GeneMark

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

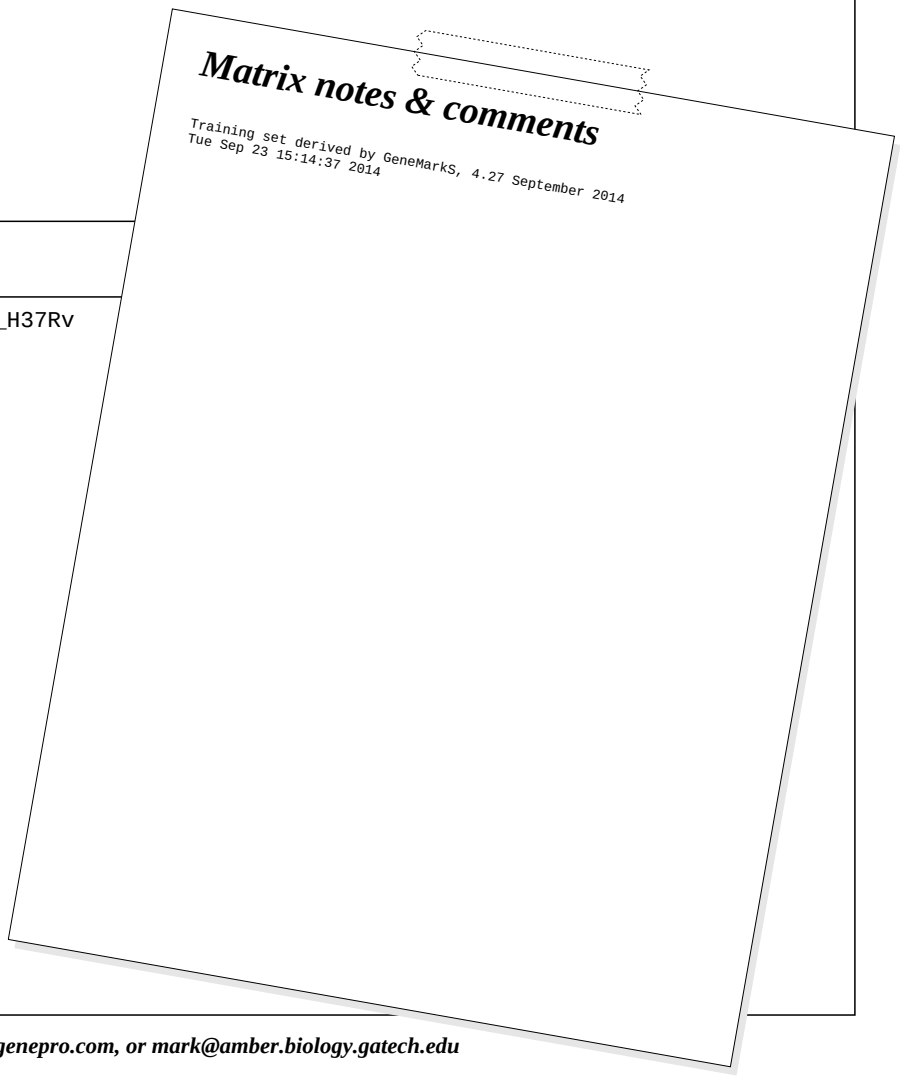
PROGRAM INFORMATION

```
Sequence         :  Mycobacterium phage Miko complete sequence, 51881 bp including 10-base 3' overhang (CGGTCGG
Analysis Date    :  3/19/24 at 5:22:27
Pages            :  26
Sequence Length  :  51881 bp
GC Content       :   63.53%

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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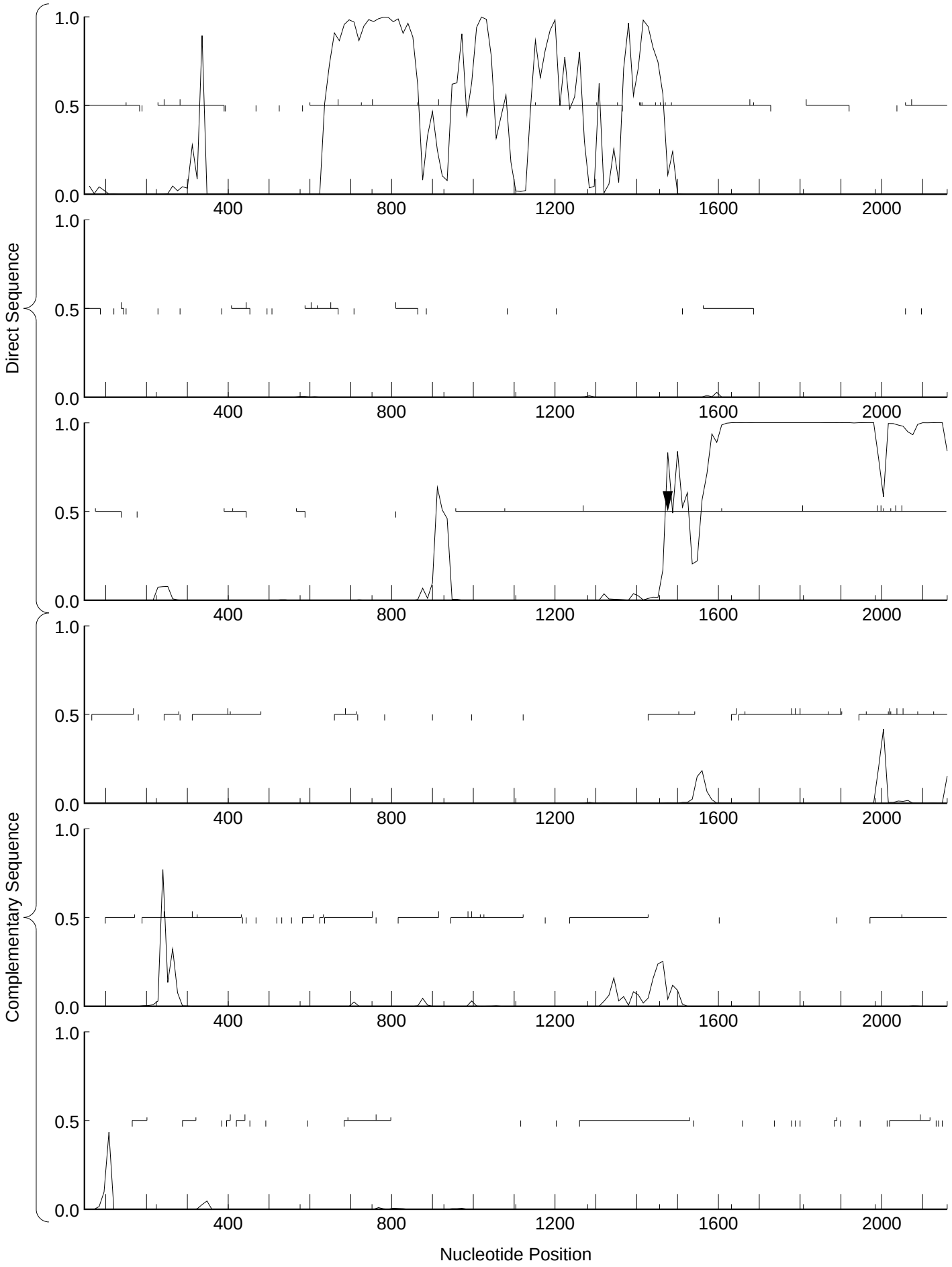
MATRIX INFORMATION

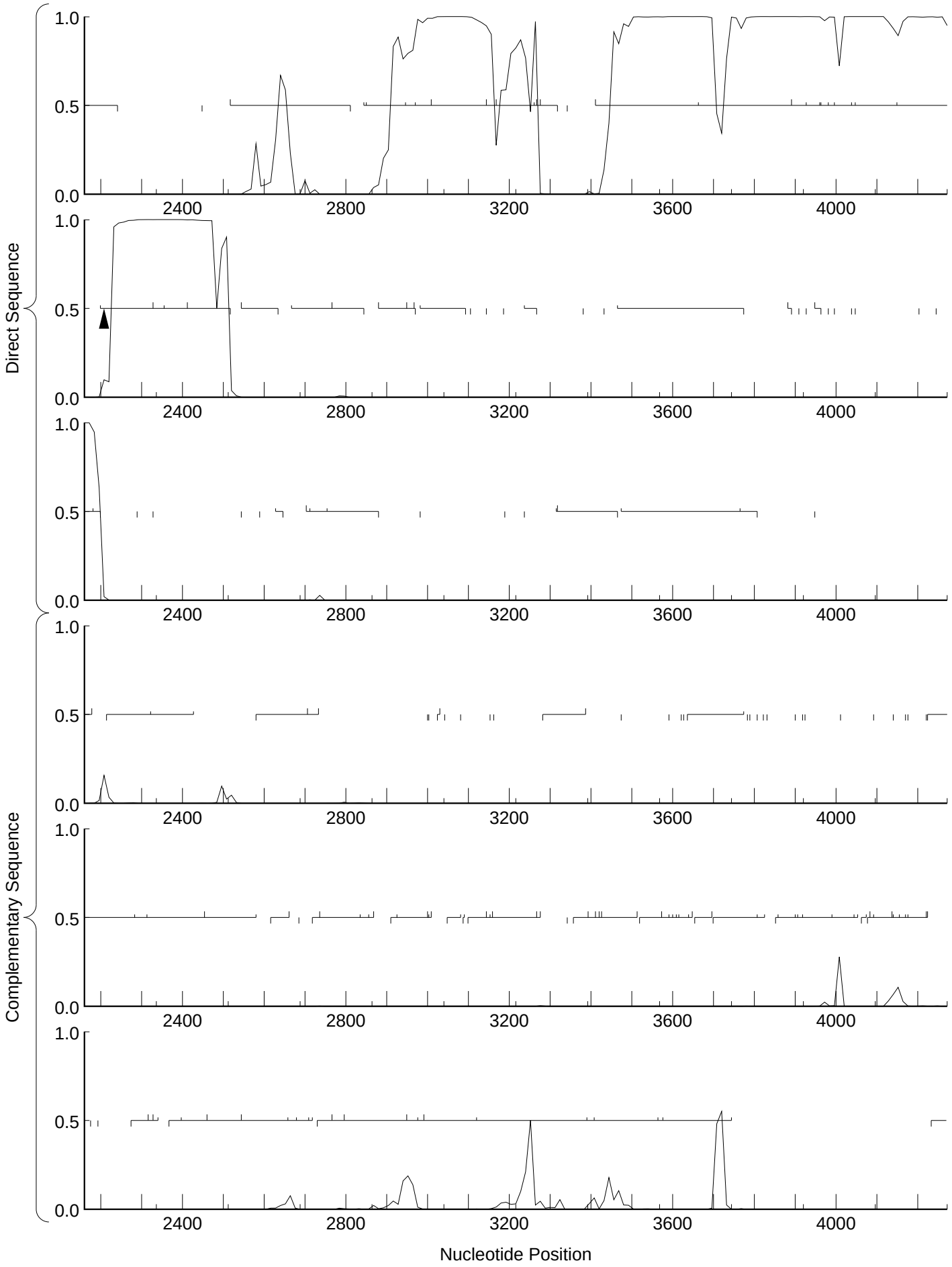
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Matrix     :  Mycobacterium_tuberculosis_H37Rv
Author     :  -

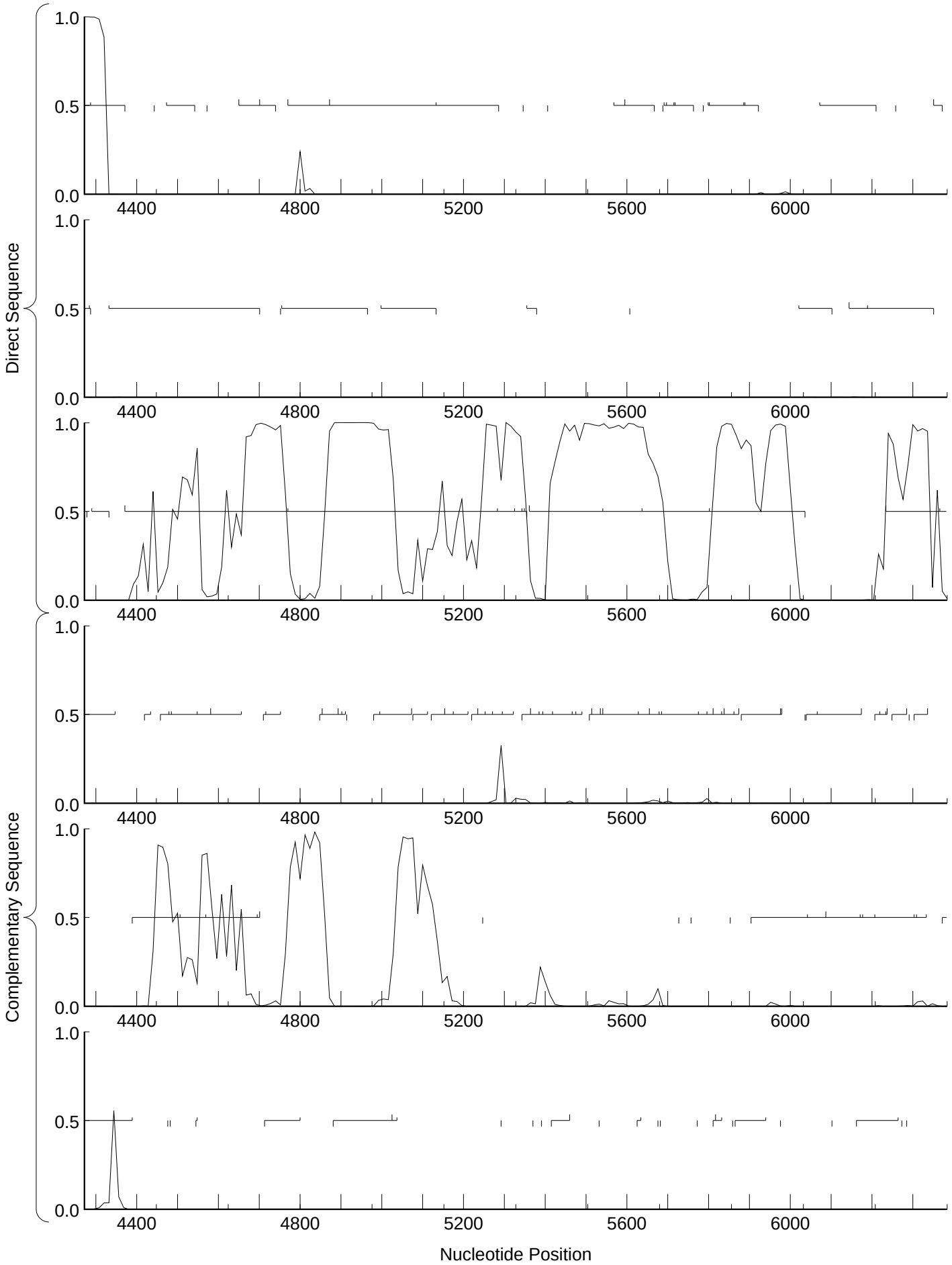
Order      :  4
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  Send questions / comments to:
      Dr. M. Borodovsky
      Georgia Institute of Technology
      School of Biology
      Atlanta, GA  30332-0230
```

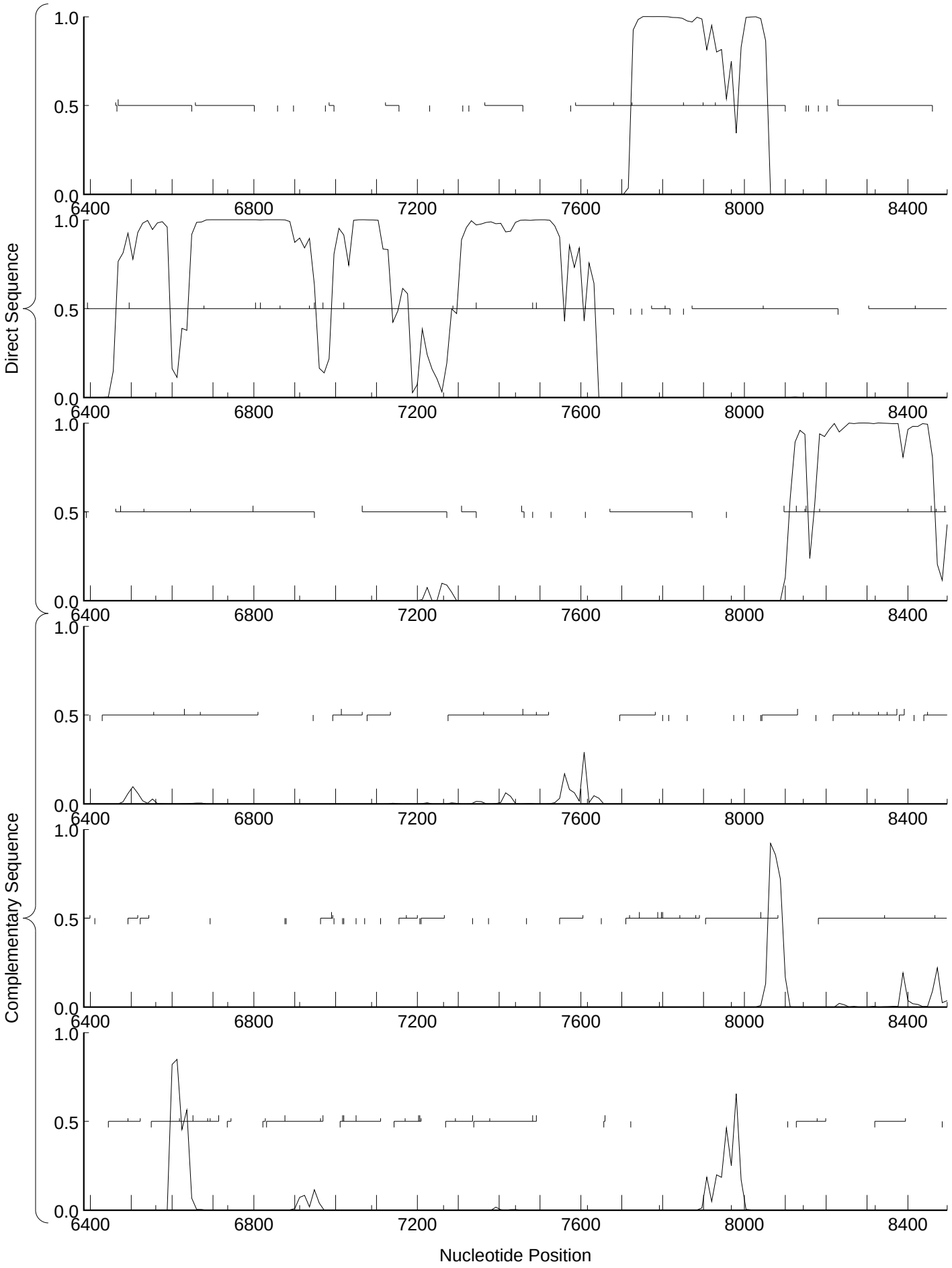

For help or information, send electronic mail to: custserv@genepro.com, or mark@amber.biology.gatech.edu

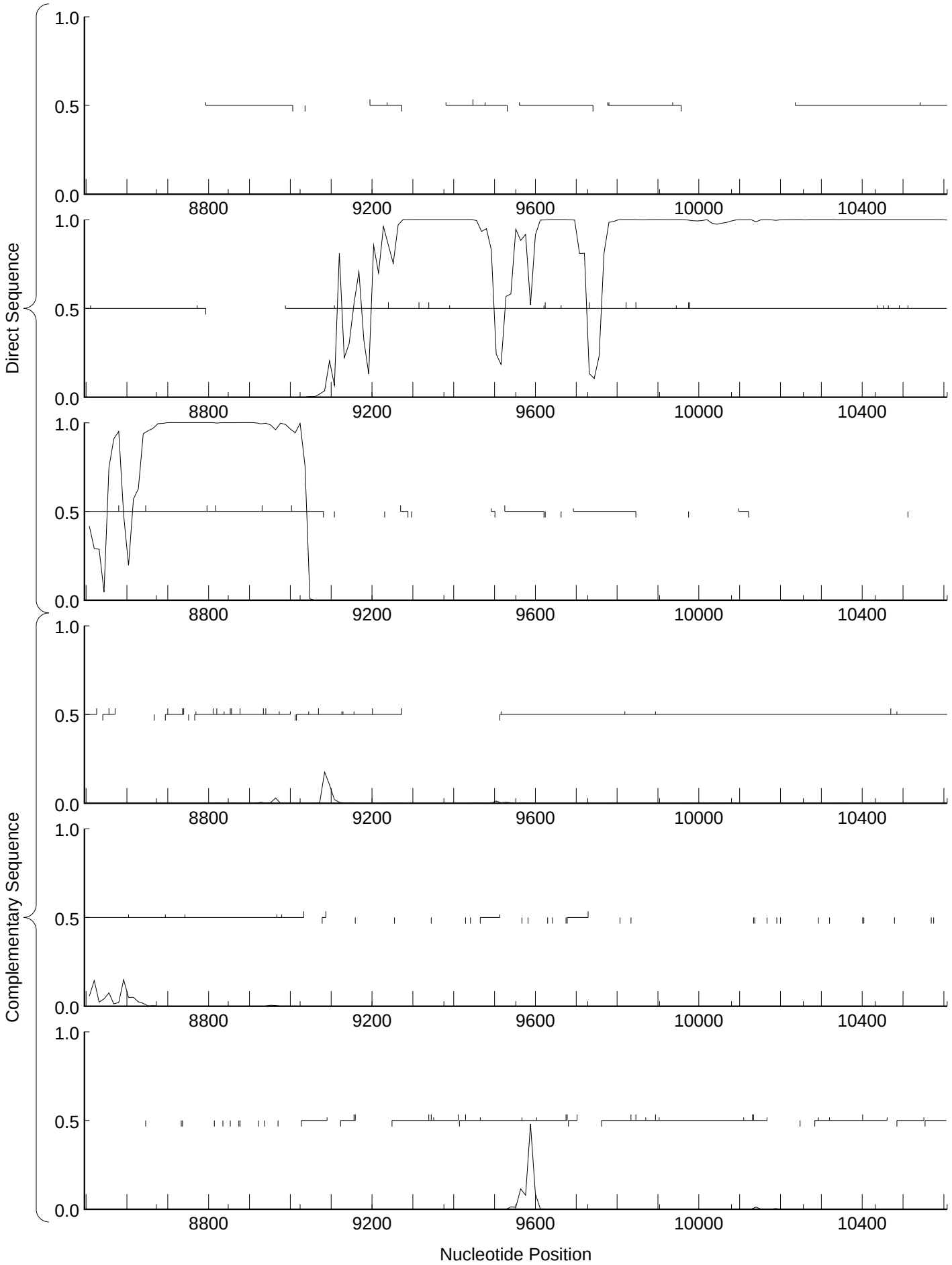

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
400
800
1200
1600
2000
Nucleotide Position

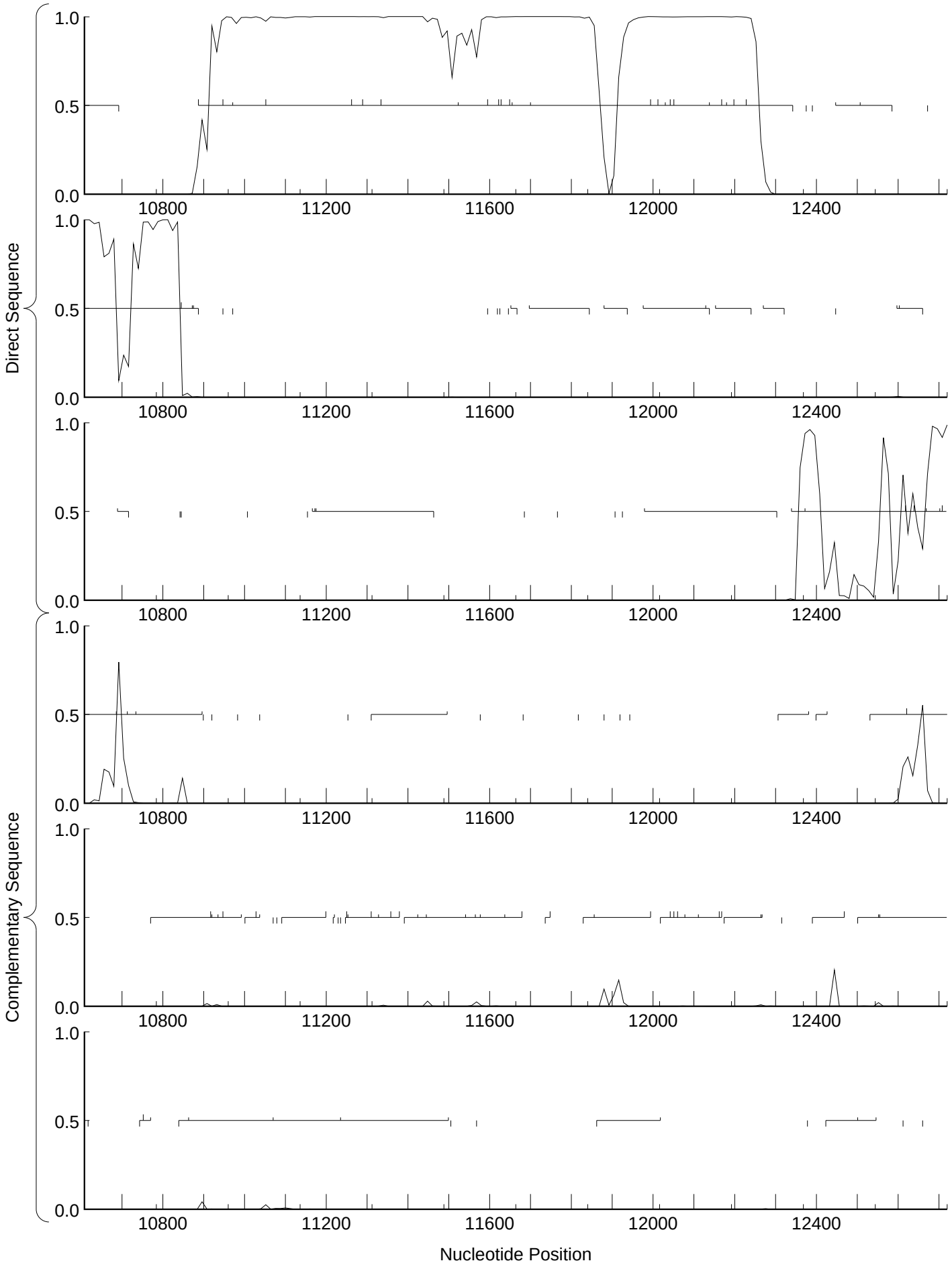

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
2400
2800
3200
3600
4000
Nucleotide Position


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
4400
4800
5200
5600
6000
Nucleotide Position

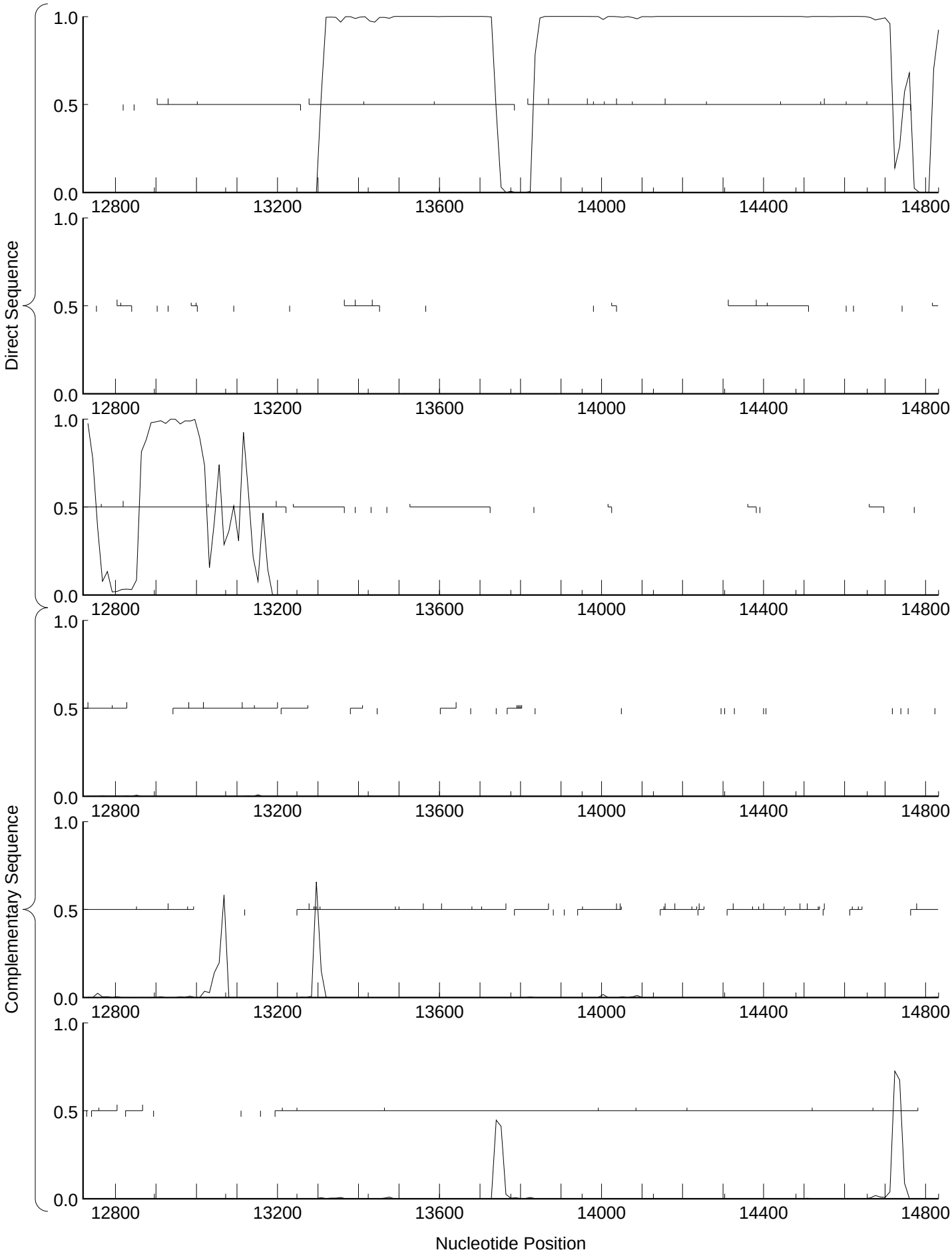
ko complete sequence, 51881 bp including 10-base 3’ overhang (CGGTCGGTTA), Cluster A2, Order 4, Window 96, Step 12, 5/26

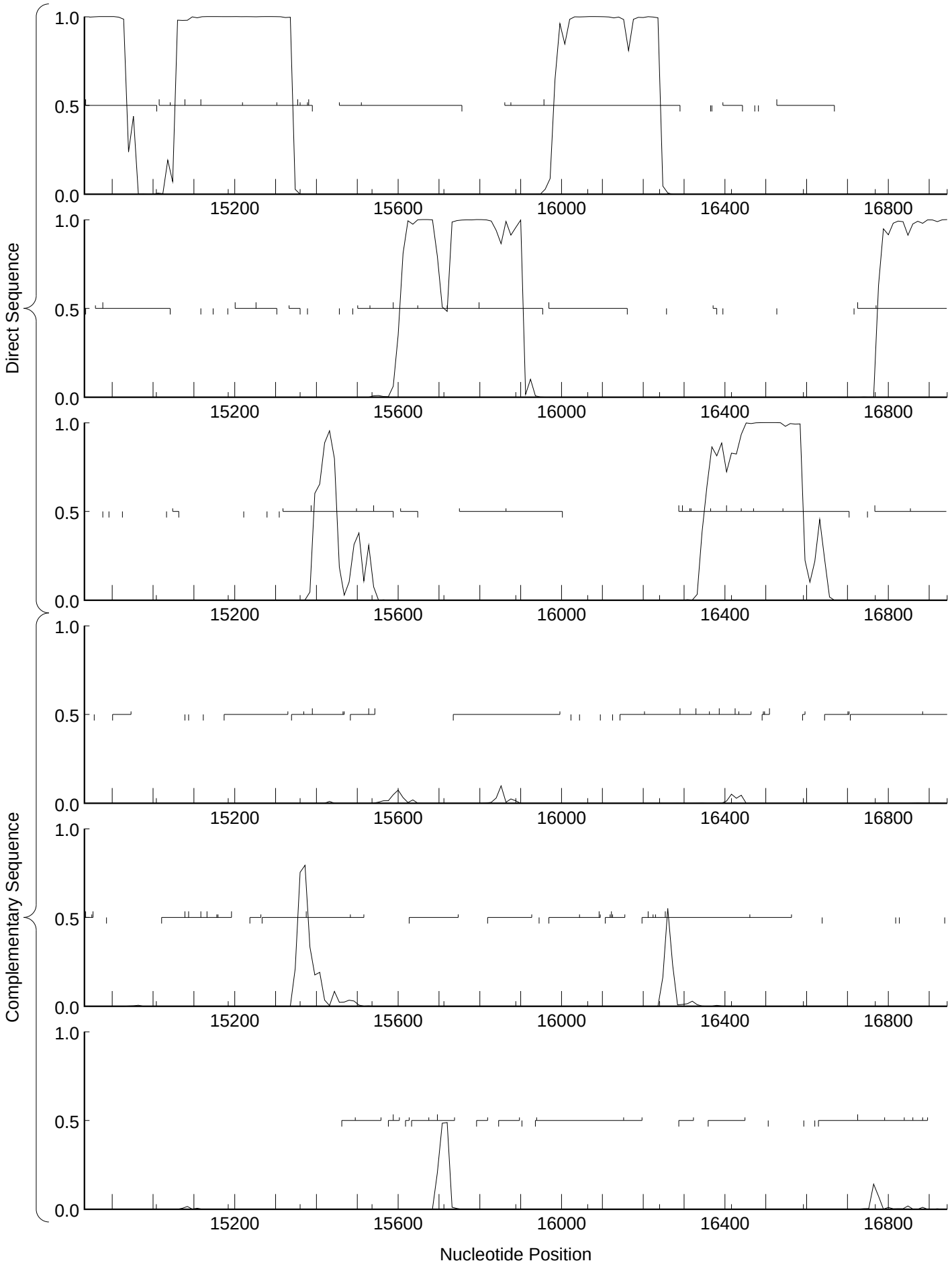


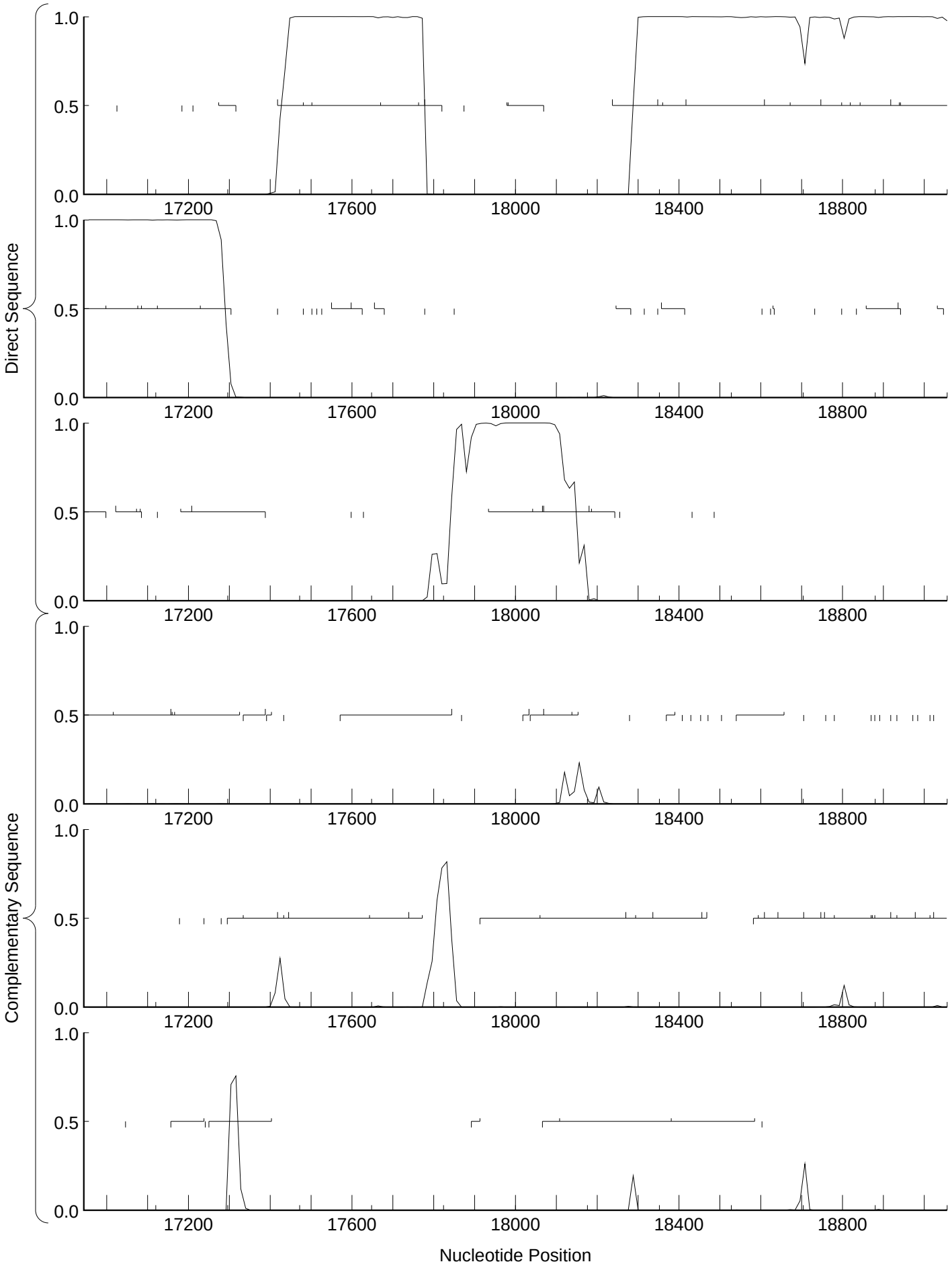

Direct Sequence
Complementary Sequence
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0.0
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9600
10000
10400
Nucleotide Position

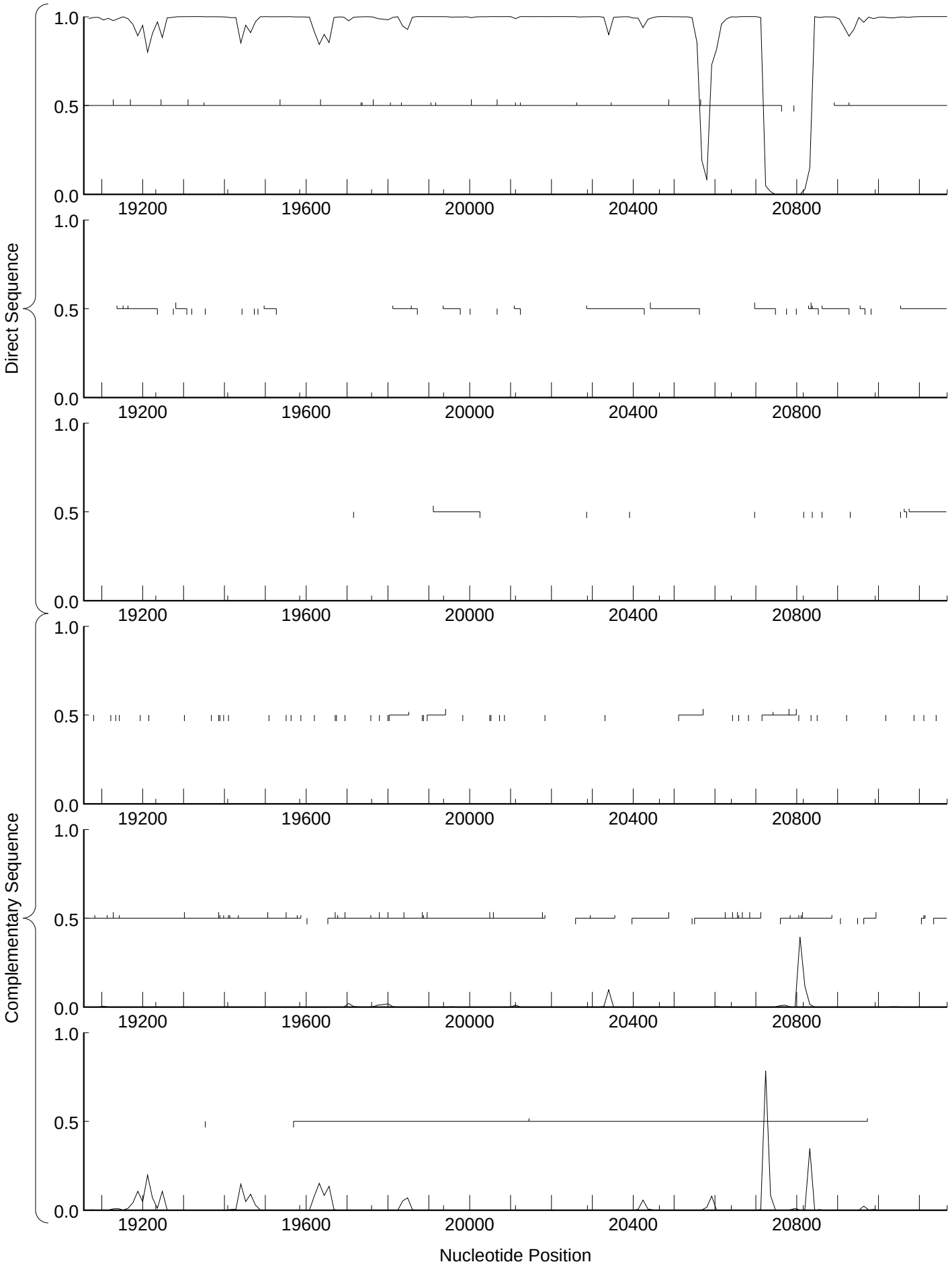

Direct Sequence
Complementary Sequence
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0.0
10800
11200
11600
12000
12400
Nucleotide Position

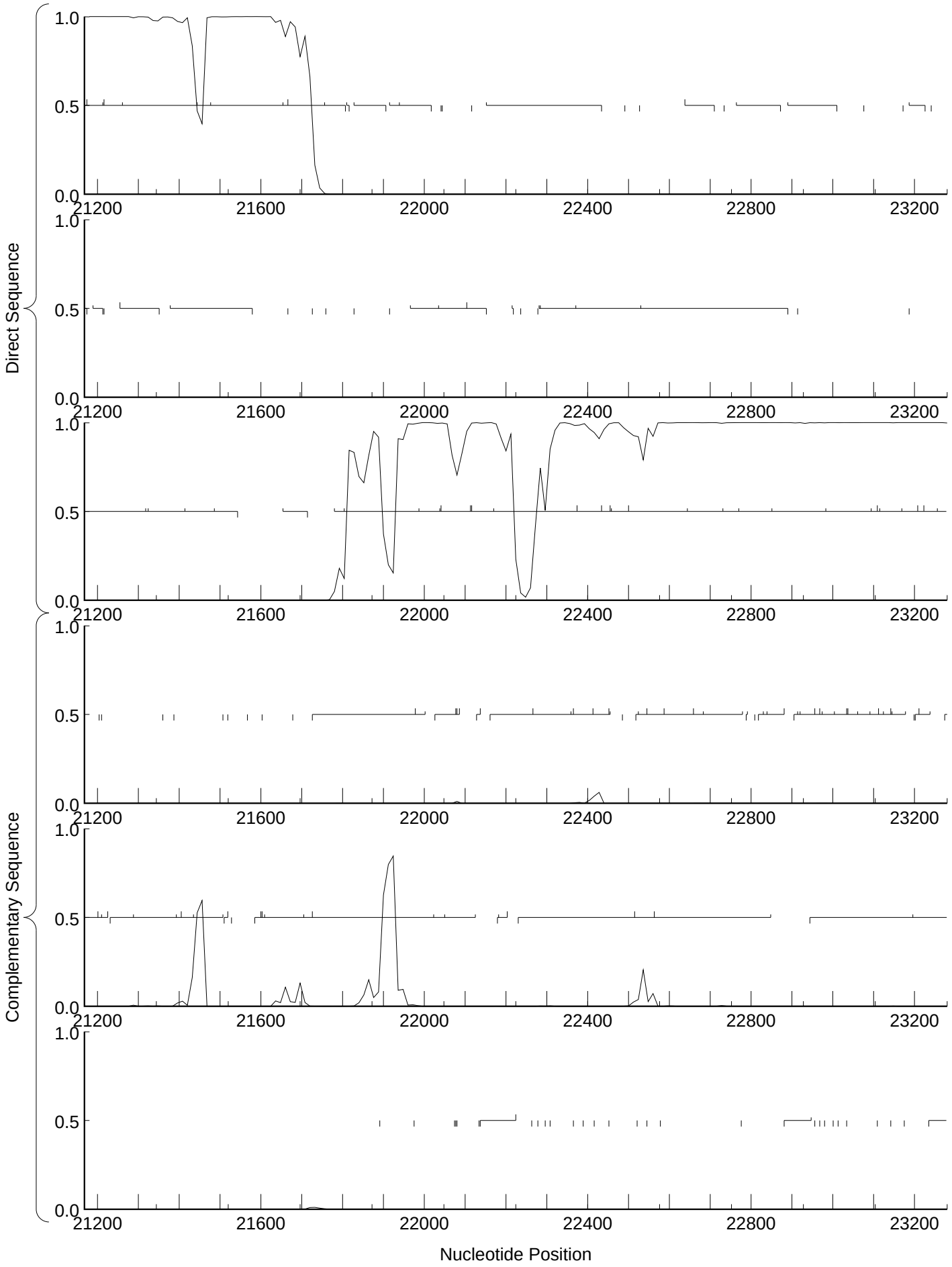
ko complete sequence, 51881 bp including 10-base 3’ overhang (CGGTCGGTTA), Cluster A2, Order 4, Window 96, Step 12, 8/26

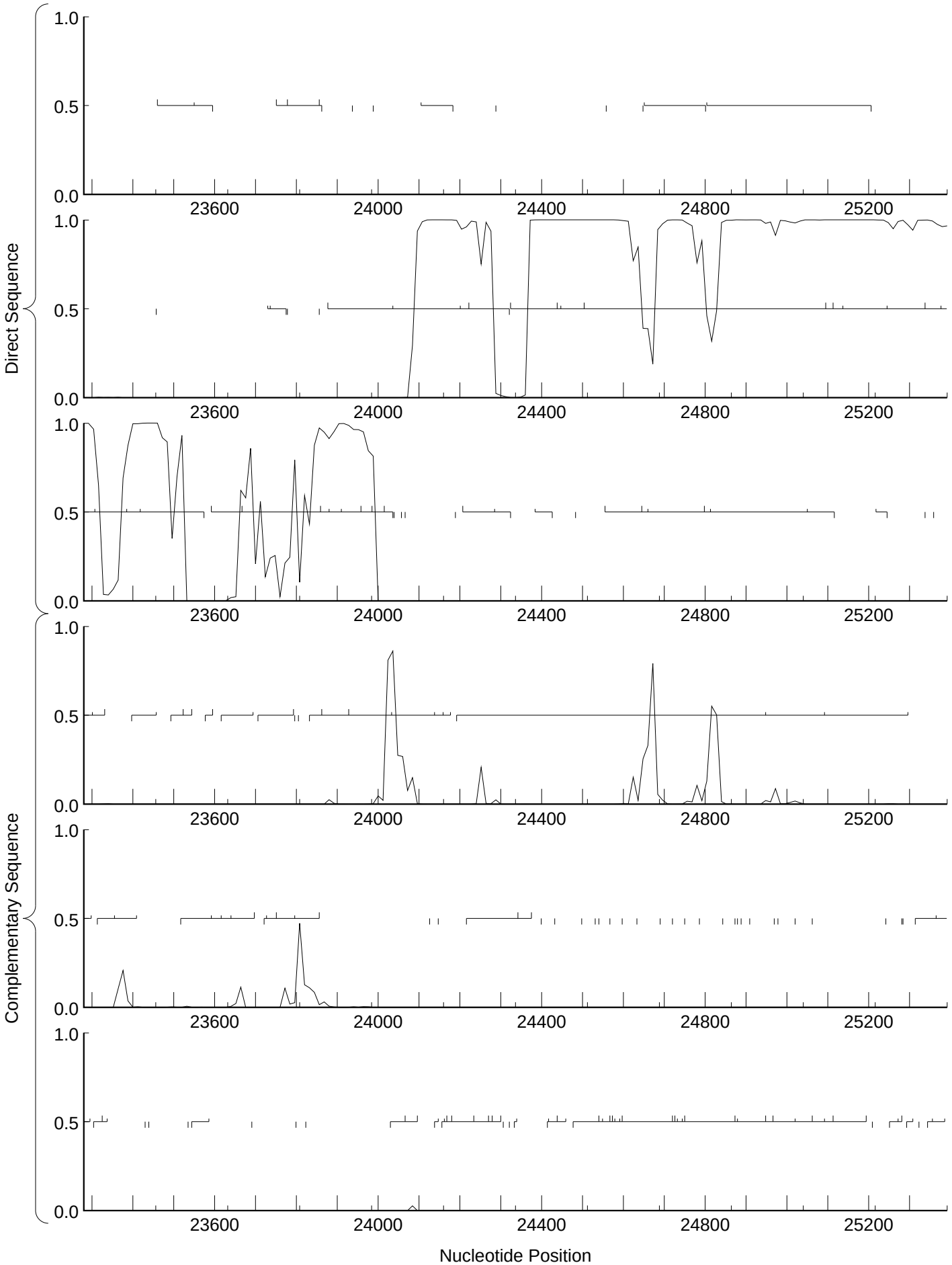


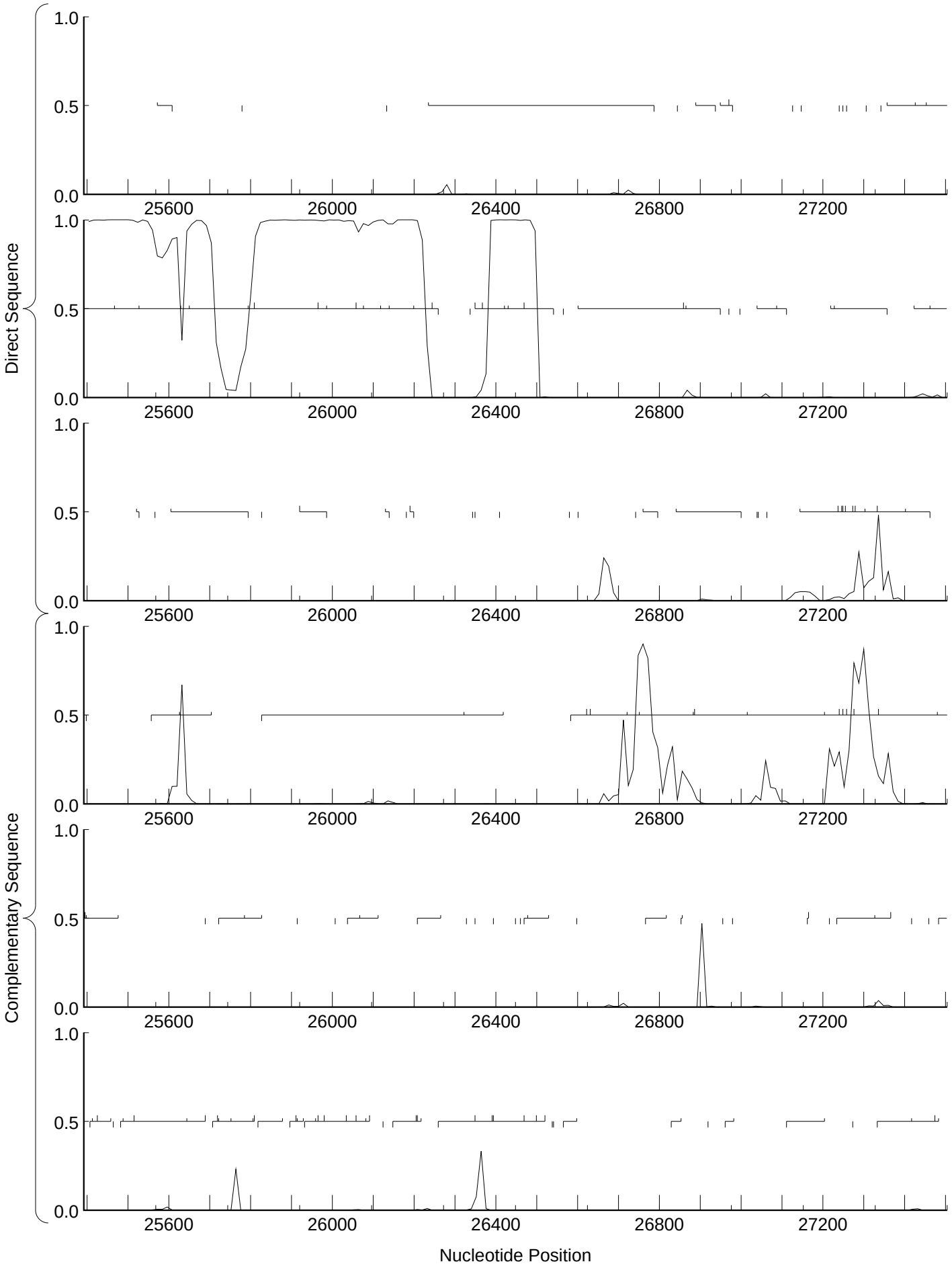

Direct Sequence
Complementary Sequence
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0.0
15200
15600
16000
16400
16800
Nucleotide Position

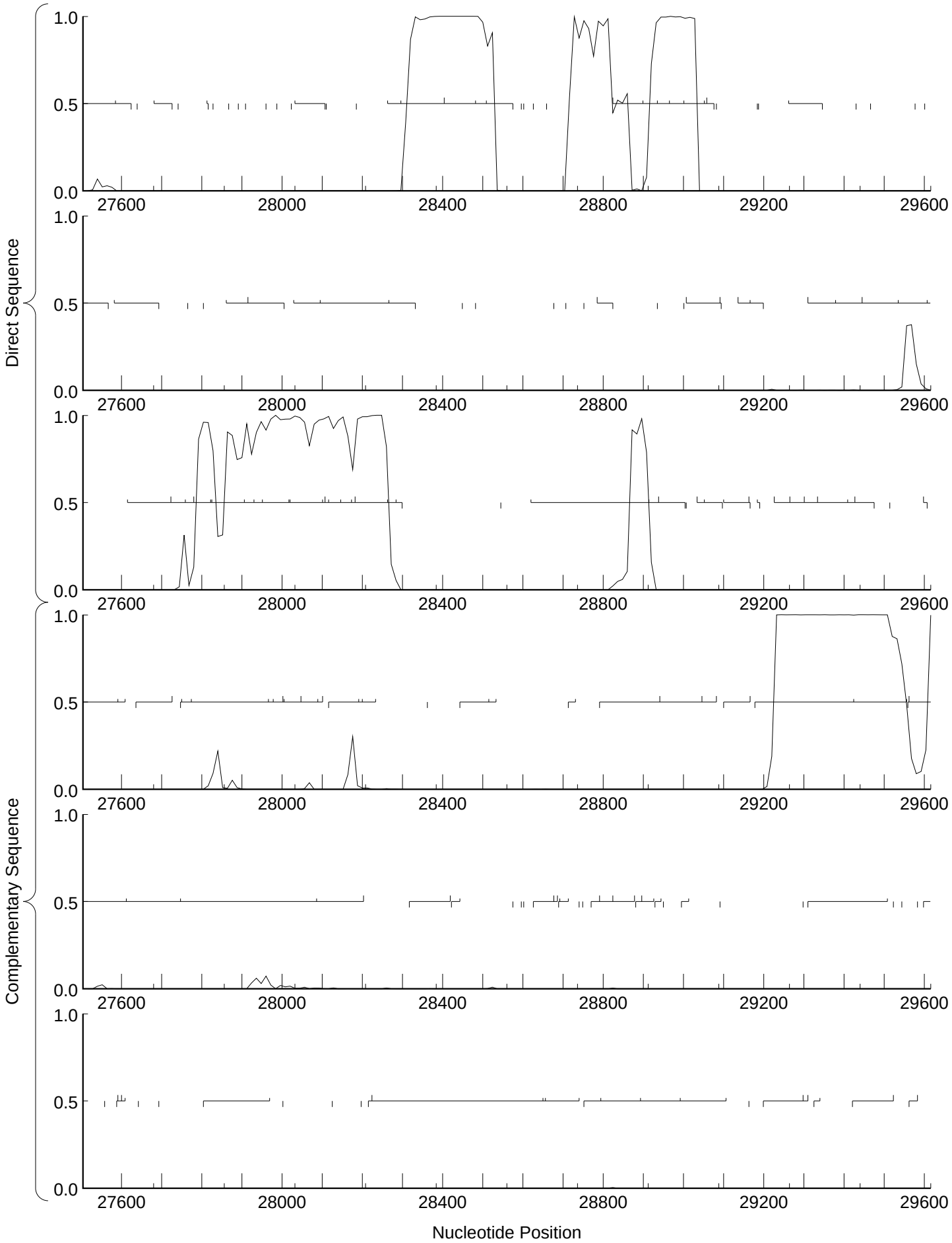

Direct Sequence
Complementary Sequence
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0.5
0.0
17200
17600
18000
18400
18800
Nucleotide Position

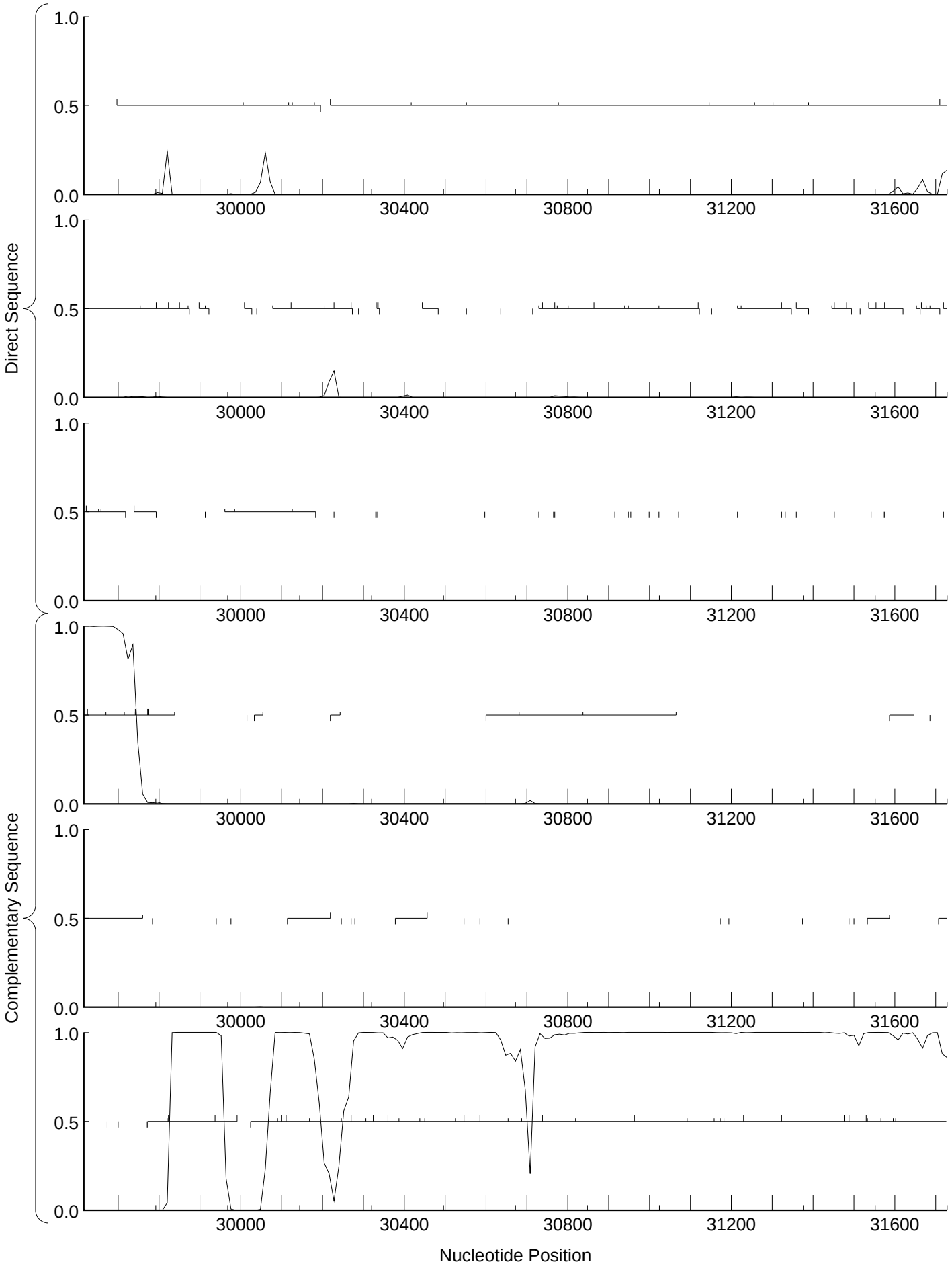

Direct Sequence
Complementary Sequence
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20400
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Nucleotide Position

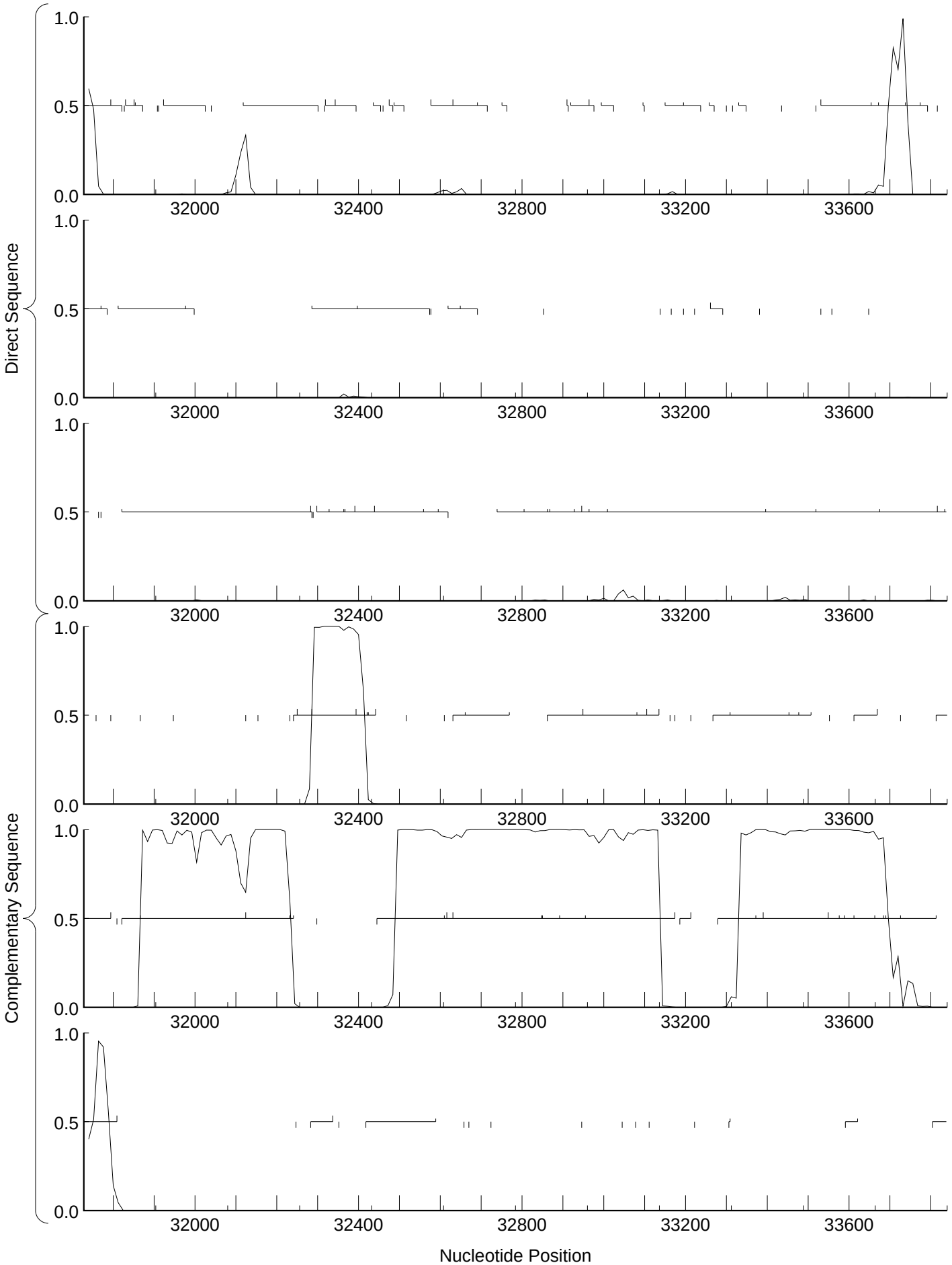

Direct Sequence
Complementary Sequence
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22400
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Nucleotide Position

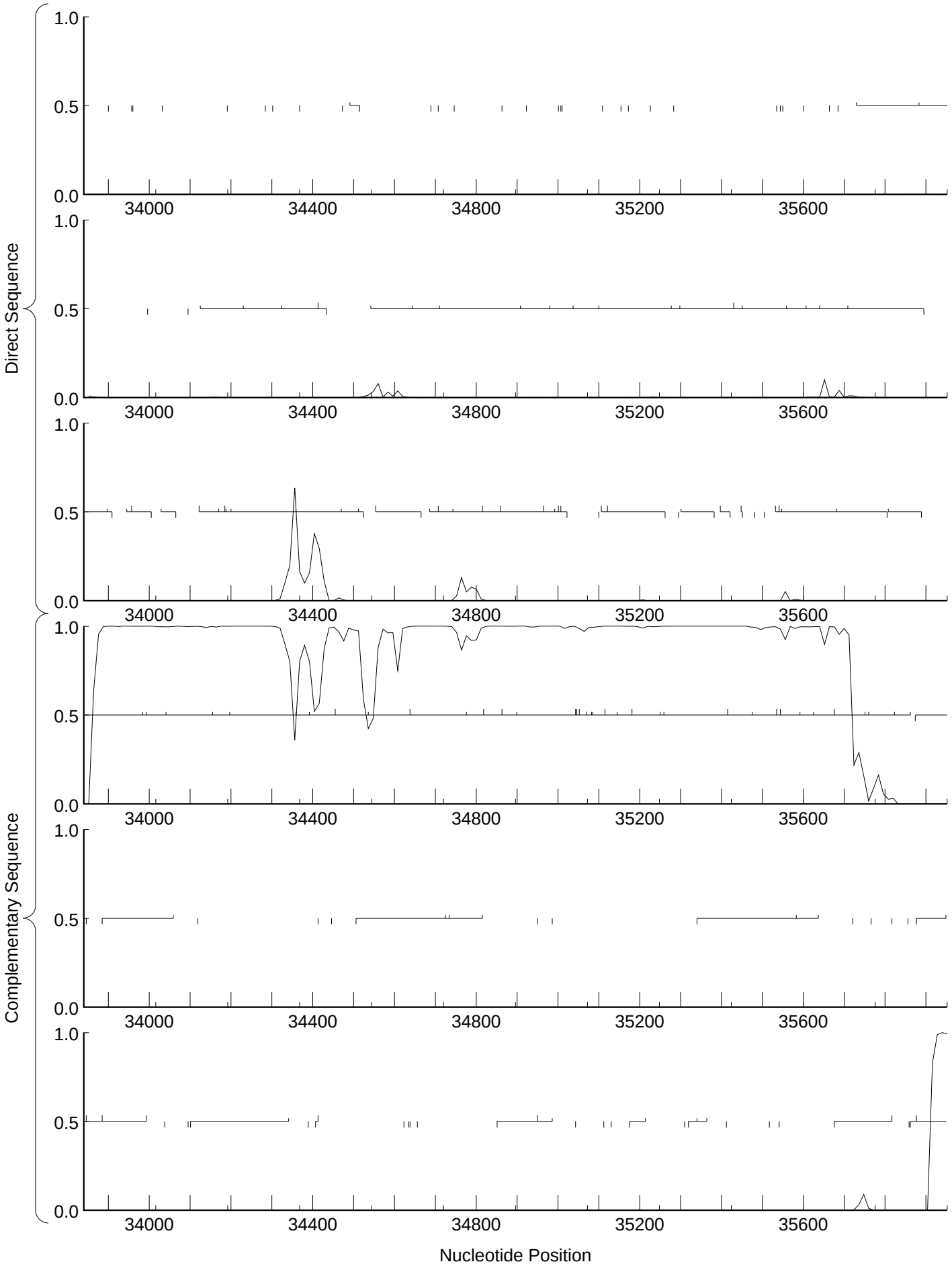

Direct Sequence
Complementary Sequence
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24400
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25200
Nucleotide Position

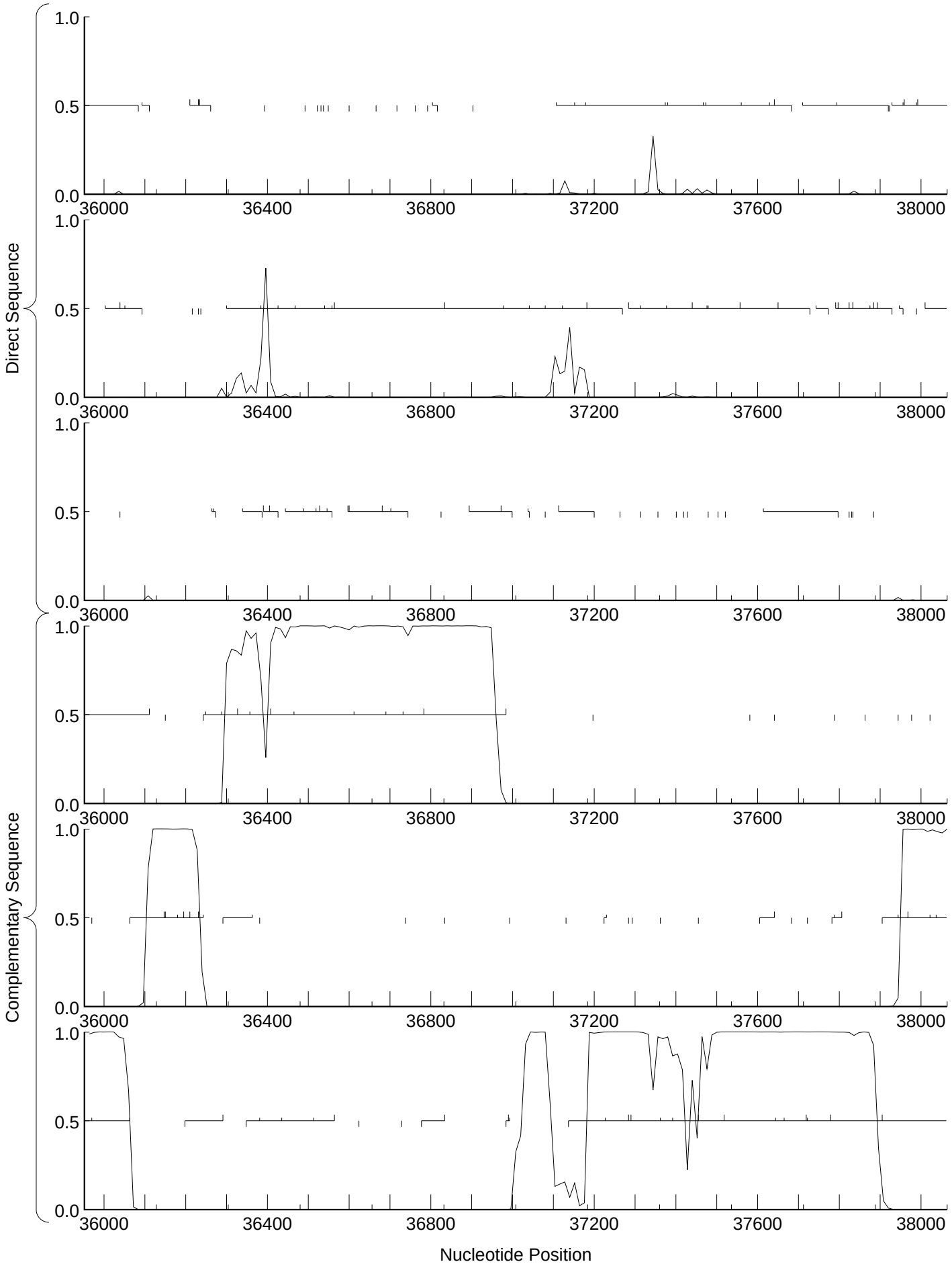

Direct Sequence
Complementary Sequence
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26400
26800
27200
Nucleotide Position

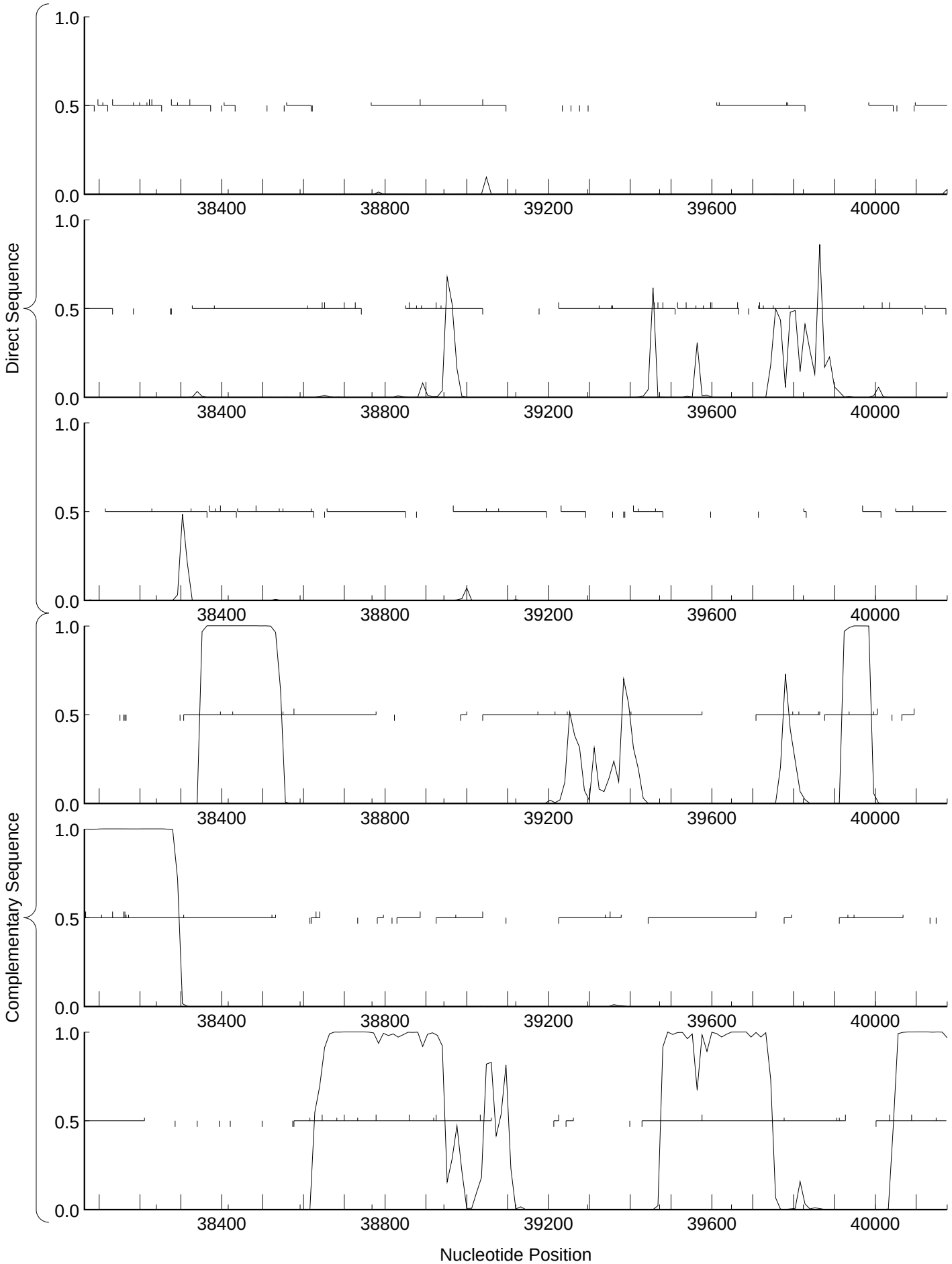

Direct Sequence
Complementary Sequence
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29200
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Nucleotide Position

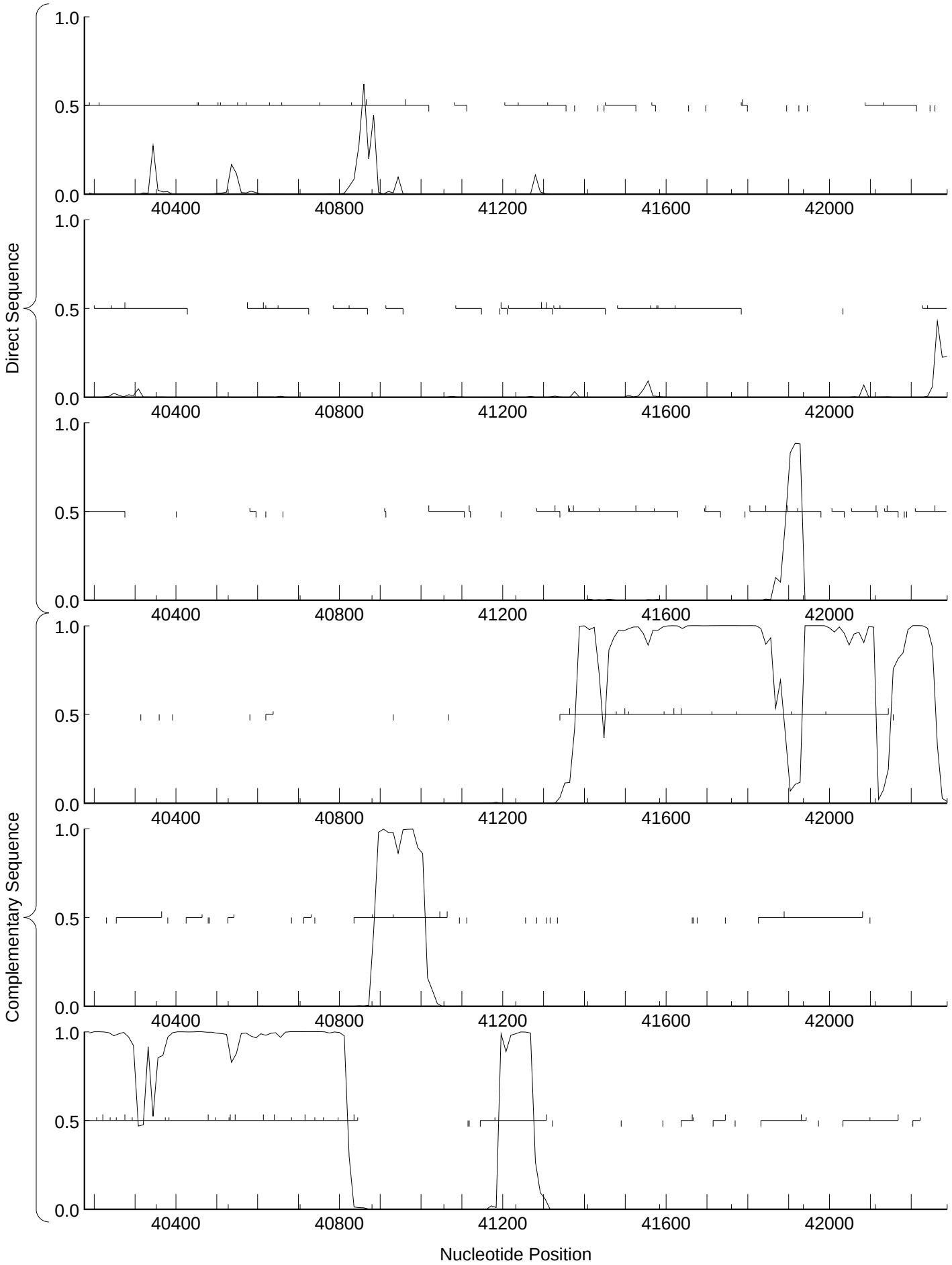

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Nucleotide Position

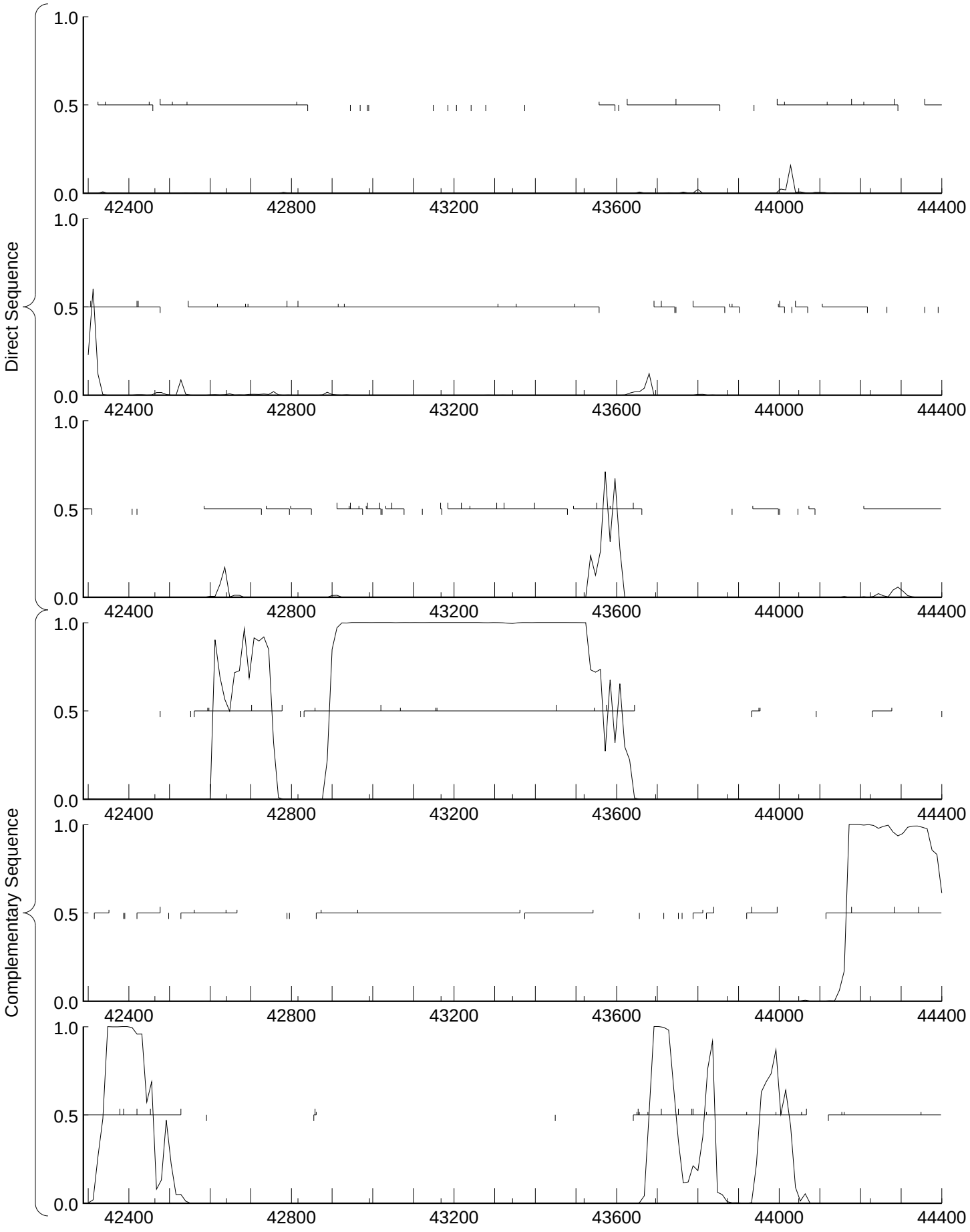

Direct Sequence
Complementary Sequence
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33200
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Nucleotide Position

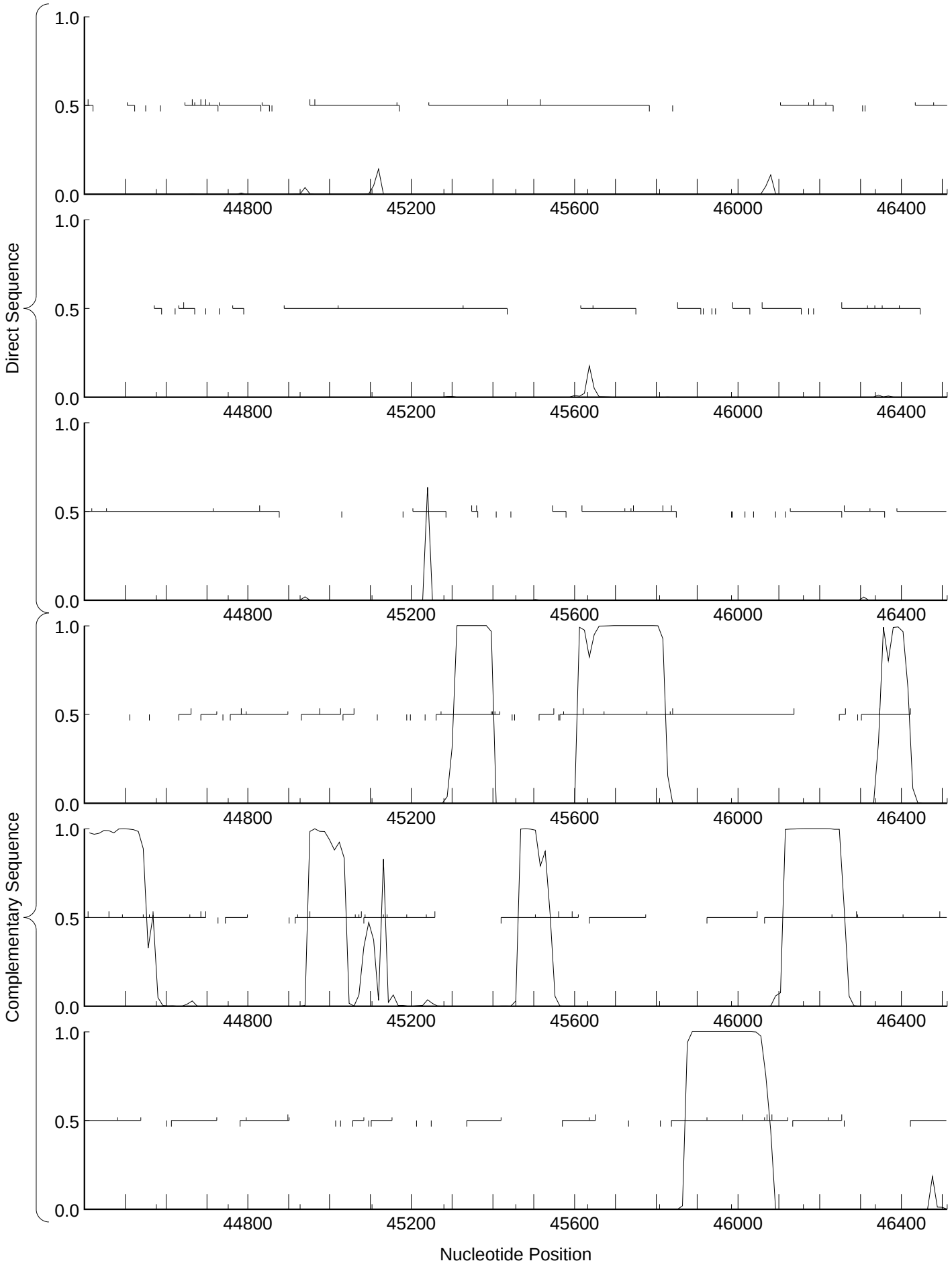

Direct Sequence
Complementary Sequence
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34800
35200
35600
Nucleotide Position

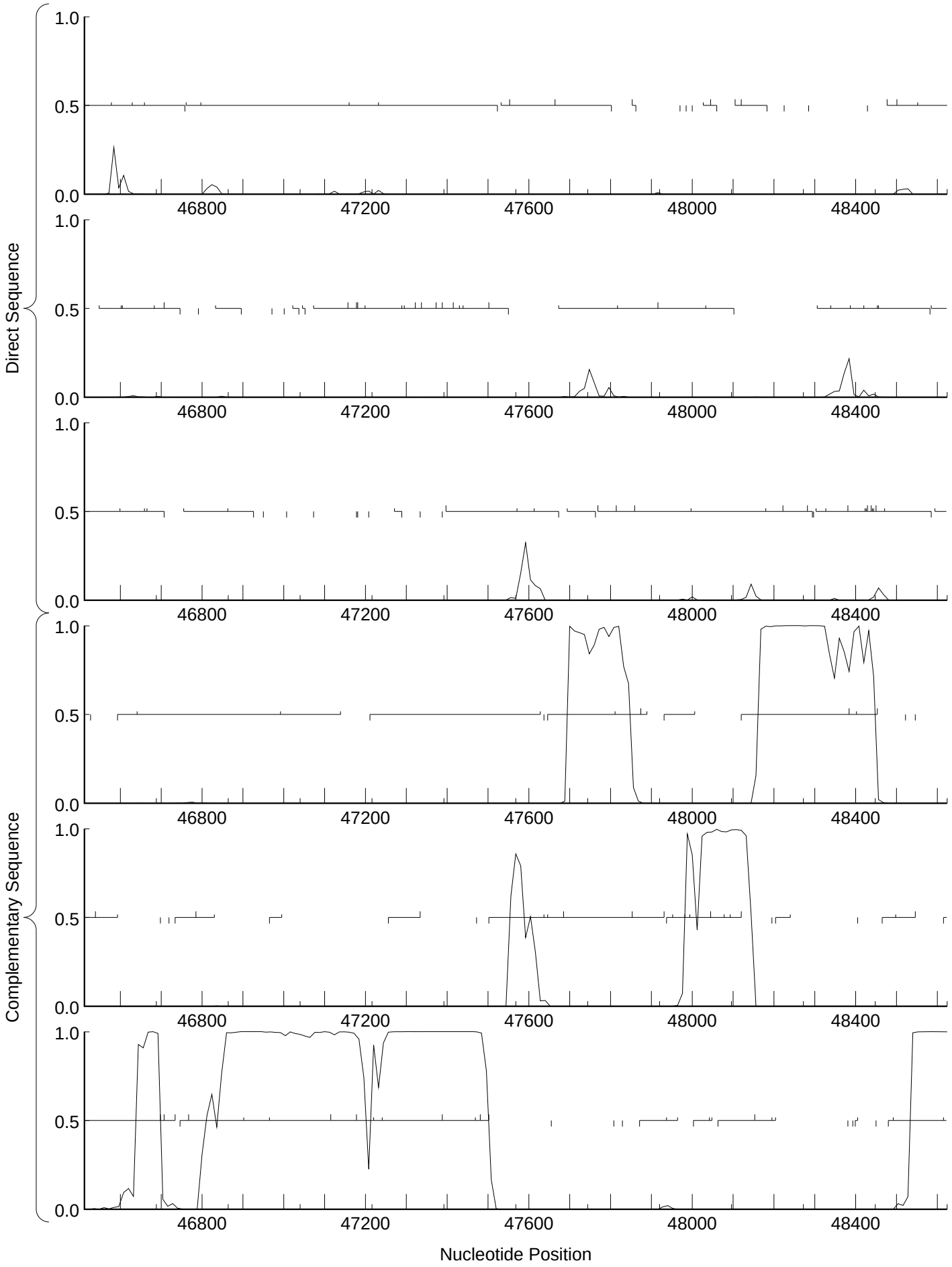

Direct Sequence
Complementary Sequence
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37600
38000
Nucleotide Position

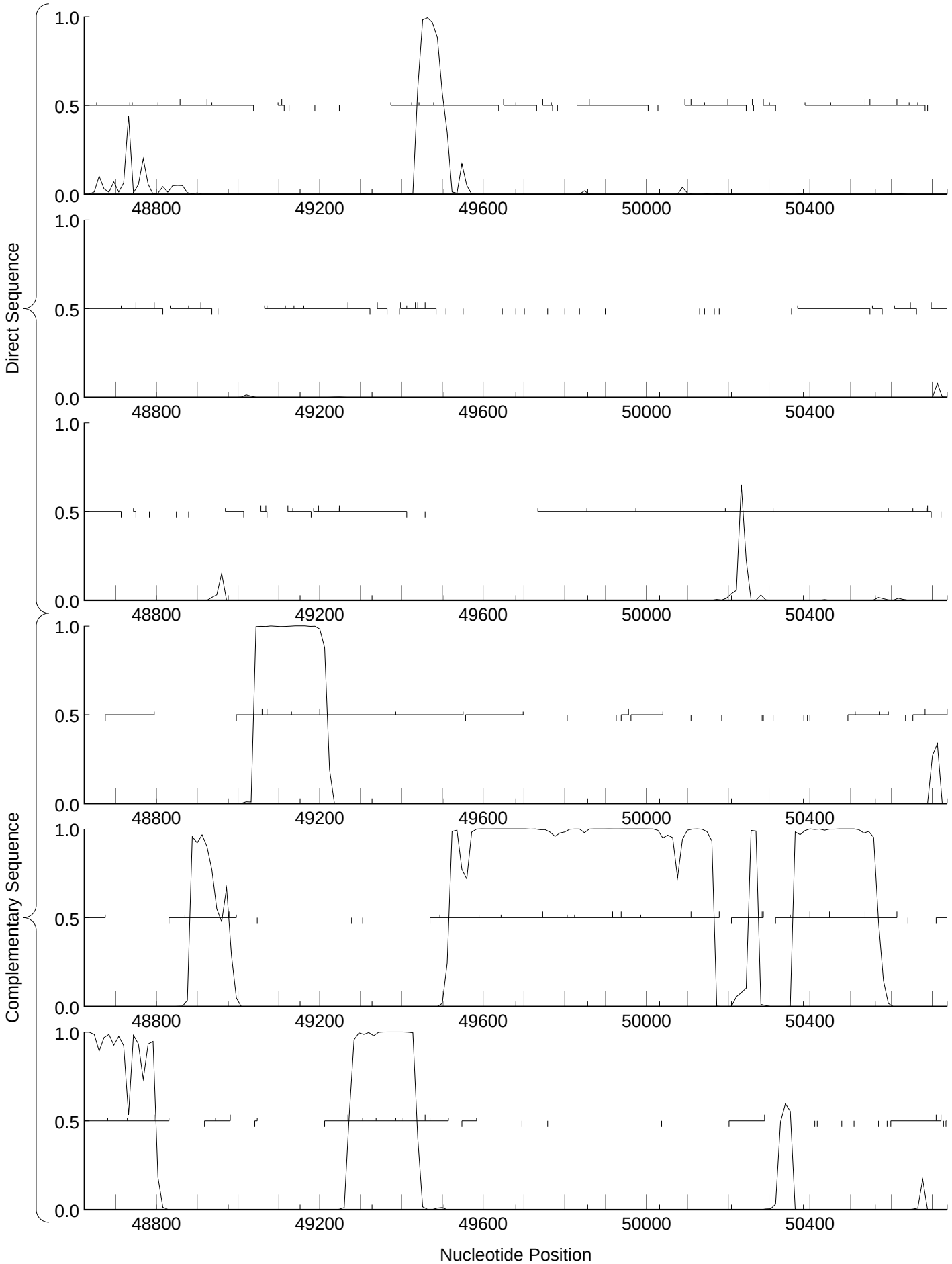

Direct Sequence
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39600
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Nucleotide Position

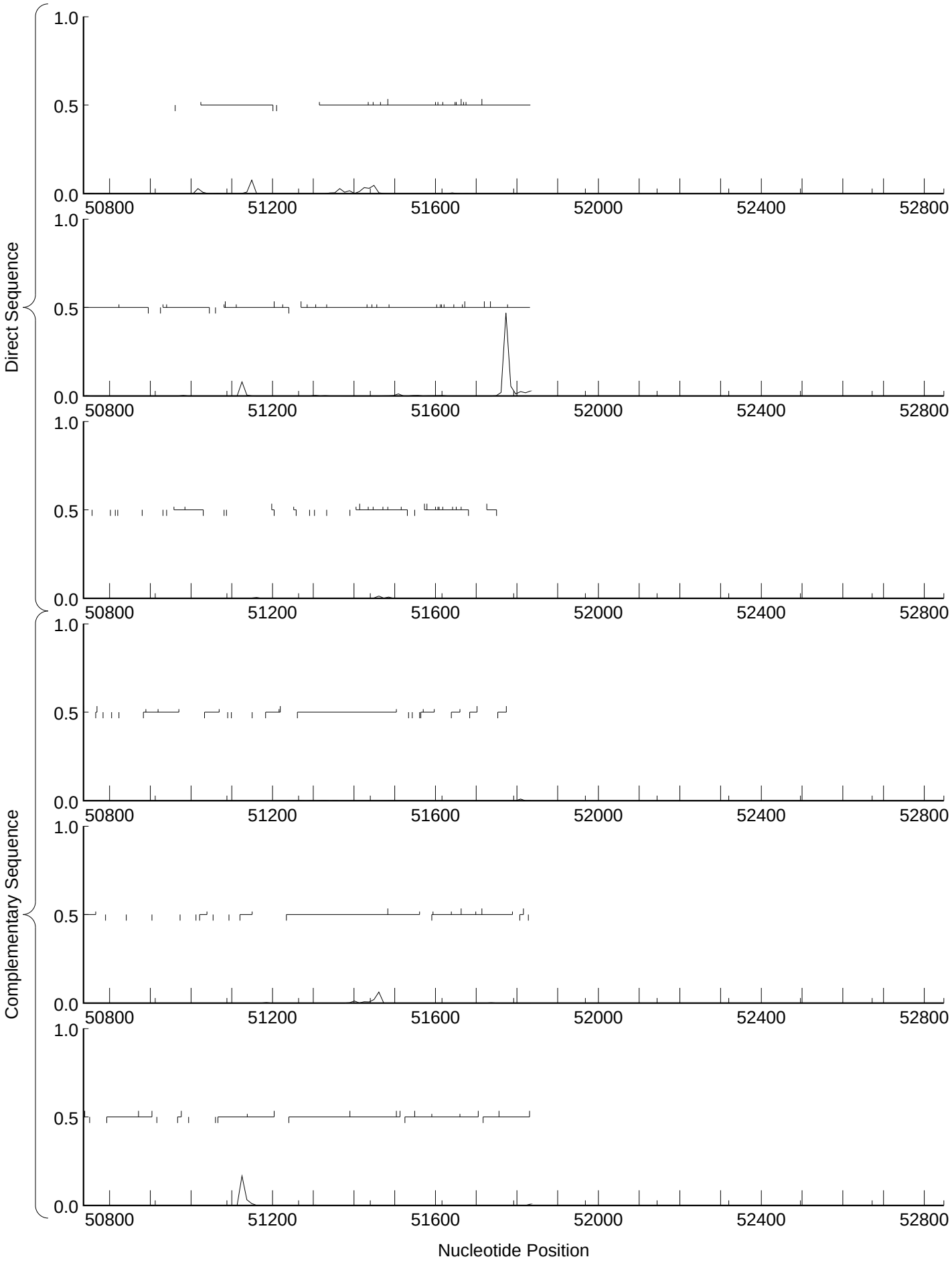

Direct Sequence
Complementary Sequence
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40400
40800
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41600
42000
Nucleotide Position


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


Direct Sequence
Complementary Sequence
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44800
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45600
46000
46400
Nucleotide Position


Direct Sequence
Complementary Sequence
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46800
47200
47600
48000
48400
Nucleotide Position


Direct Sequence
Complementary Sequence
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48800
49200
49600
50000
50400
Nucleotide Position


Direct Sequence
Complementary Sequence
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Nucleotide Position