GeneMark

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

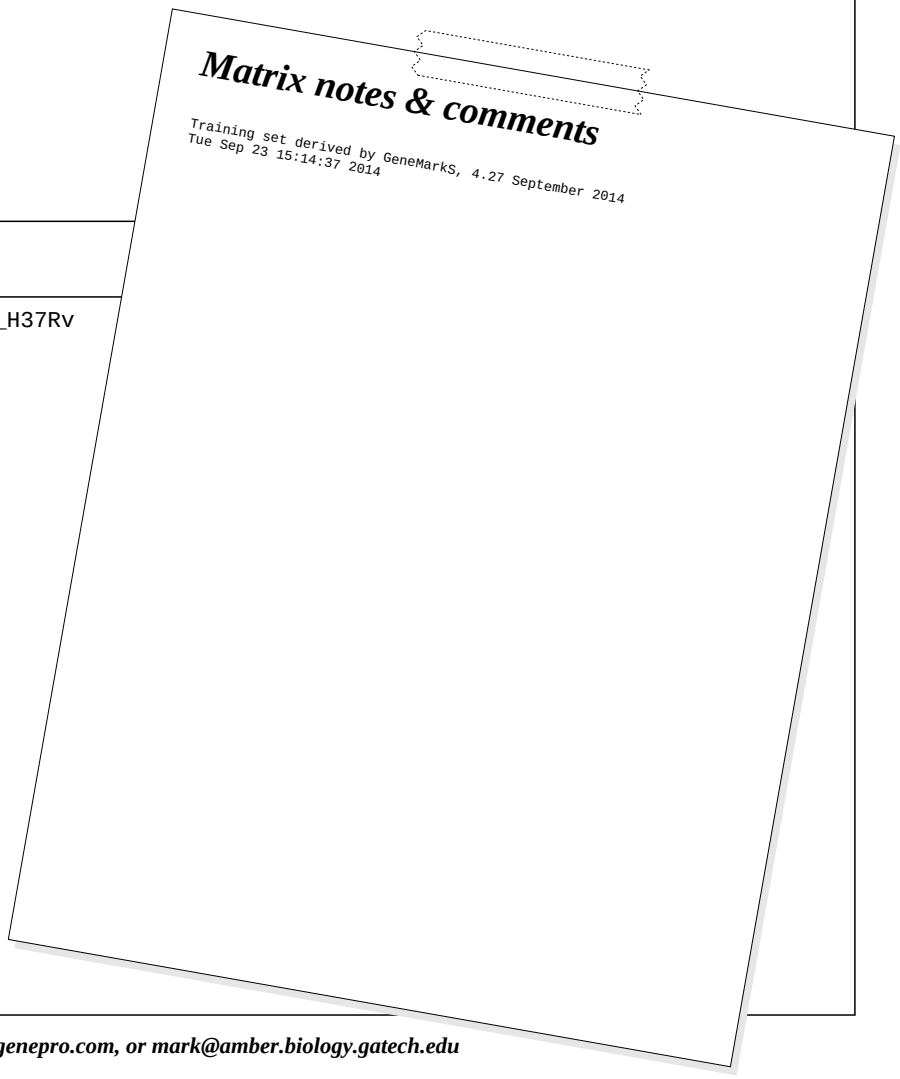
PROGRAM INFORMATION

```
Sequence         :  Mycobacterium phage Leviathan complete sequence, 53239 bp including 10-base 3’ overhang (CG
Analysis Date    :  3/29/24 at 10:25:22
Pages            :  27
Sequence Length  :  53239 bp
GC Content       :   63.25%

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

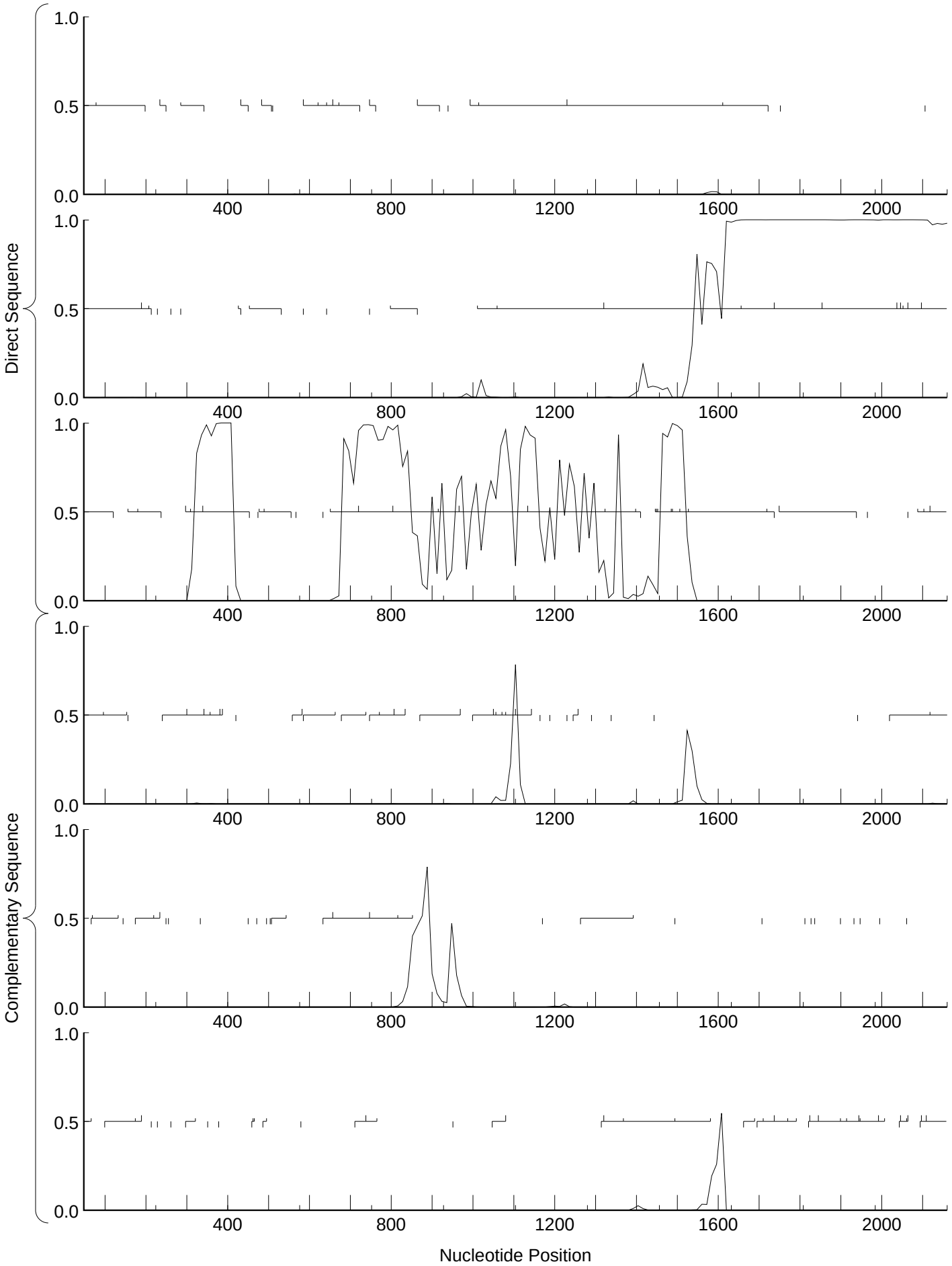
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Matrix     :  Mycobacterium_tuberculosis_H37Rv
Author     :  -

Order      :  4

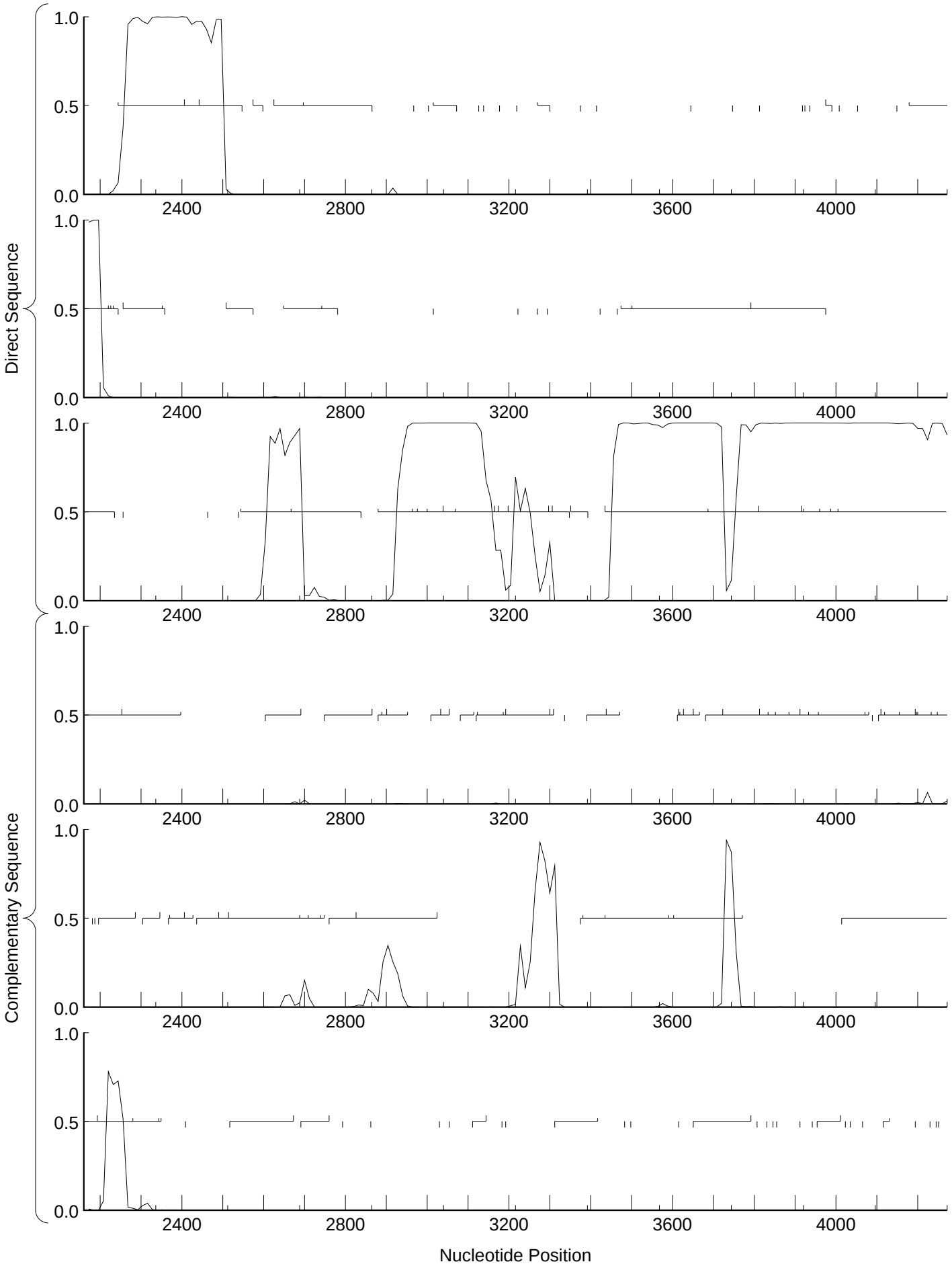

  Send questions / comments to:
      Dr. M. Borodovsky
      Georgia Institute of Technology
      School of Biology
      Atlanta, GA  30332-0230
```

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

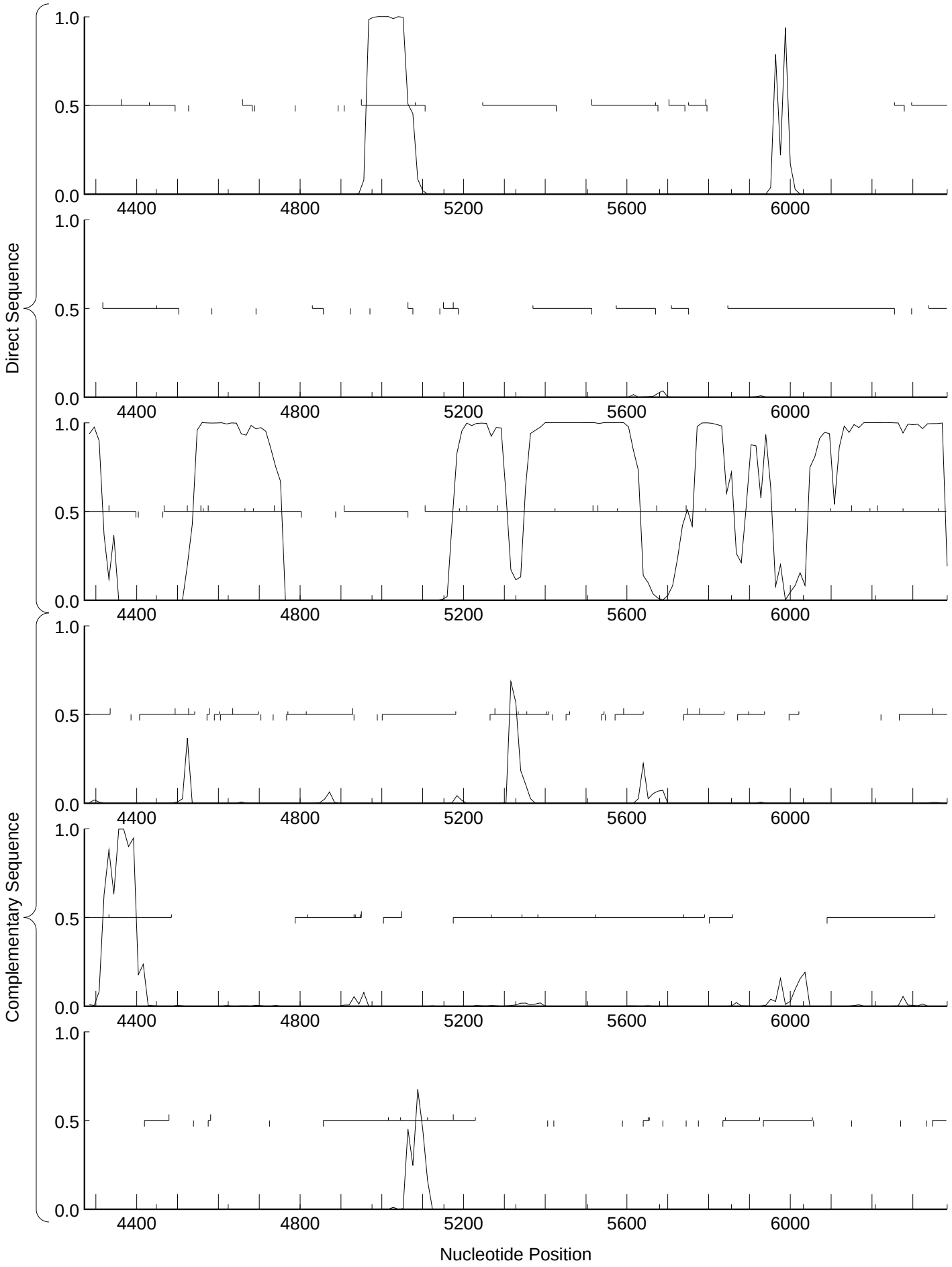
an complete sequence, 53239 bp including 10-base 3’ overhang (CGGTCGGTTA), Cluster A2, Order 4, Window 96, Step 12, 2/27



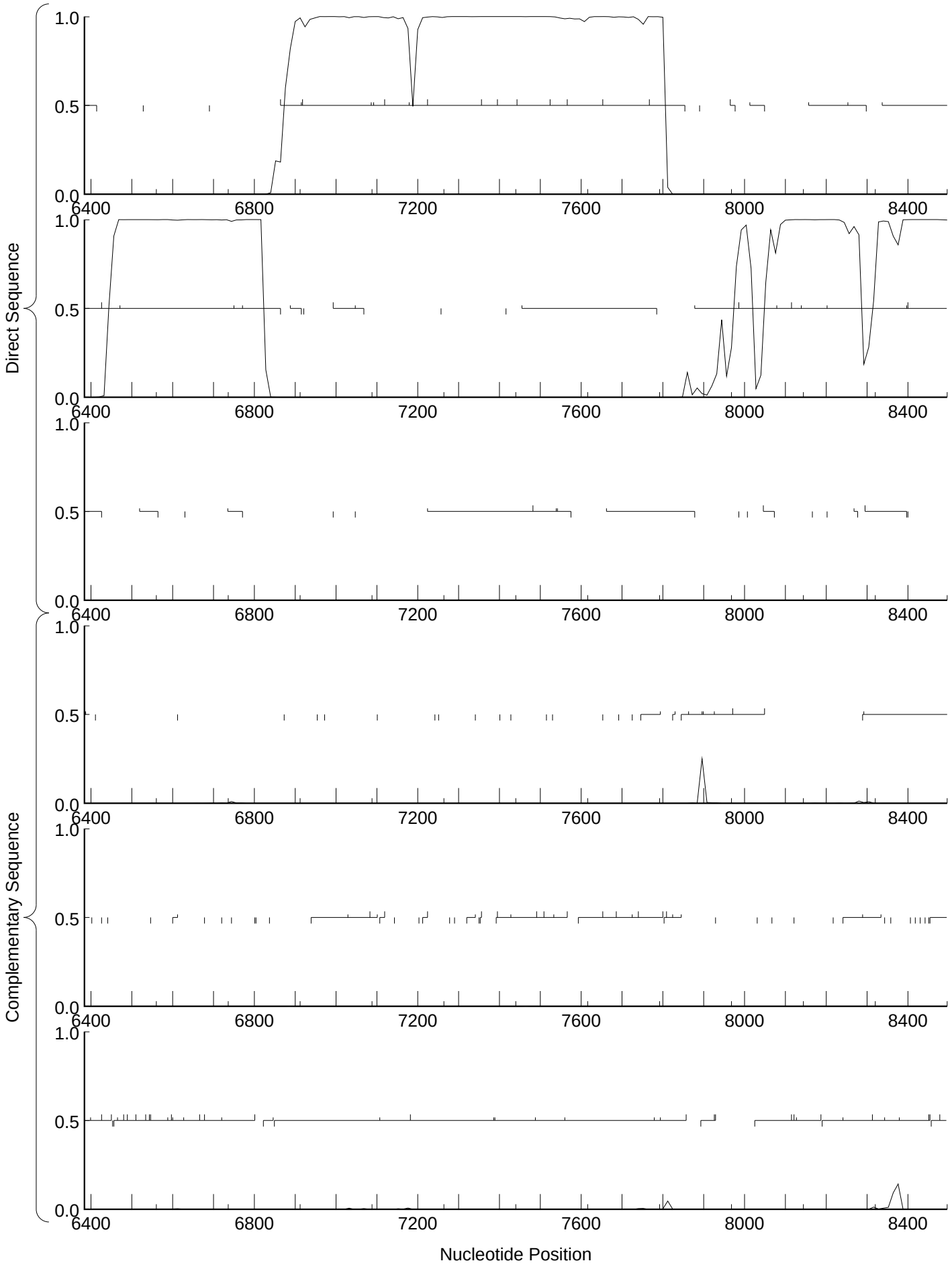
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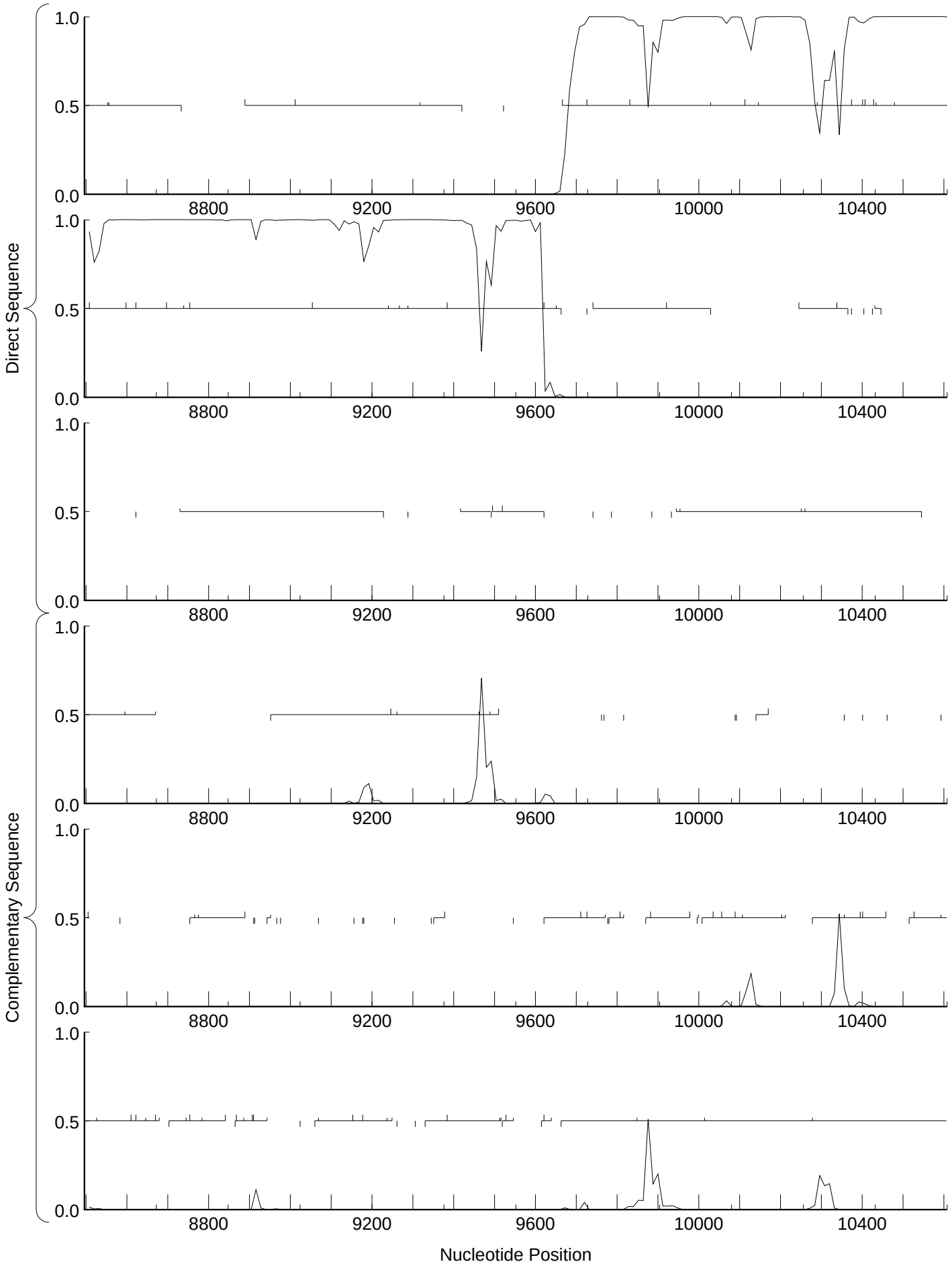
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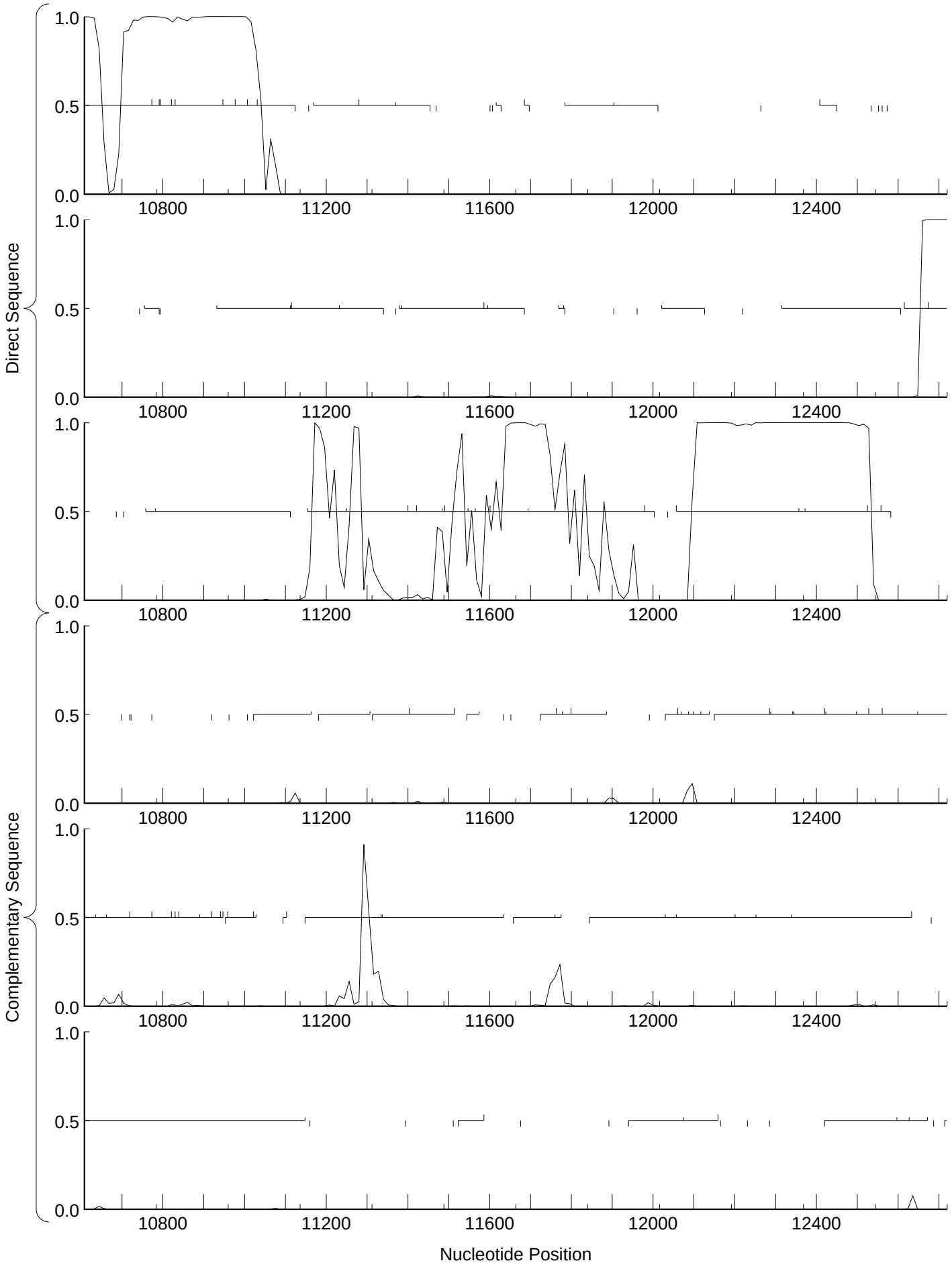
an complete sequence, 53239 bp including 10-base 3’ overhang (CGGTCGGTTA), Cluster A2, Order 4, Window 96, Step 12, 5/27



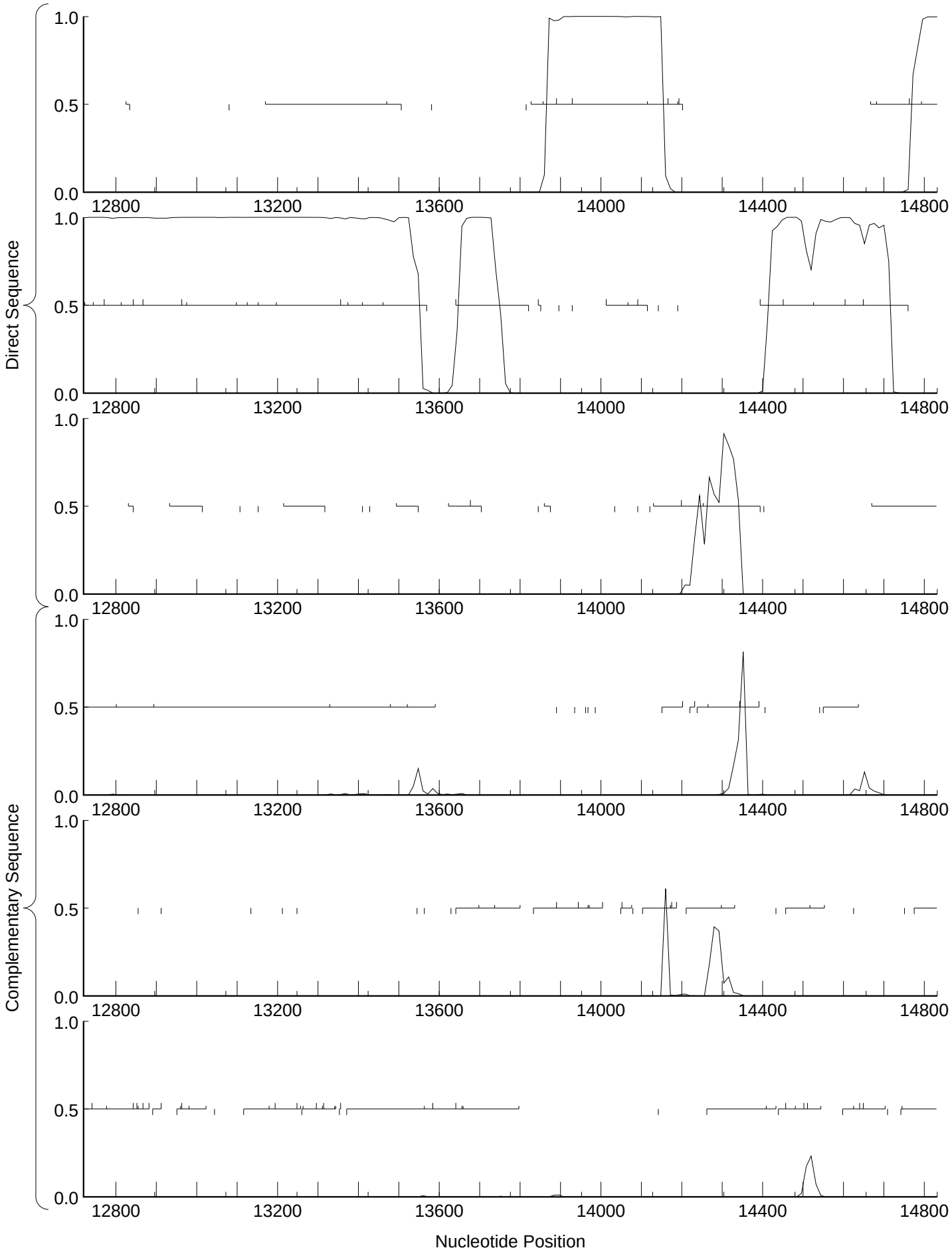
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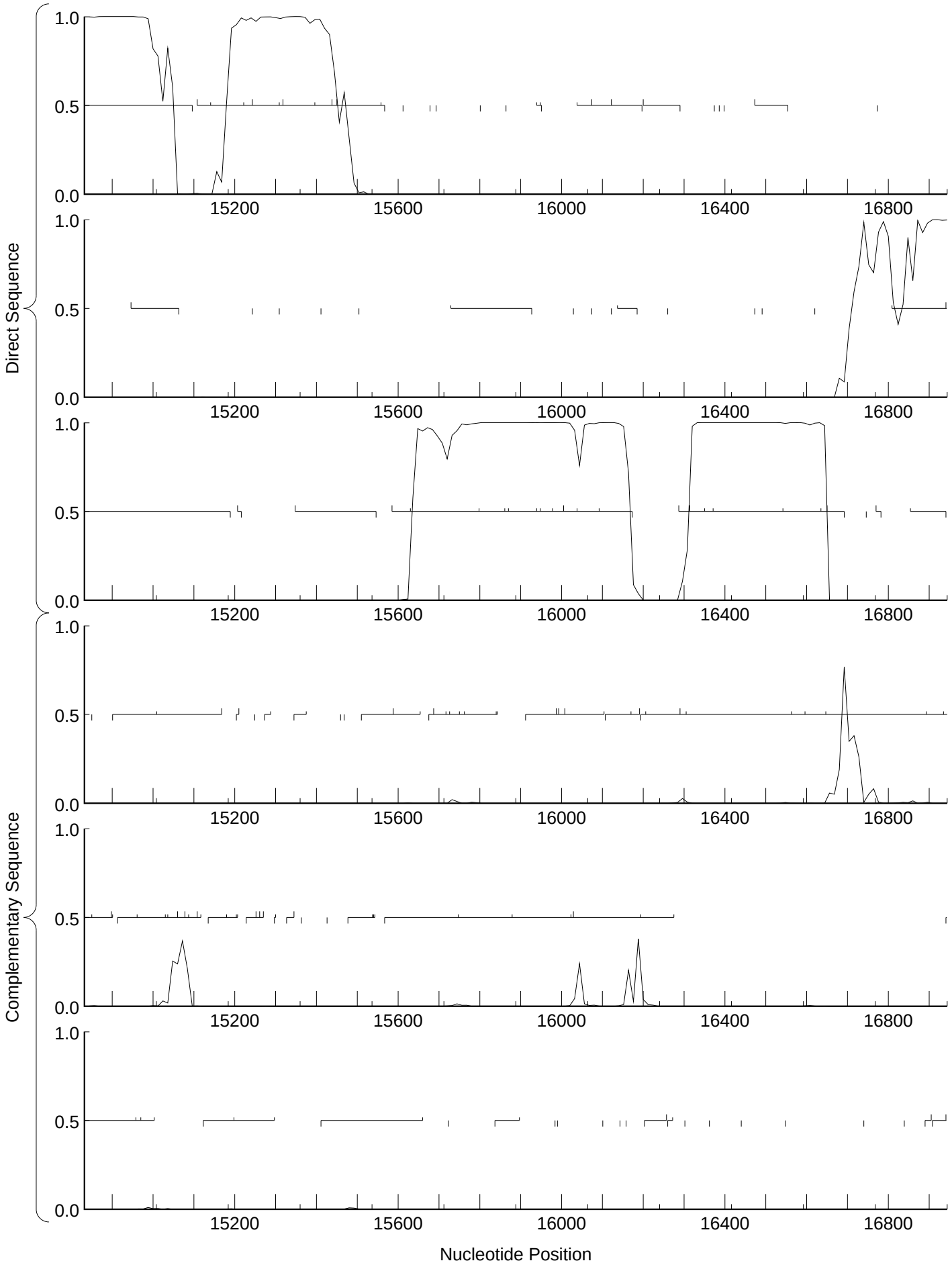
an complete sequence, 53239 bp including 10-base 3’ overhang (CGGTCGGTTA), Cluster A2, Order 4, Window 96, Step 12, 7/27



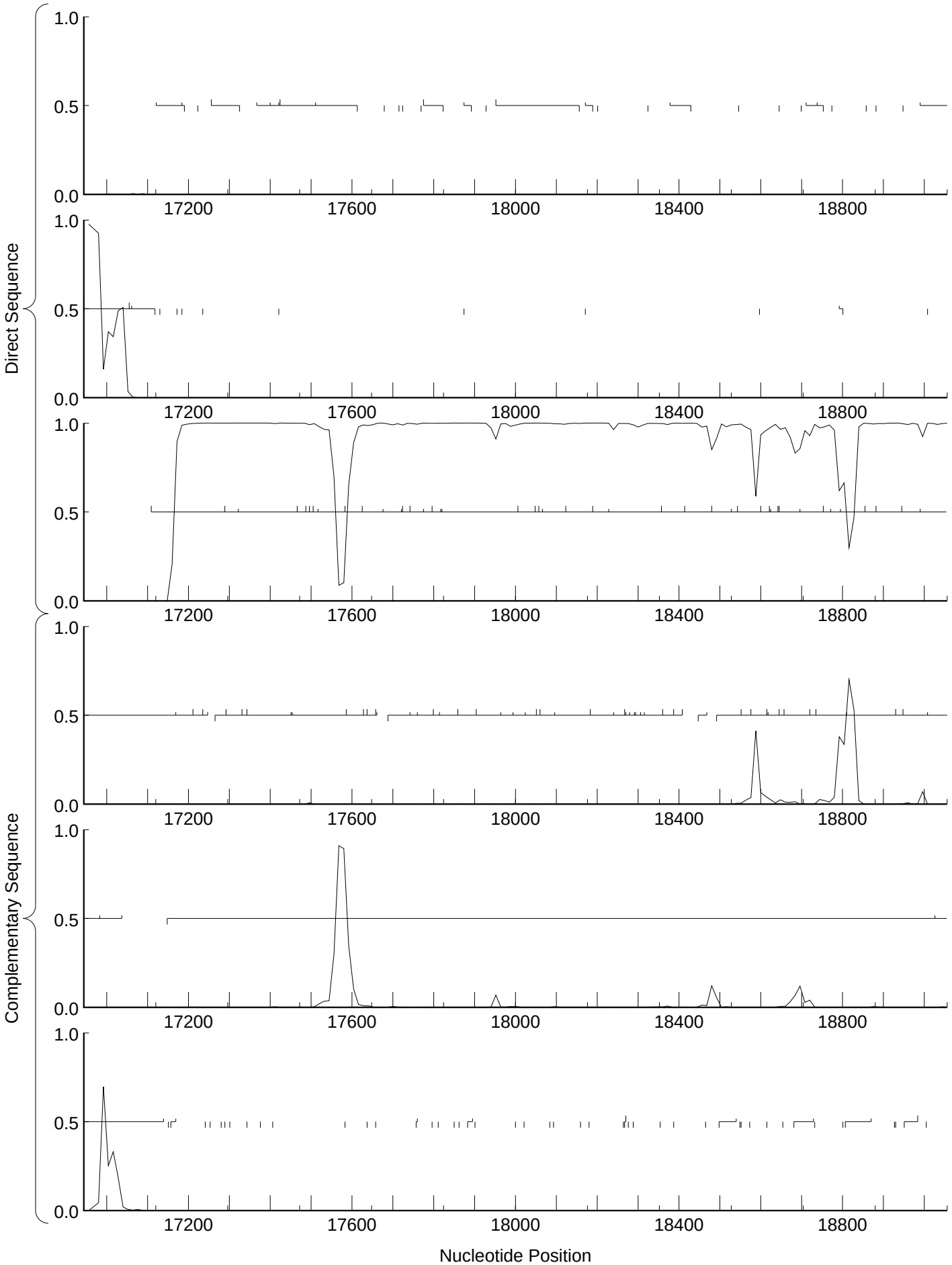
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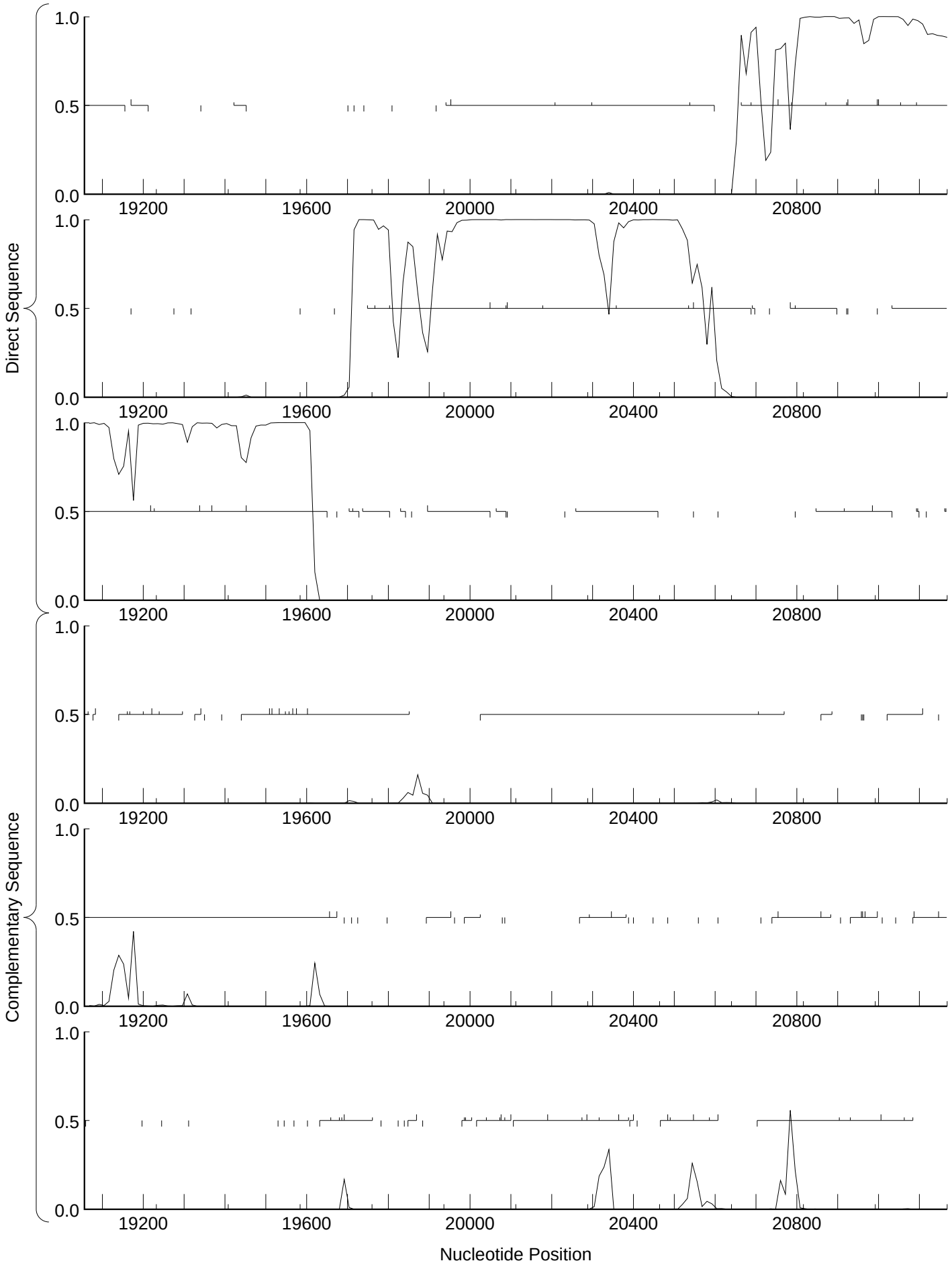
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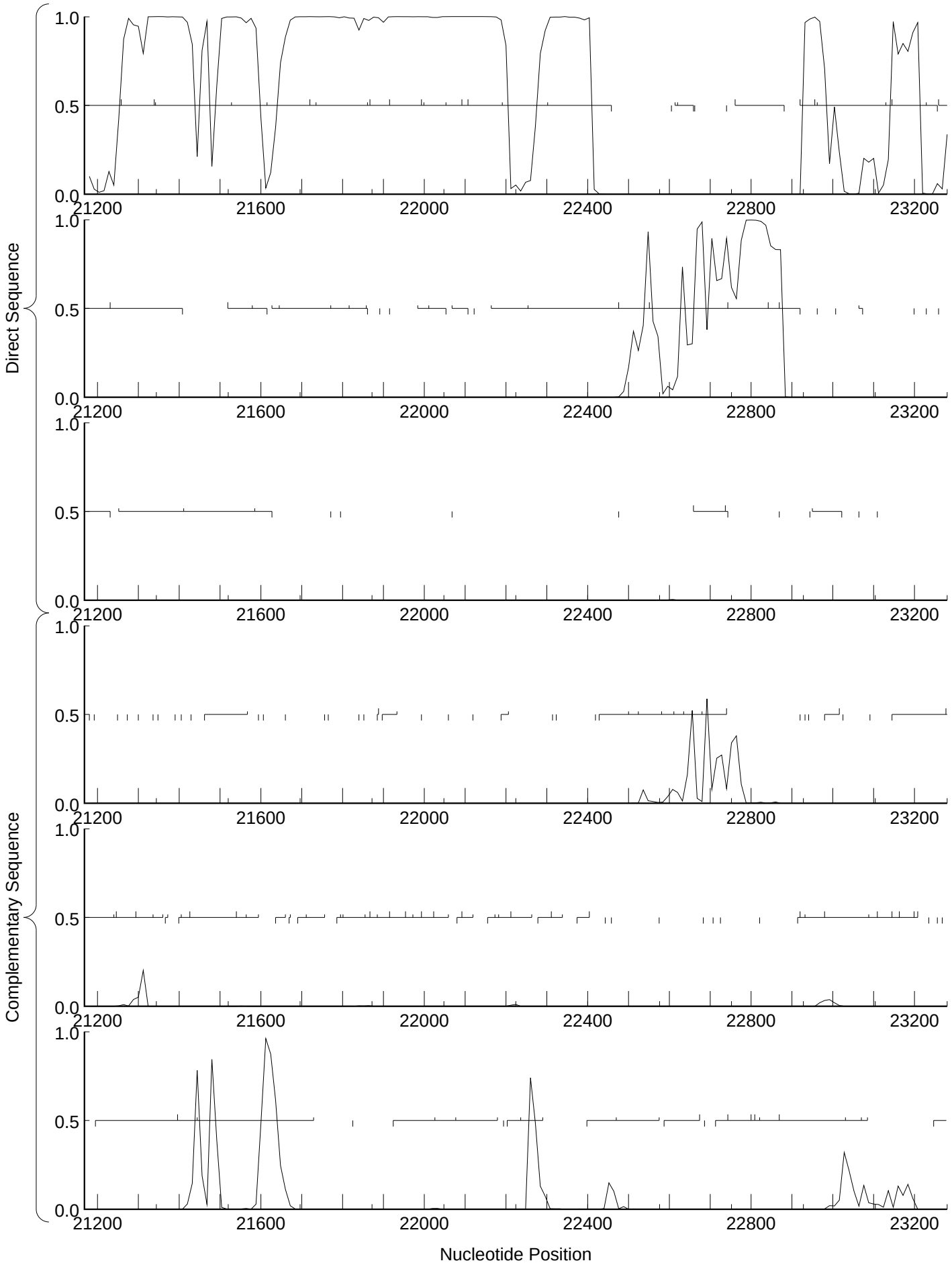
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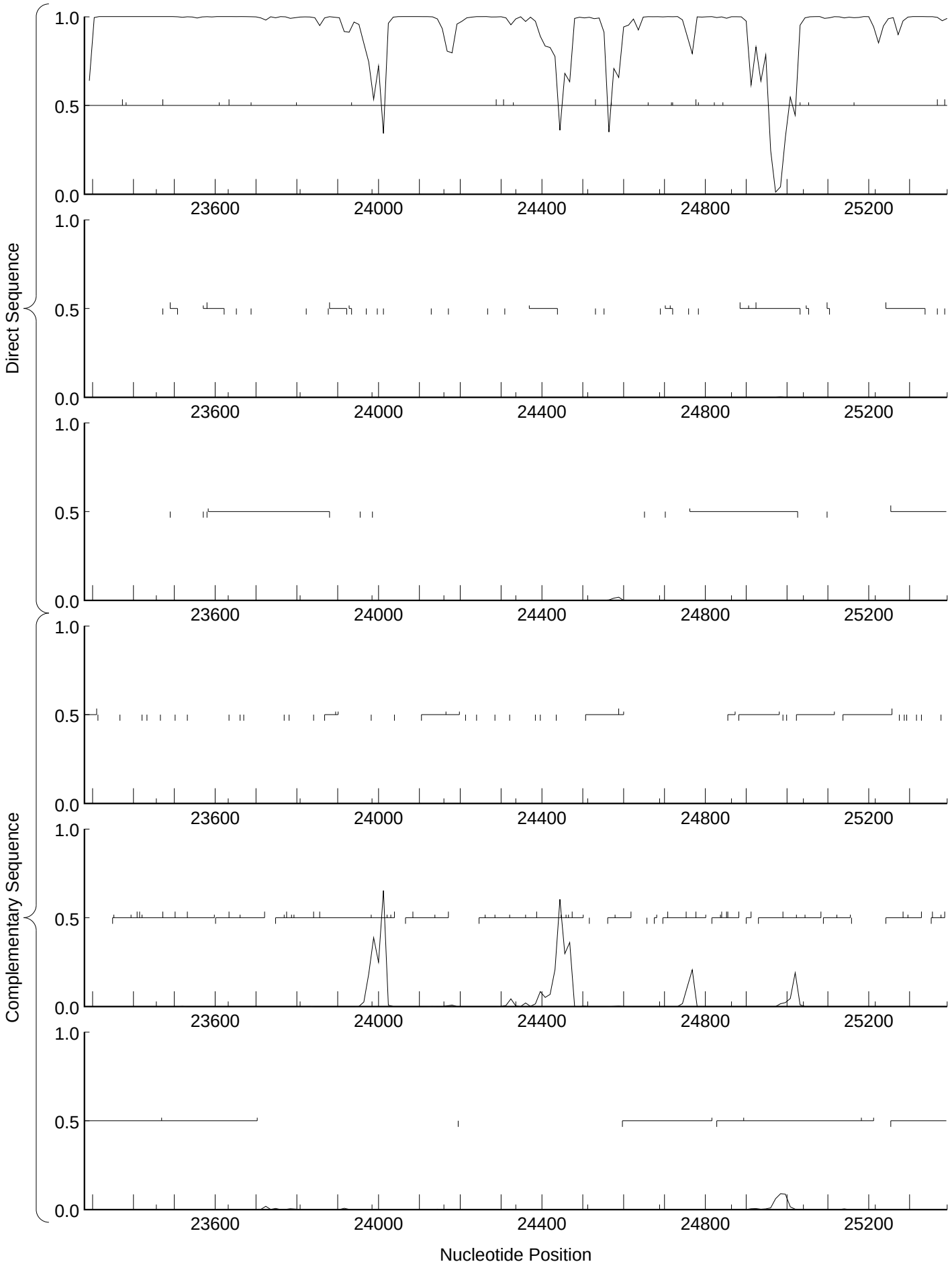
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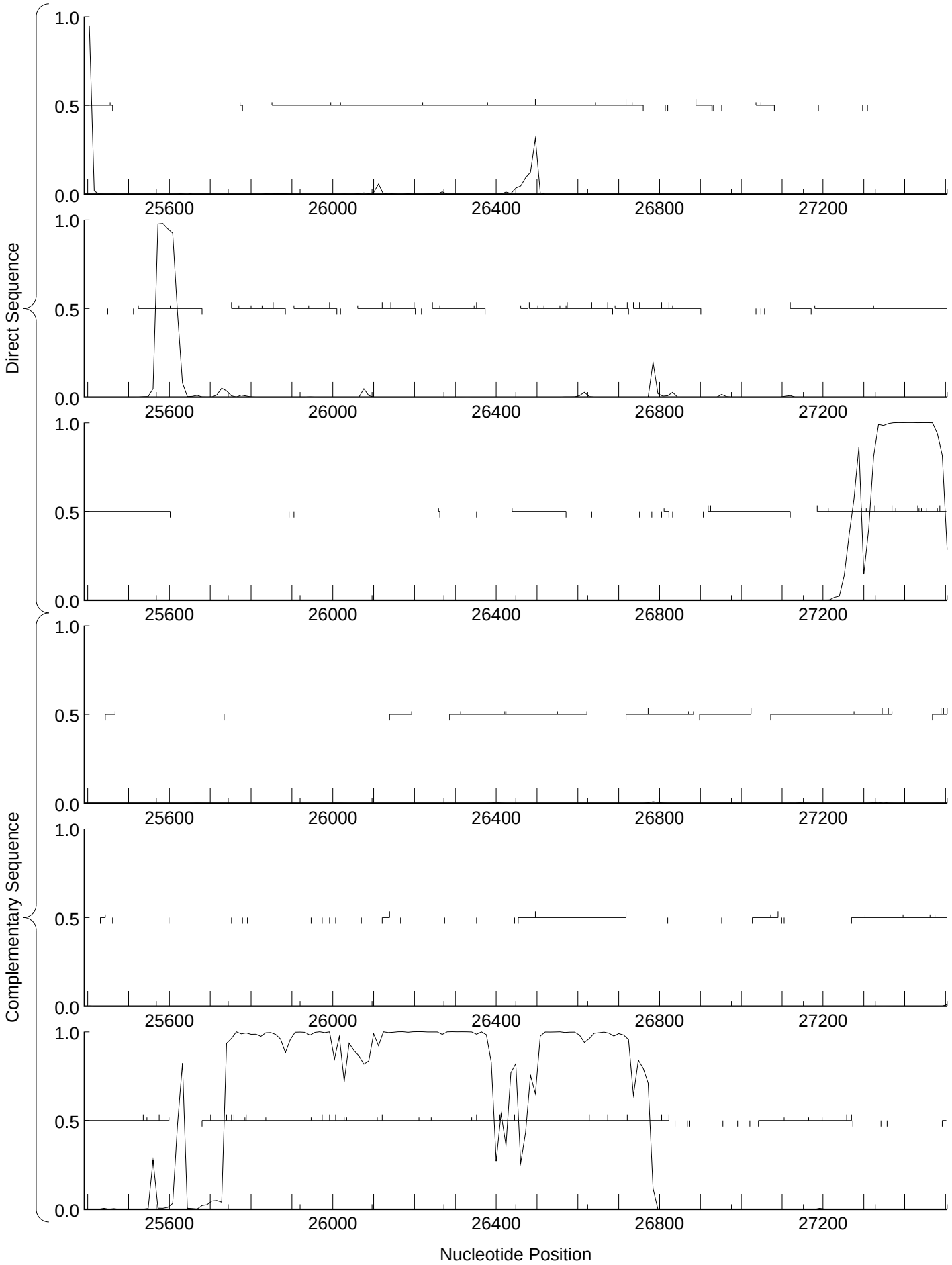


n complete sequence, 53239 bp including 10-base 3' overhang (CGGTCGGTTA), Cluster A2, Order 4, Window 96, Step 12, 12/27

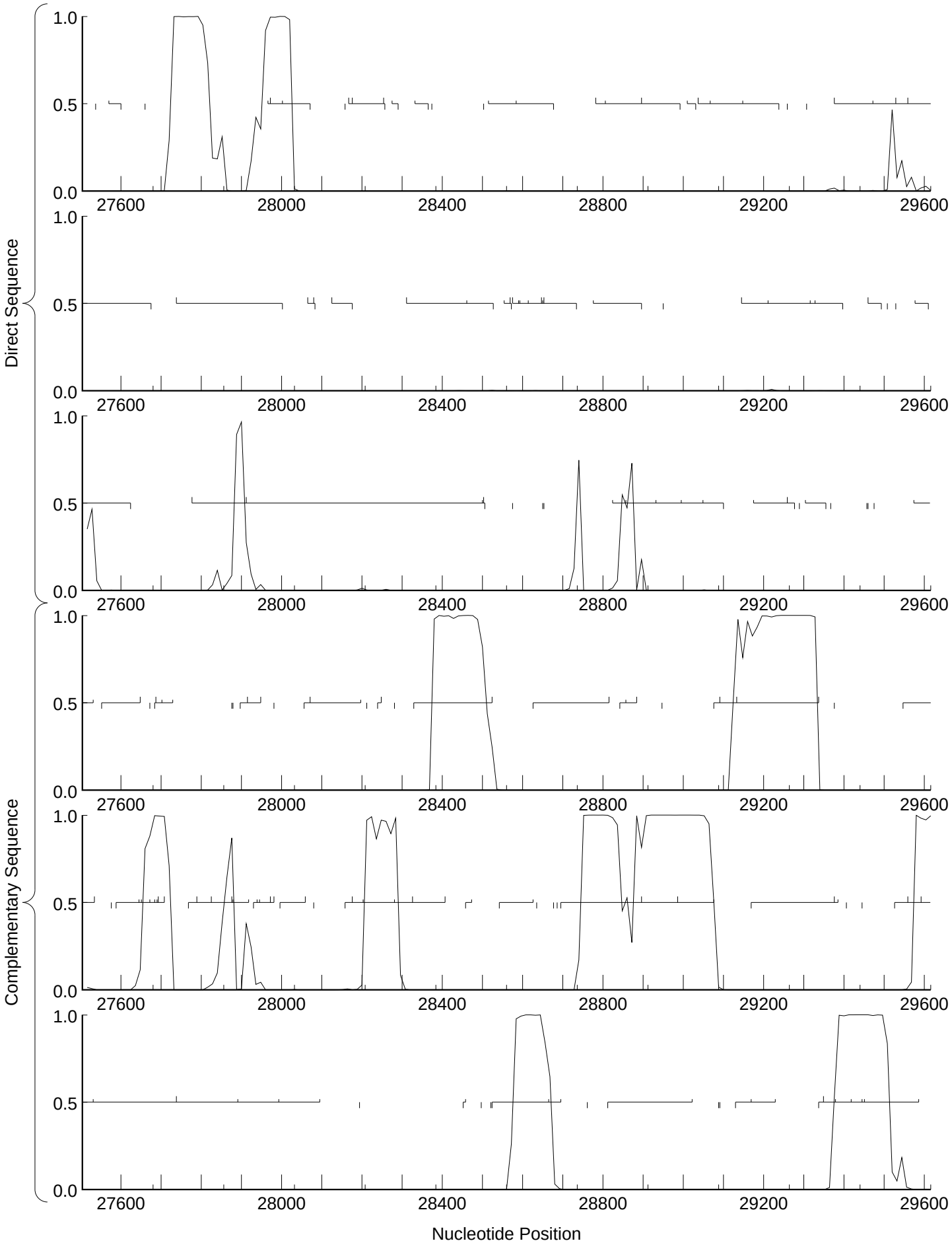


n complete sequence, 53239 bp including 10-base 3' overhang (CGGTCGGTTA), Cluster A2, Order 4, Window 96, Step 12, 13/27

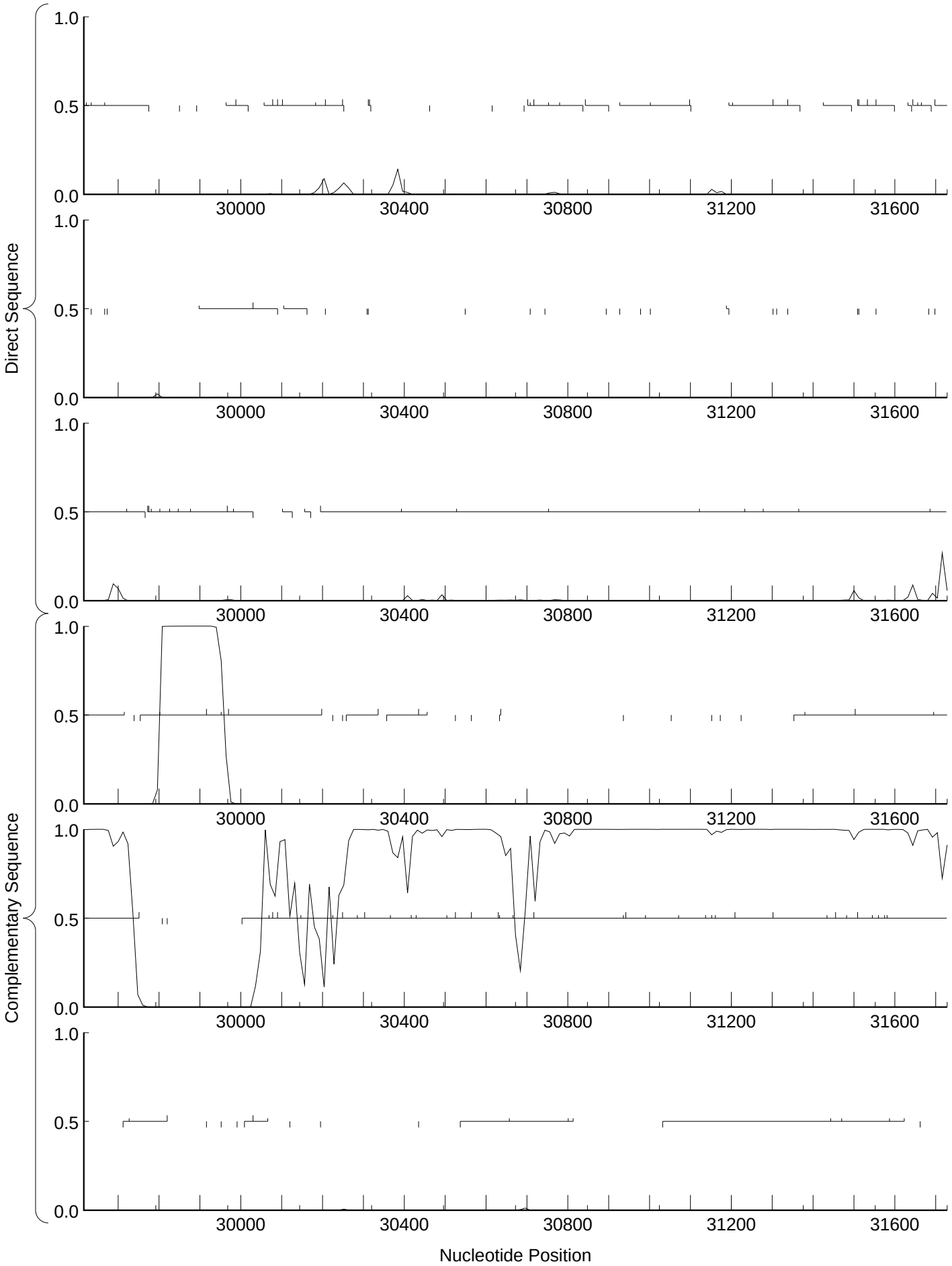


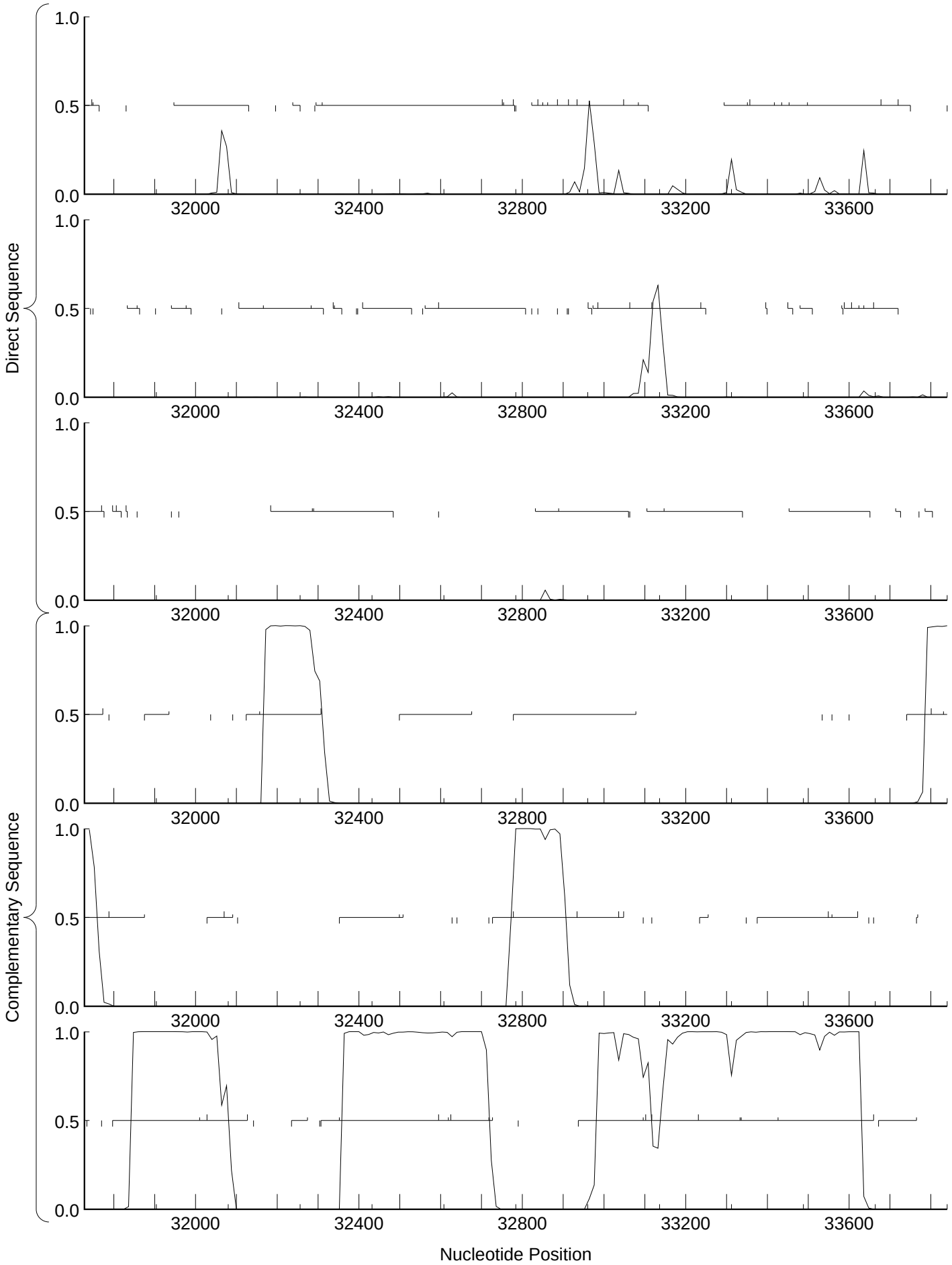

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
25600
26000
26400
26800
27200
Nucleotide Position

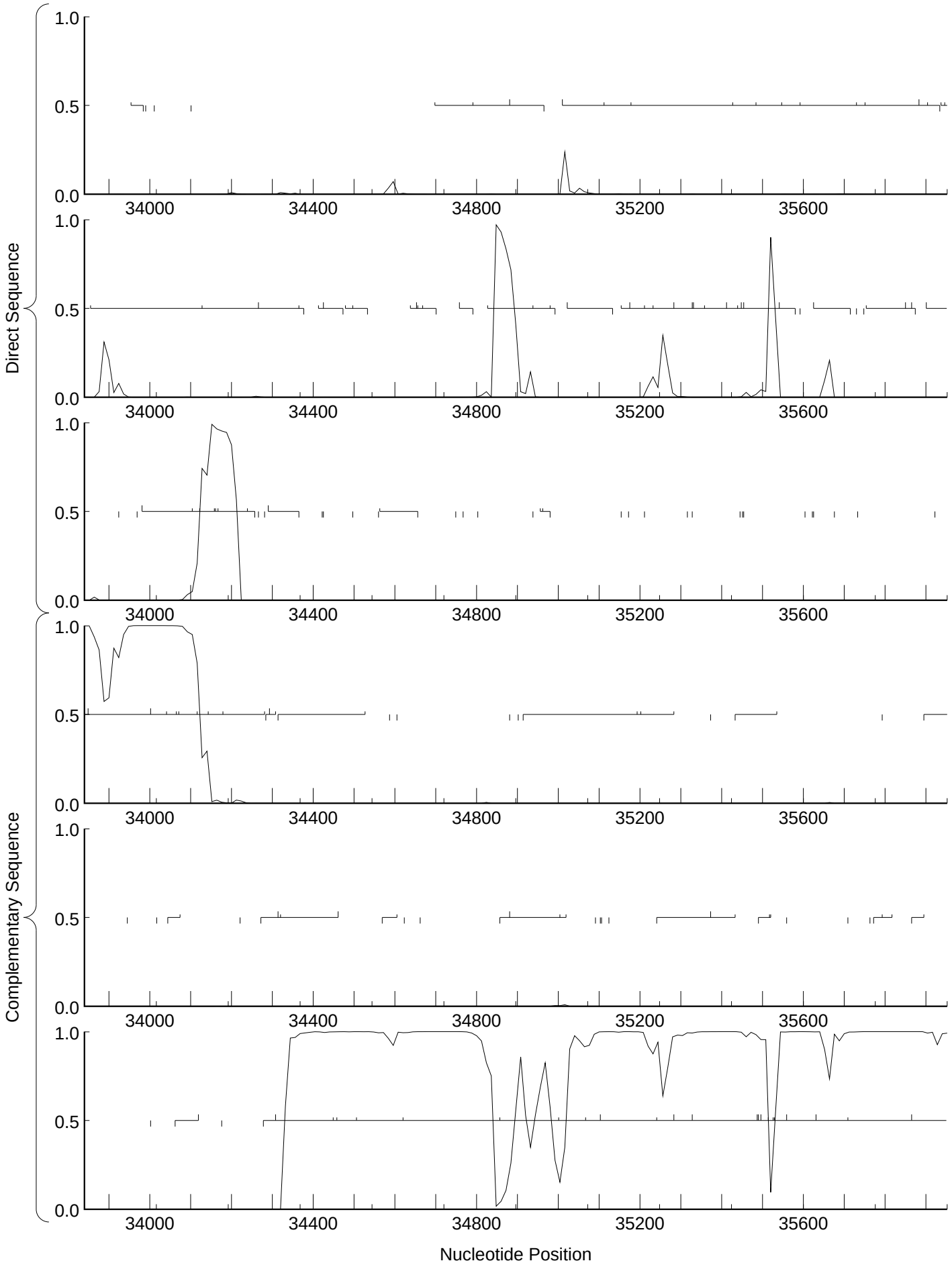
n complete sequence, 53239 bp including 10-base 3’ overhang (CGGTCGGTTA), Cluster A2, Order 4, Window 96, Step 12, 15/27



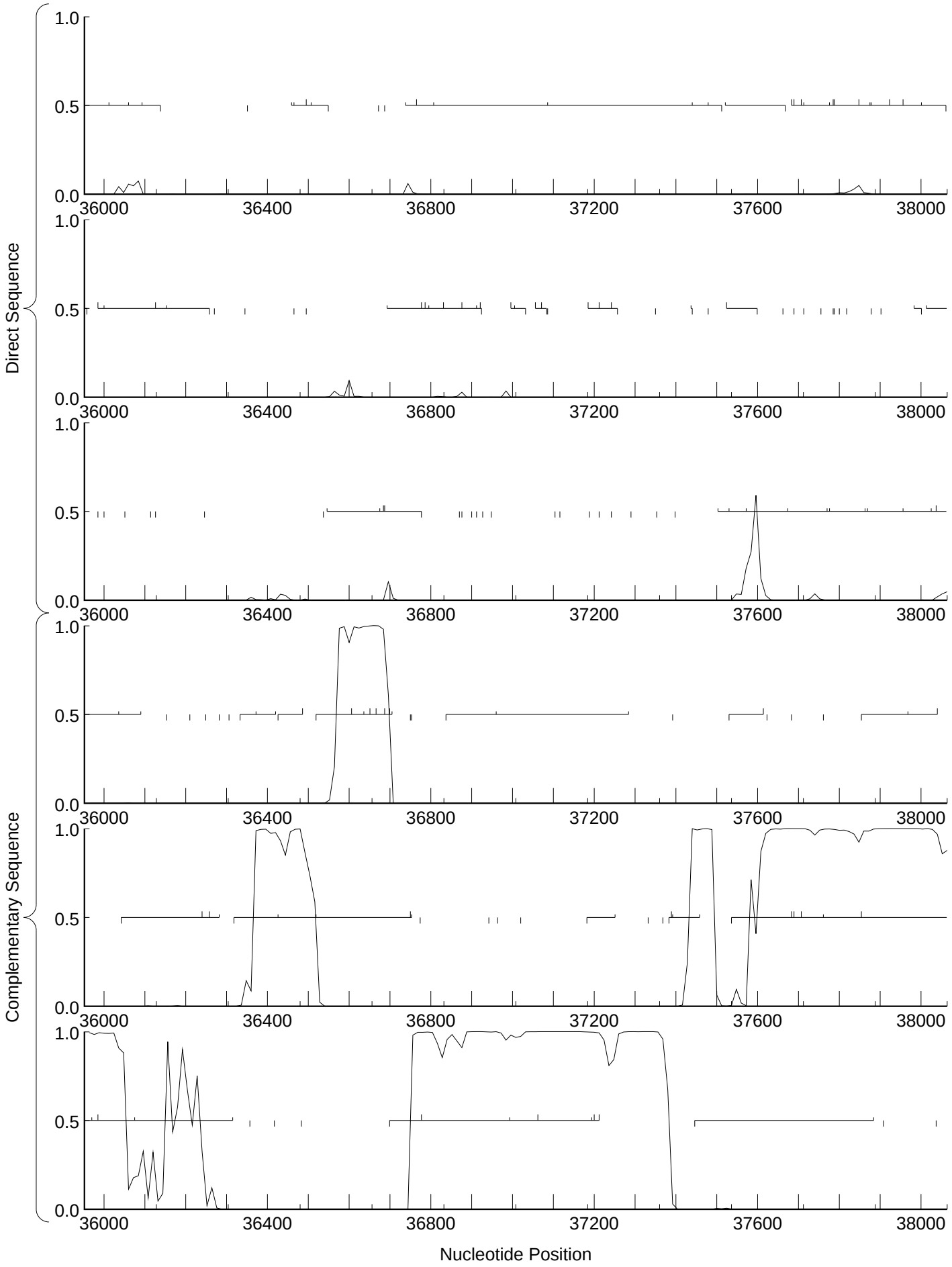
n complete sequence, 53239 bp including 10-base 3' overhang (CGGTCGGTTA), Cluster A2, Order 4, Window 96, Step 12, 16/27

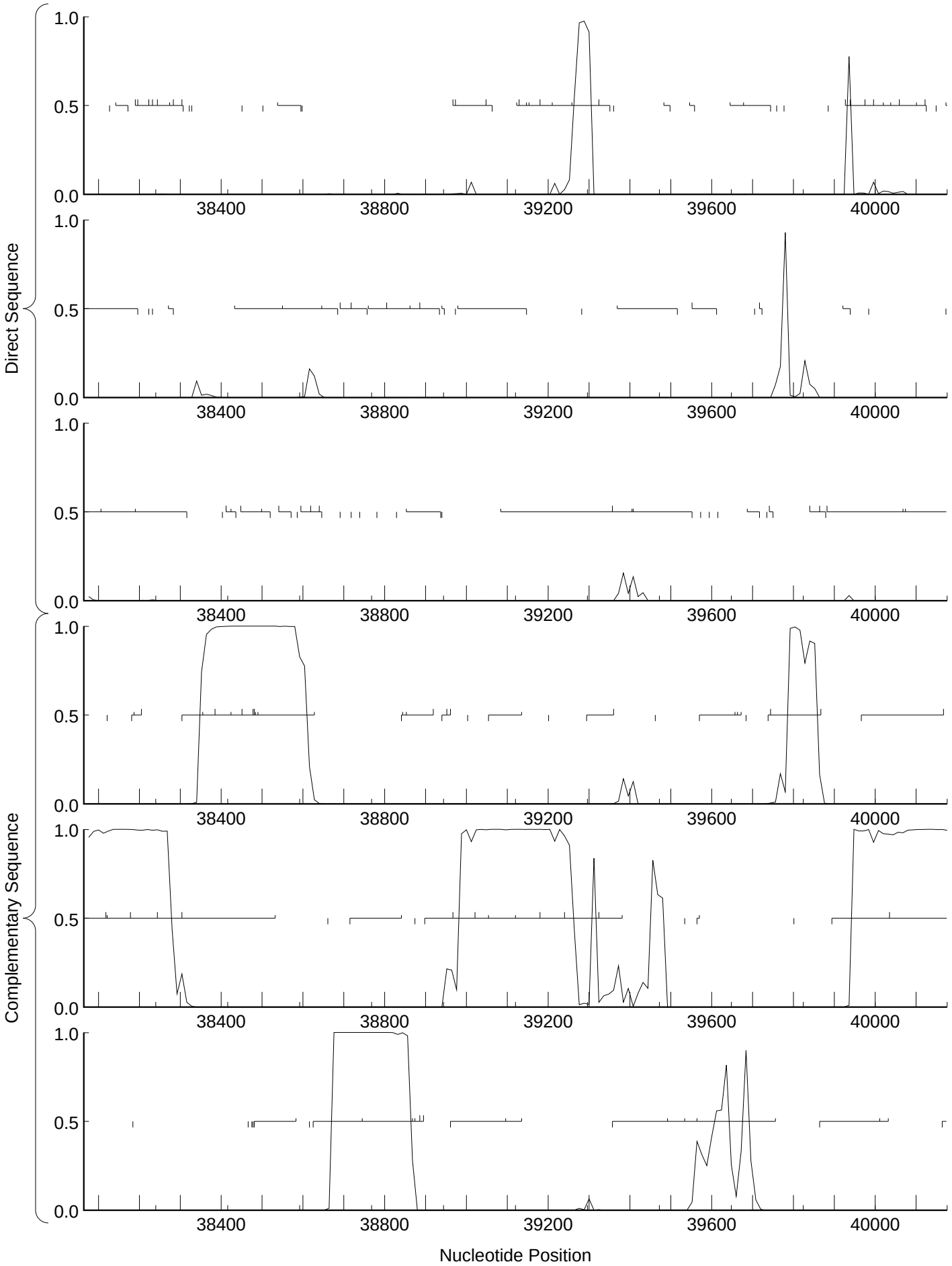



Direct Sequence
Complementary Sequence
1.0
0.5
0.0
32000
32400
32800
33200
33600
Nucleotide Position

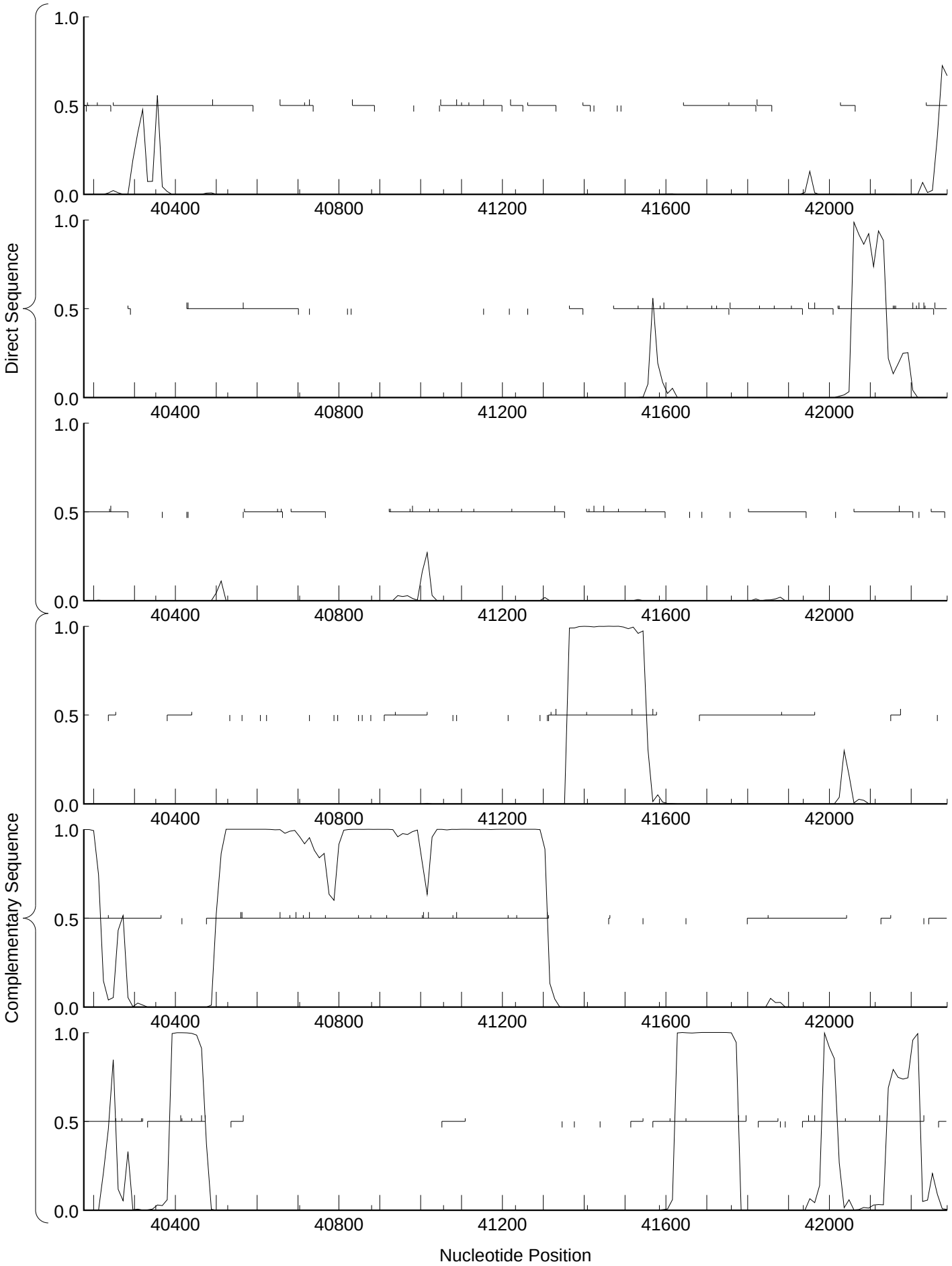

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
34000
34400
34800
35200
35600
Nucleotide Position

n complete sequence, 53239 bp including 10-base 3’ overhang (CGGTCGGTTA), Cluster A2, Order 4, Window 96, Step 12, 19/27

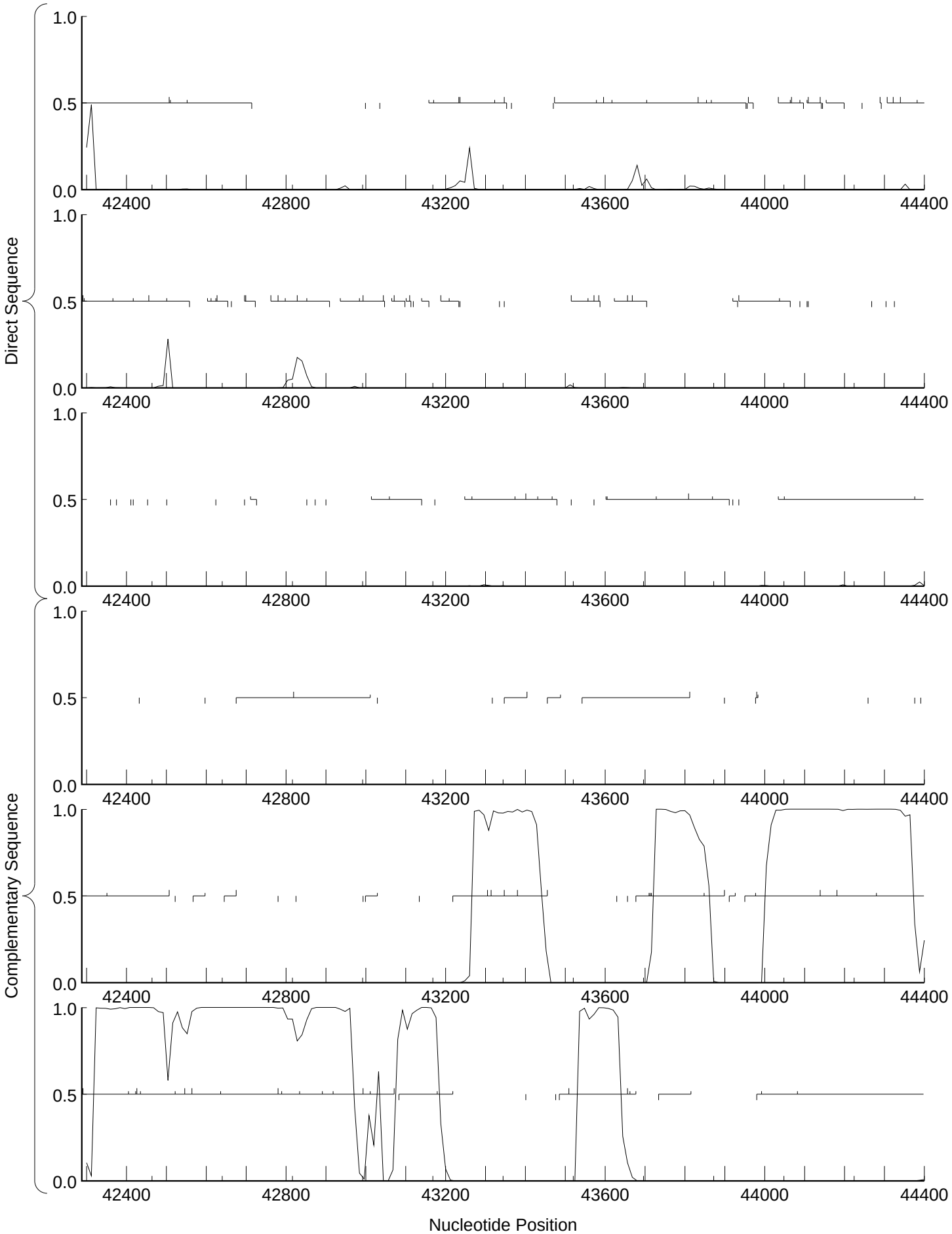



Direct Sequence
Complementary Sequence
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0.5
0.0
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38800
39200
39600
40000
Nucleotide Position

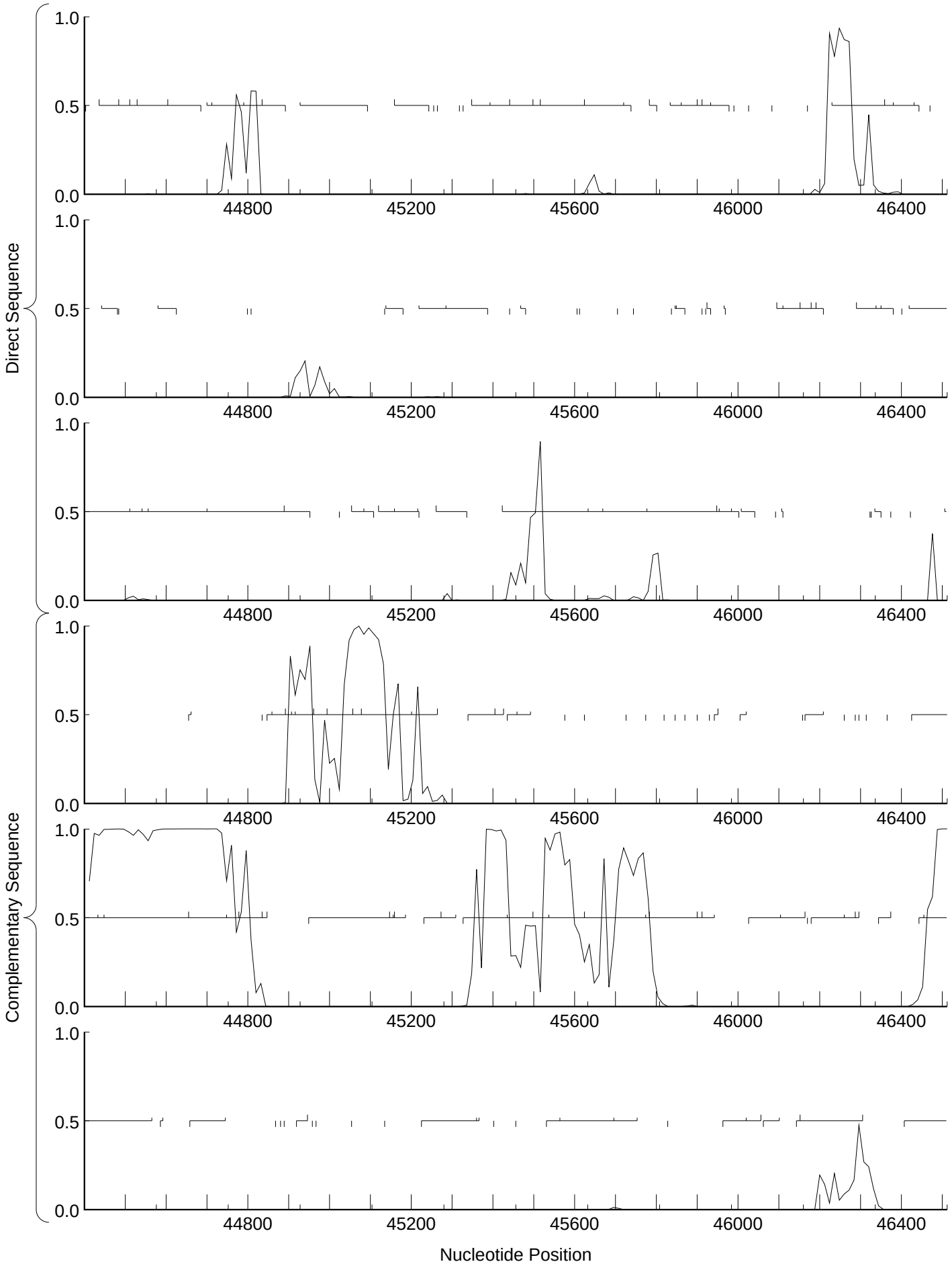
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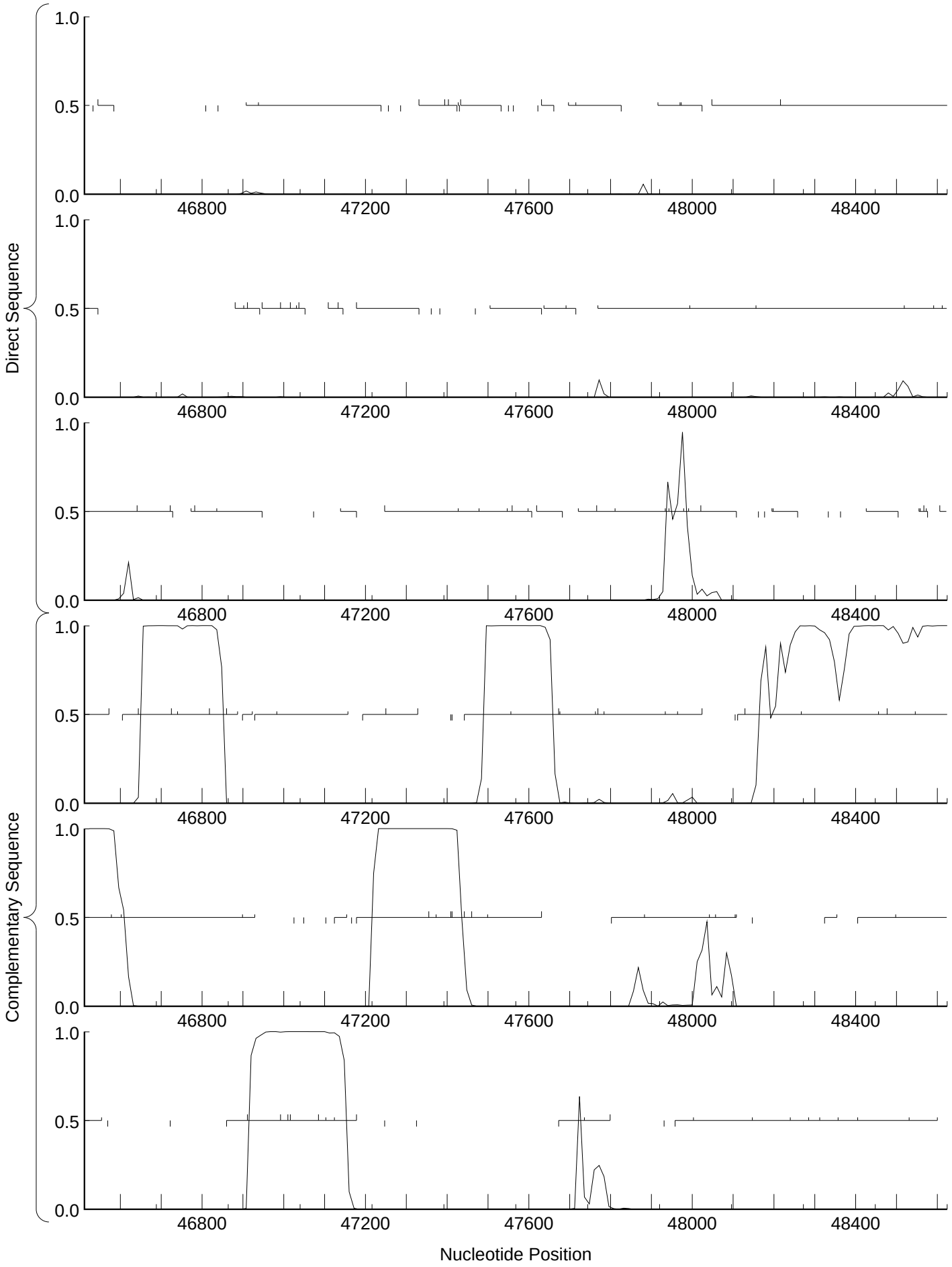


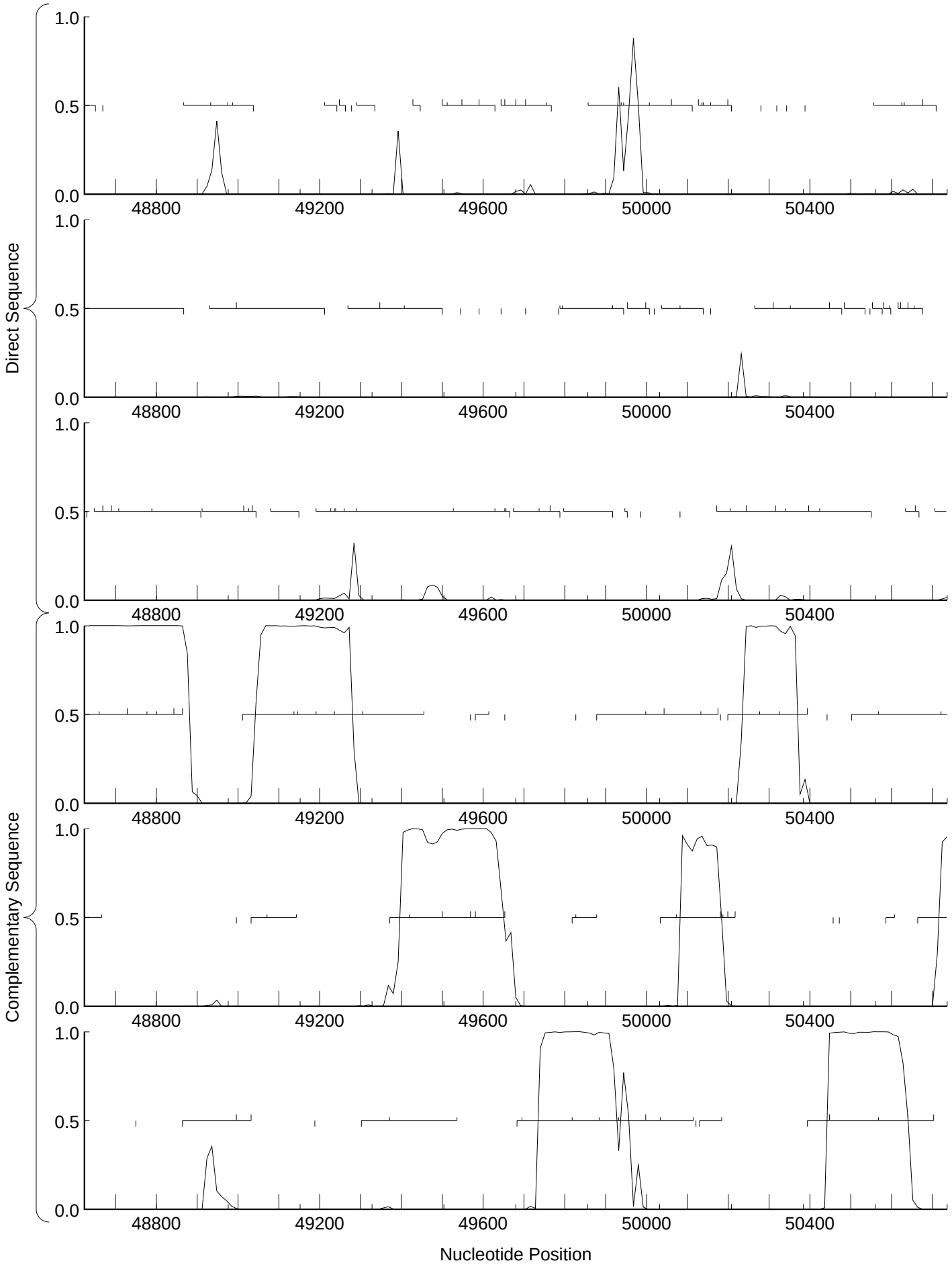
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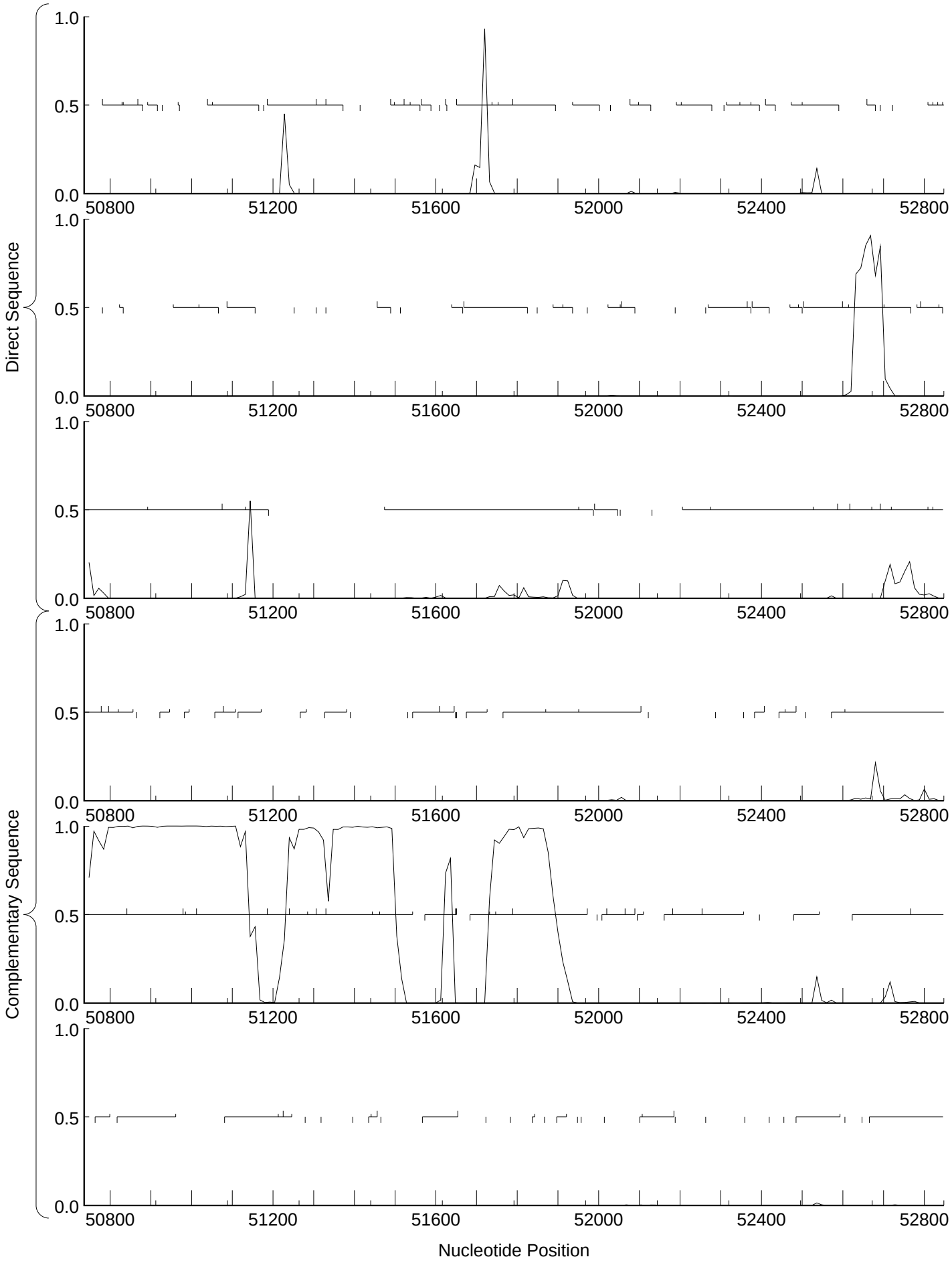
n complete sequence, 53239 bp including 10-base 3' overhang (CGGTCGGTTA), Cluster A2, Order 4, Window 96, Step 12, 23/27




Direct Sequence
Complementary Sequence
1.0
0.5
0.0
46800
47200
47600
48000
48400
Nucleotide Position


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
48800
49200
49600
50000
50400
Nucleotide Position

n complete sequence, 53239 bp including 10-base 3’ overhang (CGGTCGGTTA), Cluster A2, Order 4, Window 96, Step 12, 26/27



n complete sequence, 53239 bp including 10-base 3’ overhang (CGGTCGGTTA), Cluster A2, Order 4, Window 96, Step 12, 27/27

