Supplementary Information (SI) for Nanoscale.

Supporting Information for

Self-replication of DNA cross-tile patterns from temperature-selected species

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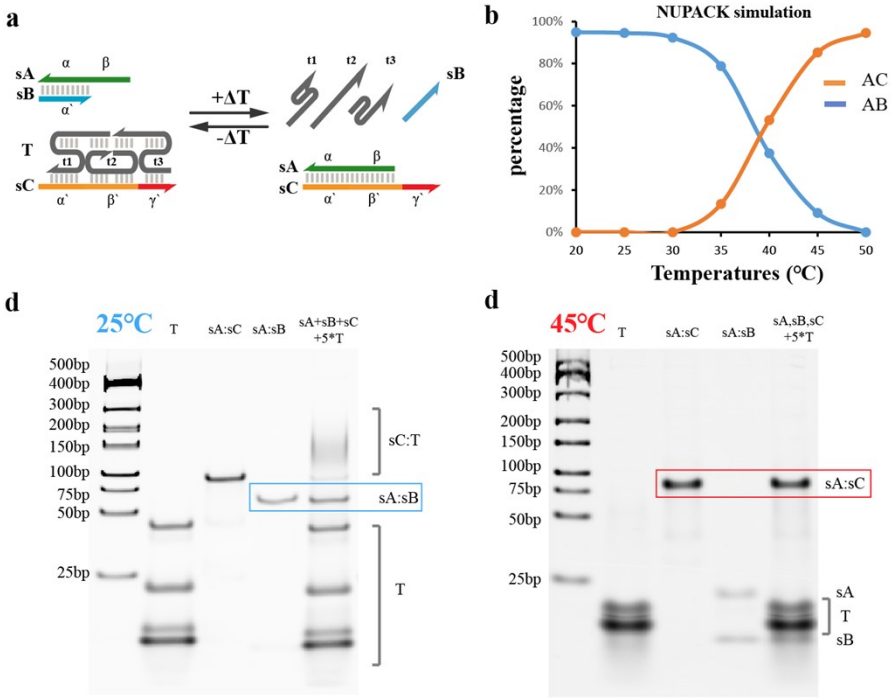

Figure S1. The DNA-based temperature-sensitive module. (a) Schematic of the temperature-dependent associative DNA strand displacement reaction. (b) The percentage of sA:sB vs. sA:sC change with temperature. Data were collected from NUPACK simulations. (c-d) Gel images of the temperature-responsive strand displacement reaction at 25°C (c) and 45°C (d). Notably, the strand sA used in these gels was extended by 15 thymine nucleotides compared to the original sA sequence (see Table S3), enabling differentiation between the sA and T strands on the gels.

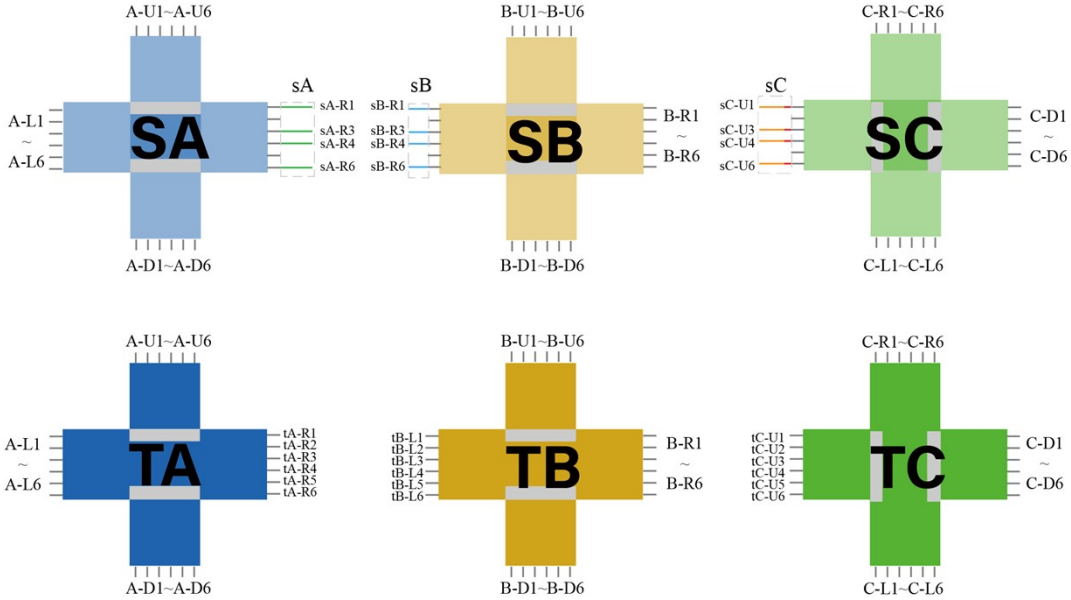

Figure S2. Schematic of origami tiles with labeled names of sticky end sequences. The upper tiles represent parental monomers used for temperature-selective dimer assembly. The temperature-sensitive sequences are located to the right side of tile SA and to the left side of tiles SB and SC. The lower tiles represent offspring monomers that participate in the specific replication induced by temperature-selective dimers.

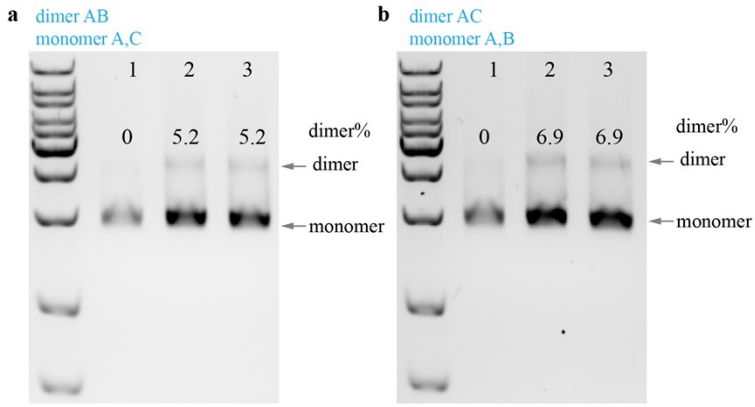

Figure S3. Gel images of one-cycle self-replication of DNA origami system with wrong seed dimer: seed AB: TA: TC (a) or seed AC: TA: TB (b). In Figure S3a, lane 1 contains monomer. Lanes 2-3 contain the mixtures of seed AC and monomers TA, TB before and after replicating, respectively. In Figure S3b, lane 1 contains monomer. Lanes 2-3 contain the mixtures of seed AC and monomers TA, TB before and after replicating, respectively.

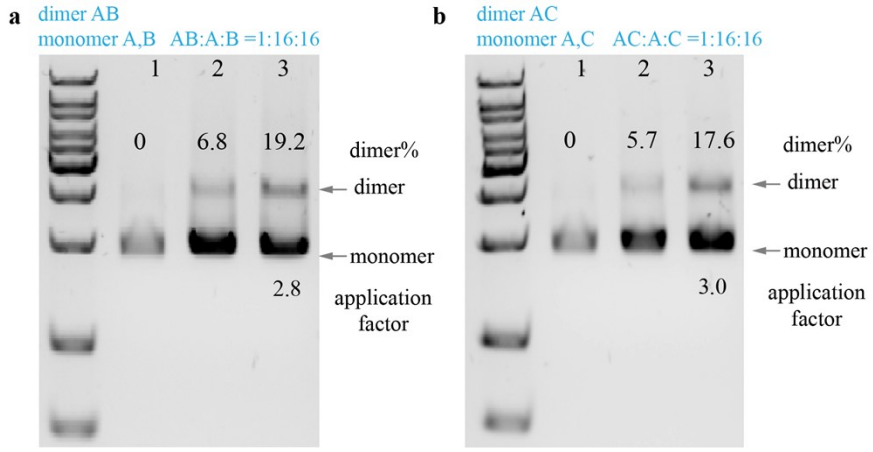

Figure S4. Gel images of one-cycle self-replication of DNA origami seed AB (a) or seed AC (b) for both the ratio of 1:16:16 between seed and monomers. In Figure S4a, lane 1 contains monomer. Lanes 2-3 contain the mixtures of seed AB and monomers TA, TB before and after replicating, respectively. In Figure S4b, lane 1 contains monomer. Lanes 2-3 contain the mixtures of seed AC and monomers TA, TC before and after replicating, respectively.

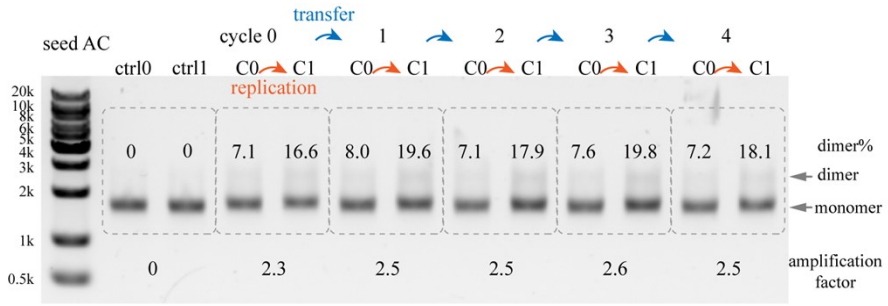

Figure S5. Gel images of five-cycle (cycle 0 to 4) self-replication of DNA origami seed AC using a serial transfer. The symbols ctrl0 and ctrl1 represent the control group before and after one replication cycle. The symbols C0 and C1 represent the beginning and end of each cycle, respectively; C0 to C1 represents the replication step, and C1 to C0 represents the transfer step.

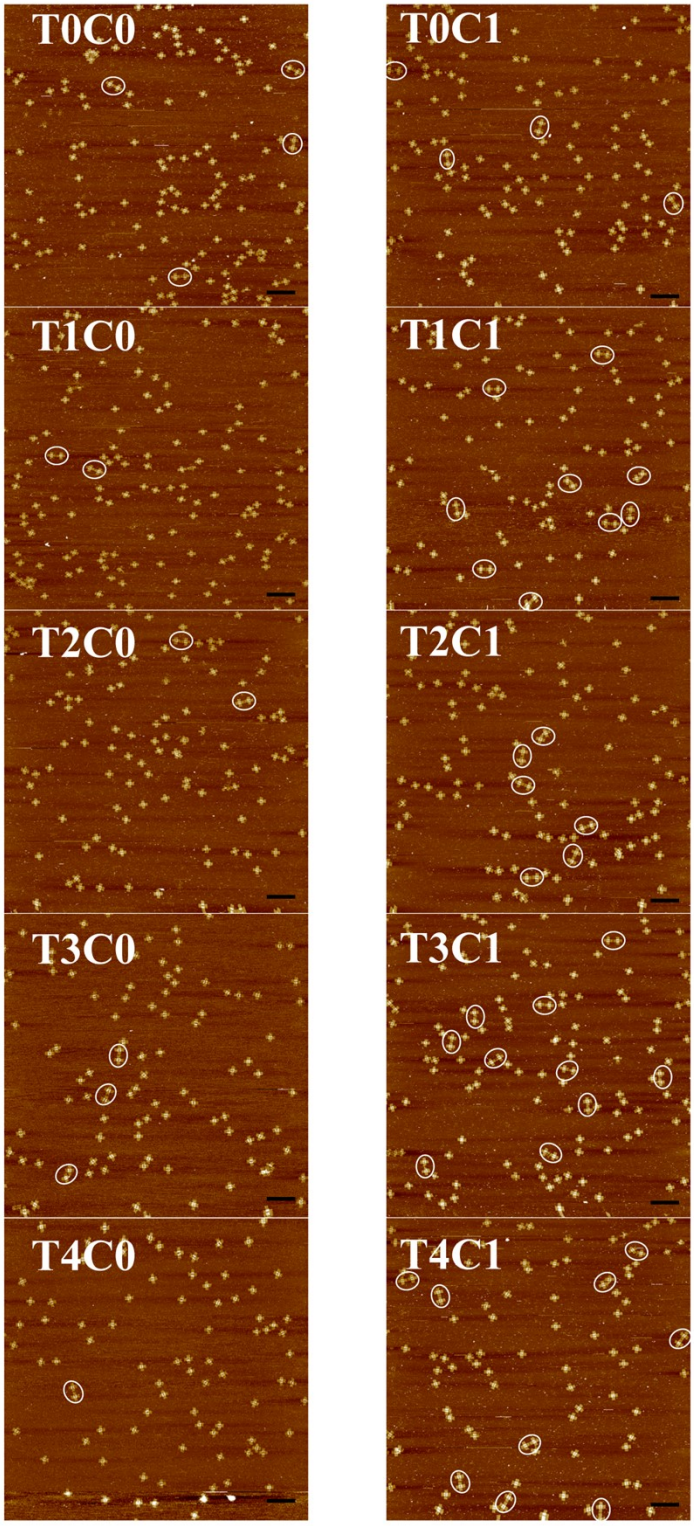

Figure S6. Representative AFM images of self-replication cycling using a ladder design in a serial transfer experiment for a ratio of 1:16:16:16 (seed AB: TA: TB: TC). The white circles represent the origami dimers. Scale bars, 400 nm.

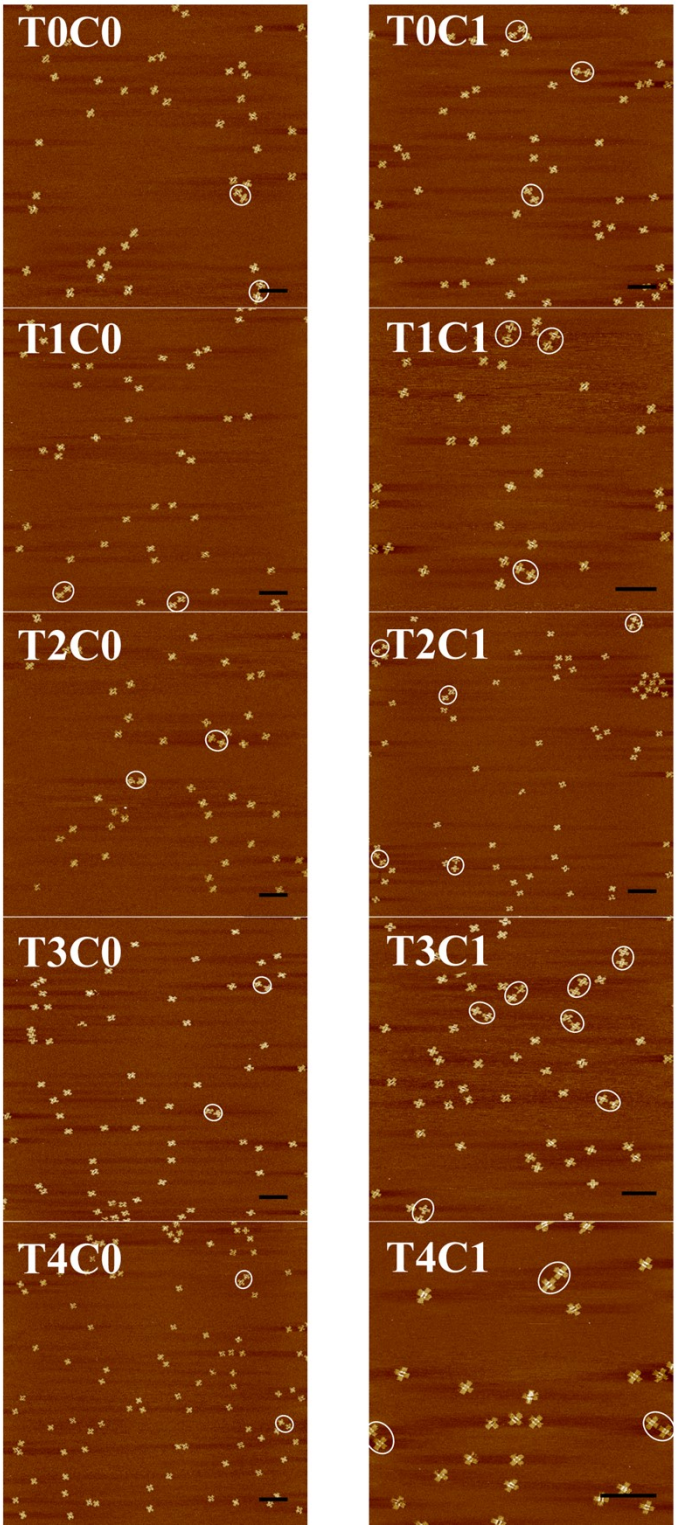

Figure S7. Representative AFM images of self-replication cycling using a ladder design in a serial transfer experiment for a ratio of 1:16:16:16 (seed AC: TA: TB: TC). The white circles represent the origami dimers. Scale bars, 400 nm.

Table S1. AFM counting data for 1:16:16:16 (seed AB: TA: TB: TC)

cycles	Monomer	Dimer AC	AC %	Application factor
T0C0	420	22	5.2	
T0C1	389	50	12.9	2.45
T1C0	356	29	8.1	
T1C1	447	49	11.0	1.35
T2C0	375	18	4.8	
T2C1	329	47	14.3	2.98
T3C0	442	28	6.3	
T3C1	402	55	13.7	2.16
T4C0	398	25	6.3	
T4C1	337	51	15.1	2.41

Table S2. AFM counting data for 1:16:16:16 (seed AC: TA: TB: TC)

cycles	Monomer	Dimer AB	AB %	Application factor
T0C0	397	27	6.8	
T0C1	377	64	17.0	2.50
T1C0	398	19	4.8	
T1C1	412	55	13.3	2.80
T2C0	372	20	5.4	
T2C1	404	44	10.9	2.03
T3C0	442	22	5.0	
T3C1	433	54	12.5	2.51
T4C0	374	19	5.1	
T4C1	391	49	12.5	2.47

Table S3. The sequences of the Thermal Sensitive Module.

sA	TTCGTCACAGATCCCGCAAATT
sB	AATTTGCGGGAT
sC	AATTTGCGGGATCTGTGACGAAACGAAACTGC
T1	GCAGTTTCCGGTCACTTGTGACCGTATGGACG
T2	CGTCCATAGTTTCGTCACAGATCCACCTCCAT
T3	ATGGAGGTCGTGGCTGCTGCCACGCGCAAATT

Table S4. The sequences of DNA origami (corresponding to Figure S2).

ST-1	AGCTAATGCAGAACGCGCCTGTTTTAATATCC
ST-2	CATCCTAATTTGAAGCCTTAAATCTTTTATCC
ST-3	TGAATCTTGAGAGATAACCCACAAAACAATGA
ST-4	AATAGCAATAGATGGGCGCATCGTACCGTATC
ST-5	GGCCTCAGCTTGCATGCCTGCAGGGAATTCGT
ST-6	AATCATGGTGGTTTTTCTTTTCACCCGCCTGG
ST-7	CGCCAGGGTCATAGCTGTTTCCTGGACGGCCA
ST-8	GTGCCAAGGAAGATCGACATCCAGATAGGTTA
ST-9	TAATATCAACCTTCGCTAACGAGCCCGACTTG
ST-10	CGGGAGGTTTTACGAGCATGTAGAACATGTTC
ST-11	AATAATCGCGTTTTAGCGAACCTCGTCTTTCC
ST-12	AGAGCCTACAAAGTCAGAGGGTAAGCCCTTTT
ST-13	TAAGAAAAGATTGACCGTAATGGGCCAGCTTT
ST-14	TGTTATCCGGGAGAGGCGGTTTGCTCCACGCT
ST-15	GGTTTGCCCCAGCAGGCGAAAATCAATCGGCC
ST-16	TTCCCAGTGCTTCTGGTGCCGGAAGTGGGAAC
ST-17	AAACGGCGGTAAGCAGATAGCCGAAACTGAAC
ST-18	ACCCTGAAATTTGCCAGTTACAAATTCTAAGA
ST-19	ACGCGAGGGCTGTCTTTCCTTATCAAGTAATT
ST-20	AATATAAAGTACCGACAAAAGGTAATTCCAAG
ST-21	AACGGGTAGAAGGCTTATCCGGTAATAAACAG
ST-22	CCATATTAATTAGACGGGAGAATTACAAAGTTACC
ST-23	GTCGGATTCTCCACCAGGCA
ST-24	AAGCGCCAATTAAGTTGGGTAACGAACATACG
ST-25	CCTGTCGTGCATAAAGTGTAAAGCGATGTGCT
ST-26	GCAAGGCGTTCGCCATTCAGGCTGCGCAACTG
ST-27	GGAAGCGCTTTATCCCAATCCAAAAAGCAAAT
ST-28	AGGCATTTTCGAGCCAGTACTCATCG
ST-29	AGAACAAGTACCGCGCCCAATAGCTAAGAAAC
ST-30	GATTTTTTACAGAGAGAATAACATAAAAACAG
ST-31	CCTAATGAACTGCCCGCTTTCCAGCCCTTATA
ST-32	TTGCGCTCGTGAGCTAACTCACATGATAGCCC
ST-33	TATTACGCGGCGATCGGTGCGGGCGAGGATTT
ST-34	GGAATCATCAAGCCGTTTTTATTTGTTATATA
ST-35	ACTATATGCTCCGGCTTAGGTTGGTCATCGTA
ST-36	ACCTGAGCAGAGGCGAATTATTCAGAAAATAG
ST-37	AGAAGTATAATAGATAATACATTTCTCTTCGC
ST-38	TAAAACATCTTTAATGCGCGAACTTAATTGCG
ST-39	CTATTAGTCGCCATTAAAAATACCATAGATTA
ST-40	GAGCCGTCTAGACTTTACAAACAATTCGACAA
ST-41	TTTTTAACTAAATGCTGATGCAAAATTGAGAA
ST-42	CAAGACAAAAATCATAGGTCTGAGACAAACAT

ST-43	CAAGAAAAATTGCTTTGAATACCAAGTTACAA
ST-44	CTCGTATTGGTGCACTAACAACTAGAACGAAC
ST-45	TGCTGGTAATATCCAGAACAATATAAGCGTAA
ST-46	GAATACGTGAAGATAAAACAGAGGATCTAAAA
ST-47	TATCTTTAAAATCCTTTGCCCGAACCGCGACCTGC
ST-48	CGAAACAAAGTAATAACGGA
ST-49	TTCGCCTGCAAAATTAATTACATTAATAGTGA
ST-50	ATATGCGTTATACAAATTCTTACCTTTTCAAA
ST-51	TATATTTTGACGCTGAGAAGAGTCTAACAATT
ST-52	TGATTTGATACATCGGGAGAAACACAACGGAG
ST-53	TCAGTATTAACCCTTCTGACCTGATACCGCCA
ST-54	GCCATTGCAACAGGAAAAACGCTCTGGCCAAC
ST-55	AGTAGAAAAGTTTGAGTAACATTA
ST-56	GTACCTTTATTACCTTTTTTAATGCGATAGCT
ST-57	TAGATTAAAGTTAATTCGATCTTCTTAGTATC
ST-58	TCATAATTACTAGAAAAAGCCTGTTGACCTAA
ST-59	ATTTAATGATCCTTGAAAACATAGGAAACAGT
ST-60	CGGAACAATATCTGGTCAGTTGGCGTGCCACG
ST-61	ACCTACATTTTGACGCTCAATCGTCAGTGCGC
ST-62	CGACCAGTCAGCAGCAAATGAAAATCAAACCC
ST-63	TCAATCAAAGAAACCACCAGAAGGATGATGGC
ST-64	AATTCATCAACCATATCAAAATTATAGATTTT
ST-65	CAGGTTTACAATATATGTGAGTGATTAATTTT
ST-66	CCCTTAGAGTTTGAAATACCGACCCACCGGAA
ST-67	ATAAGCAAAAATTCGCGTTAAATTTTTGTTAA
ST-68	CTCATATAAAAGATTCAAAAGGGTAAGATTGT
ST-69	CGAACGAGAAATGGTCAATAACCTTTAGAACC
ST-70	ATAGTCAGGGAAGCCCGAAAGACTCAATTCTG
ST-71	ACCACATTTTACGAGGCATAGTAATGACTATT
ST-72	CAAGAGTAAATCAACGTAACAAAGTTAGGAAT
ST-73	TCAGTGAAGCGCATAGGCTGGCTGACCTTCAT
ST-74	CTATCATAATTCATCAGTTGAGATCTGCTCAT
ST-75	CGCGTTTTAATCAGGTCTTTACCCGAGCAACA
ST-76	ATATTTTCTGTAACAGTTGATTCCTCAAATAT
ST-77	ATCAGCTCAAGCCCCAAAAACAGGGAGAAAGG
ST-78	ATTTCAACAGTCAAATCACCATCACGGTTGAT
ST-79	TCATTCCAATTTGGGGCGCGAGCTAAGCCTTT
ST-80	AAATCAAAAATTCGAGCTTCAAAGTGGAAGTT
ST-81	GTAGAAAGACCCTCGTTTACCAGAATGACCAT
ST-82	CAGACCAGTAAGGCTTGCCCTGACTATTACAG
ST-83	CAGAACGAGAAAGAGGACAGATGAACGGTGTA
ST-84	AAAACCAAACTAACGGAACAACATGAGAACAC
ST-85	AACCGGAAGAGTTCAGAAAACGAGACGACGATA

ST-86	GGCATCAAACTAAAGTACGGTGTCCGAACCAG
ST-87	TTCAACCGAATACTTTTGCGGGAGGAAAAGGT
ST-88	TCAAAAATTCAATCATATGTACCCATATGATA
ST-89	GACCCTGTTTCTAGCTGATAAATTTCGTAAAA
ST-90	AACAGTTAACCAGAGCCGCCGCCAGAACCGCC
ST-91	TAAAACGAAATAGCGAGAGGCTTTCTCAAATG
ST-92	CCAACTTTGTAGTAAATTGGGCTTTACGTTAA
ST-93	CATCCAATGGTGCTGTAGCTCAACATGTTT
ST-94	AGAGGGTAAATCGGTTGTACCAAAAGCATTAA
ST-95	CCAGCTTTAATCGATGAACGGTAAAATGCCGG
ST-96	AACAAGAGCATCAACATTAAATGTGAGCGAGTAACAACTTAAG GAAACCGAGGAAA
ST-97	GTCATAAATTTAATTGCTCCTTTTCTTAATTG
ST-98	AACGAGGCGCAGACGGAACTTTAATCATTGTGTTATACCA
ST-99	GCGCCGACTTTAAGAACTGGCTCAAATTACCT
ST-100	CAACGCCTGATAGCGTCCAATACTTAAAATGT
ST-101	TATTATTCTGCGGATGGCTTAGAGGATAAGAG
ST-102	CCTCAGAGATTAAGCAATAAAGCCGCAAAGAA
ST-103	CGTCACCGGTCATTGCCTGAGAGTCTACAAAG
ST-104	GCTATCAGACTTGAGCCATTTGGGATTATCAC
ST-105	TTAGCAAACCACCACCCTCAGAGCACCGCCAC
ST-106	GTCATTTTTGAAACATGAAAGTATTCGGAACC8
ST-107	TTAGACTGGTAGCATTCCACAGACACAAACTA
ST-108	TATGCGATAATGACAACAACCATCCGATAGTT
ST-109	ATAACCGATCATCTTTGACCCCCAGCGATTATACCAAGTTCATG TTACTTAGCCGG
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ST-111	CCAGCAAAAGCCGCCACCCTCAGACGCCACCA
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ST-115	TAAAACACTATATTCGGTCGCTGATTTCGAGG
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ST-117	AGCAAGGCACCAGAGCCACCACCGGCATTGAC
ST-118	AGACTCCTTTGAGGGAGGGAAGGTTTACCATT
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ST-121	AATTGTATCGTTAGTAAATGAATTCATTTTCA
ST-122	CAACCTAAAAGGCCGCTTTTGCGGGAGCCTTT
ST-123	CCCTCAGCTACGTAATGCCACTACGAAGGCAC
ST-124	GGGATTTTAAAAAGGCTCCAAAAGGATCGTCA
ST-125	CGTCGAGATCAGAGCCACCACCCTTTCTGTAT
ST-126	GATATTCAGTGTACTGGTAATAAGATAAGTGC

ST-127	CGATAGCATTTGCCATCTTTTCATTTGGCCTT
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ST-129	GTTTACCAACATACATAAAGGTGGCAACATAT
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ST-160	AGGAGGTTGCCTTGAGTAACATAATTTAGGCAG
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ST-166	TTCCACACCCAGGGTT
ST-167	CAGCCTTTGTTTAACG
ST-168	TCAAAAATTTTCAATT
ST-169	GGAAGGTTTGAGGCGG
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ST-175	AATCAGAAATTTTTTA
ST-176	ACCAATAGGAACGCCA
ST-177	GAATCCCCTGCAAAAG
ST-178	CCAGAGGGGGTAATAGGCGGAATC
ST-179	TCACCGGACGGAAACG
ST-180	TCACCAATGGCGACAT
ST-181	GGGATAGCGCTCAGTA
ST-182	CCAGGCGGTTTTAACG
sA-R1	TTCGTCACAGATCCCGCAAATTATGCTATTCGGTTAAATAAGAA TAAAGTGTGATAAATAAGGCCGAATAGCAT
sA-R2	TTTTTTTTTTAAATCGTCGCTATTAAATAACCTTGCTTCTGT
sA-R3	TTCGTCACAGATCCCGCAAATTTACGATAAGCAAATAAAGAAA TTGCGTTAGCACGTAAAACAGGCTTATCGTA
sA-R4	TTCGTCACAGATCCCGCAAATTATGCTATTCGTATTCCTGATTA TCAGAGCGGAATTATCATCACGAATAGCAT
sA-R5	TTTTTTTTTTTGCTGAACCTCAAATAATCTAAAGCATCACCT
sA-R6	TTCGTCACAGATCCCGCAAATTTACGATAAGCACATTGGCAGA TTCACCTGAAATGGATTATTTGCTTATCGTA
sB-L1	5P`- AATTTGCGGGATTTTTTTTTTTCCTGAACAAGAAAAAATCAAC AATAGATAAG
sB-L2	TTGCACCCAGCTACAAAAGATTAGTTGCTATT

sB-L3	5P`-AATTTGCGGGATTTTTTTTTTAATAATAAGAGCAAGAGAATTGAGTTAAGCCC
sB-L4	5P`-AATTTGCGGGATTTTTTTTTTGTTTGAGGGGACGACGAACCGTGCATCTGCCA
sB-L5	CCCGGGTACCGAGGTCTCGACTCTAGAGGATC
sB-L6	5P`-AATTTGCGGGATTTTTTTTTTAGCTGATTGCCCTTCACAGTGAGACGGGCAAC
sC-U1	5P`-AATTTGCGGGATCTGTGACGAAACGAAACTGCTTTGAGGACTAAAGACTTTCGGCTACAGAGGCTTT
sC-U2	ACTAAAGGAATTGCGAAGAATAGAAAGGAACA
sC-U3	5P`-AATTTGCGGGATCTGTGACGAAACGAAACTGCTTTGGTTTAGTACCGCCACATCACCGTACTCAGGA
sC-U4	5P`-AATTTGCGGGATCTGTGACGAAACGAAACTGCTTTAATTTACCGTTCCAGTGAAAGCGCAGTCTCTG
sC-U5	TGTAGCGCGTTTTCATGCCTTTAGCGTCAGAC
sC-U6	5P`-AATTTGCGGGATCTGTGACGAAACGAAACTGCTTTAATAAGTTTATTTTGTCGCAAAGACACCACGG
tA-R1	5P`-TGTCGTGGTCAGTTAAATAAGAATAAAGTGTGATAAATAAGGCTGACCACGACAGAGA
tA-R2	5P`-GCGCTTCAATAAAATCGTCGCTATTAAATAACCTTGCTTCTGTTATTGAAGCGCCCTA
tA-R3	5P`-GCCATTCACTTAAATAAAGAAATTGCGTTAGCACGTAAAACAGAAGTGAATGGCCATT
tA-R4	5P`-TGGGTCTTCTTTATTCCTGATTATCAGAGCGGAATTATCATCAAAGAAGACCCACTTC
tA-R5	5P`-TTATTGGCGTTTGCTGAACCTCAAATAATCTAAAGCATCACCTAACGCCAATAAGACT
tA-R6	5P`-GGCTTGTTCGAACATTGGCAGATTCACCTGAAATGGATTATTTTCGAACAAGCCGCCA
tB-L1	TGACCACGACATCCTGAACAAGAAAAAATCAACAATAGATAAGTGTCGTGGTCACTCT

tB-L2	TATTGAAGCGCTTGCACCCAGCTACAAAAGATTAGTTGCTATTGCGCTTCAATATAGG
tB-L3	AAGTGAATGGCAATAATAAGAGCAAGAGAATTGAGTTAAGCCCGCCATTCACTTAATG
tB-L4	AAGAAGACCCAGTTTGAGGGGACGACGAACCGTGCATCTGCCATGGGTCTTCTTGAAG
tB-L5	AACGCCAATAACCCGGGTACCGAGGTCTCGACTCTAGAGGATCTTATTGGCGTTAGTC
tB-L6	TCGAACAAGCCAGCTGATTGCCCTTCACAGTGAGACGGGCAACGGCTTGTTCGAGGCT
tC-U6	TGACCACGACAGAGGACTAAAGACTTTCGGCTACAGAGGCTTTTGTCGTGGTCACTCT
tC-U5	TATTGAAGCGCACTAAAGGAATTGCGAAGAATAGAAAGGAACAGCGCTTCAATATAGG
tC-U4	AAGTGAATGGCGGTTTAGTACCGCCACATCACCGTACTCAGGAGCCATTCACTTAATG
tC-U3	AAGAAGACCCAAATTTACCGTTCCAGTGAAAGCGCAGTCTCTGTGGGTCTTCTTGAAG
tC-U2	AACGCCAATAATGTAGCGCGTTTTCATGCCTTTAGCGTCAGACTTATTGGCGTTAGTC
tC-U1	TCGAACAAGCCAATAAGTTTATTTTGTCGCAAAGACACCACGGGGCTTGTTCGAGGCT
A-U1	TACTCTGAATAAGTTTATTTTGTCGCAAAGACACCACGG
A-U2	CATCCGTTGTAGCGCGTTTTCATGCCTTTAGCGTCAGAC
A-U3	GCACAAGAATTTACCGTTCCAGTGAAAGCGCAGTCTCTG
A-U4	GCATACAGGTTTAGTACCGCCACATCACCGTACTCAGGA
A-U5	GTCGCAAACTAAAGGAATTGCGAAGAATAGAAAGGAACA
A-U6	GAACCAAGAGGACTAAAGACTTTCGGCTACAGAGGCTTT
A-D1	CAGAGTACGTTAATATTTTGTTAATATTTAAATTGTAAA
A-D2	ACGGATGTGAGTAATGTGTAGGTTTTTAAATGCAATGCC
A-D3	CTTGTGCATTAGATACATTTCGCTAGATTTAGTTTGACC
A-D4	TGTATGCATCAAAAAGATTAAGAAAGCAAAGCGGATTGC
A-D5	TTGCGACATAACGCCAAAAGGAACAACTAATGCAGATAC
A-D6	TTGGTTCGGATATTCATTACCCAATCTTCGACAAGAACC
B-U1	GATGGATAATAAGTTTATTTTGTCGCAAAGACACCACGG
B-U2	ACGGTCGTGTAGCGCGTTTTCATGCCTTTAGCGTCAGAC
B-U3	CTCTCAAAATTTACCGTTCCAGTGAAAGCGCAGTCTCTG
B-U4	CATATCAGGTTTAGTACCGCCACATCACCGTACTCAGGA
B-U5	CGTTAGGACTAAAGGAATTGCGAAGAATAGAAAGGAACA
B-U6	TCTTCCGGAGGACTAAAGACTTTCGGCTACAGAGGCTTT
B-D1	ATCCATCCGTTAATATTTTGTTAATATTTAAATTGTAAA
B-D2	CGACCGTTGAGTAATGTGTAGGTTTTTAAATGCAATGCC
B-D3	TTGAGAGATTAGATACATTTCGCTAGATTTAGTTTGACC

B-D4	TGATATGATCAAAAAGATTAAGAAAGCAAAGCGGATTGC
B-D5	CCTAACGATAACGCCAAAAGGAACAACTAATGCAGATAC
B-D6	CGGAAGAGGATATTCATTACCCAATCTTCGACAAGAACC
C-L1	TGCCTACTCCTGAACAAGAAAAAATCAACAATAGATAAG
C-L2	TAGGTAGTTGCACCCAGCTACAAAAGATTAGTTGCTATT
C-L3	ACATACGAATAATAAGAGCAAGAGAATTGAGTTAAGCCC
C-L4	AACTCTCGTTTGAGGGGACGACGAACCGTGCATCTGCCA
C-L5	AACCAAGCCCGGGTACCGAGGTCTCGACTCTAGAGGATC
C-L6	GGATTGCAGCTGATTGCCCTTCACAGTGAGACGGGCAAC
C-R1	GTAGGCAGTTAAATAAGAATAAAGTGTGATAAATAAGGC
C-R2	CTACCTAAAATCGTCGCTATTAAATAACCTTGCTTCTGT
C-R3	CGTATGTAAATAAAGAAATTGCGTTAGCACGTAAAACAG
C-R4	GAGAGTTTATTCCTGATTATCAGAGCGGAATTATCATCA
C-R5	CTTGGTTTGCTGAACCTCAAATAATCTAAAGCATCACCT
C-R6	GCAATCCACATTGGCAGATTCACCTGAAATGGATTATTT
A-L1	TTTTTTCCTGAACAAGAAAAAATCAACAATAGATAAGTTTTT
A-L2	TTTTTTTGCACCCAGCTACAAAAGATTAGTTGCTATTTTTTT
A-L3	TTTTTAATAATAAGAGCAAGAGAATTGAGTTAAGCCCTTTTT
A-L4	TTTTTGTTTGAGGGGACGACGAACCGTGCATCTGCCATTTTT
A-L5	TTTTTCCCGGGTACCGAGGTCTCGACTCTAGAGGATCTTTTT
A-L6	TTTTTAGCTGATTGCCCTTCACAGTGAGACGGGCAACTTTTT
B-R1	TTTTTGTTAAATAAGAATAAAGTGTGATAAATAAGGCTTTTT
B-R2	TTTTTAAATCGTCGCTATTAAATAACCTTGCTTCTGTTTTTT
B-R3	TTTTTAAATAAAGAAATTGCGTTAGCACGTAAAACAGTTTTT
B-R4	TTTTTTATTCCTGATTATCAGAGCGGAATTATCATCATTTTT
B-R5	TTTTTTGCTGAACCTCAAATAATCTAAAGCATCACCTTTTTT
B-R6	TTTTTACATTGGCAGATTCACCTGAAATGGATTATTTTTTTT
C-D1	TTTTTCGTTAATATTTTGTTAATATTTAAATTGTAAATTTTT
C-D2	TTTTTTGAGTAATGTGTAGGTTTTTAAATGCAATGCCTTTTT
C-D3	TTTTTATTAGATACATTTCGCTAGATTTAGTTTGACCTTTTT
C-D4	TTTTTATCAAAAAGATTAAGAAAGCAAAGCGGATTGCTTTTT
C-D5	TTTTTATAACGCCAAAAGGAACAACTAATGCAGATACTTTTT
C-D6	TTTTTGGATATTCATTACCCAATCTTCGACAAGAACCTTTTT