GeneMark

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

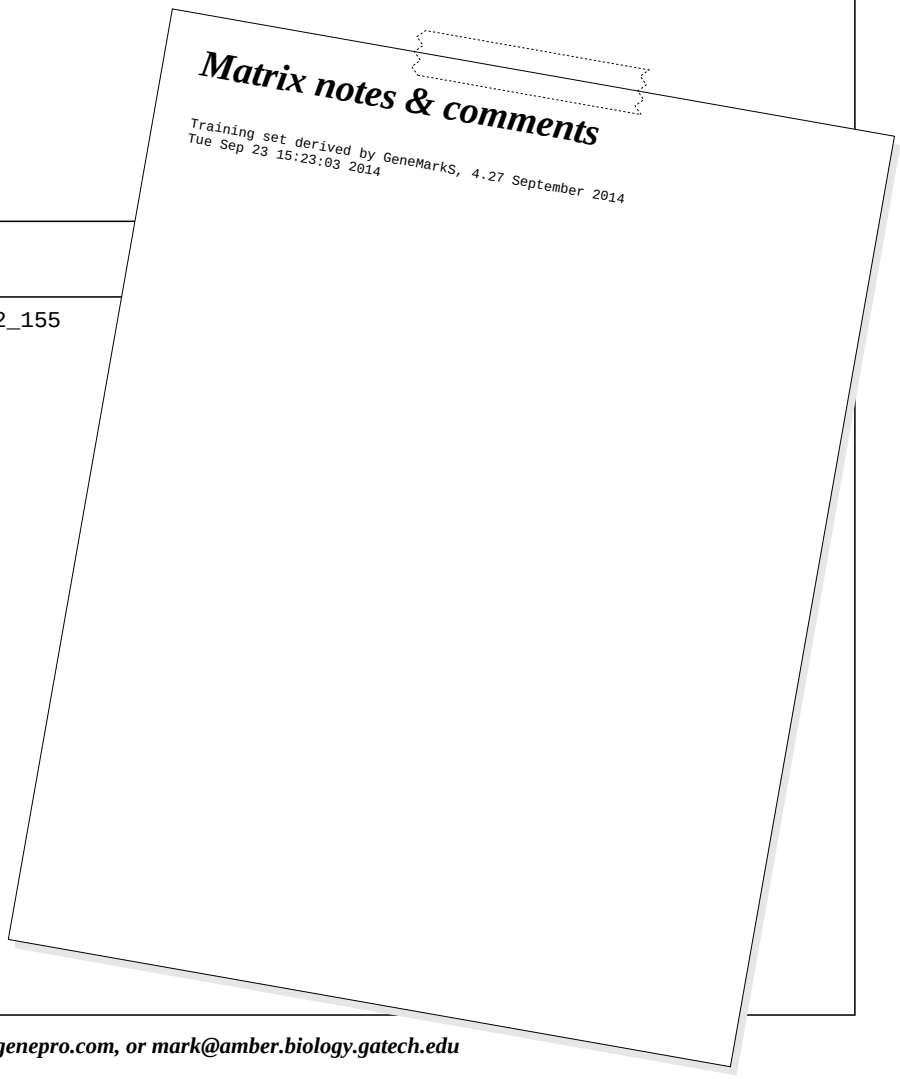
PROGRAM INFORMATION

```
Sequence         :  Mycobacterium phage Lopton complete sequence, 52394 bp including 10-base 3' overhang (CGGAT
Analysis Date    :  3/28/24 at 4:57:31
Pages            :  26
Sequence Length  :  52394 bp
GC Content       :   63.54%

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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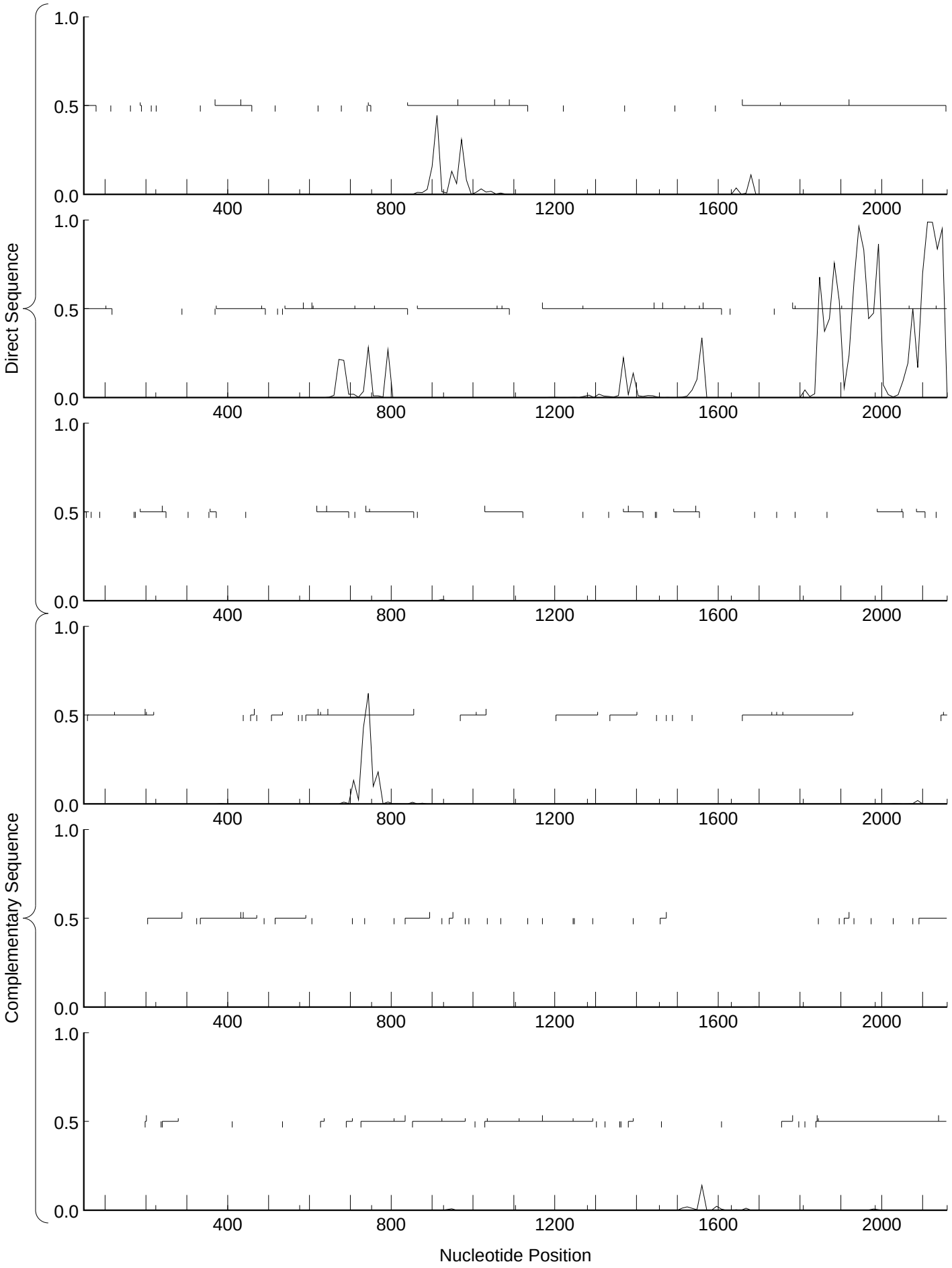
MATRIX INFORMATION

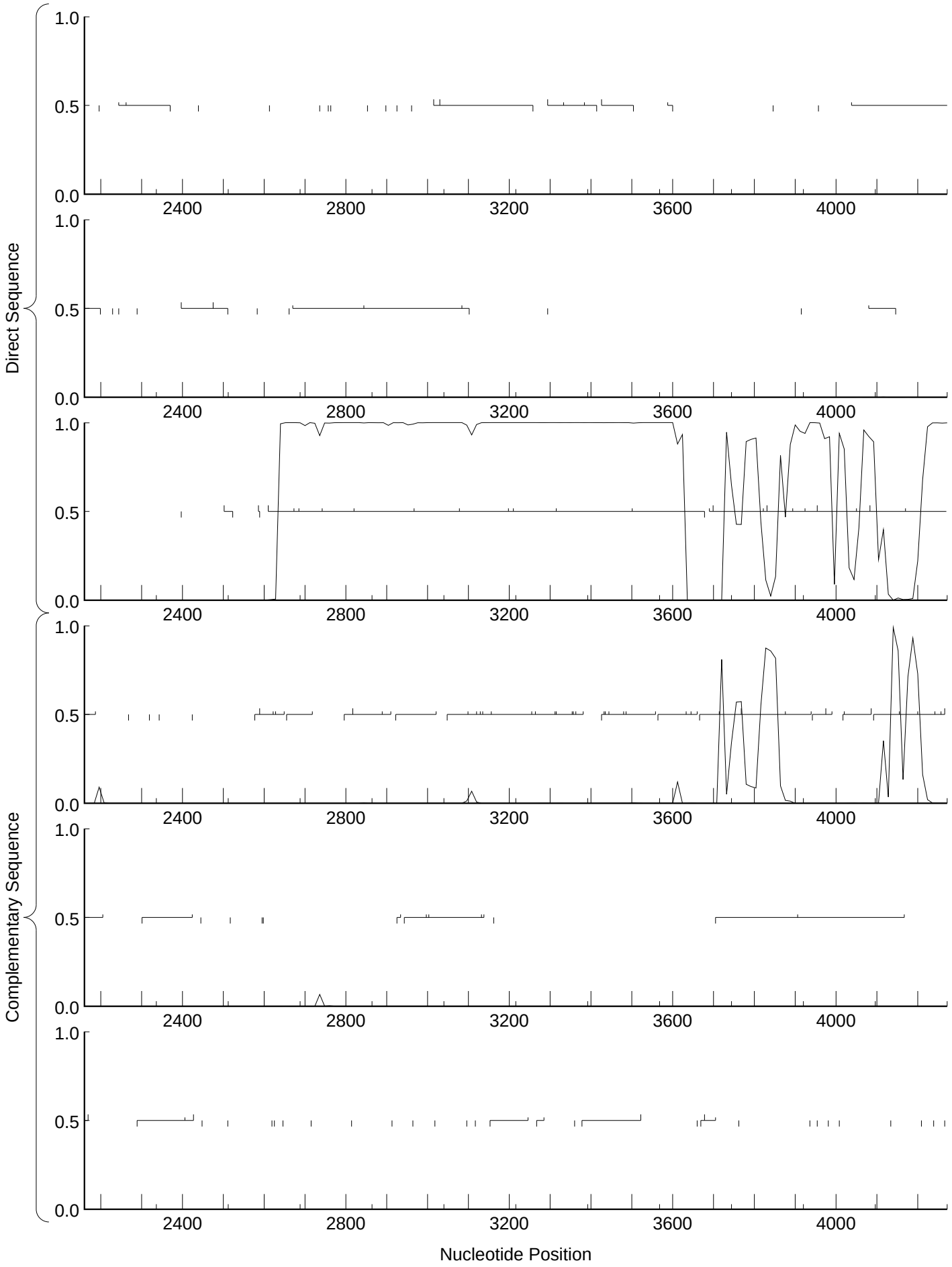
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Matrix     :  Mycobacterium_smegmatis_MC2_155
Author     :  -

Order      :  4
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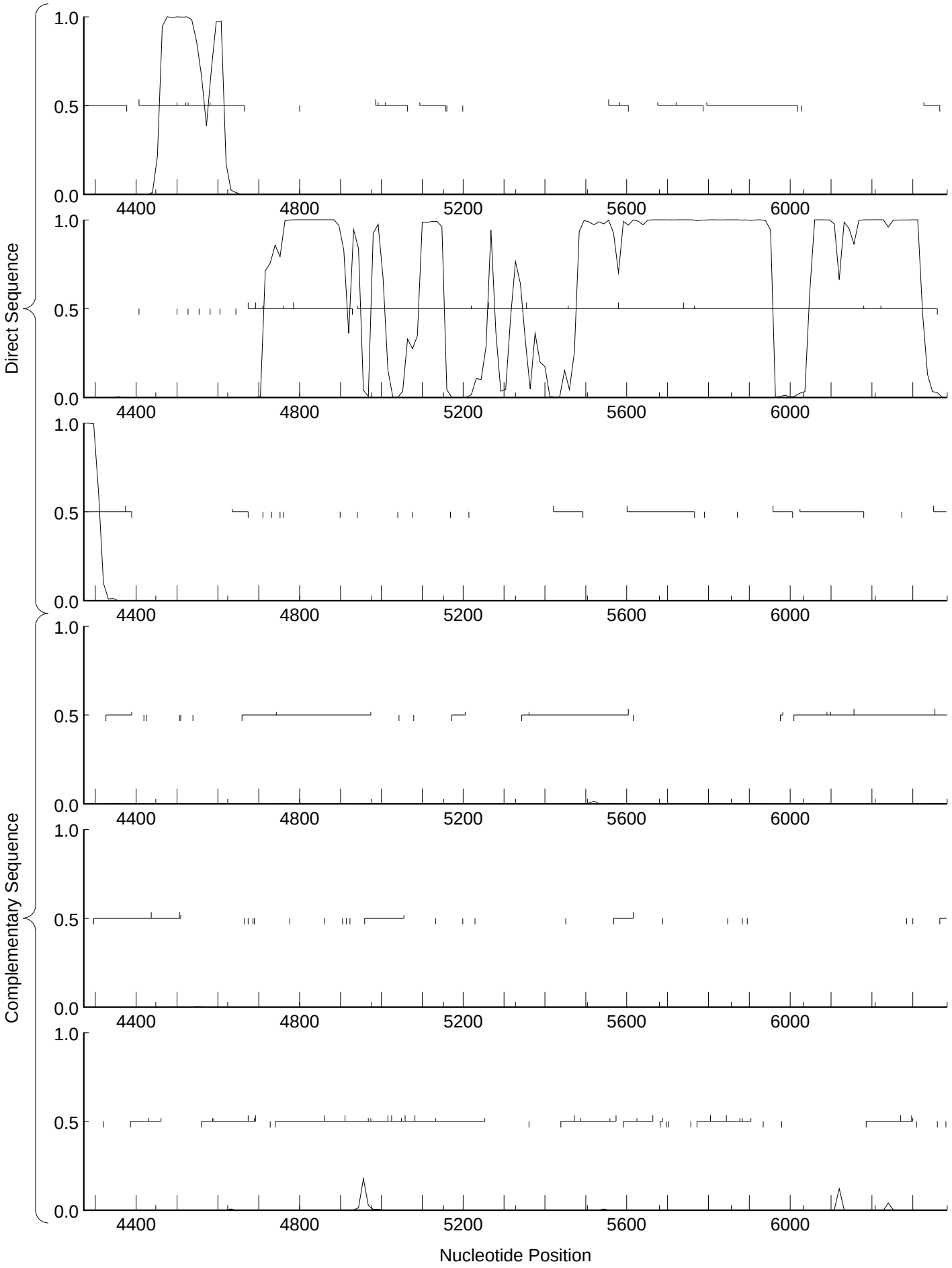

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  Send questions / comments to:
      Dr. M. Borodovsky
      Georgia Institute of Technology
      School of Biology
      Atlanta, GA  30332-0230
```

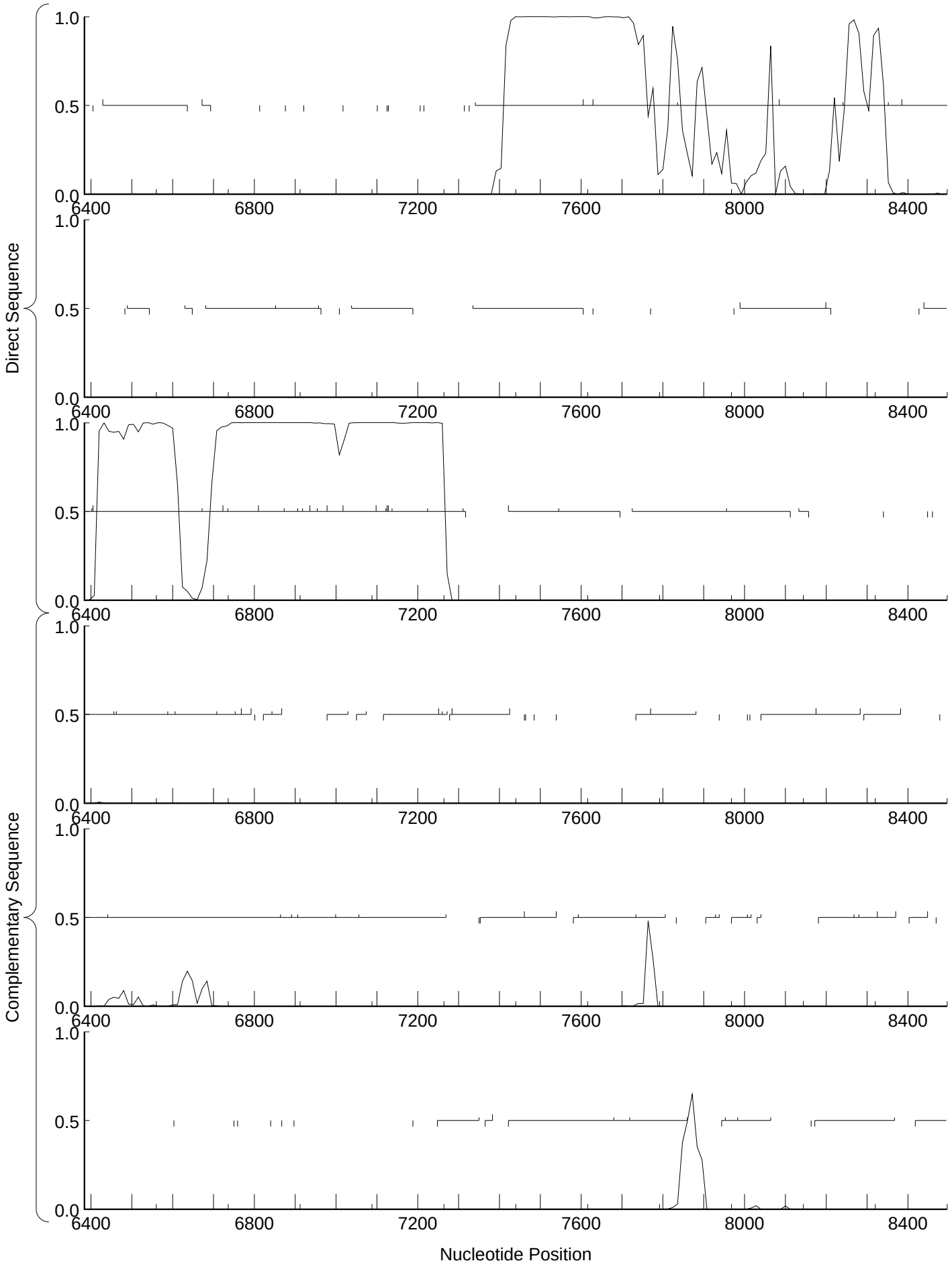

For help or information, send electronic mail to: custserv@genepro.com, or mark@amber.biology.gatech.edu

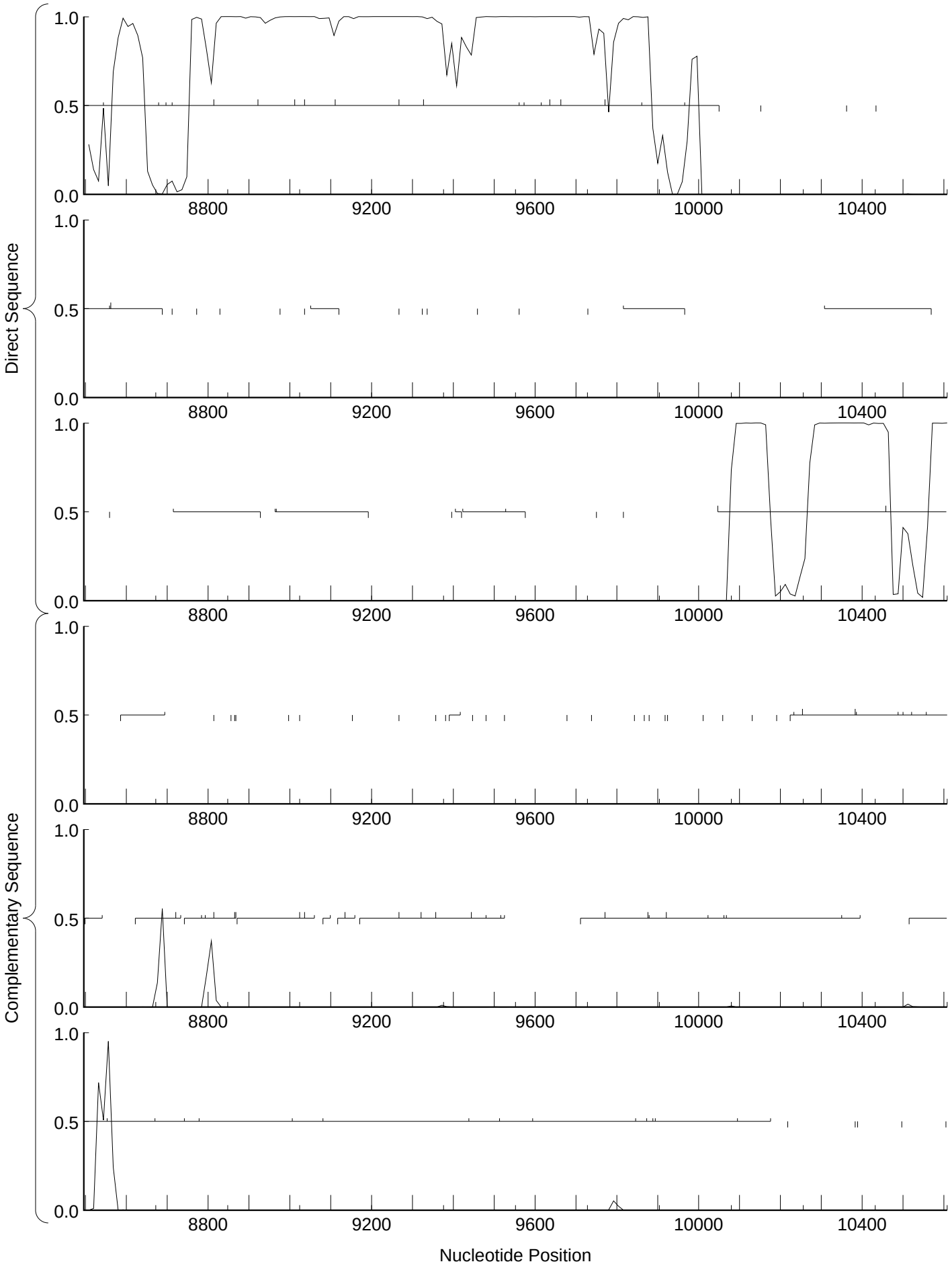

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Complementary Sequence
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0.0
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800
1200
1600
2000
Nucleotide Position

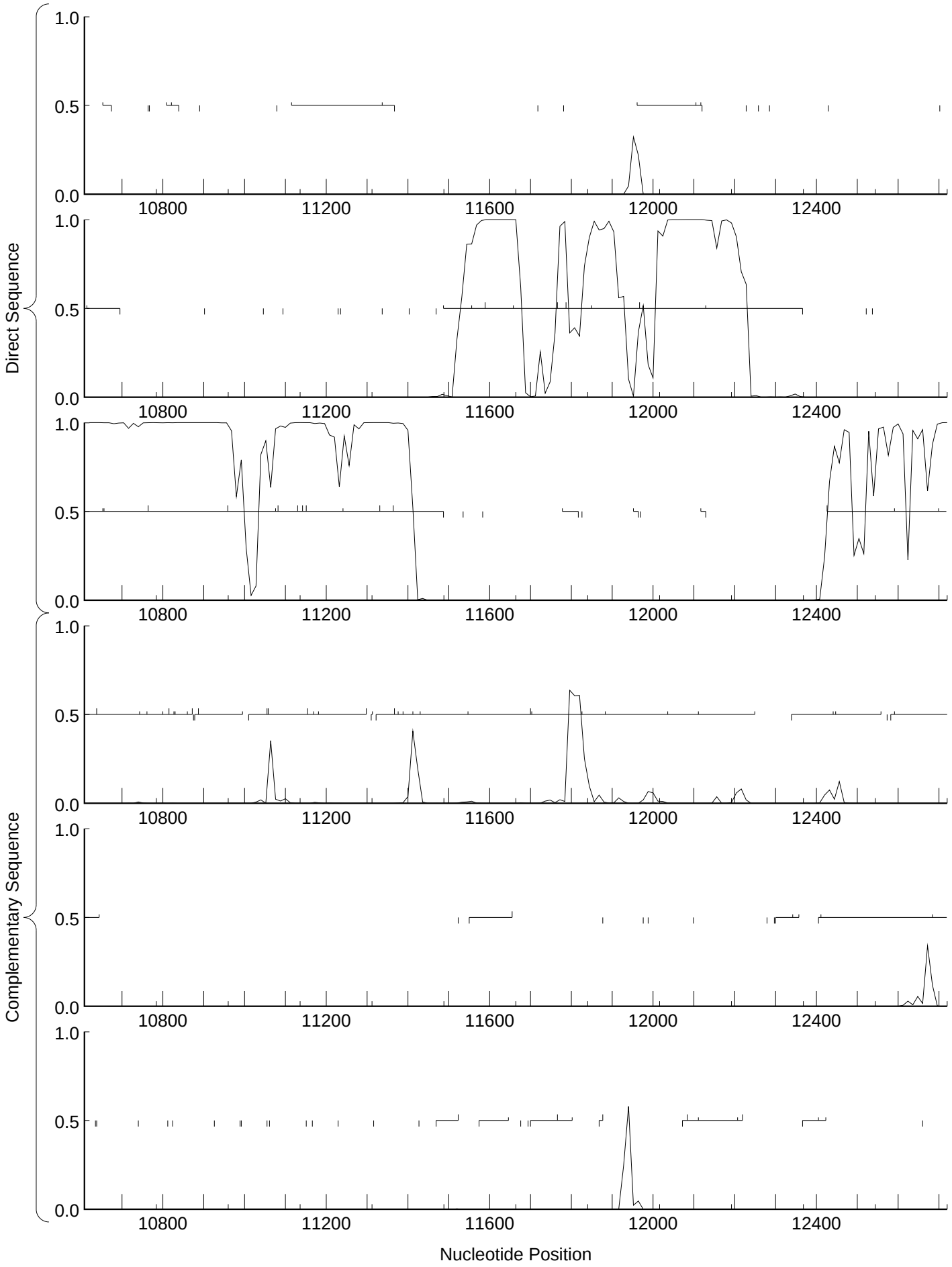

Direct Sequence
Complementary Sequence
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3200
3600
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Nucleotide Position

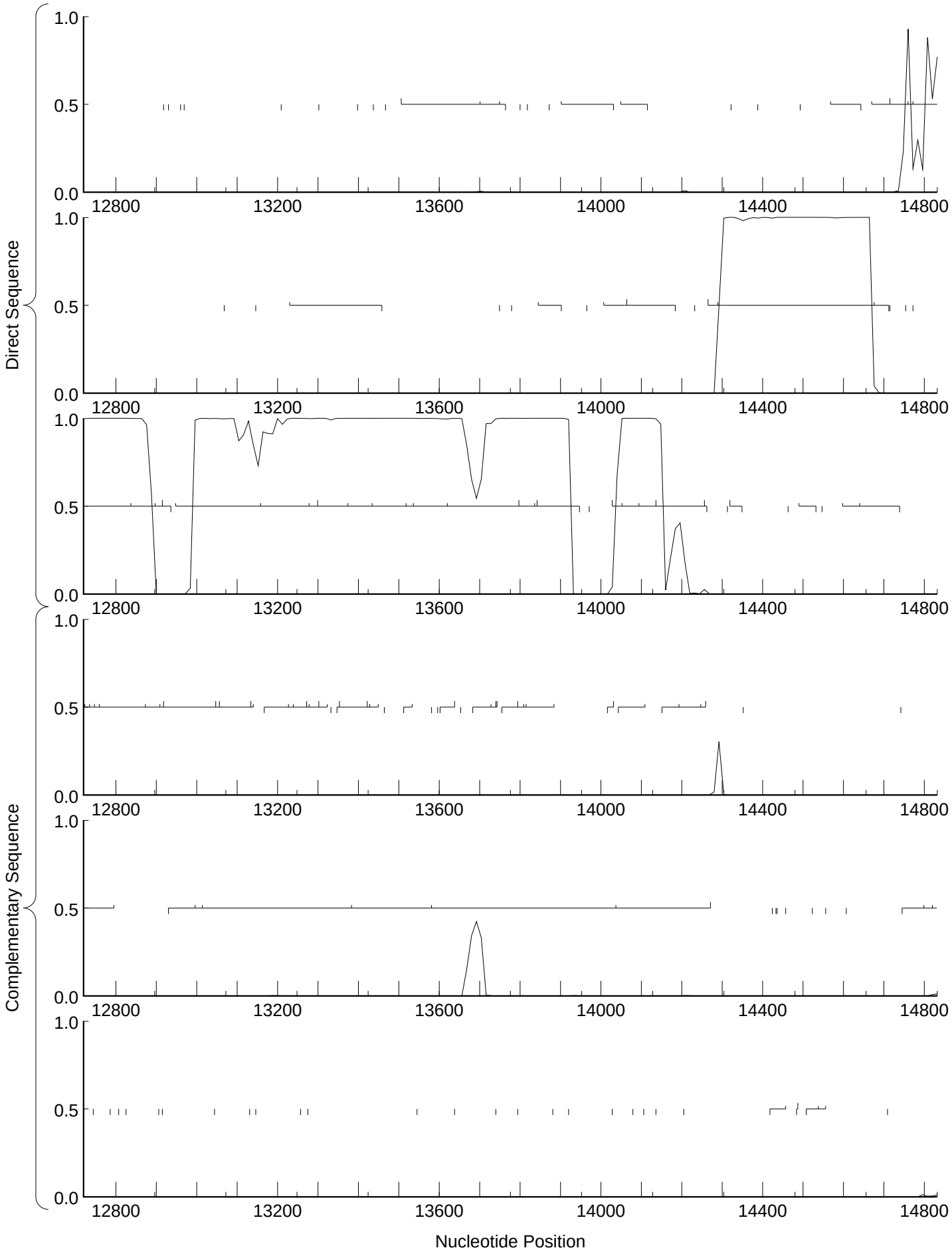
on complete sequence, 52394 bp including 10-base 3’ overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 4/26



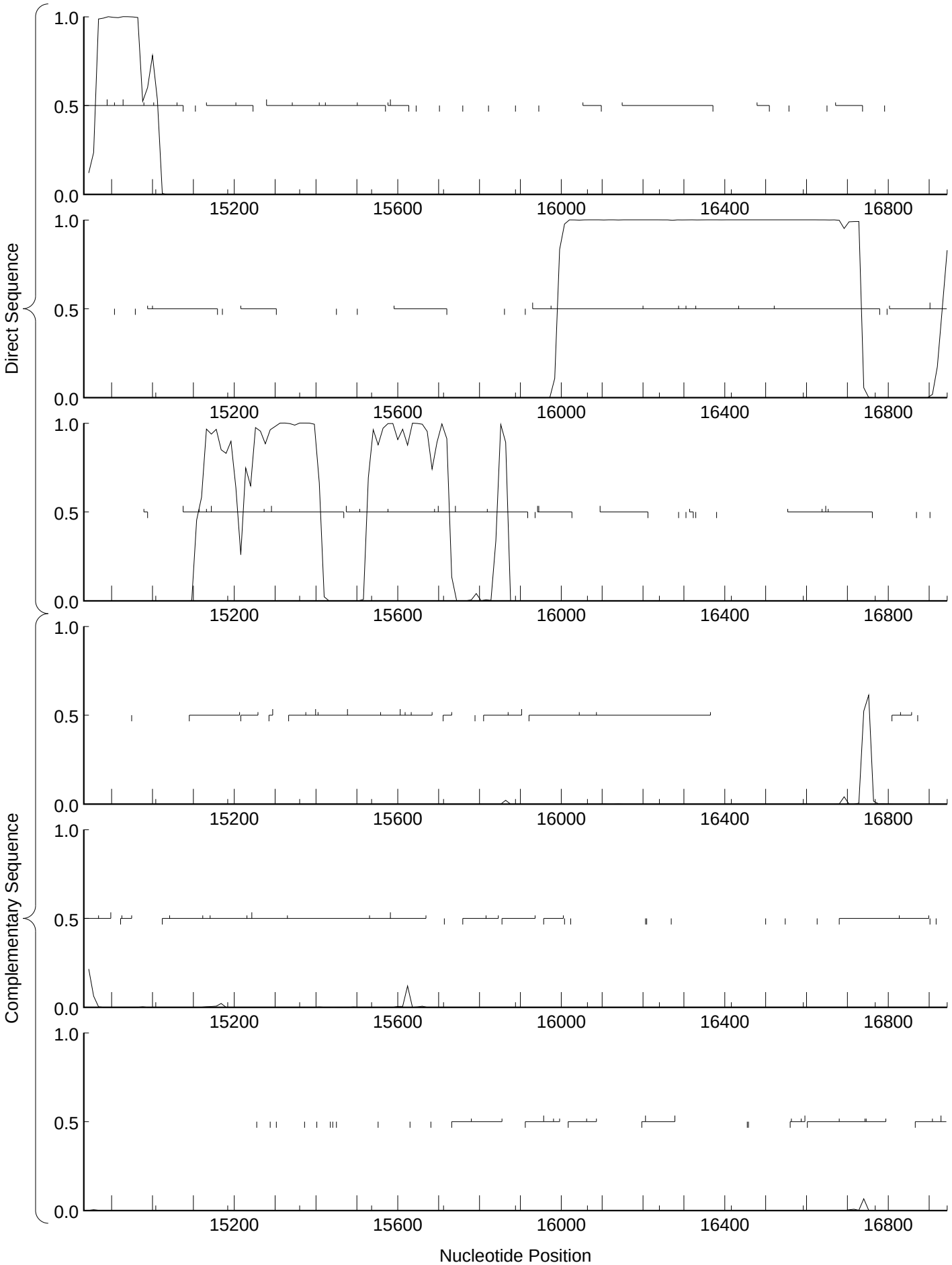

Direct Sequence
Complementary Sequence
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0.0
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6800
7200
7600
8000
8400
Nucleotide Position


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

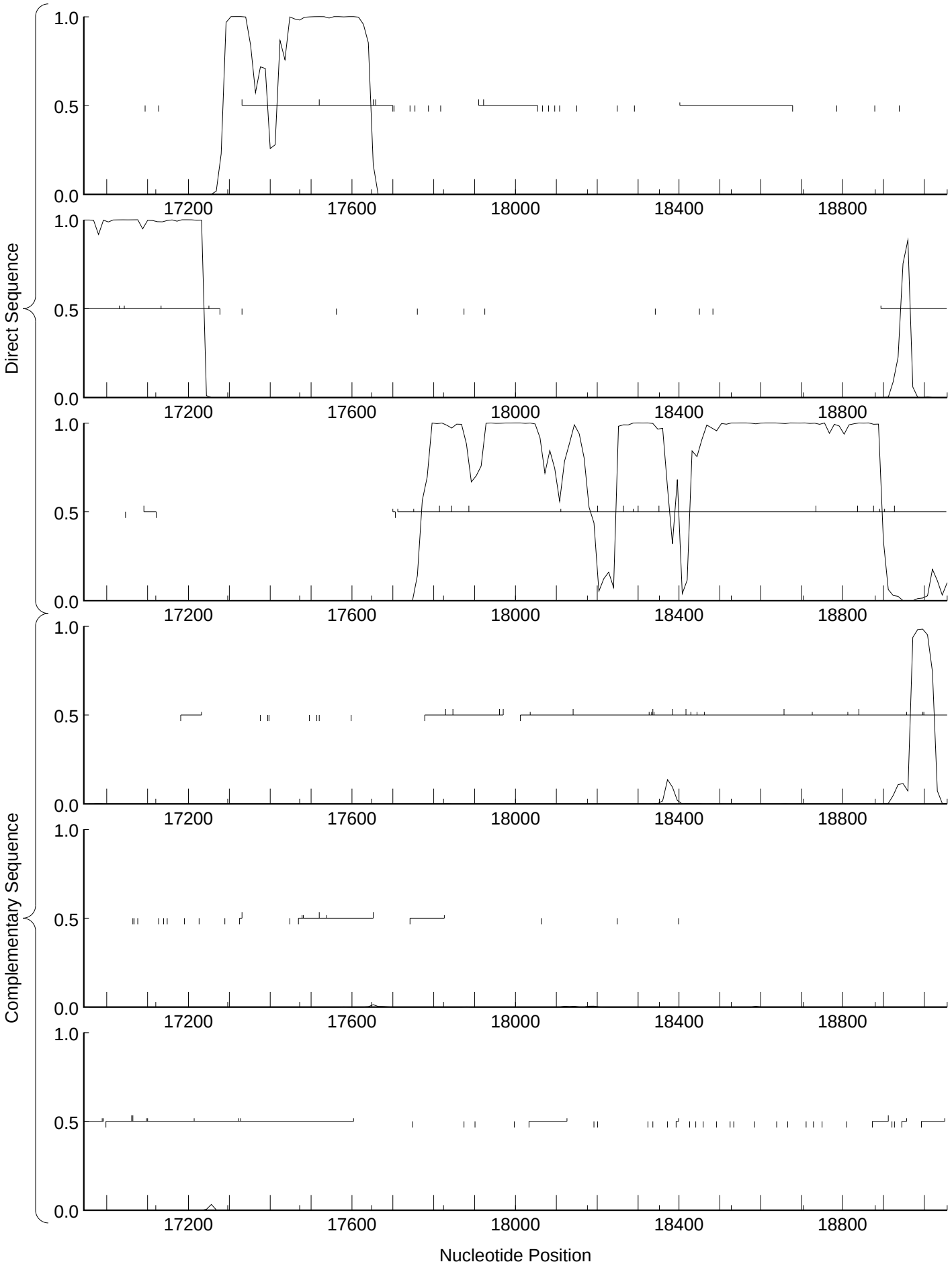

Direct Sequence
Complementary Sequence
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0.0
10800
11200
11600
12000
12400
Nucleotide Position


Direct Sequence
Complementary Sequence
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0.0
12800
13200
13600
14000
14400
14800
Nucleotide Position

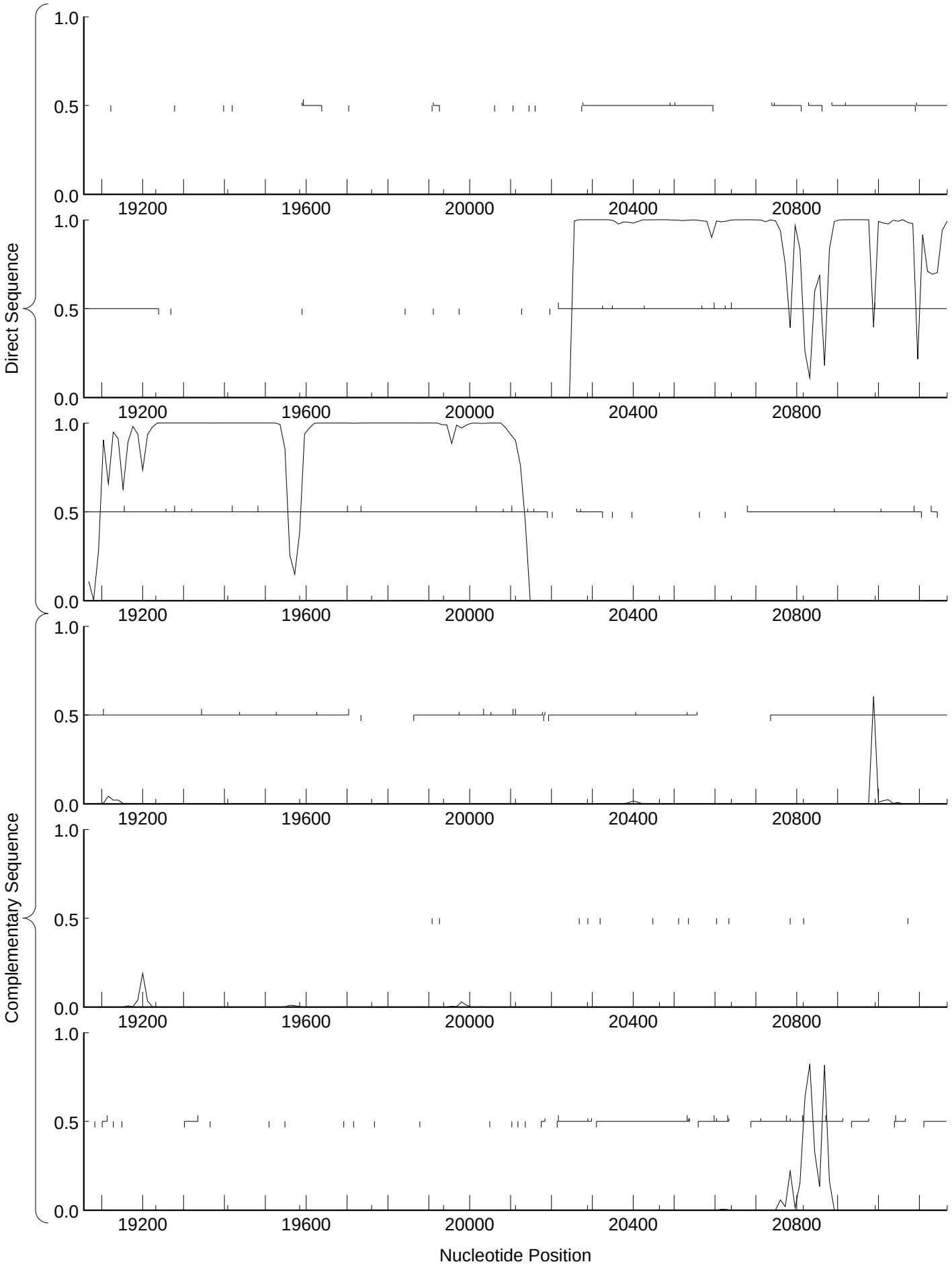
on complete sequence, 52394 bp including 10-base 3’ overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 9/26



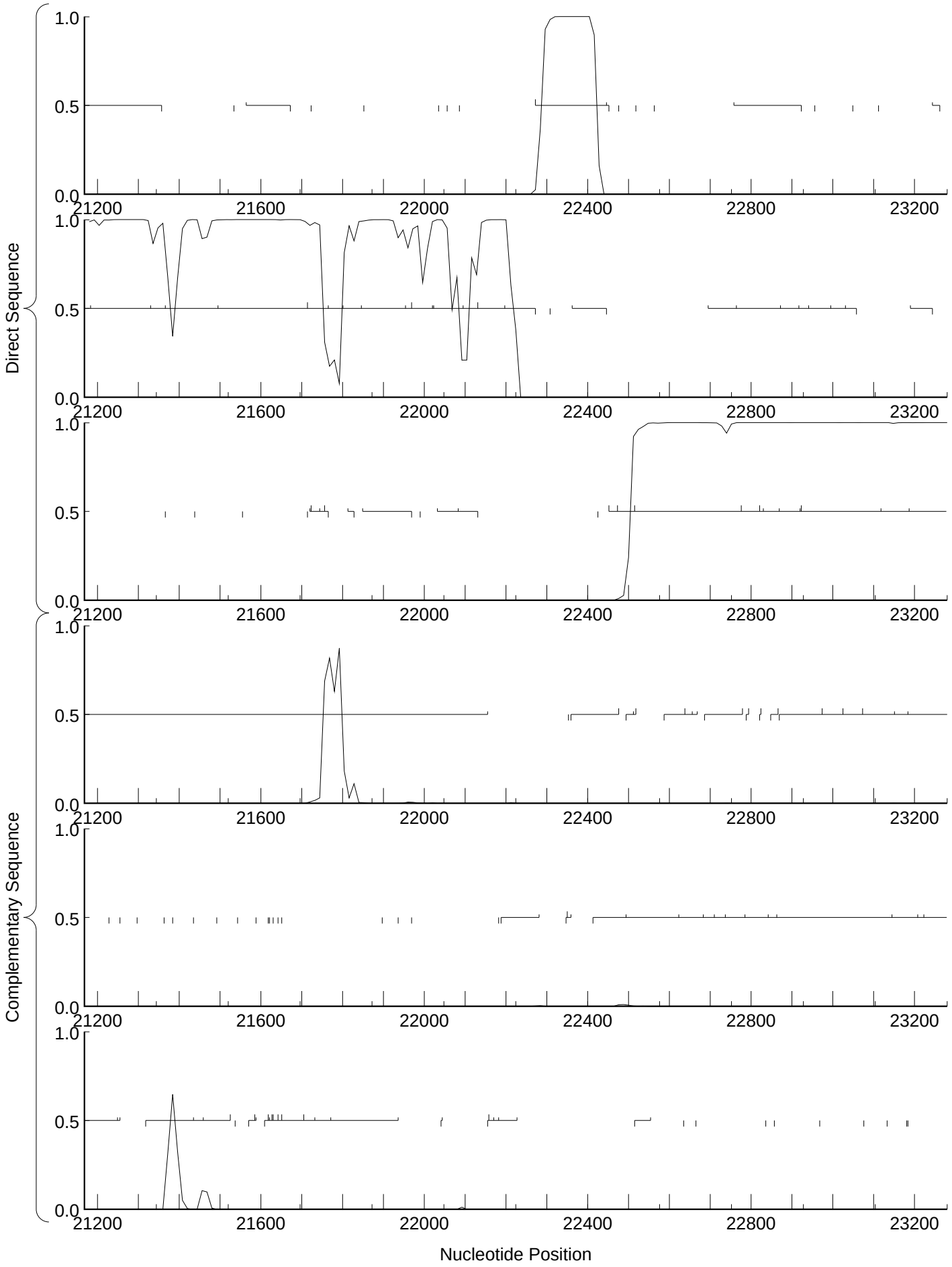
n complete sequence, 52394 bp including 10-base 3’ overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 10/26



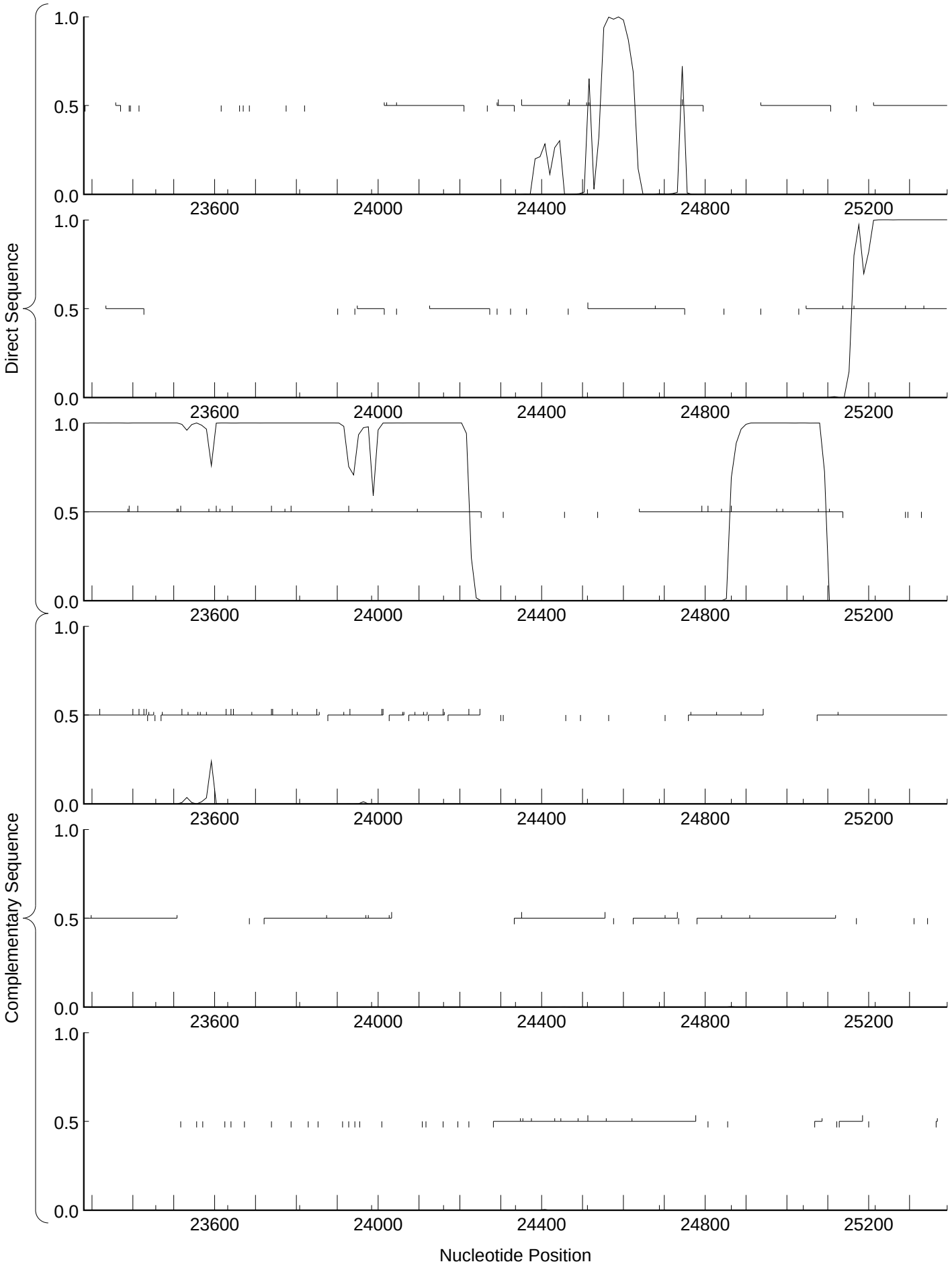
n complete sequence, 52394 bp including 10-base 3’ overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 11/26

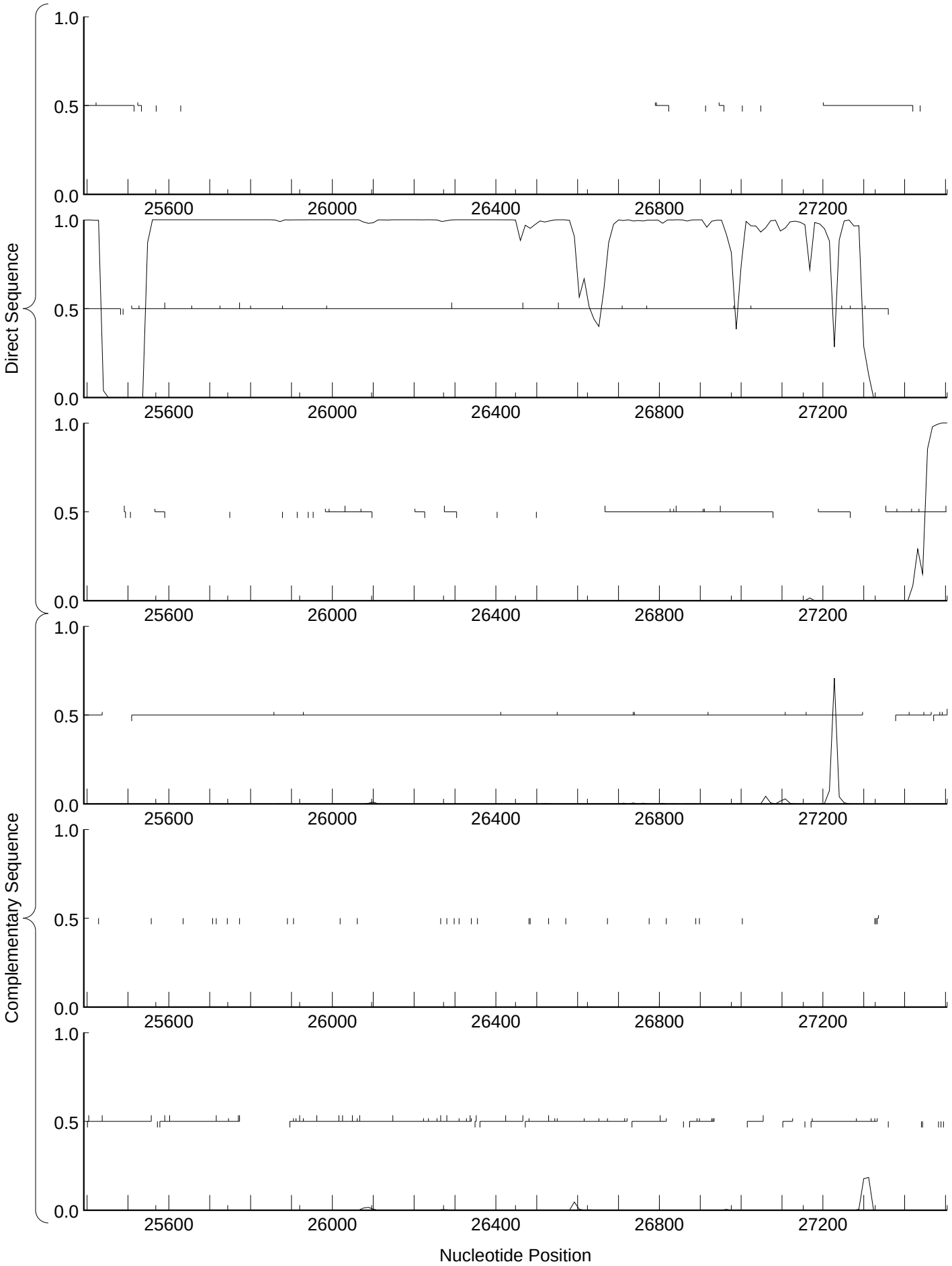


n complete sequence, 52394 bp including 10-base 3’ overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 12/26

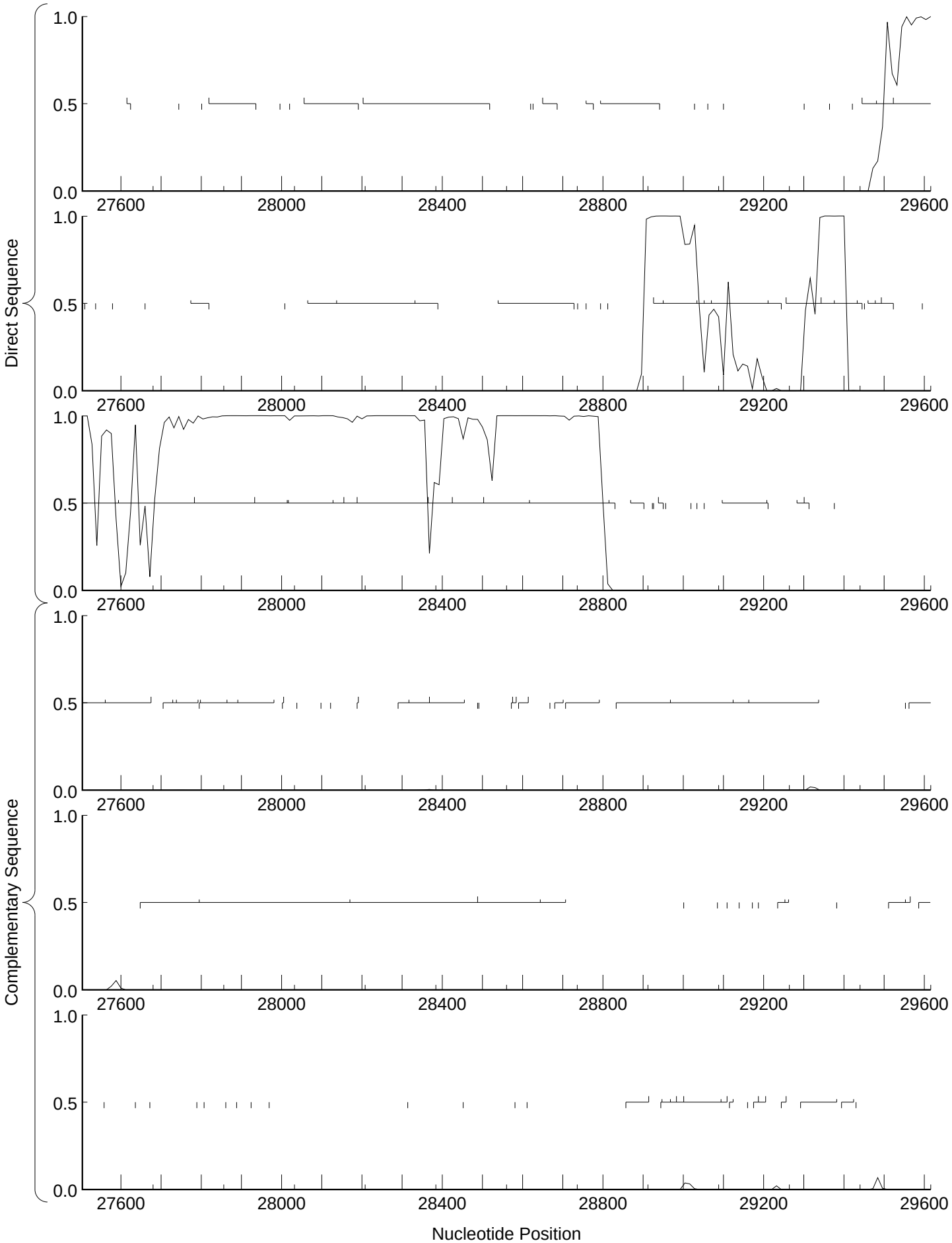


n complete sequence, 52394 bp including 10-base 3' overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 13/26

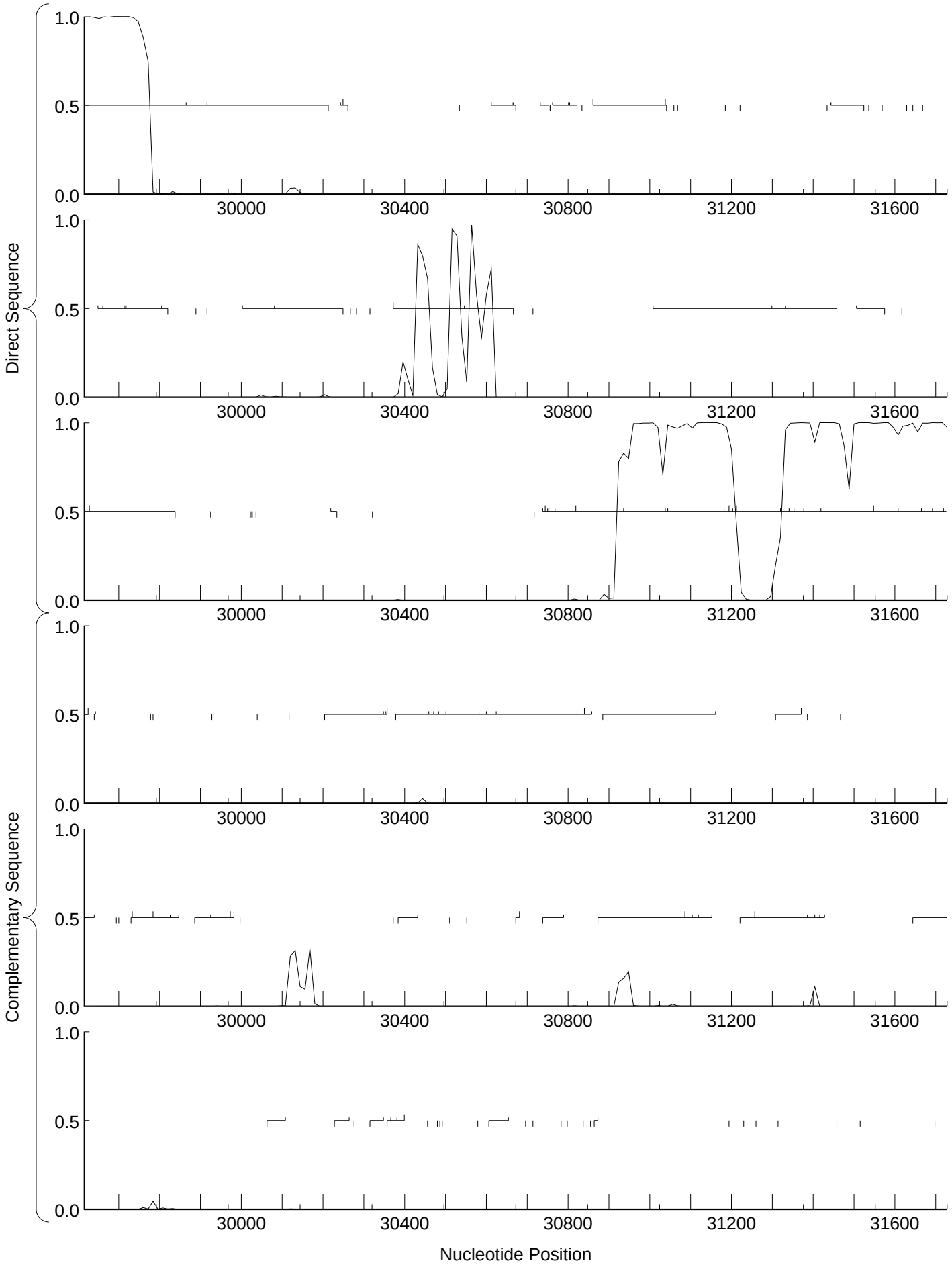


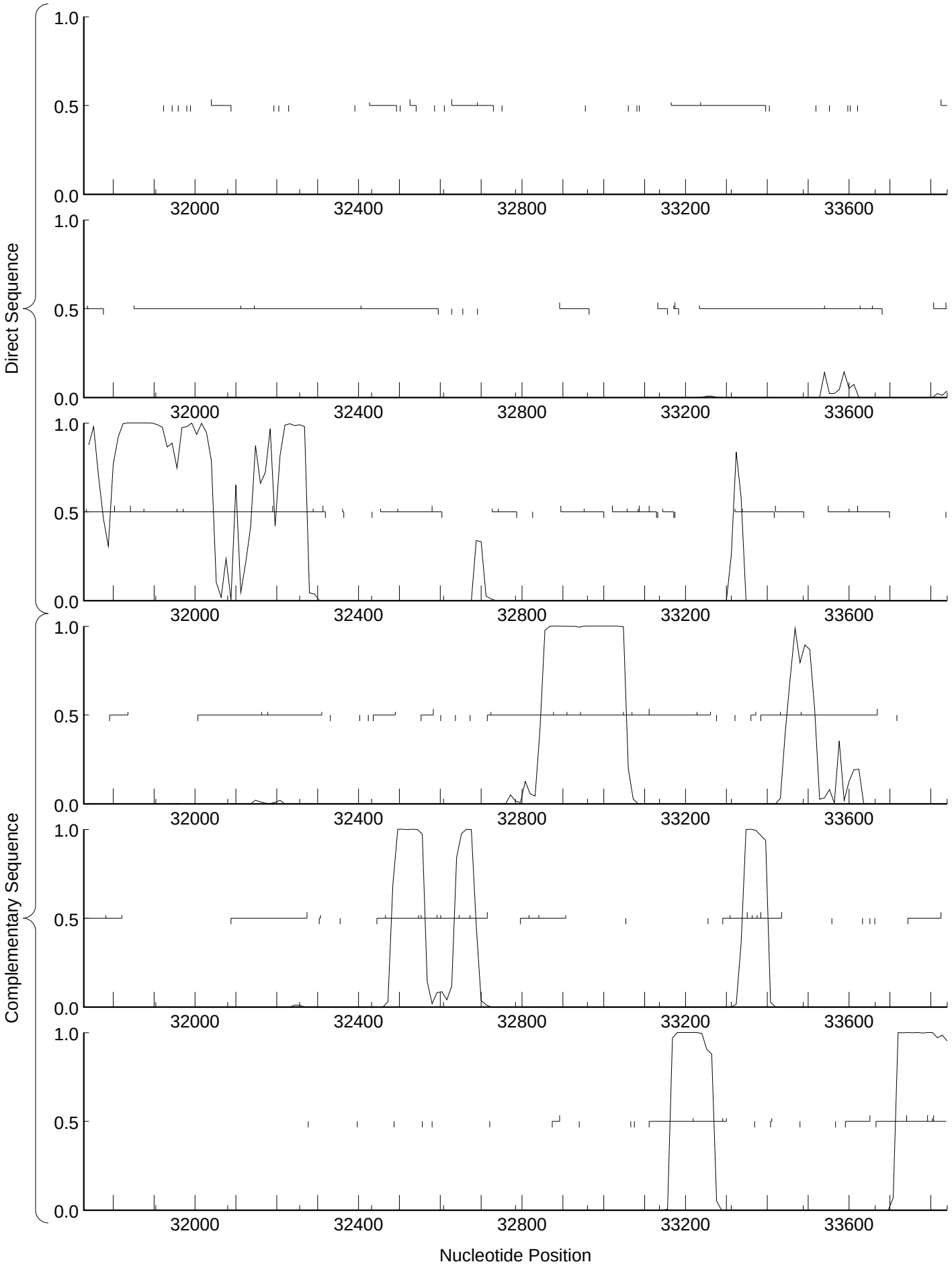

Direct Sequence
Complementary Sequence
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0.0
25600
26000
26400
26800
27200
Nucleotide Position

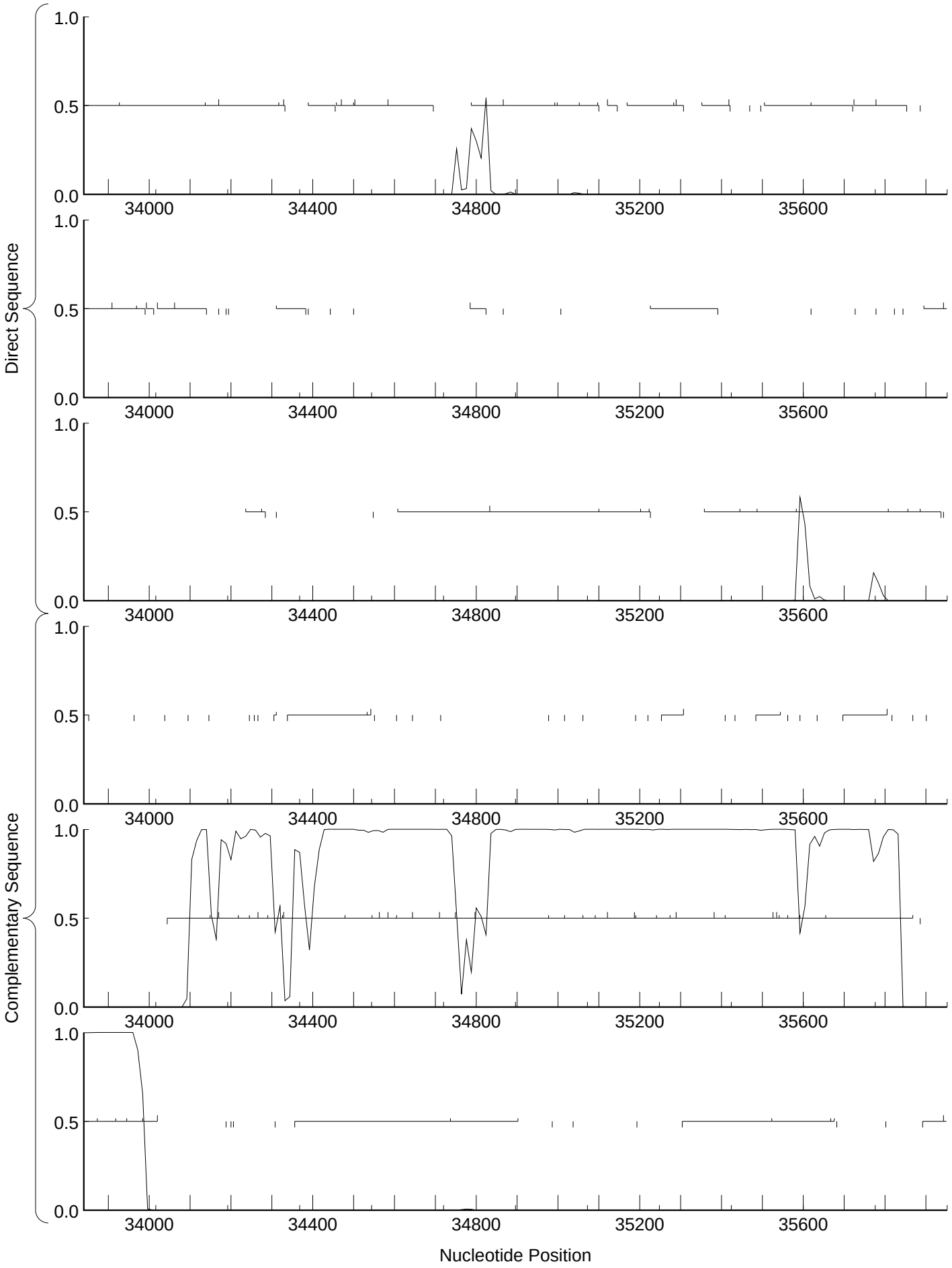
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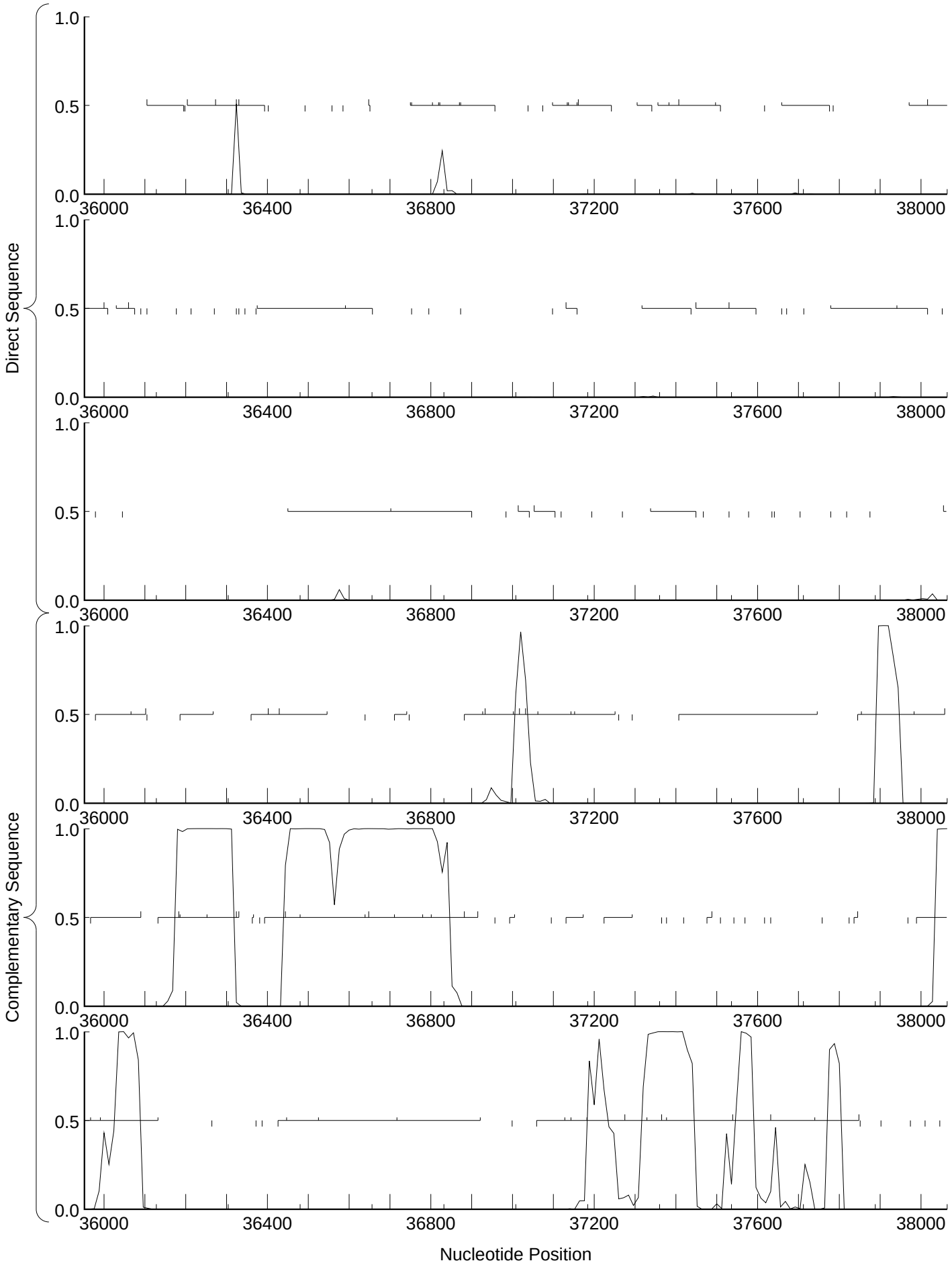
n complete sequence, 52394 bp including 10-base 3’ overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 16/26

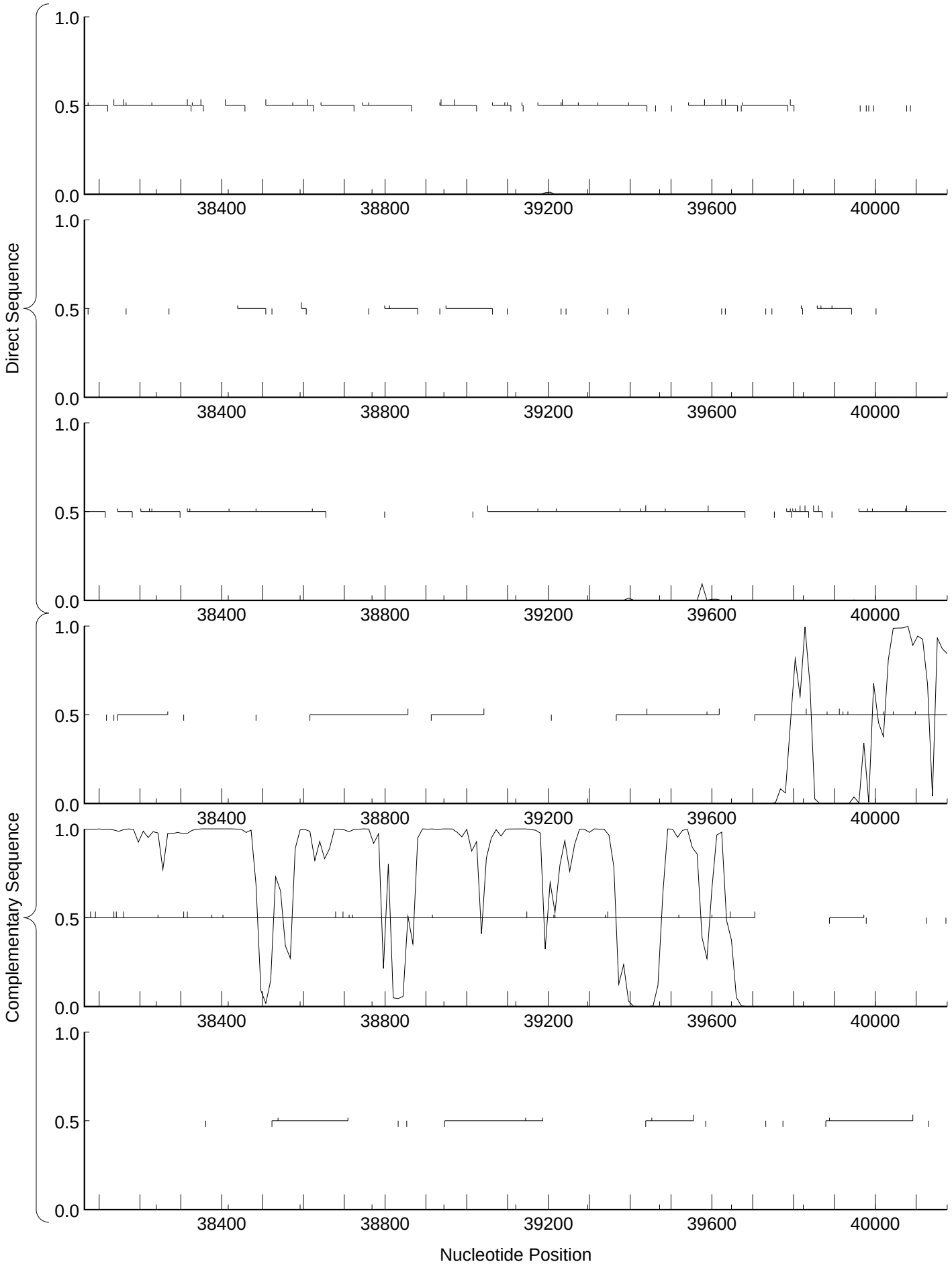


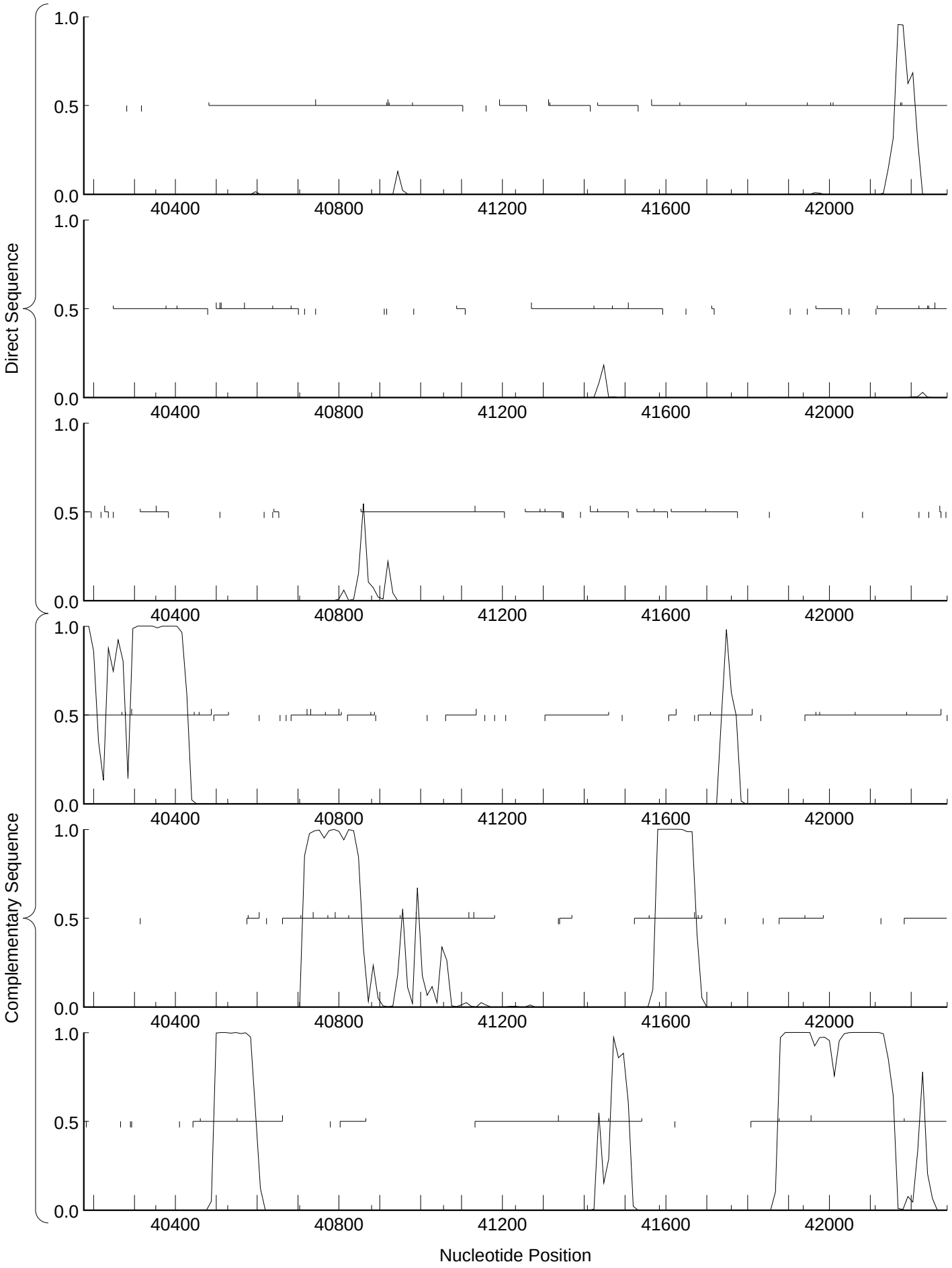

Direct Sequence
Complementary Sequence
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0.5
0.0
32000
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32800
33200
33600
Nucleotide Position

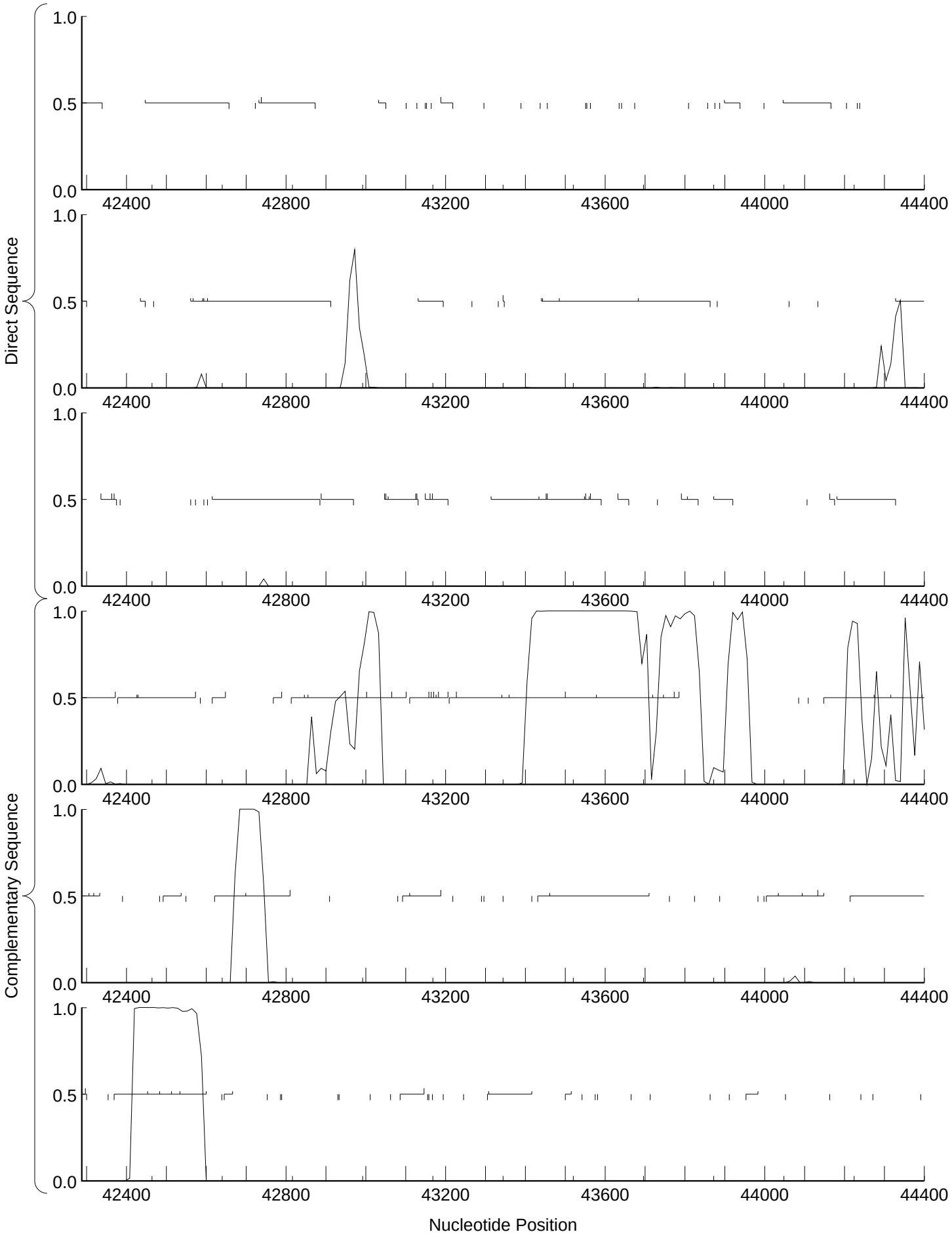

Direct Sequence
Complementary Sequence
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0.0
34000
34400
34800
35200
35600
Nucleotide Position

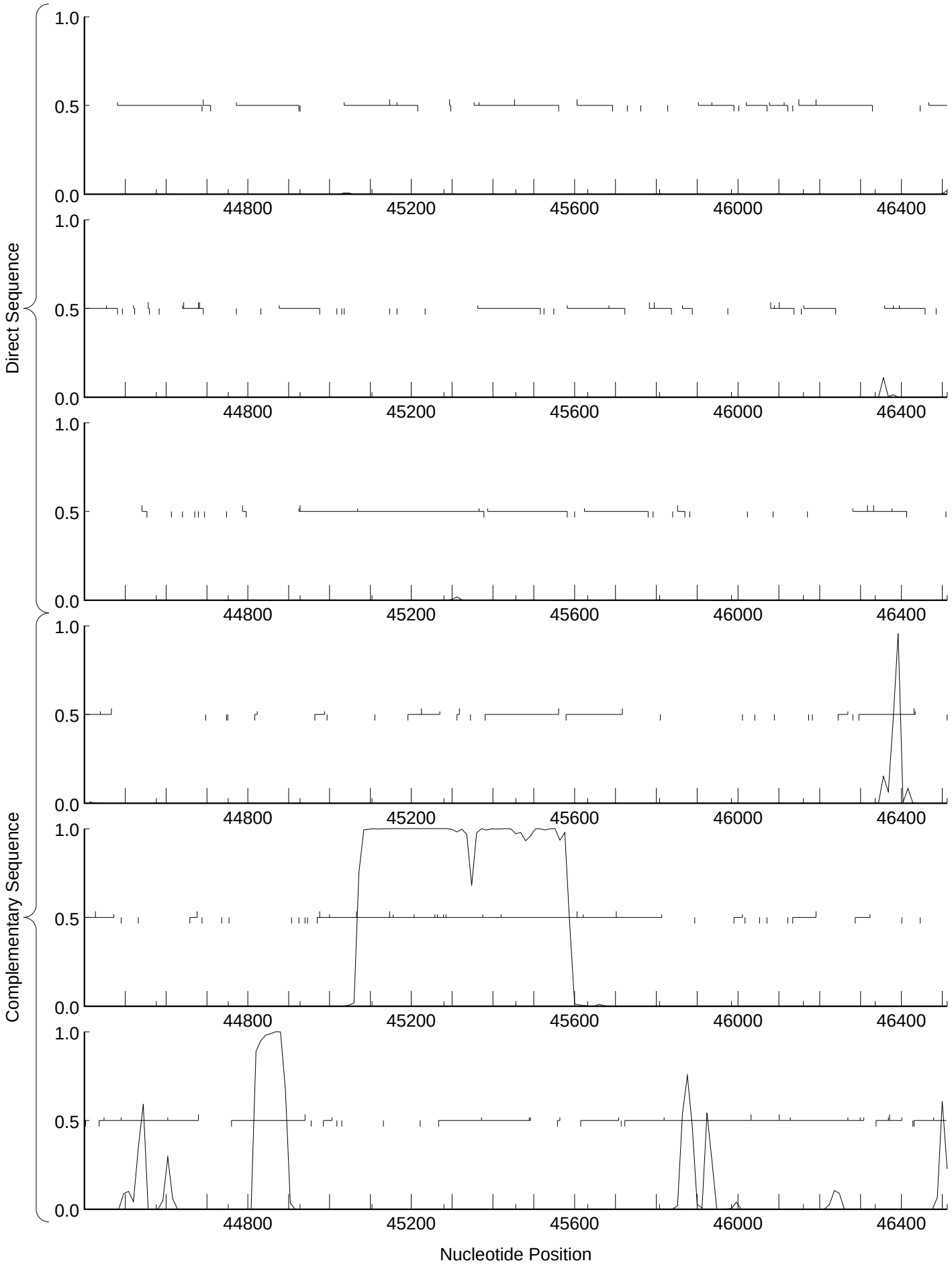
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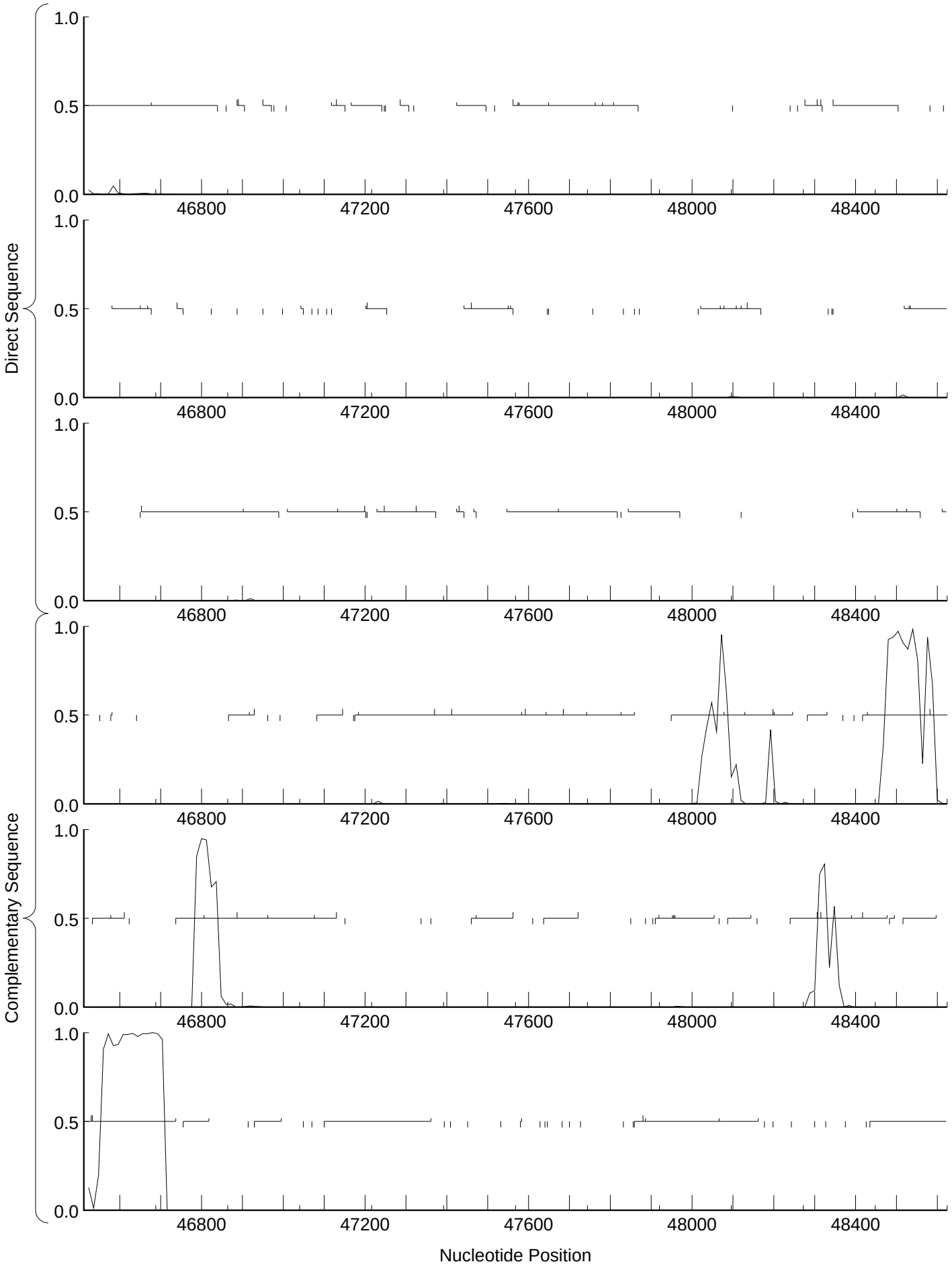

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
38400
38800
39200
39600
40000
Nucleotide Position


Direct Sequence
Complementary Sequence
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40400
40800
41200
41600
42000
Nucleotide Position

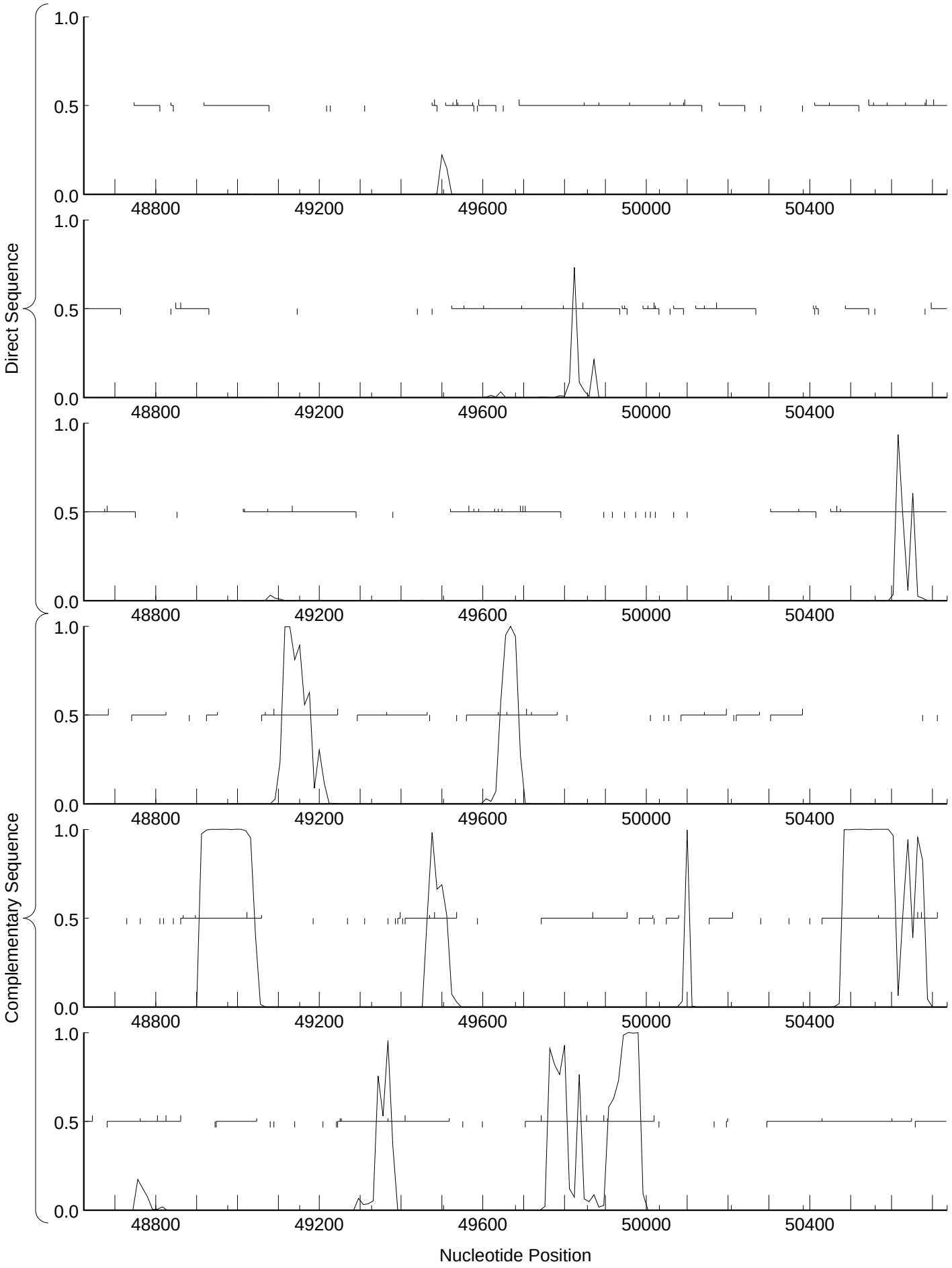

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Complementary Sequence
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0.5
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42400
42800
43200
43600
44000
44400
Nucleotide Position


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

n complete sequence, 52394 bp including 10-base 3’ overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 24/26



n complete sequence, 52394 bp including 10-base 3’ overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 25/26



n complete sequence, 52394 bp including 10-base 3’ overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 26/26

