GeneMark

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

PROGRAM INFORMATION

```
Sequence         :  Gordonia phage Lysidious complete sequence, 50948 bp including 10-base 3' overhang (TCTCCGG
Analysis Date    :  3/29/24 at 5:21:14
Pages            :  26
Sequence Length  :  50948 bp
GC Content       :   67.00%

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     :  -
Author     :  -

Order      :  4

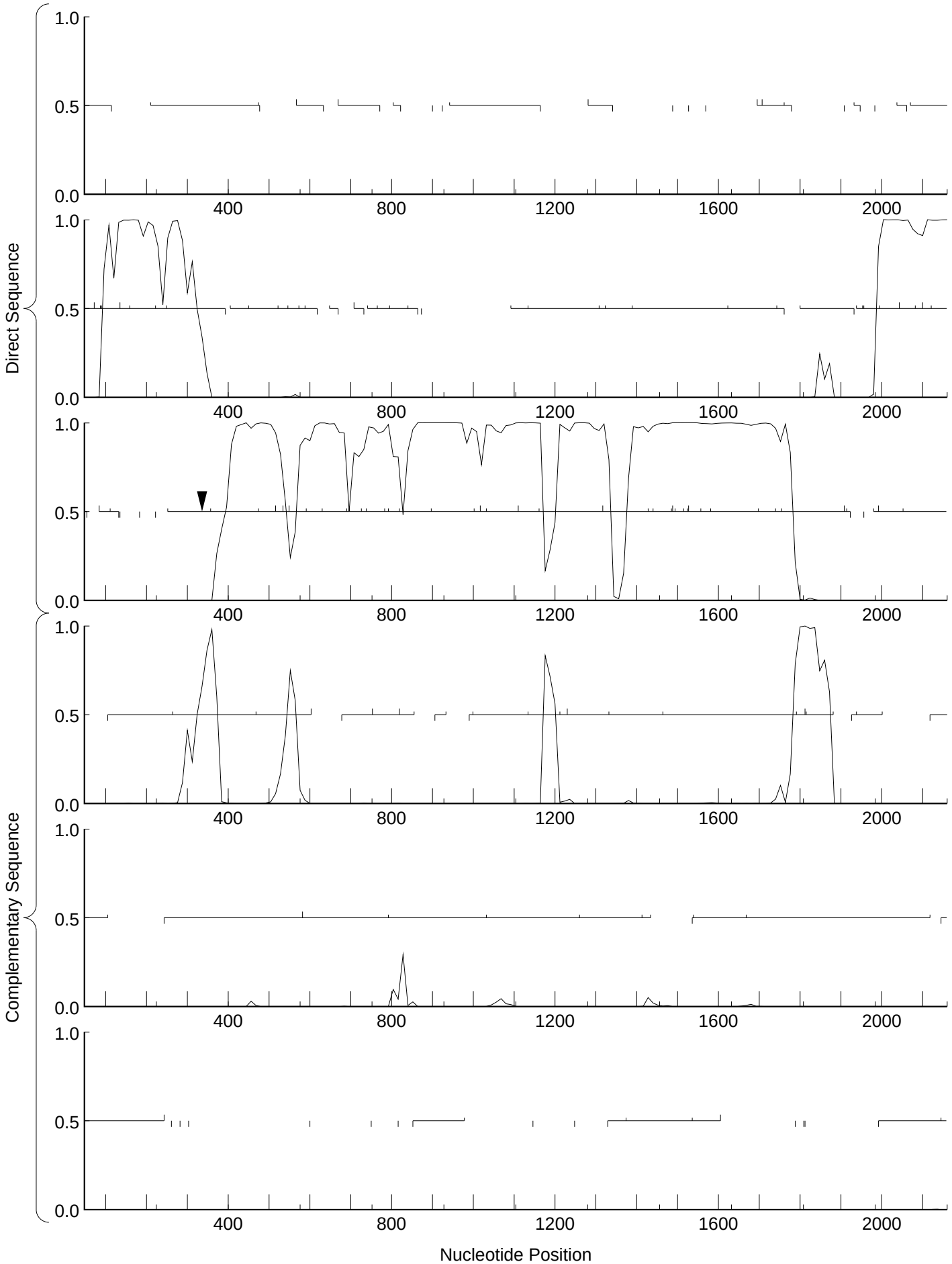

  Send questions / comments to:
      Dr. M. Borodovsky
      Georgia Institute of Technology
      School of Biology
      Atlanta, GA  30332-0230
```

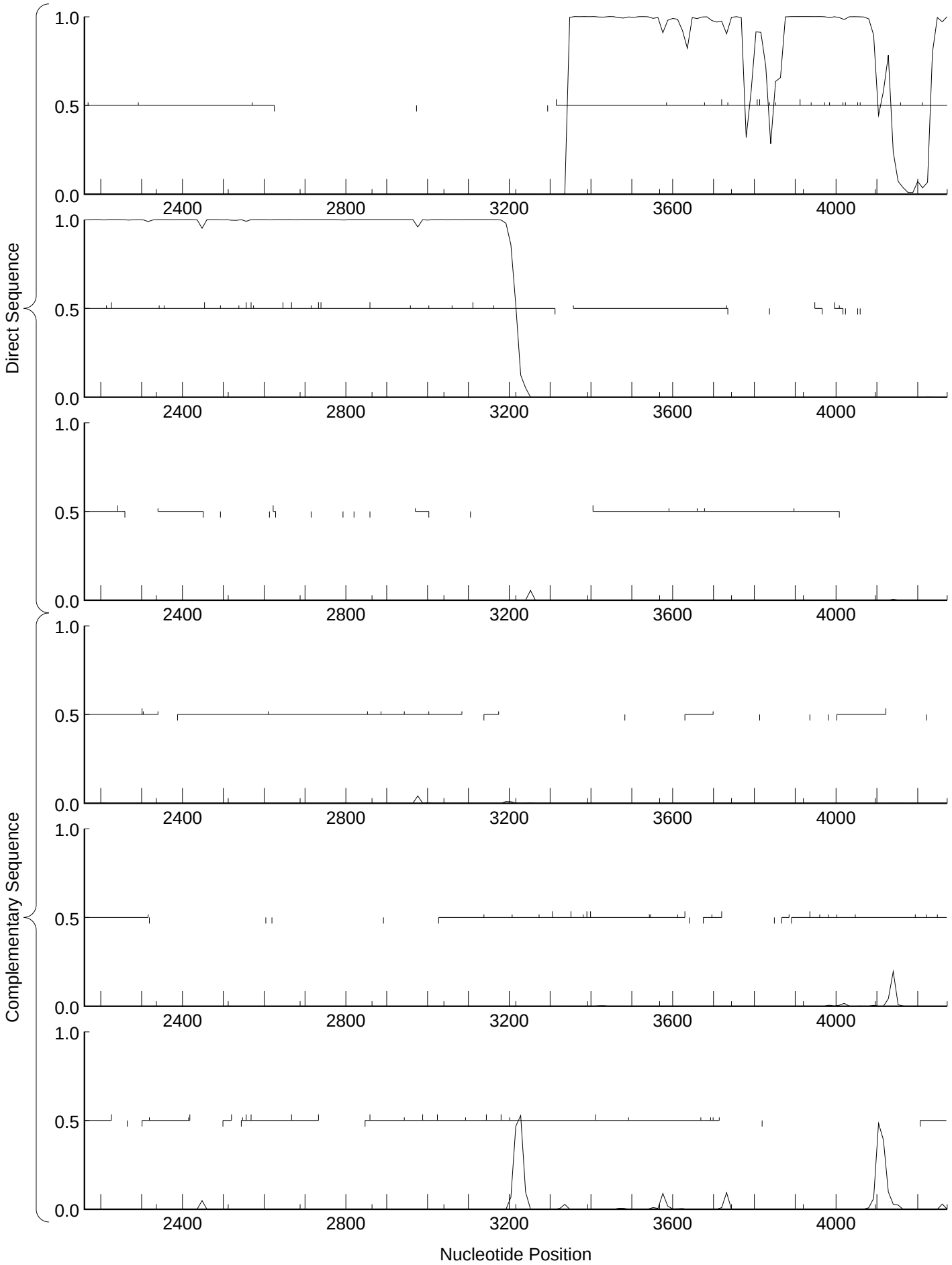
Matrix notes & comments

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Training set derived by GeneMarkS, 4.30 October 2014
Sat Sep  8 00:36:14 2018
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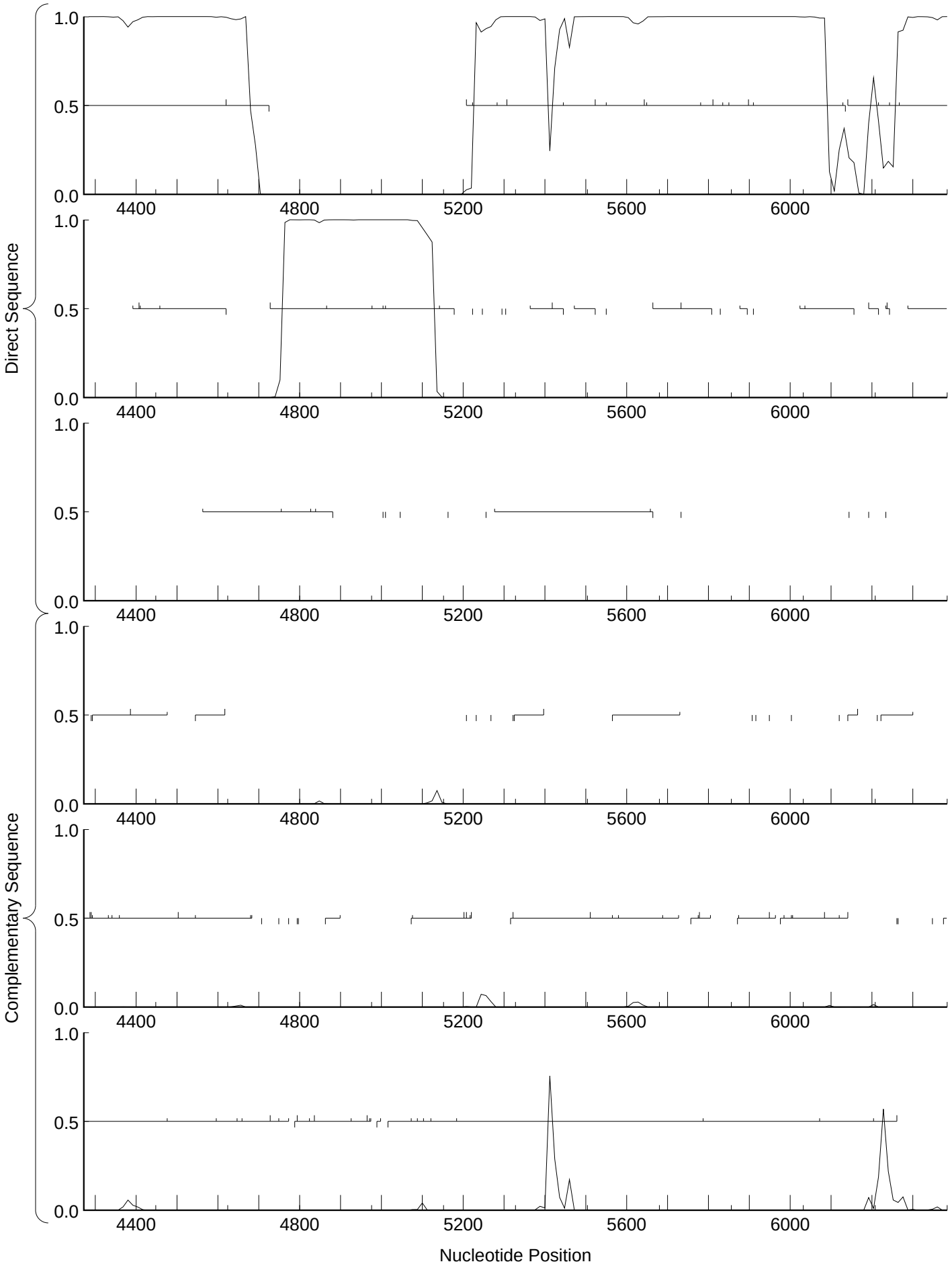
For help or information, send electronic mail to: custserv@genepro.com, or mark@amber.biology.gatech.edu

us complete sequence, 50948 bp including 10-base 3’ overhang (TCTCCGGTGA), Cluster CV, Order 4, Window 96, Step 12, 2/26

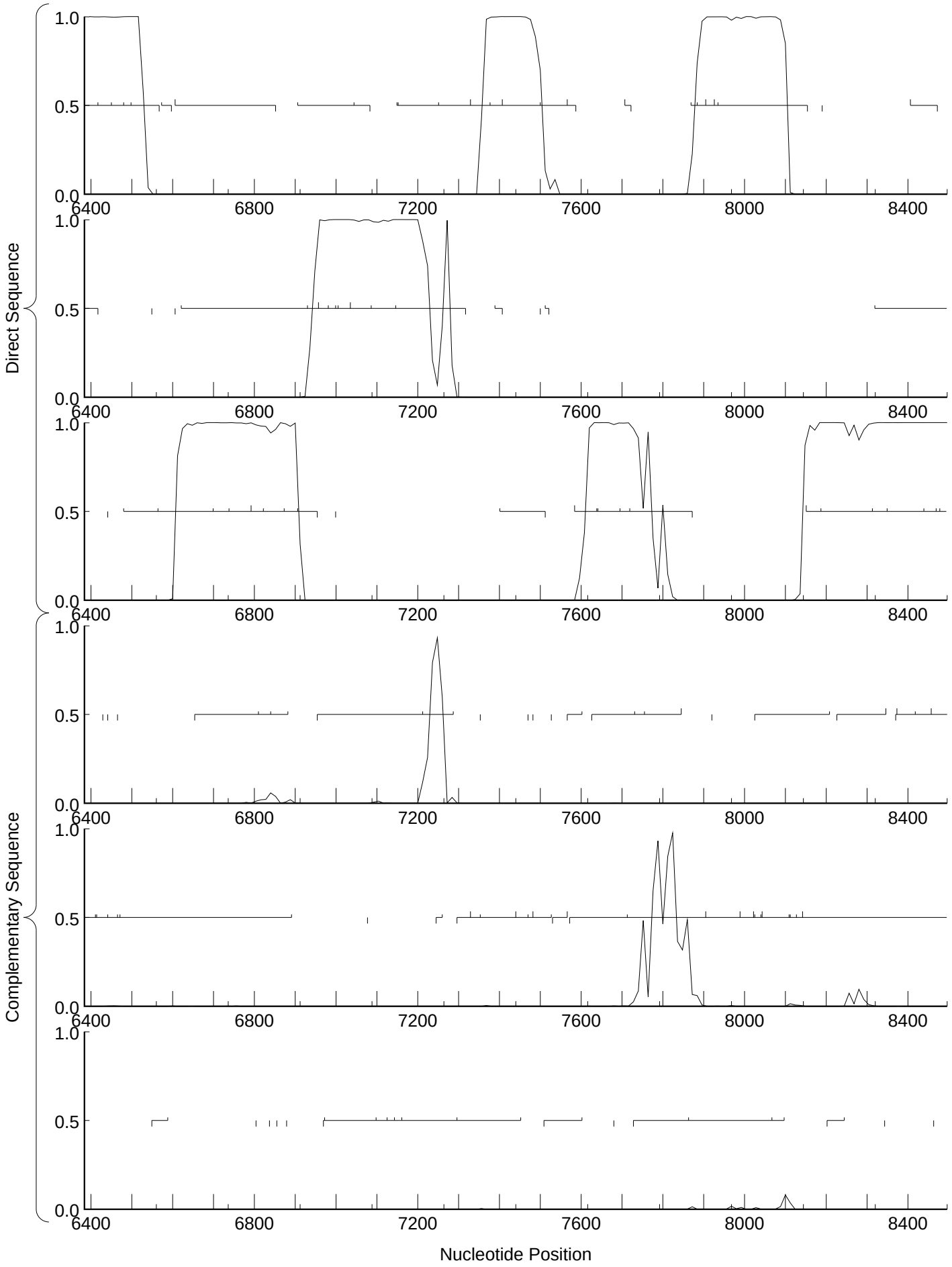


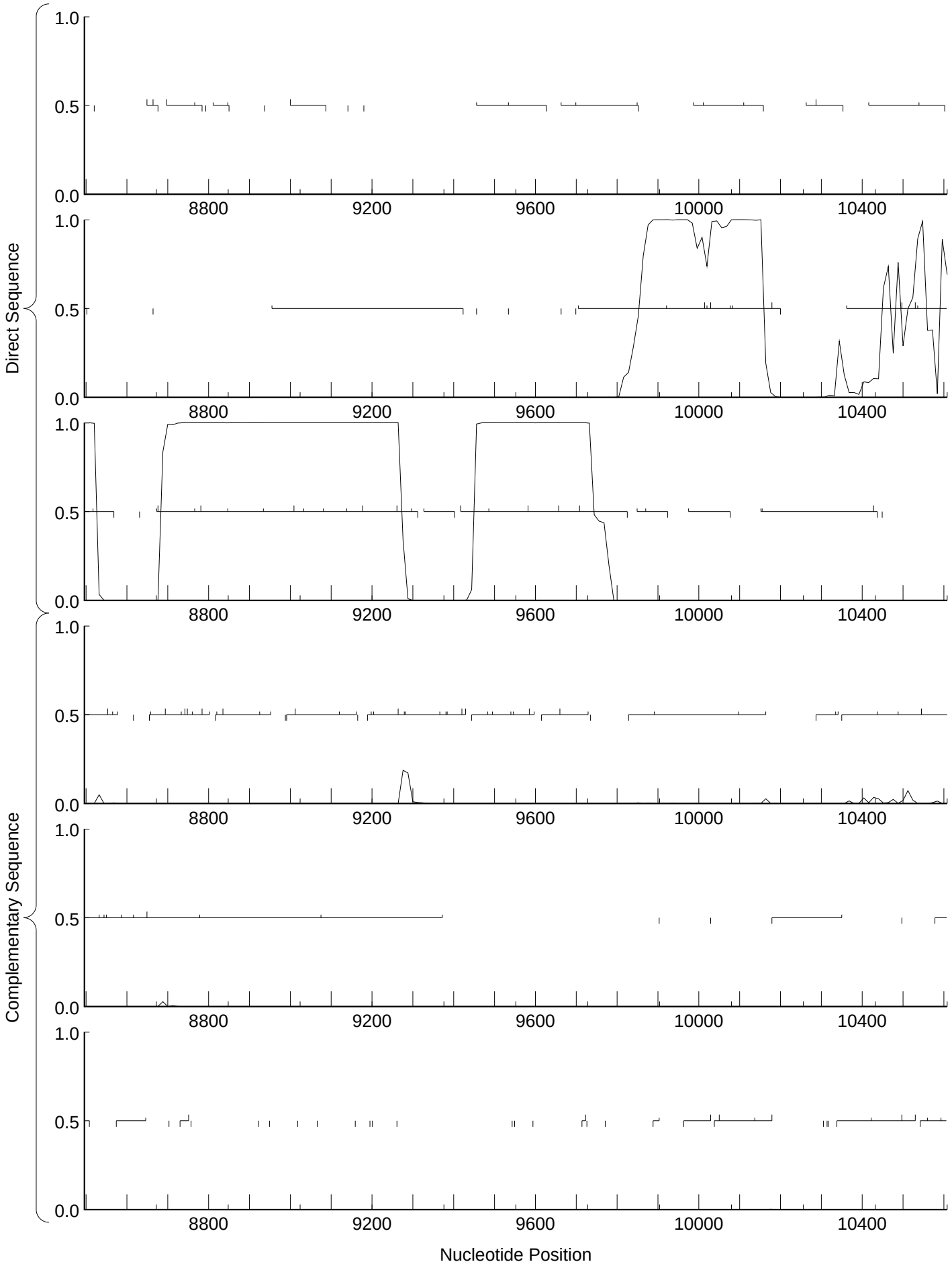

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
2400
2800
3200
3600
4000
Nucleotide Position

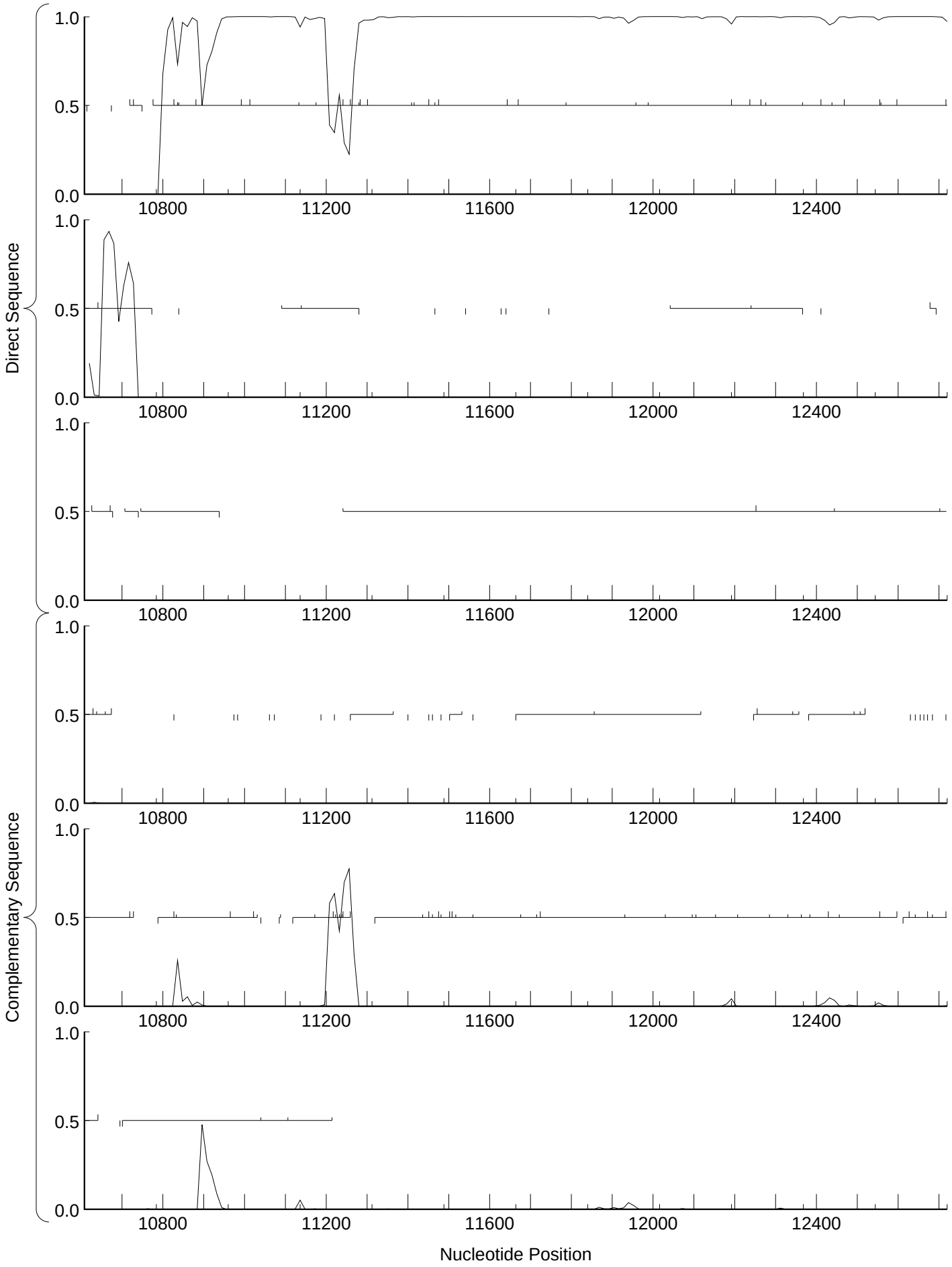
us complete sequence, 50948 bp including 10-base 3’ overhang (TCTCCGGTGA), Cluster CV, Order 4, Window 96, Step 12, 4/26

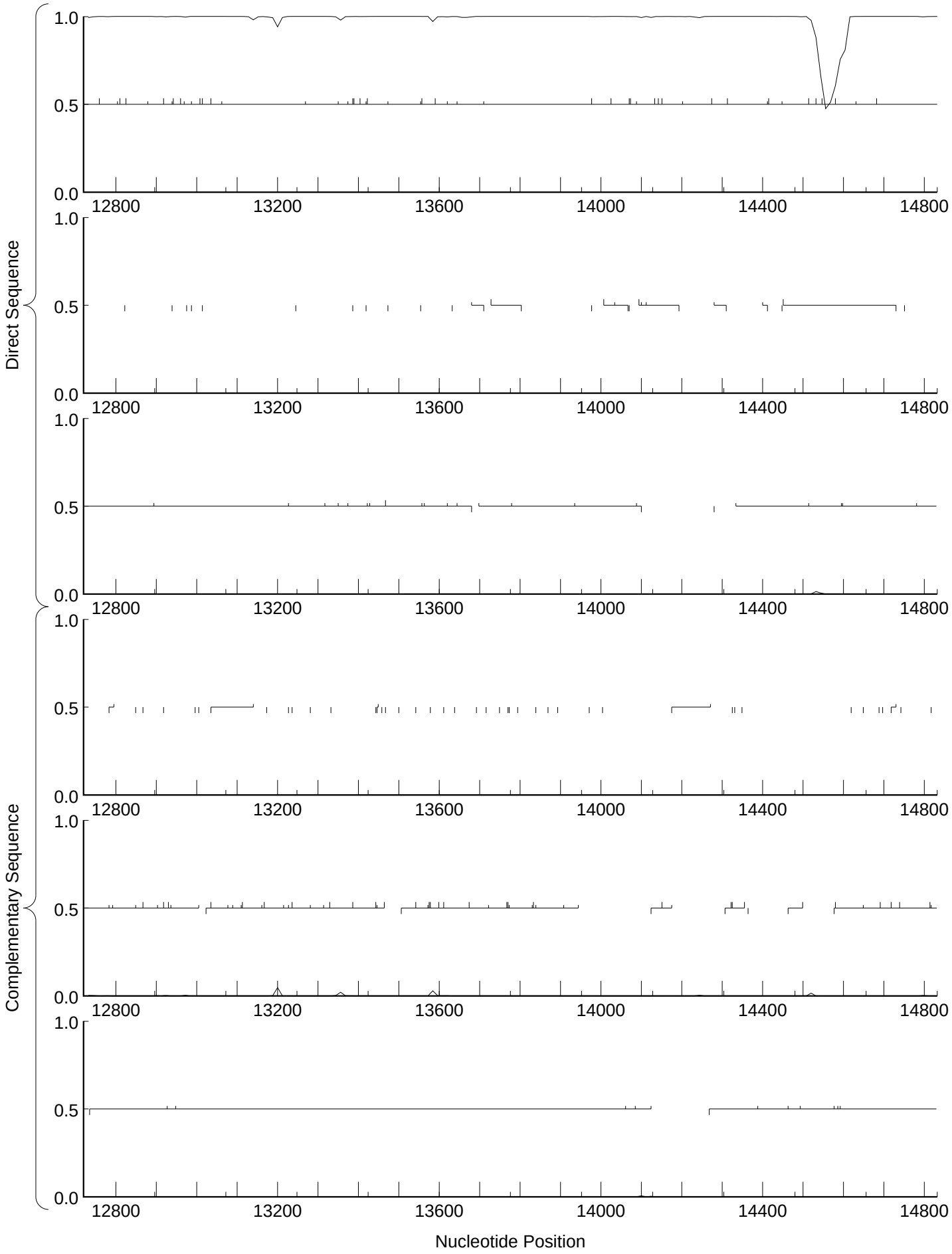


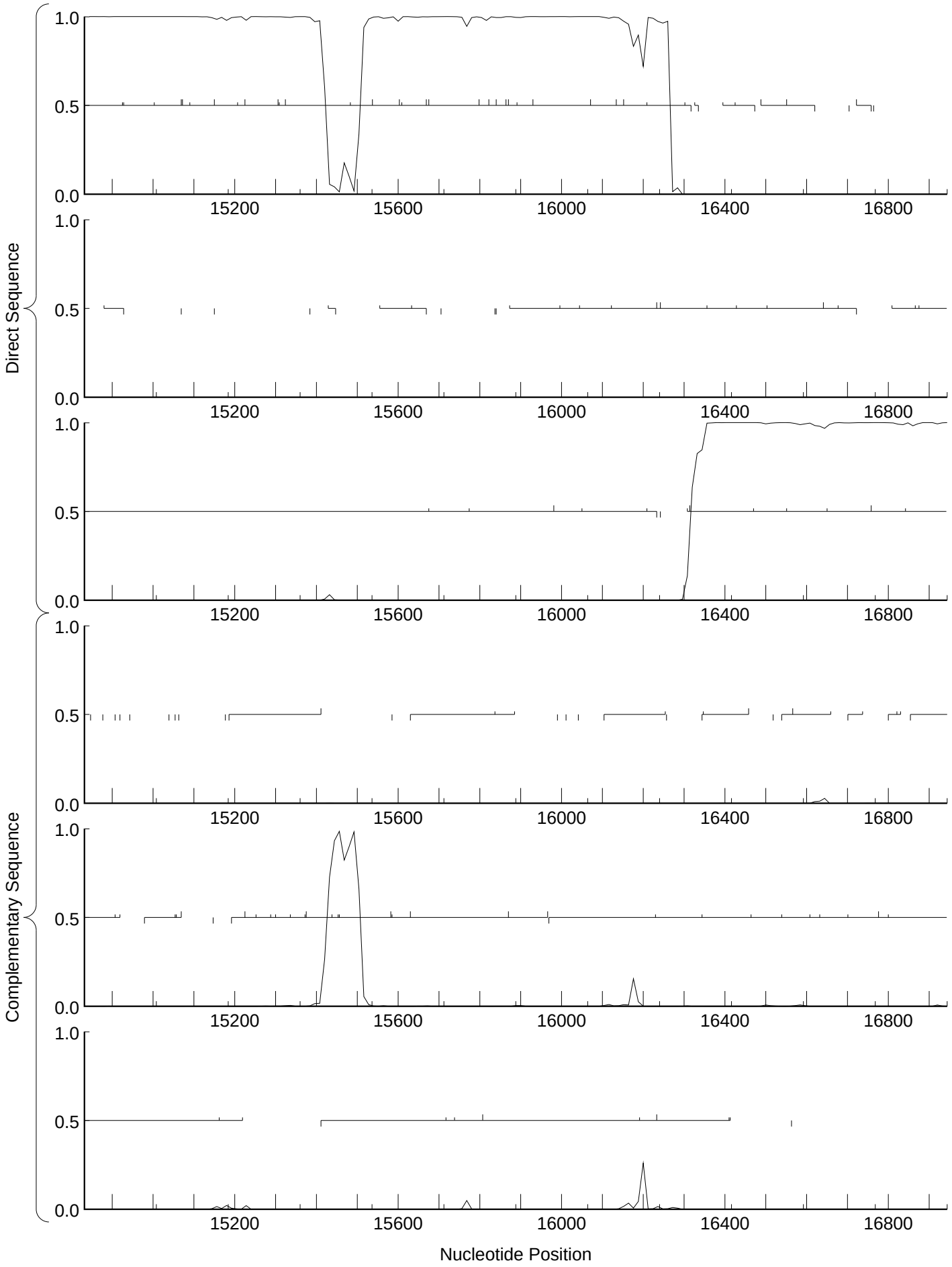
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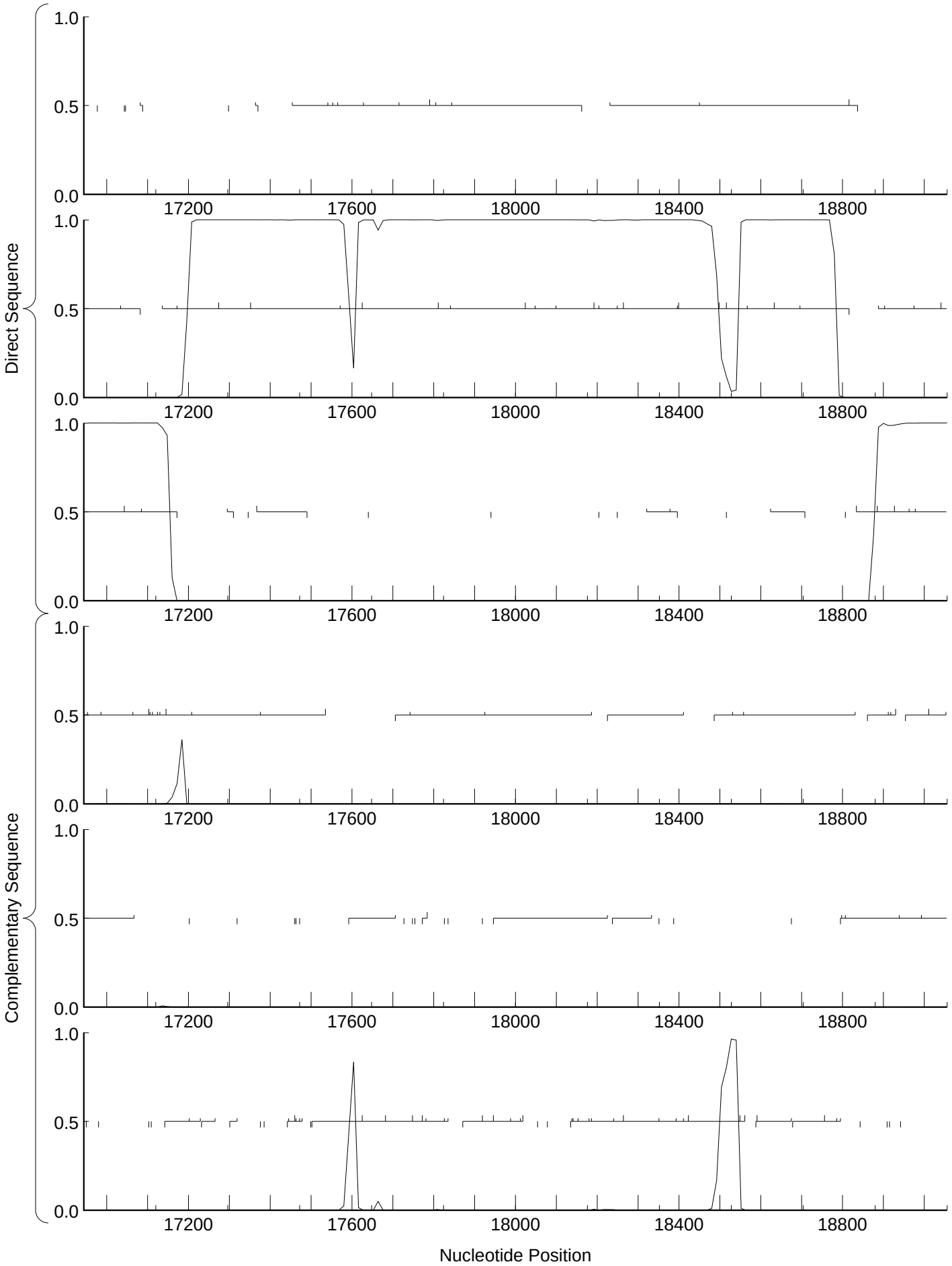

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
8800
9200
9600
10000
10400
Nucleotide Position


Direct Sequence
Complementary Sequence
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0.5
0.0
10800
11200
11600
12000
12400
Nucleotide Position

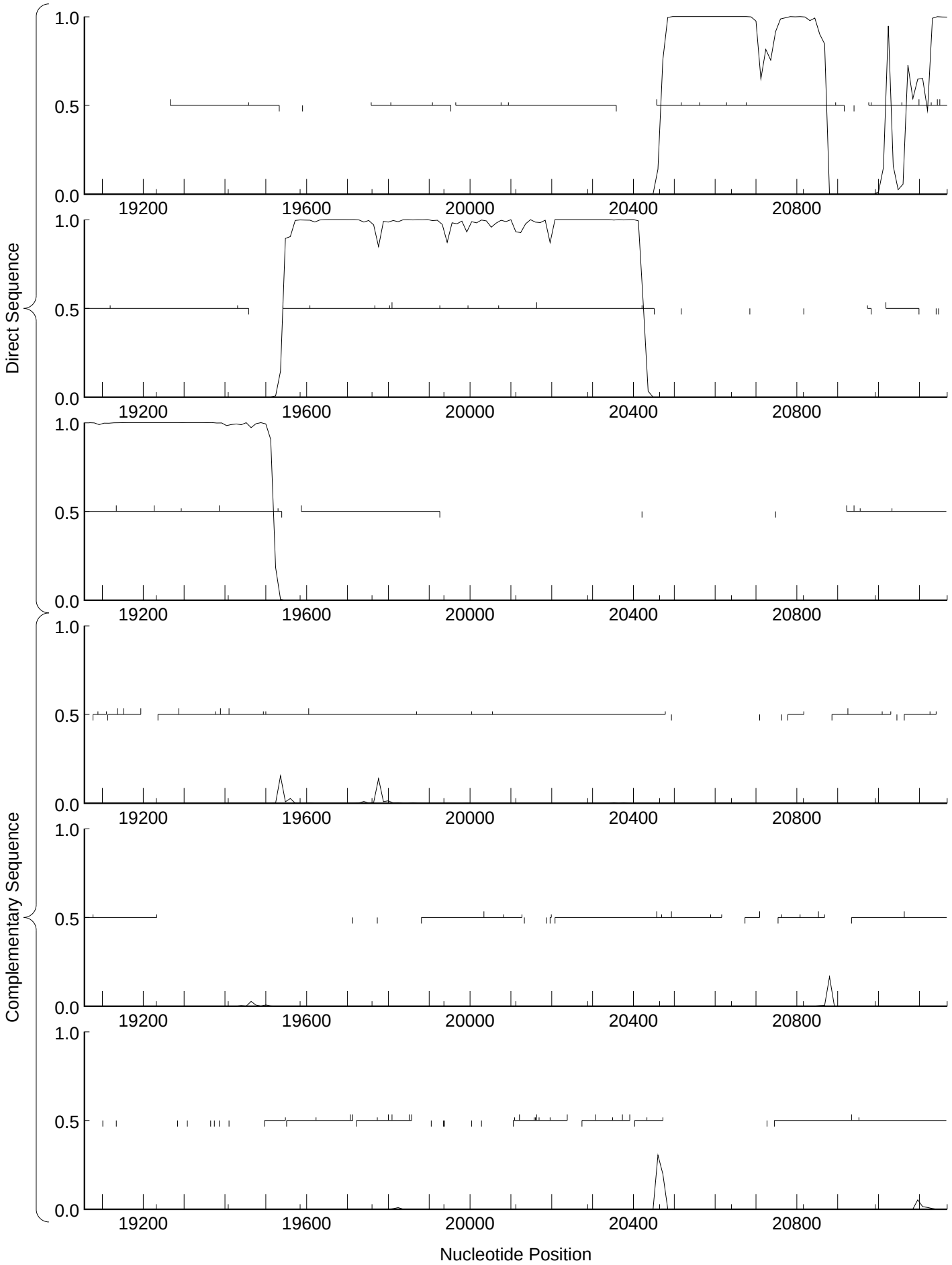

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
12800
13200
13600
14000
14400
14800
Nucleotide Position


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
15200
15600
16000
16400
16800
Nucleotide Position

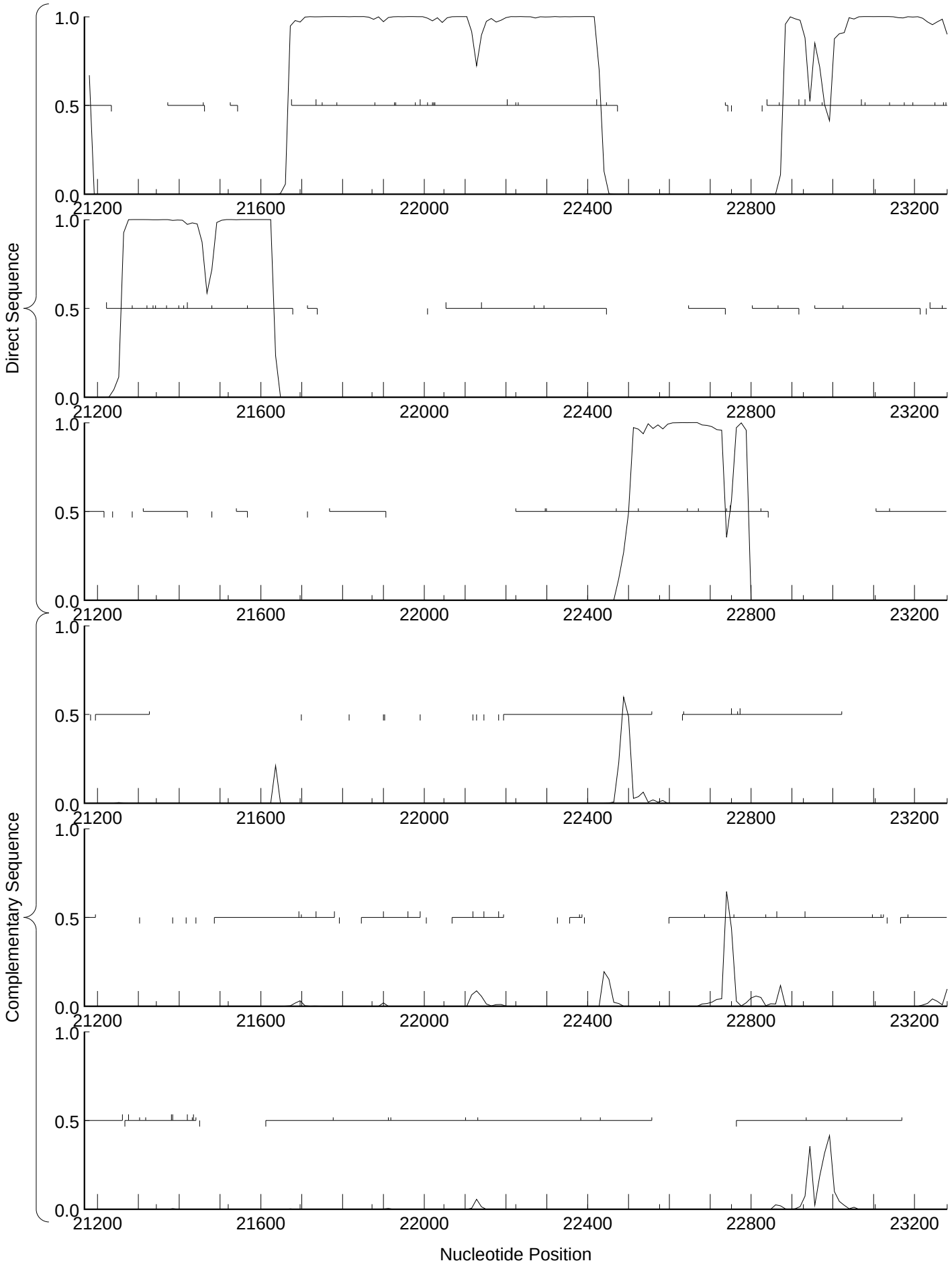
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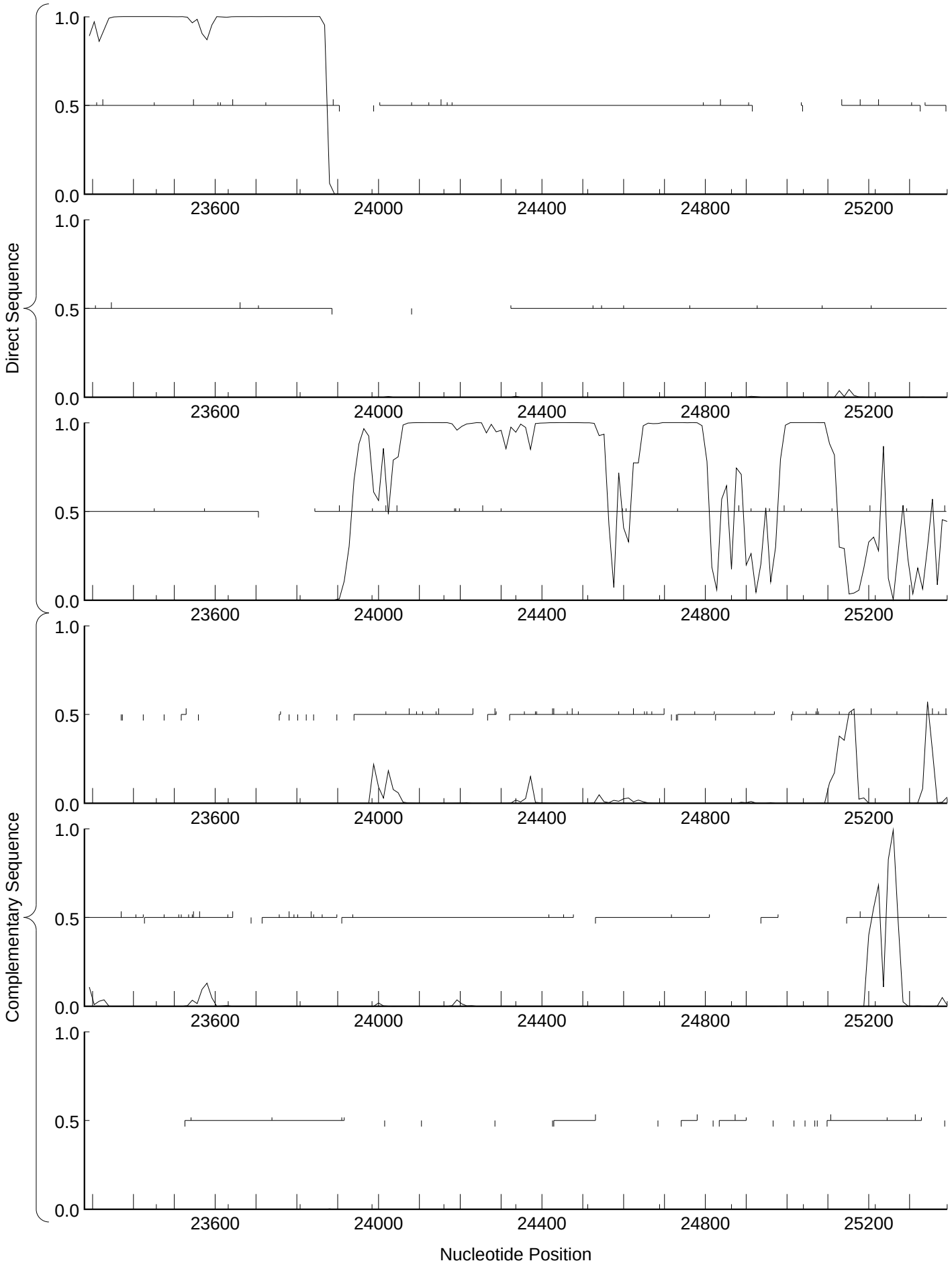
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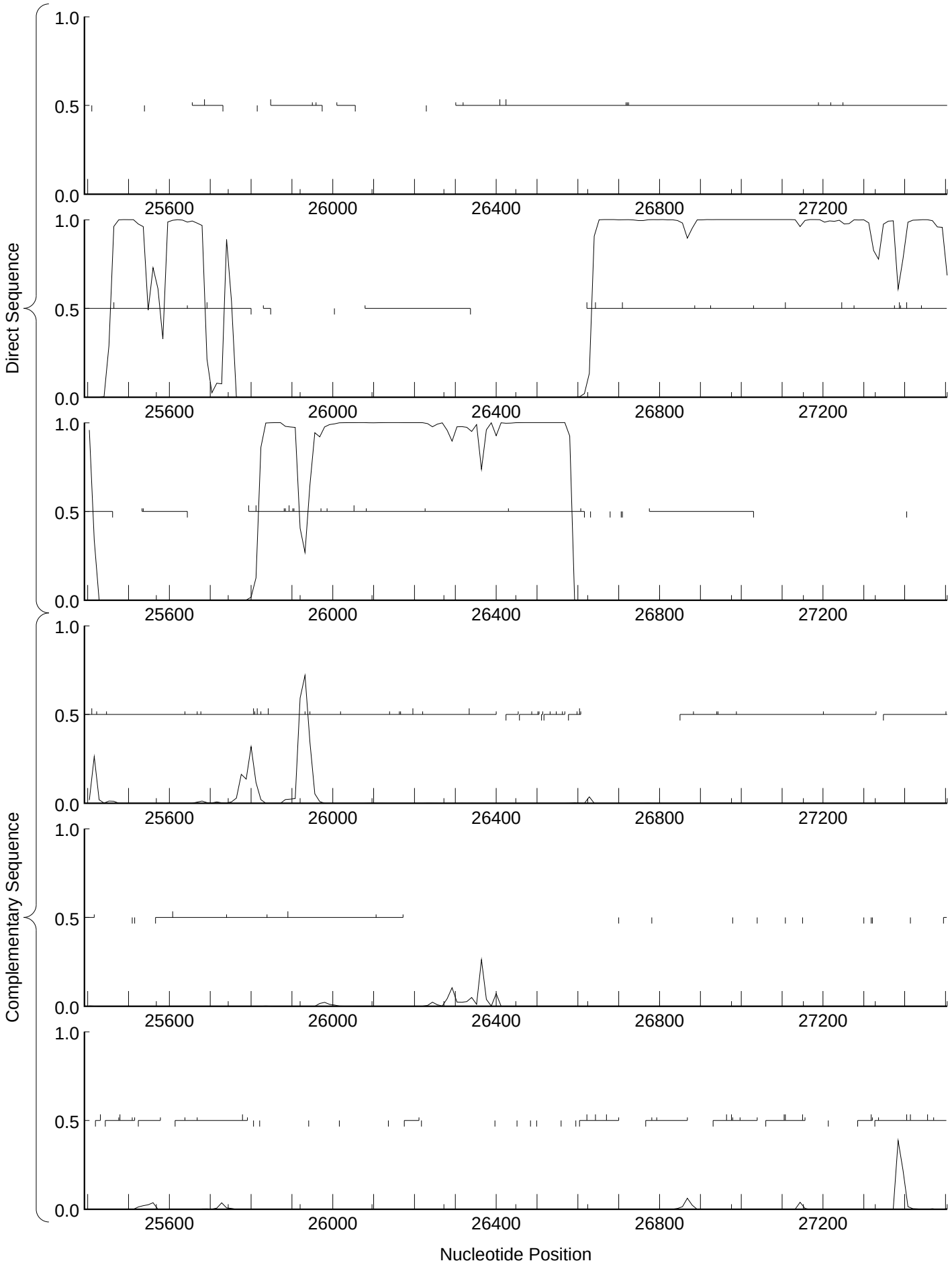
complete sequence, 50948 bp including 10-base 3’ overhang (TCTCCGGTGA), Cluster CV, Order 4, Window 96, Step 12, 12/26



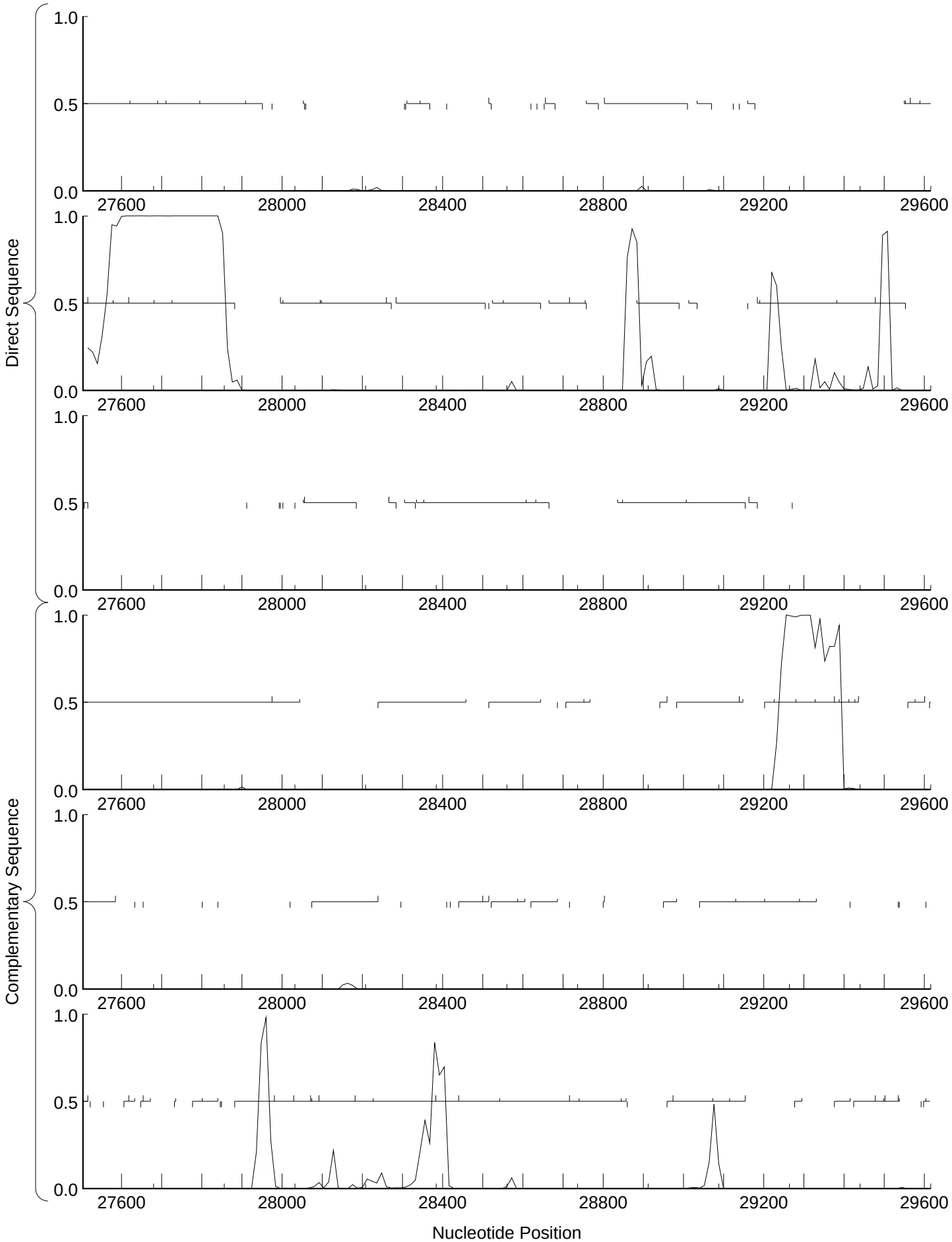
complete sequence, 50948 bp including 10-base 3’ overhang (TCTCCGGTGA), Cluster CV, Order 4, Window 96, Step 12, 13/26



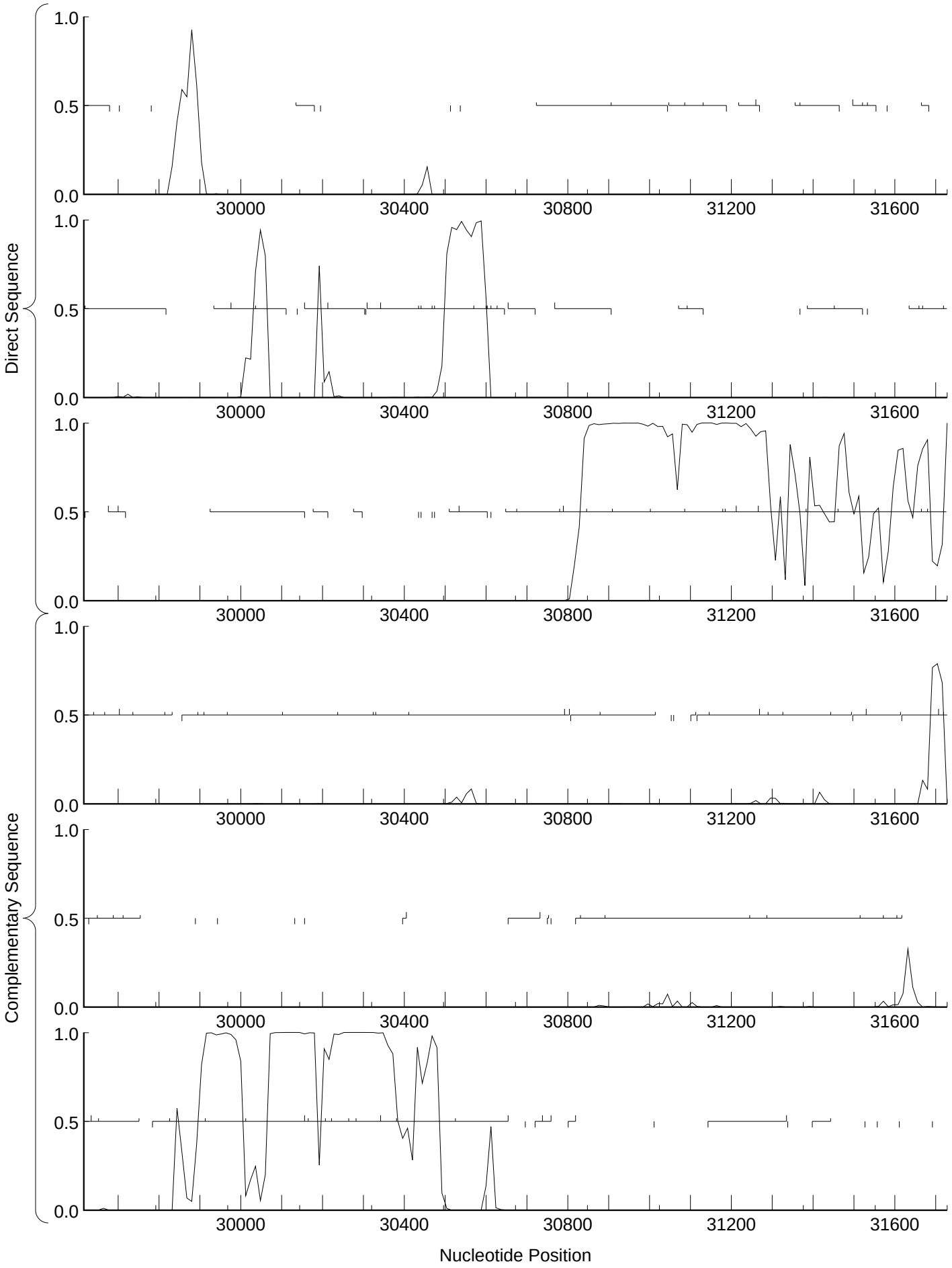
complete sequence, 50948 bp including 10-base 3’ overhang (TCTCCGGTGA), Cluster CV, Order 4, Window 96, Step 12, 14/26



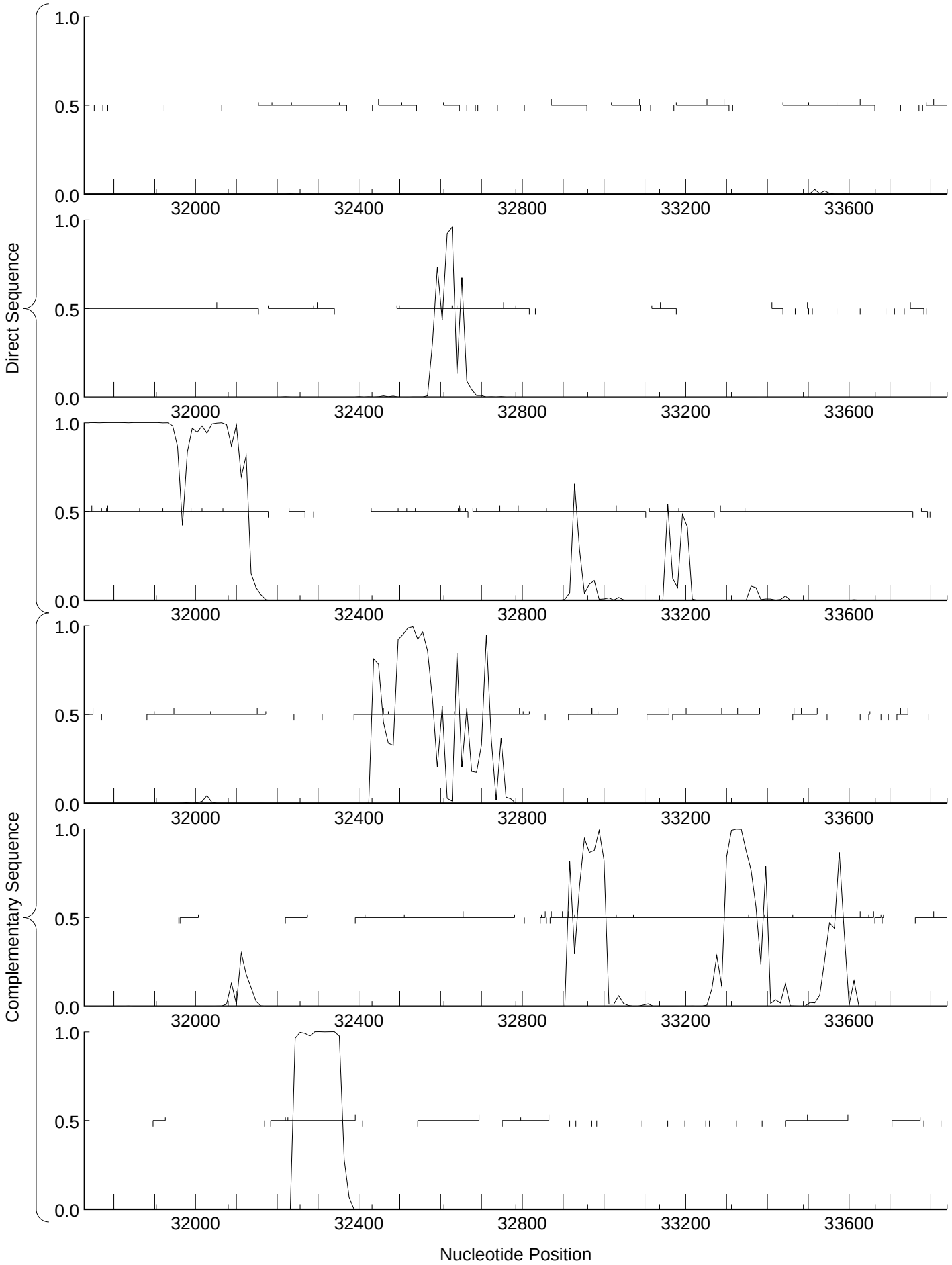
complete sequence, 50948 bp including 10-base 3’ overhang (TCTCCGGTGA), Cluster CV, Order 4, Window 96, Step 12, 15/26



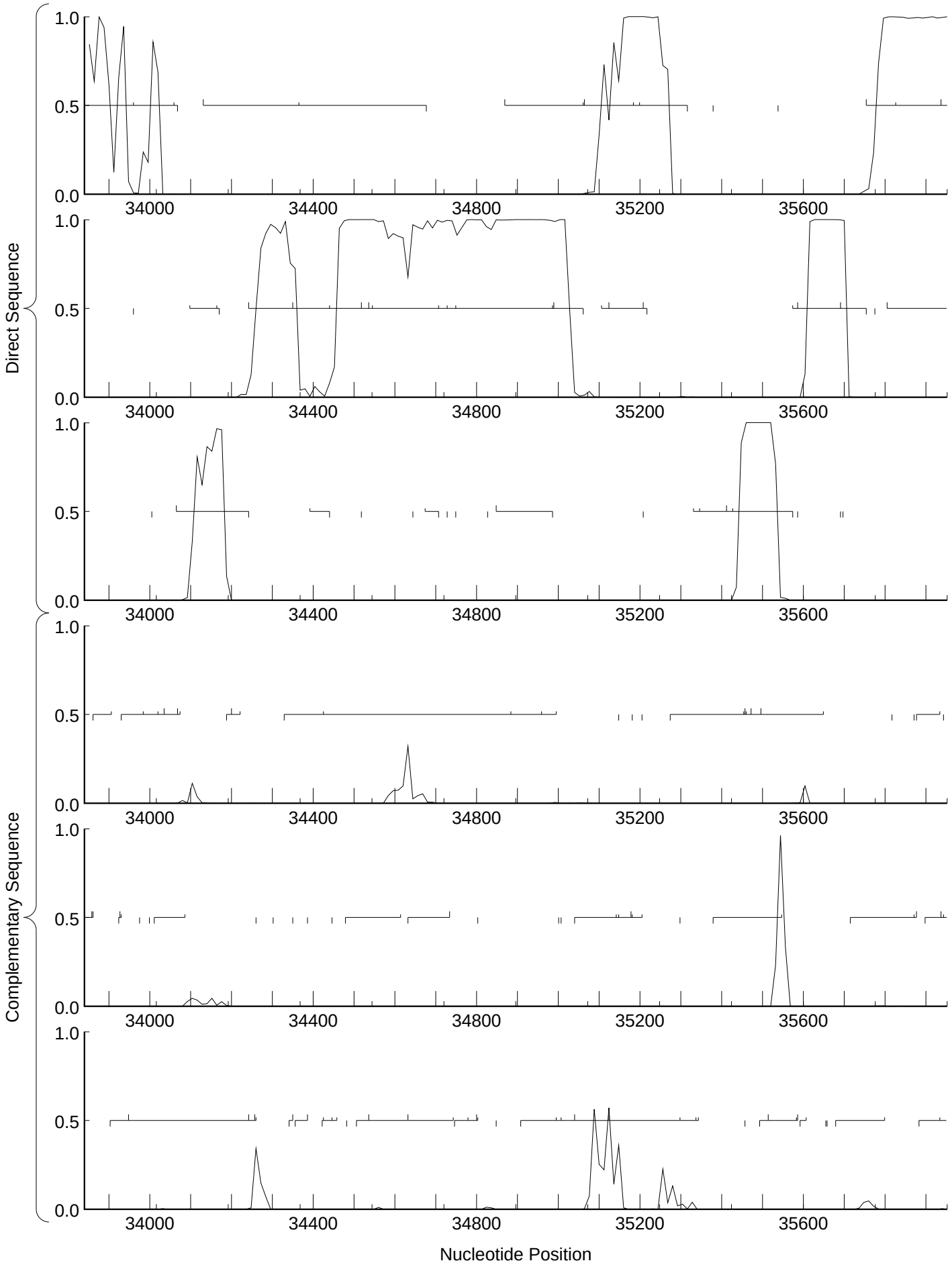
complete sequence, 50948 bp including 10-base 3’ overhang (TCTCCGGTGA), Cluster CV, Order 4, Window 96, Step 12, 16/26



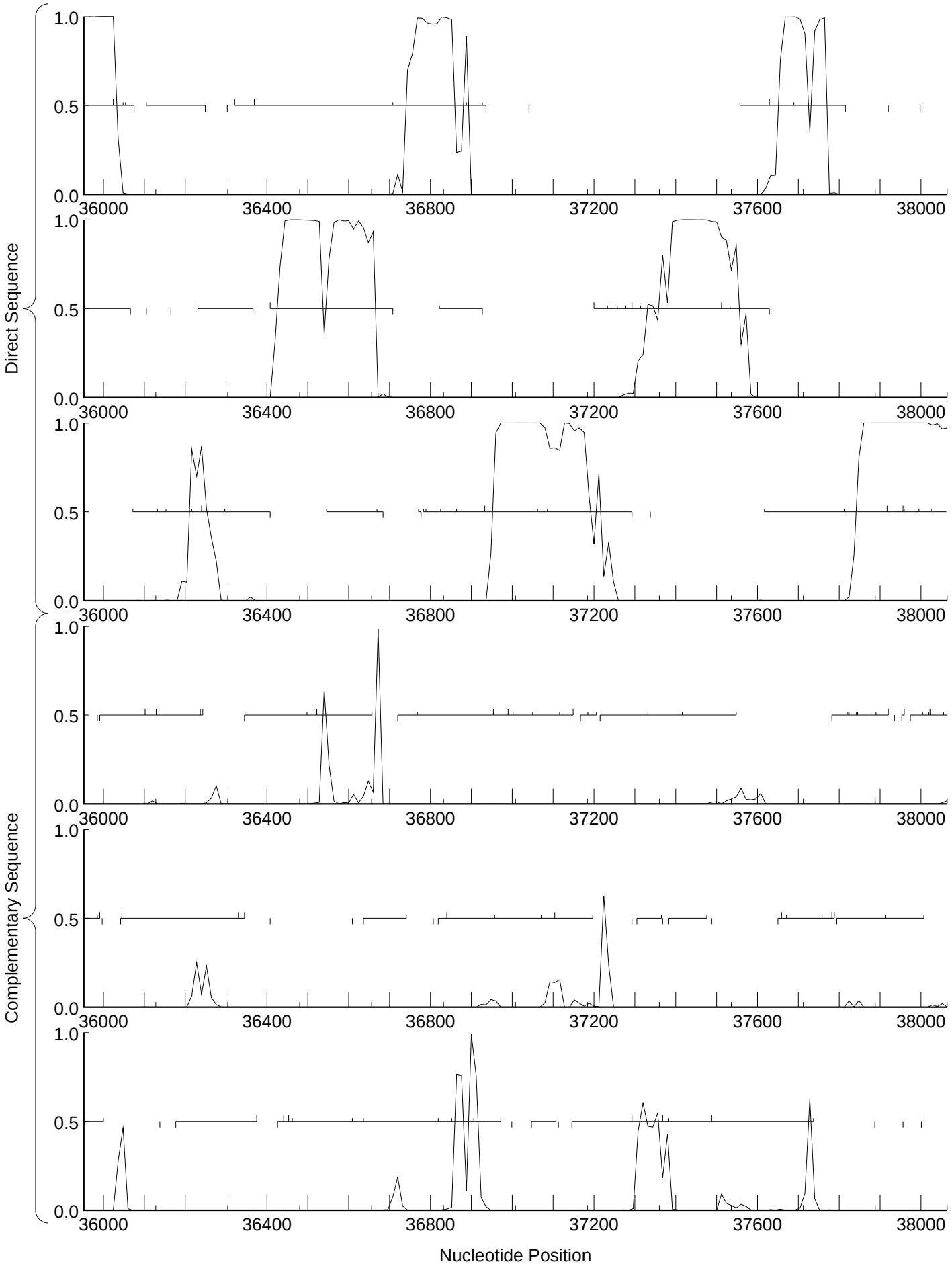
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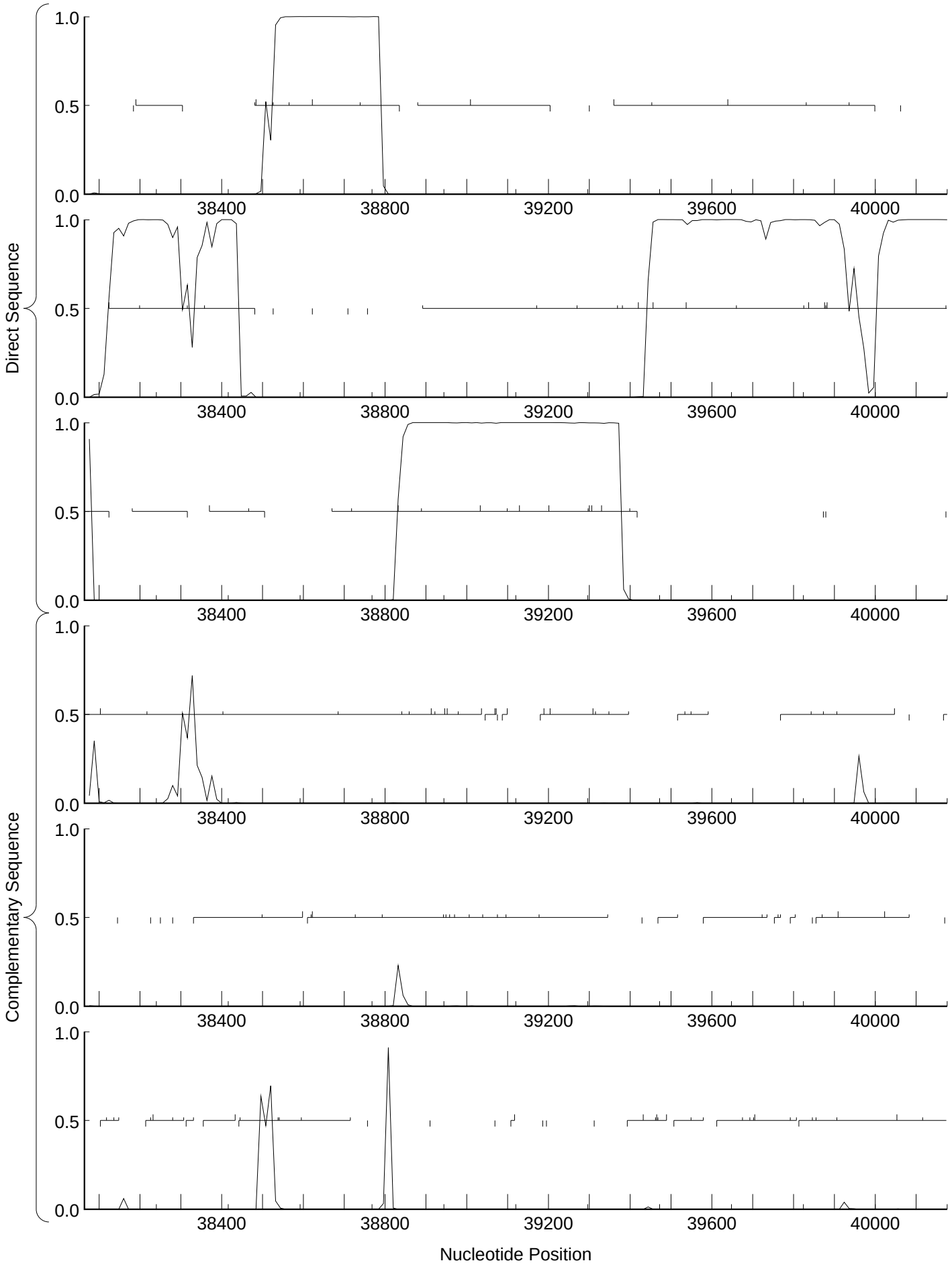
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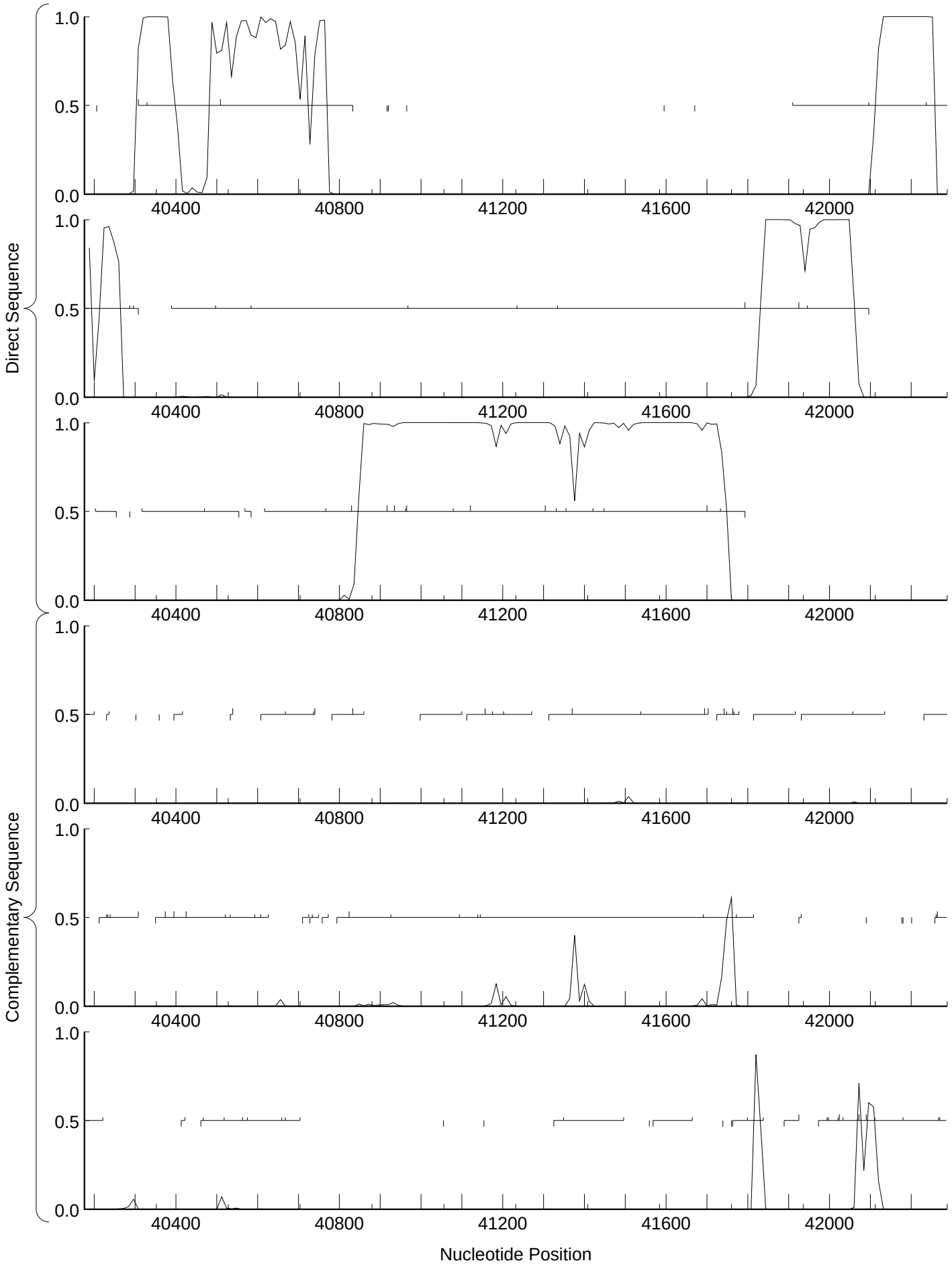
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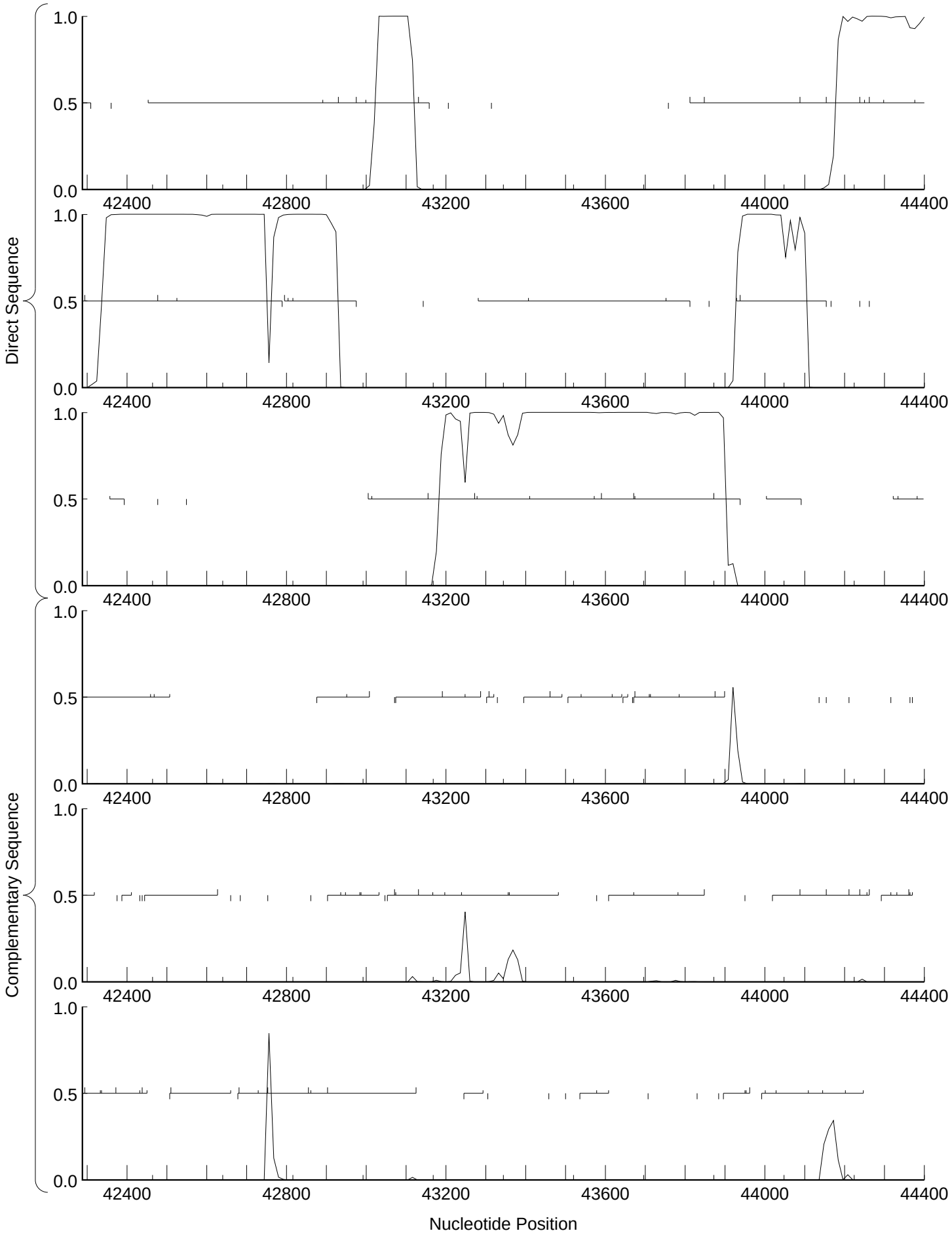
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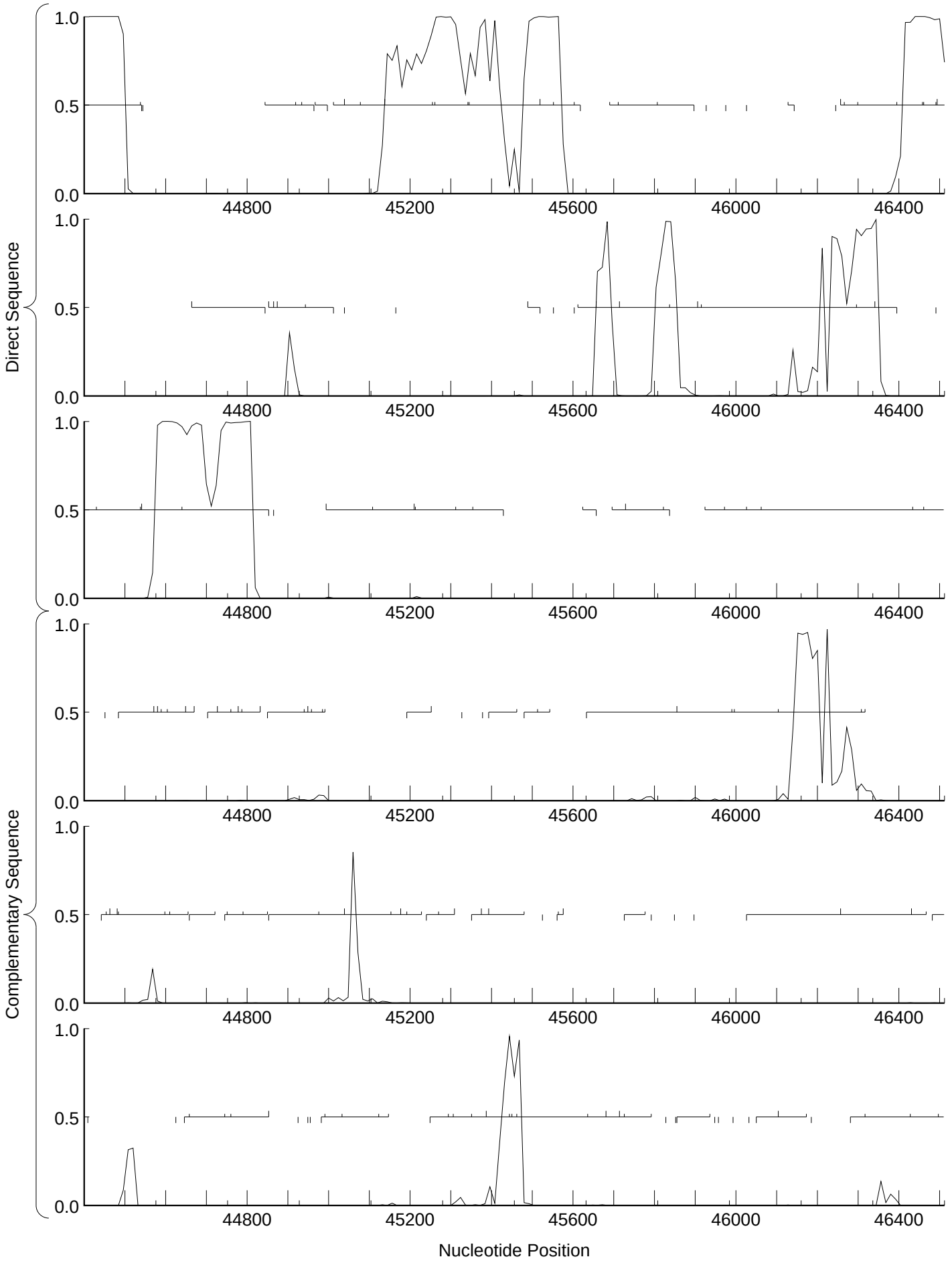
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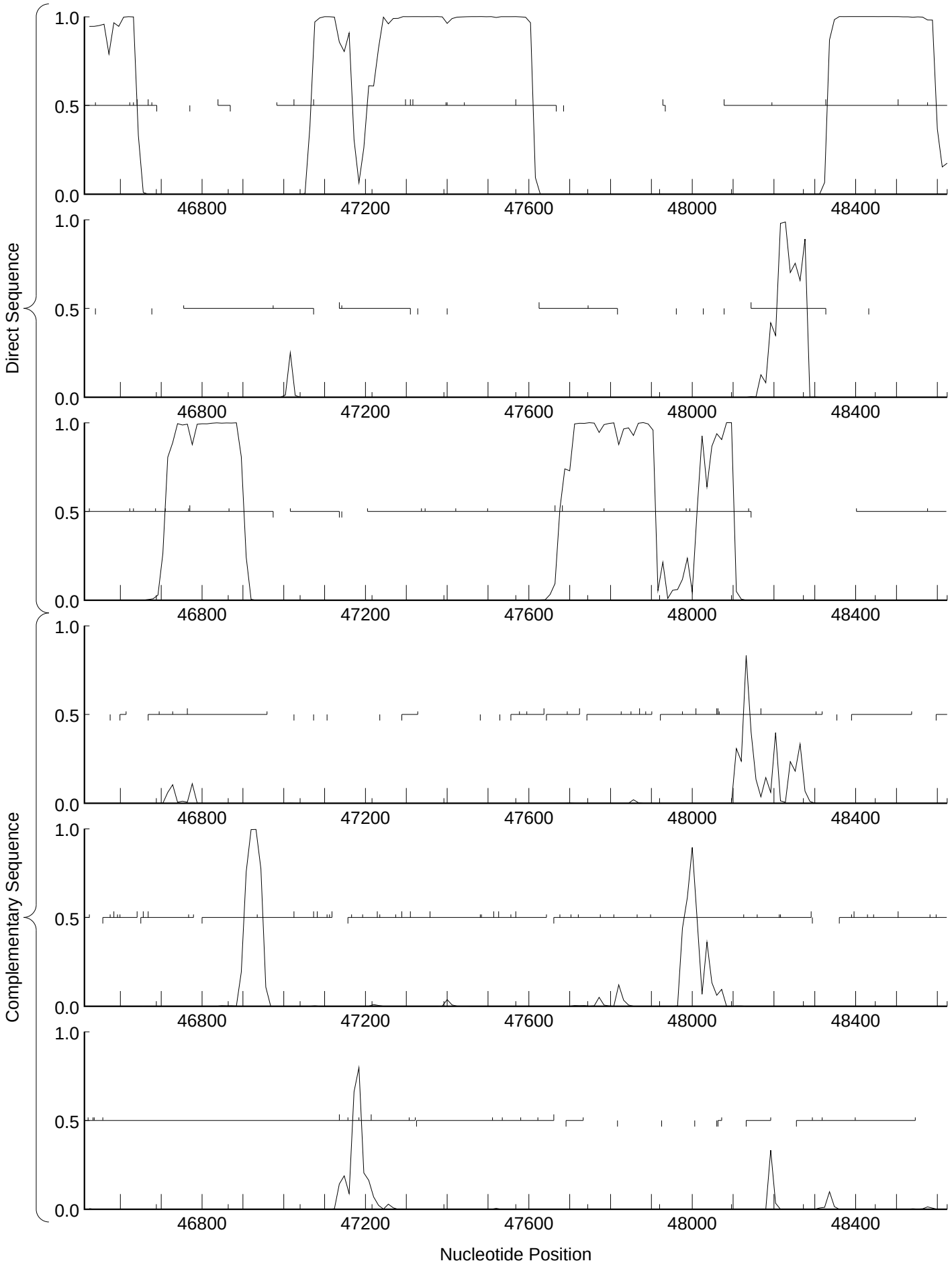
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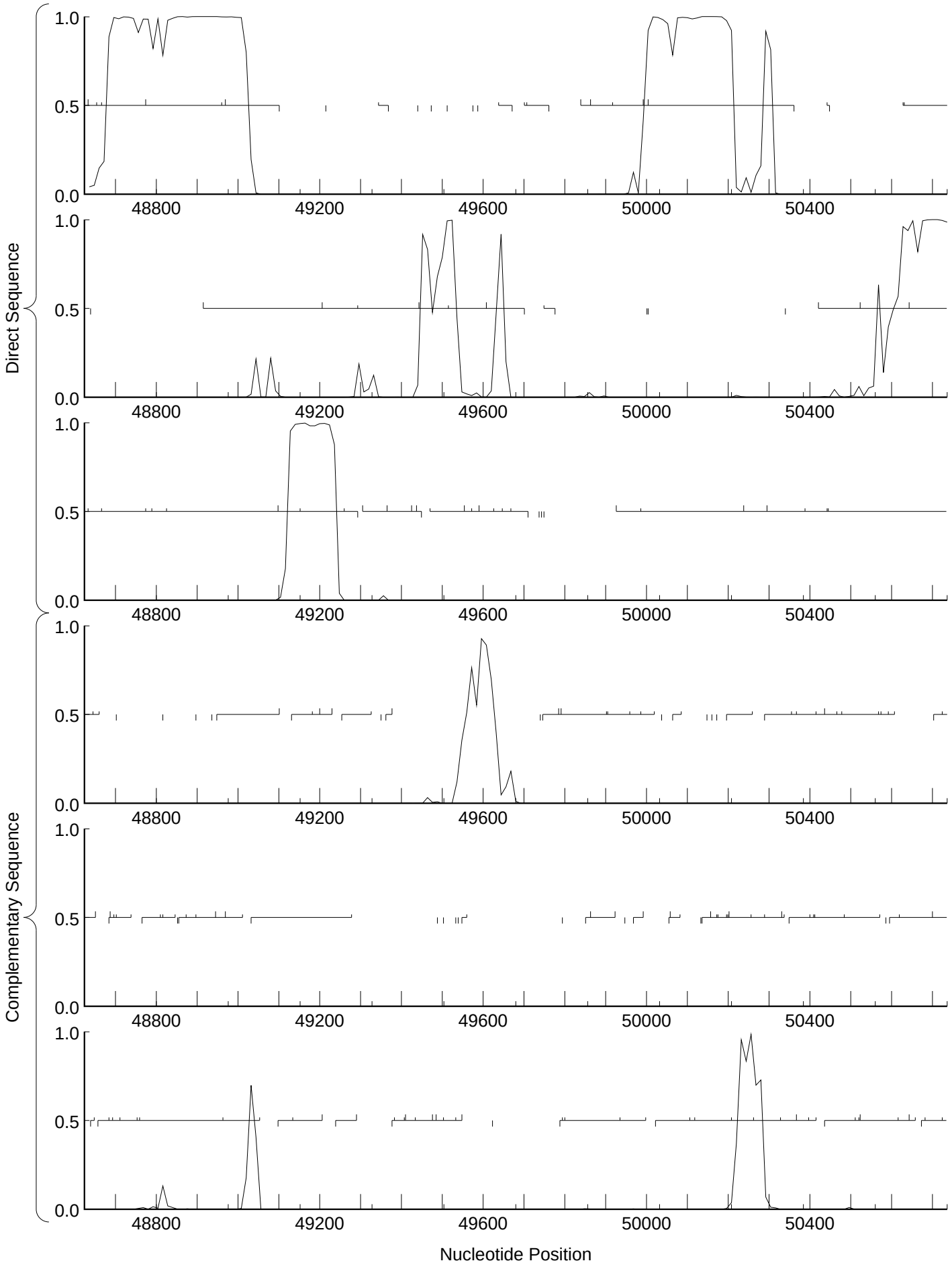
complete sequence, 50948 bp including 10-base 3’ overhang (TCTCCGGTGA), Cluster CV, Order 4, Window 96, Step 12, 23/26



complete sequence, 50948 bp including 10-base 3’ overhang (TCTCCGGTGA), Cluster CV, Order 4, Window 96, Step 12, 24/26



complete sequence, 50948 bp including 10-base 3’ overhang (TCTCCGGTGA), Cluster CV, Order 4, Window 96, Step 12, 25/26



complete sequence, 50948 bp including 10-base 3’ overhang (TCTCCGGTGA), Cluster CV, Order 4, Window 96, Step 12, 26/26

