Multilayer DNA Origami Packed on Hexagonal and Hybrid Lattices

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Assembly of DNA structures. Scaffold DNA and all the staple strands (purchased from Bioneer) were mixed together at 1:5 ratio, in 1 x Tris-Mg^{2+} buffer (Tris, 5 mM; EDTA, 1 mM; and magnesium chloride, 6-14 mM; pH 8.0). DNA structures were formed by slowly cooling the oligo mixtures from 80 °C to 24 °C over 72 hours.

Agarose gel electrophoresis and sample purification. Annealed DNA structures were purified by agarose gel (1.6% to 2%) electrophoresis. The DNA structure samples were loaded into agarose gel and allowed to run for 3 hours (running buffer: 1xTAE, 11mM $MgCl_2$; running voltage: 70 volt). The leading bands corresponding to the correctly folded structures were then visualized with ultraviolet light and cut out from the gel. Excised bands were crushed and transferred into a DNA gel extraction spin column (BIO-RAD, Catalog number: 732-6166). DNA structure solution was recovered by centrifuging the column for 10 minutes at 16000g.

TEM studies. The TEM sample was prepared by dropping 3.5μL of sample solution on a carbon-coated grid (400 mesh, Ted pella). Before depositing the sample, the grids were negatively glow discharged for 45 seconds. After 2 minutes, the sample was wicked from the grid by touching its edge with a piece of filter paper. Then the grid was touched with a drop of 2 % uranyl formate solution and excess solution was wicked away with a filter paper. Again the grid was touched with a second drop of uranyl formate solution for 20 seconds, and the excess solution was removed with a filter paper. TEM studies were conducted using a JEOL JEM-1400 transmission electron microscope, operated at 80 kV on bright field mode.

Native polyacrylamide gel electrophoresis (PAGE). Native PAGE was done by using Bio-Rad Mini-Protean Tetra Cell. Buffer: 1xTBE (89mM tris base, 89mM boric acid, 2mM EDTA). Gel electrophoresis was carried out at constant 200 V for one to two hours.

Figure S1. TEM images of 12HB-L. Scale bar: 100nm.

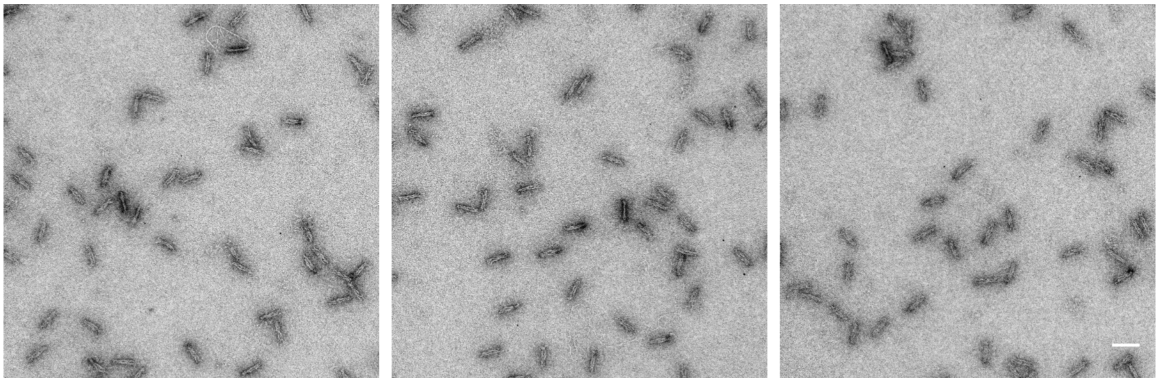


Figure S2. TEM images of 24HB-L. Scale bar: 100nm.

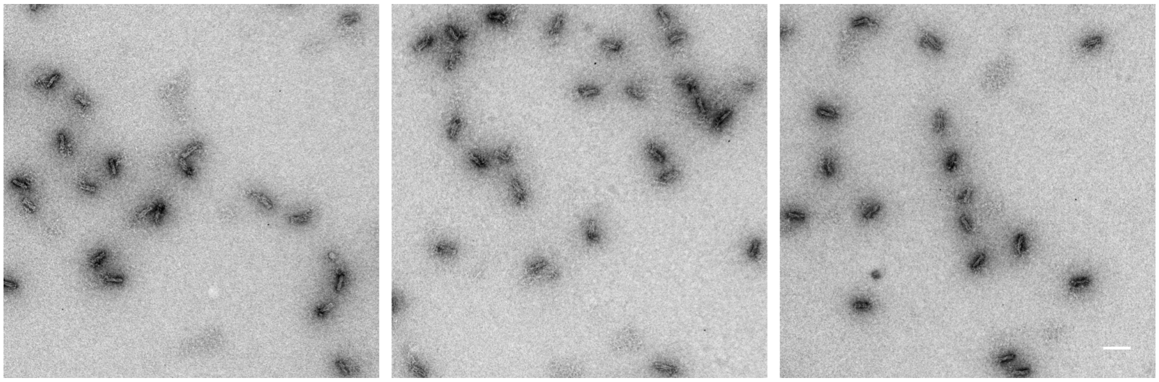


Figure S3. TEM images of 24HB-S. Scale bar: 100nm.

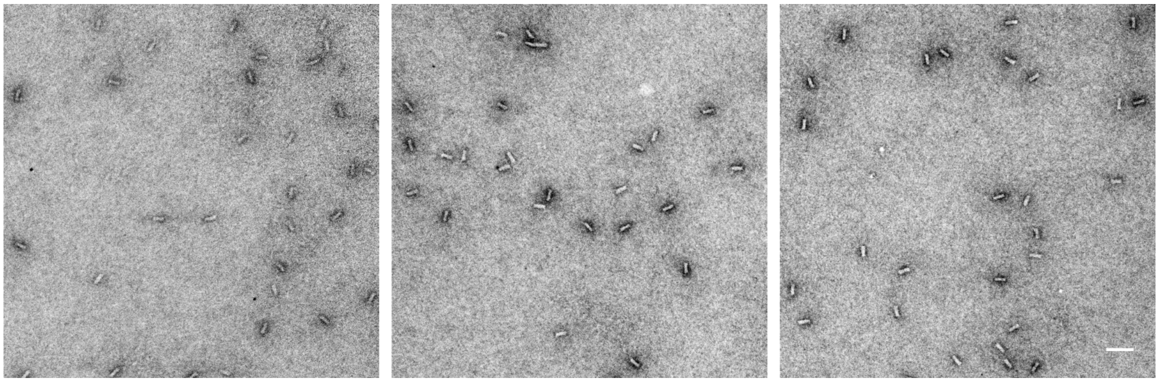


Figure S4. TEM images of 60HB-S. Scale bar:

100nm.

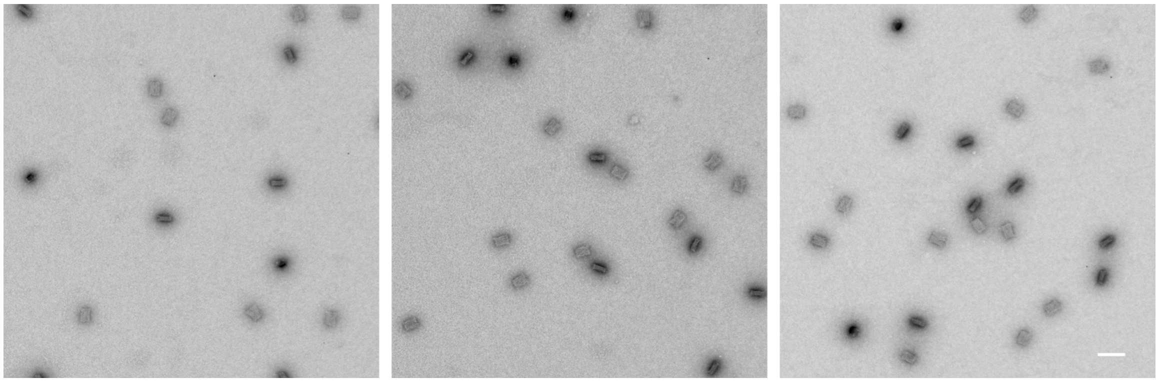


Figure S5. TEM images of 56HB Hybrid. Scale bar: 100nm.

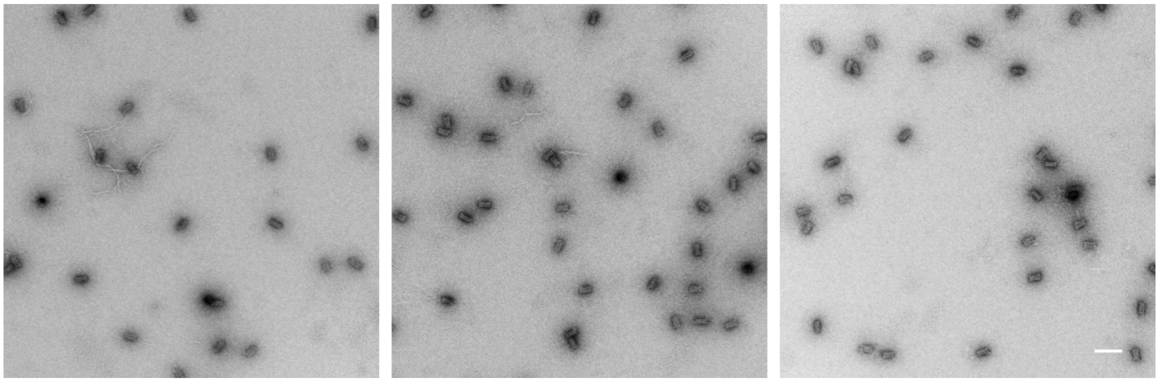


Figure S6. TEM images of 52HB Hybrid. Scale bar: 100nm.

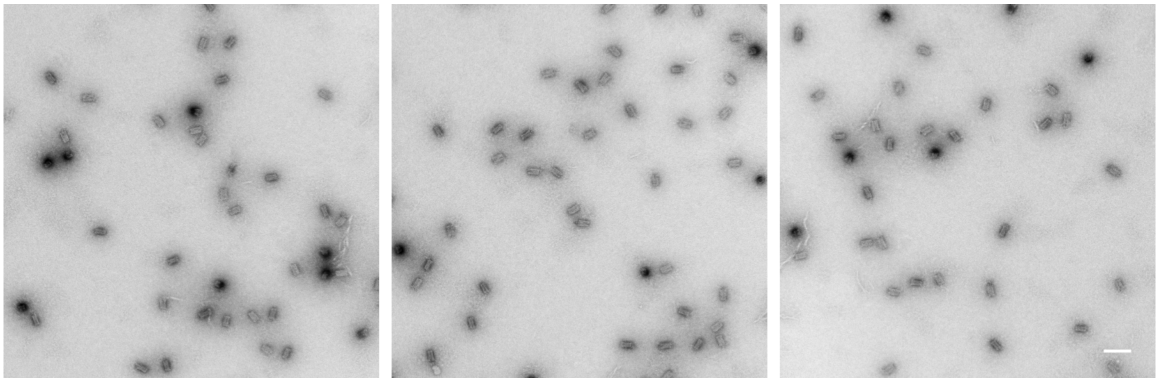
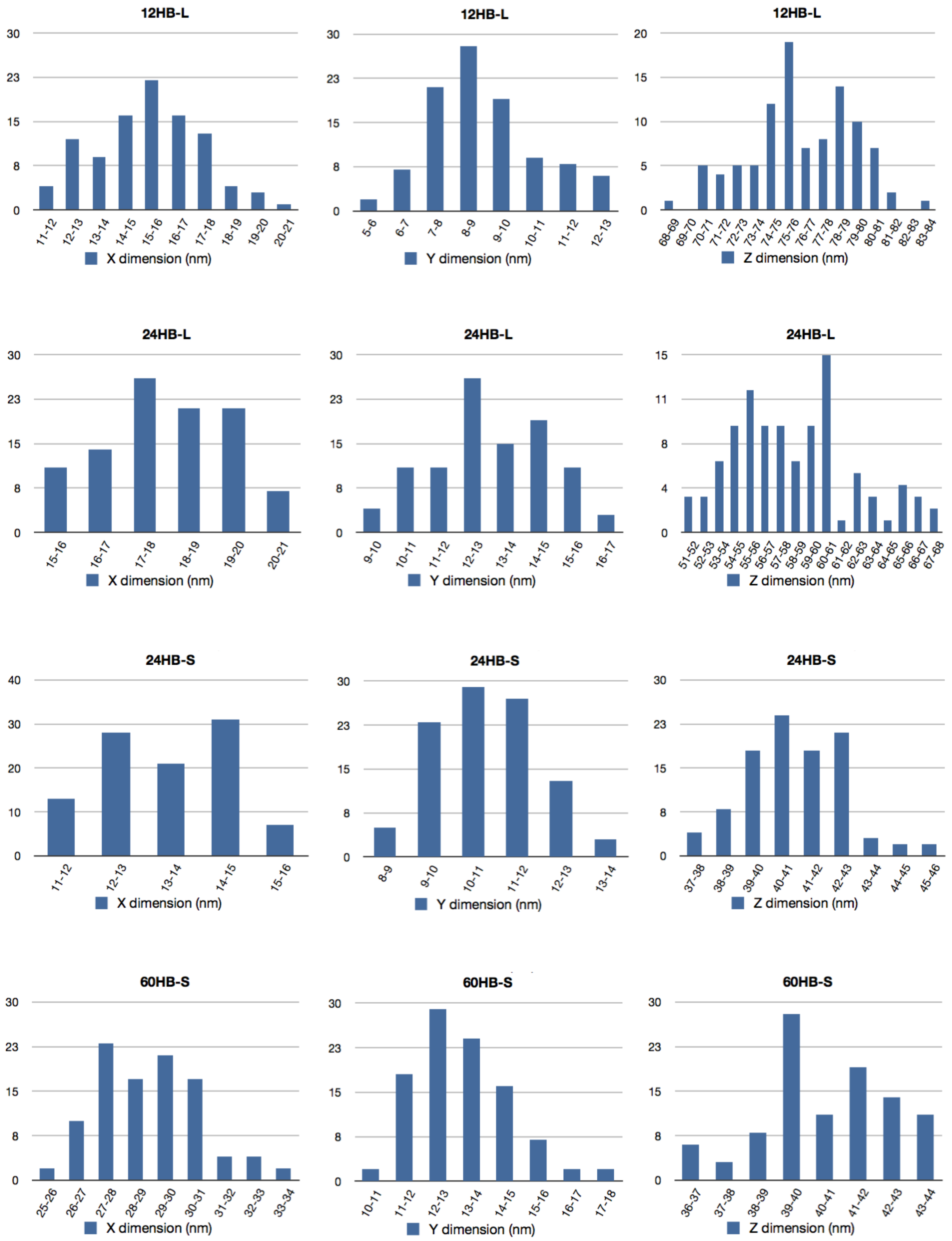
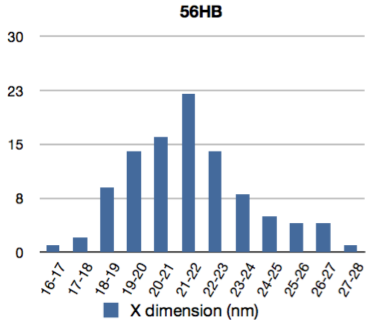
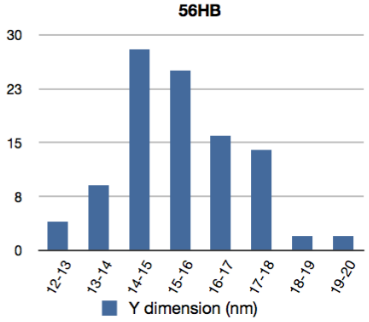
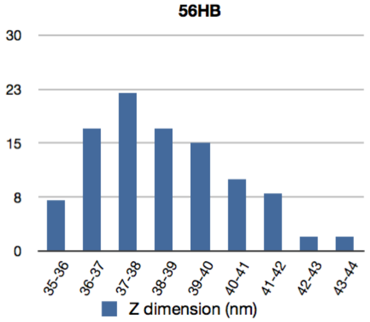


Figure S7. Histograms of measured X-, Y-, Z-dimensions of 12HB-L, 24HB-L, 24HB-S, 60HB-S, 56HB and 52HB. Data is acquired by measuring the particle sizes from TEM images. Y-axis is the number of events. Sample size: 100 particles for each dimension.




56HB
30
23
15
8
0
16-17
17-18
18-19
19-20
20-21
21-22
22-23
23-24
24-25
25-26
26-27
27-28
X dimension (nm)


56HB
30
23
15
8
0
12-13
13-14
14-15
15-16
16-17
17-18
18-19
19-20
Y dimension (nm)


56HB
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23
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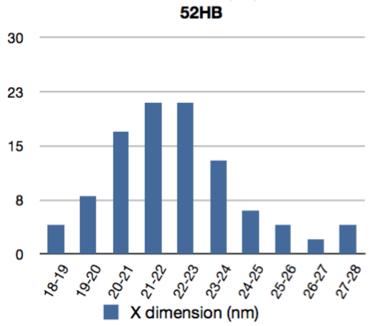
8
0
35-36
36-37
37-38
38-39
39-40
40-41
41-42
42-43
43-44
Z dimension (nm)


52HB
30
23
15
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0
18-19
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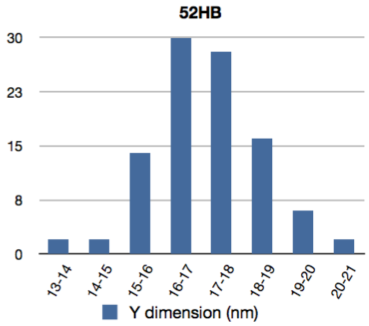
20-21
21-22
22-23
23-24
24-25
25-26
26-27
27-28
X dimension (nm)


52HB
30
23
15
8
0
13-14
14-15
15-16
16-17
17-18
18-19
19-20
20-21
Y dimension (nm)

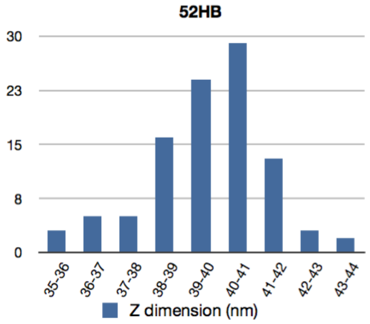
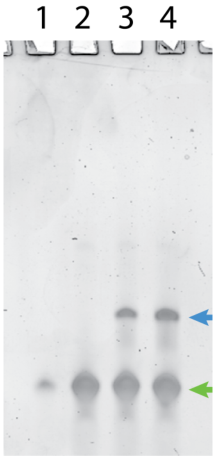

52HB
30
23
15
8
0
35-36
36-37
37-38
38-39
39-40
40-41
41-42
42-43
43-44
Z dimension (nm)

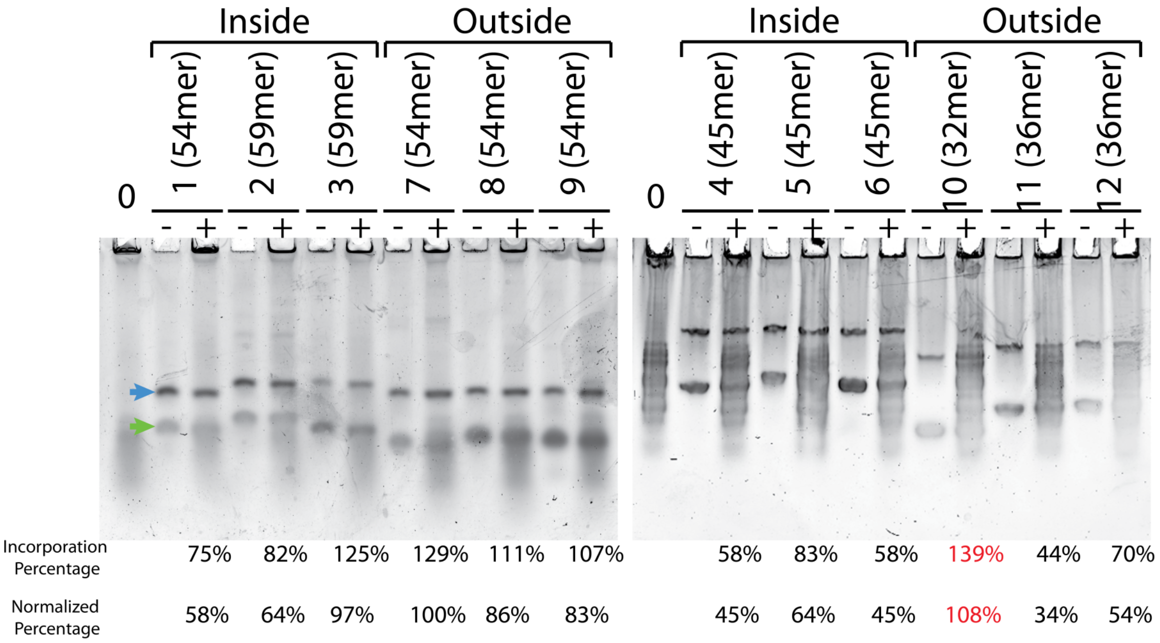
Figure S8. Analysis of staple-strand incorporation efficiency. Six inside staple strands (colored in green in Figure S11) and six outside staple strands (colored in red in Figure S11) were chosen from the 60HB-S design for the assay. Their information is shown in the table below. 60HB-S was first annealed and purified as described above. Final concentration was measured by absorbance at 260 nm wavelength assuming 50 µg/mL for $A_{260} = 1$. To estimate incorporation percentage of each staple strand, we mixed its complementary strand (800 fmol) with 40 fmol purified 60HB-S, and performed a quick annealing (90 °C to 24 °C, 20 second per °C). The DNA duplex formed by the staple strand and its complementary strand was visualized and analyzed by native PAGE assay. Incorporation percentages were obtained by comparing the integrated intensity of the resulting DNA duplex band, as measured by Image J analysis, with that from control samples made by mixing the staple strand alone with the complement. To measure integrated band intensity in ImageJ, a box was drawn around the band, and a copy of this box was placed just above the band. The integrated intensity from the control box was subtracted from the integrated intensity of the experimental box to obtain the background-corrected experimental intensity.

Shown below is a control 10% native PAGE gel demonstrating how this assay can be used to quantitate the amount of staple strand present. Lane 1 shows staple strand (inside strand 1, 54mer) alone at 40 fmol. Lane 2 shows 800 fmol of the complementary strand. Lane 3 shows 20 fmol of the staple strand mixed with 800 fmol complementary strand, representing 50% incorporation efficiency. Lane 4 shows 40 fmol staple strand mixed with 800 fmol complementary strand, representing 100% incorporation efficiency. Image J analysis comparing bands from Lane 3 and Lane 4 shows a relative band intensity of 60%, roughly in agreement with the predicted relative intensity of 50%. The DNA duplex of interest appeared on the gel as the slow migrating band pointed by a blue arrow.



Shown below to the left is a 10 percent native PAGE for analysis of longer staple strands(conditions described in Methods above). Shown below to the right is a 20 percent native PAGE for analysis of shorter staple strands (conditions described in Methods above). Lane 0 shows 40 fmol 60HB-S, while Lanes 1–12 (+) samples show 40 fmol 60HB-S and 800 fmol complementary strand, and Lanes 1–12 (-) show control samples with 40 fmol individual staple strand and 800 fmol complementary strand. Thus (+)

samples are the equivalent of Lane 3 in the control gel above, and (-) samples are the equivalent of Lane 4 in the control gel above.
All samples were subjected to the 20-minute quick annealing step before loading into the gels. Note the duplex band formed by staple 10 and its complementary strand overlapped with one band that exists in the 60HB-S-only sample (lane 0). Thus the incorporation percentage of staple 10 is likely overestimated.



Note that the measured incorporation efficiencies often exceed the theoretical maximum of 100%. We attribute this to errors in estimation of the concentration of gel purified 60HB-S and errors in estimation of concentration of control staple strands (e.g. due to errors in estimation of extinction coefficients between the different strands). We also include an incorporation percentage that is normalized to the highest reliable incorporation efficiency observed (sample 7). Also note that loss of staple strands could be due either to lack of incorporation during folding, but also from loss during purification.

As can be seen from inspection of the data, shorter strands from either inside or outside appear to have much lower incorporation efficiencies on average (51% incorporation of inside strands of mean length 45 bases versus 73% incorporation of inside strands of mean length 57 bases; 44% incorporation of outside strands of mean length 35 versus 90% incorporation of outside strands of mean length 54). Inside strands of mean length 57 bases had a 20% lower incorporation efficiency than outside strands of mean length 54. Collectively, this data suggests that greater incorporation efficiency can be obtained by increasing the length of strands, and that the requirement for longer length is greater for inside strands than for outside strands.

Inside staples	Sequence (length)	Incorporation percentage (%)	Normalized percentage (%)
1	TAAGAGAATCAGAGAGAATAACATAAAGTATAAAGCCAACGCTCATTACAAAAT (54)	75	58
2	AATAACCGAACTCTAGGAAGGTTAAAGTTTGAACGACCAGTACGCCAGAATCACGCAAA(59)	82	64
3	CGAGGCGTTGCAAGCAAAAAATATTGAGTACGGTGTCAATAACCTGGTGGCAACCCTAT (59)	125	97
4	TAATCTATTAATTGTCAATGTAAATCGAGGCTGCGCTAACGCCAG (45)	58	45
5	ATATAAGTATGCCCCCTGATATAAAAGAAACGCAAAAGCAAACGT (45)	83	64
6	AAACAGGAATTTTTGAGAATTAATTTTCCCTTAGAAAGTGAATAA (45)	58	45
Outside staples			
7	TCAGAGCCACCACCCTCAGCAAAAGAATACACTAAAGCCACTACGAAGGCACCA (54)	129	100
8	AAACAGCCATATTATTTATCCCAATCCTAGCACCATTACCATTAGGCCATTTGG (54)	111	86
9	AGTGTAGCGGTCACGCTGGAAAGCGAAAGGAGCGGGCATTAAAAATACCGAACG (54)	107	83
10	ATTTTTGCGGATGGTGCACCCAGCTTAAATCA (32)	139	108
11	TTGCTGAACCAAATGAAAGAACAAGAGTCCACTATT (36)	44	34
12	GATAAATTGTGTCGAAATACCATAAATTTAAACAGT (36)	70	54

Figure S9. Illustration of 12HB-L design. Blue strand is the scaffold strand and black strands are staple strands. Arrows indicate 3’-end of DNA.

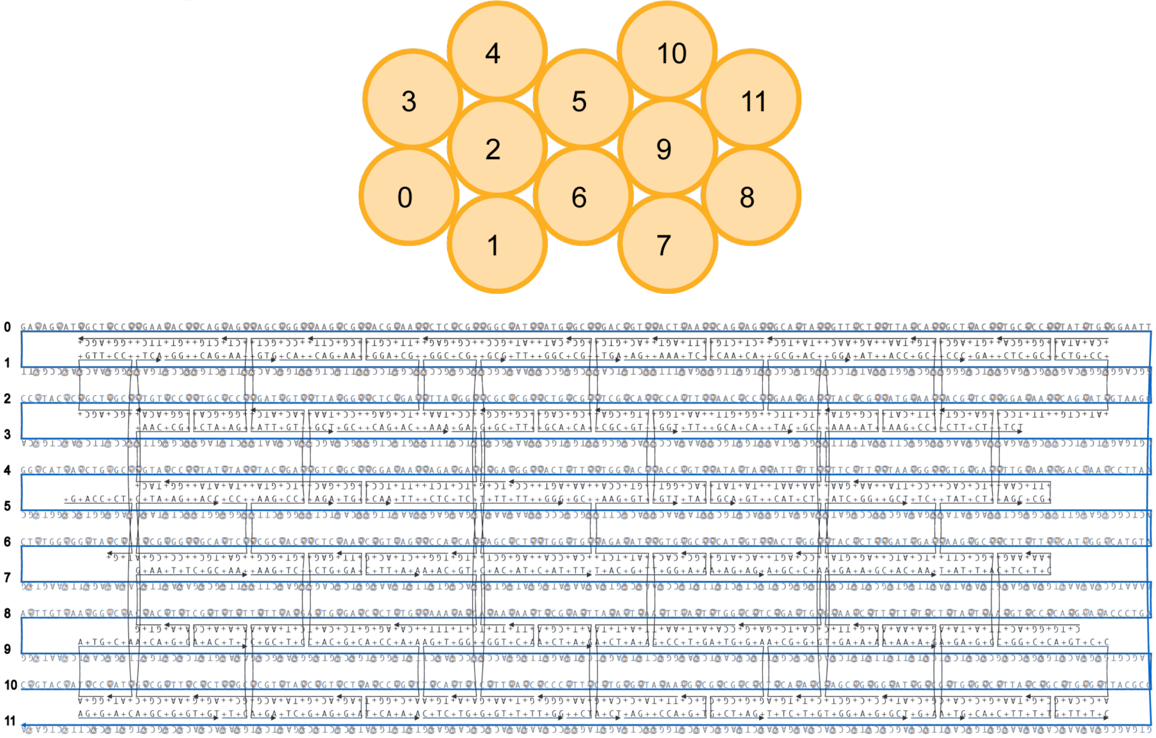
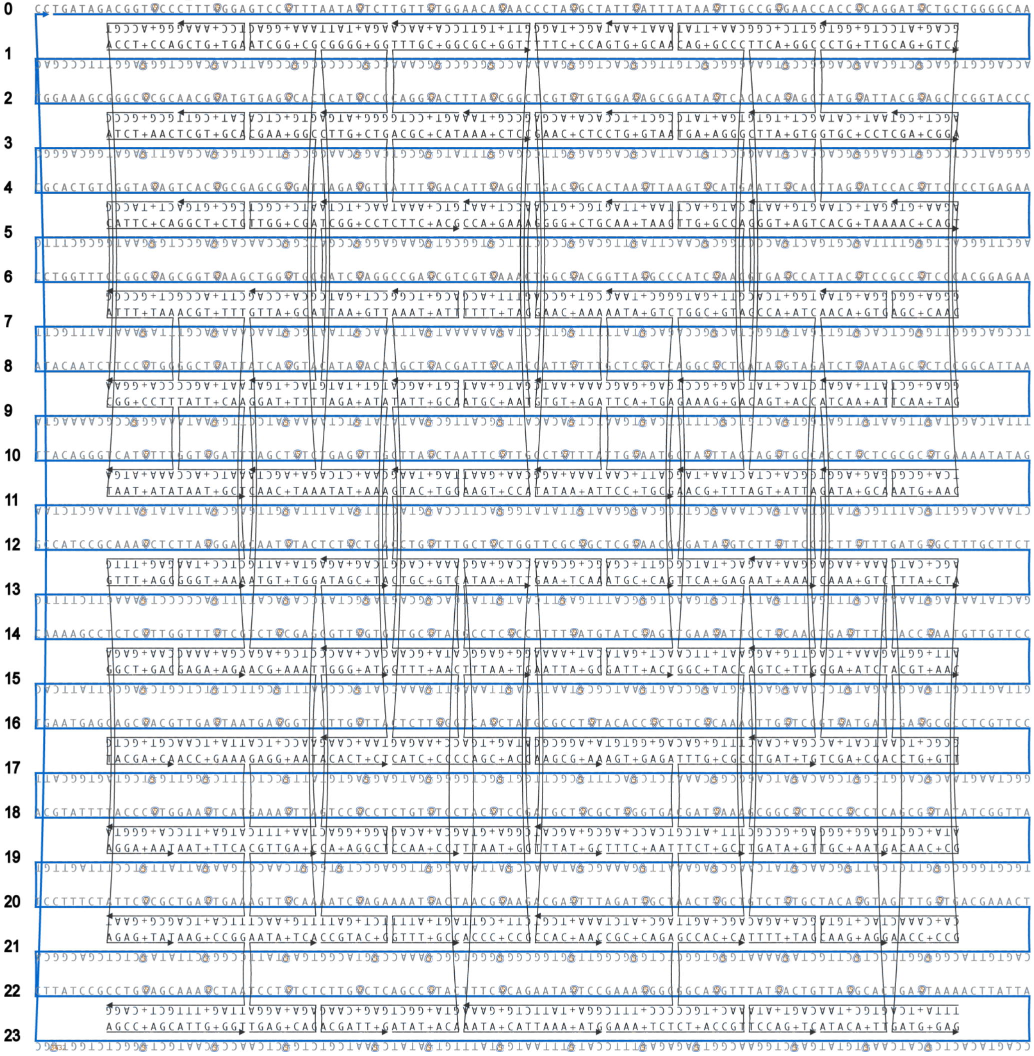


Figure S10. Illustration of 24HB-L design. Blue strand is the scaffold strand and black strands are staple strands. Arrows indicate 3'-end of DNA.



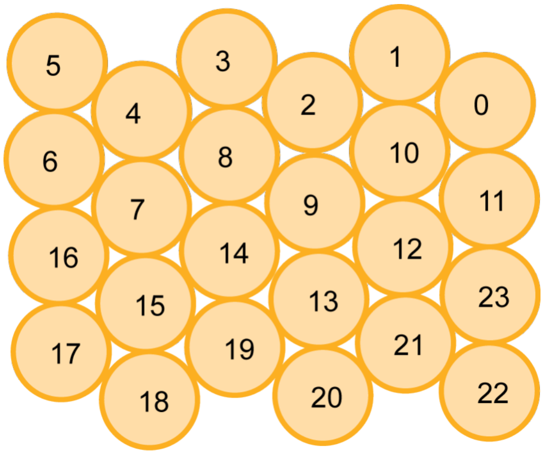


Figure S11. Illustration of 24HB-S design. Blue strand is the scaffold strand and black strands are staple strands. Arrows indicate 3’-end of DNA.

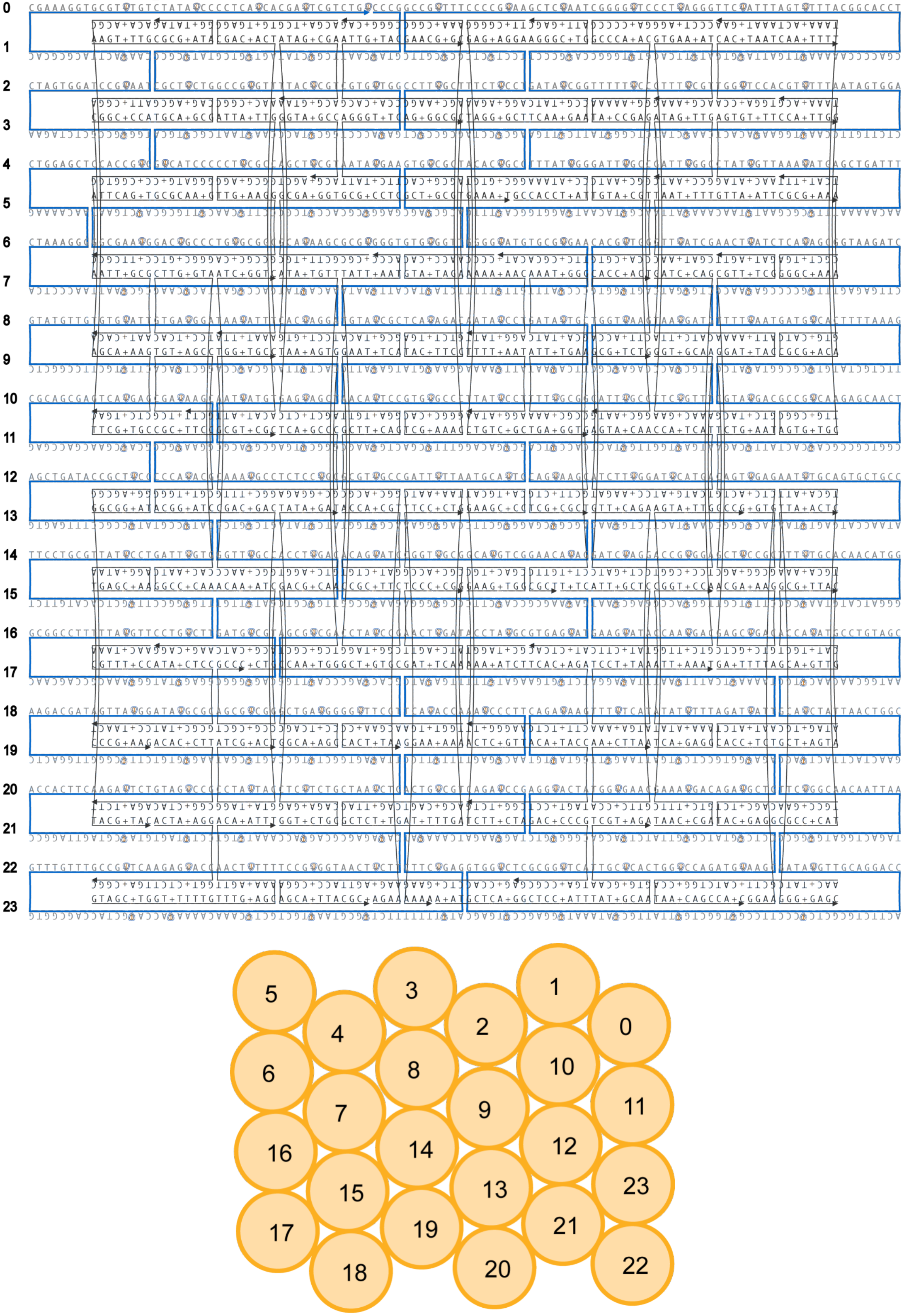


Figure S12. Illustration of 60HB-S design. Blue strand is the scaffold strand and black strands are staple strands. Arrows indicate 3’-end of DNA. Strands colored in green or red are used for incorporation efficiency assay in Figure S15.

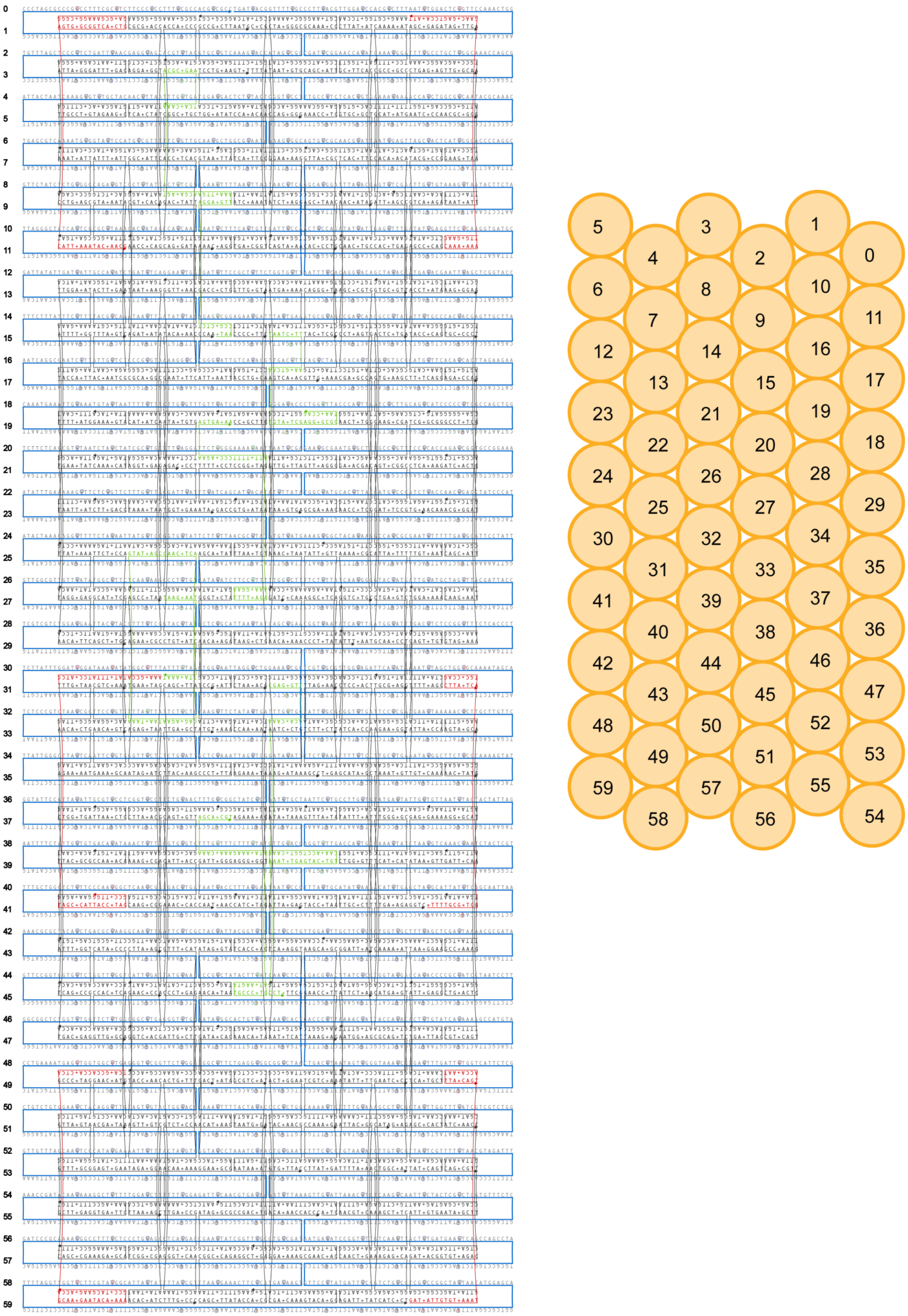


Figure S13. Illustration of 56HB hybrid design. Blue strand is the scaffold strand and black strands are staple strands. Arrows indicate 3’-end of DNA.

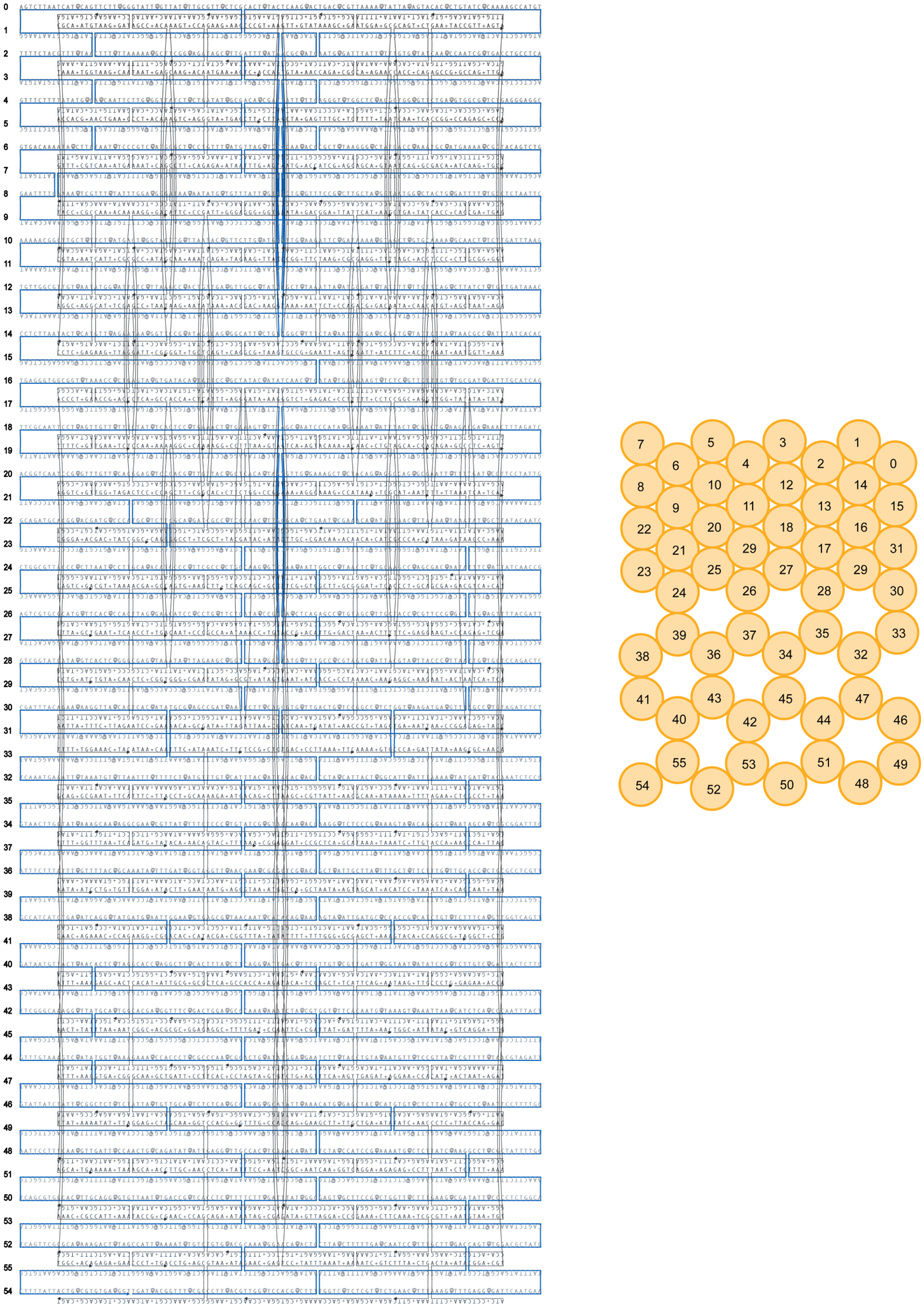
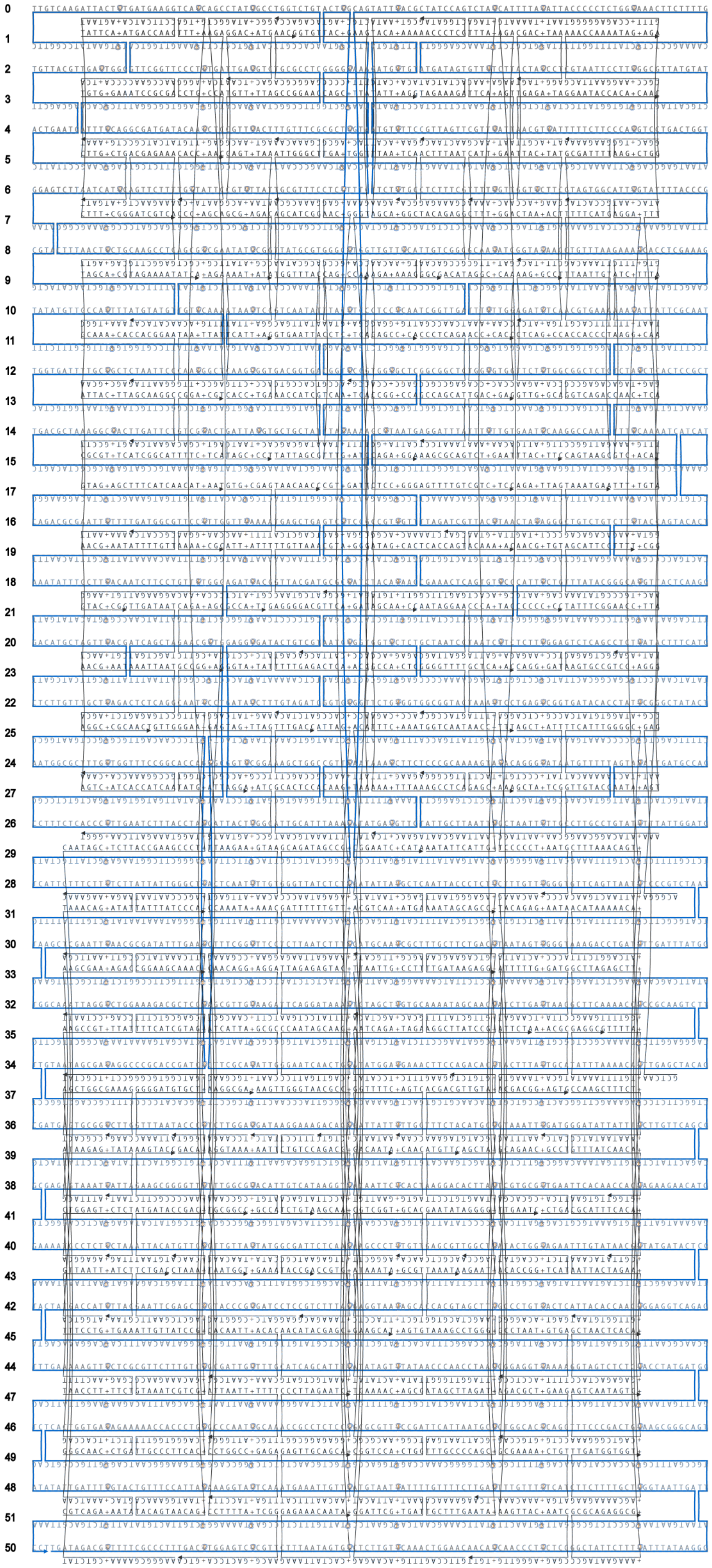


Figure S14. Illustration of 52HB hybrid design. Blue strand is the scaffold strand and black strands are staple strands. Arrows indicate 3'-end of DNA.



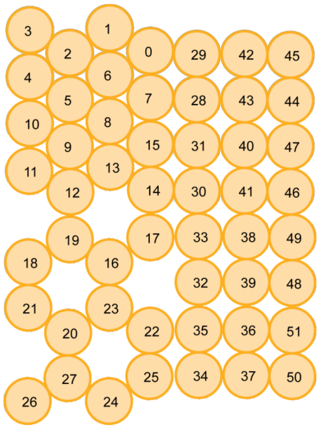


Figure S15. Explanation of the different stripe patterns of honeycomb-lattice, square-lattice and hexagon-lattice in TEM images. An 18HB honeycomb-lattice, a 20HB square-lattice and a 24HB hexagonal-lattice are used as examples for the three lattices. The red arrows point to the positions where stripes can be observed.

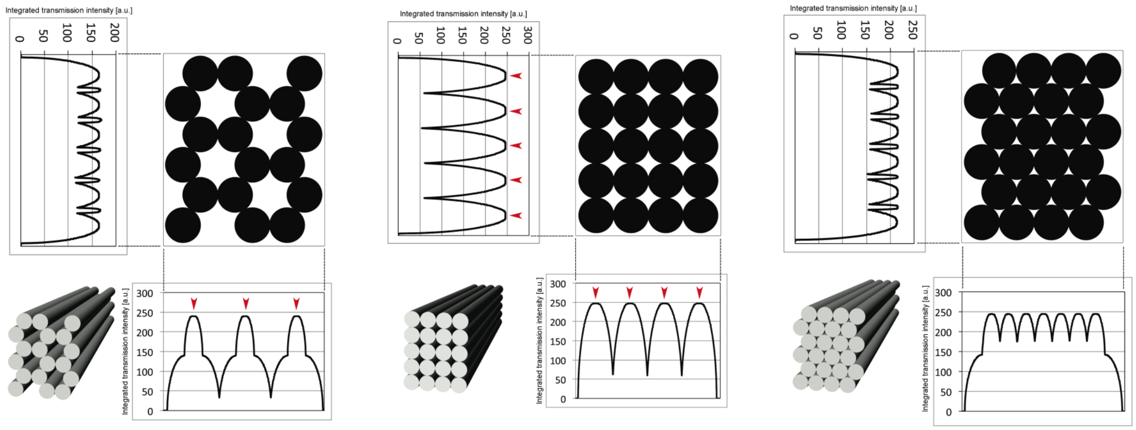


Table S1. Sequence of 12HB-L staple strands

1	CTTTCCGGCACCGCTTCTGGTGCCGG
2	AGCCGCCGCCAGCATTGACAGGAGGT
3	GGCGAAAAACCGTTAATTGCTGAATATAATGCTGTAGCT
4	AGCCCGAGATAGGTATAACAGTTGATTCCCAATTCTGCG
5	ACCTGTCGTGCCAGCTGCATTAATGATCCAACGTCAAAG
6	TTTCTTTTCACCAGTGAGACGGGCAAAAATCAAAAGAAT
7	GCGCTCACTGCCCCGGGAGAAGCCTTAAAAACATTATGA
8	GTGAGCTAACTCACGAATATAGGGGCTACCCCGGTTGAT
9	AGTGTAAAGCCTGTTTGCGTATTGGGCGCCAGGGTGGTT
10	ACACAACATACGAGTGTAGGTAAAGATAAATCATACAGG
11	TGAAATTGTTATCTGAGTAAACAGGGCAGGTCATTGCCT
12	AATCATGGTCATACCTGAGAGAGTTGCAGCAAGCGGTCC
13	ATCTGTAAGCAACTCGTCGGTGGGCACATTAATTGCGTT
14	GAACTCTGACCTCCTGGTTGGTGTAACGCTCACAATTCC
15	CTCTATGATACCGATTTAAATTGTAACCAAAAACAGGAA
16	ATCTATTTACGCTTTGGGAAGGGCGAGCACTCCAGCCAG
17	GTCCCGCCAAAATACGCATTTCACATAAATCATTTCTCC
18	TGCTGAATTGTCAGAACGCCATCAAAAAACAAGAGAATC
19	GATGTTCTTCTAAGTGCTTGTTACCTCGATAAAGACGGA
20	CATTCGCCATTCAGGCTGCGCAACTGCGCCCTGGAGTGA
21	CCTCAGGAAGATCTCGGTGCGGGCCTCTTCGCTATTACG
22	GGGAACAAACGGCAGCGAGTAACAACAGAAGCCAGGGTG
23	TGTCAATCATATGCTTGAATCGGCTGAACCCCGCTTCTA
24	GATGAACGGTAATATGCCTGAGTAATGCCGGAAGCATAA
25	CTACAAAGGCTATCTTAAGCTACGTGGTGGTTGTGAATT
26	GGAGAGGGTAGCTTCAACCGTTCTAGAGCTCGAATTCGT
27	CAATAAAGCCTCACGGGGAGAGGCGGGGGTGCCTAATGA
28	GGCATCAATTCTATTCACCGCCTGGCGCTGTTTCCTGTG
29	CAACATGTTTTAAATATGCAACTAAATCAGGATTAGAGA
30	AACGAGTAGATTTAGTTTGACCATTAGGAAGCCCGAAAG
31	GTTTTGCCAGAGGGAGGTCATTTTTGAGAGGGTTGATAT
32	ATGTTTAGACTGGTTGCTAAACAACTCGTTGAAAATCTC
33	GAATCCCCCTCAAGCTTCAAAGCGAACCACCCTCAGAAC
34	TTCAGAAAACGAGAGCCCTCATAGTTTTCTTAAACAGCT
35	GGCTTGCCCTGACCAAAATAGCGAGAAGGAATTGCGAAT
36	AATTACCTTATGCCATAACGCCAAAATTTATCAGCTTGC
37	ACCTAAAACGAAAATGAGGAAGTTTCCATTAAACGGGTA
38	AGTACAACGGAGATCACCCTCAGCAGCGAAAGACAGCAT
39	CGGAACGAGGGTAGCAACGGCTACAGCCAAAAGGAGCCT
40	ATATTCGGTCGCTGAGGCTTGCAGGGTGCGCCGACAATG
41	AATAATTTTTTCATTCAACAGTTTCAGCGGAGTGAGAAT
42	CAAAAAAAAGGCTAGGCTTTGAGGACTGGGCTTGAGATG
43	TTAATTGTATCGGGGAATTACGAGGCATAAATATTCATT
44	TTTCGAGGTGAATAGCGTAACGATCTAAAGTTTTGTCGT
45	TGATACCGATAGTAGTTAAAGGCCGCAGTCAGGACGTTG
46	ACAACAACCATCGATTATTACAGGTATTTACCCTGACTA
47	CTTTCCAGACGTTAGTAAATGAATTTGTTTAGTACCGCC
48	CACCAGTACAAACTACAACGCCTGTACAAGCCCAATAGG
49	AAGTATAGCCCGGTTAGCGGGGTTTTGCTCAGTACCAGG
50	CCGTACTCAGGAGTCTGTATGGGATTATAGCGTCCAATA
51	TTTTCAGGGATAGGCATTCCACAGACAATGACCATAAAT
52	AACCCATGTACCGAGCGGATTGCATCGATGATACAGGAG

53	GTATTAAGAGGCTGAGACTCCTCAAGACGATTGGCCTTG
54	TGAGGCAGGTCAGAGAAGGATTAGGAAATAGGTGTATCA
55	AGAGTCCACTATTAAAGAACGTGGACATCGGCCAACGCGGAGCATAAAGCTA
56	GTTCCGAAATCGGCAAAATCCCTTATCAGCTGATTGCCCCTAATAGTAGTAG
57	CATGCGCACGACTTTGGGTAACGCCAGTTGGTGTAGATGGGCGCATCGTAAC
58	CCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTAAGTGTCCTTAG
59	CGTGCATCTGCCAGTTTGAGGGGACGTTTTAACCAATAGACCTTATGACAAT
60	TGGGATAGGTCACGGGTTTTCCCAGTCACGACGTTGTAAAACGACGGCCAGT
61	AATCAGAAAAGCCACGTTAATATTTTCGACGATAAAAACGAGAAACACCAGA
62	GAGAGTCTGGAGCAATAATTCGCGTCACTAATGCAGATAGATTTTAAGAACT
63	AATCGGTTGTACCTATTTCAACGCAACTCCTTTTGATAAGGGTAATAGTAAA
64	CAAGGCAAAGAATAAGTTTCATTCCAGTTGAGTGTTGTTCCAGTTTGGAACA
65	CATTAACATCCAATTCAAAAGGGTGACGTTTTAATTCGAATGCTTTAAACAG
66	TCATTTGGGGCGCAATGGTCAATAACGCAGGCGAAAATCCTGTTTGATGGTG
67	GTACCTTTAATTGGGATAAAAATTTTTAGAACCCTCATACACTATCATAACC
68	ACTTCAAATATCGGAAAGGCCGGAGACAGTCAAATCACCGTTGAGATTTAGG
69	CTGCGGAATCGTCATAGTAAGAGCAATATTTTAAATGCACGTAAAACTAGCA
70	CAAAAATCAGGTCGAAAGATTCATCAATCAATATGATATATTTTTGAGAGAT
71	CTCGTTTACCAGAGTTAAAATTCGCATTAAATTTTTGTTTAATCTTGACAAG
72	AATACCACATTCATGGCCTTCCTGTAGCCAGCTTTCATCCGAACTGACCAAC
73	ACGAGTAGTAAATTAAAGACTTTTTCGAGGCAAAAGAATACACTAAAACACT
74	GTTTAATTTCAACCCTTCATCAAGAGAAATCAGCTCATTACGACAGTATCGG

Table S2. Sequence of 24HB-L staple strands

1	CTTTCCGGCACCGCTTCTGGTGCCGG
2	AGCCGCCGCCAGCATTGACAGGAGGT
3	GGCGAAAAACCGTTAATTGCTGAATATAATGCTGTAGCT
4	AGCCCGAGATAGGTATAACAGTTGATTCCCAATTCTGCG
5	ACCTGTCGTGCCAGCTGCATTAATGATCCAACGTCAAAG
6	TTTCTTTTCACCAGTGAGACGGGCAAAAATCAAAAGAAT
7	GCGCTCACTGCCCCGGGAGAAGCCTTAAAAACATTATGA
8	GTGAGCTAACTCACGAATATAGGGGCTACCCCGGTTGAT
9	AGTGTAAAGCCTGTTTGCGTATTGGGCGCCAGGGTGGTT
10	ACACAACATACGAGTGTAGGTAAAGATAAATCATACAGG
11	TGAAATTGTTATCTGAGTAAACAGGGCAGGTCATTGCCT
12	AATCATGGTCATACCTGAGAGAGTTGCAGCAAGCGGTCC
13	ATCTGTAAGCAACTCGTCGGTGGGCACATTAATTGCGTT
14	GAACTCTGACCTCCTGGTTGGTGTAACGCTCACAATTCC
15	CTCTATGATACCGATTTAAATTGTAACCAAAAACAGGAA
16	ATCTATTTACGCTTTGGGAAGGGCGAGCACTCCAGCCAG
17	GTCCCGCCAAAATACGCATTTCACATAAATCATTTCTCC
18	TGCTGAATTGTCAGAACGCCATCAAAAAACAAGAGAATC
19	GATGTTCTTCTAAGTGCTTGTTACCTCGATAAAGACGGA
20	CATTCGCCATTCAGGCTGCGCAACTGCGCCCTGGAGTGA
21	CCTCAGGAAGATCTCGGTGCGGGCCTCTTCGCTATTACG
22	GGGAACAAACGGCAGCGAGTAACAACAGAAGCCAGGGTG
23	TGTCAATCATATGCTTGAATCGGCTGAACCCCGCTTCTA
24	GATGAACGGTAATATGCCTGAGTAATGCCGGAAGCATAA
25	CTACAAAGGCTATCTTAAGCTACGTGGTGGTTGTGAATT
26	GGAGAGGGTAGCTTCAACCGTTCTAGAGCTCGAATTCGT
27	CAATAAAGCCTCACGGGGAGAGGCGGGGGTGCCTAATGA
28	GGCATCAATTCTATTCACCGCCTGGCGCTGTTTCCTGTG
29	CAACATGTTTTAAATATGCAACTAAATCAGGATTAGAGA
30	AACGAGTAGATTTAGTTTGACCATTAGGAAGCCCGAAAG
31	GTTTTGCCAGAGGGAGGTCATTTTTGAGAGGGTTGATAT
32	ATGTTTAGACTGGTTGCTAAACAACTCGTTGAAAATCTC
33	GAATCCCCCTCAAGCTTCAAAGCGAACCACCCTCAGAAC
34	TTCAGAAAACGAGAGCCCTCATAGTTTTCTTAAACAGCT
35	GGCTTGCCCTGACCAAAATAGCGAGAAGGAATTGCGAAT
36	AATTACCTTATGCCATAACGCCAAAATTTATCAGCTTGC
37	ACCTAAAACGAAAATGAGGAAGTTTCCATTAAACGGGTA
38	AGTACAACGGAGATCACCCTCAGCAGCGAAAGACAGCAT
39	CGGAACGAGGGTAGCAACGGCTACAGCCAAAAGGAGCCT
40	ATATTCGGTCGCTGAGGCTTGCAGGGTGCGCCGACAATG
41	AATAATTTTTTCATTCAACAGTTTCAGCGGAGTGAGAAT
42	CAAAAAAAAGGCTAGGCTTTGAGGACTGGGCTTGAGATG
43	TTAATTGTATCGGGGAATTACGAGGCATAAATATTCATT
44	TTTCGAGGTGAATAGCGTAACGATCTAAAGTTTTGTCGT
45	TGATACCGATAGTAGTTAAAGGCCGCAGTCAGGACGTTG
46	ACAACAACCATCGATTATTACAGGTATTTACCCTGACTA
47	CTTTCCAGACGTTAGTAAATGAATTTGTTTAGTACCGCC
48	CACCAGTACAAACTACAACGCCTGTACAAGCCCAATAGG
49	AAGTATAGCCCGGTTAGCGGGGTTTTGCTCAGTACCAGG
50	CCGTACTCAGGAGTCTGTATGGGATTATAGCGTCCAATA
51	TTTTCAGGGATAGGCATTCCACAGACAATGACCATAAAT
52	AACCCATGTACCGAGCGGATTGCATCGATGATACAGGAG

53	*GTATTAAGAGGCTGAGACTCCTCAAGACGATTGGCCTTG*
54	*TGAGGCAGGTCAGAGAAGGATTAGGAAATAGGTGTATCA*
55	*AGAGTCCACTATTAAAGAACGTGGACATCGGCCAACGCGGAGCATAAAGCTA*
56	*GTTCCGAAATCGGCAAAATCCCTTATCAGCTGATTGCCCCTAATAGTAGTAG*
57	*CATGCGCACGACTTTGGGTAACGCCAGTTGGTGTAGATGGGCGCATCGTAAC*
58	*CCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTAAGTGTCCTTAG*
59	*CGTGCATCTGCCAGTTTGAGGGGACGTTTTAACCAATAGACCTTATGACAAT*
60	*TGGGATAGGTCACGGGTTTTCCCAGTCACGACGTTGTAAAACGACGGCCAGT*
61	*AATCAGAAAAGCCACGTTAATATTTTCGACGATAAAAACGAGAAACACCAGA*
62	*GAGAGTCTGGAGCAATAATTCGCGTCACTAATGCAGATAGATTTTAAGAACT*
63	*AATCGGTTGTACCTATTTCAACGCAACTCCTTTTGATAAGGGTAATAGTAAA*
64	*CAAGGCAAAGAATAAGTTTCATTCCAGTTGAGTGTTGTTCCAGTTTGGAACA*
65	*CATTAACATCCAATTCAAAAGGGTGACGTTTTAATTCGAATGCTTTAAACAG*
66	*TCATTTGGGGCGCAATGGTCAATAACGCAGGCGAAAATCCTGTTTGATGGTG*
67	*GTACCTTTAATTGGGATAAAAATTTTTAGAACCCTCATACACTATCATAACC*
68	*ACTTCAAATATCGGAAAGGCCGGAGACAGTCAAATCACCGTTGAGATTTAGG*
69	*CTGCGGAATCGTCATAGTAAGAGCAATATTTTAAATGCACGTAAAACTAGCA*
70	*CAAAAATCAGGTCGAAAGATTCATCAATCAATATGATATATTTTTGAGAGAT*
71	*CTCGTTTACCAGAGTTAAAATTCGCATTAAATTTTTGTTTAATCTTGACAAG*
72	*AATACCACATTCATGGCCTTCCTGTAGCCAGCTTTCATCCGAACTGACCAAC*
73	*ACGAGTAGTAAATTAAAGACTTTTTCGAGGCAAAAGAATACACTAAAACACT*
74	*GTTTAATTTCAACCCTTCATCAAGAGAAATCAGCTCATTACGACAGTATCGG*
75	*GGCTCATTATACCTTTTGCGGGATCGTTTGTATCATCGCCTGATAAATTGTG*
76	*GGAAGAAAAATCTATCATAAGGGAACAACATTAAATGTGGGATTGACCGTAA*
77	*AACCGGATATTCATTACCCAAATCAACGTAACAAAGCTGTACGAAGGCACCA*
78	*TTTGAAAGAGGACAGATGAACGGTGTACAGACCAGGCGCAAGCGCGAAACAA*
79	*CATCTTTGACCCCCAGCGATTATACCATAGGCTGGCTGATTTAATCATTGTG*
80	*TCGAAATCCGCGACCTGCTCCATGTTGCGCAGACGGTCAACGTTAATAAAAC*
81	*ACCCTCAGAACCGCCAGACCGGAAGCAATAAATCCTCATTAAAGCCAGAATG*
82	*CGCCACCCTCAGACCCTGCCTATTTCGGAACCTATTATTCTGAAACATGAAA*
83	*TTTAACGGGGTCAGTGCCTTGAGTAACAGTGCCCGTATATCCAGTAAGCGTC*
84	*ATATTCACAAACAAAACTCCAACAGGGTACGGTGTCTGGTAGCAAAATTAAG*
85	*GAAAGCGCAGTCTCTGAATTTACCGTAACAGTTAATGCCGCCACCACCCTCA*
86	*ATACATGGCTTTTAAAAAGATTAAGAGATACATTTCGCAGAGCTGAAAAGGT*

Table S3 Sequence of 24HB-S staple strands

1	TTGACGGGGCTGTCGTGCTGACTGGTG
2	AAGTCATTGCGCGTAATAGGGCTATAG
3	GAGAAAGGAAGGGCGATGATTTAGAGC
4	AACGACGGCATTAAGTTGAAATTGTTA
5	TGGACTCCACACCCTAATCAAGTTTTT
6	AACCAATAGAGTGTTGTTCCAGTTTGG
7	CGCTGTTGAGGGCGAAAATCATTTTTT
8	GTGCTCATCCGCGCCACATAAAGAACG
9	GGCGGTAATGGCGAGCGGTACGGCTAC
10	GTTGTCAGAGTTCATCCAAATGCTTAA
11	TGAGCAAAAAGGGGATAACCCGGTAAG
12	TGGTCATGAACGAACCCCCACTGGTAA
13	ACACGACTTCGGTGCTACAGAGTTCTT
14	GGAACGAAACGCTTACCGTTCCCCCTG
15	TCAGTGAGGAAAGTATATCGGTTCCCA
16	ACTAGAAGGGGTAGCTCTTGATCCGGC
17	GGTATCTGCCAGAGCGAGTATAAAGAT
18	TAACTACGAGTCTATTTCAGTAAGTTGGCCG
19	ACAATACGCTTCGGCTGCCGCTCTTCCGCGTTGCGC
20	CCCTAAAGGGAGCCCCCGGCCCACTACGGCAAAATG
21	CGATGTAACTAATATTTTGTTAAAATTCGCGTTAAA
22	ATAGCTGTTTCGTTCGCTACGAGCATCAAGGCCAGG
23	GATCTTCAGGTCGTTTGGTATGGCTTCATAGCTCAC
24	TAATGAGTGGTCAGAGGTGGCGAAACCATCATGGTC
25	GGTGAGCAATCCTTCGGTCCTCCGATCCACCCAACT
26	GGGCGACACTCGGGAAACAAAGCCGGCCGGGGTCAG
27	CCGCAAAAAATTATTGAAGCTTTTCTGTCGTGCGCT
28	TTGCCCGGCAGTGTATGCTAAAGCACTAAATCGGAA
29	TCACTGCCCGCGGGGAGAGGCGGTTTGTGGGGTGCC
30	ACGATCAAGGTCACGCTCCGTTCTTCGGATCCAGTT
31	GAAGTTTTAGCAACGTTGCATCGTGGTGCGAGTTAC
32	ACGAATTCGTGGCTGAGGCGACTCACTACATTAATTGCTT
33	GGCAAAATCTGTAAGCGTCCACTCGTGTTCCGCGCACATTT
34	TTCTCATTCAGCTCATGAGTAAATCCTTTTAAATTAAAAAT
35	AACTTTATCGCTTACCATCTGGCCCCATAAACCAGCCAGCC
36	AGTACTCAACCAAGTCATTCATGCCATCCGTAAGATGCGTTTCTG
37	AACCGTAAACGTTTTTCCATAGGCTCCGCGCCTTATCCGGTAACT
38	GCTGTAGGTAAAGGATCTTCACCTAGACTTGGTCTGAAGGGATTT
39	GTAGCGGTGGTTTTTTTGTTTGCAAGCAAAAGAGTTACAGTATTT
40	GCCACCTAAATCCTTATAAAGGCAAGTGTAAAATAAACAGGGTTATT
41	GAAGCTCCCCAGCTGCATTCTTTTCTAGACTCCCCGTGATACCGCGA
42	GCCGCGCTTAATGCGCGATCGGTGCGGGCCTCGCTGCGCGTGAAAAGT
43	GACCCACCTCAAGAAGAAGCCAGTTACCTTCGGAAGCAGATTACGCGC
44	AGCTGGCGAAAGGTTGGGAAGGGCCGCTACAGGGCGCGTCCCATTCGCC
45	ACGCTCAGTCAGGATTAGGCTCTGCTGATCCTTTGATAATGAATCAAAA
46	CCCTGCCAAGCTGGGCTGTGTGCGATTATCAAATCTCAGTTTCCCTTCGG
47	AGGATGCTCACCGGCTCCAGATTTATCAGCAAGTGCTGCAATCGTGTAGA
48	CGGCCGCCATGCAAGGCGCAGTGAGCGATTTACGGAAGCATAAAGCTCACTGAC
49	TAGGGCGCTTCAAAAGAACCGTCTATCAGGGAAGAATTTTTCAATAGGGAATAA
50	ATTCAGGCTGCGCAACTGGGGATGTGCCCGCGGTGGAATTGCGCGAATTCCACA
51	GTCTCATGATACTCTTCCAGCGAAAGGCCAGTCACGATTGGGTACGAACGTGGC
52	GAAGCGTGGCGACCCTGCACTCACGTTACAGTTACCTAGTTGCCTCGGGGTCTG

53	ATAGTTTGCAATCAATCTCACCTATCTGCTAGAGTATGCAAAAAATTATCACTC
54	TGCCGGGAACAGCGATCTTACGGGAGGCGCCTCCATTGCATAATTGGGCCGAGC
55	GGCGAAAAATAGACCGAGCTTTCACCAGCATTTATCAAATAGGGGCTCCTGTTCCGCT
56	CCCCAACCACCACGTATTTAGAAGCGGTCACTTCGCTATTAGGGTTTTCAGCGGGCGC
57	TCCGCTCACCTTGGCGTACACAGAATCGGCCAGCAAACAAAAATCCCGACCGCTGCCC
58	GGCAGCAGCCCGTTCAGCGACGCTCAACCGCCTTTCCGGTGTAGGTATTTGAATACCC
59	AGAAGGCCAACGCGCTTTCCAGGGAAATGTTAGCTAACTCATAGGGCGAACGTTGTAA
60	GGAACTCTTACTGTCTGAGAATGTCAATACGAAACAGGAAGTGAACCATACGTCAAAG
61	CCTCGTGTAAAGCCCGTATTGGGACGGTTATCCGACAGGACGTATGTAGGATCGCCACT
62	ACCAGGCGTGATACCTGTGAATACTCAGCGGATACATCCTGTGTGGGTAACGCCACGCC
63	CAGTGGCGGTTAGCGGATAATACATTGGAAAACATCTTTTAATAGGGTTGGCCGAAATC

Table S4. Sequence of 60HB-S staple strands

1	*GCTTTCCTCAGGAACGGTAATAAAAGG*
2	*ATGGTGGTTGCCCTTCACCGTATTAAA*
3	*CAAACCCTCCAAAAGAATTCCTGTTTG*
4	*TTTAACAATAACATGTTCAGCTAATGC*
5	*TTAAGACGCTAGGCAGAGTTCTGTCCA*
6	*AAAACTTTTTTATACAAATATTTAACA*
7	*CGCCATCAACAGCTCATTGGTCACGTT*
8	*TAAAACTAGCAAGAGAATACCGCTTCT*
9	*AATAATAACTGACAGGAGGTTGAGGCA*
10	*AGCAAAATTAATCCTCATTAAAGCCAG*
11	*ACAATCAATTCAGAGCCGCCACCACCA*
12	*GAATTAGAGATTTTCGGTAGAGCCACC*
13	*TTTAATTCGGCCCGAAAGTGAATATAA*
14	*GTTTGCCATCCCTCAGAACCGCCACCC*
15	*CAAAAAGATGGTCTTTACCCTGACTAT*
16	*GGATTAGCGCTGAGACTCATTTAGTTT*
17	*GGTTTTCCCAACAAGAAACCCTCATATATTT*
18	*GACCGTGTGATAAGAAGGAGCGGTTGGTGTA*
19	*ACAAACGGCGGATGCTCGAATTAAGACGGAG*
20	*AAAGGCCGGGTAGGTAAACGAAAGGGGGATG*
21	*TTTTGATGACGTTCCAGTAGTAGCATTAACA*
22	*TACATAACGATTCATCAGACAACAACCACCC*
23	*GAAACCATCGATAGCAGAGCCTACTAAGAACG*
24	*ATTTTTGCGGATGGTGCACCCAGCTTAAATCA*
25	*GGCGAGAAAGGAAGGGAACGCGTAACCCTATTAGTC*
26	*AAAGAACGTGGACTCCAACTTATAAATAATCAATAT*
27	*ACTCACATTGCATTAATGAATCGGCCAACGCGCGGG*
28	*GACATTCTGATTTACATTTTGCACGTAACTTCTGAA*
29	*TCCTTTGCCGTTATCCGCCTGACGCATCAGGGCTTA*
30	*TTTAATGCGGTAAGAATAAGAAACAATTTTAACGTC*
31	*AACAGTTGATGAGGCGGTCGTCTATCAGGCGAACGT*
32	*CTGGTCAGTAGCACTAACTTAGTGCTGTACGCTCGC*
33	*TTGCTGAACCAAATGAAAGAACAAGAGTCCACTATT*
34	*TGTTTCCTGTGTGAAATTAAACCACCATAAATGTGA*
35	*ACCTCGATACGTAATCATTACGAGCCGAGTGAGCTA*
36	*AGATGAATAACATAGCGAAGGTCTGAGCTTAATTGA*
37	*CCTGGAGTGAAGCGCCATGACGACGACCCCGGTTGA*
38	*GAATCGCCATTCTTACCAAACAGGGAACGTCAAAAA*
39	*TAATCAGAATATTTTGTTCGCCCAATATTAGCGAAC*
40	*CATATGTACAGTATCGGCGGGCGCATCGTGCTTGTT*
41	*GTAAAGTAAGCATTTTCGCACAAGAATAACAAAGTC*
42	*ATTCAACCGAGGCTATCATTTTTAGAATCTTTCCTT*
43	*AATCACCATGAAGGGCGAAACCAGGCAACTCTATGA*
44	*TCTTACCAACGCTAACGAGCGTCTTTCATTAGAGAG*
45	*AGAGGGTAAGAATAAGTTAAAGGGCGAATCAAAATC*
46	*ATCATTCCAGCAAATGGTCTGGAAGTTGGCGGATAA*
47	*ATTAAACCATTATTTTCATGGAGCAAACATGTCAAT*
48	*ACCGGAACCCATAGCCCCCAACGCCTGGAACCCATG*
49	*GTGCCGTCGAAGCAAAGCGAAGTTTTGTCGTCATAA*
50	*TCAGTACCATCATTCCATTCAACATGTTGCGGGAGG*
51	*CCCTCAGAGCGTCACCAGTACAAACTACTTATTAGC*
52	*CATGAAAGTCGAGAGGCTTTTGCAAAAGGATTGCAT*

53	CCACCAGAACCACCCTCATTCTGTATGACGATCTAA
54	AACGGGGTCGAACCTATTGGTAGAAAGCCAAAAGGA
55	GTACTGGTATTGGGGCGCATACATTTCAGAACGGGT
56	TACCGTAACATACGTAATACACTCATCTTTGACCCC
57	ATATTCATTGGTCAATCAAGATTTGTATCATCGCCT
58	TATACCAGTACGAACTAATGAATTTACTACAGGAGT
59	CCAGAACGAGTAGTAAATTGGGCTTGACTGGCTCAT
60	CAGCGATTATACCAAGCGCCACCCTCAGCGTCCAAT
61	GATAAATTGTGTCGAAATACCATAAATTTAAACAGT
62	AAATCATTTCAACTTTAATCATTTTTTTCACGTTGAA
63	TACCGACAGGGCACGAATGTCAATAGAACAAACAATTCGA
64	CCTTGCTTCCCTTATGACACCTGAGCAAGTCACGACGTTG
65	CTTTCATCAACATATAAGGCGTTTAAATTGTATGTAAATG
66	AGAAAATACCCATCCTAAAGAAAAGTAAAGCAATAAAGCC
67	CCAACAGGTCAGGCAGCACCGTTCACCGTACTTCATTAAA
68	AGAGGAAGGAATTGTTTGAATGGACCACACCCGTATAACGT
69	AGCTACGTGGTAACCGTGAACCCGTCGCTTCCTGTAGCCAG
70	TAAAACGACGGCCATAAGTTGGGAACTGTTGGCAATATGAT
71	TAAATGCAATGCCTTCAACGCAAGGATAAAAAGGTCATTGC
72	CTCCCGACTTTTAAATATTTGCTCCTTACCGGAAGCAAACT
73	TCAGAGCATAAAGCCAGGCAAGGTATTTTCATATAAGTTTT
74	GTAAGAGCAACACTCCAAAATAGATTAAGAGGGGGTTTTGC
75	AACAAACATCAAGGAATTATTCATTTCAATTAATGTCCCGAAAC
76	GAGAATAAAGTACATATATGTGTCCTTGAAATACAGTAACCCAA
77	CGGACTTTTCATACATTCAACCTCACCGTCACAGCCTTTATCCG
78	TATACCACCACCCCAGTATGTTGACACCACGTTGAGCGCTATGT
79	TTAACCGTTTCAAACTATAAACGCTCATGGAAATACCTACATTTT
80	AAACCTGTCGACGGGCAAAGGCCACCGGGAACAAAGCGAACGTTA
81	AACCACCAGCAGAAGATAAGTACCTTTTACATCGGGCGTGGCACA
82	CAACAGTGCCACGCTGAGCGCACGACTTAAGTGTCCAACTAATAG
83	TTGGATTATAAACAGAAATGAATTTATCAAAATCATTAGCTTAGA
84	ATTTTCAGGAACGGATTCTTTTTAATGGAAACAGTATTAATTACA
85	TAATCTATTAATTGTCAATGTAAATCGAGGCTGCGCTAACGCCAG
86	GGTGCCGGATCGGTGCGGGCCTCTTCGAGTGGTTGTAGAAGCCAG
87	CTGATGCAATTTTAACCTCCGGCTTAGATCATTTCTCCCCGCTTC
88	GGTGTAGATCTCAGGAAGATCGCACTCTCGTCGGTGTGCGGCCCT
89	GCGAGTAACCATCTGCCATATAACTATAAACGTTAAAAGCCCCAA
90	AAACAGGAATTTTTGAGAATTAATTTTCCCTTAGAAAGTGAATAA
91	AGAACGCGCCTGTTTATCAATATCAGAGAGATAACCAGCCAGTAA
92	TTTGTTTAAGCGCATTAGTTACCAGCGCCAAAGACATATTTTGTC
93	AACACCCTGTGAGTTAAGCTGGCATGATTAAGACTCAGGAAACGC
94	AGAAAGAAGGCTTAGGGTAGCTAGATTGTATAACAGTAGGGAGAC
95	AATCGGCTGAATAATATCATACATAAAGTTTAGCTACAAAGAATT
96	GACCATTAGGAGCTGAAAAGGTGGCATGCGGGAGAAAACATTATG
97	GGTGAATTAGATTGAGGGAGGGAAGGTTCAGATATACCAATCAAT
98	TGCTGTAGCATAACAGTTGATTCCCAAAAGCCGTTTAGTACCGCA
99	TACCTTTAAGCAACTAAACGGAAATTATCAGGAGGTAGAGGGTTG
100	ATATAAGTATGCCCCCTGATATAAAAGAAACGCAAAAGCAAACGT
101	TTCGAGTGCCTTGAGTAACAGTAAACAAATAAGCAGATAGCCGAA
102	GGTCAGACGATTGGCCTTGACGTTAGTAAATGAATTGAACCGCCA
103	AATGGAAAGCGCAGTCTCCGGAACAACATTATTACAATTCTGAAA
104	GTTTCAGCGGAGTGAGAATAGAAAGGAAAGGCTCCATTAAACAGC
105	TACAATTCTAGCTGATAAATTAATAAGTCCTGAAAGAAGATGATGA

106	TTAATTTTAATCTAAAATGGTTGCTTTGACGAGCACGCCGCGCTTAATG
107	AAGTTTCCATTAACGGCTACAGAGGCTTTGAGTAATAGTATAATGCAGA
108	CATTGCAACAGGAACGGCCTTGCTGGTAATATCCAGAACAACCAGTCGGG
109	AGTGTAGCGGTCACGCTGGAAAGCGAAAGGAGCGGGCATTAAAAATACCGAACG
110	ATTAAAGGGATTTTAGACGTTAGAATCAGAGCGGGACCTGAAAGCCGAACTGAT
111	TTGCCTGAGTAGAAGAACGTAGCAATACTTCTTTGAAAATGGATTGCCAACAGA
112	TGCCTAATGGAAGCATAAATTGGGCGCCAGGGTGGTCTGAGAGAGTTGCAGCAA
113	TTAGACTTTTAATACATTTGCCCCAGCAGGCGAAAAAGCCCGAGATAGGGTTGA
114	GACAATATTCTACCATATCAAAATTATGGCAGATTCACCAGTCACTCATATTCC
115	ATTAGAGCCATAGGGGCCTTGAATCGGTCACAATTCCACACAACAGGTCATAGC
116	TGATTATCAGATGATGGCAATTCATCATAATTTCATCTTCTGACCGAACGCGAG
117	TAATGGAAGCAAGACAAATAAATTTAAGGAATCATAATTACTAGAAAAAGCCTG
118	TACCAAGTTACAAAATCGCGCAGAGGCAAAACAAAACATAAATCACGACAAAAG
119	TACCTATCCAATCGGGTTAGAACGACCTCCTGGAATTATCAGTAACATTACAGC
120	TAAGAGAATCAGAGAGAATAACATAAAGTATAAAGCCAACGCTCATTACAAAAT
121	CTGAGAGTCTCGTAGGAATCATTACCGAAAATTCGCATTAAATTTTATCCTGAA
122	AAACAGCCATATTATTTATCCCAATCCTAGCACCATTACCATTAGGCCATTTGG
123	TGAAAATAGCCGACTTGACAAGGCCGGCAAGTTTGCCTTTAGCGTCAGACTGTA
124	AGAAACAATGAAATAGCAATAGCTATCAGGAAACCGCTTATTACGTCAGAGCCG
125	CAAAGTTACCAGATTACCGAAGCCCTTTTTATTTACGAGCAACAATAGATGCCG
126	TCAGAGCCACCACCCTCAGCAAAAGAATACACTAAAGCCACTACGAAGGCACCA
127	GCCCAATAGTAGCATTCCCAGCAGCGAAAGACAGCAGAGTTAAAGGCCGCTTTT
128	GGATAGAACCGCCAATAGGTGTAAATCAGTAGCGACAGAATAAACGTCACCAAT
129	GTTAGCGTAGGATTTTGCGCTTTCGAGGTGAATTTCAAAGGAGCCTTTAATTGT
130	ATTACGAGGAAGAACCGGCAACTTTGAAAGAGGACAGGCGCAGACGAATCCCCC
131	AATCTCCAAAAAAACAACTAAAGGAATTGCGAGGAATACCGATATTCACGCCCG
132	CTGACCTTCATCAAGAGTATTCAGTGAATAAGGCTTGTTAATAAACAGGACGTT
133	GTTACTTAGCCGGAACGAGATGAACGGTGTACAGACCGATAAAAAATCATAACC
134	GTATTATTTGCCAGAGCAAATATTAAATAAGAATAAACACCTGGTTTGAAATACC
135	TTTATAATCAGTGCAGCTGATTCCGAAATCGGCGTACTATATCTTTAGGTGGCAAATC
136	ATGAGTAAATTCACATAAGTTGGGTTAGTTTGAGGGTCGCCATTCTCGCTATTAGATC
137	TCAAATGCTCAAAAATCATAAGAGGAAAGCTTCAAAGCGAACCAGTTGATAAGAGGTC
138	AGTTTTGTCGCTTGCAGGTCGGAACGAGGGTAGCAAACGGGTAAAACTGAGTTTGACT
139	CTTATGCGATTTTAAGAAGATGGTTTAAACGTAACAAAGCTGCTCAATCTTGACCATA
140	ACCGATATATTCGATAGTTGCGCCGACAATGTTGAGATTTAATAATAATGTGAATTAC
141	CGCCGCTACAGGGCGCAAAATCCCGTCAAAGGGCGAAAAACCAGTATTAACACCGCCTG
142	GCCCGCTTTTATTACCGCTCATTTTGCAGTAAAAGAGTCTGTCCATCCTGAGAAGTGTT
143	CAACTCGCCTGGCCTTTTCTTTTCACCAGTGAGTGCCAGCTAATTGCGTTGCGCTCACT
144	AATAACCGAACTCTAGGAAGGTTAAAGTTTGAACGACCAGTACGCCAGAATCACGCAAA
145	TGCTGCAAGGCGATGTGCCAAGCTTTCTCAGGGAATTCATGAGCCAGCAGCTCAAATAT
146	CGAGGCGTTGCAAGCAAAAAATATTGAGTACGGTGTCAATAACCTGGTGGCAACCCTAT
147	TTTTGAAGCCTACAATTTTTGTTAAATAAATAATTCGCGTCTGGCGATTCTCCGTGGGA
148	TCCAATAAATCATATAAATCGGTTGTACCAAAGCCTTTATTGAGTAATGTAGACAGTCA
149	TATAGTCAGTTAGTACCGCGAAACAAAGTACAACGGTAAGGGAACACTTTTTCATGAGG
150	ACTGCGGAACCAGAGGGGGACTAAAGCGAACTGACATATTCATTATCGCCCACGCATA
151	TTGATACCGGTCGCTGAGGTCTTTCCAACATTCAACAAATGTTTAAACAGTTAATAGCC

Table S5. Sequence of 56HB hybrid staple strands

1	GTGCCTTGATGCCGTCGAATTTTAGTT
2	CGCAGTATGTAAGCAGATCCAAAAGAA
3	AGCCCTTTTTAATAAGAGTTAATTGAG
4	AACAAATAACACCAGAACATAATATCC
5	AACCCACAACCTGAACAAGTACCGCAC
6	CCTCAGAGCTTTTCATAATACAATTTT
7	TTAAACCAAAGTCAGAGGAGGGAAGCG
8	GCACCCAGCTCAAAATCATTTTCGGTC
9	CAGTAGGGCCAAGAAACACAGAGAGAT
10	ACAAGAAAACACCACCAGAACCGCCAC
11	CTATTTCGGAAGTTACCATCTTACCGA
12	AATAAACACGCAGTCTCTATATTCACA
13	ACCCTCAGATAGTACCGCCCTGCCATC
14	CTCAGAGCCTTACGCTCGACCTTATGA
15	TTTAACCTCTAATGCCACAAAGACTTT
16	TTTTCACGTACTAAAGGACTTAGTGCT
17	CCAAAAAAATTCTTCTAAACGACGGCC
18	AACGCCTGTGCAACGGCTGGATCGTCA
19	AGGTCACGTAACGGCGGACAGTCACGA
20	AGTGCCAAGGAAAGGGGGGCTTTCCGG
21	CCCTCAGCAGCTGAGGCTCATTAAATT
22	CAATGTCCCGGGTGGATGAGGCTCCAA
23	TTCATGAGGACGAGGGTAAGCATTCCA
24	GGGCACGAACTAATCTATACCACCCTC
25	AGGCAAAAGTAAAATACGCGGCTTAGG
26	AAAAGGGTGCCCAGCGATAAATGCAAT
27	ACGAGCCGGTTTAGCTATGTGAAATTG
28	CTGGGGTGCAAGGAGCGGACACAACAT
29	CCGTCAATATTATCTAAAATATCTTTA
30	TTTTAAATAGCAGGCGAAGCTTAATTG
31	TTTGCCCCATGCAACTAAGGCCCTGAG
32	CTGAATATATATCATAACAGAGGTCAT
33	TGATGGTGGCAAACCCTCCCACGCTGG
34	AAAATCTAATGGCAAATCAACAGTTGA
35	GAGATAGAACTATTAGTCTTTAATGCG
36	ACTTGATAGCAAGGGTCTGAGAGACTACCTT
37	CAGTCAAATCACCTGACCTCCTTAAAGATTC
38	TATAAAGCCGACAAAAGGTATACAAATCAATA
39	ATTCGTGCAGGGAGACAACCATCGCCCACGCA
40	CTGGCATGACCTCAAGAGAAGGATTAGGATTAGCGG
41	GCAATAATAACGGAATACAGCCGAACAAACCTATTA
42	TACTGGTAATAAGTTTTAATGGAAAGCCGGAATCAT
43	ATAGCCCCCAGCACCGTAACCATTAGCAAGGCCGGA
44	AGCACCATTATCAGTAGCGACAGAATCAAGTTTGCC
45	ATTCAACCGATCGGTGCGAAGATCGCATGGGCGCAT
46	GTGAATTATTAAACGTTAATATTTTGTTTCGCCATT
47	CAAGCAAATCAACCCGTCGGATTCTCCAAGGGCGAC
48	TAGCGAACCCGCGTCTGGCCTTCCTGTTCATTAAAG
49	AATCGCCATCATTACCGCAAAGGAACATGAAAATCT
50	CATCCTAATTAAGAACGCTCTGTATGGACAAACTAC
51	AAGAGAATATCAGCGGAGTGAGAATAGGCCCAATAG
52	ATAAACAACACGTTAGTAAATGAATTTGAGGCGTTT

53	*TTCTGAAACCATTTTCGACAGGAGGTTACCGCCACC*
54	*AATAAGGCGGGTTTGAAATTTGATGATACAGGAGTG*
55	*GGTTTTGCTTAGGTGTATCACCGTACTGCCAGTAAT*
56	*ATTTTCAGGTCAACAGTTTAAAGTACCAACGCTCAA*
57	*TTGGGTTATTCTTTCCAGATGTTCAGCAAGTCCTGA*
58	*AAGGAGCCTAGCGAGTAACAGATATAGGAACGGGTA*
59	*CAGACAGCCAAAATAATTTCCCGACTTTGCTATTTT*
60	*CACCGCTTCGGAAGGGCGATTGAGGGAAACAGCCAT*
61	*TTTGTTAAATTTAAATTGCACCGTCACATCACCAGT*
62	*TAACCGATAAGCCCCAAAAAGCAAATATCAGCTCAT*
63	*GGCTCTGAGTTTCGGATCCCCGCTCAGAGCAAGAAG*
64	*ATAGCTTAGAGCCCGGAACAGTACCAGGCCCCCTGC*
65	*ATATTCAACCGTTCTAGCAGAAAGGCCAAACGAAAG*
66	*AATGCCGGAGCAAGACAAAAATTTAATTTAAATAAG*
67	*TTAACAATTATTTAGAAGGTGAGACGGAGATTAGAG*
68	*GCCTGAGTAGCAAGGATAAAAATTTTTCTGTAATAC*
69	*CCTGAGCAAGAAACAATAACGGATTCGGATGAATAT*
70	*CCTTGGTGCTTGTATTCTGCGATTATGCGATGTAGA*
71	*TTTTGCGGGTAAAGCTAAATCGGTTGTAGAATTAGC*
72	*ACAGTAACATACCATATCAAAATTATTTGGATTATA*
73	*CTTCTGAATCACAATTCCAATTATCATCATATTCCT*
74	*CCTGTCGTGCACATTAATTGCGTTGCGGTGTAAAGC*
75	*TGGCTCATTTTTCAACTTTAATCATTGTTCAGTGAA*
76	*TGGTTTTTCCGGCCAACGCGCGGGGAGGTCGGGAAA*
77	*GGAATACCAGGAACAACATTATTACAGTTTAAGAAC*
78	*GCATAGTAAGAGCAACACATGCTGTAGTGAGATTTA*
79	*TTTTGCGGAAGGATTAGAGAGTACCTTAAAGCGAAC*
80	*TTGCTGAACTGAGGCGGTCAGTATTAATACCGAACG*
81	*CAGACCGGAGAAAGACTTCAAATATCGAAAGCGGAT*
82	*AACCACCAGGACAATATTTTTGAATGGCCCTTCTGA*
83	*TGCATCAAAAATCAGGTCTTTACCCTGAAACAGTTC*
84	*AGAAAACGAGAATGACCAAAAGAACGTGGACTCCAA*
85	*ATCCTGAATGGAAATTATAGCCAGCTTAAAGCGCCATAAA*
86	*GCCTACAGTTAATGCGGATAAGGTAACAGTGCGAGGAAAC*
87	*TAGGGGTTGGTGTTCTGGAAGTTTCATCAGTCTCAACATG*
88	*AAACCAGGCTCATCAACATTCGAGGTGGCTTTTGCGACAGA*
89	*CGGTCGCGAAAGACGTCAATCATACGCCATCACTCATAGTT*
90	*CGTCAAAGGGTAAGAATAGAACAAGAGAATAACCTGAAGCA*
91	*CAACTAATGCAGATTGTATCATCATATATTTTTATACCAAGC*
92	*GCGAAACAACAAAGGCTAAACACTCATCTTTGACCTGATAAATT*
93	*CATTAGACGAAATAGCAGCCCAATCCAAATAAGAAACGATTTTTT*
94	*ATCGATAGCTTATTAGCGCGTCTTTCCAATATTGACCTTACCAAC*
95	*ATTATTTATCCTTTACAGAGAGAATAATTTGCCAGTAATGAAACC*
96	*AATTTCATCTTCTGACCTAGAACGCGAGAAAACTTTACGACGACA*
97	*TGTAAGCAAGTGAATAACCTTGCTTCTTTTTAATGGAAACAGTAC*
98	*AATTAATTTTCCCTTAGAATCCTTGAATATATGTGACTCGTCGGT*
99	*ATAAATCAATTTCACATAACATCAAGAAAACAAAATTTTCAATTA*
100	*TCCGAACTCCTGAGAAGACTTGAATCGGCTGACGCAAACATAGCG*
101	*AAAATTAAGAGCATTAACATCCAATAAATGAACGGTGGTGGCATC*
102	*AGAGTTGCAACAACTAATGCAACAGCTGATTGCCCTGCGCCAGGG*
103	*GGAGCACTAGCAAGCGGTAATCAATATCTGGTCAGTAGCATCACC*
104	*GCGAGAGGCCTTTTGATACCTCGTTTACCAGACGACAATTACGAG*
105	*CCTGAAAGCGCGAAAAACCGTCTATCAACCAGTCACACGACCAGT*

106	TCCCATACCTCGATACATCGGGAAAGAAGATGACAGGGCTTCCCAA
107	GACGGATCGGTTTATGAGAAGCCAGCCAAAATAAACCCATGTAAACA
108	GCTAGAAGGAAACCCCGTATAAGTTTAGTATAAAGCCAGAACGGGGTCA
109	CAGGCTGCGGTTGCGCCGACAATGACATTAAAGGCCAATTTCTTAGTCA
110	CAGGGGCCTCTTCGCTATTACGATACCGATACAACTGTTGTGGTGCCGG
111	AATTCTACTGTTTCCTGTATTTTCATTTGGGGCGCGACGTAACAACAAA
112	TGCATAAATCCTTAAACATCGCCATTAAAAACACCGCCTGCAACAGTGC
113	TTGGTCACCGCCTAGTACGGTGAATGAGTAAATGAAACAAAATCATTTC
114	AAGATTCATTCCACGGCAAAATCAACAGGTCTGGCTTAGAAATCCTGTT
115	TCATTCCAAAAGGCTTATATCGGCTGTCGCTAATATATGAAATAGTCTTA
116	AGCATAGCATCGGAAAGTTTCCAGAGAATCGAGTTTTGTCGATAACTATA
117	AACAATTAAACGGGAATACACTAATCAGGTCAAATCCAATCGAGGGTAGC
118	CTGATTGTTTGCACGTAAAACAGAAATATTTTAAAAGAGCTAACTCCAGC
119	TTATCCGCTAATGGAAGGGTAATCATGAACAGCTTGCCAGCTGGCCTTTC
120	TTACCACGAGTAGAGATAGGGTTAGGAAGCCCAGCAAACTCCCCTTATAA
121	ATCAAAAGAAAACAGAGGCTCAAATATTTCCGAAATTATAACAGTGCGTA
122	TAAACTCACTGCCACCATTAGACTCGAATTCGTTAGAACCGTACCTTTTAAA
123	TCAGCAGCTTGCTTTAAATGTGTTAATTGTAGTCACCAGTGATTTTGCTACCG
124	ACGAGAAACACCAGCAGACGGTGCAAGGCAAACCAAAAACCCATGTTACAACT
125	CACACAGAAGATAATAGCCCGATTTAGTTTGCGCTTTCCAAGGCGGTTTTGAT
126	TAAAGGTGGTAAGCCCAATAAGAAAAGTTAGCAAACAGGCAGAGGATGAAAGTA
127	CCAGTGTAGAAACCAGAGCCGCATCCTCATTCATATGCGTTAAAGTAATAAAAA
128	ACCACGGAAACTGAACACGAATTGAGTCAACATATACGTAGGAATATTTAACAA
129	GTTTAACGTCAAAAATGAGGAGAATTATAAGTTTATTACCAGCGCACAAGCAAG
130	GCCAGCAAACGACTTGAGAGCGCGTTTTCATCGGCACCGGAACCAGAGCCACCA
131	AAGATTAGTGCGGGAGGTCAGAGCCGCCACCCTCAGAGCCGCCGCCAGCATTGA
132	ACAATAGATTAATGCAGAGTCAGACGATTGGCCTTGGAATTTACCGTTCCAGTA
133	CGTAACCGTGGGGACGACGACAGTATCAAGGCGATTAAGTTGGGTAATATAATC
134	CGTTGTAAAGTGGTTGTGAATTCATGCTTTTCAGGTTTAACGTCACCTGATTGC
135	GAATTGTCACCCTGGAGTGACTCTATGGCAGAGGCGAATTATTCATAATTACAT
136	TTTGAATACAACTCGTATTTAATGAATTTTTCACCATATTAGACTAGCAAATGA
137	TAGCTAATAGTAGTCAATAAAGCGGTACCGAGTACATTTCGAGCTGCTCATGAA
138	GATTATCAGGAACAAAGAAACCACCAGCTAATGAGTGTTTGAGTATGGCCAACA
139	TAAGGCTTGTATTCATTACCCAAATCAAGCTGAAAAGTACAGACCAGGCGCATA
140	CAGTCAGGACGTTGCGACCTGCTATTATGACCAGAACCCTCGCCTGATAAAGCA
141	TAACATTGAGGACTTACGAAGGCAAAATCATAAAGCTACGTTATTTCAACATGTG
142	TGGTCTCCACTATTTAAATCAAAAAGATTAAGGAGTGTTGTTCCAGTTTGCGTGG
143	CTTAGCTAACGAGTTTGCCATCCACCACCCTCAATCAATACCGGTATTCTTACGAGCA
144	TAGGACCCCGCTTTATAGGGGCGTCAATAGTTATAAGTATATTAAGACGATCAATATG
145	GGCTGGCTGAACTTTGAAAGAGGACAGATCATACAGCAATCATAAAATCAGAAATATT
146	GGGGTAATATCGAGCTTCTAATTGCTCTTTTGCAAATTAATAAAACGAACTAACCATT
147	CCAATACTGGTCAGAAGCCGTTTTAATGTAAAATGTGGGCTTGAGATGGTTTAAATAC
148	AACGTCACCTACAAAATAGGGAAGGTAAGAGCCTAACATAAAAACGTAATTGAGCTTTC
149	TCATCGAGACAAAGACAAGTGGGAACATGGTGTAGACTCCAGCCAATGTGCTGCGGCCT
150	AATTACTAGTCTGTCCAGTTCAAATATGAGGGTTGAGAATTTATCACCAACCTAGGAGA
151	ATCCCCCTCAAATGCTTTACTATTATACGGAATCGTATCTTGACAAGAACCGGACCCTG

Table S6. Sequence of 52HB hybrid staple strands

1	ATAATAACGGGACAGATGGACGGTCAA
2	GAAGGCACCCGACGATAAAGGCATAGT
3	CACCAATGAACCGACTTGAAATTCATA
4	GTTGAGGCACCACCAGAAAAGGAGCCT
5	GAGGGGACGTTCAGGGATGATGGGCGC
6	CGAAAGAGACTTTAATGCCGACAAGGCG
7	ATCGTAACTTGTTAAACGTAATGGGCCGGA
8	ACATAGGCTCCAACCACCACCAACCGCCACC
9	ATAGAAGCCATTTGTAAGTTTATTCATTAAAG
10	TGGTTTACATATTGACATTGGGCTCGAAACAA
11	TTAATTGTTTTCACGTGCGATTTTGAAGAAAA
12	TATTAGCGACGCATAAAGCATCGGGAAACGCA
13	CAGTAAGCTTAAACAGTTTTCATGGCCACTAC
14	AGGCGTTGCTTGTTACCTCCGGAATCGTCATA
15	GAAGCCTTTATTTCAACGGCCAGCTTTTTGACC
16	CCAAATAAGAAACGGAAGCCCGAAAGTGCGGCC
17	TACAGAGAGAATAACCCTGACTATTATTGAATC
18	AAATCAGGTCTTTACATAAAAACAGGTGCGTTA
19	GAGGTTTTGAAGCGCTTAGAGCTTAAAAGTGGT
20	AGAACGCTGCAACTAAAGTAACGACGGCCAGTG
21	CCGCACTAAGCCGTTTTTATCCAGAGCCTAATT
22	AATAATCAATCAGATATAGAGCACCCAGCTACA
23	ATTTACGAAGCGAACCAGACCGTTTTAATTCGA
24	AGCAACTGGGGAGAGGCGGTCCCTTAGAATCCT
25	AGAGGCATAAACAGCCATATAAGAGCAAGAAAC
26	CTAAATTTAAGCCCAATAATTATTTATCCCAAT
27	AGAATAATCAGAGGGTAATTAAATAGCAGCCTT
28	AAGACAAAGAACGGTAAATCGTCGCTGCCAACA
29	GCTTAGGTTGGGTATAGCTTAGATTAAAAGCCA
30	TGAAAACATAGCGTATATAACTATATATAAATA
31	TTTAATGGAAACATACAGTAACAGTAACGGGTA
32	GGATTCGCCTGATAAATTAATTACATGACAATA
33	AAAGGTGGCGCAAAGACACCACGGAAGGAATTAG
34	AGCCAGCAAAACGTTAATATTTTGTTCGCCATCA
35	AAGAGCAACTTCATCAGTAATAAAACGAACTAACG
36	ATCTACGTTTGAGATTTAGGAATACCACATTCAAC
37	GAGTAGTAAGGAAATTATTTTGTCACAACATACAT
38	CCAAAAAAATCAACCGATTGAGGGAGGAGCCGCCA
39	GTGAATTACCTCCCTCAGGAAGGTAACAGCGCCAA
40	GTTTGCCTTGTAGCCAGCTTTCATCAACATTAAAT
41	CATTAAAGCCTCCGTGGGAGTTTTGTCGTCTTTCC
42	AAGCGCAGTCTCTGAATACAAACAAATGACAGGAG
43	ACCCTCAGATTTCGCAAATGGTCAATAACCTGTTT
44	AAAGAACTACGAGAAAGAGGCTTGTAGAAAATATCA
45	GATAGTTGCCATTGTGAATTACCTTATTGAAAATCT
46	GTGAGCGAGTTTTTTAACCAATAGGAAAAAATTCGC
47	AGACGTTAGCCCTCATAGTTAGCGTAAACAAACTAC
48	AGCTATATTTATGACCCTGTAATACTTGAGCATAAA
49	AATATTCATTGAATTTAGATTTACCAGAAACCTAAAA
50	GAAGTTTCATTCCATATACAACCGCCACCGATCTACA
51	GTGTTACCAGAAGTACACTAAAAACCCTCGCTGGATAG
52	CTAAAACAAACGGGCCACCCTCGGGGTTTTGTACCGCC

53	AAAGTGTAAAGCCTGGGGTTTAAGCTACGTGGTAAATA
54	AAGGGCGAAAAACCGTCTATAGCTGGCGAAAGCAAGTA
55	TAGAAAGAACTATCATACACTCATCTTAATTTCAGCAAA
56	CCAAGCTTTCTCACAAAAGAATAGCCGCGCAGAGGCGAA
57	TCCAAGACCTTTTACATCGGAACGTGGACTCCAACGTCA
58	AATTTACAAGTTACAAAATCCGAGATAGGGTTGAGTGTT
59	GAGTAAACAGGGCGCCTAATGAGTGATTTTTAACCTCCG
60	GTTCCAGTTTGGAACAAGAGGGTTTTCCCAGTCCCAATC
61	ATTAGATAACAGTTGATTCCCCAATAGCAAGCAGGCTGTC
62	AGATCGCCTGAGTAATGTGTAGGTAAAGATTCAAAAGGGT
63	CCGTGTGGTAAATGCTGATGAACATACGAGCCGGAAGCAT
64	GAGGATCCCCGGGTACCACAATTCCACACCAAATCCAATCGC
65	TAGCAAACGCAGGGAGTTATTACCATTAGCAAGGCAGAATCAA
66	AGACAAAAGTGACAACAACCGGAACCAGCCAGCATTAAATCCT
67	AAATCATACAGGCAAGGGTTGTACCAATAGTAGTTATTAAGAG
68	AAGTTGGGTAACGCCAGTCCACTATTAAAGGAGAAACAATAAC
69	TCATAAGGGCCTGCTCCAGAGATTTGTATCATCGCCTGATAAAT
70	AGTACAACGTGTTACTTAGCCGGAACCAGCGATTATATTACAGG
71	CTCAGAGCCACCACCCTAAGGAACAATAATAATTTATCGGTTTA
72	CGCGTTTTCATCGGCATTTTCGGTCAAGTAGCGACCGGAAACGT
73	CGTCGGATTTTTTCATAAATAGCAGCACCGTAATCTAGCCCCCT
74	TTTTCTGTATTTGCTAAAGATTGGCCTTGATATTCTTACCGTTC
75	GGTAGCTATATCGGCCTCCAACCGTTCCAGAAAAGCGCCAGTTT
76	GCTAAATCGCAAAGAATTAGCAAAATTAAGCAATAGAACCCTCA
77	GCTCAAGAGCCGGAATAGGTGTATCACCGTACTCAGGAATTCTA
78	GGCGCATAGGCTTTAAGAAAAGTAAACAAGAATTGAGTTAATGGT
79	CCCTCAGCAGCGAAAGACCCGATATATTCGGTCGCTCACCAGAAC
80	CAGGCGGATTCCTCAAGAGAAGGATTACCCATGTACCCCCCTGCC
81	AAAAAGATTAAGAGATTTTTTGTTTAAATTGAGAATCGCTACCGA
82	CAACAGGTCAGGATCTTACCAACGCTAGGTAAAGTAATTTATCAT
83	ATTTTTGCGGATGCTTAAATCAAGATGCAGAACGCGCCTCATCCT
84	ATTTTATCCTGAATTAGAGAGTACCTCAACCTTATGACATCTGTA
85	TTAAACGGGGATGTGCTGCGCGATCGGTGCGGGCCTCTTCGCTAT
86	TTTCCTCTGTCCAGACGACTTAACAATTTCATGAGTTGCAGCAAG
87	AACAACAGTGCTGAATTGTTTAATTGCTCCTTAGCGGATTGCATC
88	TGTGAACGCATTTCACATATCCAGTCGGGAAAAGTCAATAGTGAA
89	CTGCCAATGTCCCGCCAAACCTGGCCCTGAGATTGAATTACCTTT
90	TGTAATATGATACCGACAGACTTCAAATATCGCGGAAGCAAACTC
91	ACGCTCGAATATAGGGGCCTAGTCAGAAGCAATTGATAAGAGGTC
92	TACAAAAATTACTAGAAAACTGAGAGACTACCGCTAACTCACATT
93	TTGAAACATATTTAACAACATTAATTAATTTTTTGCGTATTGGGC
94	TTTCCTGTGTGAAATTGTTATCCGCTCGAGCTCGAATTCTCTGAC
95	TAACCTTGCTTCTCGAGAAAACTTTTGTTAATTTCATCTGTAATC
96	CTGCATTAATGAATTTGCCCCAGCAGCTTAAGTGTCCTTATGTTC
97	GGGCAACAGCTGATTCTTTTCACCAGCTGGAGTGACTCTTTAGGC
98	CGGTCCACGCTGGTCGGCCAACGCGCCGTCGGTGGGCACAACAGT
99	CGTCAGATGAATAGTACATAAATCAAATAAGAGAATATATAATCT
100	CCCTCAGAGAGCCGCCGAGCCACCAATAGGTCACTCACCAGTCGAT
101	TATTTCGGAACCTATTAAACAGTGCCCGTATAAAAGCATTCCTTTT
102	CAGTTTTTGAGACTCAGAACCCGGATTGACTCAGCTCATAACAACC
103	GCCAGGGTGGTTTTTGCCCTTCACCGATAACCCCGCTTCAAGTACC
104	AAGGCTATCAGGATCATTACCGCGCCAATTCTGCGAACAAGGCGATT
105	TATATTTTAAATGCAATGCACTCCACAAGGATAAACCCTCATTACGA

106	*GACAAAAACGAGCGTCTTTTTTCATCGTAGGATCATTGGCCGGAGAG*
107	*GAACAACATTACCAAGCGTGAGATGGTTTTGACCCCGAGGCGCAAACG*
108	*AGCTAATTAGTTGCTATTTTAGGCTTATCCGGTGGTTTAGCTCAGTAC*
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112	*GGCTGATTCATGCGCACGAGCGAAAATCCTGTATGATGAAACAAACATCA*
113	*TATTCATTATGACCAACCCTTCATCAAGAGTAATCTTTTGCGGGATCGTCA*
114	*TGTGTCGAAATCCGCGAAACCGAACCCCAAATCACTTGCCCTGGGCATGATT*
115	*GGACGTTGGAAGAACTGGCGCCAAAAGGAATTACGAAACCAAAATAGCGAGA*
116	*CGTCCAATAAGCAACGGCTACAGAGGCTTTGAGGACTAAAGACTCTTGATACC*
117	*ATTAAATTTCGTGCATCTCCCAAAAACAGGAAGATTGTATAAGCGTACCCCGG*
118	*AACGCCTGTCAGTTAATGCGTAACACTGAGTTTCGGTTGGTGTAAGCAAGCCC*
119	*GTTGGGAAGGGAGTAGATTTAGTCCGGCACCGCTTCTGGTTATGATATTAGGA*
120	*AGGGCTTACGTCAAAAATGAGAGCGCTAATATCGGTCTGCAAAGTACAGACCA*
121	*ATACGTAATAGGAAGGAATTAACTGAACCTTTAAACAGTTCTGGTTGGTGTAAT*
122	*AGAAGAAACCGAGAACGAGAGAGAGATAACCCGCAGATAGCCGAAGATAAAGACG*
123	*ACCGTCACCGTCAACCATCGTCAAAATCACCATCGCCCTTTGCCATCCAGAATGGA*
124	*AAAATAATTAACGGTAATAAATTAATCCTGAGAGTCTGGAGCAAGGCTGCGCAACT*
125	*AGAAAACATGCTTTGAATACCGAGCATGTAGAAAACGACGTTGTAAACGGTGTCTG*
126	*AACGGGAGAATAGACAGAGCCGGGTCAGACCAACTTTCAGTGAATTTCGTCATACAT*
127	*ACGGGATTTGTTTTGCCAGAGGGGGTAATAGTAAAATGTCCCCCTCAAATGACCCTG*
128	*ATGGTCACAATAGCTATCTTACCGAAGCCCTTTGGCTGATTTGAAAGAGAATACCCA*
129	*TTGATAATTAGCTGATCGTAAAACTAGTCAAATCACCATCAAGCCGGAAACCAGGCAAA*
130	*AACAAAGACACCGGAATCATTTCTTACCAGTATAGACGCTGAGAAGCCTGTCGTGCCAG*
131	*TTTTAGCAAAAATAATATCCGTTTATCAACAATTGAGCAAAAGAAGTTGATGGTGGTTC*

Sequence of P3024 scaffold
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GCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAA
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GCGAATGGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGG
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GCTGGAGCTCCACCGCGGTGGCGGCCGCTCTAGAACTAGTGGATCCGT
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Sequence of P7560 scaffold

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