GeneMark

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

PROGRAM INFORMATION

```
Sequence         :  Streptomyces phage Verse complete sequence, 49483 bp including 11-base 3' overhang (CGGTACG
Analysis Date    :  3/28/24 at 15:01:07
Pages            :  25
Sequence Length  :  49483 bp
GC Content       :   65.60%

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

PS-Version       :  1.2

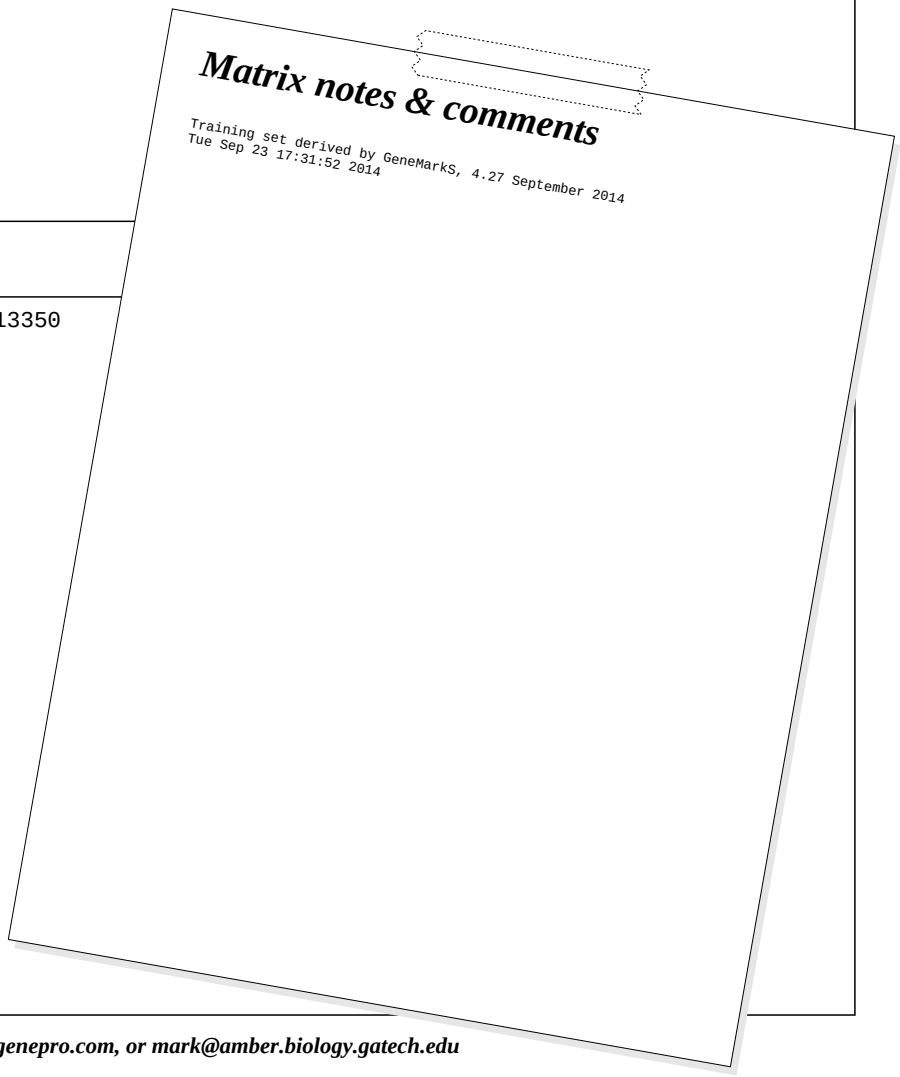
GeneMark Options :  PostScript graph,
                    Mark ORFs / splice sites,
                    List ORFs,
                    List regions and/or splice sites,
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MATRIX INFORMATION

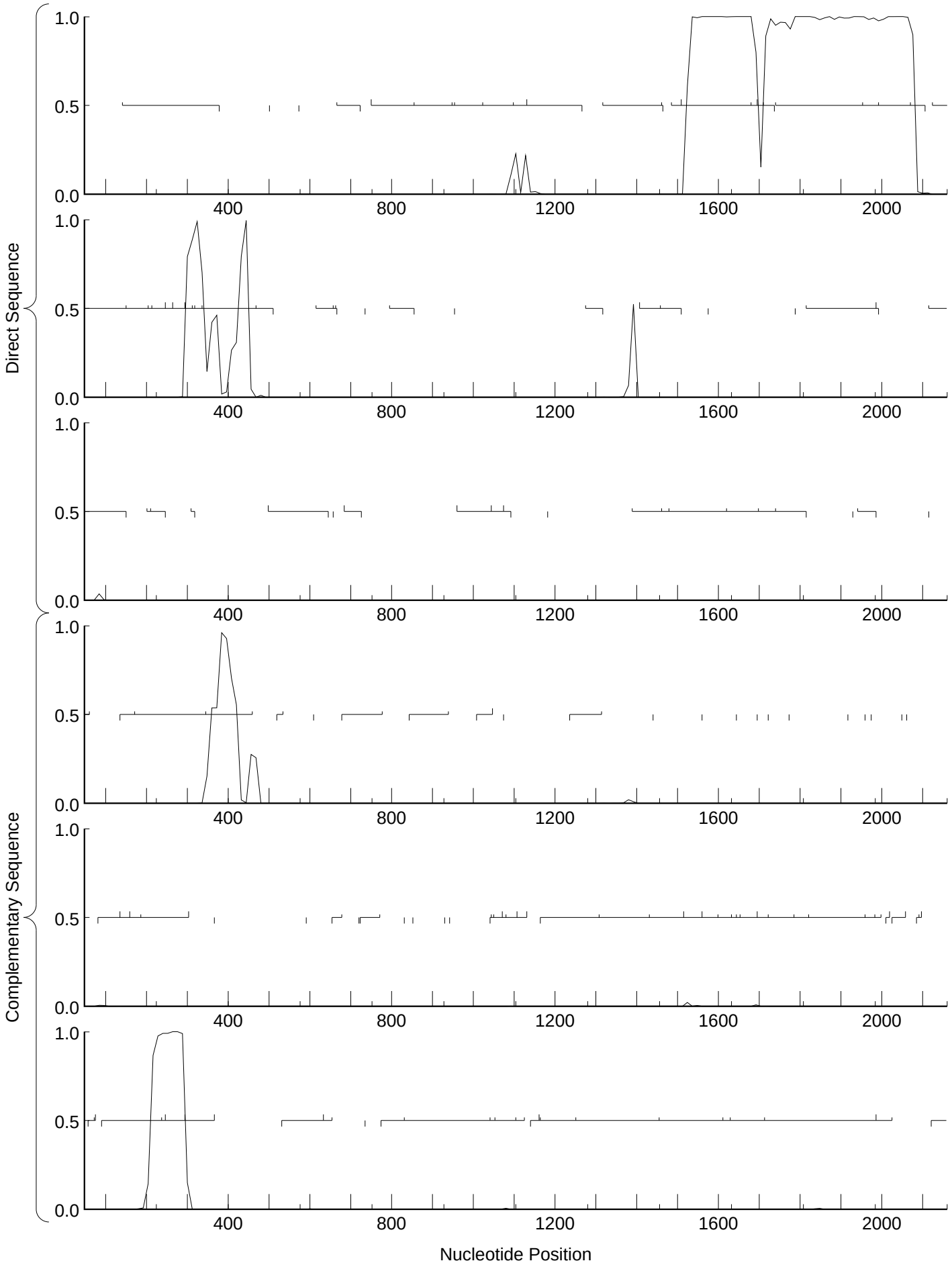
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Matrix     :  Streptomyces_griseus_NBRC_13350
Author     :  -

Order      :  4

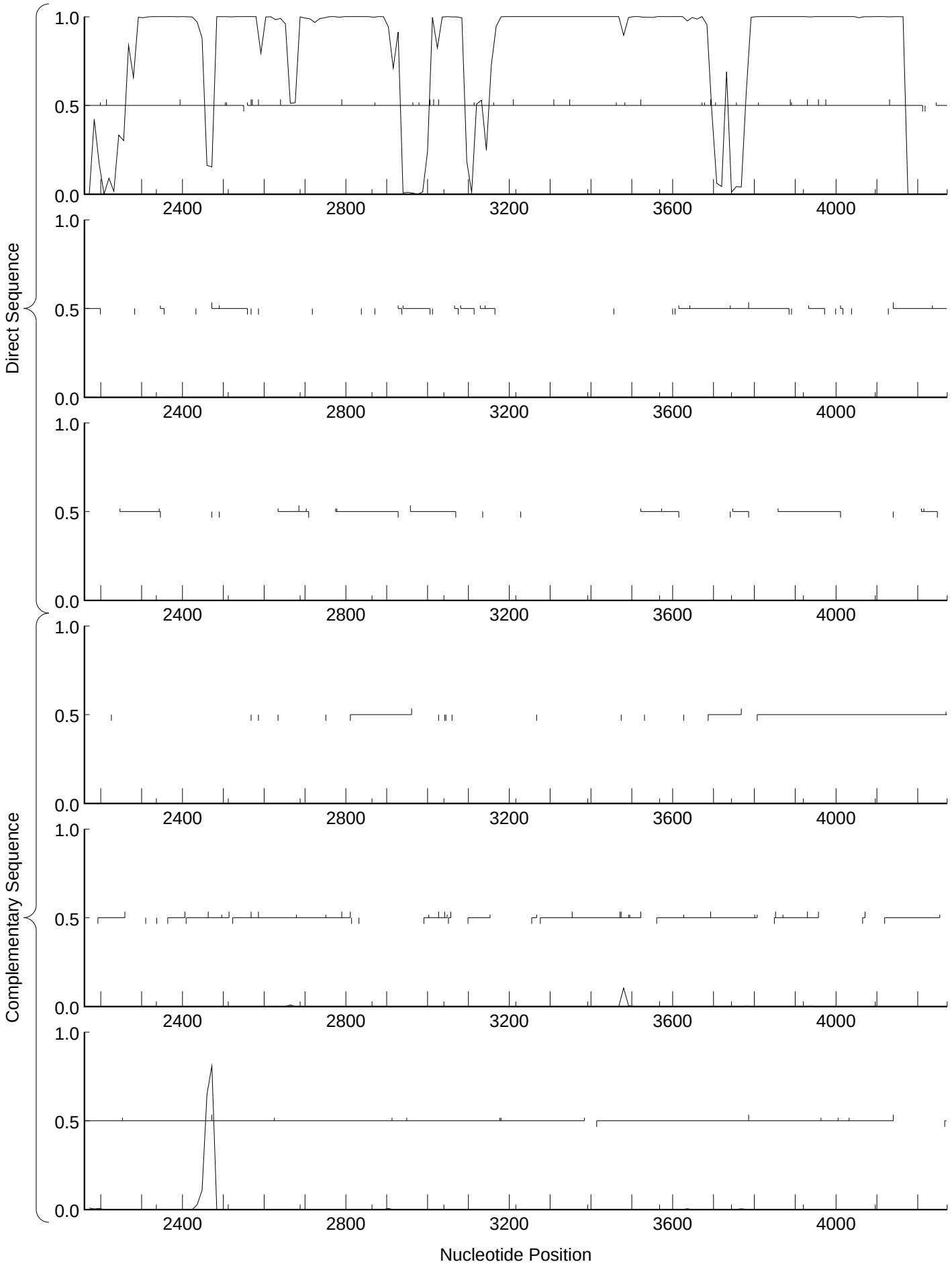

  Send questions / comments to:
      Dr. M. Borodovsky
      Georgia Institute of Technology
      School of Biology
      Atlanta, GA  30332-0230
```



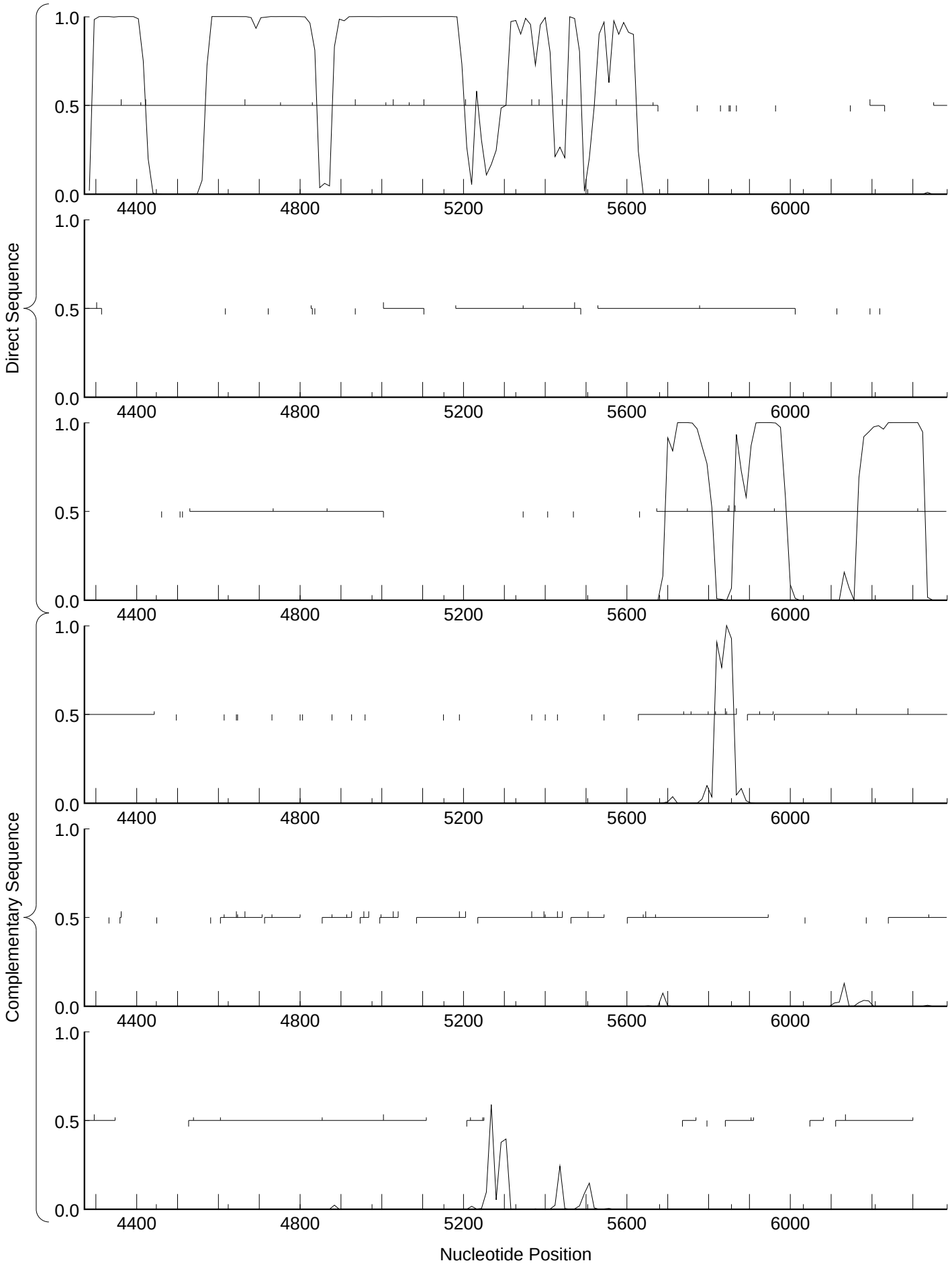
For help or information, send electronic mail to: custserv@genepro.com, or mark@amber.biology.gatech.edu

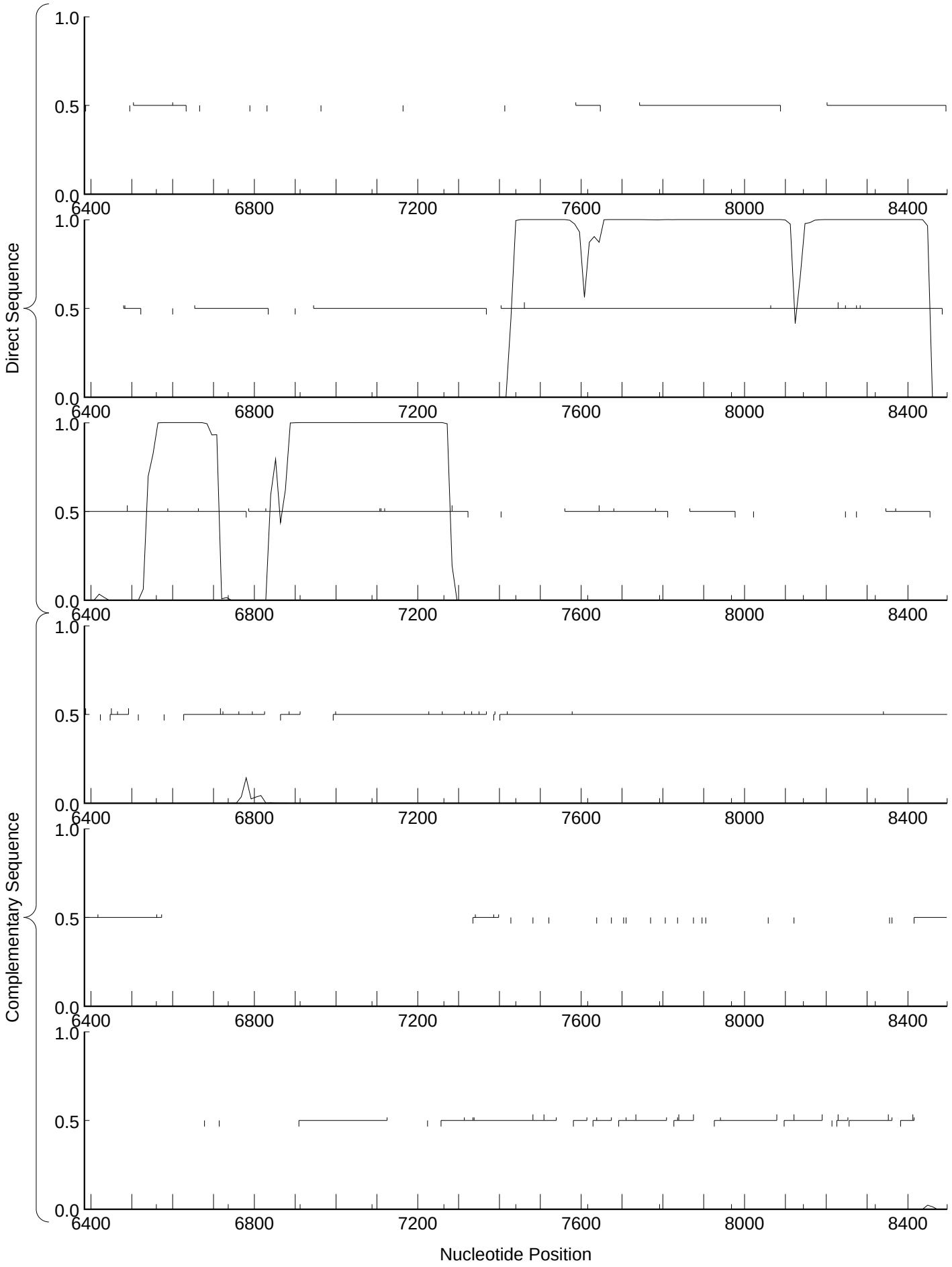

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
400
800
1200
1600
2000
Nucleotide Position

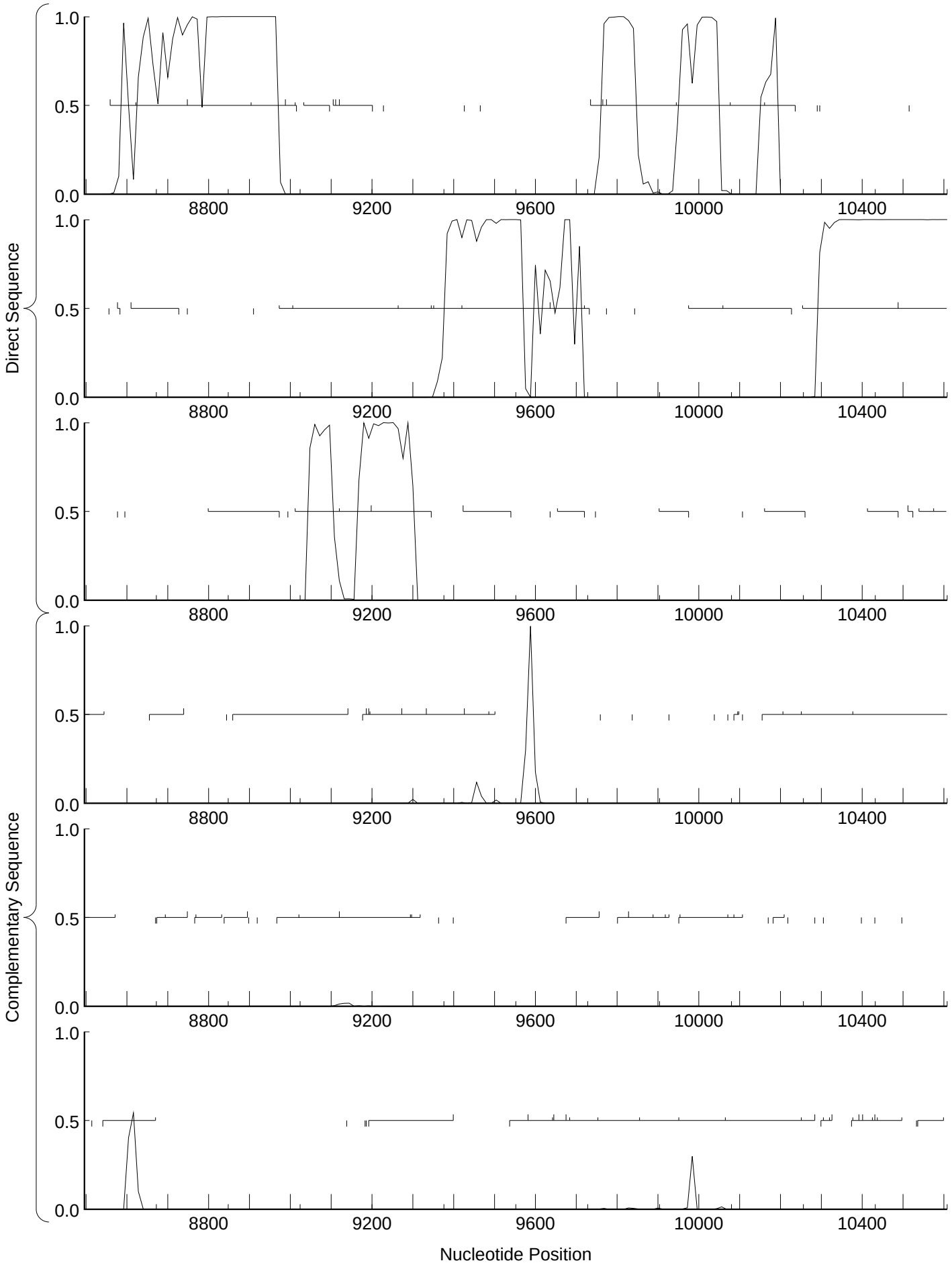
hage Verse complete sequence, 49483 bp including 11-base 3’ overhang (CGGTACGTGAT), Order 4, Window 96, Step 12, 3/25

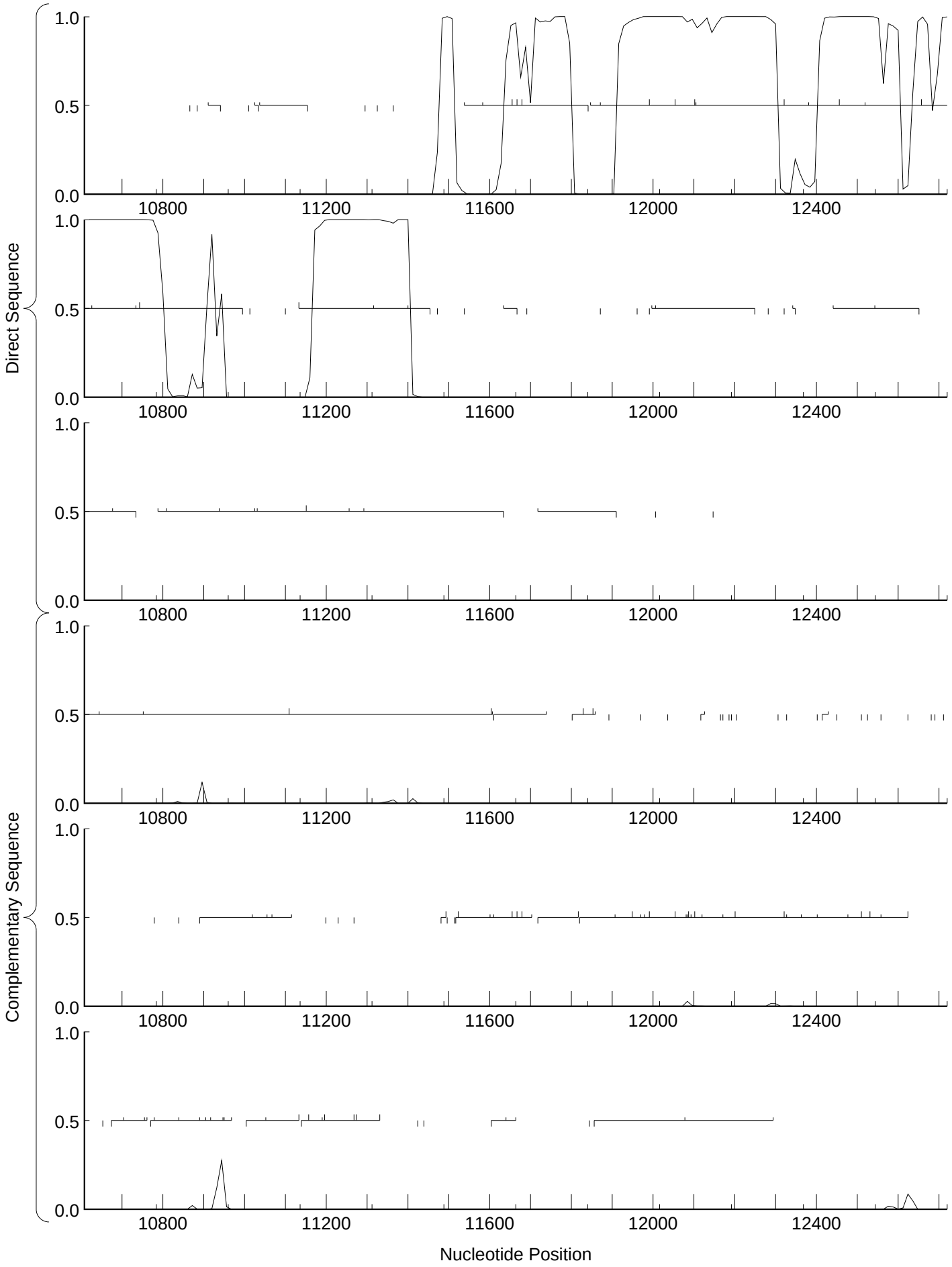


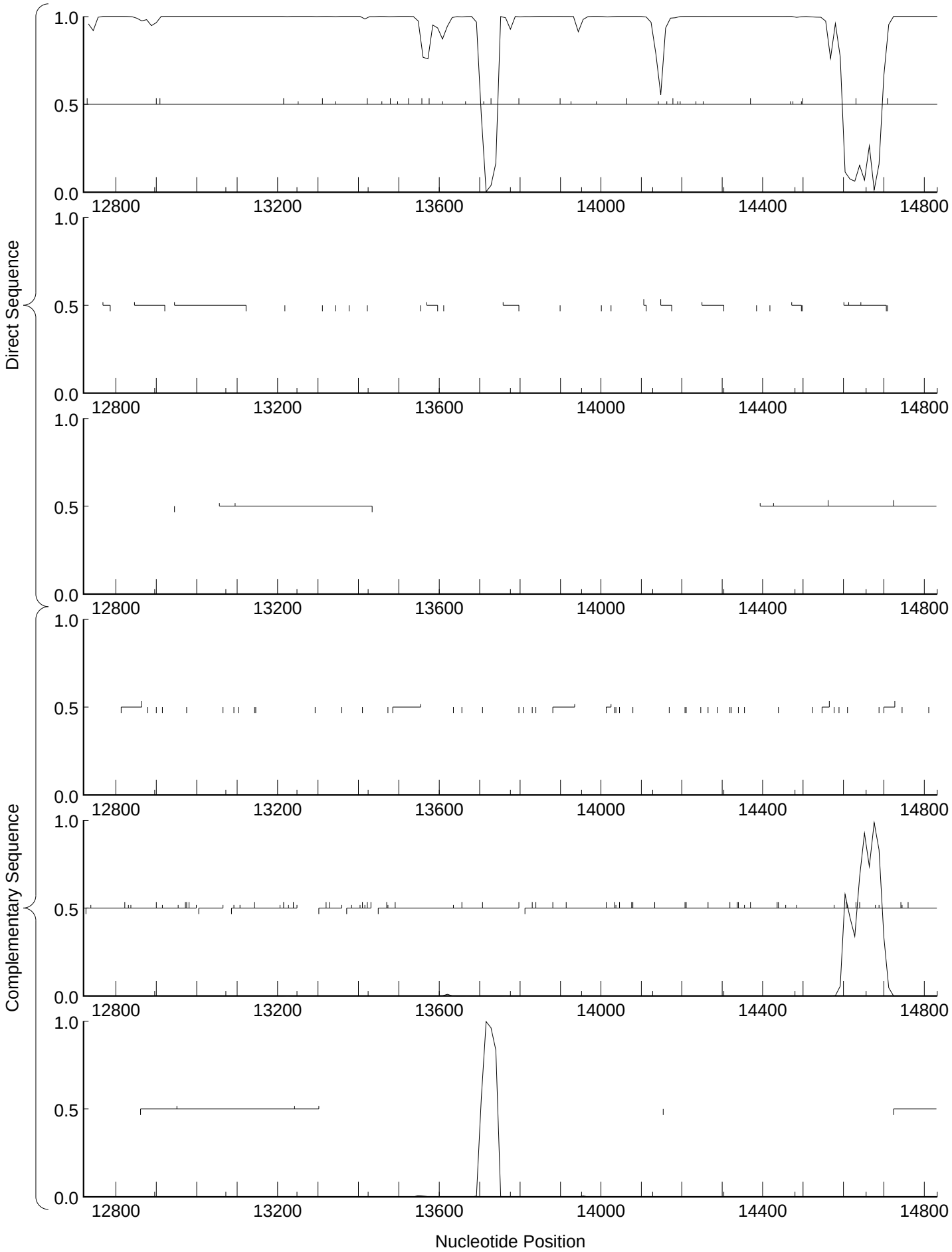
hage Verse complete sequence, 49483 bp including 11-base 3’ overhang (CGGTACGTGAT), Order 4, Window 96, Step 12, 4/25

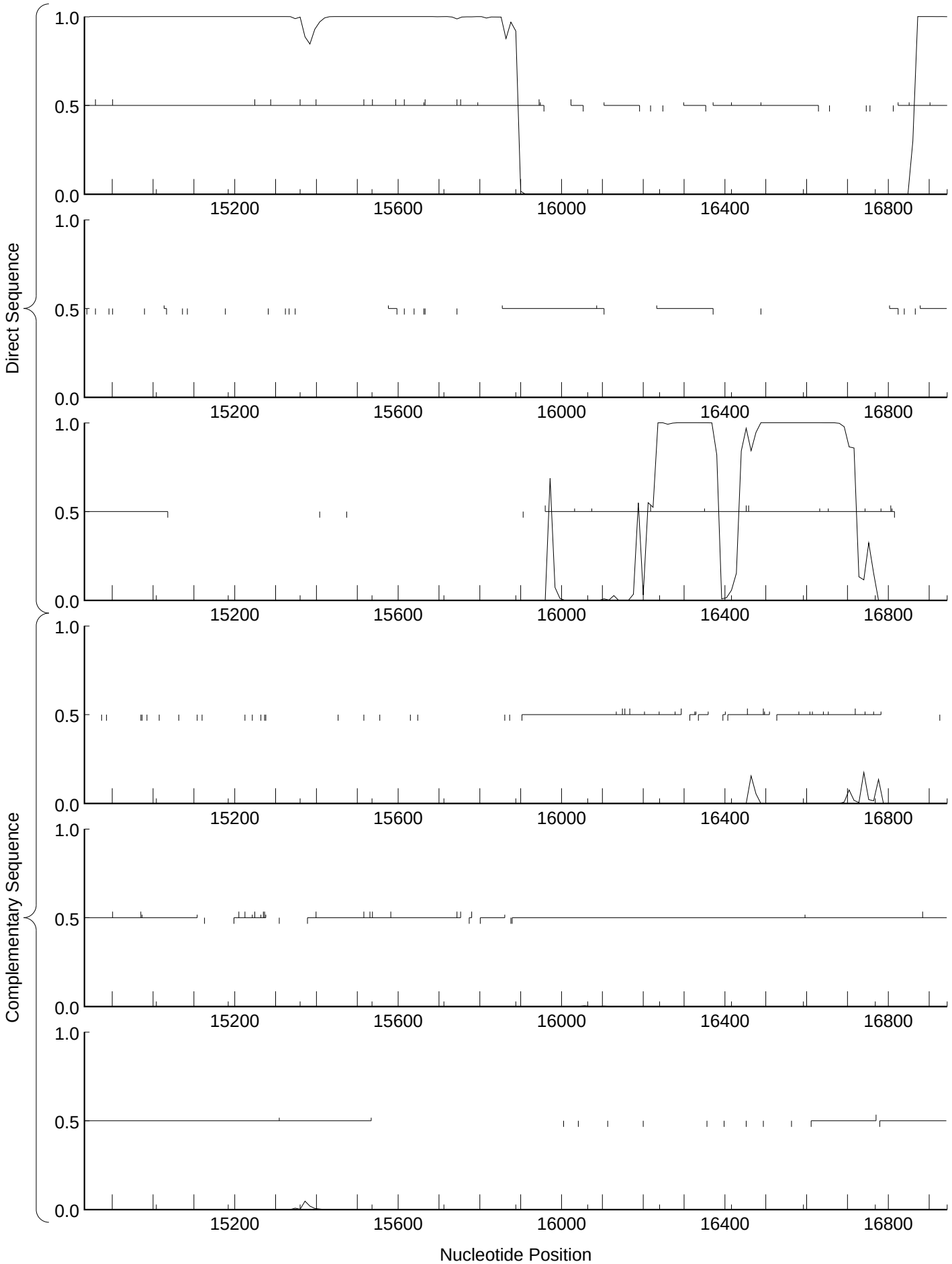


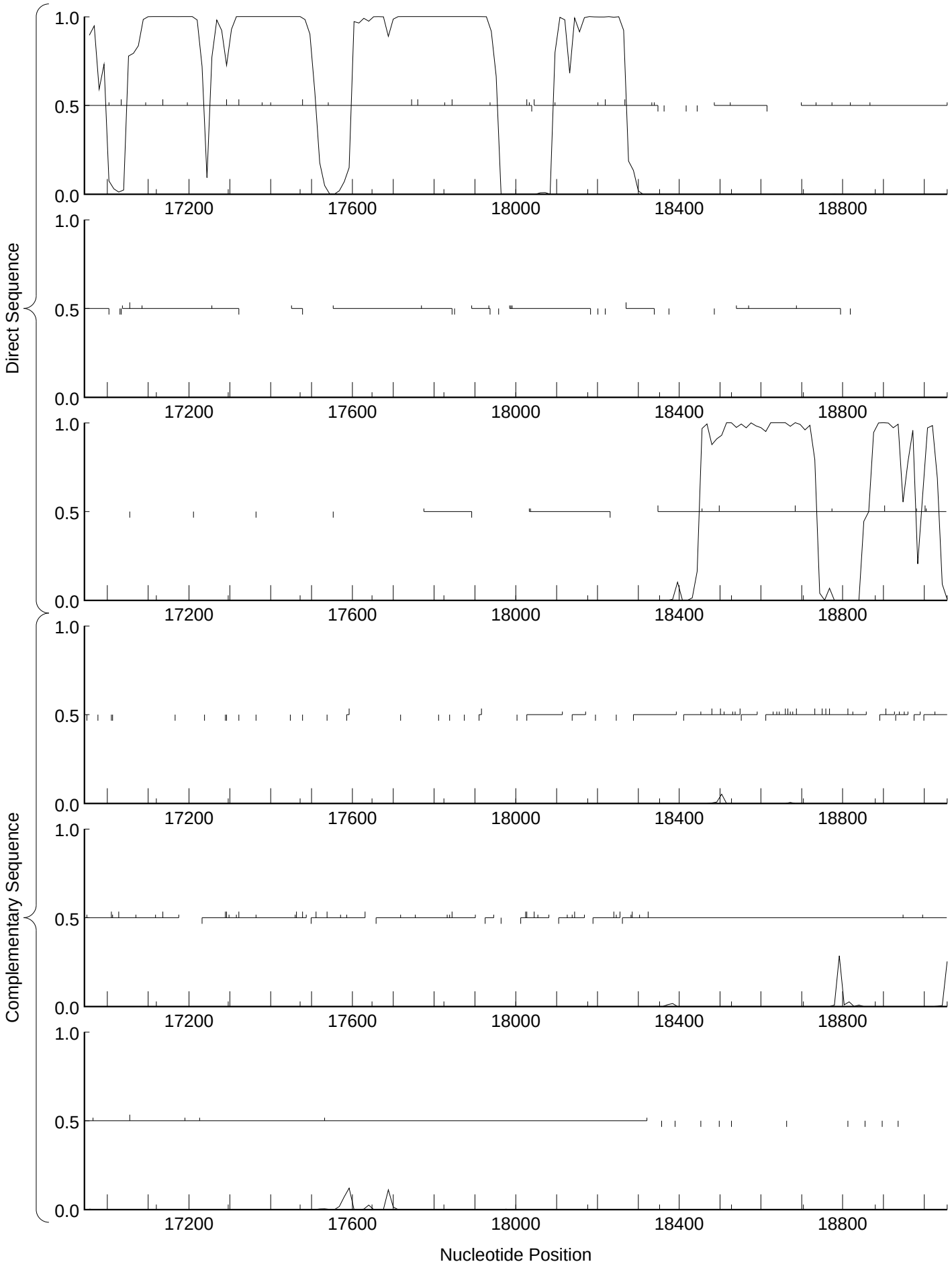

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
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6800
7200
7600
8000
8400
Nucleotide Position

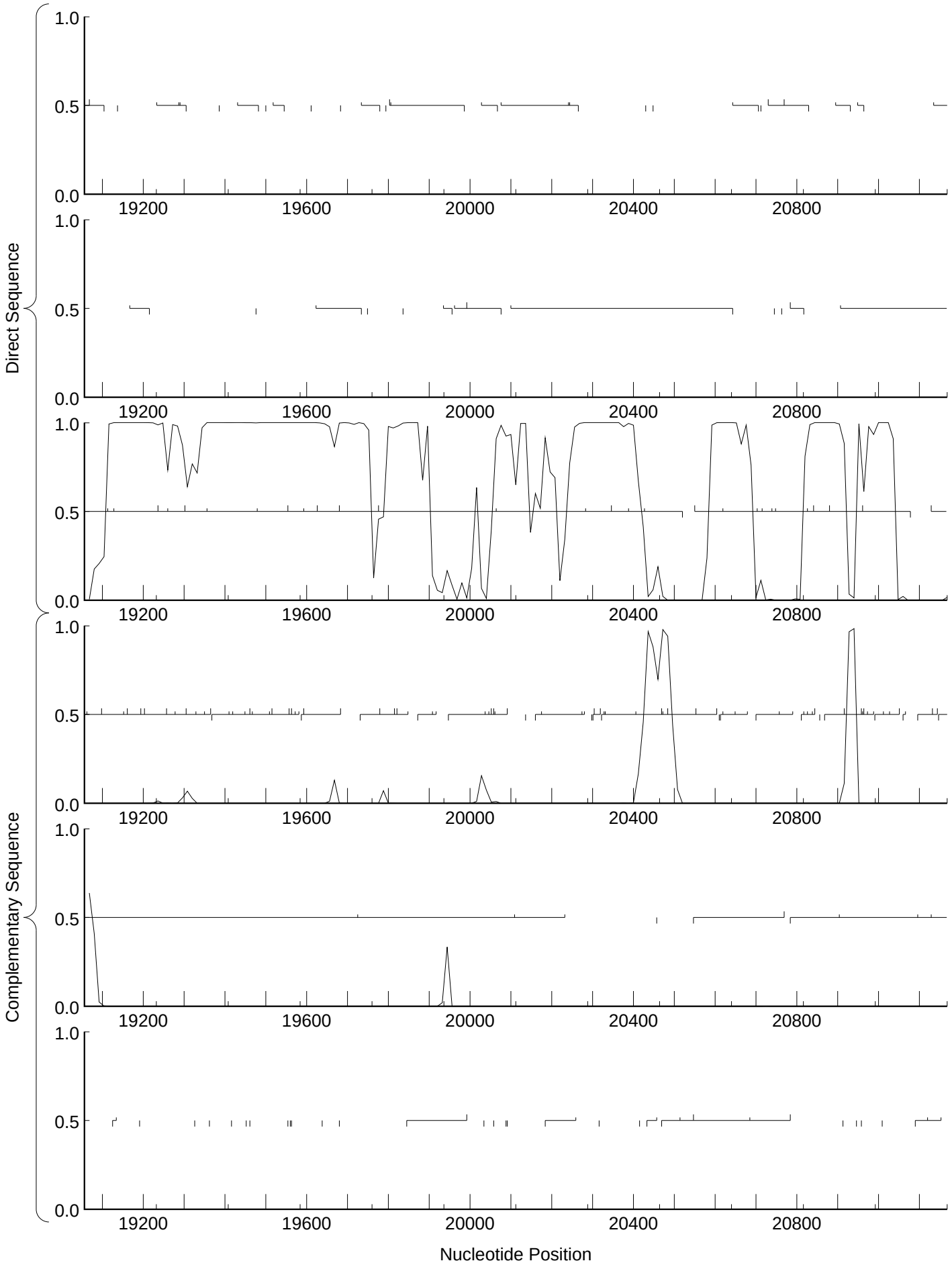

Direct Sequence
Complementary Sequence
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0.5
0.0
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9600
10000
10400
Nucleotide Position

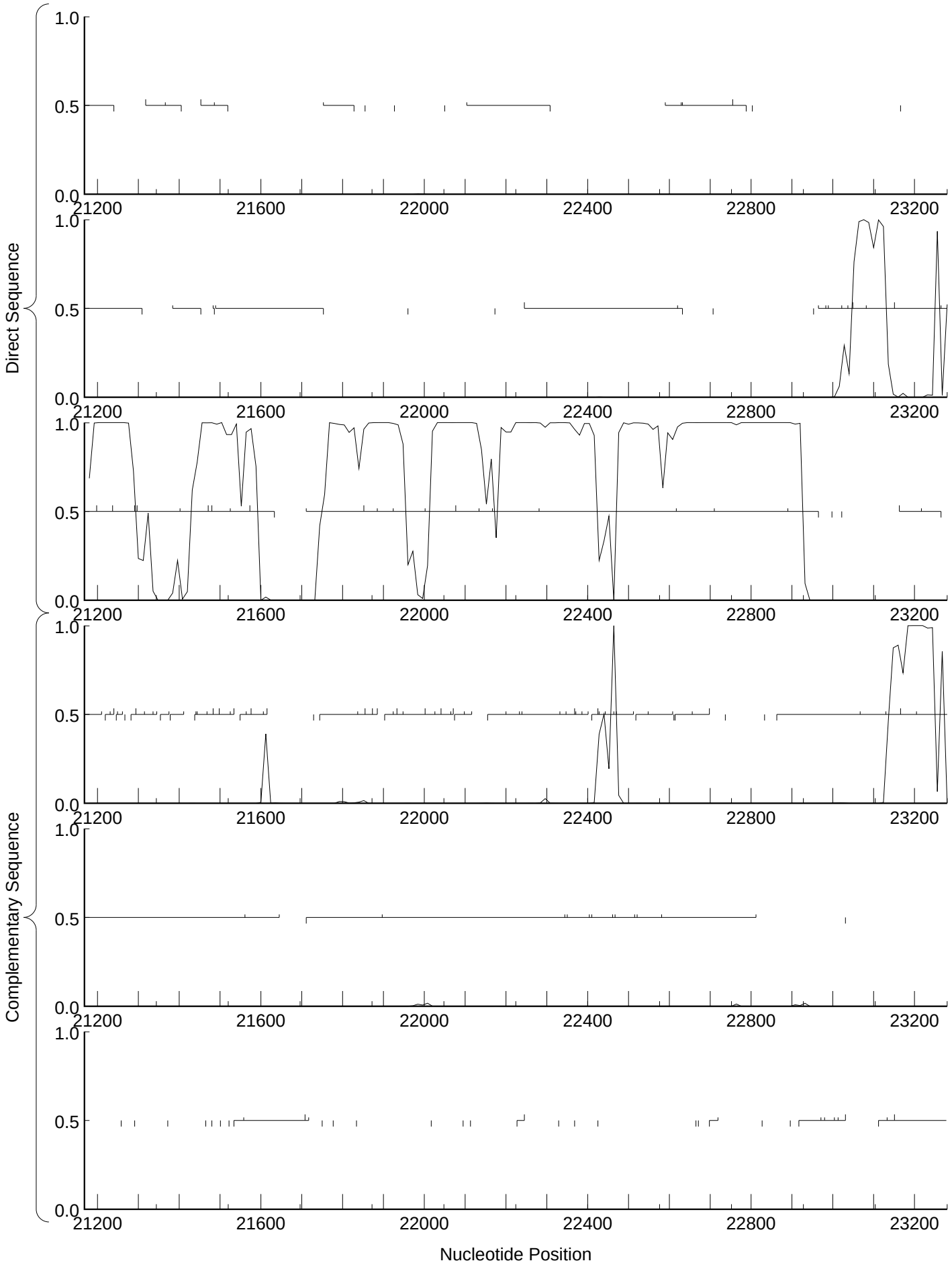

Direct Sequence
Complementary Sequence
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0.0
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11600
12000
12400
Nucleotide Position

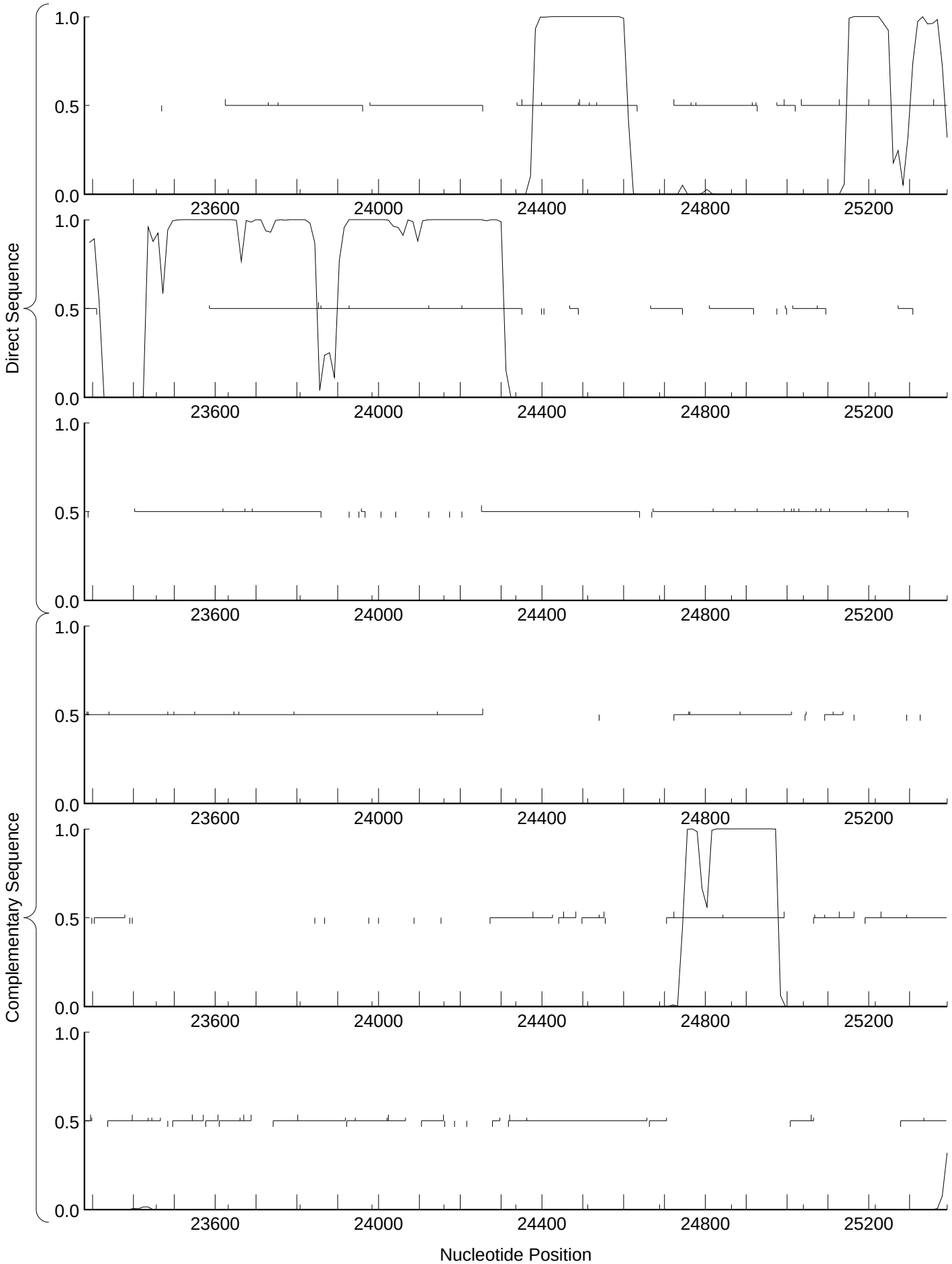

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Complementary Sequence
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0.0
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13600
14000
14400
14800
Nucleotide Position

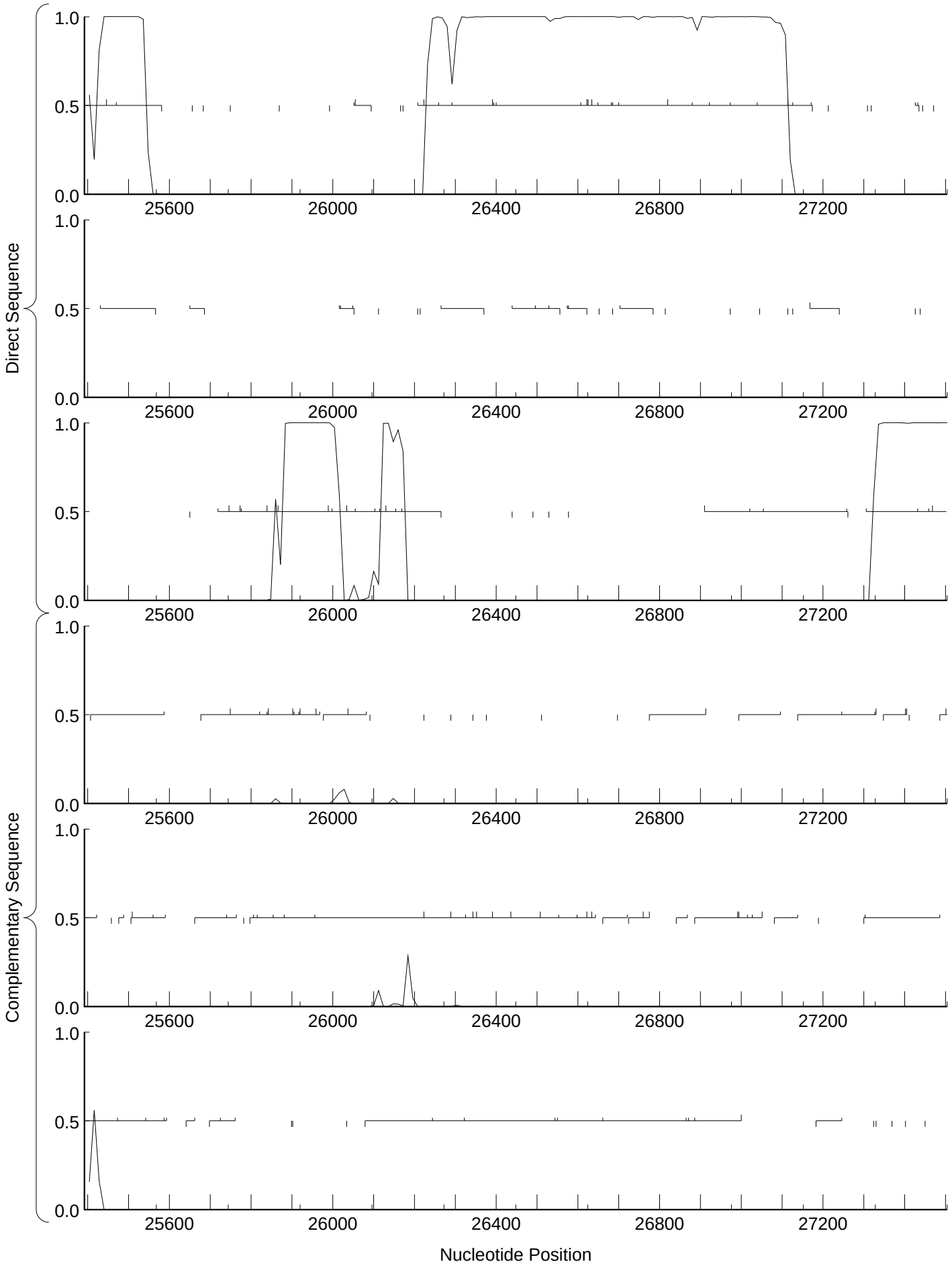

Direct Sequence
Complementary Sequence
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0.0
15200
15600
16000
16400
16800
Nucleotide Position

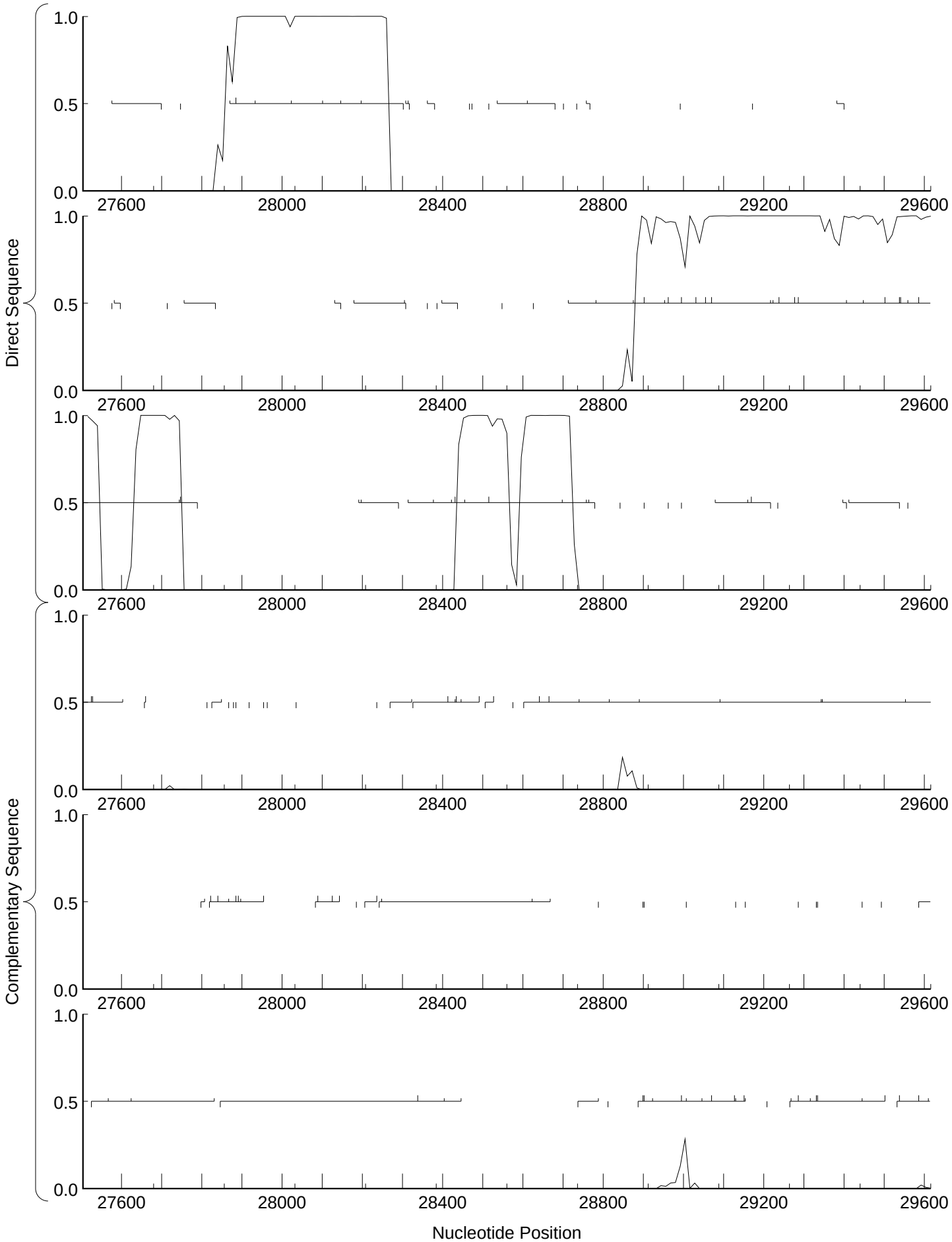

Direct Sequence
Complementary Sequence
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0.5
0.0
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17600
18000
18400
18800
Nucleotide Position

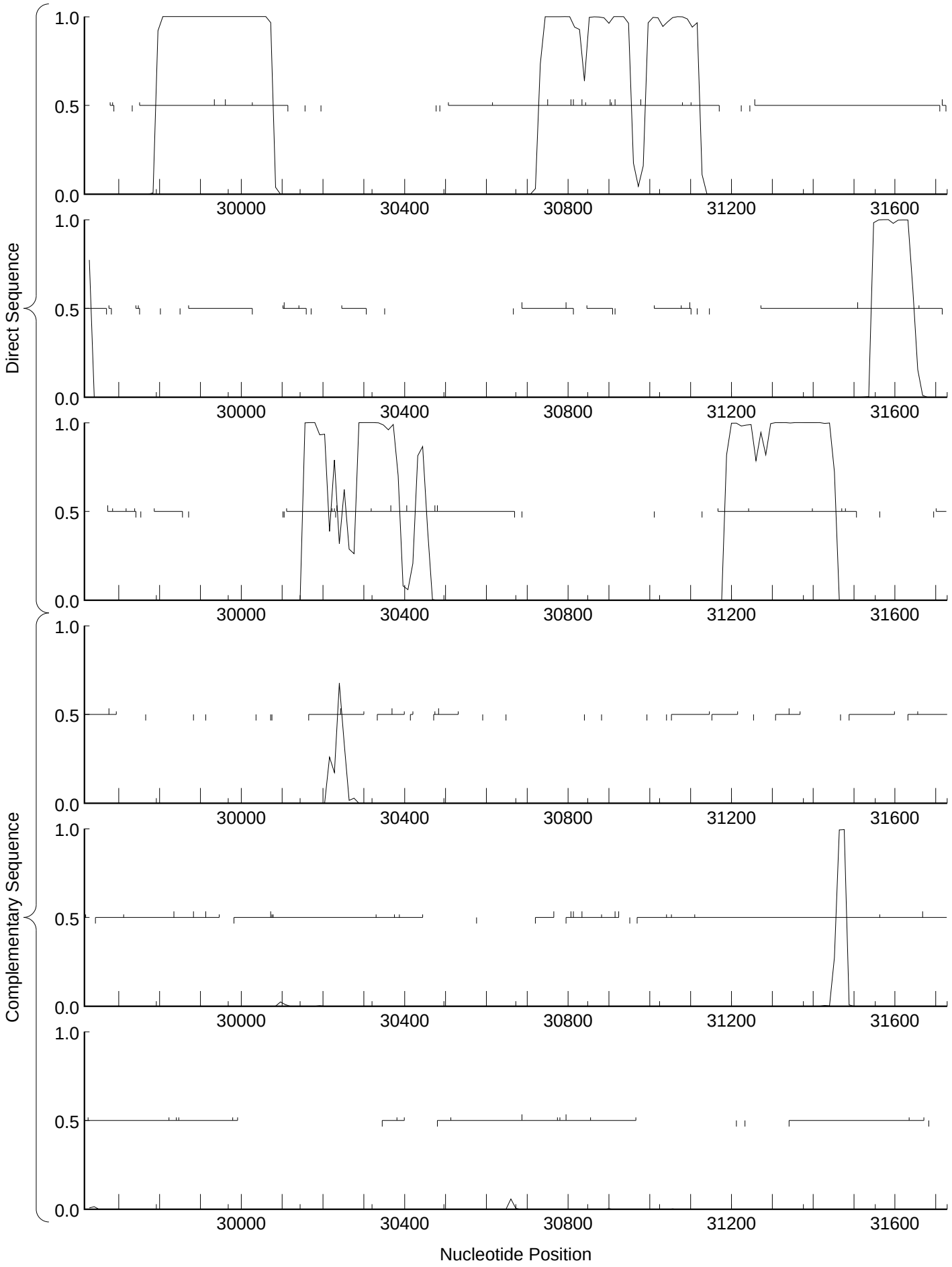

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Complementary Sequence
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20800
Nucleotide Position

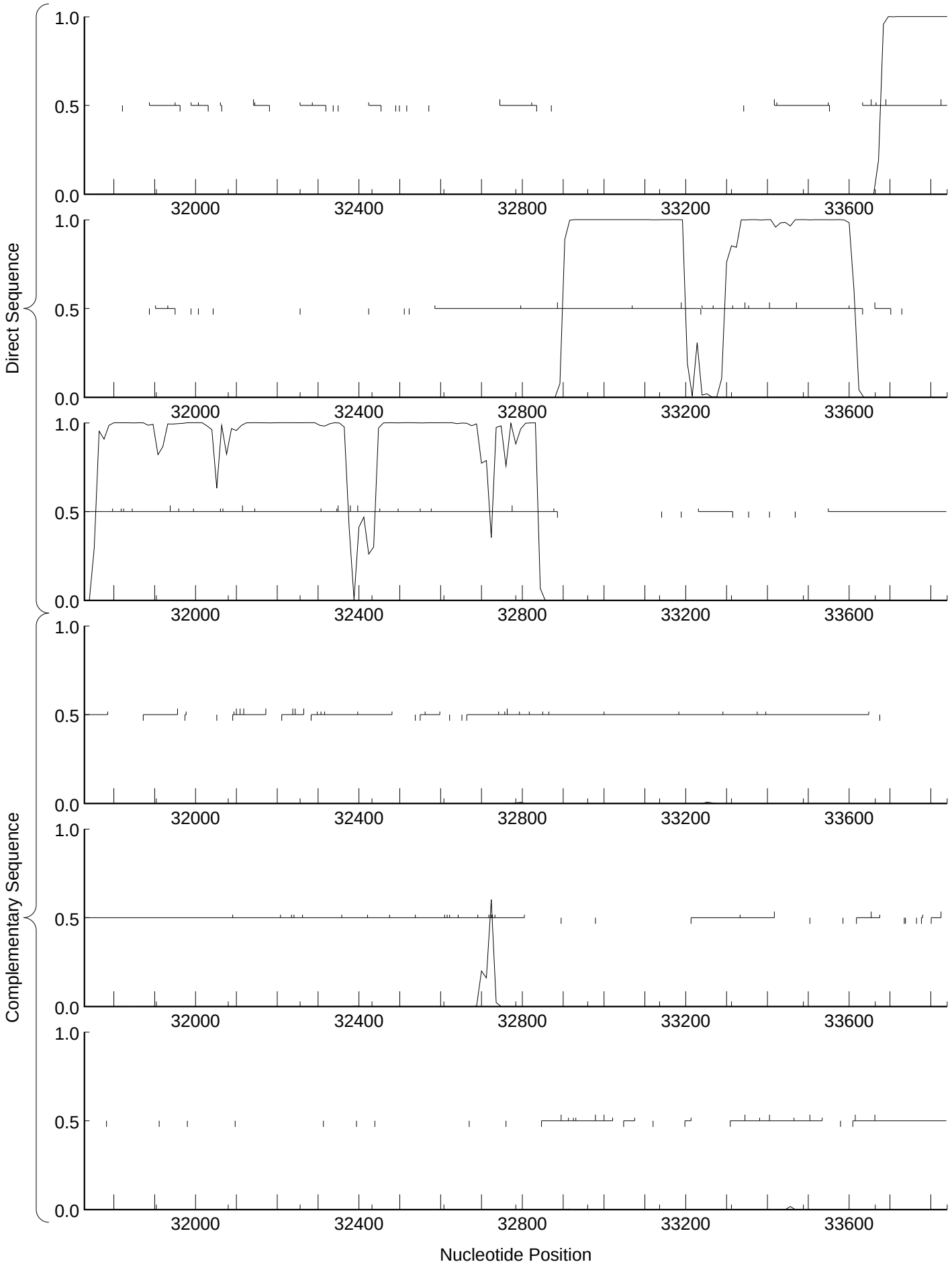

Direct Sequence
Complementary Sequence
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22400
22800
23200
Nucleotide Position

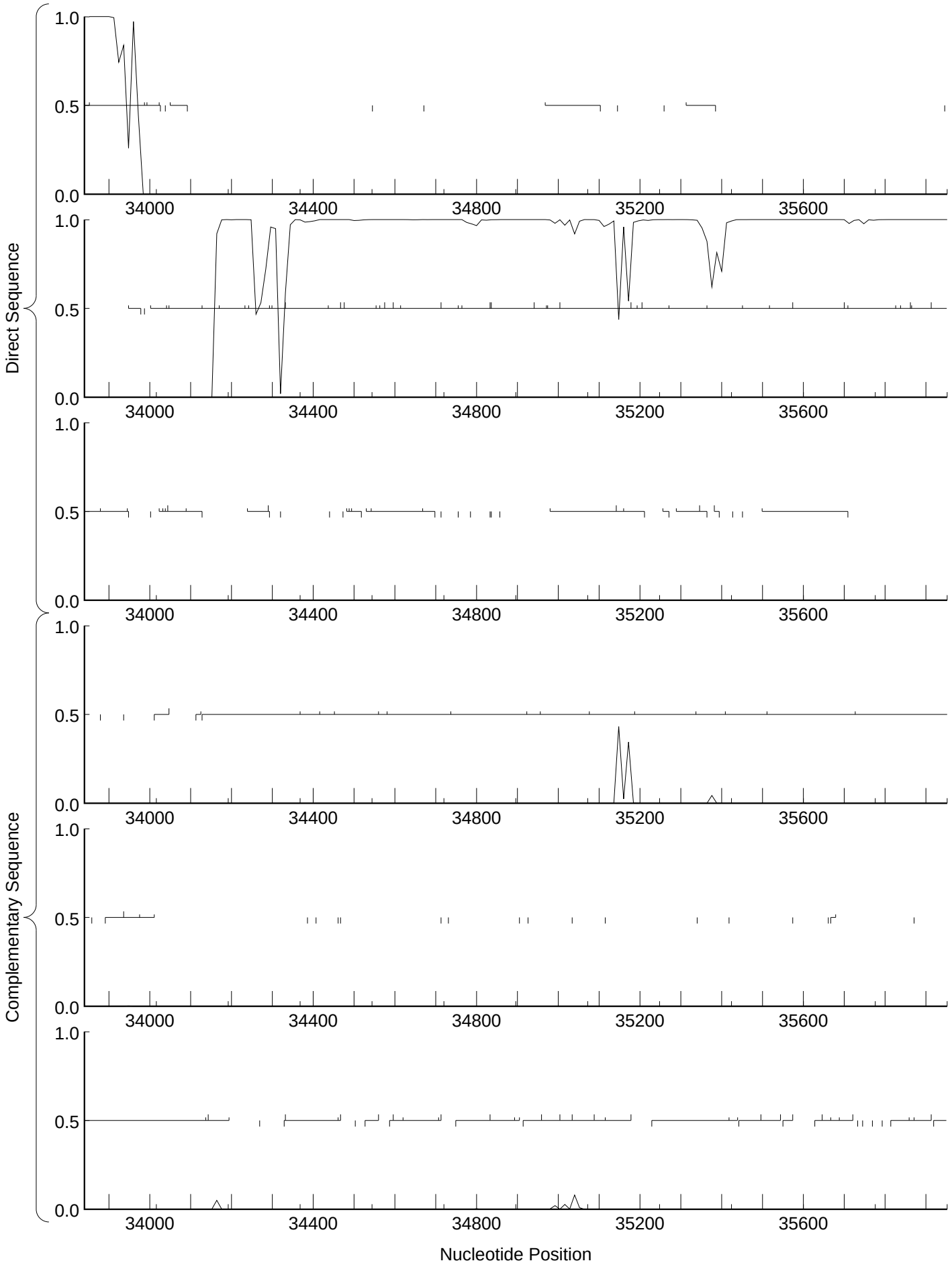

Direct Sequence
Complementary Sequence
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24800
25200
Nucleotide Position

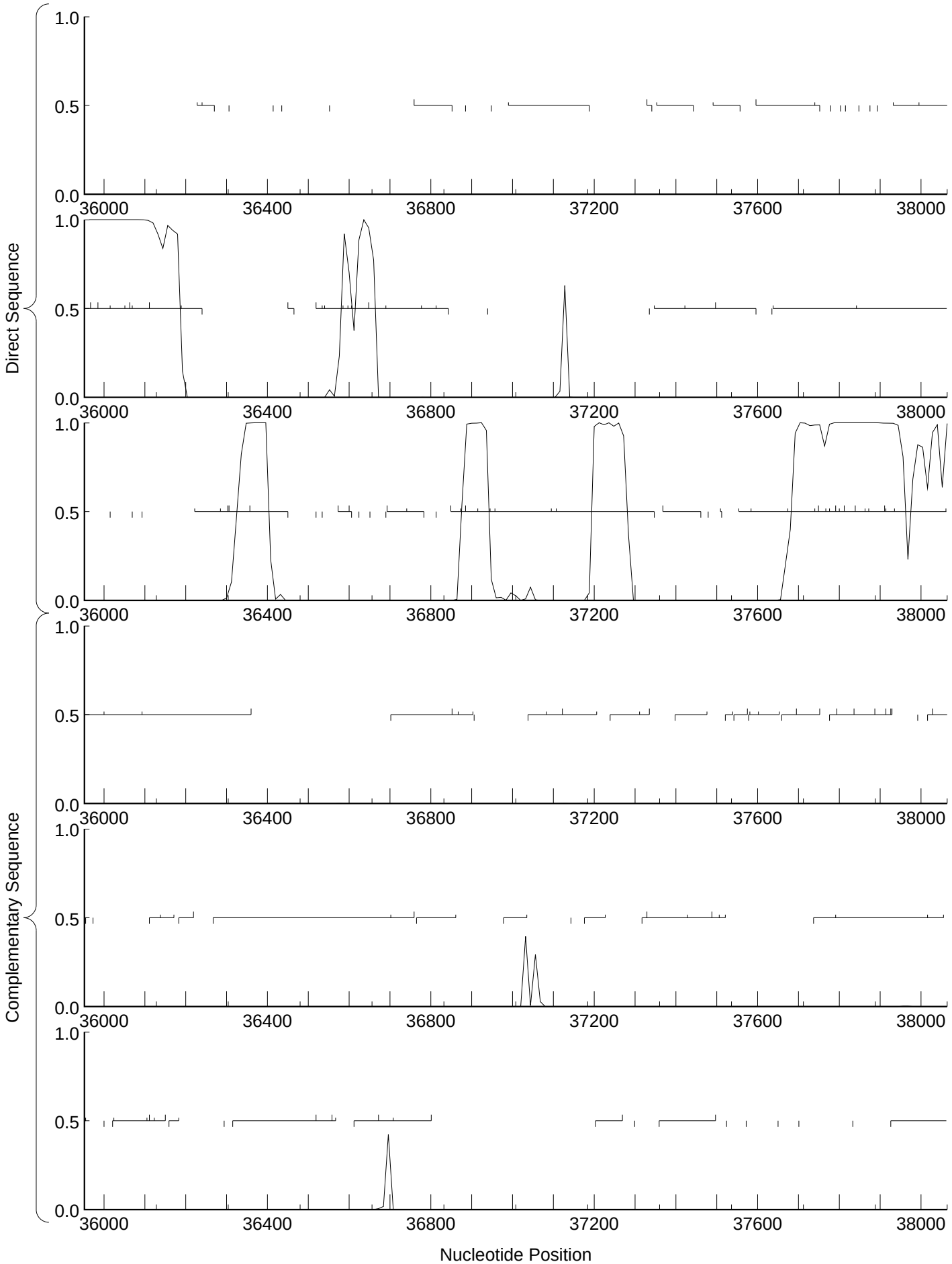

Direct Sequence
Complementary Sequence
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26800
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Nucleotide Position

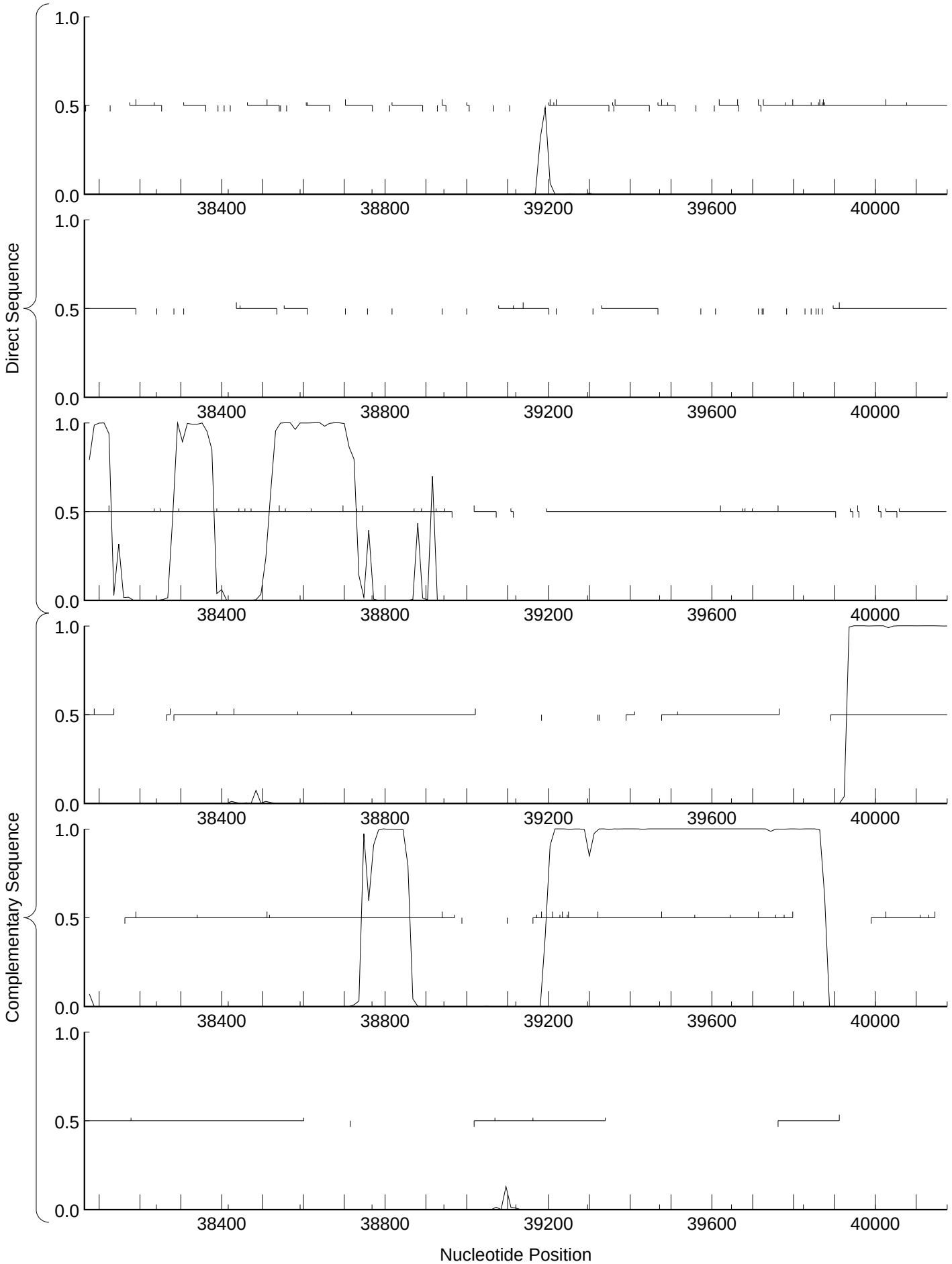

Direct Sequence
Complementary Sequence
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29200
29600
Nucleotide Position

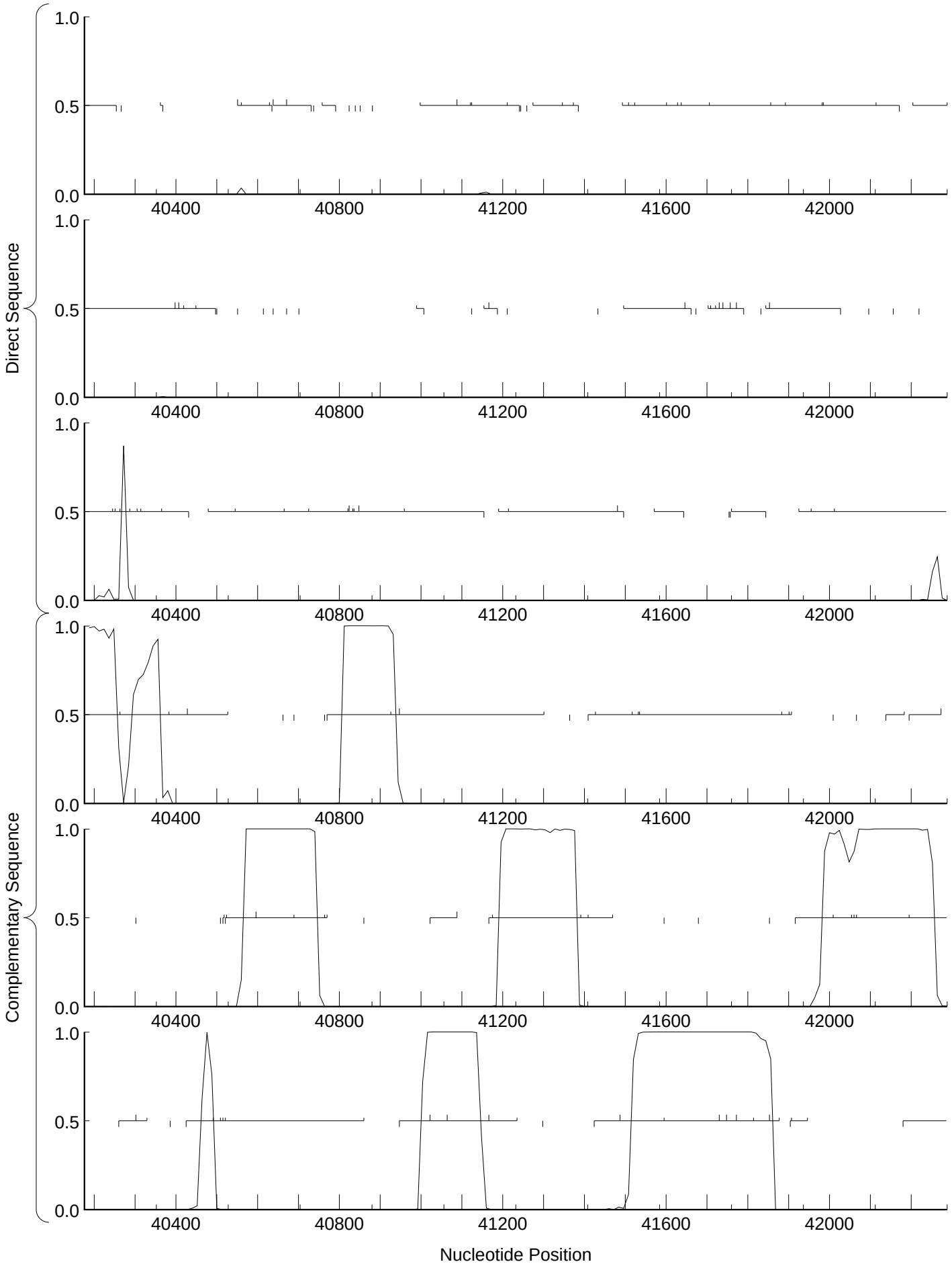

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Nucleotide Position

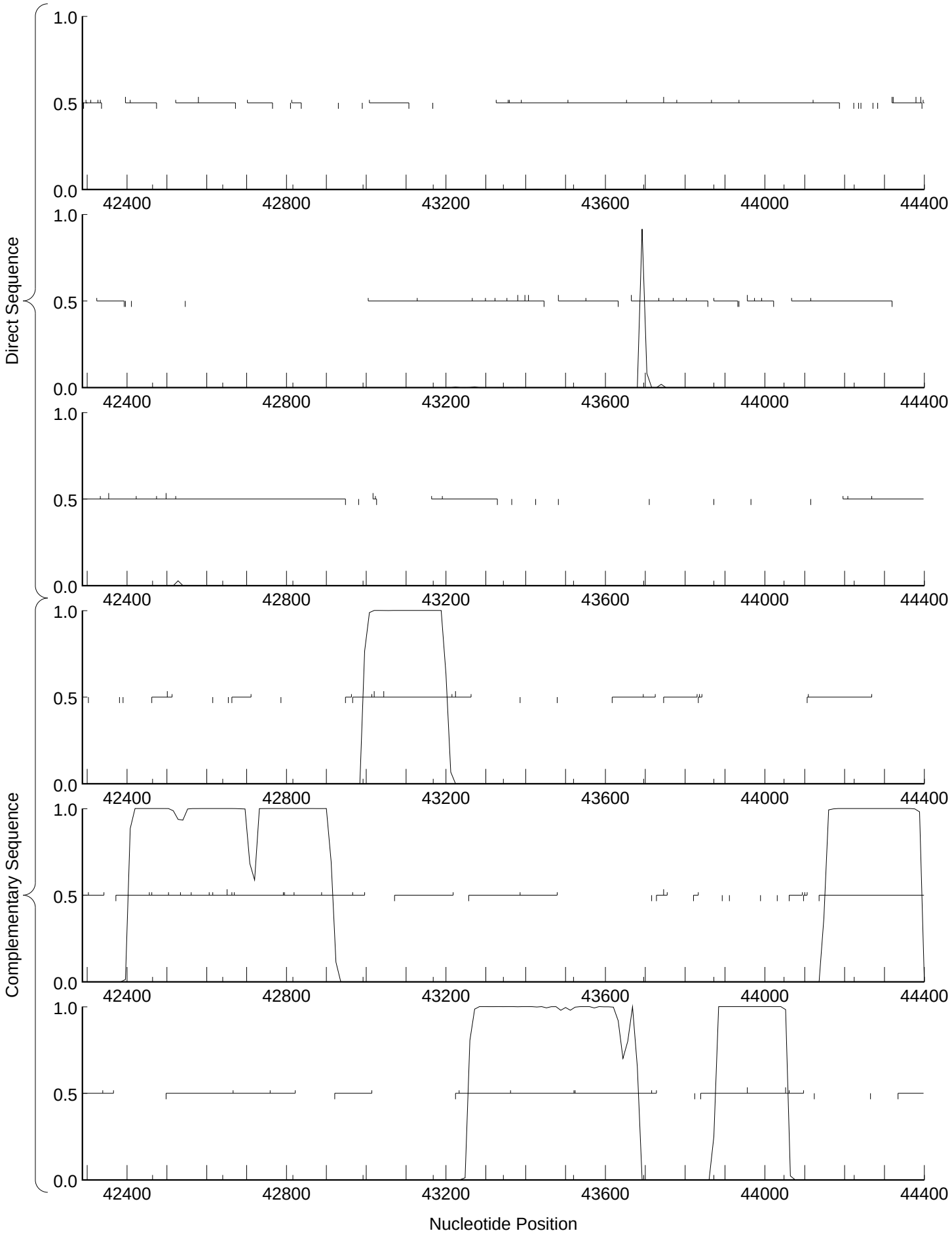

Direct Sequence
Complementary Sequence
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32800
33200
33600
Nucleotide Position

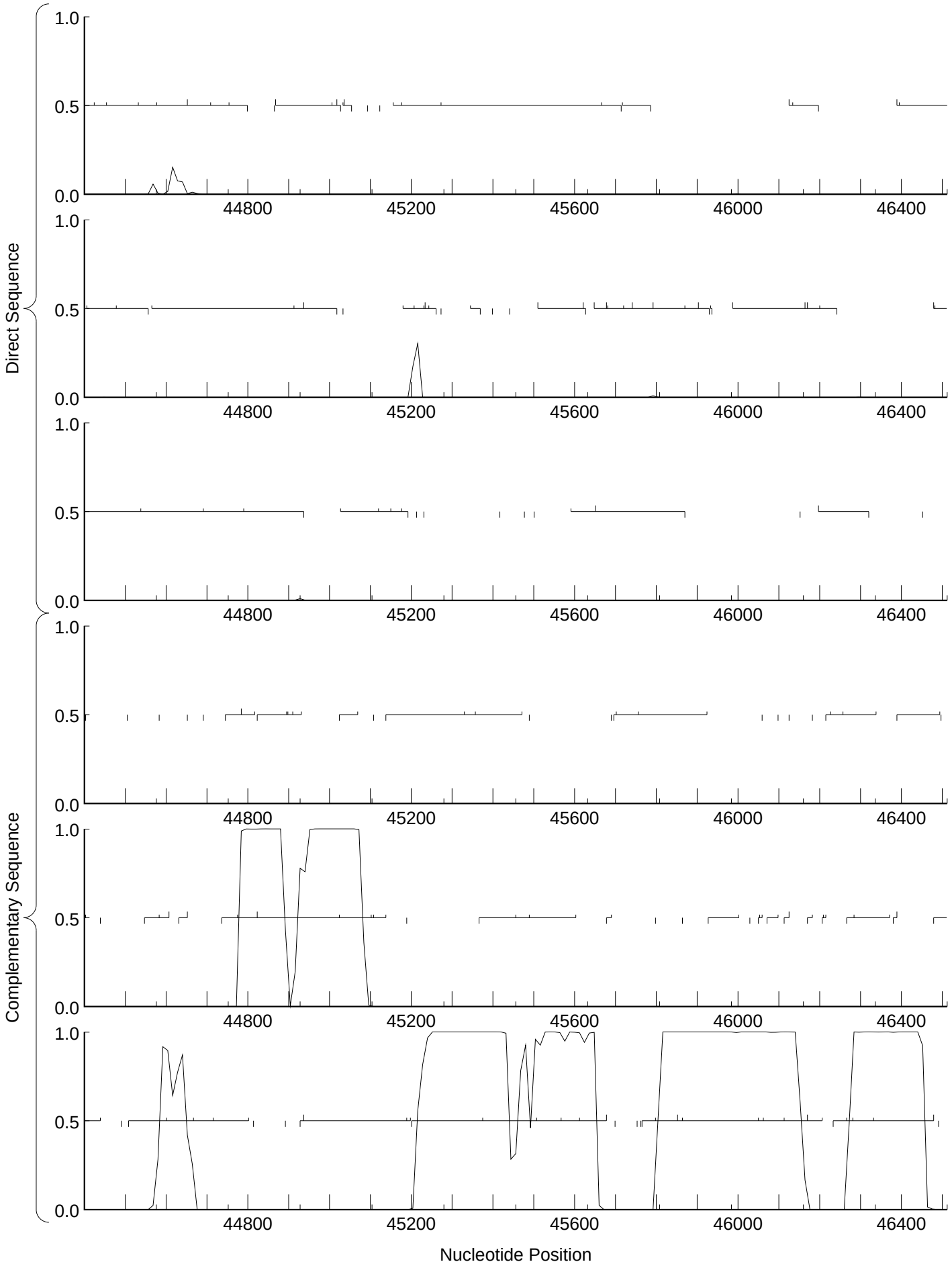

Direct Sequence
Complementary Sequence
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35200
35600
Nucleotide Position

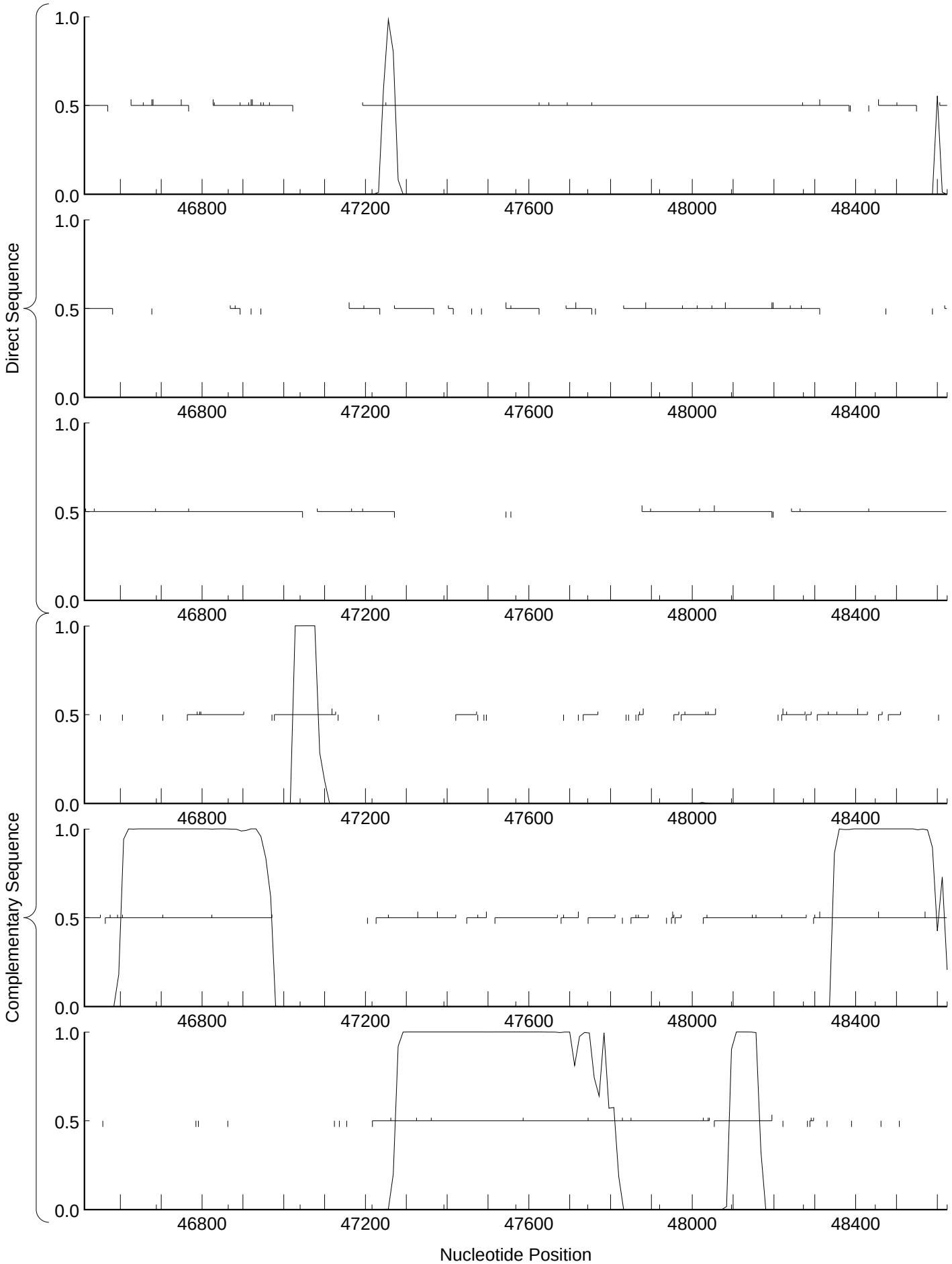

Direct Sequence
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36000
36400
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37200
37600
38000
Nucleotide Position

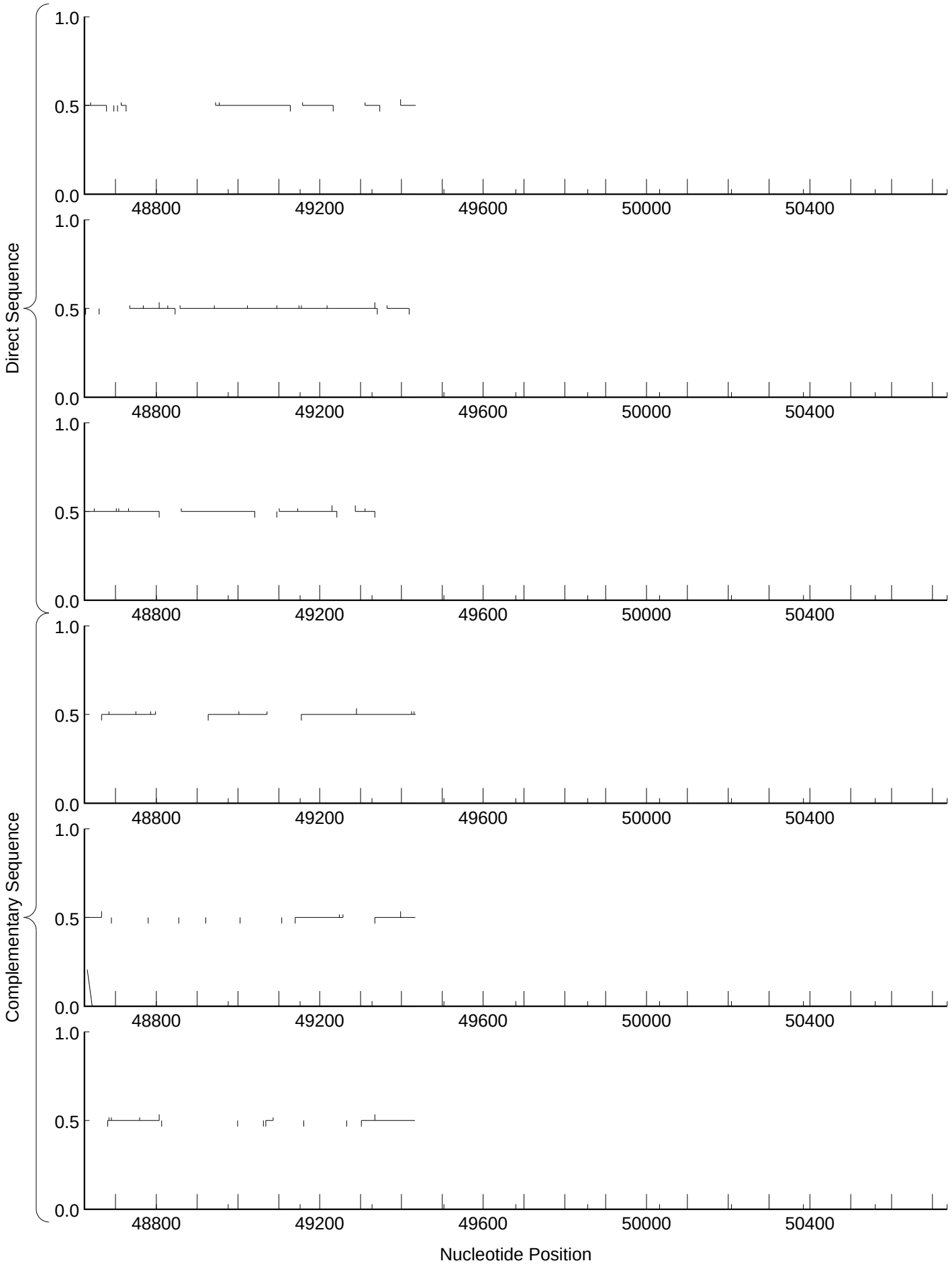

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
38400
38800
39200
39600
40000
Nucleotide Position


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


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