GeneMark

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

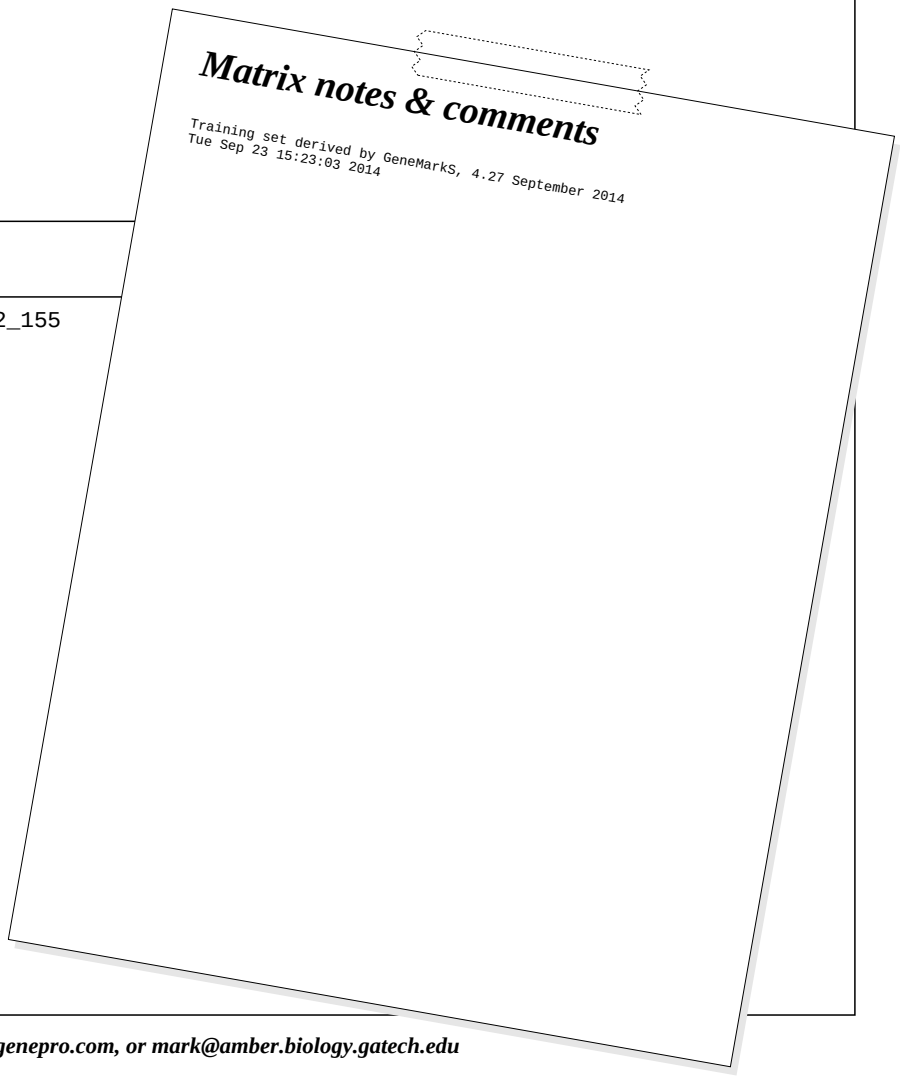
PROGRAM INFORMATION

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Sequence         :  Mycobacterium phage Avani Complete Sequence, 54470 bp including 10-base 3' overhang (CTCAGG
Analysis Date    :  3/29/24 at 6:26:25
Pages            :  27
Sequence Length  :  54470 bp
GC Content       :   60.97%

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

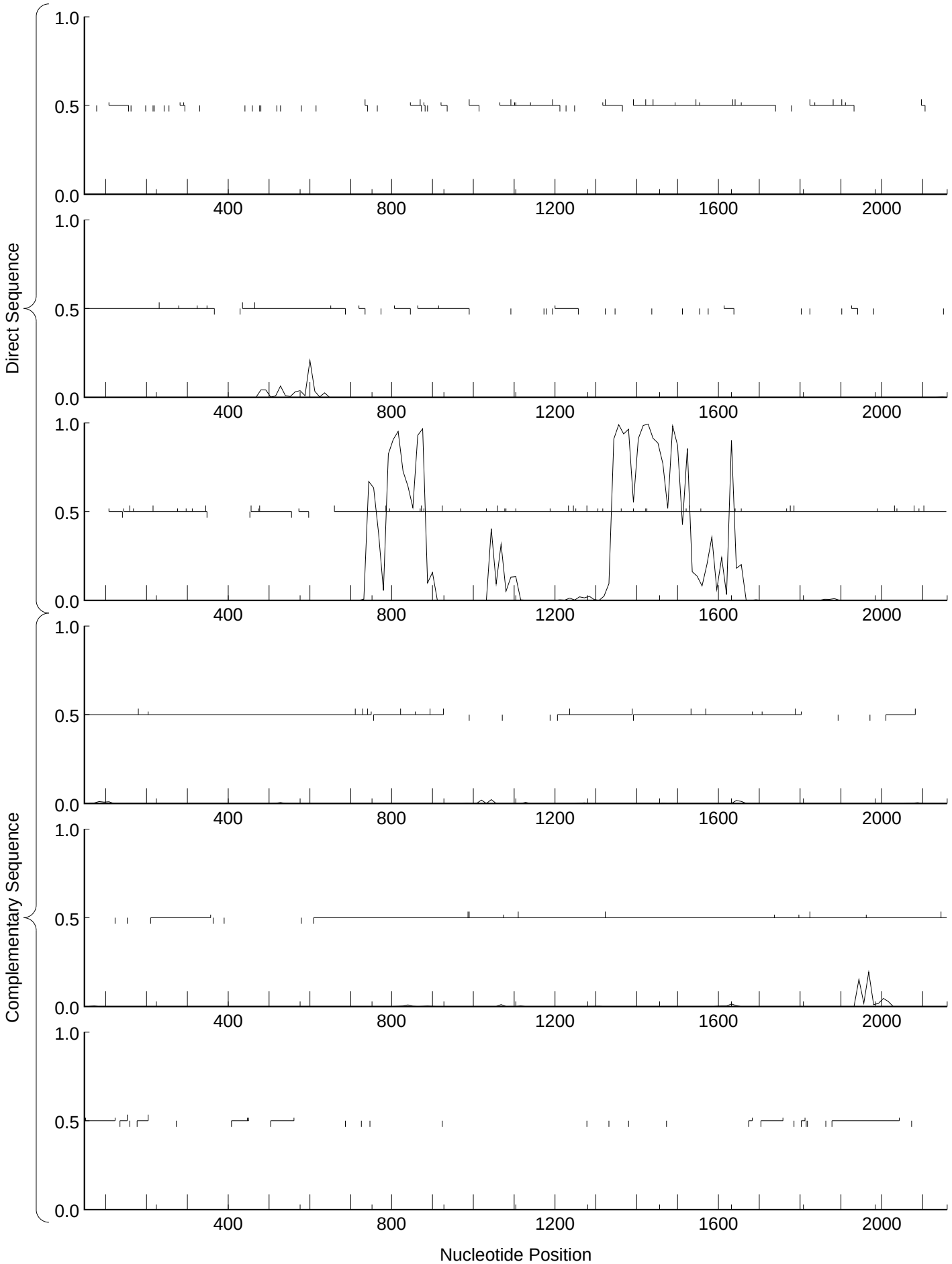
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Matrix     :  Mycobacterium_smegmatis_MC2_155
Author     :  -

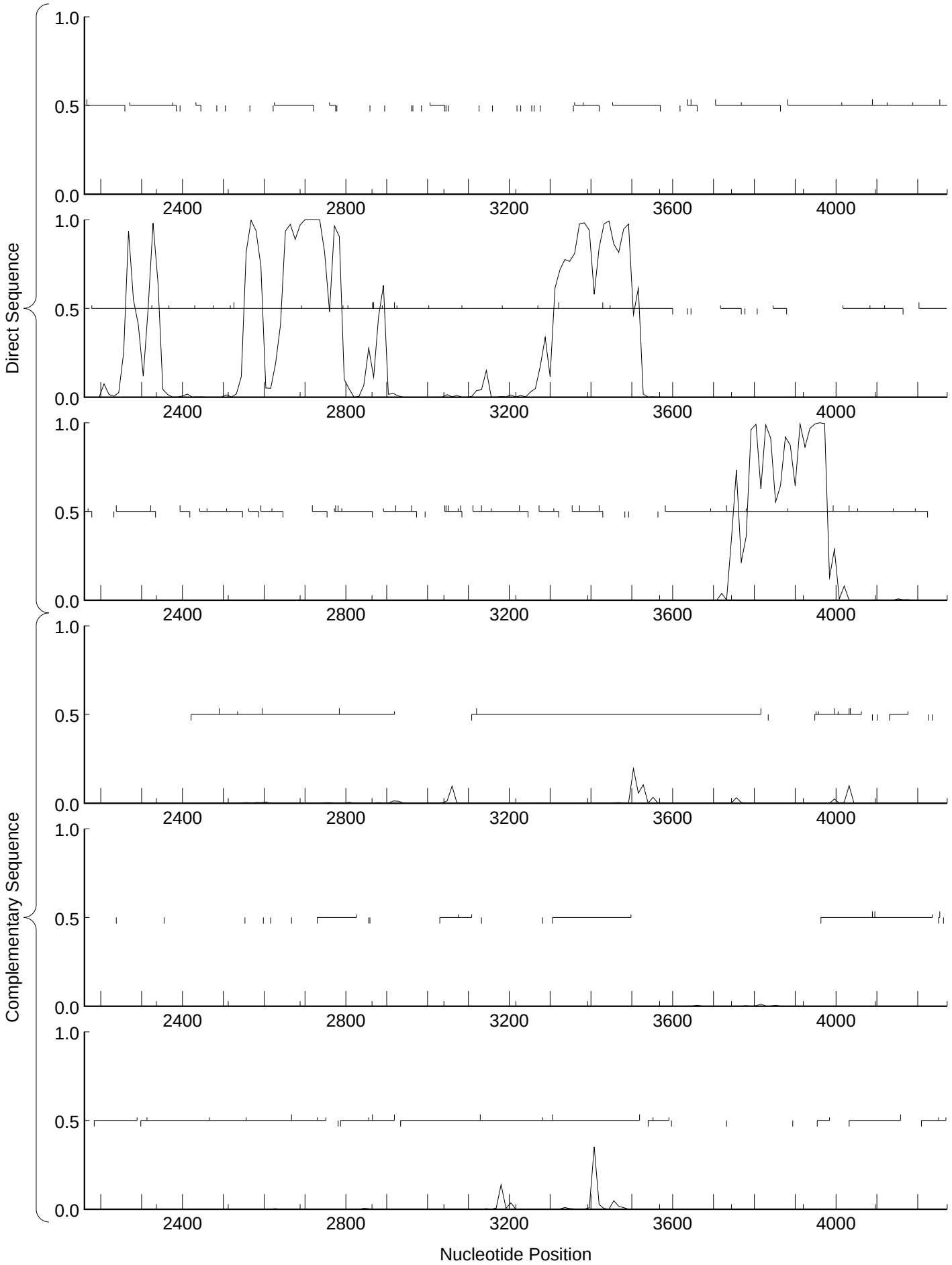
Order      :  4
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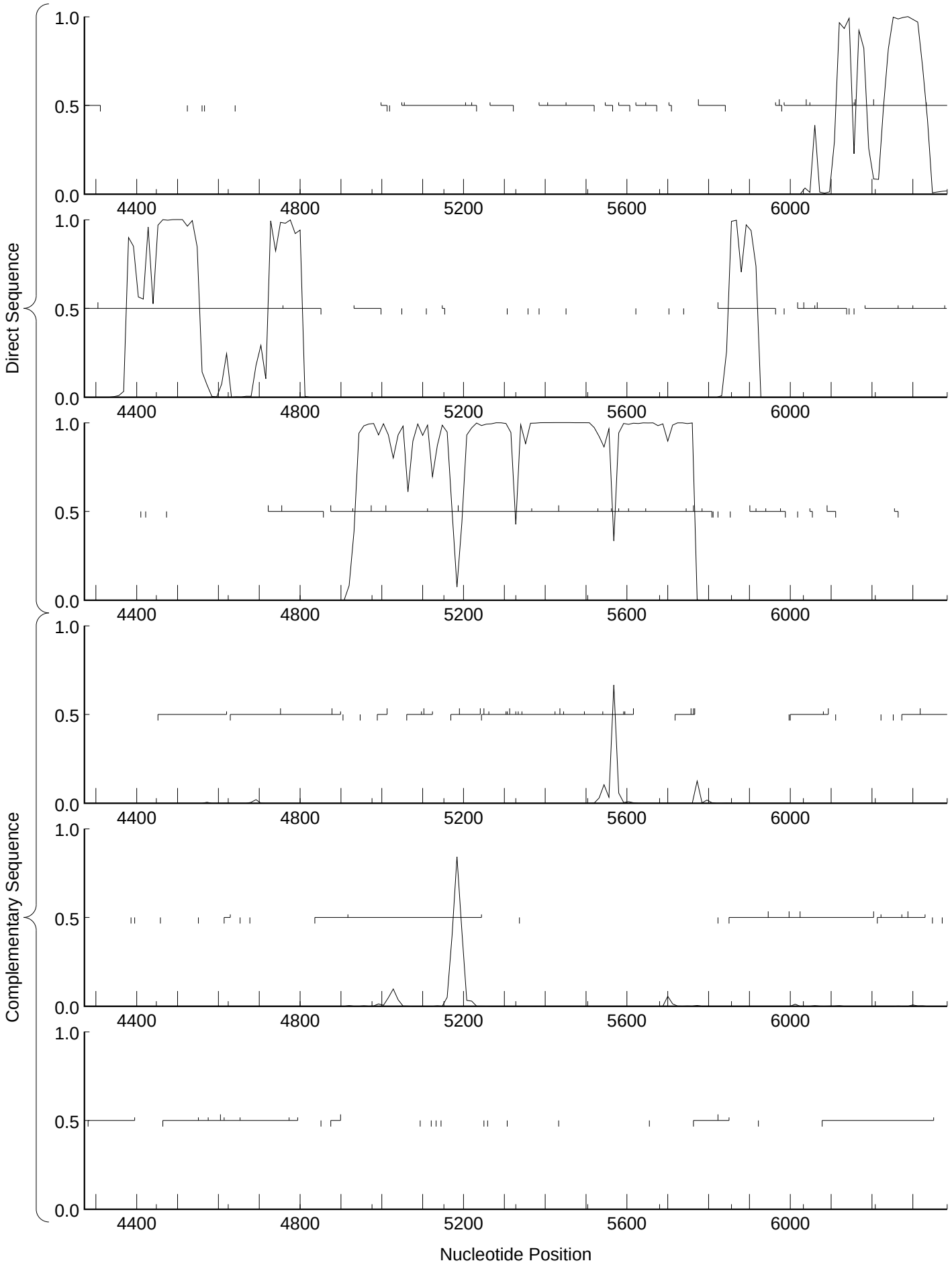

```
  Send questions / comments to:
      Dr. M. Borodovsky
      Georgia Institute of Technology
      School of Biology
      Atlanta, GA  30332-0230
```


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

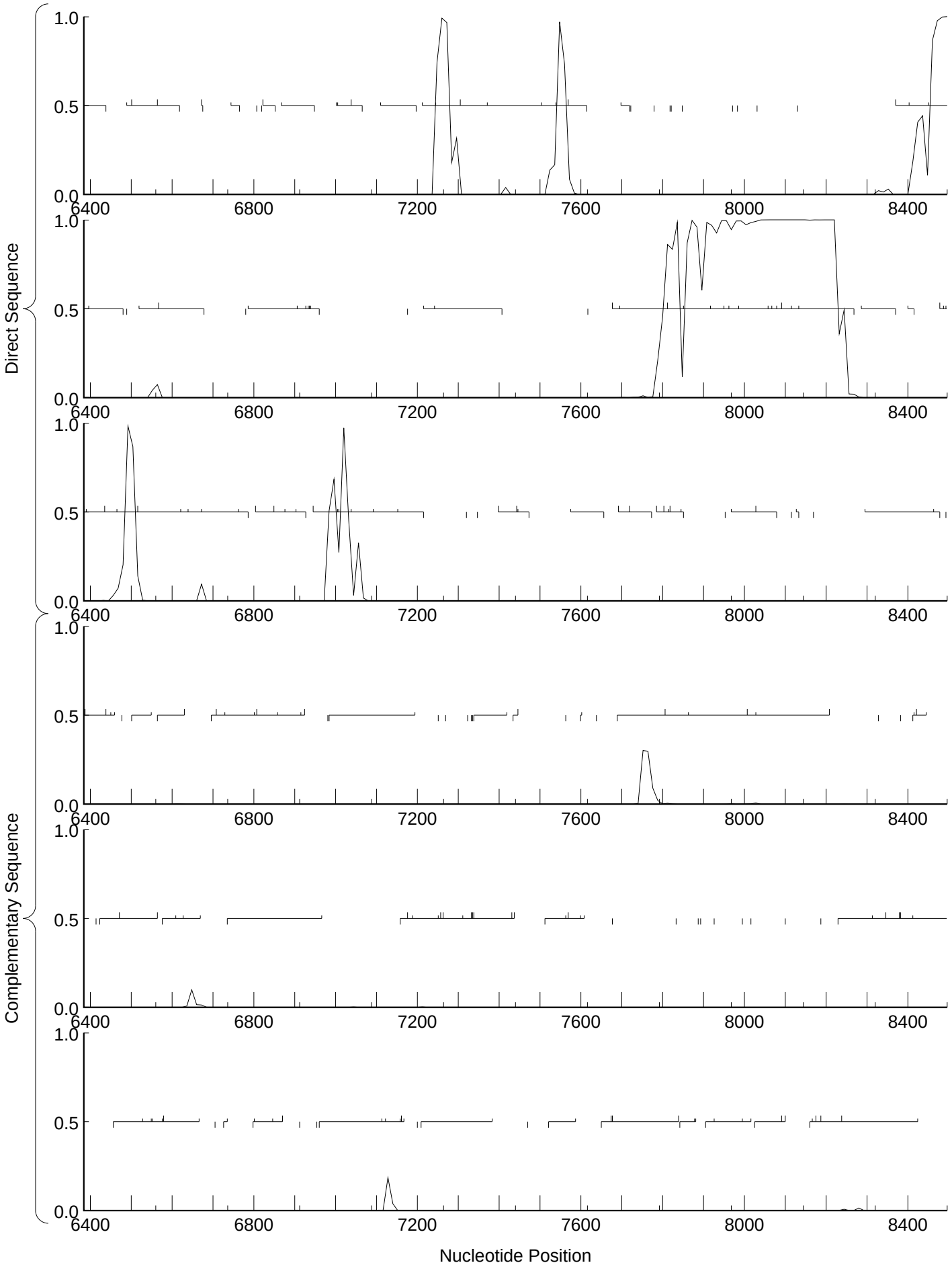
ni Complete Sequence, 54470 bp including 10-base 3’ overhang (CTCAGGGCAT), Cluster F2, Order 4, Window 96, Step 12, 2/27

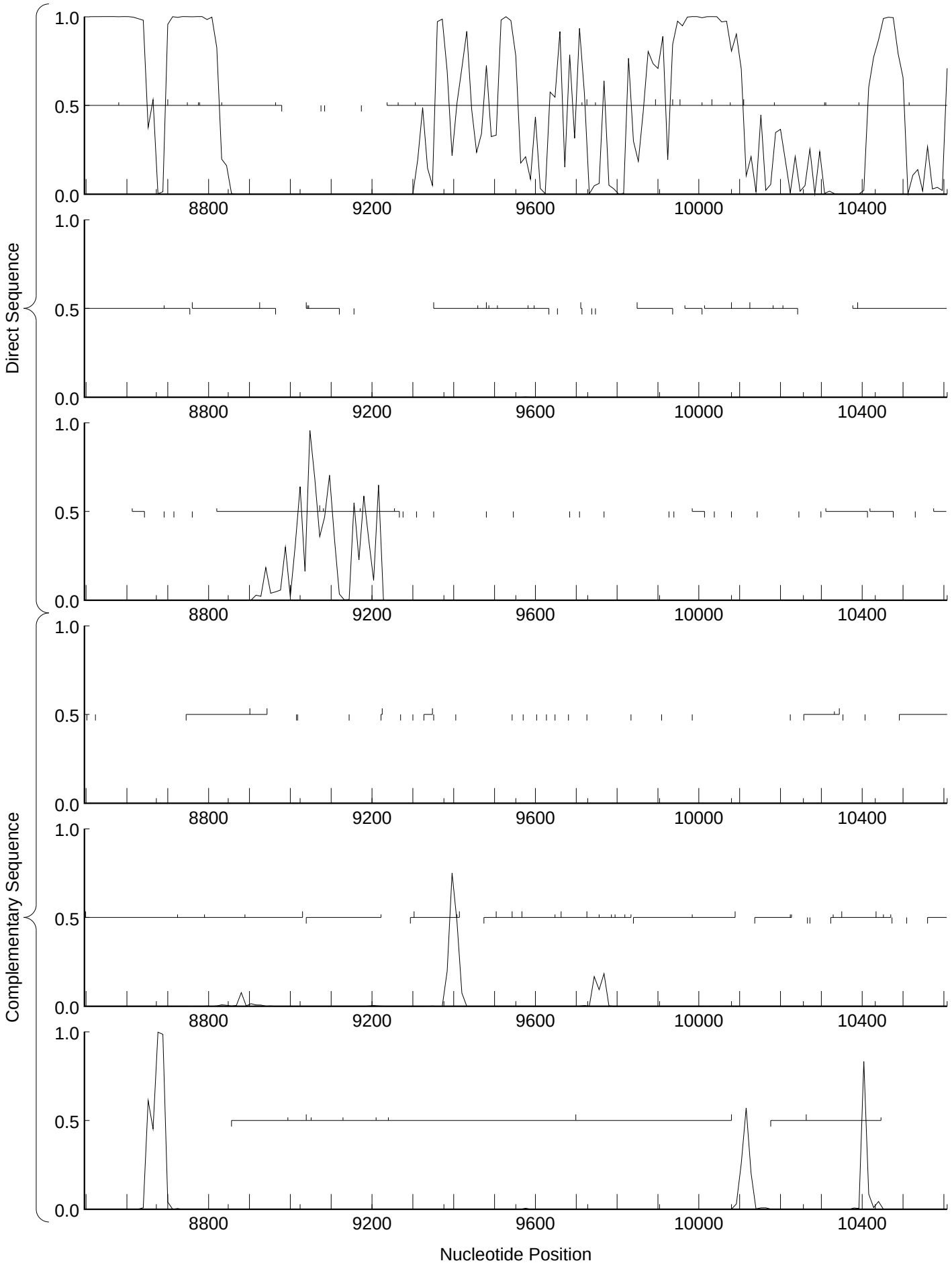



Direct Sequence
Complementary Sequence
1.0
0.5
0.0
2400
2800
3200
3600
4000
Nucleotide Position

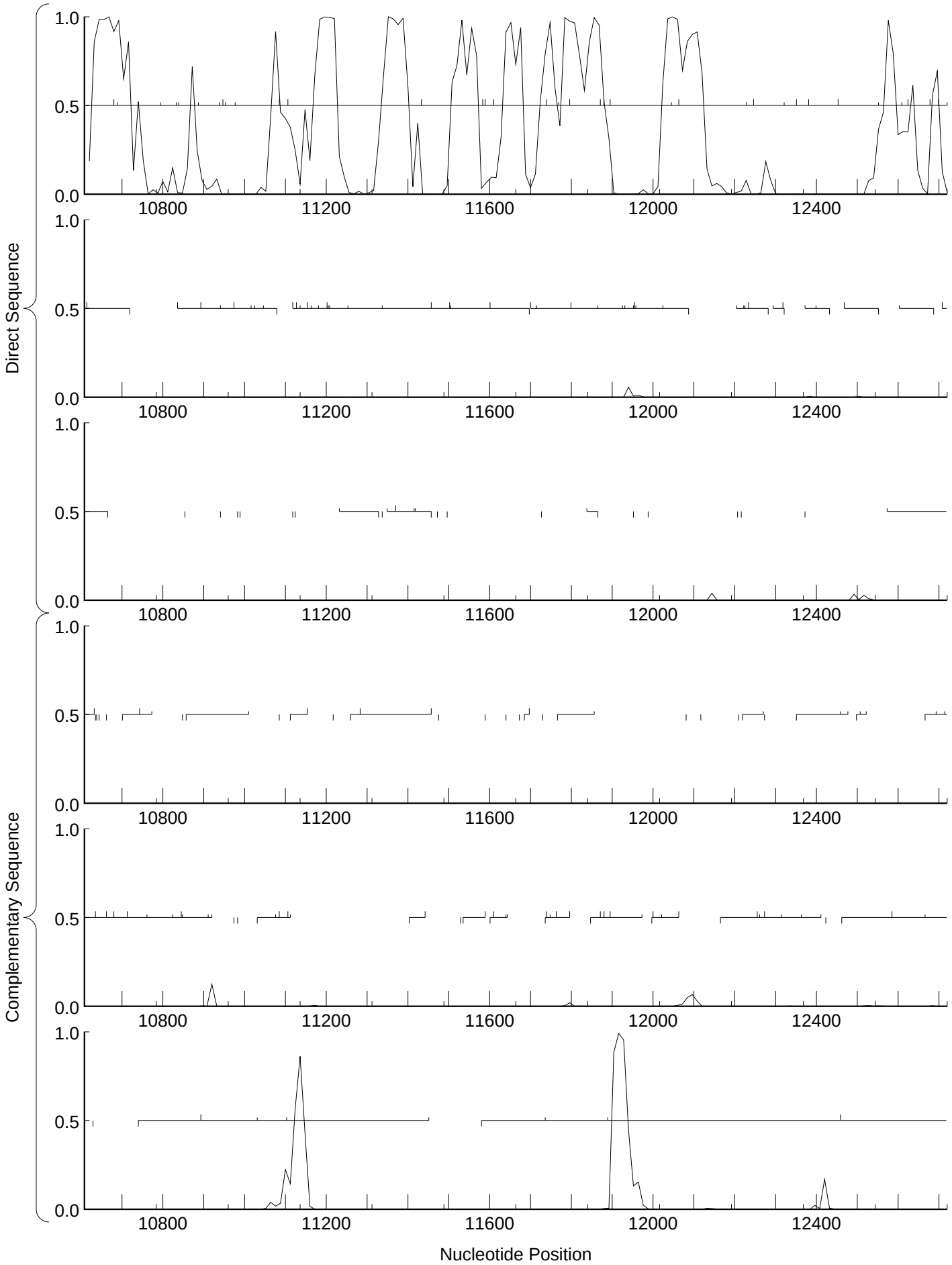

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
4400
4800
5200
5600
6000
Nucleotide Position

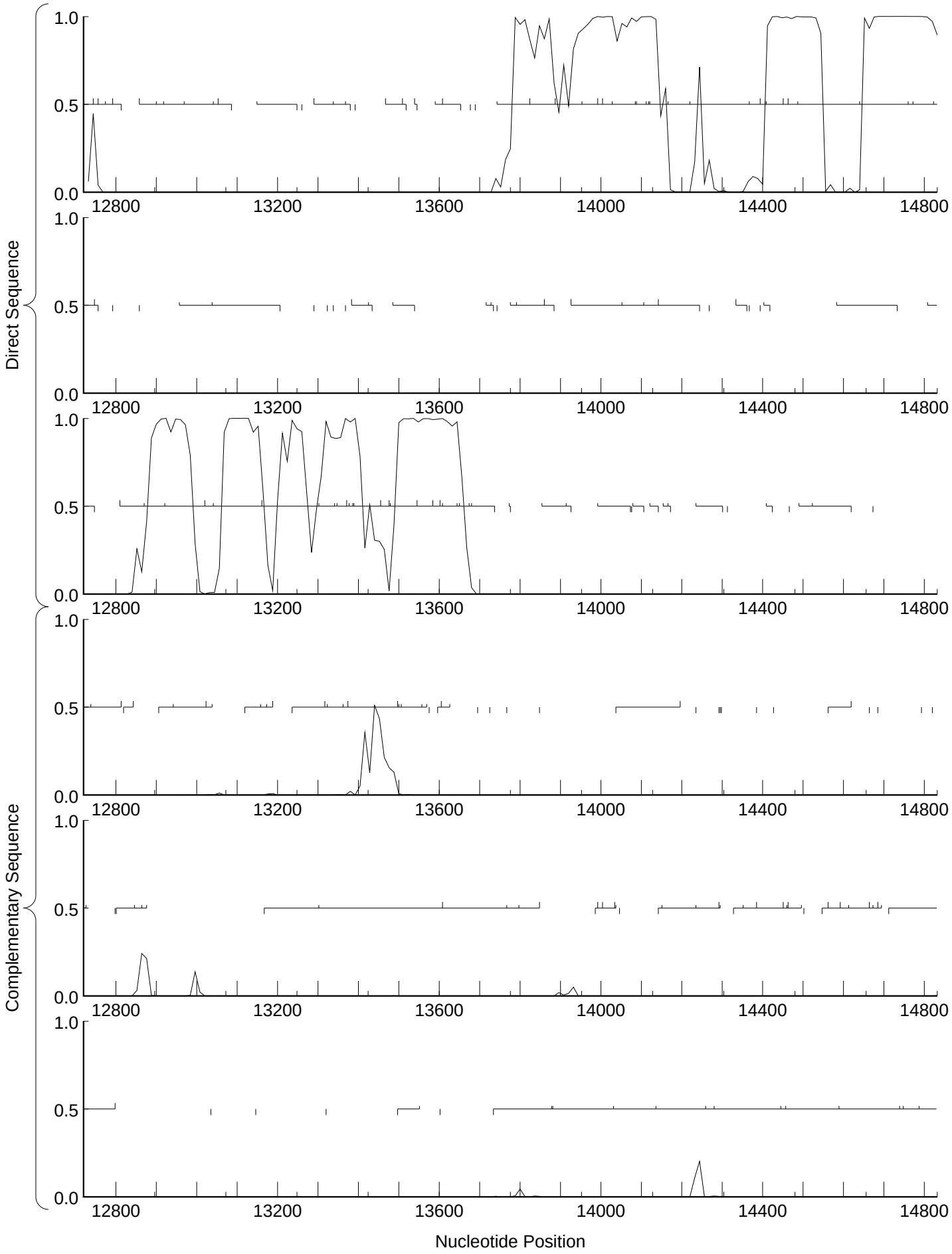
hi Complete Sequence, 54470 bp including 10-base 3’ overhang (CTCAGGGCAT), Cluster F2, Order 4, Window 96, Step 12, 5/27



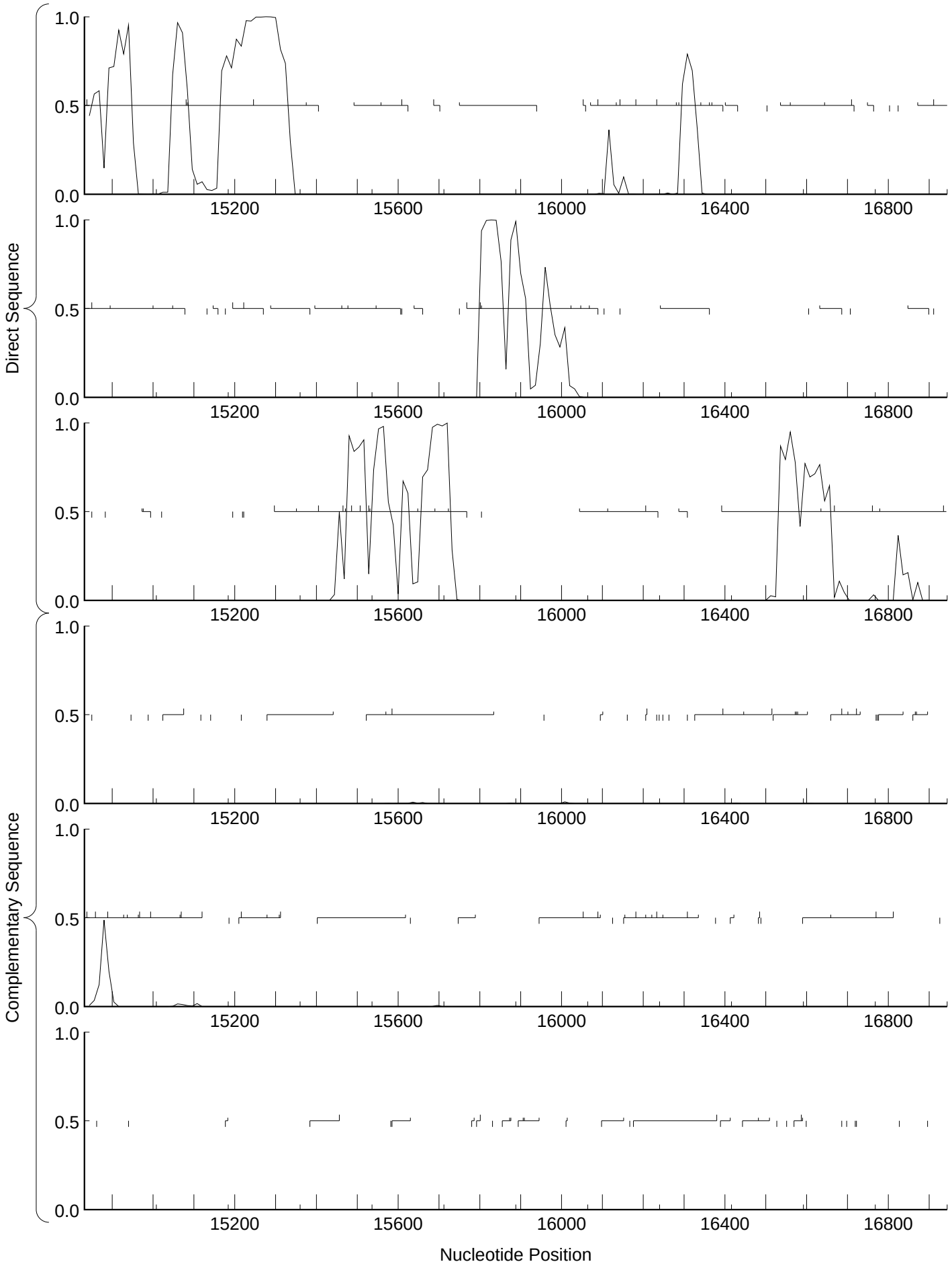

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
8800
9200
9600
10000
10400
Nucleotide Position

ni Complete Sequence, 54470 bp including 10-base 3’ overhang (CTCAGGGCAT), Cluster F2, Order 4, Window 96, Step 12, 7/27

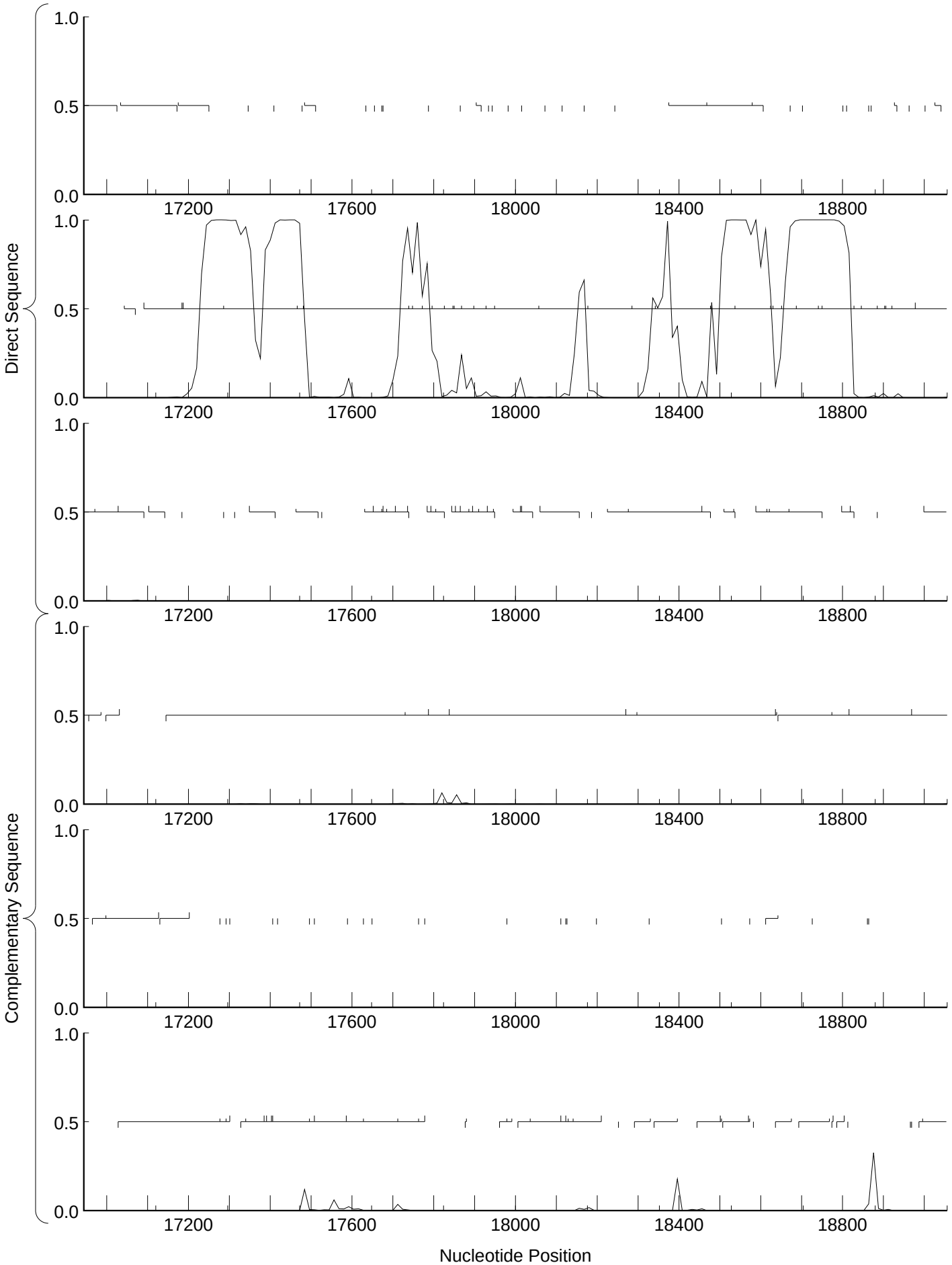



Direct Sequence
Complementary Sequence
1.0
0.5
0.0
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13200
13600
14000
14400
14800
Nucleotide Position

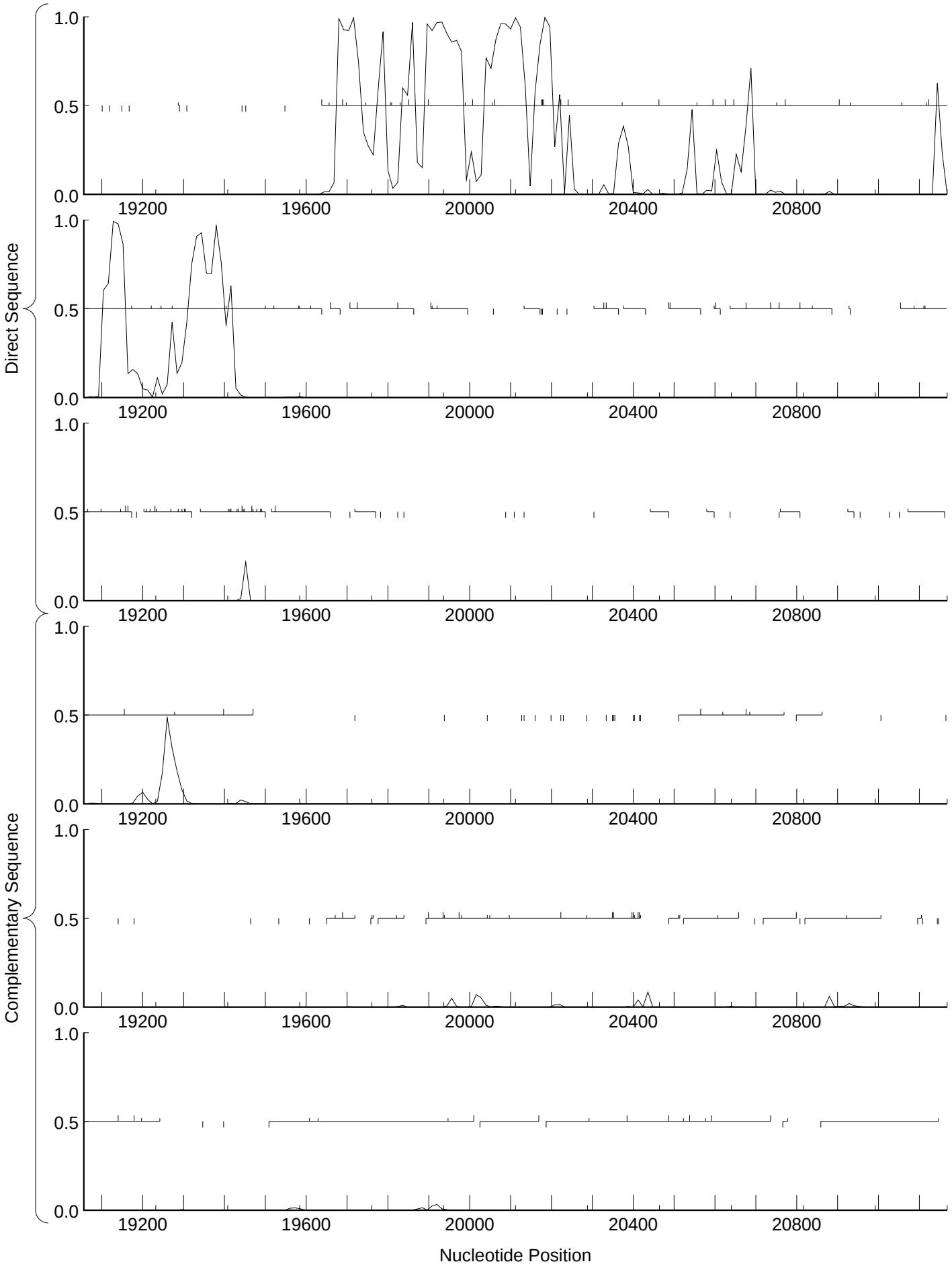
ni Complete Sequence, 54470 bp including 10-base 3’ overhang (CTCAGGGCAT), Cluster F2, Order 4, Window 96, Step 12, 9/27



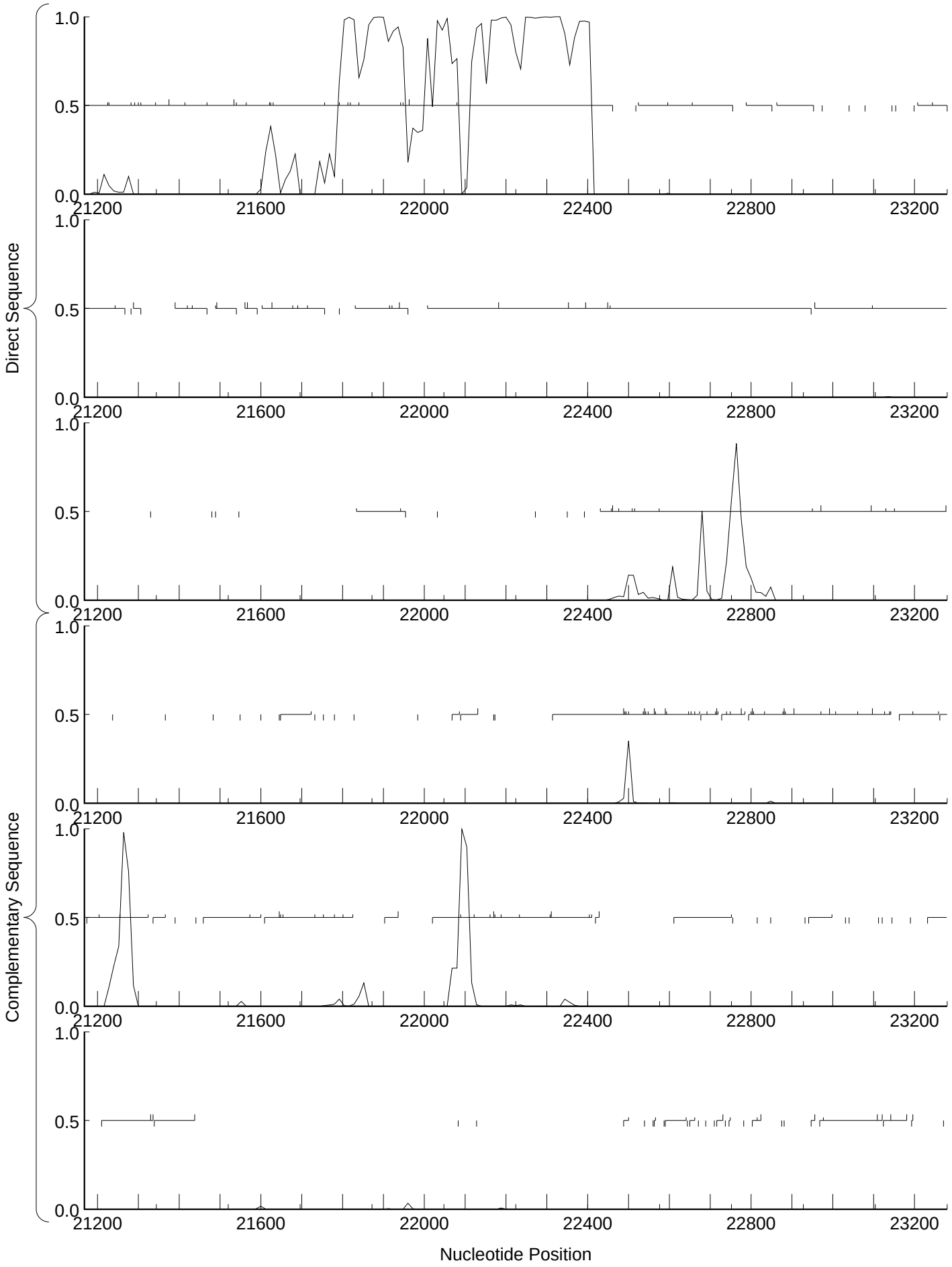
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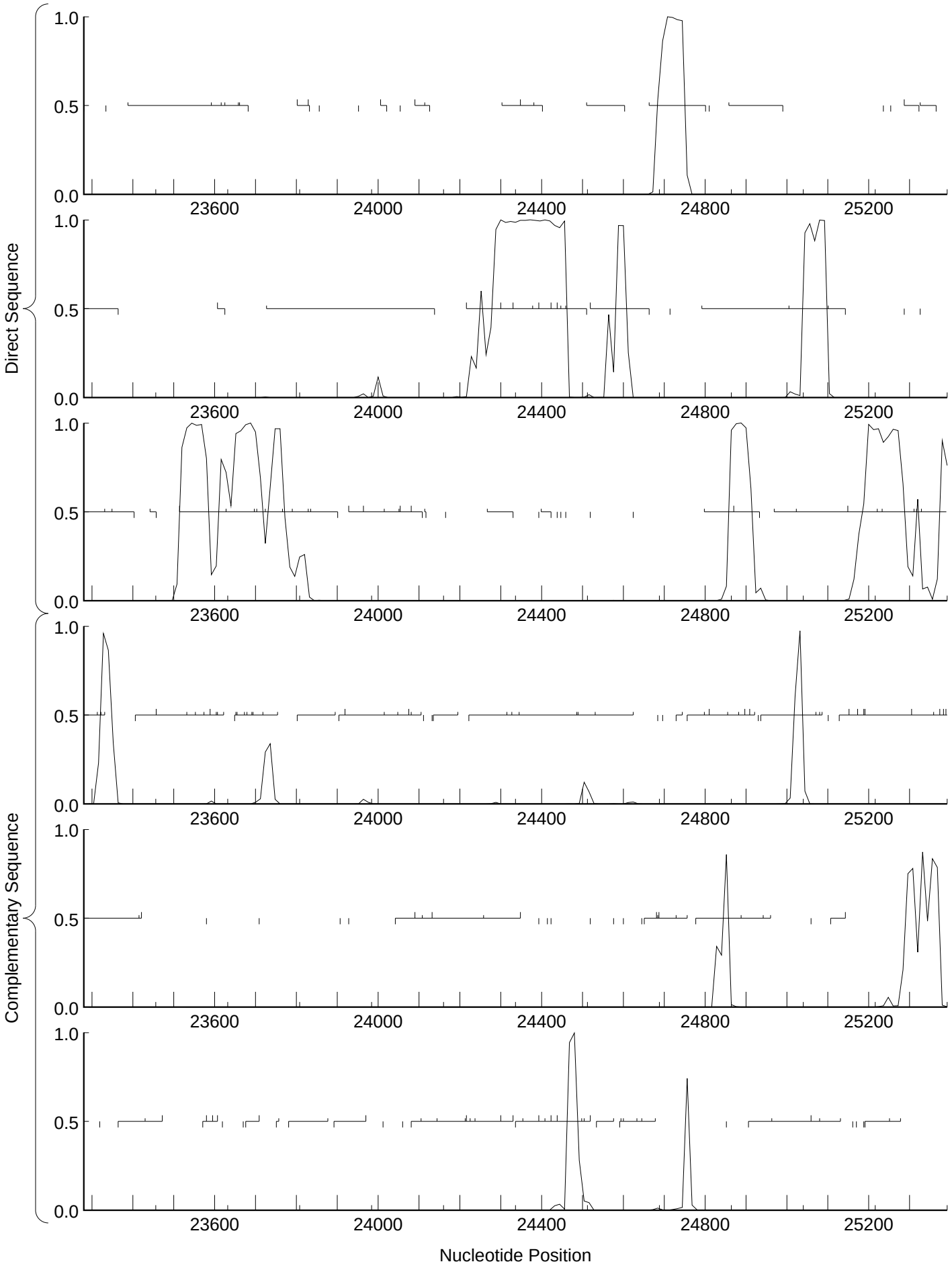
Complete Sequence, 54470 bp including 10-base 3’ overhang (CTCAGGGCAT), Cluster F2, Order 4, Window 96, Step 12, 11/27



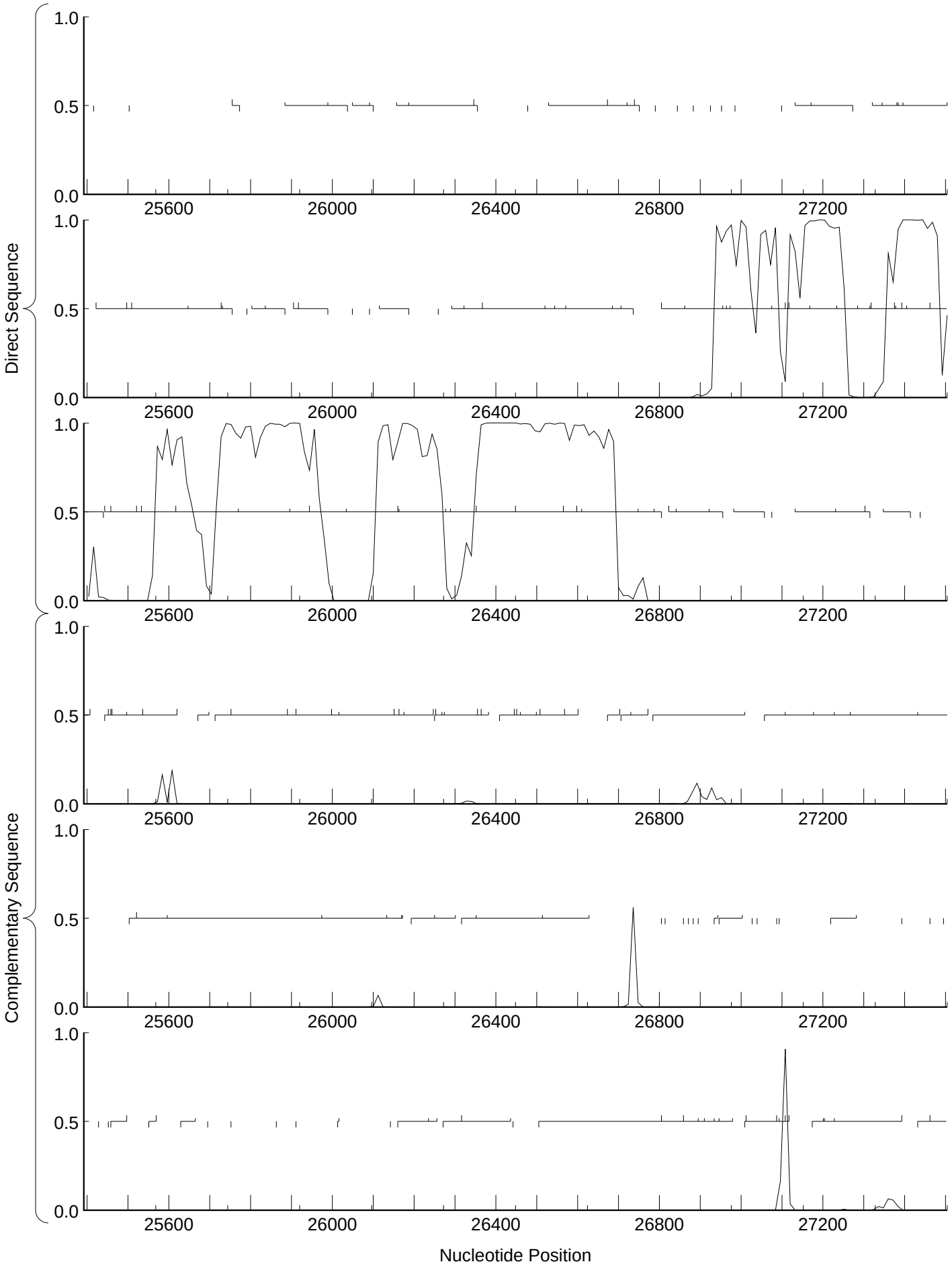
Complete Sequence, 54470 bp including 10-base 3' overhang (CTCAGGGCAT), Cluster F2, Order 4, Window 96, Step 12, 12/27



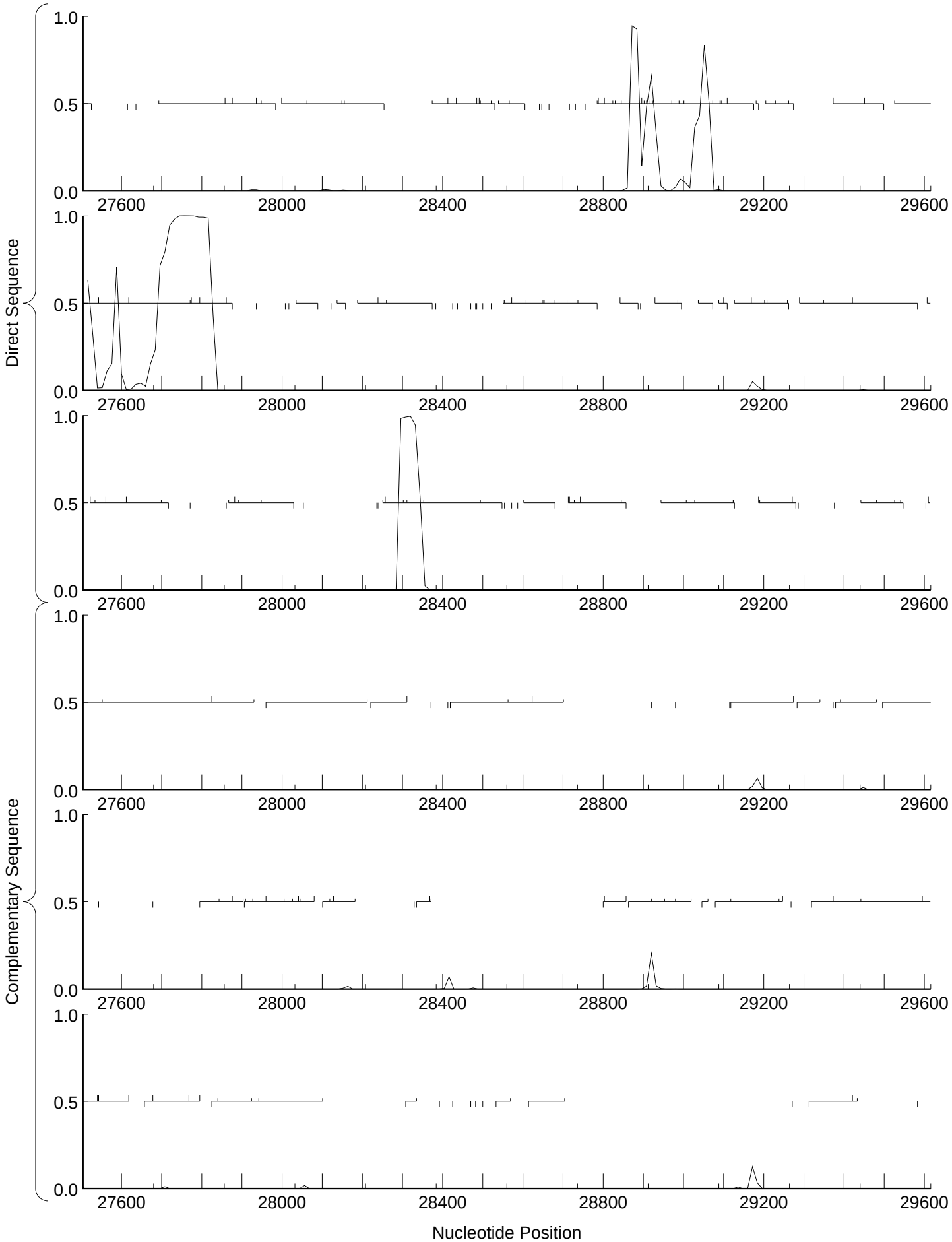
Complete Sequence, 54470 bp including 10-base 3' overhang (CTCAGGGCAT), Cluster F2, Order 4, Window 96, Step 12, 13/27



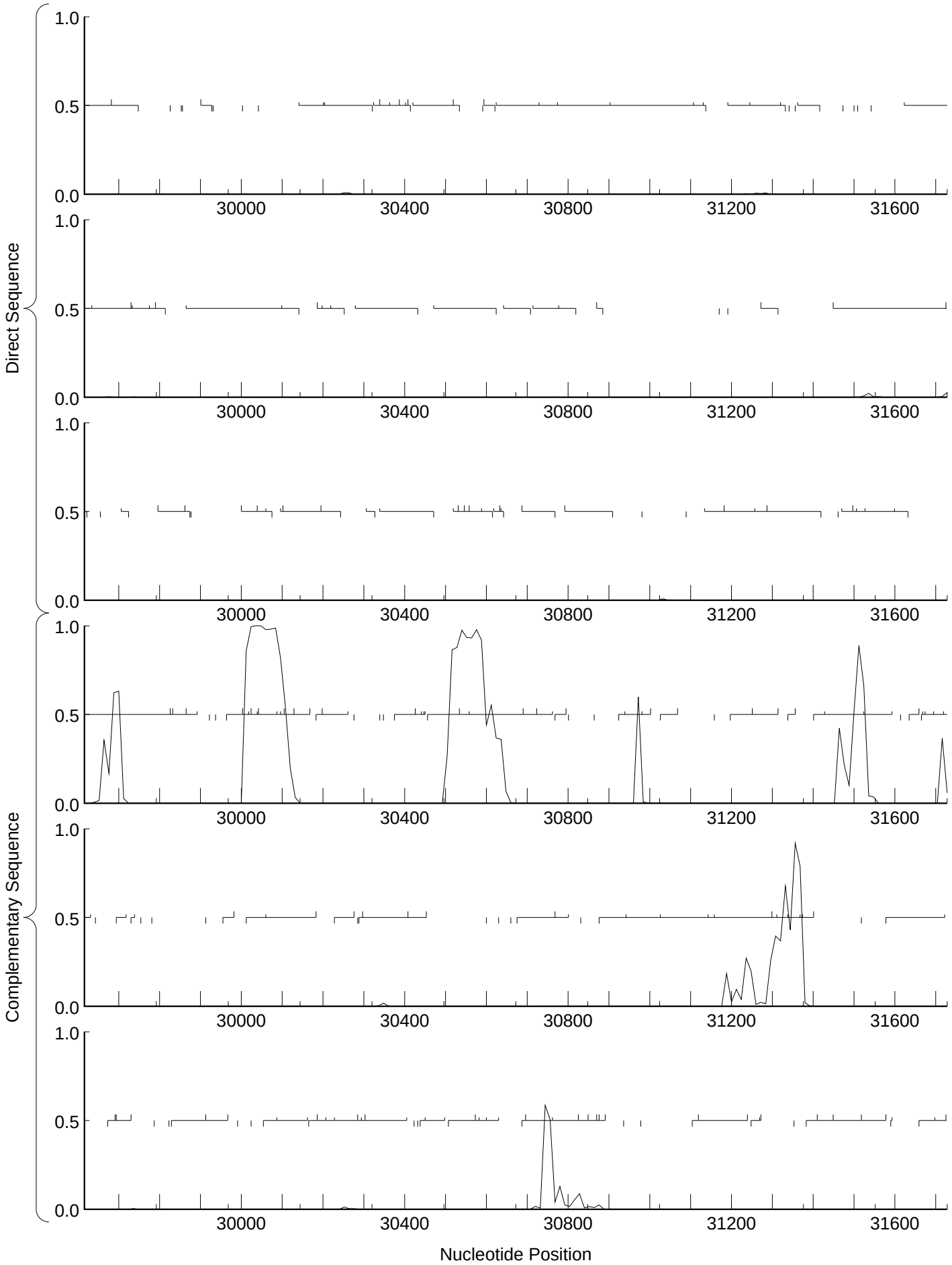
Complete Sequence, 54470 bp including 10-base 3’ overhang (CTCAGGGCAT), Cluster F2, Order 4, Window 96, Step 12, 14/27



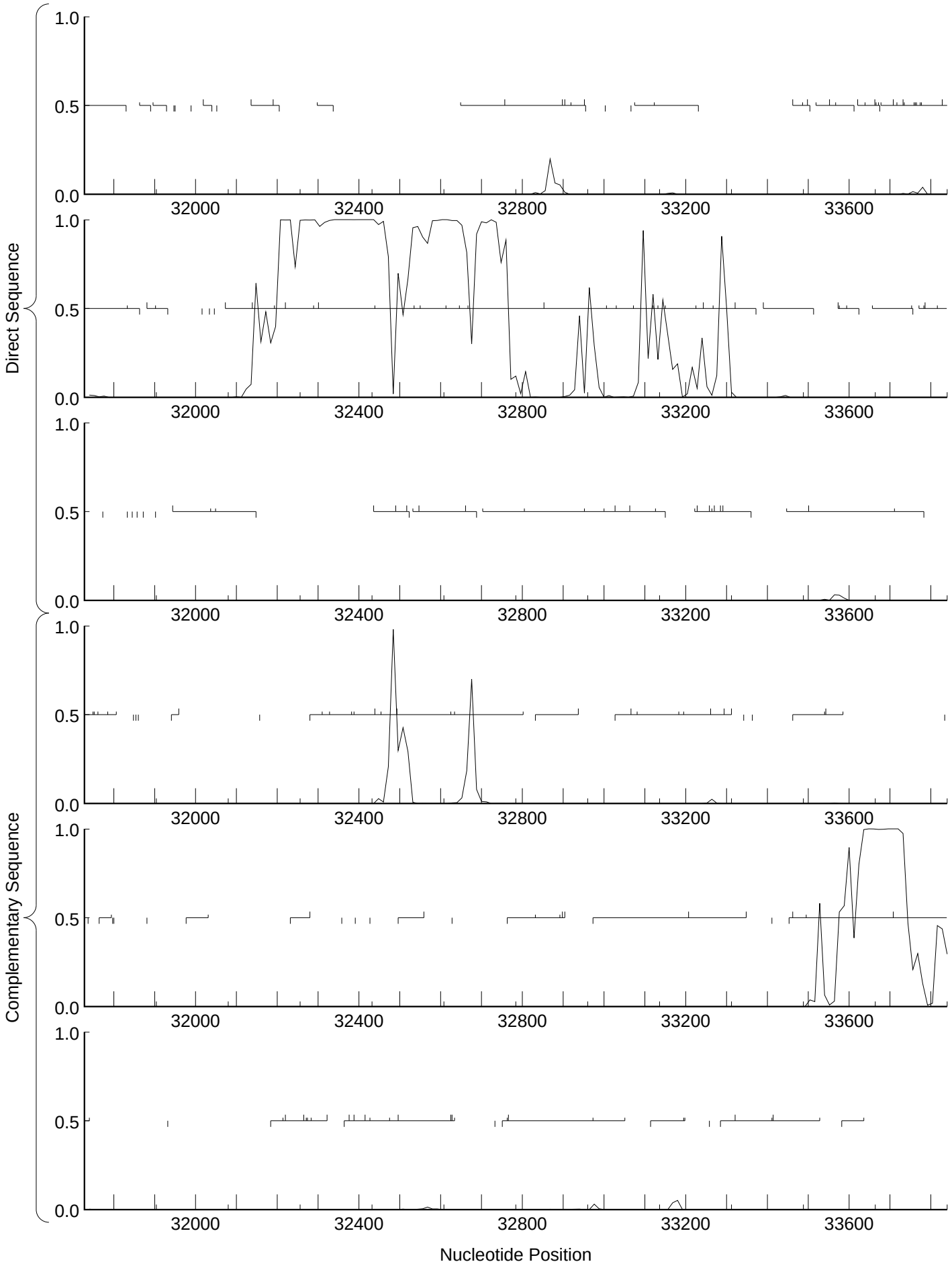
Complete Sequence, 54470 bp including 10-base 3’ overhang (CTCAGGGCAT), Cluster F2, Order 4, Window 96, Step 12, 15/27



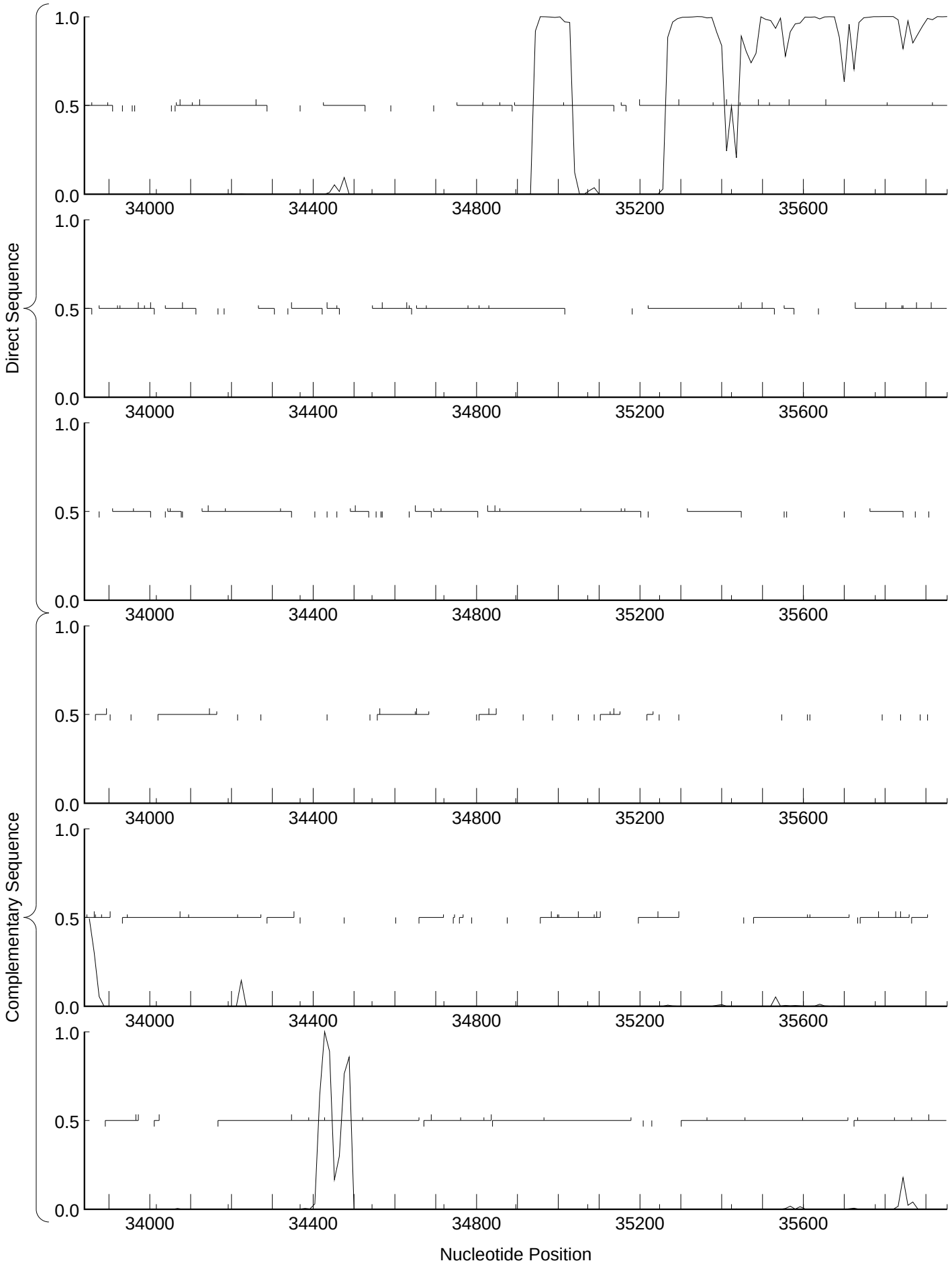
Complete Sequence, 54470 bp including 10-base 3’ overhang (CTCAGGGCAT), Cluster F2, Order 4, Window 96, Step 12, 16/27



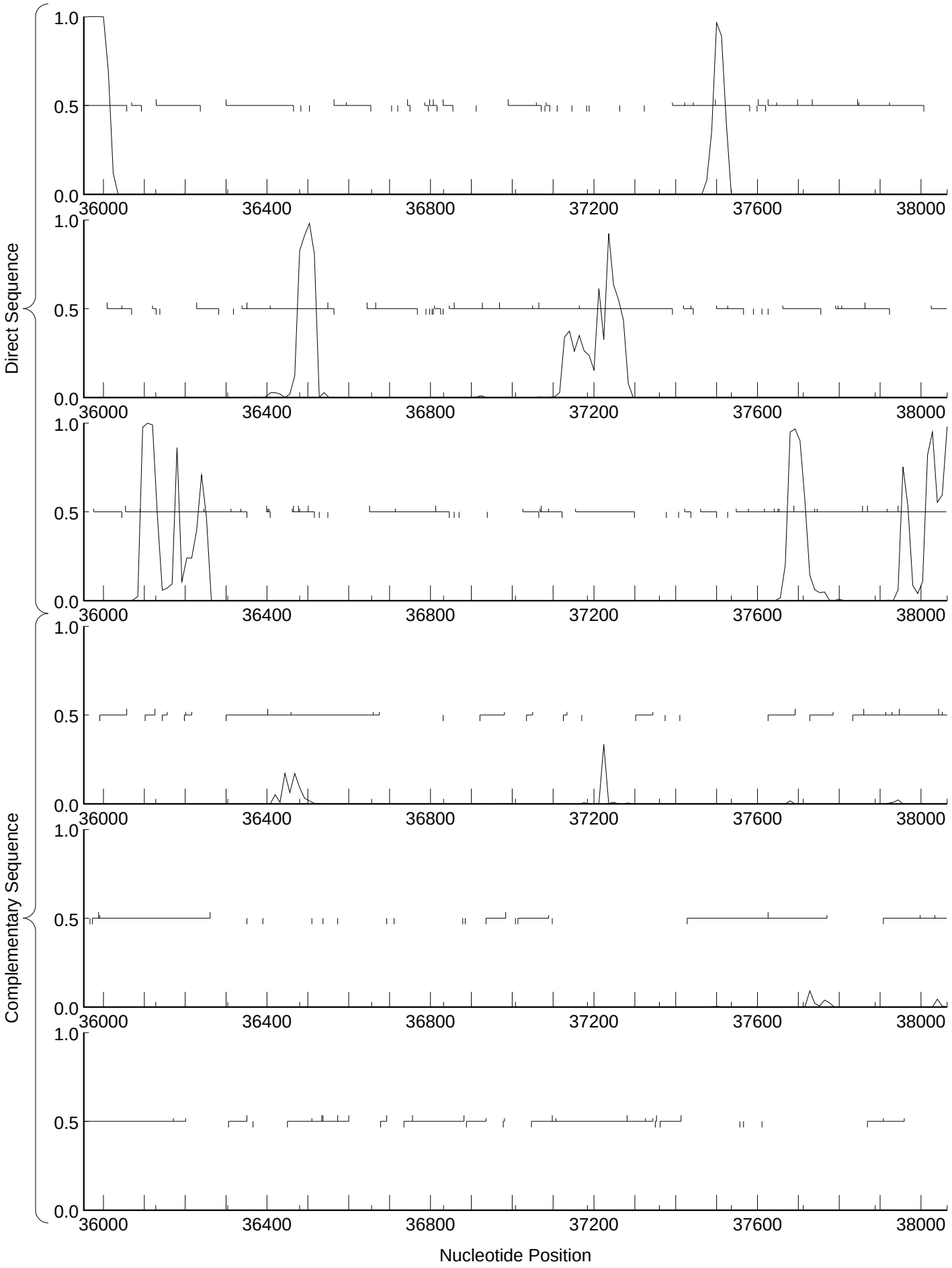
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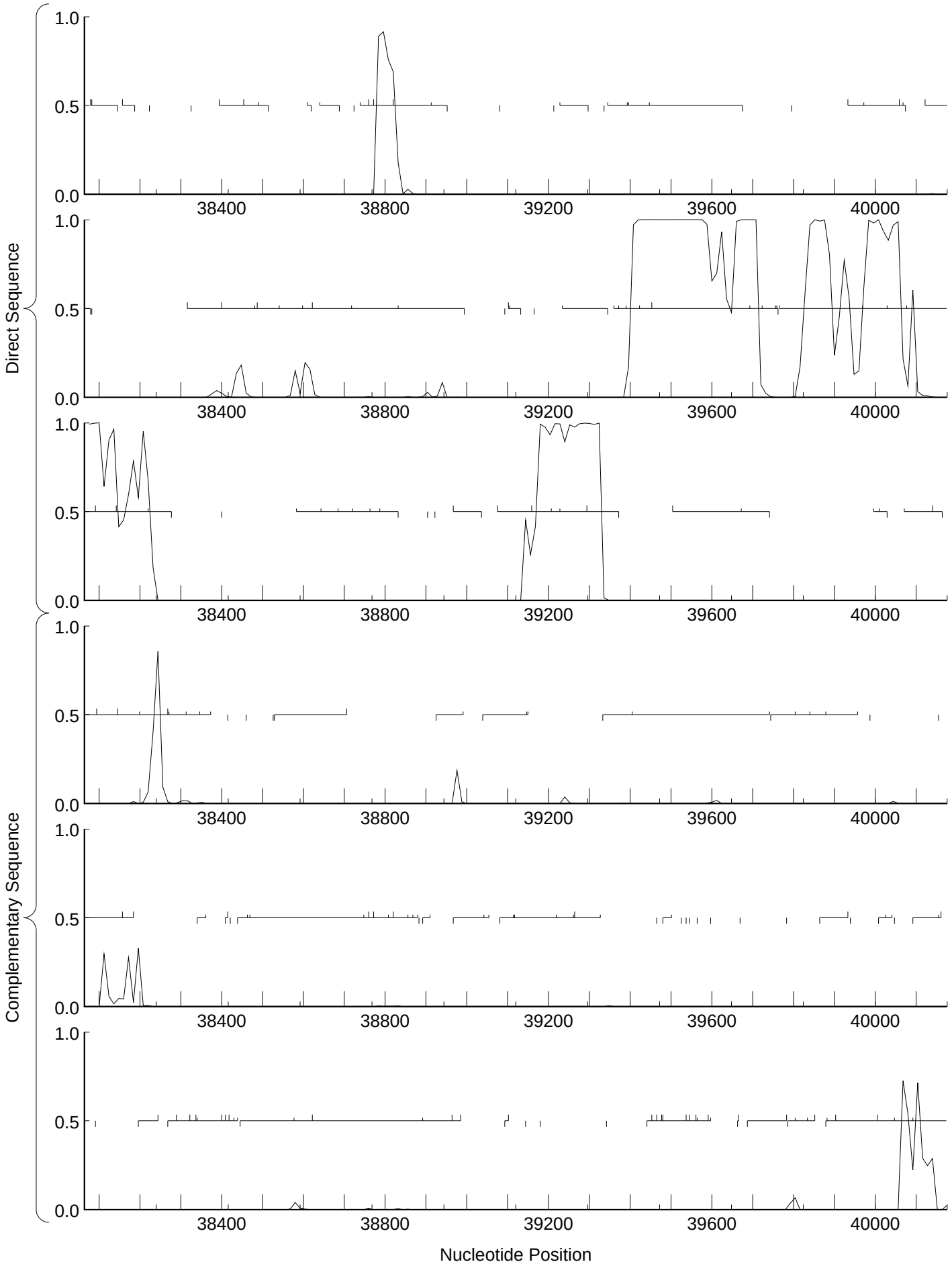
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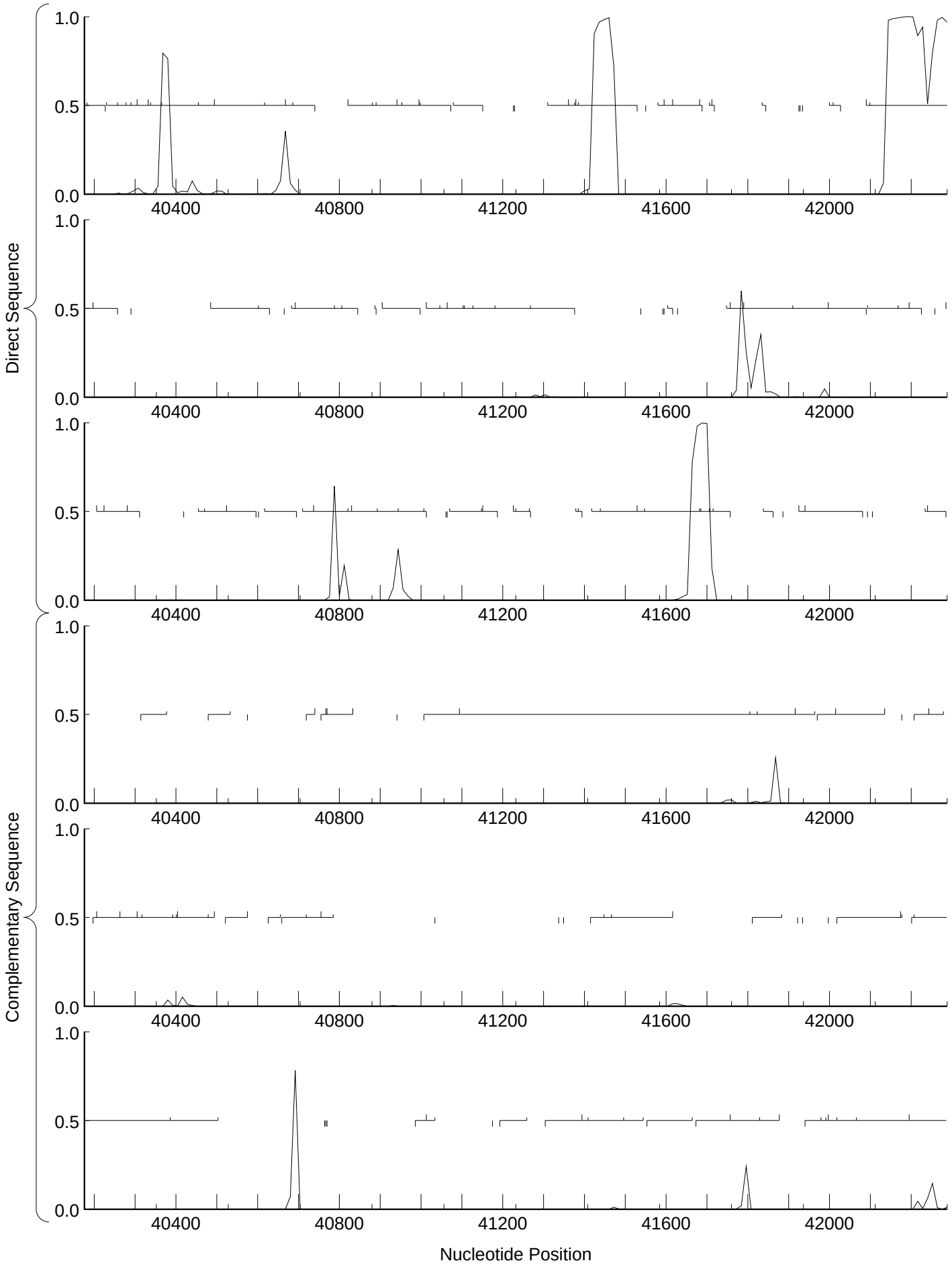
Complete Sequence, 54470 bp including 10-base 3' overhang (CTCAGGGCAT), Cluster F2, Order 4, Window 96, Step 12, 19/27



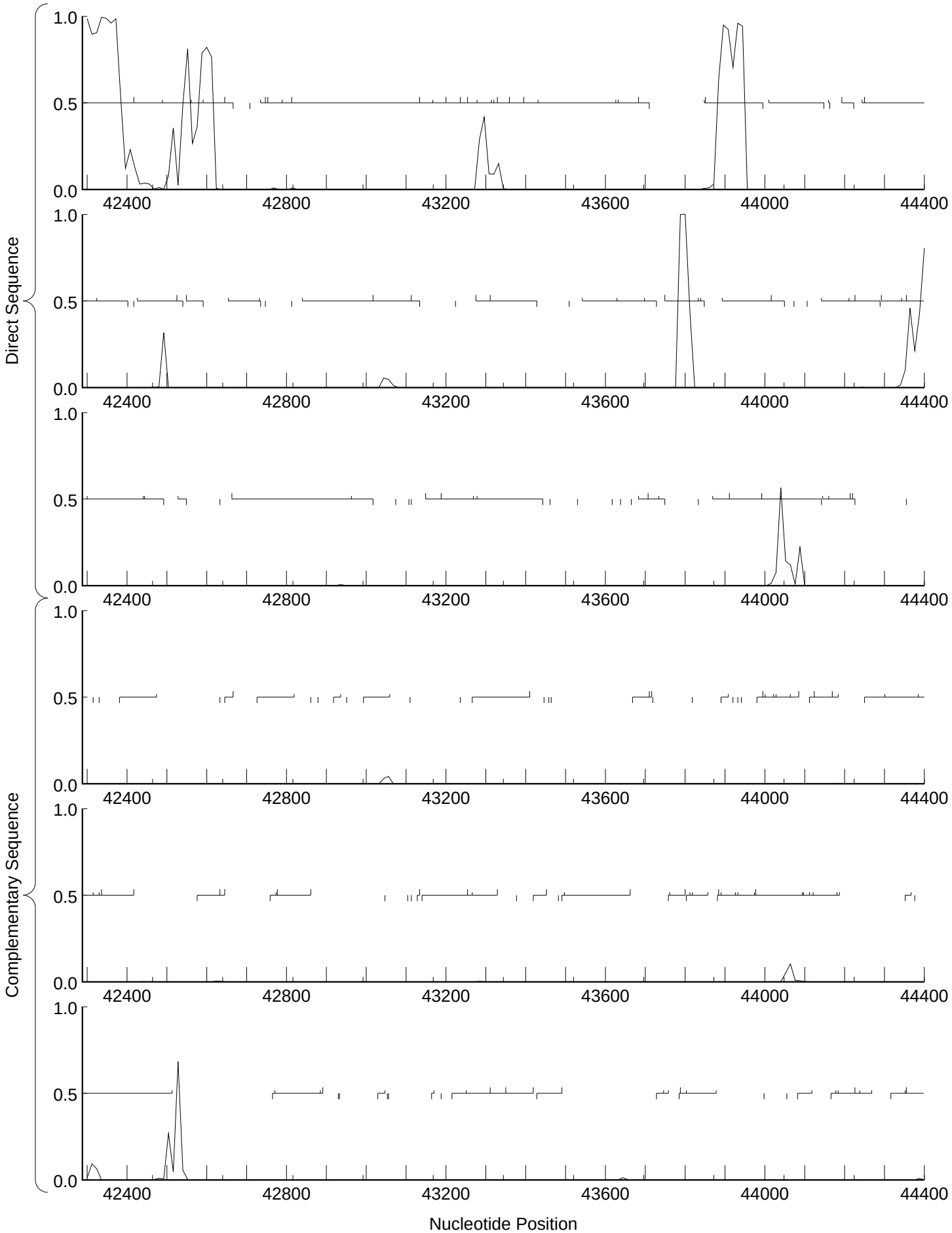
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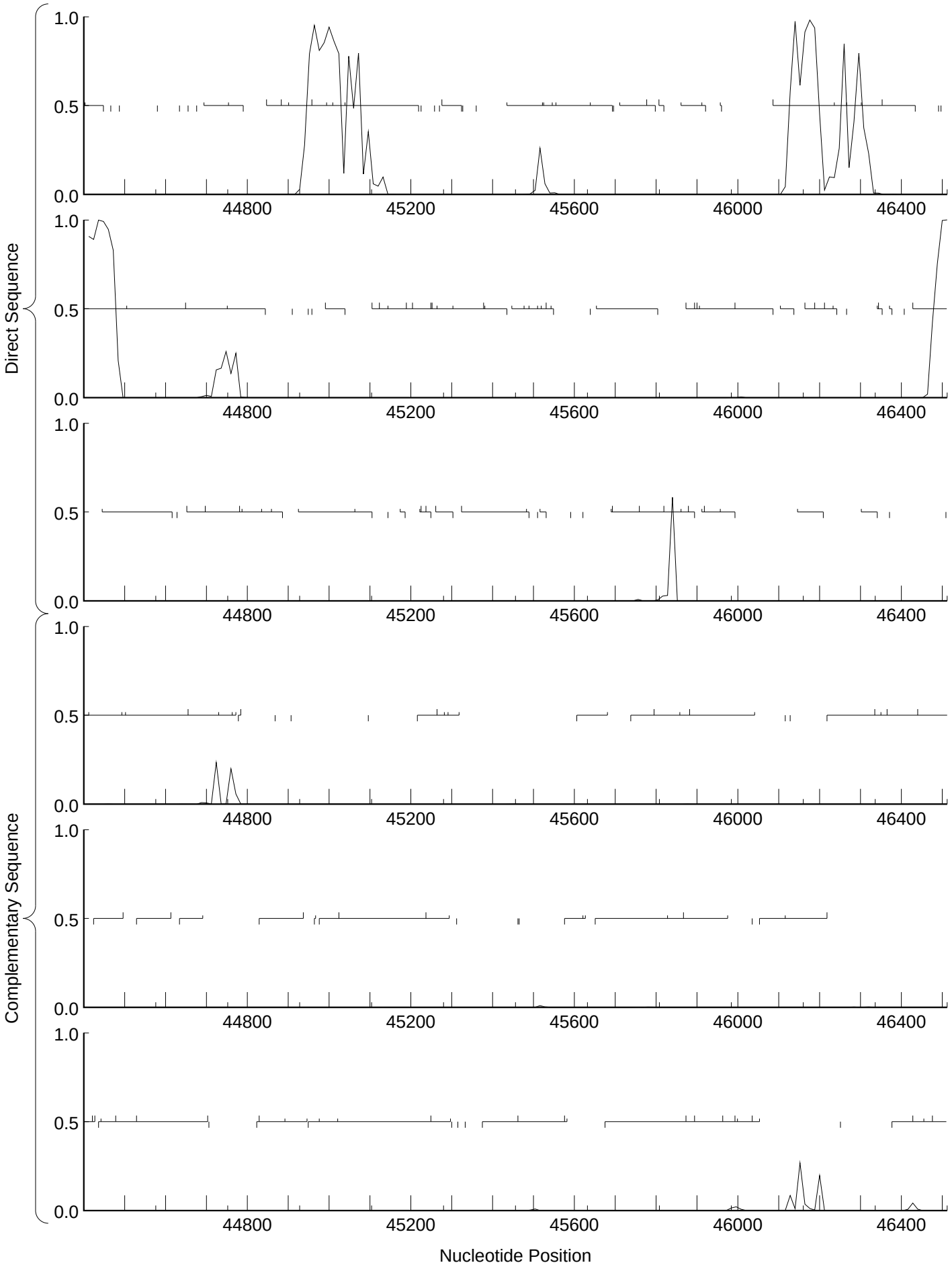
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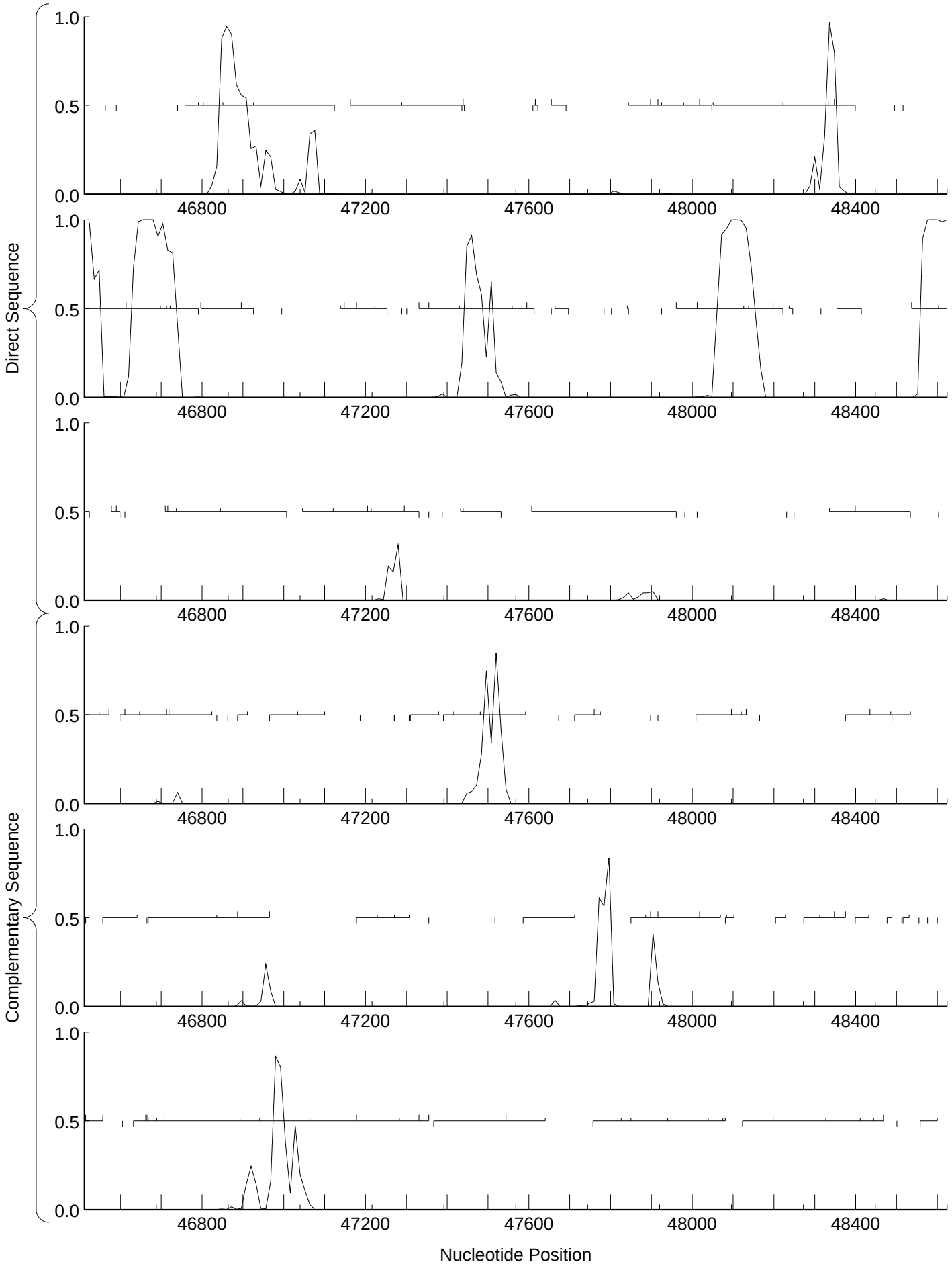
Complete Sequence, 54470 bp including 10-base 3' overhang (CTCAGGGCAT), Cluster F2, Order 4, Window 96, Step 12, 22/27



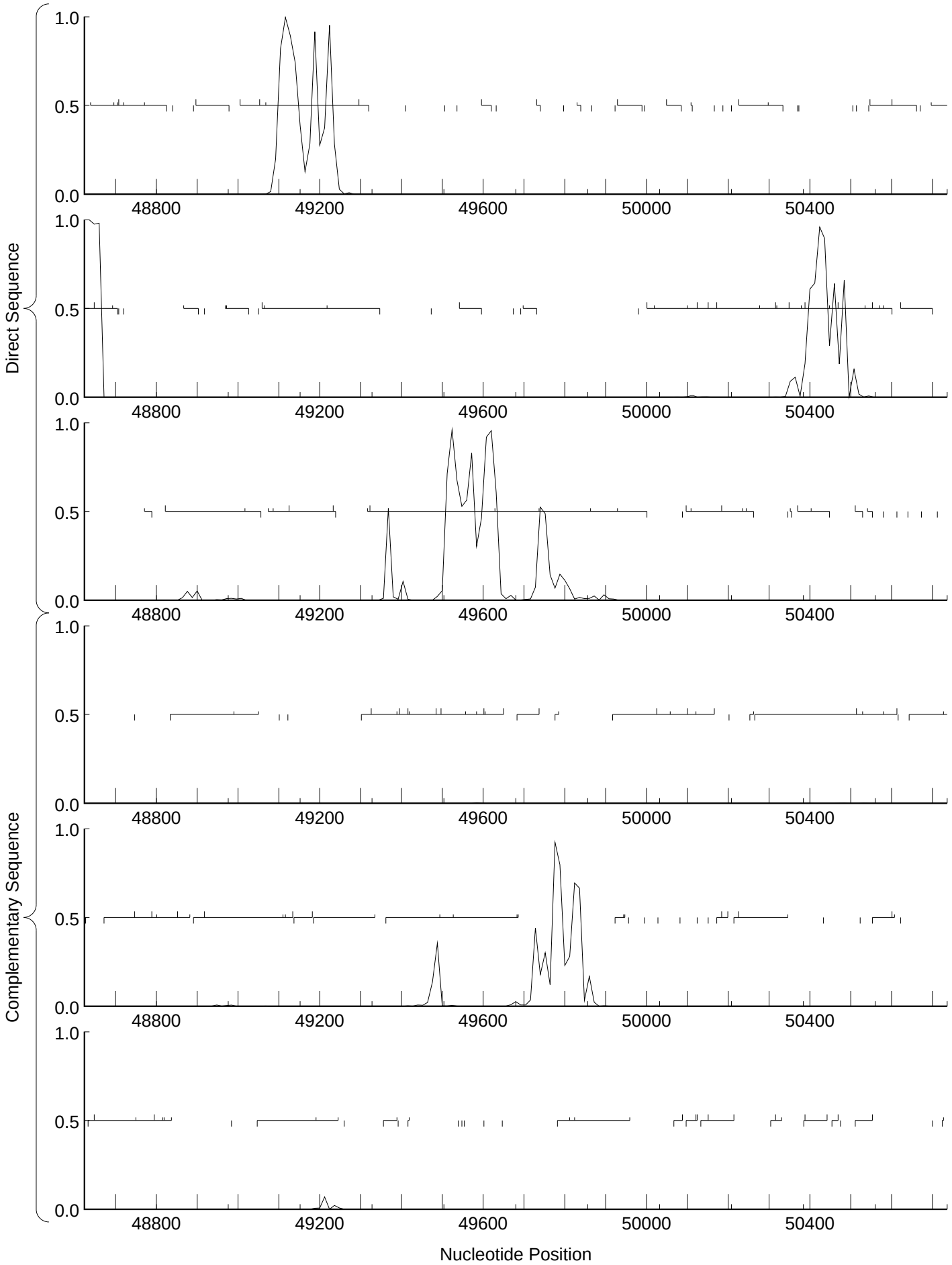
Complete Sequence, 54470 bp including 10-base 3' overhang (CTCAGGGCAT), Cluster F2, Order 4, Window 96, Step 12, 23/27



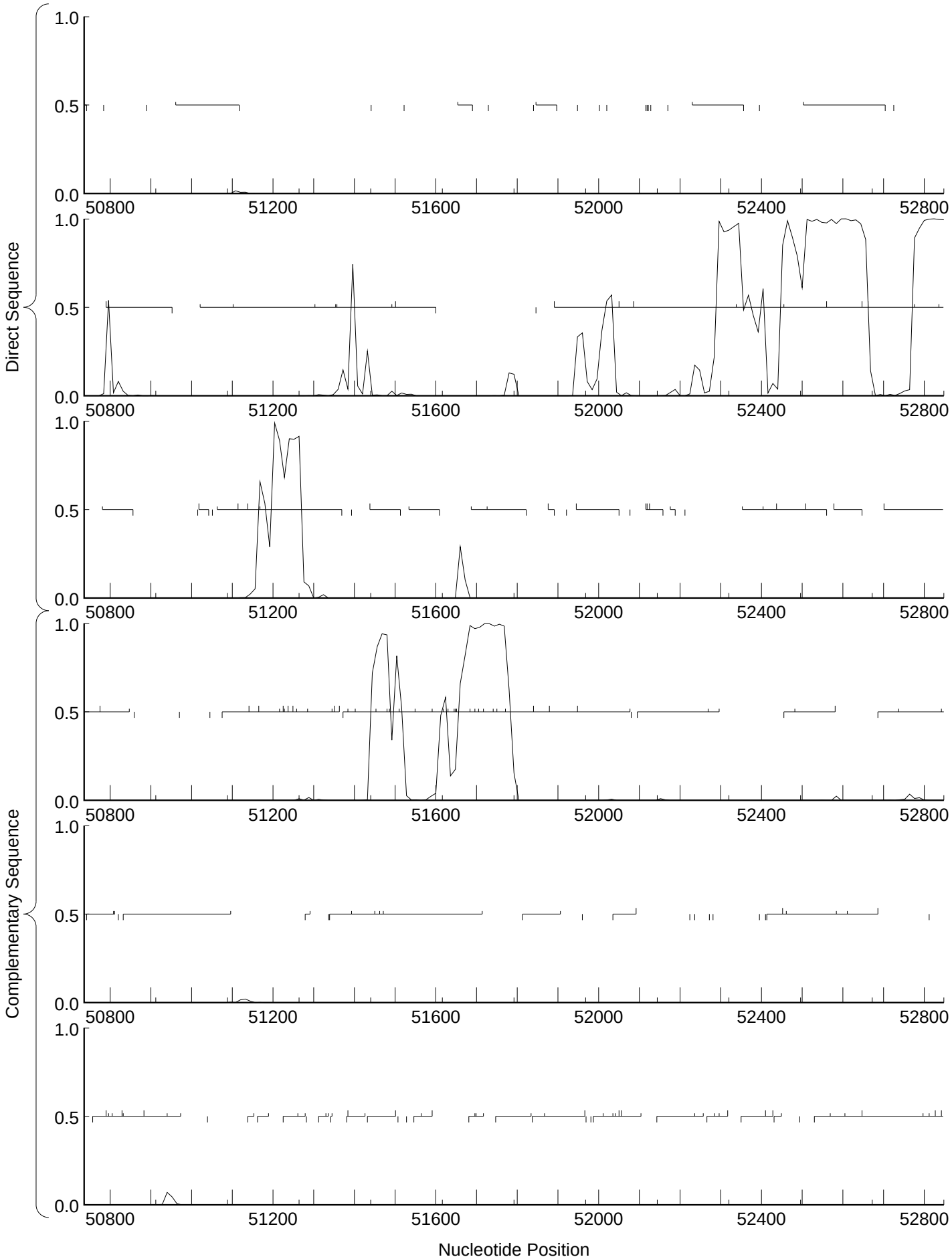
Complete Sequence, 54470 bp including 10-base 3’ overhang (CTCAGGGCAT), Cluster F2, Order 4, Window 96, Step 12, 24/27



Complete Sequence, 54470 bp including 10-base 3’ overhang (CTCAGGGCAT), Cluster F2, Order 4, Window 96, Step 12, 25/27



Complete Sequence, 54470 bp including 10-base 3’ overhang (CTCAGGGCAT), Cluster F2, Order 4, Window 96, Step 12, 26/27



Complete Sequence, 54470 bp including 10-base 3’ overhang (CTCAGGGCAT), Cluster F2, Order 4, Window 96, Step 12, 27/27

