GeneMark

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

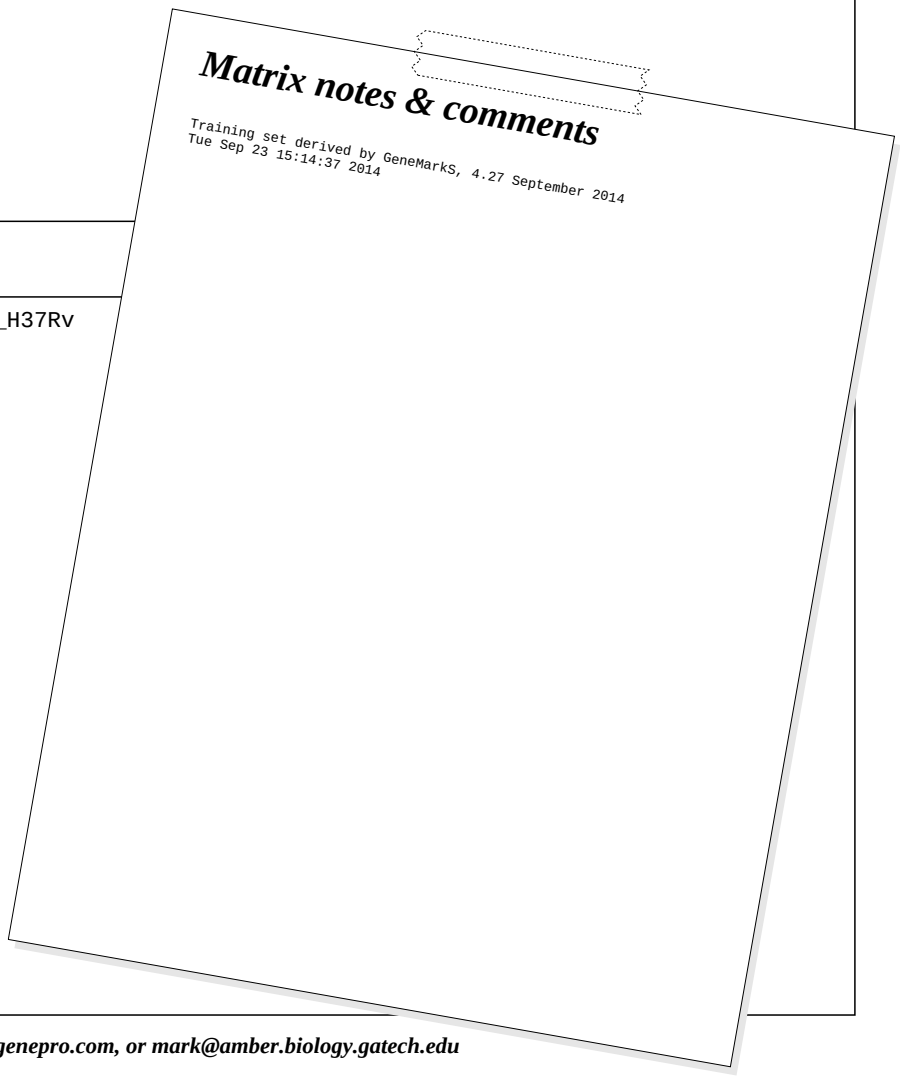
PROGRAM INFORMATION

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Sequence         :  Mycobacterium phage Marley1013 complete sequence, 69164 bp, circularly permuted, Cluster B3
Analysis Date    :  3/29/24 at 11:58:30
Pages            :  34
Sequence Length  :  69164 bp
GC Content       :   67.48%

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

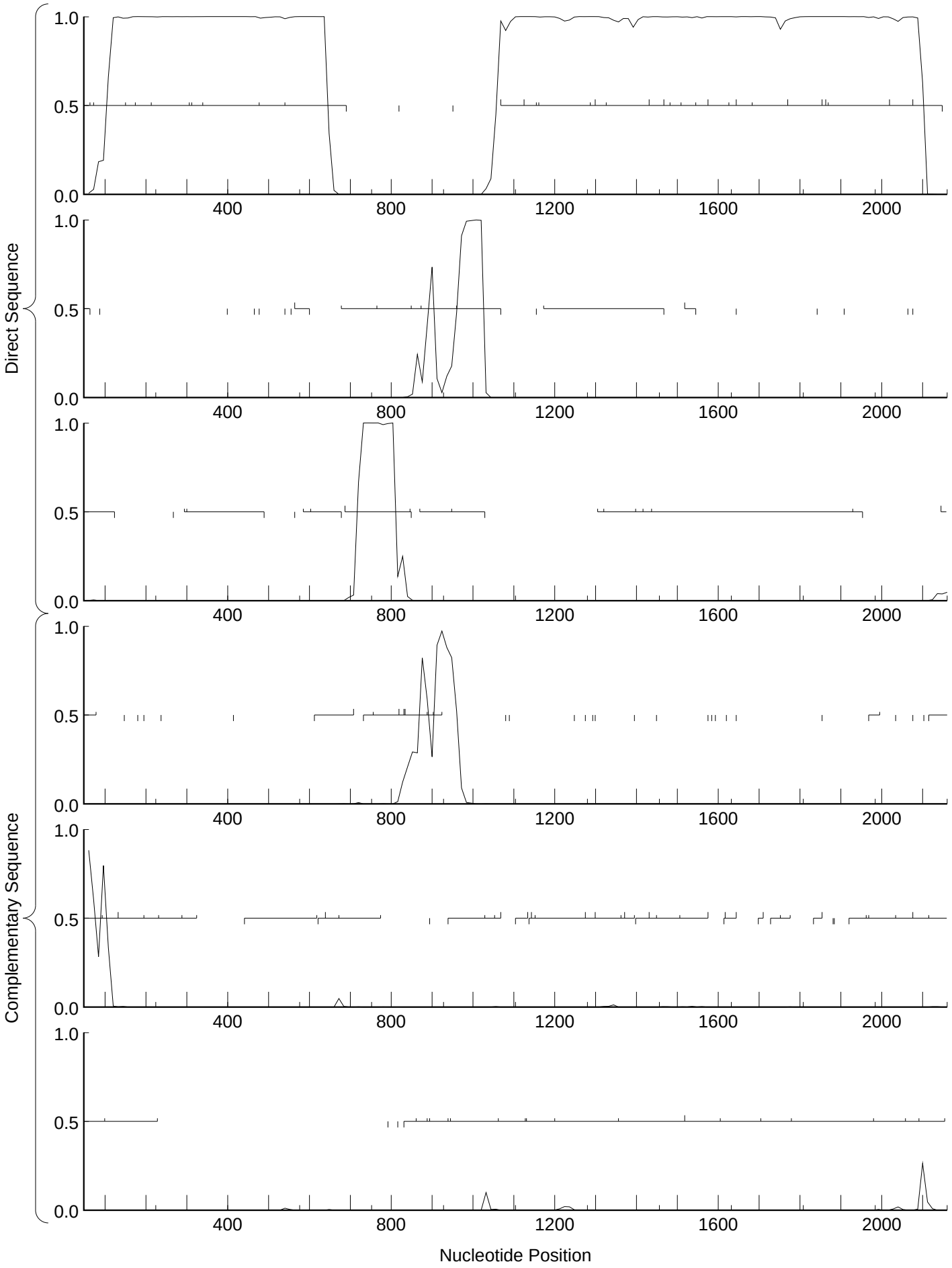
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Matrix     :  Mycobacterium_tuberculosis_H37Rv
Author     :  -

Order      :  4
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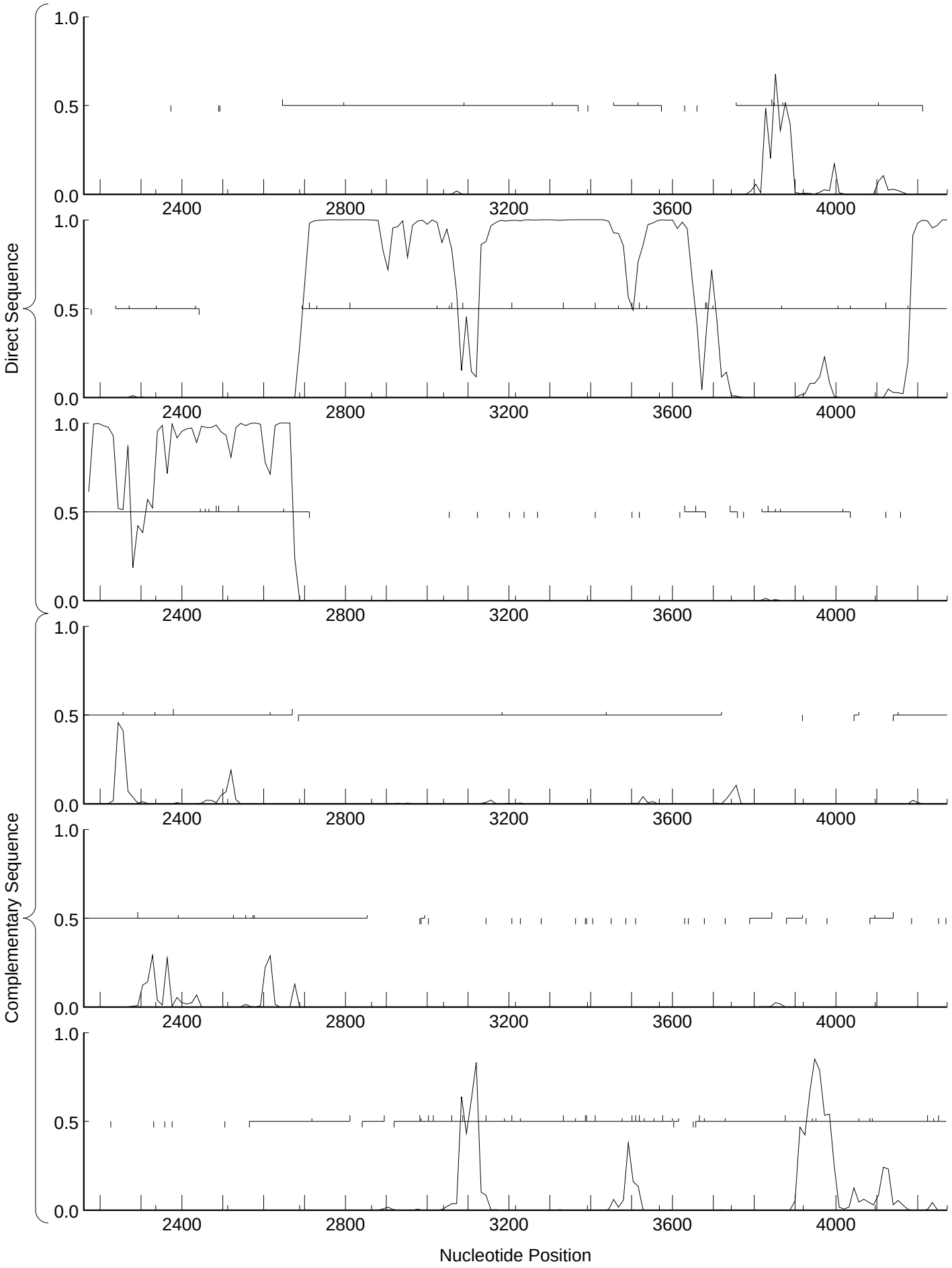

```
  Send questions / comments to:
      Dr. M. Borodovsky
      Georgia Institute of Technology
      School of Biology
      Atlanta, GA  30332-0230
```


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

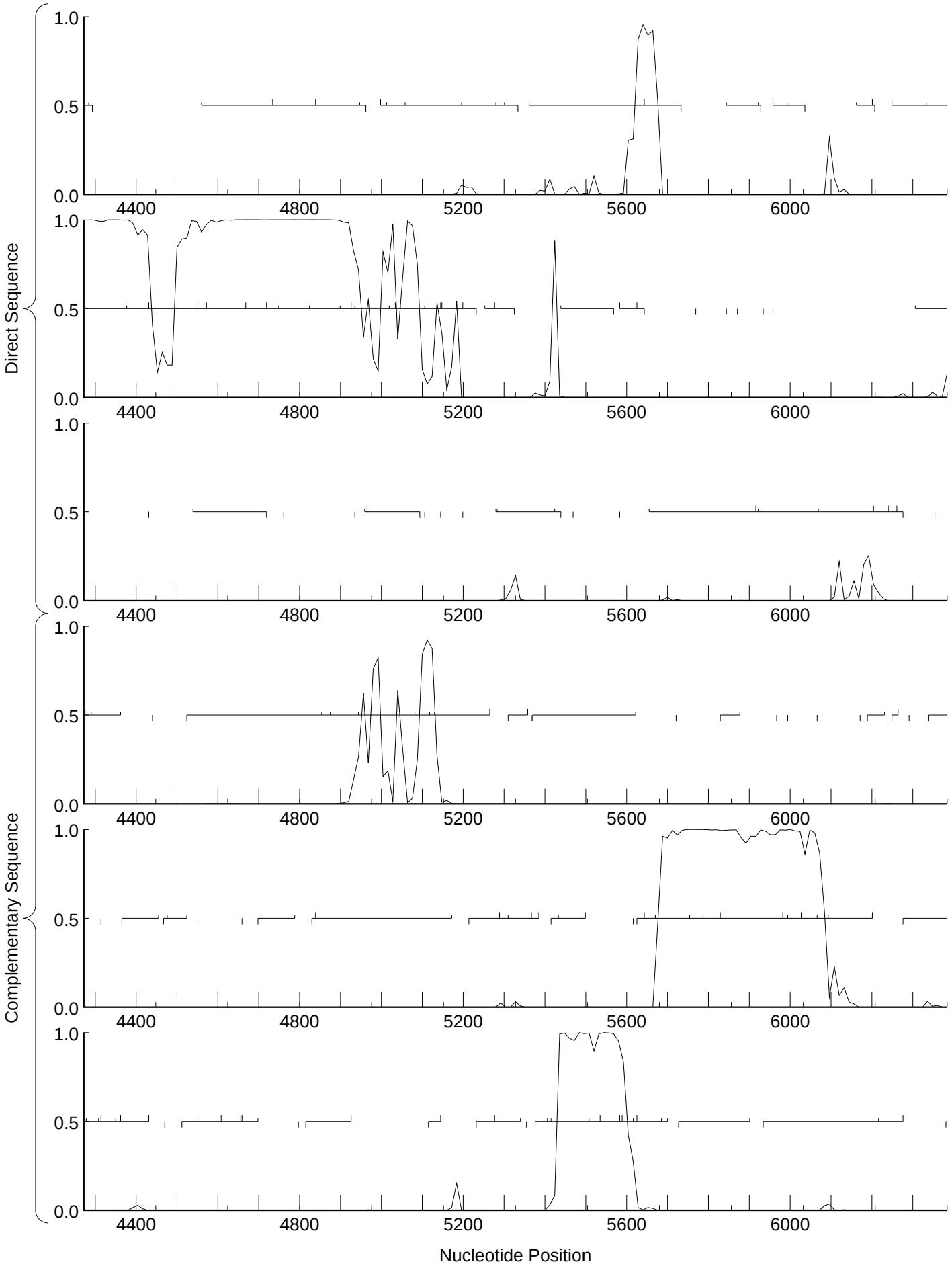
obacterium phage Marley1013 complete sequence, 69164 bp, circularly permuted, Cluster B3, Order 4, Window 96, Step 12, 2/34



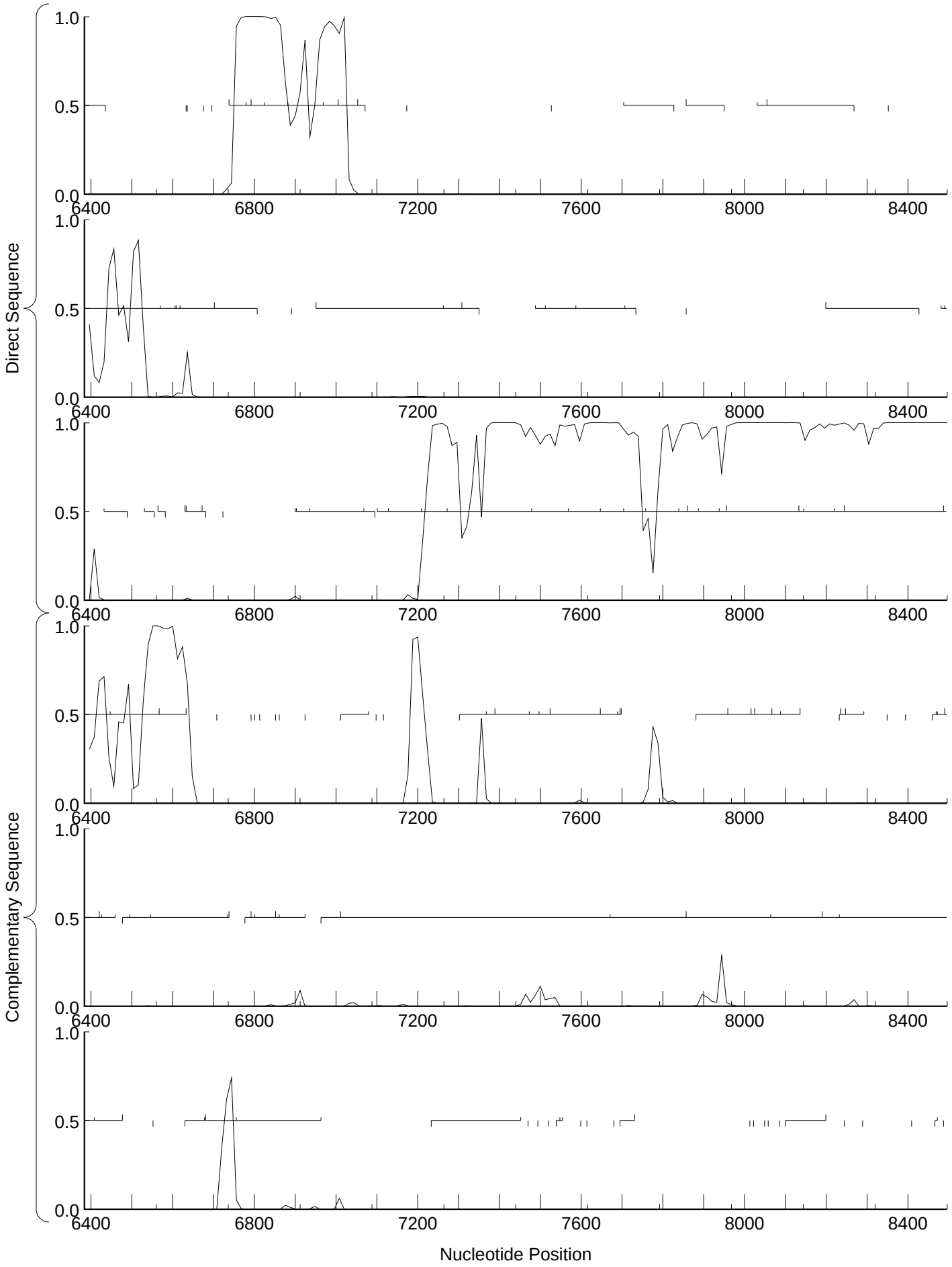
obacterium phage Marley1013 complete sequence, 69164 bp, circularly permuted, Cluster B3, Order 4, Window 96, Step 12, 3/34



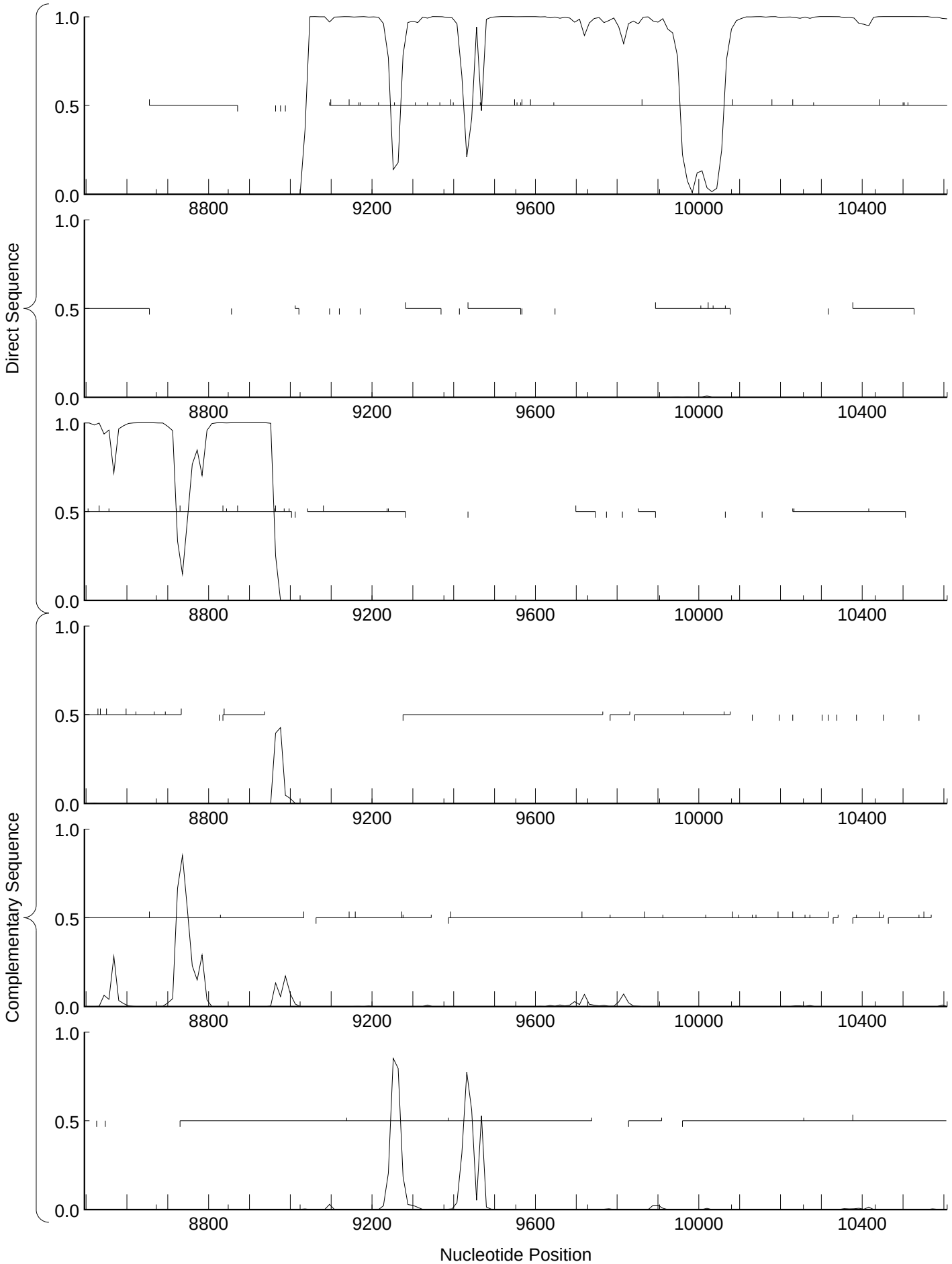
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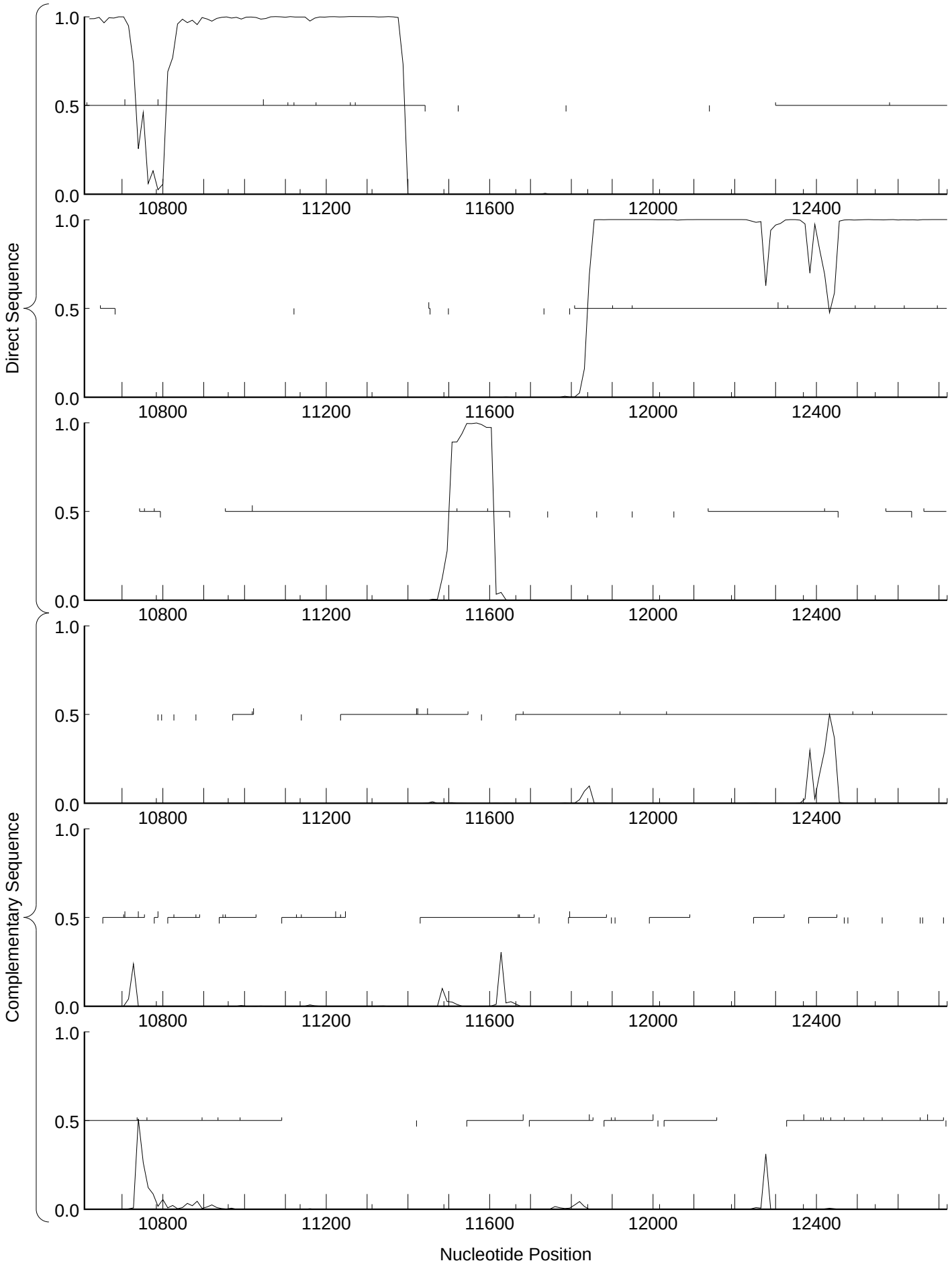
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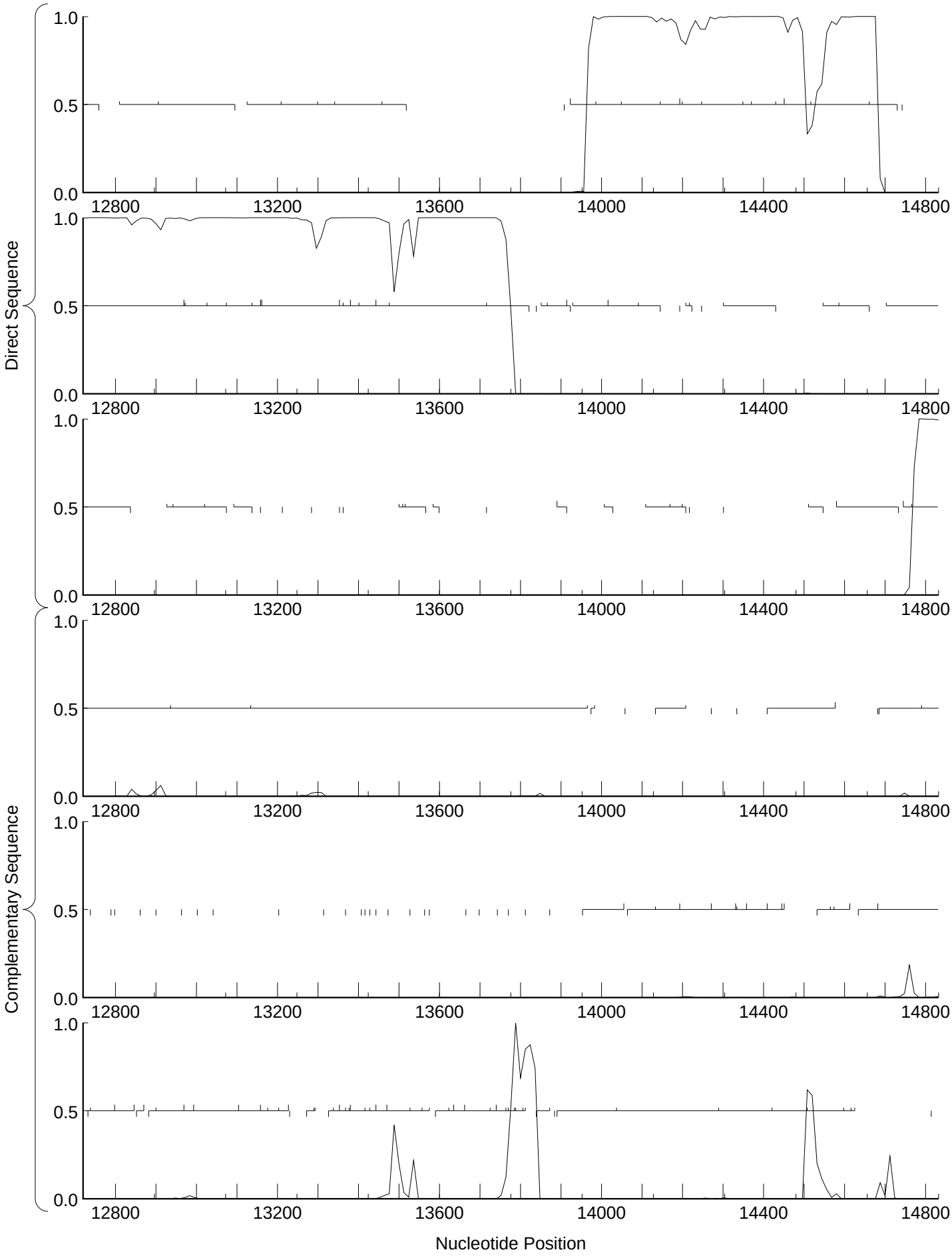
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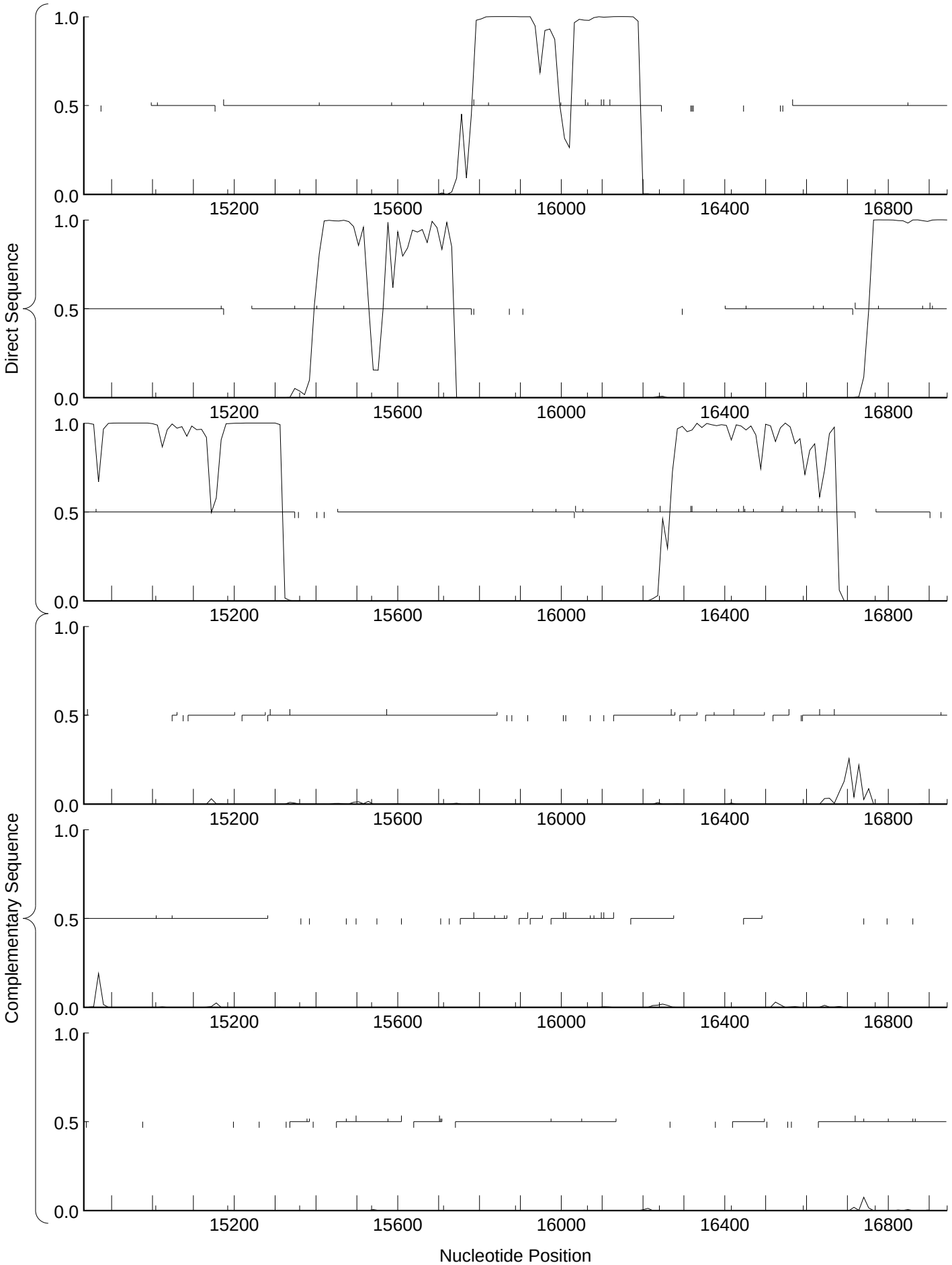
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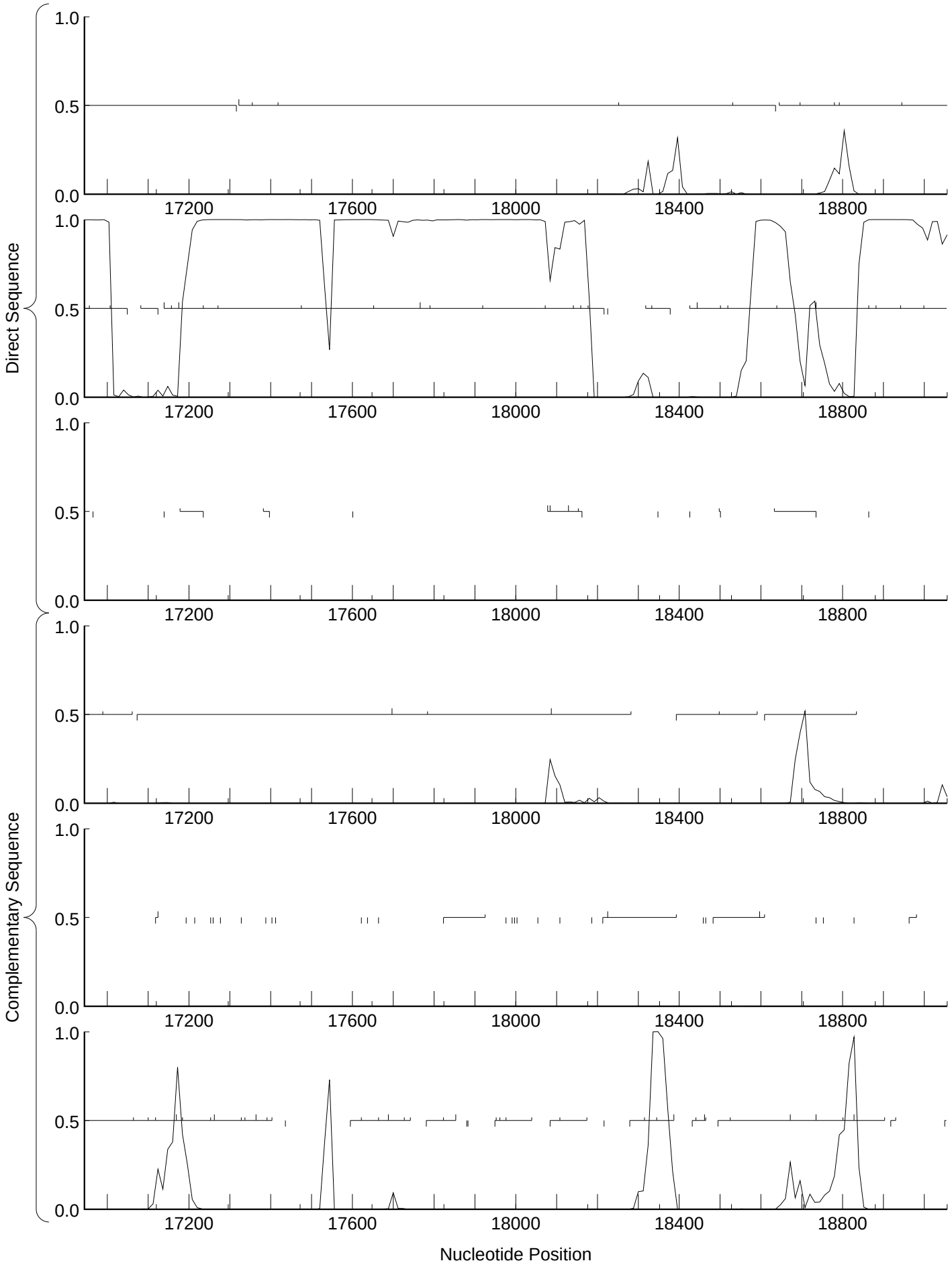
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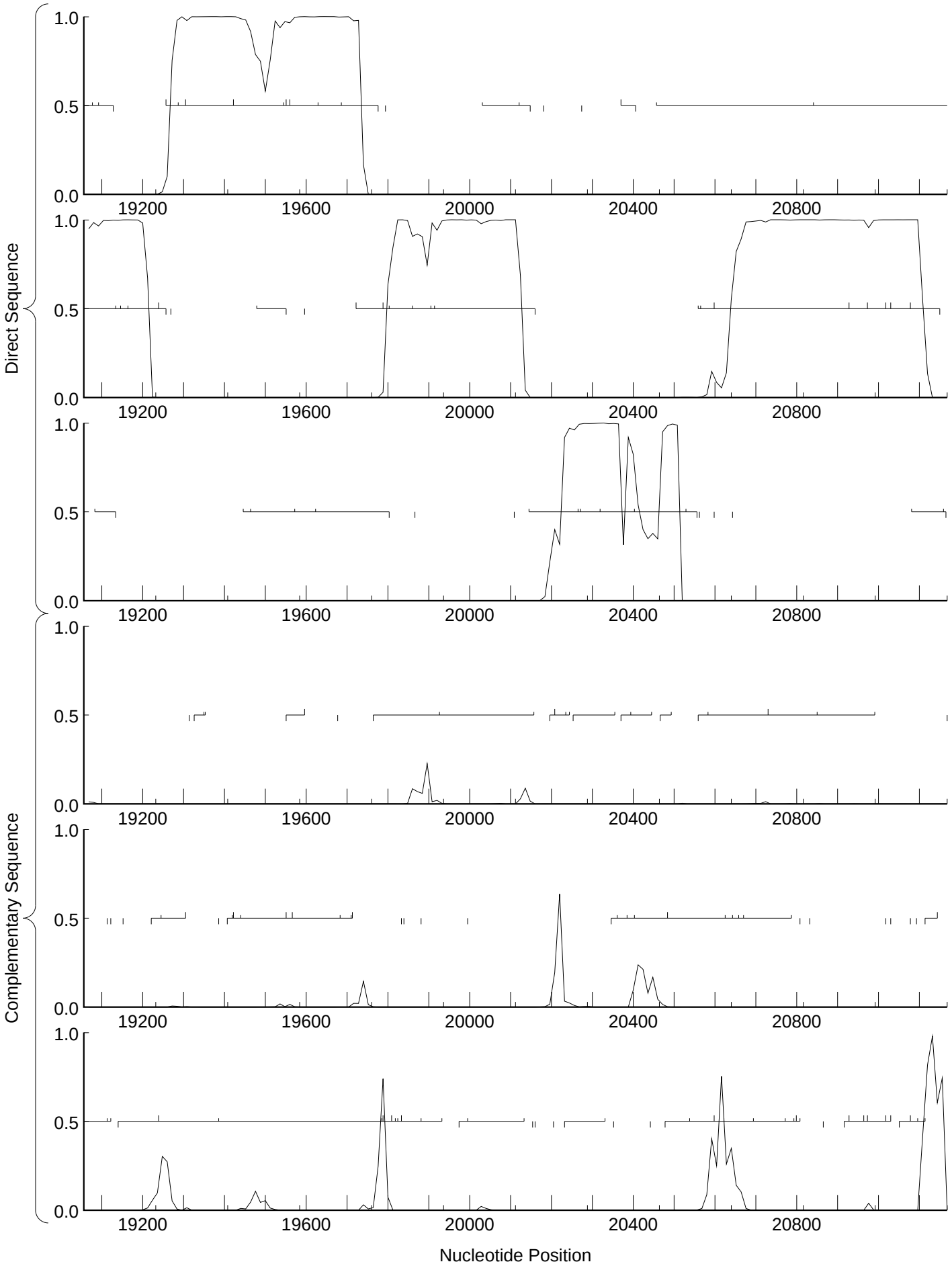


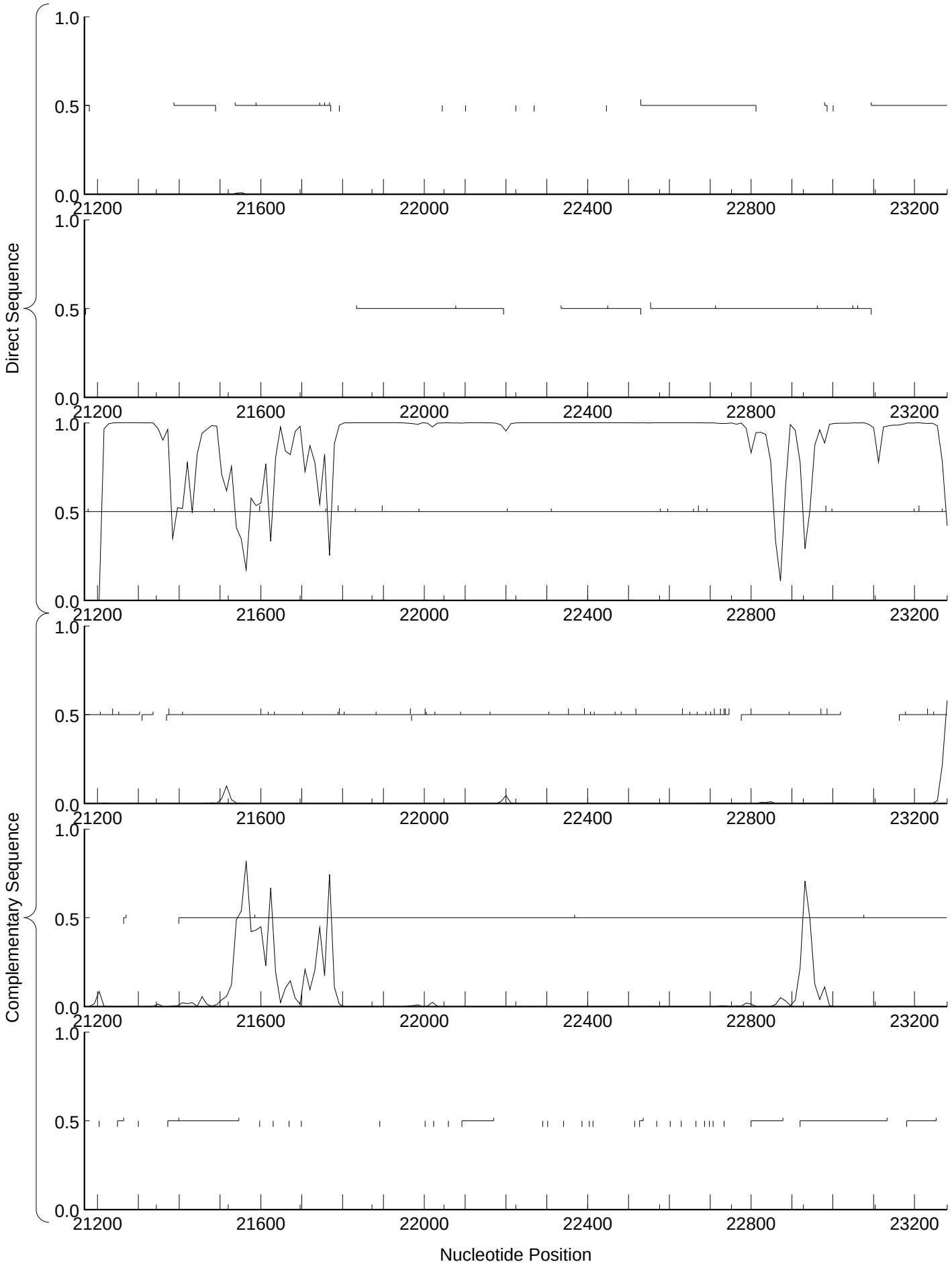
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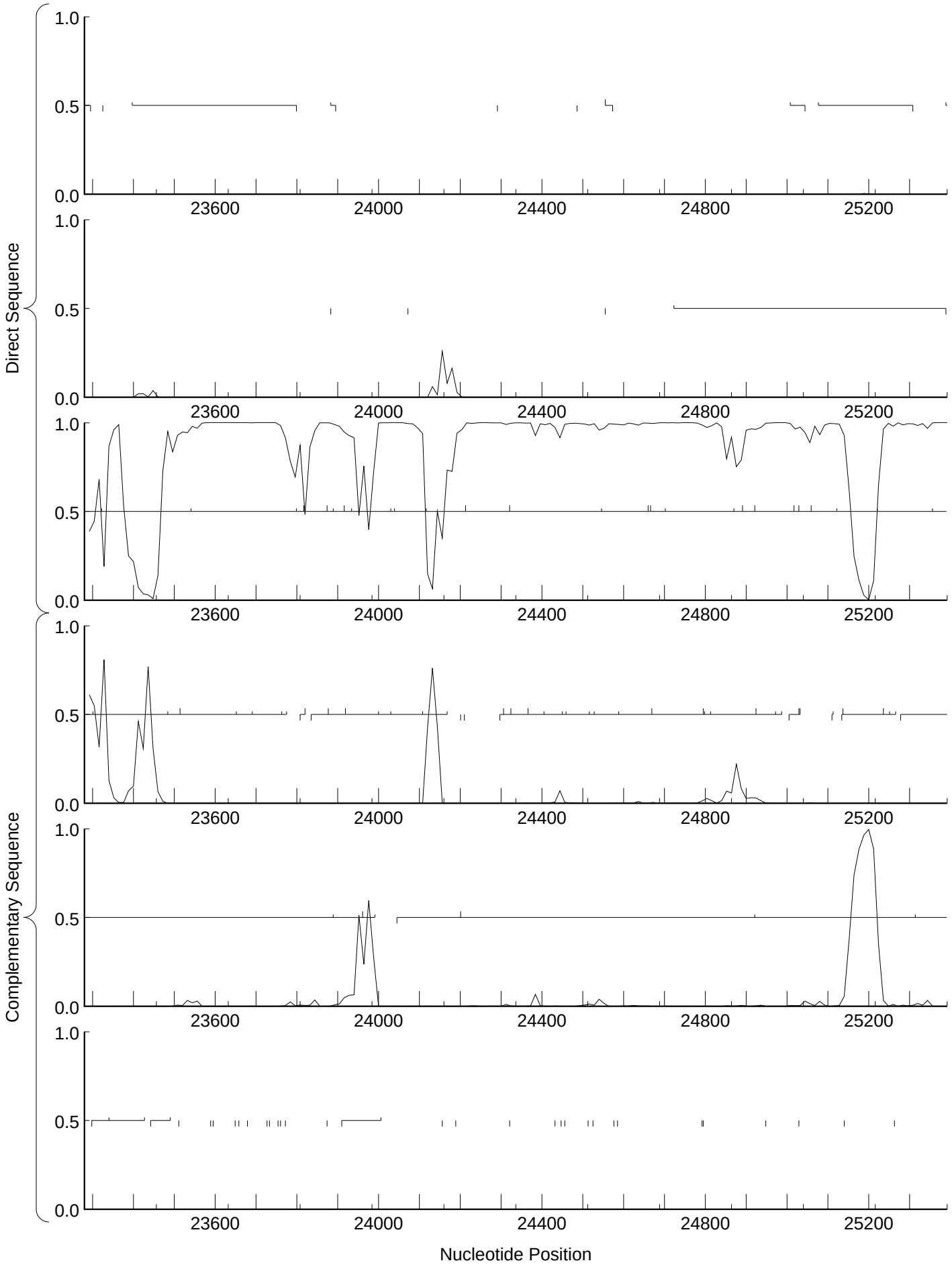
bacterium phage Marley1013 complete sequence, 69164 bp, circularly permuted, Cluster B3, Order 4, Window 96, Step 12, 10/34

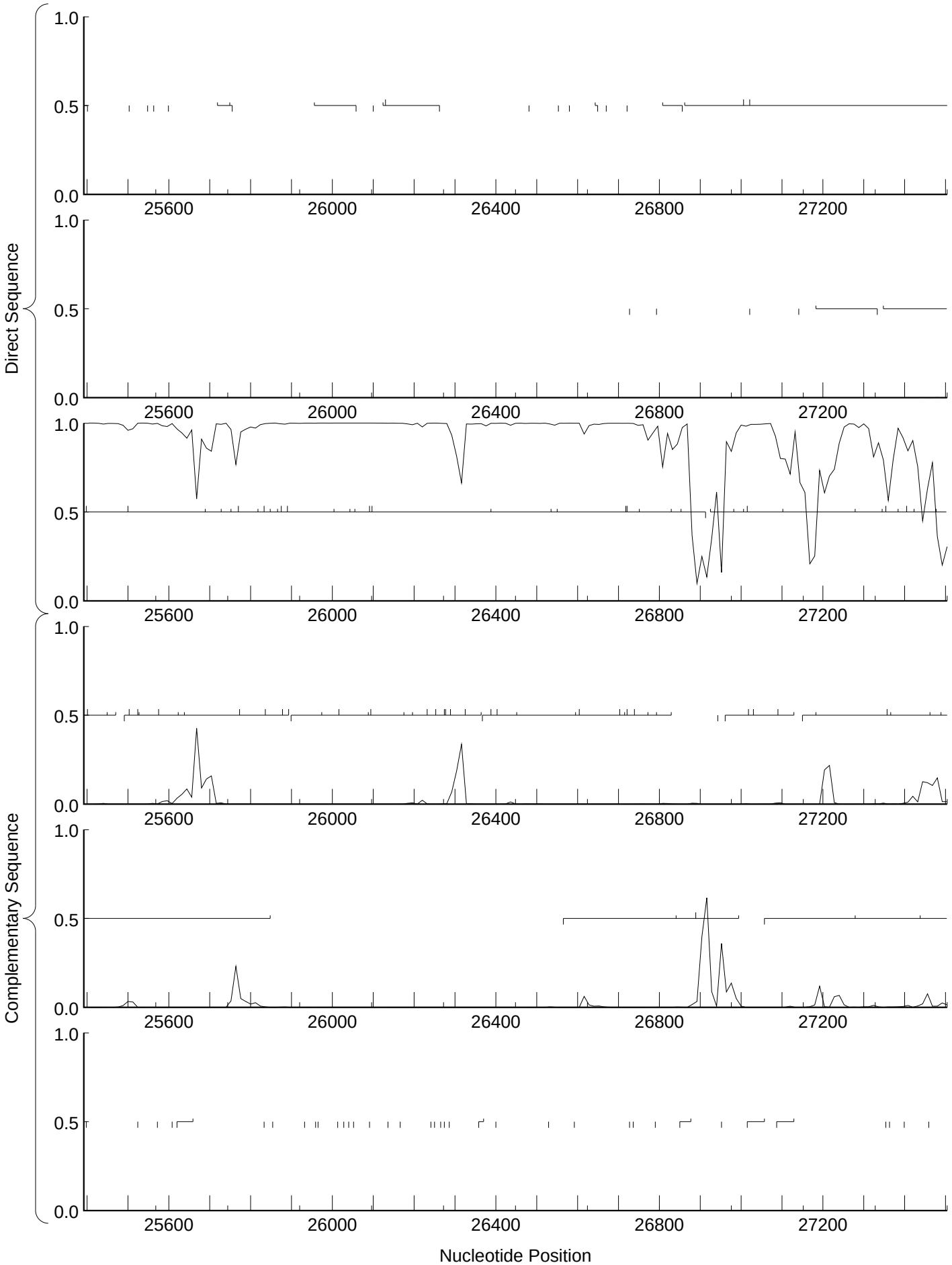


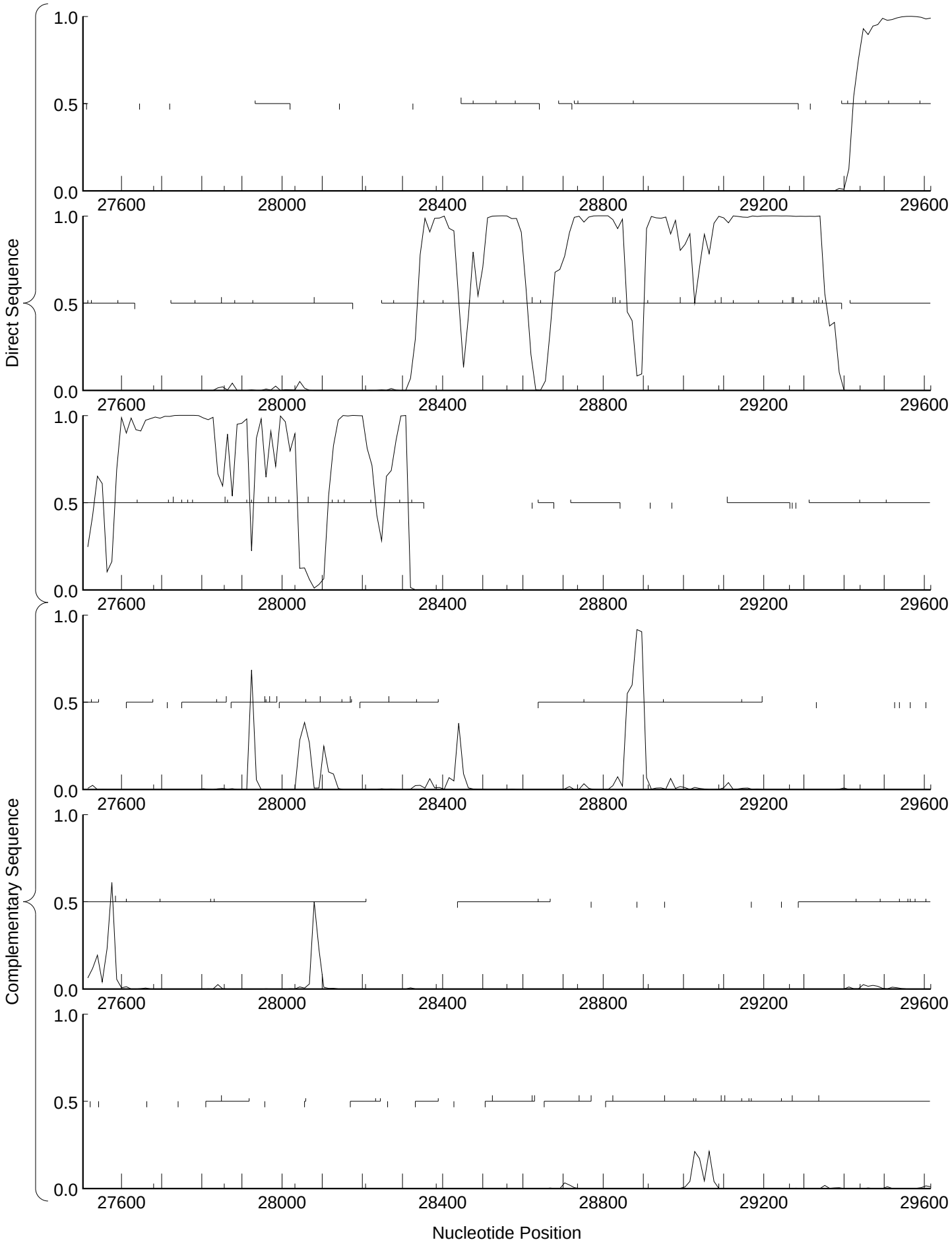

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
19200
19600
20000
20400
20800
Nucleotide Position


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
21200
21600
22000
22400
22800
23200
Nucleotide Position

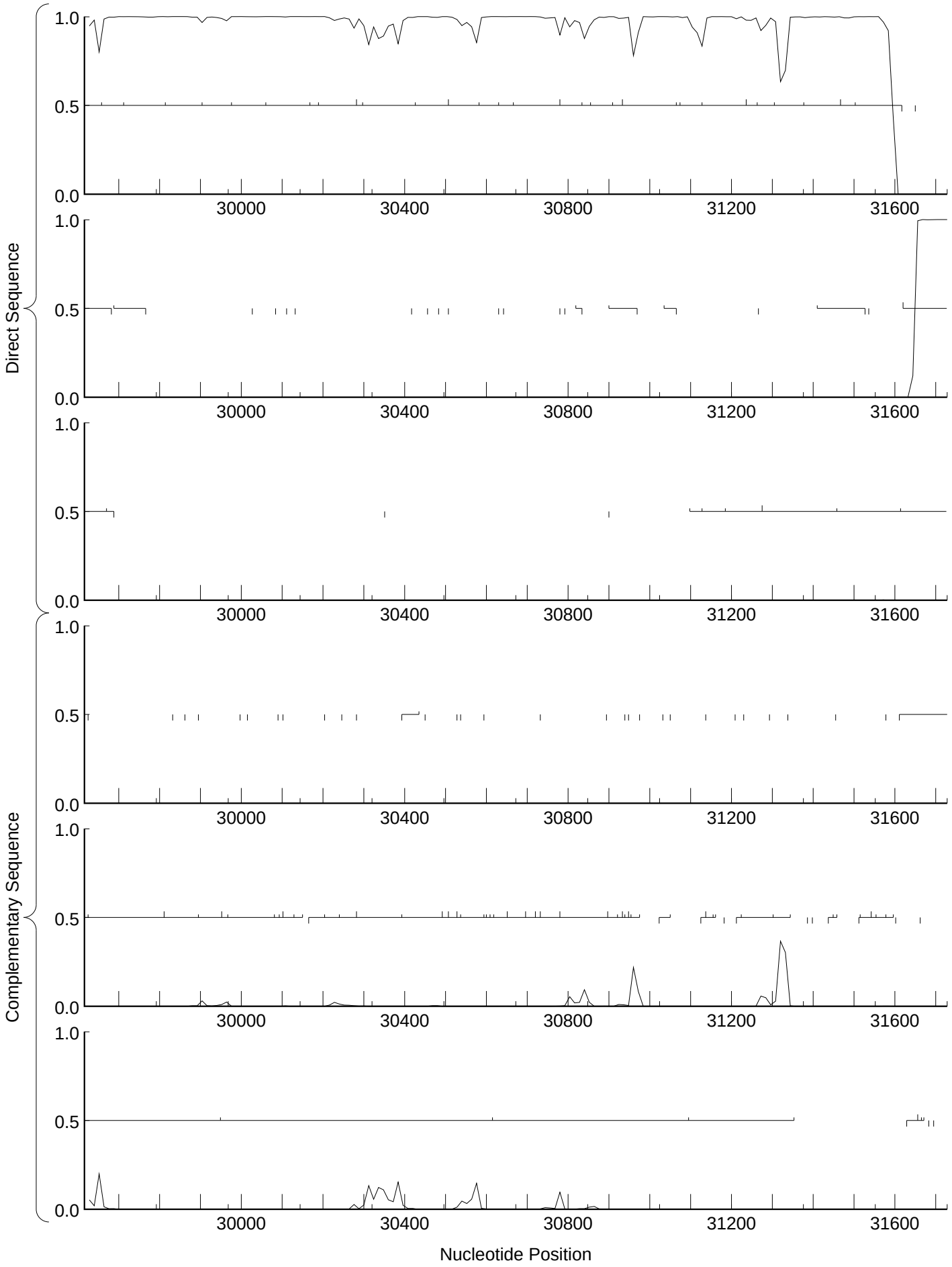
bacterium phage Marley1013 complete sequence, 69164 bp, circularly permuted, Cluster B3, Order 4, Window 96, Step 12, 13/34



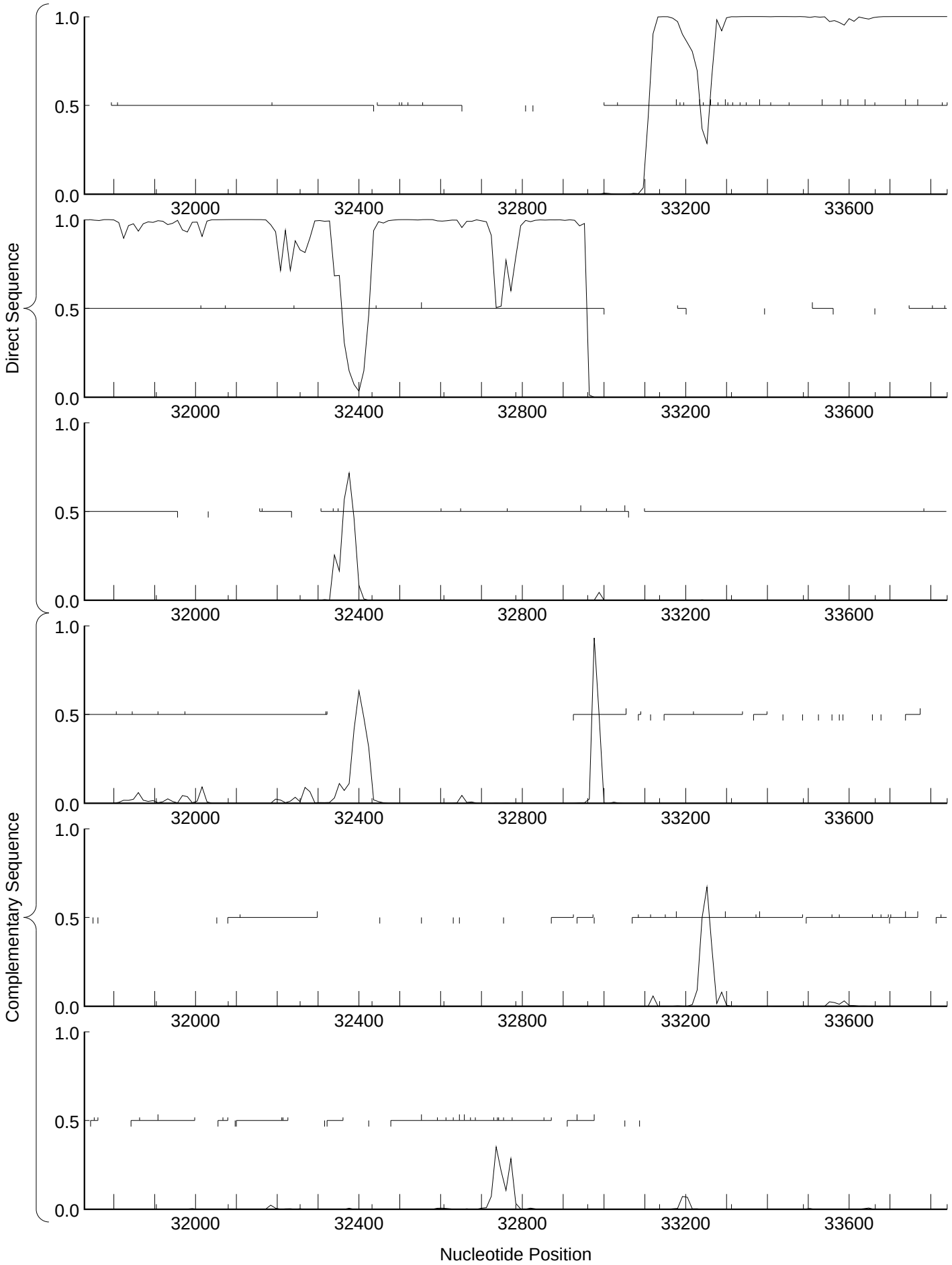

Direct Sequence
Complementary Sequence
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26400
26800
27200
Nucleotide Position

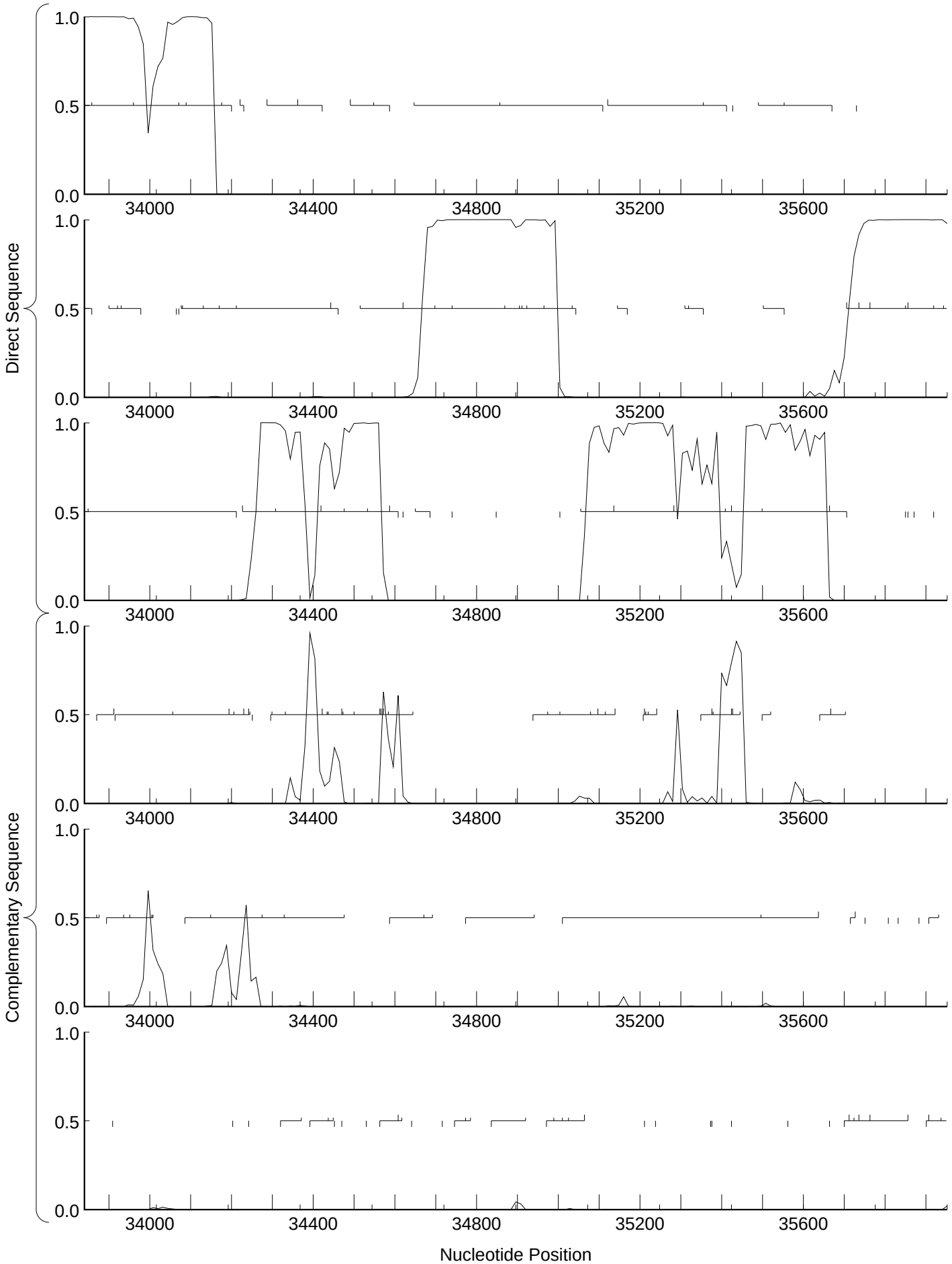

Direct Sequence
Complementary Sequence
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0.0
27600
28000
28400
28800
29200
29600
Nucleotide Position

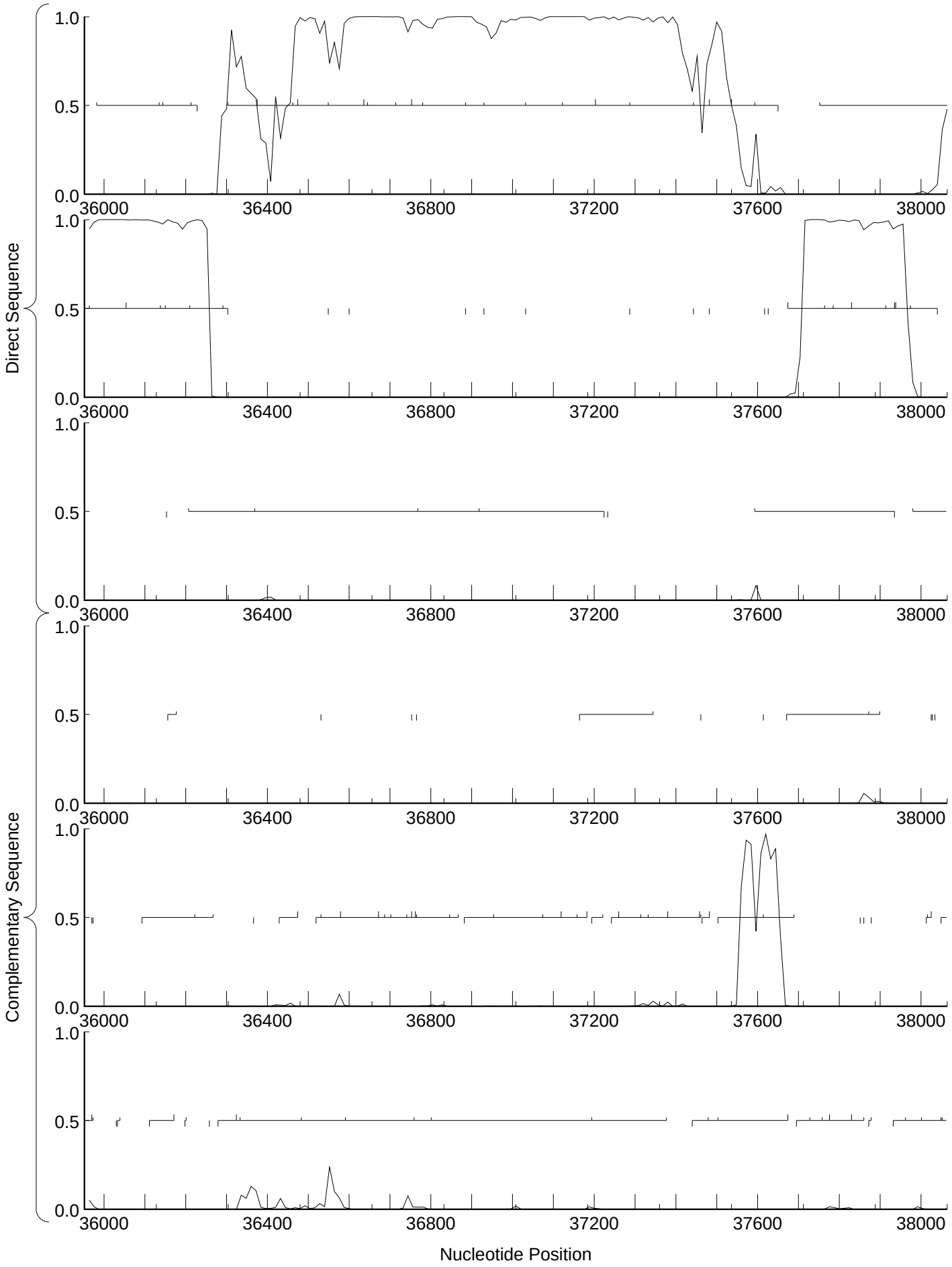
bacterium phage Marley1013 complete sequence, 69164 bp, circularly permuted, Cluster B3, Order 4, Window 96, Step 12, 16/34

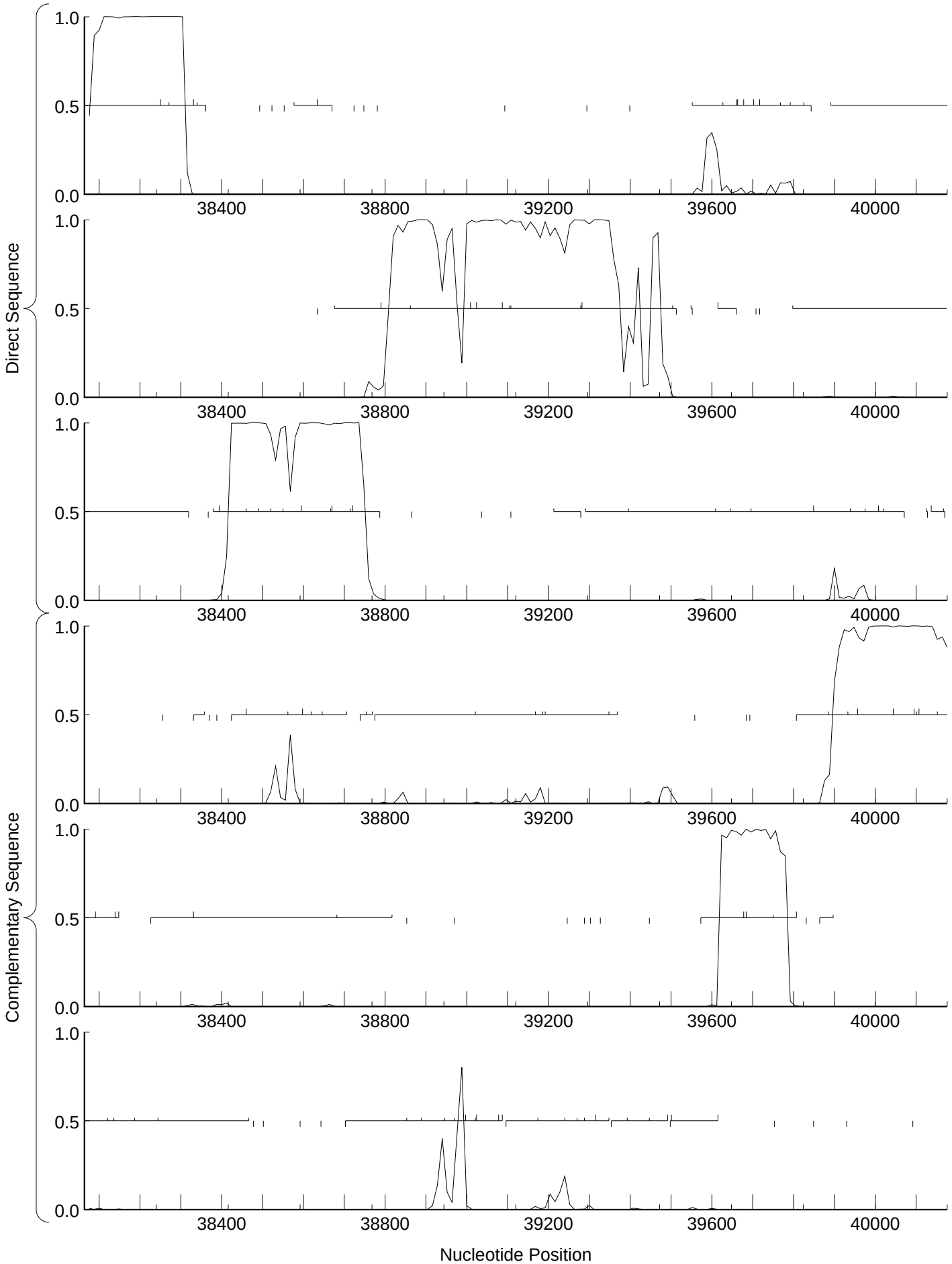


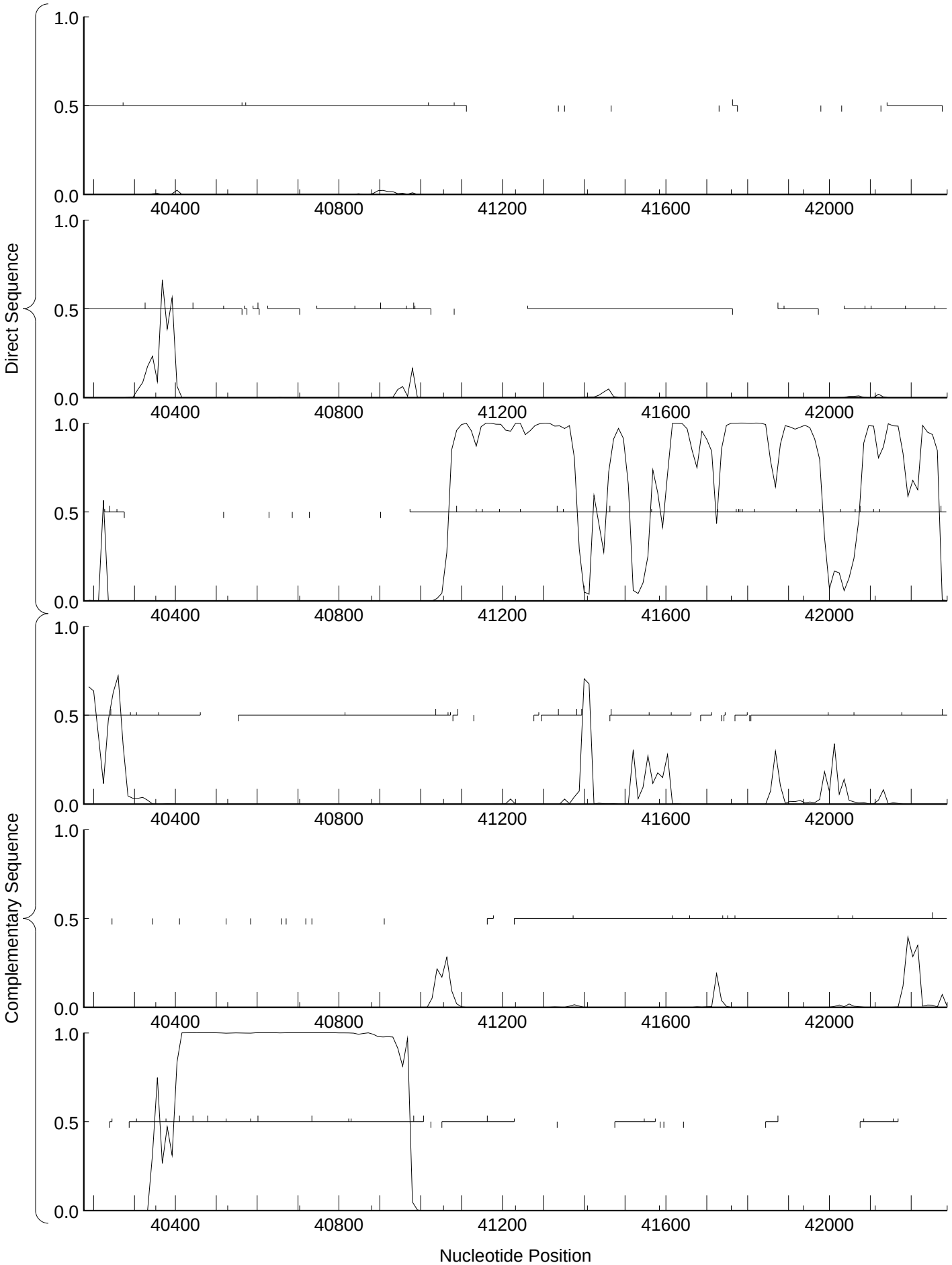
bacterium phage Marley1013 complete sequence, 69164 bp, circularly permuted, Cluster B3, Order 4, Window 96, Step 12, 17/34

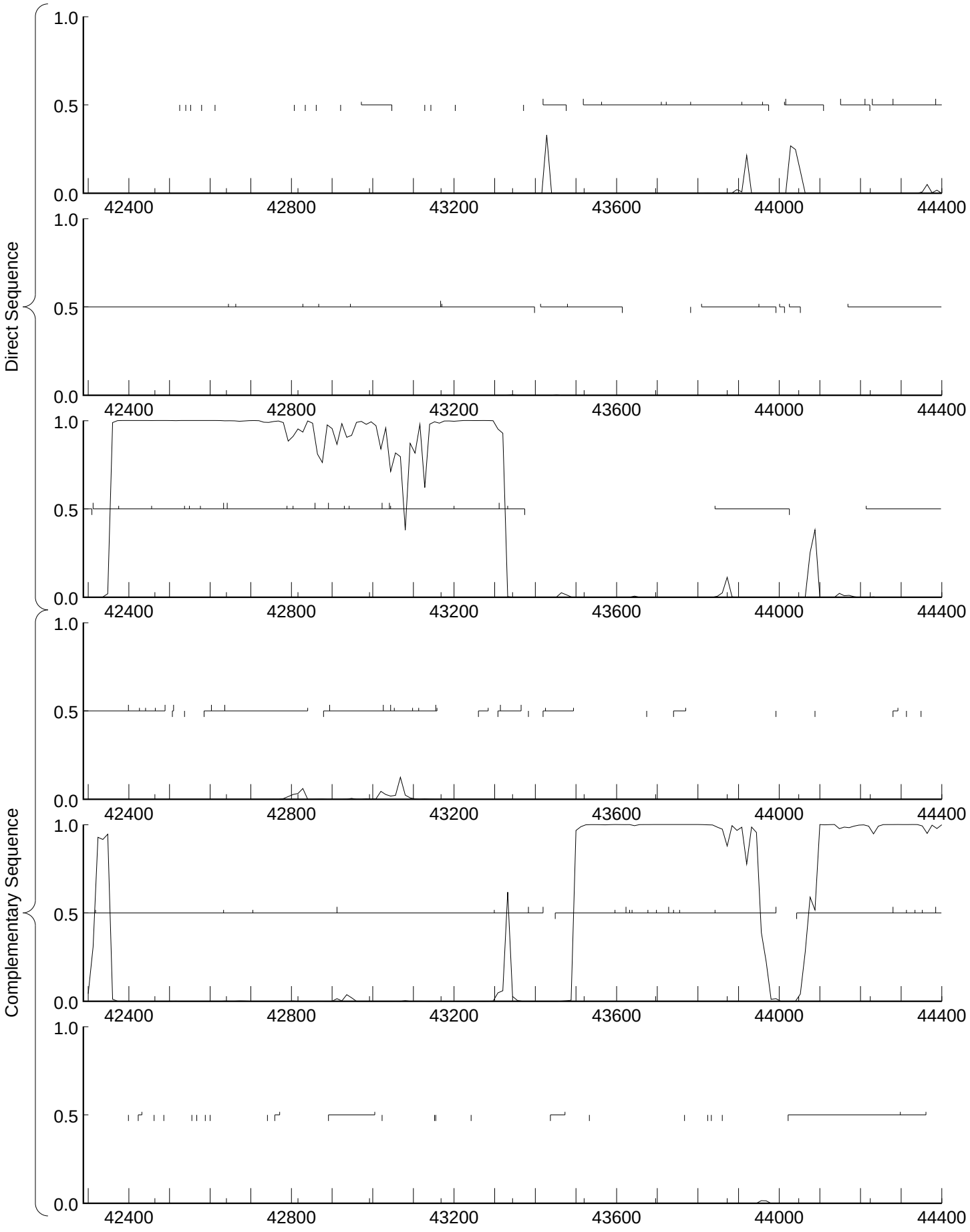


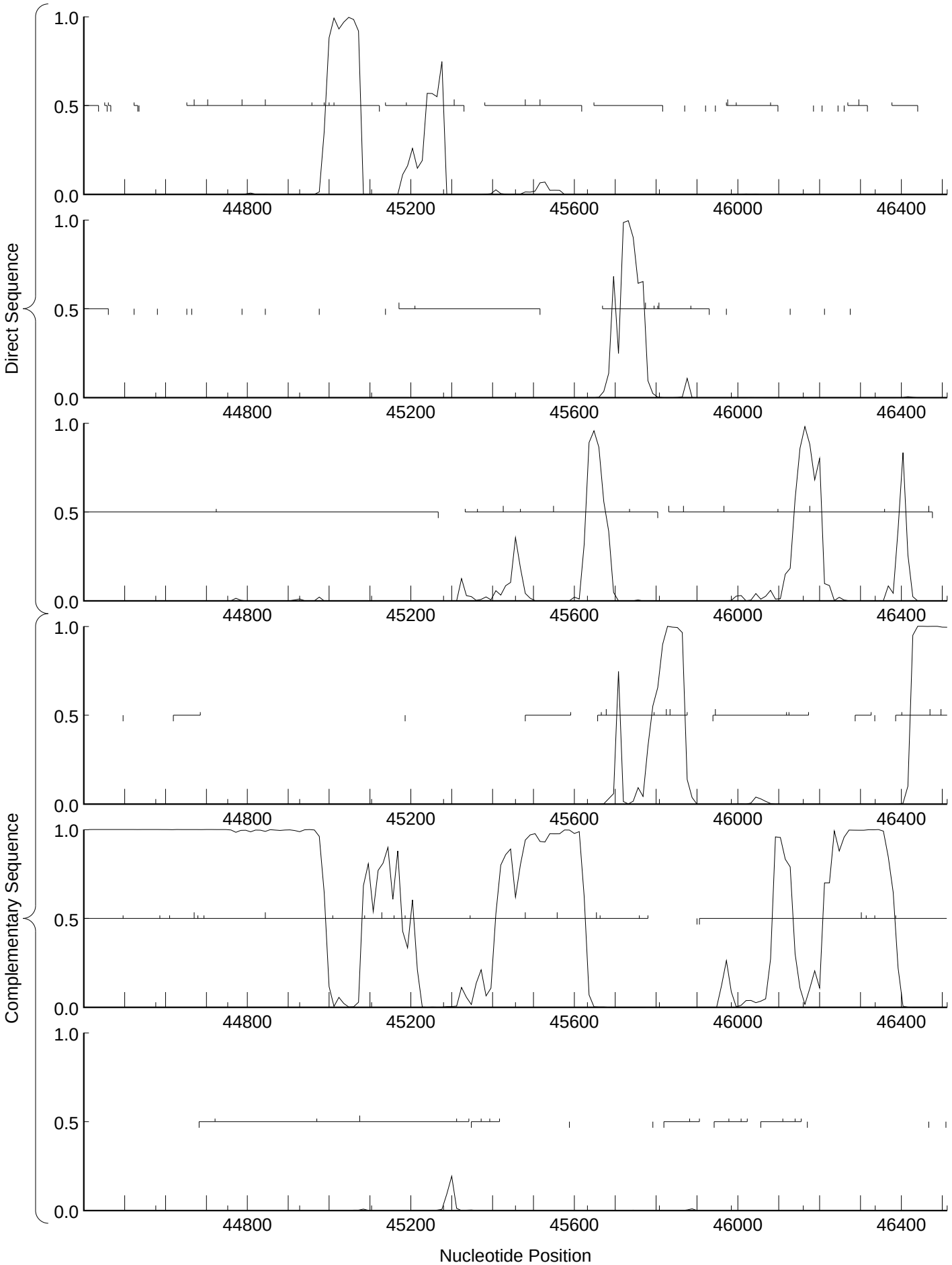

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Complementary Sequence
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0.0
34000
34400
34800
35200
35600
Nucleotide Position

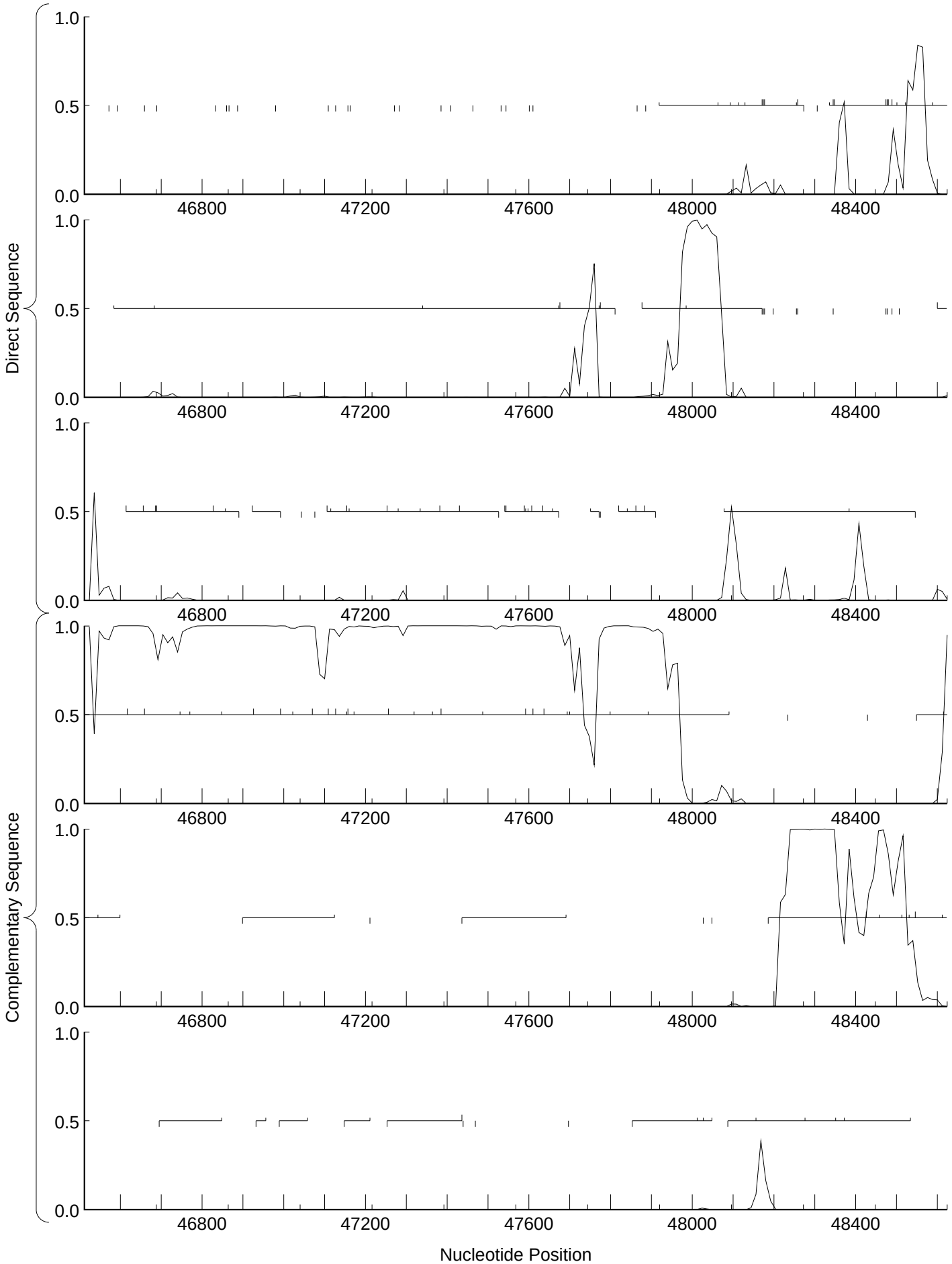

Direct Sequence
Complementary Sequence
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0.5
0.0
36000
36400
36800
37200
37600
38000
Nucleotide Position


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

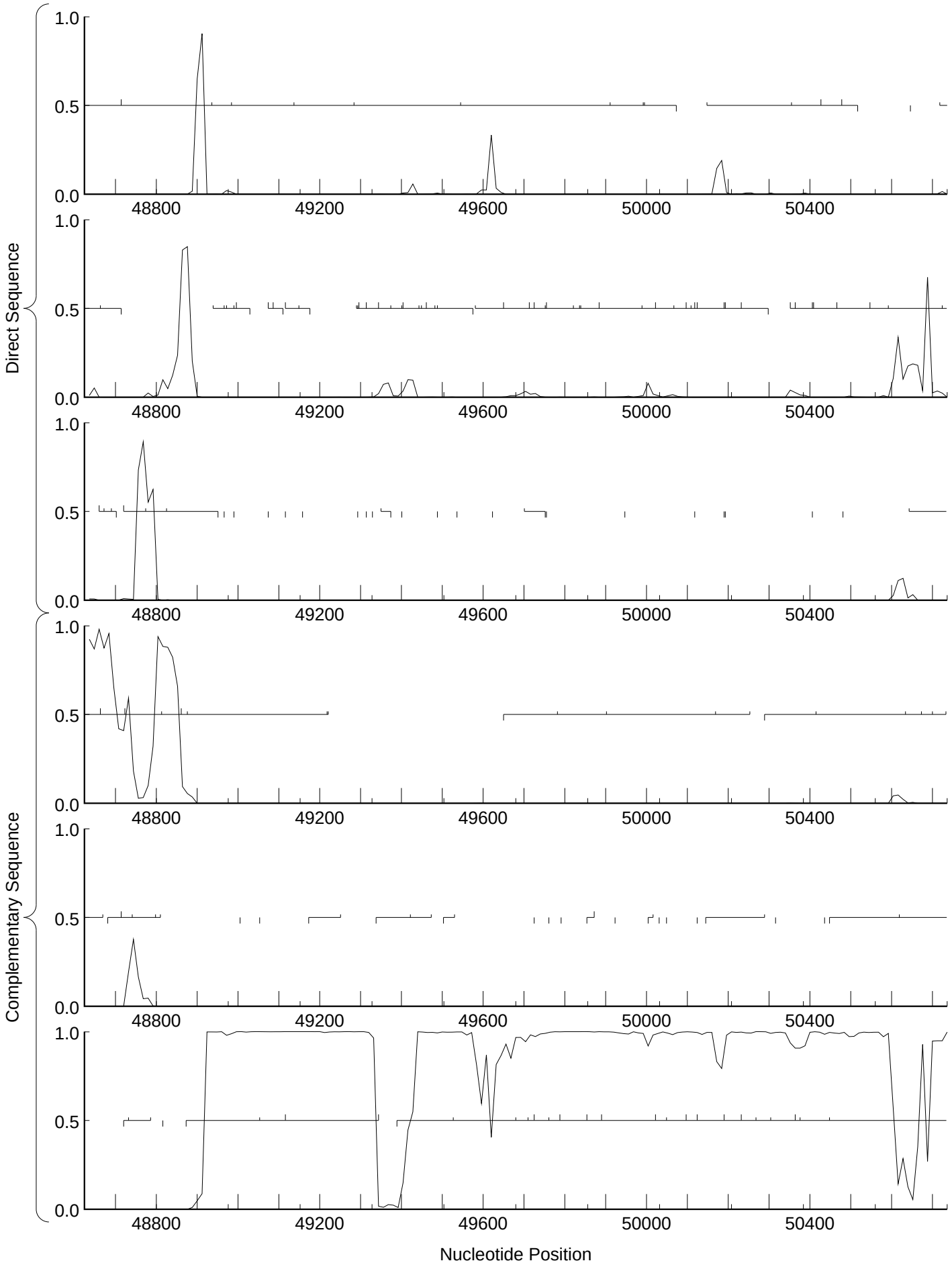

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Complementary Sequence
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41600
42000
Nucleotide Position

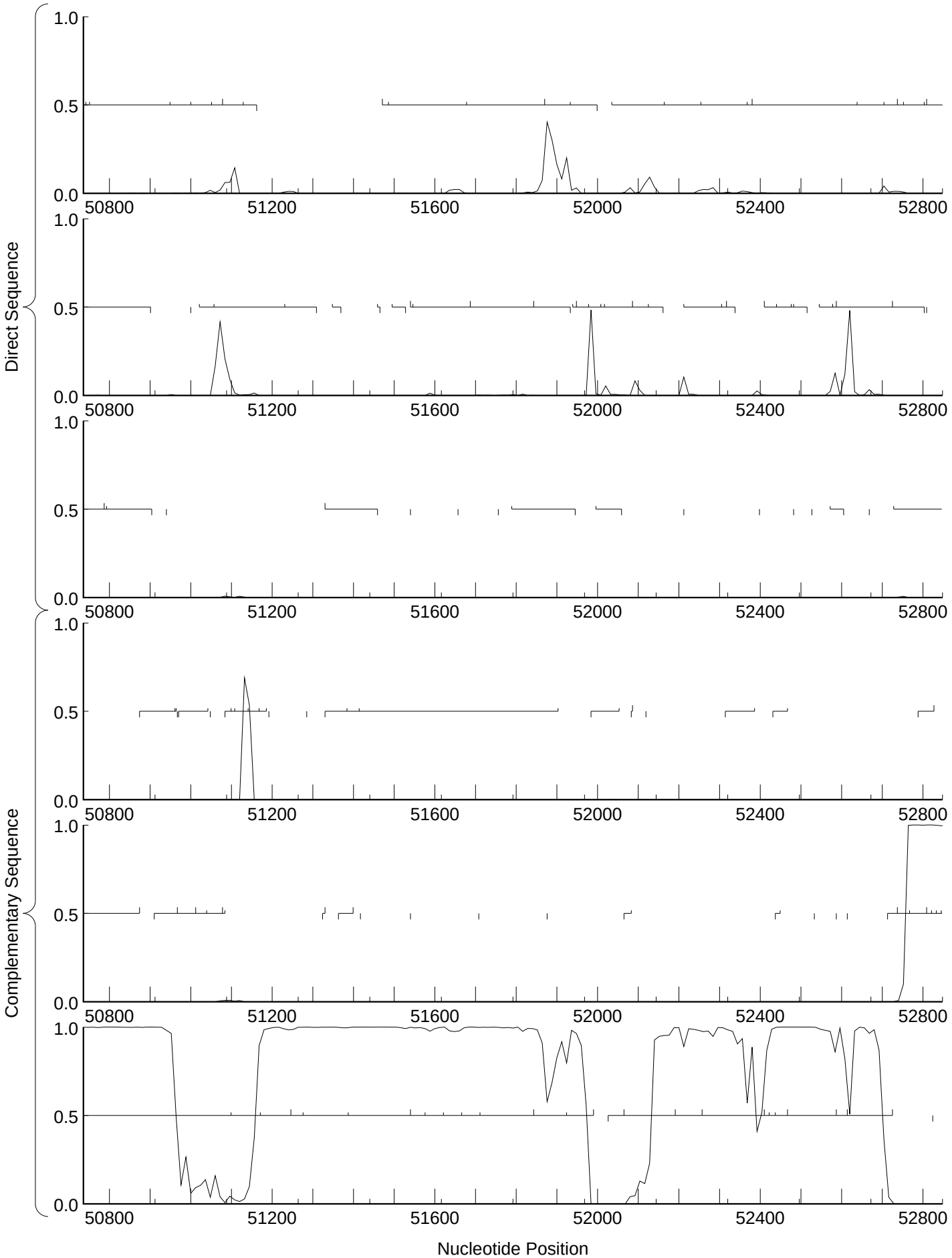

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Complementary Sequence
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0.5
0.0
42400
42800
43200
43600
44000
44400
Nucleotide Position


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

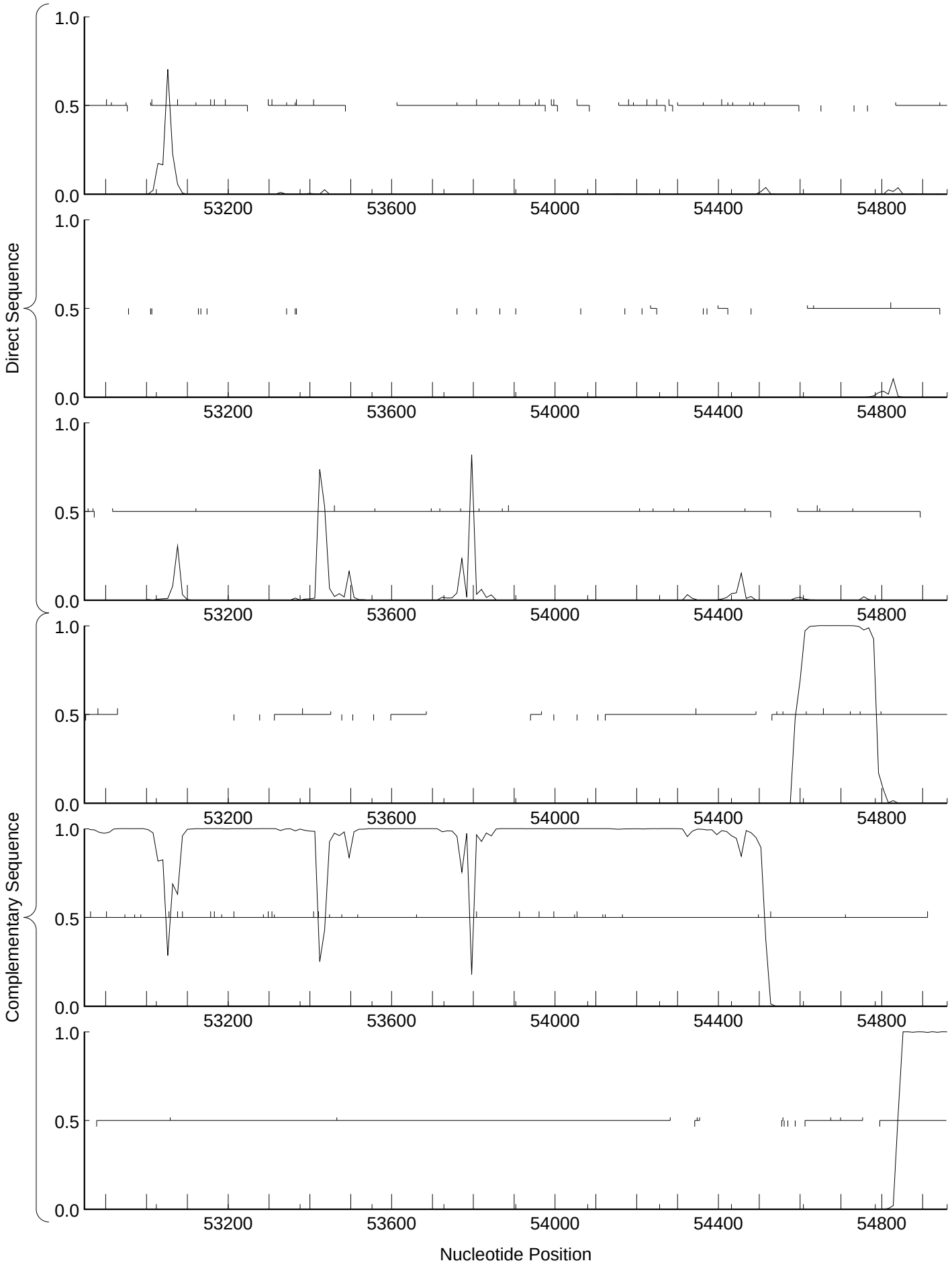

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0.0
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47600
48000
48400
Nucleotide Position

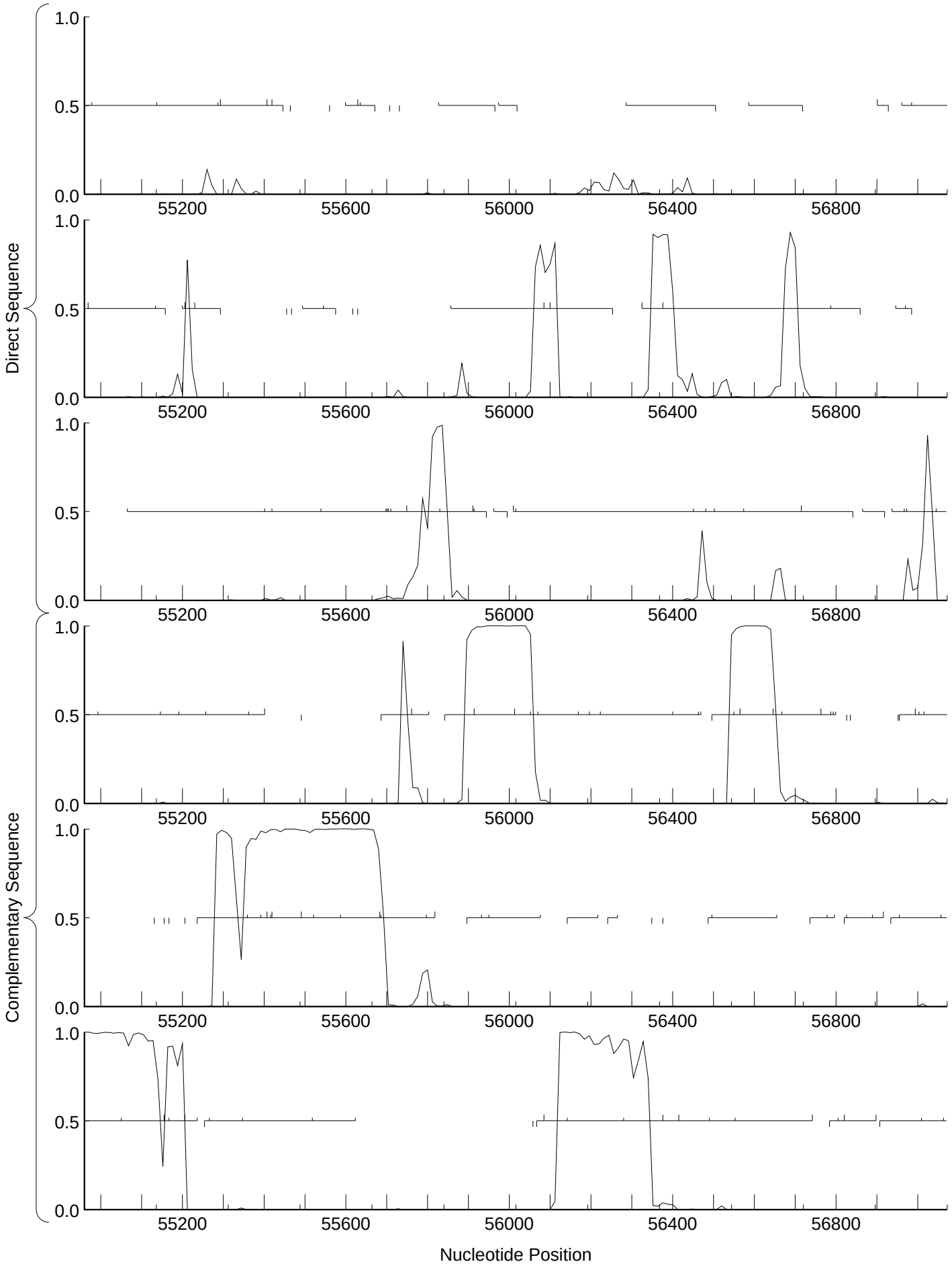
bacterium phage Marley1013 complete sequence, 69164 bp, circularly permuted, Cluster B3, Order 4, Window 96, Step 12, 25/34

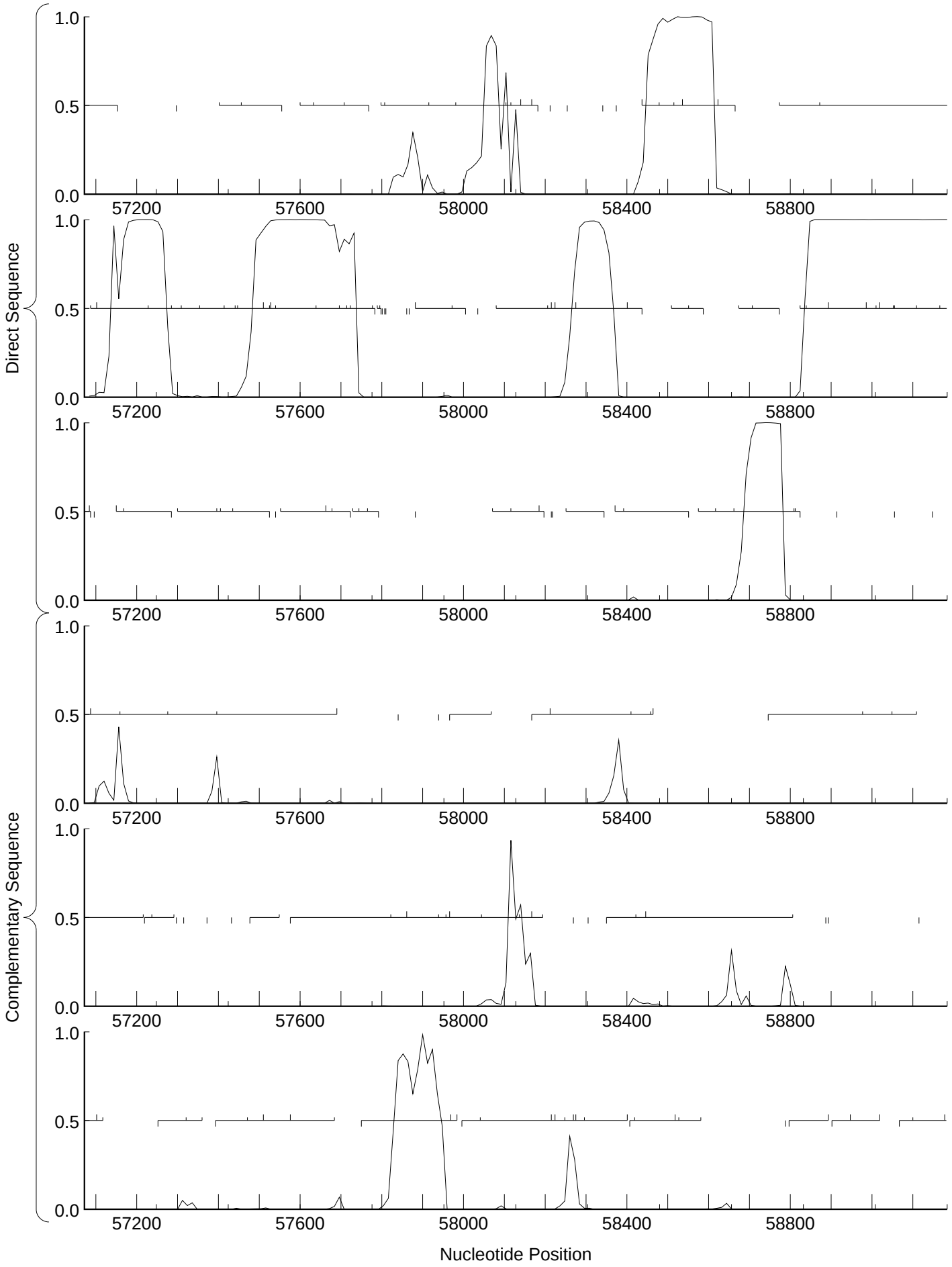


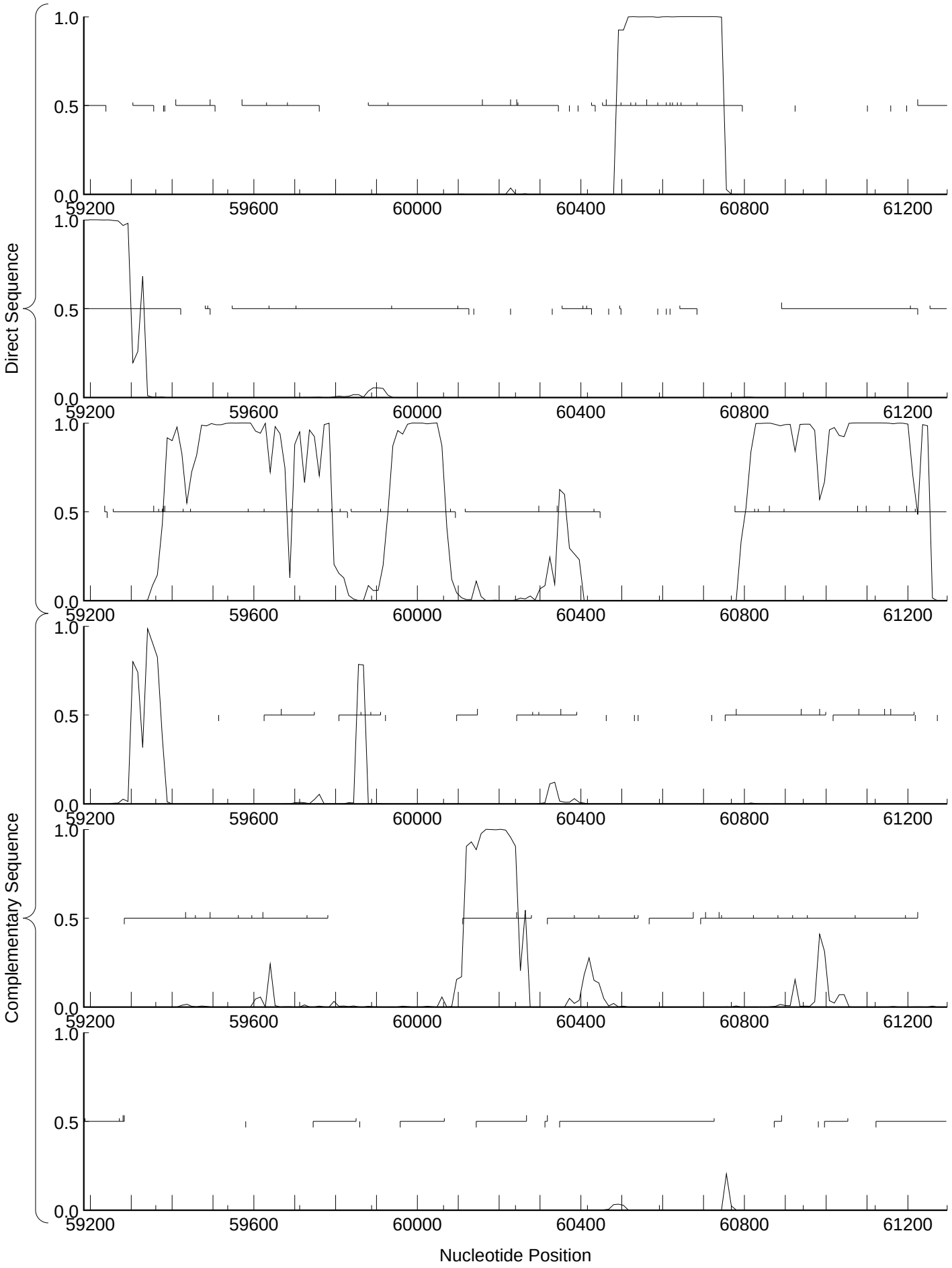

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Complementary Sequence
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0.0
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52000
52400
52800
Nucleotide Position

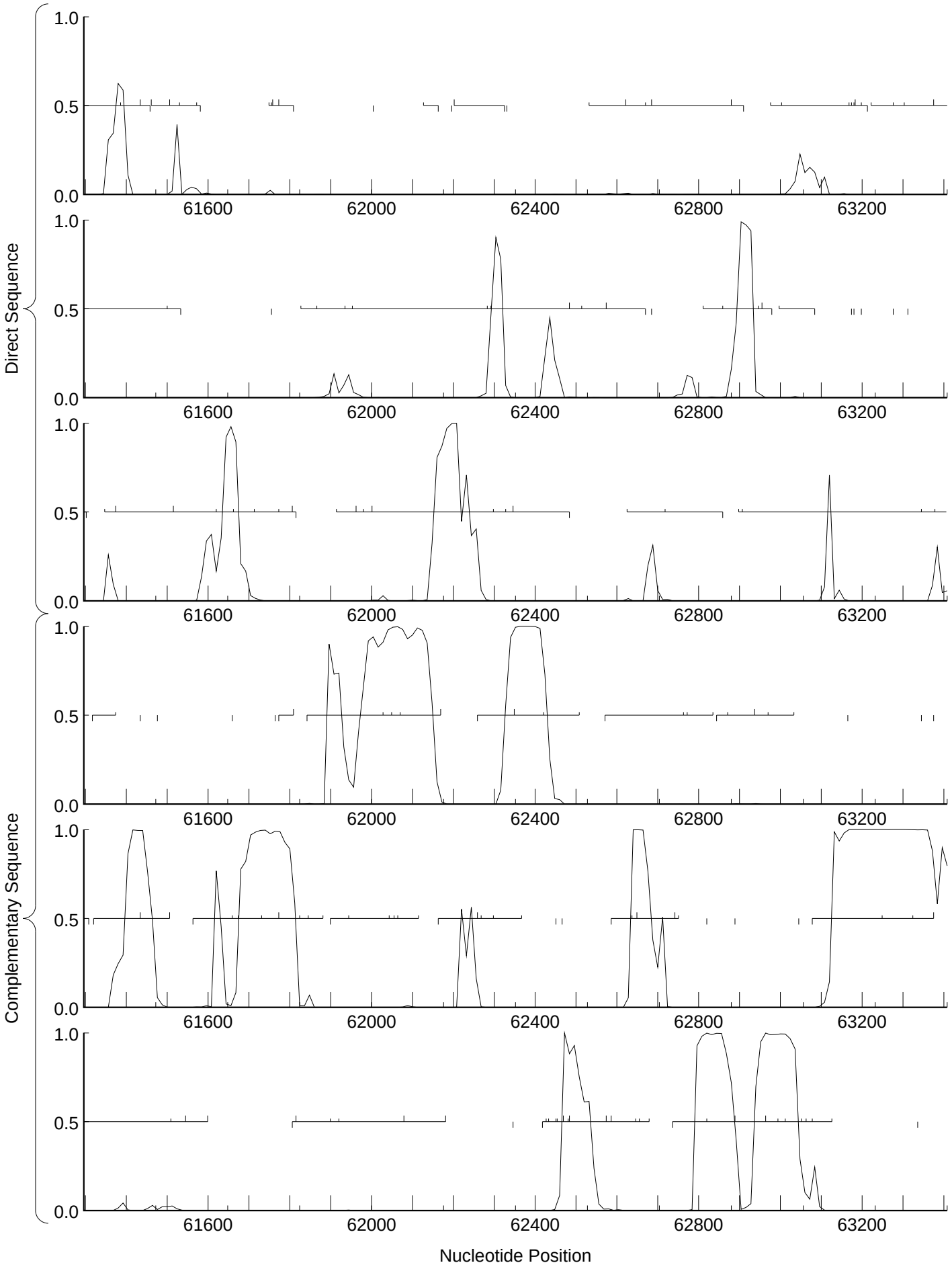
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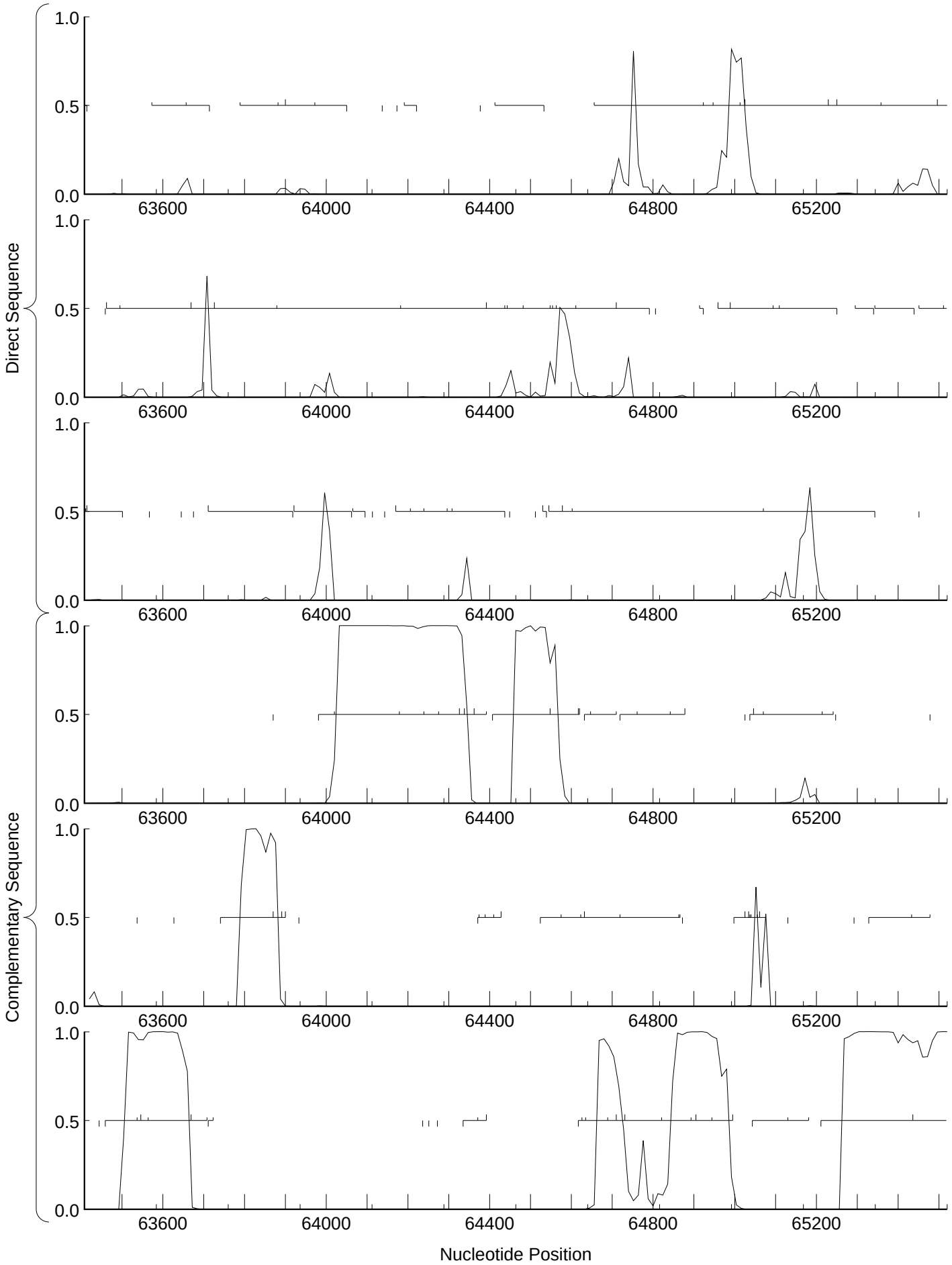



Direct Sequence
Complementary Sequence
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Nucleotide Position

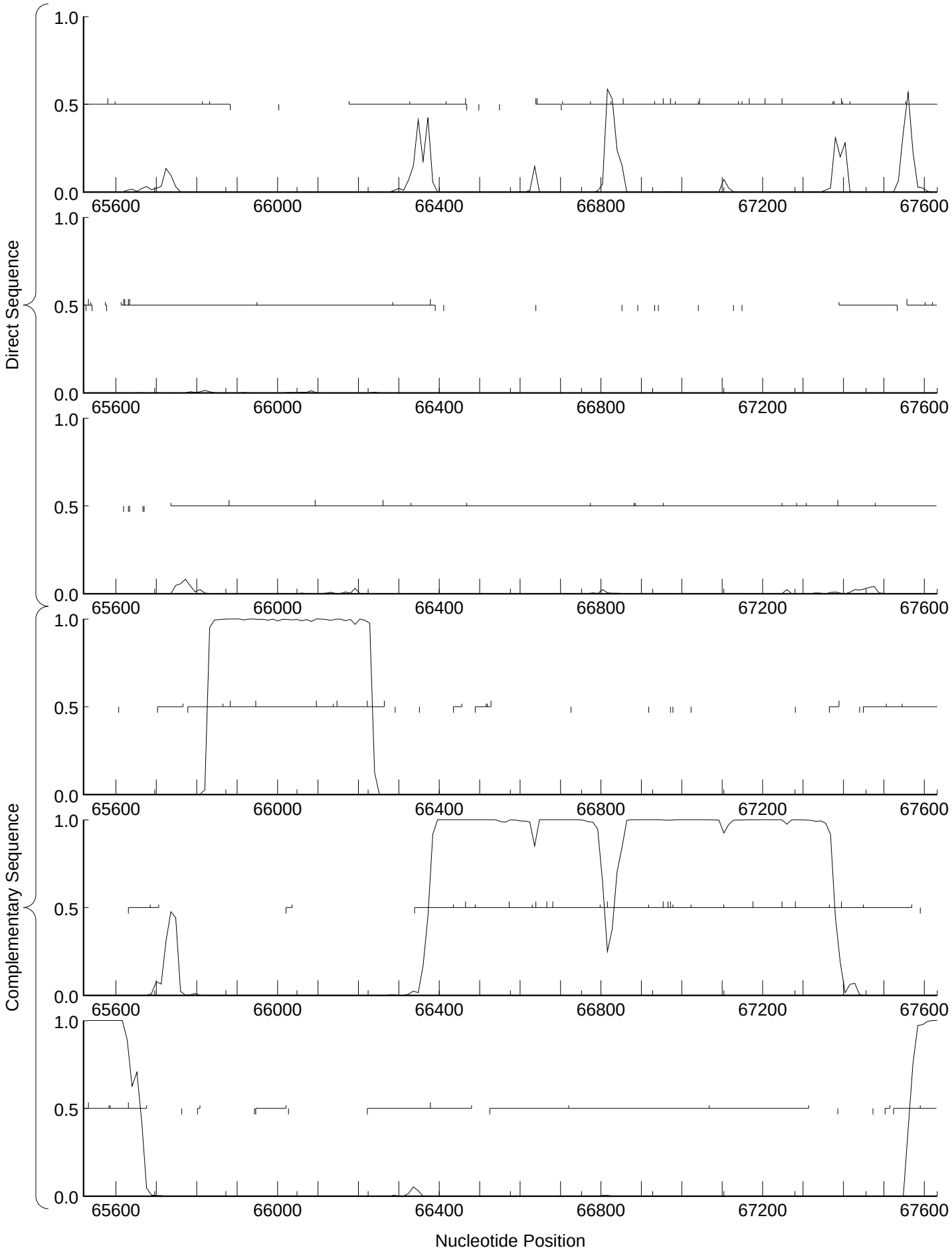

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Complementary Sequence
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0.5
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57200
57600
58000
58400
58800
Nucleotide Position


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
59200
59600
60000
60400
60800
61200
Nucleotide Position


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
61600
62000
62400
62800
63200
Nucleotide Position


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

bacterium phage Marley1013 complete sequence, 69164 bp, circularly permuted, Cluster B3, Order 4, Window 96, Step 12, 33/34



bacterium phage Marley1013 complete sequence, 69164 bp, circularly permuted, Cluster B3, Order 4, Window 96, Step 12, 34/34

