GeneMark

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

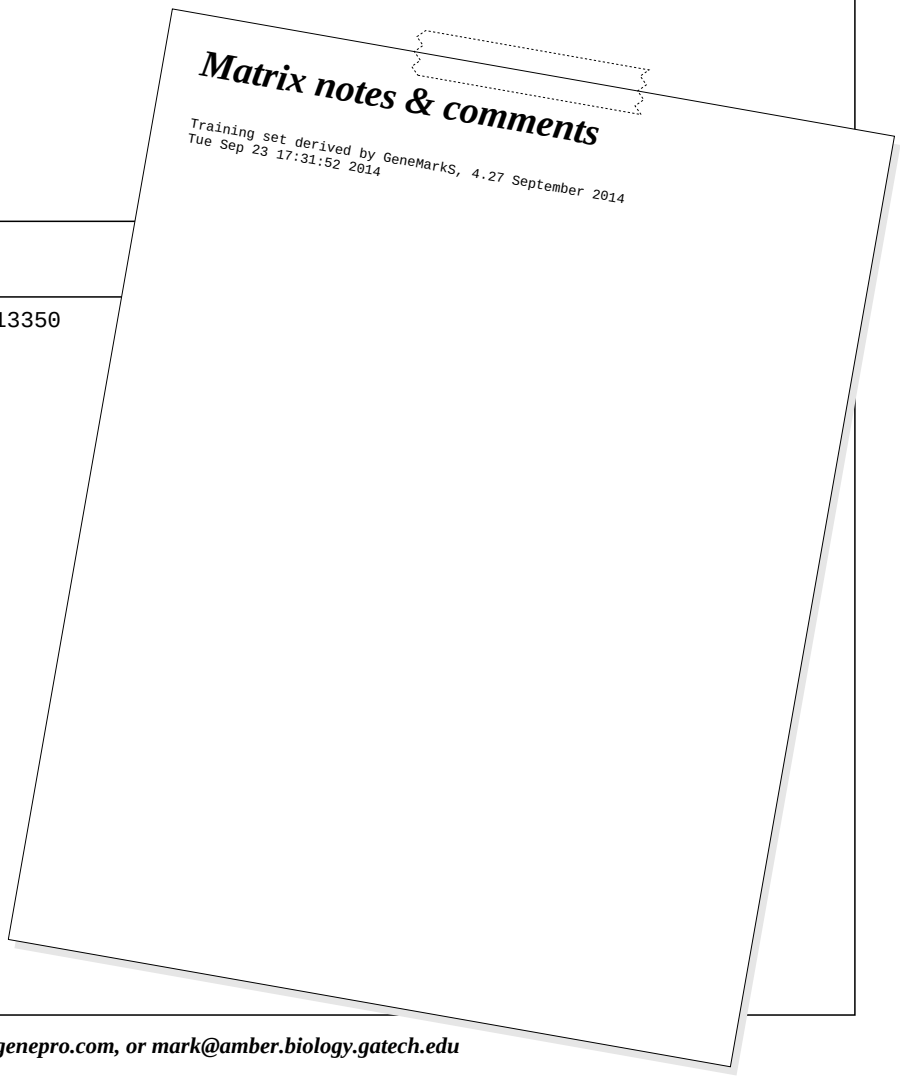
PROGRAM INFORMATION

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Sequence         :  Streptomyces phage Madamato complete sequence, 55349 bp including 9-base 3' overhang (CGCCC
Analysis Date    :  3/28/24 at 6:19:16
Pages            :  28
Sequence Length  :  55349 bp
GC Content       :   59.58%

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

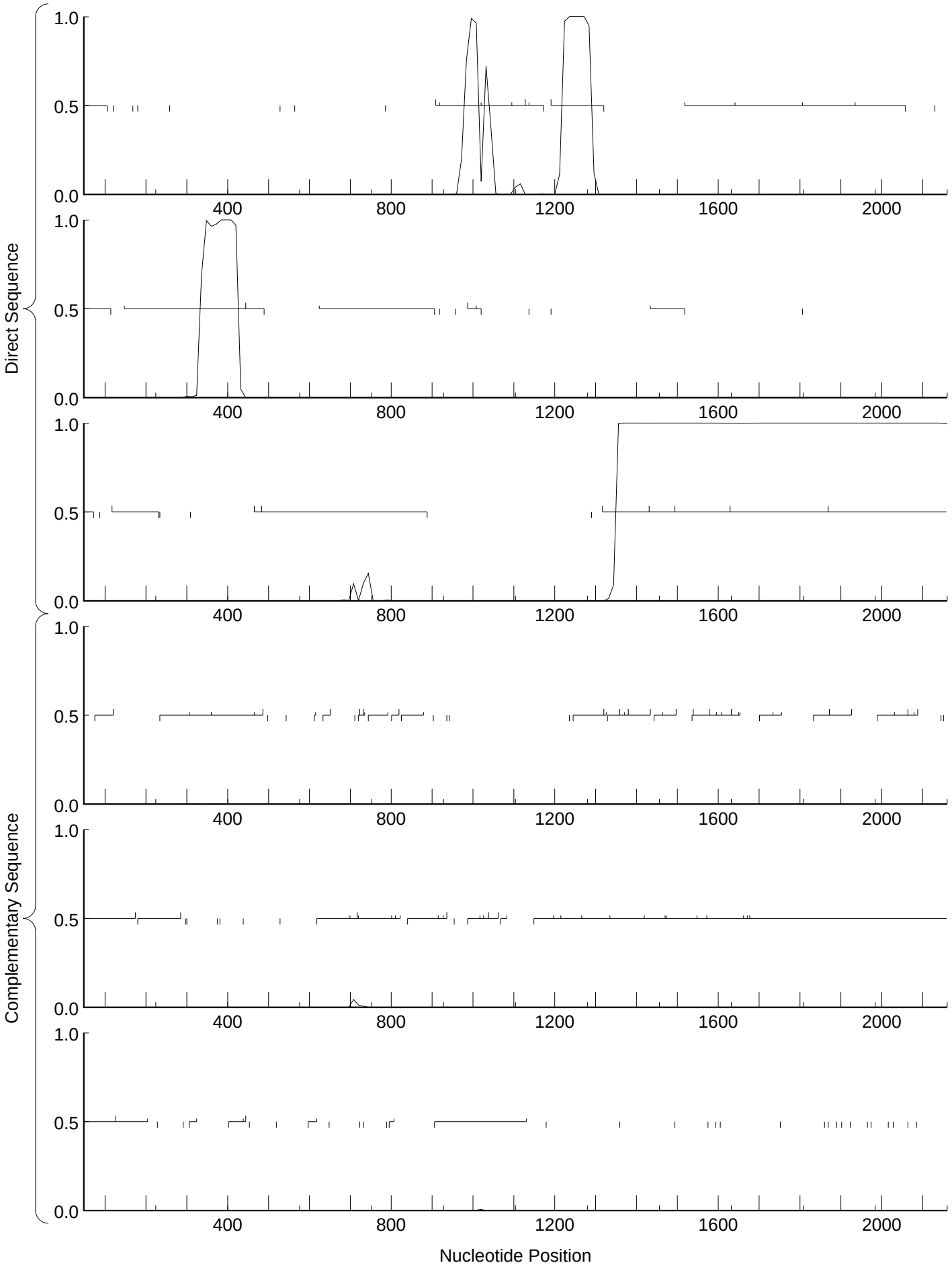
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Matrix     :  Streptomyces_griseus_NBRC_13350
Author     :  -

Order      :  4
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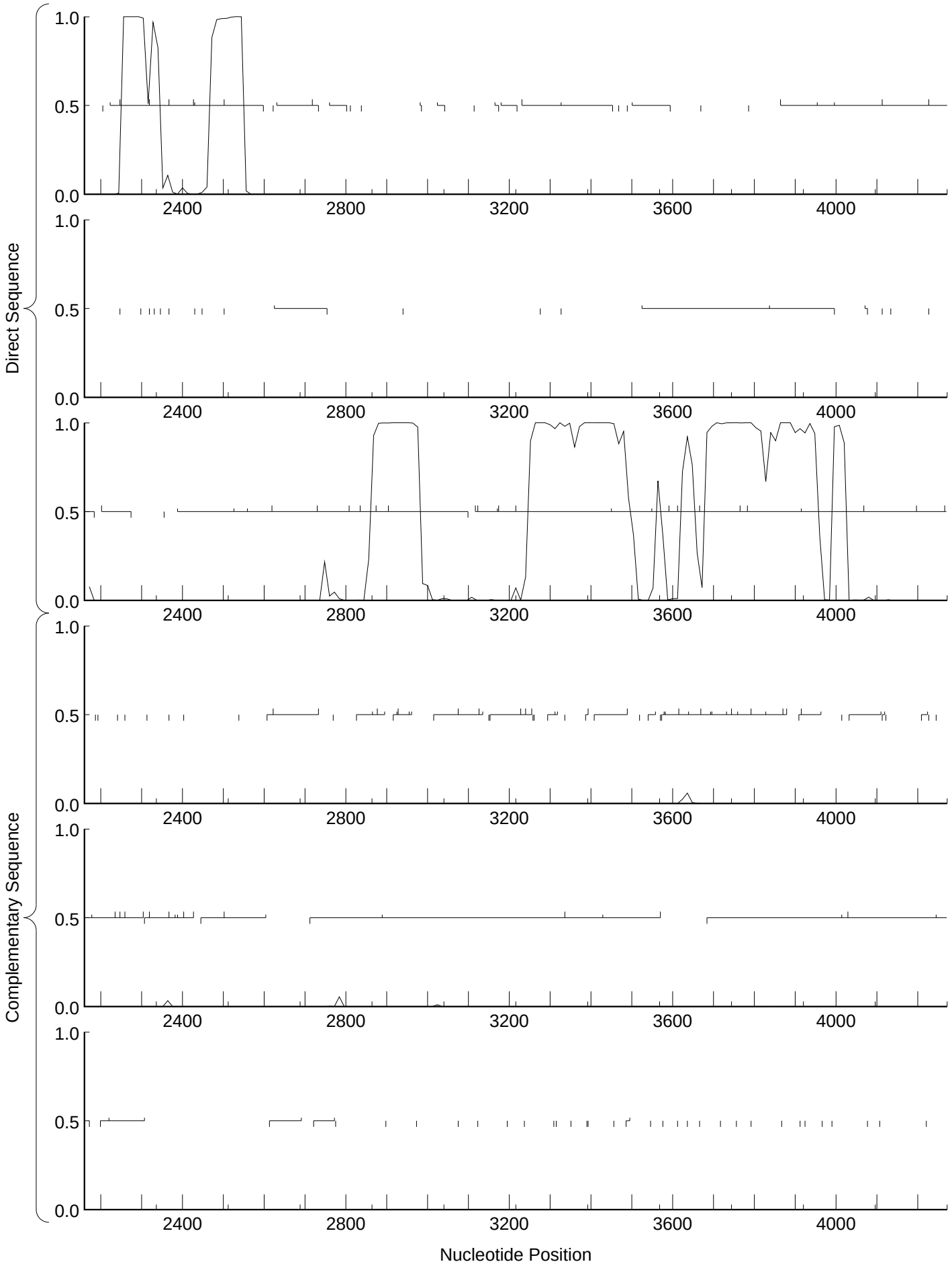

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  Send questions / comments to:
      Dr. M. Borodovsky
      Georgia Institute of Technology
      School of Biology
      Atlanta, GA  30332-0230
```

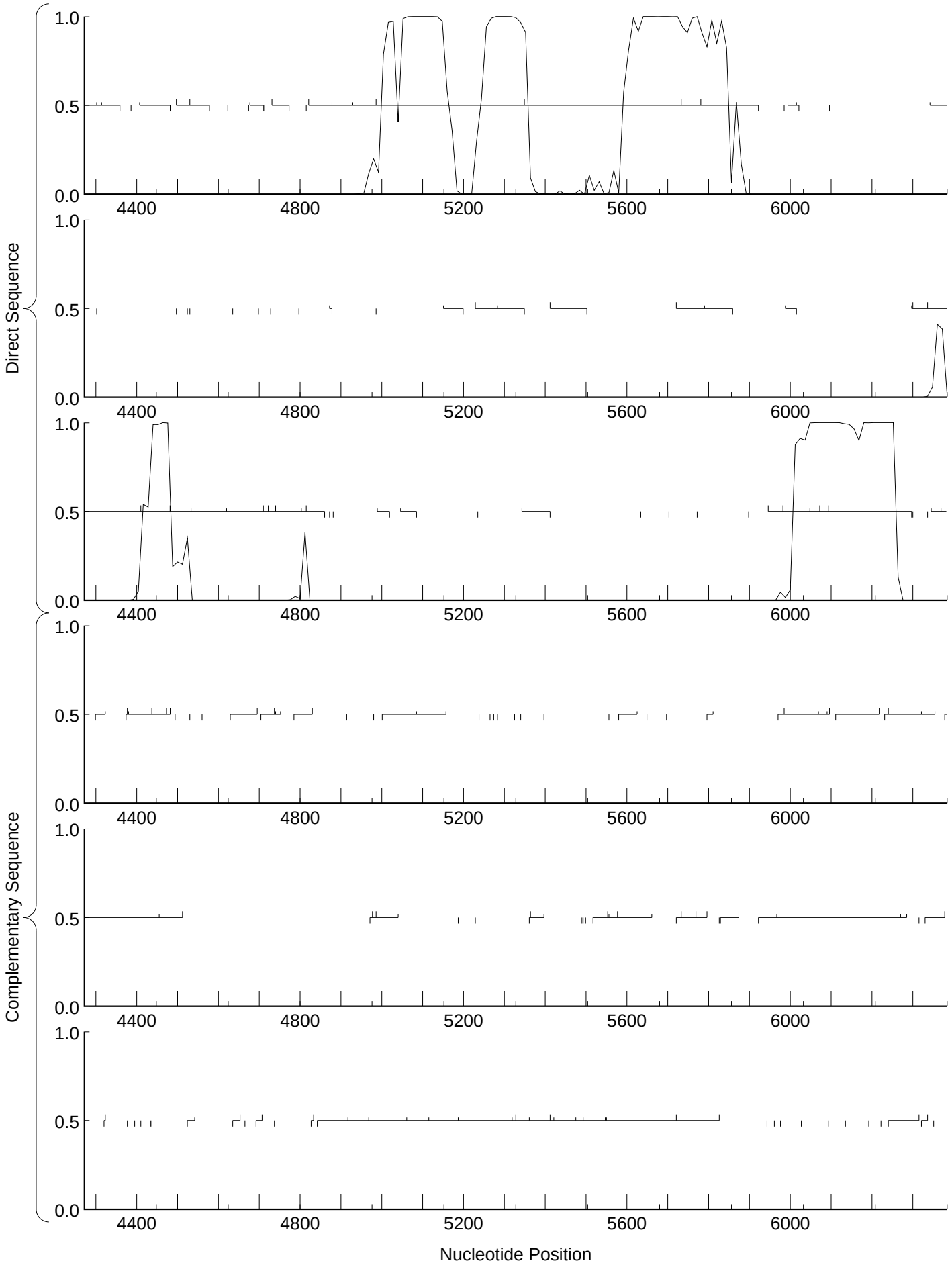

For help or information, send electronic mail to: custserv@genepro.com, or mark@amber.biology.gatech.edu

nato complete sequence, 55349 bp including 9-base 3’ overhang (CGCCCGCCT), Cluster BI1, Order 4, Window 96, Step 12, 2/28

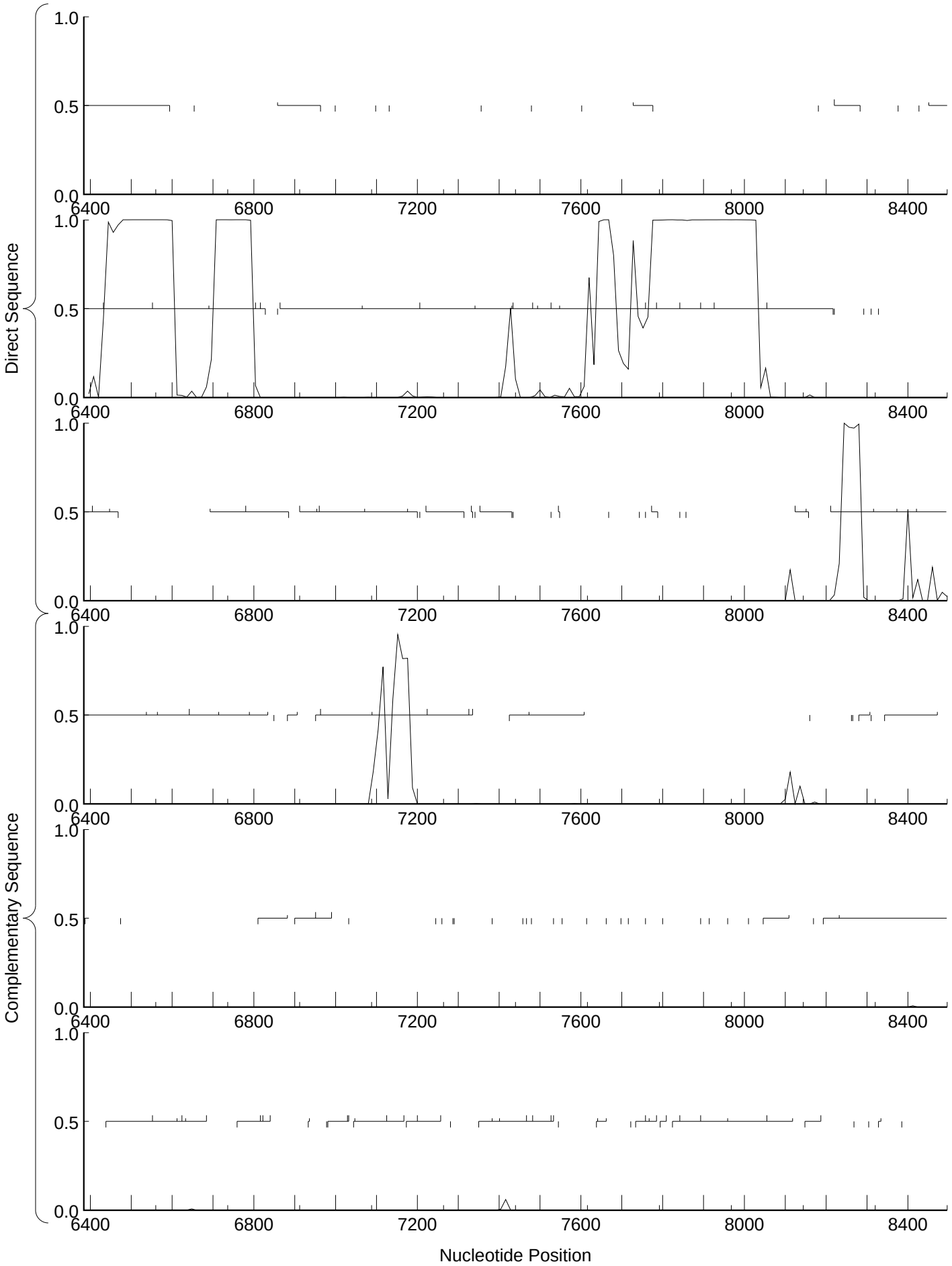


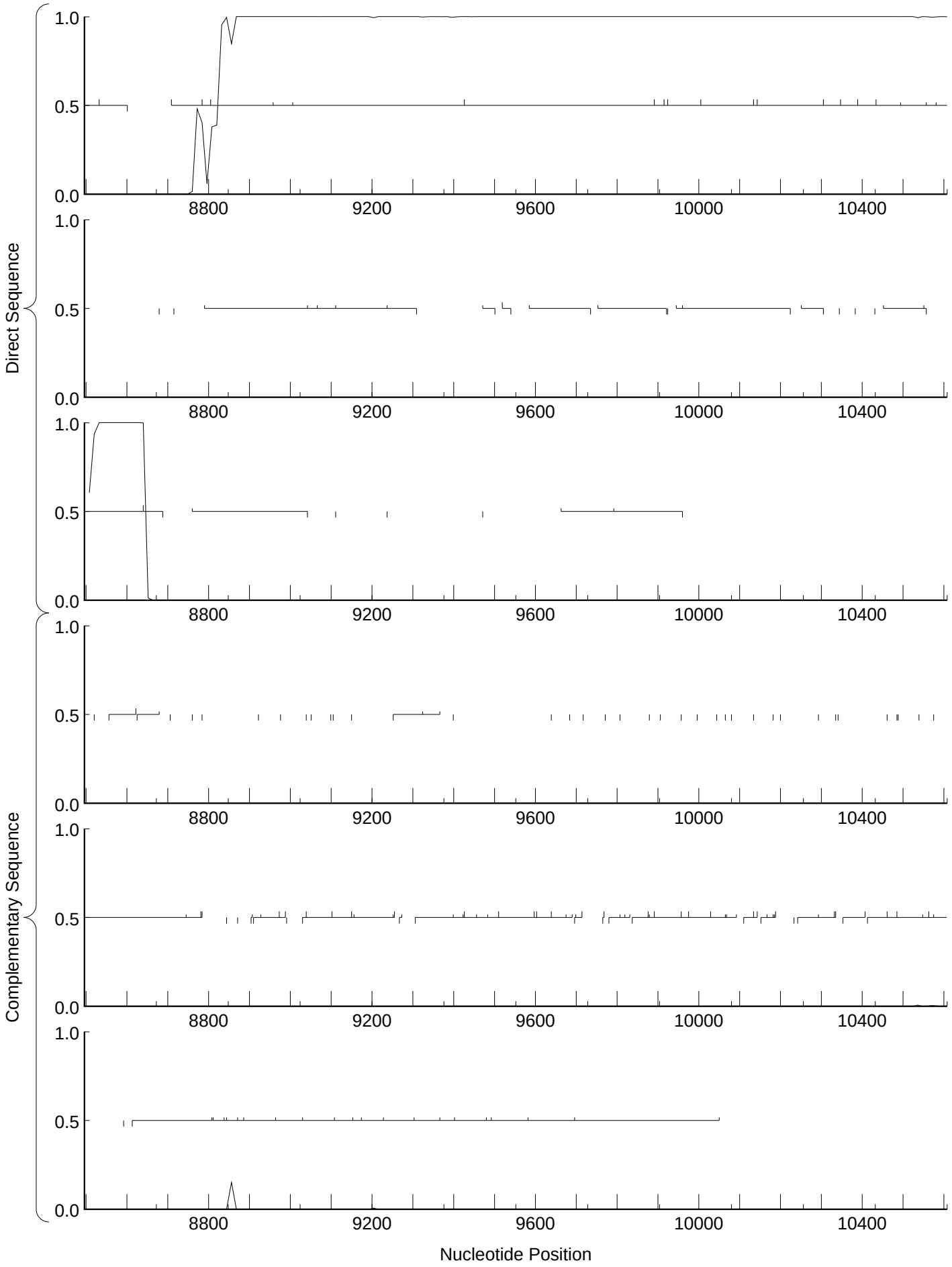
nato complete sequence, 55349 bp including 9-base 3’ overhang (CGCCCGCCT), Cluster BI1, Order 4, Window 96, Step 12, 3/28

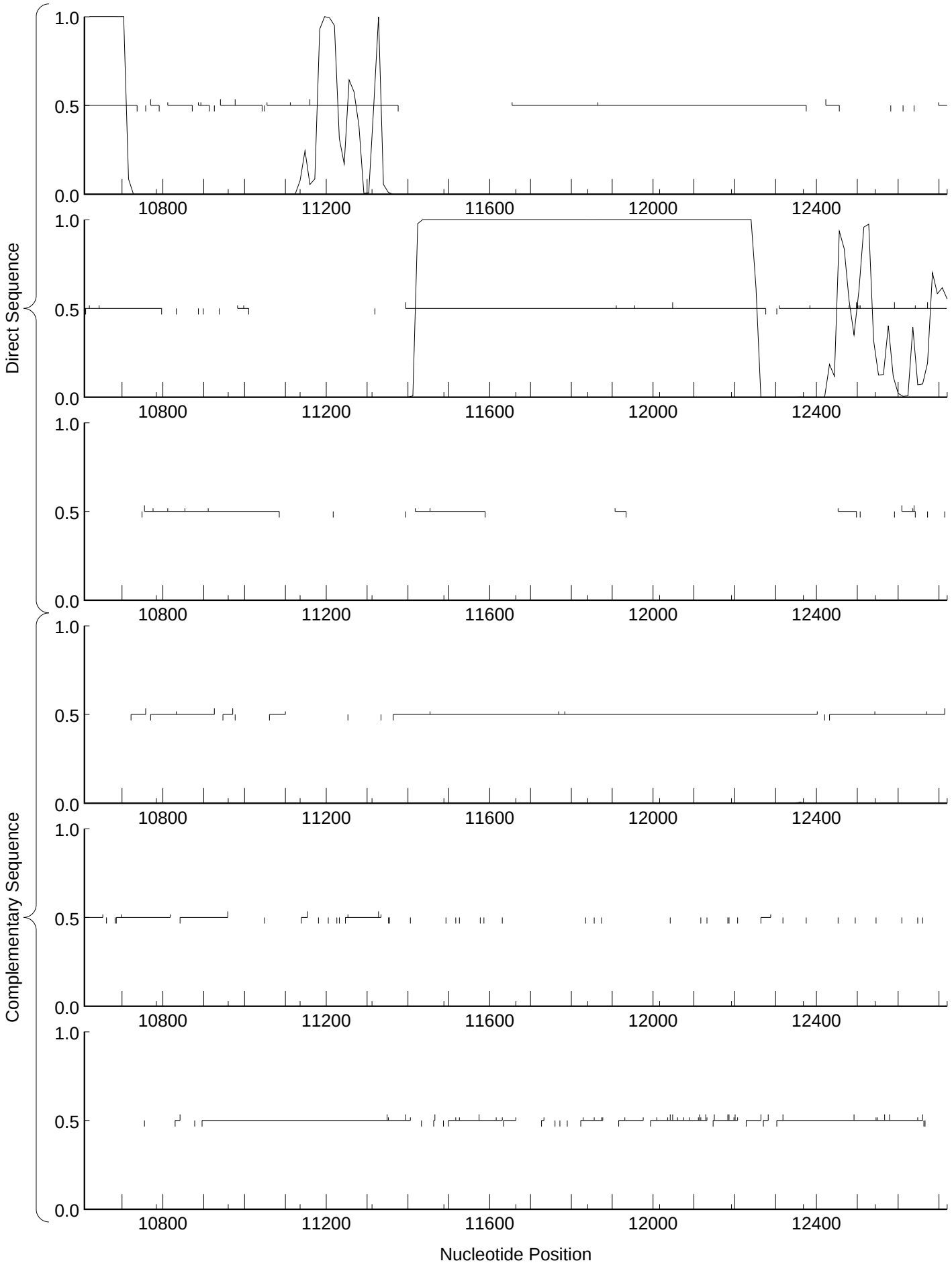



Direct Sequence
Complementary Sequence
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0.5
0.0
4400
4800
5200
5600
6000
Nucleotide Position

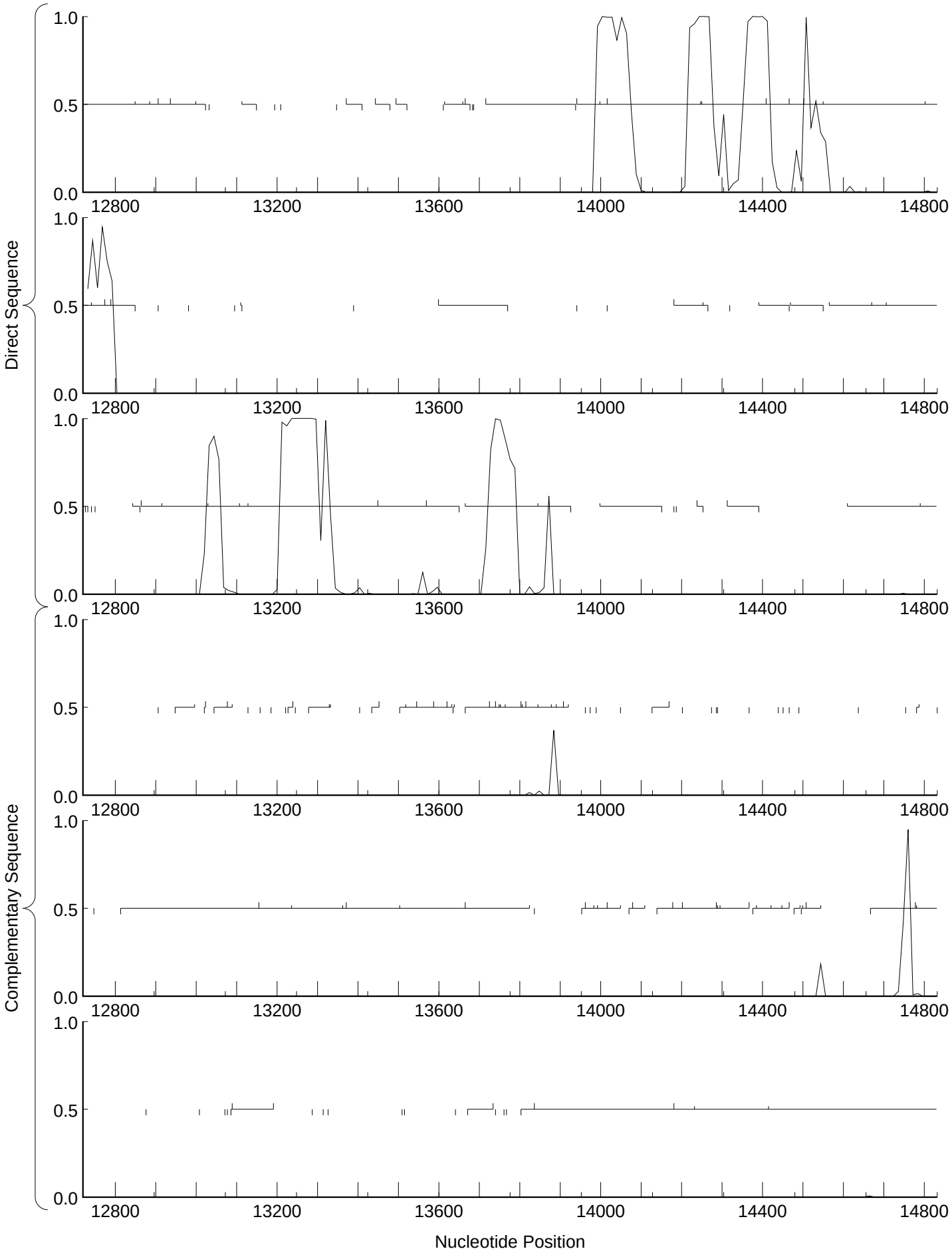
nato complete sequence, 55349 bp including 9-base 3’ overhang (CGCCCGCCT), Cluster BI1, Order 4, Window 96, Step 12, 5/28



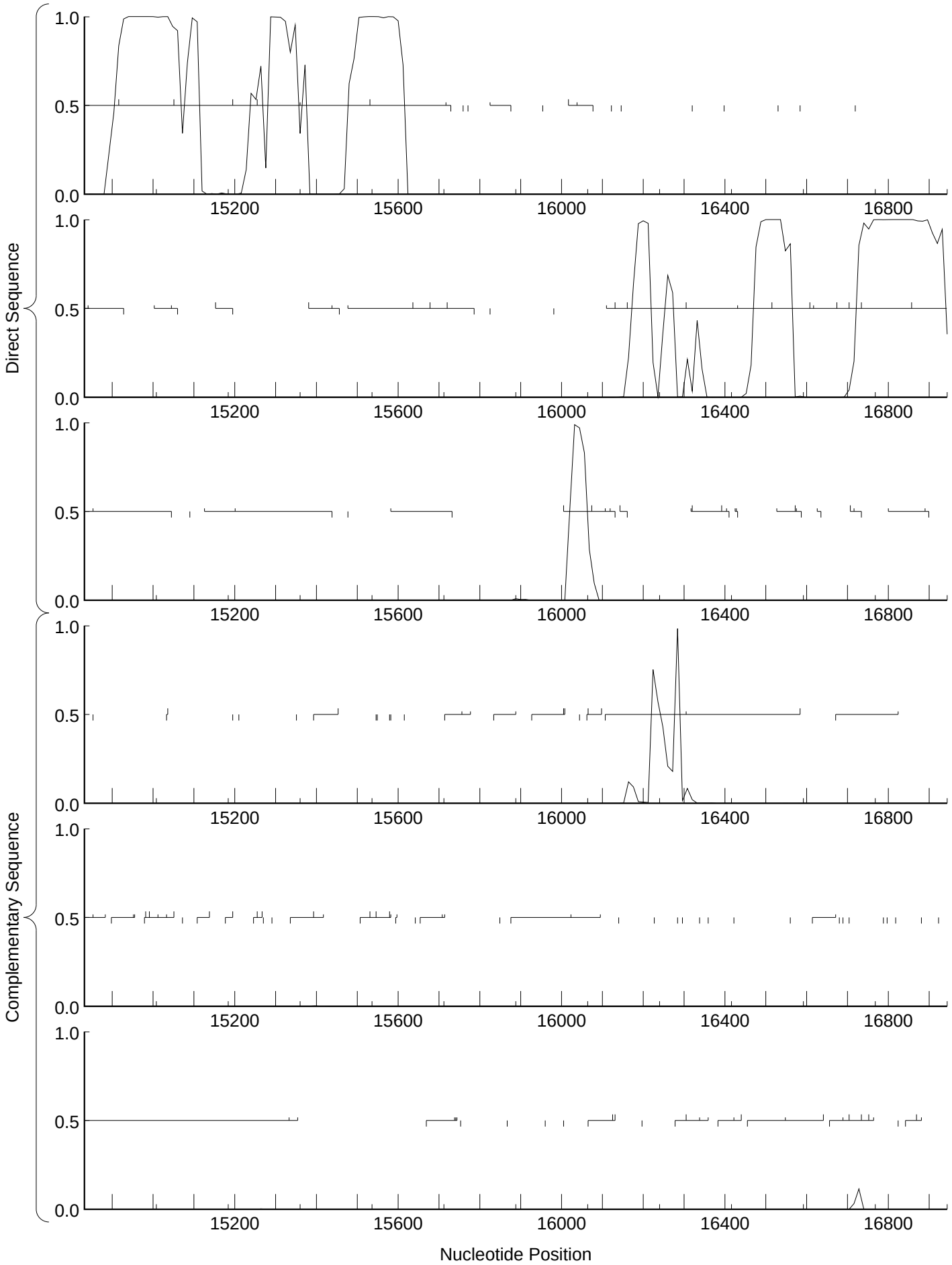

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
8800
9200
9600
10000
10400
Nucleotide Position


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

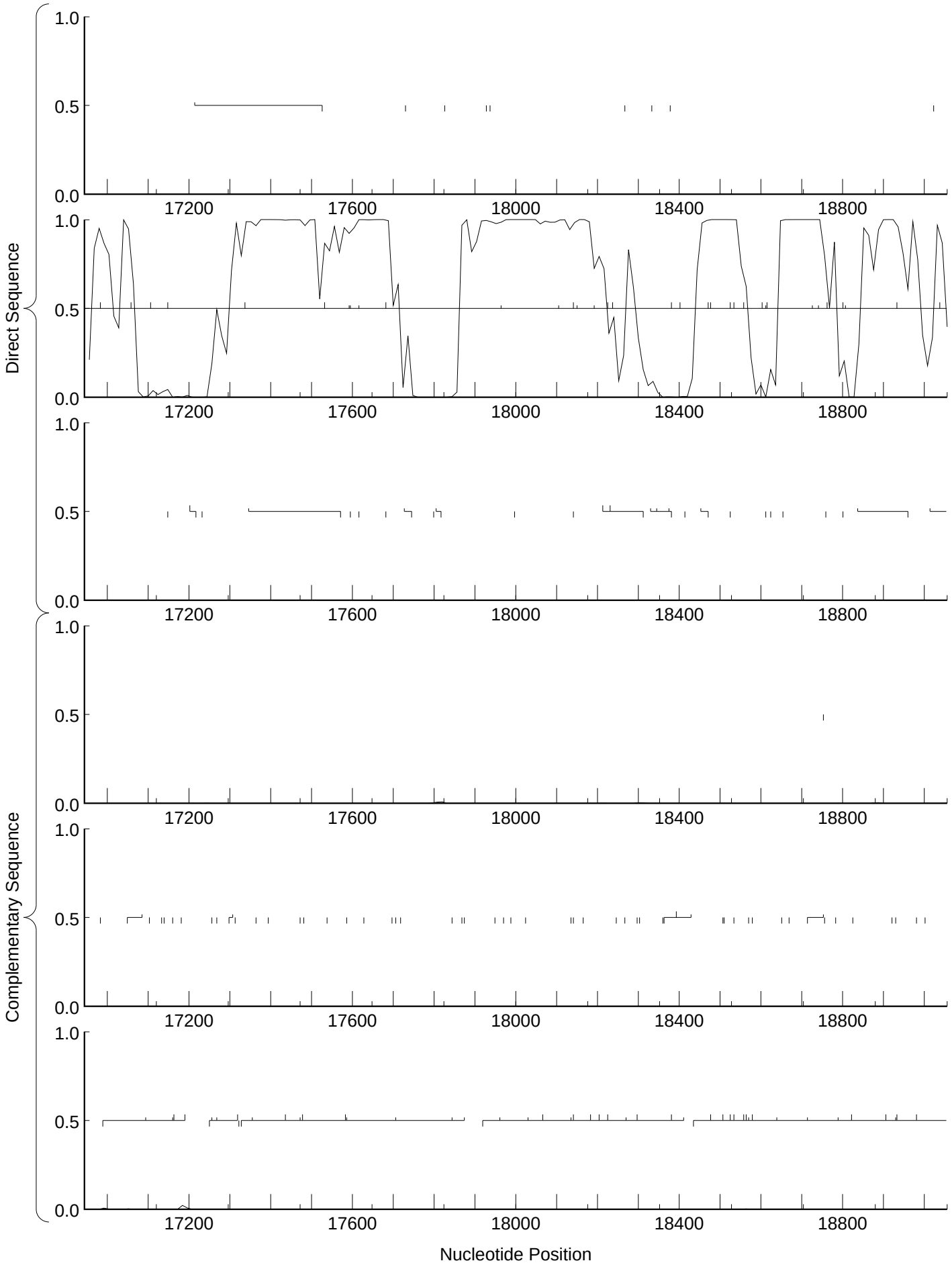
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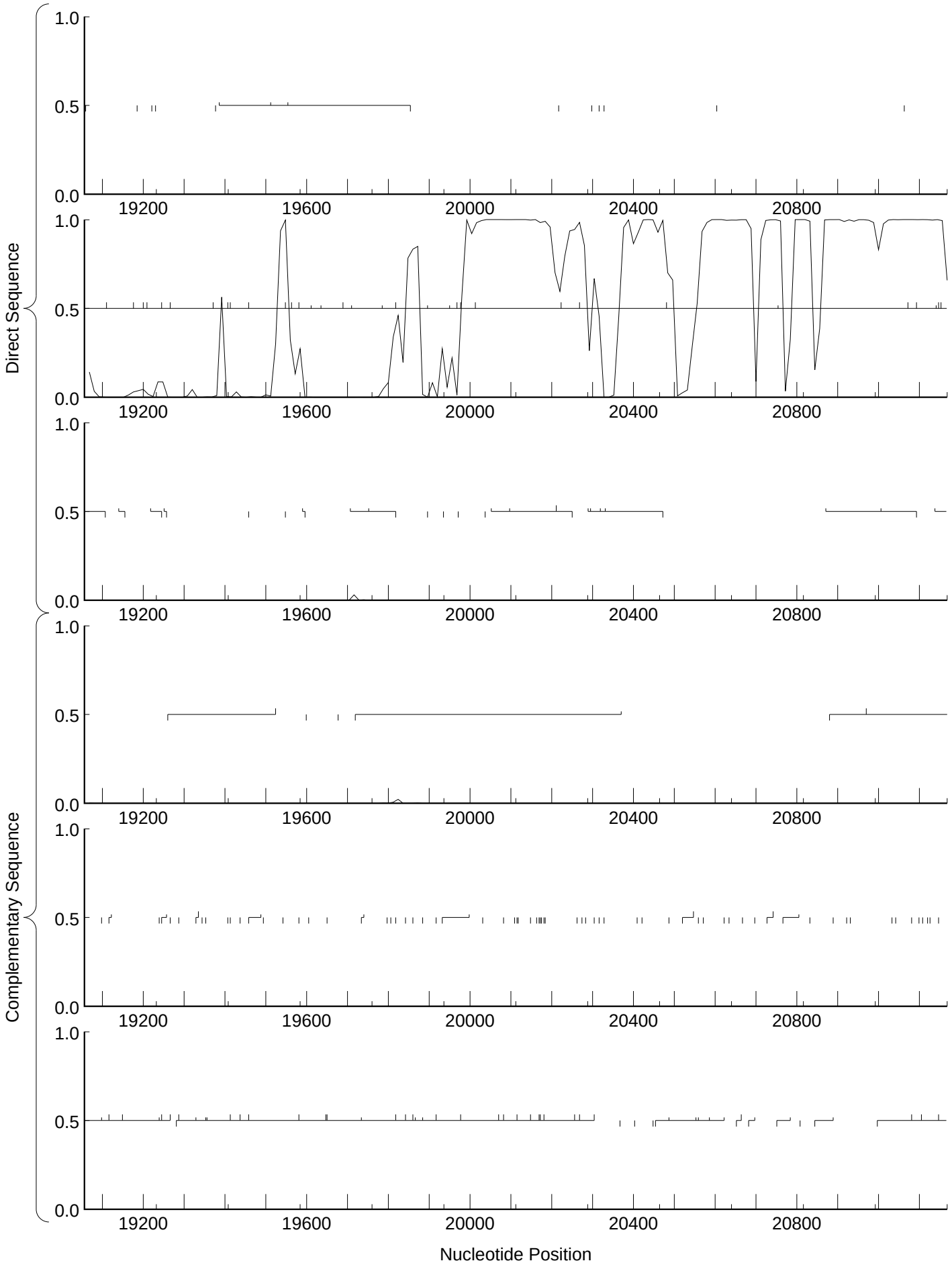
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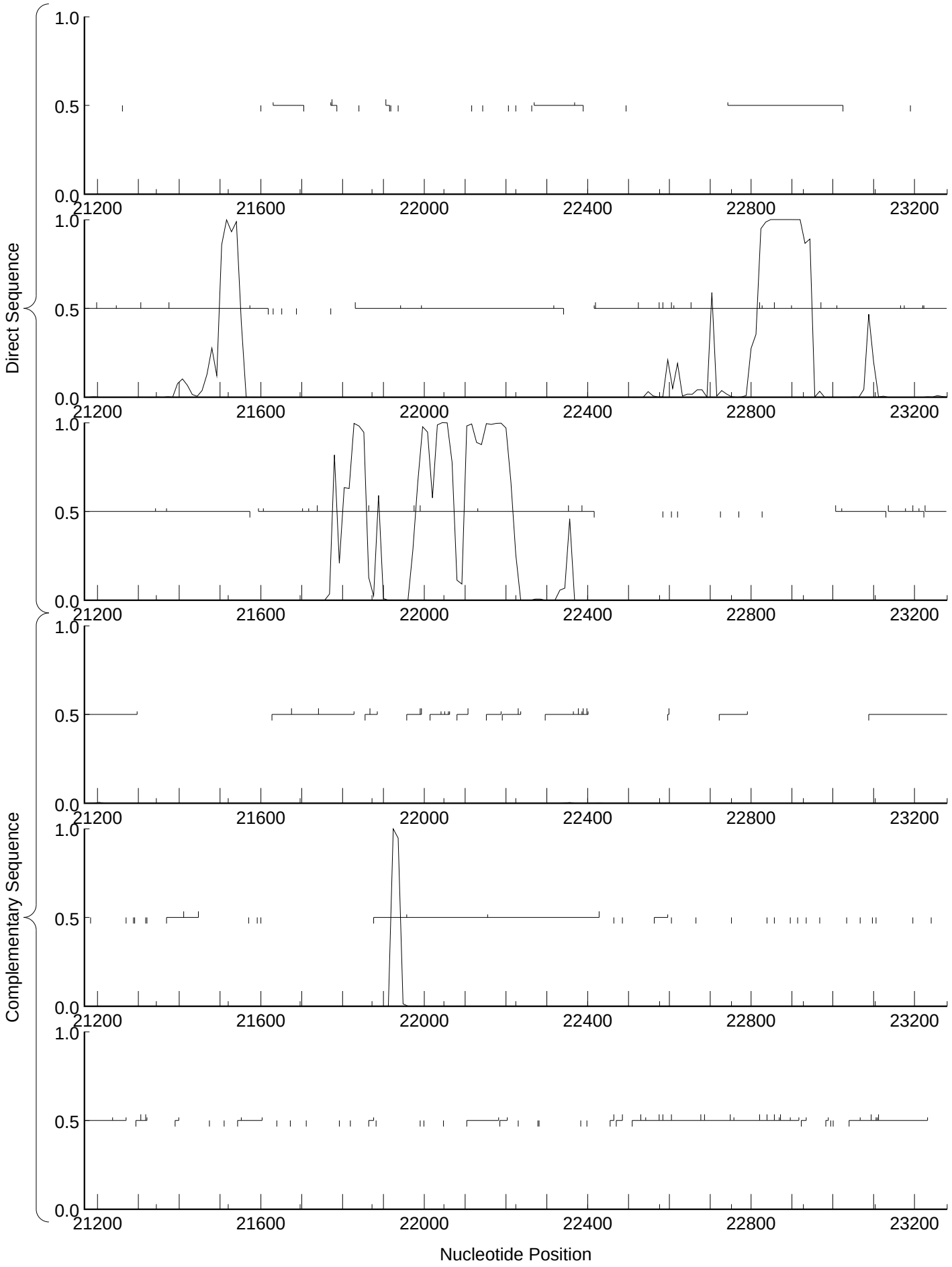


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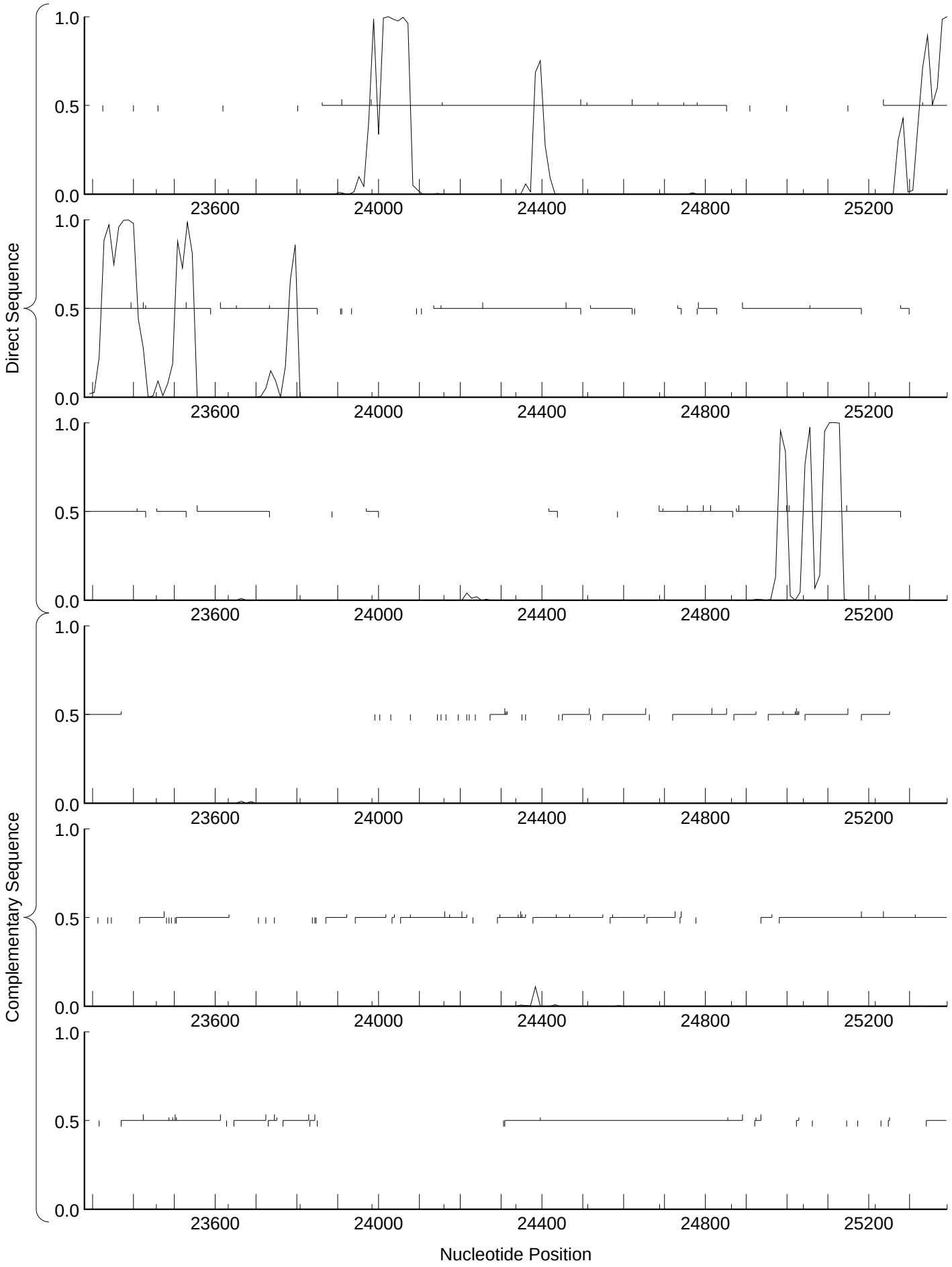


ato complete sequence, 55349 bp including 9-base 3’ overhang (CGCCCGCCT), Cluster BI1, Order 4, Window 96, Step 12, 11/28

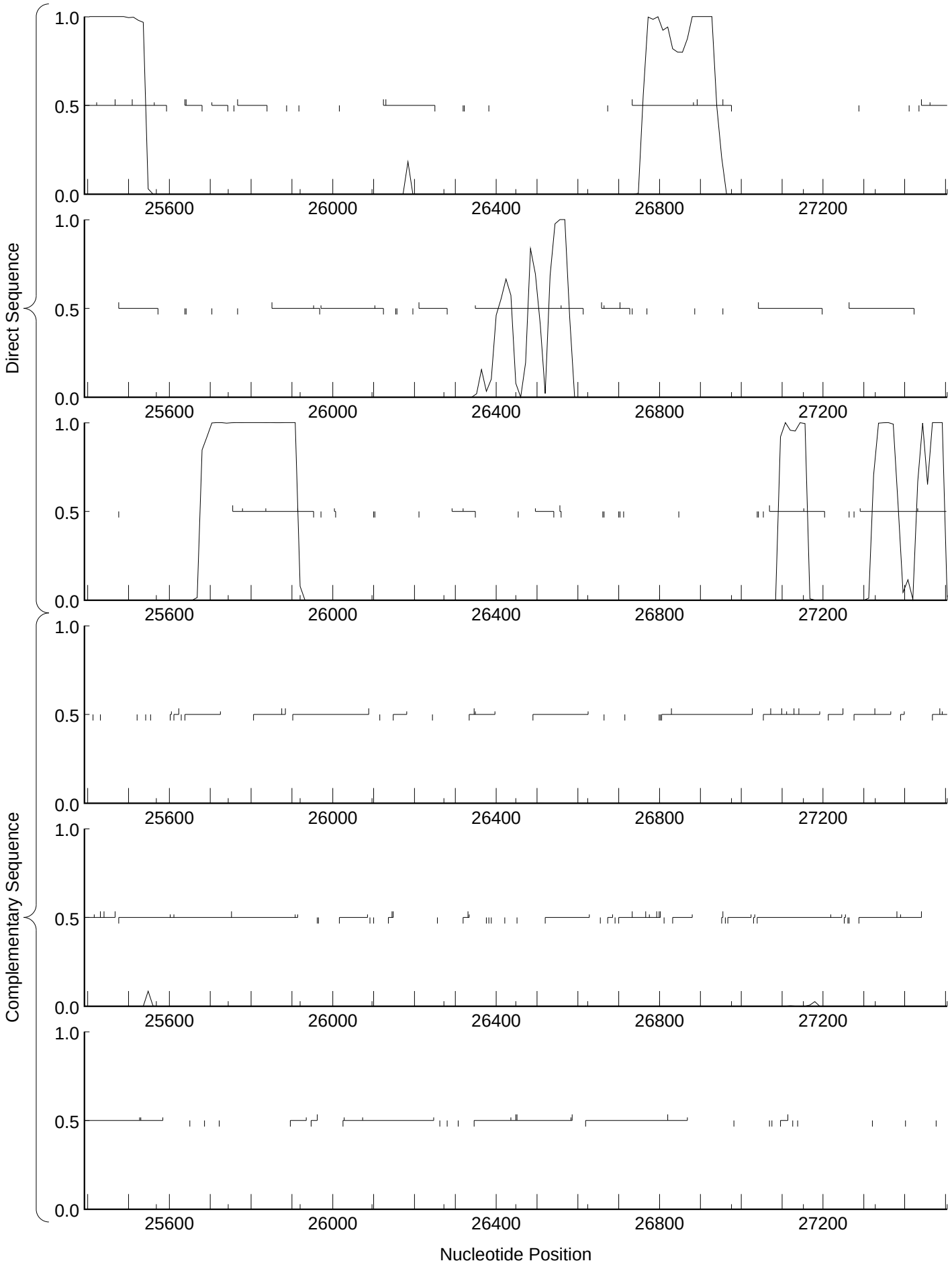



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Complementary Sequence
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0.0
21200
21600
22000
22400
22800
23200
Nucleotide Position

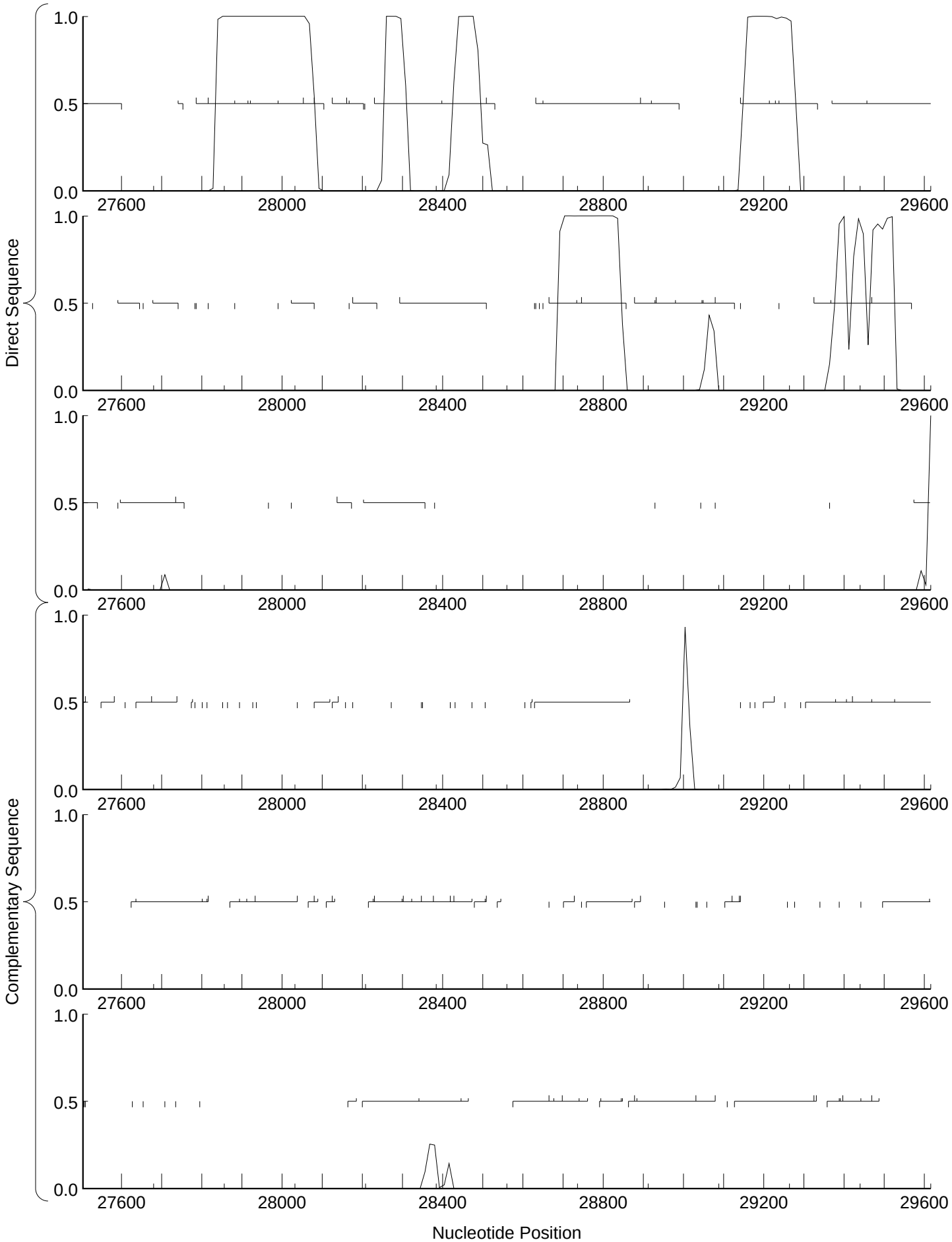
ato complete sequence, 55349 bp including 9-base 3' overhang (CGCCCGCCT), Cluster BI1, Order 4, Window 96, Step 12, 13/28

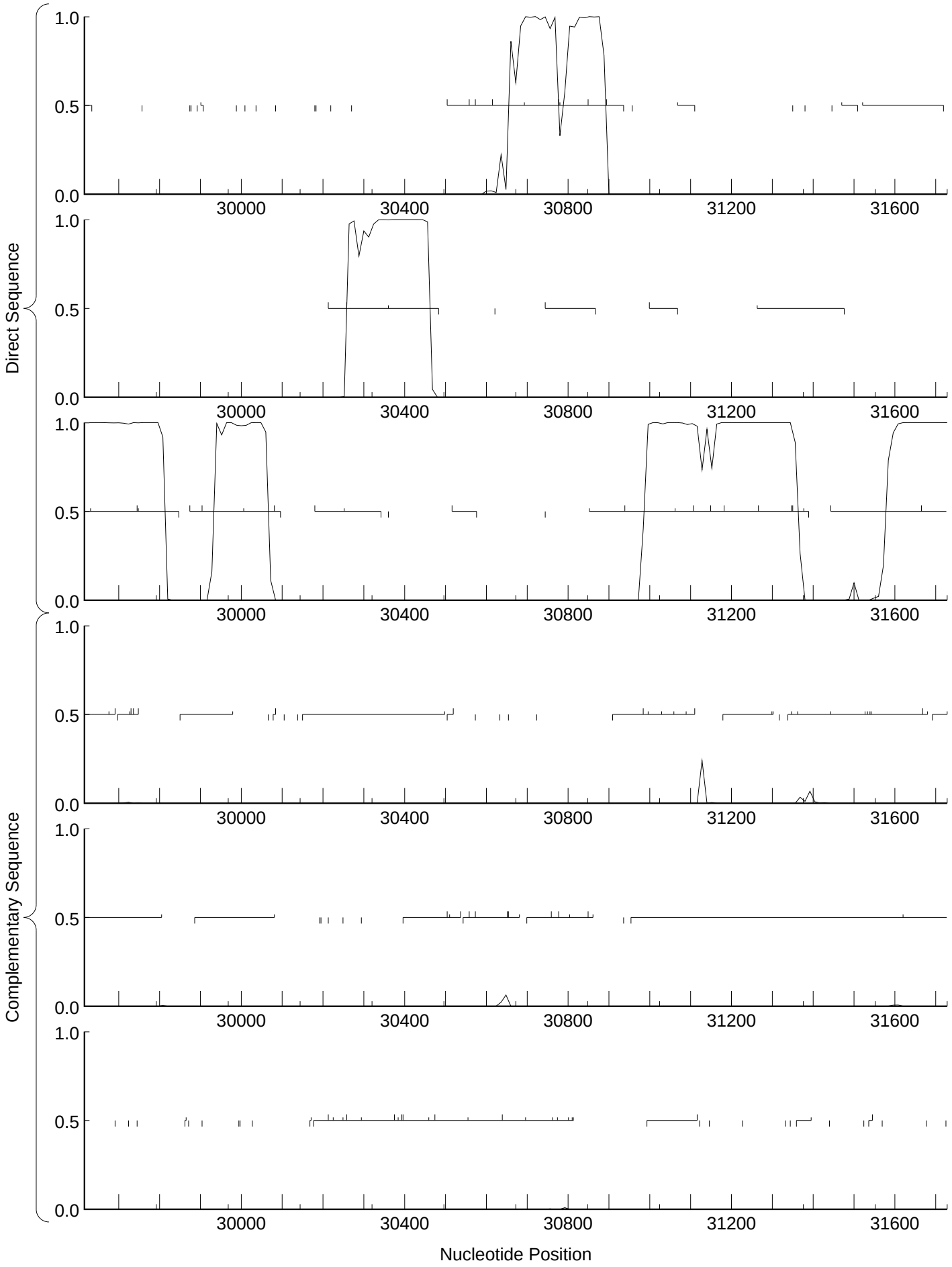


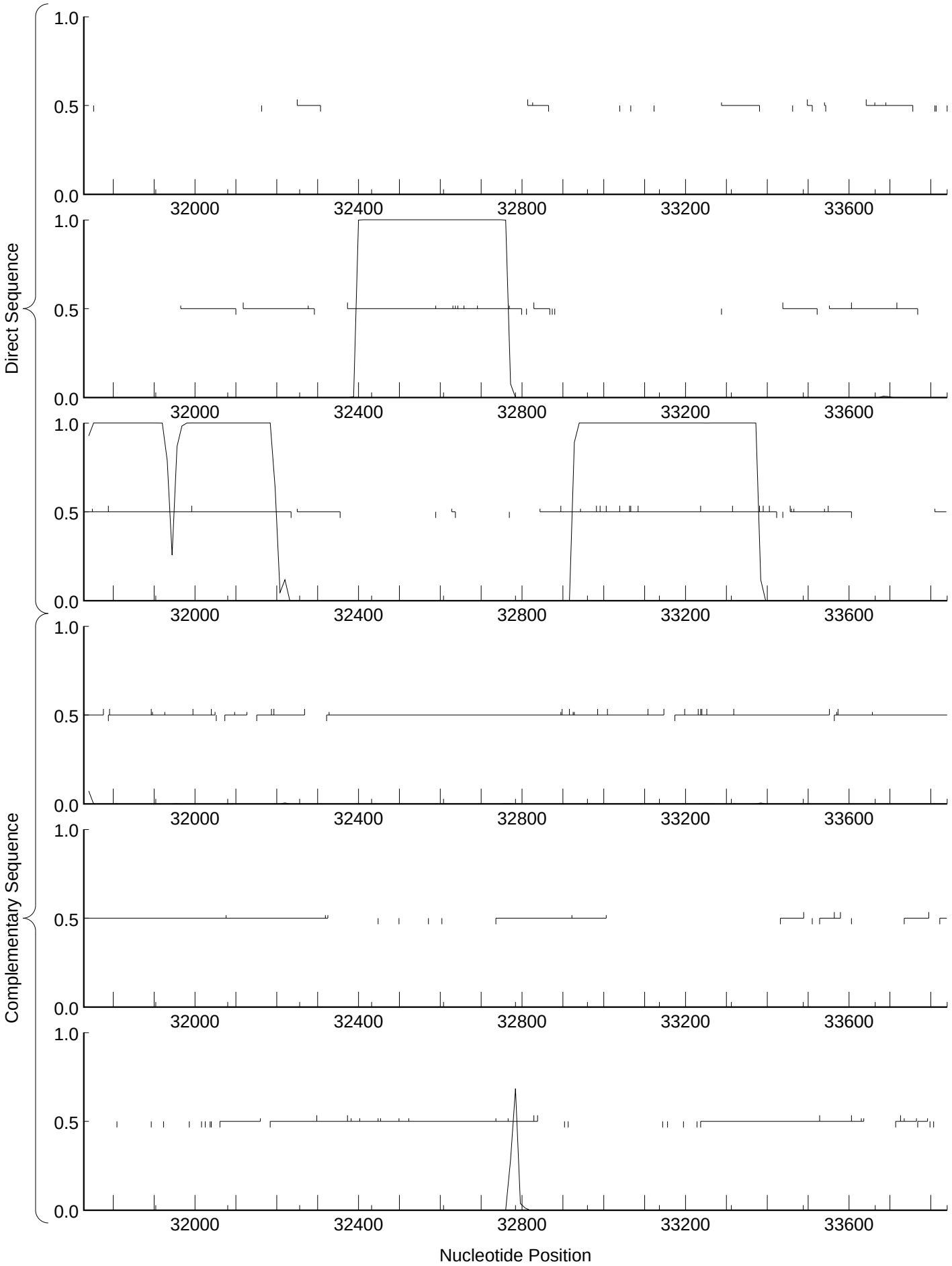
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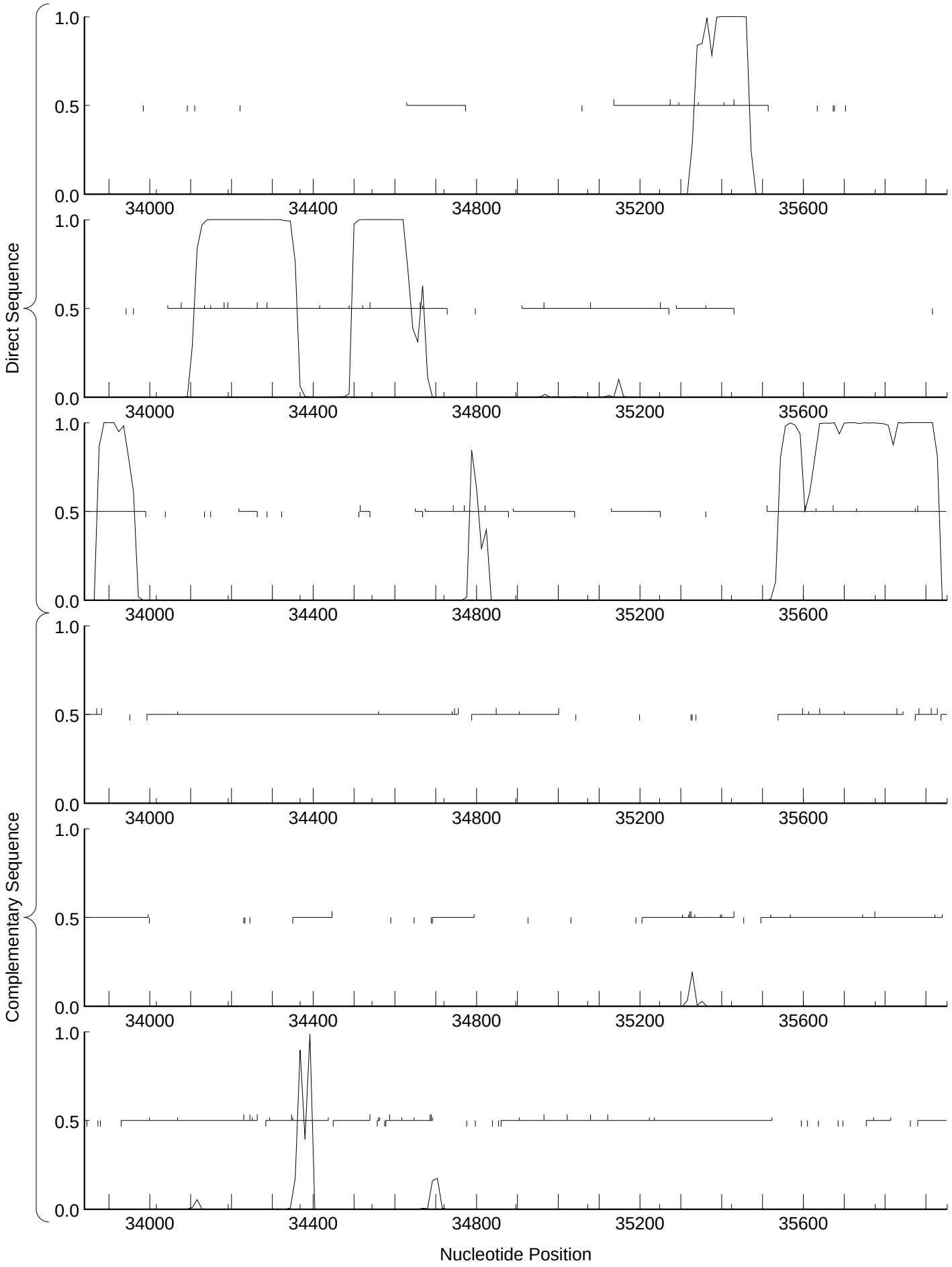


ato complete sequence, 55349 bp including 9-base 3’ overhang (CGCCCGCCT), Cluster BI1, Order 4, Window 96, Step 12, 15/28

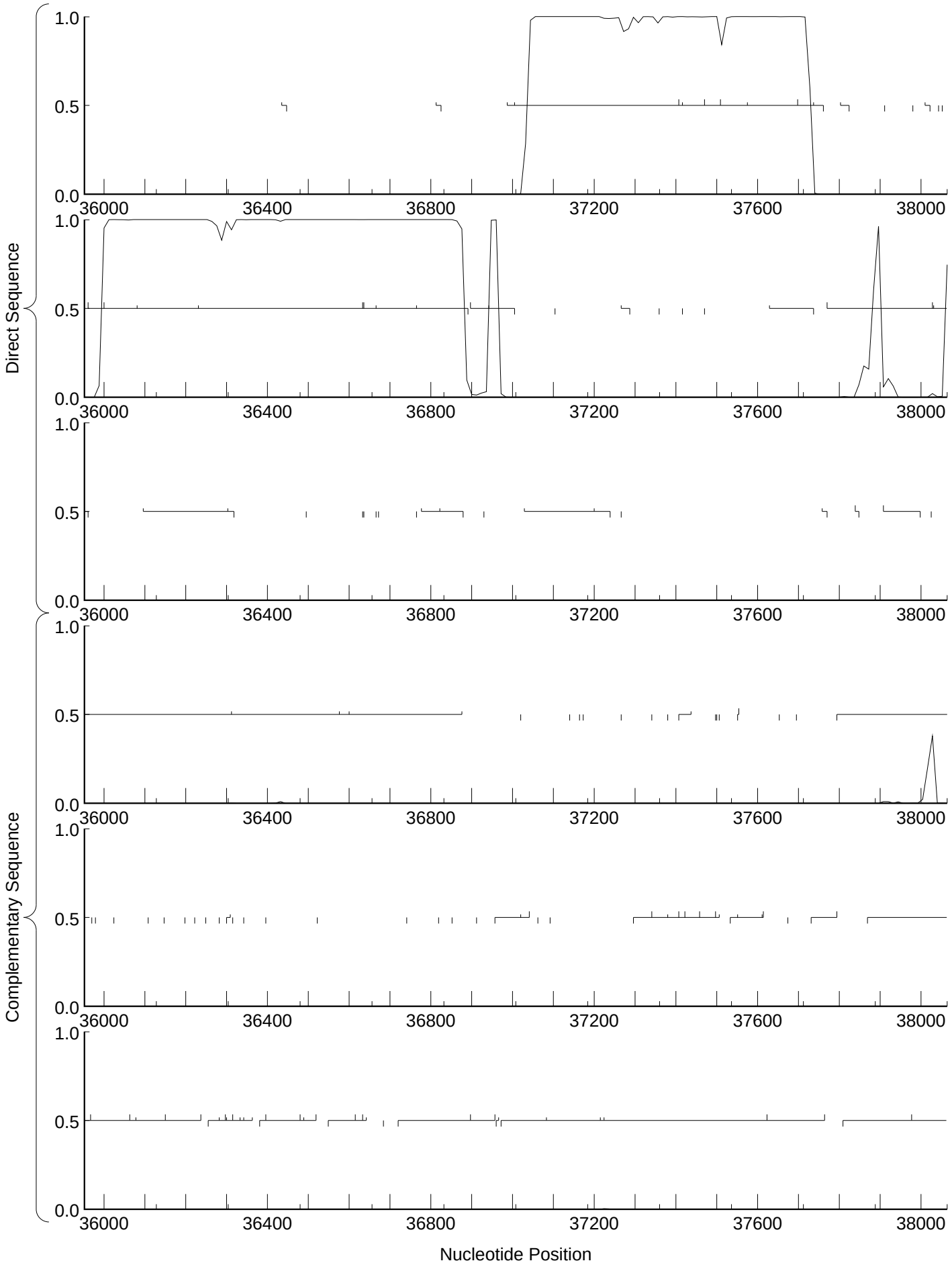


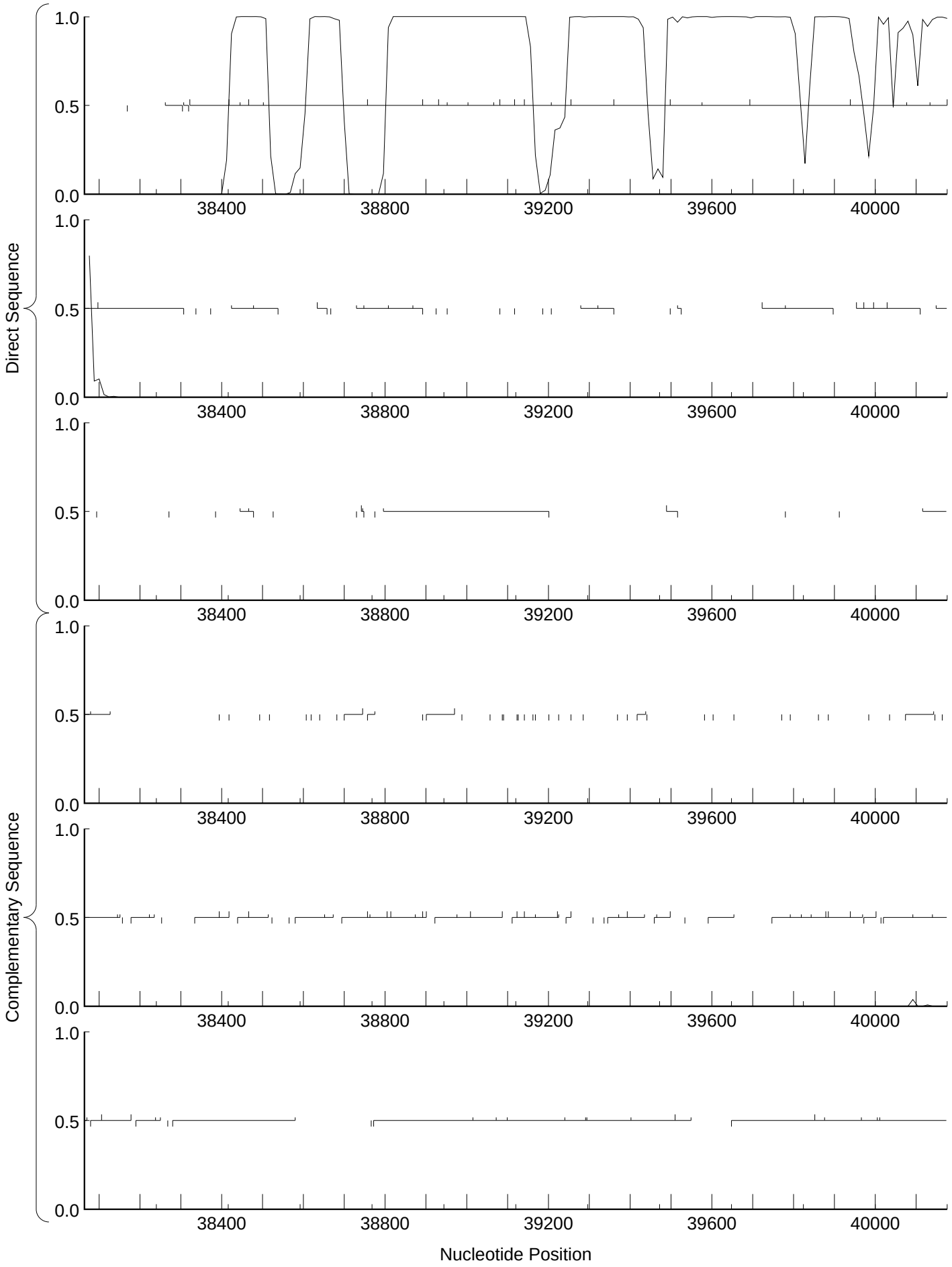

Direct Sequence
Complementary Sequence
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30000
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30800
31200
31600
Nucleotide Position

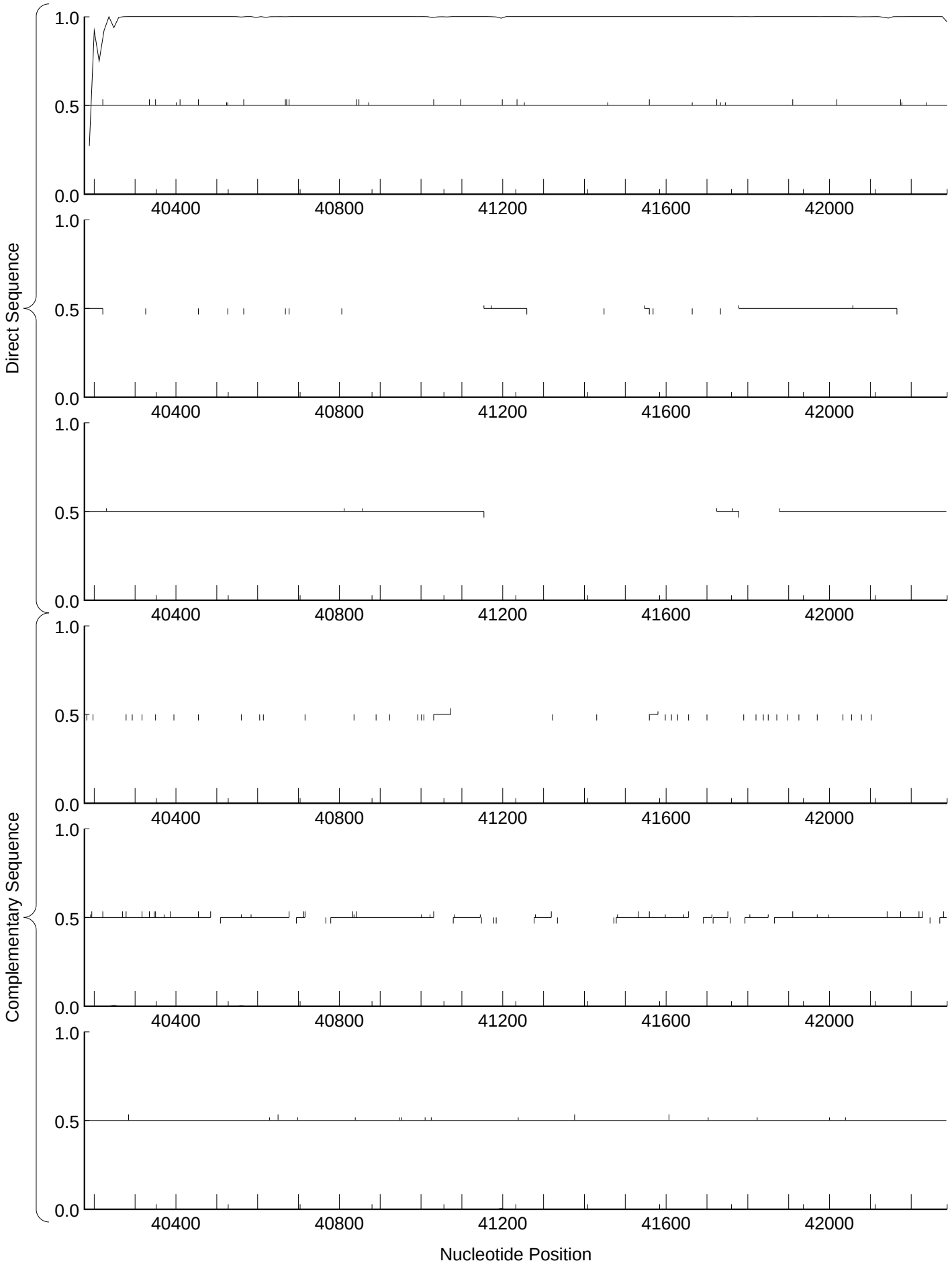

Direct Sequence
Complementary Sequence
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0.0
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32800
33200
33600
Nucleotide Position

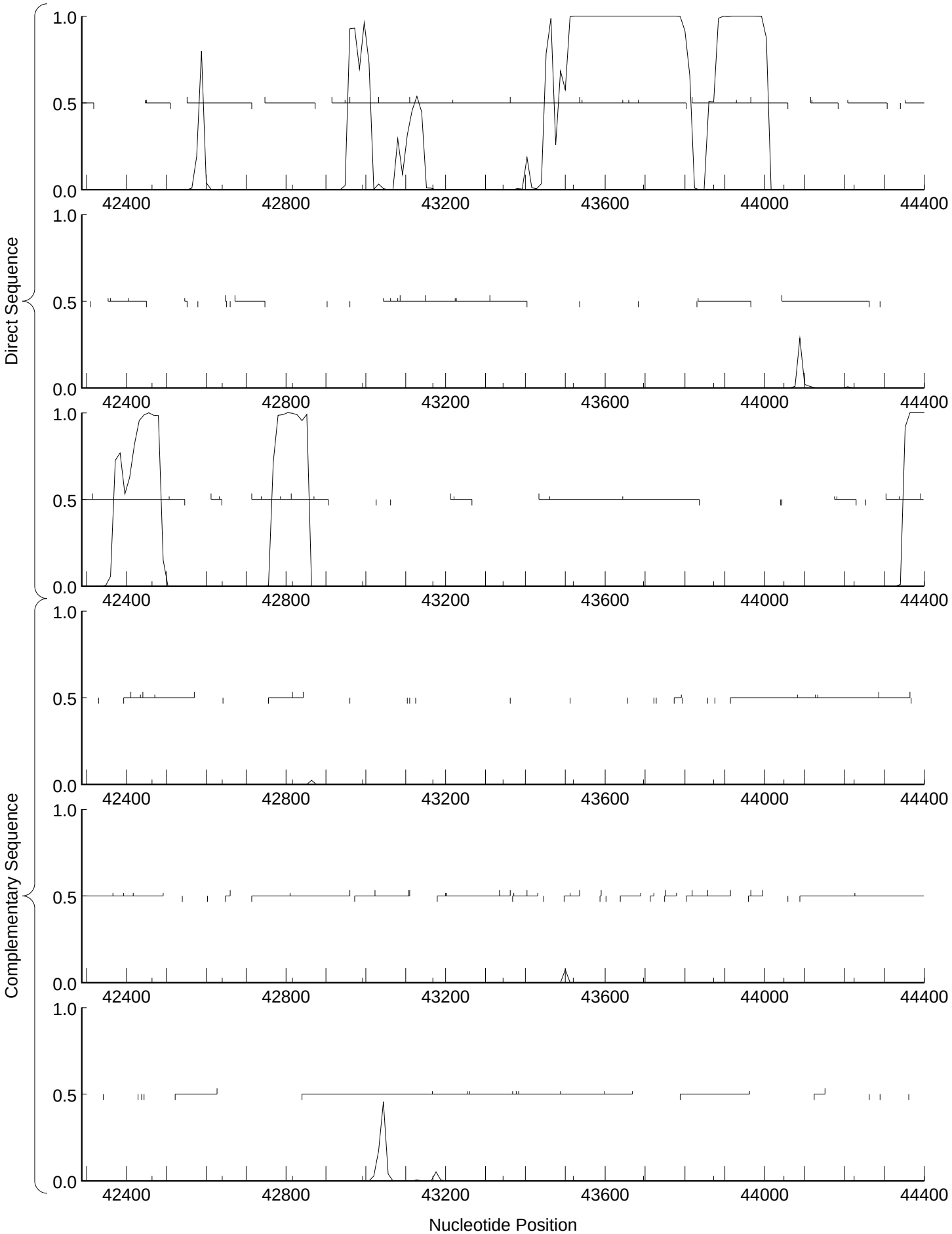

Direct Sequence
Complementary Sequence
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0.0
34000
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34800
35200
35600
Nucleotide Position

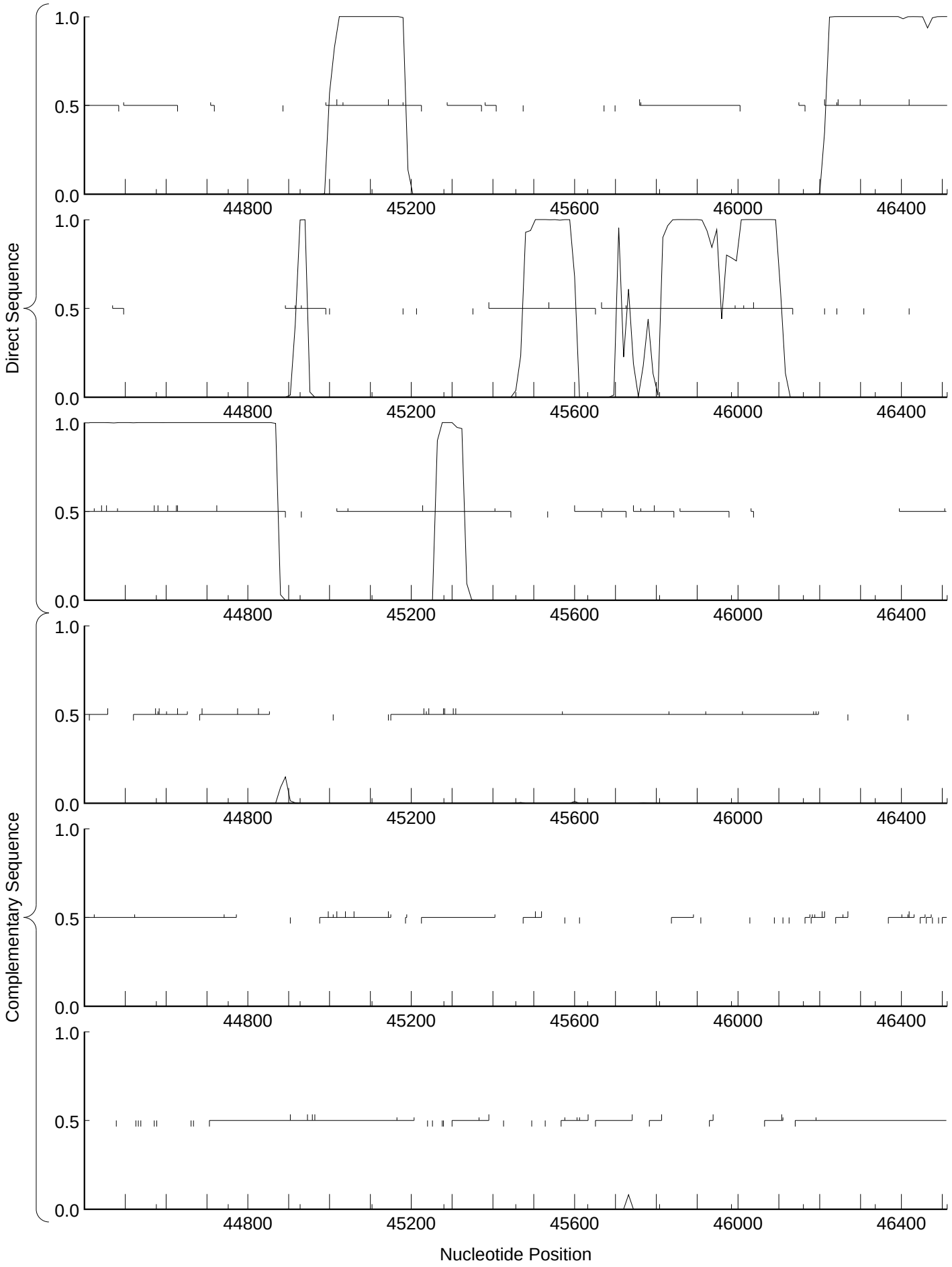
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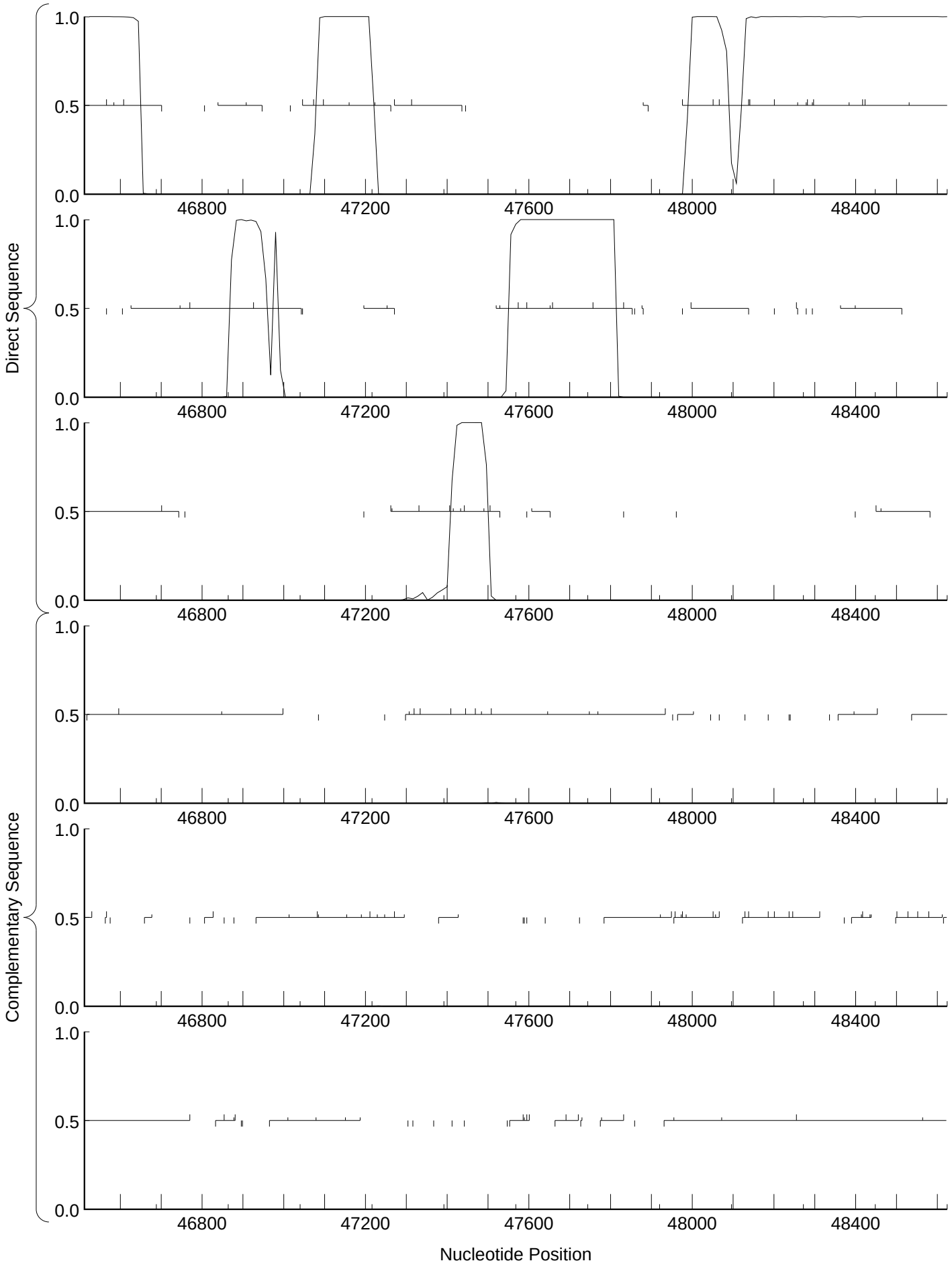

Direct Sequence
Complementary Sequence
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39200
39600
40000
Nucleotide Position

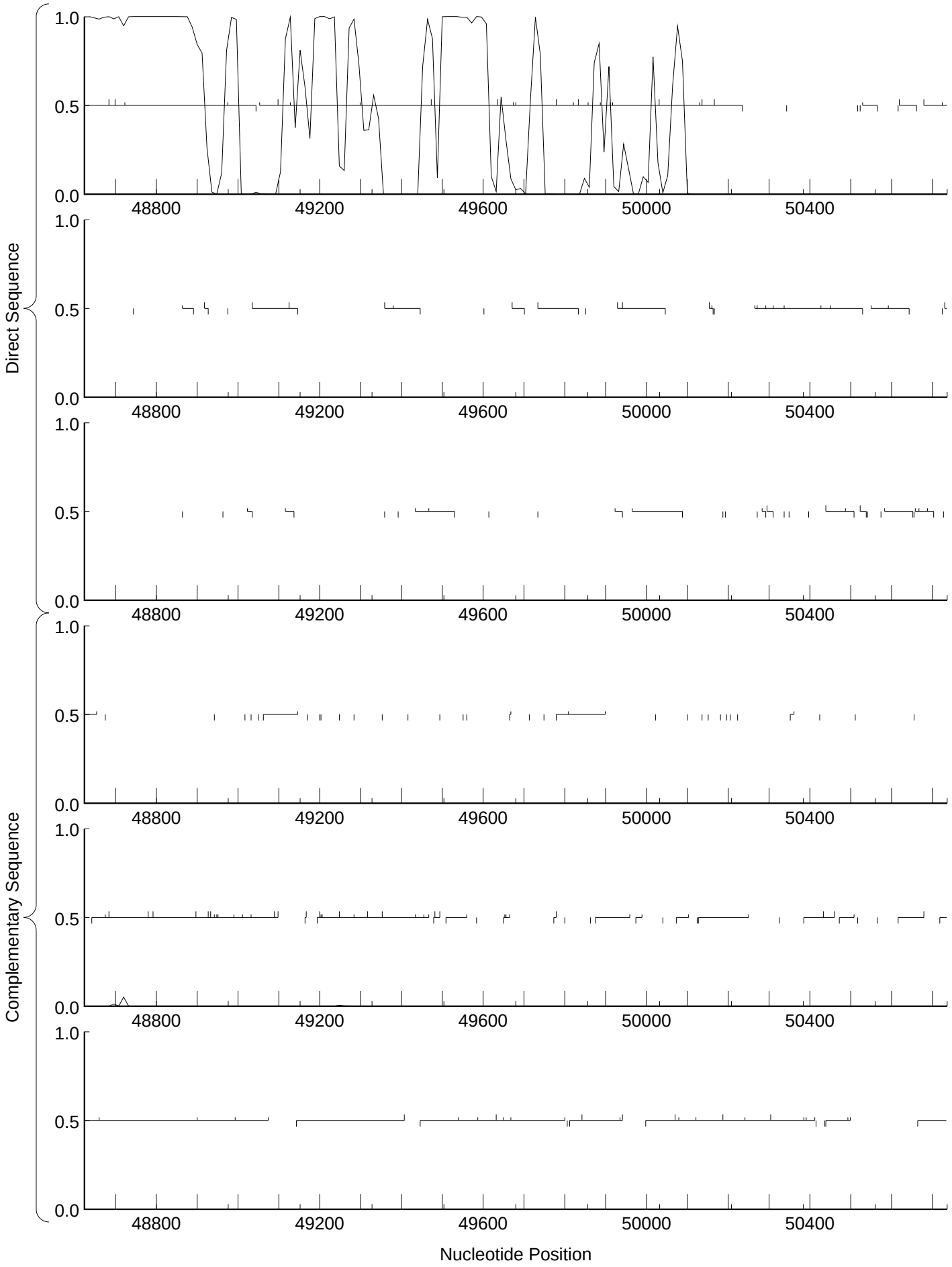

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Nucleotide Position

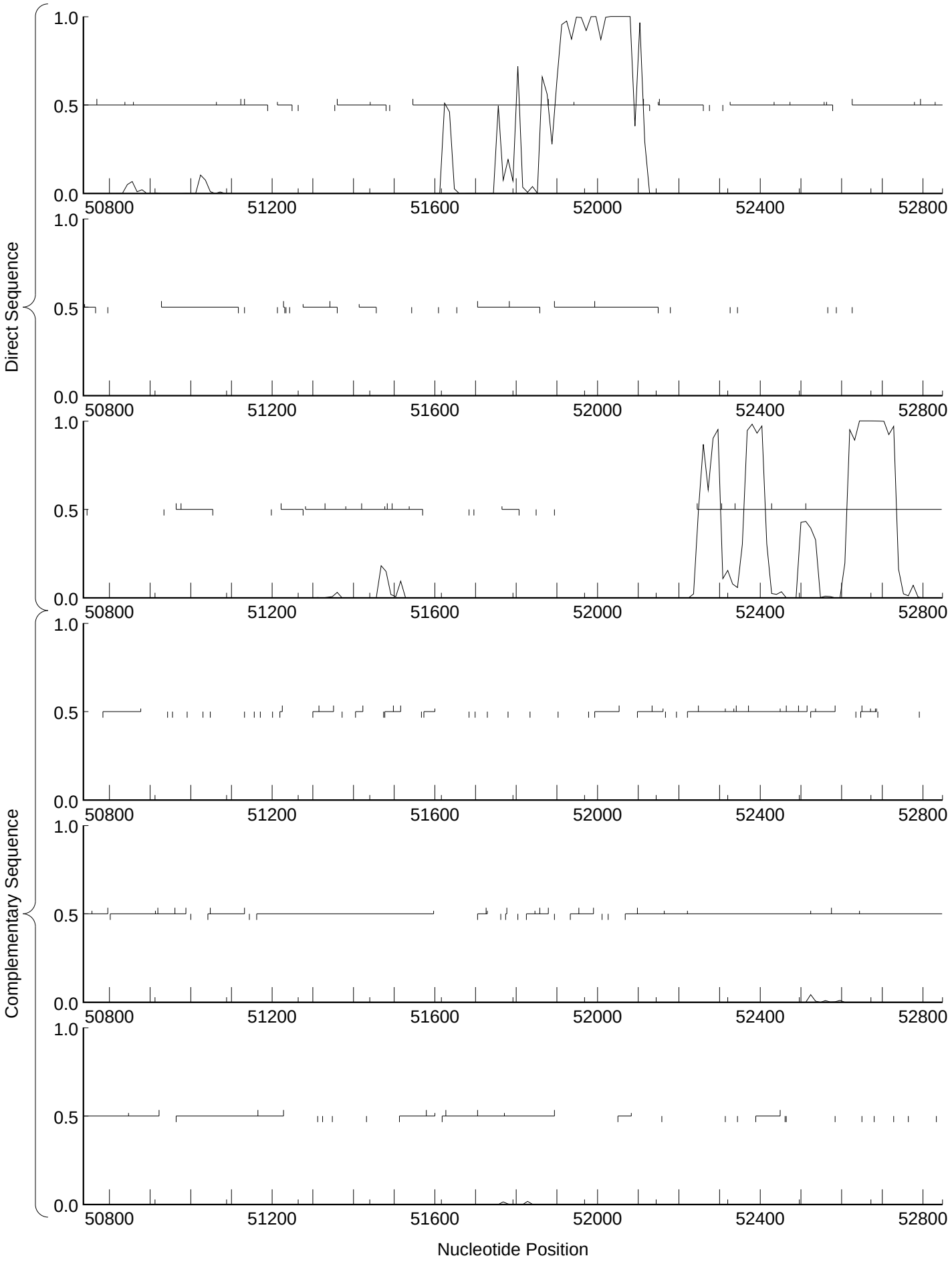

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Complementary Sequence
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42800
43200
43600
44000
44400
Nucleotide Position


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

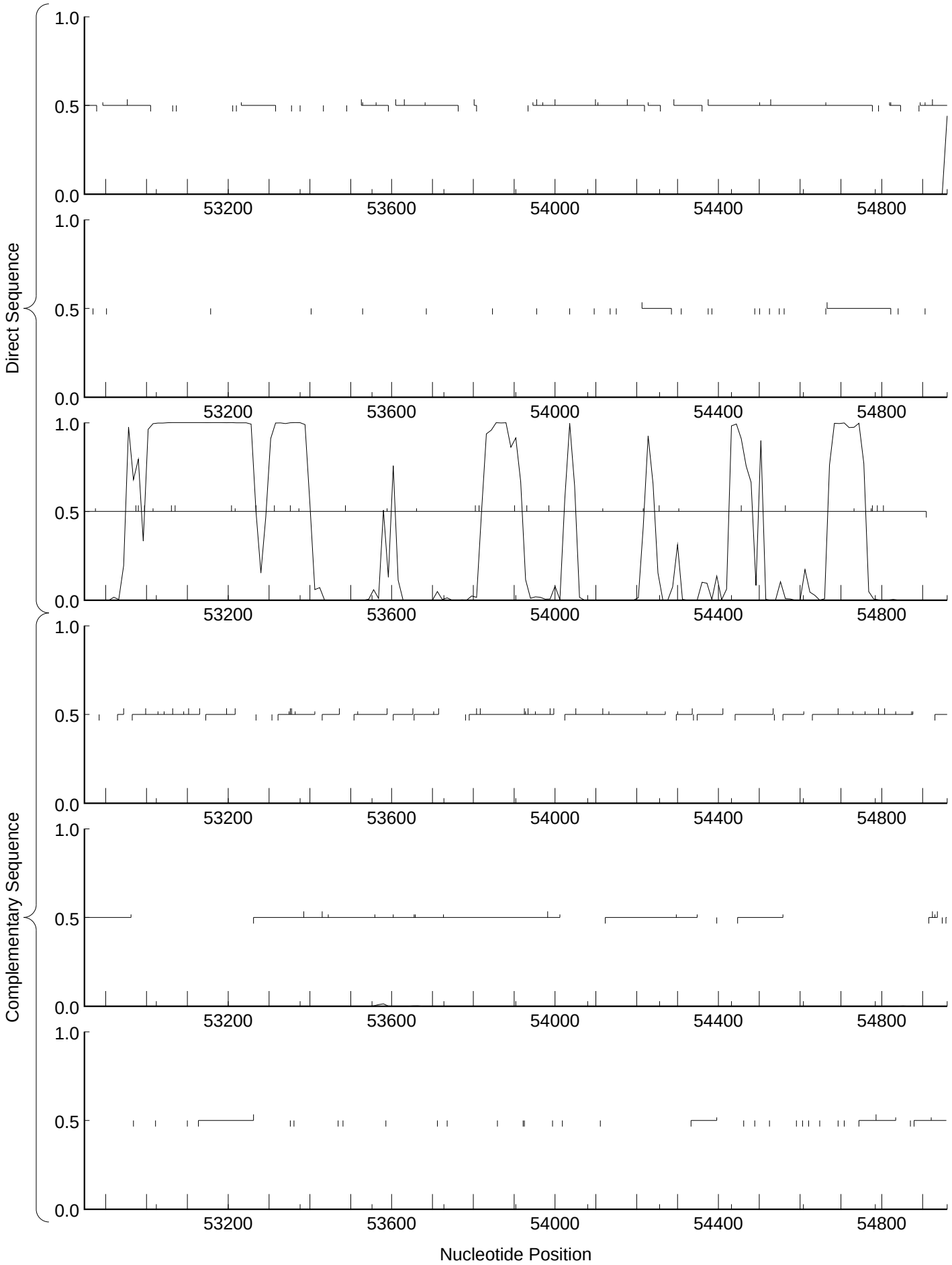
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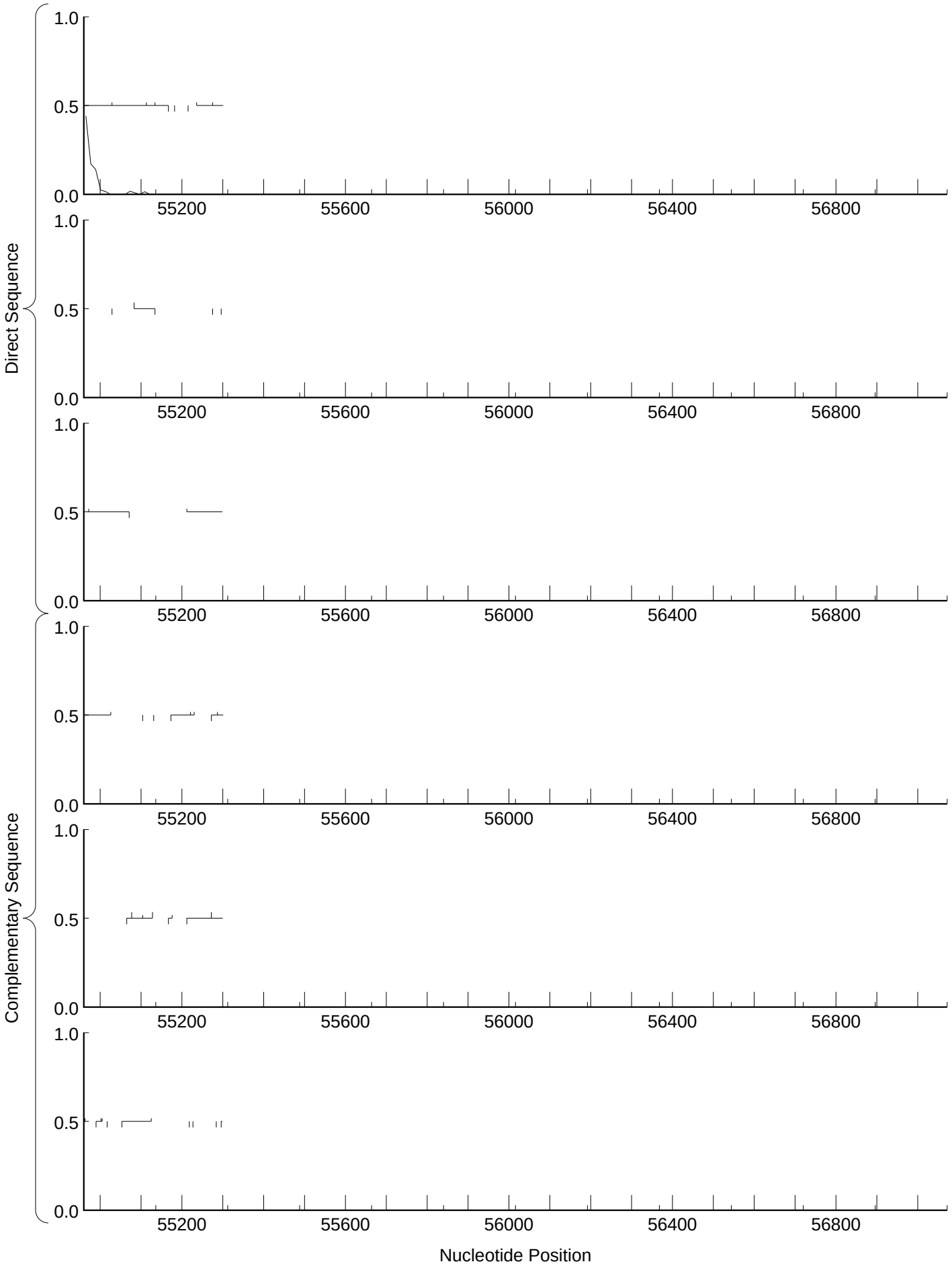



Direct Sequence
Complementary Sequence
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0.5
0.0
48800
49200
49600
50000
50400
Nucleotide Position


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

ato complete sequence, 55349 bp including 9-base 3’ overhang (CGCCCGCCT), Cluster BI1, Order 4, Window 96, Step 12, 27/28




Direct Sequence
Complementary Sequence
1.0
0.5
0.0
55200
55600
56000
56400
56800
Nucleotide Position