GeneMark

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

PROGRAM INFORMATION

```
Sequence         :  Mycobacterium phage Fenn complete sequence, 53449 bp including 10-base 3' overhang (CGGATGG
Analysis Date    :  3/29/24 at 1:01:51
Pages            :  27
Sequence Length  :  53449 bp
GC Content       :   63.67%

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

PS-Version       :  1.2

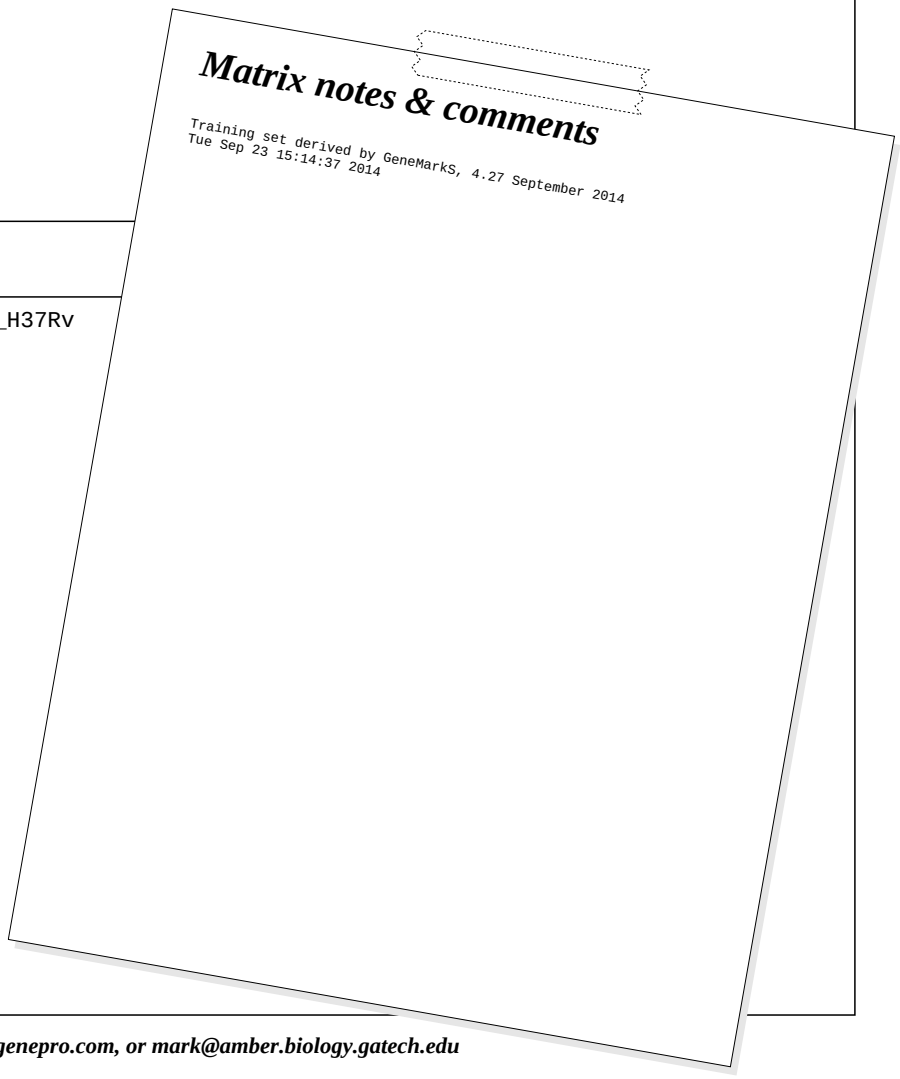
GeneMark Options :  PostScript graph,
                    Mark ORFs / splice sites,
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                    List regions and/or splice sites,
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MATRIX INFORMATION

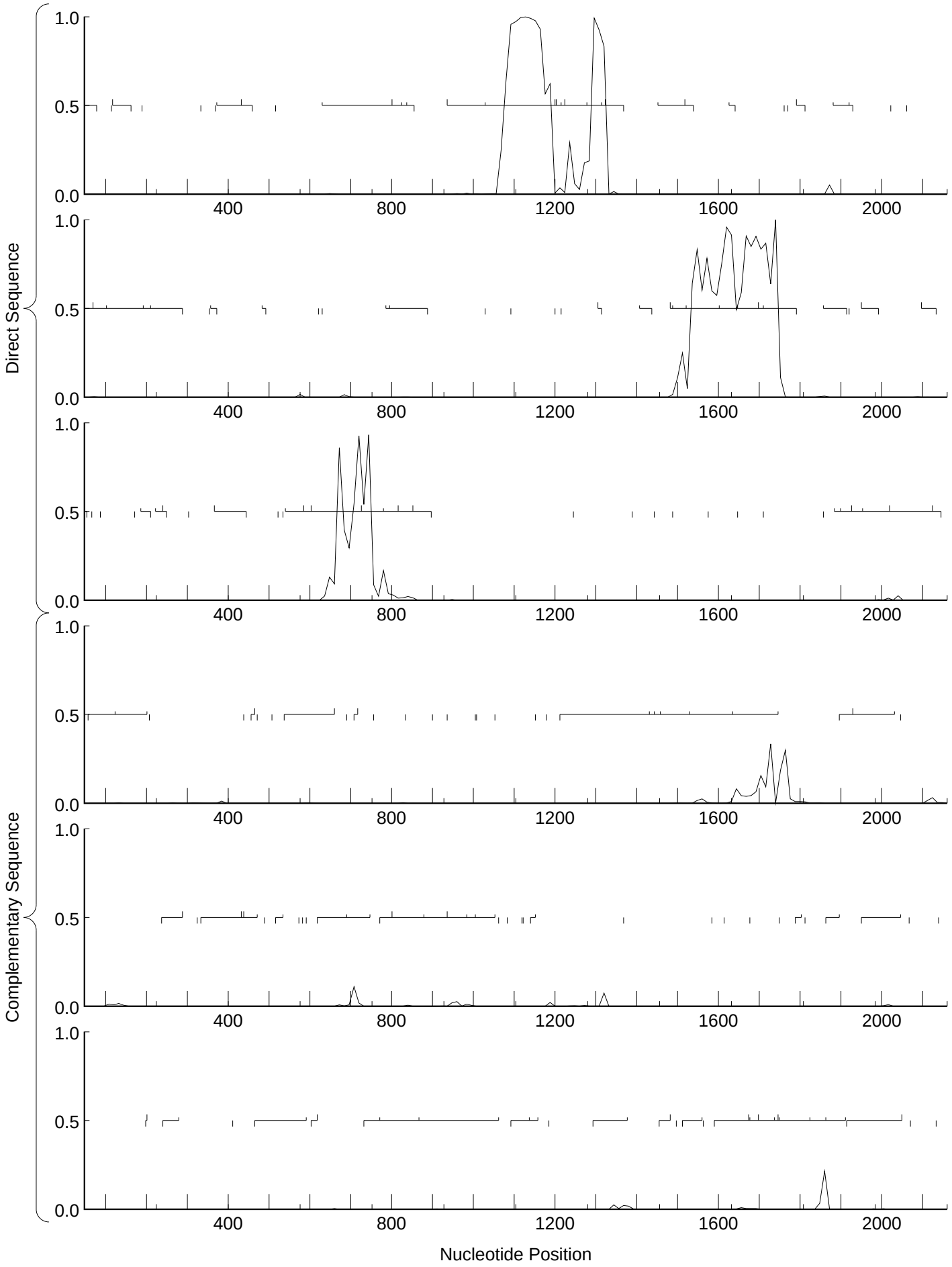
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Matrix     :  Mycobacterium_tuberculosis_H37Rv
Author     :  -

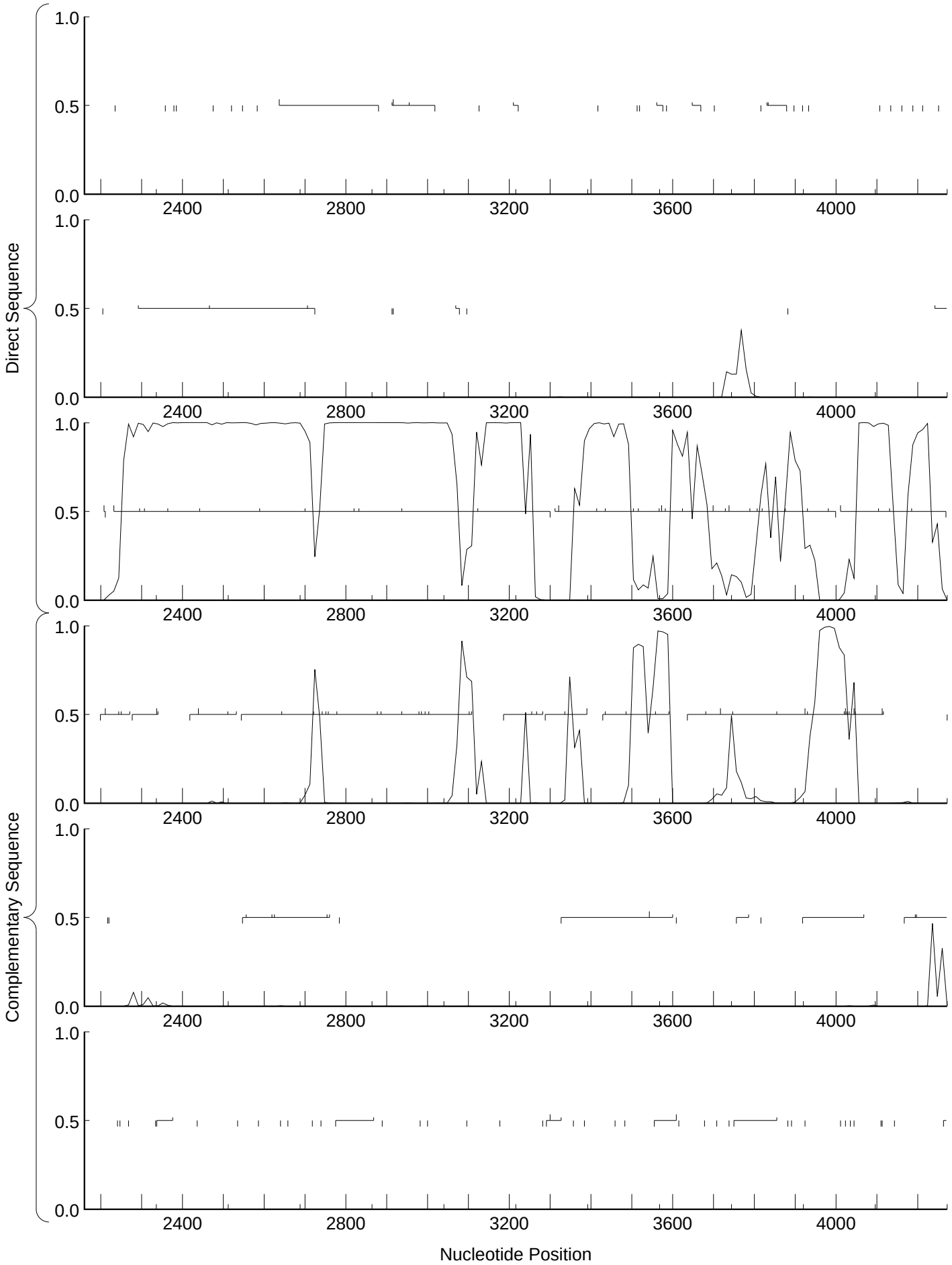
Order      :  4


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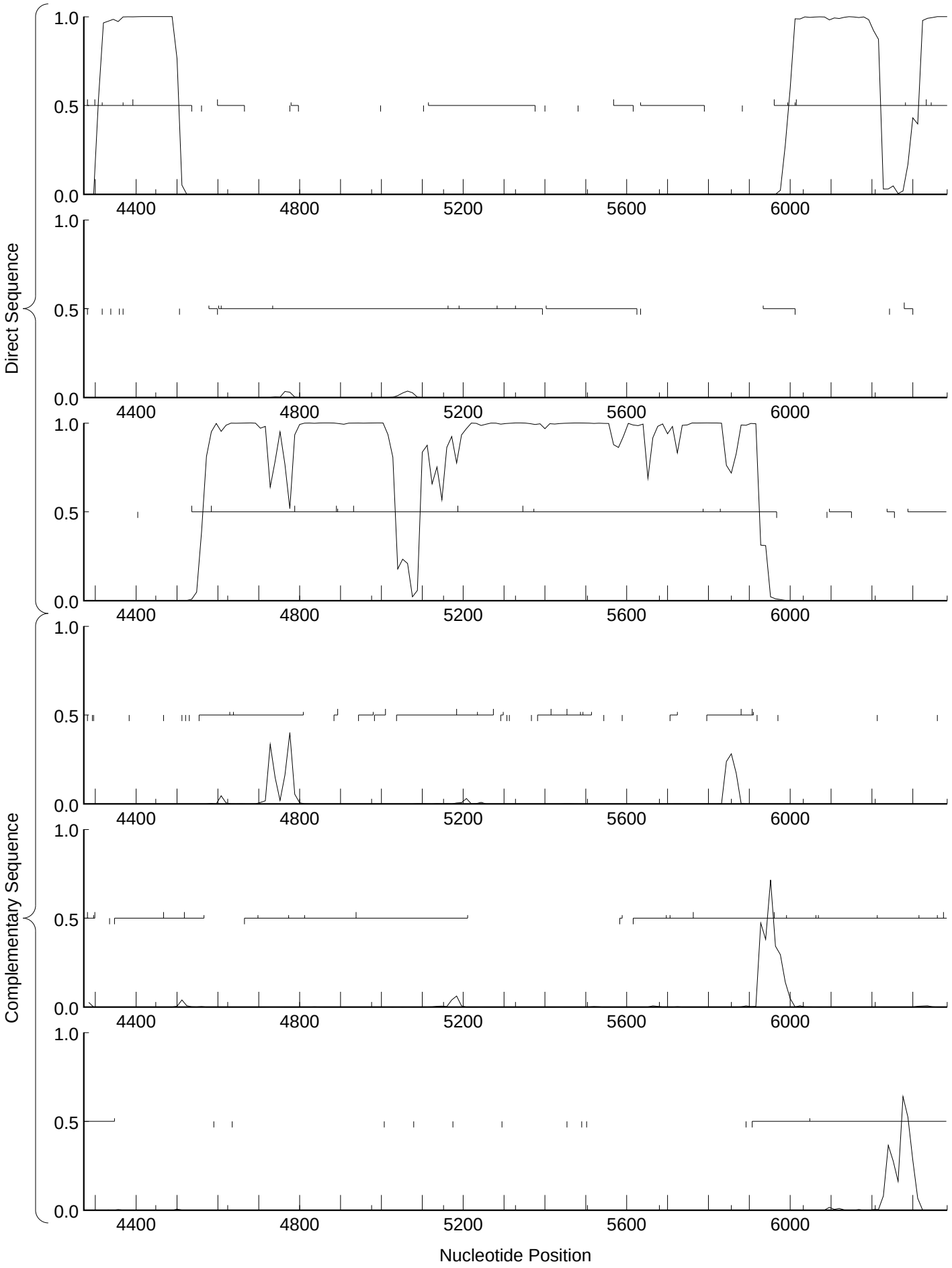


For help or information, send electronic mail to: custserv@genepro.com, or mark@amber.biology.gatech.edu

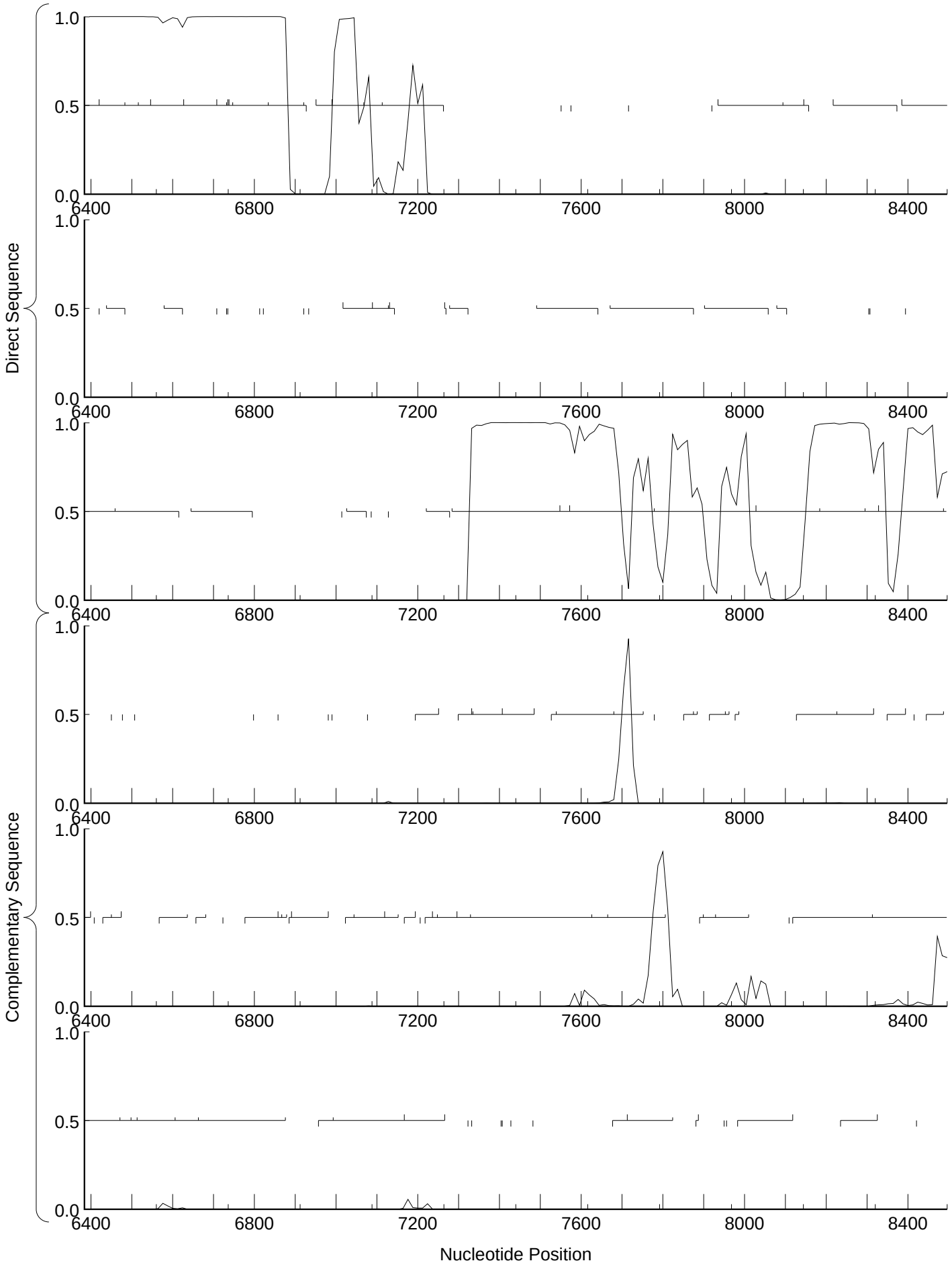

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Complementary Sequence
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800
1200
1600
2000
Nucleotide Position

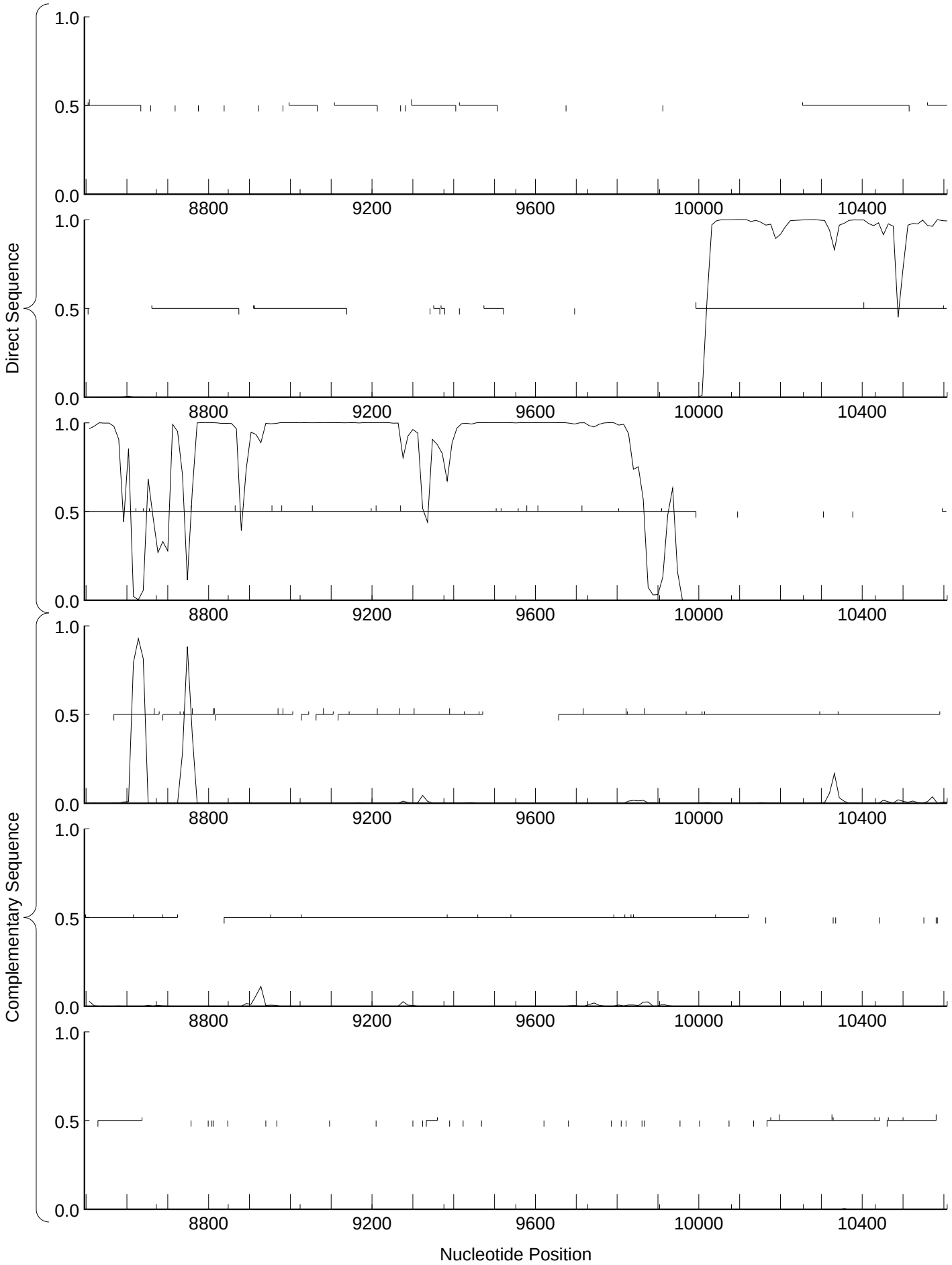

Direct Sequence
Complementary Sequence
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0.0
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3200
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4000
Nucleotide Position

n complete sequence, 53449 bp including 10-base 3’ overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 4/27

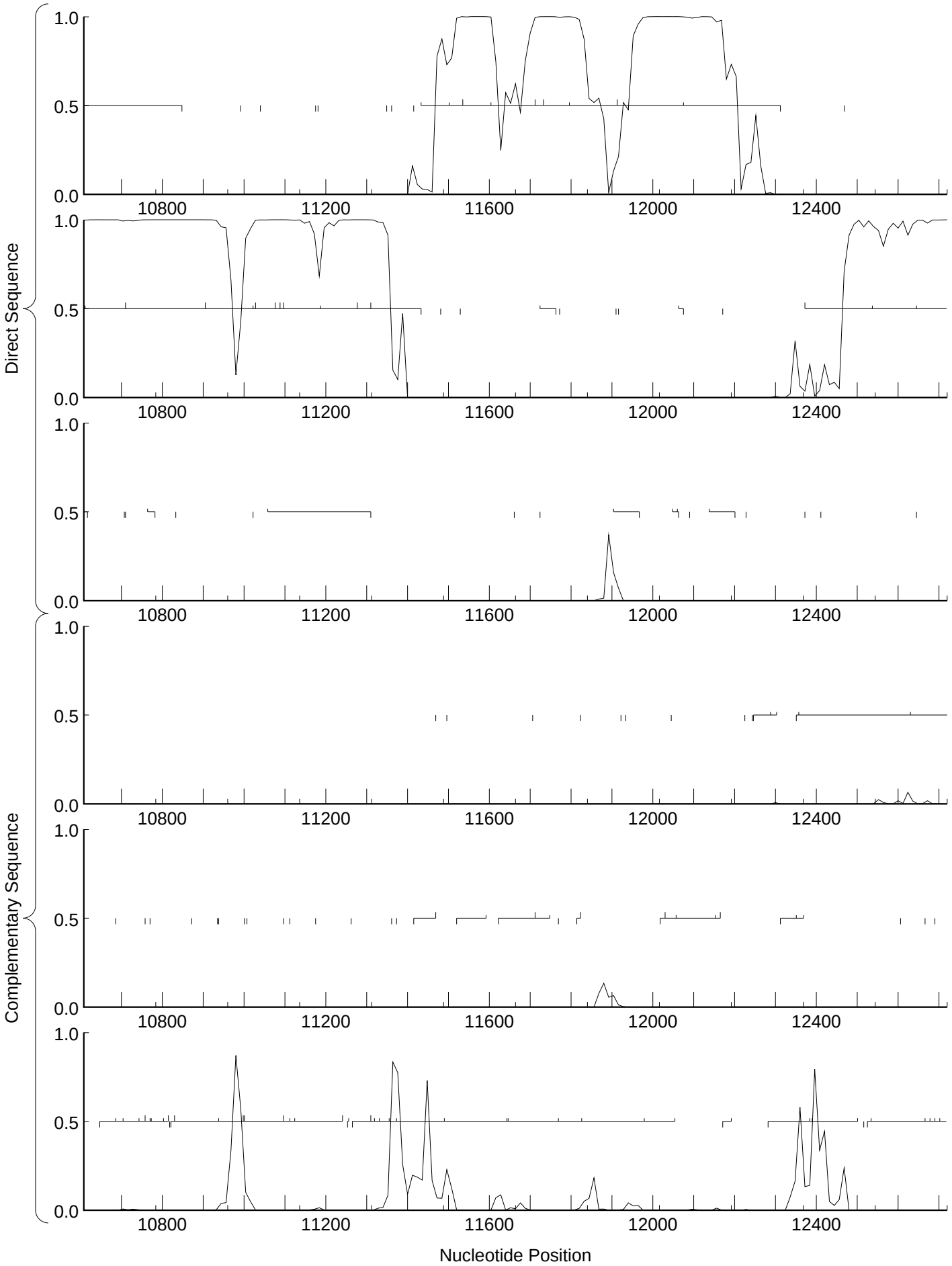


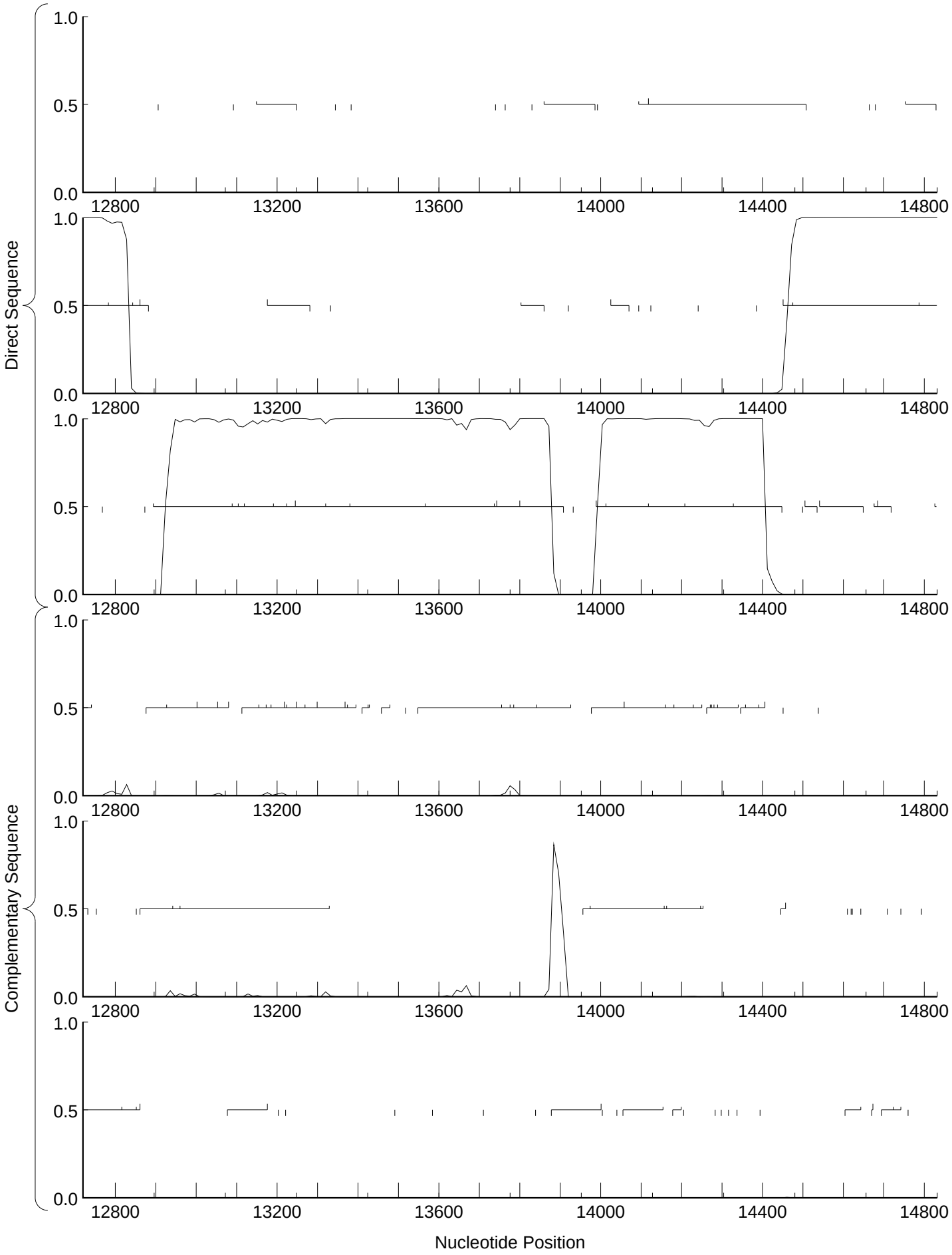
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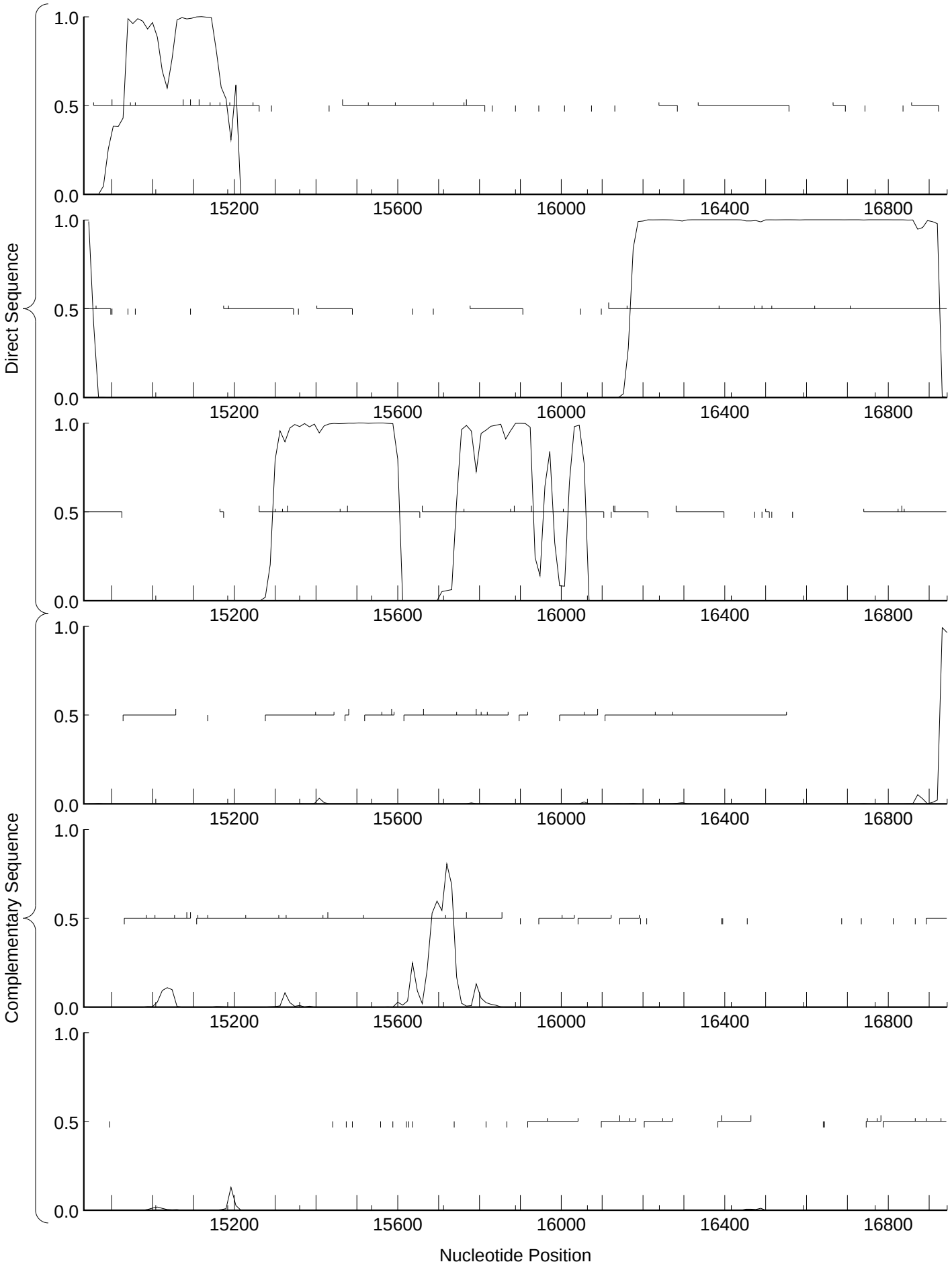

Direct Sequence
Complementary Sequence
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0.0
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10400
Nucleotide Position

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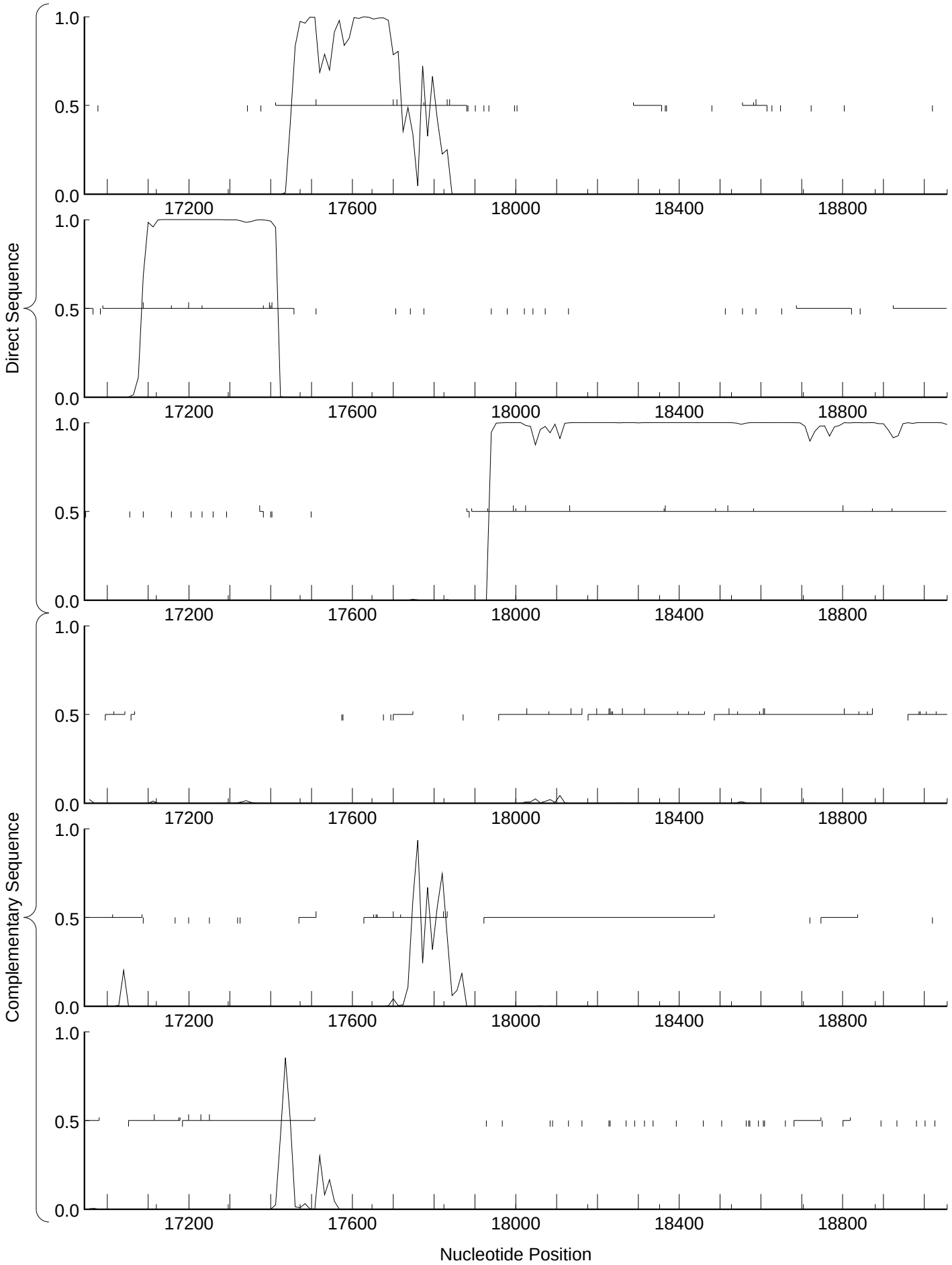



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14800
Nucleotide Position

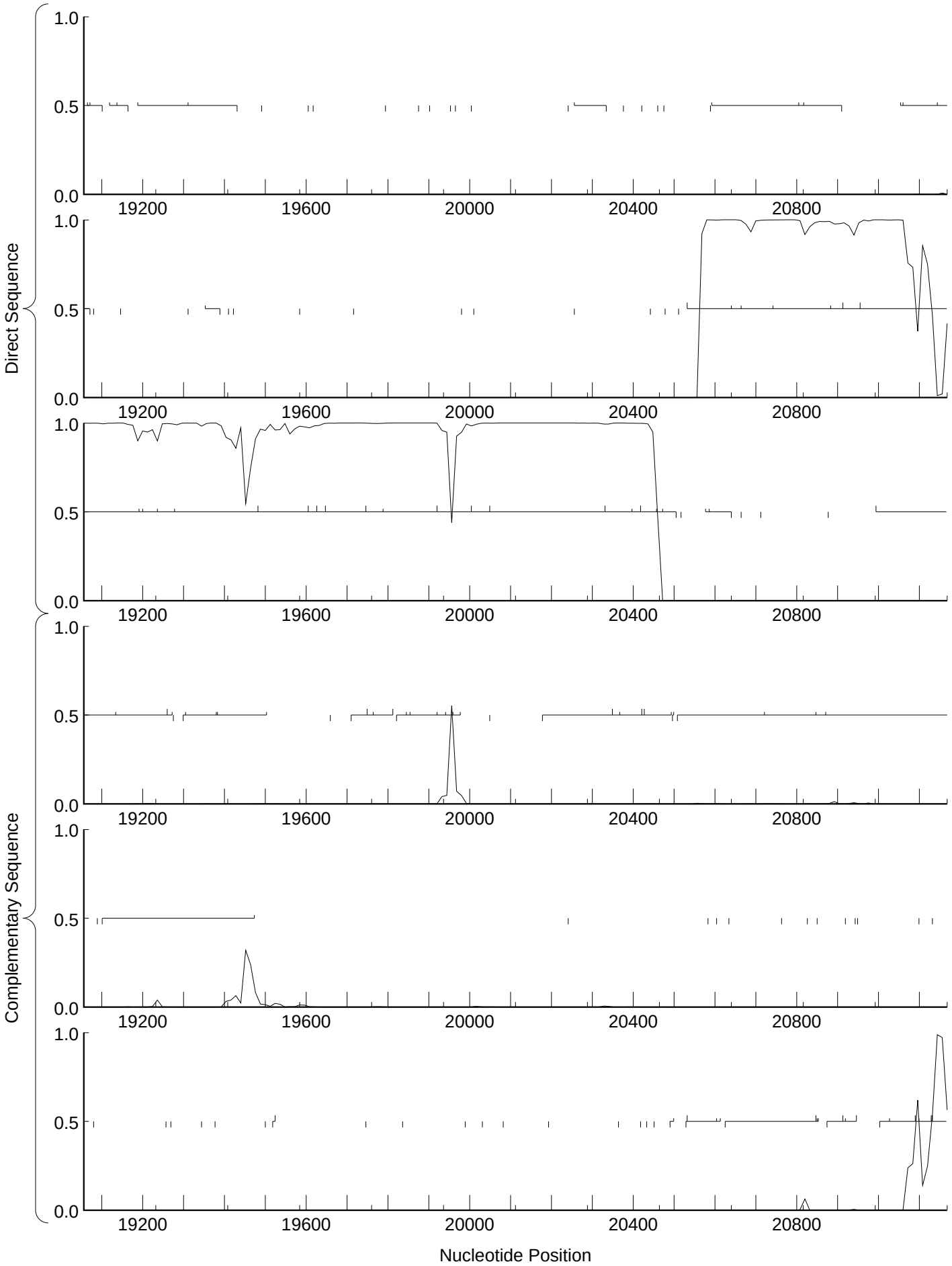
n complete sequence, 53449 bp including 10-base 3’ overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 9/27



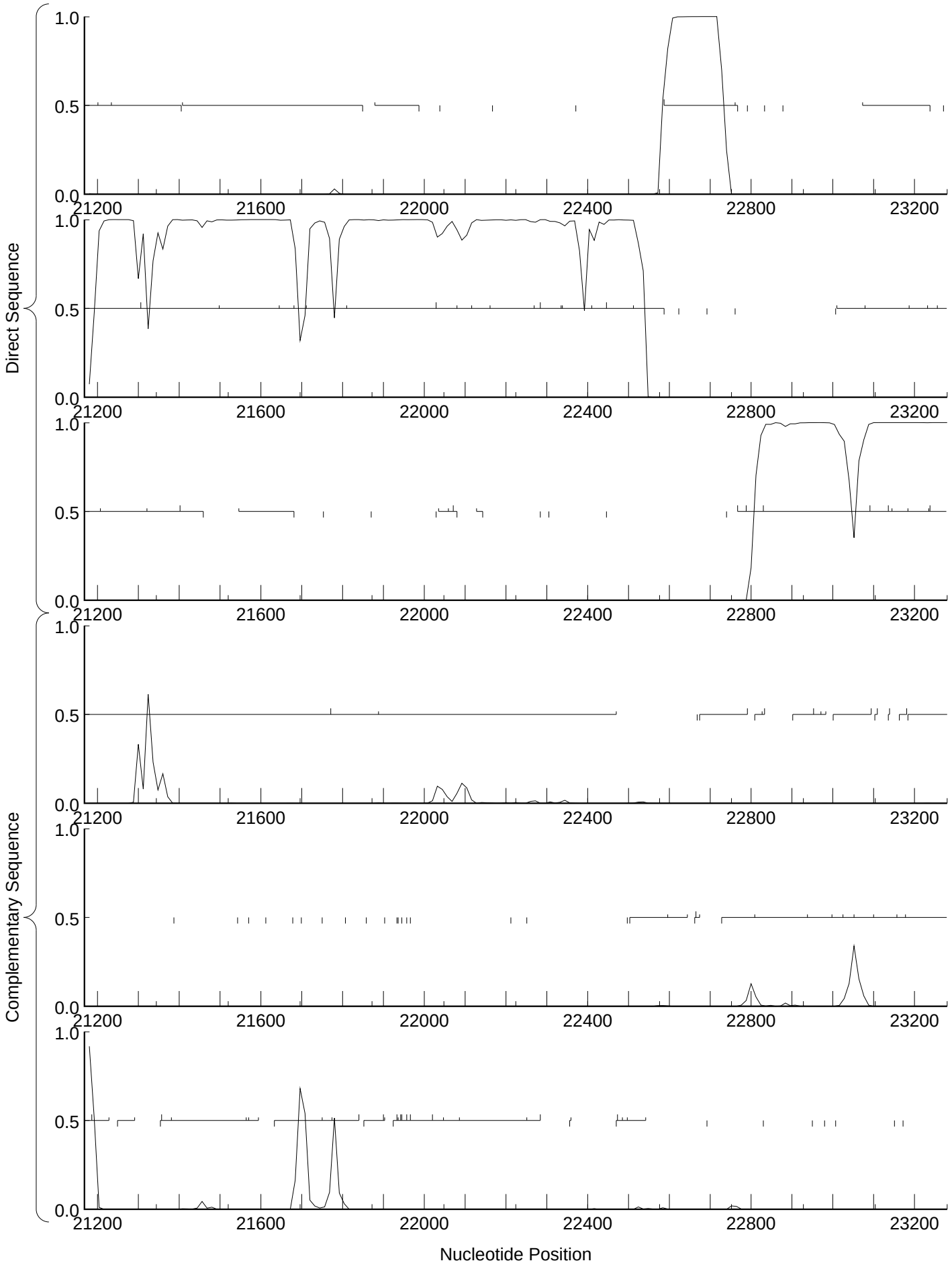
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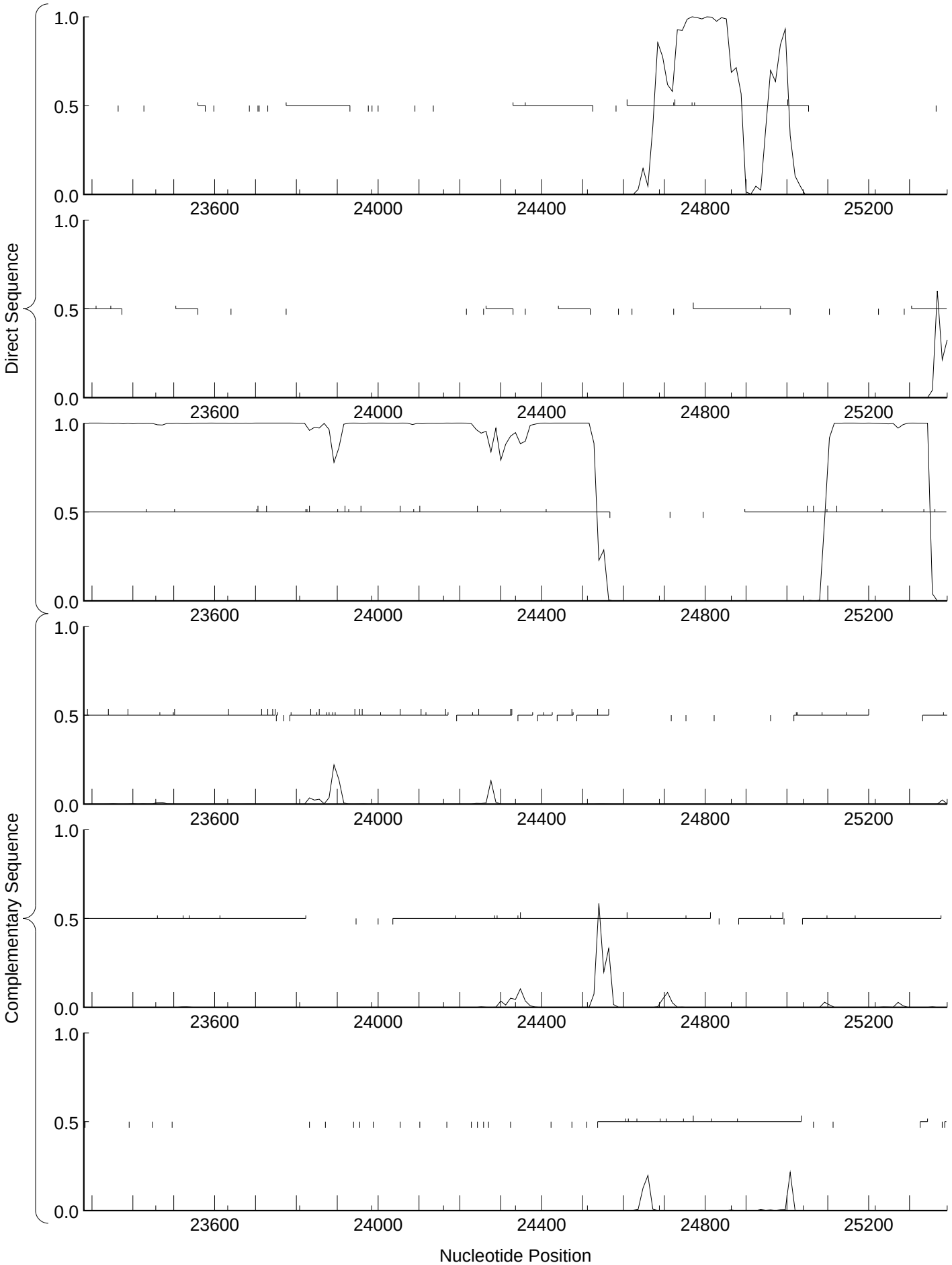
n complete sequence, 53449 bp including 10-base 3’ overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 11/27



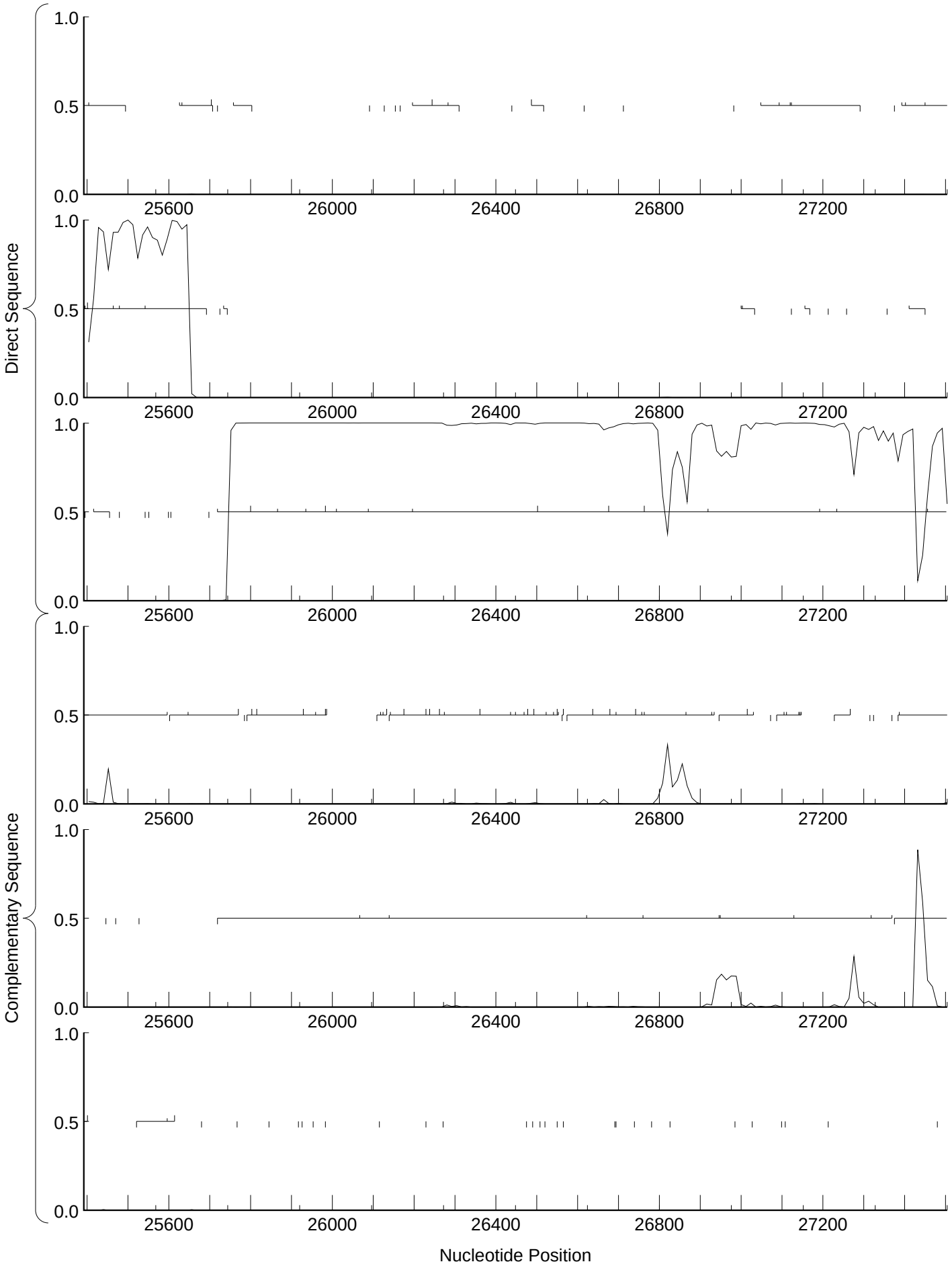
n complete sequence, 53449 bp including 10-base 3’ overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 12/27



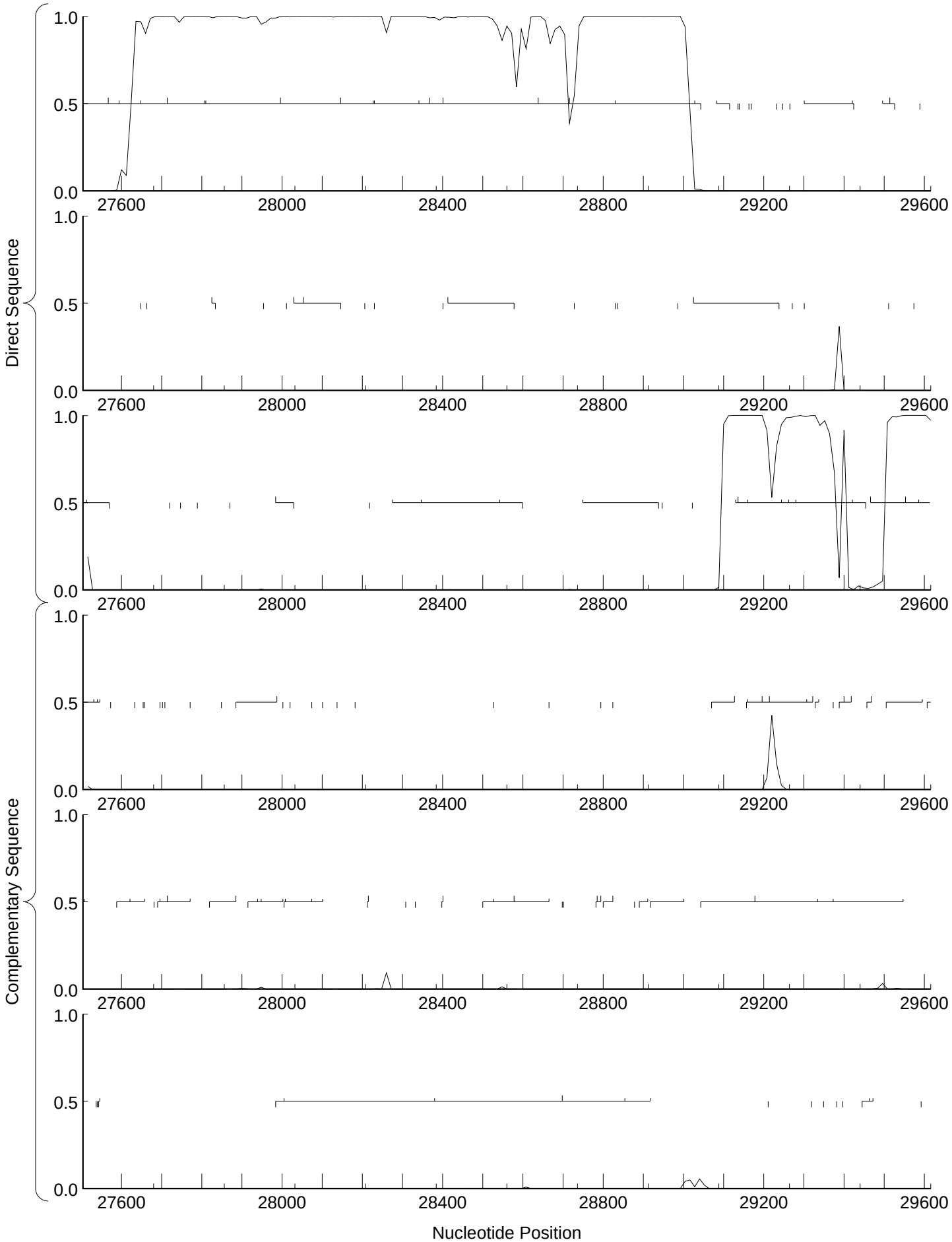
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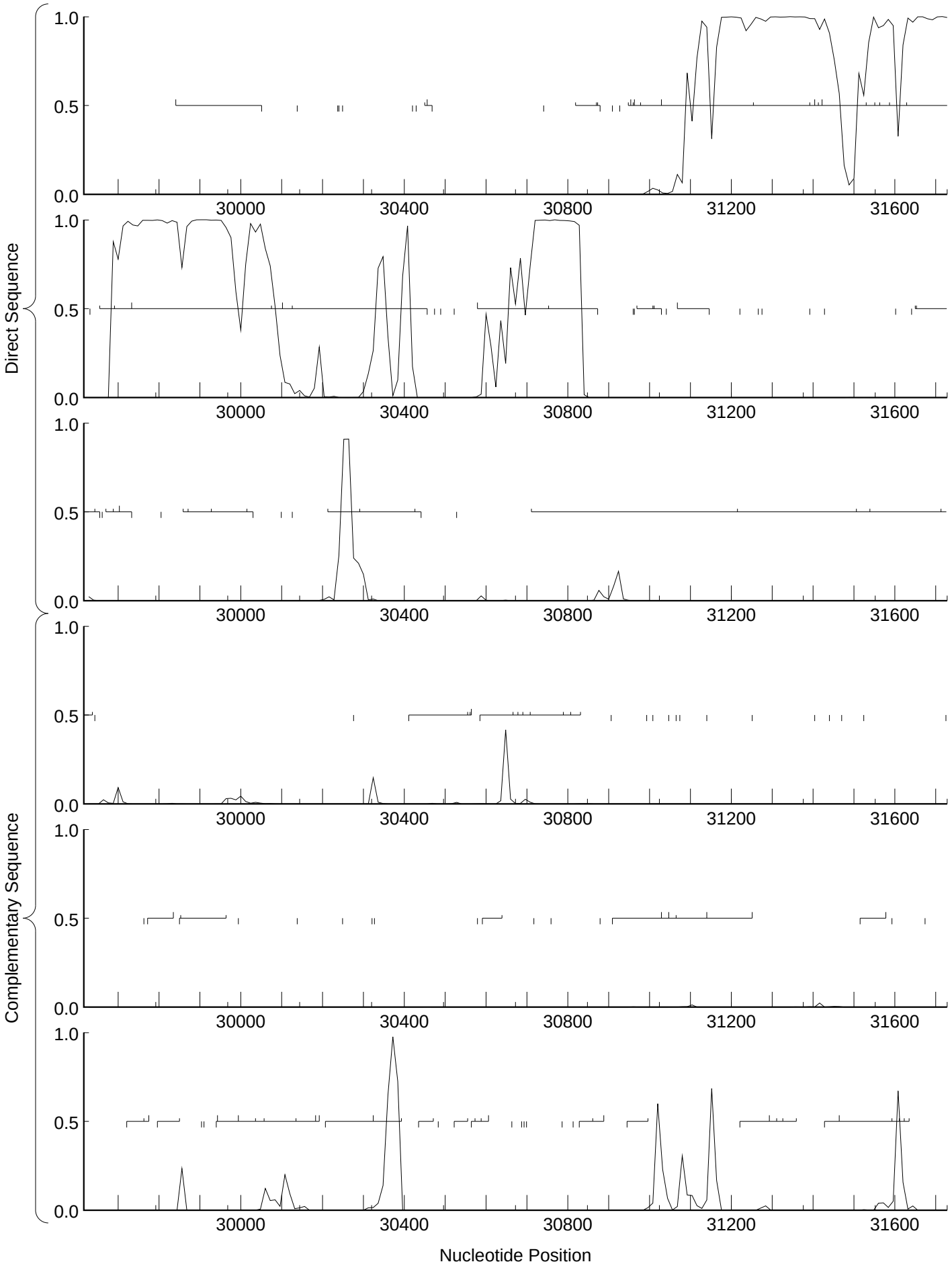
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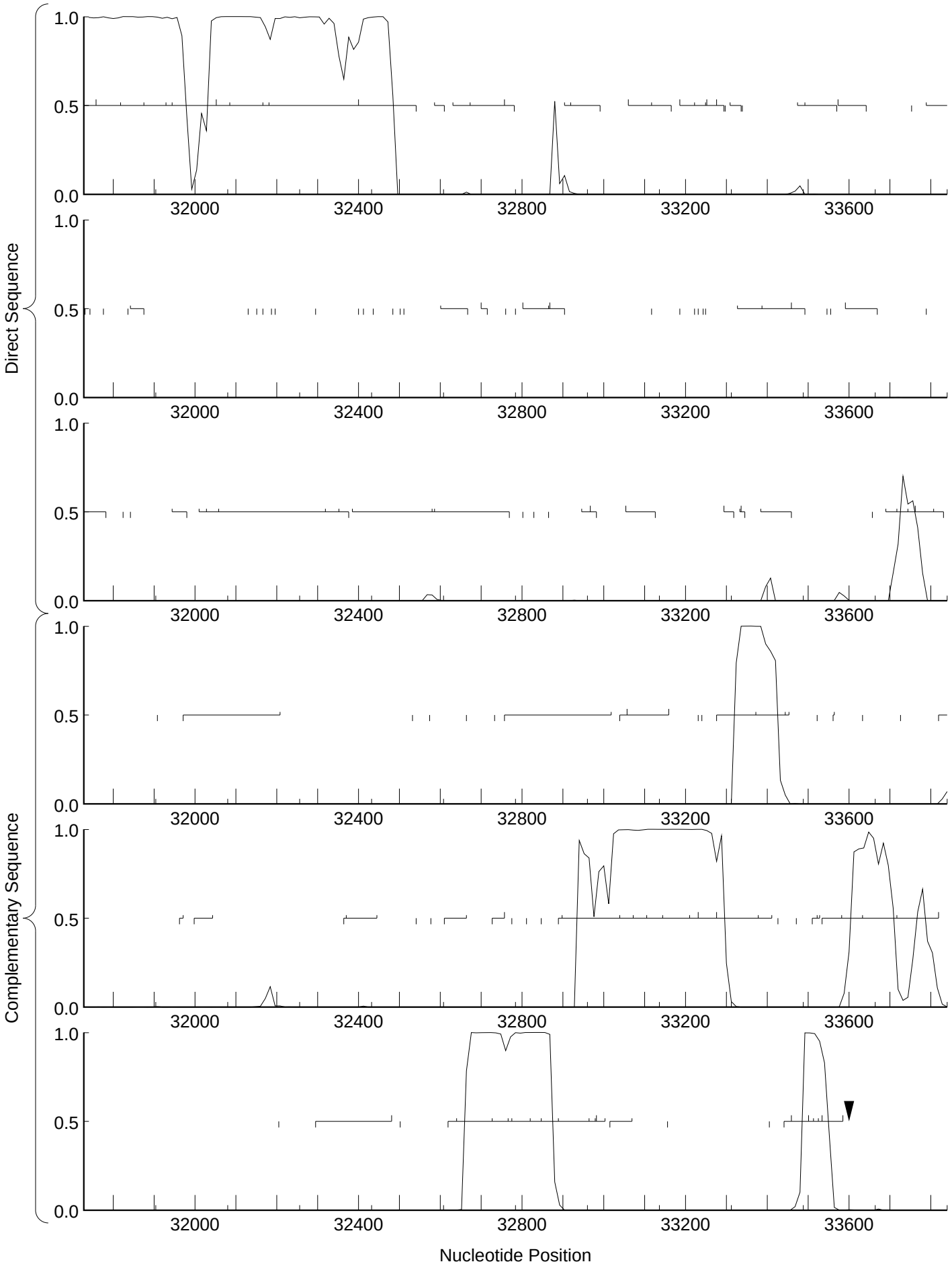
n complete sequence, 53449 bp including 10-base 3' overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 15/27

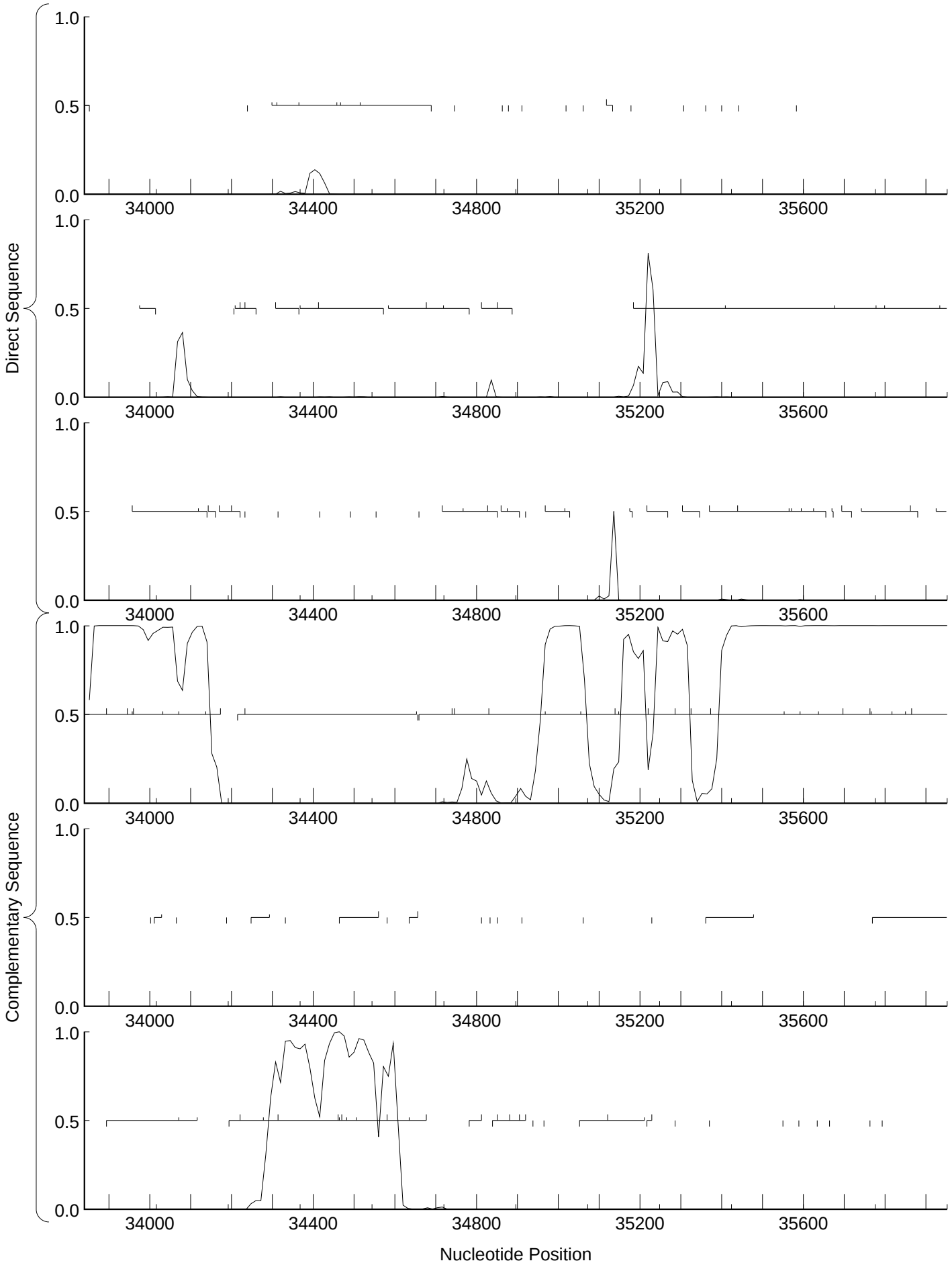


n complete sequence, 53449 bp including 10-base 3’ overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 16/27

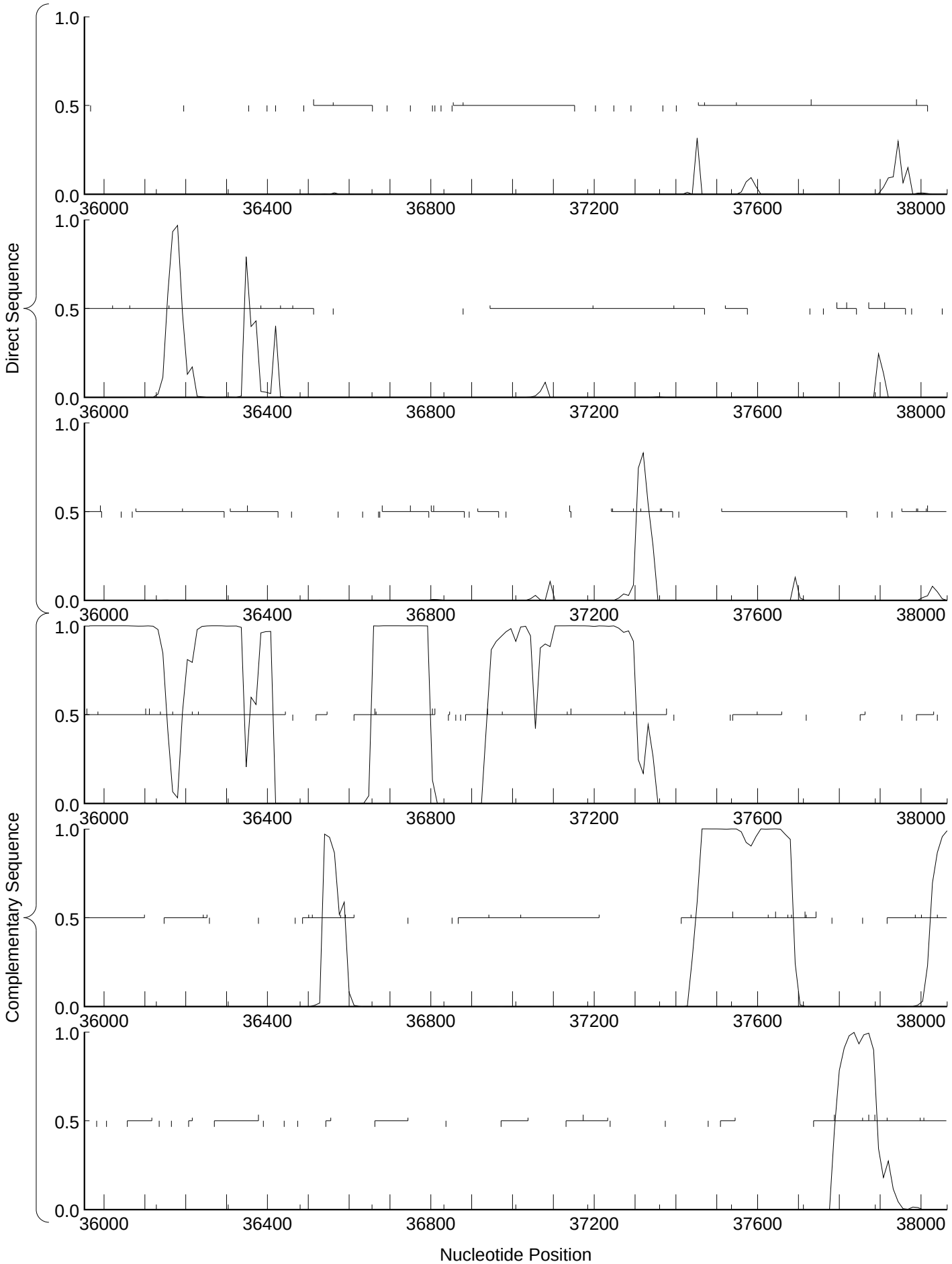


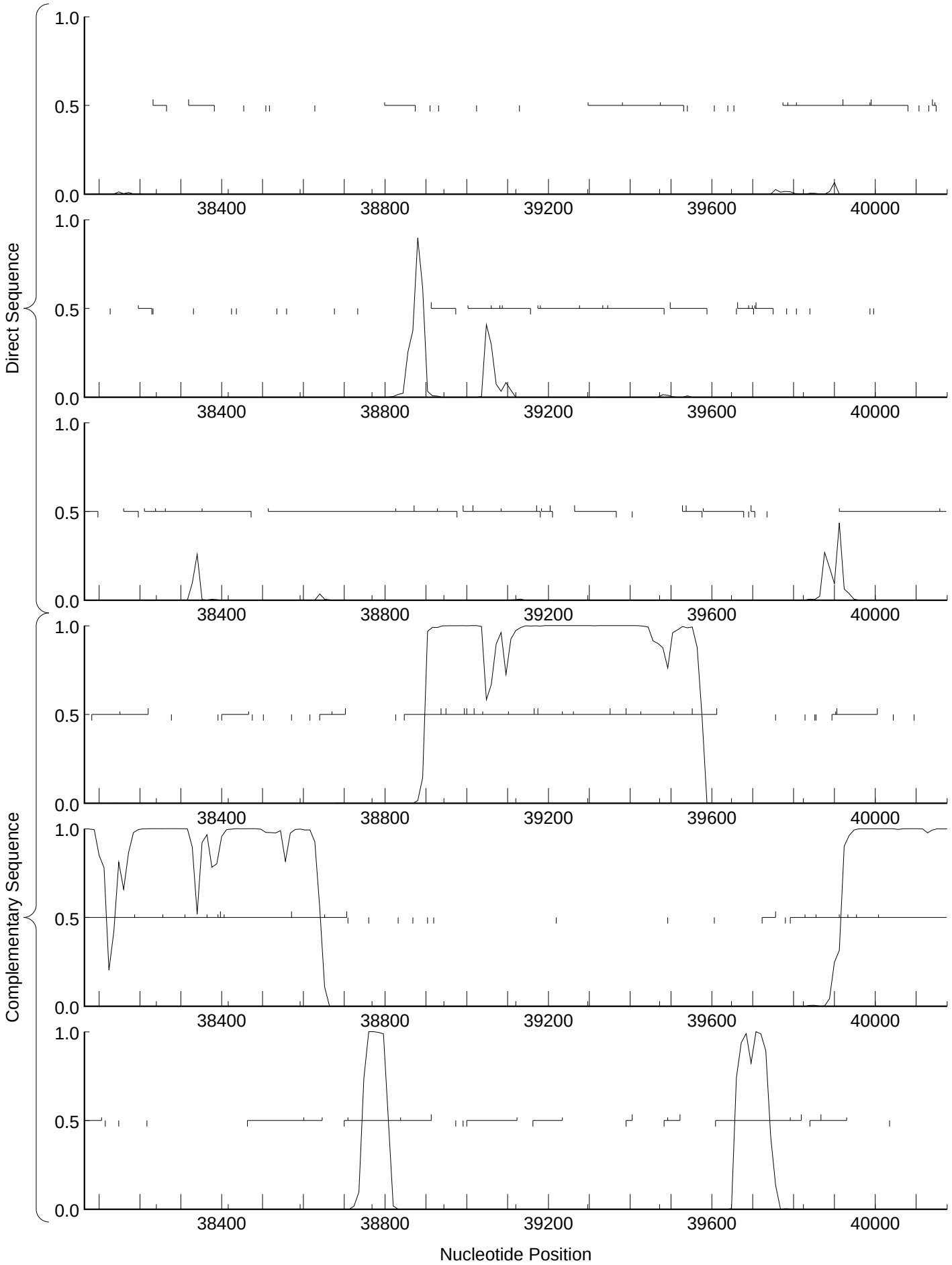
n complete sequence, 53449 bp including 10-base 3' overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 17/27



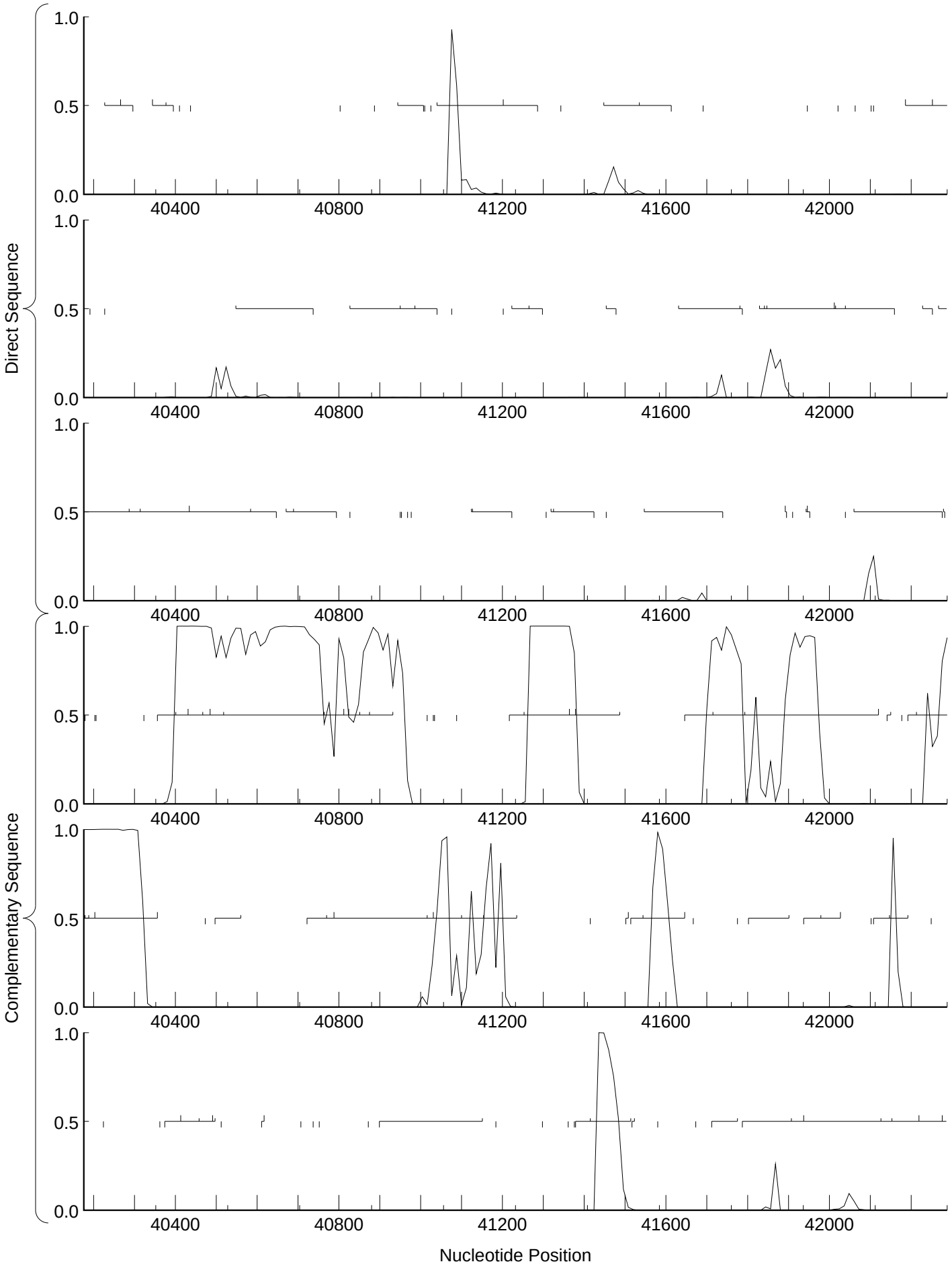

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Complementary Sequence
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0.5
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34000
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34800
35200
35600
Nucleotide Position

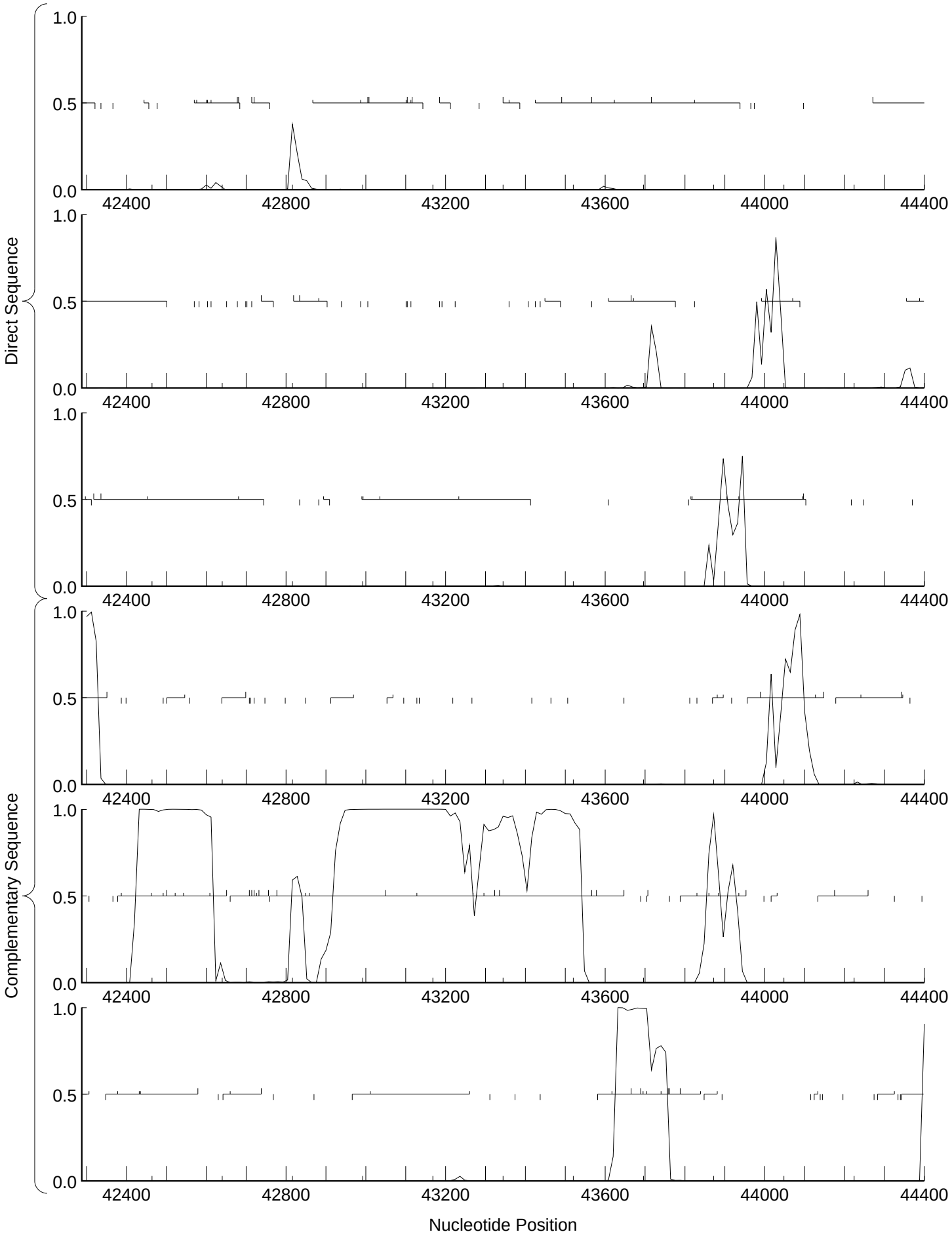
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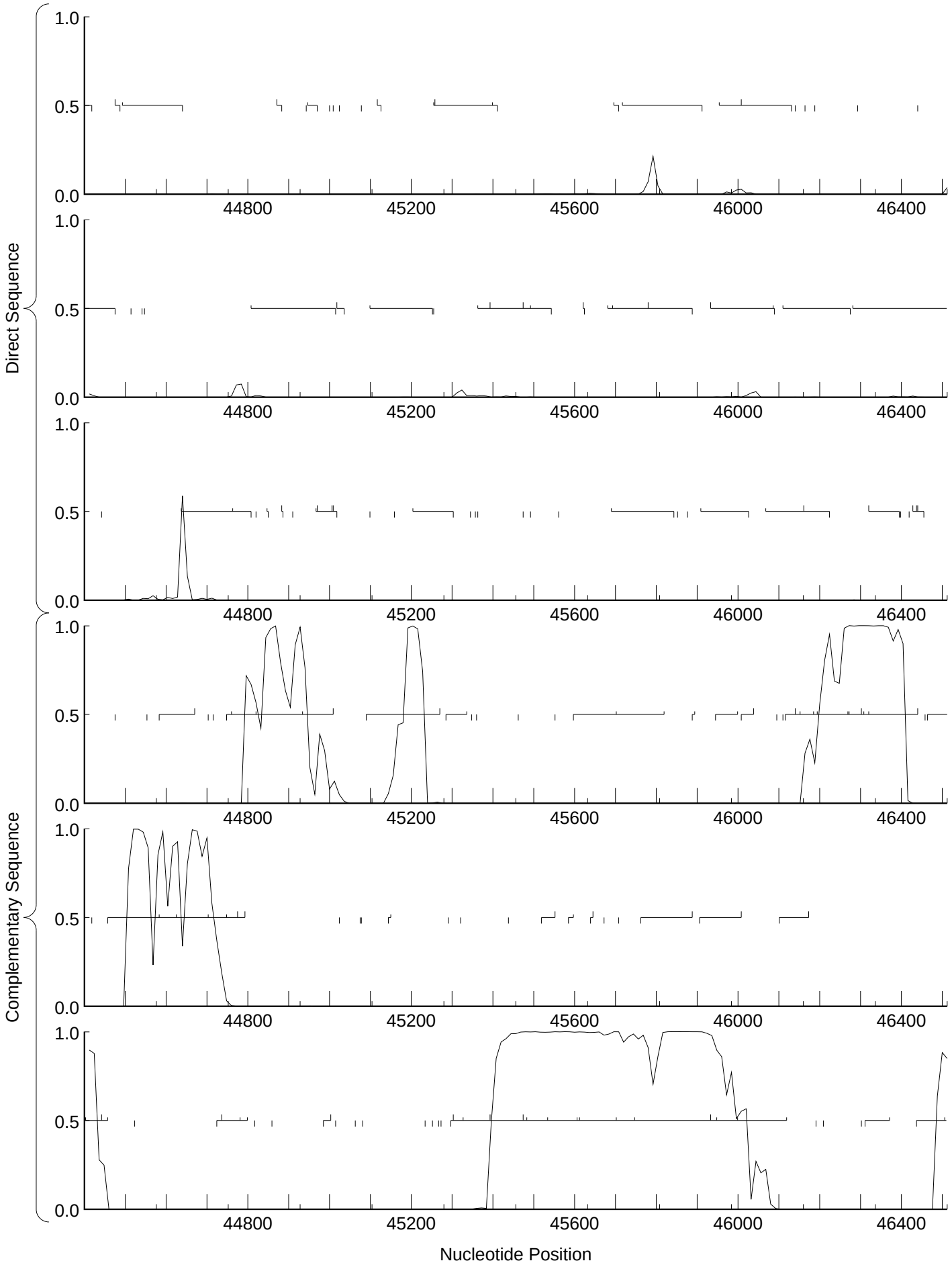

Direct Sequence
Complementary Sequence
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0.5
0.0
38400
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40000
Nucleotide Position

n complete sequence, 53449 bp including 10-base 3’ overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 21/27

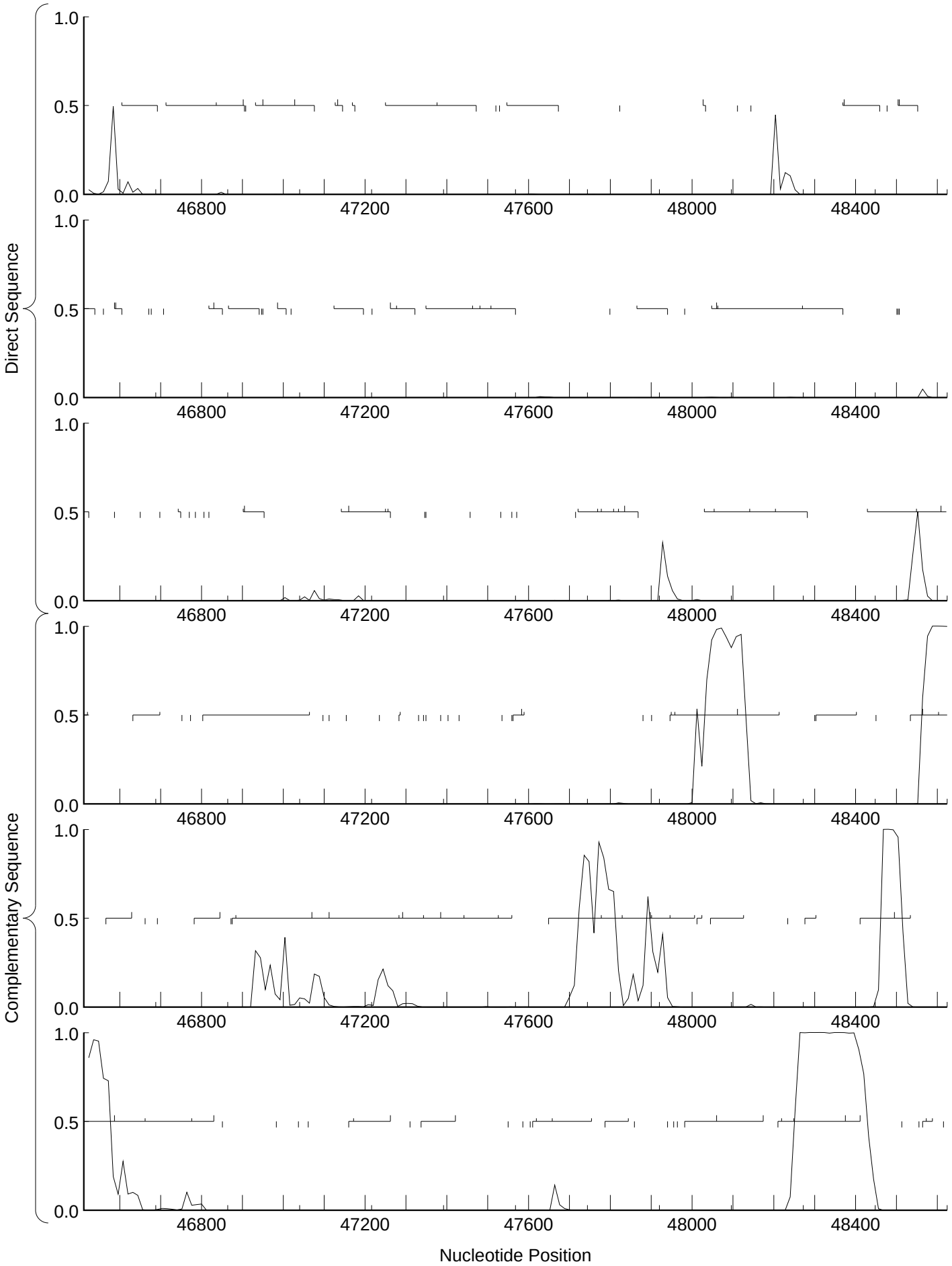



Direct Sequence
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43600
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Nucleotide Position

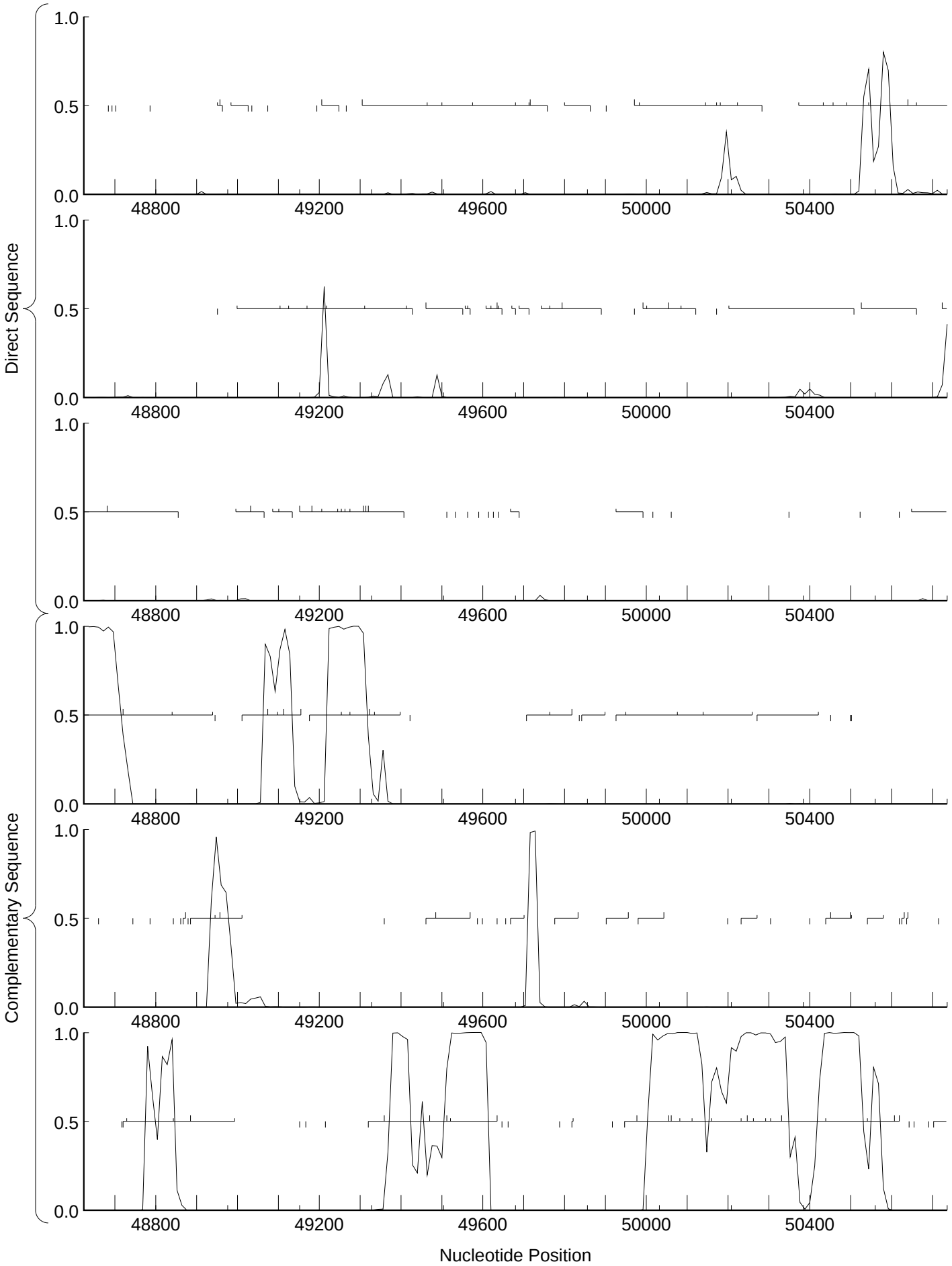
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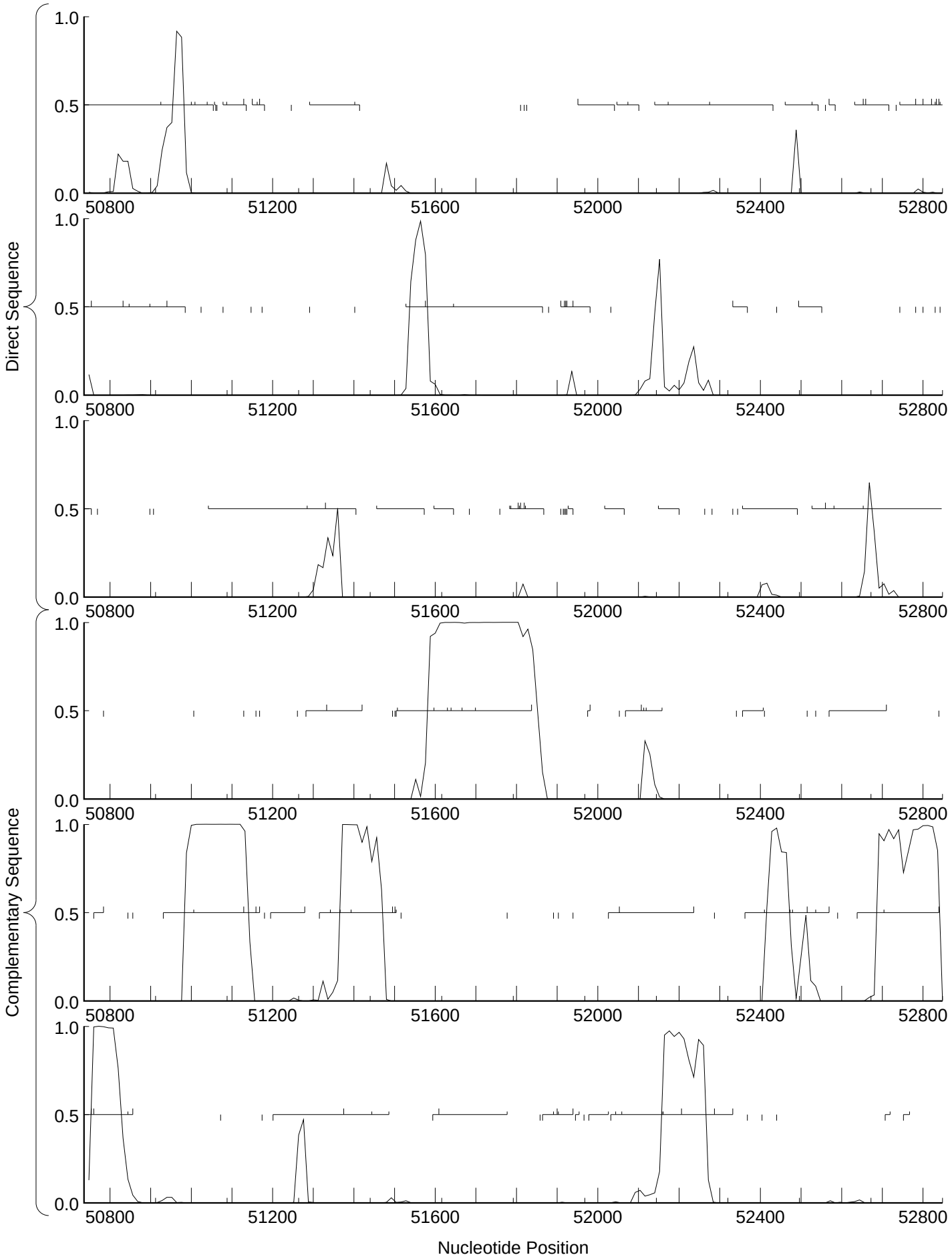
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n complete sequence, 53449 bp including 10-base 3’ overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 25/27



n complete sequence, 53449 bp including 10-base 3’ overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 26/27



n complete sequence, 53449 bp including 10-base 3’ overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 27/27

