GeneMark

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

PROGRAM INFORMATION

```
Sequence         :  Mycobacterium phage Oksu complete sequence, 59317 bp including 10-base 3' overhang (CCGATGG
Analysis Date    :  3/29/24 at 10:13:02
Pages            :  30
Sequence Length  :  59317 bp
GC Content       :   60.91%

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

PS-Version       :  1.2

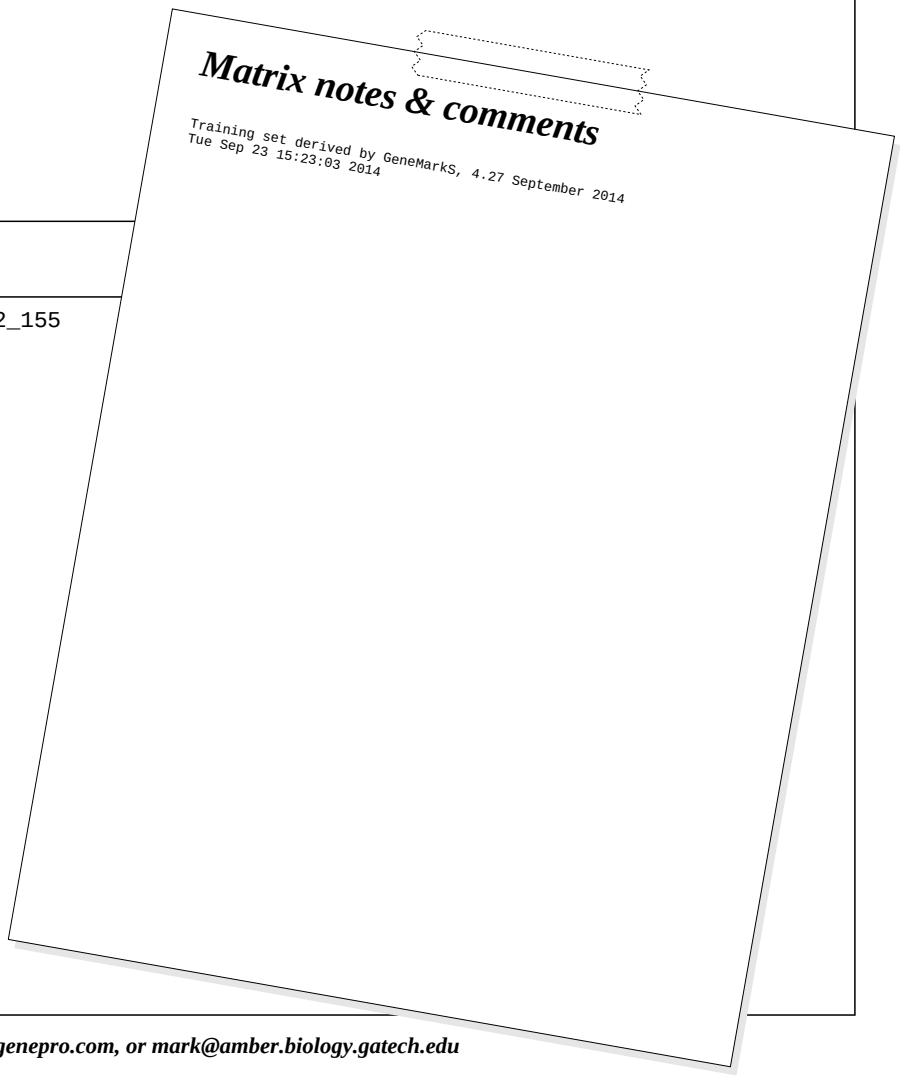
GeneMark Options :  PostScript graph,
                    Mark ORFs / splice sites,
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MATRIX INFORMATION

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Author     :  -

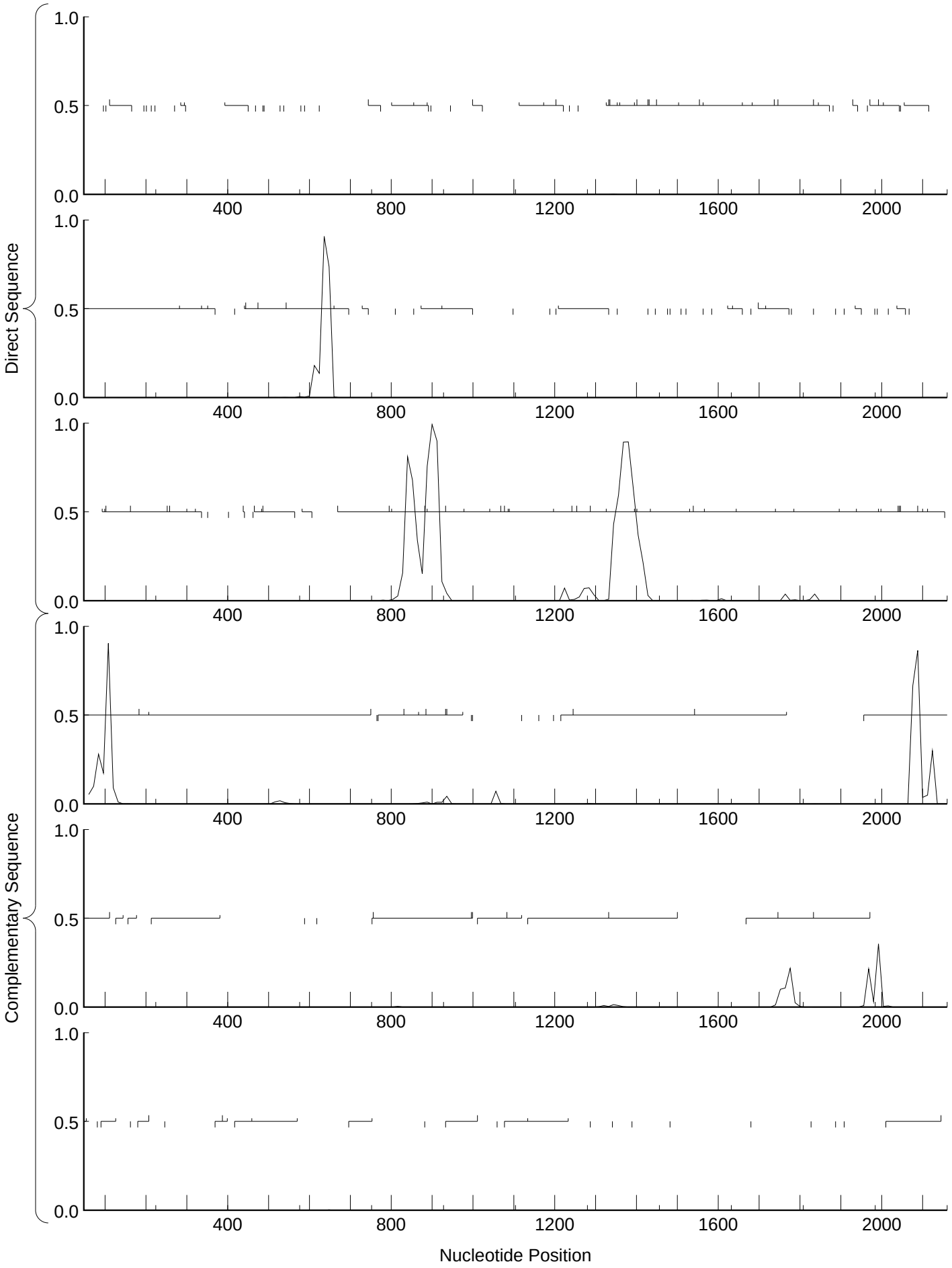
Order      :  4


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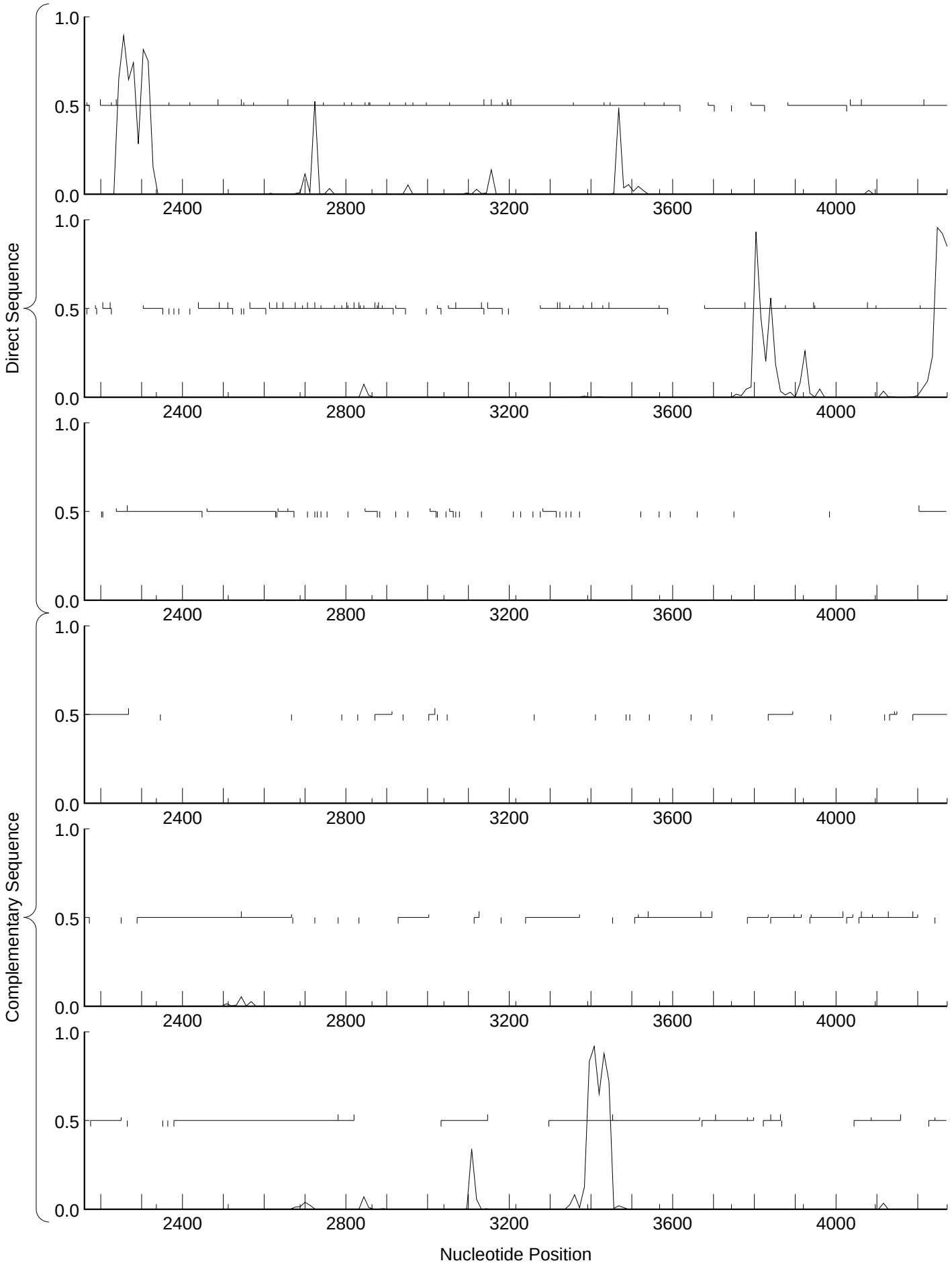


For help or information, send electronic mail to: custserv@genepro.com, or mark@amber.biology.gatech.edu

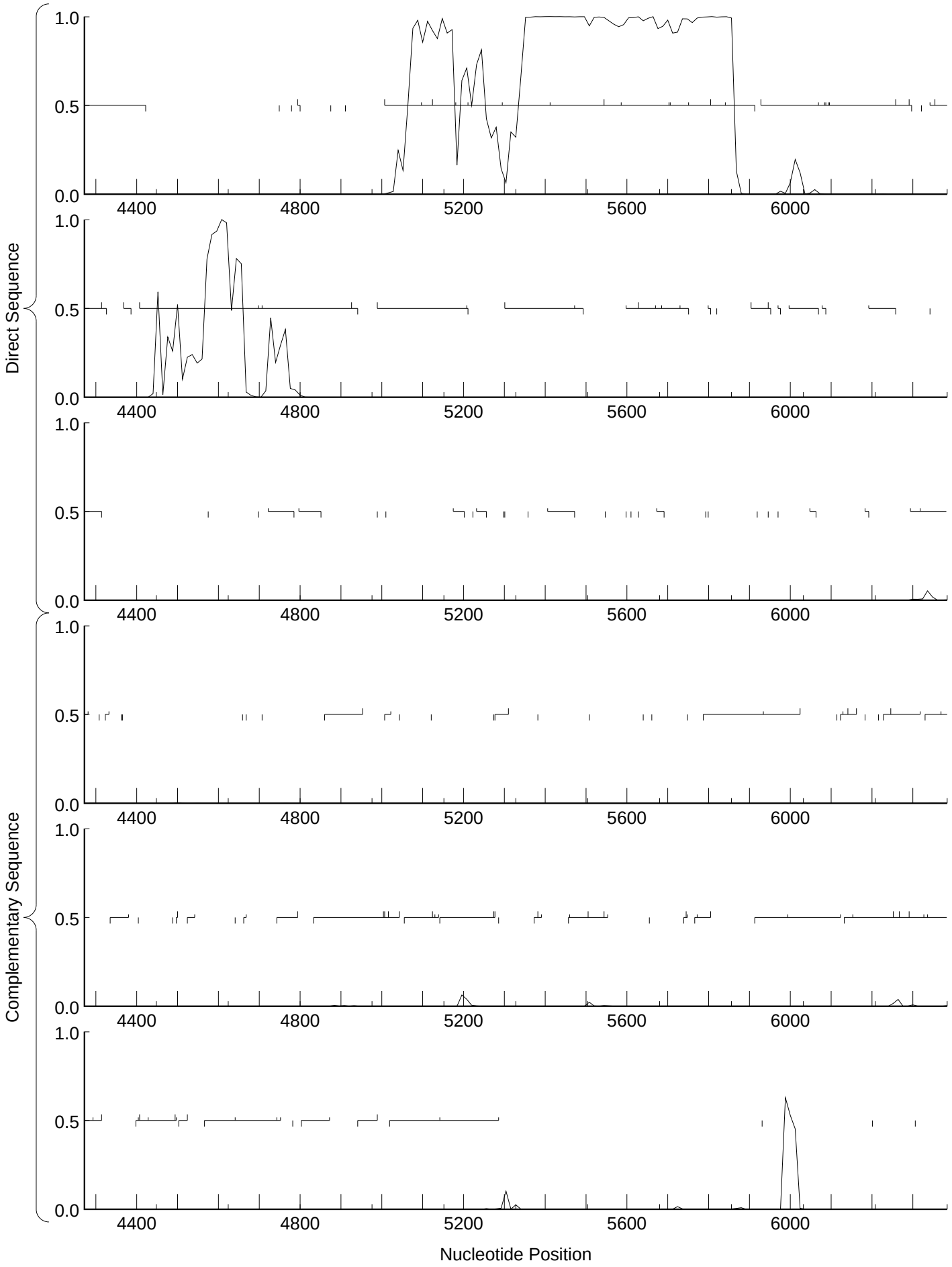
su complete sequence, 59317 bp including 10-base 3’ overhang (CCGATGGCAT), Cluster F1, Order 4, Window 96, Step 12, 2/30



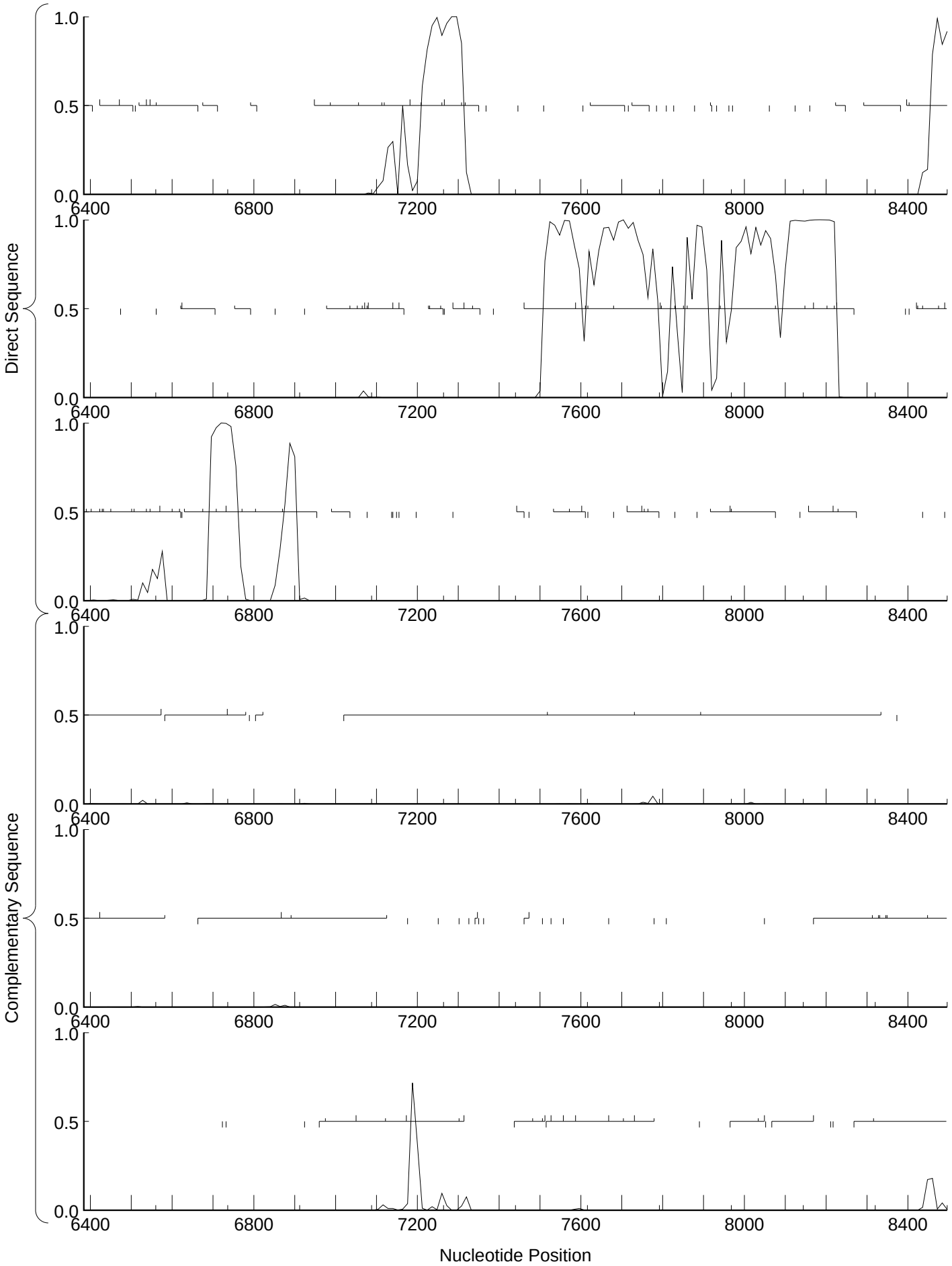
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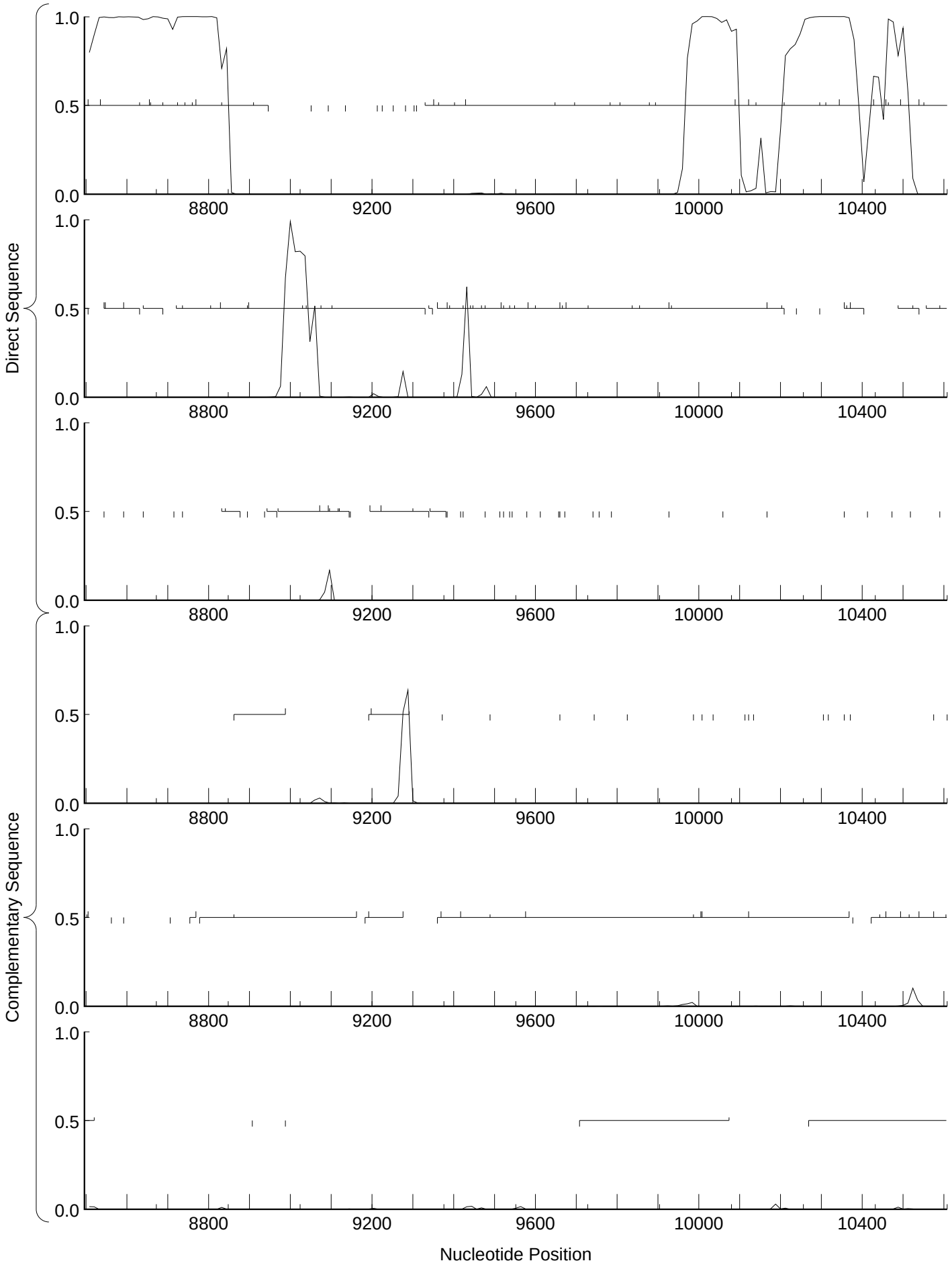
su complete sequence, 59317 bp including 10-base 3’ overhang (CCGATGGCAT), Cluster F1, Order 4, Window 96, Step 12, 4/30



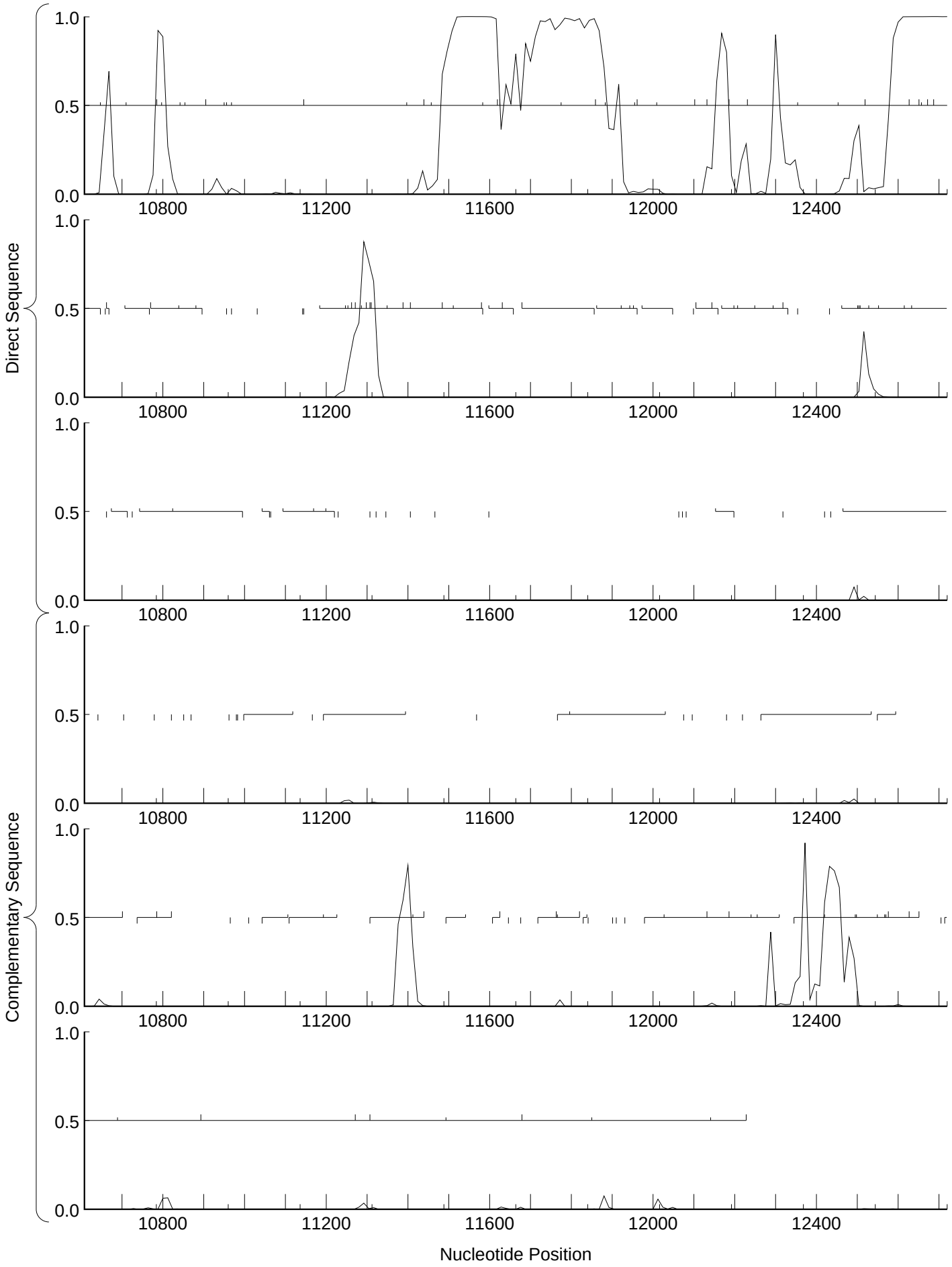
su complete sequence, 59317 bp including 10-base 3’ overhang (CCGATGGCAT), Cluster F1, Order 4, Window 96, Step 12, 5/30



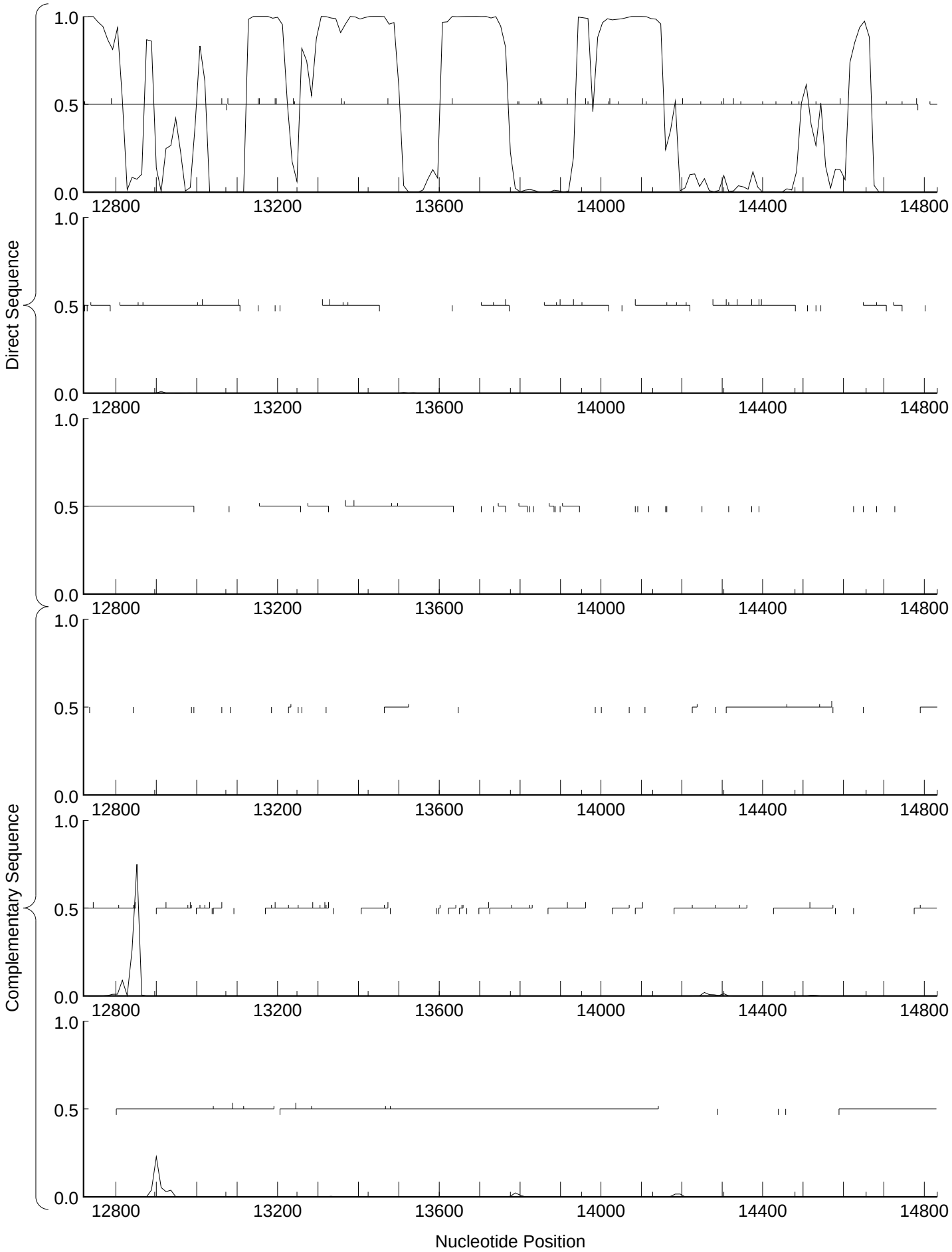
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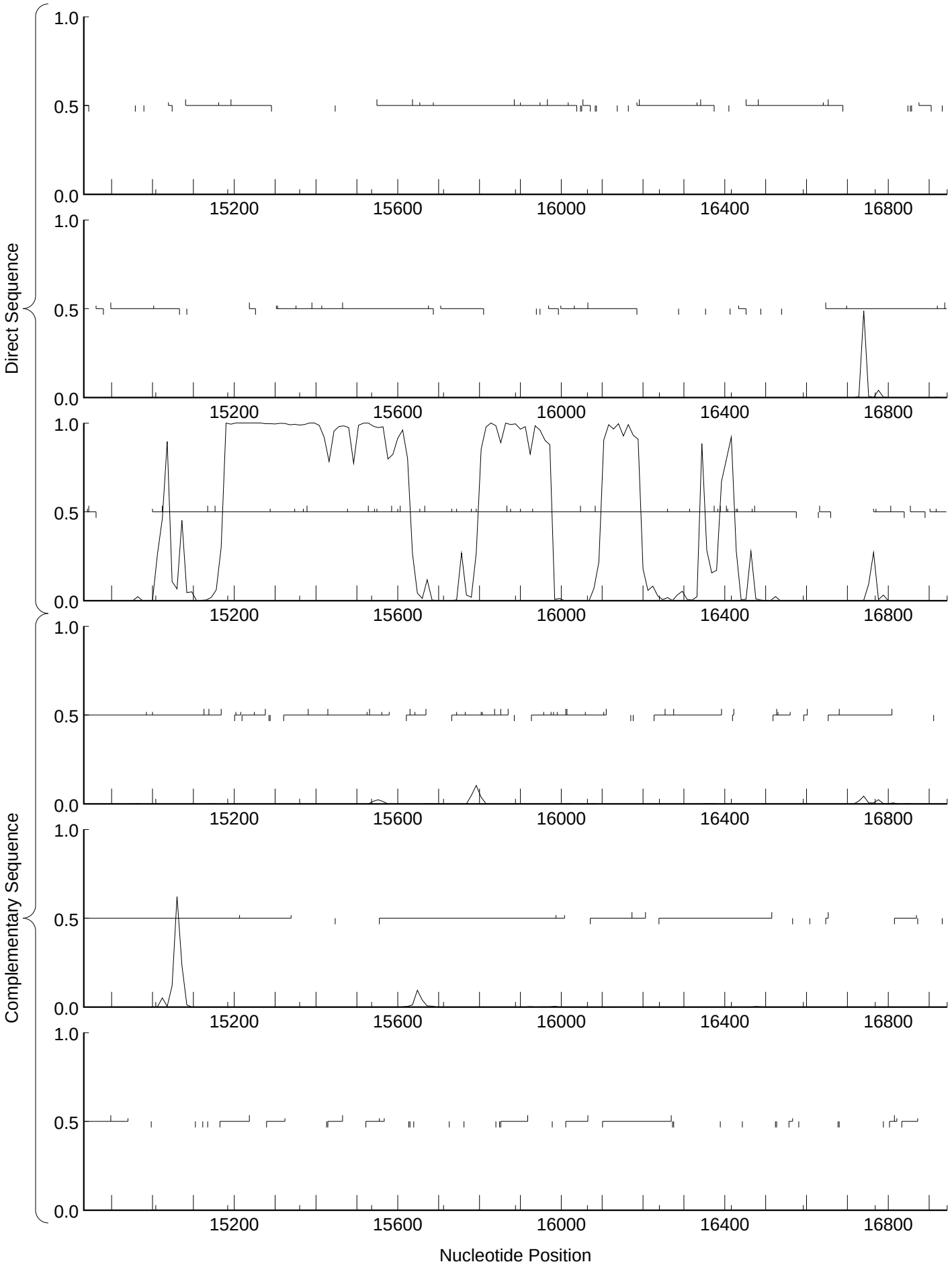
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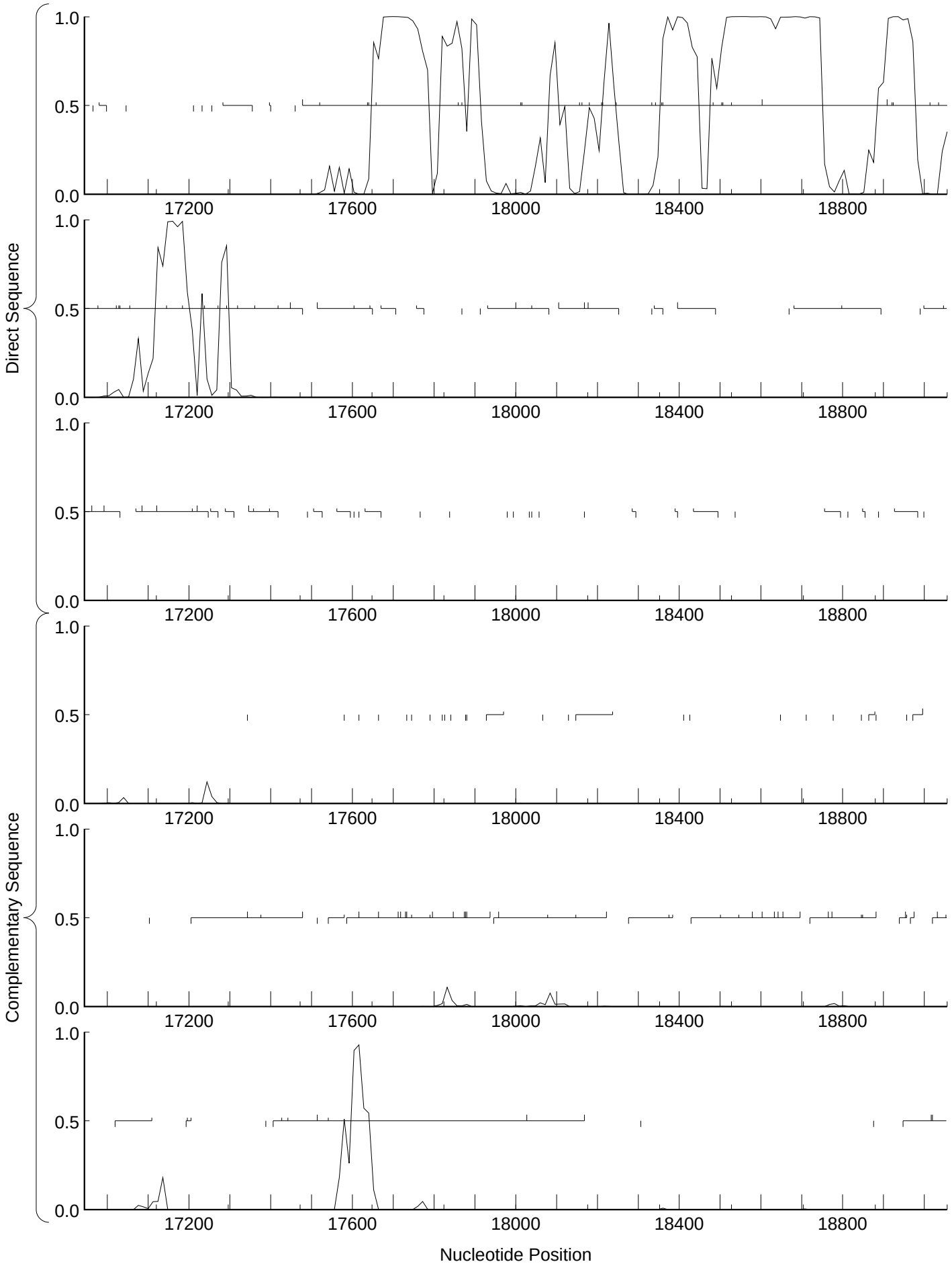
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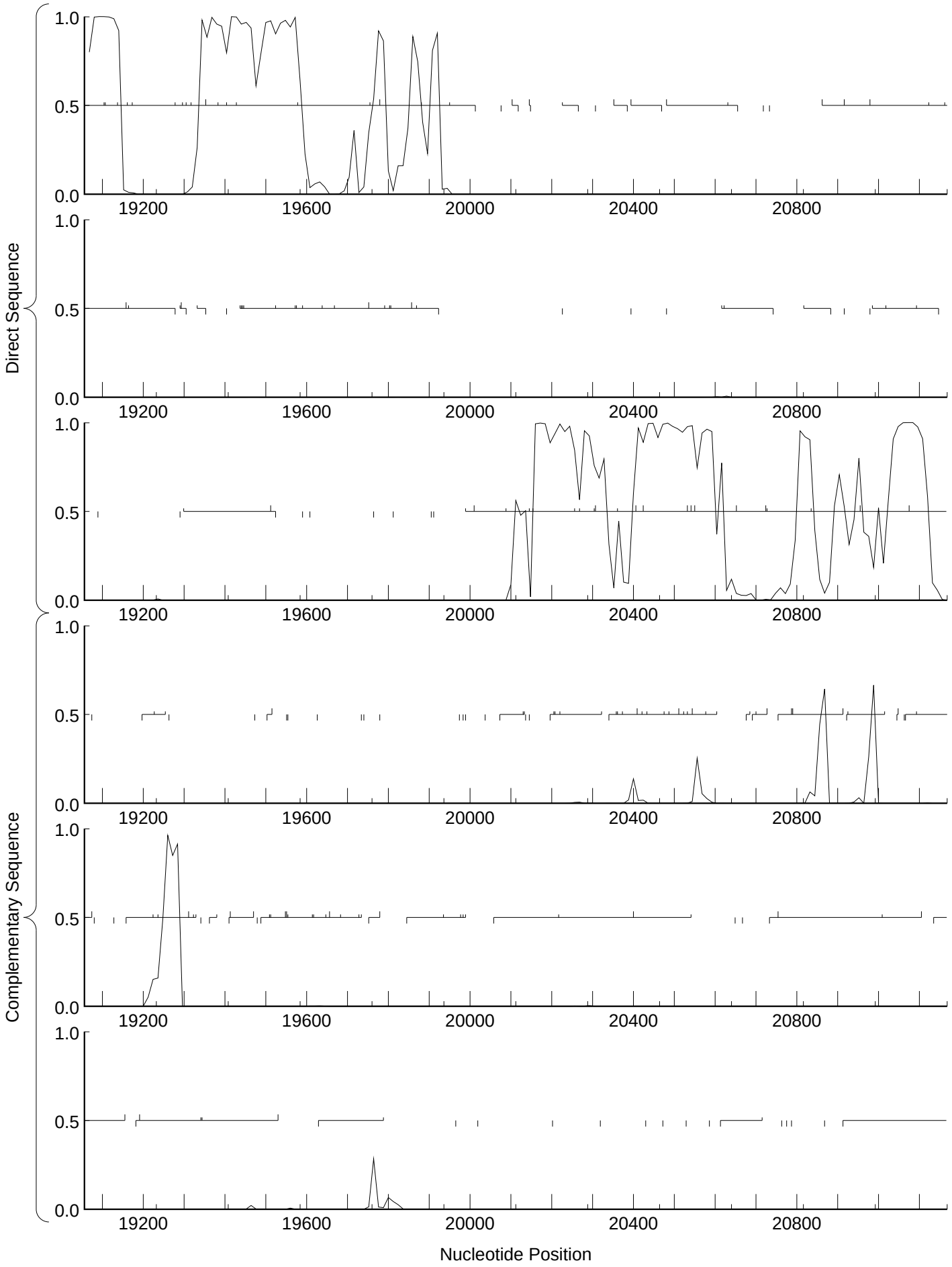


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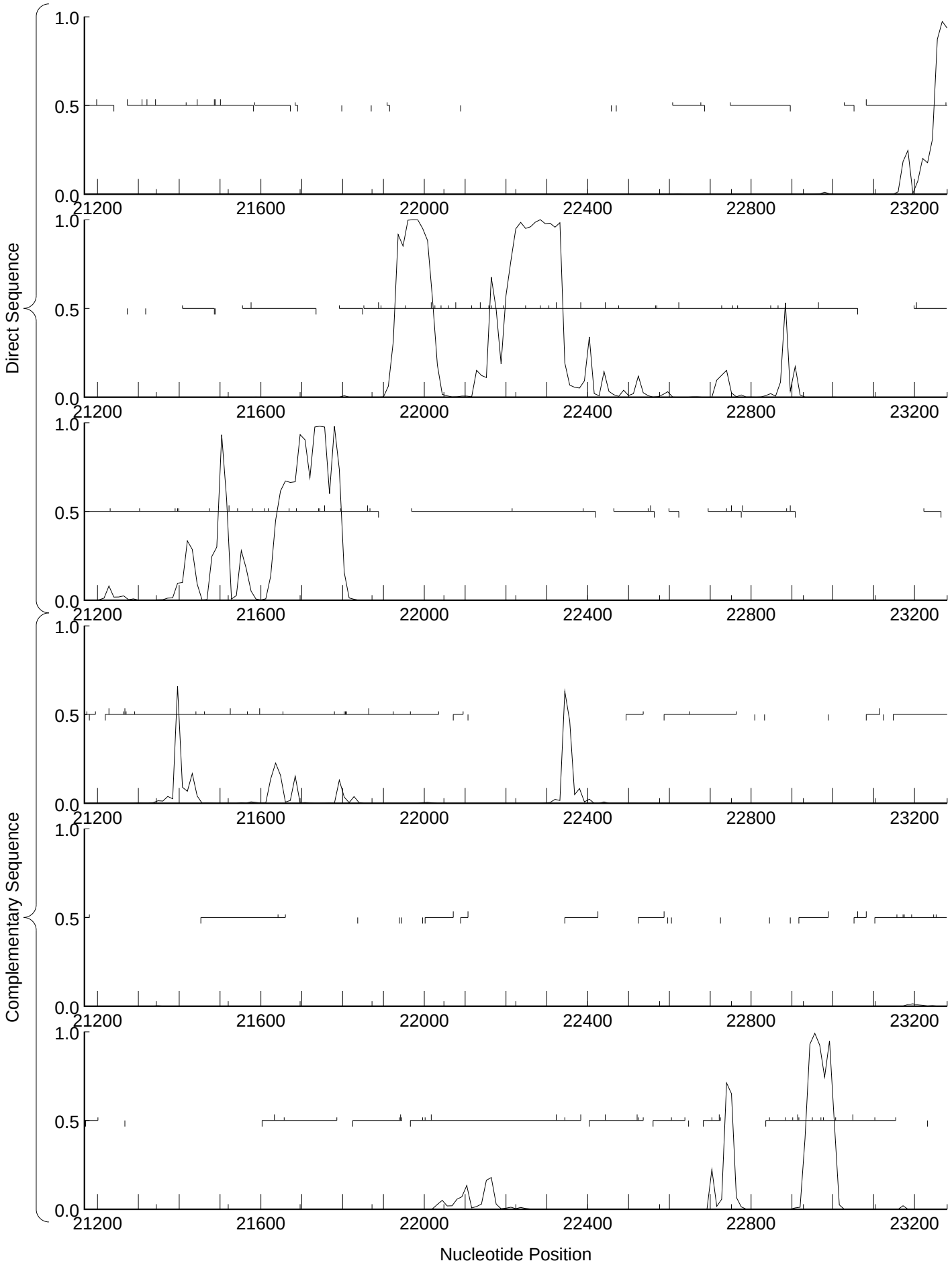


ı complete sequence, 59317 bp including 10-base 3’ overhang (CCGATGGCAT), Cluster F1, Order 4, Window 96, Step 12, 10/30

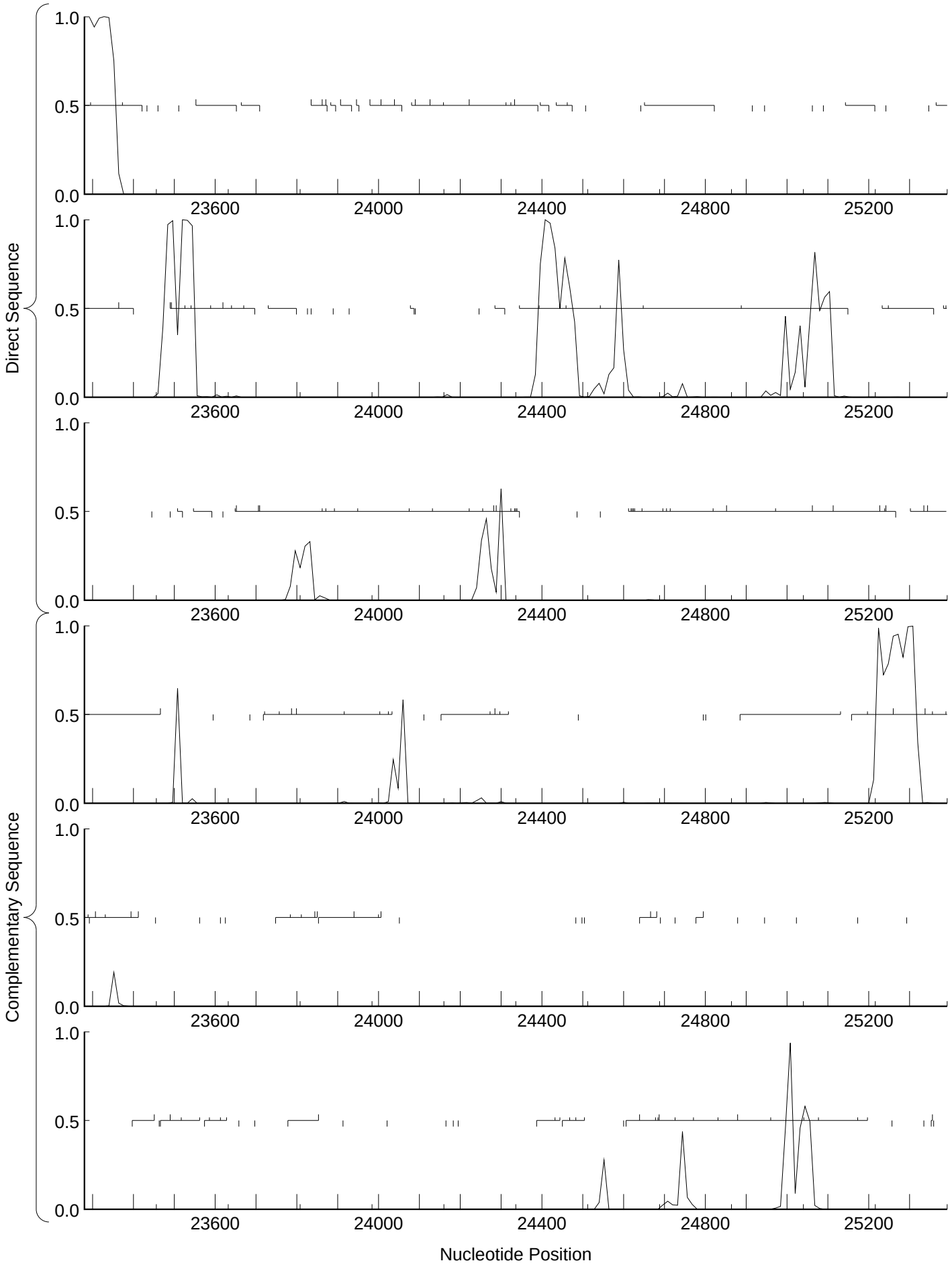



Direct Sequence
Complementary Sequence
1.0
0.5
0.0
19200
19600
20000
20400
20800
Nucleotide Position

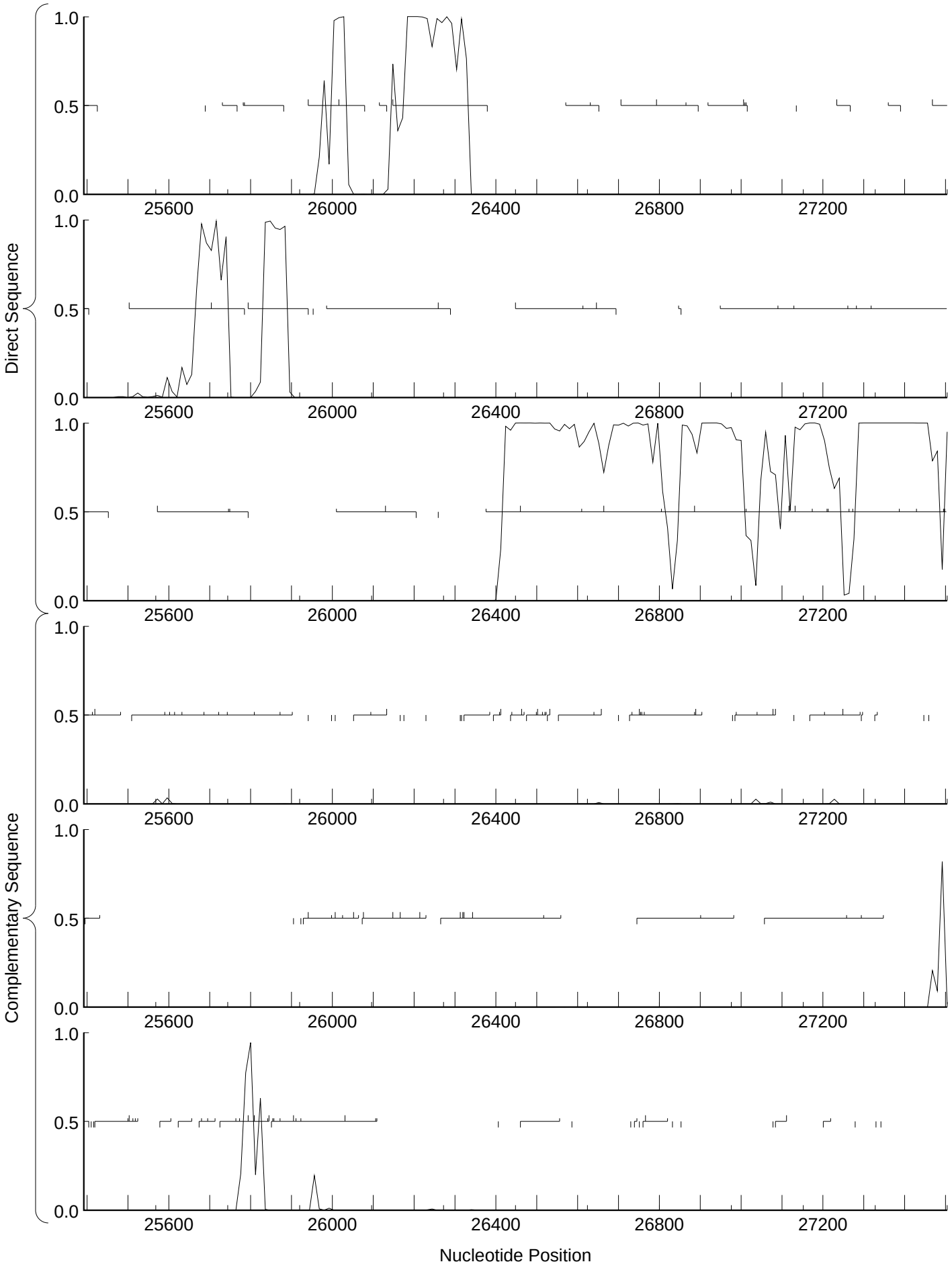
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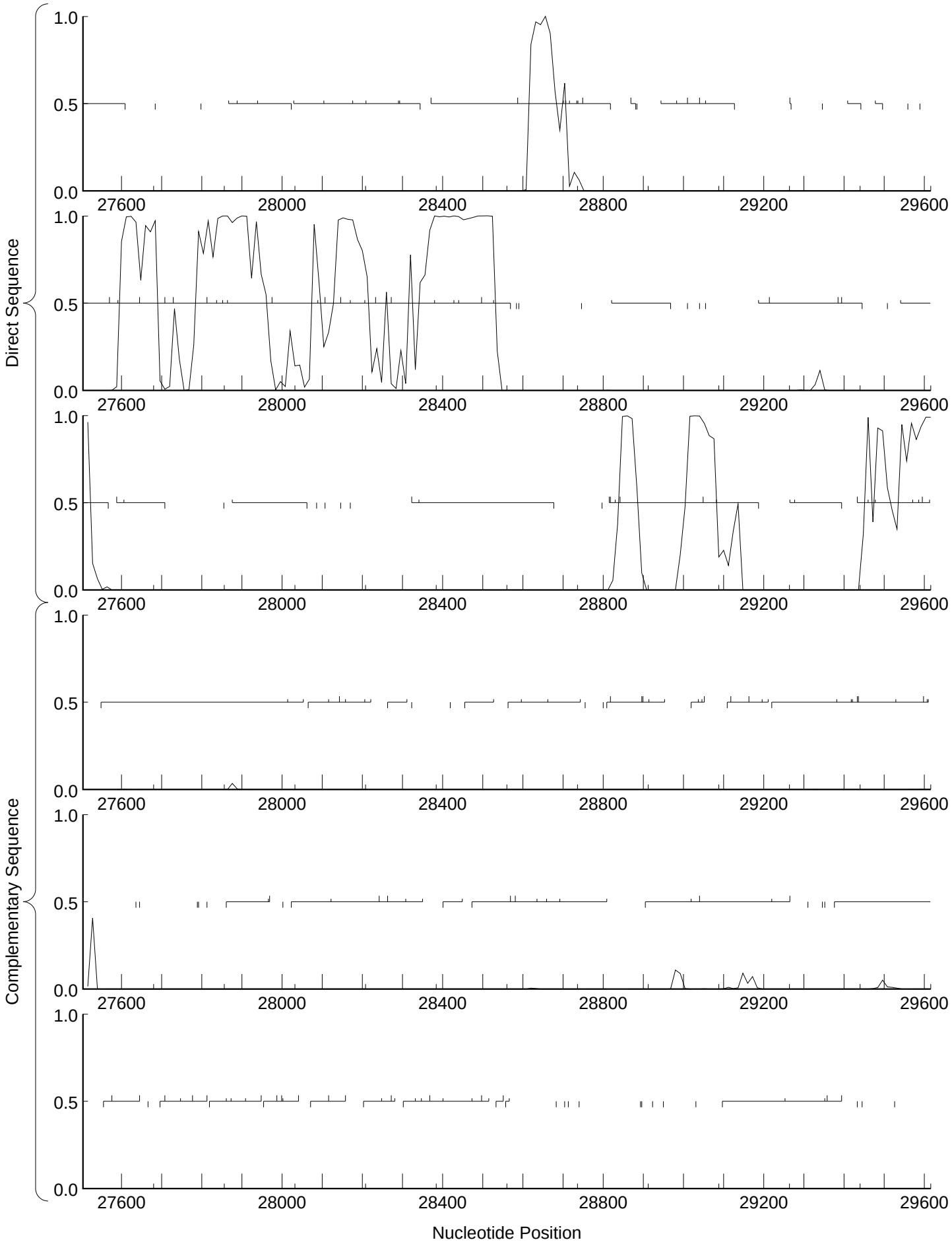
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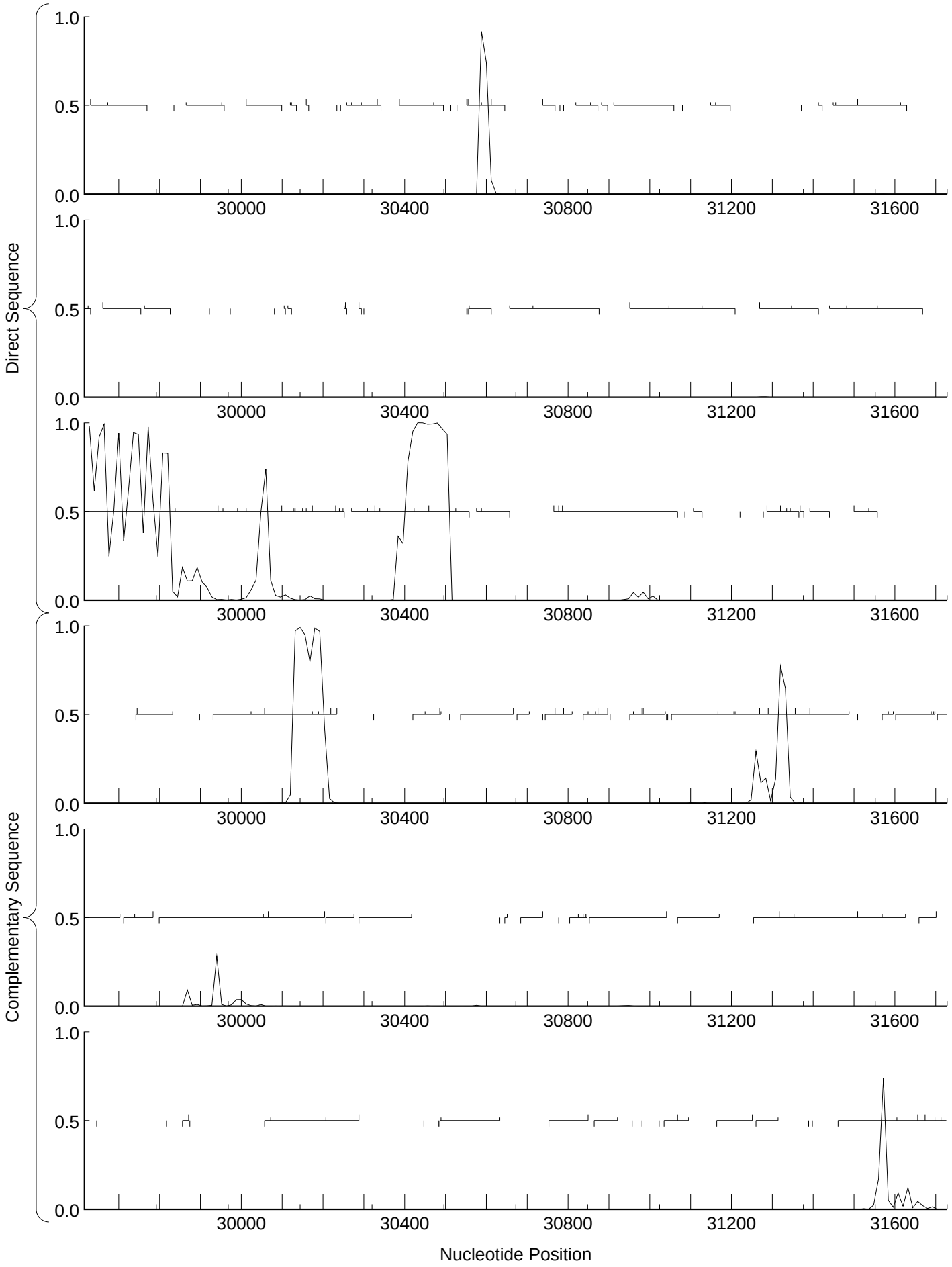


u complete sequence, 59317 bp including 10-base 3’ overhang (CCGATGGCAT), Cluster F1, Order 4, Window 96, Step 12, 14/30

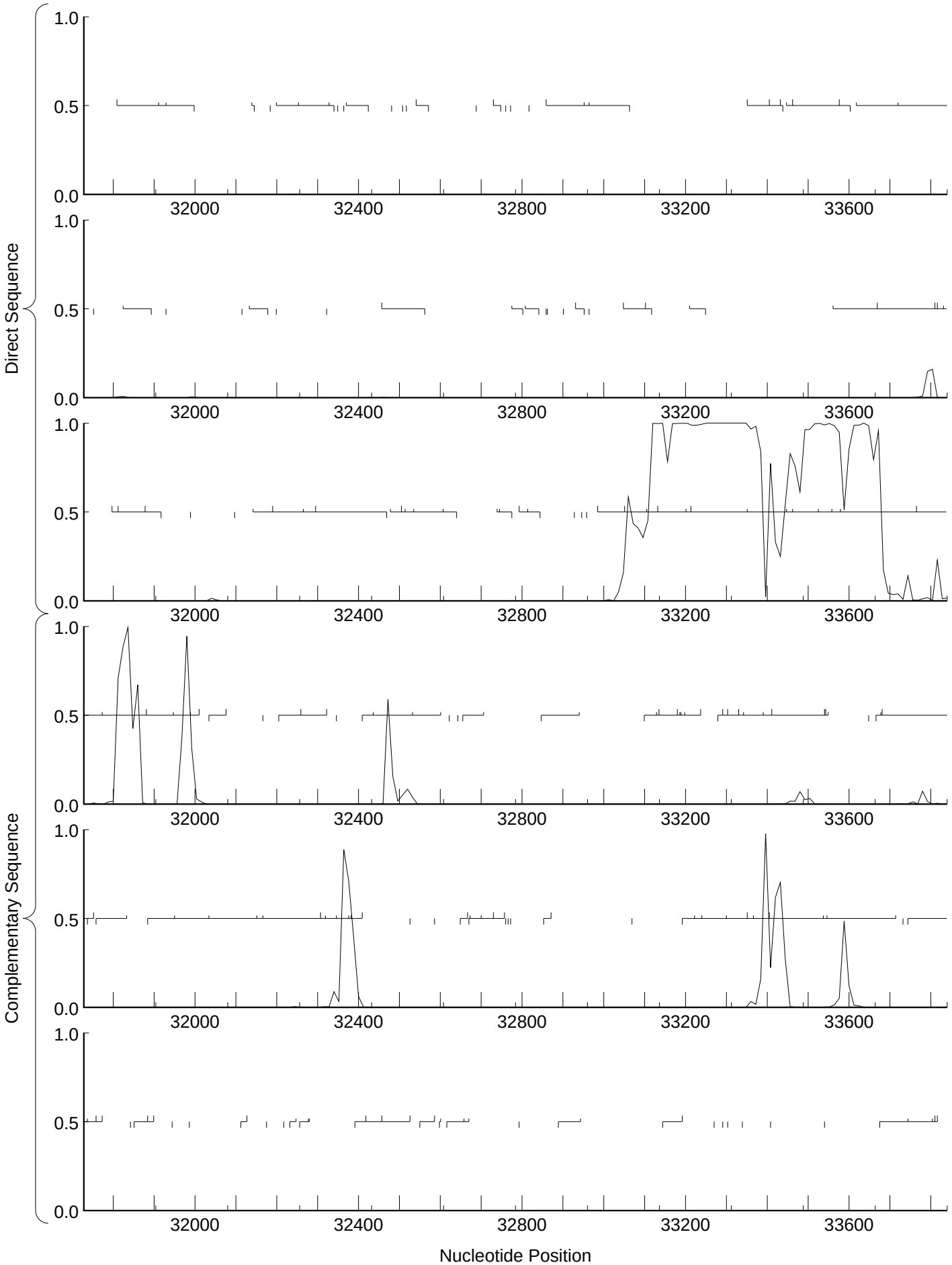


u complete sequence, 59317 bp including 10-base 3’ overhang (CCGATGGCAT), Cluster F1, Order 4, Window 96, Step 12, 15/30

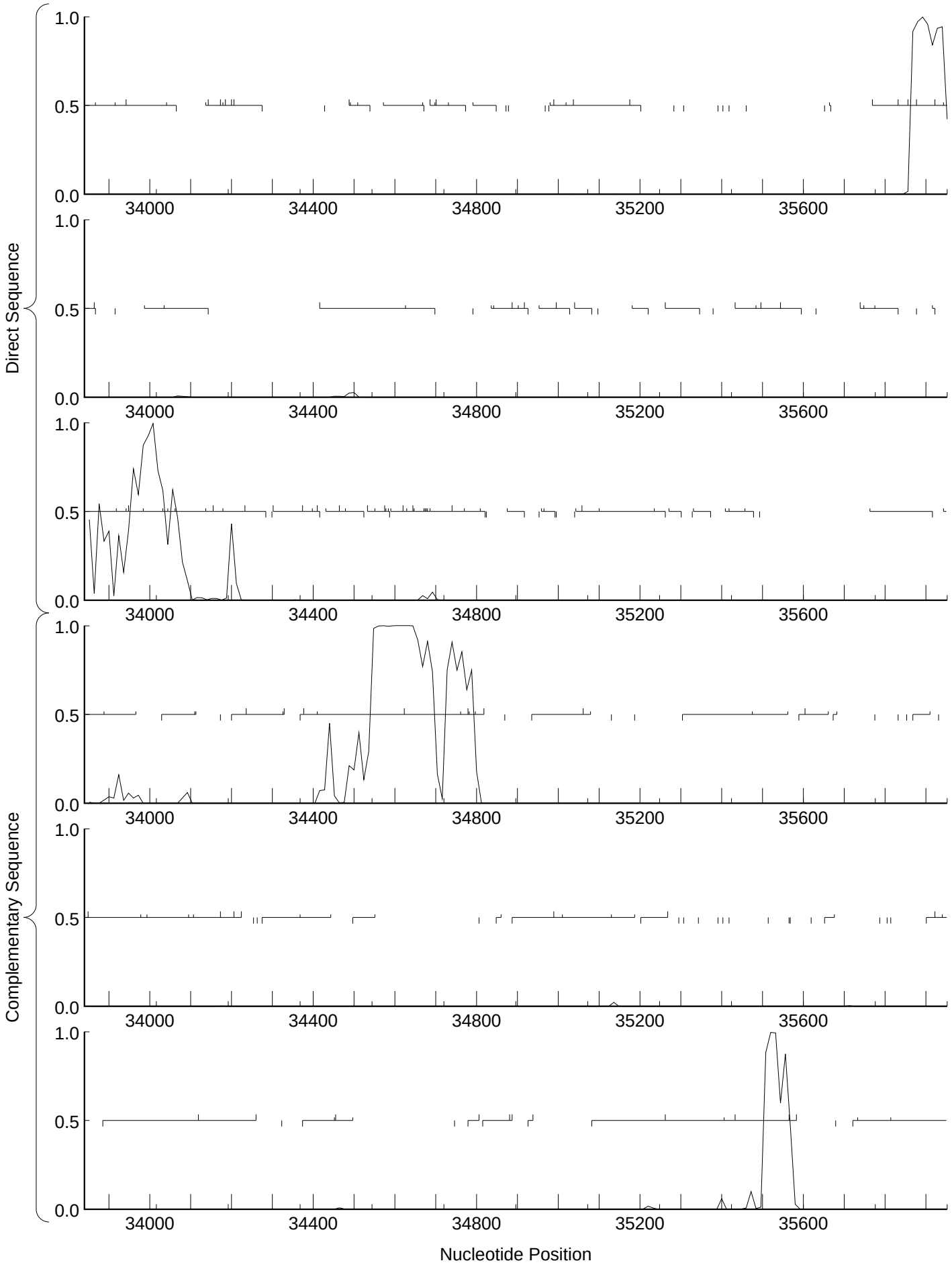


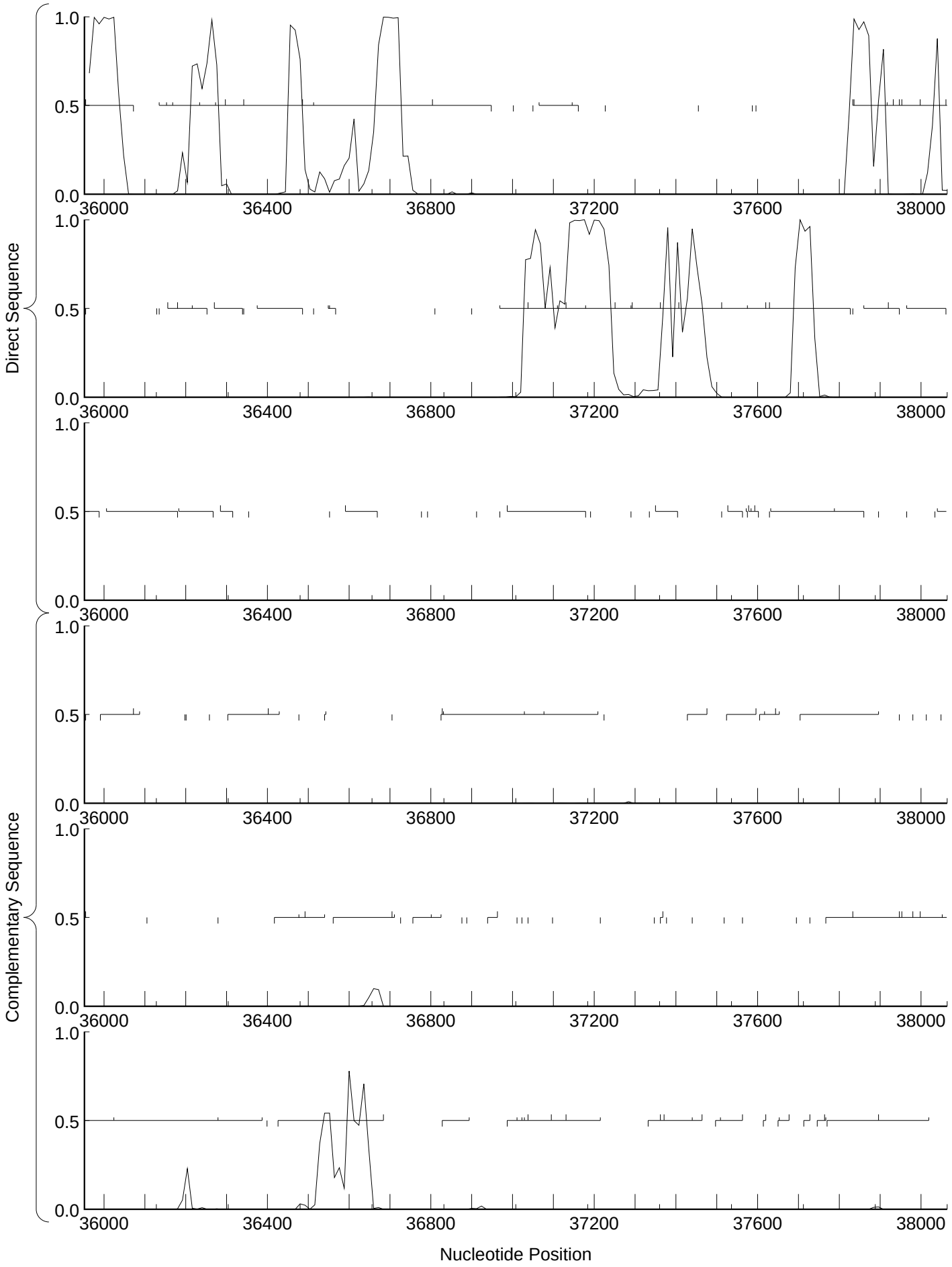

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
30000
30400
30800
31200
31600
Nucleotide Position

ı complete sequence, 59317 bp including 10-base 3’ overhang (CCGATGGCAT), Cluster F1, Order 4, Window 96, Step 12, 17/30

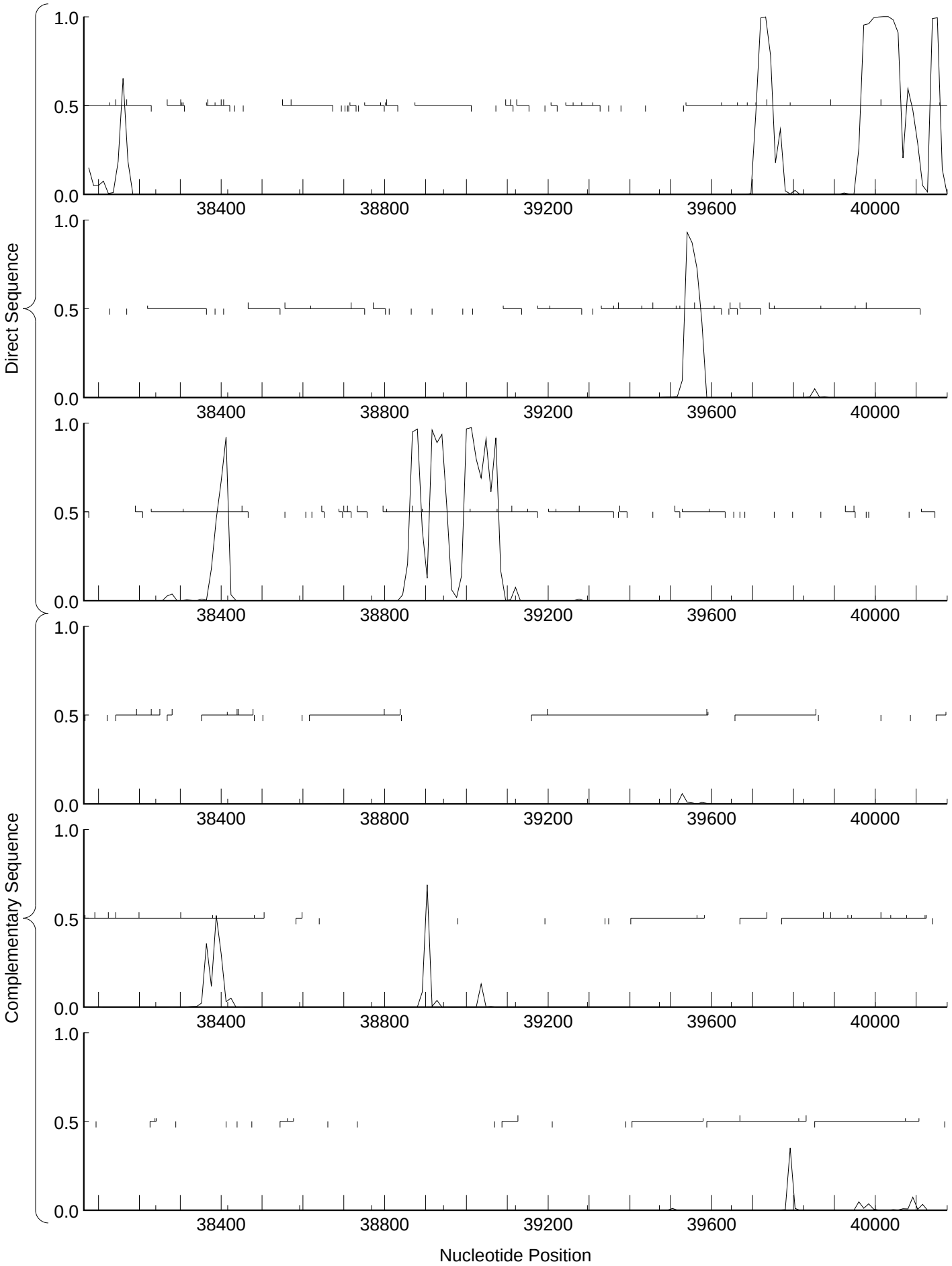


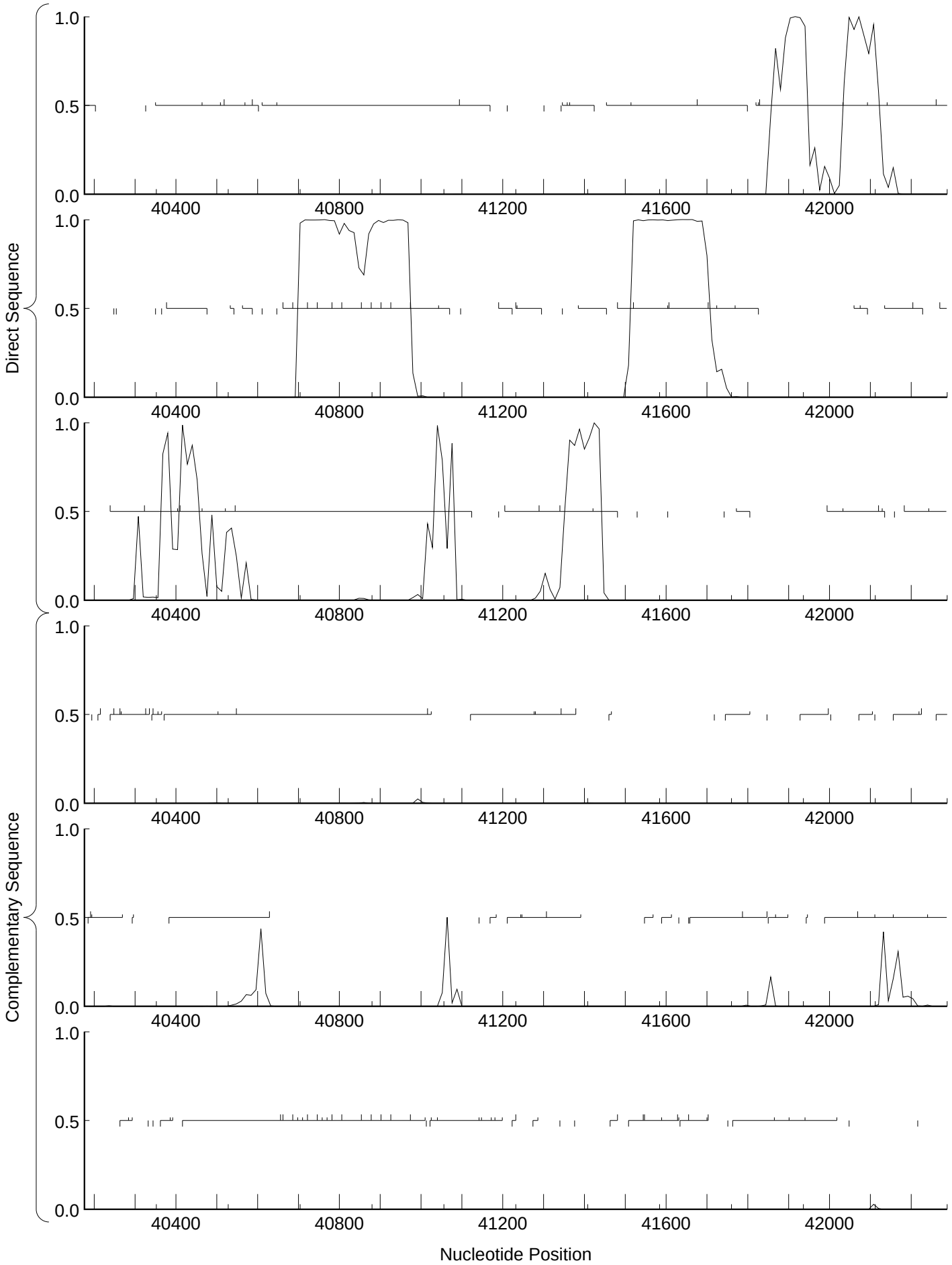
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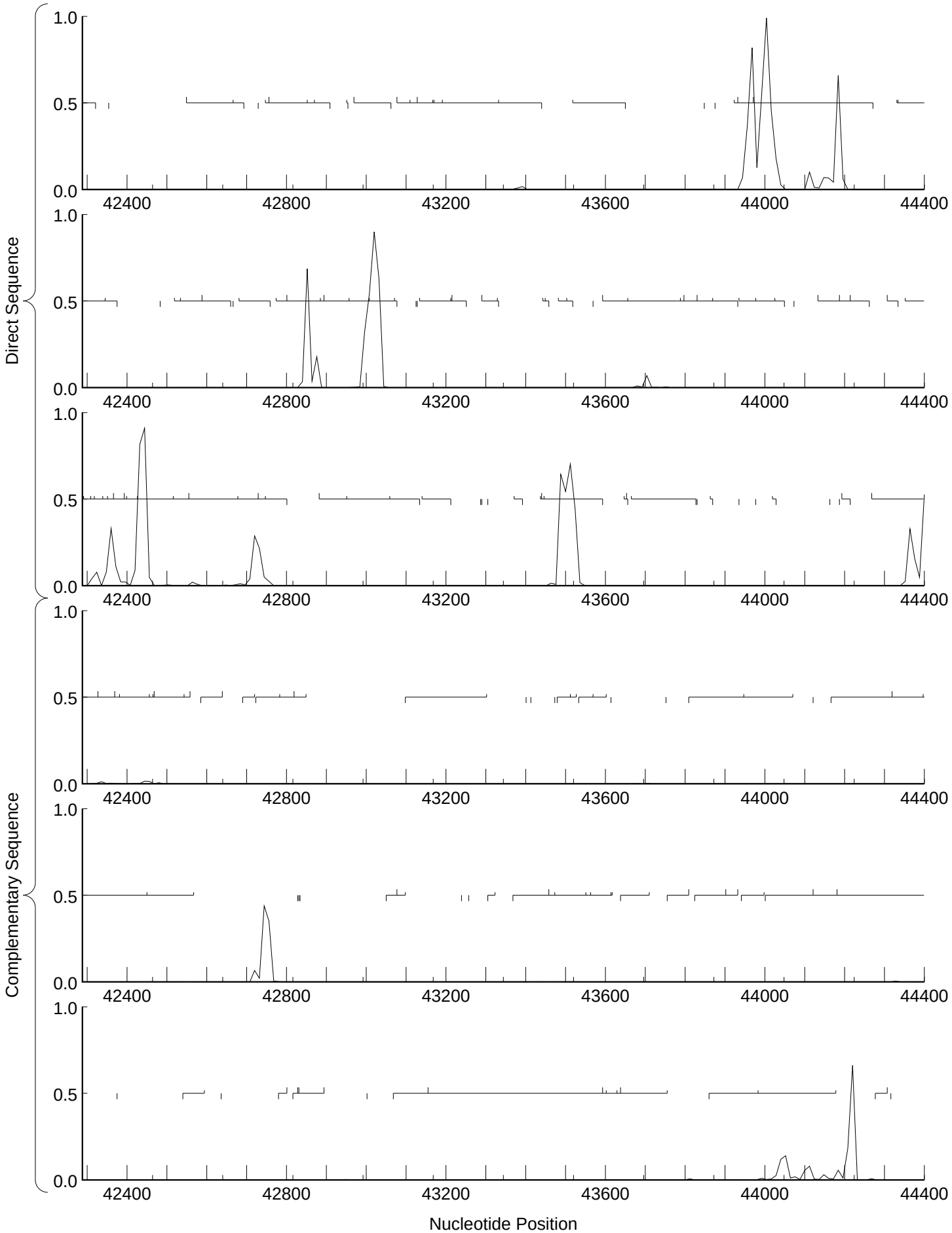



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Complementary Sequence
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0.5
0.0
36000
36400
36800
37200
37600
38000
Nucleotide Position

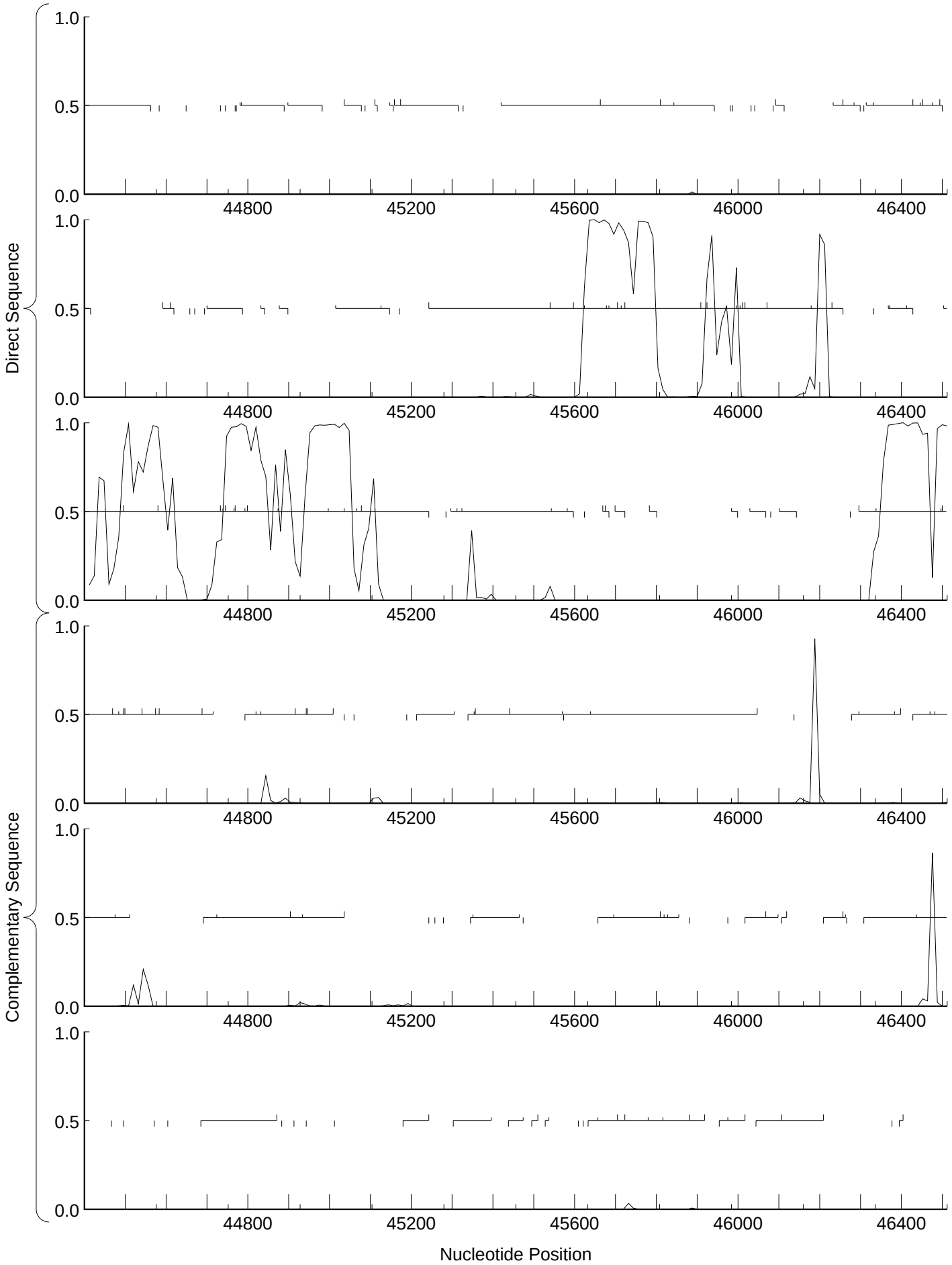
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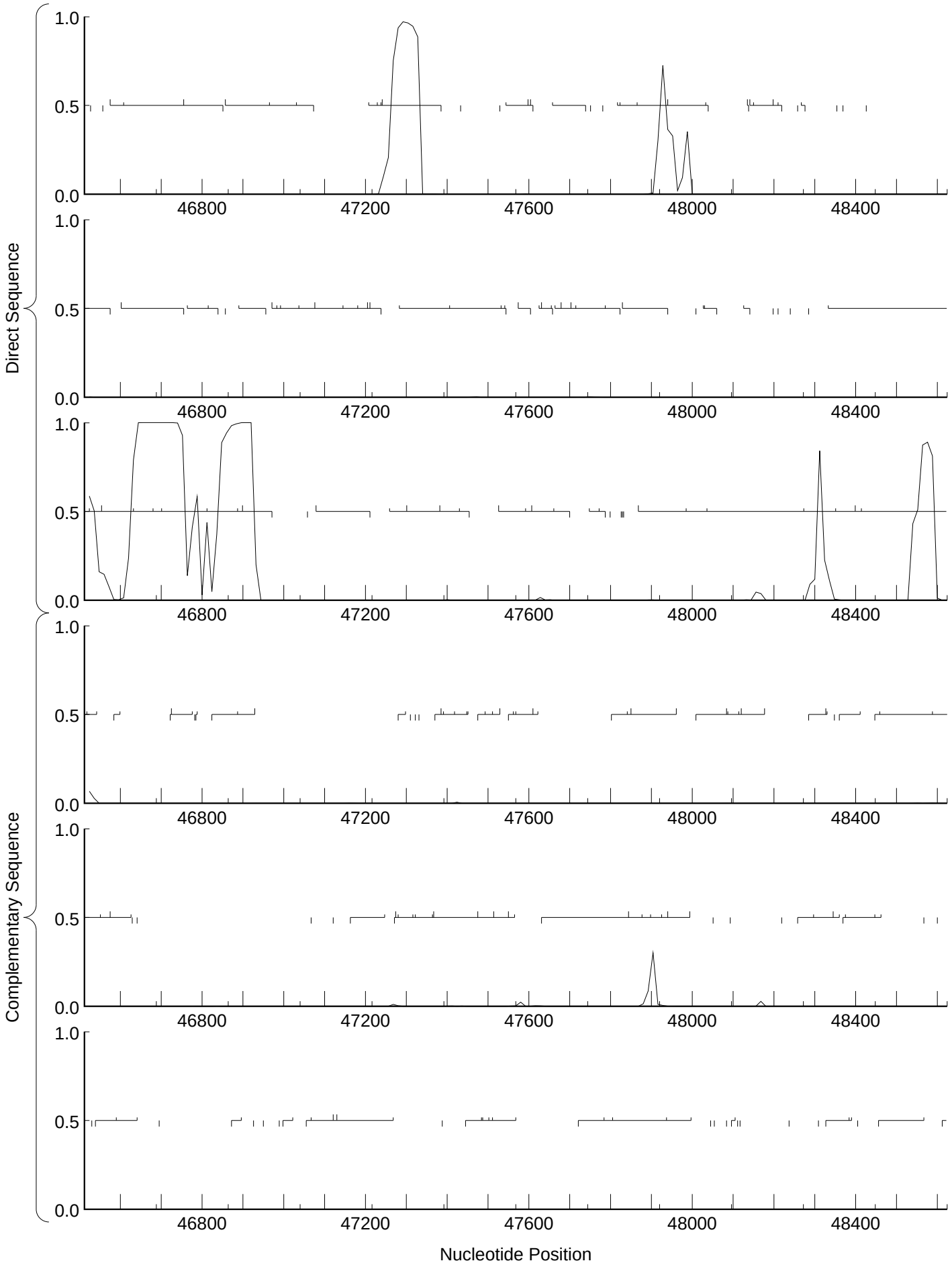



Direct Sequence
Complementary Sequence
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0.0
40400
40800
41200
41600
42000
Nucleotide Position

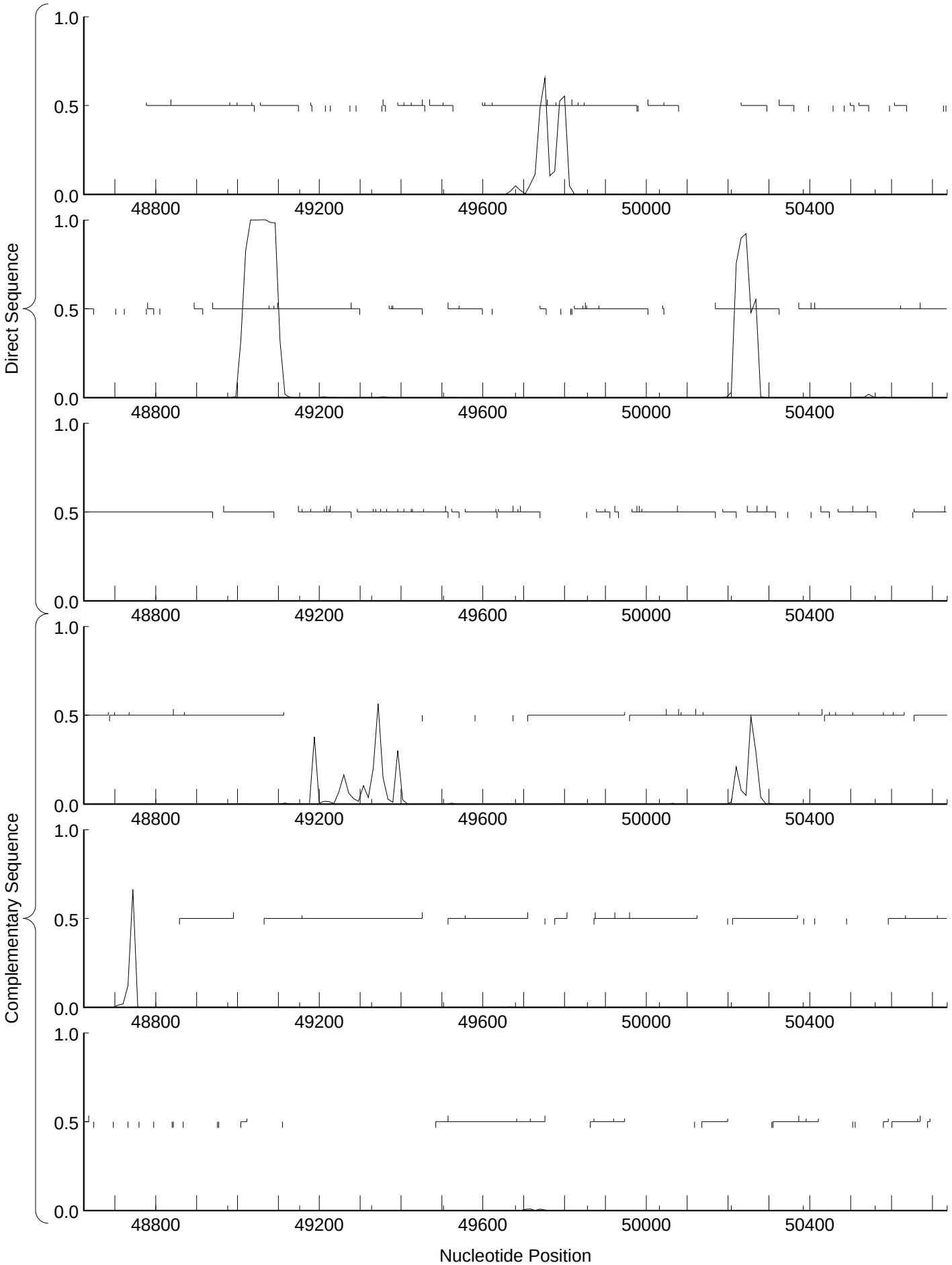

Direct Sequence
Complementary Sequence
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0.5
0.0
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42800
43200
43600
44000
44400
Nucleotide Position

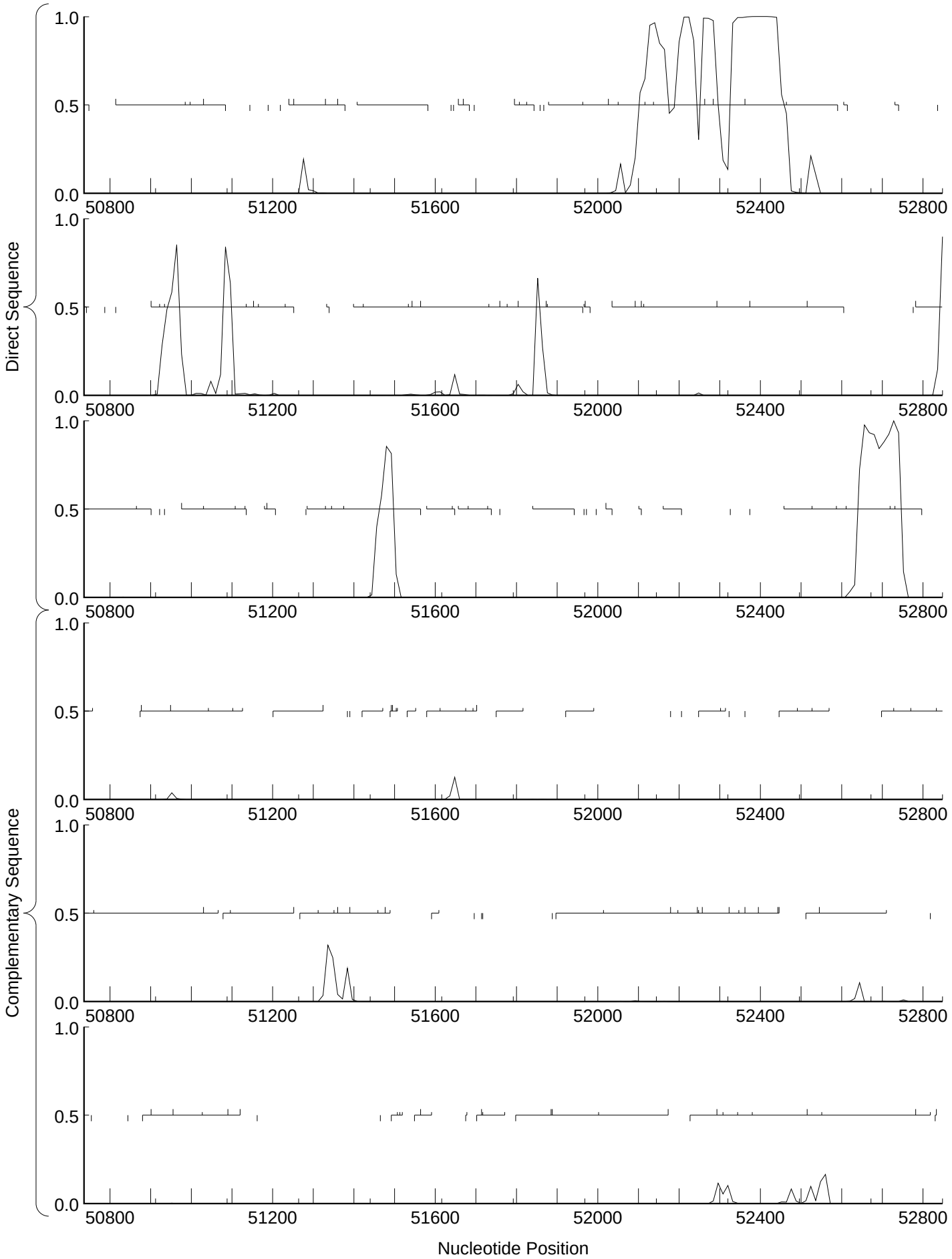
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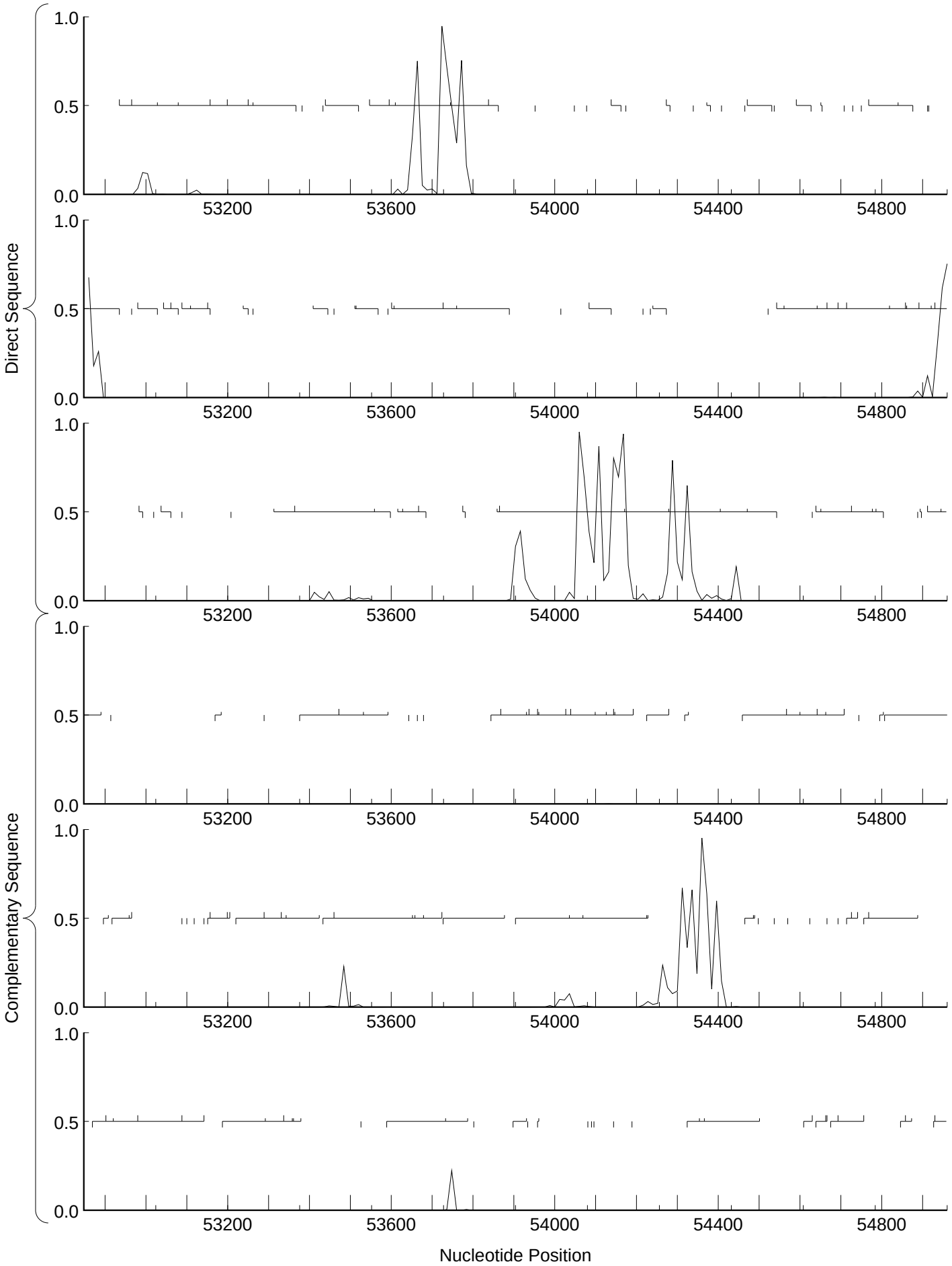

Direct Sequence
Complementary Sequence
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0.5
0.0
46800
47200
47600
48000
48400
Nucleotide Position

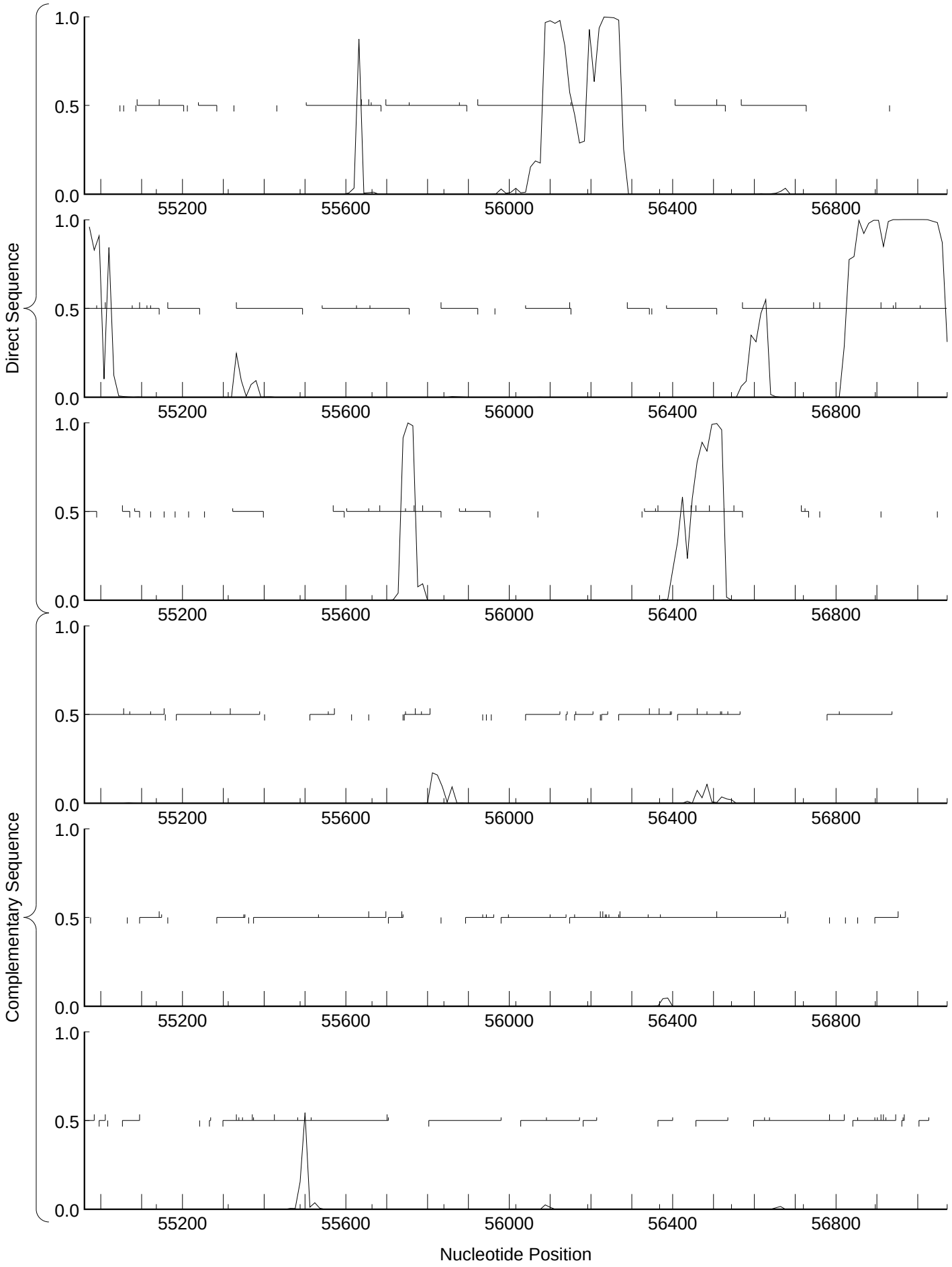
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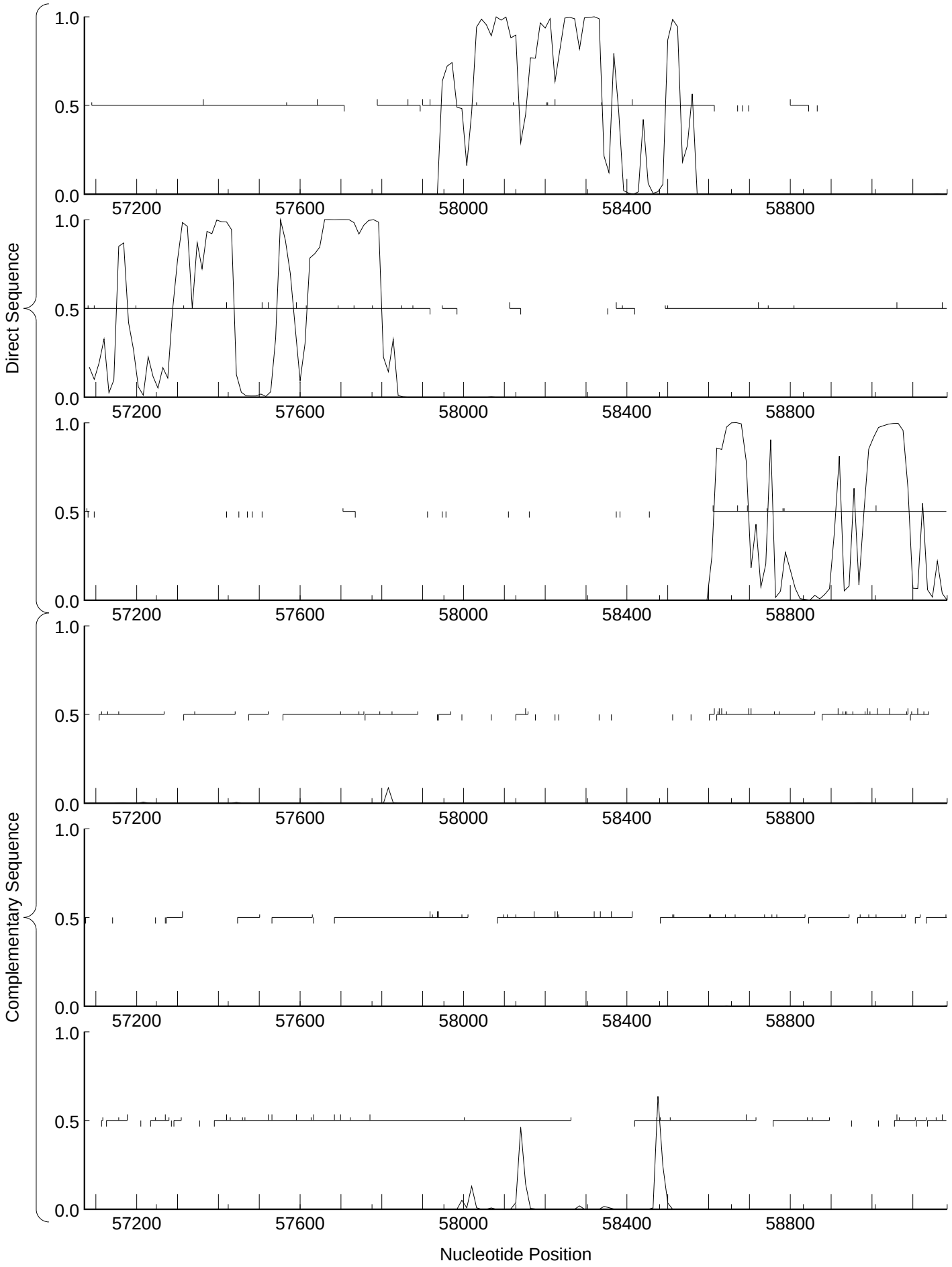



Direct Sequence
Complementary Sequence
1.0
0.5
0.0
50800
51200
51600
52000
52400
52800
Nucleotide Position

ı complete sequence, 59317 bp including 10-base 3’ overhang (CCGATGGCAT), Cluster F1, 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


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
57200
57600
58000
58400
58800
Nucleotide Position

ı complete sequence, 59317 bp including 10-base 3’ overhang (CCGATGGCAT), Cluster F1, Order 4, Window 96, Step 12, 30/30

