GeneMark

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

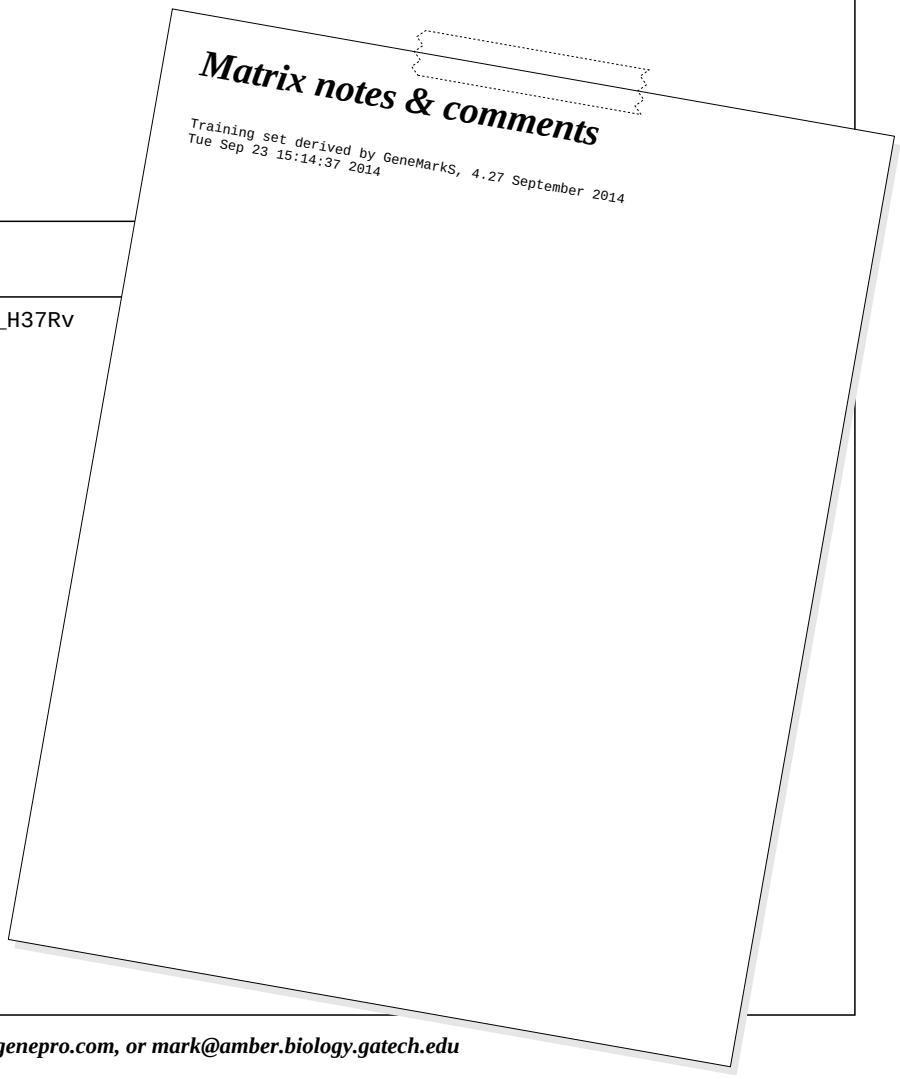
PROGRAM INFORMATION

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Sequence         :  Mycobacterium phage Avani Complete Sequence, 54470 bp including 10-base 3’ overhang (CTCAGG
Analysis Date    :  3/29/24 at 8:54:40
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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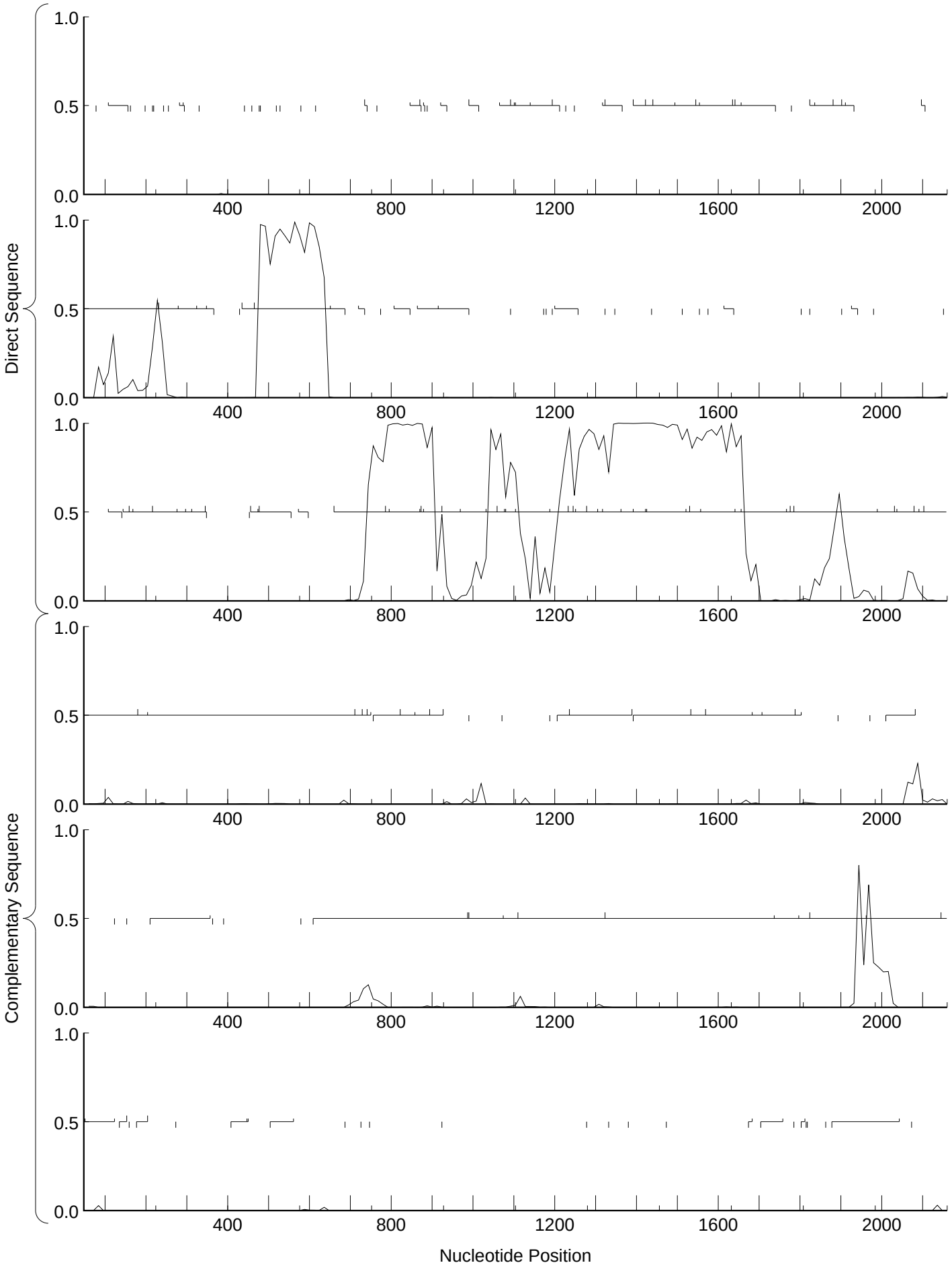
MATRIX INFORMATION

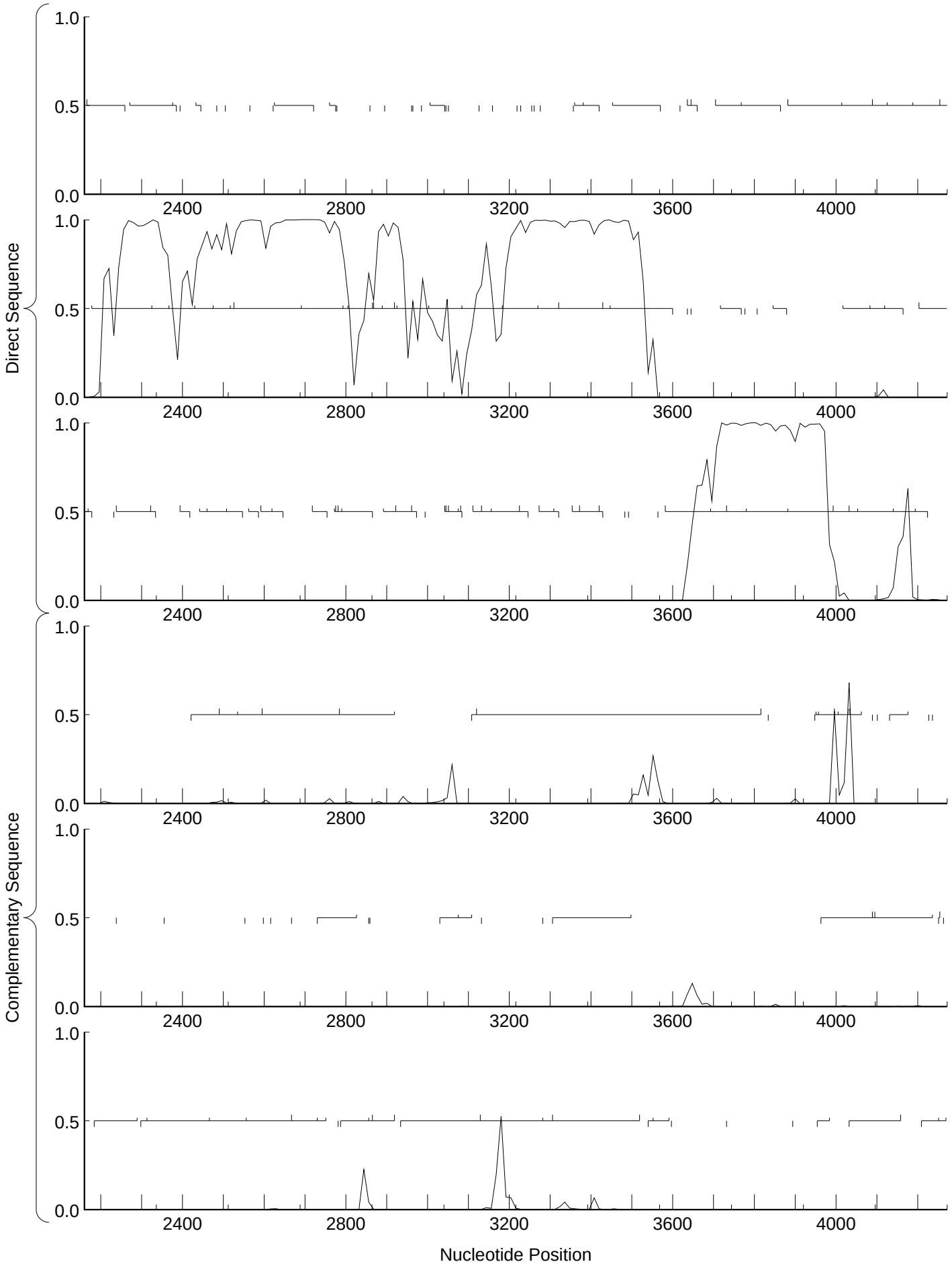
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Matrix     :  Mycobacterium_tuberculosis_H37Rv
Author     :  -

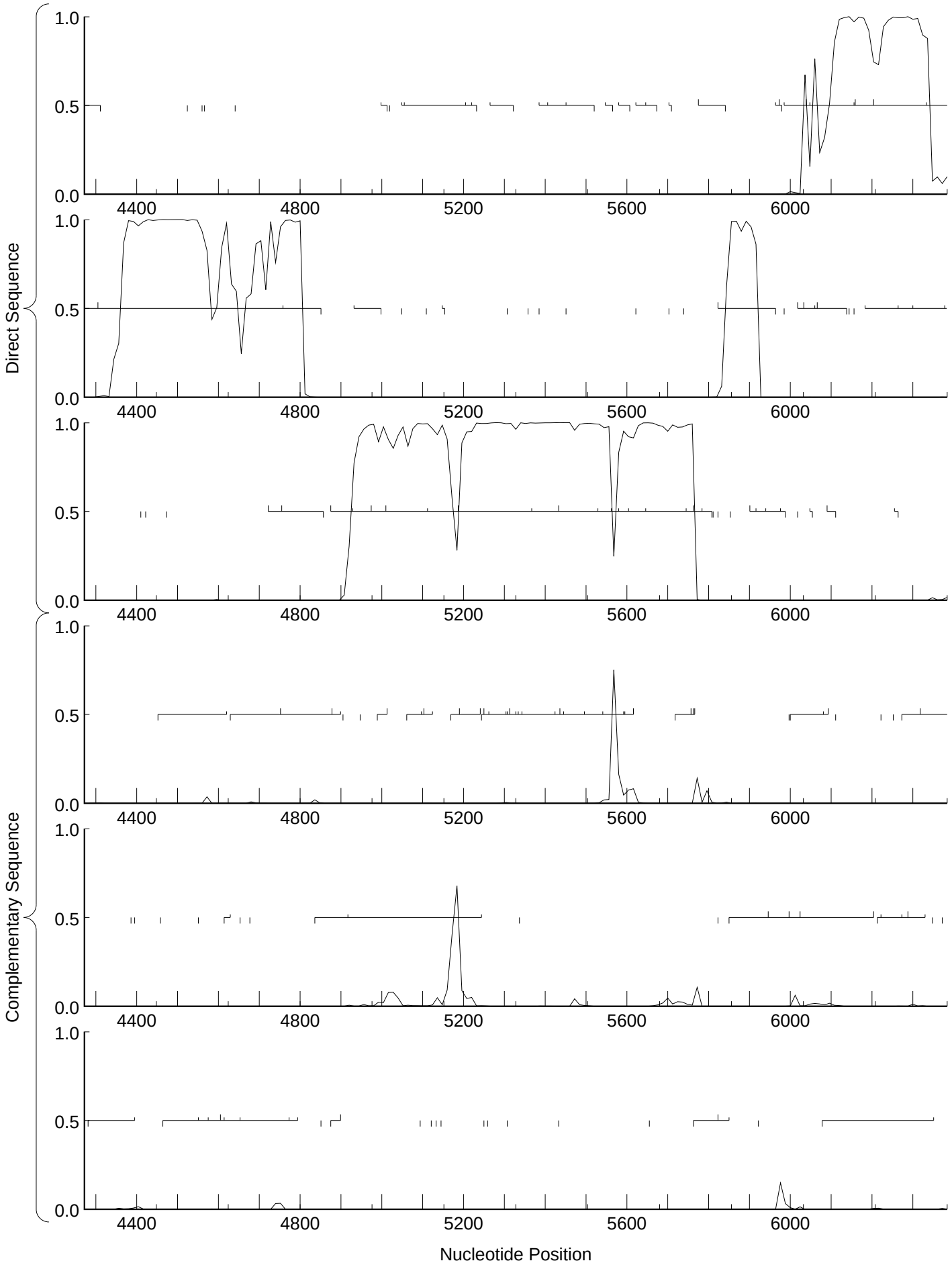
Order      :  4

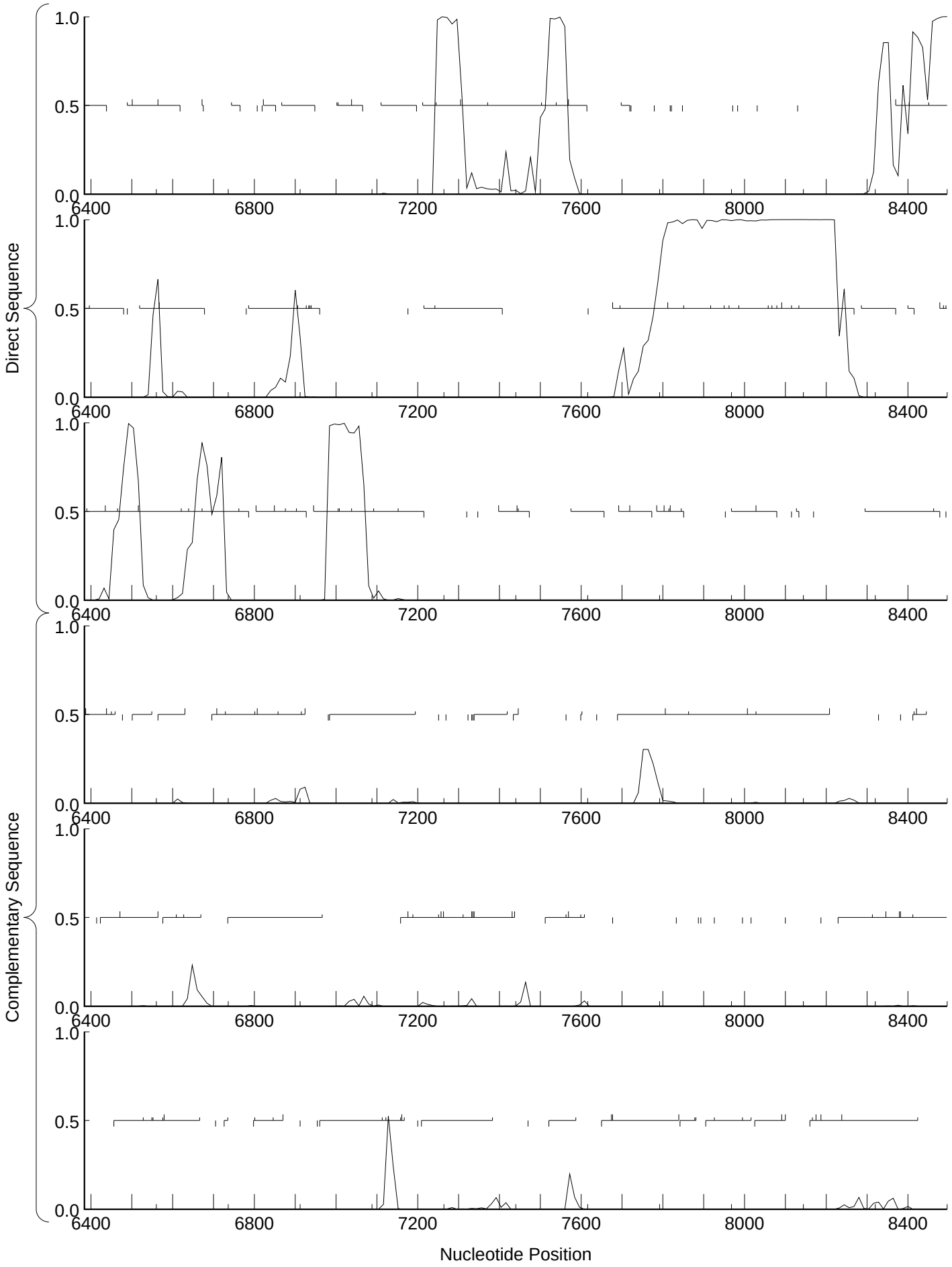

  Send questions / comments to:
      Dr. M. Borodovsky
      Georgia Institute of Technology
      School of Biology
      Atlanta, GA  30332-0230
```

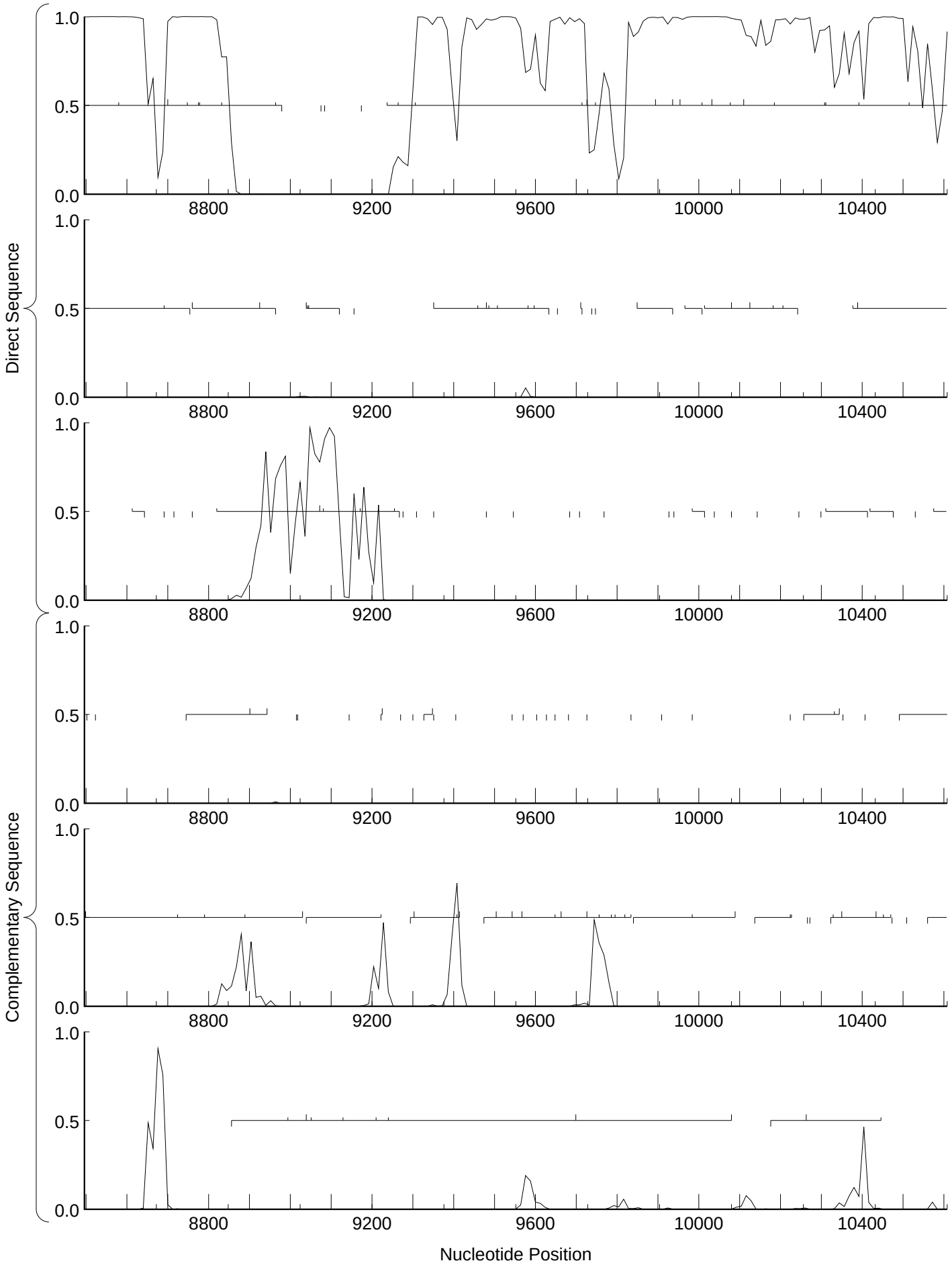
For help or information, send electronic mail to: custserv@genepro.com, or mark@amber.biology.gatech.edu

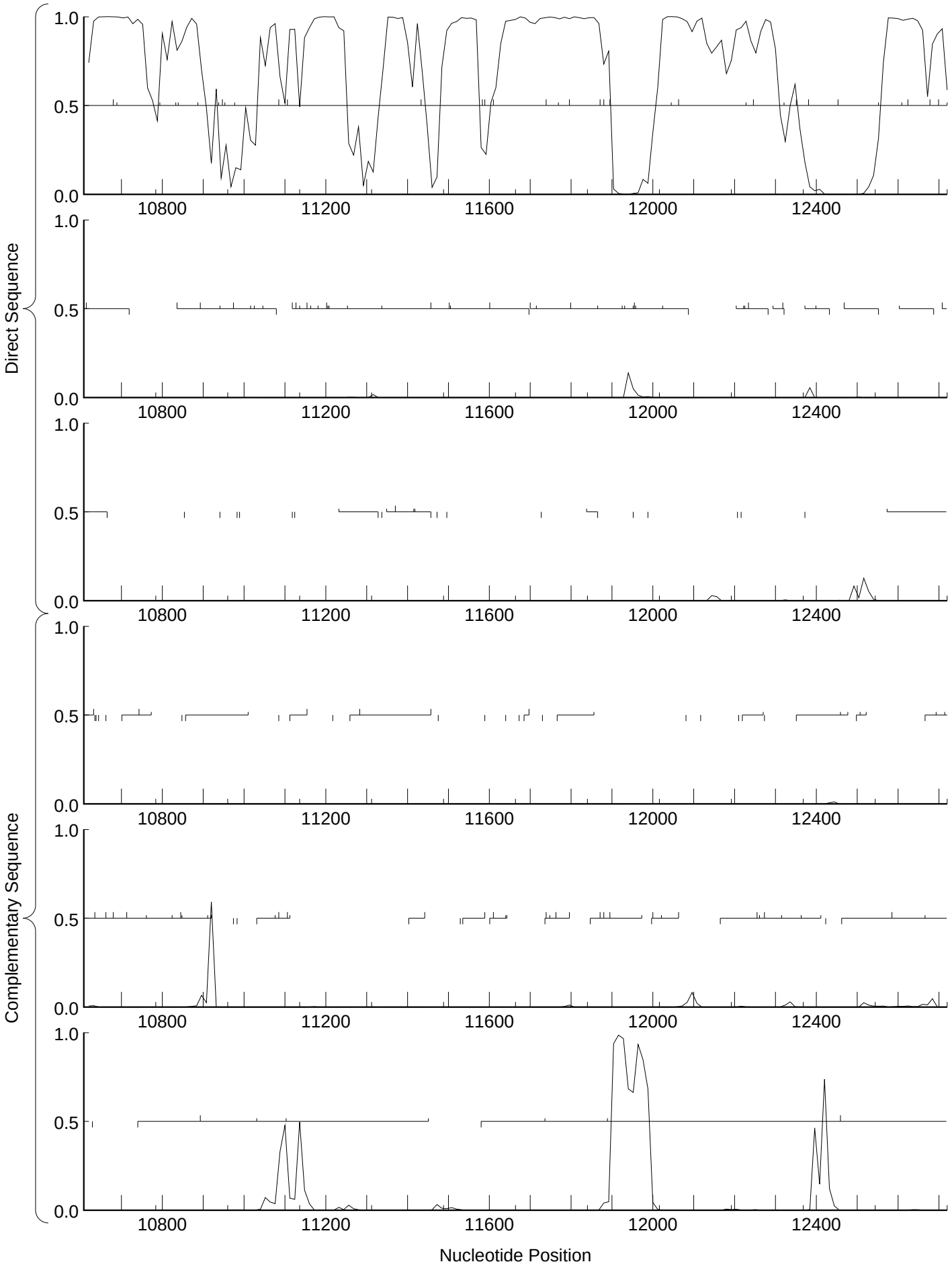

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
400
800
1200
1600
2000
Nucleotide Position

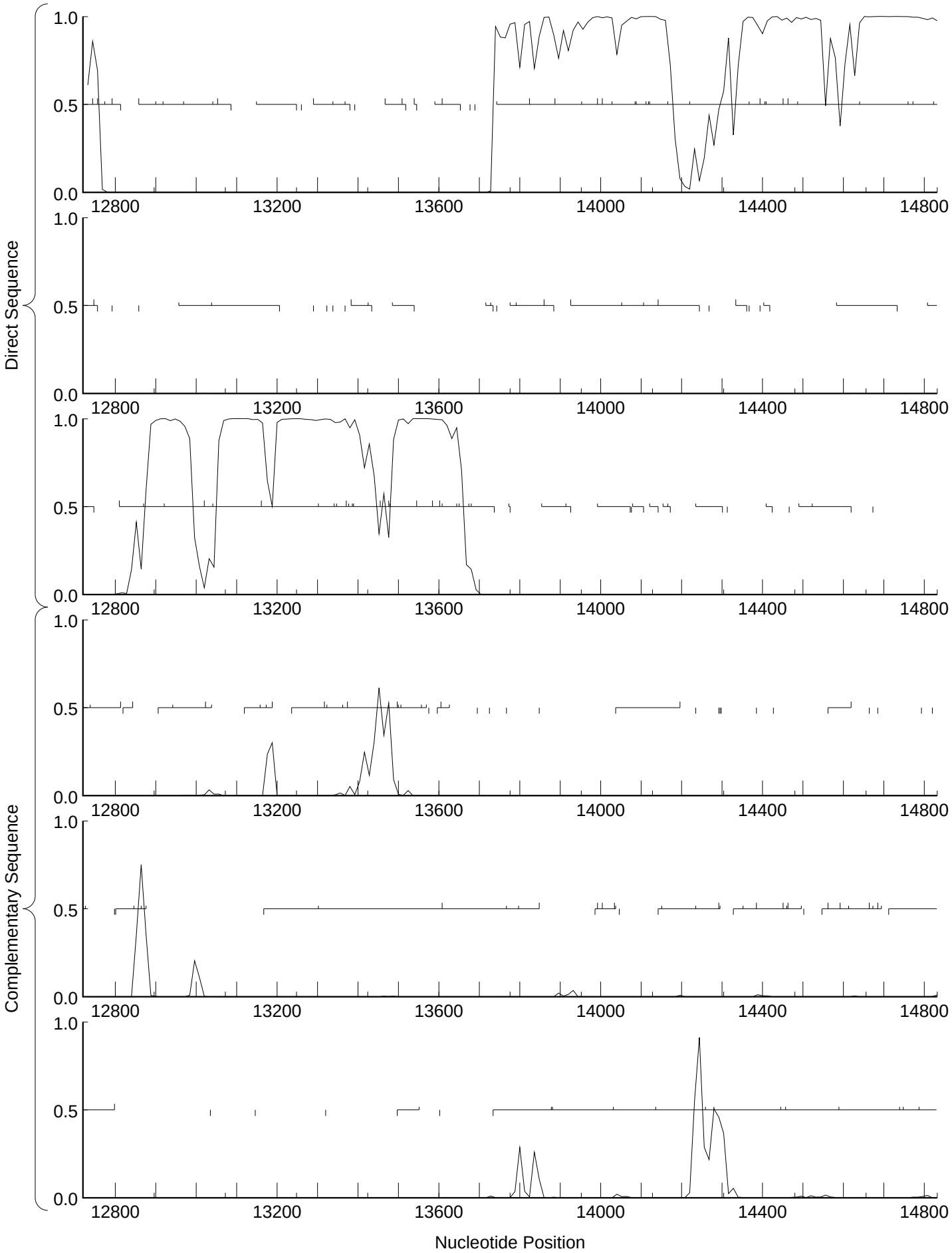

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
2400
2800
3200
3600
4000
Nucleotide Position


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

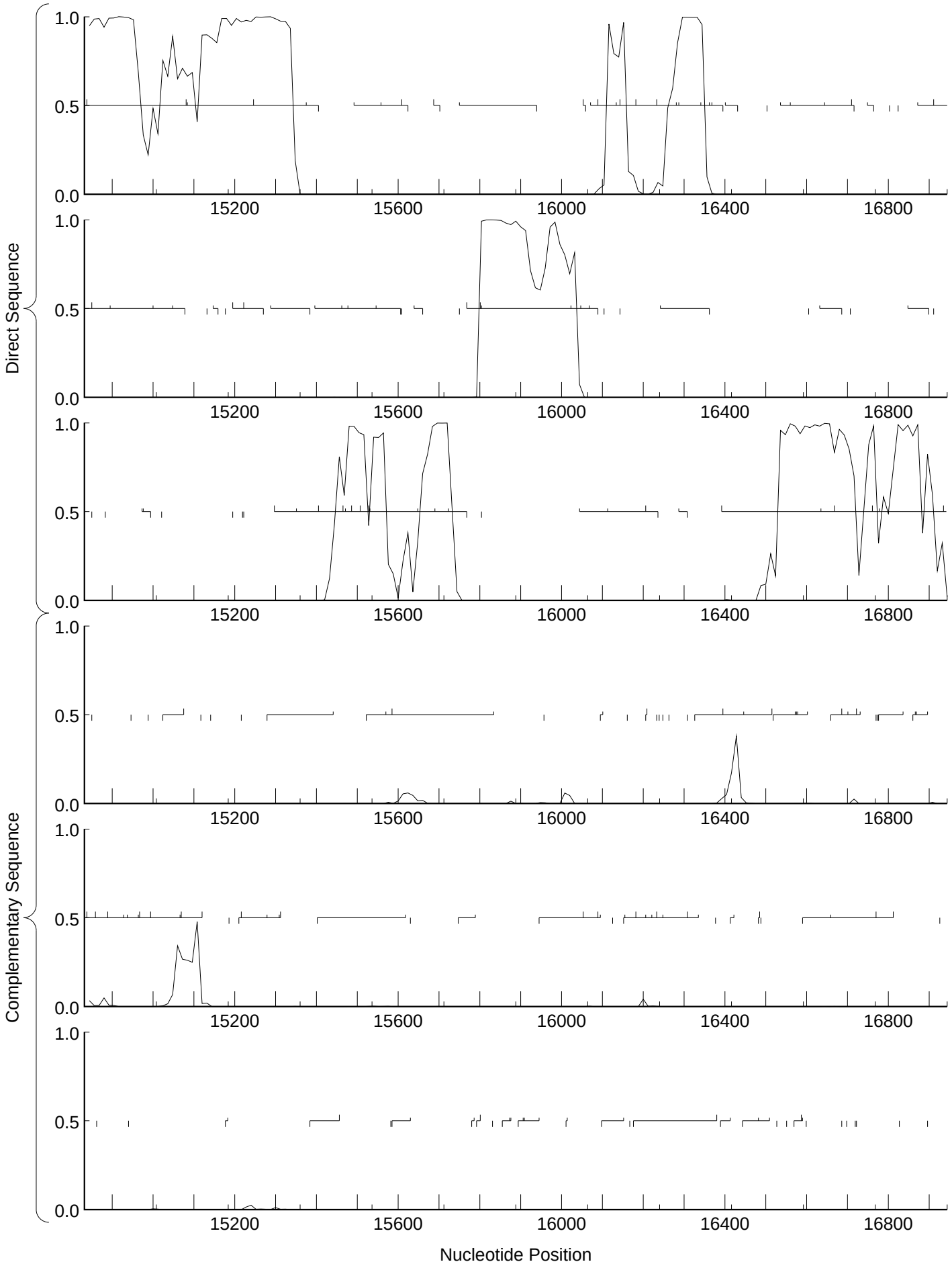

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
6400
6800
7200
7600
8000
8400
Nucleotide Position


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

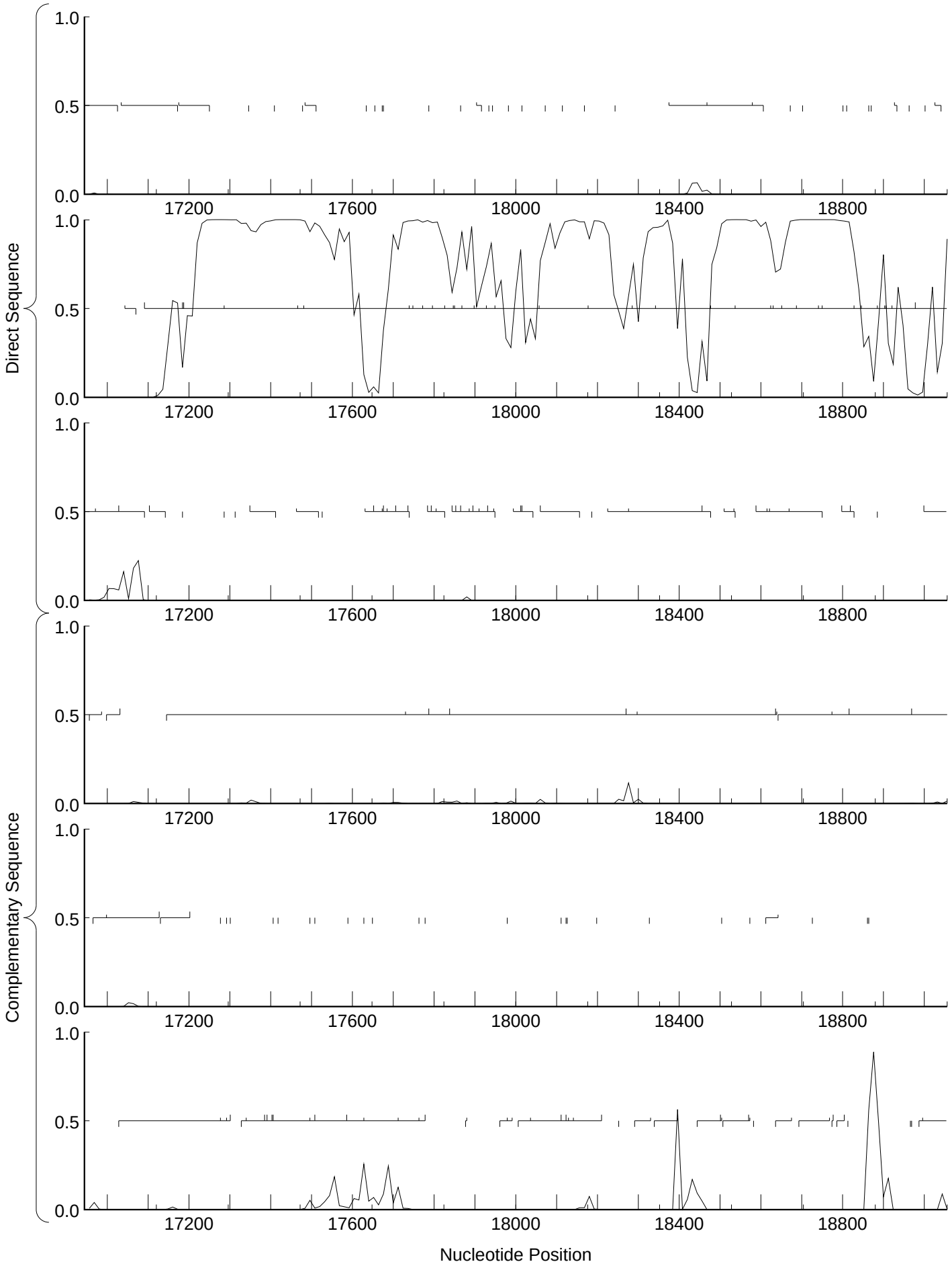

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
10800
11200
11600
12000
12400
Nucleotide Position


Direct Sequence
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12800
13200
13600
14000
14400
14800
Nucleotide Position

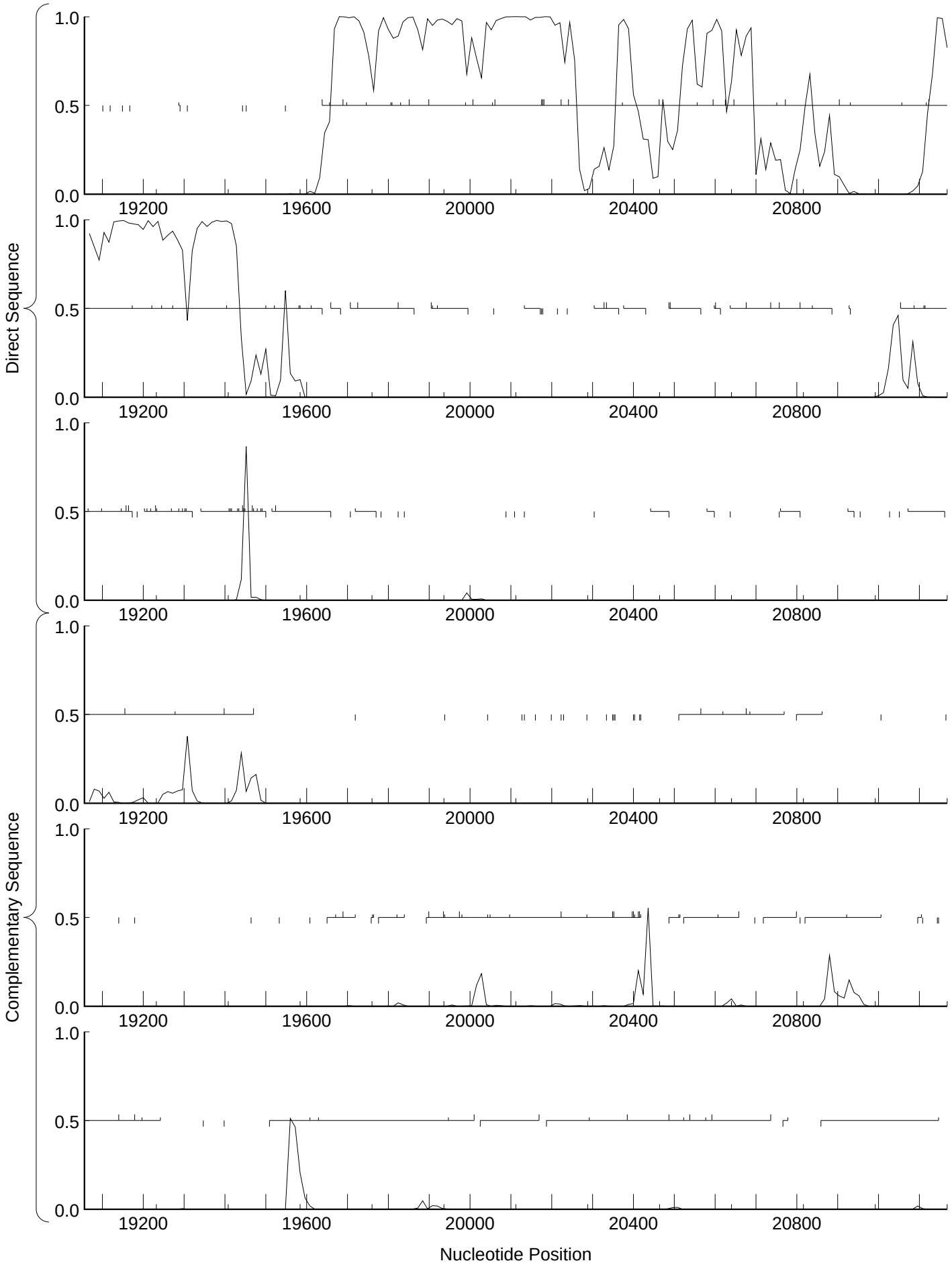
ni Complete Sequence, 54470 bp including 10-base 3’ overhang (CTCAGGGCAT), Cluster F2, Order 4, Window 96, Step 12, 9/27



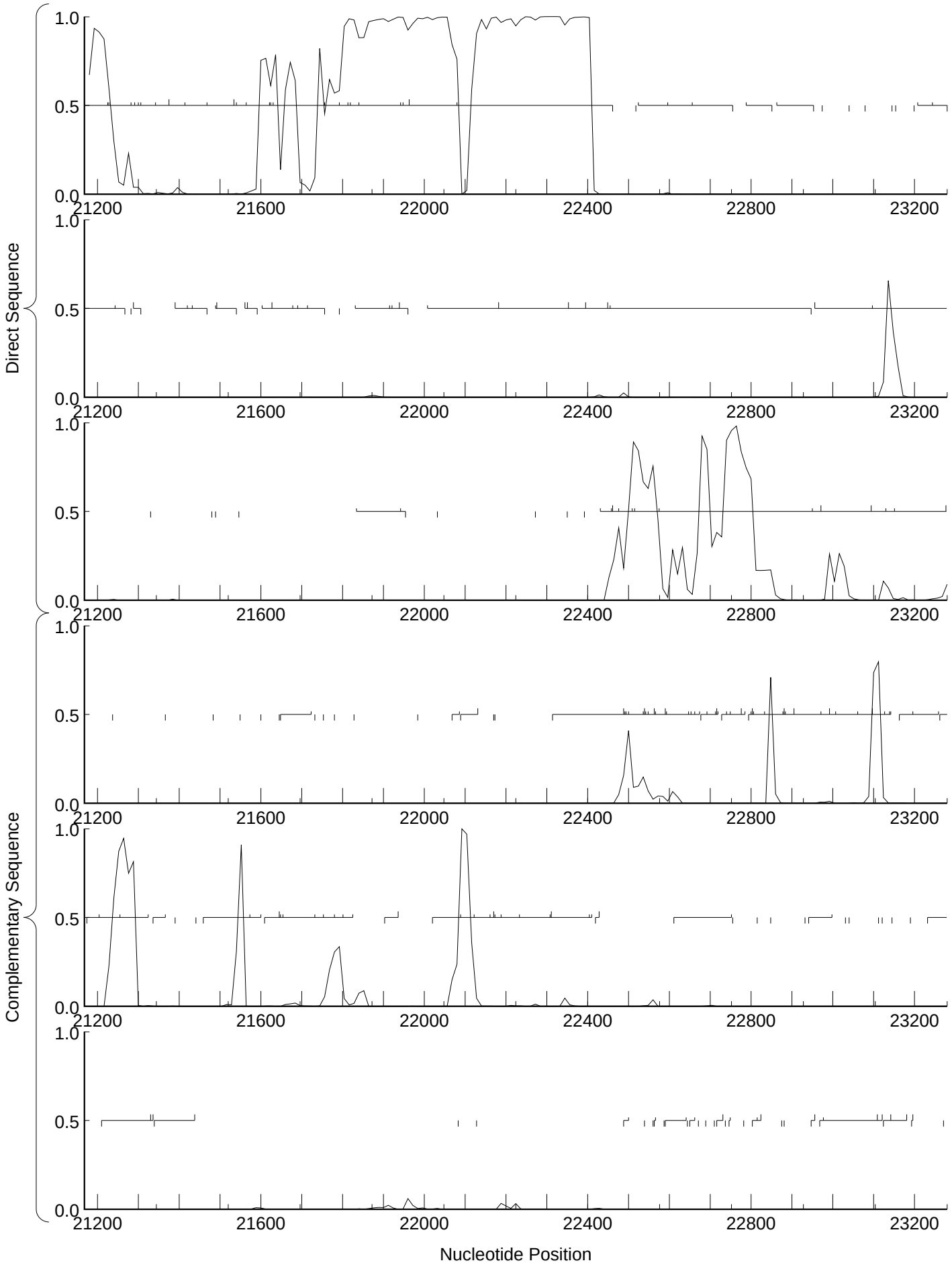
Complete Sequence, 54470 bp including 10-base 3’ overhang (CTCAGGGCAT), Cluster F2, Order 4, Window 96, Step 12, 10/27



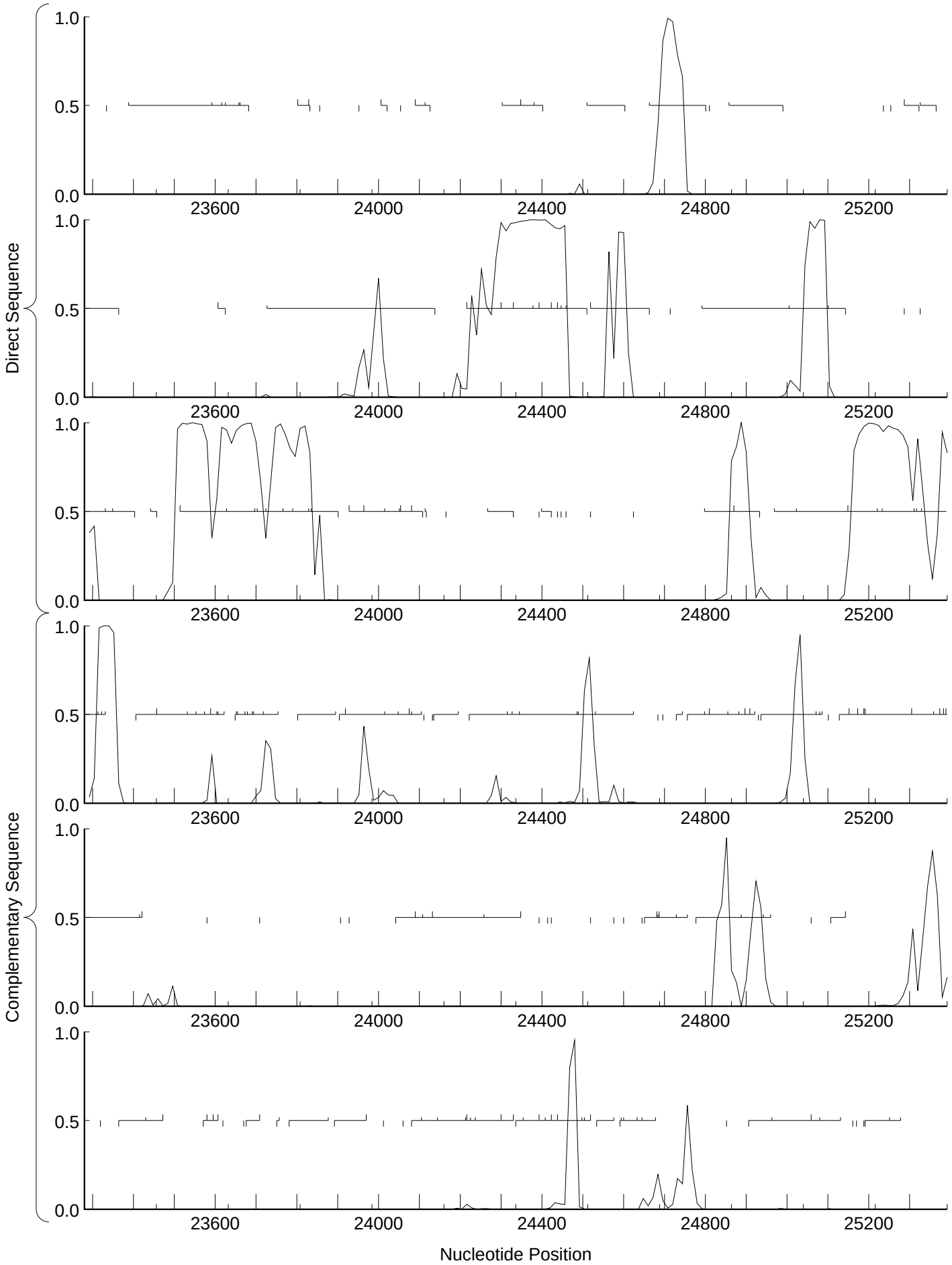
Complete Sequence, 54470 bp including 10-base 3' overhang (CTCAGGGCAT), Cluster F2, Order 4, Window 96, Step 12, 11/27



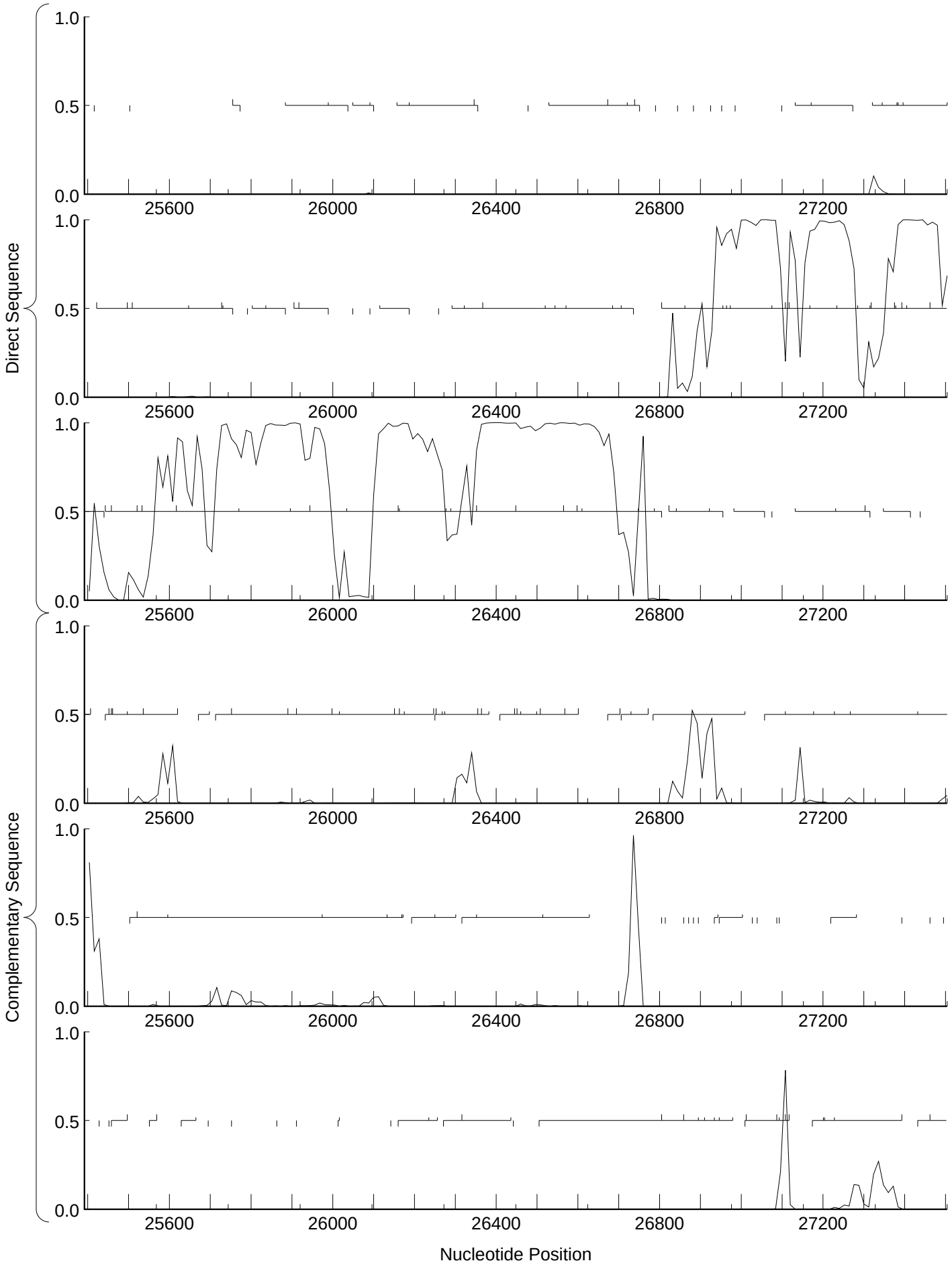
Complete Sequence, 54470 bp including 10-base 3' overhang (CTCAGGGCAT), Cluster F2, Order 4, Window 96, Step 12, 12/27



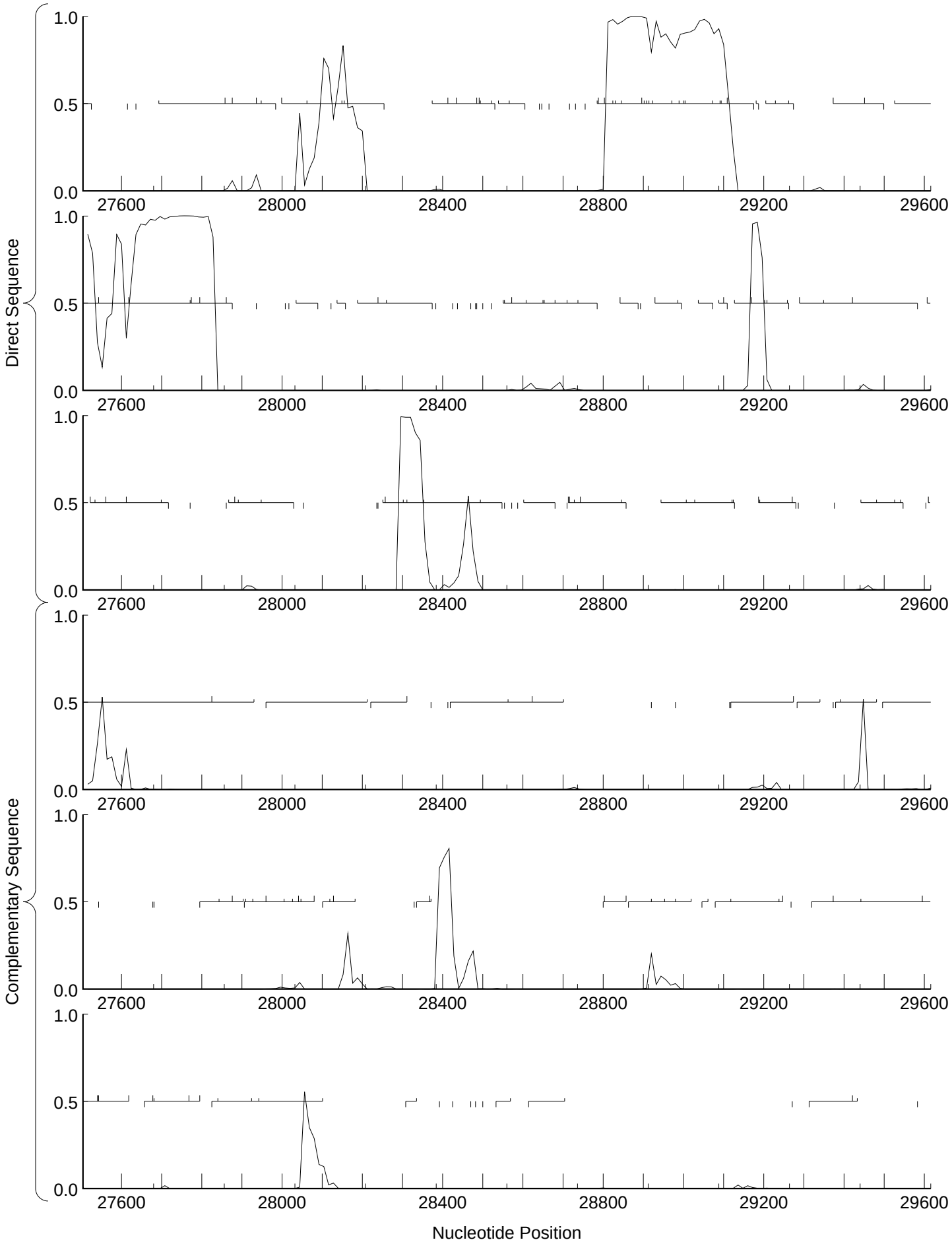
Complete Sequence, 54470 bp including 10-base 3’ overhang (CTCAGGGCAT), Cluster F2, Order 4, Window 96, Step 12, 13/27



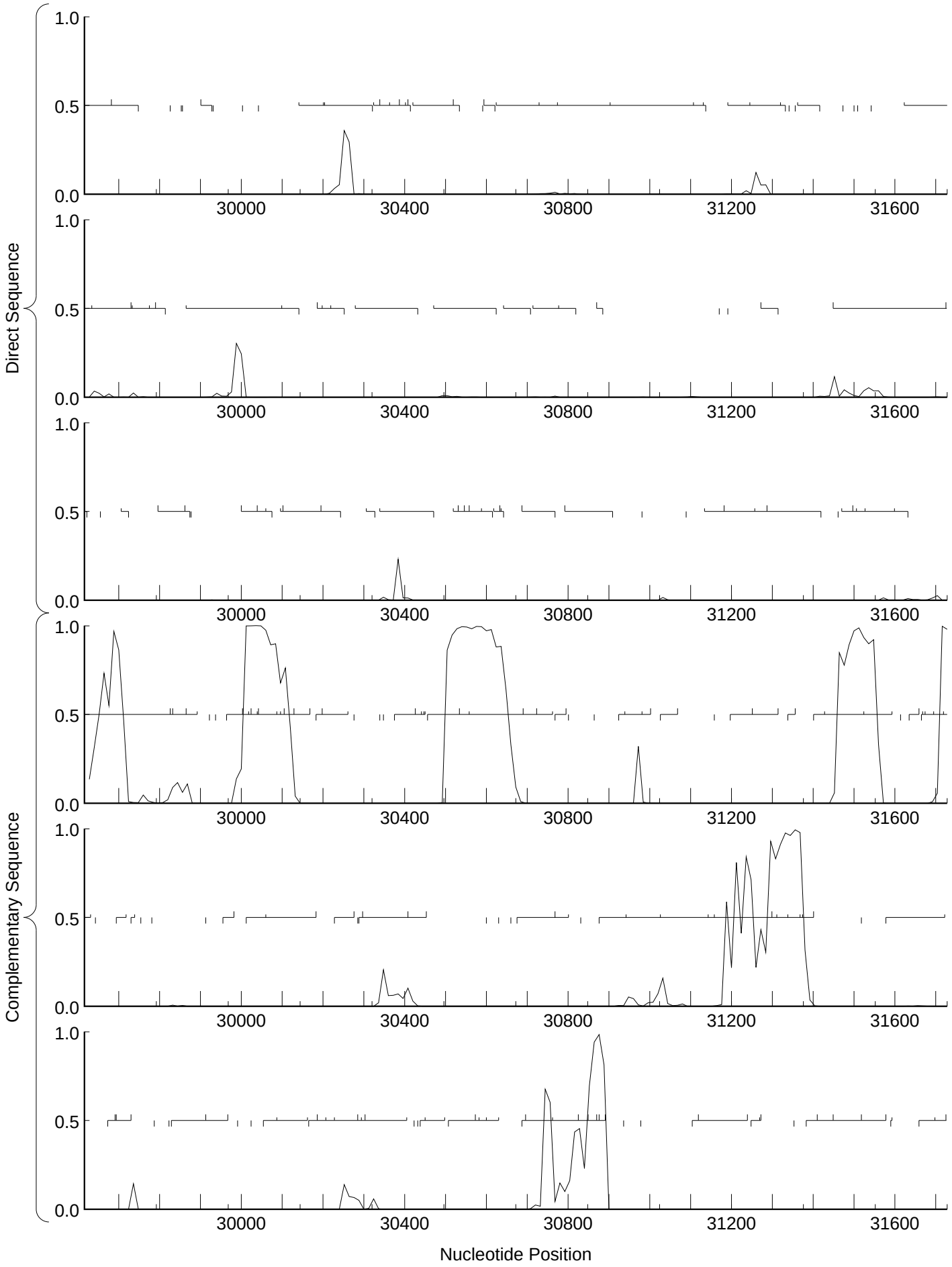
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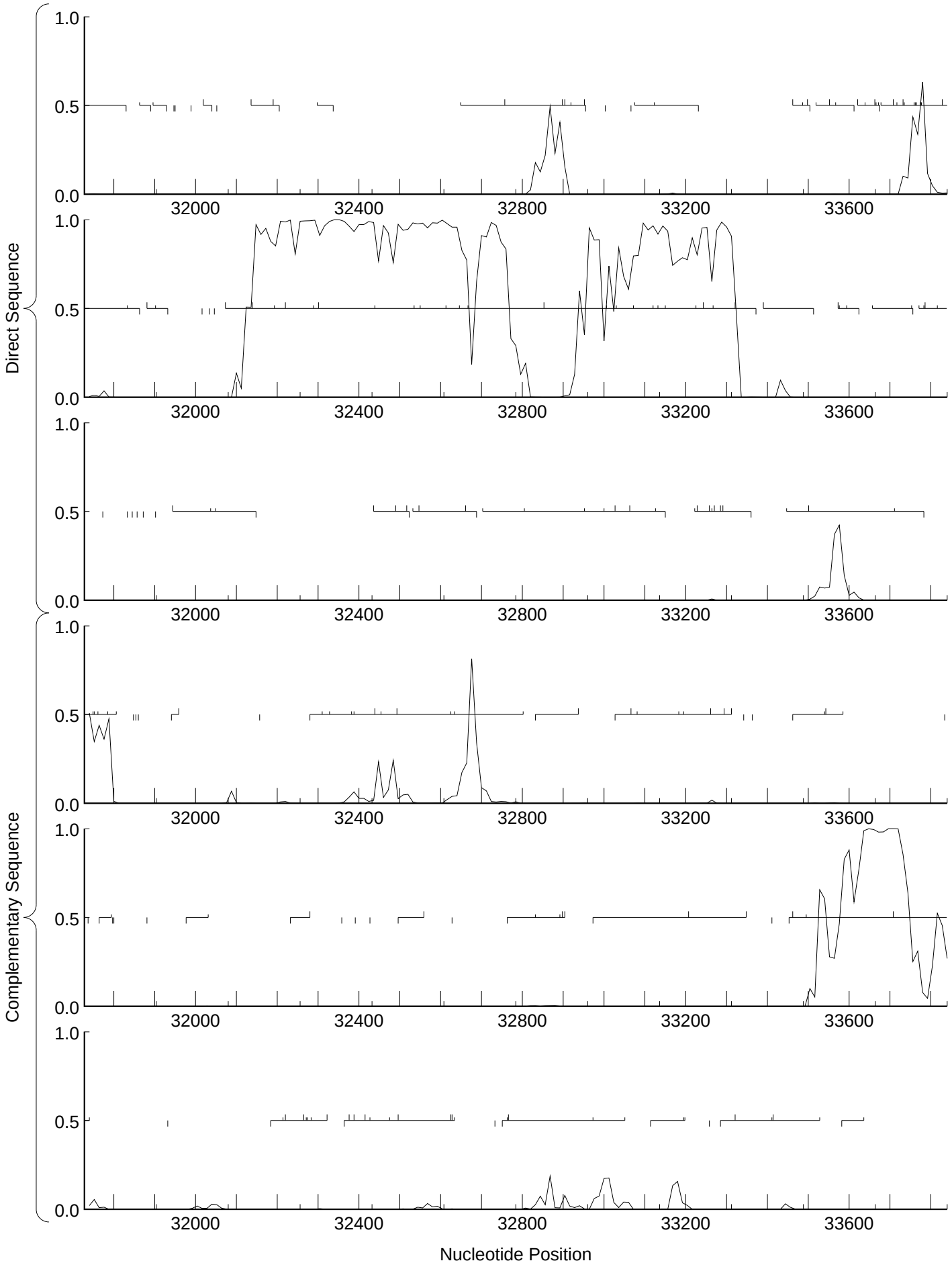
Complete Sequence, 54470 bp including 10-base 3’ overhang (CTCAGGGCAT), Cluster F2, Order 4, Window 96, Step 12, 15/27



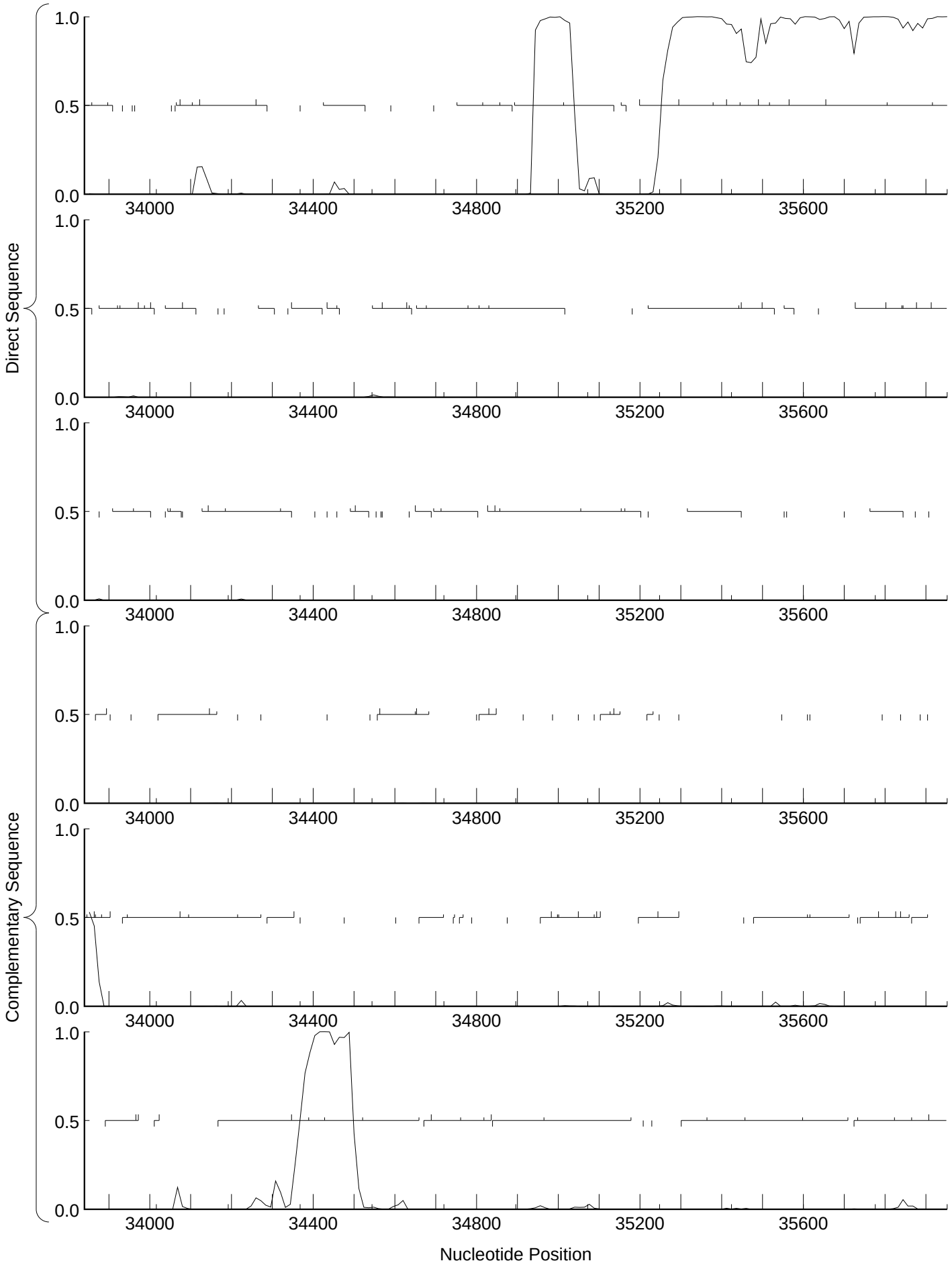
Complete Sequence, 54470 bp including 10-base 3’ overhang (CTCAGGGCAT), Cluster F2, Order 4, Window 96, Step 12, 16/27



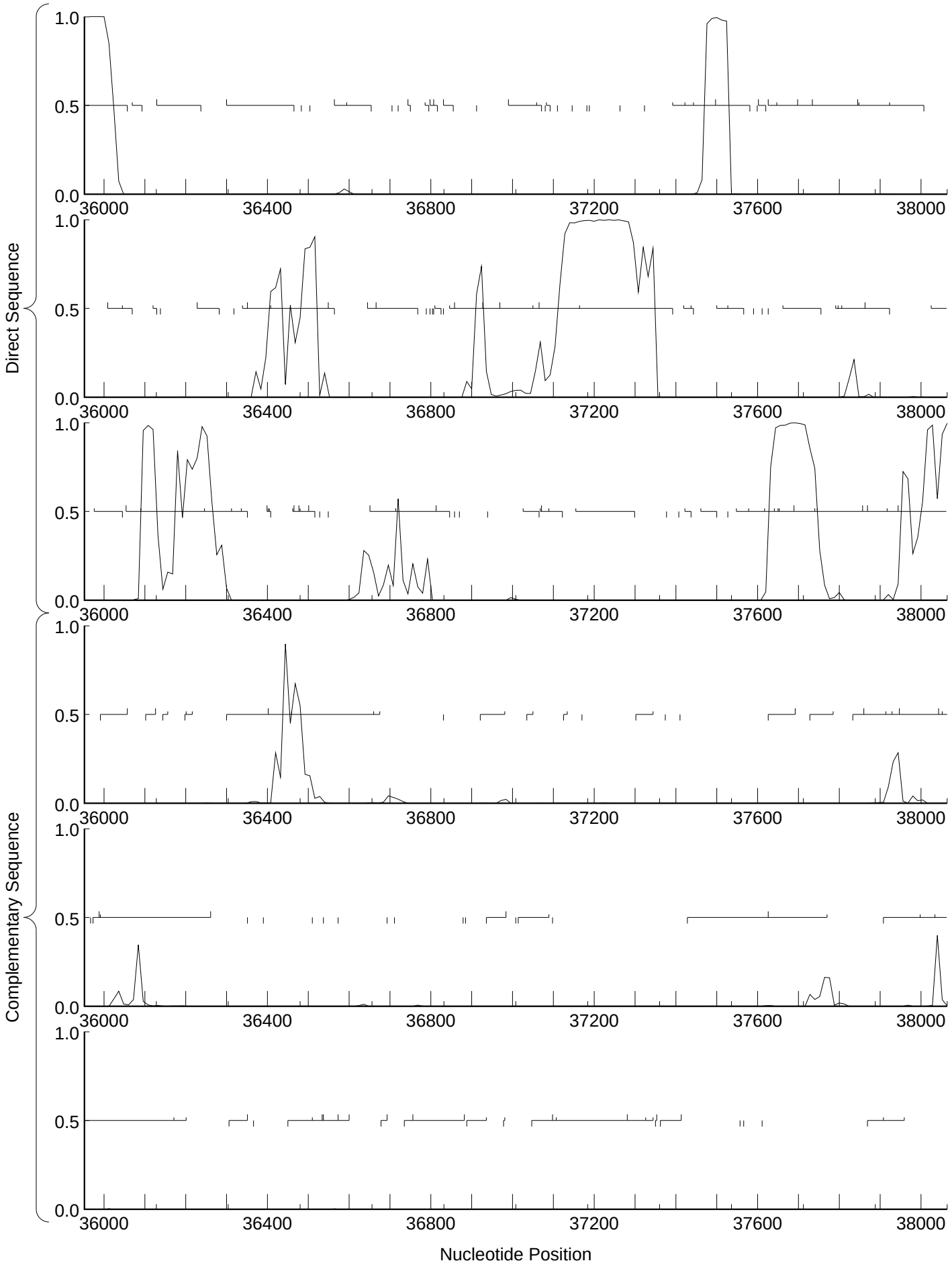
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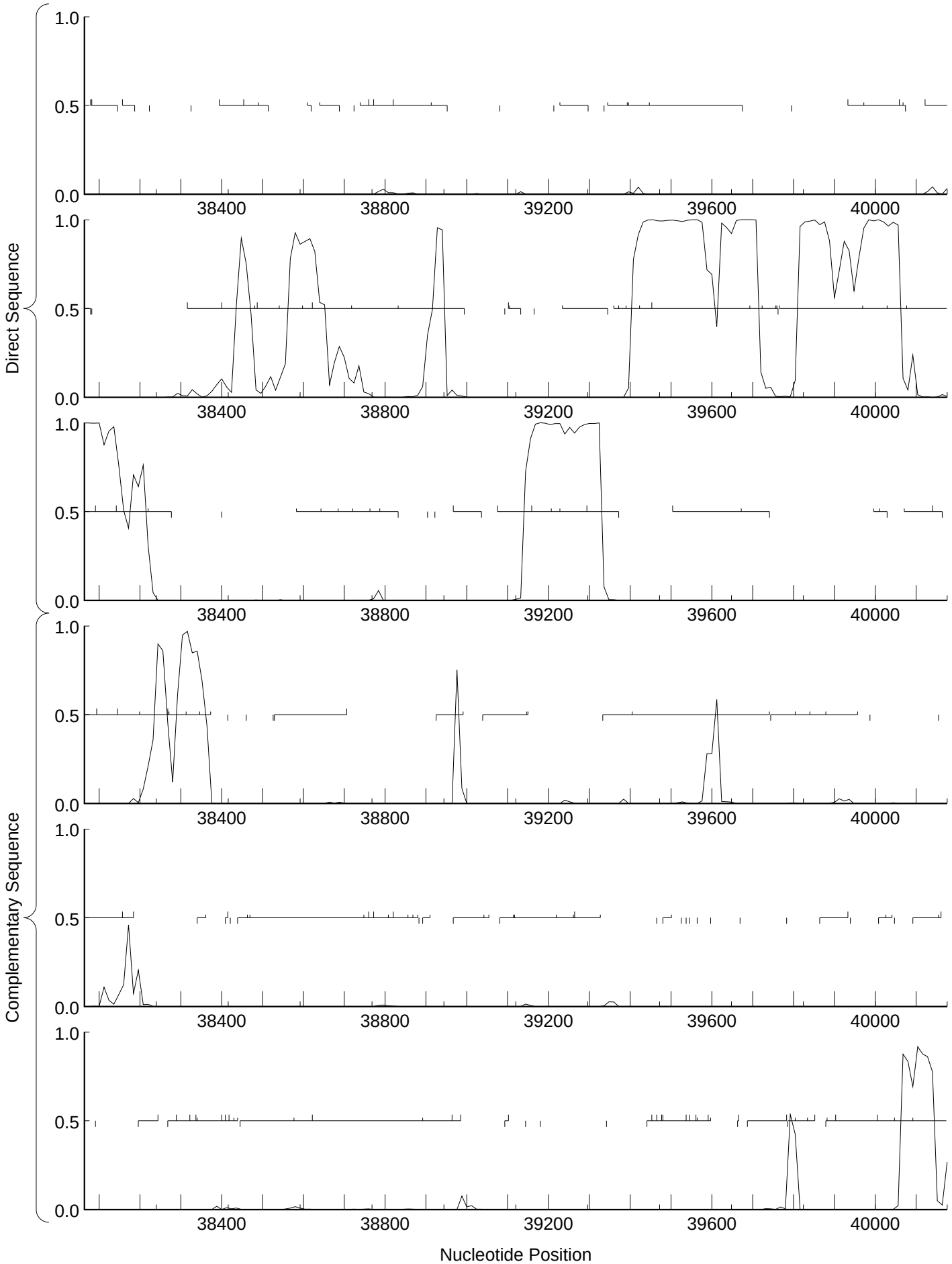
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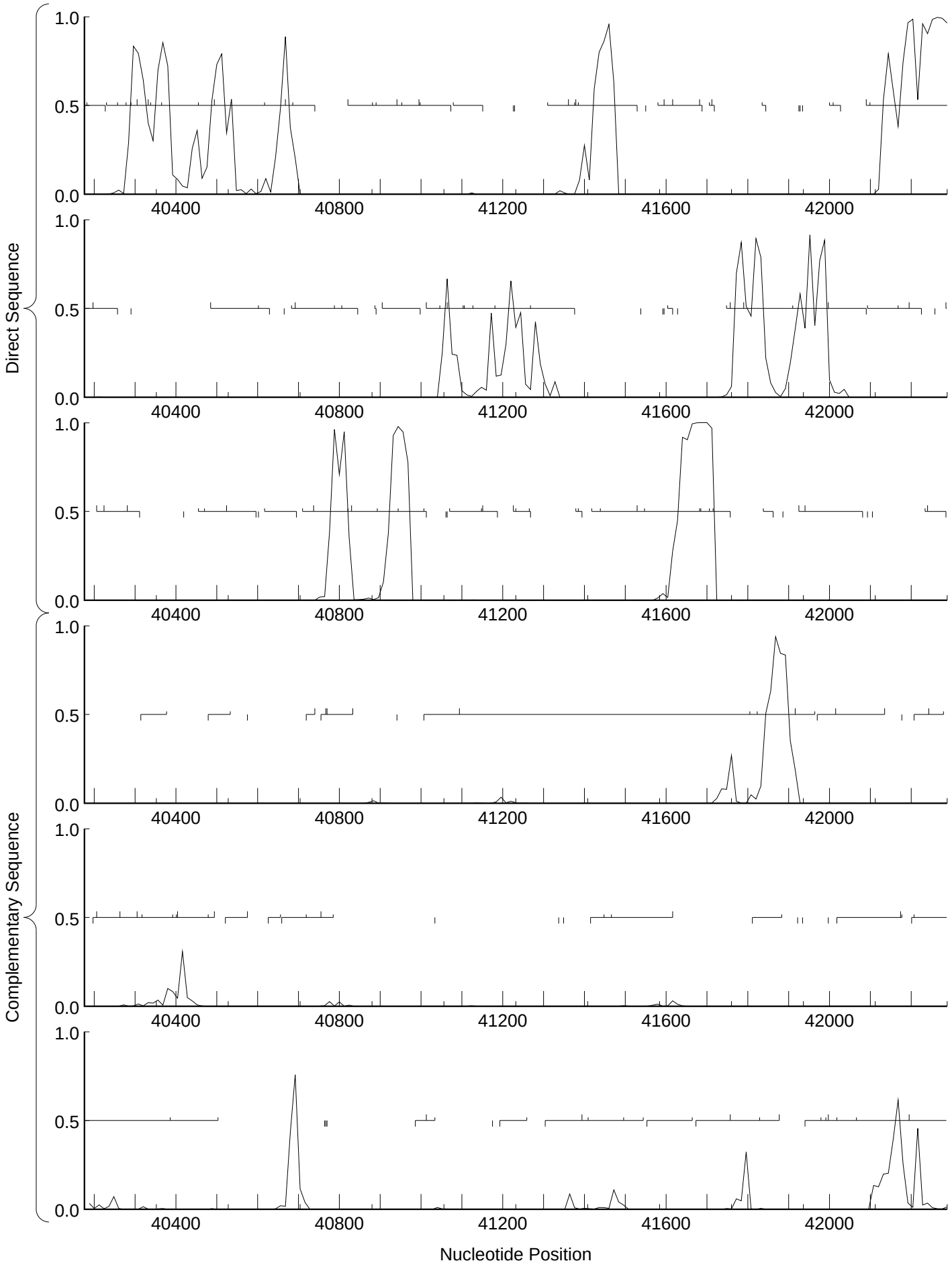
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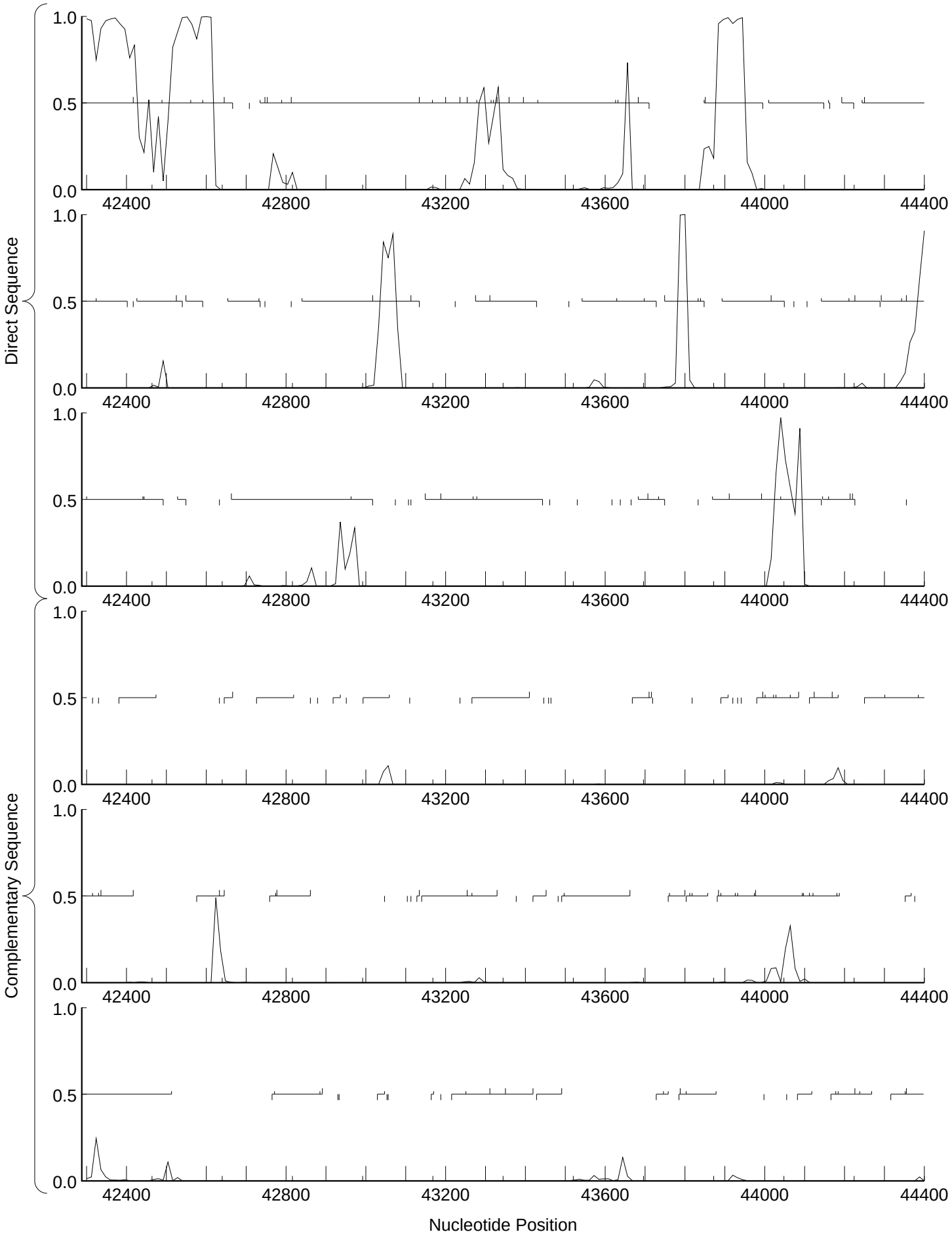
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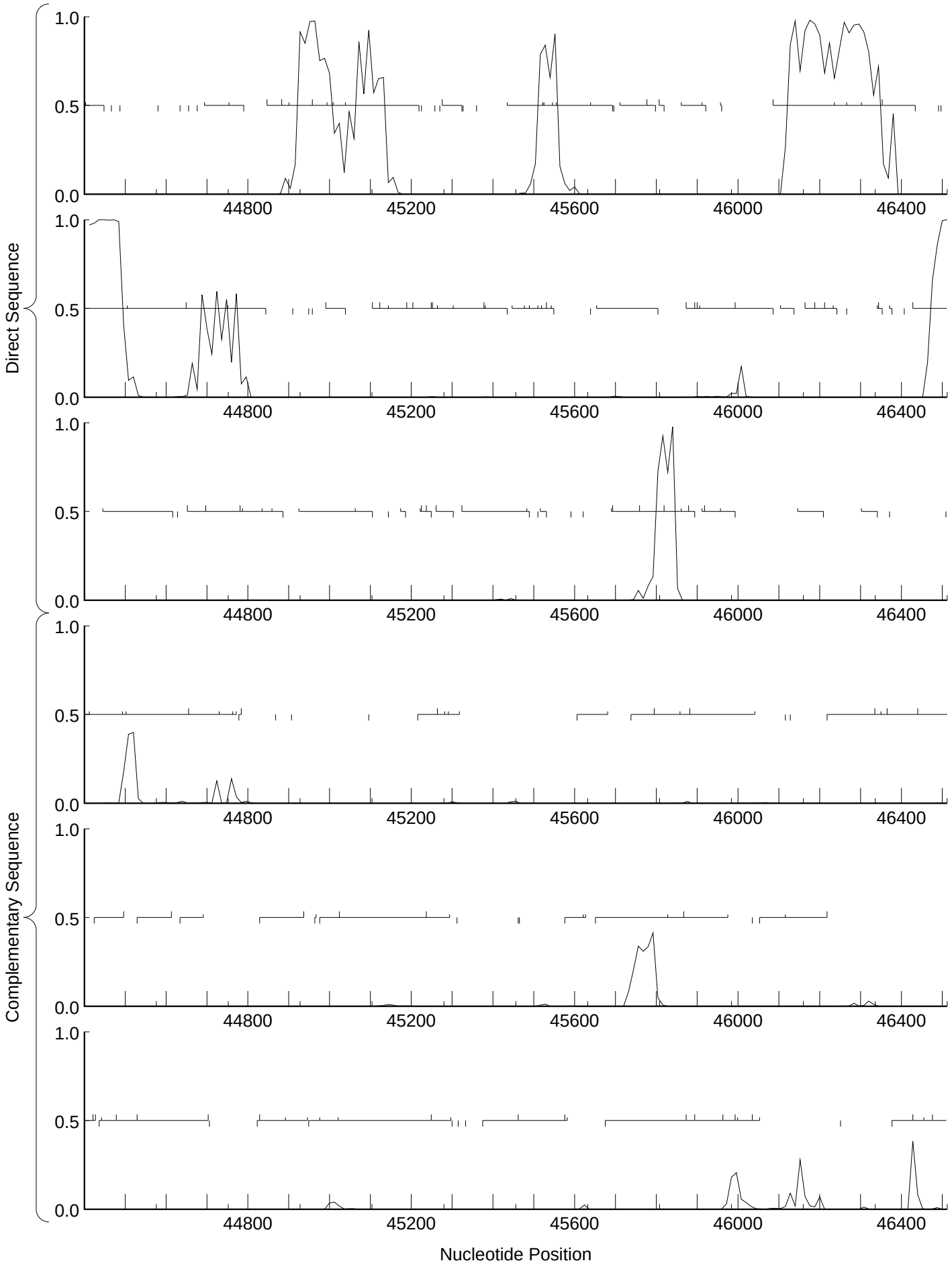
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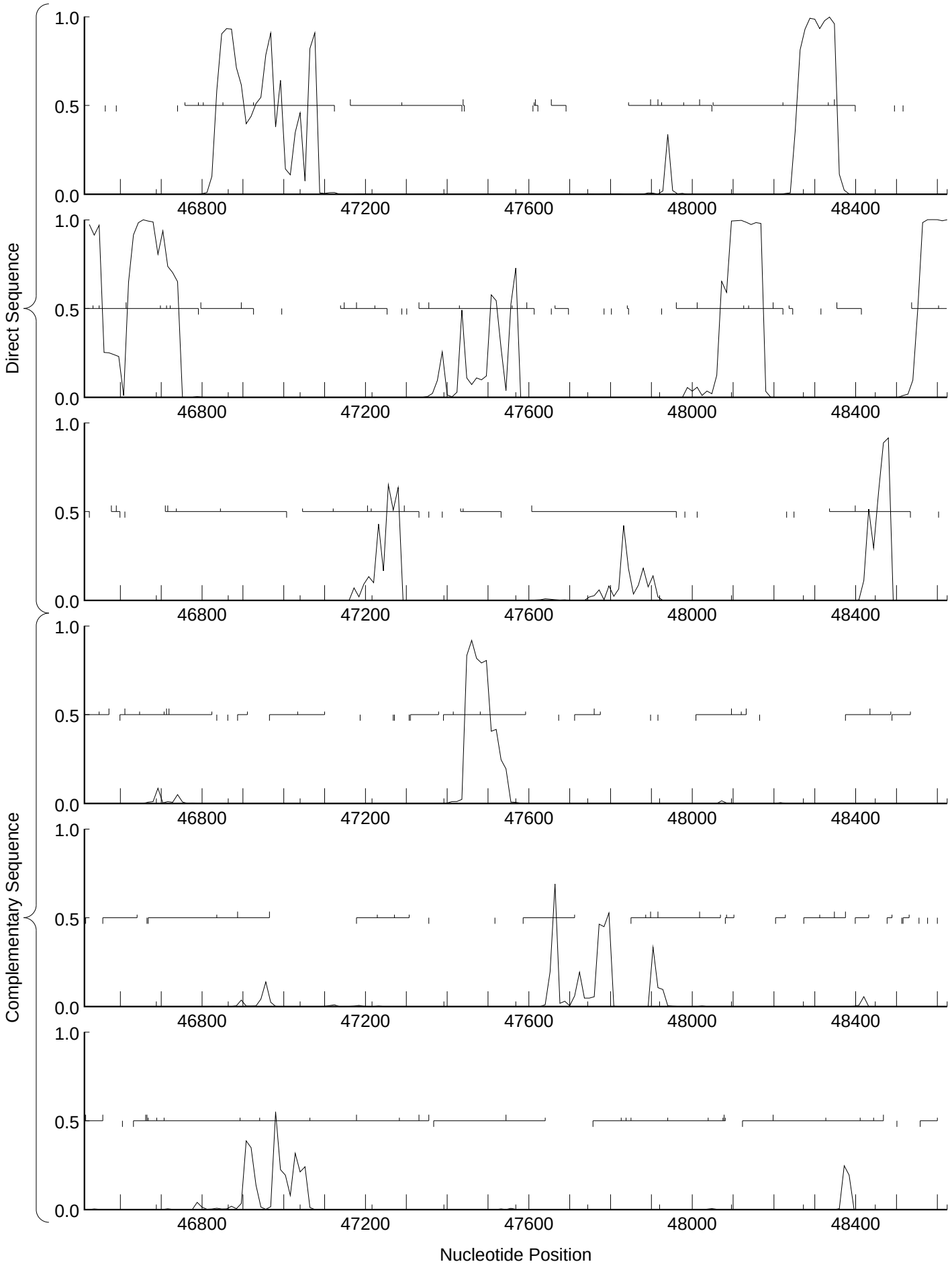
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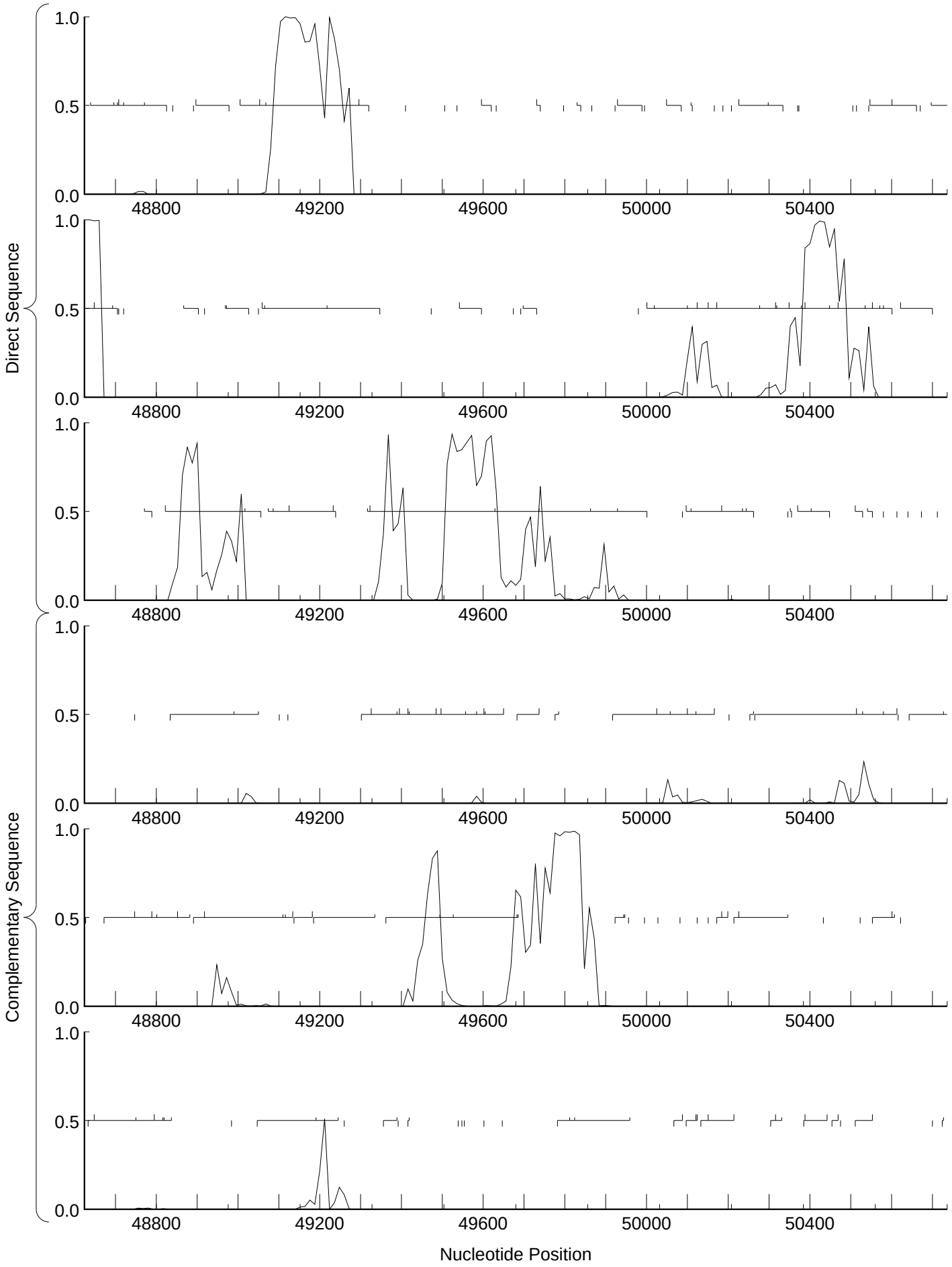
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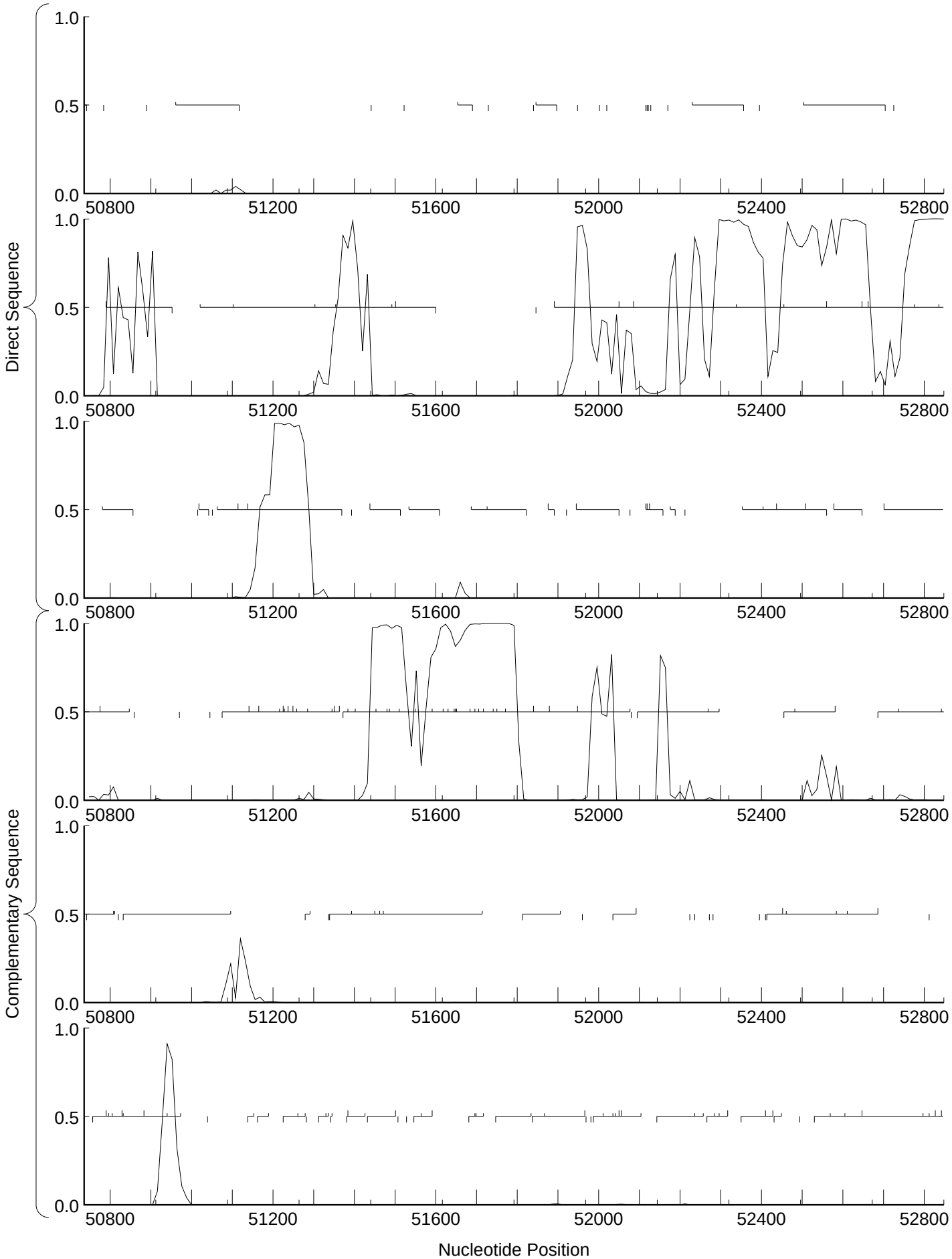
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Complete Sequence, 54470 bp including 10-base 3’ overhang (CTCAGGGCAT), Cluster F2, Order 4, Window 96, Step 12, 25/27



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

