GeneMark

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

PROGRAM INFORMATION

```
Sequence         :  Mycobacterium phage Ryadel complete sequence, 72658 bp including 4-base 3’ overhang (GTGT),
Analysis Date    :  3/28/24 at 17:29:36
Pages            :  36
Sequence Length  :  72658 bp
GC Content       :   65.21%

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_tuberculosis_H37Rv
Author     :  -

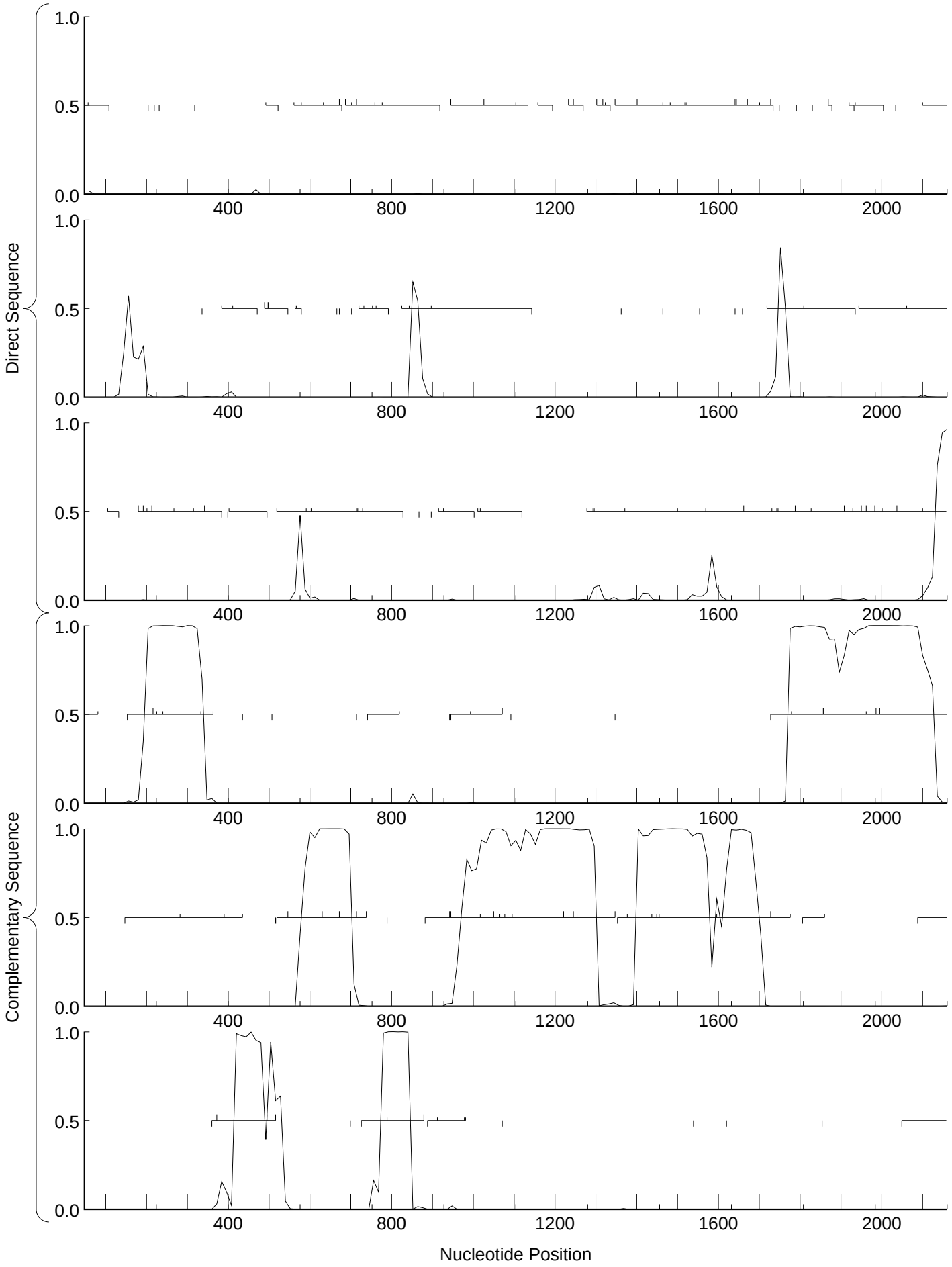
Order      :  4

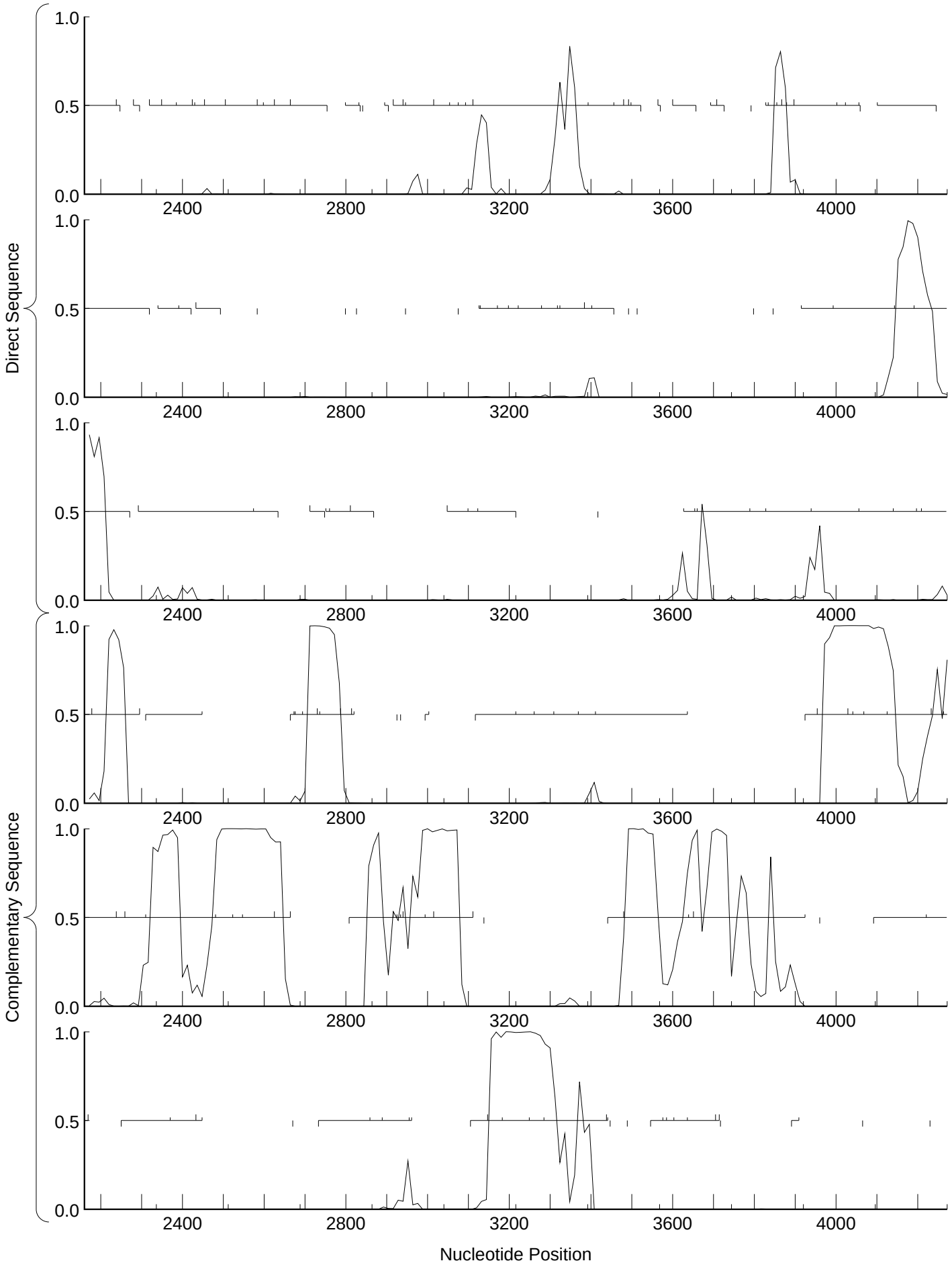

  Send questions / comments to:
      Dr. M. Borodovsky
      Georgia Institute of Technology
      School of Biology
      Atlanta, GA  30332-0230
```

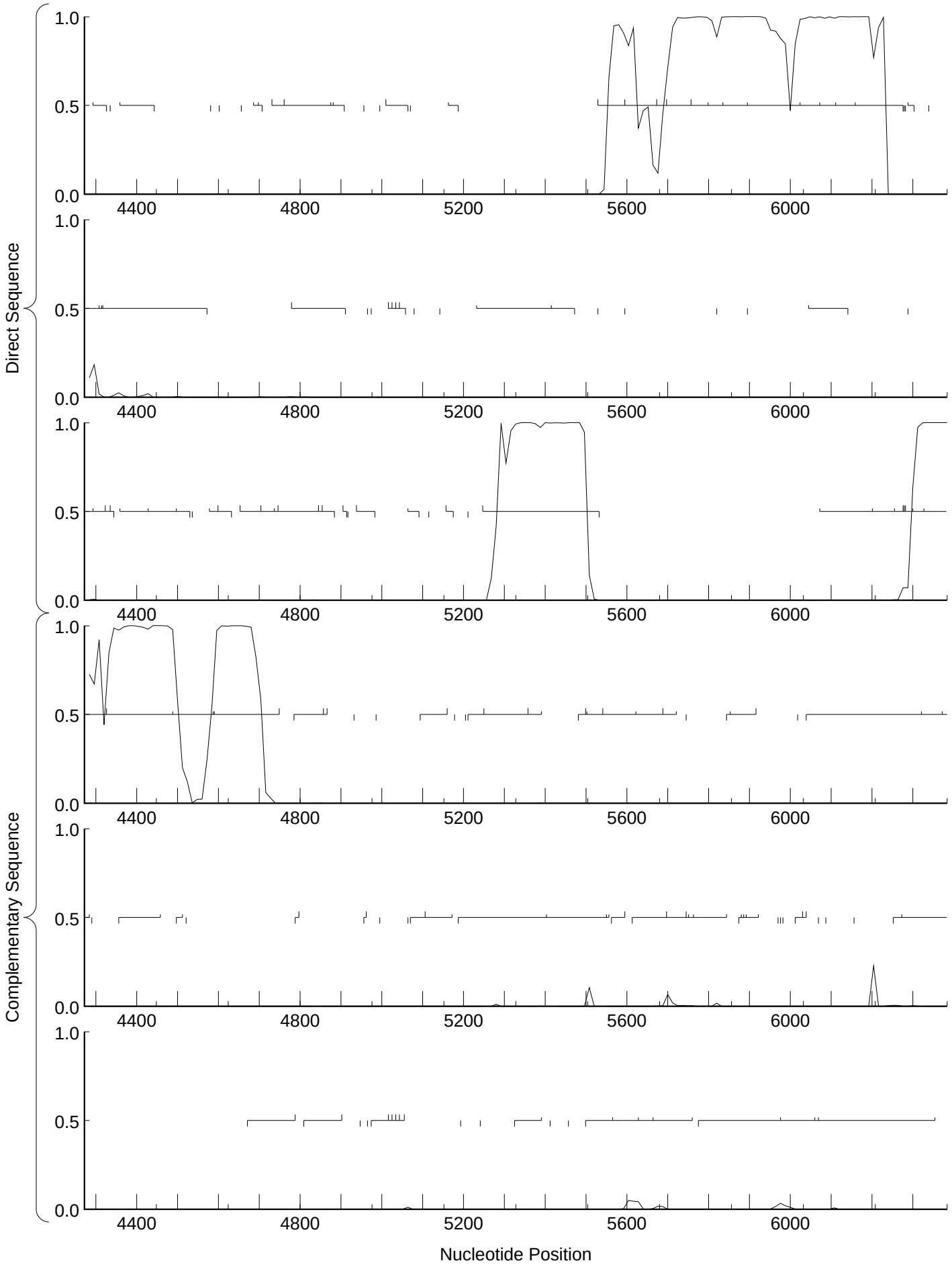
Matrix notes & comments

Training set derived by GeneMarkS, 4.27 September 2014
Tue Sep 23 15:14:37 2014

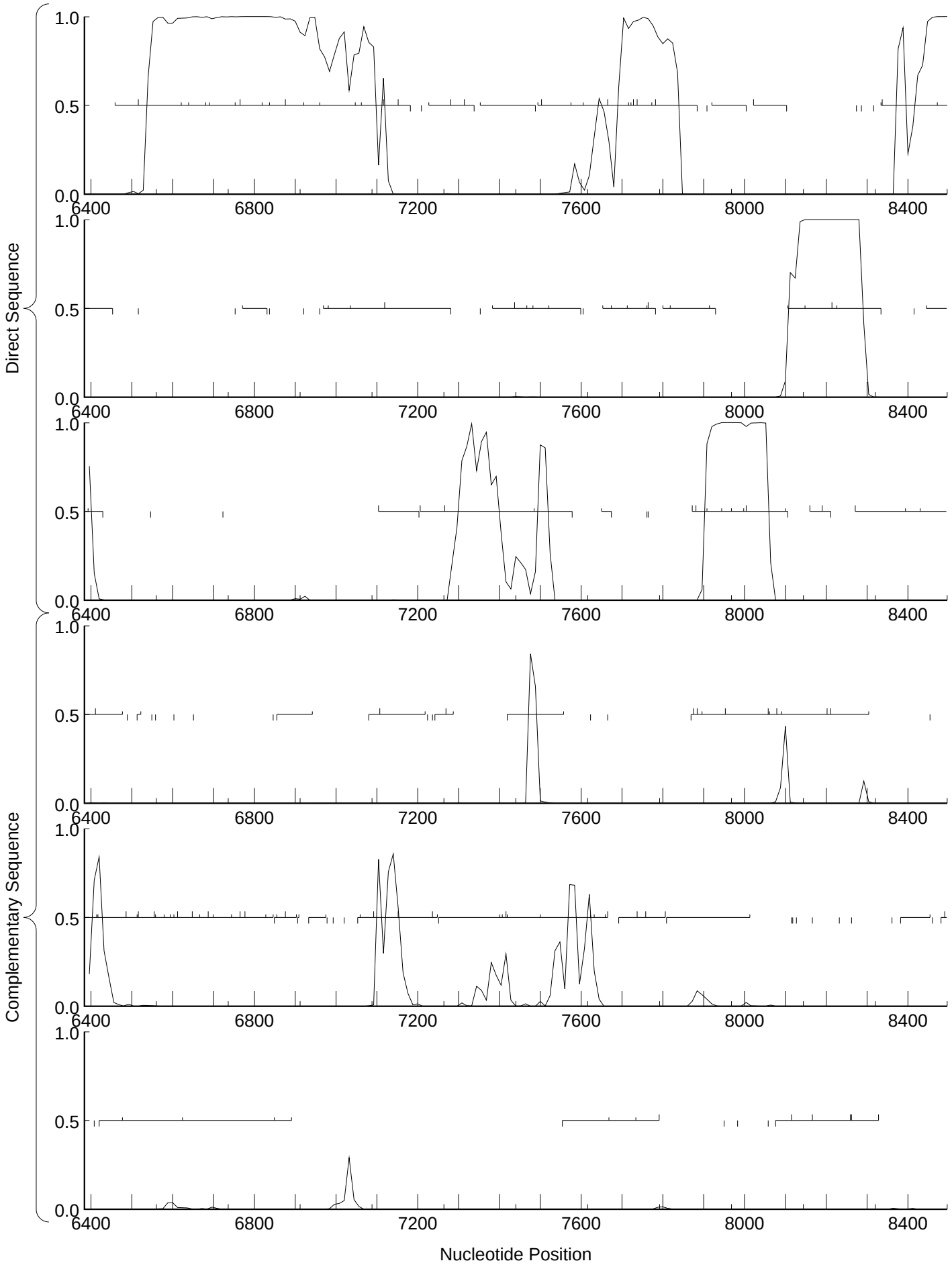
For help or information, send electronic mail to: custserv@genepro.com, or mark@amber.biology.gatech.edu


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

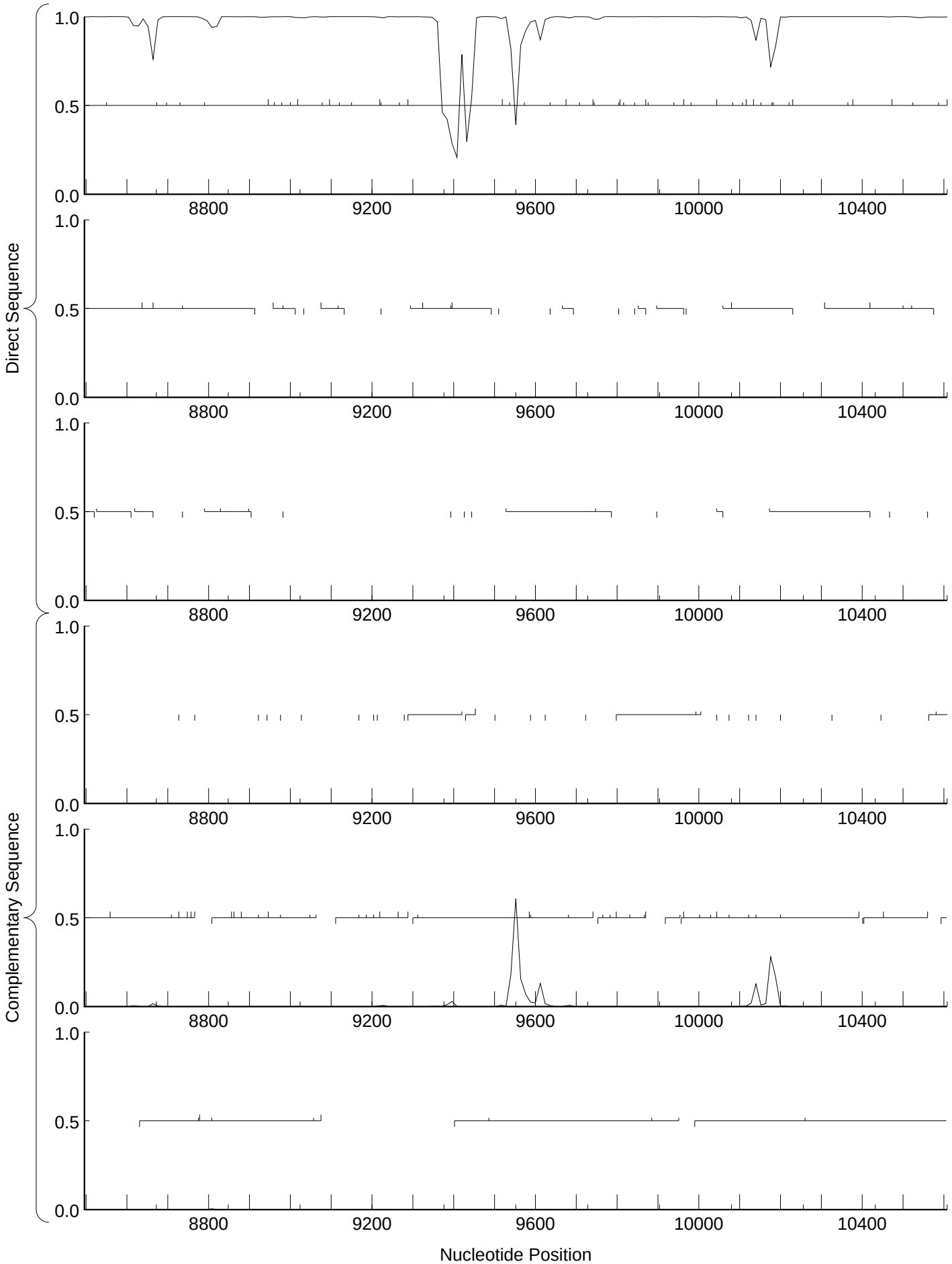

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Complementary Sequence
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3200
3600
4000
Nucleotide Position

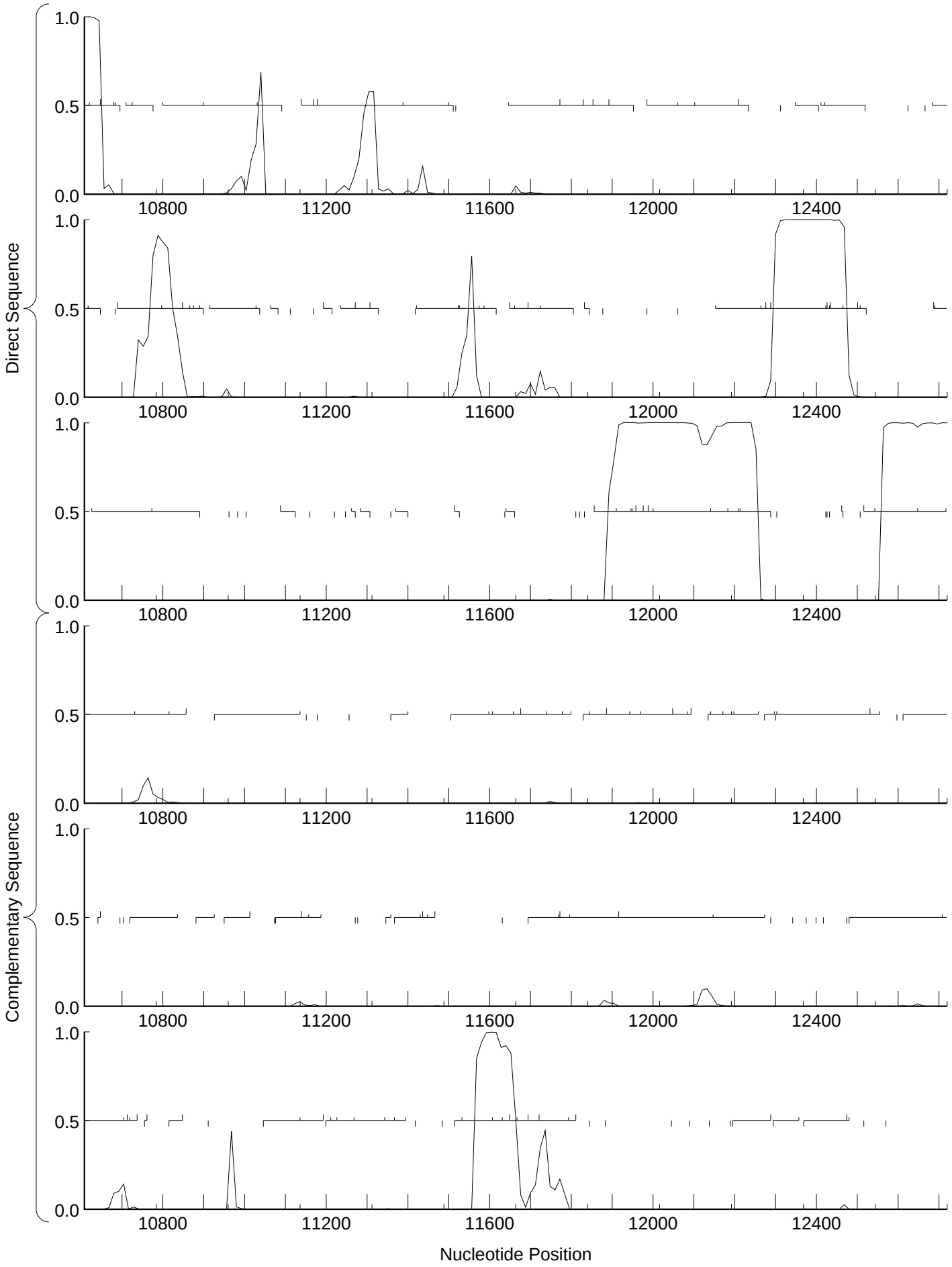

Direct Sequence
Complementary Sequence
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6000
Nucleotide Position

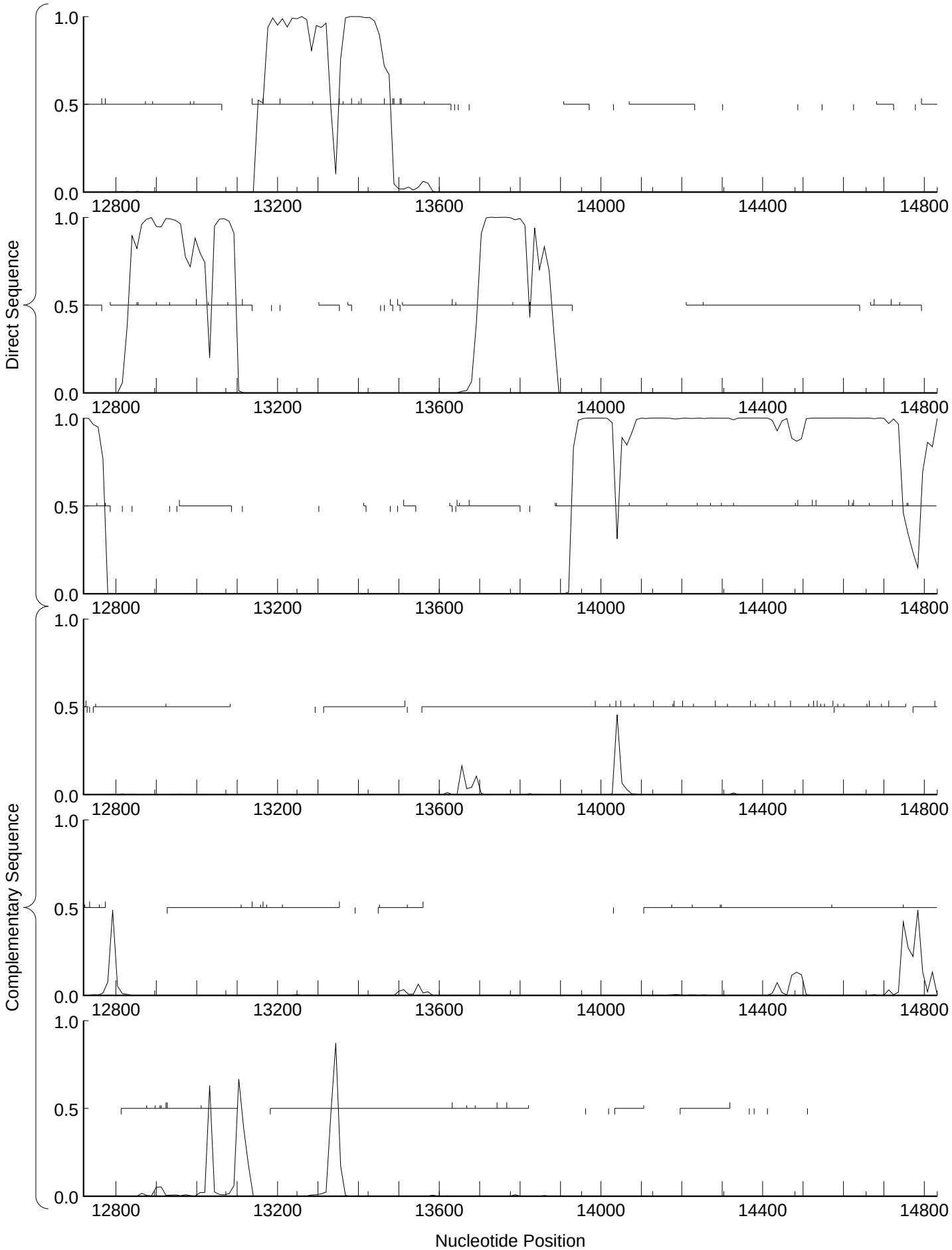
phage Ryadel complete sequence, 72658 bp including 4-base 3’ overhang (GTGT), Cluster O, Order 4, Window 96, Step 12, 5/36



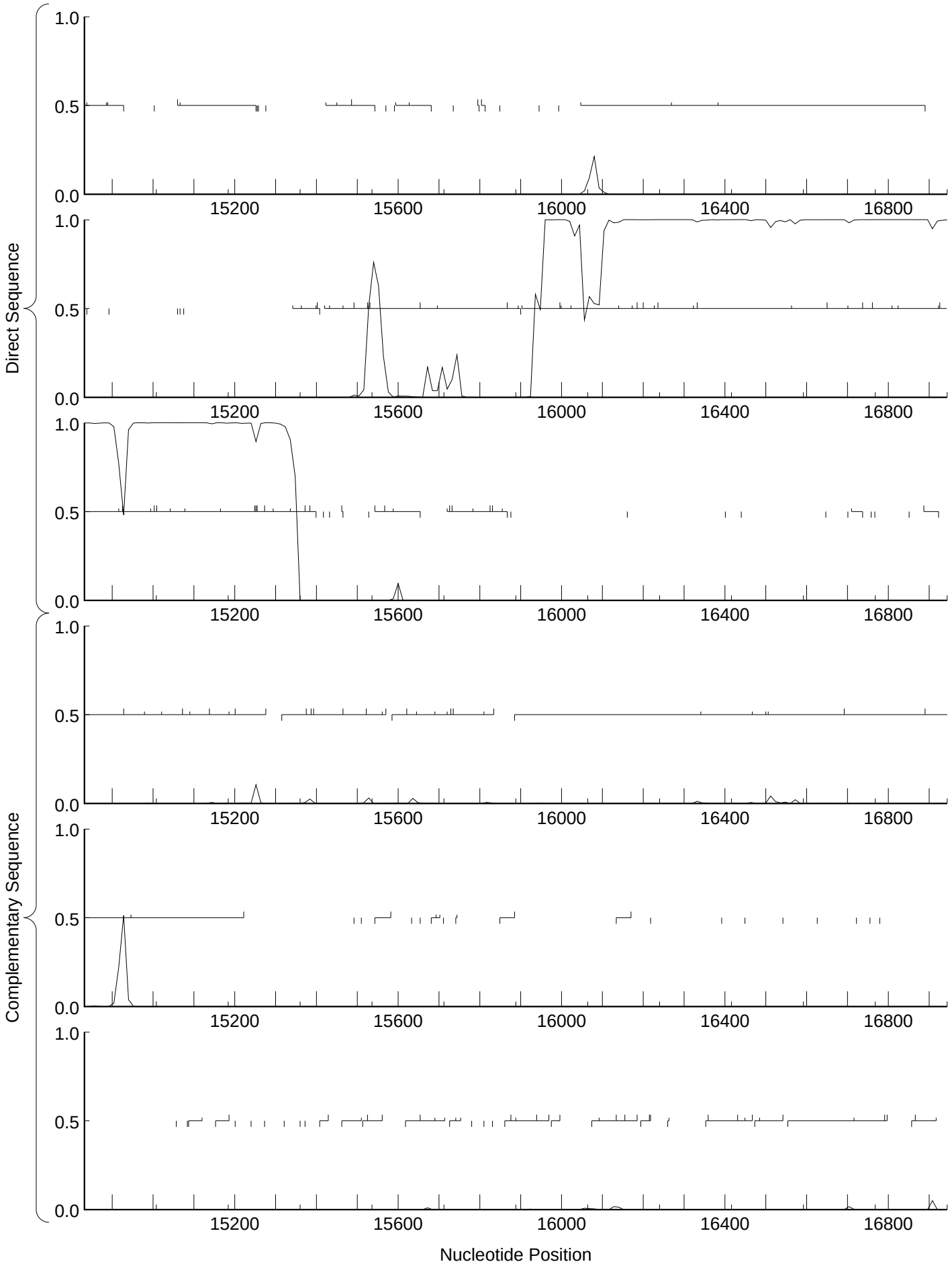
phage Ryadel complete sequence, 72658 bp including 4-base 3' overhang (GTGT), Cluster O, Order 4, Window 96, Step 12, 6/36



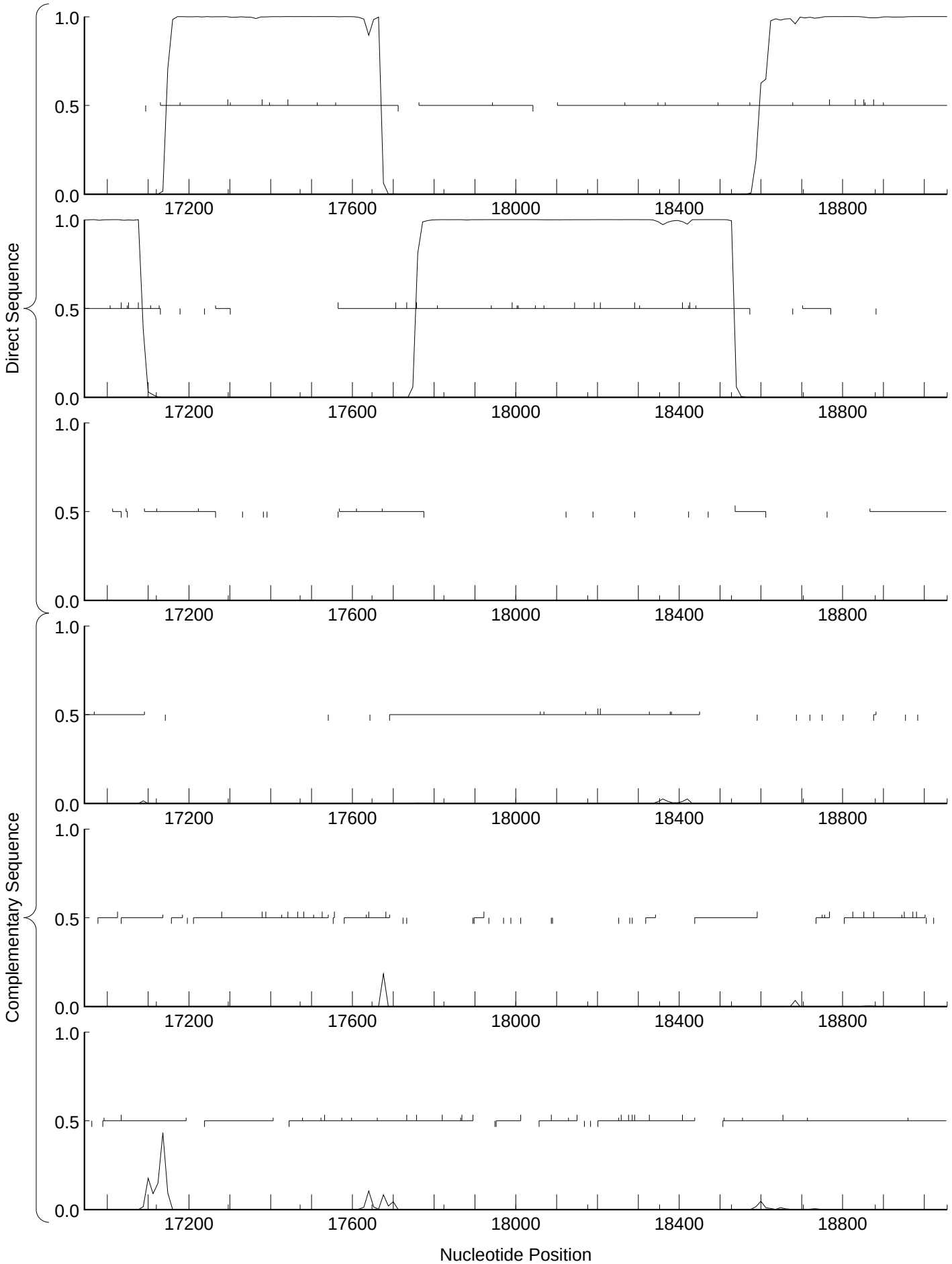

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
10800
11200
11600
12000
12400
Nucleotide Position


Direct Sequence
Complementary Sequence
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0.5
0.0
12800
13200
13600
14000
14400
14800
Nucleotide Position

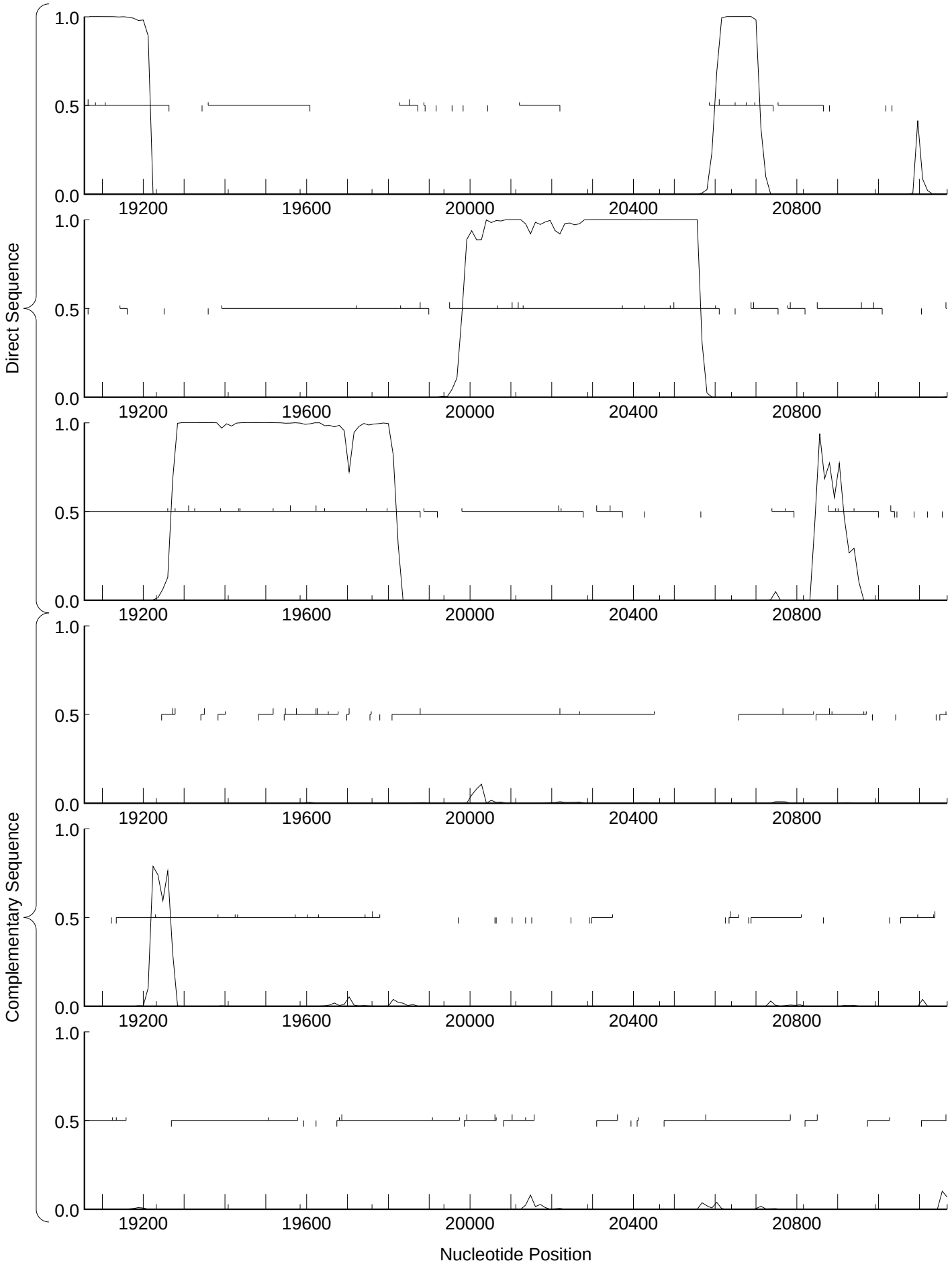
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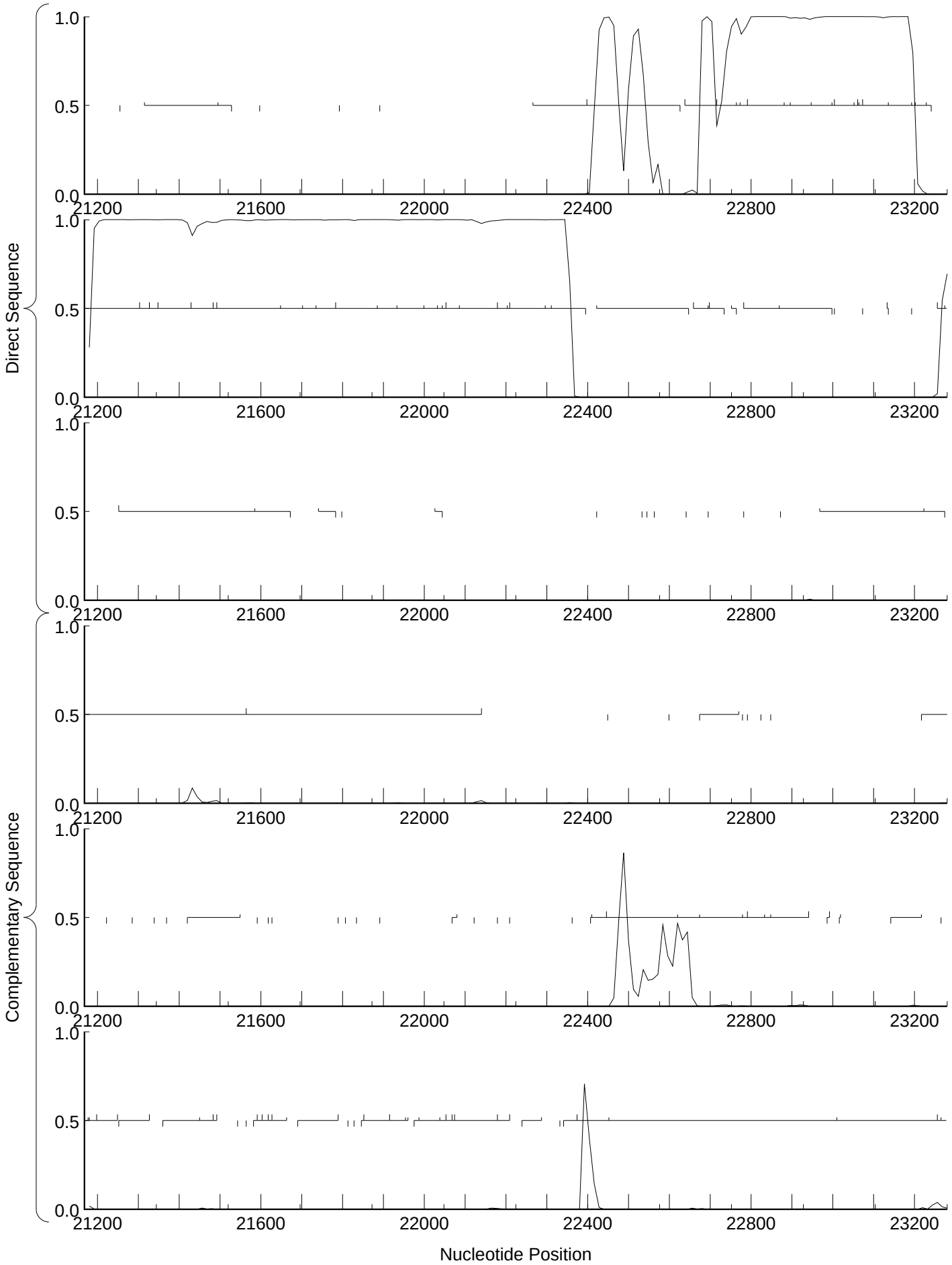


hage Ryadel complete sequence, 72658 bp including 4-base 3’ overhang (GTGT), Cluster O, Order 4, Window 96, Step 12, 10/36

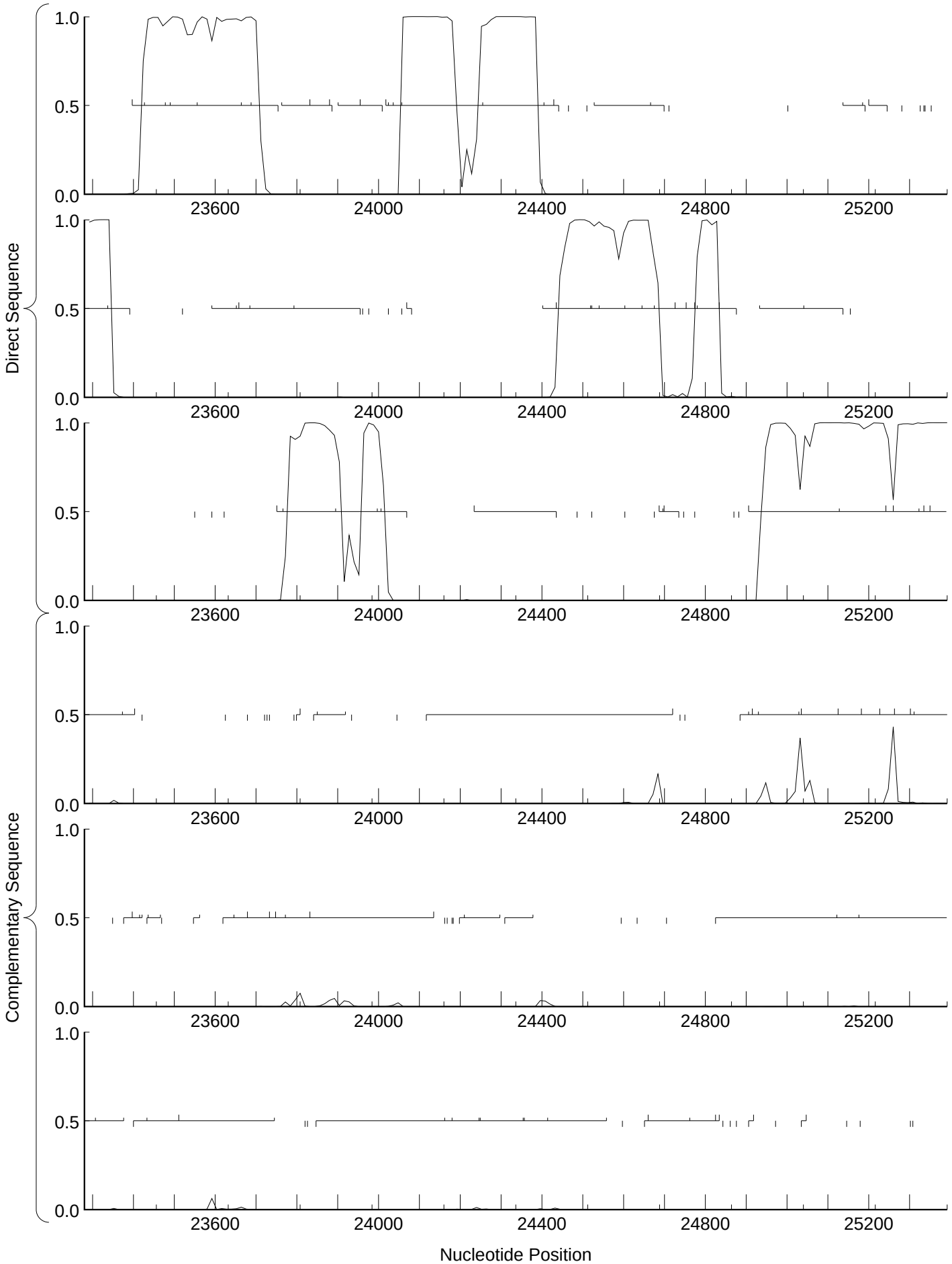


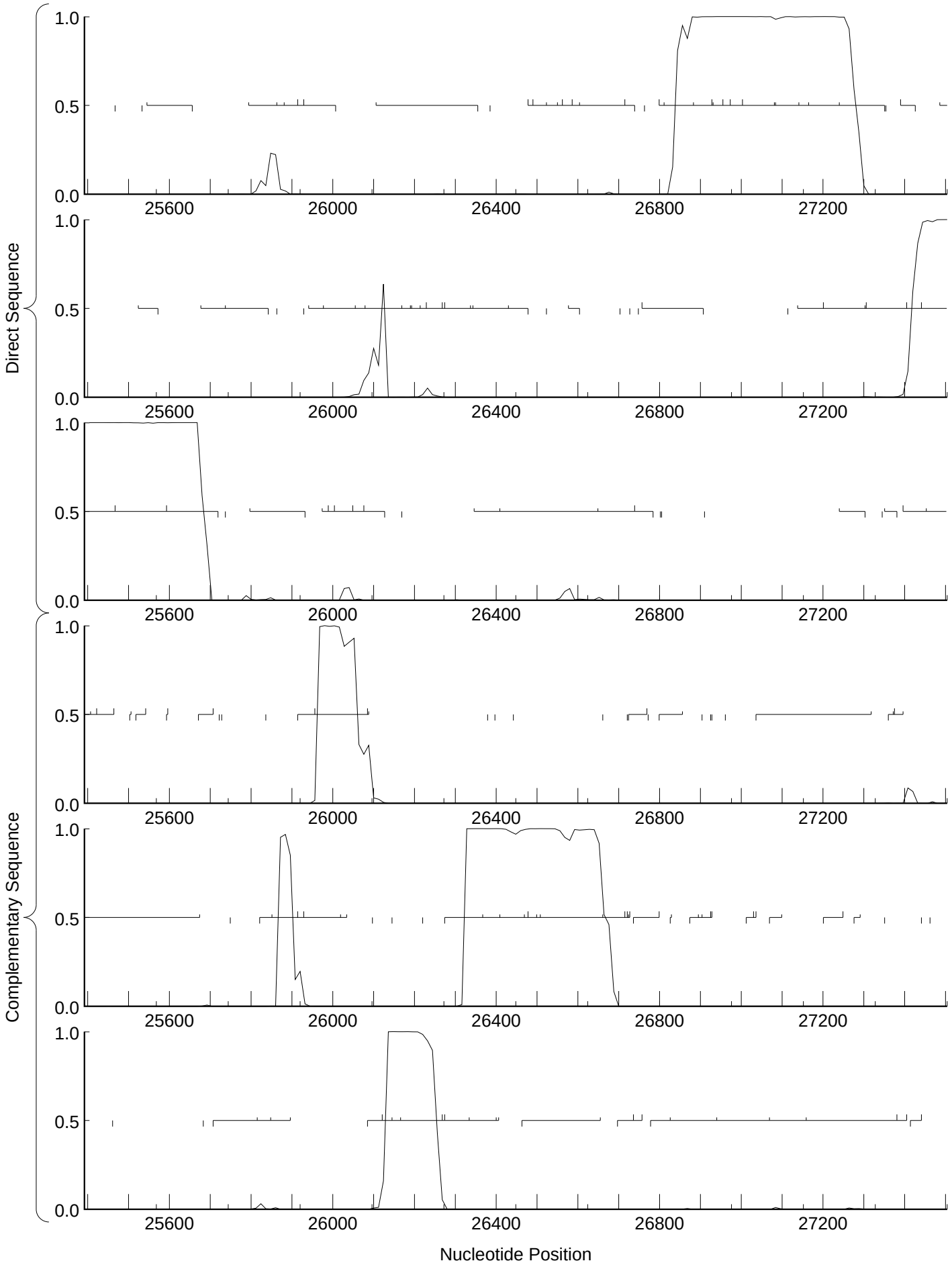
nage Ryadel complete sequence, 72658 bp including 4-base 3’ overhang (GTGT), Cluster O, Order 4, Window 96, Step 12, 11/36

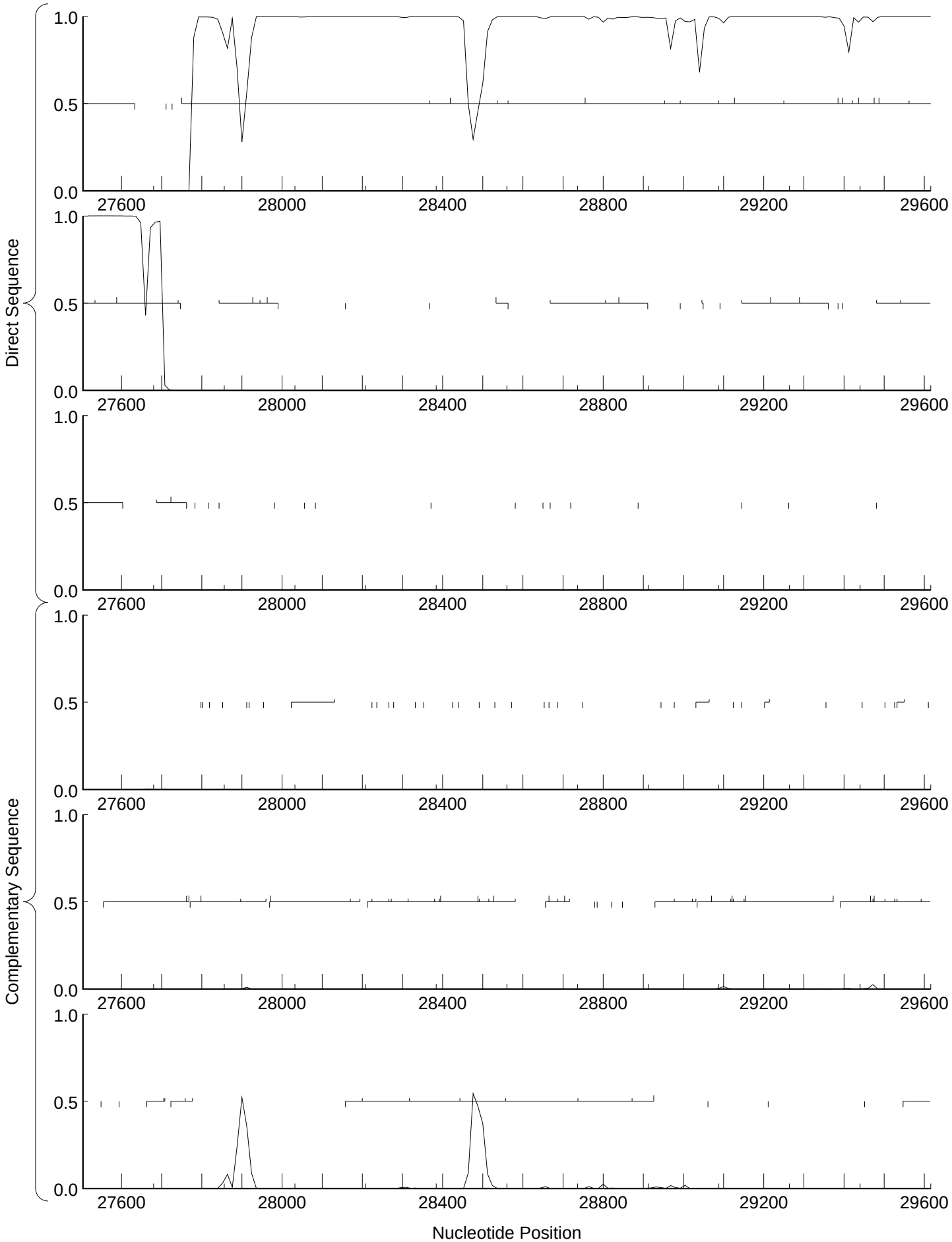


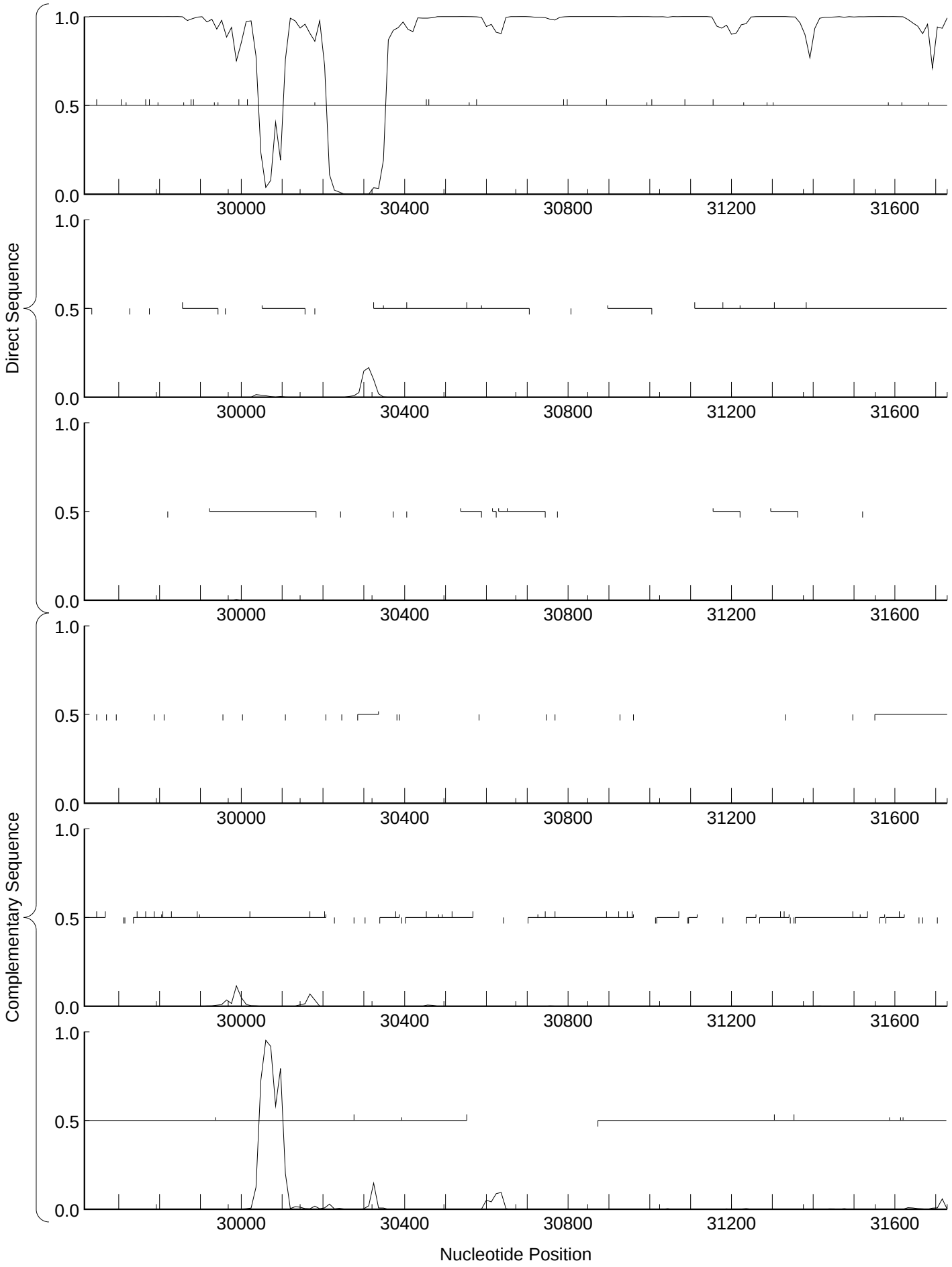

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Complementary Sequence
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22000
22400
22800
23200
Nucleotide Position

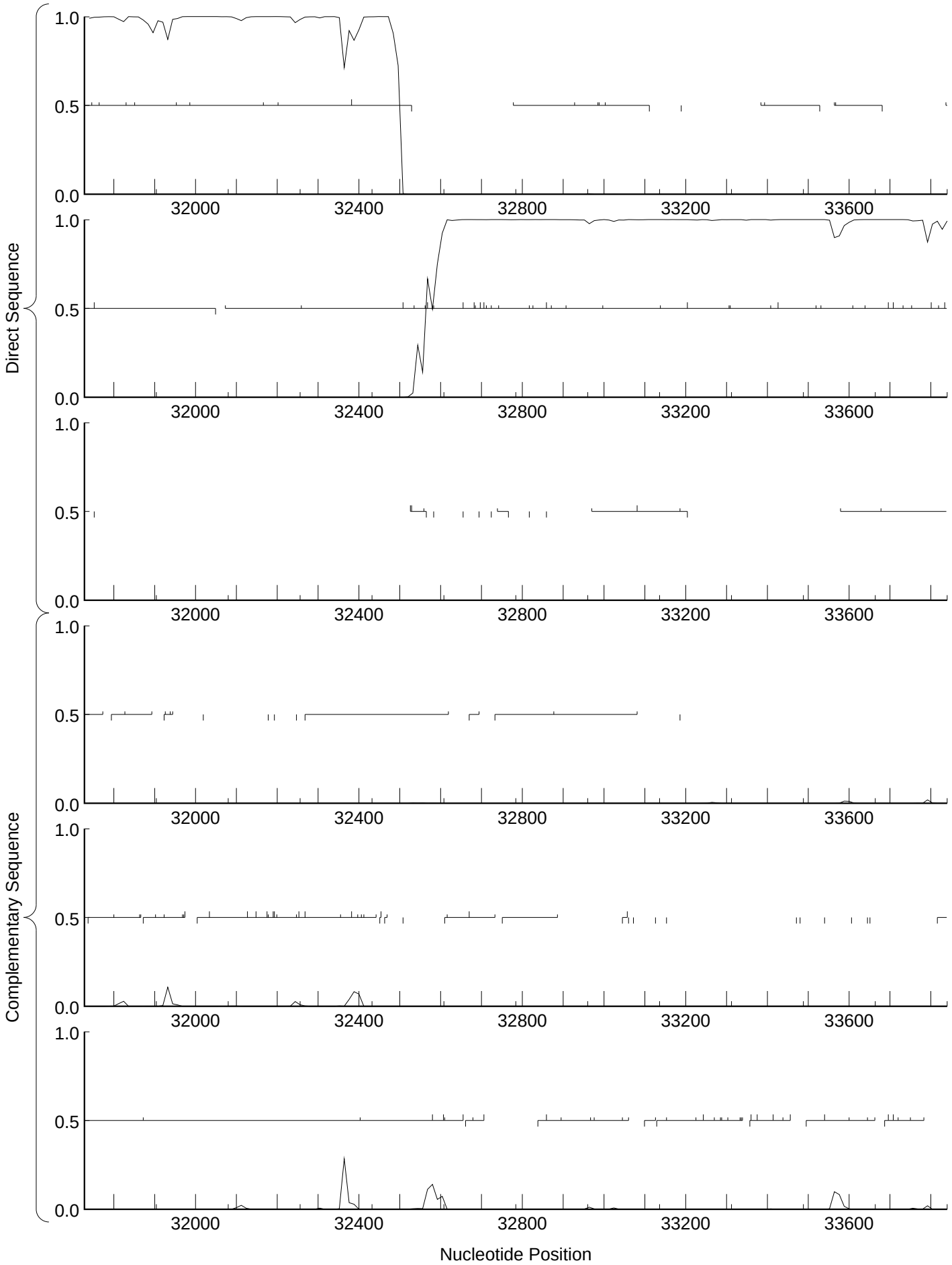
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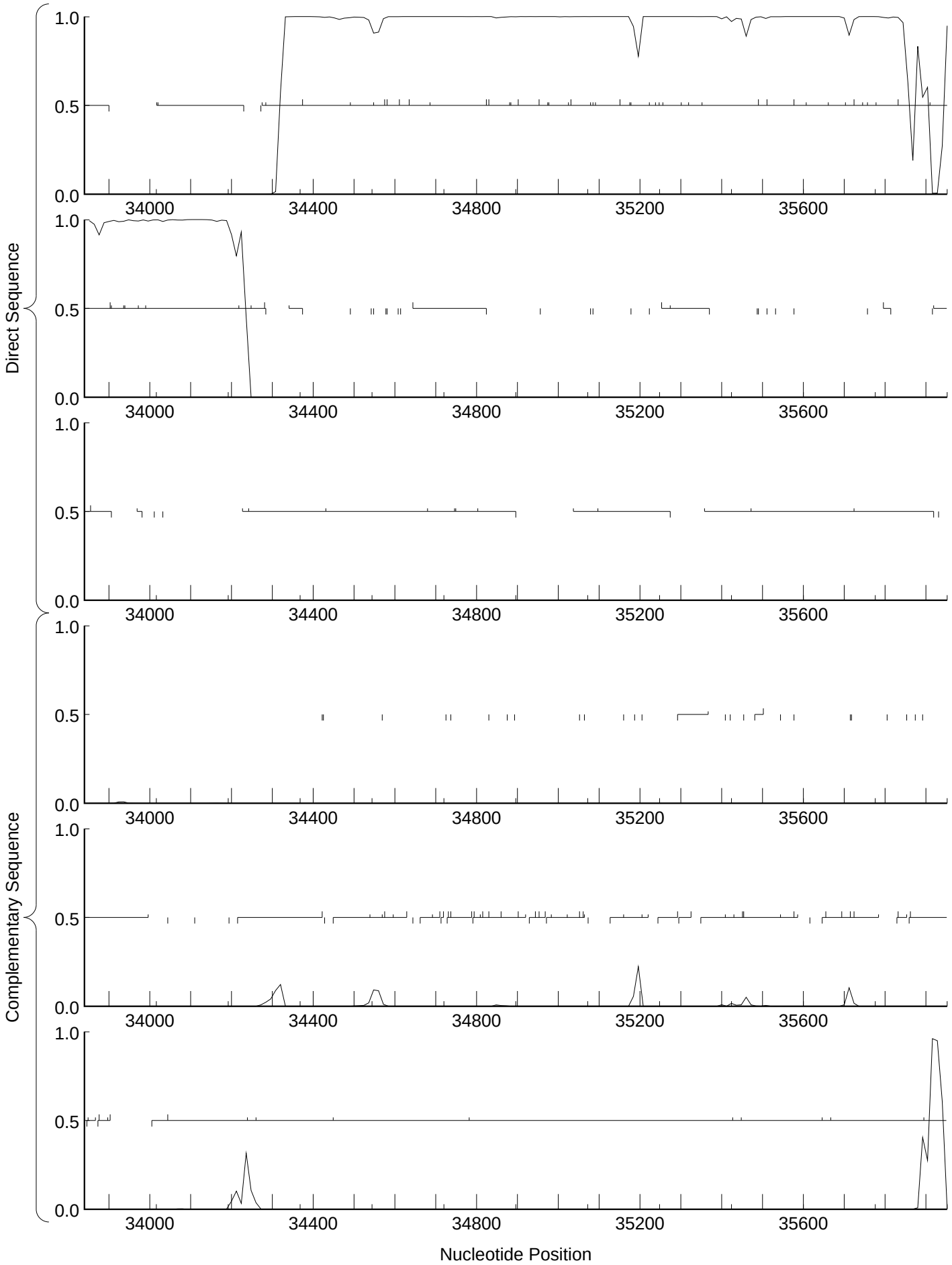


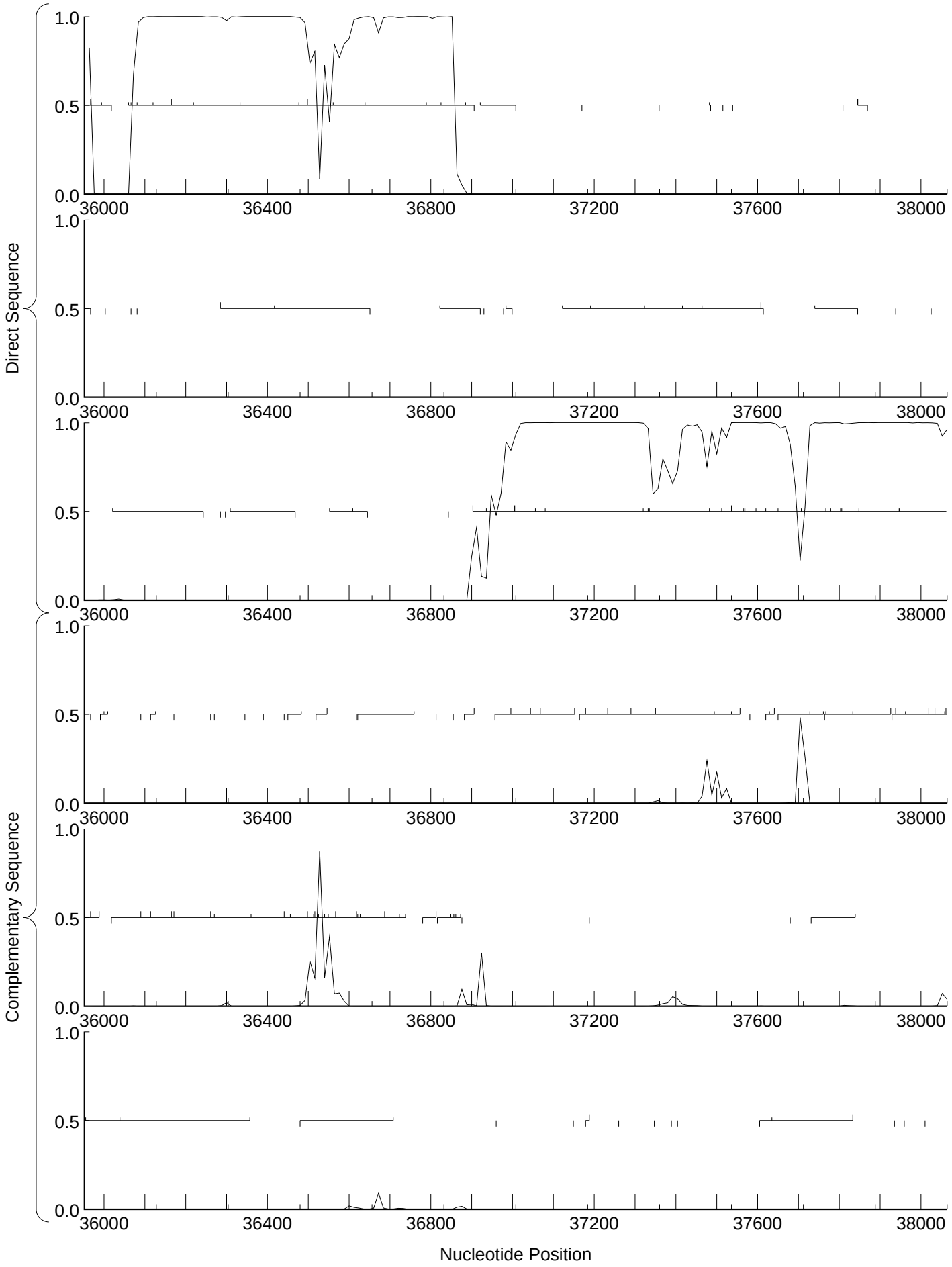

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Complementary Sequence
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26400
26800
27200
Nucleotide Position

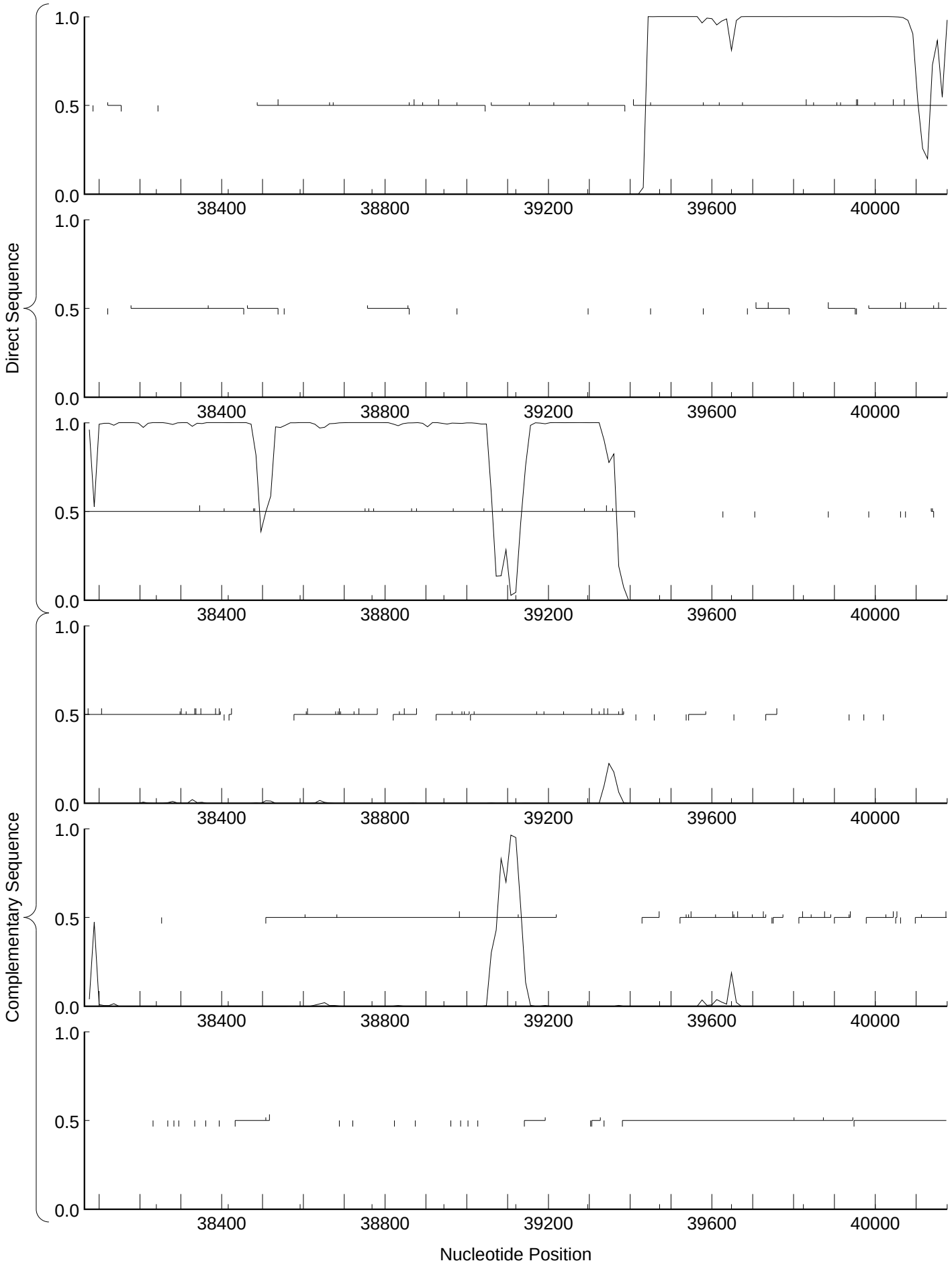

Direct Sequence
Complementary Sequence
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0.5
0.0
27600
28000
28400
28800
29200
29600
Nucleotide Position


Direct Sequence
Complementary Sequence
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30000
30400
30800
31200
31600
Nucleotide Position

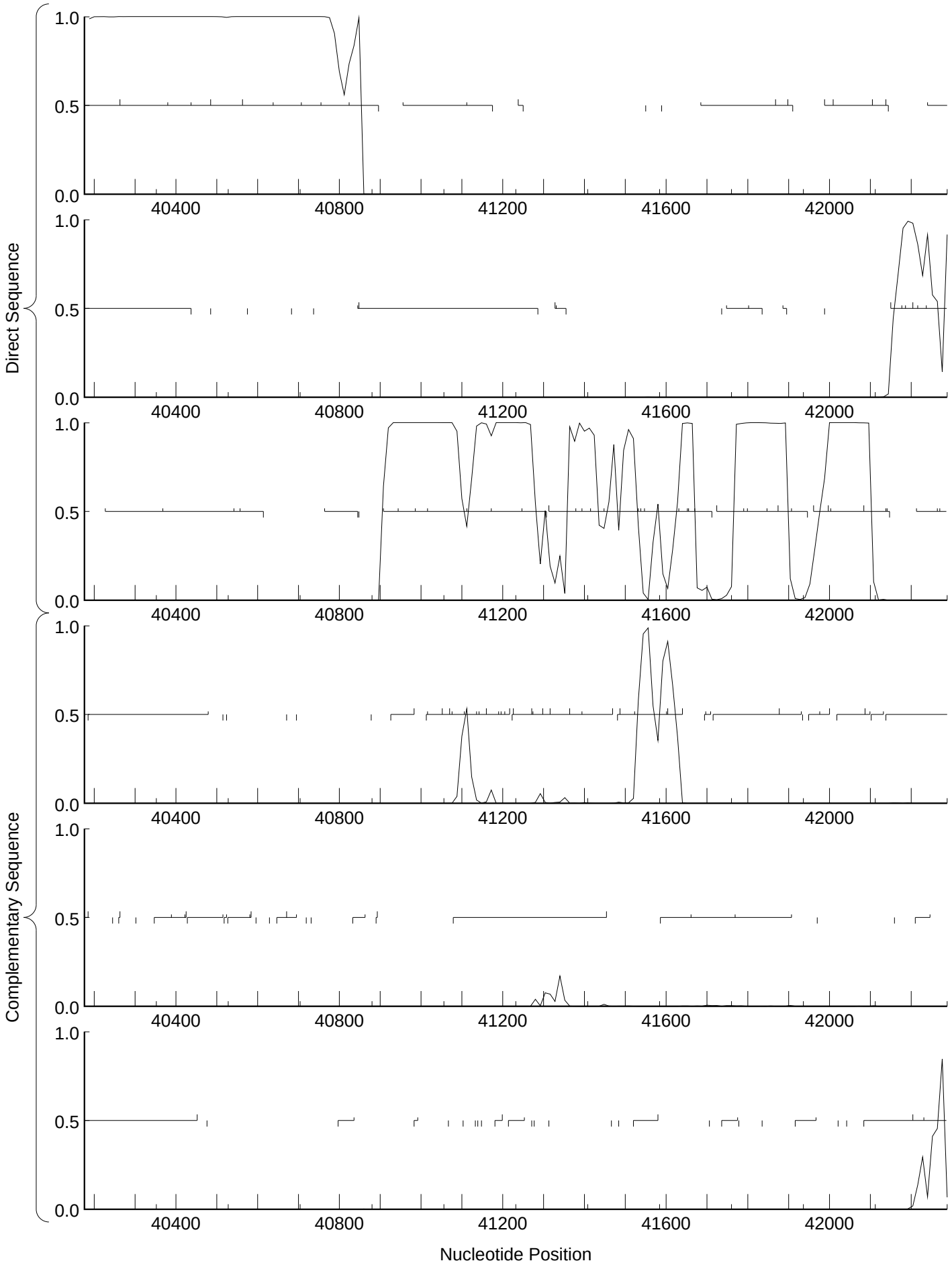

Direct Sequence
Complementary Sequence
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32800
33200
33600
Nucleotide Position

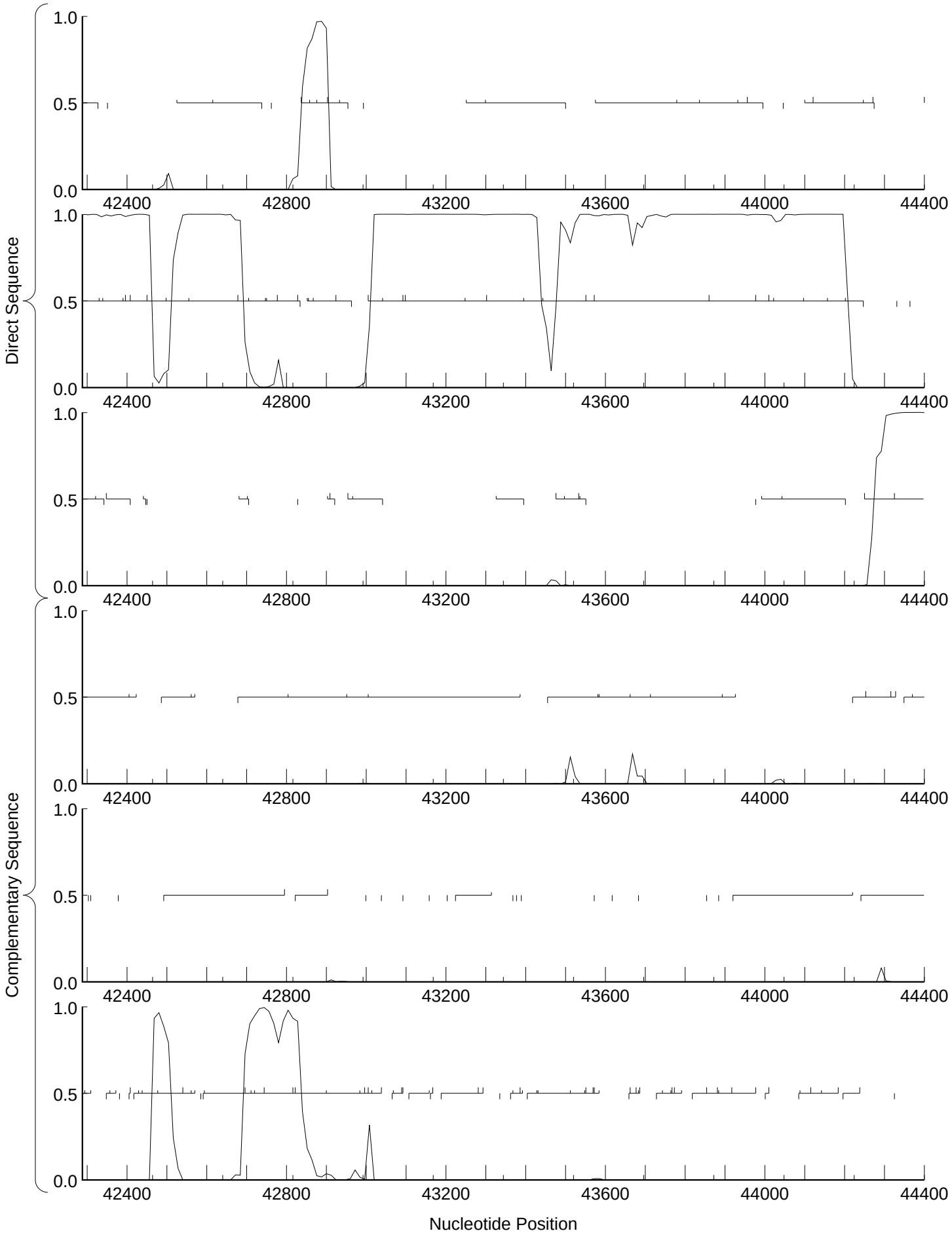

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34800
35200
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Nucleotide Position

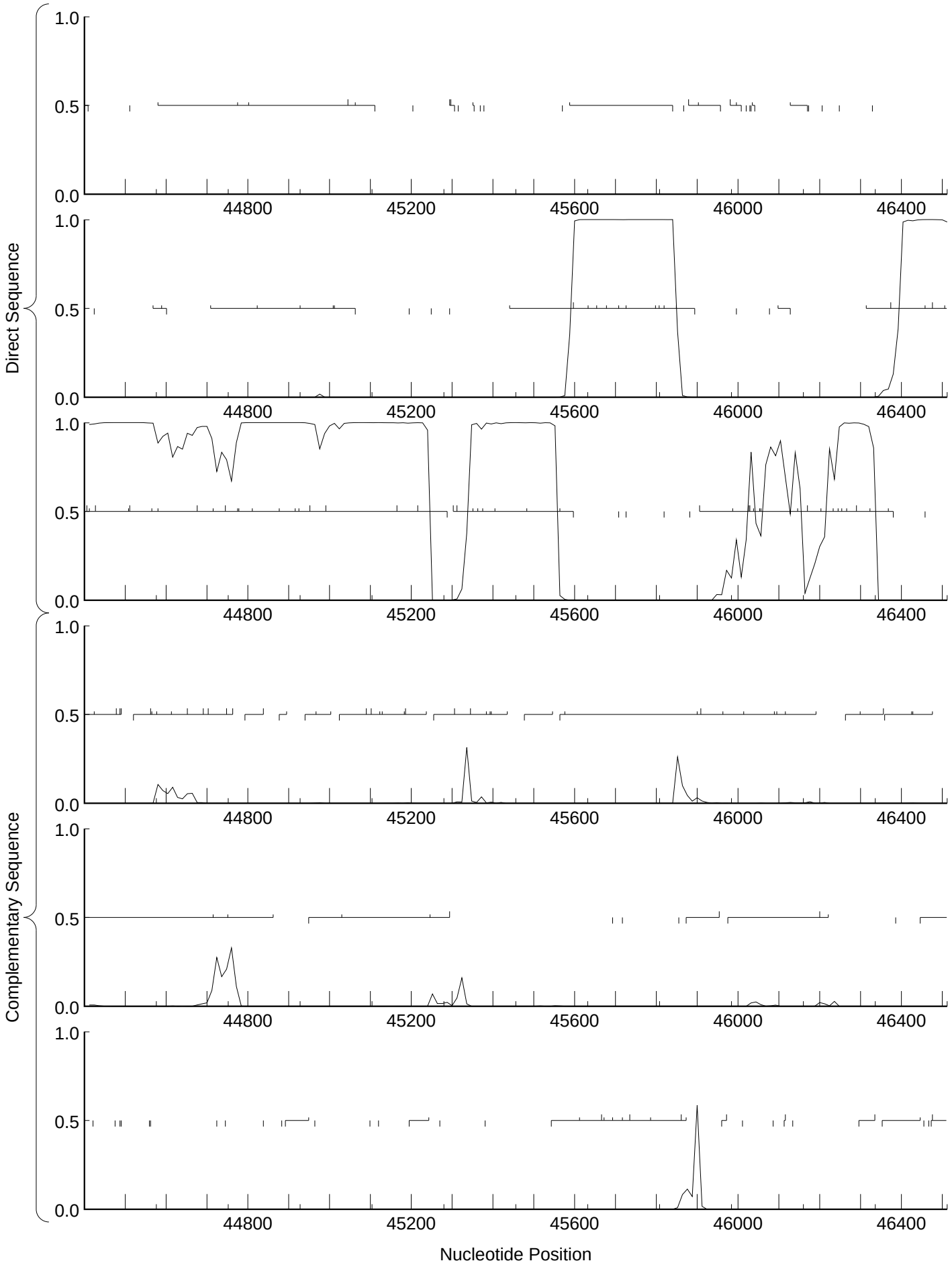

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36400
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37600
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Nucleotide Position

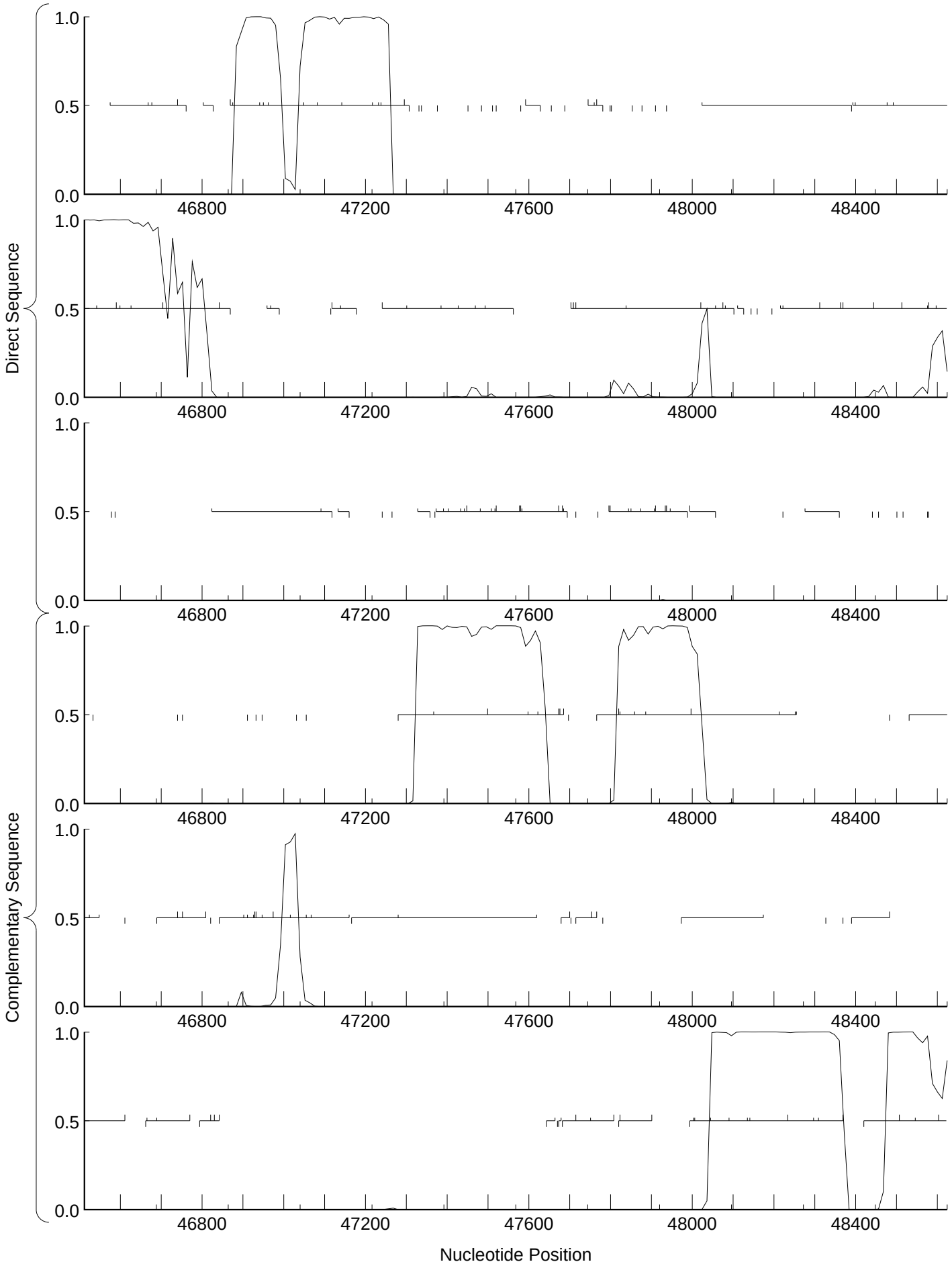

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Complementary Sequence
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Nucleotide Position

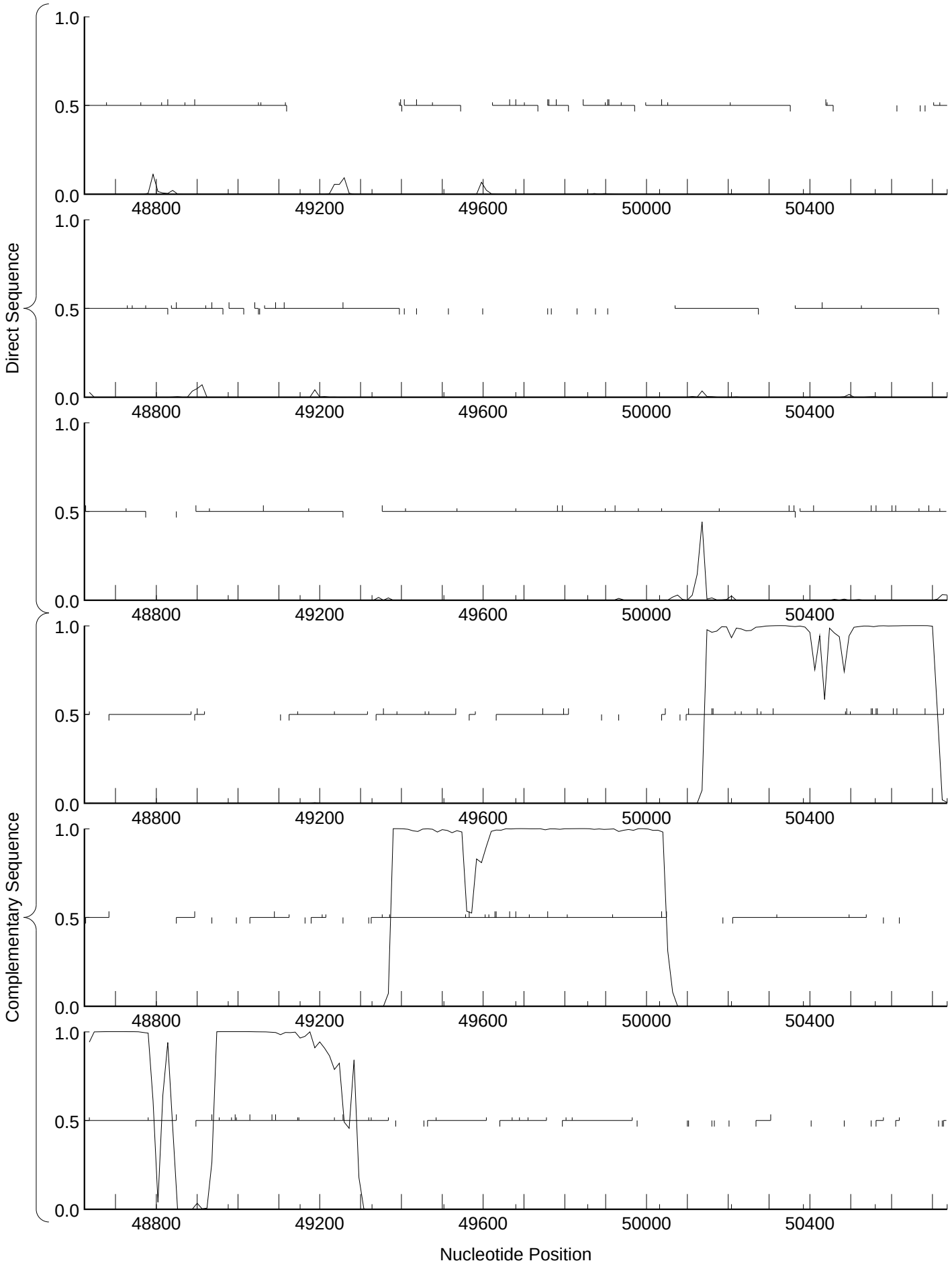
nage Ryadel complete sequence, 72658 bp including 4-base 3’ overhang (GTGT), Cluster O, Order 4, Window 96, Step 12, 21/36

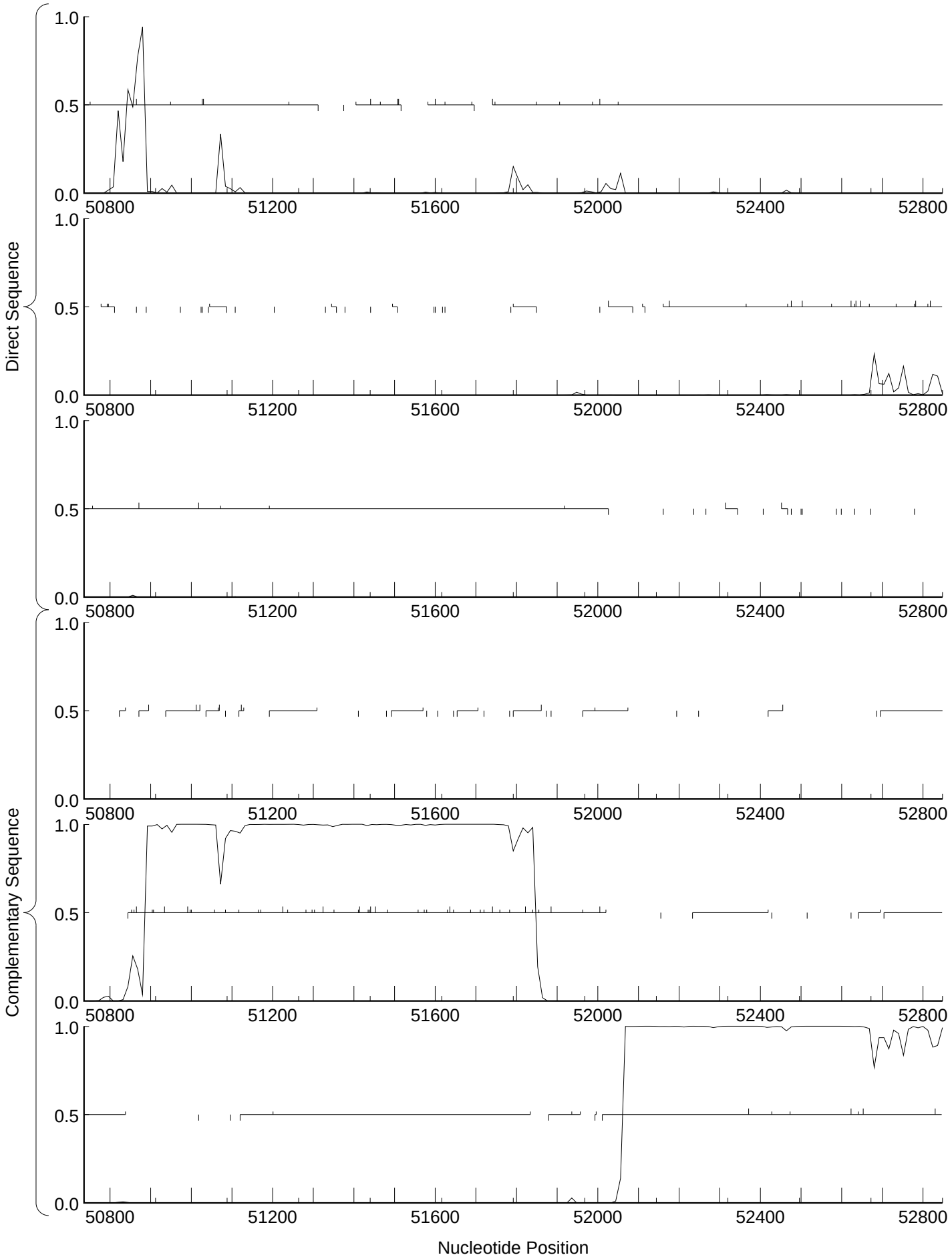



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Complementary Sequence
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43600
44000
44400
Nucleotide Position

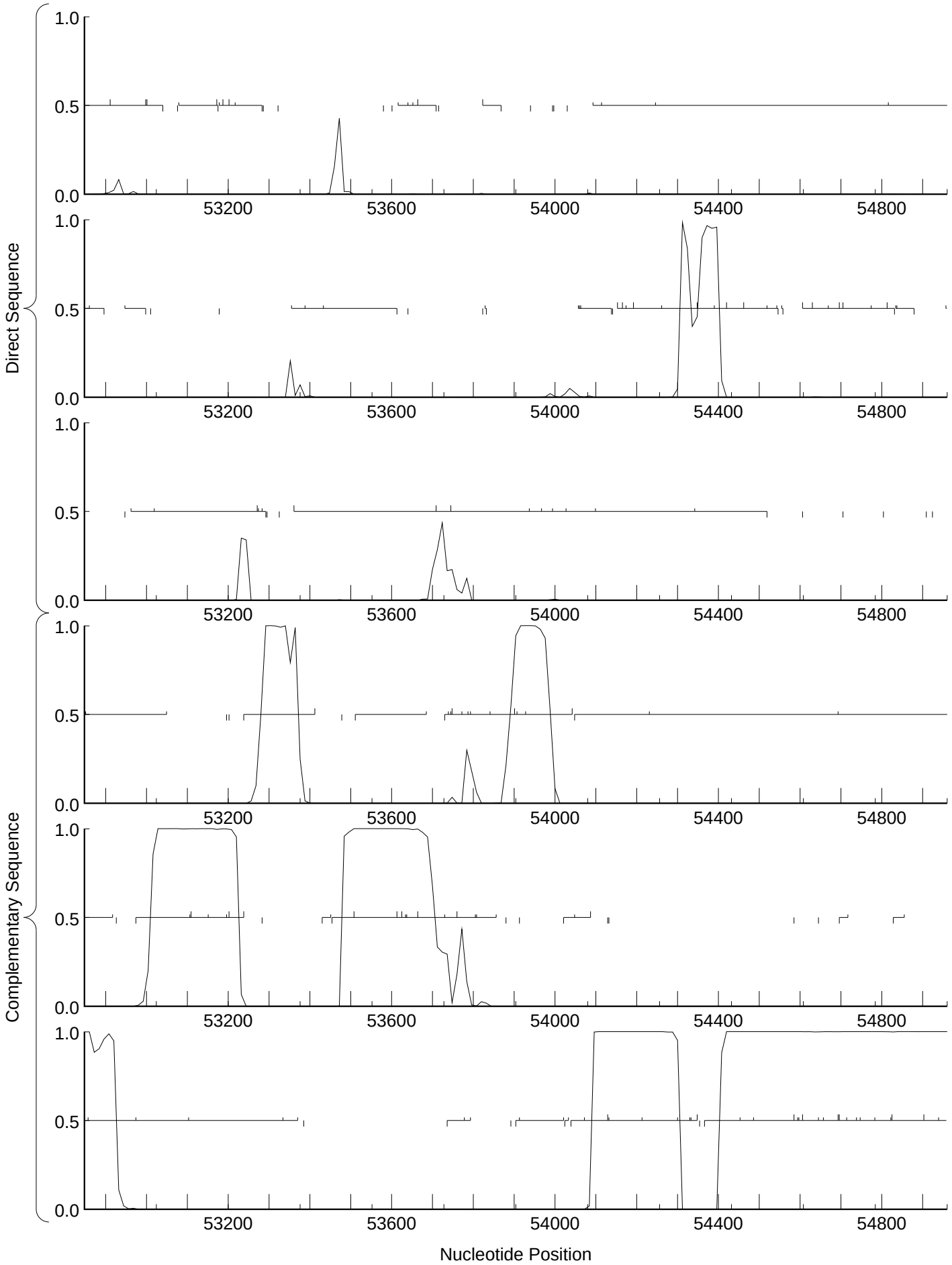

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Complementary Sequence
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45200
45600
46000
46400
Nucleotide Position

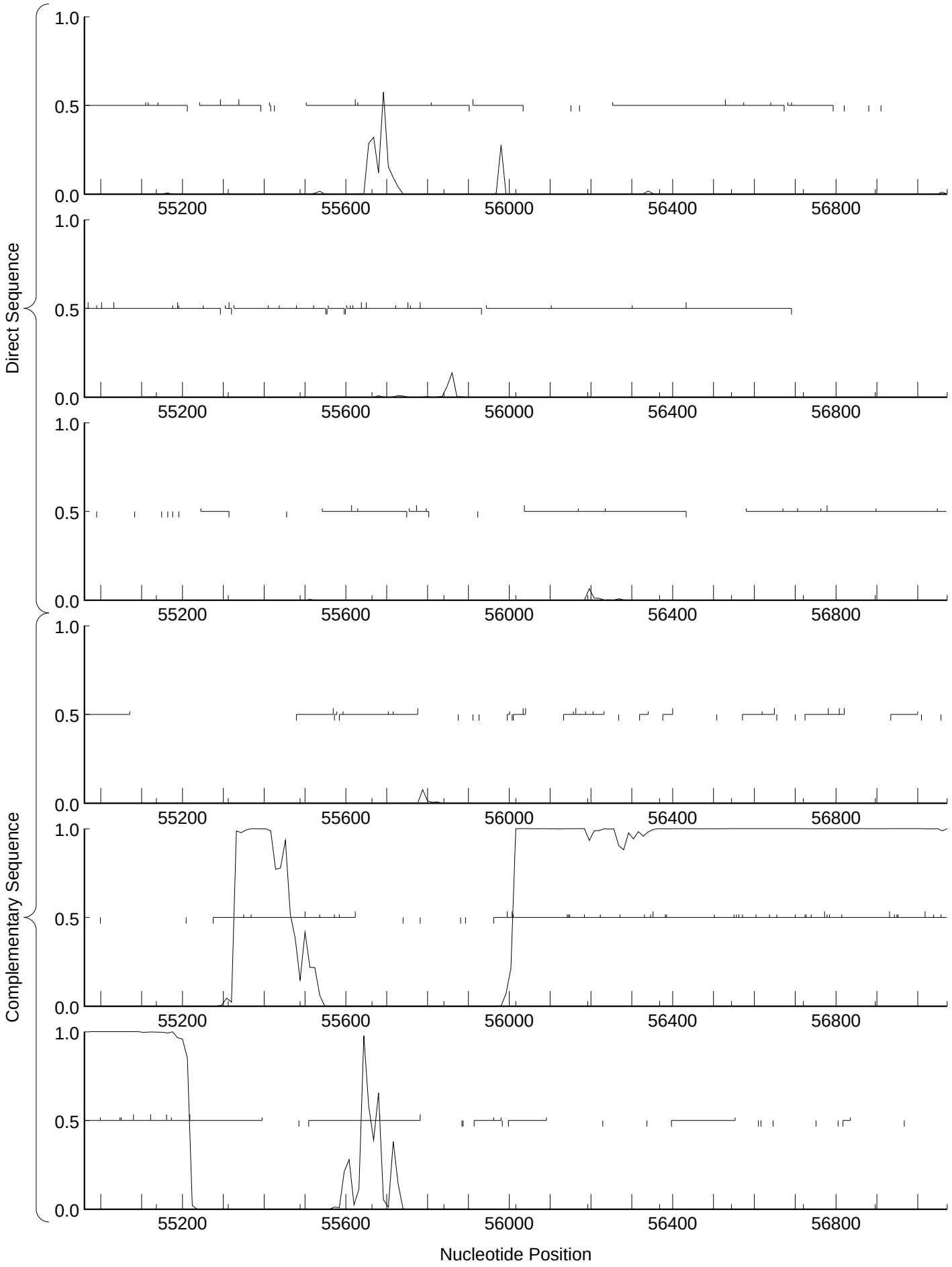

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48000
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Nucleotide Position

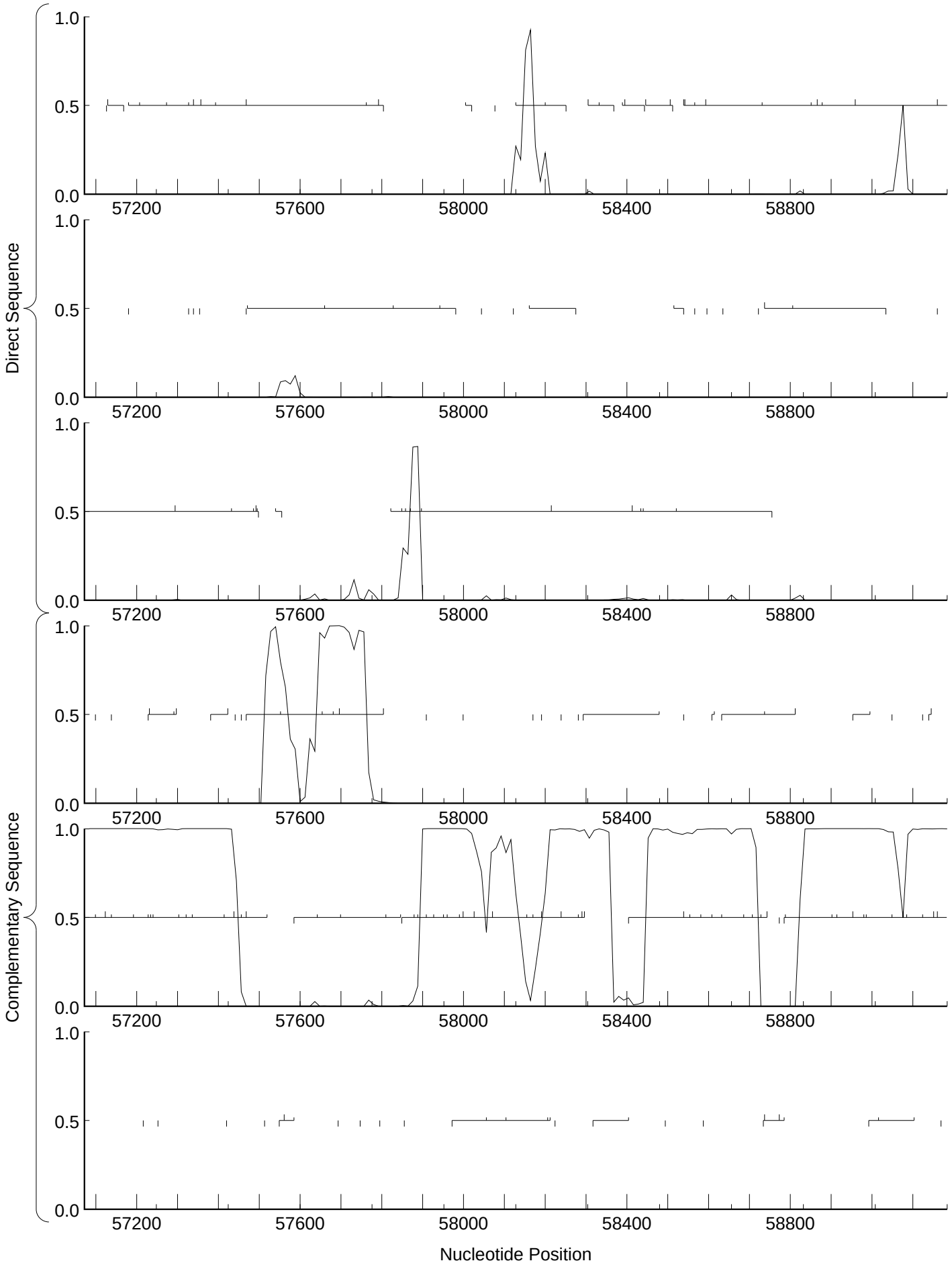

Direct Sequence
Complementary Sequence
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0.0
48800
49200
49600
50000
50400
Nucleotide Position


Direct Sequence
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52000
52400
52800
Nucleotide Position

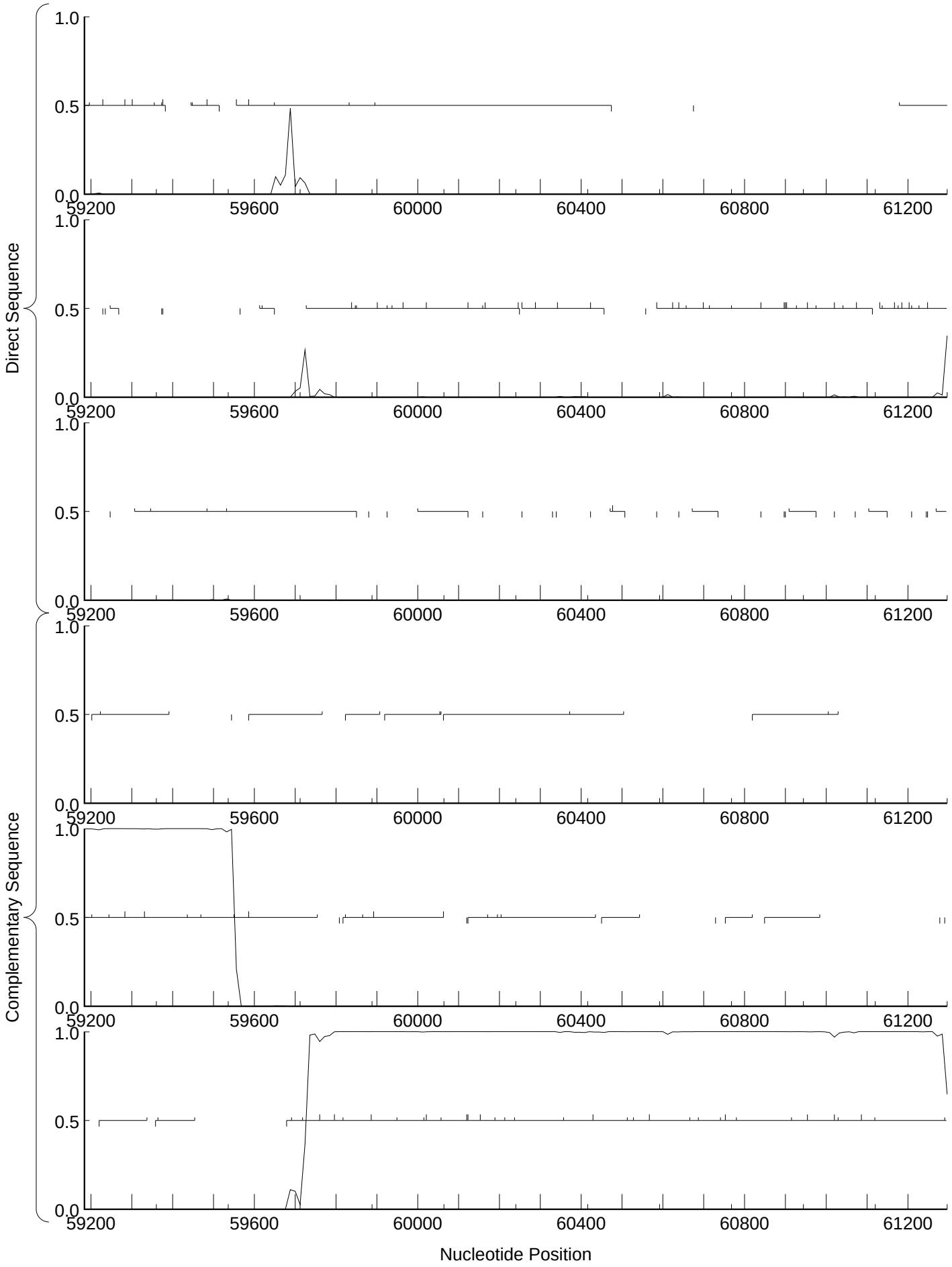
nage Ryadel complete sequence, 72658 bp including 4-base 3’ overhang (GTGT), Cluster O, Order 4, Window 96, Step 12, 27/36

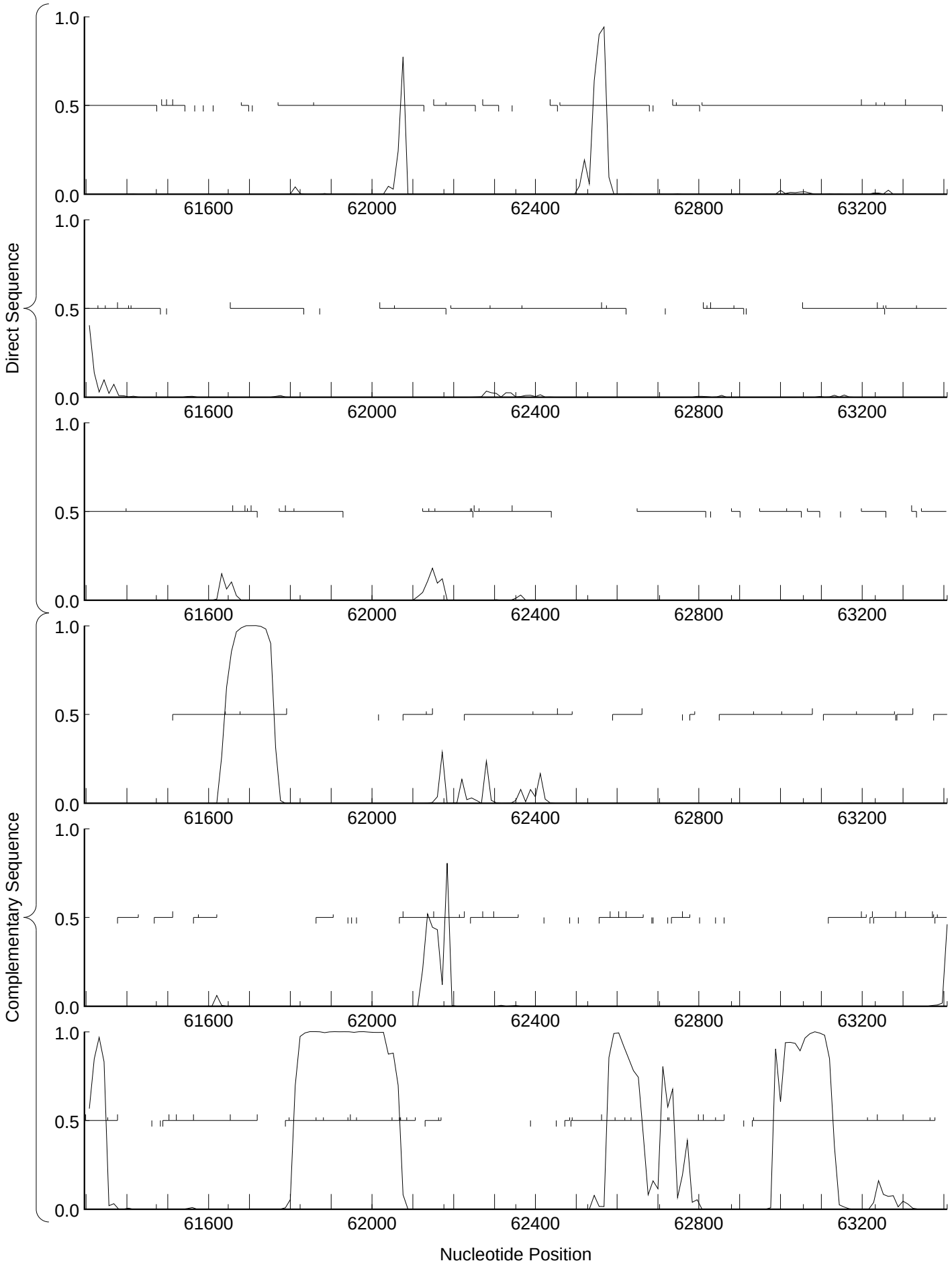


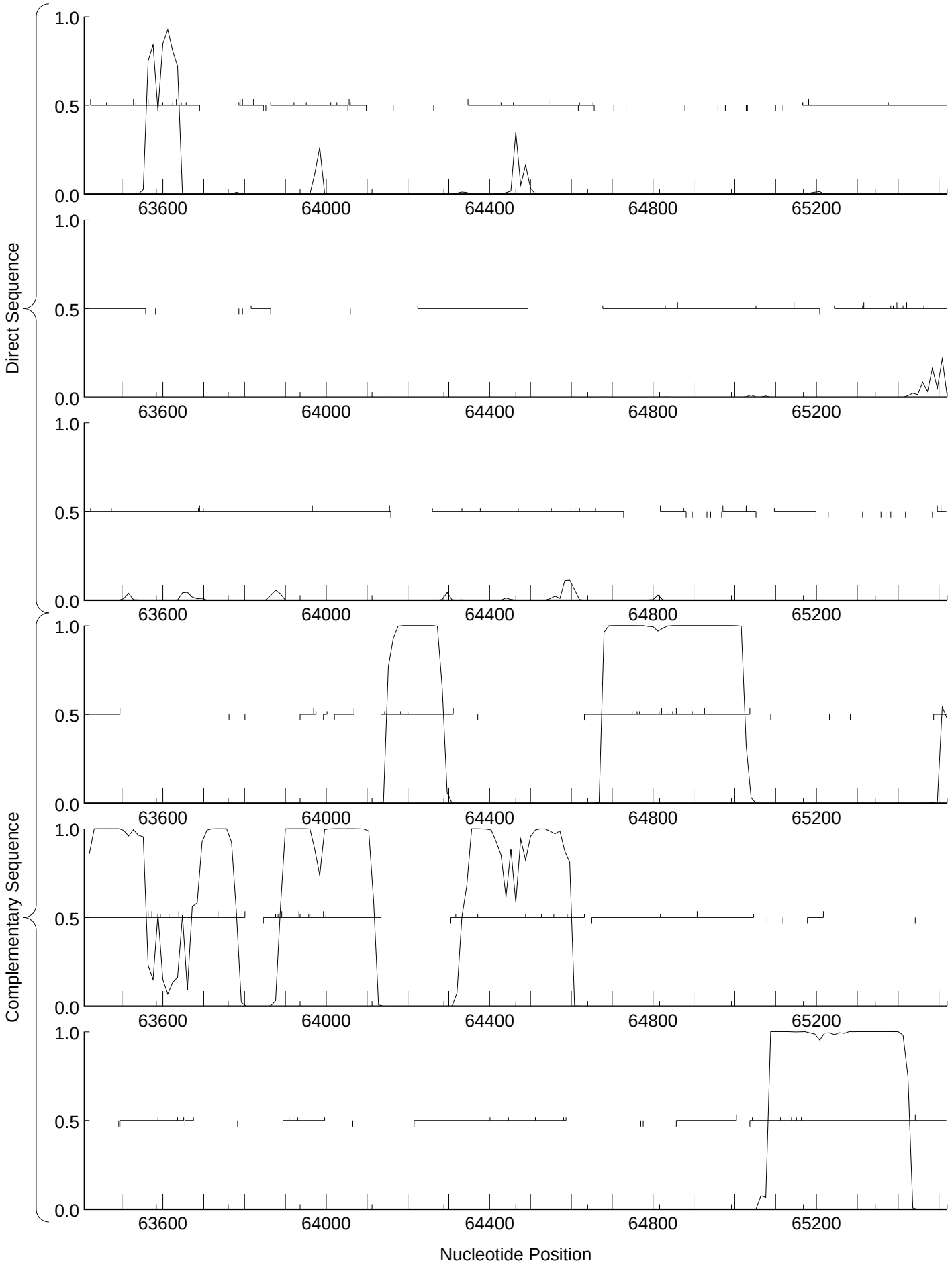

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Complementary Sequence
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56400
56800
Nucleotide Position

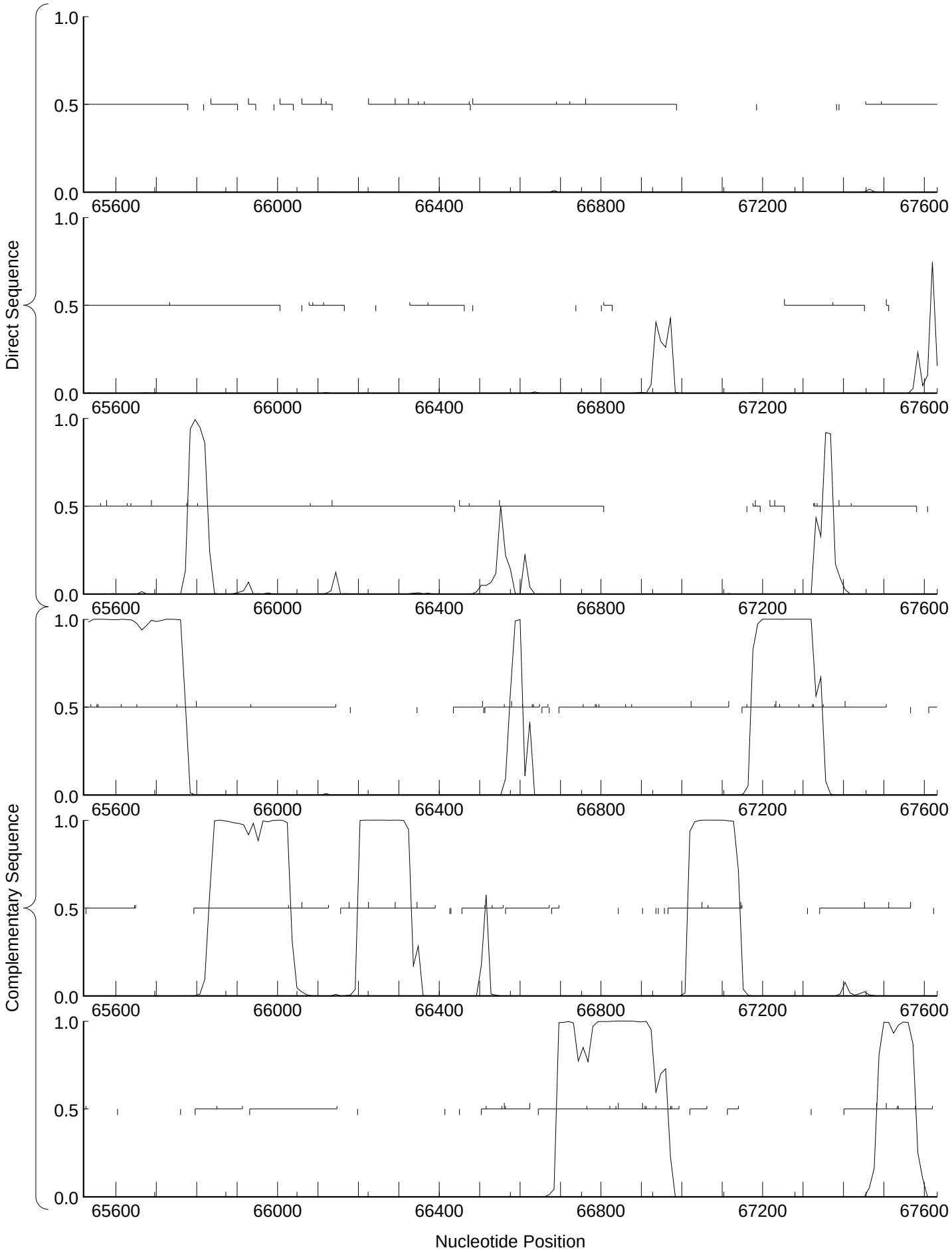

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Nucleotide Position

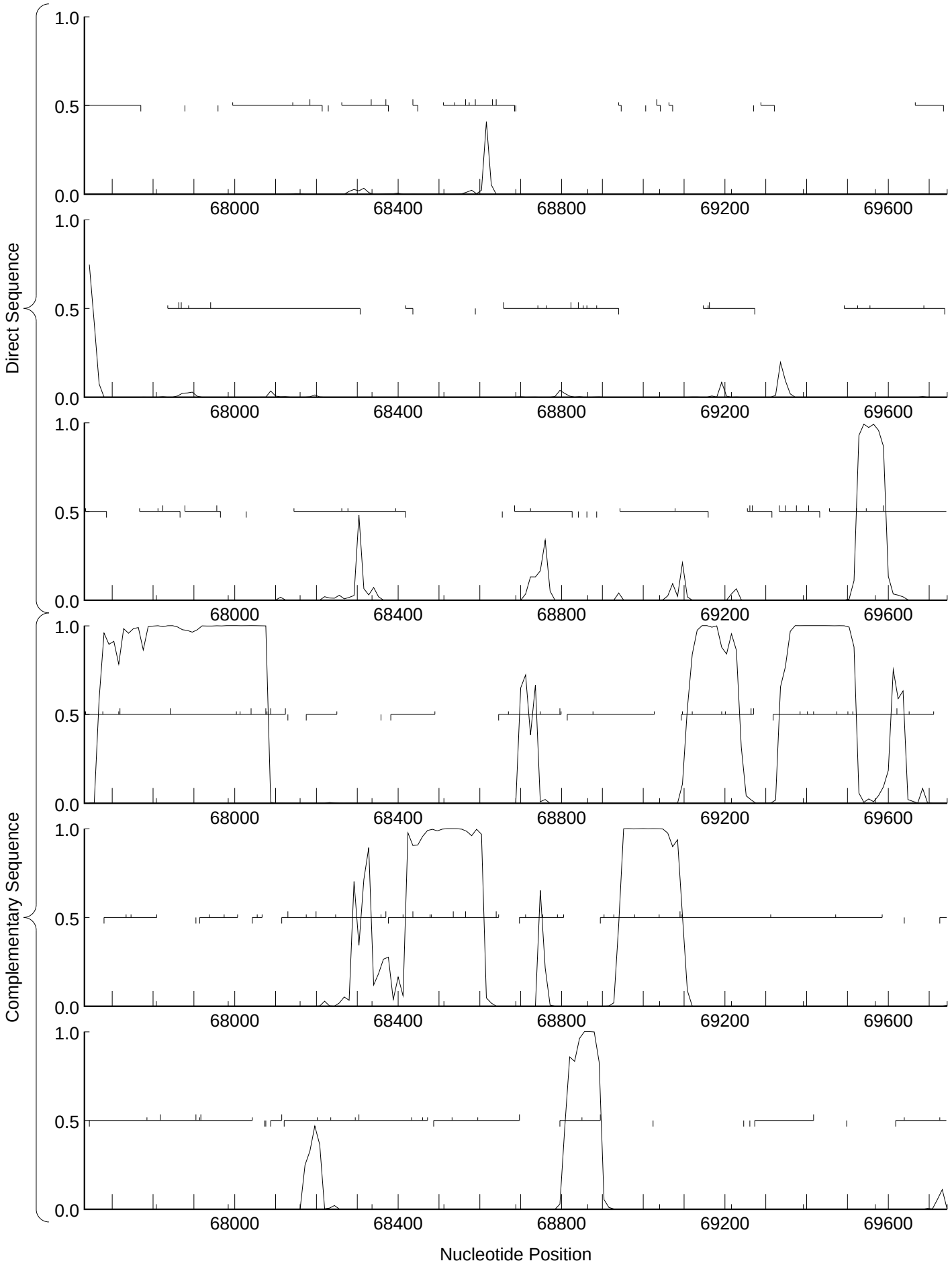
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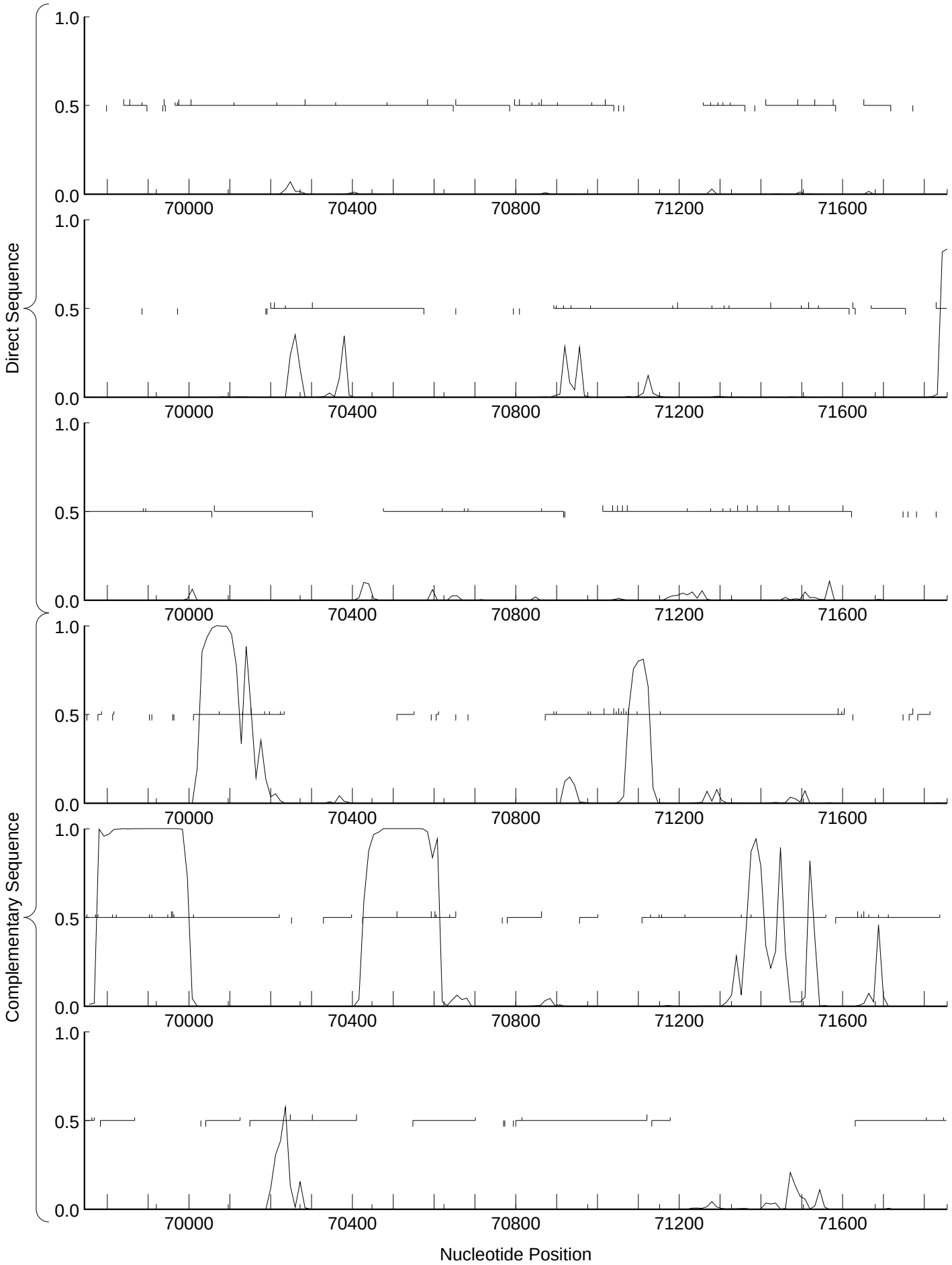



Direct Sequence
Complementary Sequence
1.0
0.5
0.0
61600
62000
62400
62800
63200
Nucleotide Position


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
63600
64000
64400
64800
65200
Nucleotide Position


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
65600
66000
66400
66800
67200
67600
Nucleotide Position


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
68000
68400
68800
69200
69600
Nucleotide Position


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
70000
70400
70800
71200
71600
Nucleotide Position

nage Ryadel complete sequence, 72658 bp including 4-base 3’ overhang (GTGT), Cluster O, Order 4, Window 96, Step 12, 36/36

