GeneMark

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

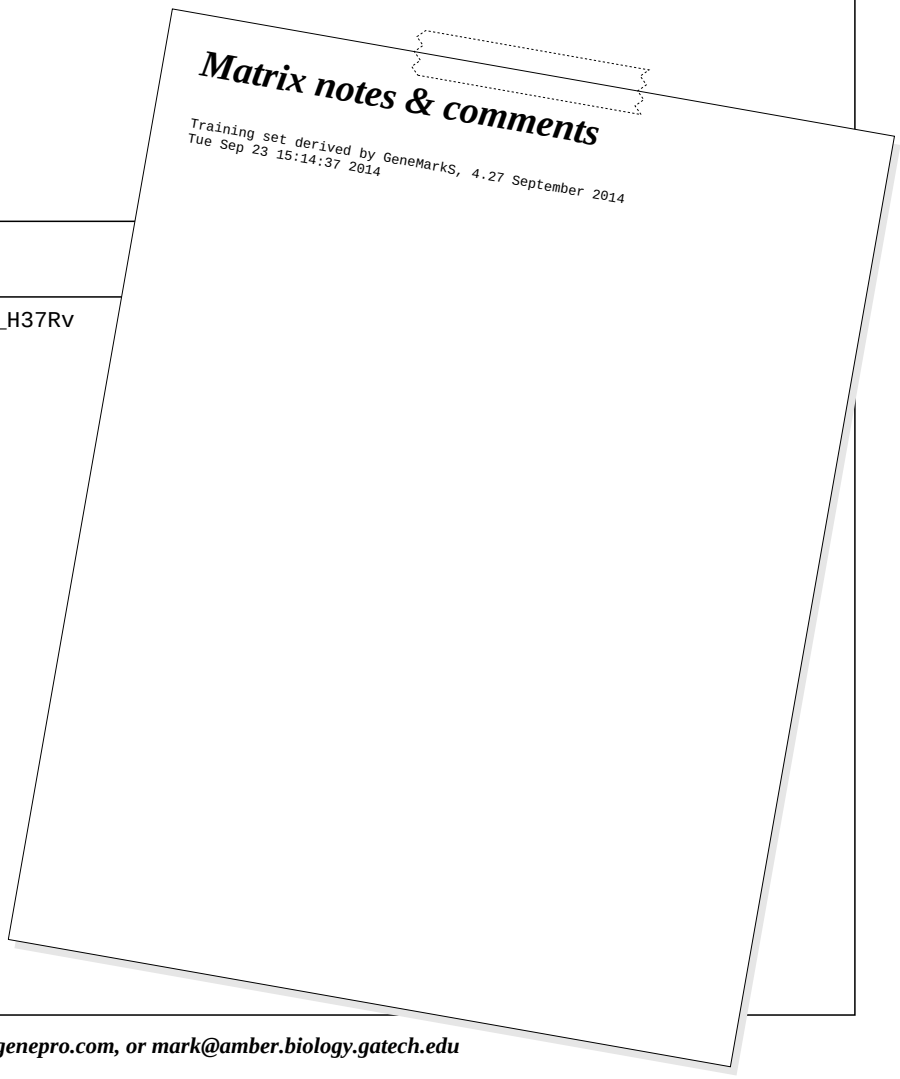
PROGRAM INFORMATION

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Sequence         :  Mycobacterium phage Coco12 complete sequence, 57693 bp including 10-base 3' overhang (CCGAT
Analysis Date    :  3/29/24 at 6:46:44
Pages            :  29
Sequence Length  :  57693 bp
GC Content       :   61.14%

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

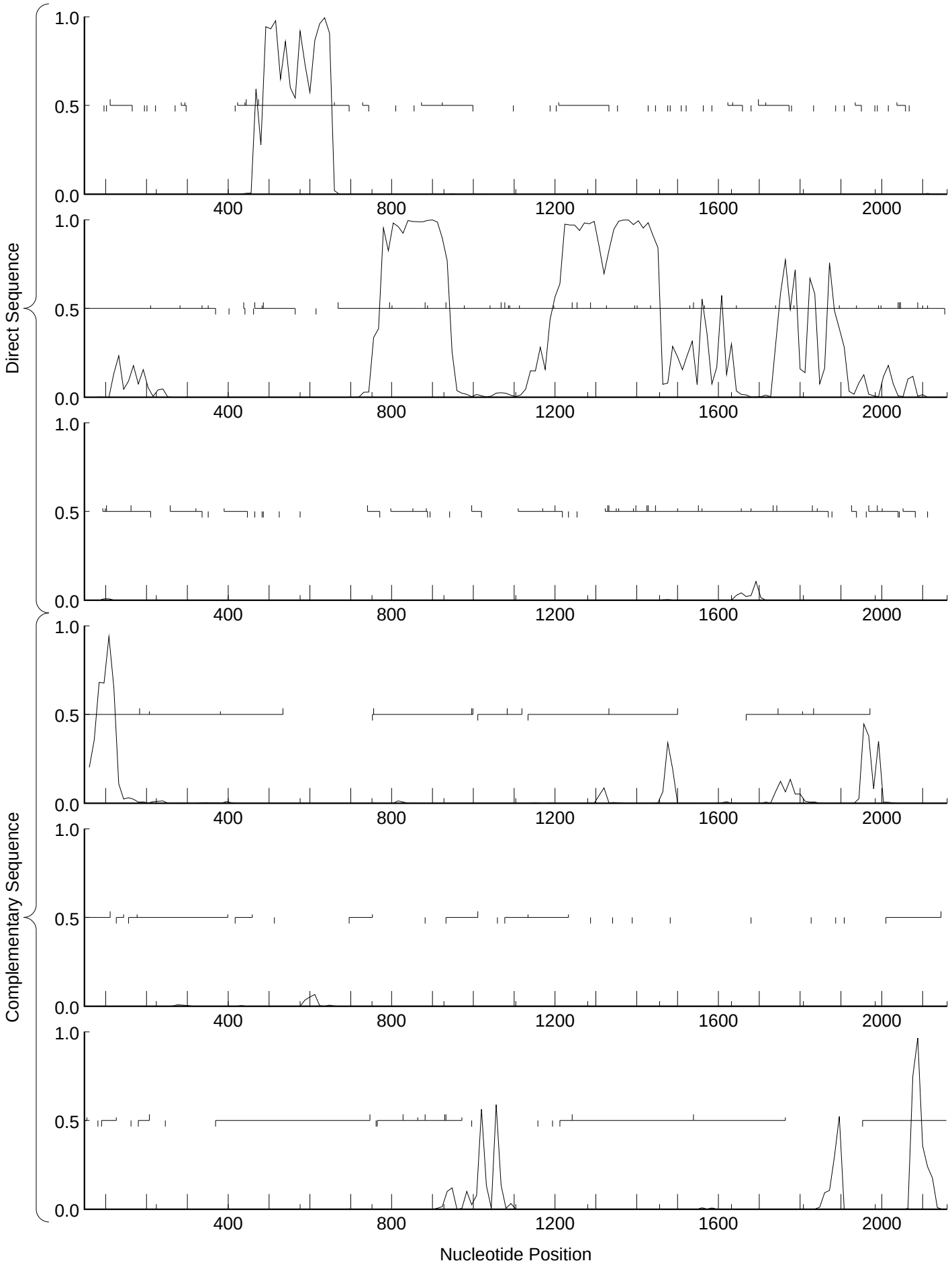
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Author     :  -

Order      :  4

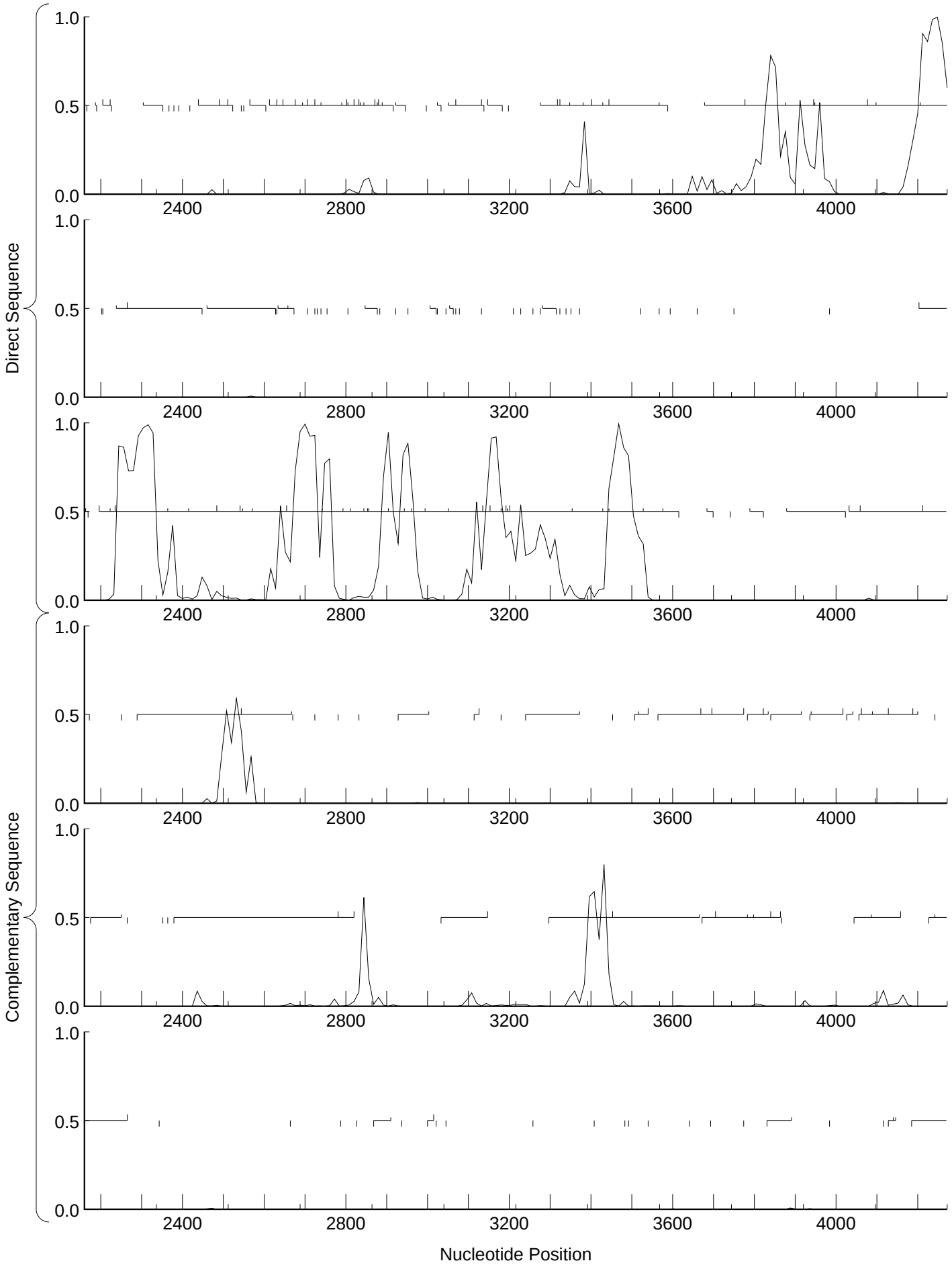

  Send questions / comments to:
      Dr. M. Borodovsky
      Georgia Institute of Technology
      School of Biology
      Atlanta, GA  30332-0230
```

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

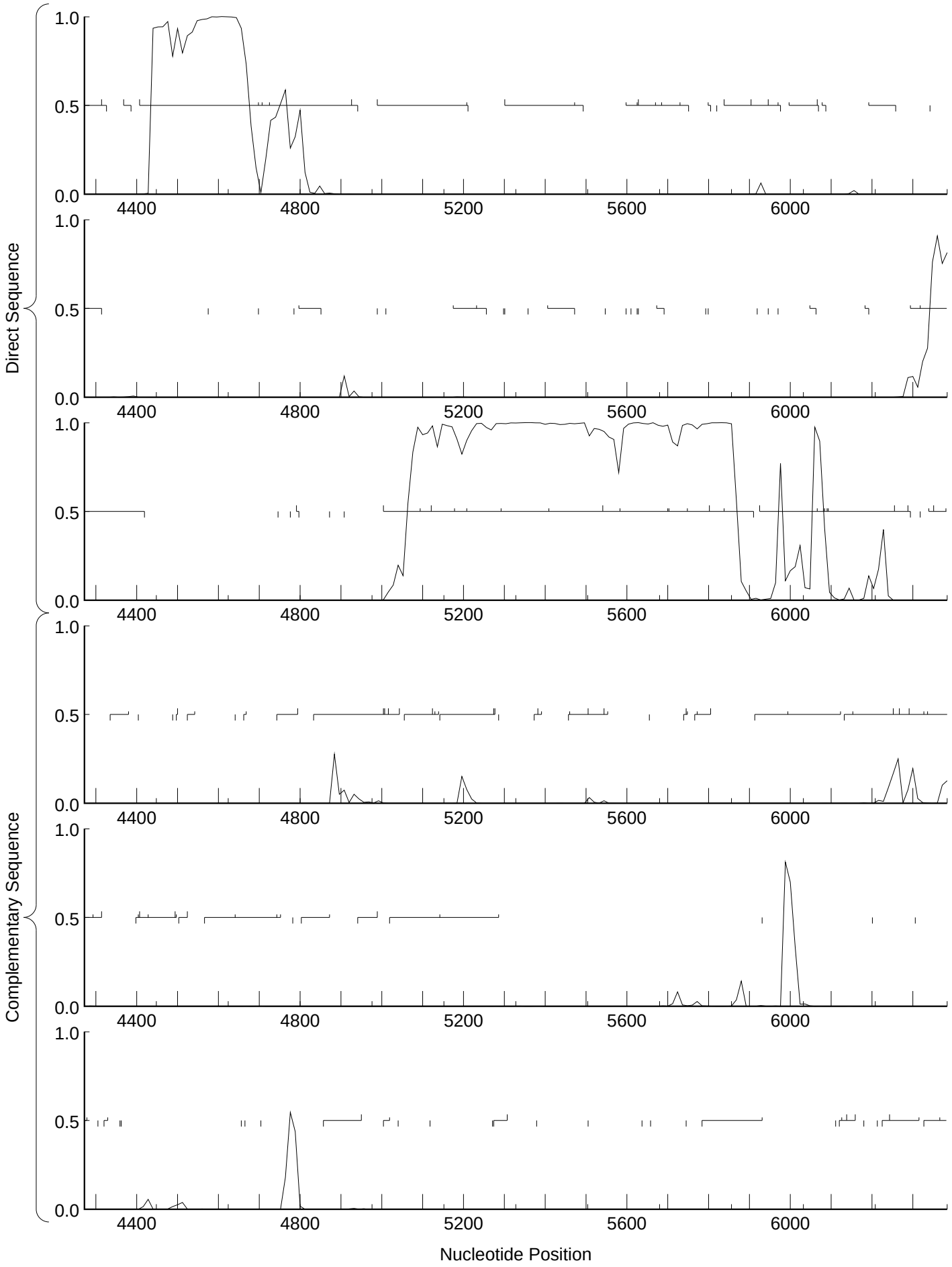
.2 complete sequence, 57693 bp including 10-base 3’ overhang (CCGATGGCAT), Cluster F1, Order 4, Window 96, Step 12, 2/29



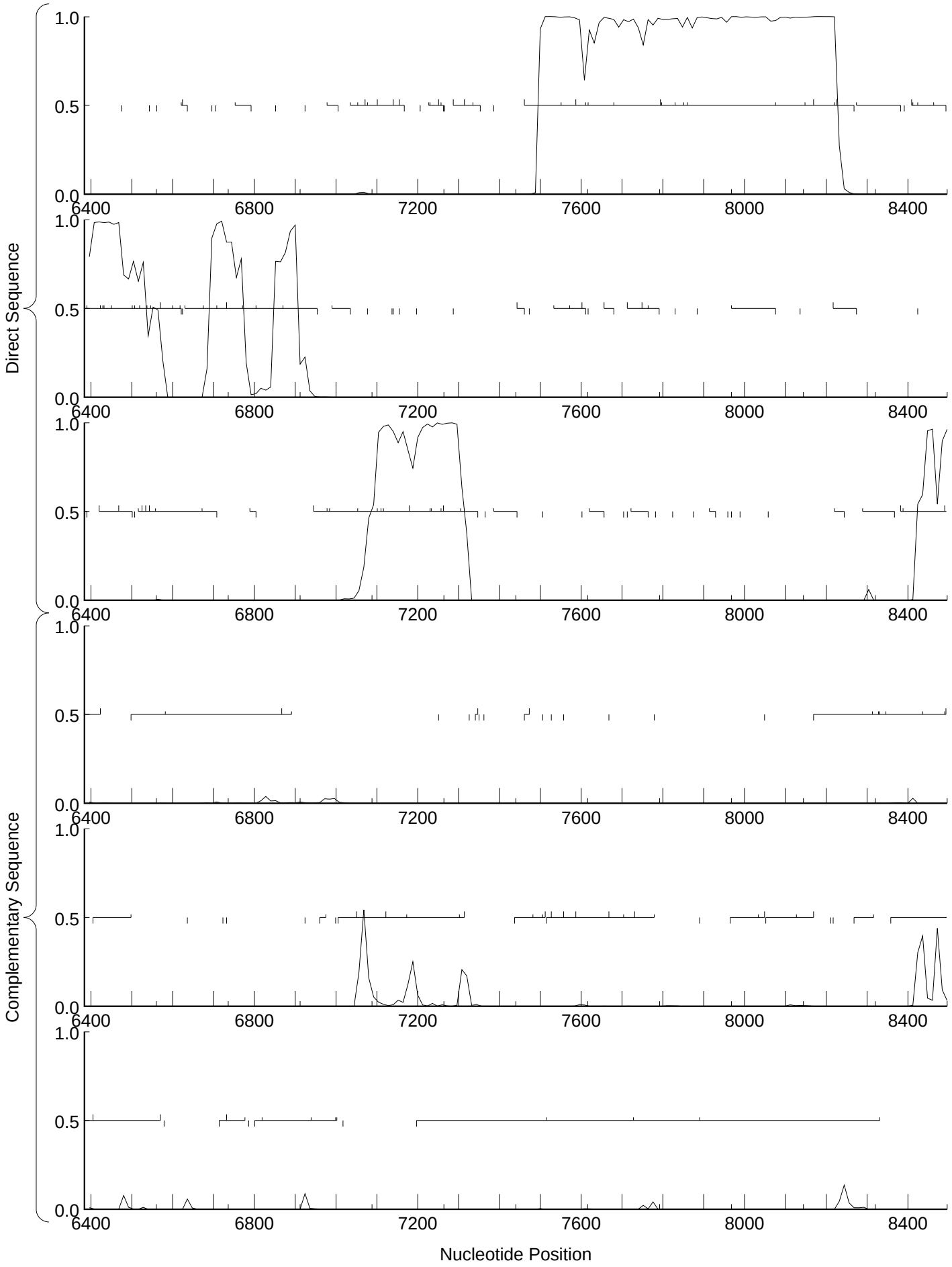
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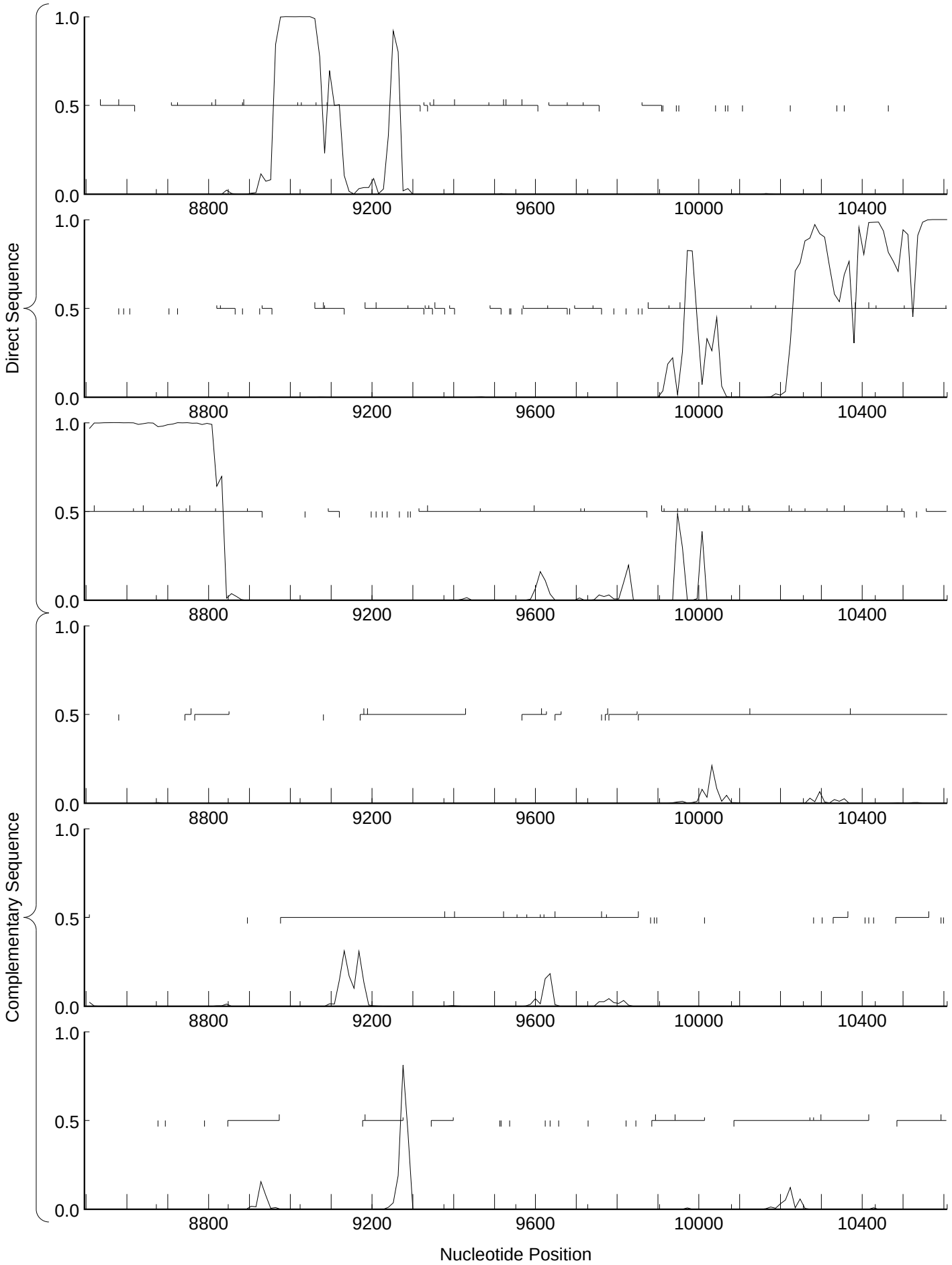


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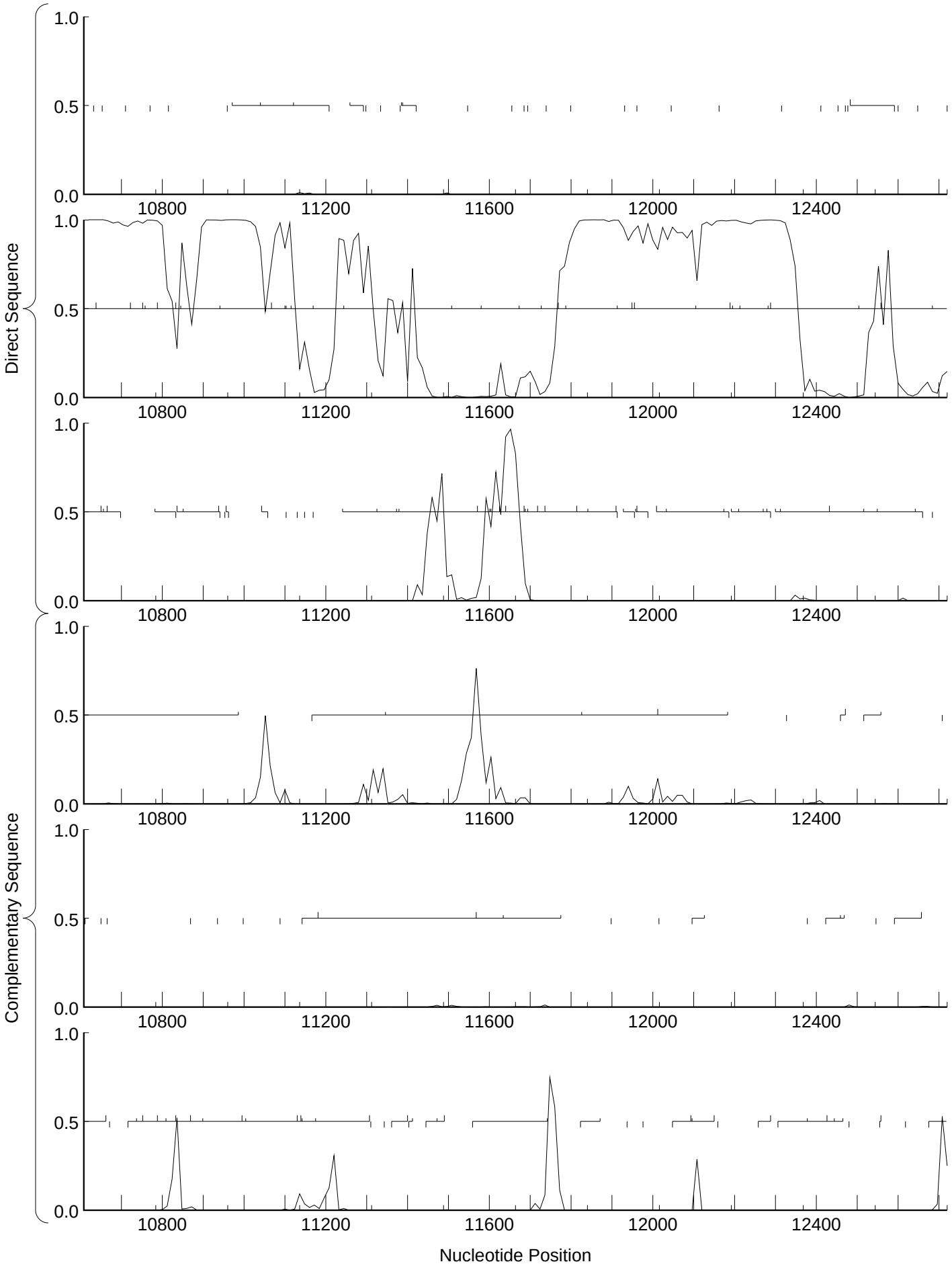


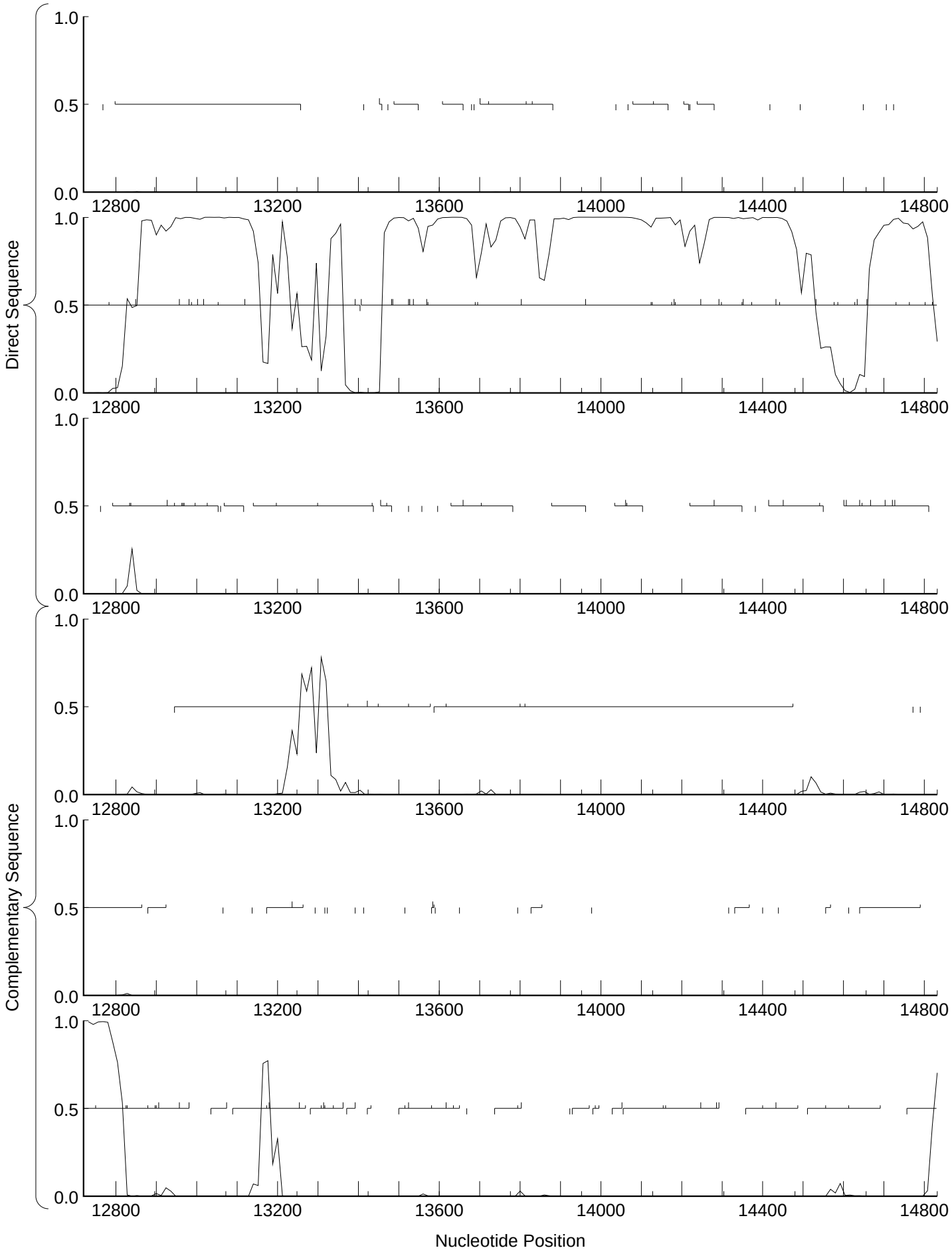
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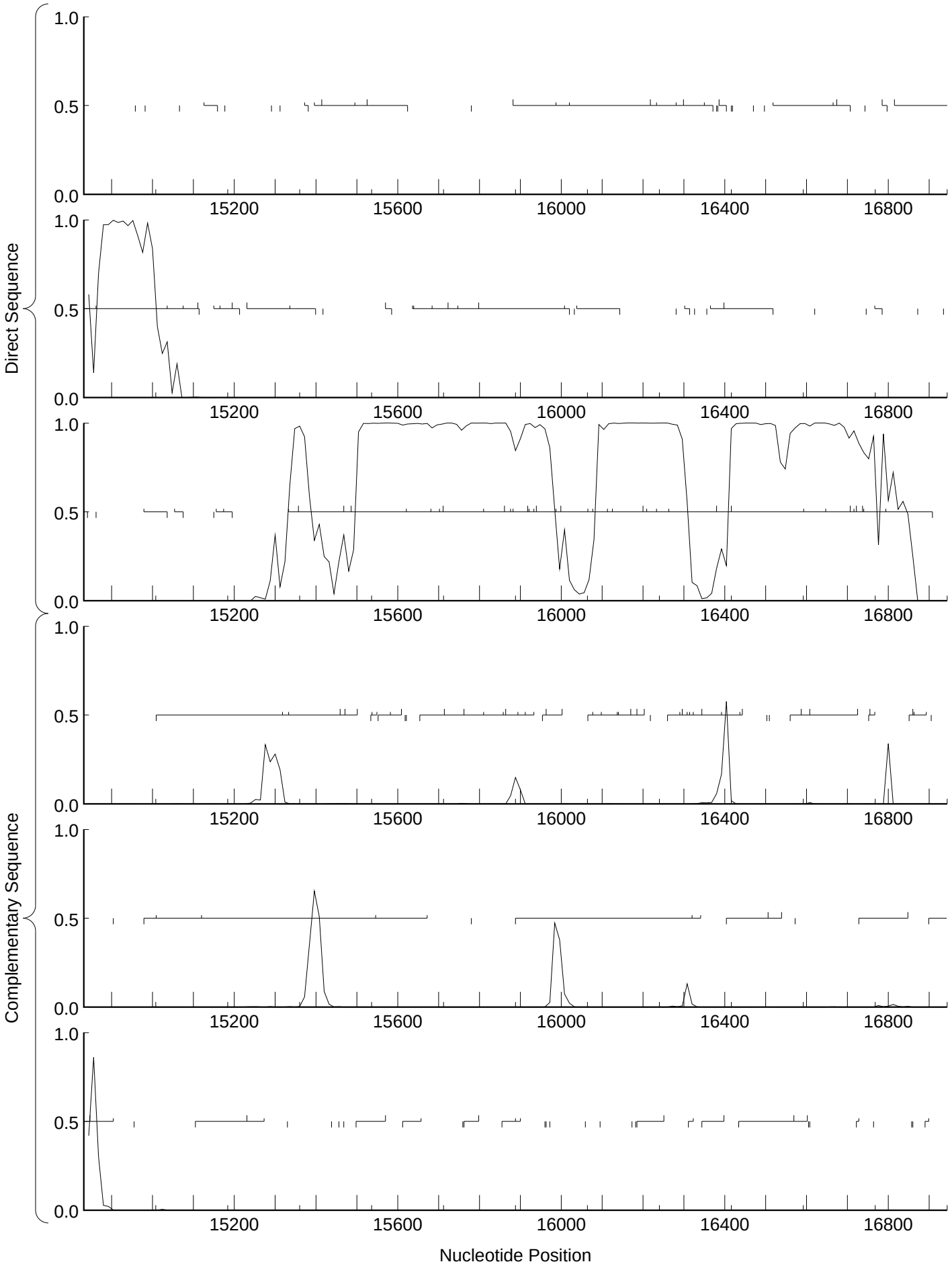

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
8800
9200
9600
10000
10400
Nucleotide Position

.2 complete sequence, 57693 bp including 10-base 3’ overhang (CCGATGGCAT), Cluster F1, Order 4, Window 96, Step 12, 7/29

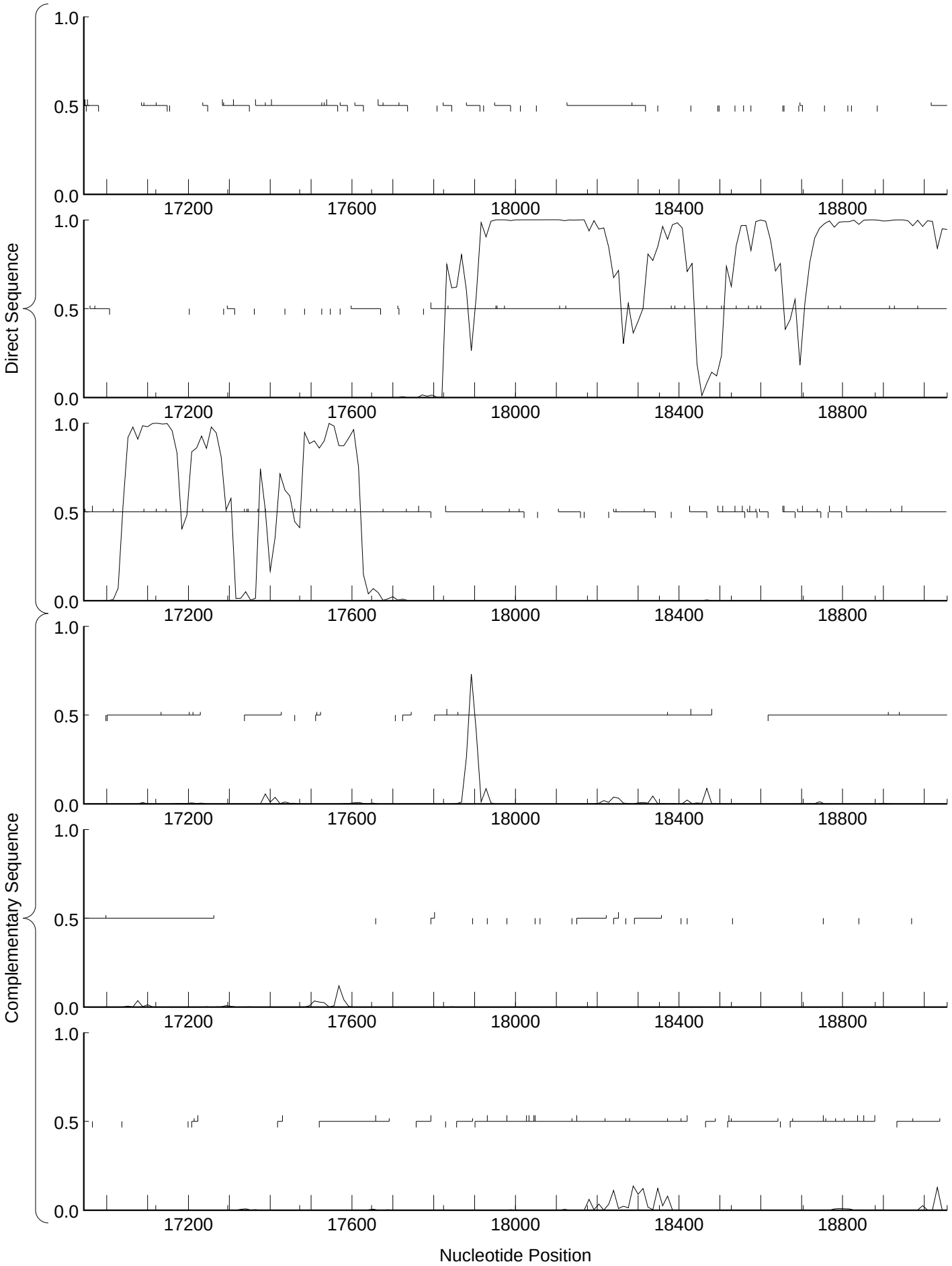



Direct Sequence
Complementary Sequence
1.0
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0.0
12800
13200
13600
14000
14400
14800
Nucleotide Position

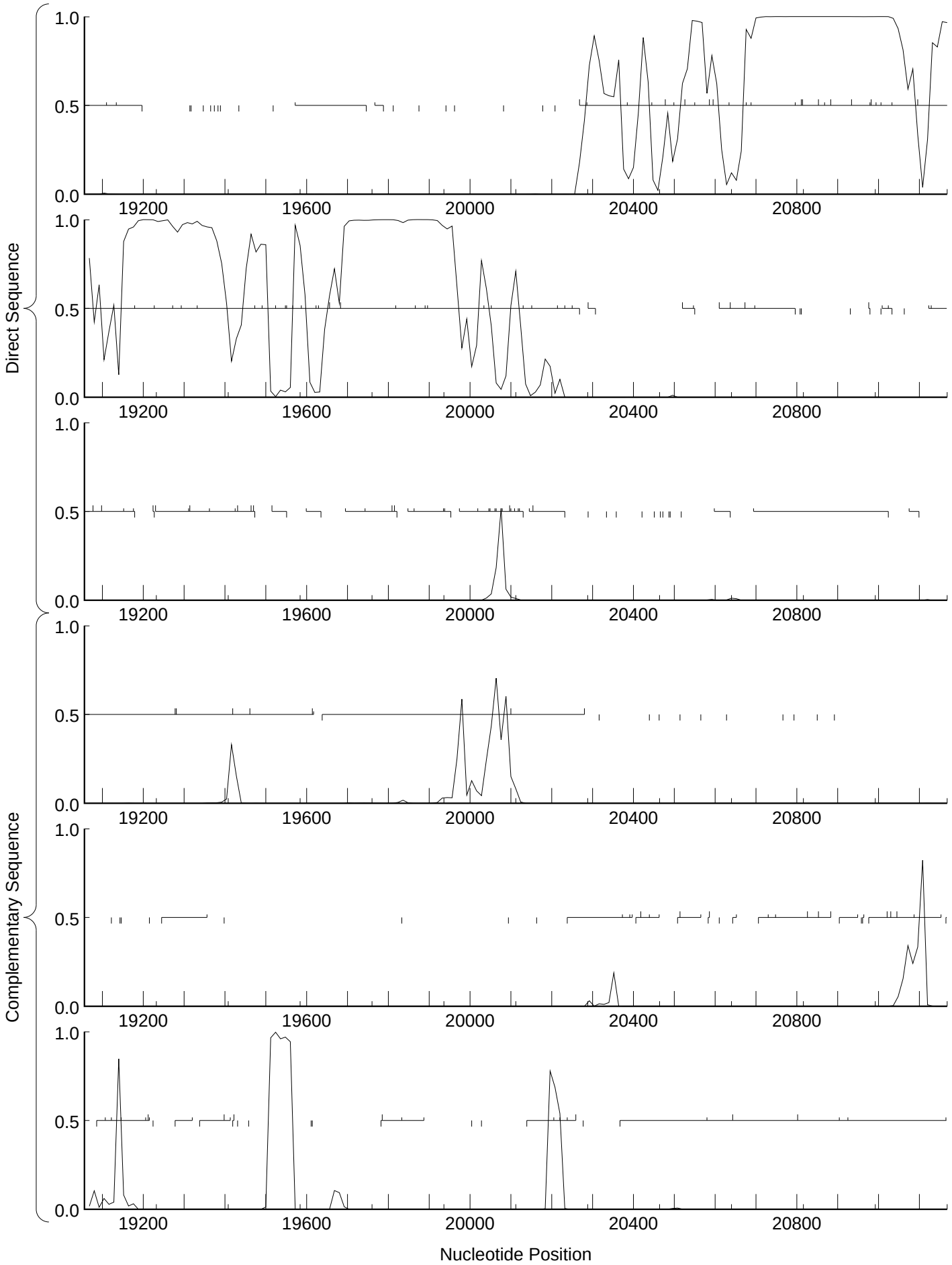
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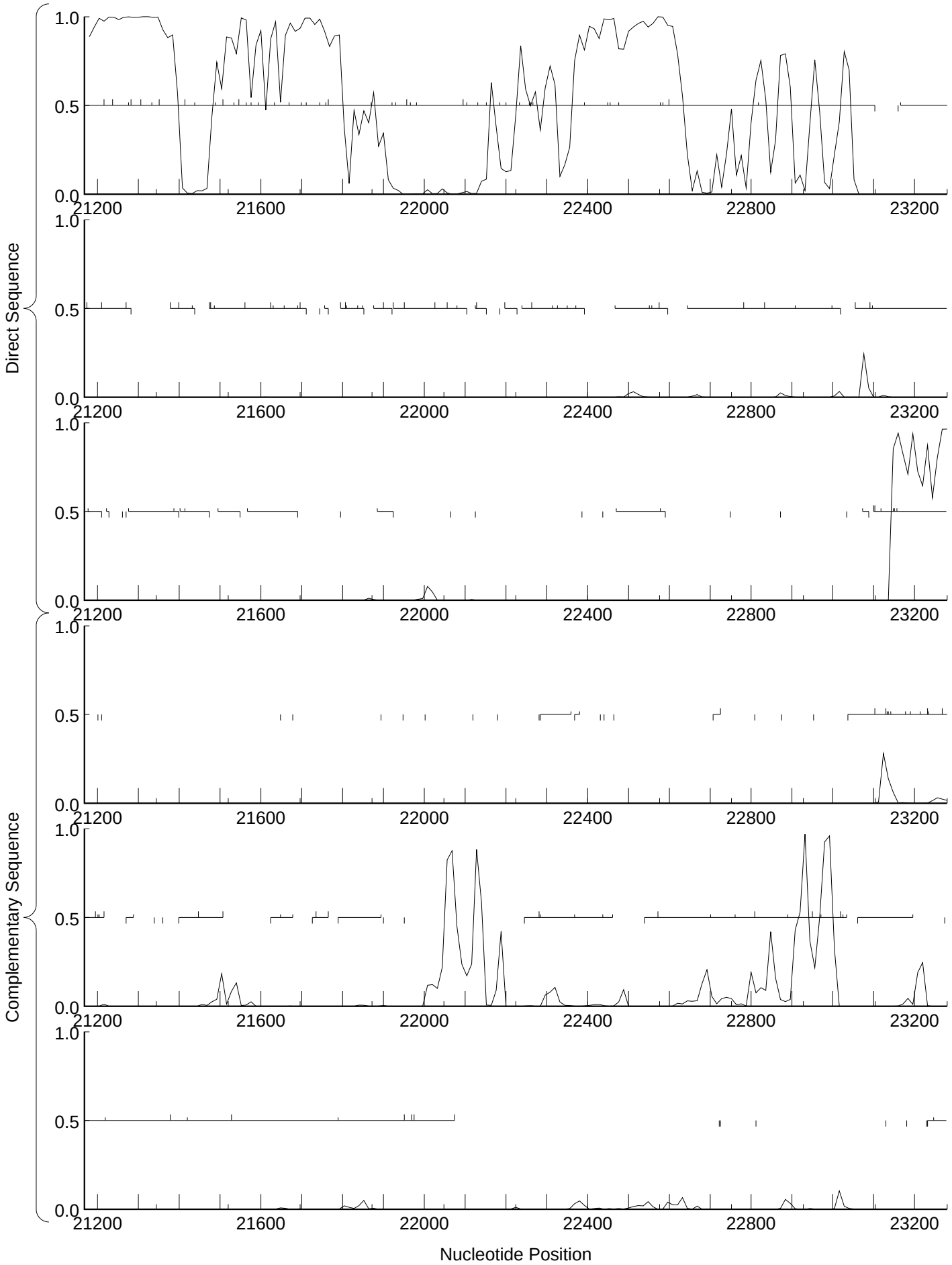
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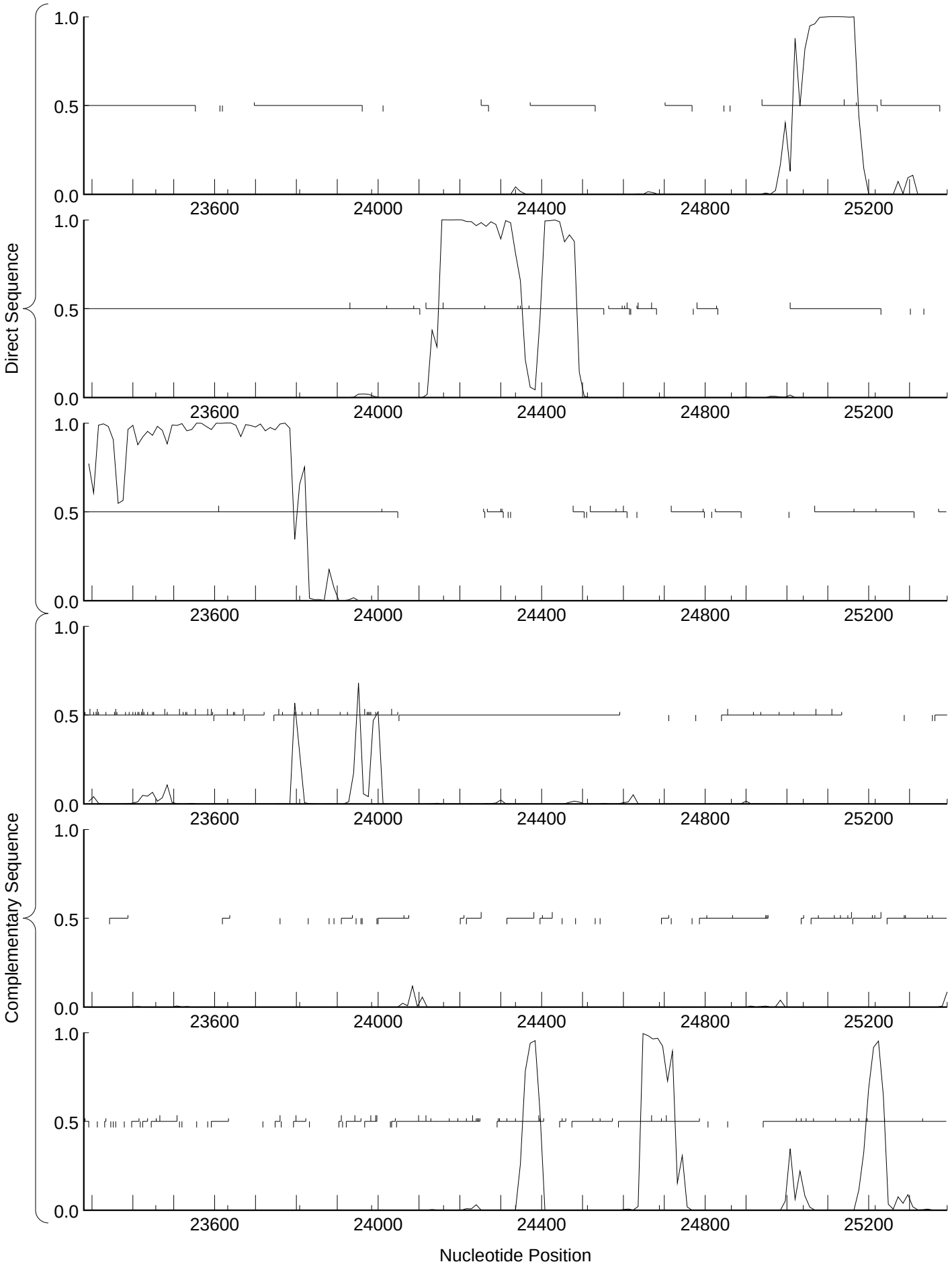
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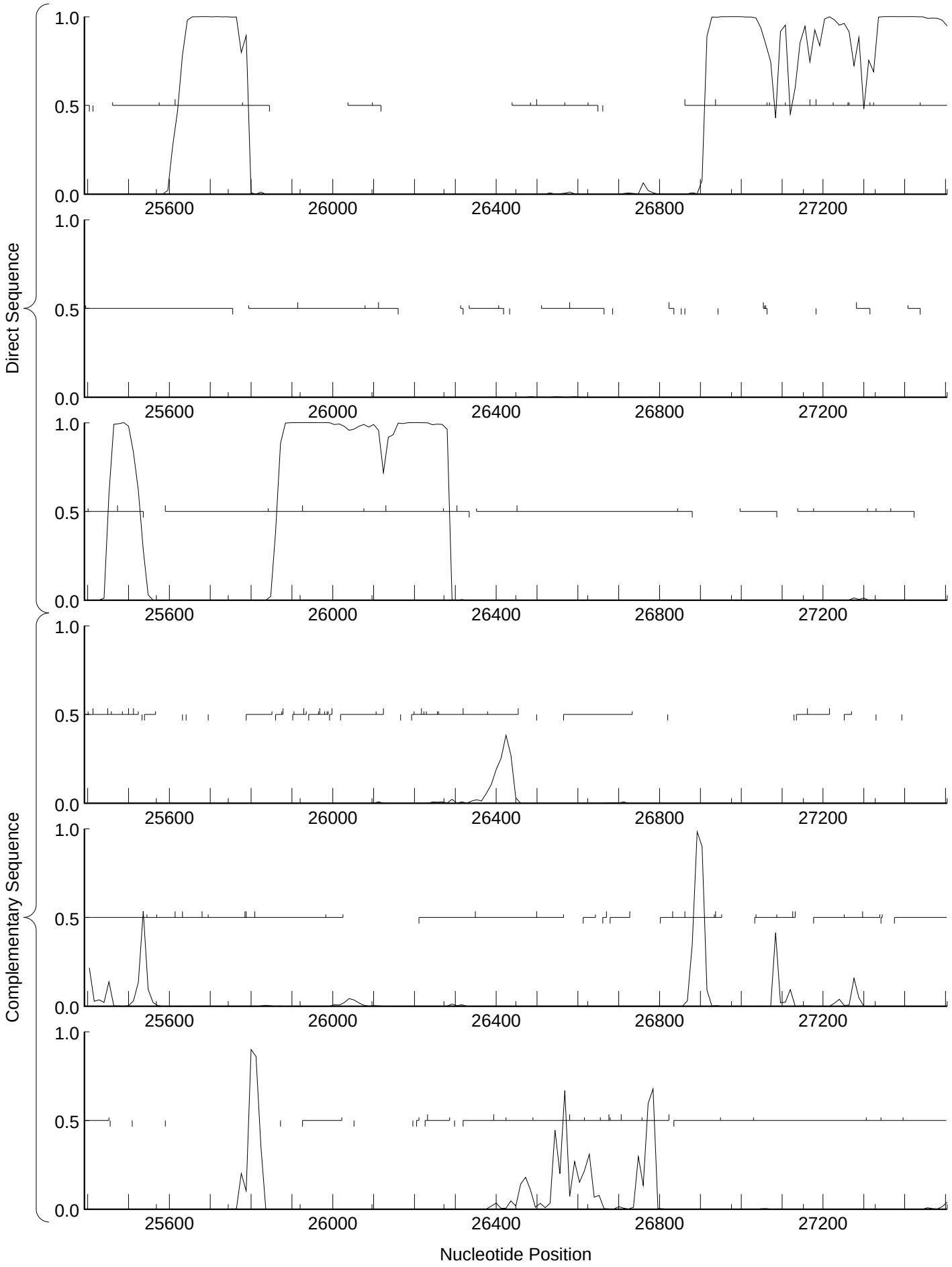
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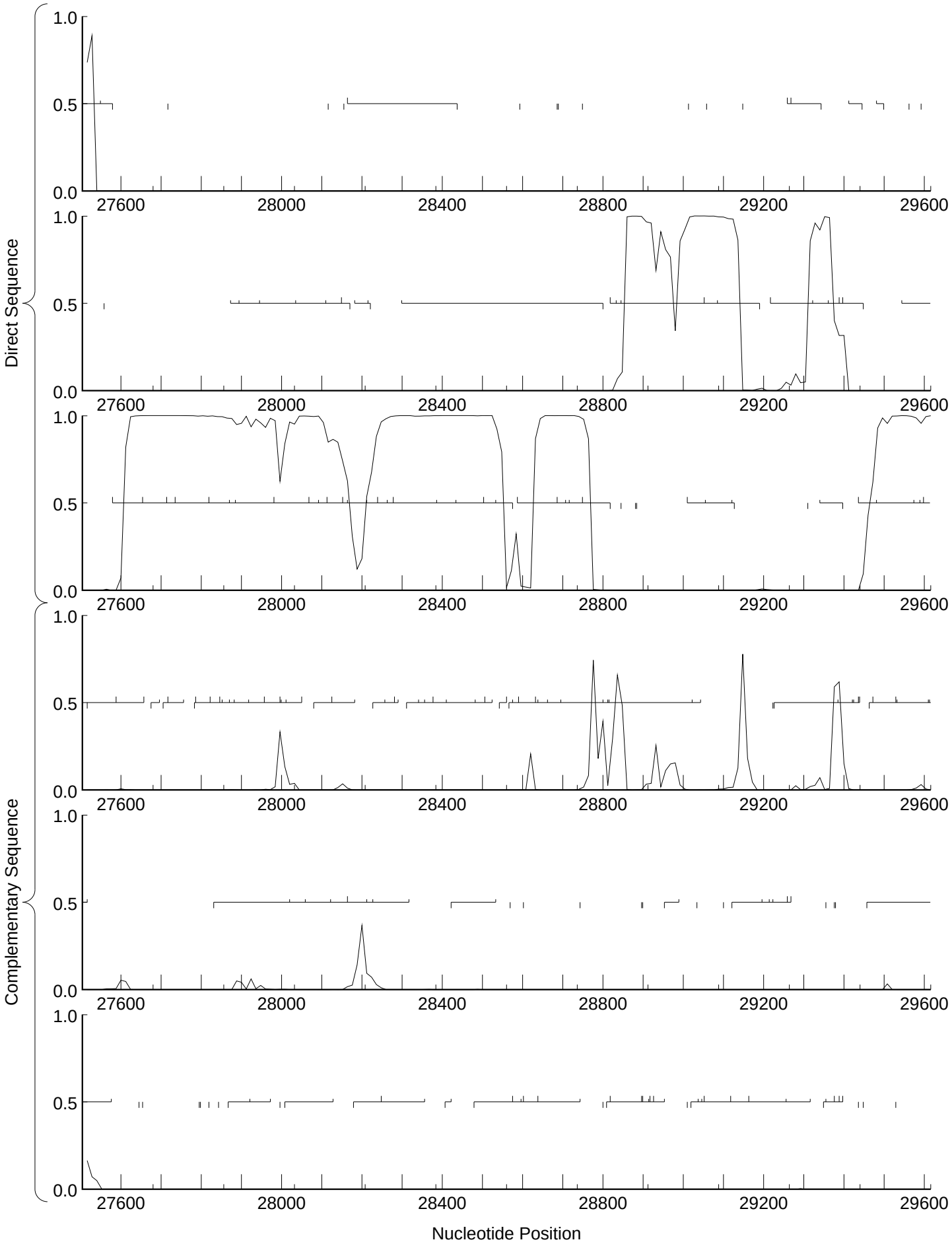
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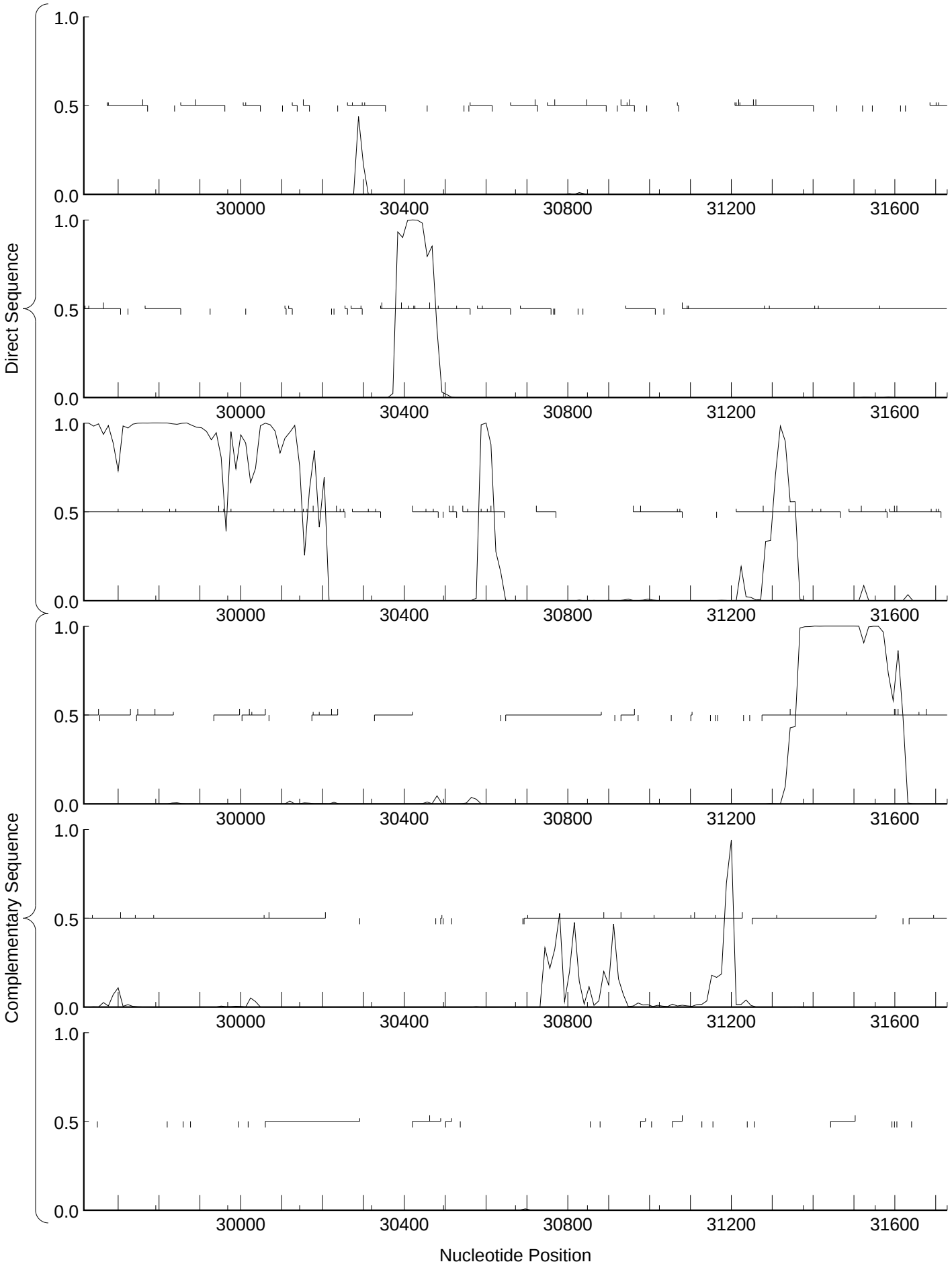
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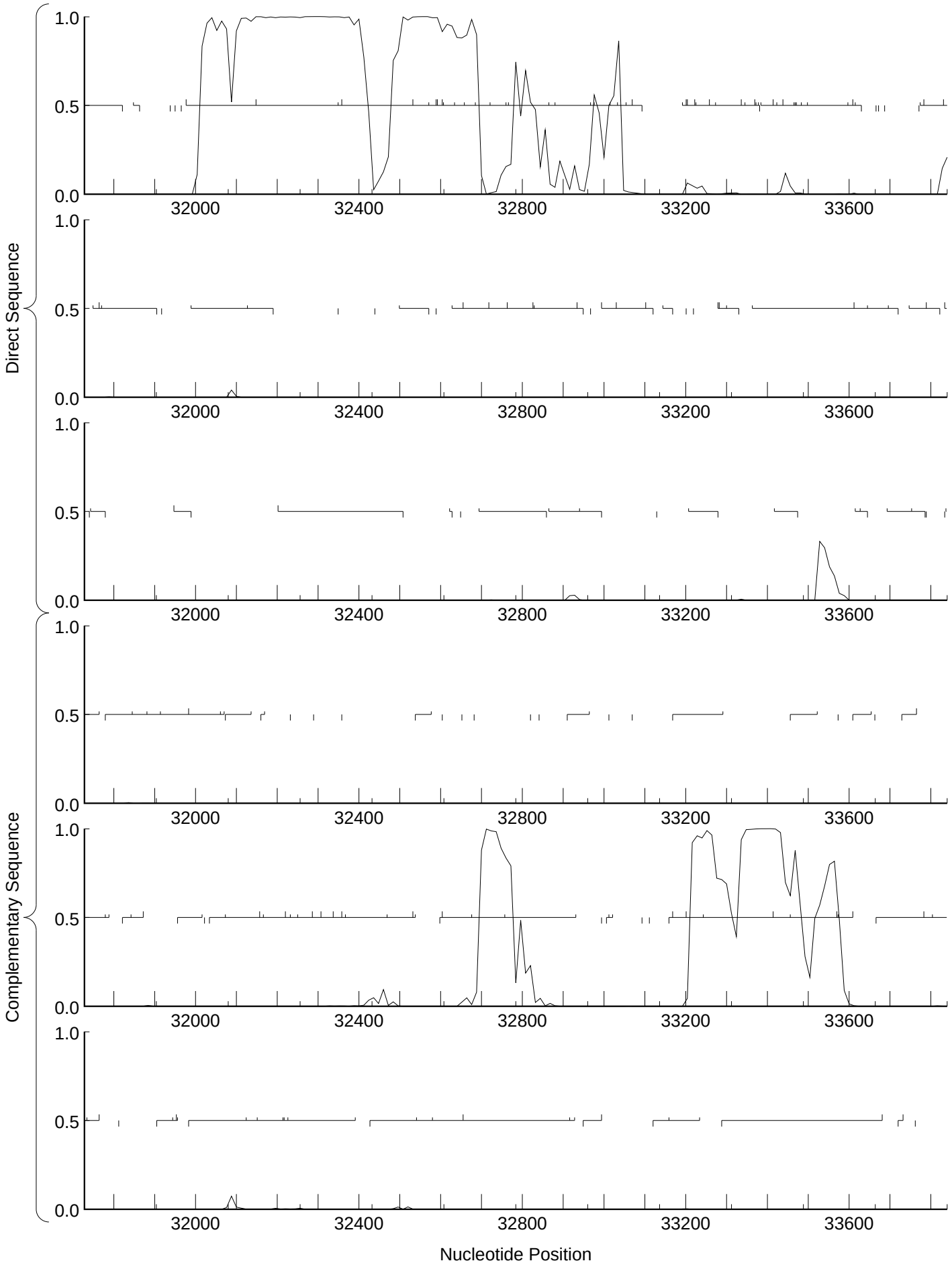
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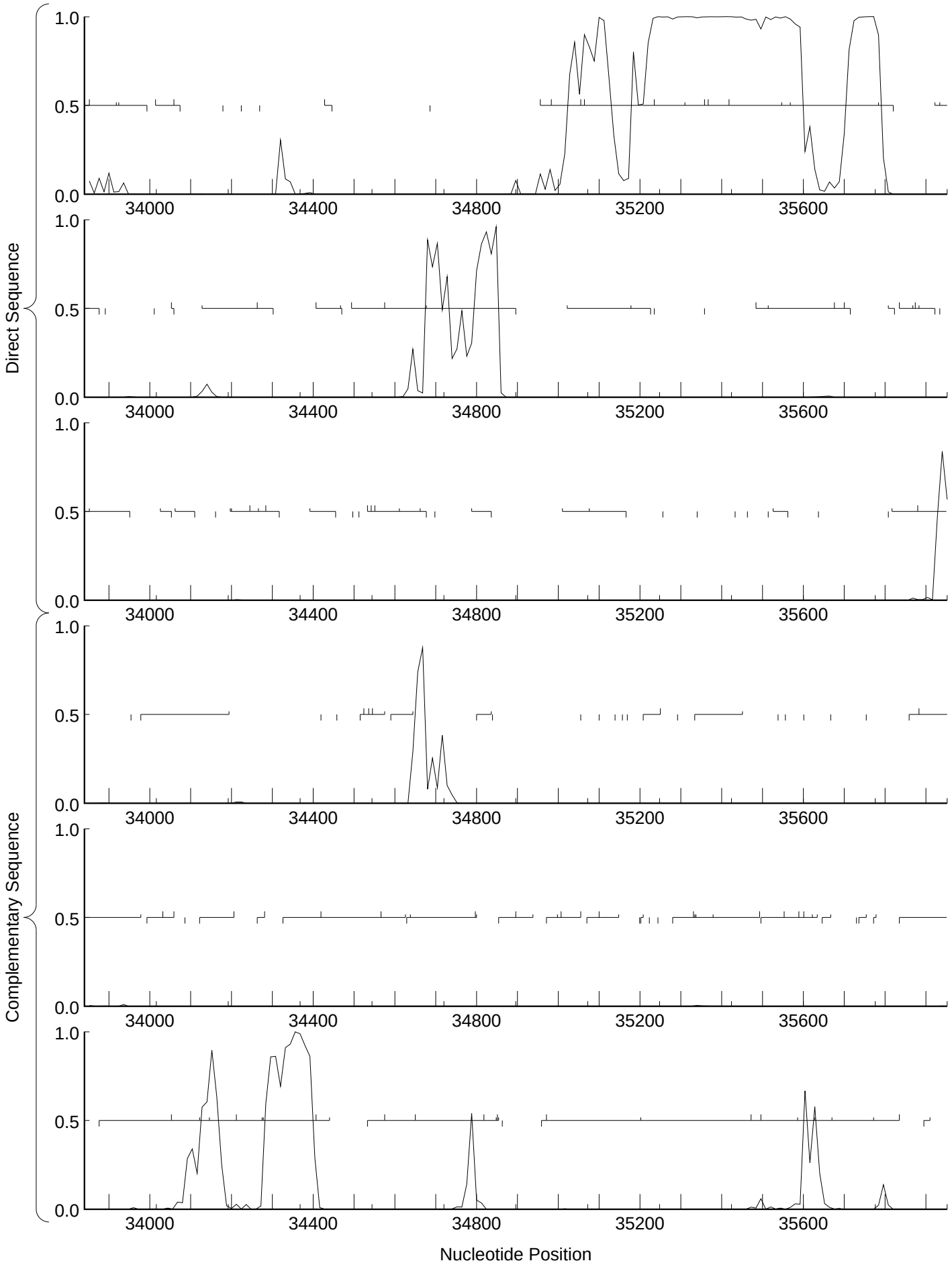
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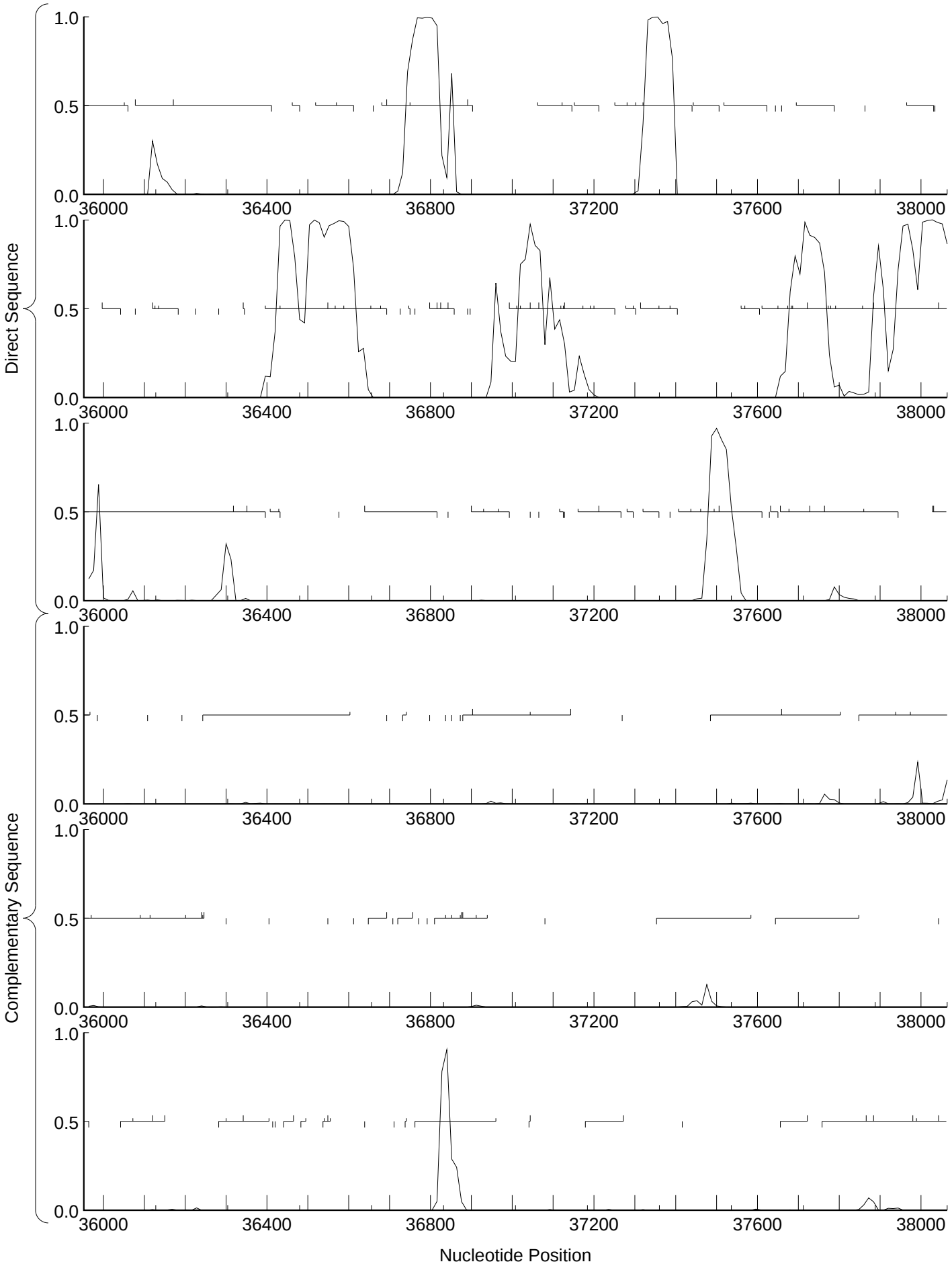
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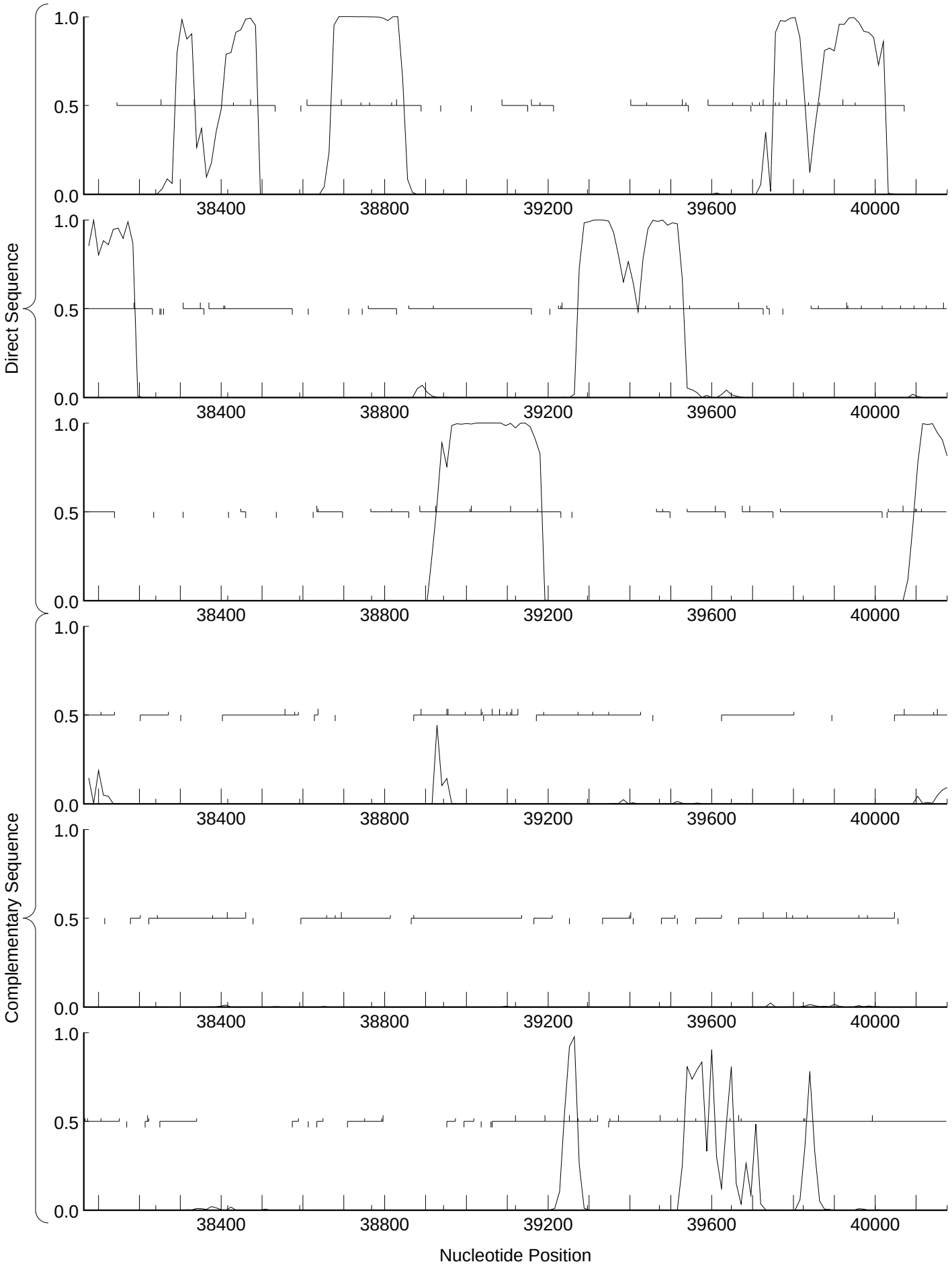
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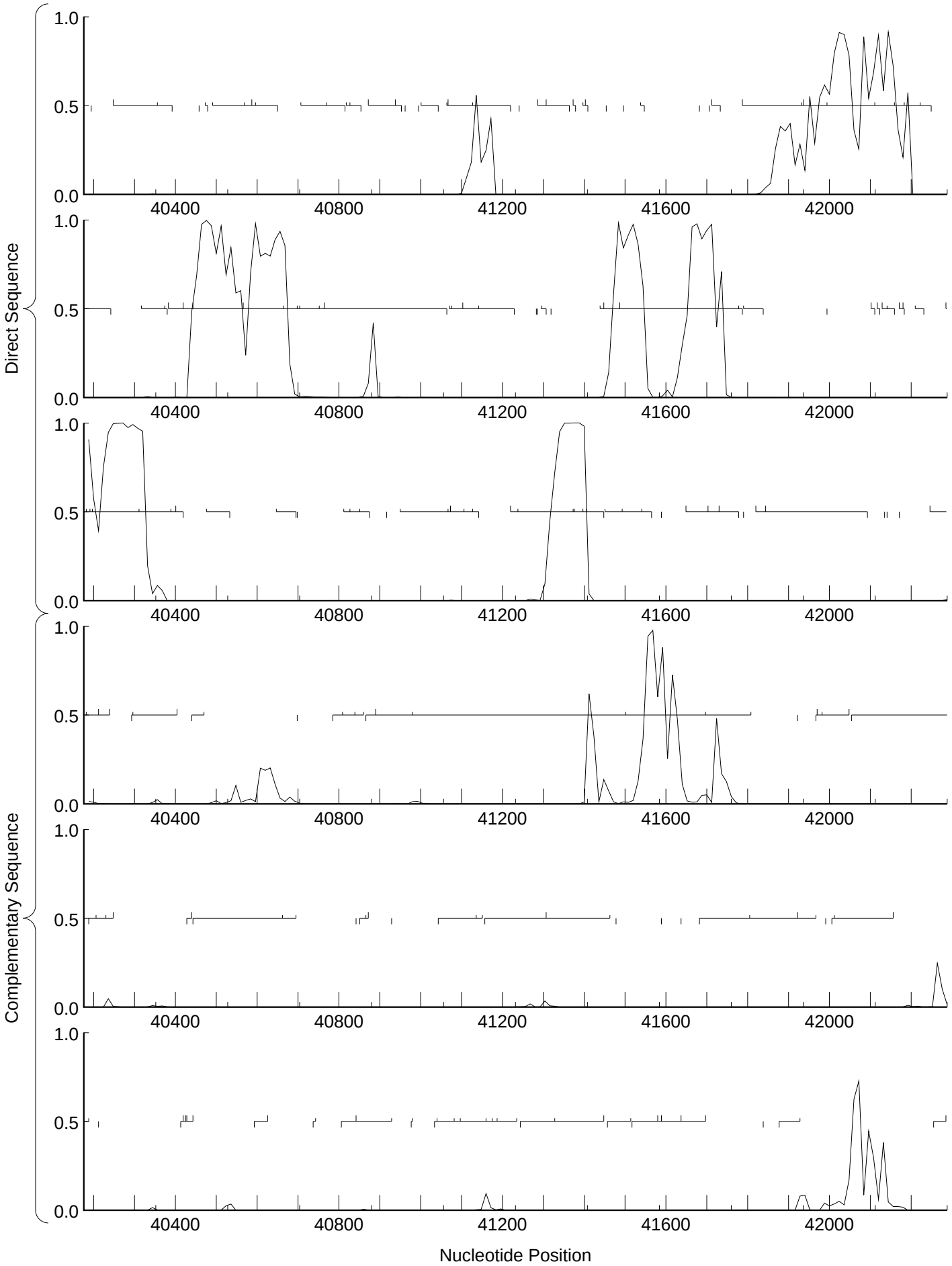
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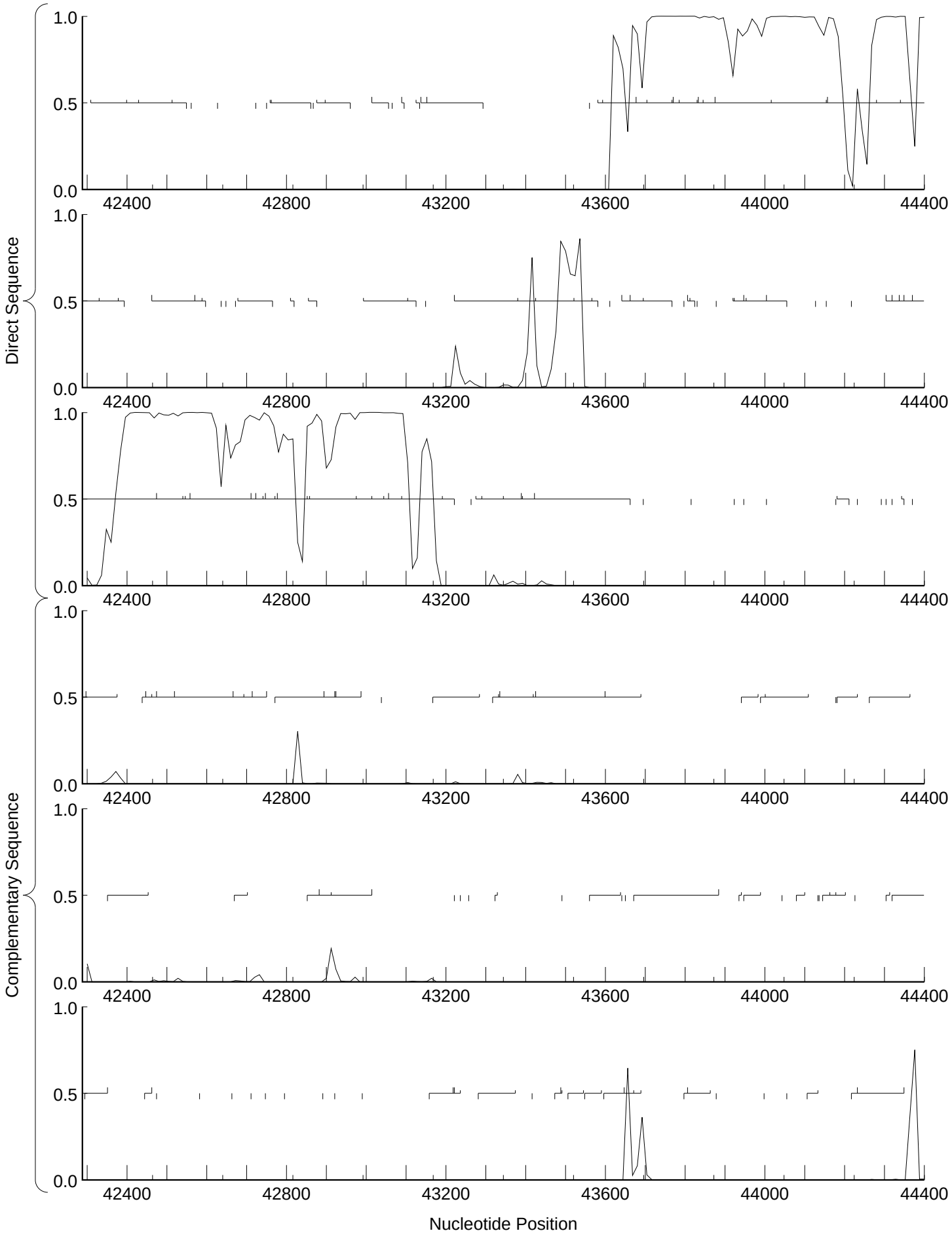
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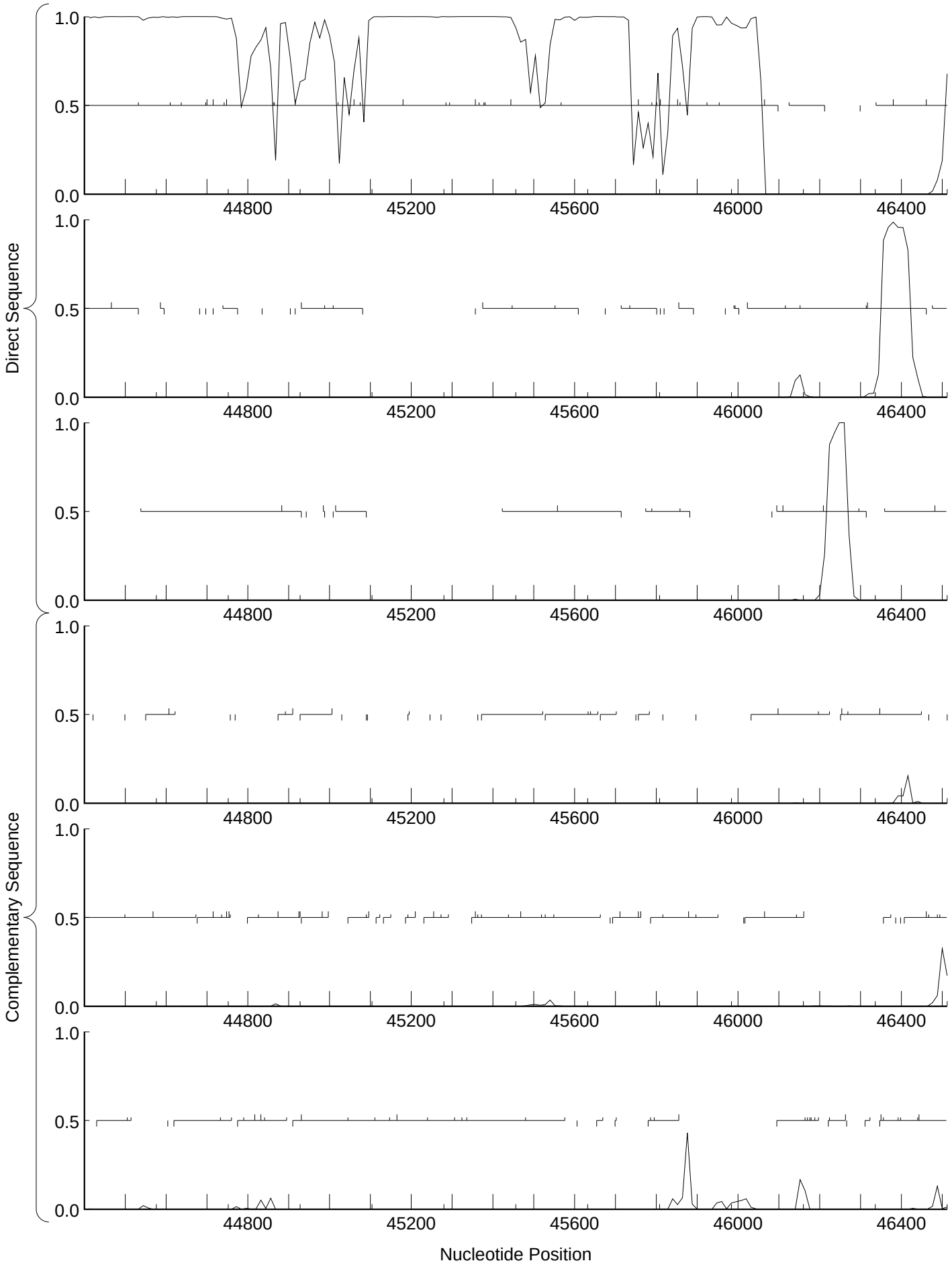
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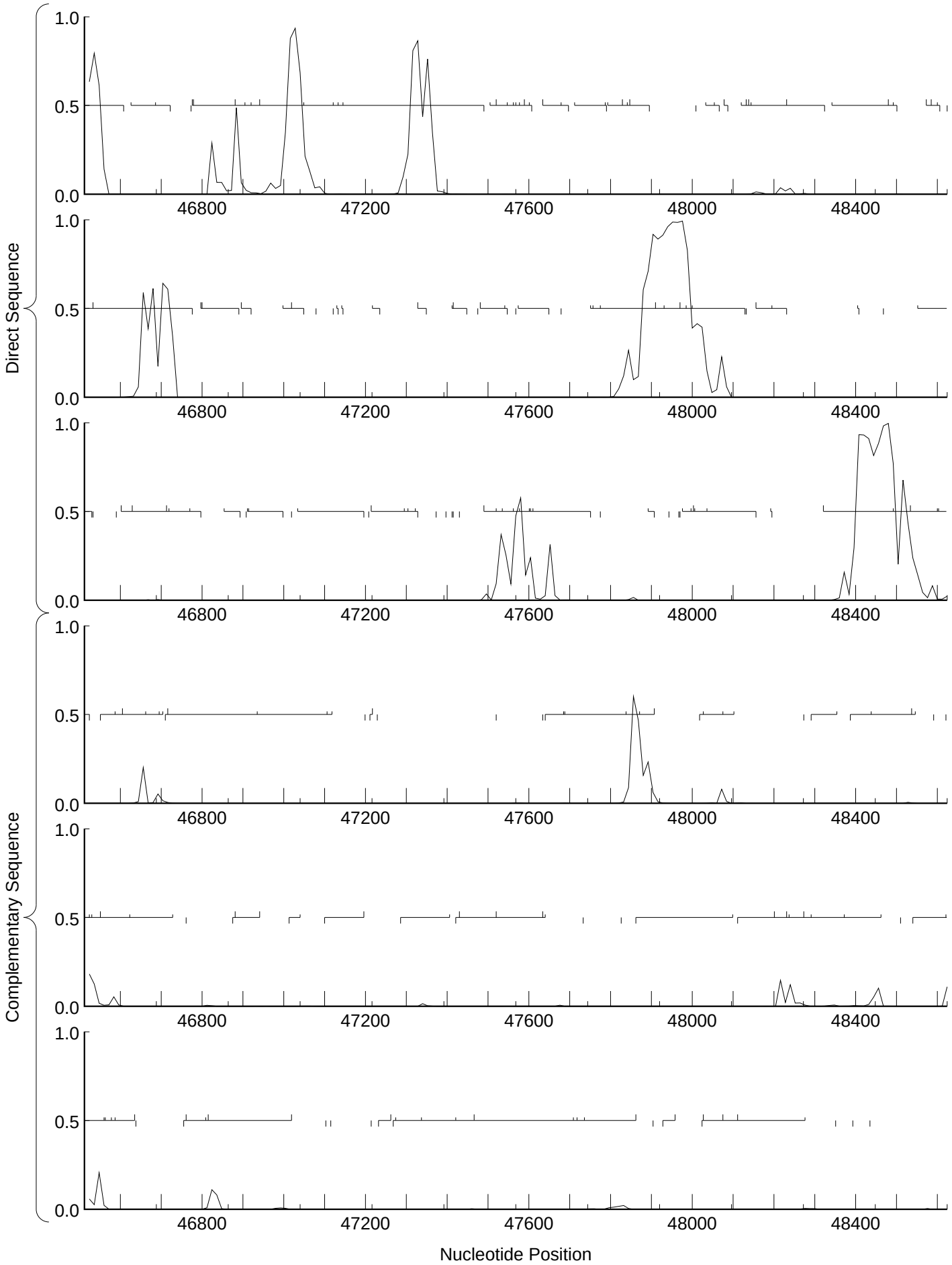
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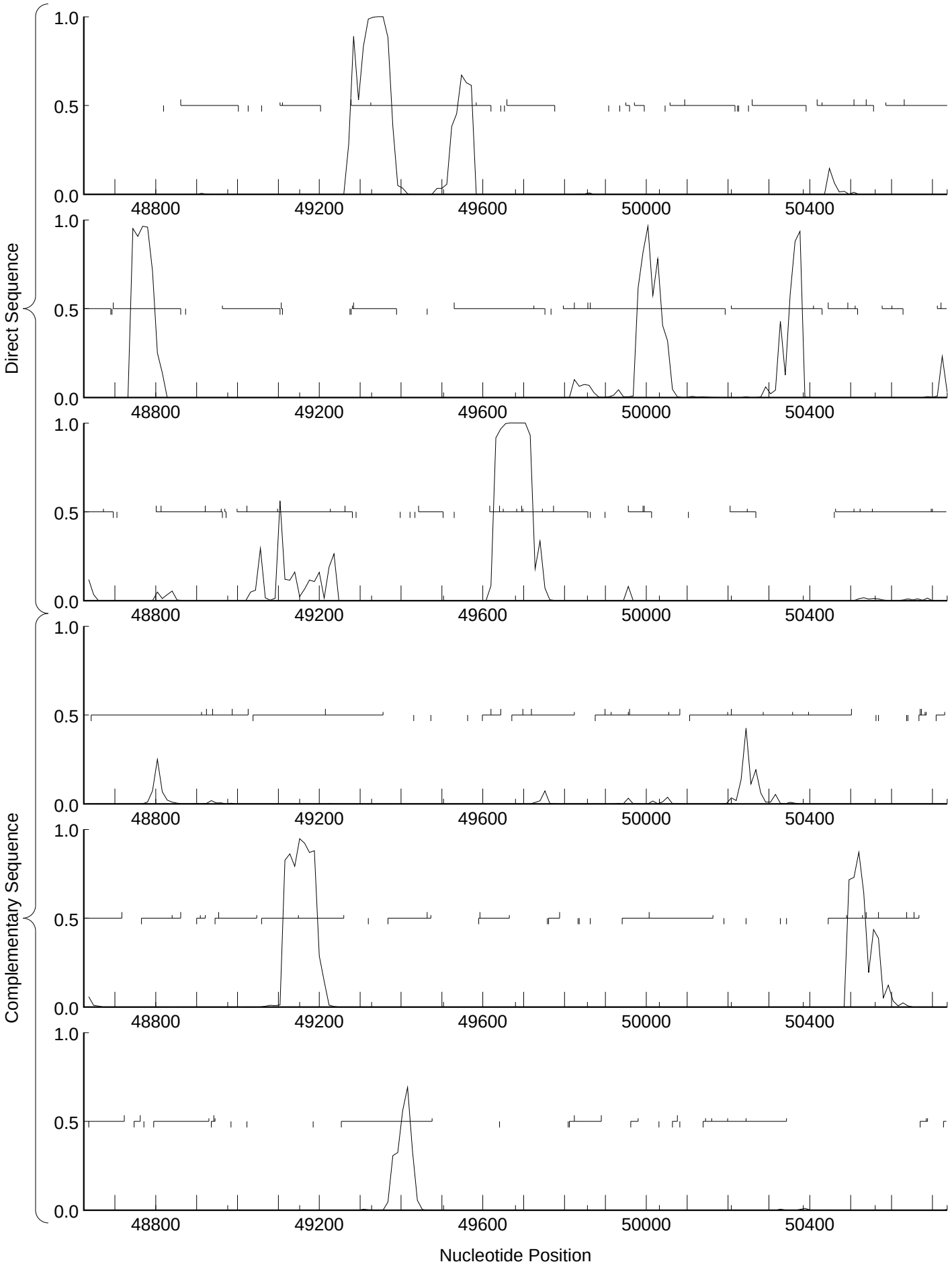
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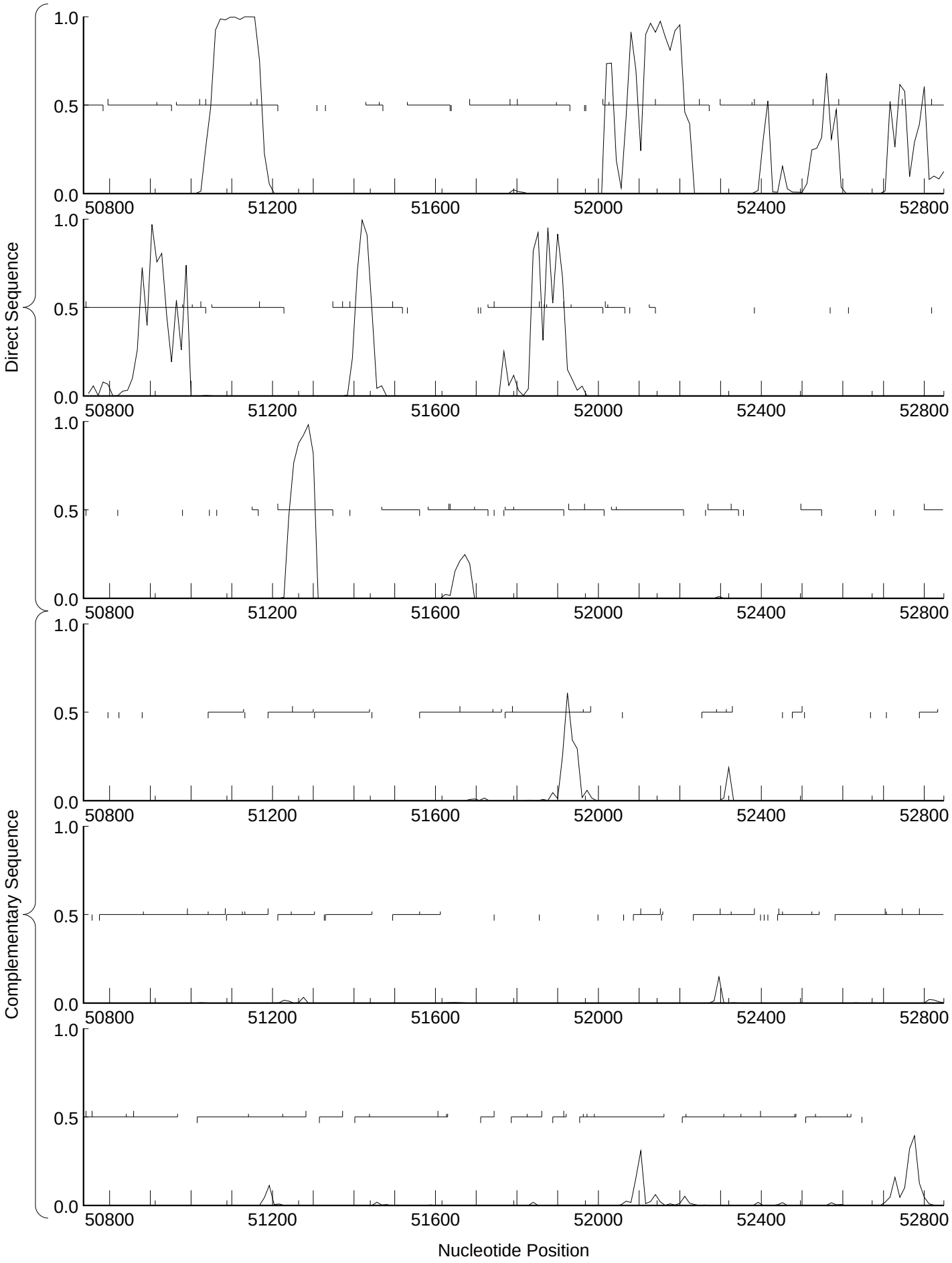
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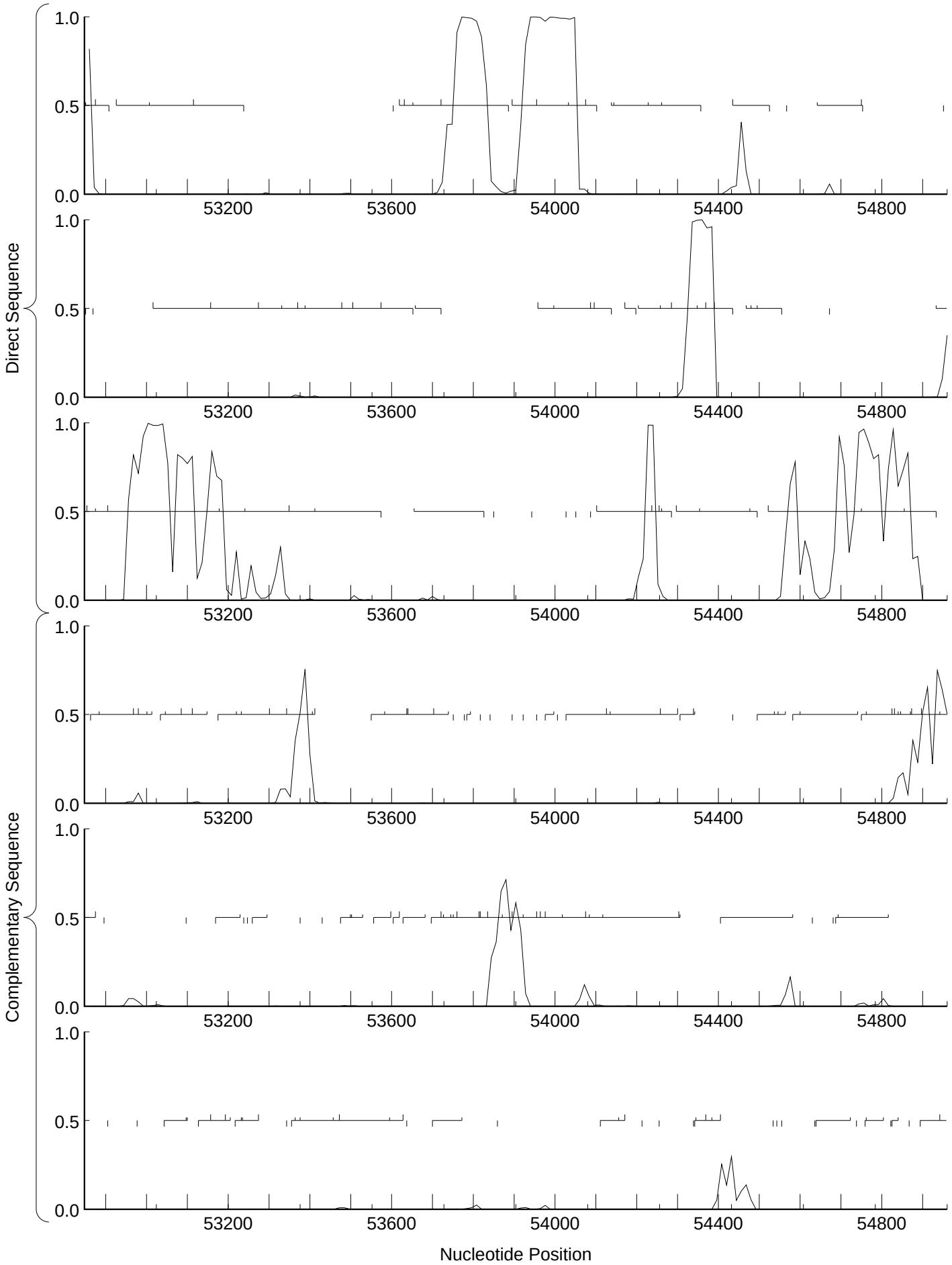
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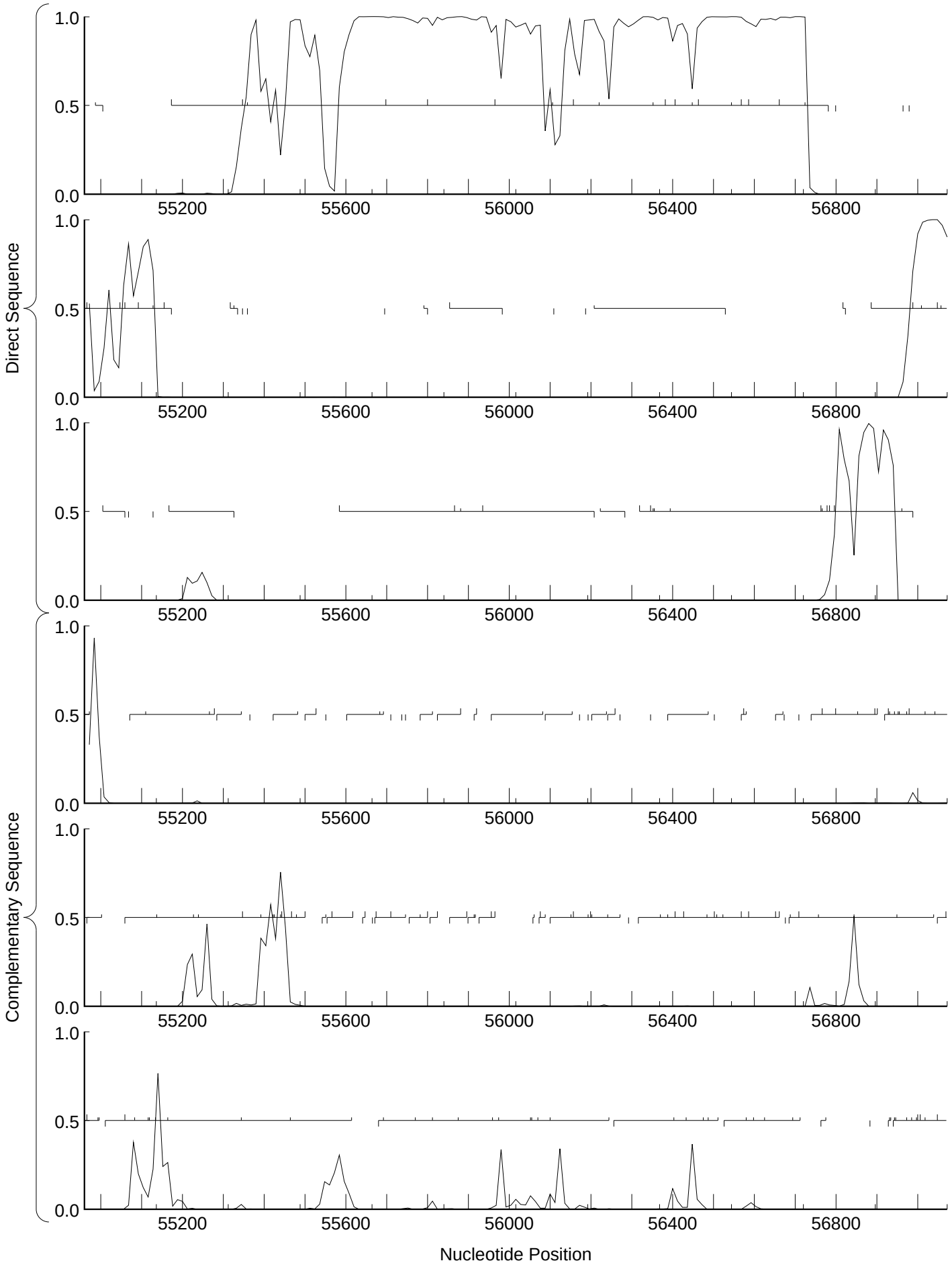
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2 complete sequence, 57693 bp including 10-base 3' overhang (CCGATGGCAT), Cluster F1, Order 4, Window 96, Step 12, 27/29



2 complete sequence, 57693 bp including 10-base 3' overhang (CCGATGGCAT), Cluster F1, Order 4, Window 96, Step 12, 28/29



2 complete sequence, 57693 bp including 10-base 3' overhang (CCGATGGCAT), Cluster F1, Order 4, Window 96, Step 12, 29/29

