GeneMark

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

PROGRAM INFORMATION

```
Sequence         :  Mycobacterium phage Superchunk complete sequence, 52772 bp including 10-base 3’ overhang (C
Analysis Date    :  3/29/24 at 10:24:23
Pages            :  26
Sequence Length  :  52772 bp
GC Content       :   62.43%

Window Length    :  96 bp
Window Step      :  12 bp
Threshold Value  :  0.500

PS-Version       :  1.2

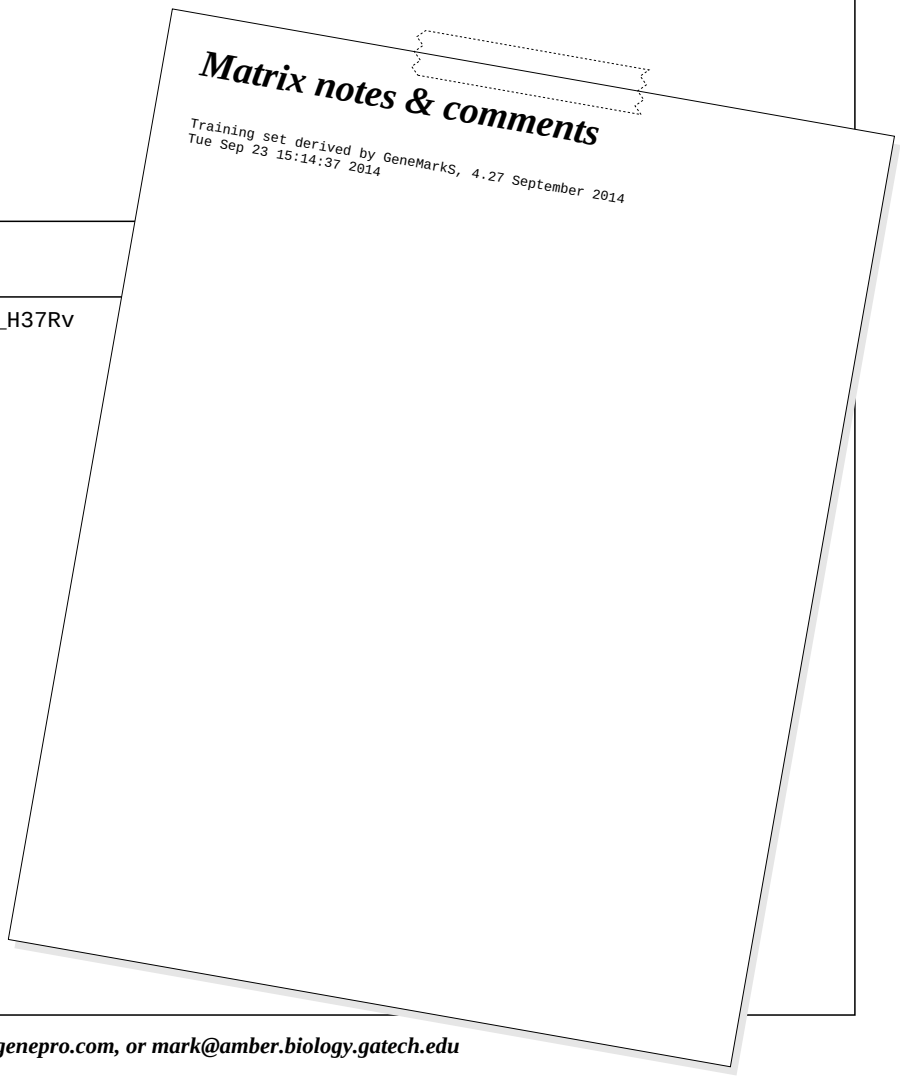
GeneMark Options :  PostScript graph,
                    Mark ORFs / splice sites,
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                    List regions and/or splice sites,
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MATRIX INFORMATION

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Matrix     :  Mycobacterium_tuberculosis_H37Rv
Author     :  -

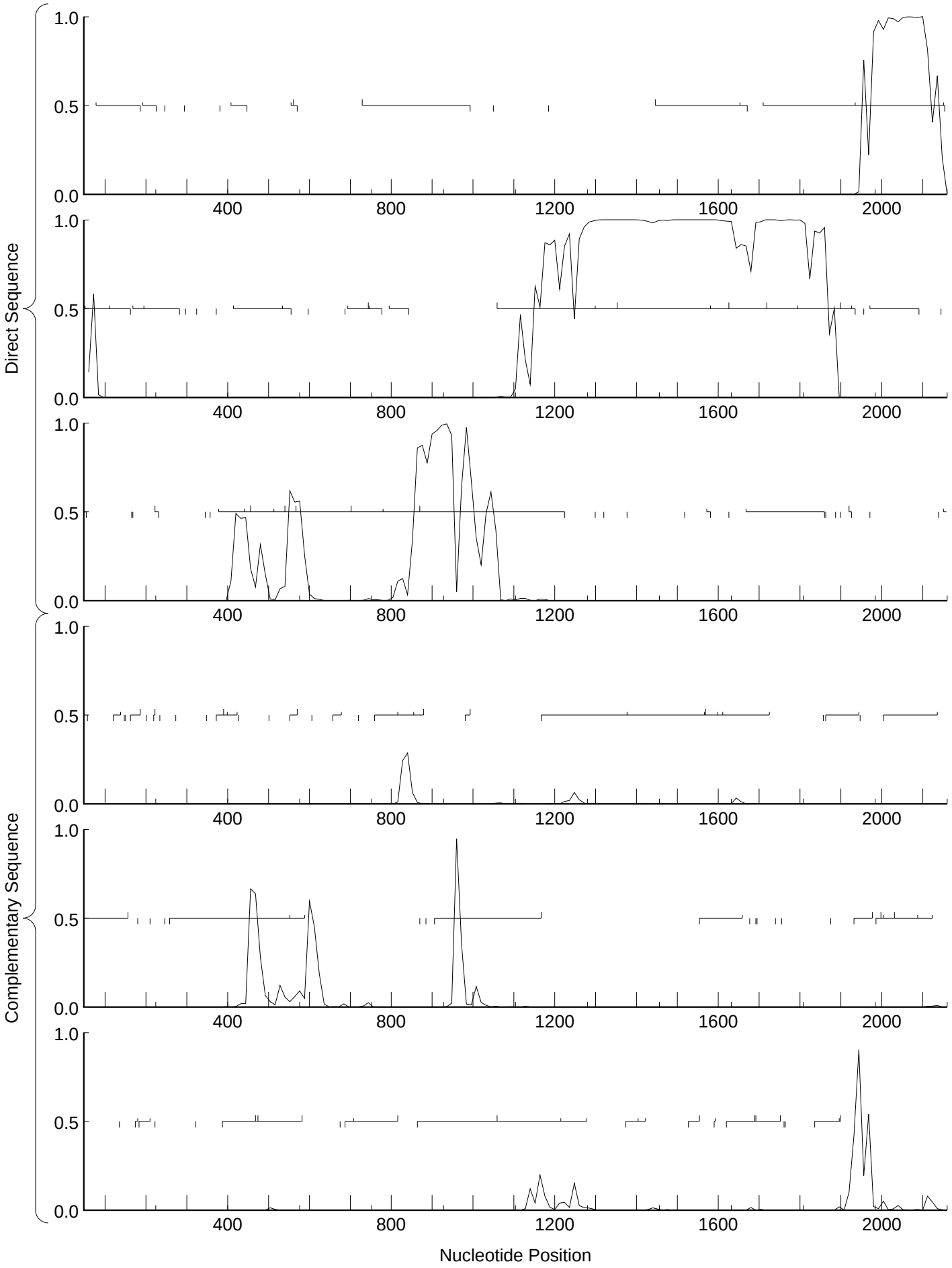
Order      :  4


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

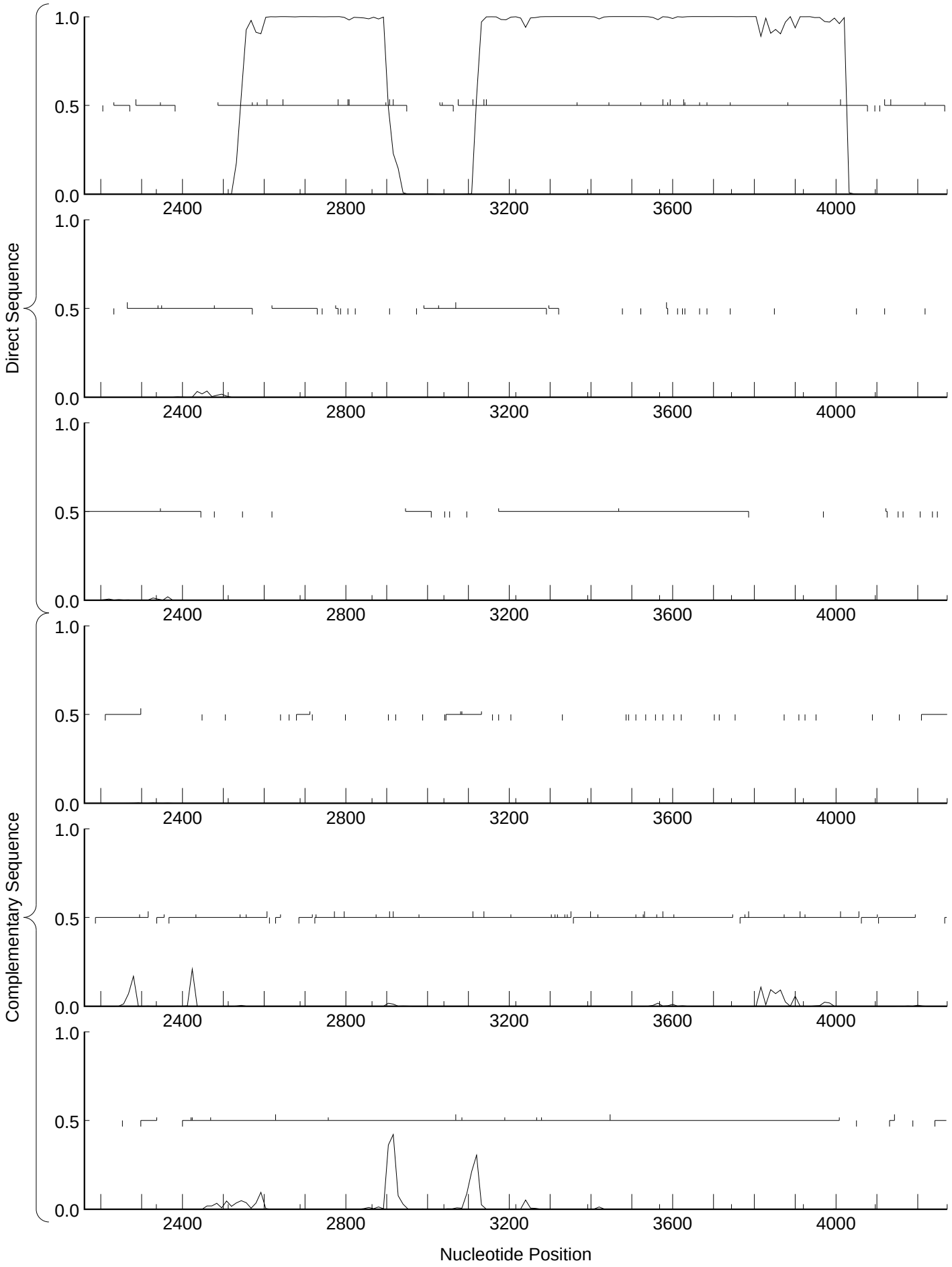


For help or information, send electronic mail to: custserv@genepro.com, or mark@amber.biology.gatech.edu

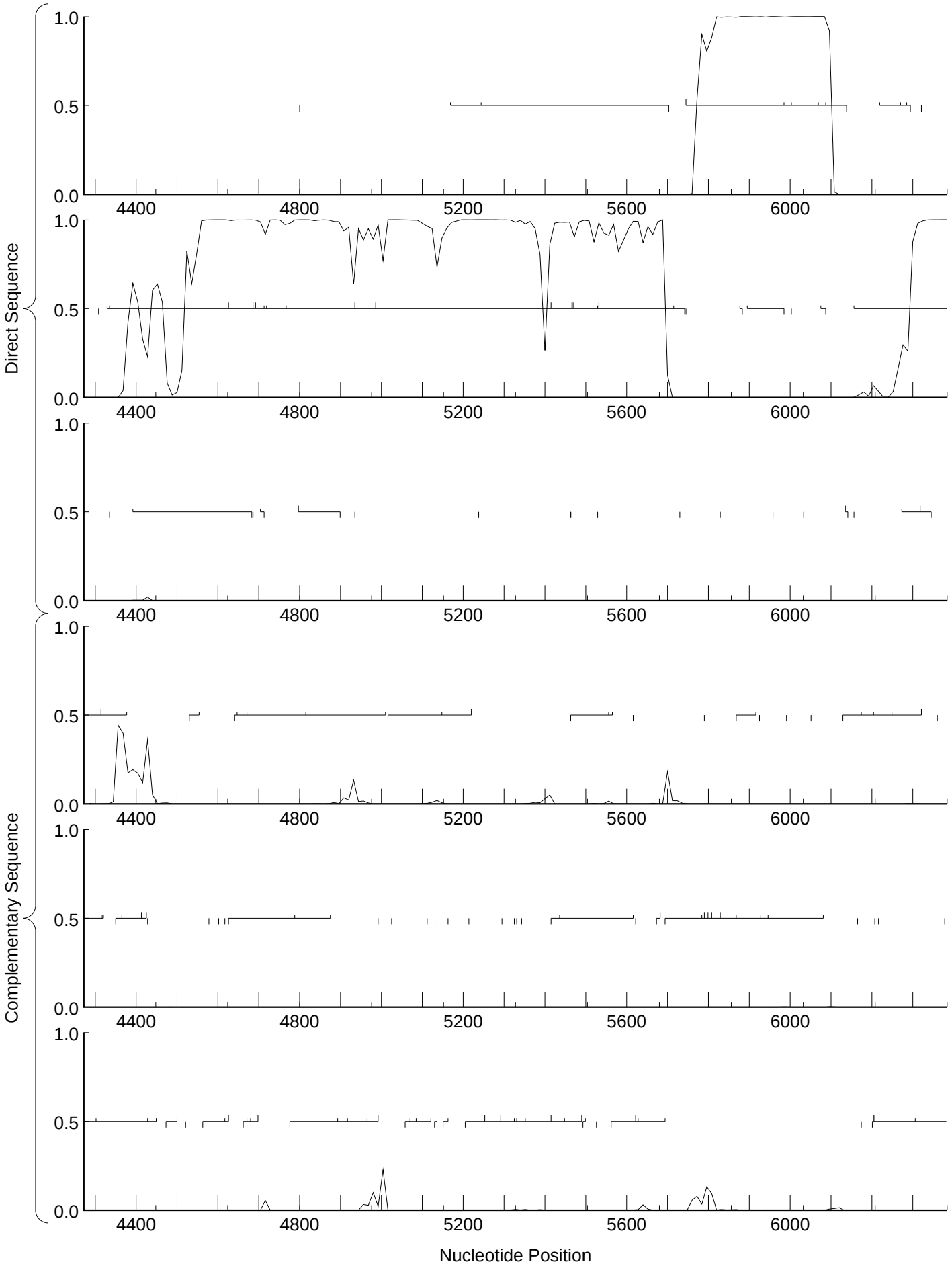
nk complete sequence, 52772 bp including 10-base 3’ overhang (CGGTCGGTTA), Cluster A2, Order 4, Window 96, Step 12, 2/26

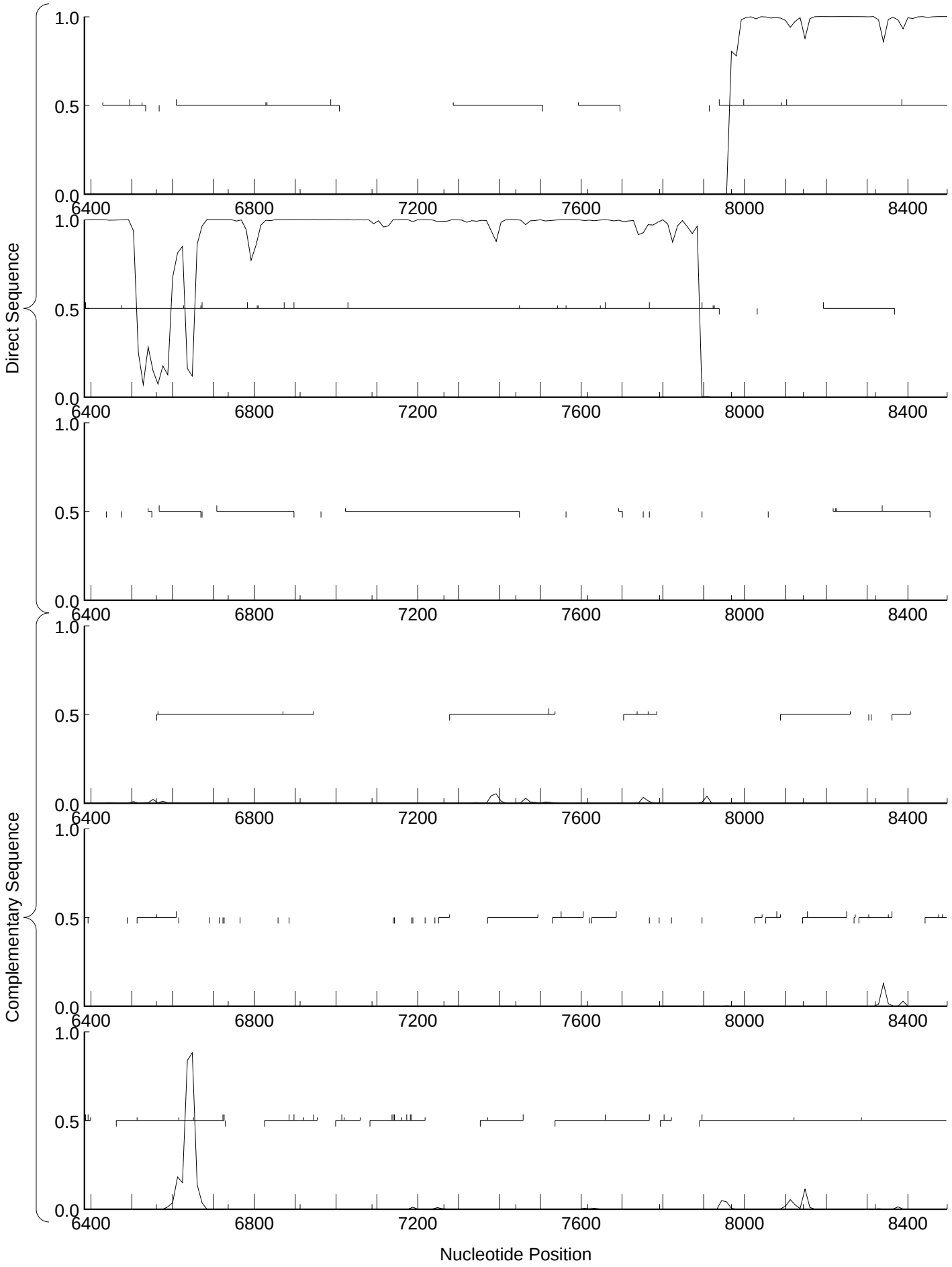


k complete sequence, 52772 bp including 10-base 3’ overhang (CGGTCGGTTA), Cluster A2, Order 4, Window 96, Step 12, 3/26

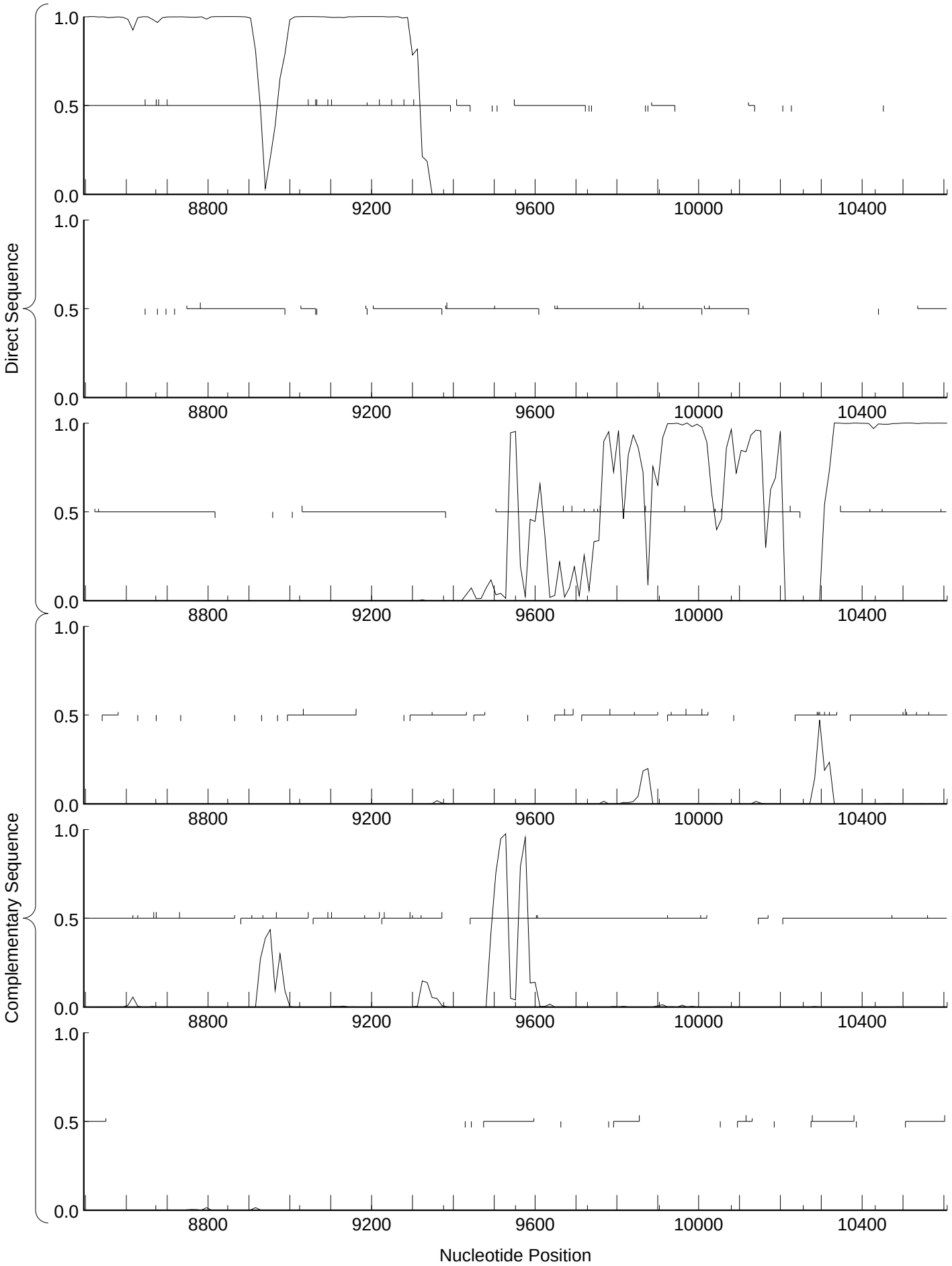


nk complete sequence, 52772 bp including 10-base 3’ overhang (CGGTCGGTTA), Cluster A2, Order 4, Window 96, Step 12, 4/26

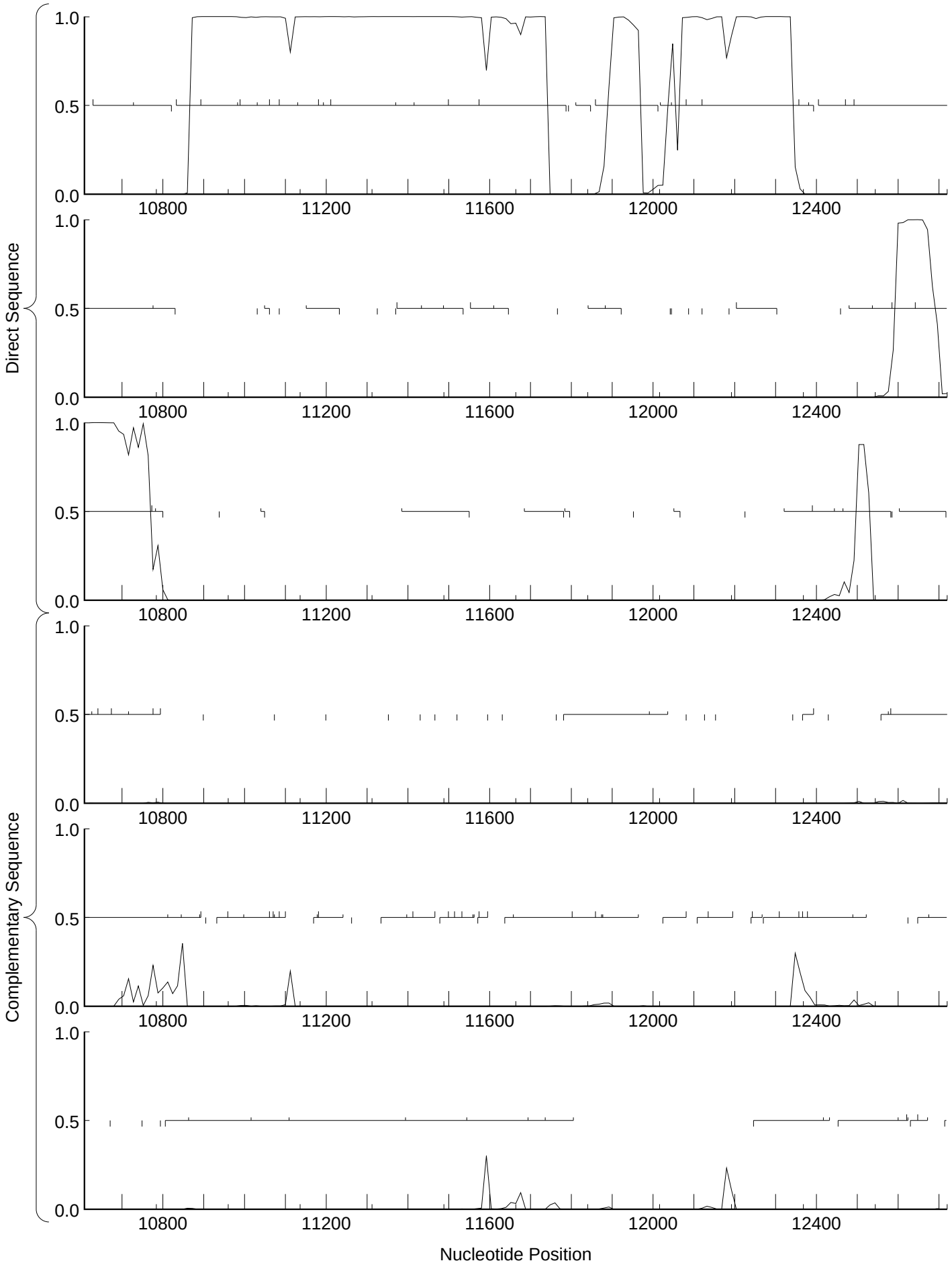



Direct Sequence
Complementary Sequence
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0.5
0.0
6400
6800
7200
7600
8000
8400
Nucleotide Position

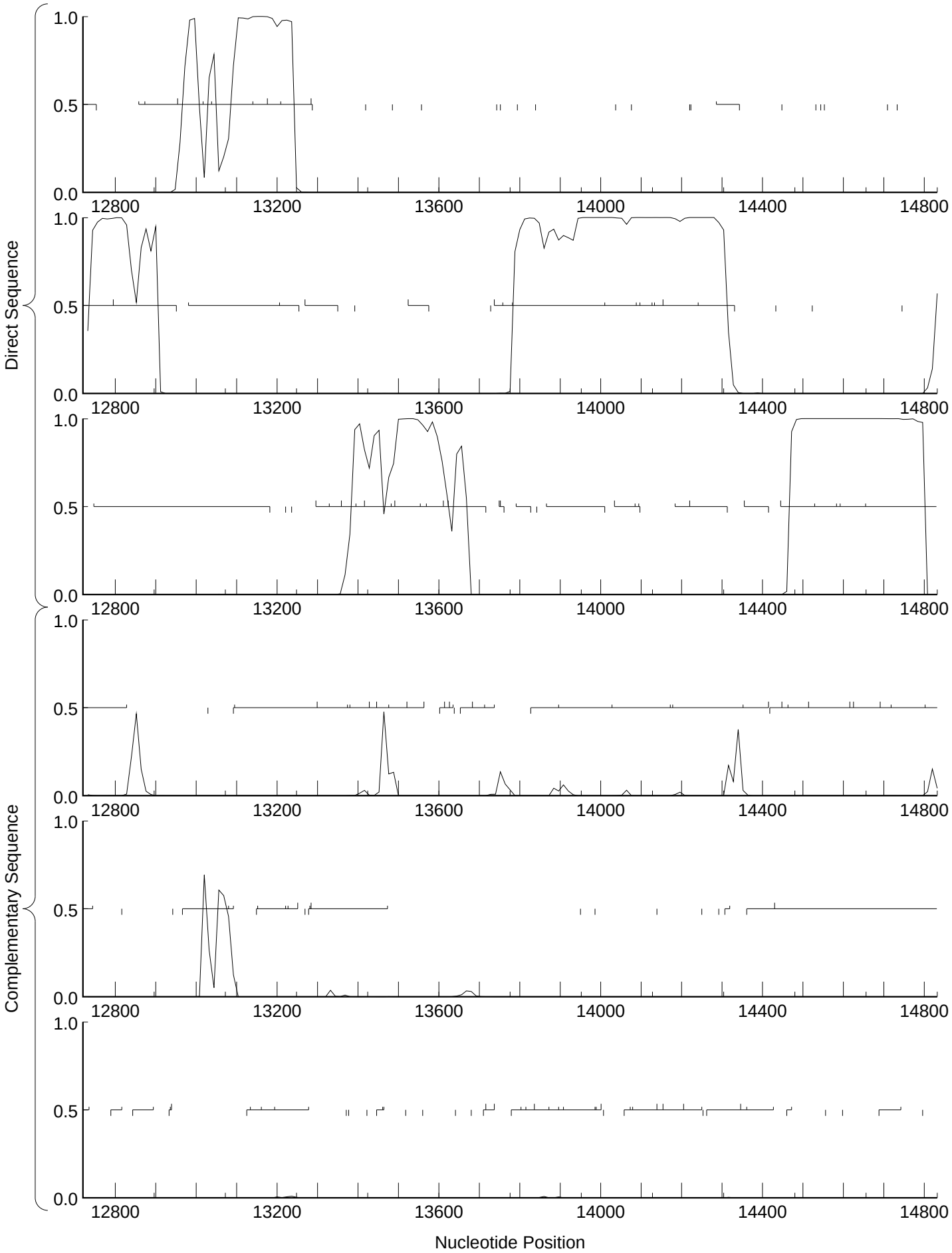
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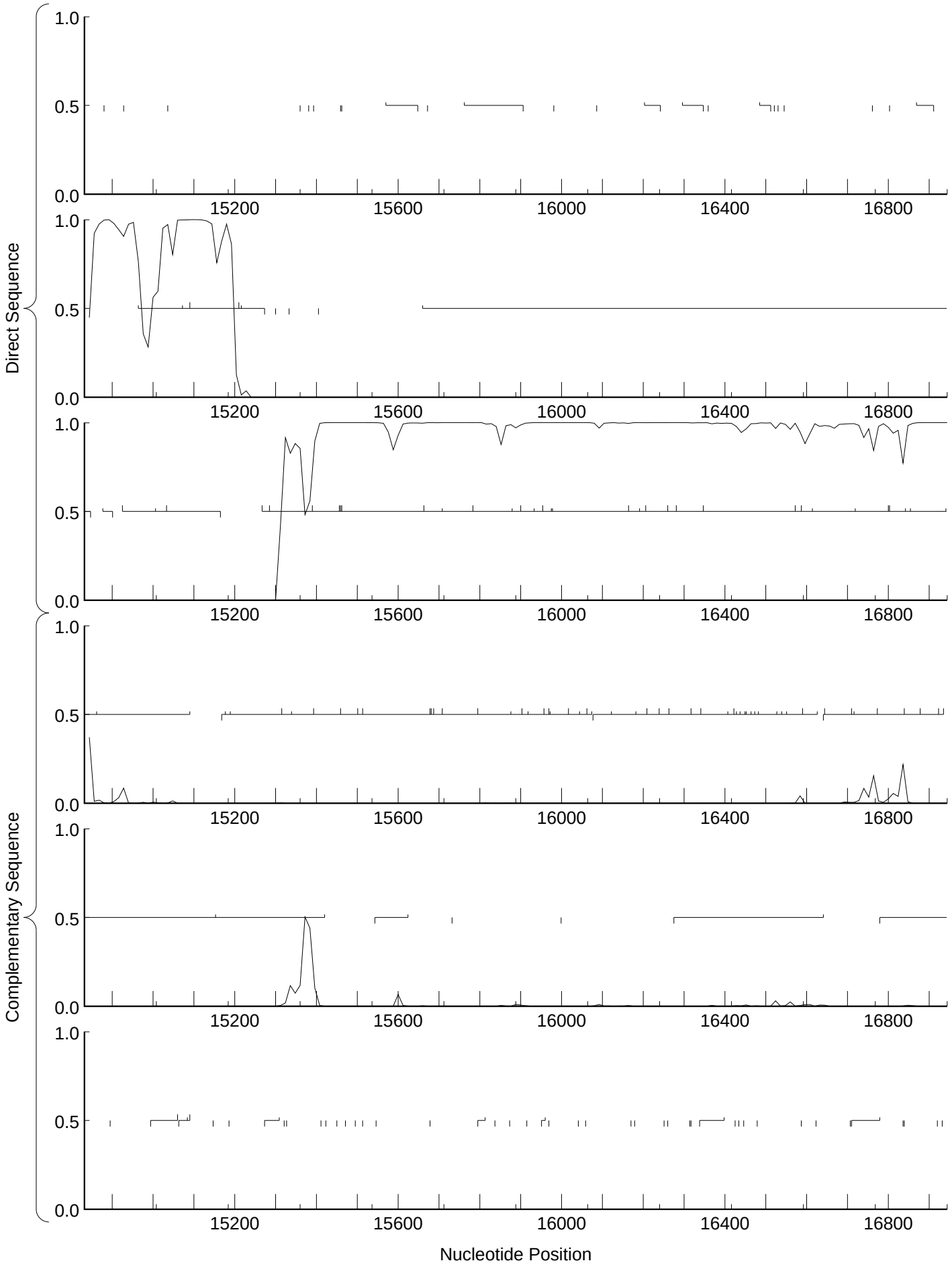
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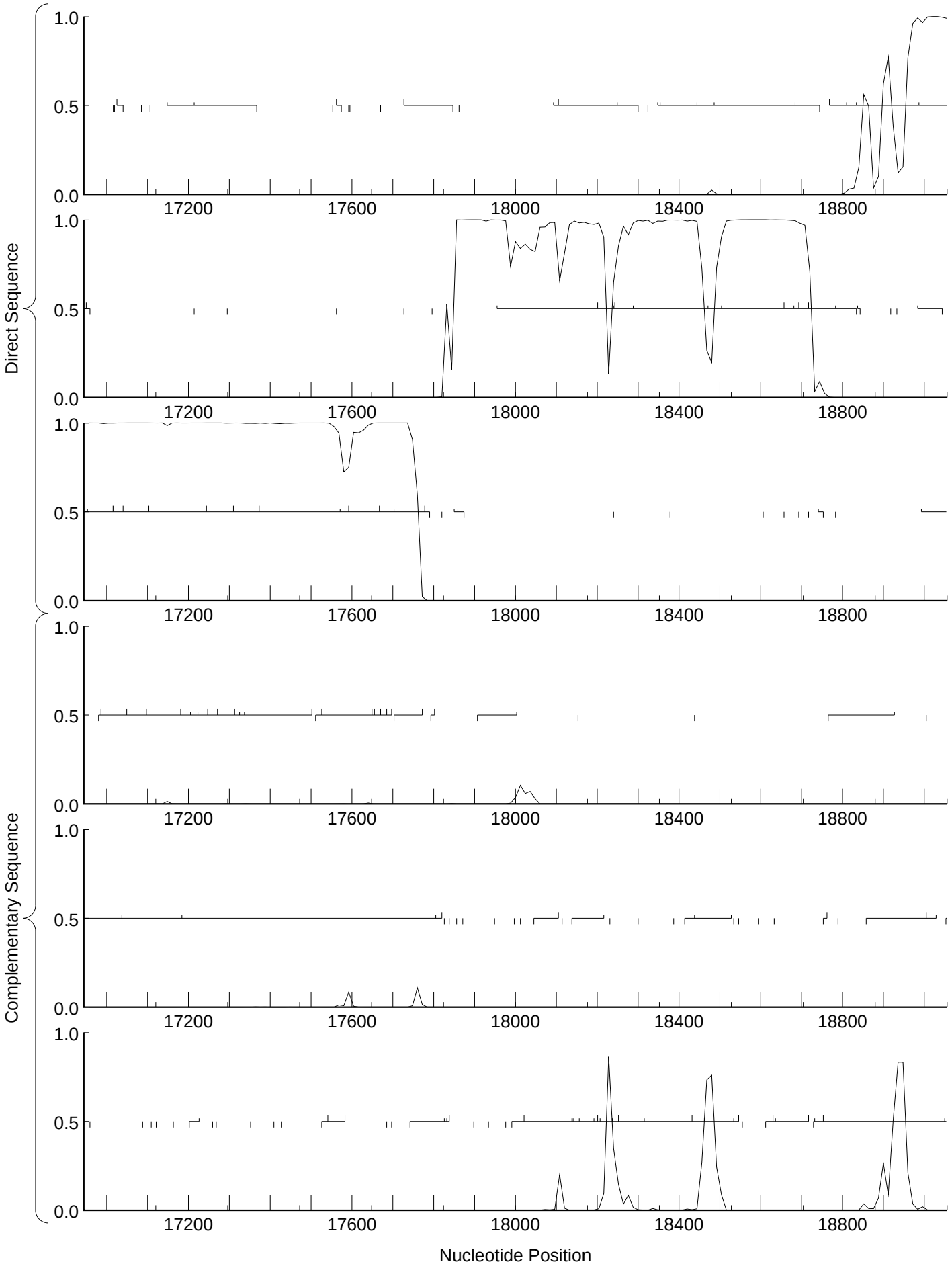
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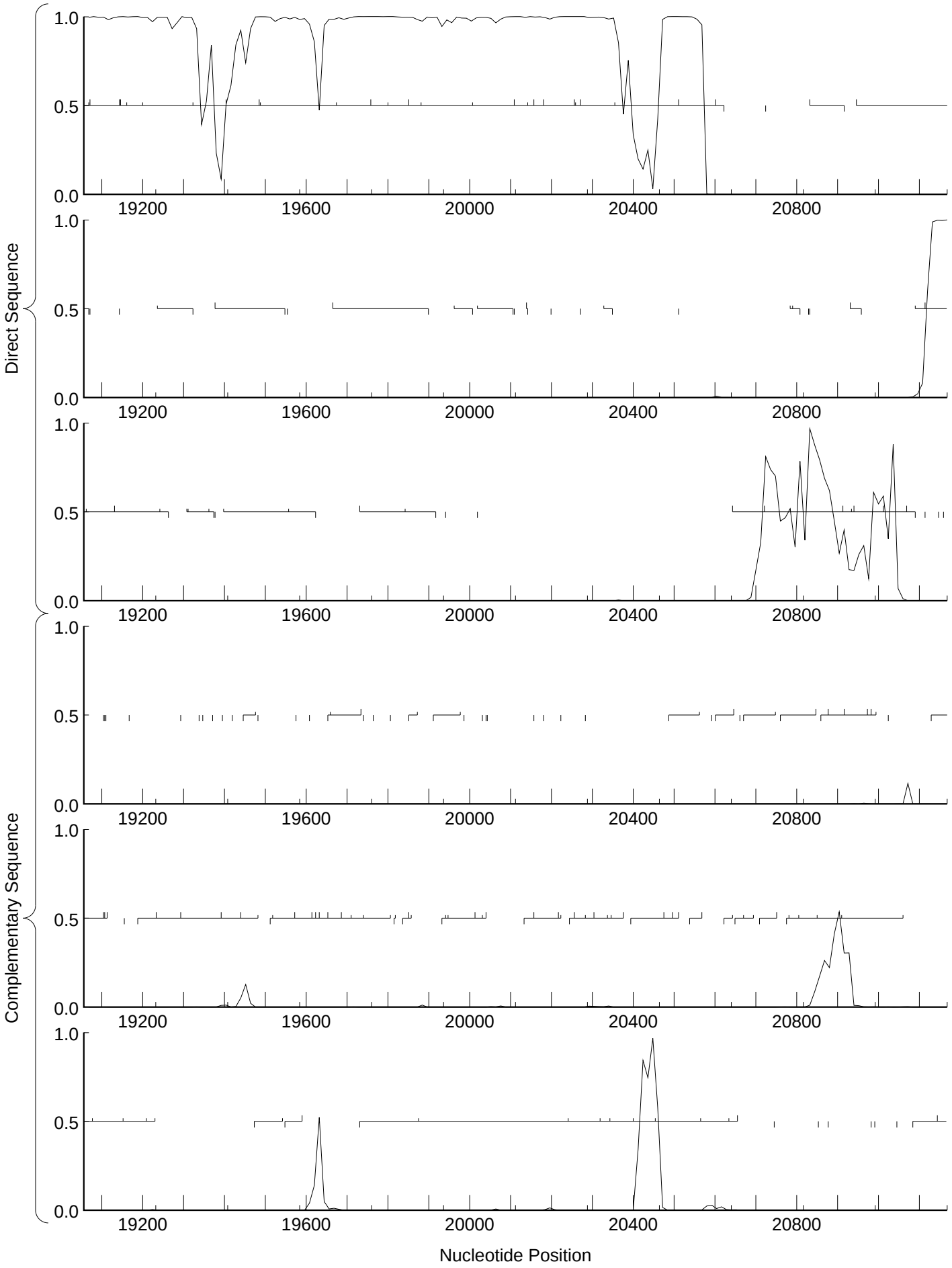


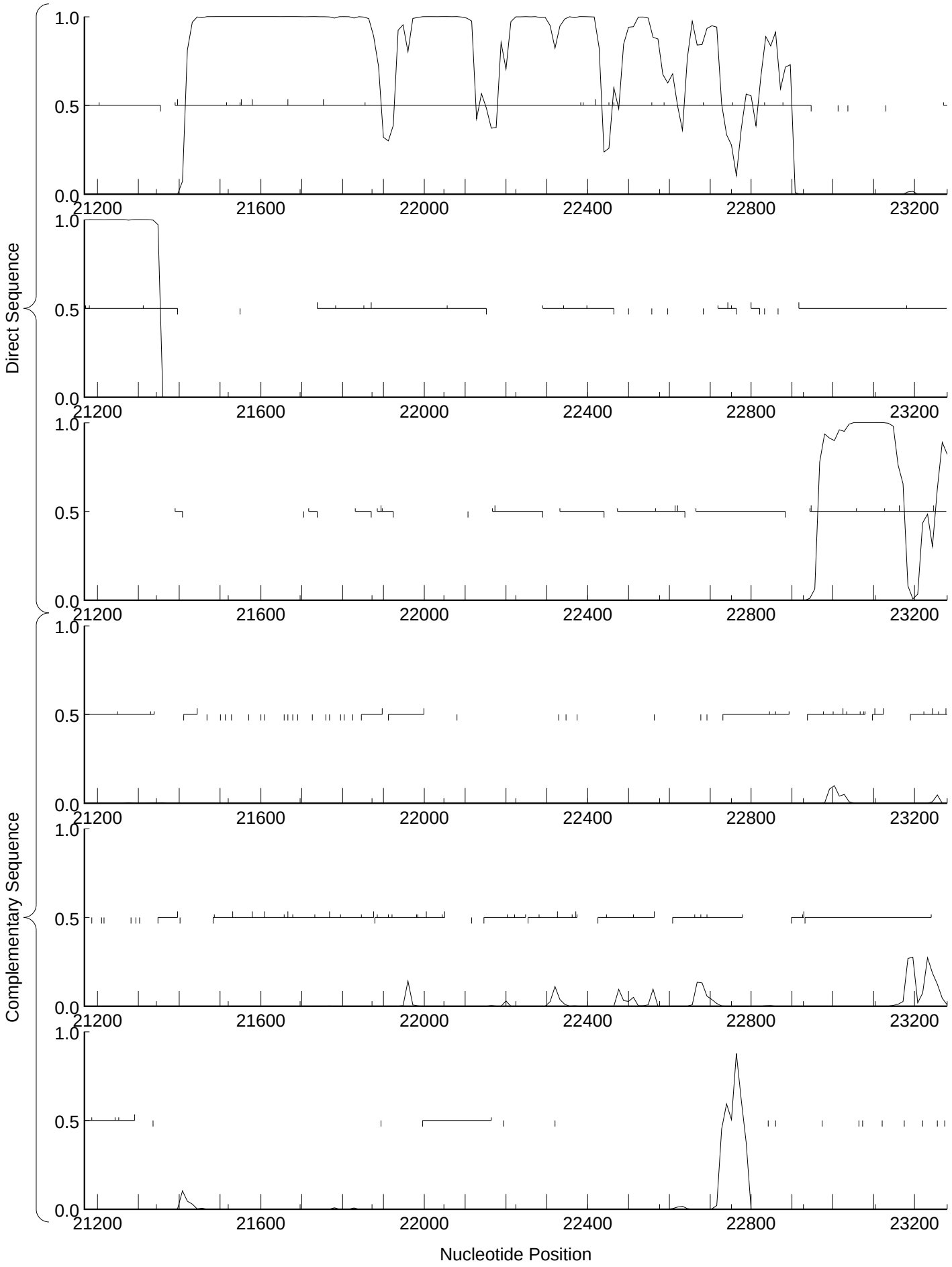
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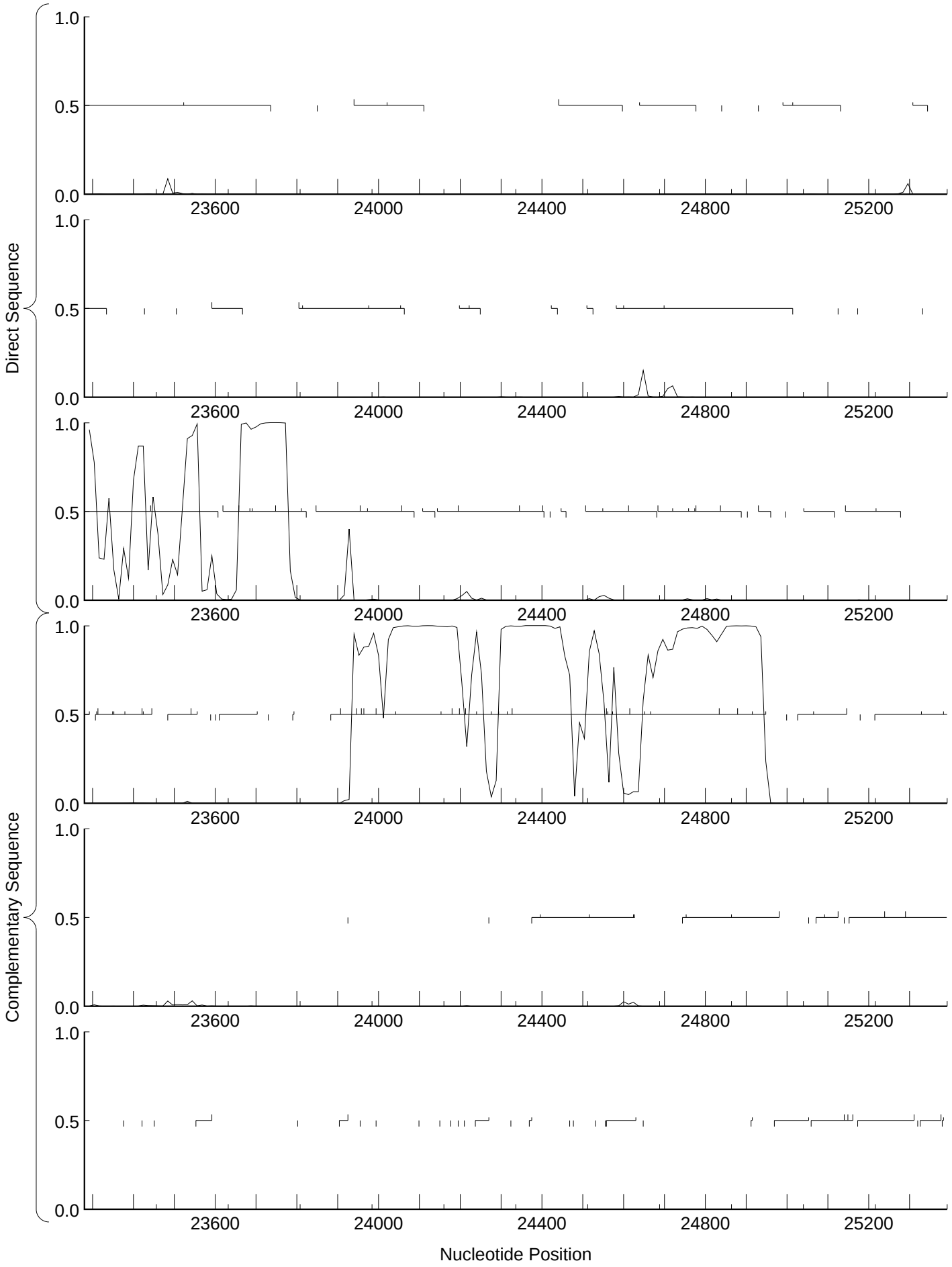


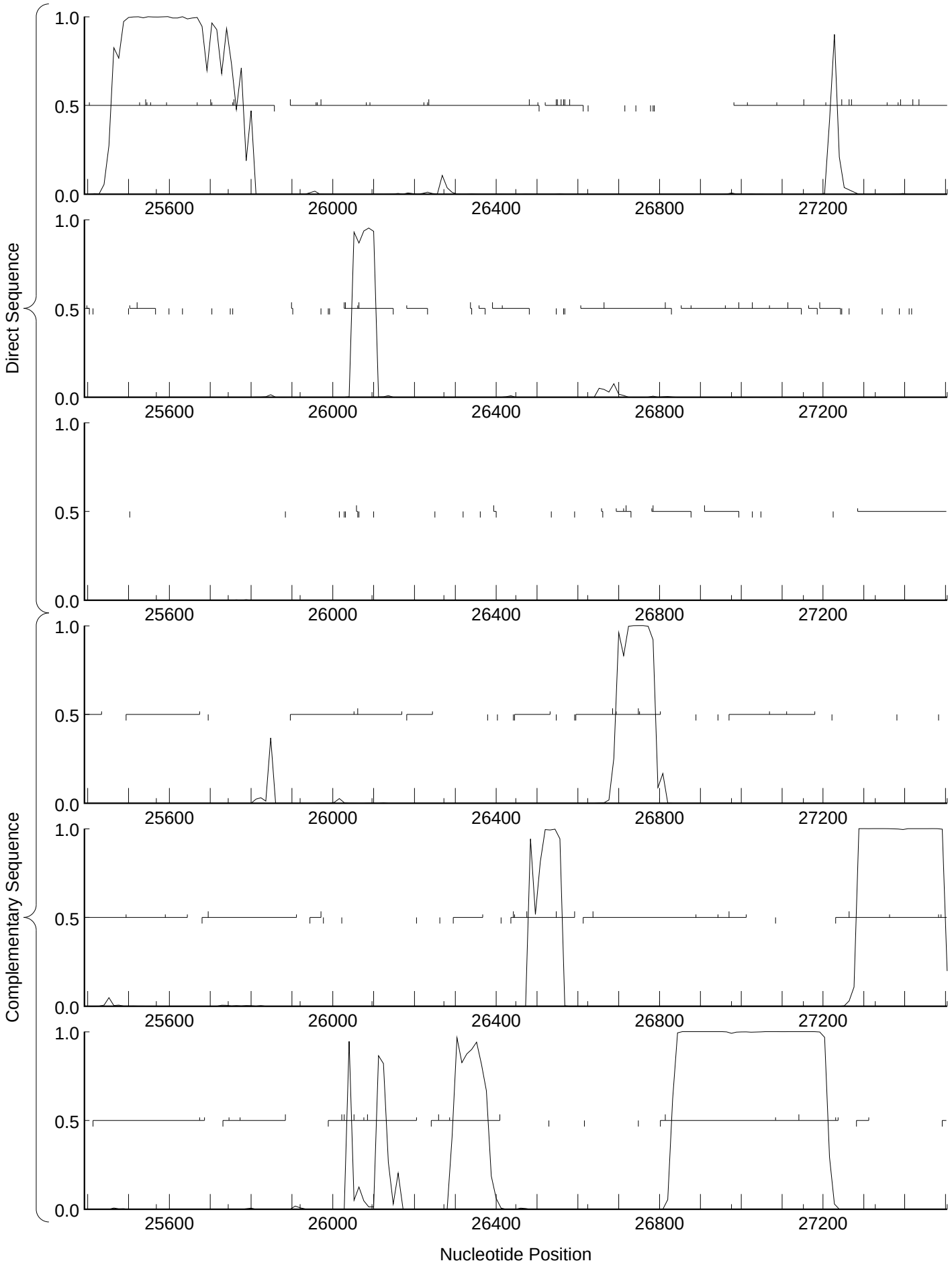
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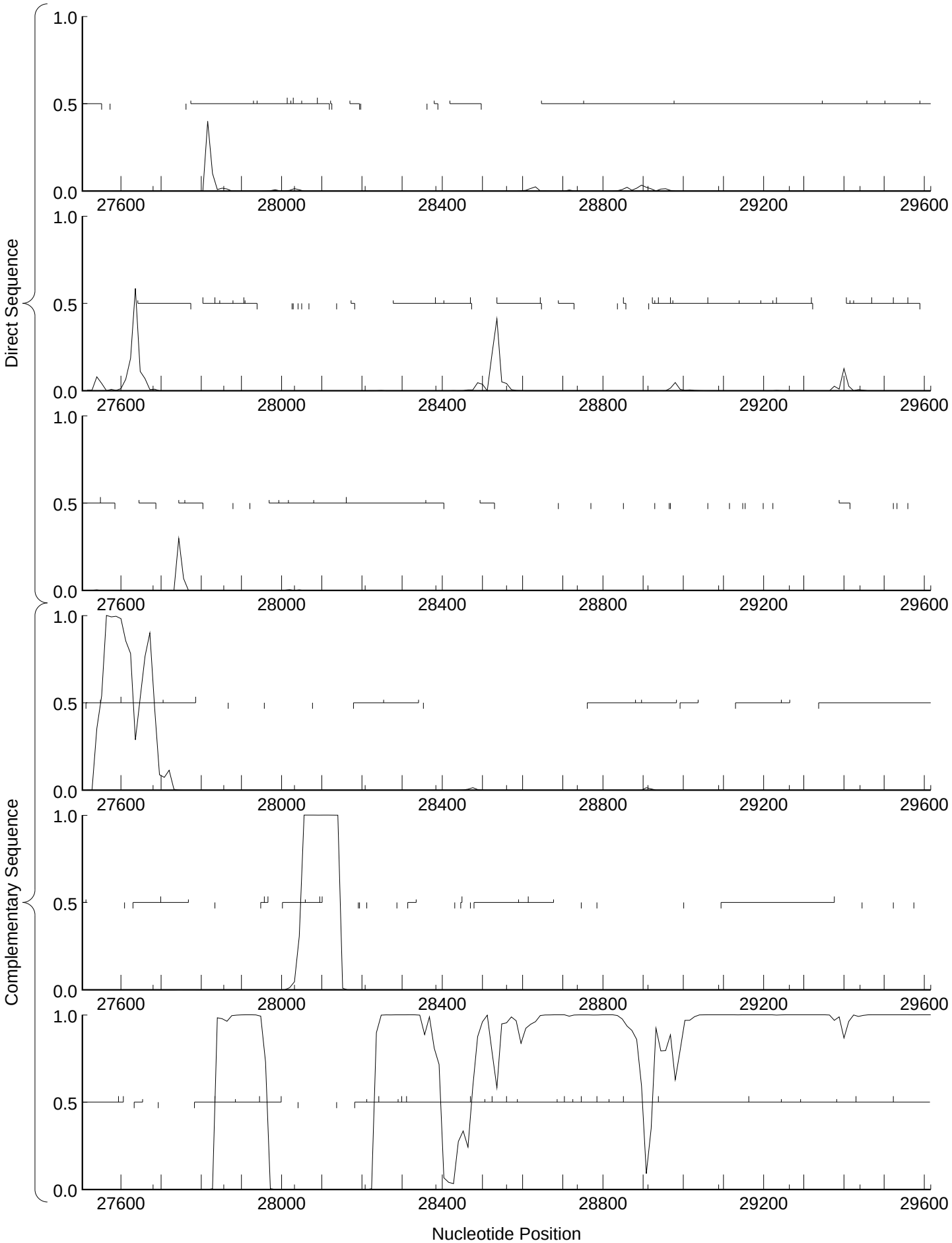

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Complementary Sequence
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Nucleotide Position

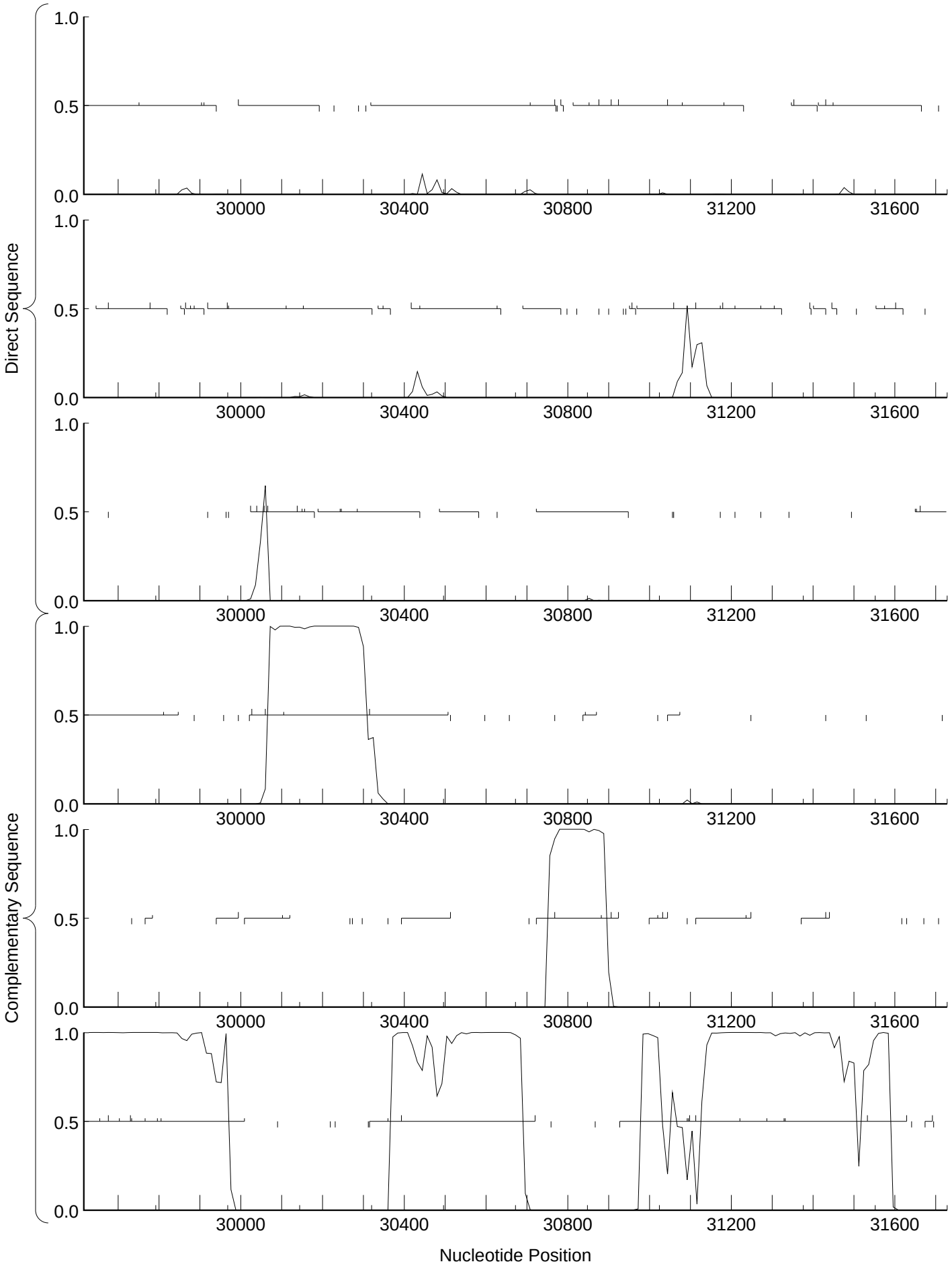

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Complementary Sequence
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21600
22000
22400
22800
23200
Nucleotide Position

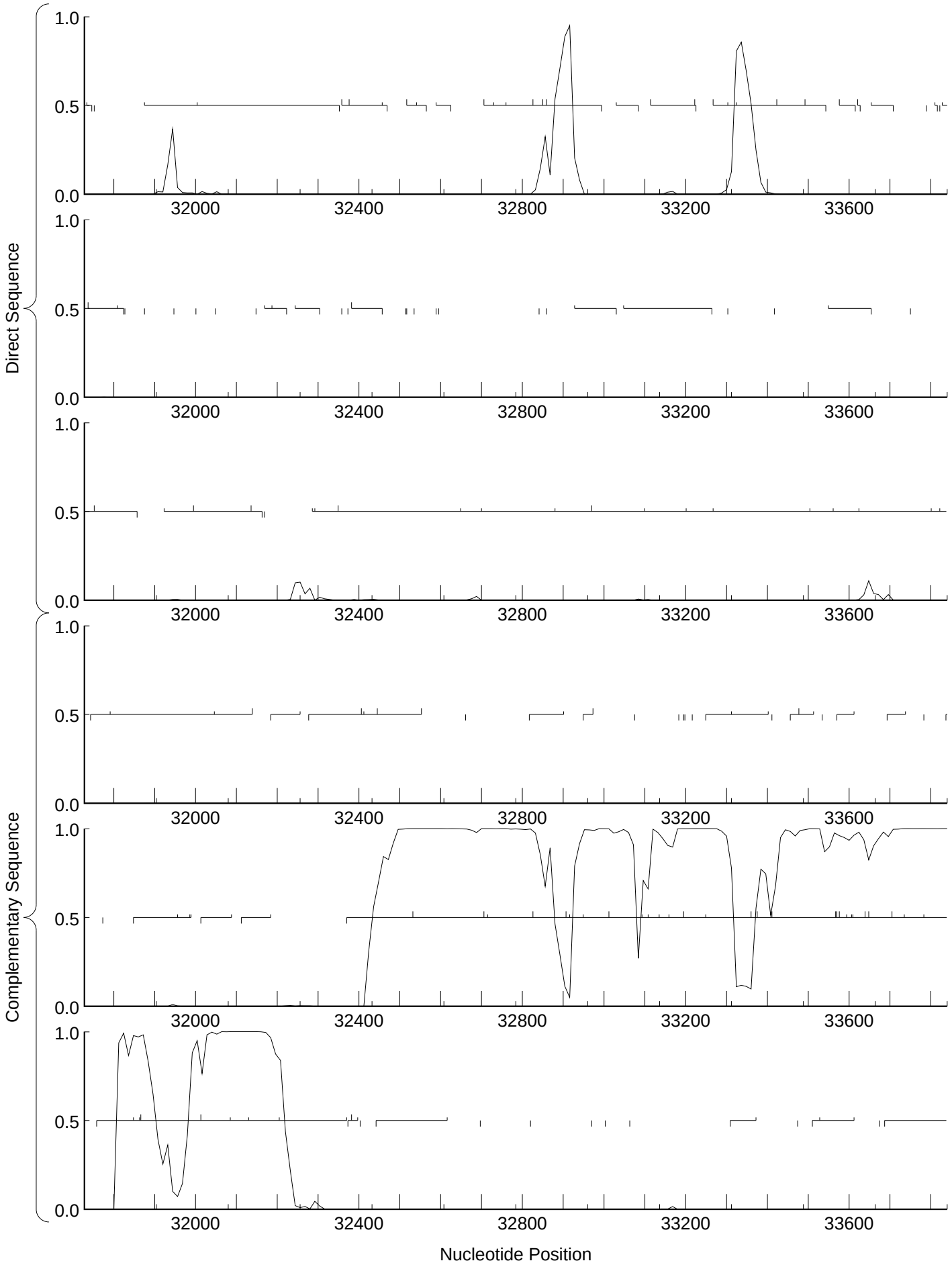

Direct Sequence
Complementary Sequence
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0.0
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24400
24800
25200
Nucleotide Position

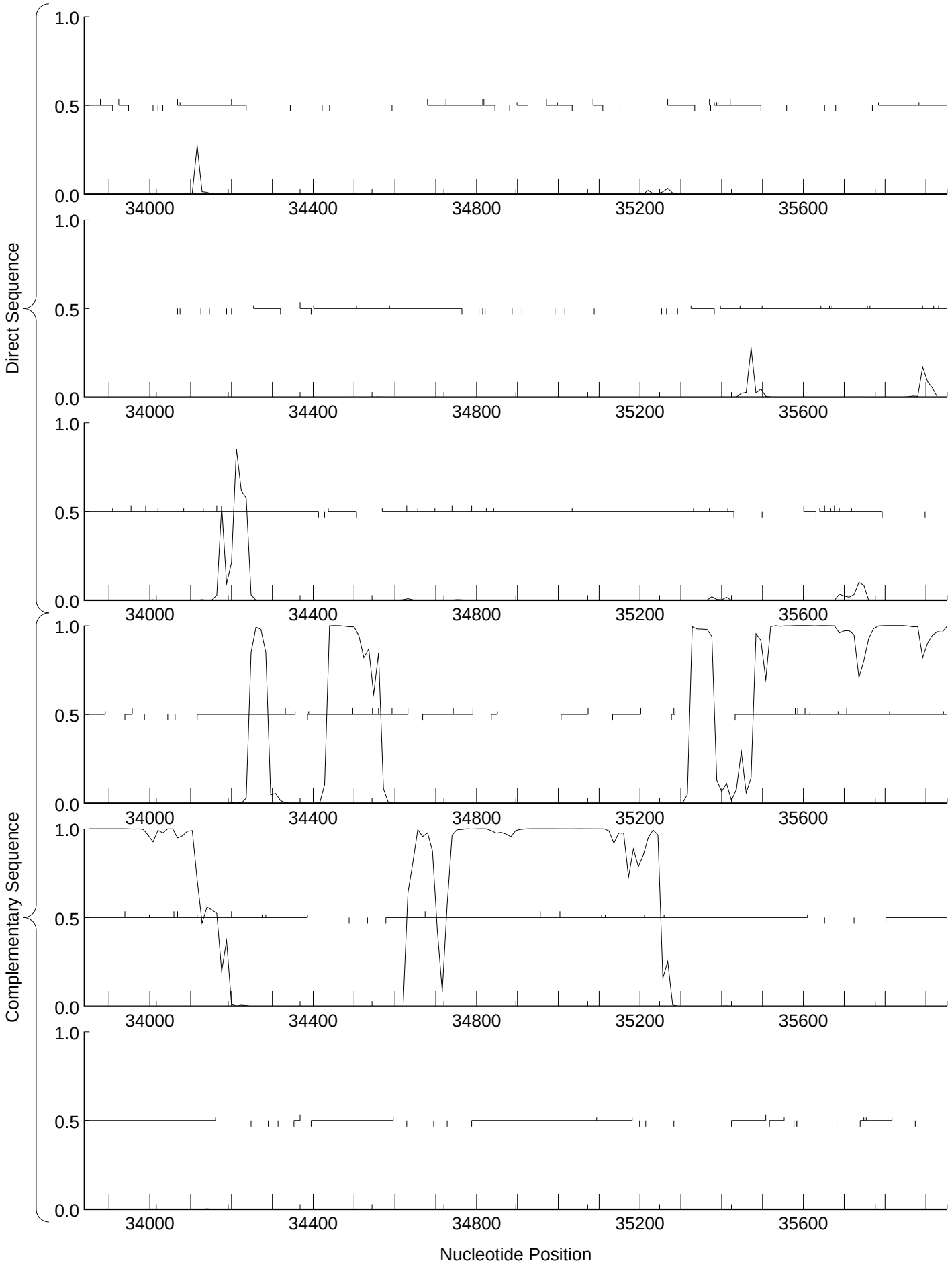

Direct Sequence
Complementary Sequence
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0.5
0.0
25600
26000
26400
26800
27200
Nucleotide Position

k complete sequence, 52772 bp including 10-base 3’ overhang (CGGTCGGTTA), Cluster A2, Order 4, Window 96, Step 12, 15/26

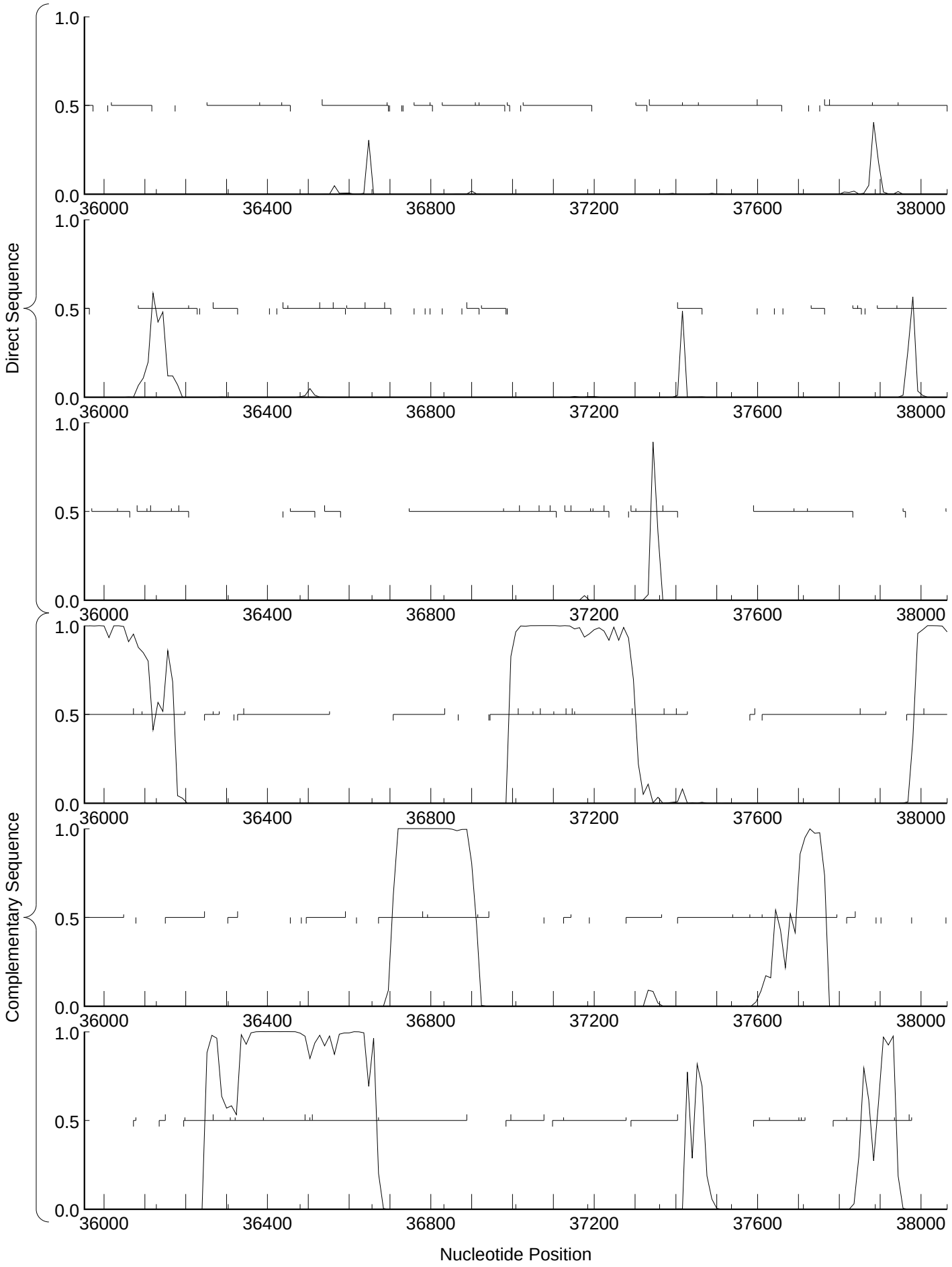


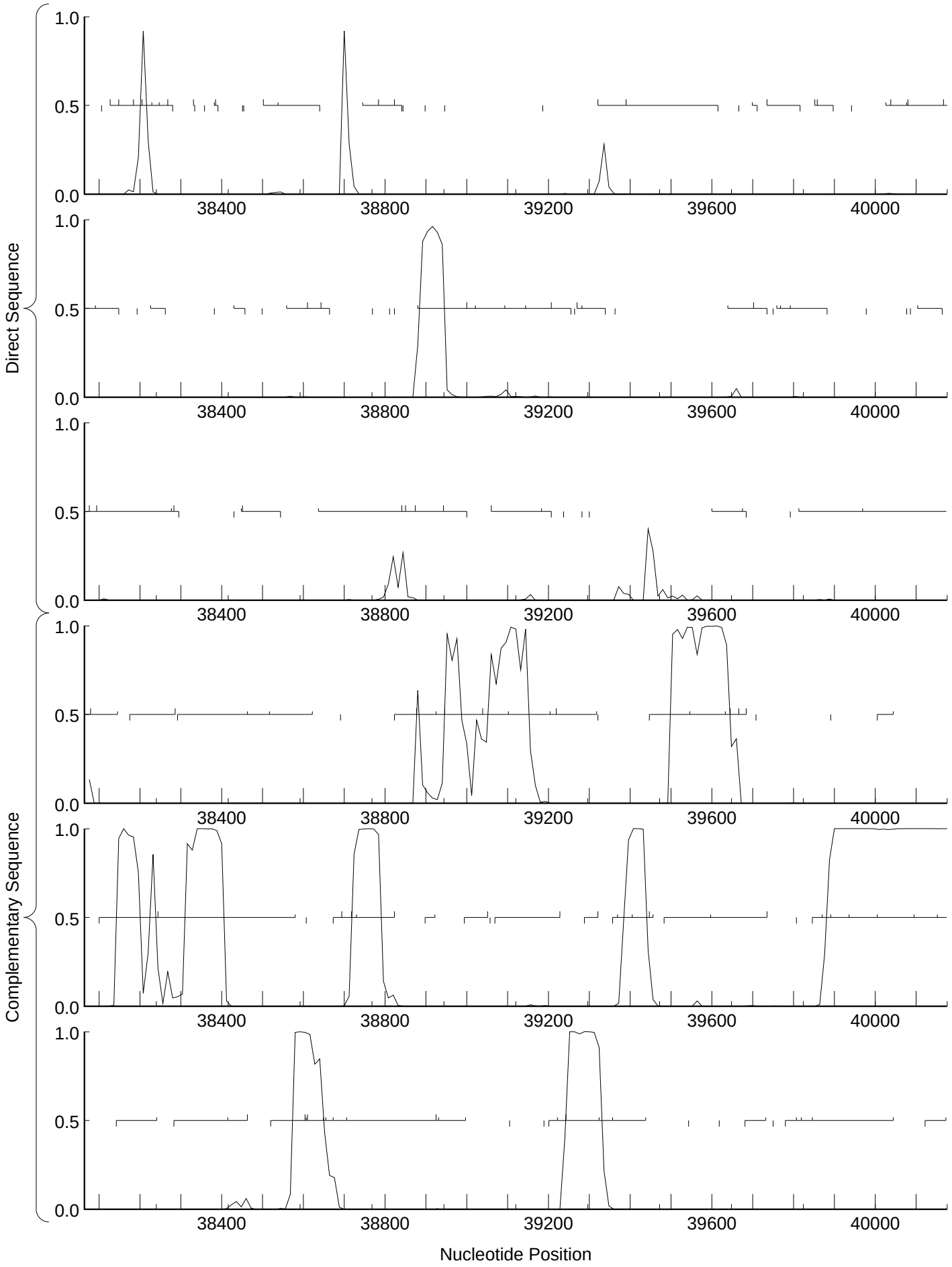

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Complementary Sequence
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31200
31600
Nucleotide Position

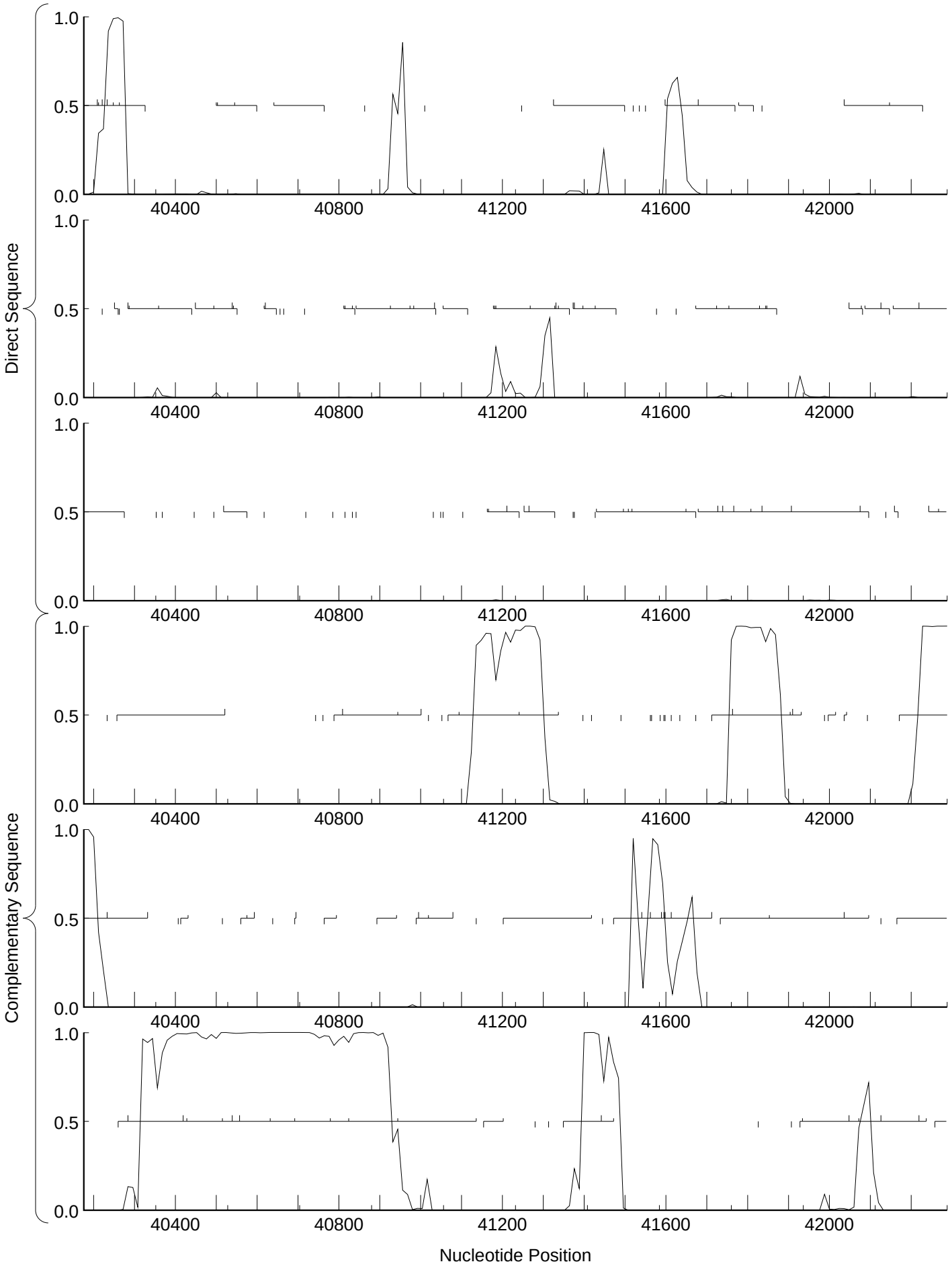

Direct Sequence
Complementary Sequence
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33200
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Nucleotide Position

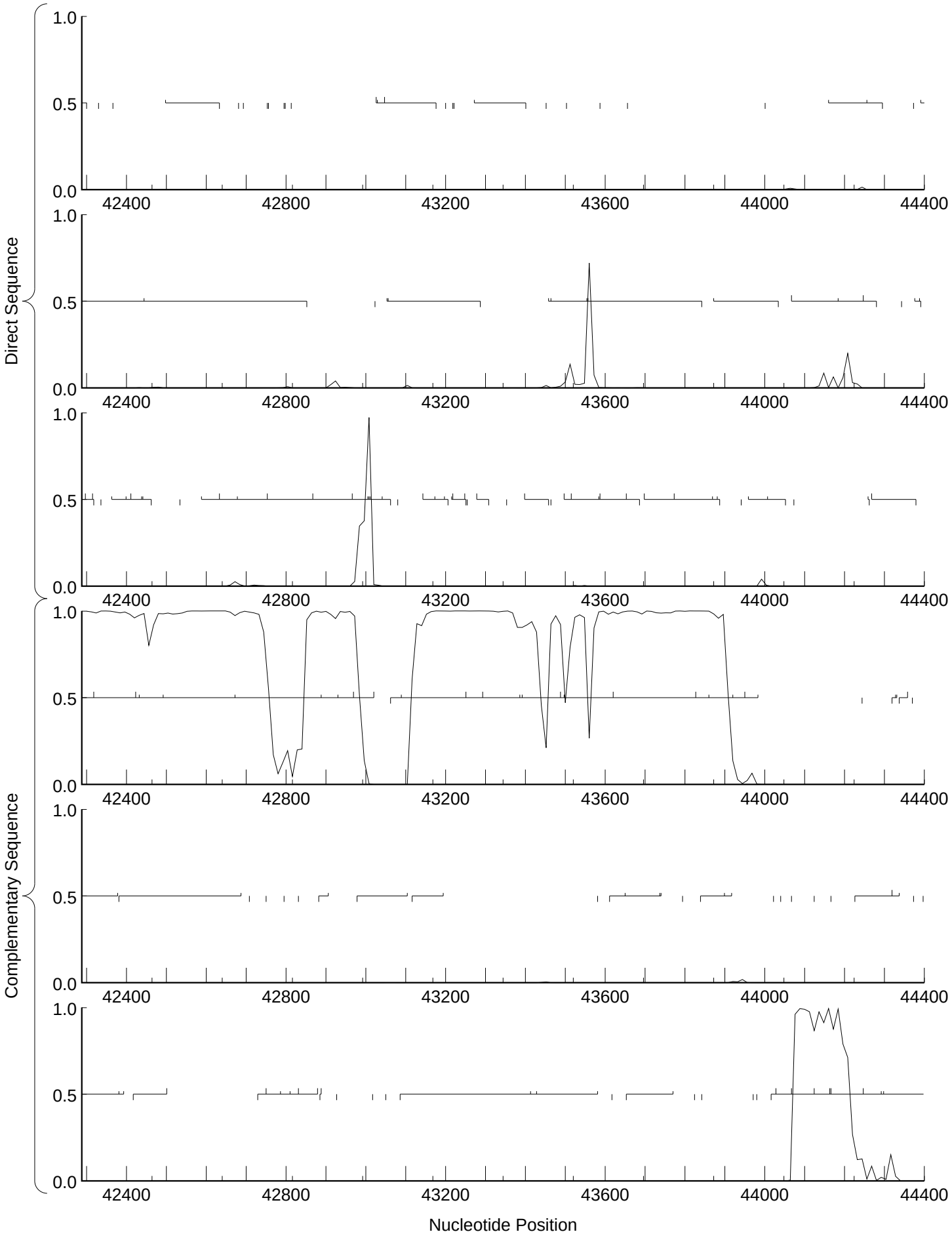

Direct Sequence
Complementary Sequence
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34800
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35600
Nucleotide Position

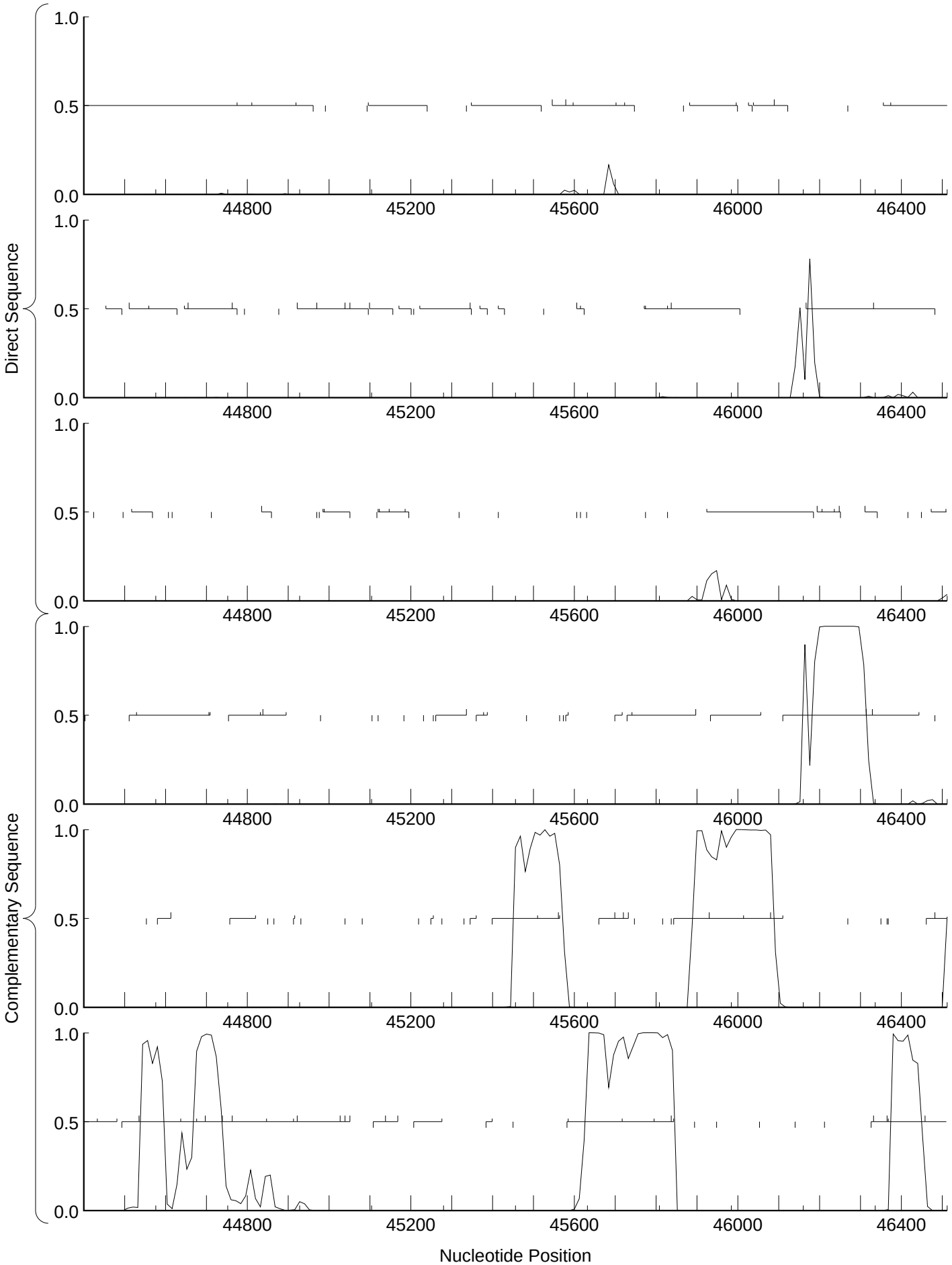
k complete sequence, 52772 bp including 10-base 3' overhang (CGGTCGGTTA), Cluster A2, Order 4, Window 96, Step 12, 19/26



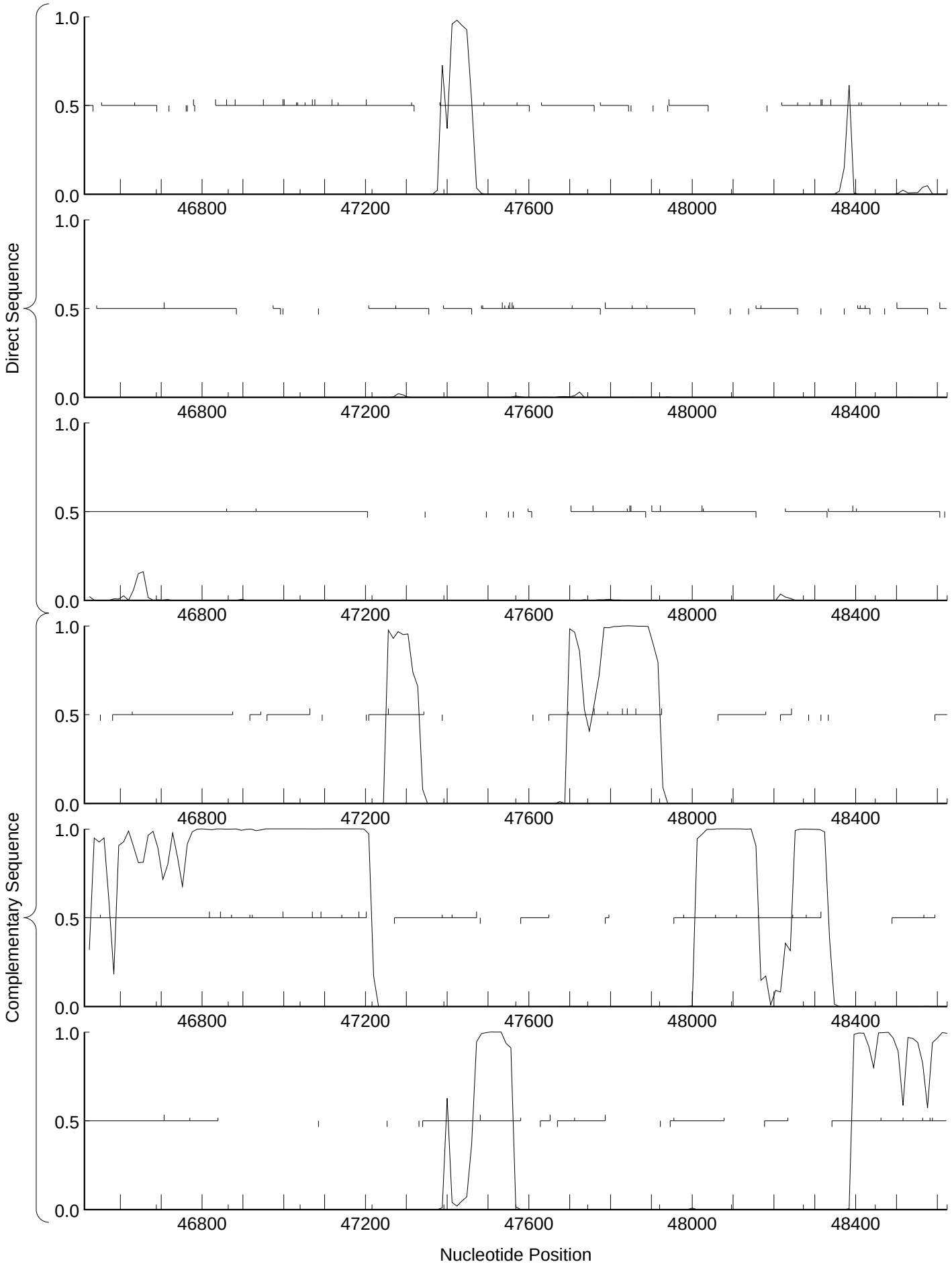

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
38400
38800
39200
39600
40000
Nucleotide Position


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

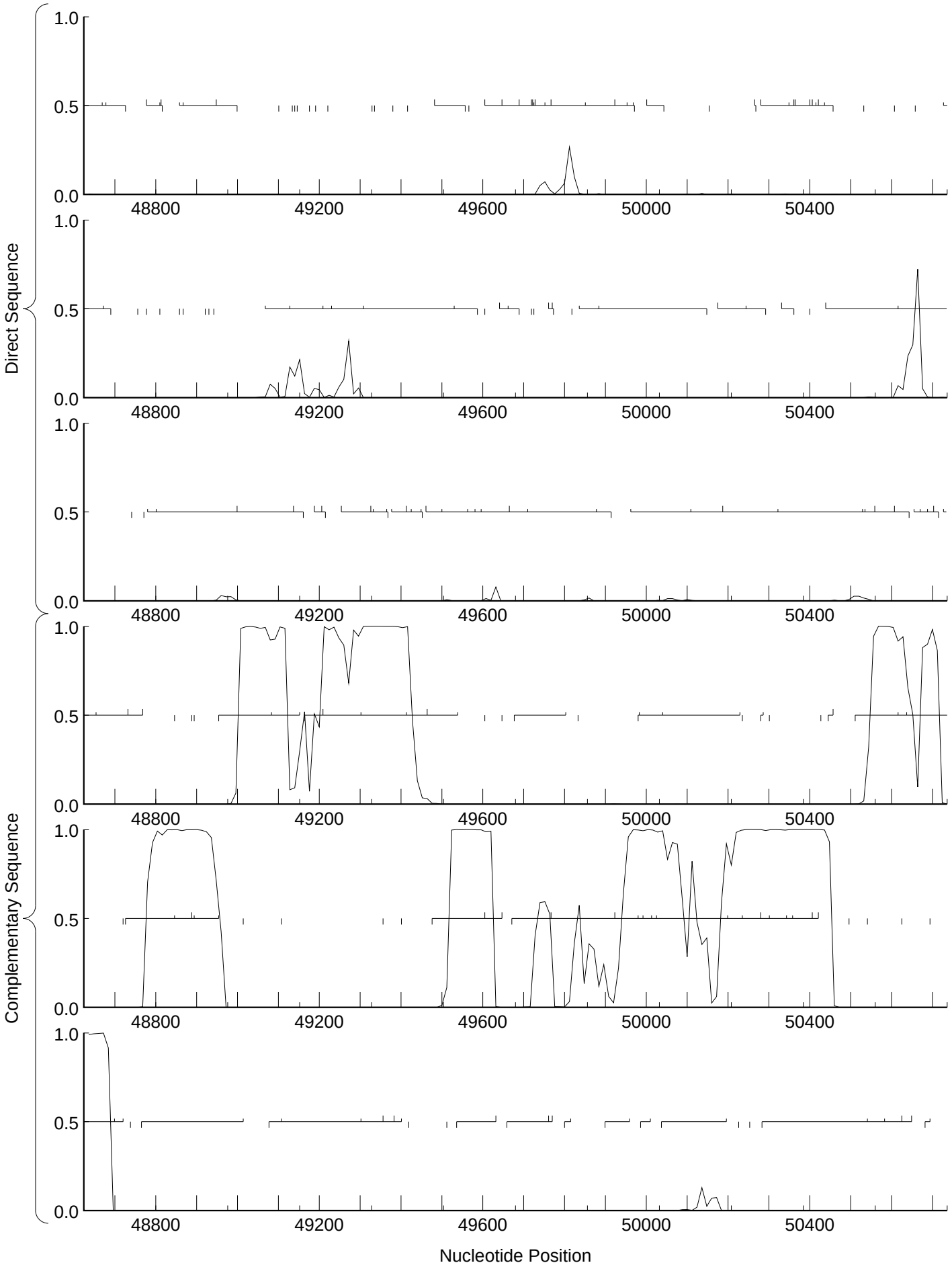

Direct Sequence
Complementary Sequence
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43600
44000
44400
Nucleotide Position

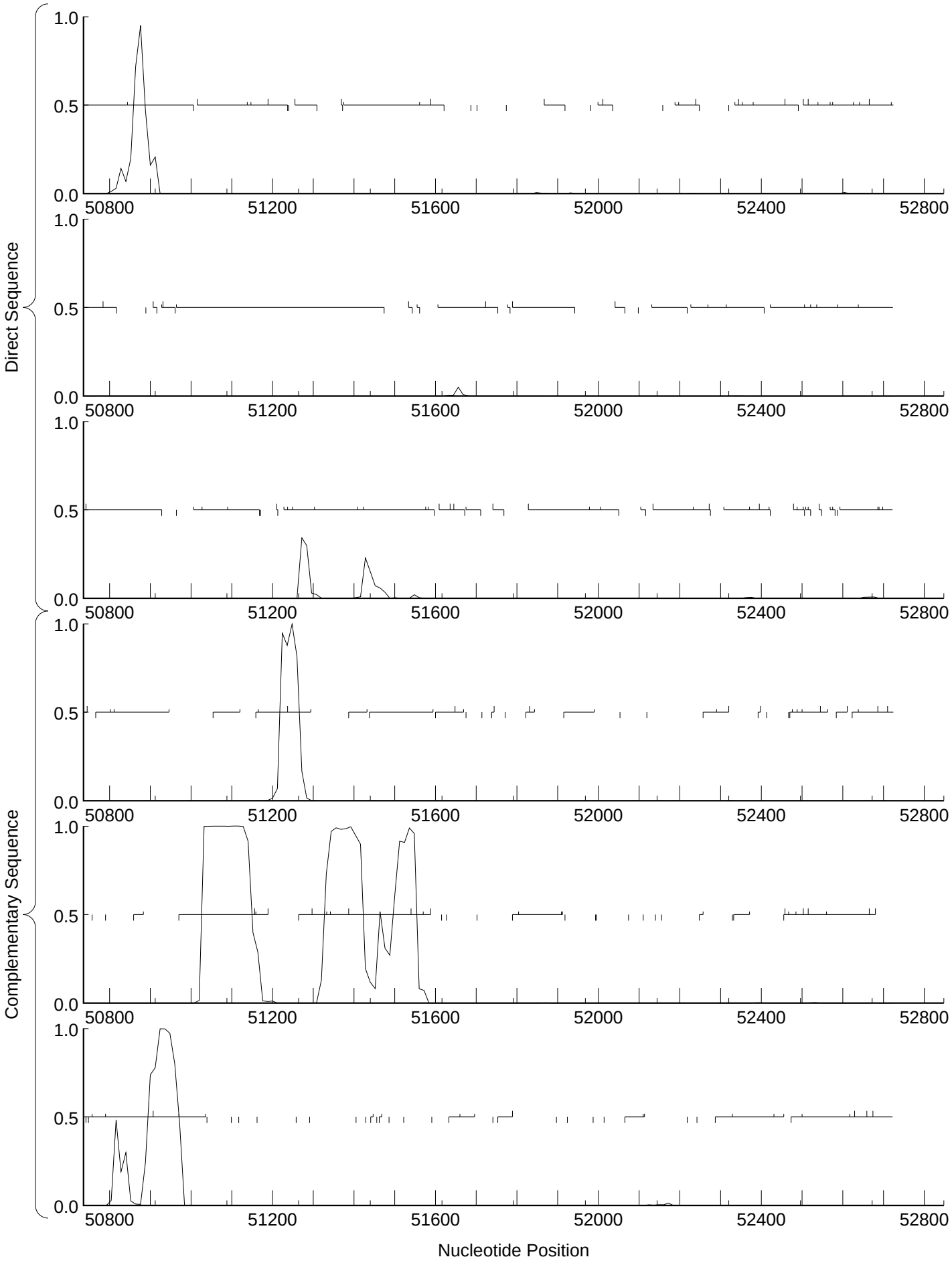

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
44800
45200
45600
46000
46400
Nucleotide Position

k complete sequence, 52772 bp including 10-base 3’ overhang (CGGTCGGTTA), Cluster A2, Order 4, Window 96, Step 12, 24/26



k complete sequence, 52772 bp including 10-base 3’ overhang (CGGTCGGTTA), Cluster A2, Order 4, Window 96, Step 12, 25/26




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