GeneMark

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

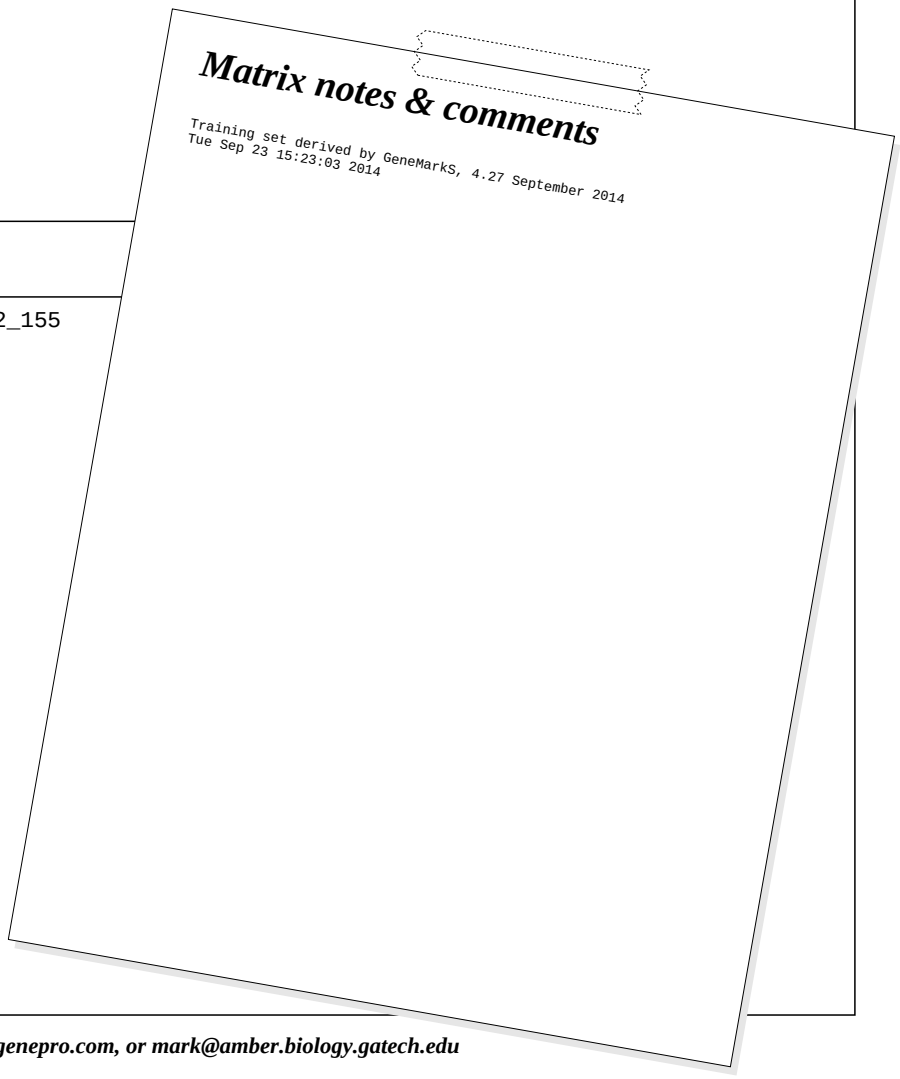
PROGRAM INFORMATION

```
Sequence         :  Mycobacterium phage Edtherson complete sequence, 51492 bp including 10-base 3’ overhang (CG
Analysis Date    :  3/29/24 at 8:12:38
Pages            :  26
Sequence Length  :  51492 bp
GC Content       :   63.98%

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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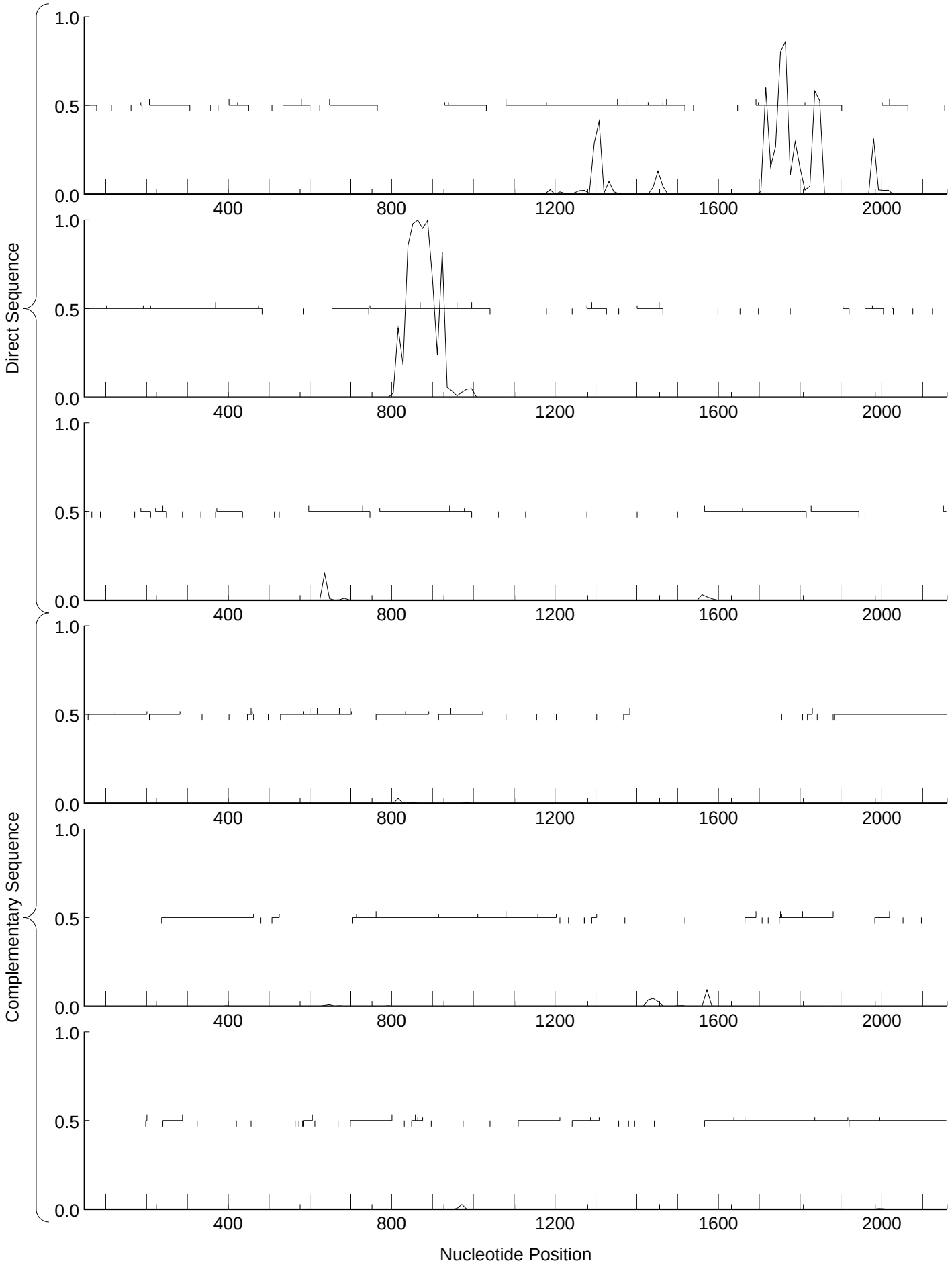
MATRIX INFORMATION

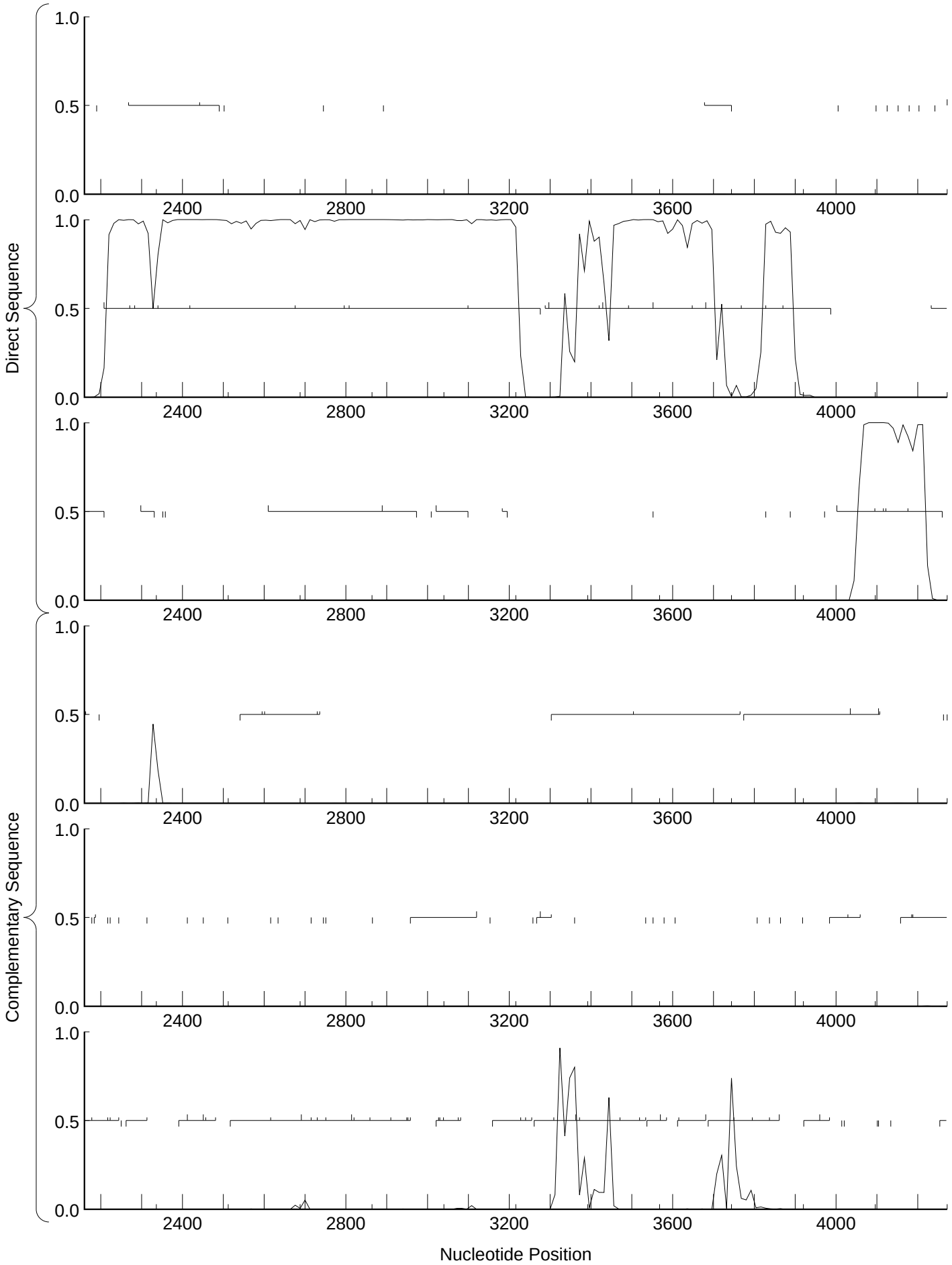
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Matrix     :  Mycobacterium_smegmatis_MC2_155
Author     :  -

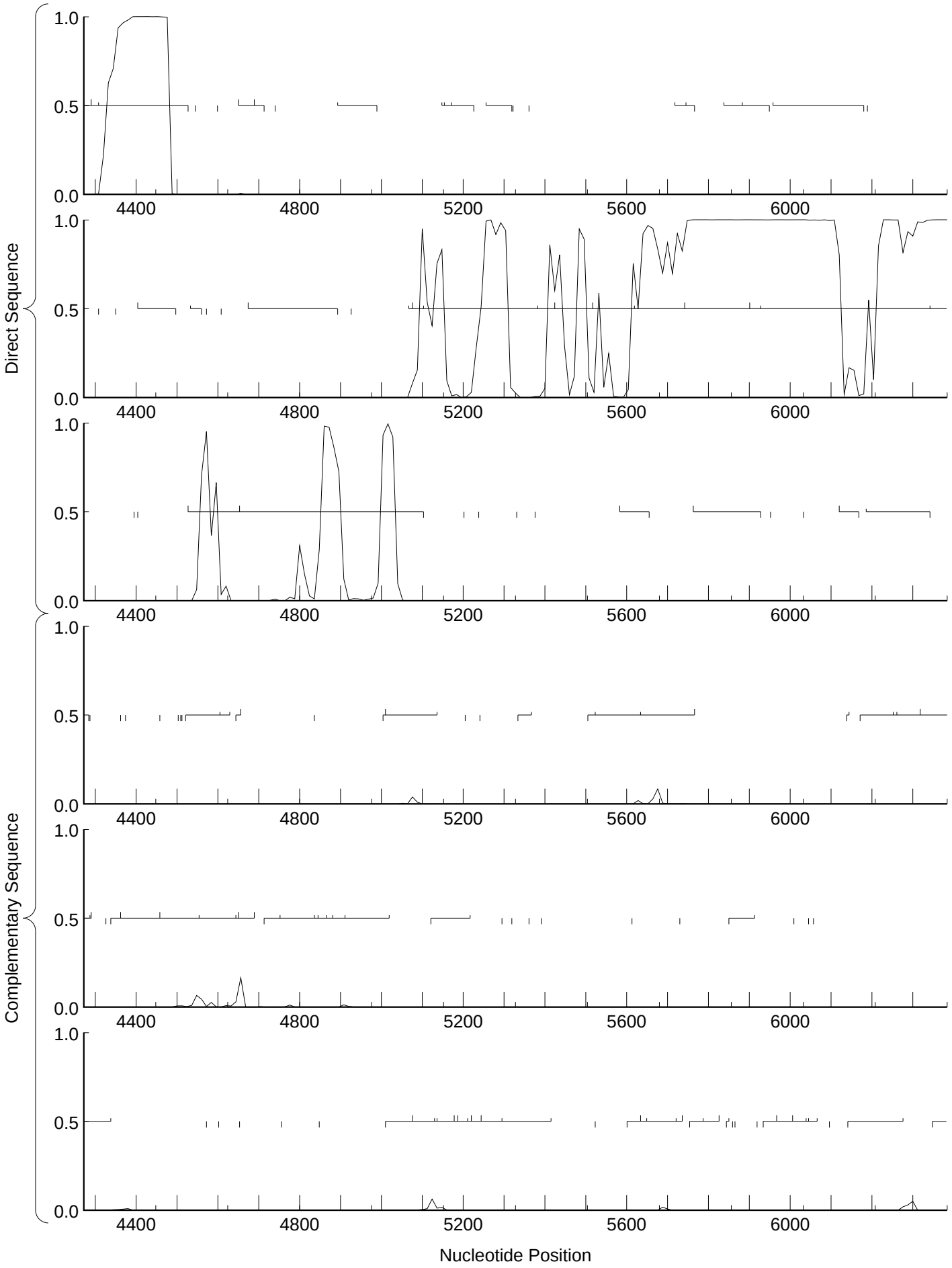
Order      :  4
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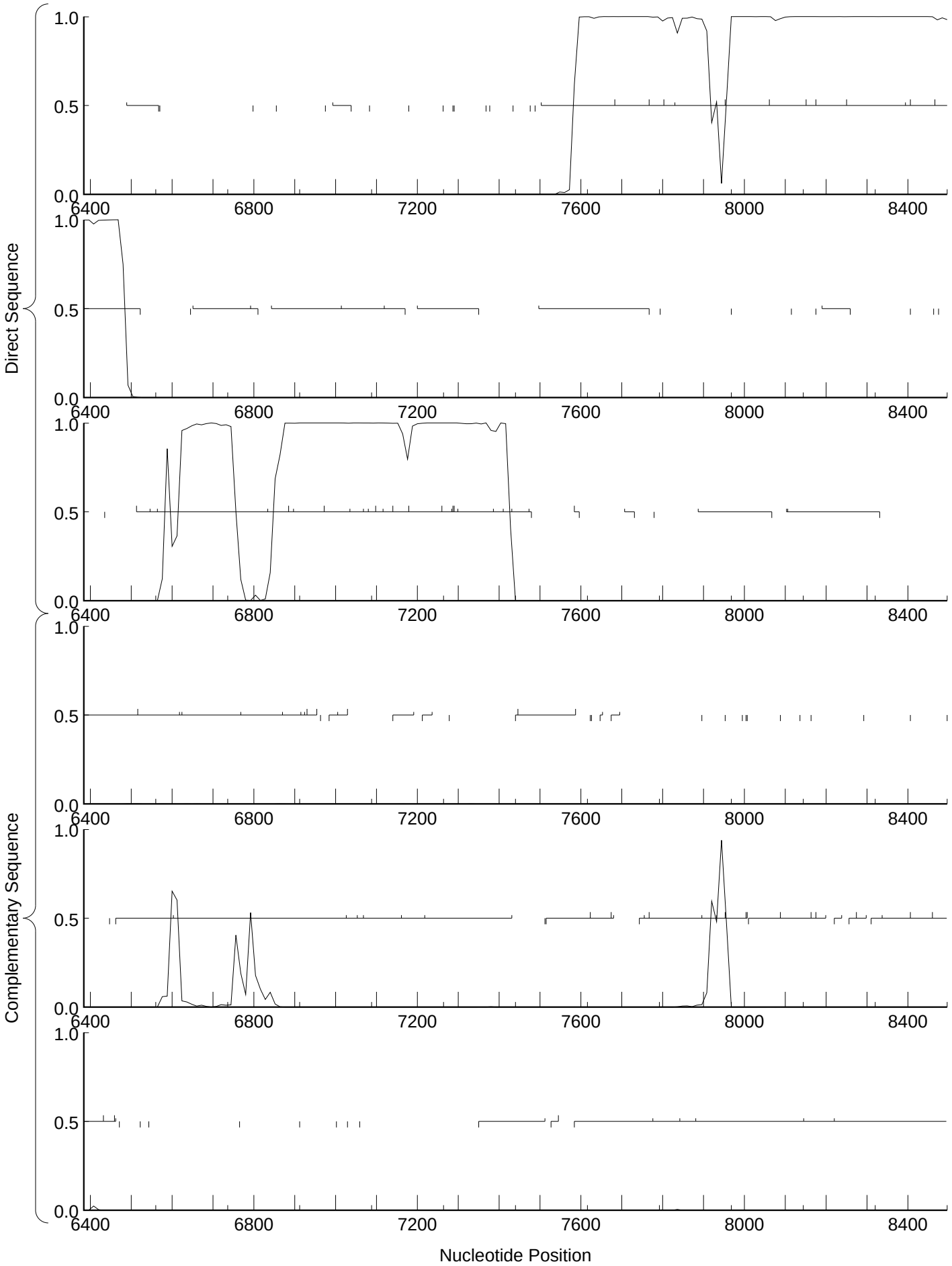

```
  Send questions / comments to:
      Dr. M. Borodovsky
      Georgia Institute of Technology
      School of Biology
      Atlanta, GA  30332-0230
```

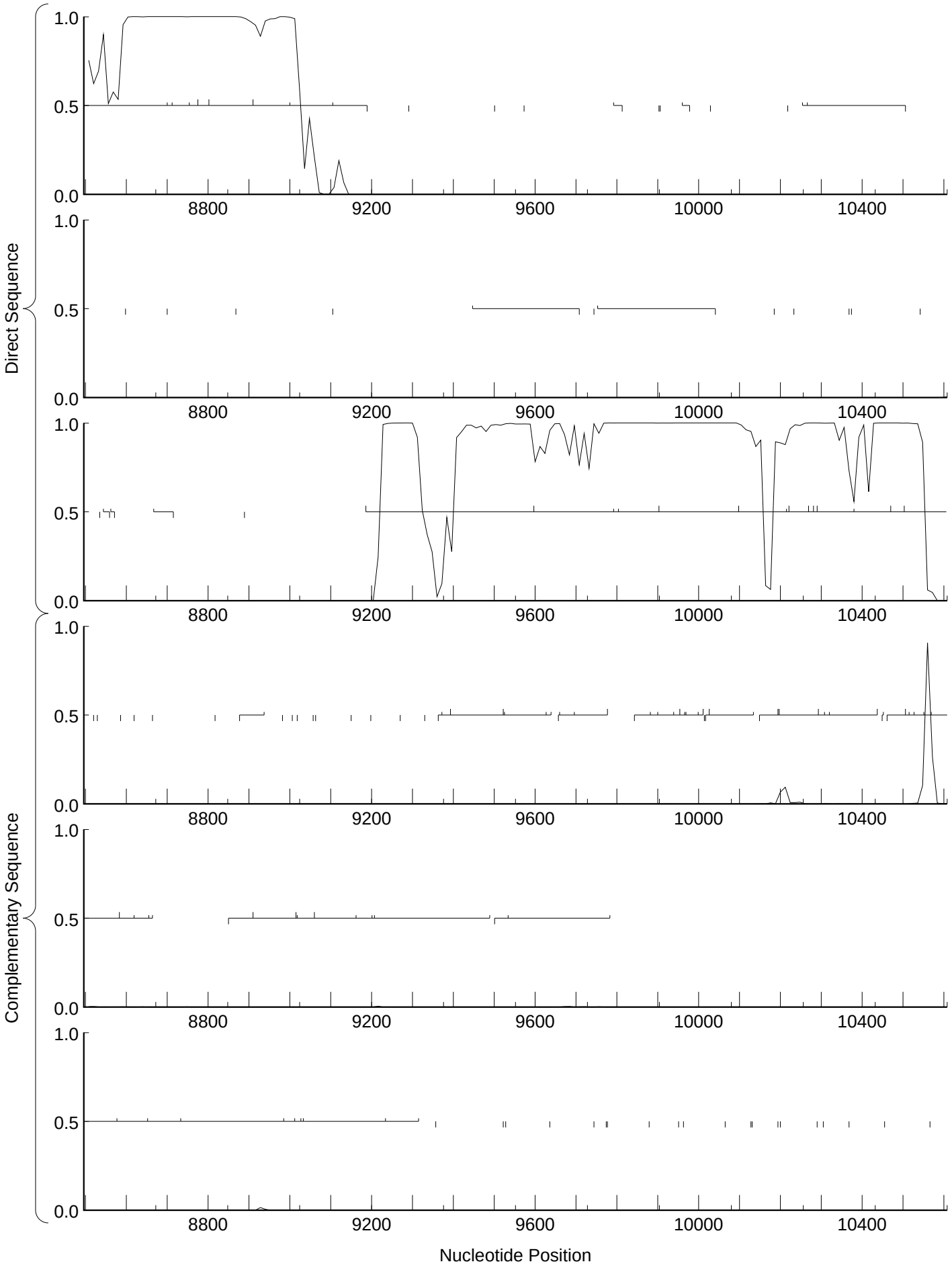

For help or information, send electronic mail to: custserv@genepro.com, or mark@amber.biology.gatech.edu

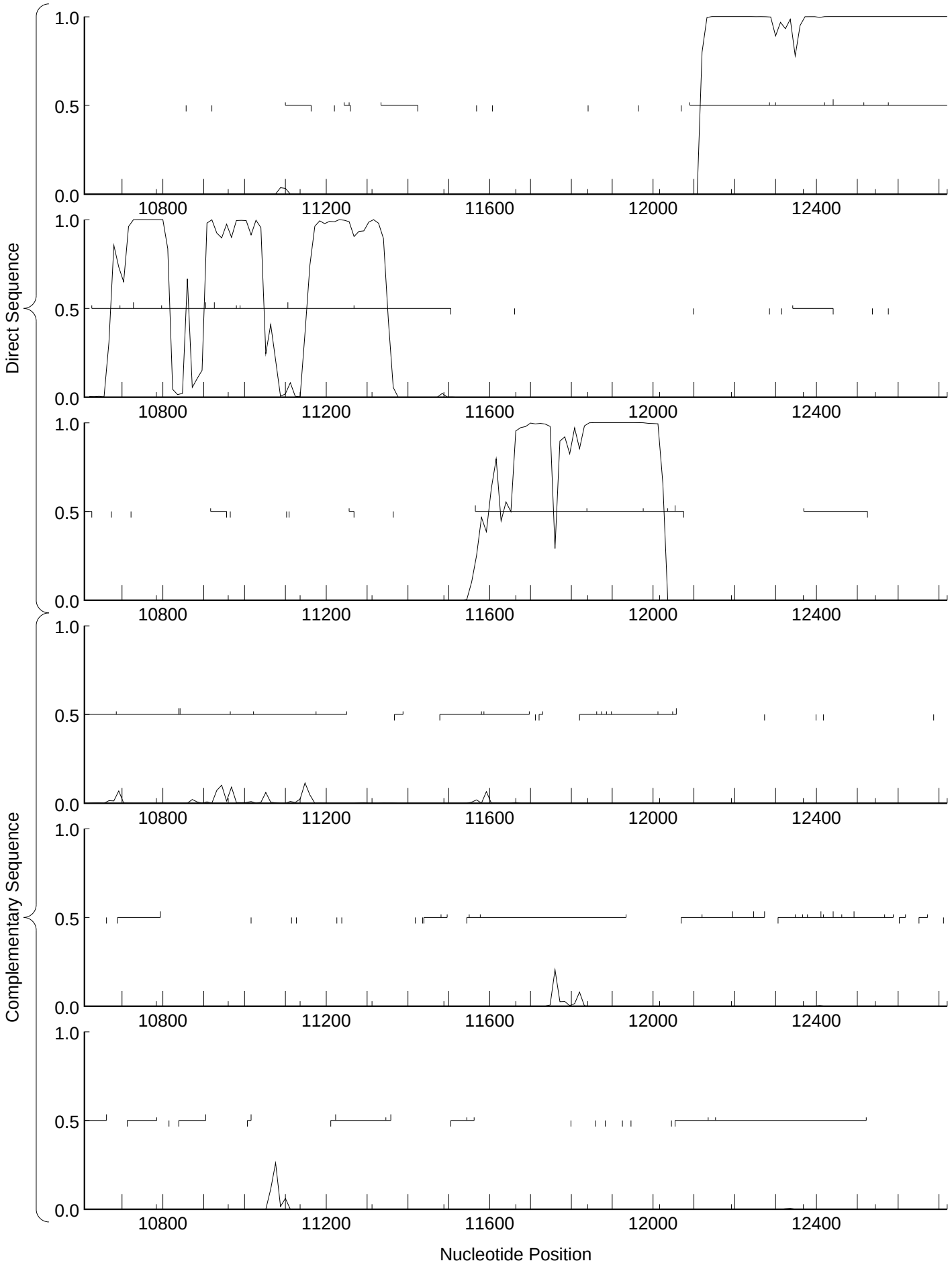

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Complementary Sequence
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0.0
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800
1200
1600
2000
Nucleotide Position

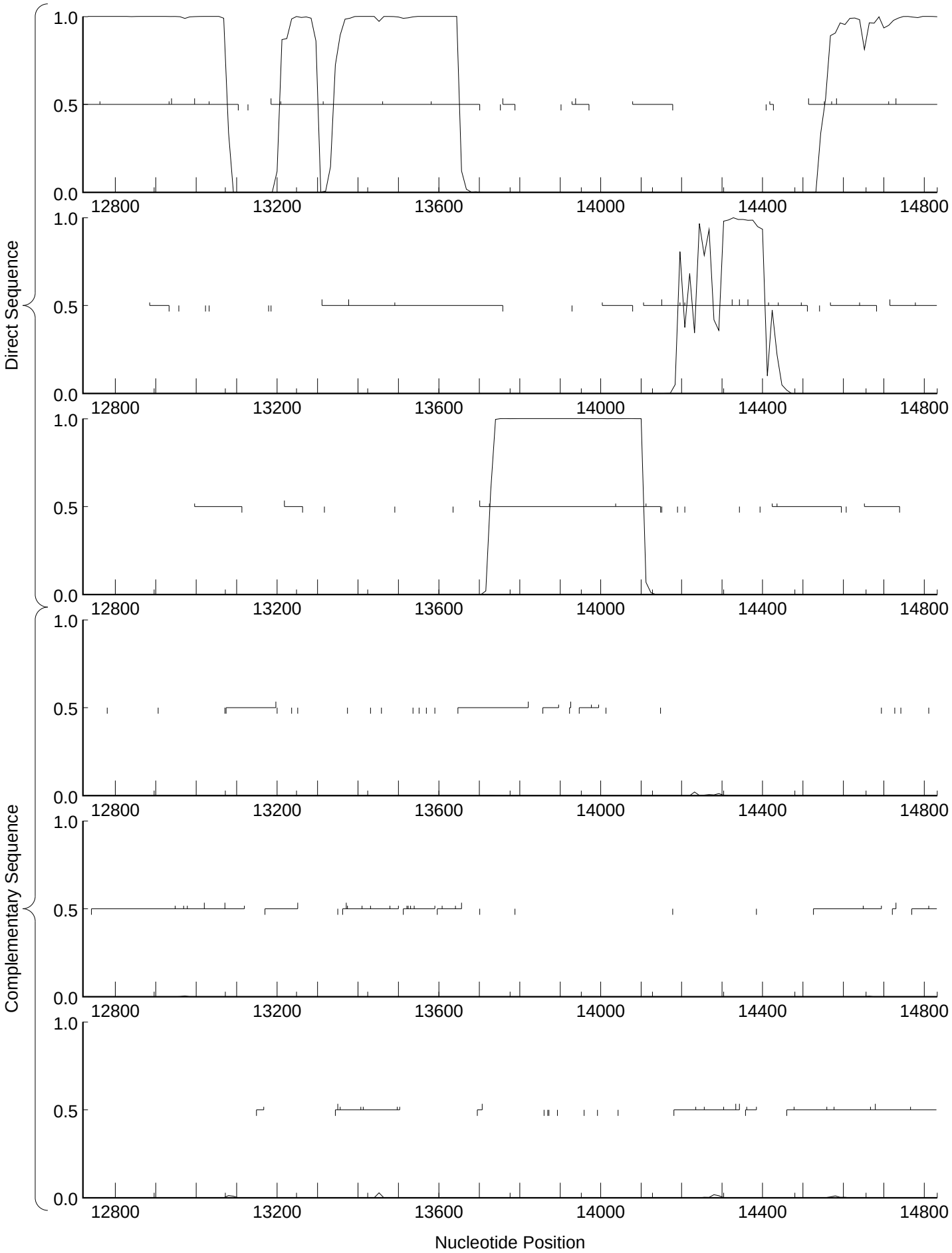

Direct Sequence
Complementary Sequence
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0.0
2400
2800
3200
3600
4000
Nucleotide Position


Direct Sequence
Complementary Sequence
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4400
4800
5200
5600
6000
Nucleotide Position

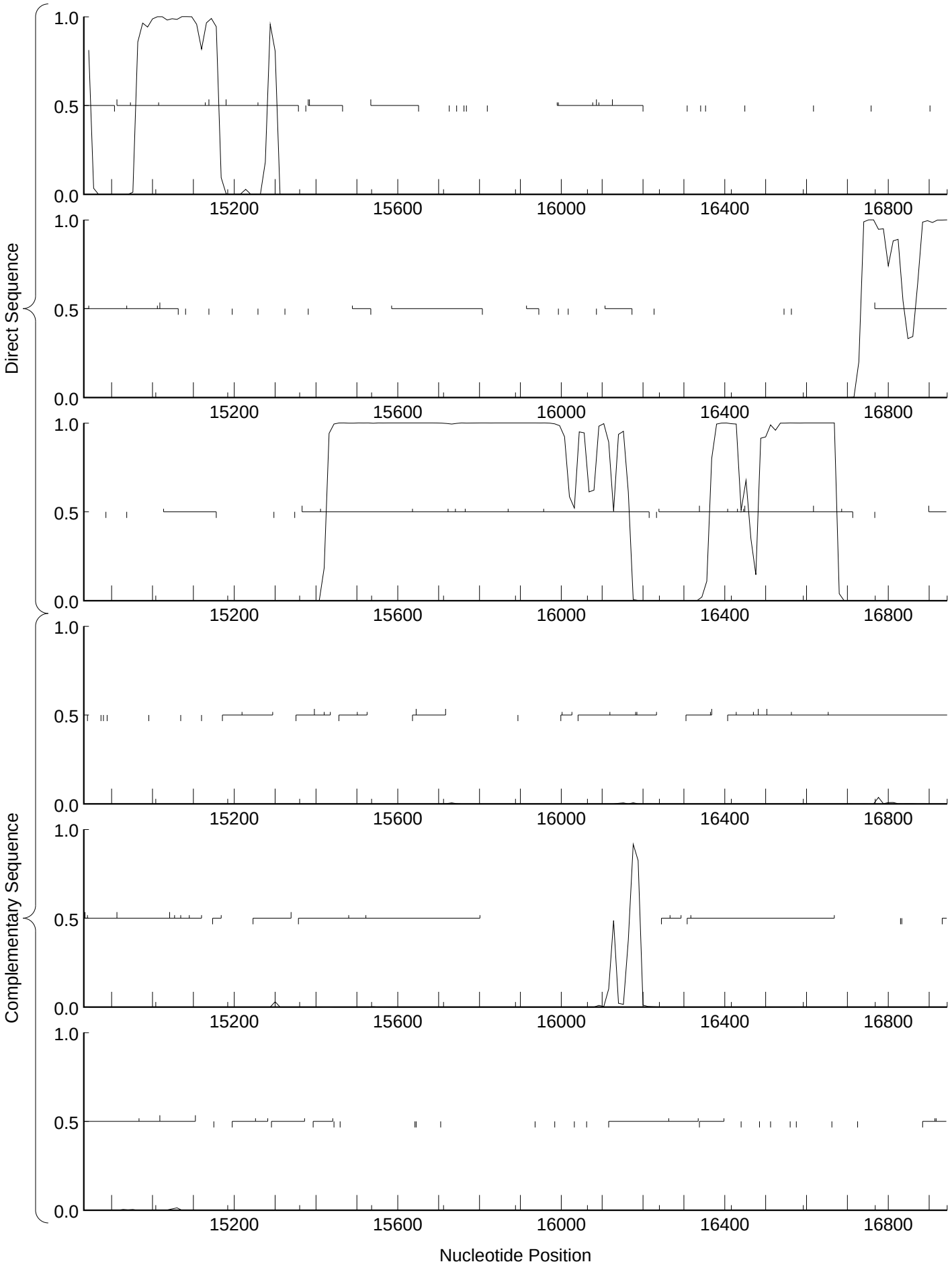

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7600
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8400
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Direct Sequence
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8800
9200
9600
10000
10400
Nucleotide Position

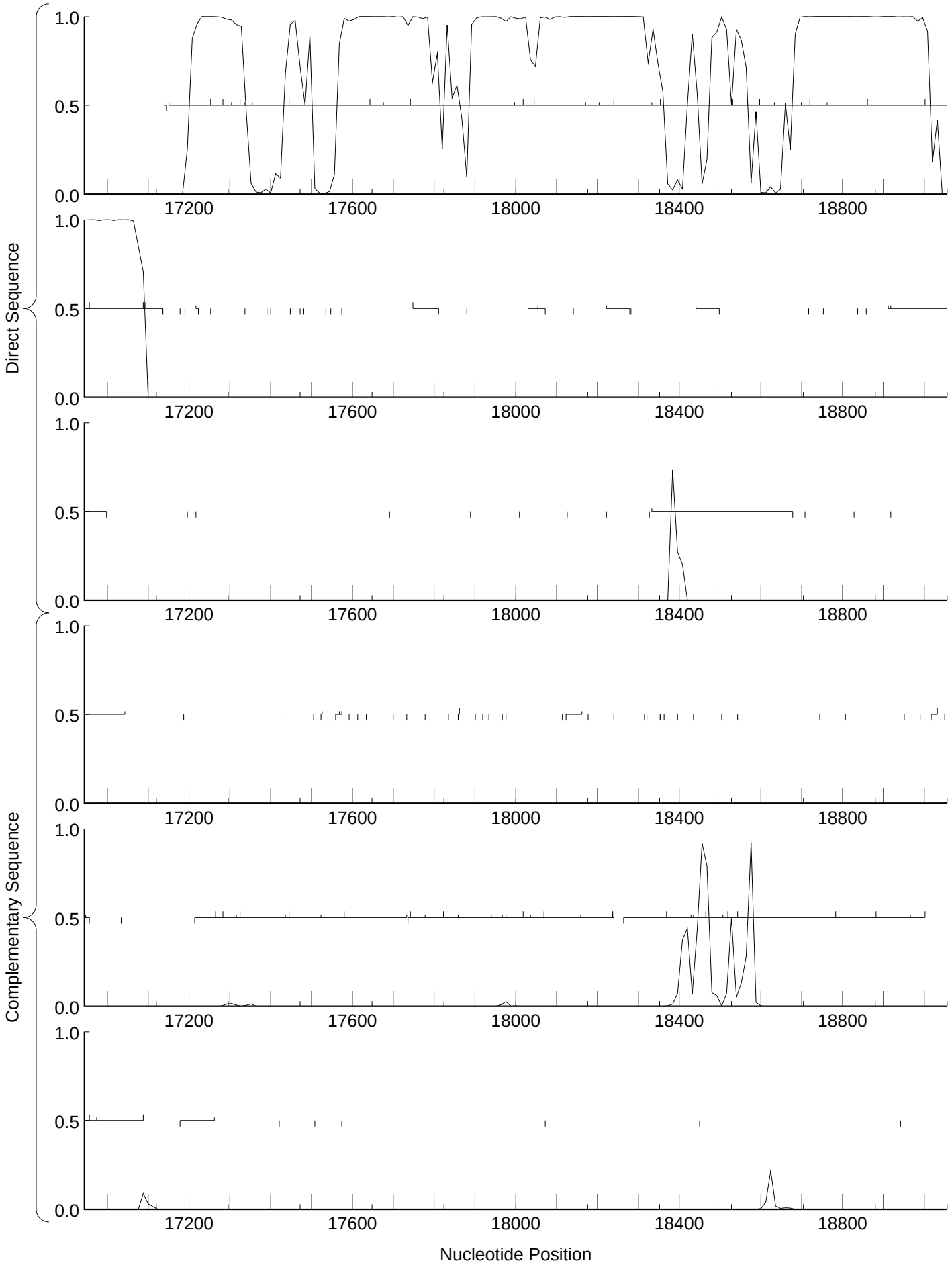

Direct Sequence
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0.0
10800
11200
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12000
12400
Nucleotide Position


Direct Sequence
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12800
13200
13600
14000
14400
14800
Nucleotide Position

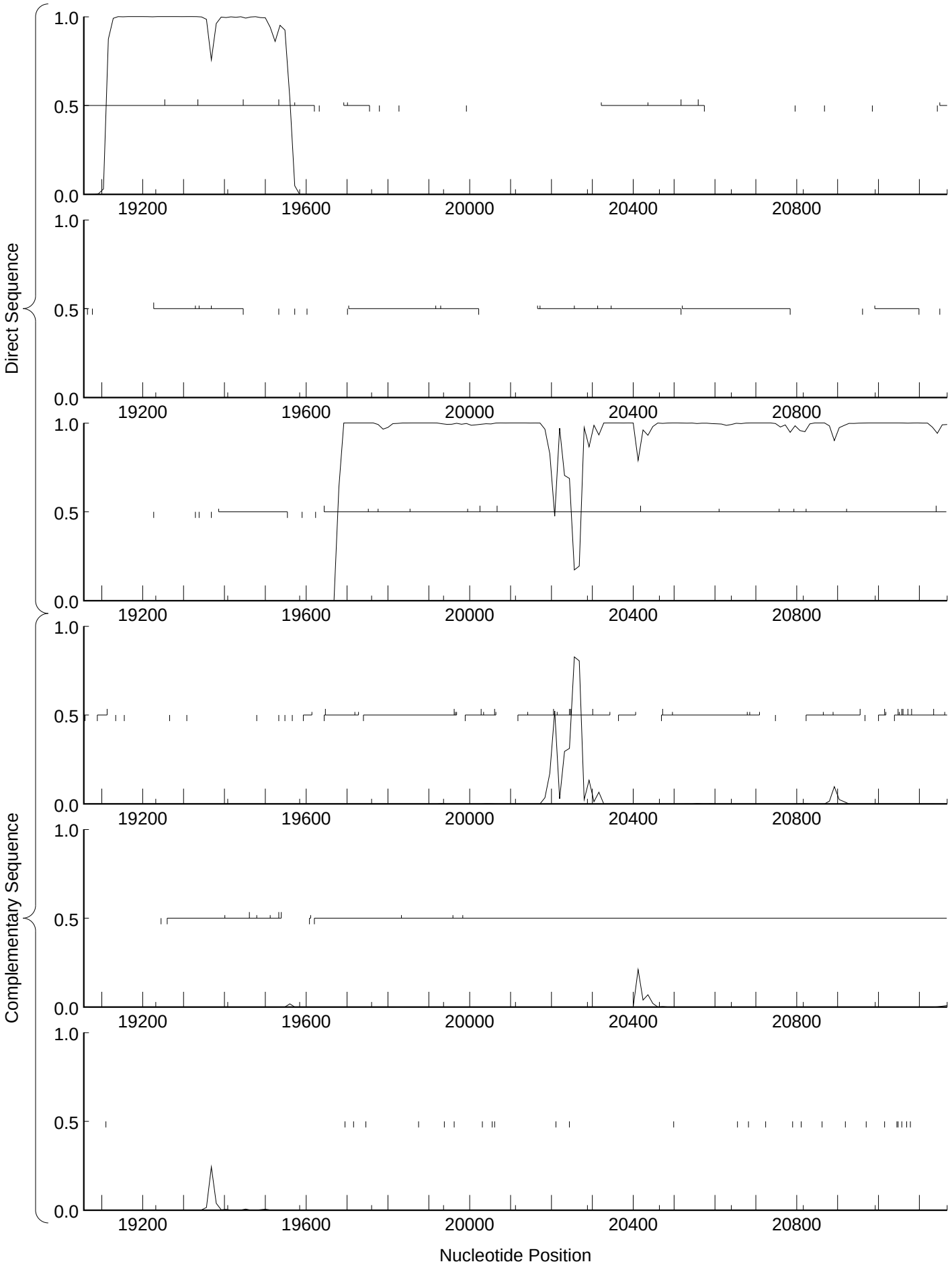
on complete sequence, 51492 bp including 10-base 3’ overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 9/26



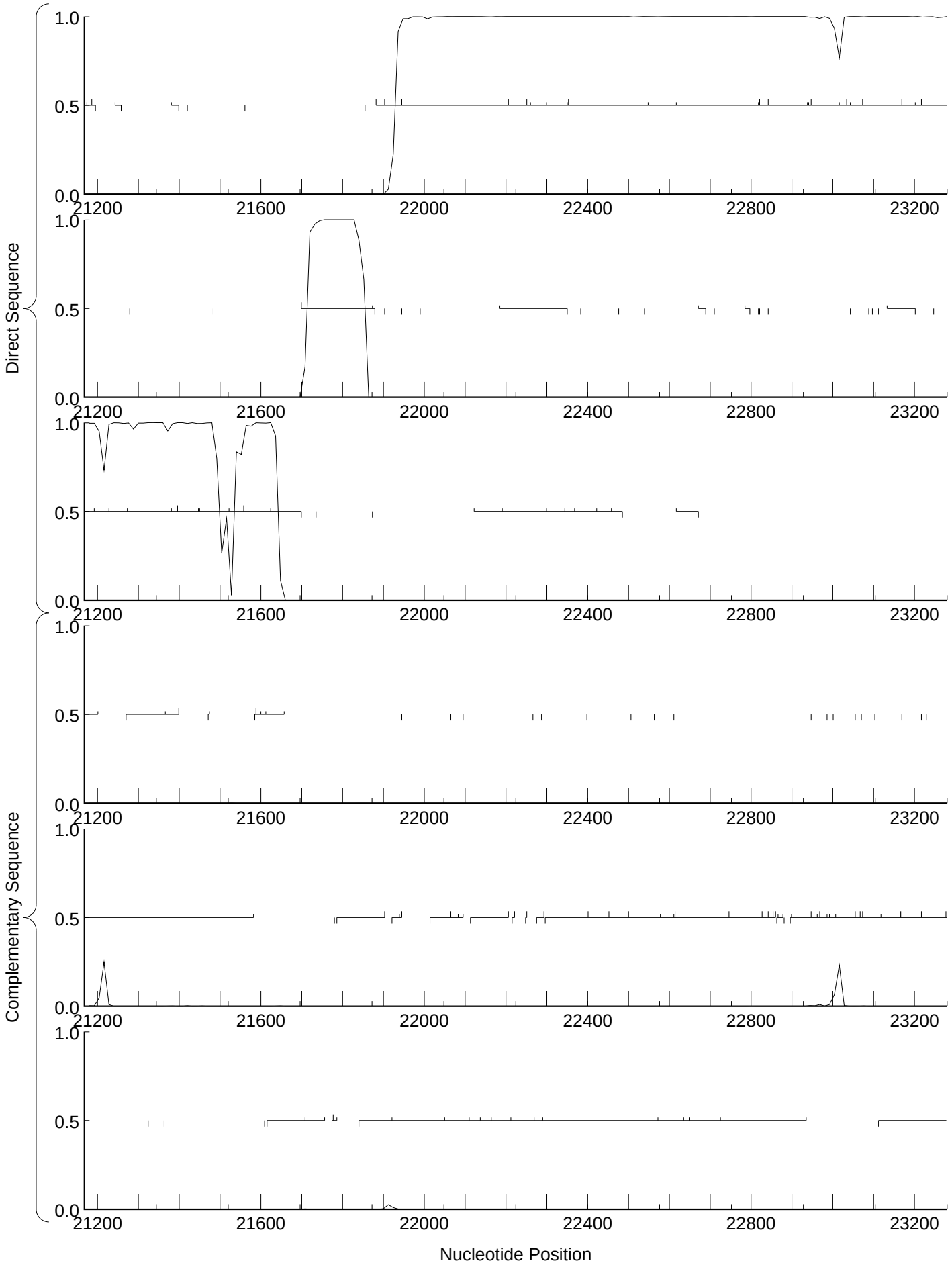
n complete sequence, 51492 bp including 10-base 3’ overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 10/26



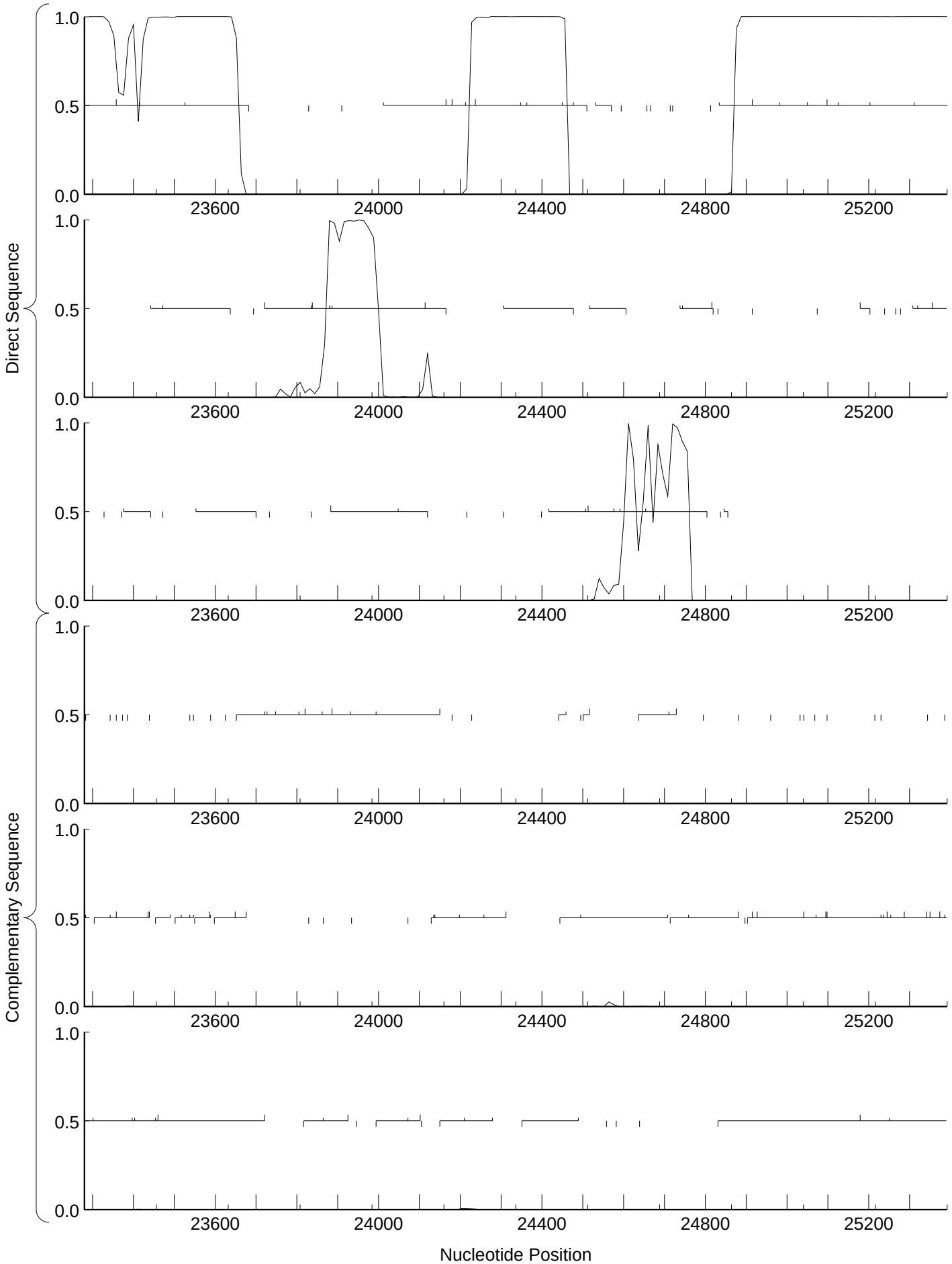
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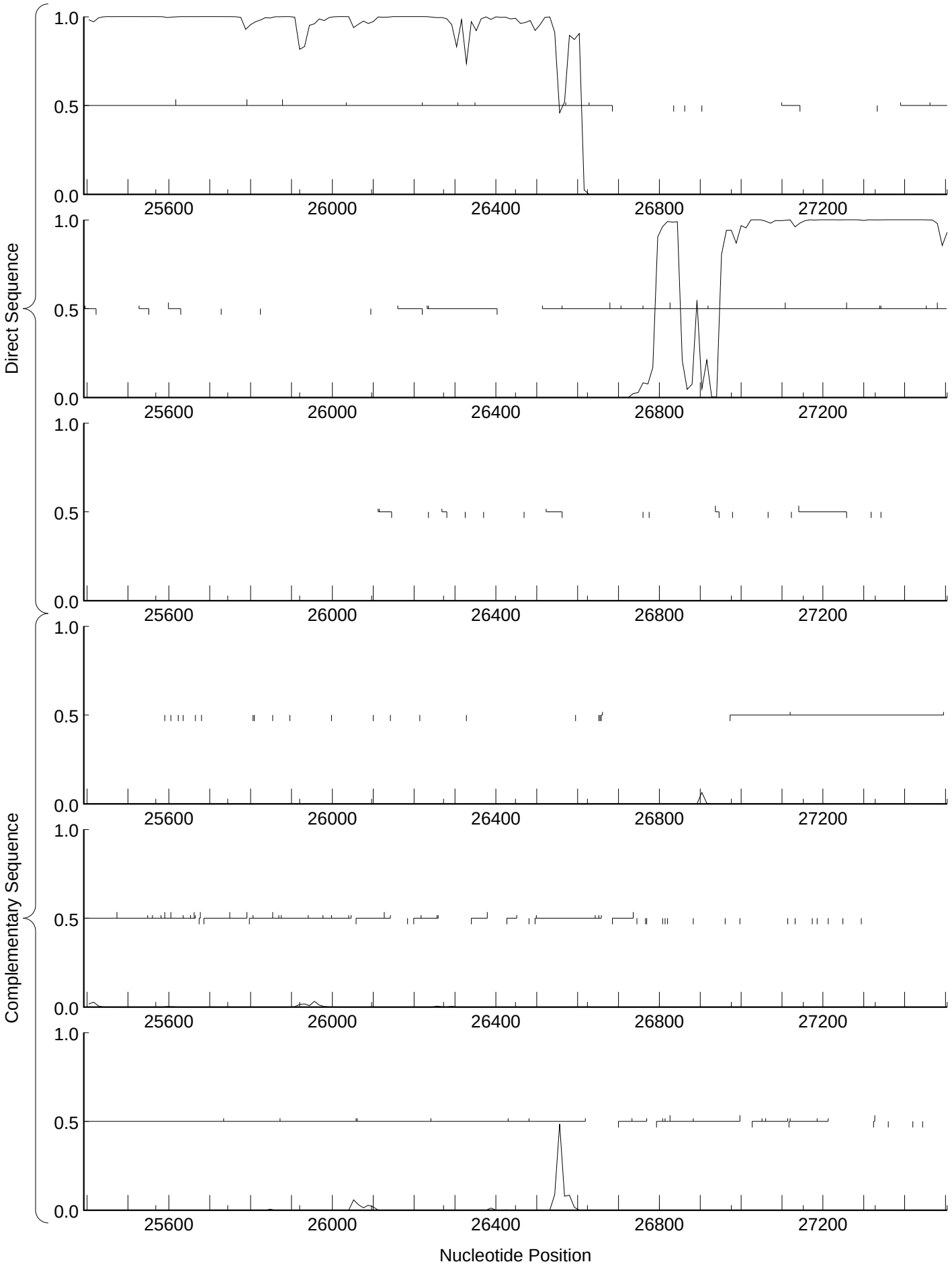
n complete sequence, 51492 bp including 10-base 3' overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 12/26



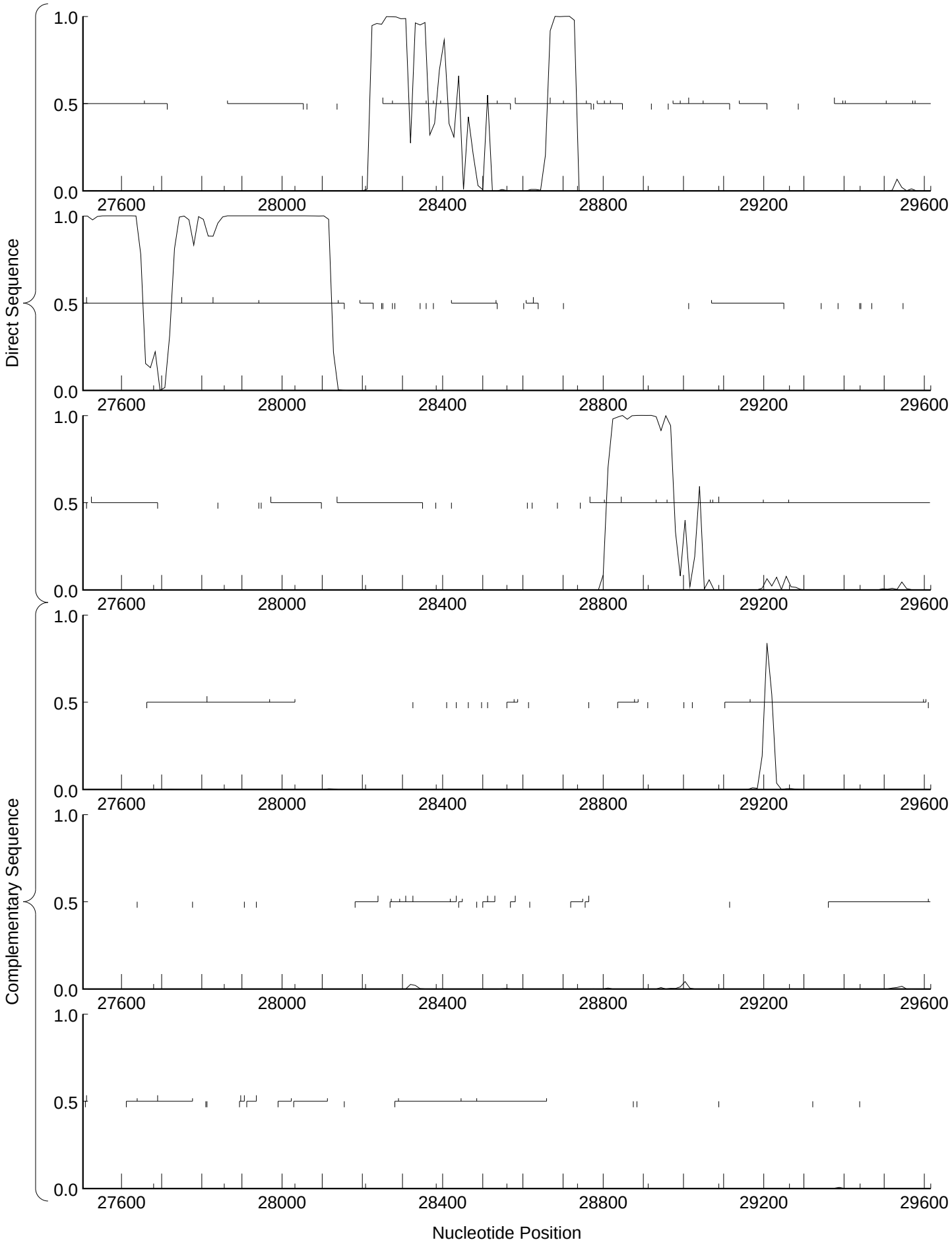
n complete sequence, 51492 bp including 10-base 3' overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 13/26

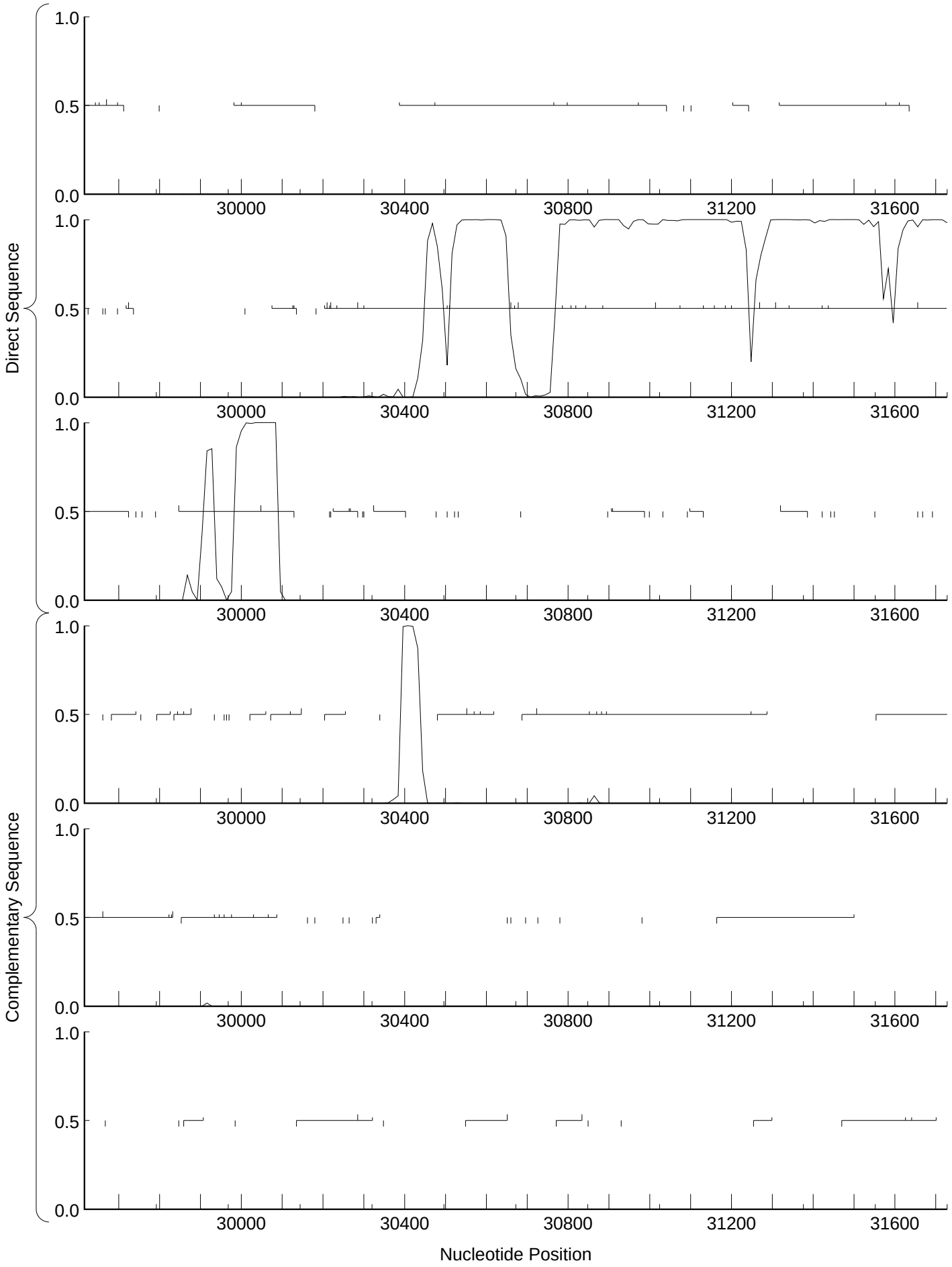


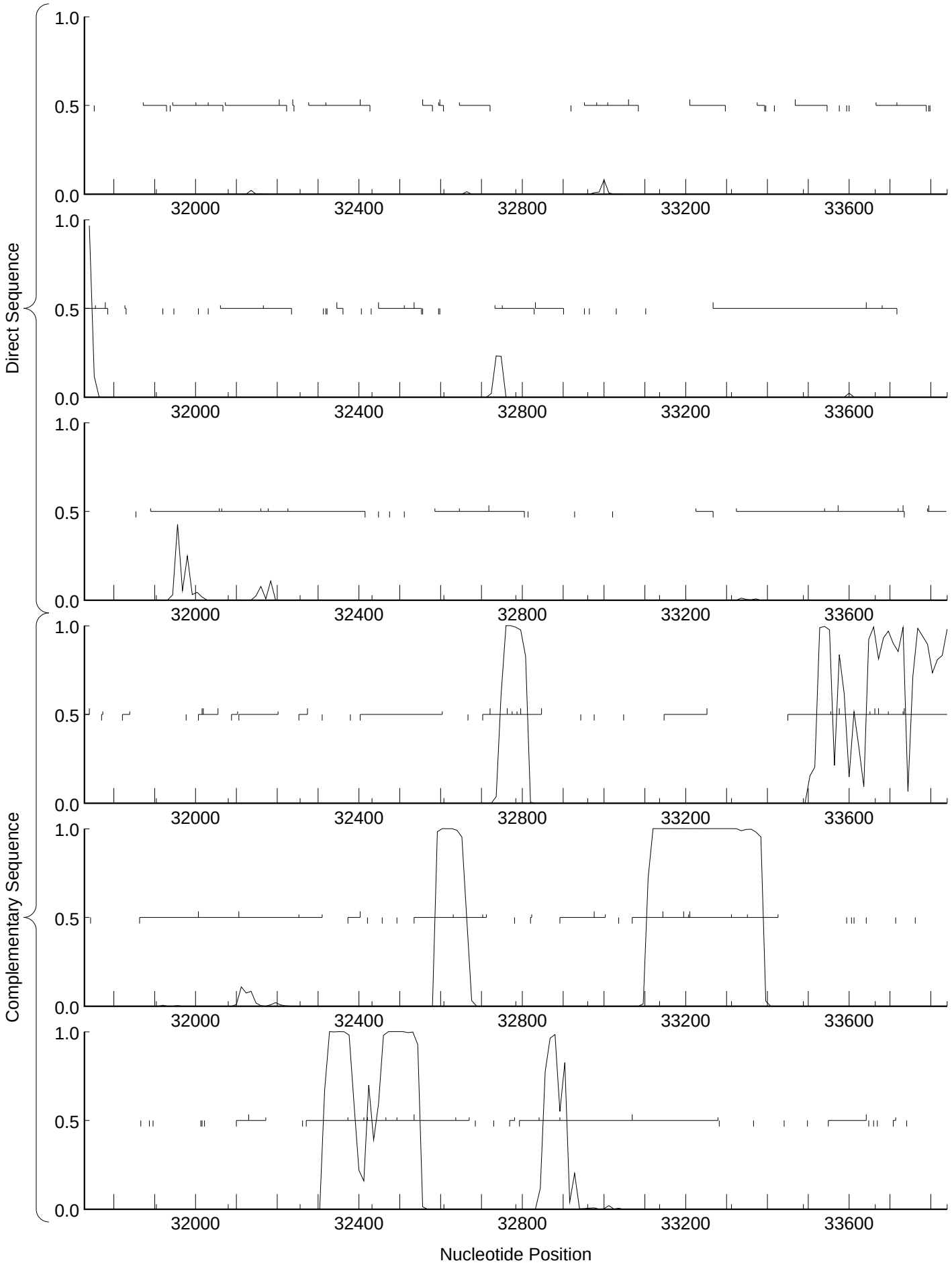
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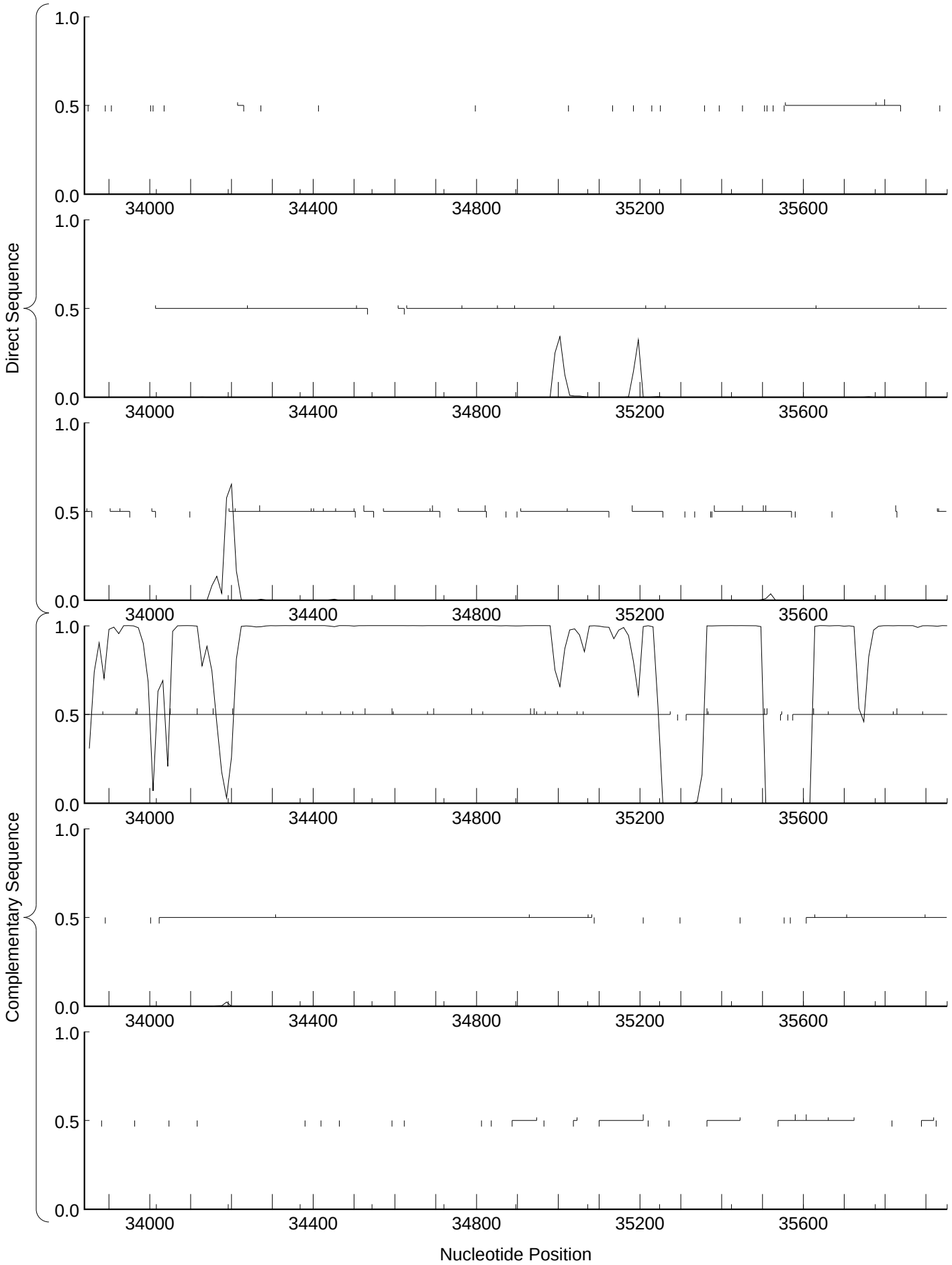


n complete sequence, 51492 bp including 10-base 3’ overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 15/26

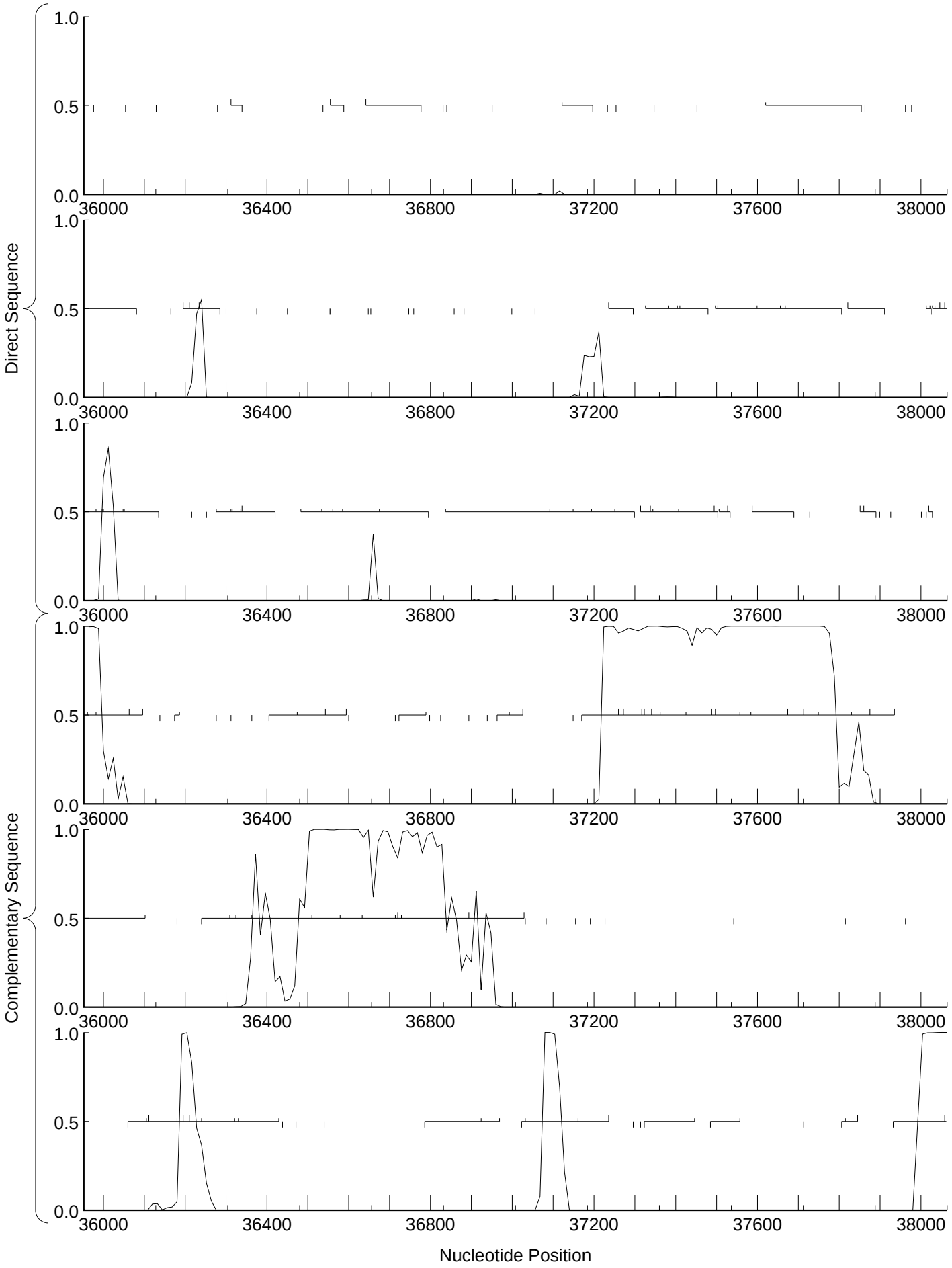


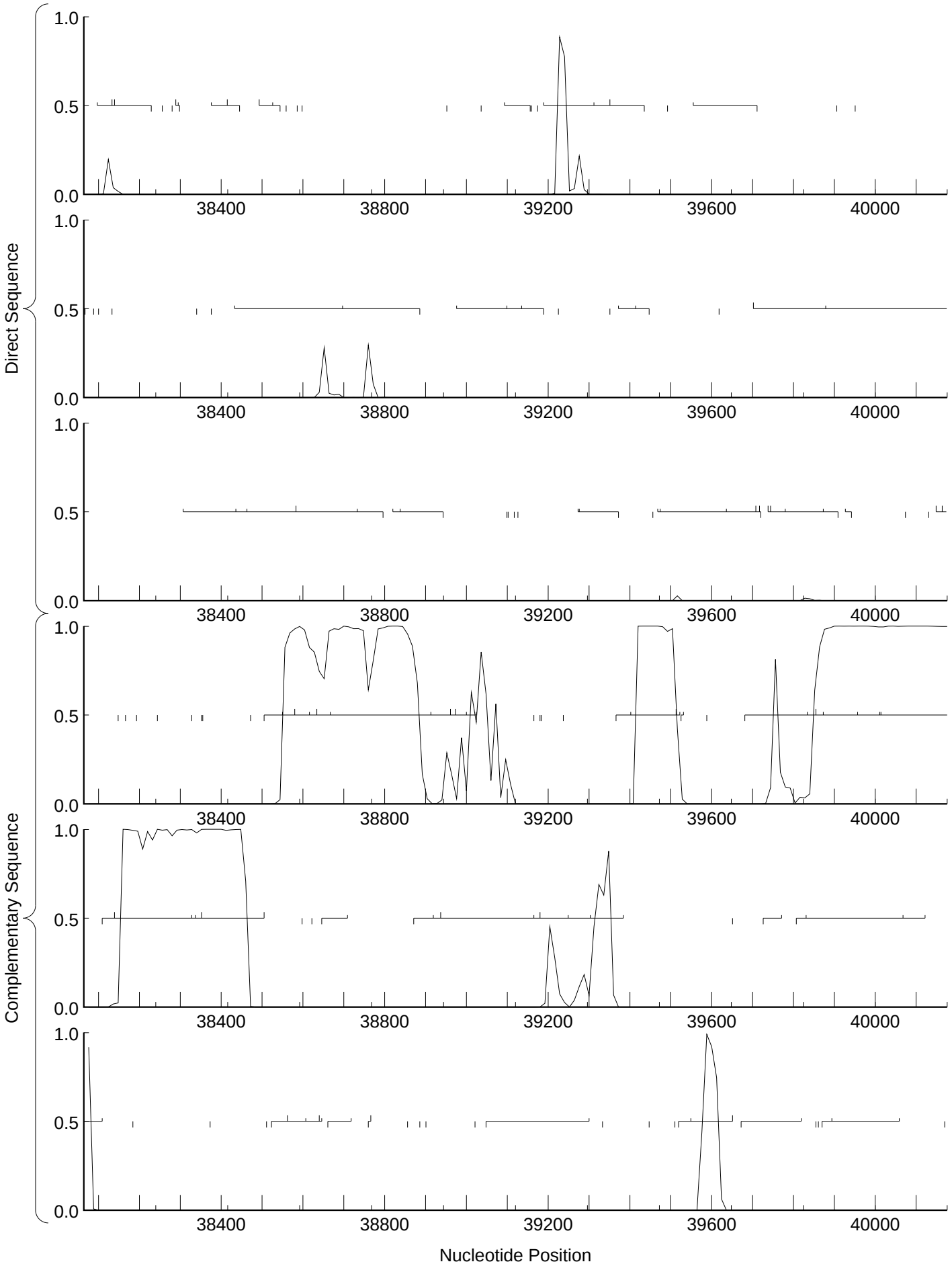

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
30000
30400
30800
31200
31600
Nucleotide Position


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

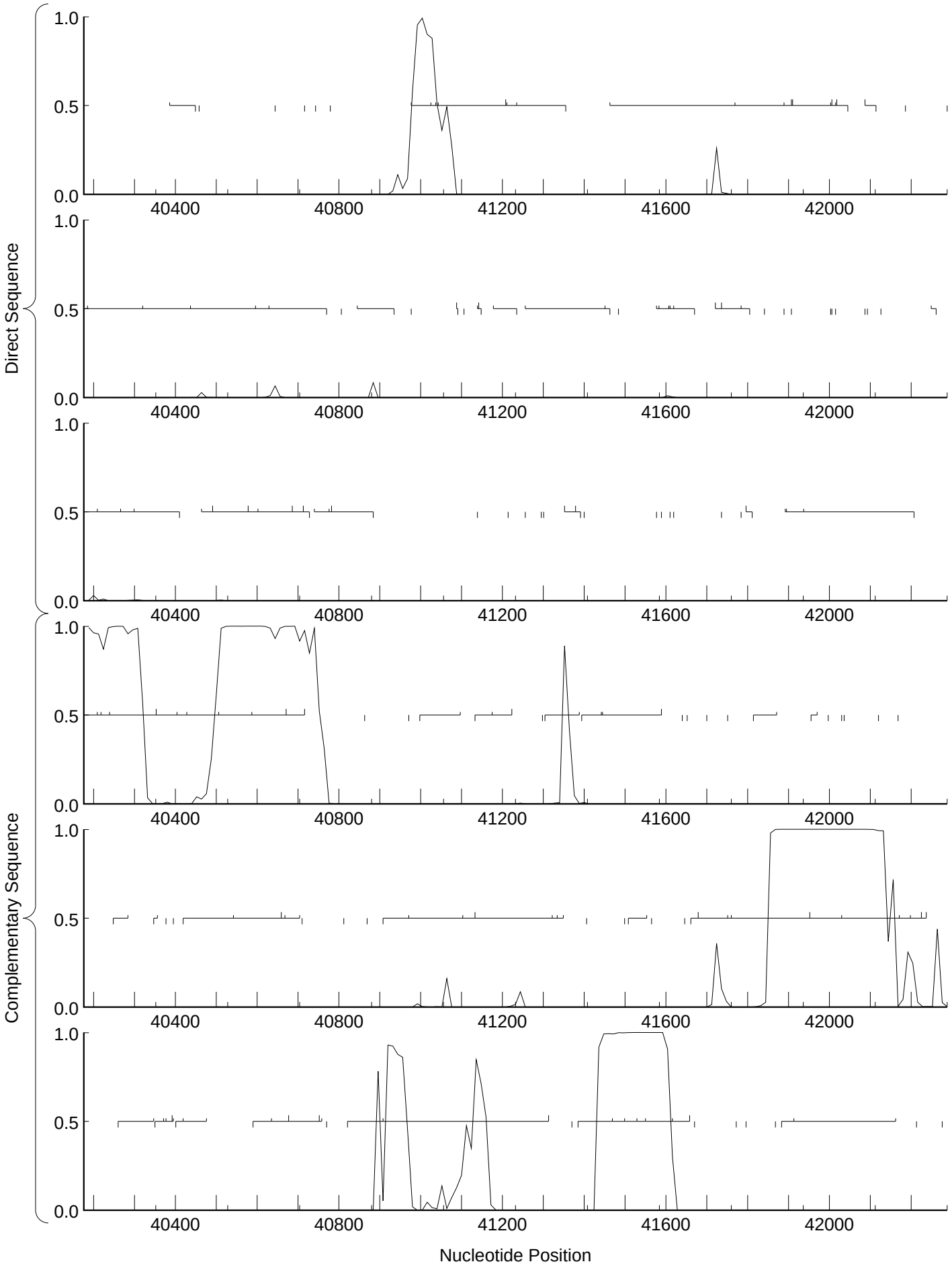

Direct Sequence
Complementary Sequence
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0.0
34000
34400
34800
35200
35600
Nucleotide Position

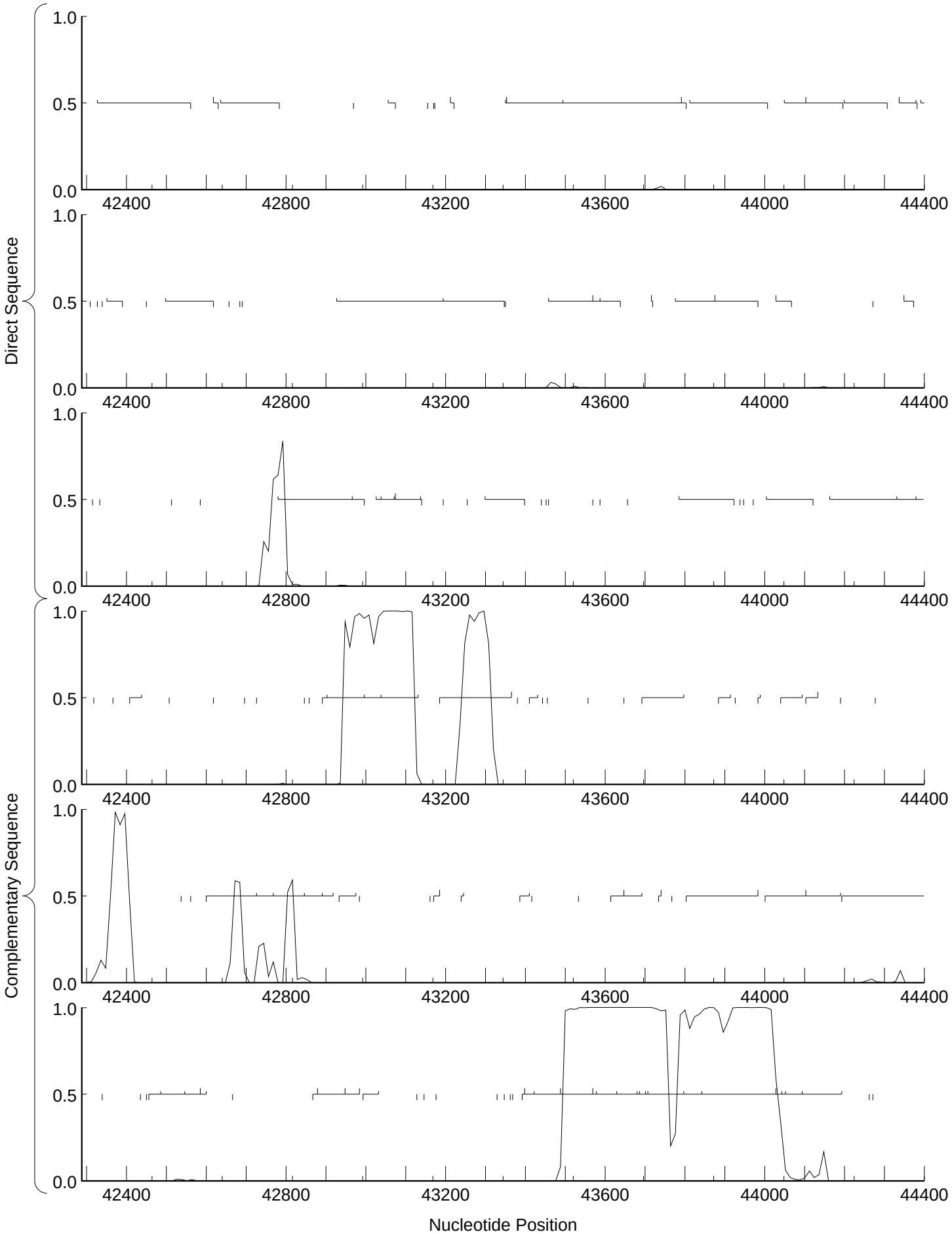
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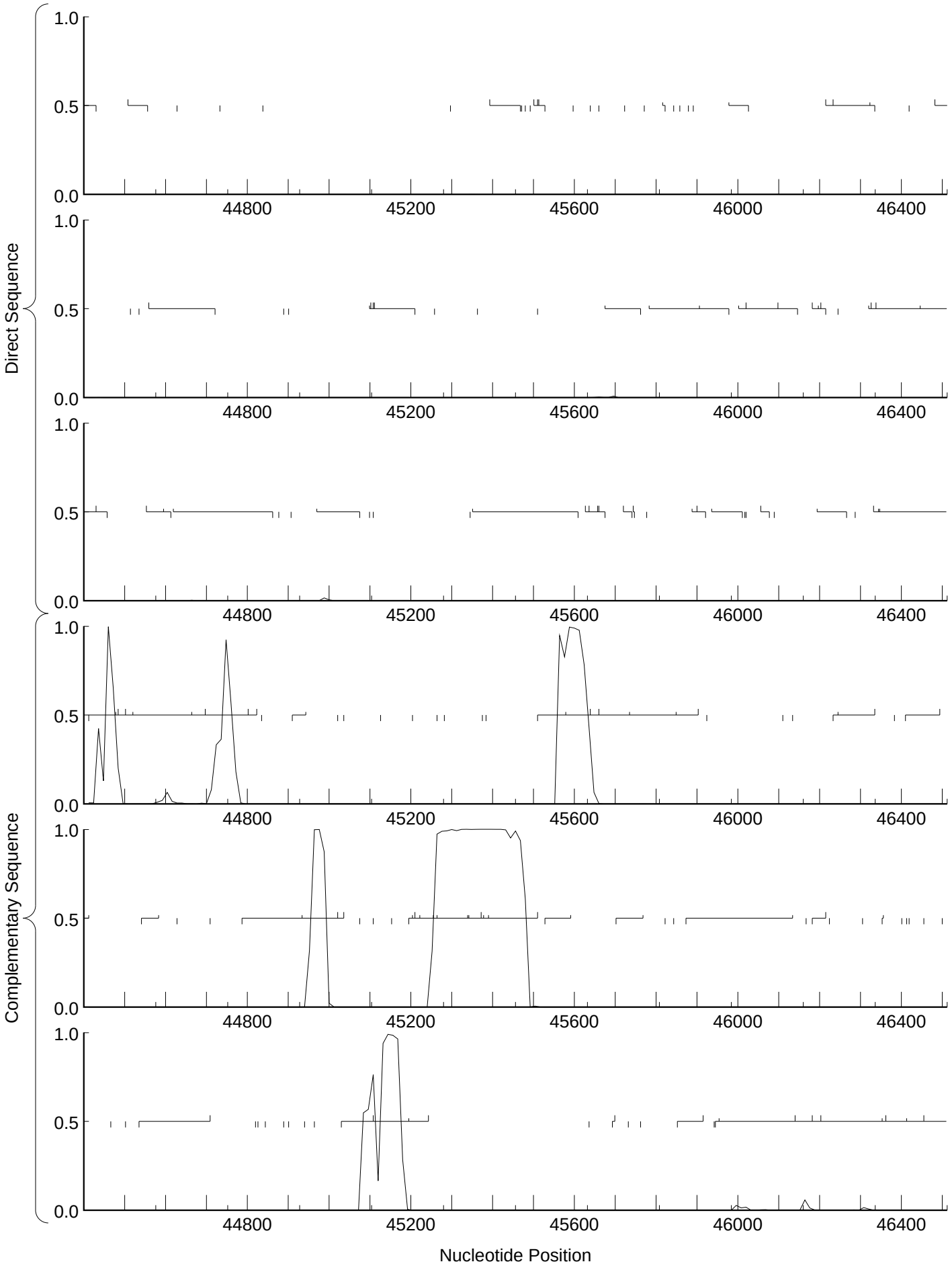


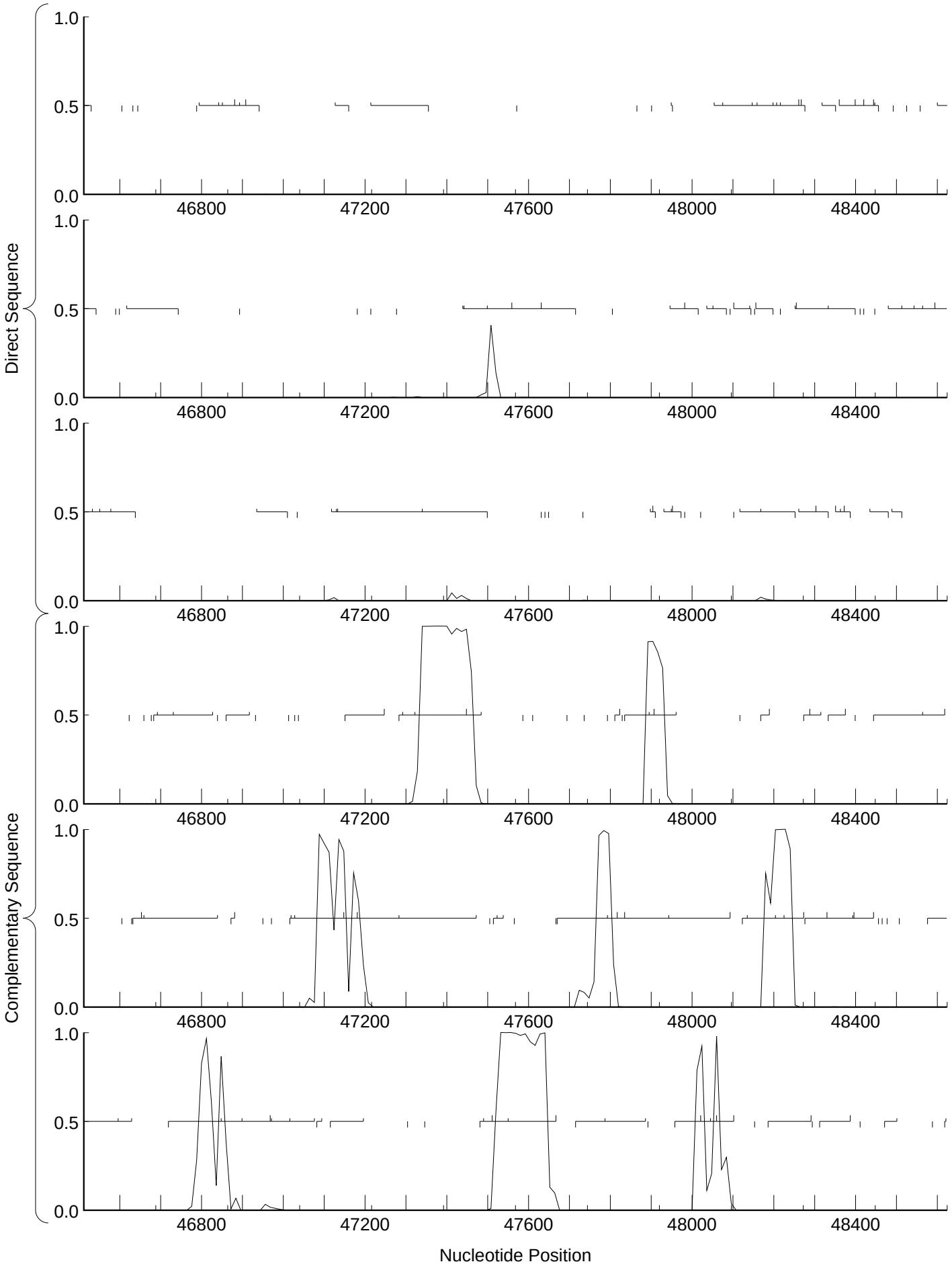

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
38400
38800
39200
39600
40000
Nucleotide Position

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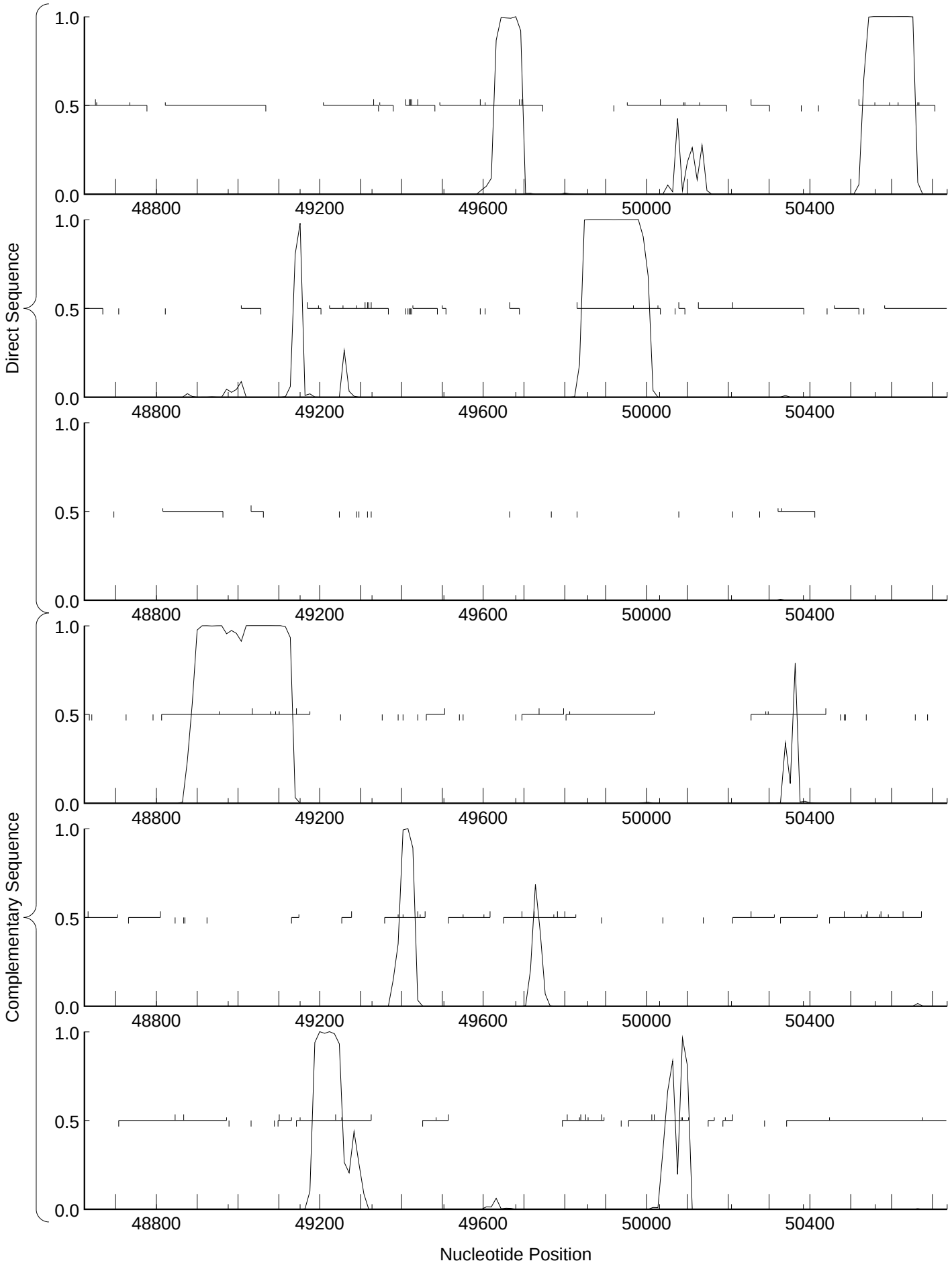



Direct Sequence
Complementary Sequence
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0.0
42400
42800
43200
43600
44000
44400
Nucleotide Position


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

n complete sequence, 51492 bp including 10-base 3’ overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 25/26



n complete sequence, 51492 bp including 10-base 3' overhang (CGGATGGTAA), Cluster A1, Order 4, Window 96, Step 12, 26/26

