GeneMark

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

PROGRAM INFORMATION

```
Sequence         :  Mycobacterium phage Megiddo complete sequence, 48783 bp including 13-base 3’ overhang (CCTG
Analysis Date    :  2/9/26 at 12:46:55
Pages            :  25
Sequence Length  :  48783 bp
GC Content       :   67.12%

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,
```

Matrix notes & comments

Training set derived by GeneMarkS, 4.27 September 2014
Tue Sep 23 15:14:37 2014

MATRIX INFORMATION

```
Matrix     :  Mycobacterium_tuberculosis_H37Rv
Author     :  -

Order      :  4
```

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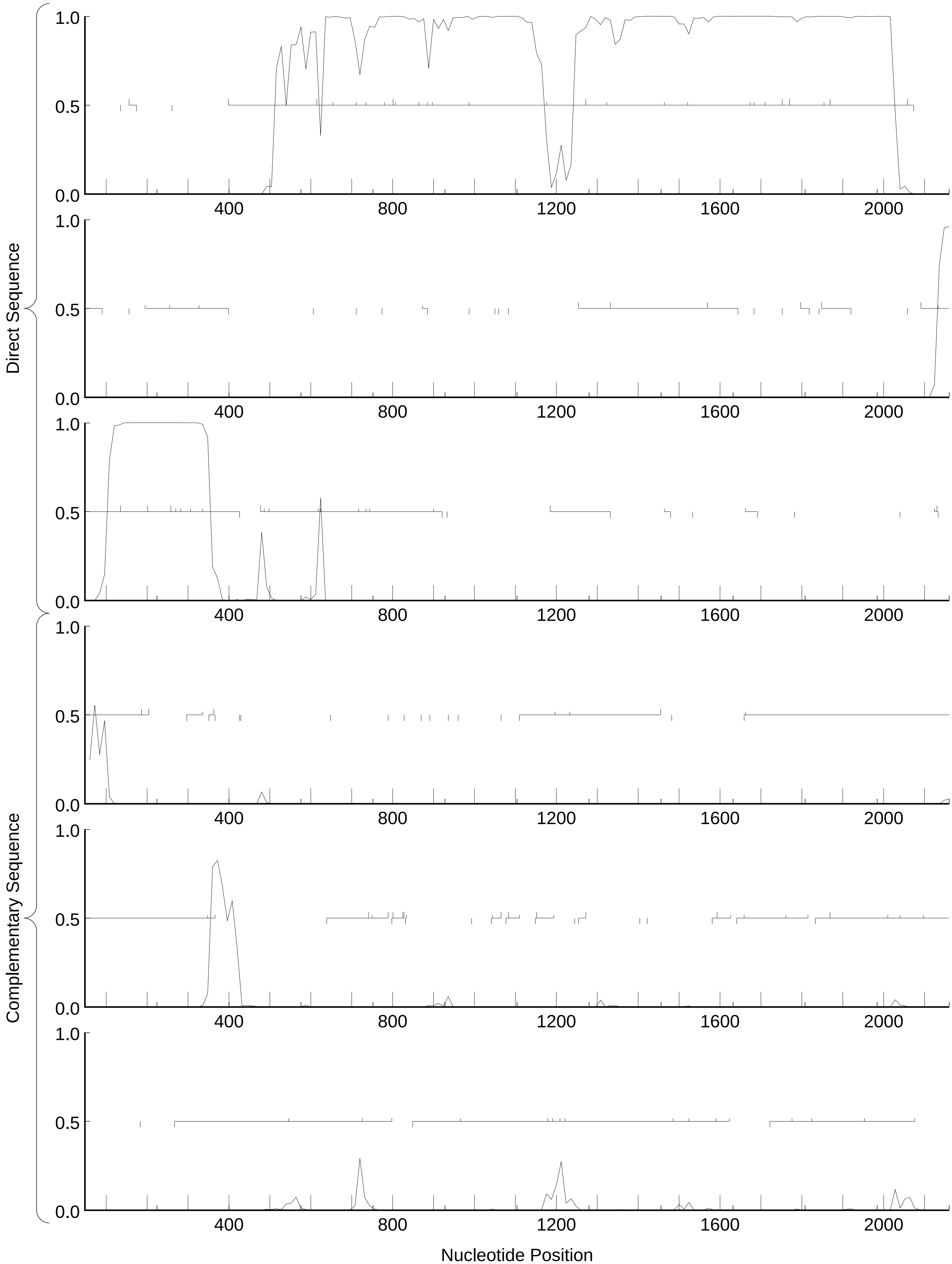
Georgia Institute of Technology
School of Biology
Atlanta, GA 30332-0230

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



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

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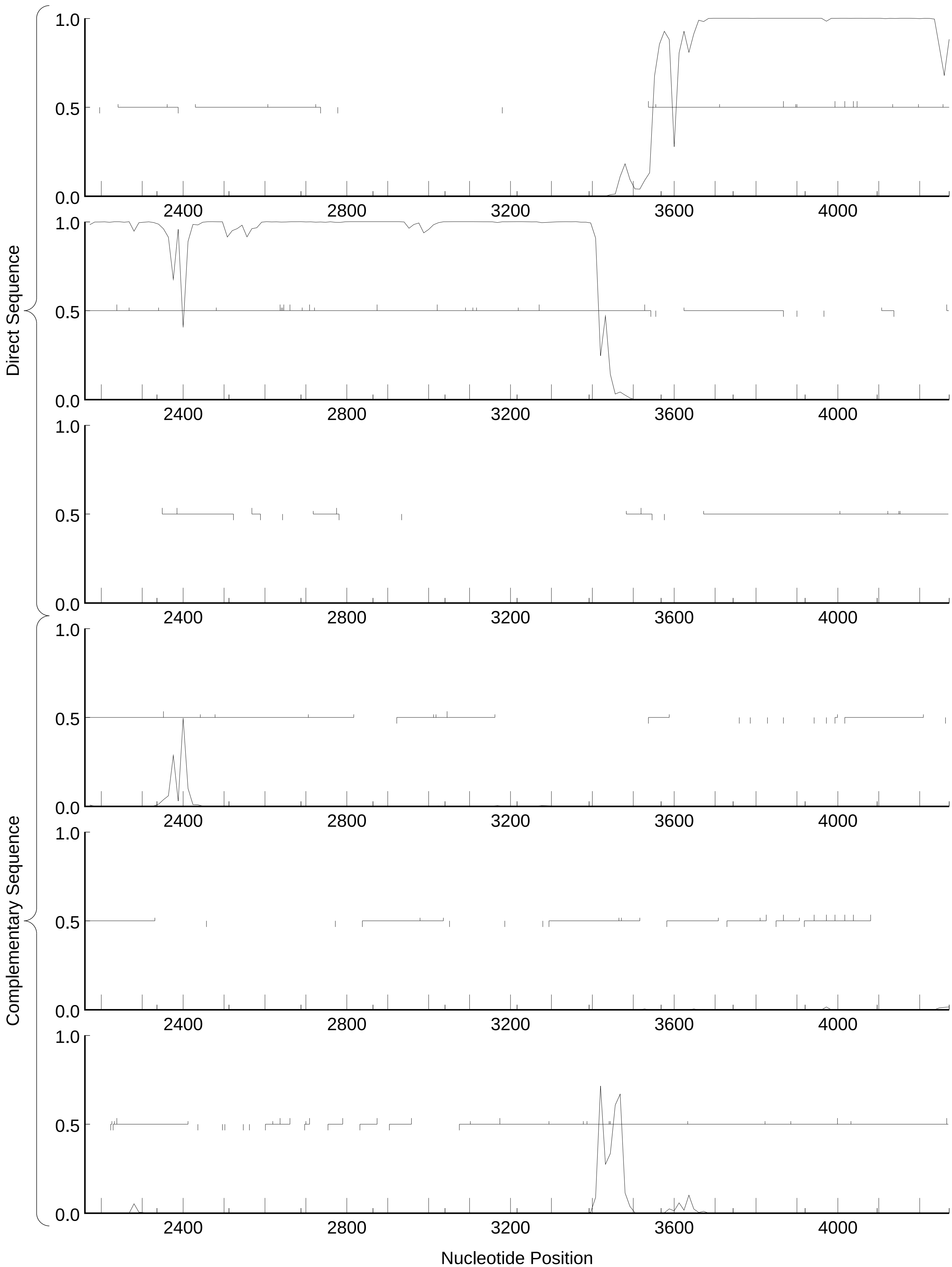

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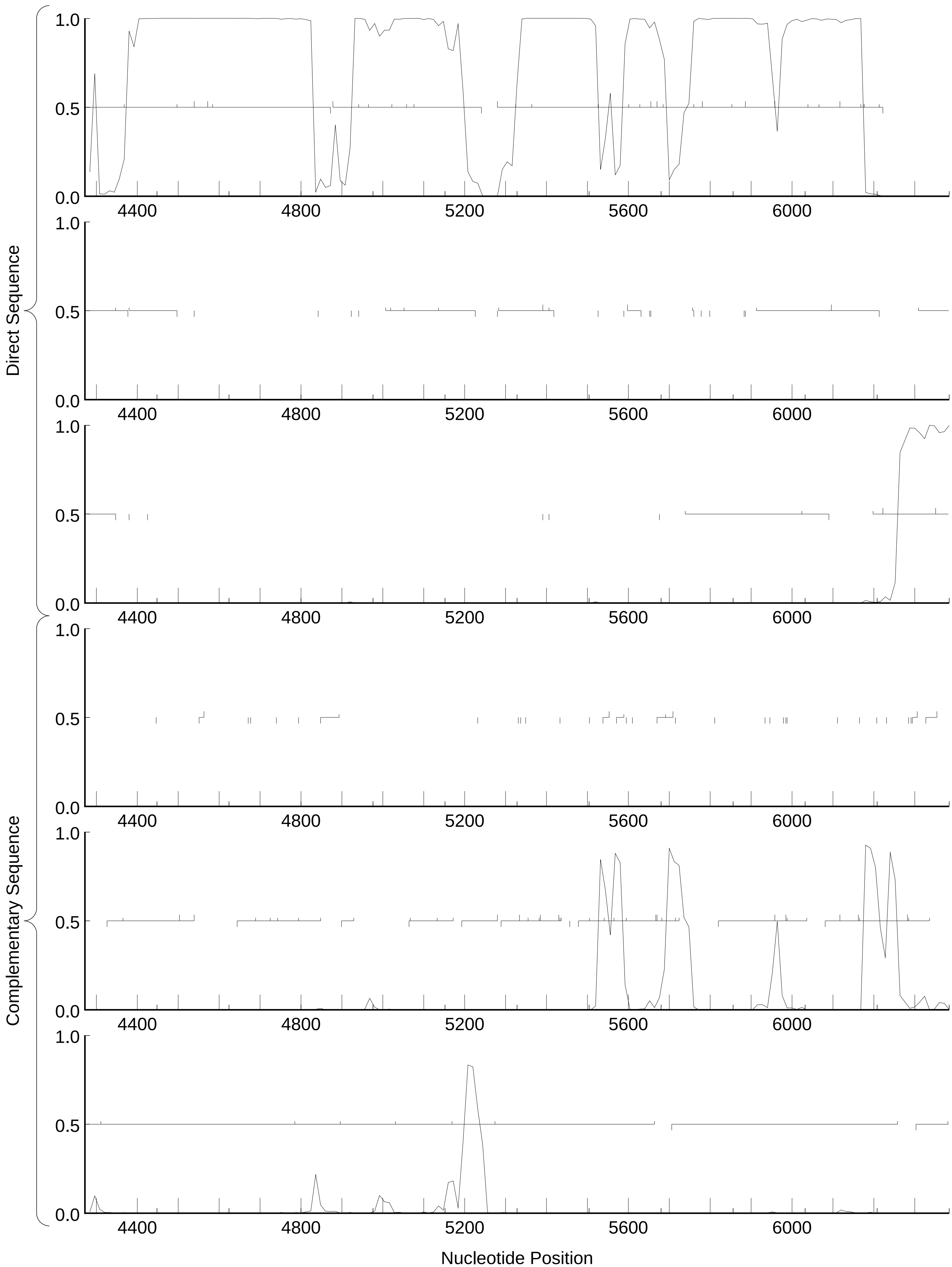

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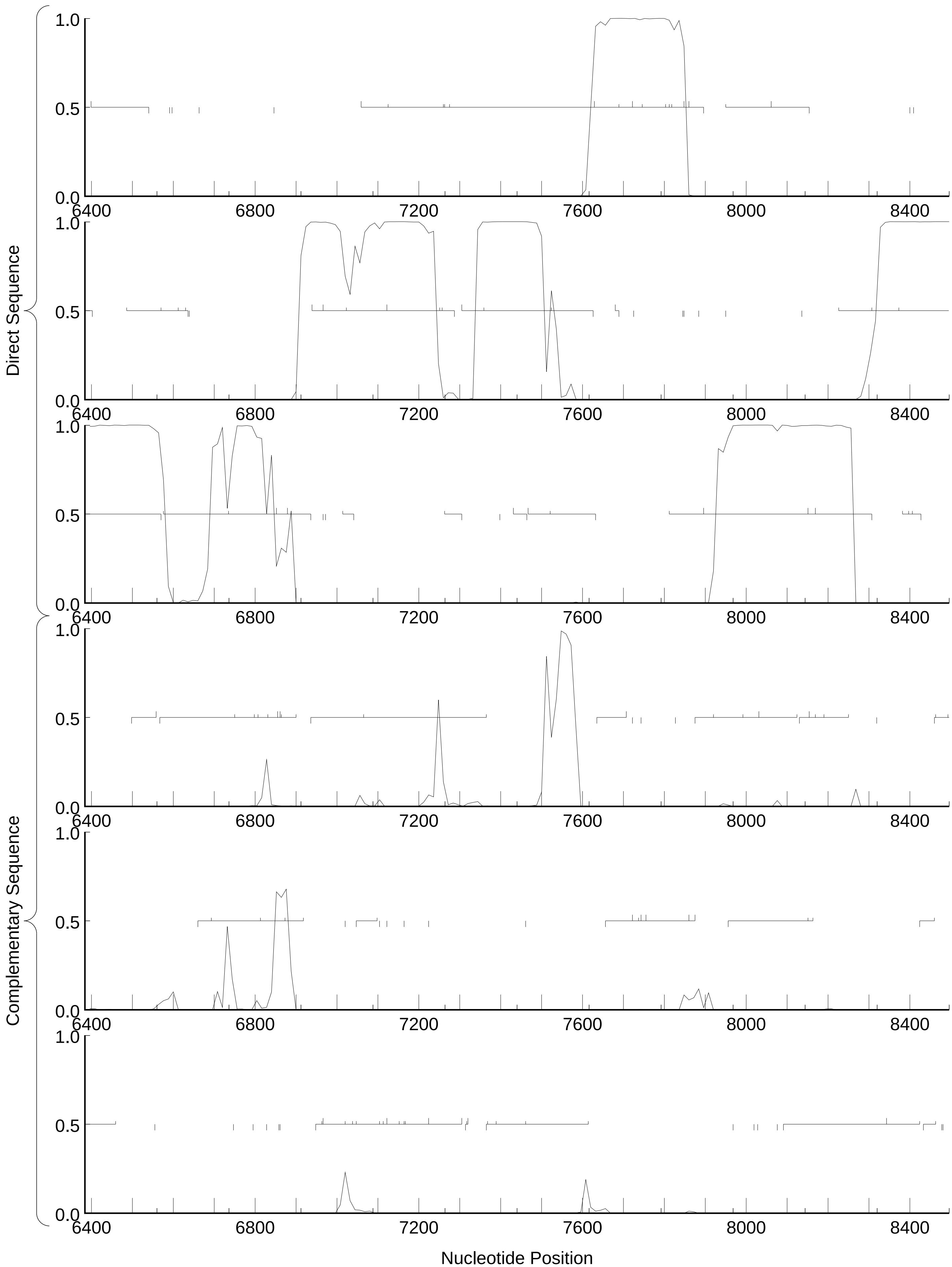

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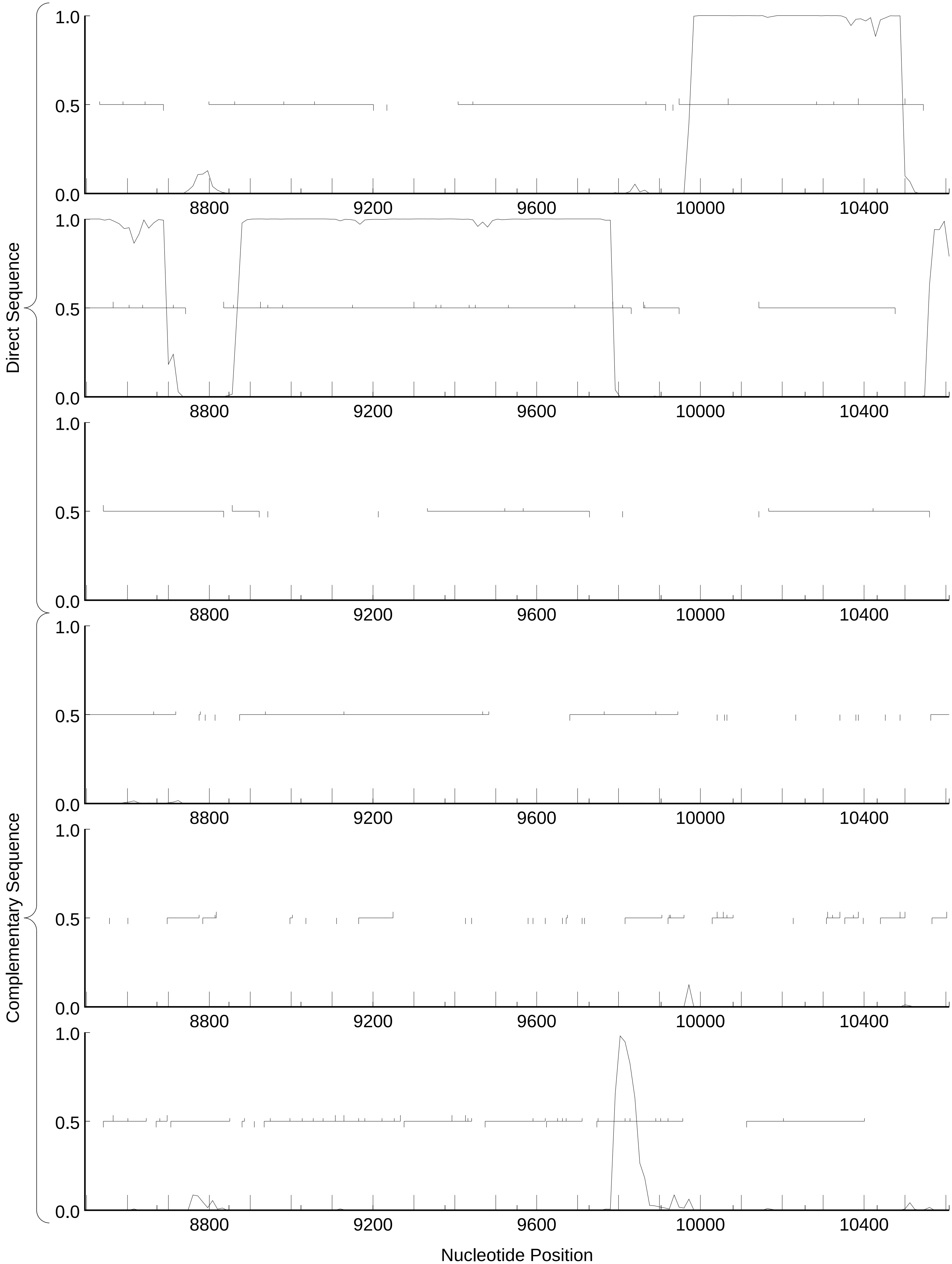

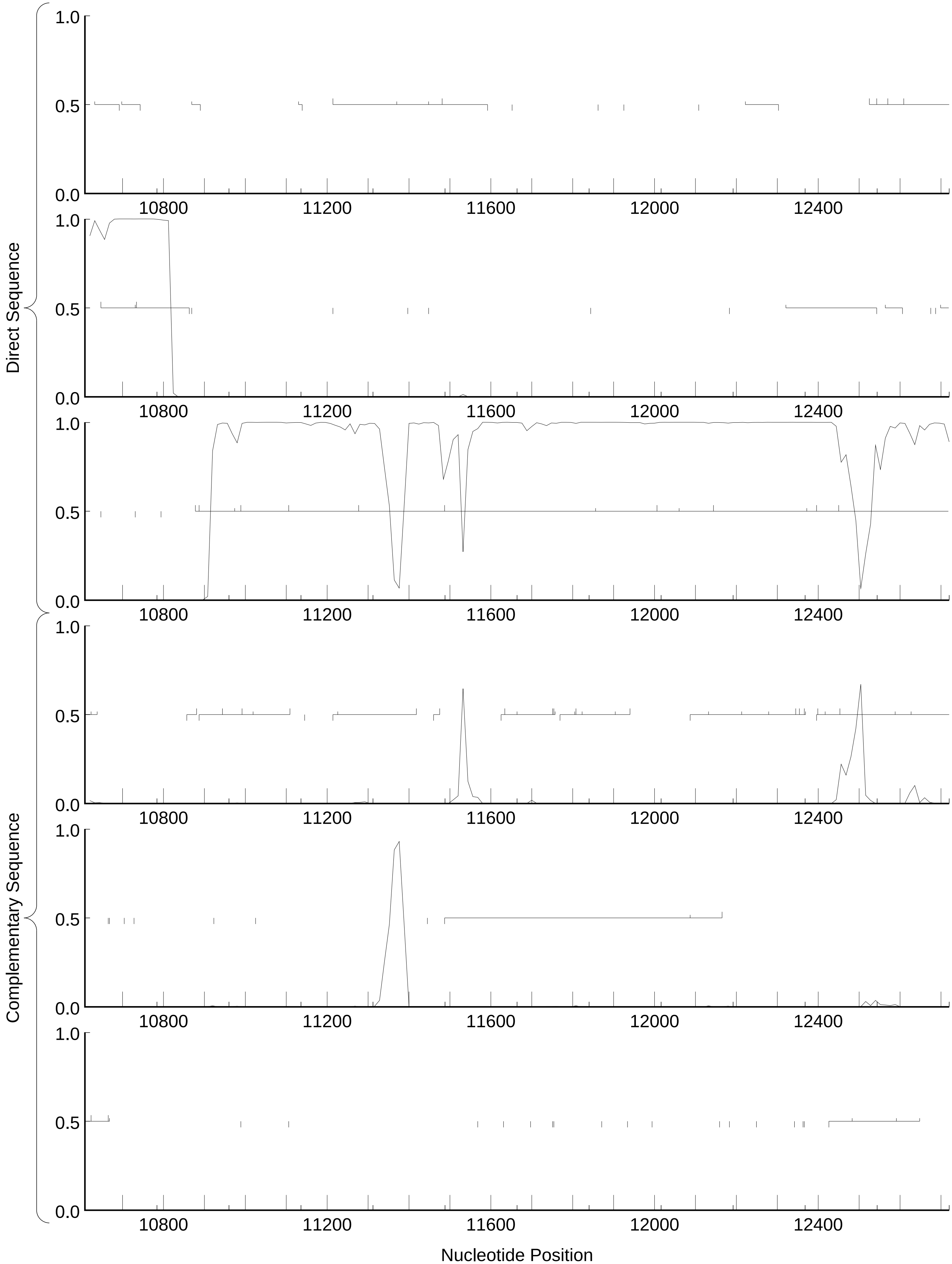
Direct Sequence
Complementary Sequence
1.0
0.5
0.0
10800
11200
11600
12000
12400
Nucleotide Position

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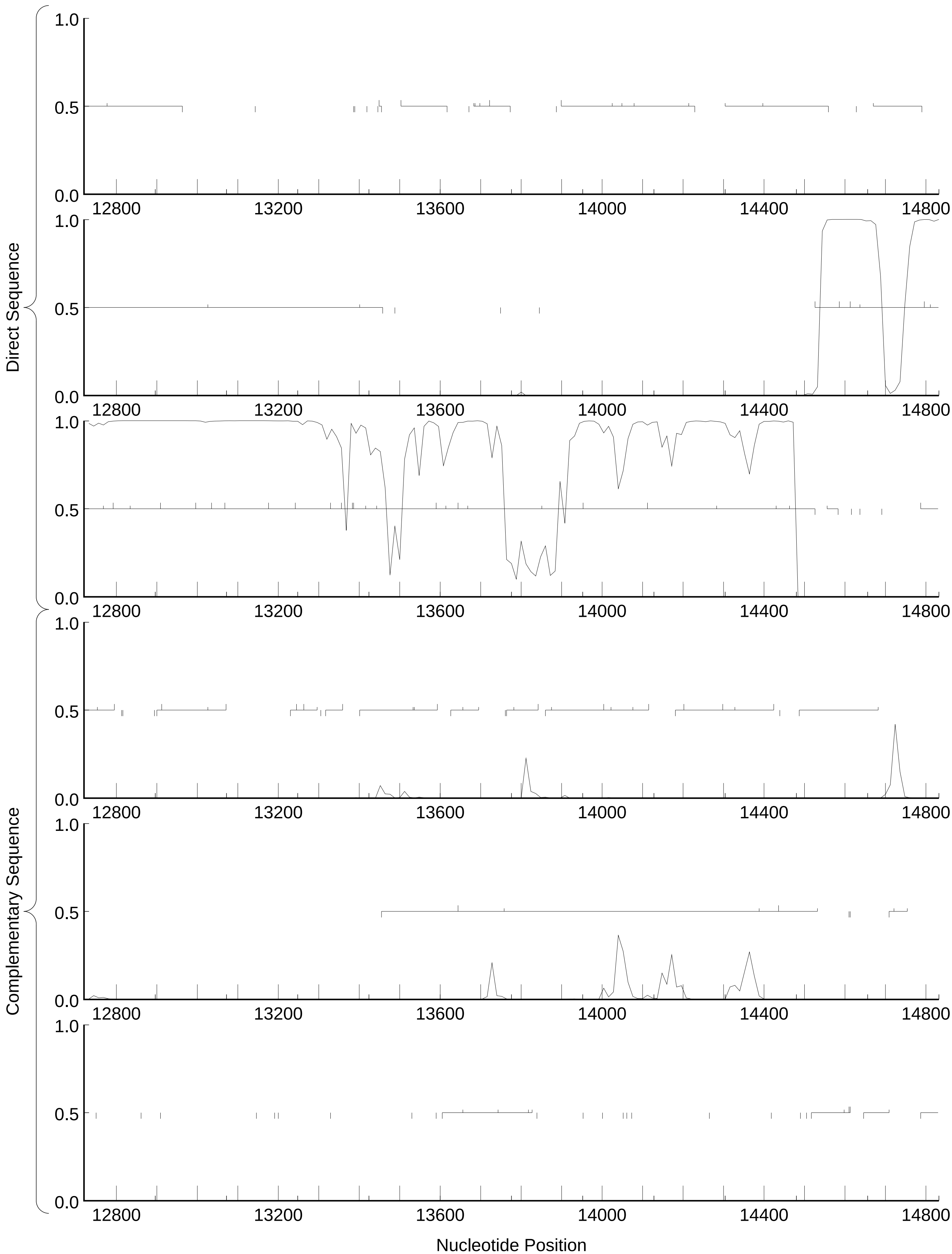

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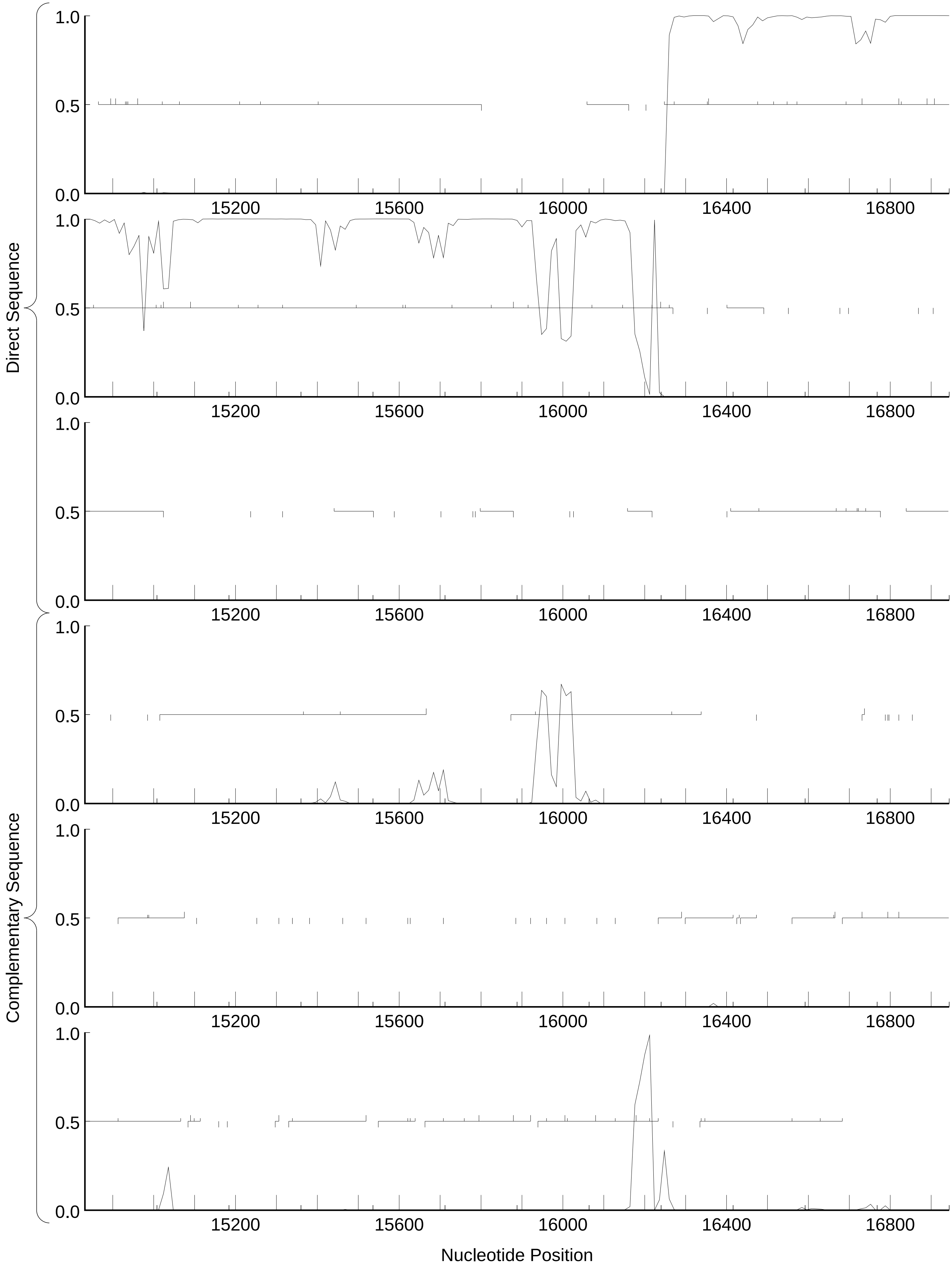
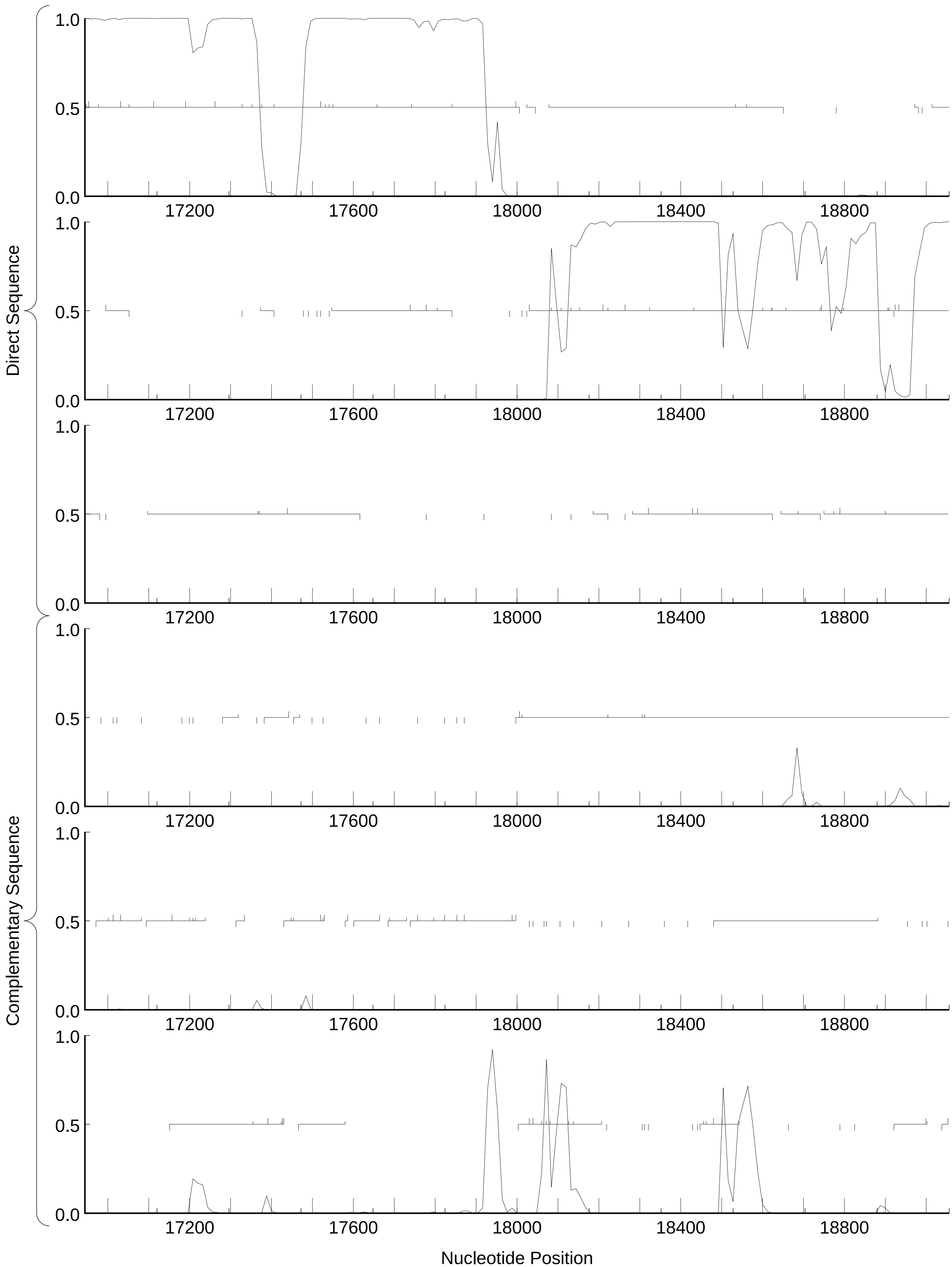
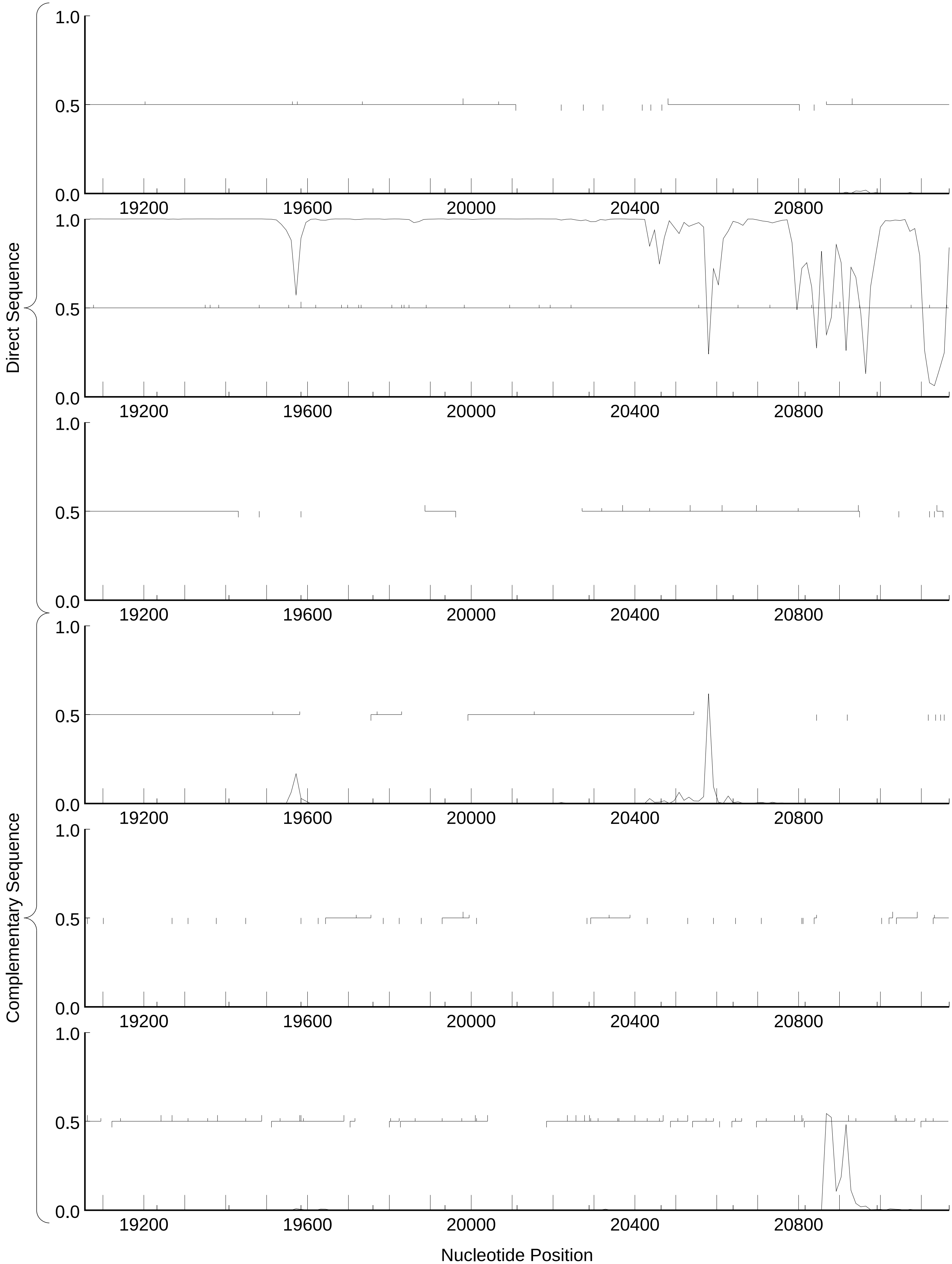


plete sequence, 48783 bp including 13-base 3’ overhang (CCTGCCGCCCCGA), Cluster P1, Order 4, Window 96, Step 12, 10/25





Direct Sequence
Complementary Sequence
1.0
0.5
0.0
19200
19600
20000
20400
20800
Nucleotide Position

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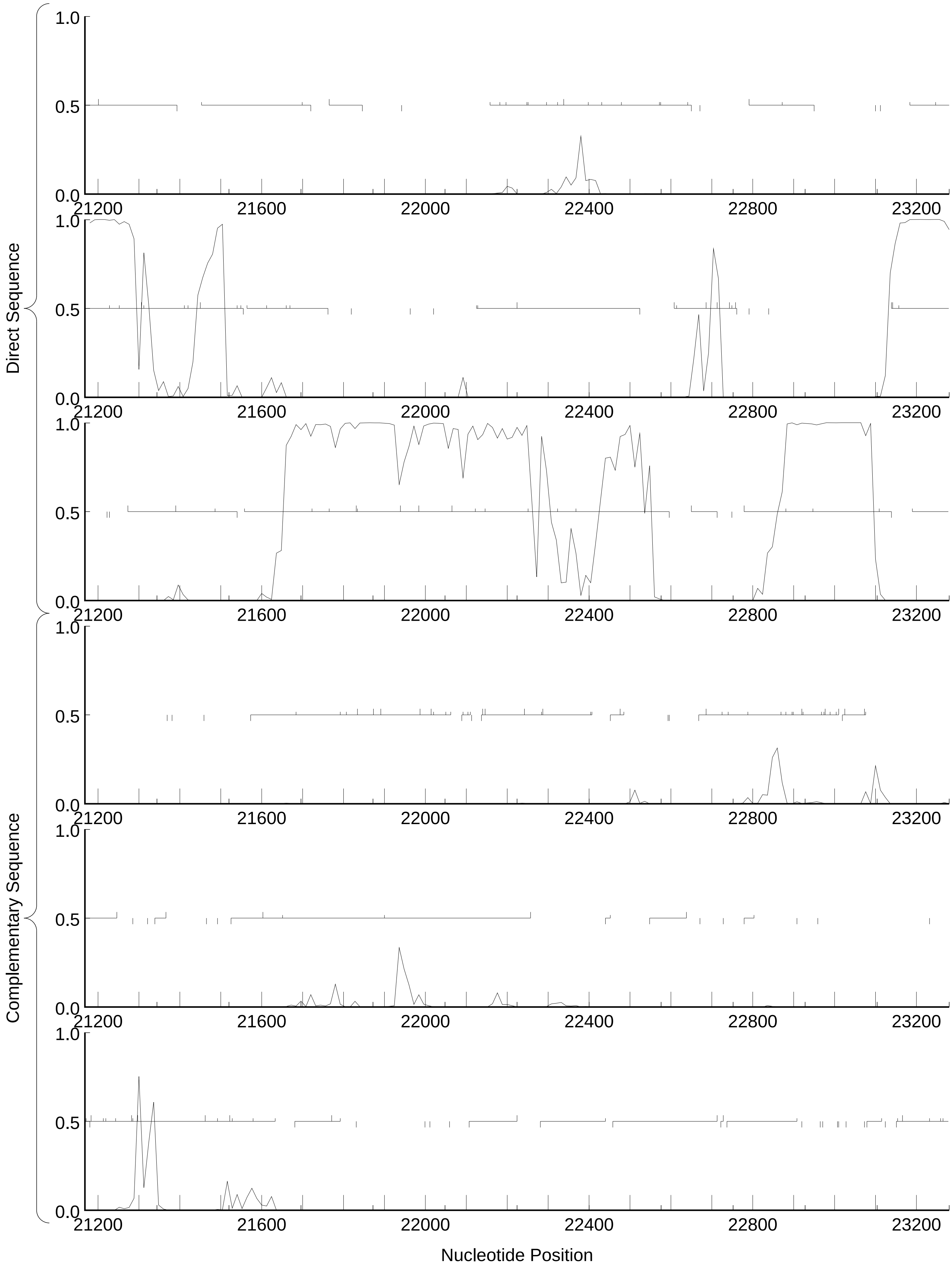
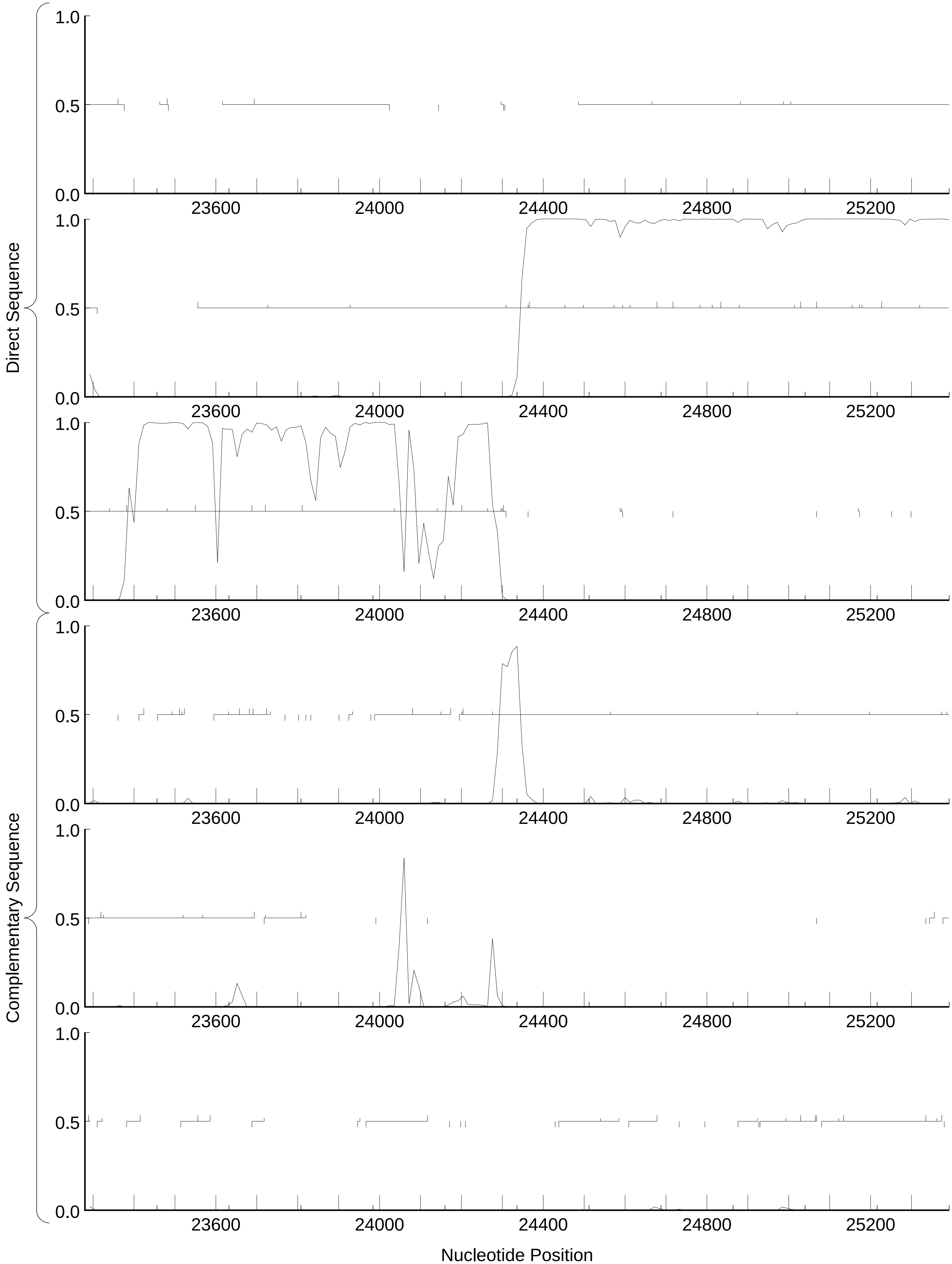
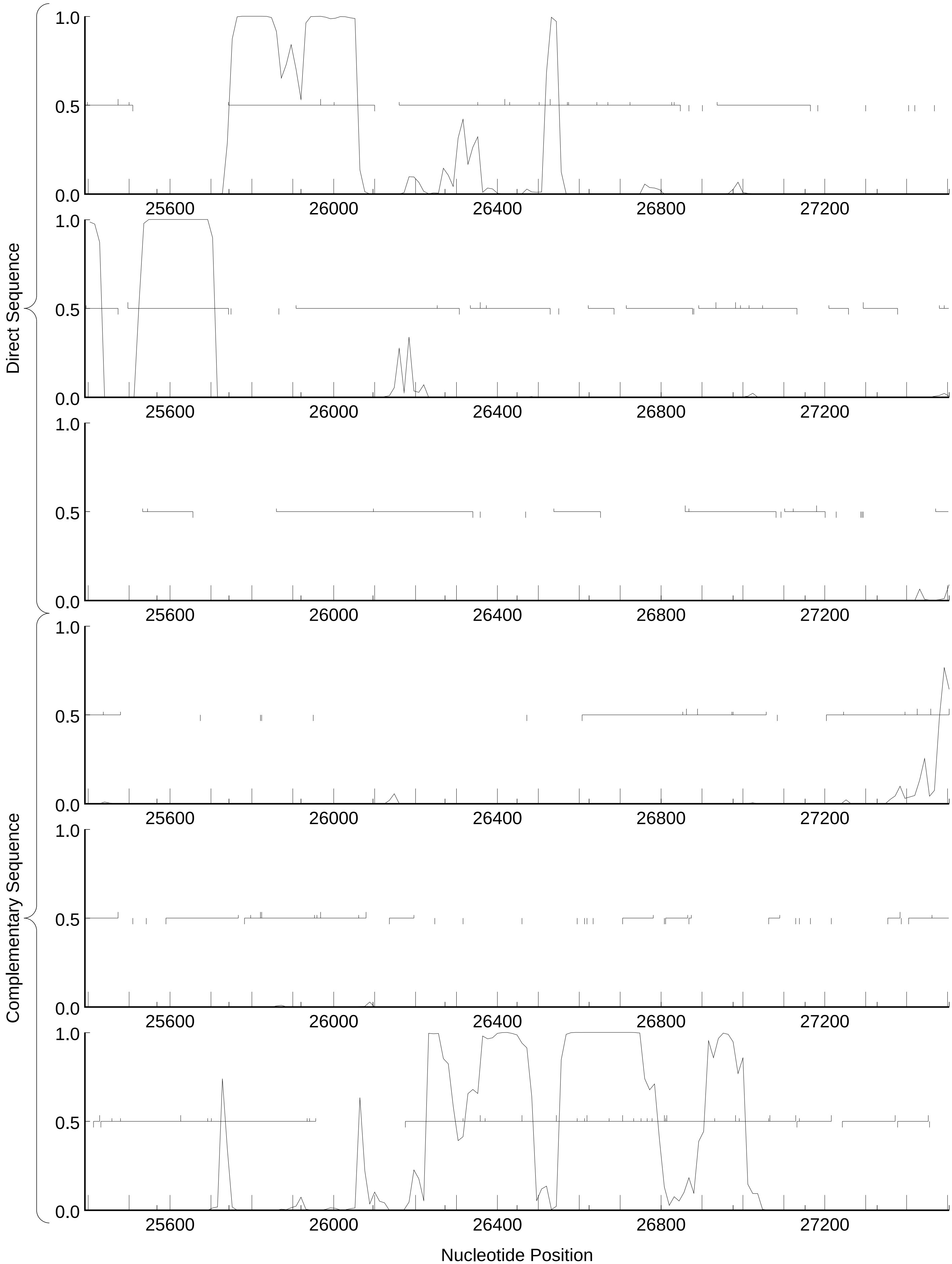




Direct Sequence
Complementary Sequence
1.0
0.5
0.0
23600
24000
24400
24800
25200
Nucleotide Position



Direct Sequence
Complementary Sequence
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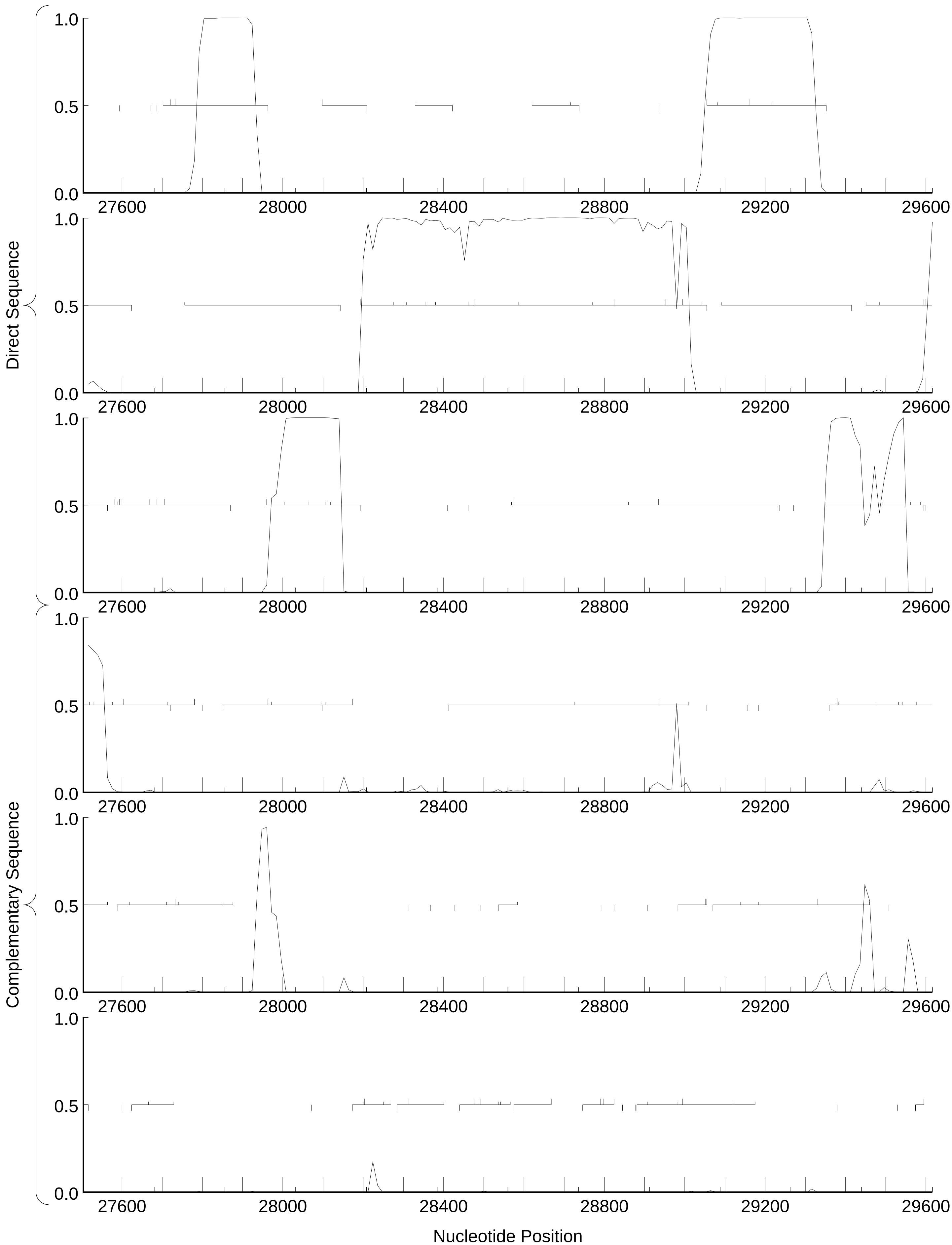
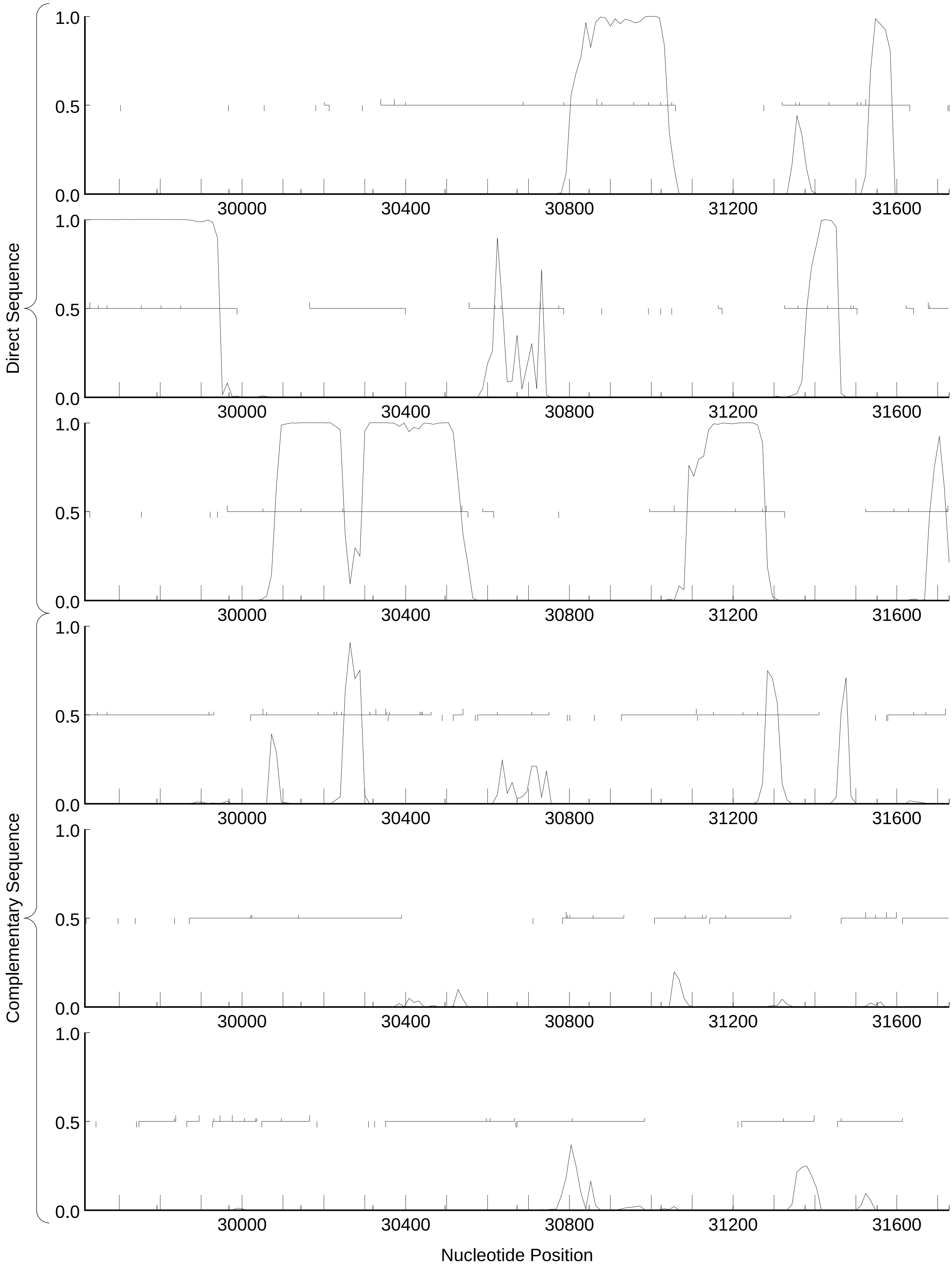
0.5
0.0
25600
26000
26400
26800
27200
Nucleotide Position

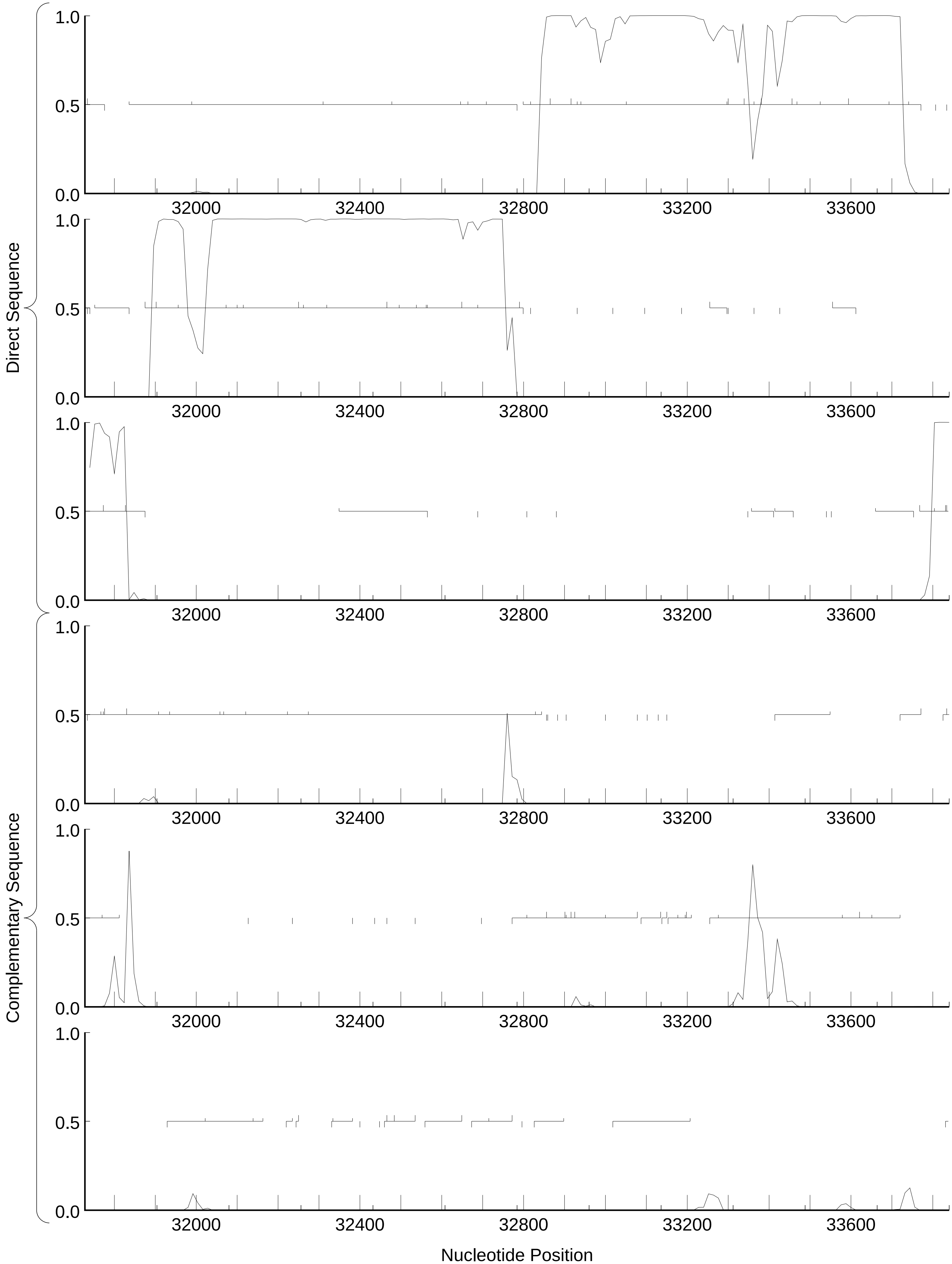


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
27600
28000
28400
28800
29200
29600
Nucleotide Position

plete sequence, 48783 bp including 13-base 3’ overhang (CCTGCCGCCCCGA), Cluster P1, Order 4, Window 96, Step 12, 16/25



plete sequence, 48783 bp including 13-base 3' overhang (CCTGCCGCCCCGA), Cluster P1, Order 4, Window 96, Step 12, 17/25



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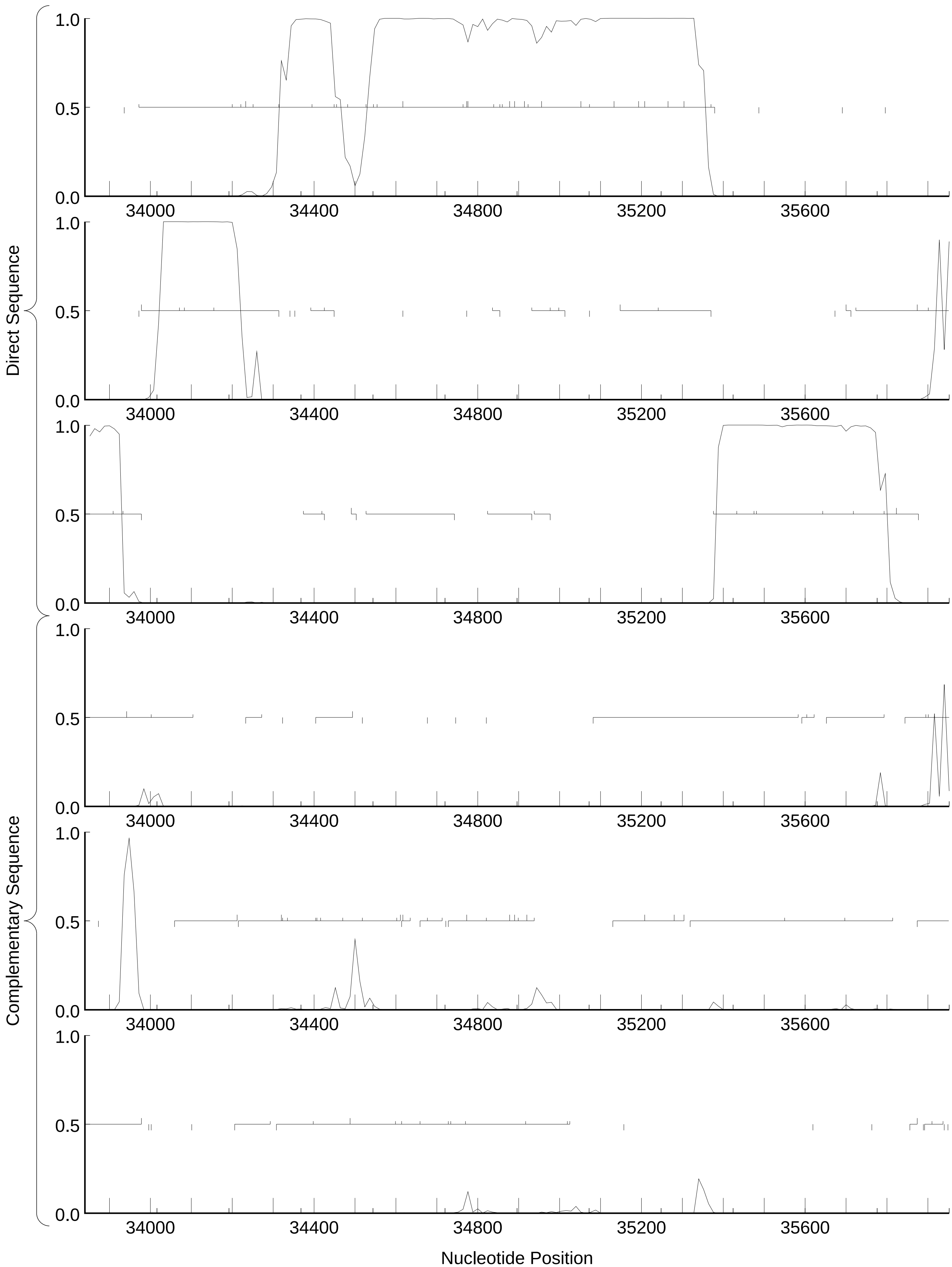

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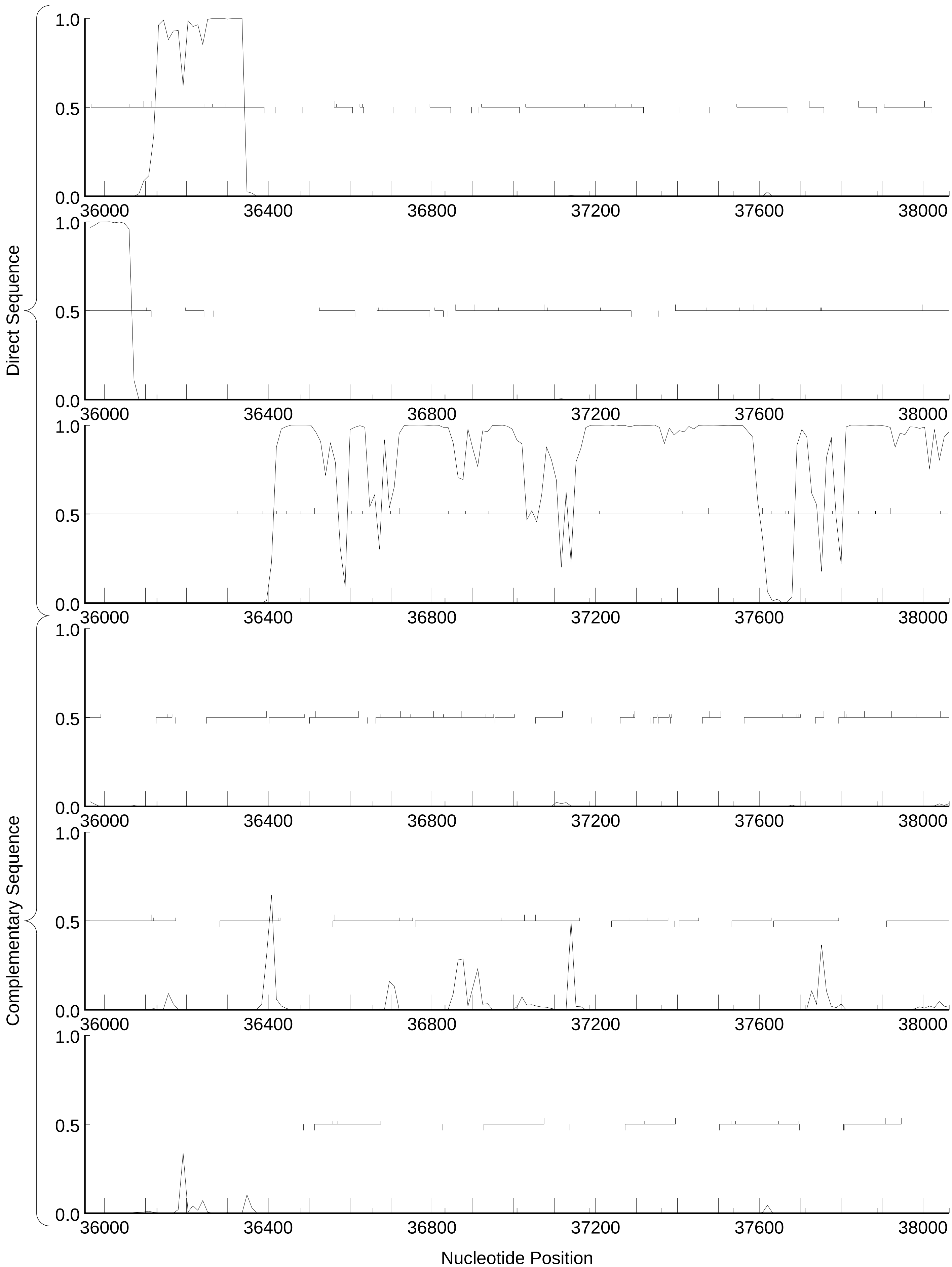

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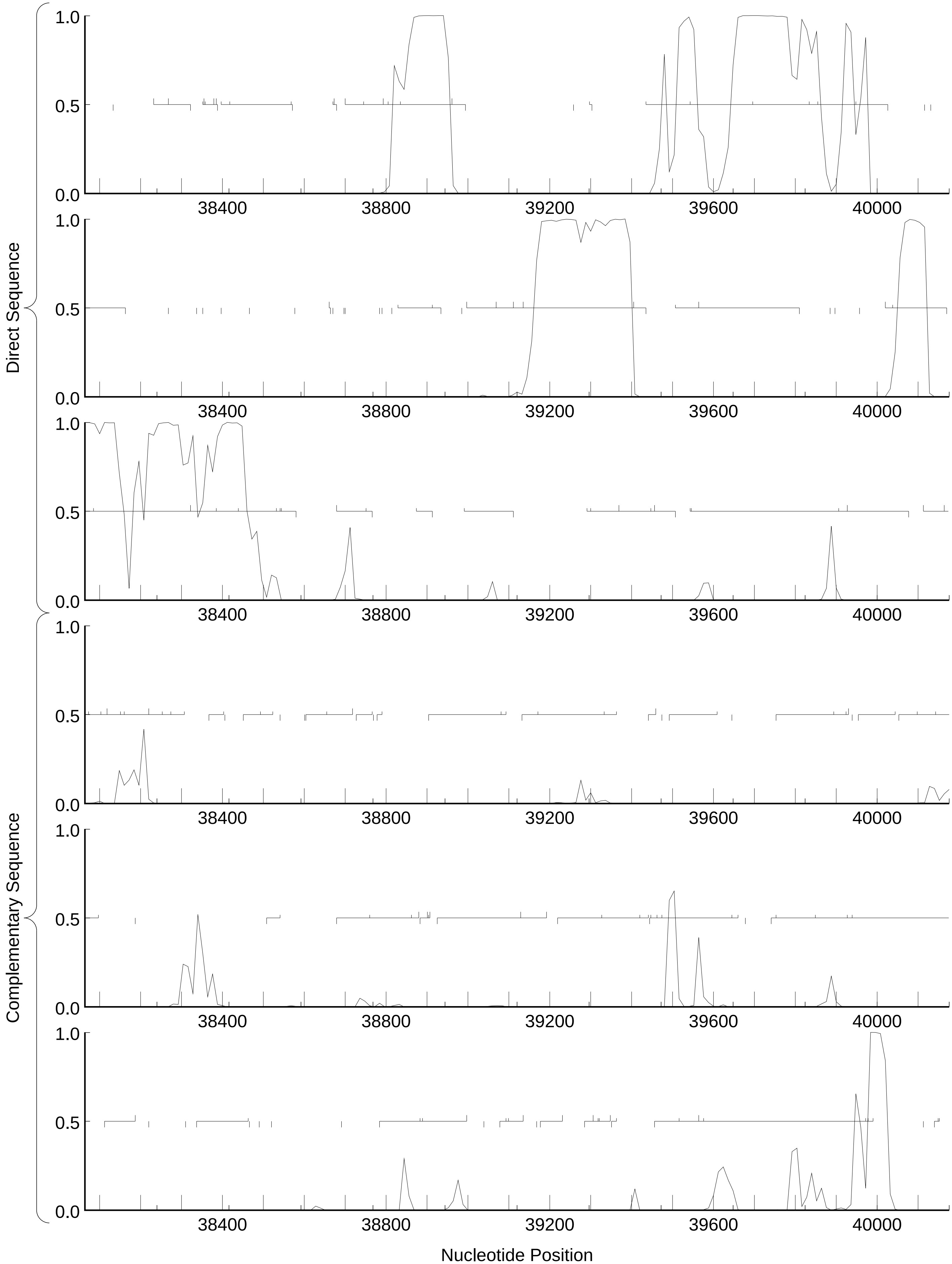

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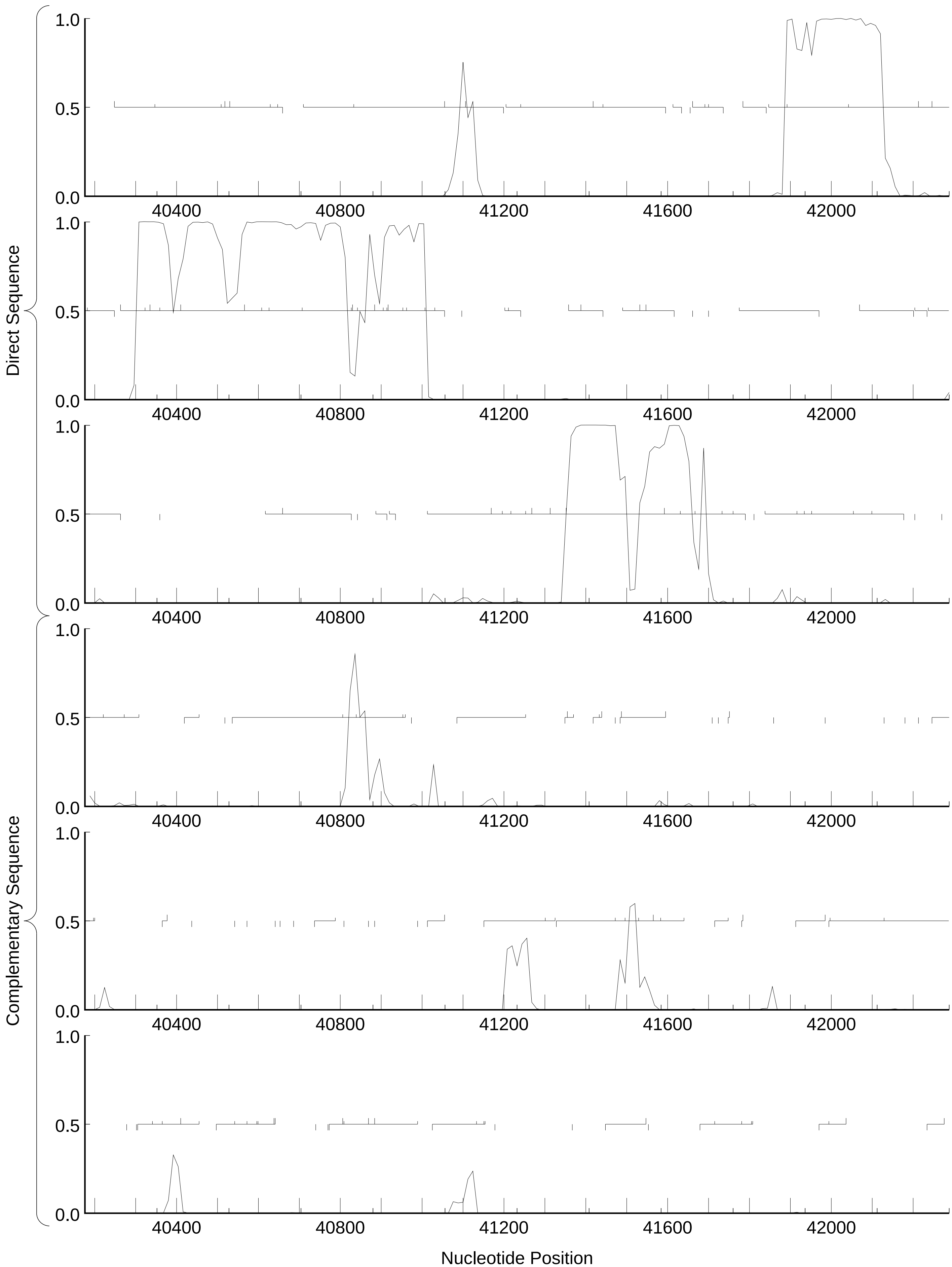

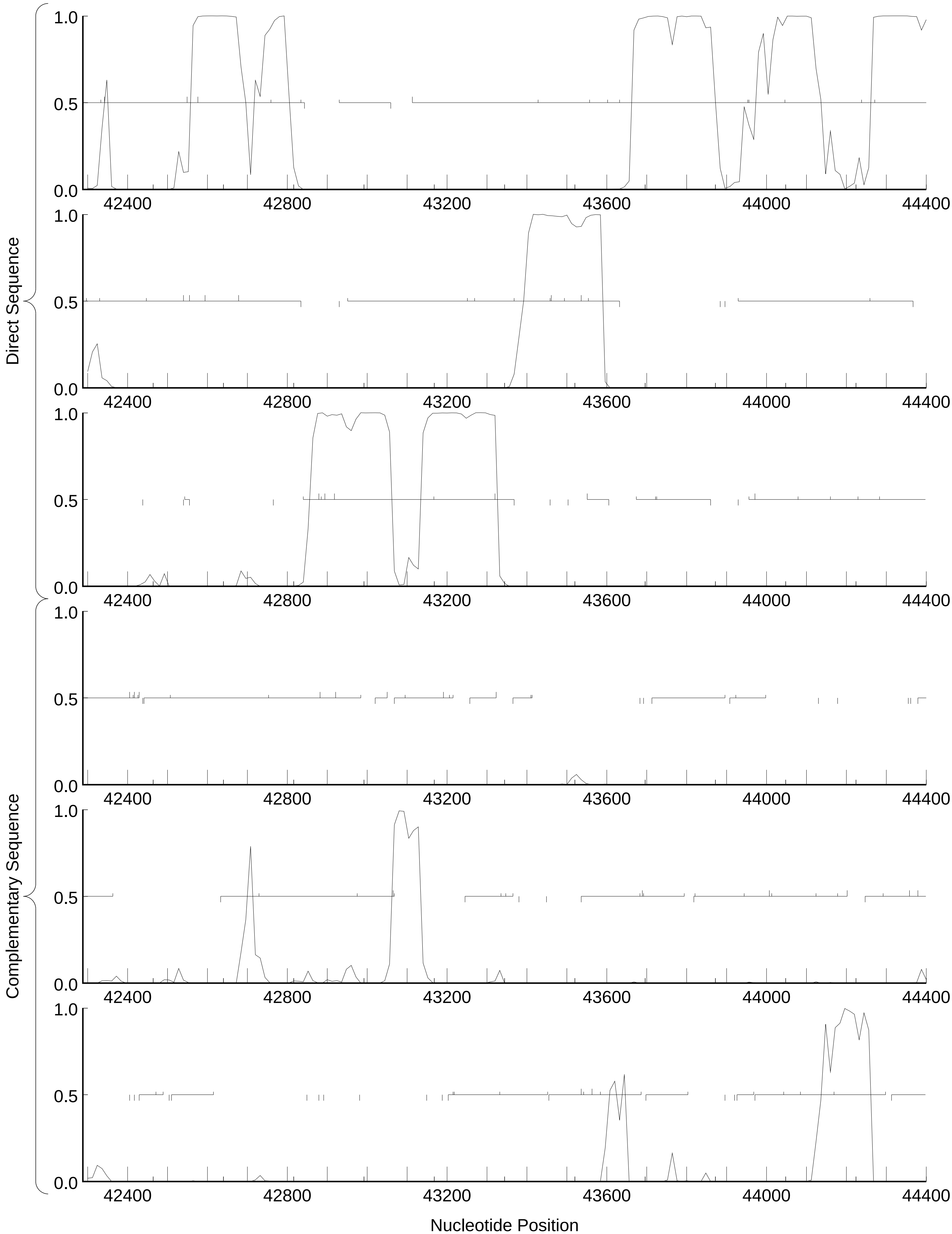
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Complementary Sequence
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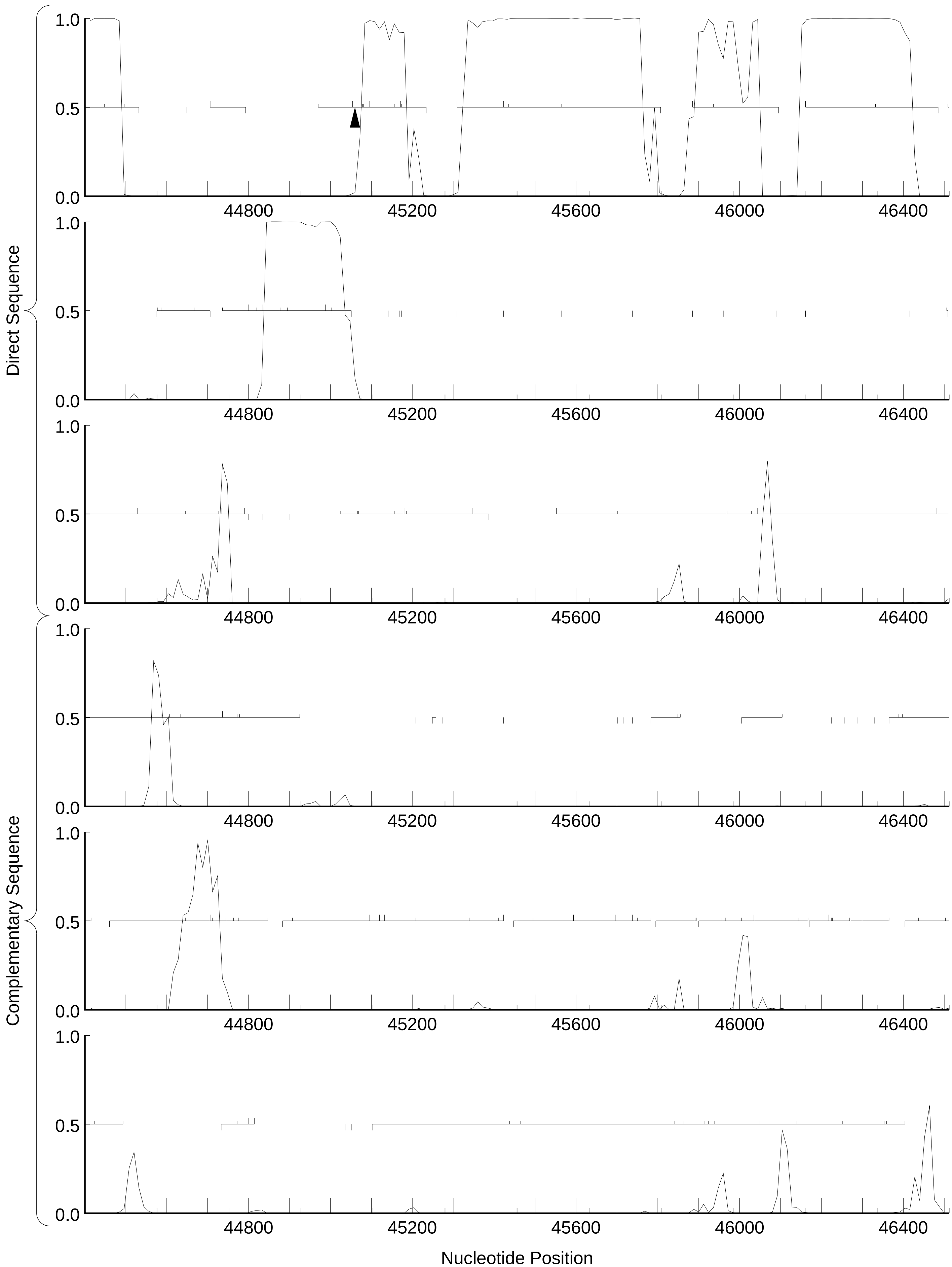
0.5
0.0
42400
42800
43200
43600
44000
44400
Nucleotide Position


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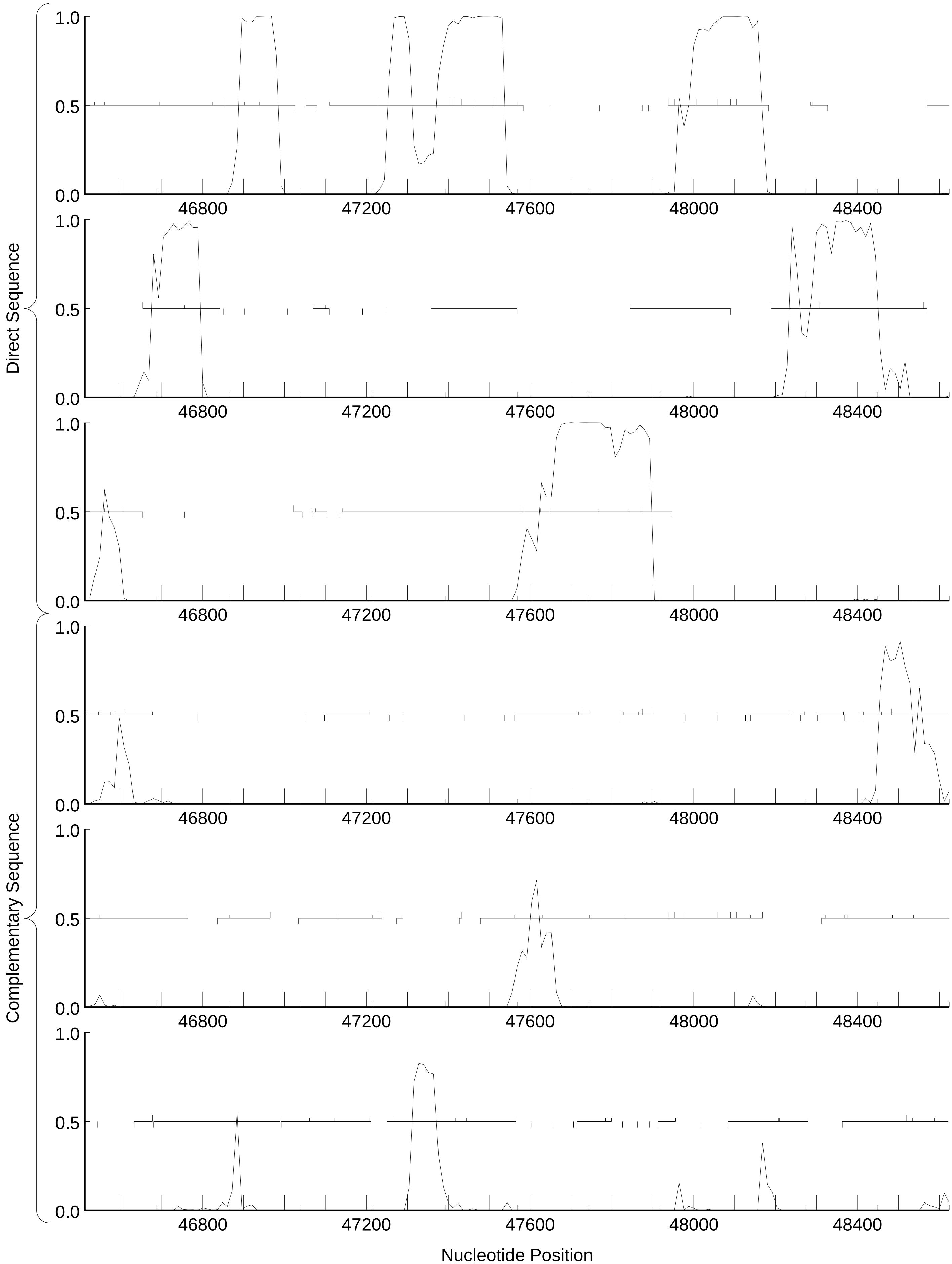
0.5
0.0
44800
45200
45600
46000
46400
Nucleotide Position



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

plete sequence, 48783 bp including 13-base 3’ overhang (CCTGCCGCCCCGA), Cluster P1, Order 4, Window 96, Step 12, 25/25