SUPPLEMENTARY INFORMATION FOR

Translation of DNA Signals into Polymer Assembly Instructions

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CONTENTS:

Experimental Methods

This section contains experimental details for procedures that are standard (*S1*), but which have been modified slightly in the work described here.

Device Assembly. The strands were designed using the program *SEQUIN* (*S2*). The component strands of diamonds I, II, III, IV and V (Figure 1b) were dissolved separately to a concentration of 1 μM in a solution containing 40 mM Tris, pH 8.0, 20 mM acetic acid, 2 mM EDTA and 12.5 mM magnesium acetate (TAEMg), and the mixtures were heated to 90 ˚C and cooled slowly to 4 ˚C. Diamonds II and III were then combined, as were diamonds IV and V; these mixtures were heated to 48 ˚C and cooled slowly to 4 ˚C. In the following, diamond I is termed U1, complex II+III is termed U2 and complex IV+V is termed

U3. The component strands of PX1, PX2, DX1, DX2, DX3, DX4, DX5, DX6, DX7, DS1, and DS2 (Figure 1c) were dissolved separately to a concentration of 2 μM in the same solution. These mixtures were heated to 90 ˚C (5 min), and cooled as follows: 65 (30 min), 45˚C (30 min), 37˚C (30 min), 4˚C (30 min). U1, PX1, U2, PX2, and U3 were combined, heated to 40 ˚C and cooled slowly to 4 ˚C.

Setting the Device State. Unset strands were added to the solution and the solution was kept at 20 ˚C 3 hours; the solution was treated with streptavidin beads at 20 ˚C for 30 minutes to remove the set-strand/unset-strand duplexes. At this point the set strands for the target JX_2 or PX states were added to the solution and kept at 20 ˚C for 3 hours to establish the device conformation.

Preparing and Purifying the Assembly Complex. DS1 and DX complexes 1-7 were added to the solution. The mixture was heated with the following thermo-cycling protocol: 35 ˚C (10 min), 33 ˚C (10 min), 30 ˚C (10 min), 25 ˚C (10 min), 20 ˚C (10 min) for 15 cycles. The solution was treated with magnetic streptavidin beads at 20 ˚C 30 minutes to bind devices with an intact left-hand side; failed assemblies are washed away and the solution containing the beads is replaced with a new solution containing 40 mM Tris, pH 8.0, 20 mM acetic acid, 2 mM EDTA, 12.5 mM magnesium acetate, 50 mM potassium acetate and 1 mM DTT. Ten units of Sma I (NEB) were added and the solution was incubated at 20 ˚C for 1 hour to release the target assembly, and the beads then removed from the solution. DS2 was then added, and the solution was incubated at 20 ˚C for 2 hr, followed by magnetic streptavidin bead treatment at 20 ˚C for 30 minutes only those with an intact right-hand side should be bound. The solution was replaced with a new solution containing 40 mM Tris, pH 8.0, 20 mM acetic acid, 2 mM EDTA, 12.5 mM magnesium acetate, 50 mM potassium acetate and 1 mM DTT.

Ten units of Apa I (NEB) were added, and the solution was incubated at 20 ˚C for 1 hour and the magnetic beads were removed.

Ligation and Analysis. The solution was brought to 1 mM in ATP and 10 units of T4 polynucleotide ligase (USB) were added. The ligation proceeded at 16 ˚C for 16 hours. Following ligation, the solution was heated at 90 ˚C for 5 minutes, and the ligation products were purified using 6% denaturing PAGE. The ligation products were sequenced to establish the correct assembly. A few missed or unknown bases are noted in the experimental sequencing, but these are far from the ligation points, and likely represent errors in the sequencing procedure.

REFERENCES

S1. N.C. Seeman, *Current Protocols in Nucleic Acid Chemistry*, Unit 12.1, John Wiley & Sons, New York (2002).

S2. N.C. Seeman, *J. Biomol. Struct. & Dyns.* **8**, 573 (1990).

LEGEND TO FIGURES S1-S3

The components used in this work are shown and the strand numbering is indicated. The coloring is used to aid the eye in distinguishing all strands, and has no further significance. Strands used twice in the same physical unit are labeled with an asterisk.

LEGEND TO FIGS. S4-S7.

These figures show the sequencing traces of the complements to the products in device states PX-PX, PX-JX_2, JX_2-PX and JX_2-JX_2, respectively.

The Sequences of the DNA Strands Used Here (See Figs. S1-S3 for Numbering).

Strand 1:

5’.GATCGGTGCTCATGTGTATGGACGCTACGGGACCGCAGTACGGCACGTTGCTATCGCTCAATGC.3’

Strand 2(2*):

5'.GTACTAGCAGTTTTTTCGCGGTCACACCGTACAGCATTTTTTGTGCATGGCACCGTGCACATGGTCGTCG.3'

Strand 3(3*):

5'.CGTCGTATCTGACGCATGGGACGATGATGGACCTACGATCCGTAGATTGGACTGTTGACCTGTGACCGCGCTGCTAGTACGTCTGTCATC.3'

Strand 4(4*):

5'.GAGATCGCCGAGCGCCGTCACCCATGCGTCTTTTTTAGATACGACGGATGACAGAC.3'

Strand 5(5*):

5'.AACGTGGTCAACAGTGGTGC.3'

Strand 6(6*):

5'.ATCGTGGCATTACCACCATC.3'

Strand 7:

5'.GTCCAGACGGTAGTCTGCTTCAGCCTGGTAATGCCTGACGGCGCTCGGCGATCTCCGTT.3'

Strand 8(8*):

5'.GTGCCGCGCATTTTTTAGTTGGCTCACCAATCTACGTTTTTTGATCGTAGGTGGCTGAAGCAGACTACCGTCTGGAC.3'

Strand 9:

5'.CTACACCCGTAGCGTGGCGT.3'

Strand 10(10*):

5'.GACAATGACGGGCAGTATCCTGTAGACGCCTGCCATGCACTGCTGTACGGACGTTGCACCTGAGCCAACTTGCGCGGCACGGATGTGCGC.3'

Strand 11:

5'.GATCCACGTGCAGCTATGCGGTGGATACTGCCTTTTTTCGTCATTGTCGCGCACATCC.3'

Strand 12:

5'.GTCATAGTTCAGTGTCACGAACGACTGCGTACACGGACAGCGCAGGACTGTCTAGCTCCAGTGGGATC.3'

Strand 13:

5'.CTACACCTGCGCTGTGGCGT.3'

Strand 14:

5'.TAGCACACTGGCGTACGACAGTGGATACTGCCTTTTTTTCGTCATTGTCGCGCACATCC.3'

Strand 15:

5'.GACCAGACGGTAGTCTGCTTCAGCCTGGTAATGCCTGACGGCGCTCGGCGATCTCTAGGC.3'

Strand 16:

5'.GTACTAGCAGTTTTTTCGCGGTCACACCGTACAGCATTTTTTGTGCATGGCACCGACTATGTCGATC.3'

Strand 17:

5'.GTAACATGATTAGCGGATCGACATAGTCGGACAGCGCAGGACACGCTGGCTACCATACATCAGTCAGTGTTCG.3'

Strand 18:

5'.GTATGGTAGCCAGCGTGTGGATACTGCCTTTTTTCGTCATTGTCGCGCACATCC.3'

Strand 19:

5'.GAGTCGACGGTAGTCTGCTTCAGCCTGGTAATGCCTGACGGCGCTCGGCGATCTCCGACC.3'

Strand 20:

5'.GATCGGTGCTCATGTGTATGGACGCTACGGGACCGCAGTACGGCACGTTGCTATCGCTTATGTCTCGAATC.3'

Strand 21:

5'.GACGGTAGTCTGCTTCAGCCTGGTAATGCCTGACGGCGCTCGGCGATCTCCGAAG.3'

Strand 22:

5'.GACACGCATCAGTGTCACGAACGACTGCGTACACGGACAGCGCAGGACTGTCTA
GCTCCAGTGGGATC.3'

Strand 23:

5'.GACGGTAGTCTGCTTCAGCCTGGTAATGCCTGACGGCGCTCGGCGATCTCGAAT
G.3'

Strand 24:

5'.AGCGCATTACTGCCCACGTAGTCTTCGATAACCTGTAAGTATCGCGTGGTCGGTA
CTTTTGTACCTACACCGCGATCCAGA.3'

Strand 25:

5'.GTCGTGCAGTATGGTATTTTTACCAGTCAGGACGACCGTGCGACGCCCTCACAT
CTGGCAACGAGTGTACG.3'

Strand 26:

5'.CGTGGCCTGACATGCGCTCGAACACTGACTGAT.3'

Strand 27:

5'.ATCACTATGACGATTCGGACCATCGTTGACTTA.3'

Strand 28:

5'.CAGGTTGGCGTAGACTAATCAGCAC.3'

Strand 29:

5'.GCTAACTGTGTGAGATCGACGCACG.3'

Strand 30:

5'.CAGGTTATCGAAGACTAGCATGAGC.3'

Strand 31:

5'.AGCCGTACTGTGAGGGCGTCGCACG.3'

Strand 32:

5'.TATTACTGCCCACGGACGGCTCGATTACCTGTAAGTGTCGCGTGGTCGGTACTTT
TGTACCTACACCGCGACTTCGA.3'

Strand 33:

5'.GTCGTGCAGTATGGTATTTTTACCACACAGAACGACCGTGCGCTGCCACTACATC
GAACAACGAGTGTACG.3'

Strand 34:

5'.CGTGGTCTGTGATAACTTGCATTGAGCGA.3'

Strand 35:

5'.ATCTGCGTGTCAGTTCGGACCATCGTTGACTTA.3'

Strand 36:

5'.CAGGTAGGCAGGCCGTCGCCAGACT.3'

Strand 37:

5'.TCGTAGCTTGTAGTATCGACGCACG.3'

Strand 38:

5'.CAGGTAATCGAGCCGTCGGTACTGG.3'

Strand 39:

5'.GGCCAAGTTGTAGTGGCAGCGCACG.3'

Unset Strand for Strand 28:

Biotin.5'.GTGCTGATTAGTCTACGCCAACCTG.3'

Unset Strand for Strand 29:

Biotin.5'.CGTGCGTCGATCTCACACAGTTAGC.3'

Unset Strand for Strand 30:

Biotin.5'.GCTCATGCTAGTCTTCGATAACCTG.3'

Unset Strand for Strand 31:

Biotin.5'.CGTGCGACGCCCTCACAGTACGGCT.3'

Unset Strand for Strand 36:

Biotin.5'.AGTCTGGCGACGGCCTGCCTACCTG.3'

Unset Strand for Strand 37:

Biotin.5'.CGTGCGTCGATACTACAAGCTACGA.3'

Unset Strand for Strand 38:

Biotin.5'.CCAGTACCGACGGCTCGATTACCTG.3'

Unset Strand for Strand 39:

Biotin.5'.CGTGCGCTGCCACTACAACTTGGCC.3'

Strand 40:

5'.GTAGTCGATGTACCACCATGCAGTCTTTTGACTGCATGGACAGCGCAGGACGAT
CAGCCAAGCTACGGTCG.3'

Strand 41:

5'.CTACACCTGCGCTGTGGCGT.3'

Strand 42:

5'.GTAGCTTGGCTGATCGTGGGCCTATACGCACGTACTGACGGCTATCACGCGGTA
TGCCATCATG.3'

Strand 43:

5'.PO_4.CATGATGGCATACCGCGTGATAGCCGTCAGTACGTGCGTATAGGCCCTGTA
GACGCCTGGTACATCGACTAC.3'

Strand 44:

5'.GCACGAACAGTAGATGCGCTAAGCAGATTGCACACATAGTTGCGTCACCGATCA
TCCAGTCGTC.3'

Strand 45:

5'.GACTCGACGACTGGATGATCGGACAGCCGTCTAGCTGGCCGCTTGTCGCGTTAC
CGTATGCAGGACGTACATCGCACCACTGCCTA.3'

Strand 46:

5'.AGCGGCCAGCTAGACGGCTGTGGCGTAGCCATGCTATCACGCTGATGGTCGGC
ATTGACTACACCTGCATACGGTAACGCGA
CA.3'

Strand 47:

5'.AGTGGTGCGATGTACGTGGGCACTCATTACTTGGCAAGGTACTAGGTCCATTCG
CTCAGTTATC.3'

Strand 48:

5'.PO_4.GATAACTGAGCGAATGGACCTAGTACCTTGCCAAGTAATGAGTGCCCTGTAG
TCAATGCCGACCATCAGCGTGATAGCATGGCTACGCCTGACGCAACTATGTGTGCA
ATCTGCTTAGCGCATCTACTGTTCGTGC.3'

Strand 49:5'.

GCACGAACAGTAGATGCGCGGAGCAGTGATGGTCGGCATTGACTACACCGATCAT
CCAGTCGTC.3'

Strand 50:

5'.GACTCGACGACTGGATGATCGGACAGCCGTCTAGCTGGCCTATTGTCGCGTTAC
CGTATGCAGGACGTACATCGCCGGATTAAGCG.3'

Strand 51:

5'.ATAGGCCAGCTAGACGGCTGTGGGCACTCATTACTTGGCAAGATTGCACACATA
GTTGCGTCACCTGCATACGGTAACGCGACA.3'

Strand 52:

5'.AATCCGGCGATGTACGTGGCGTAGCCATGCTATCGTTGGTACTAGGTCCATTCG
CTCAGTTATC.3'

Strand 53:

5'.PO_4.GATAACTGAGCGAATGGACCTAGTACCAACGATAGCATGGCTACGCCTGAC
GCAACTATGTGTGCAATCTTGCCAAGTAATGAGTGCCCTGTAGTCAATGCCGACCA
TCACTGCTCCGCGCATCTACTGTTCGTGC.3'

Strand 54:

5'.GCACGAACAGTAGATGCGCGGAGCAGTGATAAGCGGCAGACACTACACCGATCA
TCCAGTCAAC.3'

Strand 55:

5'.PO_4.TGTTAGCGCCTGACGCAACTATGTGTGCAATCTTGCCAAGTAATTGGTGCCC
TGTAGTGTCTGCCGCTTATCACTGCTCCGCGCATCTACTGTTCGTGC.3'

Strand 56:

5'.TGGTCGTTGACTGGATGATCGGACAGCCGTCTAGCTGGCCTATTGTCGCGTTAC
CGTATGCAGGACGTACATCGCCGGATTCATTC.3'

Strand 57:

5'.ATAGGCCAGCTAGACGGCTGTGGGCACCAATTACTTGGCAAGATTGCACACATA
GTTGCGTCACCTGCATACGGTAACGCGACA.3'

Strand 58:

5'.AATCCGGCGATGTACGTGGCGCTAACA.3'

Strand 59:

5'.GCACGAACAGTAGATGCGCTAAGCAGATTGCACACATAGTTGCGTCACCGATCA
TCCGTTGAAC.3'

Strand 60:

5'.PO_4.ATGAGTGCCCTGTAGTCAATGCCGAGCCTCAGCGTGATAGCATGGCTACGC
CTGACGCAACTATGTGTGCAATCTGCTTAGCGCATCTACTGTTCGTGC.3'

Strand 61:

5'.TGGTCGTTCAACGGATGATCGGACAGCCGTCTAGCTGGCCGCTTGTCGCGTTAC
CGTATGCAGGACGTACATCGCACCAGACTCG.3'

Strand 62:

5'.AGCGGCCAGCTAGACGGCTGTGGCGTAGCCATGCTATCACGCTGAGGCTCGGC
ATTGACTACACCTGCATACGGTAACGCGACA.3'

Strand 63:

5'.TCTGGTGCGATGTACGTGGGCACTCAT.3'

Strand 64:

5'.GCACACATGAGCACGATATTAGCGCAGCGTGAGTCATAGTTGCGTCACCGATCA
TCAGCATCCA.3'

Strand 65:

5'.PO_4.GAATCGACCCTGTAGTGCAATCTACTGCTATACTTGACCGCATGGCTACGCC
TGACGCAACTATGACTCACGCTGCGCTAATATCGTGCTCATGTGTGC.3'

Strand 66:

5'.TGGACTGGATGCTGATGATCGGACAGCCGTCTAGCTGGCCGCTTGTCGCGTTAC
CGTATGCAGGACGTACATCGCACCAGACATTC.3'

Strand 67:

5'.AGCGGCCAGCTAGACGGCTGTGGCGTAGCCATGCGGTCAAGTATAGCAGTAGAT
TGCACTACACCTGCATACGGTAACGCGACA.3'

Strand 68:

5'.TCTGGTGCGATGTACGTGGGTCGATTC.3'

Strand 69:

5'.GCACAATGCGGGTGGATAATGTGAGTGATATGACCATAGTTGCGTCACCGATCATCCGGCATCA.3'

Strand 70:

5'.PO_4.GAGCGTGCCCTGTAGTACCACTGCCAACAGAGGTCGATAGCATGGCTACGCCTGACGCAACTATGGTCATATCACTCACATTATCCACCCGCATTGTGC.3'

Strand 71:

5'.TGGACTGATGCCGGATGATCGGACAGCCGTCTAGCTGGCCGCTTGTCGCGTTACCGTATGCAGGACGTACATCGCACCAGACTTCG.3'

Strand 72:

5'.AGCGGCCAGCTAGACGGCTGTGGCGTAGCCATGCTATCGACCTCTGTTGGCAGTGGTACTACACCTGCATACGGTAACGCGACA.3'

Strand 73:

5'.TCTGGTGCGATGTACGTGGGCACGCTC.3'

Strand 74:

5'.CGACTCACGTACTGCACTACGATCACCCGGGATCGCACCGTCTTT.Biotin.TTT.Biotin.TGACGGTGCGATCCCGGGTGATCGTAGT.3'

Strand 75:

5'.CGCTAATCATGTTACCAGCTATCTACATCGACCGCTCAGCCTGTGTGATGCTGTCAGTCACCATACGCTGCTAGTCCACTGTAC.3'

Strand 76:

5'.GCAGTACGTGAGTCGGTACAGTGGACTAGCAGCGTATGGTGTGACAGCATCACACAGGCTGAGCGGTCGATGTAGATAGCTG.3'

Strand 77:

5'.ACGTTGGATTGGGCCCTGATCGTAGTGTTT.Biotin.TTT.Biotin.TCACTACGATCAGGGCCCAATCCAACGTCGCTAATCATGTTAC.3'

Strand 78:

5'.GTACAGTGGACTAGCAGCGTATGGTGACTGACAGCATCACACAGGCTGAGCGGTCGATGTAGATAGCTGGTAACATGATTAGCG.3'

Strand 79:

5'.CAGCTATCTACATCGACCGCTCAGCCTGTGTGATGCTGTCAGTCACCATACGCTG
CTAGTCCACTGTACGATTCGAGACATAAG.3'

Experimental Sequences of Ligation Products:

PX1-PX2:

5'.TGTTAGCGCCTGACGCAACTATGTGTGCAATCTTGCCAAGTAATTGGTGCCCTGT
AGTGTCTGCCGCTTATCACTGCTCCGCGCATCTACTGTTCGTGCGATAACTGAGCG
AATGGACCTAGTACCTTGCCAAGTAATGAGTGCCCTGTAGTCAATGCCGACCATCA
GCGTGATAGCATGGCTACGCCTGACGCAACTATGTGTGCAATCTGCTTAGCGCATC
TACTGTTCGTGCCATGATGGCATACCGCGTGATAGCCGTCAGTACGTGCGTATAGG
CCCTGTAGACGCCTGGTACATCGACTAC.3'

PX1-$JX_2$2:

5'.ATGAGTGCCCTGTAGTCAATGCCGAGCCTCAGCGTGATAGCATGGCTACGCCTG
ACGCAACTATGTGTGCAATCTGCTTAGCGCATCTACTGTTCGTGCGATAACTGAGC
GAATGGACCTAGTACCTTGCCAAGTAATGAGTGCCCTGTAGTCAATGCCGACCATC
AGCGTGATAGCATGGCTACGCCTGACGCAACTATGTGTGCAATCTGCTTAGCGCAT
CTACTGTTCGTGCCATGATGGCATACCGCGTGATAGCCGTCAGTACGTGCGTATAG
GCCCTGTAGACGCCTGGTACATCGACTAC.3'

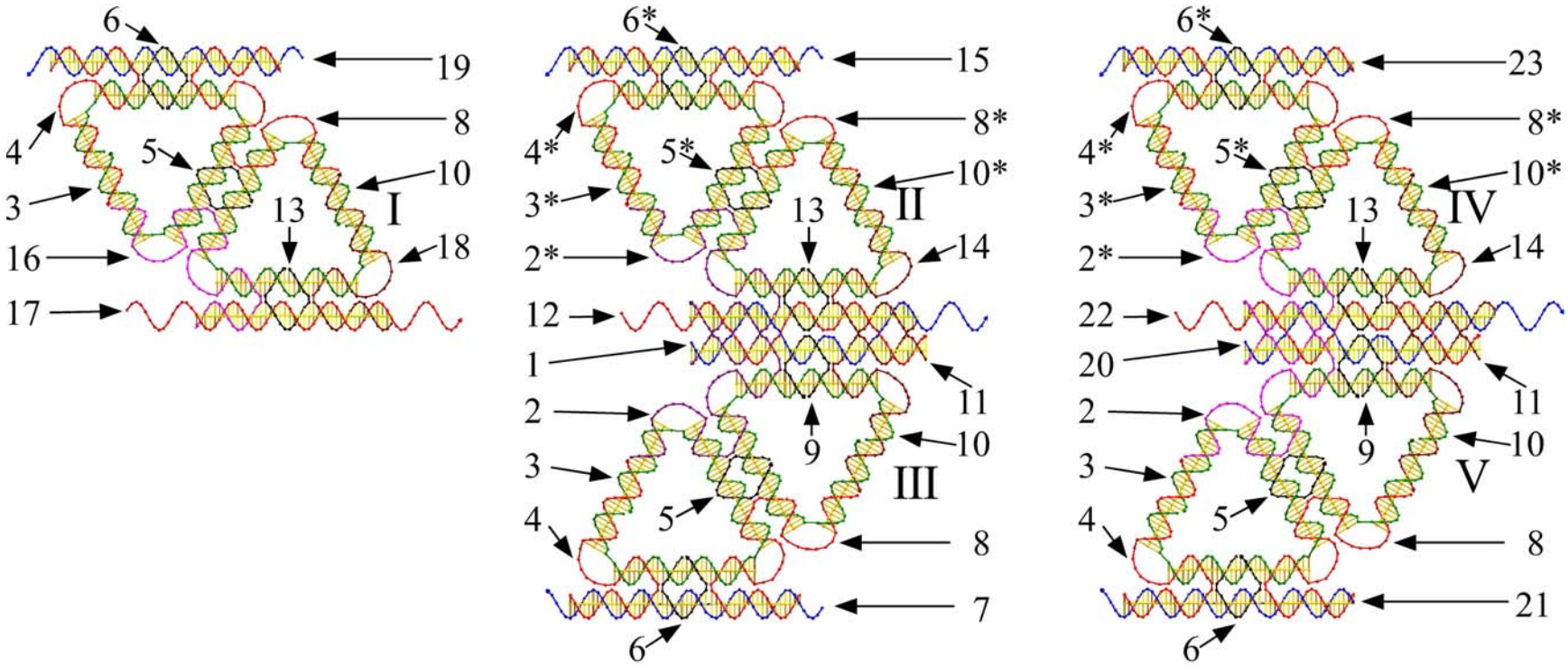
$JX_2$1-PX2:

5'.GAGCGTGCCCTGTAGTACCACTGCCAACAGAGGTCGATAGCATGGCTACGCCTG
ACGCAACTATGGTCATATCACTCACATTATCCACCCGCATTGTGCGATAACTGAGC
GAATGGACCTAGTACCAACGATAGCATGGCTACGCCTGACGCAACTATGTGTGCAA
TCTTGCCAAGTAATGAGTGCCCTGTAGTCAATGCCGACCATCACTGCTCCGCGCAT
CTACTGTTCGTGCATGATGGCATACCGCGTGATAGCCGTCAGTACGTGCGTATAGG
CCCTGTAGACGCCTGGTACATCGACTAC.3'

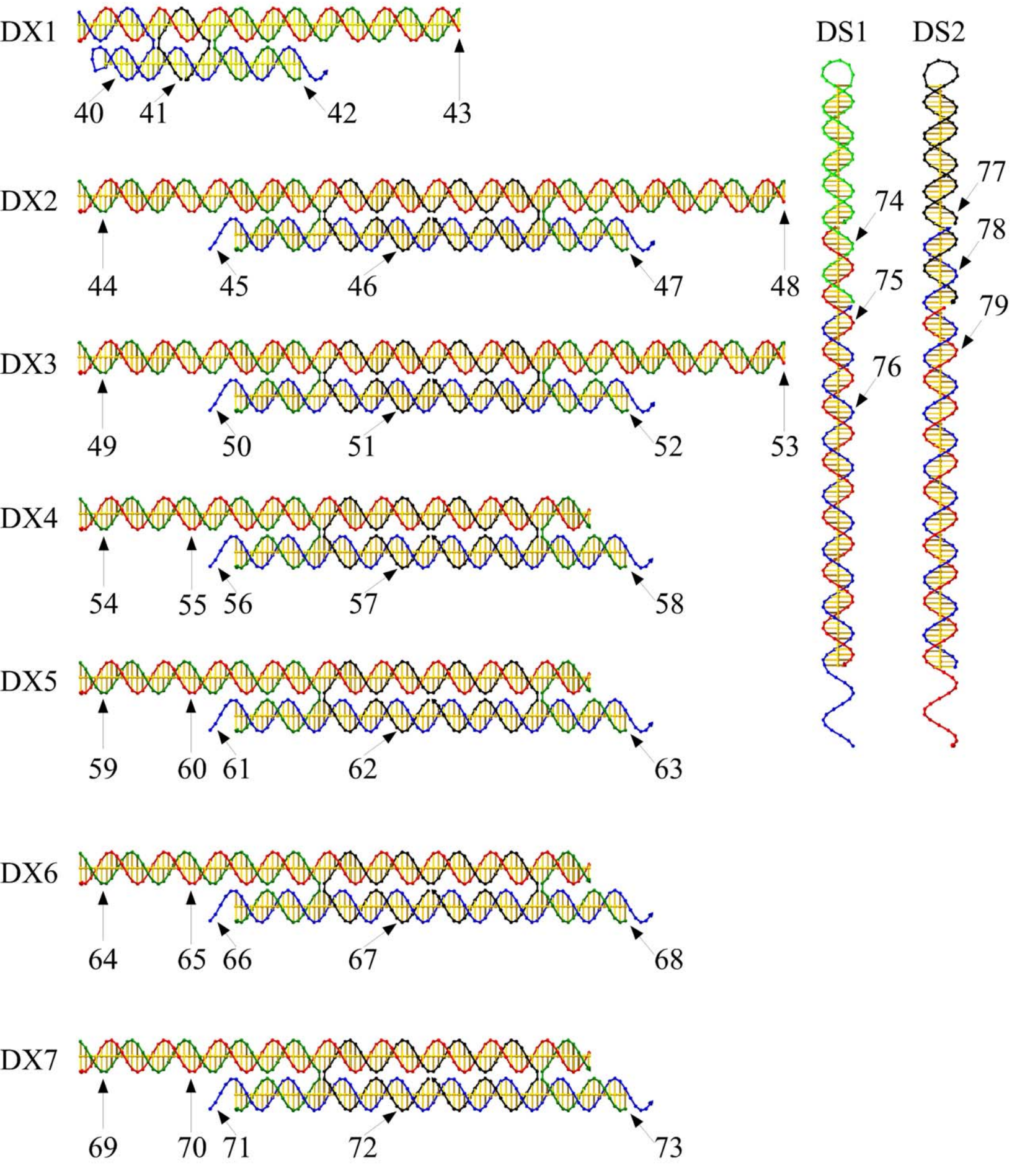
$JX_2$1-$JX_2$2:

5'.GAATCGACCCTGTAGTGCAATCTACTGCTATACTTGACCGCATGGCTACGCCTGA
CGCAACTATGACTCACGCTGCGCTAATATCGTGCTCATGTGTGCGATAACTGAGCG
AATGGACCTAGTACCAACGATAGCATGGCTACGCCTGACGCAACTATGTGTGCAAT
CTTGCCAAGTAATGAGTGCCCTGTAGTCAATGCCGACCATCACTGCTCCGCGCATC
TACTGTTCGTGCCATGATGGCATACCGCGTGATAGCCGTCAGTACGTGCGTATAGG
CCCTGTAGACGCCTGGTACATCGACTAC.3'

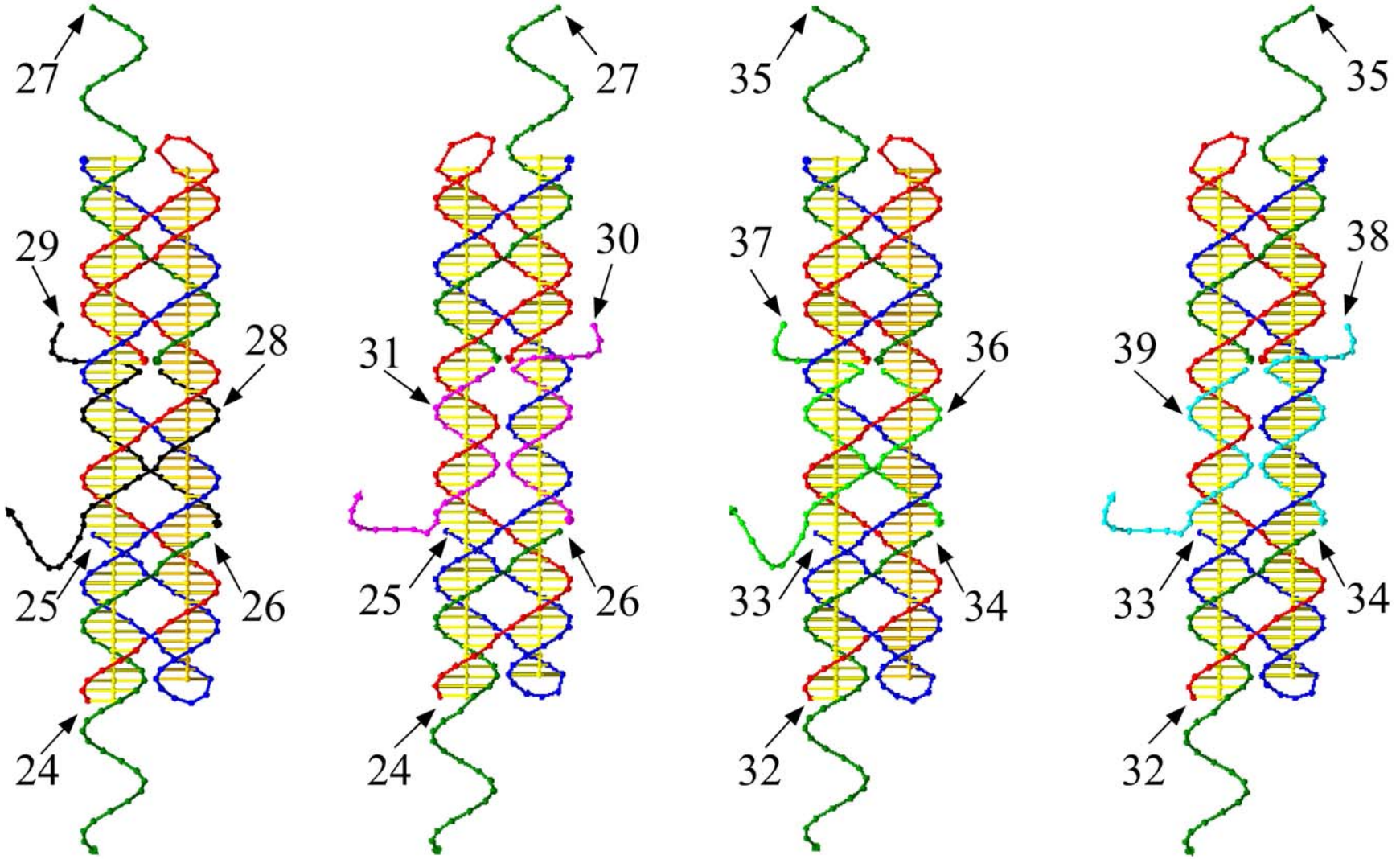
Strand Numbering for Diamond Components



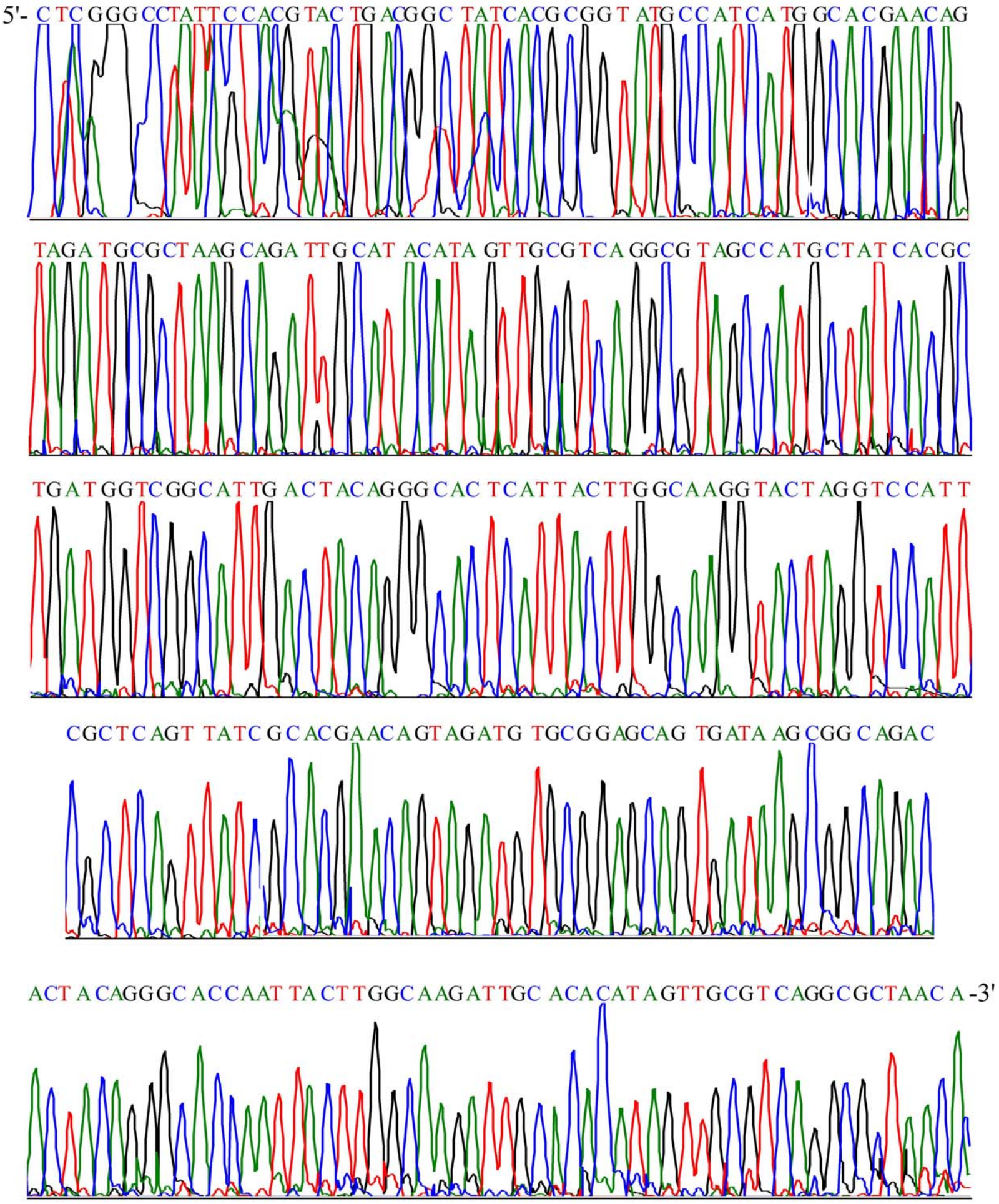
Strand Numbering for DX and DS Components



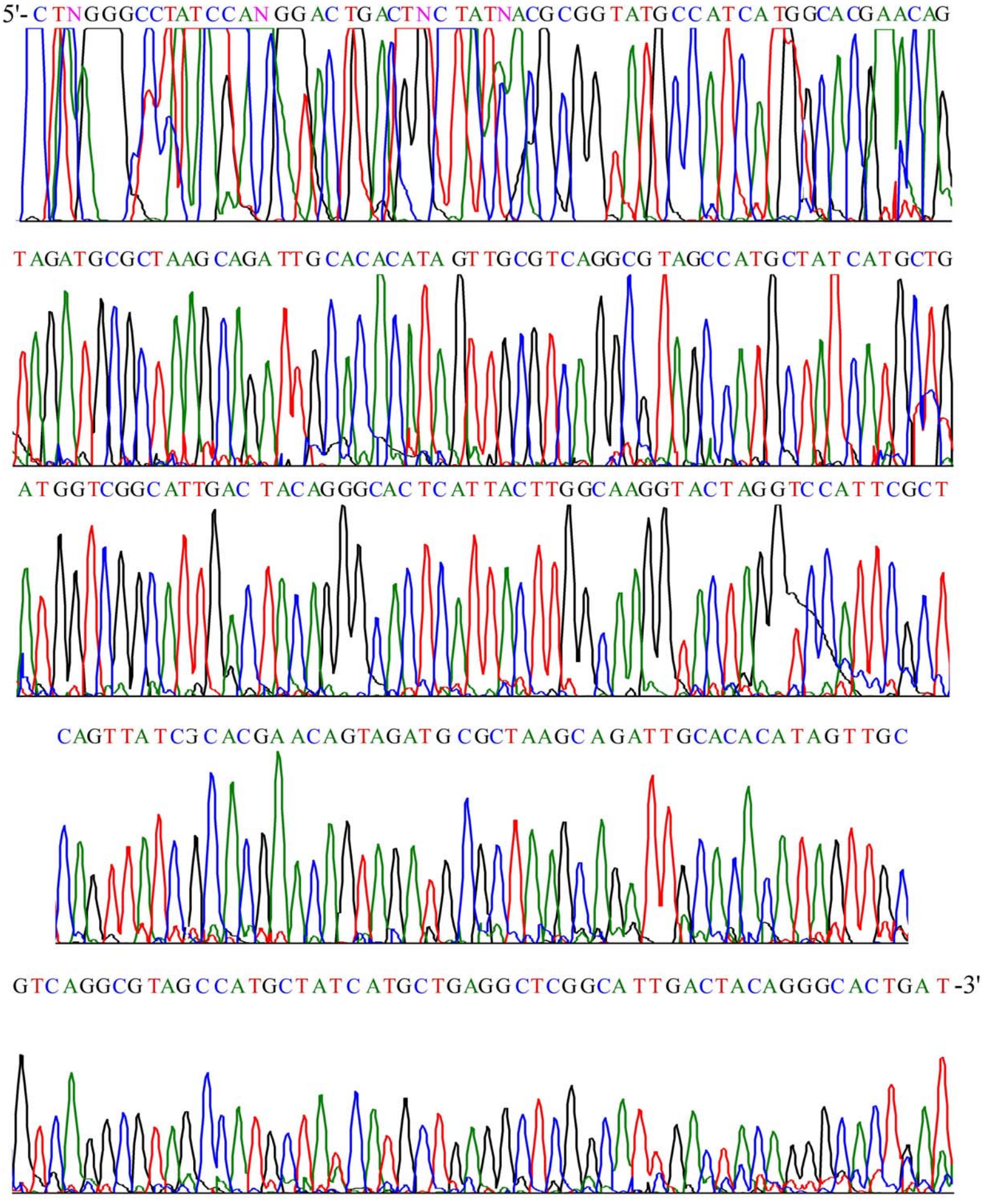
Strand Numbering for Devices (in Both States)



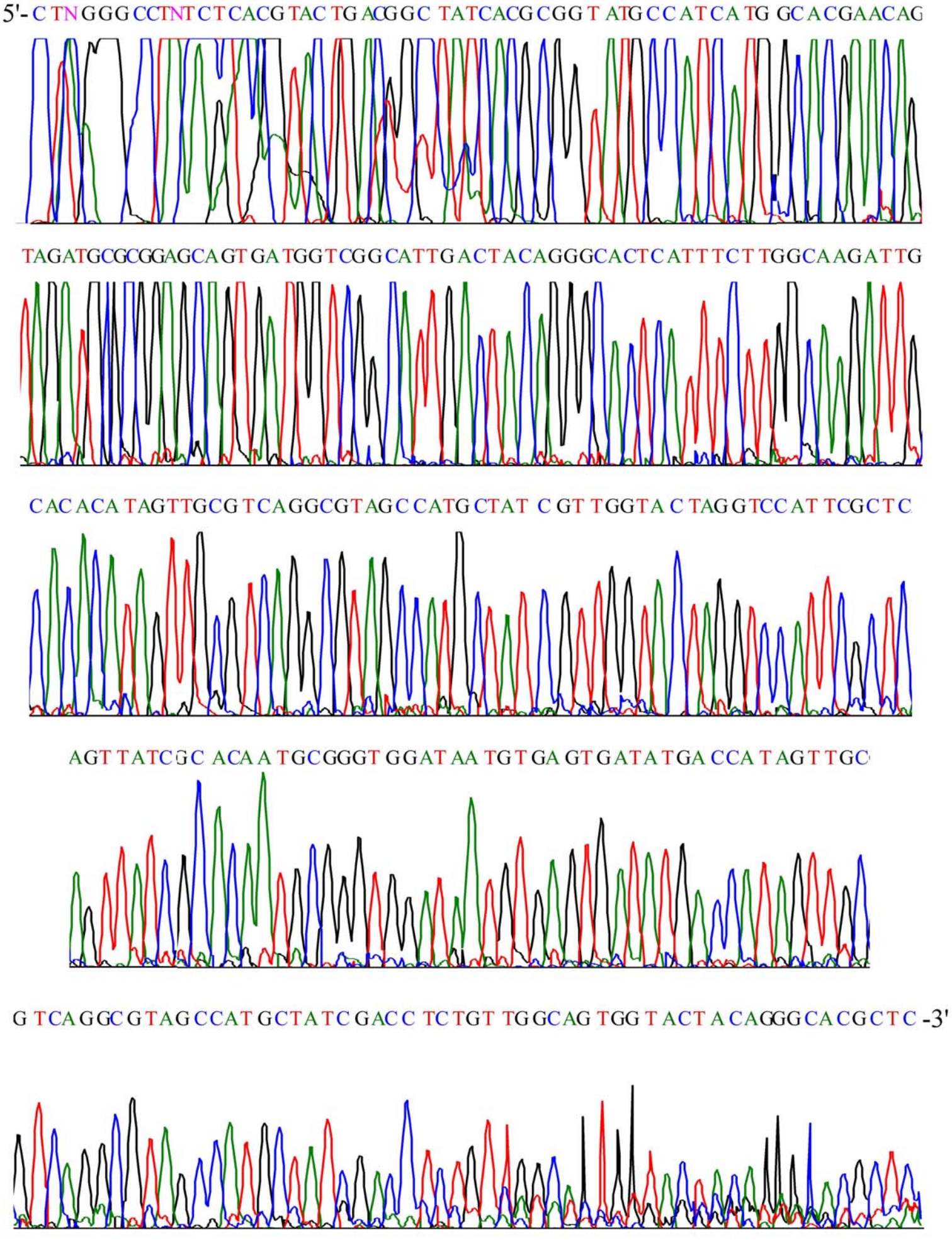
PX1 JX2 1 PX2 JX2 2



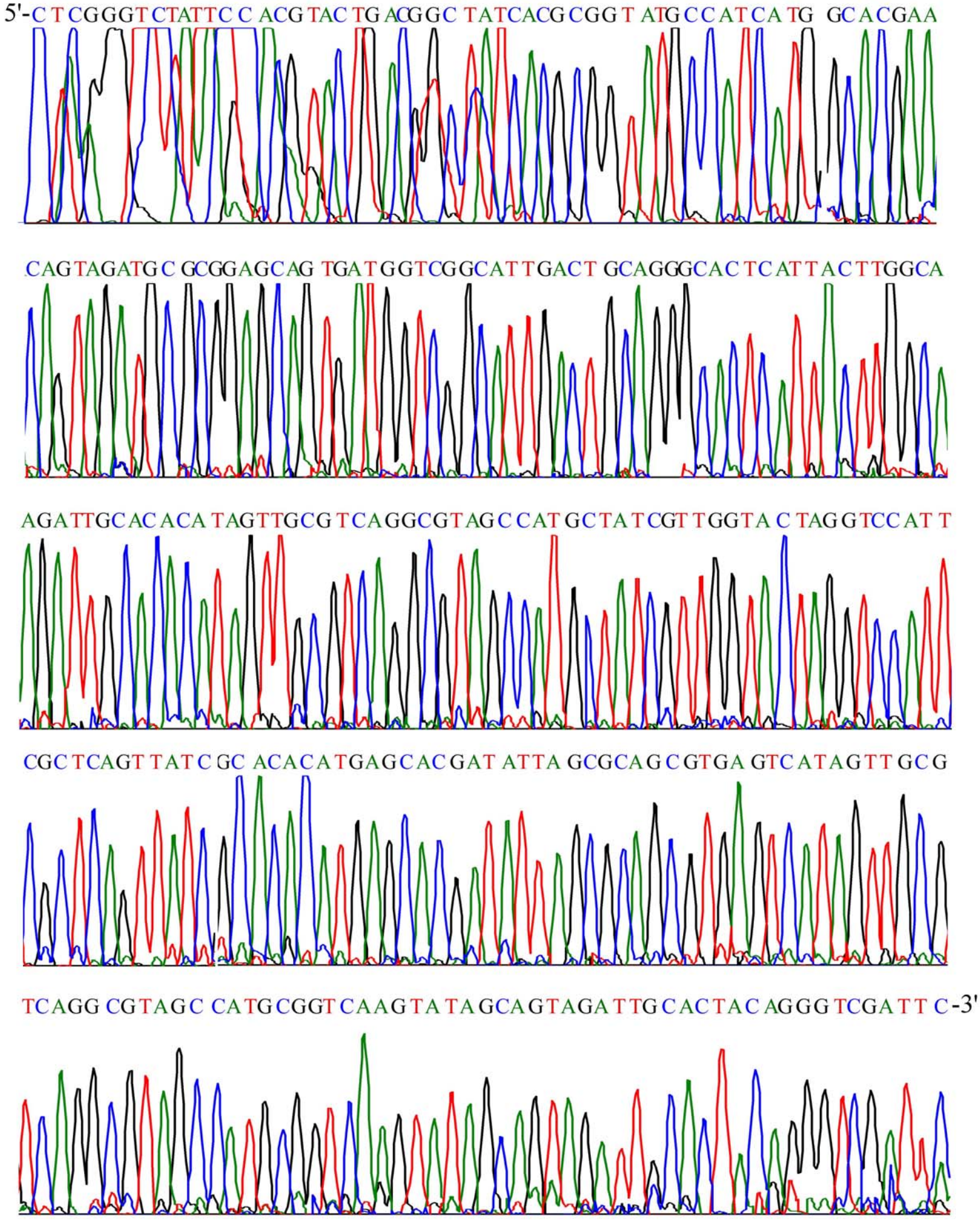
Sequencing result for the complementary strand of the PX-PX ligation product



Sequencing result for the complementary strand of the PX-JX2 ligation product



Sequencing result for the complementary strand of the JX2-PX ligation product



Sequencing result for the complementary strand of the JX2-JX2 ligation product.