
12	TTACAAAAGAAAGTCCTCCATCCCGTTGGGAGGTTCCGGAGCCTCTTTGTTAAACGATCTAAT
13	CGATGCCAGAAGTTTGTGCAACCCCTCCGTGCGGAGTTTGTACAAAGAGGCTCC
14	GAACCTCCAACGAACGCGGCCGTAAATTAGATCGTTTATCCTCCATCCAACCTTGCCCTAA

15	TCACTGAGGCTGTGACGTATATCTCTTCCTCGGGTCGTCTTGATCTTCTCACT
16	TGAGGGTCCAGAATCGAGCGCCTCGTCTATTCCGGCCAGGTCAAAGAATAAG
17	TCAAGCAGCGGATACAGCCTCAGTGATTAGGCAAGGGTTGACGACCCGAGGA
18	AGAGATATACGTCTCCTCCATCCATGGCTCTCCGGAGATGTGCTGCAAGGCACTACCTGAAG
19	AGTGAATTCAACCCGTTTGACCTCGGAACGTACGACGCTTCTTGCACGACATC
20	TCCGGAGAGCCATTTCTGGACCCTCACTTCAGGTAGTGCTCCTCCATCCCACAAATCTCCGC
21	TCTACGGCTAATCCTAATGTTTCGGTCCAGATCCTGGGCTAGCTGGCTACACG
22	AATGTAGATACGTTAGGGTCCGAGGAGTTTACCTAGCGCGAGTGCGGGCACA
23	GGTCCAAGTCCCATGATTAGCCGTAGAGCGGAGATTTGTGGCCAGGATCTGG
24	ACCGAAACATTAGTCTCCATCCCAGCCACAGCGTCGAGTTAAAGTACTTGCAGTTAAACG
25	TCTTCTGGGATCACATTCAGCAACCCGTACTCGAGTGCCTGTACTTTAACTCG
26	ACGCTGTGGGCTGACGTATCTACATTCGTTTAACTGCAATCCTCCATCCGTTGCAATTTTCC
27	GTAGGGTGAGCACTCGATATTGATTTACCGTTATCTTGCTCGATTGTTCCATT
28	ACTGAGAAAAGGATCGTTAGCGCGCGCATCCGAGGCACCTCCACGATCGAAGAT
29	AGTGGATGGGCGCTGTGCTCACCCACGAAAATTGCAACGCAAGATAACGGT
30	AAATCAATATCGATCCTCCATCCAAGACGACTAGCGCCTTGTCGTTGCAATTTCACTCCTG
31	TTGGTCTCTTATGCAAGCACCCGGATCACGTACTCGTGTGCGAACGACAAGG
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
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64	ATGGGCTTGGTTAGTAGACGACTGCTAGAGGAACAAGCCTCCTCCATCCCAAGGTCACCACT
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68	AGTGGTATTTCGAGTCTCCATCCTAAATCTGATGCTTCGCCGTGAGAGCCTAGAGTGTTC
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72	CGCCATAGTTTCGAGCCTGCATAATGAAAGGCGCCGAGGTCCTCCATCCTAGCTCACGGGT
73	ACATGAATTCCTTGATATGTGCACAAATGCGCGACGAGCTTCGTGGACCTGGC
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75	TAACGAGGTGCGTTAAGGAATTCATGTAACCCGTGAGCTAGCTCGTCGCGCAT
76	TTGTGCACATATCTCCTCCATCCTAGAAGCACCTGTAATATACGGGCCGATTCCCAGTTATG
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78	ACAGGTGCTTCTAGCGTAGGGTTATTATAACTGGGAATTCCTCCATCCAAACGCGGCGCAC
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81	AATCCTGGTGACGTTGTTCTCTAGGGTGTGCGCCGCTTTTAGCTAGAGTTGG
82	TCGCTAGTTGCAATCCTCCATCCGTGCGTCTACTCGCATTCGATGTTGCCCTGTAACCTCTA
83	CCTAAAGAAGTGTGAACCTTCGGGAAGCTATTGCAGGCTGCAACATCGAATG
84	CGAGTAGACGCACCACCGTCATTGGGTAGAAGTTACAGGTCCTCCATCCAGTGCGCGAAGCC
85	AAATACAGTGTGCTGAGTCTGATACGGCAAAGATCTTCTGCTTAGTCGATTT
86	AGGATAACTACTCTTGAAAATCATATTAATTACTCATTATACTCTATATTTAG
87	CATGCAAGGCGCATCGACACTGTATTTGGCTTCGCGCACTGAAGATCTTTGCC
88	GTATCAGAACTCATCCTCCATCCCACACTCAACTATAACCAGGCAGGCGACAGTGGTCTTTGT
89	GGCCAGTTCCTAACGACGAAATAACGGTGCAGTCTAATTTTCGCTGCCTGGT
90	ATAGTTGAGTGTGGAGTAGTTATCCTACAAAGACCACTGTCTCCATCCCCTCGCGATATAG
91	TGTATTGTCATGCTCCTCGAGGCAATAAATCGATGCCCTTATACGCAGTTCAA
92	CTCCCTCACTATTTGGCCGATCAAGCGAGGTTATACATTATATCGATCGGA
93	TCGCGGCTTCATTGCATGACAATACACTATATCGCGAGGAGGGCATCGATTT
94	ATTGCCTCGAGGATCCTCCATCCCACGGAGTAAATGAGGATAGCGTACCCTCGGAGTAAGTC
95	CCGCCATATCTAACTAAGAATAGTTATTATTACATTAATGGTACGCTATCCT
96	CATTTACTCCGTGATAGTGAGGGAAGGACTTACTCCGAGTCTCCATCCAGCACCGCTCTGT
97	AGTTGGGTTGTAGAGTCTAGACATCGTCAAGATTGTTAGTTGAAACTATAGAA
98	TTTCAATCCAGATATCGCAGAACAAGTGTAGACAAACGGAAACGAAGCTCAA
99	CCAATGGCTGTTCTCTACAACCAACTACAGAGCGGTGCTCTAACAATCTTGA
100	CGATGTCTAGACTTCTCCATCCGGGCAGTTCTTGGCCGCGCCCATTTTAGAGTGACGAGA

101	TAGCCACAGGTCTCGGCCATTACAGCCGATTAAATGATTAAATGGGCGGCCG
102	GCAAGAACTGCCCTCTGGATTGAAAATCTCGTCACTCTATCCTCCATCCGGGATGTACATGT
103	GACAGGGTTGCCAGGACTCCAGAGGCGGTTGCCATGTTATGCCATATCCCTGC
104	TTTTTTTTTTGGCAACCCTGTACATGTACATCCCTAACATGGCAACCCTCTGGAGTCCTTTTTTTT
105	TTTTTTTTTCGAAACTATGGCGGGTAGGGTCGATGCCTCGGCGCCTTTCATTATGCAGGCTTTTTTTTT
106	CTACACACCCGAGTGAATGTACGTTCCGACAGGTCACGAAGCGATATCGGTG
107	CAGACATTTATTGTTCAACCCATTGCTCGAAATGGTGGCTTAGGCGTTCTAG
108	GGTTGGGTTCTGTTCCCTCCATCCCAGACCTCGATGGTCCGATAAGTCCAGGCGTCGATGATA
109	TGCACAATGGGCCAGCGAATTAATCAACGGCGGGCTTCTTTGGACTTATCGGA
110	CCATCGAGGTCTGCTCGGGTGTGTAGTATCATCGACGCCTCCTCCATCCTAGAACCATACTG
111	AGCAGGAGTAGCAGGTGGATTTCGCTTACCAGCTGCTTTGTTATATGGGTTATT
112	ATTCTAACCGCACTGGAAGGACGTCATCACCTACTACATTTTCGTCGACCGAT
113	ATACCGGCCAAAGTTGCTACTCCTGCTCAGTATGGTCTACAAAGCAGCTGGT
114	AAGCGAATCCACCTCCTCCATCCATCGTTGAACGACGGCTACTGCGAGAAAACCAATAAGCTA
115	TAGGAGAAGCCAGAGAGAACGACCCCTCATAGATTTACGTTCTCGCAGTAGCC
116	GTCGTTCAACGATGTGCGGTTAGAATTAGCTTATTGGTTTCTCCATCCGCAGGGTAGACTA
117	GGGTAACACGAATATGTGCTCAGTCCATTGATAGCGTTTCGTCGAATCTGCC
118	CCCTTGGACGGCATAACACTTCTTTAGGAAATCGACTAAGCGCCTGCAATAGCT
119	TCCCGAAGGGTCTATTTCGTGTTACCTAGTCTACCTGCAACGCTATCAATG
120	GACTGAGGCACATTCCTCCATCCGTGCGAAAAGGGCGCCGGACTAGACTAATTGAGTTATGT
121	TTAAATAGTATCACAACTCACATCAACAGCGTGGGATGGTAGTCTAGTCCGGC
122	GCCCTTTTCGCACTGCCGTCCAAGGGACATAACTCAATTTCTCCATCCGATCCGCTTTCCC
123	ACGCACGTTTCGTGATATGTAGGCTTGTGTACCCTGTGTATTCCAGGCAGCGTA
124	CCTGAGTTCAGGTTAAGAATGGGCCTTGAACGCGTATATTAGACCGCACC
125	GTTATTTTCGTCGTTACGAACGTGCGTGGGAAAGCGGATCTACACAGGGTACA
126	CAAGCCTACATATTCCTCCATCCAAGGCGGACTTGATCCCTAGACTCACCTAACTTTACCTC
127	ACCACGCATCTGGTAAGTCGAAGCTCTACATTGGACCGATGTGAGTCTAGGGA
128	TCAAGTCCGCCTTCCTAGAACTCAGGGAGGTAAGTTAGTCCCTCCATCCACTAGGTGCGTCA
129	ACATTTTCGCATGACCGCTCTATCGGGCGCGCTCTCCAGTCACTCCCCTTGCA
130	ATGCTAATTATGCTTAGATATGGGCGGTTCTATAGTTTCATTAATGTAATAAT
131	AACTATTCCTAGTTCATGCGAAAATGTTGACGCACCTAGTCTGGAGAGCGCGC
132	CCGATAGAGCGGTTCCCTCCATCCCAATCCGCTAGCGAACAAAGCGAATAGTACGGTAGTGAA
133	CTCCTCTCGCGTCACGACCATAAATAGCGAACCCCTAAAGTTATTTCGCTTTGTT
134	CGCTAGCGGATTGGCATAATTAGCATTTCACTACCGTACTCCTCCATCCCTCGTACTCGTA
135	GTGACAGGCAGTATAGGTTTATGCC'TTCGGTTCAGCTGGTGCACCTAAGCGTGG
136	AGCCACACTGGTTTAGACCTGTGGCTAGCAGGGATATGGCATCATTAATCCG
137	GCTGTAATGGCCGTTACTGCCGTGCTACTACGAGTCACGAGCCAGCTGAACCGA
138	AGGCATAAACCTATCCTCCATCCGTGCAATTATGTTTGGCTAAGGTCAGTGACCGGCTGCAC
139	TTTTTTTTTCTGACCTTAGCCAAACATAATTGACAACAGTGTGGCTGTGCAGCCGGTCATTTTTTTTT
140	TTTTTTTTTGCCACCATTTTCGAGCAATAGGGTTGAACAGAACCAACCCTAGAACGCCTAGTTTTTTTT
141	GTCATCACGGTTATTAAGCTAAAAGCAATGCTCCACCTCTTATGGATTGTCCC
142	GATGACGGACATGTCGTATACTTTTACCTTATGCATGAGTCTCCATCCGACGCCTTATGCT
143	GCACTACATGCTTGGTTCGAGTGCAGCTTCTCGTTCCTGCTATCGTTGGCT

144	TCGCCGTTACCCATGGCCATTGTGCAAATAACCCATATAAGAAGCCCGCCGT
145	TGATTAATTCGCTTAAGCATGTAGTGCAGCATAAGGCGTCGTGAACGAGAAGC
146	TGCACTCGGAACCTCCTCCATCCGCAGACCAAGACAAACTTAAGCACCTAGATGCATAATAT
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	TTTTGTGCTCCCTTCCATCCCACATGGAGTGCCTTCTATAAAATATCTCCGGCTTAGGTT
171	TGATGACGCTGACGTGGTGATCAACATCCCTCGCGGGTGATATTTTATAGA
172	ACGACTCCATGTGATGCGCAACGCTCAACCTAAGCCGGATCCTCCATCCTGTGCGCTTTTCC
173	TGCGGACGACGGGCATTGGATCGGGCGATCTTAGCATTATGTTCAACTGTTAC
174	TTTTTTTTTCCCCTCGTCCGCAGGAAAAGGCGACATAATGCTAAGATCGCCCATCCAATGTTTTTTTT
175	TTTTTTTTTTCATGTCCGTCATCGGGACAATCCATACTCATGCATAAGGTAAAAGTATACGATTTTTTTTT
176	CACCTTGGGTGCTTAAACCGTGATGACAGCCAACGATAGCGAGGTGGAGCATT
177	GCTTTTAGCTTAATTTCTTGGTTGTAAACCTCTGTTCTCCCTAGTGCTGGTAT
178	TTAAAGCAAATCATCCTCCATCCAATTTATTCTCGCAAGAGGTGAAGGCTCCTCGGGAGAAC
179	GTCGGCGACCGCATCGTCACCCCTGGTGATAACATGGGTTGCCTTCACCTCTT
180	GCGAGAATAAAGTGACACCCAAGGTGGTTCTCCCAGGATCCTCCATCCTACCCATGCCCTC
181	GTGGTGTCGATTTAGCTCCGTCTGACCCATCCGTTATTAACTCGCGTTTCT
182	GGCCACCTGATTTTTGTTGTGCTTGTAGACGAAACTTGACCGGGATTTGACCT
183	ATACAATACGCTCTAATCGACACCCACGAGGGCATGGGTAATAAGCGGATGGG
184	TCAGACGGAGCTATCCTCCATCCAATTTCCCTTCCACACAGAACCGTCTGTCACGAATCT
185	TGATGCATTAACGTGCAGATCAATCCCTAAAGAGATGCATACGGTTCTGTGTG
186	GAAGGGAAGAATTAATCAGGTGGCCAGATTTCGTGACAGTCTCCATCCTTCATAGCAGACT

187	TGCAAGAACCCTGAACGCGCTACAGACCAACCAGGCGTTGCACCATCAAGGT
188	GTCCCTGGAATCGATAAGGCTGCCATGAAATCGTCCCTTGAGATAGATTGTCTG
189	AATTAGGCCTTGCTCAGGGTCTTGCAAGTCTGCTATGAAACGCCTGGGTGG
190	TCTGTAGCGCGTTTTCTCCATCCTCATGCCAGGGAAGTTTCGTTGAATCGTGCAGATTGACAG
191	TCGCTCCCGTTCAGGCAC TGCAAGGCTATAAATCCCTCTTCGATTCAACGAAC
192	TTCCCTGGCATGATCGATTCCAGGACCTGTCAATCTGCATCCTCCATCCGCTCGATCTTGT
193	CCATATGGTTCAC TCTCAAACAATGTTACCTTGT CAGTCTTCGCTGGGCTGCA
194	TCAGTCGGATCTCTCGAATGTG TAAAATTACCGGGTCCATAAACGCACCGTAC
195	GCGCTGTCTGCGATGTGAACCATATGGACAAAGATCGAGCGACTGACAAGGTA
196	ACATTGTTTGAGATCCTCCATCCGGTGCTGACTCTCATTGTCTCCATTTTAAAATCCATGAG
197	ACGCCTAGCTGGTGAGCGCATATCTCGTGCTTGCGTGACTAAATGGAGACAAT
198	GAGAGTCAGCACCGAGATCCGACTGACTCATGGATTTTATCCTCCATCCGATTATATCCGGT
199	CAACCCACCGTGAAGGCAGGAGCGTTAATATTGCCACCATGTAGTTAAACAAG
200	ACTACTTAGGGTGTGAAGCTCGCGTACCGGGACTACAATTCCAGCCCACGCAG
201	TCGAGAACGGCGGTTACGGTGGGTTGACCGGATATAATCTGGTGGCAATATT
202	AACGCTCGTGCTTCTCCATCCGGATAGCCACCGCCTTTTGGTGGATGTGCAAAAGCTCGT
203	CAACTACTAAAAGCGCGTCCGTATAACCATGTATCCTGT CATCCACCAAAG
204	GCGGTGGCTATCCCACCCTAAGTAGTACGAGCTTTTGCATCCTCCATCCTTAGTATCTCGCC
205	AACCACCTCCGCCAATATACTTGACCTTCGCGACCAC TACAATTCCGGAGGT
206	TCGGAGACGAGACTTCAGACGTCATCAGTAACAGTTGAACCCGCGGAGGGAT
207	GTTGATCACCACGTGGCGGAGGTGGTTGGCGAGATACTAAGTGGTCCGGAAGG
208	GTCAAGTATATTGTCTCCATCCATCCTATAGGCACTTGTA AACTCCC GGCTACCCAGGAA
209	TTTTTTTTTCGGGAGTTTACAAGTGCCTATAGGATGTCTCGTCTCCGATTCTTGGGTAGACTTTTTTTTT
210	TTTTTTTTTGAGAACAGAGGTTTACAACCAAGAATGATTTGCTTTAAATACCAGCACTAGTTTTTTTT
211	CGAAGACTCAGGCACATTCGAGAGCGTGACTTCATCTGCTCACC GTGGAACCC
212	AAAATGTTTCGTCCAGATTTTATGGGACTGTACCGTCTGCTCCTCCATCCTTTACGTCCGTTT
213	CGAGAACAAGAAAGCCTAGCACAATTGACTTAATTGTCTTAGGAATAAGTTTC
214	ACGTCCAAGTTTCTTGCGGTGCGCGACAGGAACGCGAGTTACCCATGTTATCA
215	CCAAGGTGACGATTTTCTTGTTC TCGAAACGGACGTAAAAGACAATTAAGTC
216	AATTGTGCTAGGCTCCTCCATCCTAACTCCGGCAATCATTGCCACGTCGAATAAGGAGTCAC
217	TACGGGATCTCCACTGTT CAGATCCCAGGTATACGATGTCGACGTGGCAATG
218	ATTGCCGGAGTTAGAACTTGACGCTGTGACTCCTTATTTCTCCATCCC GGCTCTTGTAC
219	CAGTCGAGCTTCTATCGCCTTTGTTCCGCATTGCTCCATTGGGAGCCTAGGG
220	TAGTCTTCAAGCCTAGTTAATGCATCAACCTTGATGGTGTGCATCTCTTTAG
221	GGATTGATCTGACTAGAAGCTCGACTGGTACAAGAGACCGTGGGAGCAATGCG
222	GAACAAAGGCGATTCTCCATCCGGCGGGCCTAGCCTCGTTGTGCGGCTCCACGTCGGCACG
223	GCCTTTTGACTCAC TACCAGCTCAACAGTCCAAAACATACGCCGACAACGA
224	GGCTAGGCCCGCCGGCTTGAAGACTACGTGCCGACGTGGTCTCCATCCGCTCAGAGACAAC
225	TATTCACTTACCTAGTAACCTTGTT CATCGGATCCCGTCTATCAATTTATCGT
226	GTGCCAAACCCATTTGAACGGGAGCGATGCAGCCCAGCGAAGAGGGATTTATA
227	GCCTTGCAGTGCTTAGGTAAGTGAATAGTTGTCTCTGAGCGACGGGATCCGAT
228	GAACAAGGTTACTTCTCCATCCCTGATTTGCCAGAGCTGTAGAGCGCCGGATTGTTCCGCGA
229	CTGCATTCATCGGGCCGCGTCTAGTAAGTAGCTTACGTTGGCGCTCTACAGC

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	TTTTTTTTTGCCTGAGTCTTCGAAACTTATCCTGCAGATGAAGTCACGCTCTCGAATGTTTTTTTTT
246	TTTTTTTTTGGAGAATCCCGTACCCTAGGCTCCCACATCGTATACCTGGGATCTGAACAGTTTTTTTTT
247	TTTTTTTTTGGAGTCAAAAGGGCACGATAAAATTGATTGTTTTGGACTGTTGAGCTGGGTAGTTTTTTTTT
248	TTTTTTTTTCCGATGAATGCAGTCTGATTTTATTAACGTGAAGCTACTTACTAGACGCGCTTTTTTTTTT
249	TTTTTTTTTGGGTATTTCACTTTTGTGCCAATGATAGATGTCACAATGCAGAGGCGTGGTTTTTTTTT
250	TTTTTTTTTAGGAGGCCTTTTCTTGAGCTGTTACATCAGCGTGAGTCAAGGATTTGTTGATTTTTTTTTT
251	TTTTTTTTTAACGGACTAATACCTAATCGCGGACTTGCCCAAGGAGAGGGTCCGGATGCGTTTTTTTTT
252	TTTTTTTTTCTGGCCGGAATAGACGAGGCGCTCGTTCGCGCTGCTTGACTTATTCTTTTGATTTTTTTTTT
253	TTTTTTTTTGGCTAGGTGAAACTCCTCGGACCCTTGGGACTTGGACCTGTGCCCGCACTCTTTTTTTTTT
254	TTTTTTTTTGGAGTGCCTCGGATGCGCGCGCTAACGGCGCCATCCACTATCTTCGATCGTGTTTTTTTTTT
255	TTTTTTTTTGGAAATACTAGCGCACGCGAGTATGGGTATCCACATGGCGAACTGAAAGGATTTTTTTTTT
256	TTTTTTTTTCGGTATACCCGGGAGACCGTTCTAACTGGTTGACTGTCTATACAGGGTTAATTTTTTTTTT
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  $\mu$ 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	GAGATAAGCCCTATGGGAACGCTCAGGCGGGAATCACATTCCTCCATCCGCAAAACTTGAGG
3	TTCGCCGCAAACGGATAAAGCAGCGGGCTAGGGTTAGGTTCCGATTCAGCAC
4	GCACTGGTCCCGTTGTAAACAGCTCAAGAAAAGGCCTCCTTCAAACAAATCCT
5	TGACTCACGCTGATAGTTTGC GGCAACCTCAAGTTTTGCCCTAACCTAGCC
6	CGCTGCTTTATCCTCCTCCATCCCTCGACTCGTAACGTGTATGGATAGAGGAAGCCCTGAG
7	CCTTGAGGGATTGCAAACGTACTTACC GTTTGTGGGAATTTCTATCCATACAC
8	GTTACGAGTCGAGCCGGGACCAGTGCCTCAAGGGCTTCCTCCTCCATCCTCTCATATATAAA

9	TAAGGACTGTTCTCTTTCTTTTGTAAAGATGCACCCCTCGATCAGTGACGTACGG
10	TTACGGCCGCGTTTAGTCCGCGATTAGGTATTAGTCCGTTTCGCATCCGGAACC
11	CTCTCCTTGGGCATAGAACAGTCCCTATTTATATATGAGATCGAGGGTGCATC
12	TTACAAAAGAAAGTCTCCATCCCCTGGGAGGTTTCGGAGCCTCTTTGTAAACGATCTAAT
13	CGATGCCAGAAGTTTGTGCAACCCCTCCGTGCGGAGTTTGTACAAAGAGGCTCC
14	GAACCTCCCAACGAACGCGGCCGTAAATTAGATCGTTTATCCTCCATCCAACCCCTGCCTAA
15	TCACTGAGGCTGTGACGTATATCTCTTCCCTCGGGTTCGTCTTGATCTTCTCACT
16	TGAGGGTCCAGAATCGAGCGCCTCGTCTATTCCGGCCAGGTCAAAGAATAAG
17	TCAAGCAGCGGATACAGCCTCAGTGATTAGGCAAGGGTTGACGACCCGAGGA
18	AGAGATATACGTCTCCTCCATCCATGGCTCTCCGGAGATGTTCGTGCAAGGCACTACCTGAAG
19	AGTGAATTCAACCCGTTTGACCTCGGAACGTACGACGCTTCTTGACAGCATC
20	TCCGGAGAGCCATTTCTGGACCCCTCACTTACAGGTAGTGCTCCTCCATCCCACAAATCTCCGC
21	TCTACGGCTAATCCTAATGTTTTCGGTCCAGATCCTGGGCTAGCTGGCTACACG
22	AATGTAGATACGTTAGGGTCCGAGGAGTTTACCTAGCGCGAGTTCGGGACACA
23	GGTCCAAGTCCCATGATTAGCCGTAGAGCGGAGATTTGTGGCCAGGATCTGG
24	ACCGAAACATTAGTCTCCATCCCAGCCACAGCGTCGAGTTAAAGTACTTGCAGTTAAACG
25	TCTTCTGGGATCACATTCAGCAACCCGTACTCGAGTGCCTGTACTTTAACTCG
26	ACGCTGTGGGCTGACGTATCTACATTCGTTTAACTGCAATCCTCCATCCGTTGCAATTTTCC
27	GTAGGGTGAGCACTCGATATTGATTTACCGTTATCTTGTCTCGATTGTTCCATT
28	ACTGAGAAAAGGATCGTTAGCGCGCGCATCCGAGGCACCTCCACGATCGAAGAT
29	AGTGGATGGGCGCTGTGCTCACCCCTACGGAAAATTGCAACGCAAGATAACGGT
30	AAATCAATATCGATCCTCCATCCAAGACGACTAGCGCCTTGTTCGTTTCGCAATTTCACTCCTG
31	TTGGTCTCTTATGCAAGCACCCCTGGATCACGTACTCGTGTGCGAACGACAAGG
32	CGCTAGTCGTCTTTCTTTTCTCAGTCAGGAGTGAAATTTCTCCATCCGGGCCACAGGCC
33	TTCTTGGCACATCAAGGACTTTTCTACCCATAGGTCTATTAGATTTTAGTCT
34	TTTTTTTTTGATGTGCAAGAAGGGCCTGTGGCCCTAGACCTATAGGGTAGAAAAGTCCTTTTTTTTT
35	TTTTTTTTTTAGGGCTTATCTCCCTCATCGAGATGATGTGATTCCCGCCTGAGCGTTCCTATTTTTTTT
36	CCCTGAAAAGTGTATACGTTGCACCCGTGCTGAATCCGAATAGGAAGTGCTT
37	ACCACCTAACCTTTCTCTCATACCTCTGTAGCTACGCCTATGCTACCTTATAG
38	GCGAGTTTTTATTATCCTCCATCCCAGATACGGTTGCGGACAACGGATTGACACAACATATCG
39	GGATTGATTGGTCACGCACCTCGTTAAGTGAAGGAACCTCAATCCGTTGTCC
40	GCAACCGTATCTGACACTTTTTCAGGGCGATATGTTGTGTTCTCCATCCCCTTAAGAAGGTC
41	AATTCGTGGTGAAGAGCATGAATATGCACCTCTGGGACCTAAGCCGTAACCC
42	CGAGCTCAAAGGTCAATCCCTCAAGGCCGTACGTCACCTGATTCCACAAACG
43	GTAAGTACGTTTGTTCACCACGAATTAGTACAGCTGGCGGGTCCAGAGTGC
44	ATATTCATGCTCTTCTCCATCCCCGCCCTCAAAGTCCACGGCCACTTGGAGCAAACCCGCC
45	AAATACGCTAGGTCGTCACCAGGATTGTTGTACCTGTAGTCAAGTGGCCGTGG
46	ACTTTGAGGGCGGCCTTTTGGAGCTCGGGCGGGTTGCTCTCCTCCATCCCCTTAAGAAGGTC
47	AATATAACTAGGAGTGTATCTCCAATAATGCTTGGCCCGTTAAATGCCGAGA
48	AACCGGTAGCTTATACCTTCTGGCATCGAGTGAGAAGATCACAACTCCGCACG
49	GAGGGTGCACAATTCCTAGTTATATTGACCTTCTTAAAGGCGGGCCAAGCATT
50	ATTGGAGATACACTCCTCCATCCTCATGGTTCCAGCTGATTAGGTTCGCGGAACACCGTTGTC
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	AGTGGTATTCGAGTCTCCATCCTAAATCTGATGCTTCGCCGTGAGAGCCTAGAGTGT'TTTC
69	TTTTTTTTTGCTCTCACGGCGAAGCATCAGATTTAGCGGTTCCAGGGCAGAAAACACTCTAGTTTTTTTT
70	TTTTTTTTTTAGGCGTAGCTACAGAGGTATGAGAGTAATAAACTCGCCTATAAGGTAGCATTTTTTTTT
71	GAACGTACATTACCAATAAATGTCTGCACCGATATCGCTTCATCGACCCTACC
72	CGCCATAGTTTCGAGCCTGCATAATGAAAGGCGCCGAGGTCTCCATCCTAGCTCACGGGTT
73	ACATGAATTCCTTGATATGTGCACAAATGCGCGACGAGCTTCGTGGACCTGGC
74	AATAACCTACGCTGACCAATCAATCCGGTTTTACGGCTTAGTTCTTCCACT
75	TAACGAGGTGCGTTAAGGAATTCATGTAACCCGTGAGCTAGCTCGTCGCGCAT
76	TTGTGCACATATCTCTCCATCCTAGAACACCTGTAATATACGGGCCGATTCCCAGTTATG
77	TGAGCGTCTTCCCTTTGGCCGGTATATCGGTCAGCGAATCGGCCCGTATATT
78	ACAGGTGCTTCTAGCGTAGGGTTATTATAACTGGGAATTCCTCCATCCAAACGCGGCGCAC
79	ACCCTAGAGAACATTGCAACTAGCGACCAACTCTAGCTATATGTAGTAGGTGA
80	CCAATGACGGTGTACCTAGCGTATTTTCTCGGCATTTTACTACAGGTACAAC
81	AATCCTGGTGACGTTGTTCTCTAGGGTGTGCGCCGCTTTTAGCTAGAGTTGG
82	TCGCTAGTTGCAATCCTCCATCCGTGCGTCTACTCGCATTCGATGTTGCCCTGTAACCTCTA
83	CCTAAAGAAGTGTGAACCTTCGGGAAGCTATTGCAGGCTGCAACATCGAATG
84	CGAGTAGACGCACCACCGTCATTGGGTAGAAGTTACAGGTCTCCATCCAGTGCAGCAAGCC
85	AAATACAGTGTGCTGAGTCTGATACGGCAAAGATCTTCTGCTTAGTCGATTT
86	AGGATAACTACTCTTGAAAATCATATTAATTACTCATTATACTCTATATTTAG
87	CATGCAAGGCGCATCGACACTGTATTTGGCTTCGCGCACTGAAGATCTTTGCC
88	GTATCAGAACTCATCTCCATCCCACACTCAACTATAACCAGGCAGGCGACAGTGGTCTTTGT
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	CCAATGGCTGTTCTCTACAACCAACTACAGAGCGGTGCTCTAACAATCTTGA
100	CGATGTCTAGACTTCCCTCCATCCGGGCAGTTCTTGCCGGCCGCCATTTTAGAGTGACGAGA
101	TAGCCACAGGTCTCGGCCATTACAGCCGATTTAATGATTAATGGGCGGCCG
102	GCAAGAACTGCCCTCTGGATTGAAAATCTCGTCACTCTATCCTCCATCCGGGATGTACATGT
103	GACAGGGTTGCCAGGACTCCAGAGGCGGTTGCCATGTTATGCCATATCCCTGC
104	TTTTTTTTTTGGCAACCCTGTCACATGTACATCCCTAACATGGCAACCCTCTGGAGTCTTTTTTTTT
105	TTTTTTTTTCGAAACTATGGCGGGTAGGGTCGATGCCTCGGGCCTTTTCATTATGCAGGCTTTTTTTTT
106	CTACACACCCGAGTGTAAATGTACGTTCCGACAGTCCACGAAGCGATATCGGTG
107	CAGACATTTATTGTTCAACCCATTGCTCGAAATGGTGGCCTAGGCGTTCTAG
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	GTGACAGGCAGTATAGGTTTATGCCTTTCGGTTTCAGCTGGTGCACCTAAGCGTGG
136	AGCCACACTGGTTTAGACCTGTGGCTAGCAGGGATATGGCATCATTAATCCG
137	GCTGTAATGGCCGTTACTGCCGTGCTACTACGAGTCACGAGCCAGCTGAACCGA



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

181	GTGGGTGTCGATTTAGCTCCGTCTGACCCATCCGCTTATTAACTCGCGTTCCT
182	GGCCACCTGATTTTTGTGTGTCGTTGTAGACGAACTTGACCGGGATTTGACCT
183	ATACAATACGCTCTAATCGACACCACGAGGGCATGGGTAATAAGCGGATGGG
184	TCAGACGGAGCTATCCTCCATCCAATTCTTCCCTTCCACACAGAACCGTCTGTCACGAATCT
185	TGATGCATTAACGTCAGATCAATCCCTAAAGAGATGCATACGGTTCGTGTG
186	GAAGGGAAGAATTAATCAGGTGGCCAGATTTCGTGACAGTCCCTCCATCCTTCATAGCAGACT
187	TGCAAGAACCCTGAACGCGCTACAGACCAACCCAGGCGTTGCACCATCAAGGT
188	GTCCTGGAATCGATAAGGCTGCCATGAAATCGTCCCTTGAGATAGATTGTCTG
189	AATTAGGCCCTTGCTCAGGGTTCCTTGCAAGTCTGCTATGAAACGCCTGGGTTGG
190	TCTGTAGCGCGTTTTCTCCATCCTCATGCCAGGGAAGTTCGTTGAATCGTGCAGATTGACAG
191	TCGCTCCCCTCAGGCCTGCAAGGCTATAAATCCCTCTTCGATTC AACGAAC
192	TTCCCTGGCATGATCGATTCCAGGACCTGTCAATCTGCATCCTCCATCCGCTCGATCTTTGT
193	CCATATGGTTCACCTCTCAAACAATGTTACCTTGTCAGTCTTCGCTGGGCTGCA
194	TCAGTCGGATCTCTCGAATGTGTAATAATACCGGGTCCATAAACGCACCGTAC
195	GCGCTGTCTGCGATGTGAACCATATGGACAAAGATCGAGCGACTGACAAGGTA
196	ACATTGTTTGAGATCCTCCATCCGGTGTGACTCTCATTGTCTCCATTTTAAATCCATGAG
197	ACGCCCTAGCTGGTGAGCGCATATCTCGTGTTCGCTGACTAAATGGAGACAAT
198	GAGAGTCAGCACCGAGATCCGACTGACTCATGGATTTTATCCTCCATCCGATTATATCCGGT
199	CAACCACCGTGAAGGCAGAGCGTTAATATTGCCACCATGTAGTTAAACAAG
200	ACTACTTAGGGTGTGAAGCTCGCGTACCGGGACTACAATTCAGCCCACGCAG
201	TCGAGAACGGCGGTTACCGTGGGTTGACCGGATATAATCTGGTGGCAATATT
202	AACGCTCGTGCCTTCTCCATCCGGATAGCCACCGCCTTTTGGTGGATGTGCAAAAGCTCGT
203	CAACTACTAAAAGCGCGTCCGTATAACCATGTATCCTGTCATCCACCAAAAG
204	GCGGTGGCTATCCCACCCTAAGTAGTACGAGCTTTTGCATCCTCCATCCTTAGTATCTCGCC
205	AACCACCTCCGCCAATATACTTGACCCTTCGCGACCCTACAATTCGGAGGT
206	TCGGAGACGAGACTTCAGACGTCATCAGTAACAGTTGAACCCGCGGAGGGAT
207	GTTGATCACCACGTGGCGGAGGTGGTTGGCGAGATACTAAGTGGTCCGGAAGG
208	GTCAAGTATATTGTCTCCATCCATCCTATAGGCACCTTGTAACCTCCCGGTCTACCCAGGAA
209	TTTTTTTTTCGGGAGTTTACAAGTGCCTATAGGATGTCTCGTCTCCGATTCTGGGTAGACTTTTTTTTT
210	TTTTTTTTTGAGAACAGAGTTTACAACCAAGAATGATTTGCTTTAAATACCAGCACTAGTTTTTTTT
211	CGAAGACTCAGGCACATTCGAGAGCGTGACTTCATCTGCTCACCCTGGAACCC
212	AAAATGTTTCGTCCAGATTTTATGGGACTGTACCGTCTGCTCCTCCATCCTTTACGTCCGTTT
213	CGAGAACAAGAAAGCCTAGCACAATTGACTTAATTGTCTTAGGAATAAGTTTC
214	ACGTCCAAGTTTCTTGCGGTCGCCGACAGGAACGCGAGTTACCCATGTTATCA
215	CCAAGGTGACGATTTTCTTGTTCCTCGAAACGGACGTAAAAGACAATTAAGTC
216	AATTGTGCTAGGCTCCTCCATCCTAACTCCGGCAATCATTGCCACGTCGAATAAGGAGTCAC
217	TACGGGATTCCTCACTGTTTCAGATCCCAGGTATACGATGTCGACGTGGCAATG
218	ATTGCCGGAGTTAGAACTTGAGCGTGTGACTCCTTATTTCTCCATCCCGGTCTCTTGTAC
219	CAGTCGAGCTTCTATCGCTTTGTTCCGCATTGCTCCATTGGGAGCCTAGGG
220	TAGTCTTCAAGCCTAGTTAATGCATCAACCTTGATGGTGTGCTGCATCTCTTTAG
221	GGATTGATCTGACTAGAAGCTCGACTGGTACAAGAGACCGTGGGAGCAATGCG
222	GAACAAAGGCGATTCTCCATCCGGCGGGCCTAGCCTCGTTGTGCGGCTCCACGTCGGCAGC
223	GCCCTTTTGACTCACTACCCAGCTCAACAGTCCAAAACATACGCCGACAACGA

224	GGCTAGGCCCGCCGGCTTGAAGACTACGTGCCGACGTGGTCCCTCCATCCGCTCAGAGACAAC
225	TATTCACCTTACCTAGTAACCTTGTTTCATCGGATCCCGTCTATCAATTTATCGT
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	GCGTGGTAGAAAGTCTCCATCCGCAATCCGCTGTTTGACAGTACTCCCTGTCTGCATACA
241	CGCTAGTATTCCAATCCTTTCAGTTCGCCATGTGGATACGGGAGTACTGTCA
242	AACAGCGGAATGCAATTCTGCGTGAATGTATGCAGGACATCCTCCATCCAGCGAATAATACG
243	CCCGGTATACCGTTAACCTGTATAGGACAGTCAACCACCATACTCGCGTG
244	TTTTTTTTTGGACGAACATTTTGGGTTCCACGGTGGCAGACGGTACAGTCCATAAAAATCTTTTTTTTT
245	TTTTTTTTTGCCTGAGTCTTCGAAACTTATTCTGCAGATGAAGTCACGCTCTCGAATGTTTTTTTT
246	TTTTTTTTTGGAGAATCCCGTACCCTAGGCTCCCACATCGTATACCTGGGATCTGAACAGTTTTTTTT
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248	TTTTTTTTTCCGATGAATGCAGTCTGATTTTATTAACGTGAAGCTACTTACTAGACGCGGCTTTTTTTTT
249	TTTTTTTTTGGGTATTTCACTTTTGTGCCAATGATAGATGTCACAATGCAGAGGCGTGGTTTTTTTT
250	TTTTTTTTTAGGAGGCCTTTTCTTGAGCTGTTACATCAGCGTGAGTCAAGGATTTGTTGATTTTTTTTT
251	TTTTTTTTTAACGGACTAATACCTAATCGCGGACTTGCCCAAGGAGAGGGTCCGGATGCGTTTTTTTT
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253	TTTTTTTTTGCCTAGGTGAAACTCCTCGGACCTTGGGACTTGGACCTGTGCCGCACTCTTTTTTTTT
254	TTTTTTTTTGAGTGCCTCGGATGCGCGGCTAACGGCGCCATCCACTATCTTCGATCGTGTTTTTTTTT
255	TTTTTTTTTGGAAATACTAGCGCACGCGAGTATGGGTATCCACATGGCGAACTGAAAGGATTTTTTTTT
256	TTTTTTTTTCCGTATACCCGGGAGACCGTTCTAACTGGTTGACTGTCTATACAGGGTTAATTTTTTTTT

### S8.5 DNA sequences for X<sub>1</sub>

Seq_ID	Sequences
1	CCCTTCTACGGGCCCTAACCTAAGACCTCAAACCTTTTCTGAATCGCTGTCGCAGGGAGA
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	TTATGTCCGTCACCCCTAACCCCTTAGCTCAGGTACTAGAGGTAGAGGTTGCTAGTTCGTCAA
20	CAATAGACTCACGTCCGCGTTGTTACAAGGCGGAGAAGTAGCCGTCTATCCAC
21	GCTAAATGCTTGAGAGTAAGTATCCCTATTTTATCGTCTCCCTAACCCCTCTCGGAGCCCGAT
22	GTCCACACACTGTGTGACGGACATAAGACTTGGACTGTATGGAAGTAACGGCC
23	TAGGCACTTTGGGCAATGTGTTACAGCAAGTCAGTTTGCCCTAACCCCTACCAGCTGCGAA
24	TAAACAGTGGGACTATTCCCTTGCGCTGCCGTGCTTGTGTTAGCGCTATAGCC
25	AACGCTGGCTACCGACGAATAACAACGTGCAGGAGCACCGCCCTAACCCCTGCGGATAGGCACC
26	ACATAAAAGTCCAGCGGATCTACCTATCCGTAACCTATTGAAATAAAAGTGA
27	CTGAGTCTCTGTGCAGGCCGGCTTAGAGCTGGGCTGAATCCCTAACCCCTACAGAGTCATCAC
28	ATGTACTTCCTTTGAAACAGTTTGGCGAATTAAGCGACTCGATCCTCCCATG
29	GCCAAACTGTTCCCTAACCCCTTGTGGCAGAGTCAGCCCTAATGACAAAGTGGTATCGCG
30	CACTACACGGGCGTGTGAGTTACCCGGCAGTAAACTATAAGGGTCATTGCAG
31	CTCATCCAATTAACCCTAACCCCTGGTGTCCATCCTTTCCGGTCTCCTAATACTTGCTCGATCC
32	TACGTATCGACCATAAAGGAAGTACATGTGATGACTCTGTGTCGCTTTAATTC
33	TAGTTCGCGCGTTAGTTGGGTAGTACGCTCTGGATGTAGCCCTAACCCCTATAGTTTACTGC
34	CGGGTAACTCAACTTAATTGGATGAGCTGCAATGACCCTTACCGTGTAGGTCA
35	TAACAACCCTAGACAGGAGAAGACCAAAACGGAGTGCACCCCTAACCCCTTCGATCAACGGC
36	TGTATAGCATGAGAAGCGTGGAGCGAGTACCGGTAGTTGTGAGAGTCAGAGCA
37	TCGCTCCACGCTTCCCTAACCCCTCTCGACTAGCGACCTTGGACCGAGTTCAGGCATGGCAG
38	AGGGATCTTGGTATGCCGCTCAACGCCCAACATGAACCTCATAATCTACTTCT
39	AACTTTCAGCCAGCCCTAACCCCTAAGATTTGCCATGCATAAACGTCACTACCCTTGTACTCC
40	TCCCTTGAGATAGTCTCATGCTATACAGCCGGTTGATCGACAACCTACCGGTAC
41	AGTACCTGAGCTACGTGAGTCTATTGTTGCAGAACTAGCCCTAACCCCTGAGGTTTATGTTG
42	GGCGTTGAGCGGCCTGGCTGAAAGTTAGAAGTAGATTATTAGGAACAGCATCG
43	TTCTATGTGATTCCACCCTCGTCATGCGACGAACTCCCTAACCCCTAACATAGTAGCG
44	AGGCCACCCCTTAATCCCTATCATGATCAGGCTAGGCGGTAACCTCTACCTCT
45	TCATGATAGGGATCCCTAACCCCTCCCAAAGTGCTTAGGCCGTTACTTCCGCAAACCTGACTTG
46	CTGTAACACATTGTCAAGGCCTGCGCGAGGAGGCTCGTGGAACGCTACAGTAA
47	CCTAAACTAAAGACCCTAACCCCTTTCACATCGGCCCTTTCGCCAGTAGGTCGTAGGTCGAG
48	TGACCGAGCCTTCTTAAGGGTGGGCCTCGCTACTATGTTACCGCCTAGCCTGA
49	ACCTGAGTCAAAGCCCTAACCCCTCACAGAGACTCAGTCACTTTTATTTTATTCAGCCCAGCT
50	CTAAGCCGGCCTGTCAACTGCTAACGGCATAATAGCGGTCCCGTCCCTGTAGGA

51	GGGCAATTCACGTCCCTAACCCCTCCGGGCAGAATCCAGTCCCTTGTGCTTCGTTTAGTCTGA
52	CTTCACGTGTCACACTGCAGACATGGGATGTGCGCTTCCGACGCCGAGCGCAGTCA
53	AAGGATGGACACCTGGTCGATACGTAGGATCGAGCAAGTCCCTAACCCCTGACCGCTATTATG
54	CCGTTAGCAGTTGACGTGAATTGCCCTCCTACAGGACGGTTCCCTAAATCCCGC
55	TCGGCTAAATCAAATATAATCGTATTTTAGAGGTCATTCCCCTAACCCCTGCGACAATGTTAC
56	CGAATTTTATCCTTGTACGGTGC GCGCCGTGATCCCACCTATTAGGAGACCGA
57	CGCGCACCGTACACCCTAACCCCTTCTAGGGTTGTTATGACCTACACGGTGTGCACTCCGTTT
58	TGGTCTTCTCCTGTGAATAGGCGGCAAGACATCCGAGTATACCCTGATAACAT
59	CCAGCCCTCTGCTCCCTAACCCCTCCTCAGAGCTACAGTCTTGGTATCTTATTCTCTCAATC
60	AATGTTTACGCACTAGGATAAAAATTCGGTAACATTGTGCGCAGTGGGATCACGG
61	CATGGCAAATCTTCTATCTCAAGGGAGGAGTACAAGGGTCCCTAACCCCTATACTCGGATGTC
62	TTGCCGCTATTTCAGCAGAGGGCTGGATGTTATCAGGGTCTATGGACTAGCG
63	TGTTTTAAATGGCGACTTAGATTTCGTCACTATGCTTCGCCCTAACCCCTGGACAGACAATC
64	CCAGAGTCCCTCAGTGGCTAGGGCACTCGAAGGAATGAGATAGTGACGTTTATG
65	AGTGCCCTAGCCACCCTAACCCCTAATCACATAGGAACGATGCTGTTCCCTGAGTTTCGTCGCA
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68	CATTCTGCTCGAGTCTGAGGACTCTGGGATTGTCTGTCCATCTCATTCCCTCG
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70	CAGGAAAGTAATCGACCTTTTACTGGTGTATGTCTGACTTGCATACACGACGA
71	CTCTGAGAAGCCCGCGACTGTGTCTGGGCTCCCTTACTGCCCTAACCCCTGCGGAGGGACCAA
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79	AGTCGGAGTCCACCCCTAACCCCTGTTTCGTGATGGGACTCATAACCCGTCTGCCATTCAA
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83	GTGCAAGGGTAACTTACAGCCCTGGCTGGAATACAGGGTCCCTAACCCCTGCTACGATAACGT
84	CAATCTACTGTTCTATCTTATGGGTACTAAAGTACGGATAGATACCAAGACT
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86	CGAATCTAAGTCGTAGCCTTATACCCAGCGCTGAATGTTGTCTTACCCACAGA
87	TCATAGTCGGGTGCCCTAACCCCTTGAAAGATAATCGACGGGACAACCACTACAGGAGTTA
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91	CCTATAGAACTCAATAAATGGACGTGTTAGGAGTCTCGCCCTAACCCCTCGGTATATGAAGC
92	ATGAGGAGTTAACAGAGGAACGCTCGGGGATACTCAAGATCACTGCTGTGTGC
93	CGAGCGTTCCTCTCCCTAACCCCTGGGCTTCTCAGAGTCGTCGTGATGCCAGTAAGGGAGCC

94	CAGACACAGTCGCTCCACATCTAGCAGCCCGTTTCAAGCGTCAAATTAGGCG
95	TCCCACAATACAACCCTAACCCCTCACTGACCTATTGGACTTGAGAATAATGTCAGTTGTGTG
96	TTCAGAGTTTGAATGTTAACTCCTCATGCTTCATATACCGTCTTGAGTATCGC
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99	GGCAGTCTGTTCCCTAACCCCTCTATCGAAGCGATTTTCTACACGATATTCACGACCACC
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106	GCCAGGGCTGTAATAAGTGGCCCAAGGATTTGAACGTCGTCTCCACATGGGC
107	AGTCACTGTAGACCCCTAACCCCTCAGACGGTCCGGGCCAGCATACTTCGGGCTTAAGTTTCGT
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124	TTGAGACCGTCTCGTCGGTTGGGTGCGCTTAACCTGCCGCCCTAACCCCTAGCAACGCCAGTC
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130	CCCGGACCGTCTGCATGTGGCTACTCACGAACTTAAGCCCCCTAACCCCTTACAGCTTTTC
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134	CTAATTTTGGATACCCTAACCCCTGCCTCAAGCTTCATTGGACAGGTCCTCTCGATATACTCG
135	ACGTTGCTGTAGTTCTAATGTTTCGAGTCCCGGTGCCGCGACACTACTTGAATG
136	TGCTATAACGTGTCCCTAACCCCTGACGCAATGGCACTACTAATCACACCGTACCTGTGGTCT

137	CCCTACGAGCCGCTGATGACGGCACGTCTAGGTGCTGGCGCTGGCCAAGCGTT
138	GGTAATGCAGTATCCAGTATGCCAATAGCTCGGGATATACCCTAACCCCTTCGCGGCACCGGG
139	ACTCGAACATTAGACACGTTATAGCACATTC AAGTAGTGTCCGCGGTTCGTGAT
140	CTCAAACGCCGGCCAAGACCGACCGTGCCGTTTGGGTCTCCCTAACCCCTTTGATTGATCGTG
141	AAGATGCTGCGACCCGAACCTTTATAGCAATACAGCTGATTGAAGGGCTACAT
142	CTATAAAGTTCGGCCCTAACCCCTCGTCGCACGGAGCAGCAGTCCGATTTCCATCGGCAGGAA
143	TTCAGTATTACCGTCGCGTTCCTAGCGAAAAGACCTGAGGTGACAGTGCCTAC
144	AAGGCTCTCTAGCCCCCTAACCCCTGGTGGCCGTACCCTGAGTTGTACTCAGAATCCGAAGGA
145	TGGGTCATCCACGTGTGCGCAGCATCTTCACGATCAATCAAATCAGCTGTATTG
146	TTTTTTTTTCCCTCAGGTCTTTTCGCTAGGAACGCGGCTAGAGAGCCTTGTAGGCCTGTCAATTTTTTTTT
147	ACATTATCCCTCGCCCTAACCCCTGAGACGGTCTCAATTTCCCATAGCTACGGCAAGTTAAGC
148	GCACCCAACCGACTCTGCGAATGGGTCTGCGCACGCCCTGCCTGGACTAAAC
149	TGAAATATACCTCCCCTAACCCCTGCCTTGCCCTCCCGGTTTGCCCTATAGCCACGGGAGCAA
150	AGCCACCAAATTGTTCTTATCGGTGTTGTGTAATTTATTTTGACGGGACTAAT
151	CAGCGTTGAGGAATAATATGACCCTCCACTATGAATACTCCCTAACCCCTAGGGCGTGCGCAG
152	GACCCATTTCGAGGAGGTATATTTTCAGTTTAGTCCAGGCTTAAATTCCTGAG
153	CGAGTTTTATGATCTATAGCAGCTTCGTGATCCAACCCCTAACCCCTCGTAATAGCGCAA
154	GAAATTACAAGTGCCTCGGGCCAGGATGTGCTAGGAAAGTAAGTCTCAGAGAC
155	TCCTGGCCCGACGCCCTAACCCCTCCATCTCGCAAATAGCCGTTGTACGTTATATAGTCGGA
156	TTGCTAACTGTGATTGTGTTATATGCCGATAATAGTAGCCATAGGTACTTCAC
157	ACTAGGCGACGGGCCCTAACCCCTTGAGGGCTGTGAATCAGGGCTAGCACGGTATTAGCATT
158	ACTTAGTGGGTCTTCACTTGTAAATTTCTTTCGCTATTACGCTTTCTTAGCACA
159	GTGCCATTGCGTCGCGGCTCGTAGGGAGACCACAGGTACCCCTAACCCCTGGCTACTATTATC
160	GGCATATAACACACCCCGTCGCTAGTGTGAAGTACCTATTCTGCCATCGGAAG
161	GATCACTGACACCCGACGCTCTCTCTGATTAGCGTTCGCTCCCTAACCCCTCGAACACAGATCG
162	CTTTTACTCAAGGCATGGGACATCTTAGCCTATTATTAGTGGTGTGATTAGTA
163	AAGATGTCCATGCCCTAACCCCTGCCGGCGTTTGAGATCACGACCGGGAGACCCAAACGGC
164	ACGGTCGGTCTTGTGACCTAGGCGGGACCACCCTCGCATATATCTTTCTTCAT
165	TCGGCATACTCAGCCCTAACCCCTTAACGGTGACGGAACAGGGCGGTGACGTGTACAGCATAA
166	CCCTCGTCATCAGTCTTGGAGTAAAAGCGATCTGTGTTGCTAATAATAGGCT
167	TGGTACGGCCACCCGTGGATGACCCATCCTTCGGATTCTCCCTAACCCCTTATGCGAGGGTGG
168	TCCCGCCTAGGTCTGAGTATGCCGAATGAAGAAAGATATCAGAGCCGACCTC
169	ACCTCACTAGATTCAGCCGTTACGGAAACGAGATTCGACCCTAACCCCTTCTGAAGTGGACT
170	GGGAGCATCTGGGTAACGGATTCAAAGATTCTCGATGCTGAGTACAACCTCAG
171	TTTTTTTTTCCAGATGCTCCAGTCCACTTCAGAGCATCGAGGAATCTTTGAATCCGTTATTTTTTTTT
172	TTTTTTTTTTATAGGGCAAACCGGGAAGGCAAGGCCAATTTGGTGGCTTTGCTCCCGTGGCTTTTTTTTT
173	TTTTTTTTTATCATAAACTCGCTCAGGGAATTTATGTTGGATCTGACGAAGCTGCTATAGTTTTTTTT
174	TTTTTTTTTTGCTAGGCCCTGATTCACAGCCCTCAAGACCCACTAAGTAATGCTAATACCGTTTTTTTT
175	TTTTTTTTTTGGTGTGATGATCCTTCCGATGGCAGACGCACGCTAATCAGAGAGAGCGTCTTTTTTTTT
176	TTTTTTTTTGTACCGCCCTGTTCCGTCACCGTTACTGATGACGAGGGTTATGCTGTACACTTTTTTTTT
177	TTTTTTTTTAATCTAGTGAGGTGAGGTGCGCTCTGTCAGAATCTCGTTTCCGTAACGGCTGTTTTTTTT
178	TTTTTTTTTTCGATTCAGAAAAGGTTTGGAGTCTTAAAGAGTTGGTAATCTCCCTGCGACATTTTTTTTT
179	TTTTTTTTTTTTCTGCAAGTCGAGGAAACCAATCCAGTAAGTAGCCTAAGGGAAGGTTAGTTTTTTTT

180	TTTTTTTTTGCCCATGAGGGACACGCGAATTTTCGAGCTTGATTGAAAGATGTAGAATTTTTTTTTTTT
181	TTTTTTTTTAACCGGCCCTAAACGCTTCGATATGTCTAGCACCGCATCCACACGTCTTTGTTTTTTTTTT
182	TTTTTTTTTGACGCCGTTTATCTAAAGGAGCCGTCCTCCTCAGCATTTGTATGTAAACAATTTTTTTTTT
183	TTTTTTTTTCAAGCATTTAGCGGCTATAGCGCTAAGACGATAAAATAGGGATACCTACTCTTTTTTTTTT
184	TTTTTTTTTAAATAAATTACACAACACCGATAAGACGAGGGATAATGTATTAGTCCCGTCATTTTTTTTTT
185	TTTTTTTTTGTAACATTAAGCCTACCCGACGATCTGCACGATGTAGACGCACCCACTATTTTTTTTTT
186	TTTTTTTTTGATGGGCTGTATCCTAGATCGTCGAGCGGTATAATTACGATTGATAGTTTCGTTTTTTTTTT
187	TTTTTTTTTGTCTAAATAGTTTCTAGTTTATCTCAGACGAATGTCTAATATGATCAGAGATTTTTTTTTTT
188	TTTTTTTTTCGTCGGAAGCGACATCCCATGTCTGCCTTTGACTCAGGTTGACTGCGCTCGGTTTTTTTTTT
189	TTTTTTTTTGGACTTTTATGTGGTGCCTATCCGCATAGGTTACGGATAGGTAGATCGCGCTTTTTTTTTTT
190	TTTTTTTTTCCCGCTGCCAAATGAACCTGTTTAGCCCGTGAGAAGGGATAACGCGTAGGGTTTTTTTTTT
191	TTTTTTTTTGTCCACTGTTTATTCGCAGCTGGTACAACAAGCACGGCAGCGCAAGGAATATTTTTTTTTTT
192	TTTTTTTTTCCACGAGCCTCCTCGCGCAGGCCTTGCTTTTAGTTTAGGTTACTGTAGCGTTTTTTTTTTTT
193	TTTTTTTTTCACGAAGAGTAATTTGGTCCCTCCGCGACTCCACGCACCCGGGACGATTTATTTTTTTTTTT
194	TTTTTTTTTGCTTGAACCGGGCTGCTAGATGTGGTTGTATTGTGGGACGCCTAATTTGACTTTTTTTTTTT
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  $\mu$ M) and rest strands (final concentration: 100 nM) are mixed together and annealed.

### S8.6 DNA sequences for X<sub>2</sub>

Seq_ID	Sequences
1	CCCTTCTCACGGGCCCTAACCTAAGACCTCAAACCTTTTCTGAATCGCTGTCGCAGGGAGA
2	TTACCAACTCTTTTTGTAAGTCCAGTCCGCGAACGTGGTTCCCGCCACATCC
3	CAGCTGATCATCTCCCTAACCTGGTAGCCAGCGTTCATGGGAGGATCGCGGTGCTCCTGAC
4	AGTTGTATTTCGTCTCTAAACAGGTTCAATTTGGCAGCGGGCCCTACGCGTTAT
5	GACTTGCAGGAACTAACCTTCCCTTAGGCTACTTACTGCCCTAACCTACCACGTTTCGCGG
6	ACTGGCAGTTACAAGATGATCAGCTGGGATGTGGCGGGATTGTCATTAGGGCT
7	GACTCTGCCACAACGCCGTGTAGTGCAGGATACCCTTCCCTAACCTTGTATCCTCGCGT
8	CAGTAGTAGGAGGTCACTCACCTGAAAGTGACGCTGGTTGATTGGTTTCCTC
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	CACTACACGGGCGTGTGAGTTACCCGGCAGTAAACTATAAGGGTCATTGCAG
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	TTCCCTATGTGATTCCACCACCTCGTTCATGCGACGAACTCCCTAACCCCTAACATAGTAGCG
44	AGGCCACCCCTTAATCCCTATCATGATCAGGCTAGGCGGTAACCTCTACCTCT
45	TCATGATAGGGATCCCTAACCCCTCCCAAAGTGCCTAGGCCGTTACTTCCGCAAACCTGACTTG
46	CTGTAACACATTGTCAAGGCCTGCGCGAGGAGGCTCGTGGAACGCTACAGTAA
47	CCTAAACTAAAGACCCCTAACCCCTCTTACATCGGCCCTTTCGCCAGTAGGTCGTAGGTCGAG
48	TGACCGAGCCTTCTTAAGGGTGGGCCTCGCTACTATGTTACCGCCTAGCCTGA
49	ACCTGAGTCAAAGCCCTAACCCCTCACAGAGACTCAGTCACTTTTATTTTATTCAGCCCAGCT
50	CTAAGCCGGCCTGTCAACTGCTAACGGCATAATAGCGGTCCCGTCTGTAGGA
51	GGGCAATTCACGTCCCTAACCCCTCCGGGCAGAATCCAGTCCCTTGTGCTTCGTTTAGTCTGA
52	CTTCACGTGTCACTGCAGACATGGGATGTGCGTTCCGACGCCGAGCGCAGTCA
53	AAGGATGGACACCTGGTCGATACGTAGGATCGAGCAAGTCCCTAACCCCTGACCGCTATTATG
54	CCGTTAGCAGTTGACGTGAATTGCCCTCCTACAGGACGGTTCCCTAAATCCCGC
55	TCGGCTAAATCAAATATAATCGTATTTTAGAGGTCATTCCCCTAACCCCTGCGACAATGTTAC
56	CGAATTTTATCCTTGTACGGTGCAGCGCCGTGATCCACTTATTAGGAGACCGA
57	CGCGCACCGTACACCCTAACCCCTCTAGGGTTGTTATGACCTACACGGTGTGCACTCCGTTT
58	TGGTCTTCTCCTGTGAATAGGCGGCAAGACATCCGAGTATAACCCCTGATAACAT
59	CCAGCCCTCTGCTCCCTAACCCCTCCTCAGAGCTACAGTCTTGGTATCTTATCTCTCAATC
60	AATGTTACGCACTAGGATAAAATTCGGTAACATTGTGCGAGTGGGATCACGG
61	CATGGCAAATCTTCTATCTCAAGGAGGAGTACAAGGTCCCTAACCCCTATACCTCGGATGTC
62	TTGCCGCTATTTCAGCAGAGGGCTGGATGTTATCAGGGTCTATGGACTAGCG
63	TGTTTTAAATGGCGACTTAGATTTCGTCACTATGCTTCGCCCTAACCCCTGGACAGACAATC

64	CCAGAGTCCTCAGTGGCTAGGGCACTCGAAGGAATGAGATAGTGACGTTTATG
65	AGTGCCCTAGCCACCCTAACCCTAATCACATAGGAACGATGCTGTTCTCGAGTTTCGTGCGCA
66	TGACGAGTGGTGGTGATTACTTTTCTGATCCTGGCTAATTAGTCAGACATACA
67	CCAGTAAAAGGTCCCCTAACCCCTTAGGGTGAGATTGCACACAGCAGTGGCTTCTTCACAAT
68	CATTCTGCTCGAGTCTGAGGACTCTGGGATTGTCTGTCCATCTCATTCTTCTCG
69	GGCCGATGTGAAGGAAGGCTCGGTCACTCGACCTACGACCCCTAACCCTAATTAGCCAGGAT
70	CAGGAAAGTAATCGACCTTTTACTGGTGTATGTCTGACTTGCATACACGACGA
71	CTCTGAGAAGCCCAGGACTGTGTCTGGGCTCCCTTACTGCCCTAACCCCTGCGGAGGGACCAA
72	ATTACTCTTCGTGATAAATCGTCCCGGGTGCCTGGAGTCTCTACTGGCGAAGA
73	GGATTCTGCCCGGGTGACACGTGAAGTCAGACTAAACGACCCCTAACCCCTTGAGATAAACTAG
74	AAACTATTTAGACATCTCTGATCATATTAGACATTTCGTCTATAAATTGACGTAC
75	TCTGTTTGAATACGACAAGTACCCGAGCCATGCCGCAGCCCTAACCCCTTGTCGAGTGGCAG
76	TCTGTGGAATAAATAGGAACTGGATAGCTTTTATACTTGTAGCACAAAGGGACT
77	TATCCAGTTCCTACCCTAACCCCTTGATTTAGCCGAGCGGGATTTAGGAGAATGACCTCTAA
78	AATACGATTATATTTCGGACTAGACGACCCGAAGGCTATCAAGCCGGCTAAACG
79	AGTCGGAGTCCCACCCTAACCCCTGTTTCGTGATGGGACTCATAACCCGTCGTCCCATTCAA
80	GCATACCTCACGGTTTTTATTCCACAGACTGCCACTCGACACAAGTATAAAAAGC
81	GTAGCTCTGAGGAGTGCCTGAACATTGATTGAGAGAATACCCTAACCCCTTGATAGCCTTGCG
82	GTCGTCTAGTCCGTGGGACTCCGACTCGTTTAGCCGGCTTGATTACTGTCCCA
83	GTGCAAGGGTAACTTACAGCCCTGGCTGGAATACAGGGTCCCTAACCCCTGCTACGATAACGT
84	CAATCTACTGTTCTTATCTTATGGGTACTAAAGTACGGATAGATACCAAGACT
85	ACCCATAAGATAGCCCTAACCCCTCCATTTTAAAACACGCTAGTCCATAGCGAAGCATAGTGA
86	CGAATCTAAGTCGTAGCCTTATAACCCAGCGCTGAATGTTGTCTTACCCACAGA
87	TCATAGTCGGGTGCCCTAACCCCTTGGAAGATAATCGACGGGACAACCCTACAGGAGTTA
88	TTATAAGTGACAATGAACAGTAGATTGACGTTATCGTAGCTCCGTACTTTAGT
89	AATCTCACCCCTAGCTCGAGCAGAAATGATTGTGAAGAAGCCCTAACCCCTCAACATTCAGCGC
90	TGGGTATAAGGCTCACCCGACTATGATCTGTGGGTAAGATATCCATGTTACTG
91	CCTATAGAACTCAATAAATGGACGTGTTAGGAGTCTCGCCCTAACCCCTCGGTATATGAAGC
92	ATGAGGAGTTAACAGAGGAACGCTCGGCGATACTCAAGATCACTGCTGTGTGC
93	CGAGCGTTCCTCTCCCTAACCCCTGGGCTTCTCAGAGTCGTGATGCCAGTAAGGGAGCC
94	CAGACACAGTCGCTCCACATCTAGCAGCCCGGTTTCAAGCGTCAAATTAGGCG
95	TCCCACAATACAACCCTAACCCCTCACTGACCTATTGGACTTGAGAATAATGTCAGTTGTGTG
96	TTCAGAGTTTGAATGTTAACTCCTCATGCTTCATATAACCGTCTTGAGTATCGC
97	CGTAATTATACCGCCCTAACCCCTGATTCGAACAGAGTACGTCAATTATCGTGCGGCATGGC
98	TCGGGTACTTGTCTCGGCATTCCGGCTACACGGCCCTAGTCGACTAATGCGCG
99	GGCCAGTCTGTTTCCCTAACCCCTTATCGAAGGCGATTTTCTACACGATATTCACGACCACC
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	CCTGGTAGTCCACTGCGGAAATTGTCCTAATGTCTATGATGGTTGTCCCGTCG
113	GACAATTTCCGCACCCTAACCCCTTGAATTCTATAGGCAGTAACATGGATGCGAGACTCCTAA
114	CACGTCCATTTATTAGTCTGGTACTGTCTCCCTGAATTGTAAATCAAGCCCT
115	AACGACGATGCTCCCTAACCCCTATACTGCATTACCATGTAGGCCCTTCTATATCCCGAGCT
116	ATTGGCATACTGGTGTGGACTACCAGGGCTAGGACACATCTCATAGACATTAG
117	CAATAGGTCAGTGTTCAAACCTCTGAACACACAACCTGACACCCTAACCCCTCAATTCAGGGAGG
118	ACAGTACCAGACTGAGCATCGTCGTTAGGGCTTGATTTATAAATCGGACTGCT
119	GCTCCGTGCGACGCGTAATACTGAATTCCTGCCGATGGCCCTAACCCCTACATGTGTTGCTT
120	AGGCAATTAACGGCTTACGTCGTGGGCCGGTGGTGTGCGGTTTATTCTCAAGTC
121	TTTTTTTTTCCGTTAATGCTAAGCAACACATGTCCGACACCACGGCCACGACGTAAGTTTTTTTTT
122	TCGCCTTCGATAGACAATGTATTCCGGGTGGTTCGTGAATCCCTAACCCCTATCGTCGGGTAGG
123	CTTTTAATGTTACTAGTGGGTGCGTCTACATCGTGCAGATTAGCTATGGGAAA
124	TTGAGACCGTCTCGTCGGTTGGGTGCGCTTAACTTGCCGCCCTAACCCCTAGCAACGCCAGTC
125	GAGTATAGGTCCTTTGATTTTATAAAGACCATTCACTTCTATCGTGTAGAAAA
126	TTTATAAAAATCAACCCTAACCCCTCACCAGTCGAATAAATCCGTGACGCCAGTGATGTCCGAA
127	ACGGAAAAGTGGGTGCGCCCTGGTTTGTGAAAAGCTGTAAGACTTCGGGAAATC
128	TCAGGACGTACGACCCTAACCCCTTCCCTCAACGCTGGTCTCTGAGACTTAGTATTCATAGTG
129	GAGGGTCATATTATAGGACCTATACTCGACTGGCGTTGCTGAAGTGAATGGTC
130	CCCGGACCGTCTGCATGTGGCTACTCACGAACCTAAGCCCCCTAACCCCTTACAGCTTTTC
131	ACAAACCAGGGCGTCTGACGTCCTGAGATTTCCCGAAGTTCGTACAACGGCTA
132	TTTGCGAGTATGGTCACAGTTAGCAATCCGACTATATAACCCTAACCCCTCGCCAGCACCTAG
133	ACGTGCCGTCTATCTCAAAAATTAGAACGCTTGCCAGTCGAAGTATGCTGG
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	GCACCAACCGACTCTGCGAATGGGTCTGCGCACGCCCTGCCTGGACTAAAC
149	TGAAATATACCTCCCTAACCCCTGCCTTGCTTCCCGGTTTGGCCCTATAGCCACGGGAGCAA

150	AGCCACCAAATTGTTCTTATCGGTGTTGTGTAATTTATTTTGACGGGACTAAT
151	CAGCGTTGAGGAATAATATGACCCTCCACTATGAATACTCCCTAACCCCTAGGGCGTGCGCAG
152	GACCCATTTCGAGGAGGTATATTTTCAGTTTAGTCCAGGCTTAAATTCCTGAG
153	CGAGTTTTATGATCTATAGCAGCTTCGTGATCCAACACCCCTAACCCCTCGTAATAGCGCAA
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	CCCTCGTCATCAGTCCTTGAGTAAAAGCGATCTGTGTTTCGCTAATAATAGGCT
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	TTTTTTTTTTTTCTGCAAGTCGAGGAAACCAATCCAGTAAGTAGCCTAAGGGAAGGTTAGTTTTTTTT
180	TTTTTTTTTGCCCATGAGGGACACGCAATTTTCGAGCTTGATTGAAAGATGTAGAATTTTTTTTTTT
181	TTTTTTTTTAACCGGCCCTAACCGTTCGATATGTCTAGCACCGCATCCACACGCTTTTGTTTTTTTTT
182	TTTTTTTTTGGACCCGTTTATCTAAAGGAGCCGTCCTCCTCAGCATTGTATGTTAAACAATTTTTTTTT
183	TTTTTTTTTCAAGCATTAGCGGCTATAGCGCTAAGACGATAAAATAGGGATACTTACTCTTTTTTTTT
184	TTTTTTTTTAAATAAATACACAACACCGATAAGACGAGGGATAATGTATTAGTCCCGTCATTTTTTTTT
185	TTTTTTTTTGTAACATTAAGGCTACCCGACGATTCCTGCACGATGTAGACGCACCCACTATTTTTTTTT
186	TTTTTTTTTGATGGGCTGTATCCTAGATCGTCGAGCGGTATAATTACGATTGATAGTTTCGTTTTTTTT
187	TTTTTTTTTGTCTAAATAGTTTCTAGTTTATCTCAGACGAATGTCTAATATGATCAGAGATTTTTTTTT
188	TTTTTTTTTCGTCGGAAGCGACATCCCATGTCTGCCTTTGACTCAGGTTGACTGCGCTCGGTTTTTTTT
189	TTTTTTTTTGGACTTTTATGTGGTGCCATCCGCATAGGTTACGGATAGGTAGATCGCGCTTTTTTTTT
190	TTTTTTTTTCCCGCTGCCAAATTGAACCTGTTTAGCCCGTGAGAAGGATAACCGGTAGGGTTTTTTTT
191	TTTTTTTTTGTCCCACTGTTTATTCGCAGCTGGTACAACAAGCACGGCAGCGCAAGGAATTTTTTTTT
192	TTTTTTTTTCCACGAGCCTCCTCGCGCAGGCCTTGCTTTTAGTTTAGGTTACTGTAGCGTTTTTTTTTT

193	TTTTTTTTTCACGAAGAGTAATTTGGTCCCTCCGCGACTCCACGCACCCGGGACGATTTATTTTTTTTT
194	TTTTTTTTTGCTTGAAACCGGGCTGCTAGATGTGGTTGTATTGTGGGACGCCTAATTTGACTTTTTTTTT

### S8.7 DNA sequences for X<sub>3</sub>

Seq_ID	Sequences
1	CCCTTCTCACGGGCCCTAACCCCTAAGACCTCAAACCTTTTCTGAATCGCTGTCGCAGGGAGA
2	TTACCAACTCTTTTTGTAAGTCCAGTCCGCGAACGTGGTTCGCCACATCC
3	CAGCTGATCATCTTGGTAGCCAGCGTTCATGGGAGGATCGCGGTGCTCCTGAC
4	AGTTGTATTTCGTCTCTAAACAGGTTCAATTTGGCAGCGGGCCCTACGCGTTAT
5	GACTTGCAGGAAACTAACCTTCCCTTAGGCTACTTACTGCCCTAACCCCTACCAGTTTCGCGG
6	ACTGGCAGTTACAAGATGATCAGCTGGGATGTGGCGGGATTGTCATTAGGGCT
7	GACTCTGCCACAACGCCCGTGTAGTGC GCGATAACCACTTTTGTATCCTCGCGT
8	CAGTAGTAGGAGGTCACCTCACCCCTGAAAAGTGACGCTGGTTGATTGGTTTCCTC
9	TCAGGGTGAGTGACCCCTAACCCCTGAAAATTCGCGTGTCCCTCATGGGCCAAATTCATATCT
10	TTCAATCAAGCTCTCTGGCGTTCCTTGAGGATGAGACAGTACTGCGTCCCGAA
11	GACTCGCGCTTCCCTAACGCGGAACCTATGCTCTGACTCTCCTACATCCAGAGC
12	GTAATAACCAACTTCCCTCCTACTACTGACGCGAGGATACAACCAGCGTCACTT
13	TTTAGGGCCGGTTACAAAGACGTGTGGATGCGGTGCTAGCCCTAACCCCTACTGTCTCATCCT
14	CAAGGAACGCCAGGGAAGCGGAGTCTTCGGGACGCAGTTAACTCGGTCCAAG
15	GTCGCTAGTCGAGTACCAAGATCCCTCTGCCATGCCTGGTTACTTCTCCGCT
16	TGTAACAACGCGGTAGTGCTCGTTCGCTGGATAGACGGCTACATATCGAAGCG
17	GGAACGAGCACTACCCTAACCCCTACGGCTCCTTTAGATAAACGGCGTCCCTGTTAACATACA
18	AATGCTGAGGAGGTACAGTGTGTGGACATCGGGCTCCGAGTACAGTCCAAGTC
19	TTATGTCCGTCACCTTAGCTCAGGTAAGTACTAGAGGTAGAGGTTGCTAGTTCTGCAA
20	CAATAGACTCACGTCCGCGTGTGTTACAAGGCGGAGAAGTAGCCGTCTATCCAC
21	GCTAAATGCTTGAGAGTAAGTATCCCTATTTTATCGTCTCCCTAACCCCTCTCGGAGCCCGAT
22	GTCCACACACTGTGTGACGGACATAAGACTTGGACTGTATGGAAGTAACGGCC
23	TAGGCACTTTGGGCAATGTGTTACAGCAAGTCAGTTTGCTTACCAGCTGCGAA
24	TAAACAGTGGGACTATTCCCTTGCCTGCGCTGCCGTGCTTGTGTTAGCGCTATAGCC
25	AACGCTGGCTACCGACGAATAACAAGTGCAGGAGCACCGCCCTAACCCCTGCGGATAGGCACC
26	ACATAAAAGTCCAGCGGATCTACCTATCCGTAACCTATTGAAATAAAAGTGA
27	CTGAGTCTCTGTGCAGGCCGGCTTAGAGCTGGGCTGAATTACAGAGTCATCAC
28	ATGTAATTCCTTTGAAACAGTTTGGCGAATTAAGCGACTCGATCCTCCCATG
29	GCCAAACTGTTTCCCCTAACCCCTTGTGGCAGAGTCAGCCCTAATGACAAAGTGGTATCGCG
30	CAC TACACGGGCGTGTGAGTTACCCGGCAGTAAACTATAAGGGTCATTGCAG
31	CTCATCCAATTAATGGTGTCCATCCTTTCGGTCTCCTAATACTTGTCTCGATCC
32	TACGTATCGACCATAAAGGAAGTACATGTGATGACTCTGTGTCGCTTTAATTC
33	TAGTTTCGCGGTTAGTTGGGTAGTACGCTCTGGATGTAGCCCTAACCCCTTATAGTTTACTGC
34	CGGGTAACTCAACTTAATTGGATGAGCTGCAATGACCCTTACCCTGTAGGTCA
35	TAACAACCCTAGACAGGAGAAGACCAAAACGGAGTGCACCTTCGATCAACCGGC
36	TGTATAGCATGAGAAGCGTGGAGCGAGTACCGGTAGTTGTGAGAGTCAGAGCA
37	TCGCTCCACGCTTCCCTAACCCCTCTCGACTAGCGACCTTGGACCGAGTTCAGGCATGGCAG
38	AGGGATCTTGGTATGCCGCTCAACGCCCAACATGAACCTCATAATCTACTTCT

39	AACTTTCAGCCAGTAAGATTTGCCATGCATAAACGTCACTACCCTTGACTCC
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	CATGGCAAATCTTCTATCTCAAGGGAGGAGTACAAGGGTCCCTAACCTATACTCGGATGTC
62	TTGCCGCCTATTCAGCAGAGGGCTGGATGTTATCAGGGTCTATGGACTAGCG
63	TGTTTTAAAATGGCGACTTAGATTCGTCACTATGCTTCGTTGGACAGACAATC
64	CCAGAGTCCCTCAGTGGCTAGGGCACTCGAAGGAATGAGATAGTGACGTTTATG
65	AGTGCCCTAGCCACCCTAACCTAATCACATAGGAACGATGCTGTTCTGAGTTTCGTGCGCA
66	TGACGAGTGGTGGTGATTACTTTCTGATCCTGGCTAATTAGTCAGACATACA
67	CCAGTAAAAGGTCTCTAGGGTGAGATTGCACACAGCAGTGGCTTCTTCACAAT
68	CATTCTGCTCGAGTCTGAGGACTCTGGGATTGTCTGTCCATCTCATTCTCTCG
69	GGCCGATGTGAAGGAAGGCTCGGTCACTCGACCTACGACCCTAACCTAATTAGCCAGGAT
70	CAGGAAAGTAATCGACCTTTTACTGGTGTATGTCTGACTTGCATACACGACGA
71	CTCTGAGAAGCCCGGACTGTGTCTGGGCTCCCTTACTGTGCGGAGGGACCAA
72	ATTACTCTTCGTGATAAATCGTCCCGGGTGCCTGGAGTCTCTACTGGCGAAGA
73	GGATTCTGCCCAGGTGACACGTGAAGTCAGACTAAACGACCCTAACCTTGAGATAAACTAG
74	AAACTATTTAGACATCTCTGATCATATTAGACATTTCGTCTATAATTGACGTAC
75	TCTGTTTGAATACGACAAGTACCCGAGCCATGCCGCACGTTGTGAGTGGCAG
76	TCTGTGGAATAAATAGGAACGGATAGCTTTTATACTTGTAGCACAAGGGACT
77	TATCCAGTTCTACCCTAACCTTTGATTTAGCCGAGCGGGATTTAGGAGAATGACCTCTAA
78	AATACGATTATATTCGGACTAGACGACCCTAAGGCTATCAAGCCGGCTAAACG
79	AGTCGGAGTCCATTGTTTTCGTGATGGGACTCATAACCCGTGCTCCATTCAA
80	GCATACCTCACGGTTTTATTCCACAGACTGCCACTCGACACAAGTATAAAAAGC
81	GTAGCTCTGAGGAGTGGTGAACATTGATTGAGAGAATACCCTAACCTTGATAGCCTTGCG

82	GTCGTCTAGTCCGTGGGACTCCGACTCGTTTAGCCGGCTTGATTACTGTCCCA
83	GTGCAAGGGTAACTTACAGCCCTGGCTGGAATACAGGGTTGCTACGATAACGT
84	CAATCTACTGTTCCCTATCTTATGGGTACTAAAGTACGGATAGATACCAAGACT
85	ACCCATAAGATAGCCCTAACCCCTCCATTTTAAAAACACGCTAGTCCATAGCGAAGCATAGTGA
86	CGAATCTAAGTCGTAGCCTTATACCCAGCGCTGAATGTTGTCTTACCCACAGA
87	TCATAGTCGGGTGTCTGGAAAGATAATCGACGGGACAACCCTACAGGAGTTA
88	TTATAAGTGACAATGAACAGTAGATTGACGTTATCGTAGCTCCGTACTTTAGT
89	AATCTCACCCCTAGCTCGAGCAGAATGATTGTGAAGAAGCCCTAACCCCTCAACATTCAGCGC
90	TGGGTATAAGGCTCACCCGACTATGATCTGTGGGTAAGATATCCATGTTACTG
91	CCTATAGAACTCAATAAATGGACGTGTTAGGAGTCTCGCTCGGTATATGAAGC
92	ATGAGGAGTTAACAGAGGAACGCTCGGCGATACTCAAGATCACTGCTGTGTGC
93	CGAGCGTTCCCTCTCCCTAACCCCTGGGCTTCTCAGAGTCGTCTGTATGCCAGTAAGGGAGCC
94	CAGACACAGTCGCTCCACATCTAGCAGCCCGGTTTCAAGCGTCAAATTAGGCG
95	TCCCACAATACAATCACTGACCTATTGGACTTGAGAATAATGTCAGTTGTGTG
96	TTCAGAGTTTGAATGTTAACTCCTCATGCTTCATATACCGTCTTGAGTATCGC
97	CGTAATTATACCGCCCTAACCCCTGTATTTCGAACAGAGTACGTCAATTATCGTGCGGCATGGC
98	TCGGGTACTTGTCTCGGCATTCCGGCTACACGGCCCTAGTCGACTAATGCGCG
99	GGCCAGTCTGTTTTCTATCGAAGGCGATTTTCTACACGATATTACAGACCACC
100	CGGAATACATTGTTCTCGACGATCTAGGATACAGCCATCCGAAACTATCAAT
101	CCATCACGAAACACCGTGAGGTATGCTTGAATGGGACGACCCTAACCCCTACTAGGGCCGTGT
102	AGCCGGAATGCCGAAACAGACTGGCCCGCGCATTAGTCGTGGCGTCACGGATT
103	TATTCGACTGGTGCCCACTTTTCCGTTTTCGGACATCACTTCGTAAGTGGAAAAG
104	TTTTGAATACTGATAAACACAACCTAACCCCTAGGACCCATCGGGTTATGAGTC
105	TTAGTTGTGTTTACCCTAACCCCTGTACCCTTGCCTGGGACAGTAATCACCCGTATTTCCA
106	GCCAGGGCTGTAATAAGTGGCCCAAGGATTTGAACGTCGTCTCCACATGGGC
107	AGTCACTGTAGACTCAGACGGTCCGGGCCAGCATACTTCGGGGCTTAAAGTTCTGT
108	GAGTAGCCACATGTTTCAAGTATTCAAACCTTTTCCAGTACGTGGGTCTAGTGG
109	ATTATCTTTCCAGTTGTCACTTATAATAACTCCTGTAGTCCCTAACCCCTACGACGTTCAAAT
110	CCTTGGGCCACTTGTCTACAGTACTGCCCATGTGGGAGTAGGACCTGTCCAA
111	TGAAGCTTGAGGCACTACAGCAACGTCGAGTATATCGAGTGATGTGTCTTAGC
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	TCAGGACGTACGATTTCCCTCAACGCTGGTCTCTGAGACTTAGTATTCATAGTGTG
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	AGCCACCAAATTGTTCTTATCGGTGTTGTGTAATTTATTTTACGGGACTAAT
151	CAGCGTTGAGGAATAATATGACCCTCCACTATGAATACTCCCTAACCCCTAGGGCGTGCGCAG
152	GACCCATTCGCAGGAGGTATATTTTCAGTTTAGTCCAGGCTTAAATTCCCTGAG
153	CGAGTTTTATGATCTATAGCAGTTTCGTCAGATCCAACATCGTAATAGCGCAA
154	GAAATTACAAGTGCCTCGGGCCAGGATGTGCTAGGAAAGTAAGTCTCAGAGAC
155	TCCTGGCCCCGACGCCCTAACCCCTCCATACTCGCAAATAGCCGTTGTACGTTATATAGTCGGA
156	TTGCTAACTGTGATTGTGTTATATGCCGATAATAGTAGCCATAGGTACTTTCAC
157	ACTAGGCGACGGGTTGAGGGCTGTGAATCAGGGCCTAGCACGGTATTAGCATT
158	ACTTAGTGGGTCTTCACTTGTAAATTTCTTGGCGCTATTACGCTTTCTAGCACA
159	GTGCCATTGCGTCGCGGCTCGTAGGGAGACCACAGGTACCCCTAACCCCTGGCTACTATTATC
160	GGCATATAACACACCCGTCGCTAGTGTGAAGTACCTATTCTGCCATCGGAAG
161	GATCACTGACACCCGACGCTCTCTCTGATTAGCGTGCCTTCGAACACAGATCG
162	CTTTTACTCAAGGCATGGGACATCTTAGCCTATTATTAGTGGTGTGATTAGTA
163	AAGATGTCCCATGCCCTAACCCCTGCCGGCGTTTGAGATCACGACCGCGGAGACCCAAACGGC
164	ACGGTCGGTCTTGTGACCTAGGCGGGACCACCCTCGCATATATCTTTCTTCAT
165	TCGGCATACTCAGTTAACGGTGACGGAACAGGGCGGTGACGTGTACAGCATAA
166	CCCTCGTCATCAGTCTTGTAGTAAAAGCGATCTGTGTTTCGCTAATAATAGGCT
167	TGGTACGGCCACCCGTGGATGACCCATCCTTCGGATTCTCCCTAACCCCTTATGCGAGGGTGG



168	TCCCGCCTAGGTCTCGAGTATGCCGAATGAAGAAAGATATCAGAGCCGACCTC
169	ACCTCACTAGATTACAGCCGTTACGGAAACGAGATTCTGATTCTGAAGTGGACT
170	GGGAGCATCTGGGTAACGGATTCAAAGATTCTCGATGCTGAGTACAACCTCAG
171	TTTTTTTTTCCAGATGCTCCAGTCCACTTCAGAGCATCGAGGAATCTTTGAATCCGTTATTTTTTTTT
172	TTTTTTTTTATAGGGCAAACCGGGAAGGCAAGGCCAATTTGGTGGCTTTGCTCCCGTGGCTTTTTTTTT
173	TTTTTTTTTATCATAAACTCGCTCAGGGAATTTATGTTGGATCTGACGAAGTCTATAGTTTTTTTT
174	TTTTTTTTTGCTAGGCCCTGATTACAGCCCTCAAGACCCACTAAGTAATGCTAATACCGTTTTTTTT
175	TTTTTTTTTGGTGTGAGTATCCTTCCGATGGCAGACGCACGCTAATCAGAGAGAGCGTCTTTTTTTTT
176	TTTTTTTTTGTACCCGCCCTGTTCCGTCACCGTACTGATGACGAGGGTTATGCTGTACACTTTTTTTTT
177	TTTTTTTTTAATCTAGTGAGGTGAGGTCTGGCTCTGTCAGAATCTCGTTTCCGTAACGGCTGTTTTTTTT
178	TTTTTTTTTGCGATTACAGAAAAGTTTGAGGTCTTAAAGAGTTGGTAATCTCCCTGCGACATTTTTTTTT
179	TTTTTTTTTTTTCTGCAAGTCGAGGAAACCAATCCAGTAAGTAGCCTAAGGGAAGTTAGTTTTTTTT
180	TTTTTTTTTGGCCCATGAGGGACACGCGAATTTTCGAGCTTGATTGAAAGATGTAGAATTTTTTTTT
181	TTTTTTTTTAACCGGCCCTAAACGCTTCGATATGCTTAGCACCCGCATCCACACGCTTTTGTTTTTTTTT
182	TTTTTTTTTGGACGCCGTTTATCTAAAGGAGCCGTCCTCCTCAGCATTTGTATGTTAAACAATTTTTTTTT
183	TTTTTTTTTCAAGCATTTAGCGGCTATAGCGCTAAGACGATAAAATAGGGATACCTACTTTTTTTTT
184	TTTTTTTTTAAATAAATTACACAACACCGATAAGACGAGGGATAATGTATTAGTCCCGTCATTTTTTTTT
185	TTTTTTTTTGTAACATTAAGAGCCTACCCGACGATTCGACGATGTAGACGCACCCACTATTTTTTTTT
186	TTTTTTTTTGATGGGCTGTATCCTAGATCGTCGAGCGGTATAATTACGATTGATAGTTTCGTTTTTTTT
187	TTTTTTTTTGTCTAAATAGTTTCTAGTTTATCTCAGACGAATGTCTAATATGATCAGAGATTTTTTTTT
188	TTTTTTTTTCGTCGGAAGCGACATCCCATGCTGCCTTTGACTCAGGTTGACTGCGCTCGGTTTTTTTT
189	TTTTTTTTTGGACTTTTATGTGGTGCCTATCCGCATAGGTTACGGATAGGTAGATCGCGCTTTTTTTTT
190	TTTTTTTTTCCCGCTGCCAAATTGAACCTGTTTAGCCCGTGAGAAGGGATAACGCGTAGGGTTTTTTTT
191	TTTTTTTTTGTCCCACTGTTTATTCGAGCTGGTACAACAAGCACGGCAGCGCAAGGAATATTTTTTTTT
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	GACTCTGCCACAACGCCCGTGTAGTGCAGGATAACCACTTTTGTATCCTCGCGT
4	GACTCGCGCTTCCCTAACGCGGAACTATGCTCTGACTCTCCTACATCCAGAGC
5	GTACTACCCAACCTCCTCCTACTACTGACGCGAGGATACAACCAGCGTCACTT
6	CAAGGAACGCCAGGGAAGCGGAGTCTTCGGGACGCAGTTAACTCGGTCCAAG
7	GTCGCTAGTCGAGTACCAAGATCCCTCTGCCATGCCTGGTTACTTCTCCGCT
8	CTGAGTCTCTGTGCAGGCCGGCTTAGAGCTGGGCTGAATTACAGAGTCATCAC
9	ATGTACTTCTTTGAAACAGTTTGGCGAATTAAGCGACTCGATCCTCCCATG
10	GCCAAACTGTTTCTTTGTGGCAGAGTCAGCCCTAATGACAAAGTGGTATCGCG
11	CACTACACGGCGTGTGAGTTACCCGGCAGTAAACTATAAGGGTCATTGACG
12	CTCATCCAATTAATGGTGTCCATCCTTTCCGGTCTCCTAATACTTGCTCGATCC
13	TACGTATCGACCATAAAGGAAGTACATGTGATGACTCTGTGTCGCTTTAATTC

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	TGTTTTAAATGGCGACTTAGATTCGTCACTATGCTTCGTTGGACAGACAATC
35	CCAGAGTCTCAGTGGCTAGGGCACTCGAAGGAATGAGATAGTGACGTTTATG
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	GGAACGAGCACTATGTATTGCAACAGAGTACGTCAATTATCGTGGGCATGGC
51	TCGGGTACTTGTCTTGTAACTGCCAGTCCGCGAACGTGGTTCCCGCCACATCC
52	AGTTGTATTTCGTCTCCGCTTGTTACAAGGCGGAGAAGTAGCCGTCTATCCAC
53	CCATCACGAAACACCGTGAGGTATGCTTGAATGGGACGATACCACGTTTCGCGG
54	CAGTAGTAGGAGGTCACTCACCCCTGAAAAGTGACGCTGGTTCCGGTTATGAGTC
55	TCAGGGTGAGTGATGTTACCCTTGCACTGGGACAGTAATCACCCGTGATTCCA
56	GCCAGGGCTGTAATCTGGCGTTCCTTGAGGATGAGACAGTACTGCGTCCCGAA

57	ATTATCTTTCCAGTTGTCACTTATAATAACTCCTGTAGTTACTGTCTCATCCT
58	TGTAACAACGCGGTAGTGCTCGTTCCGTGGATAGACGGCTGGTTGTCCCGTCG
59	AACGCTGGCTACCGACGAATACAACCTGTCAGGAGCACCGTGAGGTTTCATGTTG
60	GGCGTTGAGCGGCTGGCTGAAAGTTAGAAGTAGATTATTGAAAATAAAAGTGA
61	AGTGCCCTAGCCATCACAGAGACTCAGTCACTTTTATTTTCATTCAGCCCAGCT
62	CTTCACGTGTCACTCTGAGGACTCTGGGATTGTCTGTCCATCTCATTCCTTCG
63	GGATTCTGCCCAGGTGACACGTGAAGTCAGACTAAACGATCAACATTCAGCGC
64	TGGGTATAAGGCTCACCCGACTATGATCTGTGGGTAAGATATAAATTGACGTAC
65	TTTTTTTTGTCTAAATAGTTTCTAGTTTATCTCAGACGAATGTCTAATATGATCAGAGATTTTTTTTT
66	TTTTTTTTCGTCGGAAGCGACATCCCATGTCTGCCTTTGACTCAGGTTGACTGCGCTCGGTTTTTTTT
67	TTTTTTTTTGGACTTTTATGTGGTGCCTATCCGCATAGGTTACGGATAGGTAGATCGCGCTTTTTTTTT
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	GTGGCGCGATGCATGTTATAGATGATTGATACTGTCCGACCCGACGCATGA
6	CCTCTCGATCATTCGGGTATTGCAGCTGTCTGGCTTTTGTCCATCCTCAT
7	GGCTGACTCTTAAGGAGGATTTACTGTTCTGTGGGAGATAATGGATCCTTCA
8	TAATGAAGTGGCCATGGGCGCAAAGGCATTGTTTGTAATACTGGGAATGTAG
9	CTGAATGTTTGAATGCATCGCGCCACGACTTTGCAAGGAGTATTTGAAAGTG
10	TCTTACGTCTCATACGAAACTCGAGCTGAAGGATCCATTTGGTATTAAACCA
11	TATGAGTTACTTTACGTAGCCTCTCACTACATTCCCAGTCTACCGCAAATCT
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	TTCGCGTTTCAAACATCGATCTCTTCCGCCGC
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	ACGCGAGGTTTGAATGACAGACCTTCAGCATTA
8	CAGTACATGCAACGTAGAACTACTCAAAGCGG
9	CCCGGCAGCCTCGCGTCATATTCTTAGGTCTGT
10	CATTCAAACGAGTAACAACCTGGAGTTGCAGGTA
11	CCCGAATCAATTAAGCCGCTTTGTCATAAAGT
12	GTCTCTGATGCCTTTCTTCTGCGATTTCAGGATG
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	GTACCGCCAGGGTTAATGGGTTCGATTCCGATCAAGTGTTCGAGGCTTAACAT
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	AACAAAGTAACTCCTAAGACTCGACATCTTTTCG
3	GAGTTCCTTTATAACCGCTGCGGCCTAACTTGA
4	ATTGCAGGGCCTGCGGTGTTTACACTCCCGTAC
5	TTACCCTTTGCTTGAAAGTGATTGGGTCTGGTG
6	GTTGGTTCACCTCTGGTTTGATTTATGAATTTA
7	CTAGTATGGAATGGTGCGAAGGGATGGCGACCC
8	TCGAATGGAGCTAGCCAATAGCCTTATGGTCCA
9	CGTCGTATGAGTTTGAGCCTGTTGTGCGCCACG
10	TATCGACGGGCTGAGGGCGAACCAGCATCAGT
11	ATTCCGGAAGTTTGCGGGCCTCCCTCCAATTT
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	AAGAACTTTACGTTACTTTGTTAATCCTGAGA
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	GTGGGTACATATCGTTTTATTAATGCGTCGAAGTGACAGTGCAAC
19	GTAGCGCAGTGTAGTTTTCCCGAGTGTAGTACGAGTCTGTACGCC
20	TGATCGCGGCCAAATTTTGTGCGTAATTTCCGGATGATGAGGATCAC
21	TAGAGCAACCGATGTTTTCCAGTCACCGTGGAATGACCTCACACAC
22	GCGTAGTGTGGCTATTTTAATTTGGGCGTCCAGATTTCCCTAGTCATA
23	TTAGTTTGAGCTATTTTTGTCTTCCGCTCGCTAGAATAAAGCGAAT
24	TTAGACCAGCAATCTTTTGAATATCAACGCAATACCTGTAGCATGA
25	TACTCCTACTAGCTTAGCCGCCGAGCTGCGAACACGGCTGTA
26	TTACCTTTGCTAGGCGATATGTACCCACGAACGTGAATTGAT
27	CTGGACGCCCAATTCGGATCTGCAATTATGTGCTTGAGACAA
28	AGATGAATGTAGGGATAGCTCAAATAATATGACTAGGAAAT
29	TACTAACACTCGGGGACACGCCAGCGGTTCCTTTCTGTCCGA
30	CCGCCCGTCGCTGATTTGGCCGCGATCAGGCGTACAGACTCG
31	AGCGAGCGGAAGACCTGAAAGCCTCGGTGGTCCAAGGACGAG
32	CCATACTTGCTTACGATTGCTGGTCTAAATTCGCTTTATTCT
33	TCCACGGTGACTGGTCGTGCTGTCTGAAGTTGCACTGTCACT
34	TCGACGCATTTAATCTACACTGCGCTACGTGTGTGAGGTCAT
35	AGCGGGATTCCGGCACCAATAACGTATAGCCCTGACACAGCGC
36	CGGTCAGAGTACCTCTCCAACATACATCCAGGTTAAAGAGTT
37	GTAACGGGACATGGACGGTTACGTCGTCATCGAGGGCAATGT
38	TCTCATTGTACTTCTATCGTGACCCGTGTGAAACCAAGTTAA
39	TTGCGTTGATATTCGCATCCTGGTTCACAGTTTAGGCCGTC
40	TCCGGCCCATGCGGTAGCCACACTACGTCATGCTACAGGTA
41	ATAATAAGGATAAGGGTATAACTGAGAGAGCCTGTGGGATCG
42	ACCTACGGACCATAAGCGTGAGCCGGGTCGTATTCCTTAG
43	CCGAAATTACGCACTCCCGAATTAAGTTTAAGATACAAGC
44	TGTTTCGAGAGTGGCATCGGTTGCTCTAGTGATCCTCATCAT
45	AGTCAGCCTTGTGAGCATTGGTATGATTCAATCACGGATACG
46	CGGTGTAATGGGAGCACTATTAACGCCGTTGCGACAAGACTA
47	GTACGGGTAACATGTTACTGGAGTTTCCCGACTGATGTGCGAG
48	TTGACGTGCAGGACTTGAAGCAGTAGTAAGAGATGCAGTCCG

### S8.17 DNA sequences for icosahedron

Seq_ID	Sequences
1	ACGCCTAGAGTTTGATGCACTCAGGGCTCACTGG
2	AACGGGCTCCGTTGCTTGGCGTGGATAAAGATCT
3	TCTTGTTTAAAGTTACCAGCGTCGAGCCGGTCGGT
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	TTCACTGAAGTTTTGAGTCTACACGGCGTCGGG
17	GGGCGGACGAGTTCCATGACACTTACCACCGTGC
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	GCCCAGCTATATTTACAGGAATGAAAGGTGCCGGC
39	CACACATCCGATTAGGACACGAGAAGAAGAGGCT
40	ATGTTATGTTTTTAGGTGTTCCGGGCAACTTATTT
41	CGGAGTTGCGGTTGAAGTAATTCCGAATGTACGA
42	CCCGCGGAGACTTATCTTCTCGAAAGTAAACTC
43	TACGAATTTGGTTGCAGCTACGACGCACCATCCG
44	TAACGATAATGTTATCGCTCCGGTCTTGACCAGA
45	TCCTGAAATATTTACGTATGTATTCTGAAGCATA
46	CTTTACTGAGCTTGCCTATCAGCGCTATTCTCTCC
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	TTCTAGTTAACGTGTTGCCTCTGTATTTGGG
85	GGGAGAATTATACGCTTTGGTTTCGCATTGGGA
86	AAGTGTGATGGGGATCCTATTTGGCCTTACAG
87	ACACGAATGGGGGTGTCACCTTATTGAAAGCC
88	CGTGGGTTTCGTCAAGCAGACACGCCGGCACCT
89	TTGGTGAGGGTAAGGGATCACTAGCCTCTTCT
90	TGTAGGACTCAGGCGATCTAGTAAATAAGTTG

91	GGAATTACTTCGCTCTTCCCACAGATCTTTAT
92	TCGAGGAAGATTAATCAAGATAACCGACCGGC
93	GTCGTAGCTGCTGCTAATGAATGATGCAGGTT
94	ACCGGAGCGATTCCACCTCTTGACAGTTGGCAT
95	AATACATACGTTCTCGGCTTGCCCAGTGAGCC
96	TGACGTGTTGGAGAACAGAAATCACGATTAGT
97	ACCCAGTCACACTCGCCACAGCAAGAAGTTTG
98	CTAATGGACTTGGCACCTTGACACAAGGAGTA
99	ATCTGCTACAGATTACTGCGGTTTATAACCAC
100	CGCGGCCCAATAGTTTGAGGCCACACTGATGT
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