

Electronic Supplementary Information

DNA Nanostar Structures with Tunable Auxetic Properties

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S1. OxDNA Design of DNA Nanostars

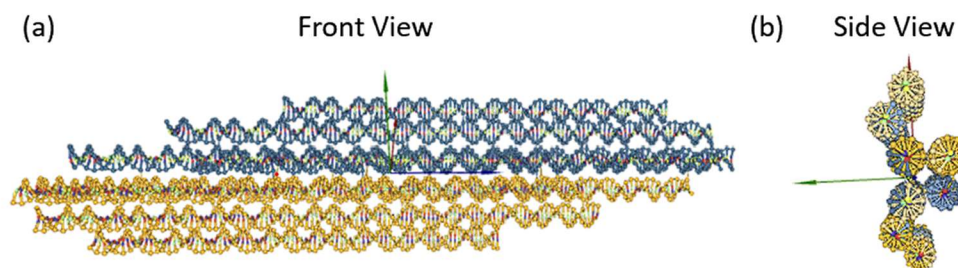


Figure S1. Schematic of edge design in oxDNA.^{1,2} (a) Front and (b) side views of the edge design of four double-stranded DNA bundles. Dark blue and yellow colors indicate two distinct edges sliding against each other.

S2. Agarose Gel Electrophoresis

Agarose gel electrophoresis was used to examine correct formations of the DNA nanostructures. The agarose gel was prepared by dissolving 500 mg of powder in 50 mL of 0.5× TBE buffer (44.5 mM tris base, 44.5 mM boric acid, 1 mM EDTA and 11 mM magnesium chloride). The solution was heated to boil and then cooled down in a mold with addition of ethidium bromide (EtBr, 0.5 μg/mL) to form a rectangular shape gel with channels. Then, DNA samples were added into the channels and electrophoresis was performed for 2 hours under 60 V. The resulting gel was visualized with an UV transilluminator to identify bands of different samples. As shown in Figure S2a, individual structures of only 9072-nt or 8064-nt scaffolds have distinct bands. The half structures based on the 9k scaffold are slower than those with the 8k scaffold due to their larger molecular weight. With 4× staples per scaffold, the bands are stronger indicating better formations of structures. Therefore, 4× were used in the experiments. Figure S2b compares the effect of the ratio between the 9k and 8k scaffolds on the assembly of three-star structures. Different ratios between 9k and 8k scaffolds (1:1, 1.5:1, and 1:2 ratios of 9k:8k) demonstrate clear bands indicating the correct formation of three-star unit cells. Note that the 1:1 ratio shows a band of half structures from the 9k scaffold. In contrast, the other two cases do not show distinctly clear bands of half structures due to individual scaffolds. Given the gel results, we chose a 1:2 ratio between 9072-nt and 8064-nt scaffolds in sliding experiments. It is noticeable that the assembled structures are faster than DNA ladders with corresponding molecular weights. This is attributed to the compact geometry of DNA origami enabling faster movement through porous agarose gel compared to free-form DNA.

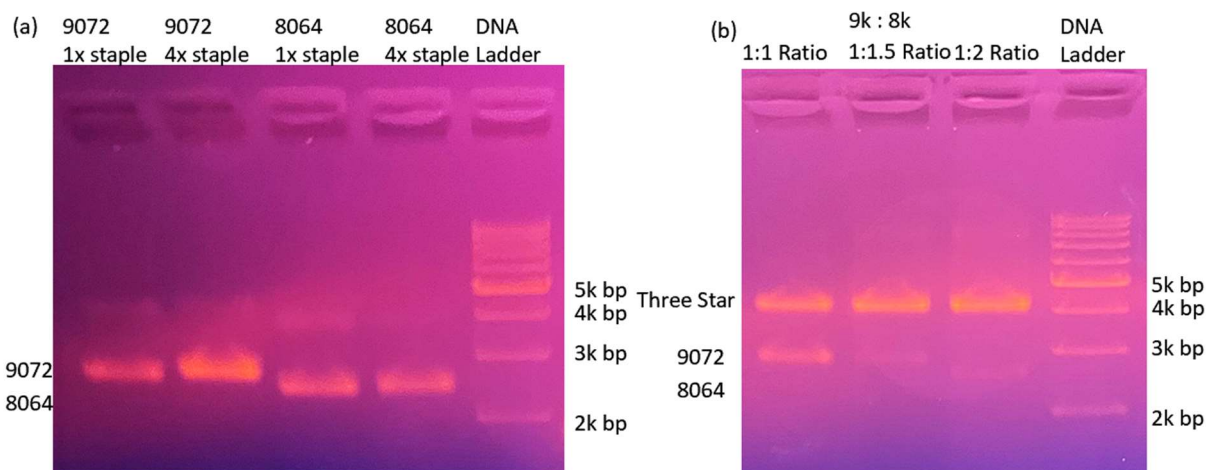


Figure S2. Agarose gel electrophoresis results. (a) Gel electrophoresis of half structures with 9072-nt or 8064-nt scaffolds with different staple concentrations. Two distinct bands of 9072-nt and 8064-nt based structures can be observed. The band with 4× staple concentration provides brighter bands. This condition is used for the formation of three-star structures. (b) Gel electrophoresis of three-star structures with various scaffold ratios between 9072-nt and 8064-nt scaffolds. It is obvious that the 1:2 and 1:1.5 ratios have stronger bands of three-star structures with weak signatures of individual half structures. Given the result, the 1:2 ratio has been used in experiments.

S3. Additional AFM Images

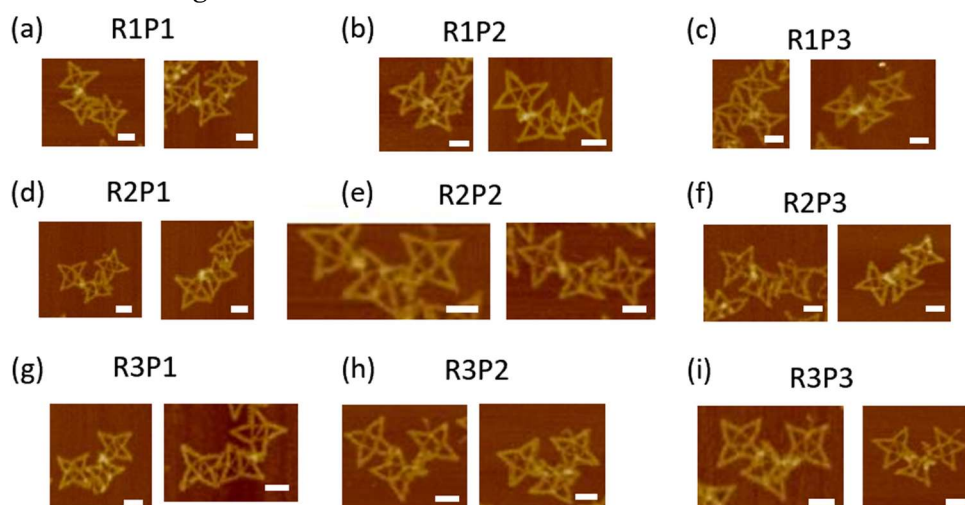


Figure S3. Additional experimental results for sliding on individual routes. The left star moves horizontally on route 1 at (a) position 1, (b) position 2, and (c) position 3. The left star moves vertically on route 2 at (d) position 1, (e) position 2, and (f) position 3. The right star moves horizontally on route 3 at (g) position 1, (h) position 2, and (i) position 3. The scale bars shown are 50 nm.

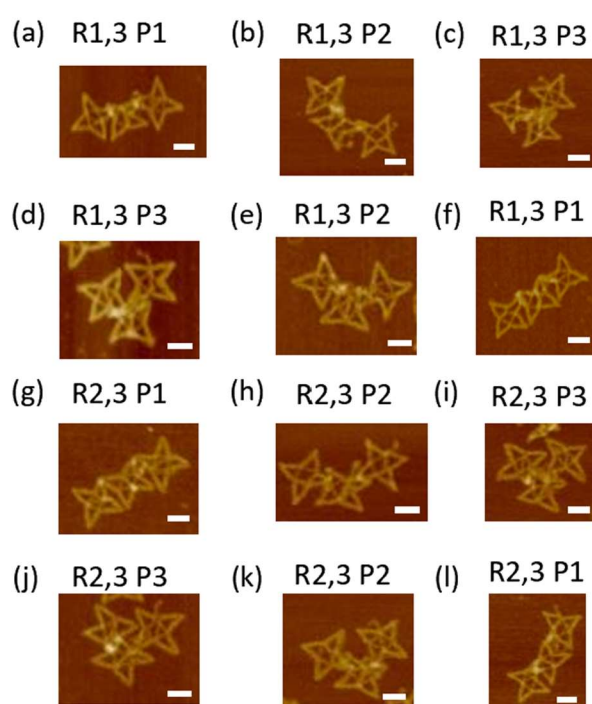


Figure S4. Additional experimental results for auxetic behaviors on combined routes. Auxetic sliding on combination between routes 1 and 3 are shown at (a) position 1, (b) position 2, and (c) position 3. Reversible movements are also demonstrated from (d) position 3 to (e) position 2, and then to (f) position 1. Similarly, for routes 2 and 3, reconfiguration is shown at (g) position 1, (h) position 2, and (i) position 3. Reversibly, sliding from (j) position 3 to (k) position 2 and finally to (l) position 1 is also demonstrated. The scale bars shown are 50 nm.

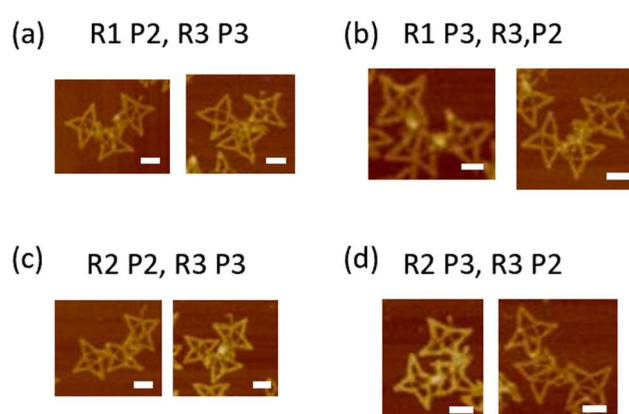


Figure S5. Additional experimental results for random positions. To show that control on individual routes is independent. Starting from undefined positions, several random reconfigurations are chosen. (a) Route 1

at position 2 and route 3 at position 3. (b) Route 1 at position 3 and route 3 at position 2. (c) Route 2 at position 2 and route 3 at position 3. (d) Route 2 at position 3 and route 3 at position 2. The scale bars shown are 50 nm.

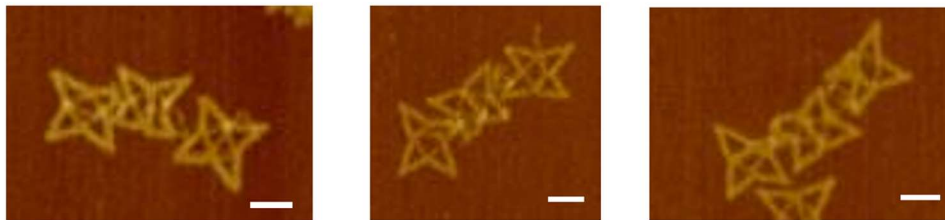


Figure S6. Additional experimental results for reconfigured, undefined positions. The AFM images show structures released from designated positions after removing positional staples. The left and right stars show detachment from the middle star as well as random orientations. The scale bars shown are 50 nm.

S4. Structural Analysis

Our unit design includes three nanostars. Each nanostar made of DNA origami has eight outer edges which are designed to have a length of 130 bp or approximately 43.2 nm. MD simulation suggests an edge length of ~ 40.0 nm. The edge lengths in AFM images are measured to be approximately 41.2 nm on average. Left and right stars slide along the edges of the middle star. A ss-loop is designed to distinguish between the left and right stars due to asymmetry, which could potentially be used to indicate sliding activities with additional mechanism designs. The sliding distance between two neighboring positional staples is designed to be 63 bp (~ 20.9 nm), while oxDNA structure shows ~ 19.9 nm. The distances measured from AFM images between 1st and 2nd positions and between 2nd and 3rd positions are approximately 20.0 and 20.1 nm on average, respectively. The measured lengths and distances from experiments are used to compute Poisson's ratios for auxetic reconfigurations for route 1 and 2 which are -0.42 and -1.01 on average, respectively. These are consistent with theoretical Poisson's ratio of $\nu = -0.414$ and -1. Overall, the analysis shows that our theoretical design, MD simulation, and experiment are in excellent agreement.

In this work, the sliding movement is enabled by toehold mediated strand displacement (TMSD) and reannealing with a new (intended) set of positional staples. The removal and insertion of positional staples work fairly well as TMSD and reannealing are well developed methods. These reactions are reported to be highly efficient while experimental conditions such as concentrations and temperatures may affect kinetically.³⁻⁵ As in any multi-step movement, however, the overall efficiency of stepwise reconfiguration in our experiment will decrease exponentially with the increased number of steps. We have characterized our initial formation efficiency of the nanostar structures from AFM images, which is approximately 68%. The efficiency of a single step movement is estimated to be roughly 35%.

S5. References

1. Snodin, B.E.K. et al. Introducing Improved Structural Properties and Salt Dependence into a Coarse-Grained Model of DNA. *Journal of Chemical Physics* **142**, 234901 (2015).
2. Shi, Z., Castro, C.E. & Arya, G. Conformational Dynamics of Mechanically Compliant DNA Nanostructures from Coarse-Grained Molecular Dynamics Simulations. *ACS Nano* **11**, 4617-4630 (2017).
3. Zhang, D.Y. & Winfree, E. Control of DNA strand displacement kinetics using toehold exchange. *Journal of the American Chemical Society* **131**, 17303-17314 (2009).
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5. Srinivas, N. et al. On the biophysics and kinetics of toehold-mediated DNA strand displacement. *Nucleic Acids Research* **41**, 10641-10658 (2013).

S6. DNA Sequences

Table S1. Sequences of staple strands for the undefined position of three-star unit cells. Lowercase letters indicate toeholds and binding domains of positional staples.

Name	Sequence
0[139]	GTACTGTTGGTAACTTCCGCAGCACAAACCACAAAAGTTCGGATGTCACC
0[153]	AGAGATTTTCGGCGTAGCTGGGGGAGTGTCTCTCGCAACAGAG
0[69]	AAGTTCACCATGGTTAGGACCTAAGTGTATTATGCAACACGGA
0[97]	CCCTACACGGCTAAACCGACTCTTGGCGTGTCTGTCTGAGAG
1[129]	GGTGCAGCGAGGCGCAAGTAAGGATCGAGCTTGAGTGAGTGG
1[154]	GTTGCCTTTTGGTTACCAGTAAGCACAC
1[45]	TTTGGAGACTTCACTCATGACACGTTGACTATCCTTAAGAGT
1[70]	CCCACCCCGCACTAGGGCTTACATACTGACACTACCTGGGAT
1[84]	CATGGATCGGCTTGCTATGGTGACAAAAGTTTAAACGAATAT
10[139]	CGCCGACTCCGCGATCACCGCCATTAGGAGCCGTGGTAATT
10[162]	ACGATATCCTCTATGTGAAGAATTCGGGACAACCGAC
10[97]	GCTCTAGAGCGATCCGTCCTACCTGTCCCCACGAAAAAGATC
100[139]	ACGAGTAGTAAATTCACCACCTTTTCGGTCATAGCTCACCGG
100[153]	CGAGAAACAGAGCCTGTAGCGGTTTTACGTACAGCG
100[90]	GTGAATTACAACGCCTGTATTTTCATAATCAACTTTAATCATT
101[126]	AAACAATCGGCGAAATCGGCAGGAACCGCCTCCCTCACCAGA
101[150]	CCATGTTTACCGTCAGACGCCACCC
101[171]	TTTGTGAGAGAAGAATCAAGTTTGCCTTTAGCAGTCCCGGAA
101[91]	GGTGGAGCCGCCACGGGAACGGATAACCCCCCTTAACCGGAA
102[104]	TTGCCATCTGCATTCCACAGACAGCCCTGCCAAGCTTTCAGA
102[62]	CGATCTACGTTGTAAAACGACGGCCAGTCATAGTTCACCAGT
103[119]	CCAGAGCGGGCTTGAGATGGTTTAATTTCAAATCTTAGCGT
103[161]	TCAGAACCGCCATTTTTAGAGCCACCACCCTCAGAG
103[57]	CACTGATGGCTCATTTTTTTTTGTCAGGA
103[77]	ACAAACTACCTTATGCGATTTTAAGAACGTTTCGTAGCGTAA
104[111]	ATGAGGAAGGGTAGTGCTAAACAACCTTGGCGAAAGGGGGAT
104[155]	CGTTGGGAAAACAACAGTCTTTCAGACGTGCCAGGG
104[76]	ATGCCACTACGAAGGCGGGATAGGAACAACCTAAAGGGAAGGG
104[97]	ATTAAACGGGTAAAGCGAAAGTTCAGCGGAGTGAGCTCTTCG
105[112]	GTGCTGCGGGATTTCAACGGCTACAGAGGCTTTTAAAACGAA
105[129]	AGTTGGGTAACTAGTAAATGAATTTTCTGTATAAGGCGATTA
105[147]	TTTTCCAGTCACGTTTTGTCTTATTACAGGTAGA
105[28]	ATTCGCCTCACGTTGAAATTTTTTTTCCAAAAAAAAGGCTCCAAAAG

105[45]	CGCAACTGTTGGAATTGCGAATAATAATTTTTATTTCAGGCTG
105[63]	CGATCGGTGCGGGCAATAGAACGTCACCCTCAGCAATACGTA
105[84]	CTATTACGCCAGCTCAACAGTACAGCATCGGAACGAGTTTCC
107[140]	CTAACGGGAAAAATCTACGTTAAGAGGACTAAAGACTTTTTTC
108[59]	CAGAACCGCCAATTCATCAGTTGAGATTTAGGCCGCCACCCT
108[80]	CACCCTCAGAAAATACCACATTCAACTAATGCTTAGTACCGC
109[101]	CGCCAAAAGGAGTATCACCGTACTCAGGAGGTAGATACATAA
109[122]	ATTACGAGGCACCGGAATAGGT
11[101]	AGTGCAAAGGTCTGGCGGATGTTCTAGATTAA
11[126]	GCAGTCTCGATGTTAGA
11[143]	CAGCACCGTTACGTCGAAAGCCACTTACGGGTAAACAAC
11[166]	TAACACTAAAGCAATTGTCGG
11[28]	CACCTTATGC
11[38]	TCAATATTCTCATATAGACTA
11[59]	CATAGTTCCCGGTTAAGCGTAGCGATGTCCAA
11[84]	GACCAAATTAGTGTGGA
110[139]	CAACCTAAAACGAACGCCACTTGCTTTCGAGGTGGAAGATC
110[90]	ACCCCAAACCAAAATAGCGATAGTTGCAACACTCATCTTTG
111[126]	GCACTCCAGCCAGCTATCAGCGCATAACCGATATATTCGGTC
111[49]	TTGGTGTAGTAAAACTATCATAACCCTCAAAGTACAACGGA
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113[119]	CAACCATAGAGGCAAAAGAATACACTAAGCCGACATAAACAG
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115[70]	ATTCGCGTTTGAGATGTAGGTAAAGATTATTGAGCGCTAATA
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36[153]	GAATTGACTTTACAATCCCACCGGCTACGGGAGTACGCATTC
36[69]	TAACGAGTCCCATATACAGGTCCATCTGGACATCTCGAATAA
37[133]	GTGCCGAATCTGTGTTACTTAGTACACAAGCAACCGCCTTTT
37[154]	CATCCTCATTGTTTCGTATAGGGACCAGTGACGGTTTTTTGAATGAGCGCACTT GCCA
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50[62]	TGAAGCTGATTATCAAAAAGGATCTTCAGCTGTTAACGAGGC
51[119]	TGGTGAGACCCACTCGTGCACCCAAGTGTGCTTTTATGGCAG
51[147]	GAATAGTGTATGCGGCTTTTTAGTTGCTCTTGCCCGGCGT
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52[162]	TTAAAAGTTTGAGTAACCAAGTTGGTTCGATCAGTGGCGGGGTC
52[90]	TCCTGATTACAGTAAGGGACACCACTTATTGCAAGCAGCAG
53[126]	TTTGATCTTTTCTAGAAGTCGGATTGCTTTGAATACATTATC
53[147]	TGACGCTCAGTGGACCTTATTACAAAATCGCGCAG
53[166]	AACTCATGTTAAGGGATTTTG
53[45]	ACAAACCACCGCGGTGTATGGGTCTGTAATTAGATCCGGCAA
53[91]	ATTACGCTCATACAACAGTACCTTTTACAATTATCATCATAT
54[104]	GCCTGGGGCAGAAAAAAGGATCTCAAGGGGGCATGAAACAA
54[34]	TCAGAATTCAGTTTTTTTTTCTAGCTTTT
54[62]	GGTTAATCTGGTAGCGGTGGTTTTTTTTGCGCCTATACGTCAG
55[119]	TAACGGAAGAAACCACCAGAAGGAGCGGATCGGGAAGATATG
55[77]	ATGAATATATCAGATGATGGCAATTCATAGGTTTAAAGTCGG
56[103]	AGTTAATTACATCAAGAAAACAAAATTAATTACACTGAGCAA
56[59]	TCATTTGAATTCGAATTATTCATTTCAATTACTTTAACAATT
57[122]	ATTTAATGGTACTTTTTTCAA

57[78]	AAGAAGATGATGAAACAATCATCTTCTGACCTAATATATTTT
58[111]	TTTAGTAAATCATAAGAAGTGTATTCTGTTAGTTACAAGTGG
58[139]	TTTGGATTATACTTGAAGGGTTTTTGTAGTTGCCGCTACGGC
58[153]	TATAATCTCAAATTCGTAGGTCTCAAGAGTATTTGGTATCT
58[90]	CAAATTCTTAAATAAGAATAAACACCGGTCATATGCGTTATA
59[112]	GGCCTAATTGAGAGATTACTAGATAATGCTGAAAAAAGCCTG
59[126]	TACACTAGAAGAAGTATGCTATAGAACCTACCATACTGATTG
59[154]	GCGCTCTCCTACTGTATTTGCACGTAACAGATTTTTAGAAATTGCGTAGAT TTTC
59[171]	GTTACCTTCGGTCTTGCACAGGTTGACGCGACGCTGAAGCCA
6[132]	GGGGCCGCGGTAGTATCGCTTCGAACGGCTCATTGGCCATG
6[90]	TACATCAAACAATTAAGAAACCCTGCCACTAGTATATCCGCG
60[62]	GTAAAGGTAACAGGATTAGCAGAGCGAGGCTTTATTGATAAA
60[83]	TTATGCCGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGT
61[57]	AATACCTCAACAGTATTTTTTTAATTGAG
61[77]	TAAGGCGTTACCAGTATAAAGCCAACGCGACCGTGAGCCTGA
62[111]	GCGGTCACAGCAGAAGATAAAACAGTAGAAGAAGTCAAATA
62[155]	AATCGCCATTGCTGGTTTACATGCCCGCATCGCCACT
62[76]	GCTGAGAGCCAGCAATAGCCCTTCCATATGCTGAATGCACGA
62[97]	CACCGCCTGCAACATAAAAAATCATAGCGAACAAACCCGACCG
63[105]	TCGTCTTGAGTCCAACCCGGTAAGACACGACTTATTGAAACC
63[147]	GGCAGCAGCCACTGGCGACGAAATATCCAGAACAA
63[28]	TAGGTCGATATAACACTTTTTTTTTAGCTAGGCGGCTAG
63[45]	GCTGGGCTGTGCCTACTCTTTTCAAGTGACCTTTCGCTCCAA
63[63]	ACCCCCCGTTCAGCCCCAAGTAAAACATCGCCATGTGCCAC
63[84]	CTGCGCCTTATCCGGTTACCGACCGAACGAACCACGTATTAA
64[132]	GCGCCGGGAGTCATCGACAAGTCAGAGGGGCACGCGTAACTA
65[140]	TCGGCCTATTTTAGTAATAACATCACTTGCCTGAGAGGTGAG
66[59]	ACAAAGAACGCTACCGCCAGCCATTGCAACAGCAATCGCAAG
66[76]	GCAAATCGAAAAACGCTCATGGAAATACCTACATTTTGACGC
67[105]	TCAATCGTAGGTTGGGTTATATAACTATATGTAAATGCTGAT
67[122]	TCTGAAATGGAAACCTCCGGCT
68[111]	AACCTCAGAACCCTGTCTCCtgggtgtg
68[139]	ATGAAAAATCTAAAGTAAGAATGAAAAC
68[69]	CAAATCAACACGACCTGCTAAaaacctga
69[112]	GTCCGCCGGCAACGTCTGACCTGAAAGCGCATCACCTTGCTG

69[140]	GCGCTTTCTCAT
69[152]	AGCTCACGC
69[49]	GTTTCCCCTAGAGGCAGATTCACCAGTCACAGTTGAAAGGAA
69[70]	CGTGCGCGGAGCGACAGTAATAAAAGGGACATTCTGGCCAAC
69[89]	ACCCTGCCGGCTGAGGTCGT
7[133]	CCGTGGGTTGATCTTCTGAGTTACGGAACGTGTGACTAATCC
7[150]	CTAAACGCGATTAGTGTCTGACGGAGCACCAACATAATAAC
7[49]	GCAGTGAGCCGTCCCCCGTAGGGCATCGGTTAGGCTCGAAAGTCGC
7[87]	CGGGGTCTCGTATGTCTCTTGATACCTATTTCTCTTAGGCAC
70[104]	AACGCGCCTTACCGGATACCT
70[125]	TAGGTTTTTCTCCCTTCGGGAAGCGTGGAACACATACGTGG
70[146]	TTGAAG
70[160]	AATTATATCGCACG
70[168]	GTGCGAGG
70[62]	AATGTTTCTGGAAGCTCCCT
70[86]	GGTATCAATTTCTCCTGTTCCG
71[140]	CACAGACAATATTTTTGAATGGCTTTTTGTCTTTAATGCGCGAACTG
71[39]	TTTACATTGGTGTAAGGTTACACAACCTTTTACCGGTCAAGAC
71[98]	AGAGATAAATATCAAACCCTCAATCAATATCTGGTCAGTTGG
72[125]	TTGACGGGGAAAGCCGGCGAAAGTGCCTATCCG
72[162]	TAAATCGGAACCCTAATTTACAGCGCG
72[76]	AAAGGAGCGGGCGCTTAGGCCACATCGTAATGCATAAGGCCA
73[105]	TCCGCCCCCTGACGAG
73[122]	egtcctccgaccCATCACAAAATCGACGCAATGTGTGAGAGCTCACAGTC
73[154]	GCGAAACGCAACCCAGTACTCGAACATG
73[161]	CCGACAGGACTTTAAAGATACCAGGC
73[28]	CTTGCTAAGG
73[38]	TGAGCAAAAGGCCAGCAA
73[63]	GGAACCGTAAAAAGGCC
73[80]	GCGTTGCTGGCGTTTTTCATTTCTGGTTGATT
74[106]	CCTCAGTAACATAGGC
74[118]	GTTTCGAGCTCACCTATCCTGCCGAGGGGATGCGA
74[148]	AGACAGTGTTCAAGTCAGAGGTG
74[34]	CGGAGACAAGGTTTTTTTTCCTAAATGGGAG
74[43]	TAAAGACGG
74[55]	AGGGCTACTGAA

74[83]	GCGGGGAAGCGCCTGCACACGGGTGAGGAAAGCG
75[140]	CCATCCAAGGGAGCCCCGATTTAGAGC
75[98]	ACGTGCCCGTGGCGAGAAAGGAAGGGAATCCGTTGCGCCCAC
76[101]	TAGATTAAGACCCTAACAAAAAGATACTGCAGAGCGATAGCT
76[59]	ATCATAGGTCTCATCTGGGAGTTTCTCACGGAATTTATCAAA
76[80]	GTCAATAGTGAAGGTACCCCTAGGCCGTTCCAGCTGAGAAGA
77[122]	GACTTAAATGCCTTGAAAACAT
78[115]	CCACACCCGCCGCGGGCTTAAGTACTGAGCACAGTCGCGTAACCA
78[136]	CGGTCACGCTGAATAAAAATCTTAAAGGACTGAAATAACTGCAACTT
78[153]	GGCGCTGGTCAAAACAAGTGG
79[126]	CGAGCGGATGCACACGGGAGACCACGCCTCCACGAGCAAGTGTAG
79[140]	TTGAGGTATCCTA
79[153]	ACTCTGGATAACTG
79[167]	GCCTCTGG
79[56]	GCTCCAGATTTAT
79[69]	CAGCAATAAACCAGCCAGCCGG
79[91]	AAGGGCCCTCCATCAGAGCTAAATTCATGCGCTTAATGAACCATACTAA
8[104]	TCGATAAGCACCTTTTGCTACTCAAGAATATTACGGAATAAT
8[62]	TCTGCTGTTCCCGATGAAGCGTATAAAACGGGATTCCGGTTC
80[104]	TATCCGCGAGCGCAGAAGTGGTCTGTCTTAGAAC
80[158]	CTAACGTGAGGCTTCTATA
80[179]	GGCGTGAAGGCACGGCGCCCC
80[74]	GCCGGGAAGCTAGAGTAAG
81[161]	GTTTCATTCATATTTTTTTGCCCCTTCGAGGGCTGTTT
81[57]	CAACATAGTAATTTATTTTTTTGTGGCAGCT
81[70]	GCAGTTACCCTTACCTTTGTCTTACAAATGTAAATGTCTAGT
81[84]	GGTGATCCAGTCTATTAATTGTT
82[115]	AGACCGAGATATAATAGAGAACCATCACCCCTACGTCTATCAGG
82[136]	TCCCTTATAAAAAGATAATCAGGGTT
82[157]	AATAGGCCGAAAGAAGTACAATATTATTGAAGATGTATTTAGA
82[178]	AAATCAGCTCACAATTCGATACTCATACTCTTAATAGGGGTTTC
82[195]	CGCGTTAATCCTTTGCCCGAACGTTAAAAGGGAATA
82[94]	TTGTTCCAGTTATCTTTATTTTTGGGGTTCGAGCAACGTCAAAG
83[109]	GCGATGGCCCCATGAGCATTGTCTACTACGT
83[126]	GGATACATATTTGACATTTATACATTTGAGGATTTATCGGCAAAA
83[151]	AAAATAAACACCTTTTTTTAGACTTTACAAATTTTTTAACC

83[172]	CGCGCACATTATGTTGAACAACCTCGTATTAAAATTTTTGTT
83[196]	CACCTAAATTGTTGTTAAAATT
83[70]	TGGACTCGTGCCGTAGGTTATCTAAAATTGGAACAAGAGTCC
83[88]	GGCGAAAAACATCAAGTGGAGCACTAACAACGGGTTGAGTG
84[139]	GGAAACGCAGAATCGGCCAACGCGCGGGGAGAGGCCAACCTGAGACGAT
84[153]	CAGAAGGCAAAAGAGCCGGGTTACCTGCGGCGCTTTCGCACT
84[576]	ATATAACAGTTCATAAATATTCATTGAATCCAGTTTCATTCC
84[597]	GGTGTCTGGACCCTCAAATGCTTTAAACAGTAACTAAAGTAC
84[69]	CAGATATCACATTAGGTGCTGCGGCCAGATGCCAACGGCAGC
84[97]	GTATTACCGCGCCCACTGCCCTGCGCGCCTGTGCGTGGTGC
85[129]	GGGTCATTGCAAGCCAGCGGTGCCGGTGCCCCAGCATCAGCG
85[154]	CAATCCGATCAGATACTGGCATGATTAA
85[45]	CAACCGCAAGAAATGCGGCGGGCCGTTTTCACTGGTCAGCAG
85[70]	ACCGTCGACTCTGTATTGCGTTGCGCTCAATAGCAAGCAAAT
85[84]	CATCCCACGCAACCAGTGTCAGCTTTCAGTCGGGGGTTTGC
86[104]	CCAGCGCAGCTTACGGCTGGAGGTGTCCCTGCATCTCGTGCC
86[34]	GGTCATAACGGTTTTTTTTTCTGCCAGCAC
87[119]	AGCTGCATTAATATAATAACGGAATACCAAACCGA
88[101]	TAATGCCCCCTATAAAGGTGGCAACATATAAATATAAACAGT
88[59]	GAAAGTATTAATCCTTATTACGCAGTATGTTATCTGAAACAT
88[80]	GAACCTATTATGCAAACGTAGAAAATACATACGCCTATTTTCG
89[122]	AGAAACGCAAAAACAGTGCCCCG
9[119]	AGTTCTGGCCGCTCTGGCATATCACGAGTTGGCGCACTGAG
9[147]	CATCCGGCACGATAATTTTTTAGCAGCAAGGTGAAGACCT
9[39]	CAGATCTACGGGAGTGTTCTGGACTTTTCACACAGCCTACAATTAT
9[77]	GTCAATCCTCCCTCAGACTCTACGAGGGATTTCAGATAGAG
90[132]	TTCTAAGACAACATTTGAGggggetctg
90[90]	GGAGGTTTTGAAGCCTTAAATCAAGATTACAATCAGACAAAA
91[122]	AGAGCACATCCTCATAACGGAatggacca
91[143]	ACGTGCCGGACTTGTAGATTCTTCGgcactagt
91[49]	AGTTAAAATTCAACAAGTTTATTTTGTGAGTTGCTATTTTGCACCCA
91[80]	ttggetcACGCGGTCCGTTTTTTTCG
92[104]	TTCGTAATCTCGTCGCTGGCAGCCTCCGGCCaaggttc
92[127]	GATCCCCGGGTACCGAGCTCACaagtagac
92[153]	CGTCCGTGAGCCTCCTCACAGACGAGCCGGAAGCAAGGCTTATCCGGTA
92[169]	cgtgcgacGCGTGCCTG

92[62]	GGGCGACCGATGCTGATTGCCGTTCCGGCAAAtcgaactc
92[85]	aacgctacGTTTACCAGCGCCAAAATAGAAA
92[97]	TCATGGTCATAGggttgctg
93[119]	ATTCCACAACGCGAGGCGTTTTAGCGAAGTTATCCGCTCGAA
93[147]	TAAAGTGTAAGCCTGTTTTTTCCTAATGAGTGAGCTAACT
93[39]	ACCACGGAATCGATTGAGGGAGGGAATTTAAATATTGACGGAAGGCG
93[77]	ATTCATATGCTGTTTTCCTGTGTGAAATTCCTCCCGACTTGCG
94[139]	TAATCTTGACAAGAGATTGGCGTCACCGACTTGAGTGTGTAC
94[162]	GGCTGGCTGACCTTCAACAAATACATTAAAGGTGAATATCCCGT
94[90]	CTGCTCAGAGCCGCACCAGTAGCACCATAAACTTAAATTTCT
95[126]	ATCGACATAAAAAATATCACCTTGATATTCACAATCAAGAG
95[147]	AAAAAAGCCGCACAATTATTAATCCTCATTAAAG
95[166]	GCCTTTTGTGATGAAGGGTAA
95[45]	TCACGGAAAAACGTCACCAATGAAACCATCGAGGGATAGCTC
95[91]	GCTCATTCAAAATCCGCCAGCATTGACATCAACGTAACAAAG
96[104]	GAGCCAGTGCCGCCAGCAGTTGGGCGGTCCATTTGGAGGCAG
96[34]	TAGCAGCACCGTTTTTTTTTCAGTAGCGAC
96[62]	CCGGAAAGAGACGCAGAAACAGCGGATCTACCATTCAGAACC
97[119]	GTCAGACACCGGATATTCATTACCCAAAGGAGGTTGGAATTA
97[77]	ACCACCATTGAGTGAATAAGGCTTGCCCCCGCCACAGCAAGG
98[59]	AGTTTTAACGGGAATGGAAAGCGCAGTCTCTGACTGGTAATA
98[79]	ACAGGAGTGTAATTTACCGT
98[87]	TTGATGATTCCAGTAAGCGTCATAGCAAGCCC
99[104]	AATAGGAACTCATTTCAGGGATACATGGCTT
99[122]	CCCATGTACCGGAGCCACCACC

Table S2. Sequences of replacement strands for sliding. The names are indicated in the order of route, position, and sequence number. Q represents complementary sequences

Name	Sequence
R1Q.0.1	GTCCAATAGCATAAGGTG
R1Q.0.2	TAGTCTATATGAGAATATTGAATACTTCT
R1Q.0.3	TTAATCTAGAACATCCGCCAGACCTTTGCACTTATATGAT
R1Q.0.4	GCTCCACGTCCACACTAATTTGGTC
R1Q.0.5	GATTCATCTCTAACATCGAGACTGC
R1Q.0.6	GTTGTTTACCCGTAAGTGGCTTTCGACGTAACGGTGCTGTCGCAGGA
R1Q.0.7	CATCACTTCAGAAAAAACGCCATCCCAGCGCCG
R1Q.0.8	CCCTGGTGGTCGTAAGCGTGTGTGCCTCCCTA
R1Q.0.9	TAAGGTGTCCTTAGCAAG
R1Q.0.10	TTGCTGGCCTTTTGCTCATCATCCTG
R1Q.0.11	TTTGACGCGGCCTTTTTACGGTTC
R1Q.0.12	AATCAACCAGAAATGAAAAACGCCAGCAACGCGCAGTTTT
R1Q.0.13	ACCCATACCTCGTCAGGGGGGCGGA
R1Q.0.14	ACACATTGCGTCGATTTTTGTGATGGTTAACCG
R1Q.0.15	CCGTCTTTATGCTGATG
R1Q.0.16	ATGGCCATTTAGTAGCCCT
R1Q.0.17	TATGTTGTCGGATAGGCACTTTCGCCG
R1Q.0.18	GCCTATGTTACTGAGGAGATCTGA
R1Q.0.19	GAGAGGCTCGCGCTGTGAAATTAGGGTCCGATTTA
R1Q.0.20	CACCTCTGACTTGAACACTGTCTGGTGTGTC
R2Q.0.1	AAGCTATCCGAGGATCTGTAG
R2Q.0.2	TAGGGCCGAGAGACCAATGTCATCAACTGA
R2Q.0.3	ACTGACTTAGTAGATGACGAC
R2Q.0.4	GTCATTCTAAGCCTTAACACCCGTCGATGA
R2Q.0.5	GGTACCAAGGCAGATCAGGTC

R2Q.0.6	ATCCTTGATTTGATCG
R2Q.0.7	TGGCTACCCCGAGCTGCGTCCCACAGGC
R2Q.0.8	GATCCGAGAAGCGGGT
R2Q.0.9	CCCTCTGATCTGTAGTACTGAGAGTTGC
R2Q.0.10	TGTATTGCACTGGATC
R2Q.0.11	GCTTTGGCATTTCGTCA
R2Q.0.12	TCGTACCCTTCGGTAAGGCCT
R2Q.0.13	GCTATGGAATAAATCTGGAGC
R2Q.0.14	CCGGCTGGCTGGTTTATTGCTGTTAATCGT
R2Q.0.15	GCGGATAAAGTTGCAGTTATTGGACAGACAATGCGGC
R2Q.0.16	ATAACGAACACTTCTGCGCTC
R2Q.0.17	CAGCAATTCAGTTATCCAGAGT
R2Q.0.18	CCAGAGGCACCGTCCG
R2Q.0.19	CAGCCTGGAACAATTAATAGACTGGATCACCTTAGTAT
R2Q.0.20	CTTACTCTAGCTTCCCGGCGCCTCCTA
R2Q.0.21	GGGGCGCCGTGCCTTCACGCCCGATCATC
R2Q.0.22	ACAAGTAACTCCCATTTAGGAAAAAAAAACCTTGTCTCCG
R3Q.0.1	ACGACCTCAGCCGGCAGGGTTCGGCGAT
R3Q.0.2	GAACAACACGGAACAGGAGAAATTGATACC
R3Q.0.3	ATTGTACTATGAGAAAGCGC
R3Q.0.4	GCGTGAGCTCATAGAAC
R3Q.0.5	TCAGGTTTTTAGCAGGTCGTGTTGATTTG
R3Q.0.6	AGGGAGCTTCCAGGAAACATTATAGCTAT
R3Q.0.7	ACACACCAGGGAGACAGGGTTCTGAGGTT
R3Q.0.8	AGGTATCCGGTAAGGCGCGTTGTGAGACC
R3Q.0.9	CTTCAAAAAGTCCCA
R3Q.0.10	GGATTTATCGTGCGATATAATT

R3Q.0.11	GCTTGCAACTAGCCGCCTAGCTAAAAAAAAAAGTGTTATATCGACCTA
R3Q.0.12	CCTCGCACACTTTCAT
R3Q.0.13	CGAAAAAACGGACCGCGTGAGCGCAA
R3Q.0.14	GAGTTCGATTGCCGGAACGGCAATCAGCATCGGTGCGCC
R3Q.0.15	TGGTCCATTCCGTTATGAGGATGTGCTCT
R3Q.0.16	ACTAGTGCCGAAGAATCTACAAGTCCGGCACGT
R3Q.0.17	GAAACCTTGGCCGGAGGCTGCCAGCGACGAGATTACGAA
R3Q.0.18	TTTCTATTTTGGCGCTGGTAAACGTAGCGTT
R3Q.0.19	CAGCCAACCTATGACCATGA
R3Q.0.20	CAGAGCCCCTCAAATGTTGTCTTAGAA
R3Q.0.21	GTCTACTTTGTGAGCTCGGTACCCGGGGATC
R3Q.0.22	TGGCTGACGTGCTGGCAGAAAAAAAAAACCGGTATGACC
R3Q.0.23	CAGGCACGCGTCGCACG
R1.1.1	CACCTTATGCcctccatagacaaactcgg
R1.1.2	gcctaccgagccgccgatcgTCAATATTCTCATATAGACTA
R1.1.4	agggtcgtaagtAGTGCAAAGGTCTGGCGGATGTTCTAGATTAA
R1.1.5	GACCAAATTAGTGTGGAcatcccatagcc
R1.1.6	GCAGTCTCGATGTTAGAAgctcgtcaaa
R1.1.7	aggctggcttatCAGCACCGTTACGTCGAAAGCCACTTACGGGTAAACAAC
R1.1.8	cgatcatcaacgaggggaaGGATGGCGTTTTTTTCTGAAGTGATG
R1.1.9	TAGGGAGGCACACACGCTTACGACTccactctttcaggaaatc
R1.1.10	CTTGCTAAGGgtctatgagggaaagcaca
R1.1.11	tcatgcctcgatcgccggctTGAGCAAAAGGCCAGCAA
R1.1.12	GGAACCGTAAAAAGGCCcccgtcgattgc
R1.1.13	cgtctccgaccGCGTTGCTGGCGTTTTTCATTTCTGGTTGATT
R1.1.14	TCCGCCCCCTGACGAGcccgtcgattgc
R1.1.15	cgtctccgaccCATCACAAAAATCGACGCAATGTGT

R1.1.16	ggttgaagtccccctcgtTAAAGACGG
R1.1.17	AGGGCTACTGAAgaaagaagtggaaagaaact
R1.1.18	CGGCGAAAGTGCCTATCCGctccttogaatg
R1.1.19	ctaaaaagtcttCCTCAGTAACATAGGC
R1.1.20	TAAATCGGAACCCTAATTTACAGCGCGcgtcaagcctag
R1.1.21	ataggcaacgctAGACAGTGTTCAGTCAGAGGTG
R1Q.1.1	cggagttgtctatggagggGCATAAGGTG
R1Q.1.2	TAGTCTATATGAGAATATTGAcgatcggcggctcggtaggc
R1Q.1.3	ttaaaccgTTGGACATCGCTACGCTTAACCGGGAACACTATG
R1Q.1.4	CATCACTTCAGAAAAAACGCCATCCtccccctcgttgatgatcg
R1Q.1.5	gattcctgaagaagtggaGTCGTAAGCGTGTGTGCCTCCCTA
R1Q.1.6	tgtgctttccctcatagacCCTTAGCAAG
R1Q.1.7	TTGCTGGCCTTTTGCTCAagccgccgatcgagcatga
R1Q.1.8	CCGTCTTTAaacgagggggaactcaacc
R1Q.1.9	agtttcttccactcttctTCAGTAGCCCT
R1.2.1	CACCTTATGC
R1.2.2	TCAATATTCTCATATAGACTAgcaatcgacggg
R1.2.3	ggtcggaggacgCATAGTTCCCGGTTAAGCGTAGCGATGTCCAA
R1.2.4	ggcaaggcaagacttttagGGATGGCGTTTTTTTCTGAAGTGATG
R1.2.5	TAGGGAGGCACACACGCTTACGACcattcgaaggagaggacggc
R1.2.6	CTTGCTAAGGggctatgggatgtaaccaga
R1.2.7	gaacagacacttacgaccctTGAGCAAAGGCCAGCAA
R1.2.8	TAAAGACGG
R1.2.9	AGGGCTACTGAA
R1Q.2.1	CATCACTTCAGAAAAAACGCCATCCctaaaaagtcttgcttgcc
R1Q.2.2	gccgtcctctccttogaatGTCGTAAGCGTGTGTGCCTCCCTA
R1Q.2.3	tctggttacatccatagccCCTTAGCAAG

R1Q.2.4	TTGCTGGCCTTTTGCTCAagggtcgtaatgtctgttc
R1Q.2.5	gactgcacgcaatcgacgggGGCCTTTTACGGTTCC
R1Q.2.6	AATCAACCAGAAATGAAAAACGCCAGCAACGCggtcggaggacggtgtacta
R1Q.2.7	cgtgctaccattcgaaggagCGGATAGGCACCTTCGCCG
R1Q.2.8	GCCTATGTTACTGAGGaagacttttaggatagtc
R1.3.1	agcgttgccatGGATGGCGTTTTTTTCTGAAGTGATG
R1.3.2	TAGGGAGGCACACACGCTTACGACctaggcttgacg
R1.3.3	CTTGCTAAGGtttgaacgagct
R1.3.4	ataagccagcctTGAGCAAAAGGCCAGCAA
R1.3.5	GGAACCGTAAAAAGGCCggtatgggatg
R1.3.6	acttacgacctGCGTTGCTGGCGTTTTTCATTTCTGGTTGATT
R1.3.7	CGGCGAAAGTGCCTATCCG
R1.3.8	CCTCAGTAACATAGGC
R2.1.1	CTACAGATCCTCGcgtcggtcgata
R2.1.2	ttgttcgtaagaTGACATTGGTCTCTCGGCCCTA
R2.1.3	GTCGTCATCTACTaggggaatcggc
R2.1.4	actaccttgagGGGTGTTAAGGCTTAGAATGAC
R2.1.5	GACCTGATCTGCCggcagactgttttcgagca
R2.1.6	ataacgcactatatttgatTCAAGGAT
R2.1.7	GCCTGTGGGACGCAGCTCGGgtcacaccgggc
R2.1.8	gagtccgcctgCTCGGATC
R2.1.9	GCAACTCTCAGTACTACAGAtcctcgacgggg
R2.1.10	gggagcactgcgGCAATACA
R2.1.11	accaacatcagcctcaagctGCCAAAGC
R2.1.12	AGGCCTTACCGAAgttgaatttaccataatca
R2.1.13	GCTCCAGATTTATgctccccgtgg
R2.1.14	attctctatgtcCAGCAATAAACCAGCCAGCCGG

R2.1.15	ccaccttaaatgGTCTGTCCAATAACTGCAACTTTATCCGC
R2.1.16	GAGCGCAGAAGTGcaccaattttcg
R2.1.17	TTGAGGTATCCTAaaacgttt
R2.1.18	ACTCTGGATAACTGaaacagtctgccccgattgcg
R2.1.19	acggtgcatcaaaatataGCCTCTGG
R2.1.20	ATACTAAGGTGATCCAGTCTATTAATTGTTatacagggtaa
R2.1.21	tattgccagcGCCGGGAAGCTAGAGTAAG
R2.1.22	CTAACGTGAGGCTTCTATAgttggtat
R2.1.23	cccgcgtagcttgaggctgGGCGTGAAGGCACGGCGCCCC
R2.1.24	CGGAGACAAGGTTTTTTTTTCTAAATGGGAGggtaaattcaac
R2Q.1.1	tgctgcgaaaacagtctgccGGCAGATCAGGTC
R2Q.1.2	ATCCTTGaatcaaaatatagtgcgttat
R2Q.1.3	GCTTTGGCagcttgaggctgatgttggt
R2Q.1.4	tgattatgggtaaattcaacTTCGGTAAGGCCT
R2Q.1.5	aaacgttTAGGATACCTCAA
R2Q.1.6	cgcaatcgggcagactgtttCAGTTATCCAGAGT
R2Q.1.7	CCAGAGGCctatattttgategcaccgt
R2Q.1.8	ataccaacTATAGAAGCCTCACGTTAG
R2Q.1.9	GGGGCGCCGTGCCTTACGCCcagcctcaagctagcgggg
R2.2.1	GACCTGATCTGCCcgaaaattggtggcggtca
R2.2.2	ccgtaagcatttaaggtggTCAAGGAT
R2.2.3	GCCAAAGCagcatag
R2.2.4	AGGCCTTACCGAAActtaattt
R2.2.5	TTGAGGTATCCTAgccgattccccttagccgca
R2.2.6	ctttggccctcaagtagtACTCTGGATAACTG
R2.2.7	GCCTCTGG
R2.2.8	atattaatcgcagtgtcccCTAACGTGAGGCTTCTATA

R2.2.9	GGCGTGAAGGCACGGCGCCCCccccgtcgaggaaaaacgac
R2Q.2.1	tgaacgccaccaattttcgGGCAGATCAGGTC
R2Q.2.2	ATCCTTGAccaccttaaatgcttaccgg
R2Q.2.3	ctatgctgGCTTTGGC
R2Q.2.4	aaattaagTTCGGTAAGGCCT
R2Q.2.5	GCGGATAAAGTTGCAGTTATTGGACAGACcatttaaggtggaggttccc
R2Q.2.6	aatcgccacgaaaattggtgCACTTCTGCGCTC
R2Q.2.7	tggcgtaaggggaatcggcTAGGATACCTCAA
R2Q.2.8	CAGTTATCCAGAGTactacctggaggggccaaag
R2Q.2.9	TATAGAAGCCTCACGTTAGgggagcactgcgattaatat
R2Q.2.10	gtcgttttctcgcacggggGGGGCGCCGTGCCTTCACGCC
R2.3.1	GACCTGATCTGCCccacggggacgc
R2.3.2	gacatagagaatTCAAGGAT
R2.3.3	gcctggcgaataGCCAAAGC
R2.3.4	AGGCCTTACCGAAttaccctgtat
R2.3.5	GTCTGTCCAATAACTGCAACTTTATCCGC
R2.3.6	GAGCGCAGAAGTG
R2.3.7	TTGAGGTATCCTAtatcgaccgacg
R2.3.8	tcttacgaacaaACTCTGGATAACTG
R2.3.9	cagggcgactcCTAACGTGAGGCTTCTATA
R2.3.10	GGCGTGAAGGCACGGCGCCCCgcccgtgtgac
R3.1.1	TAGGTTCGATATAAACTTTTTTTTTTAGCTAGGCGGCTAGcgtgtgcttgat
R3.1.2	aatgtgaatctgGTGCGAGG
R3.1.3	GGTCATACCGGTTTTTTTTTCTGCCAGCACatcaagcacacgtgagagcc
R3.1.4	gcagcgcacagattcacattGCGTGCCTG
R3Q.1.1	ATCAAGCACACGCTAGCCGCCTAGCTAAAAAAAAAAGTGTTATATCGACCTA
R3Q.1.2	CCTCGCACCAAGATTACATT

R3Q.1.3	GGCTCTCACGTGTGCTTGATGTGCTGGCAGAAAAAAAAAACCGGTATGACC
R3Q.1.4	CAGGCACGCAATGTGAATCTGTGCGCTGC
R3.2.1	GCGCTTTCTCATtcaatcggaagtatgtagac
R3.2.2	aatagcagatacaccccttgaAGCTCACGC
R3.2.3	AACCTCAGAACCCTGTCTCCCcggttagtgtaagetgctg
R3.2.4	ccactgtgtgactaagggAACGCGCCTTACCGGATACCT
R3.2.5	ccgaagtggcgactgtaacTTTGAAG
R3.2.6	AATTATATCGCACGcatctgacgaattgacacca
R3.2.7	cagcaggctcaagggtgatAGAGCACATCCTCATAACGGA
R3.2.8	TTCGTAATCTCGTCGCTGGCAGCCTCCGGCCacttccgattga
R3.2.9	TTCTAAGACAACATTTGAGattcgtcagatggtggcgat
R3.2.10	tatccgccgttacagtcgccGATCCCCGGGTACCGAGCTCACA
R3.2.11	GGTCATACCGGTTTTTTTTTCTGCCAGCACtaactaaccgcatatcat
R3.2.12	attaactccccttagtcacaGCGTGCCTG
R3Q.2.1	GTCTACATACTTCCGATTGAATGAGAAAGCGC
R3Q.2.2	GCGTGAGCTTCAAGGGTGTATCTGCTATT
R3Q.2.3	CAGCAGCTTAACACTAACCGGGGAGACAGGGTTCTGAGGTT
R3Q.2.4	AGGTATCCGGTAAGGCGCGTTCCTTAGTCACACACAGTGG
R3Q.2.5	CTTCAAAGTTACAGTCGCCAACTTCGG
R3Q.2.6	TGGTGTCAATTCGTCAGATGCGTGCGATATAATT
R3Q.2.7	TCCGTTATGAGGATGTGCTCTATACACCCTTGAGCCTGCTG
R3Q.2.8	TCAATCGGAAGTGGCCGGAGGCTGCCAGCGACGAGATTACGAA
R3Q.2.9	ATCGCCACCATCTGACGAATCTCAAATGTTGTCTTAGAA
R3Q.2.10	TGTGAGCTCGGTACCCGGGGATCGGCGACTGTAACGGCGGATA
R3Q.2.11	ATGATATGCGGTTAGTGTTAGTGCTGGCAGAAAAAAAAAACCGGTATGACC
R3Q.2.12	CAGGCACGCTGTGACTAAGGGGAGTTAAT
R3.3.1	tactaaactgcACCCTGCCGGCTGAGGTCGT

R3.3.2	GGTATCAATTTCTCCTGTTCCGatctcgatcaga
R3.3.3	GCGCTTTTCATggttcacaacta
R3.3.4	ctatttgtaaaAGCTCACGC
R3.3.5	CAAATCAACACGACCTGCTAAcggacaacctgt
R3.3.6	ccctaagcatccAATGTTTCCTGGAAGCTCCCT
R3.3.7	AACCTCAGAACCCTGTCTCCCcggttagtgta
R3.3.8	tgtgactaaggAACGCGCCTTACCGGATACCT
R3.3.9	ctgttgatcgtTTTGAAG
R3.3.10	AATTATATCGCACGgcaacctcgtg
R3.3.11	ttaacaaatagACGCGGTCCGTTTTTTCG
R3.3.12	GGGCGACCGATGCTGATTGCCGTTCCGGCAAtagttggaacc
R3.3.13	AGAGCACATCCTCATAACGGAtctgatcgagat
R3.3.14	gcacgttagtaACGTGCCGGACTTGTAGATTCTTCG
R3.3.15	acgatcaacaagGTTTACCAGCGCCAAAATAGAAA
R3.3.16	TCATGGTCATAGcacgaaggtgc
R3.3.17	TTCTAAGACAACATTTGAGtaacactaacgg
R3.3.18	cccttagtcacaGATCCCCGGGTACCGAGCTCACA
R3.3.19	GGTCATACCGTTTTTTTTTTCTGCCAGCACacaggtgtccg
R3.3.20	ggatgcttaaggGCGTGCCTG