GeneMark

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

PROGRAM INFORMATION

```
Sequence         :  Mycobacterium phage BoostSeason complete sequence, 58078 bp including 10-base 3’ overhang (
Analysis Date    :  3/29/24 at 8:35:16
Pages            :  29
Sequence Length  :  58078 bp
GC Content       :   68.21%

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

PS-Version       :  1.2

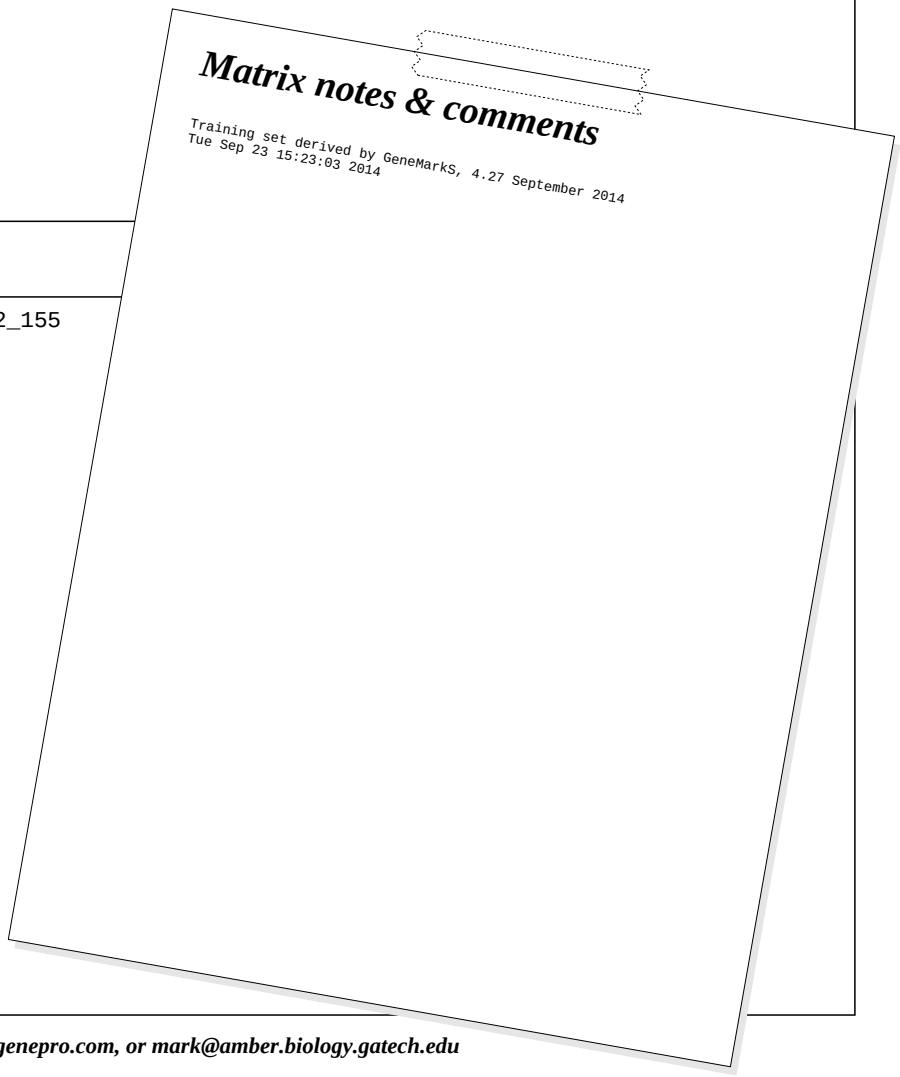
GeneMark Options :  PostScript graph,
                    Mark ORFs / splice sites,
                    List ORFs,
                    List regions and/or splice sites,
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MATRIX INFORMATION

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Matrix     :  Mycobacterium_smegmatis_MC2_155
Author     :  -

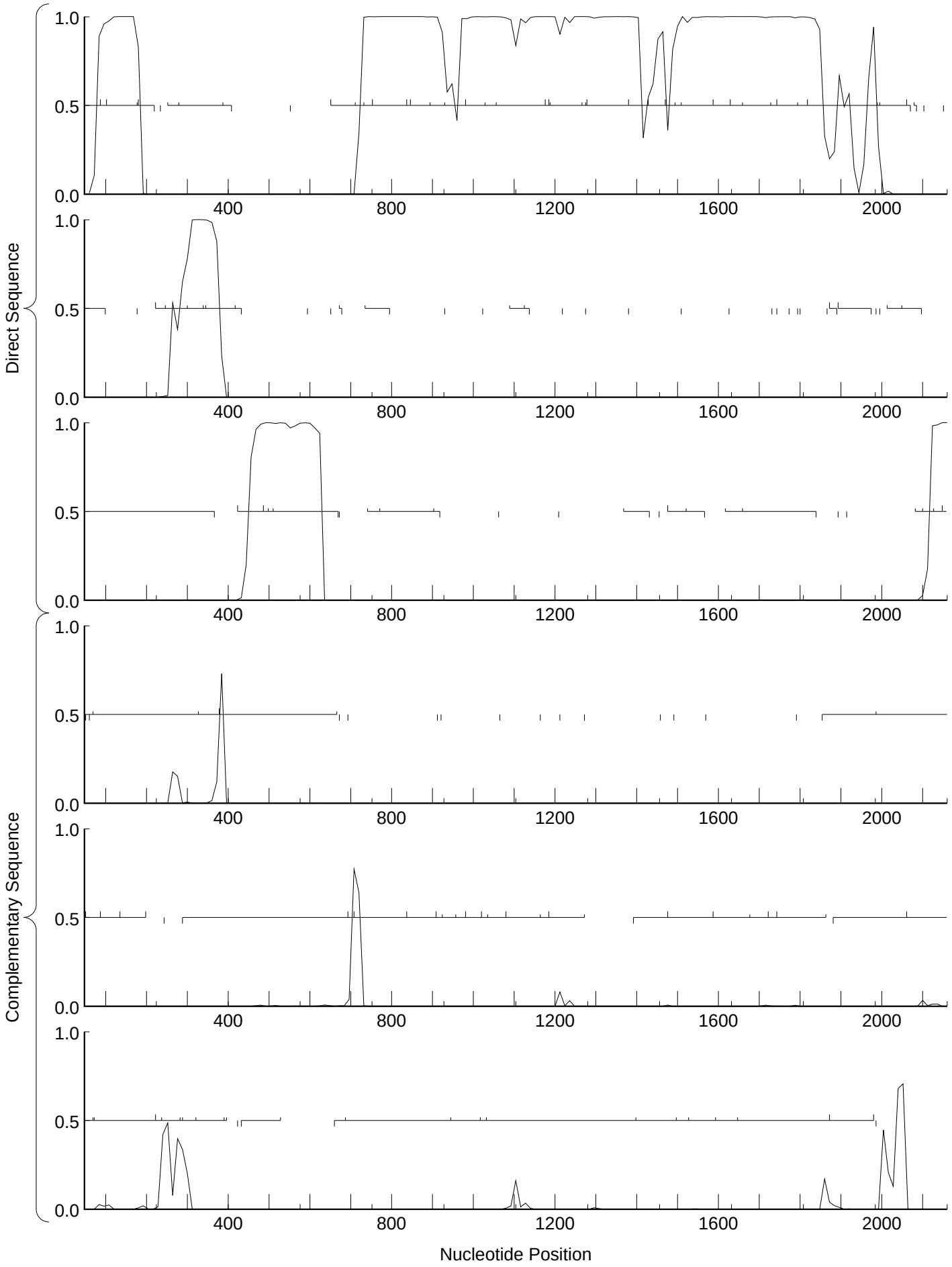
Order      :  4

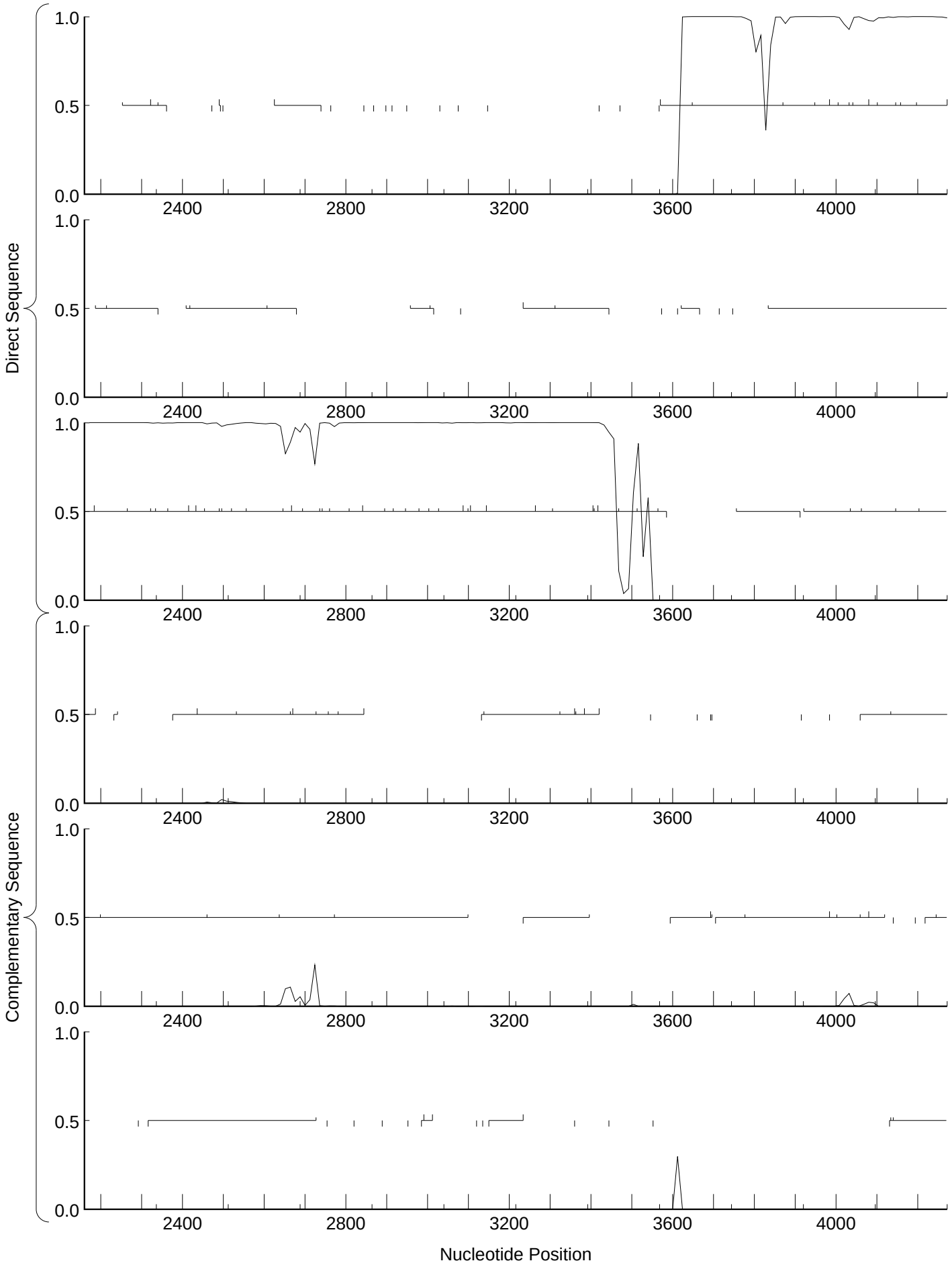

  Send questions / comments to:
      Dr. M. Borodovsky
      Georgia Institute of Technology
      School of Biology
      Atlanta, GA  30332-0230
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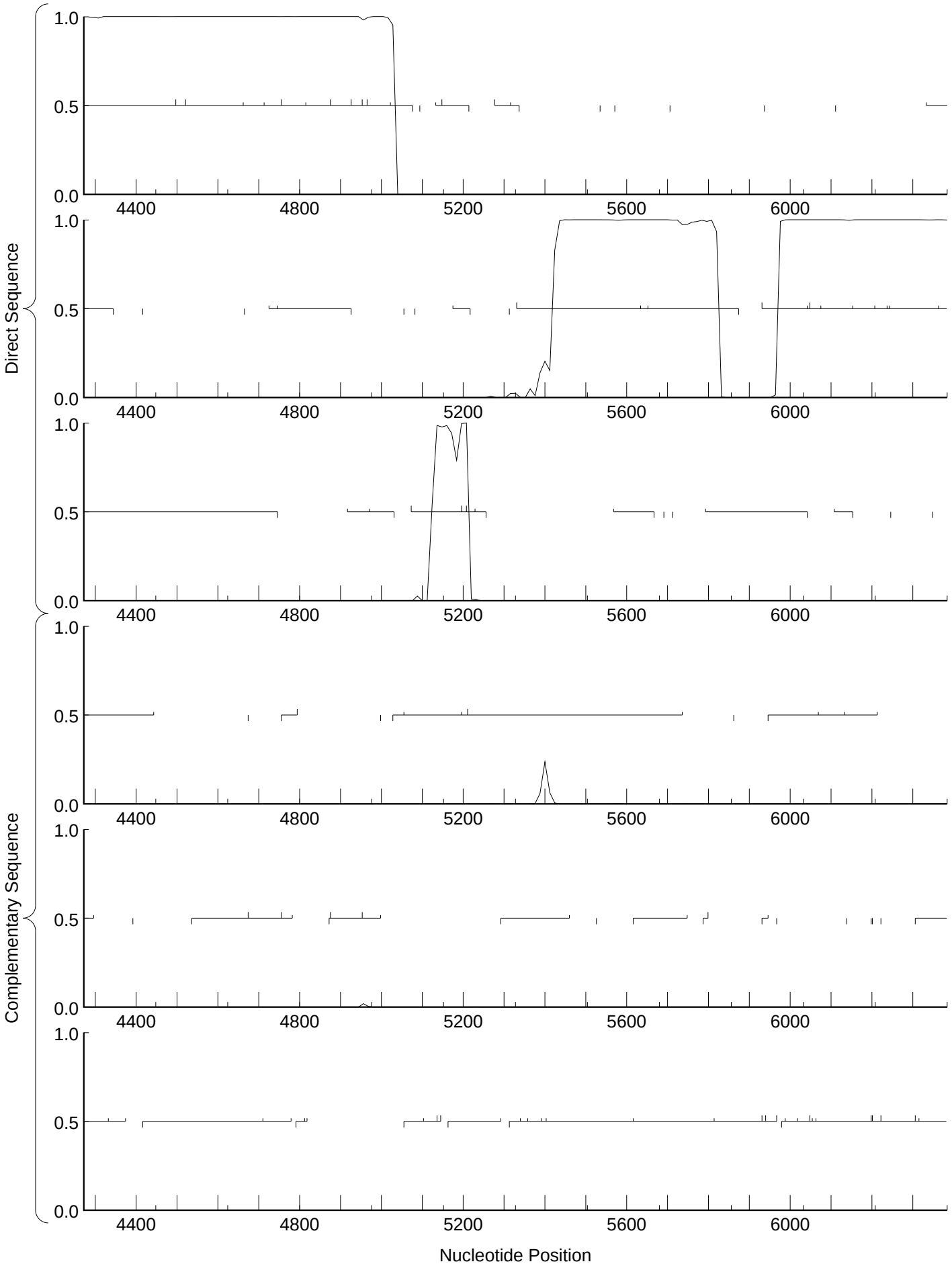


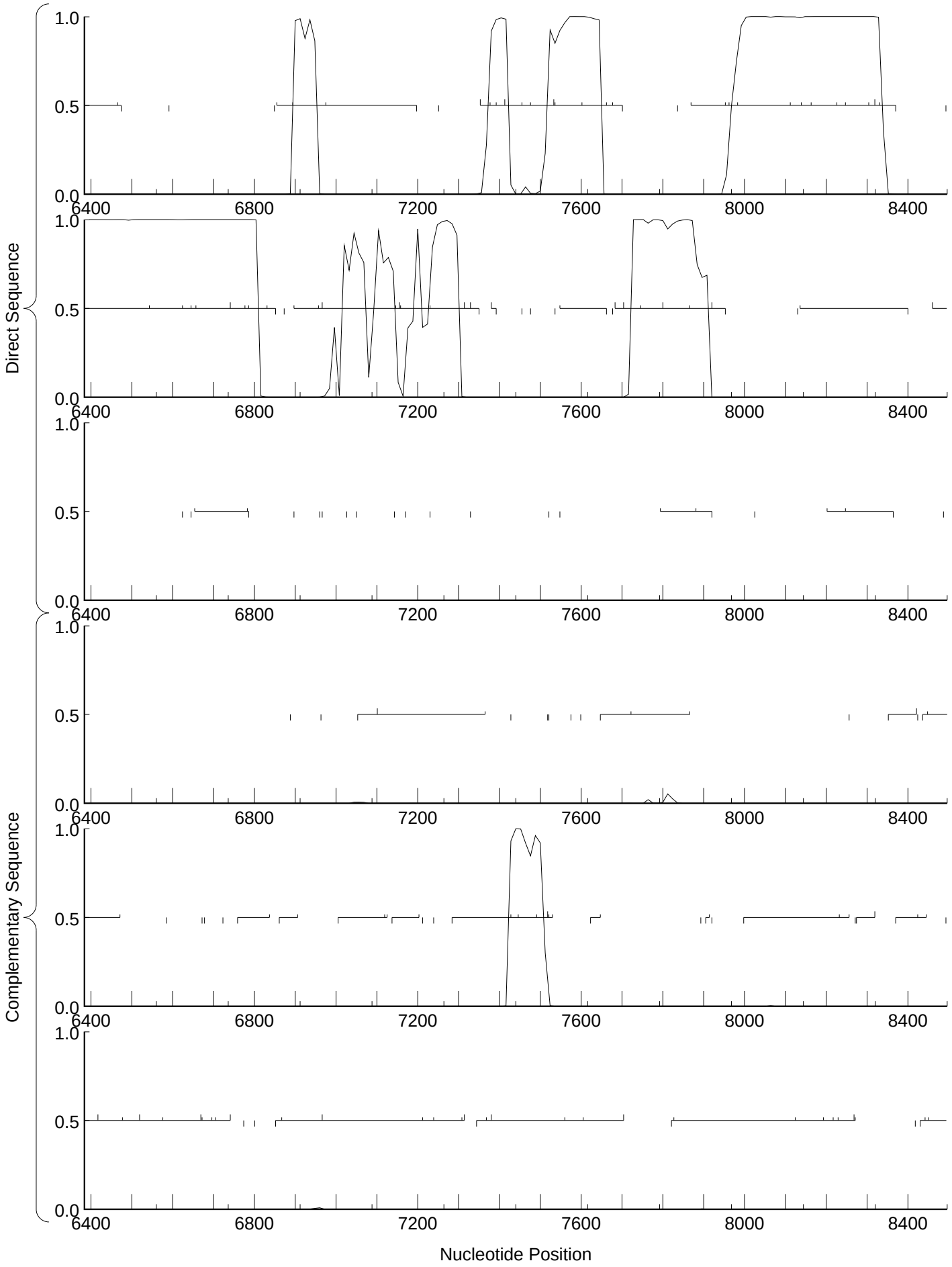
For help or information, send electronic mail to: custserv@genepro.com, or mark@amber.biology.gatech.edu

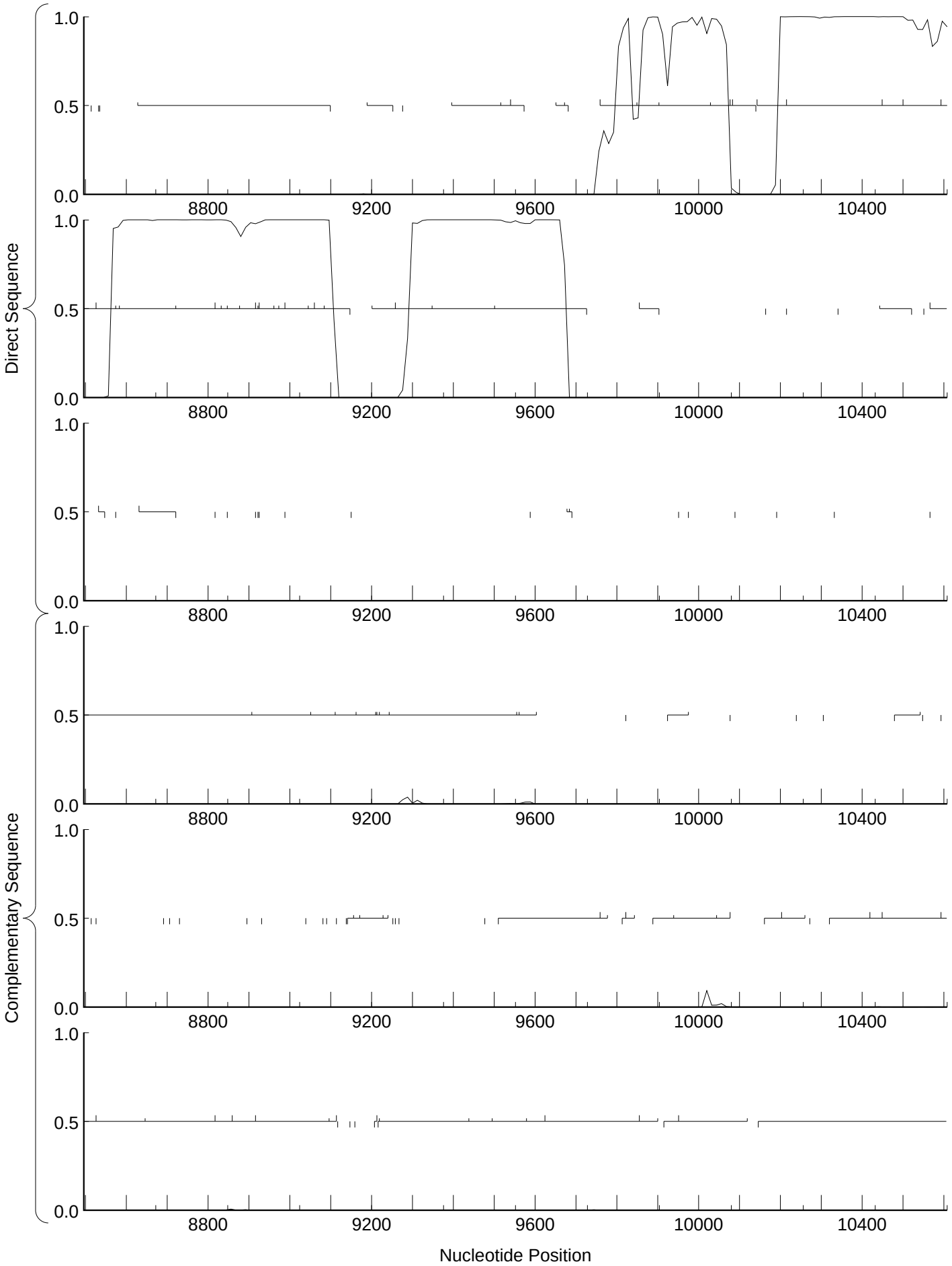
on complete sequence, 58078 bp including 10-base 3’ overhang (CTCGCGGCAT), Cluster K2, Order 4, Window 96, Step 12, 2/29

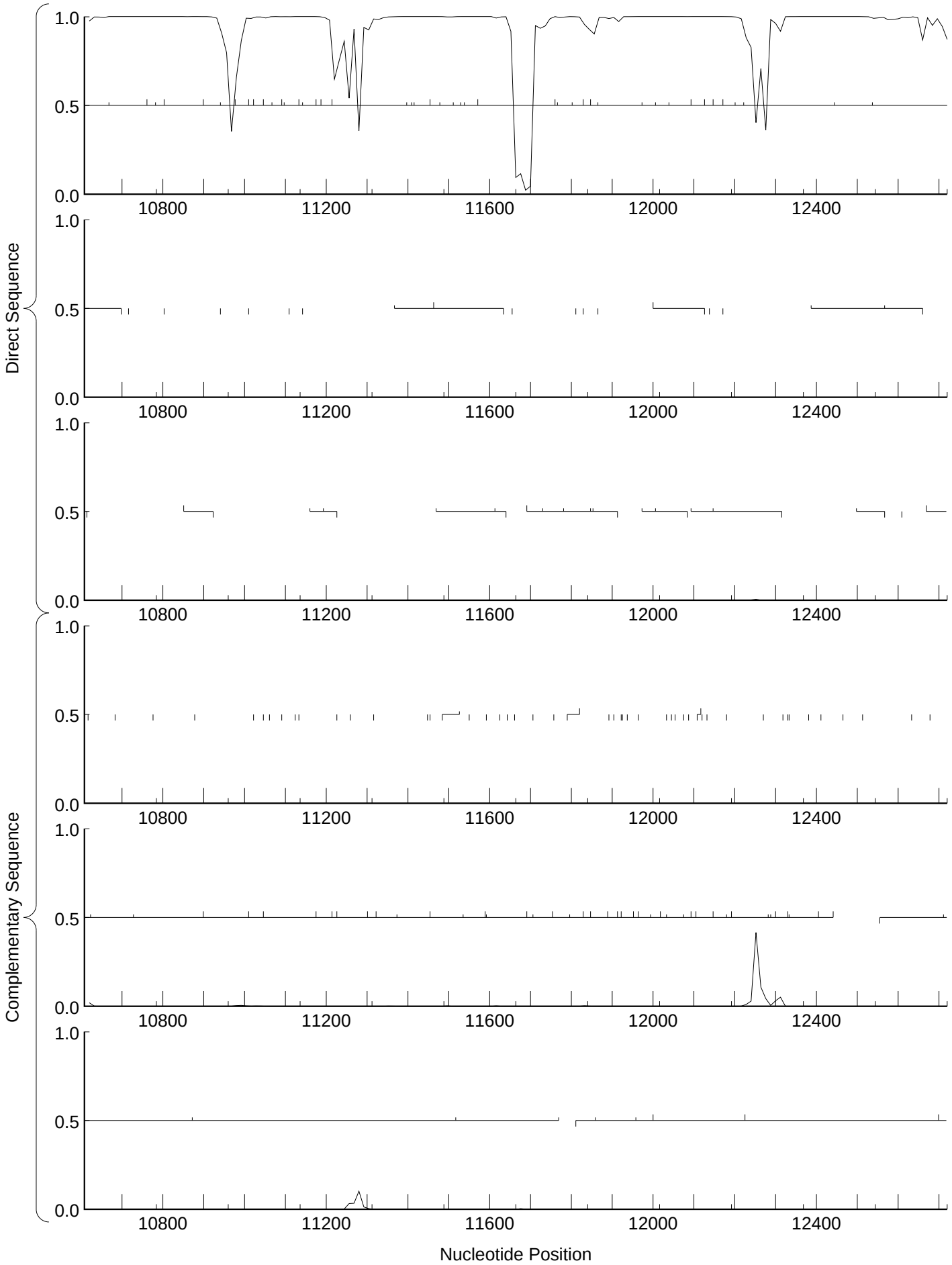


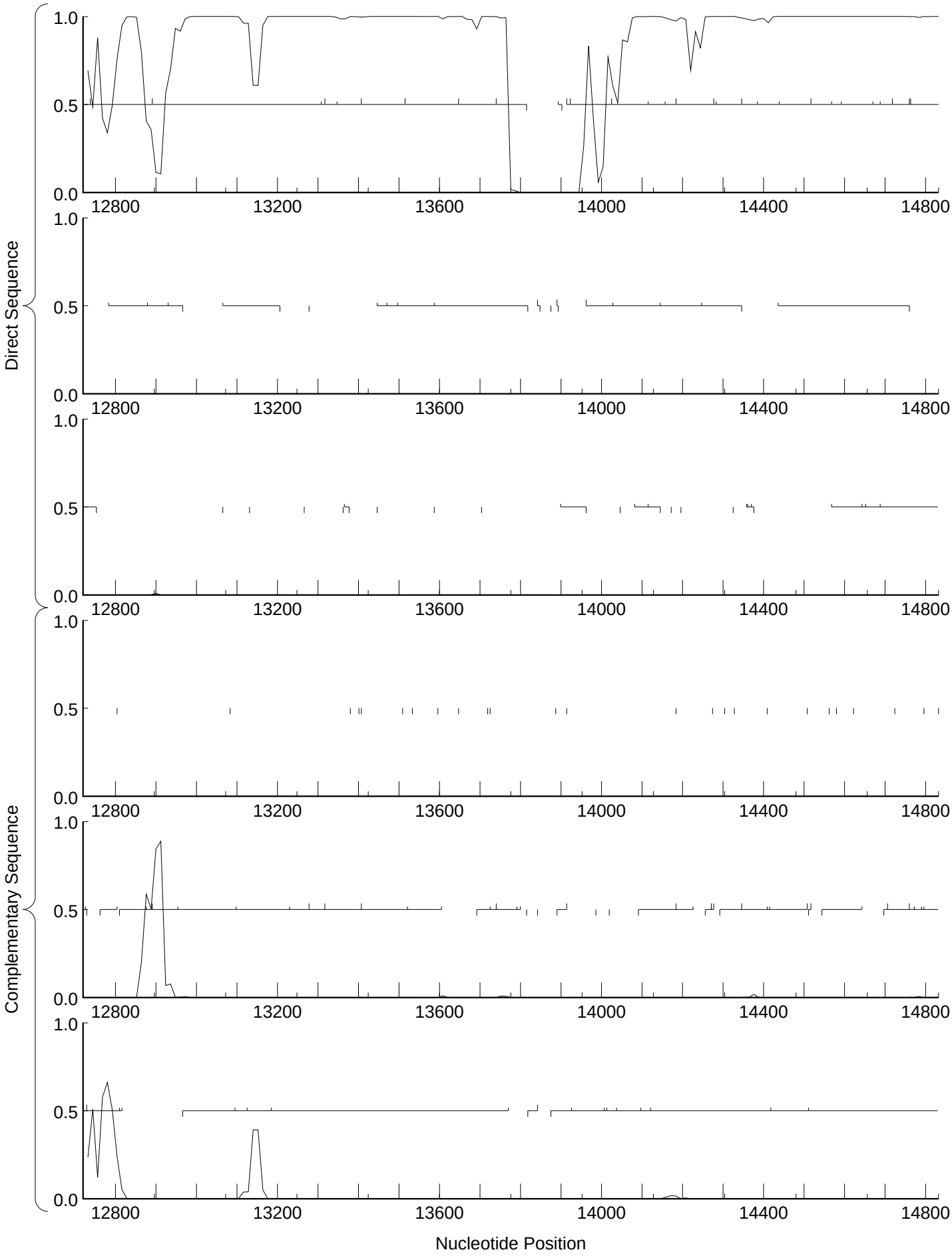

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
2400
2800
3200
3600
4000
Nucleotide Position

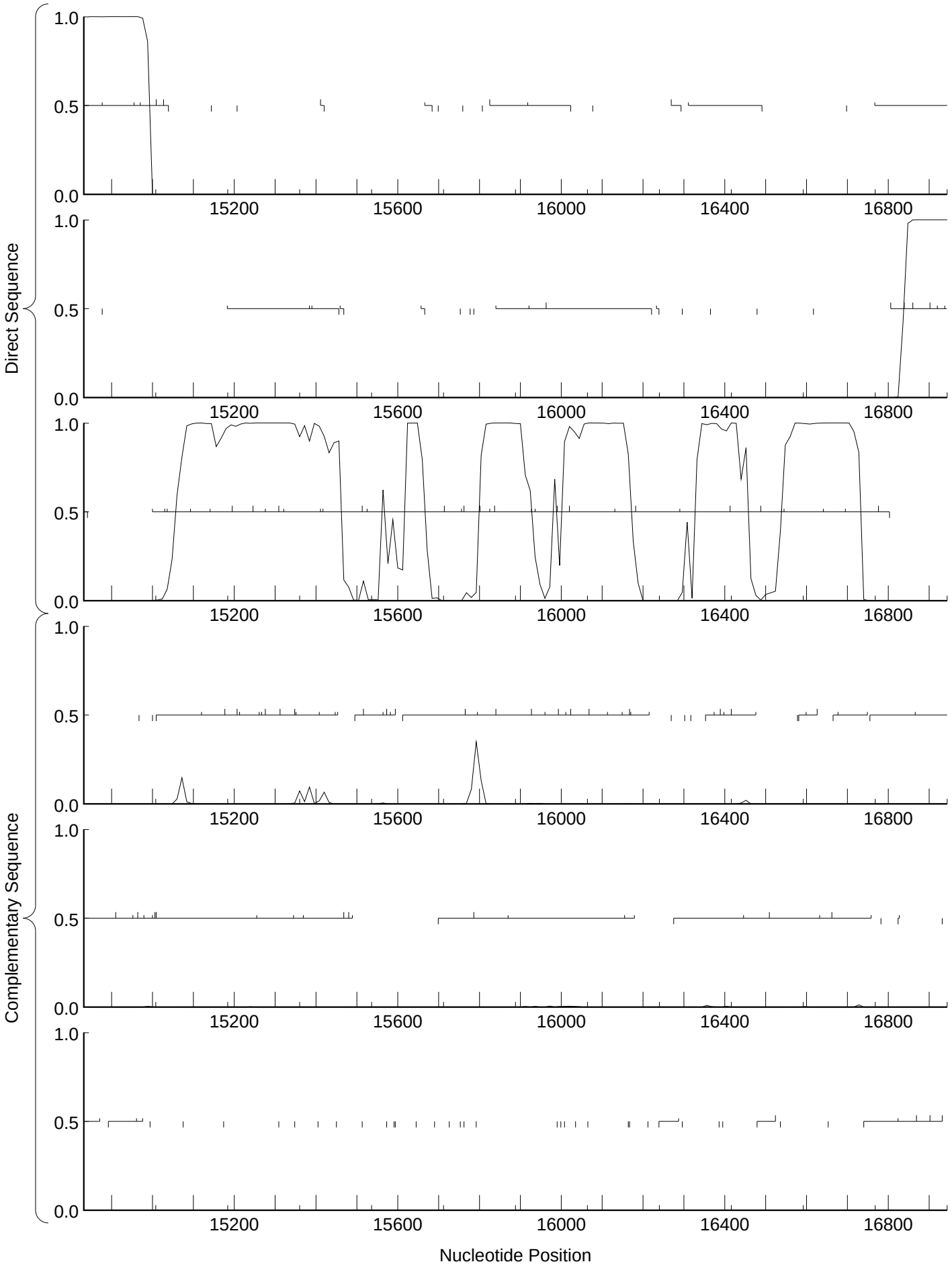

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Complementary Sequence
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5600
6000
Nucleotide Position

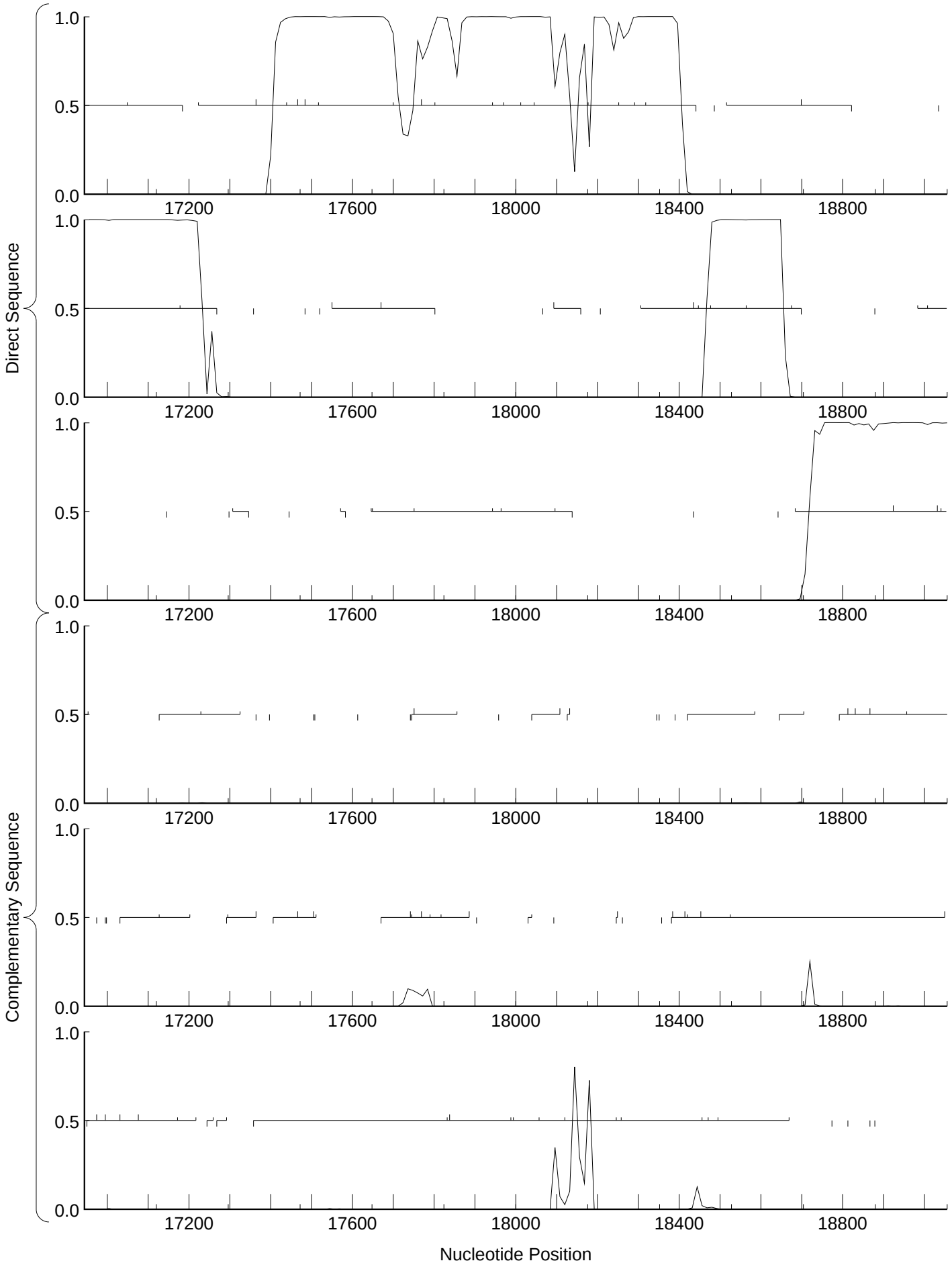

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Complementary Sequence
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8000
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Nucleotide Position

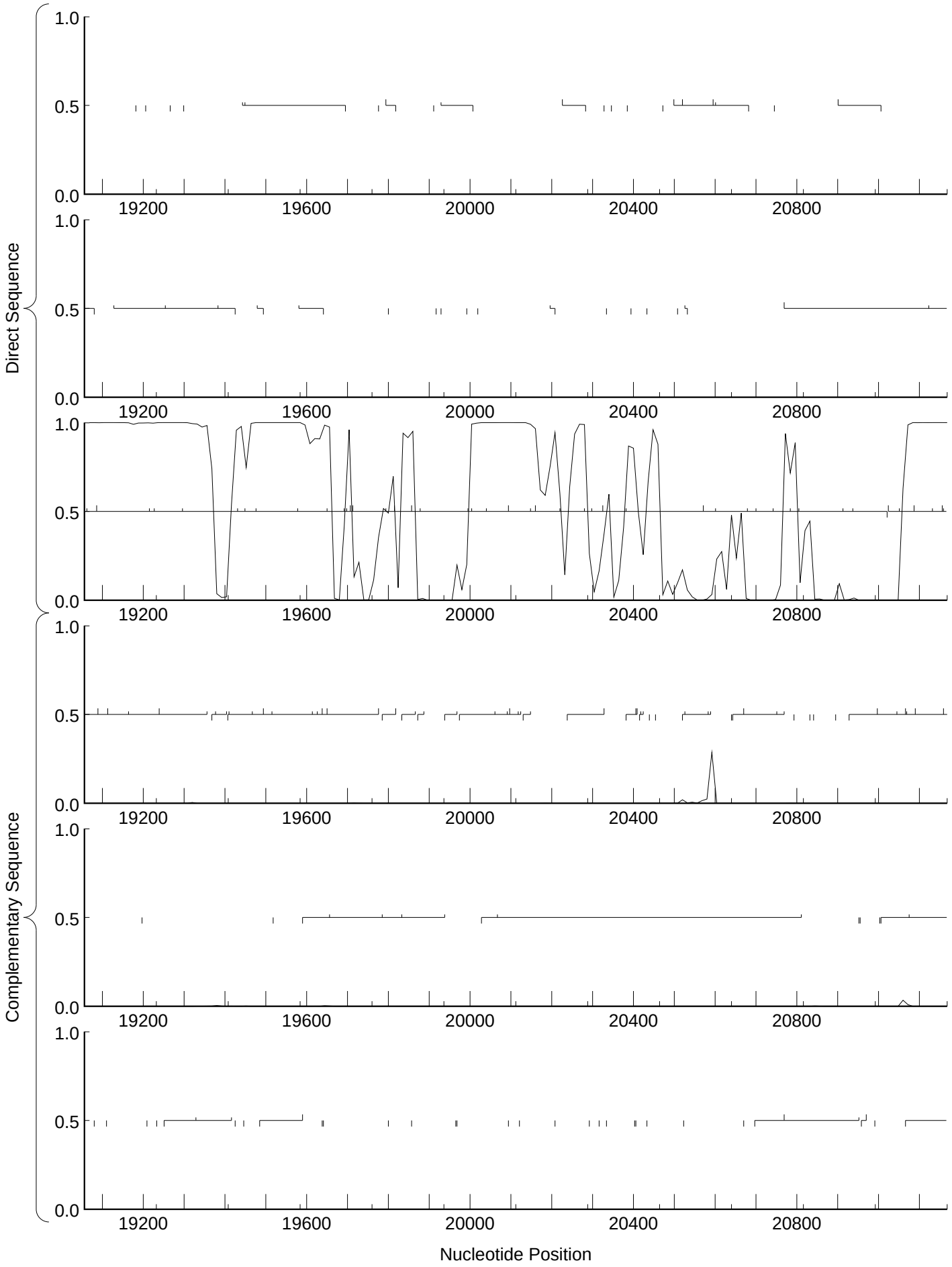

Direct Sequence
Complementary Sequence
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10000
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Nucleotide Position

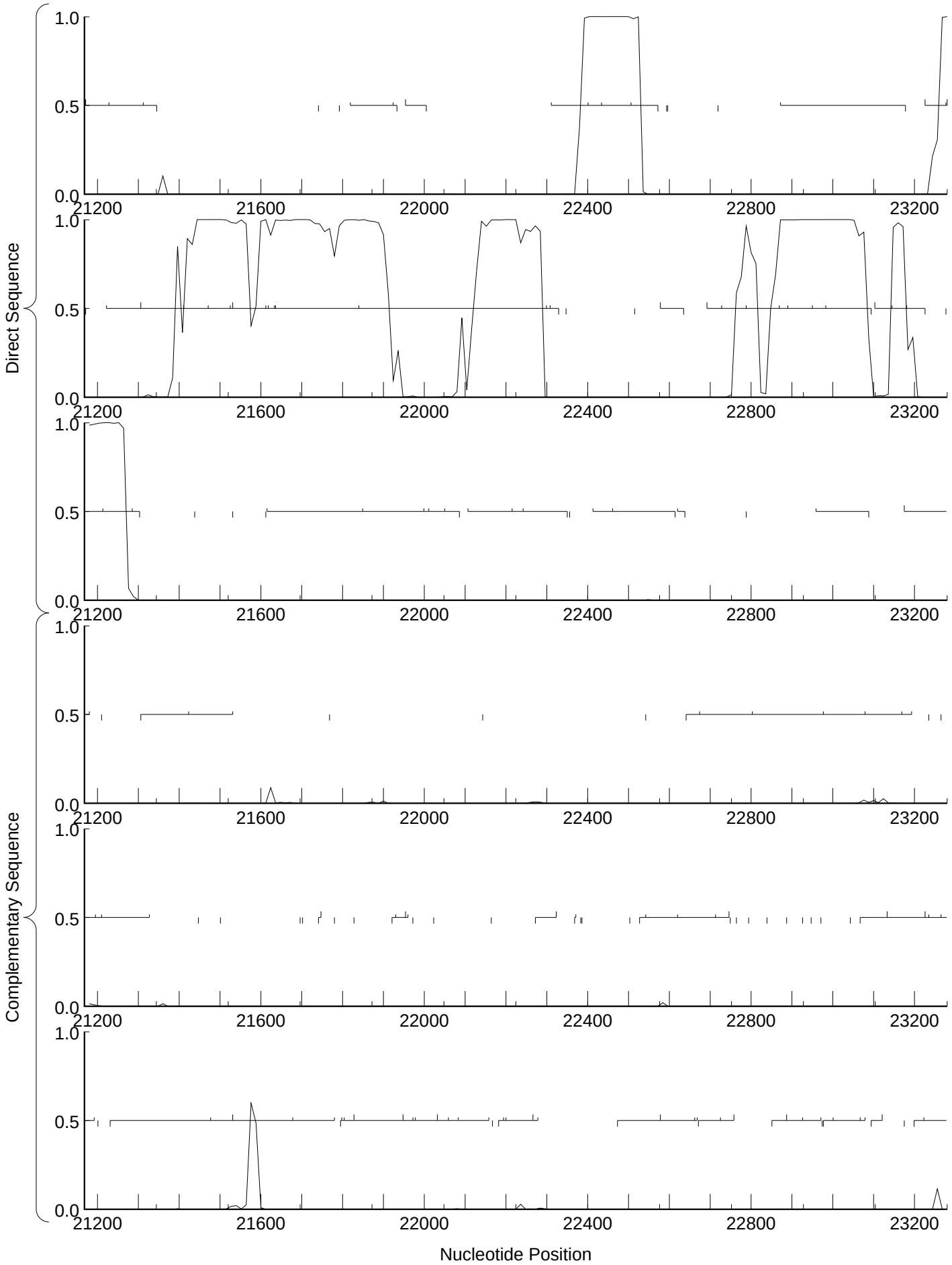

Direct Sequence
Complementary Sequence
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11600
12000
12400
Nucleotide Position

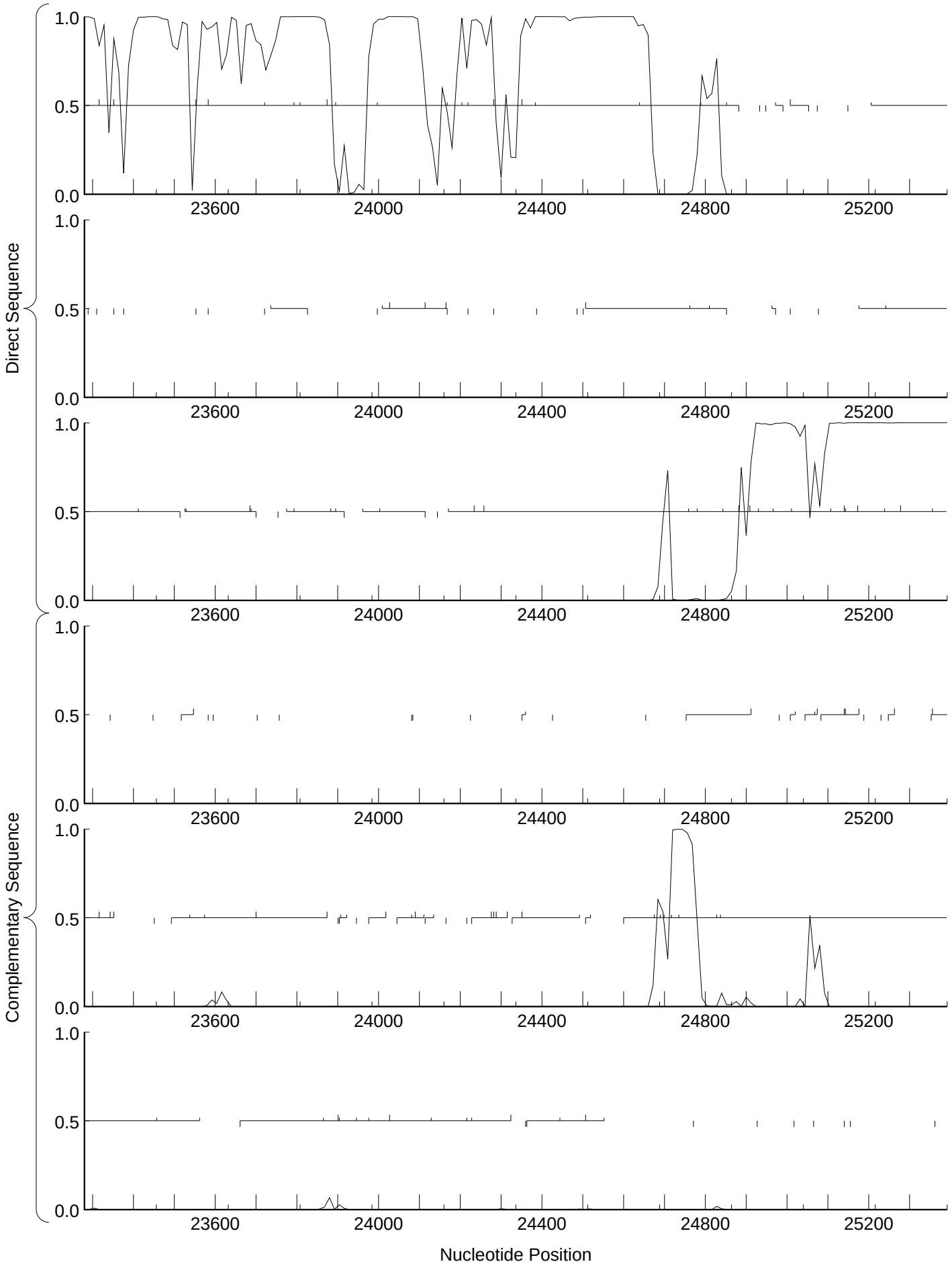

Direct Sequence
Complementary Sequence
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14400
14800
Nucleotide Position

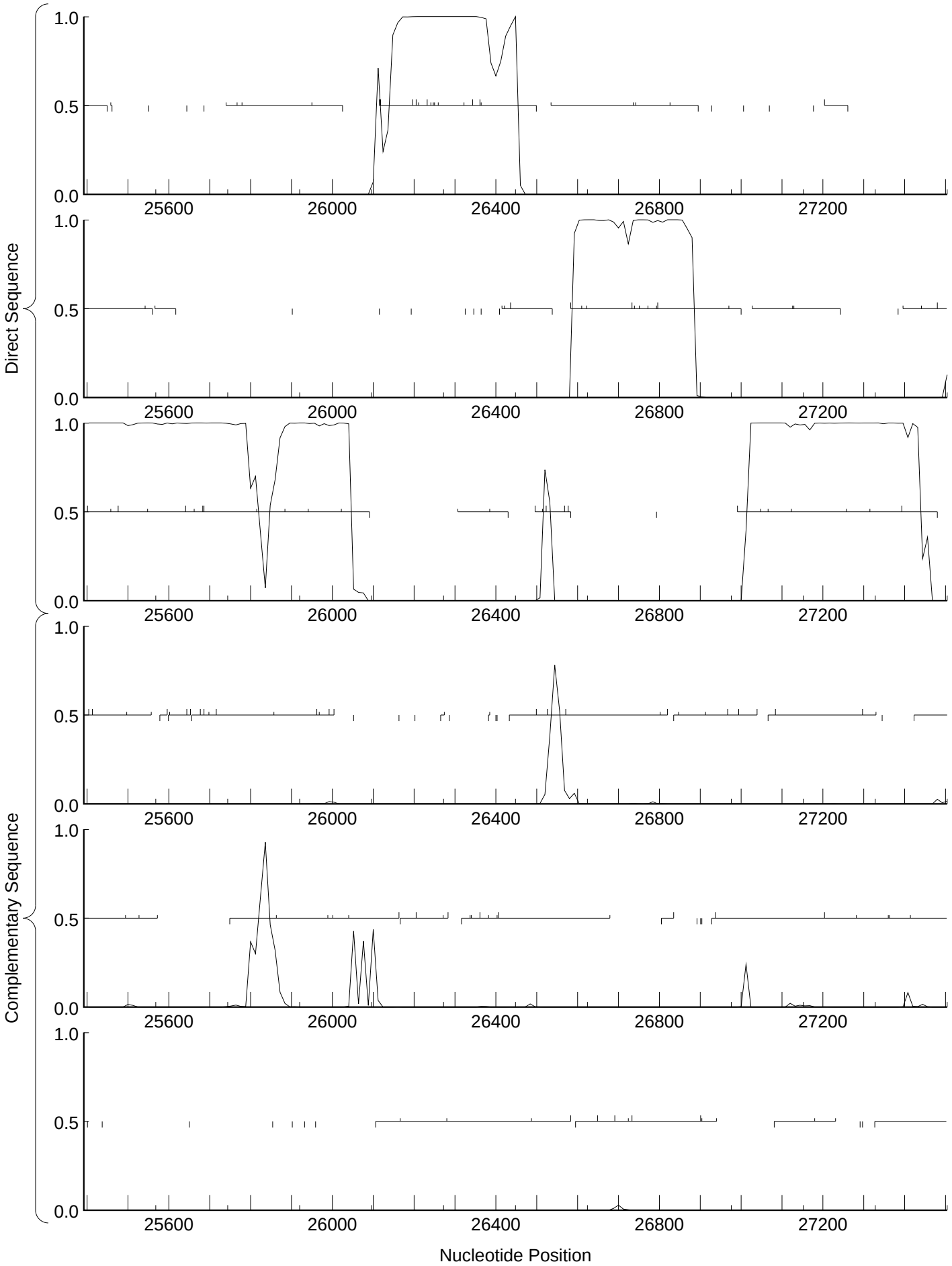

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
15200
15600
16000
16400
16800
Nucleotide Position


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
17200
17600
18000
18400
18800
Nucleotide Position

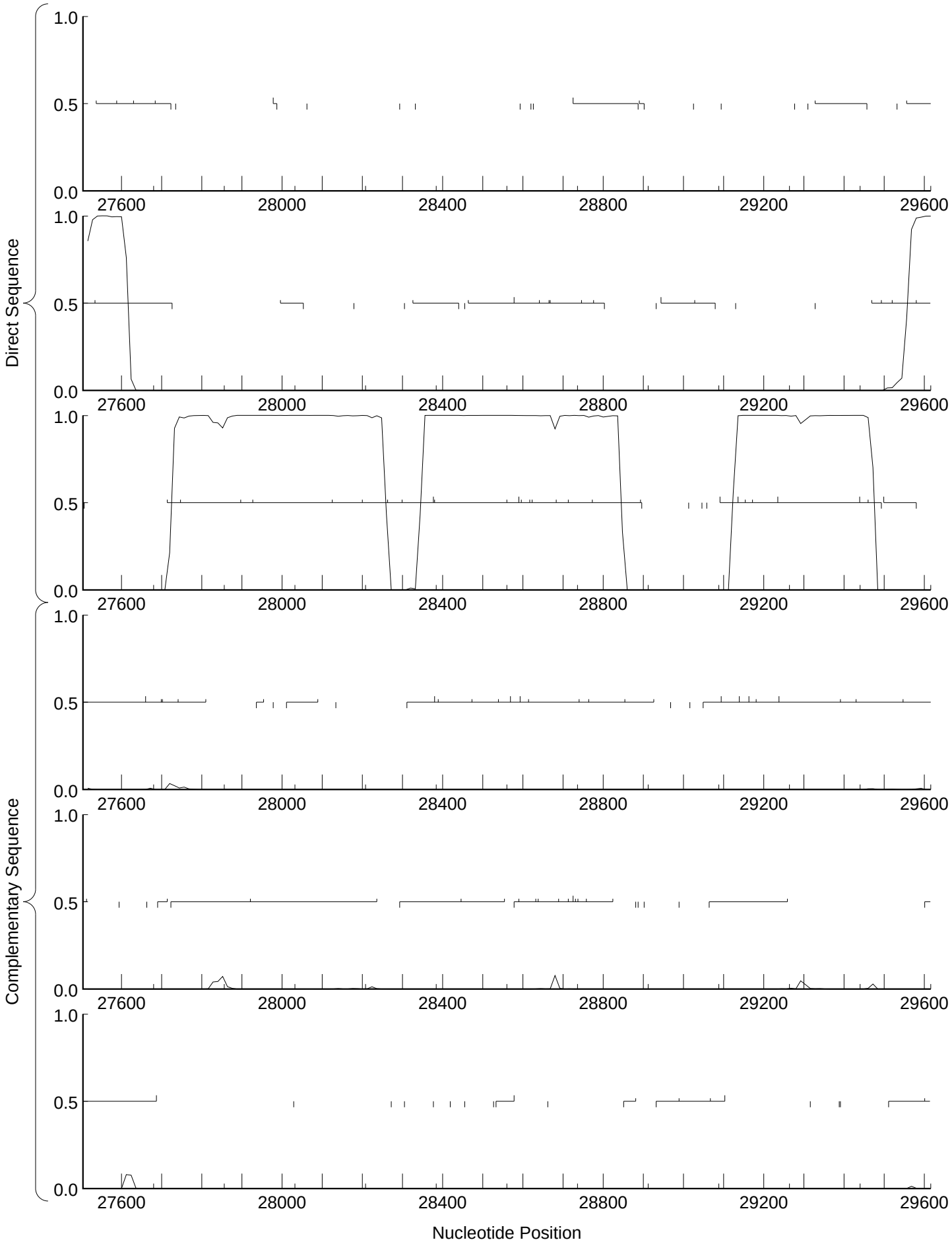

Direct Sequence
Complementary Sequence
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0.0
19200
19600
20000
20400
20800
Nucleotide Position


Direct Sequence
Complementary Sequence
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0.0
21200
21600
22000
22400
22800
23200
Nucleotide Position

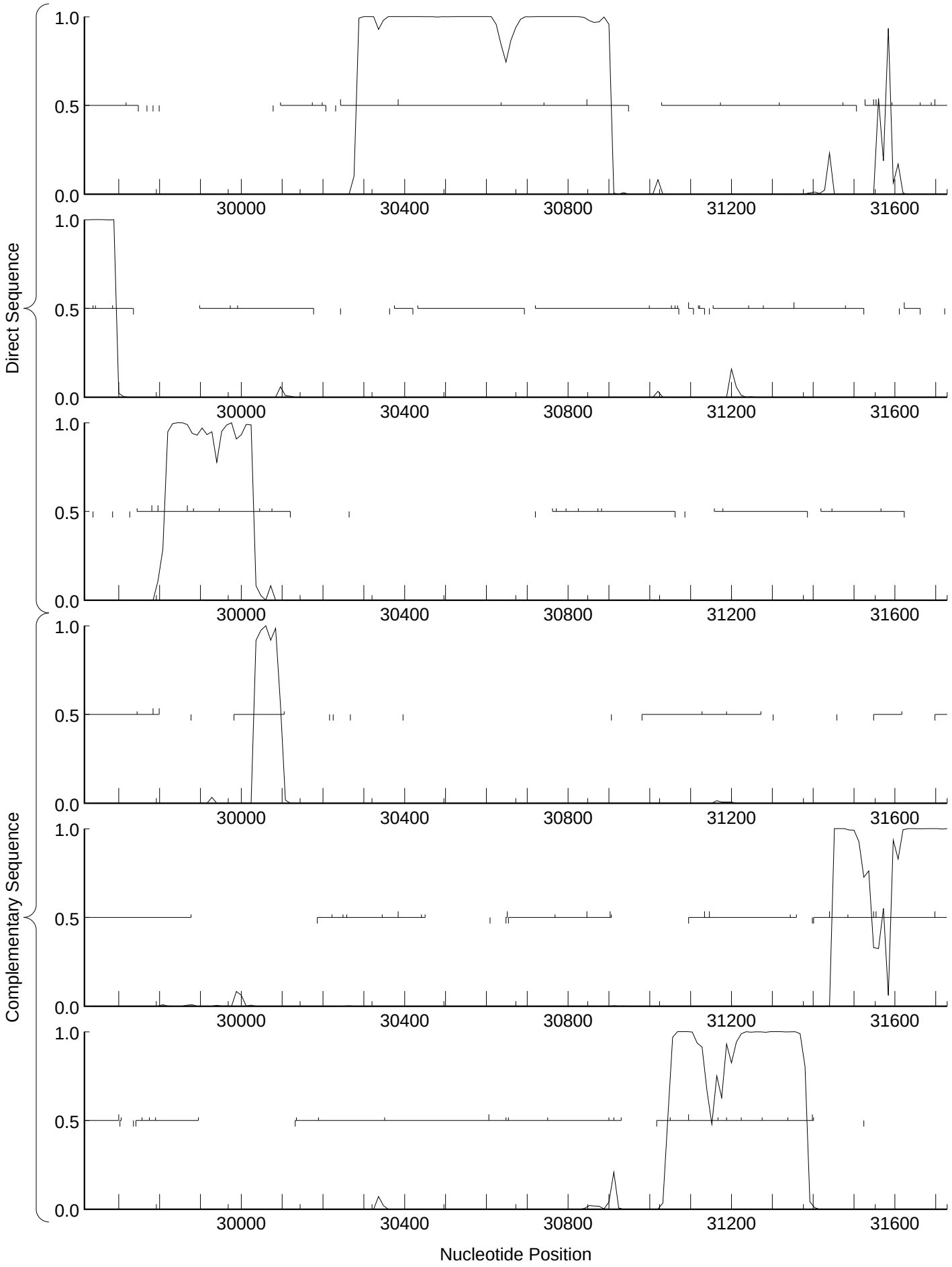

Direct Sequence
Complementary Sequence
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0.0
23600
24000
24400
24800
25200
Nucleotide Position

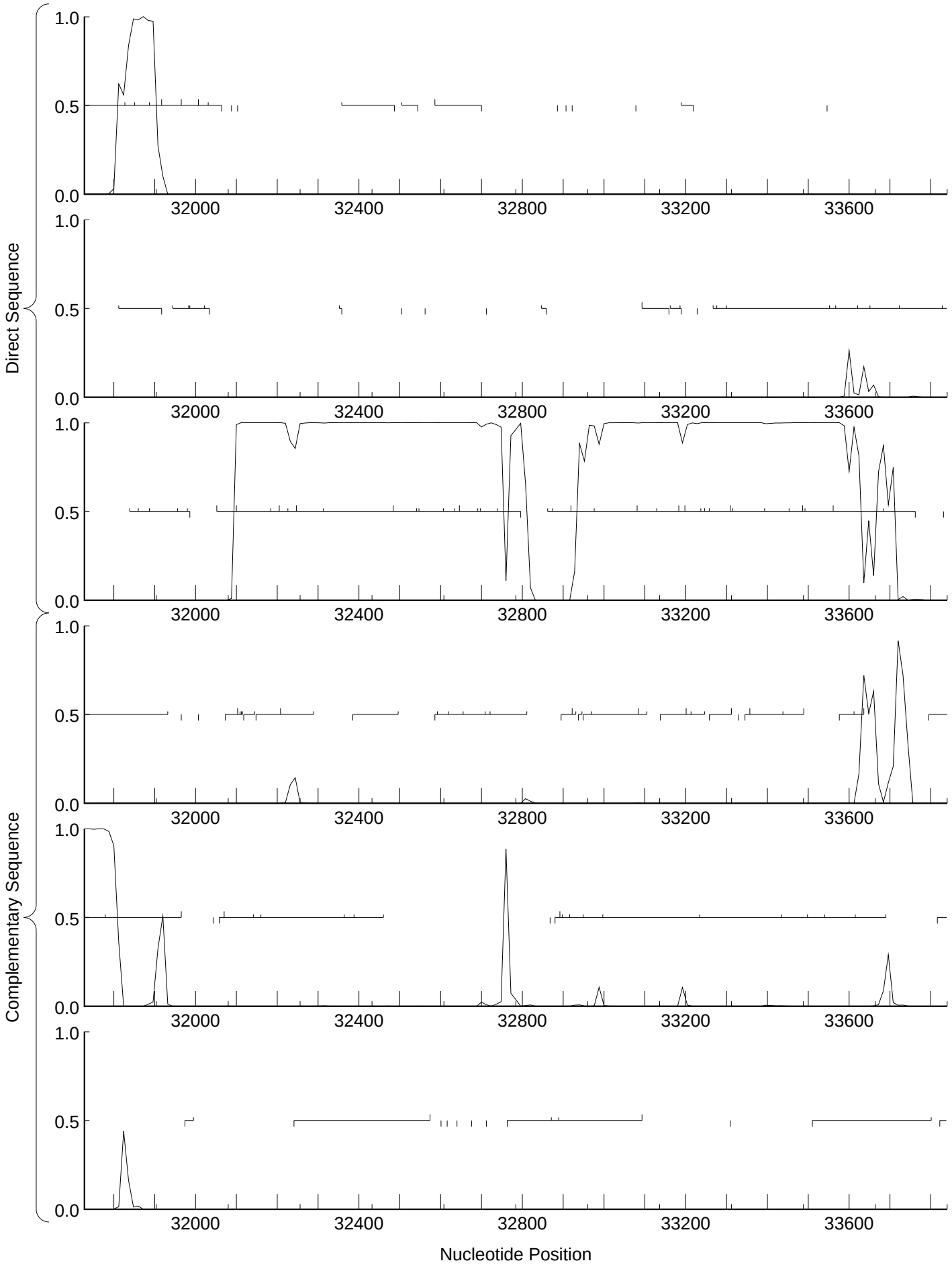

Direct Sequence
Complementary Sequence
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0.0
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26000
26400
26800
27200
Nucleotide Position

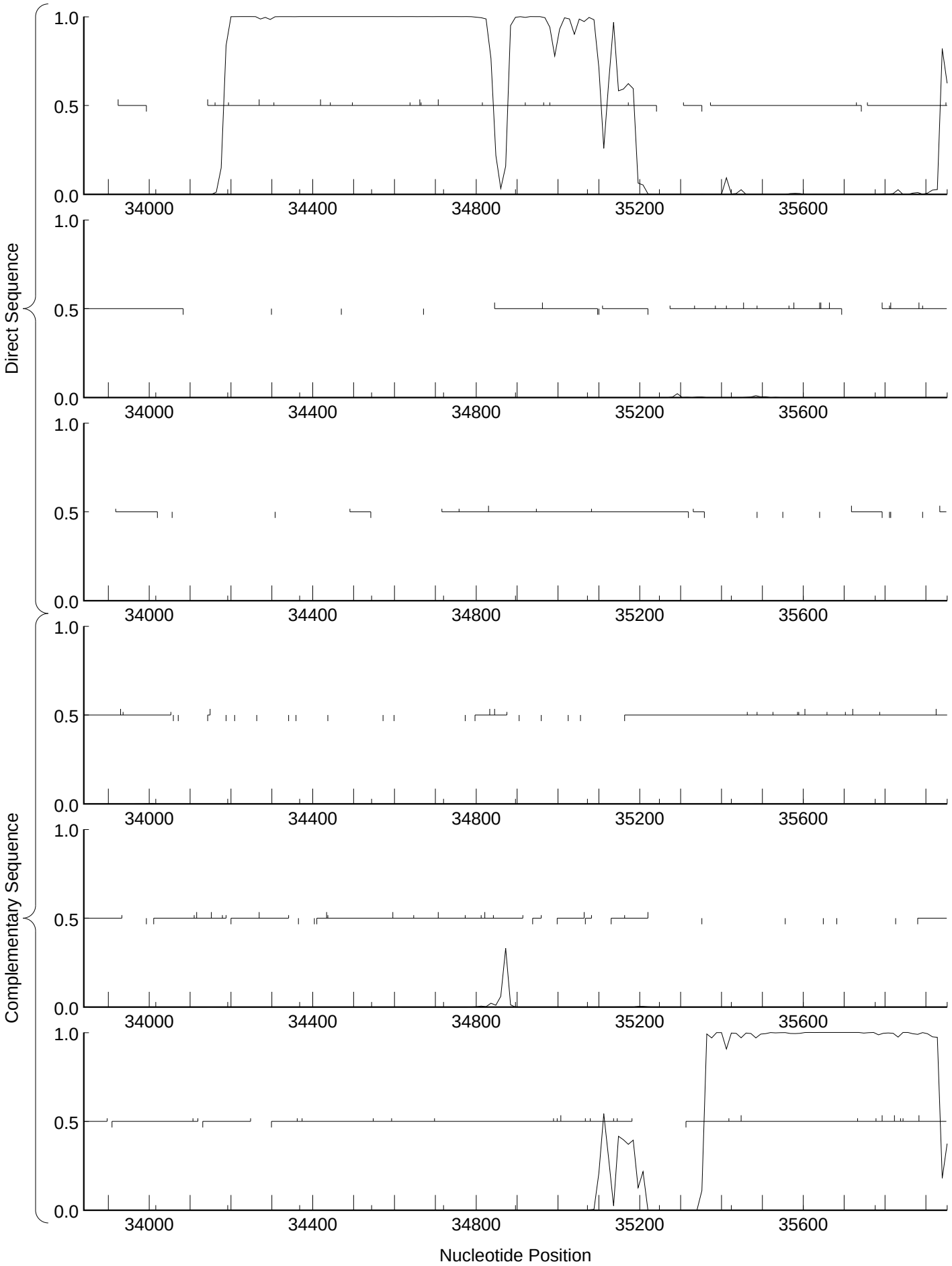
complete sequence, 58078 bp including 10-base 3’ overhang (CTCGCGGCAT), Cluster K2, Order 4, Window 96, Step 12, 15/29

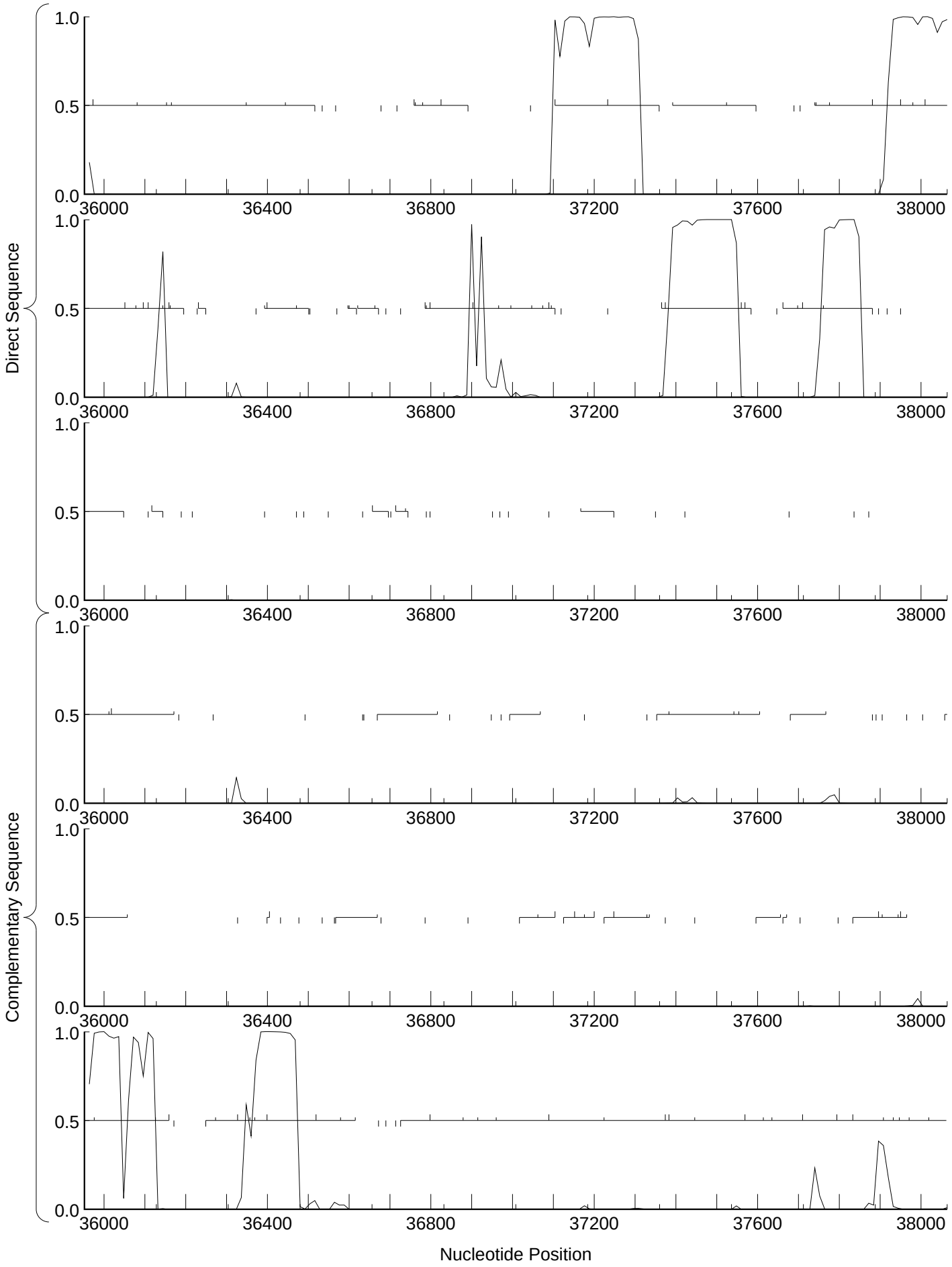


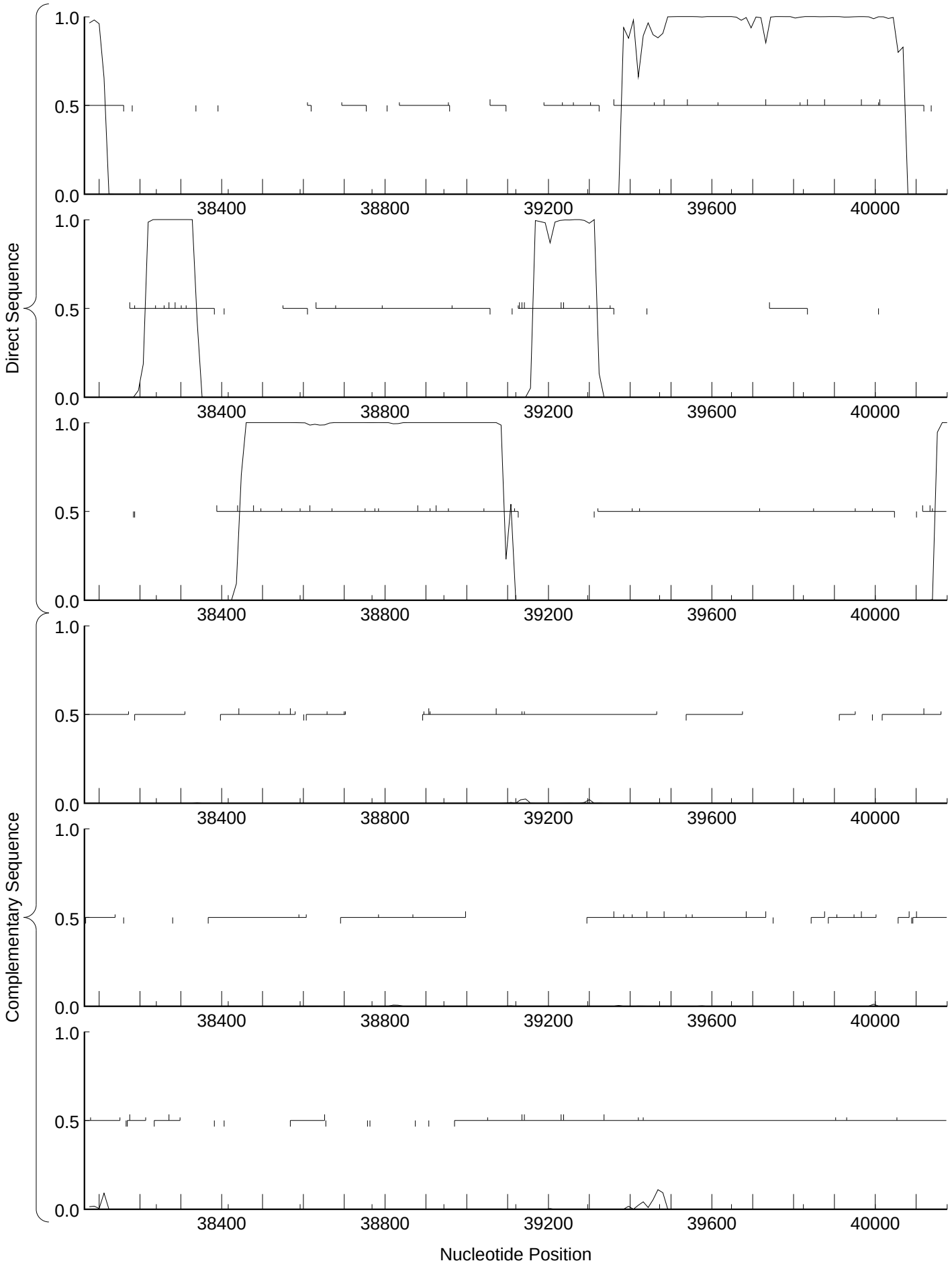
complete sequence, 58078 bp including 10-base 3’ overhang (CTCGCGGCAT), Cluster K2, Order 4, Window 96, Step 12, 16/29



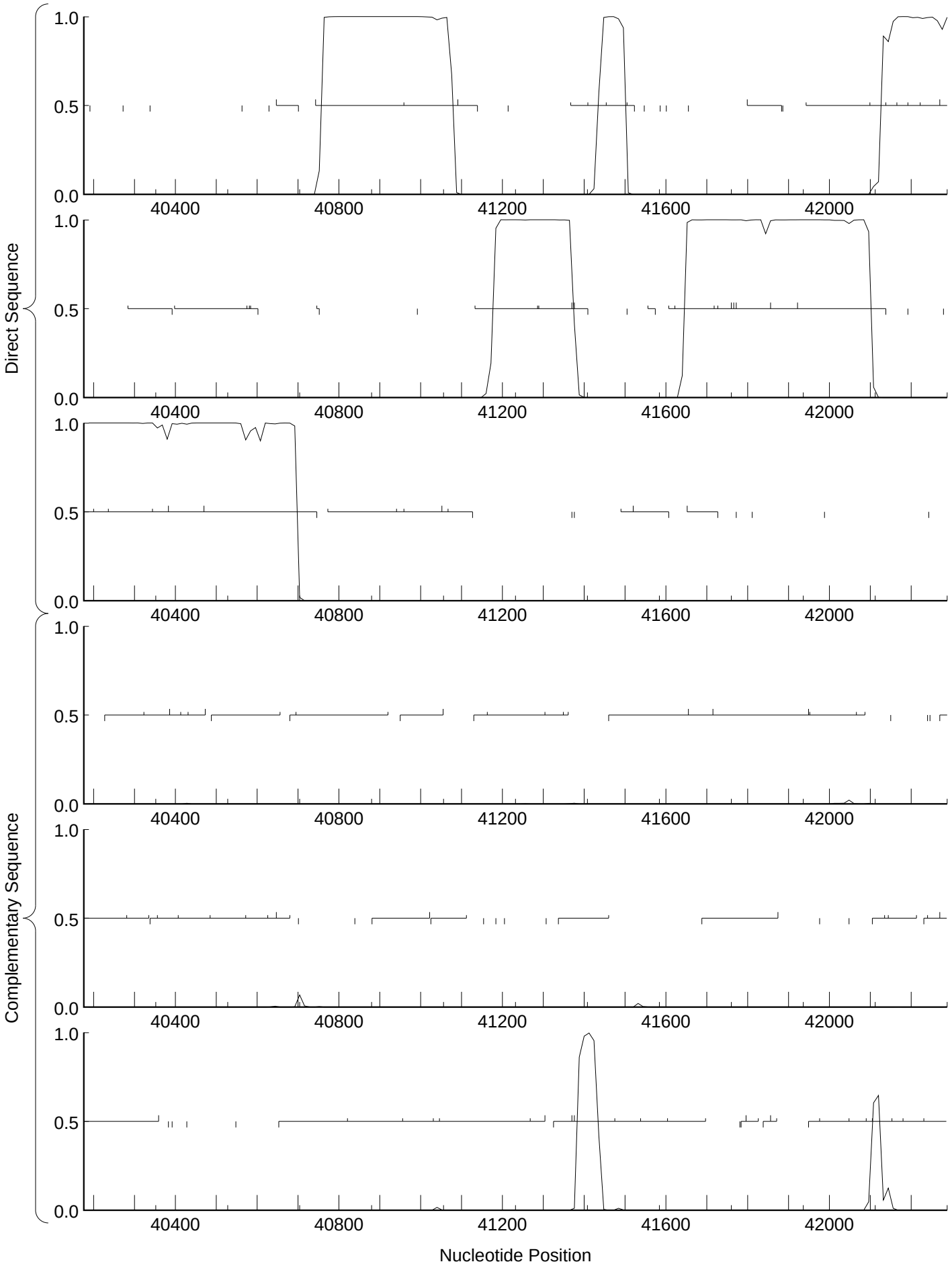

Direct Sequence
Complementary Sequence
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32800
33200
33600
Nucleotide Position

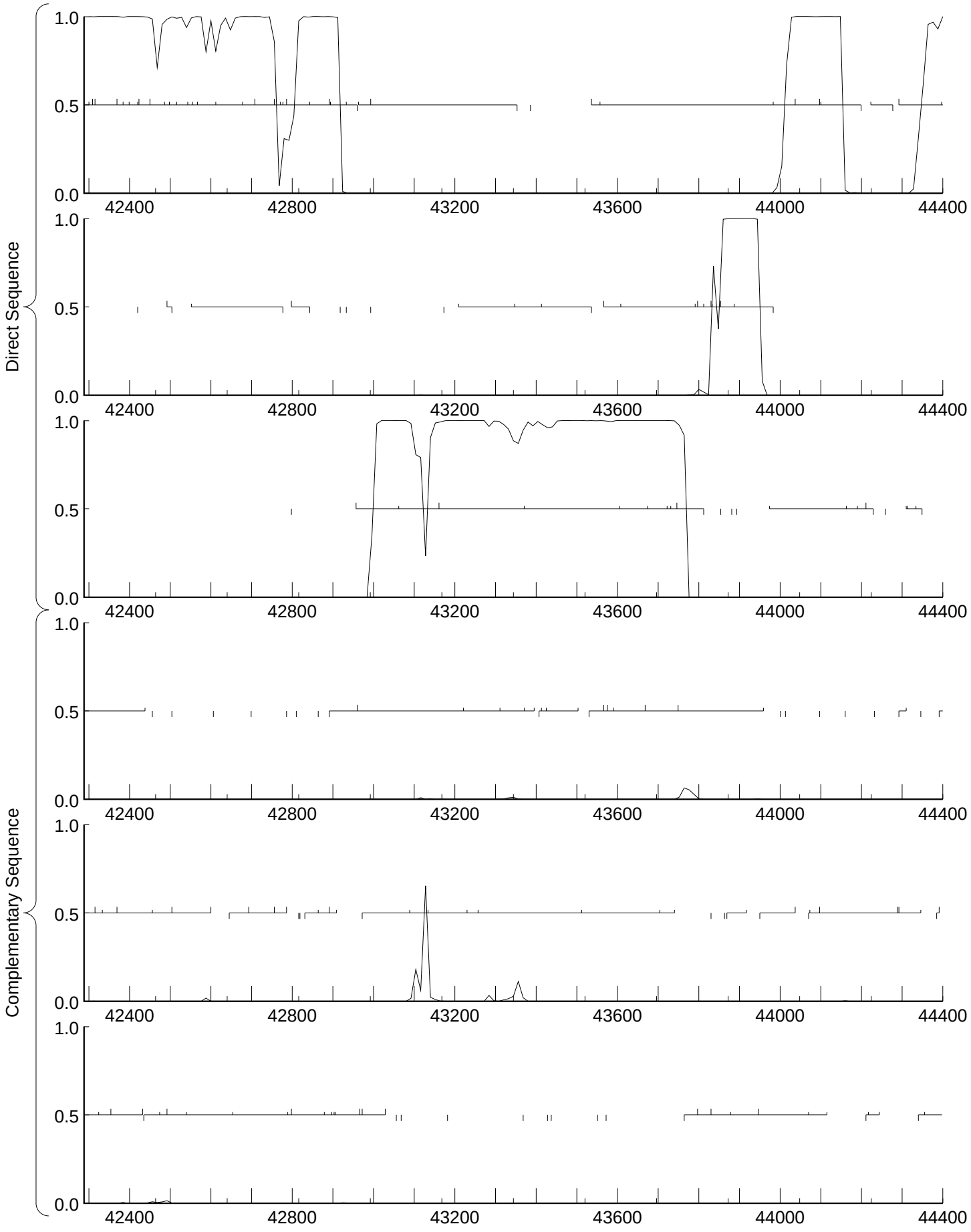

Direct Sequence
Complementary Sequence
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35200
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Nucleotide Position

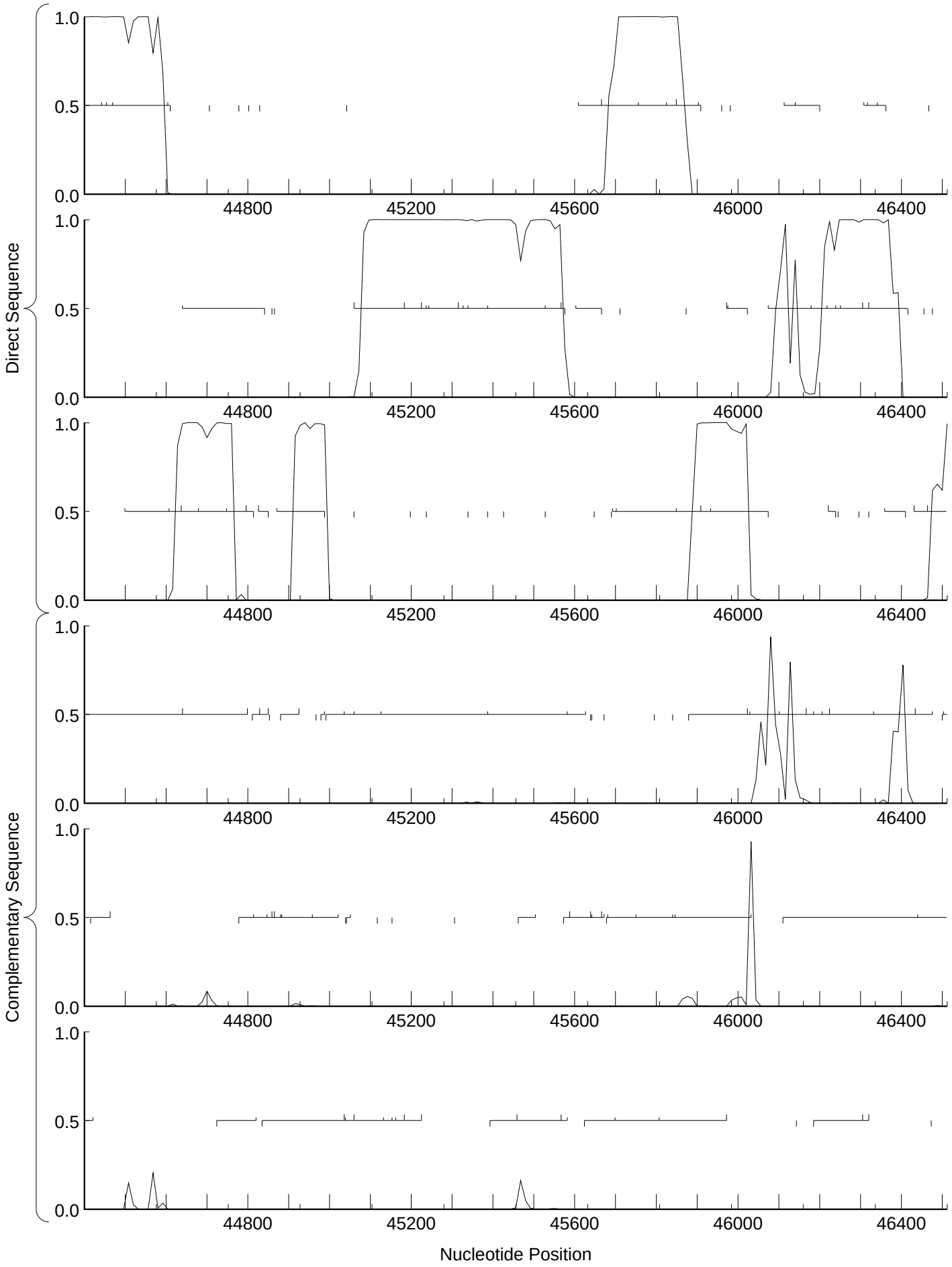

Direct Sequence
Complementary Sequence
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36400
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37200
37600
38000
Nucleotide Position

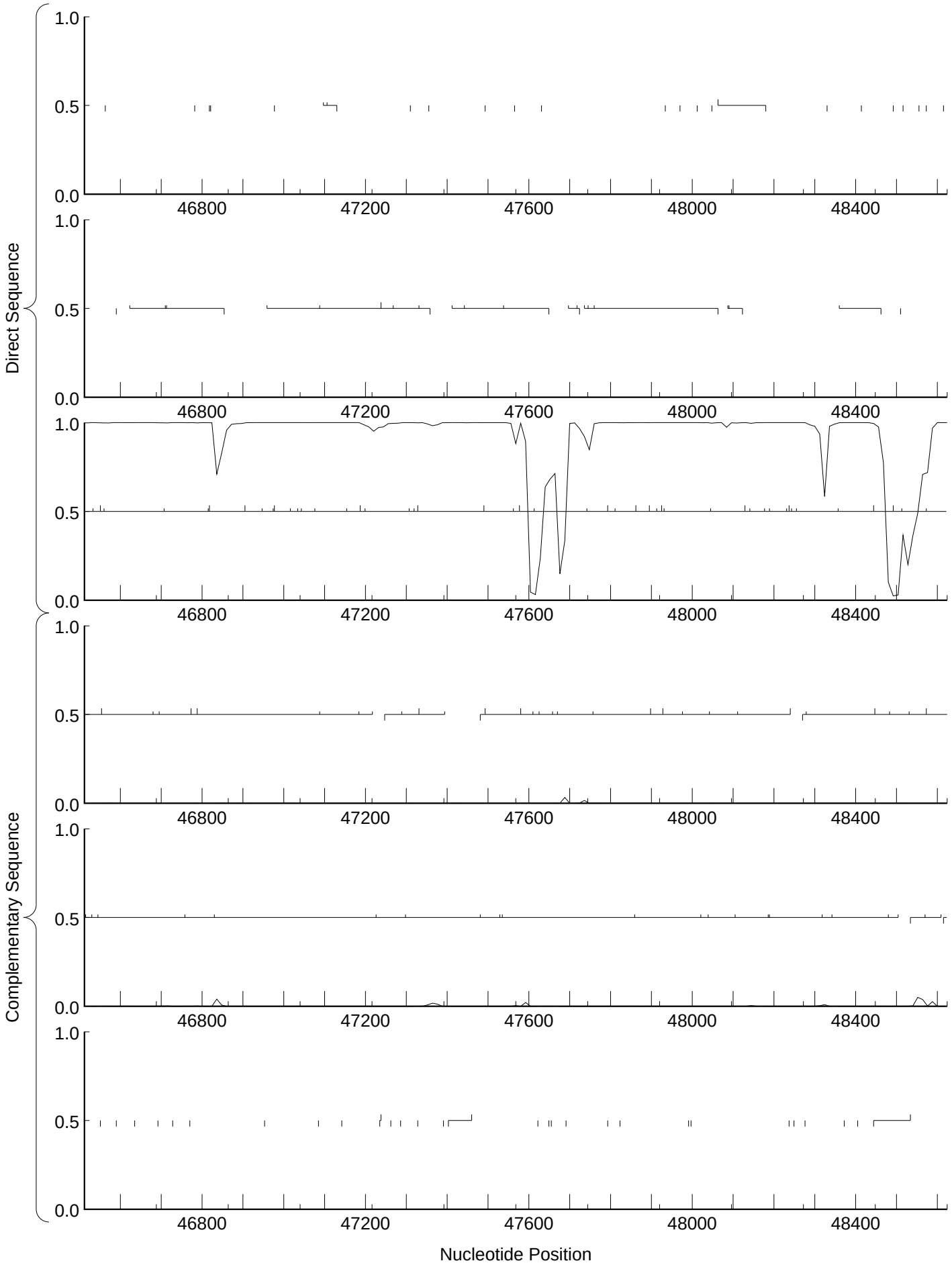

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
38400
38800
39200
39600
40000
Nucleotide Position

complete sequence, 58078 bp including 10-base 3’ overhang (CTCGCGGCAT), Cluster K2, Order 4, Window 96, Step 12, 21/29

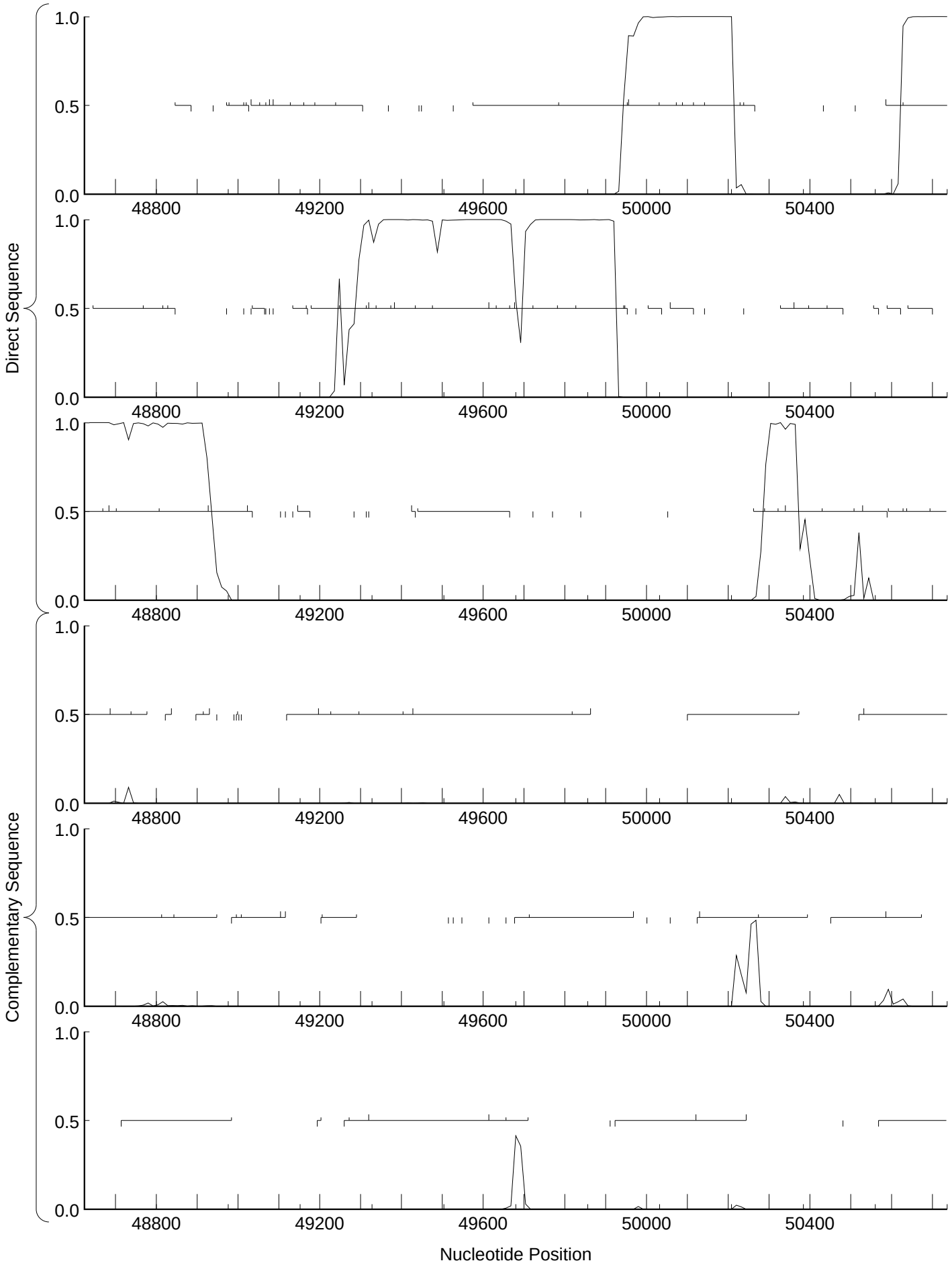


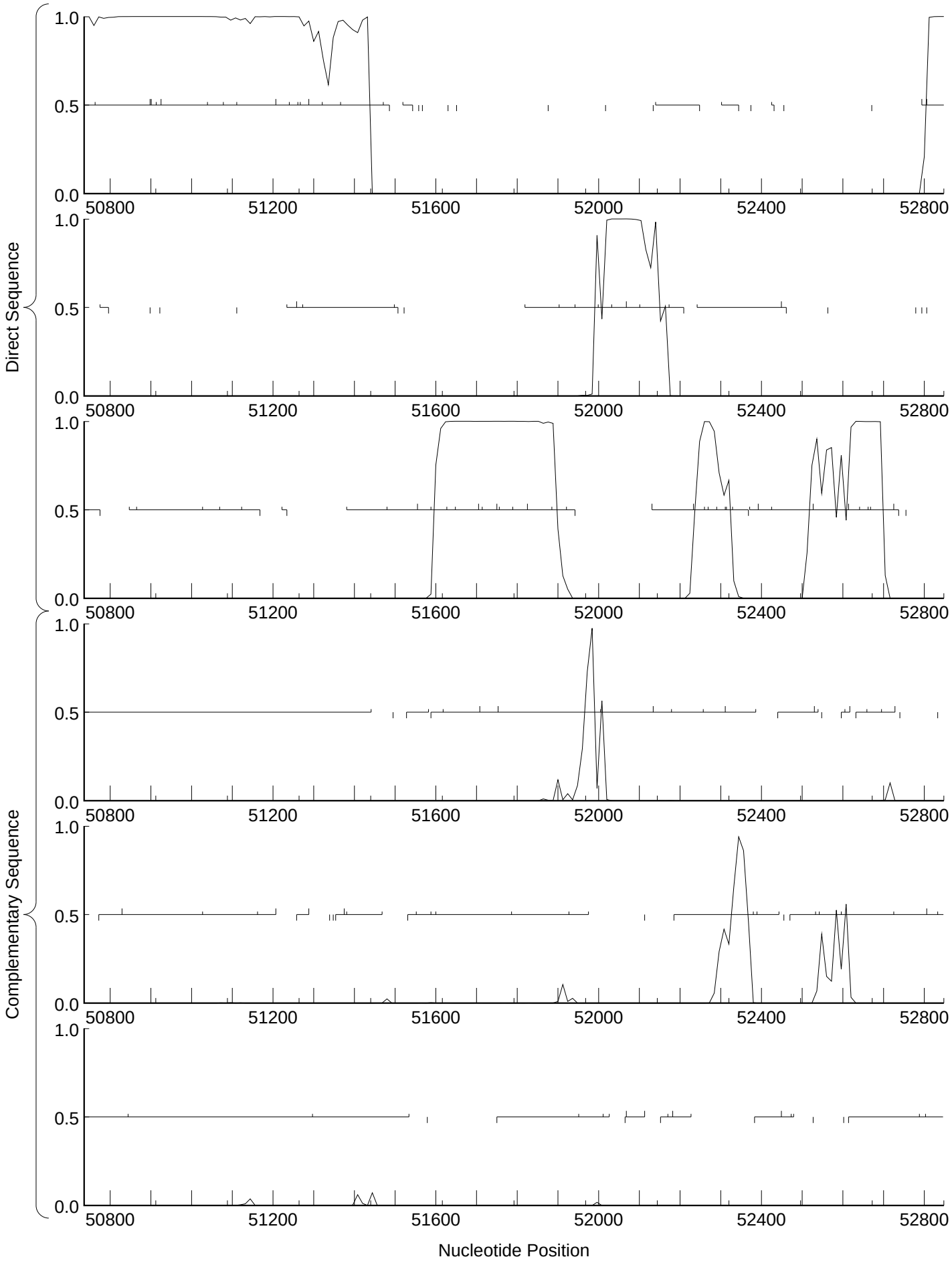

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Complementary Sequence
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0.0
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42800
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43600
44000
44400
Nucleotide Position

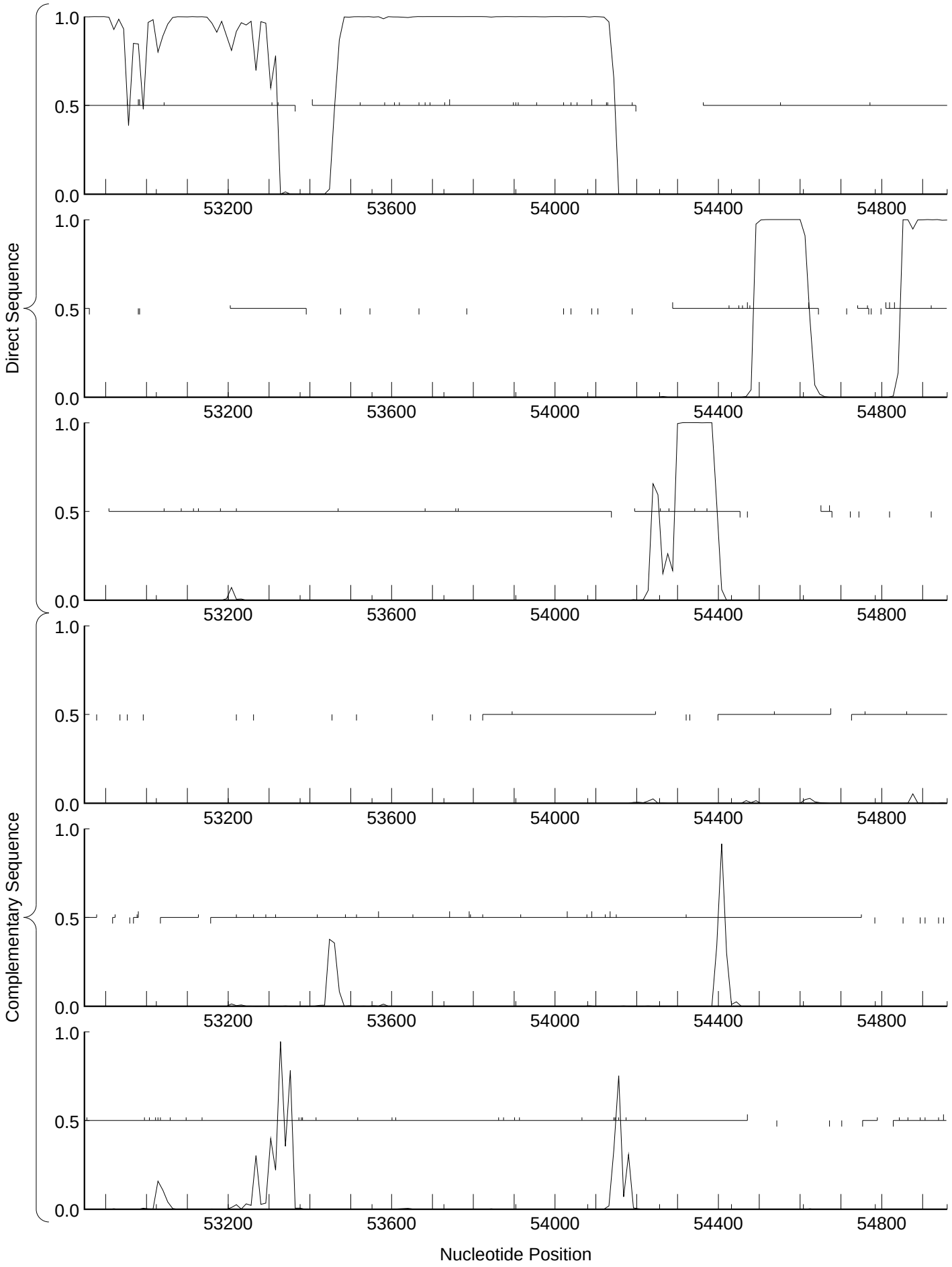

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Complementary Sequence
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46000
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Nucleotide Position

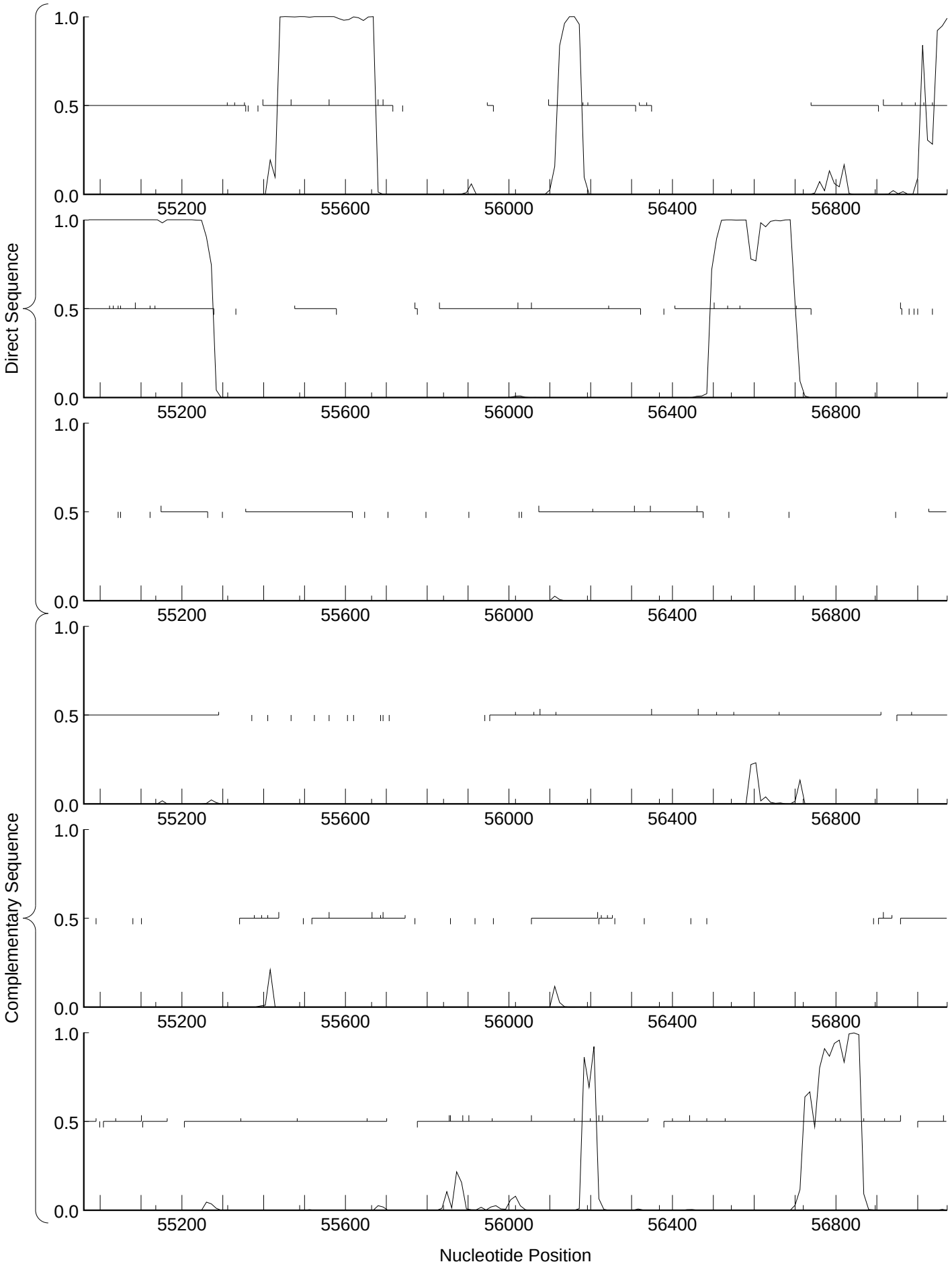

Direct Sequence
Complementary Sequence
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0.5
0.0
46800
47200
47600
48000
48400
Nucleotide Position

complete sequence, 58078 bp including 10-base 3’ overhang (CTCGCGGCAT), Cluster K2, Order 4, Window 96, Step 12, 25/29




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


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
53200
53600
54000
54400
54800
Nucleotide Position


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
55200
55600
56000
56400
56800
Nucleotide Position

complete sequence, 58078 bp including 10-base 3’ overhang (CTCGCGGCAT), Cluster K2, Order 4, Window 96, Step 12, 29/29

