GeneMark

Version 2.5p (09.08.06) *Copyright 1993 - M. Borodovsky, J. McIninch*

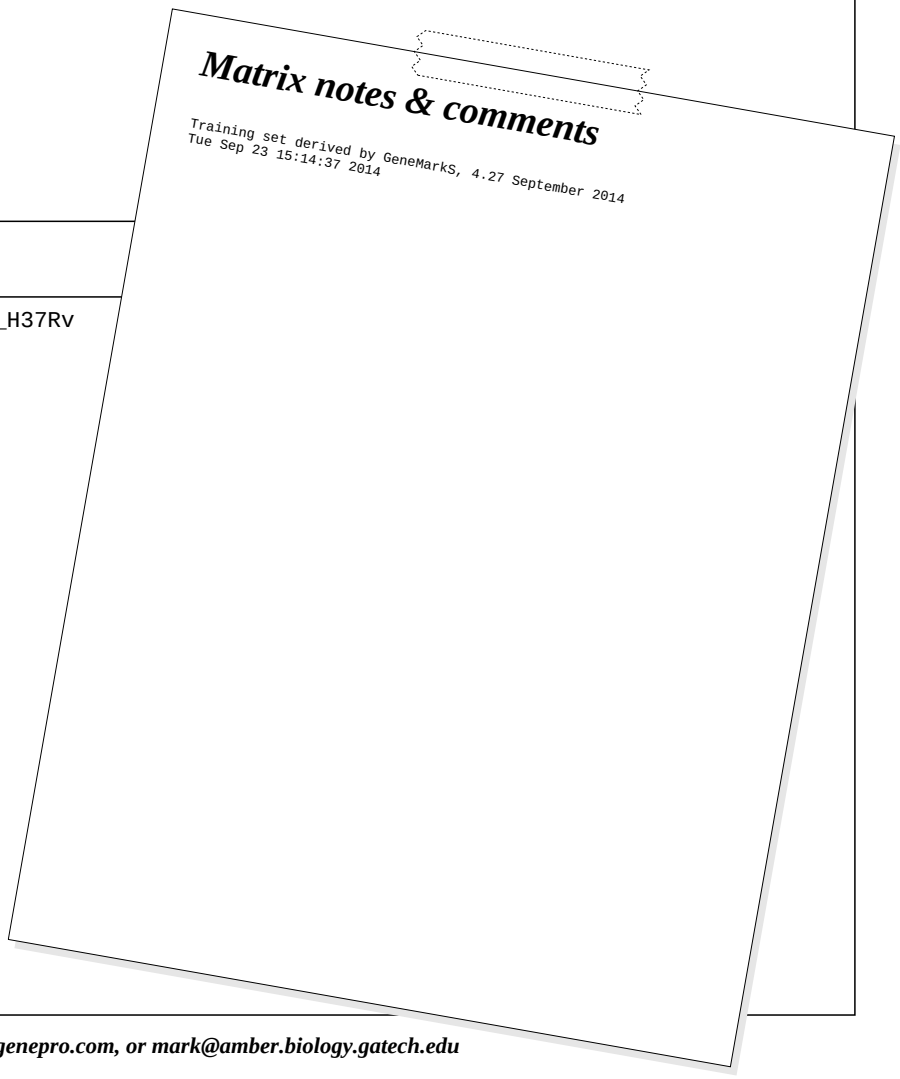
PROGRAM INFORMATION

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Sequence         :  Mycobacterium phage Astro Complete Sequence, 52494 bp including 10-base 3' overhang (CGGGAT
Analysis Date    :  3/29/24 at 9:47:38
Pages            :  26
Sequence Length  :  52494 bp
GC Content       :   61.38%

Window Length    :  96 bp
Window Step      :  12 bp
Threshold Value  :  0.500

PS-Version       :  1.2

GeneMark Options :  PostScript graph,
                    Mark ORFs / splice sites,
                    List ORFs,
                    List regions and/or splice sites,
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MATRIX INFORMATION

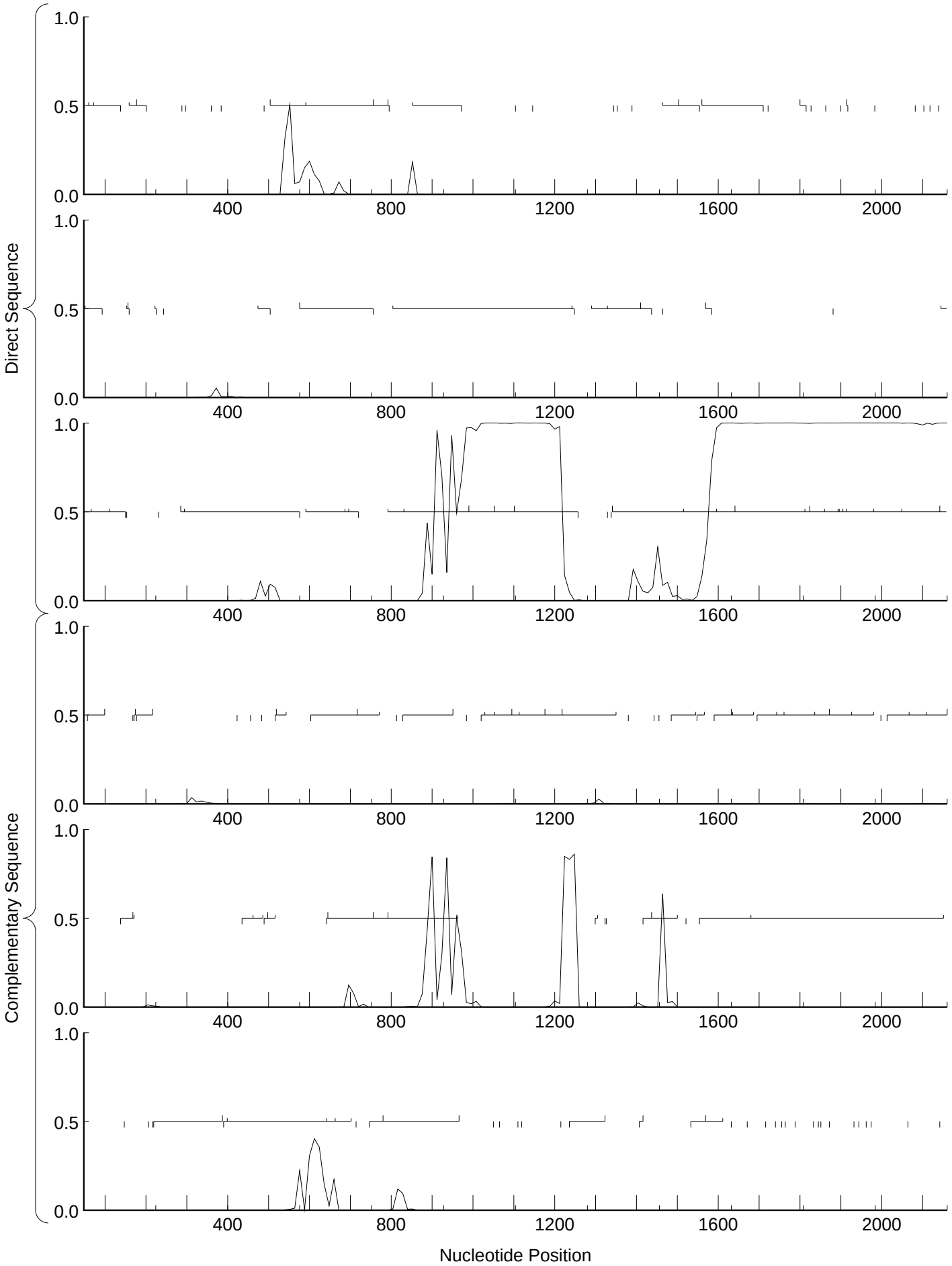
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Matrix     :  Mycobacterium_tuberculosis_H37Rv
Author     :  -

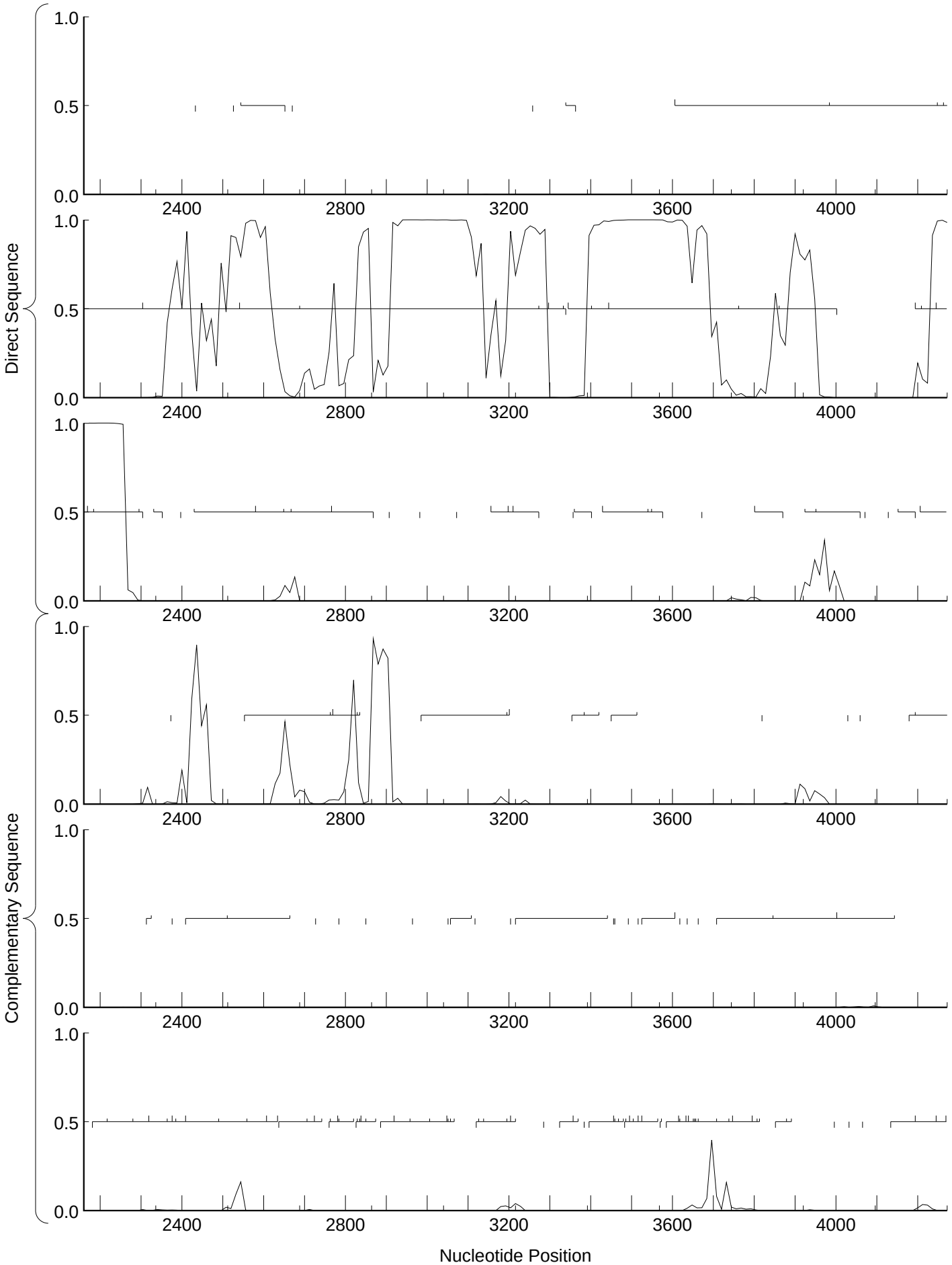
Order      :  4
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  Send questions / comments to:
      Dr. M. Borodovsky
      Georgia Institute of Technology
      School of Biology
      Atlanta, GA  30332-0230
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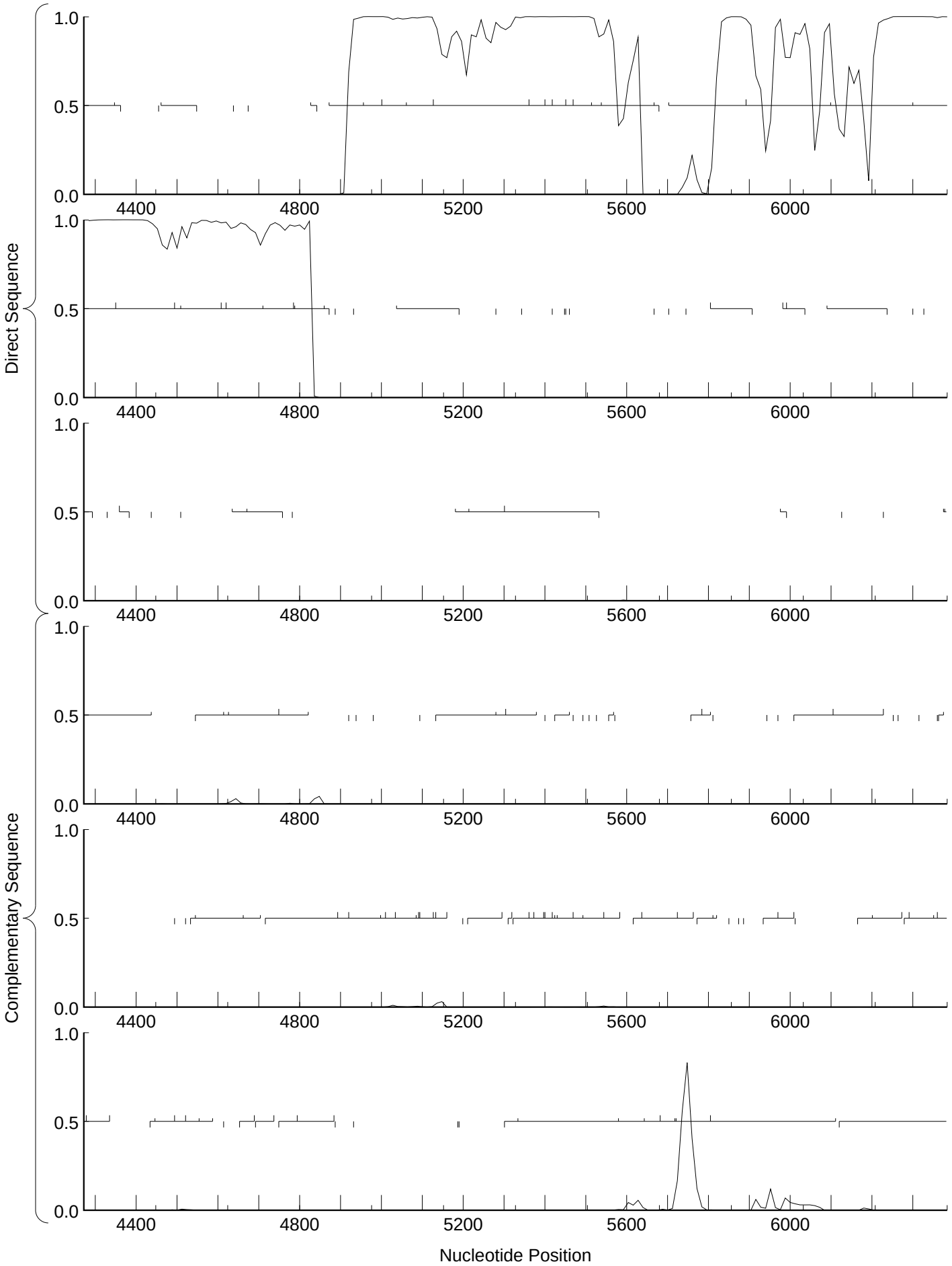

For help or information, send electronic mail to: custserv@genepro.com, or mark@amber.biology.gatech.edu

o Complete Sequence, 52494 bp including 10-base 3’ overhang (CGGGATGTAA), Cluster A8, Order 4, Window 96, Step 12, 2/26

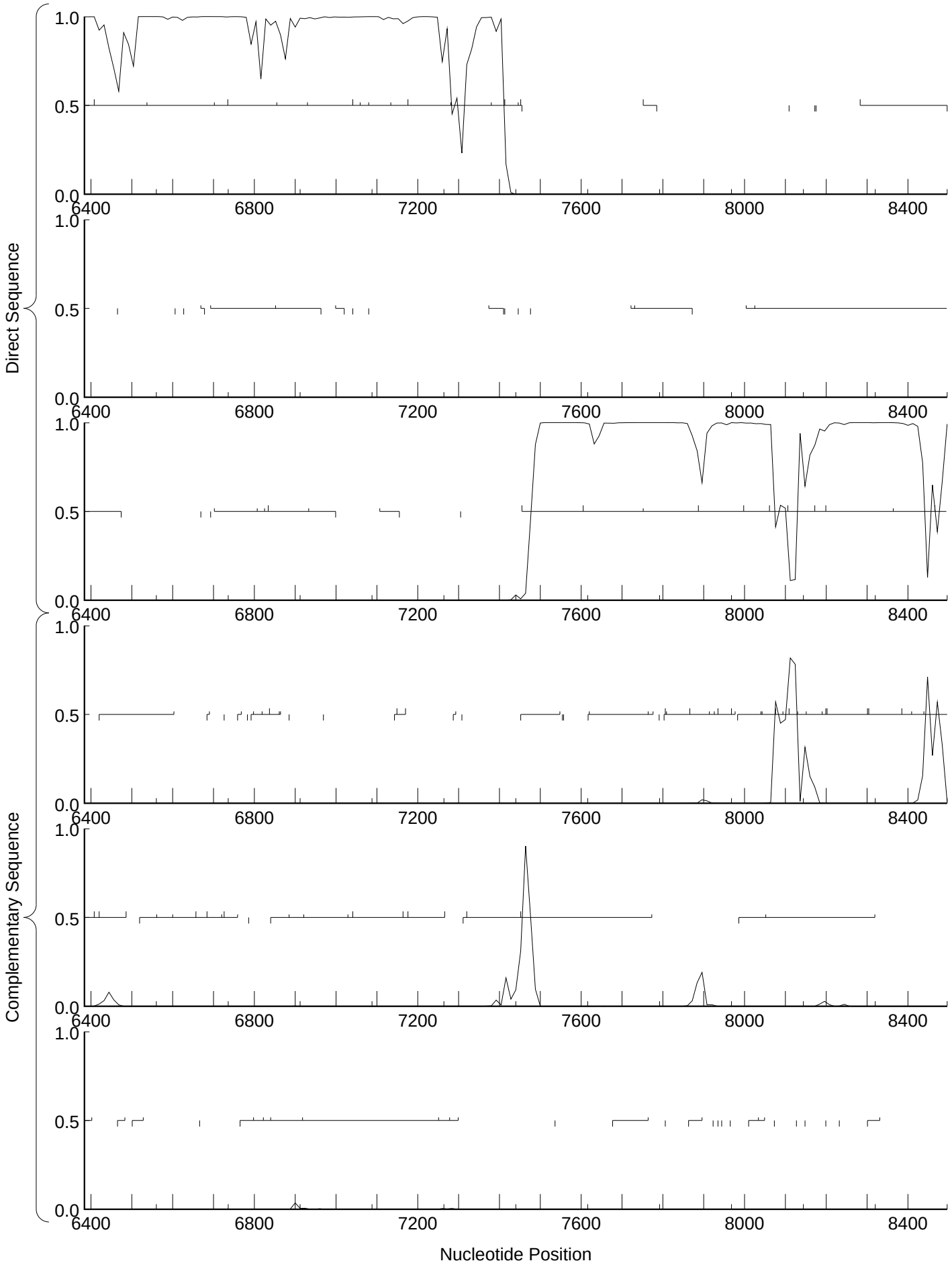


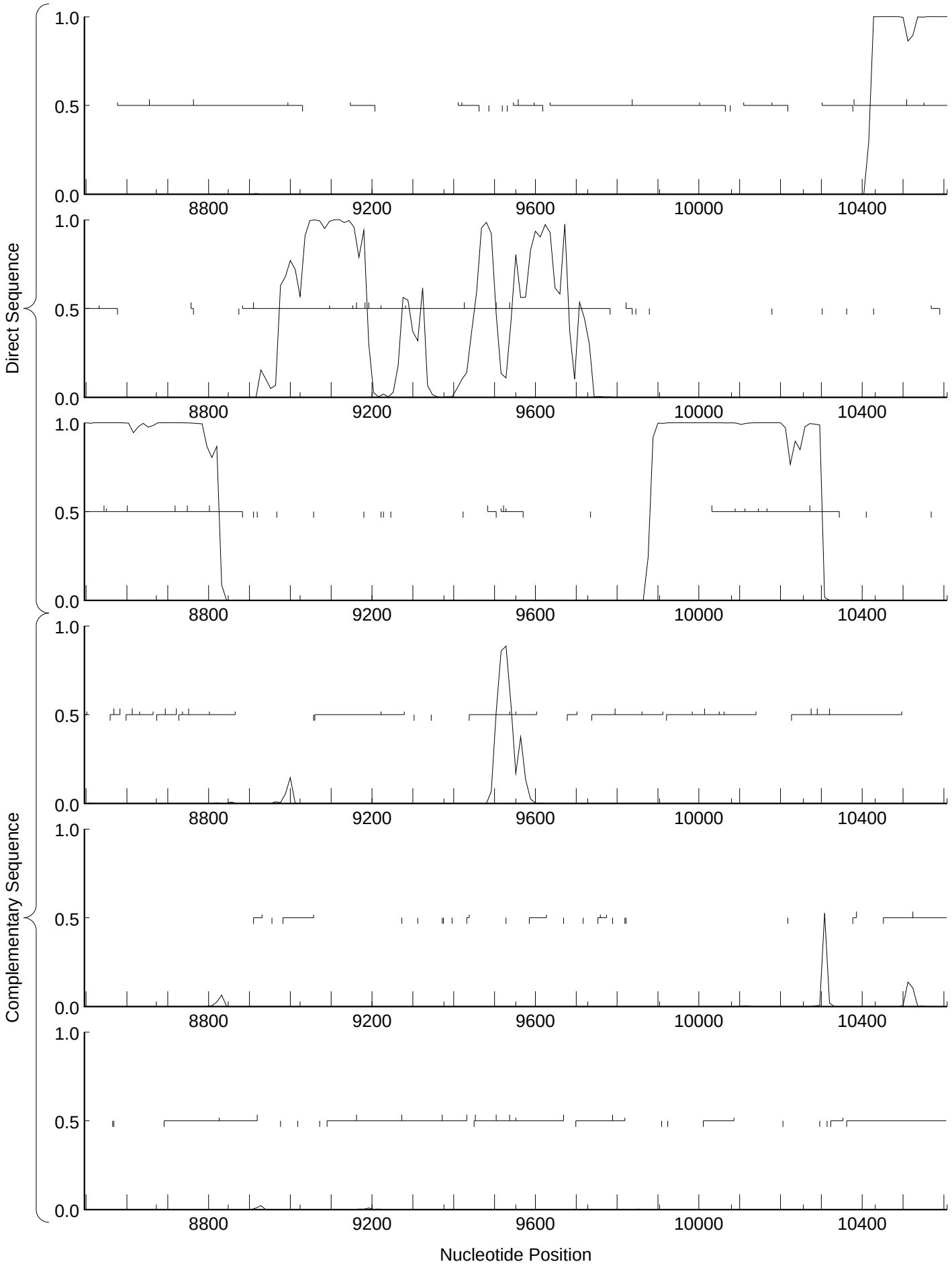

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
2400
2800
3200
3600
4000
Nucleotide Position

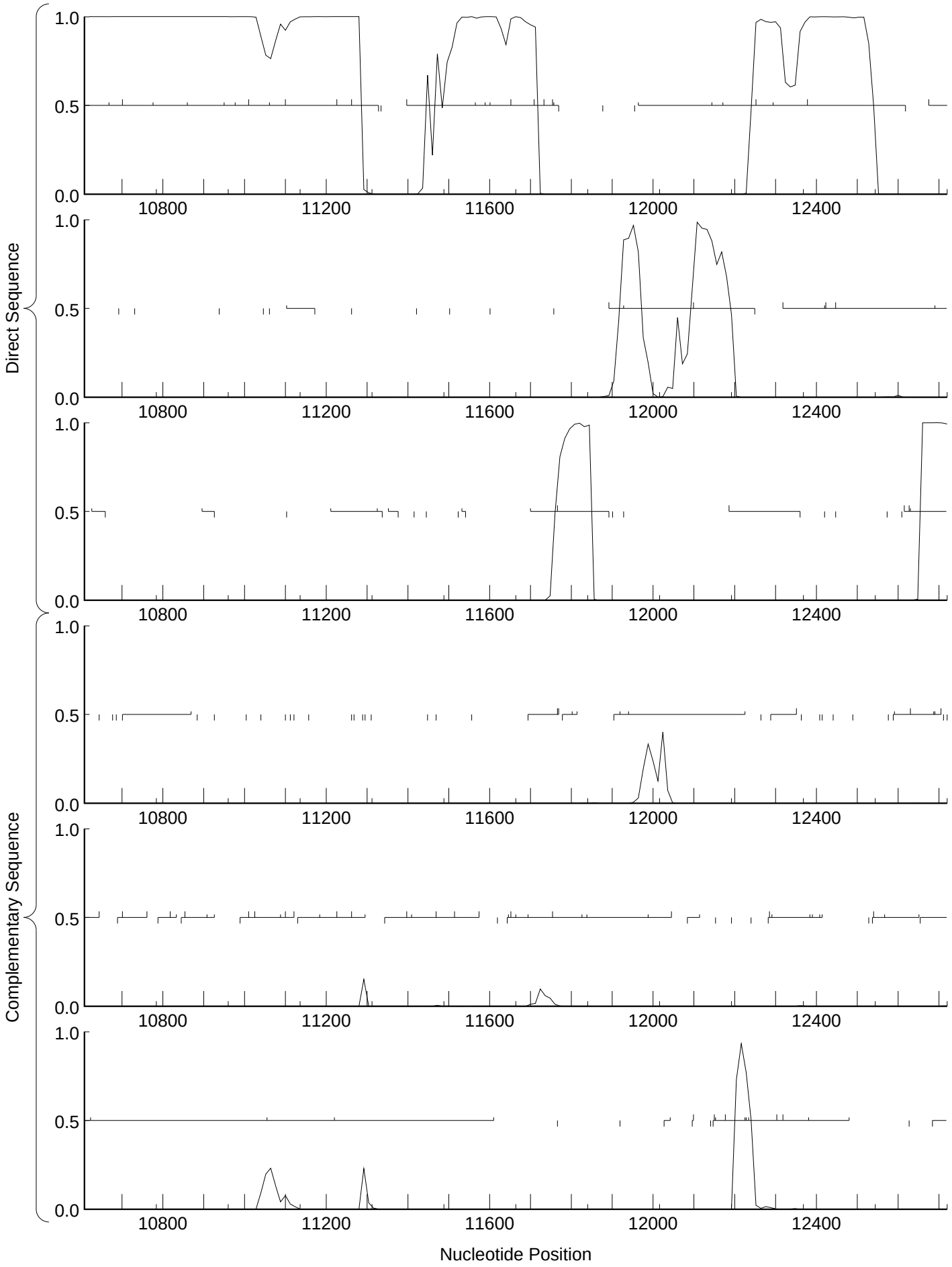
o Complete Sequence, 52494 bp including 10-base 3’ overhang (CGGGATGTAA), Cluster A8, Order 4, Window 96, Step 12, 4/26



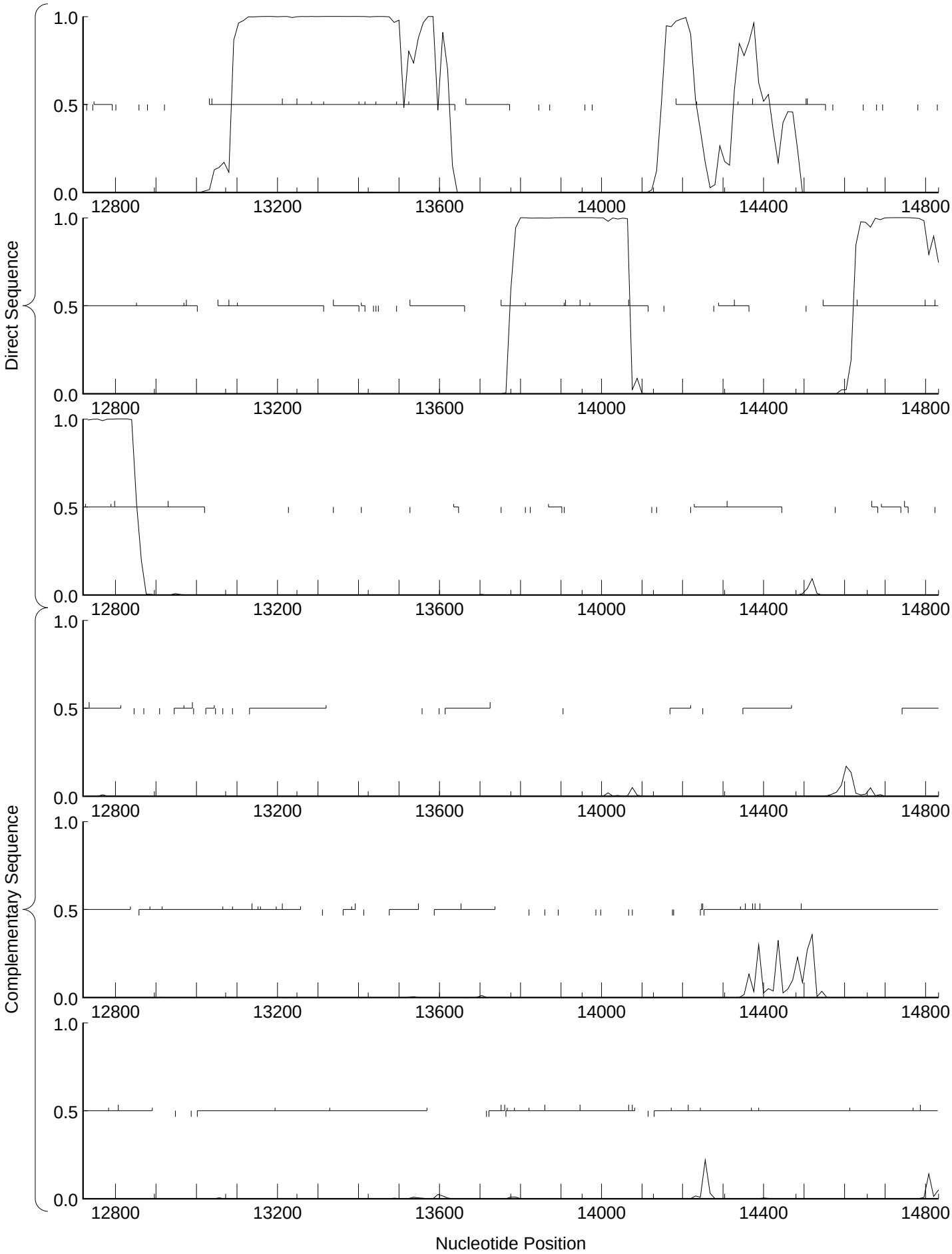
o Complete Sequence, 52494 bp including 10-base 3’ overhang (CGGGATGTAA), Cluster A8, Order 4, Window 96, Step 12, 5/26



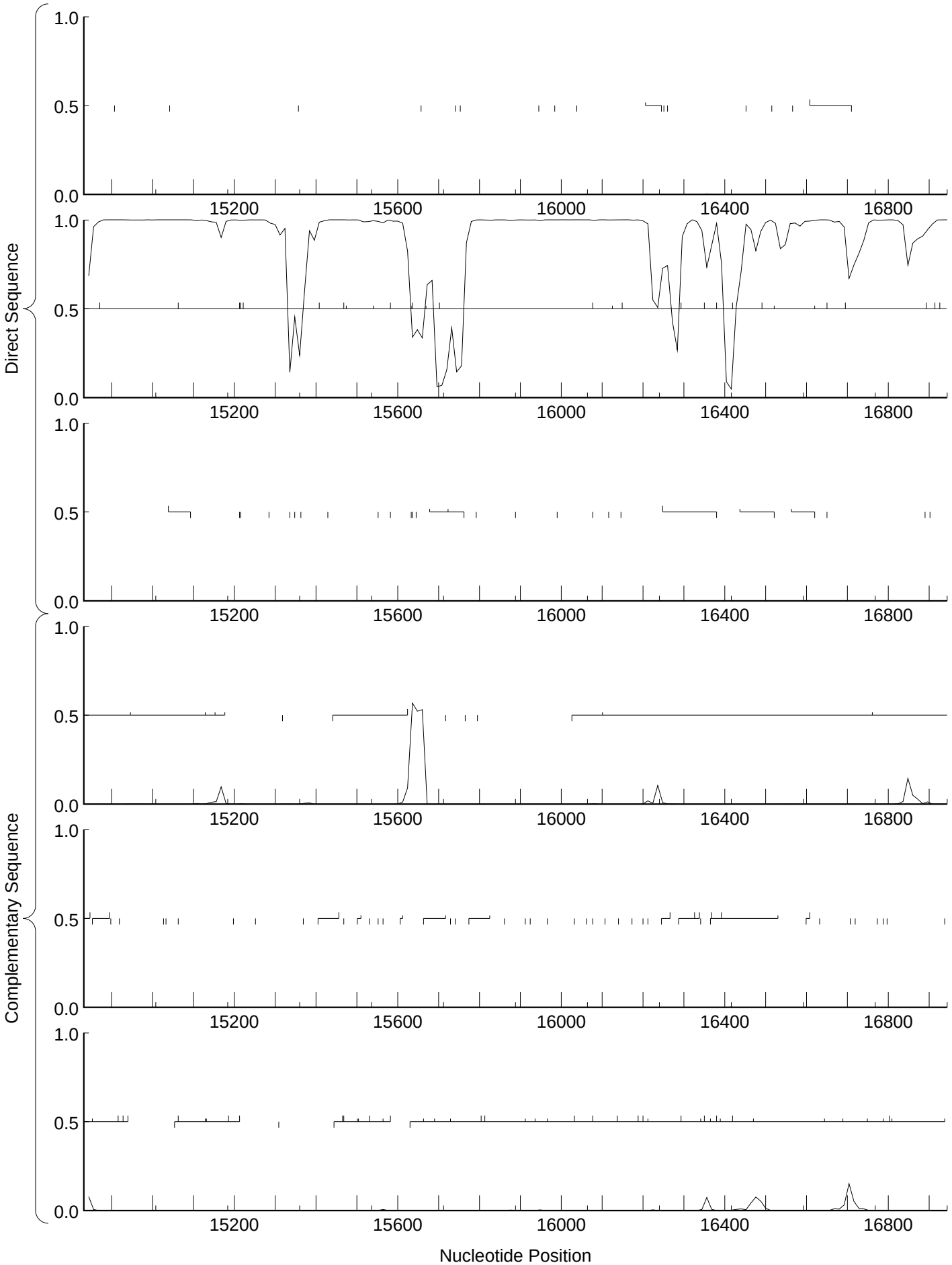

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
8800
9200
9600
10000
10400
Nucleotide Position


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
10800
11200
11600
12000
12400
Nucleotide Position

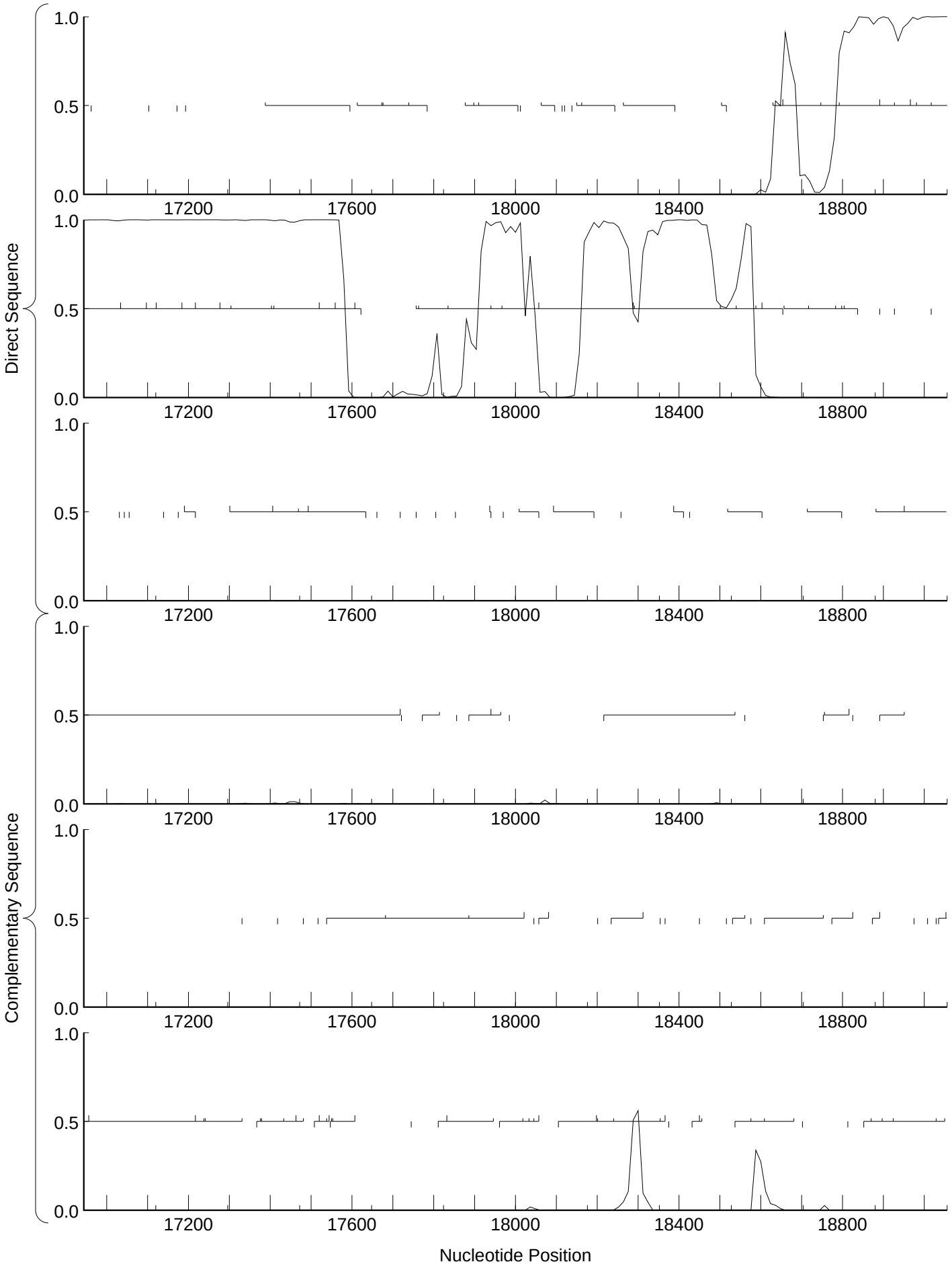
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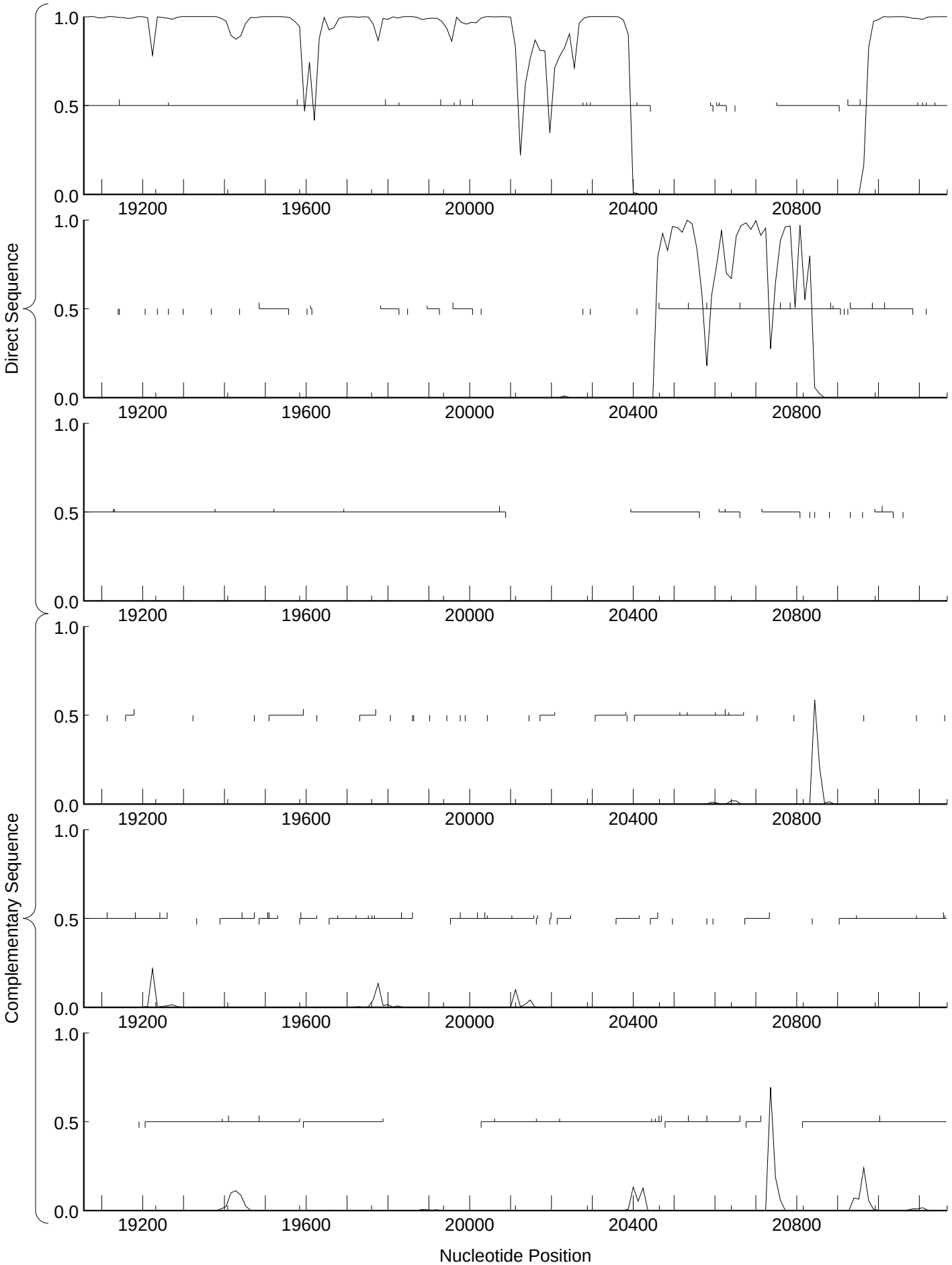
o Complete Sequence, 52494 bp including 10-base 3’ overhang (CGGGATGTAA), Cluster A8, Order 4, Window 96, Step 12, 9/26



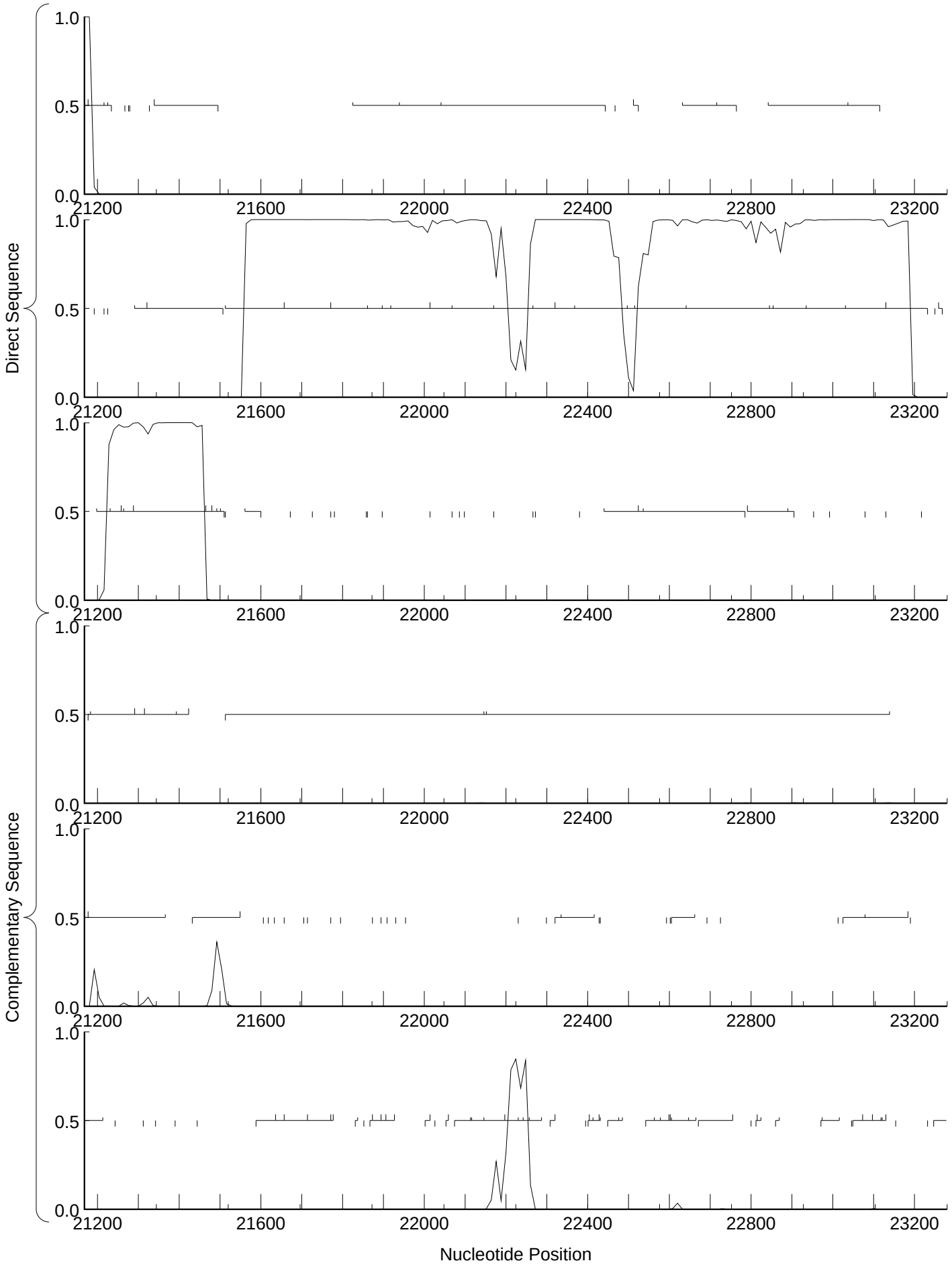
Complete Sequence, 52494 bp including 10-base 3' overhang (CGGGATGTAA), Cluster A8, Order 4, Window 96, Step 12, 10/26



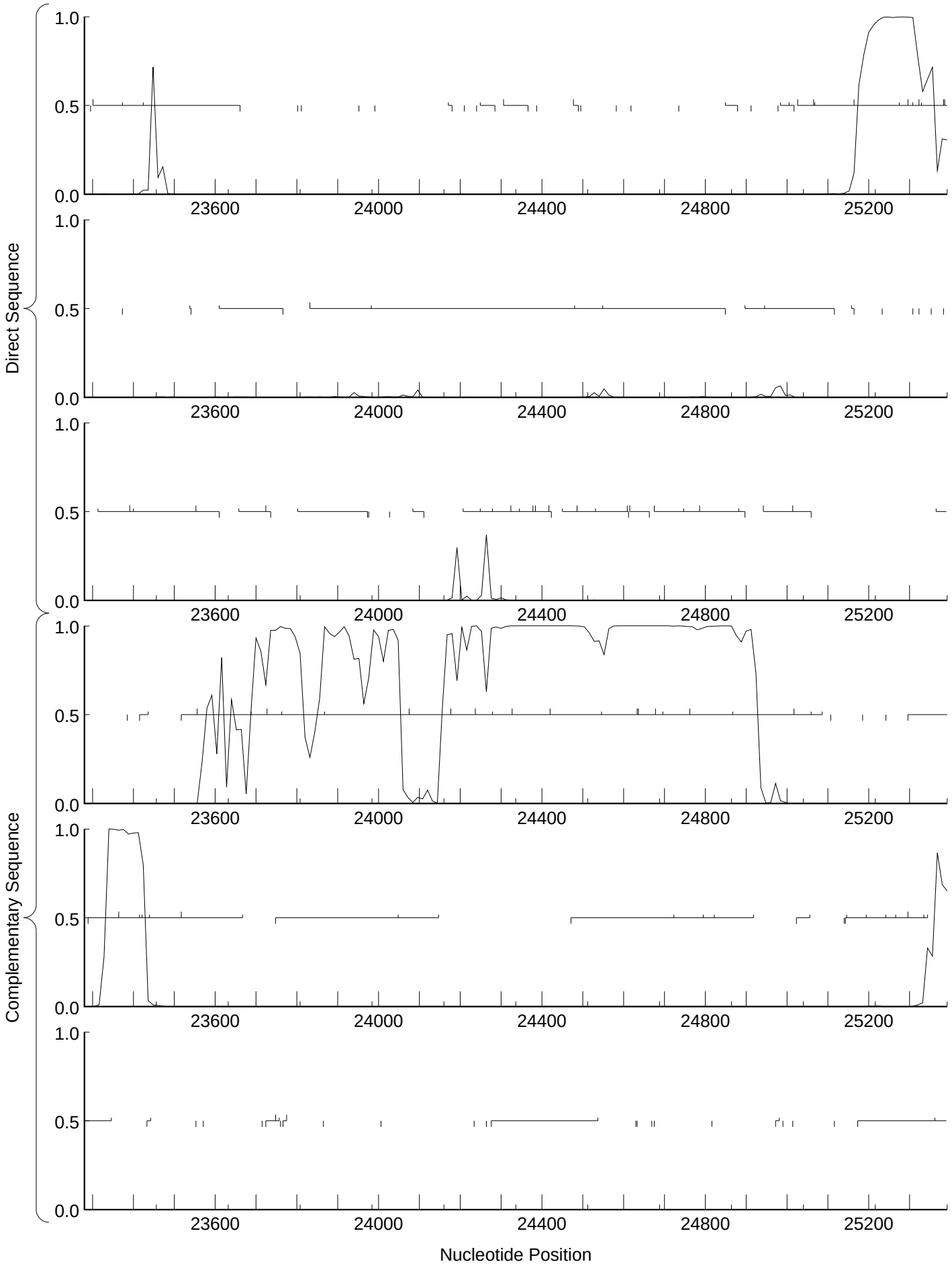
Complete Sequence, 52494 bp including 10-base 3’ overhang (CGGGATGTAA), Cluster A8, Order 4, Window 96, Step 12, 11/26



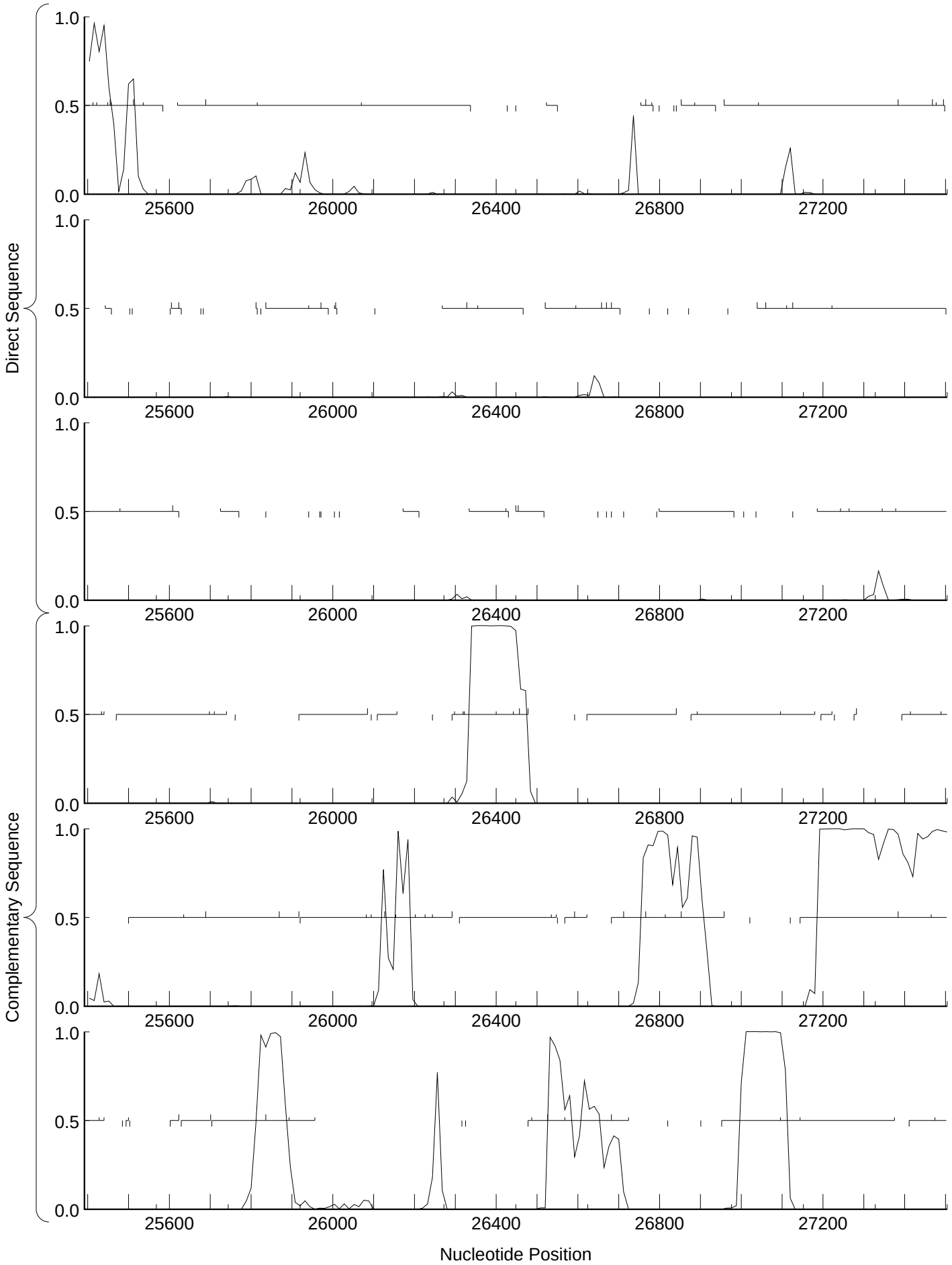
Complete Sequence, 52494 bp including 10-base 3’ overhang (CGGGATGTAA), Cluster A8, Order 4, Window 96, Step 12, 12/26



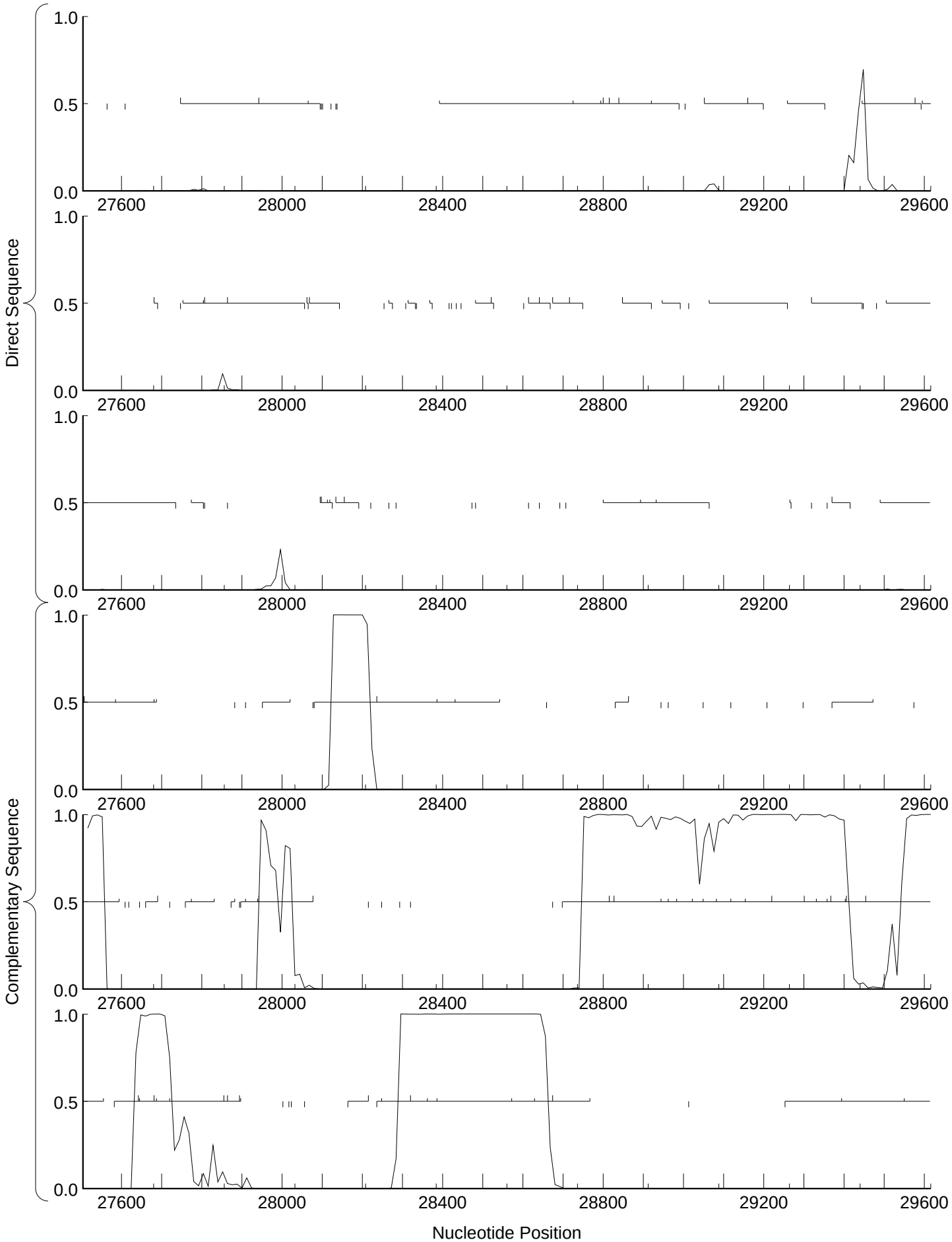
Complete Sequence, 52494 bp including 10-base 3' overhang (CGGGATGTAA), Cluster A8, Order 4, Window 96, Step 12, 13/26



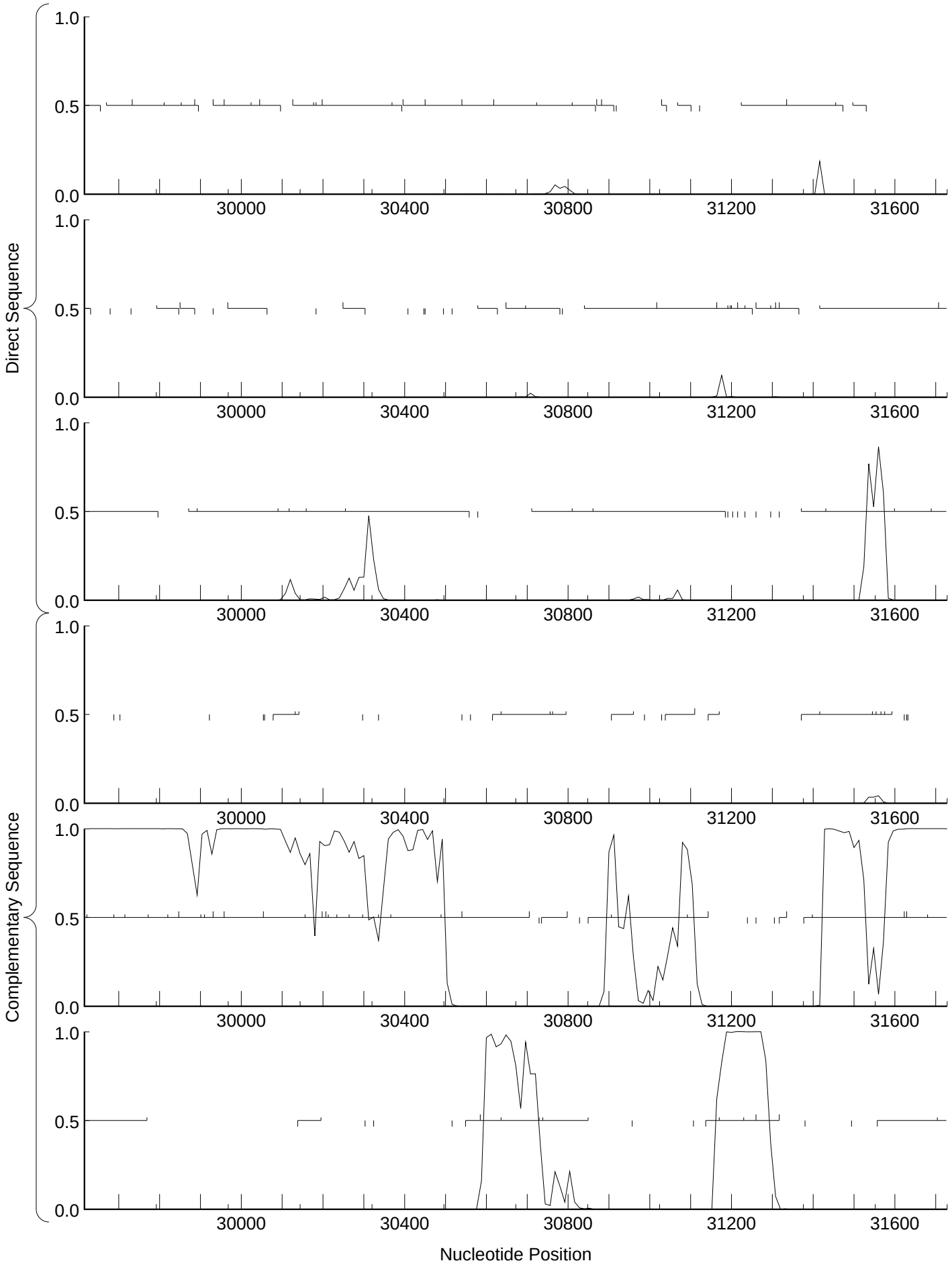
Complete Sequence, 52494 bp including 10-base 3’ overhang (CGGGATGTAA), Cluster A8, Order 4, Window 96, Step 12, 14/26



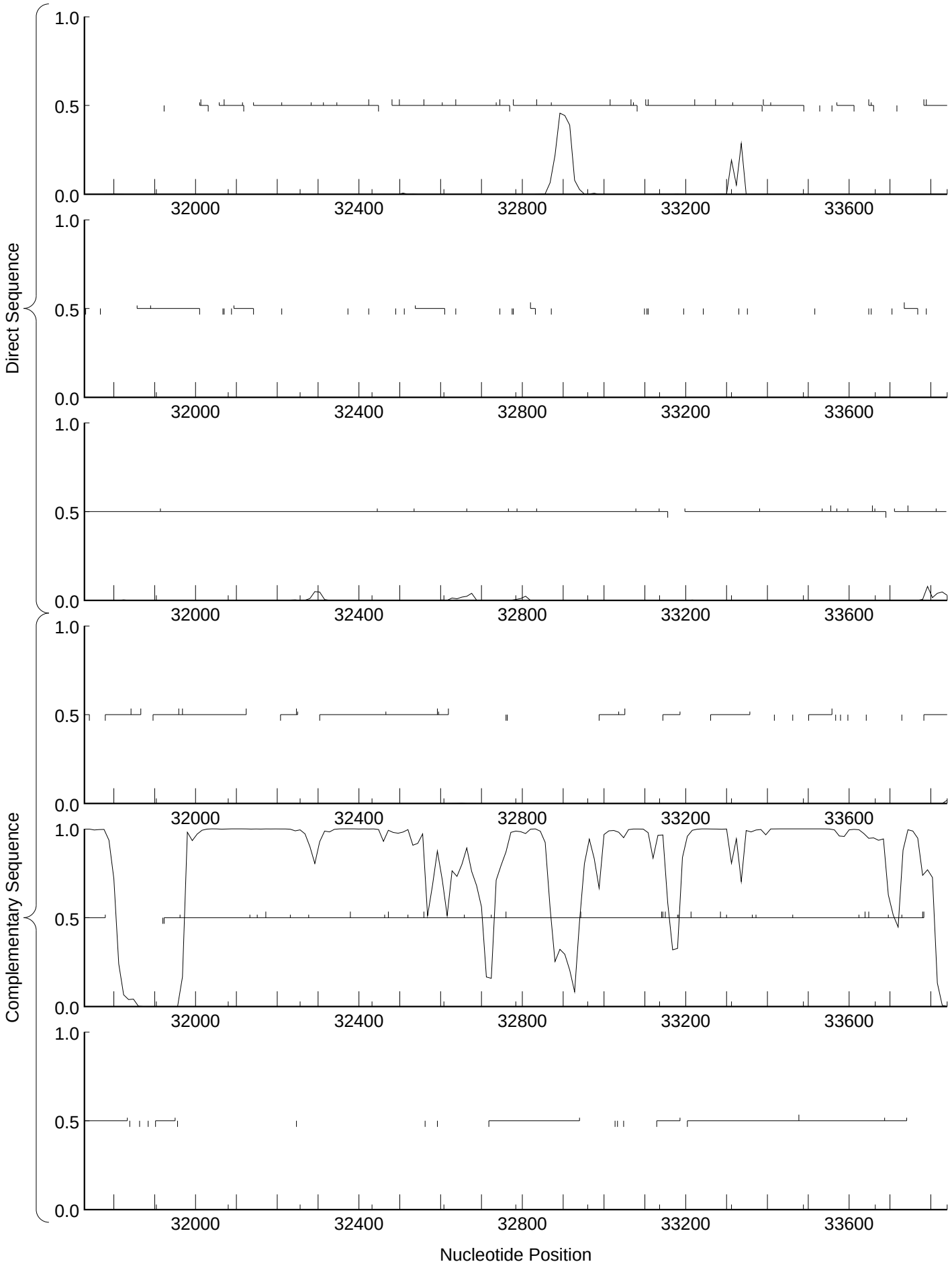
Complete Sequence, 52494 bp including 10-base 3’ overhang (CGGGATGTAA), Cluster A8, Order 4, Window 96, Step 12, 15/26



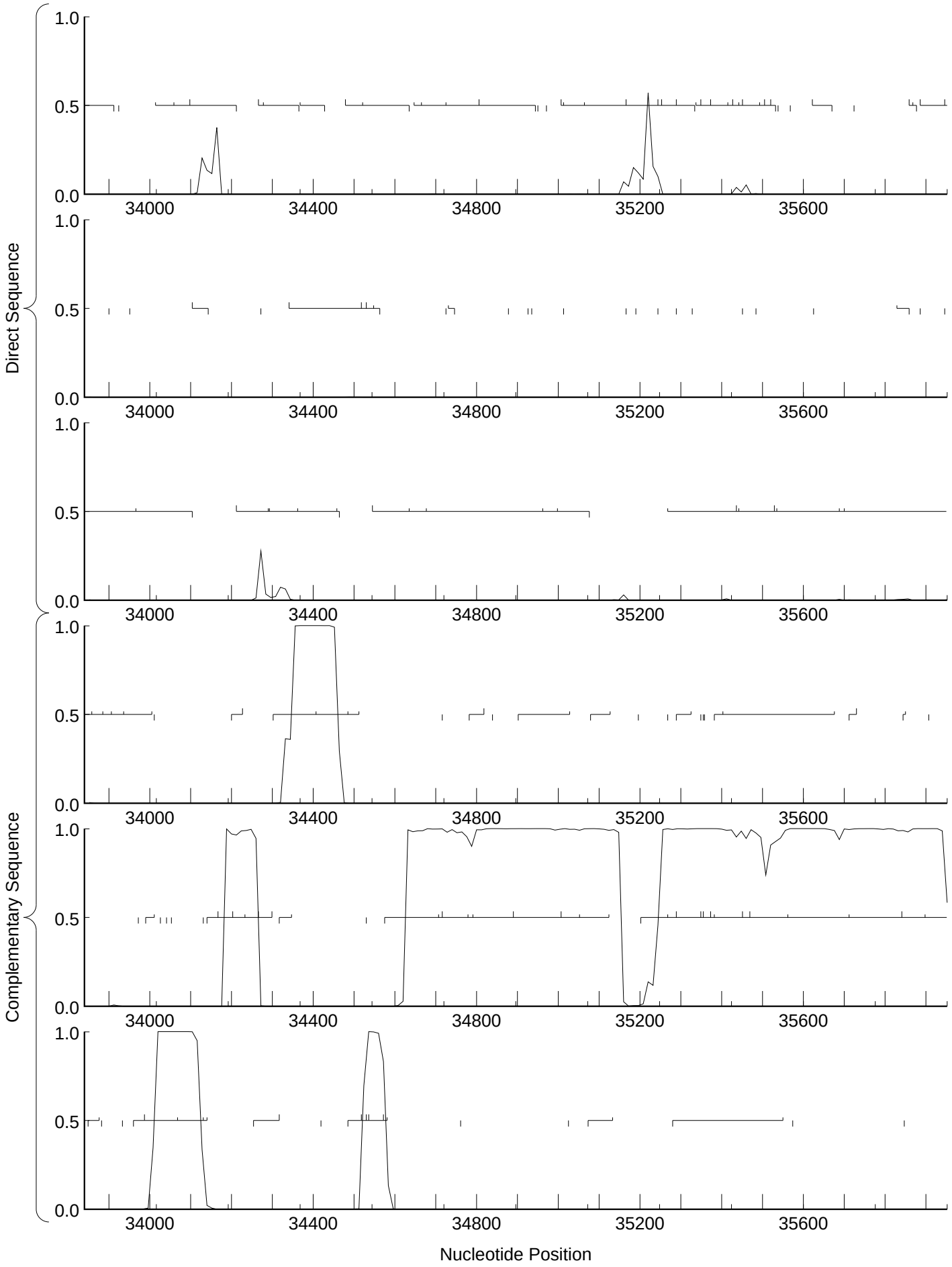
Complete Sequence, 52494 bp including 10-base 3’ overhang (CGGGATGTAA), Cluster A8, Order 4, Window 96, Step 12, 16/26



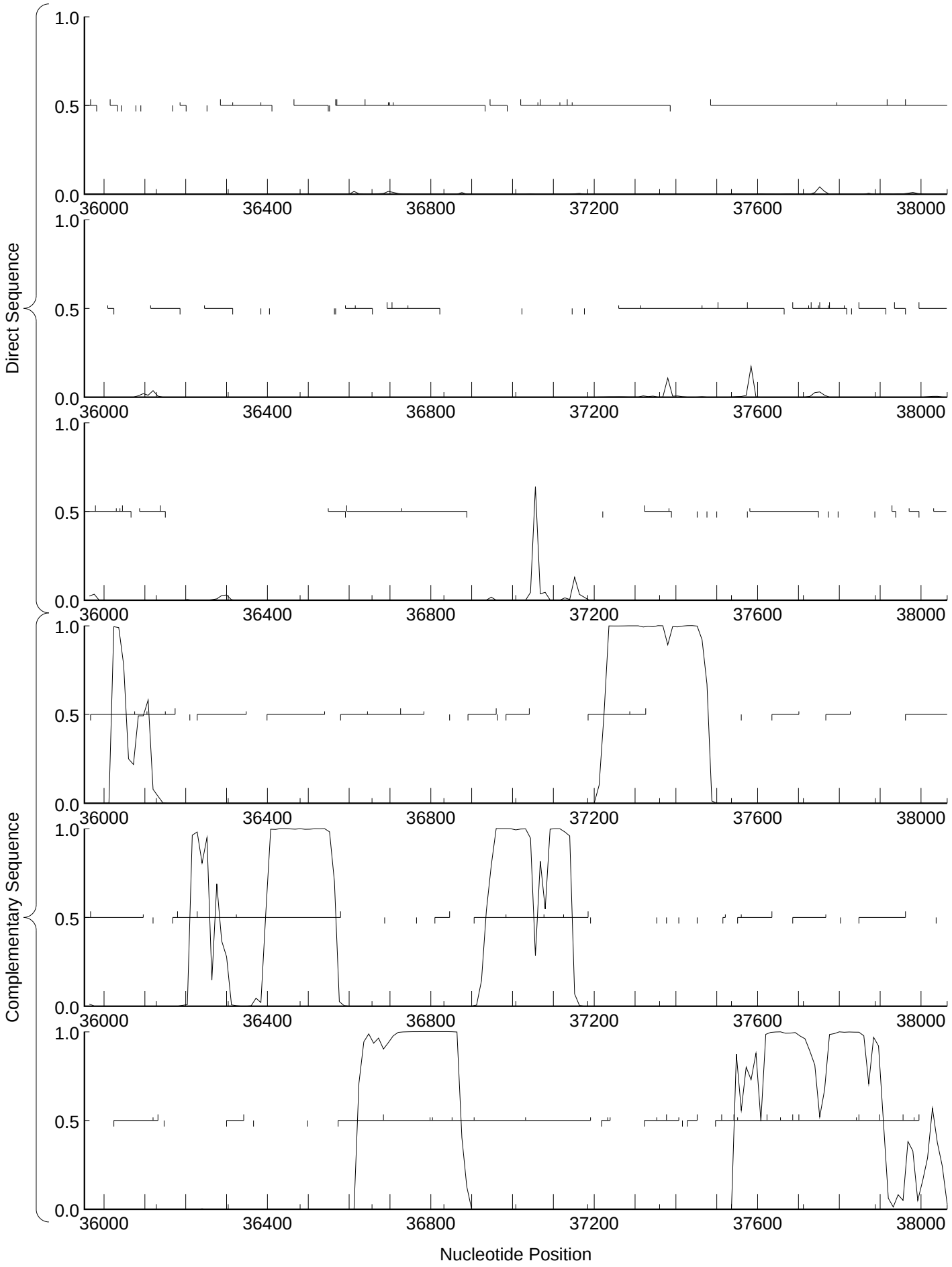
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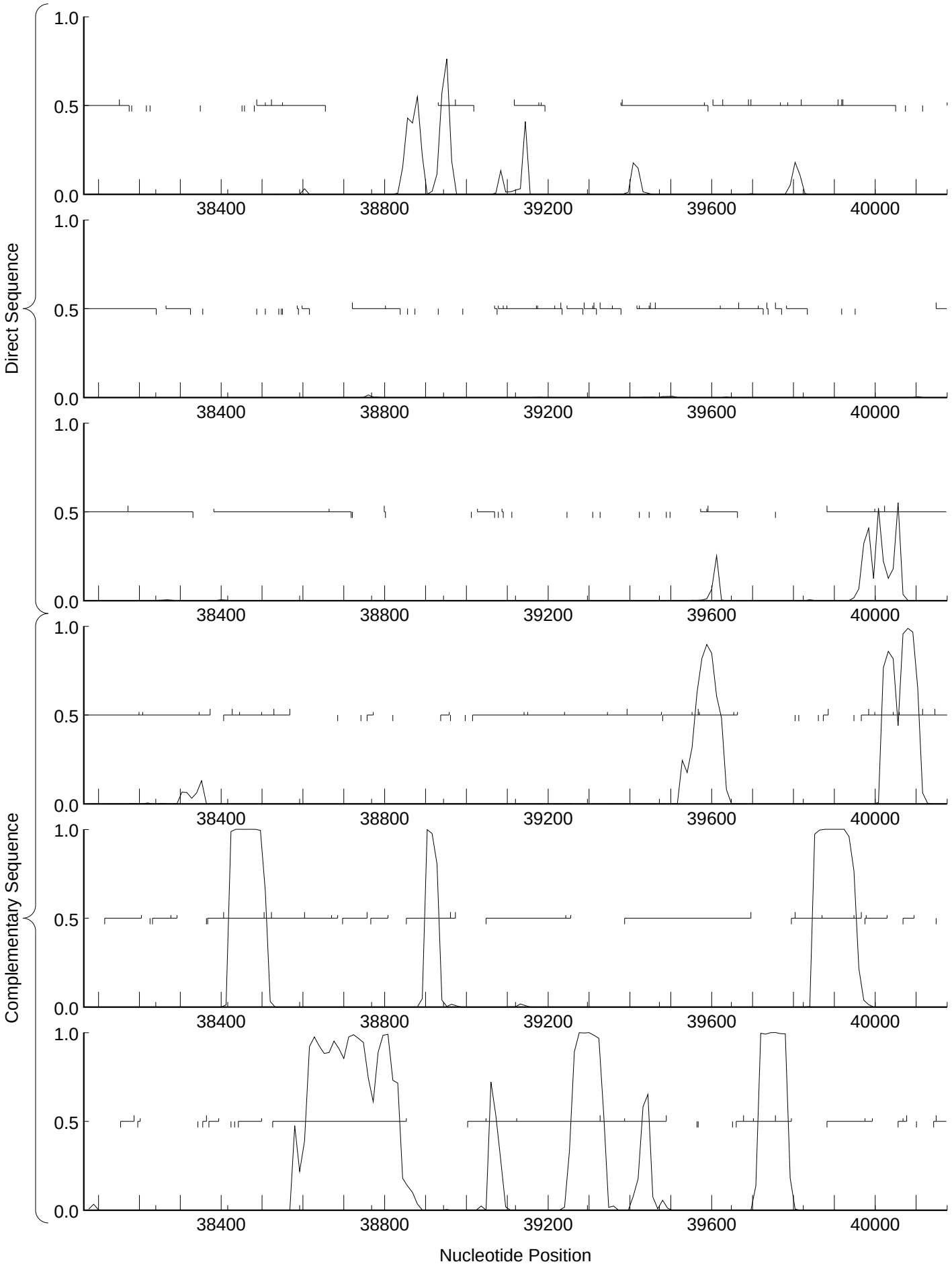
Complete Sequence, 52494 bp including 10-base 3’ overhang (CGGGATGTAA), Cluster A8, Order 4, Window 96, Step 12, 18/26



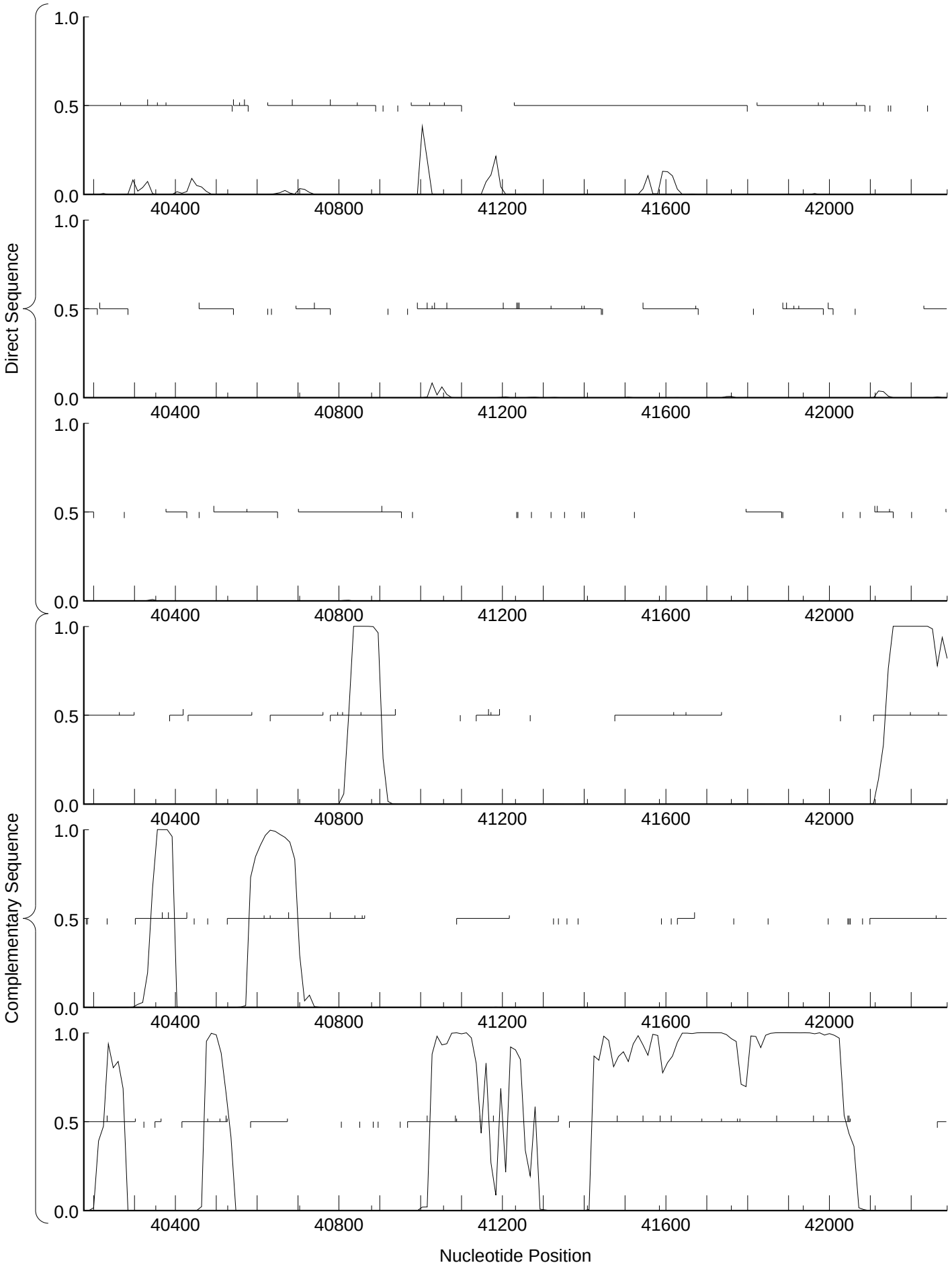
Complete Sequence, 52494 bp including 10-base 3’ overhang (CGGGATGTAA), Cluster A8, Order 4, Window 96, Step 12, 19/26



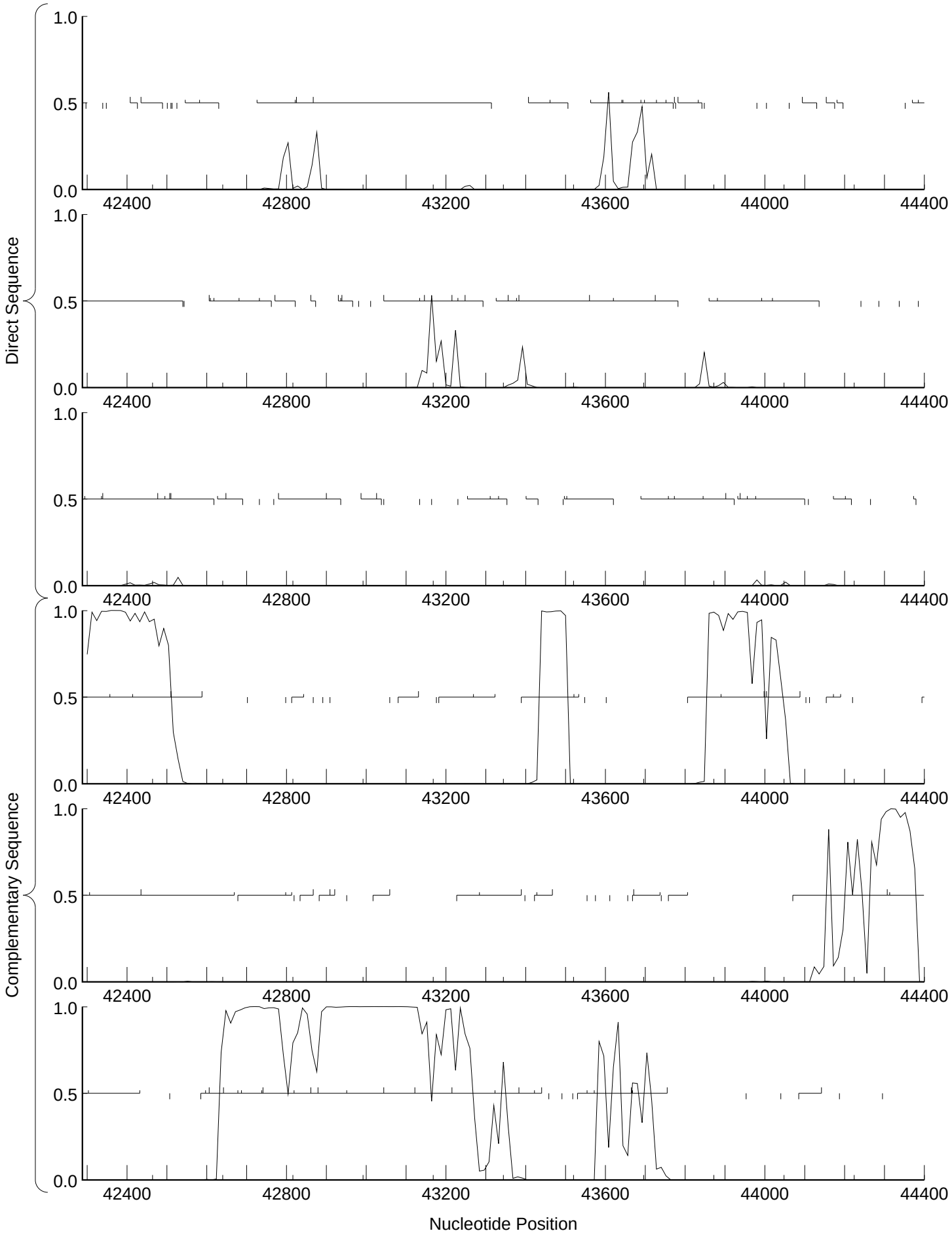
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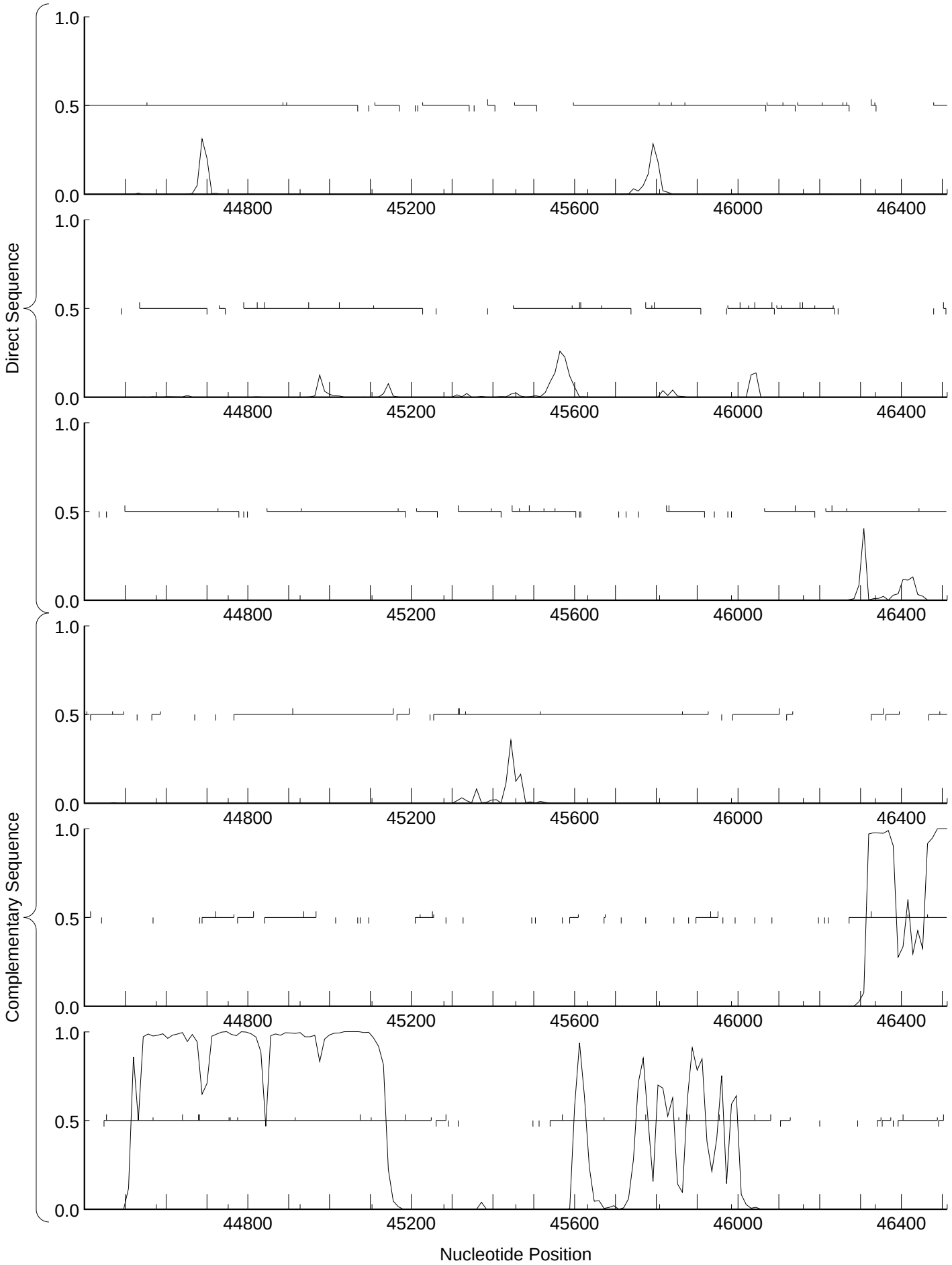
Complete Sequence, 52494 bp including 10-base 3’ overhang (CGGGATGTAA), Cluster A8, Order 4, Window 96, Step 12, 21/26



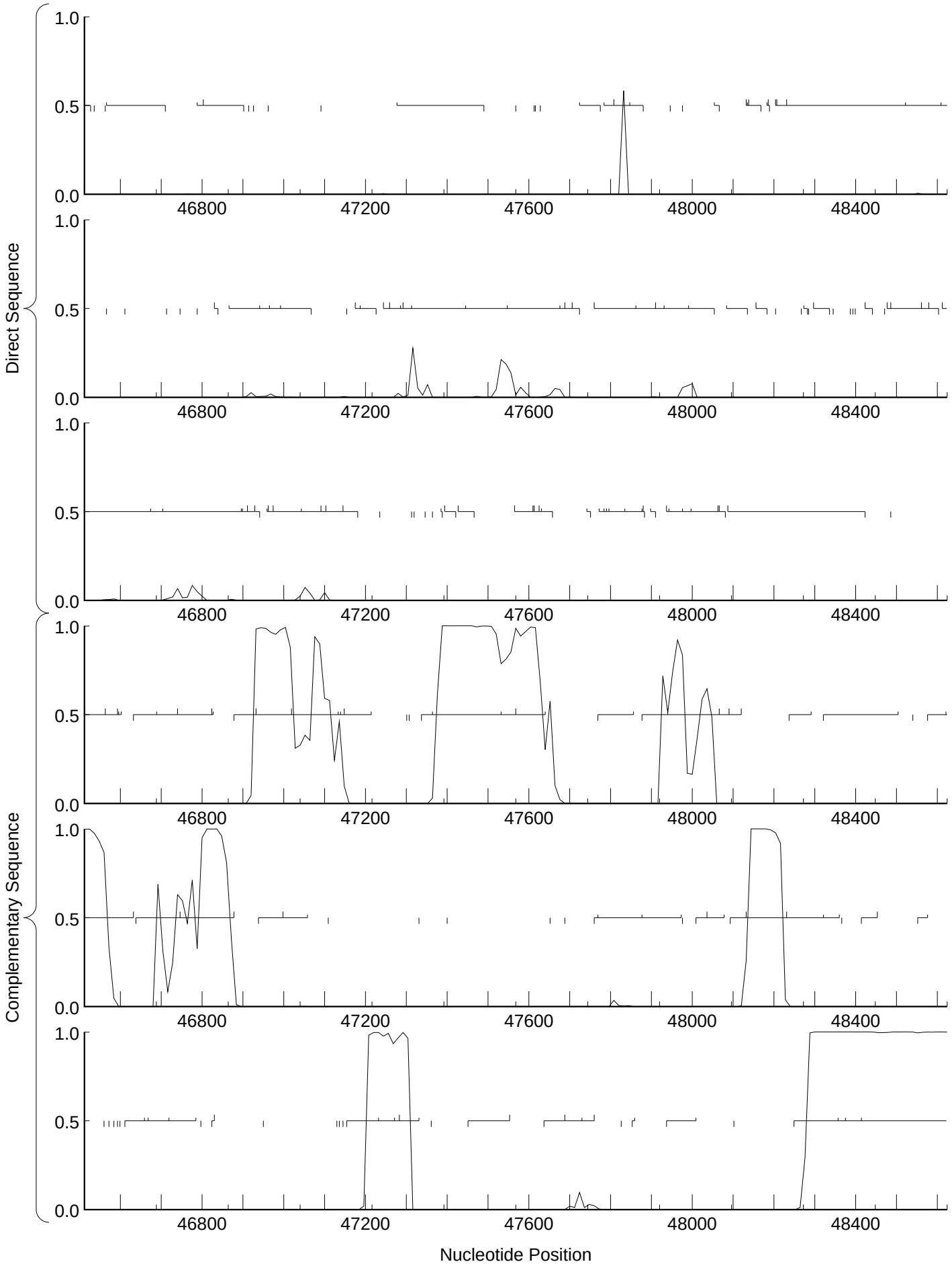
Complete Sequence, 52494 bp including 10-base 3’ overhang (CGGGATGTAA), Cluster A8, Order 4, Window 96, Step 12, 22/26



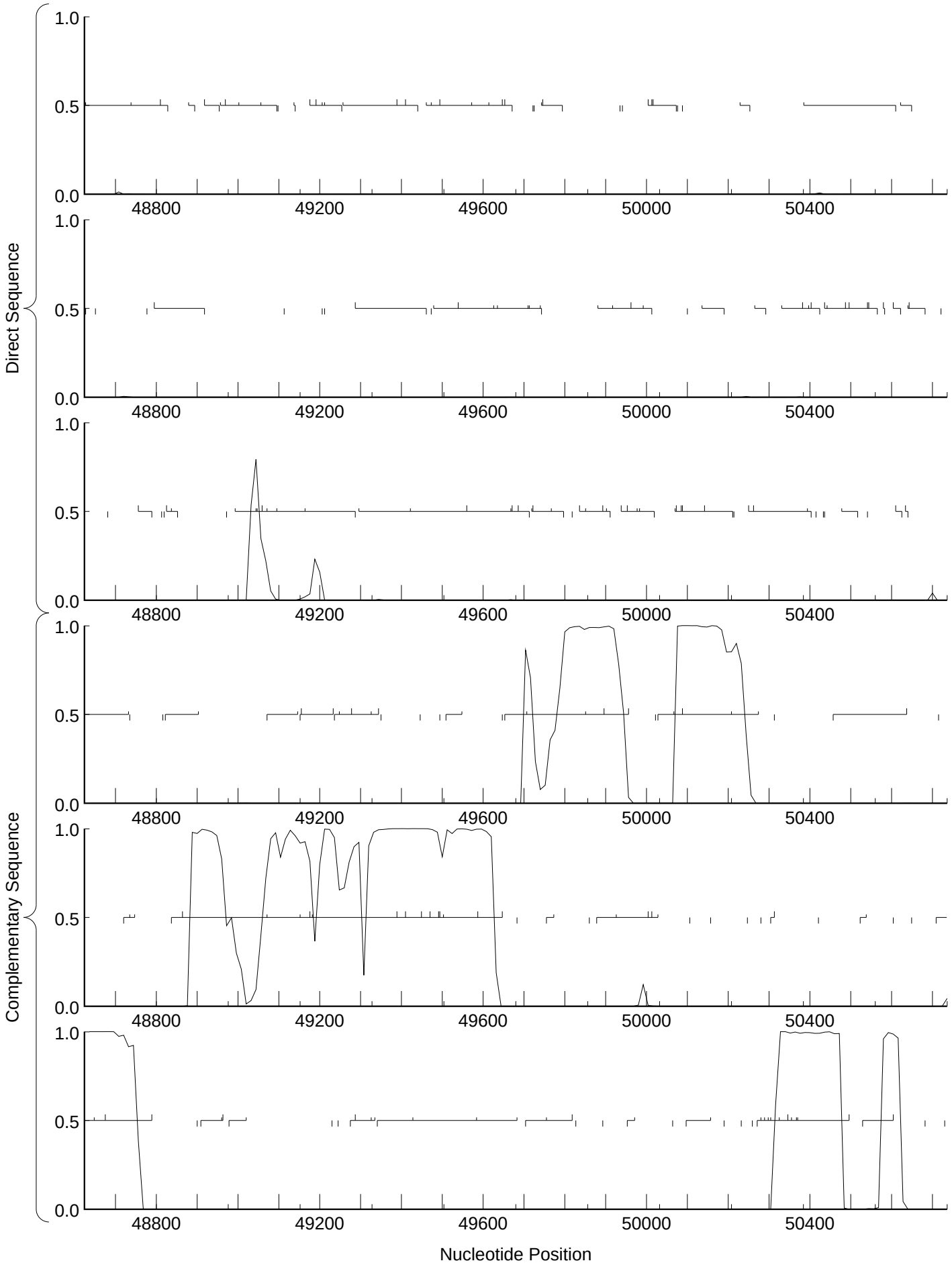
Complete Sequence, 52494 bp including 10-base 3’ overhang (CGGGATGTAA), Cluster A8, Order 4, Window 96, Step 12, 23/26



Complete Sequence, 52494 bp including 10-base 3’ overhang (CGGGATGTAA), Cluster A8, Order 4, Window 96, Step 12, 24/26



Complete Sequence, 52494 bp including 10-base 3’ overhang (CGGGATGTAA), Cluster A8, Order 4, Window 96, Step 12, 25/26



Complete Sequence, 52494 bp including 10-base 3’ overhang (CGGGATGTAA), Cluster A8, Order 4, Window 96, Step 12, 26/26

