GeneMark

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

PROGRAM INFORMATION

```
Sequence         :  Mycobacterium phage Dixon complete sequence, 52055 bp including 10-base 3’ overhang (CGGGAT
Analysis Date    :  3/28/24 at 11:40:19
Pages            :  26
Sequence Length  :  52055 bp
GC Content       :   61.39%

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

PS-Version       :  1.2

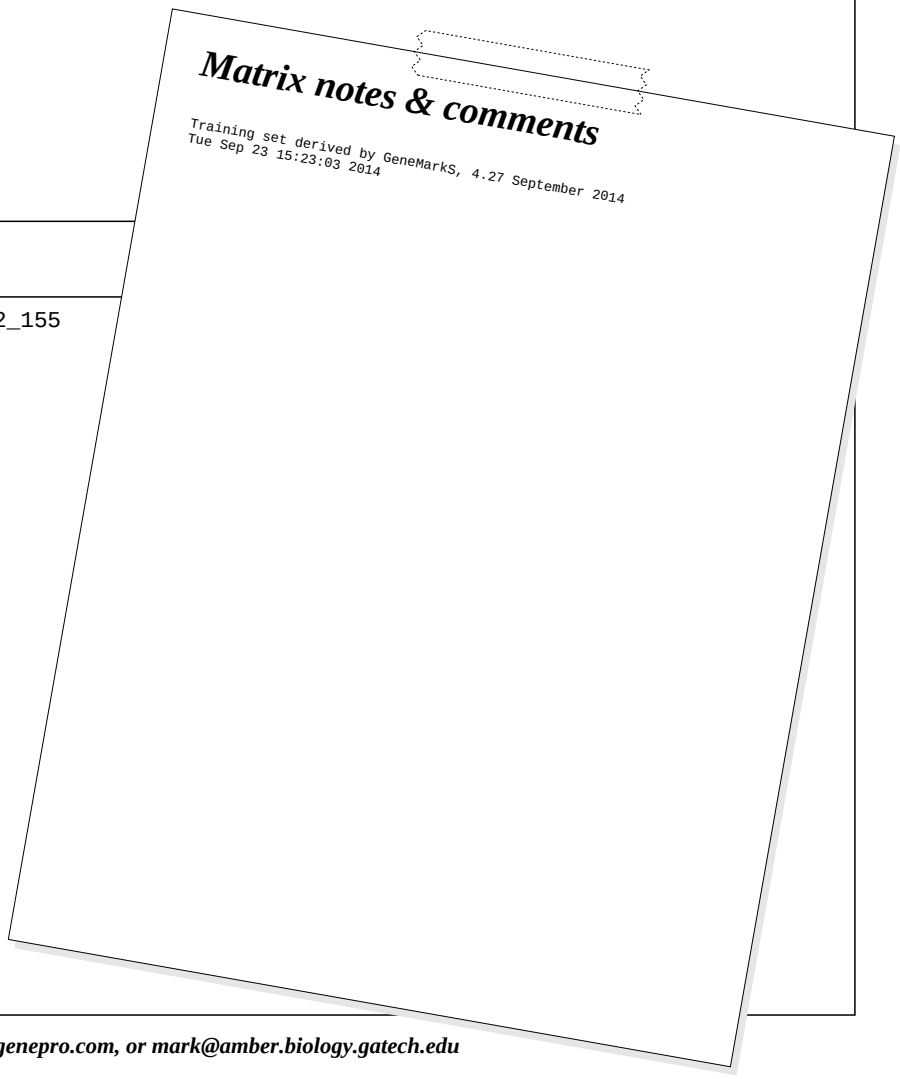
GeneMark Options :  PostScript graph,
                    Mark ORFs / splice sites,
                    List ORFs,
                    List regions and/or splice sites,
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MATRIX INFORMATION

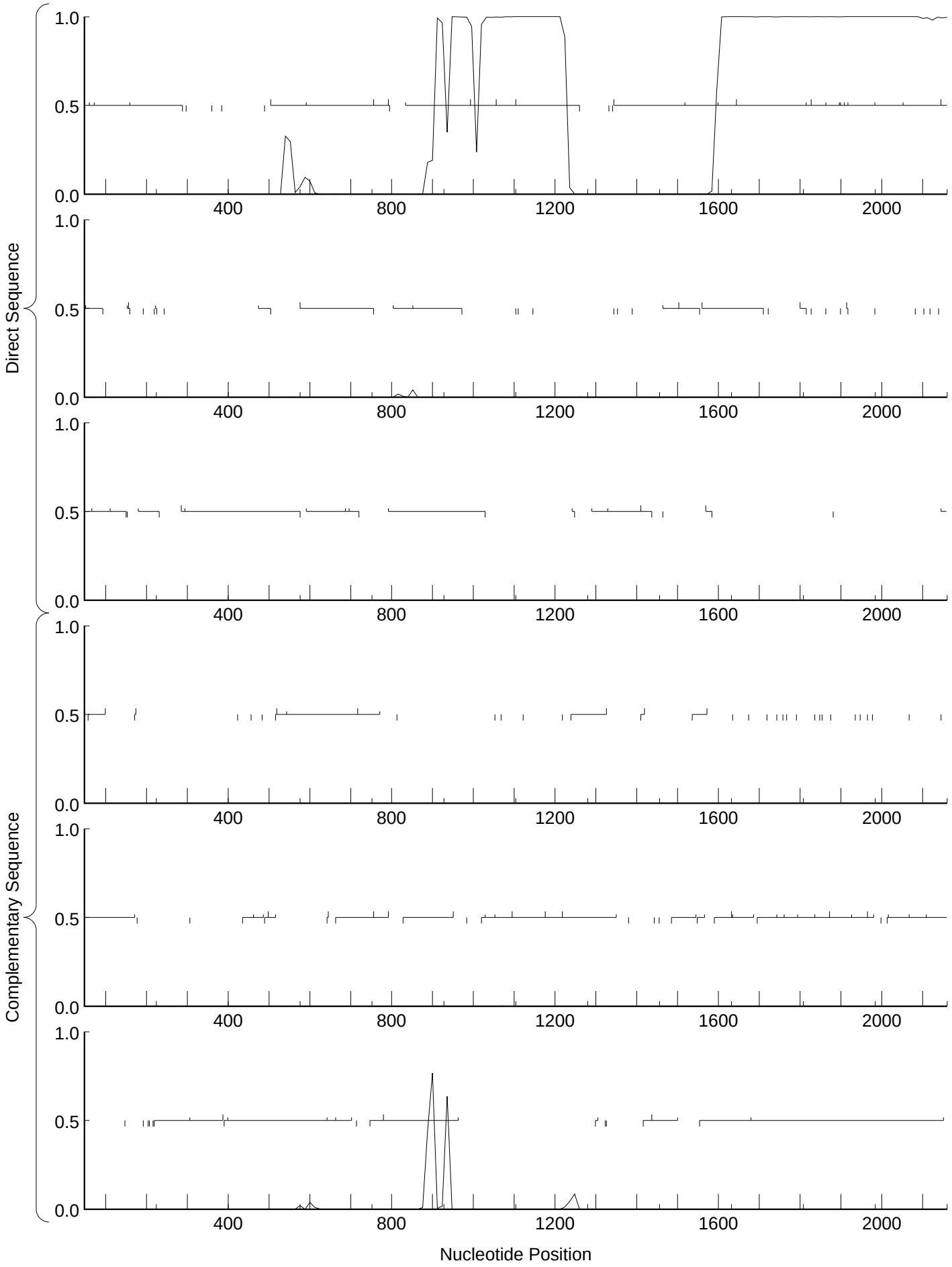
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Matrix     :  Mycobacterium_smegmatis_MC2_155
Author     :  -

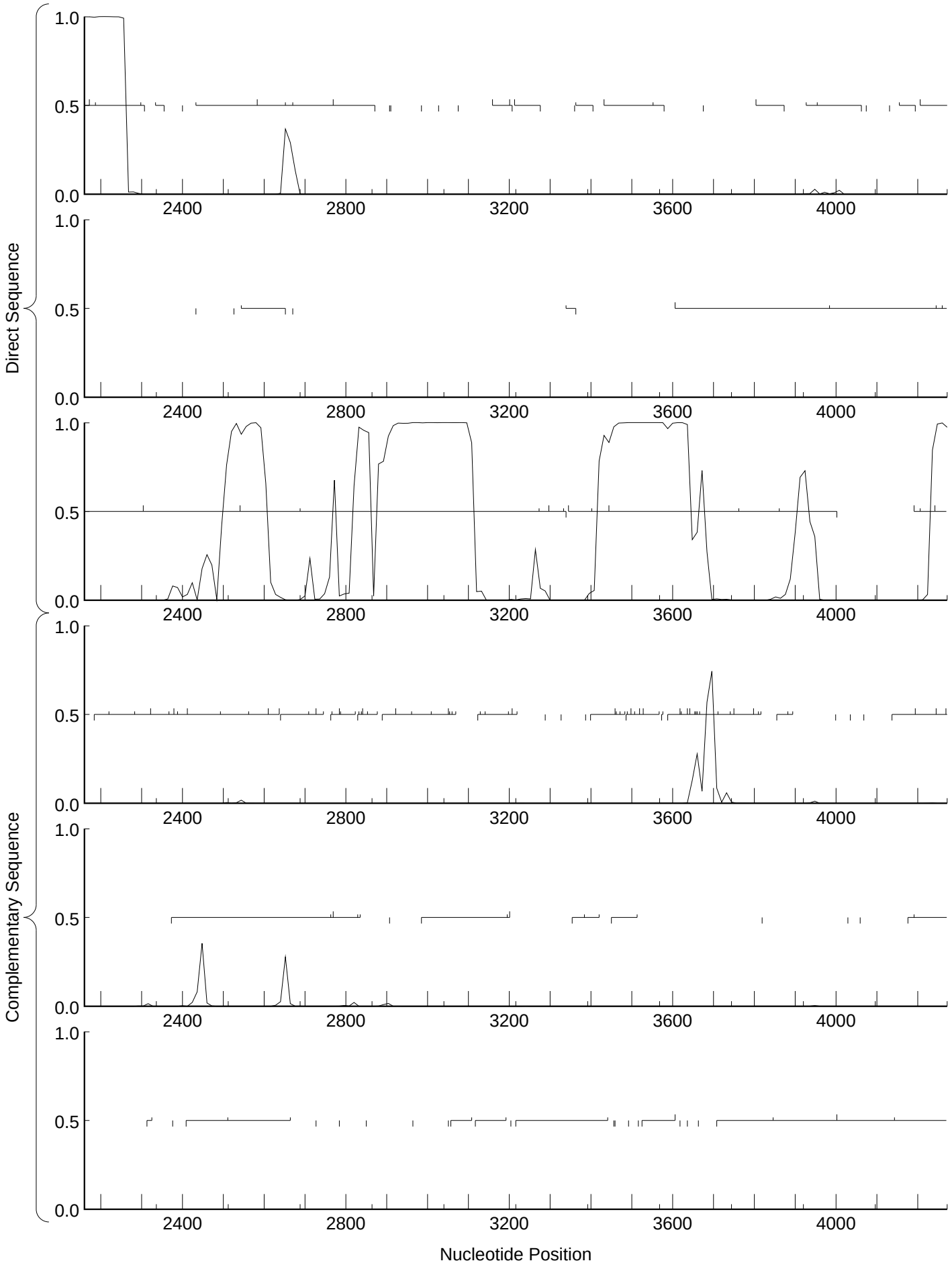
Order      :  4


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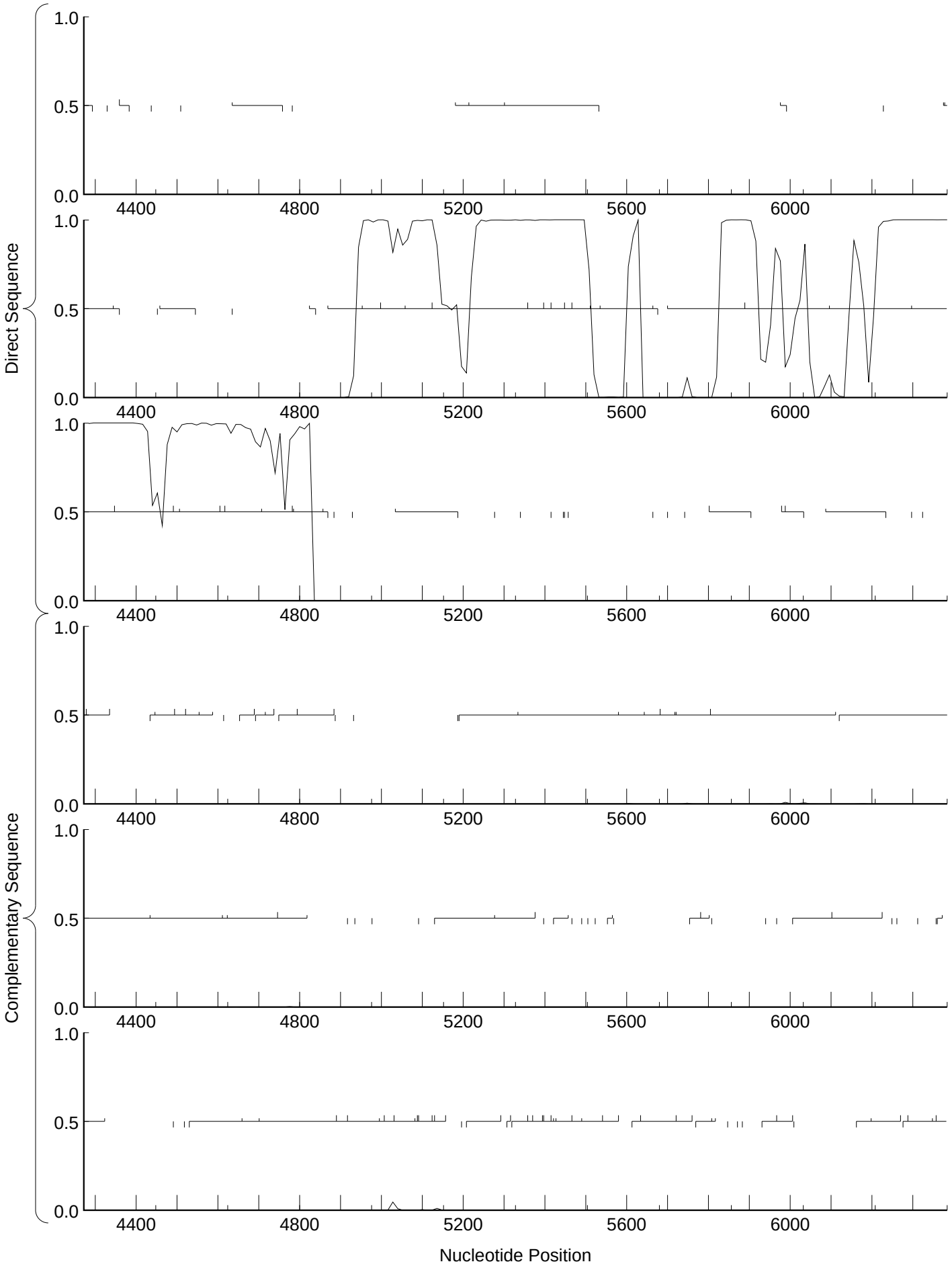


For help or information, send electronic mail to: custserv@genepro.com, or mark@amber.biology.gatech.edu

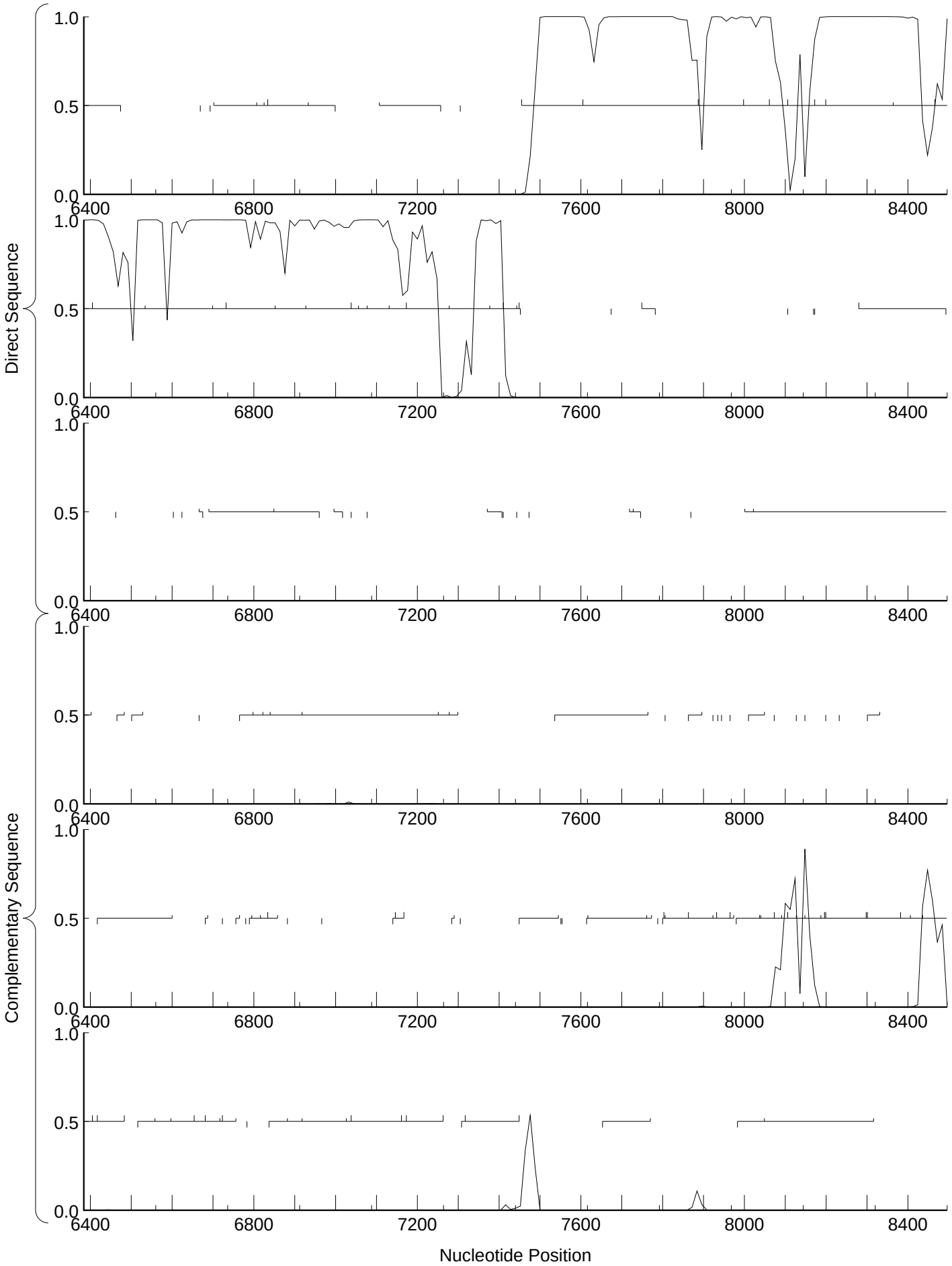

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
400
800
1200
1600
2000
Nucleotide Position

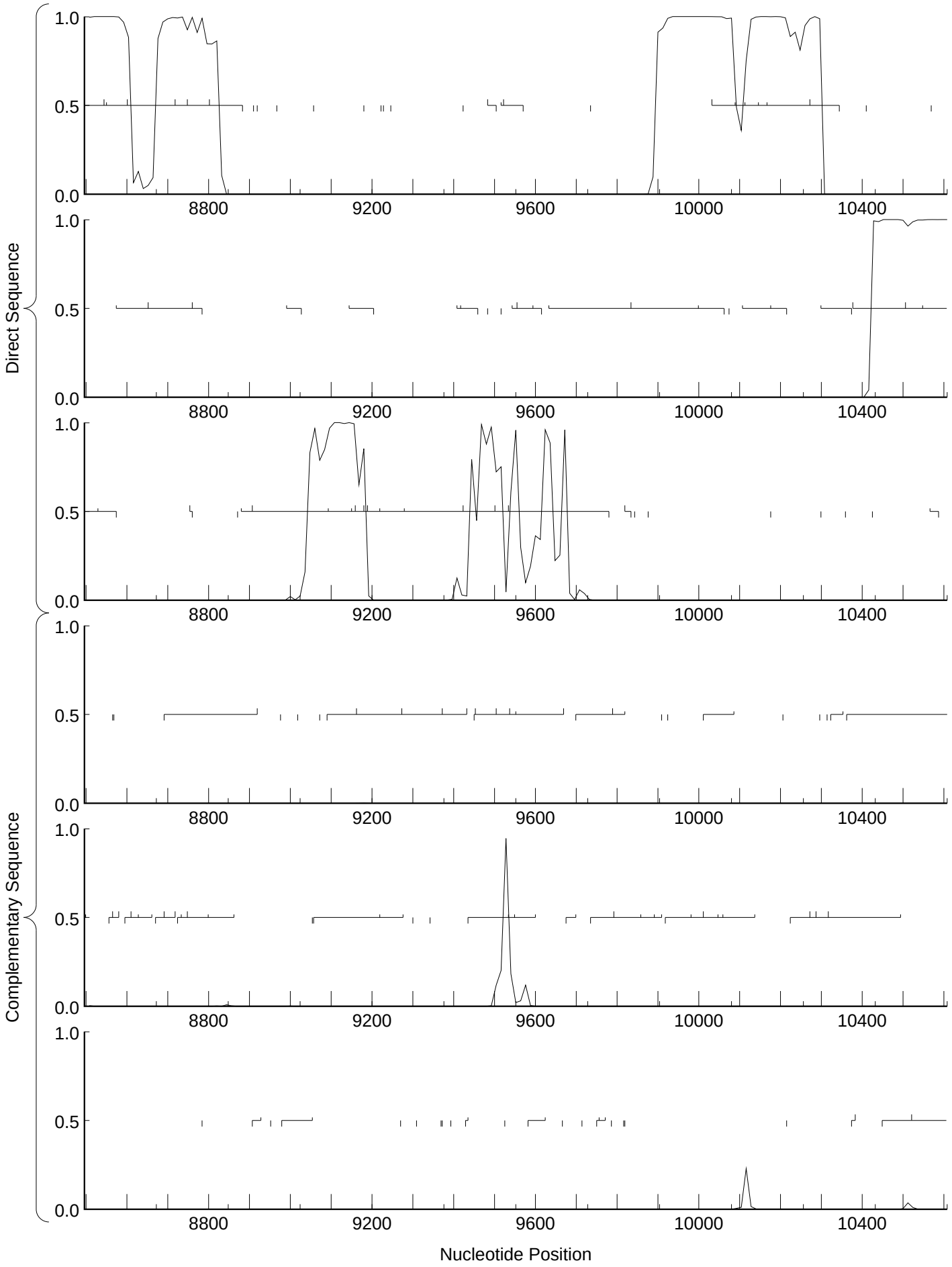

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
2400
2800
3200
3600
4000
Nucleotide Position

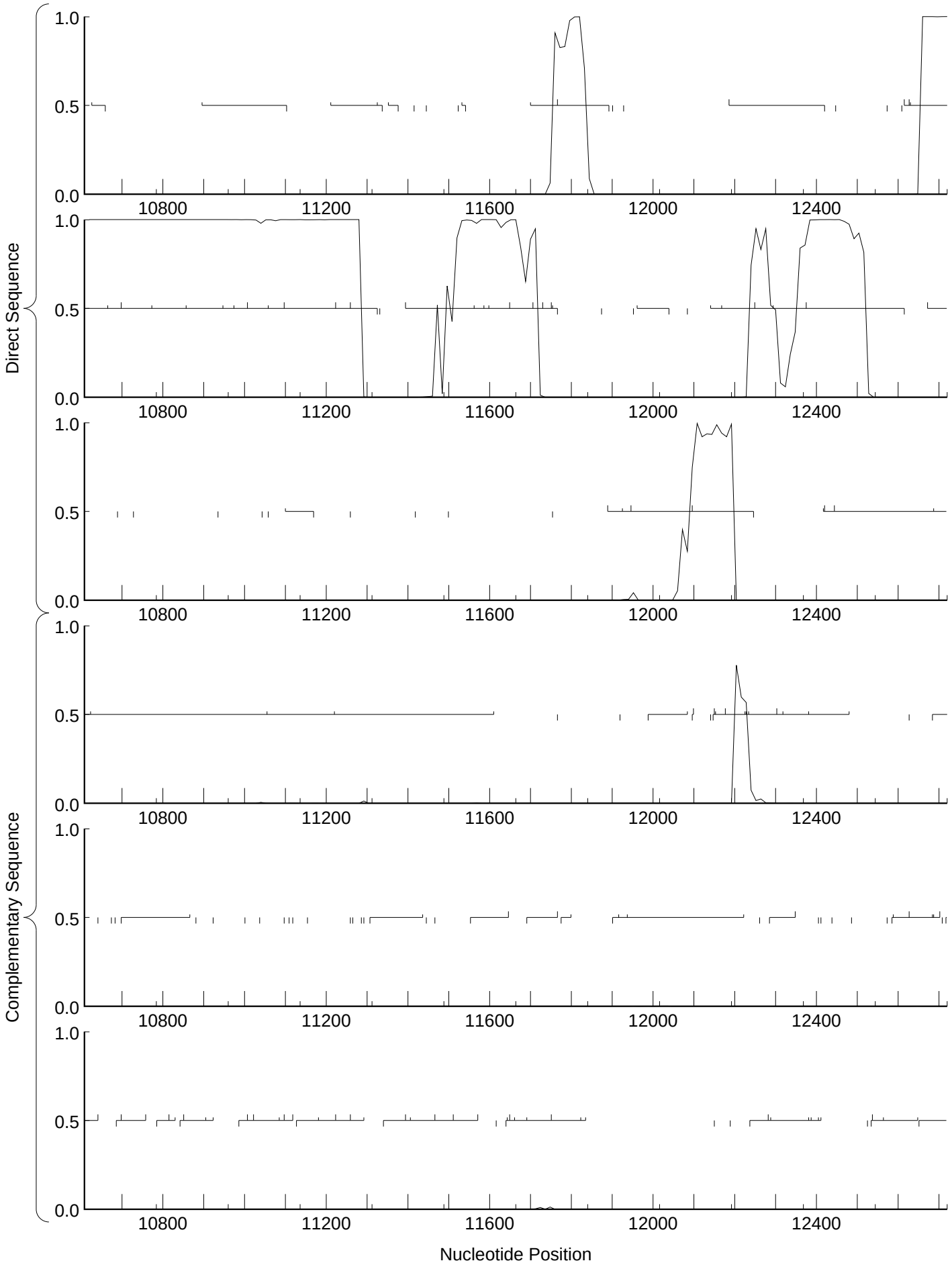
on complete sequence, 52055 bp including 10-base 3’ overhang (CGGGATGTAA), Cluster A8, Order 4, Window 96, Step 12, 4/26



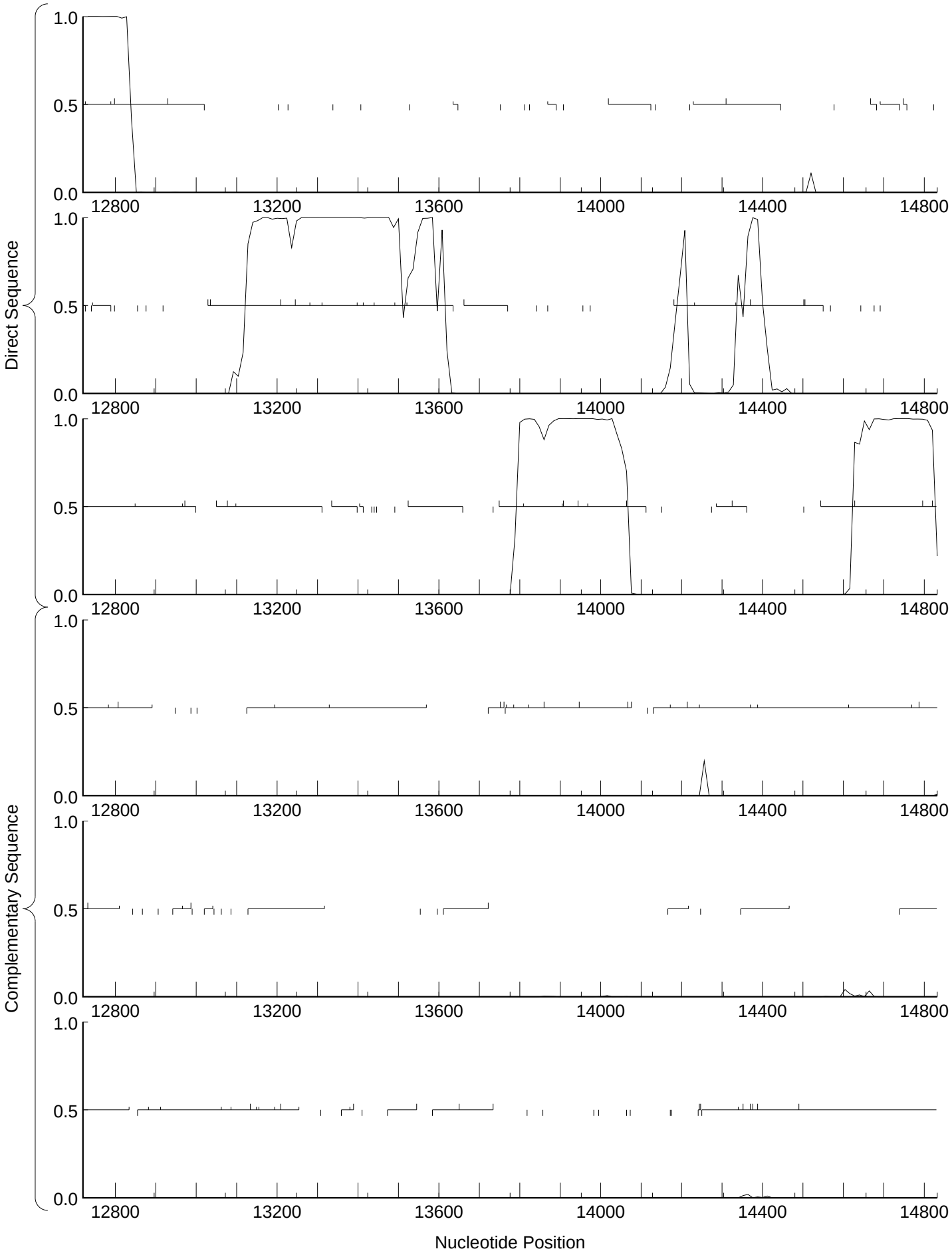
on complete sequence, 52055 bp including 10-base 3’ overhang (CGGGATGTAA), Cluster A8, Order 4, Window 96, Step 12, 5/26



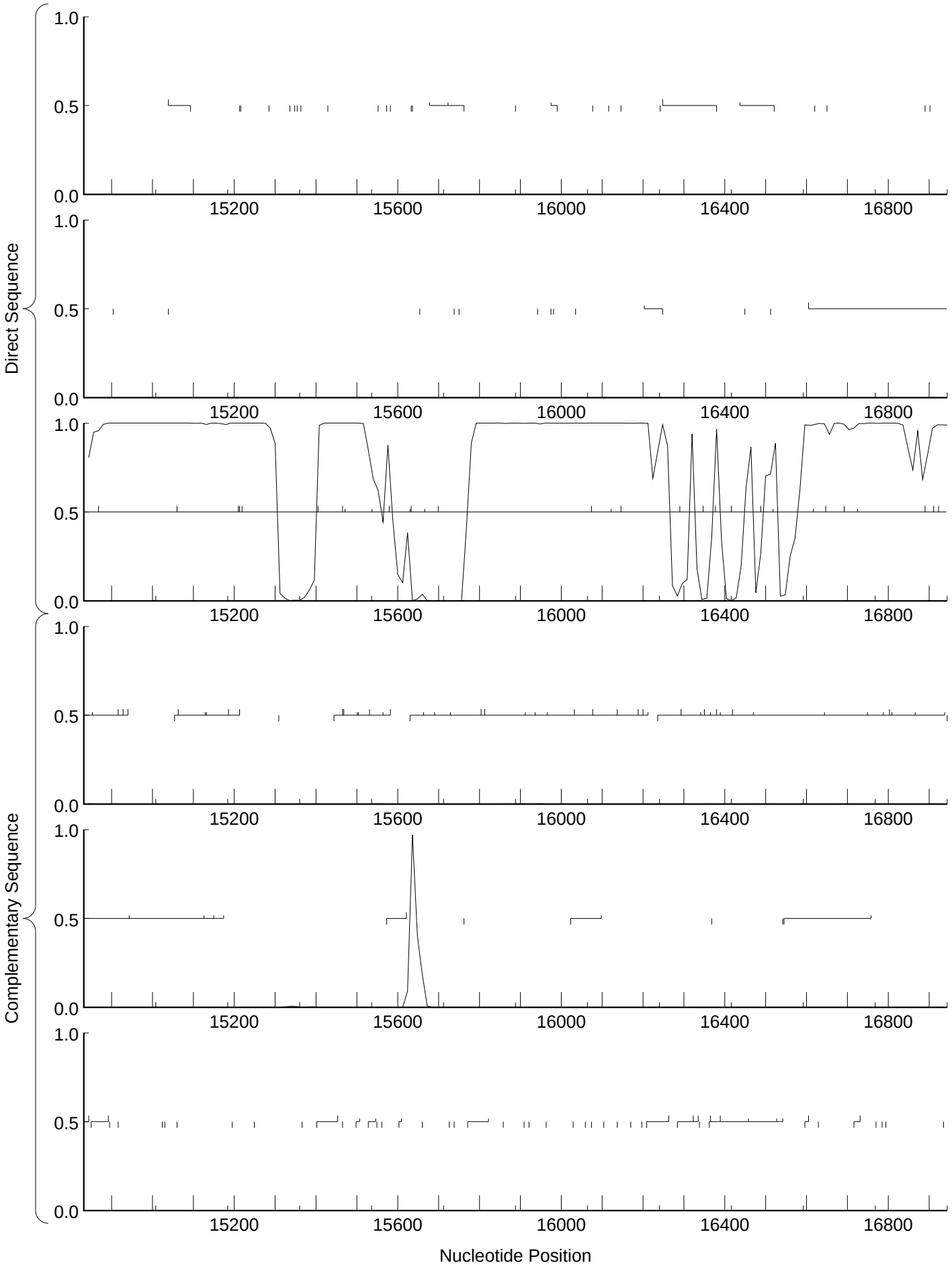

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
8800
9200
9600
10000
10400
Nucleotide Position


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

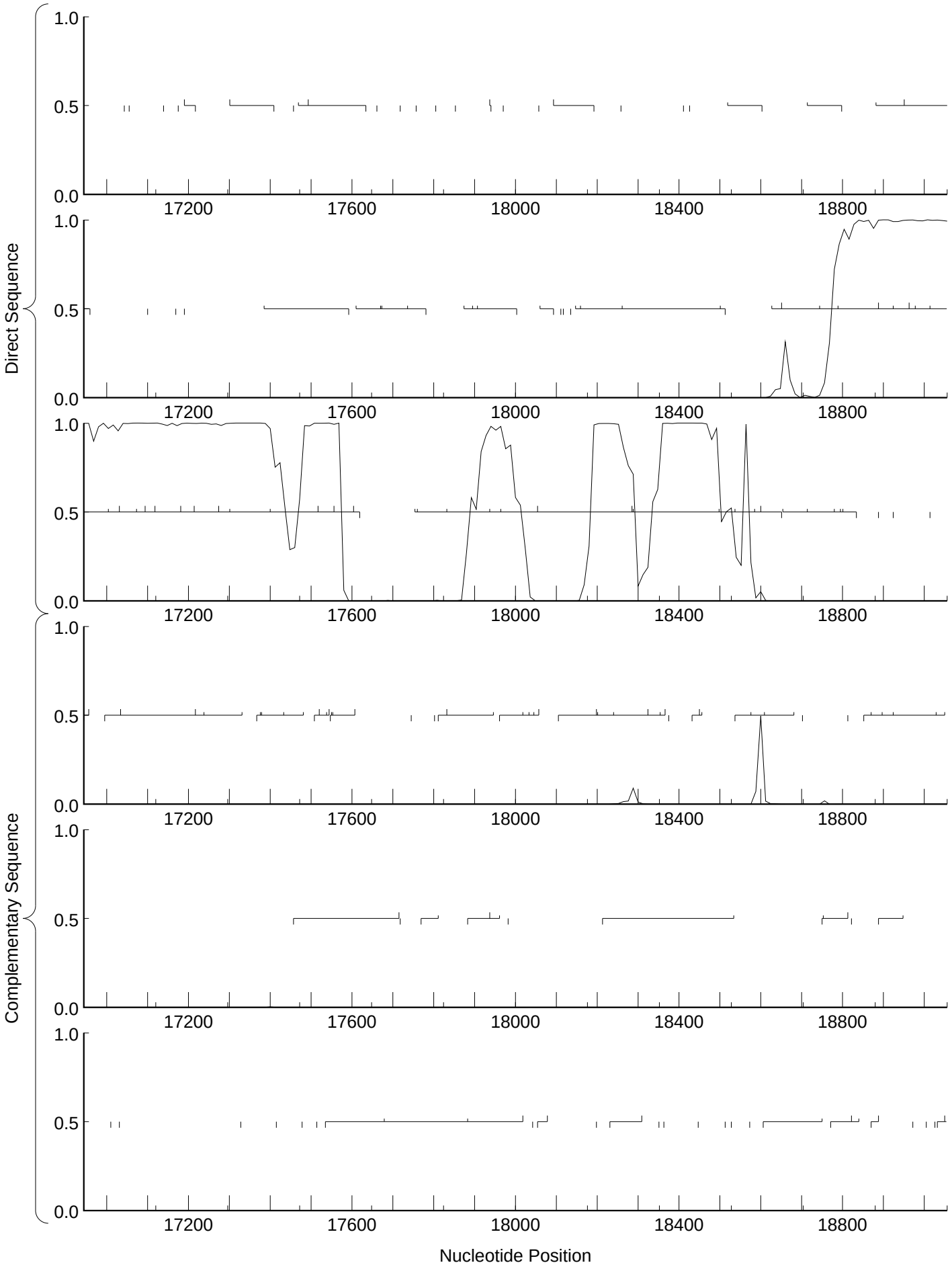
on complete sequence, 52055 bp including 10-base 3’ overhang (CGGGATGTAA), Cluster A8, Order 4, Window 96, Step 12, 8/26



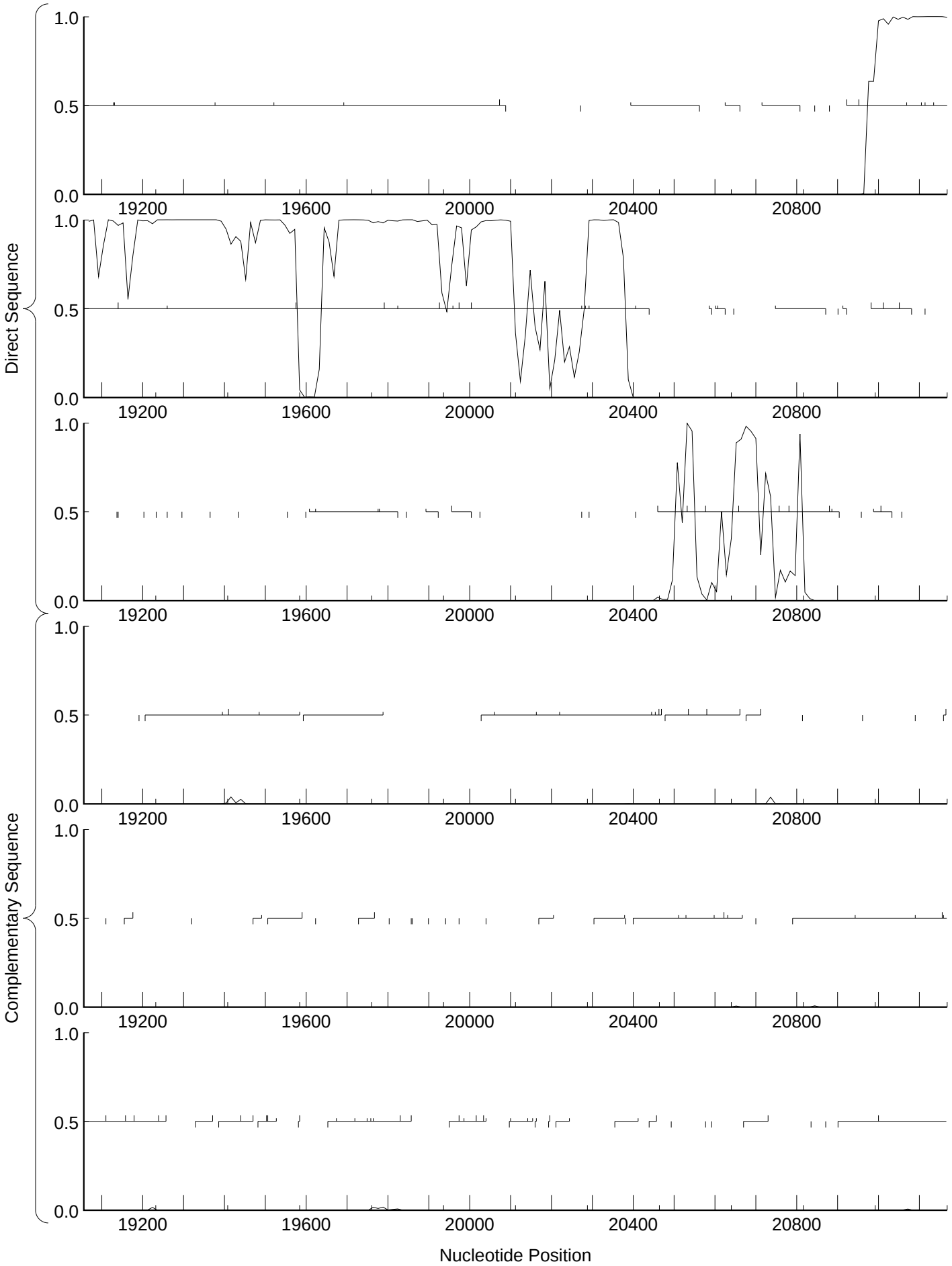
on complete sequence, 52055 bp including 10-base 3’ overhang (CGGGATGTAA), Cluster A8, Order 4, Window 96, Step 12, 9/26

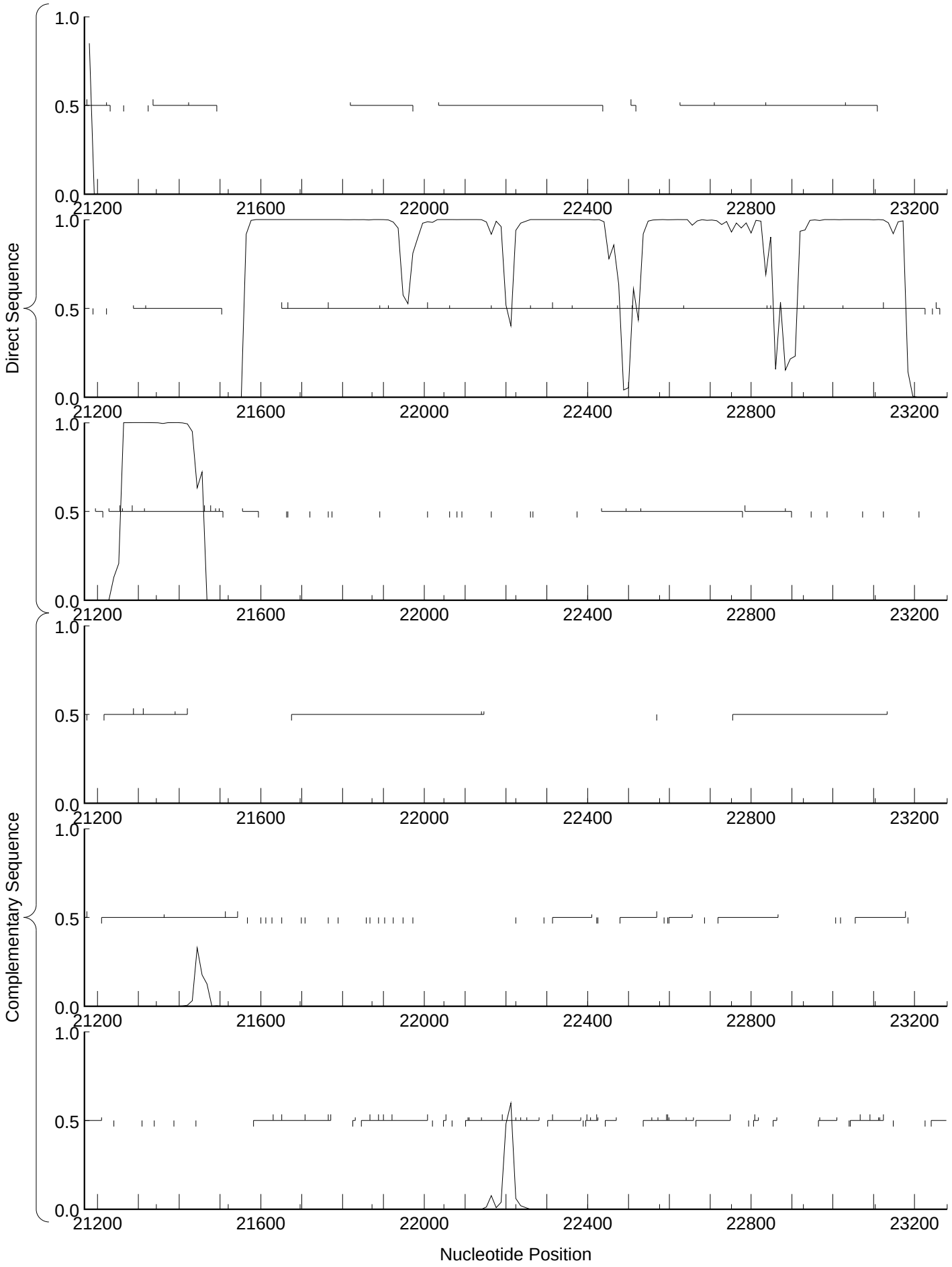


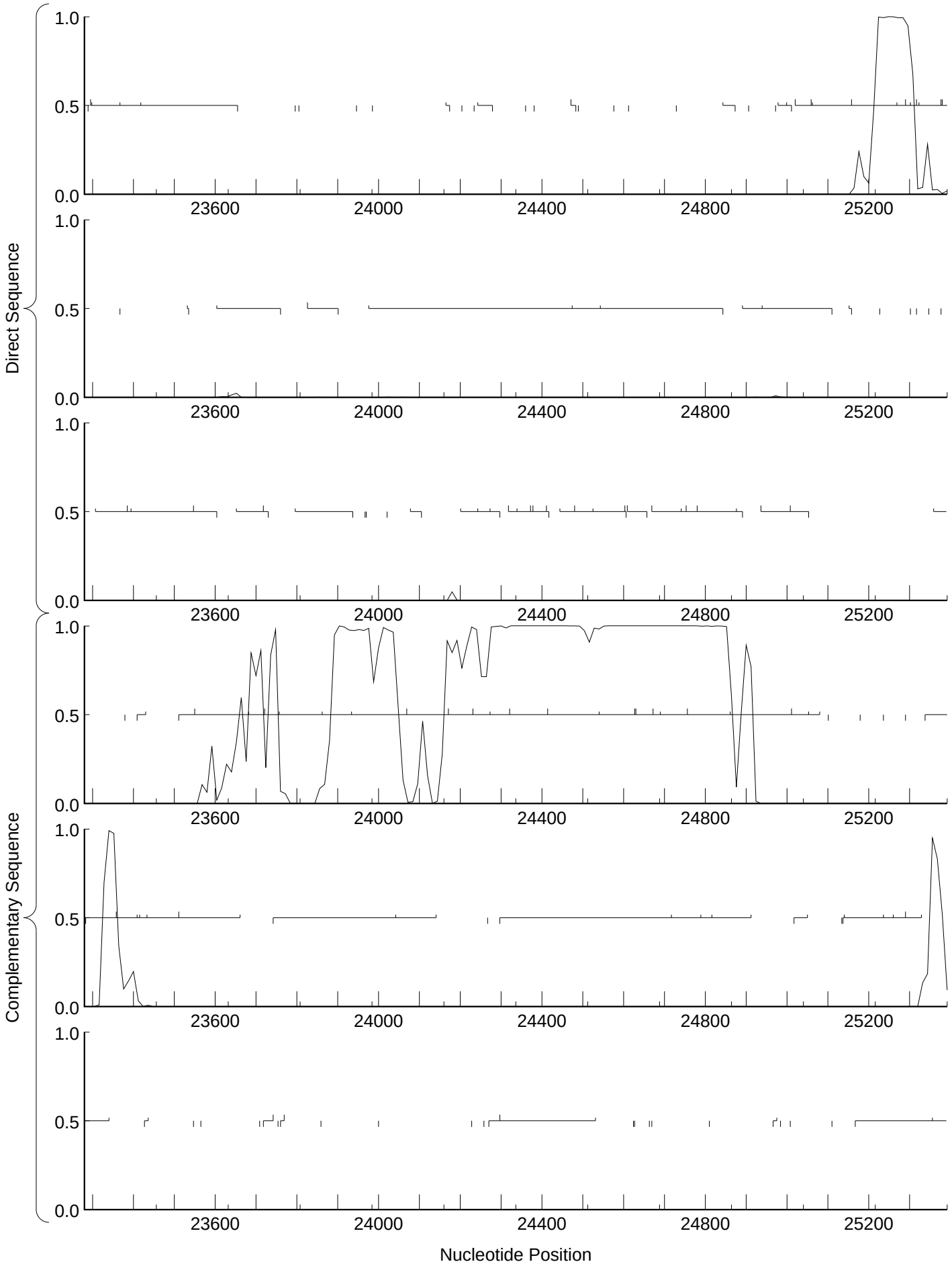
n complete sequence, 52055 bp including 10-base 3’ overhang (CGGGATGTAA), Cluster A8, Order 4, Window 96, Step 12, 10/26



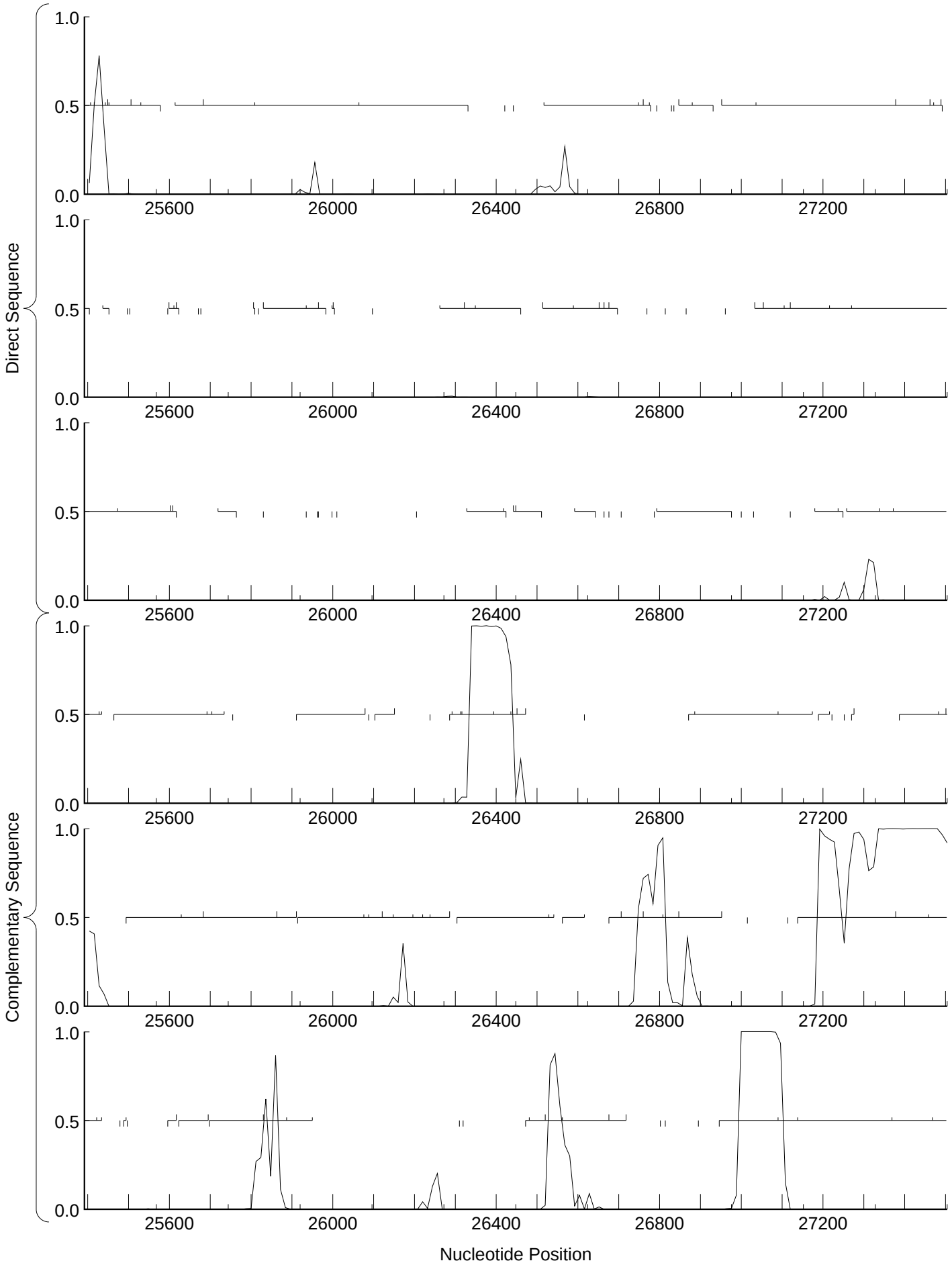
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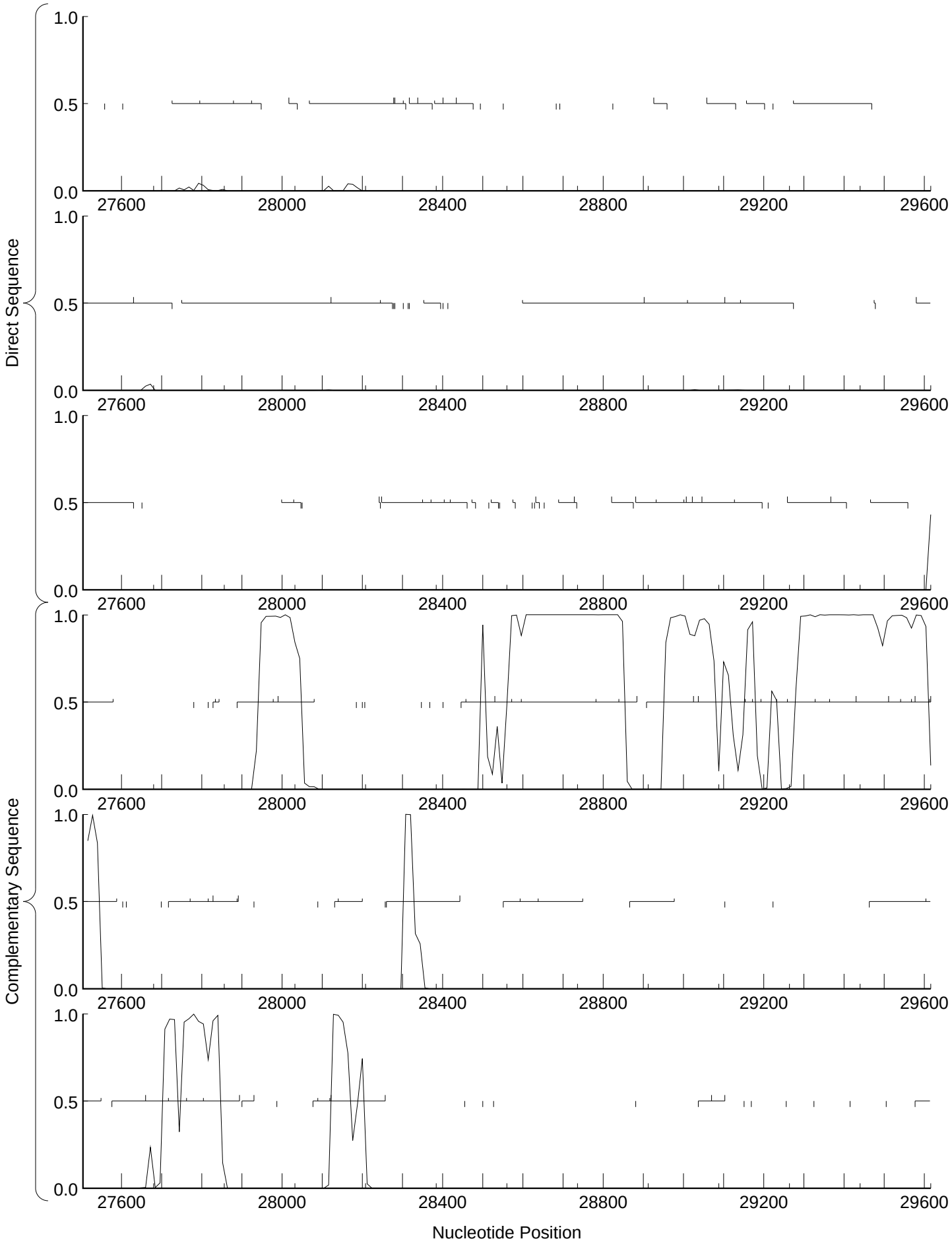

Direct Sequence
Complementary Sequence
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0.5
0.0
21200
21600
22000
22400
22800
23200
Nucleotide Position

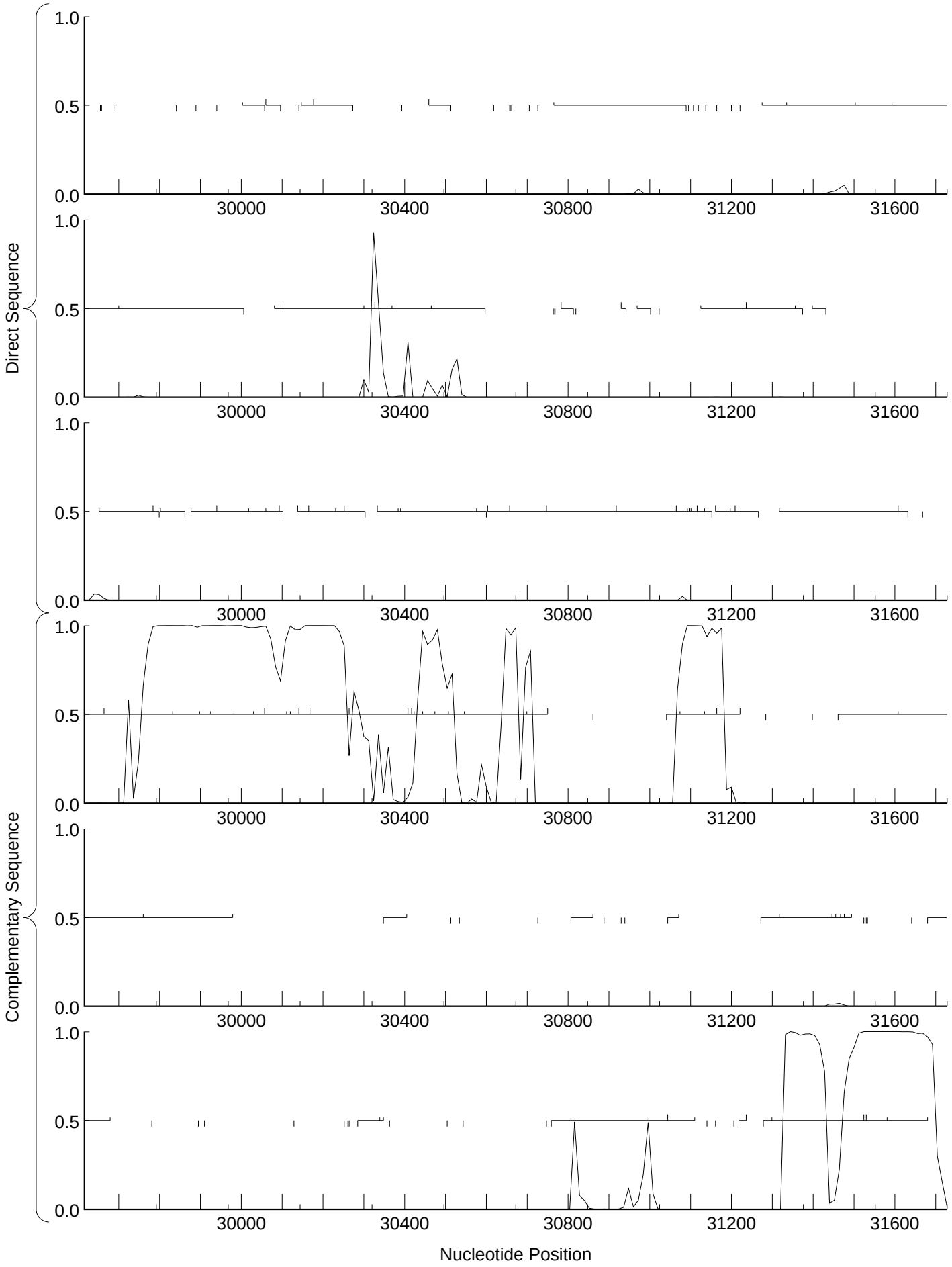

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
23600
24000
24400
24800
25200
Nucleotide Position

n complete sequence, 52055 bp including 10-base 3’ overhang (CGGGATGTAA), Cluster A8, Order 4, Window 96, Step 12, 14/26

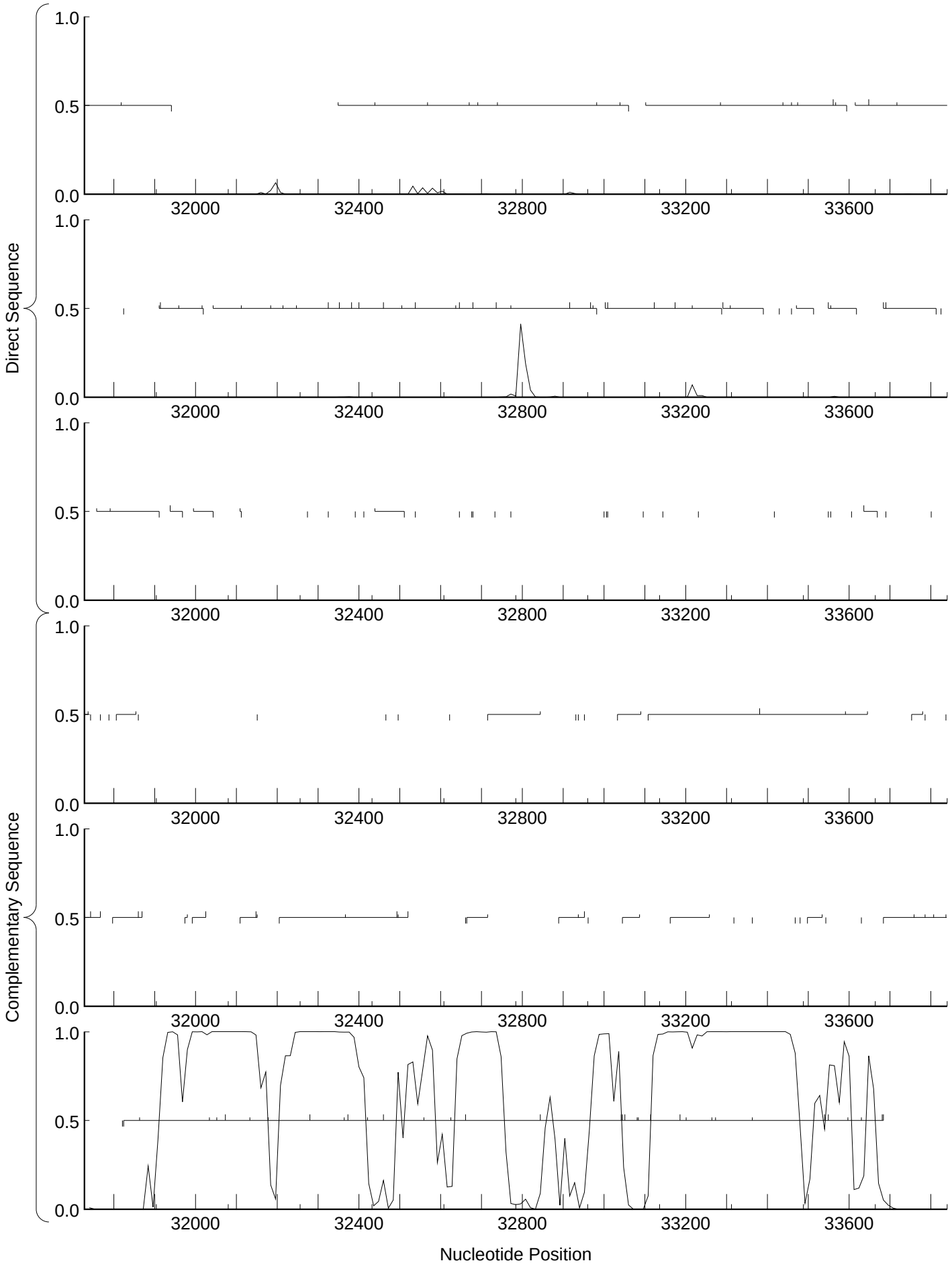


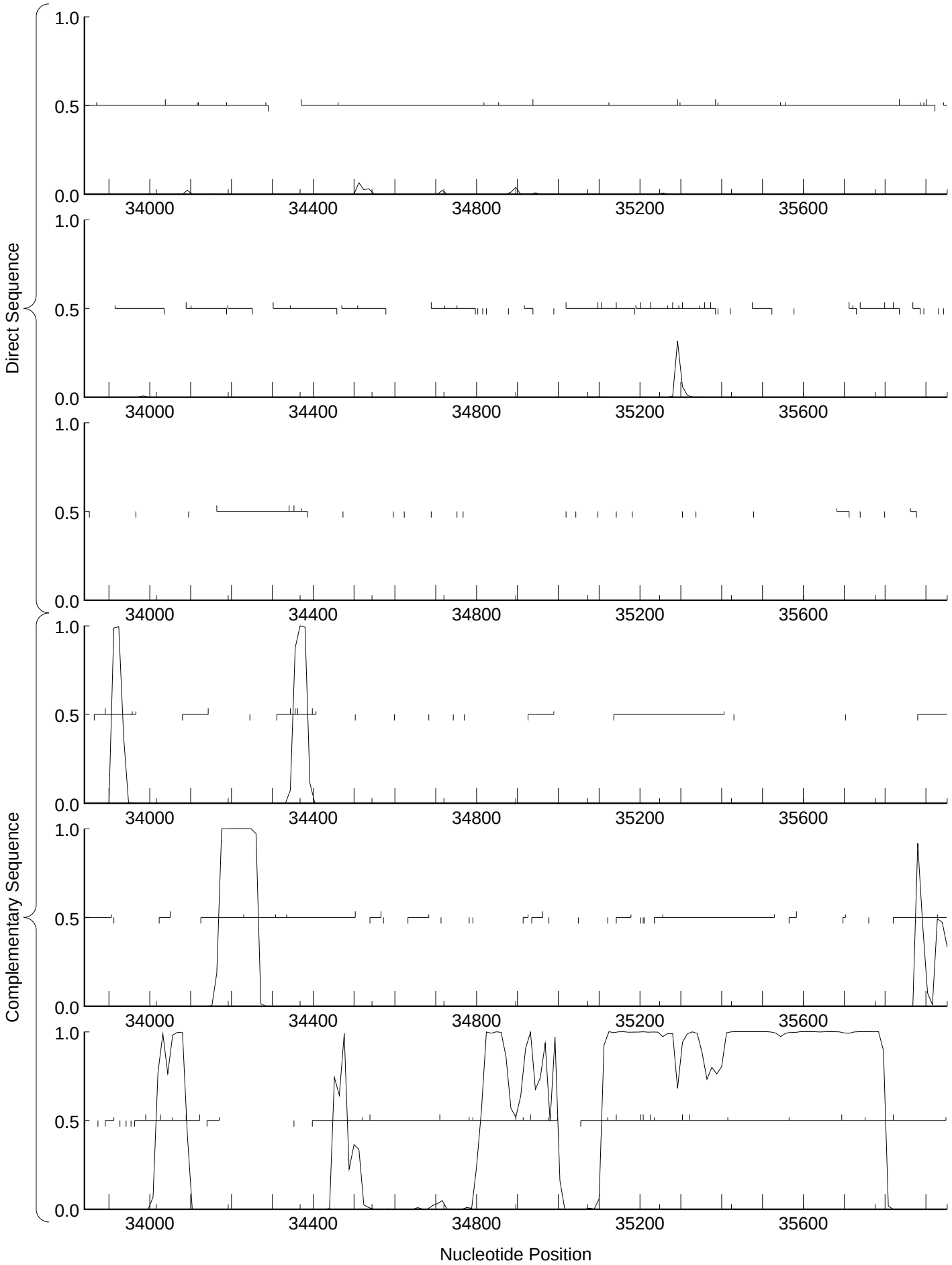
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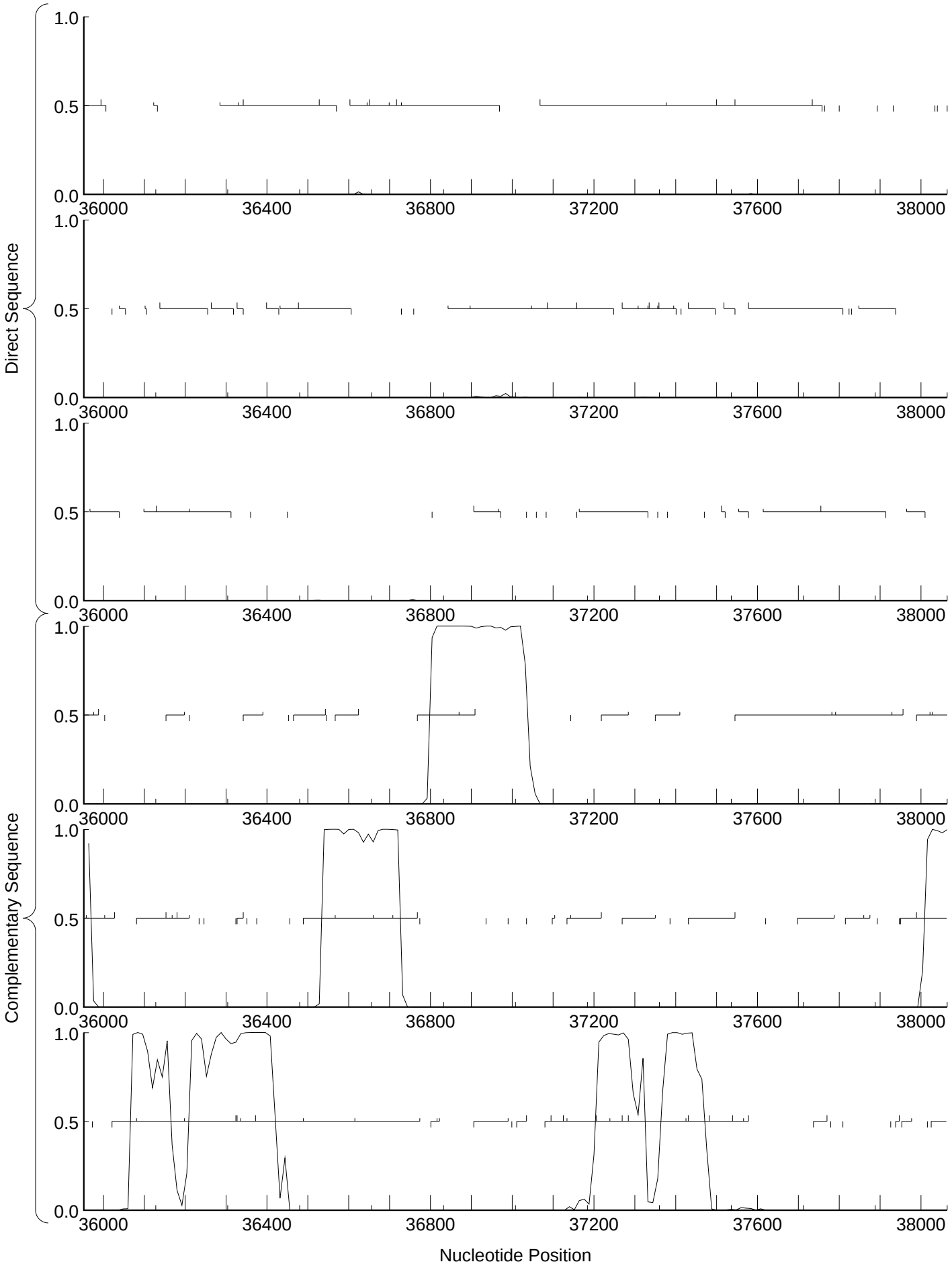

Direct Sequence
Complementary Sequence
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0.5
0.0
30000
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30800
31200
31600
Nucleotide Position

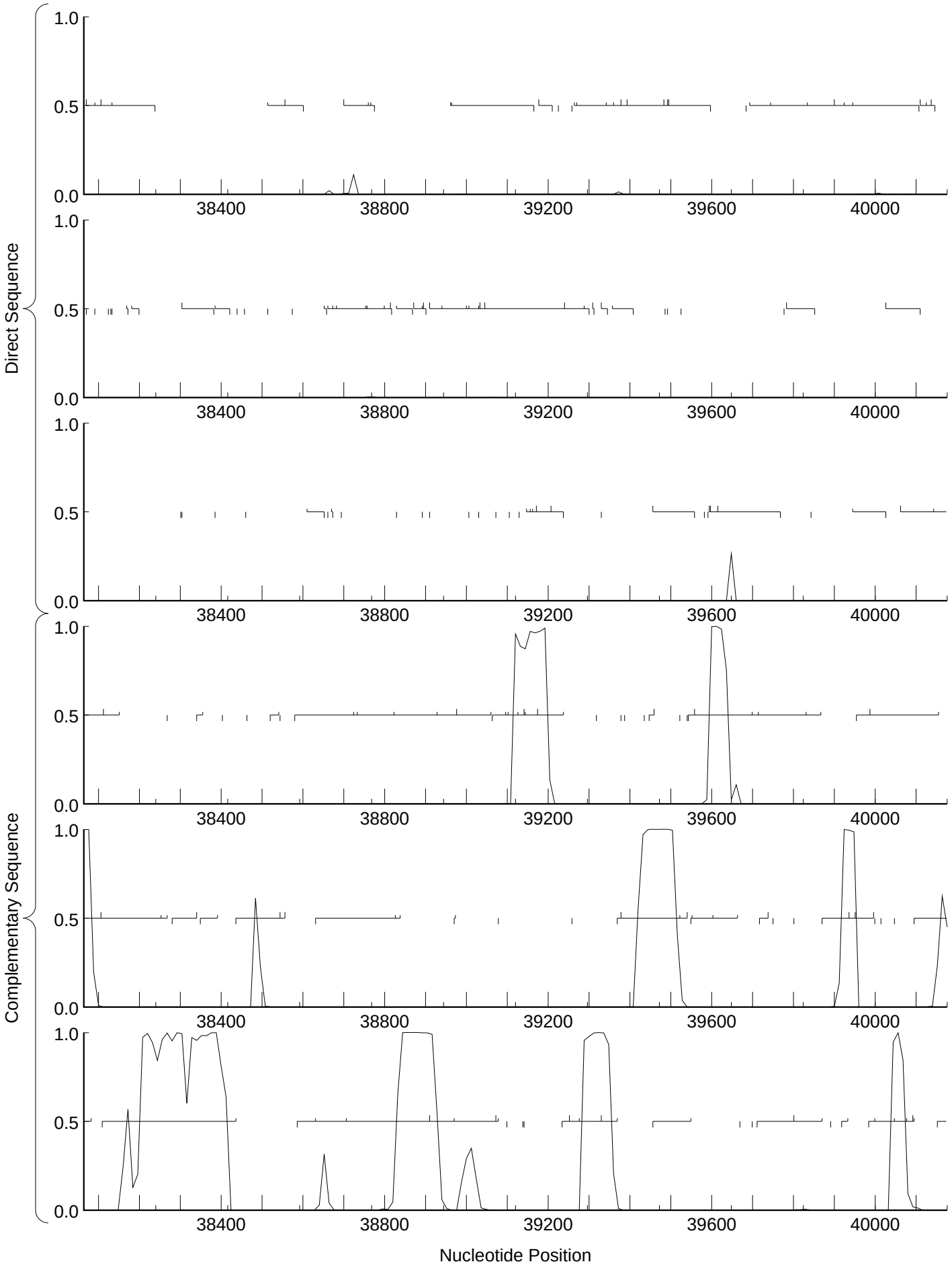
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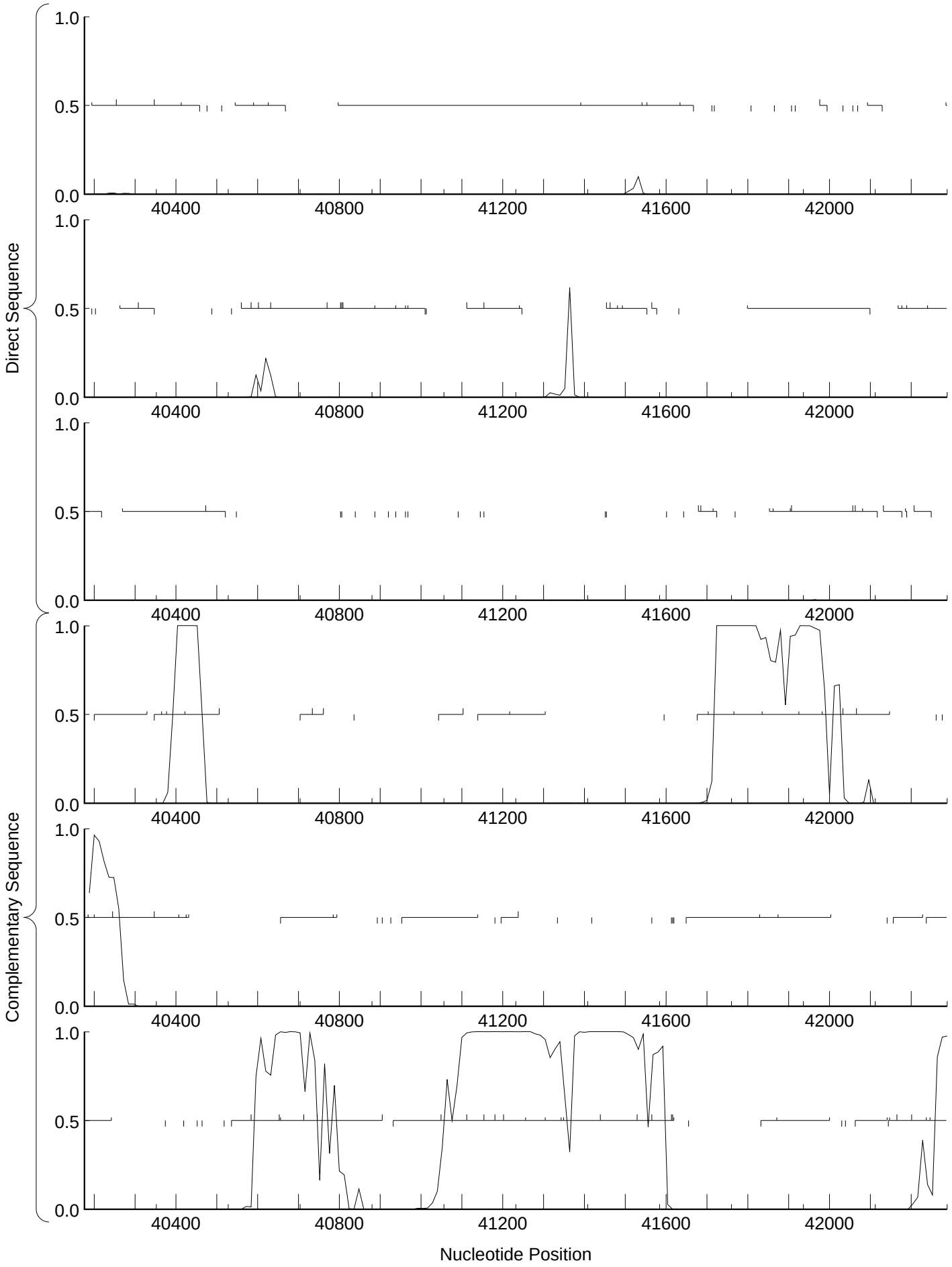


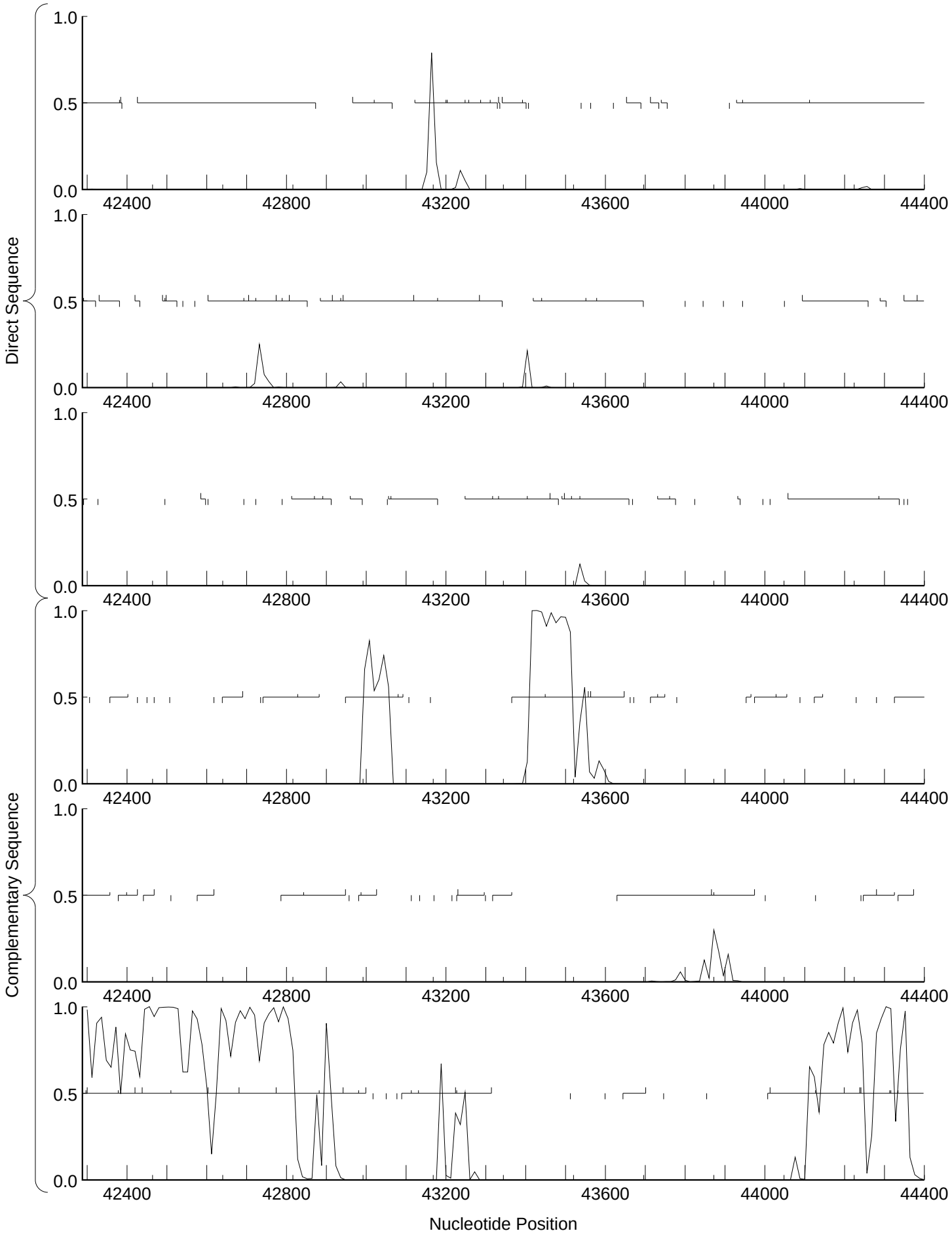

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
34000
34400
34800
35200
35600
Nucleotide Position

n complete sequence, 52055 bp including 10-base 3’ overhang (CGGGATGTAA), Cluster A8, Order 4, Window 96, Step 12, 19/26

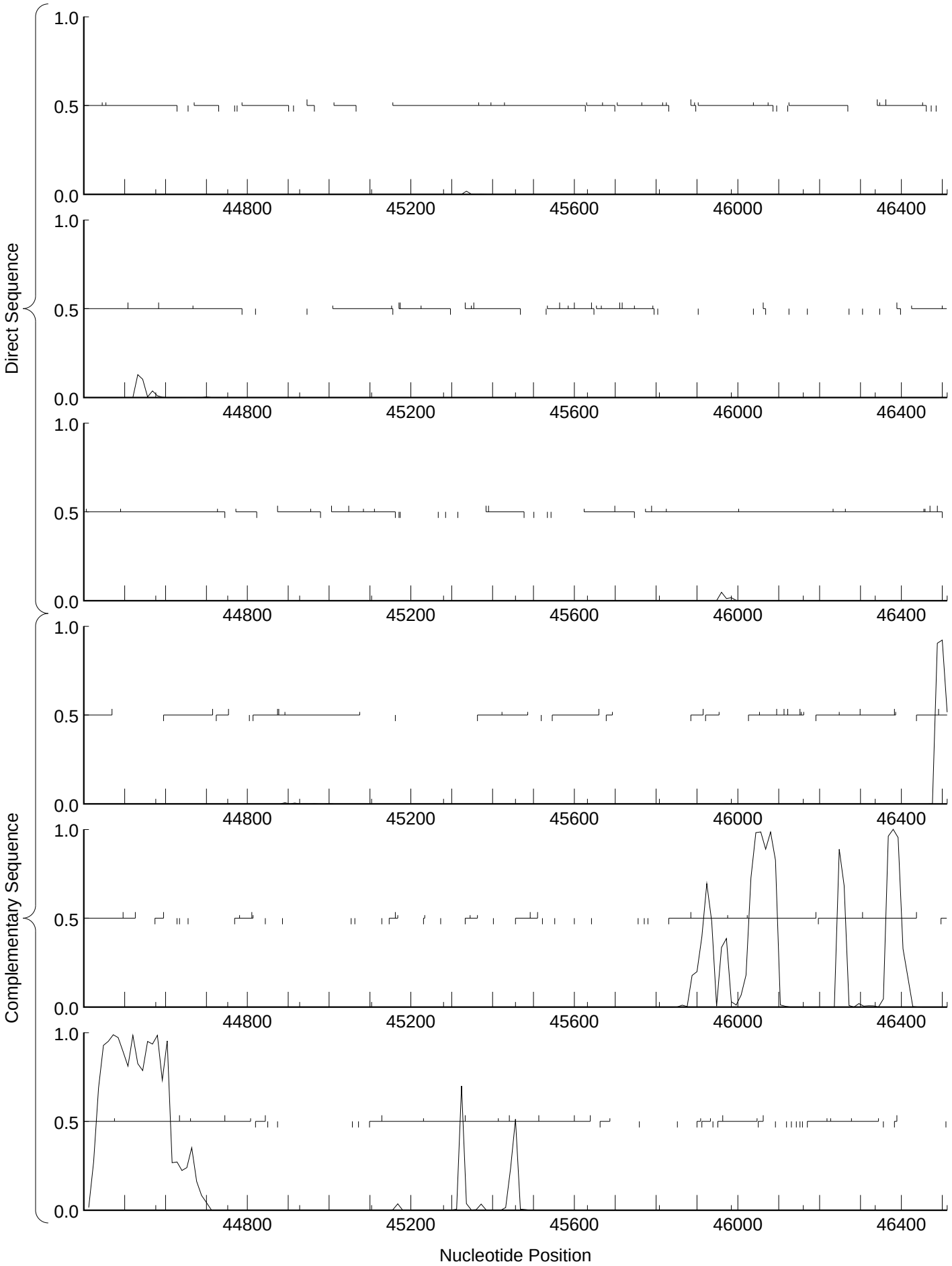


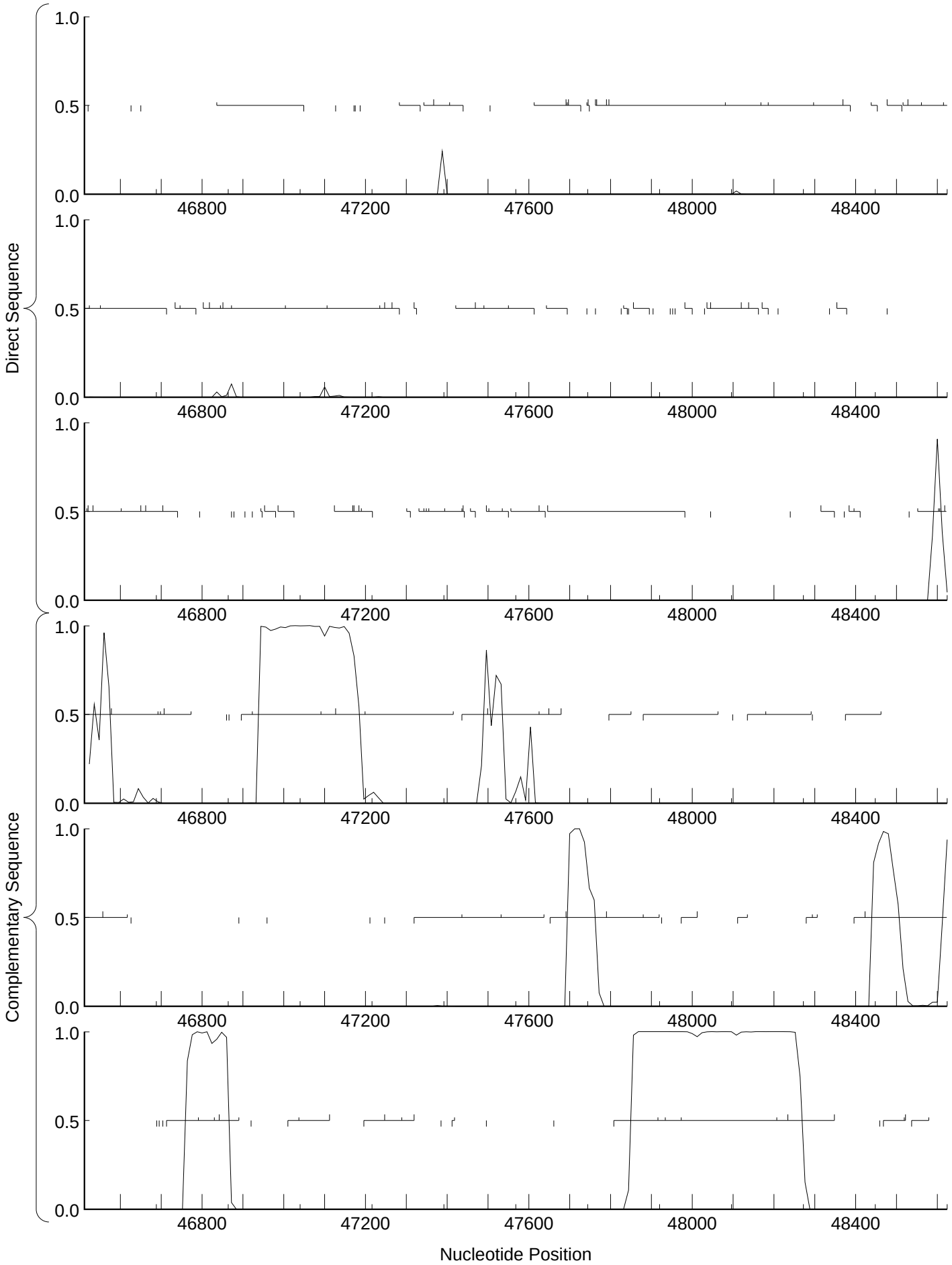

Direct Sequence
Complementary Sequence
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0.5
0.0
38400
38800
39200
39600
40000
Nucleotide Position

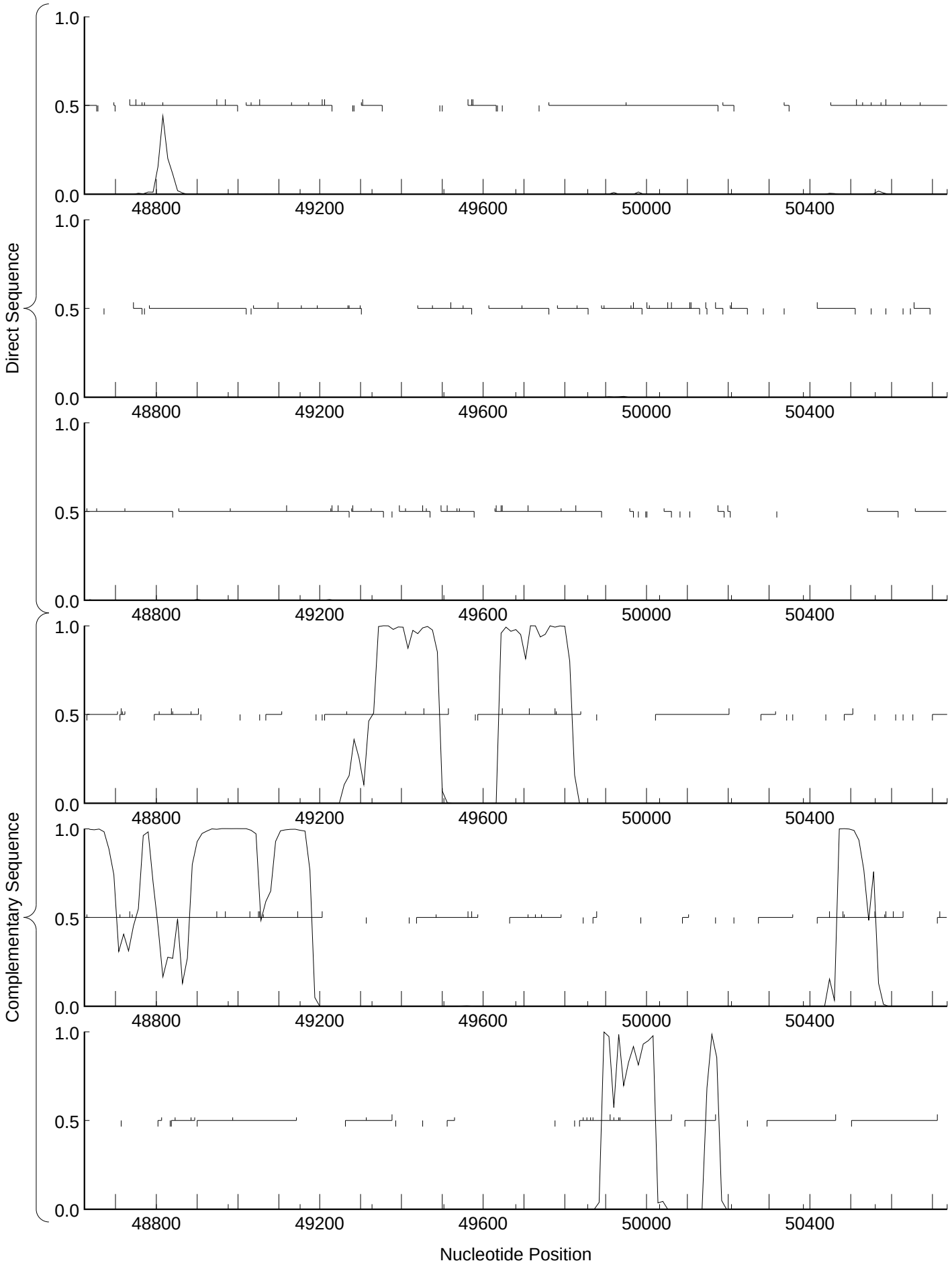

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
40400
40800
41200
41600
42000
Nucleotide Position


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
42400
42800
43200
43600
44000
44400
Nucleotide Position

n complete sequence, 52055 bp including 10-base 3’ overhang (CGGGATGTAA), Cluster A8, Order 4, Window 96, Step 12, 23/26




Direct Sequence
Complementary Sequence
1.0
0.5
0.0
46800
47200
47600
48000
48400
Nucleotide Position


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
48800
49200
49600
50000
50400
Nucleotide Position

n complete sequence, 52055 bp including 10-base 3’ overhang (CGGGATGTAA), Cluster A8, Order 4, Window 96, Step 12, 26/26

