GeneMark

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

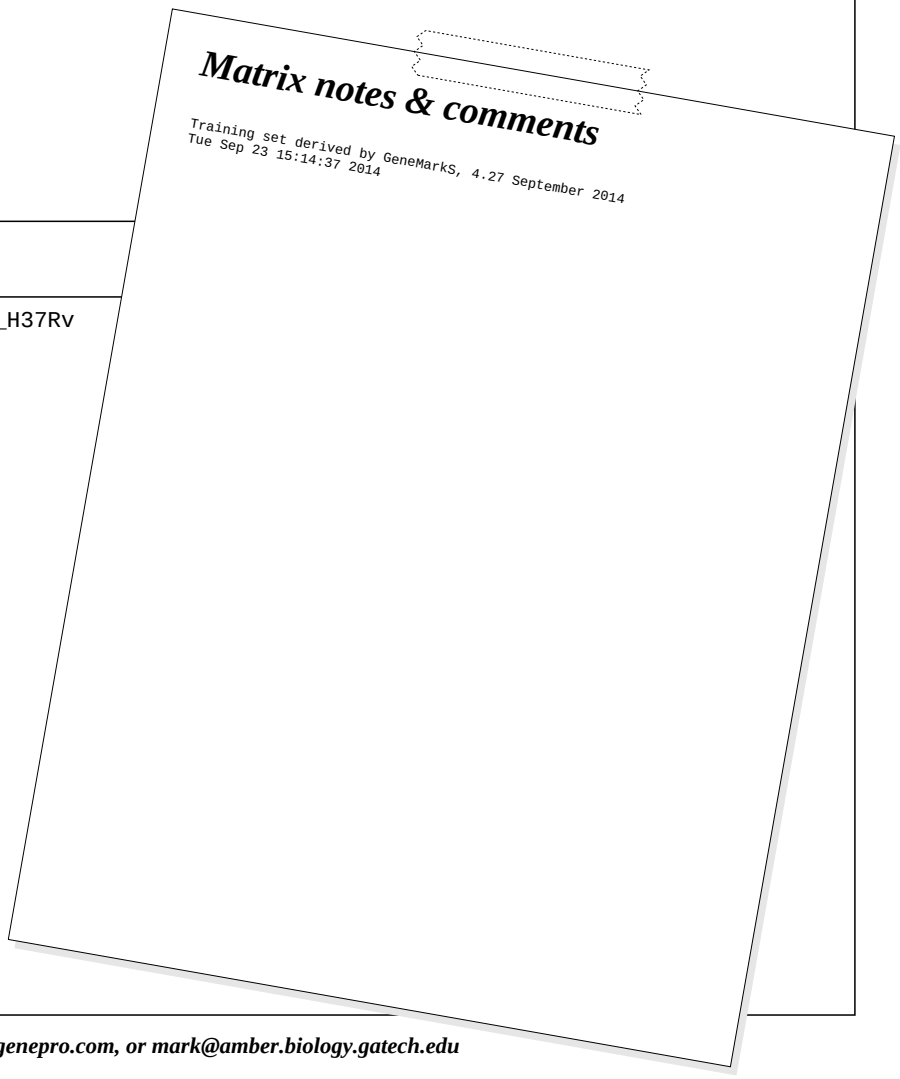
PROGRAM INFORMATION

```
Sequence         :  Mycobacterium phage Papez complete sequence, 52501 bp including 10-base 3’ overhang (CGGATG
Analysis Date    :  3/19/24 at 7:02:42
Pages            :  26
Sequence Length  :  52501 bp
GC Content       :   63.79%

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

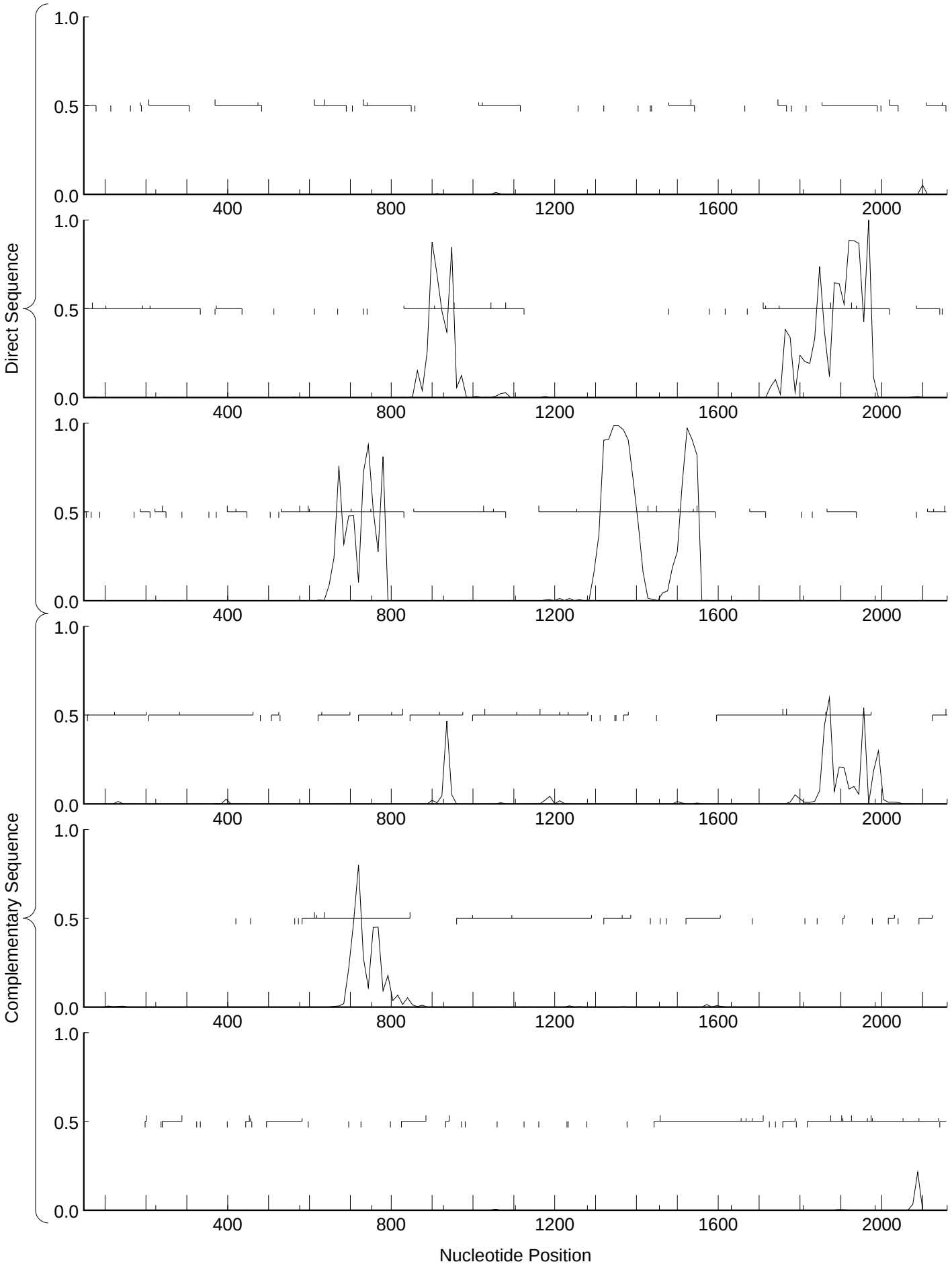
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Matrix     :  Mycobacterium_tuberculosis_H37Rv
Author     :  -

Order      :  4

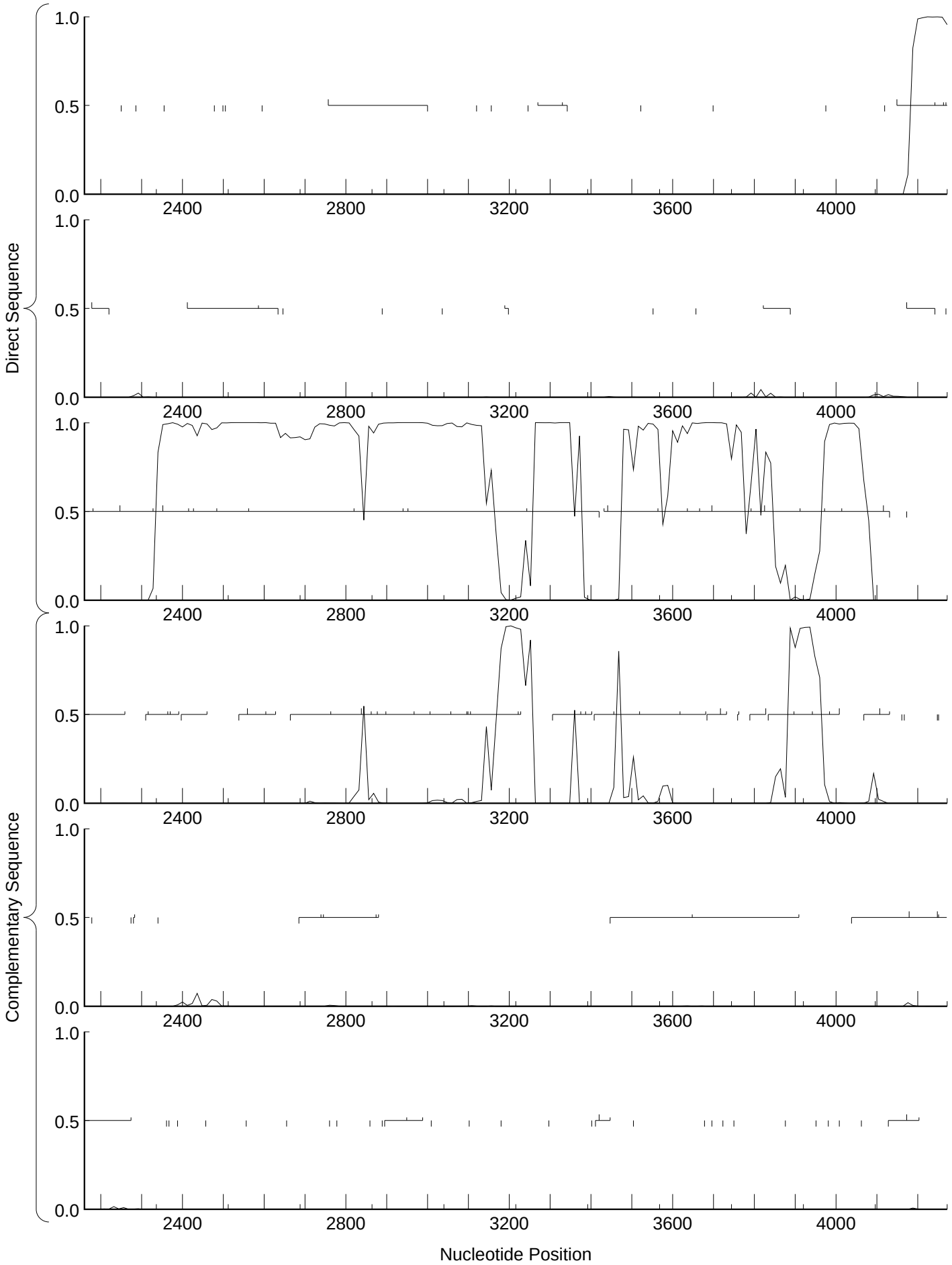

  Send questions / comments to:
      Dr. M. Borodovsky
      Georgia Institute of Technology
      School of Biology
      Atlanta, GA  30332-0230
```

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

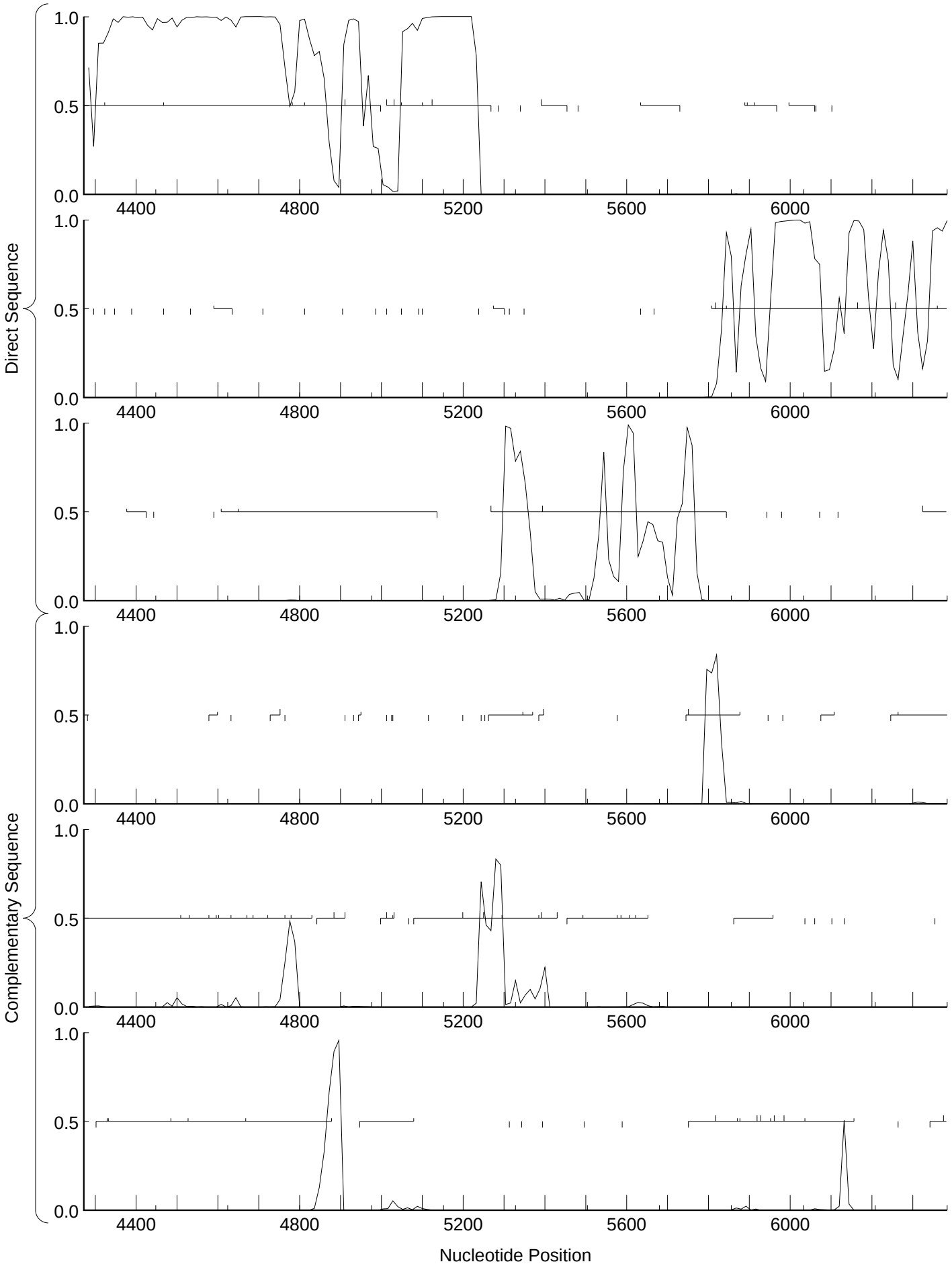
ez complete sequence, 52501 bp including 10-base 3’ overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 2/26

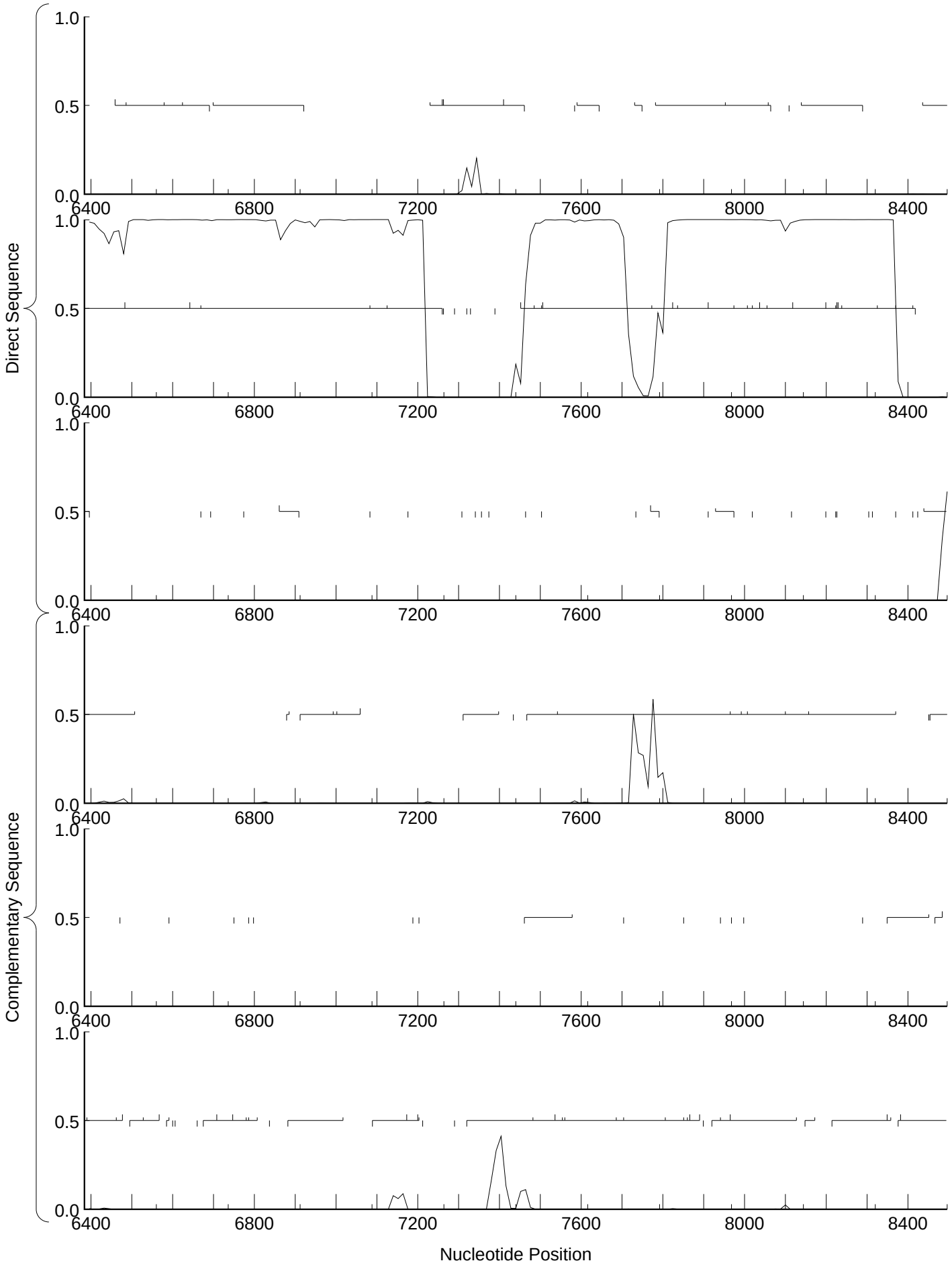


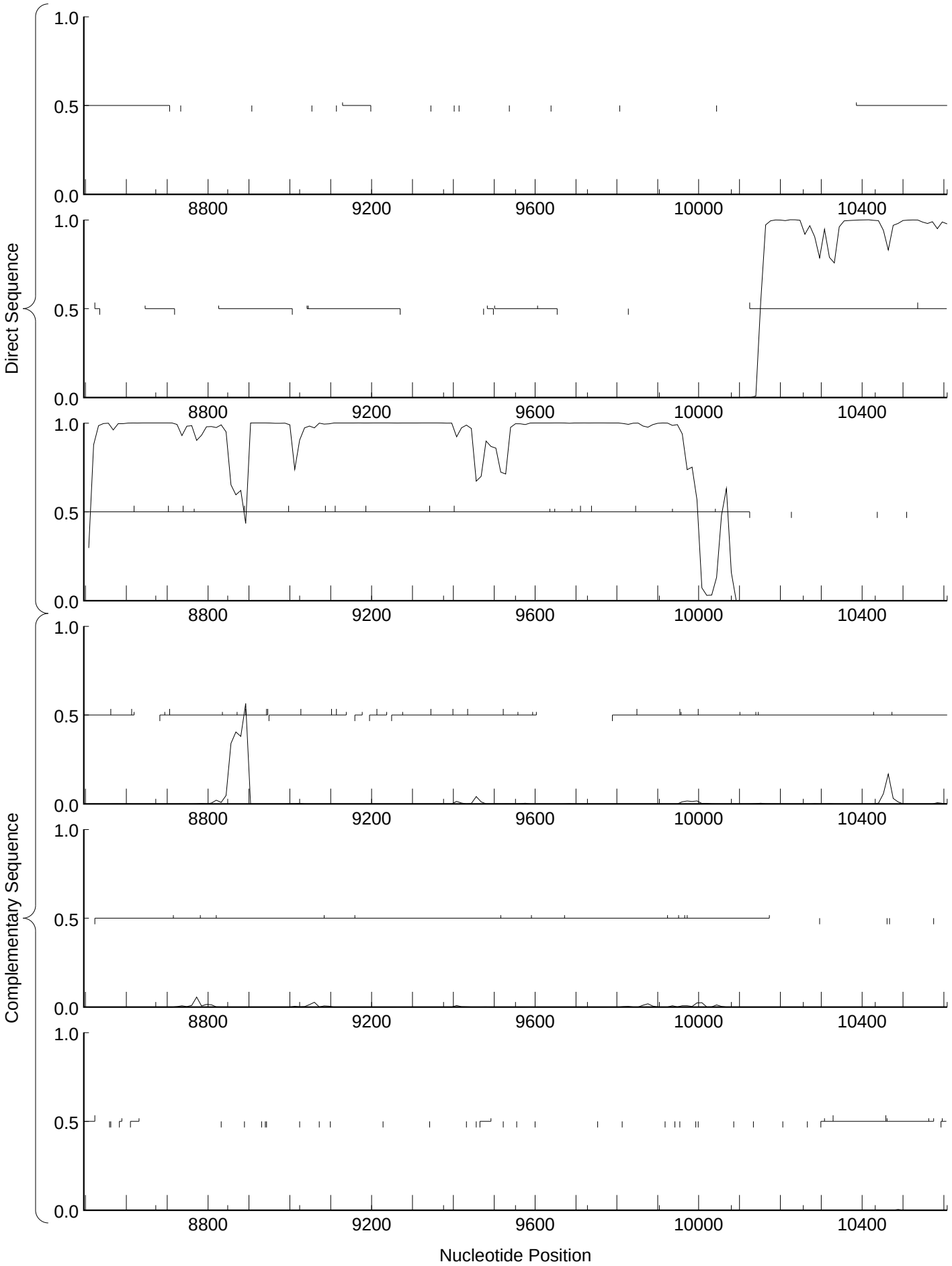
ez complete sequence, 52501 bp including 10-base 3’ overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 3/26



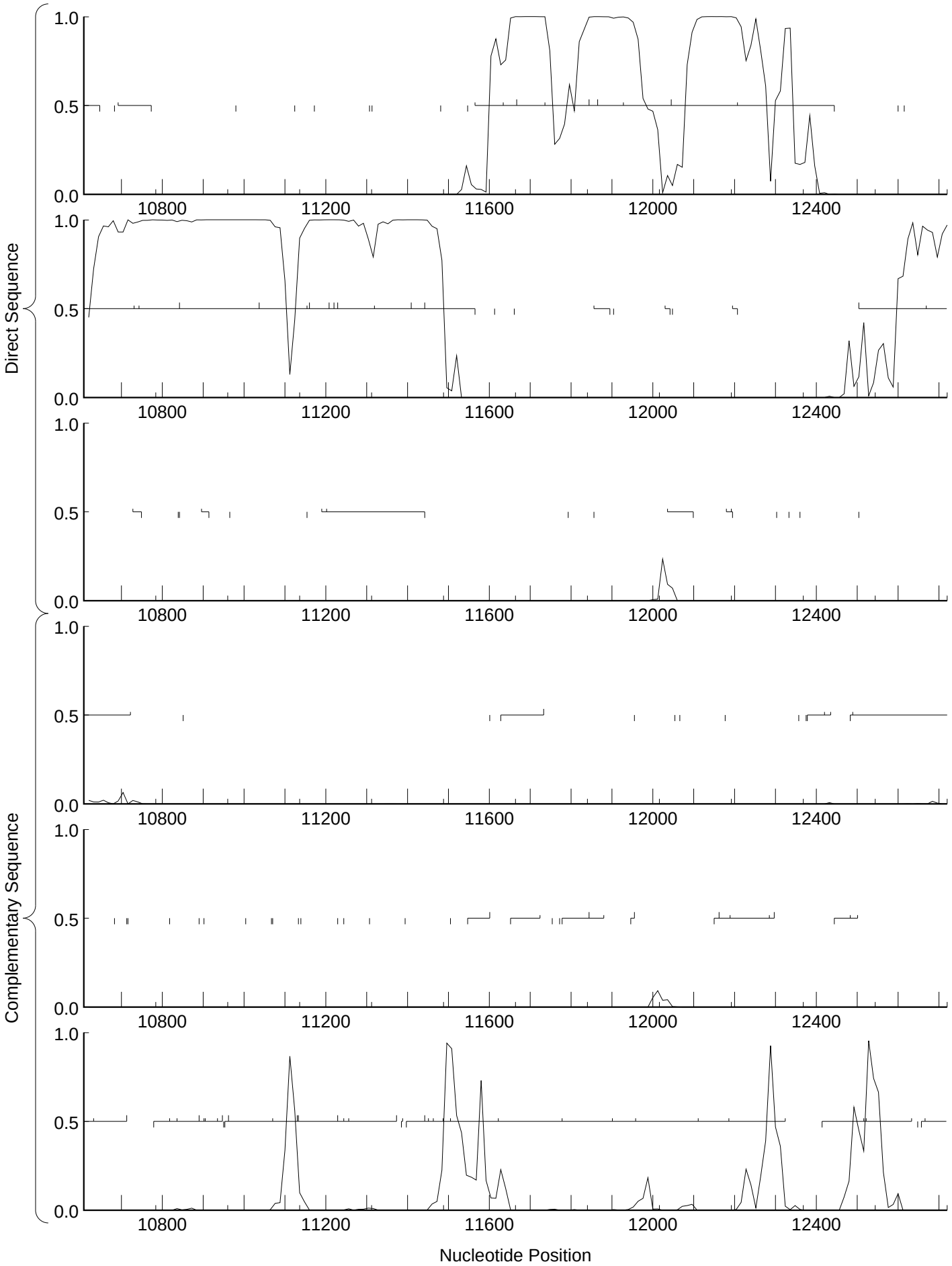
ez complete sequence, 52501 bp including 10-base 3’ overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 4/26



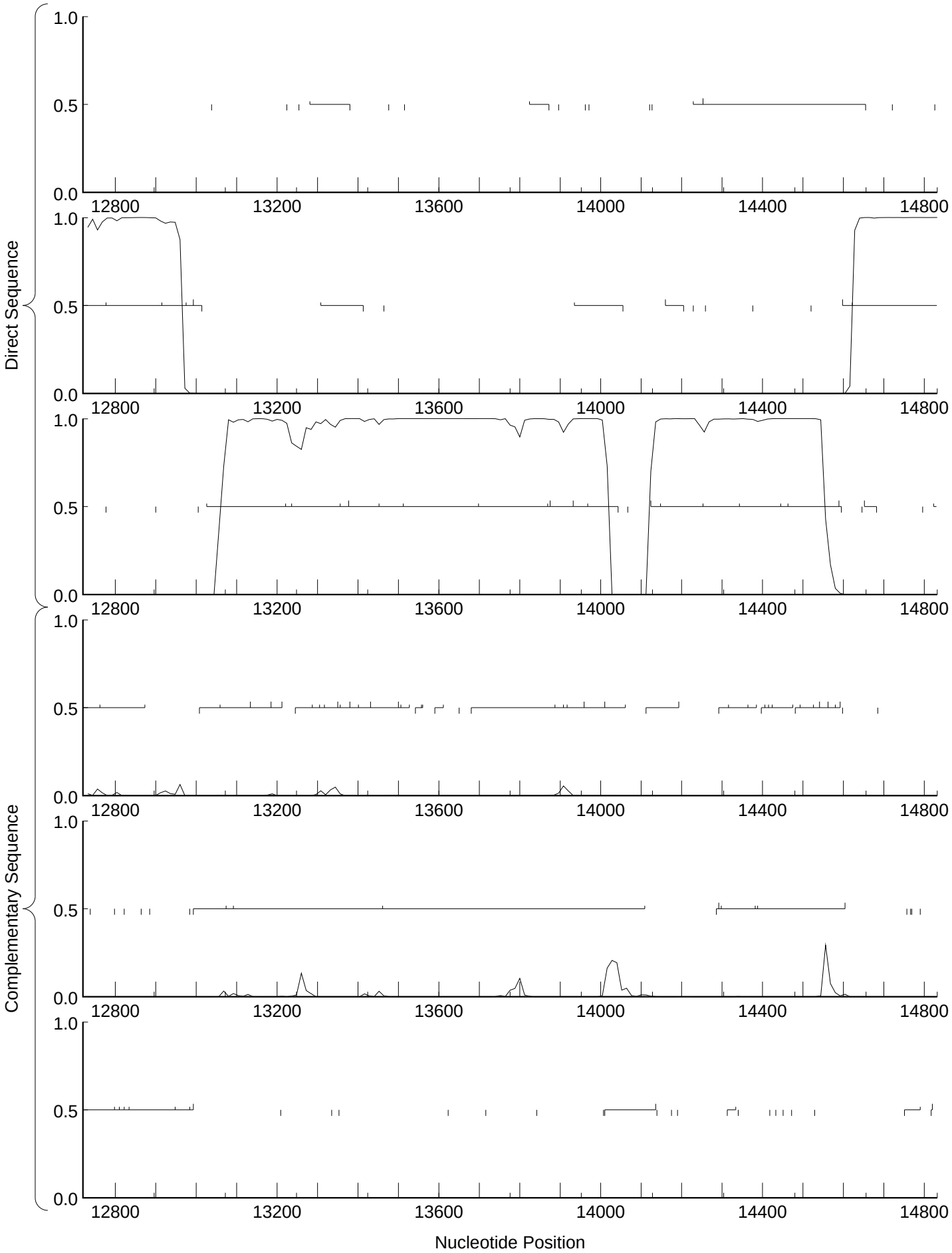

Direct Sequence
Complementary Sequence
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0.5
0.0
6400
6800
7200
7600
8000
8400
Nucleotide Position


Direct Sequence
Complementary Sequence
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0.0
8800
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9600
10000
10400
Nucleotide Position

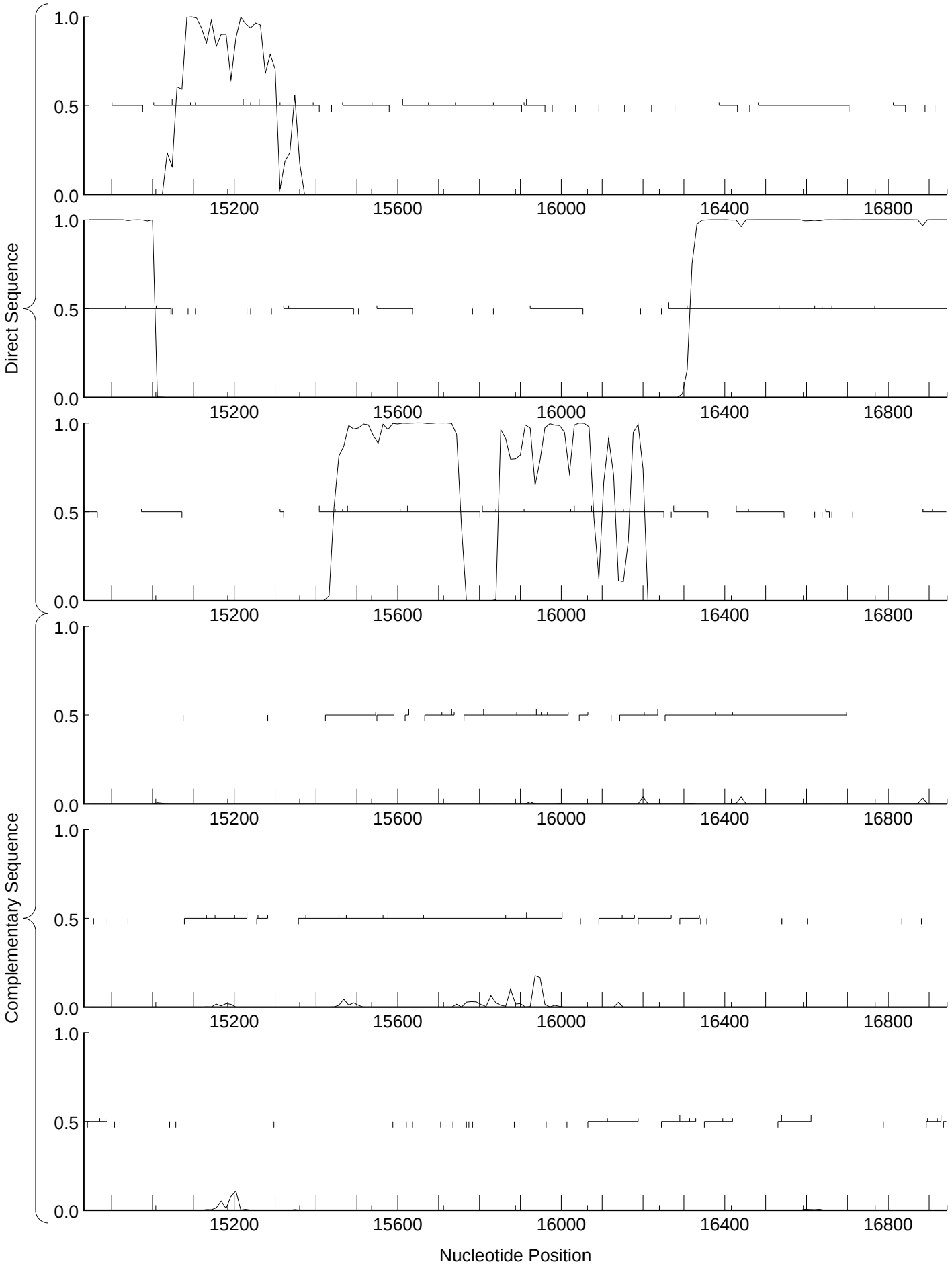
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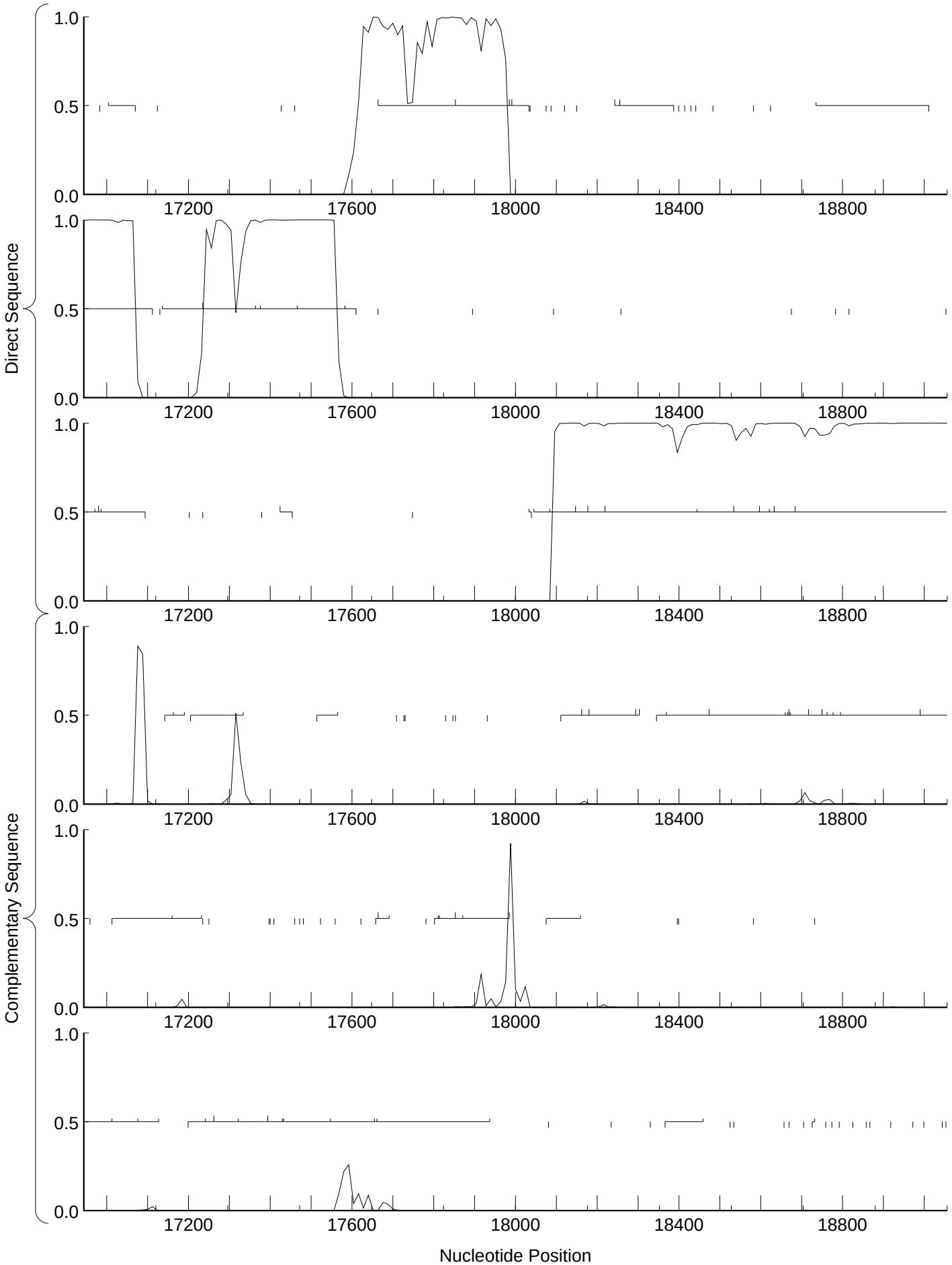


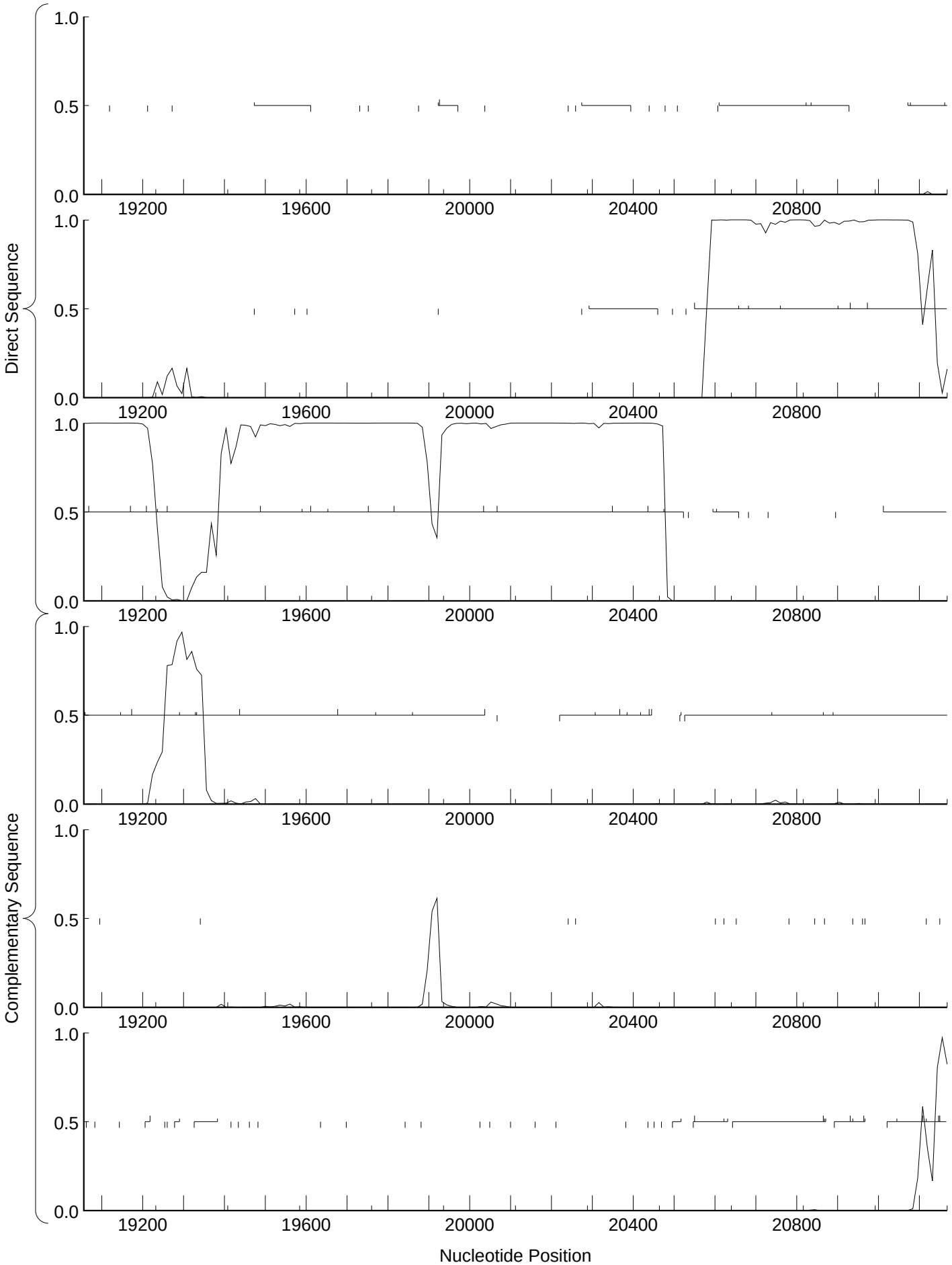
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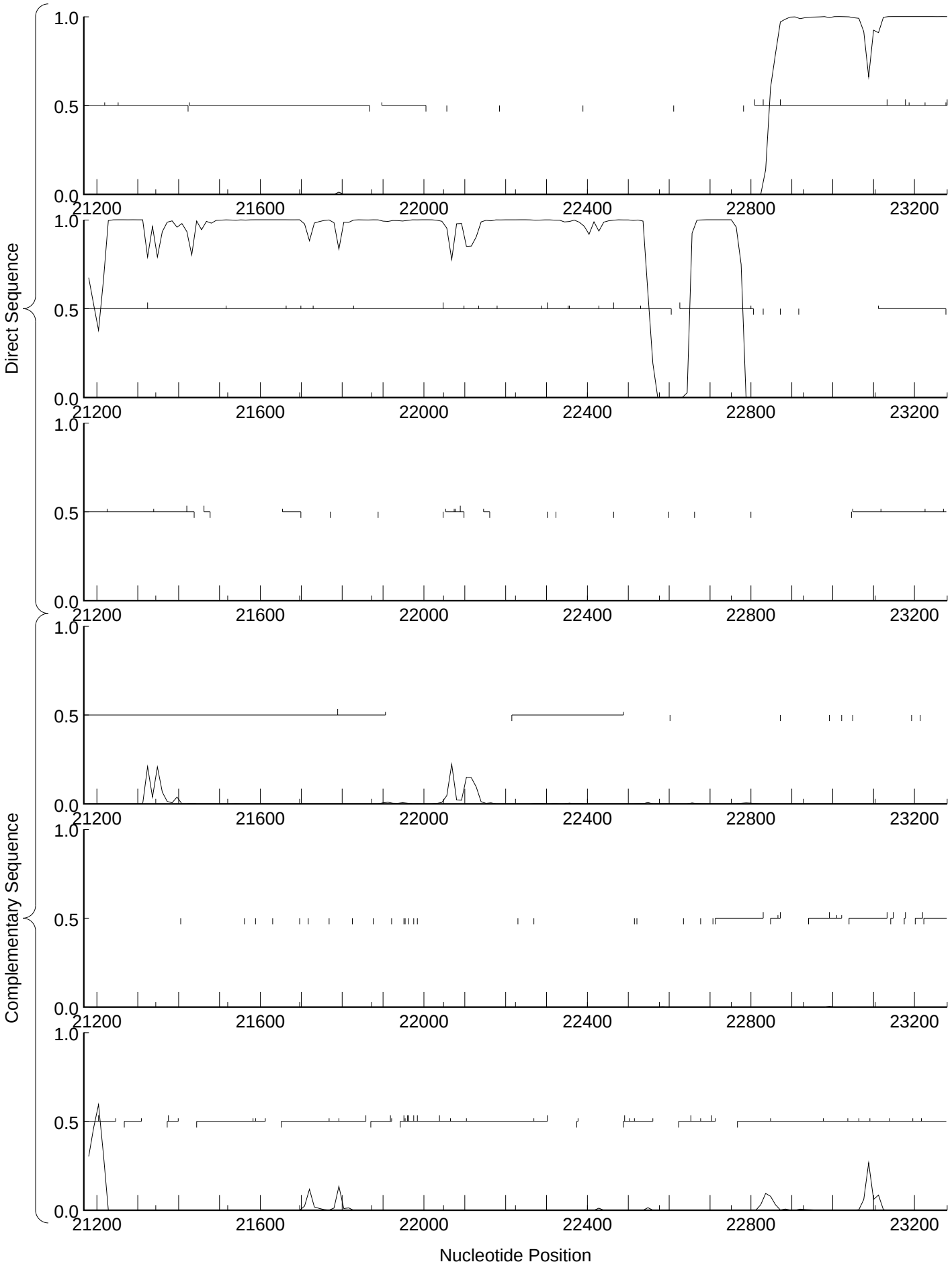


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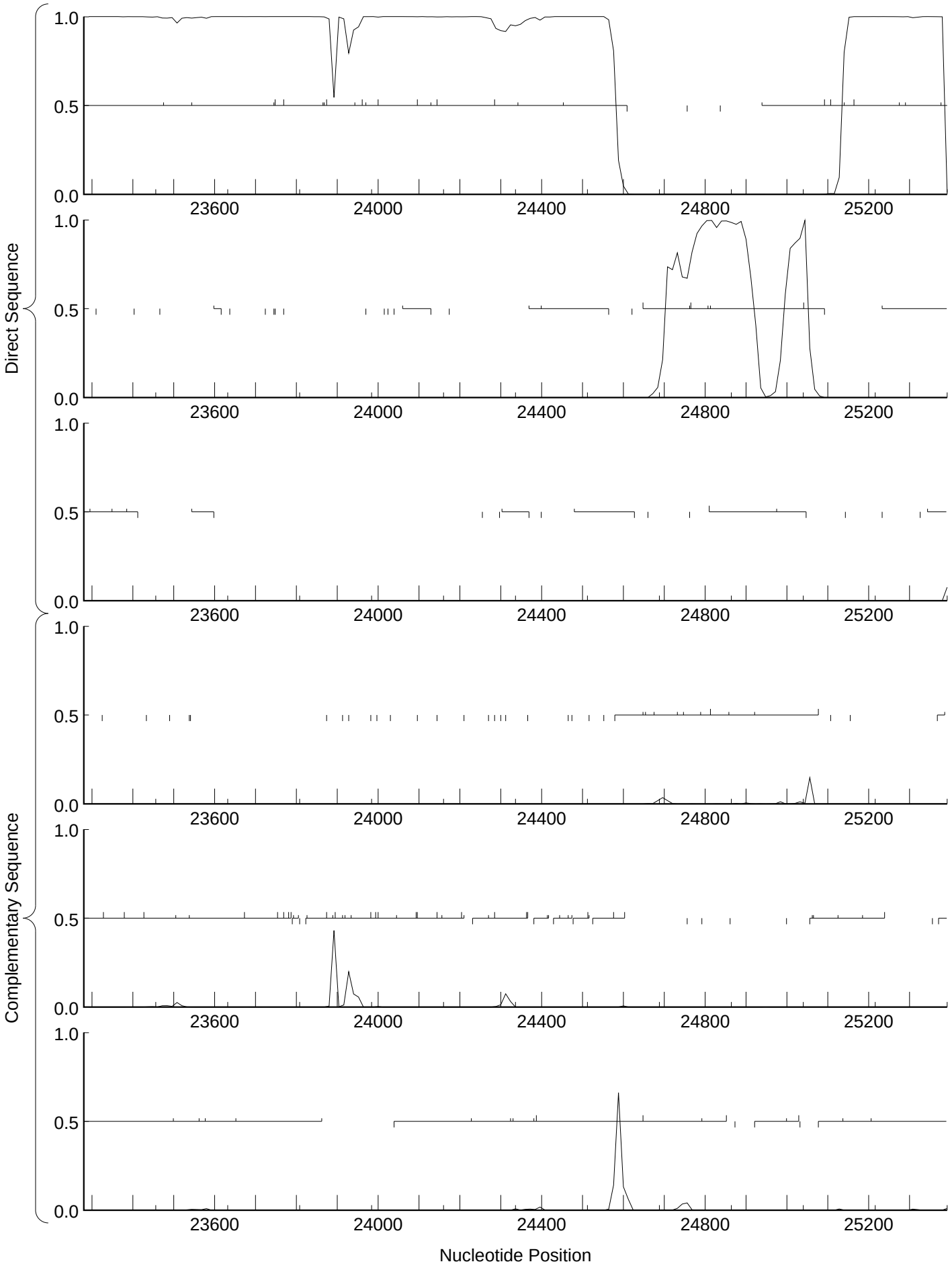


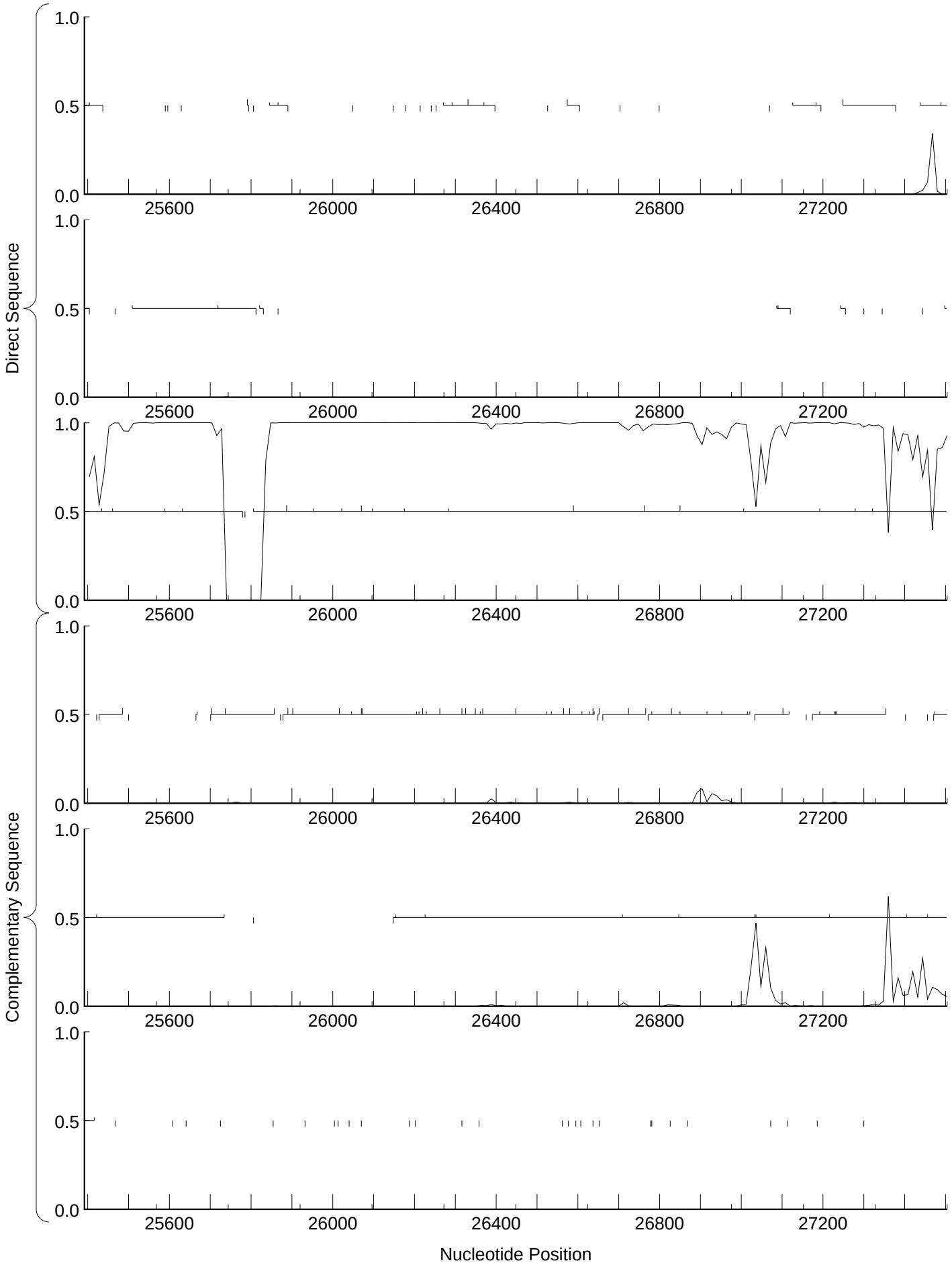

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Complementary Sequence
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18000
18400
18800
Nucleotide Position

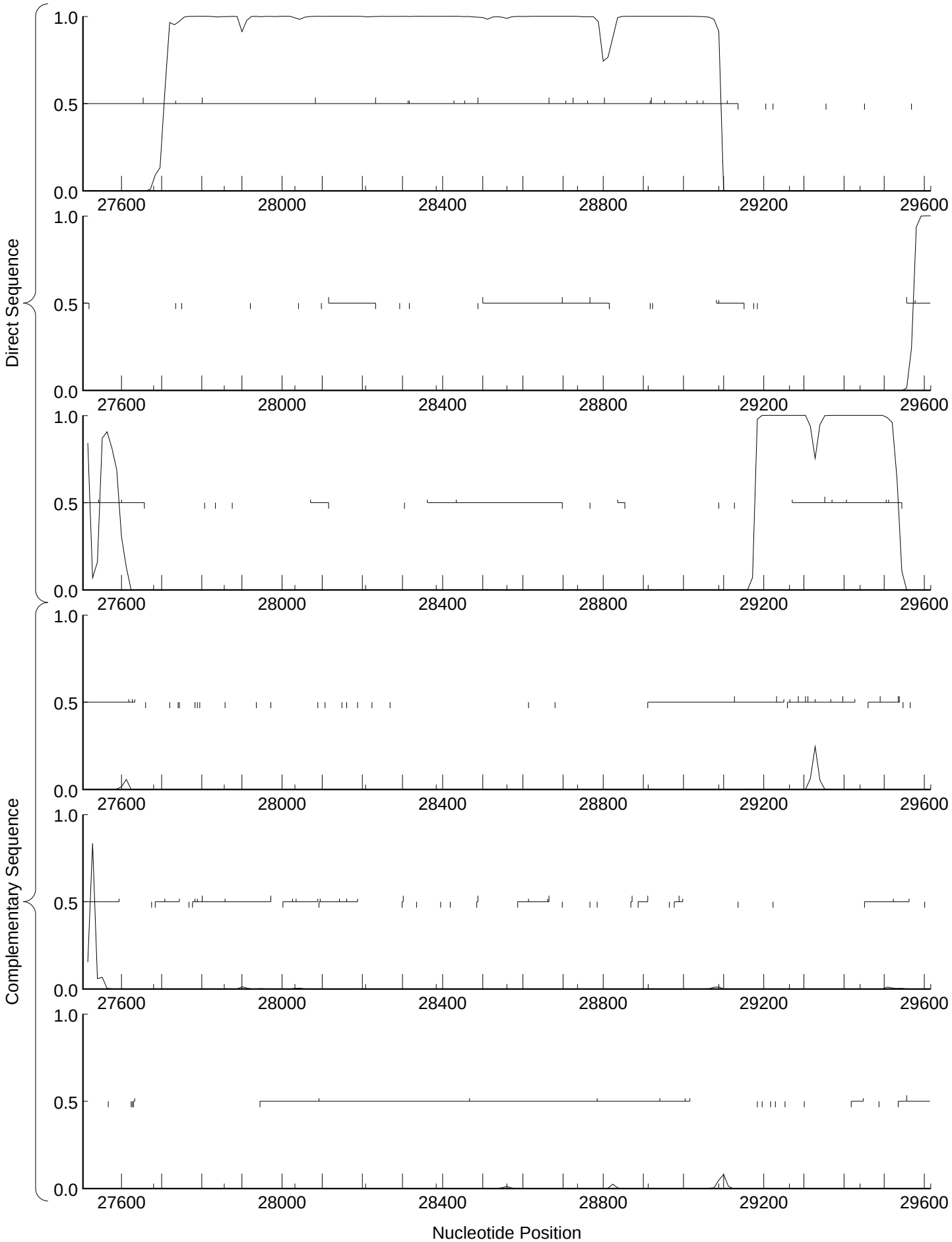

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Nucleotide Position

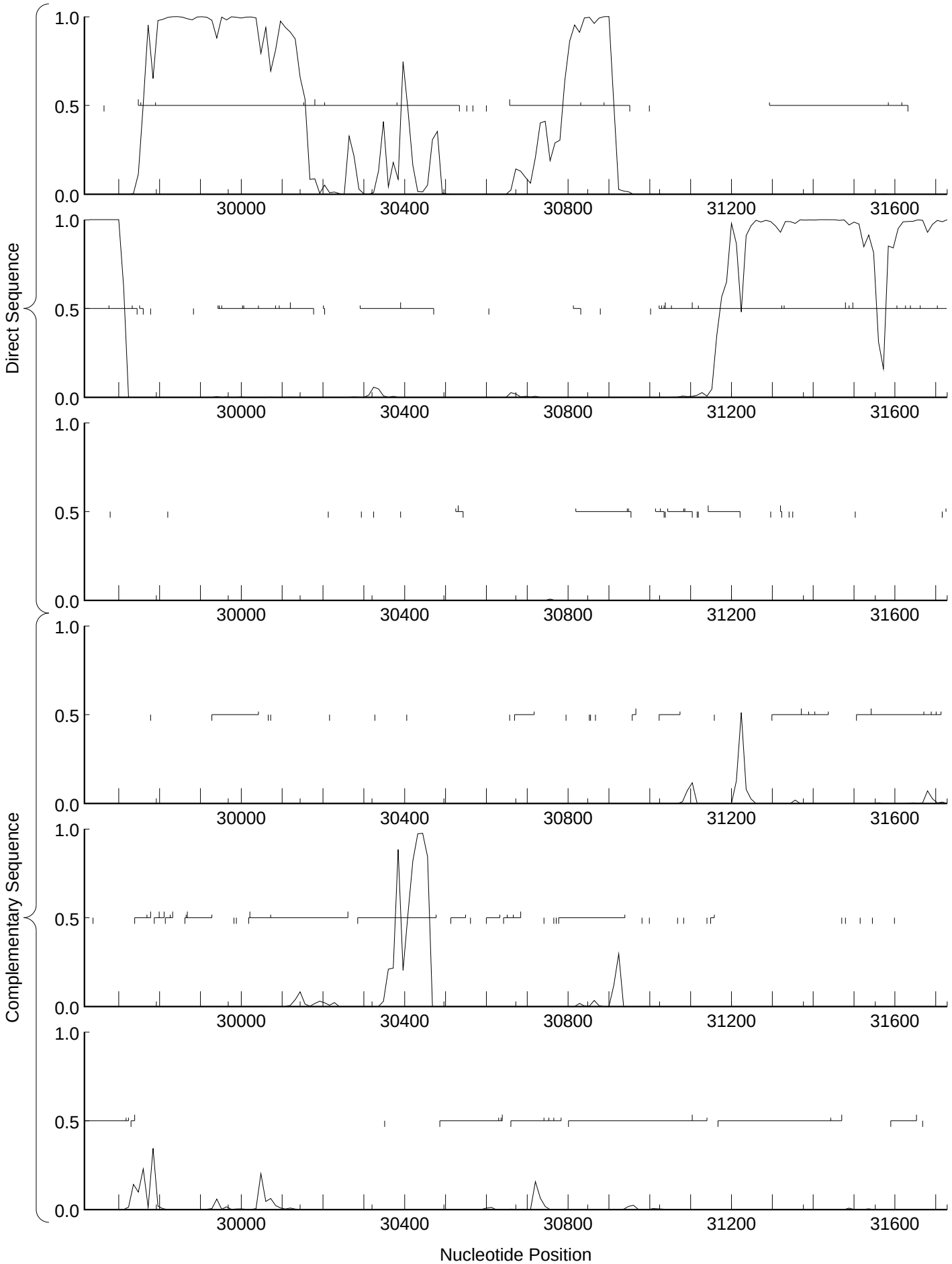

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23200
Nucleotide Position

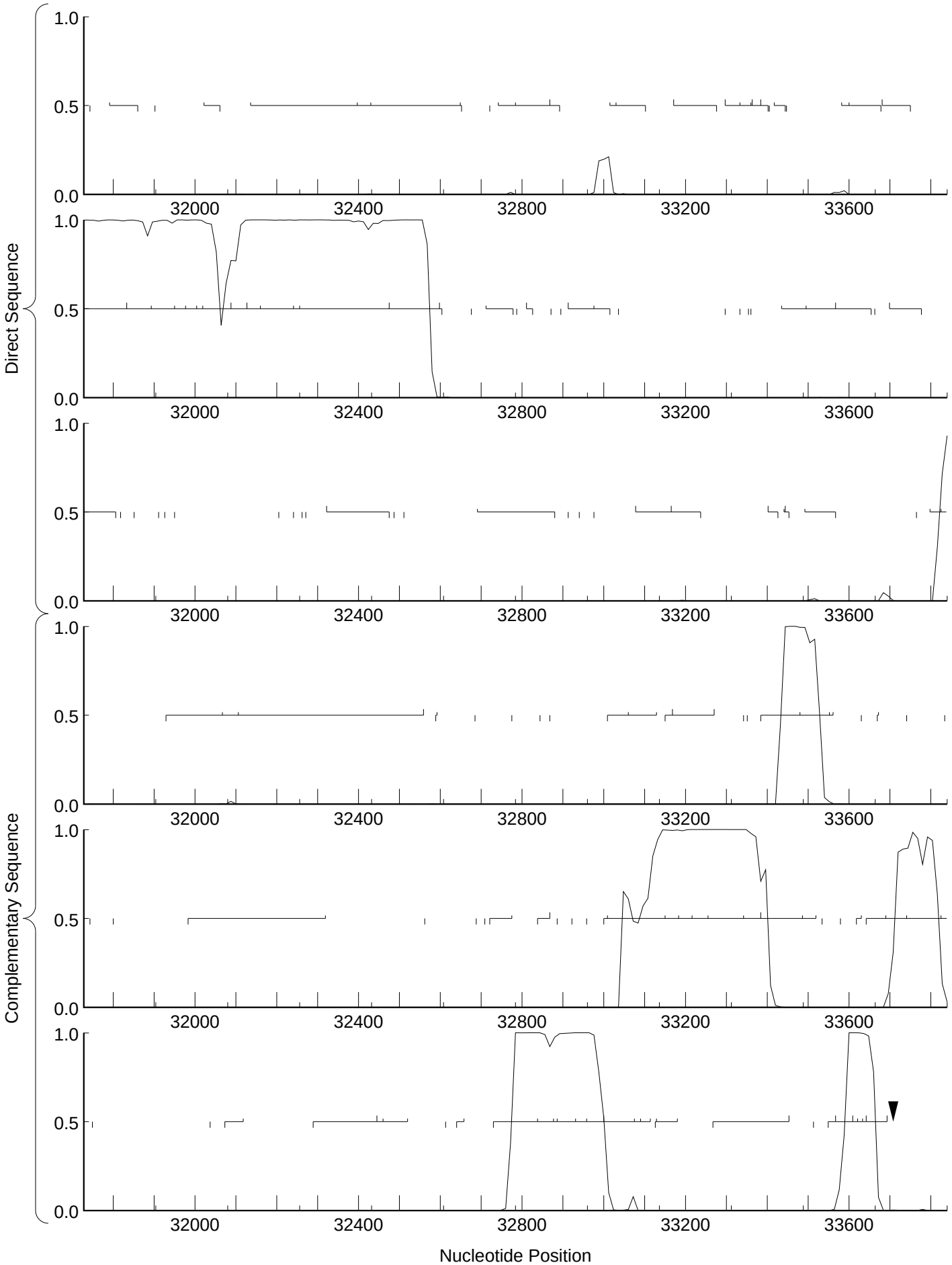
complete sequence, 52501 bp including 10-base 3' overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 13/26

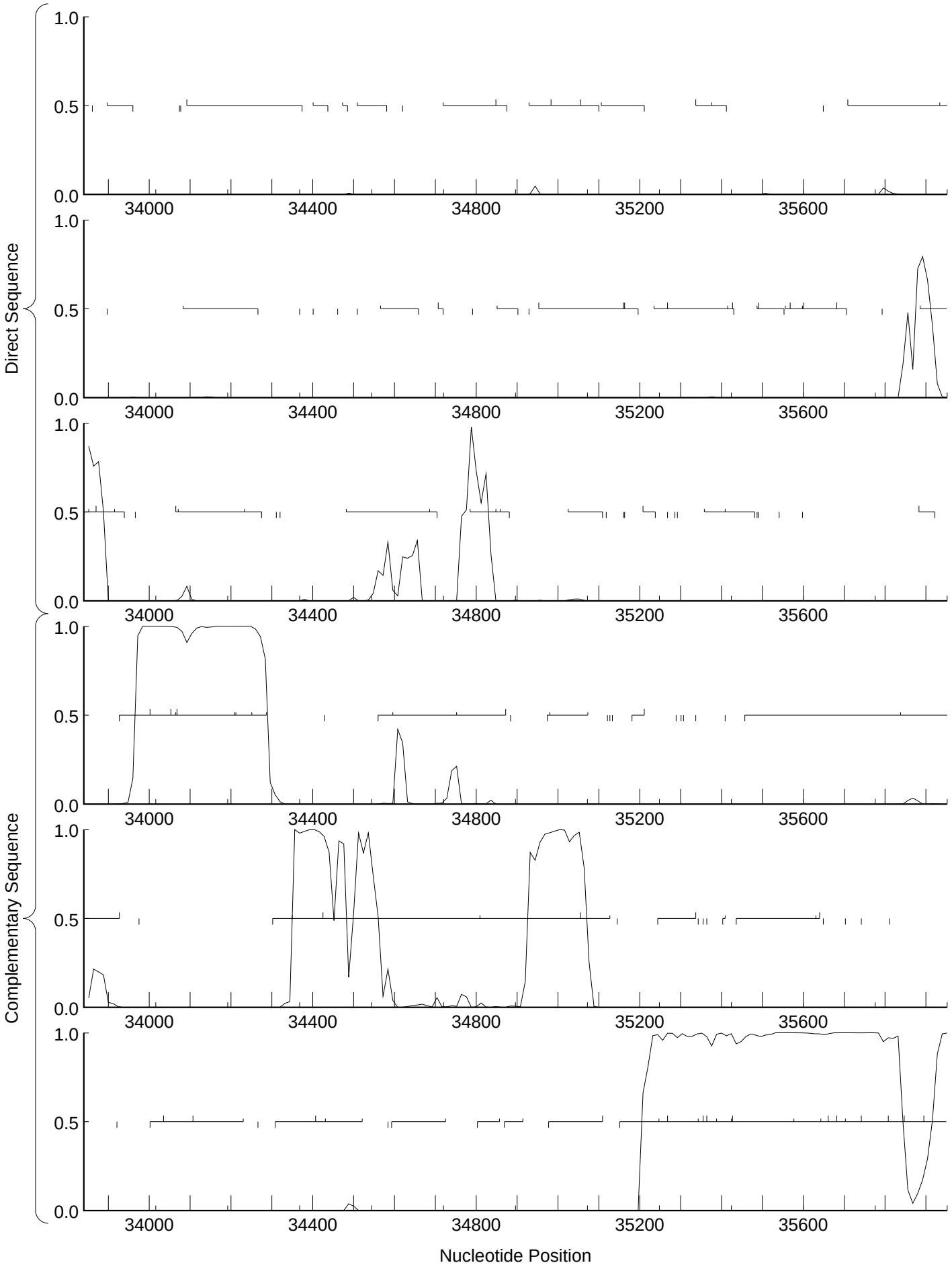



Direct Sequence
Complementary Sequence
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27200
Nucleotide Position

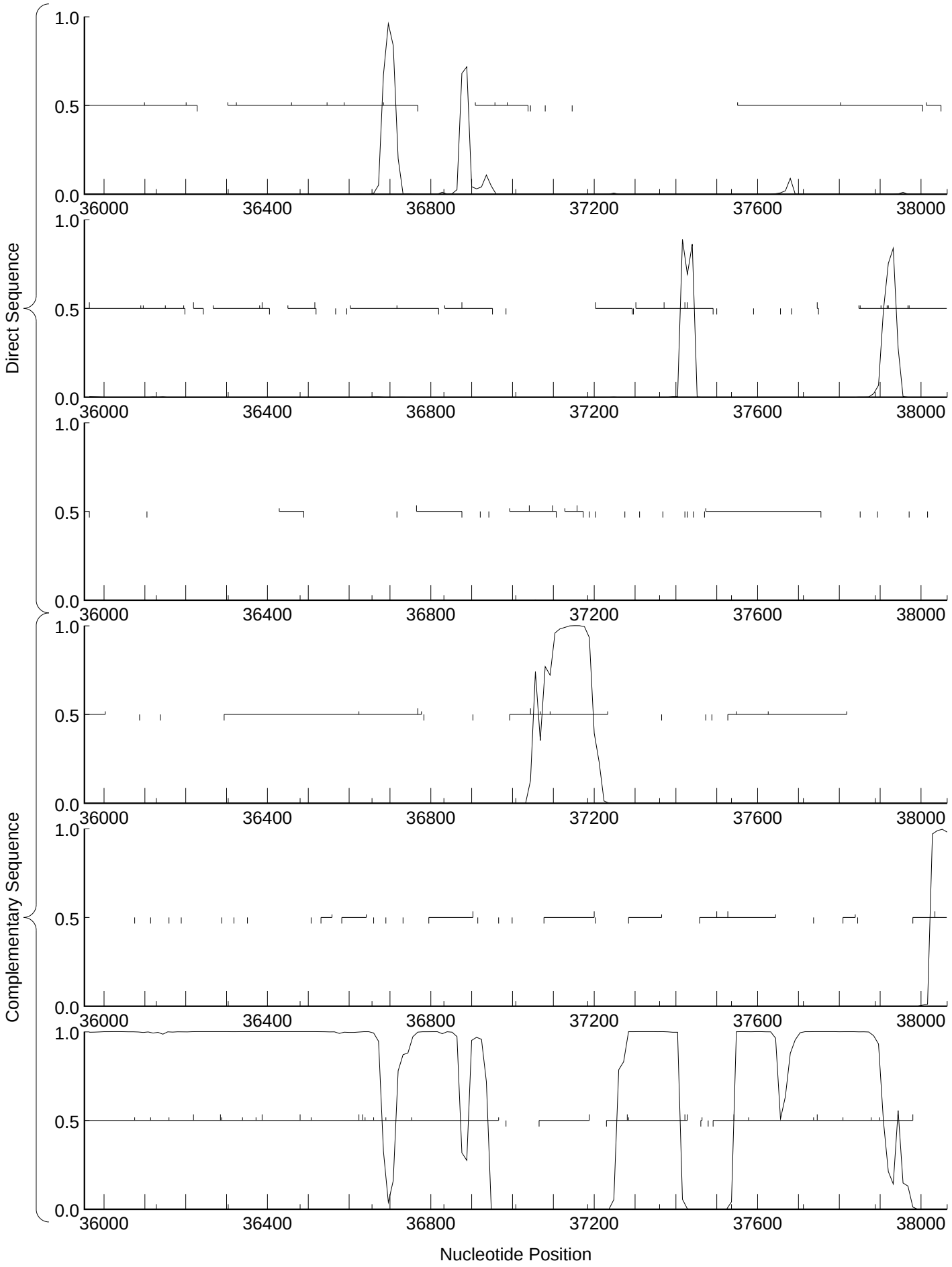

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Complementary Sequence
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Nucleotide Position

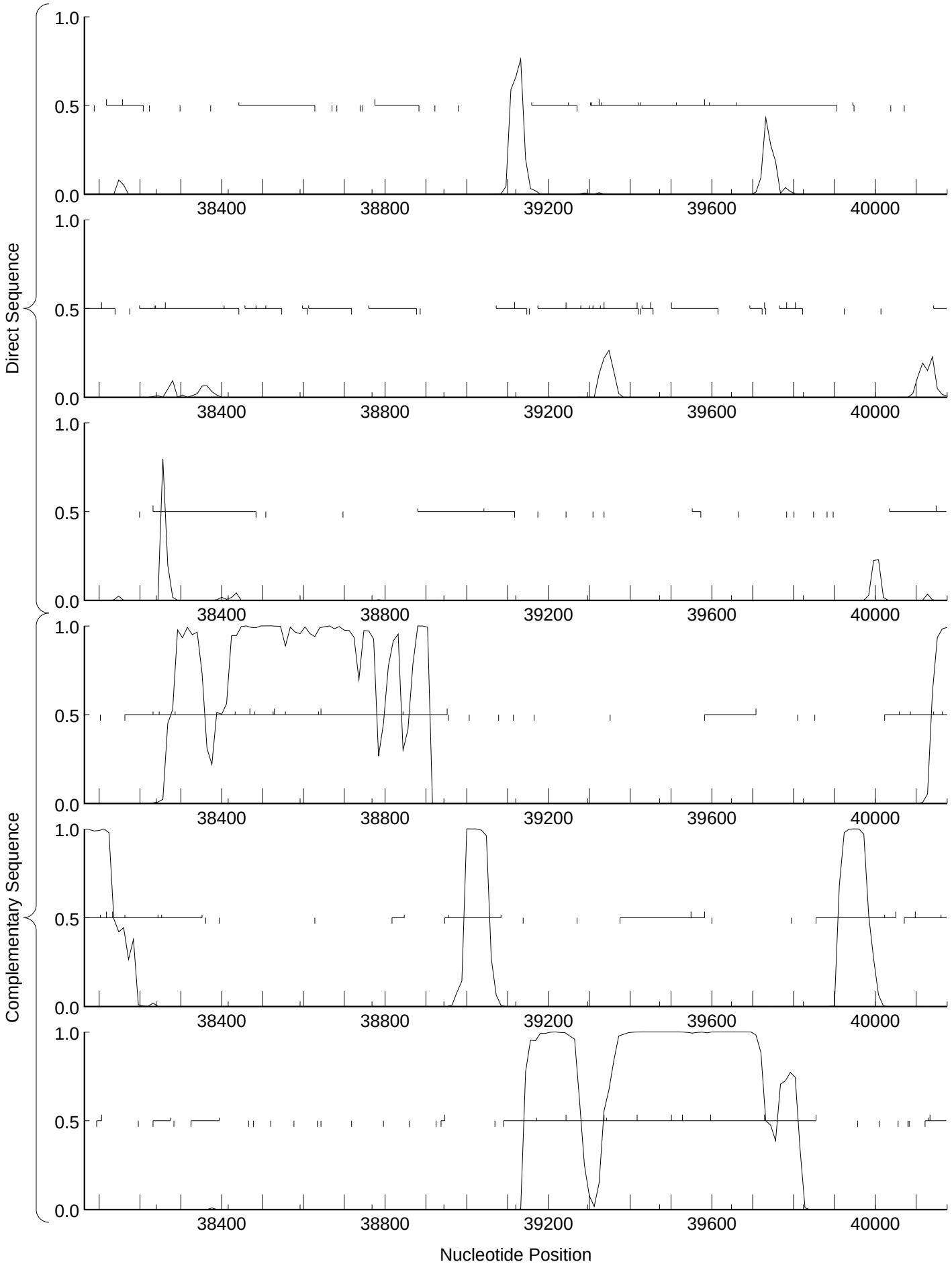

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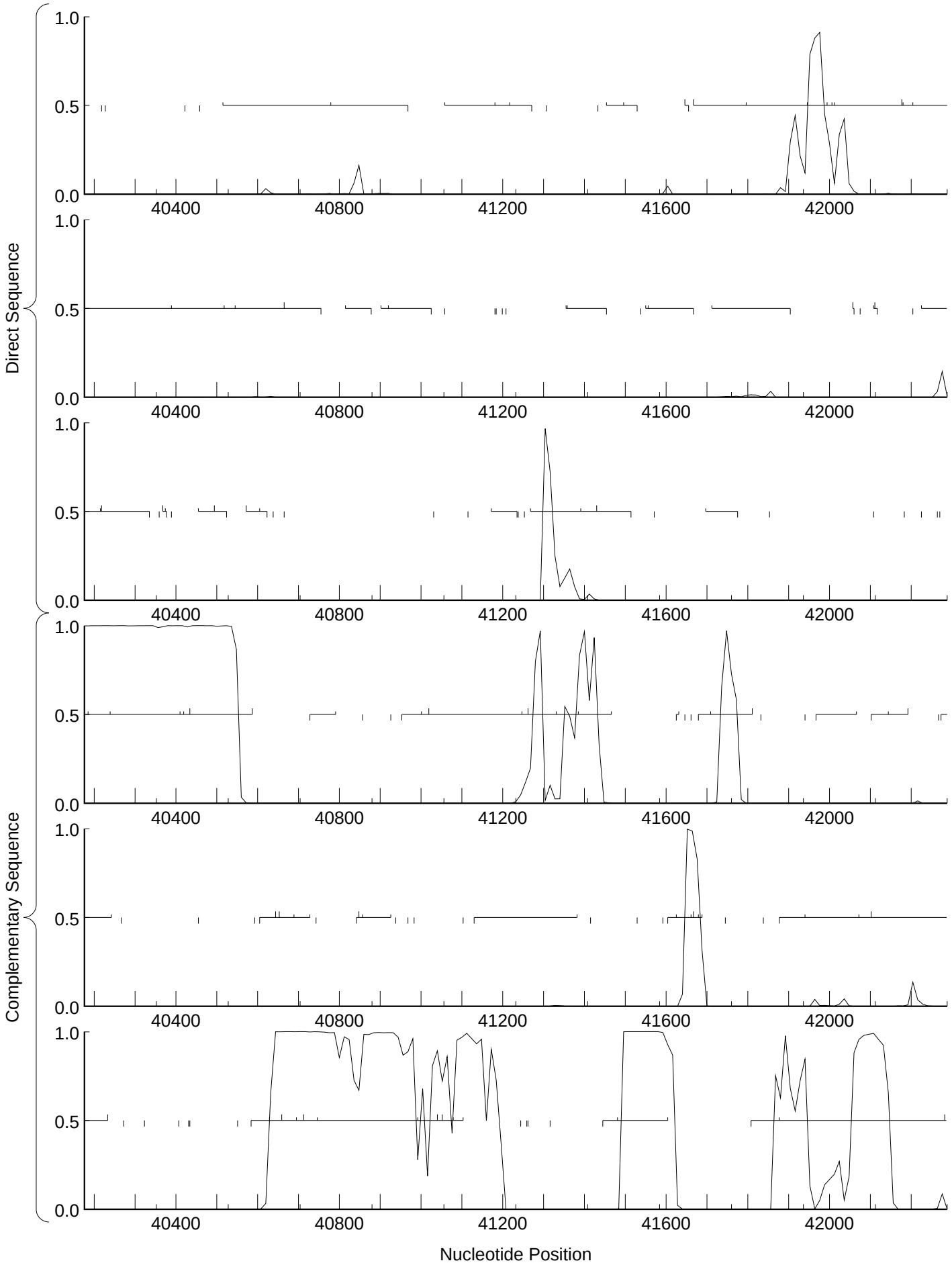

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Complementary Sequence
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33600
Nucleotide Position

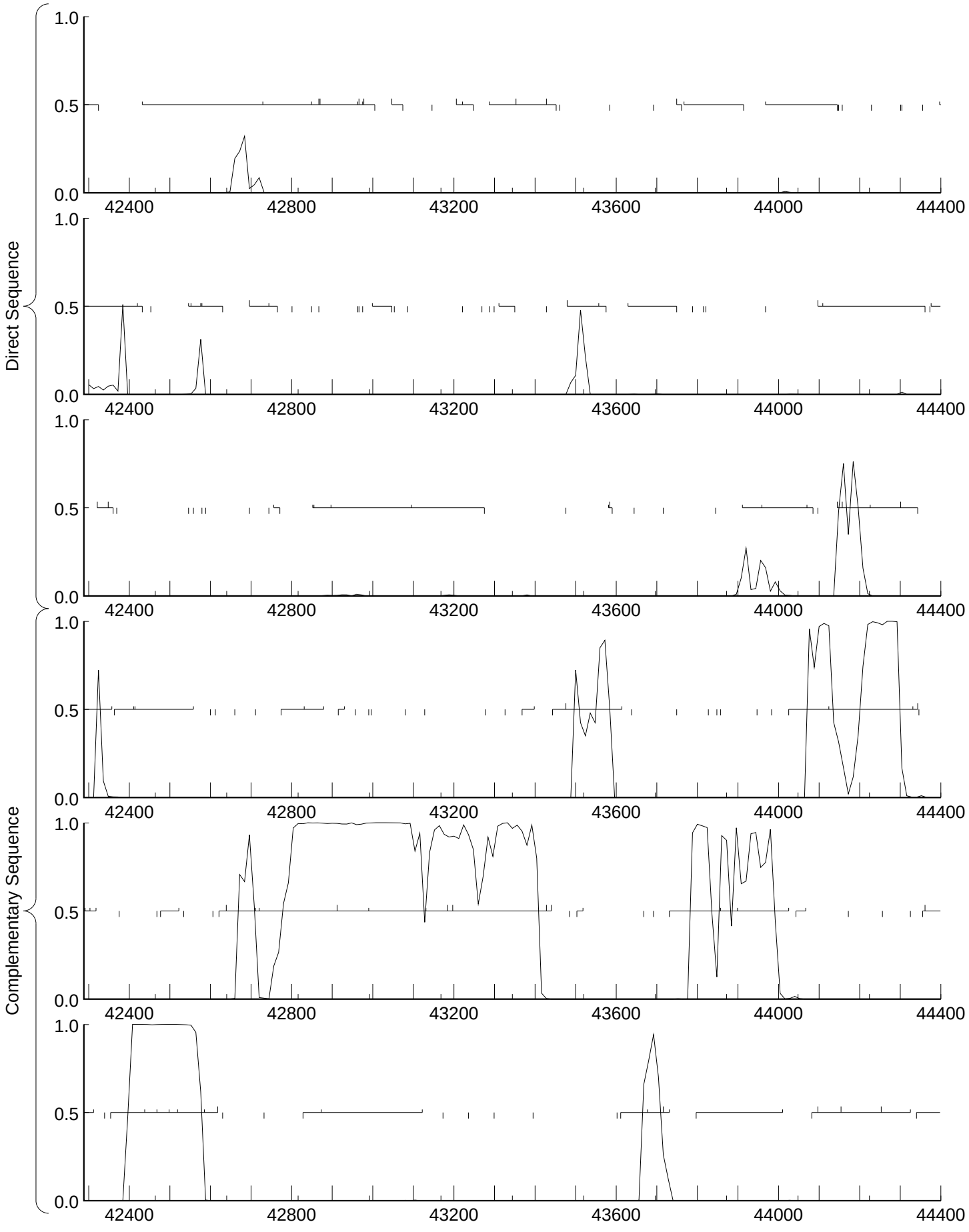

Direct Sequence
Complementary Sequence
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0.0
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35600
Nucleotide Position

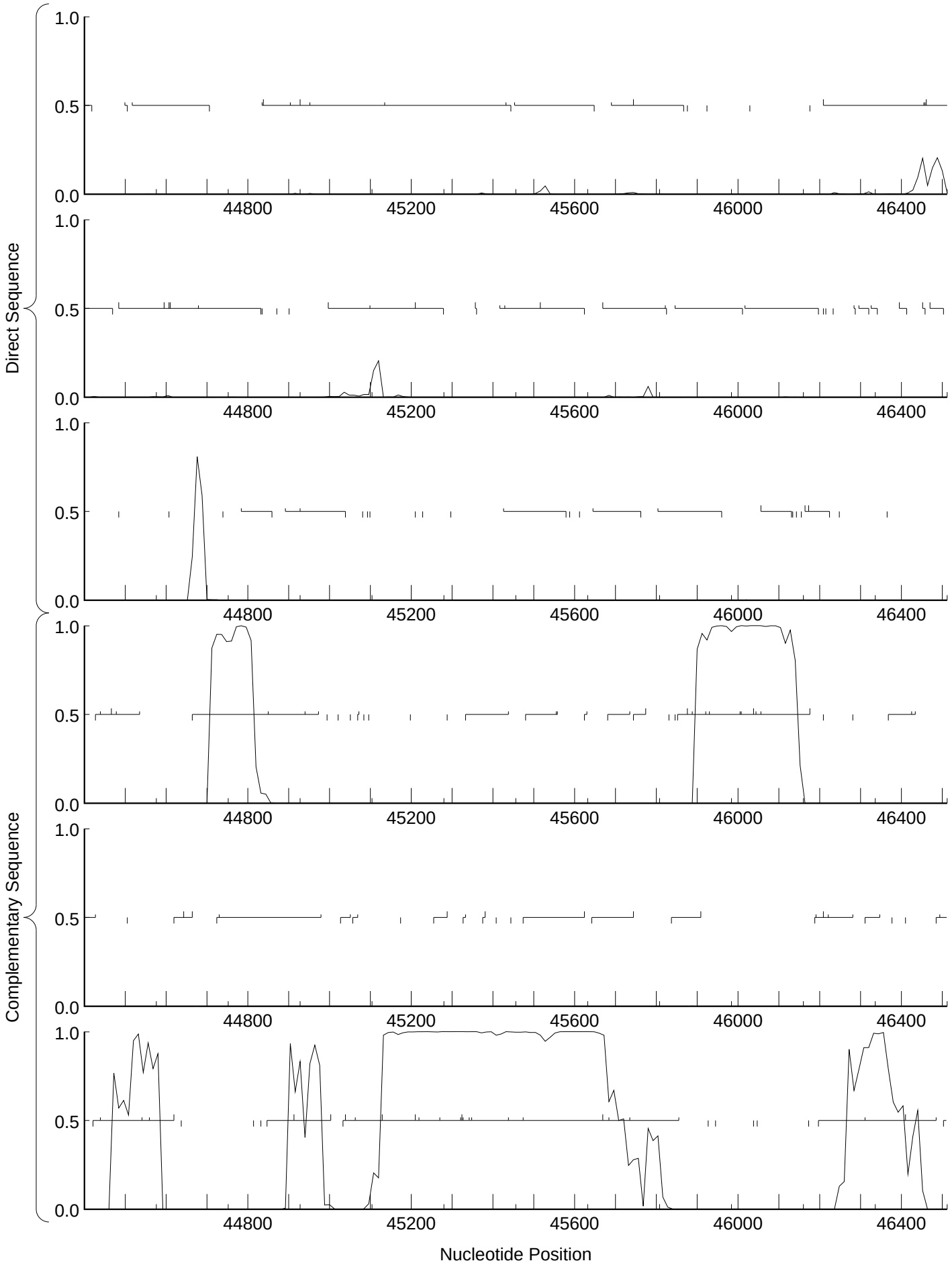
complete sequence, 52501 bp including 10-base 3' overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 19/26

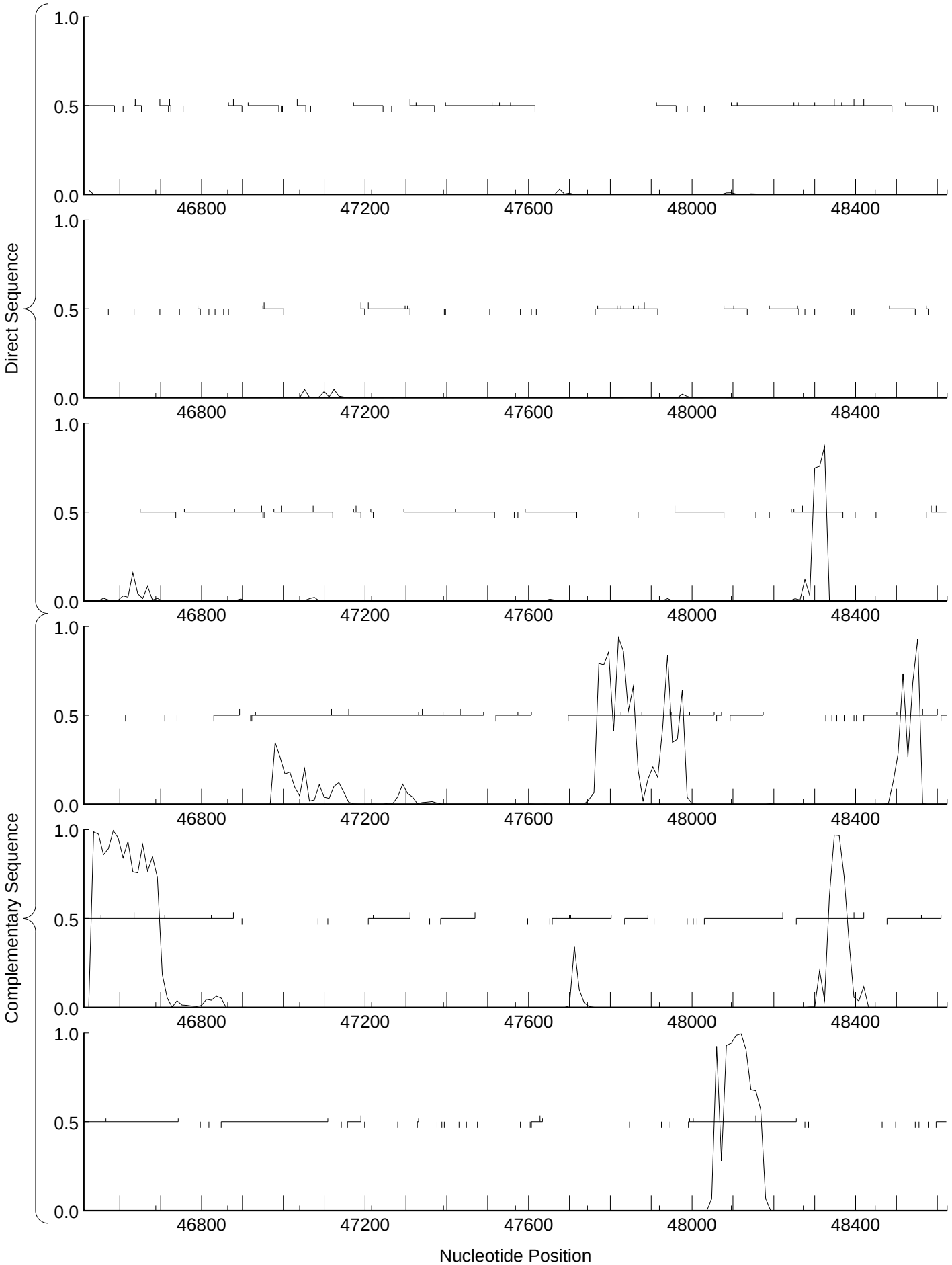


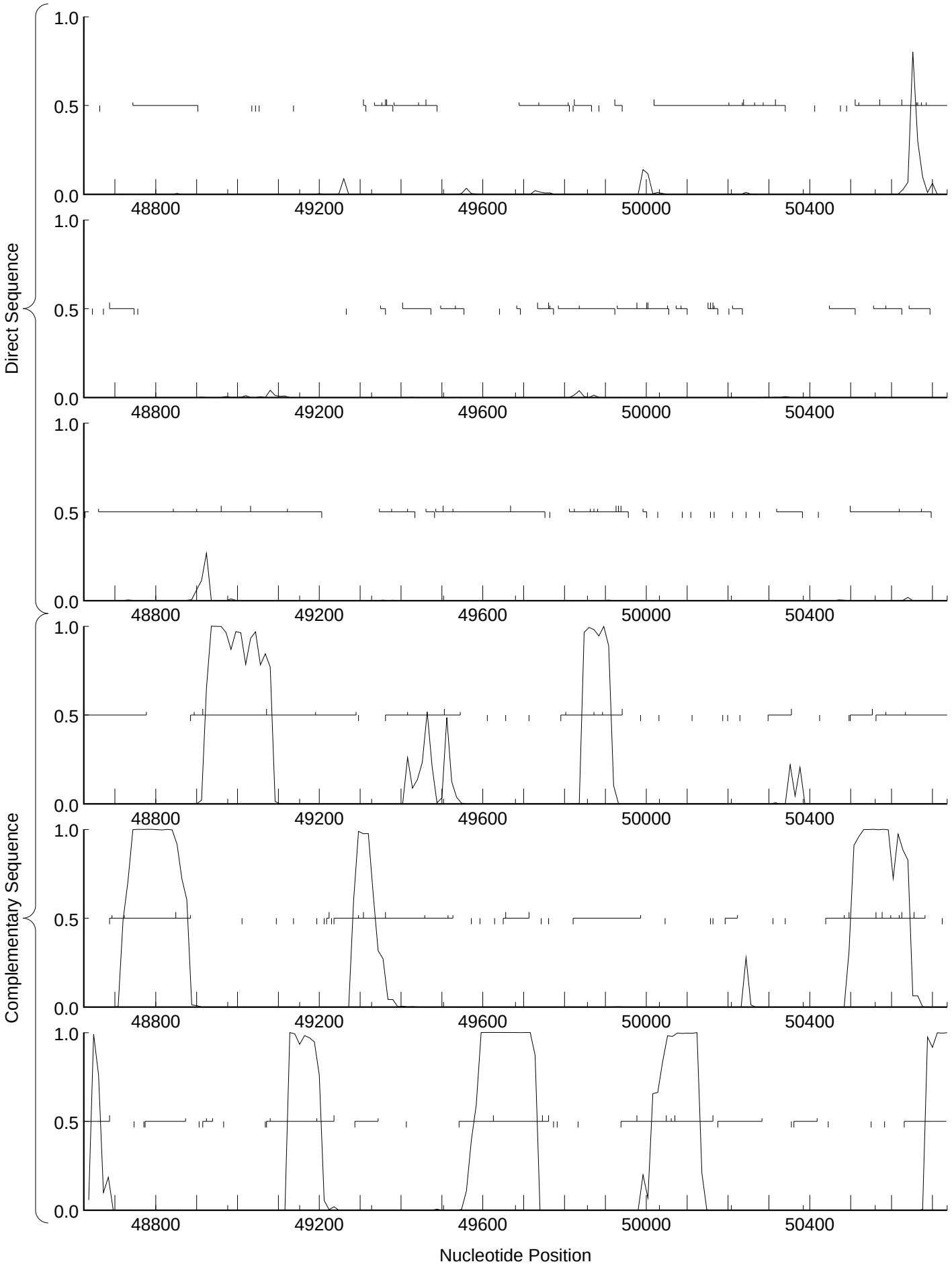

Direct Sequence
Complementary Sequence
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0.0
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38800
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39600
40000
Nucleotide Position

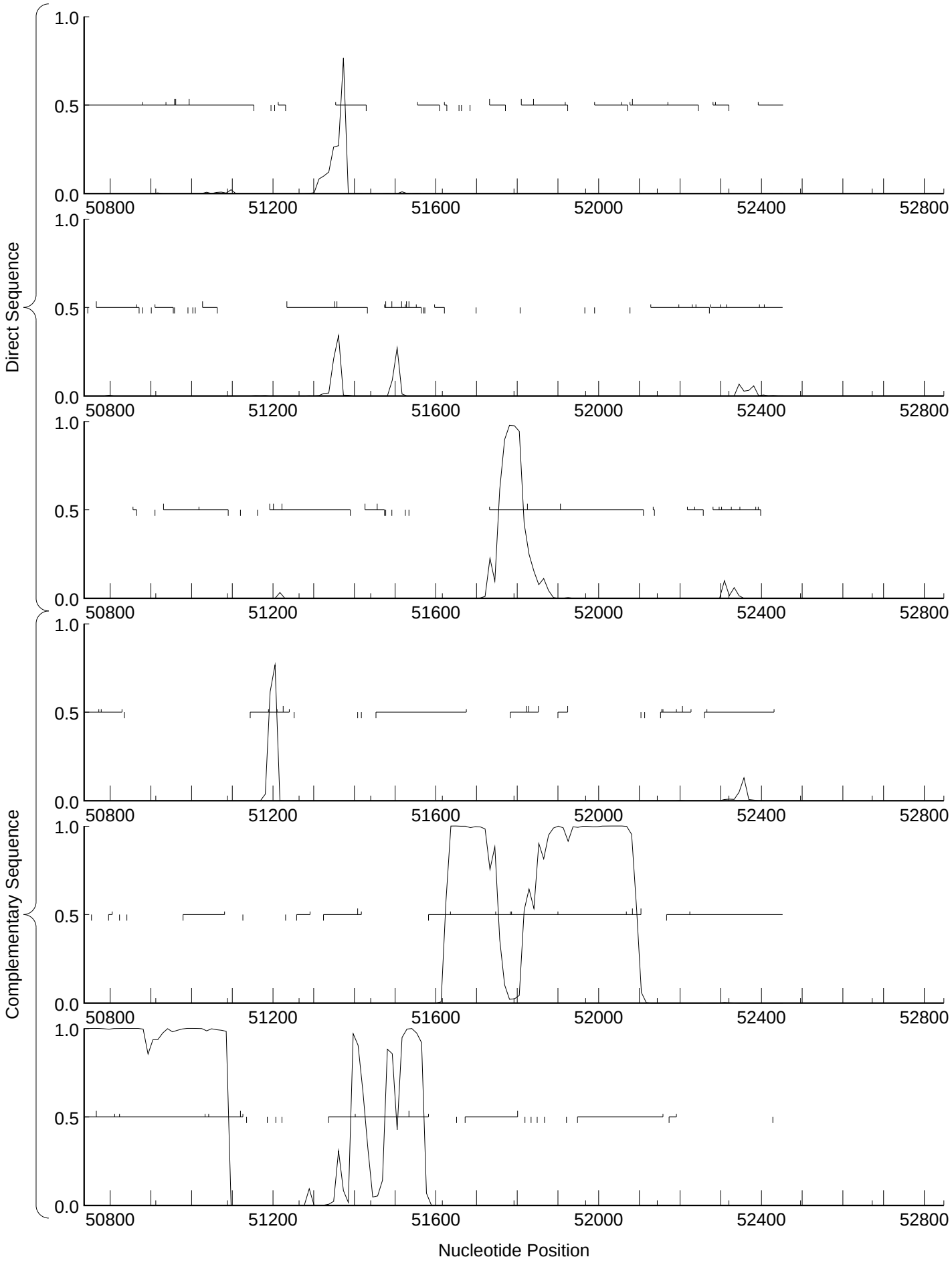

Direct Sequence
Complementary Sequence
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0.0
40400
40800
41200
41600
42000
Nucleotide Position


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


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
44800
45200
45600
46000
46400
Nucleotide Position


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


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
50800
51200
51600
52000
52400
52800
Nucleotide Position