GeneMark

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

PROGRAM INFORMATION

```
Sequence         :  Mycobacterium phage Acolyte complete sequence, 52668 bp including 10-base 3’ overhang (CGGT
Analysis Date    :  3/28/24 at 21:06:16
Pages            :  26
Sequence Length  :  52668 bp
GC Content       :   63.35%

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

PS-Version       :  1.2

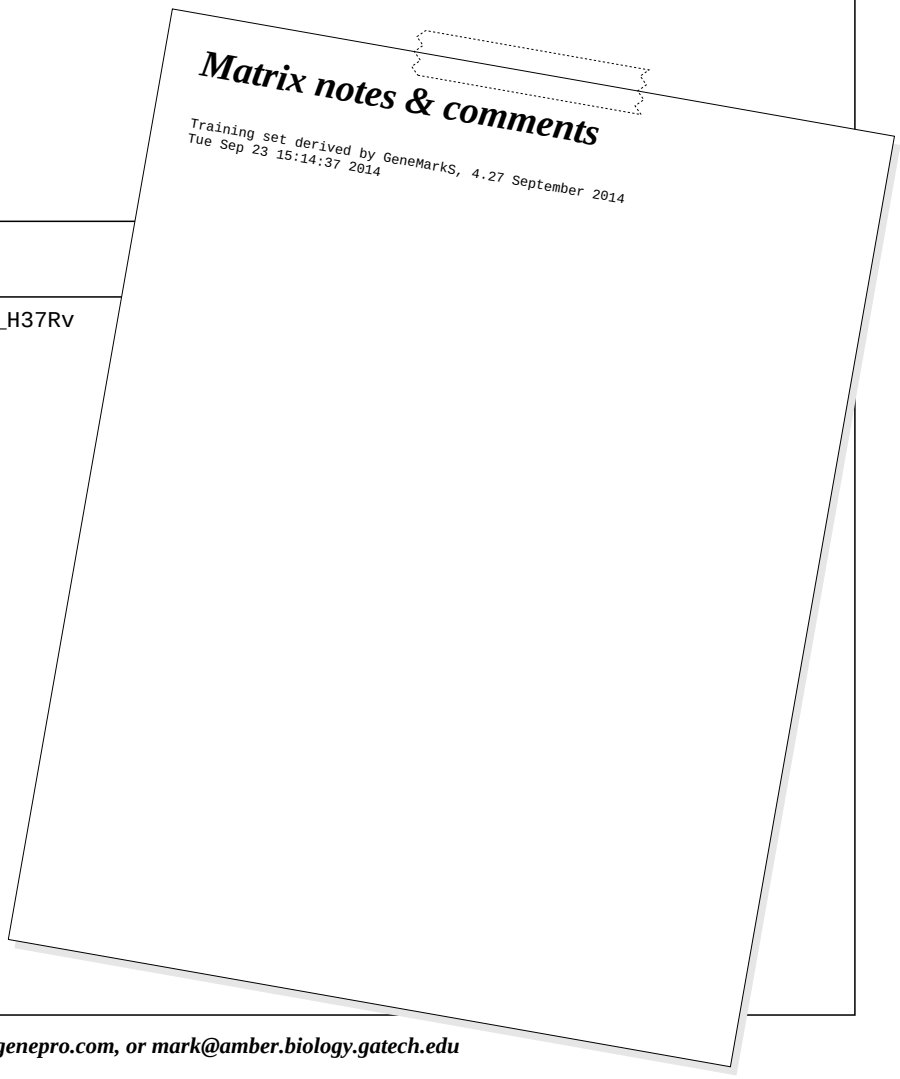
GeneMark Options :  PostScript graph,
                    Mark ORFs / splice sites,
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MATRIX INFORMATION

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Author     :  -

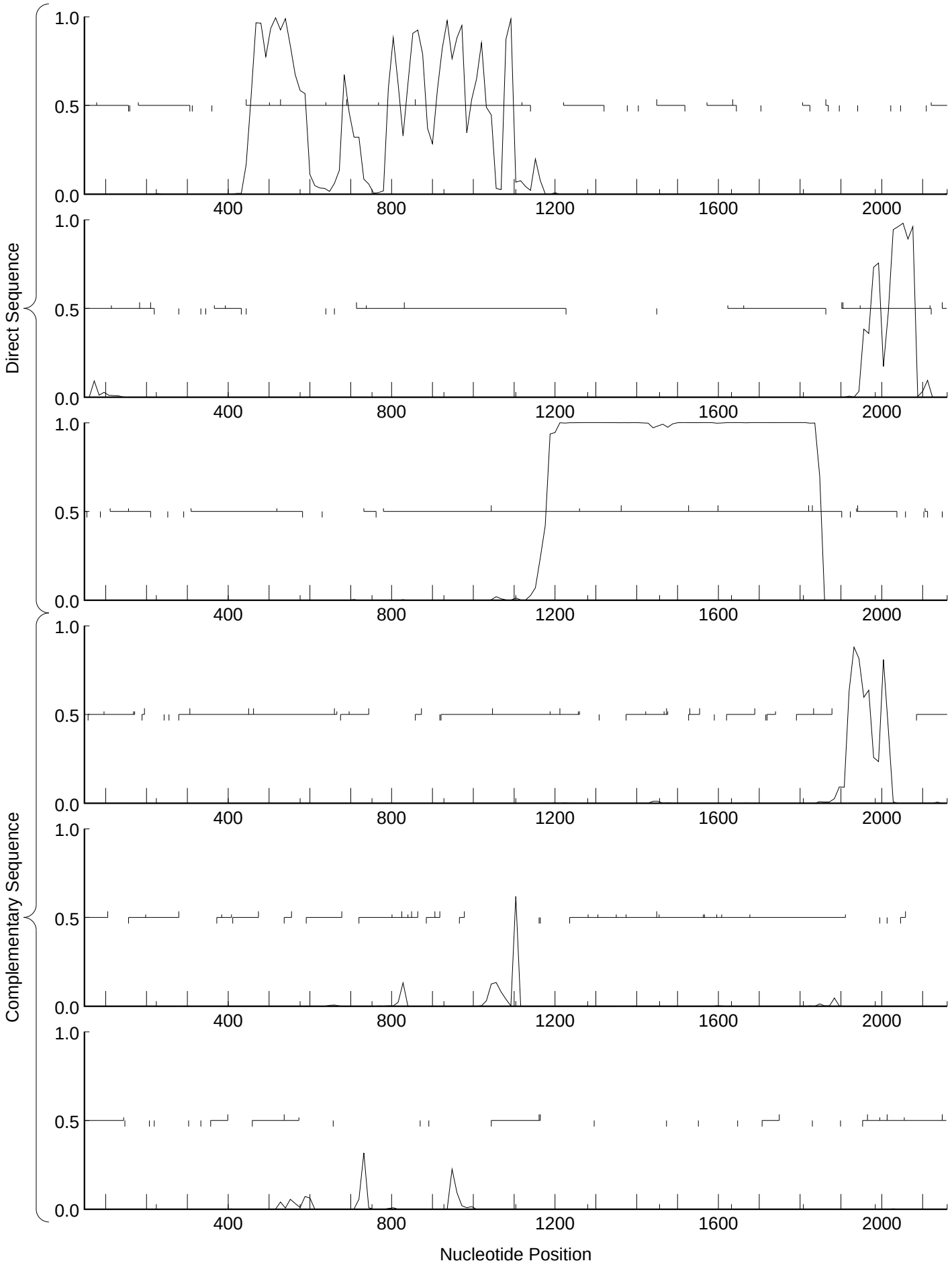
Order      :  4


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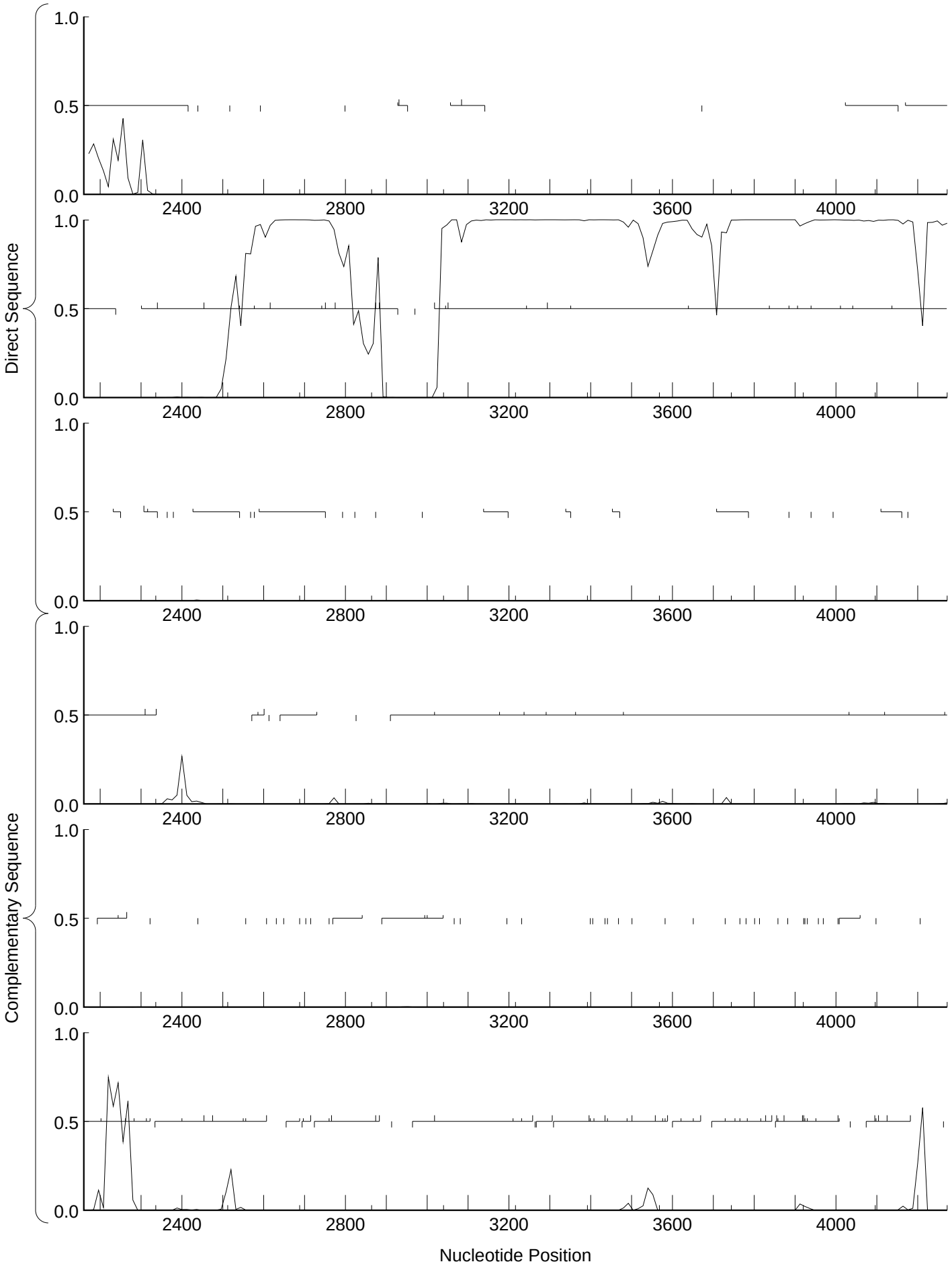


For help or information, send electronic mail to: custserv@genepro.com, or mark@amber.biology.gatech.edu

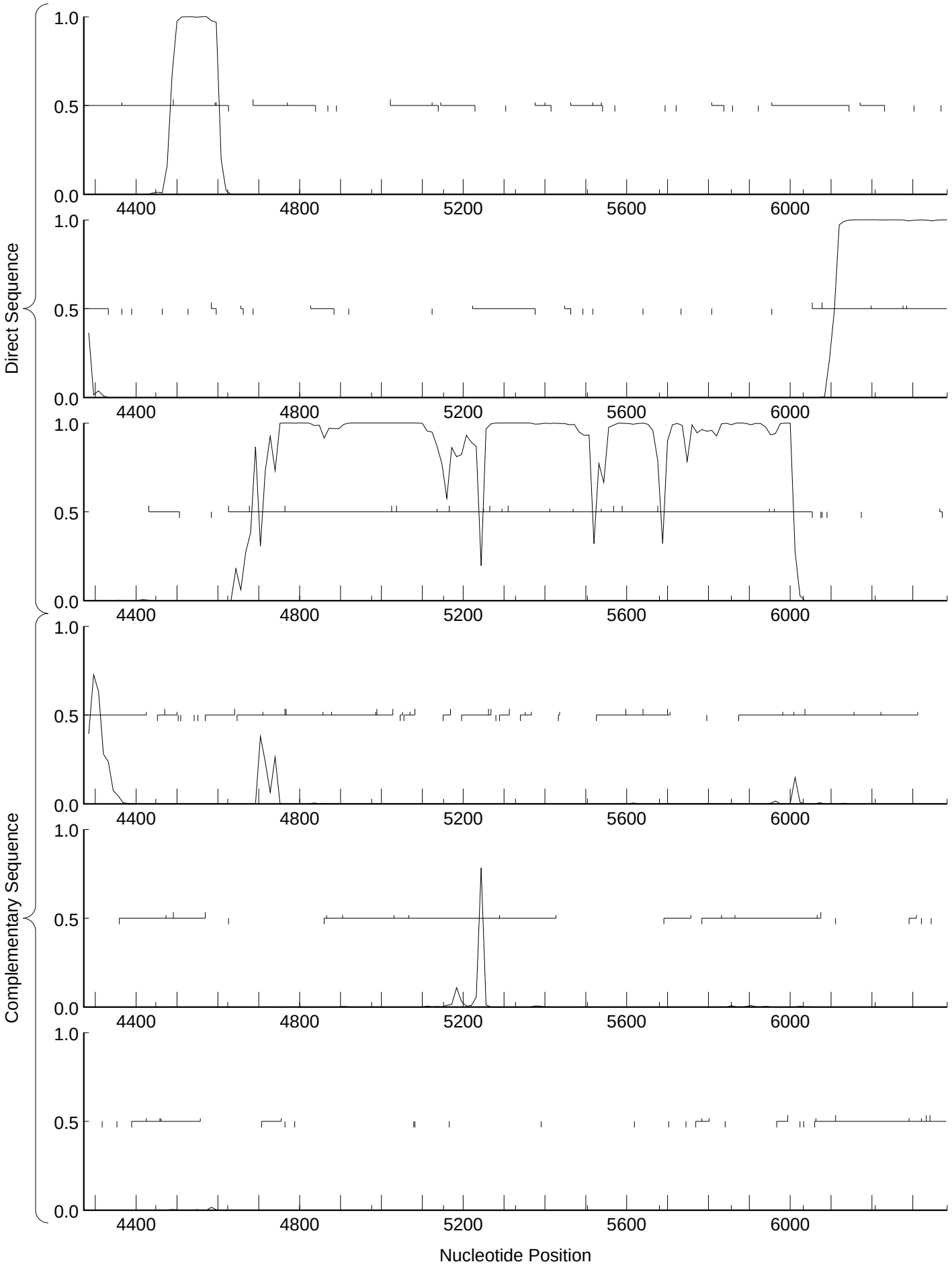
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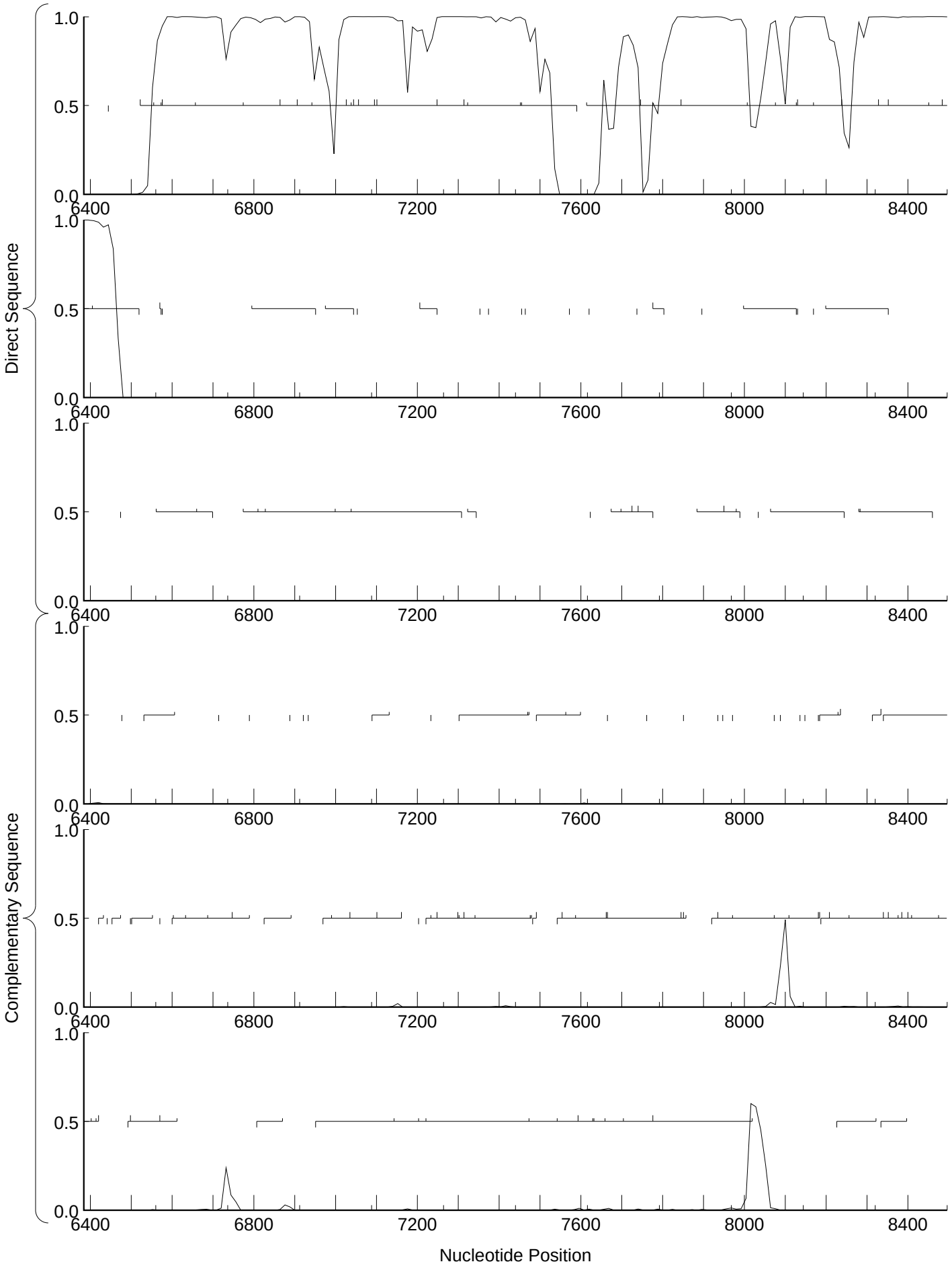
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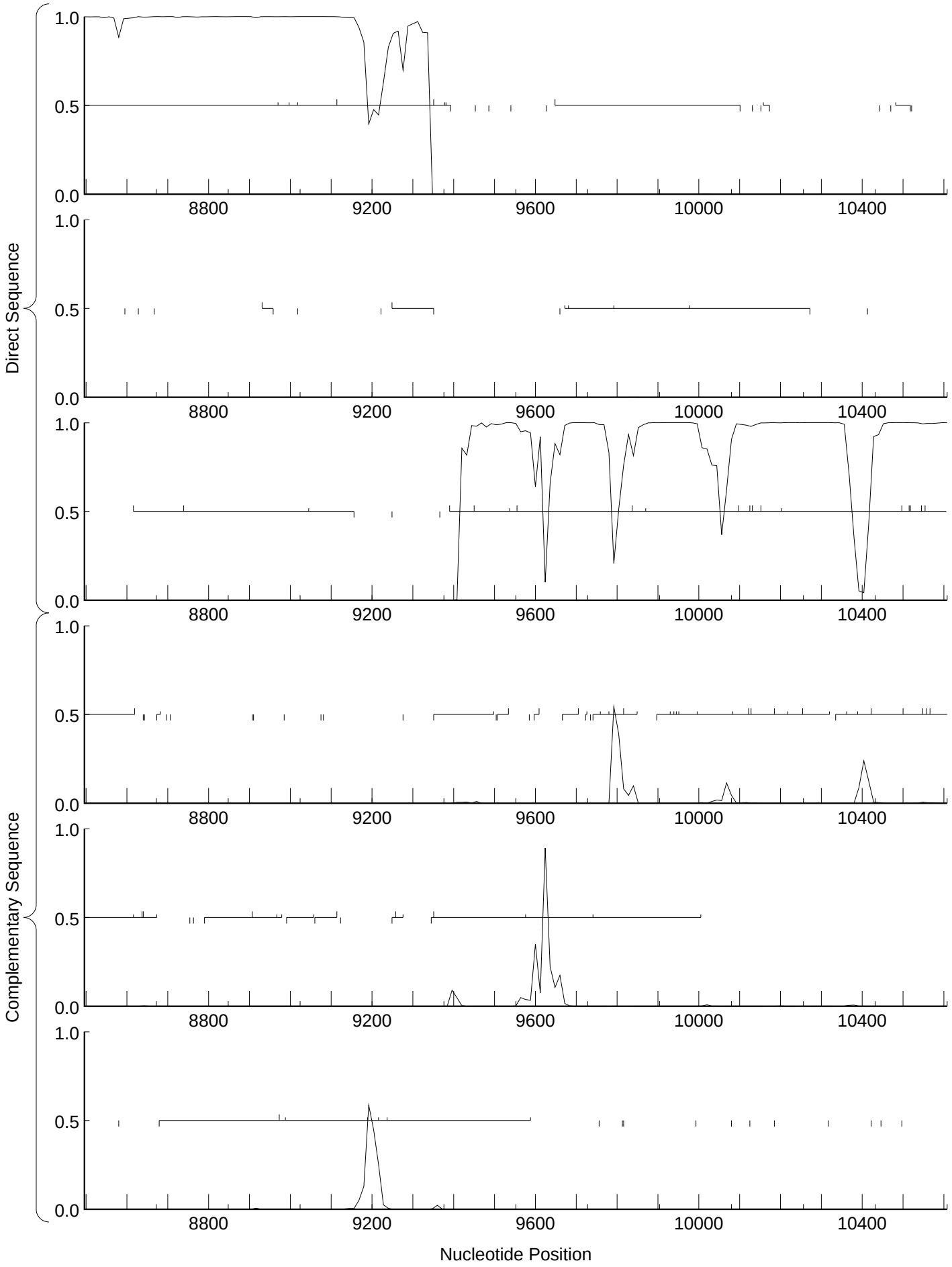
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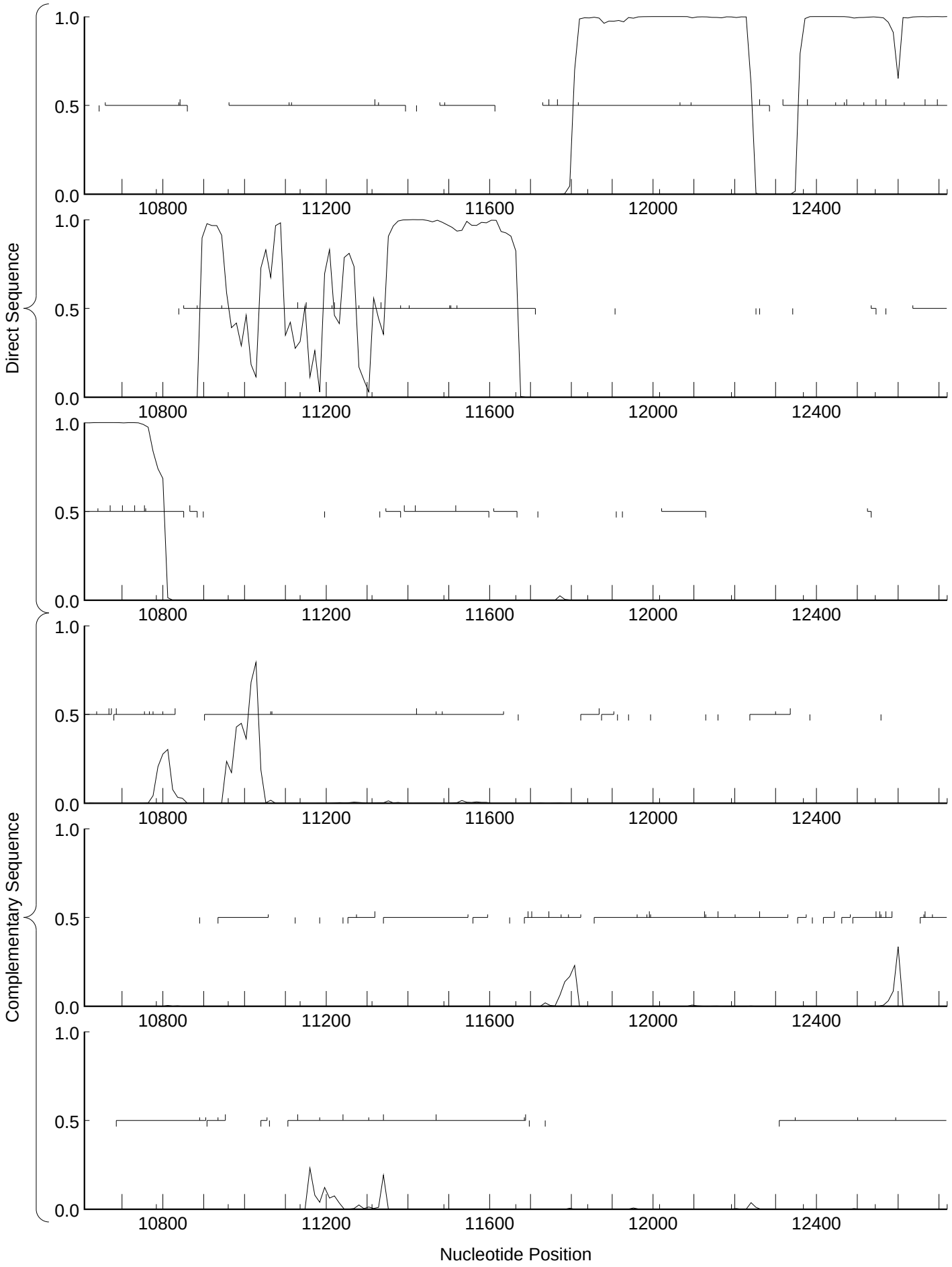
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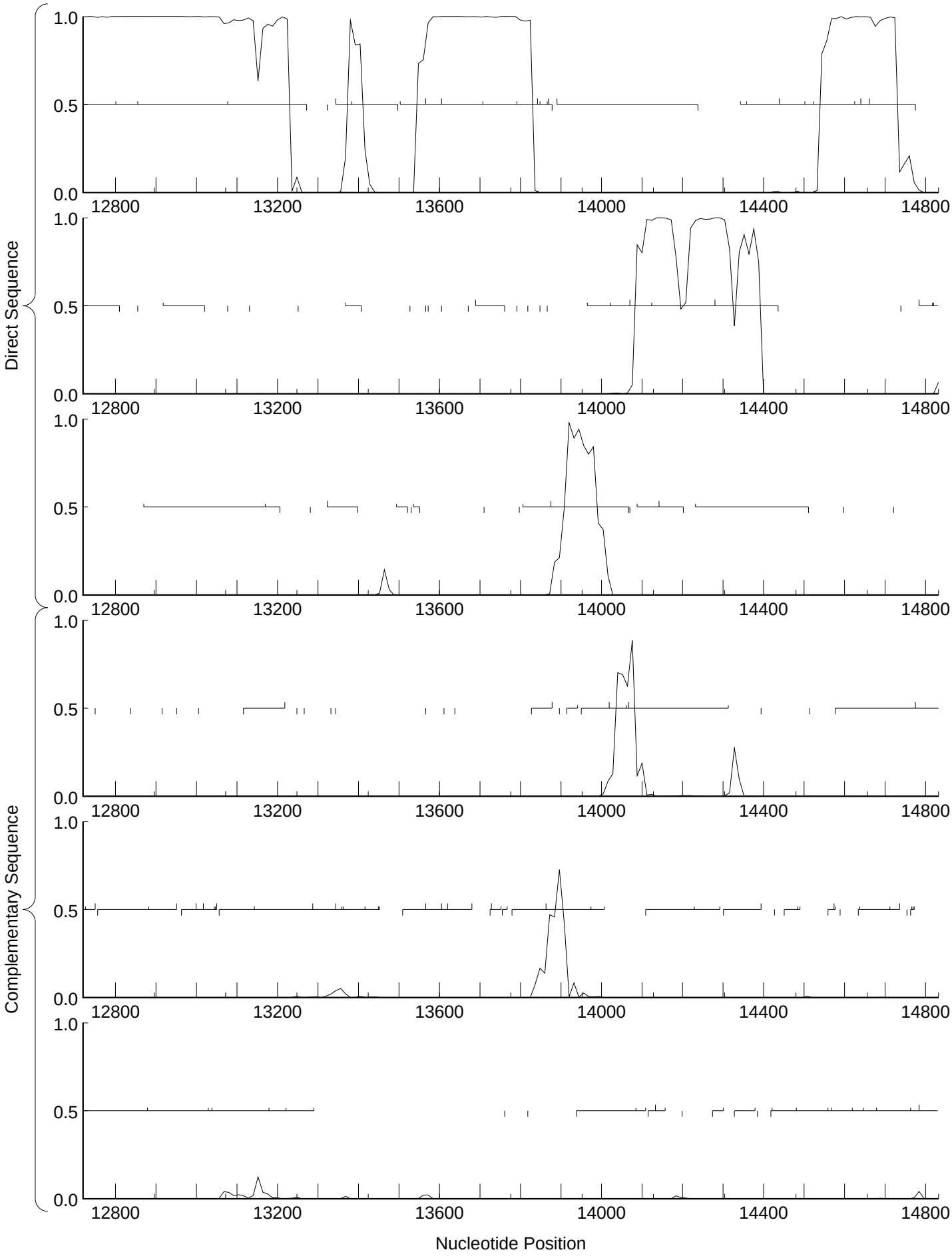
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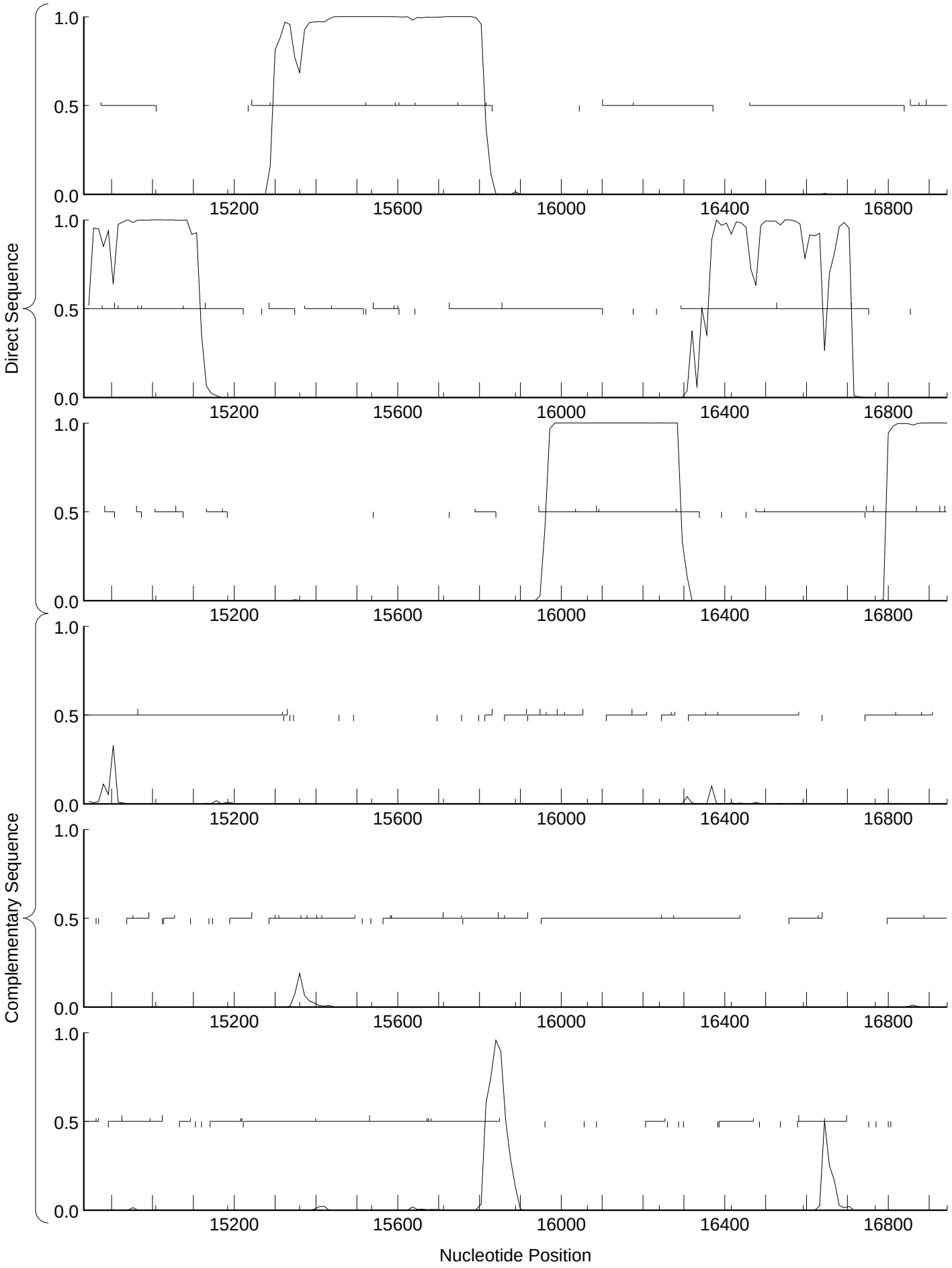
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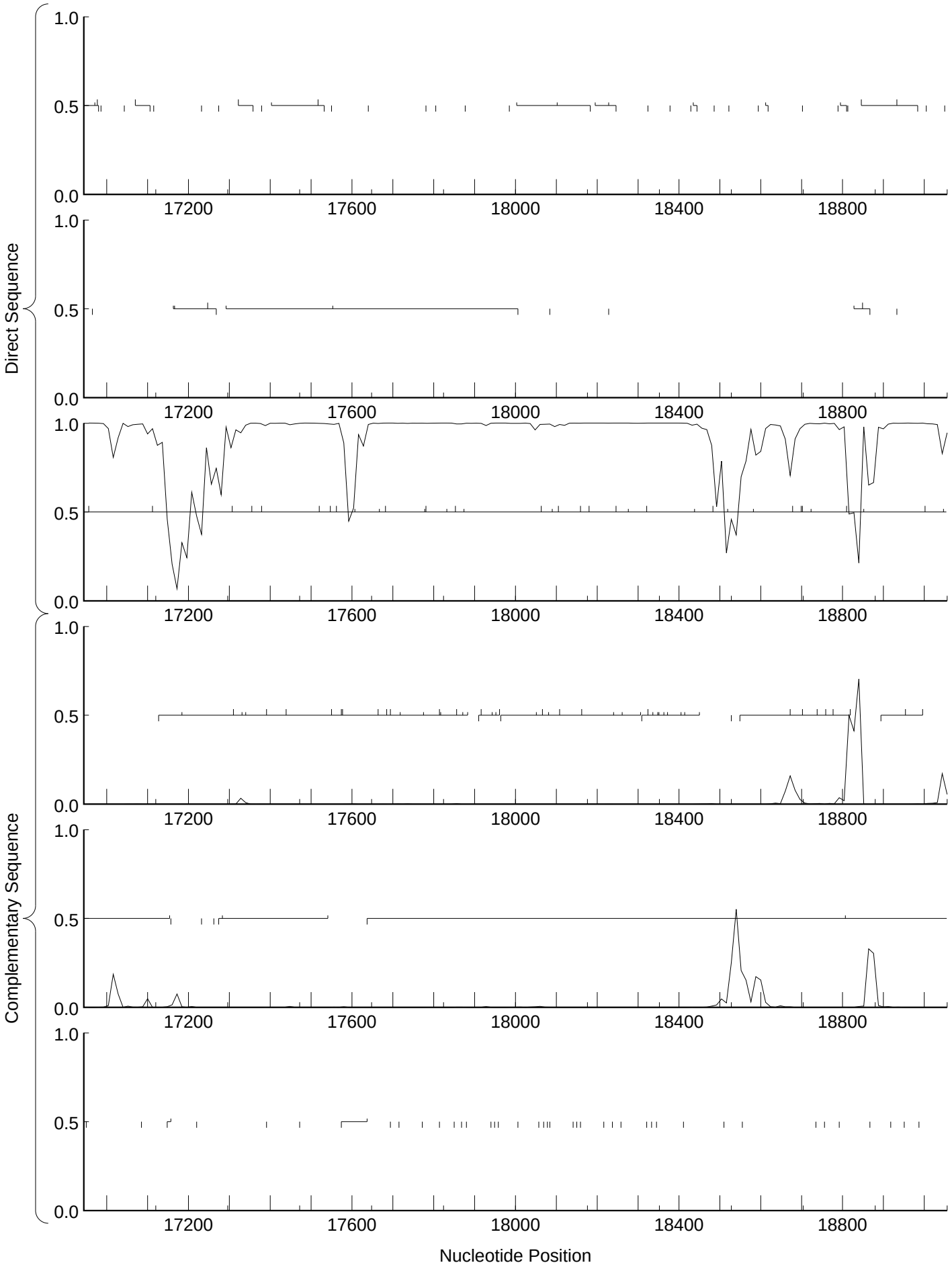
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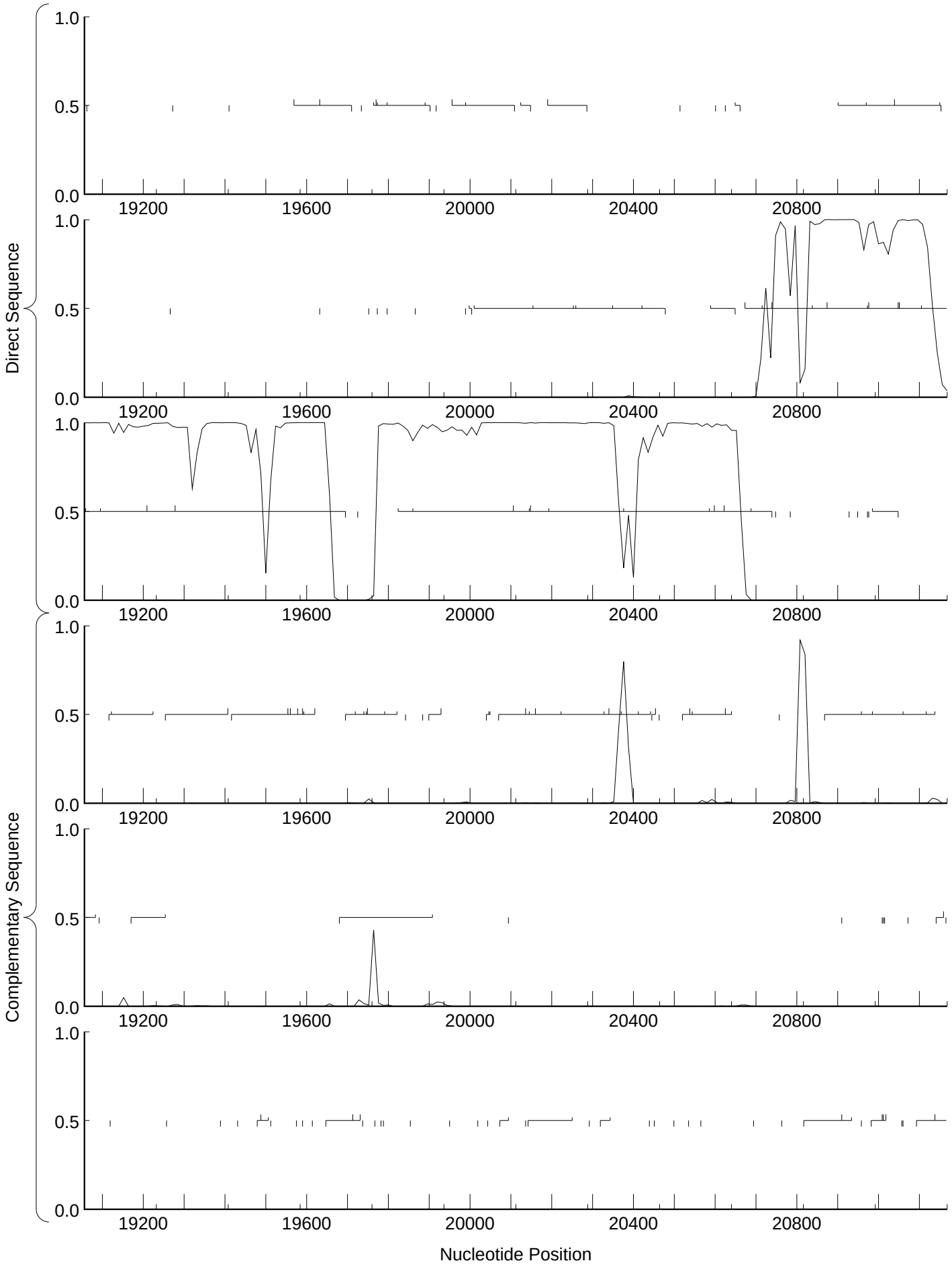
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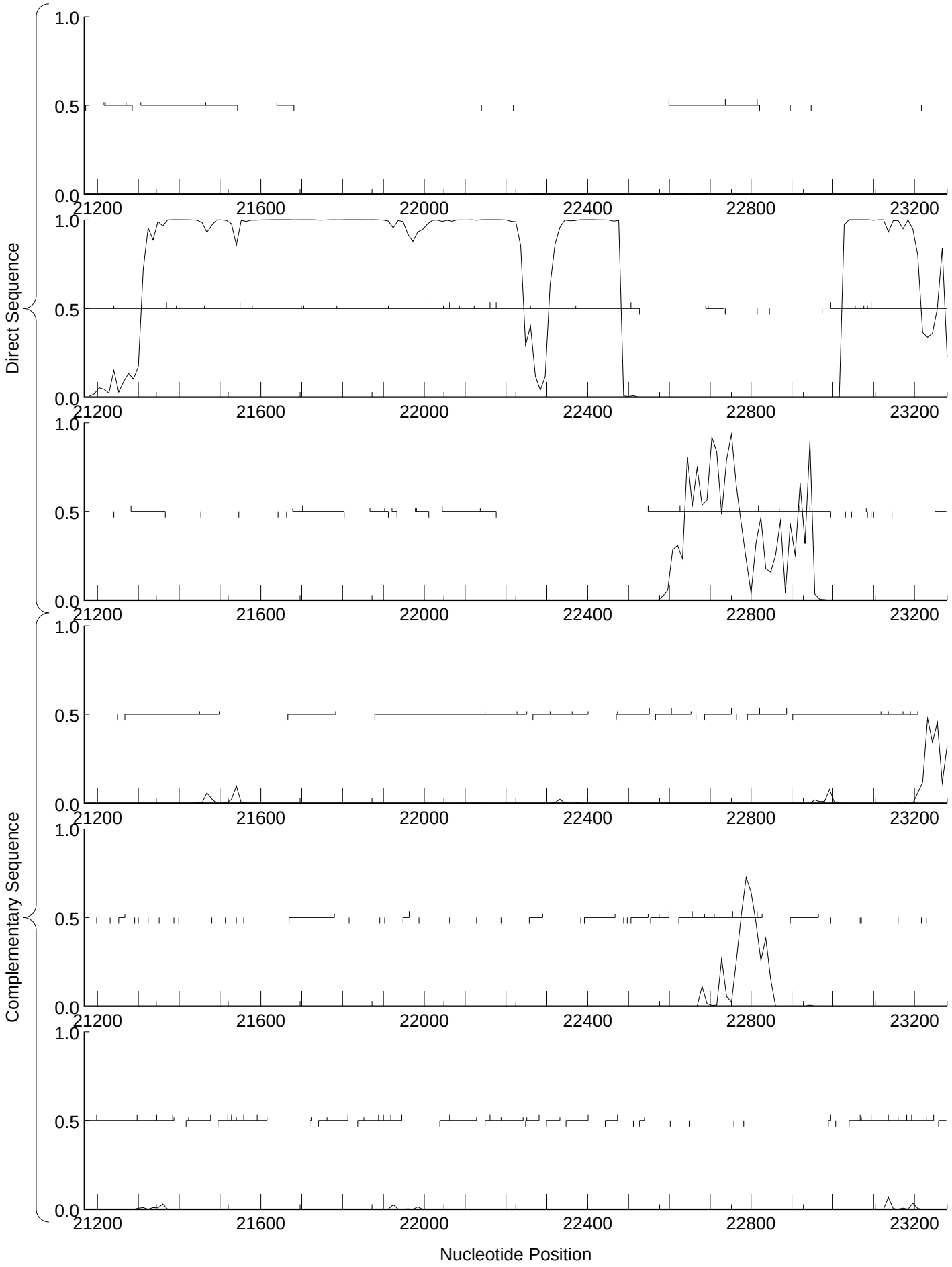
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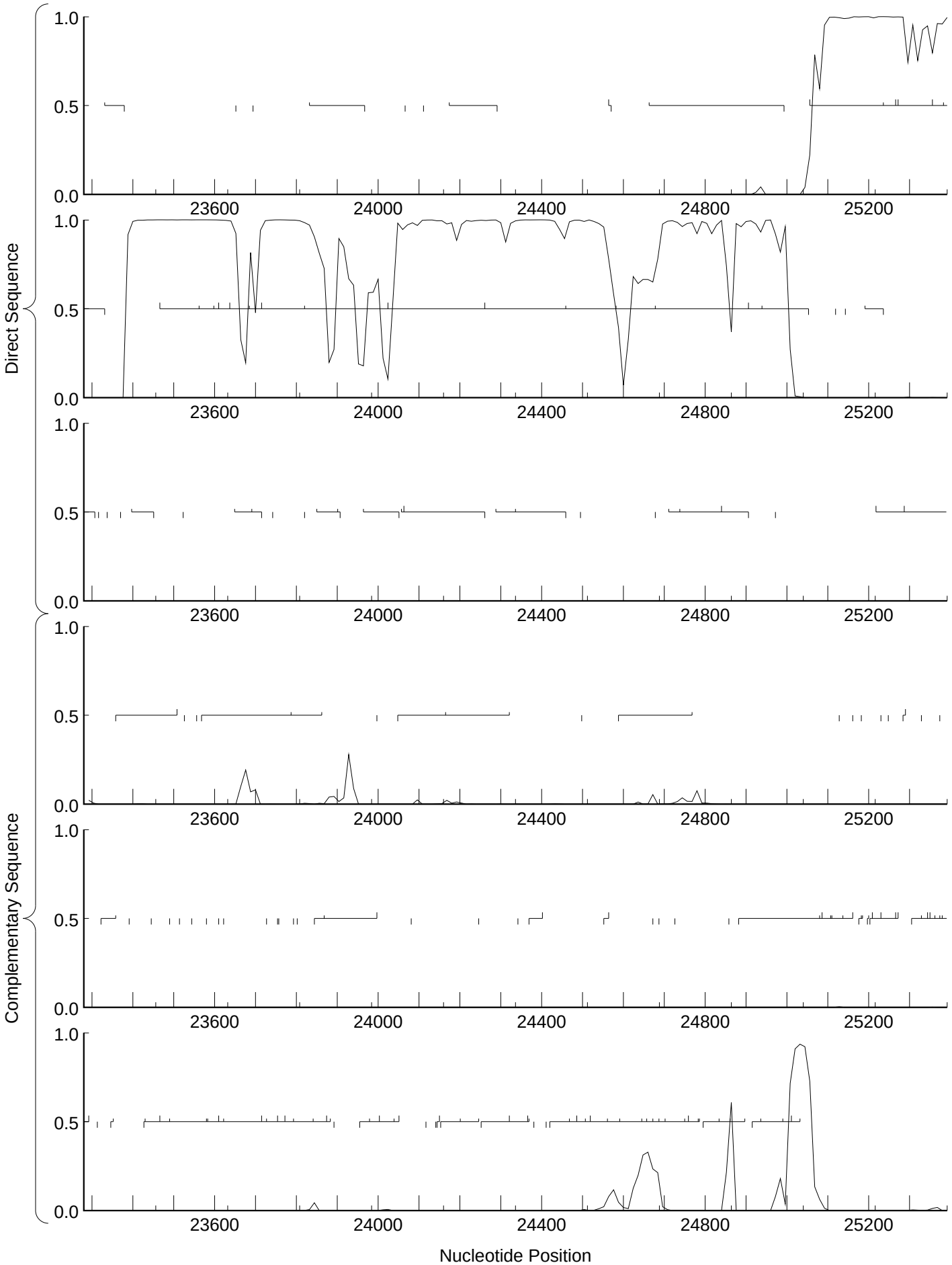
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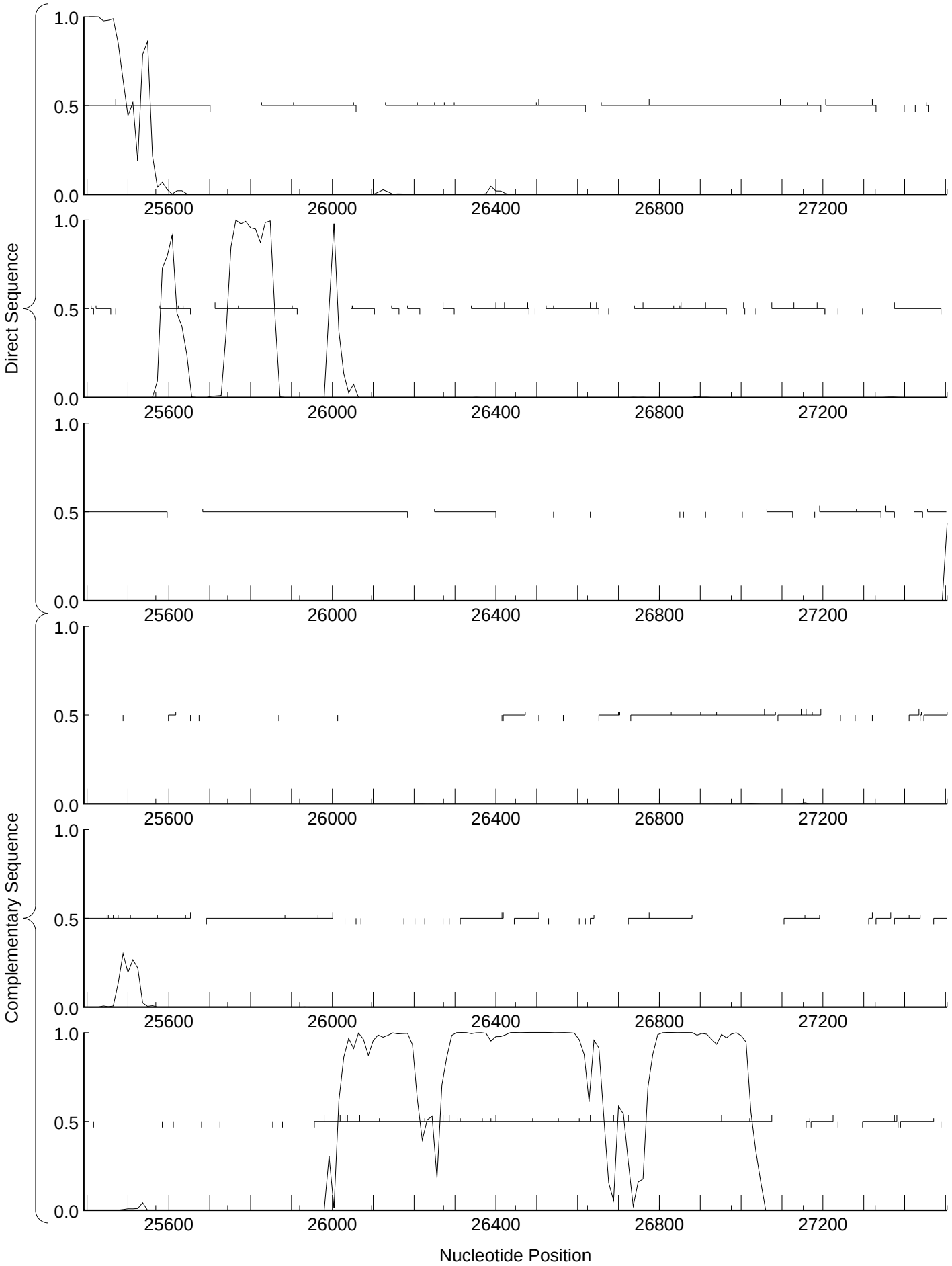
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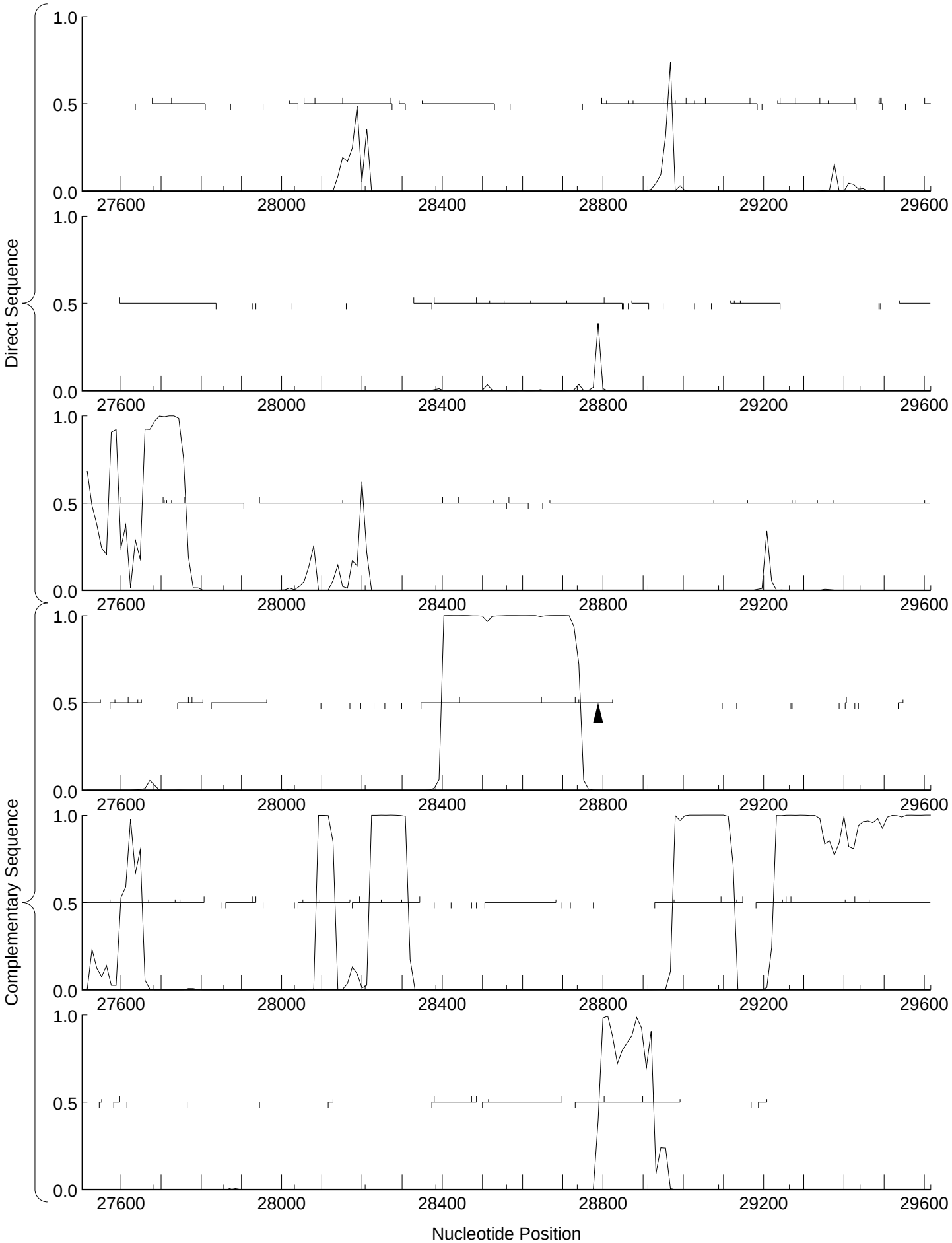
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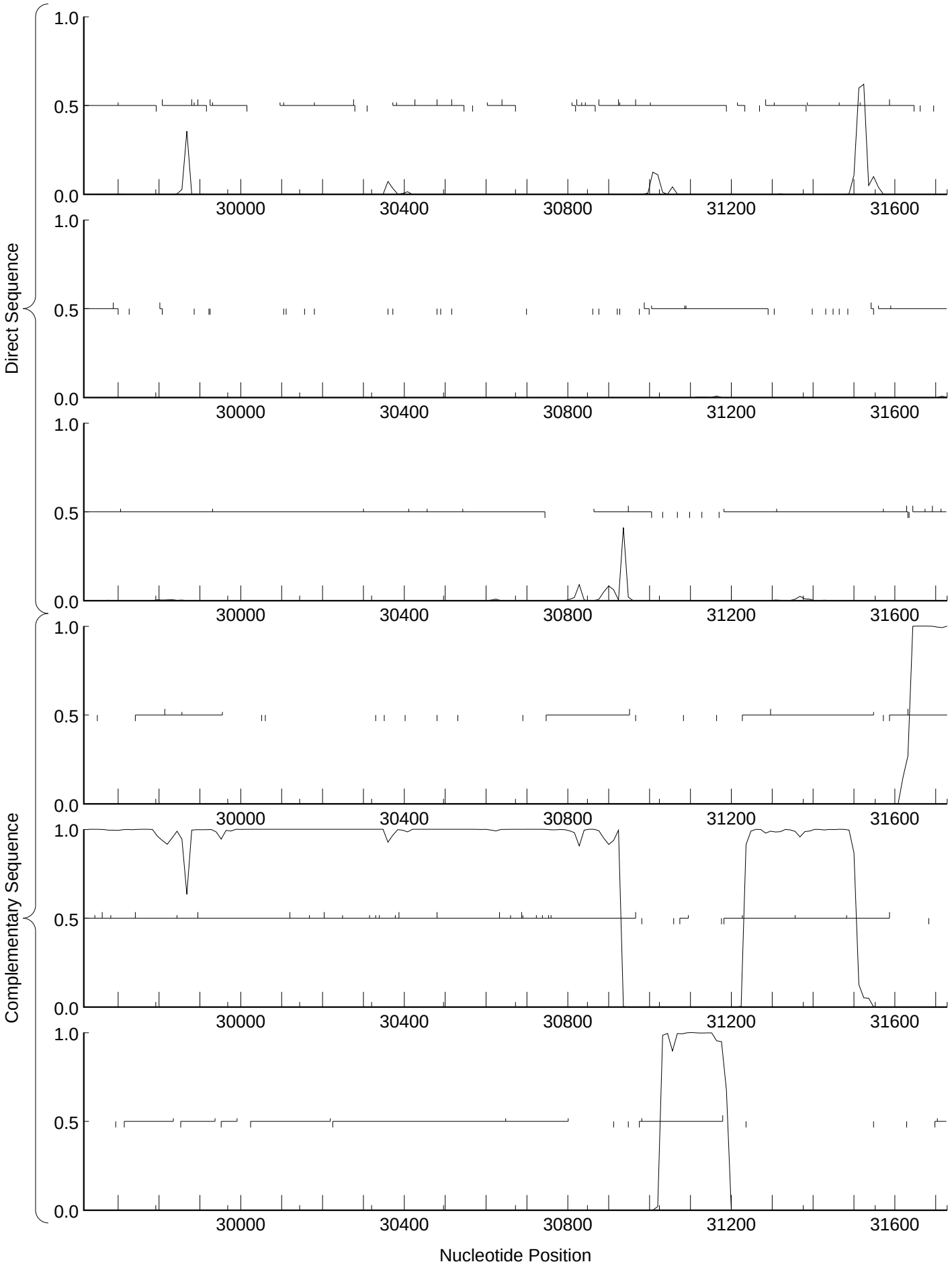
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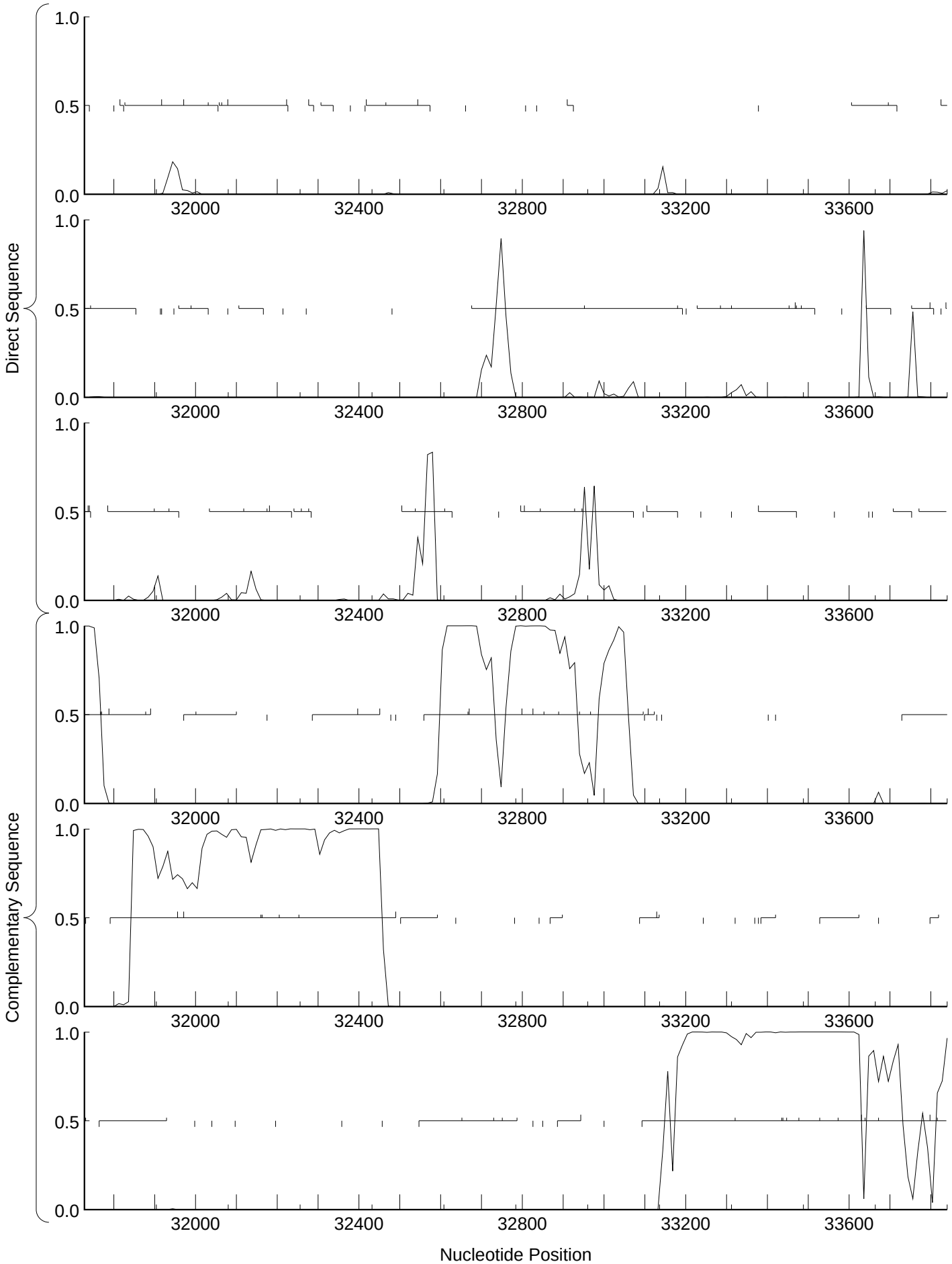
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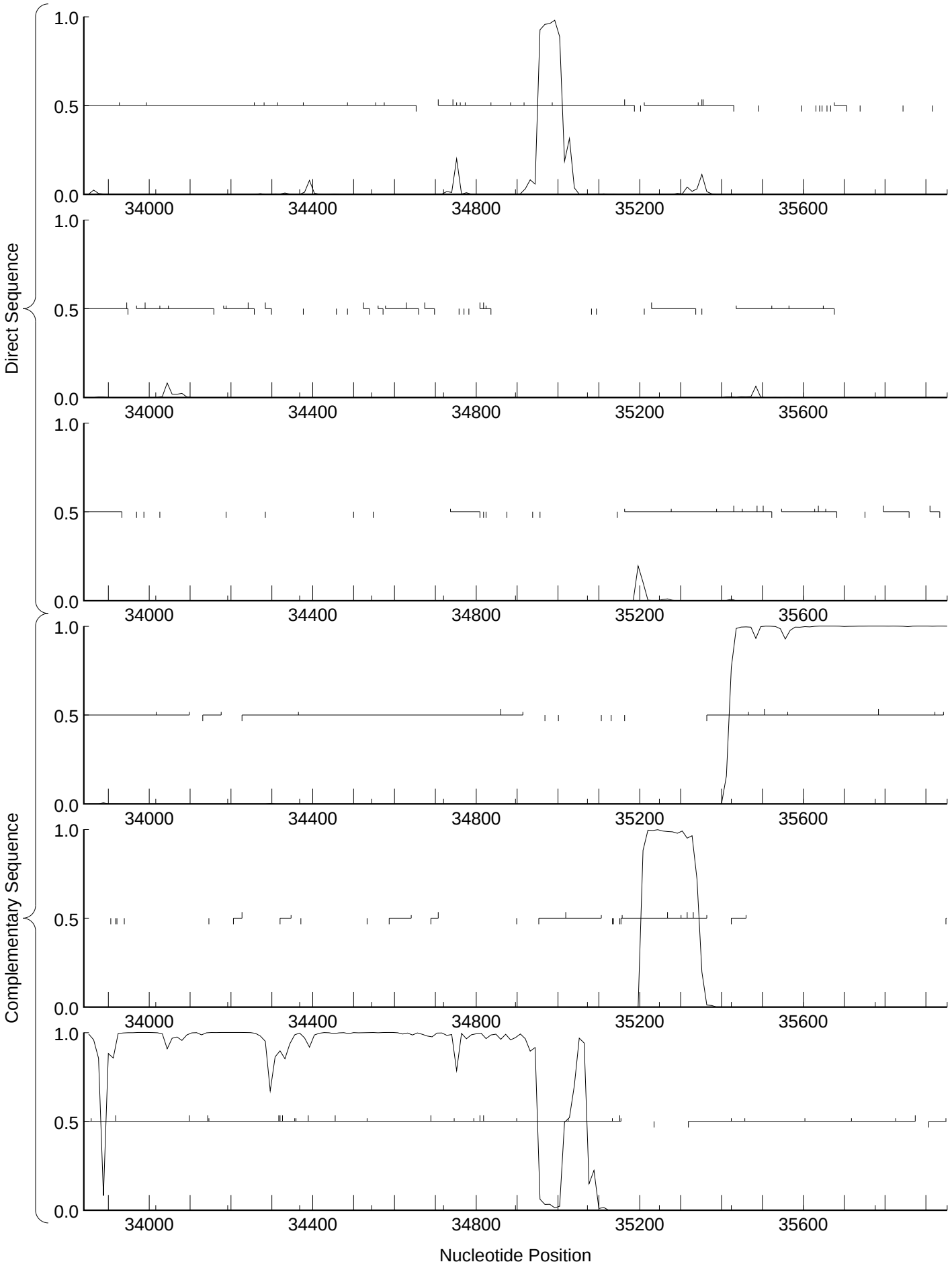


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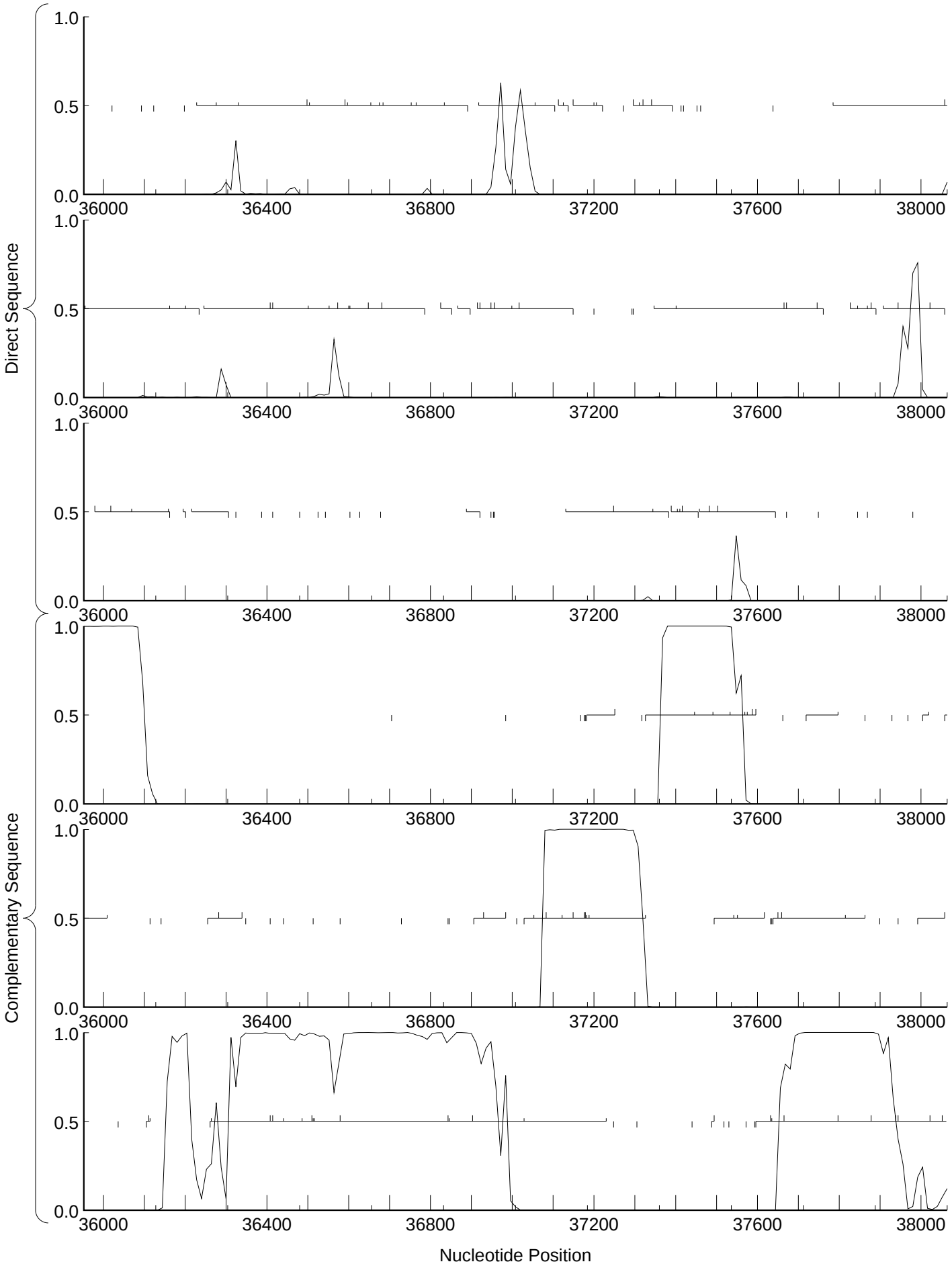


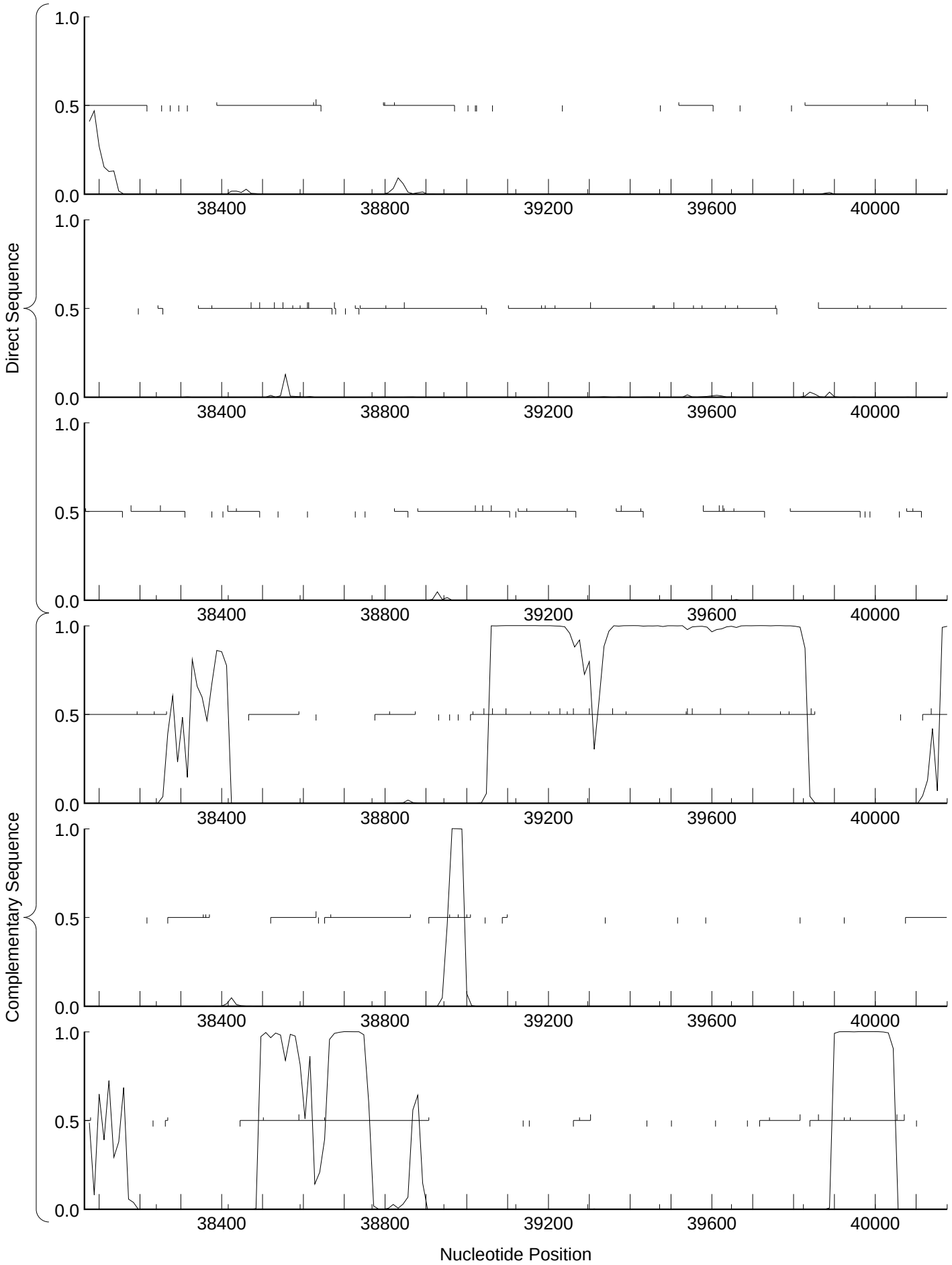
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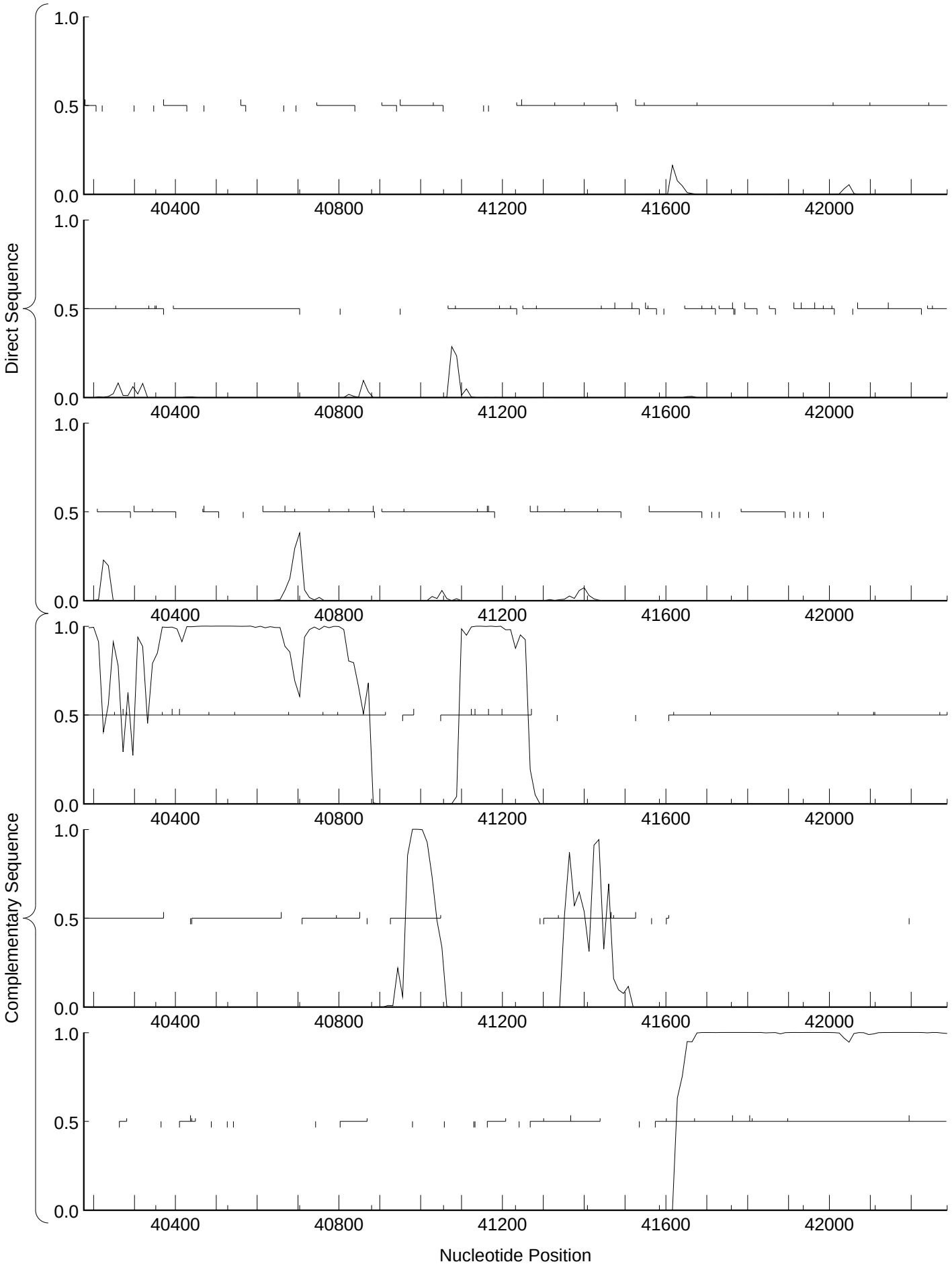

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
34000
34400
34800
35200
35600
Nucleotide Position

e complete sequence, 52668 bp including 10-base 3’ overhang (CGGTCGGTTA), Cluster A2, Order 4, Window 96, Step 12, 19/26

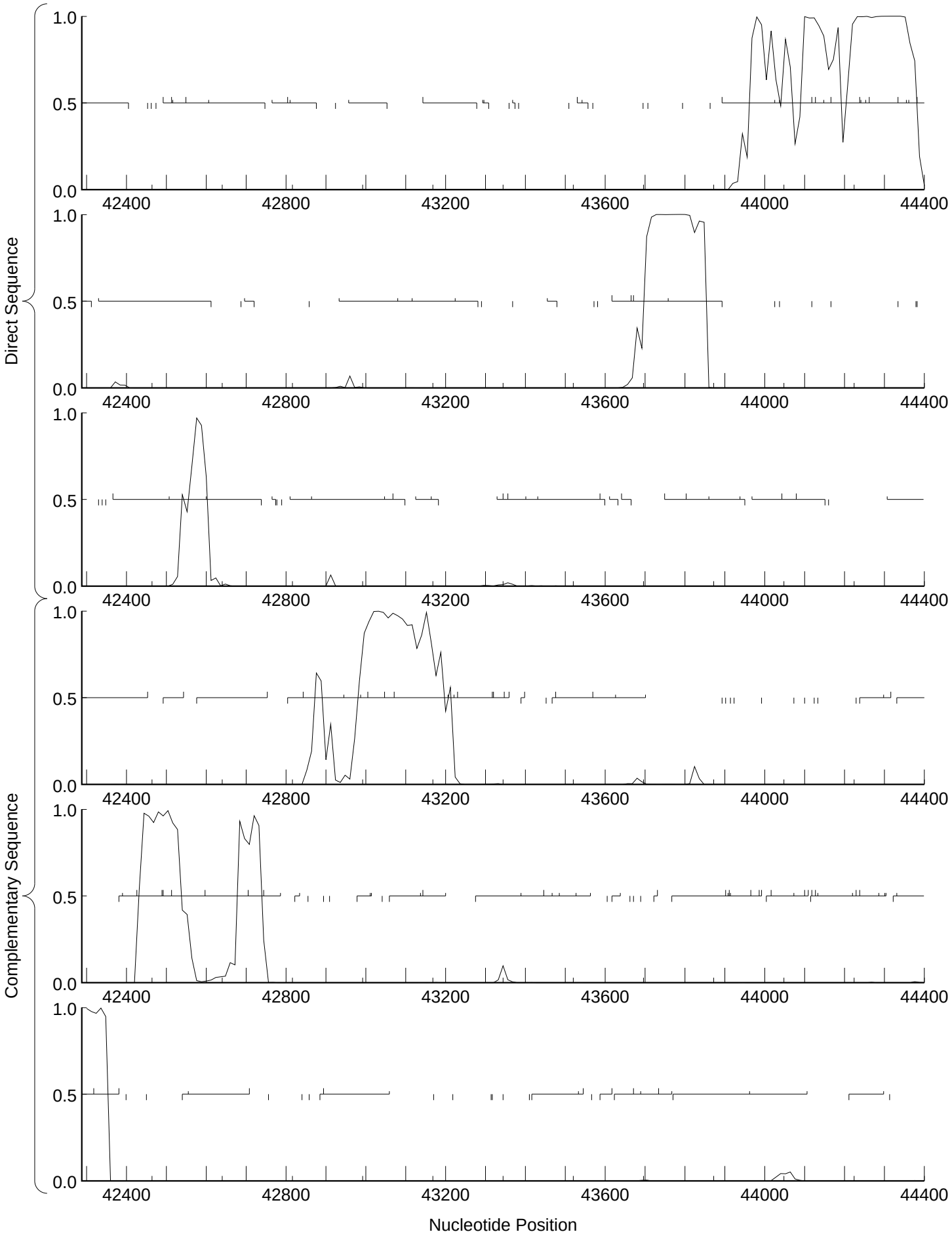


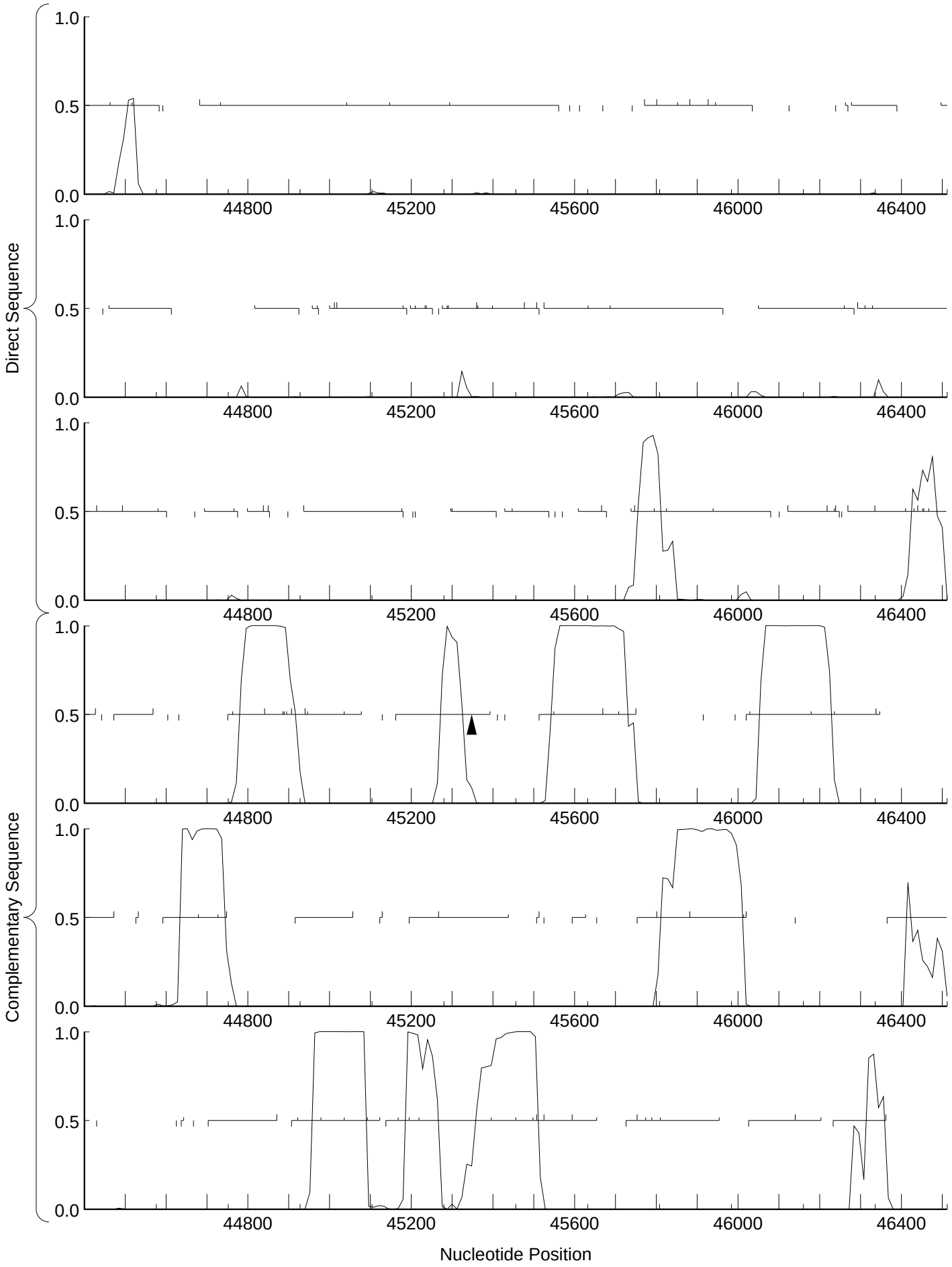

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
38400
38800
39200
39600
40000
Nucleotide Position

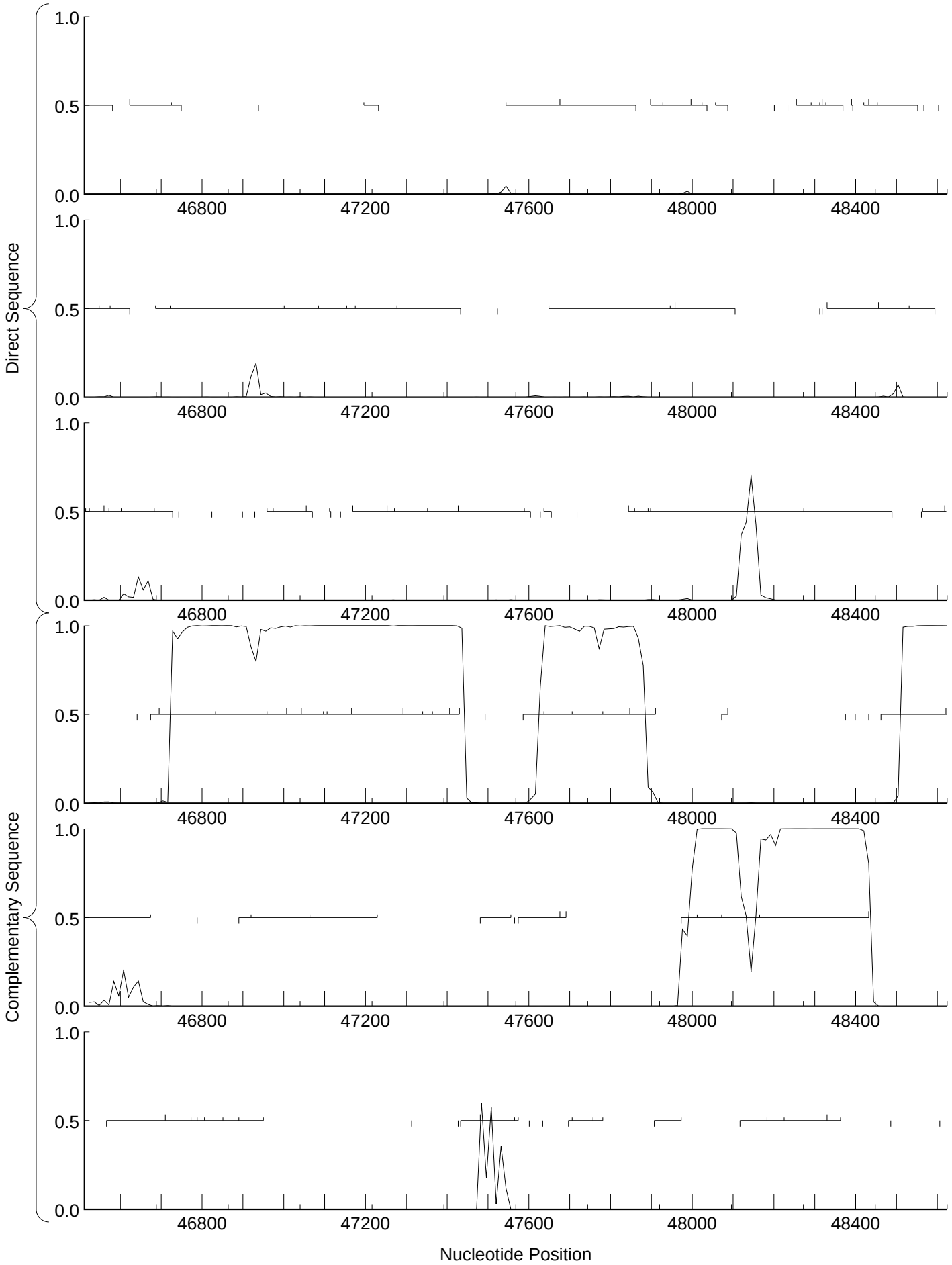
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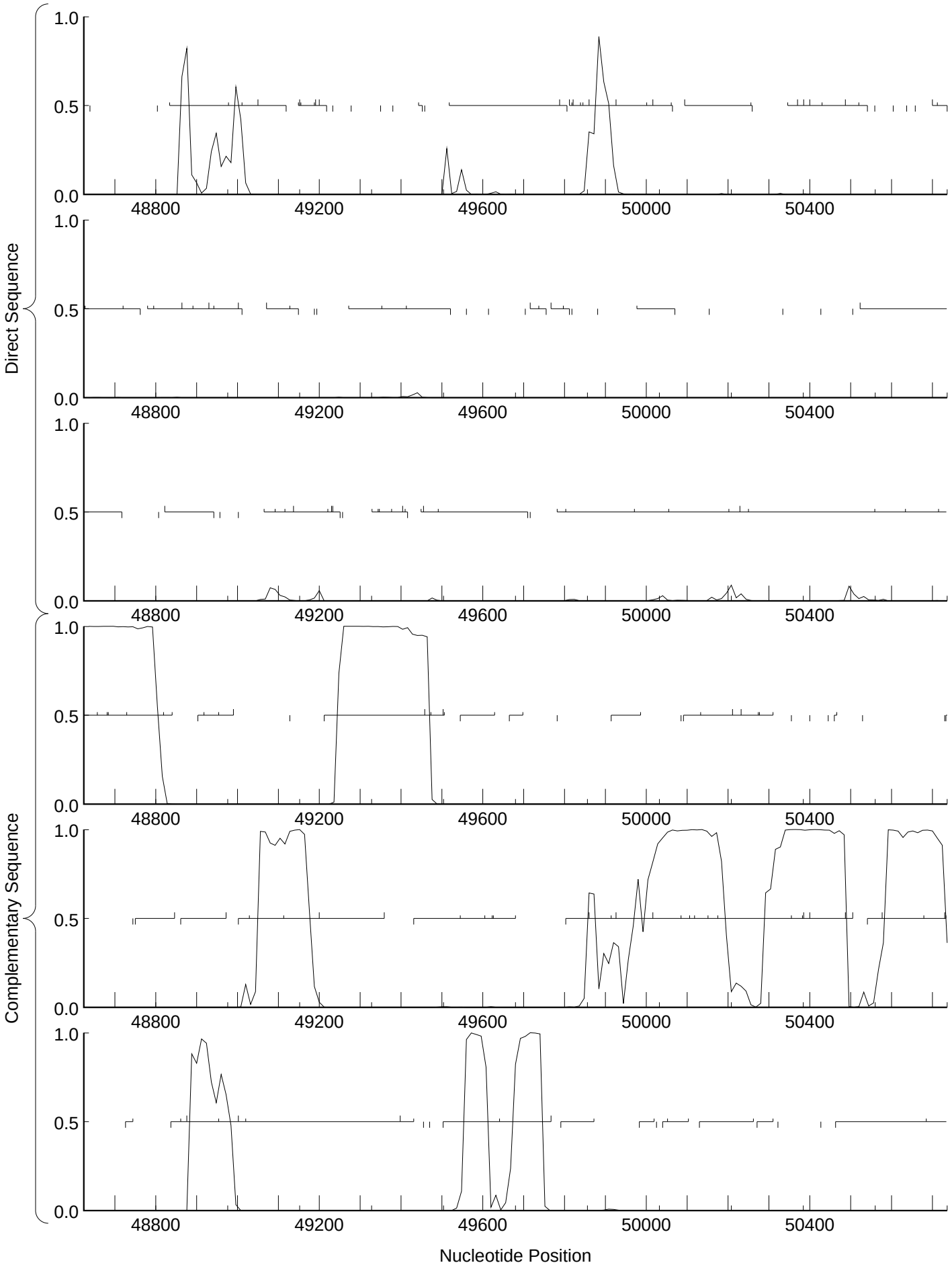
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Direct Sequence
Complementary Sequence
1.0
0.5
0.0
44800
45200
45600
46000
46400
Nucleotide Position


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
46800
47200
47600
48000
48400
Nucleotide Position

e complete sequence, 52668 bp including 10-base 3’ overhang (CGGTCGGTTA), Cluster A2, Order 4, Window 96, Step 12, 25/26



e complete sequence, 52668 bp including 10-base 3’ overhang (CGGTCGGTTA), Cluster A2, Order 4, Window 96, Step 12, 26/26

