GeneMark

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

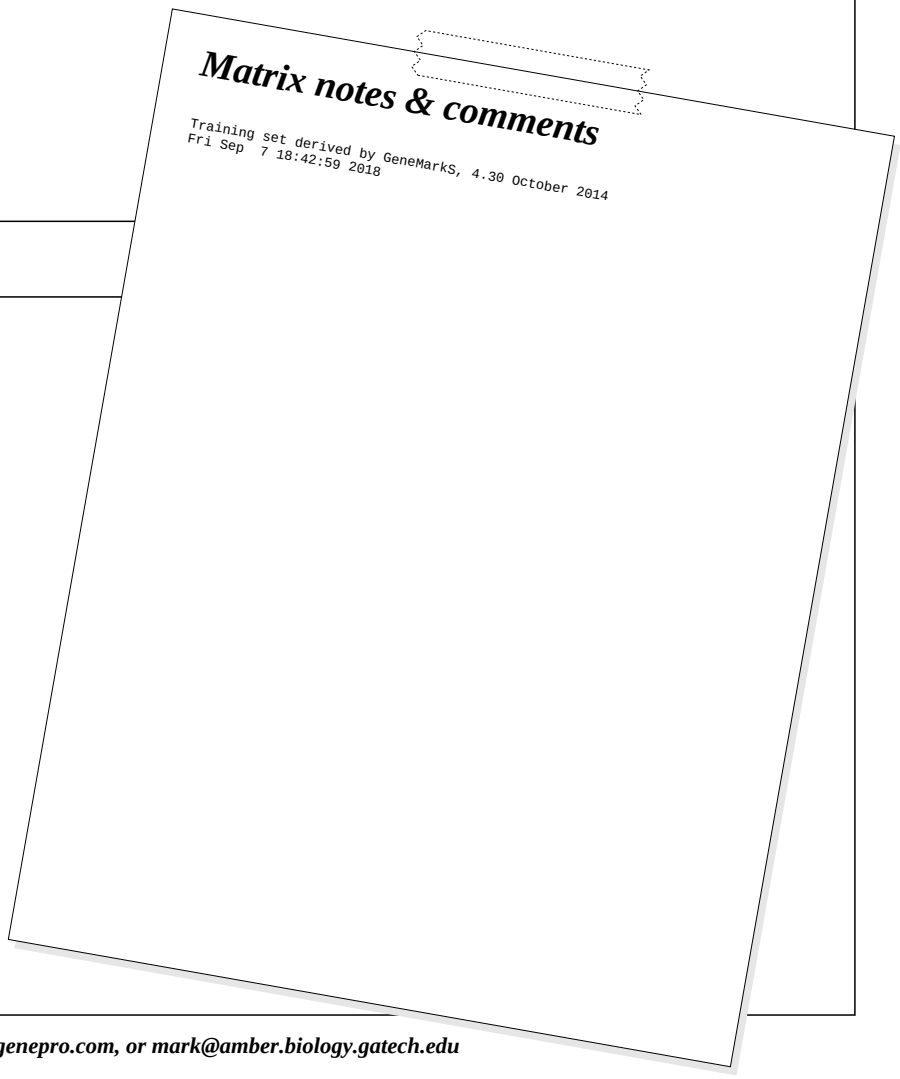
PROGRAM INFORMATION

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Sequence         :  Microbacterium phage Teagan complete sequence, 41793 bp, circularly permuted, Cluster EA1
Analysis Date    :  3/29/24 at 2:30:17
Pages            :  21
Sequence Length  :  41793 bp
GC Content       :   63.45%

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

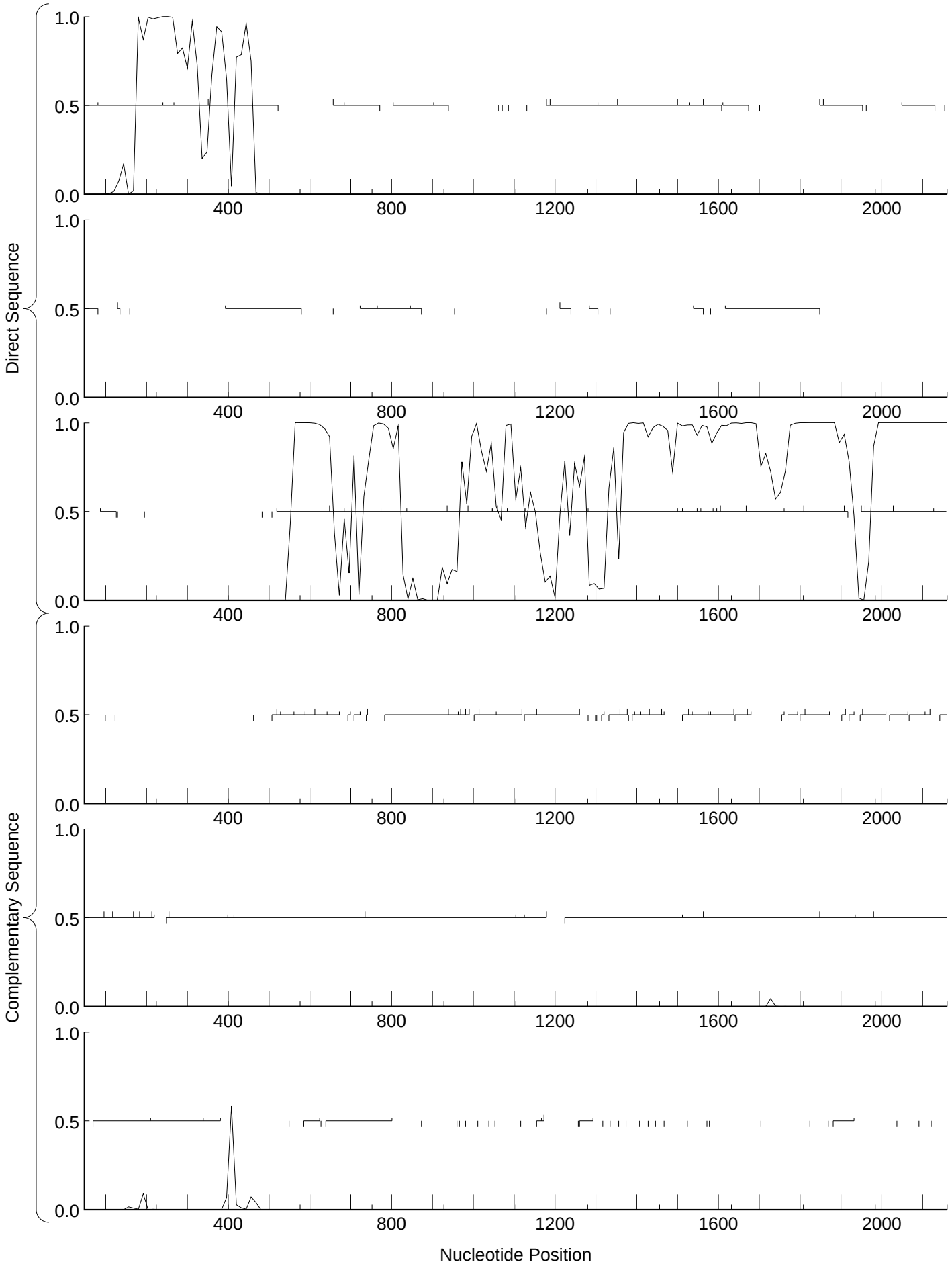
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Matrix     :  -
Author     :  -

Order      :  4
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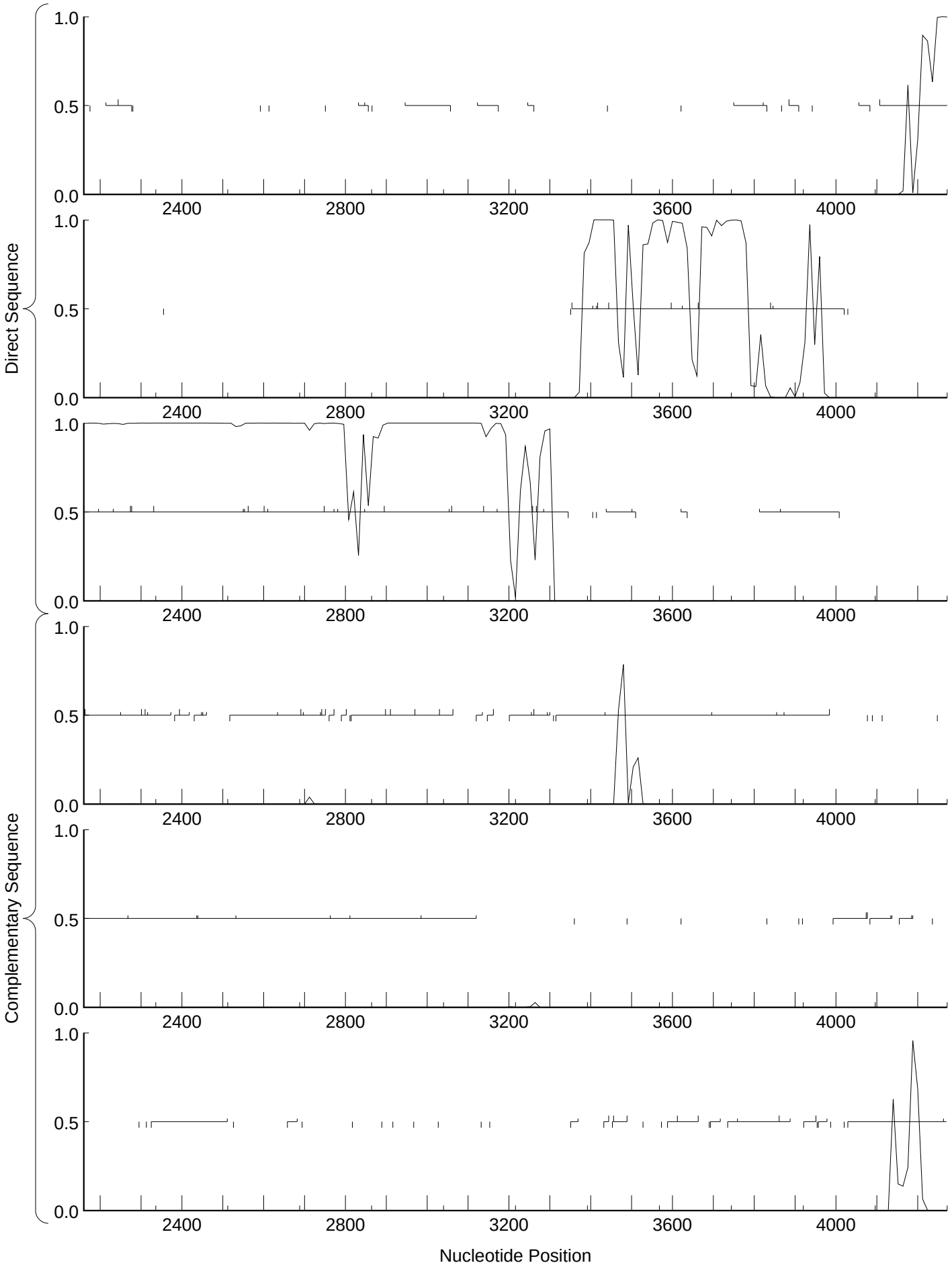

```
  Send questions / comments to:
      Dr. M. Borodovsky
      Georgia Institute of Technology
      School of Biology
      Atlanta, GA  30332-0230
```


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

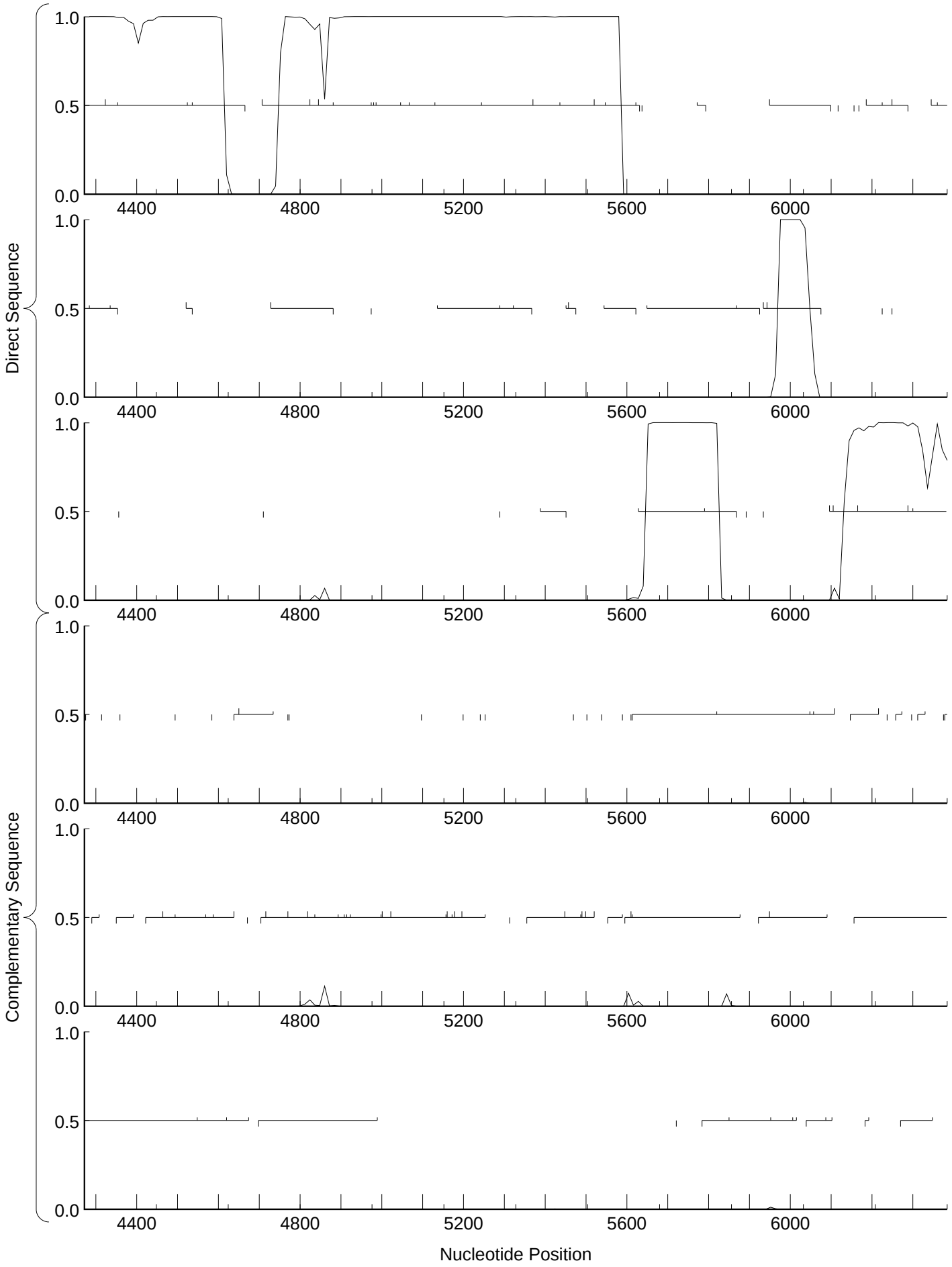
icrobacterium phage Teagan complete sequence, 41793 bp, circularly permuted, Cluster EA1, Order 4, Window 96, Step 12, 2/21



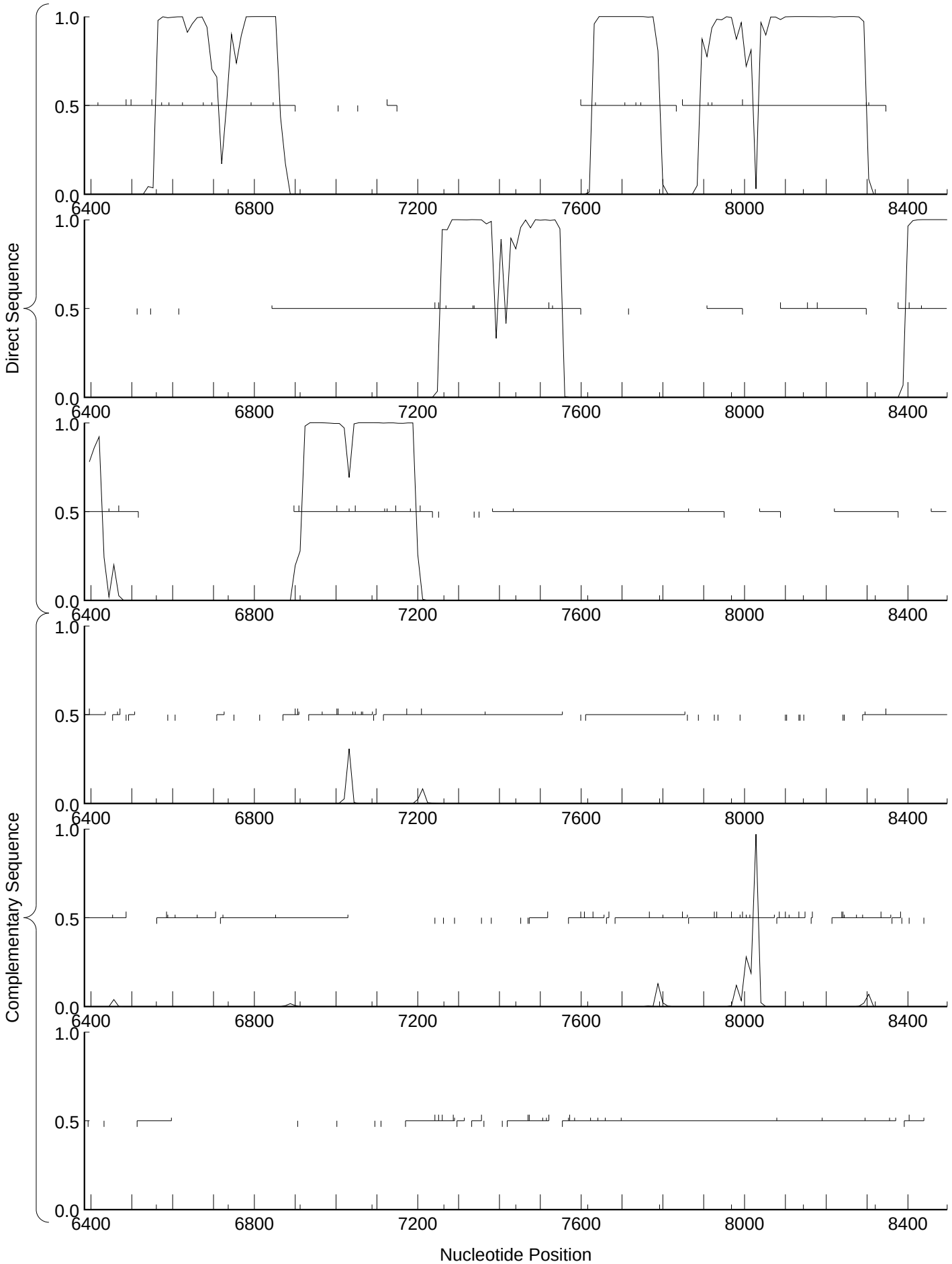
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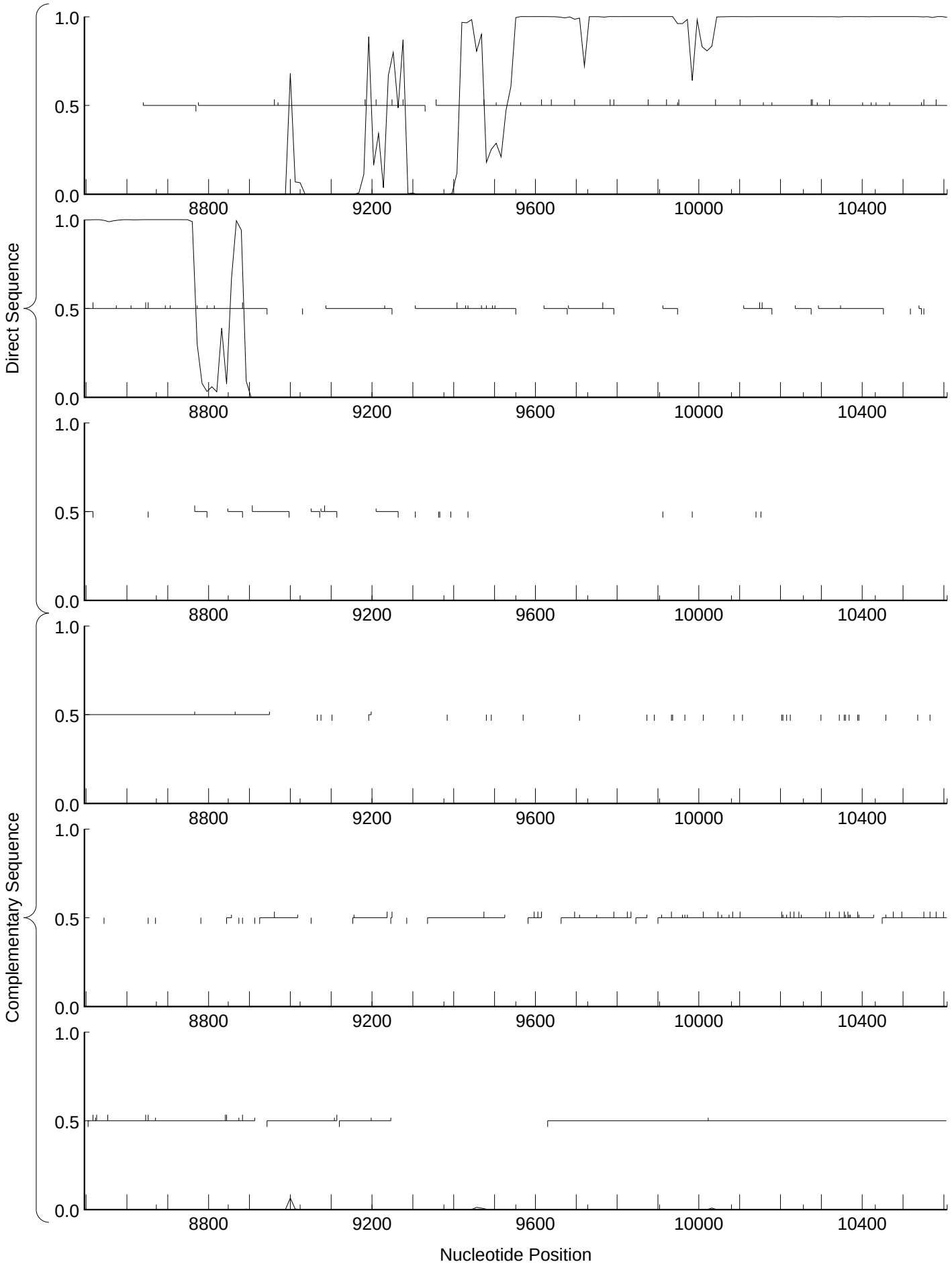
icrobacterium phage Teagan complete sequence, 41793 bp, circularly permuted, Cluster EA1, Order 4, Window 96, Step 12, 4/21



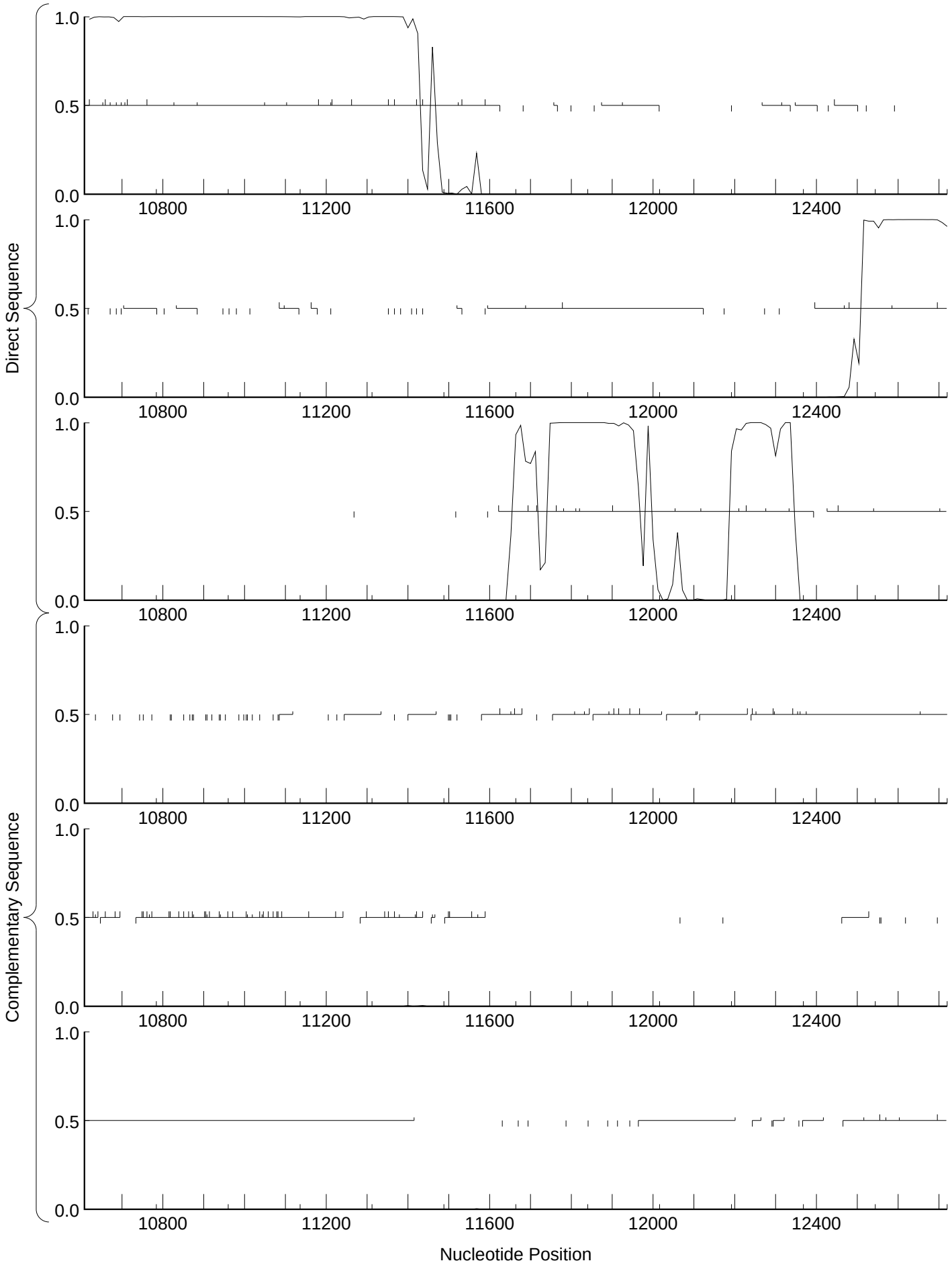
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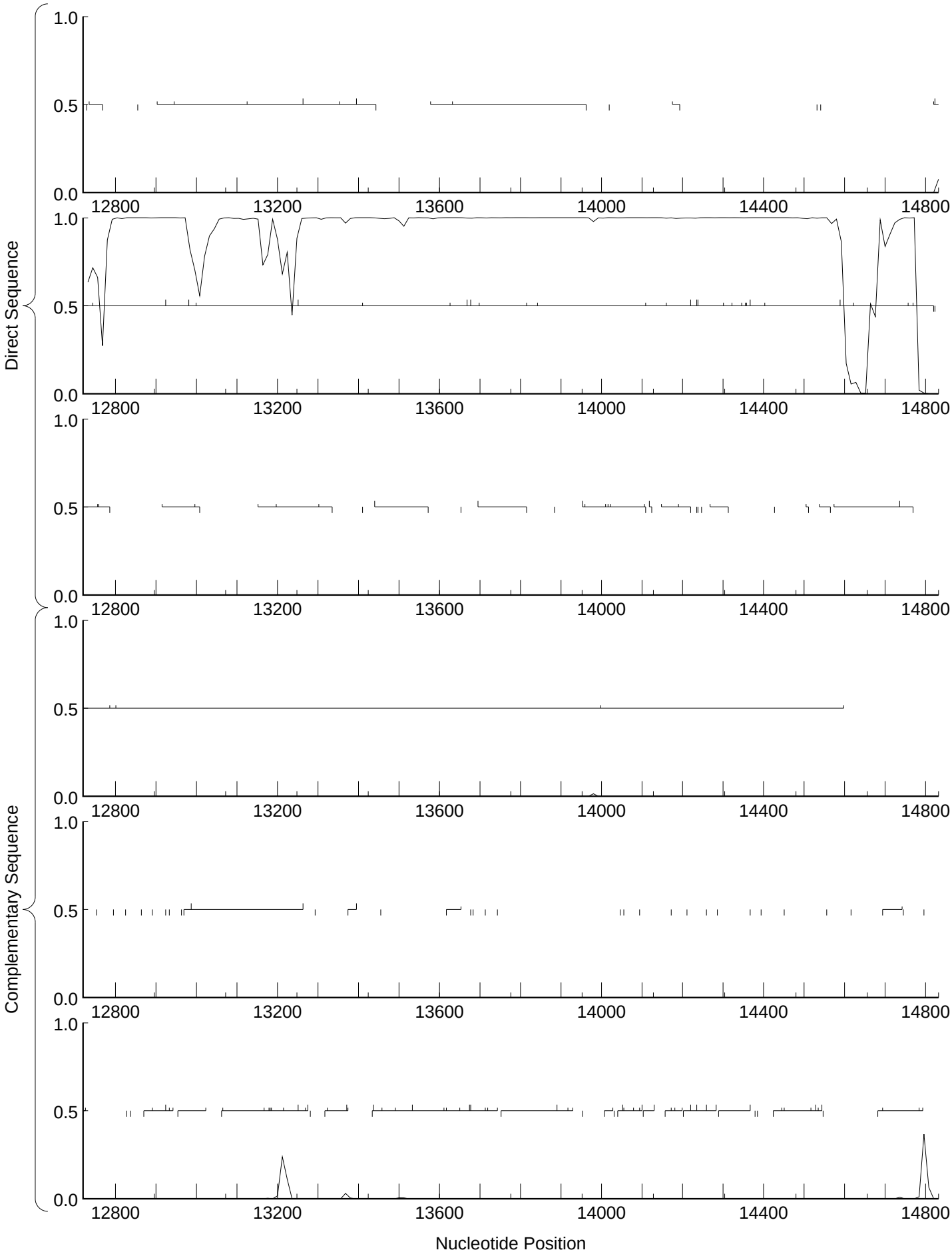
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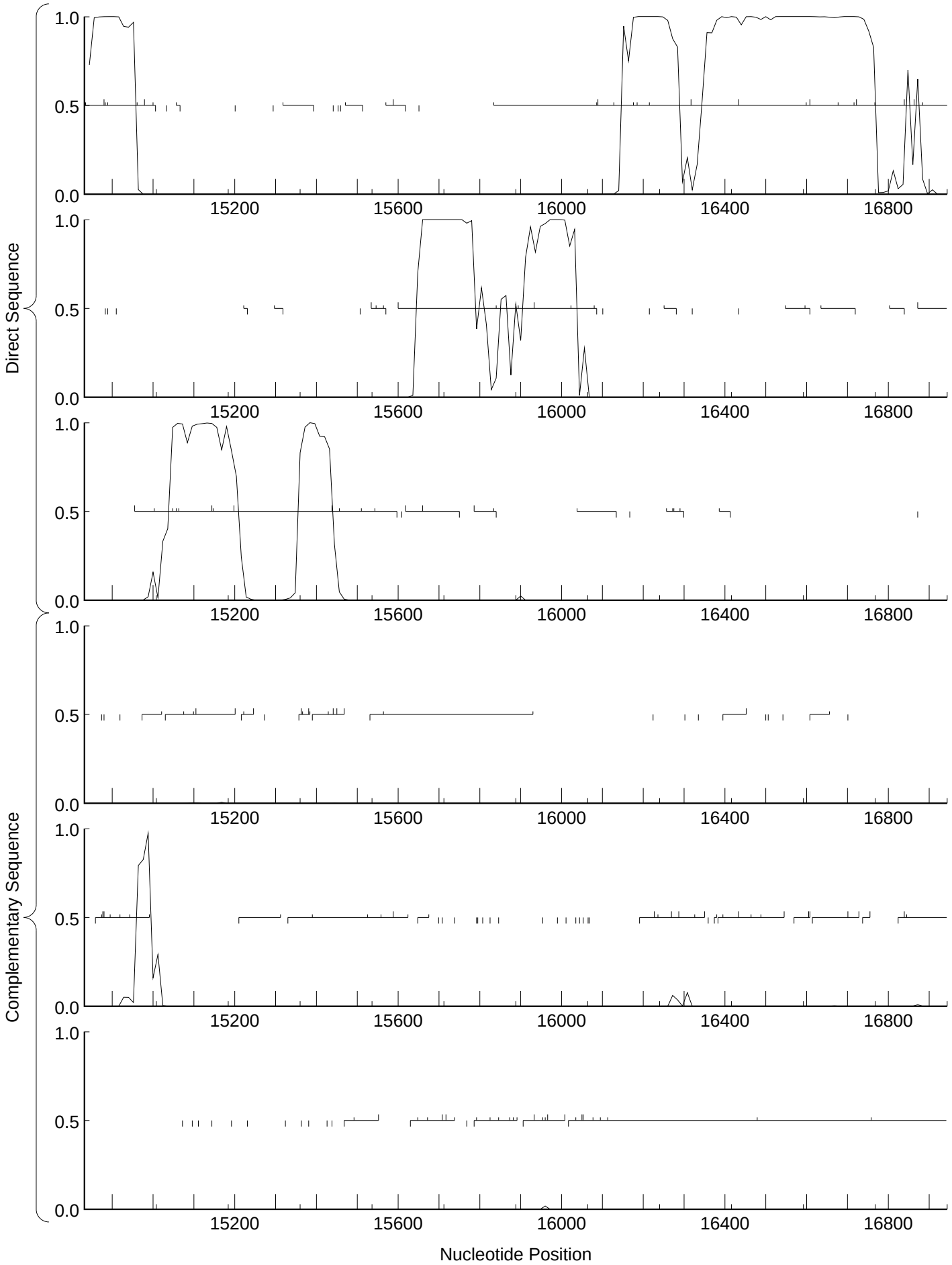
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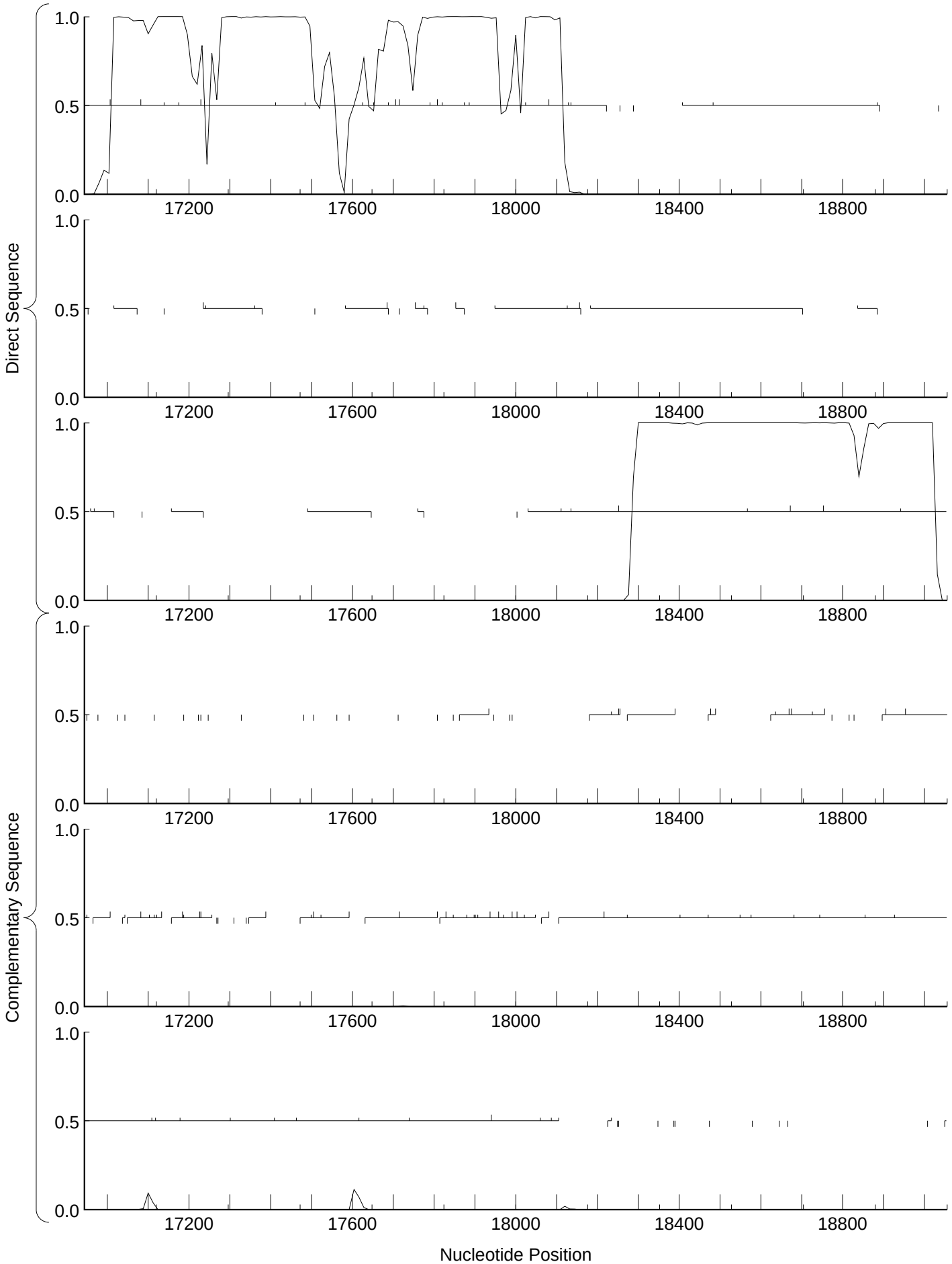
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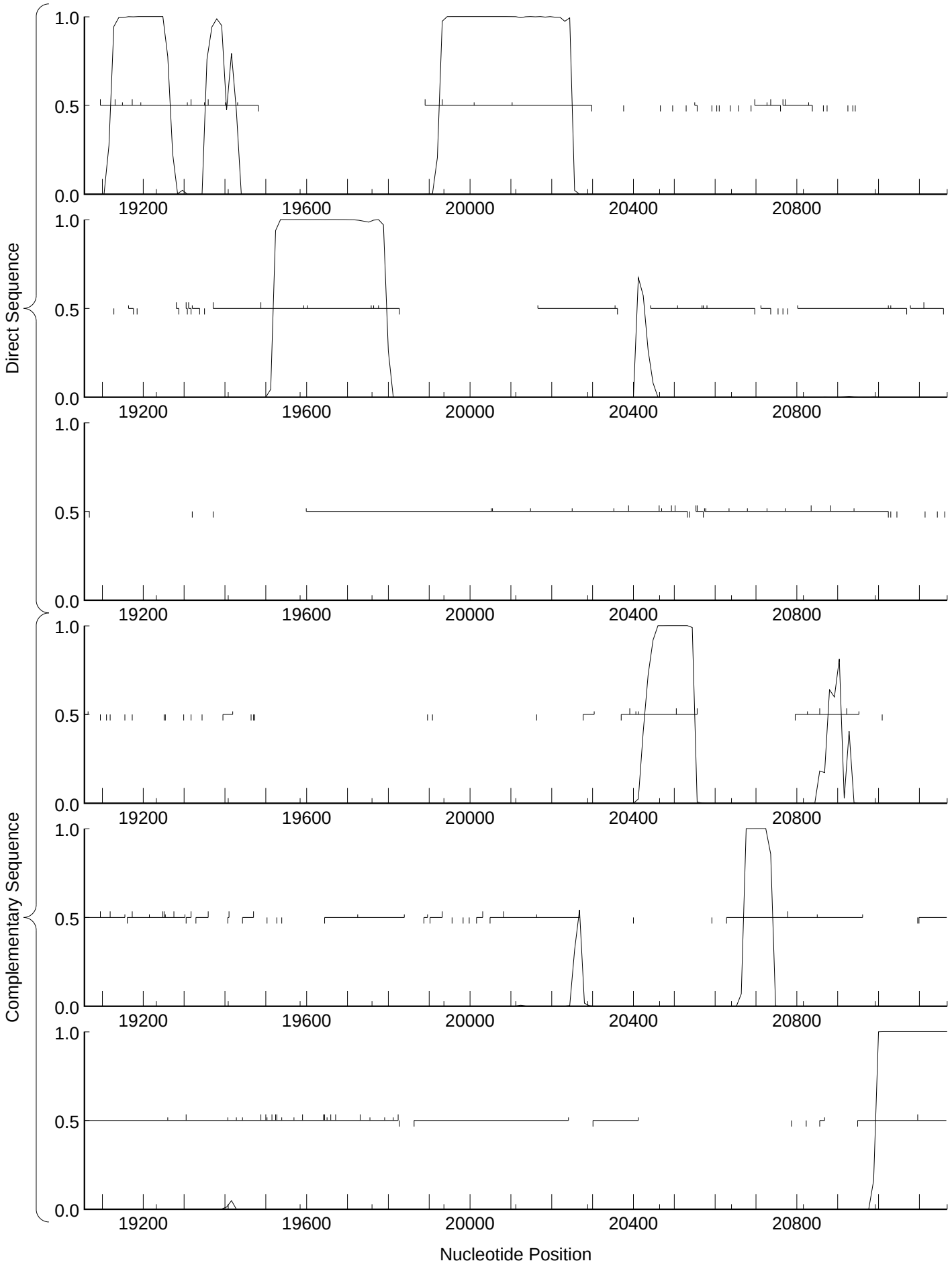
icrobacterium phage Teagan complete sequence, 41793 bp, circularly permuted, Cluster EA1, Order 4, Window 96, Step 12, 9/21



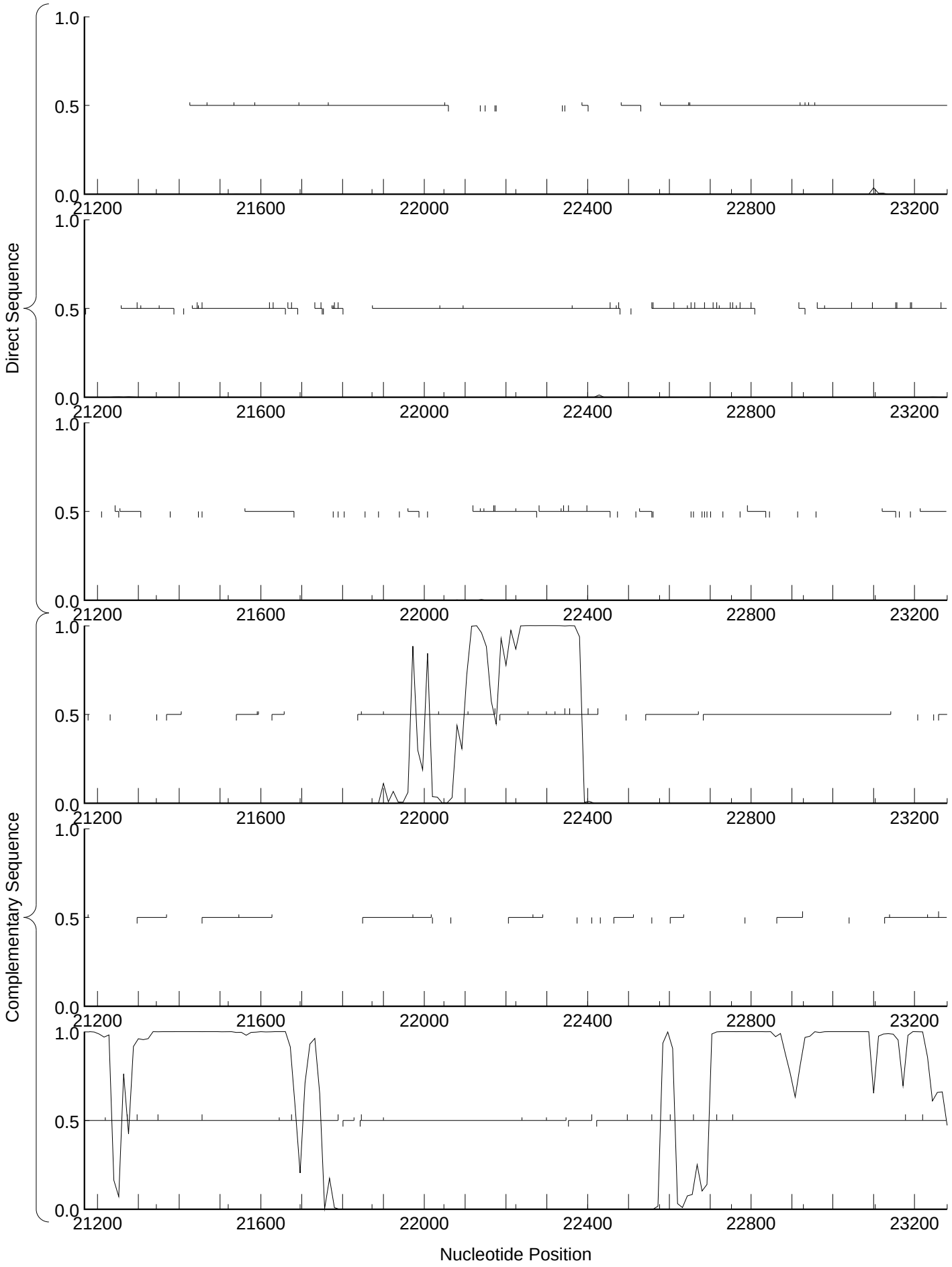
crobacterium phage Teagan complete sequence, 41793 bp, circularly permuted, Cluster EA1, Order 4, Window 96, Step 12, 10/21



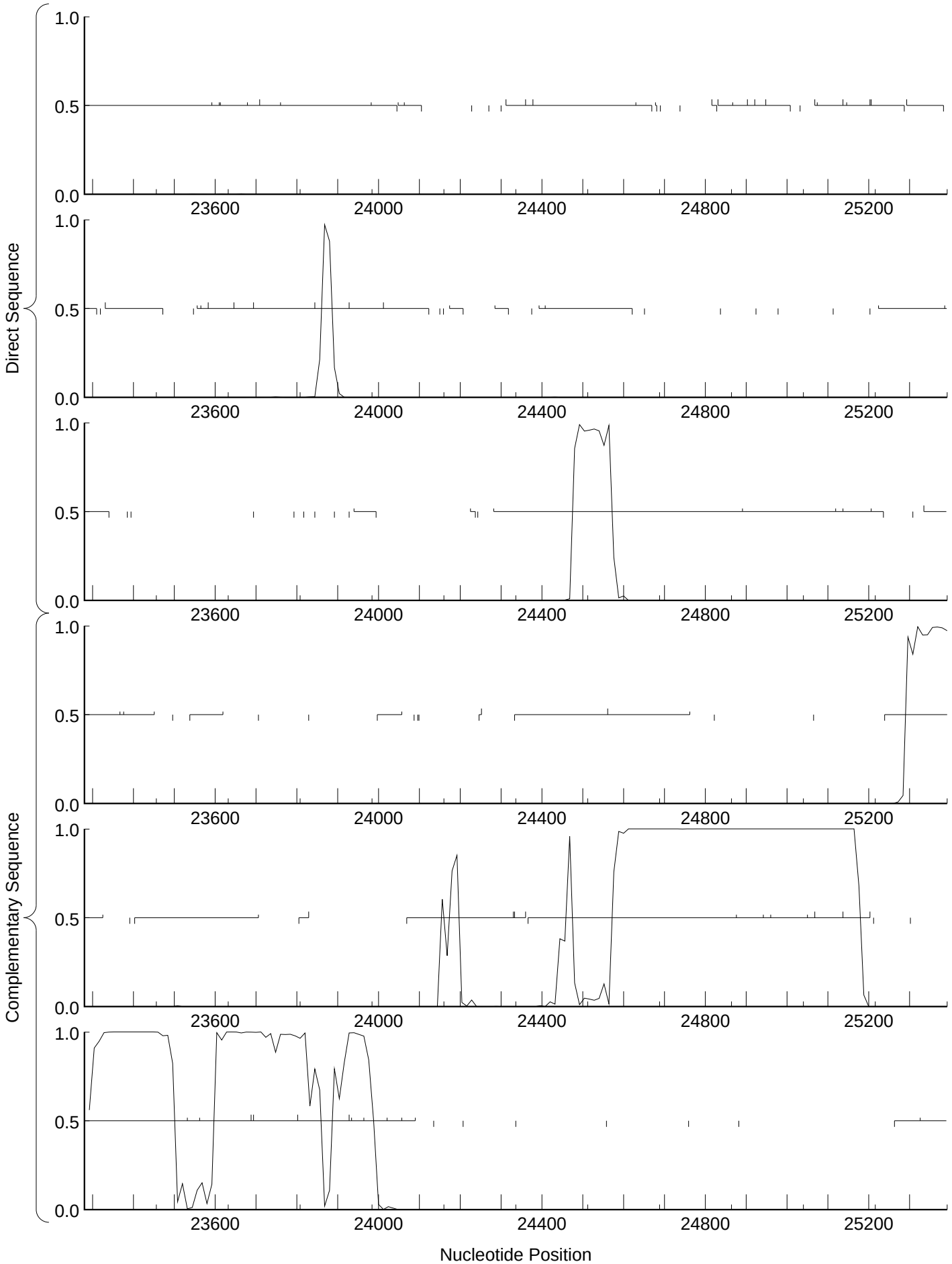
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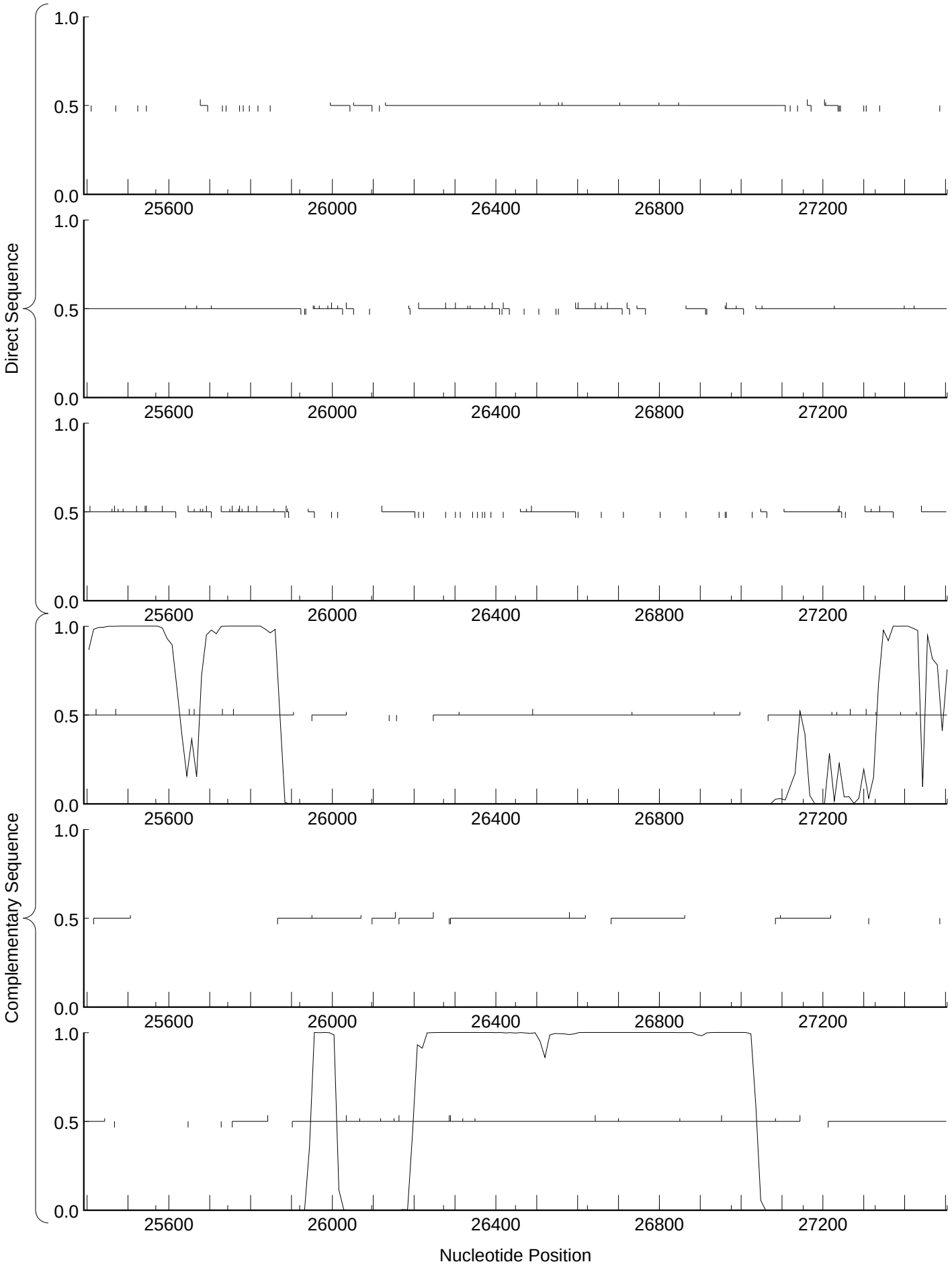


crobacterium phage Teagan complete sequence, 41793 bp, circularly permuted, Cluster EA1, Order 4, Window 96, Step 12, 12/21

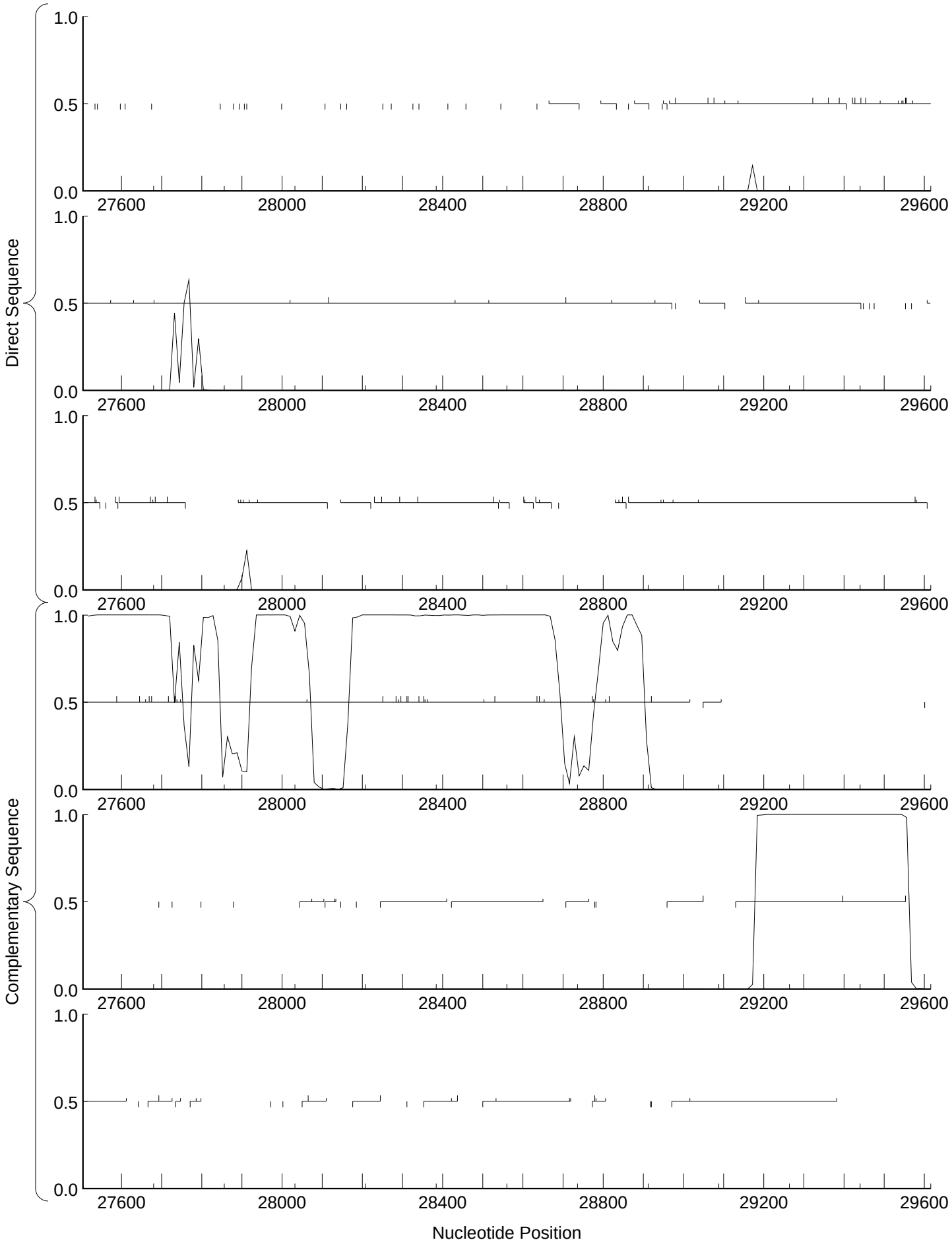


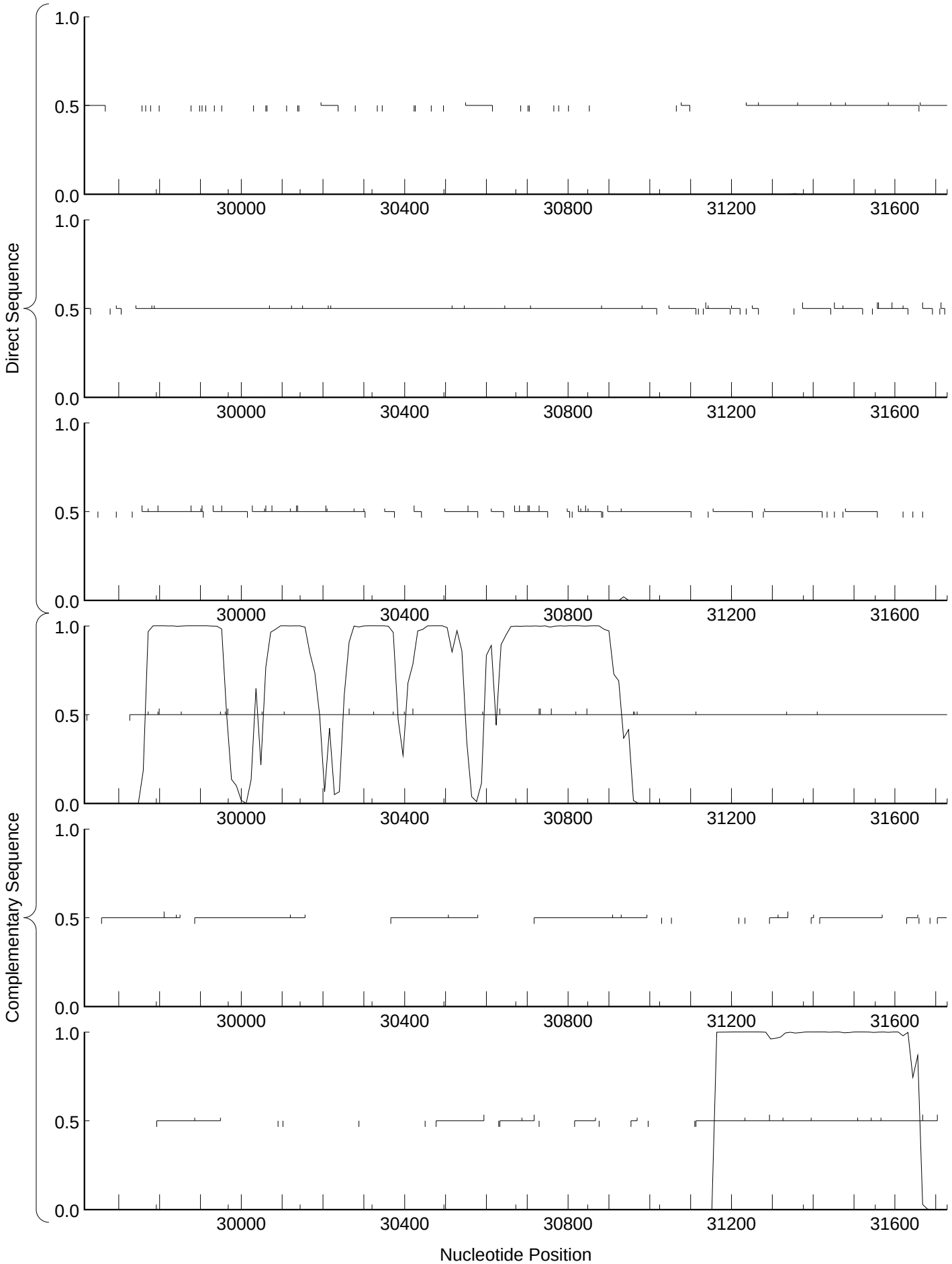
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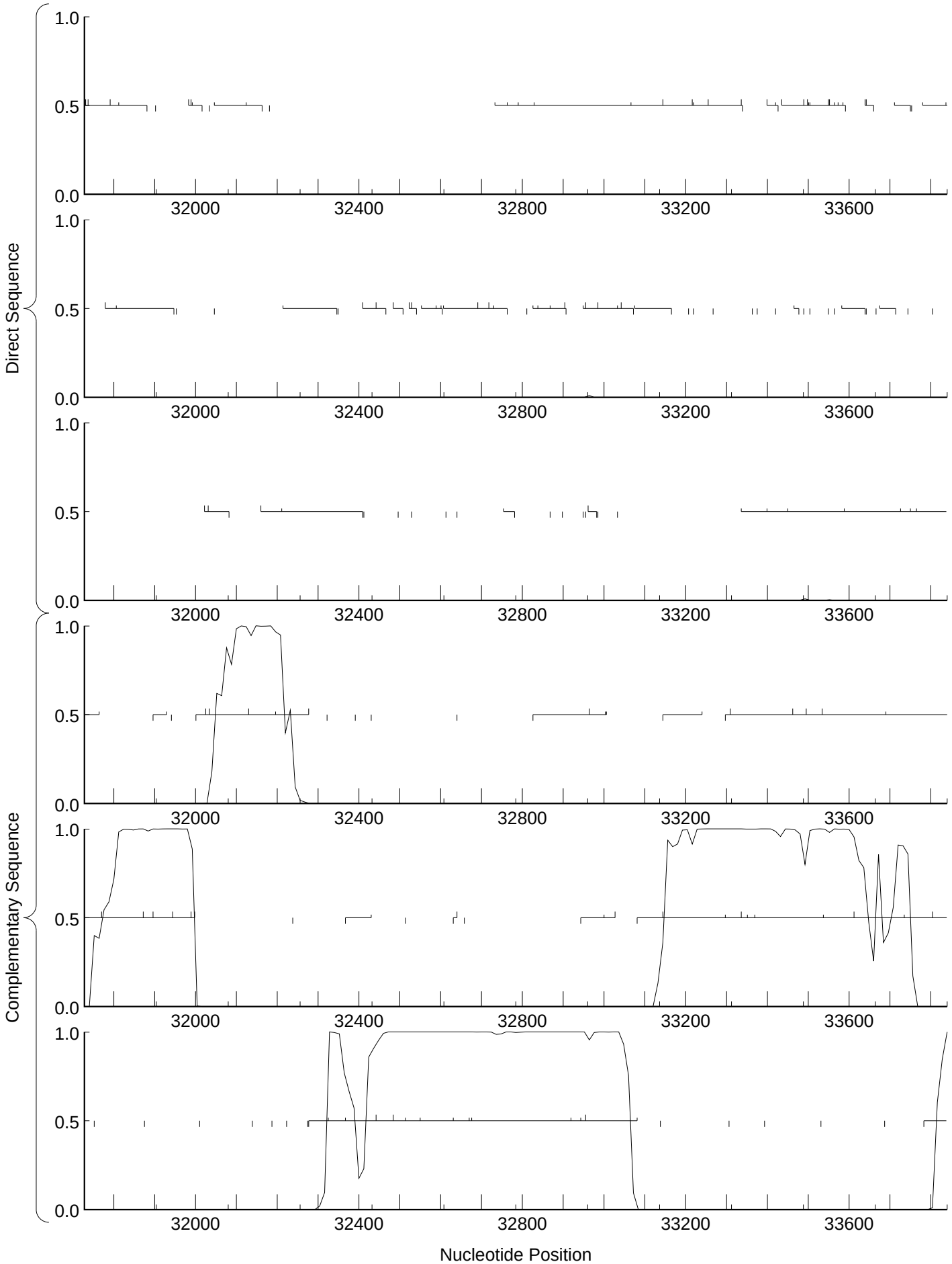


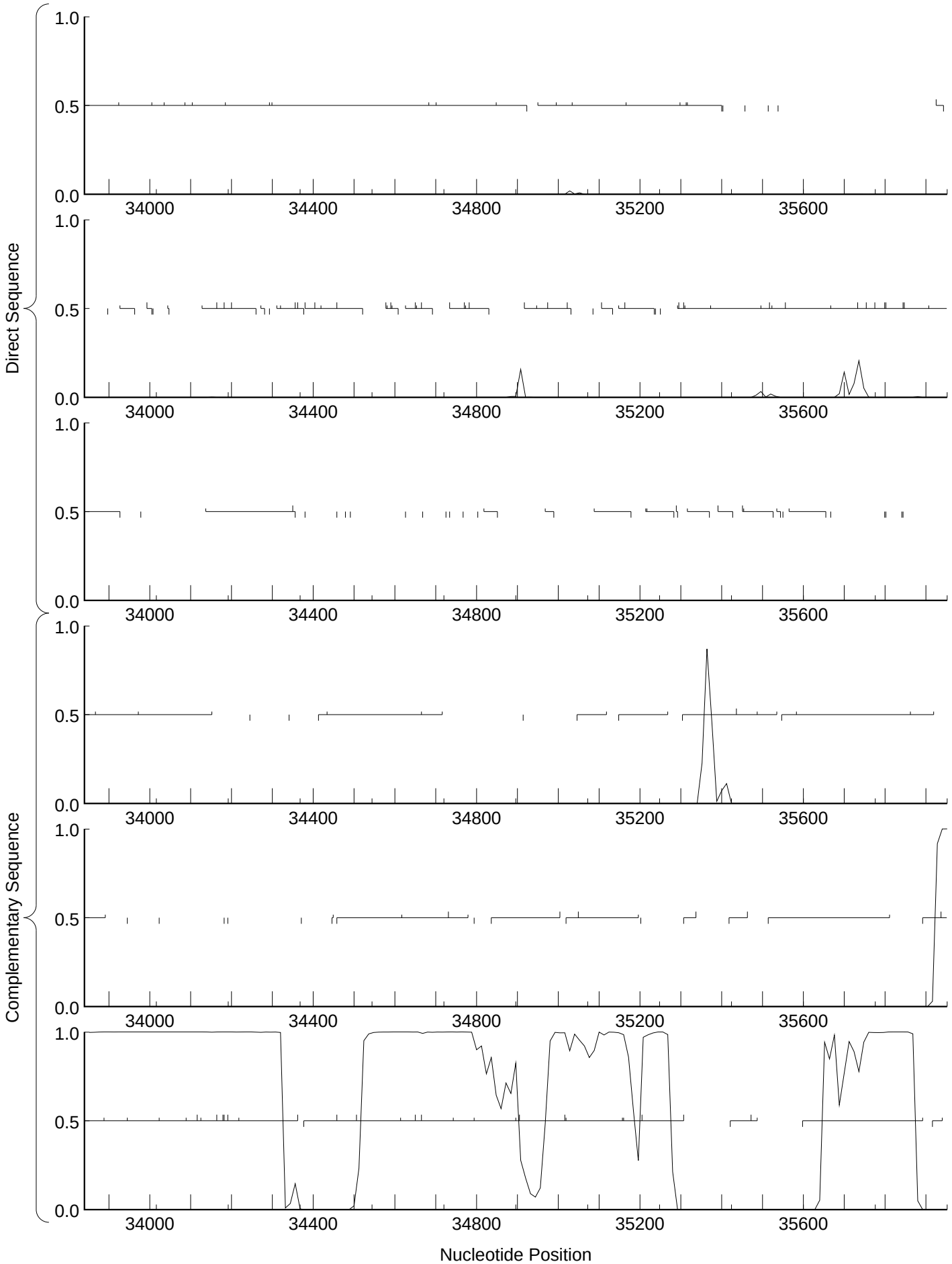

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
25600
26000
26400
26800
27200
Nucleotide Position

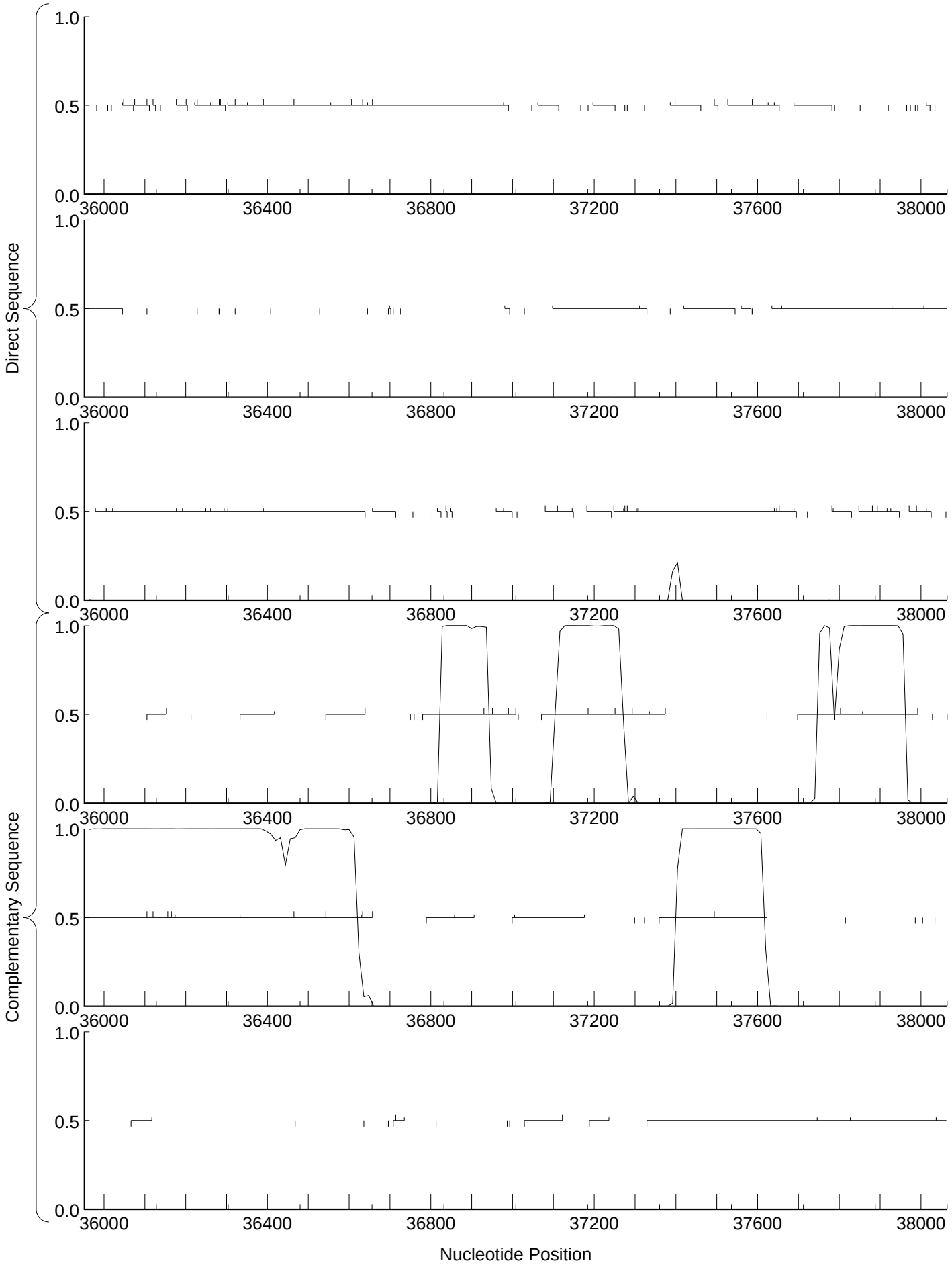
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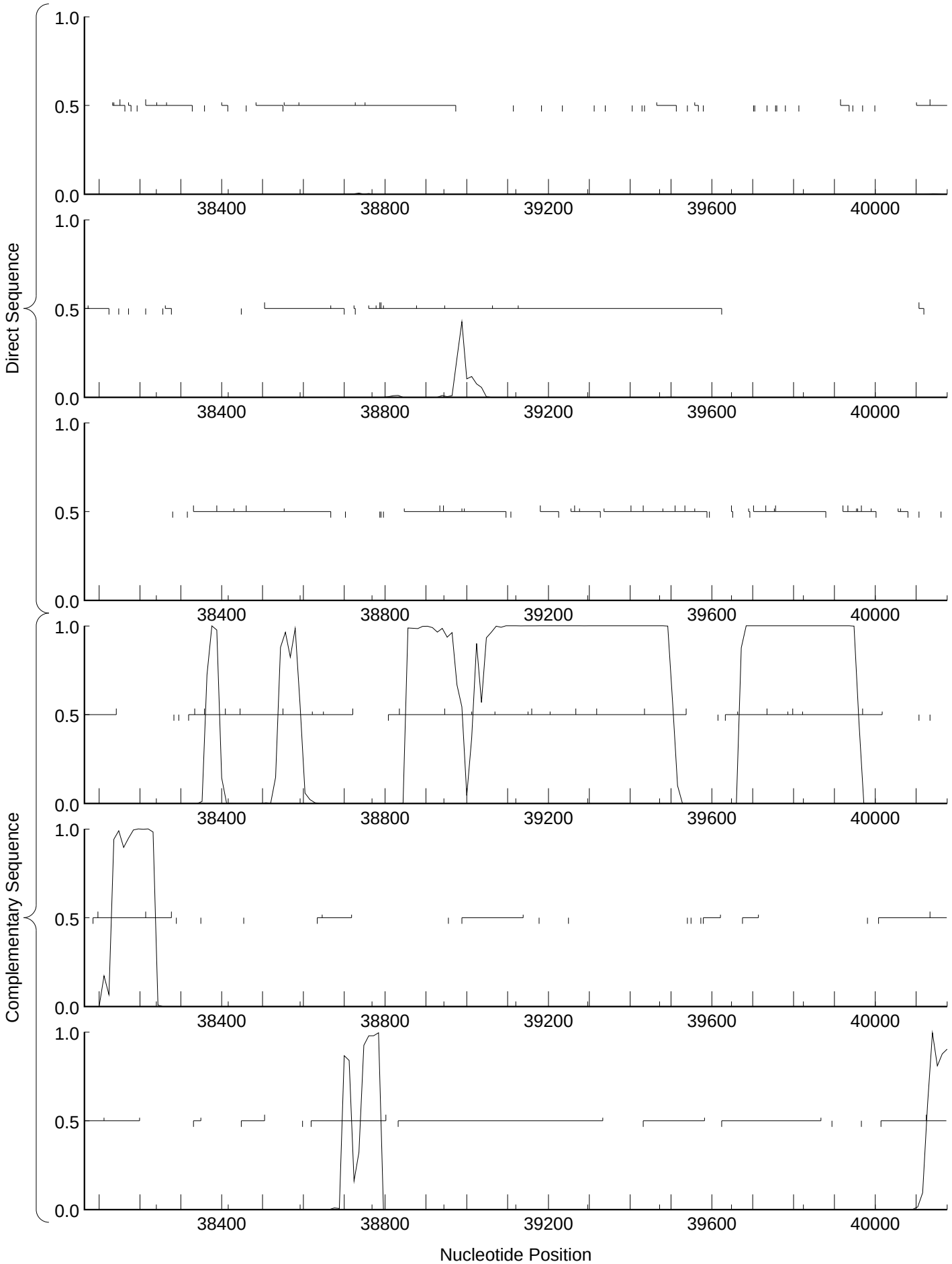


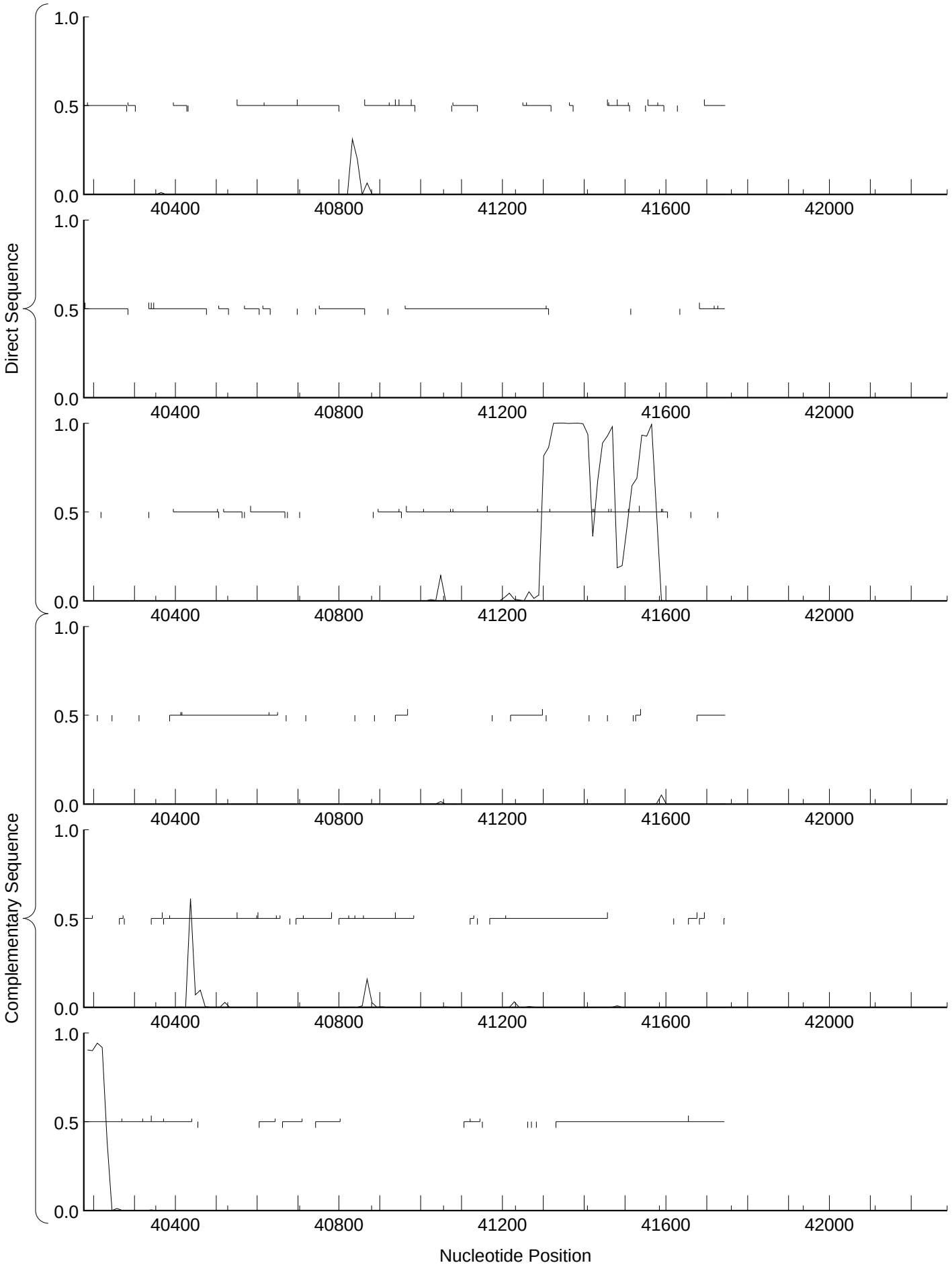

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
30000
30400
30800
31200
31600
Nucleotide Position


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


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