

Supporting Information

Controllable patterning of tannic acid on DNA origami

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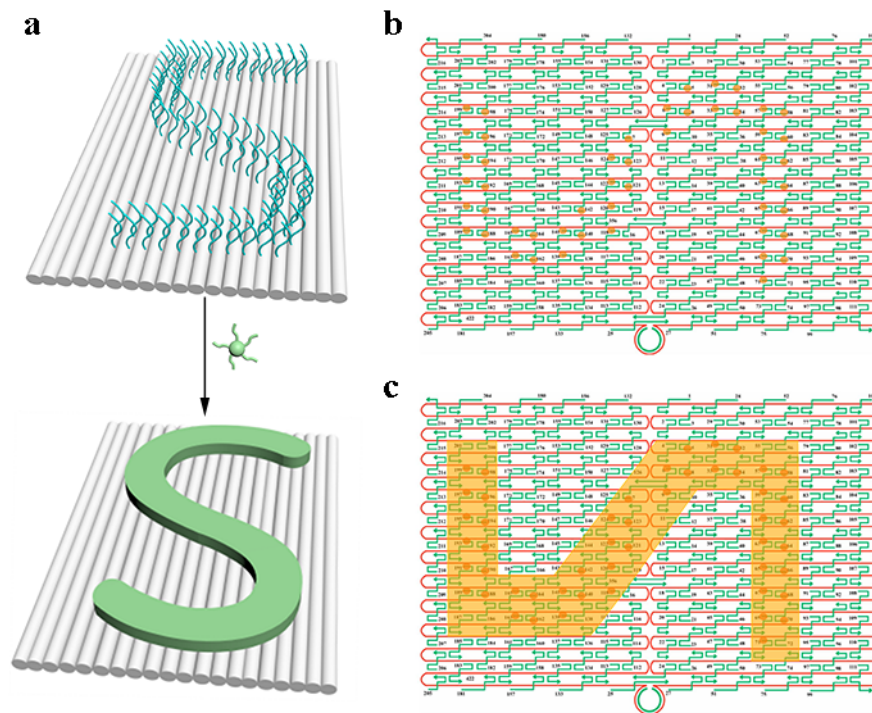
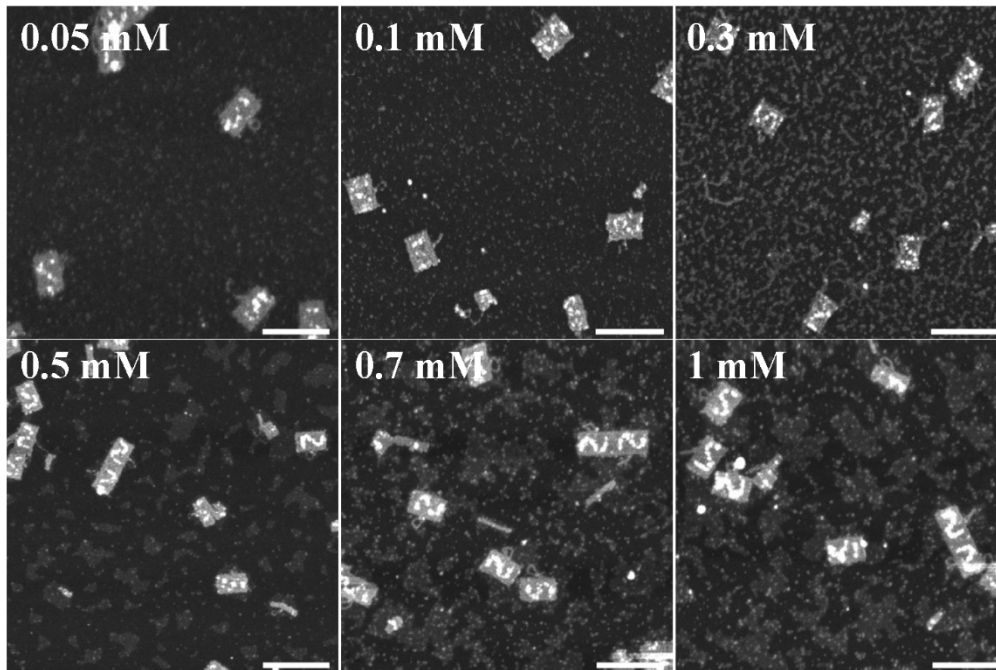


Figure S1. Calculation of theoretical deposition area ratio of TA on DNA origami.¹ (a) Schematic illustration of site-specific controllable patterning of tannic acid on a DNA origami template. (b) Description of calculation method 1: since there are 216 staples in rectangular origami, 50 of them are designed as pcDNA for TA adsorption, therefore, the TA deposition rate is $50/216=23.1\%$. (c) Description of calculation method 2: since the size of the rectangular origami tile is 7000 nm^2 , the TA deposition area is 2065 nm^2 , so the deposition ratio is $2065/7000=29.5\%$.



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Figure S2. Effect of TA concentration on the course of patterning. AFM images of “S” patterns on DNA origami at different TA concentrations. Scale bars: 200 nm.

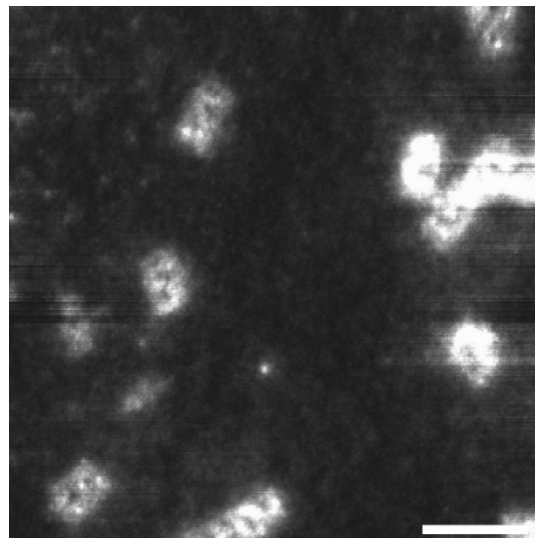


Figure S3. AFM image of “S” pattern on DNA origami at 2 mM TA. TA is adsorbed on the surface of mica to form a thin film, resulting in blurred nanopatterns. Scale bar: 200 nm.

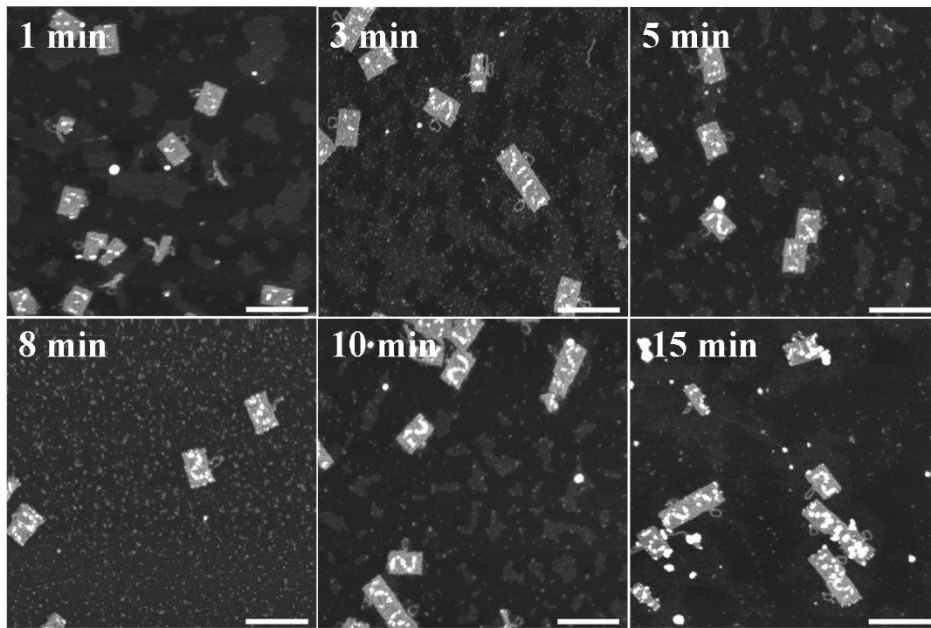


Figure S4. Effect of reaction time on the course of patterning. AFM images of “S” pattern on DNA origami at different reaction times. Scale bars: 200 nm.

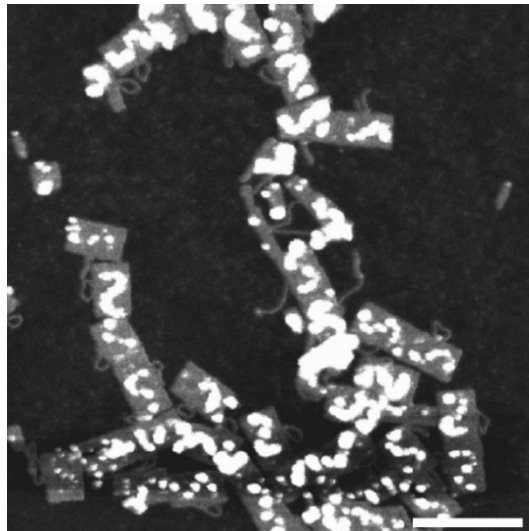


Figure S5. AFM image of the letter “S” on the DNA origami when the reaction time reaches 30 min. When the reaction time is too long, the origami will aggregate and the letter “S” overgrowth. Scale bar: 200 nm.

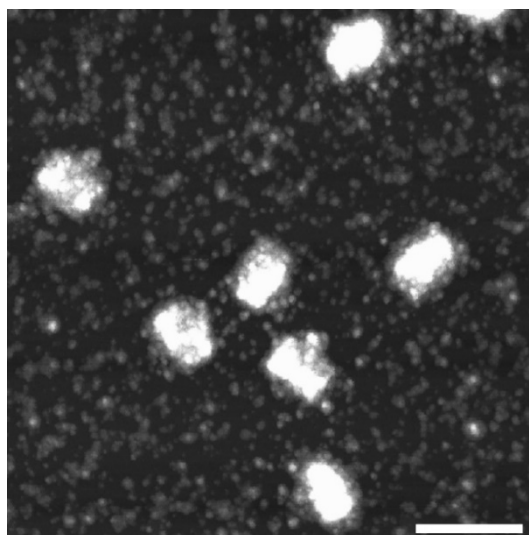


Figure S6. Representative AFM image of the TA pattern growing along the “S” shaped path on DNA origami assisted with Zn^{2+} . Scale bar: 200 nm.

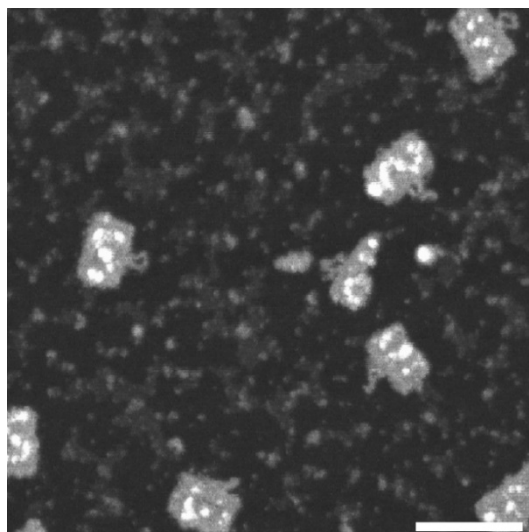


Figure S7. Representative AFM image of the TA pattern growing along the “S” shaped path on DNA origami assisted with Ca^{2+} . Scale bar: 200 nm.

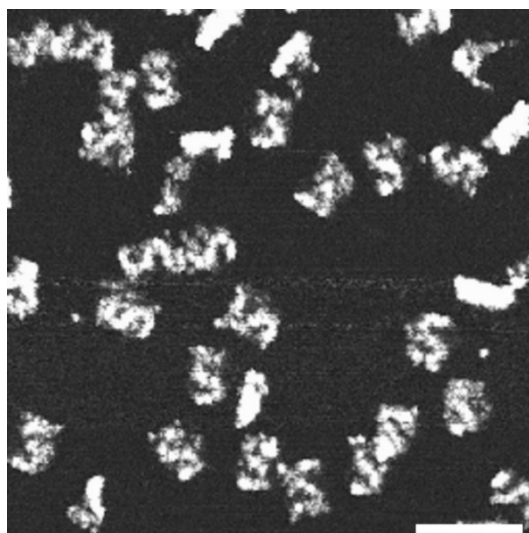


Figure S8. Representative AFM image of the “S” shaped pattern consisting of TA polymers on DNA origami after washing for three times with water. Scale bar: 200 nm.

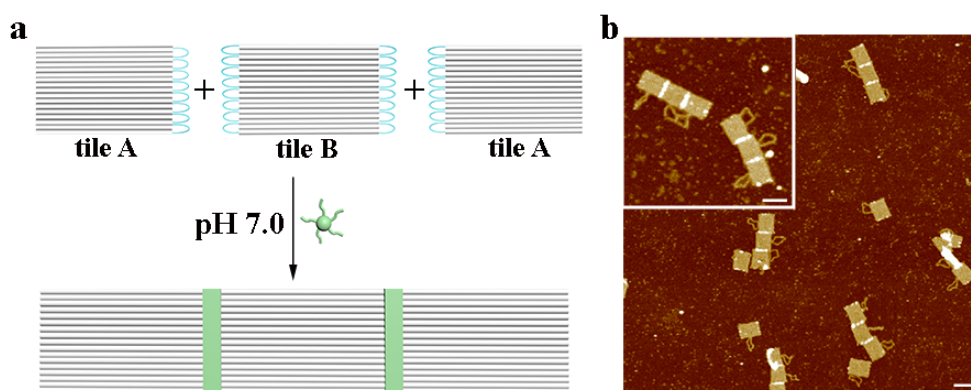


Figure S9. DNA origami trimers assembled by mixing origami tiles A and B at a ratio of 2:1 in the TA solution. (a) Assembly scheme for DNA origami trimers. (b) AFM image of DNA origami trimer. Scale bar: 100 nm.

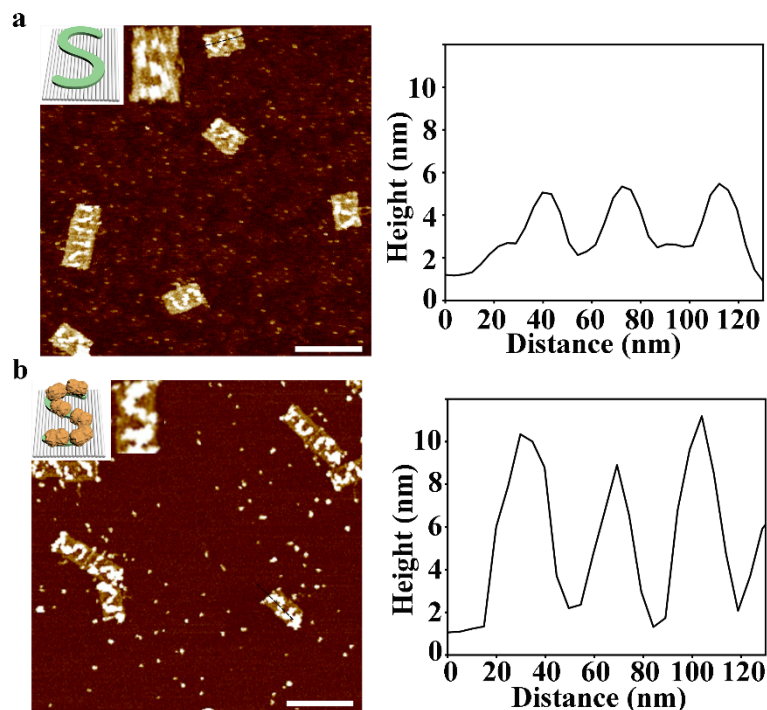


Figure S10. Glucose oxidase molecules adsorption on DNA origami along “S” shaped TA polymers. (a) “S” shaped pattern formed on DNA origami template after TA deposition and the cross-sectional analysis for TA nanopattern from AFM image. (b) The representative AFM image of glucose oxidase deposition on “S” shaped TA pattern and the corresponding cross-sectional analysis. Scale bars: 200 nm.

Table S1. Assembly yield of DNA origami dimers under pH adjustment.

pH	N (dimer)	Y (%)
7.0	0	0
7.0	103	66.4±3.1
5.5	20	17.2±4.5
7.0	97	65.1±4.2

DNA sequences:

For the letter “S” pattern on DNA origami

DNA	Sequences (5'-3')
S-005	CTTGGGTCGTAGACATCGACGACTACTAACCAGAGACCCTCAGAACC GCCAGGGGTCAG
S-006	CTTGGGTCGTAGACATCGACGACTACTTTATTCATAGGGAAGGTAATATTCATT CAGT
S-007	CTTGGGTCGTAGACATCGACGACTACTCATAACCCGAGGCATAGTAAGAGCTTTTAA G
S-008	CTTGGGTCGTAGACATCGACGACTACTATTGAGGGTAAAGGTGAATTATCAATCAC CGG

S-009	CTTGGGTCGTAGACATCGACGACTACTAAAAGTAATATCTTACCGAAGCCCTCCAGAG
S-031	CTTGGGTCGTAGACATCGACGACTACTGCCACCACTCTTTTCATAATCAAACCGTCACC
S-032	CTTGGGTCGTAGACATCGACGACTACTGTTTGCCACCTCAGAGCCGCCACCGATACAGG
S-033	CTTGGGTCGTAGACATCGACGACTACTGACTTGAGAGACAAAAGGGCGACAAGTTACCA
S-034	CTTGGGTCGTAGACATCGACGACTACTAGCGCCAACCATTTGGGAATTAGATTATTAGC
S-057	CTTGGGTCGTAGACATCGACGACTACTAATCACAAATAGAAAATTCATATATAACGGA
S-058	CTTGGGTCGTAGACATCGACGACTACTTACAATCGTAGCACCATTACCATCGTTTTCA
S-059	CTTGGGTCGTAGACATCGACGACTACTATACCCAAGATAACCCACAAGAATAAACGATT
S-060	CTTGGGTCGTAGACATCGACGACTACTATCAGAGAAAGAACTGGCATGATTTTATTTTG
S-061	CTTGGGTCGTAGACATCGACGACTACTTTTTGTTTAAGCCTTAAATCAAGAATCGAGAA
S-062	CTTGGGTCGTAGACATCGACGACTACTAGGTTTTGAACGTCAAAAATGAAAGCGCTAAT
S-063	CTTGGGTCGTAGACATCGACGACTACTCAAGCAAGACGCGCCTGTTTATCAAGAATCGC
S-064	CTTGGGTCGTAGACATCGACGACTACTAATGCAGACCGTTTTTATTTTCATCTTGCGGG
S-065	CTTGGGTCGTAGACATCGACGACTACTCATATTTAGAAATACCGACCGTGTACCTTTT
S-066	CTTGGGTCGTAGACATCGACGACTACTAATGGTTTACAACGCCAACATGTAGTTCAGCT
S-067	CTTGGGTCGTAGACATCGACGACTACTTAACCTCCATATGTGAGTGAATAAACAAAATC
S-068	CTTGGGTCGTAGACATCGACGACTACTAAATCAATGGCTTAGGTTGGGTTACTAAATTT
S-069	CTTGGGTCGTAGACATCGACGACTACTGCGCAGAGATATCAAAATTATTTGACATTATC
S-070	CTTGGGTCGTAGACATCGACGACTACTAACCTACCGCGAATTATTCATTTCCAGTACAT
S-071	CTTGGGTCGTAGACATCGACGACTACTATTTTGCCTTTTAGGAGCACTAAGCAACAGT
S-118	CTTGGGTCGTAGACATCGACGACTACTGTTAAAATTTTAAACCAATAGGAACCCGGCACC
S-120	CTTGGGTCGTAGACATCGACGACTACTAGGTAAAGAAATCACCATCAATATAATATTTT
S-121	CTTGGGTCGTAGACATCGACGACTACTTTTCATTTGGTCAATAACCTGTTTATATCGCG
S-122	CTTGGGTCGTAGACATCGACGACTACTTCGCAAATGGGGCGCGAGCTGAAATAATGTGT
S-123	CTTGGGTCGTAGACATCGACGACTACTTTTTAATTGCCGAAAGACTTCAAAACACTAT
S-124	CTTGGGTCGTAGACATCGACGACTACTAAGAGGAACGAGCTTCAAAGCGAAGATACATT
S-139	CTTGGGTCGTAGACATCGACGACTACTGAAGATCGGTGCGGGCCTCTTCGCAATCATGG
S-140	CTTGGGTCGTAGACATCGACGACTACTAAATAATTTTAAATTGTAAACGTTGATATTCA
S-141	CTTGGGTCGTAGACATCGACGACTACTGCAAATATCGCGTCTGGCCTTCTGGCCTCAG
S-142	CTTGGGTCGTAGACATCGACGACTACTACGTTCTAAATGCAATGCCTGAGAGGTGGCA
S-162	CTTGGGTCGTAGACATCGACGACTACTCAGCTGGCGGACGACGACAGTATCGTAGCCAG
S-163	CTTGGGTCGTAGACATCGACGACTACTGTTTGAGGGAAAGGGGGATGTGCTAGAGGATC
S-164	CTTGGGTCGTAGACATCGACGACTACTCTTTCATCCCCAAAACAGGAAGACCGGAGAG
S-165	CTTGGGTCGTAGACATCGACGACTACTAGAAAAGCAACATTAATGTGAGCATCTGCCA
S-188	CTTGGGTCGTAGACATCGACGACTACTACCGTCGTCATATGTACCCCGGTAAAGGCTA
S-189	CTTGGGTCGTAGACATCGACGACTACTCATGTCAAGATTCTCCGTGGGAACCGTTGGTG
S-190	CTTGGGTCGTAGACATCGACGACTACTCAGGTCACTTTTGCGGGAGAAGCAGAATTAG

S-191	CTTGGGTCGTAGACATCGACGACTACTCTGTAATATTGCCTGAGAGTCTGGAAAAGTCTAG
S-192	CTTGGGTCGTAGACATCGACGACTACTCAAATTAAGTACGGTGTCTGGAAGAGGTCA
S-193	CTTGGGTCGTAGACATCGACGACTACTTGCAACTAAGCAATAAAGCCTCAGTTATGACC
S-194	CTTGGGTCGTAGACATCGACGACTACTTTTTGCGCAGAAAACGAGAATGAATGTTAG
S-195	CTTGGGTCGTAGACATCGACGACTACTAAACAGTTGATGGCTTAGAGCTTATTTAAATA
S-196	CTTGGGTCGTAGACATCGACGACTACTACTGGATAACGGAACAACATTATTACCTTATG
S-197	CTTGGGTCGTAGACATCGACGACTACTACGAACTAGCGTCCAATACTGCGGAATGCTTT
S-198	CTTGGGTCGTAGACATCGACGACTACTCGATTTTAGAGGACAGATGAACGGCGCGACCT
S-199	CTTGGGTCGTAGACATCGACGACTACTTTTAAAAGAACTGGCTCATTATTTAATAAA

Sequences of rectangular origami staple strands

Number	Sequences (5'-3')
001	CAAGCCAATAGGAACCCATGTACAAACAGTT
002	AATGCCCGTAACAGTGCCCGTATCTCCCTCA
003	TGCCTTGACTGCCTATTTTCGGAACAGGGATAG
004	GAGCCGCCCCACCACCGGAACCGCGACGGAAA
005	AACCAGAGACCTCAGAACCGCCAGGGGTCAG
006	TTATTCATAGGGAAGGTAAATATTCATTCAGT
007	CATAACCCGAGGCATAGTAAGAGCTTTTTAAG
008	ATTGAGGGTAAAGGTGAATTATCAATCACCGG
009	AAAAGTAATATCTTACCGAAGCCCTCCAGAG
010	GCAATAGCGCAGATAGCCGAACAATTCAACCG
011	CCTAATTTACGCTAACGAGCGTCTAATCAATA
012	TCTTACCAGCCAGTTACAAAATAAATGAAATA
013	ATCGGCTGCGAGCATGTAGAAACCTATCATAT
014	CTAATTTATCTTTCCTTATCATTATCCTGAA
015	GCGTTATAGAAAAAGCCTGTTTAGAAGGCCGG
016	GCTCATTTCGCATTAAATTTTGGAGCTTAGA
017	AATTACTACAAATTCCTTACCAGTAATCCCATC
018	TTAAGACGTTGAAAACATAGCGATAACAGTAC
019	TAGAATCCCTGAGAAGAGTCAATAGGAATCAT
020	CTTTTACACAGATGAATATACAGTAAACAATT
021	TTTAACGTTCCGGGAGAAACAATAATTTCCCT
022	CGACAATAAGTATTAGACTTTACAATACCGA
023	GGATTTAGCGTATTAATCCTTTGTTTTCAGG
024	ACGAACCAAAACATCGCCATTAATGGTGGTT
025	GAACGTGGCGAGAAAGGAAGGGAACAACTAT

026	TAGCCCTACCAGCAGAAGATAAAAAACATTTGA
027	CGGCCTTGCTGGTAATATCCAGAACGAAGTGA
028	CTCAGAGCCACCACCCTCATTTTCCTATTATT
029	CTGAAACAGGTAATAAGTTTTAACCCCTCAGA
030	AGTGTAAGTAAAGTATTAAGAGGCCGCCACC
031	GCCACCACTCTTTTCATAATCAAACCGTCACC
032	GTTTGCCACCTCAGAGCCGCCACCGATACAGG
033	GACTTGAGAGACAAAAGGGCGACAAGTTACCA
034	AGCGCCAACCATTTGGGAATTAGATTATTAGC
035	GAAGGAAAATAAGAGCAAGAAACAACAGCCAT
036	GCCCAATACCGAGGAAACGCAATAGGTTTACC
037	ATTATTTAACCCAGCTACAATTTTCAAGAACG
038	TATTTTGCTCCAATCCAAATAAGTGAGTTAA
039	GGTATTAAGAACAAGAAAAATAATTAAGCCA
040	TAAGTCCTACCAAGTACCGCACTCTTAGTTGC
041	ACGCTCAAATAAGAATAAACACCGTGAATTT
042	AGGCGTTACAGTAGGGCTTAATTGACAATAGA
043	ATCAAATCGTCGCTATTAATTAACGGATTTCG
044	CTGTAAATCATAGGTCTGAGAGACGATAAATA
045	CCTGATTGAAAGAAATTGCGTAGACCCGAACG
046	ACAGAAATCTTTGAATACCAAGTTCCTTGCTT
047	TTATTAATGCCGTCAATAGATAATCAGAGGTG
048	AGATTAGATTTAAAAGTTTGAGTACACGTAAA
049	AGGCGGTCATTAGTCTTTAATGCGCAATATTA
050	GAATGGCTAGTATTAACACCGCCTCAACTAAT
051	CCGCCAGCCATTGCAACAGGAAAAATATTTTT
052	CCCTCAGAACCGCCACCCTCAGAAGTACTGACT
053	CCTCAAGAATACATGGCTTTTGATAGAACCAC
054	TAAGCGTCGAAGGATTAGGATTAGTACCGCCA
055	CACCAGAGTTCGGTCATAGCCCCGCCAGCAA
056	TCGGCATTCCGCCGCCAGCATTGACGTTCCAG
057	AATCACCAAATAGAAAATTCATATATAACGGA
058	TCACAATCGTAGCACCATTACCATCGTTTTCA
059	ATACCCAAGATAACCCACAAGAATAAACGATT
060	ATCAGAGAAAGAACTGGCATGATTTTATTTTG
061	TTTTGTTAAGCCTTAAATCAAGAATCGAGAA
062	AGGTTTTGAACGTCAAAAATGAAAGCGCTAAT

063	CAAGCAAGACGCGCCTGTTTATCAAGAATCGC
064	AATGCAGACCGTTTTTATTTTCATCTTGCGGG
065	CATATTTAGAAATACCGACCGTGTACCTTTT
066	AATGGTTTACAACGCCAACATGTAGTTCAGCT
067	TAACTCCATATGTGAGTGAATAAACAAAATC
068	AAATCAATGGCTTAGGTTGGGTTACTAAATTT
069	GCGCAGAGATATCAAAATTATTTGACATTATC
070	AACCTACCGCAATTATTCATTTCCAGTACAT
071	ATTTTGCCTCTTAGGAGCACTAAGCAACAGT
072	CTAAATAGAACAAGAAACCACCAGGGTTAG
073	GCCACGCTATACGTGGCACAGACAACGCTCAT
074	GCGTAAGAGAGAGCCAGCAGCAAAAAGGTTAT
075	GGAAATACCTACATTTTGACGCTCACCTGAAA
076	TATCACCGTACTCAGGAGGTTTAGCGGGGTTT
077	TGCTCAGTCAGTCTCTGAATTTACCAGGAGGT
078	GGAAAGCGACCAGGCGGATAAGTGAATAGGTG
079	TGAGGCAGGCGTCAGACTGTAGCGTAGCAAGG
080	TGCCTTTAGTCAGACGATTGGCCTGCCAGAAT
081	CCGAAAACACACCACGGAATAAGTAAGACTCC
082	ACGCAAAGGTCACCAATGAAACCAATCAAGTT
083	TTATTACGGTCAGAGGGTAATTGAATAGCAGC
084	TGAACAAACAGTATGTTAGCAAATAAAAGAA
085	CTTTACAGTTAGCGAACCTCCCGACGTAGGAA
086	GAGGCGTTAGAGAATAACATAAAAGAACACCC
087	TCATTACCCGACAATAAACAACATATTTAGGC
088	CCAGACGAGCGCCCAATAGCAAGCAAGAACGC
089	AGAGGCATAATTTTCATCTTCTGACTATAACTA
090	TTTTAGTTTTTCGAGCCAGTAATAAATTCTGT
091	TATGTAAACCTTTTTTAATGGAAAAATTACCT
092	TTGAATTATGCTGATGCAAATCCACAAATATA
093	GAGCAAAAATTCTGAATAATGGAAGAAGGAG
094	TGGATTATGAAGATGATGAAACAAAATTTTCAT
095	CGGAATTATTGAAAGGAATTGAGGTGAAAAAT
096	ATCAACAGTCATCATATTCCTGATTGATTGTT
097	CTAAAGCAAGATAGAACCCTTCTGAATCGTCT
098	GCCAACAGTCACCTTGCTGAACCTGTTGGCAA
099	GAAATGGATTATTTACATTGGCAGACATTCTG

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101	AGGGTTGATTTTATAAATCCTCATTAAATGATATTC
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104	TACATACATTTTGACGGGAGAATTAACACAGGGAA
105	GCGCATTATTTTGCTTATCCGGTATTCTAAATCAGA
106	TATAGAAGTTTTCGACAAAAGGTAAAGTAGAGAATA
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136	GTGAGCTAGTTTCTGTGTGAAATTTGGGAAG

137	TCATAGCTACTCACATTAATTGCGCCTGAGA
138	GGCGATCGCACTCCAGCCAGCTTTGCCATCAA
139	GAAGATCGGTGCGGGCCTCTTCGCAATCATGG
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162	CAGCTGGCGGACGACGACAGTATCGTAGCCAG
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167	CAACGCAATTTTGGAGAGATCTACTGATAATC
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171	CAAAAATCATTGCTCCTTTTGATAAGTTTCAT
172	TTTGCCAGATCAGTTGAGATTTAGTGGTTTAA
173	AAAGATTCAGGGGGTAATAGTAAACCATAAAT

174	TTTCAACTATAGGCTGGCTGACCTTGTATCAT
175	CCAGGCGCTTAATCATTGTGAATTACAGGTAG
176	CGCCTGATGGAAGTTTCCATTAAACATAACCG
177	TTTCATGAAAATTGTGTCGAAATCTGTACAGA
178	ATATATTCTTTTTTCACGTTGAAAATAGTTAG
179	AATAATAAGGTCGCTGAGGCTTGCAAAGACTT
180	CGTAACGATCTAAAGTTTTGTCGTGAATTGCG
181	ACCCAAATCAAGTTTTTTGGGGTCAAAGAACG
182	TGGACTCCCTTTTCACCAGTGAGACCTGTCGT
183	TGGTTTTTAACGTCAAAGGGCGAAGAACCATC
184	GCCAGCTGCCTGCAGGTCGACTCTGCAAGGCG
185	CTTGATGCATTAATGAATCGGCCCGCCAGGG
186	ATTAAGTTCGCATCGTAACCGTGCAGTAACA
187	TAGATGGGGGGTAACGCCAGGGTTGTCCAAG
188	ACCCGTCGTCATATGTACCCCGGTAAAGGCTA
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190	TCAGGTCACTTTTGCGGGAGAAGCAGAATTAG
191	CTGTAATATTGCCTGAGAGTCTGGAAACTAG
192	CAAAATTAAGTACGGTGTCTGGAAGAGGTCA
193	TGCAACTAAGCAATAAAGCCTCAGTTATGACC
194	TTTTTGCAGAAAACGAGAATGAATGTTTAG
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206	TATCAGGGTTTTCGGTTTGCCTATTGGGAACGCGC
207	GGGAGAGGTTTTTGTAACGACGGCCATTCCCAGT
208	CACGACGTTTTTGTAATGGGATAGGTCAAACGGCG
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211	GCTAAATCTTTTCTGTAGCTCAACATGTATTGCTGA
212	ATATAATGTTTTTCATTGAATCCCCCTCAAATCGTCA
213	TAAATATTTTTTTGGAAGAAAAATCTACGACCAGTCA
214	GGACGTTGTTTTTCATAAGGGAACCGAAAGGCGCAG
215	ACGGTCAATTTTGACAGCATCGGAACGAACCCTCAG
216	CAGCGAAAATTTTACTTTCAACAGTTTCTGGGATTTTGCTAAACTTTT
Loop1	AACATCACTTGCCTGAGTAGAAGAACT
Loop2	TGTAGCAATACTTCTTTGATTAGTAAT
Loop3	AGTCTGTCCATCACGCAAATTAACCGT
Loop4	ATAATCAGTGAGGCCACCGAGTAAAAG
Loop5	ACGCCAGAATCCTGAGAAGTGTTTTT
Loop6	TTAAAGGGATTTTAGACAGGAACGGT
Loop7	AGAGCGGGAGCTAAACAGGAGGCCGA
Loop8	TATAACGTGCTTTCCTCGTTAGAATC
Loop9	GTAATATGGTTGCTTTGACGAGCACG
Loop10	GCGCTTAATGCGCCGCTACAGGGCGC

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