GeneMark

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

PROGRAM INFORMATION

```
Sequence         :  Mycobacterium phage Hyperbowlee complete sequence, 59905 bp including 11-base 3’ overhang (
Analysis Date    :  3/28/24 at 15:58:45
Pages            :  30
Sequence Length  :  59905 bp
GC Content       :   66.56%

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

PS-Version       :  1.2

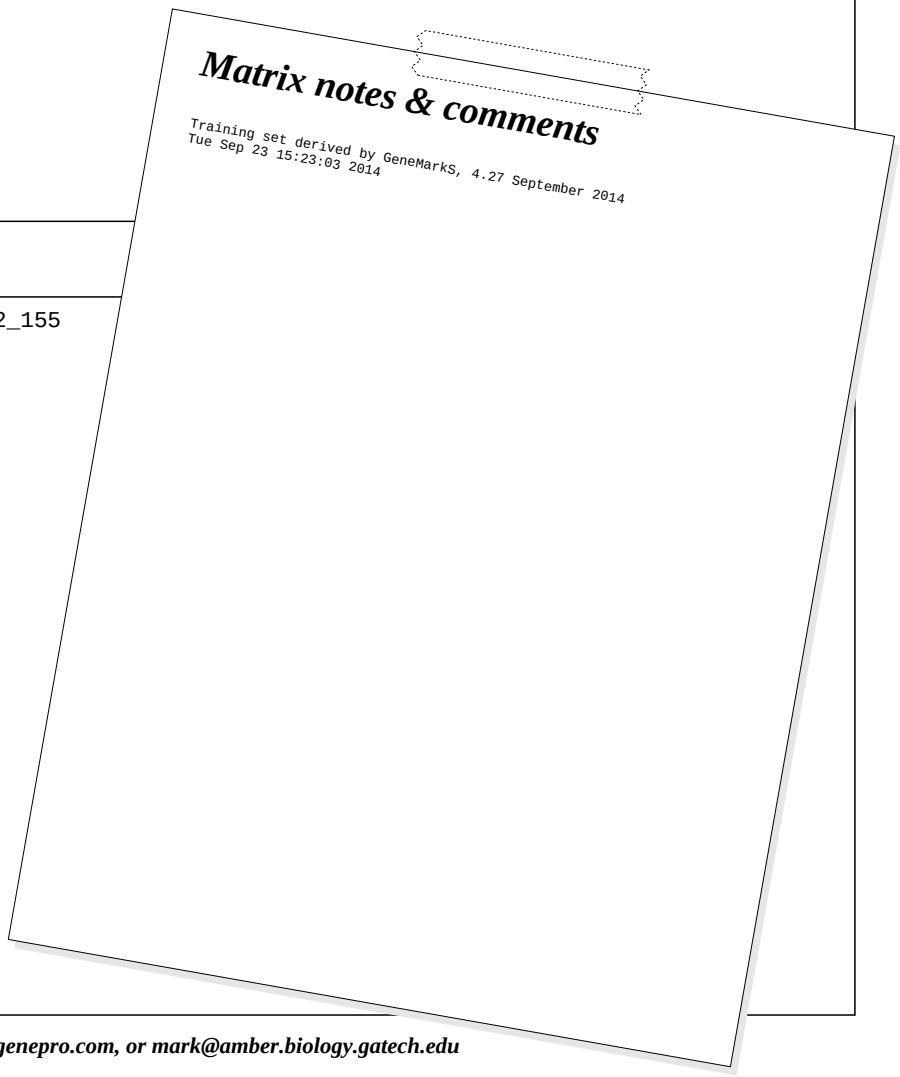
GeneMark Options :  PostScript graph,
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MATRIX INFORMATION

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Author     :  -

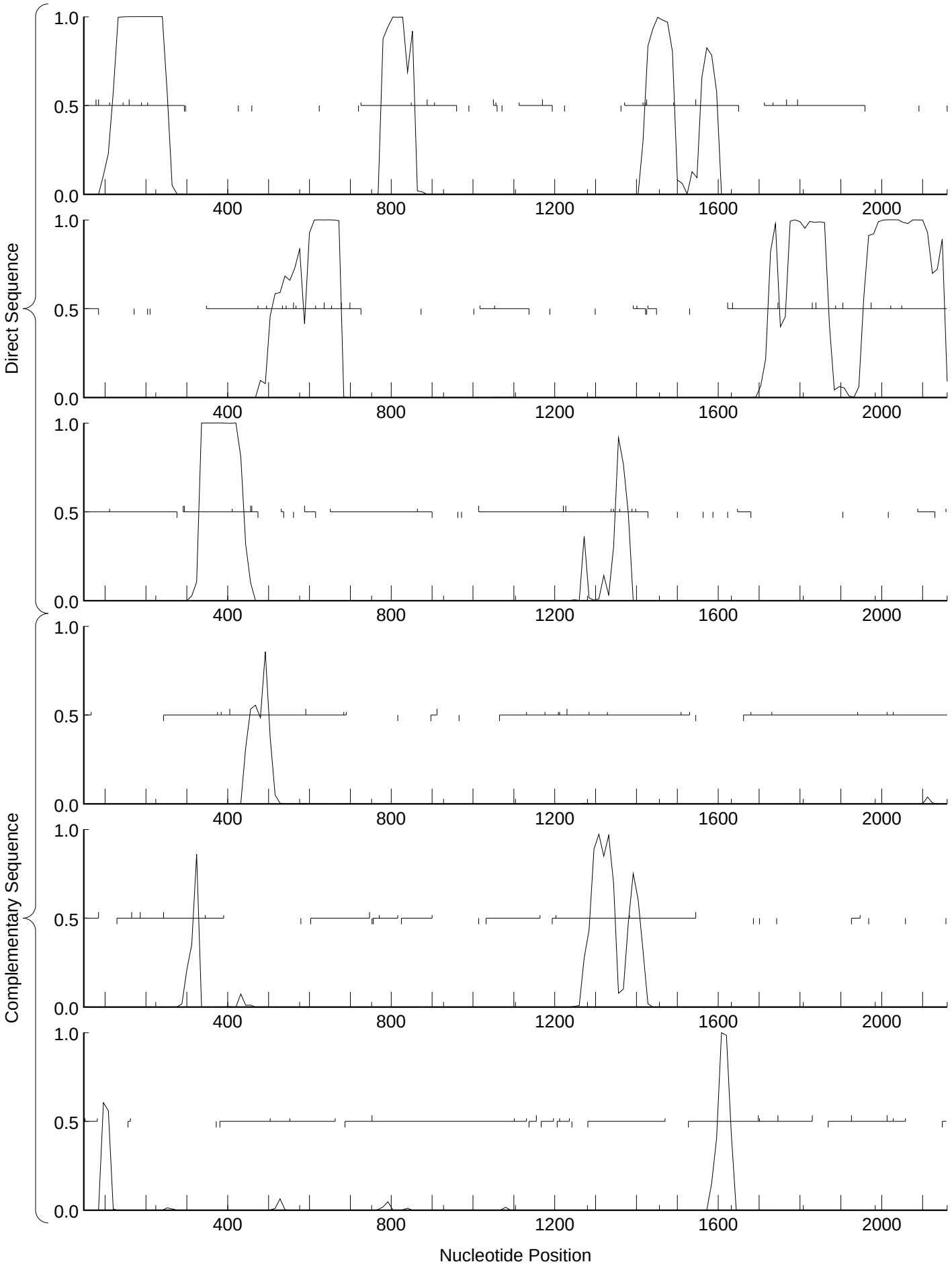
Order      :  4


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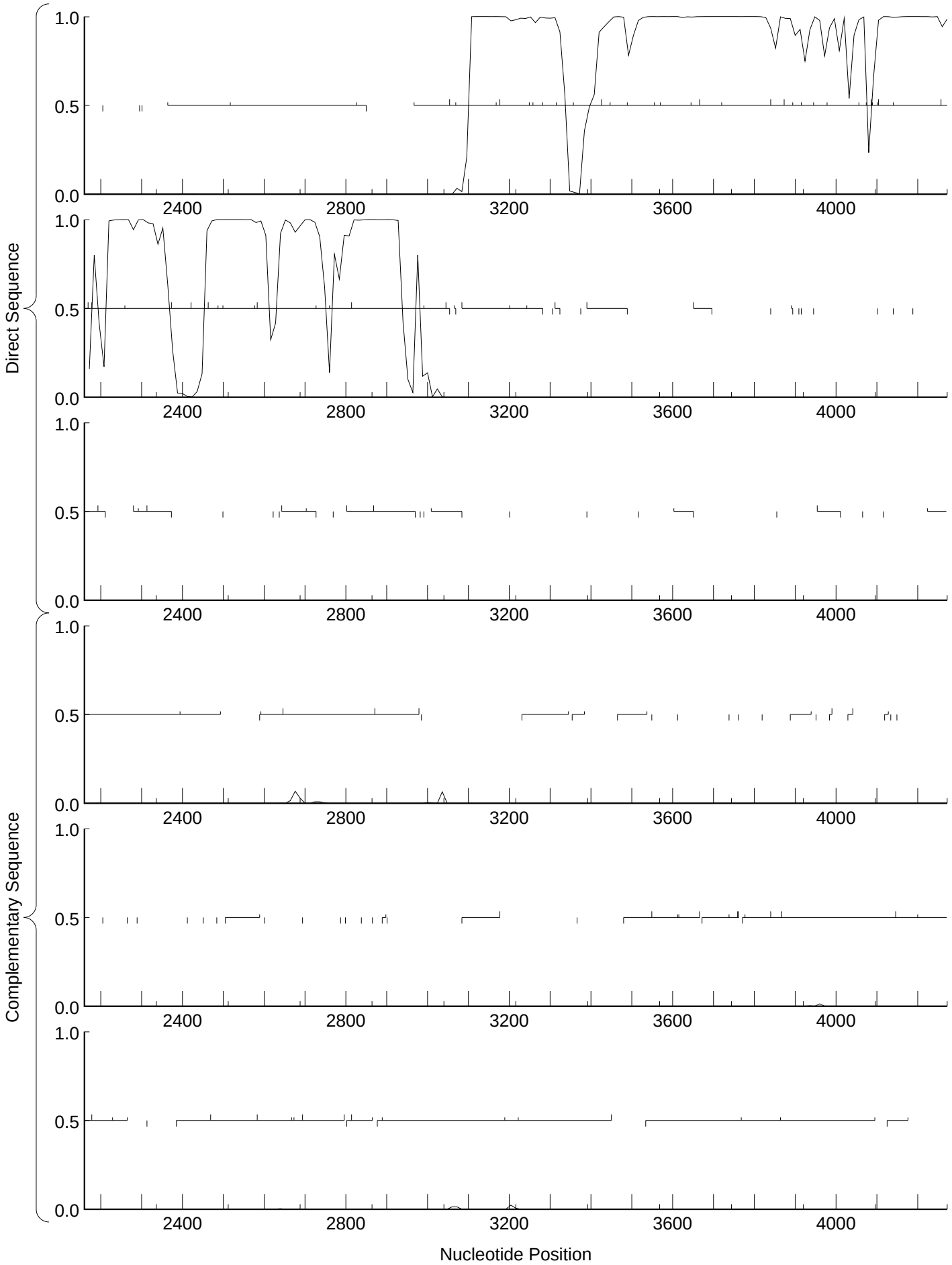


For help or information, send electronic mail to: custserv@genepro.com, or mark@amber.biology.gatech.edu

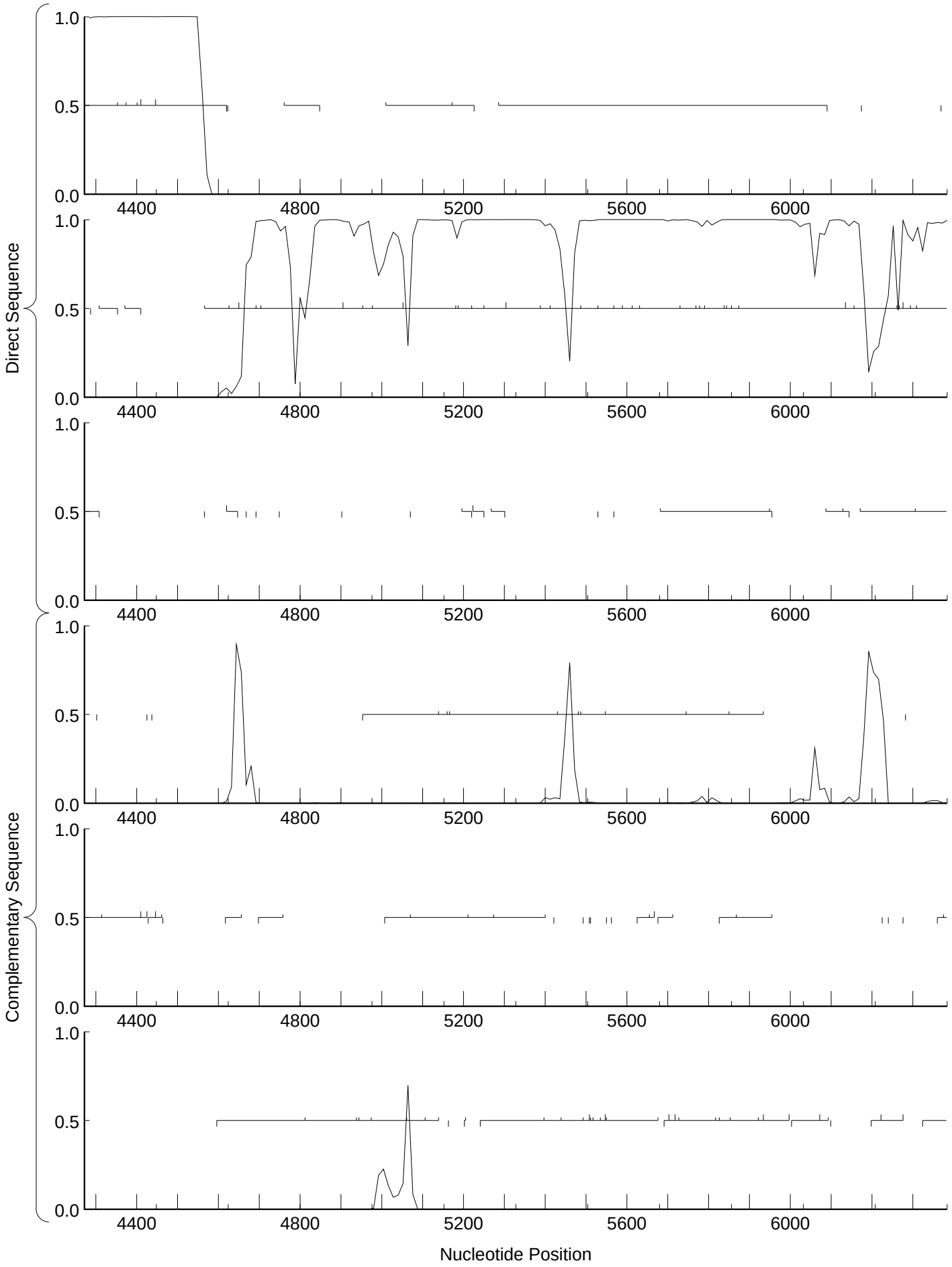
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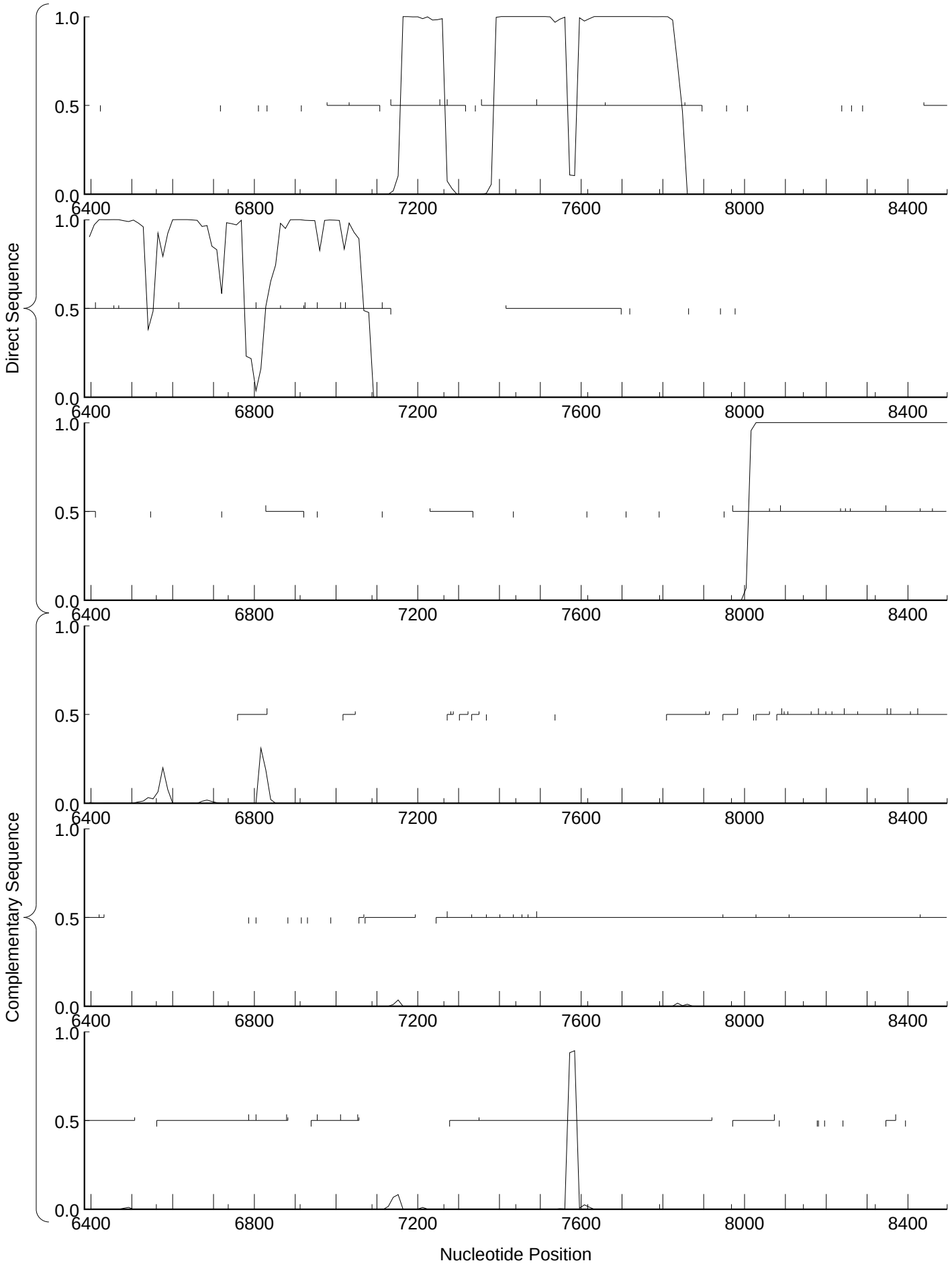
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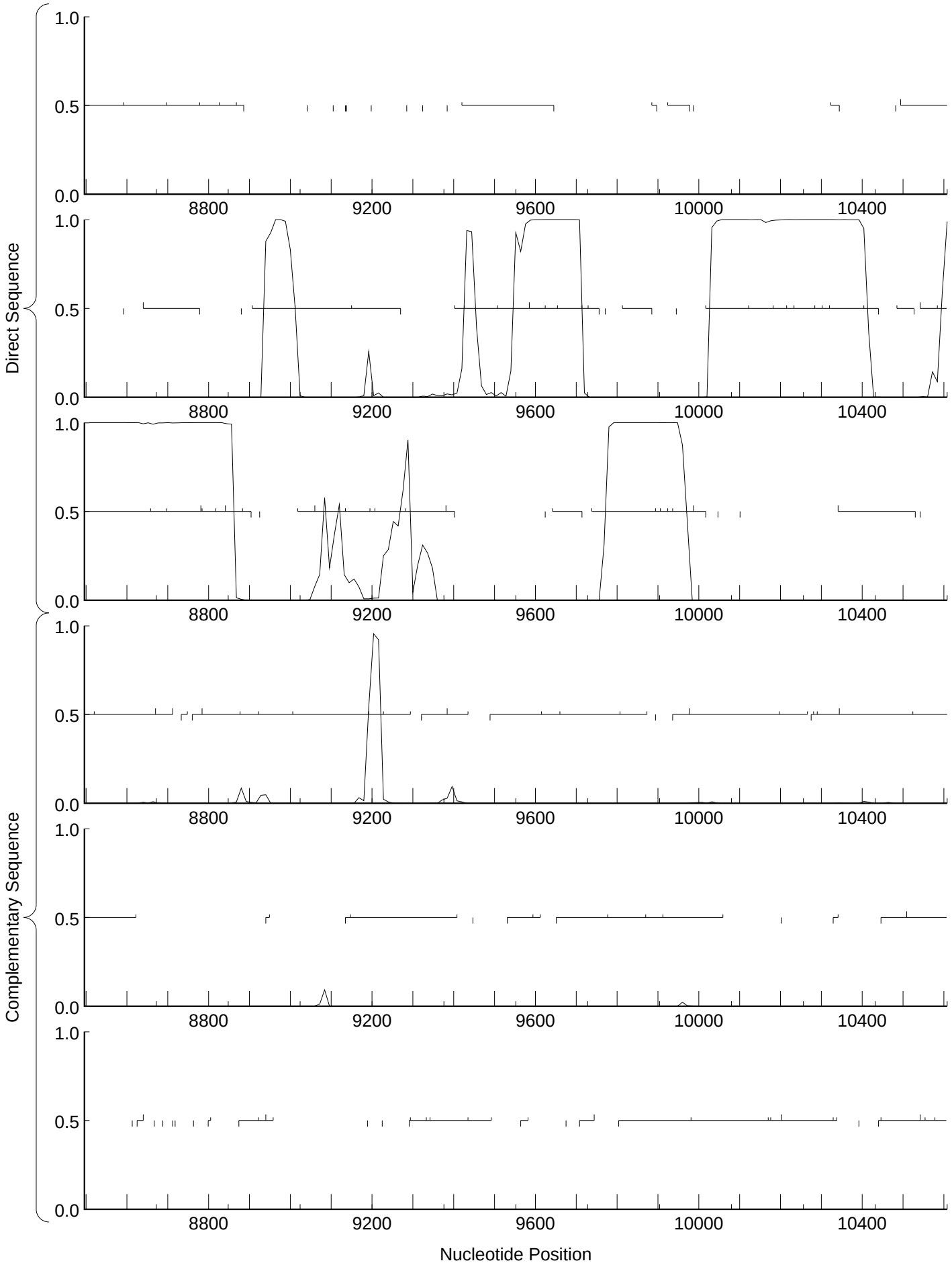
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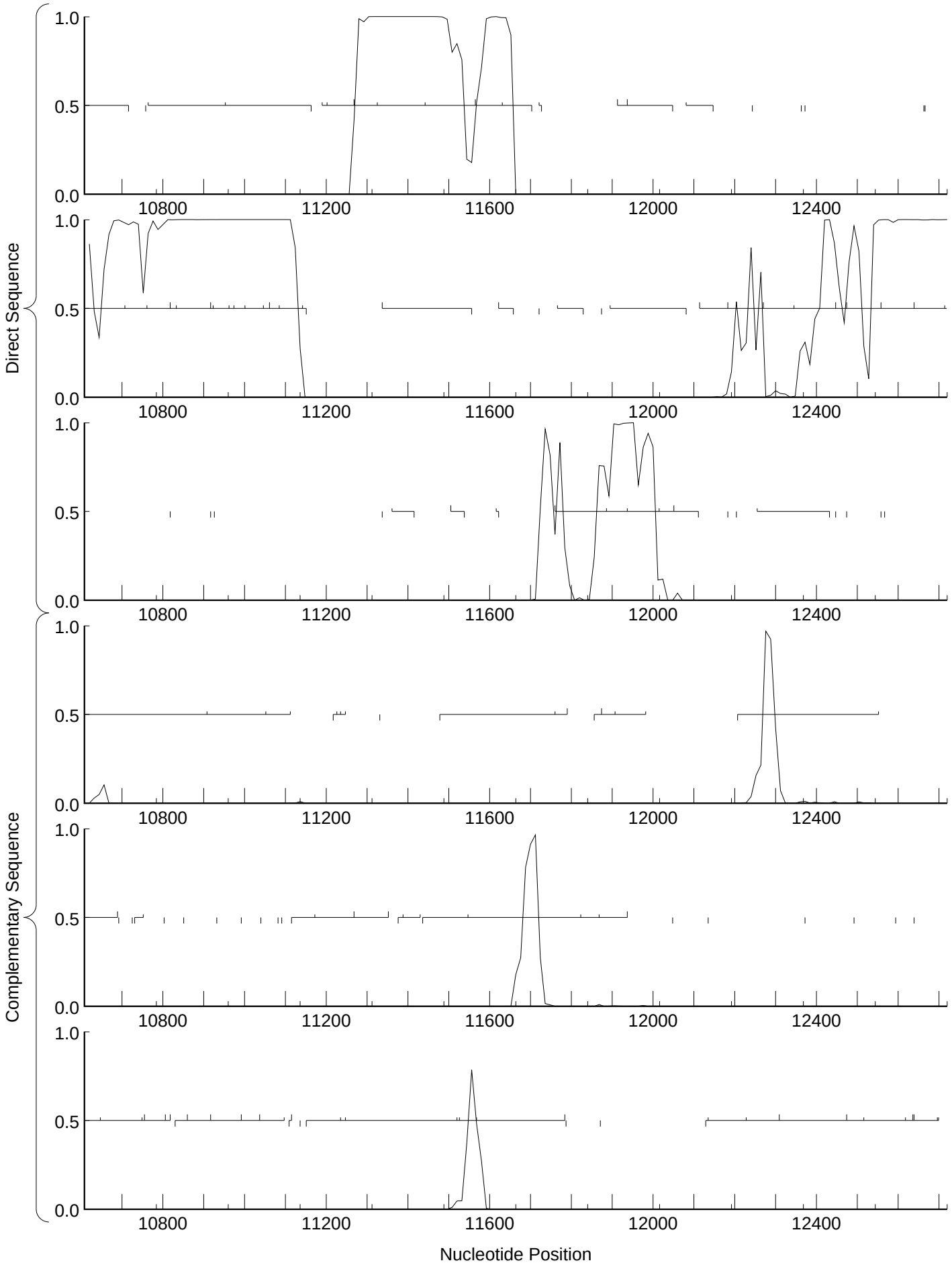
e complete sequence, 59905 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K1, Order 4, Window 96, Step 12, 5/30



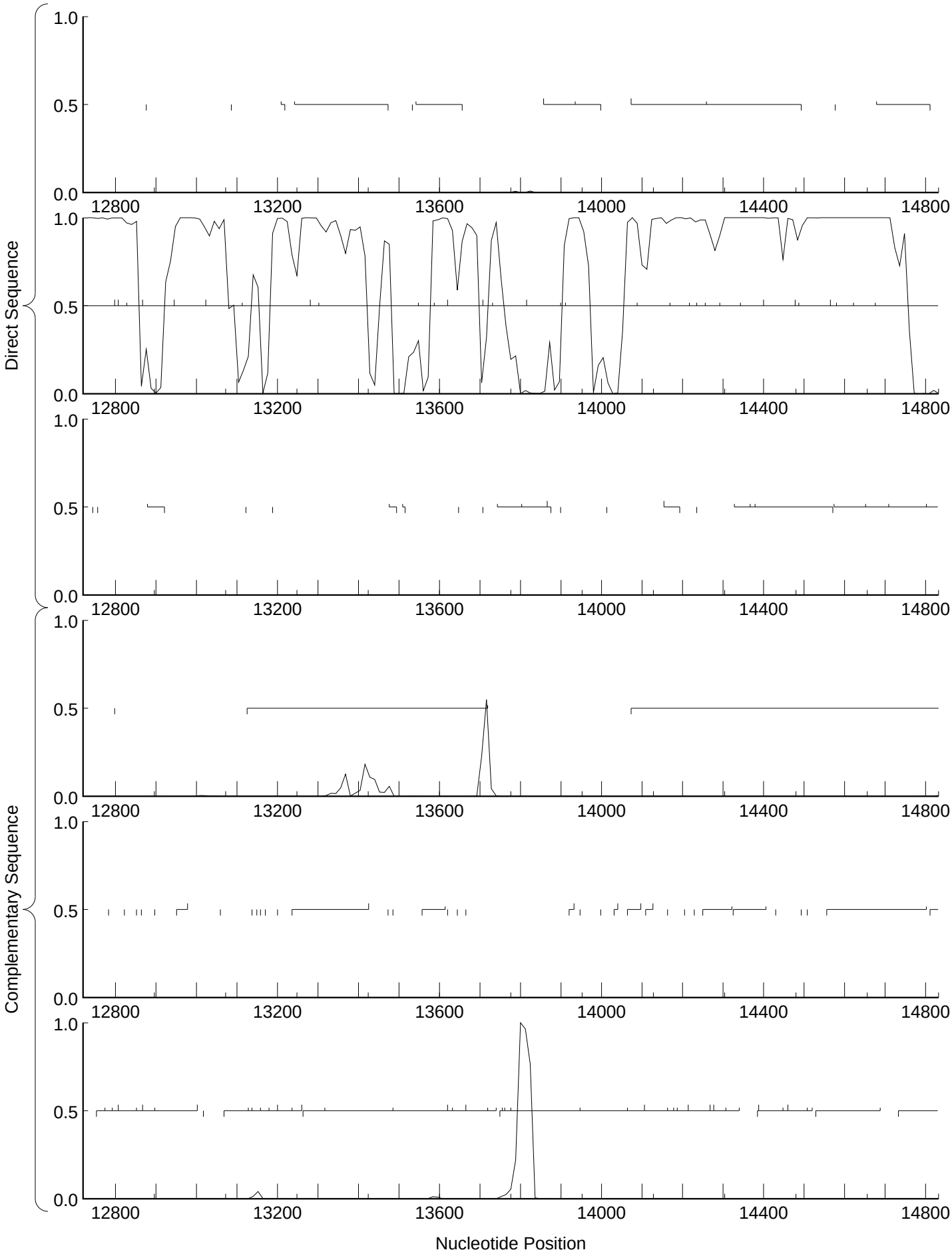
e complete sequence, 59905 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K1, Order 4, Window 96, Step 12, 6/30



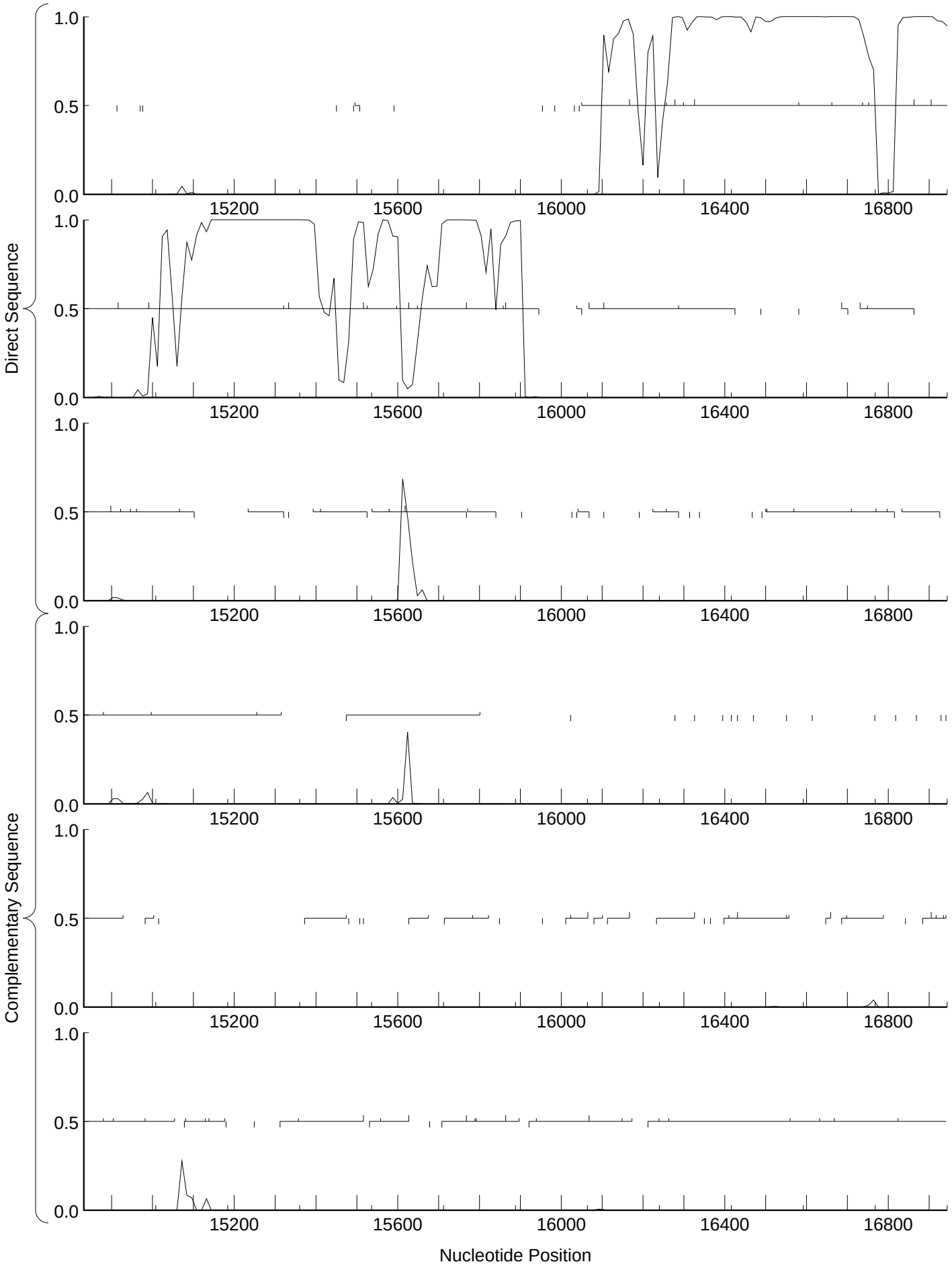
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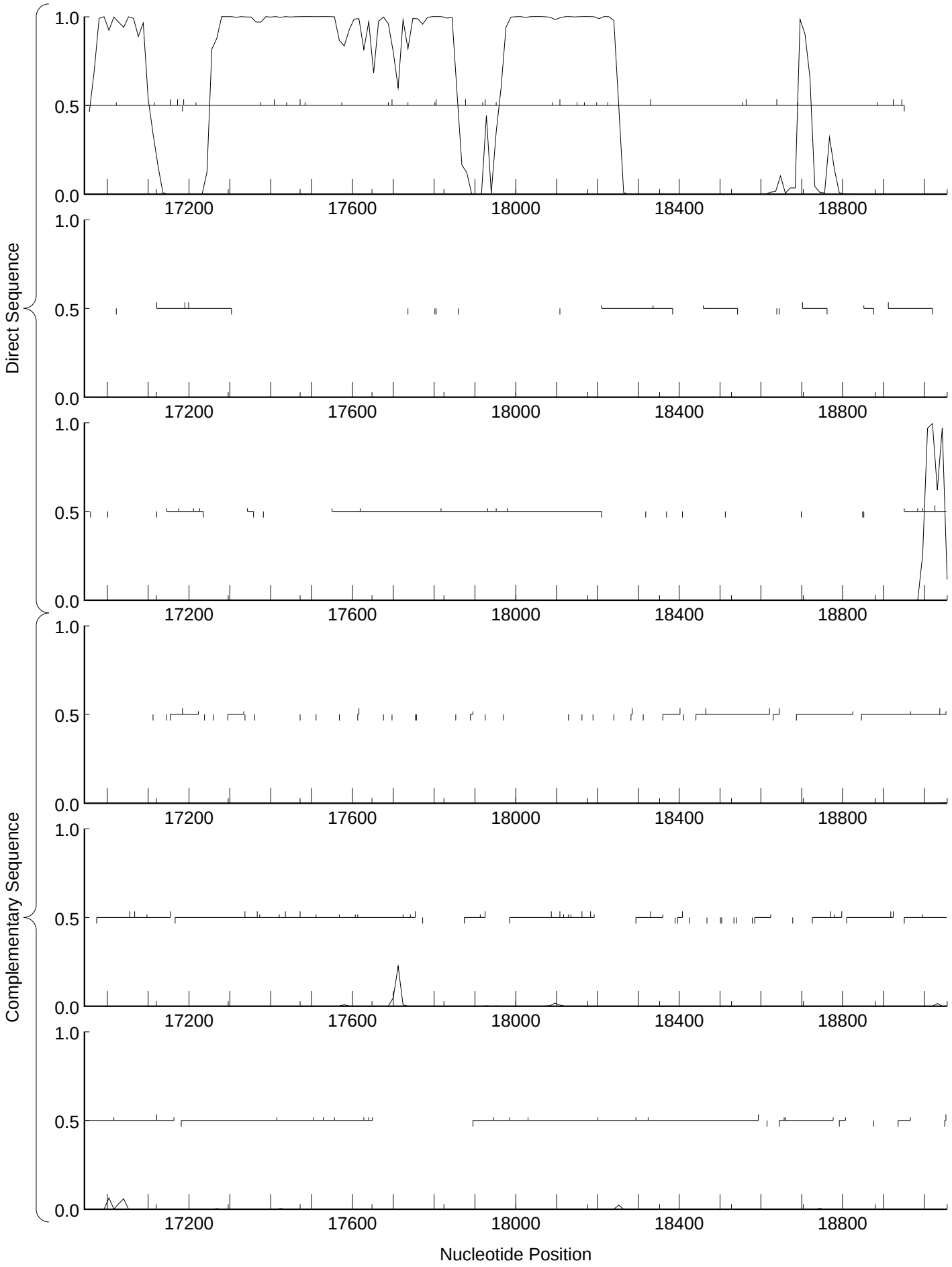
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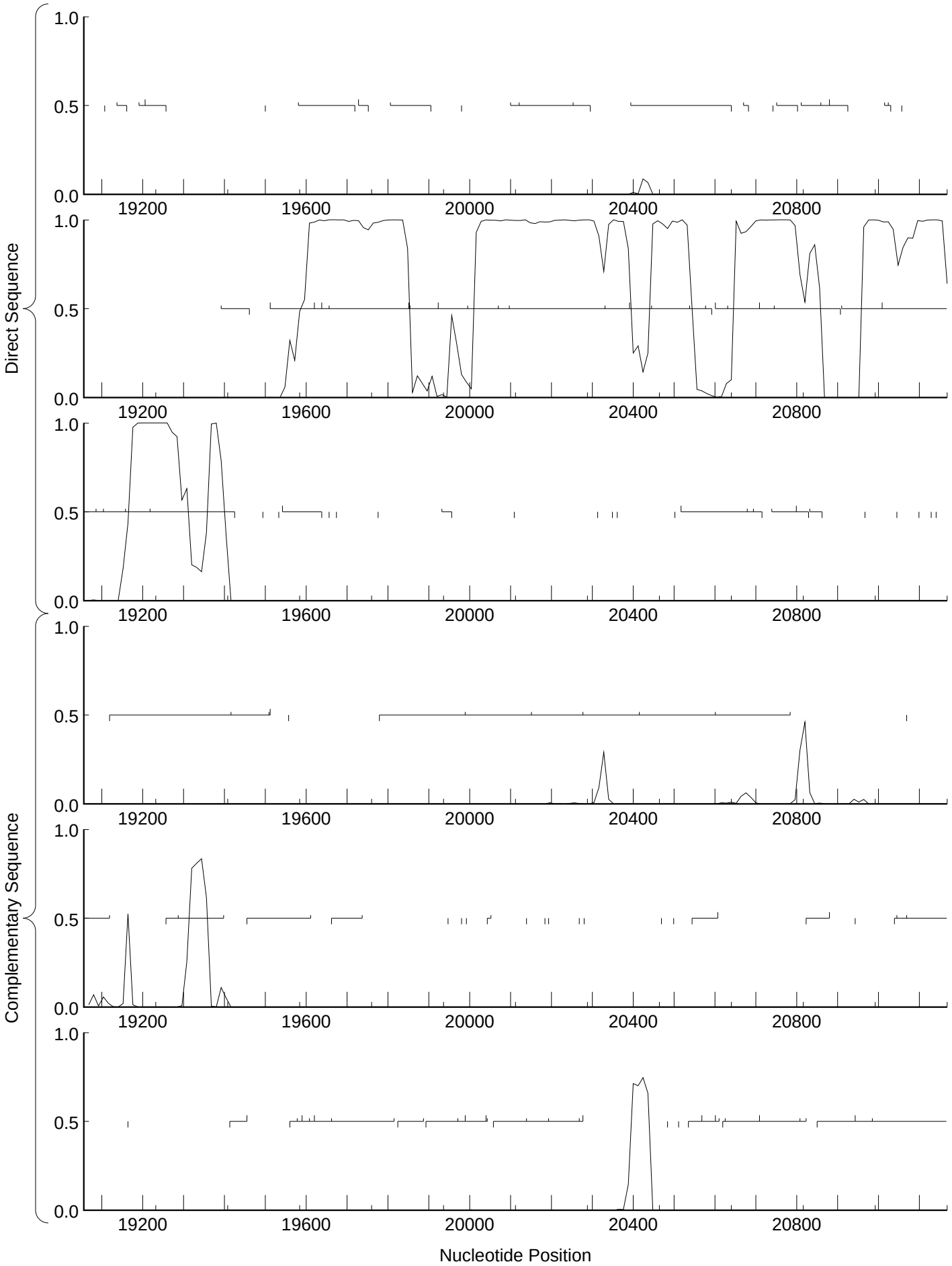
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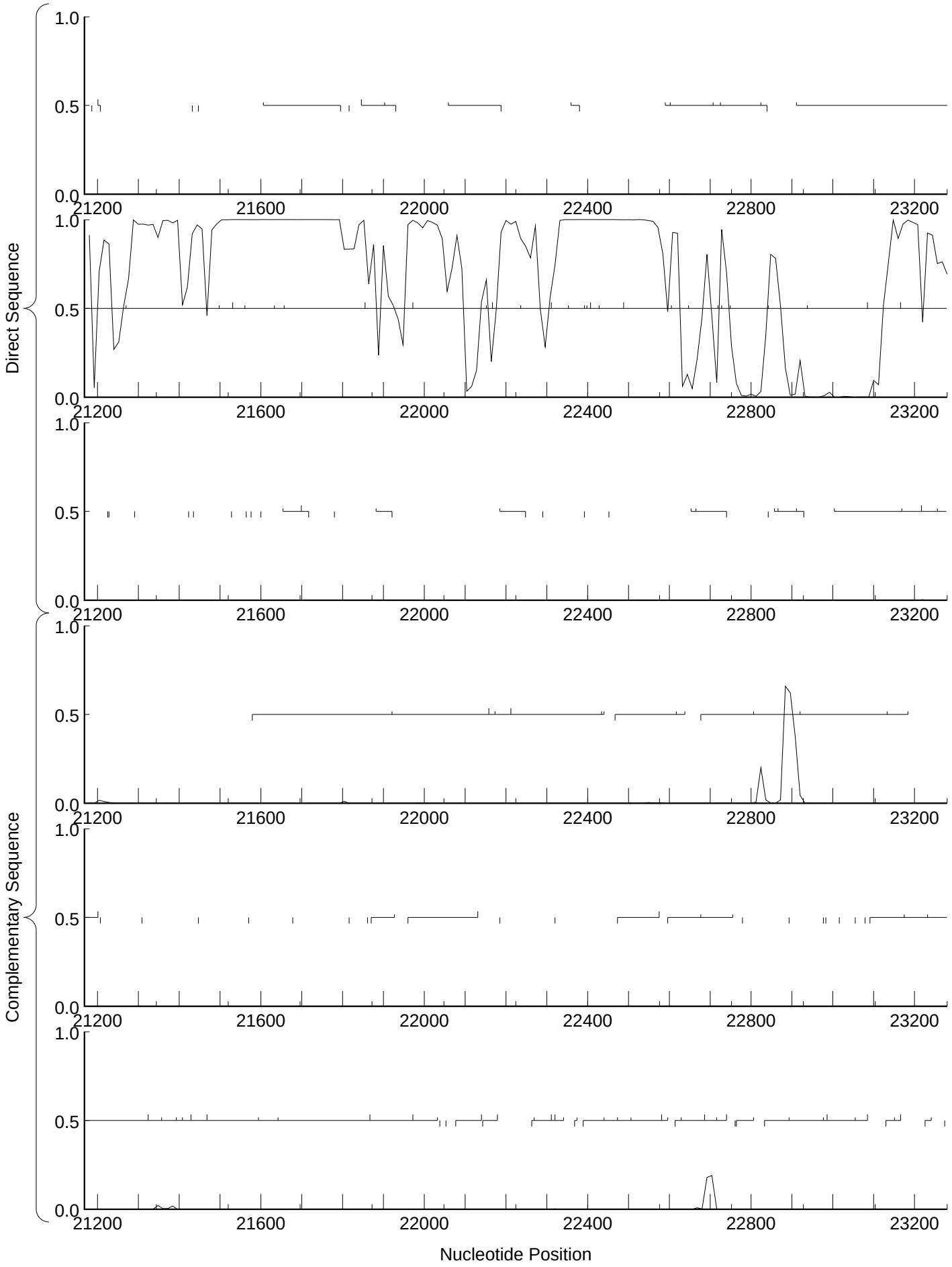
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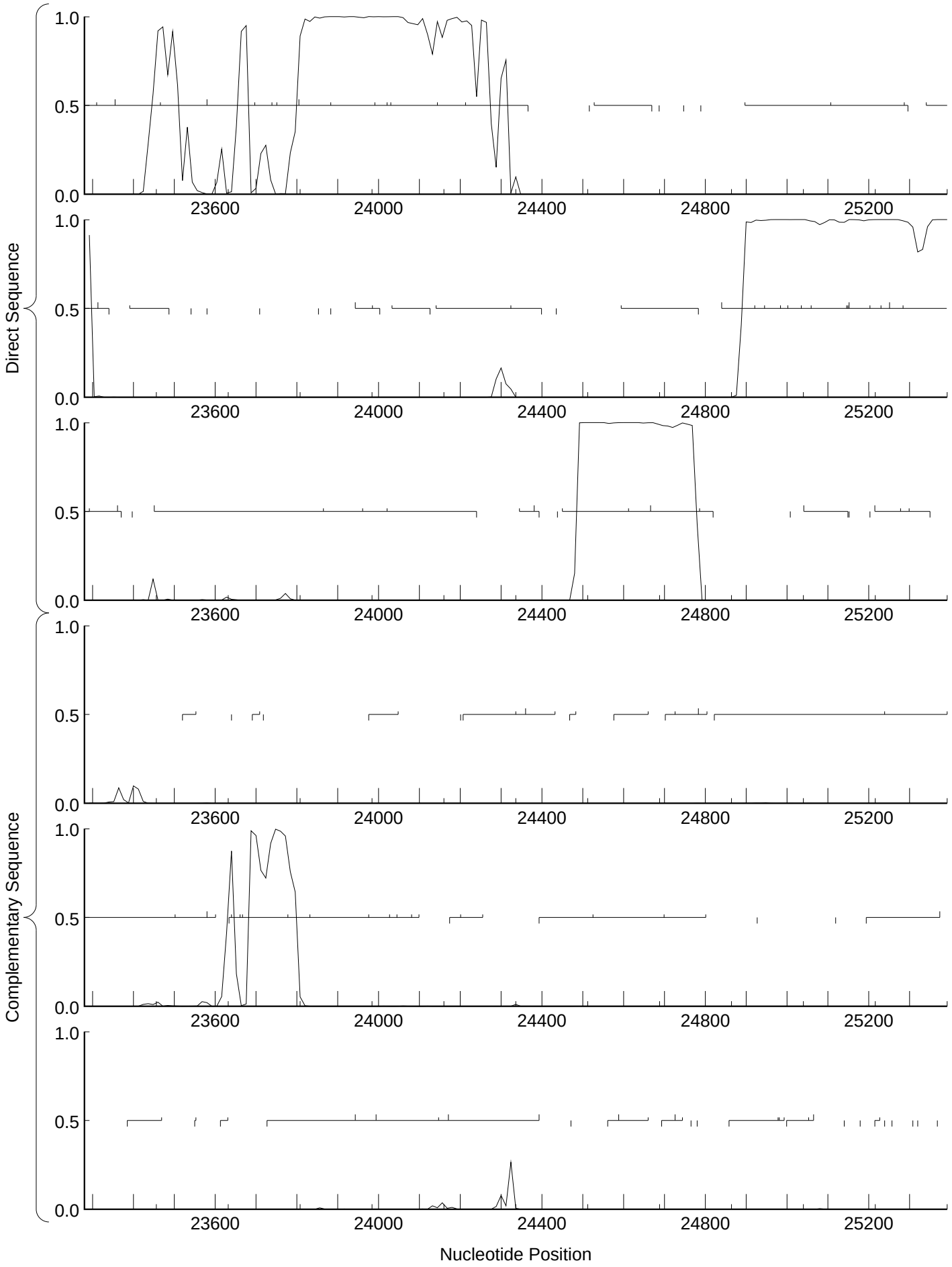
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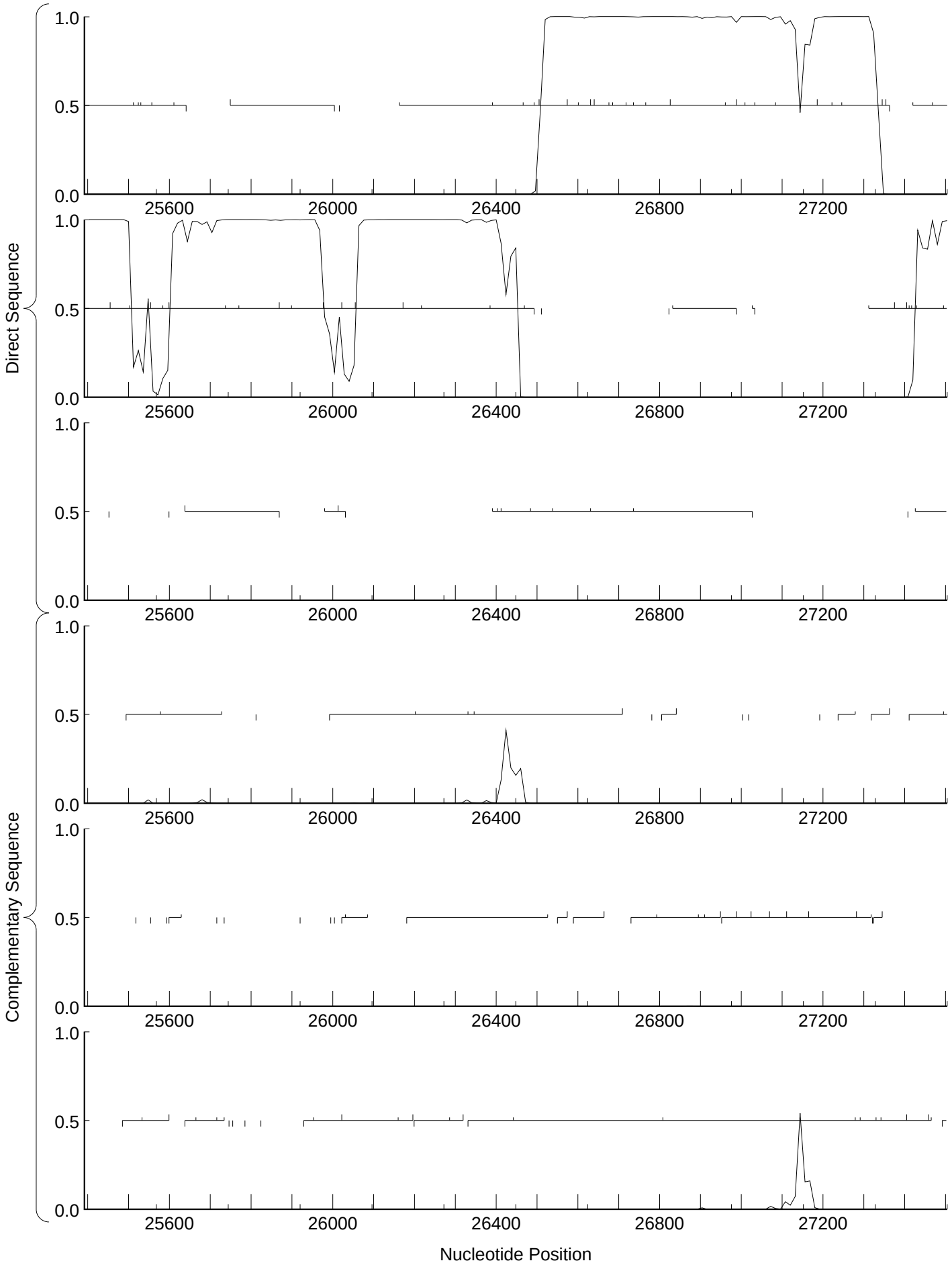


complete sequence, 59905 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K1, Order 4, Window 96, Step 12, 12/30

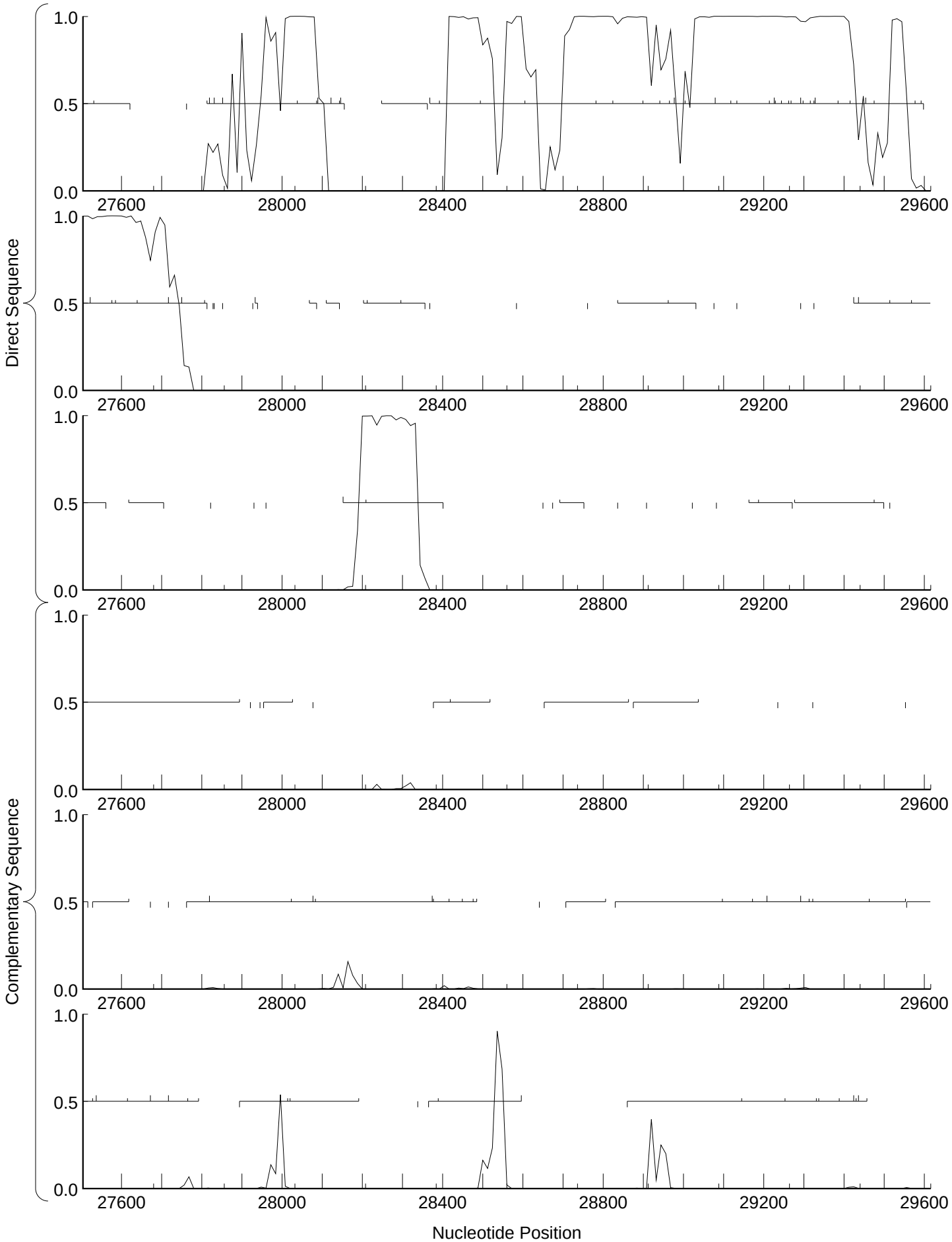


complete sequence, 59905 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K1, Order 4, Window 96, Step 12, 13/30

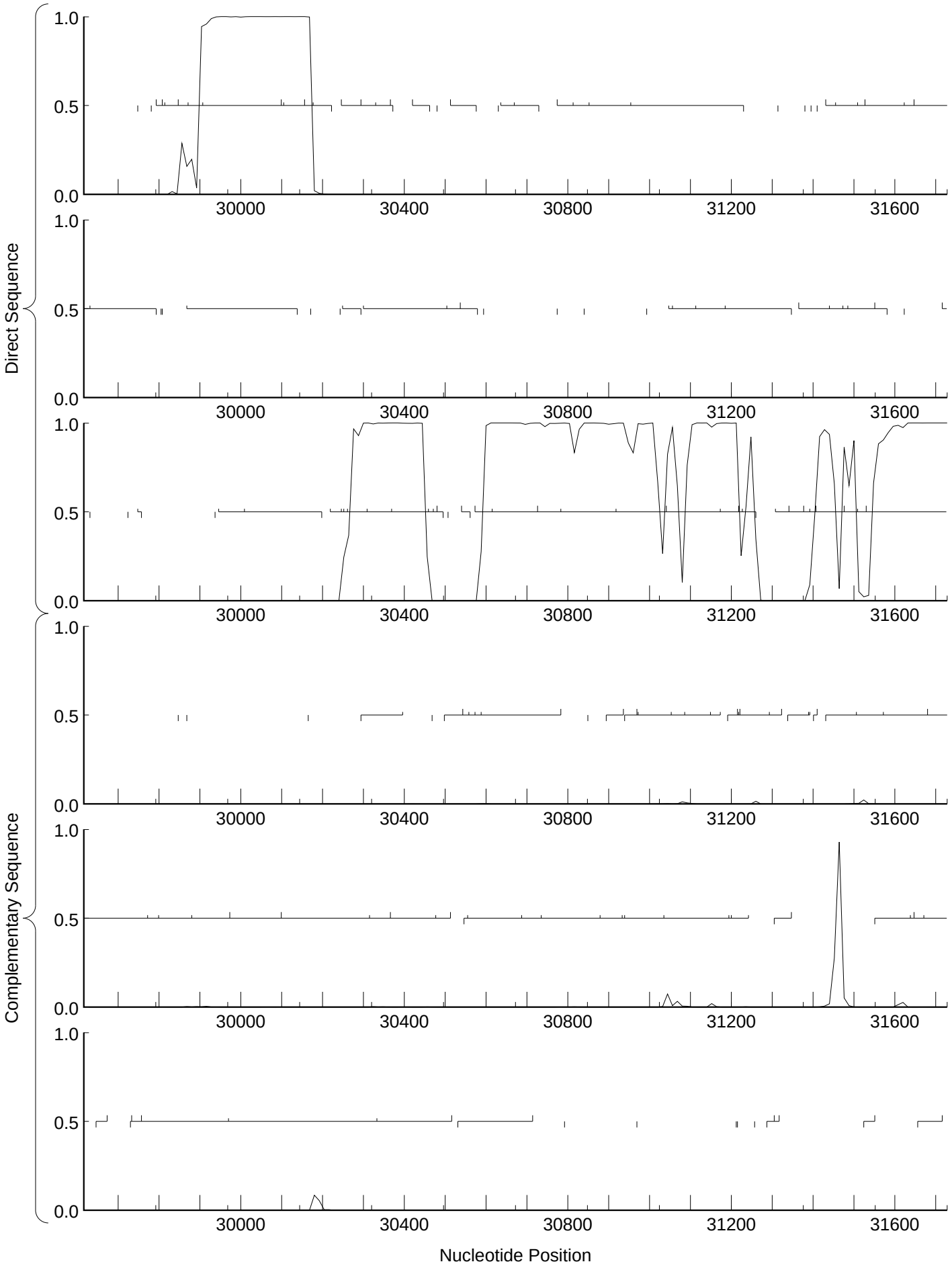



Direct Sequence
Complementary Sequence
1.0
0.5
0.0
25600
26000
26400
26800
27200
Nucleotide Position

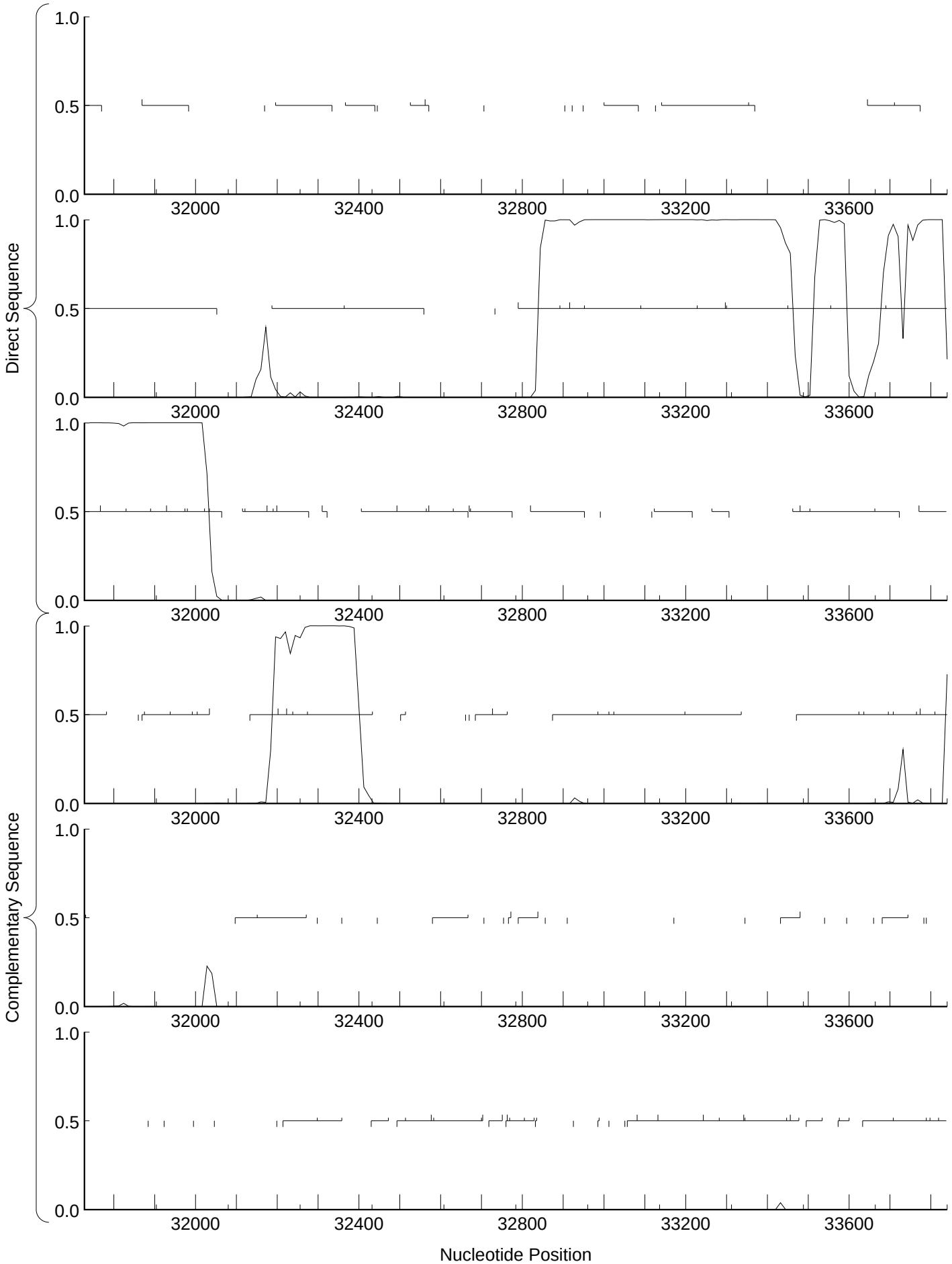
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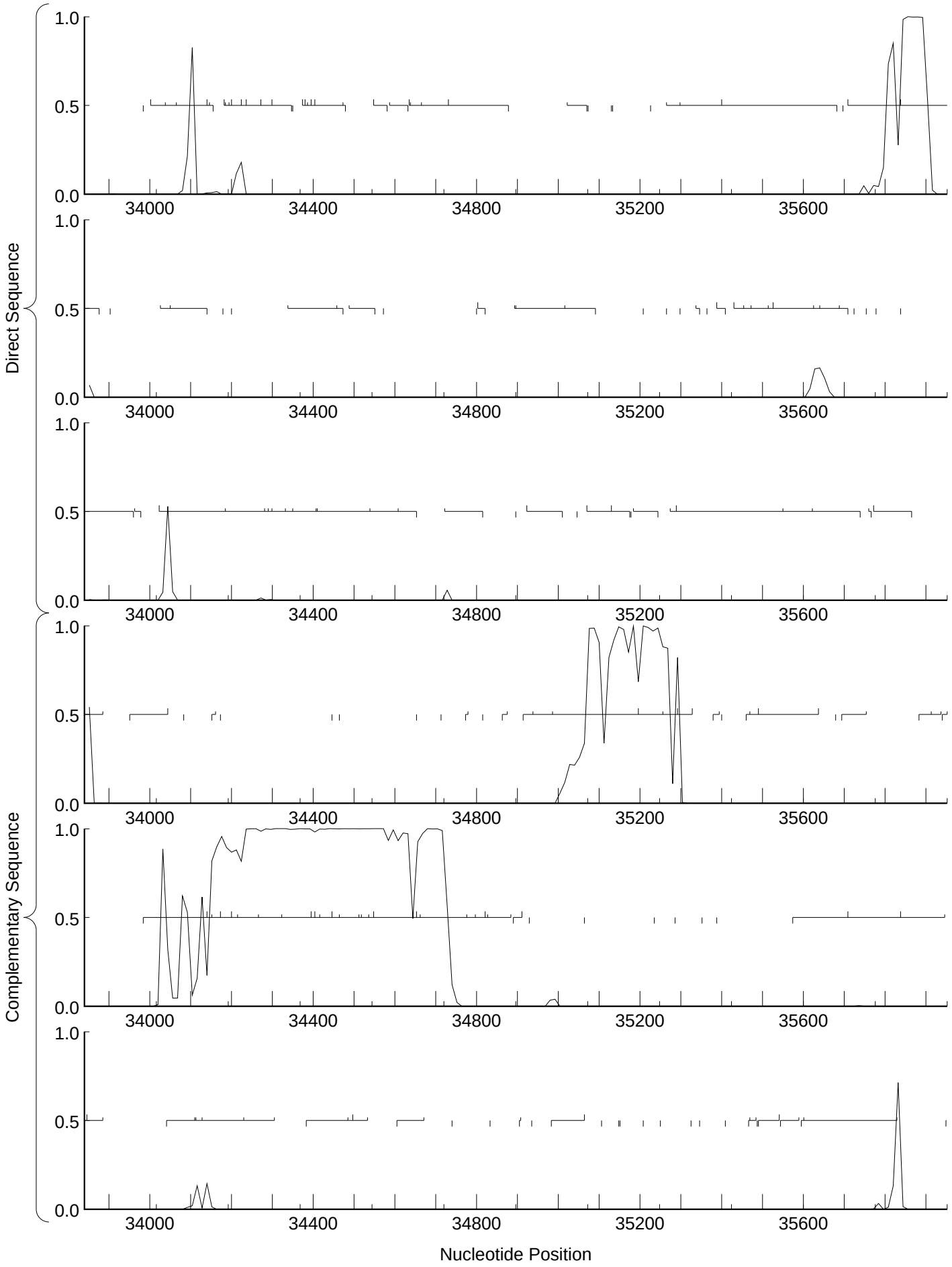
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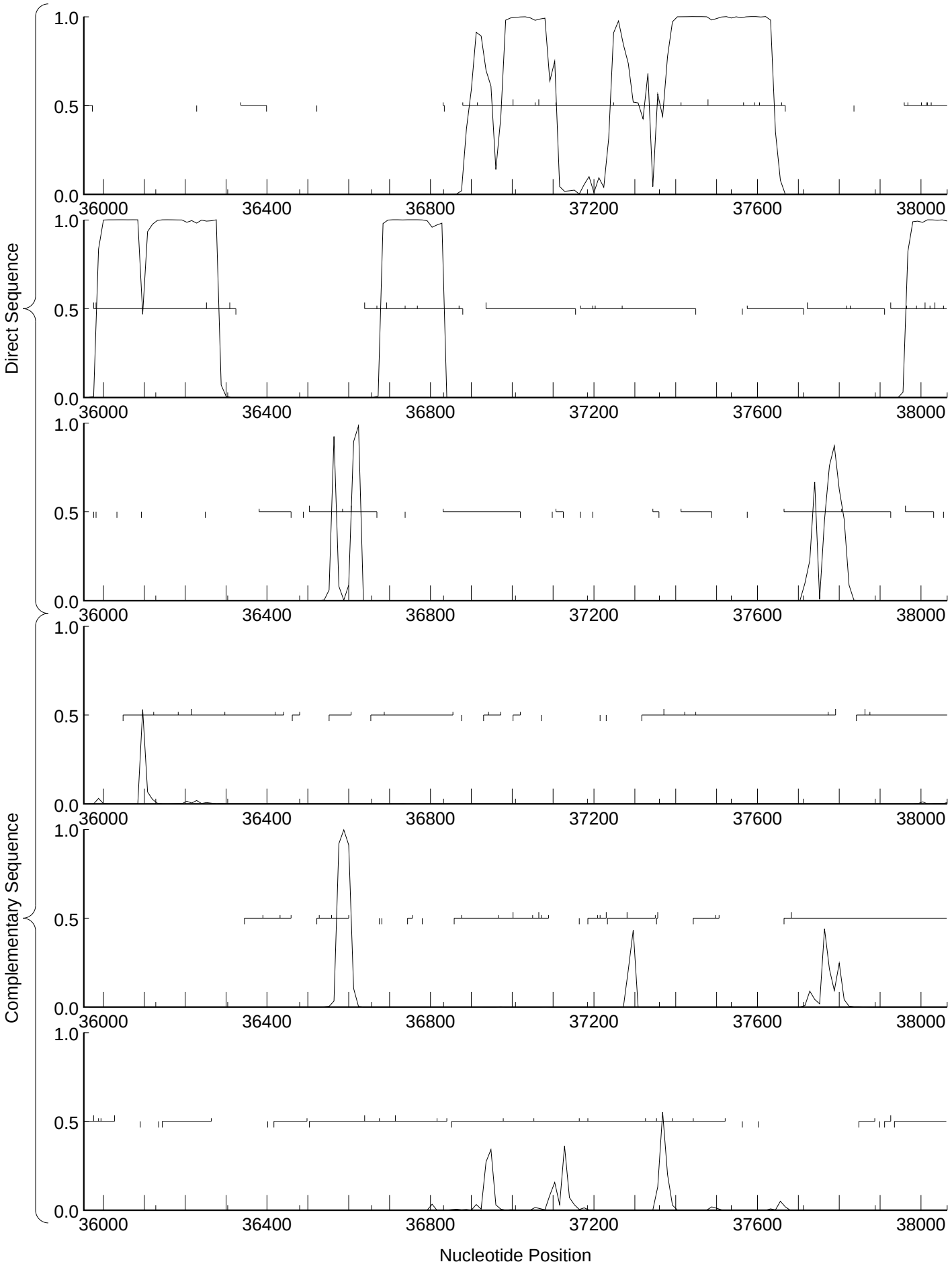
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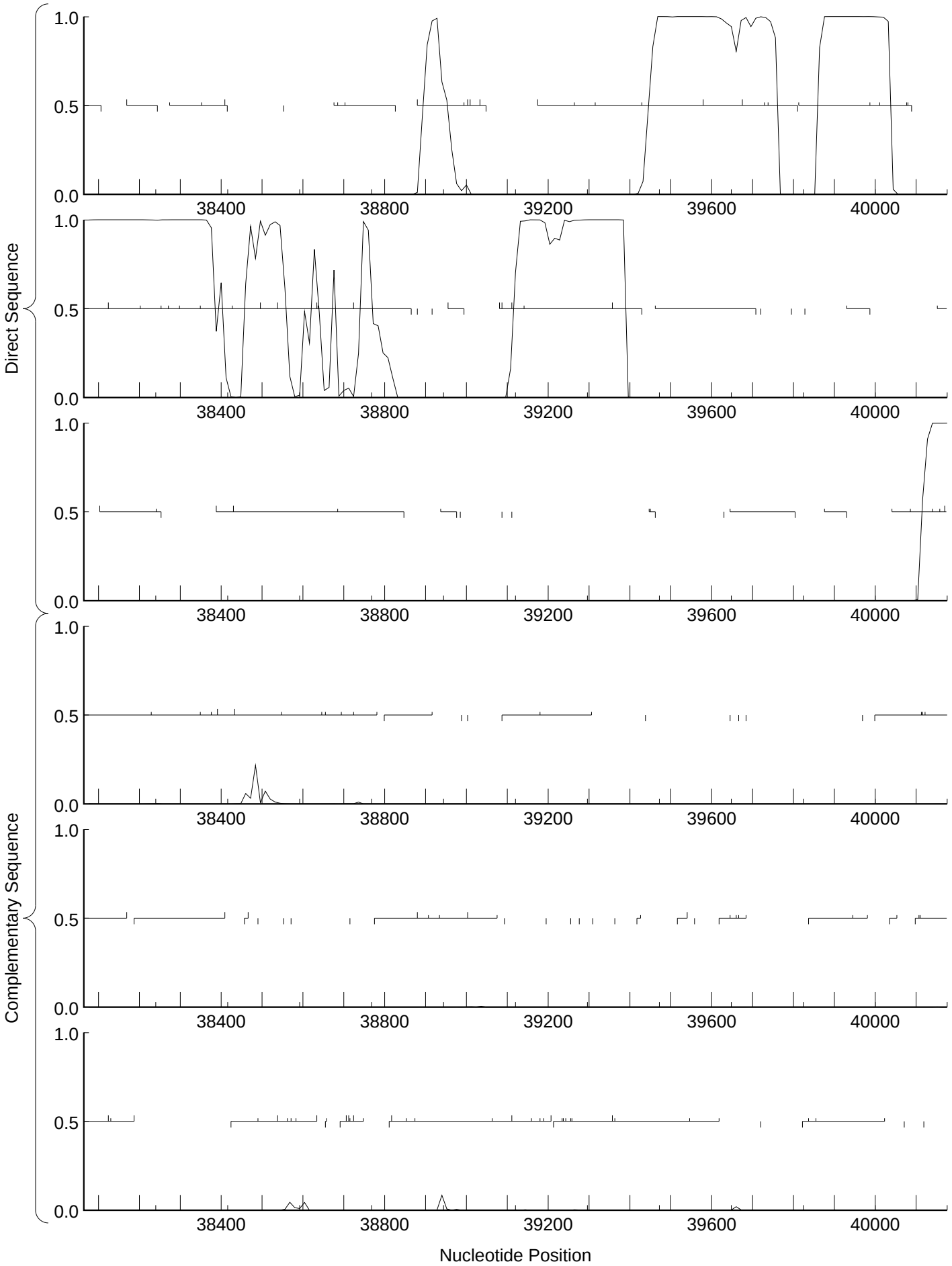
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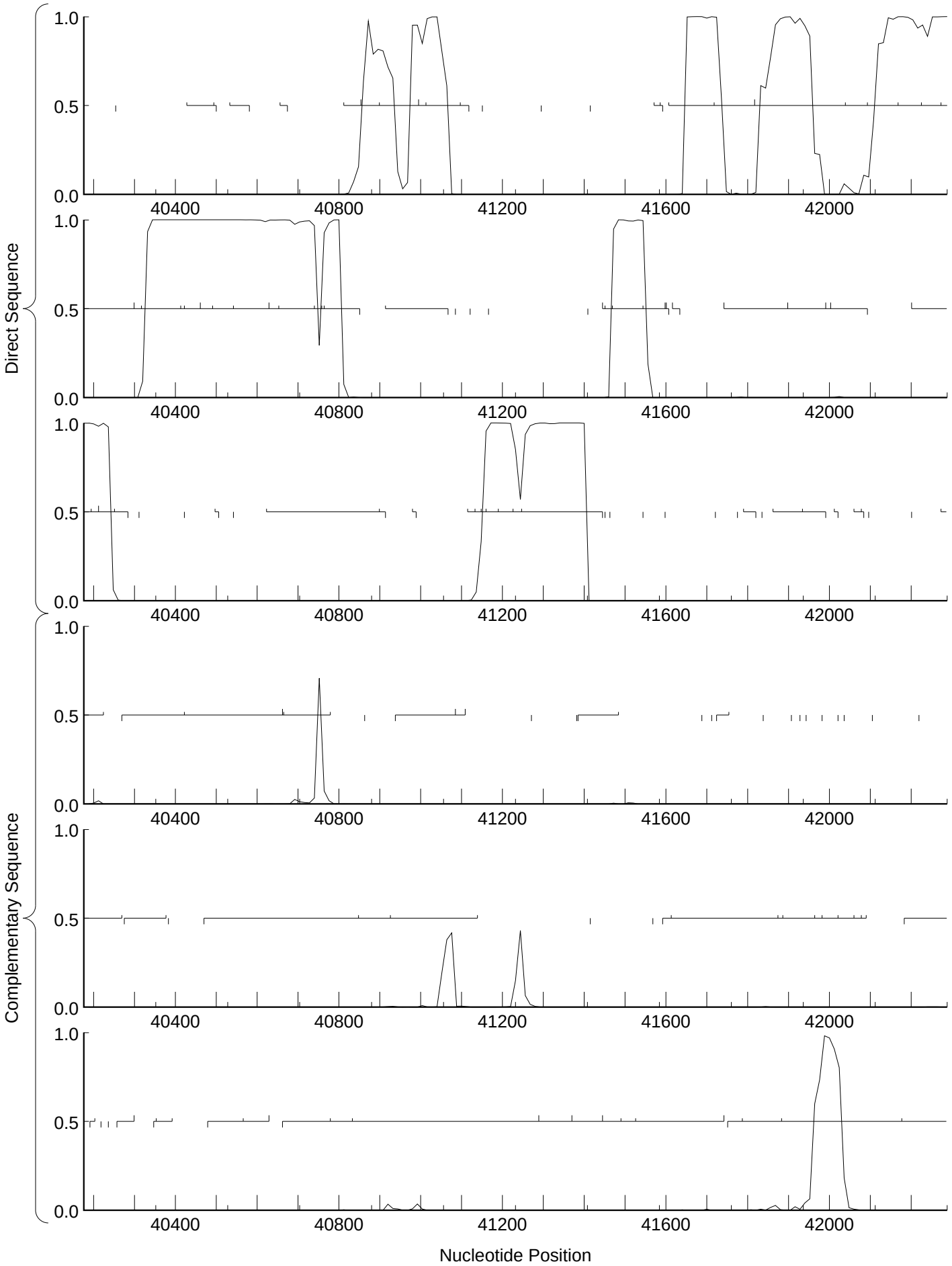
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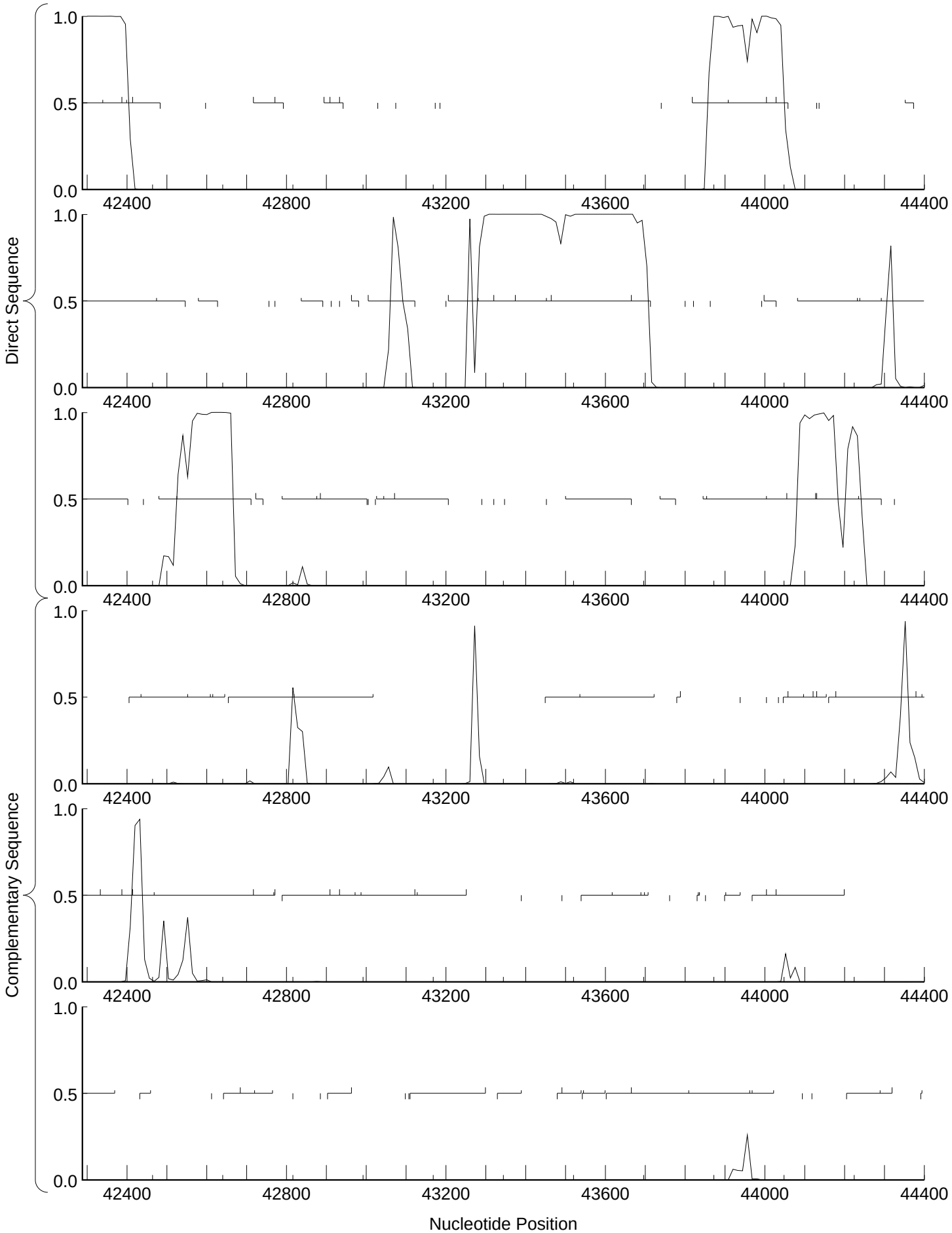


complete sequence, 59905 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K1, Order 4, Window 96, Step 12, 20/30

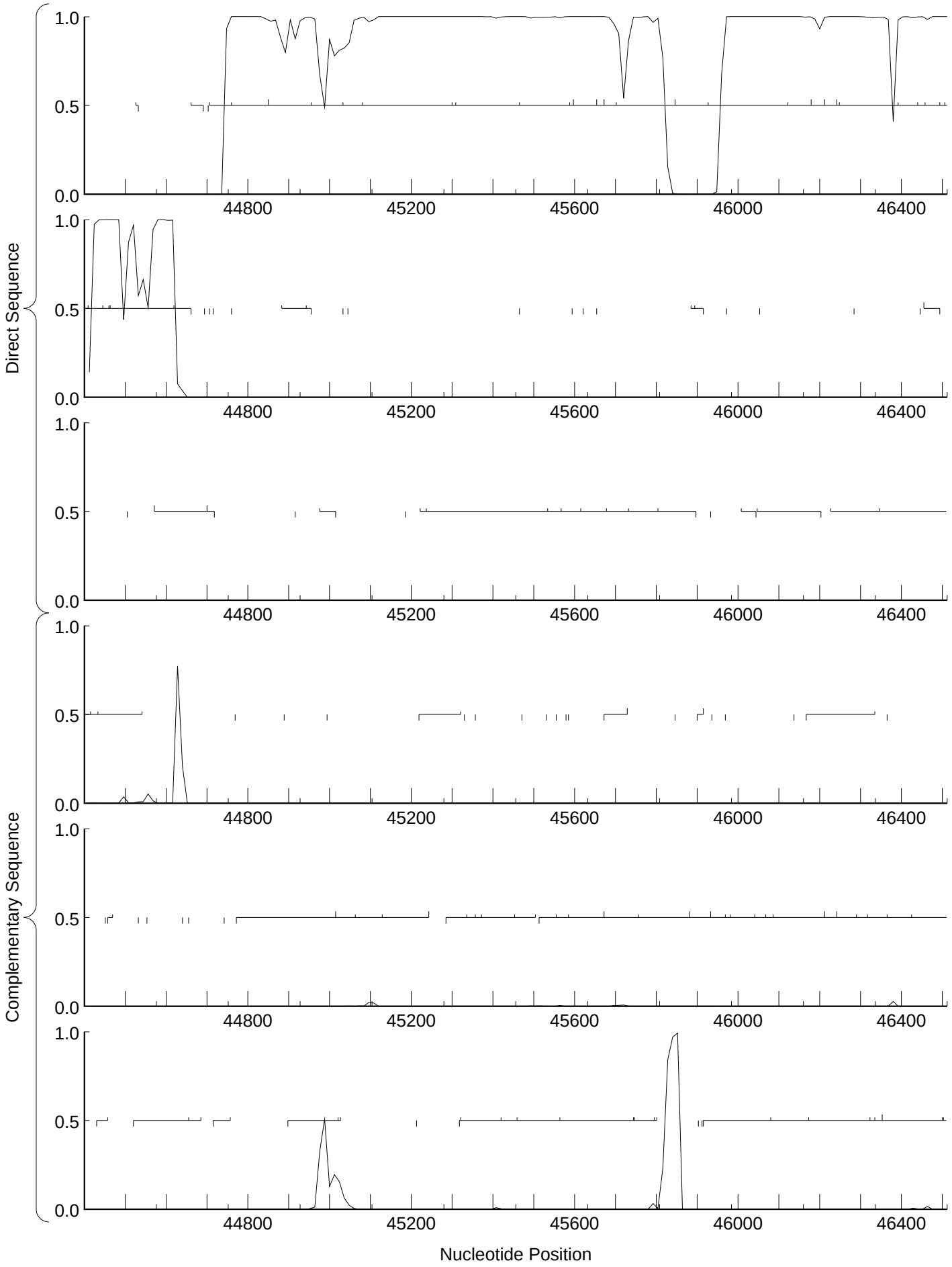


complete sequence, 59905 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K1, Order 4, Window 96, Step 12, 21/30

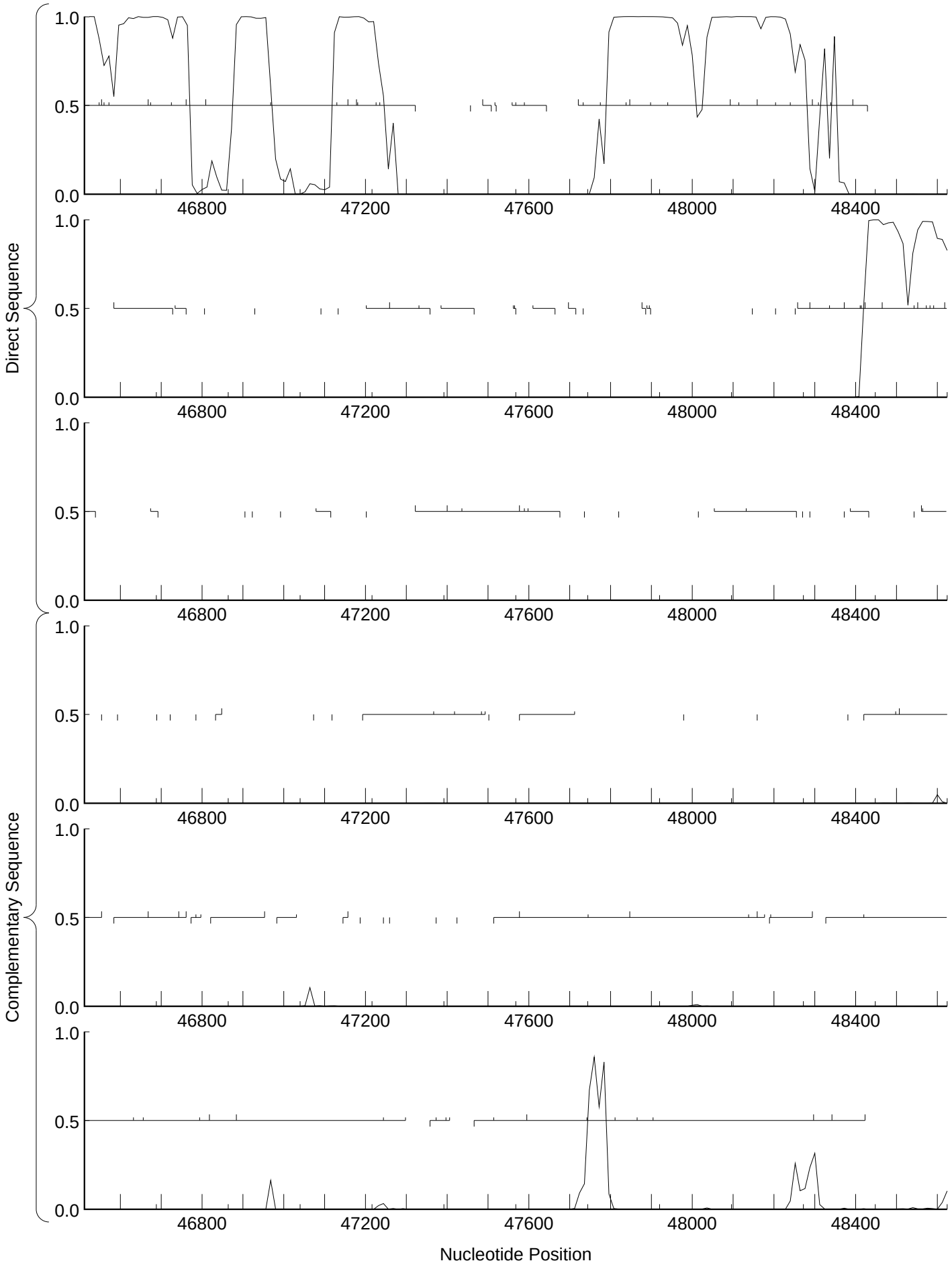



Direct Sequence
Complementary Sequence
1.0
0.5
0.0
42400
42800
43200
43600
44000
44400
Nucleotide Position

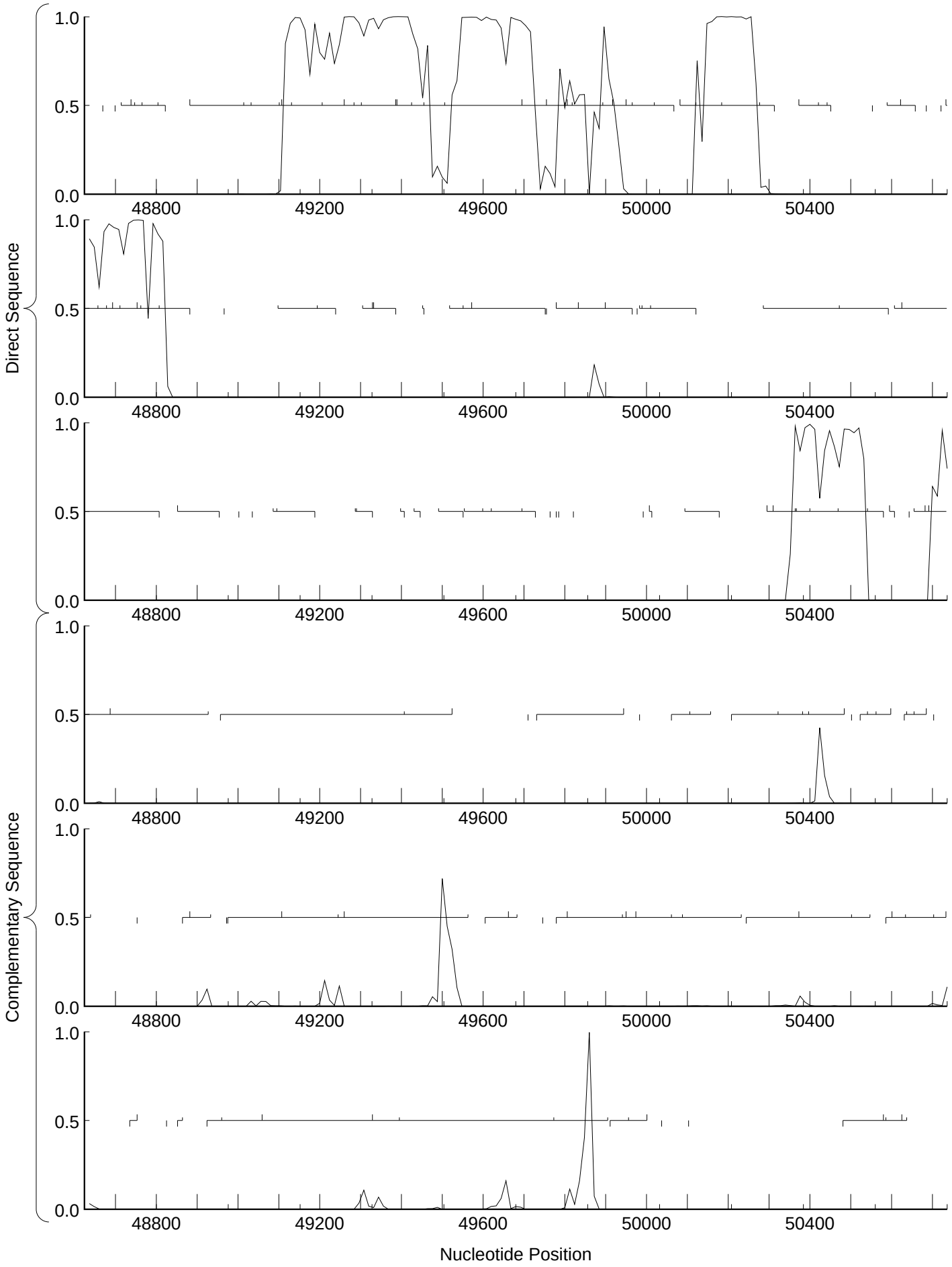
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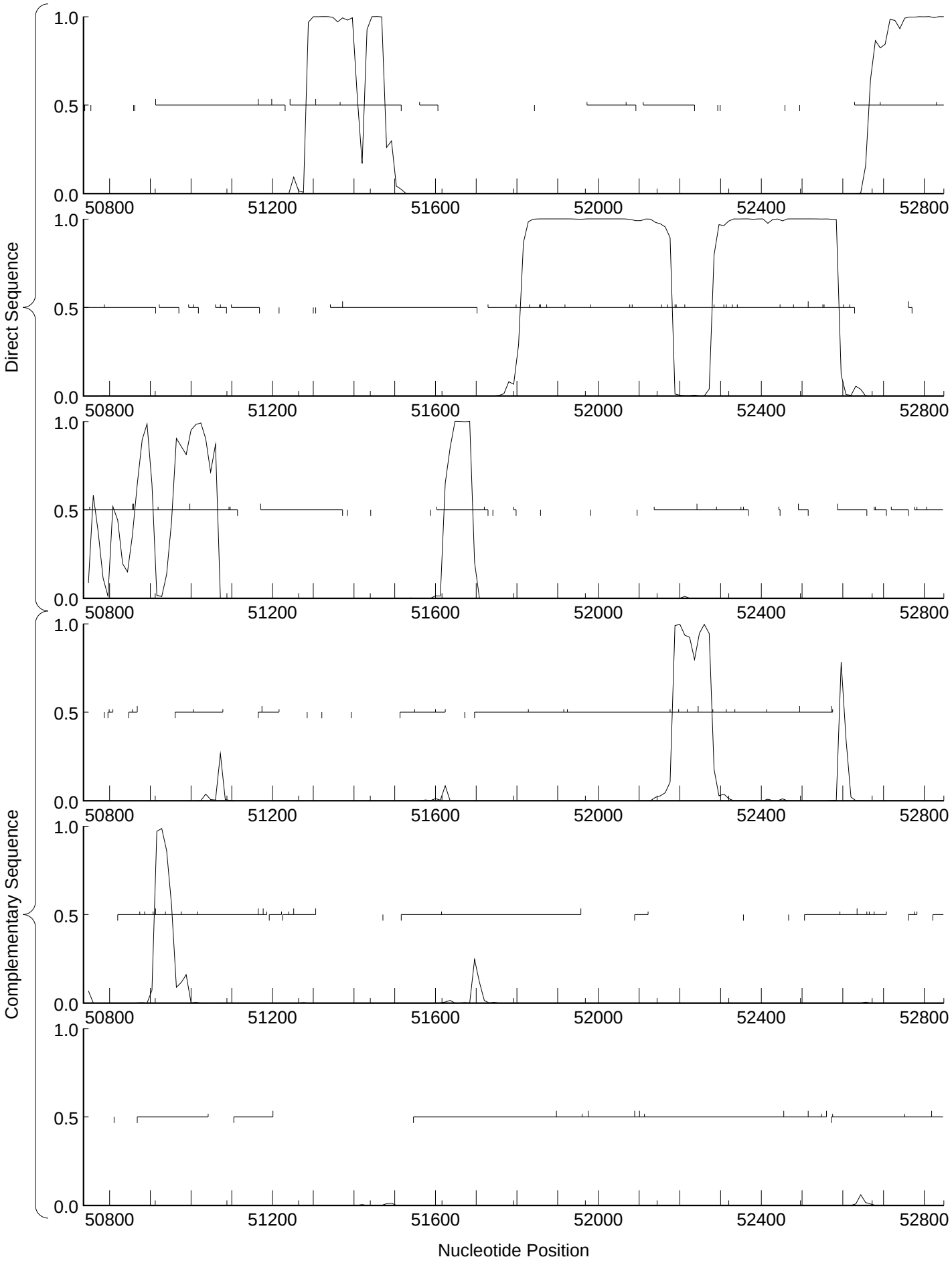
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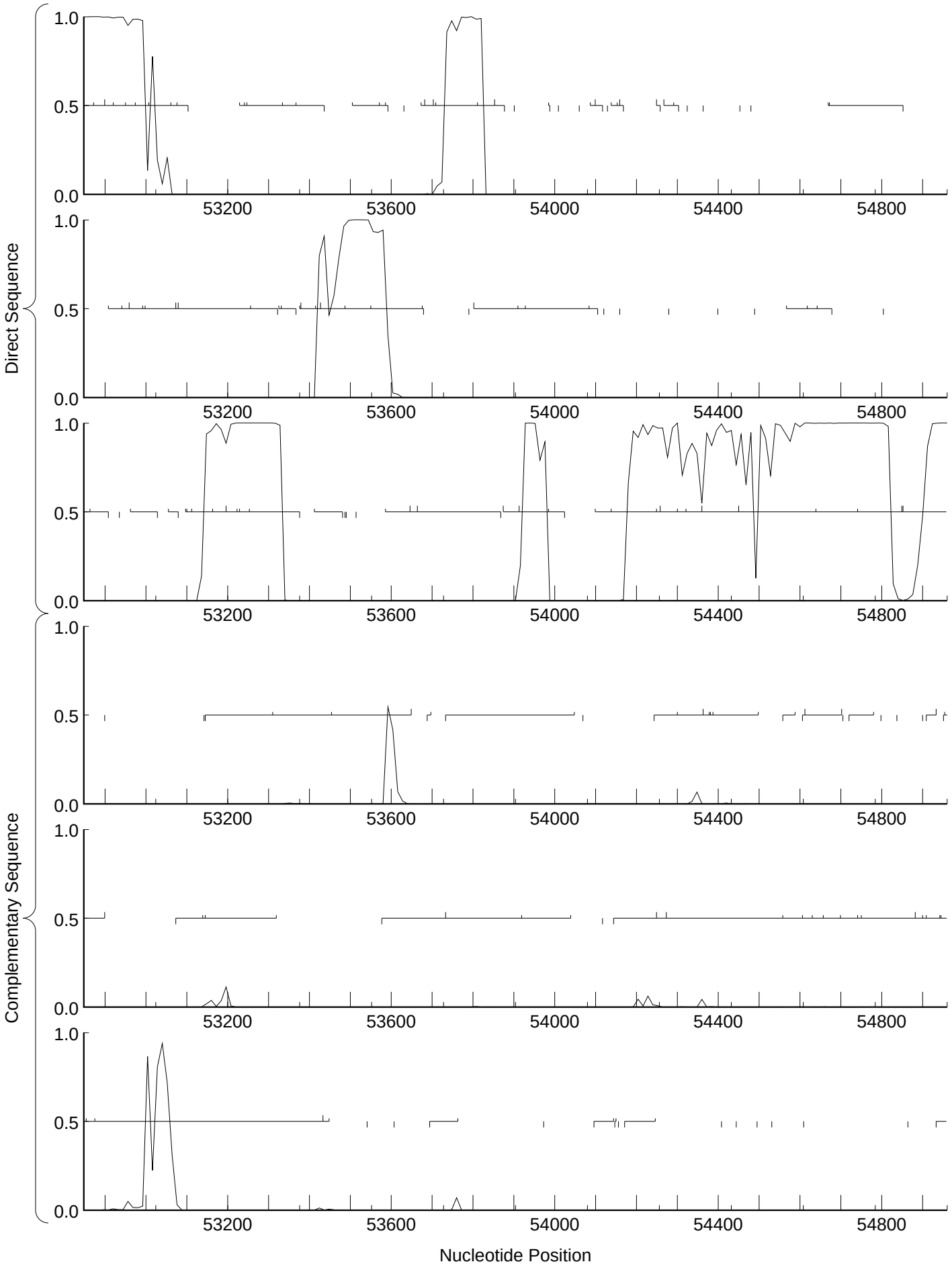
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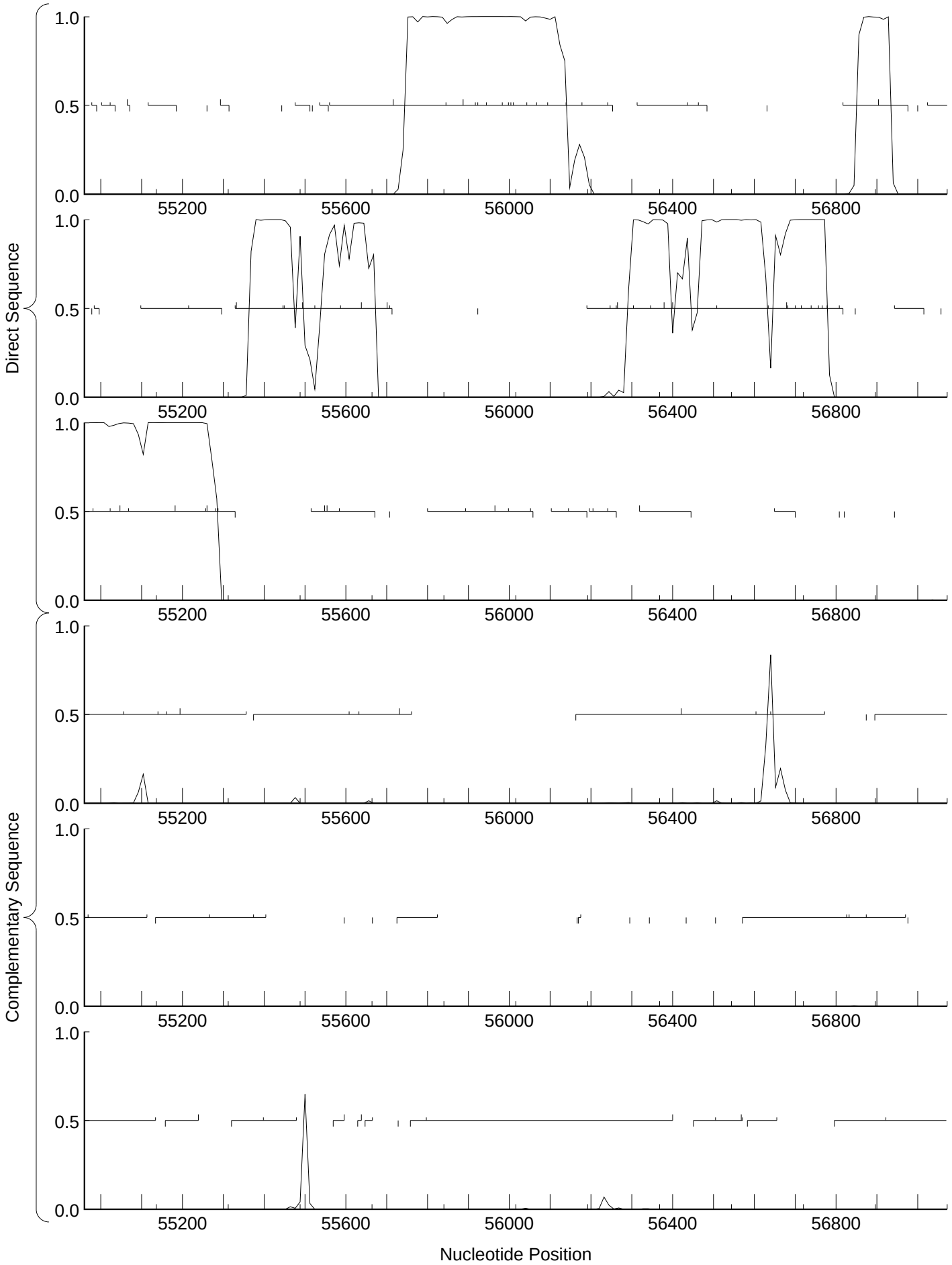


complete sequence, 59905 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K1, Order 4, Window 96, Step 12, 26/30

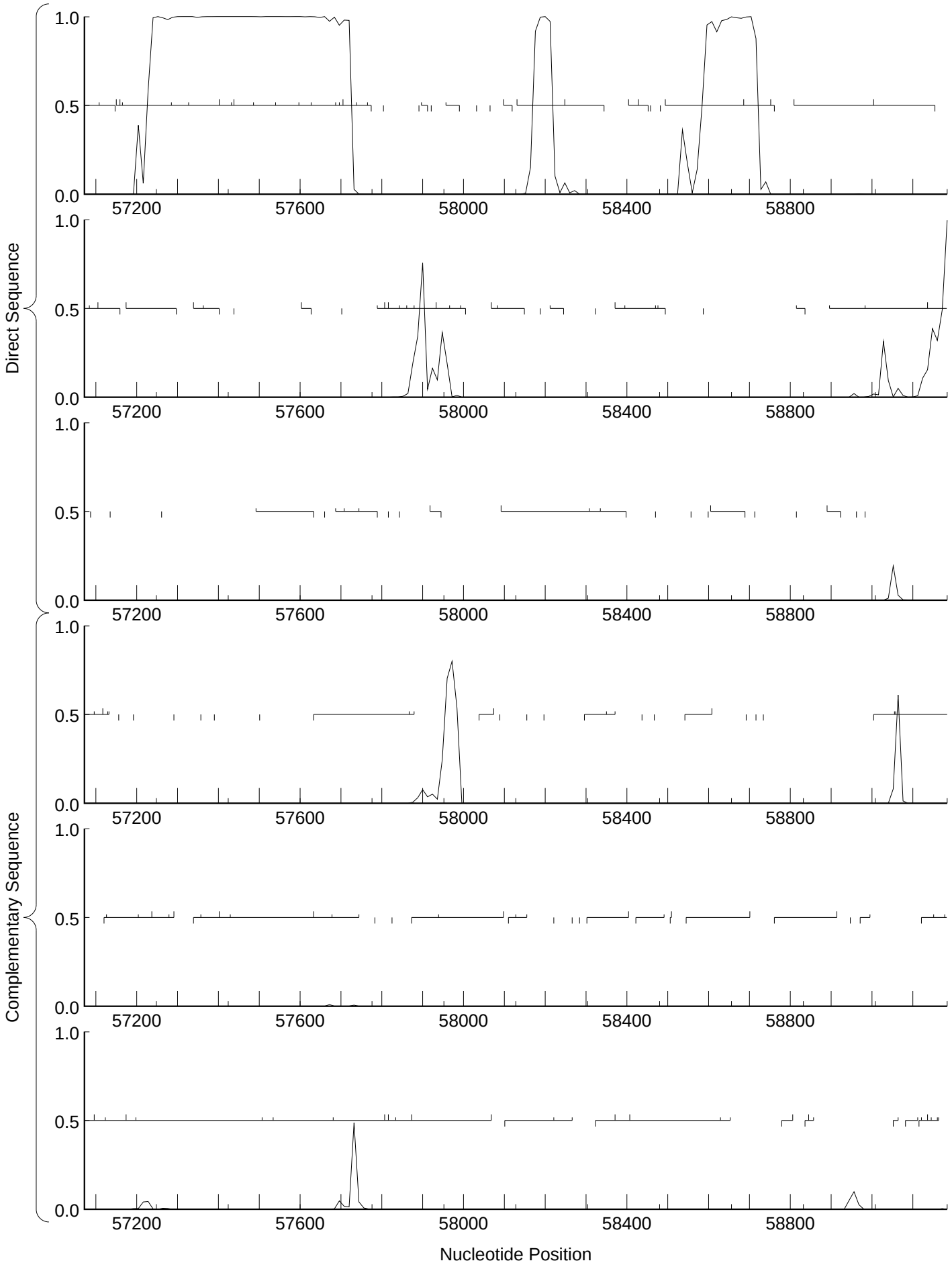


complete sequence, 59905 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K1, Order 4, Window 96, Step 12, 27/30




Direct Sequence
Complementary Sequence
1.0
0.5
0.0
55200
55600
56000
56400
56800
Nucleotide Position

complete sequence, 59905 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K1, Order 4, Window 96, Step 12, 29/30



complete sequence, 59905 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K1, Order 4, Window 96, Step 12, 30/30

