Supporting Information

Experimental section

Reagents and Materials. The mammalian cell lysis kit, phosphate buffered saline (PBS), hydrocortisone, insulin, cholera toxin and calcium chloride were obtained from Sigma-Aldrich (Saint Louis, MI). M13mp18 single-stranded DNA and Lambda DNA were purchased from New England Biolabs Inc (Ipswich, MA). All of the DNA helper strands were synthesized by Integrated DNA Technologies (Coralville, IA) and normalized to 100 µM in 96 well plates without further purification. Synthetic β-actin RNA was also purchased from IDT and purified by RNase-free HPLC in factory. Total RNA isolation kit, RNase-free DNase, and RNA fragmentation reagent were obtained from Ambion (Austin, TX). Dulbecco's Modified Eagle's Medium (DMEM), DMEM: F12 medium, keratinocyte serum-free medium, horse serum, human recombinant Epidermal Growth Factor (hrEGF), fetal bovine (FBS), serum penicillin/streptomysin solution, Bovine Pituitary Extract (BPE), trypsin, agarose and SYBR Green I were purchased from Invitrogen (Carlsbad, CA).

Assembly of DNA Origami. M13 viral ssDNA (10 nM or 20 nM) was mixed with the corresponding set of helper strands at a molar ratio of 1:5 or 1:10 in 1 x TAE/Mg buffer containing 100 mM Tris, 50 mM acetic acid, 5 mM EDTA and 12.5 mM magnesium acetate (pH 8.0) to form the 2D rectangular, 2D triangular, or 3D cuboid origami, respectively. The origami samples were annealed and assembled in an Eppendorf thermocycler (Hauppauge, NY) from 94 °C to room temperature over 12 h or 24 h for the 2D or 3D origami. Excess helper strands were removed using Microcon centrifuge filters YM-100 (Millipore, Bedford, MA).

Cell Lines. CP-A cells (metaplastic human esophageal epithelial cell line) were kindly provided by Dr. Brian J. Reid at the Fred Hutchison Cancer Research Center. MCF-10A (non-tumorigenic mammary epithelial cell line) and MDA-MB-231 cells (metastatic breast cancer cell line) were provided by Dr. Thea Tlsty, University of California, San Francisco. HeLa (human cervical cancer cell line) and End1/E6E7 (normal endocervical epithelial cell line) were purchased from American Type Culture Collection (ATCC, Manassas, VA).

Cell Cultures: CP-A cells were cultured in keratinocyte serum-free medium supplemented with BPE and hrEGF. End1/E6E7 cells were grown in the same medium for CP-A cells plus calcium chloride (0.013 g/L). HeLa and MDA-MB-231 cells were cultured in DMEM medium supplemented with 10% FBS and 100 unit/mL penicillin: 100 μ g/mL streptomycin solutions. MCF-10A cells were cultured in DMEM: F12 medium supplemented with 5% horse serum, 0.5 μ g/mL hydrocortisone, 20 ng/mL hrEGF, 10 μ g/mL insulin, 100ng/mL cholera toxin and 100 unit/mL penicillin:100 μ g/mL streptomycin solutions. All the cells were cultured in 25 or 75 cm² flasks to ~ 80% confluency and incubated at 37 °C under 5% CO₂ atmosphere.

Cell Lysis. The lysis solution contains 50 mM Tris-HCl, 150 mM NaCl, 0.1% SDS, 0.5% deoxycholic acid and protease inhibitor at the ratio of 1:100. Cells were washed with PBS and detached from the flask with 0.05% trypsin for CP-A, MDA-MB-231 and MCF-10A cells and with 0.25% trypsin for HeLa and End1/E6E7 cells. After trypsin treatment, cells were centrifuged at 900 rpm for 3 minutes and resuspended in 1mL of 1X PBS. Cells (10⁶) were lysed in 500 uL of the lysis solution and incubated on ice for 20 min on a shaker. The lysates were then centrifuged at 17000 x g at 4 °C for 30 min. Finally, the supernatant was removed and stored on ice or -20 °C for the following steps.

Separation of Rectangular Origami from CP-A Cell Lysates. Purified rectangular DNA origami was mixed with various concentrations of CP-A cell lysate for 1 h and 12 h on a shaker. The stability of origami was first verified by gel electrophoresis. 1% agarose slab gel containing SYBR Green I dye was prepared in 1X TAE/Mg buffer, and then immersed in the same buffer. The origami-cell lysate mixture was loaded in the gel sample wells, followed by electrophoresis for 2 h at 80 V. After electrophoresis, the gel was rinsed and imaged with a Gel Doc XR system (Bio-Rad, Hercules, CA). The band intensity was measured using Image J (National Institutes of Health, <u>http://rsb.info.nih.gov/ij</u>). The migration bands corresponding to assembled origami were excised from the gel for AFM imaging. Gel bands were crushed and transferred into DNA gel extraction spin column (Bio-Rad). DNA origami was recovered by centrifuging the column for 5 minutes at 13000 g.

Mixing Triangular and 3D Cuboid Origami with Cell Lysates. Purified triangular and 3D cuboid origami were mixed with CP-A cell lysates at room temperature for 1 h and 12 h, respectively. The sample mixtures were analyzed by agarose gel electrophoresis. The origami bands were subsequently excised from the gel and recovered. The structural integrity of the triangular and 3D cuboid origami was confirmed by AFM and TEM imaging, respectively.

Separation of Rectangular Origami, M13 ssDNA and λ DNA from Cell Lysates. 10 nM of rectangular origami and M13 viral ssDNA and 100 nM λ DNA were added to CP-A cell lysates (5,000 or 10,000 cells) at room temperature for 1 h and 12 h respectively. Agarose gel electrophoresis was used to separate them from the cell lysate components to determine their stability (Figure 4 in the main text). In addition, these three DNA samples were mixed with other cell lysates, including HeLa, End1/E6E7, MDA-MB-231 and MCF-10A. The mixtures were

loaded into agarose slab gels followed by electrophoresis. The gel images of three DNA structures after incubation with the various cell lysates are shown in **Figure S2**. The results show that only DNA origami can be separated from the cell lysate in all cell lines. λ DNA showed a strong interaction with all types of cell lysate, nonspecifically shifting the bands into the gel loading wells, while the ssDNA smeared and displayed some degree of random degradation.

Preparation of Total Cellular RNA. Total RNA was extracted from HeLa cell lines and prepared by total RNA isolation kit, according to the manufacturer's instructions. Genomic DNA was removed by treating samples with RNase-free DNase. The purified RNA was kept at -80 °C for future use or fragmentized using RNA fragmentation reagent.

AFM Imaging. The rectangular and triangular origami extracted from the gel (2 μ L) was deposited onto a freshly cleaved mica (Ted Pella) and left to adsorb for 2 minutes. 1 X TAE/Mg buffer (30 μ L) was added to the AFM liquid cell, and the samples were scanned in tapping mode under fluid on an AFM (Digital Instruments, Veeco, Bruker, Santa Barbara, CA) with SNL-tips (Veeco).

TEM Imaging. The TEM sample was prepared by dropping 2 μ L of 3D origami sample solution on carbon-coated grid (400 mesh, Ted Pella). Before depositing the sample, the grids were negatively glow discharged using Emitech K100X machine. After 45 seconds, the sample was wicked from the grid by filter paper. The grid was then washed with a drop of water to remove excess salt. A drop of 0.7 % uranyl formate solution was added to the grid, and excess solution was again wicked away with filter paper. The grid was treated with a second drop of uranyl formate solution for 15 seconds, and the excess solution wicked away. The grid was evaporated to dryness at room temperature. Low resolution TEM studies were carried out by using a Philips CM12 transmission electron microscope, operated at 80 kV in the bright field mode.



Figure S1. Additional AFM images of rectangular origami extracted from gels of Figure 2a. The top row is origami-cell lysate mixture incubated at 4°C and bottom row is incubation at room temperature. Left to right: 5000 lysed cells incubated with origami for 12 h, 10000 lysed cells incubated with origami for 12 h, 5000 lysed cells incubated with origami for 1 h and 10000 lysed cells incubated with origami for 1 h. Scale bar= 300 nm.



Figure S2. Eeffects of cell line on the stability of M13, rectangular origami, viral ss DNA and λ DNA as determined by agarose gel electrophoresis Leftmost lane: 1 kbp DNA marker; Lane 1: 10 nM M13 ssDNA; Lane 2: 10 nM origami; Lane 3: 100 nM λ DNA; Lane 4: cell lysate; Lane 5-7: M13, origami and λ DNA incubated with cell lysate for 1 h at 25°C; Lane 8-10: M13, origami and λ DNA incubated with cell lysate for 12 h at 25°C.



Figure S3. Schematic rectangular DNA origami with staple strands numbered. Single stranded, M13 viral DNA is shown in red, and staple strands are shown in green.



Figure S4. Schematic 2D triangular DNA origami with staple strands numbered. Single stranded, M13 viral DNA is shown in red, and staple strands are shown in green. The complex consists of three major domains which are labeled A, B and C.



Figure S5. Schematic design of 8-layer 3D origami.







Figure S6. Schematic layout of the origami/probes showing the positions of Index (initiate with 'I'), Control probes (initiate with 'C'), and β -actin probes (initiate with 'B'). The 3D structures of the origami/probes are also shown below each design.



Figure S7. AFM images of origami bearing control probe reacted with (a) Synthetic RNA, (b) Fragmentized total cellular RNA, and (c) total cellular RNA. Scale bar= 300 nm. (image insets are 250 nm by 250 nm)

Staple strand sequence

Table S1. Staple sequences for 2D rectangular origami

Name	Sequence
1	
1	
2	
3 1	
4	
5	
07	
0	
0	
9	
10	
11	
12	
13	
14	
15	
10	
17	
10	
20	ΩΤΤΤΤΑΓΑΓΑΘΑΤΘΑΑ ΤΑΤΑΓΑΘΤΑΑΙΑΘΑΑΤΕΑΙ
20	
21	CGACAACTAAGTATTA GACTTTACAATACCGA
22	GGATTTAGCGTATTAA ATCCTTTGTTTTCAGG
23	
25	GAACGTGGCGAGAAAG GAAGGGAA CAAACTAT
26	TAGCCCTACCAGCAGA AGATAAAAACATTTGA
27	CGGCCTTGCTGGTAAT ATCCAGAACGAACTGA
28	CTCAGAGCCACCACCC TCATTTTCCTATTATT
29	CTGAAACAGGTAATAA GTTTTAACCCCTCAGA
30	AGTGTACTTGAAAGTA TTAAGAGGCCGCCACC
31	GCCACCACTCTTTTCA TAATCAAACCGTCACC
32	GTTTGCCACCTCAGAG CCGCCACCGATACAGG
33	GACTTGAGAGACAAAA GGGCGACAAGTTACCA
34	AGCGCCAACCATTTGG GAATTAGATTATTAGC
35	GAAGGAAAATAAGAGC AAGAAACAACAGCCAT
36	GCCCAATACCGAGGAA ACGCAATAGGTTTACC
37	ATTATTTAACCCAGCT ACAATTTTCAAGAACG
38	TATTTTGCTCCCAATC CAAATAAGTGAGTTAA
39	GGTATTAAGAACAAGA AAAATAATTAAAGCCA

40	TAAGTCCTACCAAGTA CCGCACTCTTAGTTGC
41	ACGCTCAAAATAAGAA TAAACACCGTGAATTT
42	AGGCGTTACAGTAGGG CTTAATTGACAATAGA
43	ATCAAAATCGTCGCTA TTAATTAACGGATTCG
44	CTGTAAATCATAGGTC TGAGAGACGATAAATA
45	CCTGATTGAAAGAAAT TGCGTAGACCCGAACG
46	ACAGAAATCTTTGAAT ACCAAGTTCCTTGCTT
47	TTATTAATGCCGTCAA TAGATAATCAGAGGTG
48	AGATTAGATTTAAAAG TTTGAGTACACGTAAA
49	AGGCGGTCATTAGTCT TTAATGCGCAATATTA
50	GAATGGCTAGTATTAA CACCGCCTCAACTAAT
51	CCGCCAGCCATTGCAA CAGGAAAAATATTTTT
52	CCCTCAGAACCGCCAC CCTCAGAACTGAGACT
53	CCTCAAGAATACATGG CTTTTGATAGAACCAC
54	TAAGCGTCGAAGGATT AGGATTAGTACCGCCA
55	CACCAGAGTTCGGTCA TAGCCCCCGCCAGCAA
56	TCGGCATTCCGCCGCC AGCATTGACGTTCCAG
57	AATCACCAAATAGAAA ATTCATATATAACGGA
58	TCACAATCGTAGCACC ATTACCATCGTTTTCA
59	ATACCCAAGATAACCC ACAAGAATAAACGATT
60	ATCAGAGAAAGAACTG GCATGATTTTATTTTG
61	TTTTGTTTAAGCCTTA AATCAAGAATCGAGAA
62	AGGTTTTGAACGTCAA AAATGAAAGCGCTAAT
63	CAAGCAAGACGCGCCT GTTTATCAAGAATCGC
64	AATGCAGACCGTTTTT ATTTTCATCTTGCGGG
65	CATATTTAGAAATACC GACCGTGTTACCTTTT
66	AATGGTTTACAACGCC AACATGTAGTTCAGCT
67	TAACCTCCATATGTGA GTGAATAAACAAAATC
68	AAATCAATGGCTTAGG TTGGGTTACTAAATTT
69	GCGCAGAGATATCAAA ATTATTTGACATTATC
70	AACCTACCGCGAATTA TTCATTTCCAGTACAT
71	ATTTTGCGTCTTTAGG AGCACTAAGCAACAGT
72	CTAAAATAGAACAAAG AAACCACCAGGGTTAG
73	GCCACGCTATACGTGG CACAGACAACGCTCAT
74	GCGTAAGAGAGAGCCA GCAGCAAAAAGGTTAT
75	GGAAATACCTACATTT TGACGCTCACCTGAAA
76	TATCACCGTACTCAGG AGGTTTAGCGGGGTTT
77	TGCTCAGTCAGTCTCT GAATTTACCAGGAGGT
78	GGAAAGCGACCAGGCG GATAAGTGAATAGGTG
79	TGAGGCAGGCGTCAGA CTGTAGCGTAGCAAGG
80	TGCCTTTAGTCAGACG ATTGGCCTGCCAGAAT
81	CCGGAAACACACCACG GAATAAGTAAGACTCC
82	ACGCAAAGGTCACCAA TGAAACCAATCAAGTT
83	TTATTACGGTCAGAGG GTAATTGAATAGCAGC
84	TGAACAAACAGTATGT TAGCAAACTAAAAGAA

85	CTTTACAGTTAGCGAA CCTCCCGACGTAGGAA
86	GAGGCGTTAGAGAATA ACATAAAAGAACACCC
87	TCATTACCCGACAATA AACAACATATTTAGGC
88	CCAGACGAGCGCCCAA TAGCAAGCAAGAACGC
89	AGAGGCATAATTTCAT CTTCTGACTATAACTA
90	TTTTAGTTTTTCGAGC CAGTAATAAATTCTGT
91	TATGTAAACCTTTTTT AATGGAAAAATTACCT
92	TTGAATTATGCTGATG CAAATCCACAAATATA
93	GAGCAAAAACTTCTGA ATAATGGAAGAAGGAG
94	TGGATTATGAAGATGA TGAAACAAAATTTCAT
95	CGGAATTATTGAAAGG AATTGAGGTGAAAAAT
96	ATCAACAGTCATCATA TTCCTGATTGATTGTT
97	CTAAAGCAAGATAGAA CCCTTCTGAATCGTCT
98	GCCAACAGTCACCTTG CTGAACCTGTTGGCAA
99	GAAATGGATTATTTAC ATTGGCAGACATTCTG
100	TTTT TATAAGTA TAGCCCGGCCGTCGAG
101	AGGGTTGA TTTT ATAAATCC TCATTAAATGATATTC
102	ACAAACAA TTTT AATCAGTA GCGACAGATCGATAGC
103	AGCACCGT TTTT TAAAGGTG GCAACATAGTAGAAAA
104	TACATACA TTTT GACGGGAG AATTAACTACAGGGAA
105	GCGCATTA TTTT GCTTATCC GGTATTCTAAATCAGA
106	TATAGAAG TTTT CGACAAAA GGTAAAGTAGAGAATA
107	TAAAGTAC TTTT CGCGAGAA AACTTTTTATCGCAAG
108	ACAAAGAA TTTT ATTAATTA CATTTAACACATCAAG
109	AAAACAAA TTTT TTCATCAA TATAATCCTATCAGAT
110	GATGGCAA TTTT AATCAATA TCTGGTCACAAATATC
111	AAACCCTC TTTT ACCAGTAA TAAAAGGGATTCACCA GTCACACG TTTT
112	CCGAAATCCGAAAATC CTGTTTGAAGCCGGAA
113	CCAGCAGGGGCAAAATCCCTTATAAAGCCGGC
114	GCATAAAGTTCCACAC AACATACGAAGCGCCA
115	GCTCACAATGTAAAGCCTGGGGTGGGTTTGCC
116	TTCGCCATTGCCGGAA ACCAGGCATTAAATCA
117	GCTICTGGTCAGGCTGCGCAACTGTGTTATCC
118	GITAAAATTITTAACCAATAGGAACCCGGCACC
119	AGACAGTCATTCAAAA GGGTGAGAAGCTATAT
120	AGGTAAAGAAATCACCATCAATATATATTTT
121	
122	
123	
124	
125	GGAATTACTCGTTTACCAGACGACGACAAAAGATT
126	
127	
128	
129	AAACGAAATGACCCCCAGCGATTATTCATTAC

130	CTTAAACATCAGCTTG CTTTCGAGCGTAACAC
131	TCGGTTTAGCTTGATACCGATAGTCCAACCTA
132	TGAGTTTCGTCACCAGTACAAACTTAATTGTA
133	CCCCGATTTAGAGCTTGACGGGGAAATCAAAA
134	GAATAGCCGCAAGCGGTCCACGCTCCTAATGA
135	GAGTTGCACGAGATAGGGTTGAGTAAGGGAGC
136	GTGAGCTAGTTTCCTGTGTGAAATTTGGGAAG
137	TCATAGCTACTCACATTAATTGCGCCCTGAGA
138	GGCGATCGCACTCCAGCCAGCTTTGCCATCAA
139	GAAGATCGGTGCGGGCCTCTTCGCAATCATGG
140	AAATAATTTTAAATTGTAAACGTTGATATTCA
141	GCAAATATCGCGTCTGGCCTTCCTGGCCTCAG
142	ACCGTTCTAAATGCAATGCCTGAGAGGTGGCA
143	TATATTTTAGCTGATAAATTAATGTTGTATAA
144	TCAATTCTTTTAGTTTGACCATTACCAGACCG
145	CGAGTAGAACTAATAGTAGTAGCAAACCCTCA
146	GAAGCAAAAAAGCGGATTGCATCAGATAAAAA
147	GCTTCTGGTCAGGCTGCGCAACTGTGTTATCC
148	CCAAAATATAATGCAGATACATAAACACCAGA
149	CATTCAACGCGAGAGGCTTTTGCATATTATAG
150	ACGAGTAGTGACAAGAACCGGATATACCAAGC
151	AGTAATCTTAAATTGGGCTTGAGAGAATACCA
152	GCGAAACATGCCACTACGAAGGCATGCGCCGA
153	ATACGTAAAAGTACAACGGAGATTTCATCAAG
154	CAATGACACTCCAAAAGGAGCCTTACAACGCC
155	AAAAAAGGACAACCATCGCCCACGCGGGTAAA
156	TGTAGCATTCCACAGACAGCCCTCATCTCCAA
157	GTAAAGCACTAAATCGGAACCCTAGTTGTTCC
158	AGTTTGGAGCCCTTCACCGCCTGGTTGCGCTC
159	AGCTGATTACAAGAGTCCACTATTGAGGTGCC
160	ACTGCCCGCCGAGCTCGAATTCGTTATTACGC
161	CCCGGGTACTTTCCAGTCGGGAAACGGGCAAC
162	CAGCTGGCGGACGACGACGACAGTATCGTAGCCAG
163	GTTTGAGGGAAAGGGGGGATGTGCTAGAGGATC
164	CITTCATCCCCAAAAACAGGAAGACCGGAGAG
165	AGAAAAGCAACATTAAATGTGAGCATCTGCCA
166	GGTAGCTAGGATAAAAATTTTTAGTTAACATC
16/	
168	
169	
1/0	
1/1	
172	
1/3	
1/4	TITCAACTATAGGCTGGCTGACCTTGTATCAT

175	CCAGGCGCTTAATCATTGTGAATTACAGGTAG
176	CGCCTGATGGAAGTTTCCATTAAACATAACCG
177	TTTCATGAAAATTGTGTCGAAATCTGTACAGA
178	ATATATTCTTTTTCACGTTGAAAATAGTTAG
179	AATAATAAGGTCGCTGAGGCTTGCAAAGACTT
180	CGTAACGATCTAAAGTTTTGTCGTGAATTGCG
181	ACCCAAATCAAGTTTTTTGGGGTCAAAGAACG
182	TGGACTCCCTTTTCACCAGTGAGACCTGTCGT
183	TGGTTTTTAACGTCAAAGGGCGAAGAACCATC
184	GCCAGCTGCCTGCAGGTCGACTCTGCAAGGCG
185	CTTGCATGCATTAATGAATCGGCCCGCCAGGG
186	ATTAAGTTCGCATCGTAACCGTGCGAGTAACA
187	TAGATGGGGGGTAACGCCAGGGTTGTGCCAAG
188	ACCCGTCGTCATATGTACCCCGGTAAAGGCTA
189	CATGTCAAGATTCTCCGTGGGAACCGTTGGTG
190	TCAGGTCACTTTTGCGGGAGAAGCAGAATTAG
191	CTGTAATATTGCCTGAGAGTCTGGAAAACTAG
192	CAAAATTAAAGTACGGTGTCTGGAAGAGGTCA
193	TGCAACTAAGCAATAAAGCCTCAGTTATGACC
194	TTTTTGCGCAGAAAACGAGAATGAATGTTTAG
195	AAACAGTTGATGGCTTAGAGCTTATTTAAATA
196	ACTGGATAACGGAACAACATTATTACCTTATG
197	ACGAACTAGCGTCCAATACTGCGGAATGCTTT
198	CGATTTTAGAGGACAGATGAACGGCGCGACCT
199	CTTTGAAAAGAACTGGCTCATTATTTAATAAA
200	GCTCCATGAGAGGCTTTGAGGACTAGGGAGTT
201	ACGGCTACTTACTTAGCCGGAACGCTGACCAA
202	AAAGGCCGAAAGGAACAACTAAAGCTTTCCAG
203	GAGAATAGCTTTTGCGGGGATCGTCGGGTAGCA
204	ACGTTAGTAAATGAATTTTCTGTAAGCGGAGT
205	TTTTCGATGGCCCACTACGTAAACCGTC
206	TATCAGGGTTTTCGGTTTGCGTATTGGGAACGCGCG
207	GGGAGAGGTTTTTGTAAAACGACGGCCATTCCCAGT
208	CACGACGTTTTTGTAATGGGATAGGTCAAAACGGCG
209	GATTGACCTTTTGATGAACGGTAATCGTAGCAAACA
210	AGAGAATCTTTTGGTTGTACCAAAAACAAGCATAAA
211	AGAGAATCTTTTGGTTGTACCAAAAACAAGCATAAA
212	ATATAATGTTTTCATTGAATCCCCCTCAAATCGTCA
213	TAAATATTTTTTGGAAGAAAAATCTACGACCAGTCA
214	GGACGTTGTTTTCATAAGGGAACCGAAAGGCGCAG
215	ACGGTCAATTTTGACAGCATCGGAACGAACCCTCAG
216	CAGCGAAAATTTTACTTTCAACAGTTTCTGGGATTTTGCTAAACTTTT
Loop1	AACATCACTTGCCTGAGTAGAAGAACT
Loop2	TGTAGCAATACTTCTTTGATTAGTAAT
Loop3	AGTCTGTCCATCACGCAAATTAACCGT

Loop4	ATAATCAGTGAGGCCACCGAGTAAAAG
Loop5	ACGCCAGAATCCTGAGAAGTGTTTTT
Loop6	TTAAAGGGATTTTAGACAGGAACGGT
Loop7	AGAGCGGGAGCTAAACAGGAGGCCGA
Loop8	TATAACGTGCTTTCCTCGTTAGAATC
Loop9	GTACTATGGTTGCTTTGACGAGCACG
Loop10	GCGCTTAATGCGCCGCTACAGGGCGC

Name	Sequence
A01	CGGGGTTTCCTCAAGAGAAGGATTTTGAATTA
A02	AGCGTCATGTCTCTGAATTTACCGACTACCTT
A03	TTCATAATCCCCTTATTAGCGTTTTTCTTACC
A04	ATGGTTTATGTCACAATCAATAGATATTAAAC
A05	TTTGATGATTAAGAGGCTGAGACTTGCTCAGTACCAGGCG
A06	CCGGAACCCAGAATGGAAAGCGCAACATGGCT
A07	AAAGACAACATTTTCGGTCATAGCCAAAATCA
A08	GACGGGAGAATTAACTCGGAATAAGTTTATTTCCAGCGCC
A09	GATAAGTGCCGTCGAGCTGAAACATGAAAGTATACAGGAG
A10	TGTACTGGAAATCCTCATTAAAGCAGAGCCAC
A11	CACCGGAAAGCGCGTTTTCATCGGAAGGGCGA
A12	CATTCAACAAACGCAAAGACACCAGAACACCCTGAACAAA
A13	TTTAACGGTTCGGAACCTATTATTAGGGTTGATATAAGTA
A14	CTCAGAGCATATTCACAAACAAATTAATAAGT
A15	GGAGGGAATTTAGCGTCAGACTGTCCGCCTCC
A16	GTCAGAGGGTAATTGATGGCAACATATAAAAGCGATTGAG
A17	TAGCCCGGAATAGGTGAATGCCCCCTGCCTATGGTCAGTG
A18	CCTTGAGTCAGACGATTGGCCTTGCGCCACCC
A19	TCAGAACCCAGAATCAAGTTTGCCGGTAAATA
A20	TTGACGGAAATACATACATAAAGGGCGCTAATATCAGAGA
A21	CAGAGCCAGGAGGTTGAGGCAGGTAACAGTGCCCG
A22	ATTAAAGGCCGTAATCAGTAGCGAGCCACCCT
A23	GATAACCCACAAGAATGTTAGCAAACGTAGAAAATTATTC
A24	GCCGCCAGCATTGACACCACCCTC
A25	AGAGCCGCACCATCGATAGCAGCATGAATTAT
A26	CACCGTCACCTTATTACGCAGTATTGAGTTAAGCCCAATA
A27	AGCCATTTAAACGTCACCAATGAACACCAGAACCA
A28	ATAAGAGCAAGAAACATGGCATGATTAAGACTCCGACTTG
A29	CCATTAGCAAGGCCGGGGGGAATTA
A30	GAGCCAGCGAATACCCAAAAGAACATGAAATAGCAATAGC
A31	TATCTTACCGAAGCCCAAACGCAATAATAACGAAAATCACCAG
A32	CAGAAGGAAACCGAGGTTTTTAAGAAAAGTAAGCAGATAGCCG
A33	CCTTTTTTCATTTAACAATTTCATAGGATTAG
A34	TTTAACCTATCATAGGTCTGAGAGTTCCAGTA
A35	AGTATAAAATATGCGTTATACAAAGCCATCTT
A36	CAAGTACCTCATTCCAAGAACGGGAAATTCAT
A37	AGAGAATAACATAAAAACAGGGAAGCGCATTA
A38	AAAACAAAATTAATTAAATGGAAACAGTACATTAGTGAAT
A39	TTATCAAACCGGCTTAGGTTGGGTAAGCCTGT
A40	TTAGTATCGCCAACGCTCAACAGTCGGCTGTC
A41	TITCCTFAGCACTCATCGAGAACAATAGCAGCCTTTACAG

Table S2. Staple sequences for 2D triangular origami

A42	AGAGTCAAAAATCAATATATGTGATGAAAACAAACATCAAG
A43	ACTAGAAATATATAACTATATGTACGCTGAGA
A44	TCAATAATAGGGCTTAATTGAGAATCATAATT
A45	AACGTCAAAAATGAAAAGCAAGCCGTTTTTATGAAACCAA
A46	GAGCAAAAGAAGATGAGTGAATAACCTTGCTTATAGCTTA
A47	GATTAAGAAATGCTGATGCAAATCAGAATAAA
A48	CACCGGAATCGCCATATTTAACAAAATTTACG
A49	AGCATGTATTTCATCGTAGGAATCAAACGATTTTTTGTTT
A50	ACATAGCGCTGTAAATCGTCGCTATTCATTTCAATTACCT
A51	GTTAAATACAATCGCAAGACAAAGCCTTGAAA
A52	CCCATCCTCGCCAACATGTAATTTAATAAGGC
A53	TCCCAATCCAAATAAGATTACCGCGCCCAATAAATAATAT
A54	TCCCTTAGAATAACGCGAGAAAACTTTTACCGACC
A55	GTGTGATAAGGCAGAGGCATTTTCAGTCCTGA
A56	ACAAGAAAGCAAGCAAATCAGATAACAGCCATATTATTTA
A57	GTTTGAAATTCAAATATATTTTAG
A58	AATAGATAGAGCCAGTAATAAGAGATTTAATG
A59	GCCAGTTACAAAATAATAGAAGGCTTATCCGGTTATCAAC
A60	TTCTGACCTAAAATATAAAGTACCGACTGCAGAAC
A61	GCGCCTGTTATTCTAAGAACGCGATTCCAGAGCCTAATTT
A62	TCAGCTAAAAAAGGTAAAGTAATT
A63	ACGCTAACGAGCGTCTGGCGTTTTAGCGAACCCAACATGT
A64	ACGACAATAAATCCCGACTTGCGGGAGATCCTGAATCTTACCA
A65	TGCTATTTTGCACCCAGCTACAATTTTGTTTTGAAGCCTTAAA
B01	TCATATGTGTAATCGTAAAACTAGTCATTTTC
B02	GTGAGAAAATGTGTAGGTAAAGATACAACTTT
B03	GGCATCAAATTTGGGGGCGCGAGCTAGTTAAAG
B04	TTCGAGCTAAGACTTCAAATATCGGGAACGAG
B05	ACAGTCAAAGAGAATCGATGAACGACCCCGGTTGATAATC
B06	ATAGTAGTATGCAATGCCTGAGTAGGCCGGAG
B07	AACCAGACGITTAGCTATATTITCTICTACTA
B08	GAATACCACATTCAACTTAAGAGGAAGCCCGATCAAAGCG
B09	AGAAAAGCUCUAAAAAGAGTUTGGAGUAAACAATUAUCAT
BIO	CAATATGACCCTCATATATTTTAAAGCATTAA
BII	CATCCAATAAATGGTCAATAACCTCGGAAGCA
B12	AACTCCAAGATTGCATCAAAAAGATAATGCAGATACATAA
BI3	
BI4	
BI5	GATTAGAGATTAGATACATTICGCAAATCATA
BI6	
BI/	
BI8 D10	
B19	
B20	
B21	AIAAAGCUIIIGCGGGAGAAGCCIGGAGAGGGIAG

B22	TAAGAGGTCAATTCTGCGAACGAGATTAAGCA
B23	AACACTATCATAACCCATCAAAAATCAGGTCTCCTTTTGA
B24	ATGACCCTGTAATACTTCAGAGCA
B25	TAAAGCTATATAACAGTTGATTCCCATTTTTG
B26	CGGATGGCACGAGAATGACCATAATCGTTTACCAGACGAC
B27	TAATTGCTTGGAAGTTTCATTCCAAATCGGTTGTA
B28	GATAAAAACCAAAATATTAAACAGTTCAGAAATTAGAGCT
B29	ACTAAAGTACGGTGTCGAATATAA
B30	TGCTGTAGATCCCCCTCAAATGCTGCGAGAGGCTTTTGCA
B31	AAAGAAGTTTTGCCAGCATAAATATTCATTGACTCAACATGTT
B32	AATACTGCGGAATCGTAGGGGGGTAATAGTAAAATGTTTAGACT
B33	AGGGATAGCTCAGAGCCACCACCCATGTCAA
B34	CAACAGTTTATGGGATTTTGCTAATCAAAAGG
B35	GCCGCTTTGCTGAGGCTTGCAGGGGAAAAGGT
B36	GCGCAGACTCCATGTTACTTAGCCCGTTTTAA
B37	ACAGGTAGAAAGATTCATCAGTTGAGATTTAG
B38	CCTCAGAACCGCCACCCAAGCCCAATAGGAACGTAAATGA
B39	ATTTTCTGTCAGCGGAGTGAGAATACCGATAT
B40	ATTCGGTCTGCGGGATCGTCACCCGAAATCCG
B41	CGACCTGCGGTCAATCATAAGGGAACGGAACAACATTATT
B42	AGACGTTACCATGTACCGTAACACCCCTCAGAACCGCCAC
B43	CACGCATAAGAAAGGAACAACTAAGTCTTTCC
B44	ATTGTGTCTCAGCAGCGAAAGACACCATCGCC
B45	TTAATAAAACGAACTAACCGAACTGACCAACTCCTGATAA
B46	AGGTTTAGTACCGCCATGAGTTTCGTCACCAGGATCTAAA
B47	GTTTTGTCAGGAATTGCGAATAATCCGACAAT
B48	GACAACAAGCATCGGAACGAGGGTGAGATTTG
B49	TATCATCGTTGAAAGAGGACAGATGGAAGAAAAATCTACG
B50	AGCGTAACTACAAACTACAACGCCTATCACCGTACTCAGG
B51	TAGTTGCGAATTTTTTCACGTTGATCATAGTT
B52	GTACAACGAGCAACGGCTACAGAGGATACCGA
B53	ACCAGTCAGGACGTTGGAACGGTGTACAGACCGAAACAAA
B54	ACAGACAGCCCAAATCTCCAAAAAAAAATTTCTTA
B55	AACAGCTTGCTTTGAGGACTAAAGCGATTATA
B56	CCAAGCGCAGGCGCATAGGCTGGCAGAACTGGCTCATTAT
B57	CGAGGTGAGGCTCCAAAAGGAGCC
B58	ACCCCCAGACTTTTTCATGAGGAACTTGCTTT
B59	ACCTTATGCGATTTTATGACCTTCATCAAGAGCATCTTTG
B60	CGGTTTATCAGGTTTCCATTAAACGGGAATACACT
B61	AAAACACTTAATCTTGACAAGAACTTAATCATTGTGAATT
B62	GGCAAAAGTAAAATACGTAATGCC
B63	TGGTTTAATTTCAACTCGGATATTCATTACCCACGAAAGA
B64	ACCAACCTAAAAAATCAACGTAACAAATAAATTGGGCTTGAGA
B65	CCTGACGAGAAACACCAGAACGAGTAGGCTGCTCATTCAGTGA
C01	TCGGGAGATATACAGTAACAGTACAAATAATT

C02	CCTGATTAAAGGAGCGGAATTATCTCGGCCTC
C03	GCAAATCACCTCAATCAATATCTGCAGGTCGA
C04	CGACCAGTACATTGGCAGATTCACCTGATTGC
C05	TGGCAATTTTTAACGTCAGATGAAAACAATAACGGATTCG
C06	AAGGAATTACAAAGAAACCACCAGTCAGATGA
C07	GGACATTCACCTCAAATATCAAACACAGTTGA
C08	TTGACGAGCACGTATACTGAAATGGATTATTTAATAAAAG
C09	CCTGATTGCTTTGAATTGCGTAGATTTTCAGGCATCAATA
C10	TAATCCTGATTATCATTTTGCGGAGAGGAAGG
C11	TTATCTAAAGCATCACCTTGCTGATGGCCAAC
C12	AGAGATAGTTTGACGCTCAATCGTACGTGCTTTCCTCGTT
C13	GATTATACACAGAAATAAAGAAATACCAAGTTACAAAATC
C14	TAGGAGCATAAAAGTTTGAGTAACATTGTTTG
C15	TGACCTGACAAATGAAAAATCTAAAATATCTT
C16	AGAATCAGAGCGGGAGATGGAAATACCTACATAACCCTTC
C17	GCGCAGAGGCGAATTAATTATTTGCACGTAAATTCTGAAT
C18	AATGGAAGCGAACGTTATTAATTTCTAACAAC
C19	TAATAGATCGCTGAGAGCCAGCAGAAGCGTAA
C20	GAATACGTAACAGGAAAAACGCTCCTAAACAGGAGGCCGA
C21	TCAATAGATATTAAATCCTTTGCCGGTTAGAACCT
C22	CAATATTTGCCTGCAACAGTGCCATAGAGCCG
C23	TTAAAGGGATTTTAGATACCGCCAGCCATTGCGGCACAGA
C24	ACAATTCGACAACTCGTAATACAT
C25	TTGAGGATGGTCAGTATTAACACCTTGAATGG
C26	CTATTAGTATATCCAGAACAATATCAGGAACGGTACGCCA
C27	CGCGAACTAAAACAGAGGTGAGGCTTAGAAGTATT
C28	GAATCCTGAGAAGTGTATCGGCCTTGCTGGTACTTTAATG
C29	ACCACCAGCAGAAGATGATAGCCC
C30	TAAAACATTAGAAGAACTCAAACTTTTTATAATCAGTGAG
C31	GCCACCGAGTAAAAGAACATCACTTGCCTGAGCGCCATTAAAA
C32	TCTTTGATTAGTAATAGTCTGTCCATCACGCAAATTAACCGTT
C33	CGCGTCTGATAGGAACGCCATCAACTTTTACA
C34	AGGAAGATGGGGACGACGACAGTAATCATATT
C35	CTCTAGAGCAAGCTTGCATGCCTGGTCAGTTG
C36	CCTTCACCGTGAGACGGGCAACAGCAGTCACA
C37	CGAGAAAGGAAGGGAAGCGTACTATGGTTGCT
C38	GCTCATTTTTTAACCAGCCTTCCTGTAGCCAGGCATCTGC
C39	CAGITIGACGCACTCCAGCCAGCTAAACGACG
C40	GCCAGTGCGATCCCCGGGTACCGAGTTTTTCT
C41	TTTCACCAGCCTGGCCCTGAGAGAAAGCCGGCGAACGTGG
C42	GTAACCGTCTTTCATCAACATTAAAATTTTTGTTAAATCA
C43	
C44	
C45	TAGAGCITGACGGGGAGTIGCAGCAAGCGGTCATTGGGCG
C46	GTTAAAATTCGCATTAATGTGAGCGAGTAACACACGTTGG

C47TGTAGATGGGTGCCGGAAACCAGGAACGCCAGC48GGTTTTCCATGGTCATAGCTGTTTGAGAGGCGC49GTTTGCGTCACGCTGGTTGTGCCCAAGGAGCCCCCGATTC50GGATAGGTACCCGTCGGATTCTCCTAAACGTTAATATTTC51AGTTGGGTCAAAGCGCCATTCGCCCGTAATGC52CGCGCGGGCCTGTGTGAAATTGTTGGCGAATAC53CTAAATCGGAACCCTAAGCAGCGCAAAATCCTTCGGCCAAC54CGGCGGATTGAATTCAGGCTGCGCAACGGGGGATGC55TGCTGCAAATCCGCTCACAATTCCCAGCTGCAC56TTAATGAAGTTTGATGGTGGTTCCGAGGTGCCGTAAAGCAC57TGGCGAAATCTGGGAAGGGCGATC58TGTCGTGCACACAACATACGAGCCAAGCCAGCCAGCC60TCTTCGCTATTGGAGCATAAAGTGTATGCCGGAAAACCC61TTCCAGTCCTTATAAATCAAAAAGAGAACCATCACCAAAATC62GCGCTCACAAGCCTGGGGTGCCTAC63CGATGGCCCACTACGTATAGCCCGAGATAGGGATTGCGTTC64AACTCACATTATTGAGCTGAAAAGGGTATGCGTCAL-A2CTTAATTTATTTTACCATATCAAAL-A2CTTAATTTATTTTACCATATCAAAL-A3CCTGTCCAGACGTATACCGAACGAL-B1ATGTAGCATTCCTTTAAACAGTTL-B3AACTACGAAGGCTTAGCACCATTAL-B4AATAAGGCTTGCAACAAAGTTACL-C3BATGAGTGAGCTTTCAAAAACATTL-C3BATGAGGAGCTTCCAAAAAGCGTCC		
C48GGTTTTCCATGGTCATAGCTGTTTGAGAGGCGC49GTTTGCGTCACGCTGGTTAGCCCAAGGGAGCCCCCGATTC50GGATAGGTACCCGTCGGATTGCCCCAAAGGGACCCCCGATTC51AGTTGGGTCAAAGCGCCATTCGCCCCGTAATGC52CGCGCGGGCCTGTGGAAATTGTTGGCGATTAC53CTAAATCGGAACCCTAAGCAGGCGAAAATCCTTCGGCCAAC54CGGCGGATTGAATTCAGGCTGCGCAACGGGGGATGC55TGCTGCAAATCCGCTCACAATTCCCAGCTGCAC56TTAATGAAGTTTGATGGTGGTCCGAGGTGCCGTAAAGCAC57TGGCGAAATGTTGGGAAGGGCGATC58TGTCGTGCACAACAACATACGAGCCACGCCAGCC59CAAGTTTTTTGGGGTCGAAATCGGCAAAATCCGGGAAACCC60TCTTCGCTATTGGAAGCATAAAGTGTATGCCCGCTC61TTCCAGTCCTTATAAATCAAAAGAGAACCATCACCCAAATC62GCGCTCACAAGCCTGGGGTGCCTAC63CGATGGCCCACTACGTATAGCCCGAGAAACCGTCTATCAGGGC65ACGTGGACTCCAACGTCAAAGGGCGAATTTGGAACAAGAGTCCL-A1CTTAATTAATTTTTACCATATCAAAL-A2CTTAATTAATTTTTAACCATATCAAAL-A3CCTGTCCAGACGTATACCGAACGAL-A4CTCAAGATTAGTGTAGCACATACTL-B1ATGTAGCATTCCTTTATAAACCAGTTL-B3AACTACGAAGGCTAGCACCATTAL-B4AATAAGGCTTGCAACAAGAGTACL-C1BGTGGGAACAAATTCTATTTTGAGTATCL-C2BCGGTGCGGGCCTTCCAAAAACATTL-C2BACTATAAAGAGGATAGCGTCC	C47	TGTAGATGGGTGCCGGAAACCAGGAACGCCAG
C49GTTTGCGTCACGCTGGTTTGCCCCAAGGGAGCCCCCGATTC50GGATAGGTACCCGTCGGATTCTCCTAAACGTTAATATTTC51AGTTGGGTCAAAGCGCCATTCGCCCGTAATGC52CGCGCGGGCCTGTGTGAAATTGTTGGCGATTAC53CTAAATCGGAACCCTAAGCAGCGGAAAATCCTTCGGCCAAC54CGGCGGATTGAATTCAGGCTGCGCAACGGGGGATGC55TGCTGCAAATCGGCTCACAATTCCCAGCTGCAC56TTAATGAAGTTTGATGGTGGTTCTCGAGGTGCCGTAAAGCAC57TGGCGAAATGTTGGAAGGGCGATC58TGTCGTGCACACAACATACGAGGCCACGCCAGCC60TCTTCGCTATTGGAAGCATAAAGTGTATGCCCGCTC61TTCCAGTCCTTATAAATCAAAAGAGAACCATCACCCAAATC62GCGCTCACAAGCCTGGGGTGCCTAC64AACTCACATTATGAGTGTTGTTCCAGAAACGTCAGGGGC65ACGTGGACCCAACGTCAAAGGGCGAATTTGGAACAAGAGTCCL-A1CTTAATTAATTTTTACACATACAAAL-A2CTTAATTAATTTTTACACATAACGAACCL-B1ATGTAGCATTCCTTATAAACGAGCL-B3AACTACGAAGGCTTAGCACACAACGTTL-B3AACTACGAAGGCTTAGCACACAAGTACCL-C3BATGAGTGAGCTTCCAAAAGTTACCAL-C4BACTATTAAAGAGGATAGCGTCC	C48	GGTTTTCCATGGTCATAGCTGTTTGAGAGGCG
C50GGATAGGTACCCGTCGGATTCTCCTAAACGTTAATATTTC51AGTTGGGTCAAAGCGCCATTCGCCCCGTAATGC52CGCGCGGGCCTGTGTGAAAATGTTGGCGATTAC53CTAAATCGGAACCCTAAGCAGGCGCAACGGGGGATGC54CGGCGGATTGAATTCAGGCTGCCGCAACGGGGGATGC55TGCTGCAAATCCGCTCACAATTCCCAGCTGCAC56TTAATGAAGTTTGATGGTGGTTCCGAGGTGCCGTAAAGCAC57TGGCGAAATCTGGGACACACAACATACGAGCCACGCCAGCC59CAAGTTTTTTGGGGACGACAACATACGAGCCACGCCAGCC60TCTTCGCTATTGGAAGCATAAAGTGTATGCCCGGCTC61TTCCAGTCCTTATAAATCAAAAGAGAAACCATCACCCAAATC62GCGCTCACAAGCCTGGGGTGCCTAC63CGATGGCCCACTACGTATAGCCCGAGAAACCGTCTATCAGGGC65ACGTGGACTCCAACGTCAAAGGGCGAATTTGGAACAAGAGGCC64AACTCACATTATTGAGTGTTGTTCCAGAAACCGTCTATCAGGGC65ACGTGGACTCCAACGTCAAAAGGGCGAATTTGGAACAAGAGTCCL-A1CTTAATTAATTTTTACCATATCAAAL-A2CTTAATTAATTTTAAGCATAACCAAAAL-A4CTCAAGATTAGTGTAGCAATACTL-B1ATGTAGCATTCCTTTAGAACTAAL-B3AACTACGAAGGCTTAGCAACAAGTTACL-B4AATAAGGCTTGCAACAAAGTTACL-C1BGTGGGAACAAAATTCTATATTTTGAGL-C2BCGGTGCGGCCTTCCAAAAACATTL-C3BATGAGTGAGCTTTTAAAAACAGTTL-C4BACTATTAAAGGGATAGCGTCC	C49	GTTTGCGTCACGCTGGTTTGCCCCAAGGGAGCCCCCGATT
C51AGTTGGGTCAAAGCGCCATTCGCCCCGTAATGC52CGCGCGGGCCTGTGTGAAATTGTTGGCGATTAC53CTAAATCGGAACCCTAAGCAGGCGAAATCCTTCGGCCAAC54CGGCGGATTGAATTCAGGCTGCCAACGGGGGATGC55TGCTGCAAATCCGCTCACAATTCCCAGGTGCCGTAAAGCAC56TTAATGAAGTTTGATGGTGGTTCCGAGGTGCCGTAAAGCAC57TGGCGAAATGTTGGGAAGGGCGATC58TGTCGTGCACACAACATACGAGCCACGCCAGCC59CAAGTTTTTTGGGAGGTCGAAATCGGCAAATCCGGGAAACCC60TCTTCGCTATTGGAAGCATAAAGTGTATGCCCGCTC61TTCCAGTCCTTATAAATCAAAAGAGAAACCATCACCCAAATC62GCGCTCACAAGCCTGGGGGTGCCTAC63CGATGGCCCACTACGTATAGCCCGAGATAGGGATTGCGTTC64AACTCACATTATTGAGTGTTGTTCCAGAAACCGTCTATCAGGGC65ACGTGGACTCCAACGTCAAAGGGCGAATTTGGAACAAGAGTCCL-A1CTTAATTAATTTTTACCATATCAAAL-A2CTTAATTAGTCTTTAAAACAGAGAL-A3CCTGTCCAGACGTATACCGAACGAL-A4CTCAAGATTAGTGTAGCACCATTAL-B1ATGTAGCATTCCTTTTAAAACAGTTL-B3AACTACGAAGGCTTAGCACCATTAL-C1BGTGGGAACAAATTCTAAAACAGTTAL-C3BATGAGTGAGCTTTCAAAAACAGTTCL-C4BACTATTAAAGAGGATAGCGTCC	C50	GGATAGGTACCCGTCGGATTCTCCTAAACGTTAATATTTT
C52CGCGCGGGCCTGTGTGTGAAATTGTTGGCGATTAC53CTAAATCGGAACCCTAAGCAGGCGAAAATCCTTCGGCCAAC54CGGCGGATTGAATTCAGGCTGCGCAACGGGGGATGC55TGCTGCAAATCCGCTCACAATTCCCAGCTGCAC56TTAATGAAGTTTGATGGTGGTCCGAAGGTGCCGTAAAGCAC57TGGCGAAATGTTGGGAAGGGCGATC58TGTCGTGCACACAACATACGAGCCACGCCAGCC59CAAGTTTTTTGGGAGGCGAAATCGGCAAAATCCGGGAAACCC60TCTTCGCTATTGGAAGCATAAAGTGTATGCCCGCTC61TTCCAGTCCTTATAAATCAAAAGAGAAACCATCACCCAAATC62GCGCTCACAAGCTGGGGTGCCTAC63CGATGGCCCACTACGTATAGCCCGAGATAGGGATTGCGTTC64AACTCACATTATTGAGTGTTGTTCCAGAAACCGTCTATCAGGGC65ACGTGGACTCCAACGTCAAAGGCGAATTTGGAACAAGAGTCCL-A2CTTAATTAATTTTTACCATATCAAAL-A2CTTAATTGATGTAGGCGAATACTL-B1ATGTAGCATTACTTAGACTTACAAAL-B2ATTTAATTGTATTCCACCAGAGCCL-B3AACTACGAAGGCTTAGCACCATTAL-B4AATAAGGCTTGCAACAAGATACL-C2BCGGTGCGGGCCTTCCAAAAACATTL-C3BATGAGTGAGACTATCCACL-C4BACTATTAAAGAGGATAGCGTCC	C51	AGTTGGGTCAAAGCGCCATTCGCCCCGTAATG
C53CTAAATCGGAACCCTAAGCAGGCGAAAATCCTTCGGCCAAC54CGGCGGATTGAATTCAGGCTGCGCAACGGGGGATGC55TGCTGCAAATCCGCTCACAATTCCCAGCTGCAC56TTAATGAAGTTTGATGGTGGTTCCGAGGTGCCGTAAAGCAC57TGGCGAAATGTTGGGAAGGGCGATC58TGTCGTGCACAACATACGAGCCACGCCAGCC59CAAGTTTTTGGGATCGAAATCGGCAAAATCCGGGAAACCC60TCTTCGCTATTGGAAGCATAAAGTGATATGCCCGCTC61TTCCAGTCCTTATAAATCAAAAGAGAACCATCACCCAAATC62GCGCTCACAAGCCTGGGGTGCCTAC63CGATGGCCCACTACGTATAGCCCGAGATAGGGATTGCGTTC64AACTCACATTATTGAGTGTTGTTCCAGAAACCGTCTATCAGGGC65ACGTGGACTCCAACGTCAAAGGGCGAATTTGGAACAAGAGTCCL-A1CTTAATTAATTTTTTACCATATCAAAL-A2CTTAATTAATTTTTAACATATCAAAL-A3CCTGTCCCAGACGTATACCGAACGAL-A4CTCAAGATTAGTGTAGCAATACTL-B1ATGTAGCATTCCTTTAAAACAGTTL-B3AACTACGAAGGCTTAGCACCATTAL-B4AATAAGGCTTGCAACAAAGTTACL-C1BGTGGGAACAAATTTCAAAAACATTL-C2BCGGTGCGGGCCTTCCAAAAACATTL-C4BACTATTAAAGAGGATAGCGTCC	C52	CGCGCGGGCCTGTGTGAAATTGTTGGCGATTA
C54CGGCGGATTGAATTCAGGCTGCGCAACGGGGGATGC55TGCTGCAAATCCGCTCACAATTCCCAGCTGCAC56TTAATGAAGTTTGATGGTGGTTCCGAGGTGCCGTAAAGCAC57TGGCGAAATGTTGGGAAGGGCGATC58TGTCGTGCACACAACATACGAGCCACGCCAGCC59CAAGTTTTTTGGGGTCGAAATCGGCAAAATCCGGGAAACCC60TCTTCGCTATTGGAAGCATAAAGAGAACCATCACCCAAATC62GCGCTCACAAGCCTGGGGTGCCTAC63CGATGGCCCACTACGTATAGCCCGAGATAGGGATTGCGTTC64AACTCACATTATTGAGTGTTGTTCCAGAAACCGTCTATCAGGGC65ACGTGGACTCCAACGTCAAAGGGCGAATTTGGAACAAGAGTCCL-A1CTTAATTAATTTTTACCATATCAAAL-A2CTTAATTCATCTTAGACTTTACAAL-A3CCTGTCCCAGACGTAACCGAACGAL-A4CTCAAGATTAGTGAGCAATACTL-B1ATGTAGCATTCCTTTAAAACAGTTL-B2ATTTAATTGTATTCCACCAGAGCCL-B3AACTACGAAGGCTTAGCACATACL-B4AATAAGGCTTGCAACAAAGTTACL-C1BGTGGGAACAAATTTCTATTTTGAGL-C2BCGGTGCGGGCCTTCCAAAAACATTL-C4BACTATTAAAGAGGATAGCGTCC	C53	CTAAATCGGAACCCTAAGCAGGCGAAAATCCTTCGGCCAA
C55TGCTGCAAATCCGCTCACAATTCCCAGCTGCAC56TTAATGAAGTTTGATGGTGGTTCCGAGGTGCCGTAAAGCAC57TGGCGAAATGTTGGGAAGGCCGATC58TGTCGTGCACACAACATACGAGCCACGCCAGCC59CAAGTTTTTTGGGGTCGAAATCGGCAAAATCCGGGAAACCC60TCTTCGCTATTGGAAGCATAAAGTGTATGCCCGCTC61TTCCAGTCCTTATAAATCAAAAGAGAACCATCACCCAAATC62GCGCTCACAAGCCTGGGGTGCCTAC63CGATGGCCCACTACGTATAGCCCGAGATAGGGATTGCGTTC64AACTCACATTATTGAGTGTTGTTCCAGAAACCGTCTATCAGGGC65ACGTGGACTCCAACGTCAAAGGCGAAATTTGGAACAAGAGTCCL-A1CTTAATTAATTTTTACCATATCAAAL-A2CTTAATTAATTTTTACATATCAAAAGAGAACCAL-A3CCTGTCCAGACGTATAGCGAACATL-B1ATGTAGCATTACTTAGACTTAAAACAGTTL-B1ATGTAGCATTGCTATGCAACAGTAL-B1ATGTAGCATGCAACAAAGTTACL-B3AACTACGAAGGCTTAGCACCATTAL-B4AATAAGGCTTGCAACAAAGTTACL-C1BGTGGGAACAAATTTCTATTTTGAGL-C2BCGGTGCGGGCCTTCCAAAAACATTL-C4BACTATTAAAGGGATAGCGTCC	C54	CGGCGGATTGAATTCAGGCTGCGCAACGGGGGATG
C56TTAATGAAGTTTGATGGTGGTTCCGAGGTGCCGTAAAGCAC57TGGCGAAATGTTGGGAAGGGCGATC58TGTCGTGCACACAACATACGAGCCACGCCAGCC59CAAGTTTTTTGGGGGTCGAAATCGGCAAAATCCGGGAAACCC60TCTTCGCTATTGGAAGCATAAAGTGTATGCCCGCTC61TTCCAGTCCTTATAAATCAAAAGAGAACCATCACCCAAATC62GCGCTCACAAGCCTGGGGTGCCTAC63CGATGGCCCACTACGTATAGCCCGAGATAGGGATTGCGTTC64AACTCACATTATTGAGTGTTGTTCCAGAAACCGTCTATCAGGGC65ACGTGGACTCCAACGTCAAAGGGCGAATTTGGAACAAGAGTCCL-A1CTTAATTAATTTTTACCATATCAAAL-A2CTTAATTACTTAGGTATACCGAACGAL-A3CCTGTCCAGACGTATACCGAACGAL-A4CTCAAGATTAGTGTAGCAATACTL-B1ATGTAGCATTCCTTTTAAACAGTTL-B2ATTTAATTGTATTTCCACCAGAGCCL-B3AACTACGAAGGCTTAGCACCATTAL-B4AATAAGGCTTGCAACAAAGTTACL-C1BGTGGGAACAAATTTCTATTTTGAGL-C2BCGGTGCGGGCCTTCCAAAAACATTL-C4BACTATTAAAGAGGATAGCGTCC	C55	TGCTGCAAATCCGCTCACAATTCCCAGCTGCA
C57TGGCGAAATGTTGGGAAGGGCGATC58TGTCGTGCACACAACATACGAGCCACGCCAGCC59CAAGTTTTTTGGGGGTCGAAATCGGCAAAATCCGGGAAACCC60TCTTCGCTATTGGAAGCATAAAGTGTATGCCCGCTC61TTCCAGTCCTTATAAATCAAAAGAGAACCATCACCCAAATC62GCGCTCACAAGCCTGGGGTGCCTAC63CGATGGCCCACTACGTATAGCCCGAGATAGGGATTGCGTTC64AACTCACATTATTGAGTGTTGTTCCAGAAACCGTCTATCAGGGC65ACGTGGACTCCAACGTCAAAGGGCGAATTTGGAACAAGAGTCCL-A1CTTAATTAATTTTTACCATATCAAAL-A2CTTAATTACTCTTAGACTTTACAAL-A3CCTGTCCAGACGTATACCGAACGAL-A4CTCAAGATTAGTGTAGCAATACTL-B1ATGTAGCATTCCTTTTAAAACAGTTL-B2ATTTAATTGTATTTCCACCAGAGCCL-B3AACTACGAAGGCTTAGCACCATTAL-B4AATAAGGCTTGCAACAAAGTTACL-C1BGTGGGAACAAATTTCTATTTTGAGL-C2BCGGTGCGGGCCTTCCAAAAACATTL-C4BACTATTAAAGAGGATAGCGTCC	C56	TTAATGAAGTTTGATGGTGGTTCCGAGGTGCCGTAAAGCA
C58TGTCGTGCACACACACATACGAGCCACGCCAGCC59CAAGTTTTTTGGGGTCGAAATCGGCAAAATCCGGGAAACCC60TCTTCGCTATTGGAAGCATAAAGTGTATGCCCGCTC61TTCCAGTCCTTATAAATCAAAAGAGAACCATCACCCAAATC62GCGCTCACAAGCCTGGGGTGCCTAC63CGATGGCCCACTACGTATAGCCCGAGATAGGGATTGCGTTC64AACTCACATTATTGAGTGTTGTTCCAGAAACCGTCTATCAGGGC65ACGTGGACTCCAACGTCAAAGGGCGAATTTGGAACAAGAGTCCL-A1CTTAATTAATTTTTTACCATATCAAAL-A2CTTAATTCATCTTAGACTTTACAAL-A3CCTGTCCAGACGTATACCGAACGAL-A4CTCAAGATTAGTGTAGCAATACTL-B1ATGTAGCATTCCTTTATAAACAGTTL-B2ATTTAATTGTATTTCCACCAGAGCCL-B3AACTACGAAGGCTTAGCACCATTAL-B4AATAAGGCTTGCAACAAAGTTACL-C1BGTGGGAACAAATTTCTATTTTGAGL-C2BCGGTGCGGGCCTTCCAAAAACATTL-C3BATGAGTGAGCTTTAAAATATGCAL-C4BACTATTAAAGAGGATAGCGTCC	C57	TGGCGAAATGTTGGGAAGGGCGAT
C59CAAGTTTTTTGGGGTCGAAATCGGCAAAATCCGGGAAACCC60TCTTCGCTATTGGAAGCATAAAGTGTATGCCCGCTC61TTCCAGTCCTTATAAATCAAAAGAGAACCATCACCCAAATC62GCGCTCACAAGCCTGGGGTGCCTAC63CGATGGCCCACTACGTATAGCCCGAGATAGGGATTGCGTTC64AACTCACATTATTGAGTGTTGTTCCAGAAACCGTCTATCAGGGC65ACGTGGACTCCAACGTCAAAGGGCGAATTTGGAACAAGAGTCCL-A1CTTAATTAATTTTTACCATATCAAAL-A2CTTAATTAATTTTTACCATATCAAAL-A3CCTGTCCAGACGTATACCGAACGAL-A4CTCAAGATTAGTGTAGCAATACTL-B1ATGTAGCATTCCTTTTAAAACAGTTL-B2ATTTAATTGTATTTCCACCAGAGCCL-B3AACTACGAAGGCTTAGCACCATTAL-B4AATAAGGCTTGCAACAAAGTTACCL-C1BGTGGGAACAAATTTCTATTTTGAGL-C2BCGGTGCGGGCCTTCCAAAAACATTL-C3BATGAGTGAGCATTAGCACCATTAL-C4BACTATTAAAGAGGATAGCGTCC	C58	TGTCGTGCACACAACATACGAGCCACGCCAGC
C60TCTTCGCTATTGGAAGCATAAAGTGTATGCCCGCTC61TTCCAGTCCTTATAAATCAAAAGAGAAACCATCACCCAAATC62GCGCTCACAAGCCTGGGGTGCCTAC63CGATGGCCCACTACGTATAGCCCGAGATAGGGATTGCGTTC64AACTCACATTATTGAGTGTTGTTCCAGAAACCGTCTATCAGGGC65ACGTGGACTCCAACGTCAAAGGGCGAATTTGGAACAAGAGTCCL-A1CTTAATTAATTTTTACCATATCAAAL-A2CTTAATTCATCTTAGACTTTACAAL-A3CCTGTCCAGACGTATACCGAACGAL-A4CTCAAGATTAGTGTAGCAATACTL-B1ATGTAGCATTCCTTTATAAACAGTTL-B2ATTTAATTGTATTTCCACCAGAGCCL-B3AACTACGAAGGCTTAGCACCATTAL-B4AATAAGGCTTGCAACAAAGTTACL-C1BGTGGGAACAAATTTCTATTTTGAGL-C2BCGGTGCGGGCCTTCCAAAAACATTL-C3BATGAGTGAGCATTAGCACCATTAL-C4BACTATTAAAGAGGATAGCGTCC	C59	CAAGTTTTTTGGGGTCGAAATCGGCAAAATCCGGGAAACC
C61TTCCAGTCCTTATAAATCAAAAGAGAACCATCACCCAAATC62GCGCTCACAAGCCTGGGGTGCCTAC63CGATGGCCCACTACGTATAGCCCGAGATAGGGATTGCGTTC64AACTCACATTATTGAGTGTTGTTCCAGAAACCGTCTATCAGGGC65ACGTGGACTCCAACGTCAAAGGGCGAATTTGGAACAAGAGTCCL-A1CTTAATTAATTTTTACCATATCAAAL-A2CTTAATTCATCTTAGACTTTACAAL-A3CCTGTCCAGACGTATACCGAACGAL-A4CTCAAGATTAGTGTAGCAATACTL-B1ATGTAGCATTCCTTTTATAAACAGTTL-B2ATTTAATTGTATTTCCACCAGAGCCL-B3AACTACGAAGGCTTAGCAACATTACL-C1BGTGGGAACAAATTTCTATTTTGAGL-C2BCGGTGCGGGCCTTCCAAAAACATTL-C3BATGAGTGAGCTTTAAAATATGCAL-C4BACTATTAAAGAGGATAGCGTCC	C60	TCTTCGCTATTGGAAGCATAAAGTGTATGCCCGCT
C62GCGCTCACAAGCCTGGGGTGCCTAC63CGATGGCCCACTACGTATAGCCCGAGATAGGGATTGCGTTC64AACTCACATTATTGAGTGTTGTTCCAGAAACCGTCTATCAGGGC65ACGTGGACTCCAACGTCAAAGGGCGAATTTGGAACAAGAGTCCL-A1CTTAATTAATTTTTTACCATATCAAAL-A2CTTAATTCATCTTAGACTTTACAAL-A3CCTGTCCAGACGTATACCGAACGAL-A4CTCAAGATTAGTGTAGCAATACTL-B1ATGTAGCATTCCTTTTATAAACAGTTL-B2ATTTAATTGTATTTCCACCAGAGCCL-B3AACTACGAAGGCTTAGCACCATTAL-B4AATAAGGCTTGCAACAAAGTTACL-C1BGTGGGAACAAATTCTATTTTGAGL-C2BCGGTGCGGGCCTTCCAAAAACATTL-C3BATGAGTGAGCTTTAAATATGCAL-C4BACTATTAAAGAGGATAGCGTCC	C61	TTCCAGTCCTTATAAATCAAAAGAGAACCATCACCCAAAT
C63CGATGGCCCACTACGTATAGCCCGAGATAGGGATTGCGTTC64AACTCACATTATTGAGTGTTGTTCCAGAAACCGTCTATCAGGGC65ACGTGGACTCCAACGTCAAAGGGCGAATTTGGAACAAGAGTCCL-A1CTTAATTAATTTTTTACCATATCAAAL-A2CTTAATTCATCTTAGACTTTACAAL-A3CCTGTCCAGACGTATACCGAACGAL-A4CTCAAGATTAGTGTAGCAATACTL-B1ATGTAGCATTCCTTTTATAAACAGTTL-B2ATTTAATTGTATTTCCACCAGAGCCL-B3AACTACGAAGGCTTAGCACCATTAL-B4AATAAGGCTTGCAACAAAGTTACL-C1BGTGGGAACAAATTTCTATTTTGAGL-C2BCGGTGCGGGCCTTCCAAAAACATTL-C3BATGAGTGAGCTTTAAATATGCAL-C4BACTATTAAAGAGGATAGCGTCC	C62	GCGCTCACAAGCCTGGGGTGCCTA
C64AACTCACATTATTGAGTGTTGTTCCAGAAACCGTCTATCAGGGC65ACGTGGACTCCAACGTCAAAGGGCGAATTTGGAACAAGAGTCCL-A1CTTAATTAATTTTTTACCATATCAAAL-A2CTTAATTCATCTTAGACTTTACAAAL-A3CCTGTCCAGACGTATACCGAACGAL-A4CTCAAGATTAGTGTAGCAATACTL-B1ATGTAGCATTCCTTTTATAAACAGTTL-B2ATTTAATTGTATTTCCACCAGAGCCL-B3AACTACGAAGGCTTAGCACCATTAL-B4AATAAGGCTTGCAACAAAGTTACL-C1BGTGGGAACAAATTTCTATTTTGAGL-C2BCGGTGCGGGCCTTCCAAAAACATTL-C3BATGAGTGAGCTTTAAATATGCAL-C4BACTATTAAAGAGGATAGCGTCC	C63	CGATGGCCCACTACGTATAGCCCGAGATAGGGATTGCGTT
C65ACGTGGACTCCAACGTCAAAGGGCGAATTTGGAACAAGAGTCCL-A1CTTAATTAATTTTTACCATATCAAAL-A2CTTAATTTCATCTTAGACTTTACAAL-A3CCTGTCCAGACGTATACCGAACGAL-A4CTCAAGATTAGTGTAGCAATACTL-B1ATGTAGCATTCCTTTTATAAACAGTTL-B2ATTTAATTGTATTTCCACCAGAGCCL-B3AACTACGAAGGCTTAGCACCATTAL-B4AATAAGGCTTGCAACAAAGTTACL-C1BGTGGGAACAAATTTCTATTTTGAGL-C2BCGGTGCGGGCCTTCCAAAAACATTL-C3BATGAGTGAGCTTTAAATAGCAL-C4BACTATTAAAGAGGATAGCGTCC	C64	AACTCACATTATTGAGTGTTGTTCCAGAAACCGTCTATCAGGG
L-A1CTTAATTAATTTTTTACCATATCAAAL-A2CTTAATTTCATCTTAGACTTTACAAL-A3CCTGTCCAGACGTATACCGAACGAL-A4CTCAAGATTAGTGTAGCAATACTL-B1ATGTAGCATTCCTTTTATAAACAGTTL-B2ATTTAATTGTATTTCCACCAGAGCCL-B3AACTACGAAGGCTTAGCACCATTAL-B4AATAAGGCTTGCAACAAAGTTACL-C1BGTGGGAACAAATTTCTATTTTGAGL-C2BCGGTGCGGGCCTTCCAAAAACATTL-C3BATGAGTGAGCTTTTAAATATGCAL-C4BACTATTAAAGAGGATAGCGTCC	C65	ACGTGGACTCCAACGTCAAAGGGCGAATTTGGAACAAGAGTCC
L-A2CTTAATTTCATCTTAGACTTTACAAL-A3CCTGTCCAGACGTATACCGAACGAL-A4CTCAAGATTAGTGTAGCAATACTL-B1ATGTAGCATTCCTTTTATAAACAGTTL-B2ATTTAATTGTATTTCCACCAGAGCCL-B3AACTACGAAGGCTTAGCACCATTAL-B4AATAAGGCTTGCAACAAAGTTACL-C1BGTGGGAACAAATTTCTATTTTGAGL-C2BCGGTGCGGGCCTTCCAAAAACATTL-C3BATGAGTGAGCTTTAAATATGCAL-C4BACTATTAAAGAGGATAGCGTCC	L-A1C	TTAATTAATTTTTACCATATCAAA
L-A3CCTGTCCAGACGTATACCGAACGAL-A4CTCAAGATTAGTGTAGCAATACTL-B1ATGTAGCATTCCTTTTATAAACAGTTL-B2ATTTAATTGTATTTCCACCAGAGCCL-B3AACTACGAAGGCTTAGCACCATTAL-B4AATAAGGCTTGCAACAAAGTTACL-C1BGTGGGAACAAATTTCTATTTTGAGL-C2BCGGTGCGGGCCTTCCAAAAAACATTL-C3BATGAGTGAGCTTTTAAATATGCAL-C4BACTATTAAAGAGGATAGCGTCC	L-A2C	TTAATTTCATCTTAGACTTTACAA
L-A4CTCAAGATTAGTGTAGCAATACTL-B1ATGTAGCATTCCTTTTATAAACAGTTL-B2ATTTAATTGTATTTCCACCAGAGCCL-B3AACTACGAAGGCTTAGCACCATTAL-B4AATAAGGCTTGCAACAAAGTTACL-C1BGTGGGAACAAATTTCTATTTTTGAGL-C2BCGGTGCGGGCCTTCCAAAAACATTL-C3BATGAGTGAGCTTTAAATATGCAL-C4BACTATTAAAGAGGATAGCGTCC	L-A3C	CTGTCCAGACGTATACCGAACGA
L-B1ATGTAGCATTCCTTTTATAAACAGTTL-B2ATTTAATTGTATTTCCACCAGAGCCL-B3AACTACGAAGGCTTAGCACCATTAL-B4AATAAGGCTTGCAACAAAGTTACL-C1BGTGGGAACAAATTTCTATTTTTGAGL-C2BCGGTGCGGGCCTTCCAAAAACATTL-C3BATGAGTGAGCTTTTAAATATGCAL-C4BACTATTAAAGAGGATAGCGTCC	L-A4C	TCAAGATTAGTGTAGCAATACT
L-B2ATTTAATTGTATTTCCACCAGAGCCL-B3AACTACGAAGGCTTAGCACCATTAL-B4AATAAGGCTTGCAACAAAGTTACL-C1BGTGGGAACAAATTTCTATTTTTGAGL-C2BCGGTGCGGGCCTTCCAAAAACATTL-C3BATGAGTGAGCTTTTAAATATGCAL-C4BACTATTAAAGAGGATAGCGTCC	L-B1A	TGTAGCATTCCTTTTATAAACAGTT
L-B3AACTACGAAGGCTTAGCACCATTAL-B4AATAAGGCTTGCAACAAAGTTACL-C1BGTGGGAACAAATTTCTATTTTTGAGL-C2BCGGTGCGGGCCTTCCAAAAACATTL-C3BATGAGTGAGCTTTTAAATATGCAL-C4BACTATTAAAGAGGATAGCGTCC	L-B2A	TTTAATTGTATTTCCACCAGAGCC
L-B4AATAAGGCTTGCAACAAAGTTACL-C1BGTGGGAACAAATTTCTATTTTGAGL-C2BCGGTGCGGGCCTTCCAAAAACATTL-C3BATGAGTGAGCTTTTAAATATGCAL-C4BACTATTAAAGAGGATAGCGTCC	L-B3A	ACTACGAAGGCTTAGCACCATTA
L-C1BGTGGGAACAAATTTCTATTTTTGAGL-C2BCGGTGCGGGCCTTCCAAAAACATTL-C3BATGAGTGAGCTTTTAAATATGCAL-C4BACTATTAAAGAGGATAGCGTCC	L-B4A	ATAAGGCTTGCAACAAAGTTAC
L-C2BCGGTGCGGGCCTTCCAAAAACATTL-C3BATGAGTGAGCTTTTAAATATGCAL-C4BACTATTAAAGAGGATAGCGTCC	L-C1B	GTGGGAACAAATTTCTATTTTGAG
L-C3B ATGAGTGAGCTTTTAAATATGCA L-C4B ACTATTAAAGAGGATAGCGTCC	L-C2B	CGGTGCGGGCCTTCCAAAAACATT
L-C4B ACTATTAAAGAGGATAGCGTCC	L-C3B	ATGAGTGAGCTTTTAAATATGCA
	L-C4B	ACTATTAAAGAGGATAGCGTCC

Name	Sequence
1	ТААТАСТААТААТССТТТТТСАСС
2	TGGCTTAGAAAATCAGCAGCATCG
3	GAAAACGAAATTACGAATTGTGTC
4	ATGCAGATGAGTAGTATGCCCTGA
5	AGTTTCGTAGGAACCCTCAAGAGATTATCCGG
6	AAAAGGCTAAAGTATTAAACAAATCGTCAAAA
7	GGCTACAGCAGACGATGGCATTTTAGATAGCC
8	TCCATGTTGTCAGACTTGAGGGAGACAAAAGG
9	AGTCCTGAGCGCCTGTGTTATACAACATTTTG
10	GGCGTTTTAAAAGCCTACCTCCGGAGCAGAAG
11	TTACAGAGTAGGTCTGAACAAAATCGTCAATA
12	AGGAAACCAGATGATGCCTACCATTTCTGAAT
13	AAGTGTTTGGAACGGTGGGAAGAAGAGAGGGGTTCTACAAA
14	AATGGATTCCGGCGAATGAGTGTTAATCAGCTGGAACGCC
15	GCGGTCAGCAAAAGAACGGCCAACCTCAGGAAGCTTTCCG
16	ATTTAGAAGTCGTGCCACTCTAGACCAAGCTTGCATGCCT
17	AGCCCAATCACCAGTATAATAATTGTAGCTCATTTGCGGA
18	GCGAAAGAGTCTTTACACAGTTCA
19	CCTGATAAGGCATAGTTTCAACTA
20	AAGTAAGCCGGTCATACCTTTAGCACTTAGCCATAAGGCTAATTGGGCTTGAGATG
21	TGCAGAACACAAGAAATAGAAGGCAGGATTAGGAAACATGCCAAAAGG
22	TTGTTTAAAAATCCTCAGGCAGGTAGGCTTTG
23	ATTAGAGCTAATTACAGCAAAAGAGAGGAAACCGCCAAAGGGAAGGTA
24	TTTAGACATTATAATCAAATACCTAATTCTTATTACTAGAAGCGAACC
25	GAACCACCCTTAGGTTCAAAATCAAGAATAAC
26	CGACGACAGTATCGGCGCGCGGGGGGGGAAACCTGTATTAGAGATTATACATCAAAAT
27	TGACCCTGTAATGCCGAGCGAAAGGGGGGAAAGATTTACAT
28	CATTAAATTTTTGTTAGTTCCAGTTTATAAATTATTAACA
29	GCACCGCTGGCCAGTGGGATCCCC
30	TCCCGACTATTATTCTGATTAGCGATTGCGAACAAACTACGTGGCATCAATTCTAC
31	AGCCTTTAAGGTCATTACATGTTT
32	AGGACTAATGCTTTAACCTGACTA
33	AATATTGATTCAGTGAGGAACGAGATACCACAAAGAGCAA
34	TGGCAGATAATCATAACCAGTATAATCAGATAAATAATATGGATAGCA
35	ATAAAAACGGAGGTTGATTAAAGCCCTCAGCA
36	TATTTGCATTTACCAGGCAATAATCAAGTTTGGCCCCCTTTATCATCG
37	GGCTATCAGGTCATTGAGCTTGACGAGCGGGGGGCGCTCATGGAGTGAGGCTCAGCTAA
38	CCGCCTGCGAATTTATGGGTTATAACGATTTT
39	GGGTACCGATTGTTTGCTTTACAATTACCTGATTTAACAATTTAAGAA
40	TGATAAATTAATACTTAAAGGGAT
41	ATCAAAAATAATTCGCAAAATCCCTTGGAACATACCGAAC
42	AAAACGACTCTGGTGCTCCAGTCGAGAGGCGGACTAATAG
43	TAAATATGCTGAAAAGAACGCCTG
44	TTATAGTCTTGATAAGATTGTATC
45	CACTATCACCCTCAAAAGACTTTT

Table S3. Staple sequences for 3D cuboid origami

46	GTTTAATTATTAGGAGCGCAGAC
47	CTAAAGGAGGGTTTTGATTTTCAGCCCATCCT
48	ATCGTCACCAGAATGGCGGAACCTTGCGGGAG
49	GAGATTTGATTAGCGTCATTGACAAGGGAAGC
50	GCTGCTCACGGAAATTGACAGAATAACGGAAT
51	GCAAGCAAAAGCCAACCAACATGTCACCGAGT
52	AATAAGAATAACTATAAACACCGGTCACCAGT
53	AAGCCCTTTTTCATTTTCAATAGTAACAGTGC
54	TCATATGGCGTAAAACCATTTCAAACAATTCG
55	GGAAAAACGCTAGGGCGGCCGATTTTGCGGGAGAAGCCTT
56	ATTAAAAAAGAGTCCACGATTTAGCCTGAGAGGTTCTAGC
57	CACTAACATTTGCGTAAAATCGGCGTCTGGCCAAAATTCG
58	TAATCCTGAGCTCGAAGCCCGCTTCGGAAACCTGAGGGGA
59	GGCGCGAGCAACTAAAAGGAACAA
60	TGCTCCTTAGAAGCAATTTGCGGG
61	TTGAATCCTAACCCTCGTACAACG
62	CAGTTGAGTCAACTTTGTAACAAA
63	TAGCATTCCCACCCTCCTCAGTACGCCCAATA
64	GGTTTATCGCCTATTTAAAGCGCACCAATCCA
65	TCATGAGGGCCGCCAGTTGCCATCTCTTACCG
66	GGTCAATCTCAGTAGCATTCATTATAGAAAAT
67	AATTTACGACAATAAAGCTCAACATTGCAACA
68	GTTTTGAATAAGAATATGTAAATGACATCGCC
69	GCATTAGAGAGAAGAGGAATTACCTTTAGGAG
70	ACCCAAAAGAATTATTAGAAATAACATCAATA
71	AAAAGAGTAAACAGGAGCTGGCAAATTCAACCTCTGGAGC
72	CACACGACGGAGCCCCCTATTAAAATTTTGTTTTCCTGTA
73	CACGCTGATGGTTCCGTTGGGCGCTGCCAGTTAGGCAAAG
74	ACAACTCGCGCTCACTTTCGTAATCCAGTCACGACGTTGT
75	CAGAGCCACACAGACAGAATAGAAGTACGGTGCCTTTAAT
76	AGGCCGCTAGCGGATTAATATTCA
77	GAAACAAAGTTTACCAAGATTCAT
78	AATAGCTATTTTCATACACCGTAAATAAGGGAAAATCAACAATCATTGTGAATTAC
79	AGACGACGAGCATGTAATTACCGCCAGGCGGATGCCCCCTAGCTTGCT
80	TATTTATCGTCTCTGACCAGAGCCAAGTTTCC
81	AAAATATCTTTTTTAAGCAGAGGCGAACTGGCACAATCAAAAGGTGAA
82	CGGGAGCTCTGTCCATGCCAGCCAGTAGGGCTGCGTTAAAGCCTTAAA
83	GCCCTAAACTGATGCAAAGACGCTCGGGAGAA
84	ATCGTAACCGTGCATCCAGGGTGGTTGCGTTGTATTAAATTGGCAATTAGAAATTG
85	TATTTCAAAATATGATGTGTAGCGCCCTAAAGCAGTAATA
86	AATTGTAAACGTTAATGAACGTGGTTTGATGGGAGCCAGC
87	CGCCATTCGGGTTTTCCATGGTCA
88	TCAAGATTACAGTTAATAAGTGCCCGGAGTGAGCCCTCATCTATATTTTCATTTGG
89	TTCGAGGTAGAGAGTATCTGGAAG
90	ATTAAACGTCGTCATAGCATCAAA
91	TTATCACCCATTACCCACCGAACTAGGTAGAAGACGACGA
92	AAAGGGACTAAATAAGTAATTGAGTAGGAATCGAAACCAAGCCACCCT
93	TTAACTGAAACCACCAATTTACCGGGAGTTAA
94	CGTAGATTATTTTGTCATGATTAAGATAGCAGATCAAAATCCAAGCGC

95	AAACAAGAGAATCGATAATCGGAAGTCACGCTATATTACCCACGCAAATTCTGTCC
96	AGCAAATGCTTAGATTAATCCAATAGCCATAT
97	TAGCTGTTTCAGATGACCTTTGCCAAAATCGCTGGAAACAGAAATAGC
98	TCACCATCCGCAAGGAAATCAGAG
99	GCCAGCTTTCATCAACAAATCCTGACTCCAACAACTGATA
100	TAACGCCAGCCATTCACACATTAATTTTTCTTGGTTATCT
101	TTTCATTCCTGTTTAGAGTTAGCG
102	AAGATTAATCAGGATTGAATTTCT
103	TAAAAACCCTGCGGAAGGTAAAAT
104	CTTATGCGATTATTACGACCAACT
105	AGTTTCAGGTCGAGAGTCAGAACCTCAATAAT
106	GCTTGCAGTTCCAGTACCGTATAAAGTTGCTA
107	CGATTATACACCGGAAGCCACCAGACACCCTG
108	CGGATATTGTCACCGAAAACCATCGACTCCTT
109	TTTCATCGAATCGCCATAAAGTAATTAACCGT
110	AAATAAACCGCAAGACCCGTGTGAATTCTGGC
111	GAAACAATGTACATAAAGCGATAGAAAAATCT
112	ATAAGTTTTTCAGGTTCAAGTTACCGAACGTT
113	CCAGAACAGCGCGTAACTCGTTAGTAAAAATTTTTAGAAC
114	AATGCGCGGTCAAAGGAAGCACTAGAACGGTACAGTCAAA
115	TTGAGGAATTCACCAGGCAGGCGAATTAAATGAATATTTA
116	CCTGATTATCCTGTGTAGCTAACTGGCTGCGCATGGGCGC
117	TCAATAACCATATAACCTTTCAAC
118	CCAACAGGGAGGAAGCTCGCTGAG
119	GTCCAATAAAAATAGCACCCCAG
120	GGAACAACATTTTAAGACAAGAAC
121	TAACGATCCGCCACCCGGTTGATAGTTTTTAT
122	TAAACAGCAACAGTGCAGCGTCATCAGTTACA
123	ACGTAATGTCAGAGCCCAGAGCCAAGAGCAA
124	TTGAAAGACACCAATGCTTGAGCCACCACGGA
125	CGGCTGTCACAAAAGGTATTTAACGGTAATAT
126	TTTTGCACAATACCGAAAAGAACGTAGTCTTT
127	AACAAAGTGAAAACATATCAATATGAAAGGAA
128	ATTACGCATTGAATACTAACGTCAATCATATT
129	TGTAGCAAGTGCTTTCCCACCACAGCCGGAGAATCGTAAA
130	CAACAGAGGTGCCGTAGCGAAAAATATAAGCATGAGCGAG
131	AAAGCATCTTGCCCCATGAGACGGTGGTGTAGAACTGTTG
132	ATTAATTTAATGAGTGGAAATTGTAGGCGATTAAGTTGGG
133	CTCAGAACTAAAGTTTCTAAACAAAGTTGATTAGCAAACT
134	ATATTCGGCCGAAAGATGGATAGC
135	CATCTTTGGAGAGGCTGAACTAAC
136	CCAATAATACCACCGGGGAAACGTGGACAGATTAATCTTGAACTGGCTCATTATAC
137	AAGTACCGTTTCCTTAAGCAAGCCTAAGTATACCTTGAGTTTGATACC
138	TAATTTGCACATGGCTCACCACCCCCACTACG
139	CAACAGTTATGTGAGTTGATTGCTGTATGTTAGCAAAGACATTTGGGA
140	CGTATAACTACTTCTTGCCTTGCTAACGCCAATGGTTTGACCAGCTAC
141	ATGGCTATCGAGAAAAGAATCCTTCAGAGGGT
142	ATGGGATAGGTCACGTGCAACAGCGGGTGCCTTAAAAGTTGAATTATCGATGAATA
143	CCTCATATTGAGAAAGCCCGCCGCGGGTCGAGATAGAACC

144	AAAAACAGGAAGATTGCCGTCTATACGCTGGTACCTTGCT
145	GGAAGGGCGTGCTGCATATCCGCT
146	AATTTTATGGTCAGTGGCCCGGAAGGATTTTGTGTCGTCTTACATTTCGCAAATGG
147	GATAGTTGAGACCGGACCCAATTC
148	AAGGCACCGTTTAGACCTTCAAAT
149	ATTAGAGCATCAAGAGGAACGGTGAATAAAACTTTGCAAA
150	CTTCTGACAAATTTAACATGTAATCGAGAACATCATTCCACCGCCACC
151	AATTGAGCCTCAGAGCTTTGATGATAACCGAT
152	TACAGTAAAAAGAAACGCAAACGTGCAAGGCCAACCGCCTAAAACACT
153	ACTAGCATGTCAATCAGTTTTTTGGCTTAATGAACTATCGTGATTAGTAGAATATA
154	GAACCTCATTCCCTTACTTTTTCACCAGAGCC
155	CACAATTCAAGGAGCGTGAGTAACGATTCGCCGAATAACCAGTTAAGC
156	CAAAAGGGATTTTAAAGACGAGCA
157	TAACAACCCGTCGGATAGCGGTCCCAGGGCGAATTTTTGA
158	AGGGGGATGATCGGTGAAAGCCTGTGATTGCCTGGCAAAT
159	TGCGAACGCCATTAGATTCCAGAC
160	ATCGCGTTAGCGAACCCGCCGACA
161	AGAAGTTTAGTAAAATAACCTAAA
162	CAGTCAGGTCTACGTTTACAGACC
163	TCTGTATGTAGGTGTAGTTTAGTAAGAACGGG
164	CCCACGCATACAGGAGTTTAACGGCCTGAATC
165	AATACACTCCCTCAGACCGCCACCGCTAATAT
166	TGACCTTCCAGCAAAATACCATTAAGAAAATA
167	GCACTCATTTAGGCAGGTAATAAGAATAACAT
168	GCGTCTTTAATATATTTCTGACCTCTGAAAGC
169	AAGAATTGTTGCTTCTAATTAATTAATATCAA
170	AACATATACAGTACCTCAATAACGATTATCAT
171	AGAACTCACGCCGCTAGTTGCTTTTGCAATGCCTGAGTAA
172	CAGACAATTGGCCCACCAAATCAATATGTACCTAAAGATT
173	TGGTCAGTCTTCACCGTTGCAGCATCTCCGTGAAAGCCCC
174	ACCACCAGCACAACTAAAGTGTCGGGCCTCTGACCGTA

Table S4. Sequences of the Probe/Index strands for 2D rectangular origami (Given below are the sequences of all the modified strands. Note that unmodified helper strands are replaced by these modified helper strands to assemble the rectangular origami for functional assay)

B-93-1 GAGCAAAAACTTCTGA TGAGGTAGTCTGTCAGGTCC B-93-2 ACGCTCGGTCAGGATCTTCA ATAATGGAAGAAGGAG B-95-1 CGGAATTATTGAAAGG TGAGGTAGTCTGTCAGGTCC B-95-2 ACGCTCGGTCAGGATCTTCA AATTGAGGTGAAAAAT B-97-1 CTAAAGCAAGATAGAA TGAGGTAGTCTGTCAGGTCC B-97-2 ACGCTCGGTCAGGATCTTCA CCCTTCTGAATCGTCT

Name

Sequence

I-175 CCAGGCGCTTAATCATTCCTCTTTTGAGGAACAAGTTTTCTTGT TGTGAATTACAGGTAG I-177 TTTCATGAAAATTGTGTCCTCTTTTGAGGAACAAGTTTTCTTGT TCGAAATCTGTACAGA I-198 CGATTTTAGAGGACAGTCCTCTTTTGAGGAACAAGTTTTCTTGT ATGAACGGCGCGACCT I-199 CTTTGAAAAGAACTGGTCCTCTTTTGAGGAACAAGTTTTCTTGT СТСАТТАТТТААТААА GCTCCATGAGAGGCTTTCCTCTTTTGAGGAACAAGTTTTCTTGT I-200 TGAGGACTAGGGAGTT I-201 ACGGCTACTTACTTAGTCCTCTTTTGAGGAACAAGTTTTCTTGT CCGGAACGCTGACCAA C-76-1 TATCACCGTACTCAGG CTGGCTCAAC GAACTGAACC C-76-2 ACTTGCATCA GGTTCTCGGC AGGTTTAGCGGGGTTT C-77-1 TGCTCAGTCAGTCTCT CTGGCTCAAC GAACTGAACC C-77-2 ACTTGCATCA GGTTCTCGGC GAATTTACCAGGAGGT C-79-1 TGAGGCAGGCGTCAGA CTGGCTCAAC GAACTGAACC C-79-2 ACTTGCATCA GGTTCTCGGC CTGTAGCGTAGCAAGG C-81-1 CCGGAAACACACCACG CTGGCTCAAC GAACTGAACC C-81-2 ACTTGCATCA GGTTCTCGGC GAATAAGTAAGACTCC C-83-1 TTATTACGGTCAGAGG CTGGCTCAAC GAACTGAACC C-83-2 ACTTGCATCA GGTTCTCGGC GTAATTGAATAGCAGC CTTTACAGTTAGCGAA CTGGCTCAAC GAACTGAACC C-85-1 C-85-2 ACTTGCATCA GGTTCTCGGC CCTCCCGACGTAGGAA C-87-1 TCATTACCCGACAATA CTGGCTCAAC GAACTGAACC C-87-2 ACTTGCATCA GGTTCTCGGC AACAACATATTTAGGC C-89-1 AGAGGCATAATTTCAT CTGGCTCAAC GAACTGAACC C-89-2 ACTTGCATCA GGTTCTCGGC CTTCTGACTATAACTA C-91-1 TATGTAAACCTTTTTT CTGGCTCAAC GAACTGAACC C-91-2 ACTTGCATCA GGTTCTCGGC AATGGAAAAATTACCT C-93-1 GAGCAAAAACTTCTGA CTGGCTCAAC GAACTGAACC C-93-2 ACTTGCATCA GGTTCTCGGC ATAATGGAAGAAGGAG C-95-1 CGGAATTATTGAAAGG CTGGCTCAAC GAACTGAACC C-95-2 ACTTGCATCA GGTTCTCGGC AATTGAGGTGAAAAAT C-97-1 CTAAAGCAAGATAGAA CTGGCTCAAC GAACTGAACC C-97-2 ACTTGCATCA GGTTCTCGGC CCCTTCTGAATCGTCT B-76-1 TATCACCGTACTCAGG GGTGAGCTGGCGGCGGGTGT

B-76-2	CGCGGCGATATCATCATCCA AGGTTTAGCGGGGTTT
B-77-1	TGCTCAGTCAGTCTCT GGTGAGCTGGCGGCGGGTGT
B-77-2	CGCGGCGATATCATCATCCA GAATTTACCAGGAGGT
B-79-1	TGAGGCAGGCGTCAGA GGTGAGCTGGCGGCGGGTGT
B-79-2	CGCGGCGATATCATCATCCA CTGTAGCGTAGCAAGG
B-81-1	CCGGAAACACACCACG GGTGAGCTGGCGGCGGGTGT
B-81-2	CGCGGCGATATCATCATCCA GAATAAGTAAGACTCC
B-83-1	TTATTACGGTCAGAGG GGTGAGCTGGCGGCGGGTGT
B-83-2	CGCGGCGATATCATCATCCA GTAATTGAATAGCAGC
B-85-1	CTTTACAGTTAGCGAA GGTGAGCTGGCGGCGGGTGT
B-85-2	CGCGGCGATATCATCATCCA CCTCCCGACGTAGGAA
B-87-1	TCATTACCCGACAATA GGTGAGCTGGCGGGGGGGTGT
B-8/-2	CGCGGCGATATCATCATCCA AACAACATATTTAGGC
B-89-1	AGAGGCATAATTTCAT GGTGAGCTGGCGGCGGGTGT
B-89-2	CGCGGCGATATCATCATCCA CTTCTGACTATAACTA
B-91-1	TATGTAAACCTTTTTT GGTGAGCTGGCGGCGGGTGT
B-91-2	CGCGGCGATATCATCATCCA AATGGAAAAATTACCT
B-93-1	GAGCAAAAACTTCTGA GGTGAGCTGGCGGCGGGTGT
B-93-2 D 05 1	CGCGGCGATATCATCATCCA ATAATGGAAGAAGGAG
D-93-1 D 05 2	CGGAATTATTGAAAGG GGTGAGCTGGCGGCGGGTGT
D-93-2 D 07 1	CGCGGCGATATCATCATCCA AATTGAGGTGAAAAAT
D-7/-1 D 07 2	CTAAAGCAAGATAGAA GGTGAGCTGGCGGCGGGTGT
D-9/-2	CGCGGCGATATCATCATCCA CCCTTCTGAATCGTCT

Sequence of synthetic β -actin RNA:

rArCrA rCrCrC rGrCrC rGrCrC rArGrC rUrCrA rCrCrA rUrGrG rArUrG rArUrG rArUrA rUrCrG rCrCrG rCrG