GeneMark

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

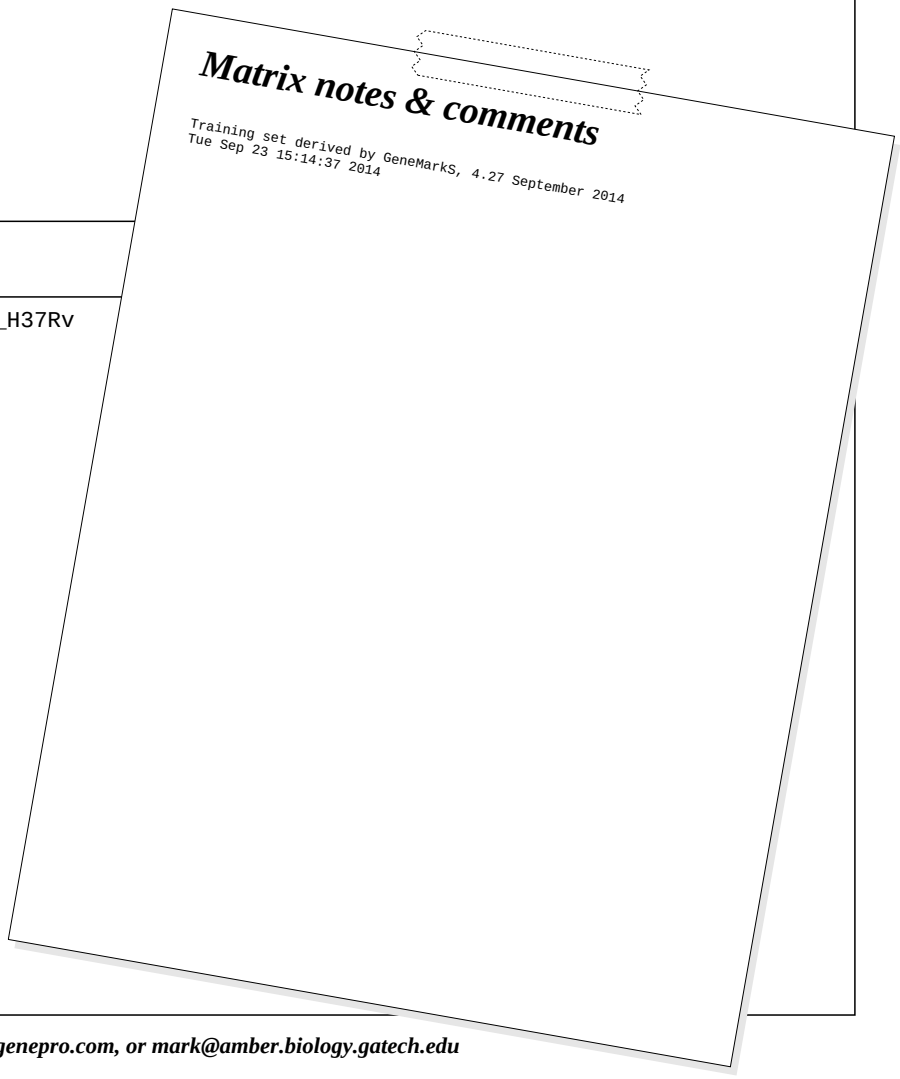
PROGRAM INFORMATION

```
Sequence         :  Mycobacterium phage Findley complete sequence, 58150 bp including 10-base 3’ overhang (CTCG
Analysis Date    :  3/29/24 at 8:46:39
Pages            :  29
Sequence Length  :  58150 bp
GC Content       :   68.34%

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

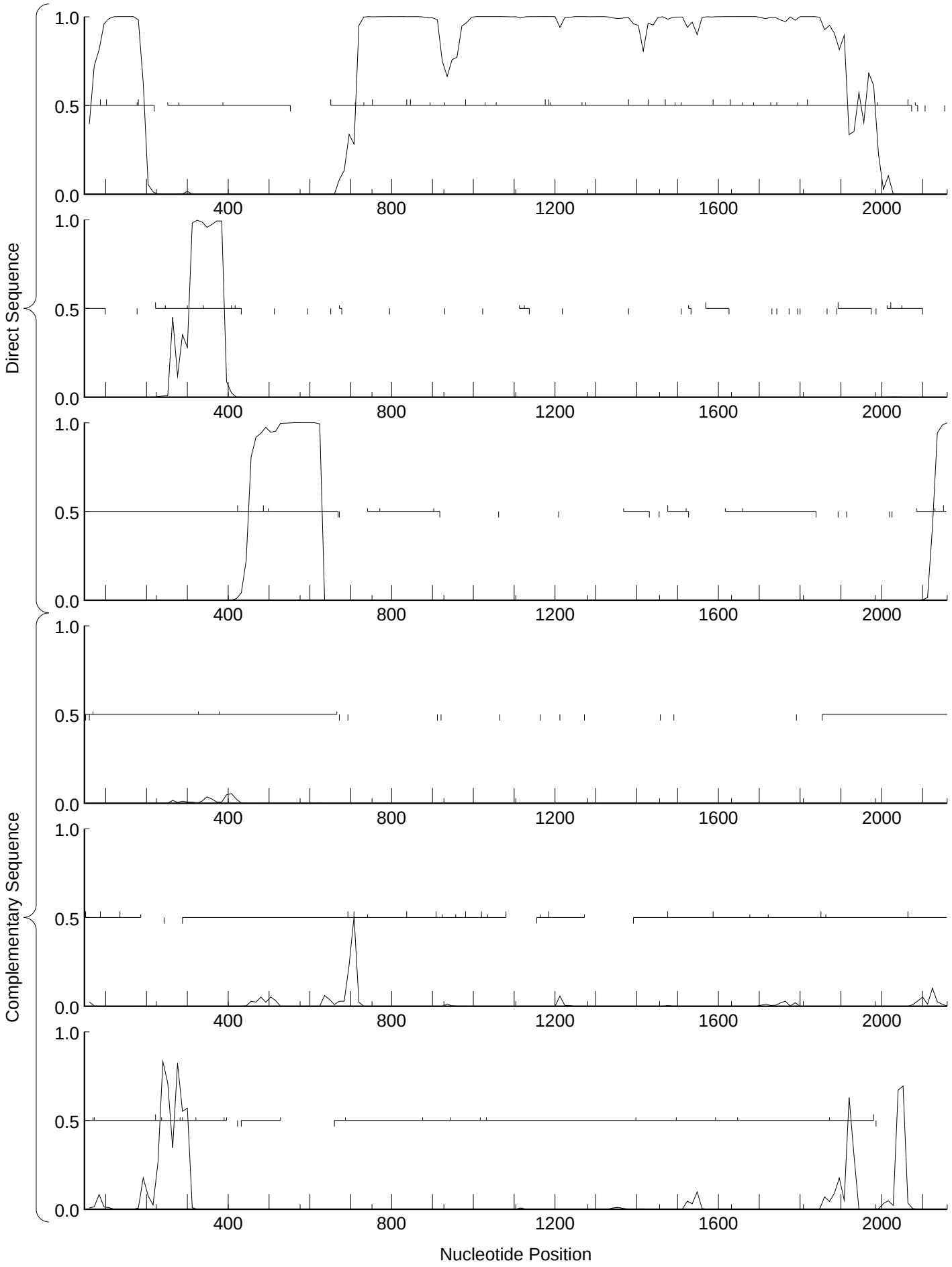
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Matrix     :  Mycobacterium_tuberculosis_H37Rv
Author     :  -

Order      :  4
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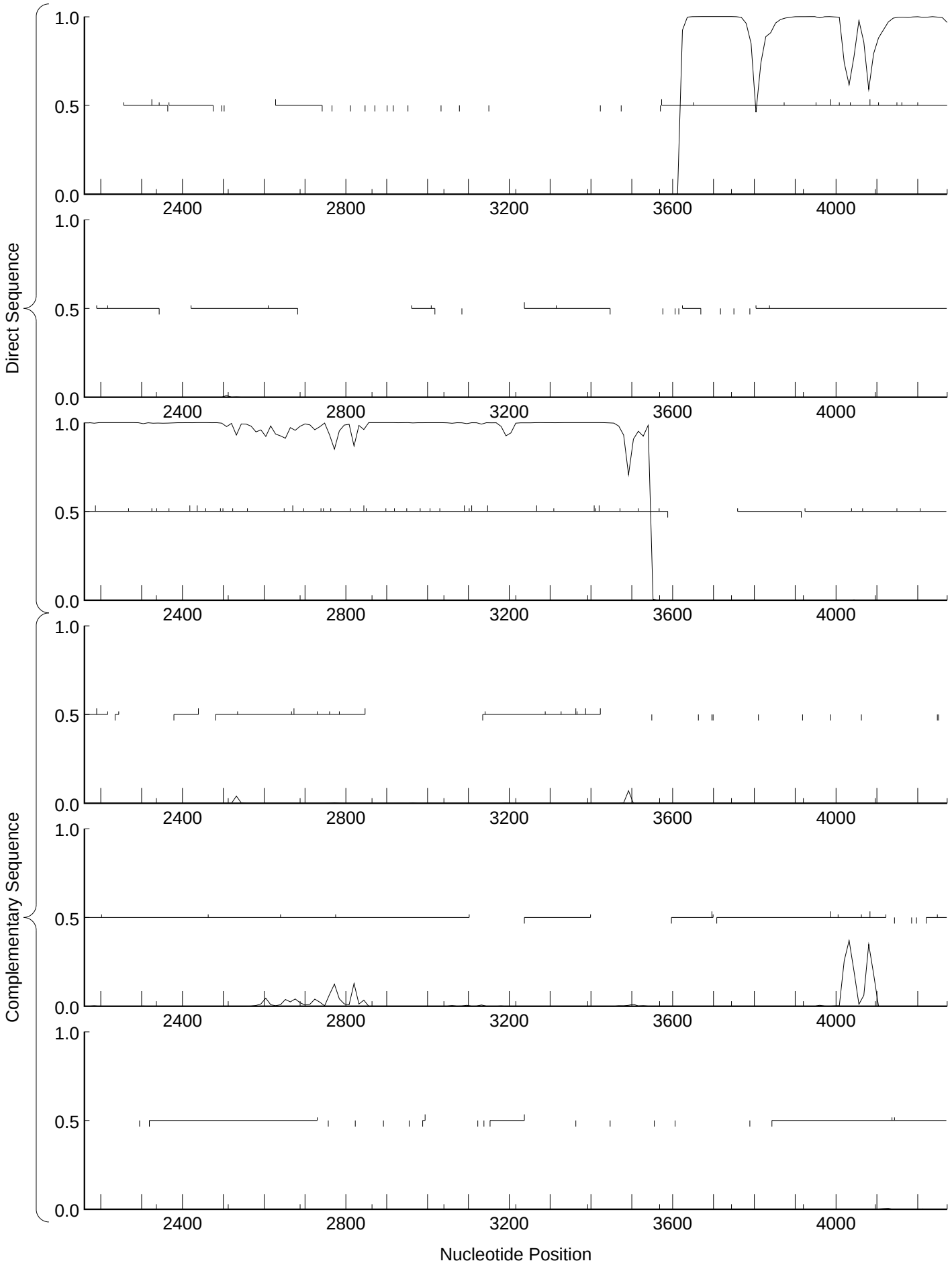

```
  Send questions / comments to:
      Dr. M. Borodovsky
      Georgia Institute of Technology
      School of Biology
      Atlanta, GA  30332-0230
```


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

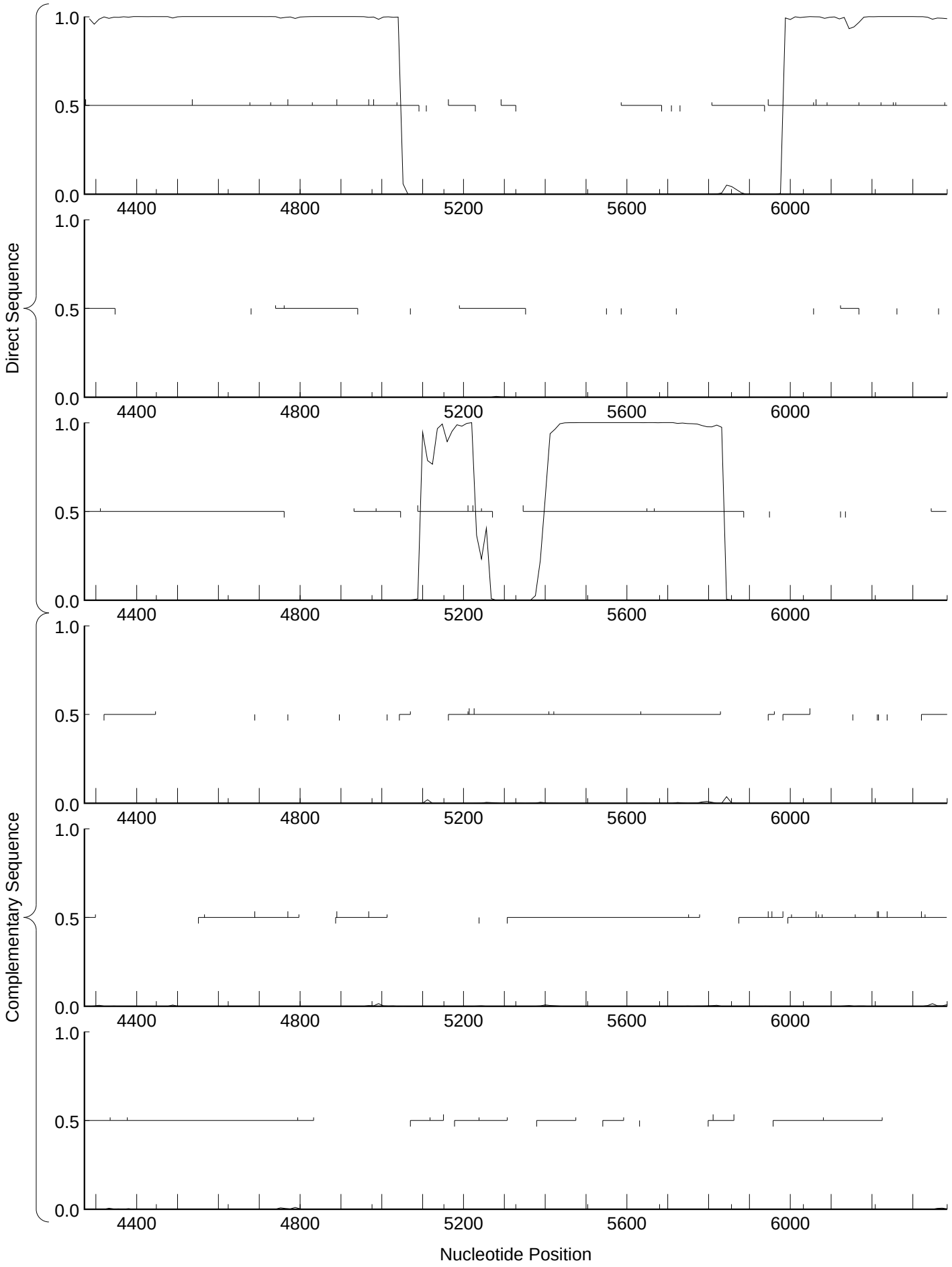
ey complete sequence, 58150 bp including 10-base 3’ overhang (CTCGCGGCAT), Cluster K2, Order 4, Window 96, Step 12, 2/29



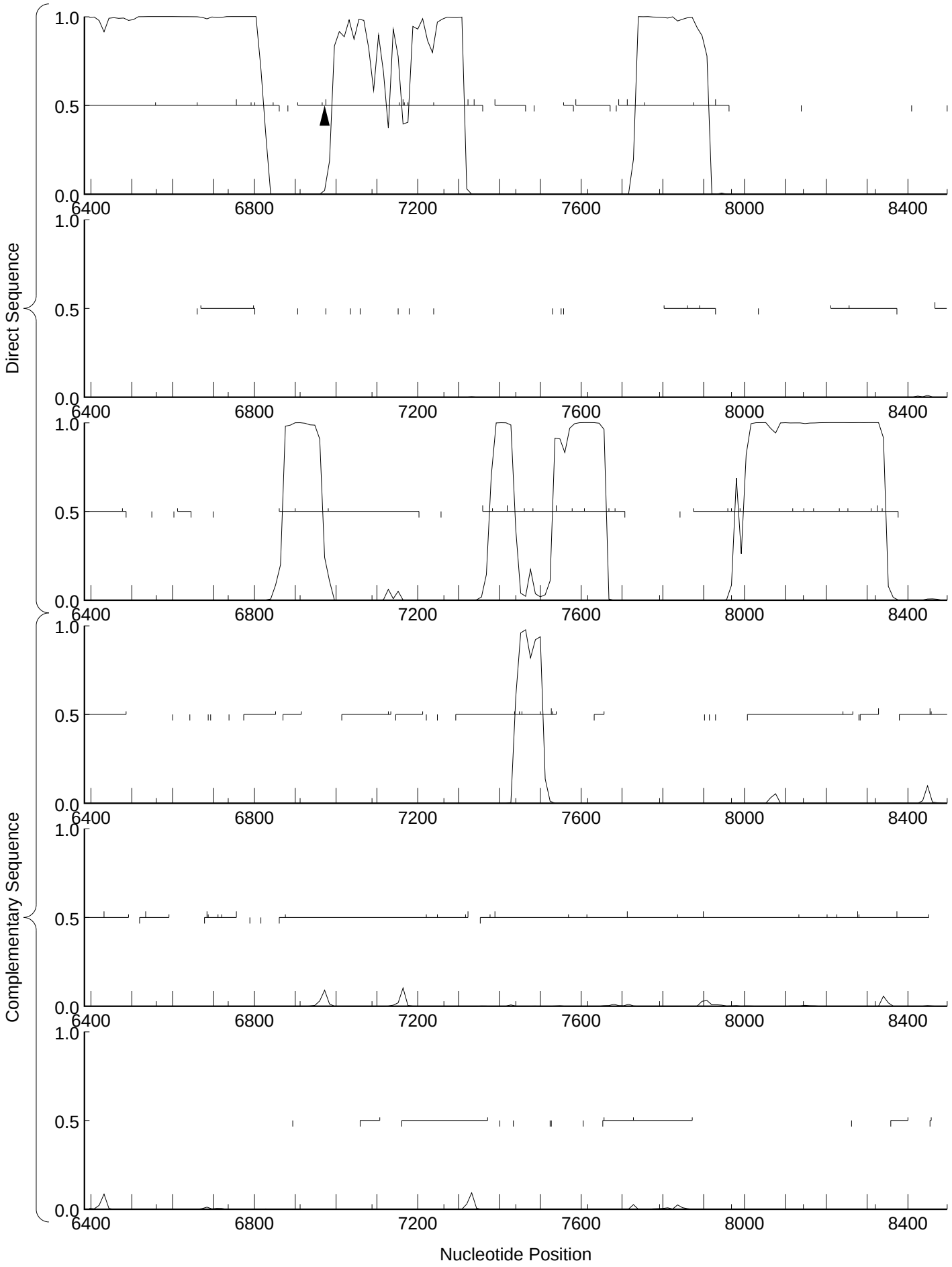
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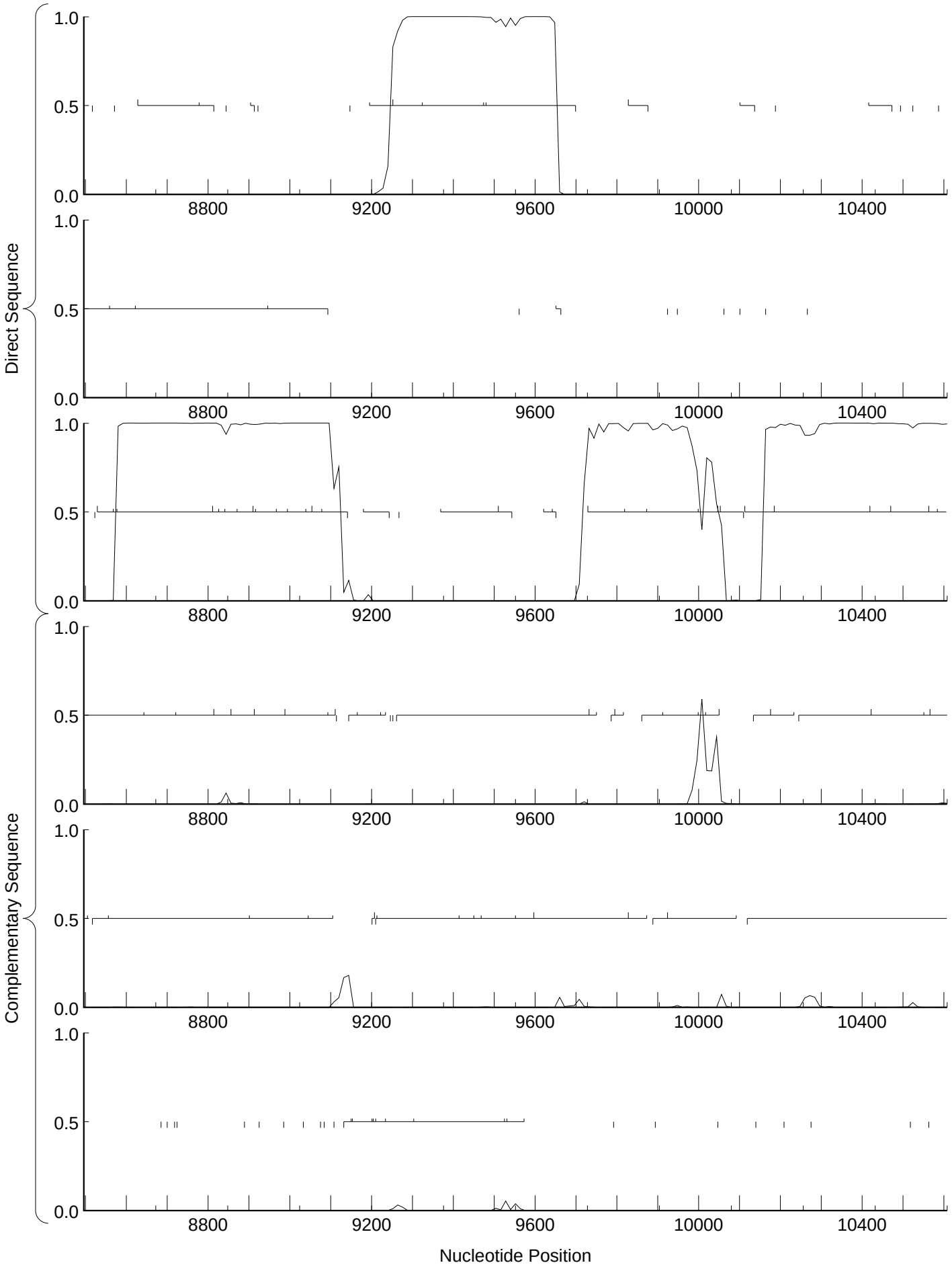
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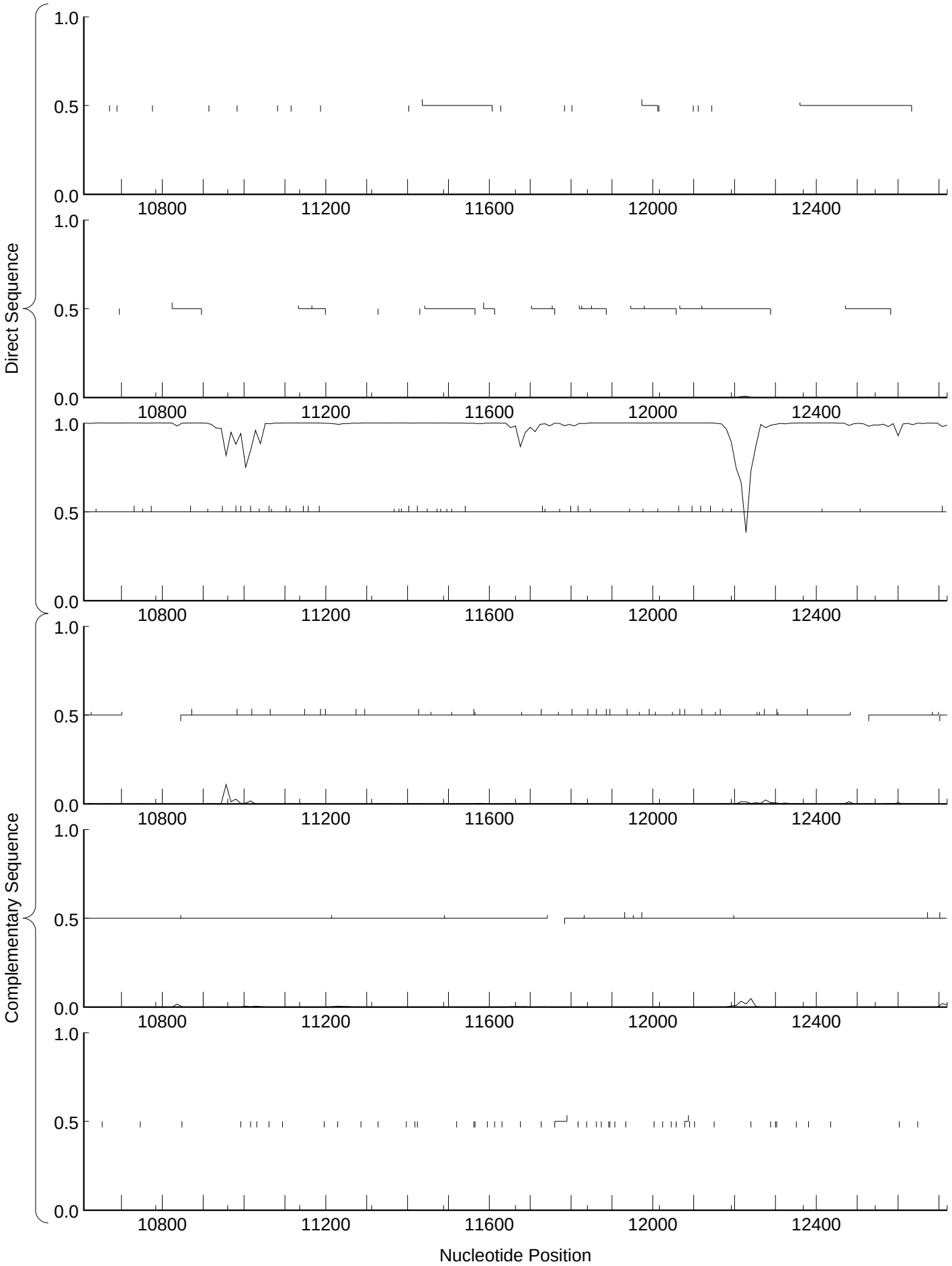
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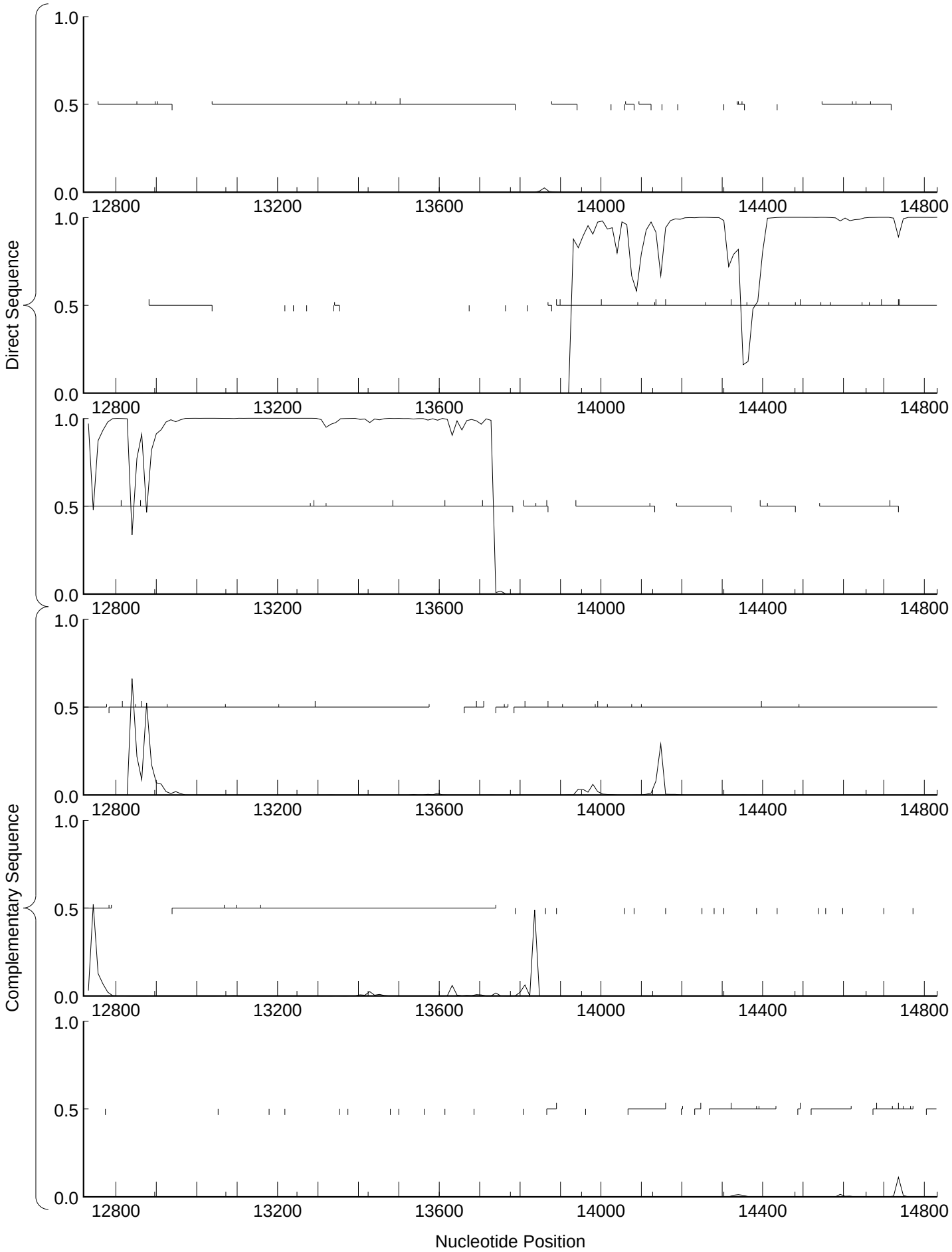
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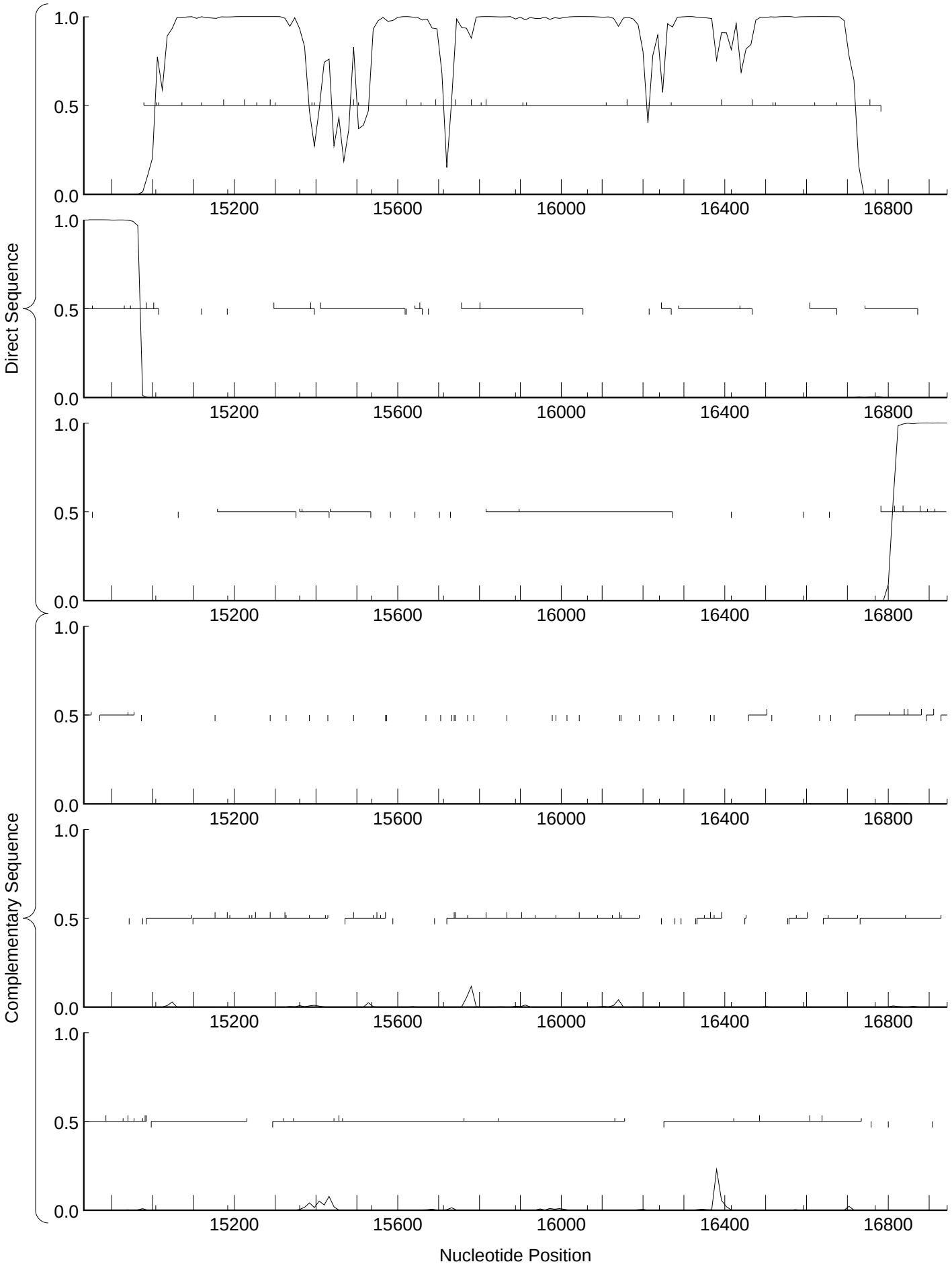
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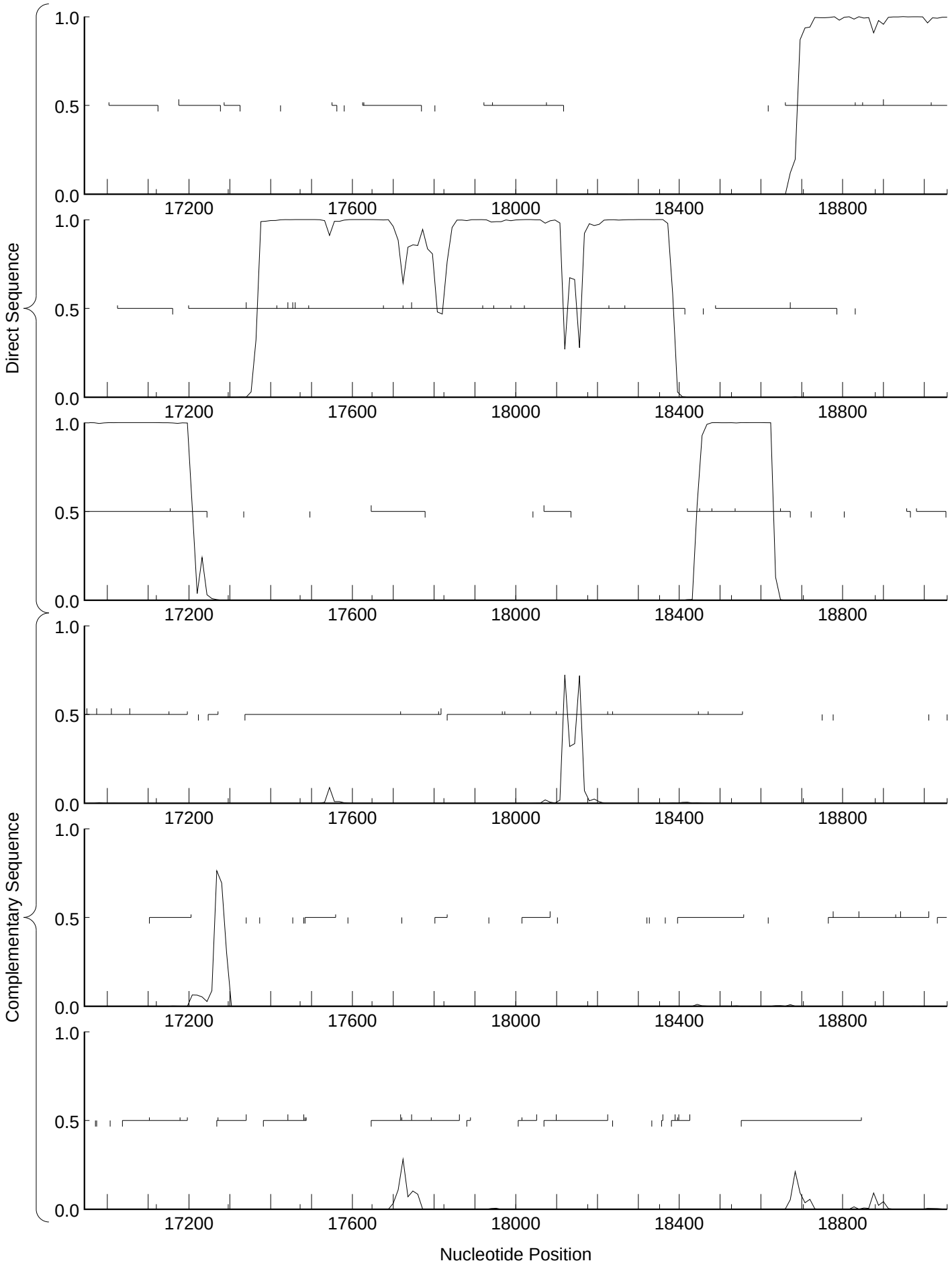


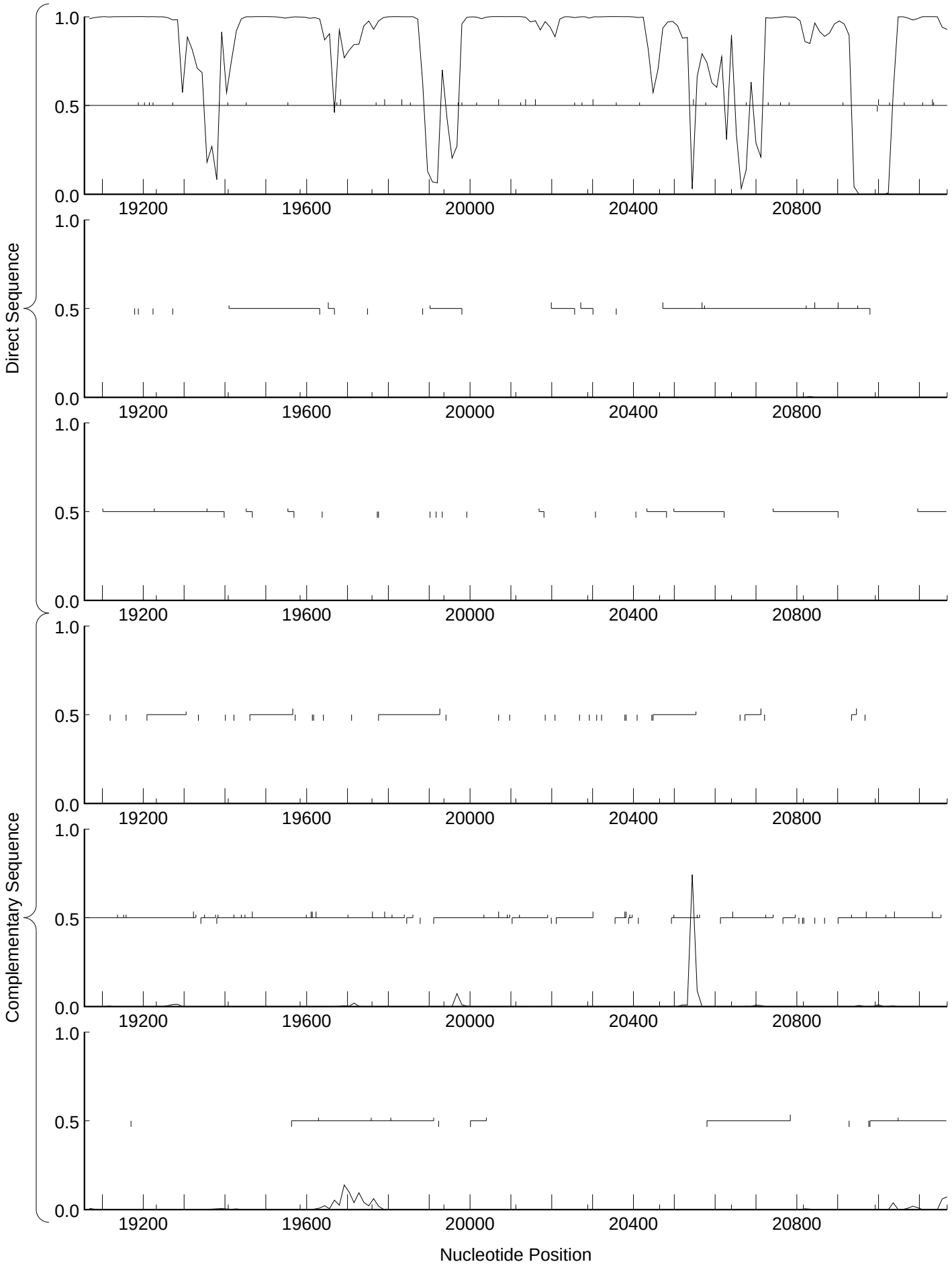
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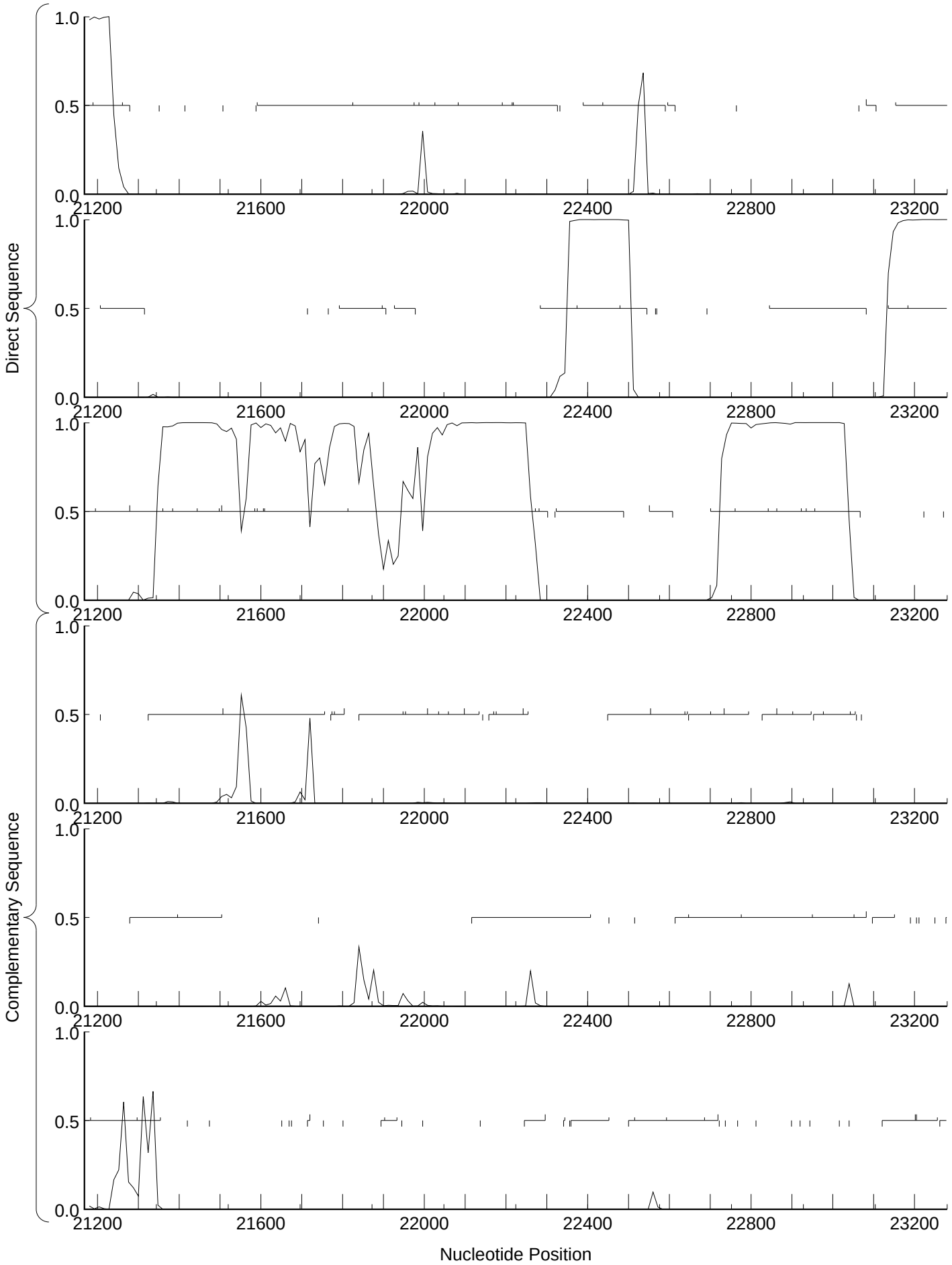


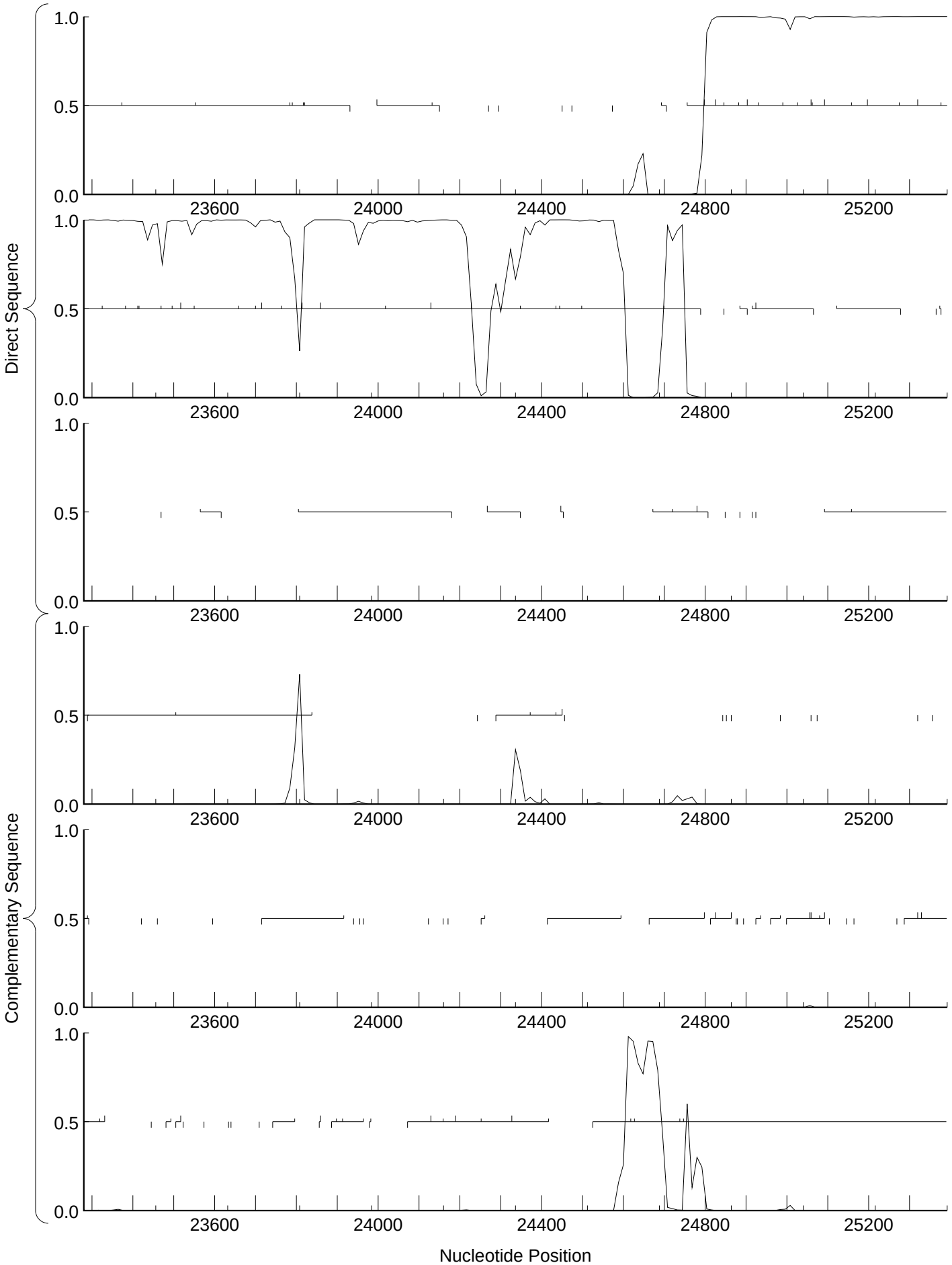
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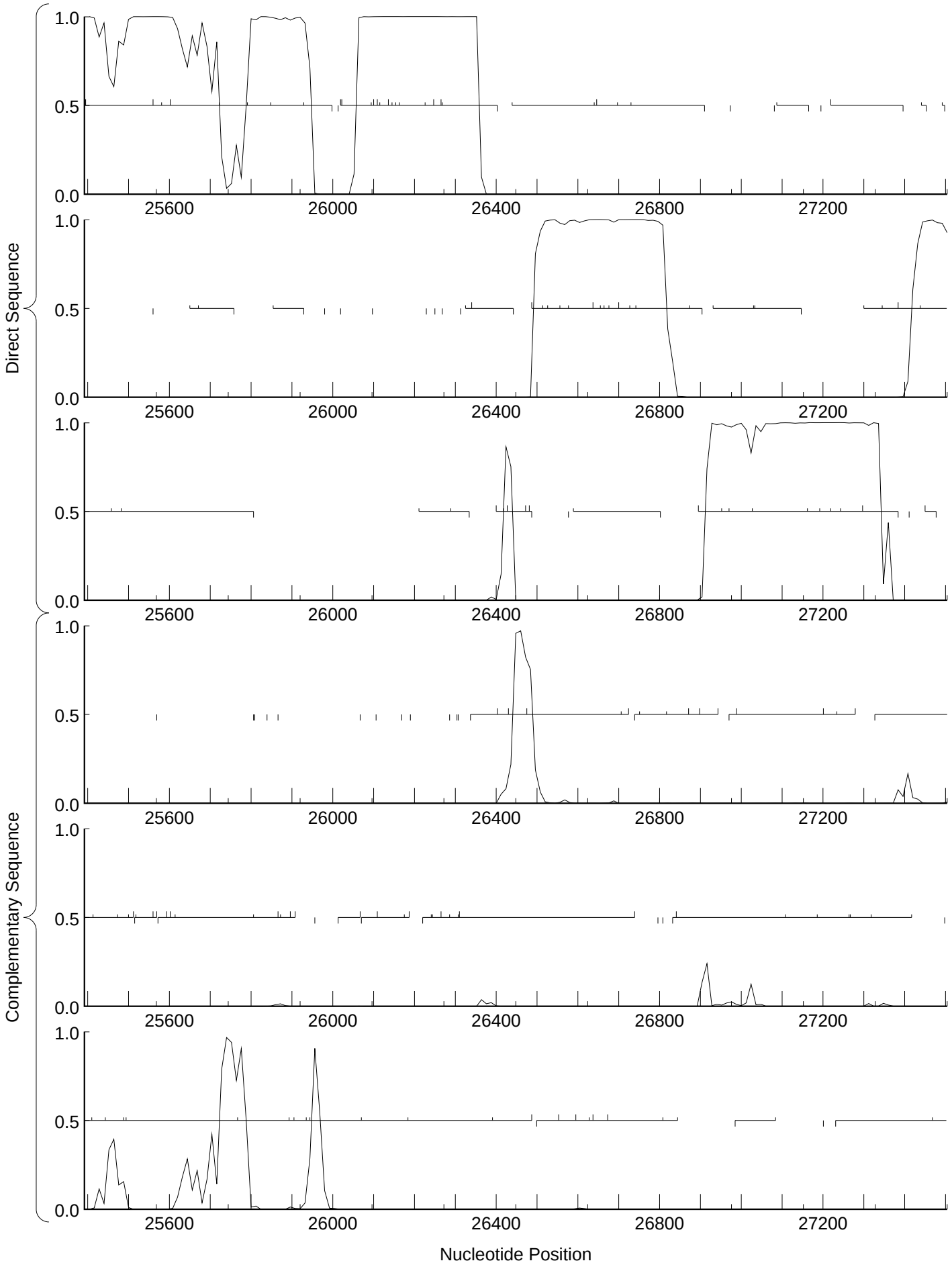


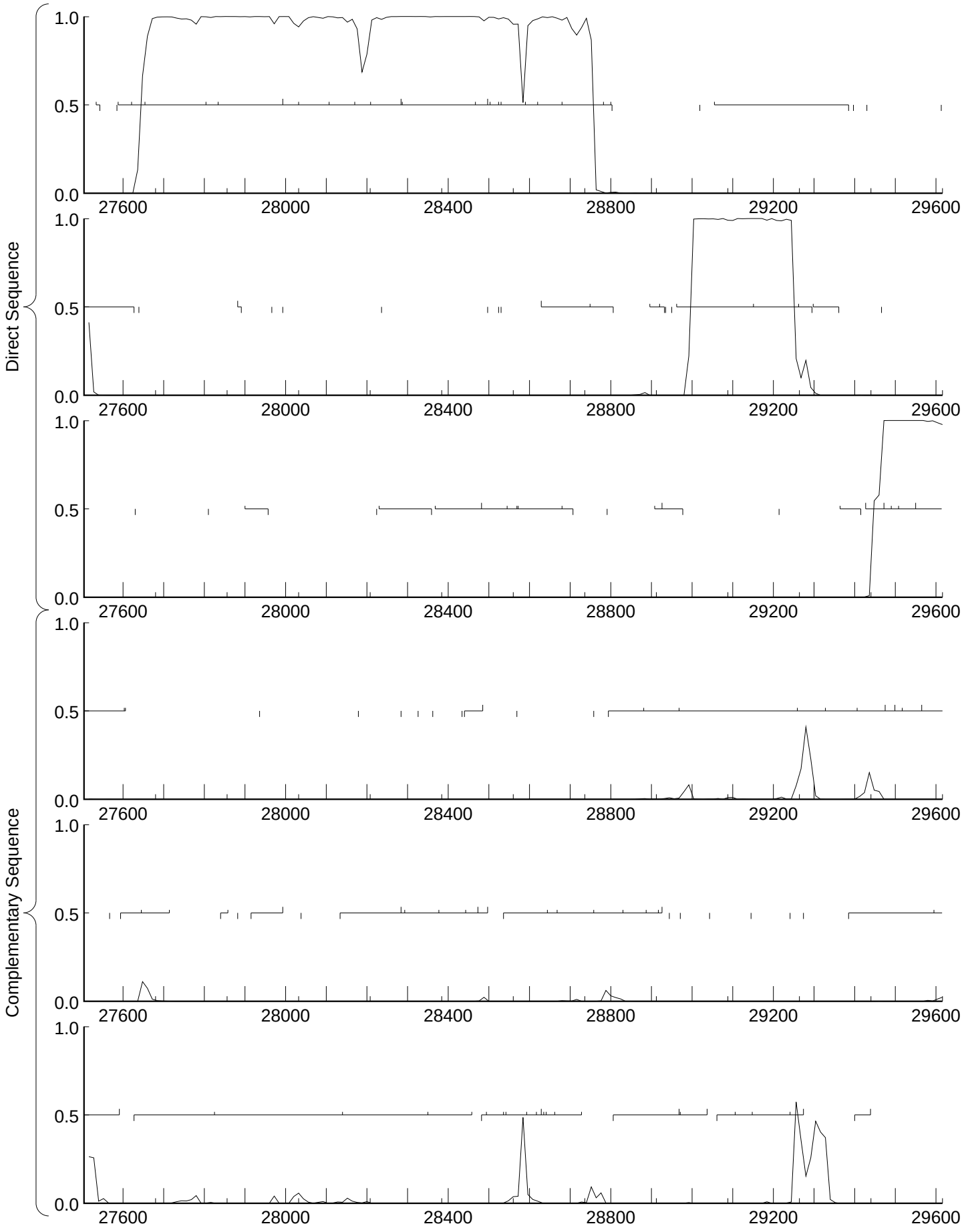

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Complementary Sequence
1.0
0.5
0.0
17200
17600
18000
18400
18800
Nucleotide Position

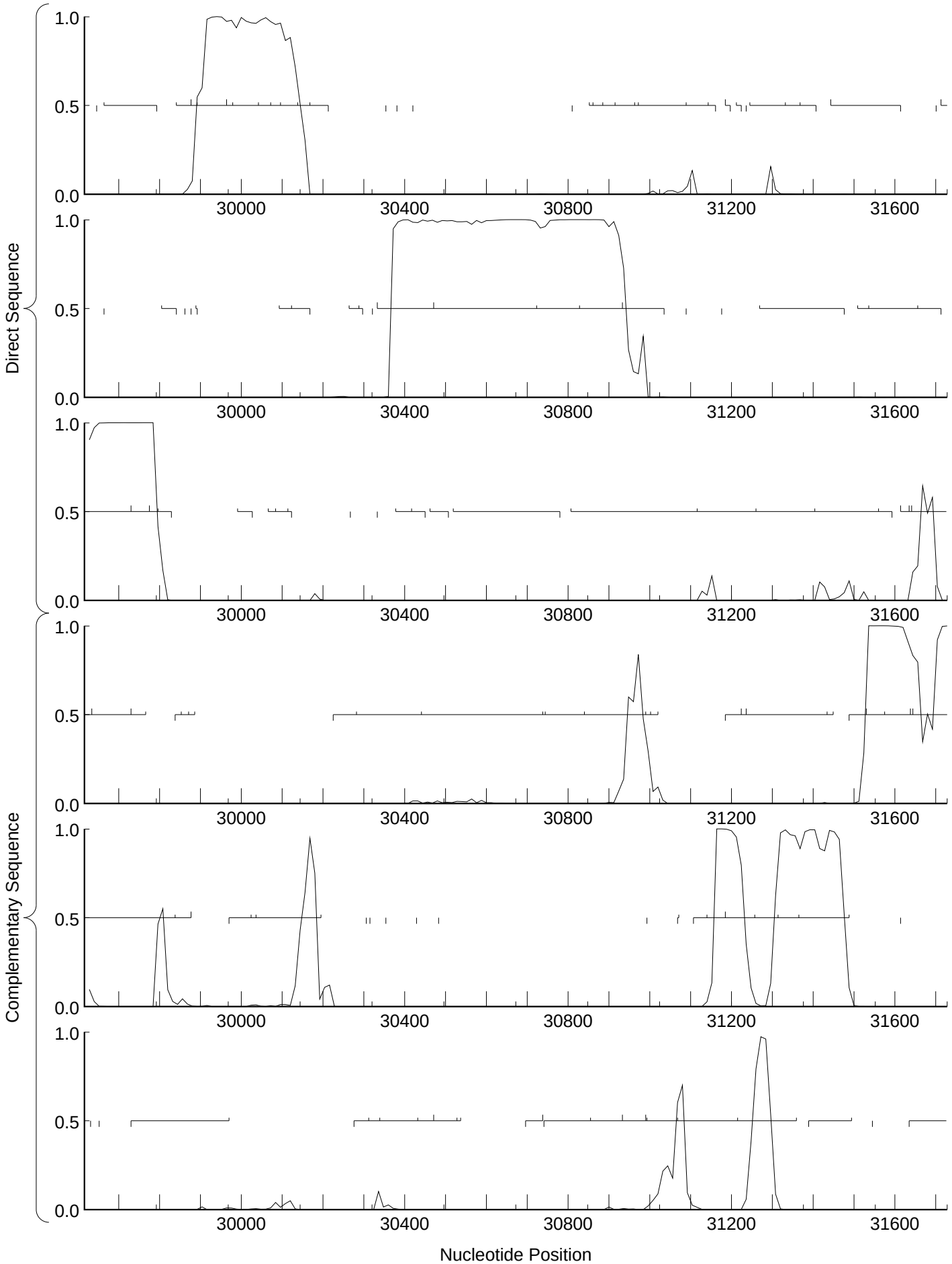

Direct Sequence
Complementary Sequence
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0.0
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19600
20000
20400
20800
Nucleotide Position

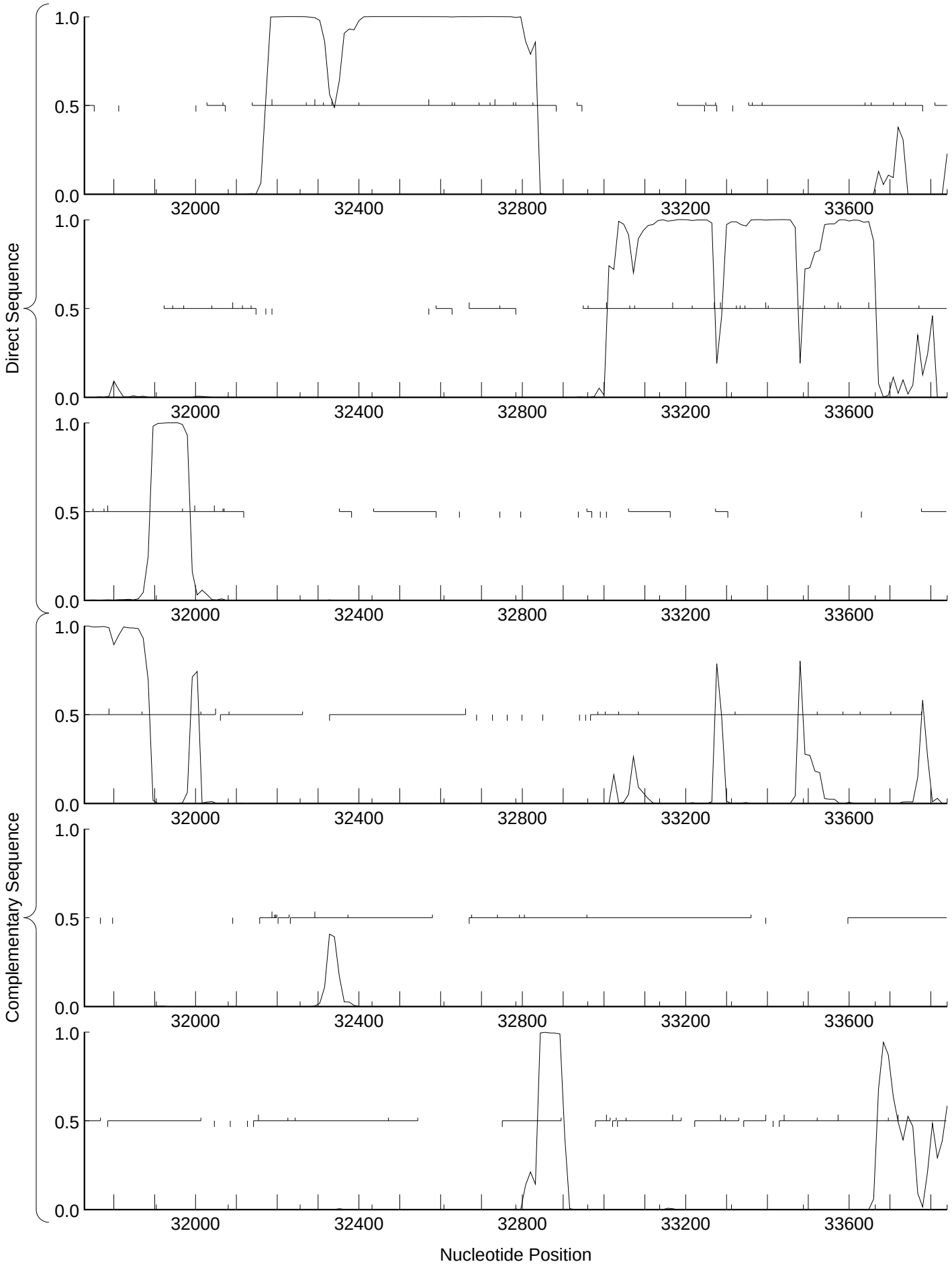

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Complementary Sequence
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21600
22000
22400
22800
23200
Nucleotide Position

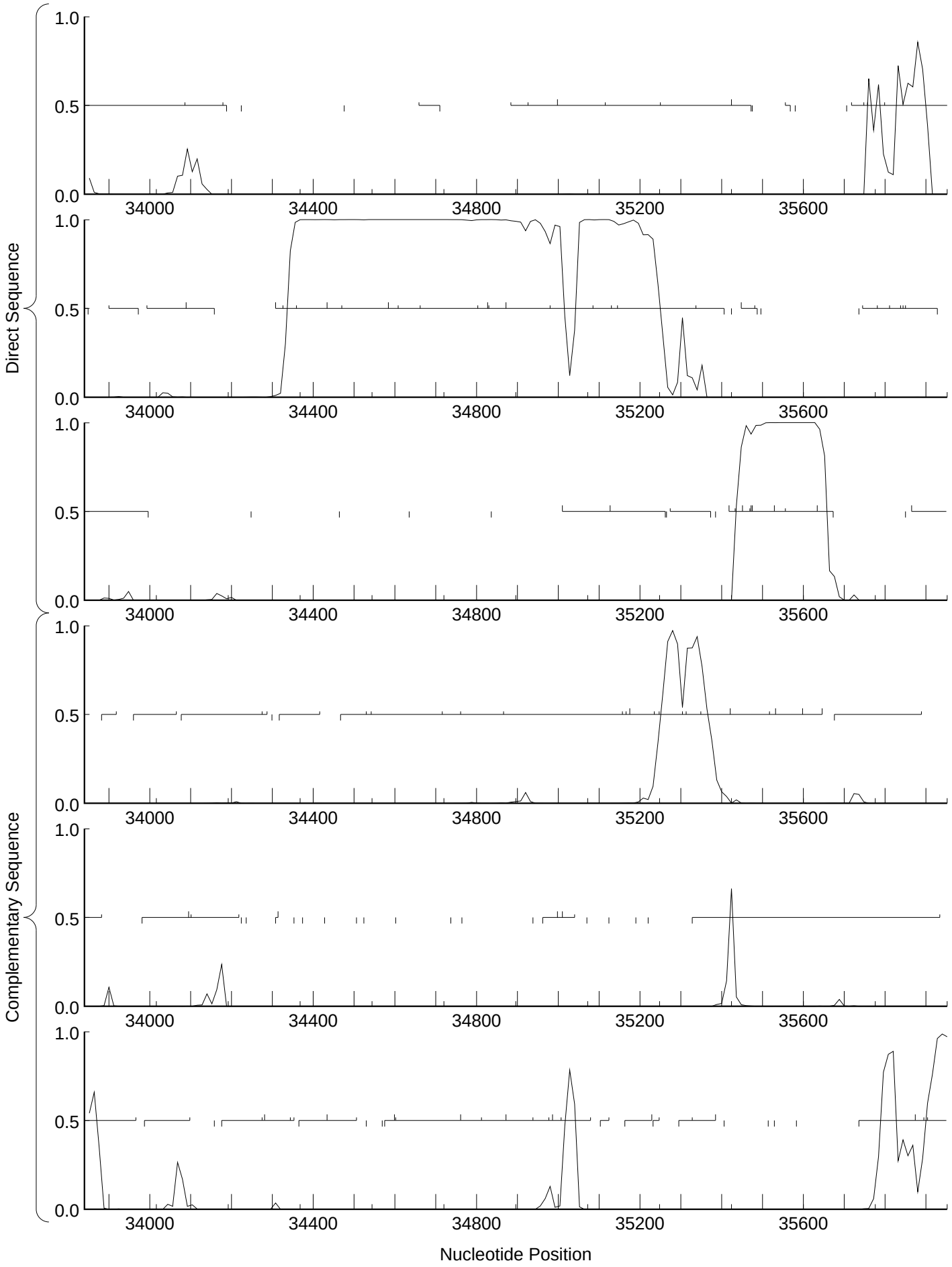

Direct Sequence
Complementary Sequence
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0.5
0.0
23600
24000
24400
24800
25200
Nucleotide Position

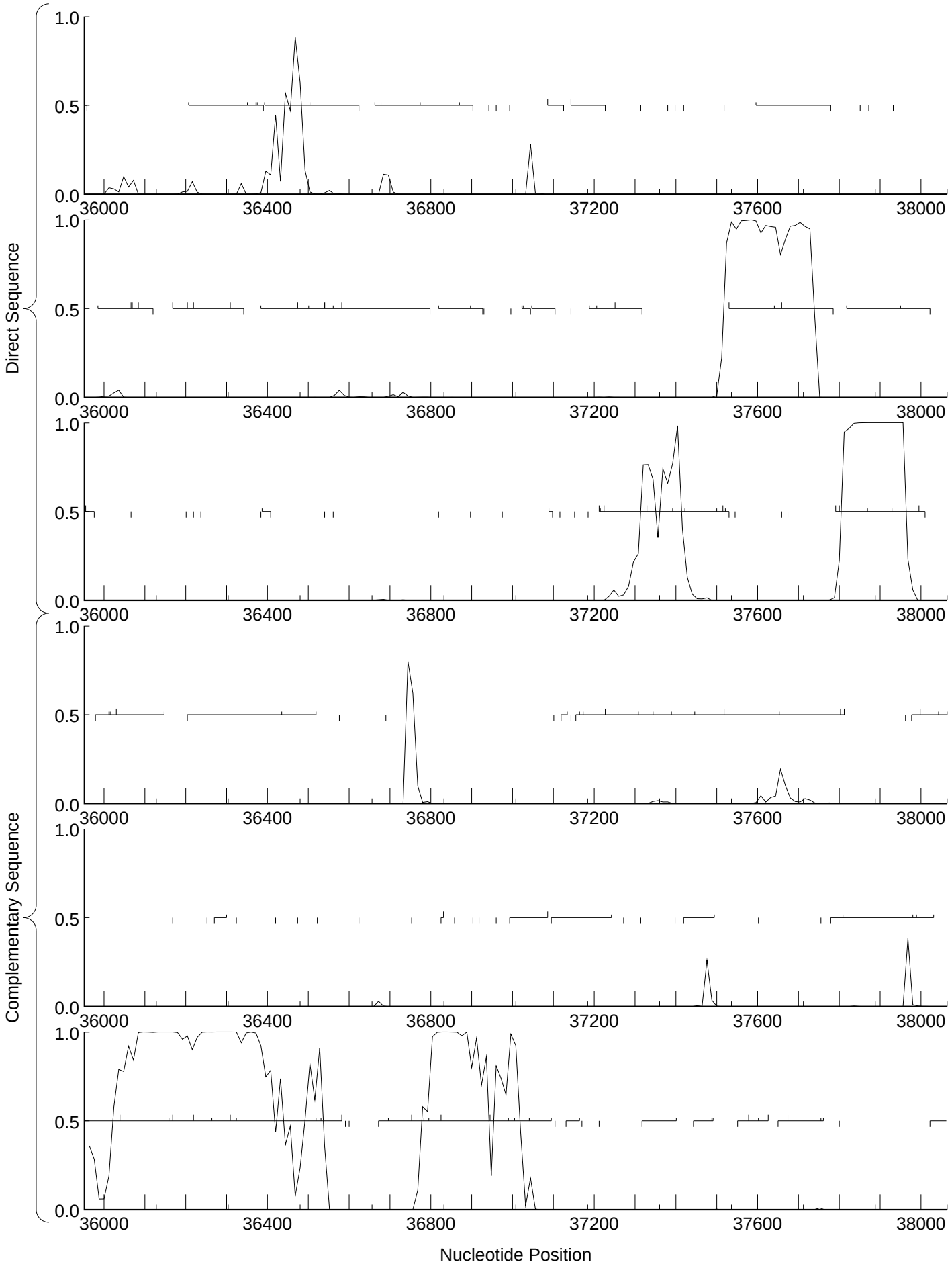

Direct Sequence
Complementary Sequence
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0.0
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26400
26800
27200
Nucleotide Position

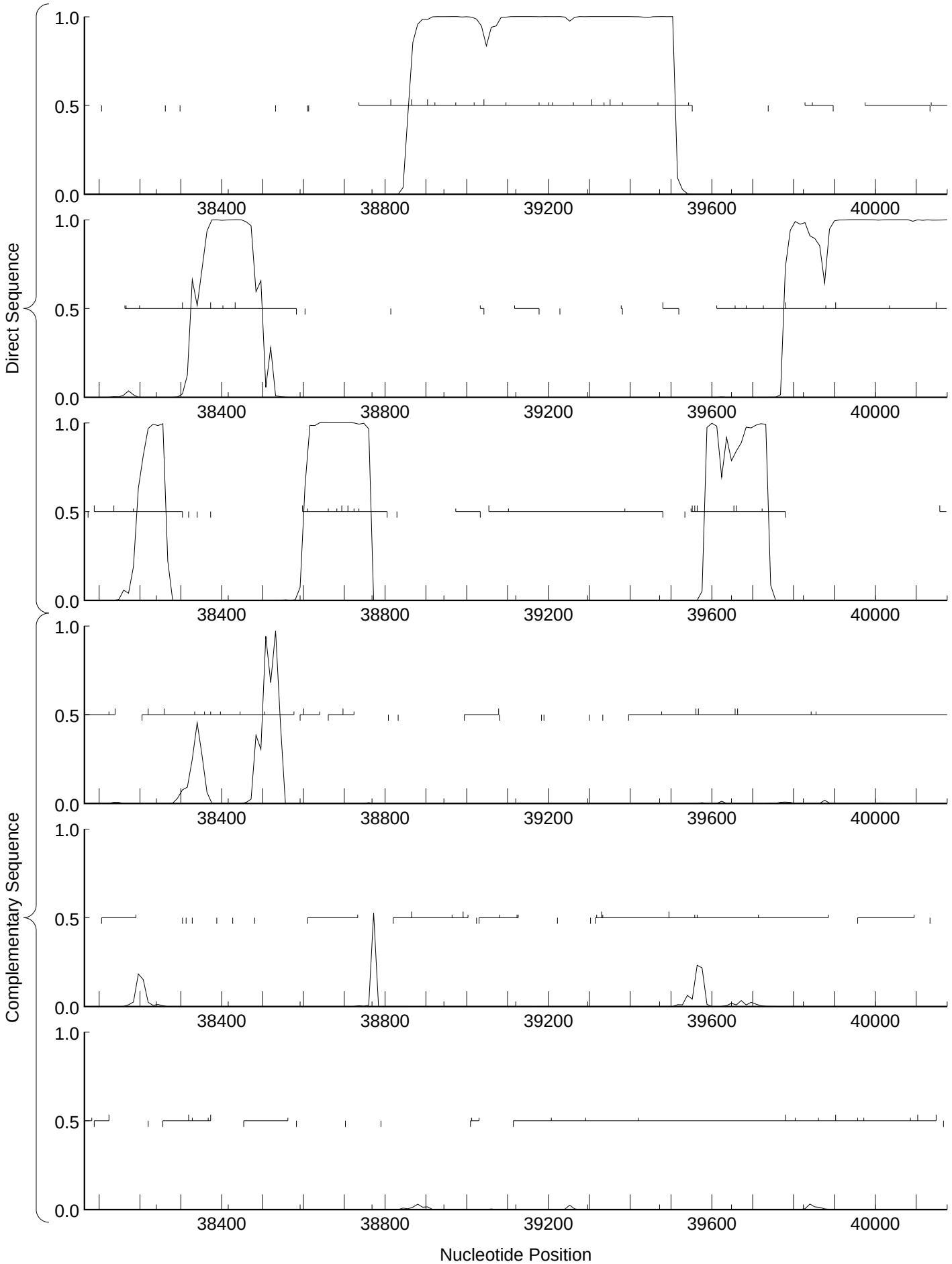

Direct Sequence
Complementary Sequence
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0.0
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29200
29600
Nucleotide Position

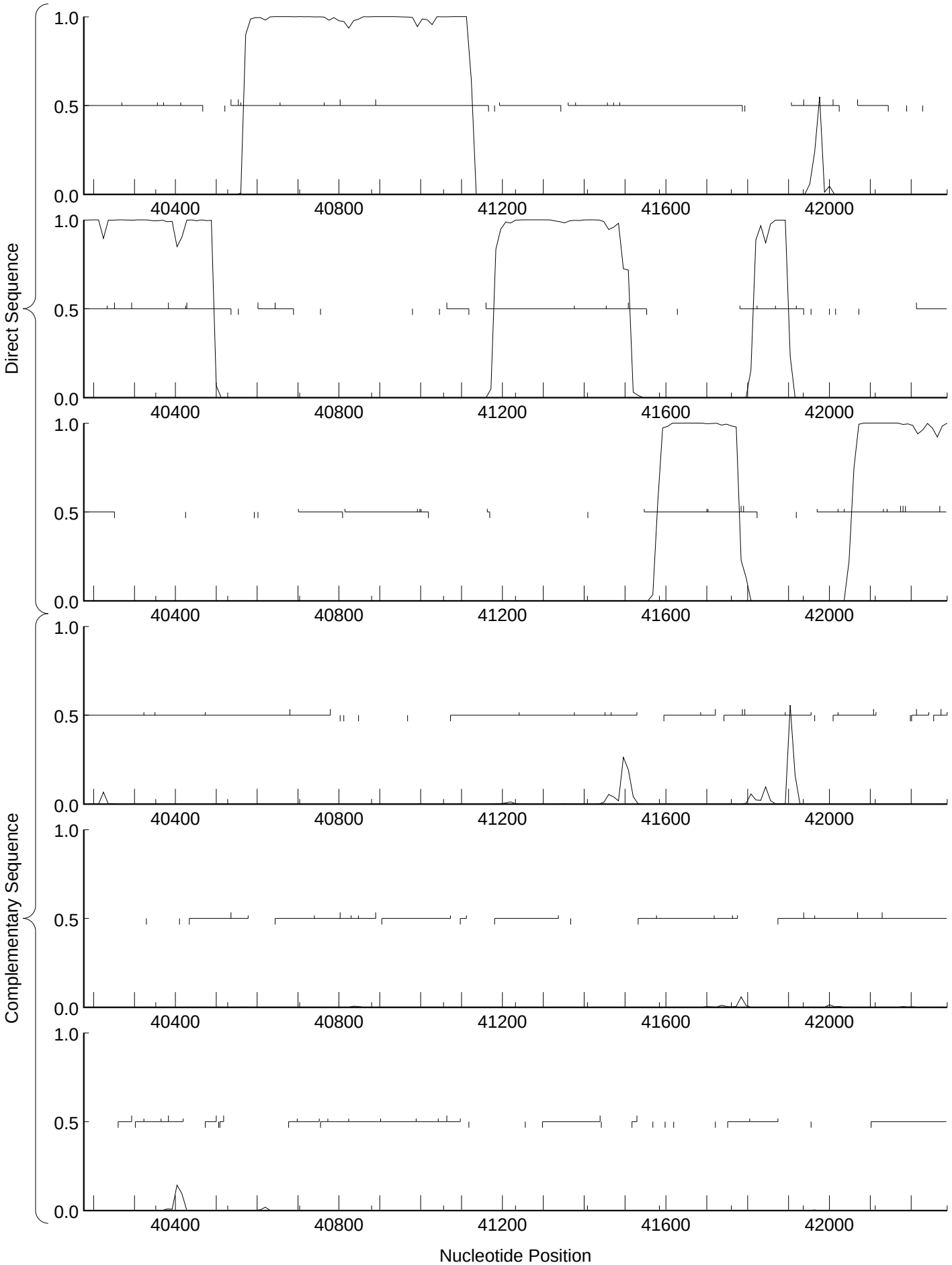

Direct Sequence
Complementary Sequence
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0.0
30000
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31200
31600
Nucleotide Position

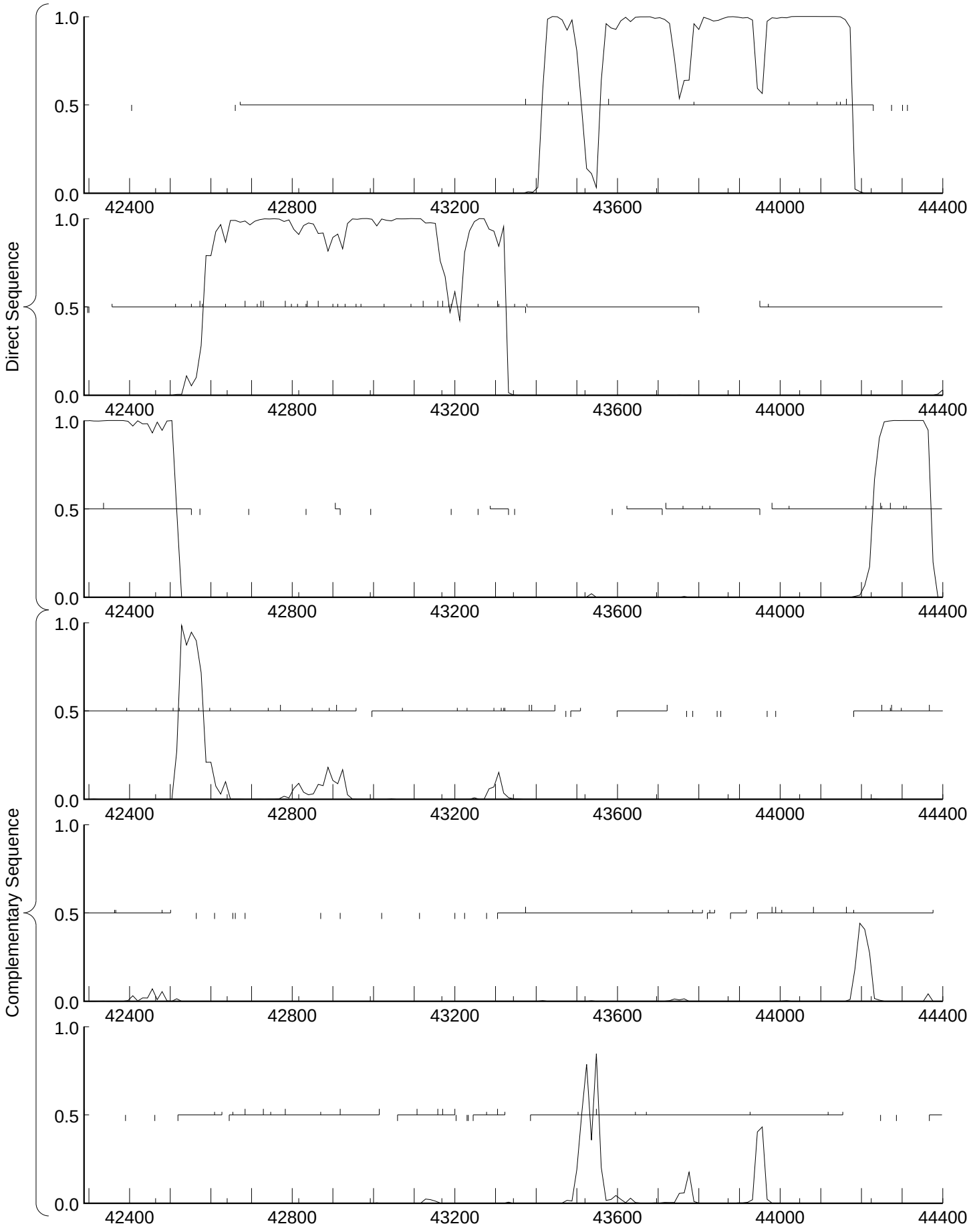

Direct Sequence
Complementary Sequence
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32800
33200
33600
Nucleotide Position

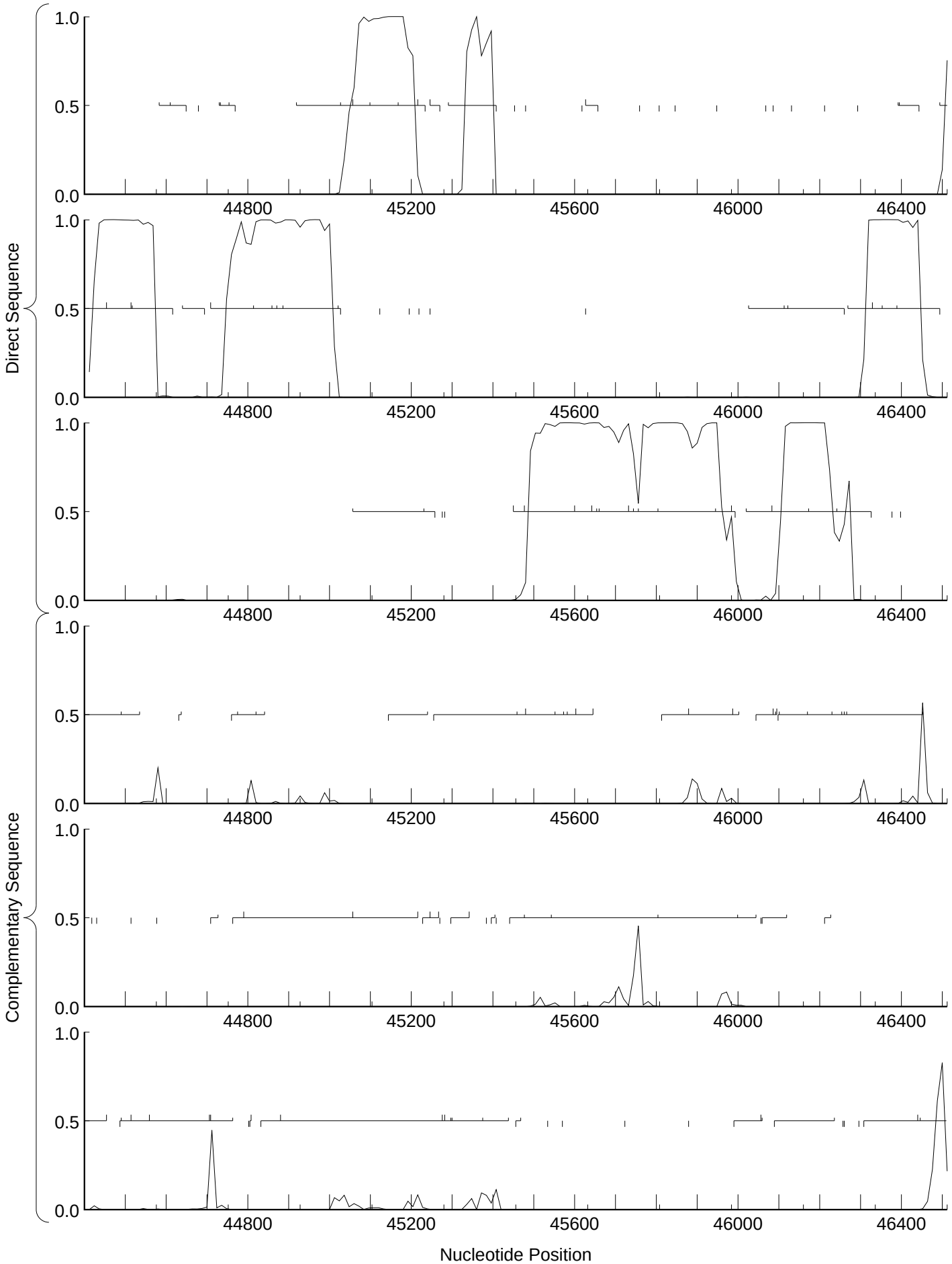

Direct Sequence
Complementary Sequence
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0.0
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34400
34800
35200
35600
Nucleotide Position

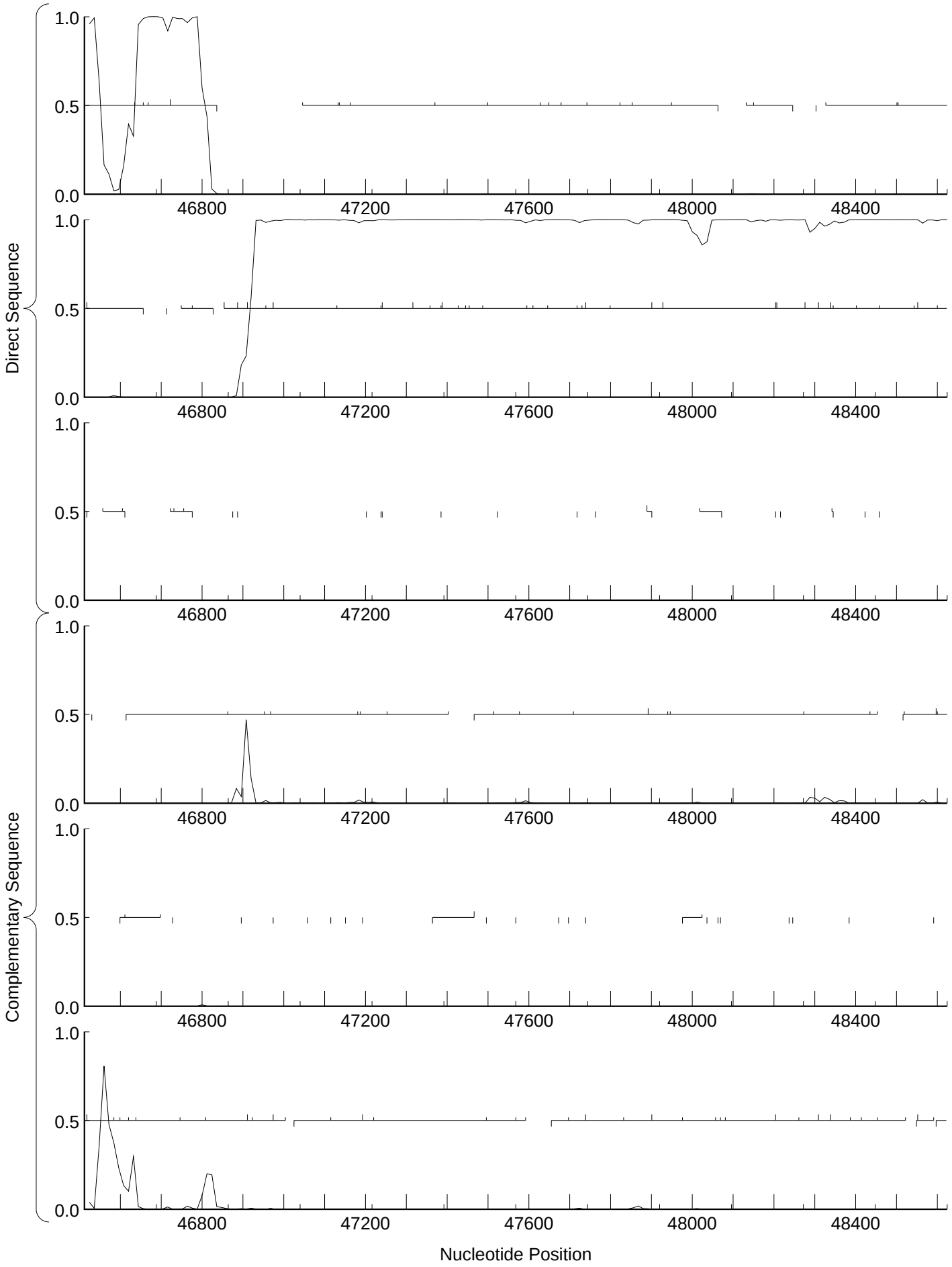

Direct Sequence
Complementary Sequence
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0.0
36000
36400
36800
37200
37600
38000
Nucleotide Position

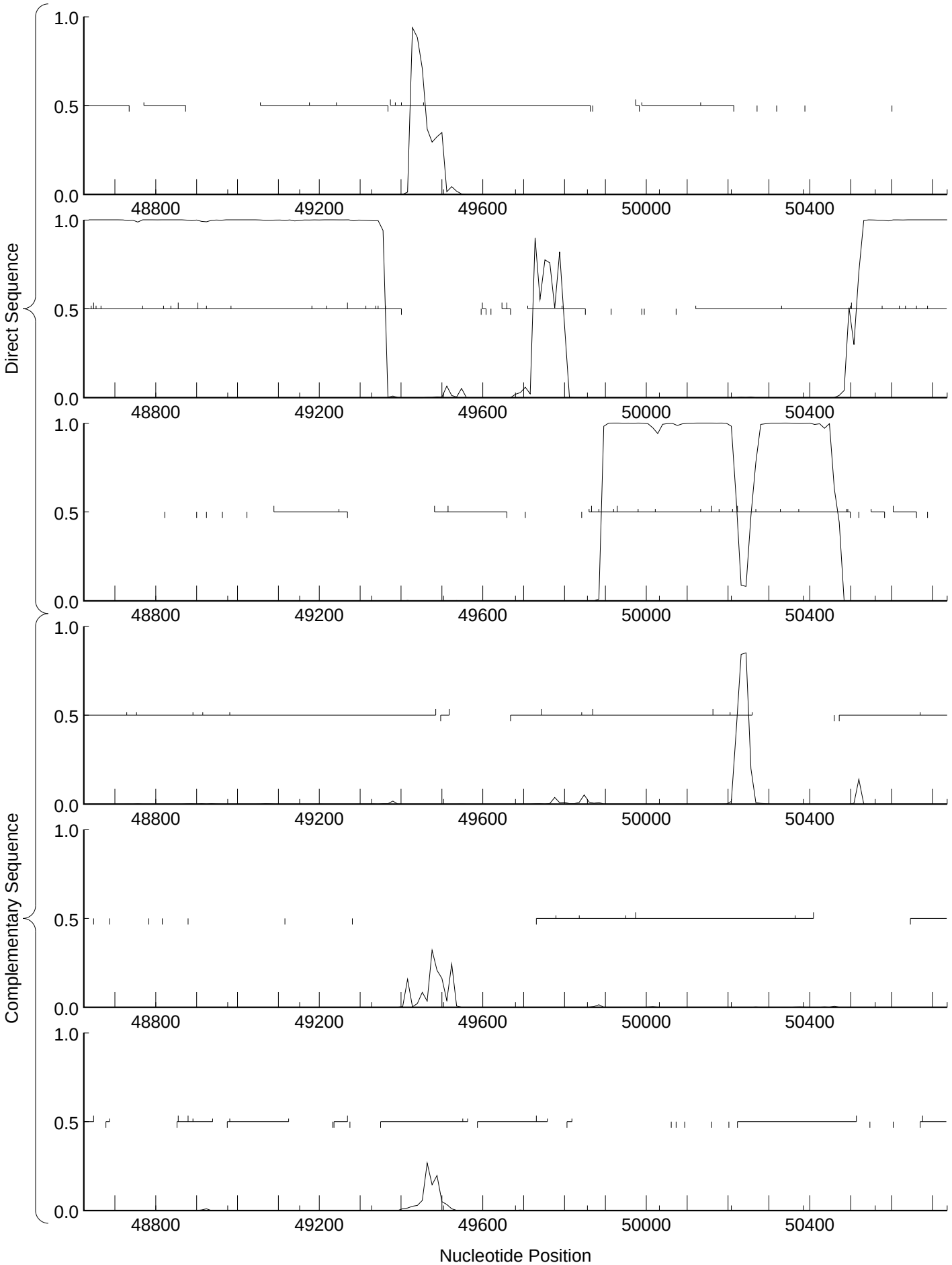

Direct Sequence
Complementary Sequence
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0.5
0.0
38400
38800
39200
39600
40000
Nucleotide Position

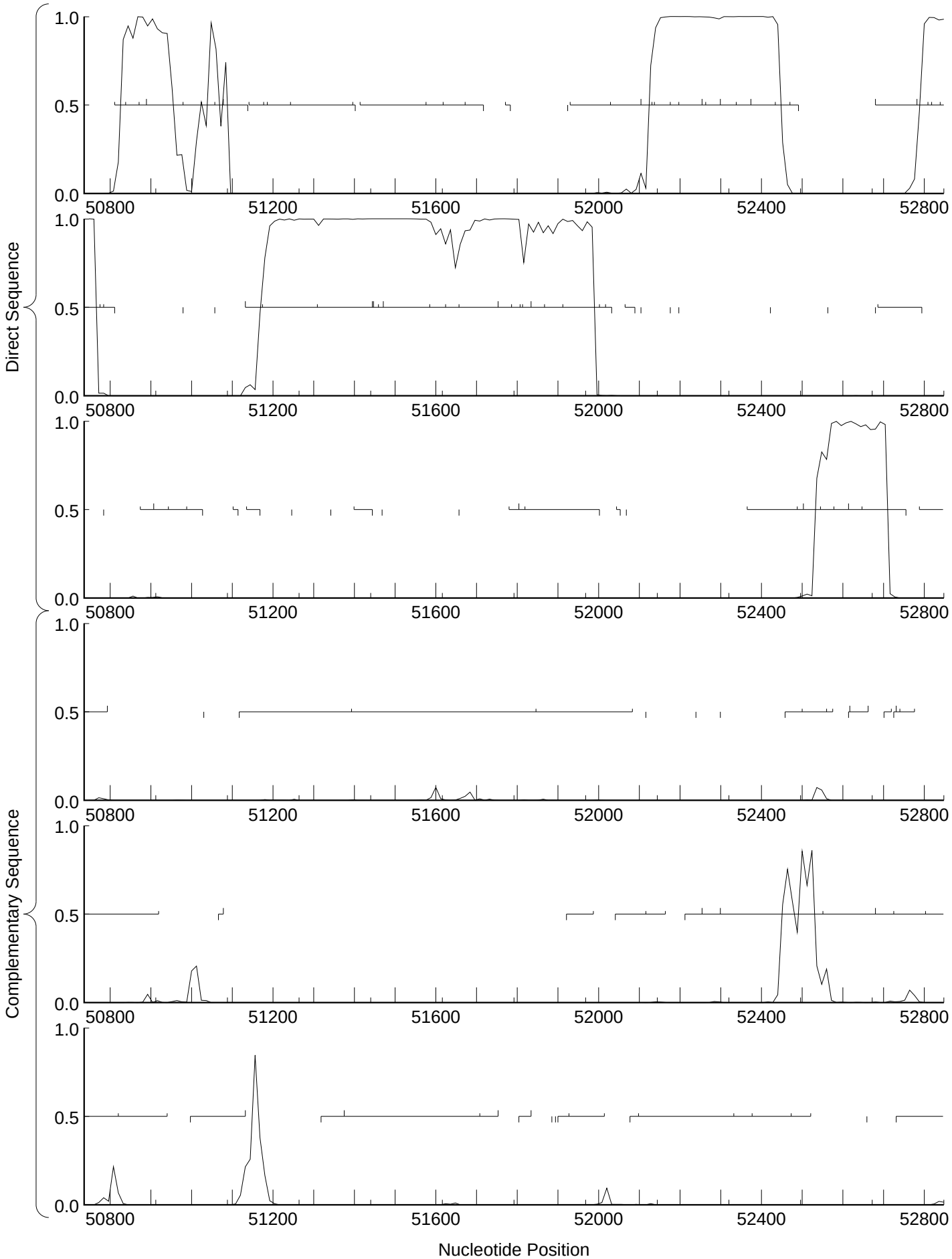

Direct Sequence
Complementary Sequence
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40800
41200
41600
42000
Nucleotide Position

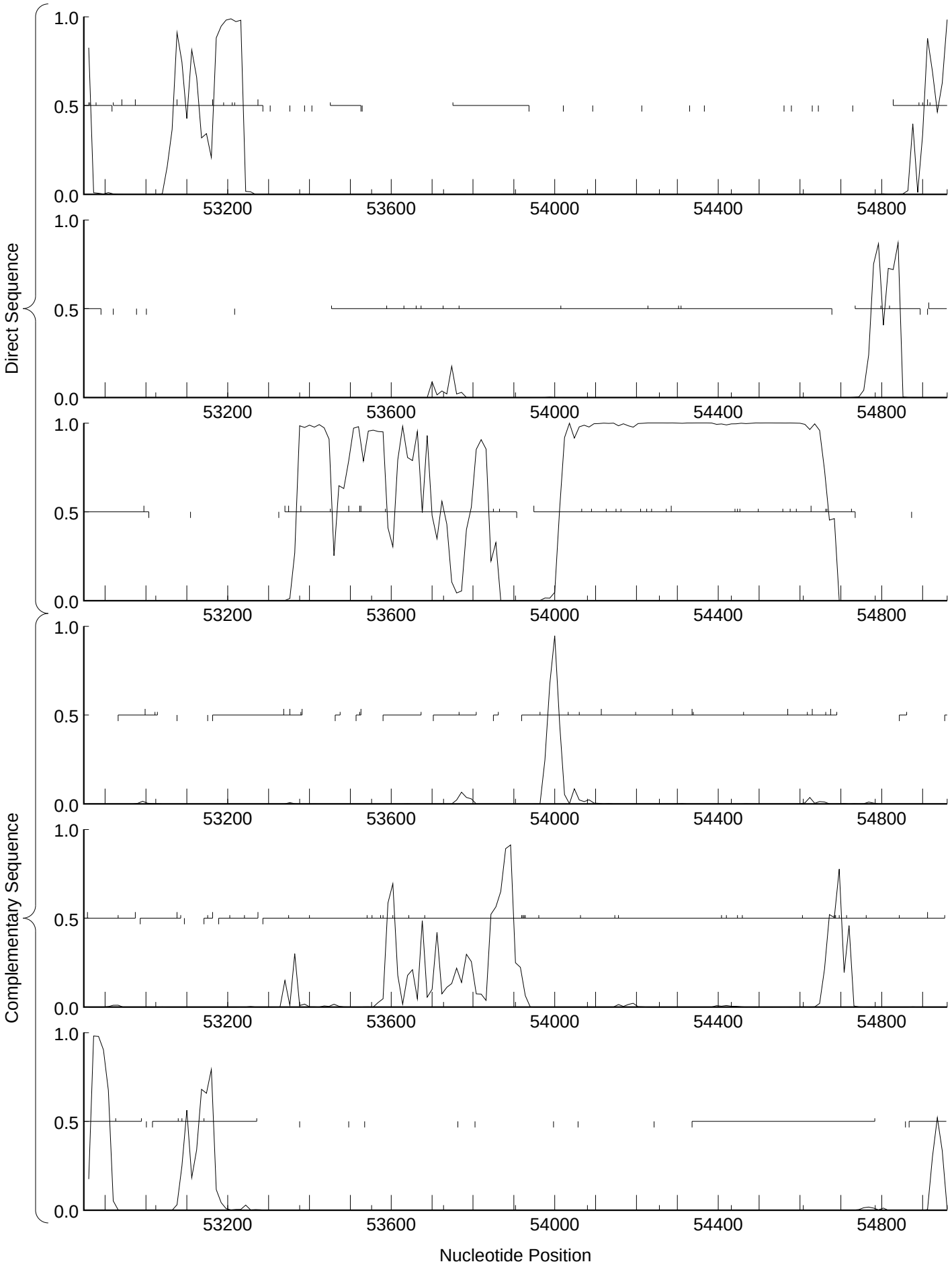

Direct Sequence
Complementary Sequence
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0.0
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43200
43600
44000
44400
Nucleotide Position

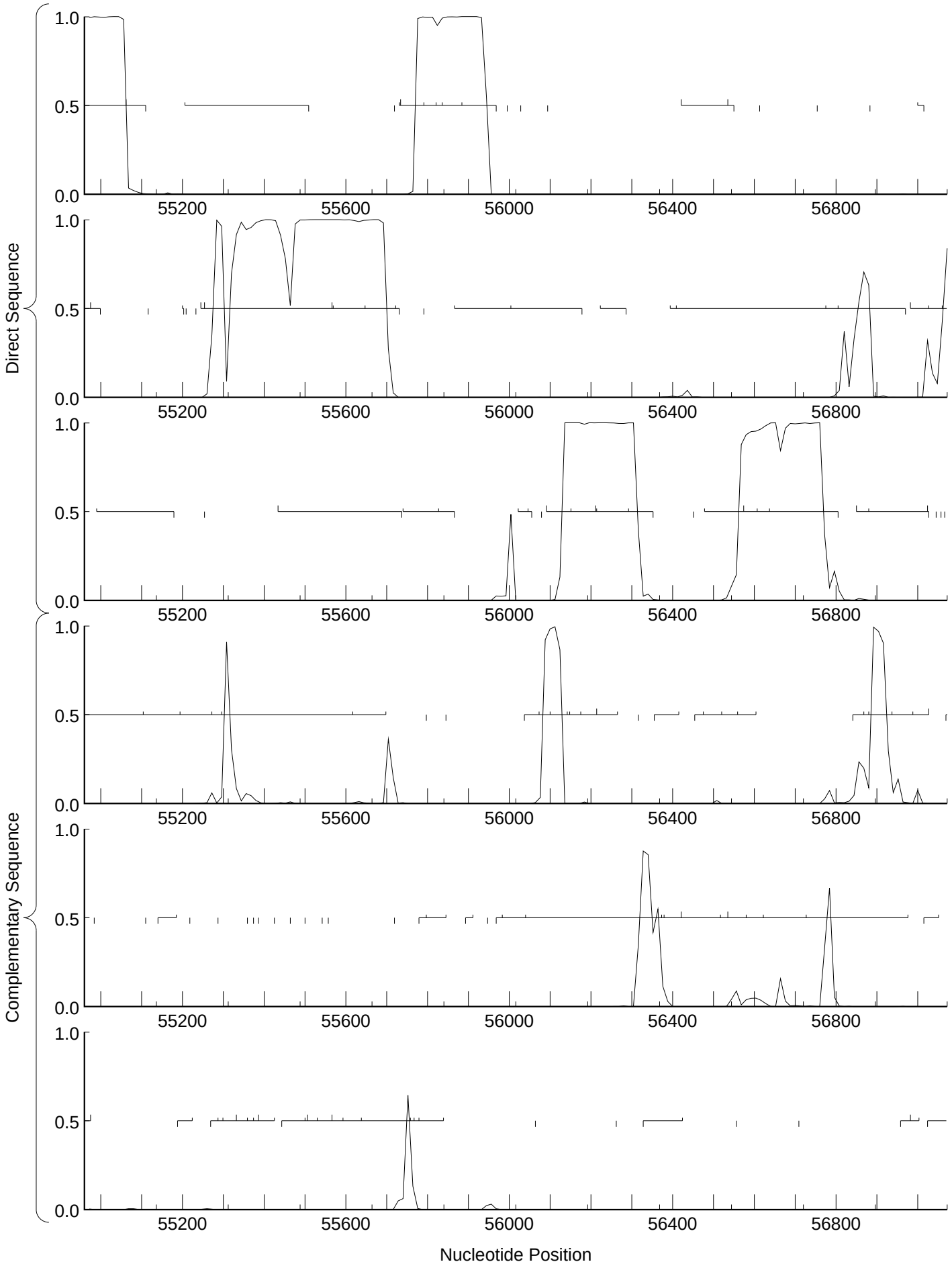

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
44800
45200
45600
46000
46400
Nucleotide Position


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


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, 58150 bp including 10-base 3’ overhang (CTCGCGGCAT), Cluster K2, Order 4, Window 96, Step 12, 29/29

