Supplementary information

Multiple-unit interlocking enhance single stranded tiles assembly of DNA nanostructures

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Materials and experimental methods

1. Materials

The DNA strands for the assembling DNA bricks were purchased from Beijing Xianghong Biotechnology Co., Ltd at 10 nmol synthesis scales with concentrations normalized to 500 μM. Scaffold single-stranded Foundation ssDNA™ 7249(M13mp18) was purchased from Guild BioSciences. All single-stranded DNA with multiple-unit and all DNA staple strands were purchased from SupraDNA Technology (Beijing, China). GeneRuler Express DNA Ladder, agarose, 50×TAE buffer and SYBR Gold were purchased from Thermo Fisher Scientific. All the other chemicals were from Sigma-Aldrich (St. Louis, MO, USA).

2. DNA assembly process

The MUD-square, MUA-rectangle, MUD-triangle, MUD-cross, MUD-xU (x=2~24) samples were assembled by mixing the multiple-unit DNA strands in an equimolar stoichiometric ratio with 5-fold staple DNA strands, which were generated in the 1×TAE buffer (40 mM Tris, 20 mM glacial acetic acid, 1 nM EDTA, 20 mM magnesium acetate or magnesium acetate with concentration gradient). The final concentration of each MUD strand was adjusted to roughly 10 nM. The square-shaped DNA bricks and MUD-1U were assembled by mixing the entire DNA strands in an equimolar stoichiometric ratio, which were generated in the 0.5×TE-$MgCl_2$ buffer (5 mM Tris, 1 mM EDTA, 20 mM $MgCl_2$ or $MgCl_2$ with concentration gradient). The final concentration of each strand was adjusted to roughly 100 nM. For modifying the assembly yields, a gradient of magnesium ion concentrations was utilized, ranging from 0 mM to 30 mM in increments of 2.5 mM. The conventional DNA origami with a square shape was assembled with a ultralong scaffold M13mp18 circular DNA and 5-fold staple strands. The final concentration of M13mp18 circular DNA was adjusted to roughly 10 nM. All the DNA assemblies above were annealed in a PCR thermal cycler.

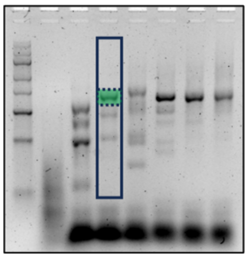
The MUD-square, MUA-rectangle, MUD-triangle, MUD-cross, MUD-xU (x=2~24) were heated to 95 °C with staying 5 min, then cooled to 75 °C at a rate of 5 °C/1 min, continued to 25 °C at a rate of 1 °C/y min (y=2, 10, 30, 60), and was finally held at 4

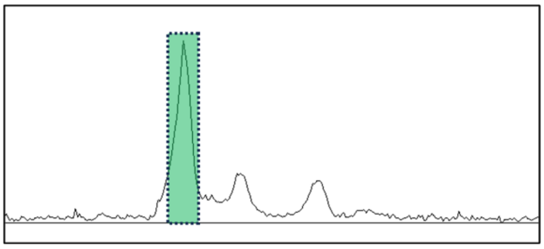
°C. The square-shaped DNA bricks and MUD-1U were heated to 90 °C with staying 5 min, then cooled to 65 °C at a rate of 1 °C/5 min, continued to 25 °C at a rate of 1 °C/y min (y=2, 10, 30, 60), and was finally held at 4 °C. The CDO-square was cooling from 85 °C to 25 °C at a rate of 1 °C/2 min, and was finally held at 4 °C. In DNA origami and MUD preparations, the use of longer scaffold strands incurs an entropic penalty, which consequently raises the melting temperature of the DNA assembly. This increase is attributed to an enthalpic effect. Therefore, the starting point of the precise cooling process of DNA bricks (65 °C) is lower than those of MUD structures (75 °C) and CDO-square structure (rapid uniform cooling rates starting from 85 °C).

3. Agarose gel electrophoresis

We run 2% agarose gels containing 1× TAE-Mg buffer (40 mM Tris, 20 mM glacial acetic acid, 1 nM EDTA, 12.5 mM magnesium acetate) or 0.5×TBE buffer (4.45 mM Tris, 4.45 mM boric acid, 1 mM EDTA). to characterize the DNA nanostructure samples. All of the samples were kept on ice throughout the experiment. Each sample, prepared at a concentration of 10 nM for the target structure and with a volume of 5 μl, was mixed with a 6 × loading in a 1 μl volume and then loaded into each lane. After sample loading, the gels were subjected to an electric field of 60 V across a distance of 18 cm for 1-2 h on ice bath. SYBR-Gold were premixed with the gel buffer during gel preparation and stained the samples during the electrophoresis process. We used the Gel doc XR+ with image lab software (Biorad) to capture and analyze the agarose gel images.

4.The calculation method for analyzing the intact assembly proportion though gel images





Capture clear images of the gel after electrophoresis. Use ImageJ software to subtract the background and then to generate an intensity curve corresponding to the selected area. Next, use a python code to calculate the intensity of the bands corresponding to the intact assembly marked by a green mask. For excluding the effect of excess short DNA strands, we calculated the intensity of the selected lane area within black-boxed region. Divide the of the intensity of intact assembly band by the intensity of total the black-boxed area to obtain the proportion of the intact assembly. Multiply the value by 100 to express the result as a percentage.

5.AFM imaging

All samples were imaged using a Multimode VIII microscope (Bruker) in the ScanAsyst mode in fluid with ScanAsyst fluid tips. The AFM samples were prepared as follows, dropping 2.5 μl (10 nM) sample solution onto the freshly cleaved mica, keeping 2-min for adsorption, adding 1×TAE-Mg^{2+}-$NiCl_2$ buffer (40 mM Tris, 20 mM glacial acetic acid, 1 nM EDTA, 12.5 mM magnesium acetate, 8 mM NiCl2) onto mica for enhancing sample adsorption. After 5-min adsorption, samples were scanned with a peak force setpoint of 0.1 N, peak force frequency of 2 kHz. AFM images were analyzed by Gwyddion 2.63 software.

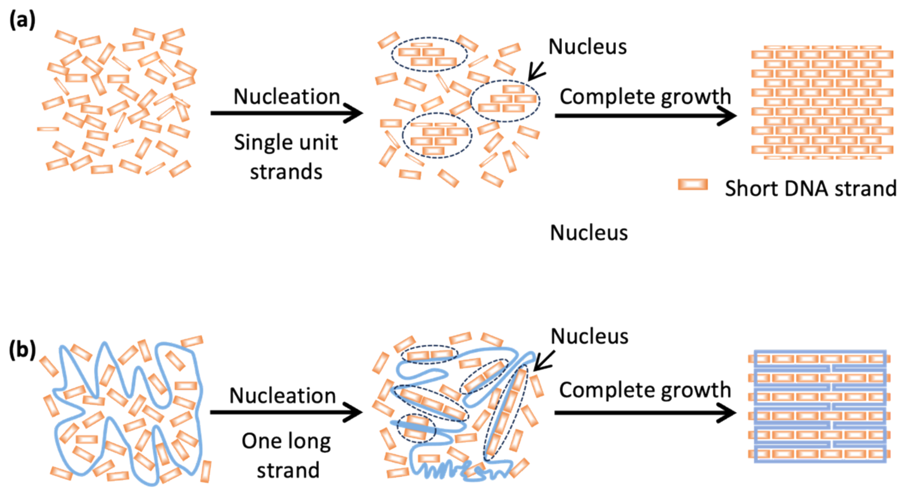


Fig. S1. Schematic illustrations of a) the DNA bricks assembly and b) the conventional DNA origami assembly, which has the same design as square shaped MUD in Scheme. 1b. In the conventional square shaped DNA origami, only one ultra-long ssDNA exists in the assembly system, all the nucleuses are arranged in the long ssDNA.

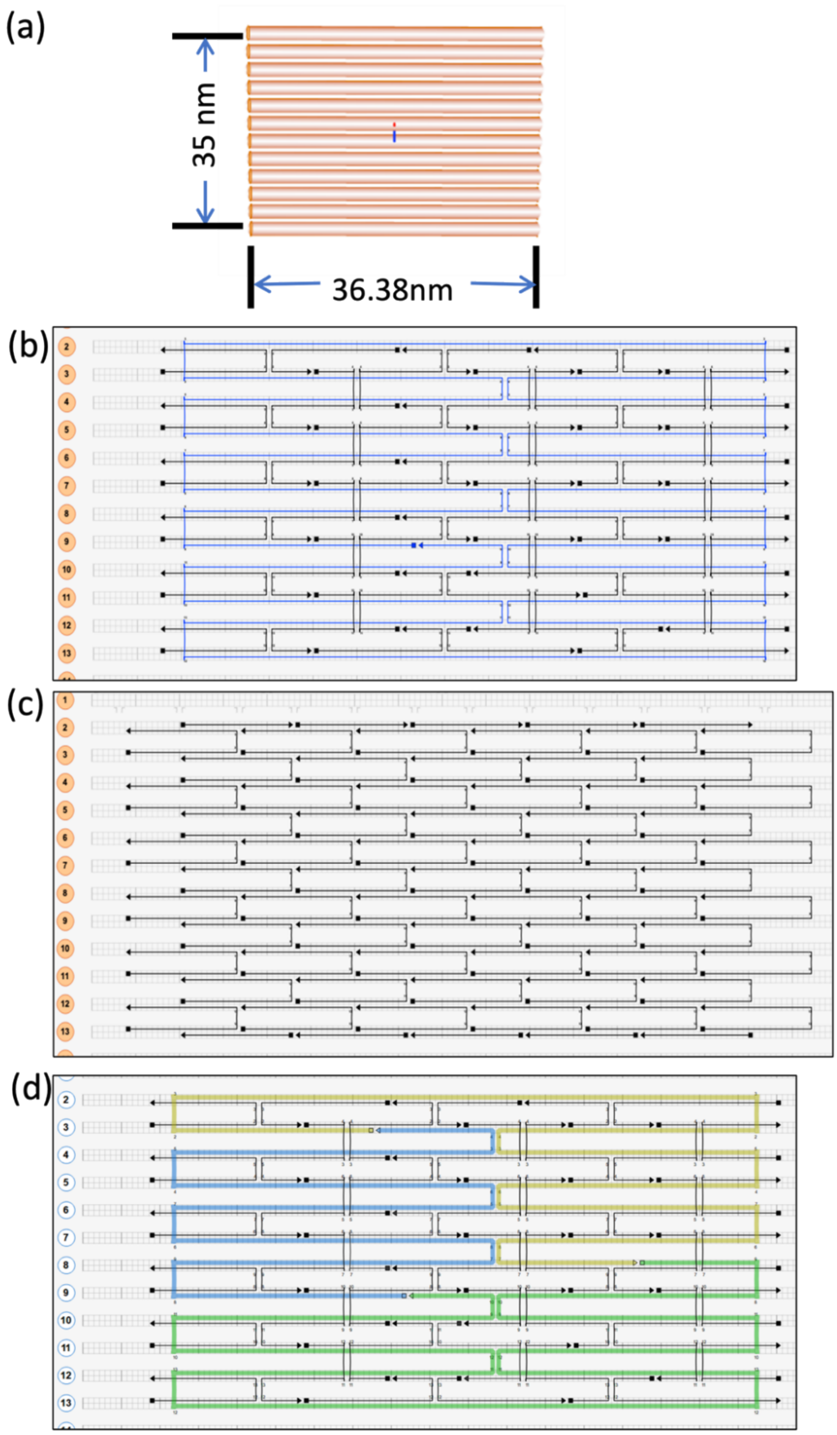


Fig. S2. a) the size details of square shaped DNA nanostructure. b-d) The arrangement of DNA strands within DNA nanostructure with square shaped designed in caDNAno. b) The conventional origami with a square shape. Only the first 1384 bases of M13mp18 were used as scaffold, which are marked by blue colors. c) DNA bricks with a square shape. All the ssDNA tiles are marked by black color. d) MUD-square. The scaffold of MUD-square is totally 1384 bases long, consisting of one 360 nt, one 410 nt and one 614 nt DNA strands which are marked by blue, olive and green colors. The staples are all marked by black color. The sequences are listed in Table S1-3.

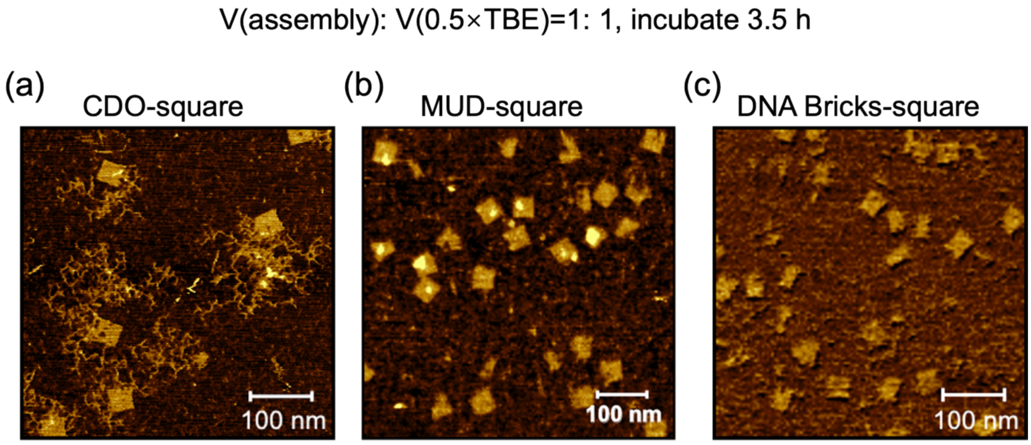


Fig. S3. The AFM results after incubating 0.5×TBE with a) CDO-square, b) MUD-square, c) DNA bricks-square for 3.5 h.

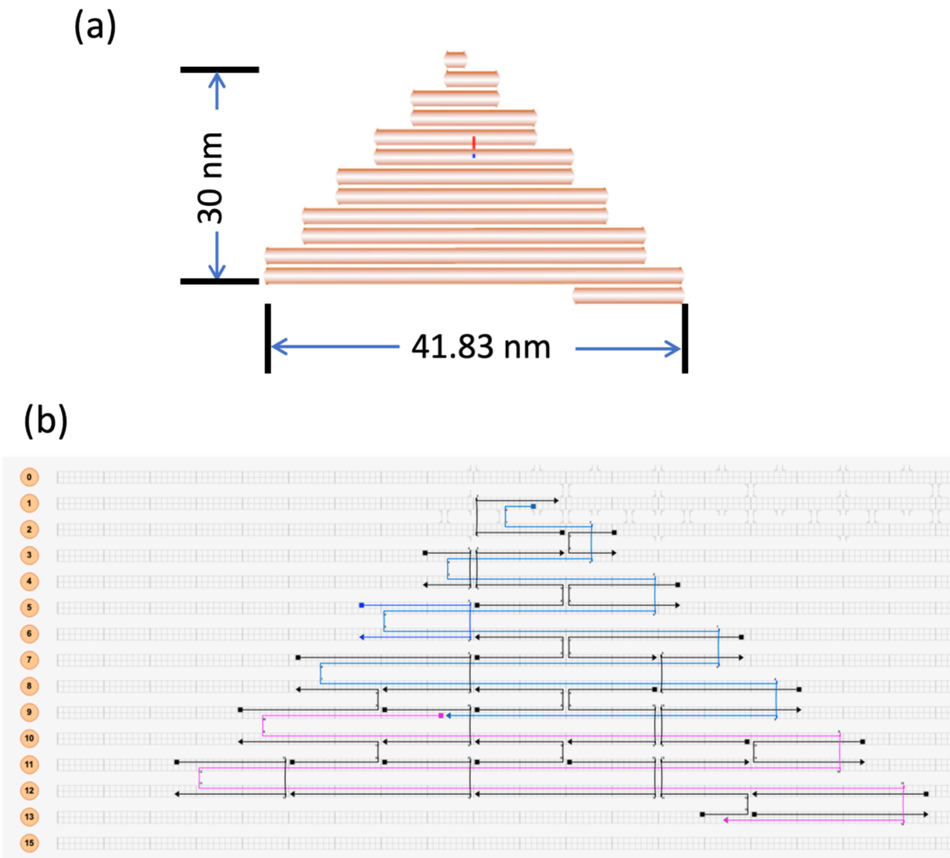
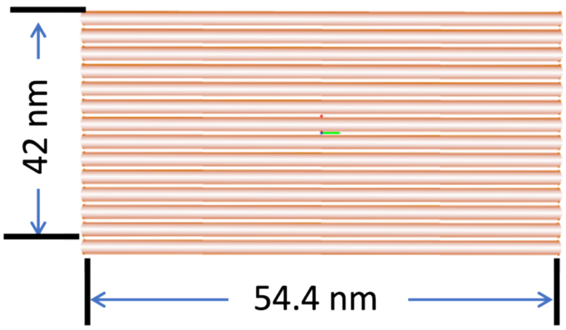


Fig. S4. a) The size details of triangle shaped DNA nanostructure. b) The arrangement of DNA strands within triangle shaped DNA nanostructure designed in caDNAno. The scaffold of MUD-triangle is totally 800 bases long, consisting of two 400 nt (8 units) DNA strands which are marked by blue and magenta colors. The staples are all marked by black color. The sequences are listed in Table S4.

(a)



(b)

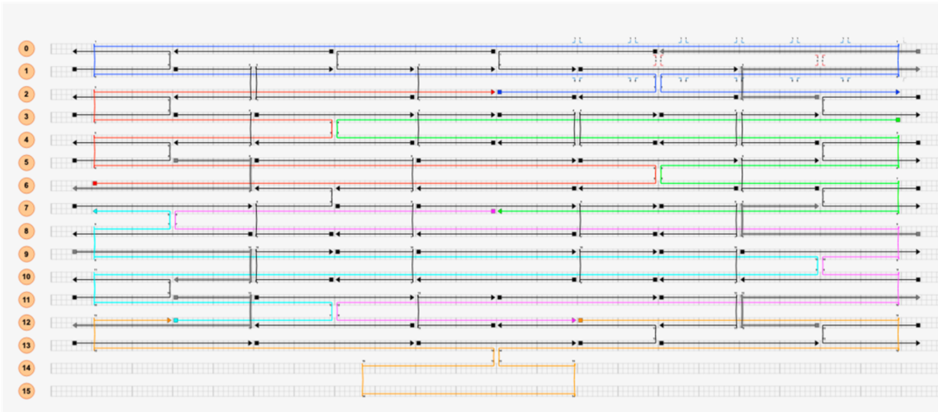


Fig. S5. a) The size details of rectangle shaped DNA nanostructure. b) The arrangement of DNA strands within rectangle shaped DNA nanostructure designed in caDNAno. The scaffold of MUD-rectangle is totally 2328 bases long, consisting of five 400 nt (8 units) and one 326 nt (6 units) DNA strands which are marked by blue, brown, green, cyan, orange and magenta colors. The staples are all marked by black color. The sequences are listed in Table S5.

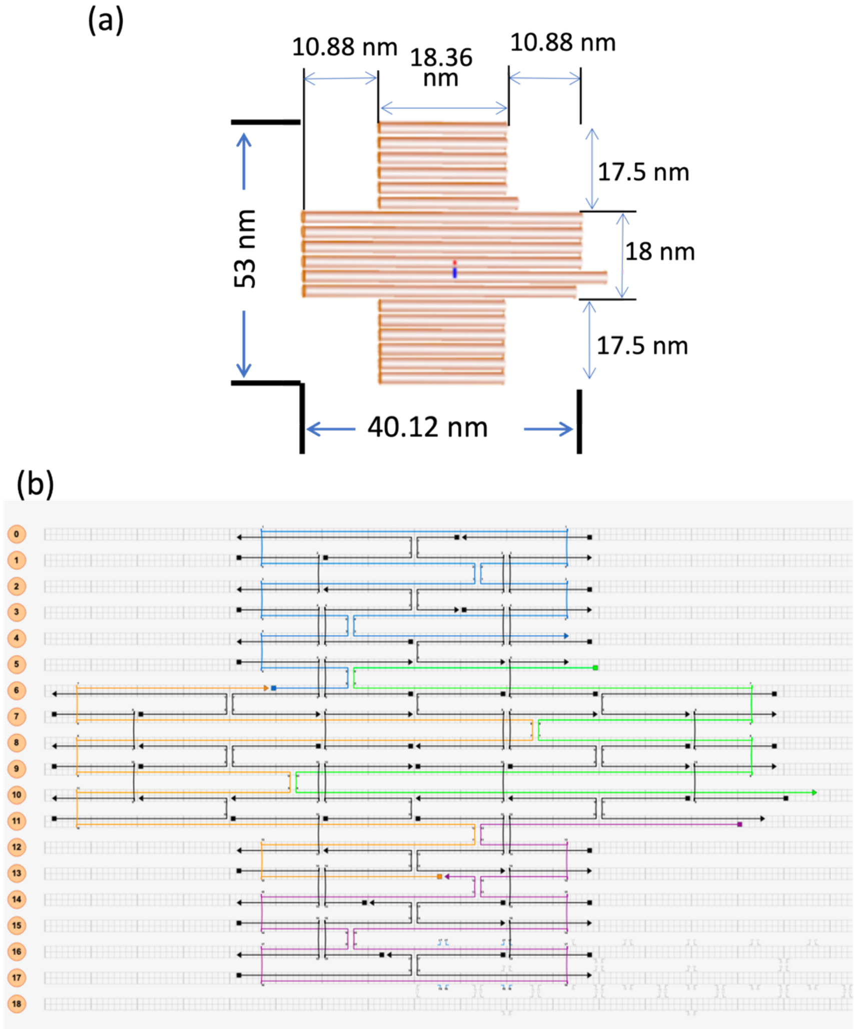


Fig.S6. a) The size details of cross shaped DNA nanostructure. b) The arrangement of DNA strands within cross shaped DNA nanostructure designed in caDNAno. The scaffold of MUD-cross is totally 1370 bases long, consisting of two 300 nt (6 units), one 360 nt (7 units) and one 410 nt (8 units) DNA strands which are marked by blue, purple, green and orange colors. The staples are all marked by black color. The sequences are listed in Table S6.

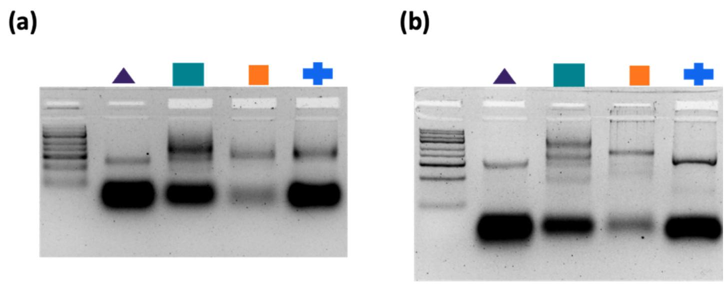


Fig. S7. The agarose gel electrophoresis (AGE, 2% w/v) images of four shapes nanostructures in the buffers containing a) 1×TAE-Mg^{2+} (12.5 mM Mg^{2+}) under 60 V,1 h and b) 0.5×TBE under 60 V, 1 h. Lane 1-4: triangle shape MUD-triangle, MUD-rectangle, MUD-square, MUD-cross. The makers are GeneRuler Express DNA Ladder, Thermo Fisher Scientific.

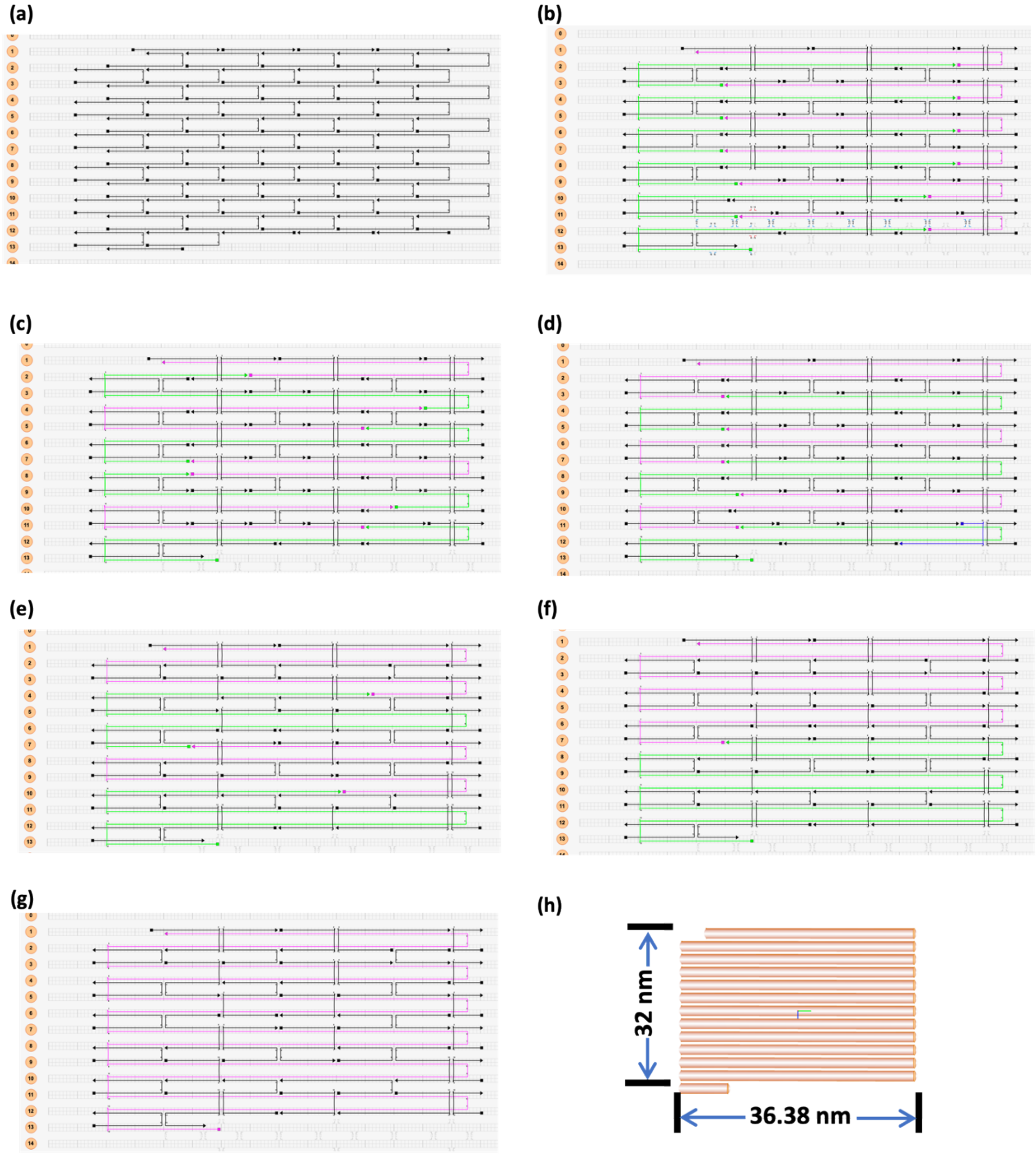


Fig. S8. The arrangement of DNA strands in MUD-xU (x=1~4, 6, 12, 24) with gradually increasing in length designed in caDNAno software. The MUD-xU (x=1~4, 6, 12, 24) were consisted of a) all short ssDNA bricks MUD-1U marked by black color, staples marked by black color with b) twelve MUD-2U of length of nearly 100 nt , c) eight MUD-3U of length of nearly 150 nt, d) six MUD-4U of length of nearly 200 nt , e) four MUD-6U of length of nearly 300 nt , f) two MUD-12U of length of nearly 600 nt , g) one MUD-24U of length of 1228 nt , which are marked by magenta and adjacent green colors. The corresponding sequences are listed in Table S7-13. h) The size details of the MUD-xU series DNA nanostructures.

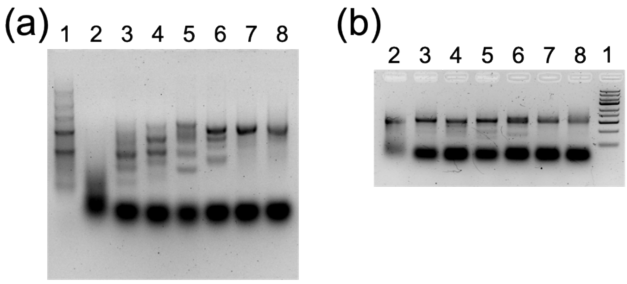


Fig. S9. The images of MUD-xU series samples under agarose gel electrophoresis with a) 1 × TAE-Mg^{2+} (2 mM Mg^{2+}) and b) 1 × TAE-Mg^{2+} (7 mM Mg^{2+}). All the MUD-xU samples were assembled with a 20 mM Mg^{2+} in buffer. Lane 1-8: double stranded DNA ladder (GeneRuler Express DNA Ladder, Thermo Fisher Scientific), MUD-1U, MUD-2U, MUD-3U, MUD-4U, MUD-6U, MUD-12U, MUD-24U.

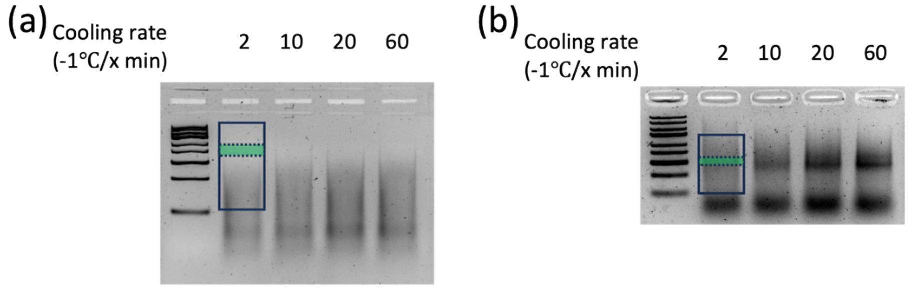


Fig. S10. The gel images of MUD-1U at cooling rate of -1 ℃/2 minutes, -1 ℃/10 minutes, -1 ℃/20 minutes, -1 ℃/60 minutes under agarose gel electrophoresis with a) 0.5×TBE and b) 1×TAE-12.5 mM Mg^{2+} buffers. The intact assembly bands were masked in green, the total areas excluding the bands of excess short DNA strands were marked by blacked boxes.

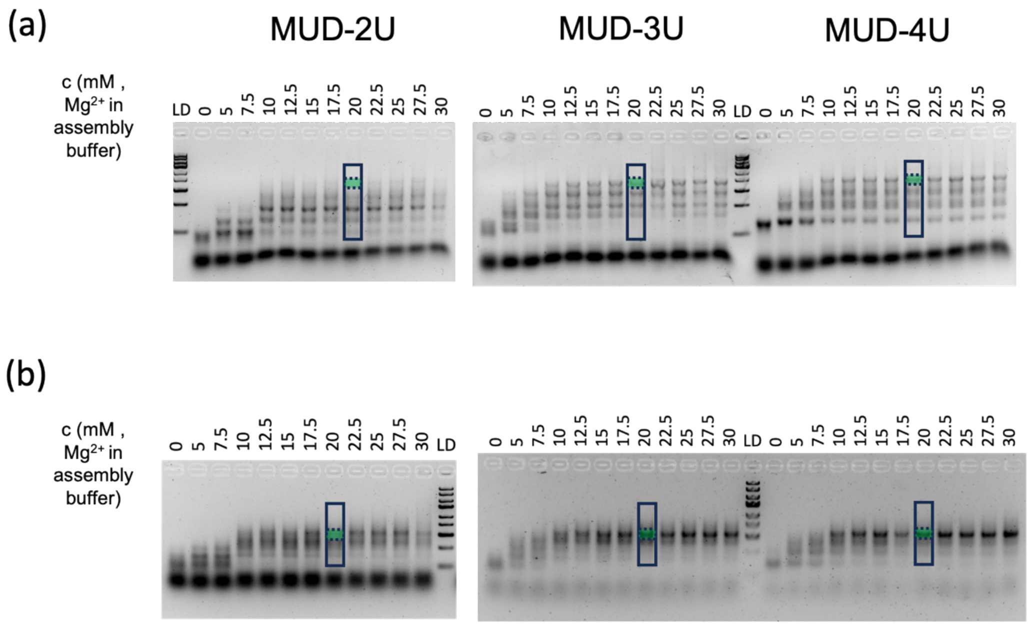


Fig. S11. The gel images of MUD-2U, MUD-3U, MUD-4U with gradient Mg^{2+} ion assembly concentrations and a cooling rate with -1 ℃/2 minutes under agarose gel electrophoresis with a) 0.5×TBE and b) 1×TAE-12.5 mM Mg^{2+} buffers. The intact assembly bands were masked in green, the total areas excluding the bands of excess short DNA strands were marked by blacked boxes.

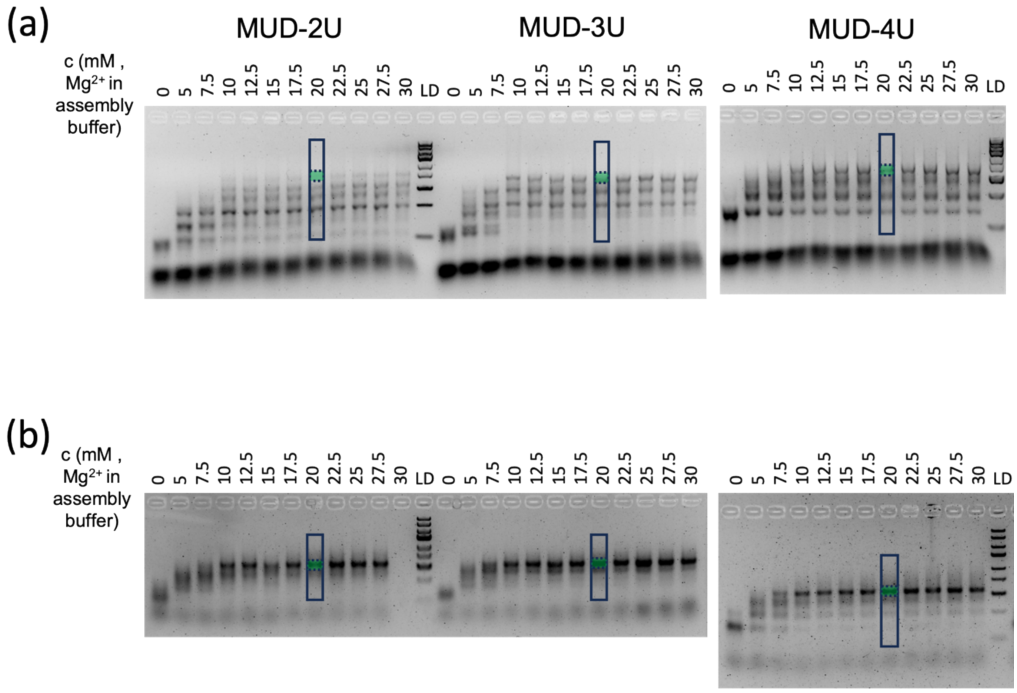


Fig. S12. The gel images of MUD-2U, MUD-3U, MUD-4U with gradient Mg^{2+} ion assembly concentrations and a cooling rate with -1 ℃/10 minutes under agarose gel electrophoresis with a) 0.5×TBE and b) 1×TAE-12.5 mM Mg^{2+} buffers. The intact assembly bands were masked in green, the total areas excluding the bands of excess short DNA strands were marked by blacked boxes.

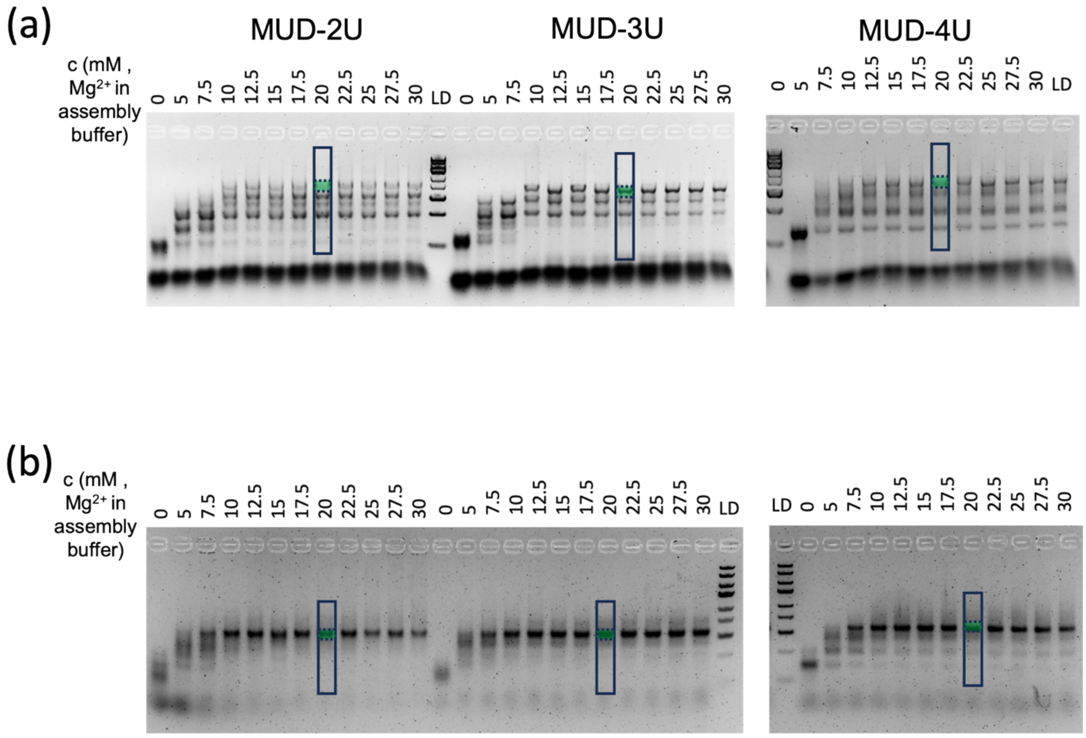


Fig. S13. The gel images of MUD-2U, MUD-3U, MUD-4U with gradient Mg^{2+} ion assembly concentrations and a cooling rate with -1 ℃/30 minutes under agarose gel electrophoresis with a) 0.5×TBE and b) 1×TAE-12.5 mM Mg^{2+} buffers. The intact assembly bands were masked in green, the total areas excluding the bands of excess short DNA strands were marked by blacked boxes.

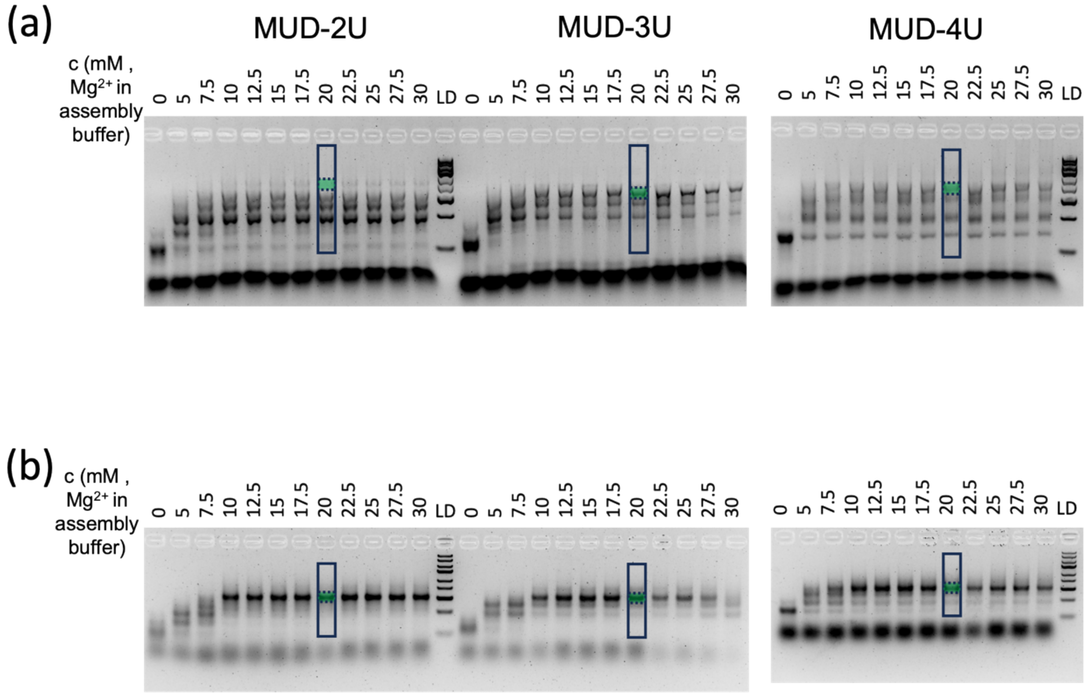


Fig. S14. The gel images of MUD-2U, MUD-3U, MUD-4U with gradient Mg^{2+} ion assembly concentrations and a cooling rate with -1 °C/60 minutes under agarose gel electrophoresis with a) 0.5×TBE and b) 1×TAE-12.5 mM Mg^{2+} buffers. The intact assembly bands were masked in green, the total areas excluding the bands of excess short DNA strands were marked by blacked boxes.

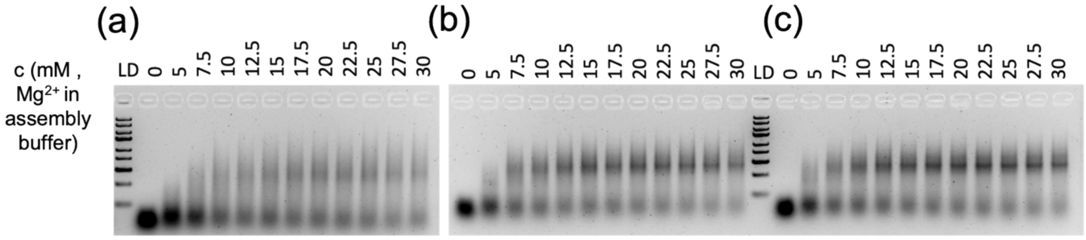


Fig. S15. The gel images of MUD-1U with gradient Mg^{2+} ion assembly concentrations and a cooling rate with a) -1 ℃/2 minutes, b) -1 ℃/10 minutes, c) -1 ℃/30 minutes under agarose gel electrophoresis with 1×TAE-12.5 mM Mg^{2+} buffer.

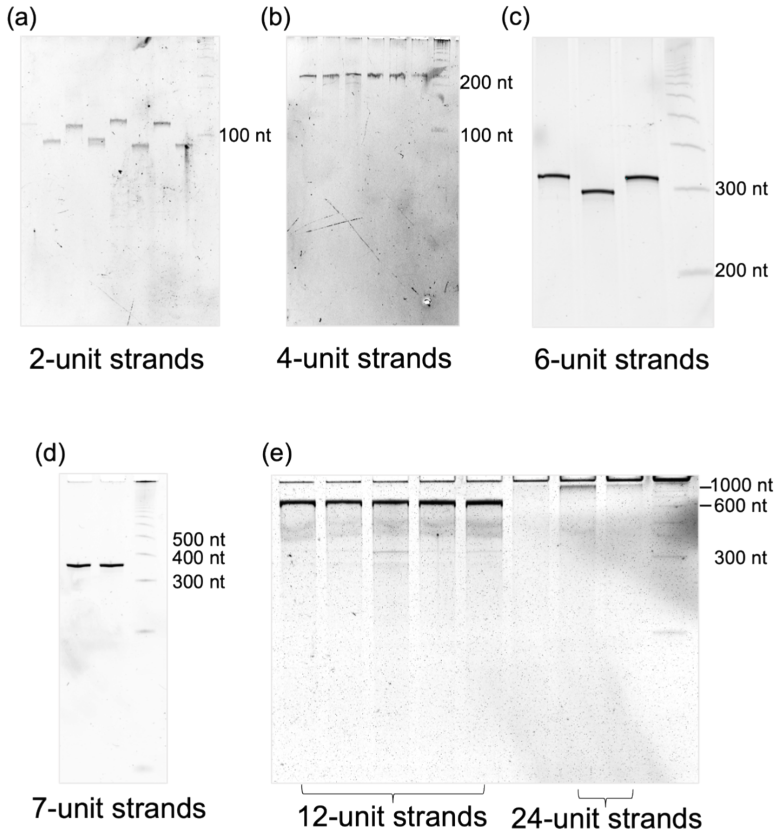


Fig.S16. The denatured Polyacrylamide gel electrophoresis of the multiple-unit DNA strands. a) the 2-unit strands, b) the 4-unit strands, c) the 6-unit strands, d) the 7-unit strands, e) the 12-unit strands and the 24-unit strands.

Sequences (5’→3’)

Table S1. Sequences of the DNA bricks with a square shape, where the italicized parts are shared by MUD-1U.

a13.1-b13.1	CCCGAAGTACCTCTGCAGGAT
a13.2-b13.2	CGTTACCAGGCTACGATGAGT
a13.3-b13.3	CTGTCCCACTCTCCTTCAAAT
a13.4-b13.4	CATTATATTGCTCCTGAGGGT
a13.5-b13.5	CGTGCATGCCCTCCCAAACTT
T10-b14.1-a13.1-T10*	*TTTTTTTTTTTGTTACTTGATGGTACTTCGGGTTTTTTTTTT*
a14.2-b14.2-a13.2-b13.1**	*CCGATGCGACTTGATATGTCTGCCTGGTAACGATCCTGCAGA*
a14.3-b14.3-a13.3-b13.2**	*CGCTGCCAGCTTCAGGGCCTTGAGTGGGACAGACTCATCGTA*
a14.4-b14.4-a13.4-b13.3**	*CAGAAGGGTCTGTGTAACTGTGCAATATAATGATTTGAAGGA*
a14.5-b14.5-a13.5-b13.4**	*CGAGCGCCGCTGCGGCTATTTGGGCATGCACGACCCTCAGGA*
a14.6-T11-T11-b13.5*	CAGGAGGCTCTTTTTTTTTTTTTTTTTTTTTTAAGTTTGGGA
a15.1-b15.1-a14.2-b14.1**	*CTGGGCAAGCCTTATTGCGATGTCGCATCGGATCAAGTAACA*
a15.2-b15.2-a14.3-b14.2**	*CGTGCGGTCCCTACGCGCAGTGCTGGCAGCGAGACATATCAA*
a15.3-b15.3-a14.4-b14.3**	*CGCGGGCCGCCTTTCAATTATGACCCTTCTGAAGGCCCTGAA*
a15.4-b15.4-a14.5-b14.4**	*CTATCTTGTACTGCACCGGTTGCGGCGCTCGACAGTTACACA*
a15.5-b15.5-a14.6*-b14.5*	CCAAACCGTCCTCCTACGTTTGAGCCTCCTGAAATAGCCGCA
T10-b16.1-a15.1-T10*	*TTTTTTTTTTTGGCCCATCATGGCTTGCCCAGTTTTTTTTTT*
a16.2-b16.2-a15.2-b15.1**	*CAAGACATACTATTCTGTATTGGGACCGCACGATCGCAATAA*
a16.3-b16.3-a15.3-b15.2**	*CTAGACCACCTCTTTCTTTATGGCGGCCCGCGACTGCGCGTA*
a16.4-b16.4-a15.4-b15.3**	*CCCTTGTGGCTAAGGAGGTCTGTACAAGATAGATAATTGAAA*
a16.5-b16.5-a15.5-b15.4**	*CACCGAACCCTTCCGCTCGCTGGACGGTTTGGAACCGGTGCA*
a16.6-T11-T11-b15.5*	CCTGAAGTTCTTTTTTTTTTTTTTTTTTTTTTAAACGTAGGA
a17.1-b17.1-a16.2-b16.1**	*CTTTGGGTACCTAGACGGGTTGTATGTCTTGATGATGGGCCA*
a17.2-b17.2-a16.3-b16.2**	*CGCATGTCCGCTCCAGAAAGTGGTGGTCTAGAATACAGAATA*

a17.3-b17.3-a16.4-b16.3**	*CTAAGGACGTCTCCAATTCATGCCACAAGGGATAAAGAAAGA*
a17.4-b17.4-a16.5-b16.4**	*CAAATGCATACTTTGTTTAGTGGGTTCGGTGAGACCTCCTTA*
a17.5-b17.5-a16.6*-b16.5*	CACTTAGAGTCTGGGCCCGGTGAACTTCAGGAGCGAGCGGAA
T10-b18.1-a17.1-T10*	*TTTTTTTTTTTTCCAGACTATGGTACCCAAAGTTTTTTTTTT*
a18.2-b18.2-a17.2-b17.1**	*CGTTCGCTTCTGCTGGGCCGTGCGGACATGCGAACCCGTCTA*
a18.3-b18.3-a17.3-b17.2**	*CACCCTTACCTTTCTGCCAATGACGTCCTTAGACTTTCTGGA*
a18.4-b18.4-a17.4-b17.3**	*CGCCTCACACTGTCAGAGTTTGTATGCATTTGATGAATTGGA*
a18.5-b18.5-a17.5-b17.4**	*CTAACCTGCCTGACCGATCGTGACTCTAAGTGACTAAACAAA*
a18.6-T11-T11-b17.5*	CGACGATACCTTTTTTTTTTTTTTTTTTTTTTACCGGGCCCA
a19.1-b19.1-a18.2-b18.1**	*CTGAGATGATCTCAAACGAATGAAGCGAACGATAGTCTGGAA*
a19.2-b19.2-a18.3-b18.2**	*CCCTTCCCGCCTTAGGCGGCTGGTAAGGGTGACGGCCCAGCA*
a19.3-b19.3-a18.4-b18.3**	*CCTGGCTAGTCTATTGTTAATGTGTGAGGCGATTGGCAGAAA*
a19.4-b19.4-a18.5-b18.4**	*CTACGTGGAGCTATTAGGGATGGCAGGTTAGAAACTCTGACA*
a19.5-b19.5-a18.6*-b18.5*	CTGACATTACCTCACAATCCTGGTATCGTCGACGATCGGTCA
T10-b20.1-a19.1-T10*	*TTTTTTTTTTTTACCTTGCTTGATCATCTCAGTTTTTTTTTT*
a20.2-b20.2-a19.2-b19.1**	*CGCTTAAGTCTTGGCGCTAATGGCGGGAAGGGATTCGTTTGA*
a20.3-b20.3-a19.3-b19.2**	*CCCTAGGCCCTAGCTGCATGTGACTAGCCAGGAGCCGCCTAA*
a20.4-b20.4-a19.4-b19.3**	*CTAAGCCTTCTGTTAATTCTTGCTCCACGTAGATTAACAATA*
a20.5-b20.5-a19.5-b19.4**	*CGGGCTCCACTGTAAGTGCTTGGTAATGTCAGATCCCTAATA*
a20.6-T11-T11-b19.5*	CTCTGTTATCTTTTTTTTTTTTTTTTTTTTTTAGGATTGTGA
a21.1-b21.1-a20.2-b20.1**	*CTTGCTTTGCCTCCTAACGATGACTTAAGCGAAGCAAGGTAA*
a21.2-b21.2-a20.3-b20.2**	*CAATACACCGCTGCAAGACCTGGGCCTAGGGATTAGCGCCAA*
a21.3-b21.3-a20.4-b20.3**	*CTTGGGACGGCTTTGGAAATTGAAGGCTTAGACATGCAGCTA*
a21.4-b21.4-a20.5-*	*CCAATTAGGACTAATTTAGATGTGGAGCCCGAAGAATTAACA*

b20.4*	
a21.5-b21.5-a20.6*-b20.5*	CTTTGGCCATCTTATCCAAATGATAACAGAGAAGCACTTACA
T10-b22.1-a21.1*-T10	TTTTTTTTTTTGTTGTTTGTTGGCAAAGCAAGTTTTTTTTTT
a22.2-b22.2-a21.2*-b21.1*	CTCTGACGGCTACATTGAGGTGCGGTGTATTGATCGTTAGGA
a22.3-b22.3-a21.3*-b21.2*	CGGAAGTGCCTCCATGATTGTGCCGTCCCAAGAGGTCTTGCA
a22.4-b22.4-a21.4*-b21.3*	CTACCATGGCTGCTCACGAGTGTCCTAATTGGAATTTCCAAA
a22.5-b22.5-a21.5*-b21.4*	CTTAGTCGGCTGCCGATAGTTGATGGCCAAAGATCTAAATTA
a22.6-T11-T11-b21.5*	CGCAAGCGCCTTTTTTTTTTTTTTTTTTTTTTATTTGGATAA
a23.1-b23.1-a22.2*-b22.1*	CATGCCTGCCCTTGCTAACTTGCCGTCAGAGAACAAACAACA
a23.2-b23.2-a22.3*-b22.2*	CAAGACTATACTCAGGACGCTGGCACTTCCGACCTCAATGTA
a23.3-b23.3-a22.4*-b22.3*	CACGCGCATCCTCCGTTTATTGCCATGGTAGACAATCATGGA
a23.4-b23.4-a22.5*-b22.4*	CGTAAAGCTGCTATGGTCTATGCCGACTAAGACTCGTGAGCA
a23.5-b23.5-a22.6*-b22.5*	CGTGAATGCACTCGGTAGACTGGCGCTTGCGAACTATCGGCA
T10-b24.1-a23.1*-T10	TTTTTTTTTTTCAGTATGTATGGGCAGGCATGTTTTTTTTTT
a24.2-b24.2-a23.2*-b23.1*	CTGTATCGGCTTTAGTATAATGTATAGTCTTGAAGTTAGCAA
a24.3-b24.3-a23.3*-b23.2*	CATCTGGGTCTACAAGACCCTGGATGCGCGTGAGCGTCCTGA
a24.4-b24.4-a23.4*-b23.3*	CACAGATGTCTATTTGCGAGTGCAGCTTTACGAATAAACGGA
a24.5-b24.5-a23.5*-b23.4*	CAGCGTGGACTCGTAACAATTGTGCATTCACGATAGACCATA
a24.6-T11-T11-b23.5*	CCGGCTCGCCTTTTTTTTTTTTTTTTTTTTTTAGTCTACCGA
a24.2*-b24.1*	GCCGATACAGATACATACTGA
a24.3*-b24.2*	GACCCAGATGATTATACTAAA
a24.4*-b24.3*	GACATCTGTGAGGGTCTTGTA
a24.5*-b24.4*	GTCCACGCTGACTCGCAAATA
a24.6*-b24.5*	GGCGAGCCGGAATTGTTACGA

Table S2. Sequences of conventional square-shaped DNA origami, which scaffold is the former 1384 bases of M13mp18 viral DNA as follows.

M13mp18-1384	AATGCTACTACTATTAGTAGAATTGATGCCACCTTTTCAGCTCG CGCCCCAAATGAAAATATAGCTAAACAGGTTATTGACCATTTG CGAAATGTATCTAATGGTCAAACTAAATCTACTCGTTCGCAGA ATTGGGAATCAACTGTTATATGGAATGAAACTTCCAGACACCG TACTTTAGTTGCATATTTAAAACATGTTGAGCTACAGCATTATA TTCAGCAATTAAGCTCTAAGCCATCCGCAAAAATGACCTCTTA TCAAAAGGAGCAATTAAAGGTACTCTCTAATCCTGACCTGTTG GAGTTTGCTTCCGGTCTGGTTCGCTTTGAAGCTCGAATTAAAA CGCGATATTTGAAGTCTTTCGGGCTTCCTCTTAATCTTTTTGAT GCAATCCGCTTTGCTTCTGACTATAATAGTCAGGGTAAAGACC TGATTTTTGATTTATGGTCATTCTCGTTTTCTGAACTGTTTAAA GCATTTGAGGGGGATTCAATGAATATTTATGACGATTCCGCAG TATTGGACGCTATCCAGTCTAAACATTTTACTATTACCCCCTCT GGCAAAACTTCTTTTGCAAAAGCCTCTCGCTATTTTGGTTTTTA TCGTCGTCTGGTAAACGAGGGTTATGATAGTGTTGCTCTTACT ATGCCTCGTAATTCCTTTTGGCGTTATGTATCTGCATTAGTTGA ATGTGGTATTCCTAAATCTCAACTGATGAATCTTTCTACCTGTA ATAATGTTGTTCCGTTAGTTCGTTTTATTAACGTAGATTTTTCTT CCCAACGTCCTGACTGGTATAATGAGCCAGTTCTTAAAATCGC ATAAGGTAATTCACAATGATTAAAGTTGAAATTAAACCATCTCA AGCCCAATTTACTACTCGTTCTGGTGTTTCTCGTCAGGGCAAG CCTTATTCACTGAATGAGCAGCTTTGTTACGTTGATTTGGGTA ATGAATATCCGGTTCTTGTCAAGATTACTCTTGATGAAGGTCA GCCAGCCTATGCGCCTGGTCTGTACACCGTTCATCTGTCCTCT TTCAAAGTTGGTCAGTTCGGTTCCCTTATGATTGACCGTCTGC GCCTCGTTCCGGCTAAGTAACATGGAGCAGGTCGCGGATTTC GACACAATTTATCAGGCGATGATACAAATCTCCGTTGTACTTT GTTTCGCGCTTGGTATAATCGCTGGGGGTCAAAGATGAGTGT TTTAGTGTATTCTTTTGCCTCTTTCGTTTTAGGTTGGTGCCTTC GTAGTGGCATTACGTATTTTACCCGTTTAATGGAAACTTCCTCA TGAAAAAGTCTTTAGTCCTCAAAGCCTCTGTAGCCGTTGCTAC CCTCGTTCCGATGCTGTCTTTCGCTGCTGAGGGTGACGAT
M13-sq-Origa-St1	AACATACGAGCCGGAAGCATAAAGACTCACAT
M13-sq-Origa-St2	TGTTATCCGCTCACAACTTTC
M13-sq-Origa-St3	TTTTCTCGAATTCGTAATCATGGTCATAGCTGACTCTAG
M13-sq-Origa-St4	TTTTCCTAATGAGTGAGCTATGTAAAGCCTGGGGTGTTTT
M13-sq-Origa-St5	TAATTGCGTGAATCGGCCAACGCGGGTGGTTT
M13-sq-Origa-St6	CAGTCGAAGCTGTGCCGGAAACCTGTCACAGC
M13-sq-Origa-St7	TGCAGGTCGTTTCCTGTGTGAAAT
M13-sq-Origa-St8	AGGATCCCTTCCCAGTCACGACGTTGTGCTGC
M13-sq-Origa-St9	TGCATTAATTGCGCTCACTGCCCGTTCCACAC

M13-sq-Origa-St10	TTTTACGCCAGGGTTCGGGTACCGAGTTTT
M13-sq-Origa-St11	TTTTGCGTATTGGGCGCCAGCGGGGAGAGGCGGTTTTTTT
M13-sq-Origa-St12	TTCTTTTCTGCAGCAAGCGGTCCATTGATGGT
M13-sq-Origa-St13	TGATTGCGCCATATTACCCTTCACCGCTATAA
M13-sq-Origa-St14	AAGGGGGATGTAAAACGACGGCCATGCATGCC
M13-sq-Origa-St15	AAGGCGATTTGGGAAGGGCGATCGCAGGCAAA
M13-sq-Origa-St16	GAGAGAGTACCAGTGAGACGGGCAGTGCCAGC
M13-sq-Origa-St17	TTTTCTGCGCAACTGTAAGTTGGGTATTTT
M13-sq-Origa-St18	TTTTCAGGCGAAAATCCTGTCGCTGGTTTGCCCCAGTTTT
M13-sq-Origa-St19	GGTTCCGATGTTCCAGTTTGGAACCGTCAAAG
M13-sq-Origa-St20	ATCAAAACCGCCCGGCAGAATAGCCCGTCAAA
M13-sq-Origa-St21	CCGGAAACGTGCGGGCCTCTTCGCGCTGGCGA
M13-sq-Origa-St22	GCGCCATTGGCCTCAGGAAGATCGCCGTGCAT
M13-sq-Origa-St23	TTGAGTGTAATCGGCAAAATCCCTCTGGCCCT
M13-sq-Origa-St24	TTTTACGACAGTATCCGCCATTCAGGTTTT
M13-sq-Origa-St25	TTTTAGAACGTGGACTCCAAAAGAGTCCACTATTAATTTT
M13-sq-Origa-St26	GGCGAAAAGATAAATTAATGCCGGGCTATCAG
M13-sq-Origa-St27	TCACCAGTGTACGTTGTCAATA
M13-sq-Origa-St28	CATCGTAACACTCCAGCCAGCTTTTTCTGGTG
M13-sq-Origa-St29	CTGCCAGTAAACGGCGGATTGACCGTGAGCGAGTAACAACGC CATCAA
M13-sq-Origa-St30	TTCTAGCTACCGTCTATCAGACAGAGATAGGG
M13-sq-Origa-St31	TGATAAACAAGAGAATCAGCTGTAGCCGATGA
M13-sq-Origa-St32	TTTTTCCGTGGGAACTTGAGGGGACGTTTT
M13-sq-Origa-St33	TTTTTGAGAGATCTACAAAGAGAGGGTAGCTATTTTTTTT
M13-sq-Origa-St34	GTCATTGCTGTCAATCATATGTACGGAAGATT
M13-sq-Origa-St35	ATTAAATGTAATGGGATAGGTCAGATGGGCG
M13-sq-Origa-St36	AACTAGCACTGAGAGTCTGGAGCATTCAACCG
M13-sq-Origa-St37	ACGGTAACGTTAATATTTTGTTAAAATTC
M13-sq-Origa-St38	AAATAATTTTTTTGTTAAATCAGCTCATTTTTTAATTTT
M13-sq-Origa-St39	TTTTCCAATAGGAACCCGTCGGATTCTTTT
M13-sq-Origa-St40	TTTTAAAAGCCCCAAAAACACCCGGTTGATAATCAGTTTT
M13-sq-Origa-St41	GTATAAGCAAATATTTAAATTGTAAATCGTAA
M13-sq-Origa-St42	GCATTAAACGCGTCTGGCCTTCCTTTCATCAAC

Table S3. Sequences of square-shaped DNA origami with multiple-unit DNA strands in length of 360 nt (7 units), 410 nt (8 units) and 614 nt (12units).

ACTB-GFP-L (410 nt)	CCTCGGCTCACAGCGCGCCCGGCTATTCTCGCAACTGACAATGG TGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCT GGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGT CCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCT GAAGTTCATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCA CCCTCGTGACCACCCTGACCTACGGCGTGCAGTGCTTCAGCCGC TACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATG CCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGA CGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGAC ACCCTGGTGAACCGCA
CAR-3 (360 nt)	GTTTTCTTAAAAATGAACAGTCTGCAAACTGACGACACAGCCATTT ACTACTGTGCCAAACATTATTACTACGGTGGTAGCTACGCTATGG ACTACTGGGGCCAAGGAACCTCAGTCACCGTCTCCTCAACCACG ACGCCAGCGCCGCGACCACCAACACCGGCGCCCACCATCGCGT CGCAGCCCCTGTCCCTGCGCCCAGAGGCGTGCCGGCCAGCGGC GGGGGGCGCAGTGCACACGAGGGGGCTGGACTTCGCCTGTGAT ATCTACATCTGGGCGCCCTTGGCCGGGACTTGTGGGGTCCTTCT CCTGTCACTGGTTATCACCCTTTACTGCAAACGGGGCAGAAAGAA ACTCCTG
Gfc-R (614 nt)	TGGGCGTAGATCATTCGCTAAACTAACTCGGACGCAGGGGCACC CAGGCCAGCGTGCAGACGAAGTAGTCGTCTACCCCATTTTCGTGT TTGAGAGACTGCAACCGGTTTTTAAGCAGTCCCCTTGGGTGGAAA GCGGAGTAATAGTTGGCAGCAAAATGTAGCCGATCCGCATGCGC ACTTCACTCCGTGGTGACCGTAAAGTTCCACGGCGAGTCTGATCG CGATGCTATGTGAATCCCACCGACACGTTGCGGCATTAACAGCCT AAGTCAATTACTCACACAATCTCTTTGTTGATTATTCTATTGTCACG CGGTACCTACGCCCTAGAGCTTTTGGACTTGTATTTAGTACGGTG TGTACTAGTGGCGGGCCGCCTGCCGGGACCCGGATTCAGTGCGT CCTGGTAAGAAGCTACTGTGCCTTTCTTCCTTAGCGCTGAAGATA ATCGGTCTTAATTCCCTCATATAACCTCCAGTTAAATCAAGTGTCT CGATAGCTCGTTCTGGATGAGGTAGTGTTGGTTTATTGAATAGGT GTGAAGAAAATATTTGTTAATTAGGTGATATAAAGTAGAGTTAAAT AAAGTGTATGGATAGGTGGTTGTGTATG
2-9-r-seam-1	CCACCCCGGTGAACAGCTCCTCGCCGGGCGCG
2-9-r-seam-2	CGTCCAGCTCGACCAGTTCTG
2-9-r-seam-3	TTTTTCGCCCTCGCCGGACACGCTGAACTTGGTCAGCTT
2-9-r-seam-4	TTTTCAGTTGCGAGAATAGCCCTTGCTCACCATTGTTTTT
2-9-r-seam-5	CTGTGAGCAGGAGAAGGACCCCACTCACAGGC
2-9-r-seam-6	CCCCGTGTGGTTGCCGTTGCAGTAAAGTGCGC
2-9-r-seam-7	ACTTCAGGTGGCCGTTTACGTCGC
2-9-r-seam-8	GCCGTAGGGGTCACGAGGGTGGGCGGGTAGCG

2-9-r-seam-9	CCAGTGACCGAGGCAGGAGTTTCTGATGGGCA
2-9-r-seam-10	TTTTTAGGTCAGGGTTGGCATCGCCCTTTT
2-9-r-seam-11	TTTTCGCCCAGATGTAGATAAAGTCCCGGCCAAGGGTTTT
2-9-r-seam-12	GAAGTCCAGGGACAGGGGCTGCGAGCGCTGGC
2-9-r-seam-13	CCCCCGTCGTGAGAAGCCGCTGGCCGGGAGGT
2-9-r-seam-14	TGTGGTCGCAGGGCACGGGCAGCTGCAGATGA
2-9-r-seam-15	GCTGAAGCCTGGACGTAGCCTTCGTTGTAGTT
2-9-r-seam-16	TGGGCGCAGCCCCCTCGTGTGCACGGTGATAA
2-9-r-seam-17	TTTTATGGTGCGCTCACTGCACGCCGTTTT
2-9-r-seam-18	TTTTGGTGTTGGTGGTCGCGCGCGATGGTGGGCGCCTTTT
2-9-r-seam-19	GTCGTGGTACCGTAGTAATAATGTTTGCAGAC
2-9-r-seam-20	TCCTTGAACTTCCTCGGCCCCAGTAGTAGAAC
2-9-r-seam-21	CGCGGGTCGGCATGGCGGACTTGACTGCTTCA
2-9-r-seam-22	GCCGTCGTATCTACGCCCATGCGGGCCTGGGT
2-9-r-seam-23	TAGCTACCTGAGGAGACGGTGACTCACGCCTC
2-9-r-seam-24	TTTTTTTAGCGAATGCCTTGAAGAAGTTTT
2-9-r-seam-25	TTTTTGGCTGTGTCGTCAGTTTGGCACAGTAGTAAATTTT
2-9-r-seam-26	TGTTCATTATATGAGGGAATTAAGACAGTAGC
2-9-r-seam-27	GAGCTAGACTATAGACTCGAGA
2-9-r-seam-28	GCACGCTGTTCACCAGGGTGTCGCCACCTCGG
2-9-r-seam-29	GCCCCTGCCCGGTTGCAGTCTCTCTATTACTCCGCTTTCCCTTTA CGG
2-9-r-seam-30	TGGAGGTTTTTAAGAAAACCATCCCCATAGCG
2-9-r-seam-31	CACTTGGGTCCCGGCACGGCTCGGATGGCGGC
2-9-r-seam-32	TTTTCTGCTTAAAAAGTCCGAGTTAGTTTT
2-9-r-seam-33	TTTTGCTAAGGAAGAAAGGCACCGATTATCTTCAGCTTTT
2-9-r-seam-34	TTCTTACCCTAAATACAAGTCCAAGAATAATC
2-9-r-seam-35	TGCCAACAAACACGAAAATGGGGCTTCGTCT
2-9-r-seam-36	ACACCGTAAGGACGCACTGAATCCGATTTAAC
2-9-r-seam-37	CCGCCGACTTAGGCTGTTAATGCCGCAAC
2-9-r-seam-38	TCACCACGGGGATTCACATAGCATCGCGATCAGACTTTT
2-9-r-seam-39	TTTTTCGCCGTGGAAACCCAAGGGGATTTT
2-9-r-seam-40	TTTTGTACCGCGTGACAATAAAGCTCTAGGGCGTAGTTTT
2-9-r-seam-41	AACAAAGAGATTGTGTGAGTAATTACTAGTAC
2-9-r-seam-42	GTGTCGGTGAGTGAAGTGCGCATGACATTTTGC

Table S4. Sequences of MUD-triangle with two multiple-unit DNA strands in length of 400 nt (8 units).

sma4(400 nt)	TGTATCTGAATGGTCGTCGTCTTCTACCAGGTGGACTCATGGTTT ATGAGGATGAAGTCTGGACCAAAGAAGATGAAGAGGAATACTCTA ACCCTGACAACCATCTCCCTCCTATGGAAGTCGGGTCTGAGTCCC TCTAAACCCTTTCCCAAACCCTTTCTTACTTTTTCTGTTGTCTGTTG TCCCTTGTCTGATCCTATCATTCCTTCTGTGAGCGAAGCGAACCC CTATACCCGCACCCCAGCCTAACGTGTCTAATTTCAGACATTTTGT CGGATTTCAGACATTTTGCTCCCATGAAACCCGGGGTTTAAAAGA ATATAATAAAAGATATTAGGGCGCAAGGCGGGAGTATTACGCGGT AGCGCCCAAGCCTTGCGCTTATTTCGCGAGCTGTACT
sma5(400 nt)	AGACCTAGCTCGCCCGGTGCCCAAAACCTGAACCGGTCTTCTGA CAGCAGGTCGTATTTTGGATATTCATTTGTAAAAACAAACACTCTT GGACTTTCTATCCACATTTCTTCCCAGCTATACCTGTCGTCCCACA TGTACCCATTTTTGATGCTTTCAATTGCTGACCATGTTTCCTTTGC TTGCTTGCTTCCTGCTCTTGGGATGTCGAAAATGTATGTACCAAG CTTTGCTCGTTTCATACACATACGCATTATATCTTTCCCTGTAAGA CCAGATGGAATATTGATTGCCATATTCTTCATACACATATACTTTG TAACAAACGACTTTCCAGTGTTTCCACGCAGGTCTATAATACAGTC TACTTCTCTGTCGTTTTGTTTCAGGTCTACTAAGT
2-400-tri-st1	ACGACCATTCATTTTTTTTTTGATACATTTT
2-400-tri-st2	TTTTAGACGGTAGATTTT
2-400-tri-st3	TTTTCATAAATCCTTTTT
2-400-tri-st4	TTTTTATTCCTCTTCATCTTGTTGTCAGGGTTAGAGTTTT
2-400-tri-st5	TTTTGACTCAGACCCGACTTGGAAAGGGTTTAGAGGTTTT
2-400-tri-st6	CCATAGGAGGGAGATGCTTTGGTCCAGACTTCACCATGAGTCCAC CTG
2-400-tri-st7	TTTTAGACAAGGGACAACAGACAACAGAAAATTCGCTCACAGAAG GA
2-400-tri-st8	TTTTGAAATTAGACACGTTAGGCTGGGGTGCAAATGTCTGAAATC CG
2-400-tri-st9	GGGTATAGGGGTTCGCAGTAAGAAAGGGTTTG
2-400-tri-st10	TATTCTTTTAAACCCCGCAAGGCTTGGGCGCTATAGAAAGTCCAA GAG
2-400-tri-st11	TTTTGCGCCCTAATATCTTTTATTAATGATAGGATCTTTT
2-400-tri-st12	TTTTTTCAGGTTTTGGGCACCGGGCACAAAATGTCTTTTT
2-400-tri-st13	GAGCTAGGTCTAGTACTGAATATCCAAAATAC
2-400-tri-st14	AGCTCGCGAAATAAGCGGGTTTCATGGGAGCA
2-400-tri-st15	CTGGGAAGAAATGTGGACCGCGTAATACTCCCGCCTTTTTT
2-400-tri-st16	TTTTGGGACGACAGGTATAGAAAAATGGGTACATGTTTTT
2-400-tri-st17	TTTTTGTATGAAACGAGCAAAGATATAATGCGTATGTTTT
2-400-tri-st18	AGCTTGGTACATACATGACCTGCTGTCAGAAGACCGGTTTT
2-400-tri-st19	TTTCGACATCCCAAGAGCAATCAATATTCCATCTGGTCTTACAGG

	GAA
2-400-tri-st20	GCAGGAAGCAAGCAAGTGTTTGTTTTTACAAA
2-400-tri-st21	CAAAGGAAACATGGTCTTGTTACAAAGTATATGTGTATGAAGAATATG
2-400-tri-st22	TTTTGTAGACTGTATTATAGACCTGCGTGGA
2-400-tri-st23	TTTTACTTAAACACTGGAAAGTCGTAGCAATTGAAAGCATC
2-400-tri-st24	GTAGACCTGAAACAAAACGACAGAGAATTTT

Table S5. Sequences of MUD-square with multiple-unit DNA strands in length of five 400 nt (8 units) and one 328 nt (6 units).

Sma-1	AAGTCTTAAGTACCCCTCCCCTTATATAGAGTCTATGTCTTATTACAGACGCTCTTATTACCCTCGTAGGCGATCCTACGGTAGGCGCAGATATTACAGACGTAGGAGATACTAAACATGGCCTATCAGACTGGATTGTACGCTTTACCTATTGCAGGACGTTTCATTTACGAATATGACCGCATGAAGGACTACGGTAAGATGGCAAAAGACTACAGACGTAATACTGGCCGTACCTCTAAGTATGCAACCCAGGGATATGAAGCTCAGATGTACCGGCAAGCTGGTCAATTATATGATTCTGCTCTTTCGTTTGGTACGTCTGTTGCTGGACGTGTTGGAAGATCAACCAAGGATGTGACGAAACTATGGATGCAATGAAGAGAGGGCTCTGCTGTGT
Sma-2	GCTGCTGCTGTGTGGAGCAGTCTTCGTTTCGGCCAGCAGAGTGCAGCCCACCGAGAGCATCGTGCGGTTCCCCAACATCACCAATCTGTGCCCTTTCGGCGAGGTGTTCAACGCCACCAGATTCGCCTCTGTGTACGCCTGGAACCGGAAGCGGATCAGCAATTGCGTGGCCGACTACAGCGTGCTGTACAACAGCGCCAGCTTCAGCACCTTCAAGTGCTACGGCGTGTCCCCTACCAAGCTGAACGACCTGTGCTTCACCAACGTGTACGCCGACAGCTTCGTGATCAGAGGCGACGAAGTGCGGCAGATTGCCCCTGGACAGACAGGCAAGATCGCCGATTACAACTACAAGCTGCCCGACGACTTCACCGGCTGTGTGATTGCCTGGAACAGCAAC
Sma-3	AACCTGGACAGCAAAGTCGGCGGCAACTACAACTACCTGTACCGGCTGTTCCGGAAGTCCAACCTGAAGCCTTTCGAGCGGGACATCAGCACCGAGATCTATCAGGCCGGCAGCACCCCTTGCAATGGCGTGGAAGGCTTCAACTGCTACTTCCCACTGCAGTCCTACGGCTTCCAGCCTACAAACGGCGTGGGCTACCAGCCTTACAGAGTGGTGGTGCTGAGCTTCGAGCTGCTGCATGCTCCTGCCACAGTGTGCGGCCCTAAGAAAAGCACCAACCTGGTCAAGAACAAATGCGTGAACTTCGGCTATATCCCCGAGGCTCCTAGAGATGGCCAGGCCTATGTTCGGAAGGATGGCGAATGGGTGCTGCTGAGCACCTTCCTTTAAATGGCATATG
Sma-4	TGTATCTGAATGGTCGTCGTCTTCTACCAGGTGGACTCATGGTTTATGAGGATGAAGTCTGGACCAAAGAAGATGAAGAGGAATACTCTAACCCTGACAACCATCTCCCTCCTATGGAAGTCGGGTCTGAGTCCCTCTAAACCCTTTCCCAAACCCTTTCTTACTTTTTCTGTTGTCTGTTGTCCCTTGTCTGATCCTATCATTCCTTCTGTGAGCGAAGCGAACCCCTATACCCGCACCCCAGCCTAACGTGTCTAATTTCAGACATTTTGTCGGATTTCAGACATTTTGCTCCCATGAAACCCGGGGTTTAAAAGAATATAATAAAAGATATTAGGGCGCAAGGCGGGAGTATTACGCGGTAGCGCCCAAGCCTTGCGCTTATTTCGCGAGCTGTACT
Sma-5	AGACCTAGCTCGCCCGGTGCCCAAAACCTGAACCGGTCTTCTGACAGCAGGTCGTATTTTGGATATTCATTTGTAAAAACAAACACTCTTGGACTTTCTATCCACATTTCTTCCCAGCTATACCTGTCGTCCCACA

	TGTACCCATTTTTGATGCTTTCAATTGCTGACCATGTTTCCTTTGCTTGCTTGCTTCCTGCTCTTGGGATGTCGAAAATGTATGTACCAAGCTTTGCTCGTTTCATACACATACGCATTATATCTTTCCCTGTAAGACCAGATGGAATATTGATTGCCATATTCTTCATACACATATACTTTGTAACAAACGACTTTCCAGTGTTTCCACGCAGGTCTATAATACAGTCTACTTCTCTGTCGTTTTGTTTCAGGTCTACTAAGT
Sma-6	GCTGTTGCCAGGGTCTTAACTGAGCATTTCGGATAGCGTCTGGTACTTTGATCCATGAACATATGAAGTCACCTTCTTTCAGAACATAGTCAAAATTTCTAACACTAGTAGGGCTACAATGACCACTATGCCCCCATATTTCCCGCATTGTTTCCCAGCTTGTAGGATTGCGTAATACAACTCTGACTTGGAAATGTTCGTATCCGTCTTCTCCTCGTTCTCTTCCGTAAGCATATCTTTCTCCATTTTCATCTAACCACTTCCTTAGTATTTCTTCAGGACATTTTGCCTTAGAAACGGTTATATCGTACCATTTAGGCTCTGTCAT
2328-rec-st1	CACGCCGTTTGTAGGCTGGAAGCCGTAGGACT
2328-rec-st2	CTCAGCACCACCACTCTGTAAGGCTGGTAGCCCTCGGTGCTGATGTCC
2328-rec-st3	ACACTGTGGCAGGAGCATGCAGCAGCTCGAAGGGTTGGACTTCCGGAA
2328-rec-st4	TTTTAGTTCACGCATTTGTTCTTGACCAGGTTGGTGCTTTTCTTAGGGCCGC
2328-rec-st5	TTTTGTTGAAGCCTTCCACGGCAGTGGGAAGTAGCATTTT
2328-rec-st6	CCATTGCAAGGGGTGCGTAGTTGTAATCGGCG
2328-rec-st7	CAGCCGGTACAGGTAGTCCGAACATAGGCCTG
2328-rec-st8	ATCACACAGCCGGTGAAGTCGTCGGGCAGCTTTGCCGGCCTGATAGAT
2328-rec-st9	CTTTGCTGTCCAGGTTGTTGCTGTTCCAGGCACGCTCGAAAGGCTTCA
2328-rec-st10	ACCCATTCGCCATCCTTTGTAGTTGCCGCCGA
2328-rec-st11	GAAGGTGCTCAGCAGCGCCATCTCTAGGAGCCTCGGGGATATAGCCGATTTT
2328-rec-st12	TTTTCATATGCCATTTAAAGCGACCATTCAGATACATTTT
2328-rec-st13	TTTTCAGGGGCAATCTGCCGATCTTGCCTGTCTGTCTTTT
2328-rec-st14	CACTTCGTCGCCTCTGGCACAGGTCGTTCAGC
2328-rec-st15	ATCACGAAGCTGTCGGGGAGGGAGATGGTTGT
2328-rec-st16	CTCTTCATCTTCTTTGGAAAGGGTTTGGGAAA
2328-rec-st17	CATAAACCATGAGTCCAGACAAGGGACAACAG
2328-rec-st18	AGACCCGACTTCCATACGTACACGTTGGTGAA
2328-rec-st19	GGGTTTAGAGGGACTCCAGGGTTAGAGTATTC
2328-rec-st20	ACAACAGAAAAAGTAAGTCCAGACTTCATCCT
2328-rec-st21	AAGGAATGATAGGATCACCTGGTAGAAGACGA
2328-rec-st22	TTTTTTCGCTTCGCTCACAGGGTGCGGGTATAGGGGTTTT
2328-rec-st23	TTTTCGTAGCACTTGAAGGTTTGGTAGGGGACACGCTTTT

2328-rec-st24	GCTGAAGCTGGCGCTGCCGAAACGAAGACTGCTCCACACAGCAGCAGCTTTT
2328-rec-st25	TTGTACAGCACGCTGTAGTCGGCCACGCAATTCACGATGCTCTCGGTG
2328-rec-st26	GCTGATCCGCTTCCGGTTCCAGGCGTACACAG
2328-rec-st27	AGGCGAATCTGGTGGCCAAAATGTCTGAAATT
2328-rec-st28	AAAGGGCACAGATTGGTGATGTTGGGGAACCG
2328-rec-st29	AATGTCTGAAATCCGAGTTGAACACCTCGCCG
2328-rec-st30	GGTTTCATGGGAGCAAAGACACGTTAGGCTGG
2328-rec-st31	TTTTATTCTTTTAAACCCCGTAATATCTTTTATTATTTTT
2328-rec-st32	TTTTACACAGCAGAGCCCTCATCCAAAATACGACCT
2328-rec-st33	TTCAGGTTTTGGGCACAAGAAATGTGGATAGA
2328-rec-st34	CGGGCGAGCTAGGTCTAGTACAGCTCGCGAAA
2328-rec-st35	GCGCTACCGCGTAATAGAAACATGGTCAGCAA
2328-rec-st36	GTTTTTACAAATGAATTCTTCATTGCATCCATTTTT
2328-rec-st37	AAGTCCAAGAGTGTTTGCTGTCAGAAGACCGGGGCTGCACTCTGCTGG
2328-rec-st38	TGGGTACATGTGGGACGACAGGTATAGCTGGG
2328-rec-st39	TTGAAAGCATCAAAAATAAGCGCAAGGCTTGG
2328-rec-st40	TTTTACATCCCAAGAGCAGGAAGCAAGCAAGCAAAGCTCCCGCCTTGCGCCC
2328-rec-st41	TTTTAGTTTCGTCACATCCTTGGTTGATCTTCCAACGTATCTCCTACGTCTG
2328-rec-st42	GTACCAAACGAAAGAGAGCGTACAATCCAGTC
2328-rec-st43	CAGAATCATATAATTGACCAGCTTGCCGGTAC
2328-rec-st44	CCTGGGTTGCATACTTTTGCCATCTTACCGTA
2328-rec-st45	AGAGGTACGGCCAGTAGGTACATACATTTTCGTTTT
2328-rec-st46	TGATAGGCCATGTTTAACGTCCAGCAACAGAC
2328-rec-st47	TATTCGTAAATGAAACGTCCTGCAATAGGTAA
2328-rec-st48	GTCCTTCATGCGGTCAATCTGAGCTTCATATC
2328-rec-st49	TTTTGAAACGAGCAAAGCTTTTACGTCTGTAGTCTT
2328-rec-st50	TTTTCGTAGGATCGCCTACGTAATATCTGCGCCTACTTTT
2328-rec-st51	AGGGTAATAAGAGCGTGGGGTACTTAAGACTTATGACAGAGCCTAAATTTTT
2328-rec-st52	CTGTAATAAGACATAGACCTGCGTGGAAACAC
2328-rec-st53	ACAAAGTATATGTGTATGAAGAATATGGCAAT
2328-rec-st54	CAATATTCCATCTGGTCCGAAATGCTCAGTTA
2328-rec-st55	GTAGACTGTATTATAGACTCTATATAAGGGGA
2328-rec-st56	ACAAAACGACAGAGAATGGAAAGTCGTTTGTT
2328-rec-st57	AAGTACCAGACGCTATCTTACAGGGAAAGATATAATGCGTATGTGTATTTTT
2328-rec-st58	TTTTATATGTTCATGGATCAGAAAGAAGGTGACTTCTTTT
2328-rec-st59	TTTTGGTACGATATAACCGTTTCTAAGGCAAAATGT

2328-rec-st60	CCTGAAGAAATACTAAGGAAGTGGTTAGATGA
2328-rec-st61	AAATGGAGAAAGATATGGGAAATATGGGGGCA
2328-rec-st62	TAGTGGTCATTGTAGCAGACCCTGGCAACAGCACTTAGTAGACCTGAA
2328-rec-st63	CCTACTAGTGTTAGAAATTTTGACTATGTTCT

Table S6. Sequences of MUD-cross with multiple-unit DNA strands in length of two 300 nt (6 units), one 360 nt (7 units) and one 410 nt (8 units).

Gfc-2 (300)	GCTCAACTTTACATGGAGAAAACACCTTCTCCCGTTTATGACAAGGTTCGGGGGATCTTGACTATACGTGAGCCCCCGAACAAACCATCGACTCTAGCATCACCAAATTGCCACTACAACATCTGCTTATAGAACTGGGAAGGGTAGGGCTAGGATATGCATAGGCAATATTAGACCTGTAACGCTCCTCGCAAGCCATAAGGCTGCGAATGGCCCAAGAGGTCCAATGCCCGCTTGCACGATTTCCGAGGAACGAGCGACGTCAGCTGTCCGGCTTCGAGATTGAACCCTGACGGGTTG
ACTB-GFP-L (410)	CCTCGGCTCACAGCGCGCCCGGCTATTCTCGCAACTGACAATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGACCTACGGCGTGCAGTGCTTCAGCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCA
Gfc-4 (300)	GCGGTACCTACGCCCTAGAGCTTTTGGACTTGTATTTAGTACGGTGTGTACTAGTGGCGGGCCGCCTGCCGGGACCCGGATTCAGTGCGTCCTGGTAAGAAGCTACTGTGCCTTTCTTCCTTAGCGCTGAAGATAATCGGTCTTAATTCCCTCATATAACCTCCAGTTAAATCAAGTGTCTCGATAGCTCGTTCTGGATGAGGTAGTGTTGGTTTATTGAATAGGTGTGAAGAAAATATTTGTTAATTAGGTGATATAAAGTAGAGTTAAATAAAGTGTATGGATAGGTGGTTGTGTATG
CAR-2 (360)	CAGGGTAATACGCTTCCGTACACGTTCGGAGGGGGGACCAAGCTGGAGATCACAGGTGGCGGTGGCTCGGGCGGTGGTGGGTCGGGTGGCGGCGGATCTGAGGTGAAACTGCAGGAGTCAGGACCTGGCCTGGTGGCGCCCTCACAGAGCCTGTCCGTCACATGCACTGTCTCAGGGGTCTCATTACCCGACTATGGTGTAAGCTGGATTCGCCAGCCTCCACGAAAGGGTCTGGAGTGGCTGGGAGTAATATGGGGTAGTGAAACCACATACTATAATTCAGCTCTCAAATCCAGACTGACCATCATCAAGGACAACTCCAAGAGCCAAGTTTTCTTAAAAATGAACAGTCTGCAAACT
cross-st1	GATTTAACGCACAGTAGCTCACTAACCAATCTTACCAGGACCTAATTA
cross-st2	TTTTACGAGCTATCGAGACACTT
cross-st3	TTTTGATTATCTTCACCCGGCAGGCGTTTT
cross-st4	GCGCTAAGGAAGAAAGTGGAGGTTATATGAGGGAATTAAGACCTTTT
cross-st5	TTTTCTATTCAATAACCTCATCCAGATTTT
cross-st6	TTTTGCCCGCCACTATACTAAATACATTTT

cross-st7	ACAAATATACCTATCCATACACTTCCTCCGAACGTGTACG
cross-st8	TATTTAACTCTCACCGGTACAACTTTATATCACGCACTGAATCCGGGT
cross-st9	TTTTCATACACAACCTTTCTTCACACTTTT
cross-st10	TTTTAGTCCAAAAGCAGGTACCGCTGCGGTTGTCCTTGAAGAAGATG
cross-st11	TGTGATCTCCAGGCGTTCTAGGCTTGGTCCCC
cross-st12	CCGAGCCACCGCCACCAGCCTTCGGGCATGGCAAGTCGTGCTGCTTCA
cross-st13	CCCGACCCACCACCGCGAAGCGTATTAC
cross-st14	TTTTTGCAGTTTCACCTCAGATCCGCCGCCAGGCGCCACCAGGCCAG
cross-st15	TTTTCTCGGCGCGGGTCACGAGGGTGTTTT
cross-st16	TCTTGTAGTTGCCGTCCACCAGGGTGTCGCCCTCGAACTTCACTTTT
cross-st17	GCTGAAGCACTGCACGGTGCAGATGAAGTGGTAGTATCTTCAGGGTCA
cross-st18	TGTGGTCGGGGTAGCGGTGCGCTCCTGGACGT
cross-st19	CCCCTGAGACAGTGCACTGGCGAATCCAGCTT
cross-st20	TTTTGGGTAATGAGAGTCCTGACTCCTTTT
cross-st21	TTTTGGCCAGGGCACATCGCCCTCGCTTTT
cross-st22	GGGCAGCTTGCCGGTGCCGTAGGTCAGGGTGG
cross-st23	ACTCCCAGCCACTCCAGATGGTCAGTCTGGAT
cross-st24	GACCCTTTCGTGGAGGTGTGACGGACATGAAGGGACTGGCTCTGTGAG
cross-st25	AAGAAAACTTGGCTCTGTGTTTTCTCCATGTAAAGTTGAGCTTTTT
cross-st26	GCAGACTGTTCATTTTTACACCATAGTCTTTT
cross-st27	TTTTCCTCGCCGGACACGCTGAACTTGTGGCGCTTGCCGTAGGTGGC
cross-st28	CGTTTACGTCGCCGTCCATTGTCAGTTTTTT
cross-st29	CAGCTCGACCAGGATGTTGAGAGCTGAATTATTTCACTACCCCATATT
cross-st30	GGCACCACCCCCCTTGCCGAAGGTGAACAGCTCGAGGCAACCCCGGGG
cross-st31	TTTTGTCAAGATCCCTCATAAACGGGAGAAGTGGAGTTGTCCTTGAT
cross-st32	TTTTGCGAGAATAGCGCTGACGTCGCTTTT
cross-st33	GCCGGACACGGGCGCGCTGTGAGCCCTCGCCCTTGCTCAC
cross-st34	TTGTTGTCAGGGTTCATGTTGTAGTGGCAATT
cross-st35	TTTTGAGTCGATGGTGCTCACGTATATTTT
cross-st36	TTTTTCGTTCCTCGGAGCGGGCATTGTTTT
cross-st37	CCAGTTGTGCAAAATCCTATAAGCAGAATCTCGAA
cross-st38	CATATCCTAGCCCTACGGCTTGCGAGGAGCGTTACAGGTCTAATT

	TT
cross-st39	TTTTTATTGCCTATGTGGTGATGCTATTTT
cross-st40	TTTTGACCTCTTGGGCCATTCGCAGCCTTATCCTTC

Table S7. Sequences of the MUD-1U, a portion of which is displayed and marked in italics in Table S2.

a13.1-b13.1-a12.2*	CCCGAAGTACCTCTGCAGGATGCGTCGCCAG
a13.2-b13.2-a12.3*-b12.2*	CGTTACCAGGCTACGATGAGTGTAGACCAAGACACGGTCAGA
a13.3-b13.3-a12.4*-b12.3*	CTGTCCCACTCTCCTTCAAATGTGGCGCGCGATCTATAAACA
a13.4-b13.4-a12.5*-b12.4*	CATTATATTGCTCCTGAGGGTGTAAATCTGGACTCCTAATGA
a13.5-T10-T10-b12.5*	CGTGCATGCCCTTTTTTTTTTTTTTTTTTTTACTGGGTACAA
T4-a12.2-b12.2	TTTTCTGGCGACGCTCTGACCGTGT
a12.3-b12.3	CTTGGTCTACTGTTTATAGAT
a12.4-b12.4	CGCGCGCCACTCATTAGGAGT
a12.5-b12.5	CCAGATTTACTTGTACCCAGT
a15.5-T10-T10-b14.5*	CCAAACCGTCCTTTTTTTTTTTTTTTTTTTTAAATAGCCGCA
a17.5-T10-T10-b16.5*	CACTTAGAGTCTTTTTTTTTTTTTTTTTTTTAGCGAGCGGAA
a19.5-T10-T10-b18.5*	CTGACATTACCTTTTTTTTTTTTTTTTTTTTACGATCGGTCA
a21.5-T10-T10-b20.5*	CTTTGGCCATCTTTTTTTTTTTTTTTTTTTTAAGCACTTACA
a23.5-T10-T10-b22.5*	CGTGAATGCACTTTTTTTTTTTTTTTTTTTTAACTATCGGCA
a24.2-T11-a23.2*-b23.1*	CTGTATCGGCTTTTTTTTTTTTATAGTCTTGAAGTTAGCAA
a23.3*-b23.2*	GGATGCGCGTGAGCGTCCTGA
a23.4*-b23.3*	GCAGCTTTACGAATAAACGGA
a23.5*-b23.4*	GTGCATTCACGATAGACCATA

Table S8. Sequences of MUD-2U. The short DNA strands are marked by italic.

Gfc-100-1 (112 nt)	AGTGTAGGTAGGGGGTATAGGTTTTTGAGTTGTATTTATTAAAGTGTGTAGAAGTTGATGGAATAGTGGGGGTAAAGTTATTGTGTTAGTGATGTTATGAGATGGTTATCAG
Gfc-100-2 (94 nt)	AGTTTCATGTCGCCAACGGAATACTTACCACAGGAGGGAGCACATACACTGAGGCGCGCCGTCGGCCTCTGTTCAAAGGACATTGGTCATCCTA
Gfc-100-3 (108 nt)	TCCATGAAACGTATGGGGTCGAAATAAAAAGACAGTATATCTAATGATGTTAGGTATCGTACAGATGAGTGATACCGCGTTACGACCAGAATTTGCTGGCTCTCAGGT
Gfc-100-4 (94 nt)	GCTCAACTTTACATGGAGAAAACACCTTCTCCCGTTTATGACAAGGTTCGGGGGATCTTGACTATACGTGAGCCCCCGAACAAACCATCGACTC
Gfc-100-5 (116 nt)	TAGCATCACCAAATTGCCACTACAACATCTGCTTATAGAACTGGGAAGGGTAGGGCTAGGATATGCATAGGCAATATTAGACCTGTAACGCTCCTCGCAAGCCATAAGGCTGCGAA
Gfc-100-6 (90 nt)	ATGGCCCAAGAGGTCCAATGCCCGCTTGCACGATTTCCGAGGAACGAGCGACGTCAGCTGTCCGGCTTCGAGATTGAACCCTGACGGGTT
Gfc-100-7(112 nt)	TGGGCGTAGATCATTCGCTAAACTAACTCGGACGCAGGGGCACCCAGGCCAGCGTGCAGACGAAGTAGTCGTCTACCCCATTTTCGTGTTTGAGAGACTGCAACCGGTTTTT
Gfc-100-8 (90 nt)	AAGCAGTCCCCTTGGGTGGAAAGCGGAGTAATAGTTGGCAGCAAAATGTAGCCGATCCGCATGCGCACTTCACTCCGTGGTGACCGTAAA
Gfc-100-9 (112 nt)	GTTCCACGGCGAGTCTGATCGCGATGCTATGTGAATCCCACCGACACGTTGCGGCATTAACAGCCTAAGTCAATTACTCACACAATCTCTTTGTTGATTATTCTATTGTCAC
Gfc-100-10 (90 nt)	GCGGTACCTACGCCCTAGAGCTTTTGGACTTGTATTTAGTACGGTGTGTACTAGTGGCGGGCCGCCTGCCGGGACCCGGATTCAGTGCGT
Gfc-100-11 (112 nt)	CCTGGTAAGAAGCTACTGTGCCTTTCTTCCTTAGCGCTGAAGATAATCGGTCTTAATTCCCTCATATAACCTCCAGTTAAATCAAGTGTCTCGATAGCTCGTTCTGGATGAG
Gfc-100-12 (98 nt)	GTAGTGTTGGTTTATTGAATAGGTGTGAAGAAAATATTTGTTAATTAGGTGATATAAAGTAGAGTTAAATAAAGTGTATGGATAGGTGGTTGTGTATG
Gfc-6-12-St_1	*TTTTCATACACAACCACCTATTAAGACC*
Gfc-6-12-St_2	*AACTCTACTTTATATCCACTTGATTTAACTGGGGCGGCCC*
Gfc-6-12-St_3	*ACACCTATAACACTACCTCATCCATACAAGTC*
Gfc-6-12-St_4	*GATTATCTTTACCAGGACGCACTGTGCCGCAA*
Gfc-6-12-St_5	*TATCGAGAACCTAATTAACAAATATTTTCTTC*
Gfc-6-12-St_6	*TTTTAAACCTCAATTTTT*

Gfc-6-12-St_7	*TTTTAAGGCACAGTAGCTTCTCAGCGCTAAGGAAGATTTT*
Gfc-6-12-St_8	*TCCCGGCAAGGTTATATGAGGGAATCCATACACTTTATTT*
Gfc-6-12-St_9	*GCCACTAGAGATTGTGTGAGTAATGCGCATGC*
Gfc-6-12-St_10	*CAAAAGCTGGTACCGCGTGACAATCTATTACT*
Gfc-6-12-St_11	*CGTGTCGGCGTGGAACTTTACGGTCACGCTGG*
Gfc-6-12-St_12	*CAACAAAGTACACACCGTACTAAAGAACGAGC*
Gfc-6-12-St_13	*TTTTGCGTACTAGGTTTT*
Gfc-6-12-St_14	*TTTTTCGCGATCAGACTCGCTGGGATTCACATAGCATTTT*
Gfc-6-12-St_15	*AGTGAAGTTGACTTAGGCTGTTAAAATCCGGG*
Gfc-6-12-St_16	*GGATCGGCCACGAAAATGGGGTAGGCCGGACA*
Gfc-6-12-St_17	*CCGCTTTCGACTGCTTAAAAACCGATCGTGCA*
Gfc-6-12-St_18	*CCTGGGTGTACGCCCAAACCCGTCCCTAGCCC*
Gfc-6-12-St_19	*CTCTCAAATACATTTTGCTGCCAAAGAATAAT*
Gfc-6-12-St_20	*TTTTAAGGGCACCCTTTT*
Gfc-6-12-St_21	*TTTTAGTTTAGCGAATGATCCCCCTGCGTCCGAGTTTTTT*
Gfc-6-12-St_22	*ATCTCGAAACGACTACTTCGTCTGCACCACGG*
Gfc-6-12-St_23	*GCTGACGTAGCGTTACAGGTCTAAGGCTCACG*
Gfc-6-12-St_24	*AGCGGGCATGGGCCATTTCGCAGCGTCATAAA*
Gfc-6-12-St_25	*TACCCTTCTTGGTGATGCTAGAGTCGATGGTT*
Gfc-6-12-St_26	*TTGCGAGGCGCTCGTTCCTCGGAAGTTGCAGT*
Gfc-6-12-St_27	*TTTTCCTCTTTGGATTTT*
Gfc-6-12-St_28	*TTTTATGTTGTAGTGGCAATCCAGTTCTATAAGCAGTTTT*
Gfc-6-12-St_29	*TGTTCGGGTATTGCCTATGCATATAGGGTTCA*
Gfc-6-12-St_30	*TATAGTCAATTCTGGTCGTAACGCGAACAGAG*
Gfc-6-12-St_31	*CGGGAGAACCATGTAAAGTTGAGCACCTGAGA*
Gfc-6-12-St_32	*CCTAACATCAACGTTTCATGGATAGGATGACC*
Gfc-6-12-St_33	*GCCAGCAAAGATCCCCCGAACCTTCTTATGGC*
Gfc-6-12-St_34	*TTTTTTTCTGGTGTTTTT*
Gfc-6-12-St_35	*TTTTTTTATTTCGACCCCATTTAGATATACTGTCTTTTTT*
Gfc-6-12-St_36	*AATGTCCTTTGGTATCACTCATCTGTACGATA*
Gfc-6-12-St_37	*GCCGACGGAACATCACTAACACAATAACTTTA*
Gfc-6-12-St_38	*CTGTGGTTTGGCGACATGAAACTCTGATAAC*
Gfc-6-12-St_39	*CCCCCACTATTCCATCAACTTCTAACCCCCTACCTA*
Gfc-6-12-St_40	*CATCTCATCGCGCCTCAGTGTATGTGCTCCCTC*
Gfc-6-12-St_41	*TTTTTTCCGAAGTATTTT*
Gfc-6-12-St_42	*TTTTCAACTCAAAAACCTATCACACTTTAATAAATATTTT*

Table S9. Sequences of MUD-3U.

Gfc-1-1(162 nt)	GCTCAACTTTACATGGAGAAAACACCTTCTCCCGTTTATGACAAG GTTCGGGGGATCTTGACTATACGTGAGCCCCCGAACAAACCATC GACTCTAGCATCACCAAATTGCCACTACAACATCTGCTTATAGAA CTGGGAAGGGTA
Gfc-1-2(152 nt)	GCTCAACTTTACATGGAGAAAACACCTTCTCCCGTTTATGACAAG GTTCGGGGGATCTTGACTATACGTGAGCCCCCGAACAAACCATC GACTCTAGCATCACCAAATTGCCACTACAACATCTGCTTATAGAA CTGGGAAGGGTA
Gfc-2-1(146 nt)	GGGCTAGGATATGCATAGGCAATATTAGACCTGTAACGCTCCTC GCAAGCCATAAGGCTGCGAATGGCCCAAGAGGTCCAATGCCCG CTTGCACGATTTCCGAGGAACGAGCGACGTCAGCTGTCCGGCTT CGAGATTGAACCCTG
Gfc-2-2(154 nt)	GGGCTAGGATATGCATAGGCAATATTAGACCTGTAACGCTCCTC GCAAGCCATAAGGCTGCGAATGGCCCAAGAGGTCCAATGCCCG CTTGCACGATTTCCGAGGAACGAGCGACGTCAGCTGTCCGGCTT CGAGATTGAACCCTGACGGGTTG
Gfc-3-1(154 nt)	TGGGCGTAGATCATTCGCTAAACTAACTCGGACGCAGGGGCACC CAGGCCAGCGTGCAGACGAAGTAGTCGTCTACCCCATTTTCGTG TTTGAGAGACTGCAACCGGTTTTTAAGCAGTCCCCTTGGGTGGAA AGCGGAGTAATAGTTGGCAGC
Gfc-3-2(160 nt)	TGGGCGTAGATCATTCGCTAAACTAACTCGGACGCAGGGGCACC CAGGCCAGCGTGCAGACGAAGTAGTCGTCTACCCCATTTTCGTG TTTGAGAGACTGCAACCGGTTTTTAAGCAGTCCCCTTGGGTGGAA AGCGGAGTAATAGTTGGCAGC
Gfc-4-1(154 nt)	AAAATGTAGCCGATCCGCATGCGCACTTCACTCCGTGGTGACCG TAAAGTTCCACGGCGAGTCTGATCGCGATGCTATGTGAATCCCA CCGACACGTTGCGGCATTAACAGCCTAAGTCAATTACTCACACAA TCTCTTTGTTGATTATTCTAT
Gfc-4-2(146 nt)	CCGCATGCGCACTTCACTCCGTGGTGACCGTAAAGTTCCACGGC GAGTCTGATCGCGATGCTATGTGAATCCCACCGACACGTTGCGG CATTAACAGCCTAAGTCAATTACTCACACAATCTCTTTGTTGATTA TTCTATTGTCAC
1228-St1	TTTTCATACACAACCACCTATTAAGACC
1228-St2	AACTCTACTTTATATCCACTTGATTTAACTGGGGCGGCCC
1228-St3	ACACCTATAACACTACCTCATCCATACAAGTC
1228-St4	GATTATCTTTACCAGGACGCACTGTGCCGCAA
1228-St5	TATCGAGAACCTAATTAACAAATATTTTCTTC
1228-St6	TTTTAAACCTCAATTTTT
1228-St7	TTTTAAGGCACAGTAGCTTCTCAGCGCTAAGGAAGATTTT
1228-St8	TCCCGGCAAGGTTATATGAGGGAATCCATACACTTTATTT
1228-St9	GCCACTAGAGATTGTGTGAGTAATGCGCATGC
1228-St10	CAAAAGCTGGTACCGCGTGACAATCTATTACT

1228-St11	CGTGTCGGCGTGGAACTTTACGGTCACGCTGG
1228-St12	CAACAAAGTACACACCGTACTAAAGAACGAGC
1228-St13	TTTTGCGTACTAGGTTTT
1228-St14	TTTTTCGCGATCAGACTCGCTGGGATTCACATAGCATTTT
1228-St15	AGTGAAGTTGACTTAGGCTGTTAAAATCCGGG
1228-St16	GGATCGGCCACGAAAATGGGGTAGAGCCGGAC
1228-St17	CCGCTTTCGACTGCTTAAAAACCGAATCGTGC
1228-St18	CCTGGGTGTACGCCCACAACCCGTCCTAGCCCTACCCTTCTTGG TGAT
1228-St19	CTCTCAAATACATTTTGCTGCCAAAGAATAAT
1228-St20	TTTTAAGGGCACCCTTTT
1228-St21	TTTTAGTTTAGCGAATGATCCCCCTGCGTCCGAGTTTTTT
1228-St22	AATCTCGAACGACTACTTCGTCTGCACCACGG
1228-St23	AGCTGACGAGCGTTACAGGTCTAAGGCTCACG
1228-St24	AAGCGGGCTTGGGCCATTCGCAGCGTCATAAA
1228-St25	TTGCGAGGTCGCTCGTTCCTCGGAGTTGCAGT
1228-St26	TTTTACCTCATTGGTTTT
1228-St27	TTTTATGTTGTAGTGGCAATCCAGTTCTATAAGCAGTTTT
1228-St28	GCTAGAGTACGATACCTAACATCAACGTTTCA
1228-St29	TGTTCGGGTATTGCCTATGCATATCAGGGTTC
1228-St30	TATAGTCAATTCTGGTCGTAACGCGAACAGAG
1228-St31	CGGGAGAACCATGTAAAGTTGAGCACCTGAGA
1228-St32	GCCAGCAAAGATCCCCCGAACCTTCTTATGGC
1228-St33	TTTTTTTCTGGTGTTTTT
1228-St34	TTTTTTTATTTCGACCCCATTTAGATATACTGTCTTTTTT
1228-St35	TGGATAGGATTCCATCAACTTCTAACCCCCTACCTA
1228-St36	TGTCCTTTGGTATCACTCATCTGTCGATGGTT
1228-St37	GCCGACGGAACATCACTAACACAA
1228-St38	CTGTGGTTTGGCGACATGAAACTCTGATAAC
1228-St39	TAACTTTACCCCCACTATGACCAA
1228-St40	CATCTCATCGCGCCTCAGTGTATGTGCTCCCTC
1228-St41	TTTTTTCCGAAGTATTTT
1228-St42	TTTTCAACTCAAAAACCTATCACACTTTAATAAATATTTT

Table S10. Sequences of MUD-4U. The short DNA strands are same with MUD-2U. marked by italic in Table S8.

Gfc-200-1 (206 nt)	AGTGTAGGTAGGGGGTATAGGTTTTTGAGTTGTATTTATTAAAGTGTGTAGAAGTTGATGGAATAGTGGGGGTAAAGTTATTGTGTTAGTGATGTTATGAGATGGTTATCAGAGTTTCATGTCGCCAACGGAATACTTACCACAGGAGGGAGCACATACACTGAGGCGCGCCGTCGGCCTCTGTTCAAAGGACATTGGTCATCCTA
Gfc-200-2 (202 nt)	TCCATGAAACGTATGGGGTCGAAATAAAAAGACAGTATATCTAATGATGTTAGGTATCGTACAGATGAGTGATACCGCGTTACGACCAGAATTTGCTGGCTCTCAGGTGCTCAACTTTACATGGAGAAAACACCTTCTCCCGTTTATGACAAGGTTCGGGGGATCTTGACTATACGTGAGCCCCCGAACAAACCATCGACTC
Gfc-200-3 (206 nt)	TAGCATCACCAAATTGCCACTACAACATCTGCTTATAGAACTGGGAAGGGTAGGGCTAGGATATGCATAGGCAATATTAGACCTGTAACGCTCCTCGCAAGCCATAAGGCTGCGAAATGGCCCAAGAGGTCCAATGCCCGCTTGCACGATTTCCGAGGAACGAGCGACGTCAGCTGTCCGGCTTCGAGATTGAACCCTGACGGGTT
Gfc-200-4 (202 nt)	TGGGCGTAGATCATTCGCTAAACTAACTCGGACGCAGGGGCACCCAGGCCAGCGTGCAGACGAAGTAGTCGTCTACCCCATTTTCGTGTTTGAGAGACTGCAACCGGTTTTTAAGCAGTCCCCTTGGGTGGAAAGCGGAGTAATAGTTGGCAGCAAAATGTAGCCGATCCGCATGCGCACTTCACTCCGTGGTGACCGTAAA
Gfc-200-5 (202 nt)	GTTCCACGGCGAGTCTGATCGCGATGCTATGTGAATCCCACCGACACGTTGCGGCATTAACAGCCTAAGTCAATTACTCACACAATCTCTTTGTTGATTATTCTATTGTCACGCGGTACCTACGCCCTAGAGCTTTTGGACTTGTATTTAGTACGGTGTGTACTAGTGGCGGGCCGCCTGCCGGGACCCGGATTCAGTGCGT
Gfc-200-6 (210 nt)	CCTGGTAAGAAGCTACTGTGCCTTTCTTCCTTAGCGCTGAAGATAATCGGTCTTAATTCCCTCATATAACCTCCAGTTAAATCAAGTGTCTCGATAGCTCGTTCTGGATGAGGTAGTGTTGGTTTATTGAATAGGTGTGAAGAAAATATTTGTTAATTAGGTGATATAAAGTAGAGTTAAATAAAGTGTATGGATAGGTGGTTGTGTATG

Table S11. Sequences of MUD-6U. The short DNA strands are marked by italic.

Gfree-c-1 (314 nt)	AGTGTAGGTAGGGGGTATAGGTTTTTGAGTTGTATTTATTAAAGTGTGTAGAAGTTGATGGAATAGTGGGGGTAAAGTTATTGTGTTAGTGATGTTATGAGATGGTTATCAGAGTTTCATGTCGCCAACGGAATACTTACCACAGGAGGGAGCACATACACTGAGGCGCGCCGTCGGCCTCTGTTCAAAGGACATTGGTCATCCTATCCATGAAACGTATGGGGTCGAAATAAAAAGACAGTATATCTAATGATGTTAGGTATCGTACAGATGAGTGATACCGCGTTACGACCAGAATTTGCTGGCTCTCAGGT
Gfree-c-2 (300 nt)	GCTCAACTTTACATGGAGAAAACACCTTCTCCCGTTTATGACAAGGTTCGGGGGATCTTGACTATACGTGAGCCCCCGAACAAACCATCGACTCTAGCATCACCAAATTGCCACTACAACATCTGCTTATAGAACTGGGAAGGGTAGGGCTAGGATATGCATAGGCAATATTAGACCTGTAACGCTCCTCGCAAGCCATAAGGCTGCGAATGGCCCAAGAGGTCCAATGCCCGCTTGCACGATTTCCGAGGAACGAGCGACGTCAGCTGTCCGGCTTCGAGATTGAACCCTGACGGGTTG
Gfree-c-3 (314 nt)	TGGGCGTAGATCATTCGCTAAACTAACTCGGACGCAGGGGCACCCAGGCCAGCGTGCAGACGAAGTAGTCGTCTACCCCATTTTCGTGTTTGAGAGACTGCAACCGGTTTTTAAGCAGTCCCCTTGGGTGGAAAGCGGAGTAATAGTTGGCAGCAAAATGTAGCCGATCCGCATGCGCACTTCACTCCGTGGTGACCGTAAAGTTCCACGGCGAGTCTGATCGCGATGCTATGTGAATCCCACCGACACGTTGCGGCATTAACAGCCTAAGTCAATTACTCACACAATCTCTTTGTTGATTATTCTATTGTCAC
Gfree-c-4 (300 nt)	GCGGTACCTACGCCCTAGAGCTTTTGGACTTGTATTTAGTACGGTGTGTACTAGTGGCGGGCCGCCTGCCGGGACCCGGATTCAGTGCGTCCTGGTAAGAAGCTACTGTGCCTTTCTTCCTTAGCGCTGAAGATAATCGGTCTTAATTCCCTCATATAACCTCCAGTTAAATCAAGTGTCTCGATAGCTCGTTCTGGATGAGGTAGTGTTGGTTTATTGAATAGGTGTGAAGAAAATATTTGTTAATTAGGTGATATAAAGTAGAGTTAAATAAAGTGTATGGATAGGTGGTTGTGTATG
Gfree-c-st_1	CATACACAACCACCTATTAAGACCGATTATCT
Gfree-c-st_2	AACTCTACTTTATATCCACTTGATTTAACTGG
Gfree-c-st_3	GAACGAGCTATCGAGAACCTAATTAACAAATATTTTCTTCACACCTAT
Gfree-c-st_4	AACACTACCTCATCCATACAAGTCCAAAAGCT
Gfree-c-st_5	TTTTAAACCTCAATTTTT
Gfree-c-st_6	TTTTAAGGCACAGTAGCTTCTCAGCGCTAAGGAAGATTTT
Gfree-c-st_7	TTACCAGGACGCACTGTGCCGCAACGTGTCGGCGTGGAACTTTACGGT
Gfree-c-st_8	AATCCGGGTCCCGGCAAGGTTATATGAGGGAATCCATACACTTTATTT
Gfree-c-st_9	GGCGGCCCGCCACTAGAGATTGTGTGAGTAAT
Gfree-c-st_10	GGTACCGCGTGACAATCTATTACTCCGCTTTC
Gfree-c-st_11	TTTTGCGTACTAGGTTTT

Gfree-c-st_12	TTTTTCGCGATCAGACTCGCTGGGATTCACATAGCATTTT
Gfree-c-st_13	GCGCATGCGGATCGGCCACGAAAATGGGGTAG
Gfree-c-st_14	TACATTTTGCTGCCAAAGAATAATCAACAAAGTACACACCGTACTAAA
Gfree-c-st_15	CACGCTGGCCTGGGTGTACGCCCACAACCCGTCCTAGCCCTACCCTTC
Gfree-c-st_16	ACGACTACTTCGTCTGCACCACGGAGTGAAGTTGACTTAGGCTGTTAA
Gfree-c-st_17	GACTGCTTAAAAACCGAATCGTGCAAGCGGGC
Gfree-c-st_18	TTTTAAGGGCACCCTTTT
Gfree-c-st_19	TTTTAGTTTAGCGAATGATCCCCCTGCGTCCGAGTTTTTT
Gfree-c-st_20	AGCCGGACAGCTGACGAGCGTTACAGGTCTAAGGCTCACGTATAGTCA
Gfree-c-st_21	TCGCTCGTTCCTCGGAGTTGCAGTCTCTCAAA
Gfree-c-st_22	TTGGGCCATTCGCAGCGTCATAAACGGGAGAACCATGTAAAGTTGAGC
Gfree-c-st_23	TTTTACCTCATTGGTTTT
Gfree-c-st_24	TTTTATGTTGTAGTGGCAATCCAGTTCTATAAGCAGTTTT
Gfree-c-st_25	TTGGTGATGCTAGAGTACGATACCTAACATCA
Gfree-c-st_26	CGATGGTTTGTTCGGGTATTGCCTATGCATATCAGGGTTCAATCTCGA
Gfree-c-st_27	AGATCCCCCGAACCTTCTTATGGCTTGCGAGG
Gfree-c-st_28	TTTTTTTCTGGTGTTTTT
Gfree-c-st_29	TTTTTTTATTTCGACCCCATTTAGATATACTGTCTTTTTT
Gfree-c-st_30	ACGTTTCATGGATAGGATTCCATCAACTTCTAACCCCCTACCTACACT
Gfree-c-st_31	GAACAGAGGCCGACGGAACATCACTAACACAA
Gfree-c-st_32	CGCGCCTCAGTGTATGACCTGAGAGCCAGCAAATTCTGGTCGTAACGC
Gfree-c-st_33	TGCTCCCTCCTGTGGTTTGGCGACATGAAACTCTGATAACCATCTCAT
Gfree-c-st_34	TAACTTTACCCCCACTATGACCAATGTCCTTTGGTATCACTCATCTGT
Gfree-c-st_35	TTTTTTCCGAAGTATTTT
Gfree-c-st_36	TTTTCAACTCAAAAACCTATCACACTTTAATAAATATTTT

Table S12. Sequences of MUD-12U. The short DNA strands are same with MUD-6U, marked by italic in Table S11.

Gfc-L (614 nt)	AGTGTAGGTAGGGGGTATAGGTTTTTGAGTTGTATTTATTAAAGTG TGTAGAAGTTGATGGAATAGTGGGGGTAAAGTTATTGTGTTAGTG ATGTTATGAGATGGTTATCAGAGTTTCATGTCGCCAACGGAATACT TACCACAGGAGGGAGCACATACACTGAGGCGCGCCGTCGGCCTC TGTTCAAAGGACATTGGTCATCCTATCCATGAAACGTATGGGGTC GAAATAAAAAGACAGTATATCTAATGATGTTAGGTATCGTACAGAT GAGTGATACCGCGTTACGACCAGAATTTGCTGGCTCTCAGGTGCT CAACTTTACATGGAGAAAACACCTTCTCCCGTTTATGACAAGGTTC GGGGGATCTTGACTATACGTGAGCCCCCGAACAAACCATCGACT CTAGCATCACCAAATTGCCACTACAACATCTGCTTATAGAACTGG GAAGGGTAGGGCTAGGATATGCATAGGCAATATTAGACCTGTAAC GCTCCTCGCAAGCCATAAGGCTGCGAATGGCCCAAGAGGTCCAA TGCCCGCTTGCACGATTTCCGAGGAACGAGCGACGTCAGCTGTC CGGCTTCGAGATTGAACCCTGACGGGTTG
Gfc-R (614 nt)	TGGGCGTAGATCATTCGCTAAACTAACTCGGACGCAGGGGCACC CAGGCCAGCGTGCAGACGAAGTAGTCGTCTACCCCATTTTCGTGT TTGAGAGACTGCAACCGGTTTTTAAGCAGTCCCCTTGGGTGGAAA GCGGAGTAATAGTTGGCAGCAAAATGTAGCCGATCCGCATGCGC ACTTCACTCCGTGGTGACCGTAAAGTTCCACGGCGAGTCTGATCG CGATGCTATGTGAATCCCACCGACACGTTGCGGCATTAACAGCCT AAGTCAATTACTCACACAATCTCTTTGTTGATTATTCTATTGTCACG CGGTACCTACGCCCTAGAGCTTTTGGACTTGTATTTAGTACGGTG TGTACTAGTGGCGGGCCGCCTGCCGGGACCCGGATTCAGTGCGT CCTGGTAAGAAGCTACTGTGCCTTTCTTCCTTAGCGCTGAAGATA ATCGGTCTTAATTCCCTCATATAACCTCCAGTTAAATCAAGTGTCT CGATAGCTCGTTCTGGATGAGGTAGTGTTGGTTTATTGAATAGGT GTGAAGAAAATATTTGTTAATTAGGTGATATAAAGTAGAGTTAAAT AAAGTGTATGGATAGGTGGTTGTGTATG

Table S13. Sequences of MUD-24U. The short DNA strands are same with MUD-6U, marked by italic in Table S11.

Gfc (1228 nt)	AGTGTAGGTAGGGGGTATAGGTTTTTGAGTTGTATTTATTAAAGTG TGTAGAAGTTGATGGAATAGTGGGGGTAAAGTTATTGTGTTAGTG ATGTTATGAGATGGTTATCAGAGTTTCATGTCGCCAACGGAATACT TACCACAGGAGGGAGCACATACACTGAGGCGCGCCGTCGGCCTC TGTTCAAAGGACATTGGTCATCCTATCCATGAAACGTATGGGGTC GAAATAAAAAGACAGTATATCTAATGATGTTAGGTATCGTACAGAT GAGTGATACCGCGTTACGACCAGAATTTGCTGGCTCTCAGGTGCT CAACTTTACATGGAGAAAACACCTTCTCCCGTTTATGACAAGGTTC GGGGGATCTTGACTATACGTGAGCCCCCGAACAAACCATCGACT CTAGCATCACCAAATTGCCACTACAACATCTGCTTATAGAACTGG GAAGGGTAGGGCTAGGATATGCATAGGCAATATTAGACCTGTAAC GCTCCTCGCAAGCCATAAGGCTGCGAATGGCCCAAGAGGTCCAA TGCCCGCTTGCACGATTTCCGAGGAACGAGCGACGTCAGCTGTC CGGCTTCGAGATTGAACCCTGACGGGTTGTGGGCGTAGATCATT CGCTAAACTAACTCGGACGCAGGGGCACCCAGGCCAGCGTGCA GACGAAGTAGTCGTCTACCCCATTTTCGTGTTTGAGAGACTGCAA CCGGTTTTTAAGCAGTCCCCTTGGGTGGAAAGCGGAGTAATAGTT GGCAGCAAAATGTAGCCGATCCGCATGCGCACTTCACTCCGTGG TGACCGTAAAGTTCCACGGCGAGTCTGATCGCGATGCTATGTGAA TCCCACCGACACGTTGCGGCATTAACAGCCTAAGTCAATTACTCA CACAATCTCTTTGTTGATTATTCTATTGTCACGCGGTACCTACGCC CTAGAGCTTTTGGACTTGTATTTAGTACGGTGTGTACTAGTGGCG GGCCGCCTGCCGGGACCCGGATTCAGTGCGTCCTGGTAAGAAG CTACTGTGCCTTTCTTCCTTAGCGCTGAAGATAATCGGTCTTAATT CCCTCATATAACCTCCAGTTAAATCAAGTGTCTCGATAGCTCGTTC TGGATGAGGTAGTGTTGGTTTATTGAATAGGTGTGAAGAAAATATT TGTTAATTAGGTGATATAAAGTAGAGTTAAATAAAGTGTATGGATA GGTGGTTGTGTATG