GeneMark

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

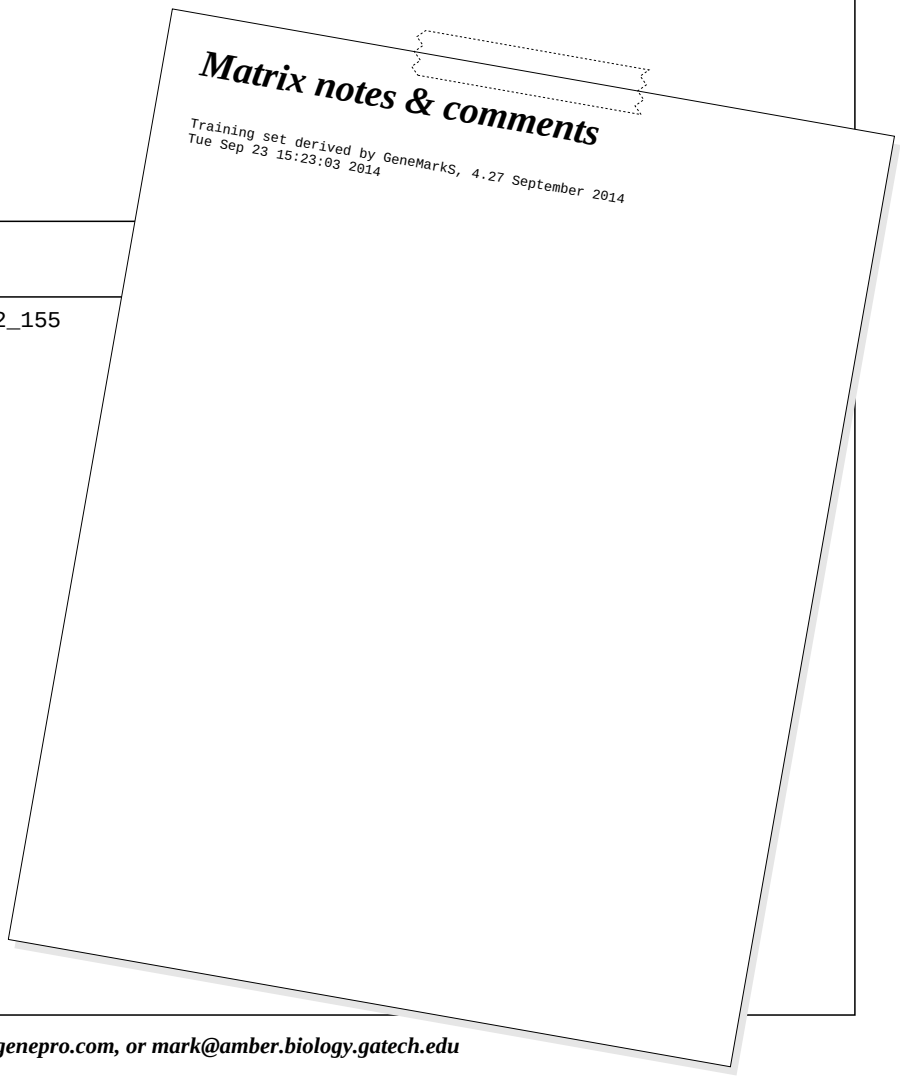
PROGRAM INFORMATION

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Sequence         :  Mycobacterium phage Roary complete sequence, 52521 bp including 10-base 3’ overhang (CGGGAT
Analysis Date    :  3/28/24 at 15:00:13
Pages            :  26
Sequence Length  :  52521 bp
GC Content       :   61.44%

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

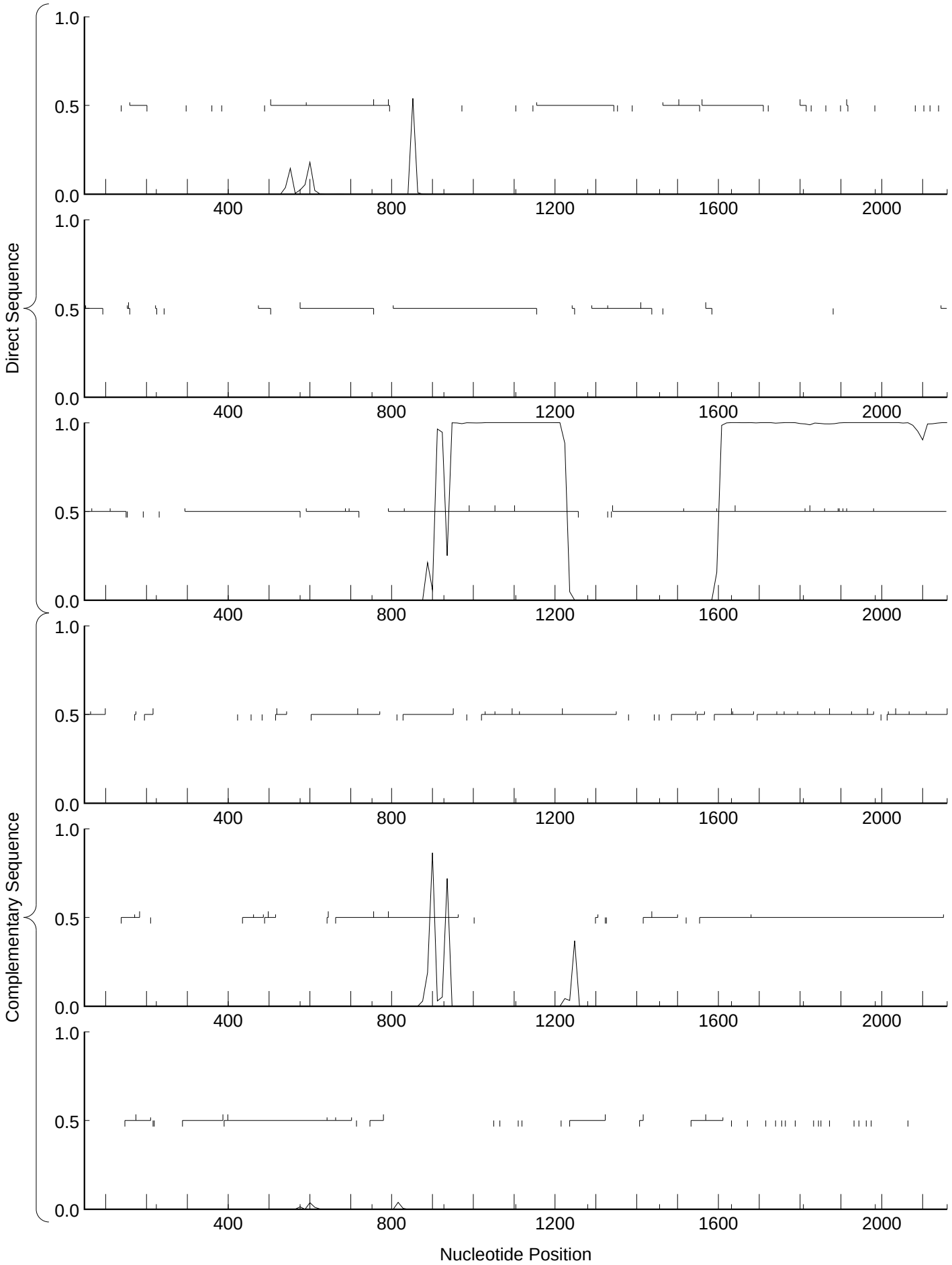
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Matrix     :  Mycobacterium_smegmatis_MC2_155
Author     :  -

Order      :  4
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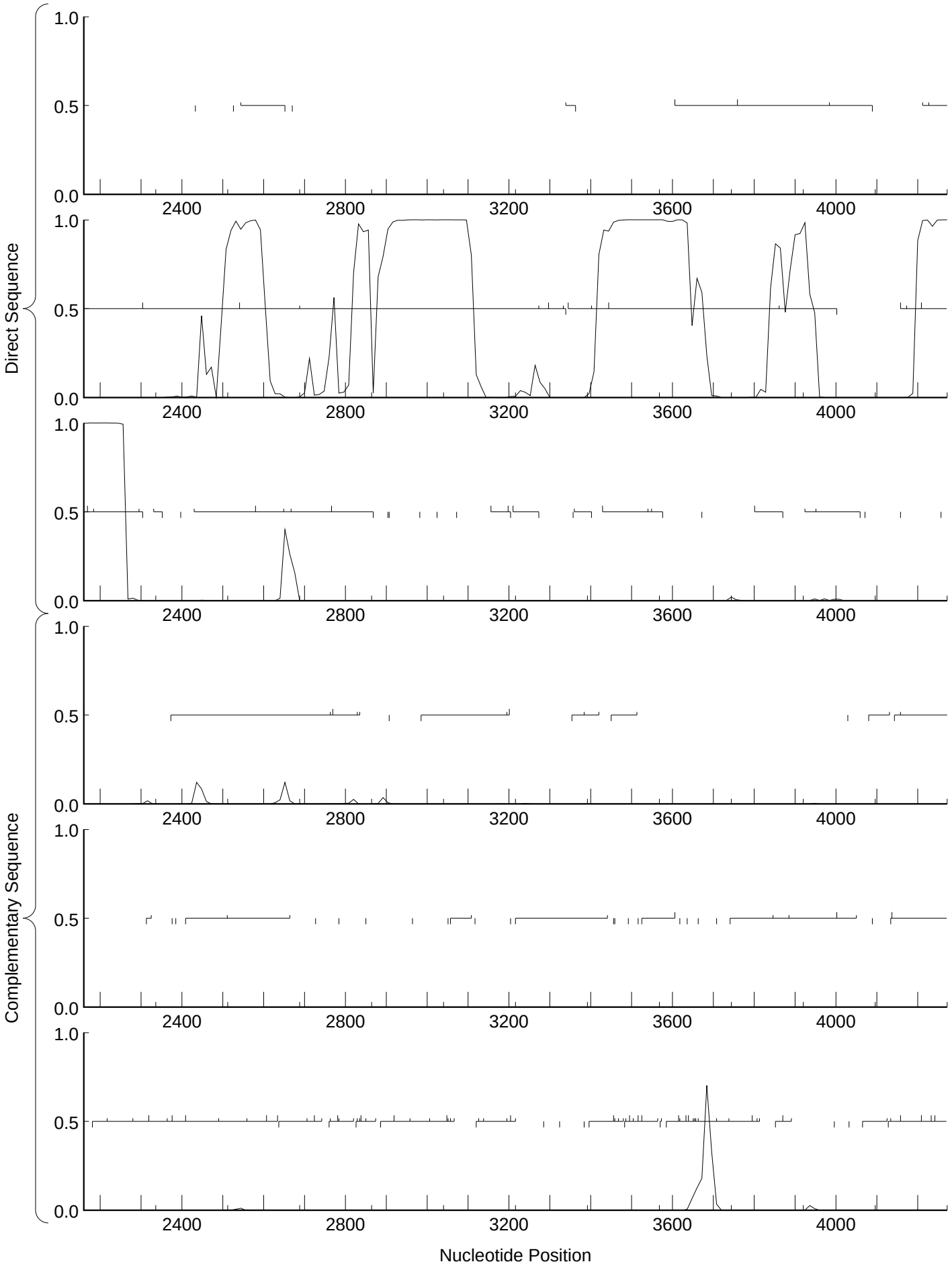

```
  Send questions / comments to:
      Dr. M. Borodovsky
      Georgia Institute of Technology
      School of Biology
      Atlanta, GA  30332-0230
```


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

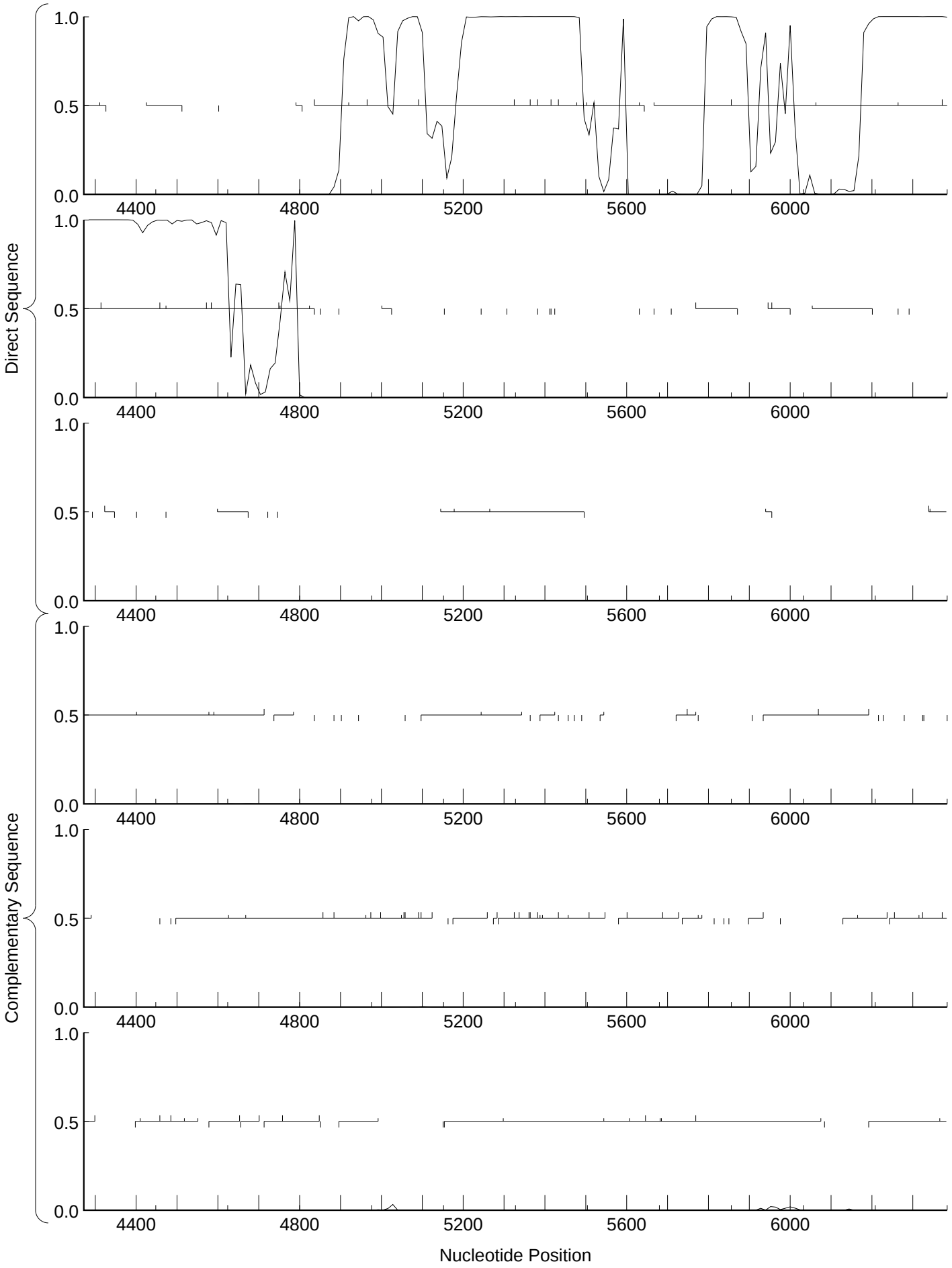
ry complete sequence, 52521 bp including 10-base 3’ overhang (CGGGATGTAA), Cluster A8, Order 4, Window 96, Step 12, 2/26



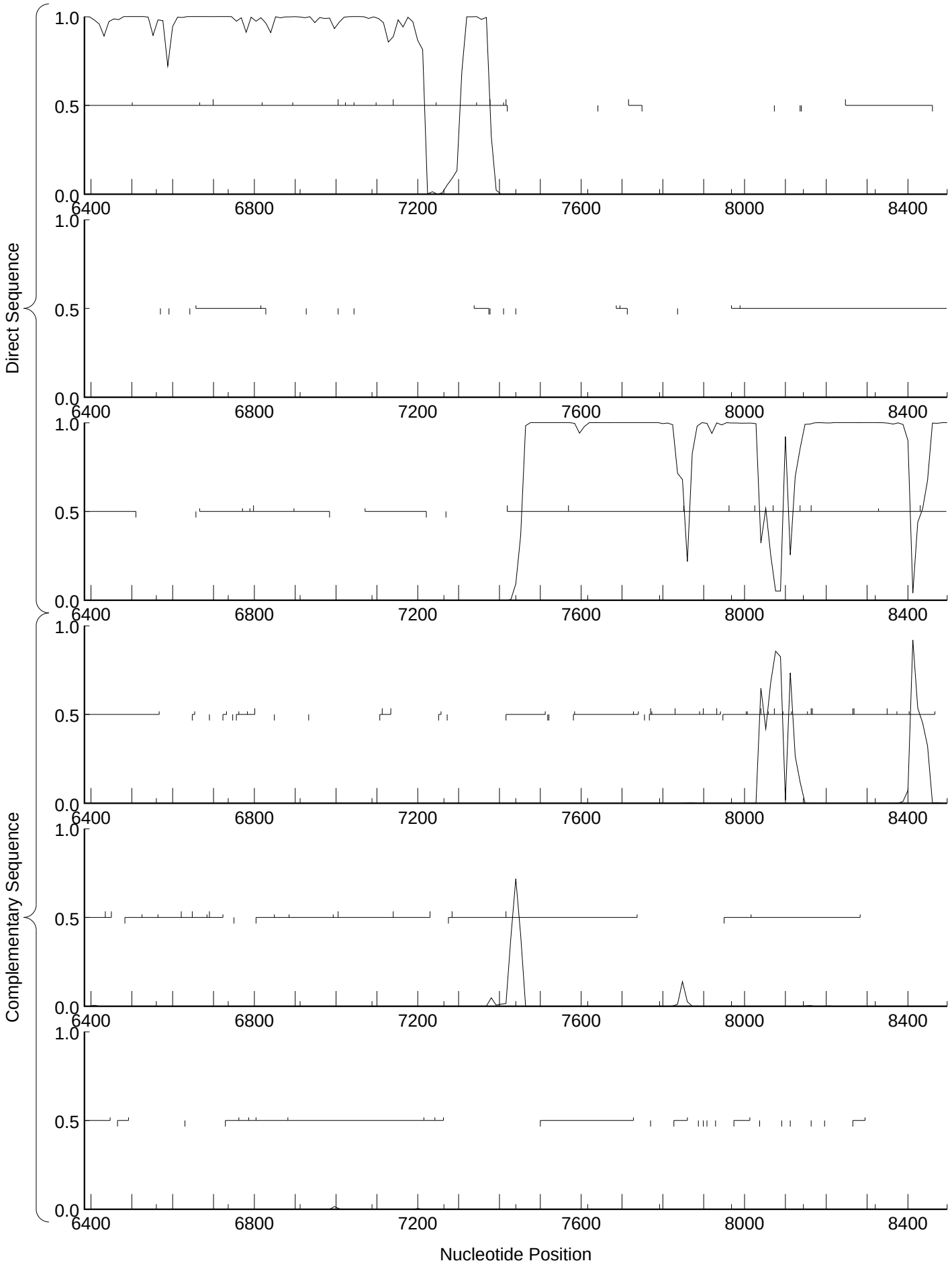
ry complete sequence, 52521 bp including 10-base 3’ overhang (CGGGATGTAA), Cluster A8, Order 4, Window 96, Step 12, 3/26



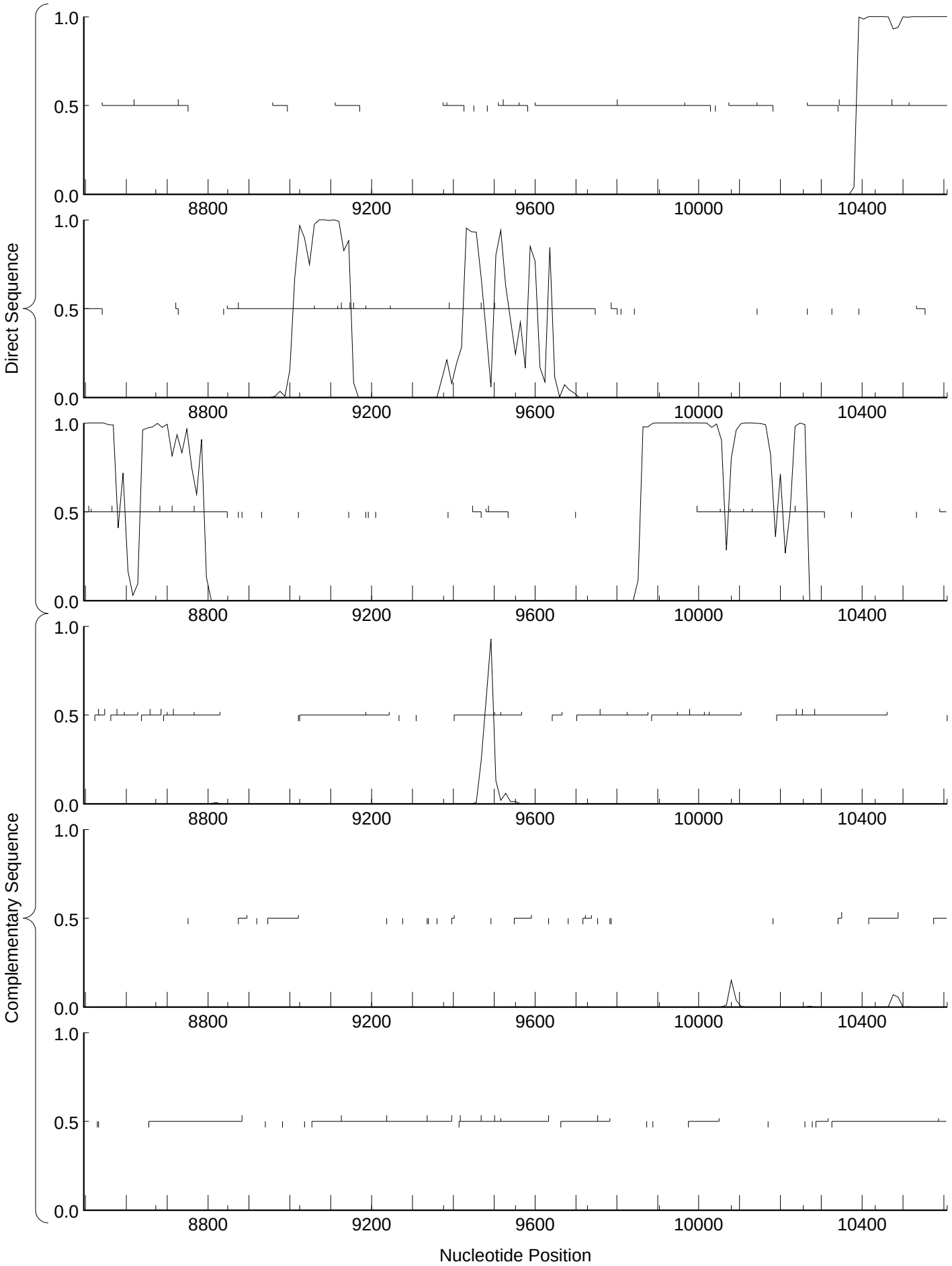
ry complete sequence, 52521 bp including 10-base 3’ overhang (CGGGATGTAA), Cluster A8, Order 4, Window 96, Step 12, 4/26



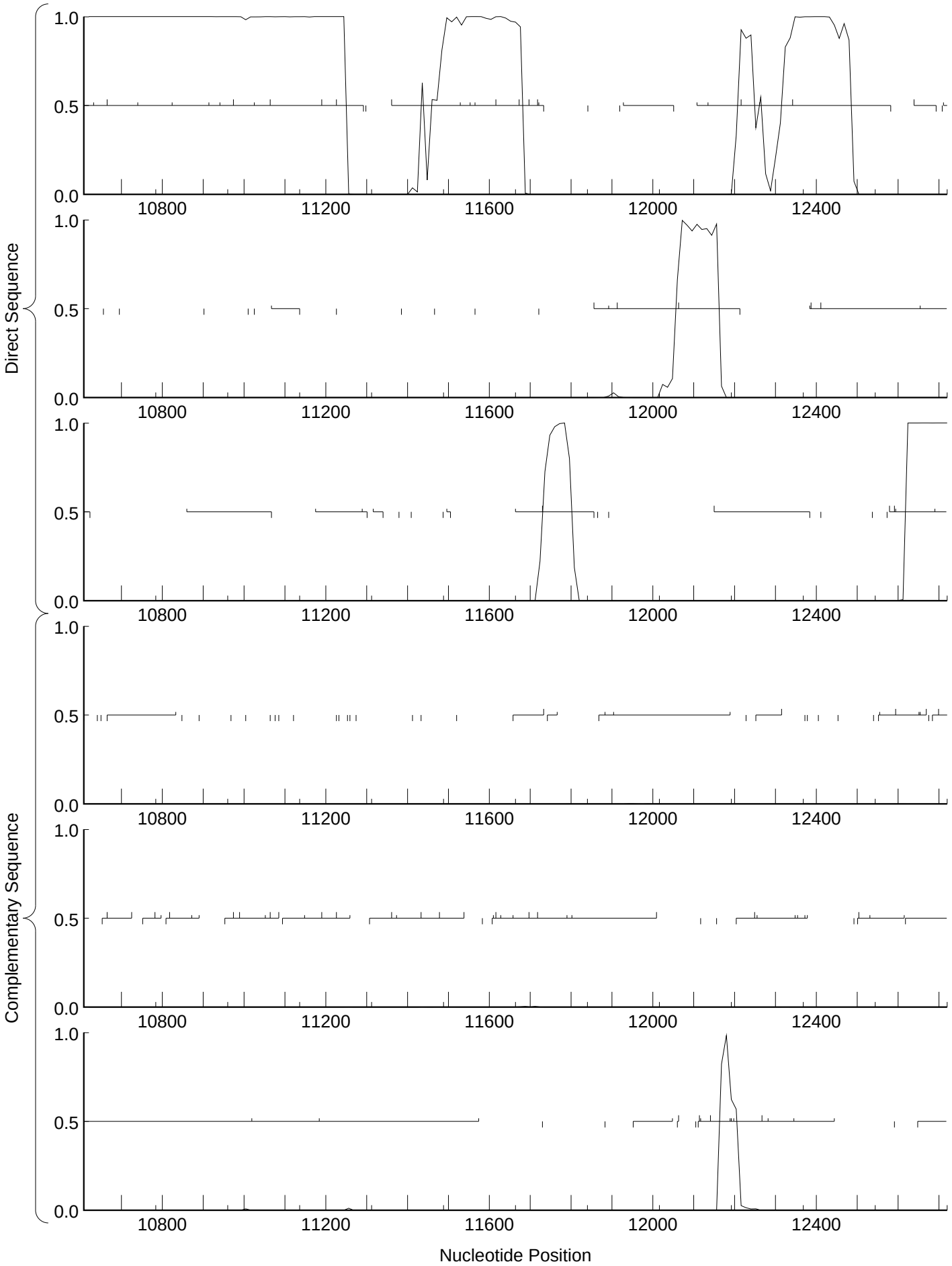
ry complete sequence, 52521 bp including 10-base 3’ overhang (CGGGATGTAA), Cluster A8, Order 4, Window 96, Step 12, 5/26



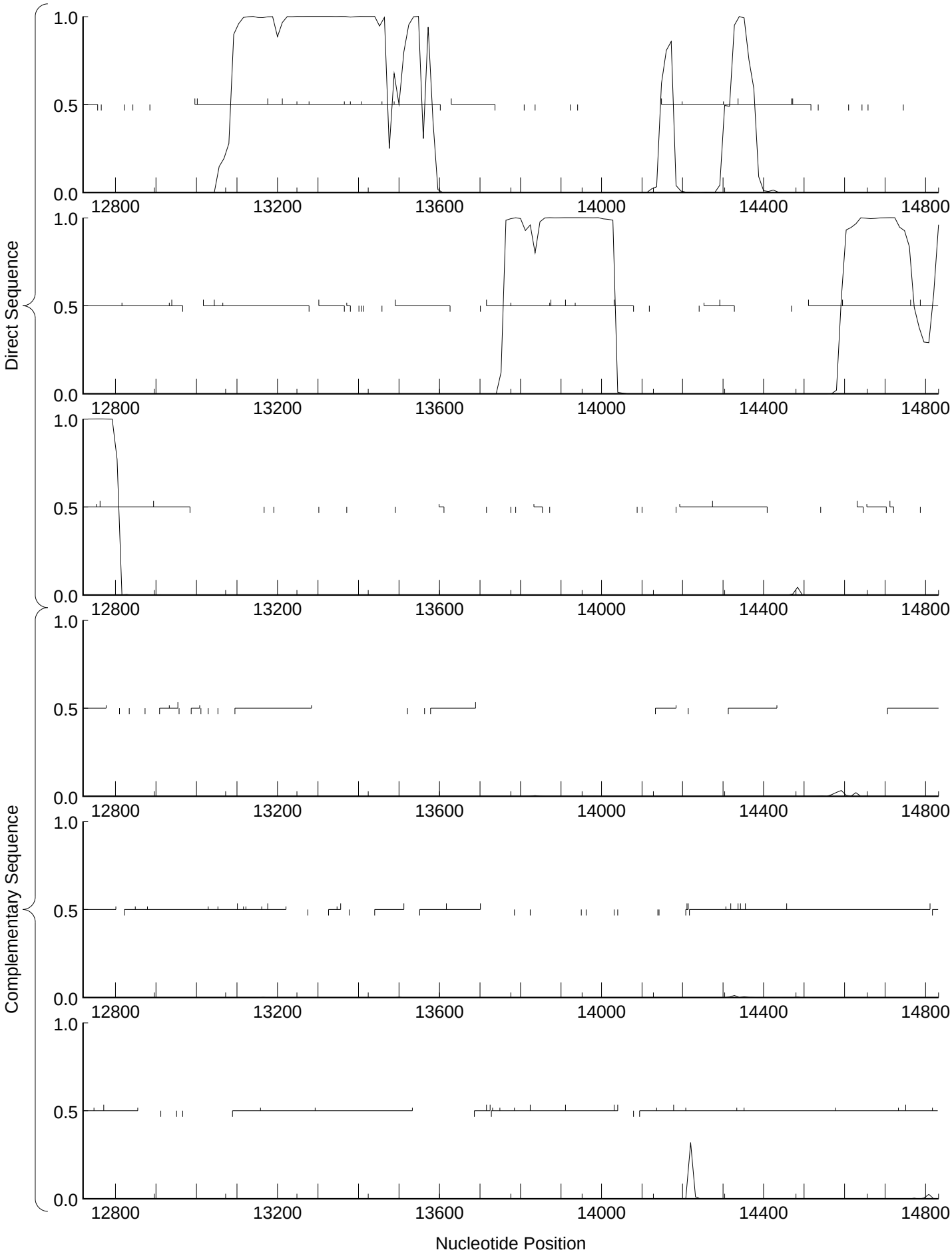
ry complete sequence, 52521 bp including 10-base 3’ overhang (CGGGATGTAA), Cluster A8, Order 4, Window 96, Step 12, 6/26



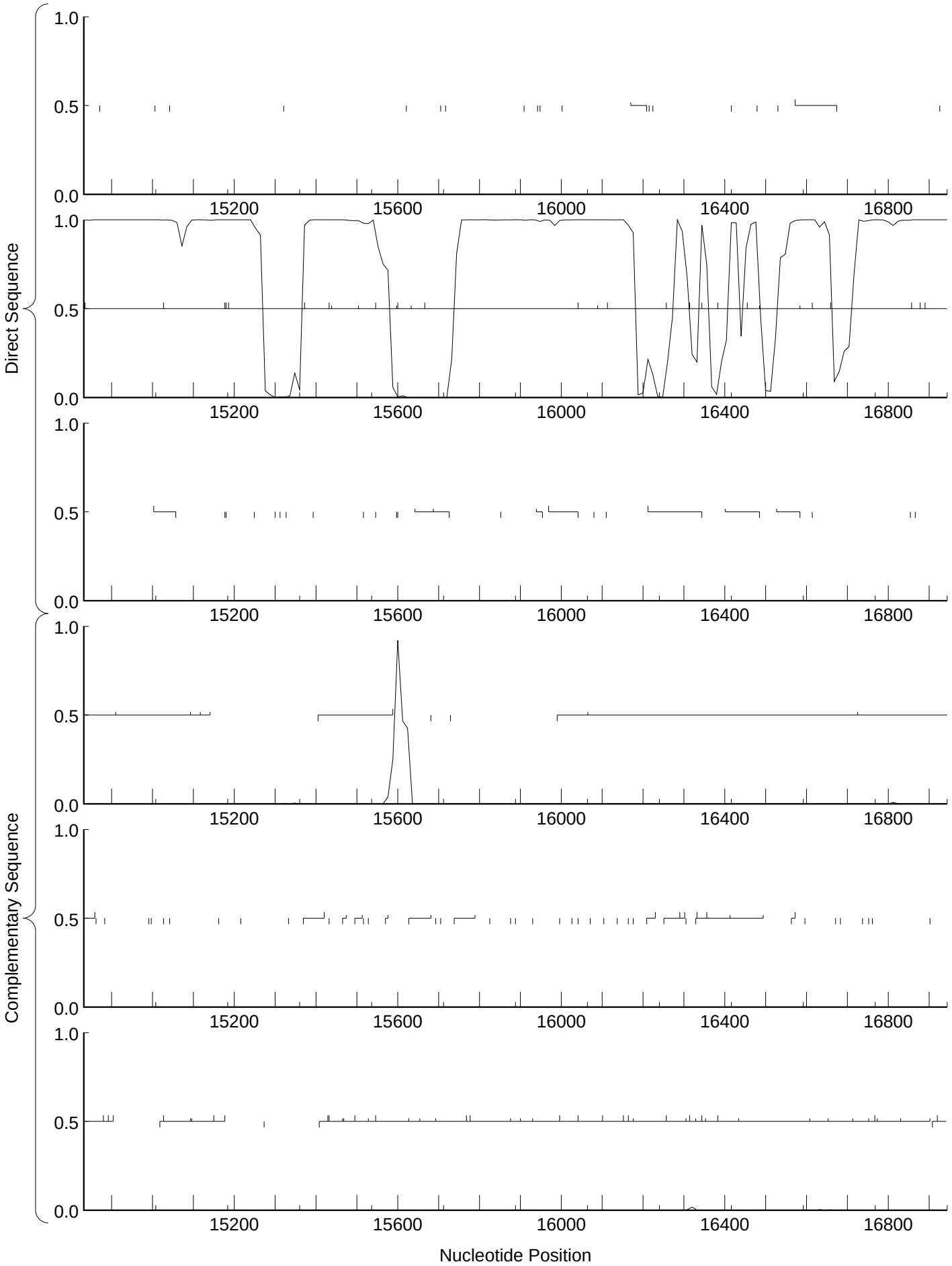
ry complete sequence, 52521 bp including 10-base 3’ overhang (CGGGATGTAA), Cluster A8, Order 4, Window 96, Step 12, 7/26

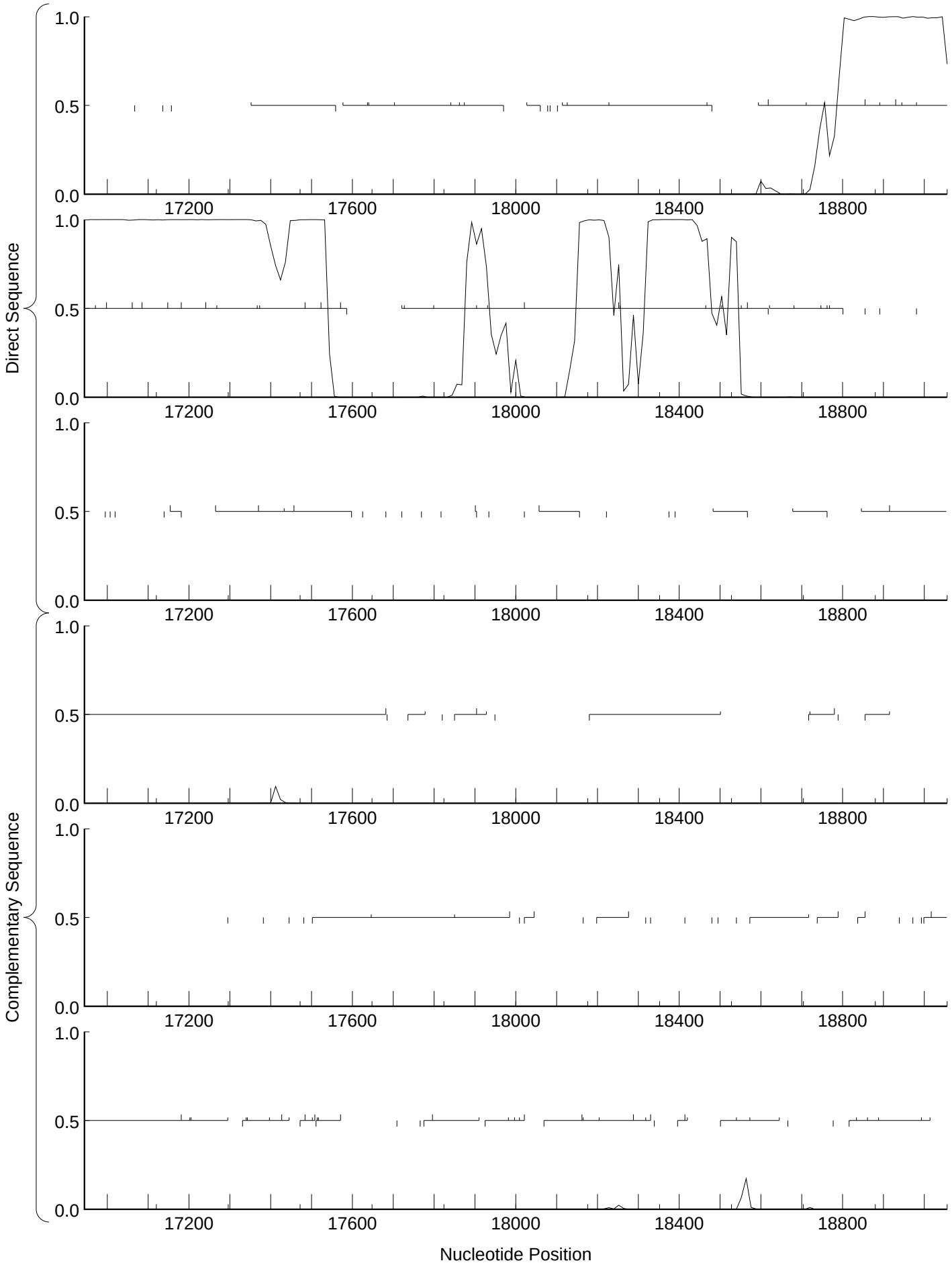


ry complete sequence, 52521 bp including 10-base 3’ overhang (CGGGATGTAA), Cluster A8, Order 4, Window 96, Step 12, 8/26

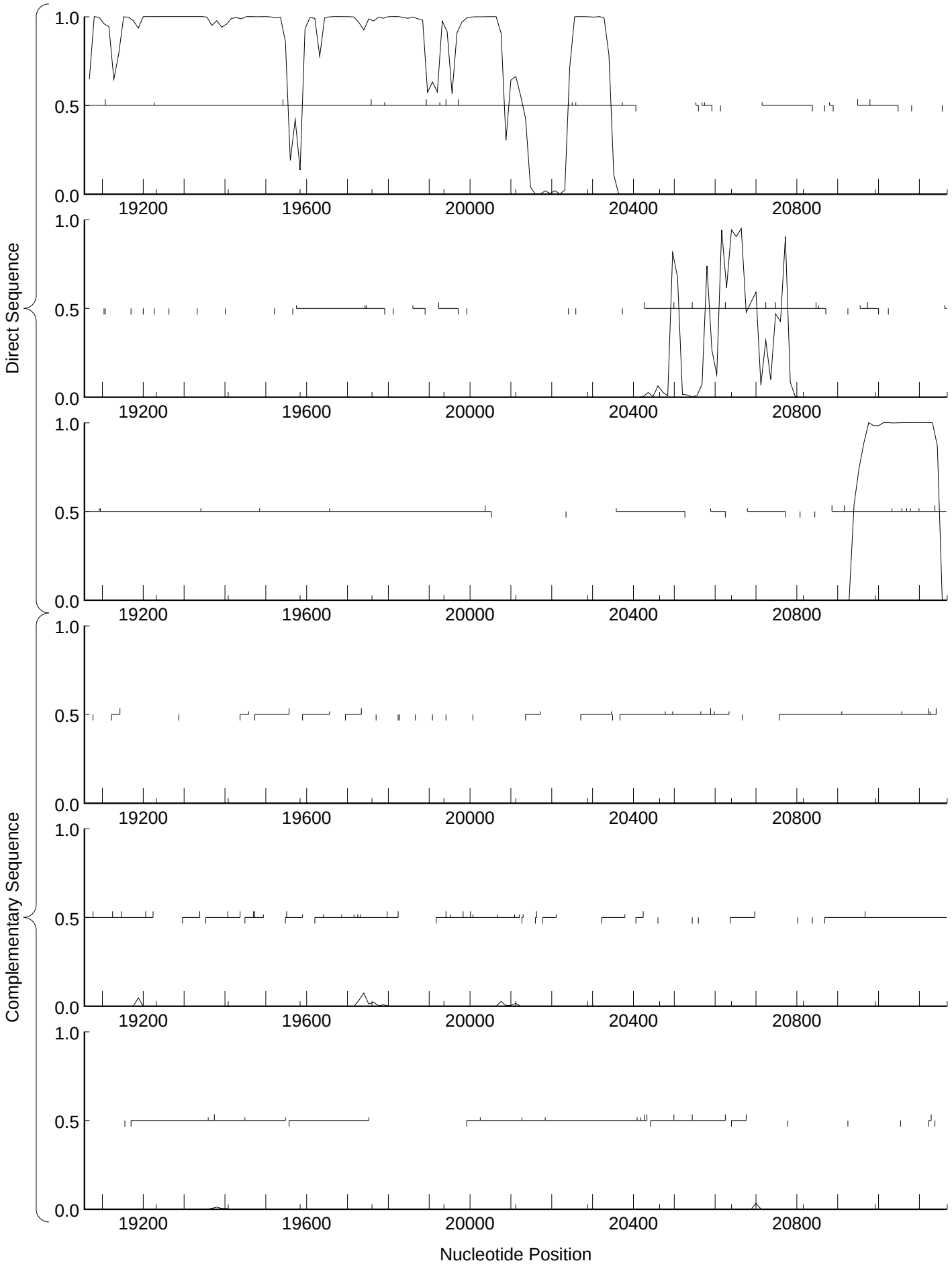


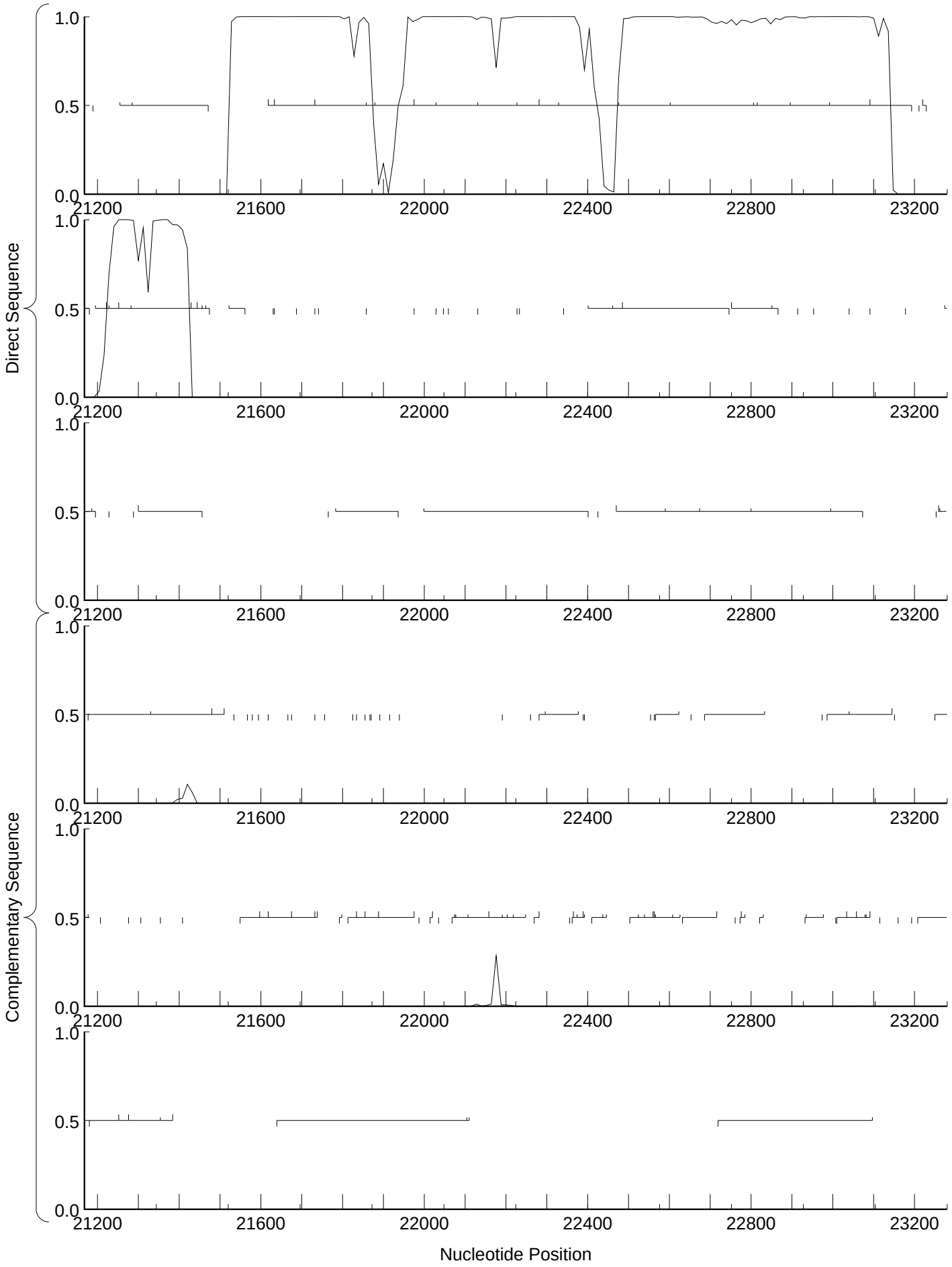
ry complete sequence, 52521 bp including 10-base 3’ overhang (CGGGATGTAA), Cluster A8, Order 4, Window 96, Step 12, 9/26



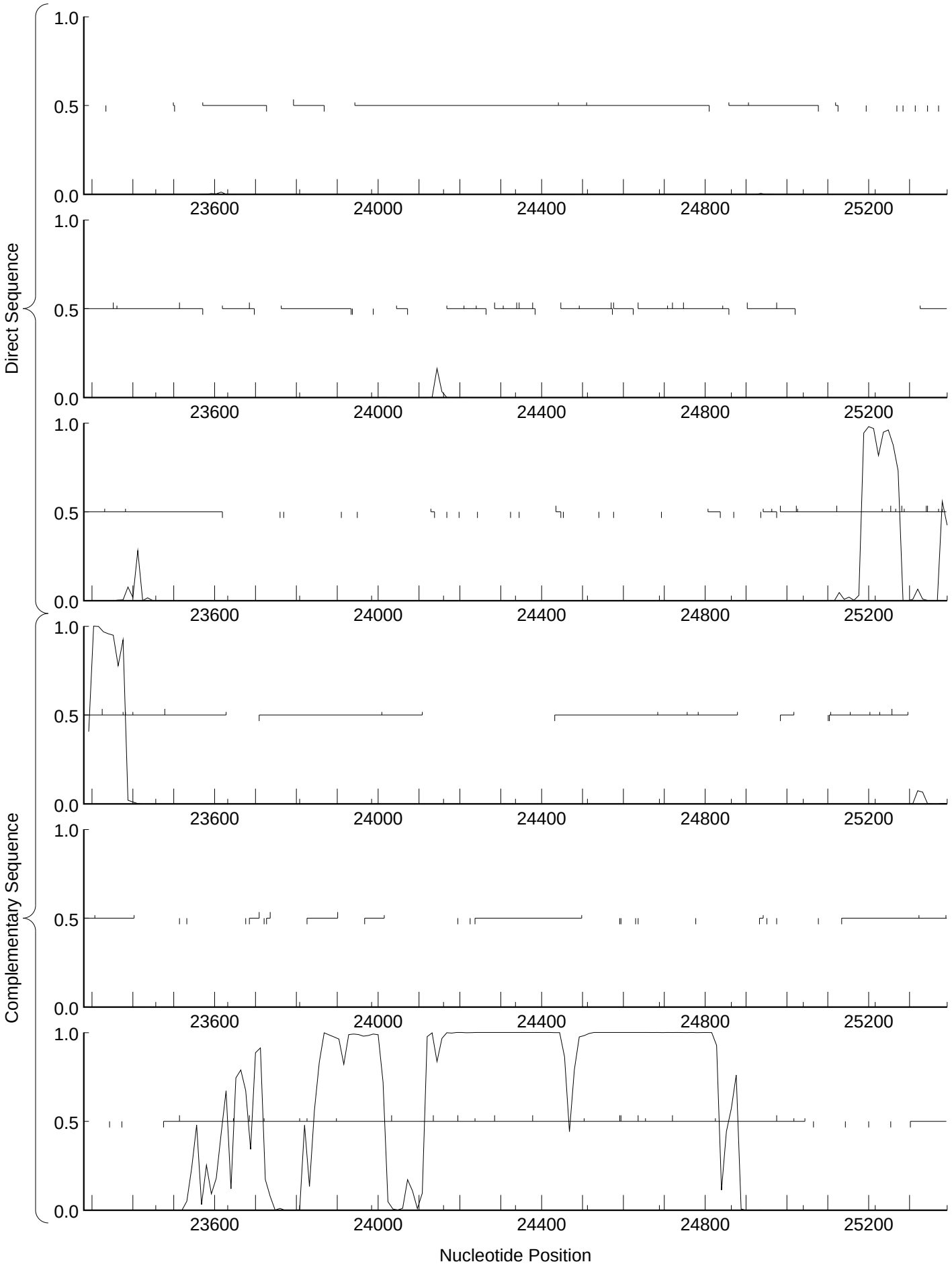

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Complementary Sequence
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0.0
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17600
18000
18400
18800
Nucleotide Position

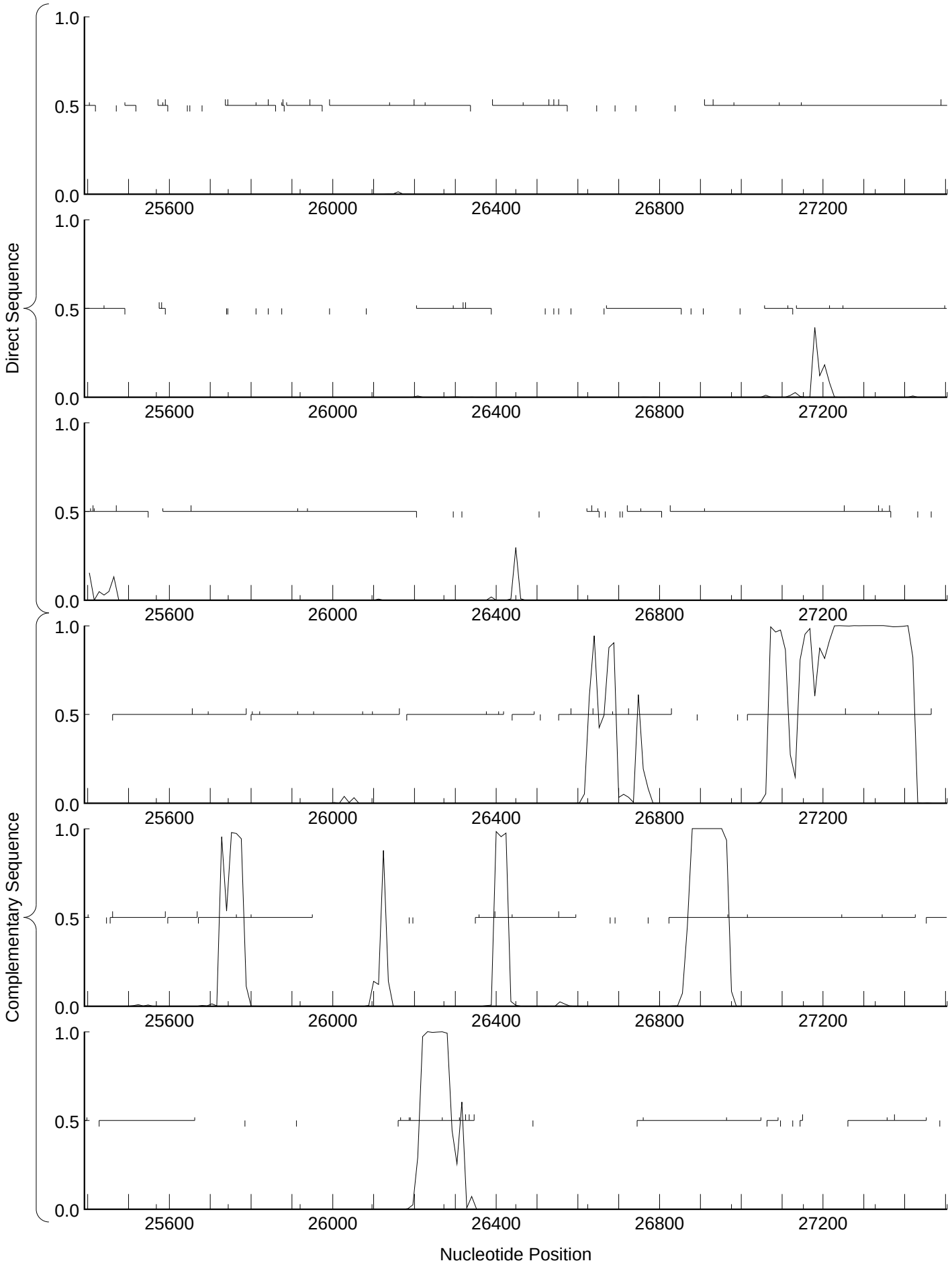
y complete sequence, 52521 bp including 10-base 3' overhang (CGGGATGTAA), Cluster A8, Order 4, Window 96, Step 12, 11/26



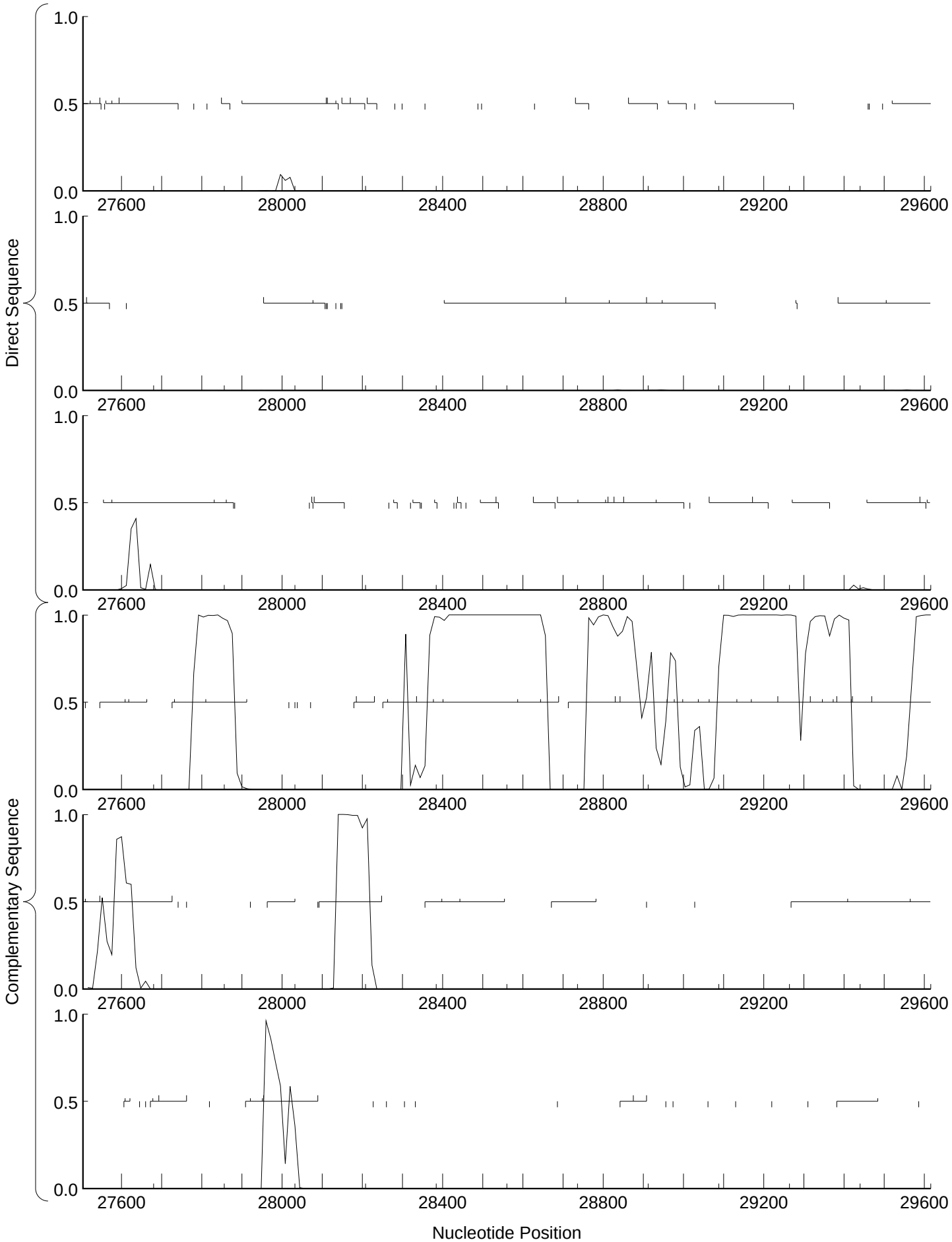

Direct Sequence
Complementary Sequence
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0.5
0.0
21200
21600
22000
22400
22800
23200
Nucleotide Position

y complete sequence, 52521 bp including 10-base 3' overhang (CGGGATGTAA), Cluster A8, Order 4, Window 96, Step 12, 13/26

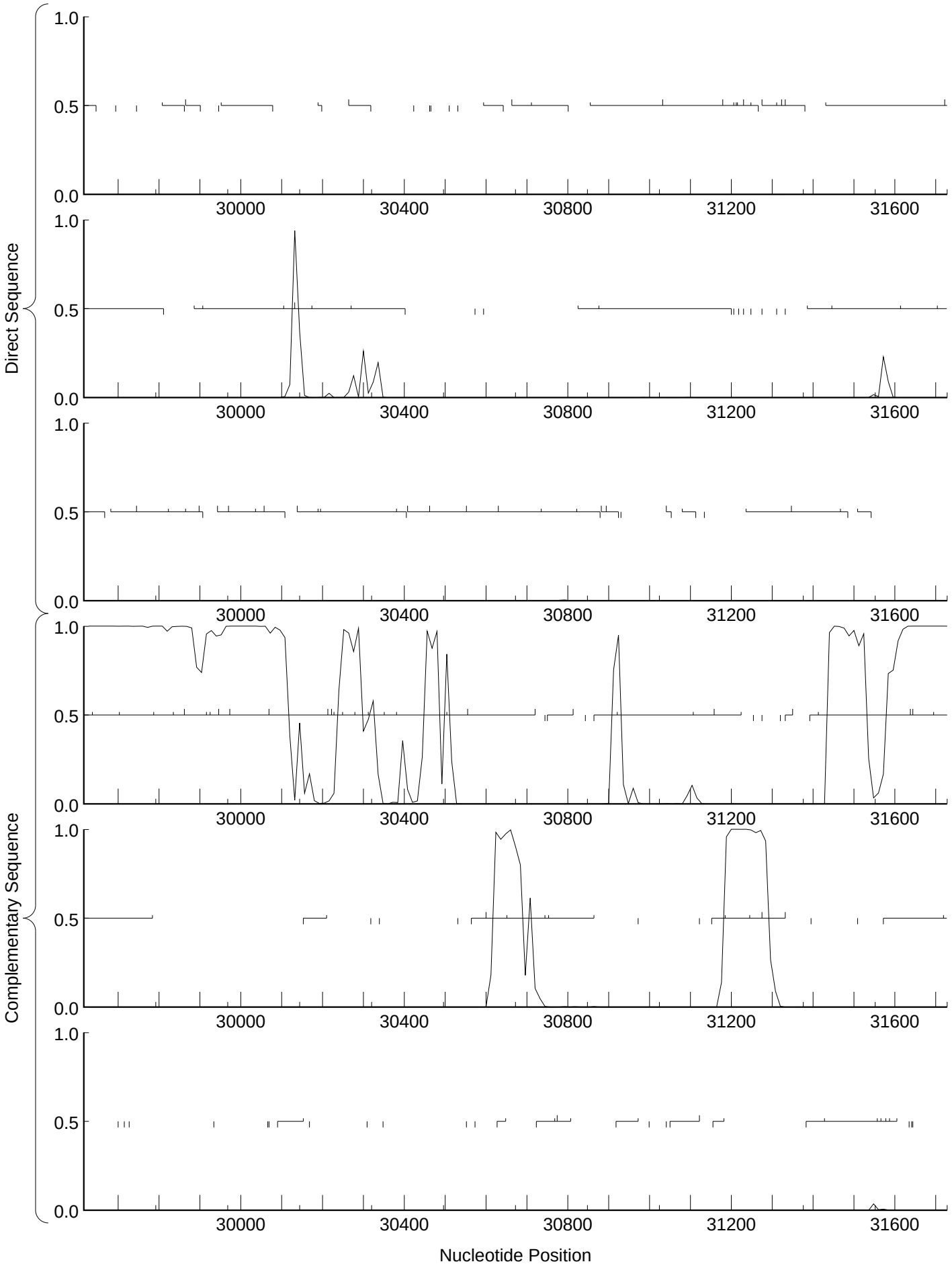


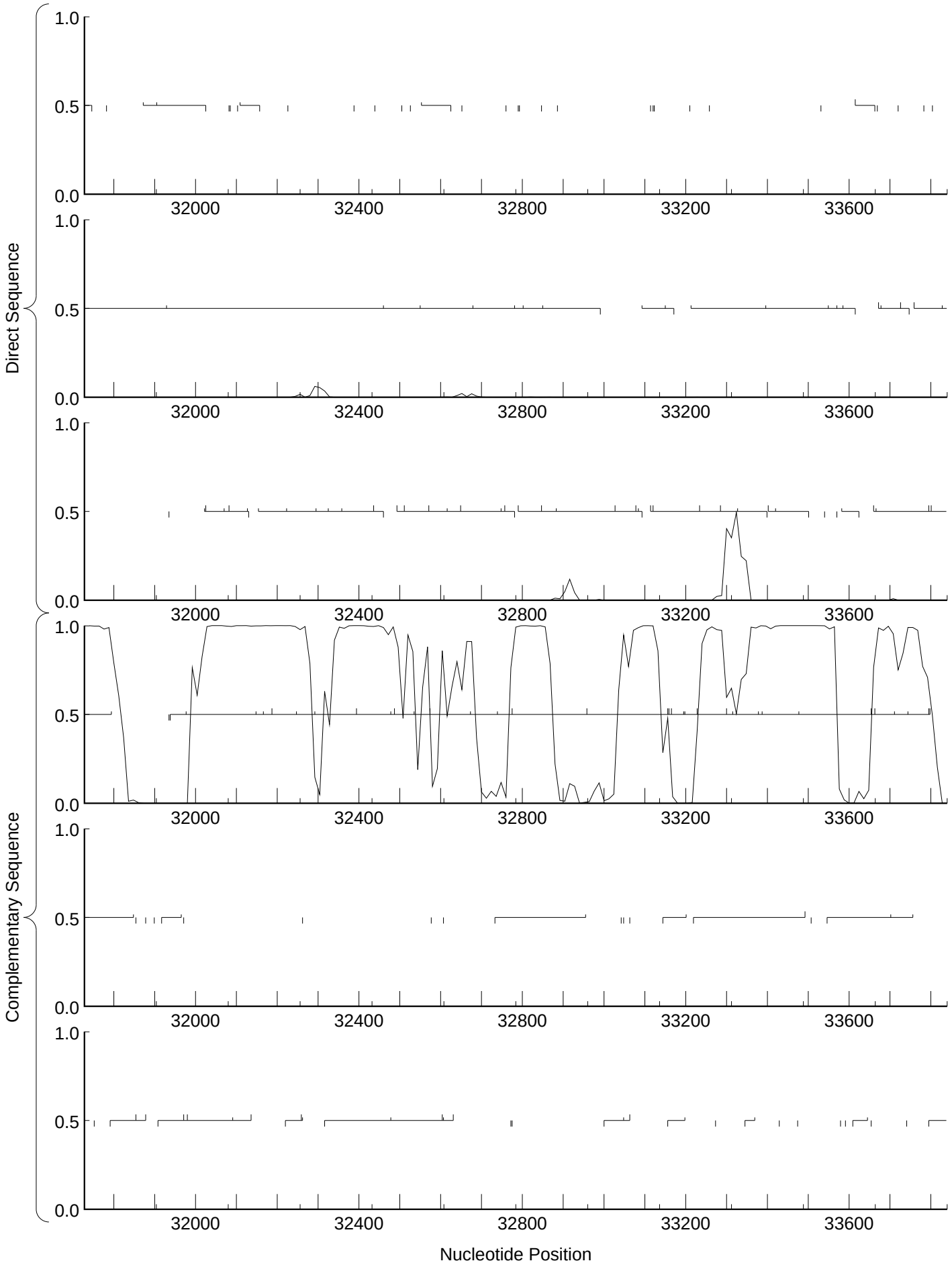

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Complementary Sequence
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26400
26800
27200
Nucleotide Position

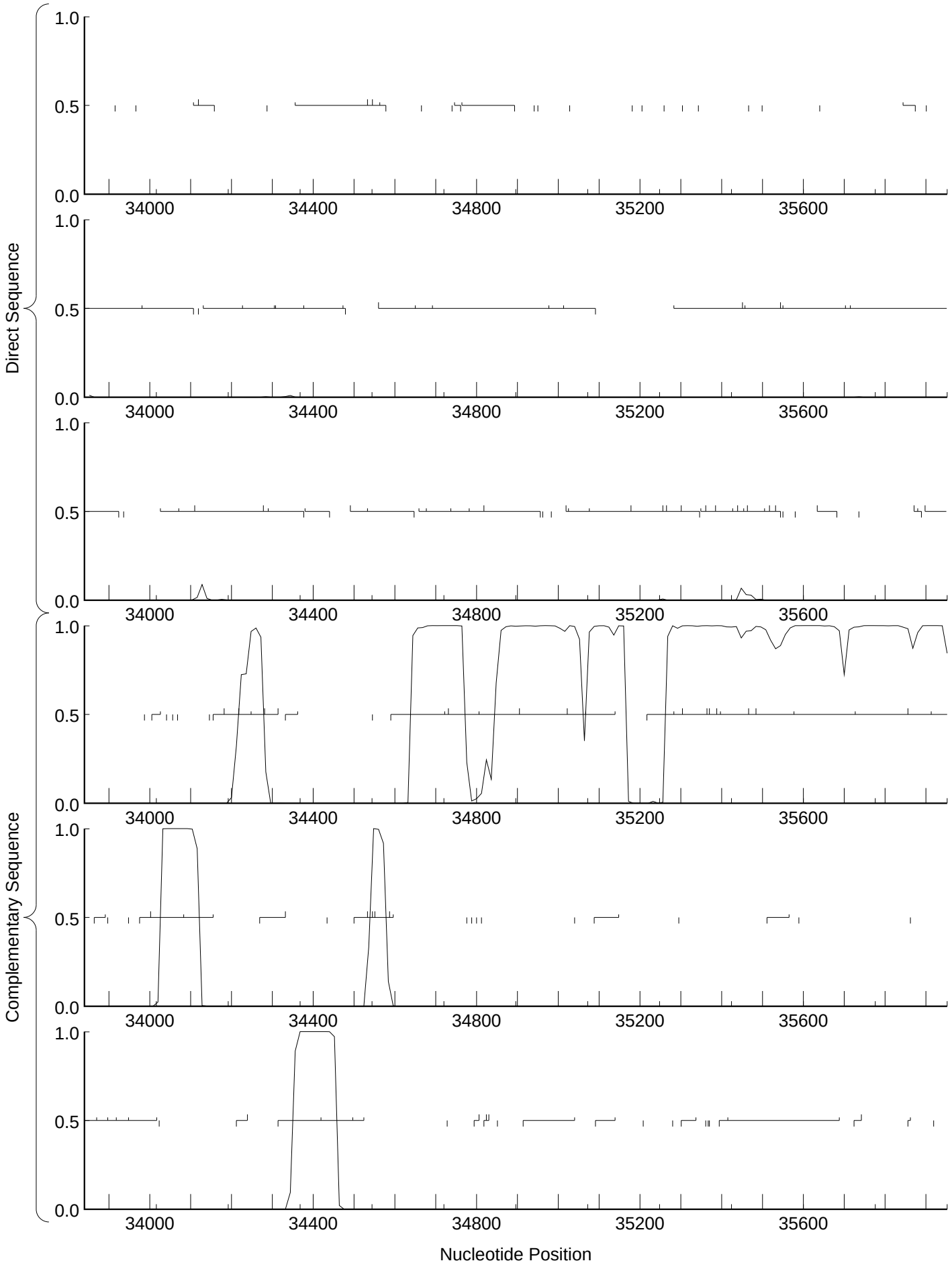
y complete sequence, 52521 bp including 10-base 3' overhang (CGGGATGTAA), Cluster A8, Order 4, Window 96, Step 12, 15/26



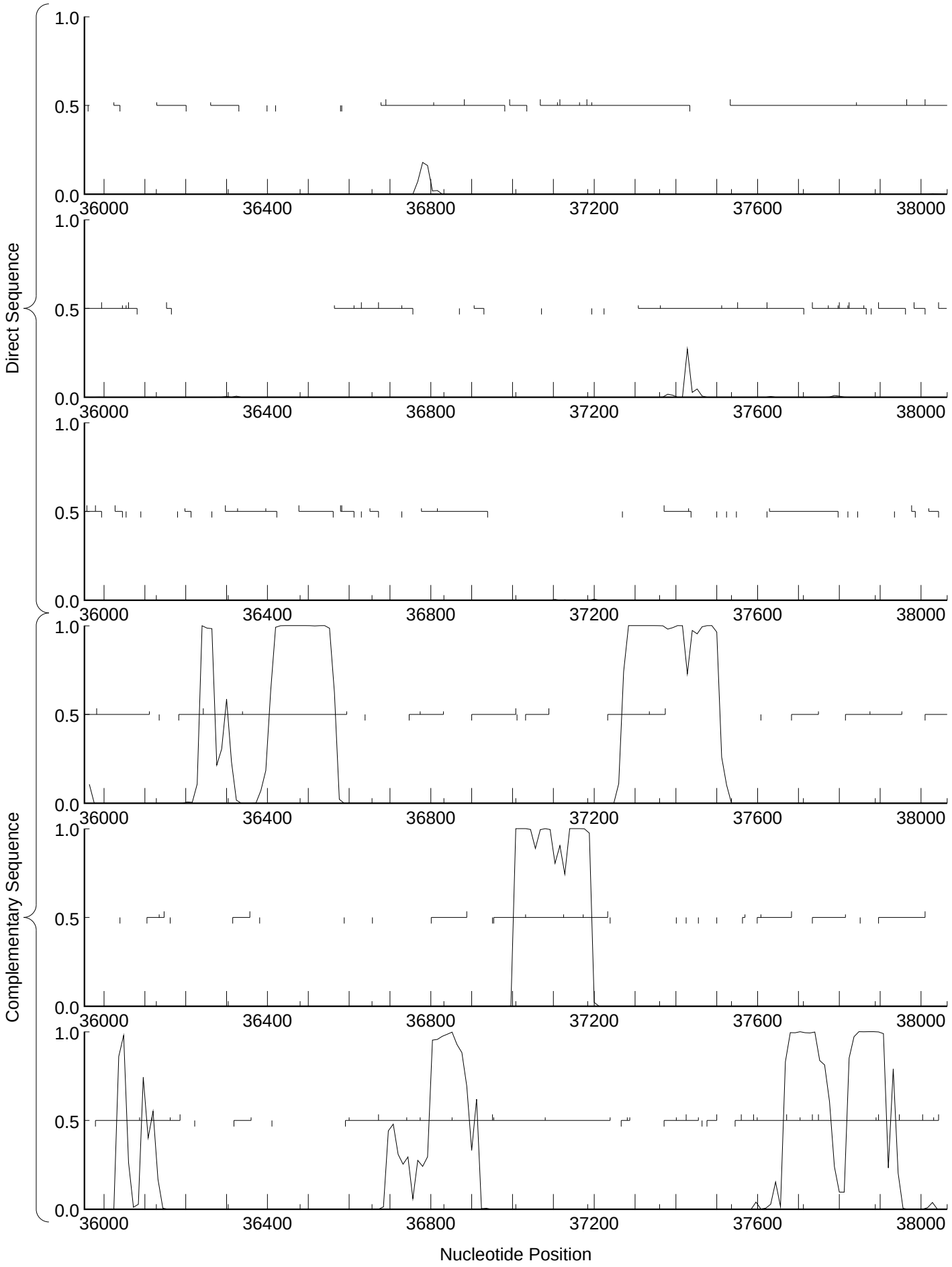
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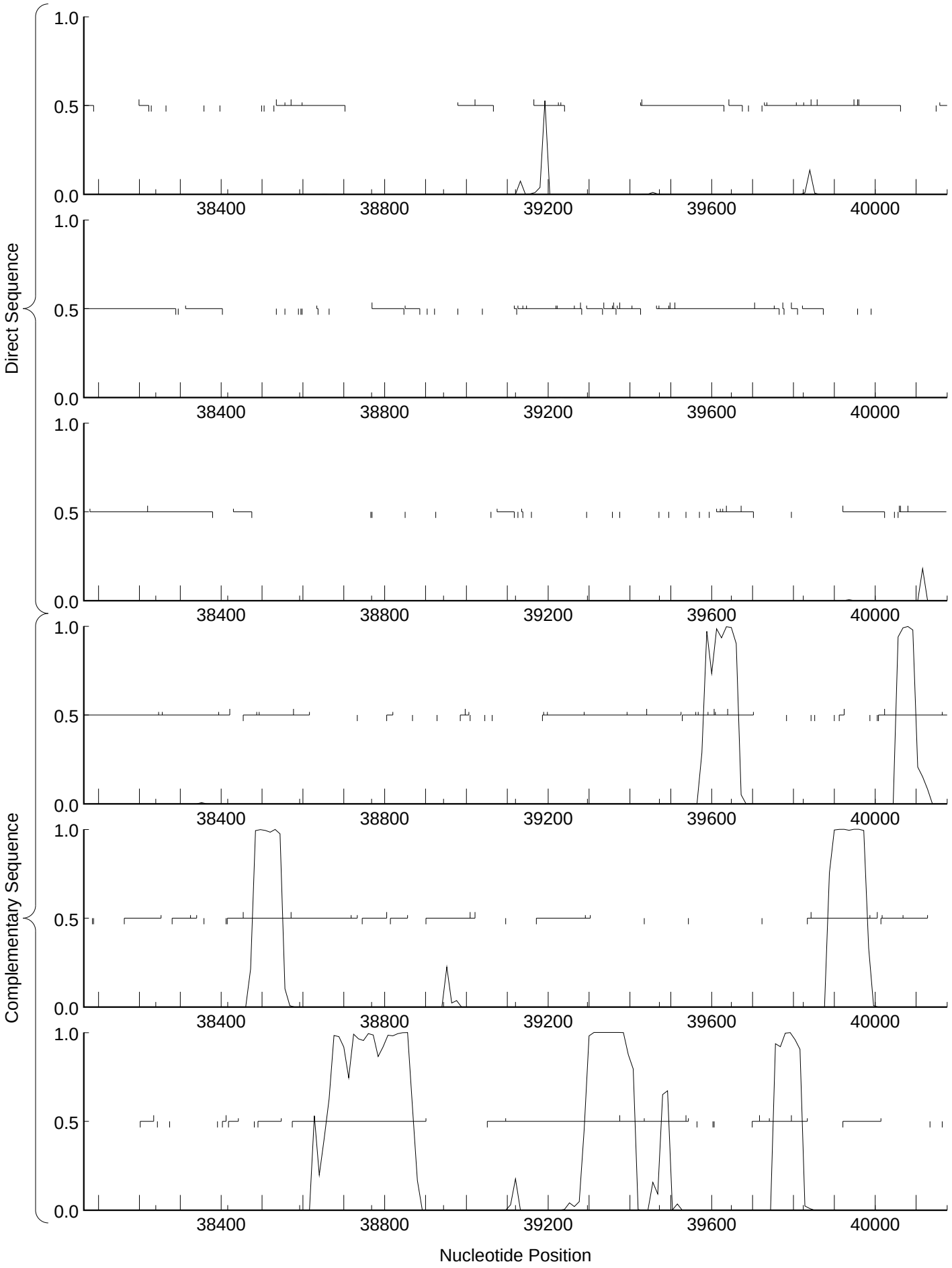

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
32000
32400
32800
33200
33600
Nucleotide Position


Direct Sequence
Complementary Sequence
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0.0
34000
34400
34800
35200
35600
Nucleotide Position

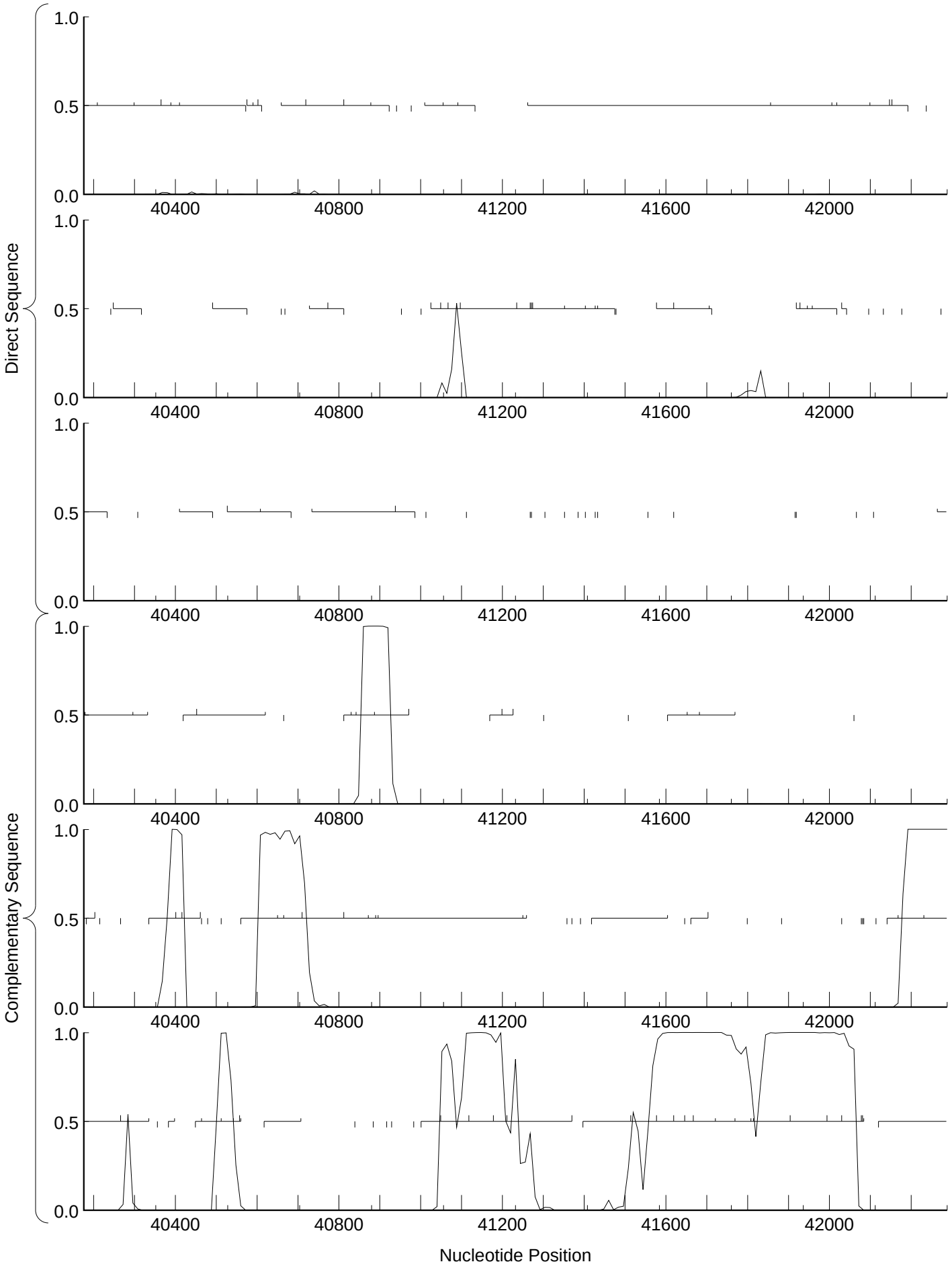
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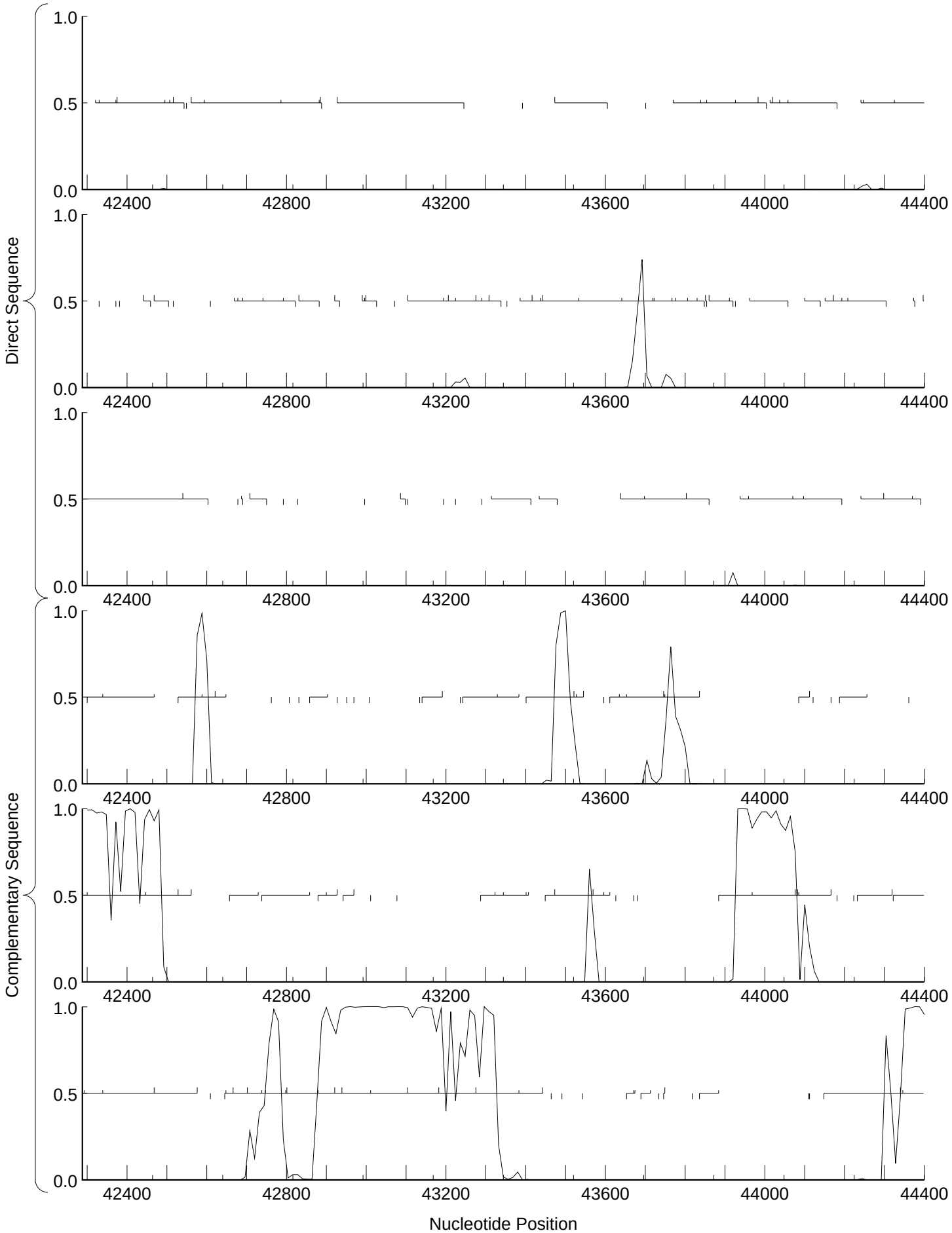


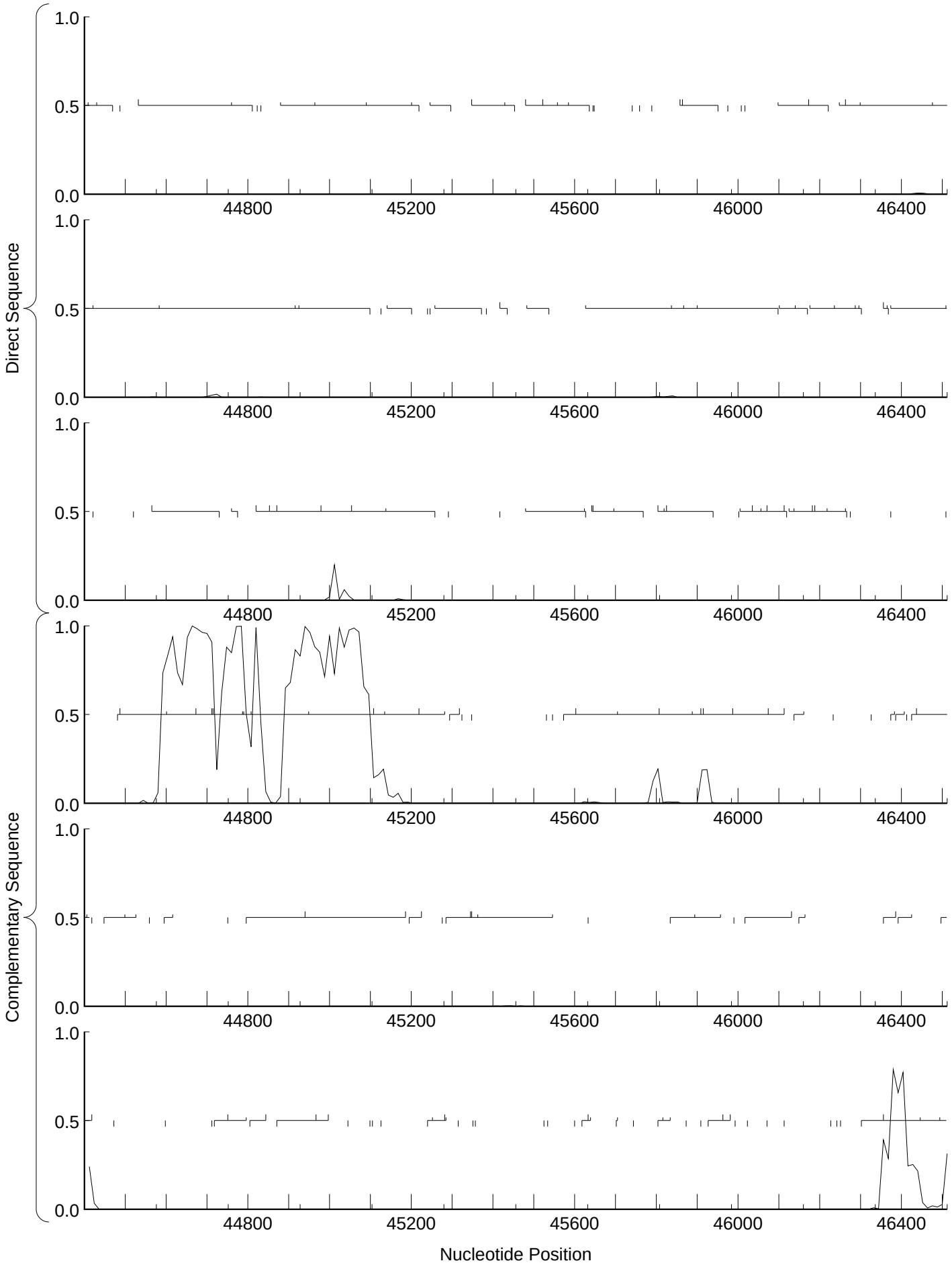
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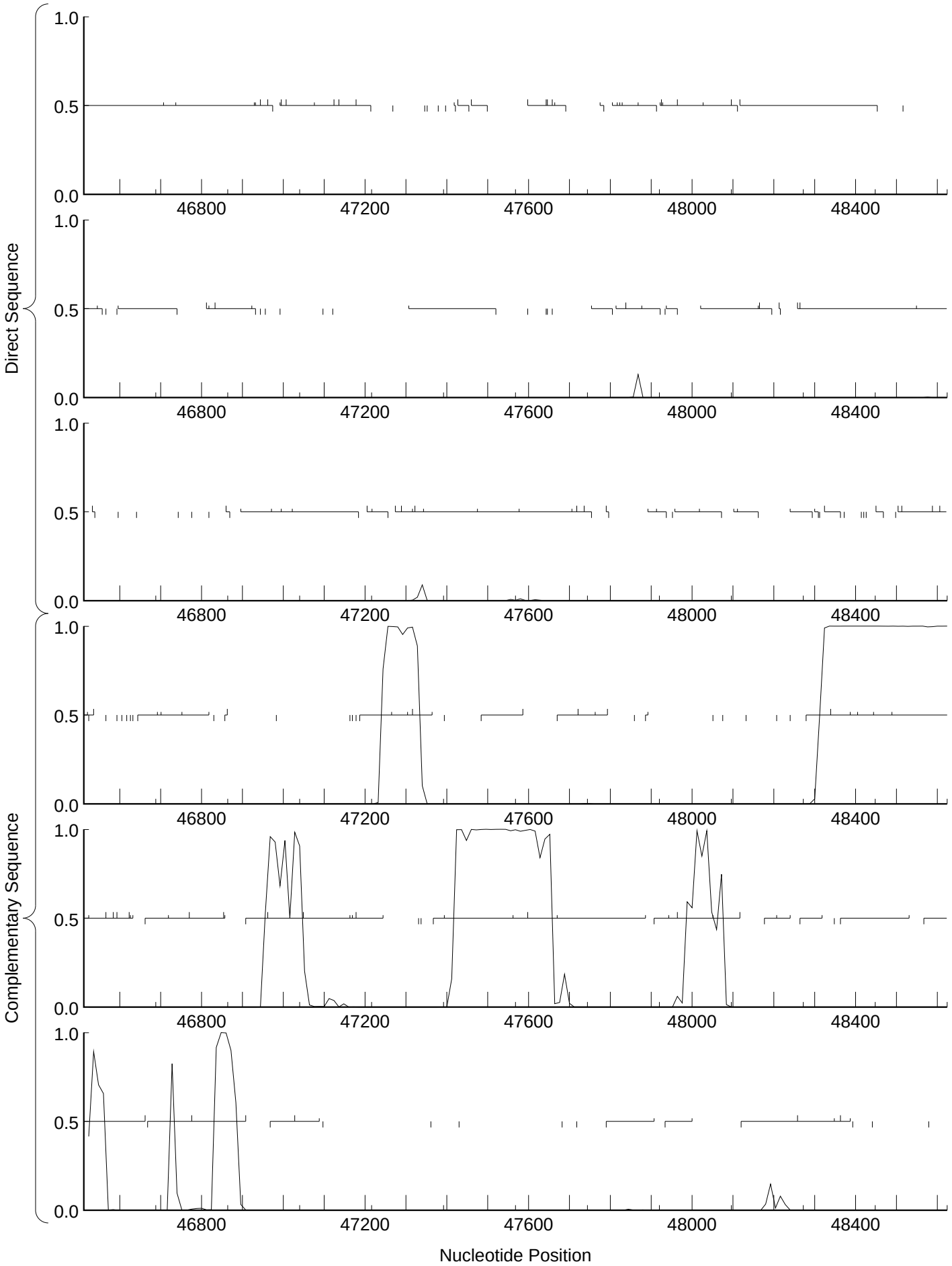
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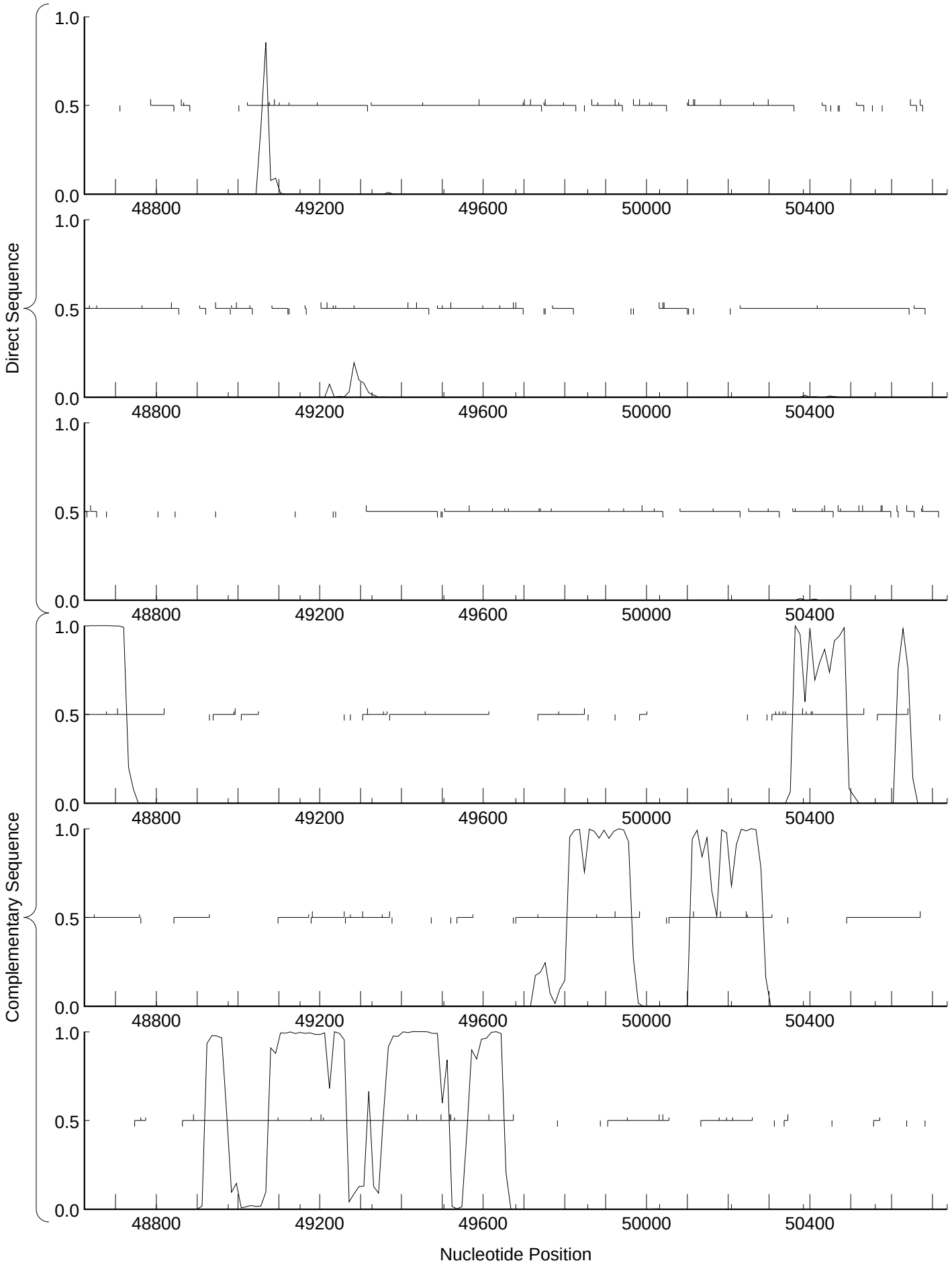

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Complementary Sequence
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44000
44400
Nucleotide Position

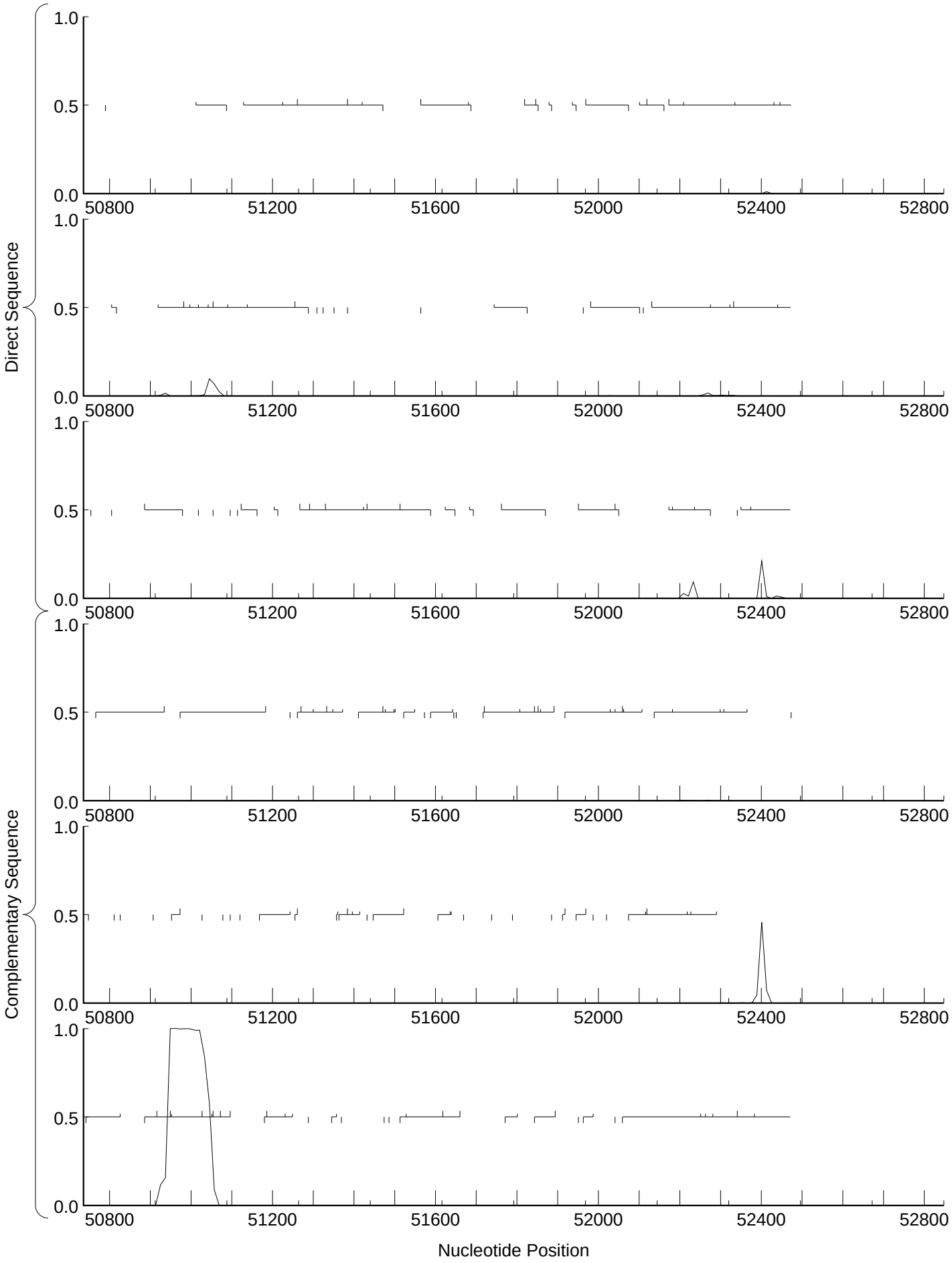

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
44800
45200
45600
46000
46400
Nucleotide Position

y complete sequence, 52521 bp including 10-base 3’ overhang (CGGGATGTAA), Cluster A8, Order 4, Window 96, Step 12, 24/26



y complete sequence, 52521 bp including 10-base 3’ overhang (CGGGATGTAA), Cluster A8, Order 4, Window 96, Step 12, 25/26




Direct Sequence
Complementary Sequence
1.0
0.5
0.0
50800
51200
51600
52000
52400
52800
Nucleotide Position