GeneMark

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

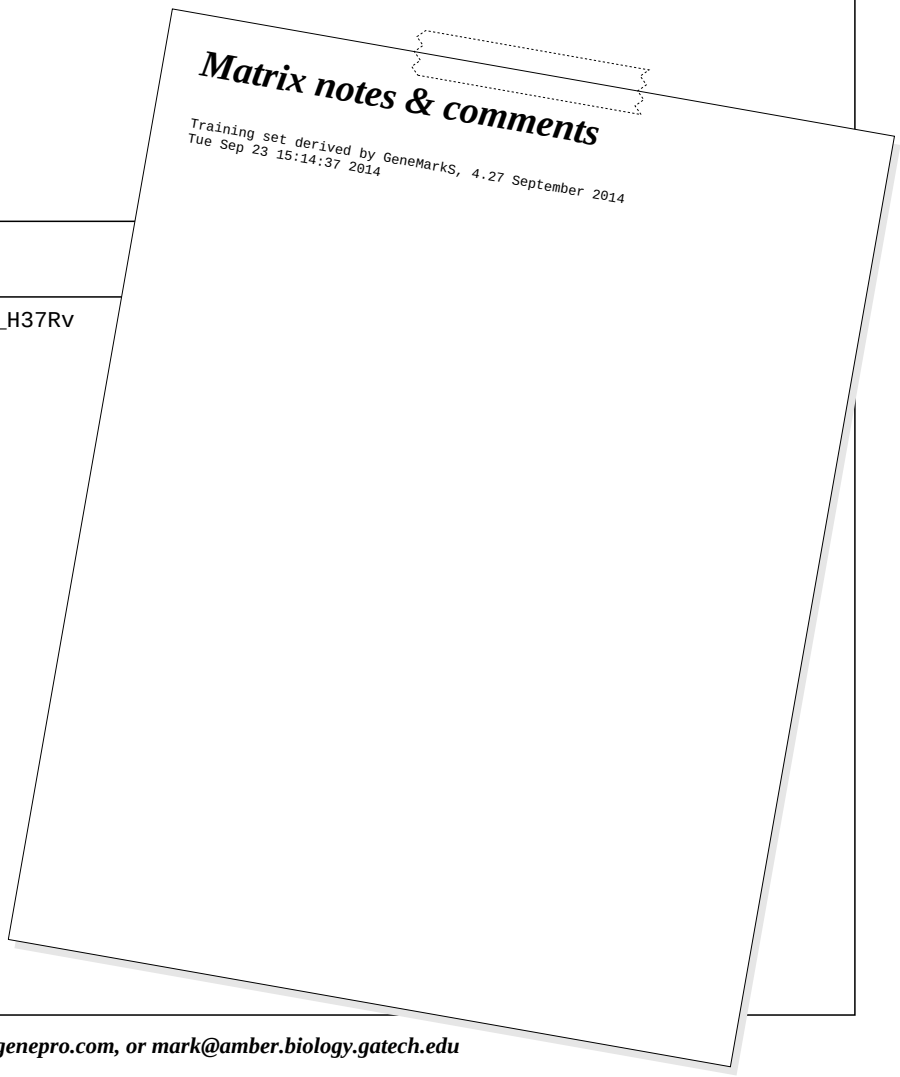
PROGRAM INFORMATION

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Sequence         :  Mycobacterium phage KayaCho complete corrected sequence, 70838 bp, circularly permuted
Analysis Date    :  3/28/24 at 9:08:40
Pages            :  35
Sequence Length  :  70838 bp
GC Content       :   70.01%

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

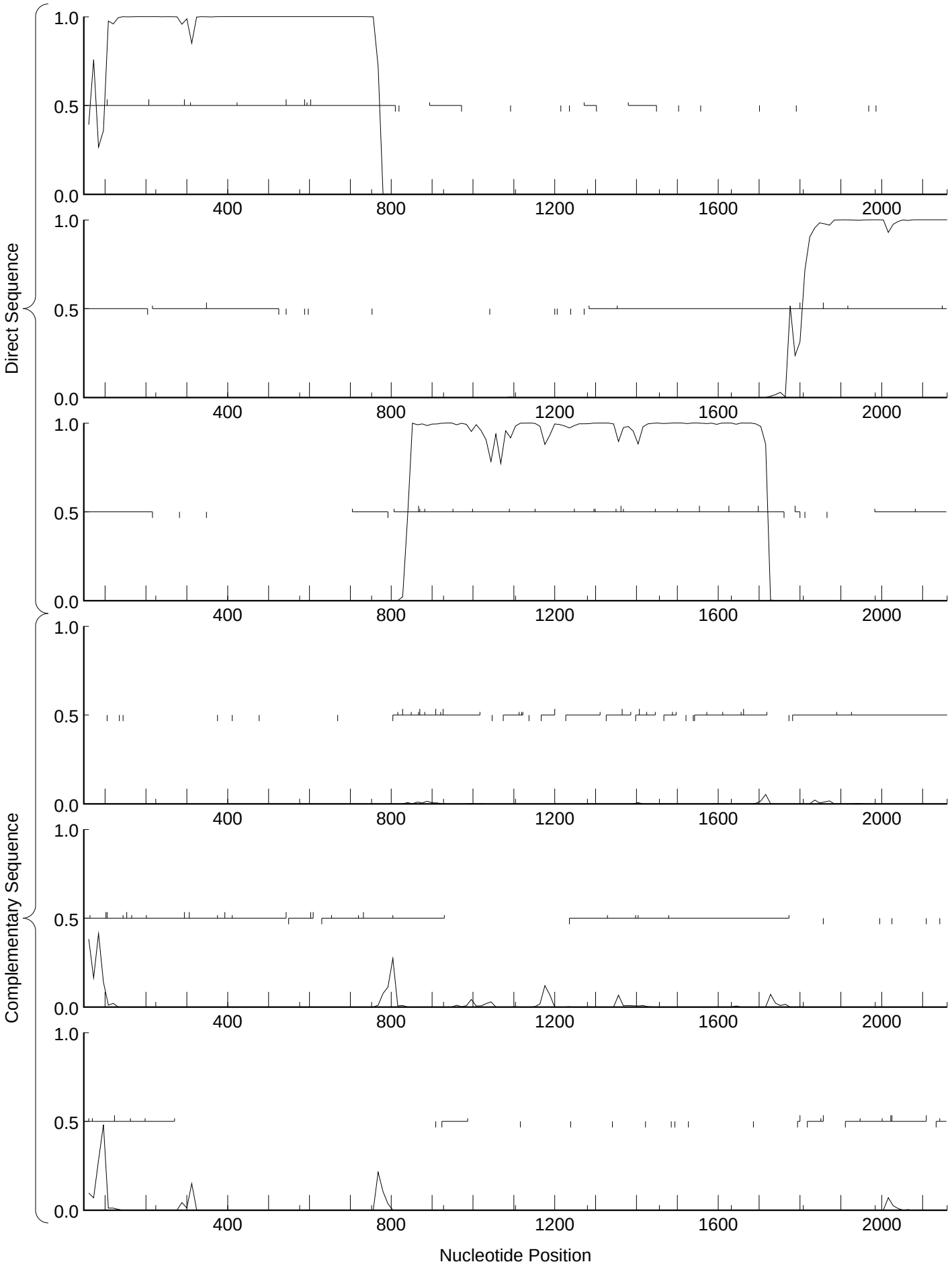
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Matrix     :  Mycobacterium_tuberculosis_H37Rv
Author     :  -

Order      :  4
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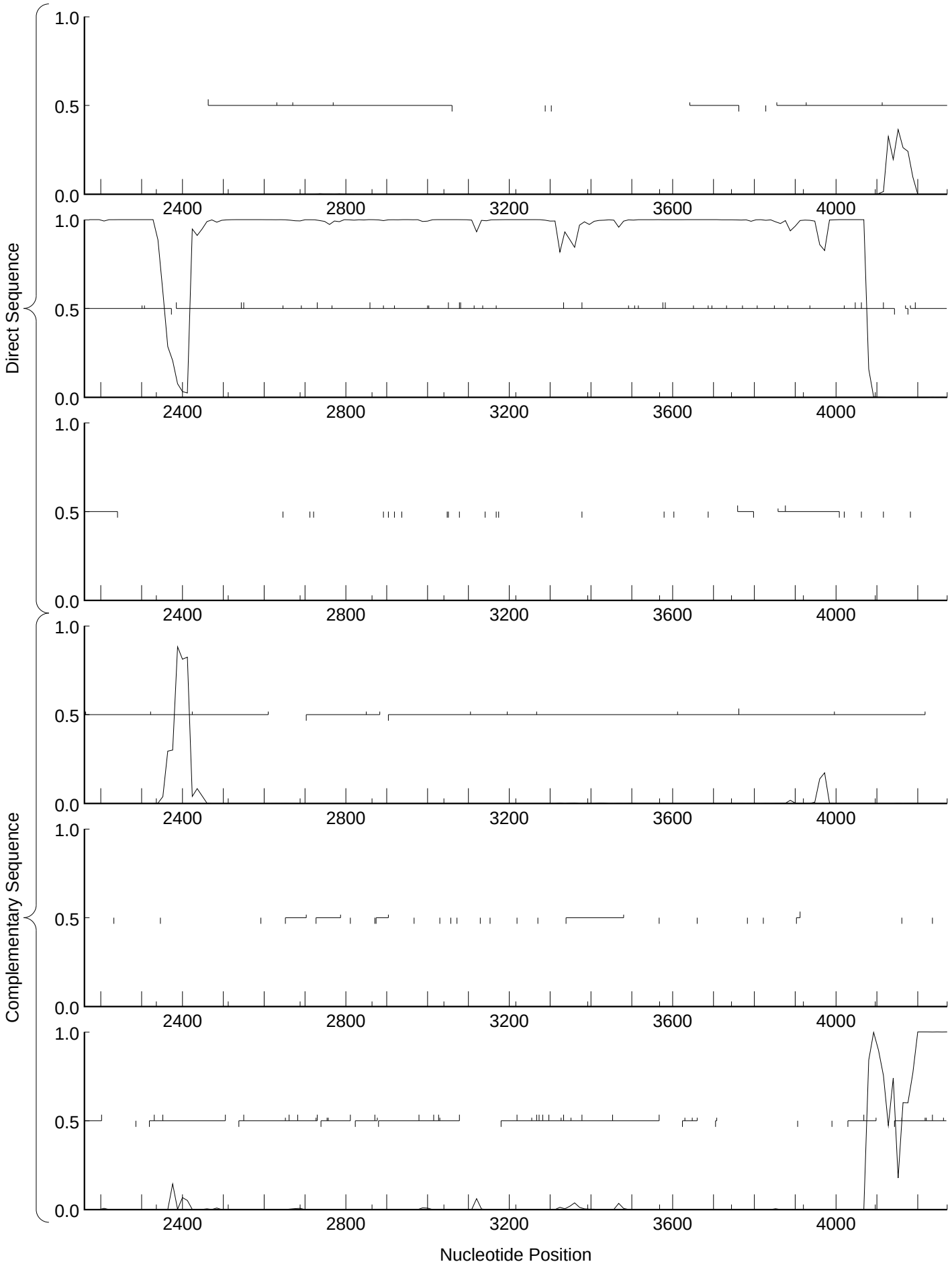

```
  Send questions / comments to:
      Dr. M. Borodovsky
      Georgia Institute of Technology
      School of Biology
      Atlanta, GA  30332-0230
```


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

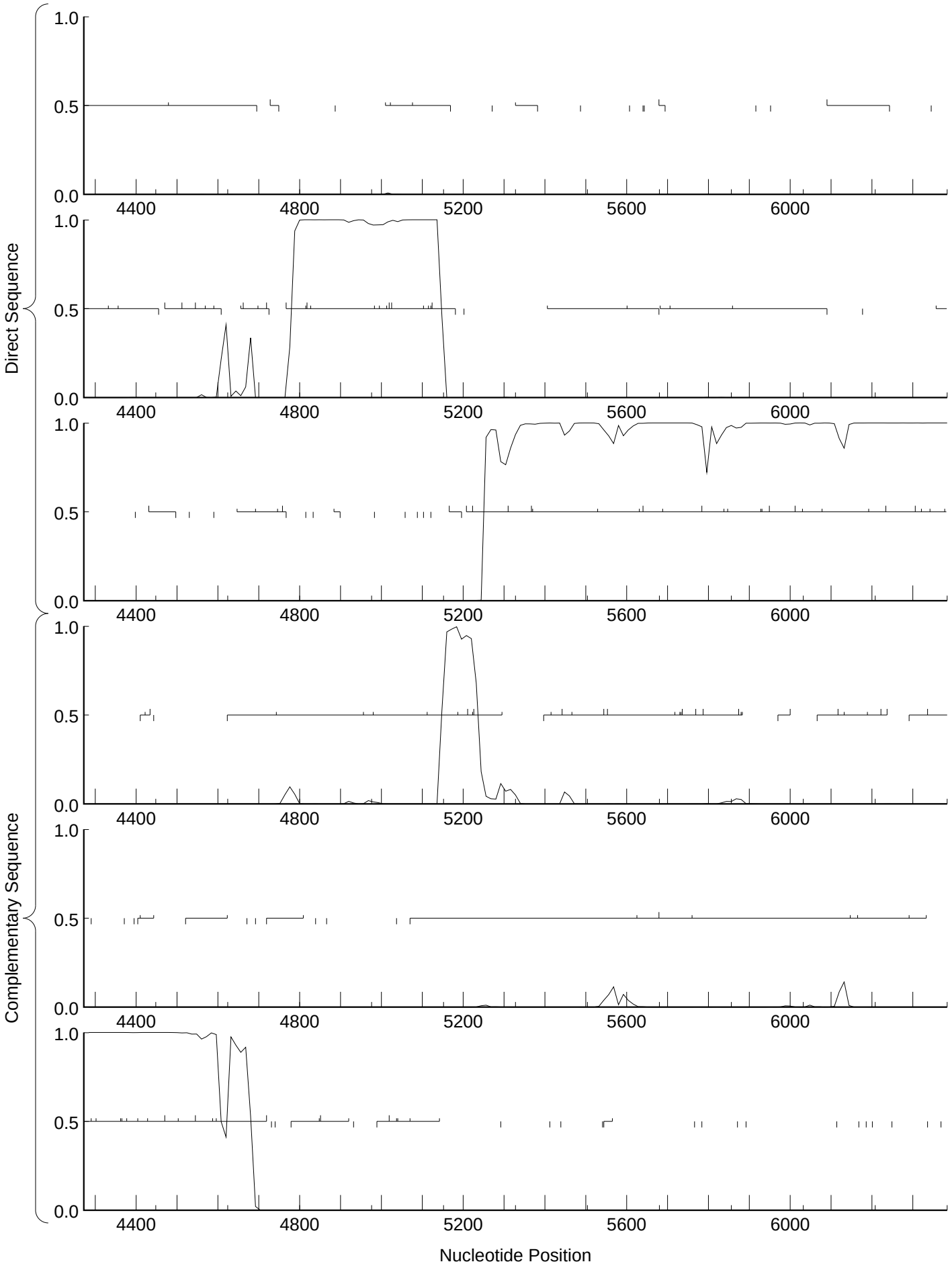
Mycobacterium phage KayaCho complete corrected sequence, 70838 bp, circularly permuted, Order 4, Window 96, Step 12, 2/35



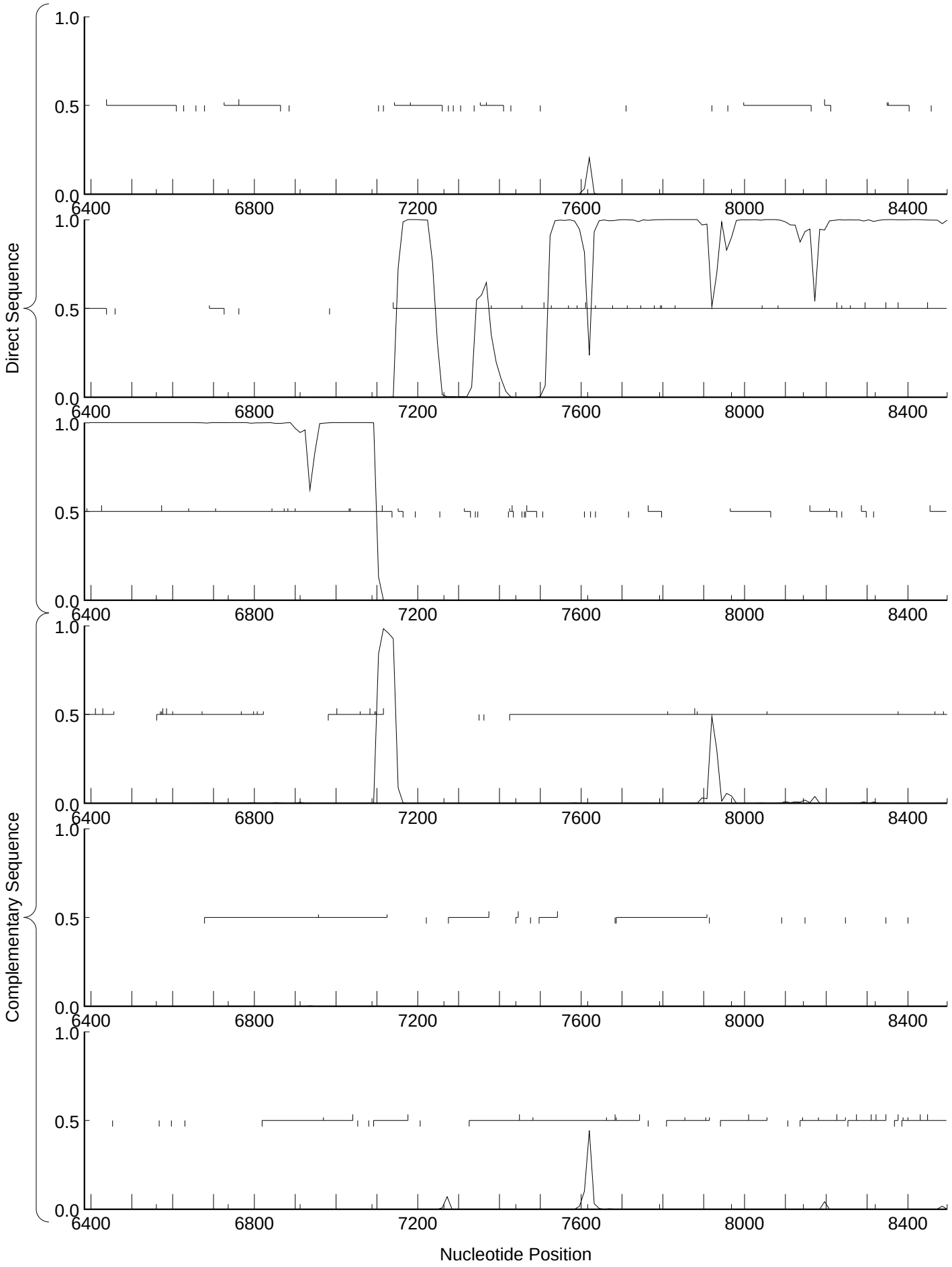
Mycobacterium phage KayaCho complete corrected sequence, 70838 bp, circularly permuted, Order 4, Window 96, Step 12, 3/35



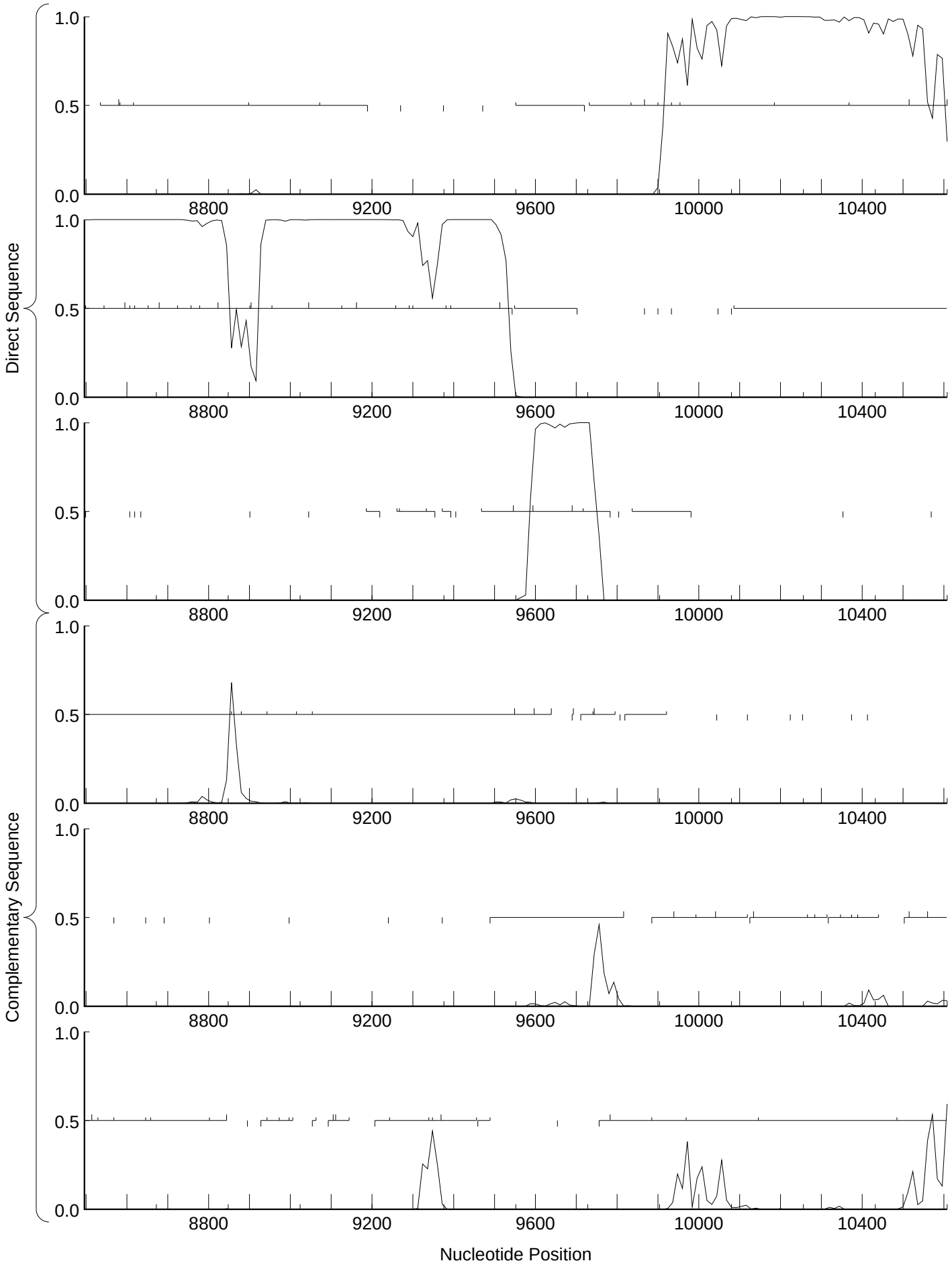
Mycobacterium phage KayaCho complete corrected sequence, 70838 bp, circularly permuted, Order 4, Window 96, Step 12, 4/35



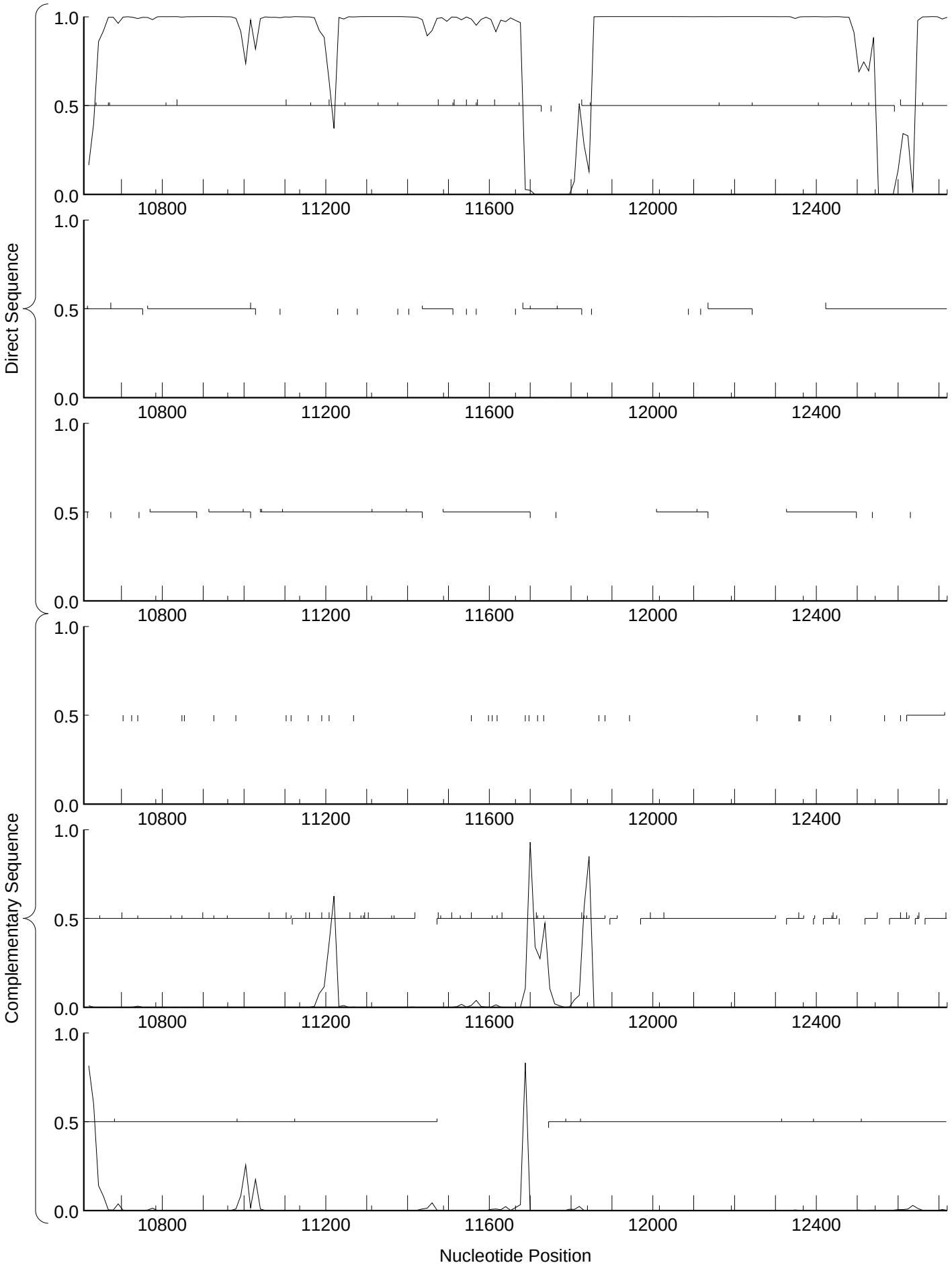
Mycobacterium phage KayaCho complete corrected sequence, 70838 bp, circularly permuted, Order 4, Window 96, Step 12, 5/35



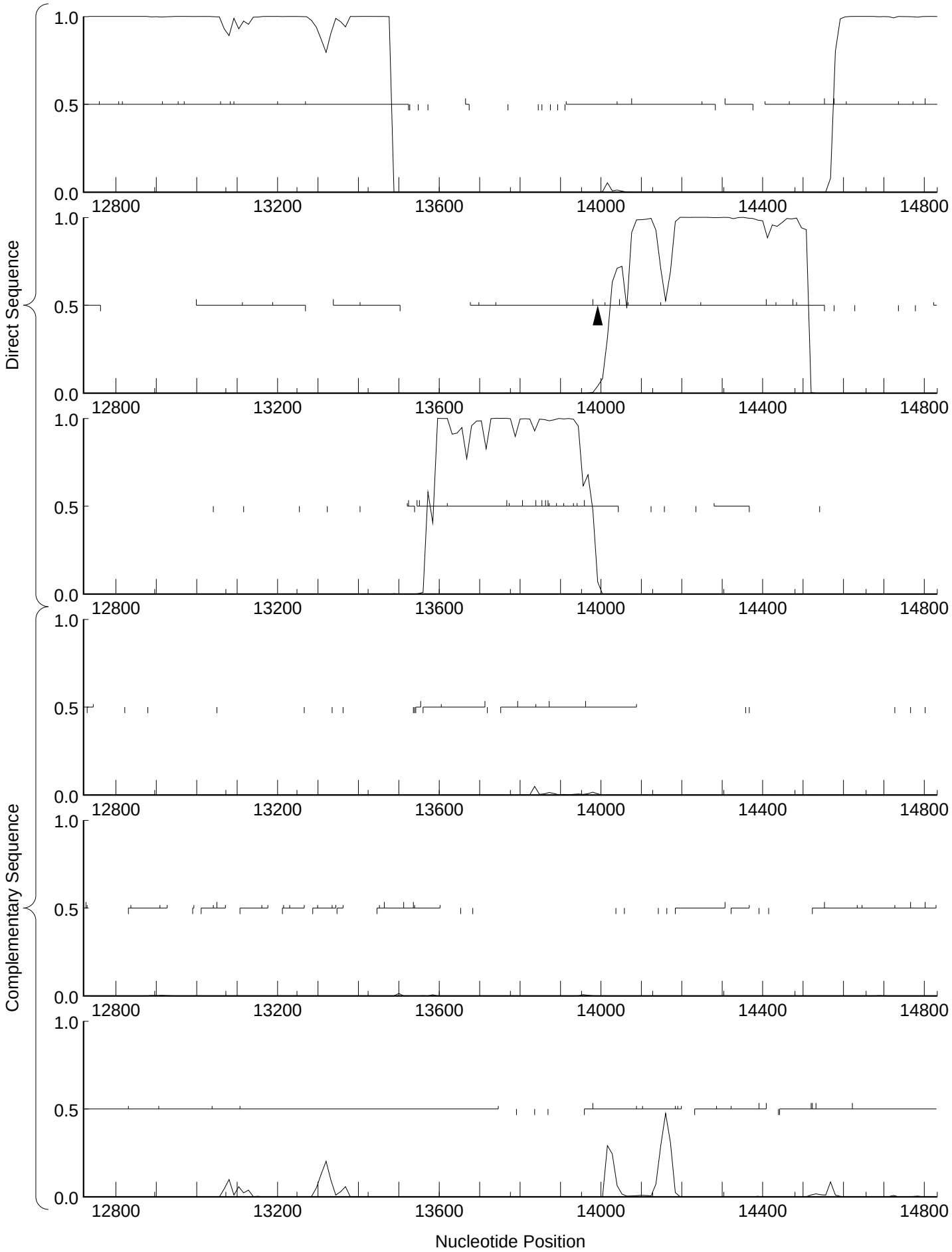
Mycobacterium phage KayaCho complete corrected sequence, 70838 bp, circularly permuted, Order 4, Window 96, Step 12, 6/35



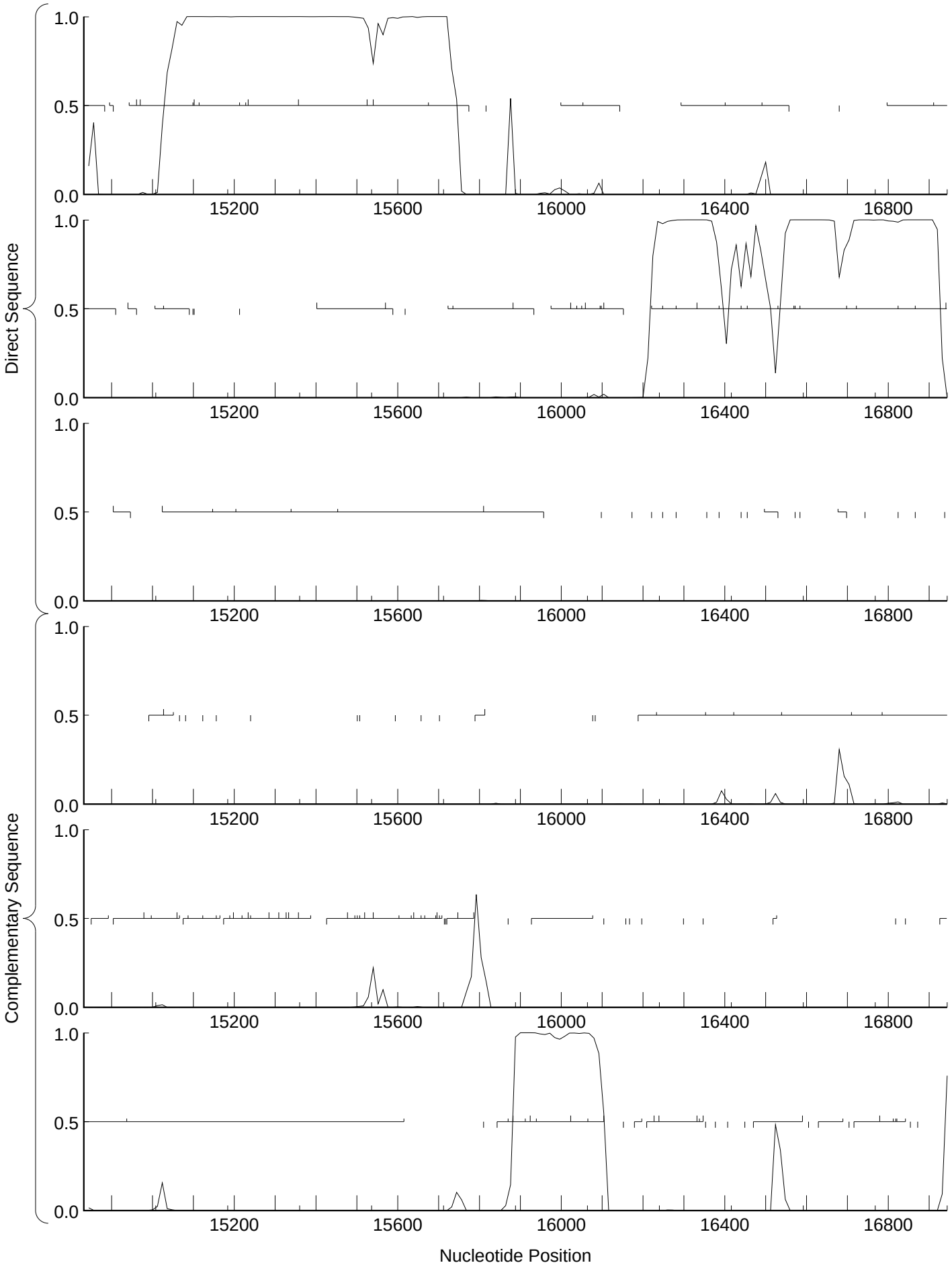
Mycobacterium phage KayaCho complete corrected sequence, 70838 bp, circularly permuted, Order 4, Window 96, Step 12, 7/35



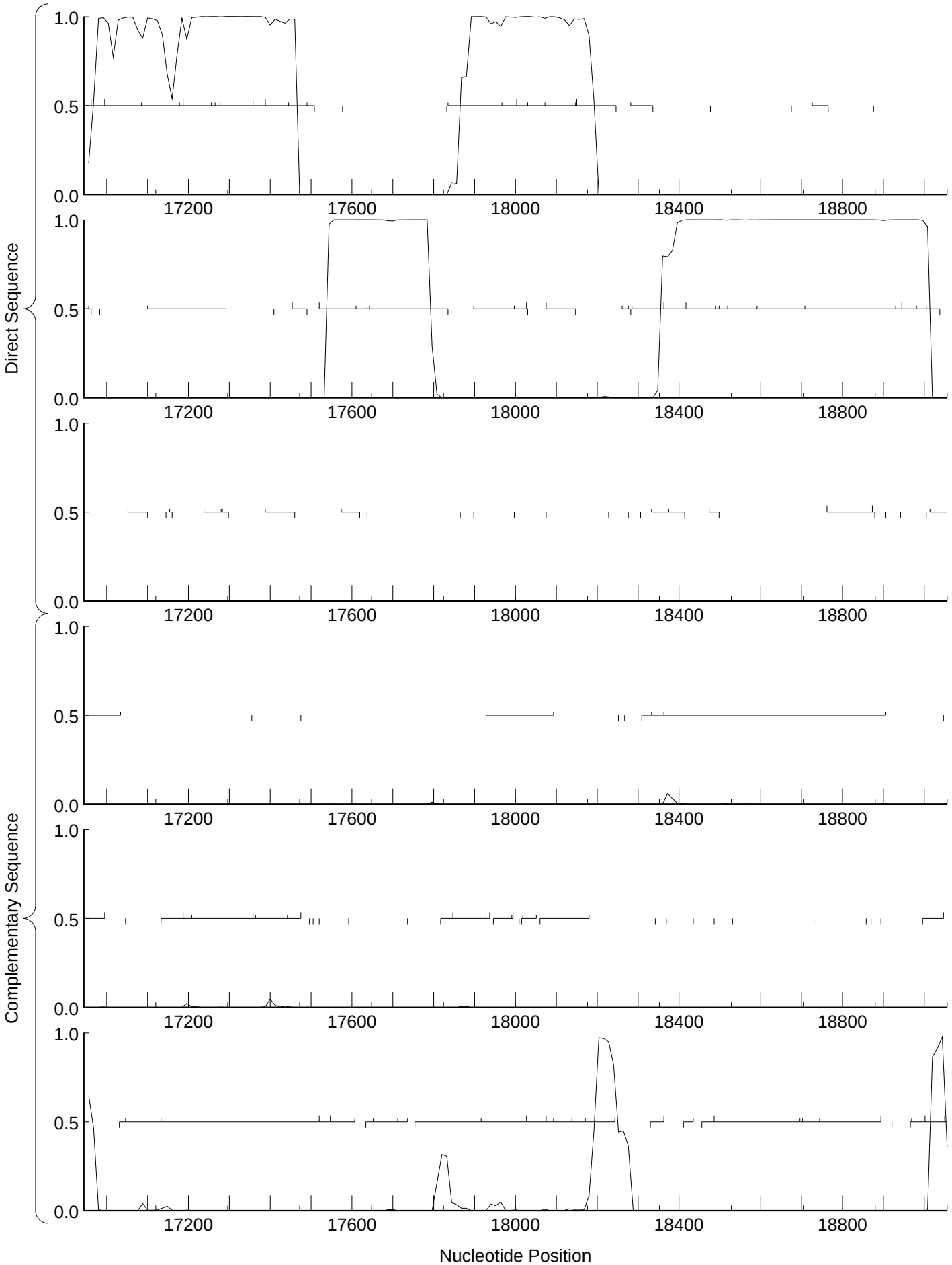
Mycobacterium phage KayaCho complete corrected sequence, 70838 bp, circularly permuted, Order 4, Window 96, Step 12, 8/35



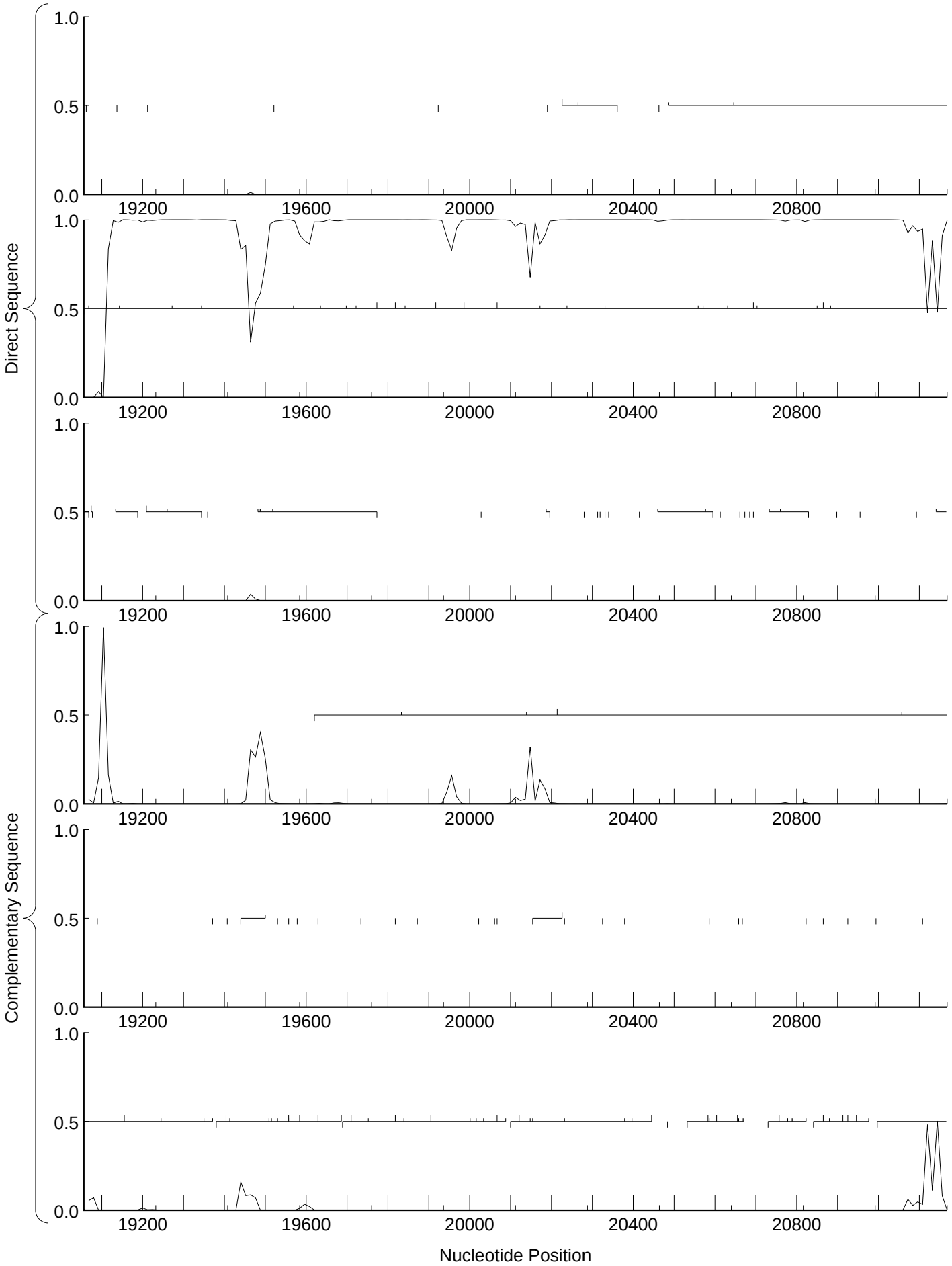
Mycobacterium phage KayaCho complete corrected sequence, 70838 bp, circularly permuted, Order 4, Window 96, Step 12, 9/35



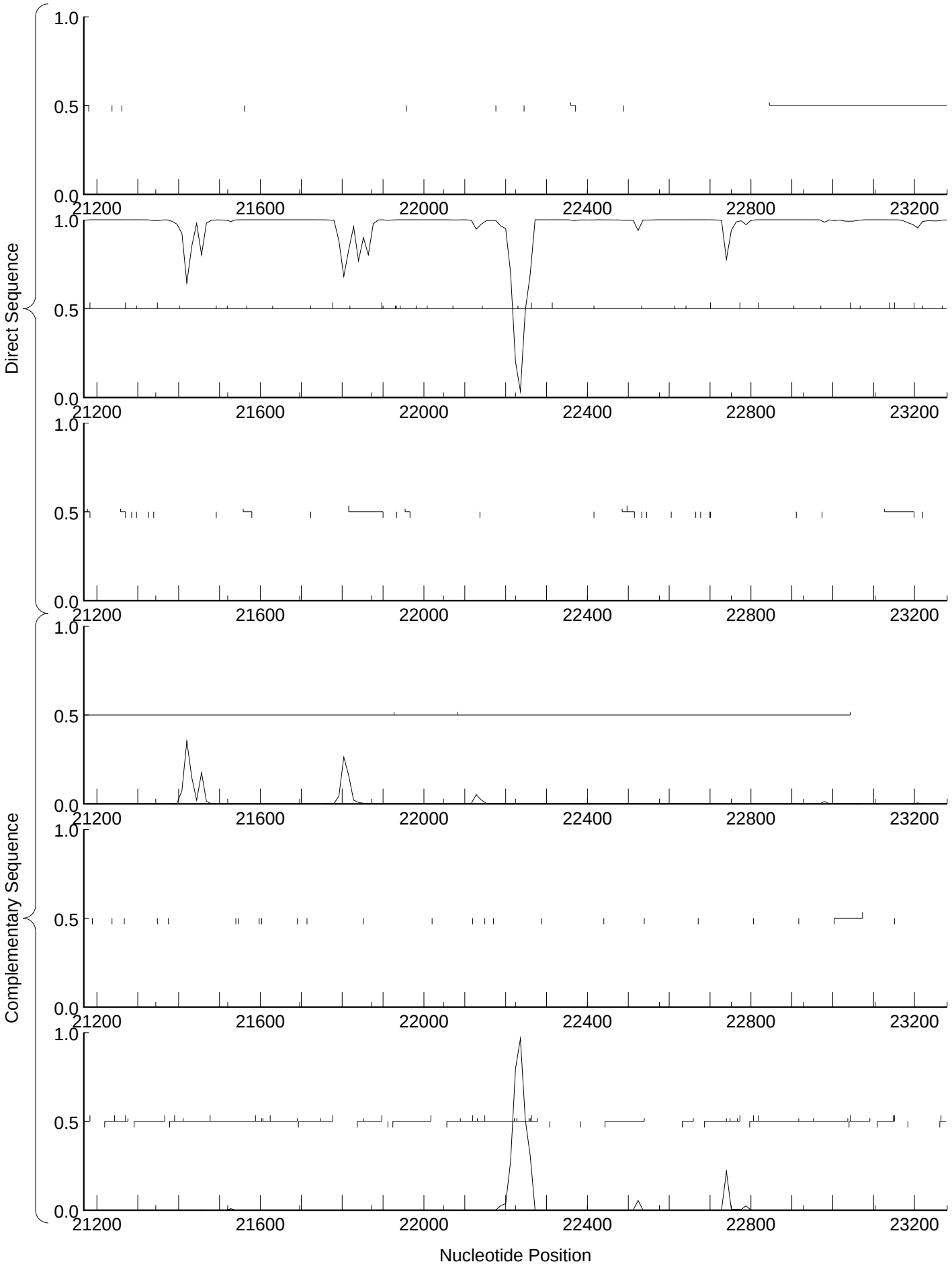
ycobacterium phage KayaCho complete corrected sequence, 70838 bp, circularly permuted, Order 4, Window 96, Step 12, 10/35



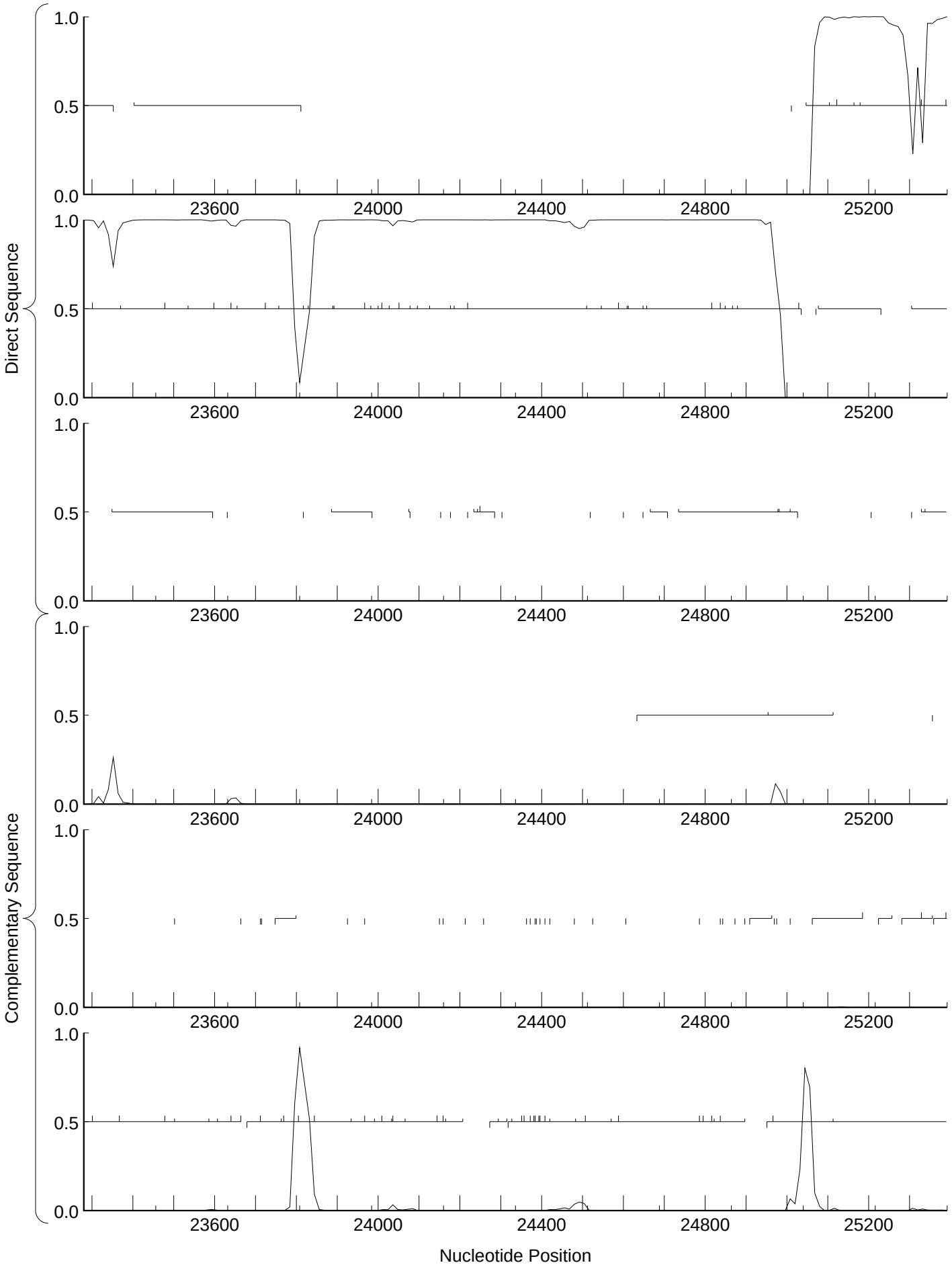
Mycobacterium phage KayaCho complete corrected sequence, 70838 bp, circularly permuted, Order 4, Window 96, Step 12, 11/35

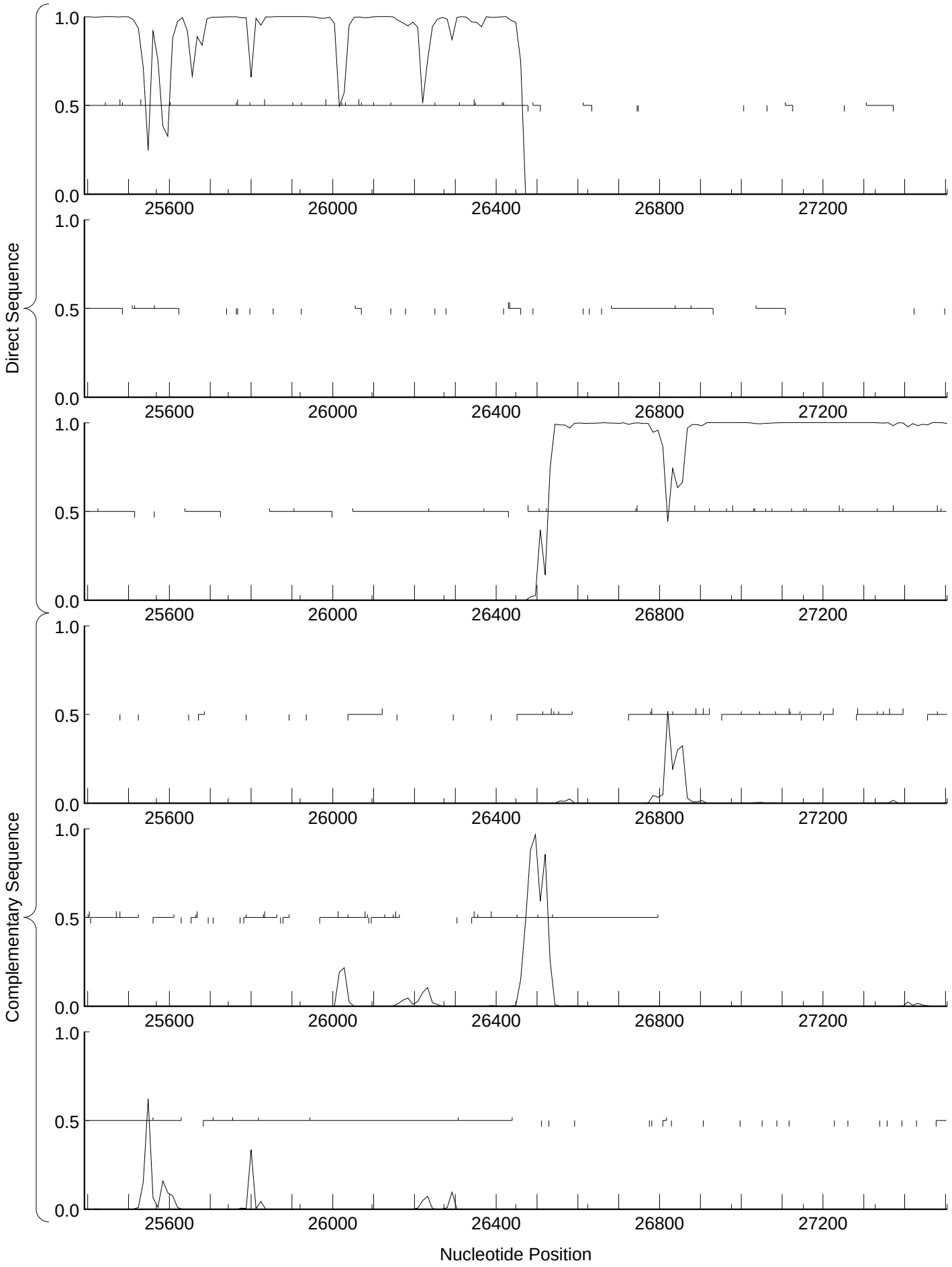


Mycobacterium phage KayaCho complete corrected sequence, 70838 bp, circularly permuted, Order 4, Window 96, Step 12, 12/35

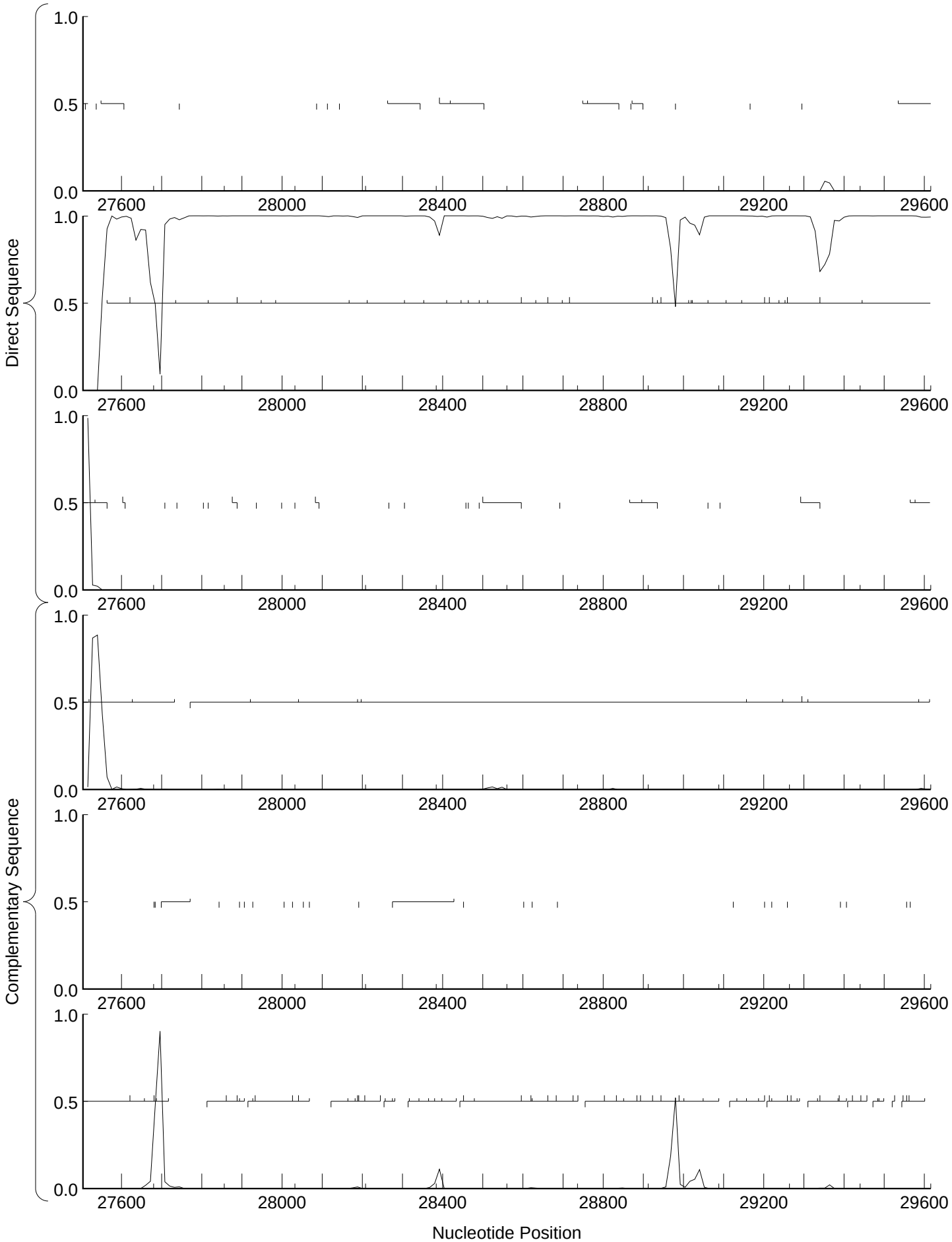


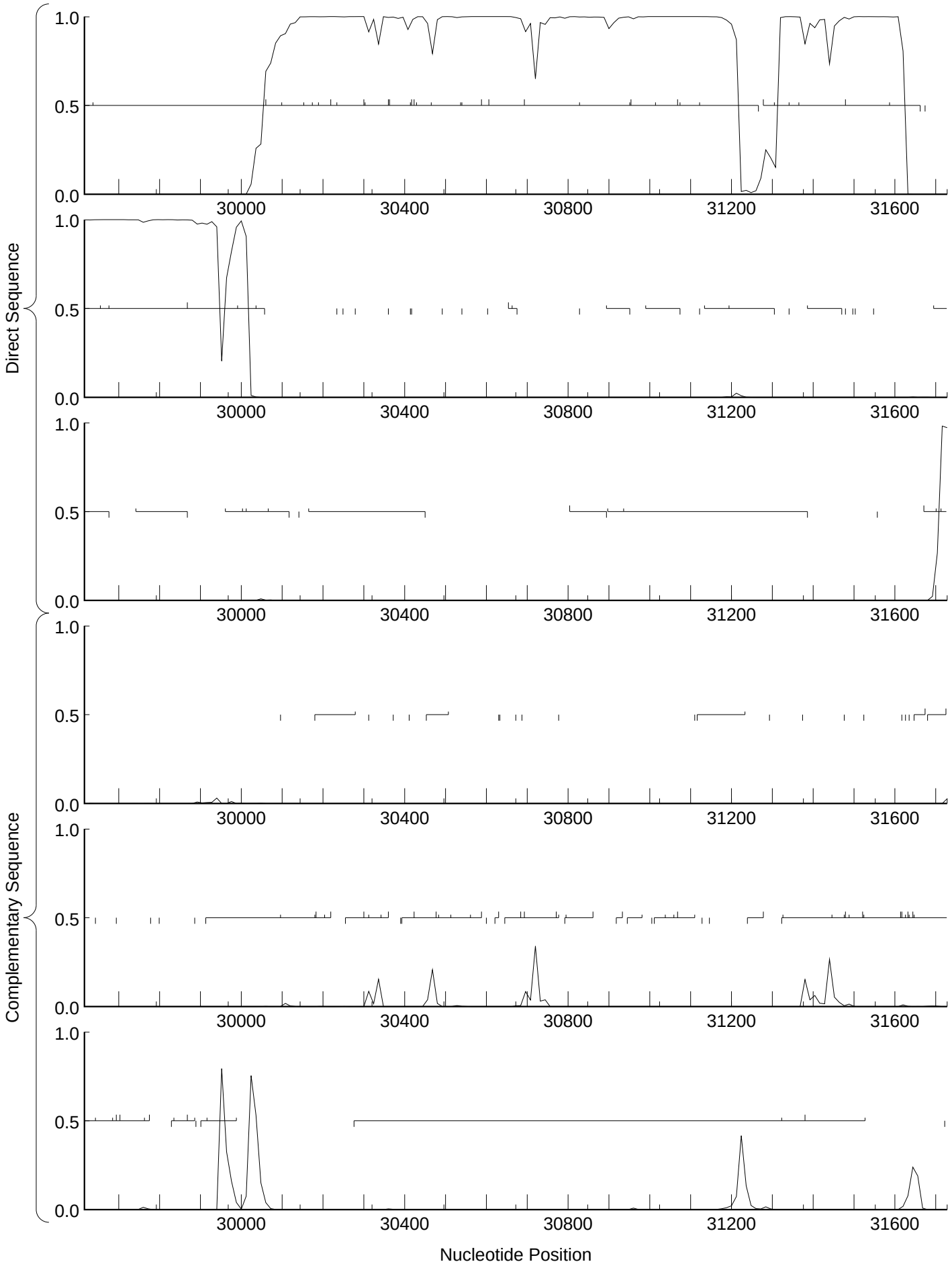
Mycobacterium phage KayaCho complete corrected sequence, 70838 bp, circularly permuted, Order 4, Window 96, Step 12, 13/35



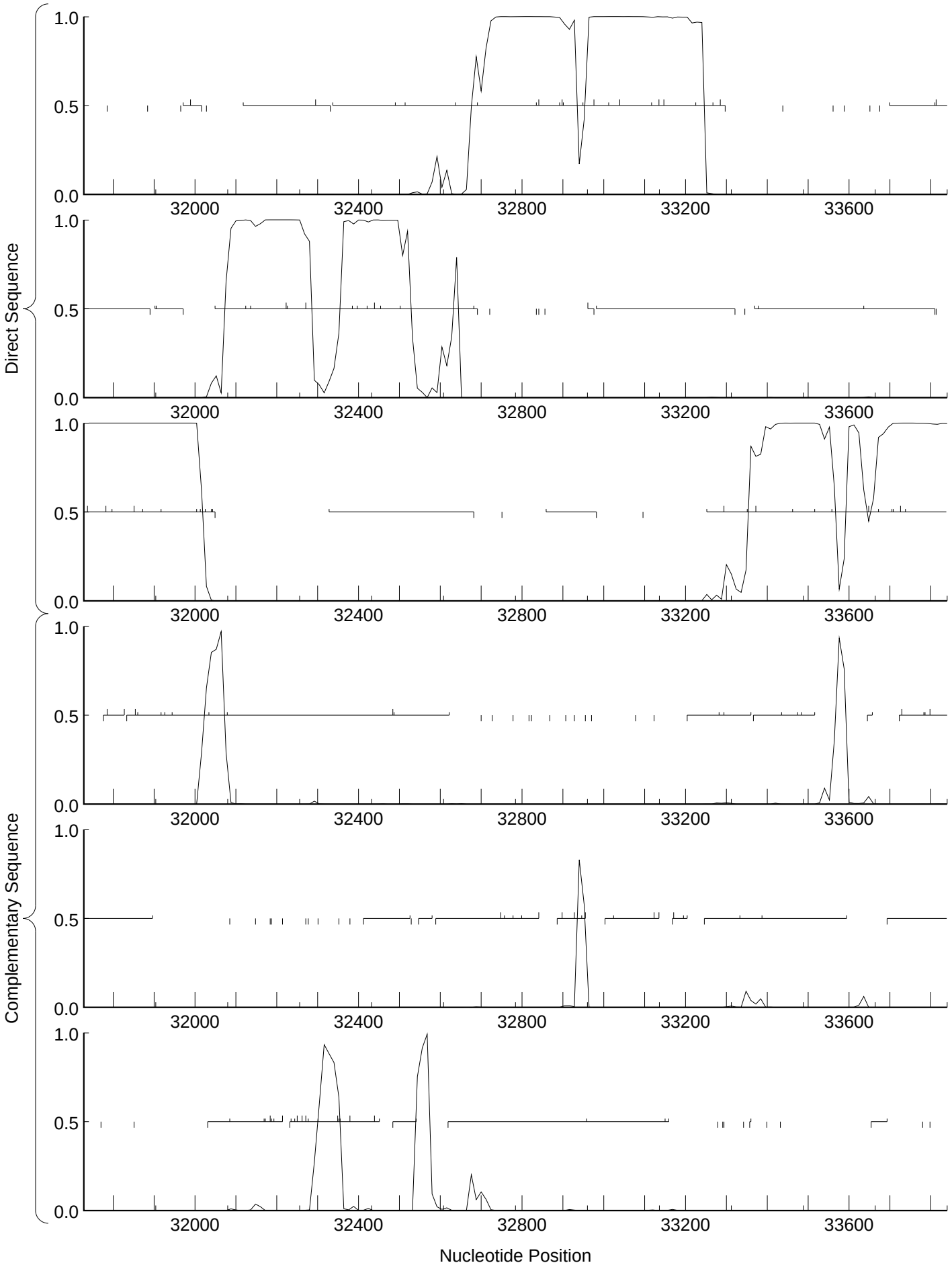

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
25600
26000
26400
26800
27200
Nucleotide Position

Mycobacterium phage KayaCho complete corrected sequence, 70838 bp, circularly permuted, Order 4, Window 96, Step 12, 15/35

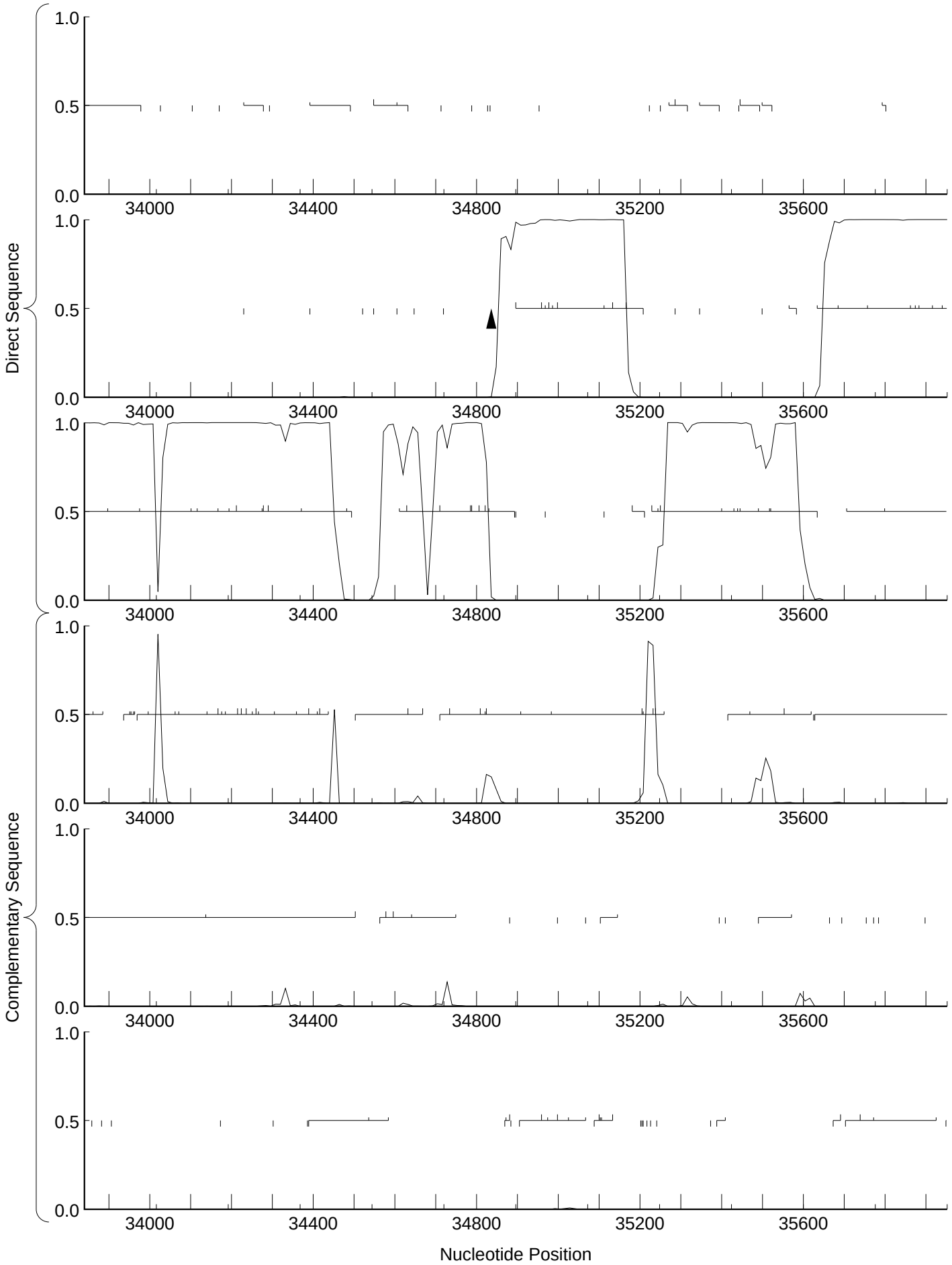


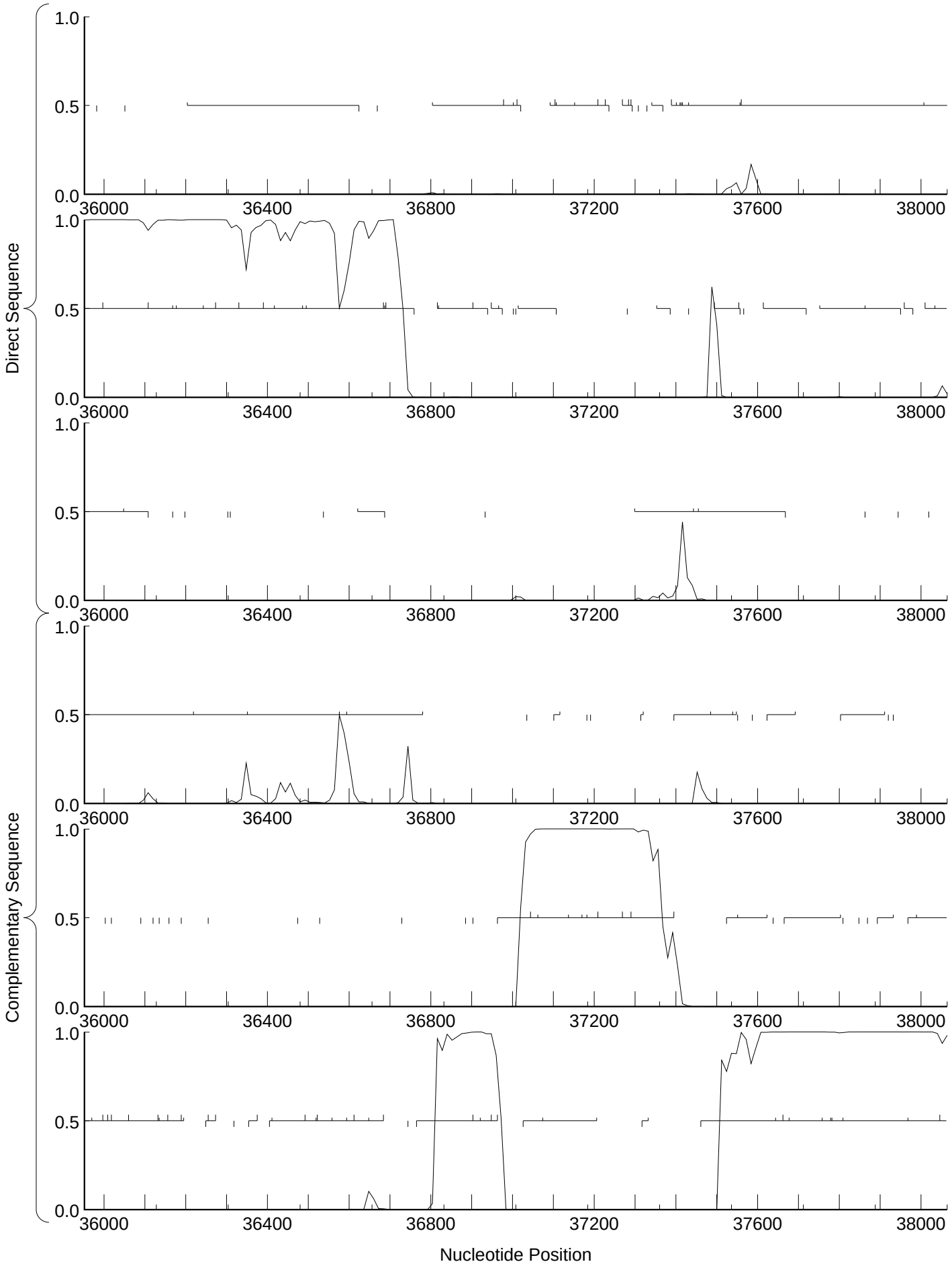

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
30000
30400
30800
31200
31600
Nucleotide Position

ycobacterium phage KayaCho complete corrected sequence, 70838 bp, circularly permuted, Order 4, Window 96, Step 12, 17/35

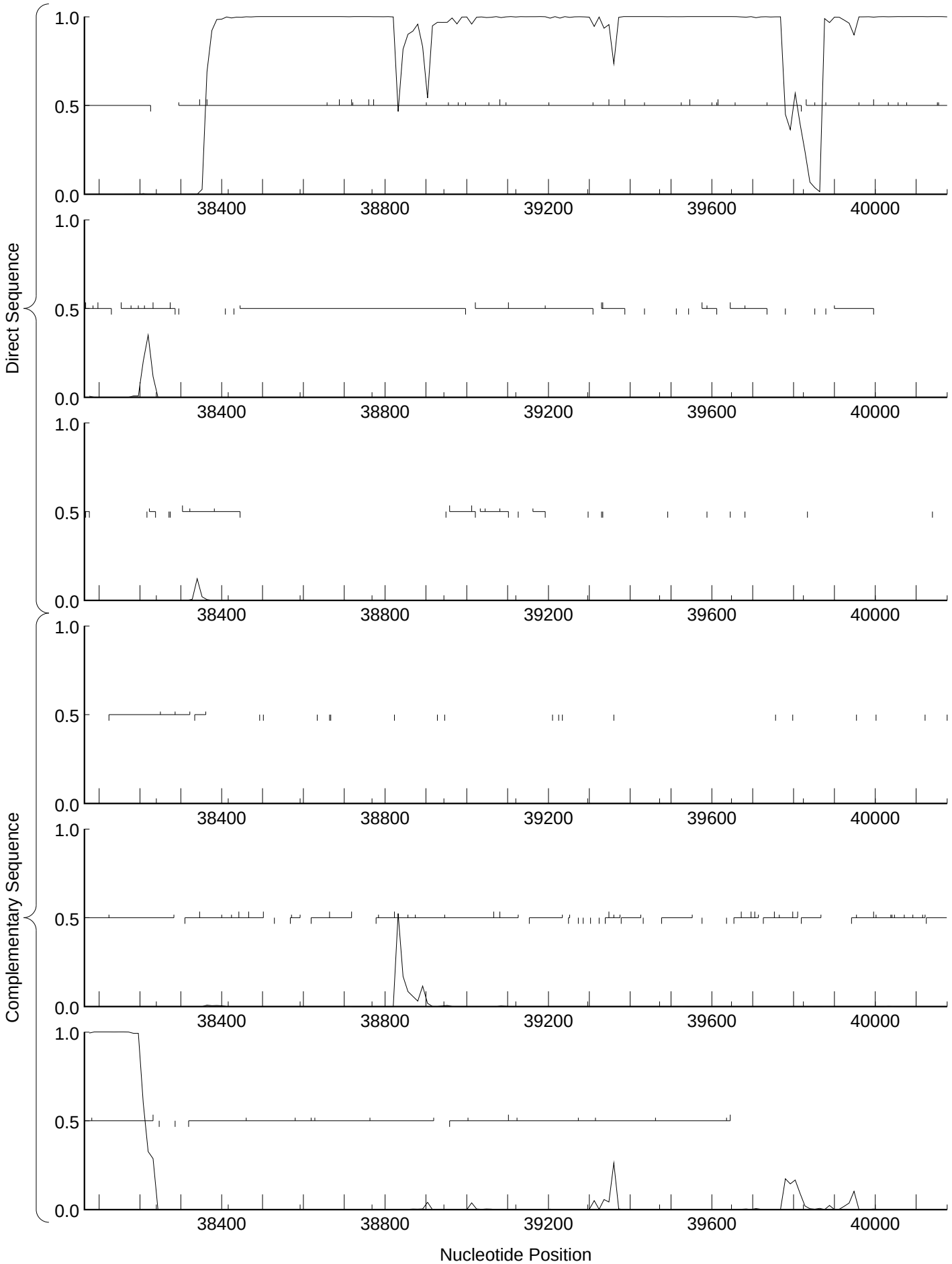


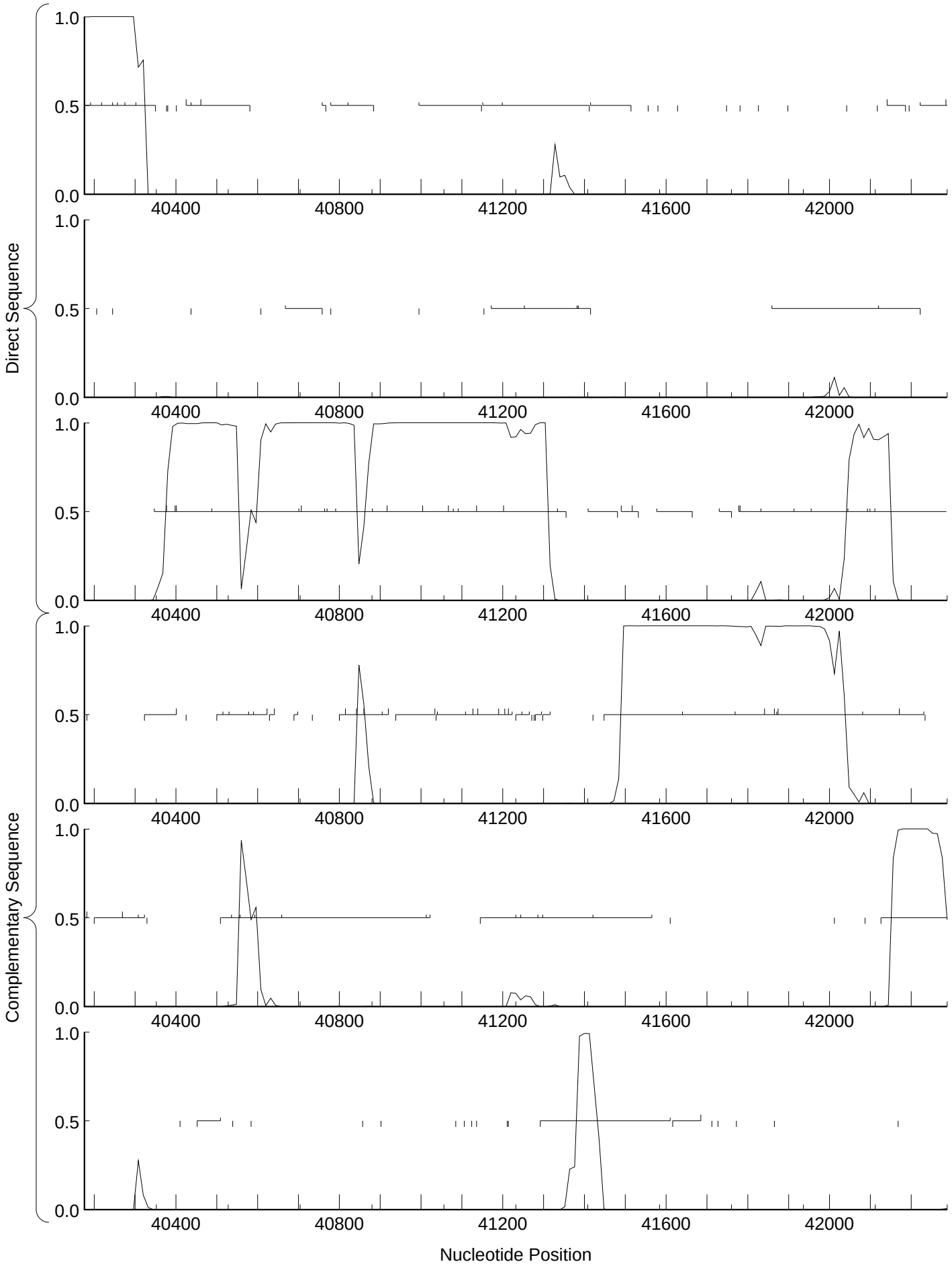
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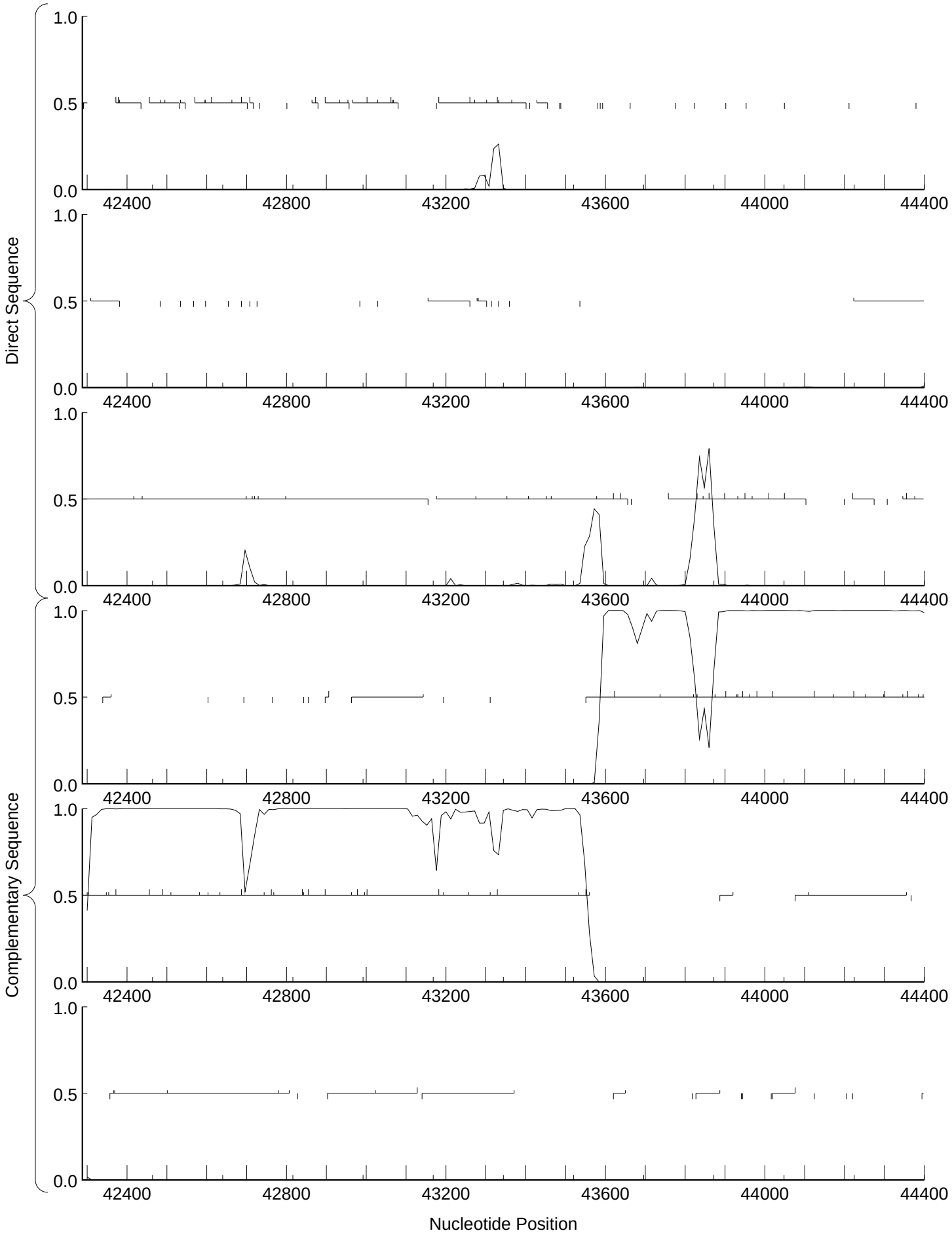


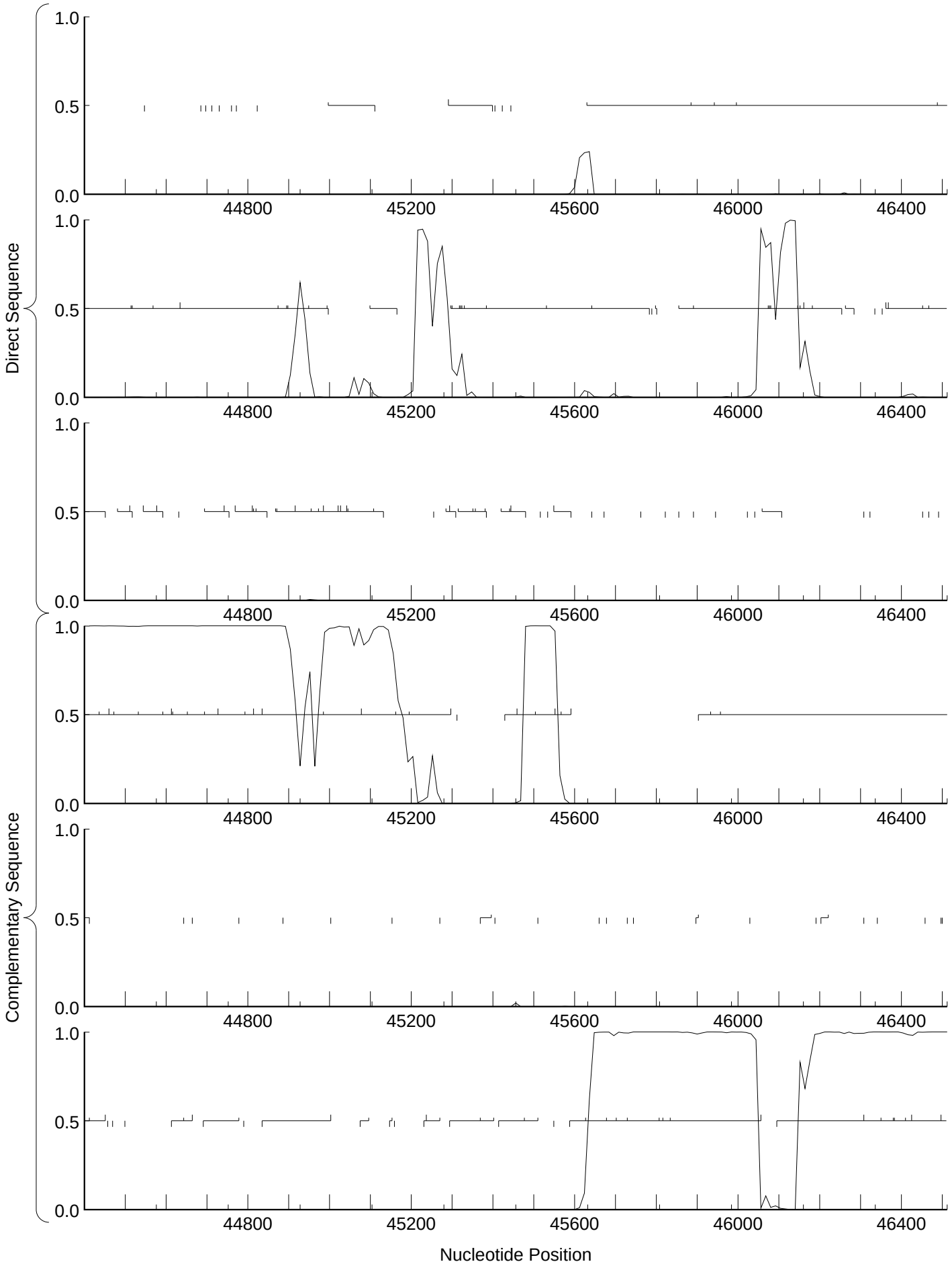

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
36000
36400
36800
37200
37600
38000
Nucleotide Position

Mycobacterium phage KayaCho complete corrected sequence, 70838 bp, circularly permuted, Order 4, Window 96, Step 12, 20/35

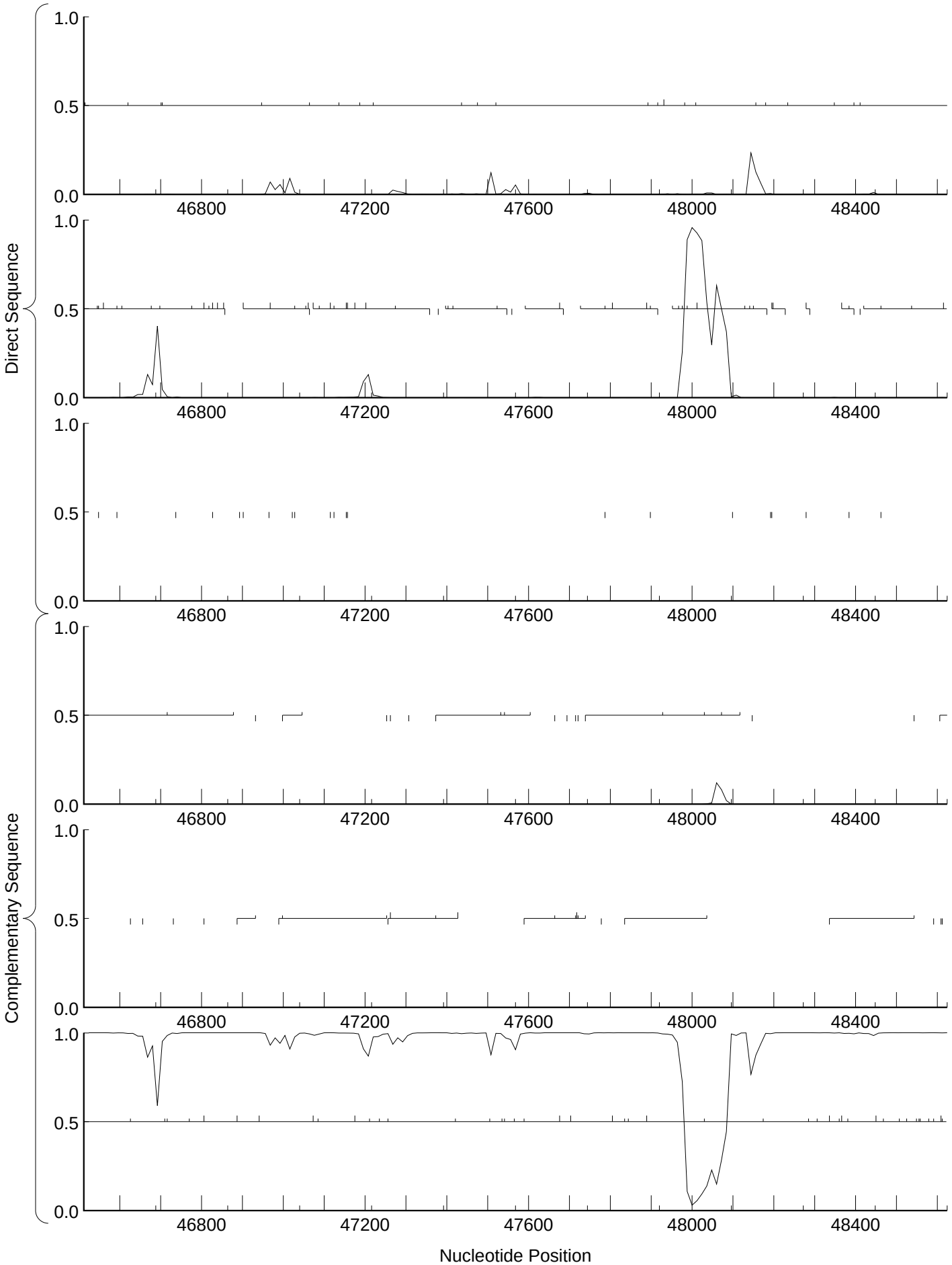


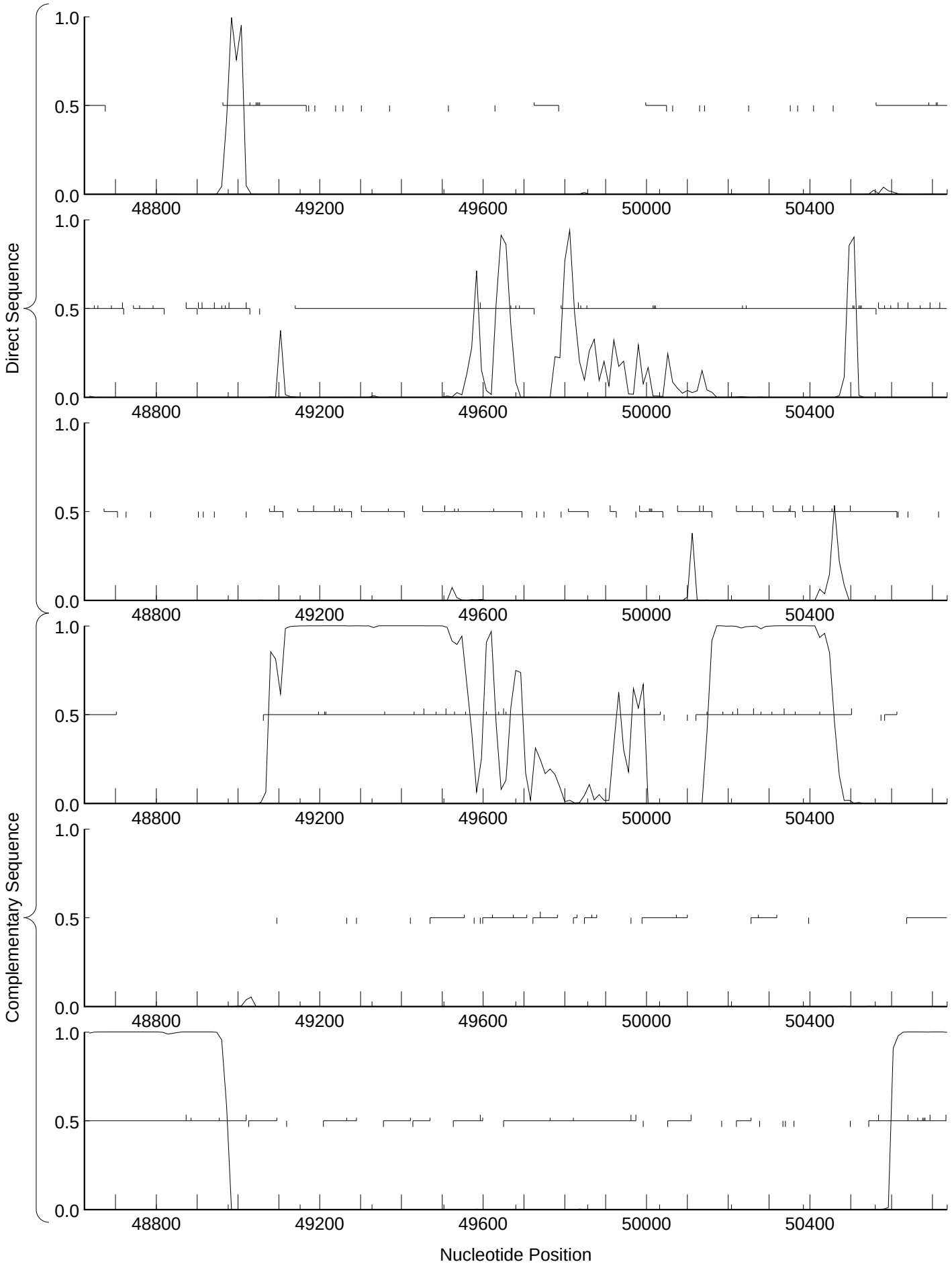

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
40400
40800
41200
41600
42000
Nucleotide Position

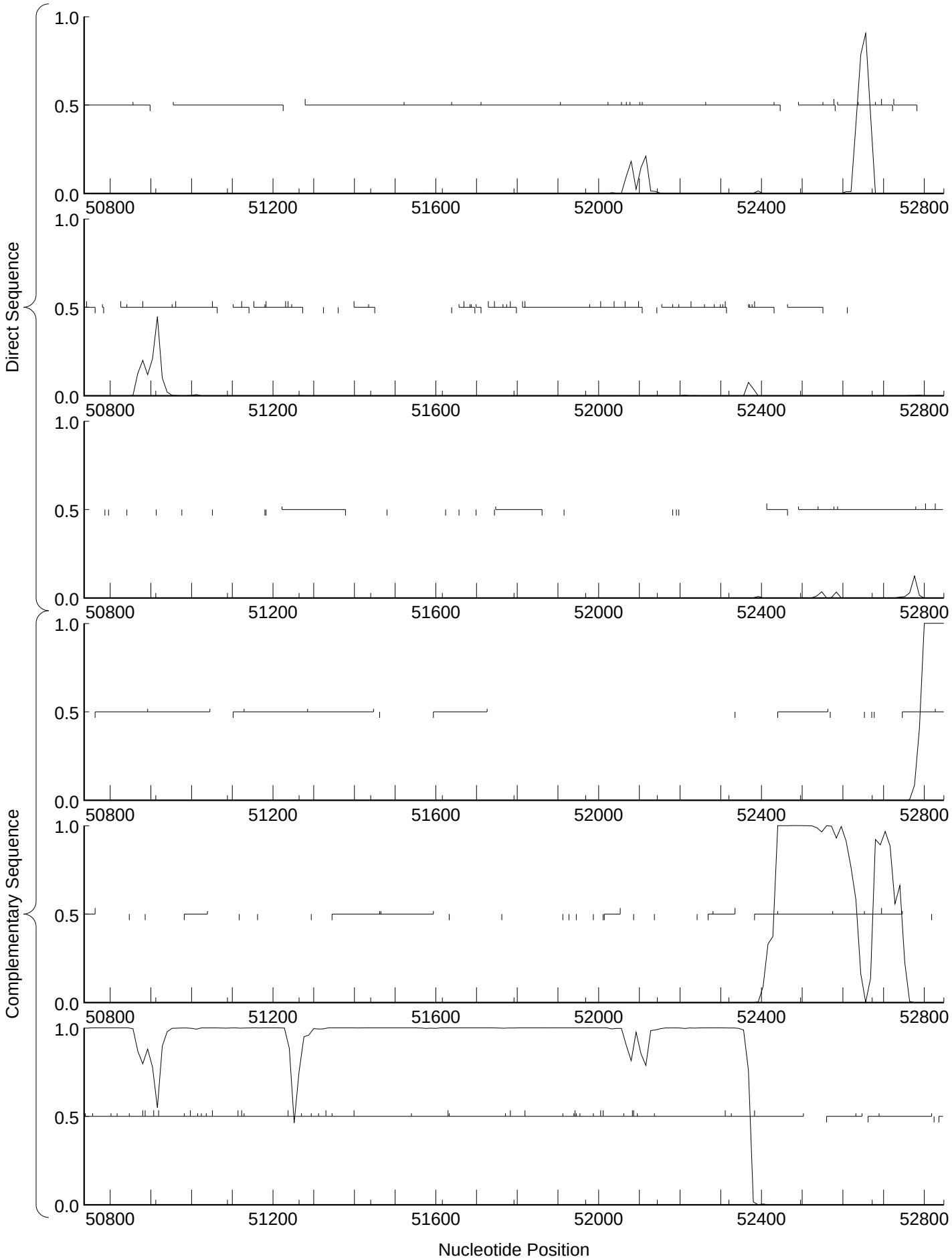

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
42400
42800
43200
43600
44000
44400
Nucleotide Position


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

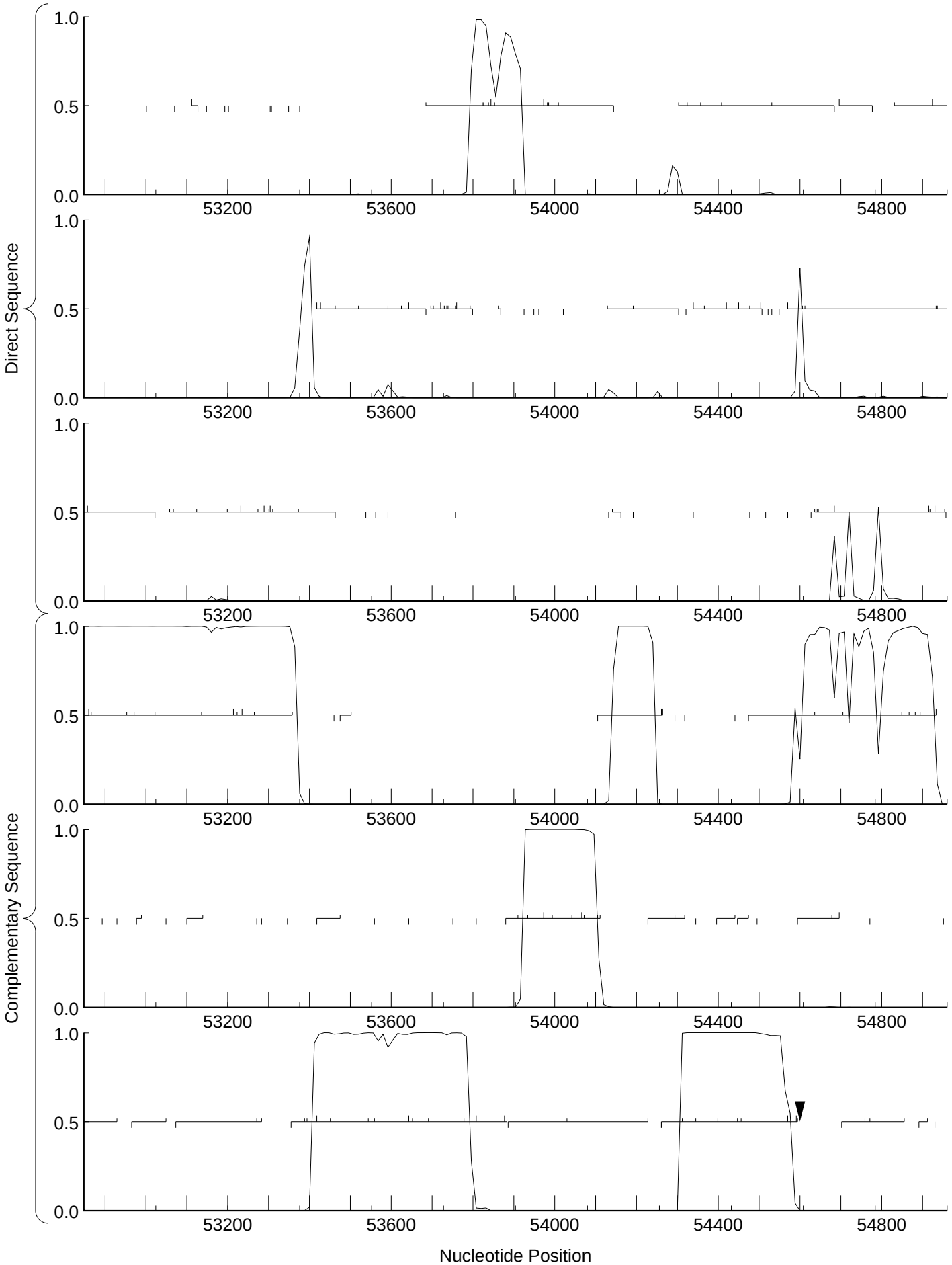
Mycobacterium phage KayaCho complete corrected sequence, 70838 bp, circularly permuted, Order 4, Window 96, Step 12, 24/35

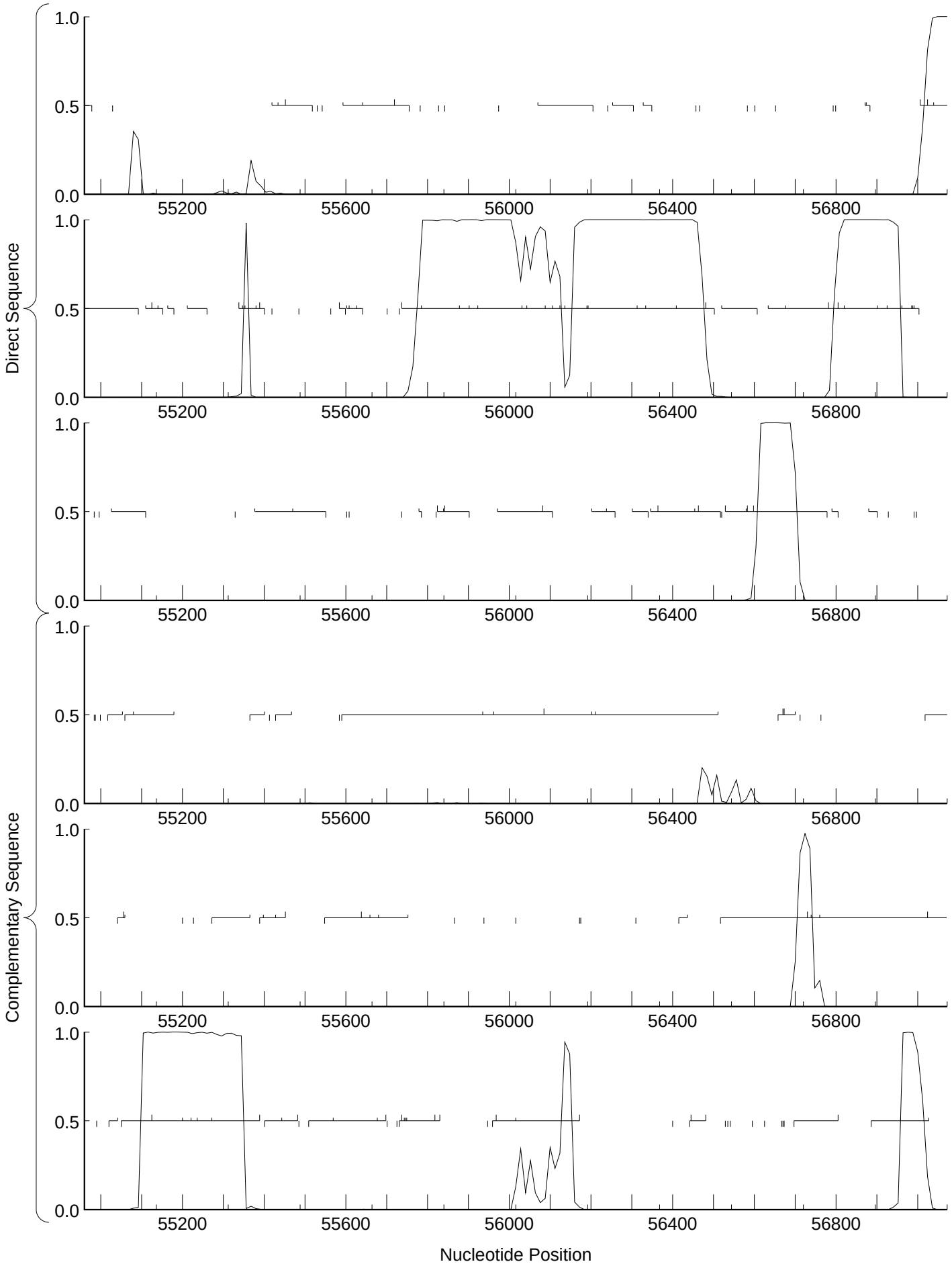


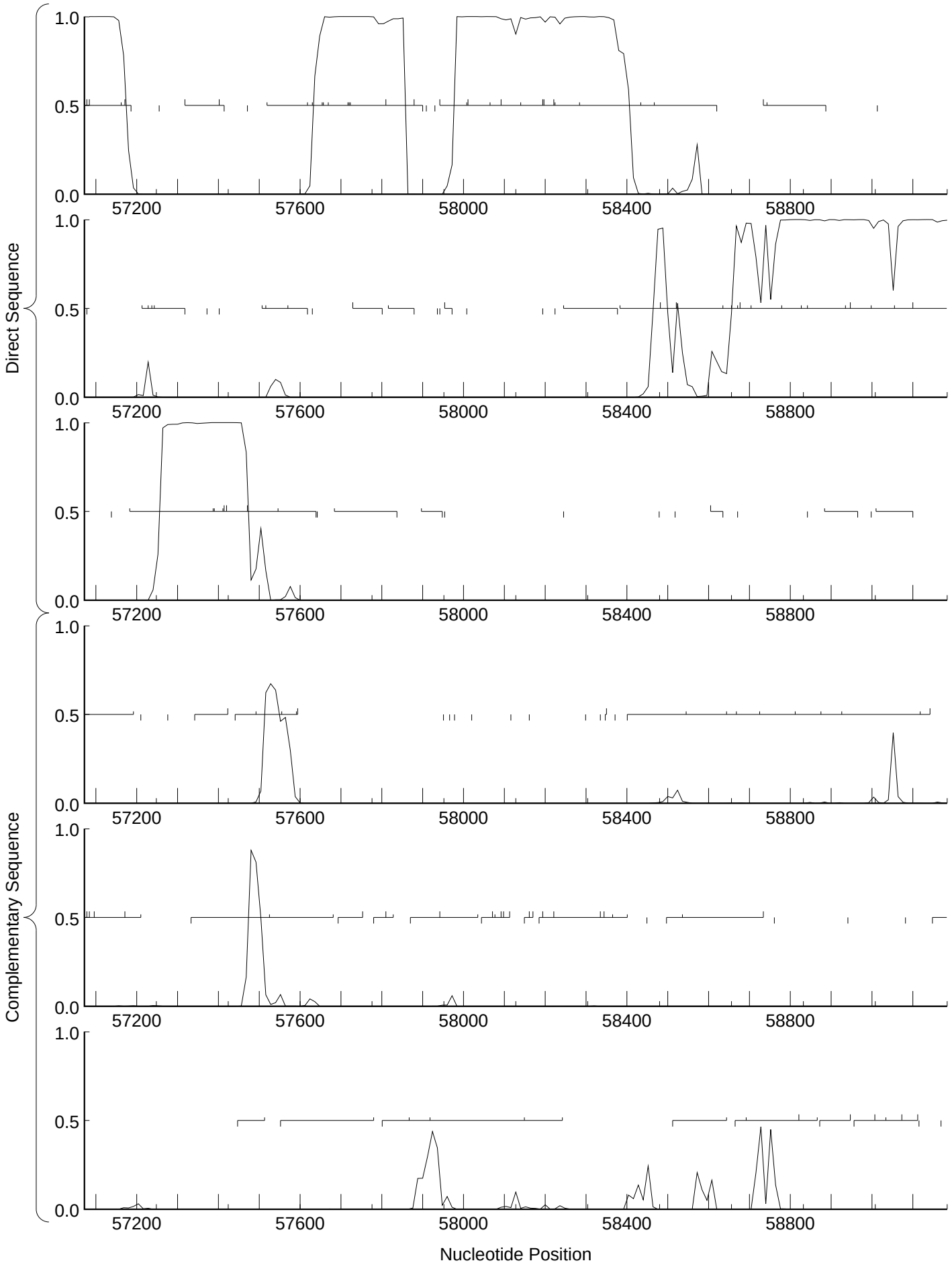

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
48800
49200
49600
50000
50400
Nucleotide Position


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

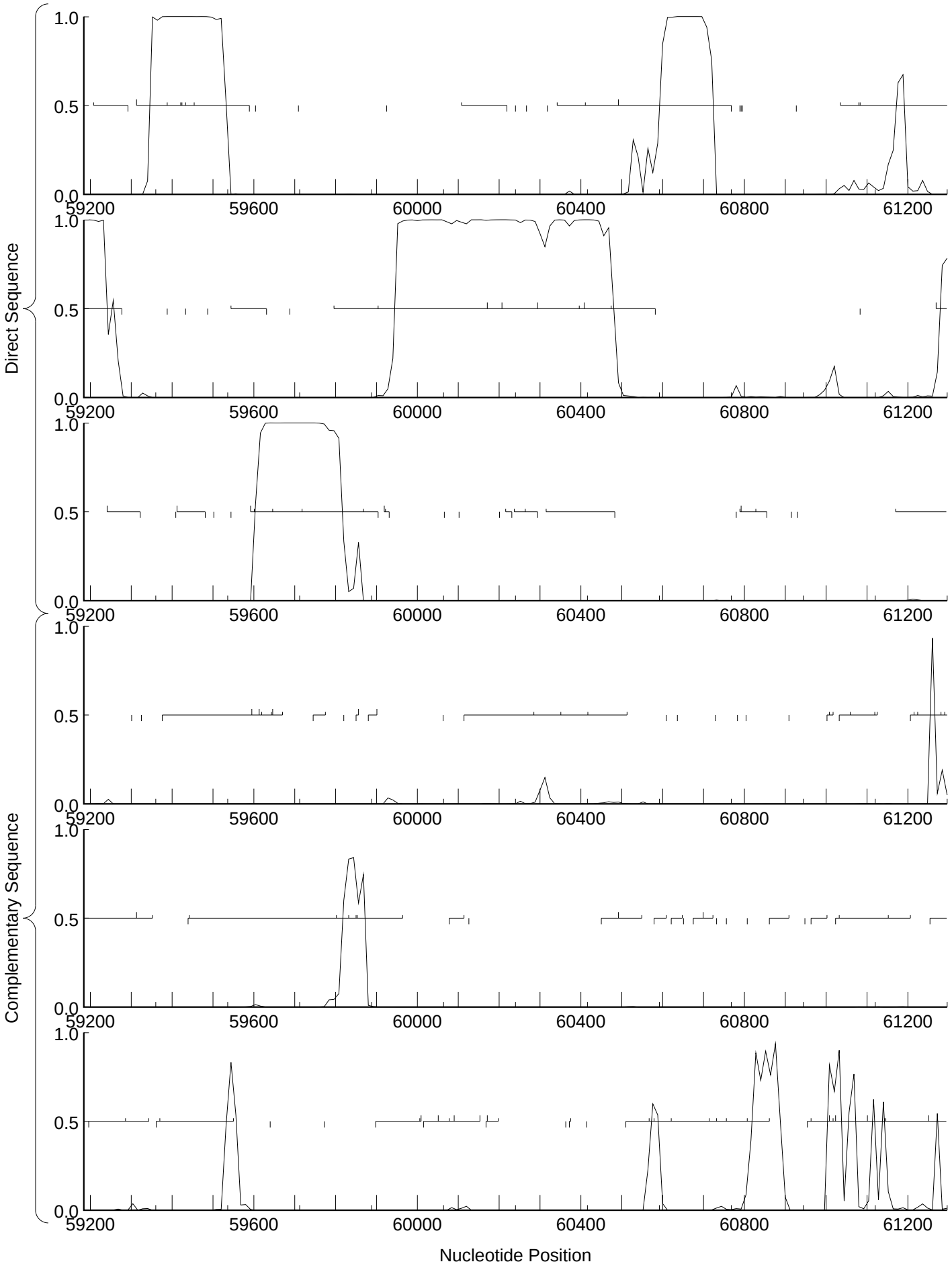
Mycobacterium phage KayaCho complete corrected sequence, 70838 bp, circularly permuted, Order 4, Window 96, Step 12, 27/35



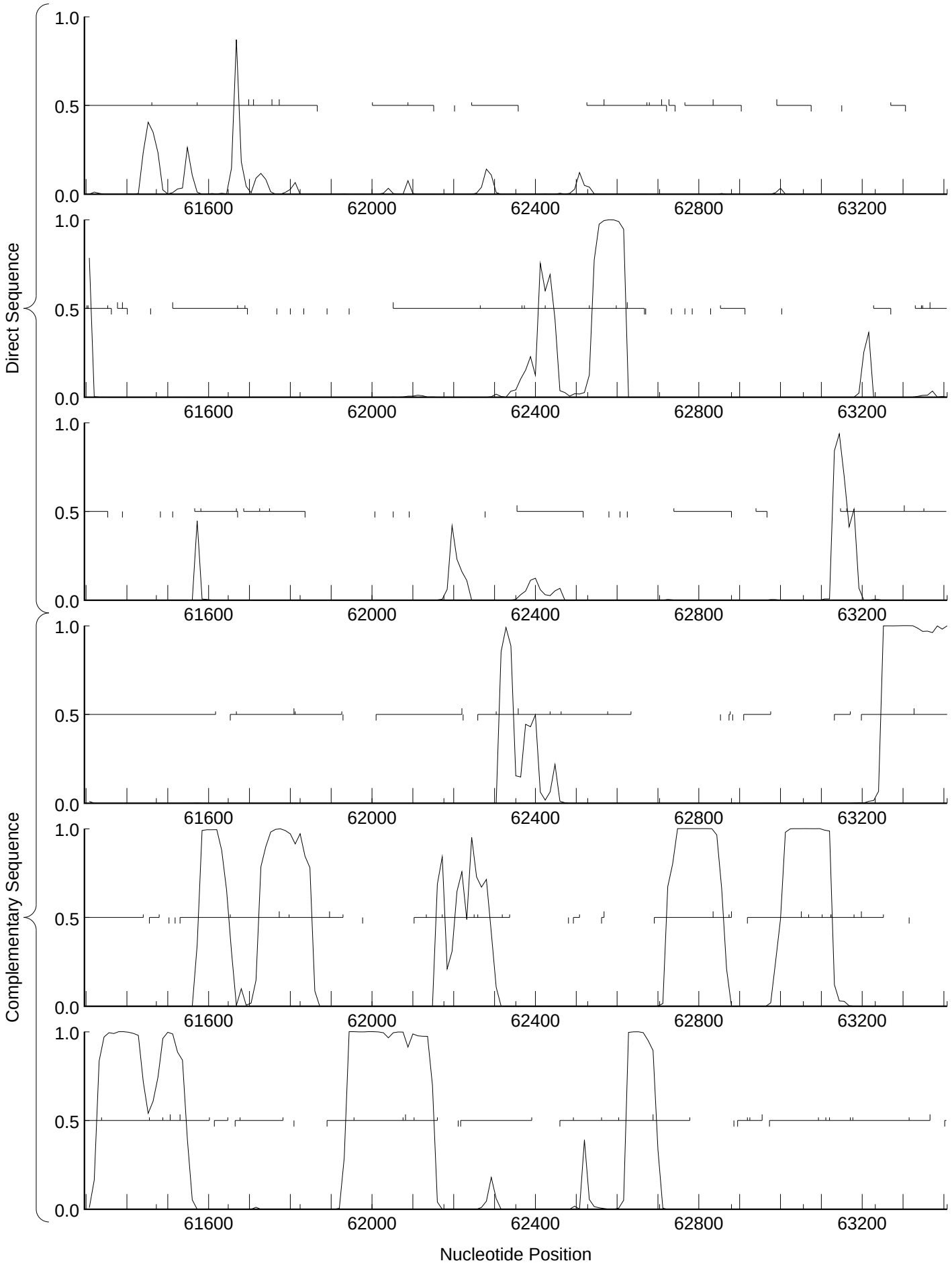

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
55200
55600
56000
56400
56800
Nucleotide Position

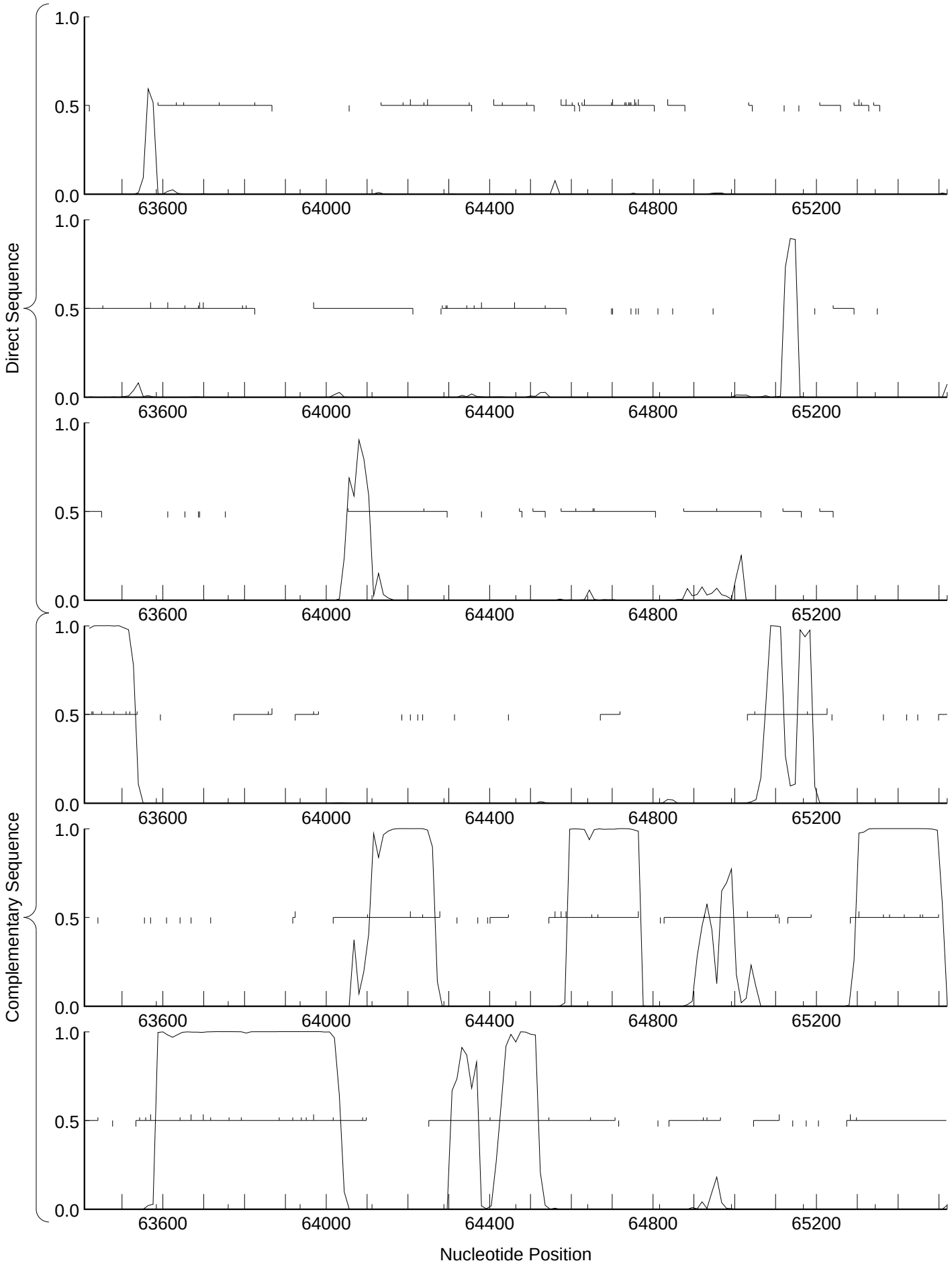

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Complementary Sequence
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0.0
57200
57600
58000
58400
58800
Nucleotide Position

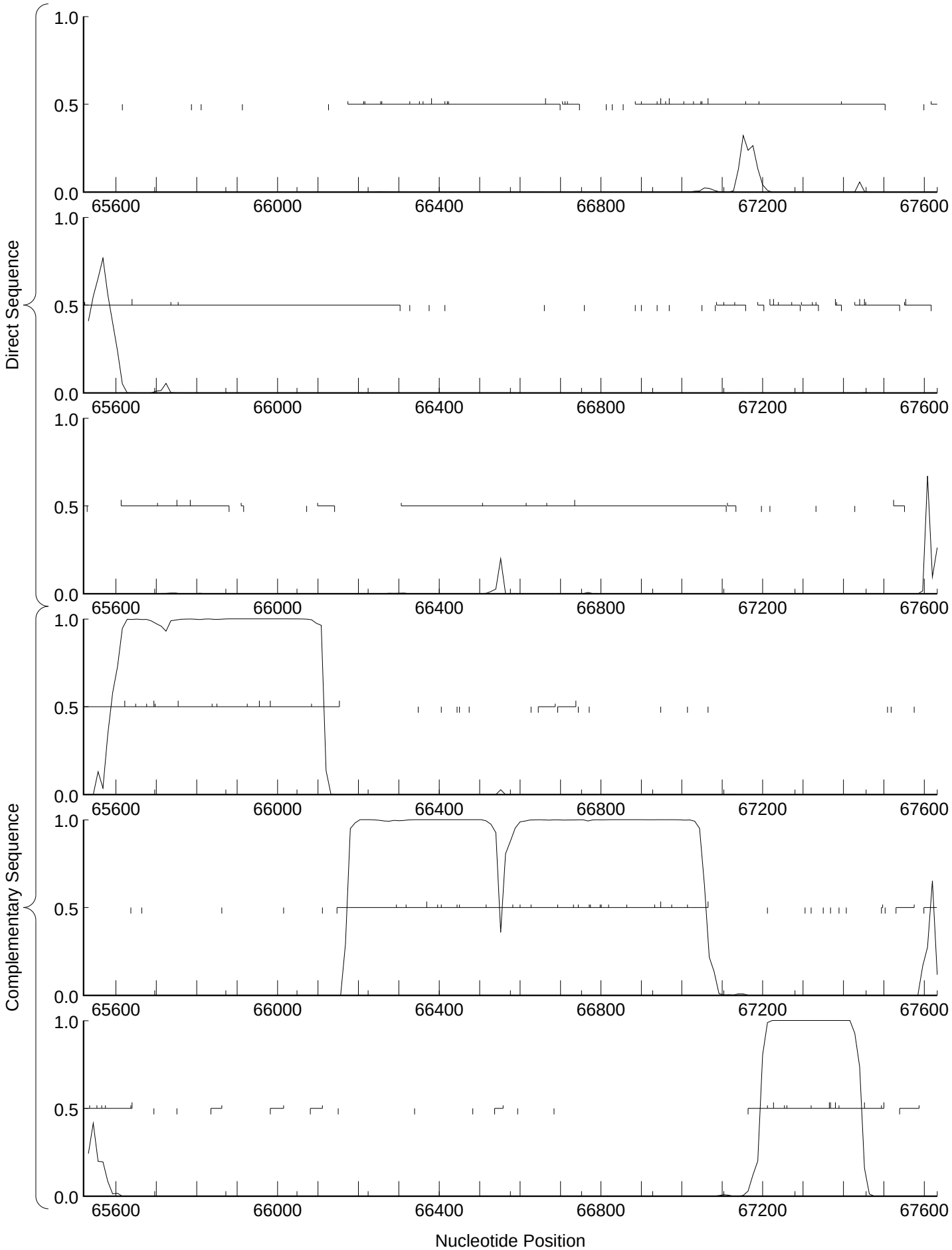
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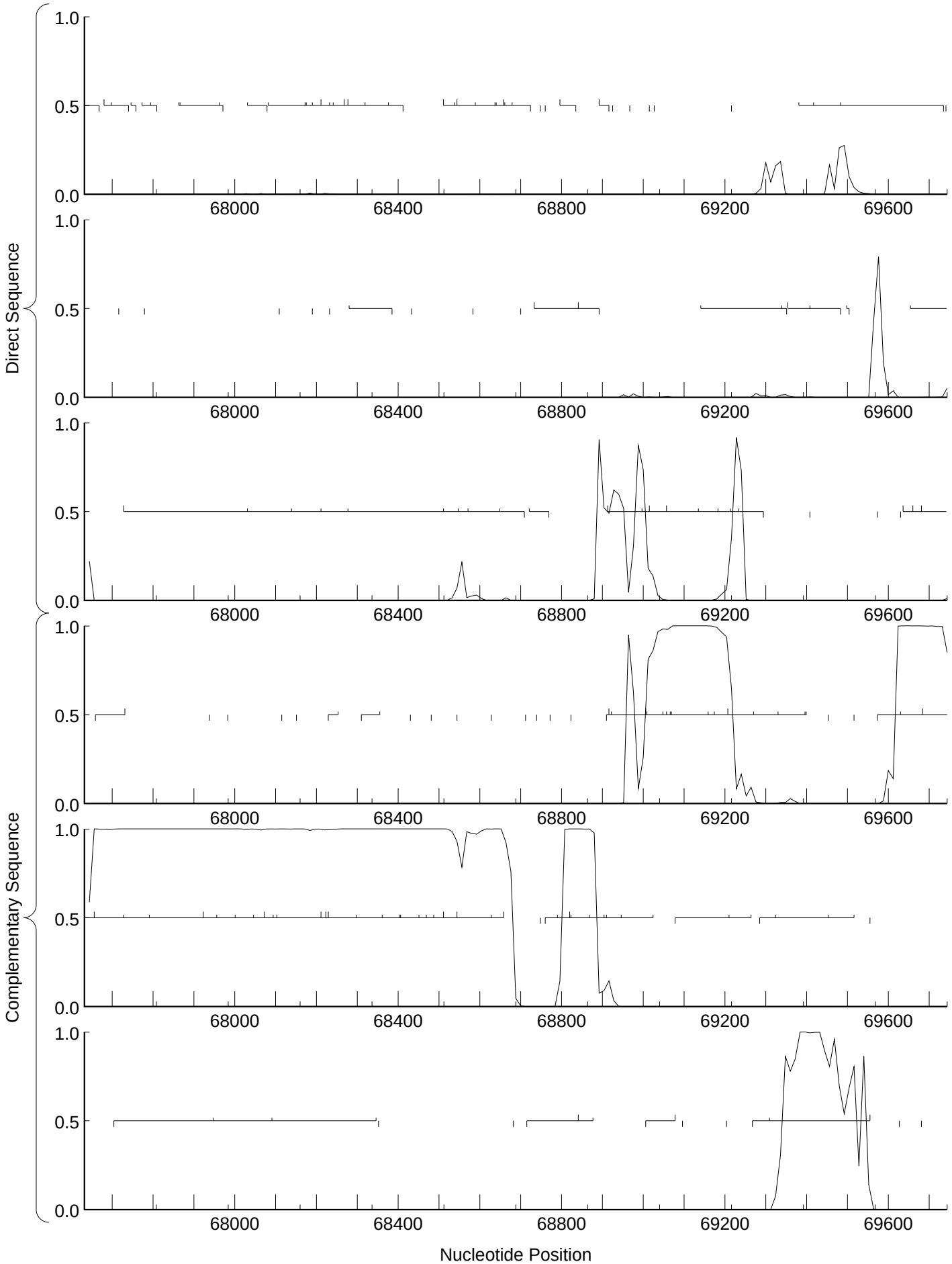


ycobacterium phage KayaCho complete corrected sequence, 70838 bp, circularly permuted, Order 4, Window 96, Step 12, 31/35




Direct Sequence
Complementary Sequence
1.0
0.5
0.0
63600
64000
64400
64800
65200
Nucleotide Position


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
65600
66000
66400
66800
67200
67600
Nucleotide Position


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
68000
68400
68800
69200
69600
Nucleotide Position

ycobacterium phage KayaCho complete corrected sequence, 70838 bp, circularly permuted, Order 4, Window 96, Step 12, 35/35

