GeneMark

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

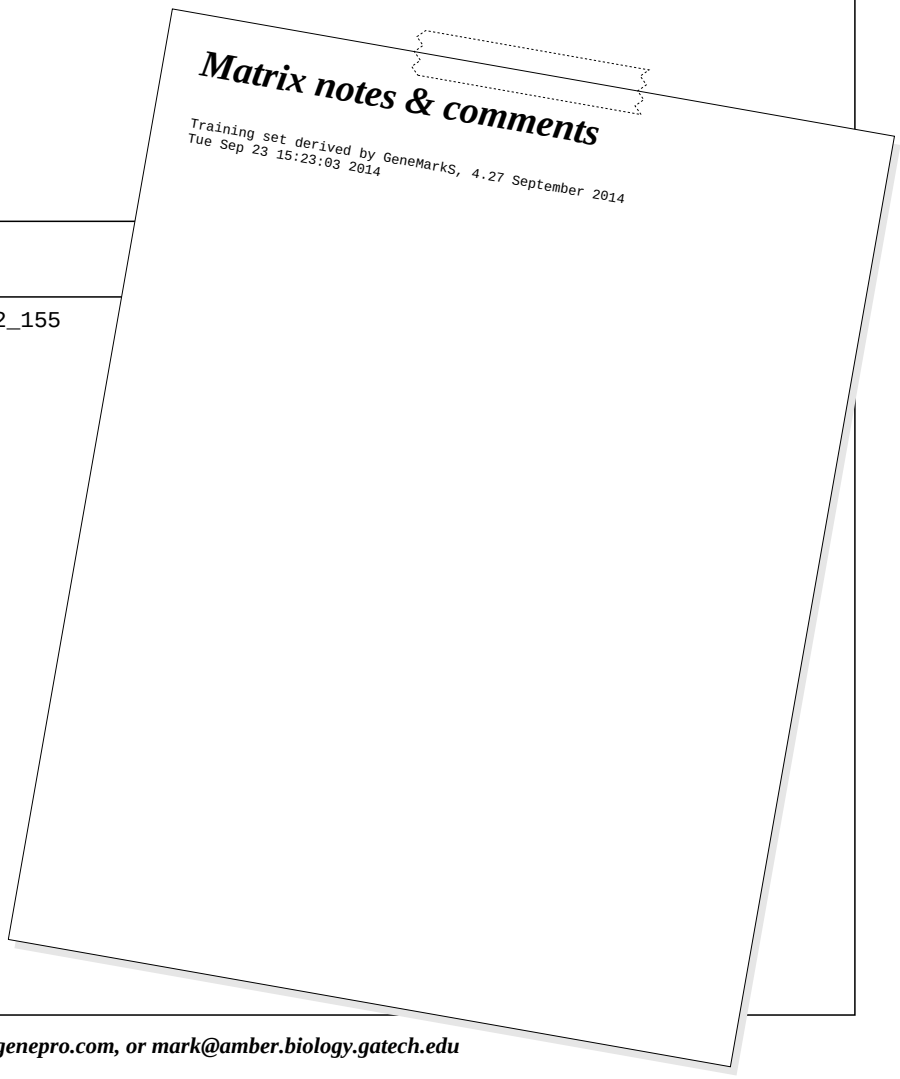
PROGRAM INFORMATION

```
Sequence         :  Mycobacterium phage Dynamix complete sequence, 50628 bp including 10-base 3’ overhang (CGGA
Analysis Date    :  3/28/24 at 21:35:05
Pages            :  25
Sequence Length  :  50628 bp
GC Content       :   63.72%

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

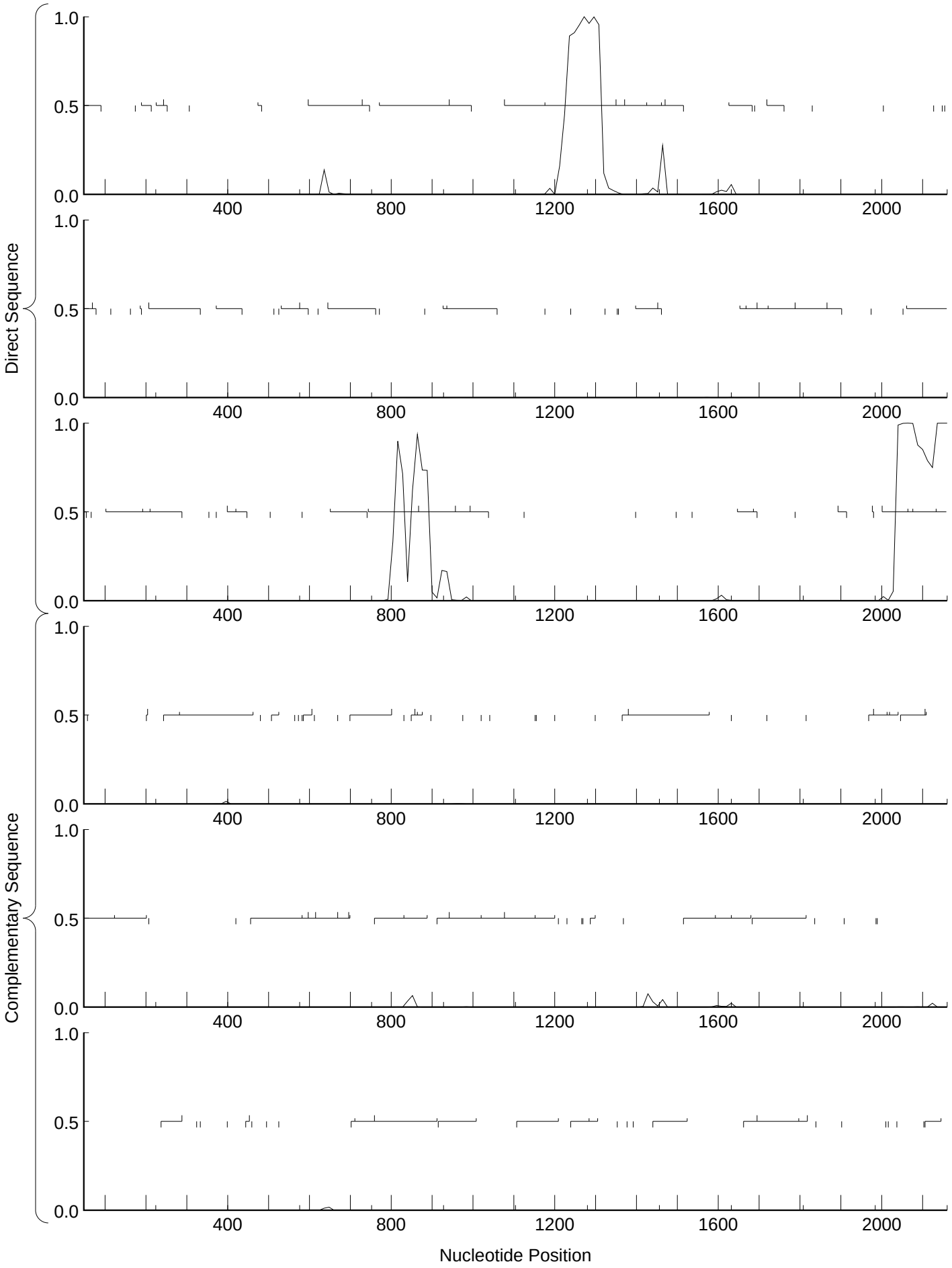
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Matrix     :  Mycobacterium_smegmatis_MC2_155
Author     :  -

Order      :  4

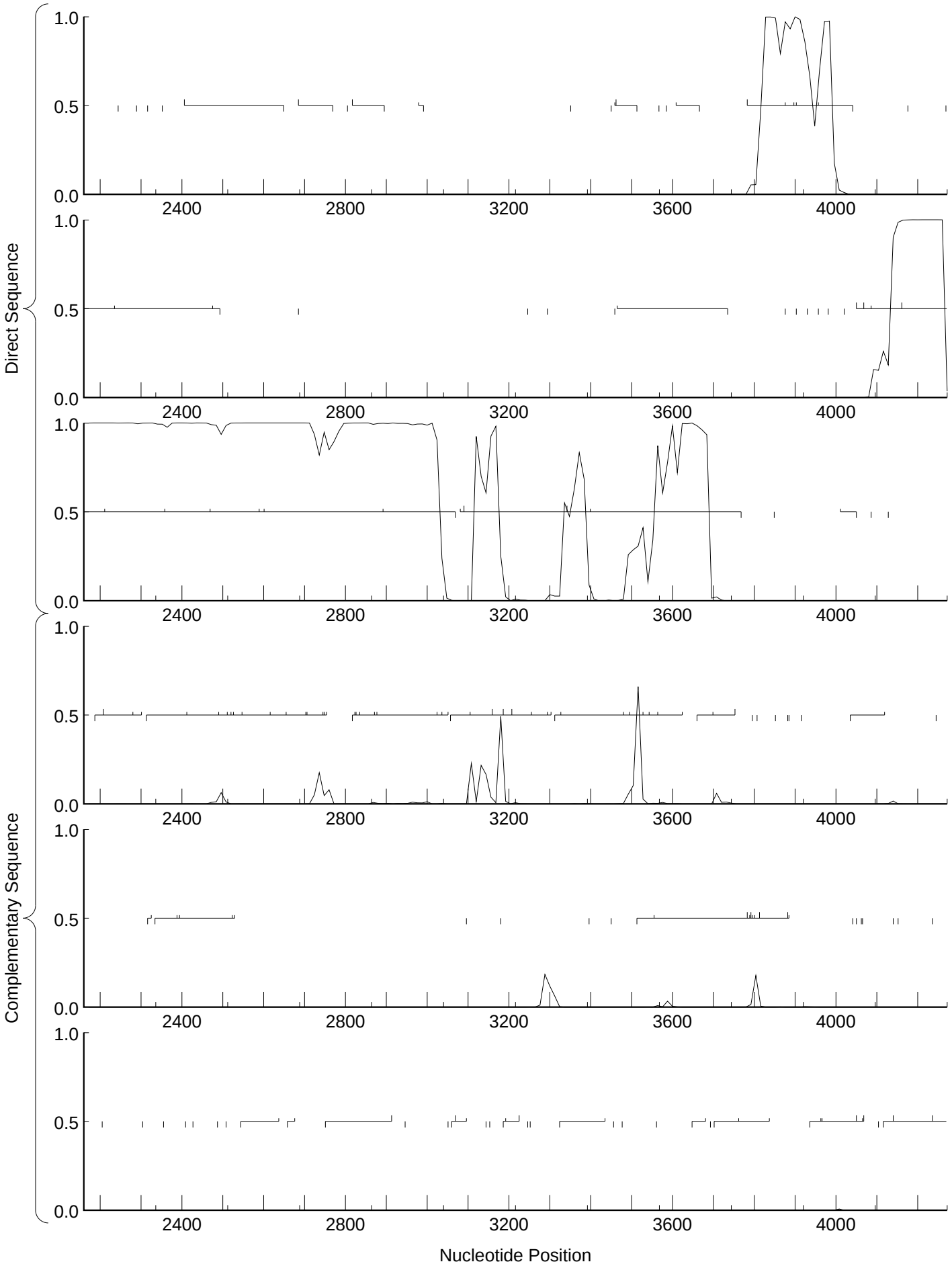

  Send questions / comments to:
      Dr. M. Borodovsky
      Georgia Institute of Technology
      School of Biology
      Atlanta, GA  30332-0230
```

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

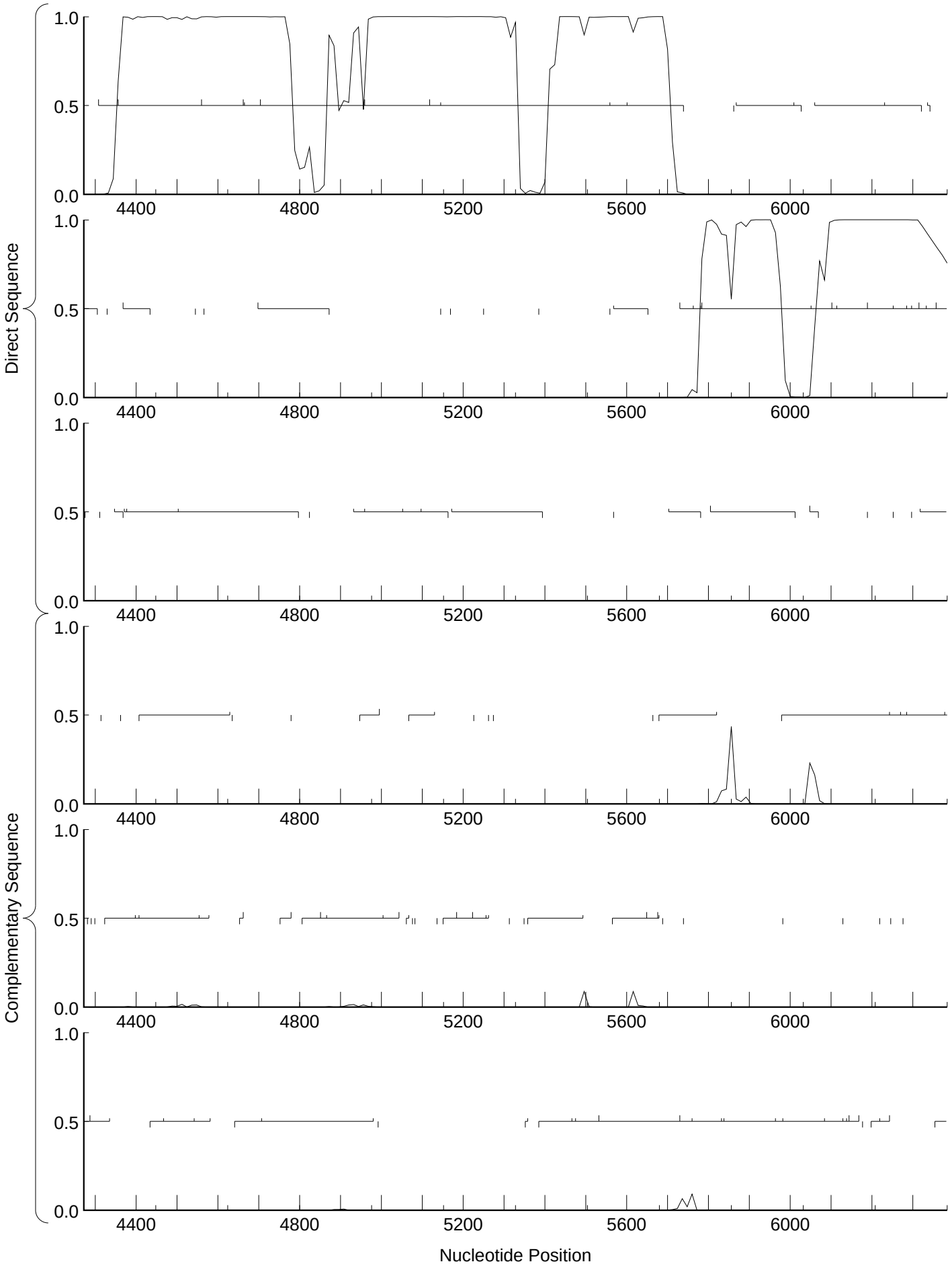
ix complete sequence, 50628 bp including 10-base 3’ overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 2/25



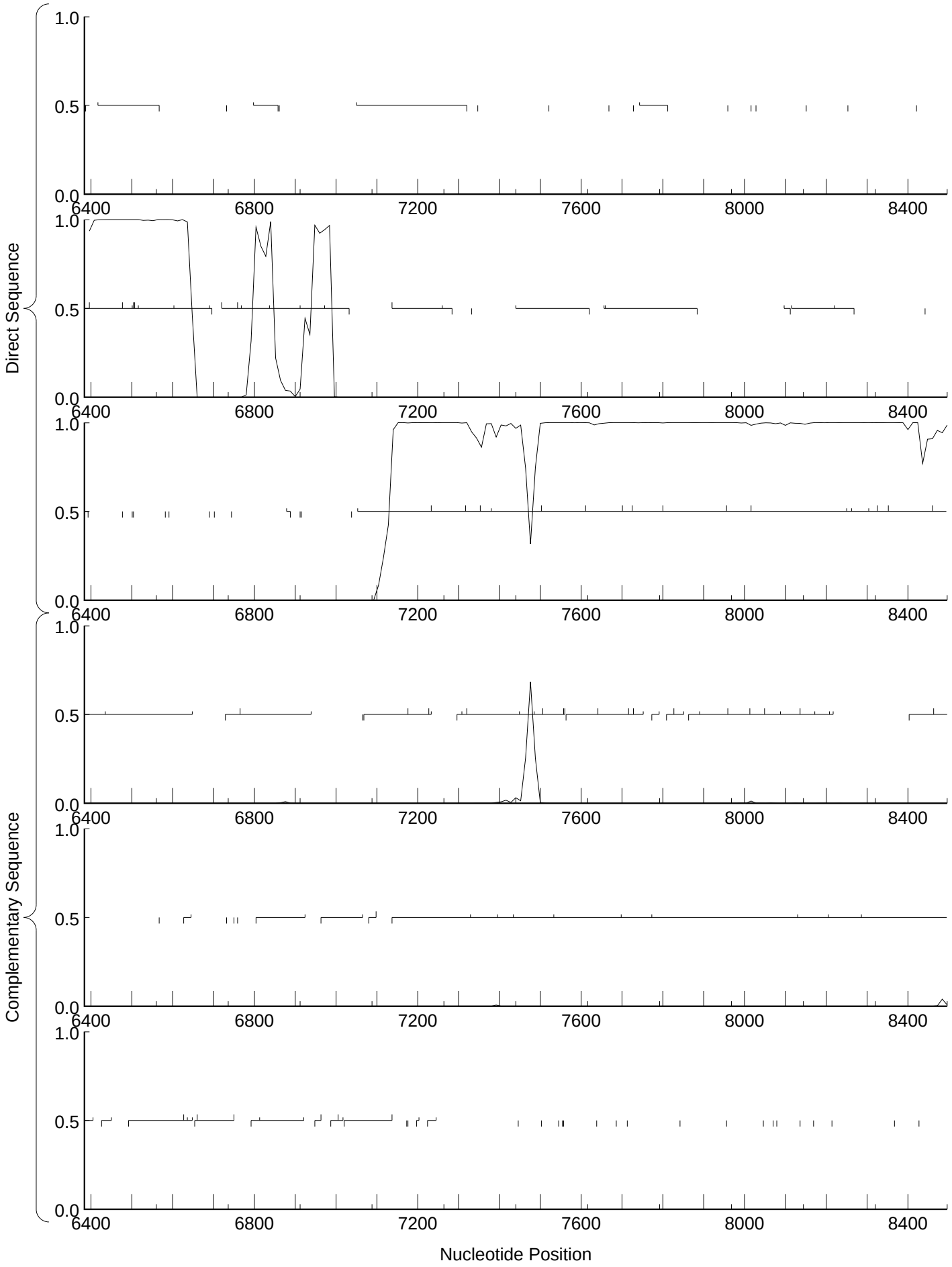
ix complete sequence, 50628 bp including 10-base 3’ overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 3/25



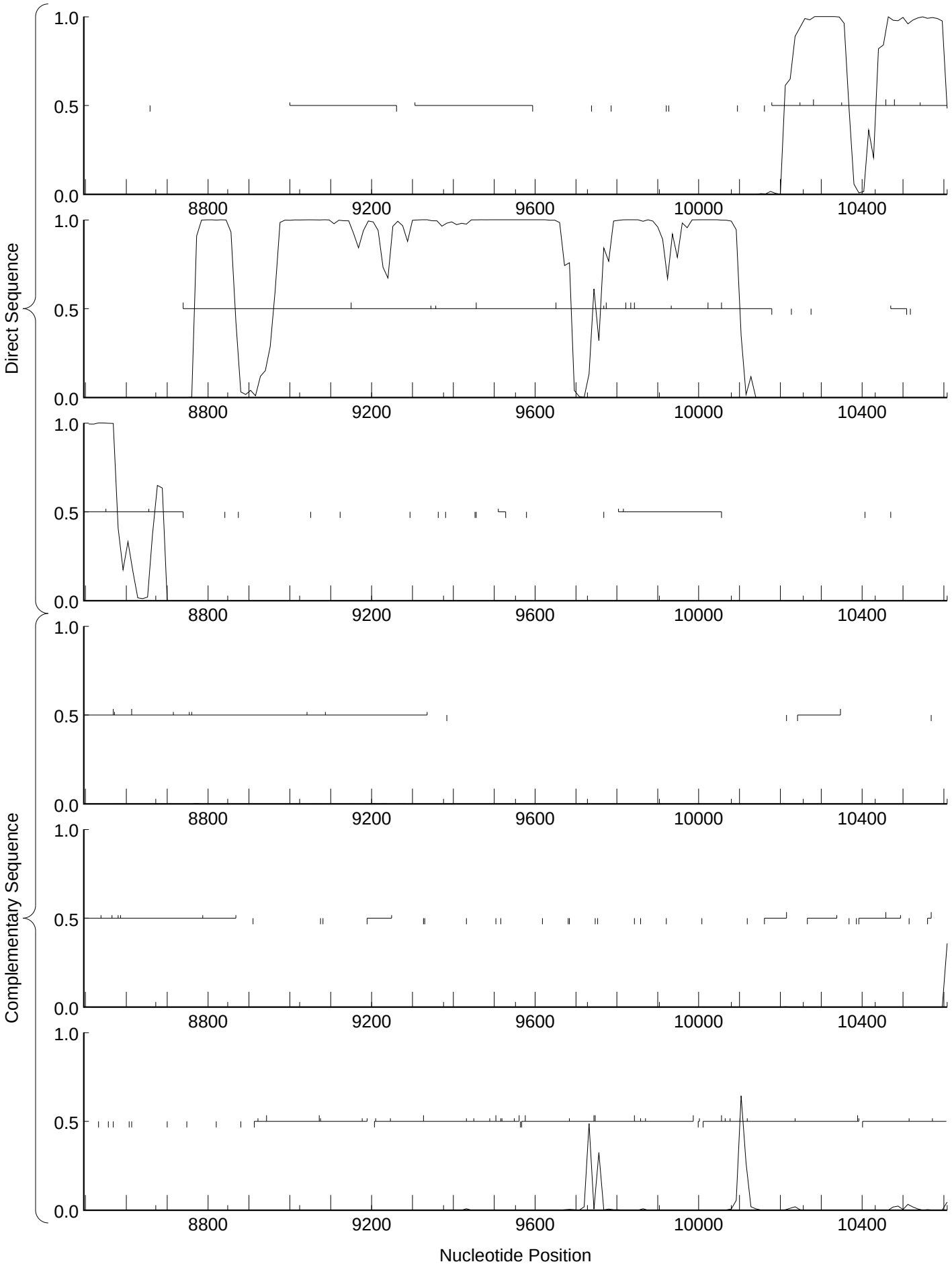
ix complete sequence, 50628 bp including 10-base 3’ overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 4/25



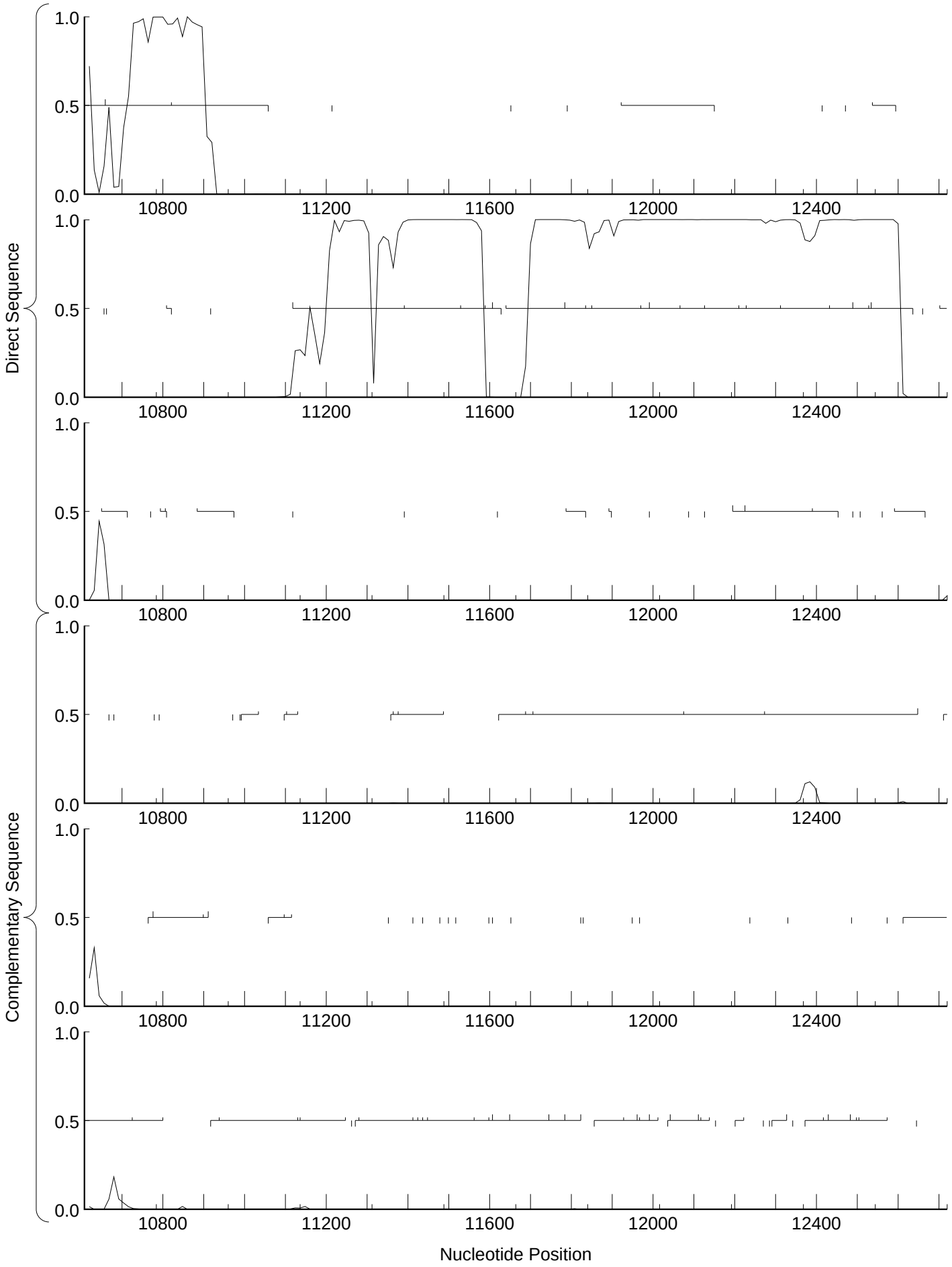
ix complete sequence, 50628 bp including 10-base 3’ overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 5/25



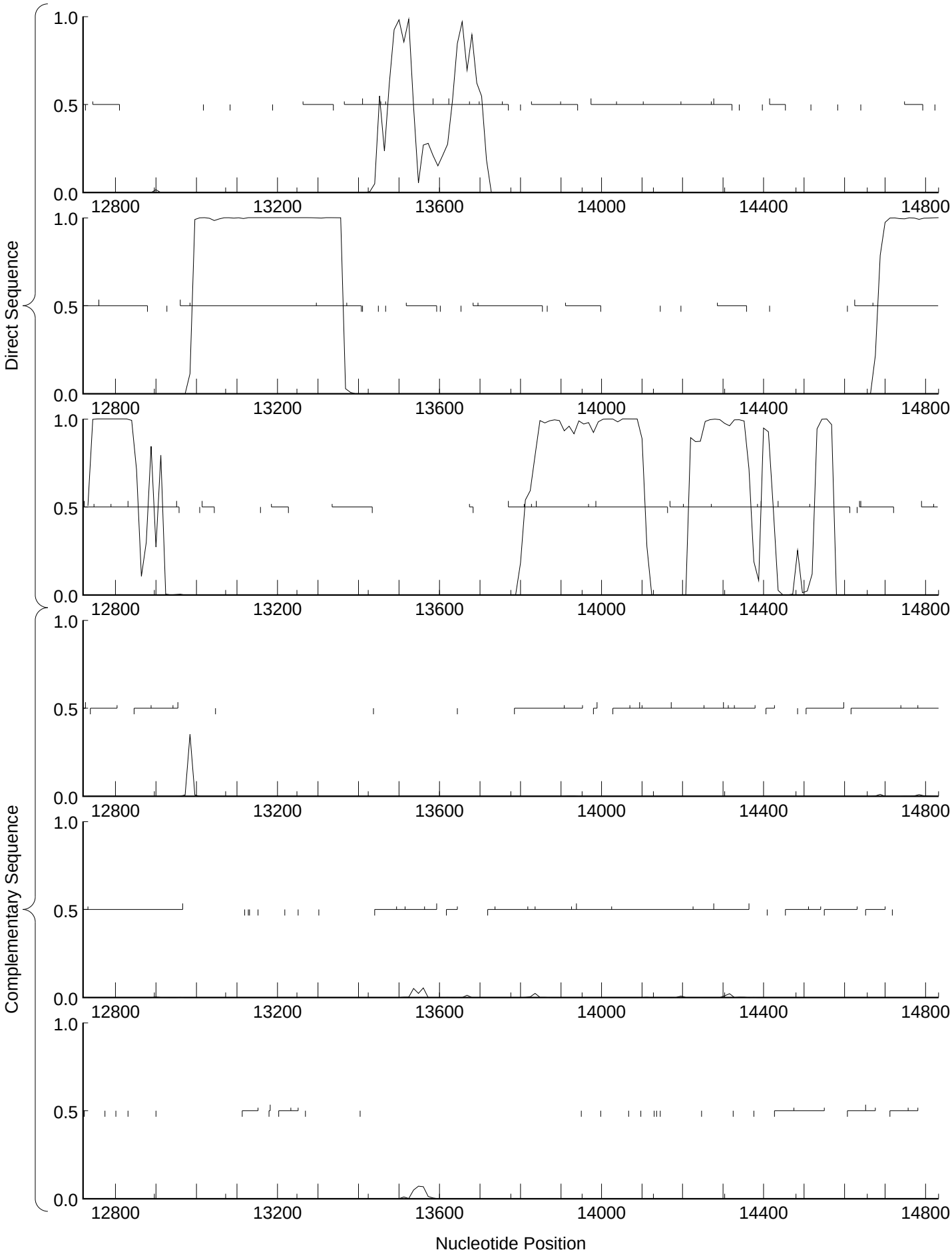
ix complete sequence, 50628 bp including 10-base 3’ overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 6/25



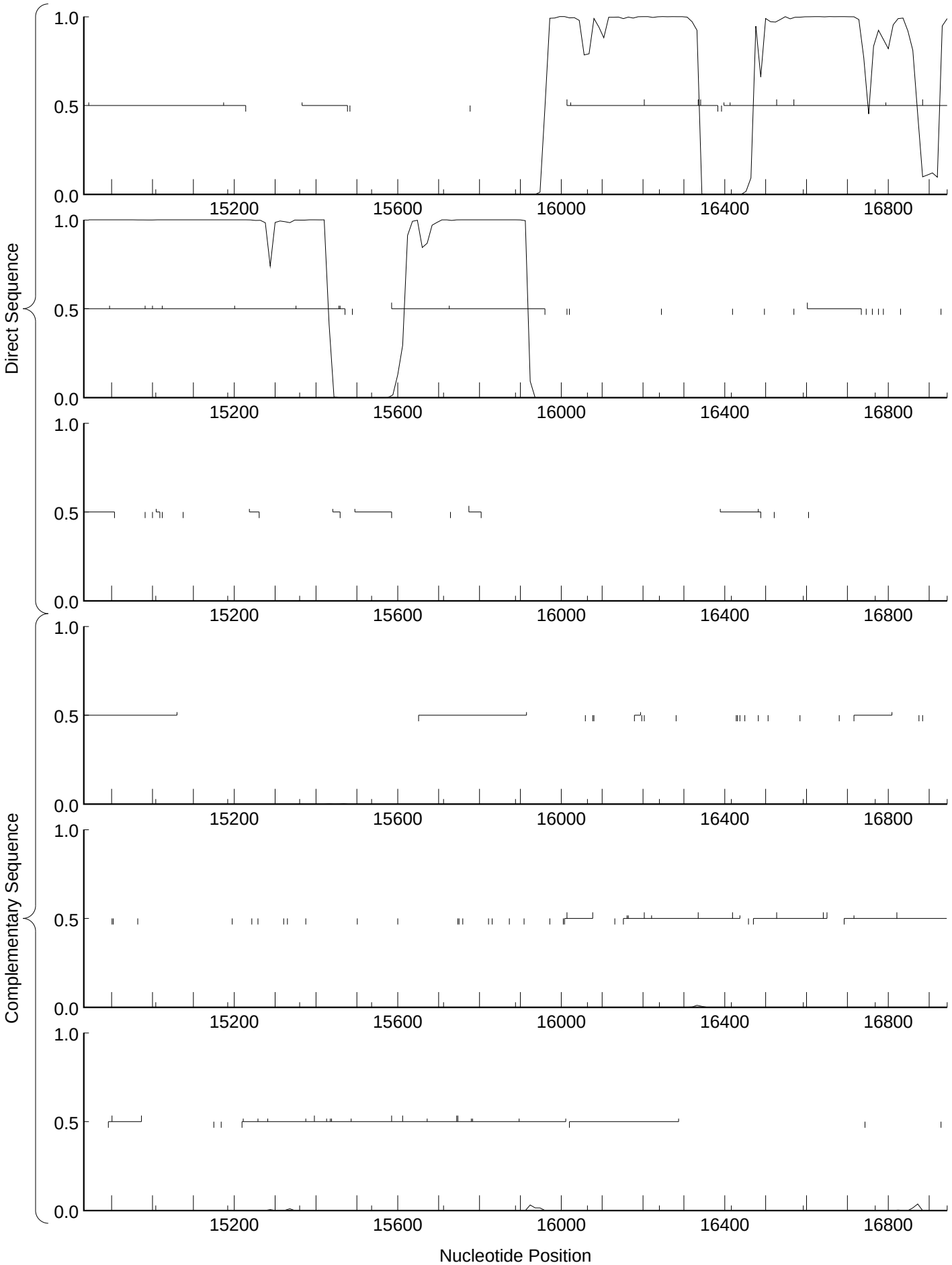
ix complete sequence, 50628 bp including 10-base 3’ overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 7/25

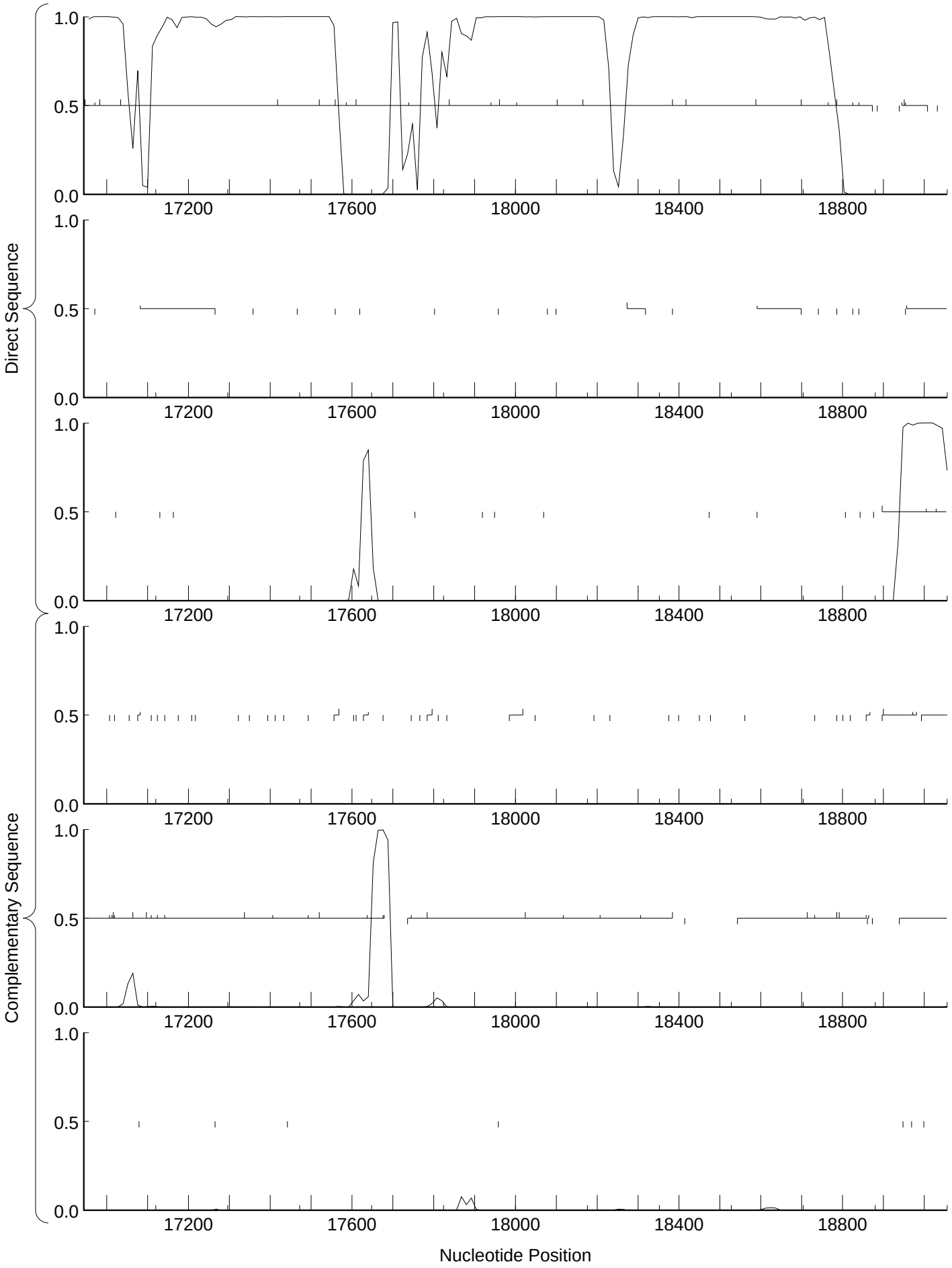


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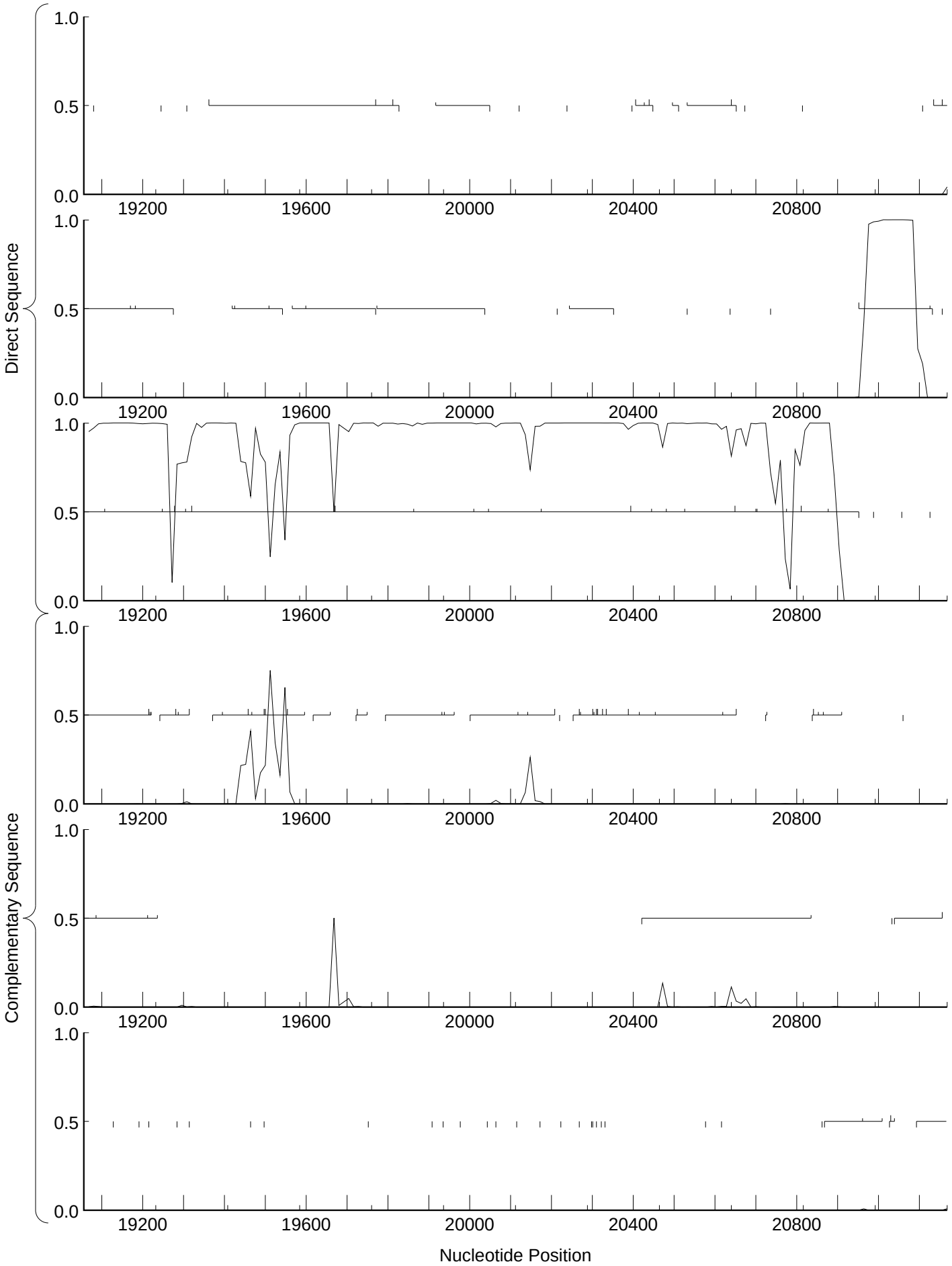


ix complete sequence, 50628 bp including 10-base 3’ overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 9/25

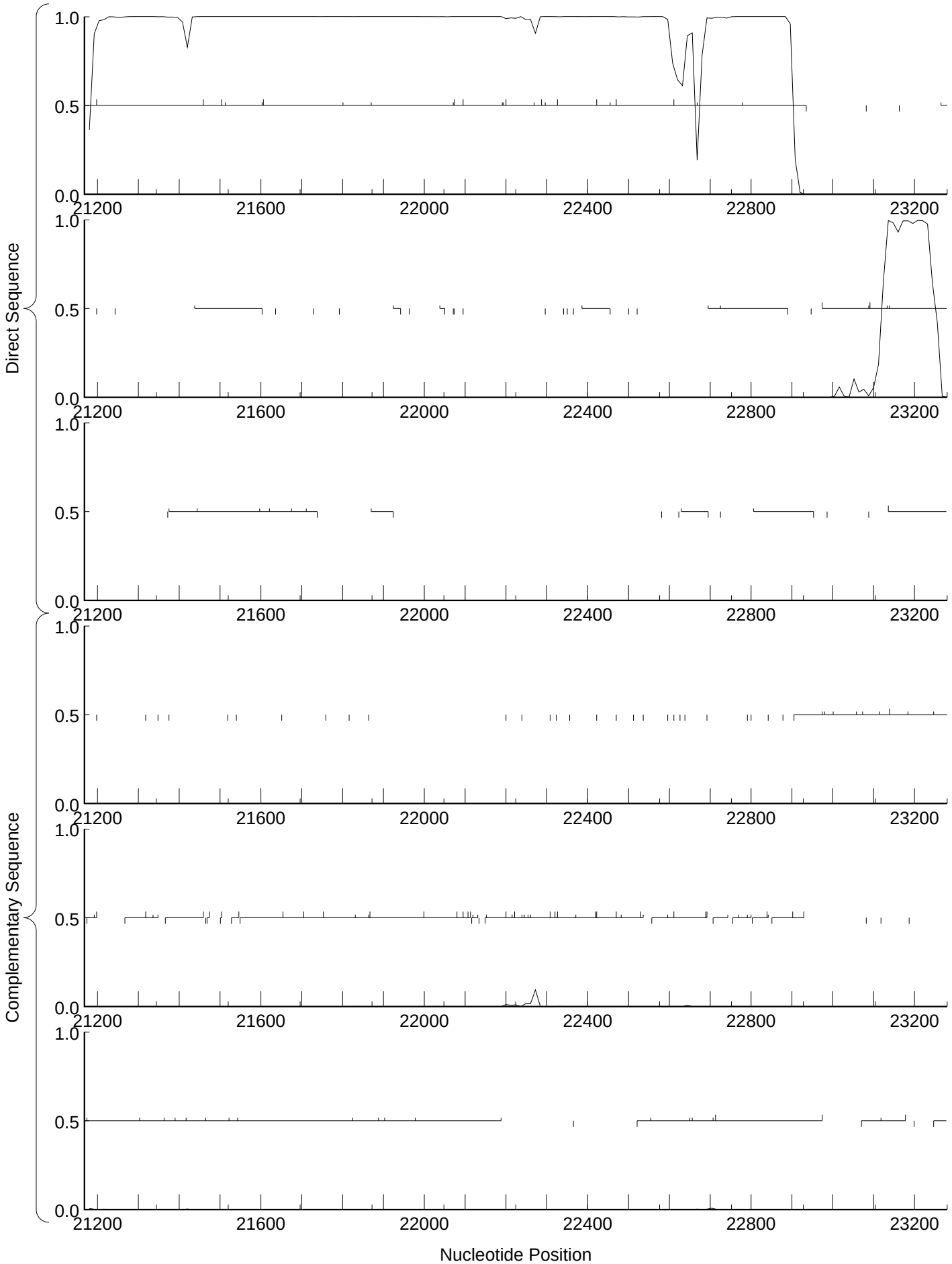



Direct Sequence
Complementary Sequence
1.0
0.5
0.0
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17600
18000
18400
18800
Nucleotide Position

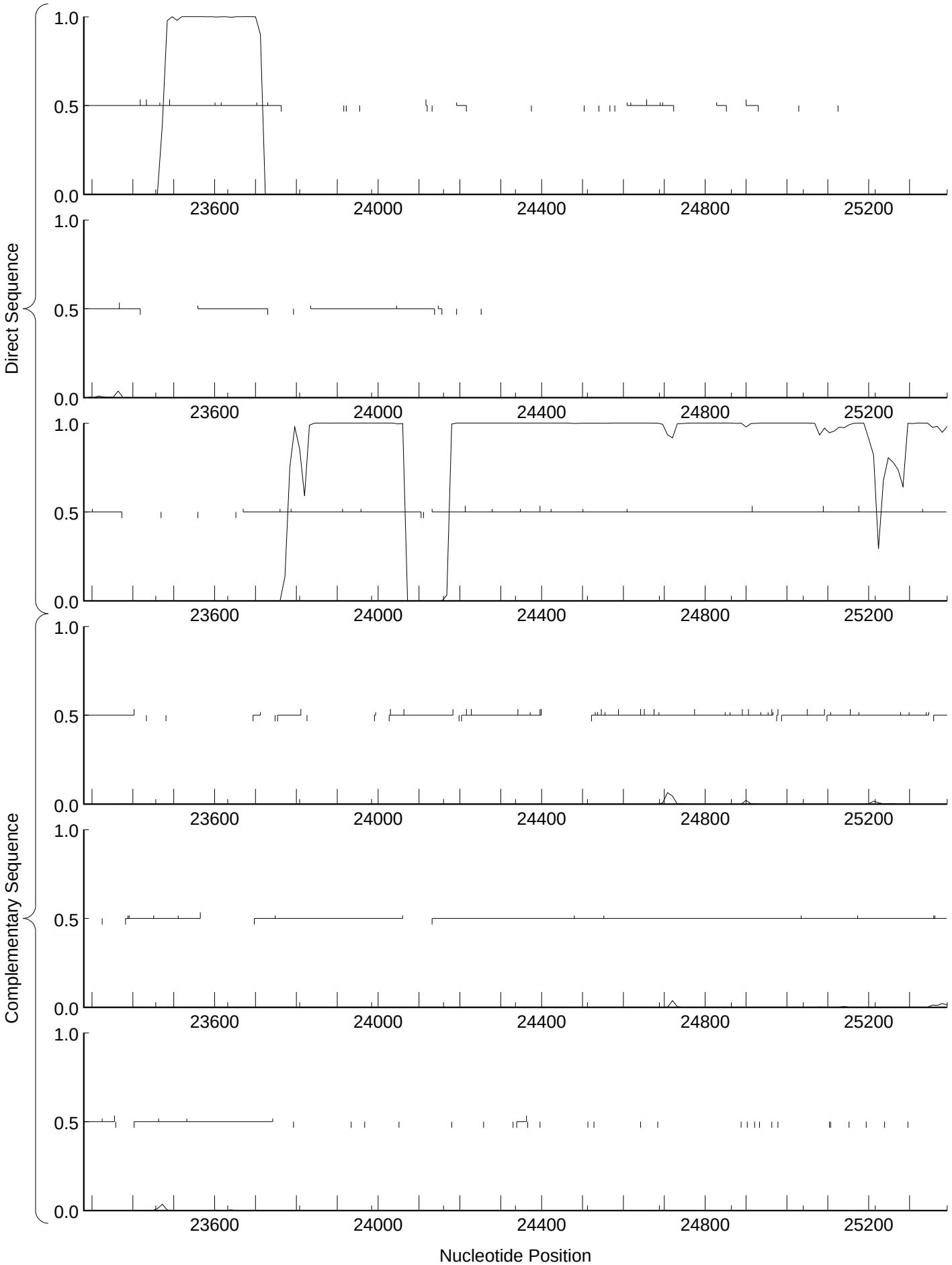
x complete sequence, 50628 bp including 10-base 3' overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 11/25



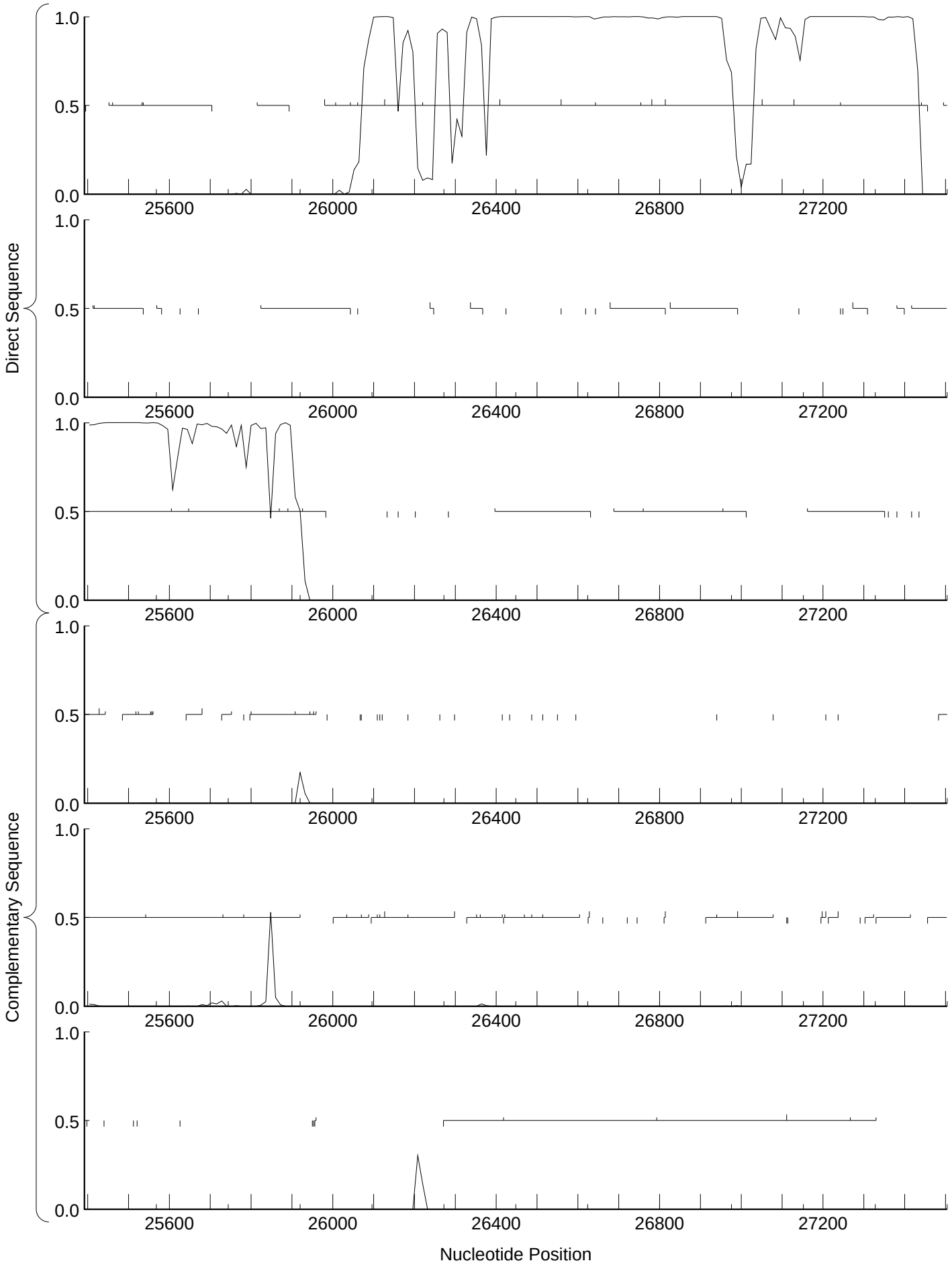
x complete sequence, 50628 bp including 10-base 3' overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 12/25



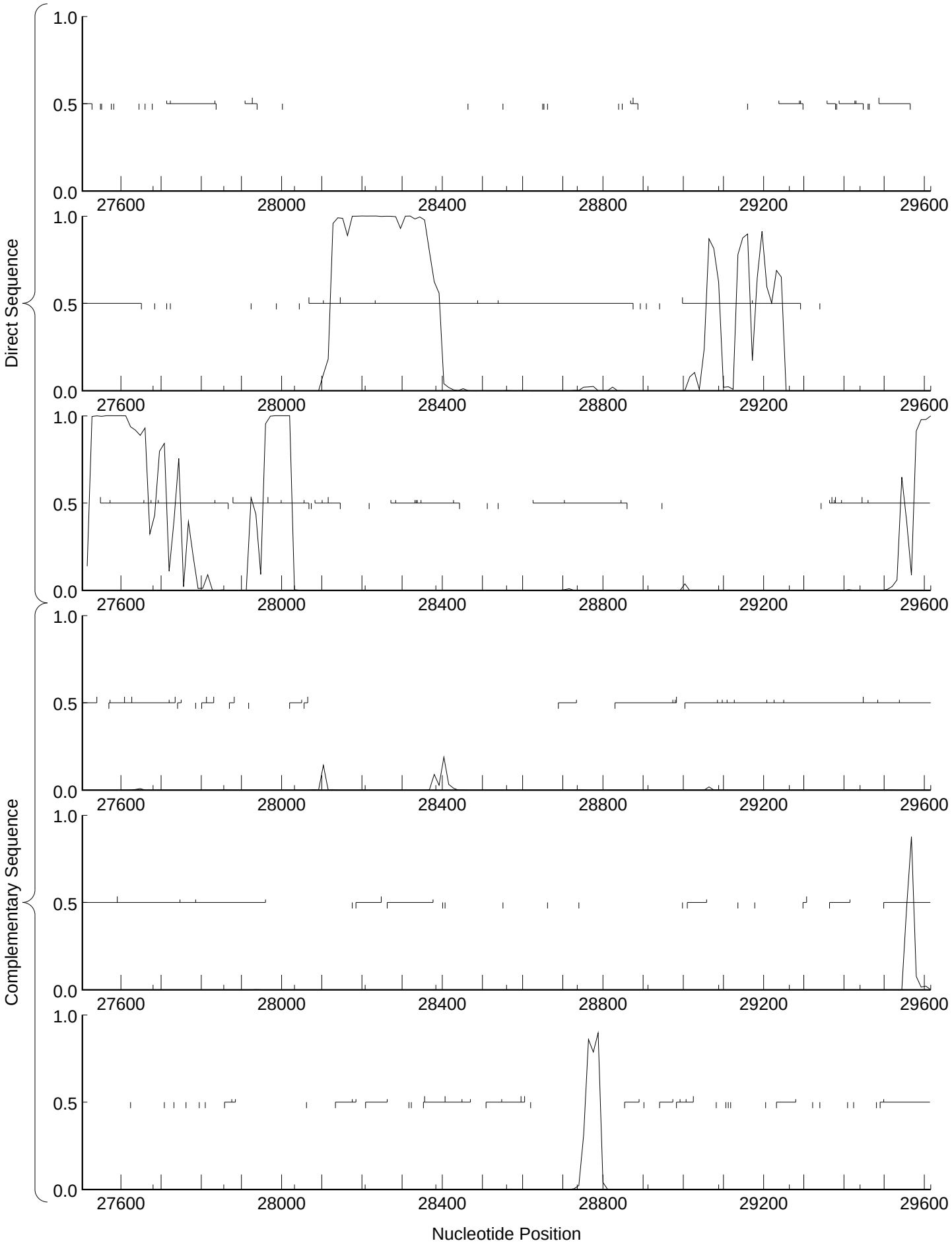
x complete sequence, 50628 bp including 10-base 3' overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 13/25

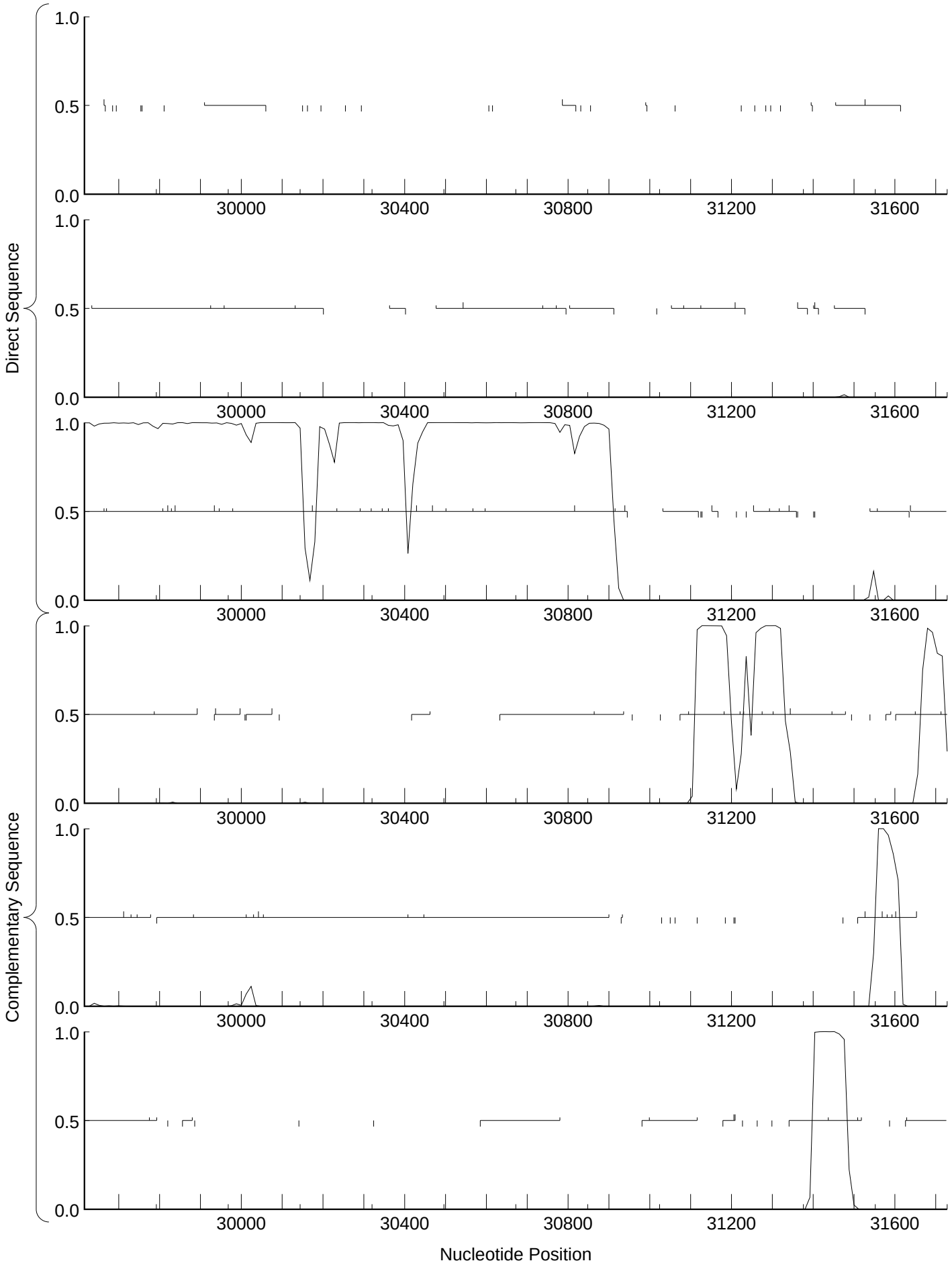


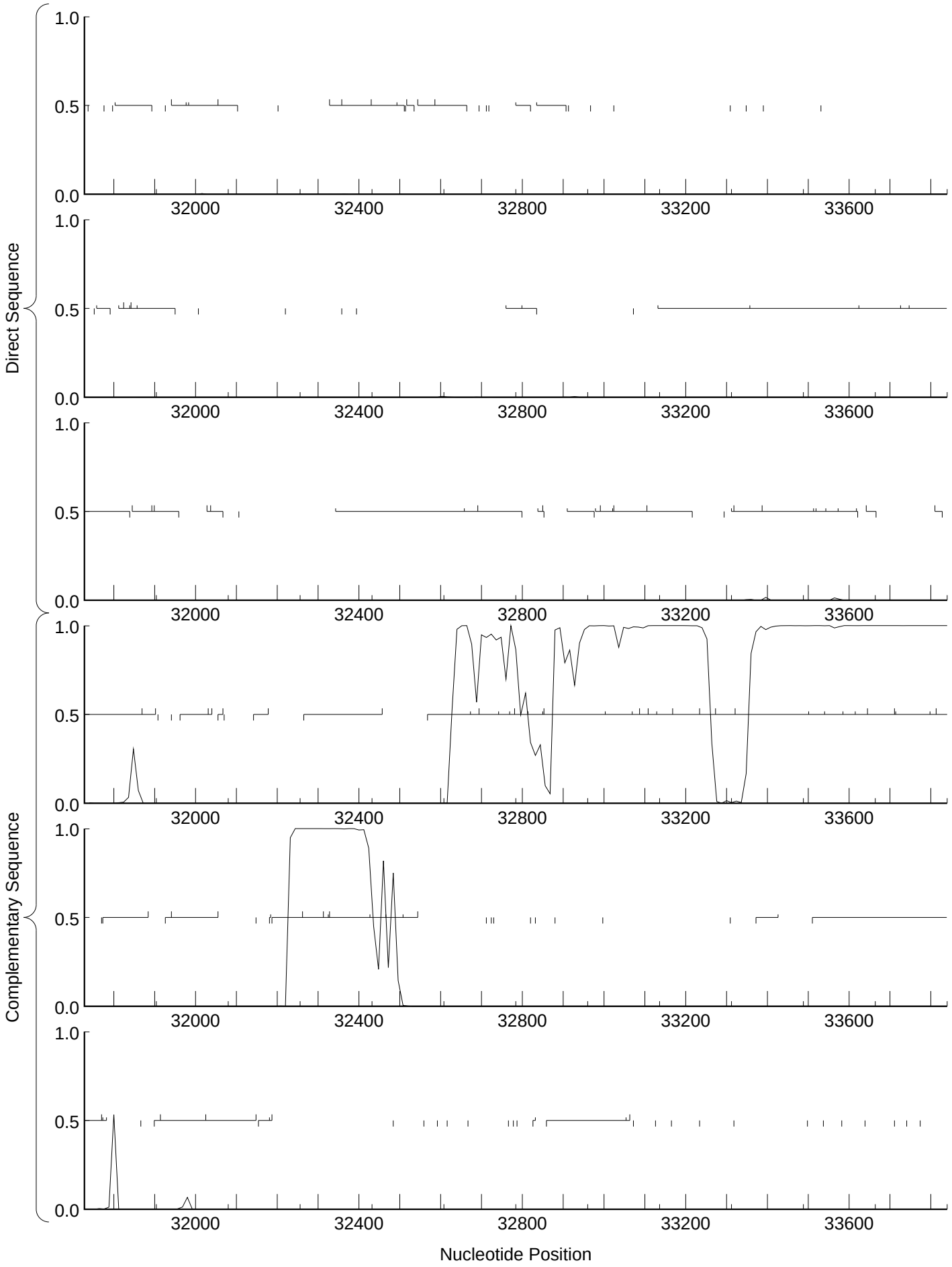
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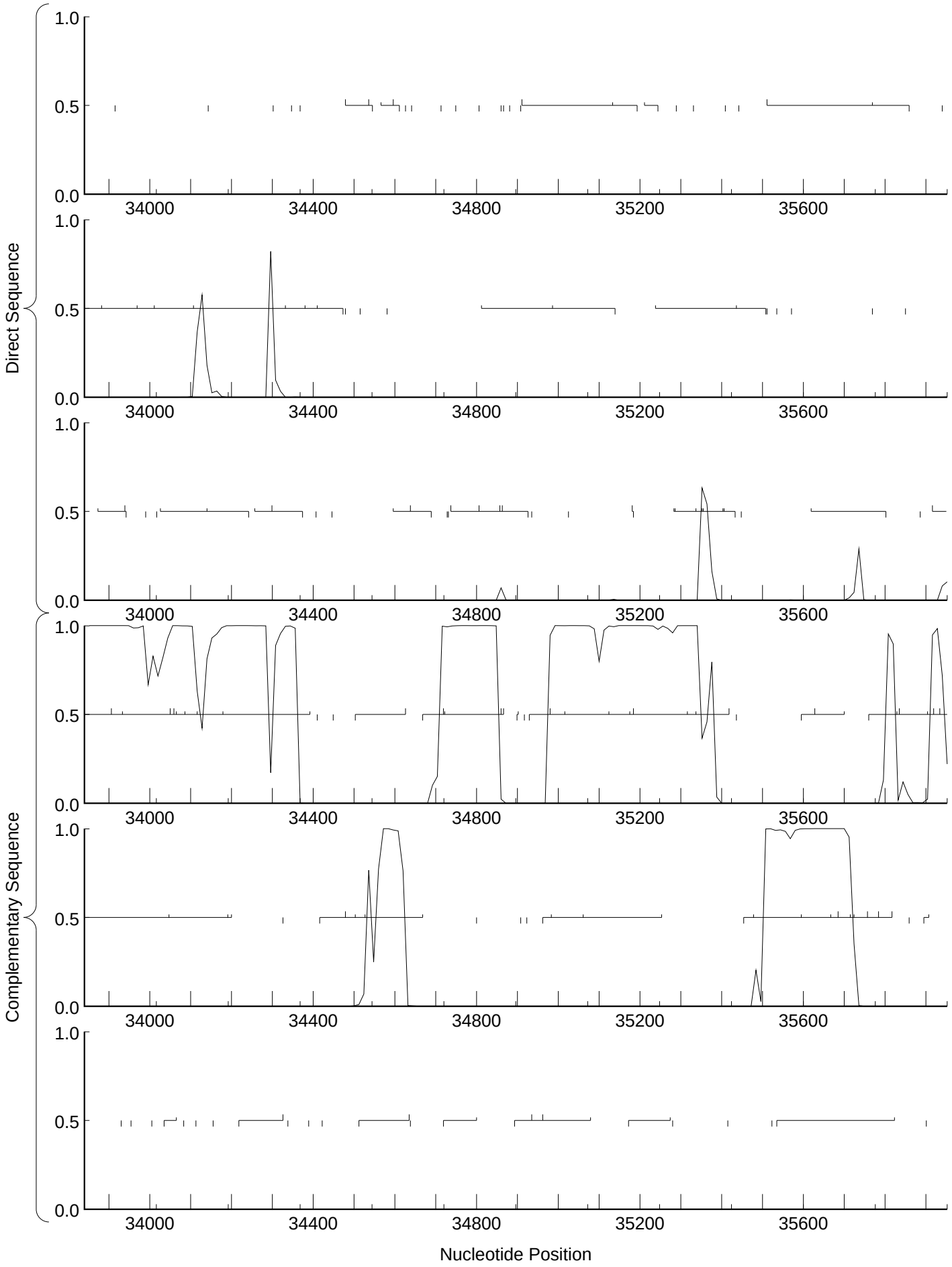


x complete sequence, 50628 bp including 10-base 3’ overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 15/25

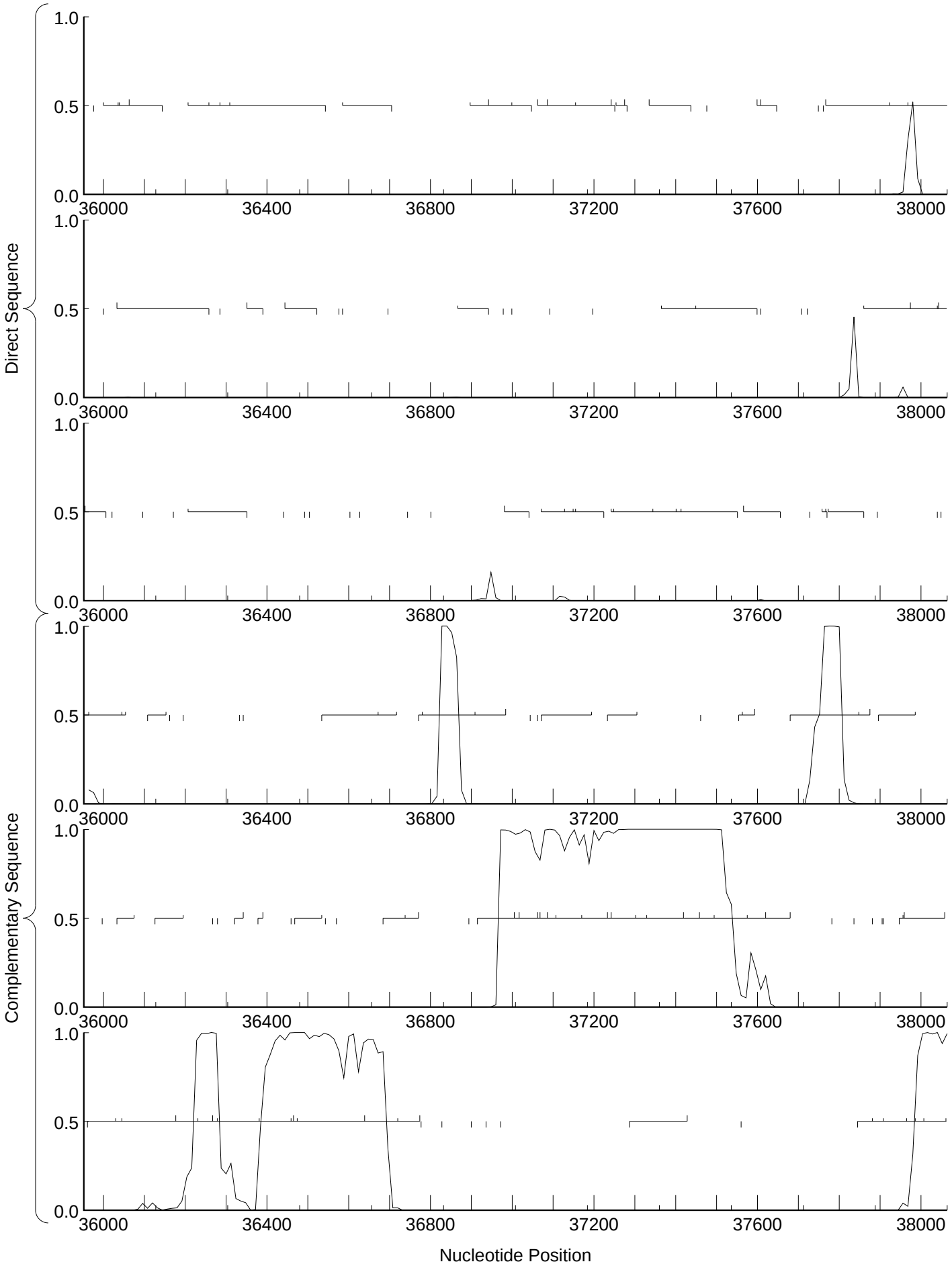


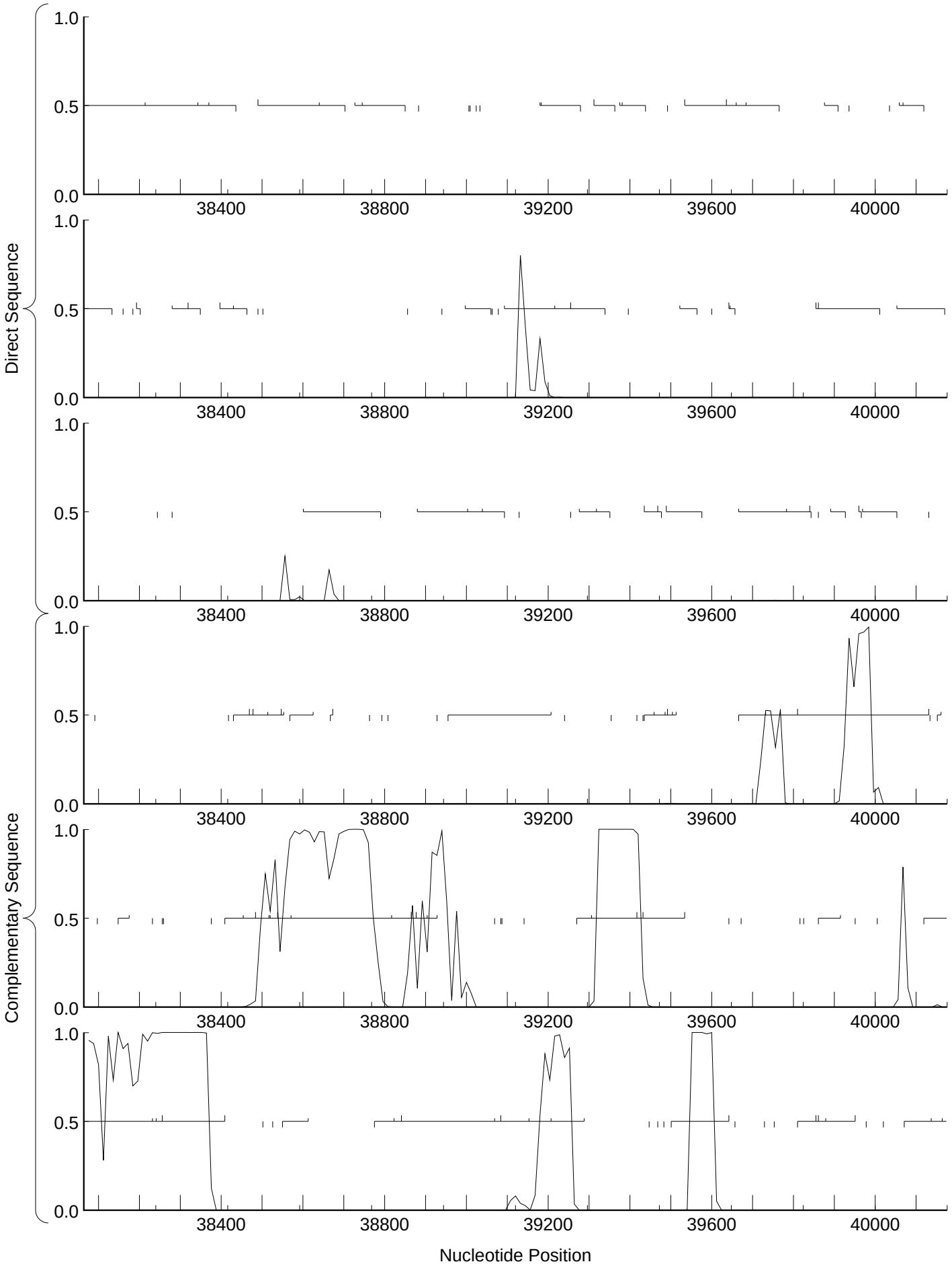

Direct Sequence
Complementary Sequence
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0.5
0.0
30000
30400
30800
31200
31600
Nucleotide Position

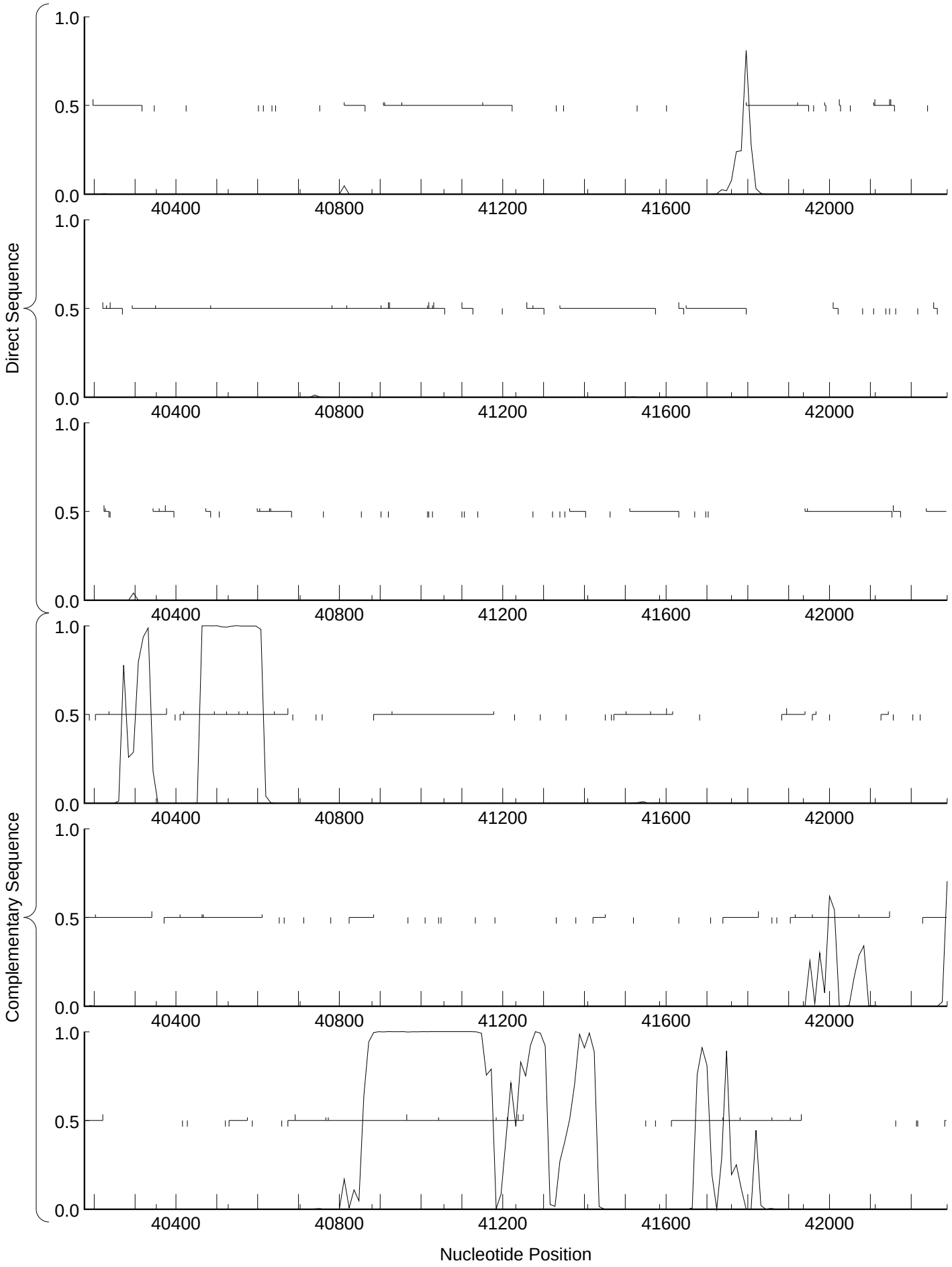

Direct Sequence
Complementary Sequence
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0.5
0.0
32000
32400
32800
33200
33600
Nucleotide Position

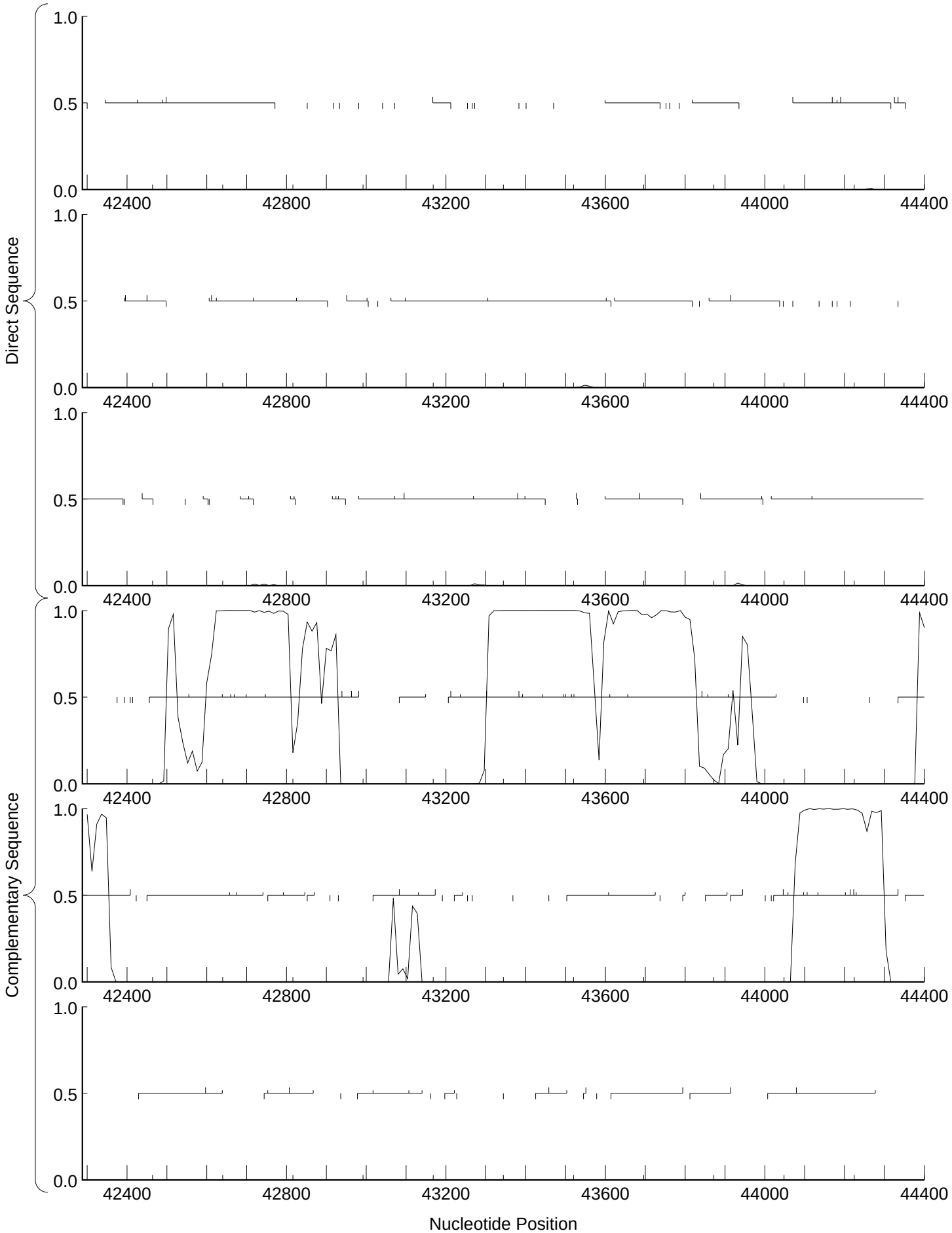

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
34000
34400
34800
35200
35600
Nucleotide Position

x complete sequence, 50628 bp including 10-base 3' overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 19/25

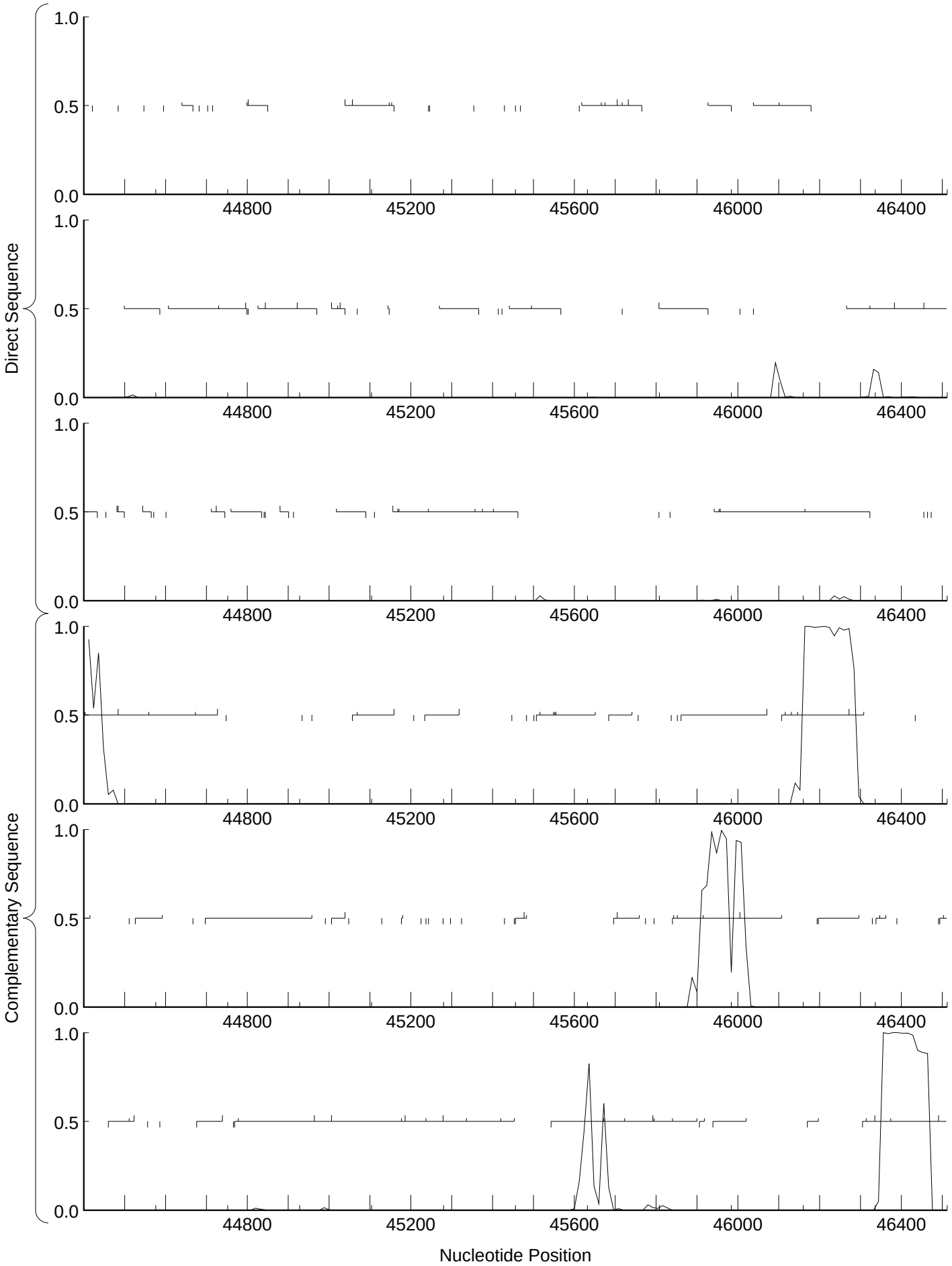



Direct Sequence
Complementary Sequence
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39200
39600
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Nucleotide Position

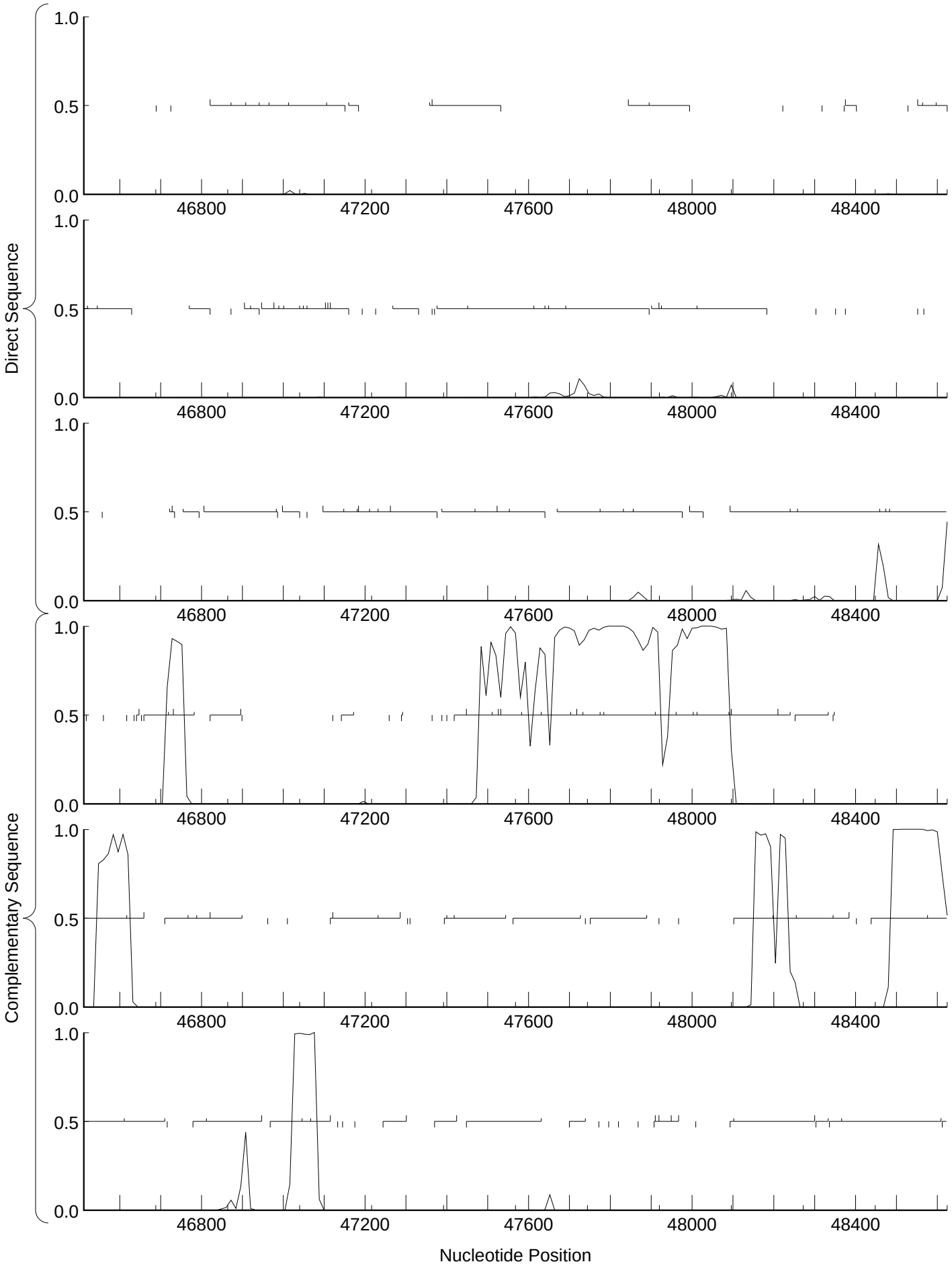

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
40400
40800
41200
41600
42000
Nucleotide Position


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
42400
42800
43200
43600
44000
44400
Nucleotide Position

x complete sequence, 50628 bp including 10-base 3’ overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 23/25



x complete sequence, 50628 bp including 10-base 3’ overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 24/25



x complete sequence, 50628 bp including 10-base 3’ overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 25/25

