GeneMark

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

PROGRAM INFORMATION

```
Sequence         :  Mycobacterium phage Beatrix complete sequence, 52295 bp including 10-base 3’ overhang (CGGA
Analysis Date    :  3/29/24 at 5:31:07
Pages            :  26
Sequence Length  :  52295 bp
GC Content       :   63.94%

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

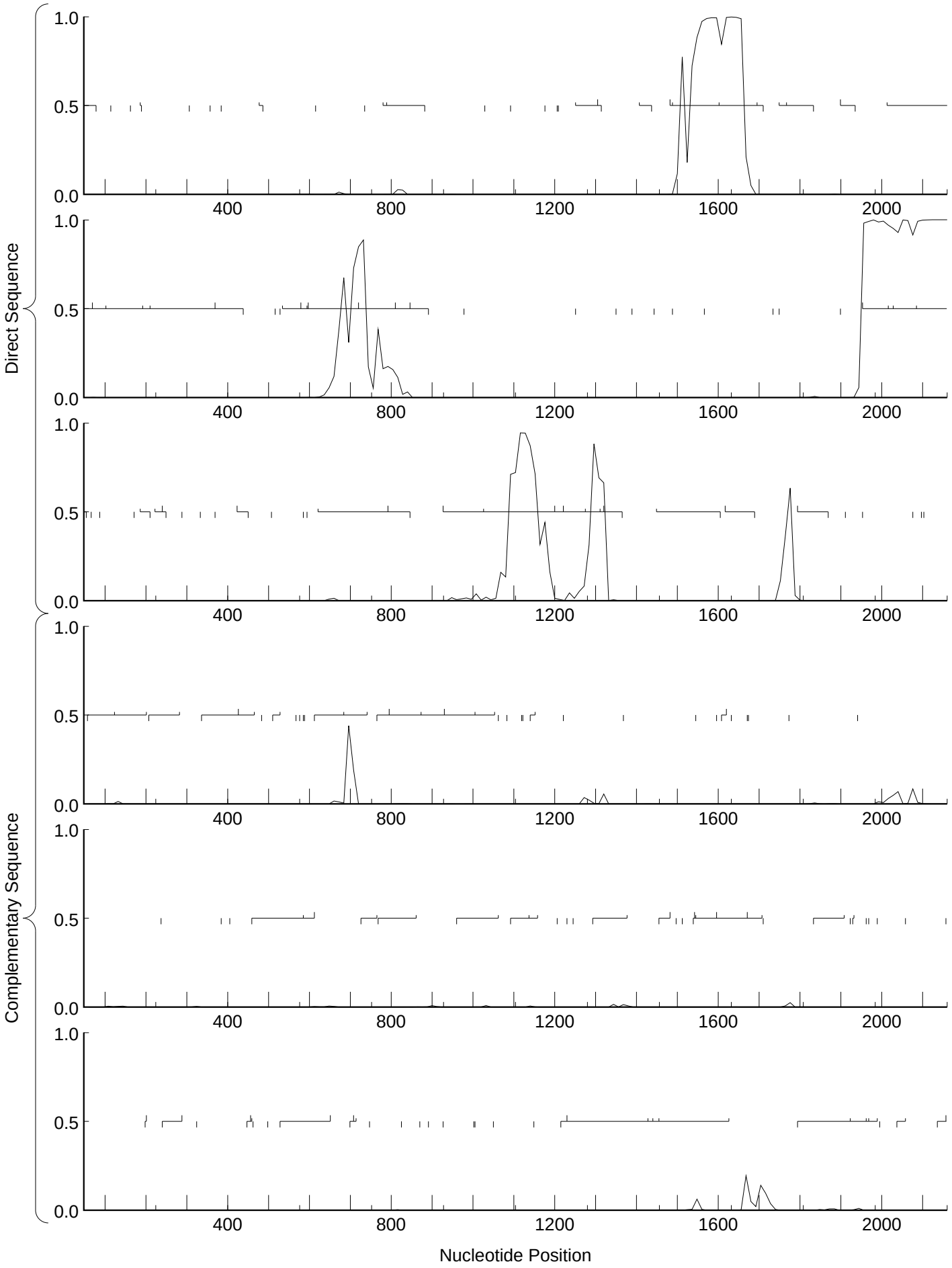

  Send questions / comments to:
      Dr. M. Borodovsky
      Georgia Institute of Technology
      School of Biology
      Atlanta, GA  30332-0230
```

Matrix notes & comments

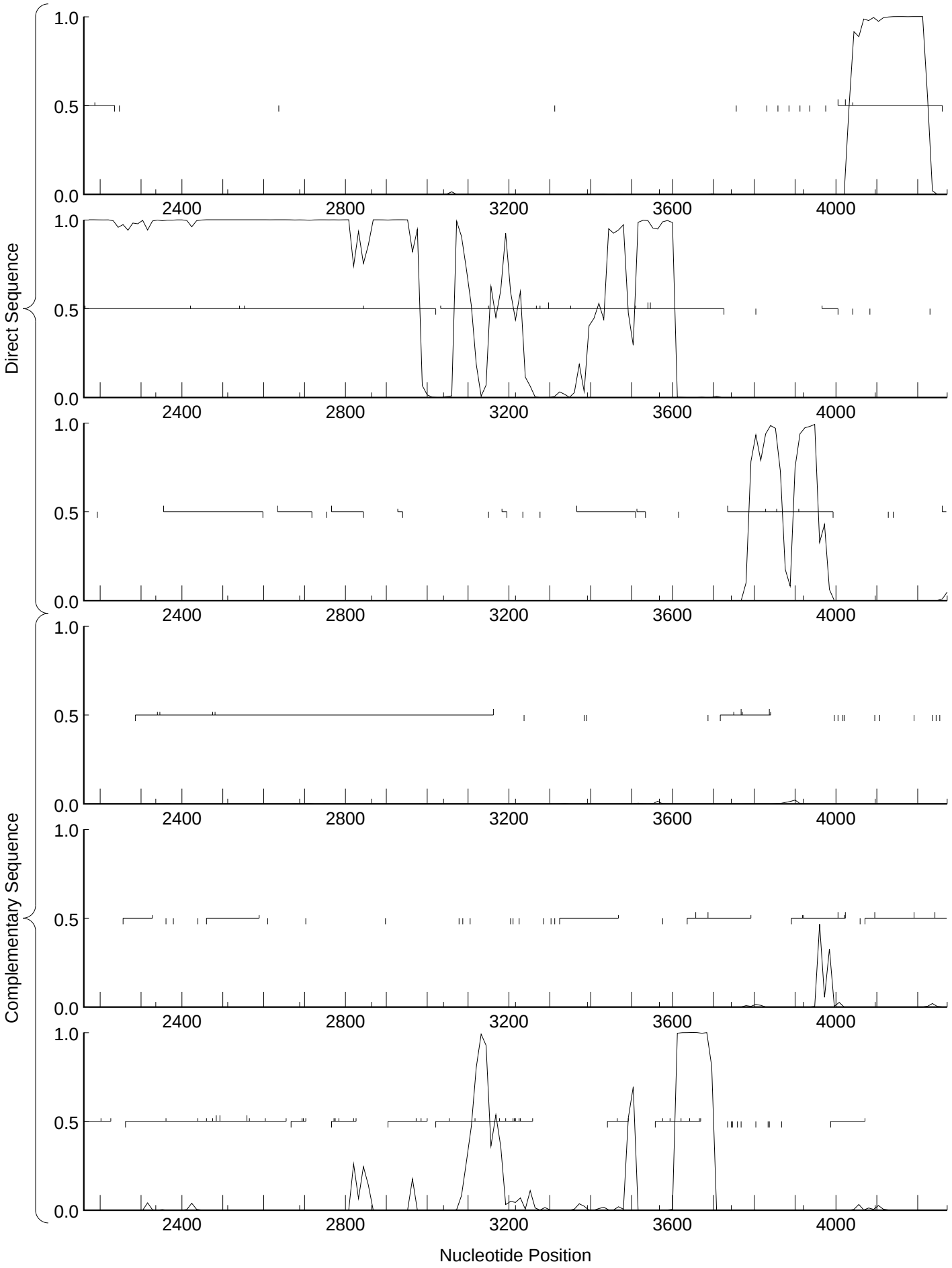
Training set derived by GeneMarkS, 4.27 September 2014
Tue Sep 23 15:14:37 2014

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

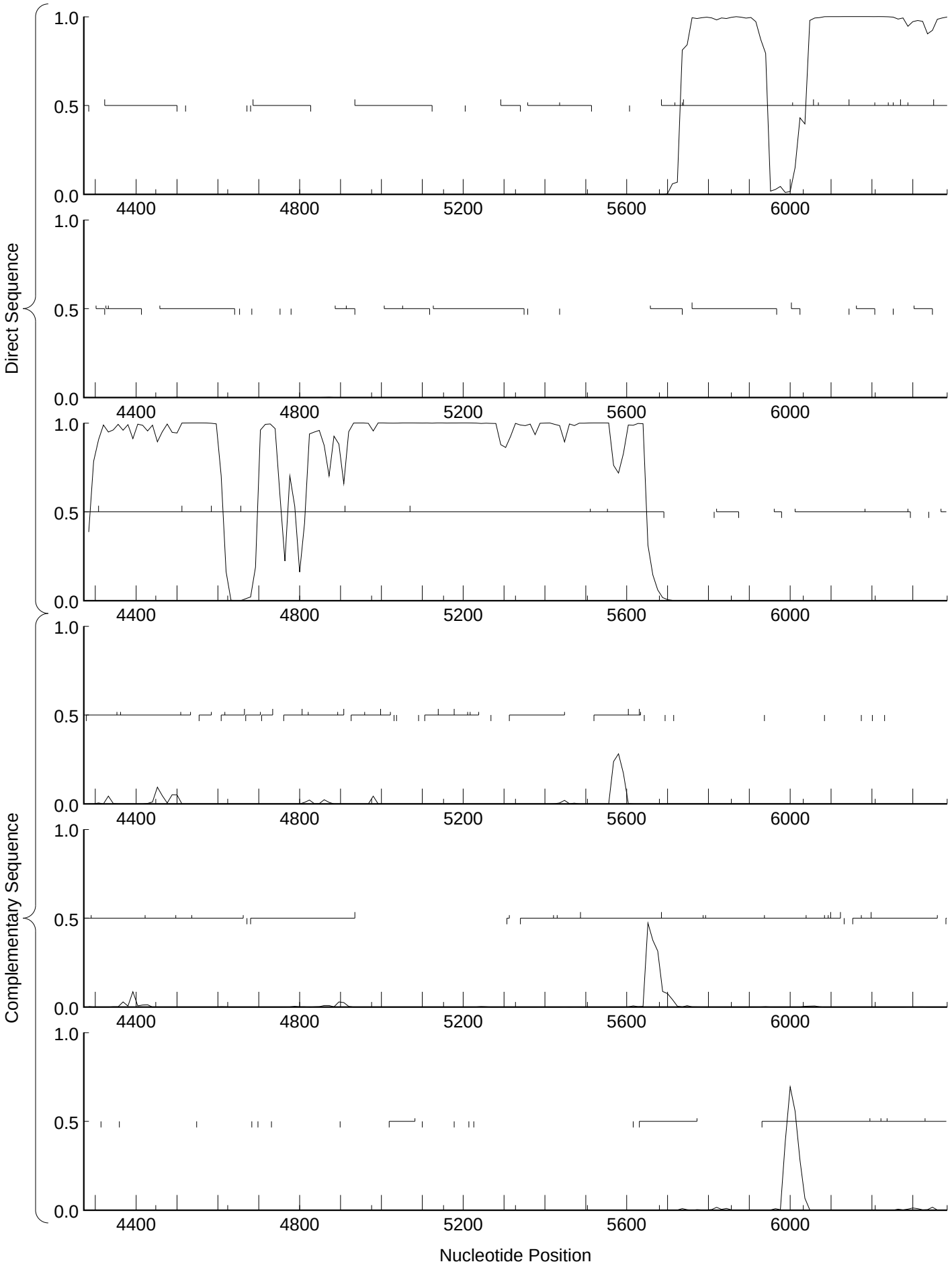
ix complete sequence, 52295 bp including 10-base 3’ overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 2/26



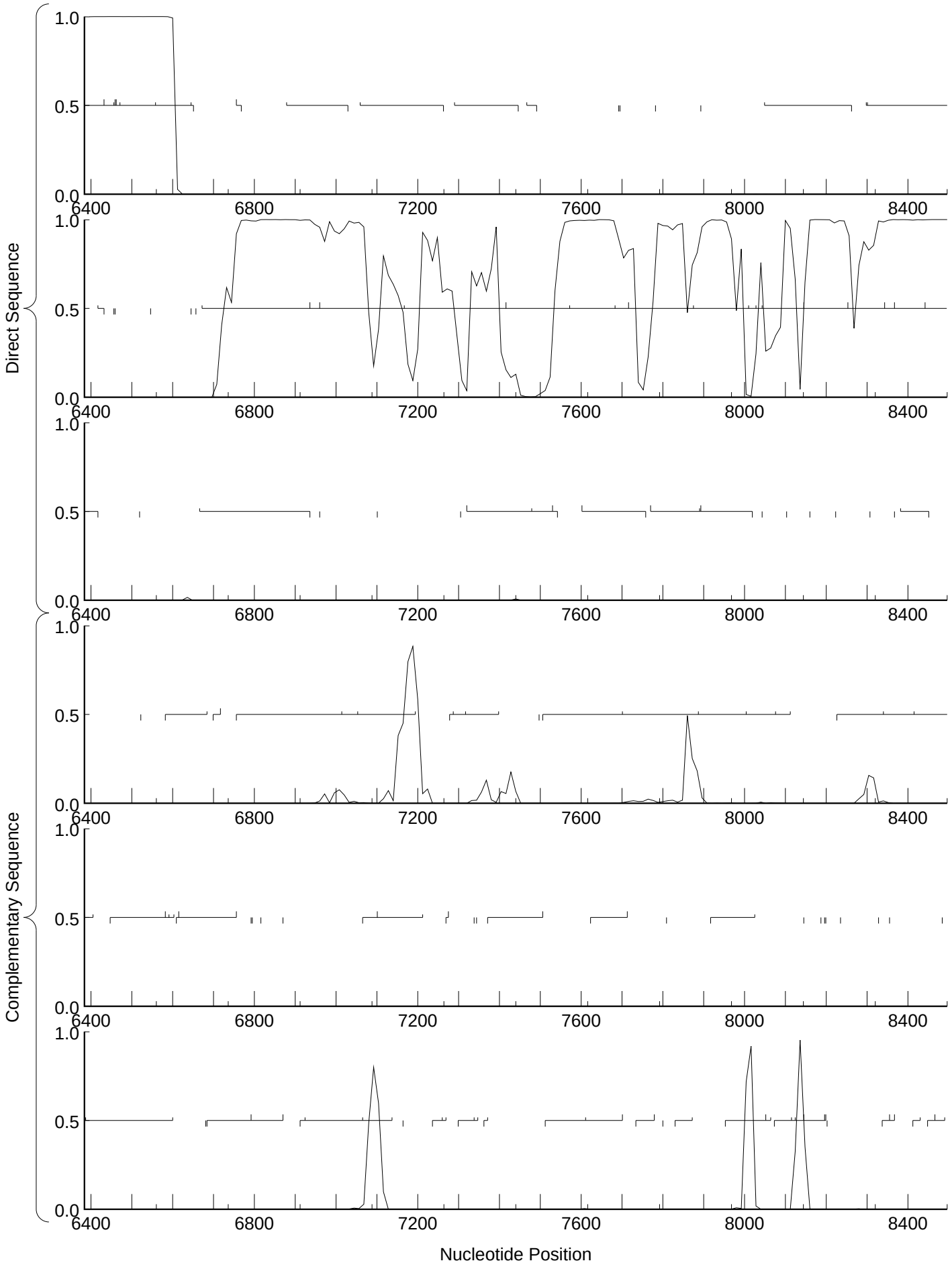
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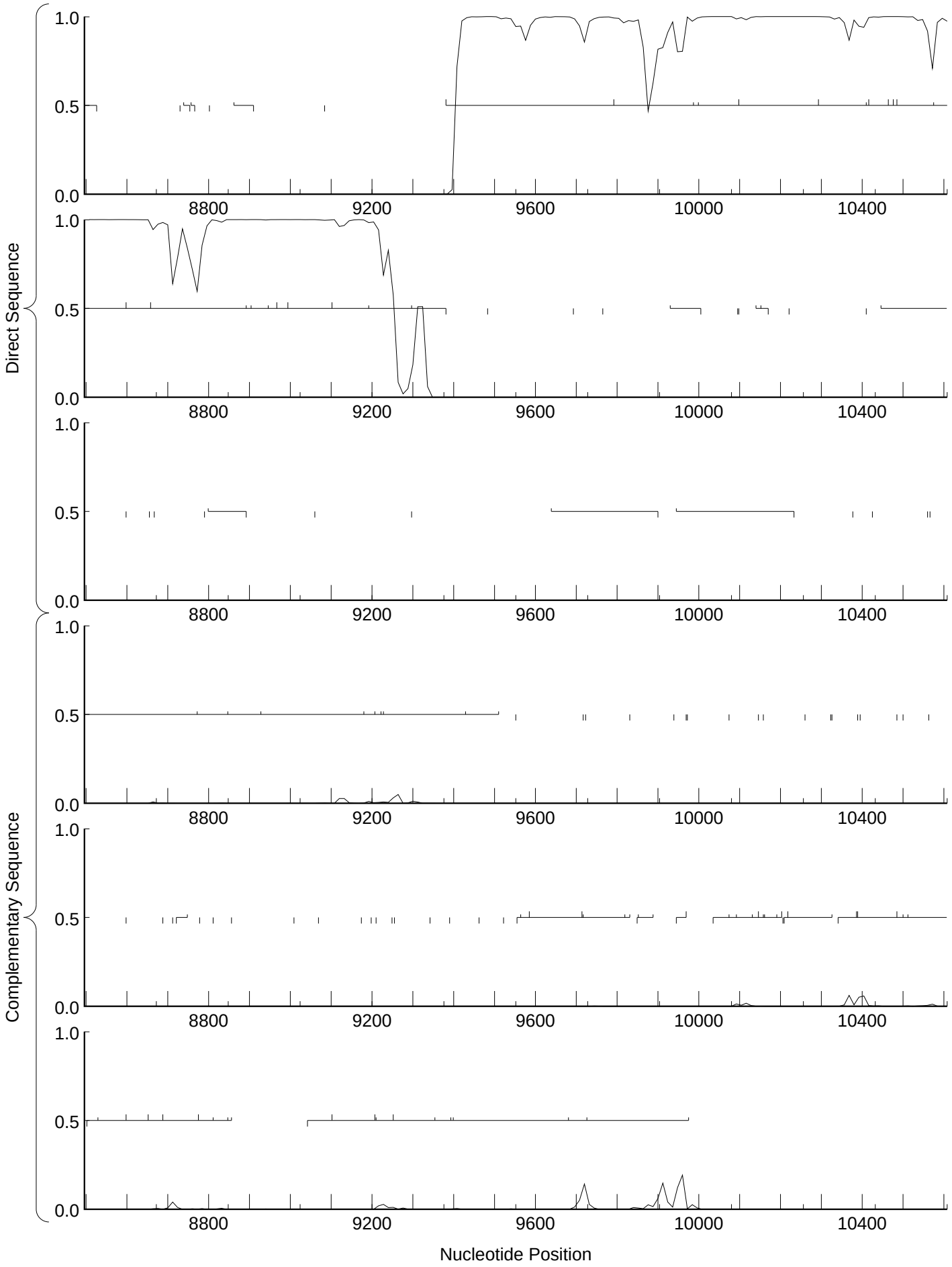
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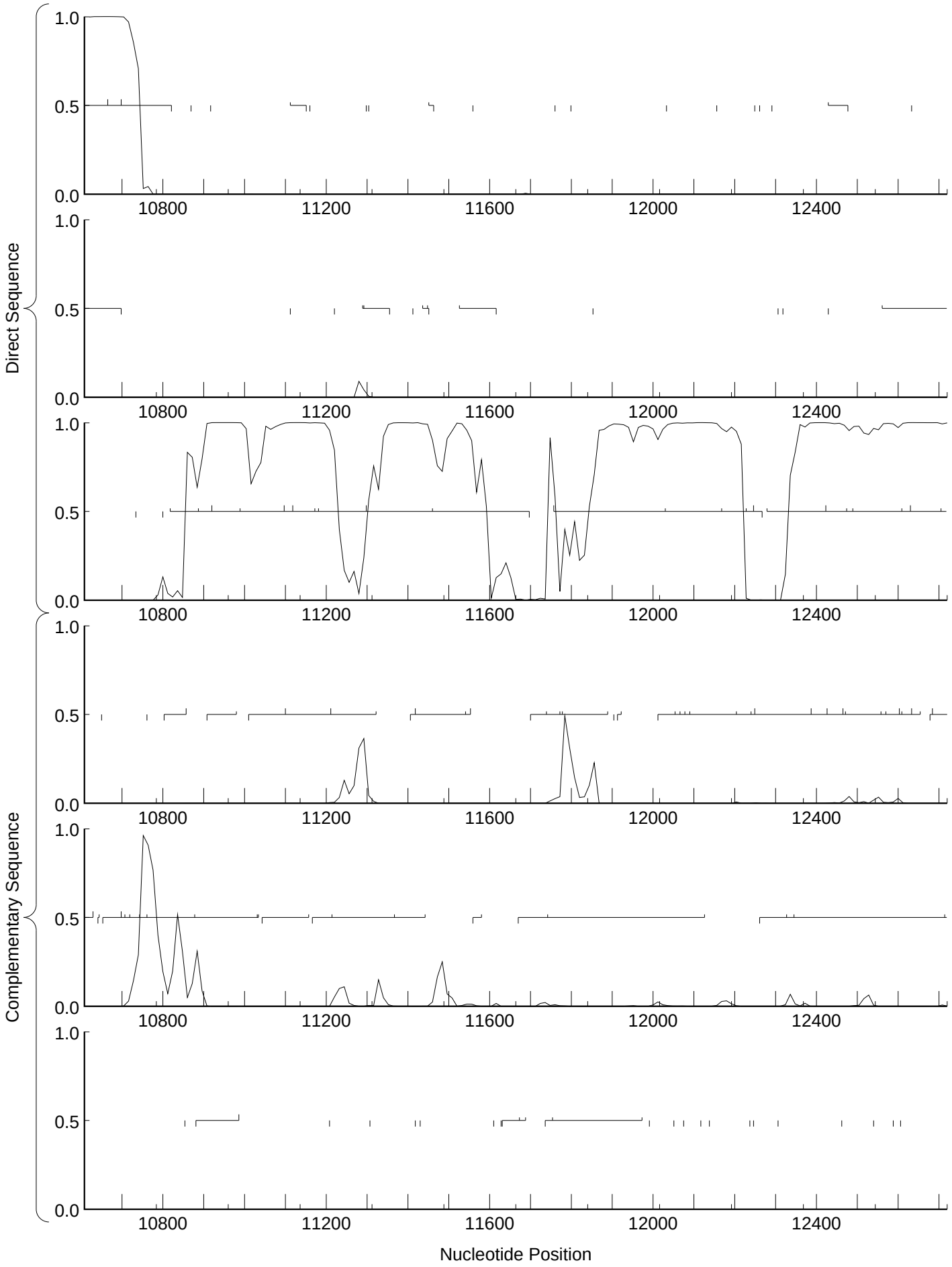
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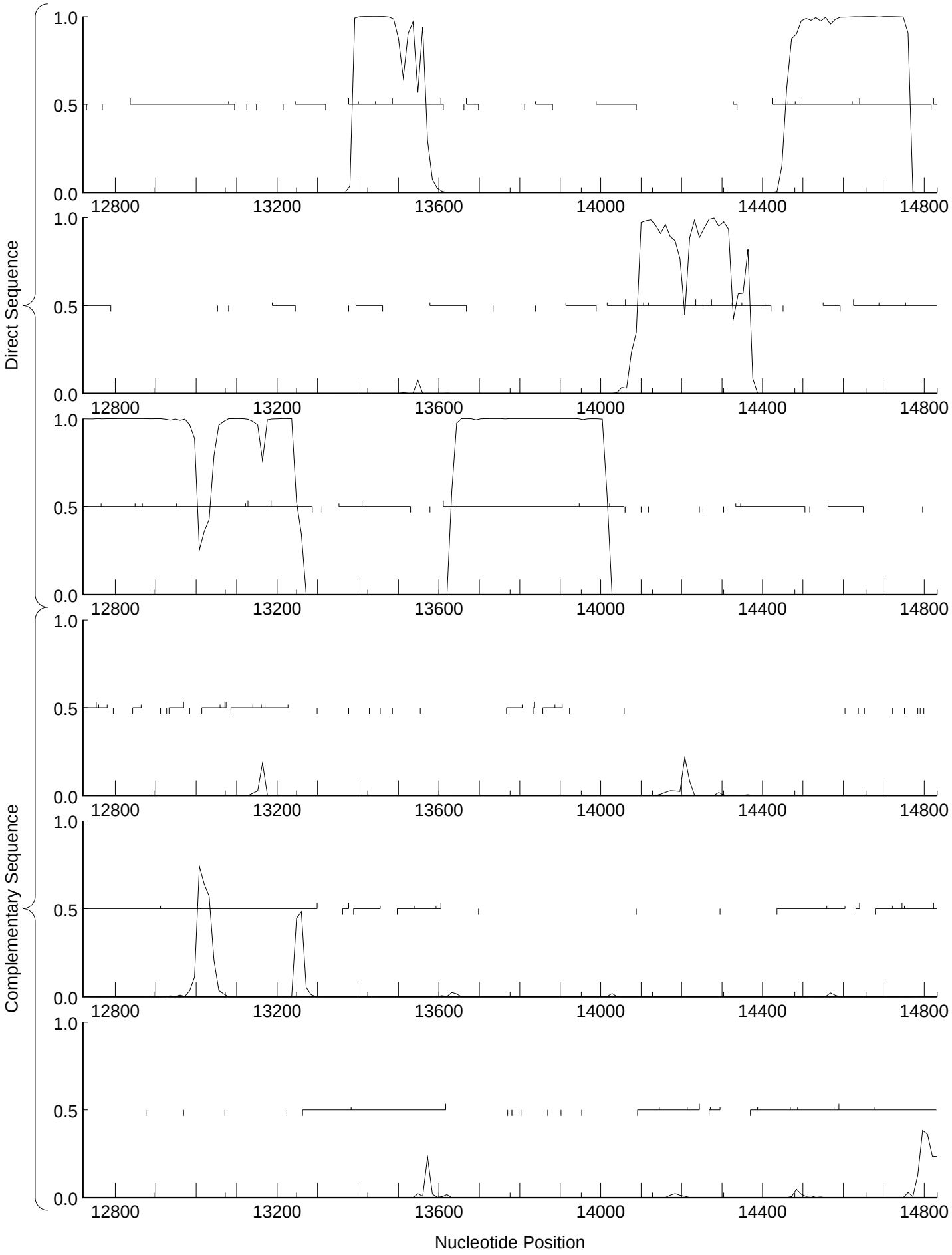
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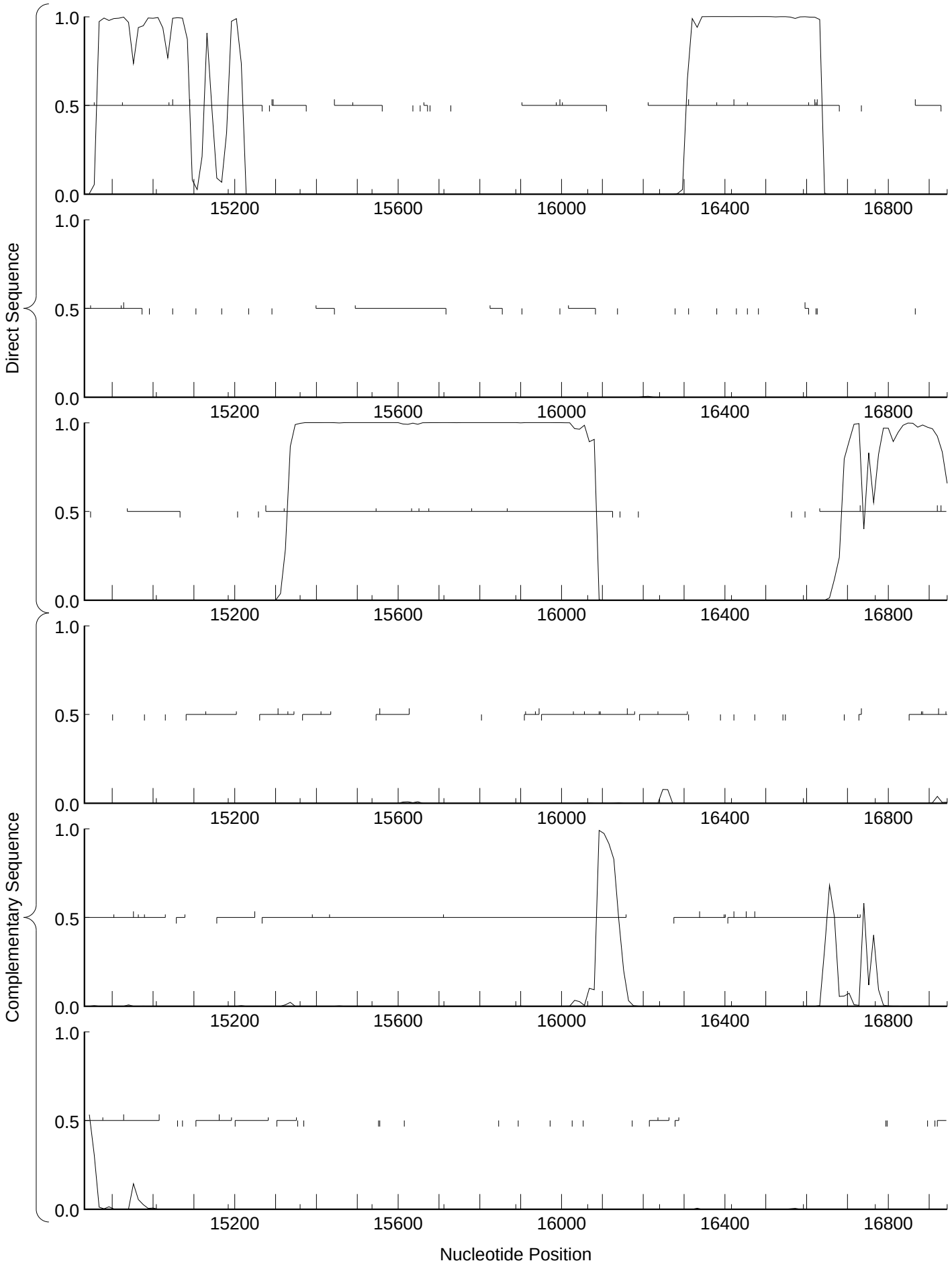
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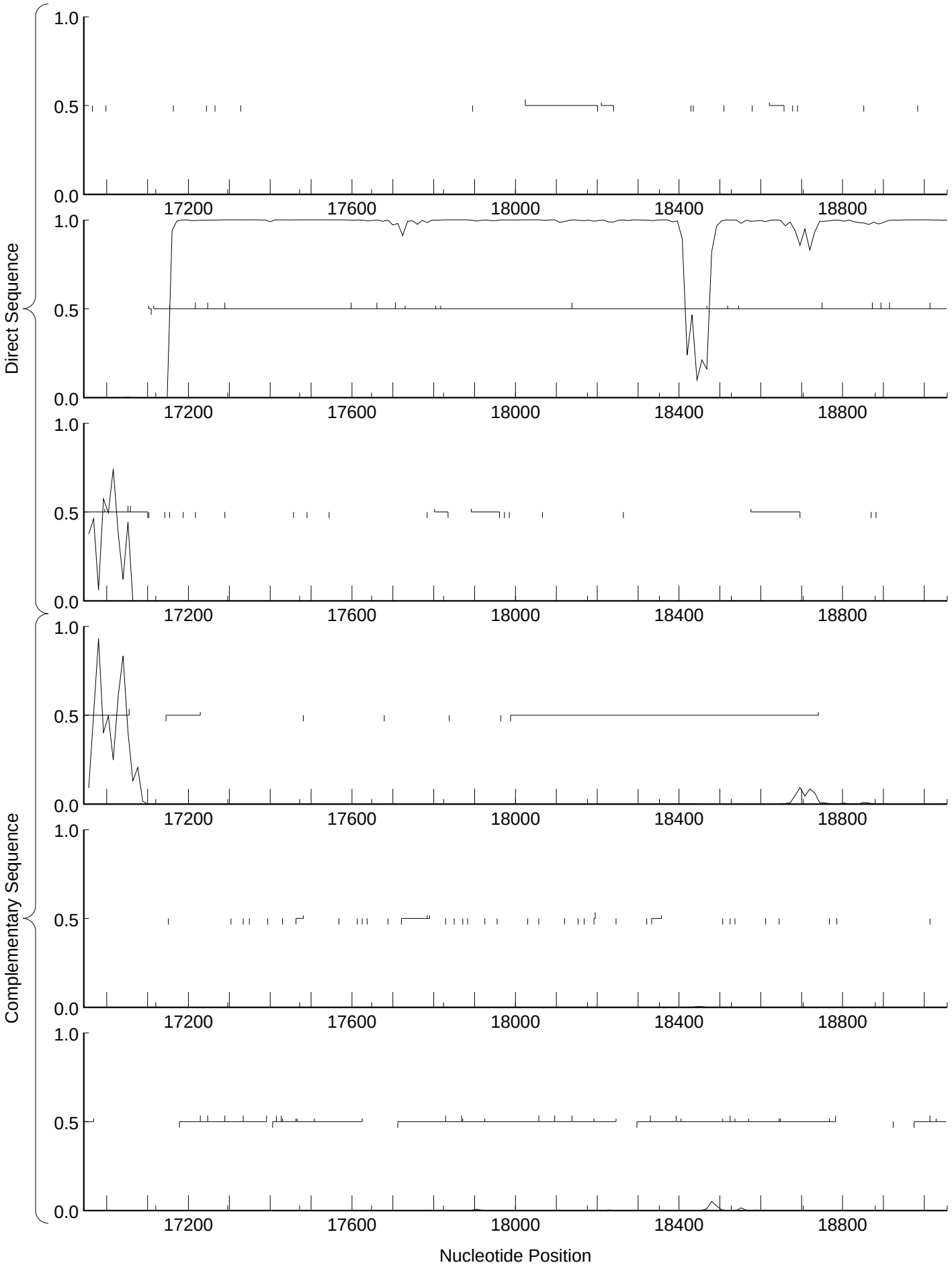
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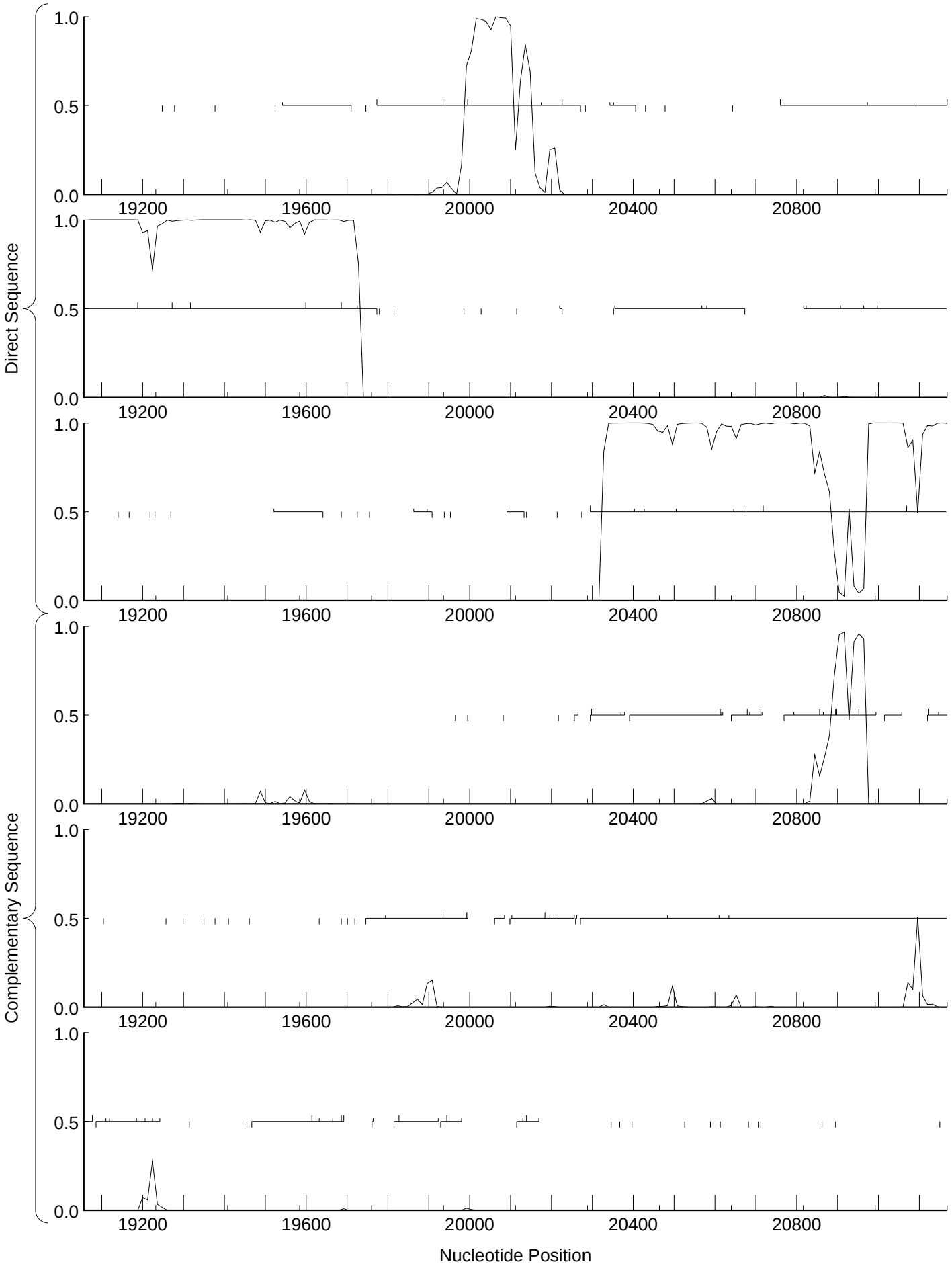
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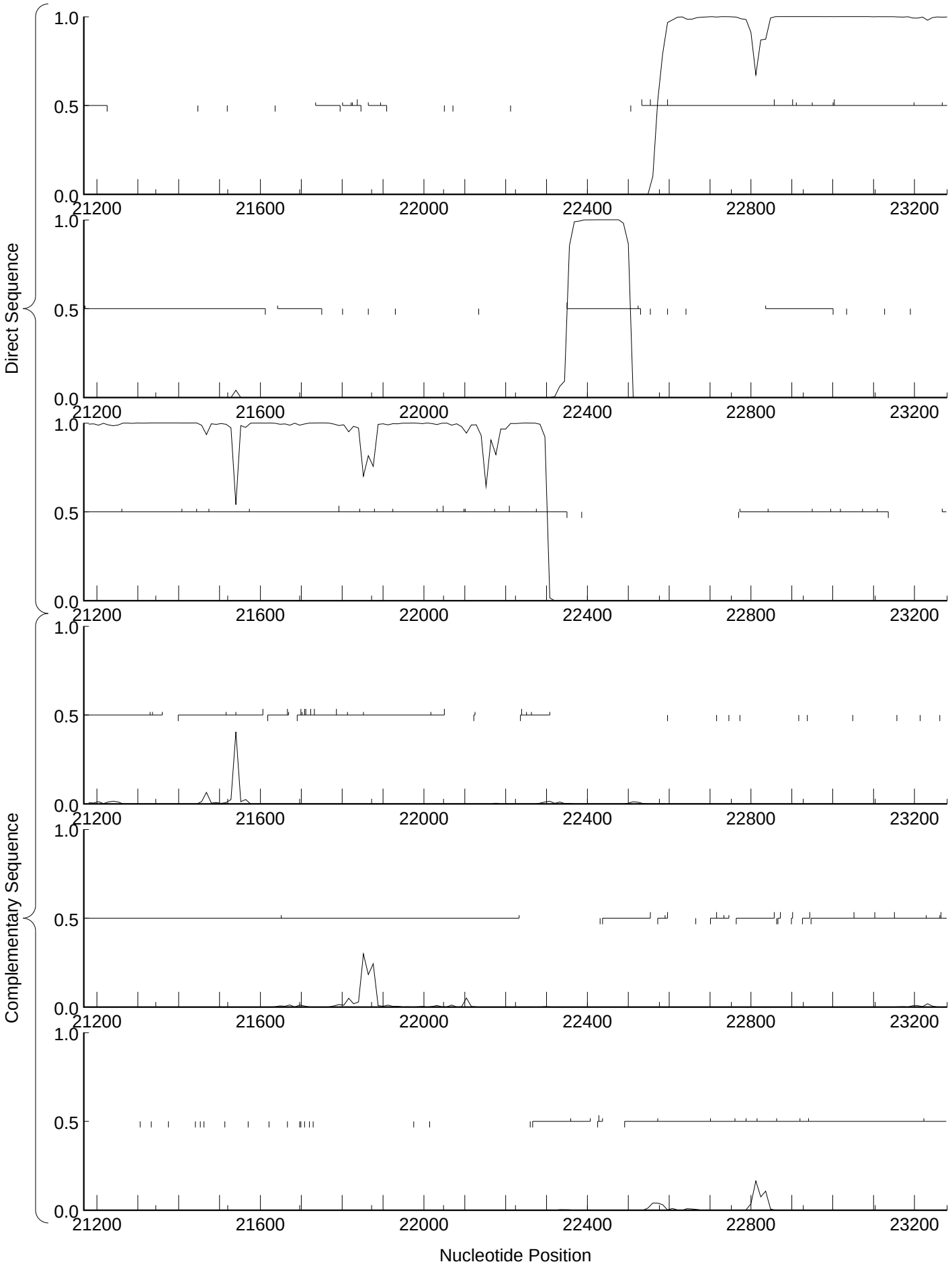
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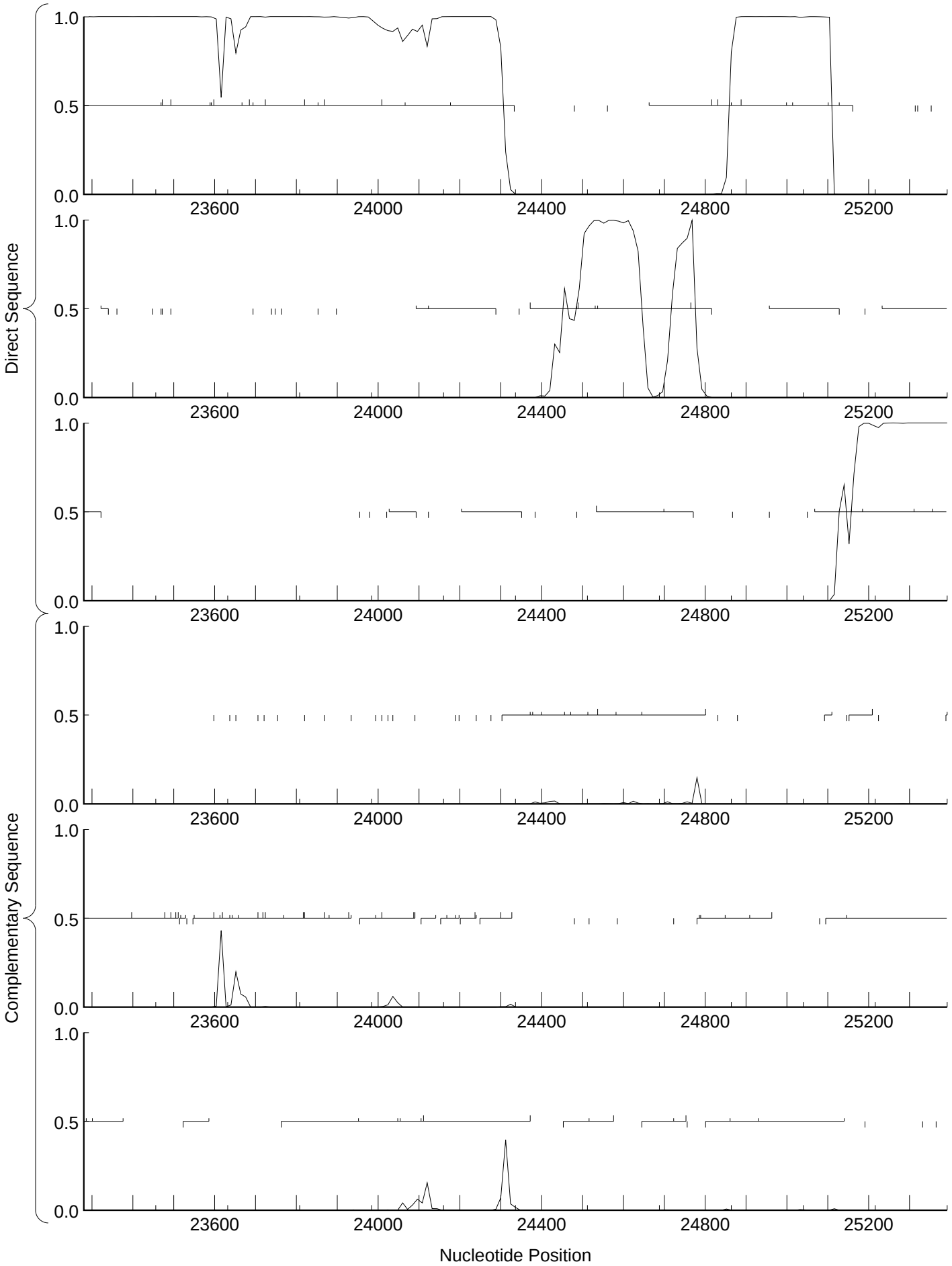
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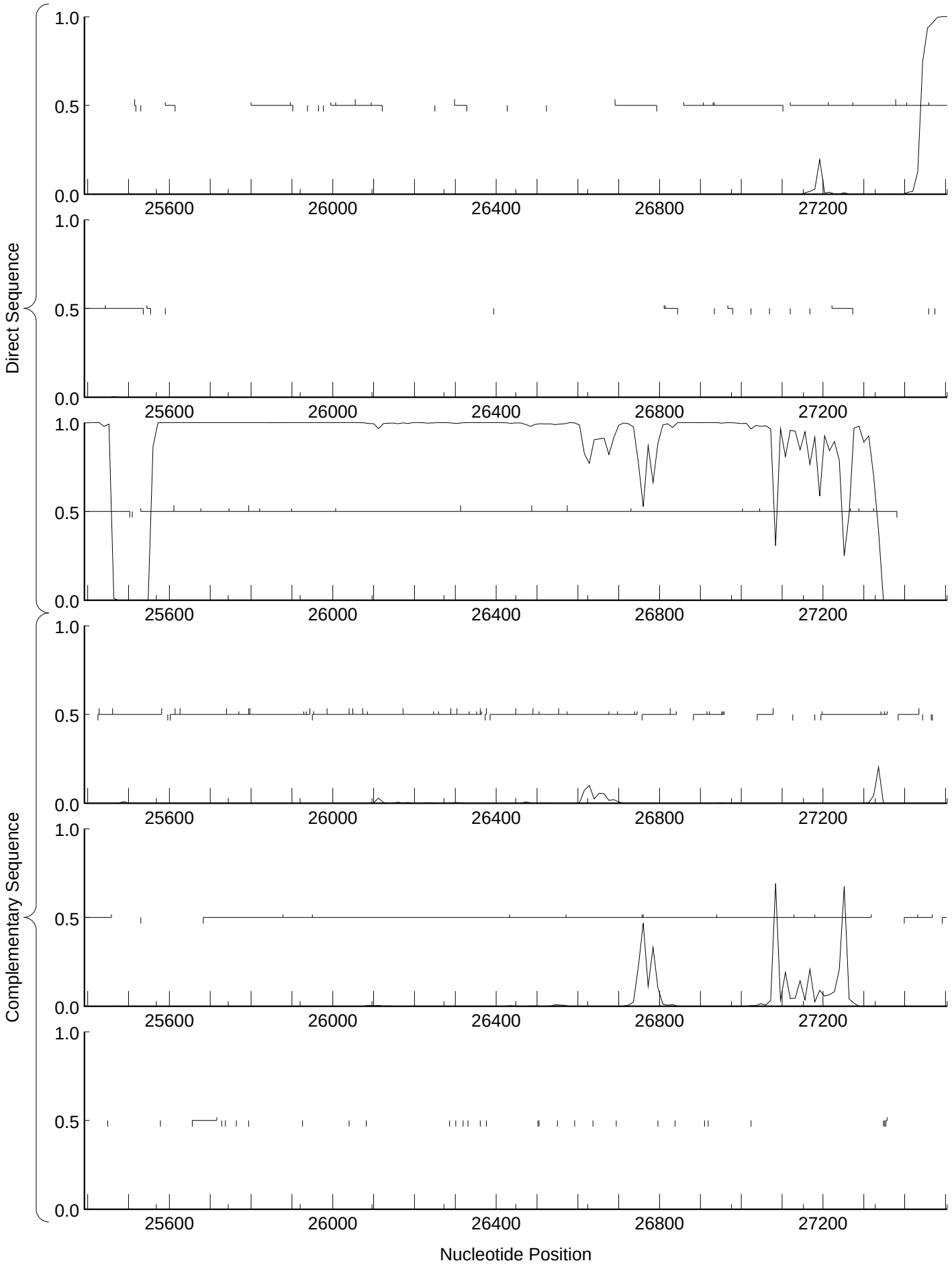


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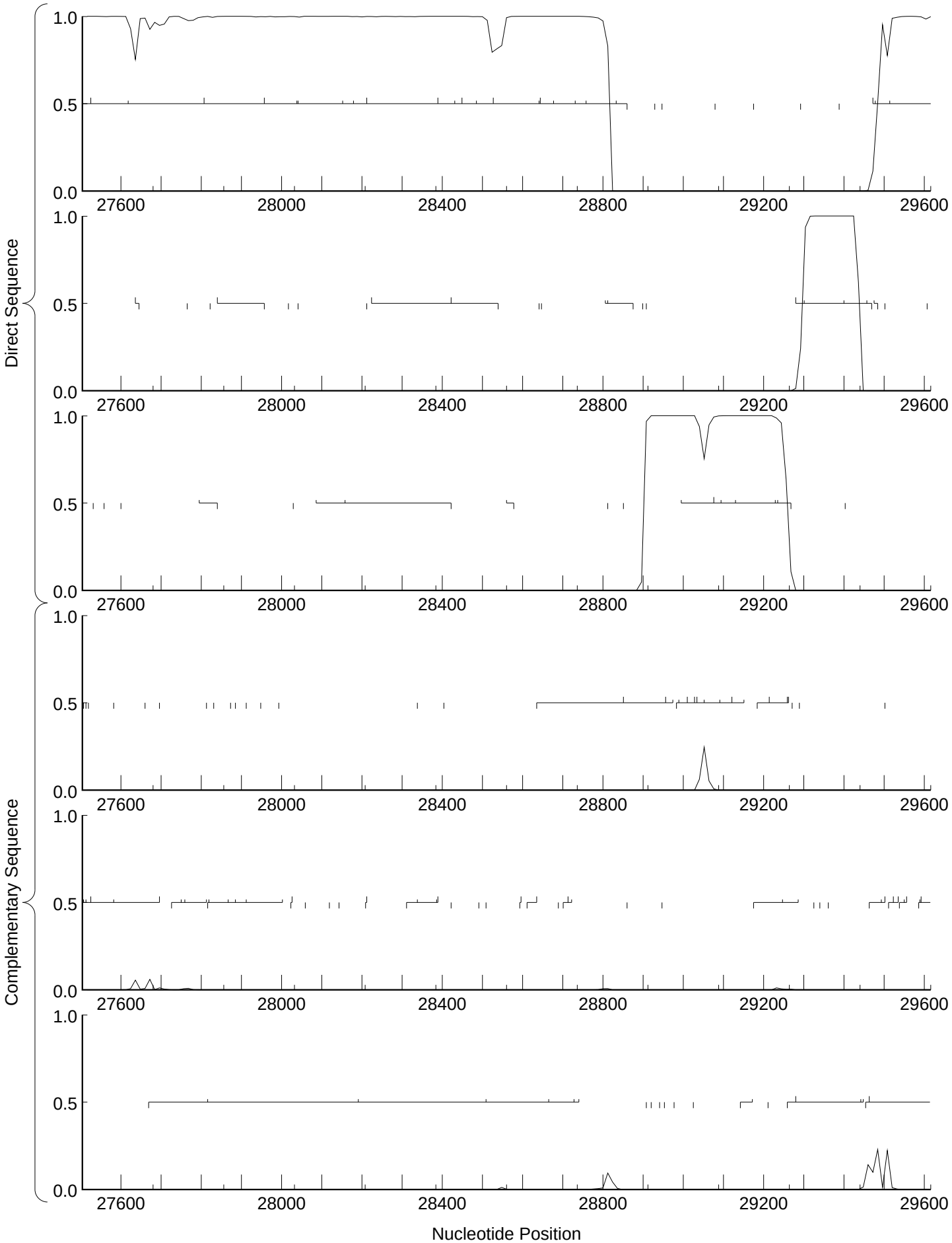


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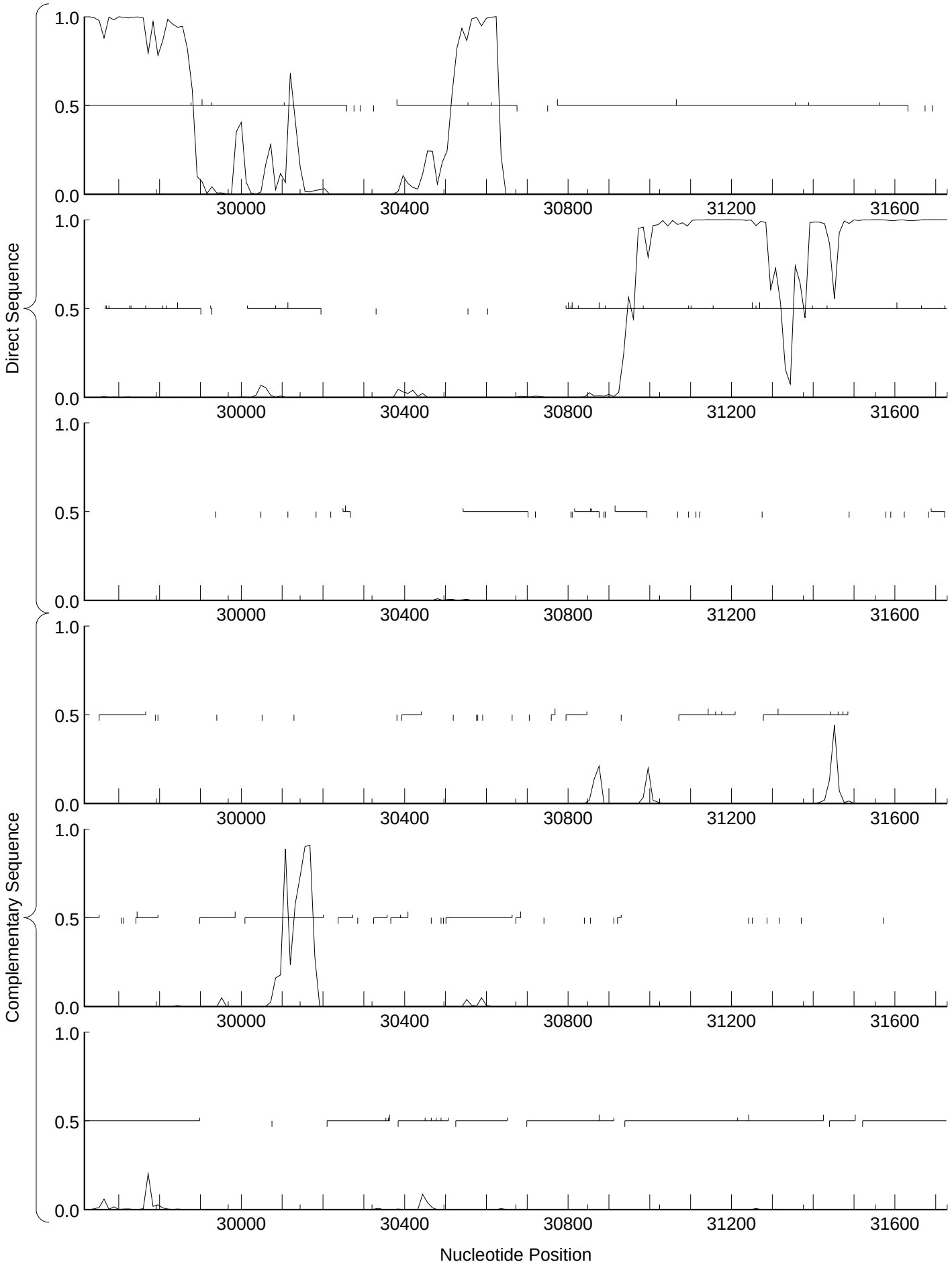



Direct Sequence
Complementary Sequence
1.0
0.5
0.0
25600
26000
26400
26800
27200
Nucleotide Position

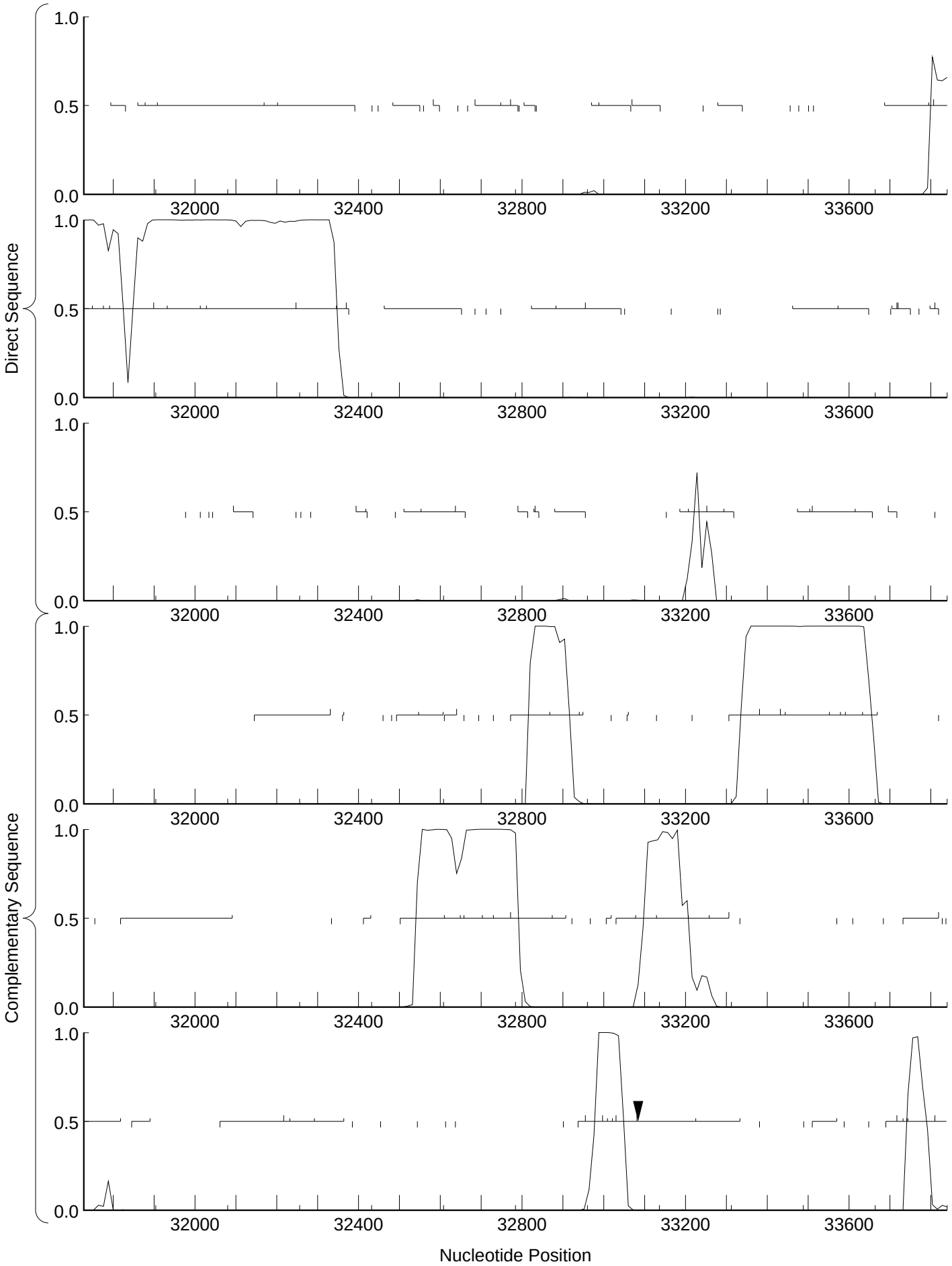
x complete sequence, 52295 bp including 10-base 3' overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 15/26

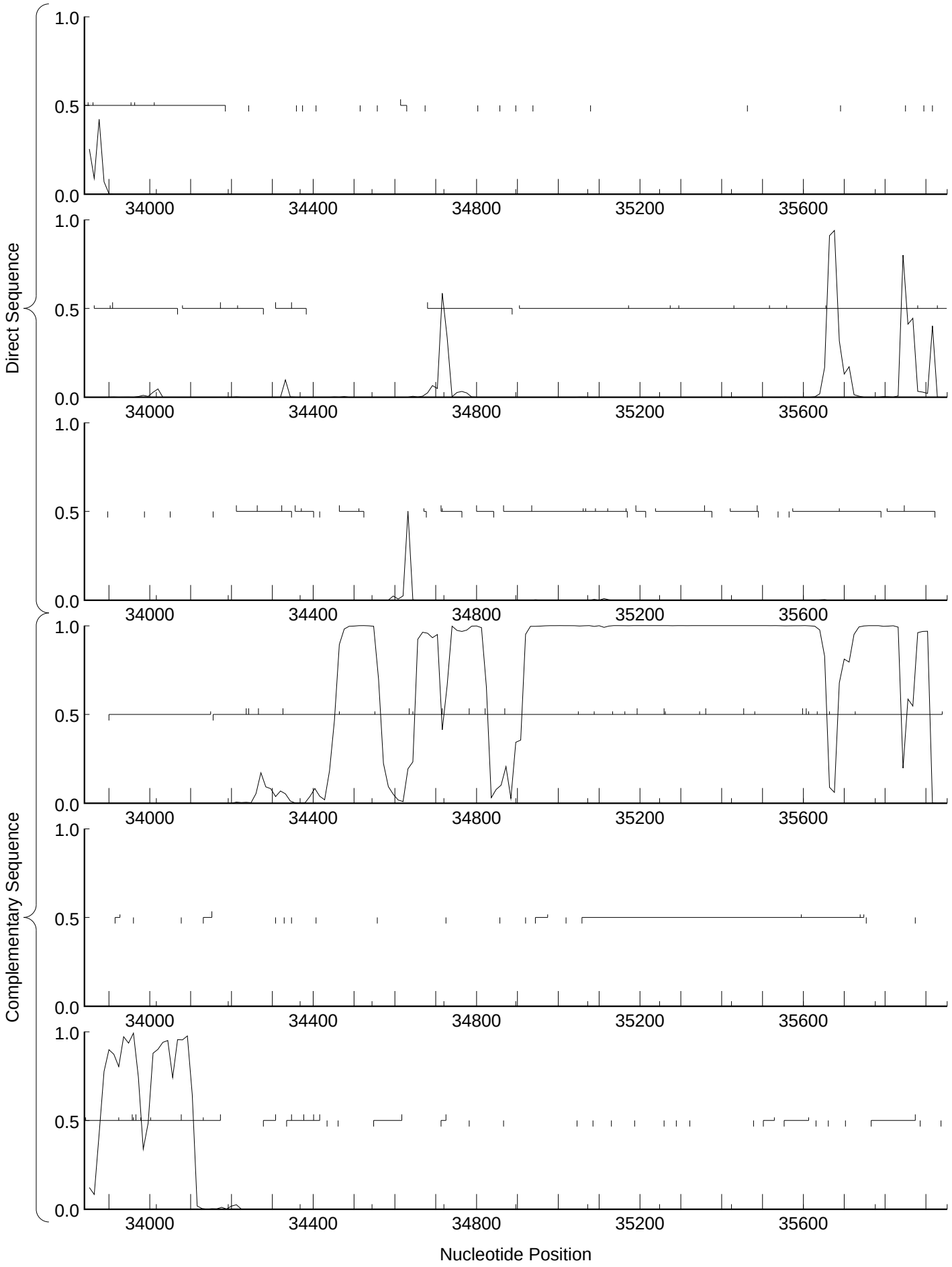


x complete sequence, 52295 bp including 10-base 3' overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 16/26

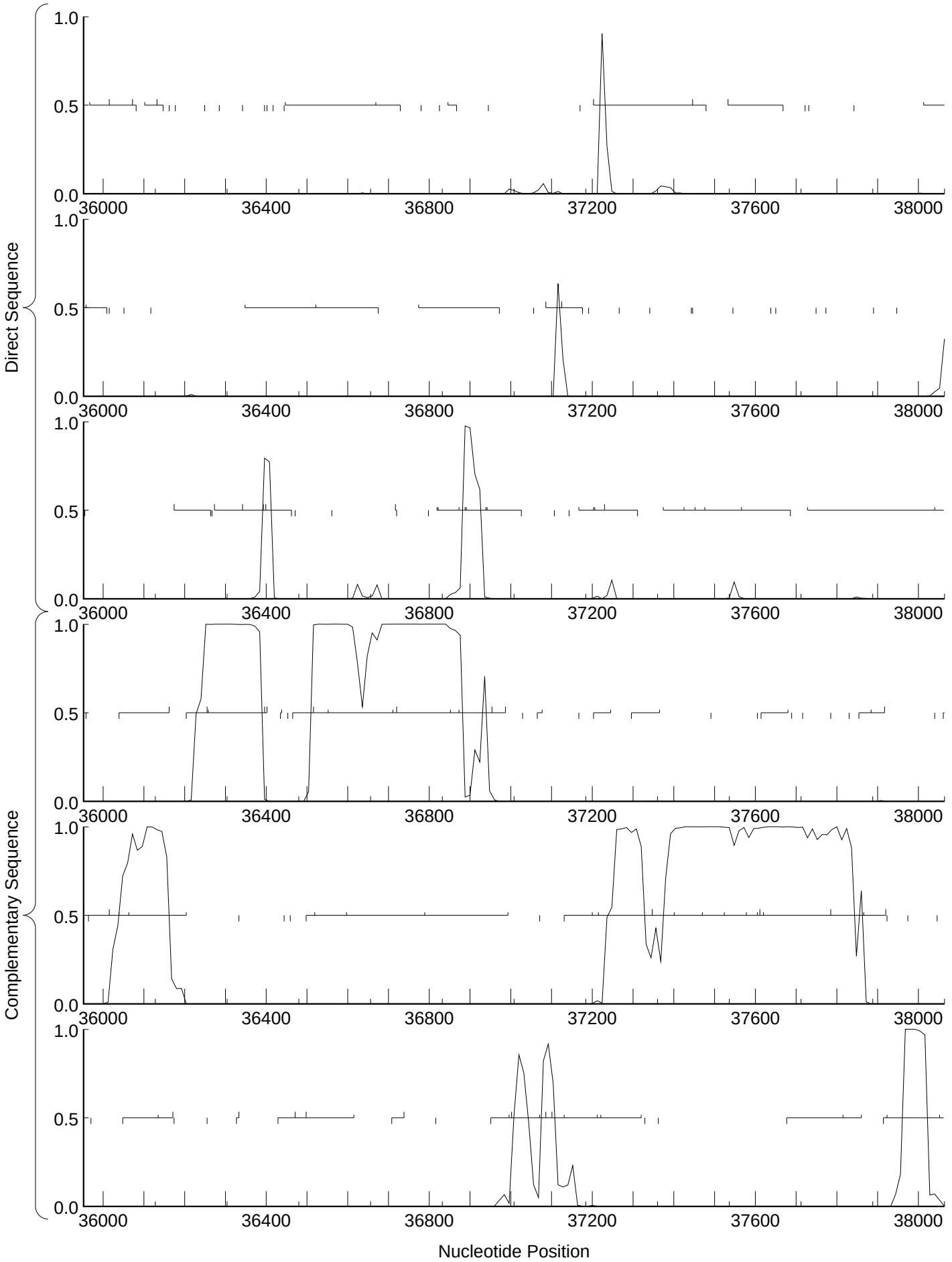


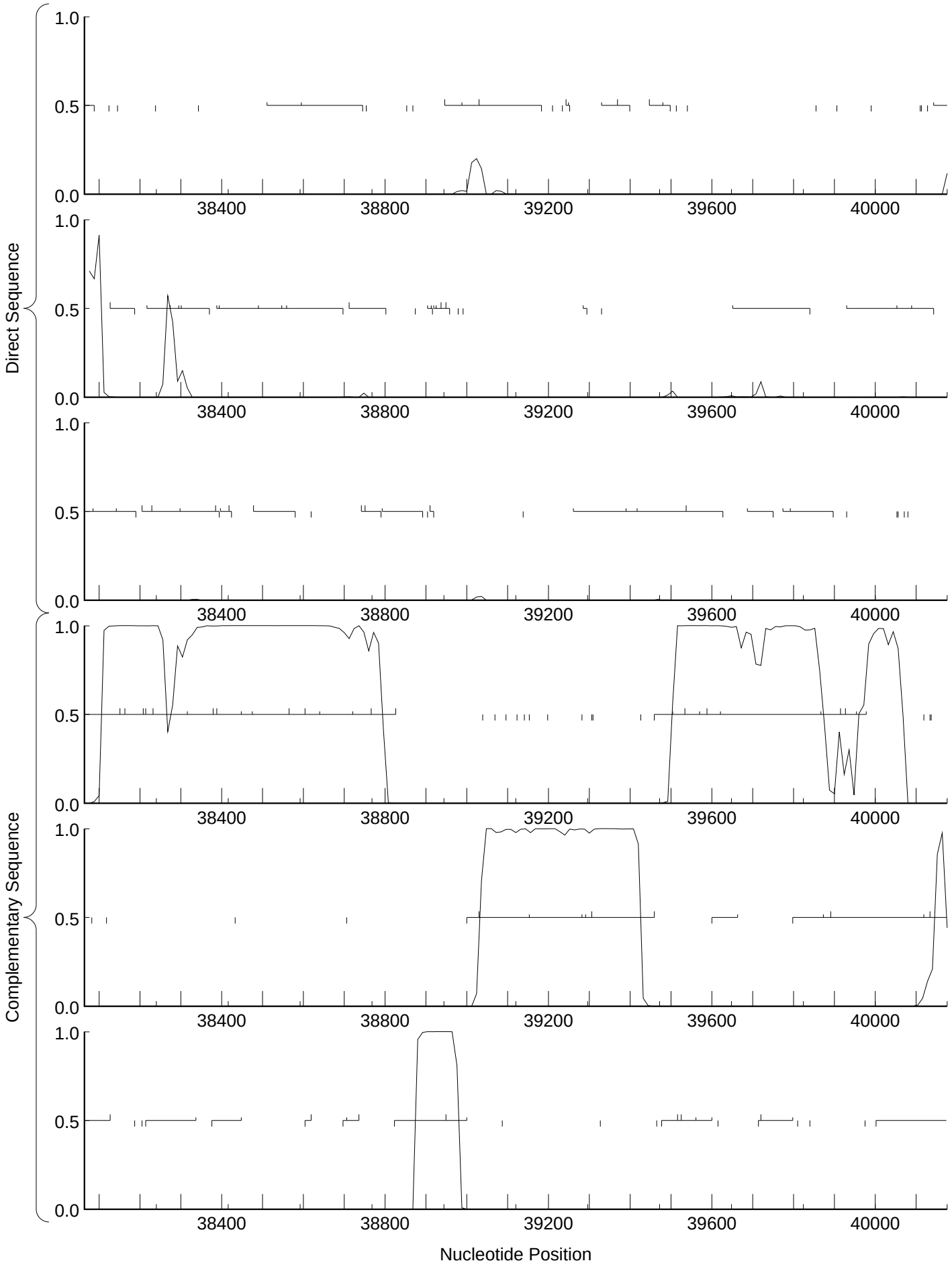
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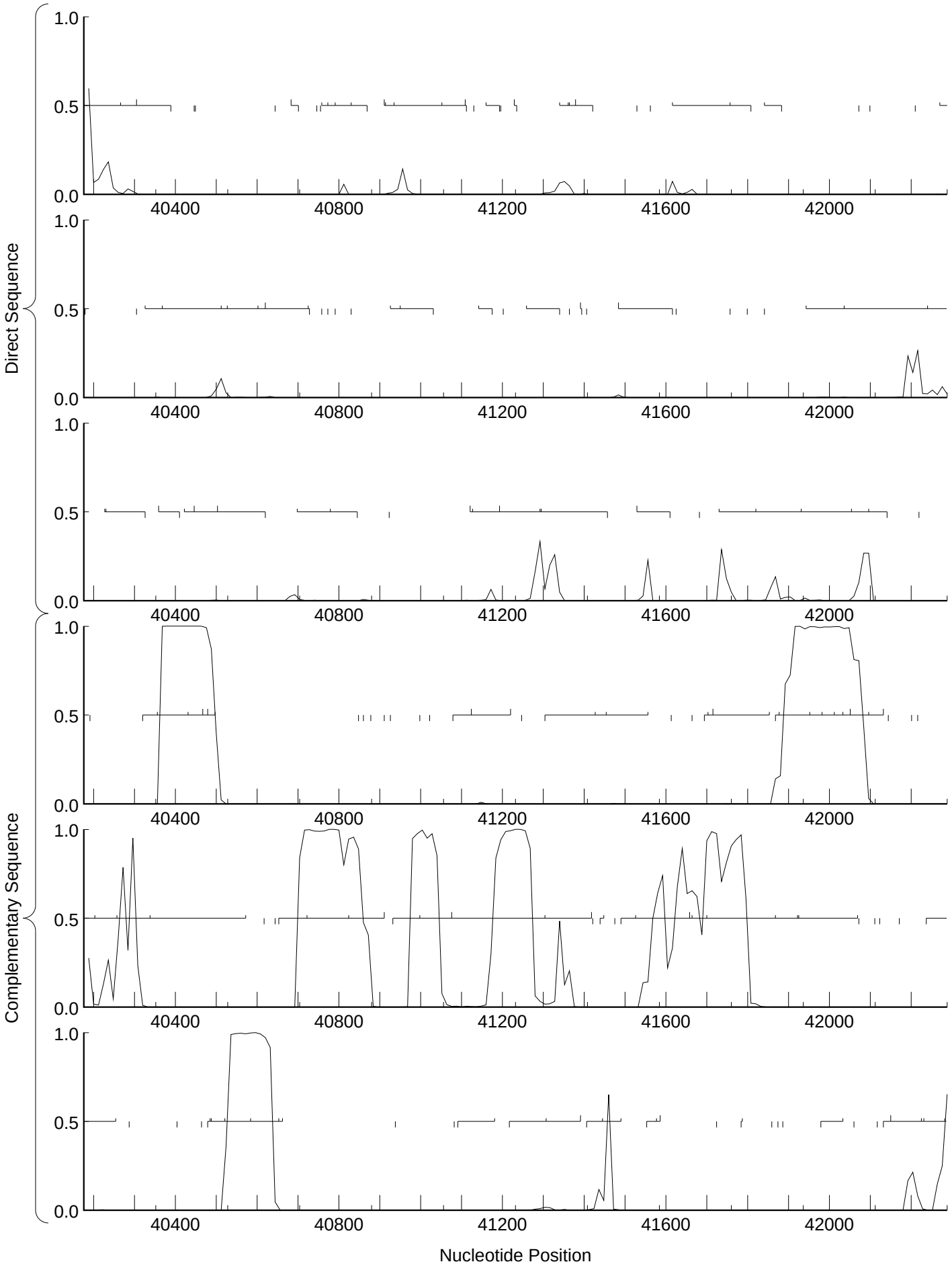

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
34000
34400
34800
35200
35600
Nucleotide Position

x complete sequence, 52295 bp including 10-base 3' overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 19/26

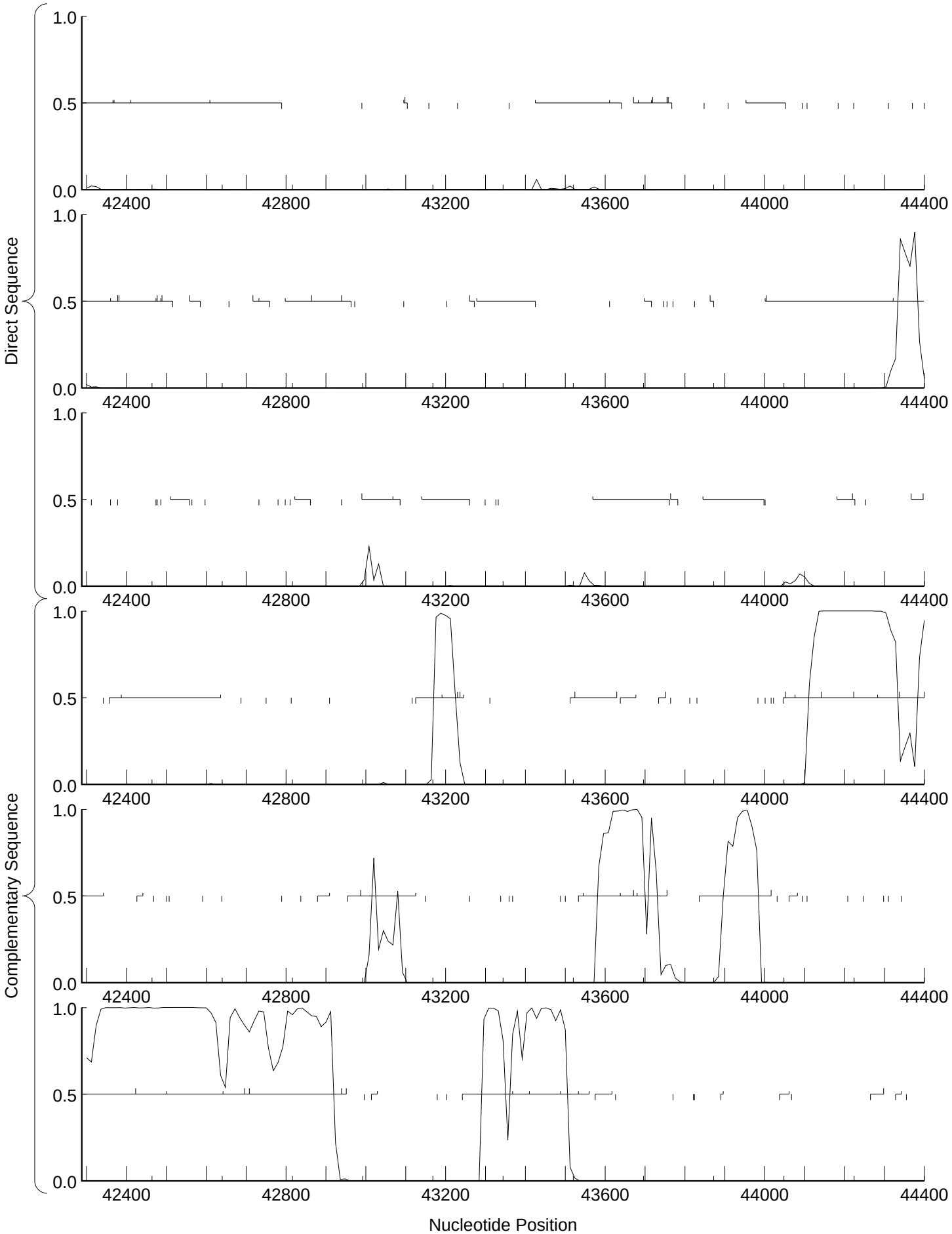


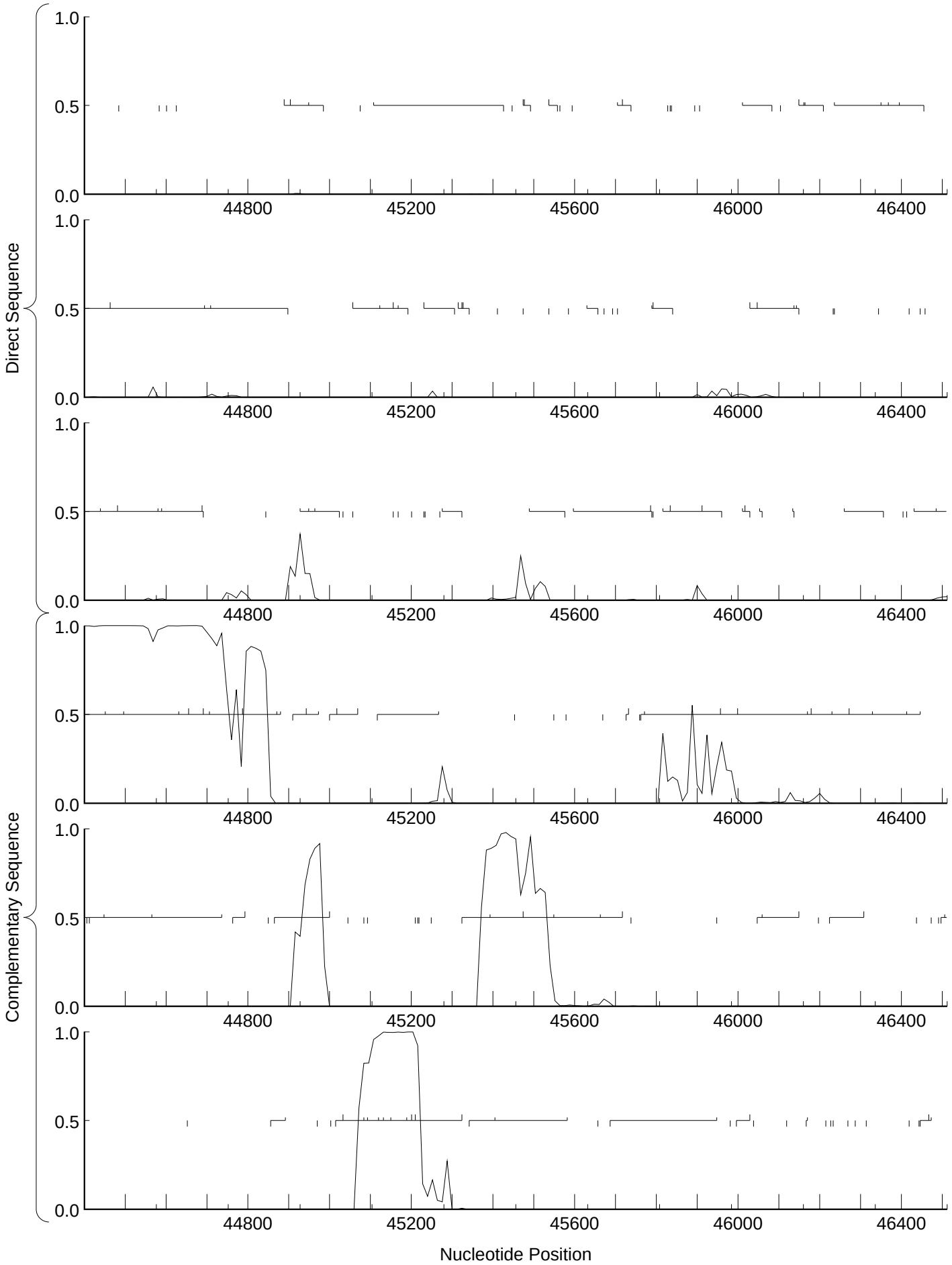

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
38400
38800
39200
39600
40000
Nucleotide Position

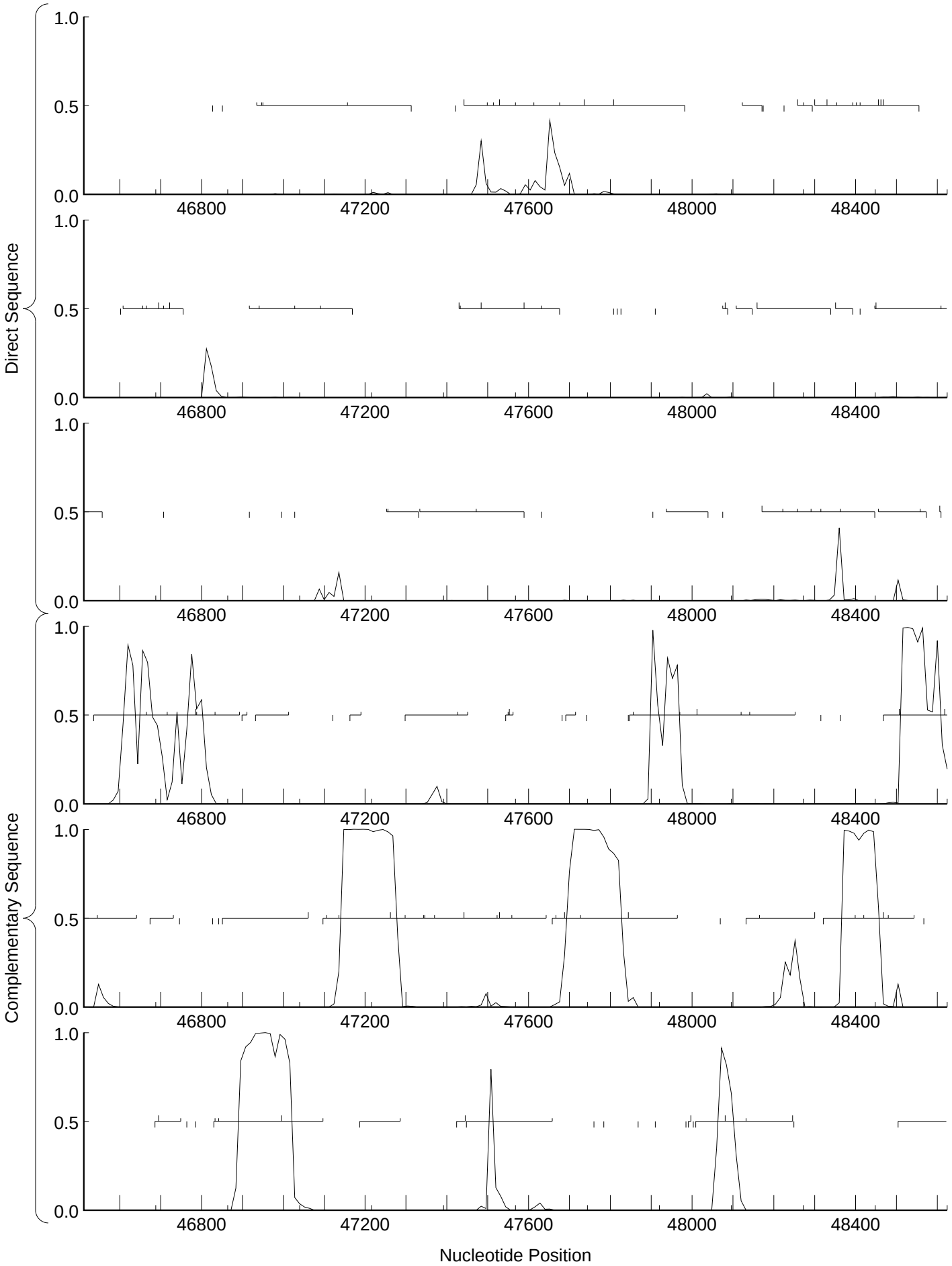
x complete sequence, 52295 bp including 10-base 3’ overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 21/26

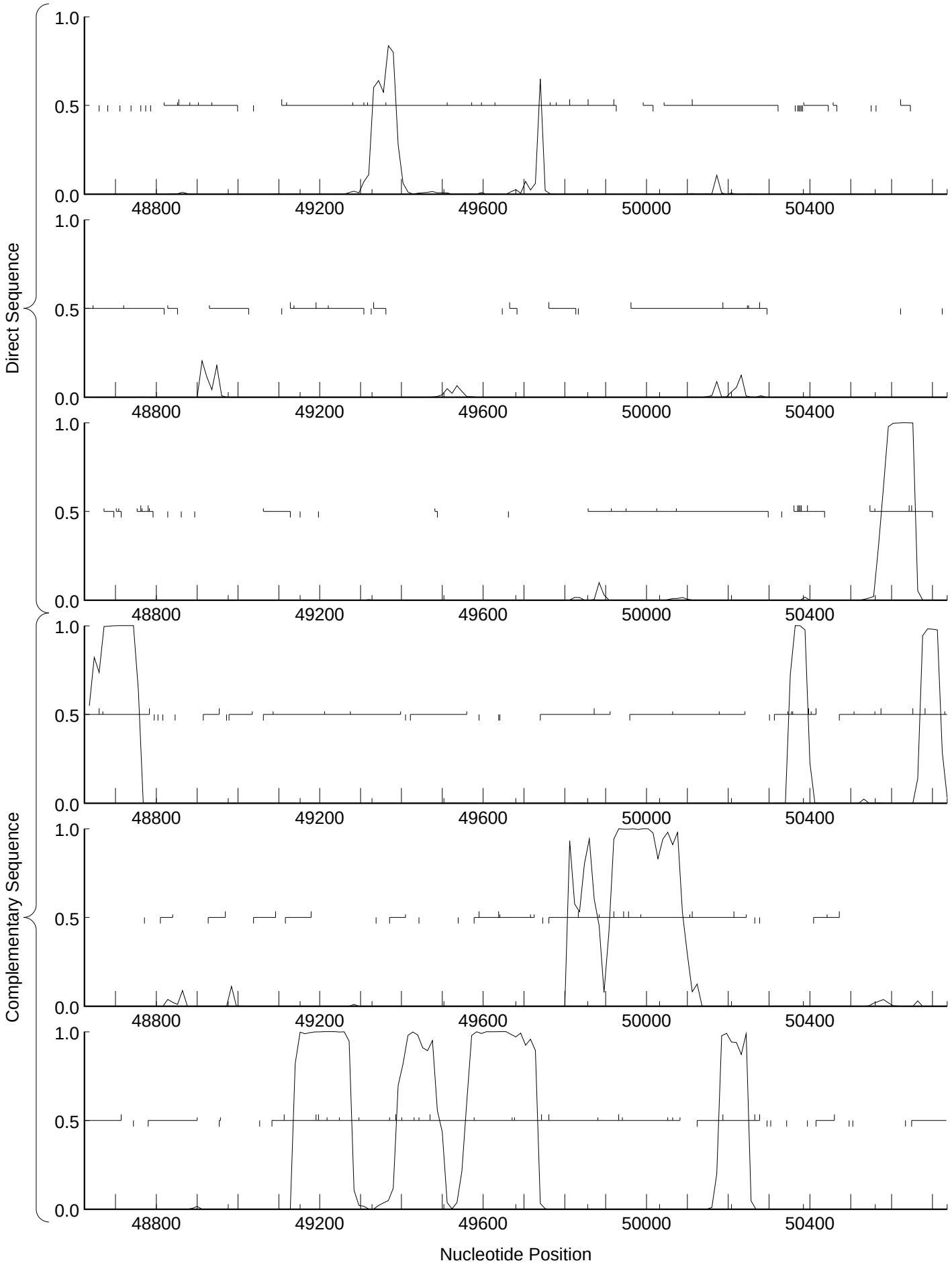


x complete sequence, 52295 bp including 10-base 3’ overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 22/26




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


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
48800
49200
49600
50000
50400
Nucleotide Position

x complete sequence, 52295 bp including 10-base 3’ overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 26/26

