

Rapid, High Yield, Directed Addition of Quantum Dots onto Surface Bound Linear DNA Origami Arrays

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Experimental Section

Materials: All staple strands and sticky-end strands were purchased from Integrated DNA Technologies Inc. Single-stranded M13mp18 DNA plasmid was purchased from Bayou Biolabs. Streptavidin (Thermo Scientific), Qdot® 525 Streptavidin Conjugate (Invitrogen) and chemicals were purchased from Aldrich.

AFM: All AFM imaging studies were performed with a Bruker Multimode8 and NanoscopeVI controller using SCANASYST-AIR mode. Circular grade V1 mica discs (10 mm, Ted Pella, Inc.) served as substrates.

Fluorescence microscope (FM): Fluorescence images were taken with a Rolera-MGi EMCCD camera (QIMAGING), with acquisition parameters: gain 2, EM gain 3500, exp. Time=100msec. A Sapphire (Coherent) 488nm laser (20mW collimated) was used for excitation and launched into a Nikon TE200 inverted epifluorescence microscope. The characteristics of the filters employed were excitation 470/40 nm and emission 515/30 nm.

Preparation of DNA Origami:

Single Rectangular DO (srDO): The sequences of staple strands for srDO were designed using the Parabon inSēquio™ program.¹ Biotin-labeled staples were used to direct the local binding of, or address, SA or SA-Qdot species. The mixture of staple strands, biotin-labeled staples and M13mp18 ssDNA plasmid was brought to a volume of 50 µl using DO buffer (1×TAE buffer solution containing 40 mM Tris-HCl, pH 8.0, 20 mM Acetic acid, 2.5 mM EDTA, and 10.5 mM Magnesium chloride). The final concentration of M13mp18 ssDNA plasmid in the solution was 10 nM, and the molar ratio of the long viral ssDNA to the staple strands was 1:5. The sample was cooled from 90°C to 16°C over the course of 13h in a thermocycling machine (Primus96, MWG Biotech).² Staple sequences are listed at the end of the supporting information.

One Dimensional Rectangular DO (1DrDO): To prepare the one dimensional DO, designed sticky-ended strands were employed. The sequences are listed at the end of ESI. The mixture of staple strands, sticky-ended strands, biotin modified strands and M13mp18 ssDNA plasmid was brought to a volume of 50 µl using DO buffer. The final concentration of ssDNA plasmid in the solution was 10 nM, and the molar ratio of the ssDNA plasmid to all the other strands was 1:5. The sample was annealed by cooling as described in the previous procedure.

Purification of DO: To remove the excess staple strands, the DO solutions were dialyzed using the drop dialysis method.³ 50 µl of DO solution was purified using 0.25 µm pore size membrane (Millipore Inc.) by dialysis for 30 min against 10 ml of DO buffer.

Silanization of glass coverslip (AP-glass):

Indexed cover glass (Eppendorf CELLocate) surfaces were cleaned with 5 minutes of sonication, first in ethanol and then in acetone then dried in a N₂ stream. The substrates were then exposed to a low pressure UV lamp at a distance of ~2-3cm (SEN light Co. UVL-20, Hg lamp, 20 watt with 254nm power = 50µW@1meter) for 5 minutes and finally reacted in an O₂ plasma (100 mtorr ~75% O₂) for 5 minutes. This cleaned coverslip was immersed in a freshly prepared 1% 3-aminopropyl-trimethoxysilane (APTES) in dry ethanol solution for 10 minutes at room temperature, rinsed by dipping and agitation in an ethanol (~10-20ml) bath, then annealed in an oven for 1hr at 120°C.

Assembly of SA and SA-Qdot on DO:

10 µl of 1 nM DO was used to cover ~ 1cm² of freshly cleaved mica for 5 minutes, then the surface was washed with 400 µl of MilliQ water and immediately blown dry with N₂. The number density and structural integrity of the immobilized origami were determined using AFM. Mica bound samples were then incubated at room temperature in 10 nM SA or SA-Qdot solutions and brought to a volume of 30 µl using DO buffer. After one minute, the sample was washed with 400µl of DO buffer and then with 400µl of MilliQ water and immediately blown dry with N₂.

sQD-1DrDO alignment using the combing method:

To align then immobilize the sQD-1DrDO complex in one direction a moving interface combing technique has been employed.⁴ A small drop (typically 5 µl) of complex solution was deposited at the edge of an AP coated glass coverslip substrate. One flat edge of an untreated coverslip was then pressed/touched on top of the drop, forcing the drop to spread by capillary action along the untreated coverslip edge. This interface is slowly moved in one direction (as illustrated in Fig. 4a). After one minute incubation, the sample was wicked dry using an absorbent paper, then subjected to analysis by fluorescence microscopy and AFM analysis.

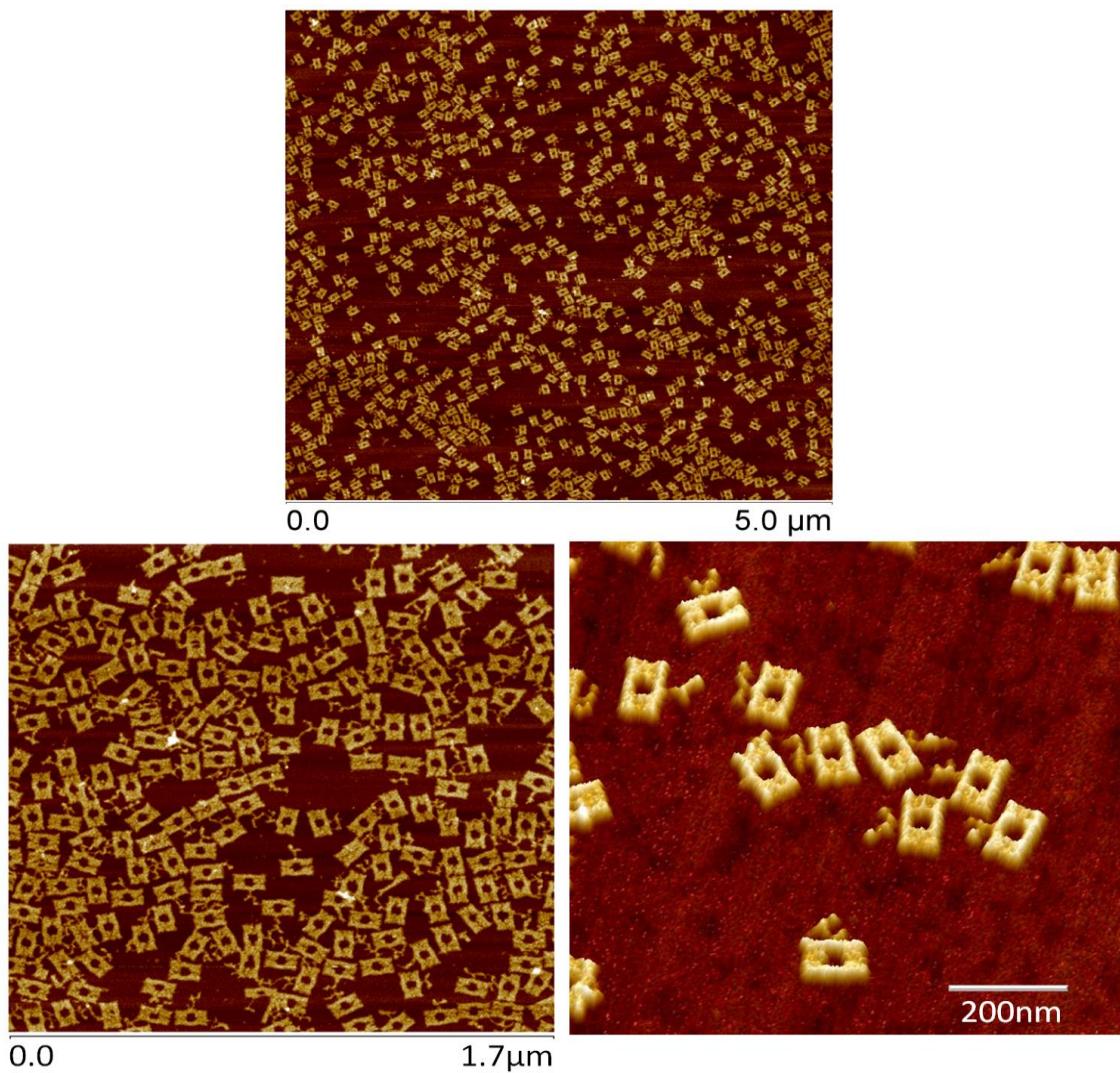


Figure S1: AFM images of single rectangular origami (srDO) platforms on mica

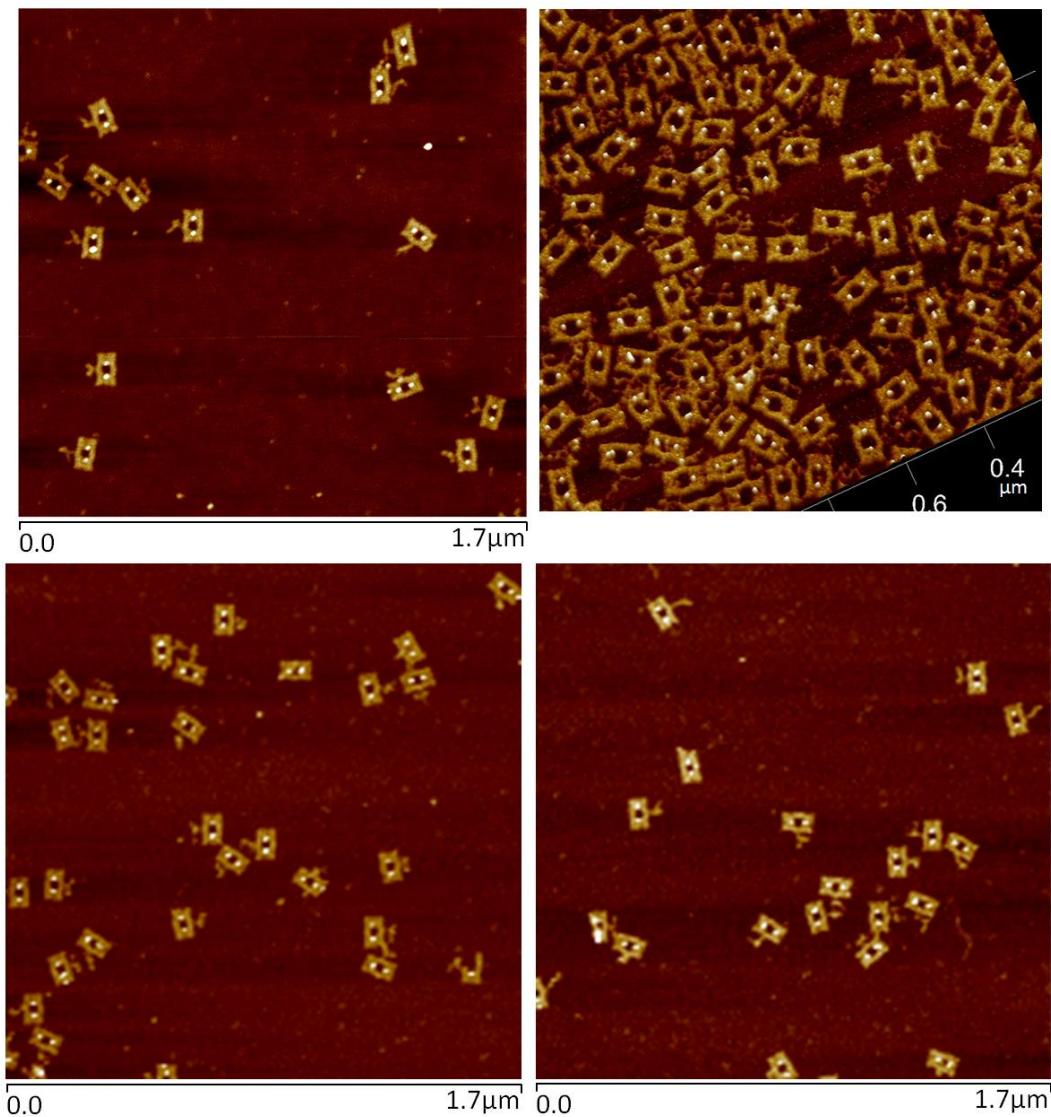


Figure S2: Directed assembly of streptavidin (SA) to addresses on srDO

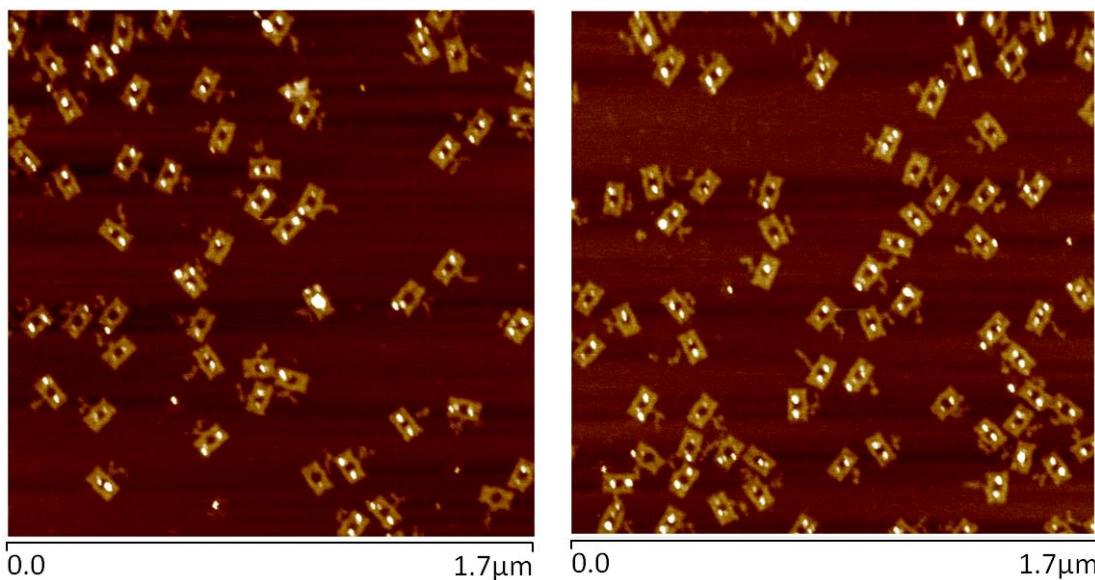


Figure S3: Directed assembly of SA-QDs to addresses on srDO

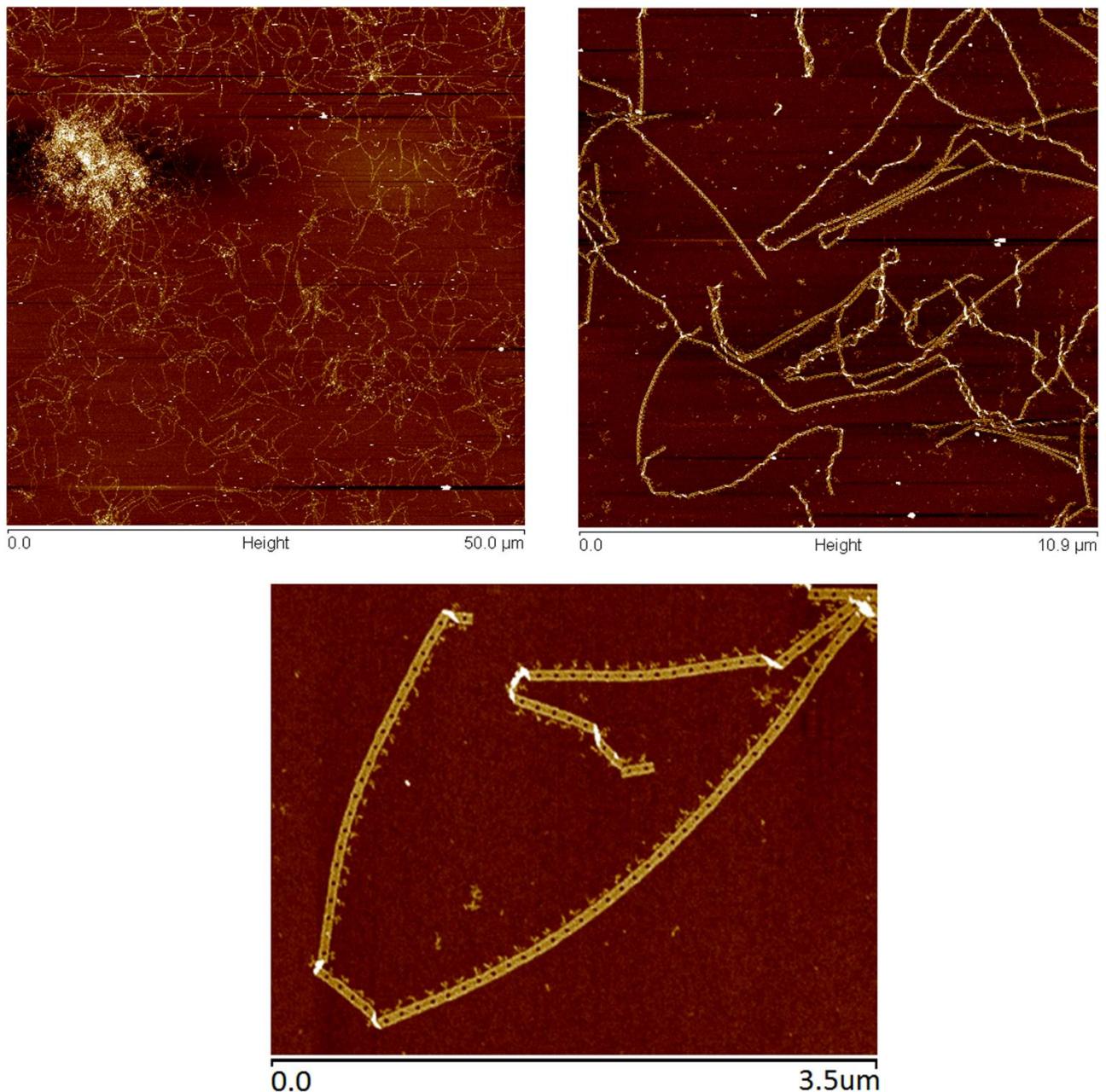


Figure S4: AFM images of one-dimensional rectangular origami (1DrDO) on mica

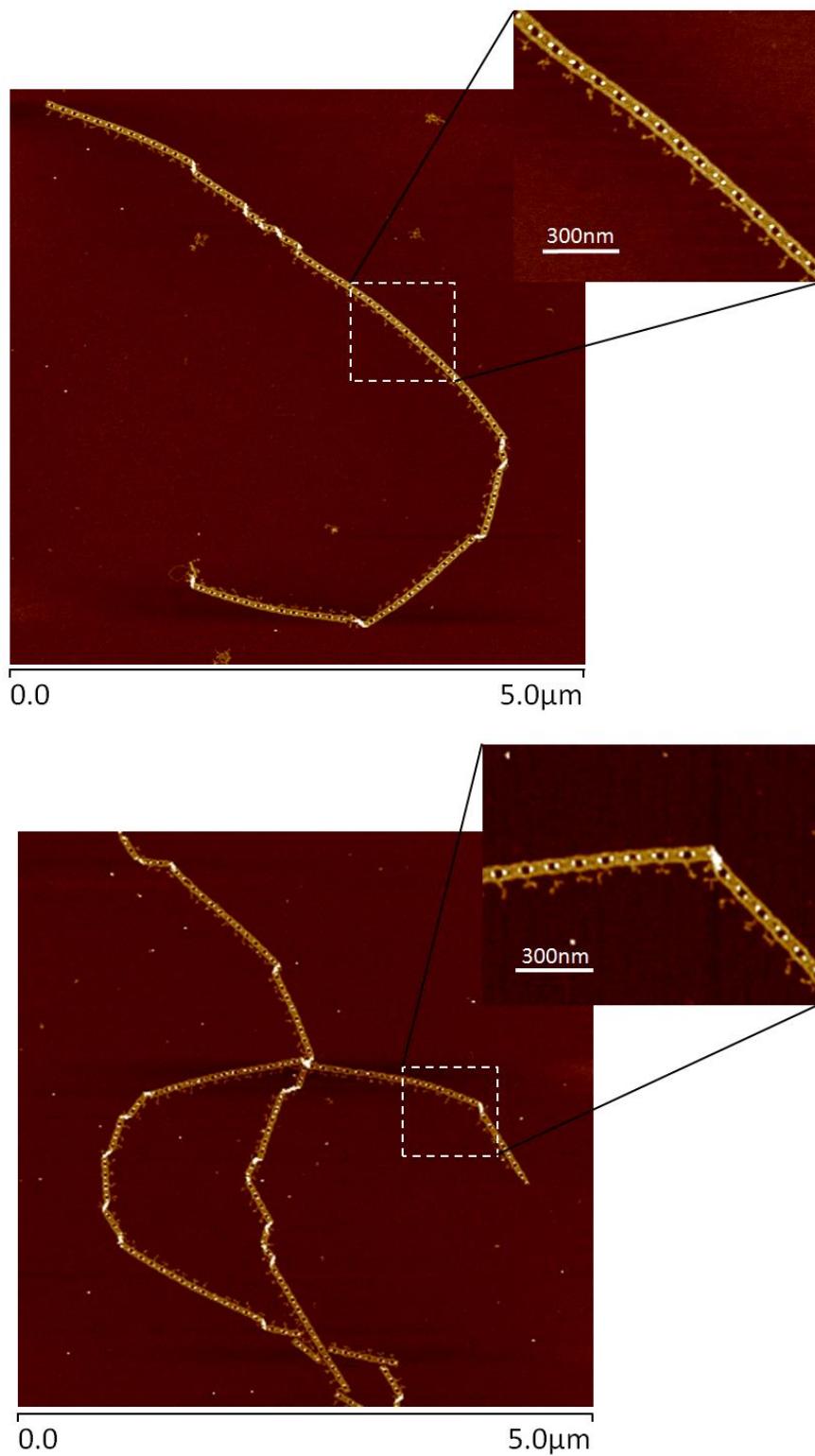


Figure S5: Directed assembly of SA to addresses on 1DrDO

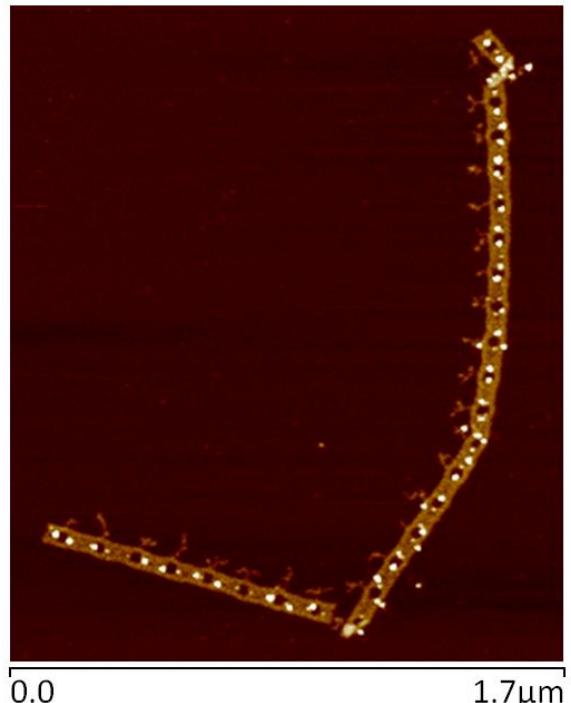
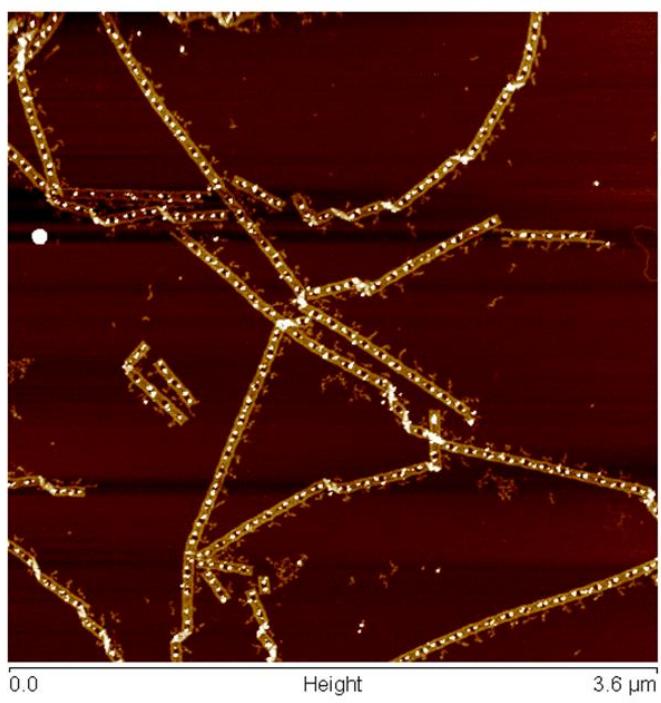
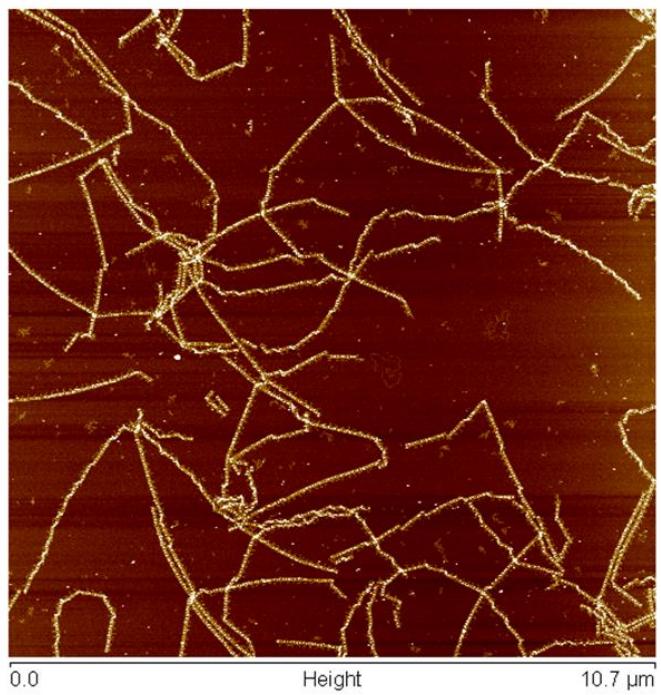


Figure S6: Directed assembly of SA-QDs to addresses on 1DrDO

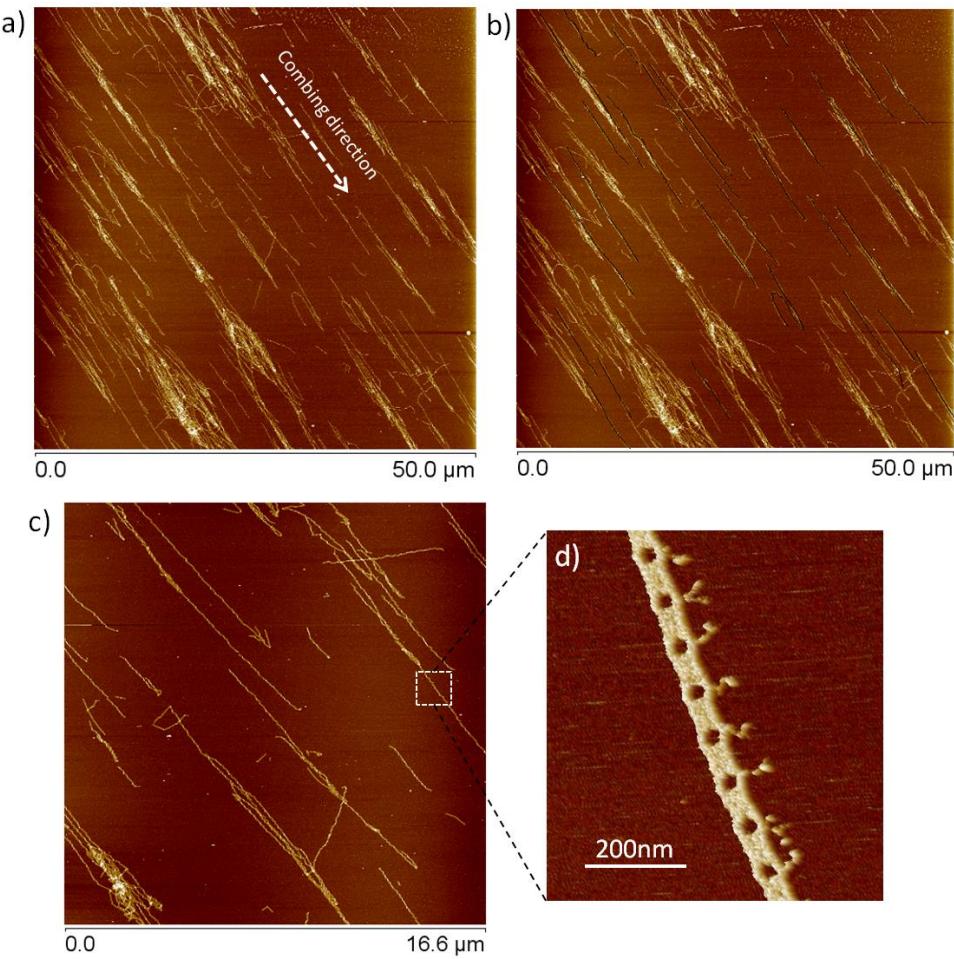


Figure S7: a) Large area AFM image of combed 1DrDO on mica; arrow indicates the combing direction; b) NIH ImageJ software was used to analyze 1DrDOs to determine length distribution (mean and standard deviation value) for apparently single constructs. Black overlay lines indicate which 1DrDO were analyzed; c) different region of combed 1DrDO; d) inset shows high resolution AFM image of the combed 1DrDO construct.

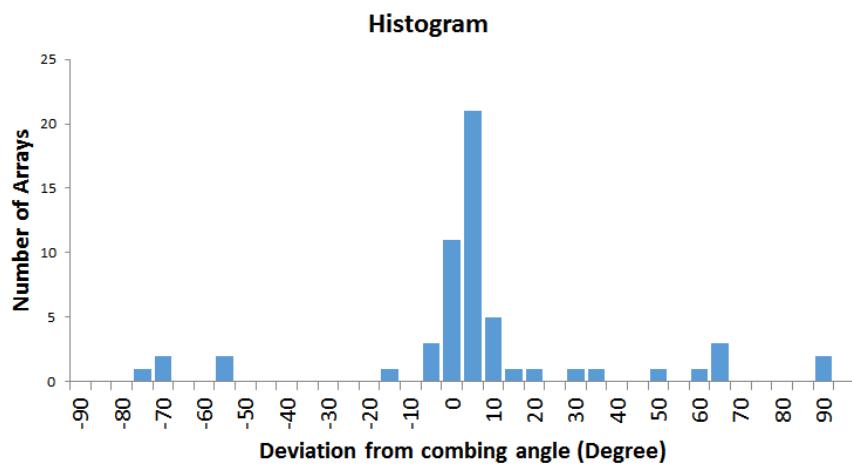


Figure S8: The bins at the center of this histogram show apparent normal distribution of the origami chain alignment dominated by combing while outliers at both extremes likely indicate other forces at work. N=58 number of origami chains were analyzed. If we take ± 10 degree as successful chain alignment than we see that 77% (40/58) are aligned along flow direction.

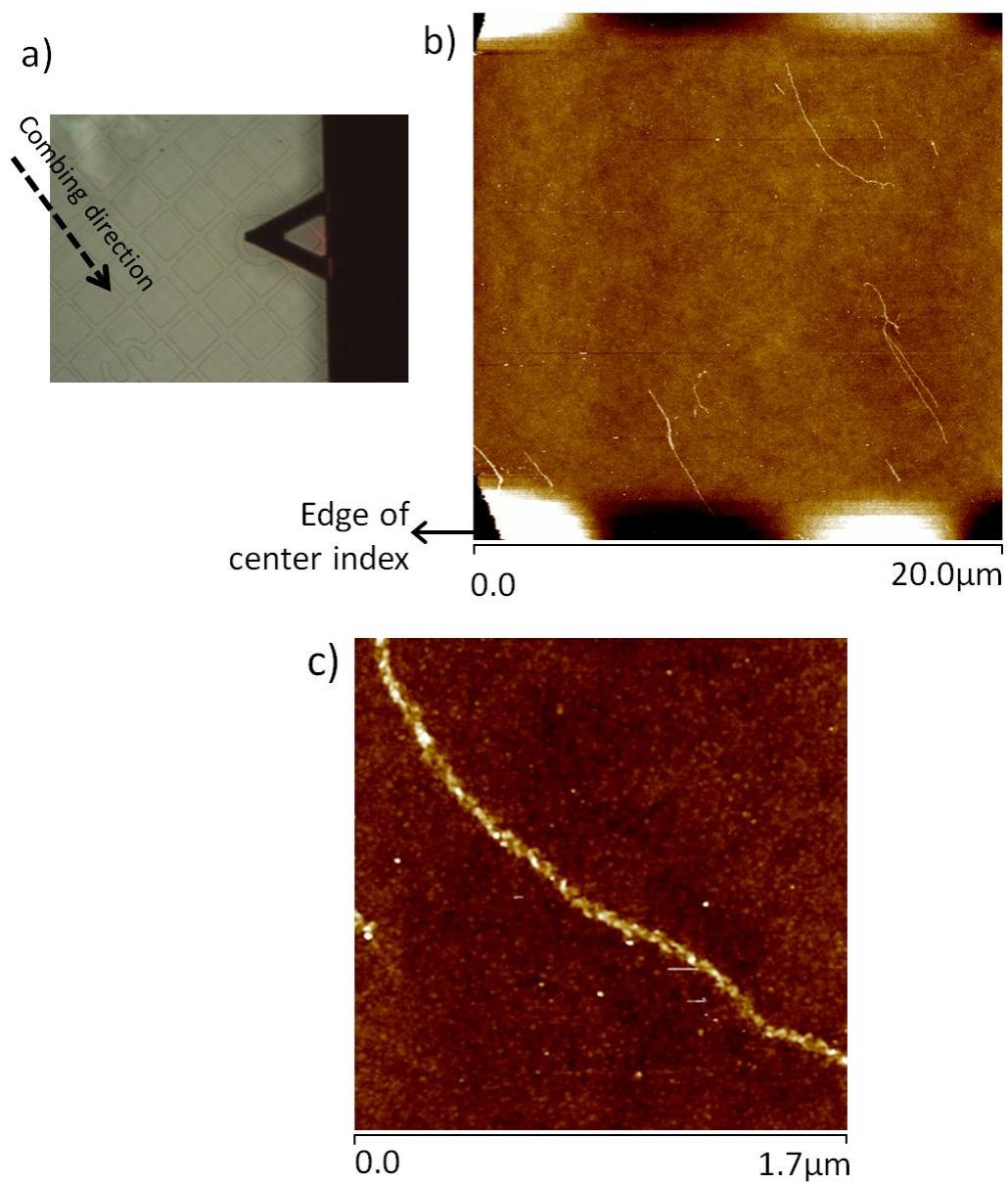


Figure S9: a) Arrow indicates the combing direction on indexed AP-glass; Light microscope image was taken during AFM imaging in air; b) low magnification AFM image of combed 1DrDO; c) high resolution AFM image showing a single 1DrDO construct.

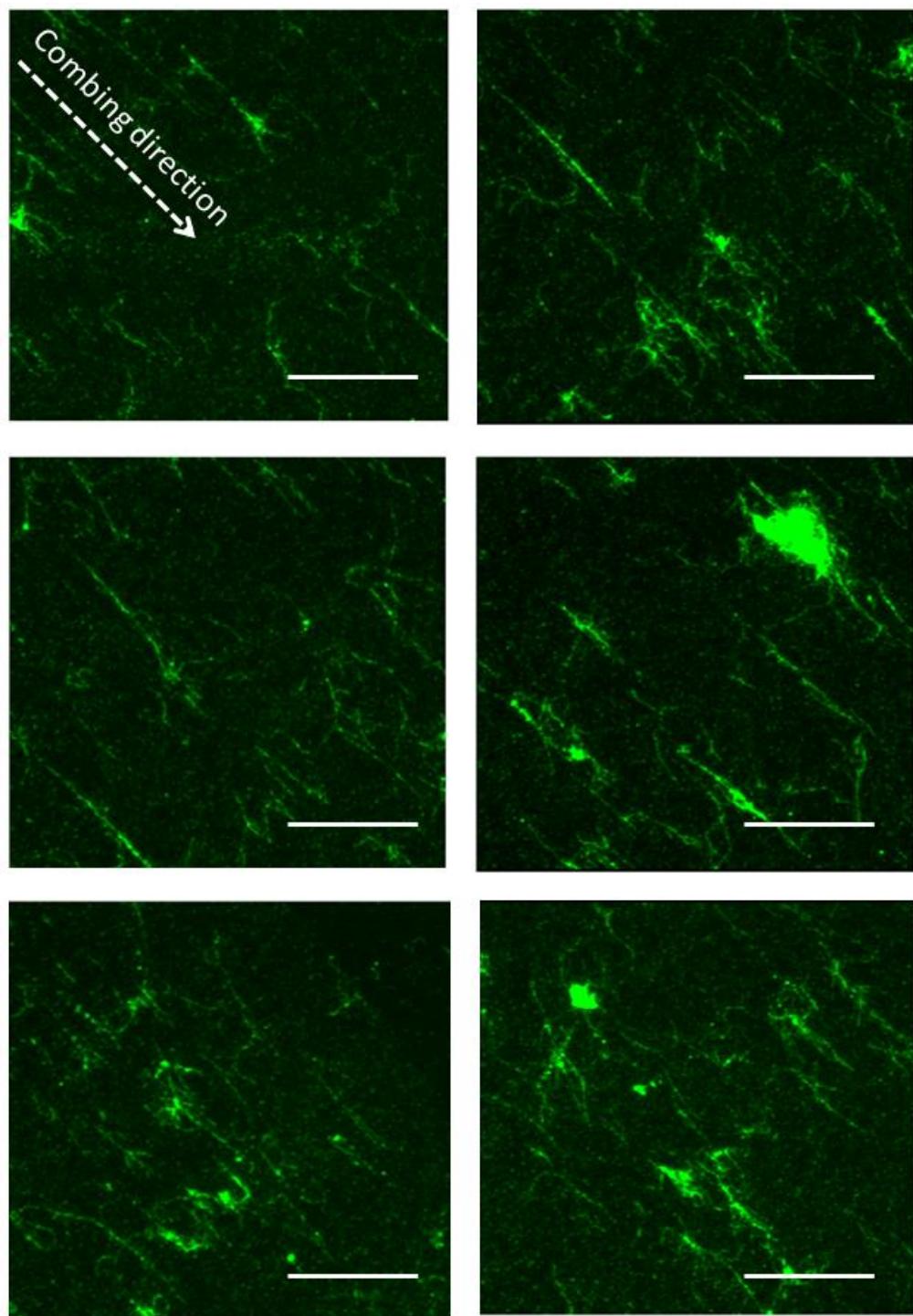


Figure S10: Fluorescence microscopy images of combed sQD-1DrDO construct on AP-glass; Scale bar 20 μ m

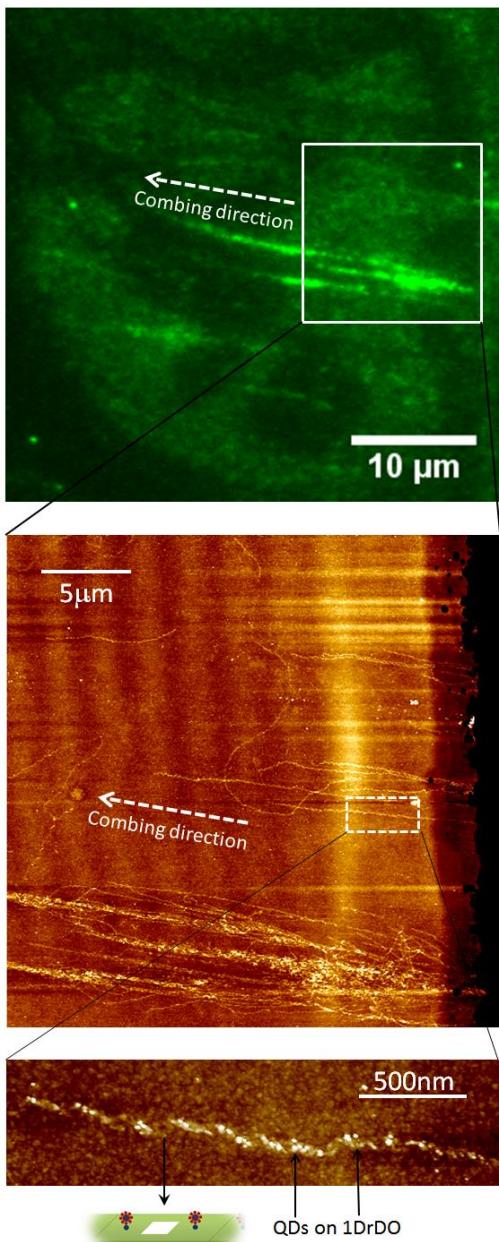


Figure S10. Wide range of Fluorescence microscopy and high resolution AFM and of the same region of combed sQD-1DrDO construct on AP-glass.

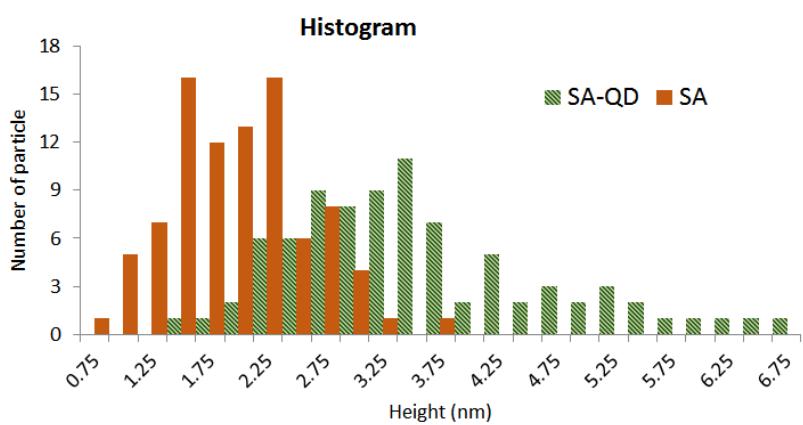


Figure S11: Histogram chart of SA and SA-QD height (excluding origami height) on origami chain.

Rectangular origami sequence (Black = m13, Ä=5' end; Å=3' end)

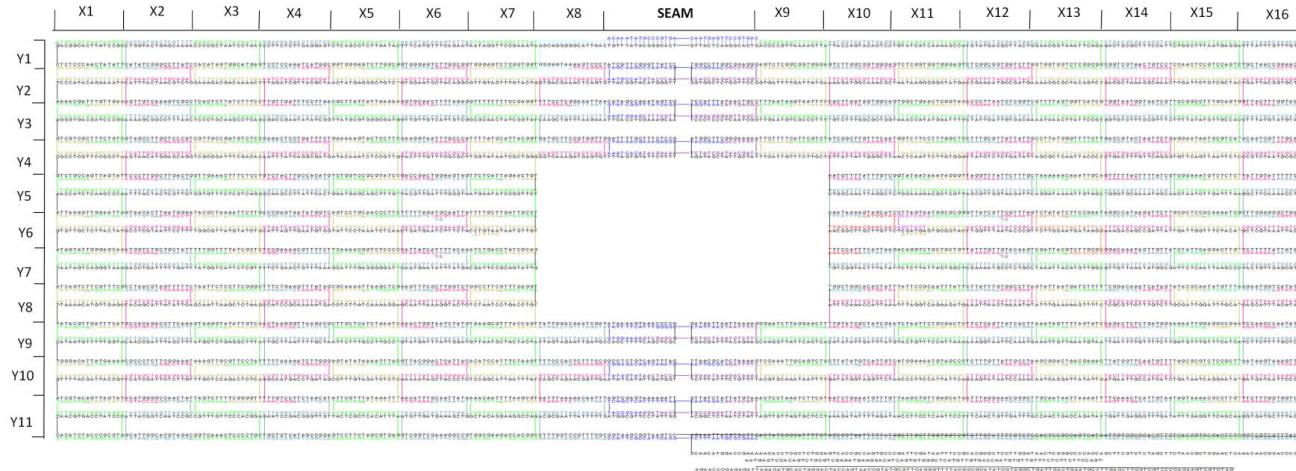


Figure S12: Rectangular origami structure and staple strand positions.

Staple strand sequences

seam-01	CAGTGCCTTGAGTAACAGTGCCCGTATAAACAA
seam-02	TACCGTAATAGCAAGCCAATAGGACCGGAAC
seam-03	CGCCTCCCCGGAACCAGAGCCACCAACCCATG
seam-04	GAGGTGAAGTATCGGTTATCAGCAGGTAAAT
seam-05	ATTGACGGCCGATTGAGGGAGGGATTGCTTTC
seam-06	ACACTAAACTAAAACGAAAGAGGCTACCGAAG
seam-07	CCCTTTTATAGCAATAGCTATCTAAAAGAAT
seam-08	AAAAGGTGTATTTCATGGGGCCTATTAAT
seam-09	TAATTTCCTCTGTAAATCGTCGGCGAGCTG
seam-10	TATGATATCGGAGACAGTCAAATCAATTGCGT
seam-11	AGATTTCAAAACAGAAATAAGAACCATCAA
seam-12	AACGCCATTCAAGCTATTTTAACAATAGAT
seam-13	AATACATTAATAGATTAGAGCCGTCCAATAGG
seam-14	CCATTGCCATTCAAGCTTAAATGCGCGAAC
x01-y01	TGATATAAGCGGATAAGTGCCTGC
x01-y02	AACAACCTAATTTCTGTATGGGAGAGAGGGT
x01-y03	AAAGACAGGCGGGATCGTCACCCTTTGCTA
x01-y04	CAATCATATAGCCGGAACGGAGGCGCAGCG
x01-y05	ACTTTAATTGGGCTTGAGATGGTCAGACGGT
x01-y06	CCCTCGTTATAGTAAGAGCAACACTAATTCA
x01-y07	AGCAAAGCTTACCCGTACTATTATCATAA
x01-y08	CTAAAGTAGCTAACATGTTTAATAGTCAGA
x01-y09	ATACTTTACCAAAAACATTATGATATGCAA
x01-y10	CAATCATAACGGTAATCGTAAACACCCCTGTA
x01-y11	GTGTAGATGGCGCATGGGATAGGTACGTTAGCATGT
x02-y01	TTTGTCTAGTACCAAGGTATAGCC
x02-y02	CGGAATAGCAGACGTTAGTAAATGTCACAGT
x02-y03	TTCAGCGGGTTAAAGGCCGTTTCATCGGAA
x02-y04	CGAGGGTACCTGCTCCATGTTACTAGGGAAC
x02-y05	GAACTGACAGAACGAGTAGTAAATCATTGTGA
x02-y06	ATTACCTTAAAGGAATTACGAGGCTACCAGAC
x02-y07	GACGATAAAATCAAAATCAGGTCGGATTGCA
x02-y08	TCAAAAAGTGAATATAATGCTGTACGGGTGTCT
x02-y09	GGAAAGTTAAAGCTAAATCGGTTGGGGAGA
x02-y10	AGCCTTAACAAGAGAACGATGATGTACCCC

x02-y11 GGGTGTAGCGGATTGACCGTAATCGTAACCGTGCATCTG
 x03-y01 CCGTACTCATTAGGATTAGCGGGG
 x03-y02 TAGAAAGGAGTTTGTCTTCGTGTATCA
 x03-y03 TACAGAGGCTGAGGCTTGAGGGAAAGTGAGAA
 x03-y04 AAAGAGGAGTGTGAAATCCCGAGCAACGGC
 x03-y05 TTAAGAACCCCTGACGAGAAACACCCAACCTTG
 x03-y06 ATAGCGAGCAGATAACGCAATGCGATT
 x03-y07 GAAGCCGAACGAGAATGACCATAAAACCAA
 x03-y08 ATAACAGTCTTAGAGCTTAATTGCATTAAGAG
 x03-y09 CAAGGATATAAAGCCTCAGAGCATCATTCCAT
 x03-y10 AGCCCCATGAGAGTCTGGAGCAATTCAACG
 x03-y11 CCAGTTGAGGGACGTCCGTGGAACAAACGATCAGAAA
 x04-y01 ACTCCTCAAGAGAAGGAGGAGGTT
 x04-y02 TAGTACCGTAGCGTAACGATCTAAACAACTA
 x04-y03 AAGGAATTCCGATATATTCCGTCGCTTGAGG
 x04-y04 ACTAAAGACATCGCCTGATAAATTCAAGATGAA
 x04-y05 CGGTGTACAGTGAATAAGGCTTGTGGCTCAT
 x04-y06 TATACCAGCCACATTCAACTAATGAGGCTTT
 x04-y07 GCAAAAGATTAAACAGTTAGAGAAAAGACTT
 x04-y08 CAAATATCTCATTTCGCGATGGTATTCCC
 x04-y09 AATTCTGCTAGCAAATTAAAGCAAAAAATT
 x04-y10 TAGAACCCCTATCAGGTATTGCCAACAGGA
 x04-y11 AGATTGTAACAACCGTCCGATTACGACAGTATCGGCCT
 x05-y01 AGAACCGCGTATTAAGAGGCTGAG
 x05-y02 TAATTTTAGACAGCCCTCATAGTCCACCCTC
 x05-y03 TGAGGAAGCATGCCACCGATAAGCGAATAA
 x05-y04 CGCATAGGCAACGGAGATTGTATCTTTCA
 x05-y05 TTGGGAAGACAAAGCTGCTCATTCAAGACCAGG
 x05-y06 CAGAGGGTTGAGATTAGGAATATCAGGACG
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 x07-y01 AGCCACCATATTCGGAACCTATT
 x07-y02 AGGCTCCACAGTACAAACTACAACACCCCTCAG
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 x07-y05 CTAACCGAAGAACCGGATATTCAAGAGTAA
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 x07-y08 AATGGTCAACAGGTCAAGGATTAGACCGGAAGC
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 x07-y10 AATTGCGAATAATTAAATGCCGGATGTAGGTA
 x07-y11 ACCGCTTCTGGTCCGCTGGCCTTCCTGTAGCTTGTAA
 x08-y01 GTTAATGCCCTGCCCCCTCATT
 x08-y02 TTCAGGGACACTGAGTTCGTCACAAAGGAGC
 x08-y03 CTTTAATTTCCTAAACAGCTTGTACGAAG
 x08-y04 GCACCAACACACTCATTTGACC
 x08-y09 ATAACCTGTTAGCTAGCATCAATTCTACTAAAAAGGGTG
 x08-y10 AGAAAGGCTAACCGTCTAGCTGTAAATT

x08-y11 TTGTTAAACAAAATAATCGCGTGAACCAGGCAAAGCG
 x09-y01 GCCACCCTTAAGTTAACGGGGT
 x09-y02 CATTAAAGTCATAATCAAATCACTCAGAGCC
 x09-y03 TAAGCAGAAAAGGGCGACATTCAAAAATTATT
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 x14-y10 GTTACAAAGATGATGGCAATTCTAACAGTTGA

x14-y11	GTAACATTATCAAACCCCTCAATCATAACACCGCCTGCAAC
x15-y01	CAGGTCA GT CTC ATT AAAGCCAG
x15-y02	AACGT CAC GT AG CG AC AGA AT CA AG GTT GAGG
x15-y03	ACGCAGTAGTGGCAACATATAAAAGGCCGGA
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x15-y10	GCGGAACAATATTCTGATTATCAATCGCGCA
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x16-y07	AATATCCCCAACGCTCAACAGTATCTTACCA
x16-y08	GTATAAAGCTATATGTAATGCTGAGGTTGGG
x16-y09	TTATATAACCTGAGCAAAGAAGATTATTCA
x16-y10	TTCAATTAGAGCGGAATTATCATCAAGAAACC
x16-y11	ACCAGAAGAATCTAAGCATCACCCAGCAGCAAATGAAA

Sticky End staples

MR-X1-Y1	ATAGAGAGGGTTGATATAAGCGGATAAGTGCC
MR-X1-Y2	GATTTTGCTAACAACTTAATTCTGTATG
MR-X1-Y3	AGACAGCAGCGAAAGACAGGGGATCGTCAC
MR-X1-Y4	AGGCAGACGGTCAATCATATAGCGGAACGAG
MR-X1-Y5	TGCTAATTCAACTTAAATTGGGCTTGAGATG
MR-X1-Y6	CCCTATCATAACCCCTCGTTAGTAAGAGCAA
MR-X1-Y7	AAGGAGTCAGAAGCAAAGCTTACCGCTGACTA
MR-X1-Y8	TAATATGCAACTAAAGTAGCTAACATGTTT
MR-X1-Y9	TTAACCTGTAATACTTTACCAAAACATT
MR-X1-Y10	AAAGTCATGTCAATCATAACGGTAATCGTAA
MR-X1-Y11	AAAGTGTAGATGGCGCATGGGATAGGTACCG
MR-X16-Y1	GTCTTCACAAACAAATAAAACGATTGGCTTG
MR-X16-Y2	GGAAAGCAGCACCGTAATCACAATGAAACCATC
MR-X16-Y3	CCTAAATACATACATAAAAGTGTAGCAAACGT
MR-X16-Y4	GCGGAAGCGCATTAGACGGATAACATAAAAAC
MR-X16-Y5	GTTGGGAGGTTTGAGCGAACCTCCGACT
MR-X16-Y6	CACATCTAATTACGAGCAGAAAAATAATAT
MR-X16-Y7	TTACCAACGCTCAACAGTATCTTACCAAGTATA
MR-X16-Y8	TAACTATATGTAATGCTGAGGTTGGTTATA
MR-X16-Y9	ATGCCTGAGCAAAGAAGATTATTCAATTCAA
MR-X16-Y10	AACGAGCGGAATTATCATCAAGAAACCACCA
MR-X16-Y11	TTGAATCTAAGCATCACCCAGCAGCAAATG

Biotin labeled staple strands

Biotin-X6-y5	CCTTCATCTACCCAAATCAACGTAAAAATCT TT/3BioTEG/
Biotin-X6-y6	ACGTTAATTAGAAAGATTCACTCAGTAATAGT TT/3BioTEG/
Biotin-X7-y6	ATAGCGTCACAACATTA CTTTT/3BioTEG/
Short-X7-y6	TTACAGGAAAACGAA
Biotin-X12-y5	AAGAAACGGAATCTTACCAACGCTCAATAGCA TT/3BioTEG/
Biotin-X12-y6	AGCAAATCACGGGTATTAAACCAAATAACAA TT/3BioTEG/
Biotin-X11-y6	CGACGACAGTACCGCAC CTTTT/3BioTEG/
Short-X11-y6	TCATCGAGAATCATT

References:

- (1) Paragon Computation Inc.
- (2) Liu, W.; Zhong, H.; Wang, R.; Seeman, N. C. *Angew Chem Int Ed Engl* **2011**, *50*, 264.
- (3) Marusyk, R.; Sergeant, A. *Anal Biochem* **1980**, *105*, 403.
- (4) Bensimon, A.; Simon, A.; Chiffaudel, A.; Croquette, V.; Heslot, F.; Bensimon, D. *Science* **1994**, *265*, 2096.