GeneMark

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

PROGRAM INFORMATION

```
Sequence         :  Microbacterium phage Phonegingi complete sequence, 39364 bp, circularly permuted, Cluster G
Analysis Date    :  3/28/24 at 12:42:16
Pages            :  20
Sequence Length  :  39364 bp
GC Content       :   67.57%

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     :  -
Author     :  -

Order      :  4

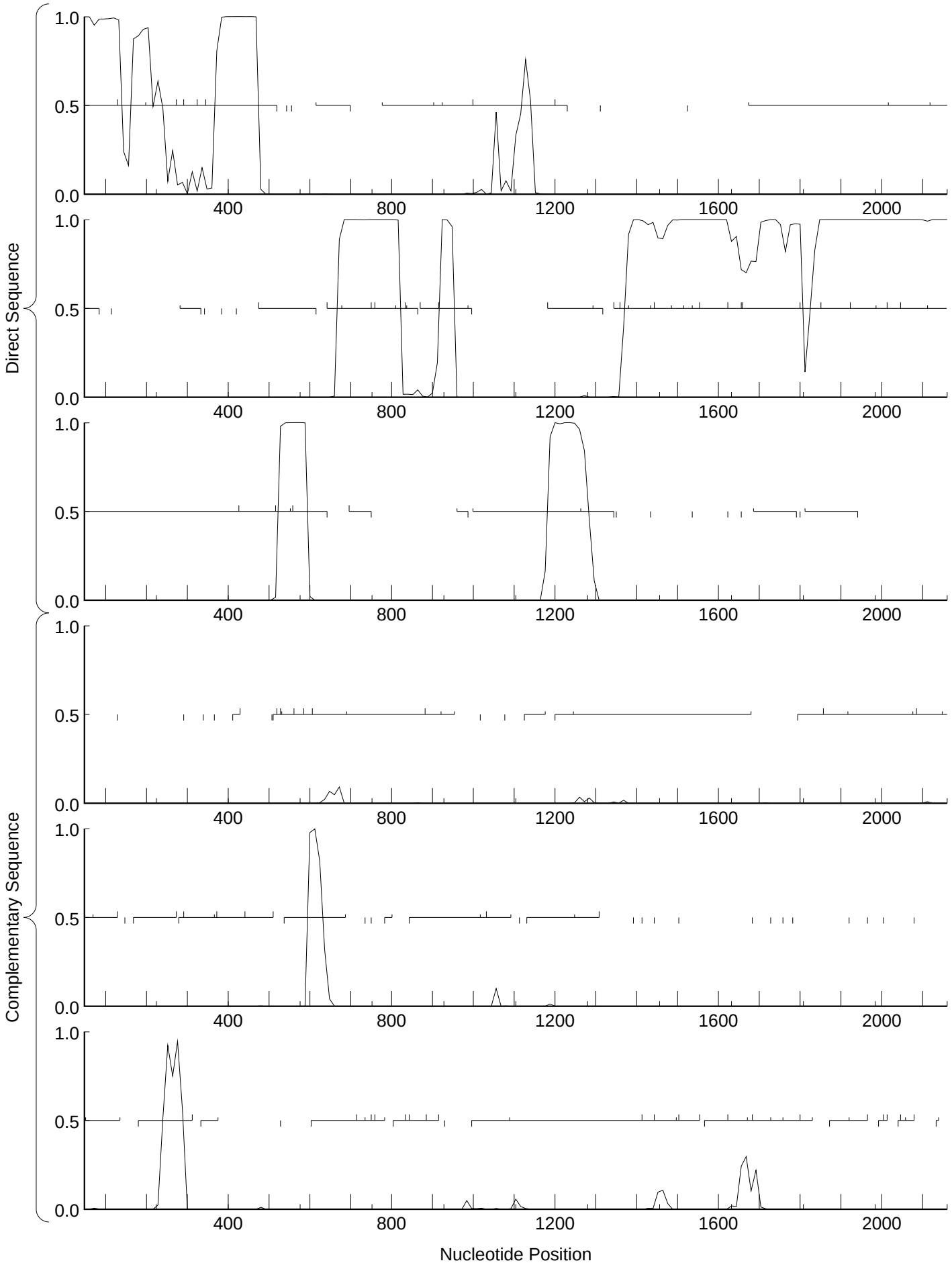

  Send questions / comments to:
      Dr. M. Borodovsky
      Georgia Institute of Technology
      School of Biology
      Atlanta, GA  30332-0230
```

Matrix notes & comments

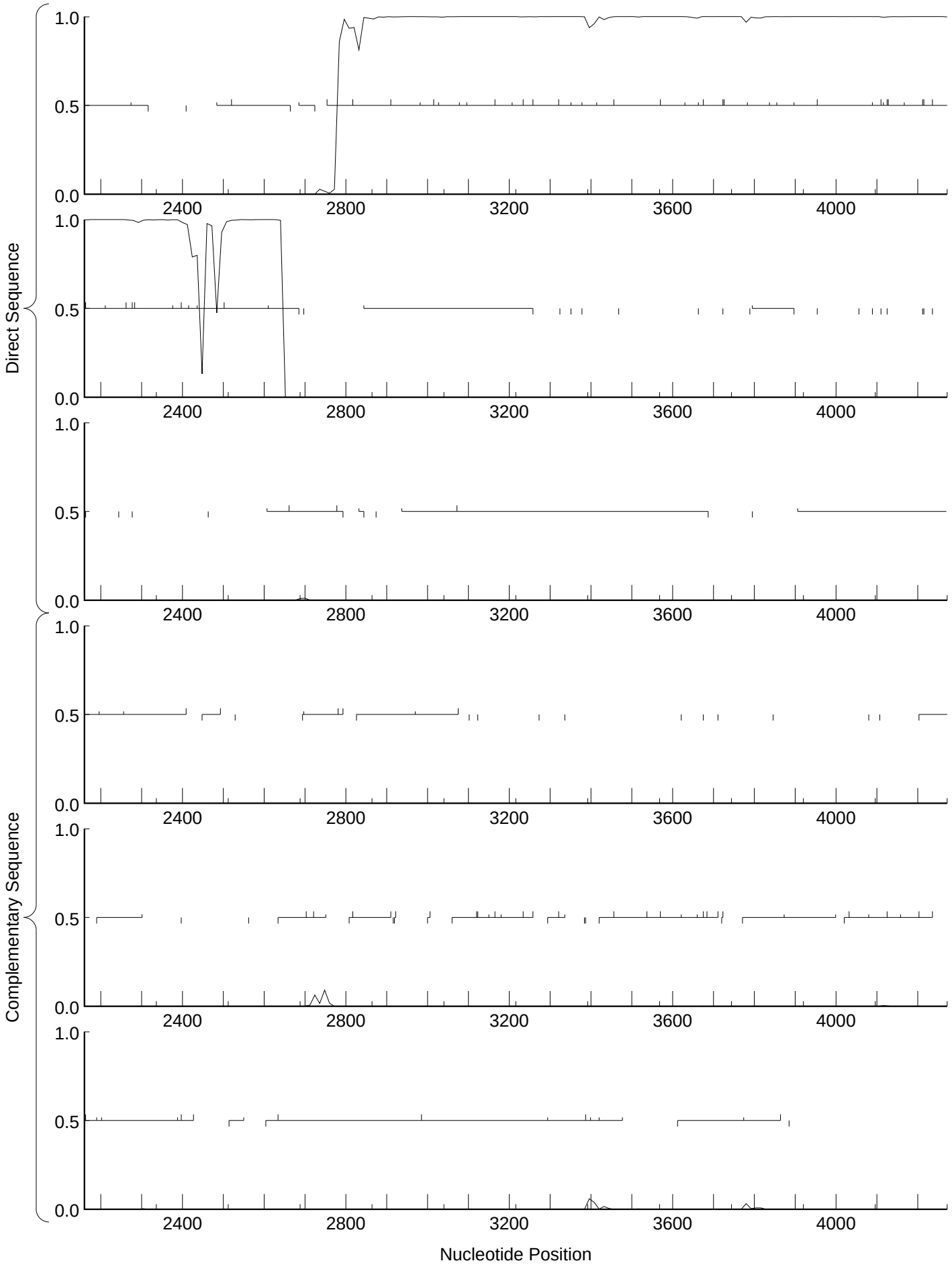
Training set derived by GeneMarkS, 4.30 October 2014
Fri Sep 7 18:42:59 2018

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

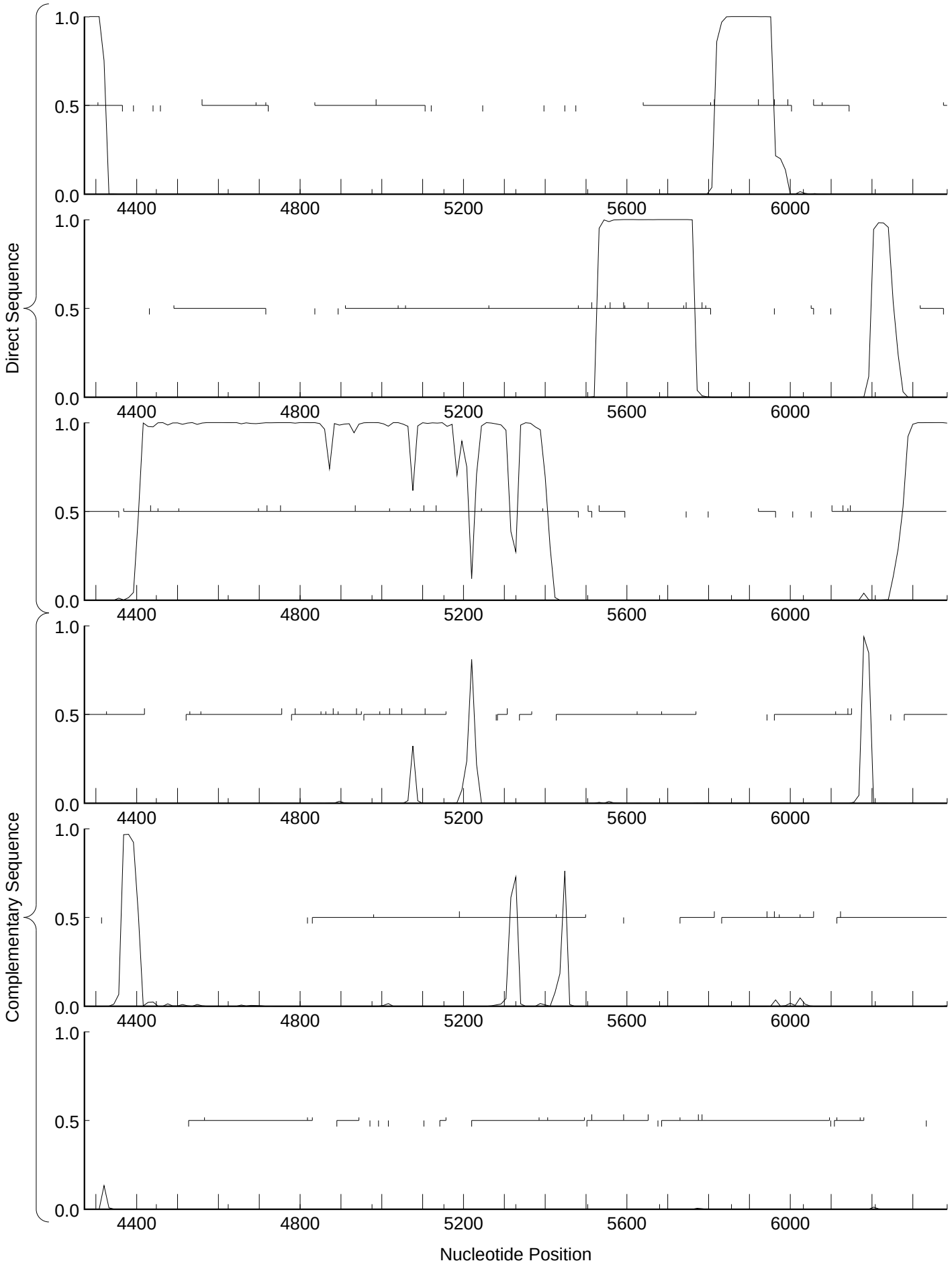
obacterium phage Phonegingi complete sequence, 39364 bp, circularly permuted, Cluster GA, Order 4, Window 96, Step 12, 2/20



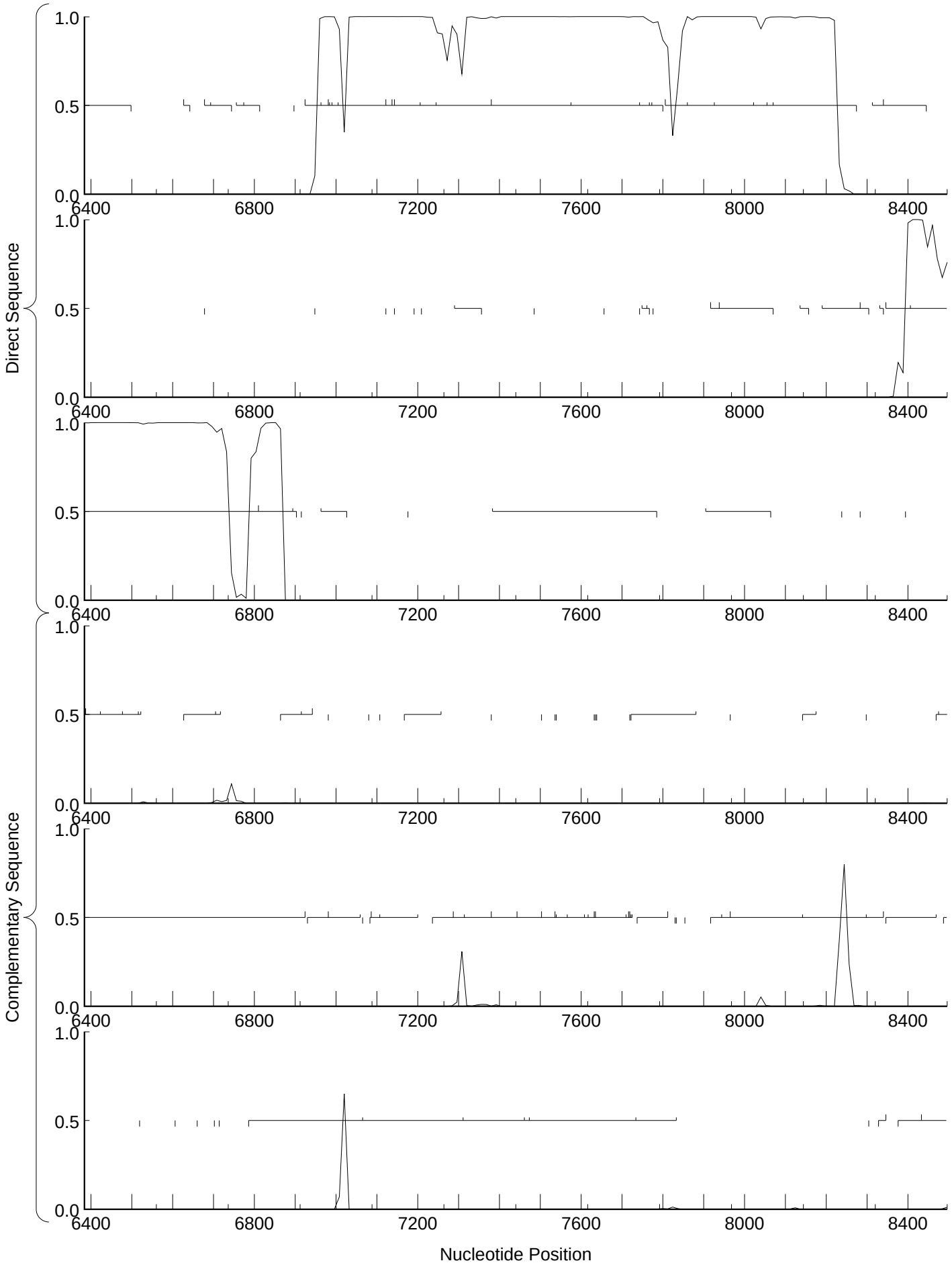
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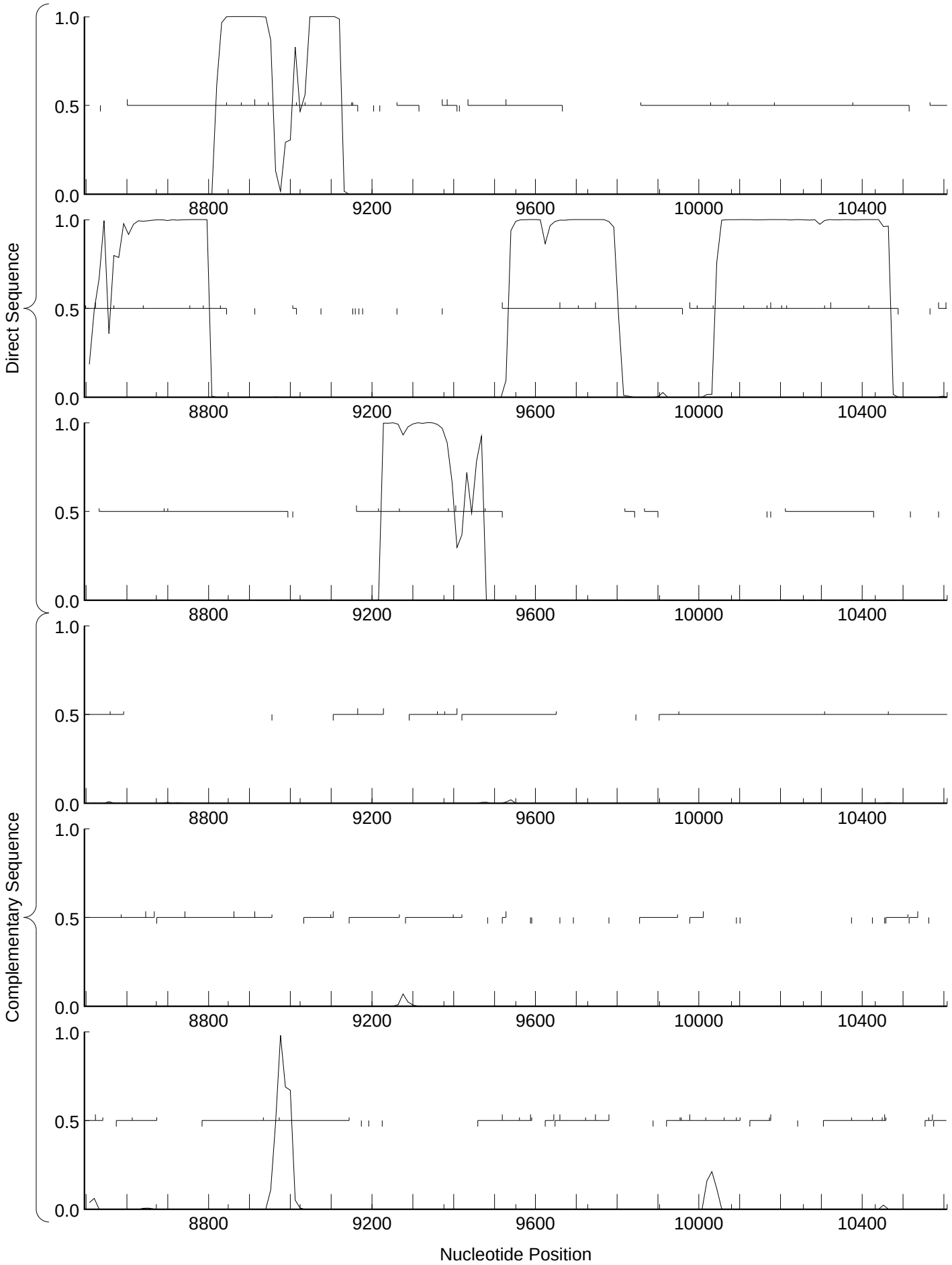
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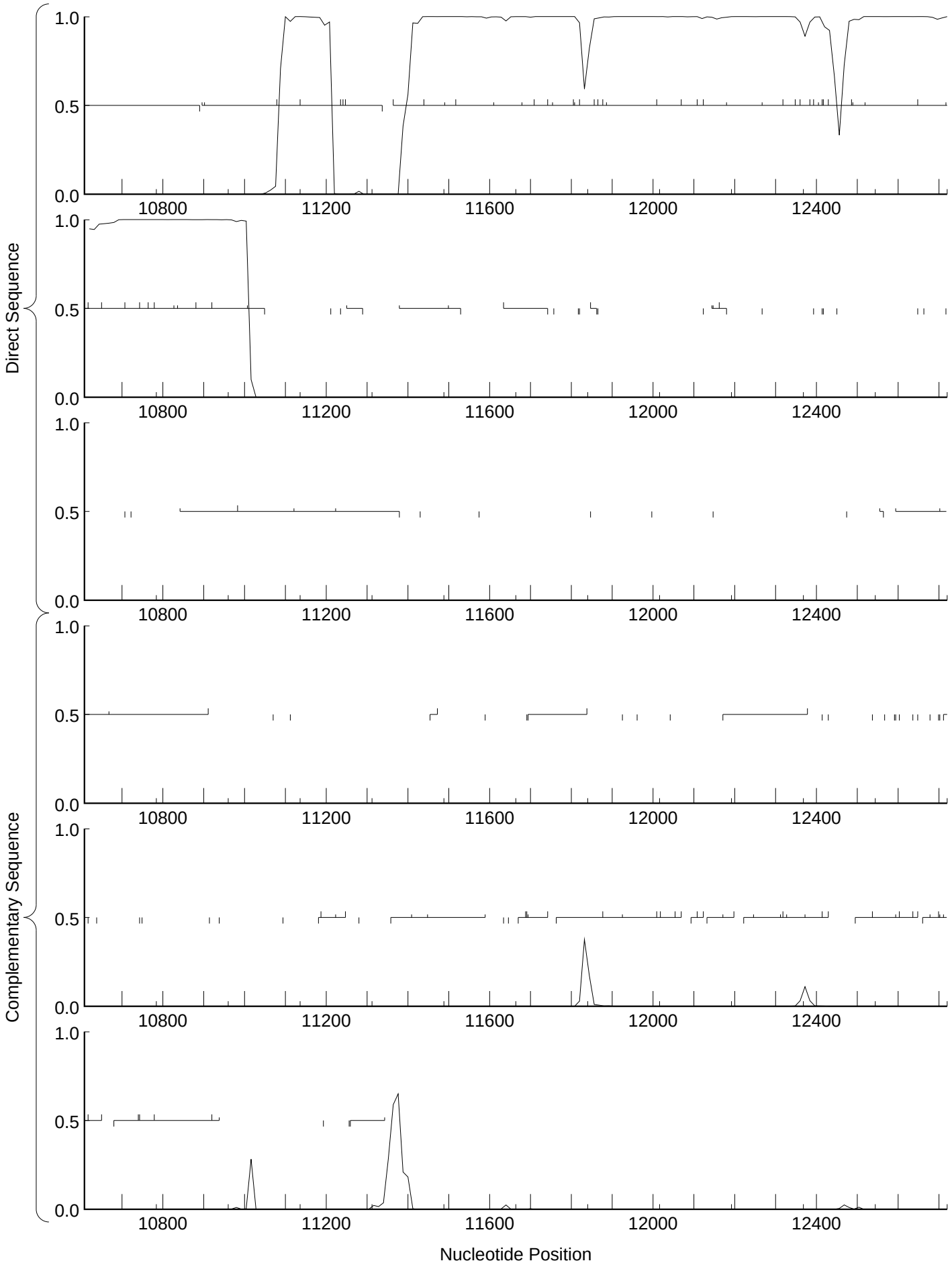
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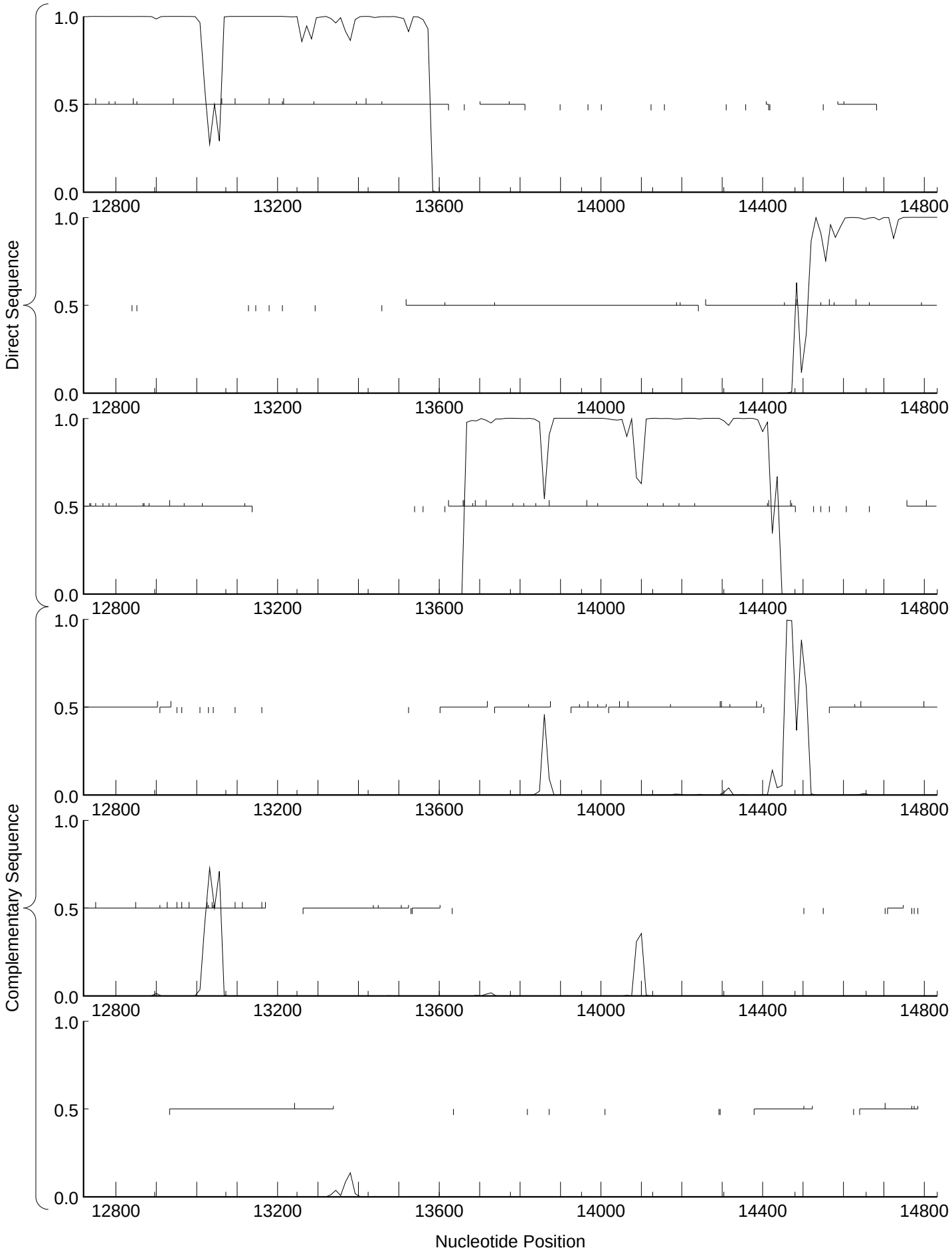
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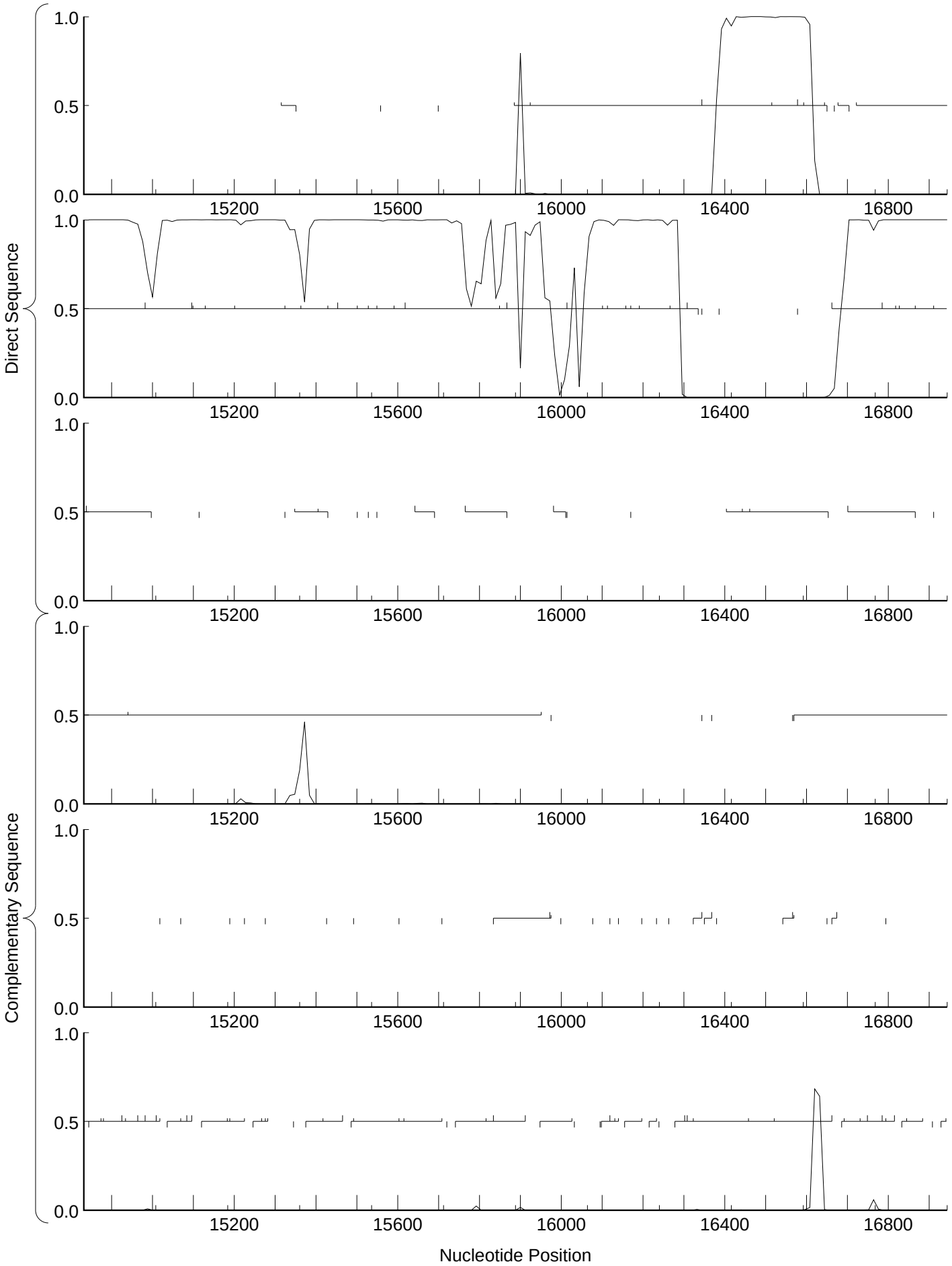
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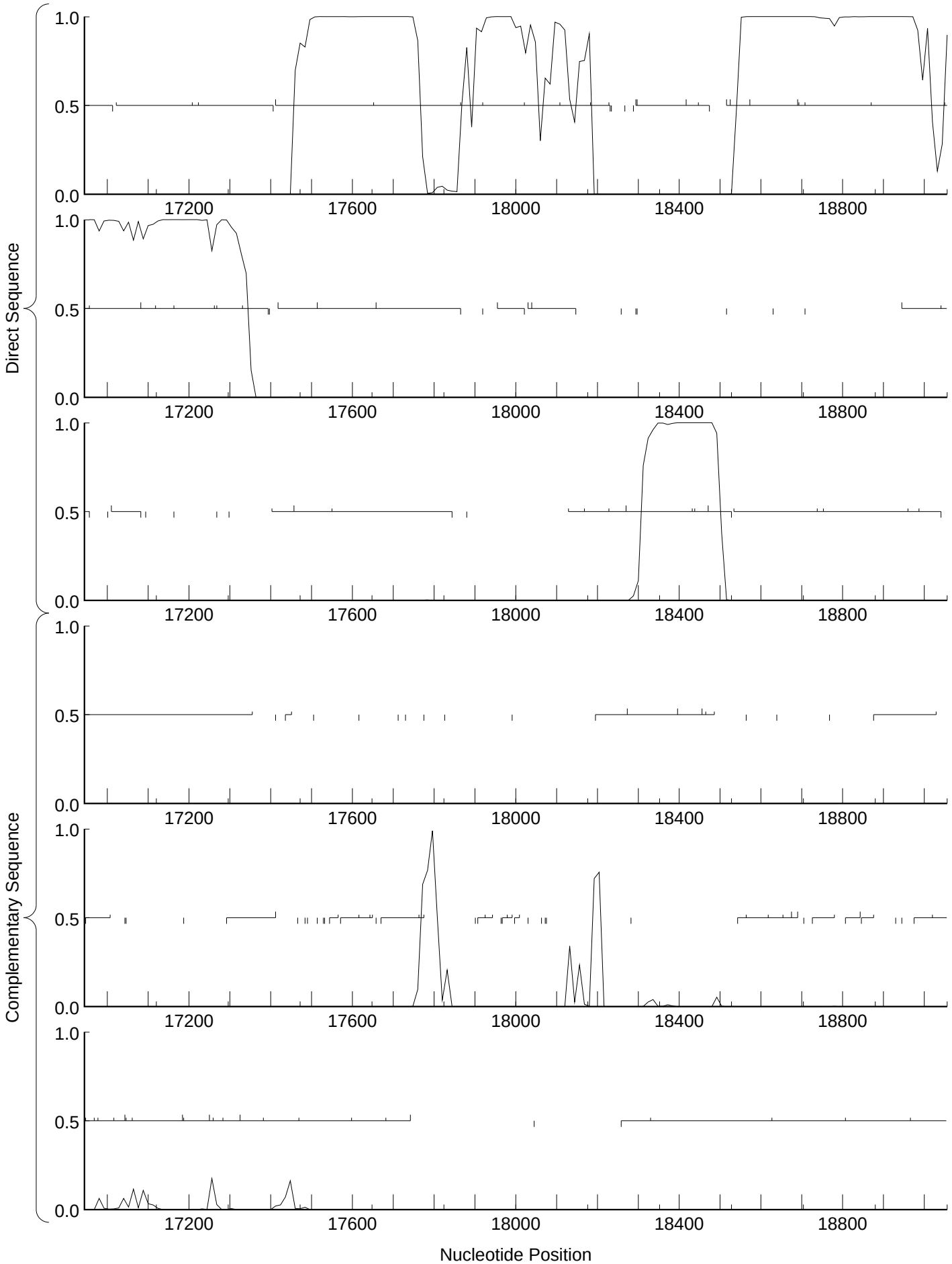


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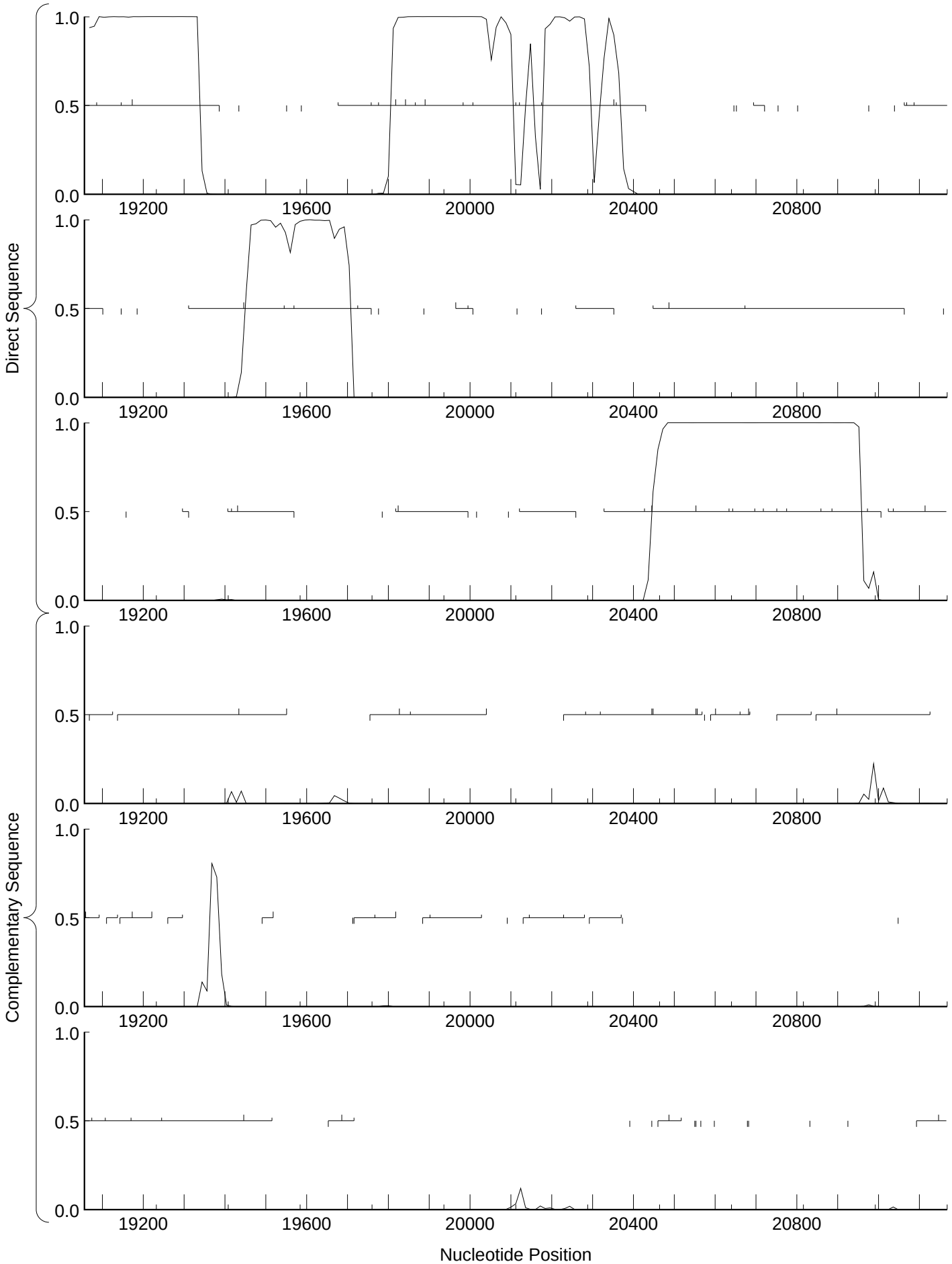


obacterium phage Phonegingi complete sequence, 39364 bp, circularly permuted, Cluster GA, Order 4, Window 96, Step 12, 9/20

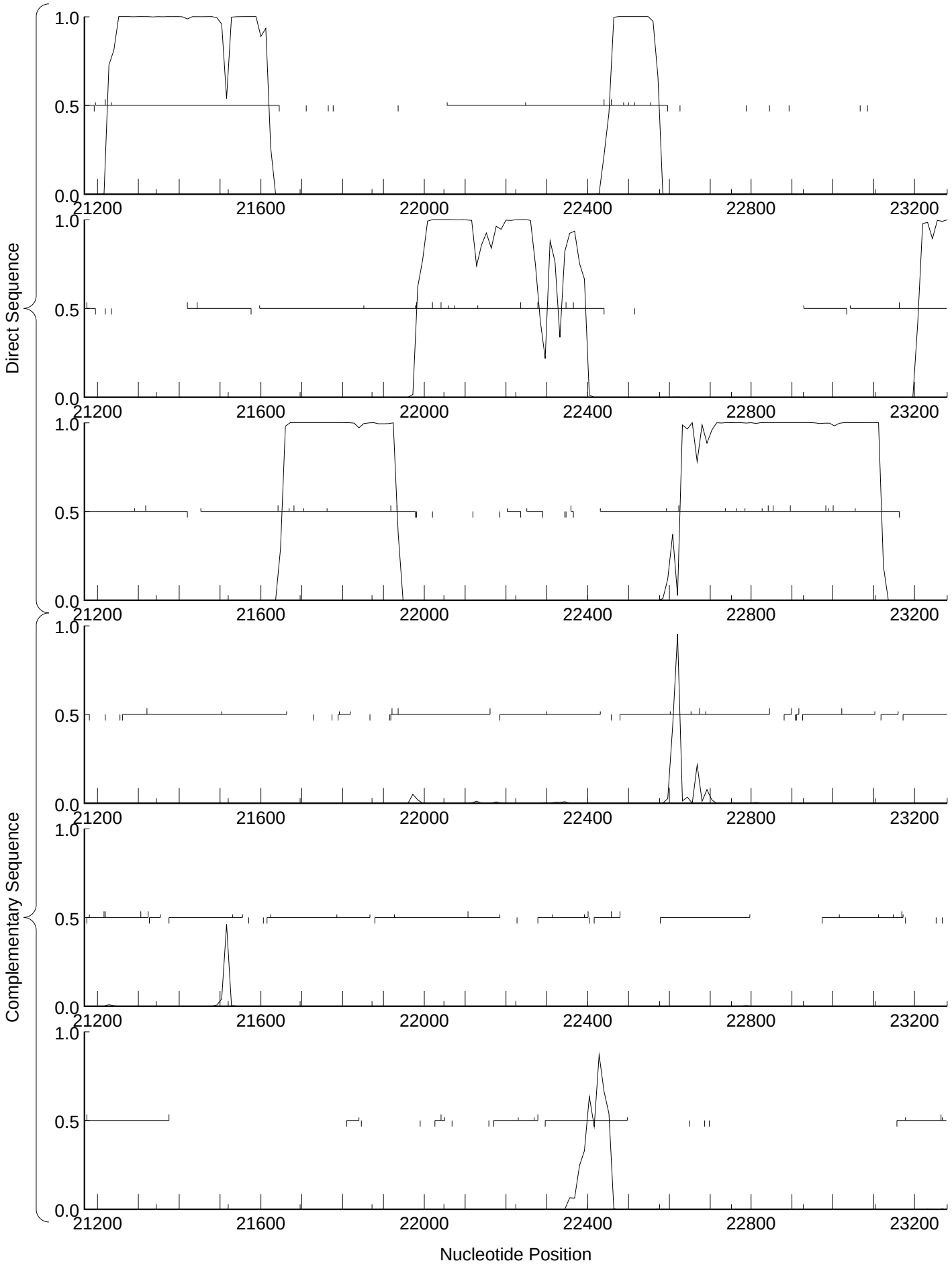



Direct Sequence
Complementary Sequence
1.0
0.5
0.0
17200
17600
18000
18400
18800
Nucleotide Position

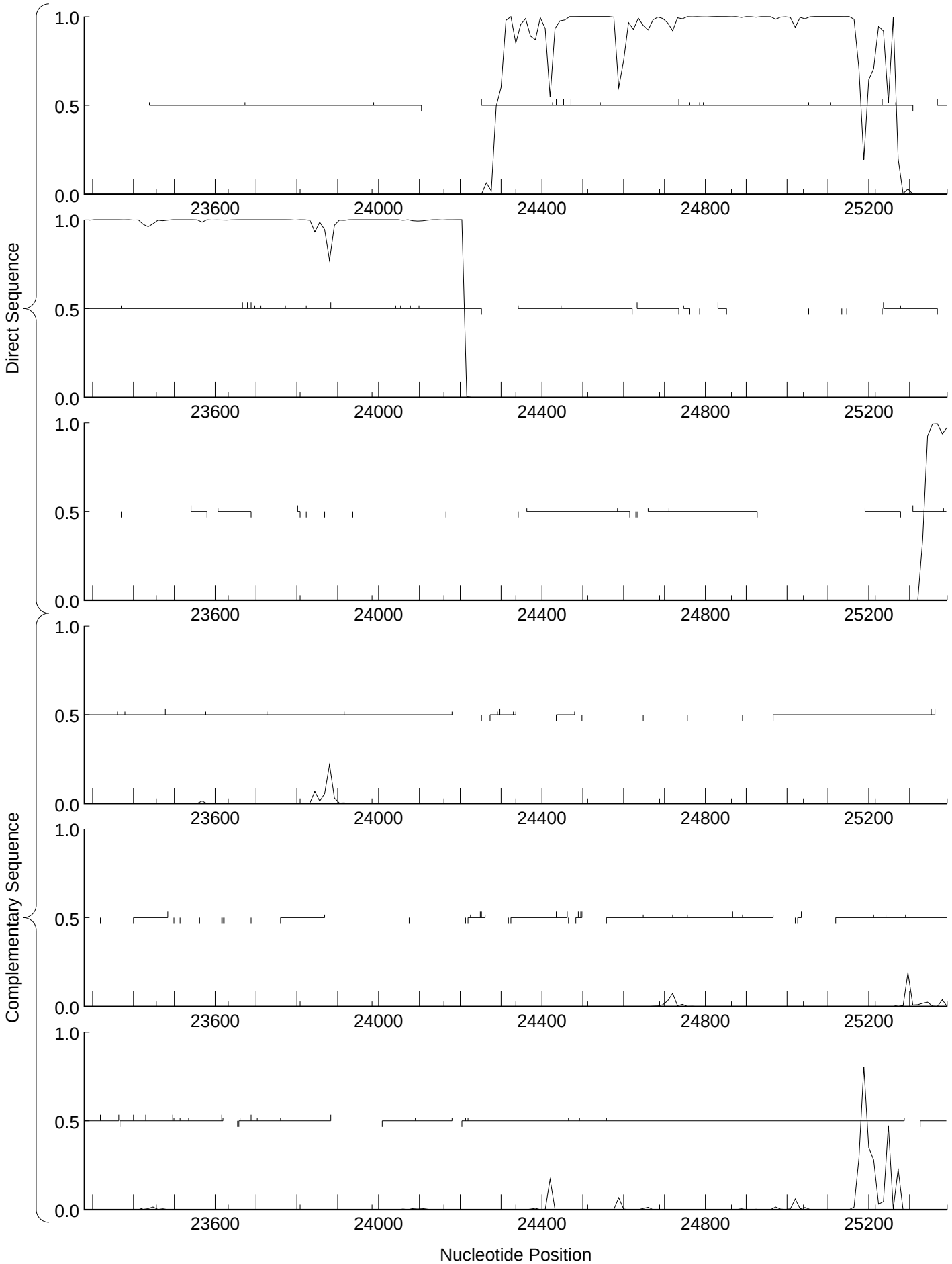
bacterium phage Phonegingi complete sequence, 39364 bp, circularly permuted, Cluster GA, Order 4, Window 96, Step 12, 11/20

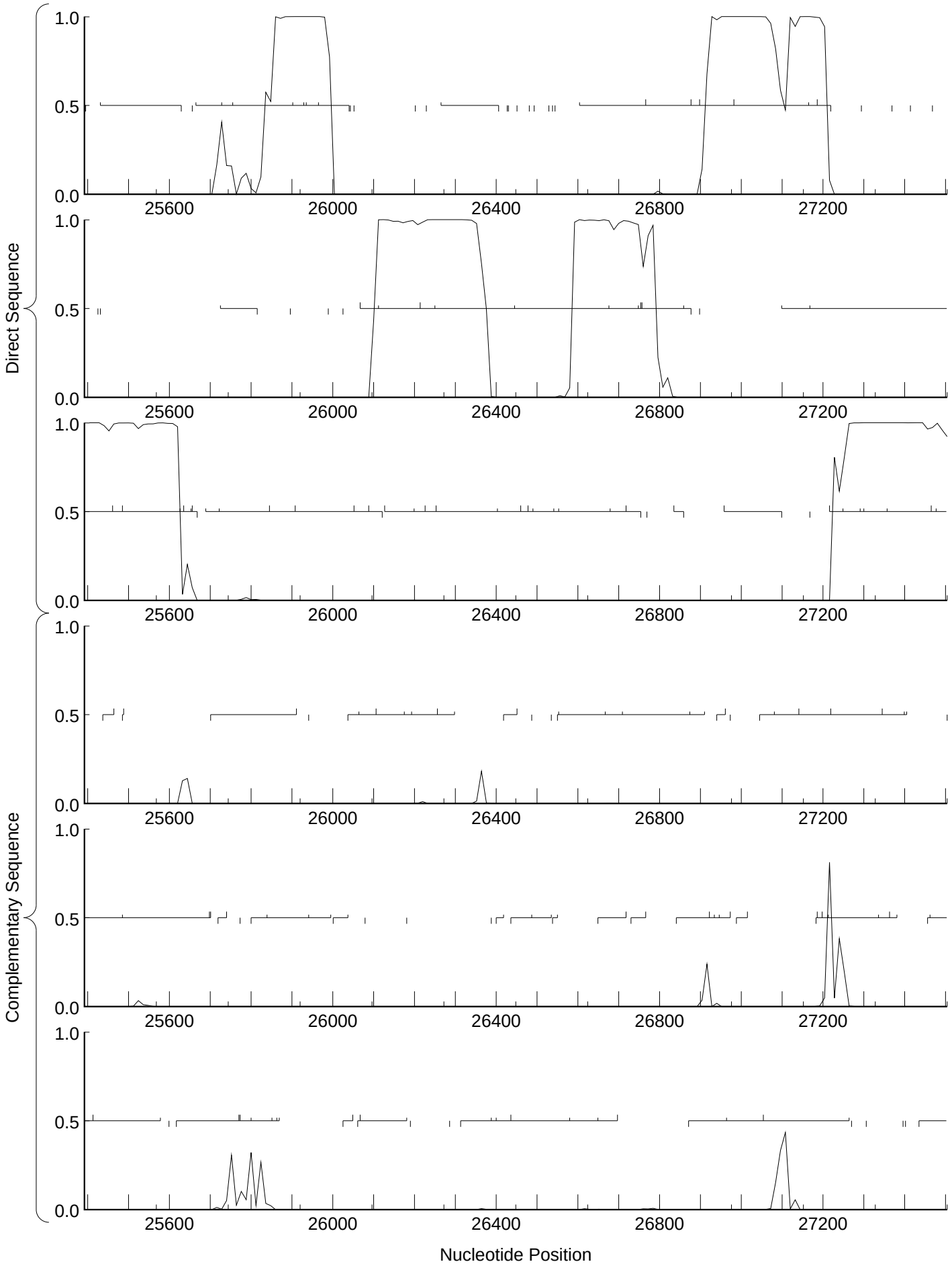


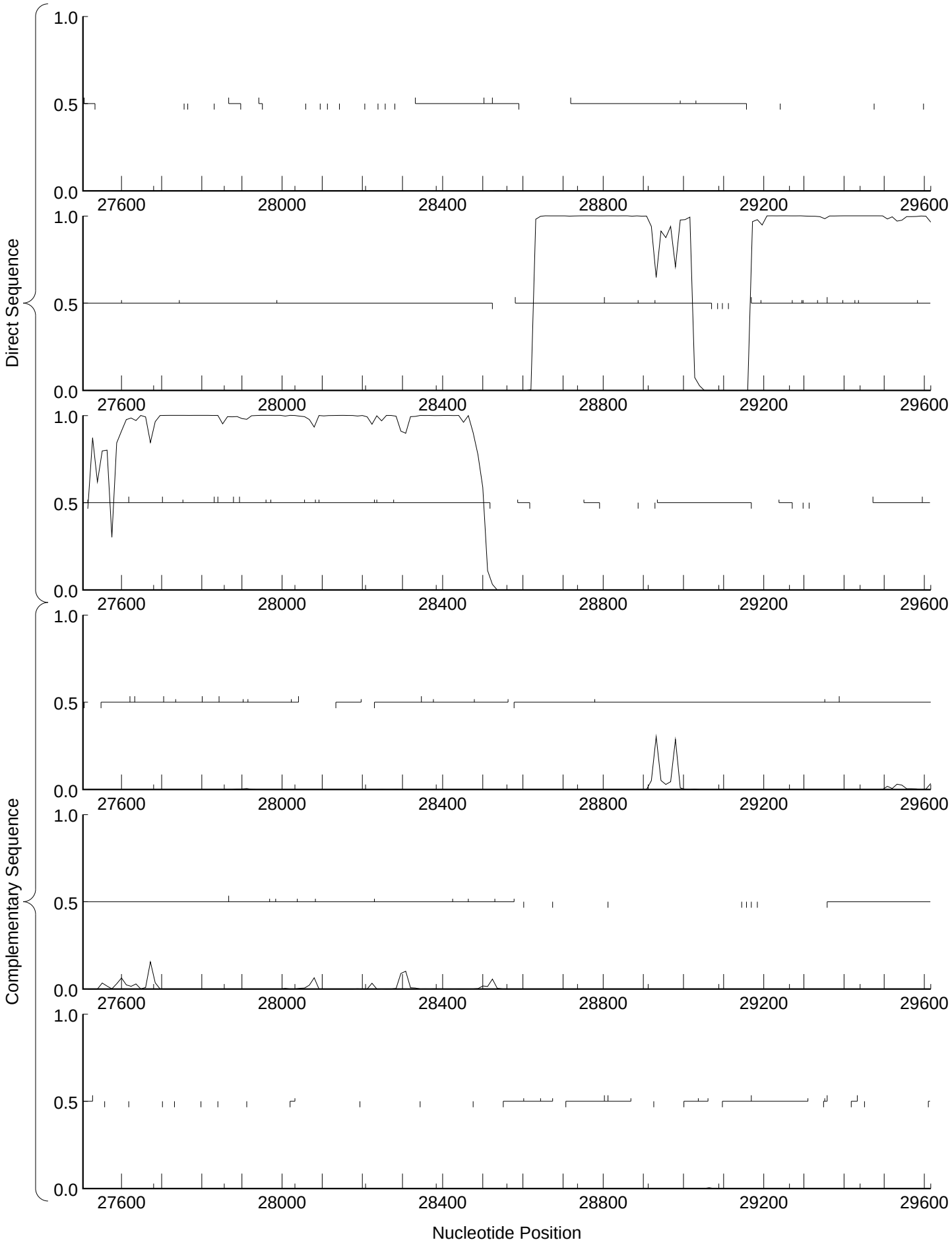
bacterium phage Phonegingi complete sequence, 39364 bp, circularly permuted, Cluster GA, Order 4, Window 96, Step 12, 12/20

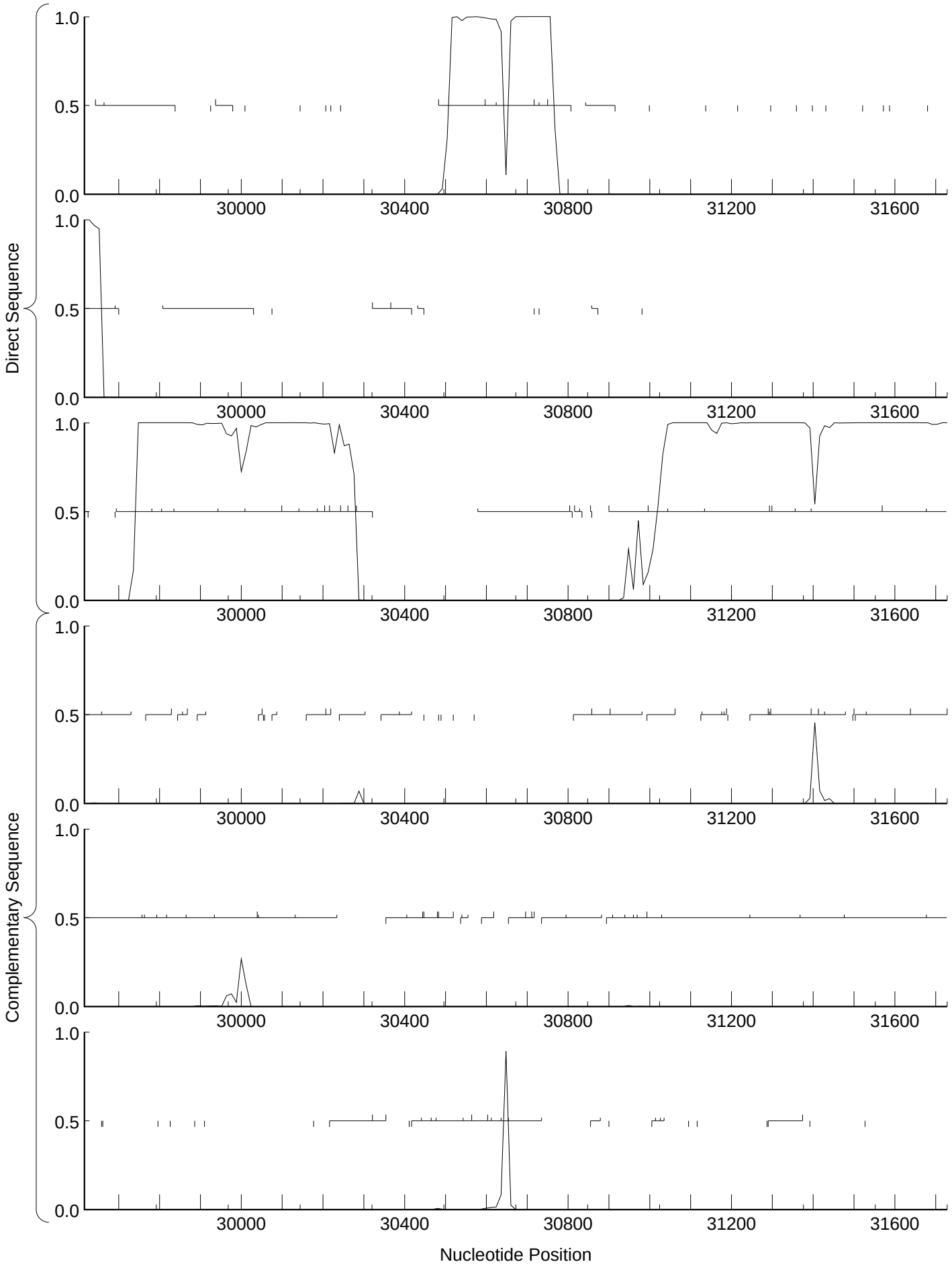


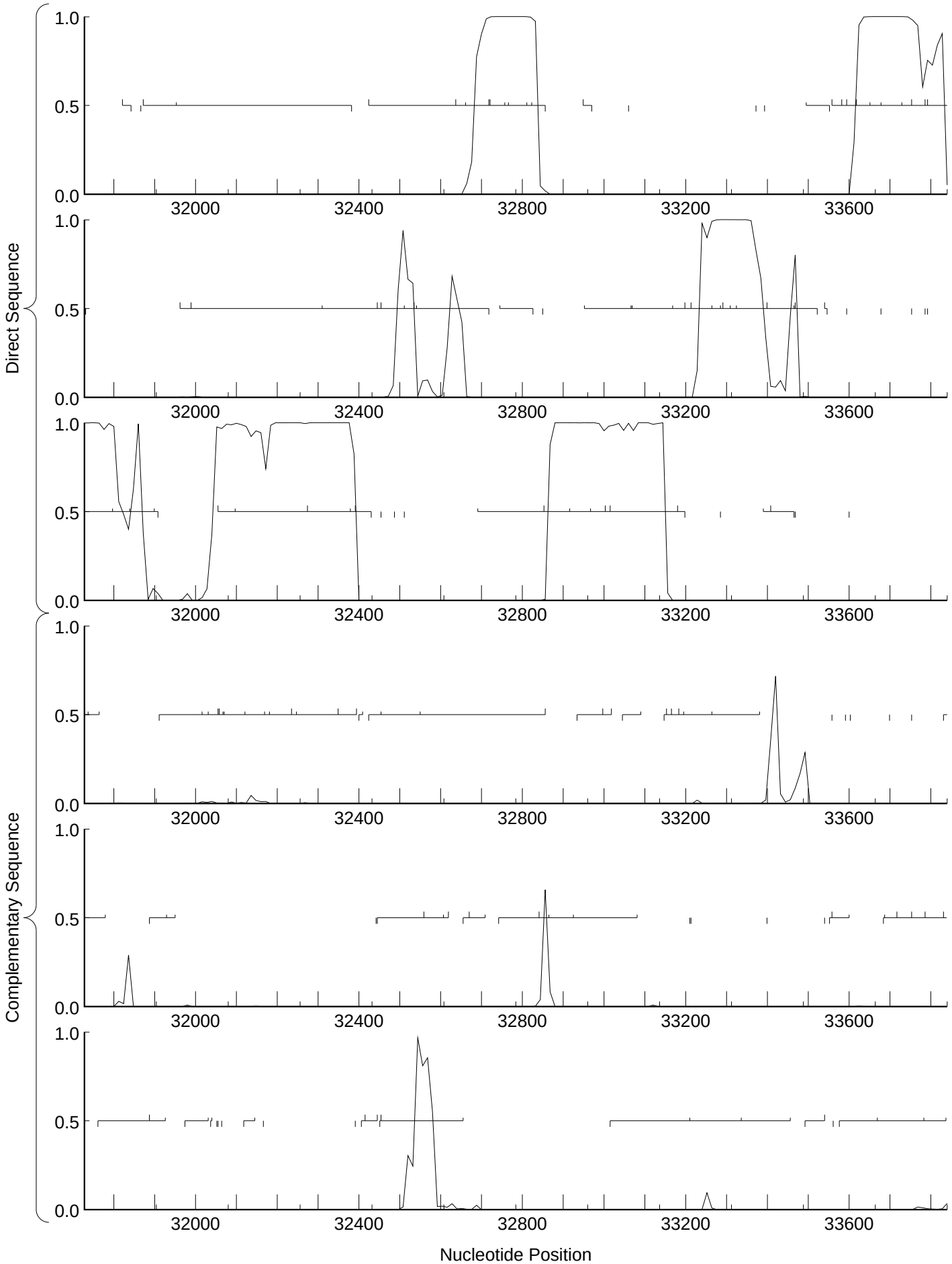
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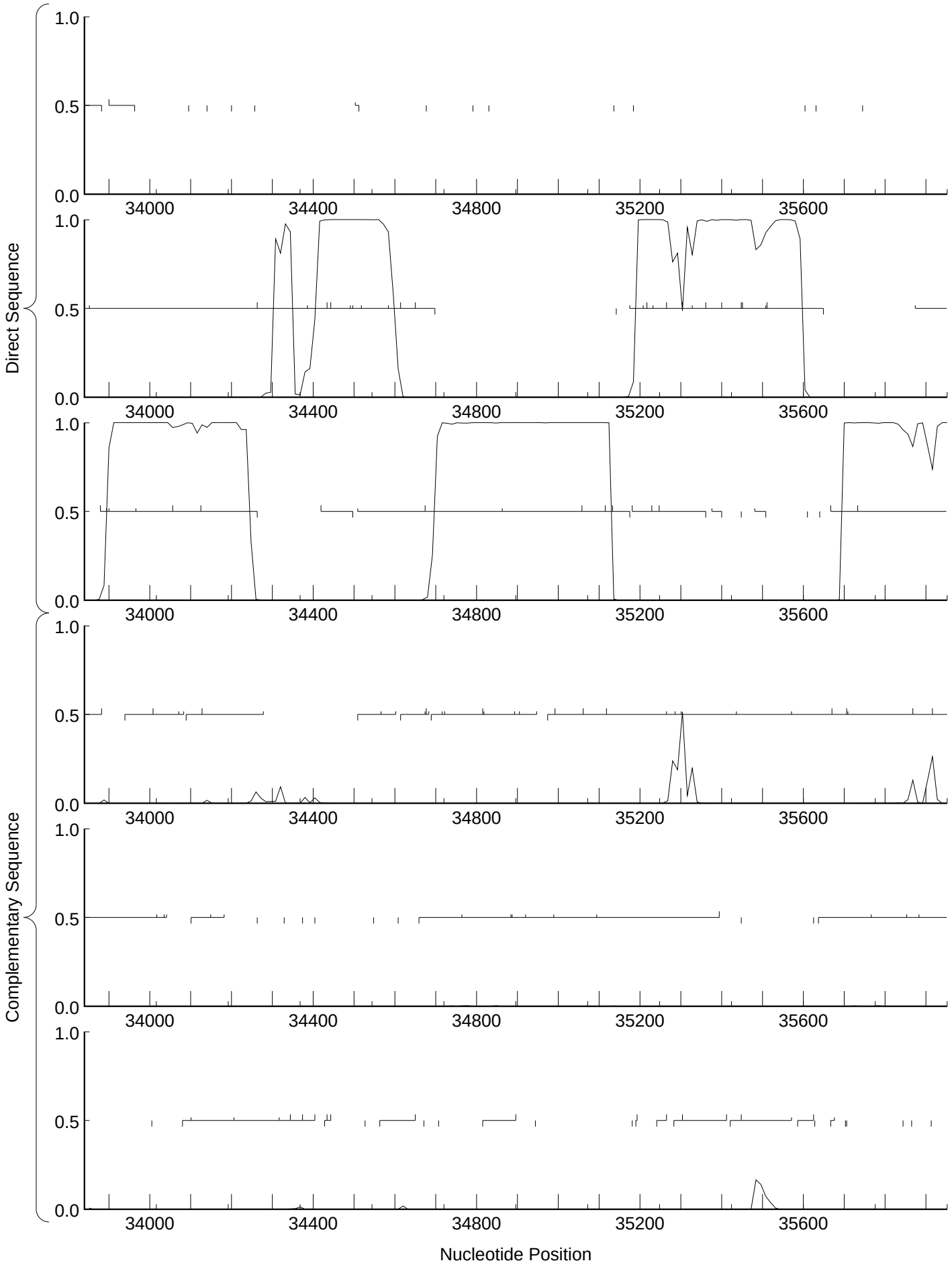


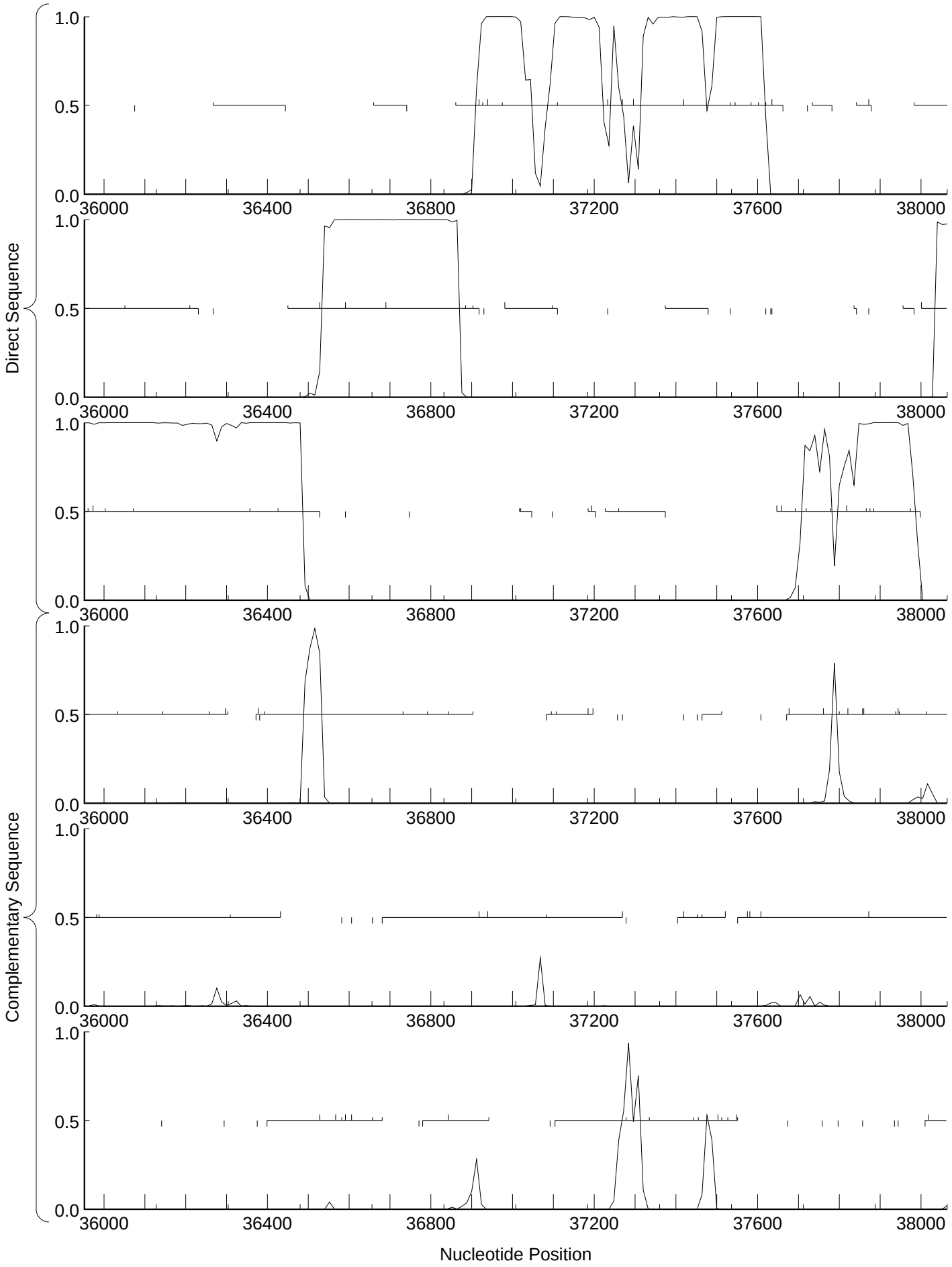

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
25600
26000
26400
26800
27200
Nucleotide Position

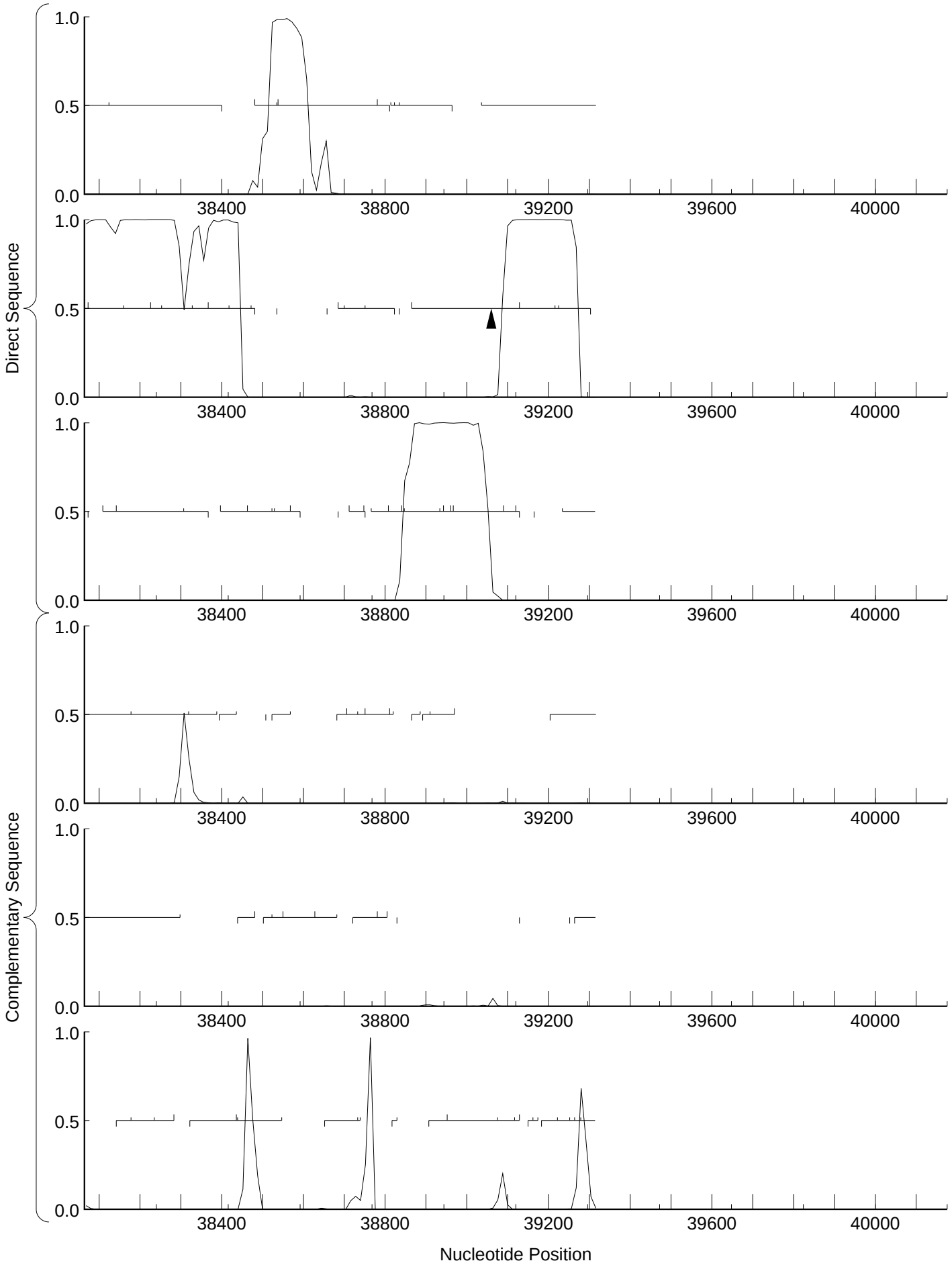

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
27600
28000
28400
28800
29200
29600
Nucleotide Position


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


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
32000
32400
32800
33200
33600
Nucleotide Position


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


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


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