GeneMark

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

PROGRAM INFORMATION

```
Sequence         :  Gordonia phage ChisanaKitsune complete sequence, 88657 bp, circularly permuted, Cluster DQ
Analysis Date    :  3/28/24 at 10:22:27
Pages            :  43
Sequence Length  :  88657 bp
GC Content       :   60.03%

Window Length    :  96 bp
Window Step      :  12 bp
Threshold Value  :  0.500

PS-Version       :  1.2

GeneMark Options :  PostScript graph,
                    Mark ORFs / splice sites,
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                    List regions and/or splice sites,
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MATRIX INFORMATION

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Matrix     :  -
Author     :  -

Order      :  4

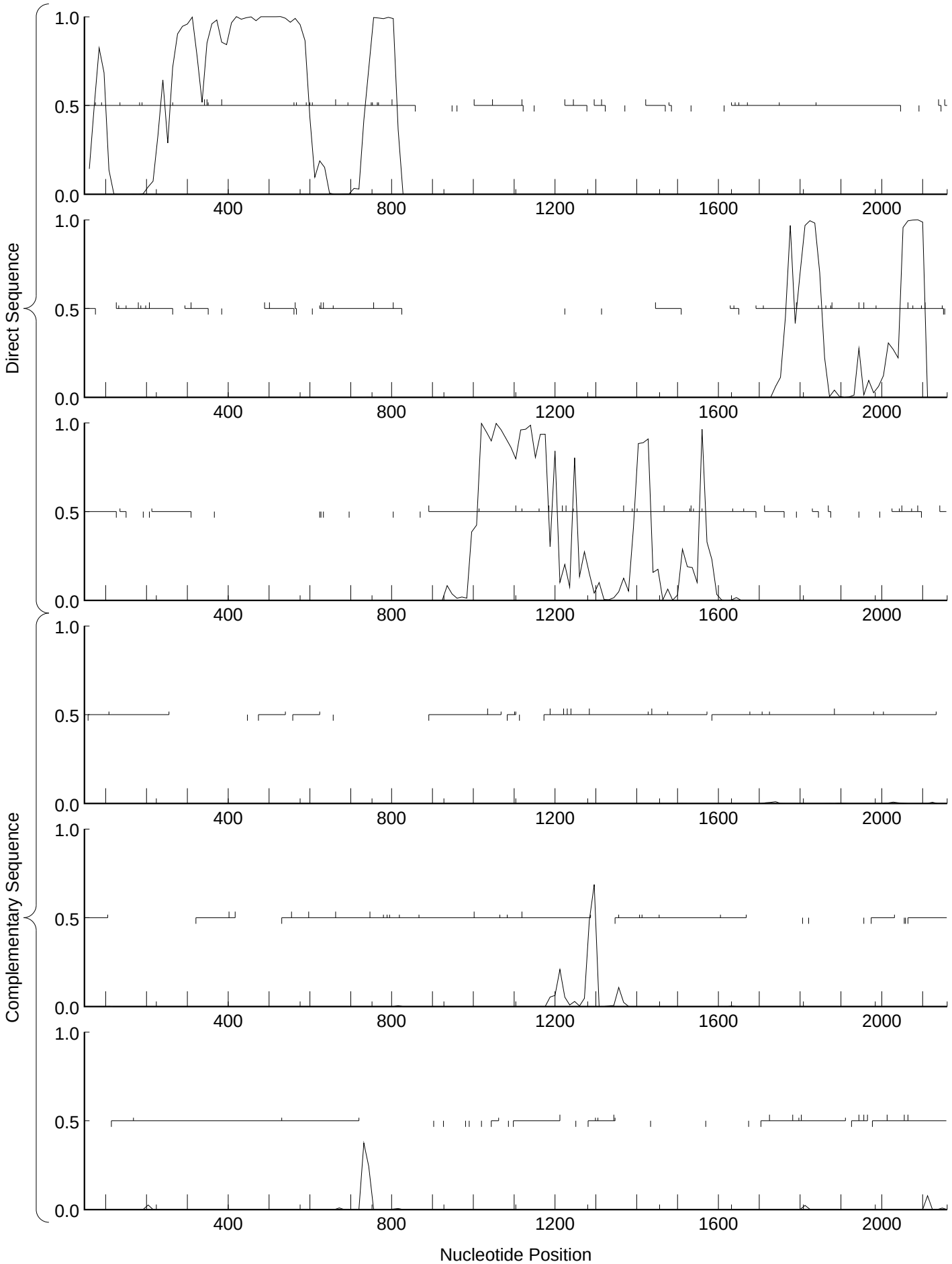

  Send questions / comments to:
      Dr. M. Borodovsky
      Georgia Institute of Technology
      School of Biology
      Atlanta, GA  30332-0230
```

Matrix notes & comments

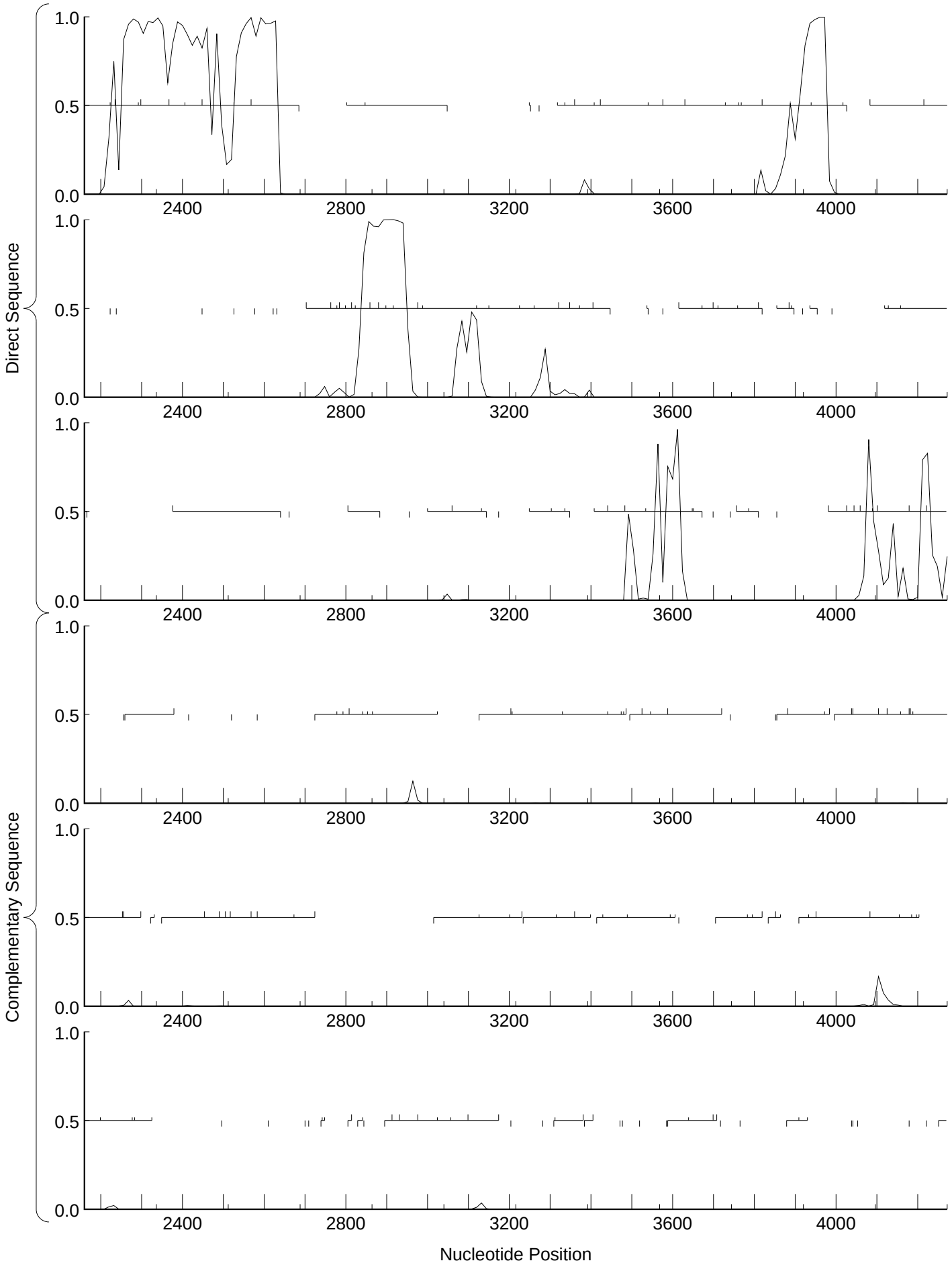
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Training set derived by GeneMarkS, 4.30 October 2014
Sat Sep  8 00:36:14 2018
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For help or information, send electronic mail to: custserv@genepro.com, or mark@amber.biology.gatech.edu

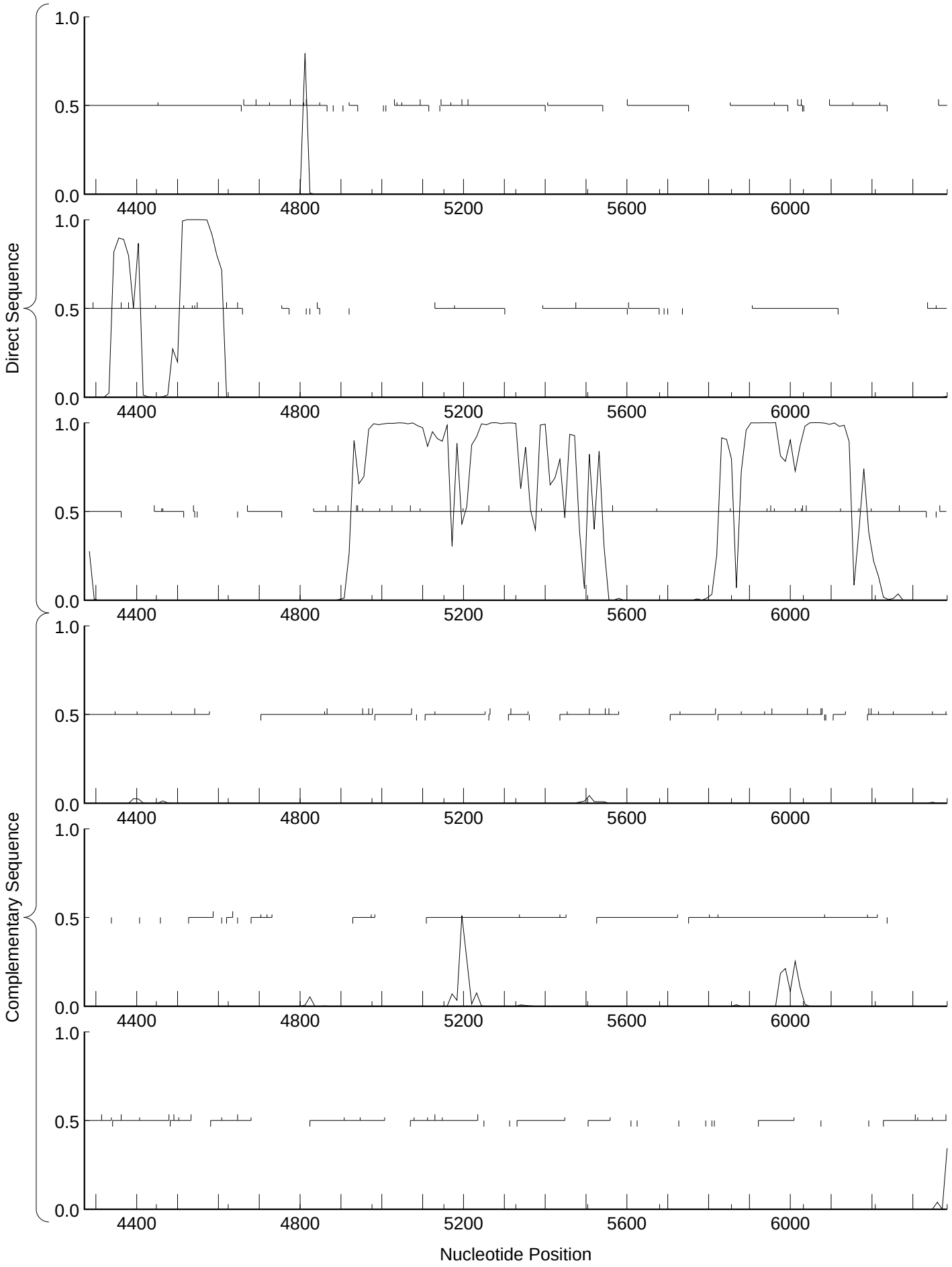
rdonia phage ChisanaKitsune complete sequence, 88657 bp, circularly permuted, Cluster DQ, Order 4, Window 96, Step 12, 2/43



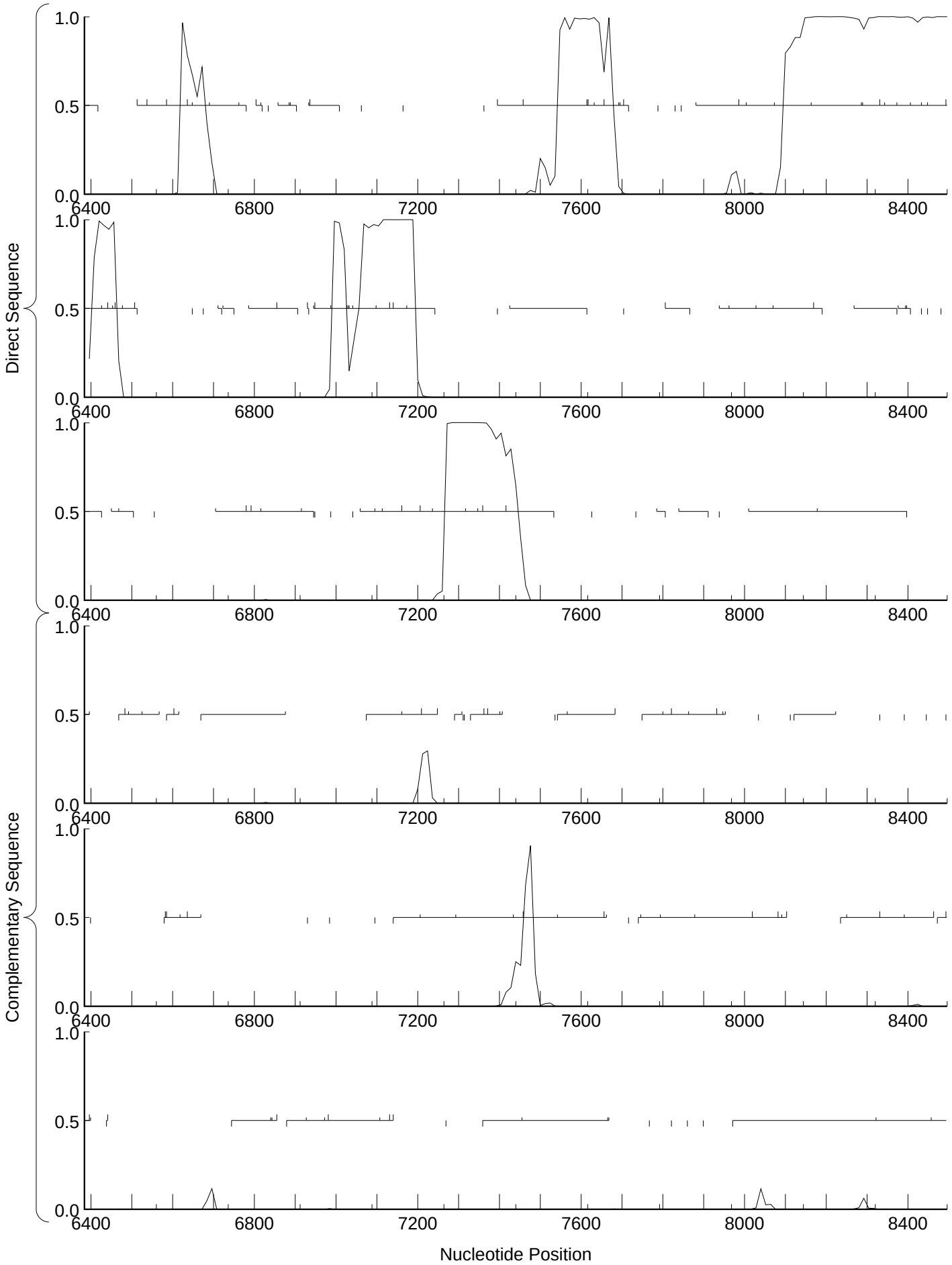
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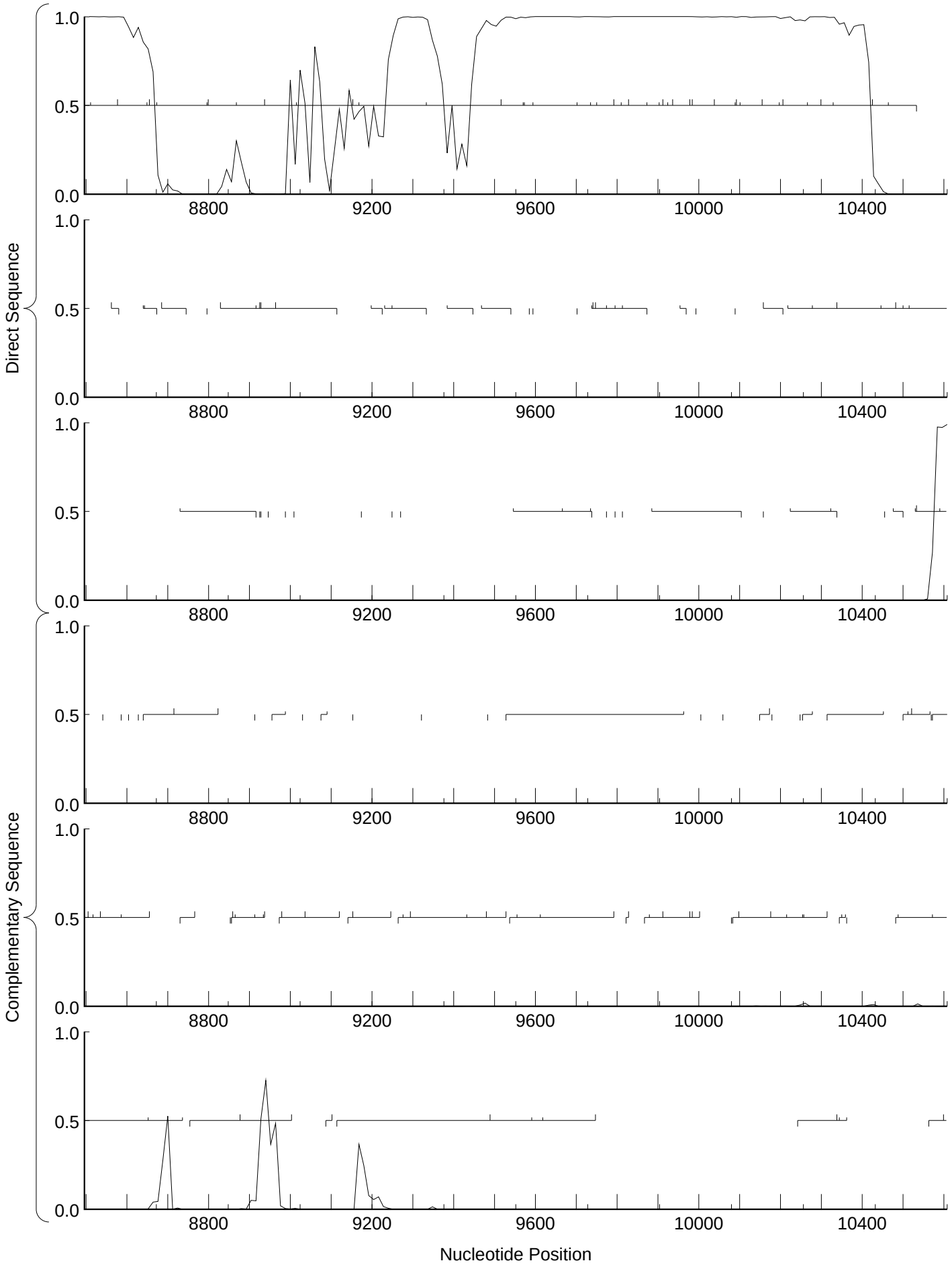
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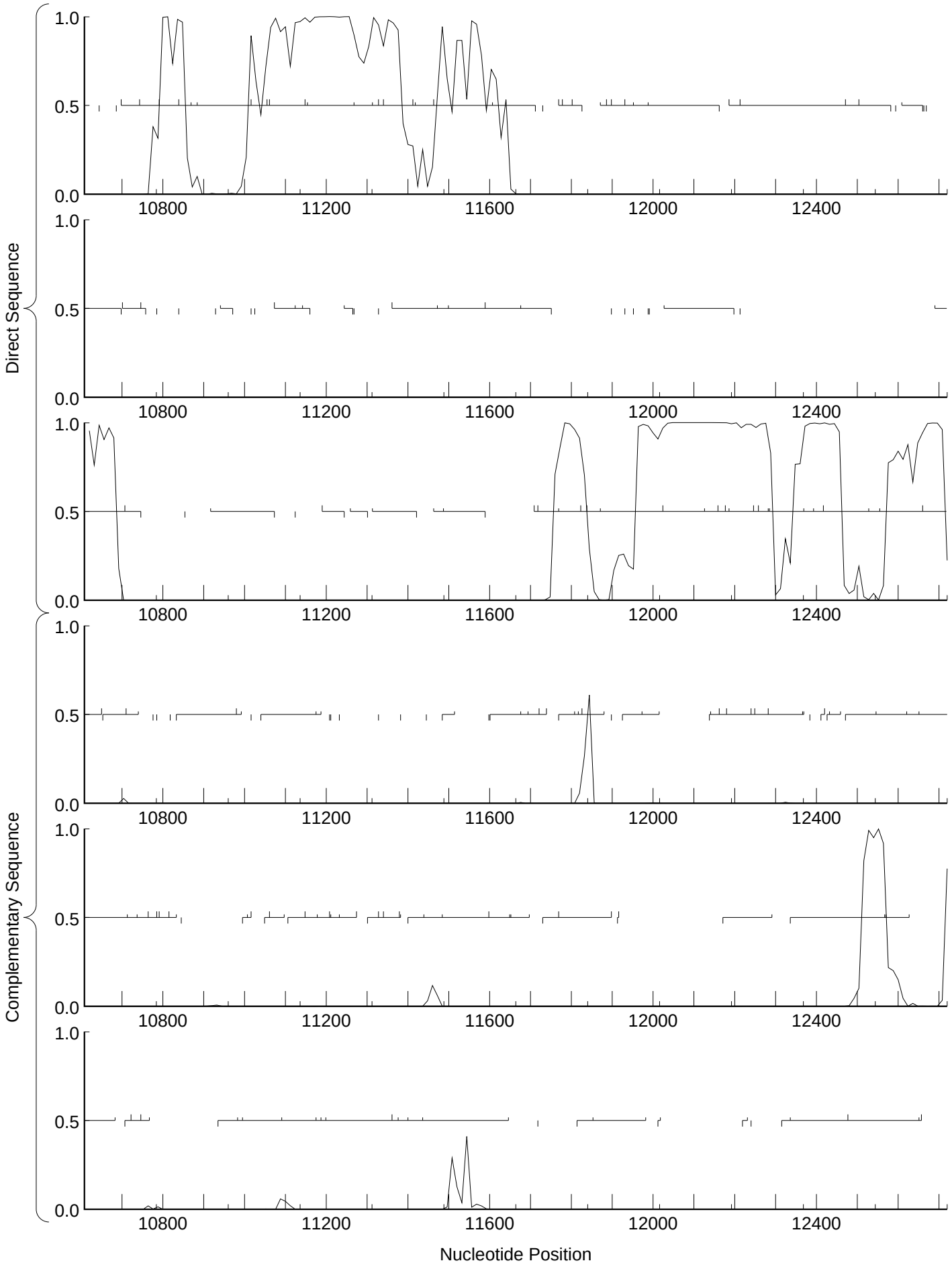
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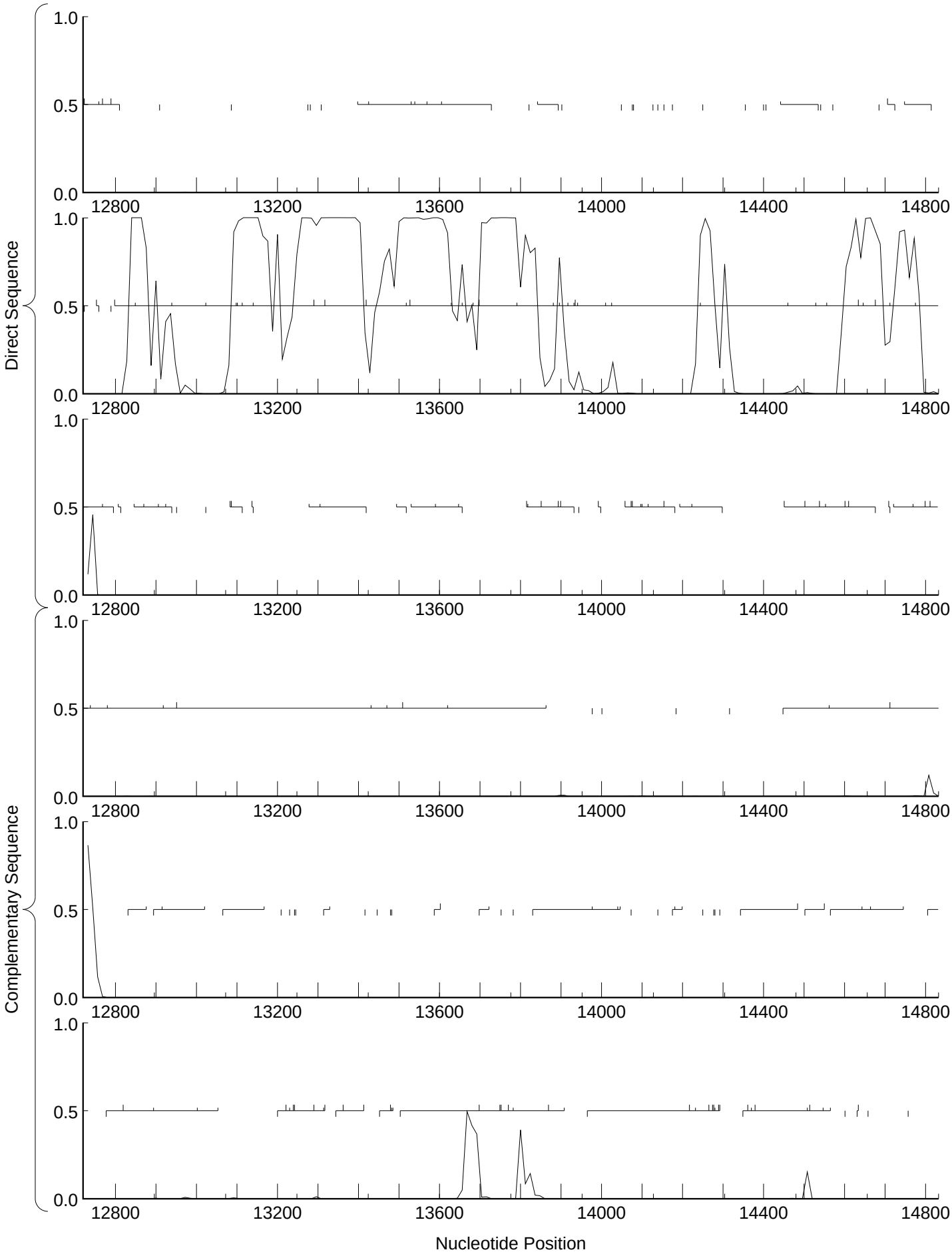
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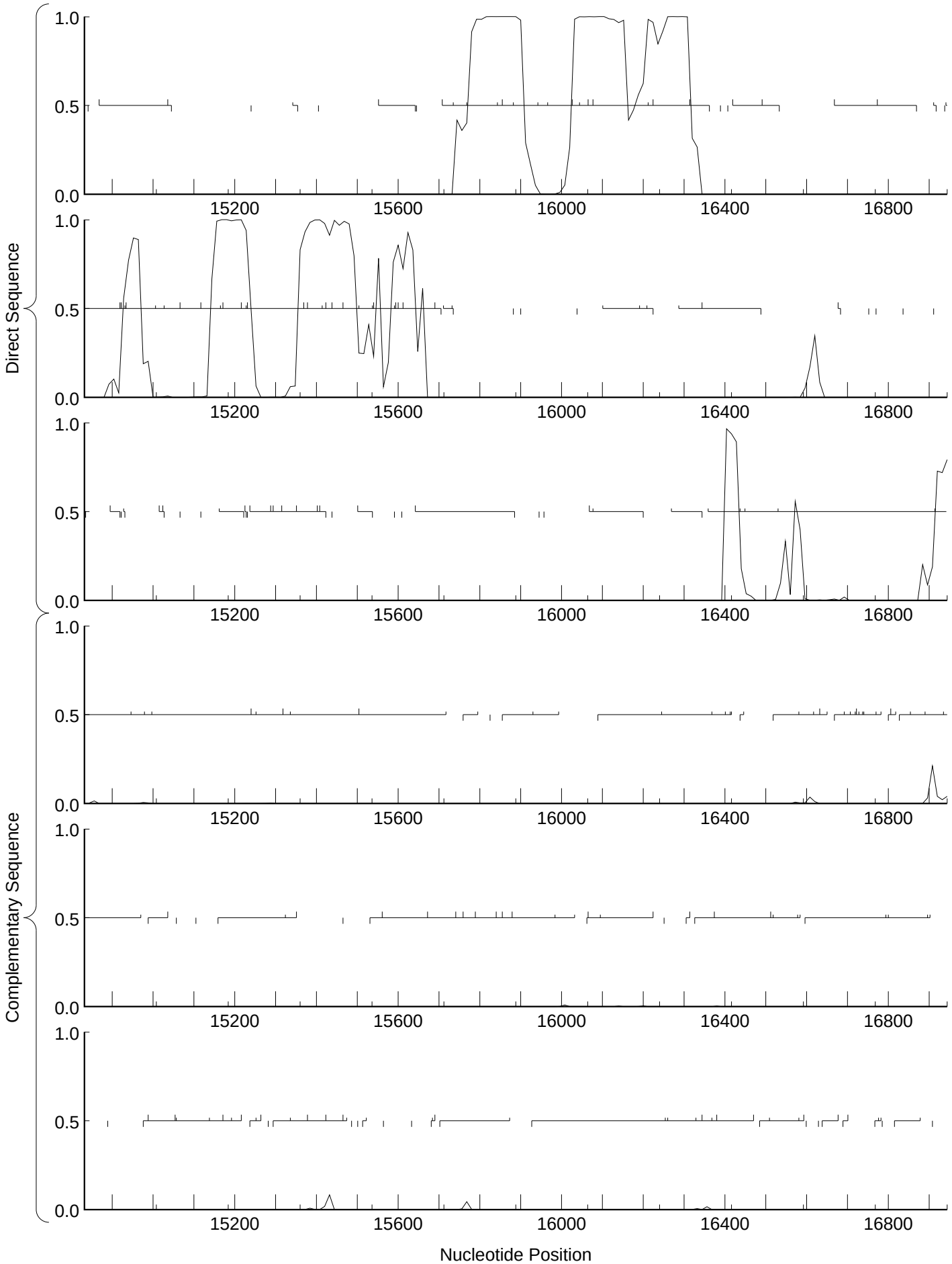
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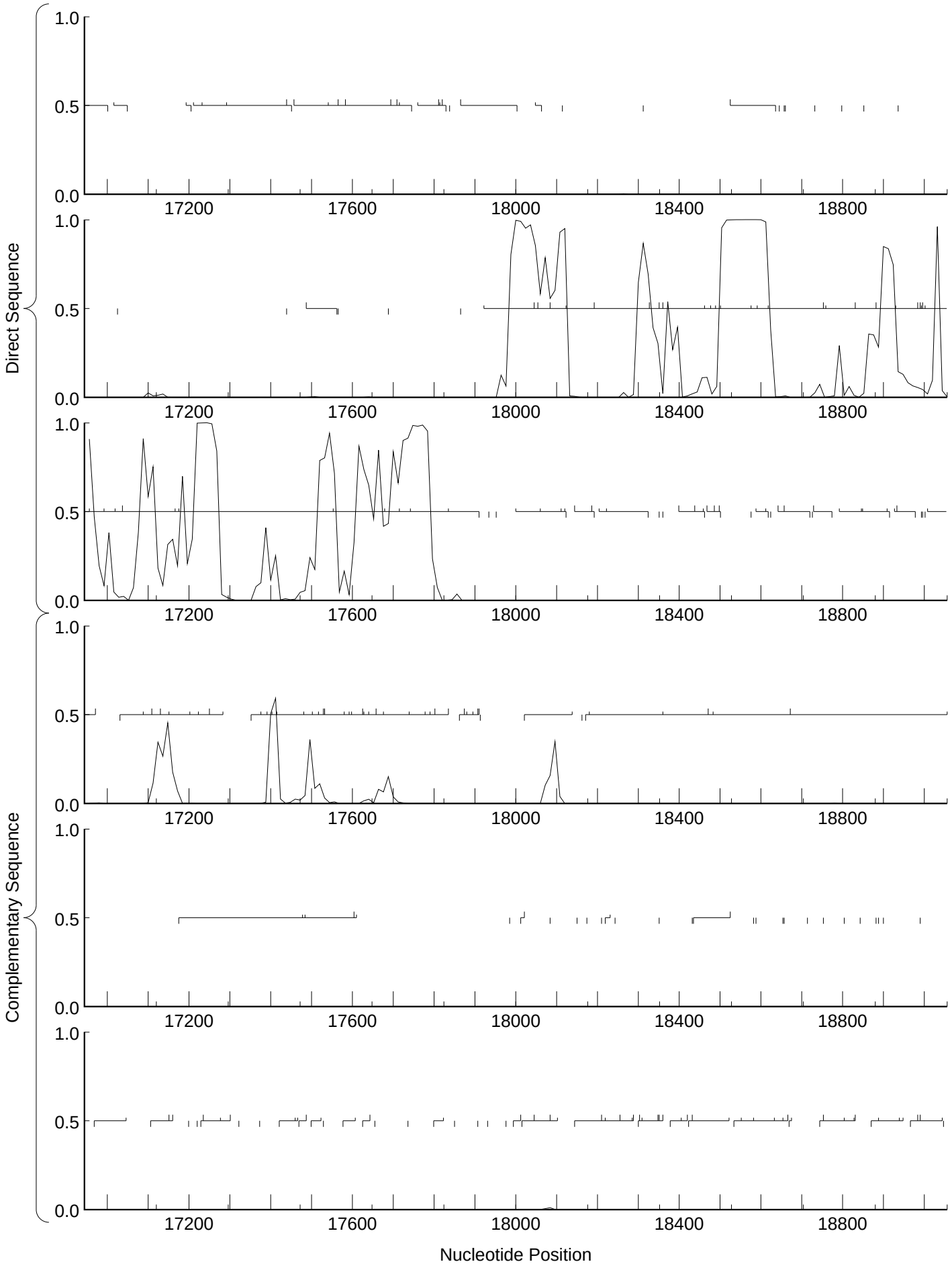


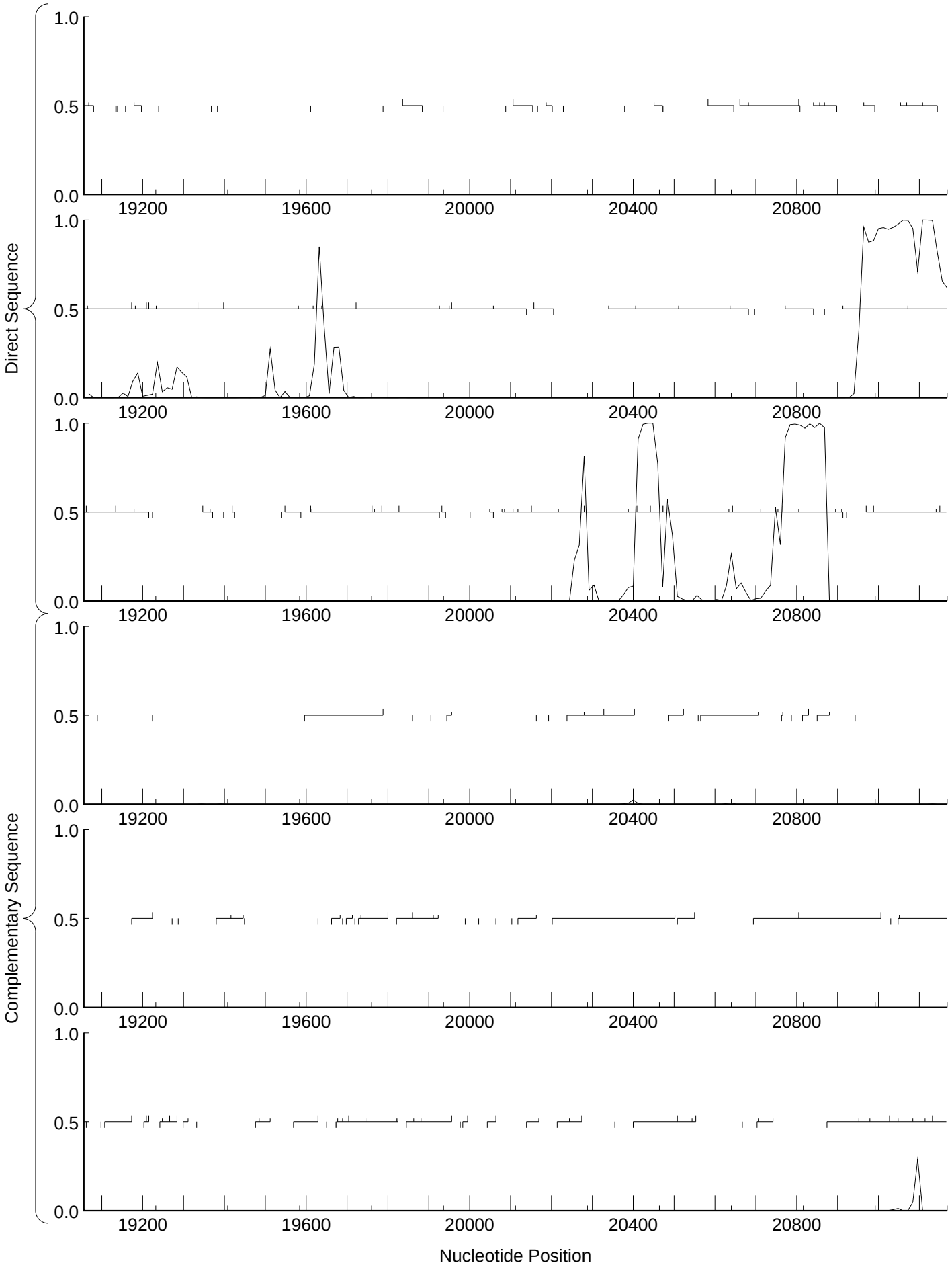
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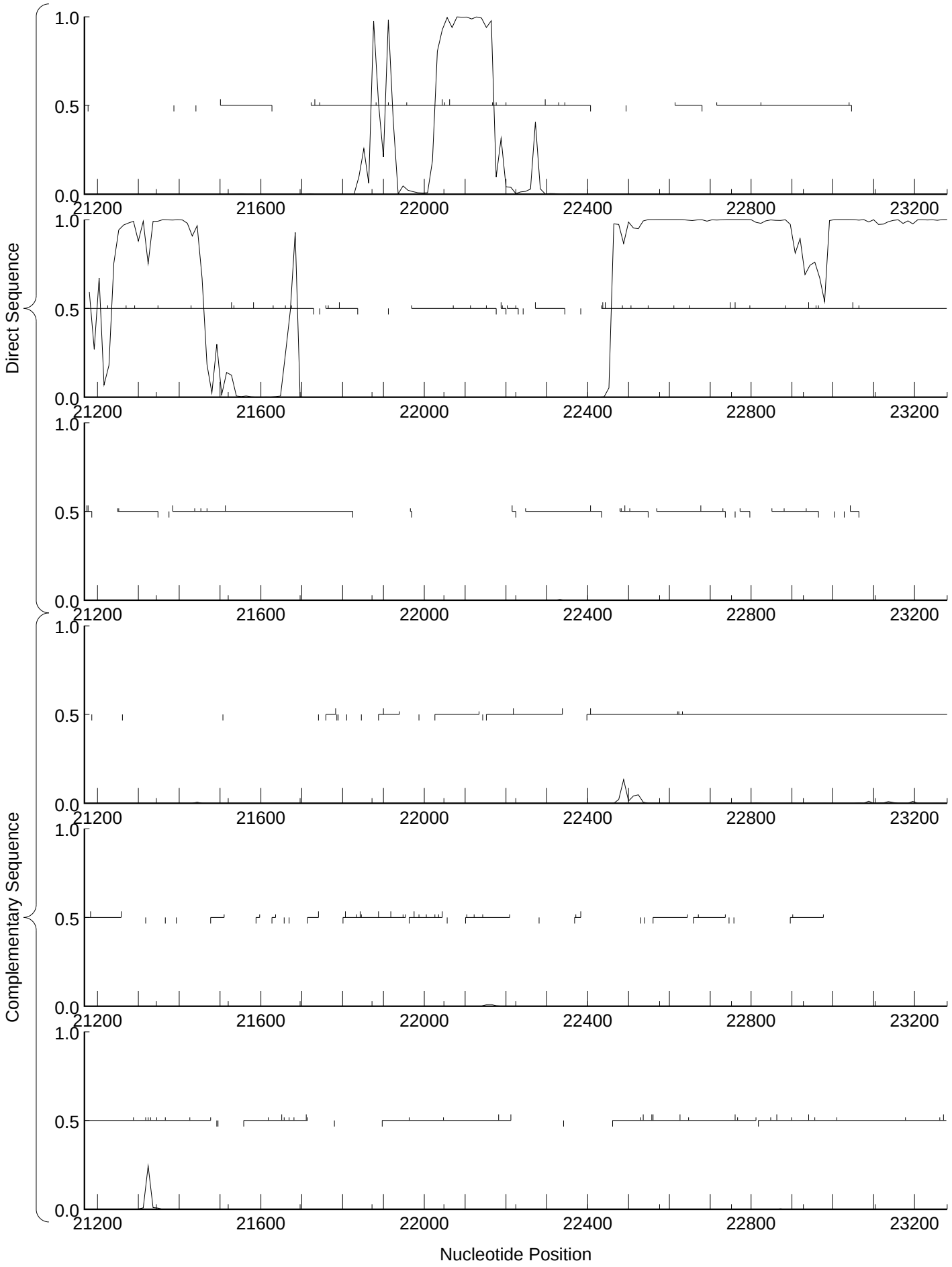
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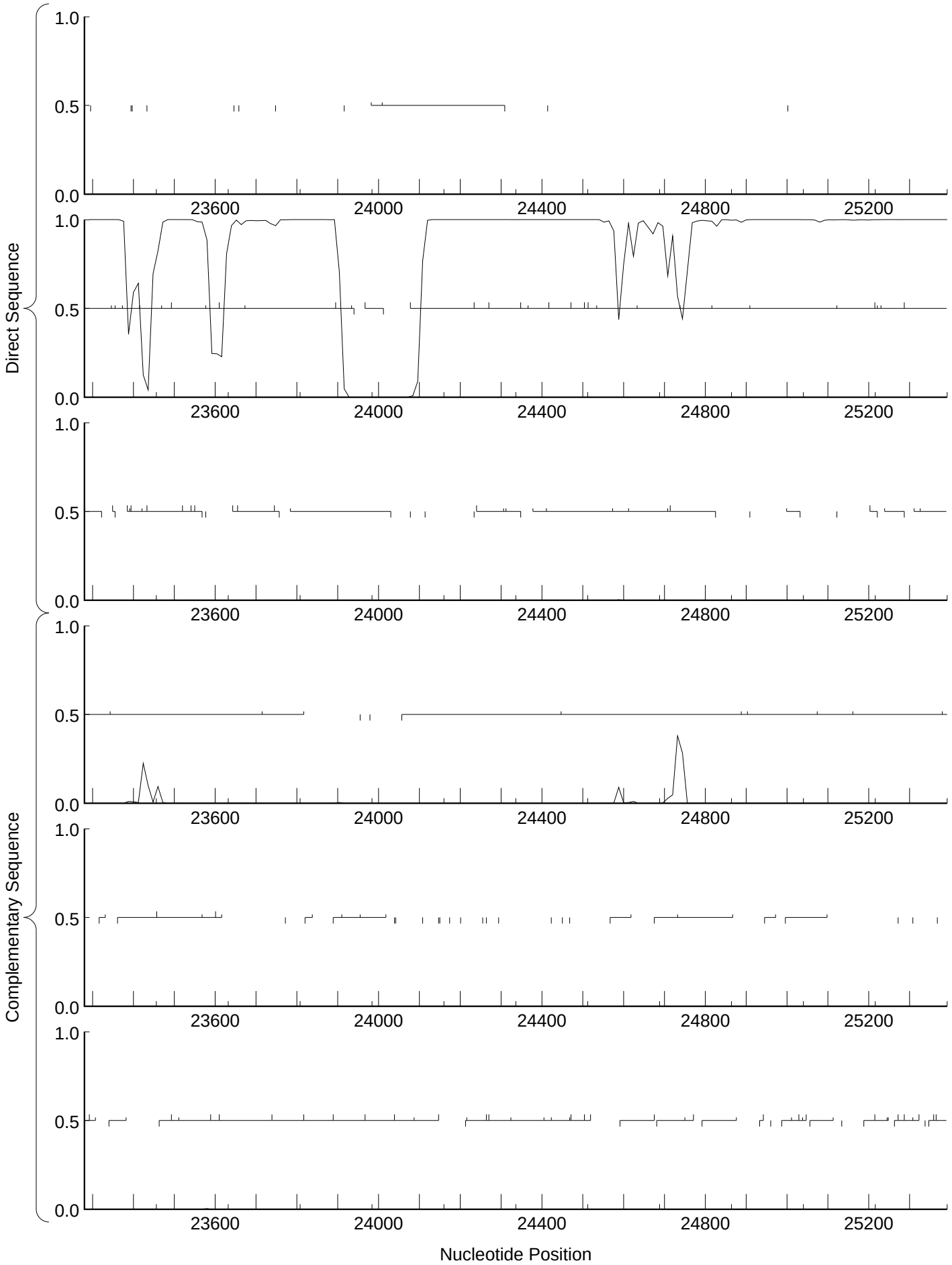

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
17200
17600
18000
18400
18800
Nucleotide Position


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

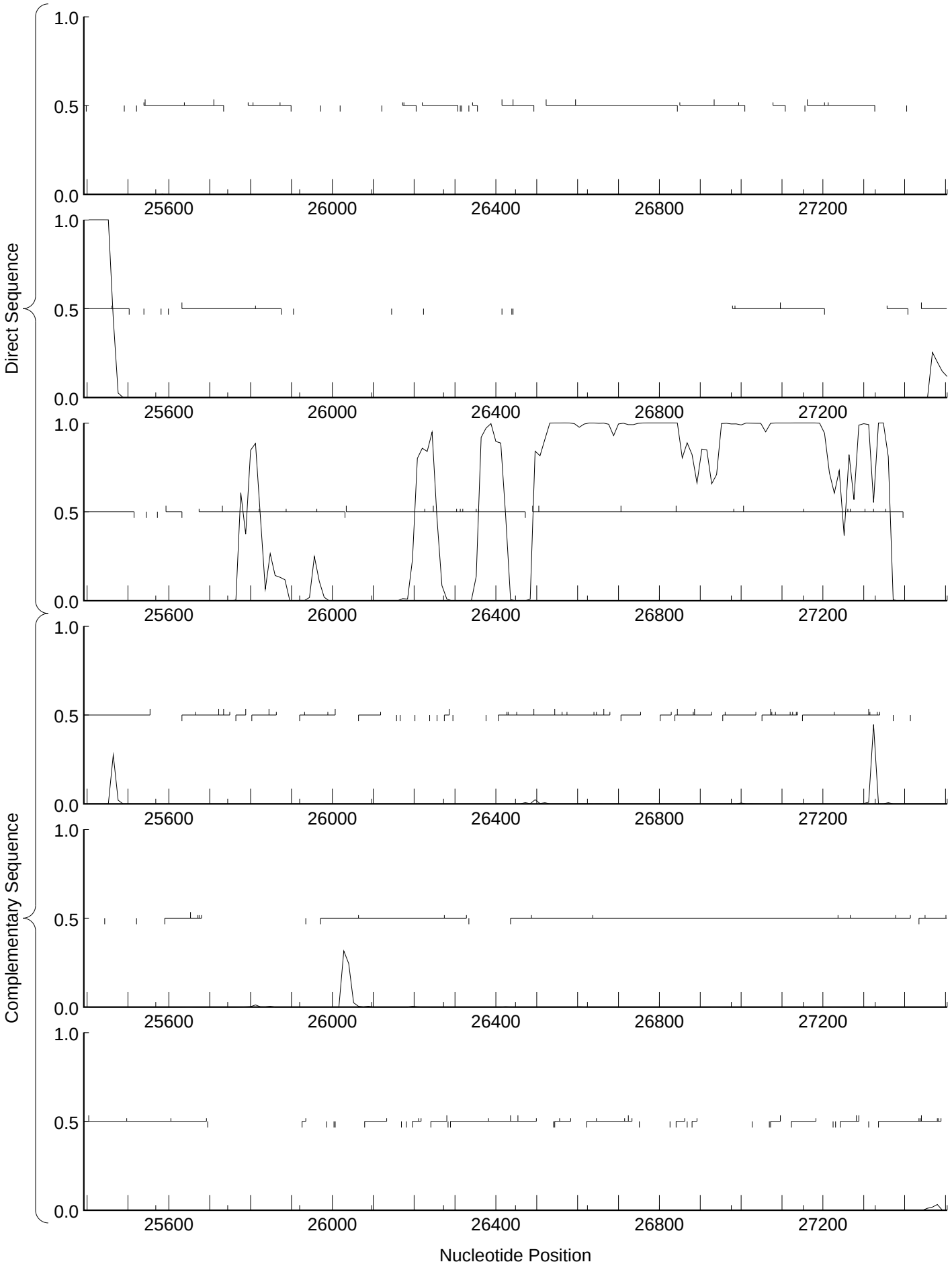
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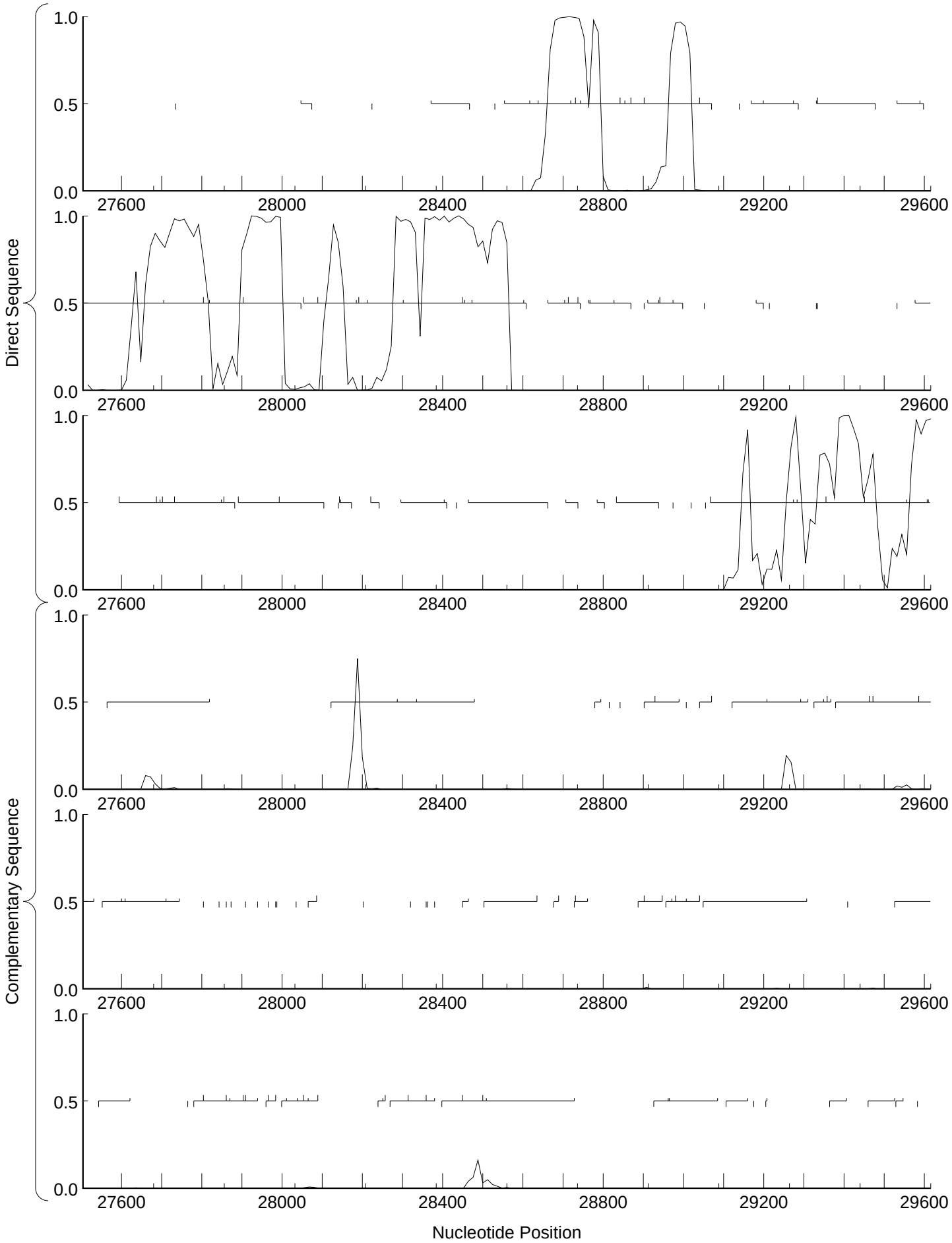
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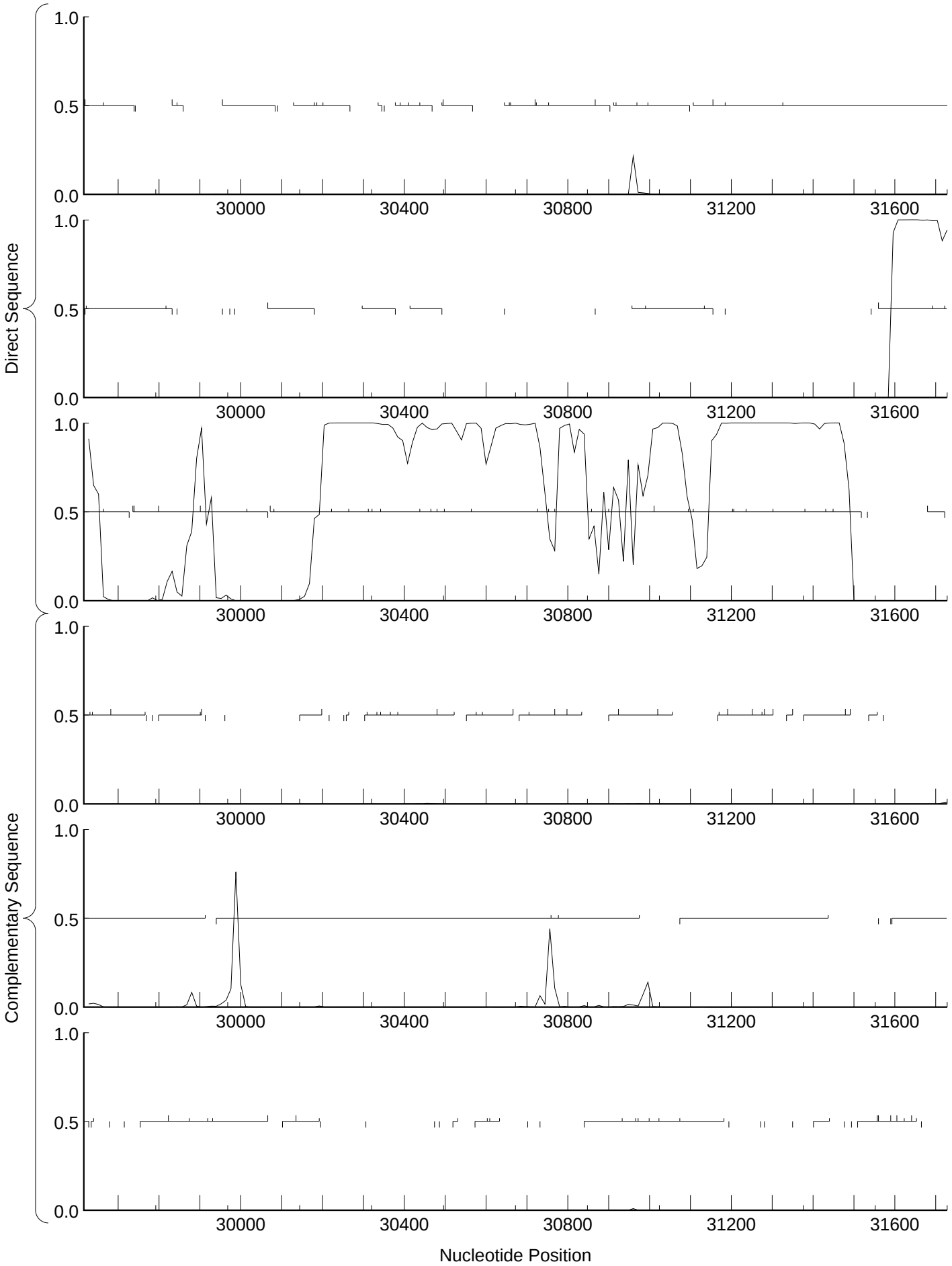
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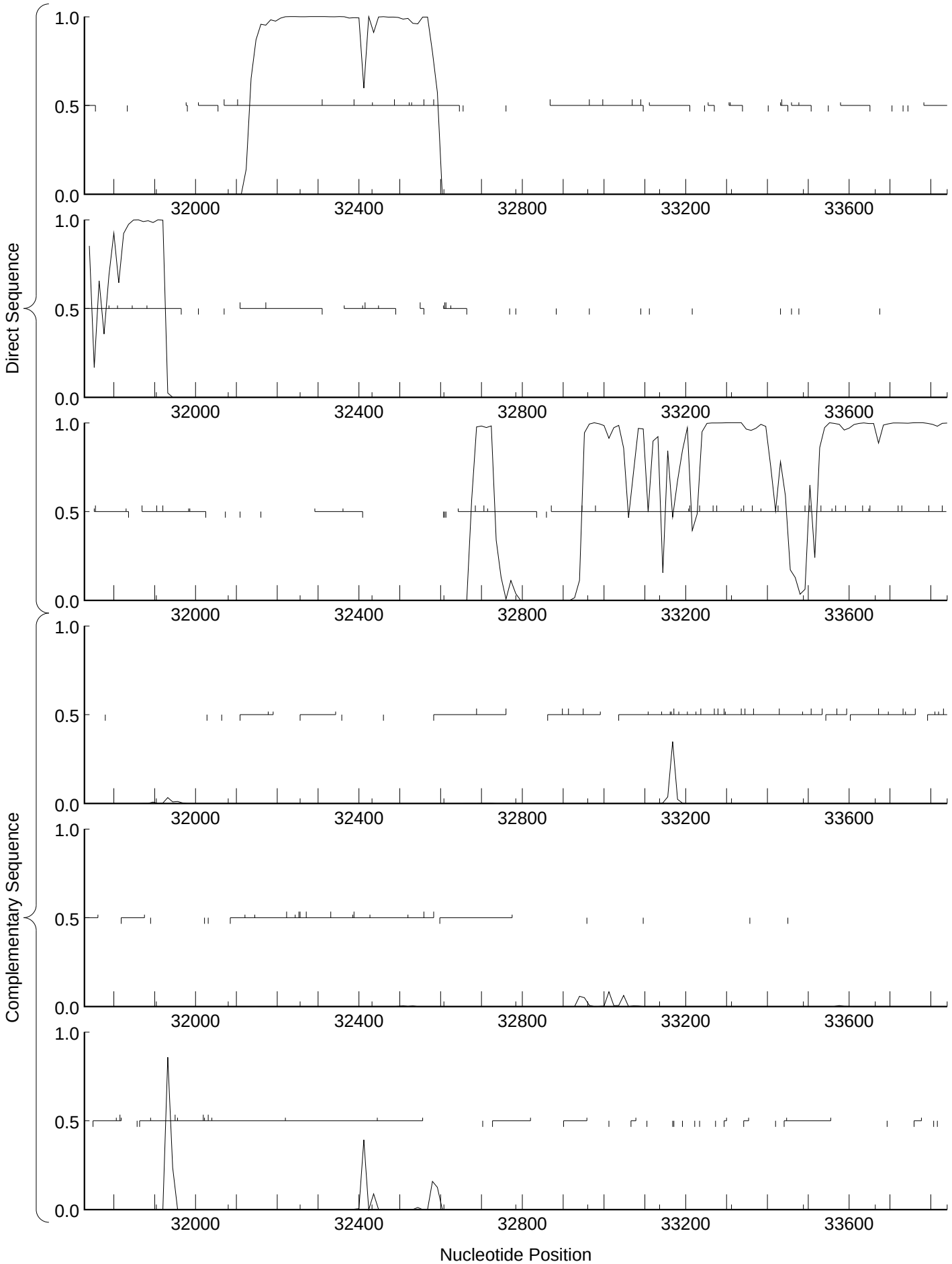


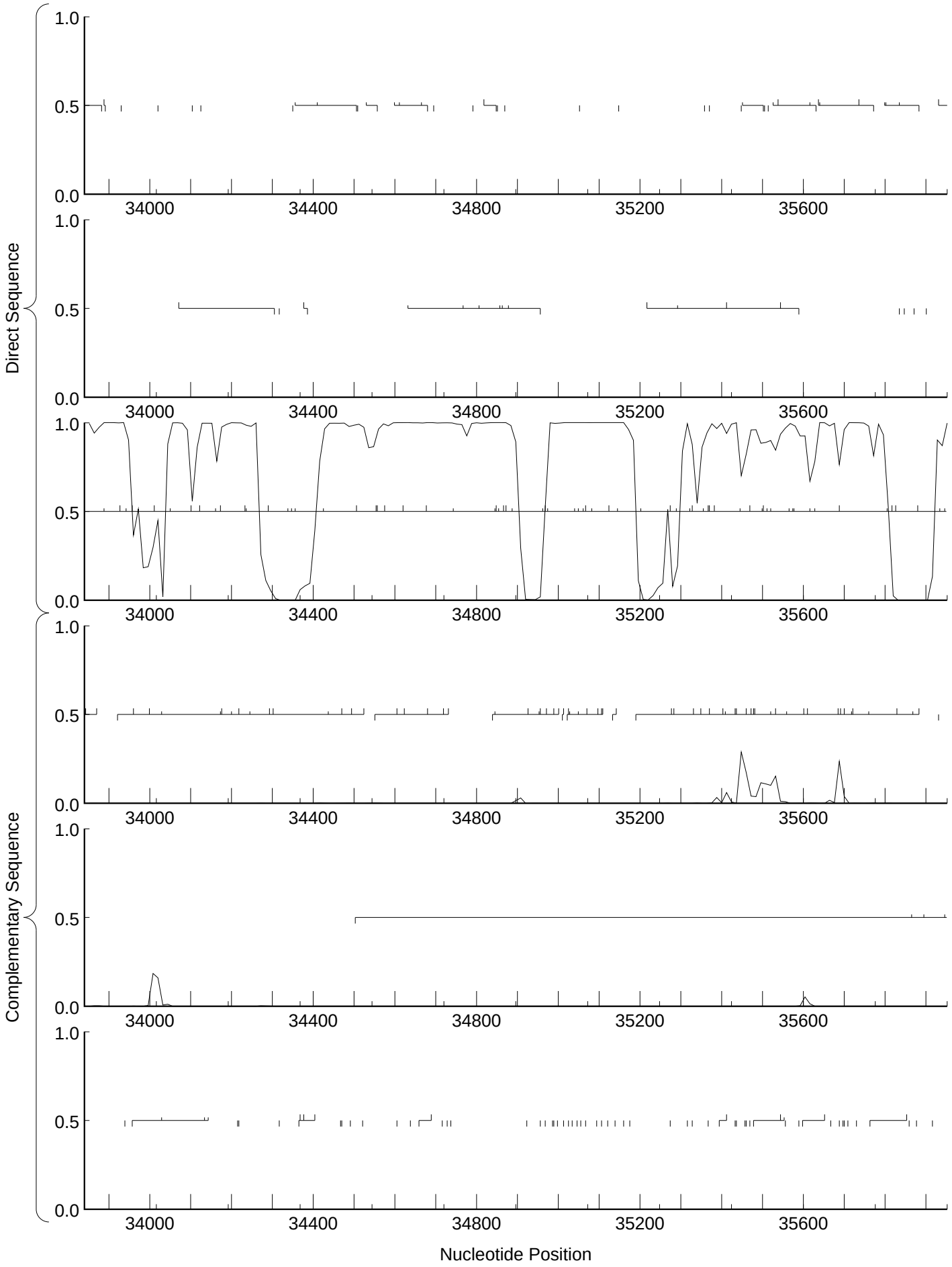
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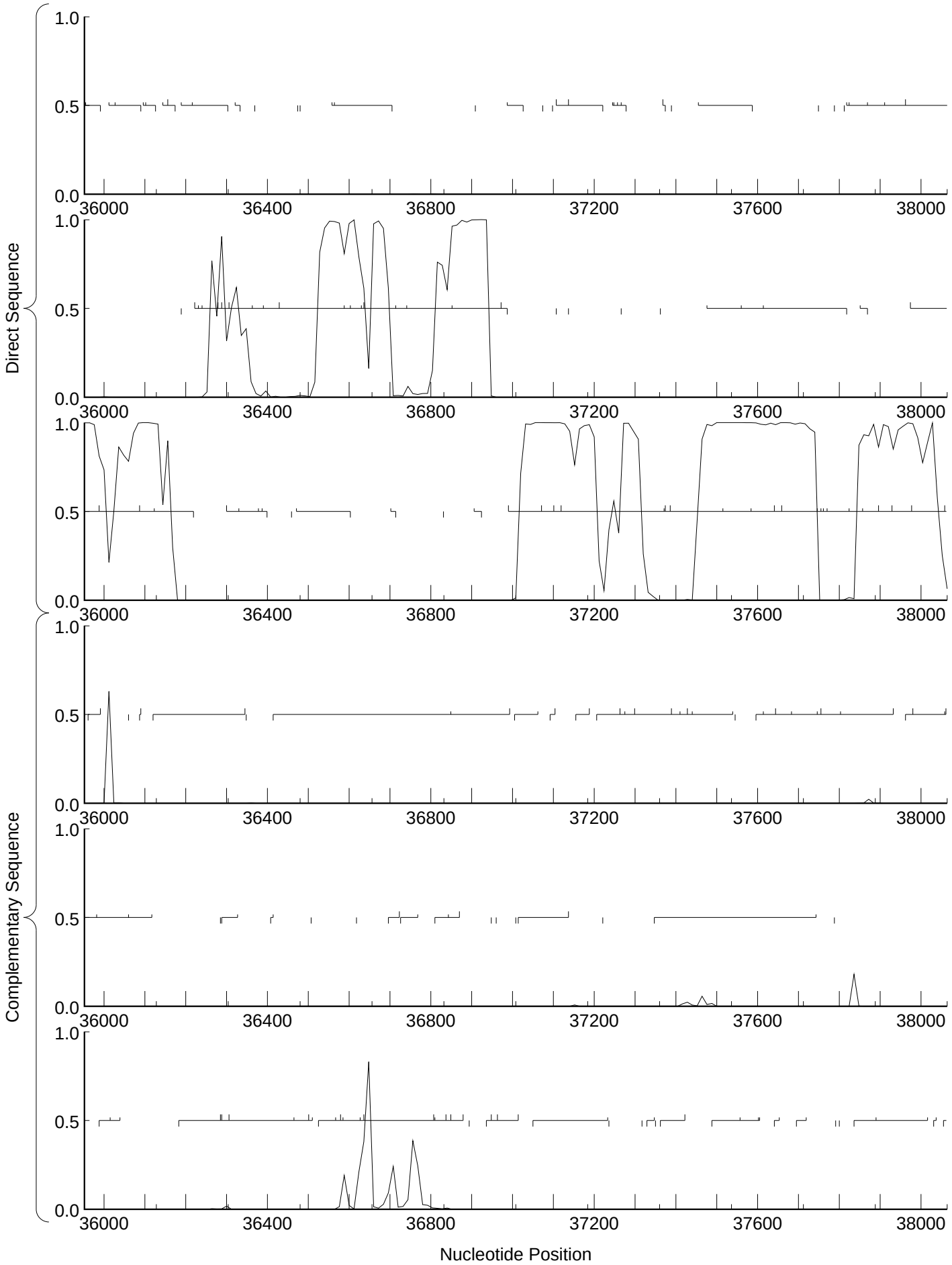


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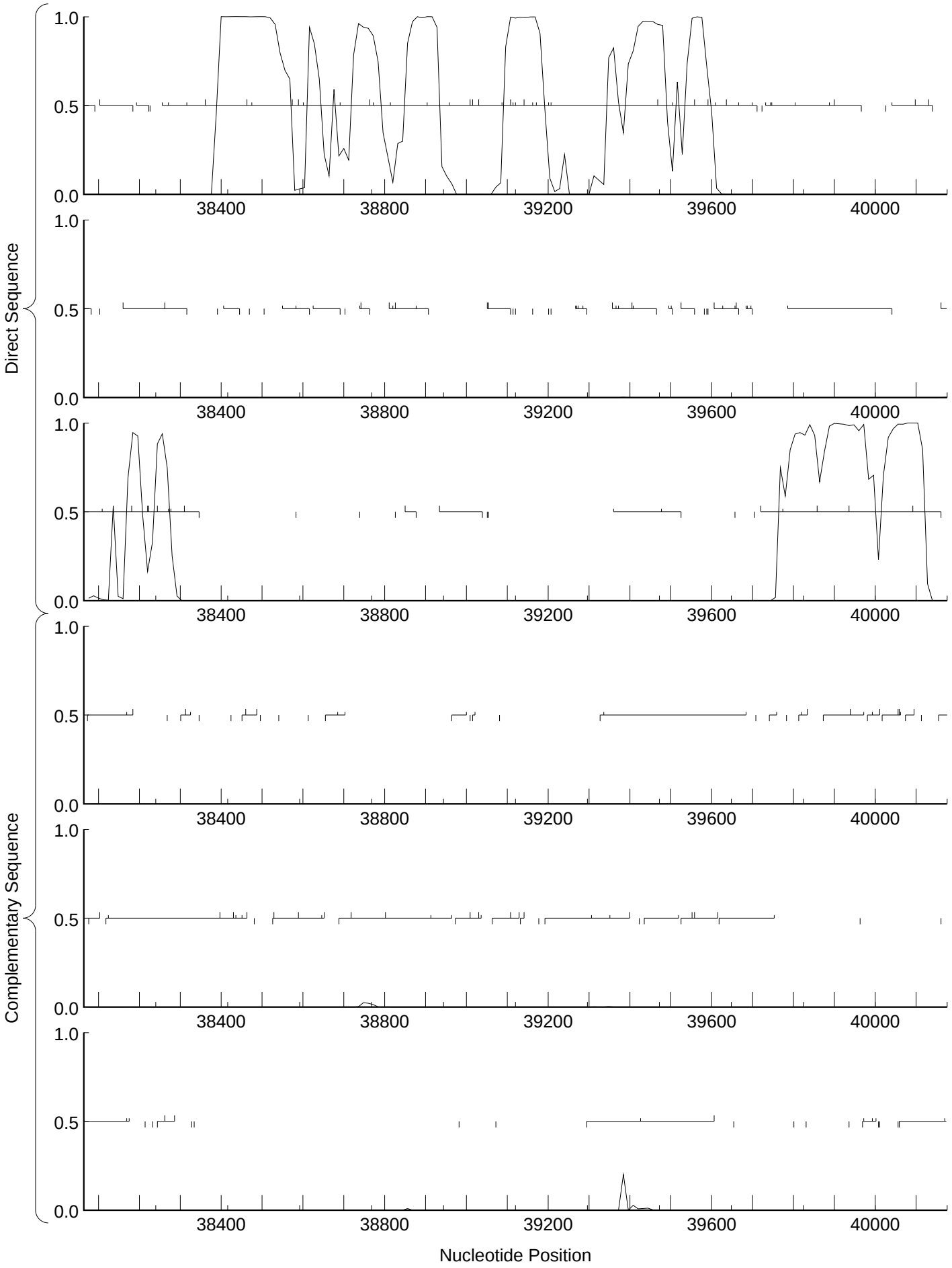



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Complementary Sequence
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32800
33200
33600
Nucleotide Position

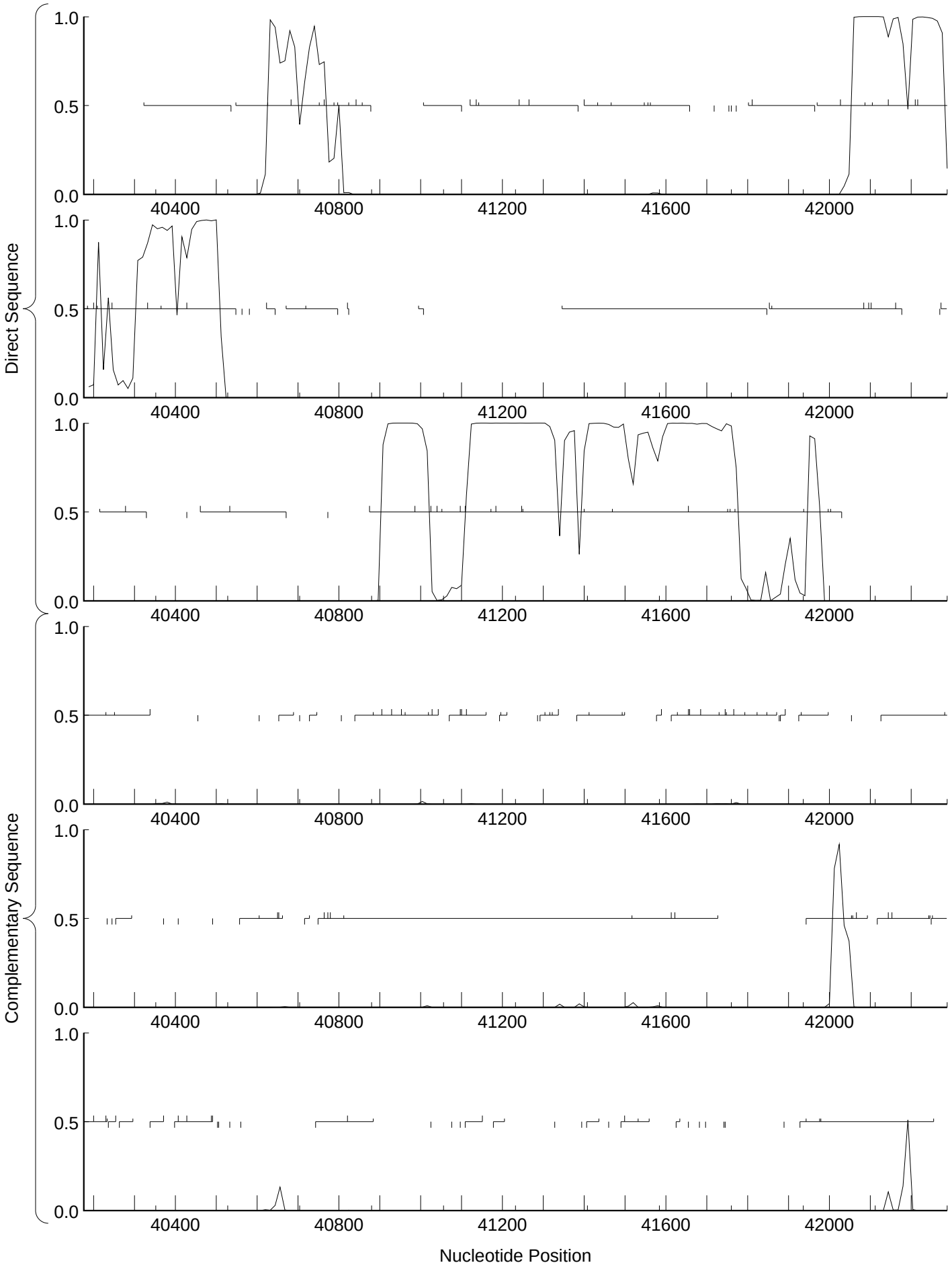

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
34000
34400
34800
35200
35600
Nucleotide Position


Direct Sequence
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0.0
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36400
36800
37200
37600
38000
Nucleotide Position

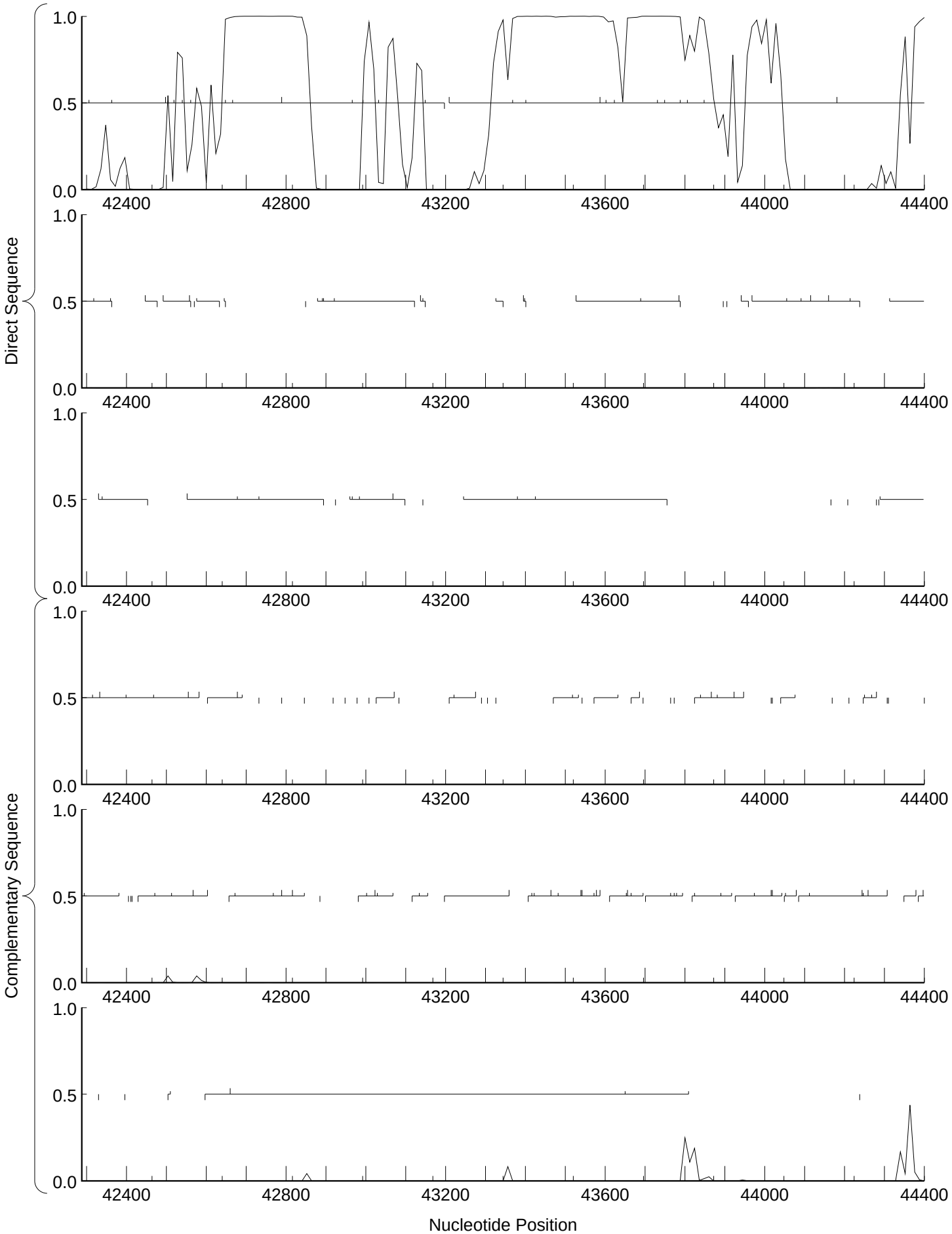
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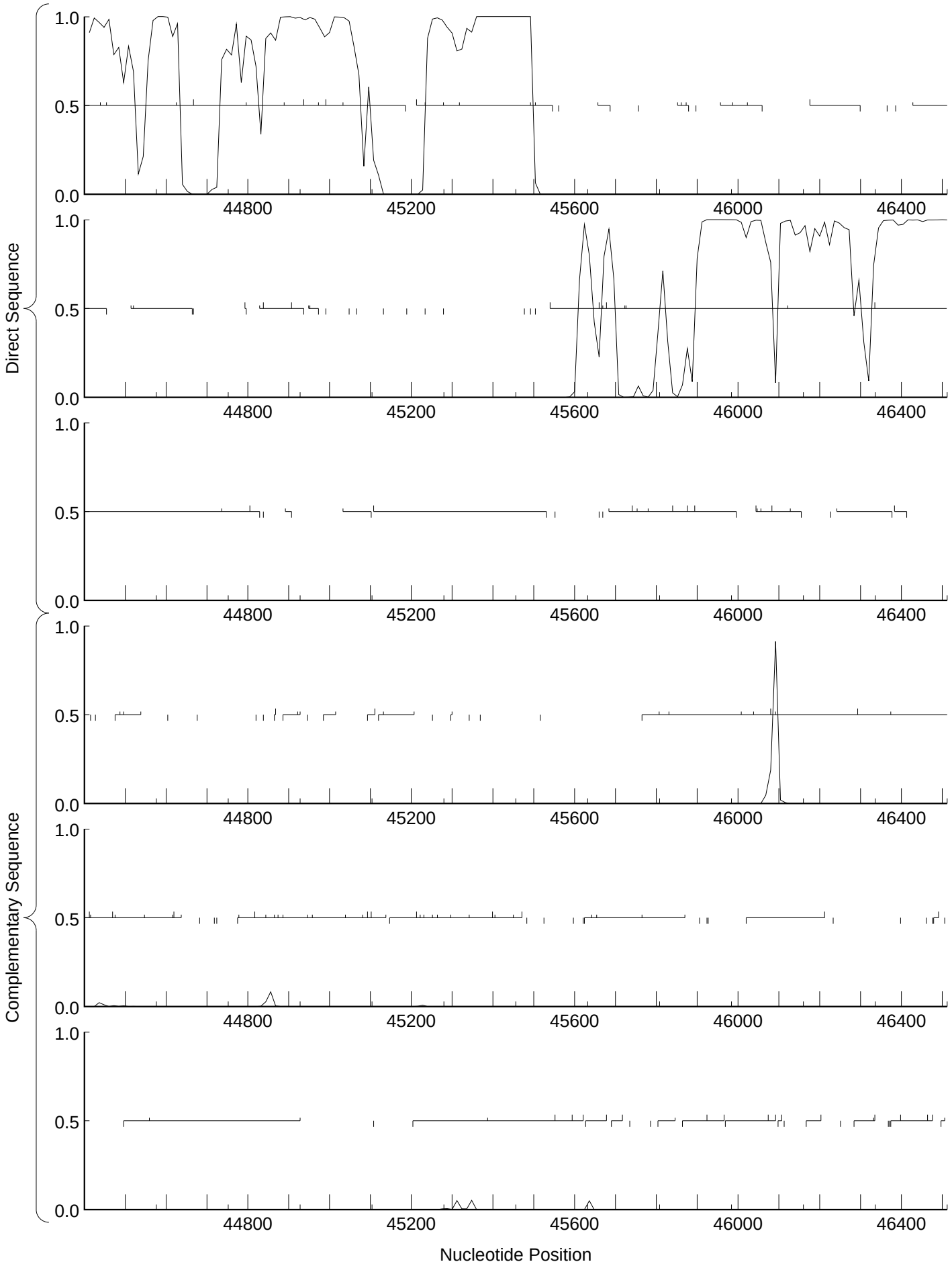


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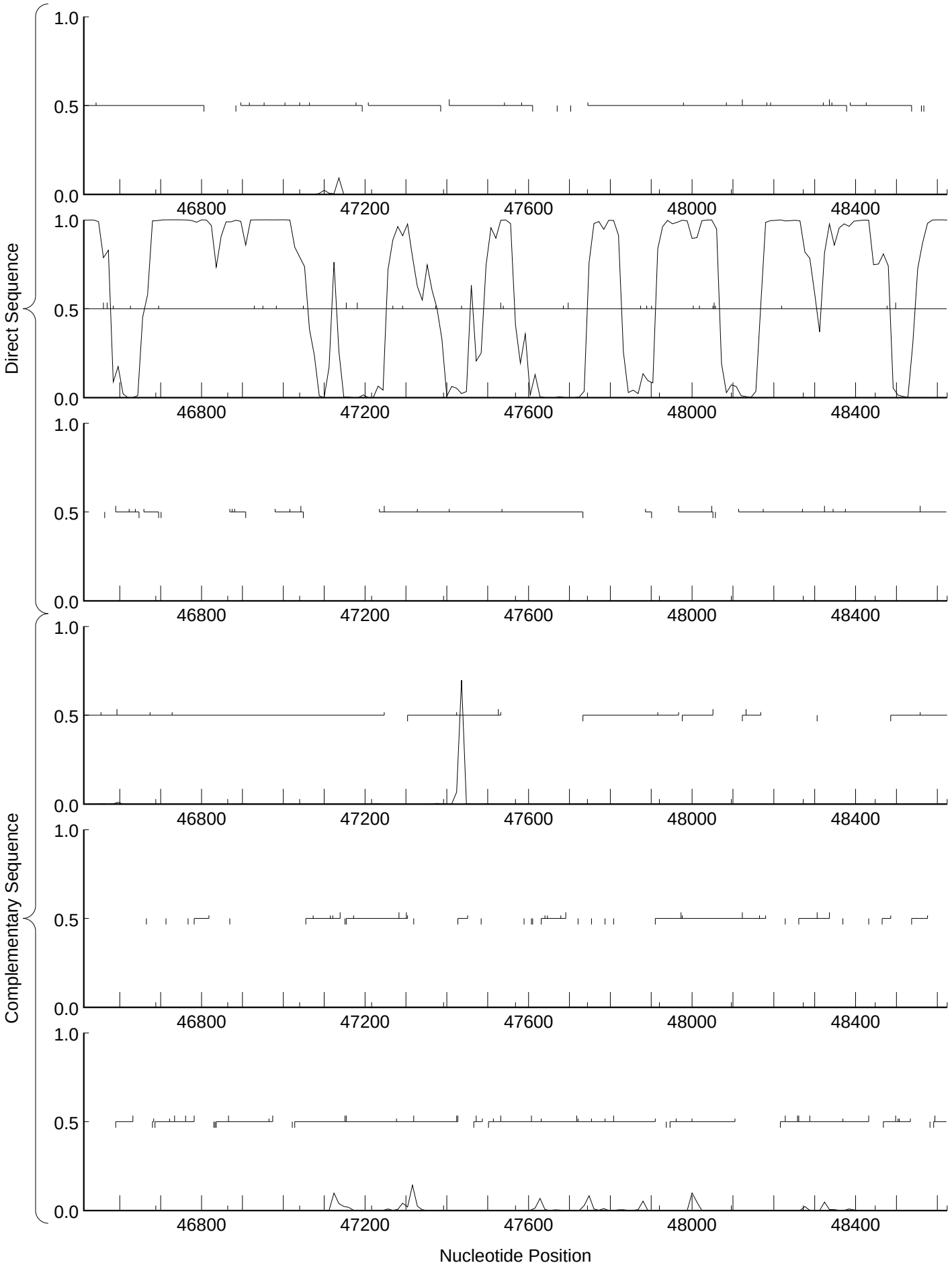


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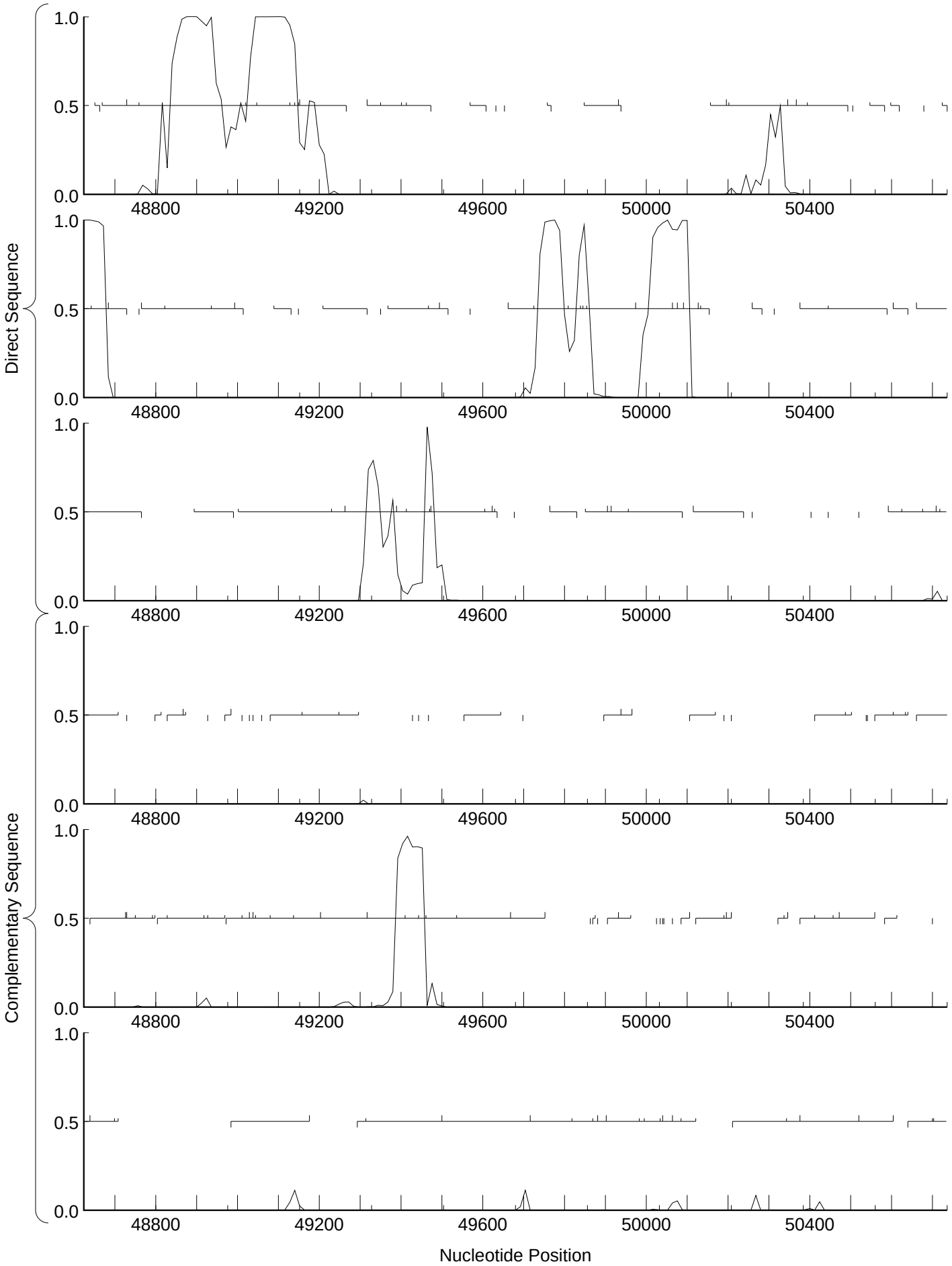


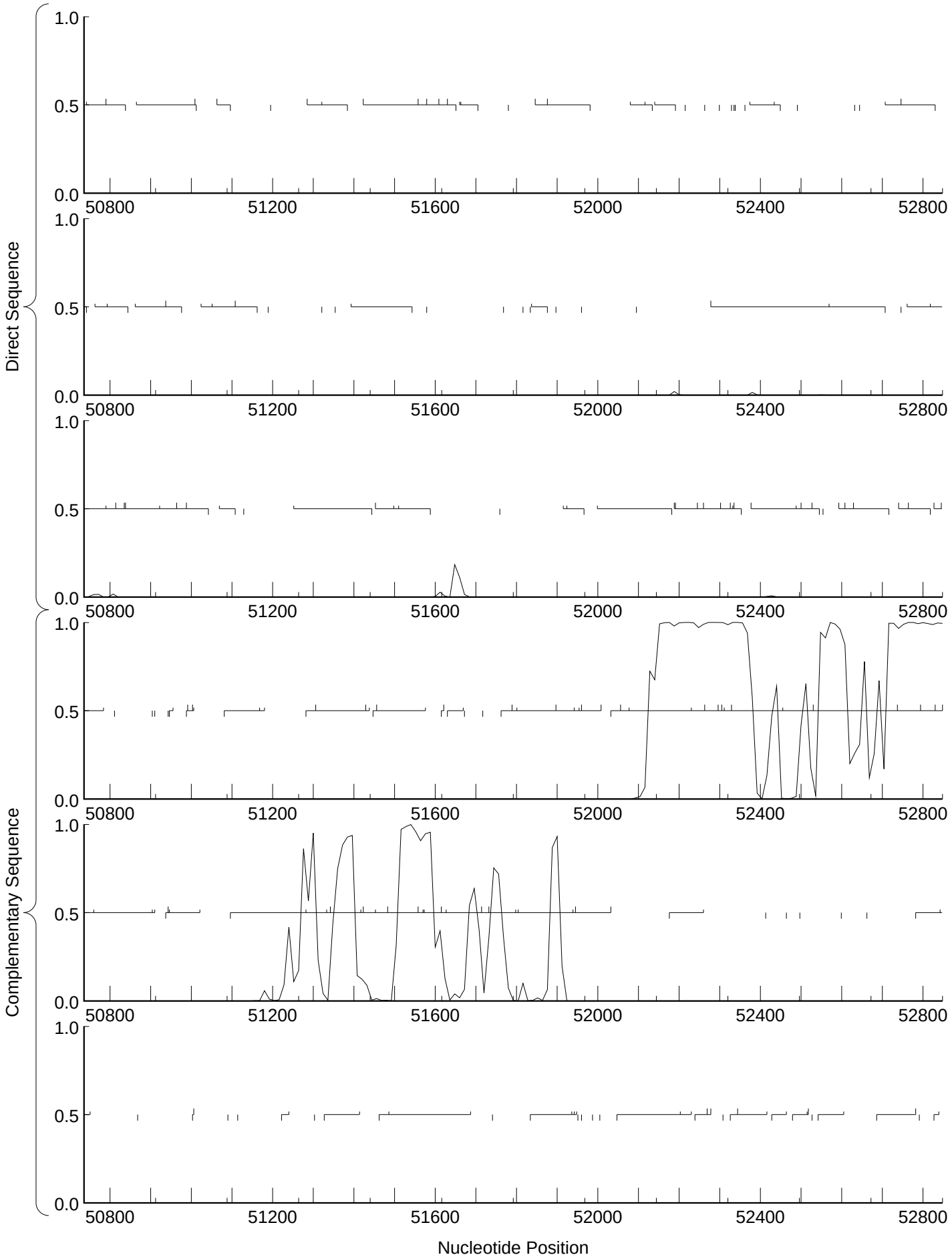

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
44800
45200
45600
46000
46400
Nucleotide Position

donia phage ChisanaKitsune complete sequence, 88657 bp, circularly permuted, Cluster DQ, Order 4, Window 96, Step 12, 24/43

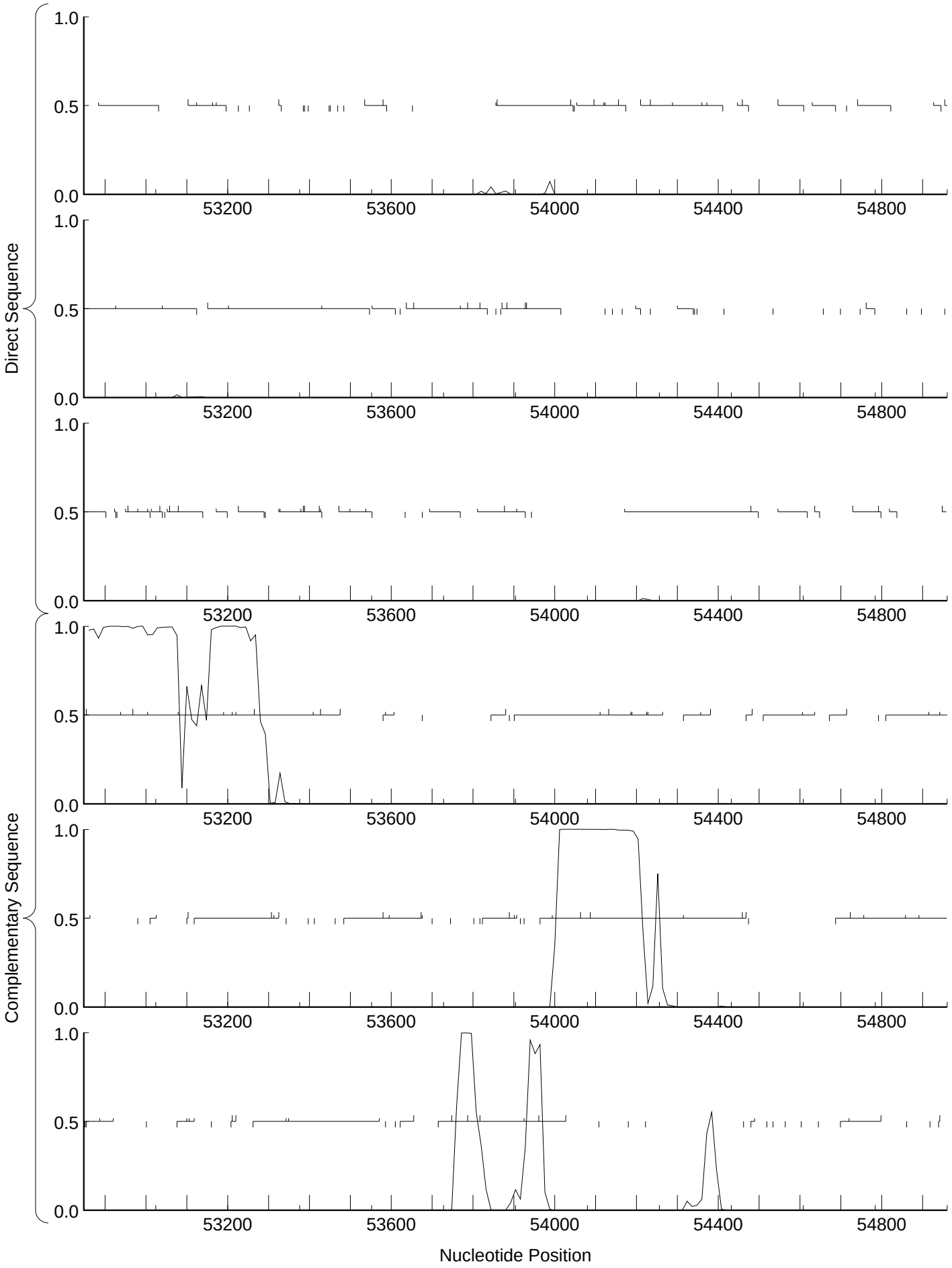


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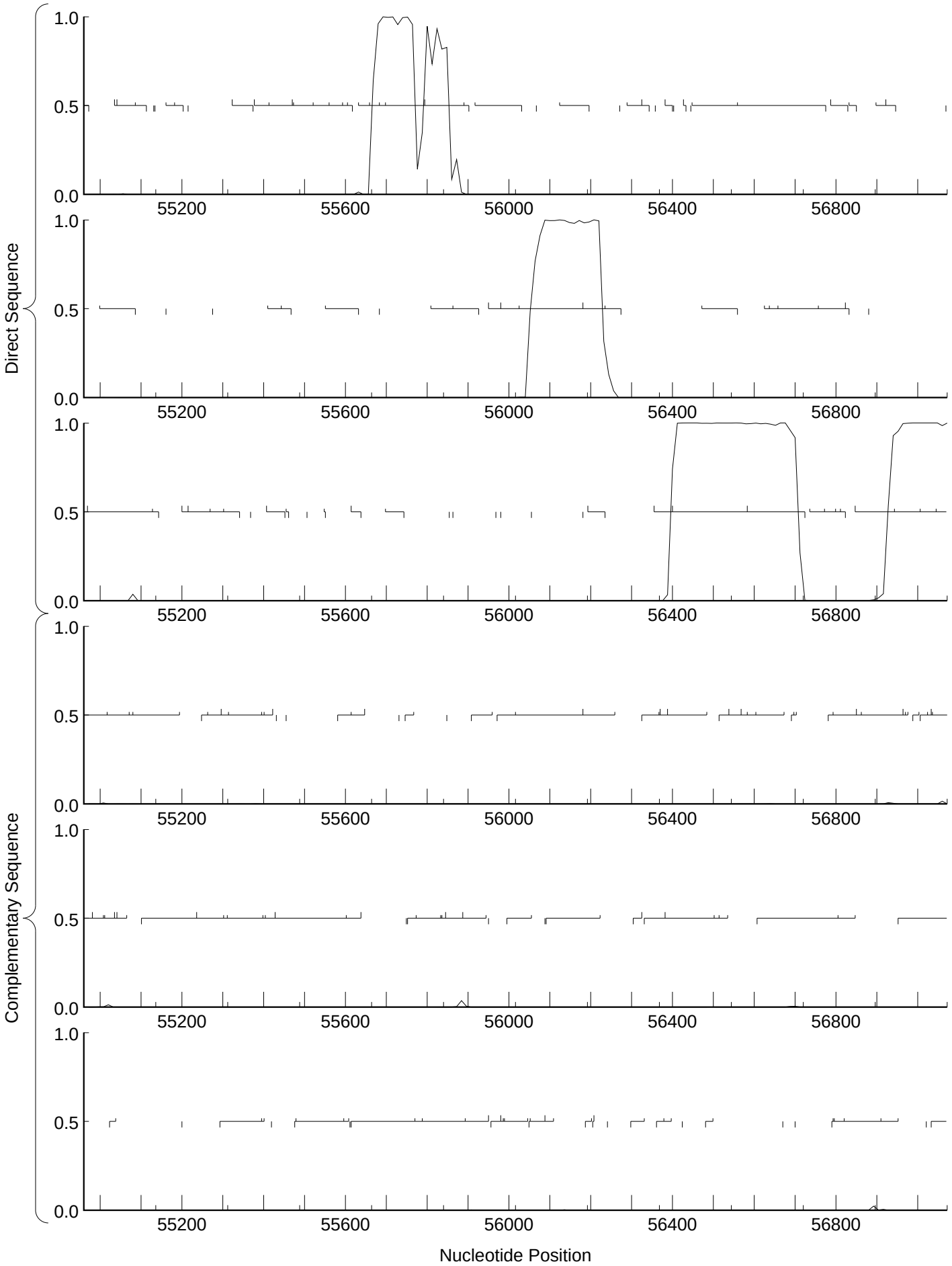



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Nucleotide Position

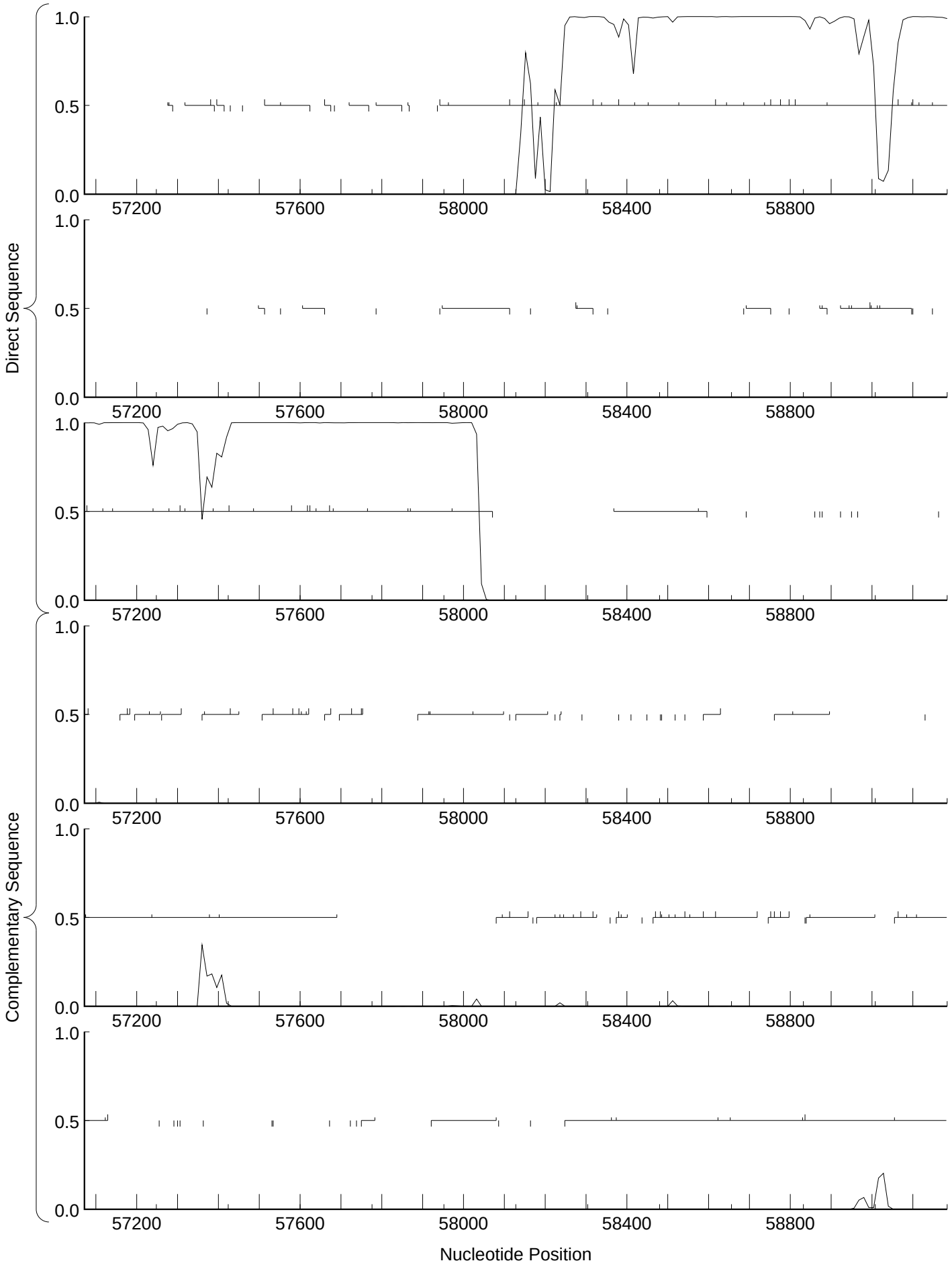
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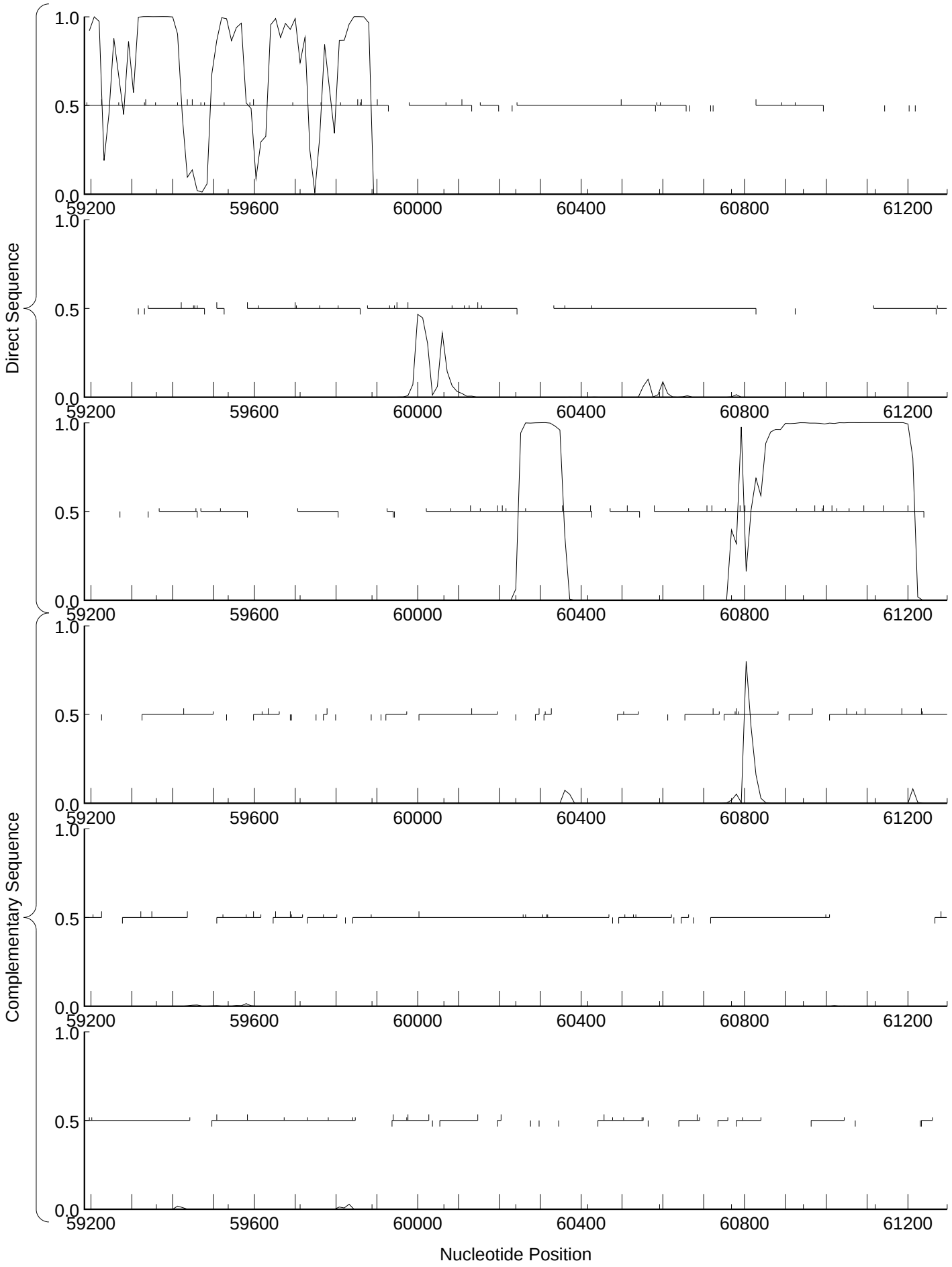
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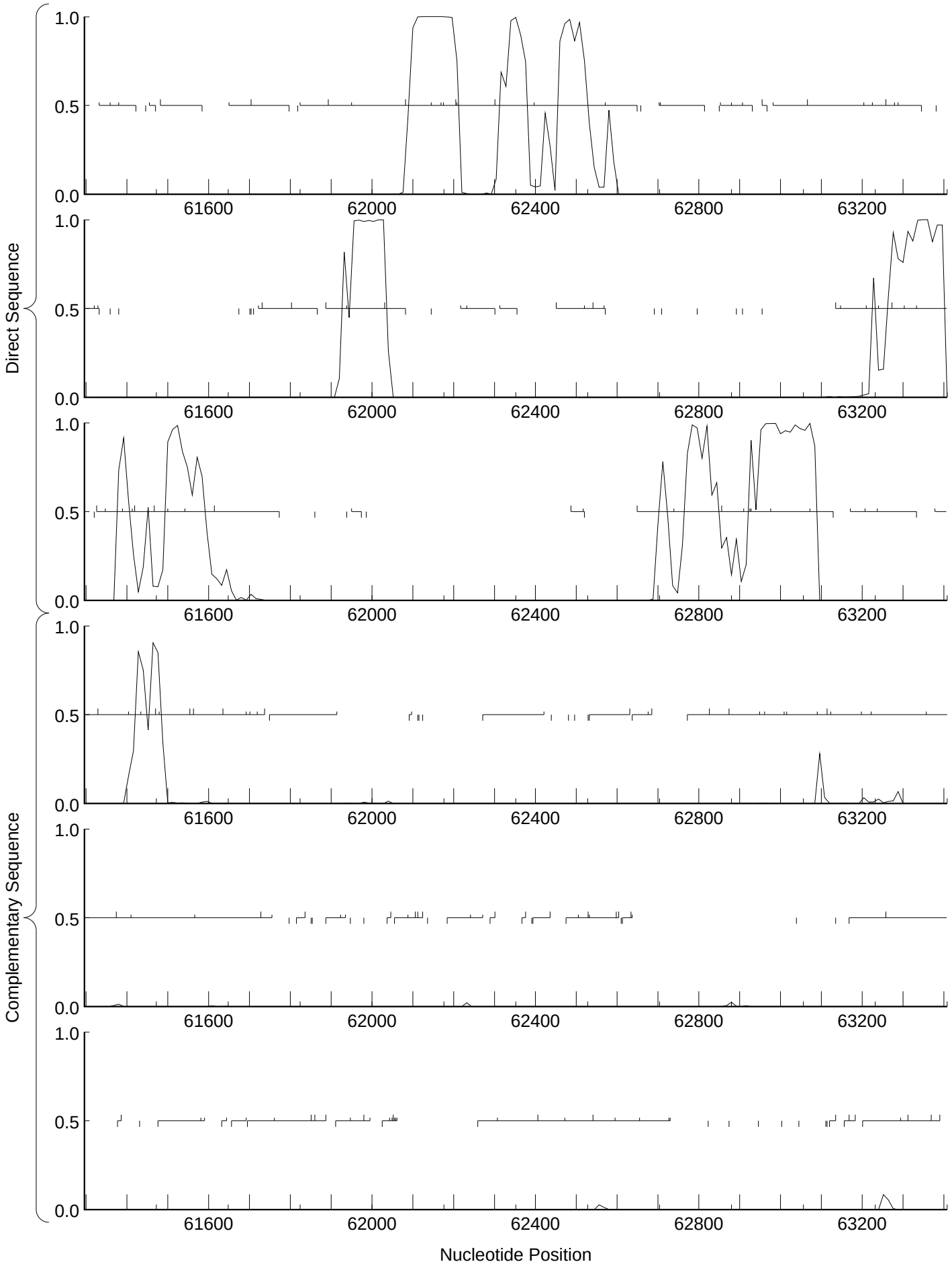


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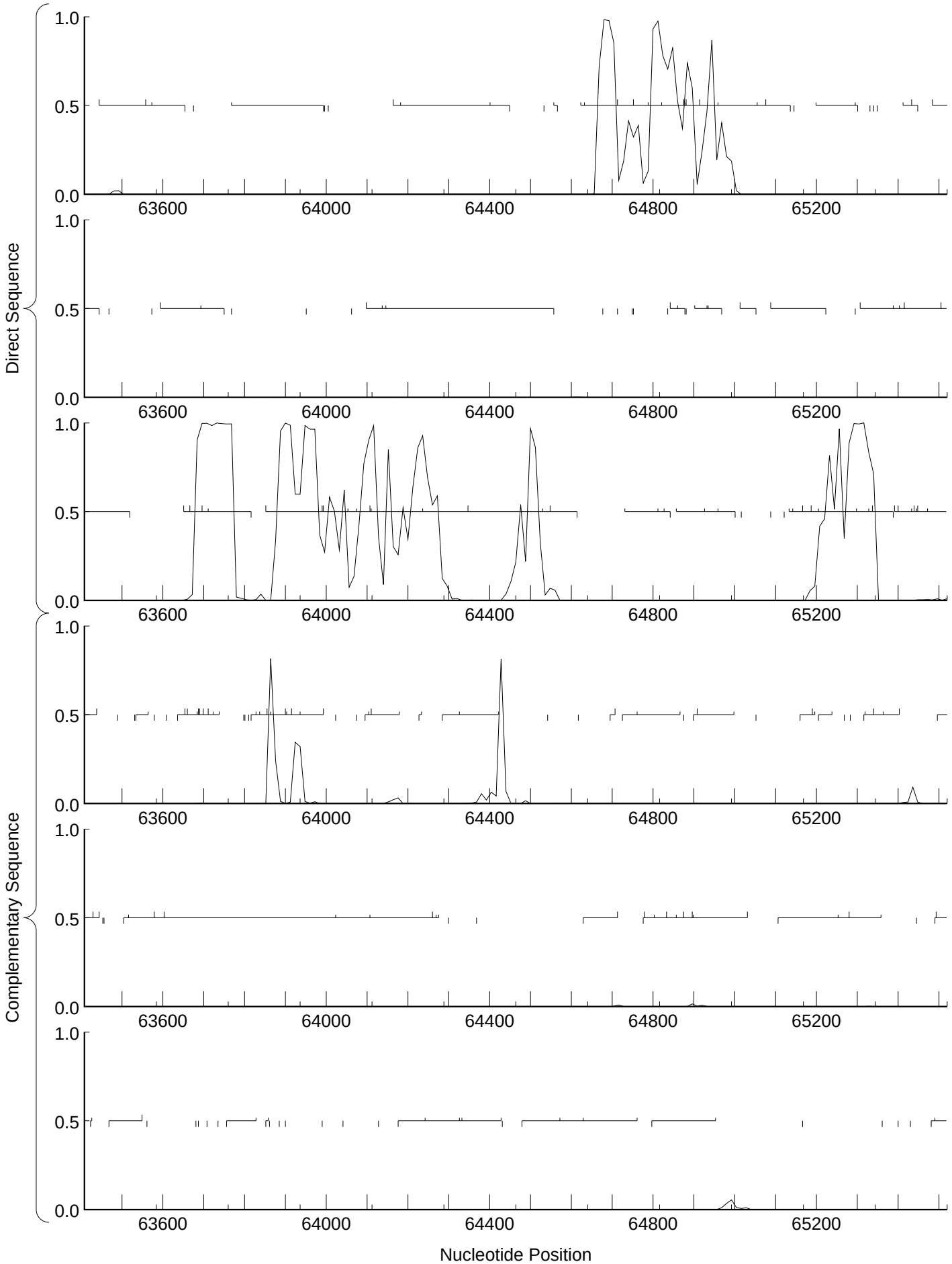


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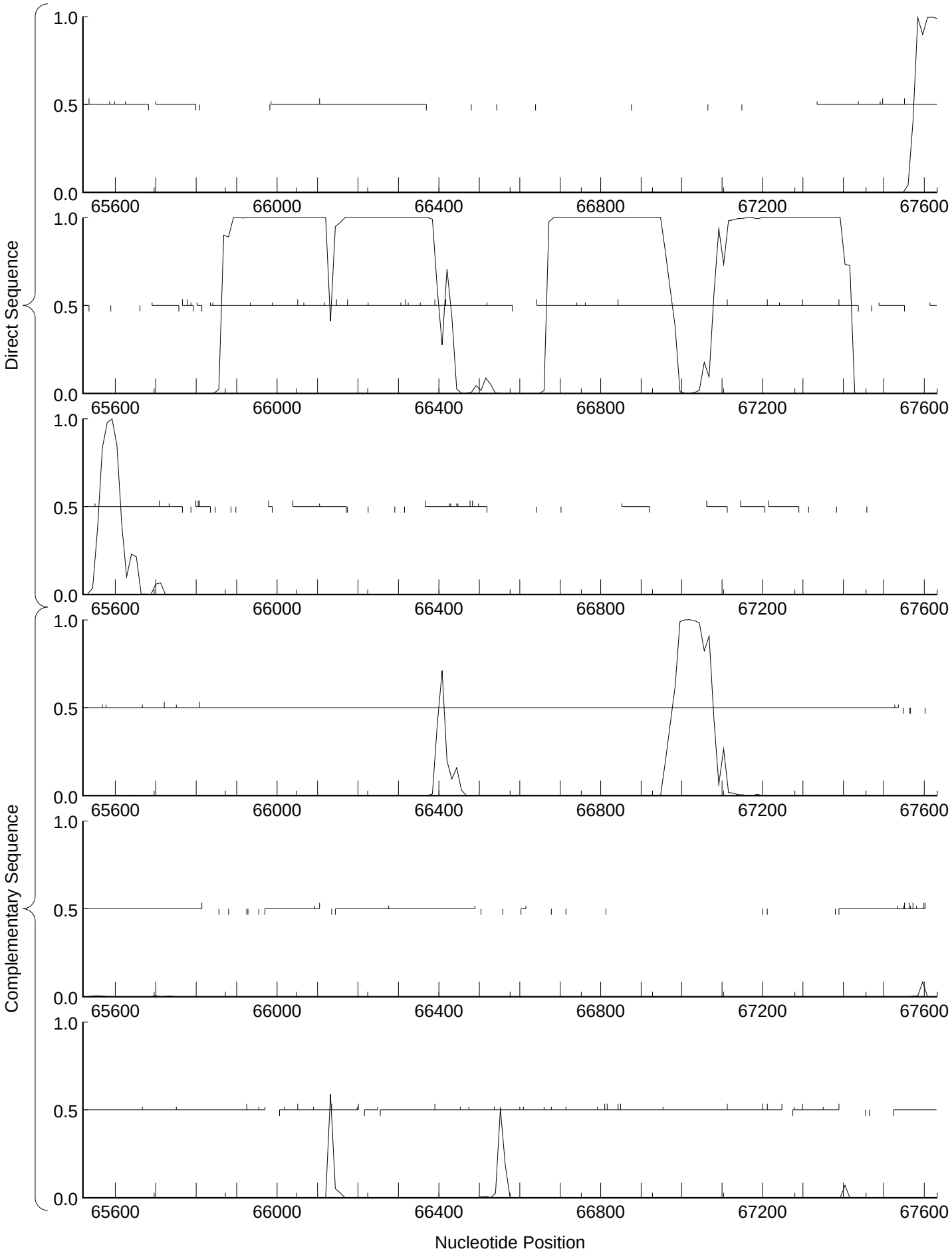



Direct Sequence
Complementary Sequence
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0.0
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62400
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63200
Nucleotide Position

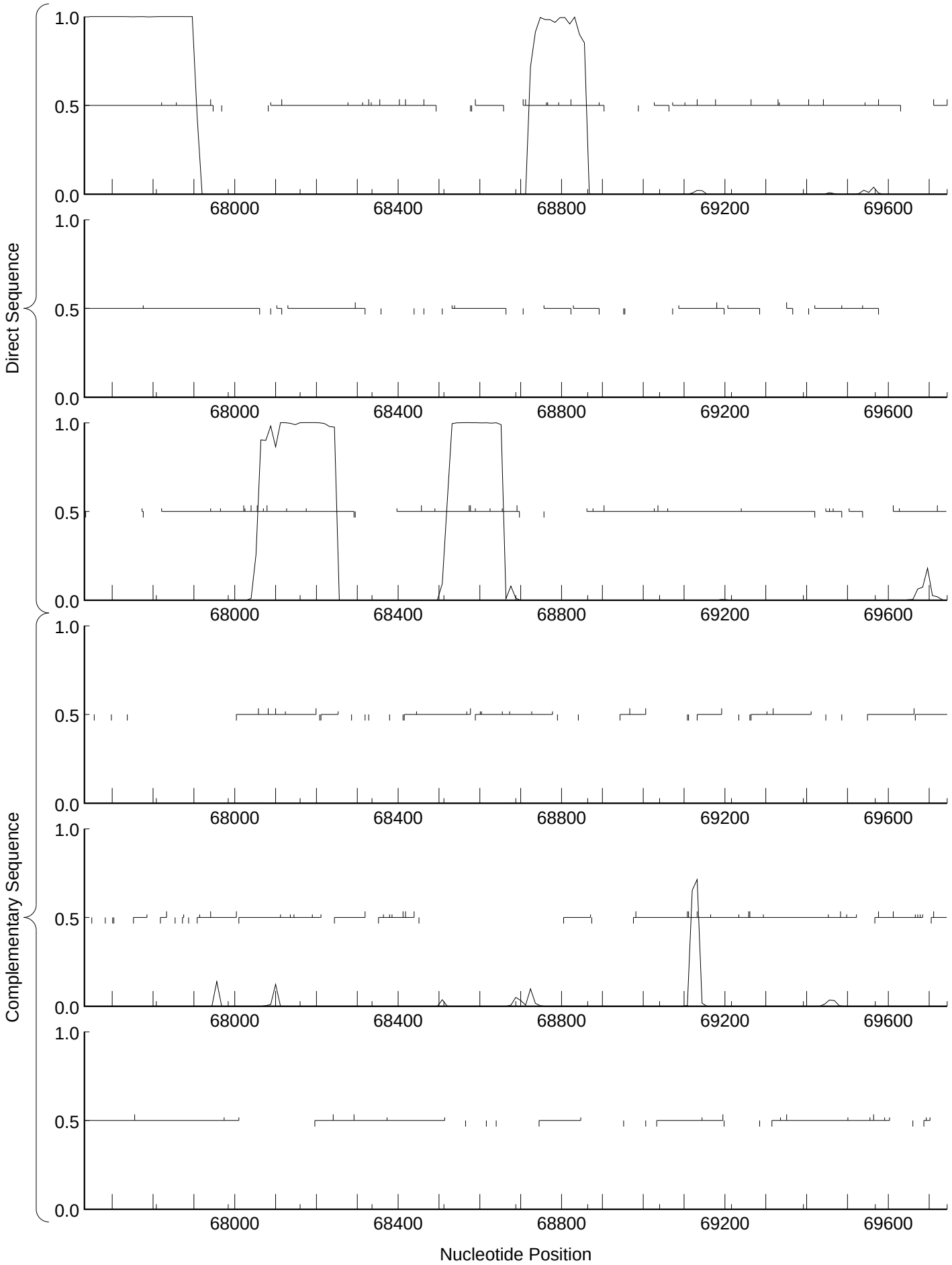
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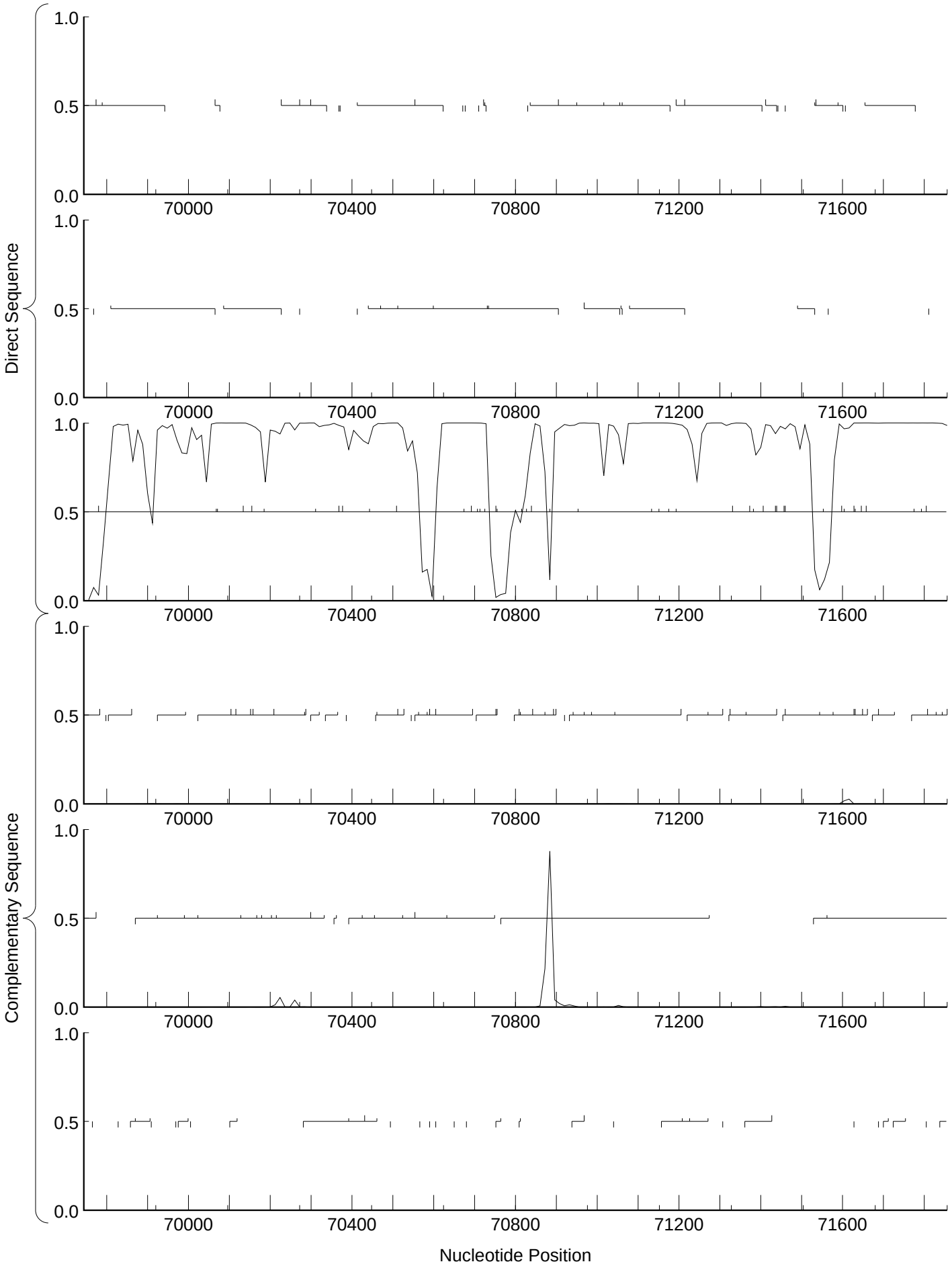
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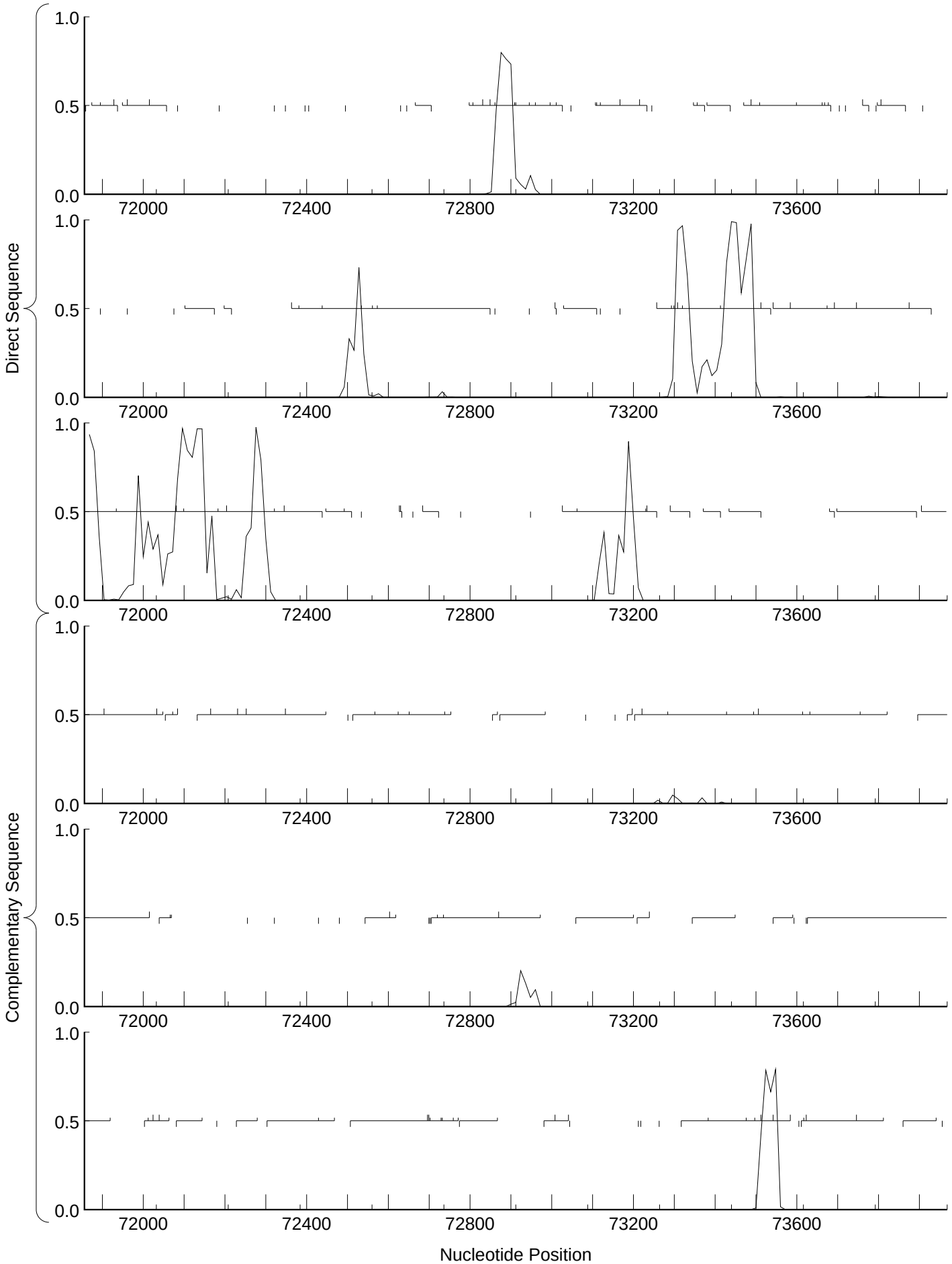


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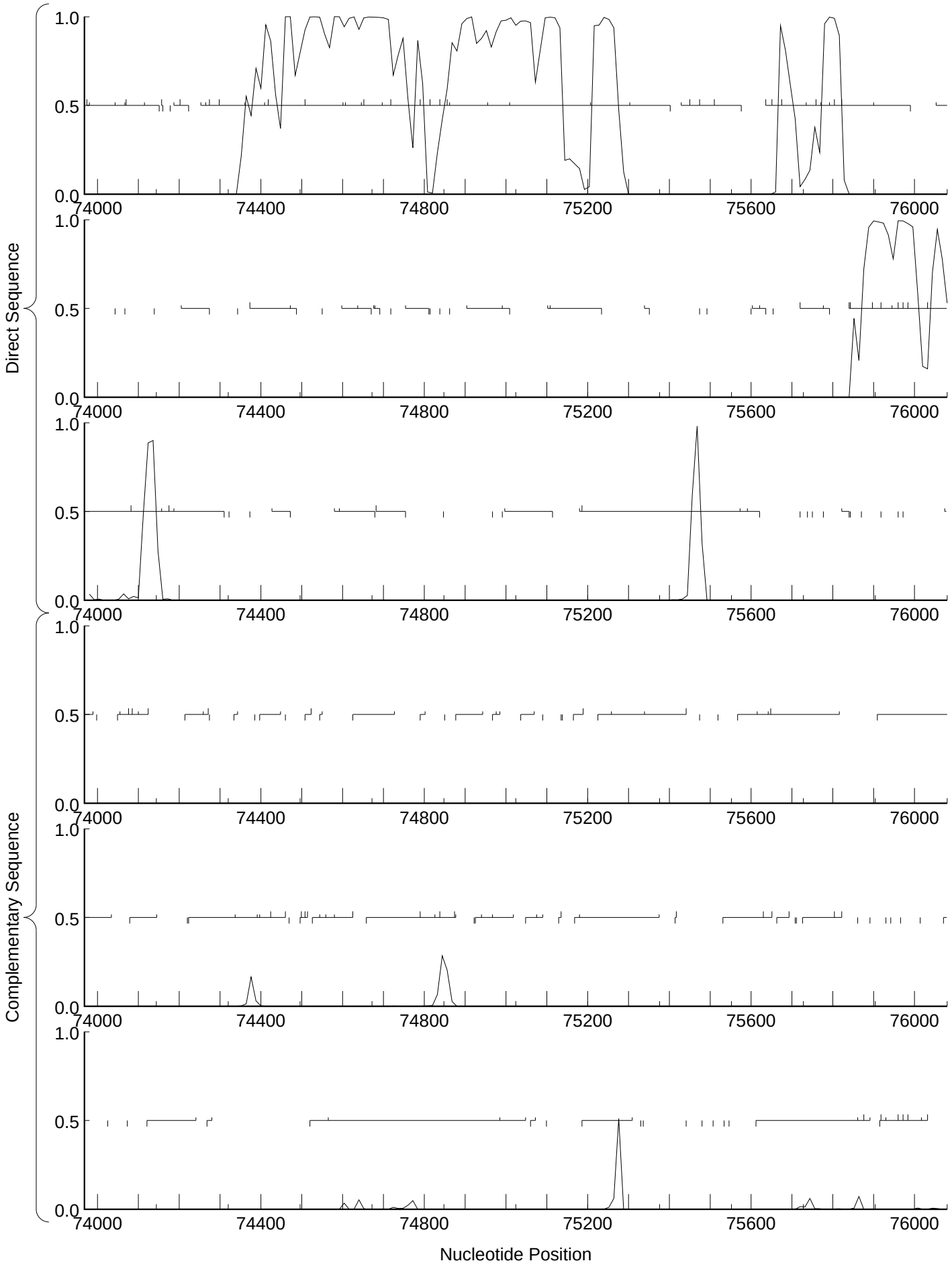


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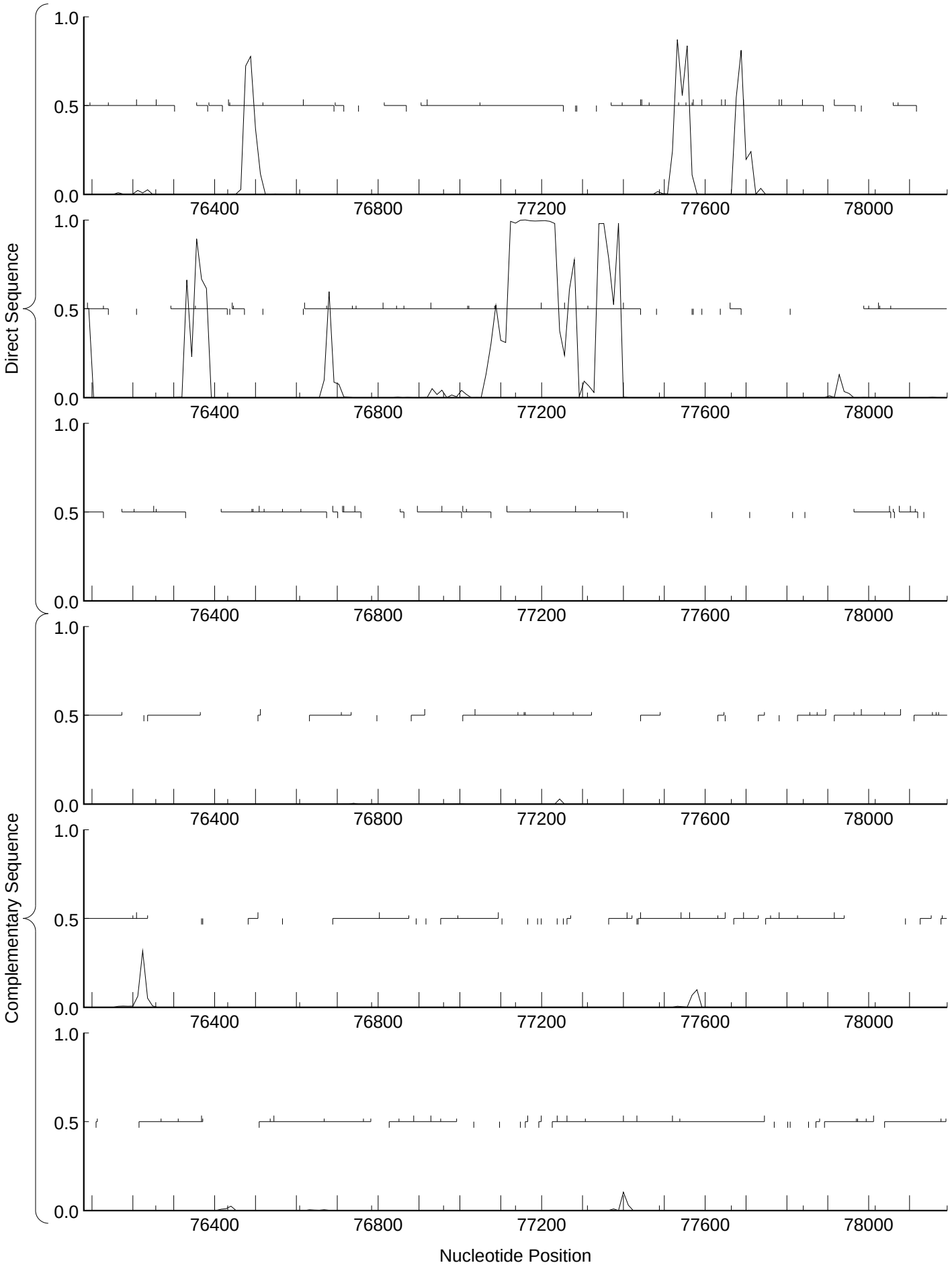



Direct Sequence
Complementary Sequence
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0.5
0.0
72000
72400
72800
73200
73600
Nucleotide Position

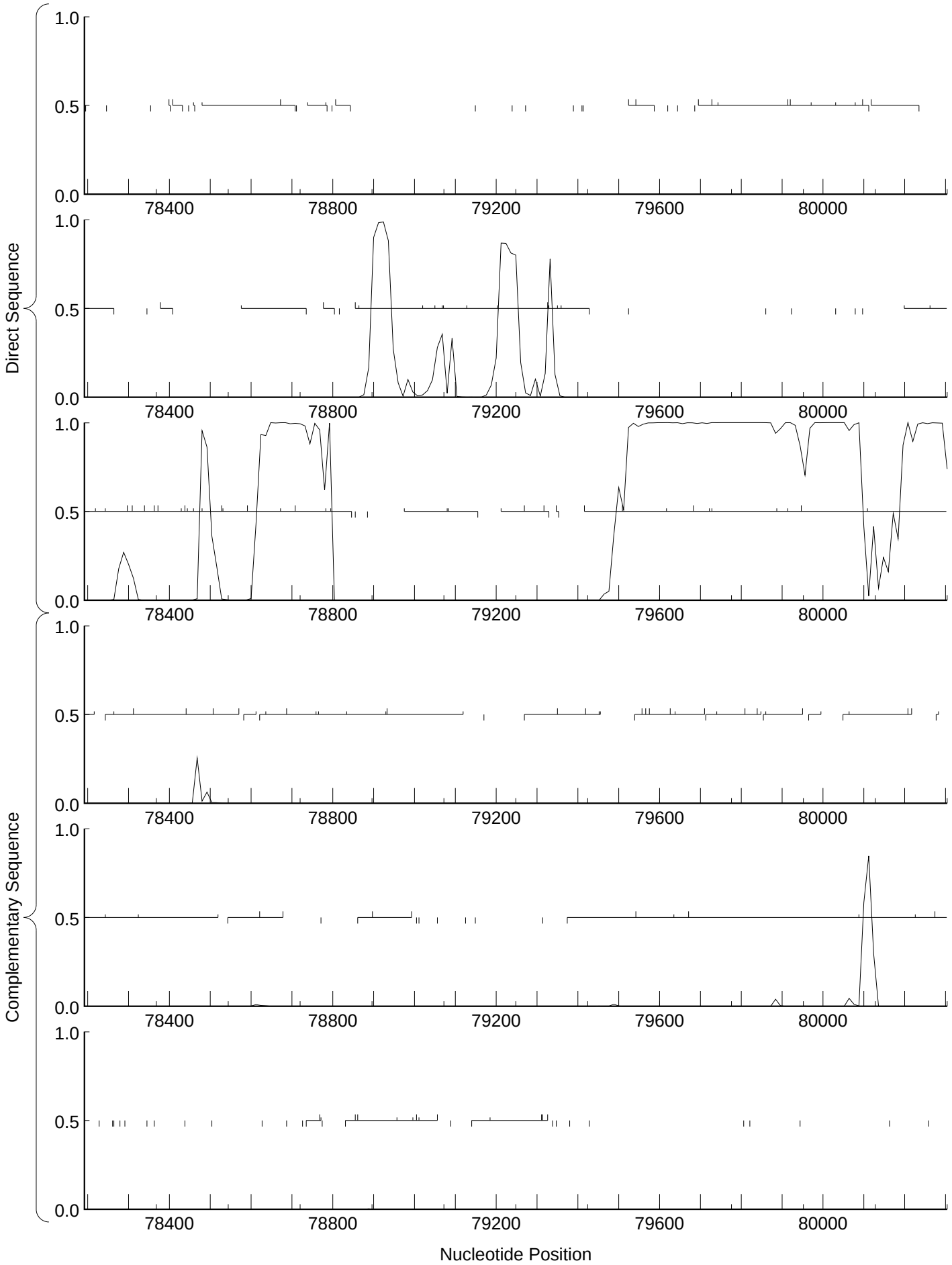
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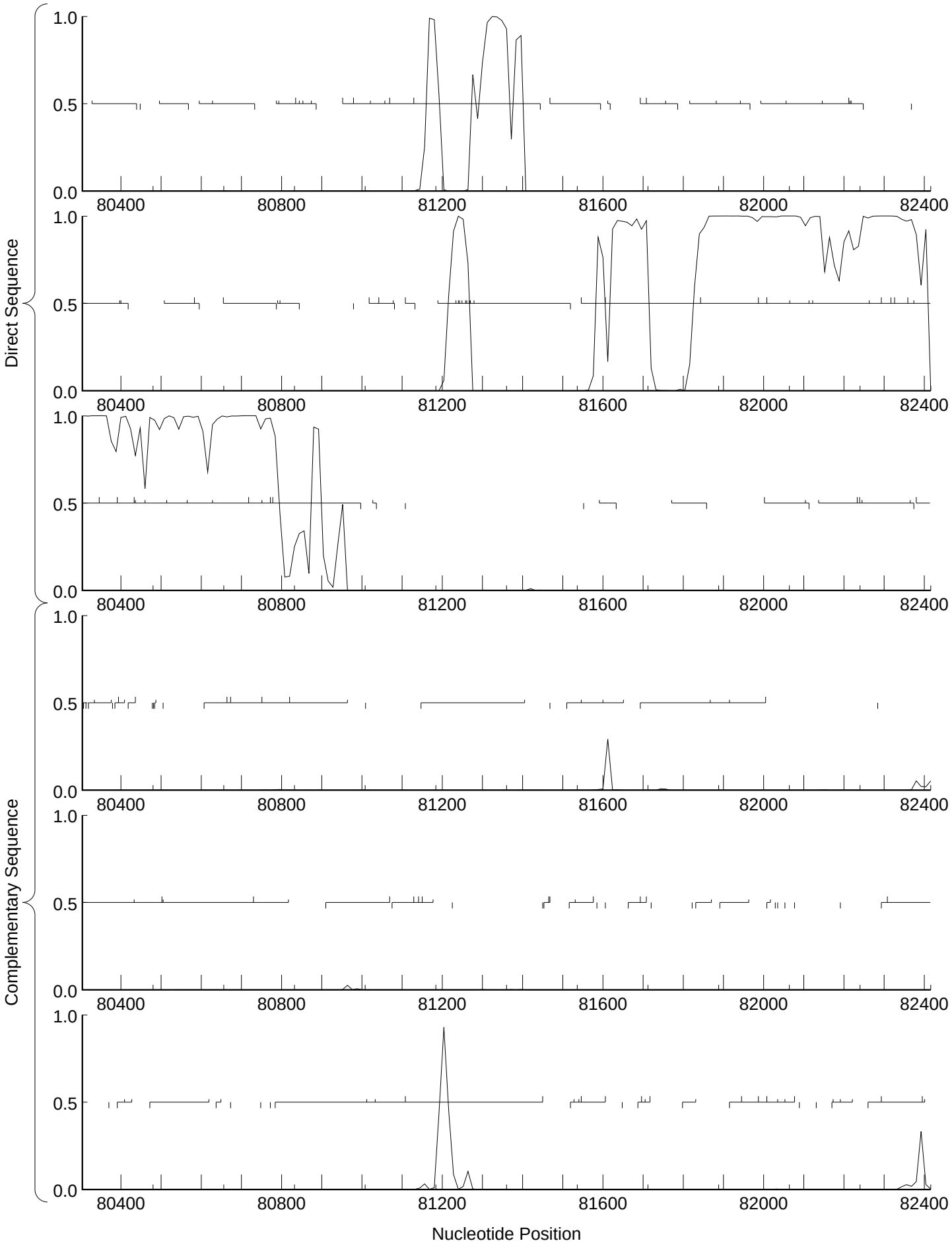
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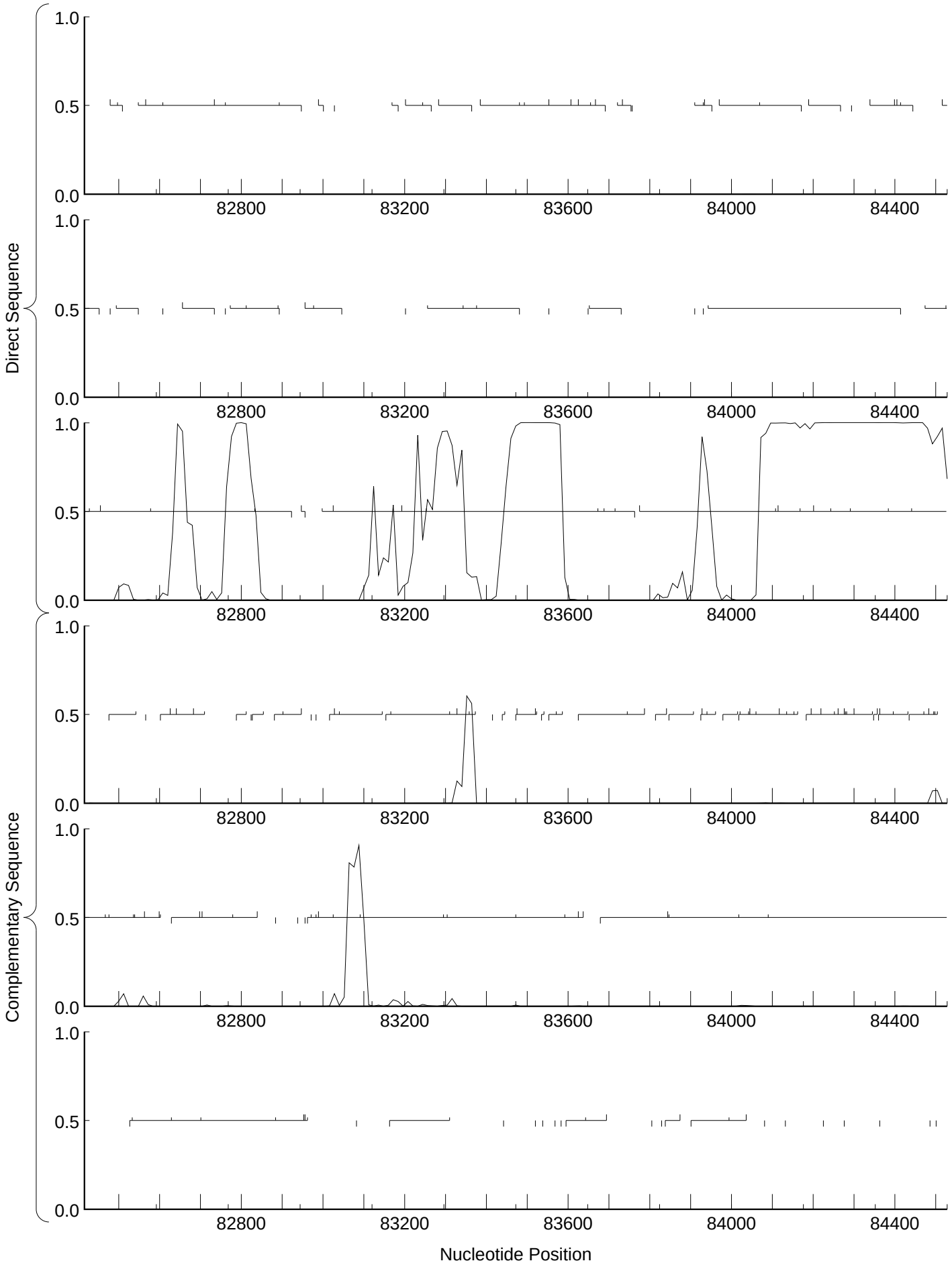
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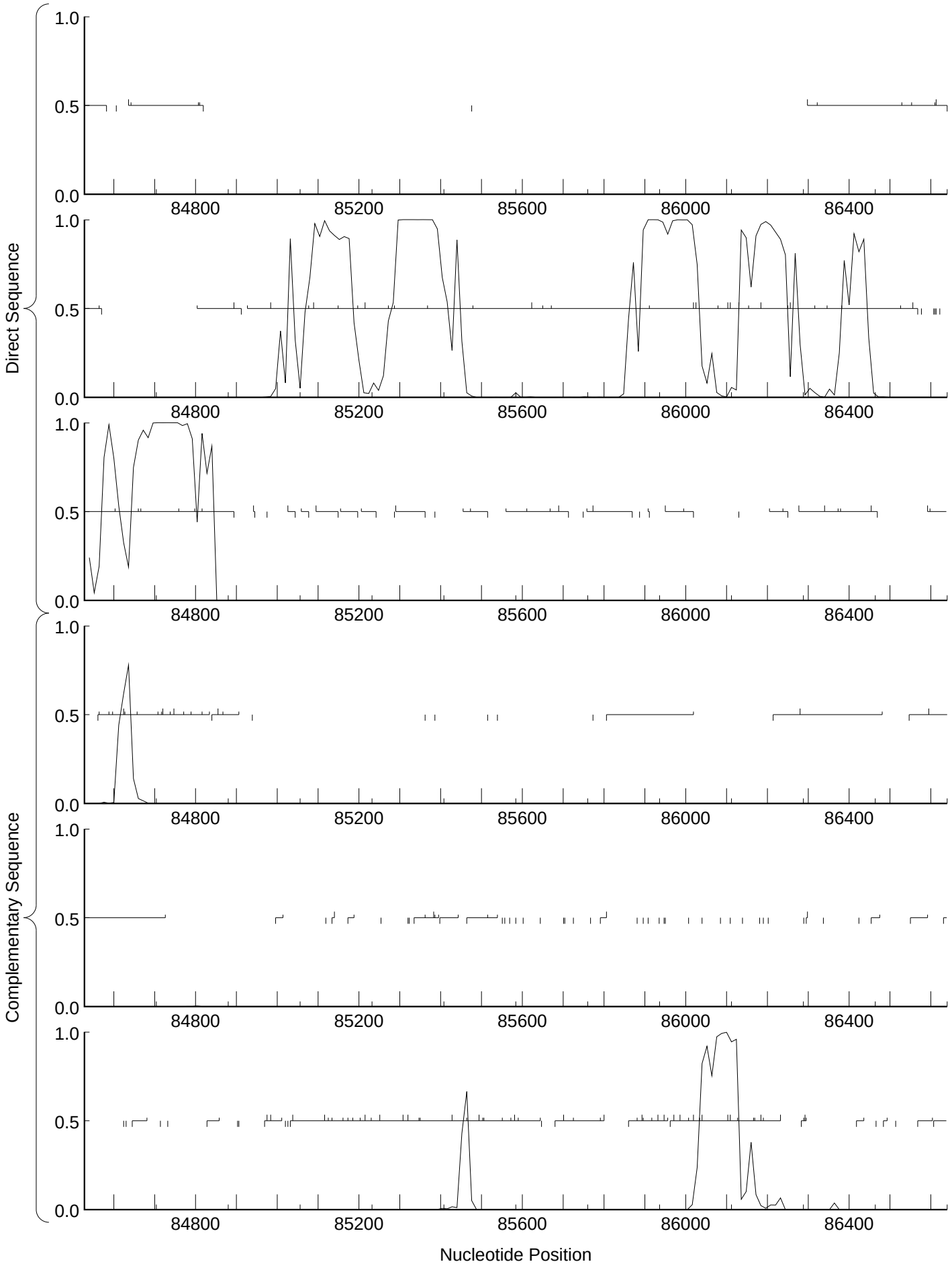
donia phage ChisanaKitsune complete sequence, 88657 bp, circularly permuted, Cluster DQ, Order 4, Window 96, Step 12, 40/43



donia phage ChisanaKitsune complete sequence, 88657 bp, circularly permuted, Cluster DQ, Order 4, Window 96, Step 12, 41/43



donia phage ChisanaKitsune complete sequence, 88657 bp, circularly permuted, Cluster DQ, Order 4, Window 96, Step 12, 42/43



donia phage ChisanaKitsune complete sequence, 88657 bp, circularly permuted, Cluster DQ, Order 4, Window 96, Step 12, 43/43

