Electronic Supplementary Material (ESI) for Nanoscale.

Supporting Information

Programmed Dissociation of Dimer and Trimer Origami Structures by Aptamer-Ligand Complexes

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Description			Origamis Counted
T_1-T_2	Prior to cleavage	Singles	30
		Dimers	248 (89%)
		In all	278
	After interaction with ATP	Singles	186
		Dimers	58 (24%)
		In all	244

Figure S1. The detailed analysis of large-area domains: the ATP -programmed cleavage of the dimer origami structure T_1-T_2.

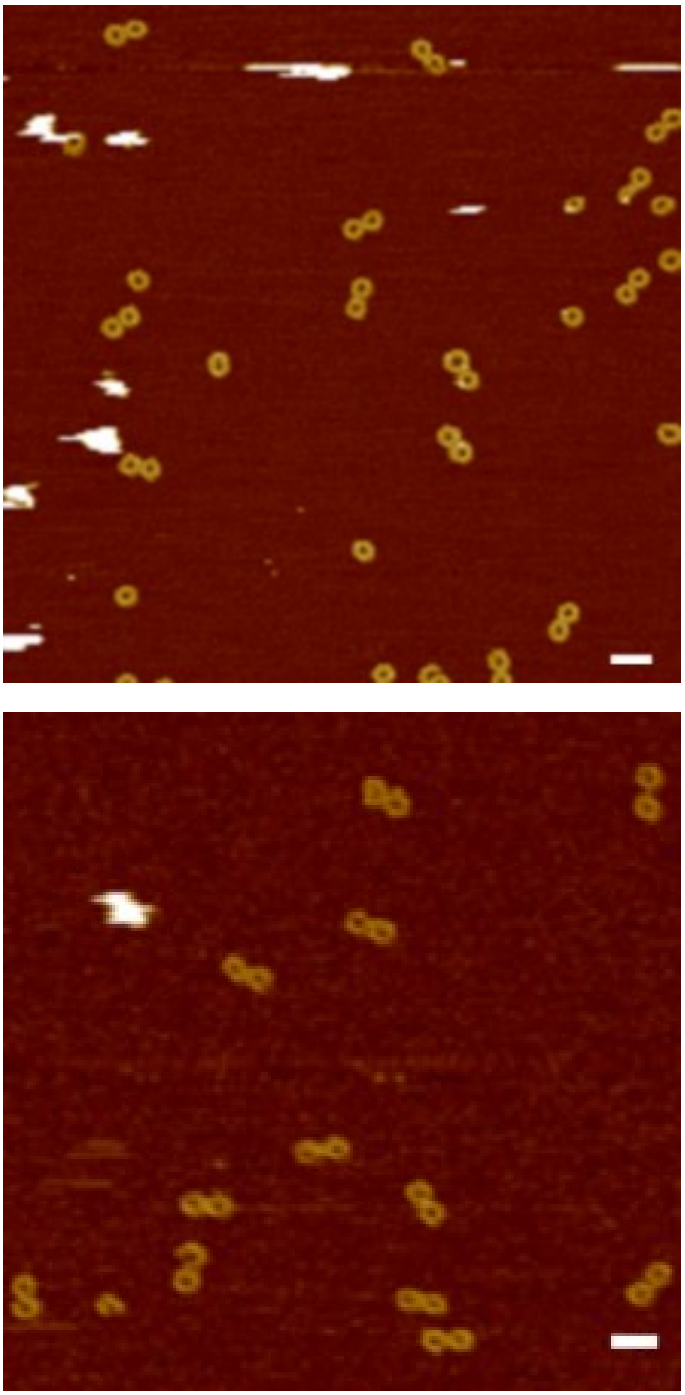

Figure S2. AFM images corresponding to the diluted sample depicted in Figure 1 (B). (3 - fold dilution). The images show that no apparent tetramers are observed, as discussed in the text. Scale bars: 200 nm.

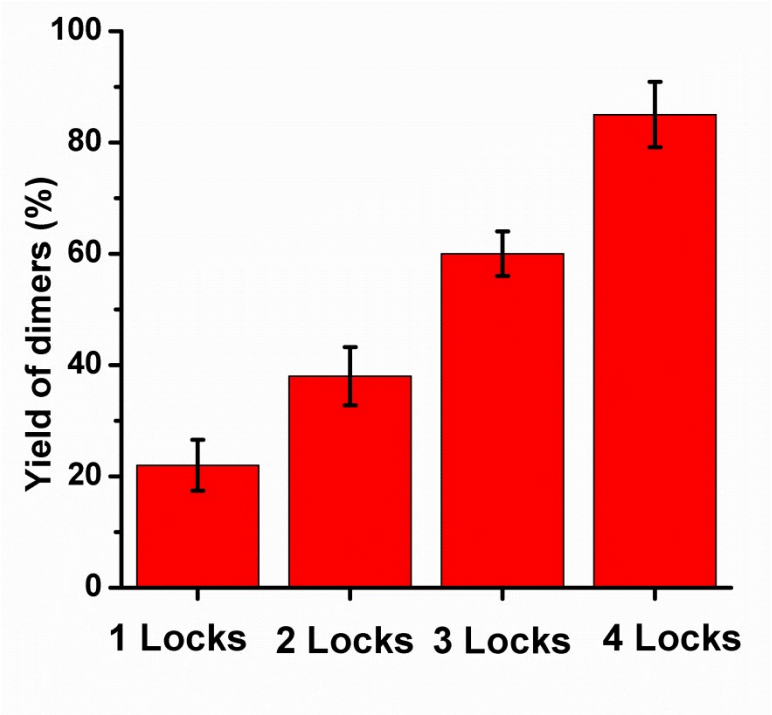

Figure S3. The yields of the origami dimers (T_1-T_2) as a function of the number of duplex crosslinking units (each duplex includes 11 base-pairs).

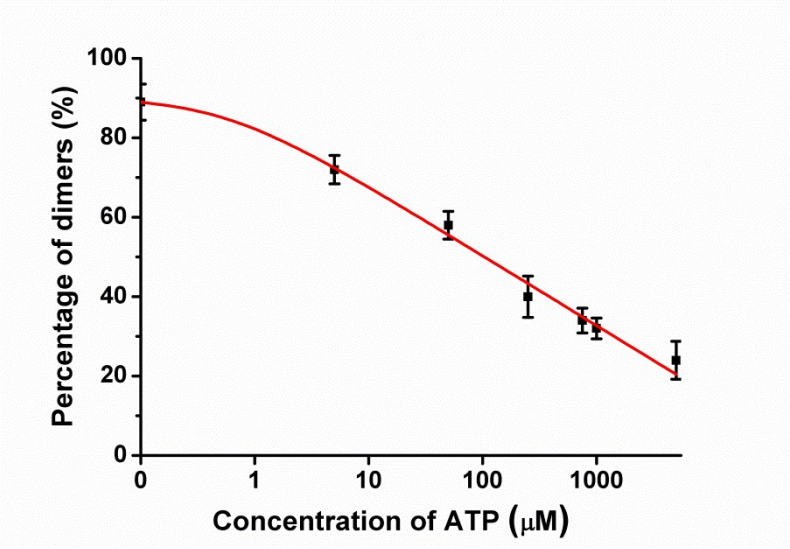

Figure S4. Percentage of AFM-imaged T_1-T_2 dimer structures upon subjecting the T_1-T_2 origami mixture to variable concentrations of ATP, for a fixed time-interval of two hours.

Description	The number of Origami tiles / Proportion		
	Singles	Dimers	In all
Prior to cleavage	30	248/89%	278
After interaction with 5 μM ATP	92	242/72%	334
After interaction with 50 μM ATP	279	392/58%	671
After interaction with 250 μM ATP	200	134/40%	334
After interaction with 750 μM ATP	338	172/34%	510
After interaction with 1 mM ATP	189	88/32%	277
After interaction with 5 mM ATP	186	58/24%	244

Table S1. The detailed analysis of large-area domains: the concentration-dependent (ATP) cleavage of the dimer origami structure T_1-T_2.

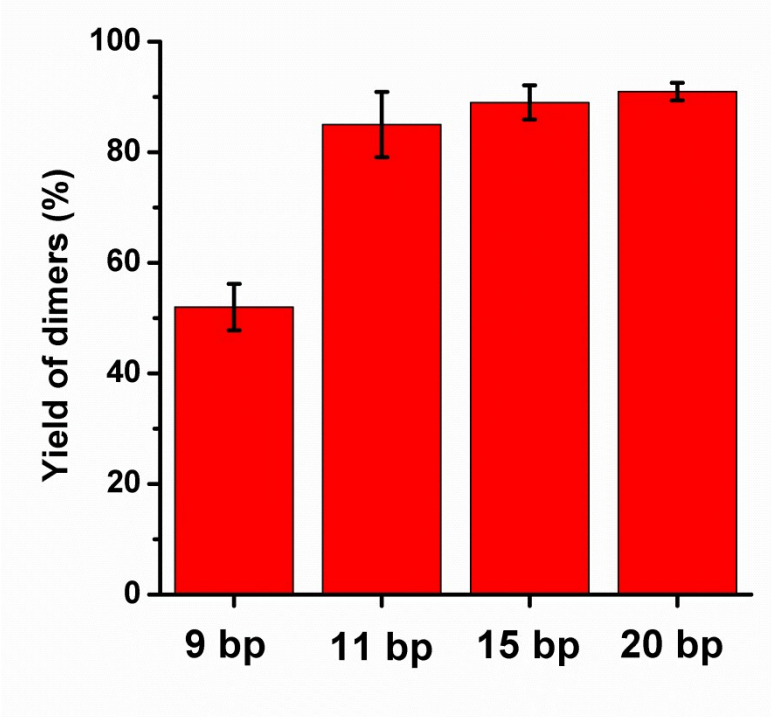

Figure S5. The yields of the origami dimers (T_1-T_2) as a function of the number of base pairs, upon applying four duplex crosslinking bridges.

Description			Origamis Counted
T_3-T_4	Prior to cleavage	Singles	53
		Dimers	340 (87%)
		In all	393
	After interaction with Cocaine	Singles	168
		Dimers	84 (33%)
		In all	252

Figure S6. The detailed analysis of large-area domains: the cocaine-programmed cleavage of the dimer origami structure T_3-T_4.

Description	The number of Origami tiles / Proportion		
	Singles	Dimers	In all
Prior to cleavage	53	340/87%	393
After interaction with 5 μM cocaine	117	238/67%	355
After interaction with 50 μM cocaine	91	134/60%	225
After interaction with 250 μM cocaine	83	94/53%	177
After interaction with 750 μM cocaine	122	104/46%	226
After interaction with 1 mM cocaine	122	92/43%	214
After interaction with 5mM cocaine	168	84/33%	252

Table S2. The detailed analysis of large-area domains: the concentration-dependent (cocaine) cleavage of the dimer origami structure T_3-T_4.

Description	The number of Origami tiles / Proportion						
	T_1-T_5-T_4	T_1-T_5	T_5-T_4	T_1	T_5	T_4	In all
Prior to cleavage	216/80%	16/5.9%	8/3.0%	10/3.7%	7/2.6%	12/4.5%	269
After interaction with ATP	66/19%	28/7.9%	142/40%	66/19%	28/7.9%	24/6.8%	354
After interaction with cocaine	60/19%	120/39%	20/6.5%	23/7.4%	22/7.1%	65/21%	310
After interaction with ATP & cocaine	6/2.8%	24/11%	28/13%	44/20%	53/25%	60/28%	215

Figure S7. The detailed analysis of large-area domains: the ATP or/and cocaine-programmed cleavage of the trimer origami structure T_1-T_5-T_4.

Experimental Section

The DNA origami tiles were assembled in a TAE buffer solution consisting of Tris buffer 20 mM that included acetic acid 20 mM, EDTA 1 mM, magnesium acetate, 12.5 mM, pH = 8.0. Single-stranded M13mp18 phage DNA, 5 nM, (New England Biolabs), was dissolved in the buffer solution, and the short staple strands (unmodified staple strands, functionalized specific edge staple strands and biotinylated staple strands) (Integrated DNA Technologies), 50 nM were added to the M13mp18 buffer solution. The mixture was heated to 95 ˚C in a thermal cycler and then allowed to cool down to 20 ˚C at a rate of 0.1 ˚C/10 seconds. The respective origami-tile samples were purified using 100 kD MWCO centrifuge filters to eliminate the excess of unreacted staple strands.

The respective origami monomers were mixed at the same concentration ratio in 1×TAE/Mg^{2+} buffer to form the corresponding dimer or trimer structures, after heating the mixture to 45 ˚C, and allowing it cooling to 15 ˚C at a rate of 0.1 ˚C/minute for the assembly of the dimers, and at a rate of 0.05 ˚C/minute for the assembly of the origami trimers. The trimer origami structure was purified by electrophoresis and

extracting from the gel using Freeze ´N Squeeze spin columns (BioRad). The separated trimer cut out of the gel is depicted in Figure 6, lane 5.

For the cleavage of the origami dimers or trimers in HEPES/Mg^{2+} buffer solution that included HEPES 20 mM, $MgCl_2$ 12.5 mM, pH = 7.0. ATP or/and cocaine was added to the origami TAE/Mg^{2+} solution, the volume of the origami solution was five – fold diluted by the added HEPES/Mg^{2+} buffer solution. The cleavage was allowed to proceed for 2 hours, at 30 °C. The dissociation yield as a function of ATP/cocaine concentration was probed in HEPES/Mg^{2+} buffer solution, for a time-interval of 2 hours, at 30 °C.

The AFM imaging of the different origami samples was performed using a Multi-mode Nanoscope VIII AFM (Bruker) and DNP-S probes (Bruker). Before imaging, streptavidin solution was added into the origami samples, incubating for 5 minutes. Then, a drop, 2 μl, of the respective origami-tiles was deposited on freshly-cleaned mica, and allowed to adsorb for 5 minutes. Imaging was performed by covering the surface with the TAE/Mg^{2+} buffer solution.

Electrophoretic experiments were performed using 1% agarose gel, subjected to a constant voltage of 80 V at 0 ºC for 1.5 h, in 1×TAE/Mg^{2+} buffer. The gel was stained by SYBR gold to identify the separated bands.

DNA sequences:

Staple Strands for Hexagonal Origami Structure and Modified Staple Strands

A01	ACAGGTCAGAACCAGACCGGAAGCCCGCTTTT
A02	TAGTCAGAATCAGGTCTTTACCCTAAACGGGT
A03	TAGACTGGCAGAGGGGGTAATAGTATTTGTAT
A04	CAGATACATAGGAATACCACATTCCGCATAGG

A05	TTCAAAGCGGATTAGAGAGTACCTTTAATTGC
A06	AATCAAAAAGCAAAGCGGATTGCAATTCGAGC
A07	AGTTTTGCATAGCGTCCAATACTGTGACCATA
A08	TTGAGATTTAACGCCAAAAGGAATGCAAAAGA
A09	CATTGTGAATTACCTTATGCGATTTTCATCAG
A10	ACTTCAAATATCGCGTTTTATCAAAAAG
A11	ATTAAGAGGTTCAGAAAACGAGAACGGAATCG
A12	TCATAAATATAGCGAGAGGCTTTTTACGAGGC
A13	ATAGTAAGATTACAGGTAGAAAGATTAAGAAC
A14	ACAACATTAGCAACACTATCATAAGACGATAA
A15	TGGCTCATTATACCAGTCAGGACGCTAACGGA
A16	GCGGGATCTGCAGGGAGTTAAAGGAAACTCCA
A17	AAAATACGTGAGGAAGTTTCCATTGACTATTA
A18	CATCGCCTACAAAGTACAACGGAGAAAATGTT
A19	CTGGCTGACGGTGTACAGACCAGGAACTAATG
A20	TGGGCTTGAGATGGTTTAATTTCAACTTTAAT
A21	CTGAGGCTGTCACCCTCAGCAGCGACTAAAGA
A22	CTTTTTCATAATGCCACTACGAAGTTATACCA
A23	AGCGCGAAGATAAATTGTGTCGAAAAAGAGGA
A24	CAGATGAACCTTCATCAAGAGTAATAGTAAAT
A25	CTAAAACGTACAGAGGCTTTGAGGAAAGACAGCATCGGAACGAG
A26	CCTGCTCCCTTTGACCCCCAGCGAGCACCAAC
A27	AGAACCGGGAACTGACCAACTTTGATCCGCGA
A28	CCTGACGAGAAACACCAGAACGAGTCTTGACA
A29	ACACTCATATGTTACTTAGCCGGACAATCATA
A30	AGGGAACCATATTCATTACCCAAAAGGCTTGC
B01	ATACCGATGAGGTGAATTTCTTAACCAGTAGC
B02	GCGAATAATAGAAAGGAACAACTAGCGCGTTT
B03	TAGCGTAACATTCCACAGACAGCCCCACCCTC
B04	CACCCTCATAGTACCGCCACCCTCGCGCAGTC
B05	TTGCTTTCAGTTGCGCCGACAATGACAACAAC
B06	AGTGAGAATAATTTTTTCACGTTGTTATCAGC
B07	GCCTGTAGCGATCTAAAGTTTTGTTTCAGCGG
B08	AGGAGGTTGAACCGCCACCCTCAGACTACAAC
B09	GTATTAAGAGGCTGAGACTCCTCACCGTACTC
B10	GAGCCTTTAATTGTATCGGTAAAATCTC
B11	CAAAAAAAAACAACTTTCAACAGTCGTCTTTC
B12	CAGACGTTTTCGTCACCAGTACAAAGCCACCA
B13	CCCTCATTCGGAATAGGTGTATCAAGAGAAGG
B14	GTATAGCCTTCAGGGATAGCAAGCTACCGTAA
B15	ATTAGGATTAGCGGGGTTTTGCTCTGATATAA
B16	ACCATTACAGAGCCAGCAAAATCAACAGCTTG
B17	TCATCGGCTTAGCGTCAGACTGTAAAGGAATT
B18	AGAGCCACGCCACCCTCAGAACCGCTCATAGT

B19	TCTGAATTAAAGCCAGAATGGAAAAGAACCGC
B20	TATTTCGGAACCTATTATTCTGAAACATGAAA
B21	TGGGAATTCATTAGCAAGGCCGGAAGAATCAA
B22	GTTTGCCTATTTTCGGTCATAGCCCGCCTCCC
B23	TCAGAGCCCACCCTCAGAGCCGCCCAAATAAA
B24	TCCTCATTTACCGTTCCAGTAAGCCCCCTGCC
B25	AGCGTTTGCGTAATCAGTAGCGACAACGTCACCAATGAAACCAT
B26	CACCACCAGAGCCACCACCGGAACCCCTTATT
B27	TGGCTTTTCCTTGATATTCACAAAACCAGAAC
B28	AGTGCCCGTATAAACAGTTAATGCGTCATACA
B29	CGGAACCAGAGCCGCCGCCAGCATCAGGTCAG
B30	ACGATTGGGATGATACAGGAGTGTTGAGTAAC
C01	AGGTAAATACATTCAACCGATTGACAACAGTA
C02	GAAACGCAACATAAAGGTGGCAACAGTAATTC
C03	CCAGAAGGTAAGCAGATAGCCGAAACCAATCA
C04	AGGGTAATACTGAACACCCTGAACAAGGCTTA
C05	AAAGGGCGATTGACGGAAATTATTCATTAAAG
C06	AAATACATAAGACACCACGGAATACAAAGACA
C07	AAGAAAAGAAACCGAGGAAACGCAAACGTAGA
C08	GAGAATTATGAGCGCTAATATCAGCCCTTTTT
C09	TTACAAAATAAACAGCCATATTATTTAGACGG
C10	TTCATATGGTTTACCAGCGCAGTTTATT
C11	TTGTCACAACGCAGTATGTTAGCAATAATAAC
C12	GGAATACCAGCTATCTTACCGAAGAGAGATAA
C13	CCCACAAGAAAACAGGGAAGCGCATTATCCCA
C14	ATAACATAAATTGAGTTAAGCCCAACAATGAA
C15	ATCCAAATAAGAAACGATTTTTTGCAGAGAGA
C16	GGGCTTAAGTATAAAGCCAACGCTGGGAGGGA
C17	TGTCCAGATACCGACAAAAGGTAAATATAAAA
C18	ATAATCGGTTACGAGCATGTAGAACAAAGTTA
C19	TCCGGTATAGCAAATCAGATATAGAAAGTCAG
C20	AACGAGCGTCTTTCCAGAGCCTAATTTGCCAG
C21	TCTTACCATTGAGAATCGCCATATATAAGAGA
C22	ATATAAAGCGACGACAATAAACAAAATATCCC
C23	ATCCTAATCTGTCTTTCCTTATCAACCGCGCC
C24	CAATAGCATCTAAGAACGCGAGGCCCAACGCT
C25	GCTAATGCCATTTTCGAGCCAGTATTAACAACGCCAACATGTAA
C26	ACGGGTATCCTGAACAAGAAAAATCATGTTCA
C27	GAACCTCCCATCGTAGGAATCATTTTCCAAGA
C28	GCTACAATTTTATCCTGAATCTTAGTTTTAGC
C29	AGATAAGTTAAACCAAGTACCGCAAAGCCGTT
C30	TTTATTTTCGACTTGCGGGAGGTTTGCACCCA
D01	GAATAAACTGTGATAAATAAGGCGCCACCAGC
D02	AAGACAAAAAATGCTGATGCAAATCCTCAAAT

D03	AGATTAAGTCCTTGAAAACATAGCAATACATT
D04	TTACATTTCAAACATCAAGAAAACTTATCATC
D05	ACCGACCGACCGGAATCATAATTACTAGAAAA
D06	CTATATGTGAACGCGAGAAAACTTTTTGAAAT
D07	CCTTAGAAACGCTGAGAAGAGTCATTATATAA
D08	TGATGAAAAACAATTTCATTTGAATAATTTTC
D09	GAATATACAGTAACAGTACCTTTTAAAGAAGA
D10	TTCTGACCTAAATTTAATGGTTTCAAAT
D11	ATATTTTATCCGGCTTAGGTTGGGATAGTGAA
D12	TTTATCAAAATCGTCGCTATTAATTTACCTTT
D13	TTTAATGGTTCAATTACCTGAGCAACATCGGG
D14	TTATTCATAAACAGTACATAAATCTAACCTTG
D15	AGAAACAATAACGGATTCGCCTGAGAGGCGAA
D16	AGAAGATAAAAAATACCGAACGAATTAAATAA
D17	ATCAAACCGCATCACCTTGCTGAACCAATCGC
D18	TGAGGATTAGAGCCGTCAATAGATGATAGCTT
D19	ATATTCCTACCAGAAGGAGCGGAAAAAATTAA
D20	AATTGCGTAGATTTTCAGGTTTAACGTCAGAT
D21	TCGCCATTAAACAGAGGTGAGGCGAAATGAAA
D22	AATCTAAACTCAATCAATATCTGGTAACAACT
D23	AATAGATTTAGAAGTATTAGACTTGCGGAACA
D24	AAGAAACCGATTATCAGATGATGGAATAAAGA
D25	CAAATCAAGCTGAGAGCCAGCAGCGTCAGTATTAACACCGCCTG
D26	ATTCGACAATATCTTTAGGAGCACTCAGTTGG
D27	CAATATAAGTAACATTATCATTTTTACAAACA
D28	AAAATTATTTGCACGTAAAACAGACAATTCAT
D29	TATCTAAAACTCGTATTAAATCCTAATTTTAA
D30	AAGTTTGATCCTGATTGTTTGGATACCATATC
E01	TCATGGAACAGCCATTGCAACAGGATGCCTGC
E02	CTTCTTTGCGCAAATTAACCGTTGACGAGCCG
E03	ACAGGAGGCGTTAGAATCAGAGCGGCCAACGC
E04	TAGGGCGCGAAGAAAGCGAAAGGAAGGCGAAA
E05	ATTACCGCACAATATTTTTGAATGGCTATTAG
E06	GTCCATCAATTAGTAATAACATCAAGAACAAT
E07	GCTTTCCTCCGATTAAAGGGATTTAAGAGTCT
E08	AAGGAAGGTGGCAAGTGTAGCGGTTATAACGT
E09	GCCCACTACGTGAACCATCACCCATGGCGAGA
E10	CGGCCTTGCTGGTAATATCCCTTGCCTG
E11	AGTAGAAGTGAGGCCACCGAGTAATAGACAGG
E12	AACGGTACTGCTTTGACGAGCACGCACGCTGC
E13	GCGTAACCGGAAAGCCGGCGAACGAATCAAGT
E14	CTTGACGGACCACACCCGCCGCGCGGGCGCGT
E15	TTTTTGGGGTCGAGGTGCCGTAAAATTTAGAG
E16	AGGTCGACCCAGTGCCAAGCTTGCAAAAACGC

E17	GAAGCATACAATTCCACACAACATTAGCAATA
E18	GCGGGGAGCTGCATTAATGAATCGGGAGCTAA
E19	ATCCTGTTGCTGGTTTGCCCCAGCGCGGGCGC
E20	CAAAGGGCGAAAAACCGTCTATCAGGGCGATG
E21	AACGACGGTCTAGAGGATCCCCGGAATTGTTA
E22	TCCGCTCAAAGTGTAAAGCCTGGGAAACCTGT
E23	CGTGCCAGAGGCGGTTTGCGTATTGCAGCAAG
E24	CGGTCCACTGATGGTGGTTCCGAATCCAACGT
E25	TGAGTGAGGCTGTTTCCTGTGTGAGTACCGAGCTCGAATTCGTA
E26	GGGTGGTTCCGCTTTCCAGTCGGGGTGCCTAA
E27	AATCCCTTTGGCCCTGAGAGAGTTGGGCGCCA
E28	AGTCCACTATTAAAGAACGTGGACATCGGCAA
E29	CTCACTGCTTTCTTTTCACCAGTGATTGCCCT
E30	TCACCGCCATAAATCAAAAGAATAGGAACAAG
F01	GGGGATGTCGCTATTACGCCAGCTATGCTGTA
F02	ACCGCTTCTCGCACTCCAGCCAGCTTAGATAC
F03	GCGGATTGTCGGATTCTCCGTGGGCAAAGAAT
F04	TTAAATTTGTTAATATTTTGTTAATTTAAATG
F05	GGCCTCTTGCTGCAAGGCGATTAAGTTGGGTA
F06	CAGGAAGATGGTGCCGGAAACCAGTCGGTGCG
F07	ACAACCCGACCGTAATGGGATAGGATCGGCCT
F08	TTGTAAACTTGTTAAATCAGCTCAAGCGAGTA
F09	TGAGAGTCTGGAGCAAACAAGAGATATTTAAA
F10	GCAACTGTTGGGAAGGGCGAGCAAAGCG
F11	CCATTCGCAGGGGACGACGACAGTTCACGTTG
F12	GTGTAGATATCAACATTAAATGTGTTTTTTAA
F13	CCAATAGGAGATTGTATAAGCAAAATCGATGA
F14	AAACAGGAAACGCCATCAAAAATACCTGTAGC
F15	ACGGTAATCGTAAAACTAGCATGTAGCCCCAA
F16	GCTCAACATTAATTGCTGAATATAGGCGAAAG
F17	ATTTCGCAAGATTTAGTTTGACCATTTCCGGC
F18	TAGCAAAAAATCATACAGGCAAGGAACAAACG
F19	CAATGCCTTAGAACCCTCATATATAATTCGCA
F20	GAGAGATCTACAAAGGCTATCAGGTCATTGCC
F21	CTTAGAGCTGTTTTAAATATGCAAAATTCTGC
F22	GAACGAGTAATGGTCAATAACCTGGCATTAAC
F23	ATCCAATATTAAGCAATAAAGCCTCAAGGATA
F24	AAAATTTTGAGTAATGTGTAGGTACTATTTTT
F25	TATTTTCAATAACAGTTGATTCCCCTAAAGTACGGTGTCTGGAA
F26	AAAGCTAATCTACTAATAGTAGTATTTAGCTA
F27	AAAGGGTGAGCCTTTATTTCAACGCAGAGCAT
F28	ATAAATTAATGCCGGAGAGGGTAGAAGATTCA
F29	GCATCAATATCGGTTGTACCAAAAATACTTTT
F30	GCGGGAGAAGAAAGGCCGGAGACATCTAGCTG

linker AB1	CATCGCCCACGCATAACCGATATATTCGGTCG
linker AB2	GGGATTTTGCTAAGGCTCCAGCAACGGCAAAGAGGCAAAA
linker AB3	CACTGAGTAGTAAATGAATTTTCTACACTAAA
linker AB4	CATGCCAATAGGCAGACGGTACGA
linker AB5	CGTCGAGAGGGTAGTACCAGGCGGATAAGCTCATTCAGTGAATATCAACGTAACAA
linker BC1	GTGAATTATCACCGTCACCGACTTGAGCCATT
linker BC2	AGACTCCTTATTATCAATAGAGCAGCACCCATCTTTTCAT
linker BC3	ATAGCAATCAAAAGAACTGGCATGAAAATCAC
linker BC4	AGAAATAATAAGGGTTGAGGTGAC
linker BC5	TAGCAGCCTTTATTTAACGTCAAAAATGAACGGGGTCAGTGCCTACTGGTAATAAG
linker CD1	AGCCTGTTTAGTATCATATGCGTTATACAAAT
linker CD2	ACCTTTTTAACCGTTAATTTGGCAGAGGAGAACGCGCCTG
linker CD3	CTTCTGTAAATCATAGGTCTGAGATCAACAAT
linker CD4	TGAAAATATATGGAACAAGCCTCA
linker CD5	CAAAATCGCGCATTGCTTTGAATACCAAAGATTAGTTGCTATTTTTGAAGCCTTAA
linker DE1	TCTTTAATGCGCGAACTGATAGCCCTAAAACA
linker DE2	TTTTATAATCAGAACTCAAAAGTGCCACCAGTTGAAAGGA
linker DE3	ACTATGGTGCCAGAATCCTGAGAAAGGAAGGT
linker DE4	TACATTAATGCGACGTTATTTTGC
linker DE5	AGGGAGCCCCCGGCACTAAATCGGAACCGGAAGGGTTAGAACCTTATACTTCTGAA
linker EF1	ACGCCAGGGTTTTCCCAGTCACGACGTTGTAA
linker EF2	TCTGCCAGTTTGCATTCAGGTGGTCATACTAACTCACATT
linker EF3	CAGCTTTCGGGCGCATCGTAACCGGCGTTGCG
linker EF4	CCTTATTCGCGTAACAGCTGAGAC
linker EF5	GATAATCAGAAACAATCATATGTACCCCAGTGTTGTTCCAGTTTGCCCGAGATAGG
linker FA1	TCCTTTTGATAAGAGGTCATTTTTGCGGATGG
linker FA2	ATGCTTTAAACAGAAGCCCGCATTCCATTTTGGGGCGCGA
linker FA3	AAACCAAAATTCATTGAATCCCCCAAAAGGTG
linker FA4	AGACCCCTCGTTACCCTGTAACAT
linker FA5	TAATAAAACGAATTGGGAAGAAAAATCTTATGATATTCAACCGTGTCAAATCACCA
loop 1	CTGACCTGAAAGCGTAAGAATACGTGGCACAG
loop 2	GTAATAAAAGGGACATTCTGGCCAACAGAGAT
loop 3	TTACATTGGCAGATTCACCAGTCACACGACCA
loop 4	ATACCTACATTTTGACGCTCAATCGTCTGAAA
L_1D09	TTGTCCACCTGGGGGAGTATTGCGGAGGAAGGTGTTTTTGAATATACAGTAACAGTACCTTTTAAAGAAGA
L_1D15	TTGTCCACCTGGGGGAGTATTGCGGAGGAAGGTGTTTTTAGAAACAATAACGGATTCGCCTGAGAGGCGAA
L_1D20	TTGTCCACCTGGGGGAGTATTGCGGAGGAAGGTGTTTTTAATTGCGTAGATTTTCAGGTTTAACGTCAGAT
L_1D28	TTGTCCACCTGGGGGAGTATTGCGGAGGAAGGTGTTTTTAAAATTATTTGCACGTAAAACAGACAATTCAT
L_1'A09	CAGGTGGACAATTTTTCATTGTGAATTACCTTATGCGATTTTCATCAG
L_1'A15	CAGGTGGACAATTTTTTGGCTCATTATACCAGTCAGGACGCTAACGGA

L_1'A20	CAGGTGGACAATTTTTTGGGCTTGAGATGGTTTAATTTCAACTTTAAT
L_1'A28	CAGGTGGACAATTTTTCCTGACGAGAAACACCAGAACGAGTCTTGACA
L_2D09	ATCTCGGGAGACAAGGATAAATCCTTCAATGAAGTGGGTCTCCCTTTTTGAATATACAGTAACAGTACCTTTTAAAGAAGA
L_2D15	ATCTCGGGAGACAAGGATAAATCCTTCAATGAAGTGGGTCTCCCTTTTTAGAAACAATAACGGATTCGCCTGAGAGGCGAA
L_2D20	ATCTCGGGAGACAAGGATAAATCCTTCAATGAAGTGGGTCTCCCTTTTTAATTGCGTAGATTTTCAGGTTTAACGTCAGAT
L_2D28	ATCTCGGGAGACAAGGATAAATCCTTCAATGAAGTGGGTCTCCCTTTTTAAAATTATTTGCACGTAAAACAGACAATTCAT
L_2'A09	GTCTCCCGAGATTTTTTCATTGTGAATTACCTTATGCGATTTTCATCAG
L_2'A15	GTCTCCCGAGATTTTTTTGGCTCATTATACCAGTCAGGACGCTAACGGA
L_2'A20	GTCTCCCGAGATTTTTTTGGGCTTGAGATGGTTTAATTTCAACTTTAAT
L_2'A28	GTCTCCCGAGATTTTTTCCTGACGAGAAACACCAGAACGAGTCTTGACA
B03-Biotin	Biotin-TTTTTTAGCGTAACATTCCACAGACAGCCCCACCCTC
C03-Biotin	Biotin-TTTTTCCAGAAGGTAAGCAGATAGCCGAAACCAATCA

L_1'A09-15bp	CCCCCAGGTGGACAATTTTTCATTGTGAATTACCTTATGCGATTTTCATCAG
L_1'A15-15bp	CCCCCAGGTGGACAATTTTTTGGCTCATTATACCAGTCAGGACGCTAACGGA
L_1'A20-15bp	CCCCCAGGTGGACAATTTTTTGGGCTTGAGATGGTTTAATTTCAACTTTAAT
L_1'A28-15bp	CCCCCAGGTGGACAATTTTTCCTGACGAGAAACACCAGAACGAGTCTTGACA
L_1'A09-20bp	ATACTCCCCCAGGTGGACAATTTTTCATTGTGAATTACCTTATGCGATTTTCATCAG
L_1'A15-20bp	ATACTCCCCCAGGTGGACAATTTTTTGGCTCATTATACCAGTCAGGACGCTAACGGA
L_1'A20-20bp	ATACTCCCCCAGGTGGACAATTTTTTGGGCTTGAGATGGTTTAATTTCAACTTTAAT
L_1'A28-20bp	ATACTCCCCCAGGTGGACAATTTTTCCTGACGAGAAACACCAGAACGAGTCTTGACA
L_1'A09-9bp	GGTGGACAATTTTTCATTGTGAATTACCTTATGCGATTTTCATCAG
L_1'A15-9bp	GGTGGACAATTTTTTGGCTCATTATACCAGTCAGGACGCTAACGGA
L_1'A20-9bp	GGTGGACAATTTTTTGGGCTTGAGATGGTTTAATTTCAACTTTAAT
L_1'A28-9bp	GGTGGACAATTTTTCCTGACGAGAAACACCAGAACGAGTCTTGACA

L_1'A-8lock-1	CAGGTGGACAATTTTTATGCGATTTTCATCAG
L_1'A-8lock-2	CAGGTGGACAATTTTTTCAGGACGCTAACGGA
L_1'A-8lock-3	CAGGTGGACAATTTTTTAATTTCAACTTTAAT
L_1'A-8lock-4	CAGGTGGACAATTTTTAGAACGAGTCTTGACA
L_1'A-8lock-5	CAGGTGGACAATTTTTCATTGTGAATTACCTT
L_1'A-8lock-6	CAGGTGGACAATTTTTTGGCTCATTATACCAG
L_1'A-8lock-7	CAGGTGGACAATTTTTTGGGCTTGAGATGGTT
L_1'A-8lock-8	CAGGTGGACAATTTTTCCTGACGAGAAACACC
L_1D-8lock-1	TTGTCCACCTGGGGGAGTATTGCGGAGGAAGGTGTTTTTTACCTTTTAAAGAAGA
L_1D-8lock-2	TTGTCCACCTGGGGGAGTATTGCGGAGGAAGGTGTTTTTTCGCCTGAGAGGCGAA

L_1D-8lock-3	TTGTCCACCTGGGGGAGTATTGCGGAGGAAGGTGTTTTTAGGTTTAACGTCAGAT
L_1D-8lock-4	TTGTCCACCTGGGGGAGTATTGCGGAGGAAGGTGTTTTTAAAACAGACAATTCAT
L_1D-8lock-5	TTGTCCACCTGGGGGAGTATTGCGGAGGAAGGTGTTTTTGAATATACAGTAACAG
L_1D-8lock-6	TTGTCCACCTGGGGGAGTATTGCGGAGGAAGGTGTTTTTAGAAACAATAACGGAT
L_1D-8lock-7	TTGTCCACCTGGGGGAGTATTGCGGAGGAAGGTGTTTTTAATTGCGTAGATTTTC
L_1D-8lock-8	TTGTCCACCTGGGGGAGTATTGCGGAGGAAGGTGTTTTTAAAATTATTTGCACGT