GeneMark

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

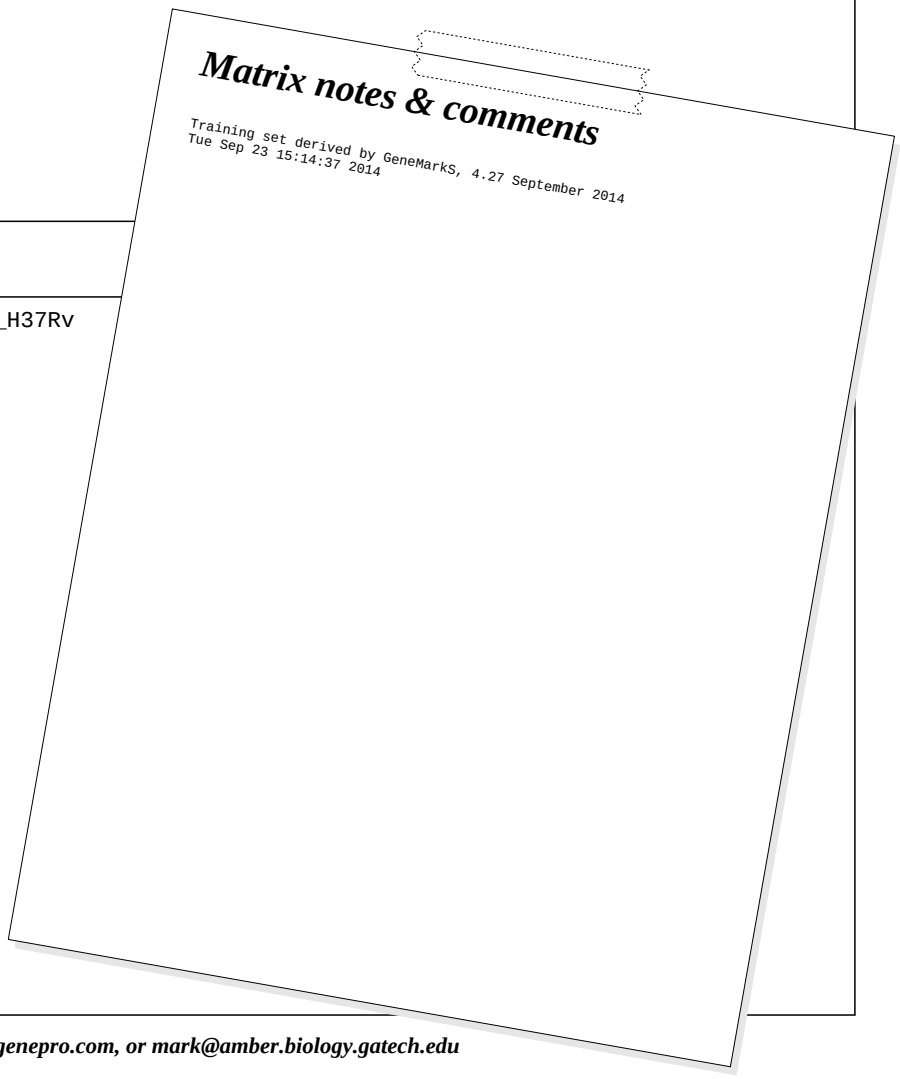
PROGRAM INFORMATION

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Sequence         :  Mycobacterium phage PhrodoBaggins complete sequence, 68873 bp, circurlarly permuted, Cluste
Analysis Date    :  3/28/24 at 6:48:44
Pages            :  34
Sequence Length  :  68873 bp
GC Content       :   66.41%

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

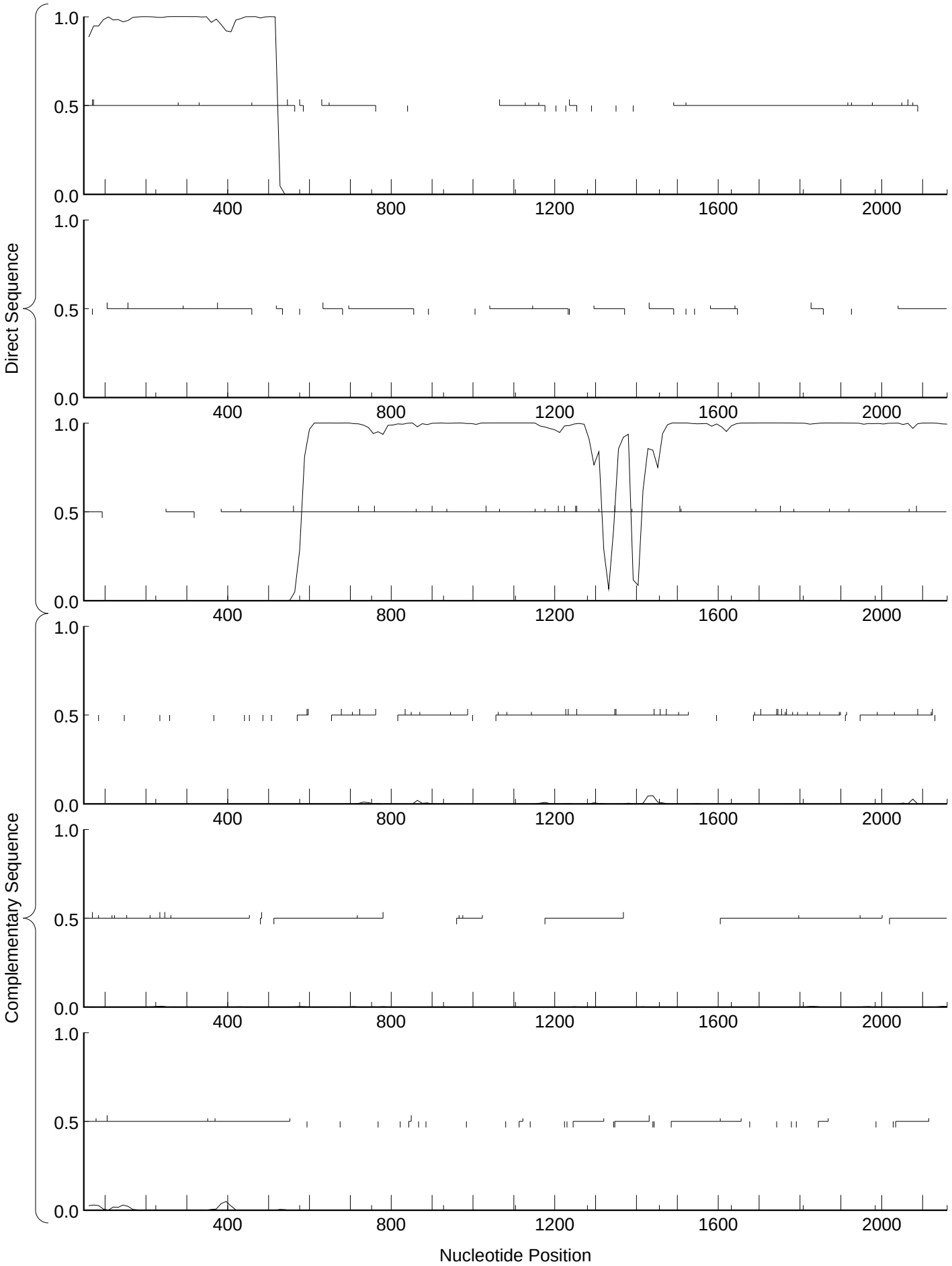
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Matrix     :  Mycobacterium_tuberculosis_H37Rv
Author     :  -

Order      :  4
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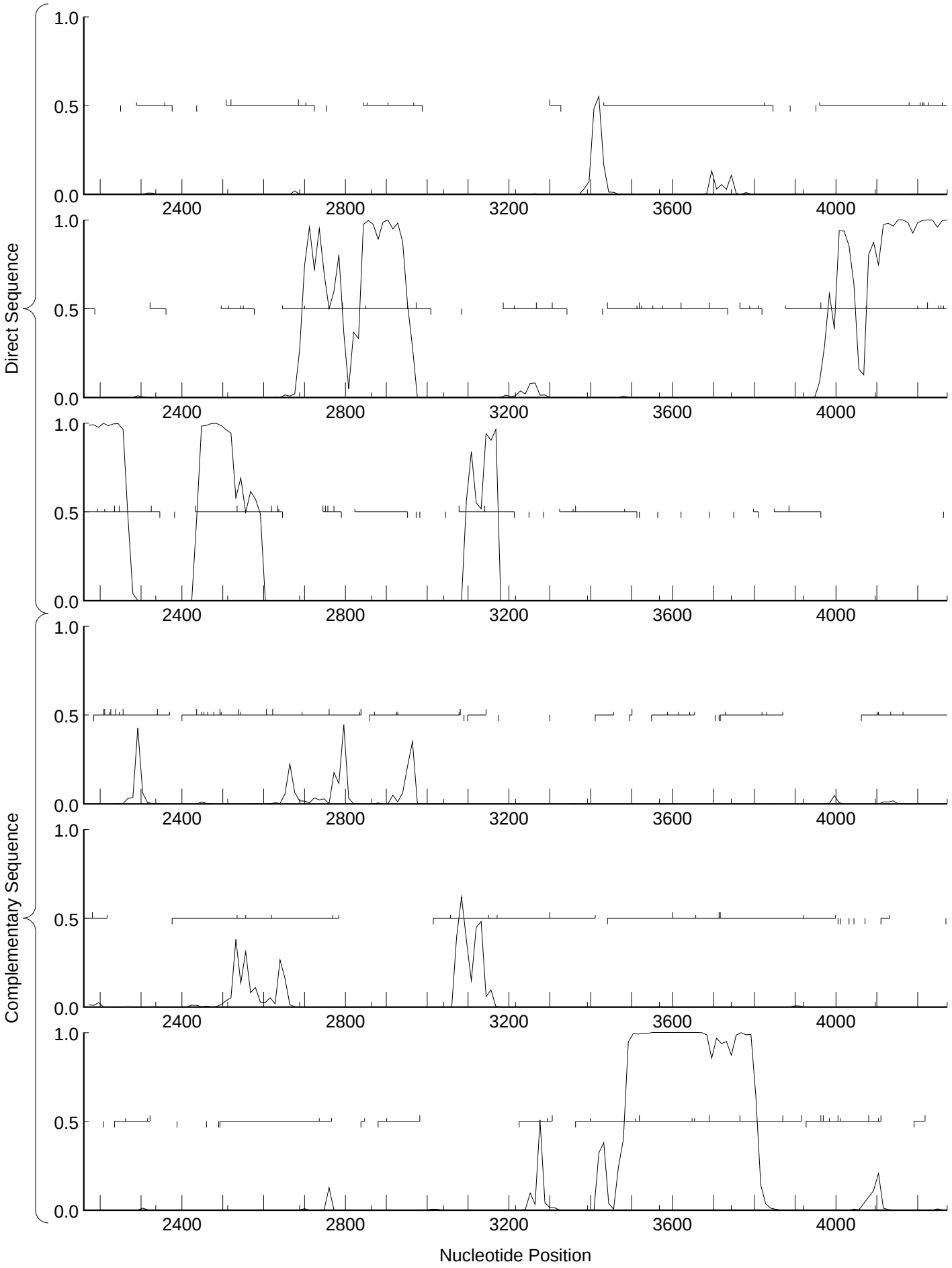

```
  Send questions / comments to:
      Dr. M. Borodovsky
      Georgia Institute of Technology
      School of Biology
      Atlanta, GA  30332-0230
```


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

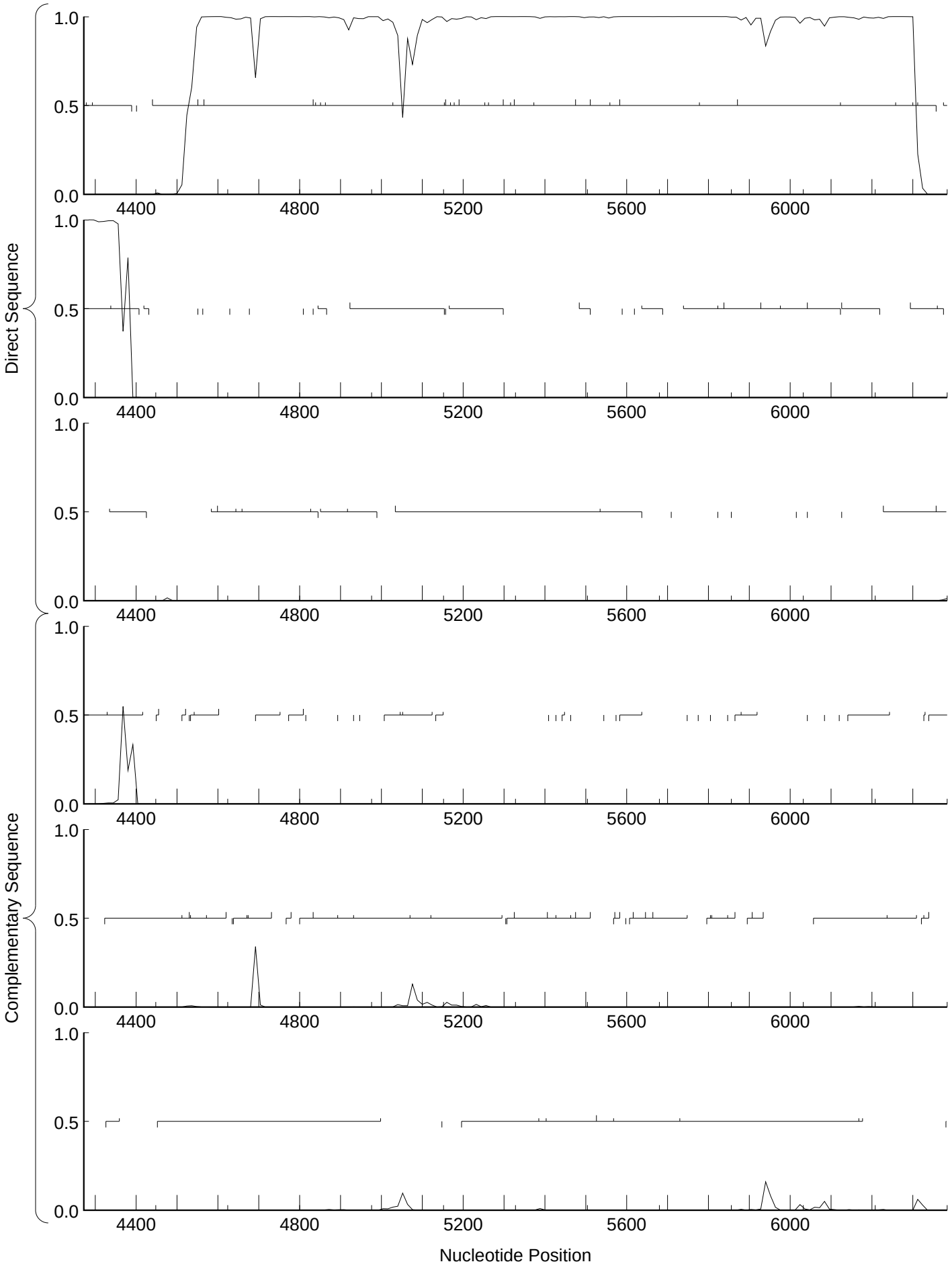
terium phage PhrodoBaggins complete sequence, 68873 bp, circurlarly permuted, Cluster B1, Order 4, Window 96, Step 12, 2/34



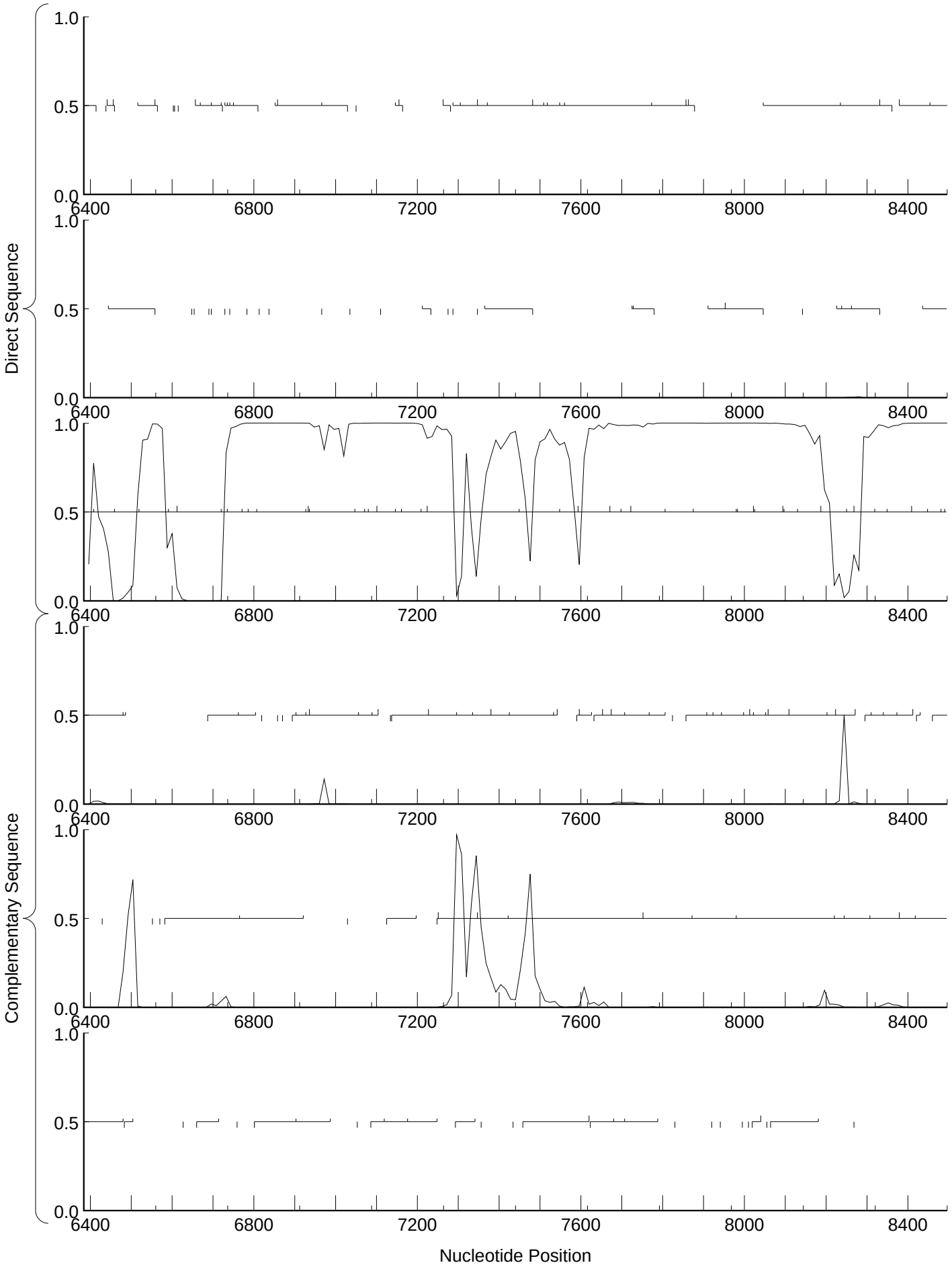
terium phage PhrodoBaggins complete sequence, 68873 bp, circurlarly permuted, Cluster B1, Order 4, Window 96, Step 12, 3/34



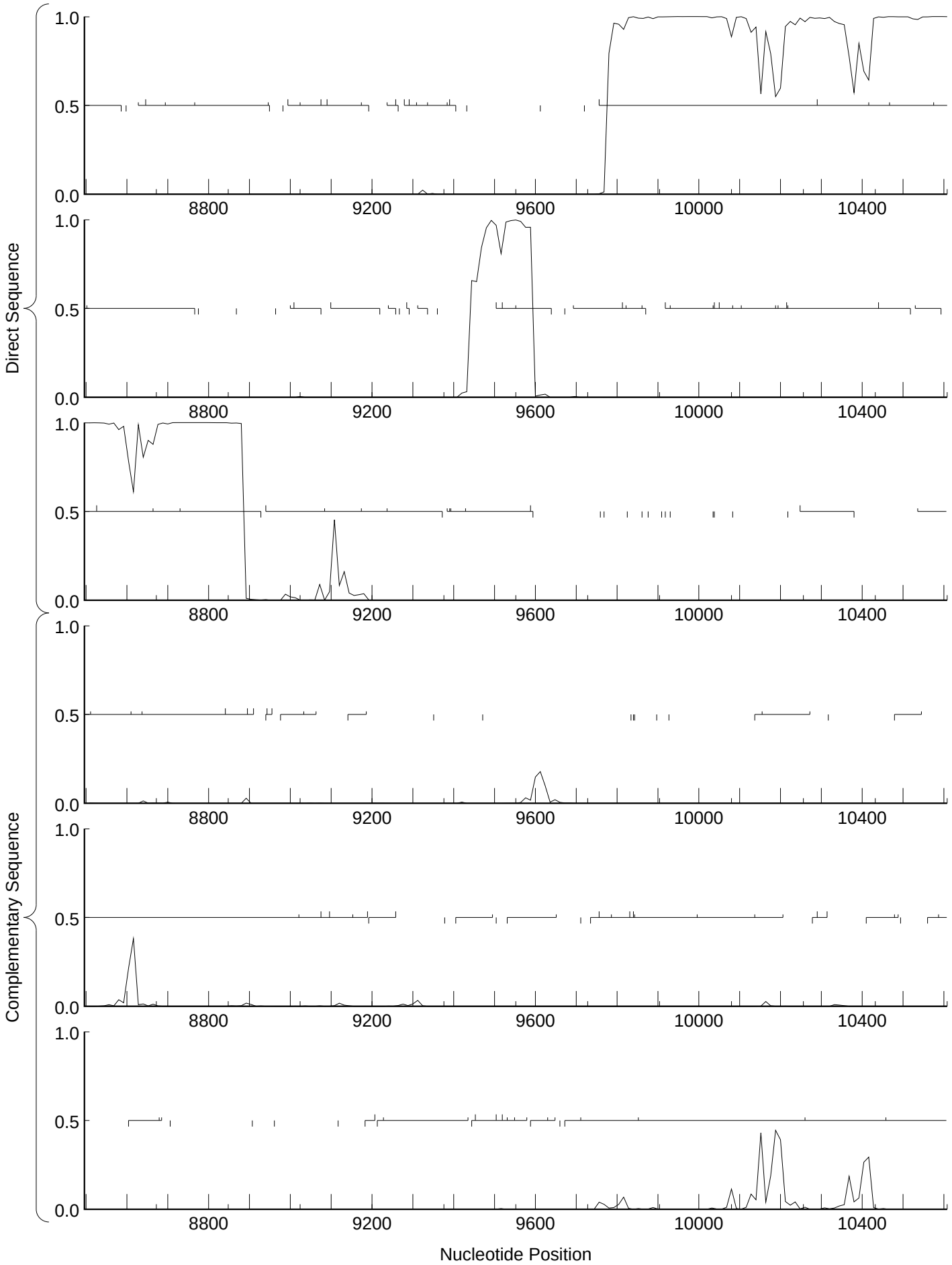
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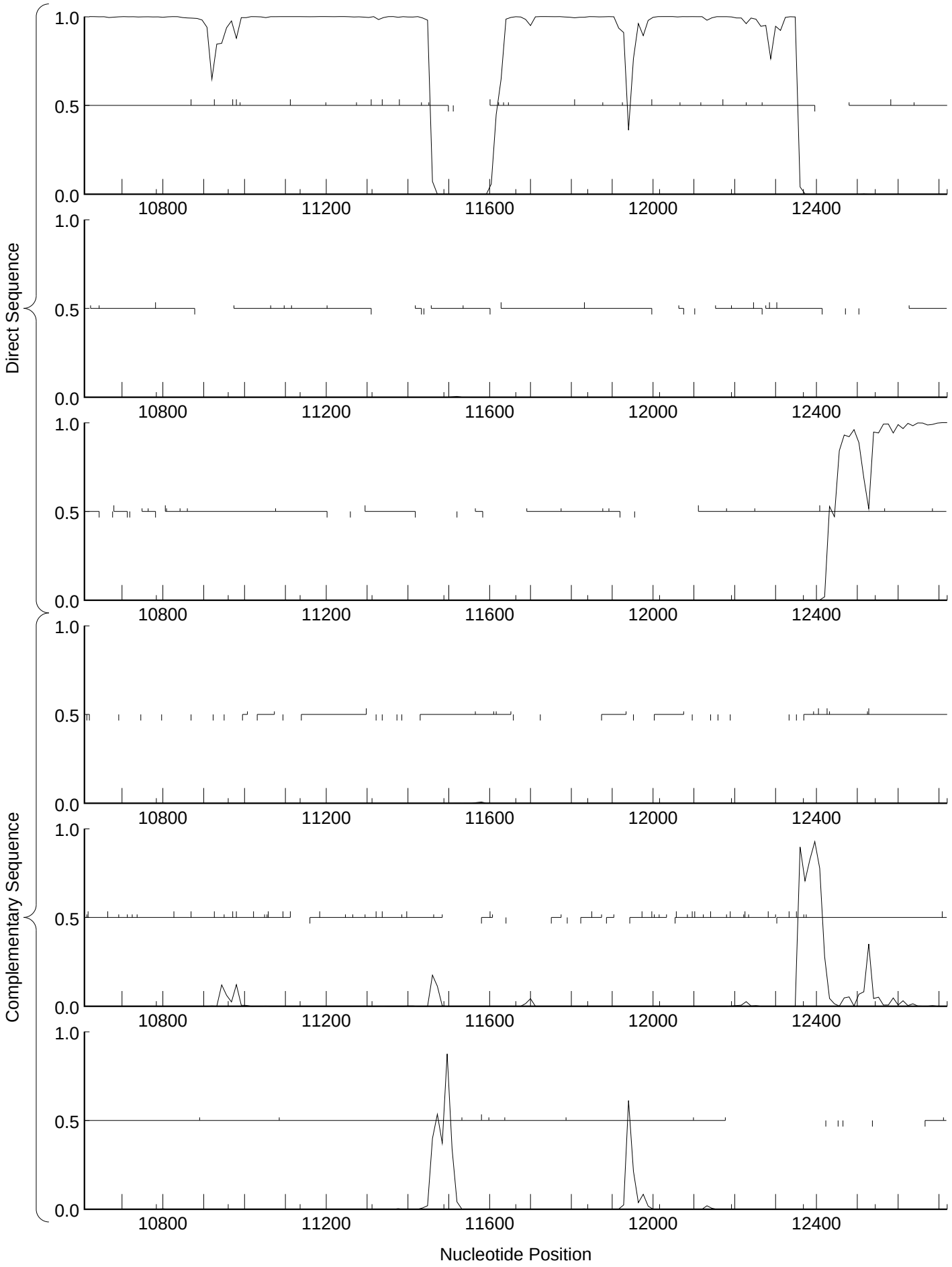
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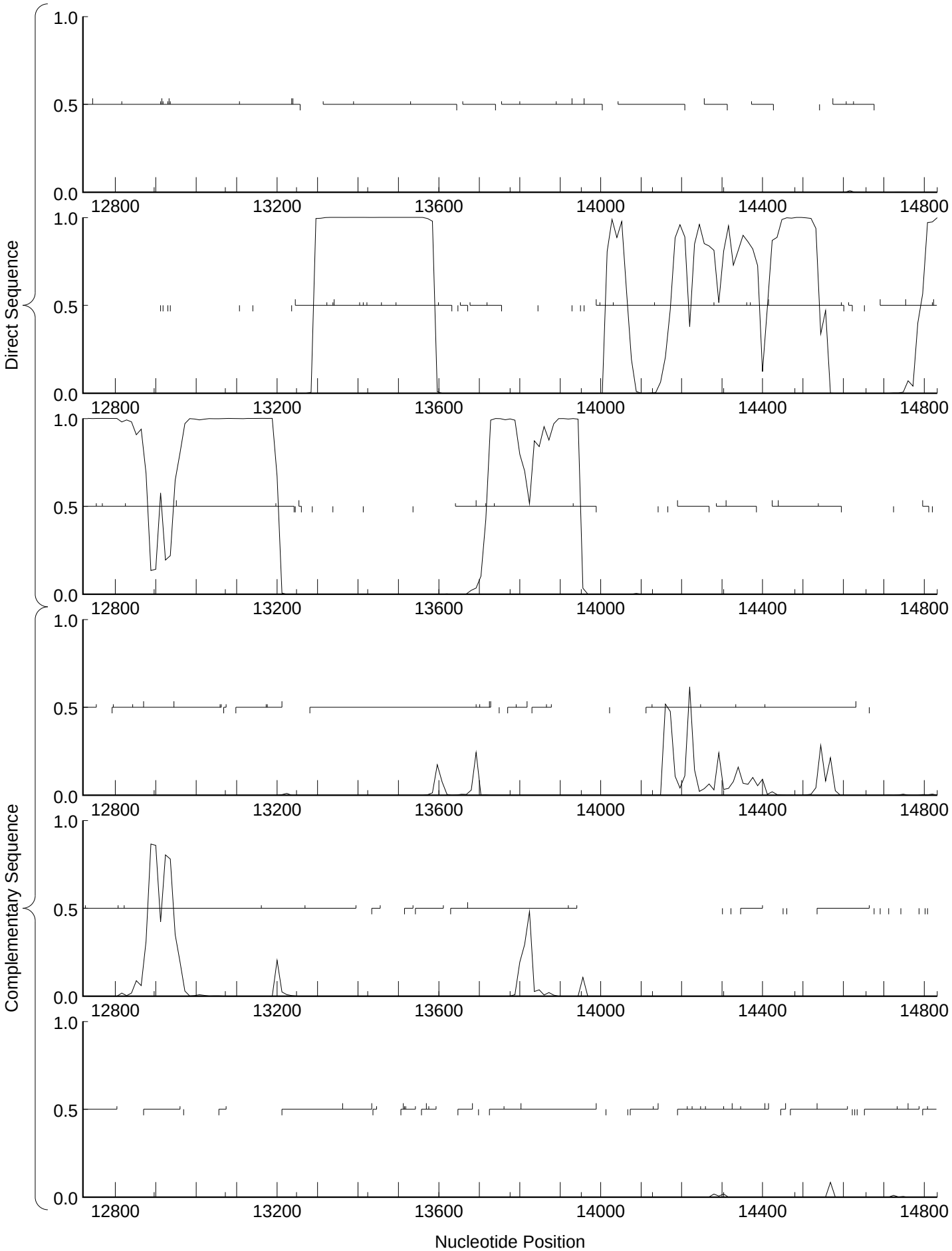
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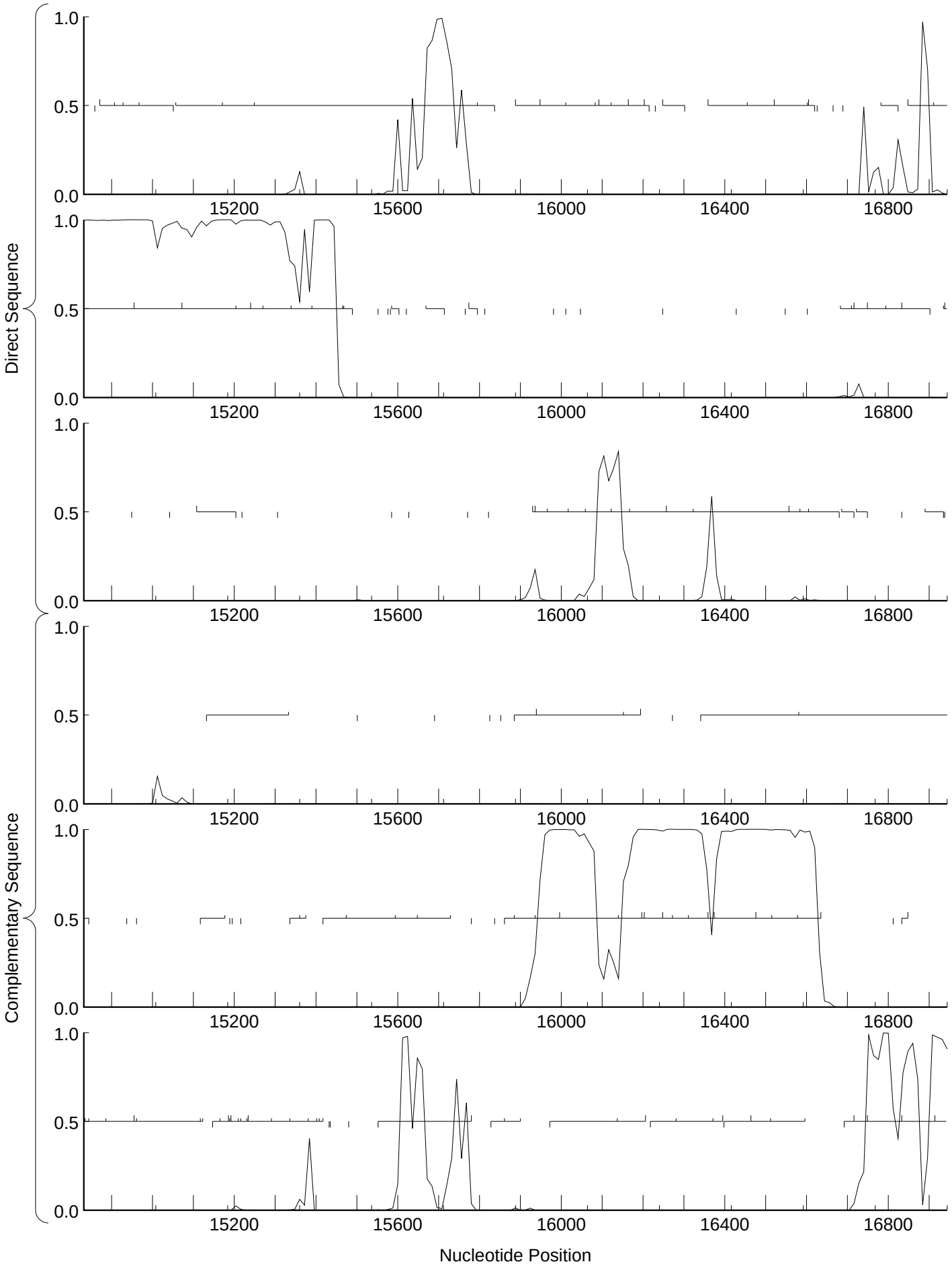
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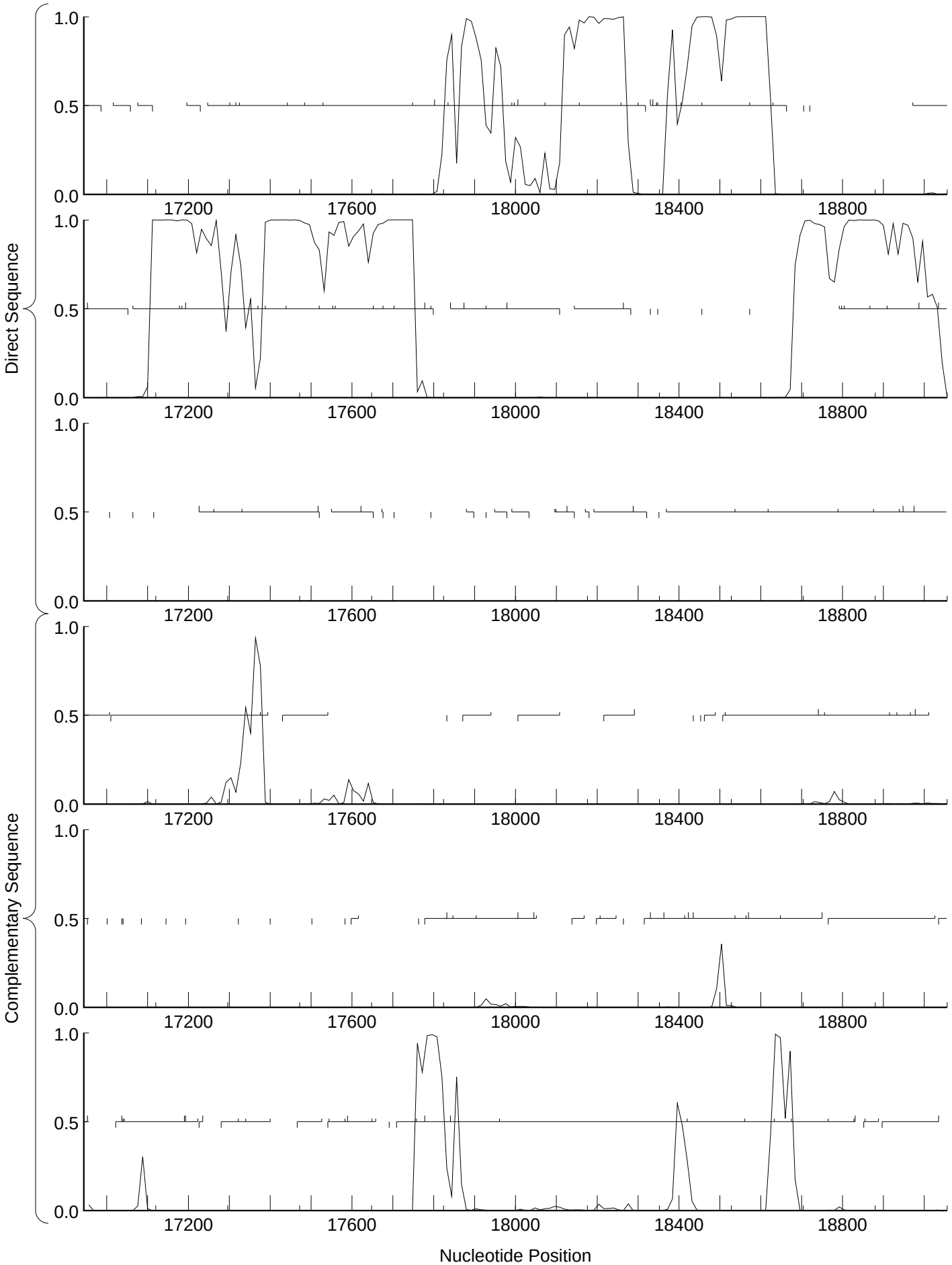
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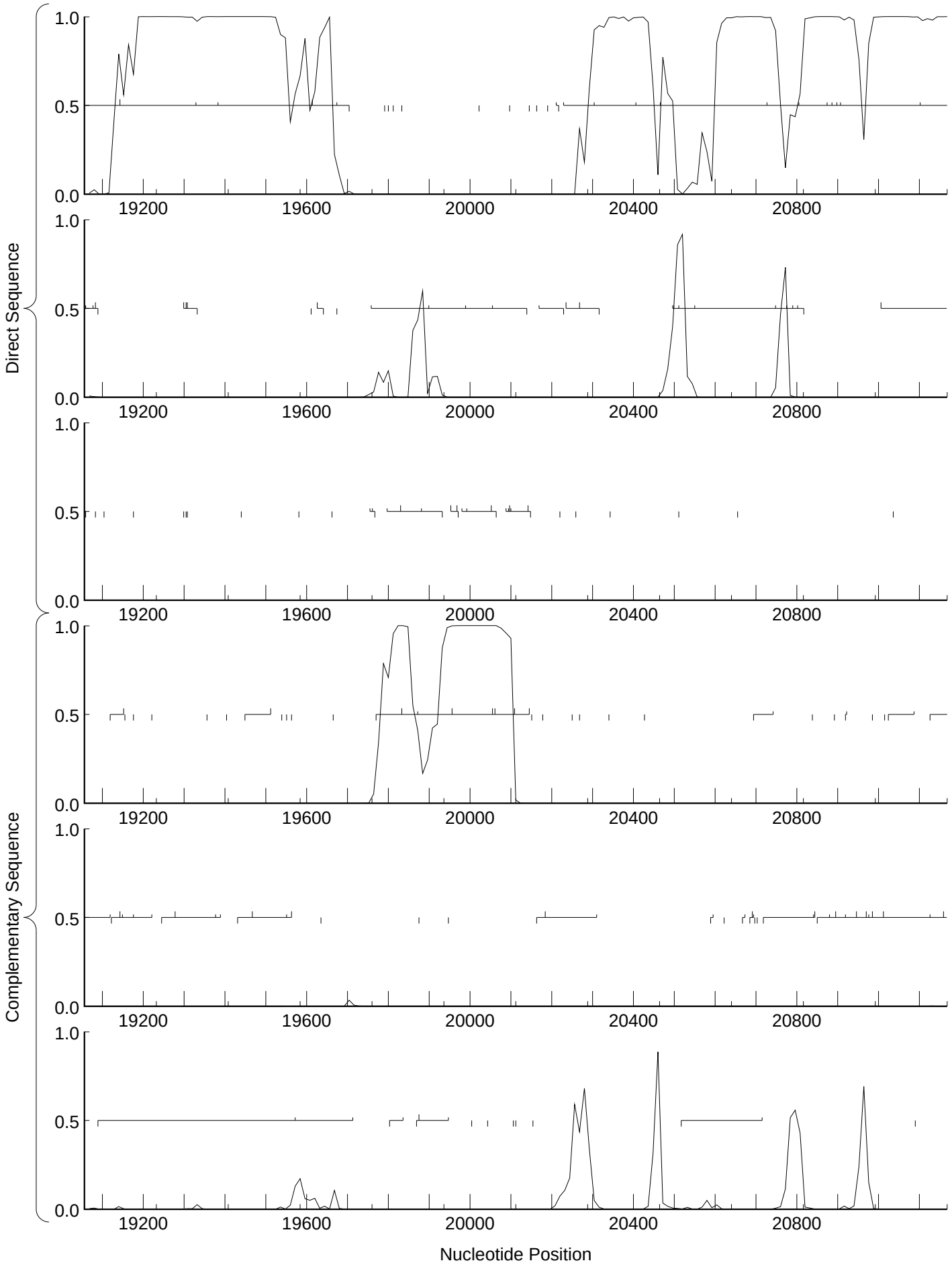
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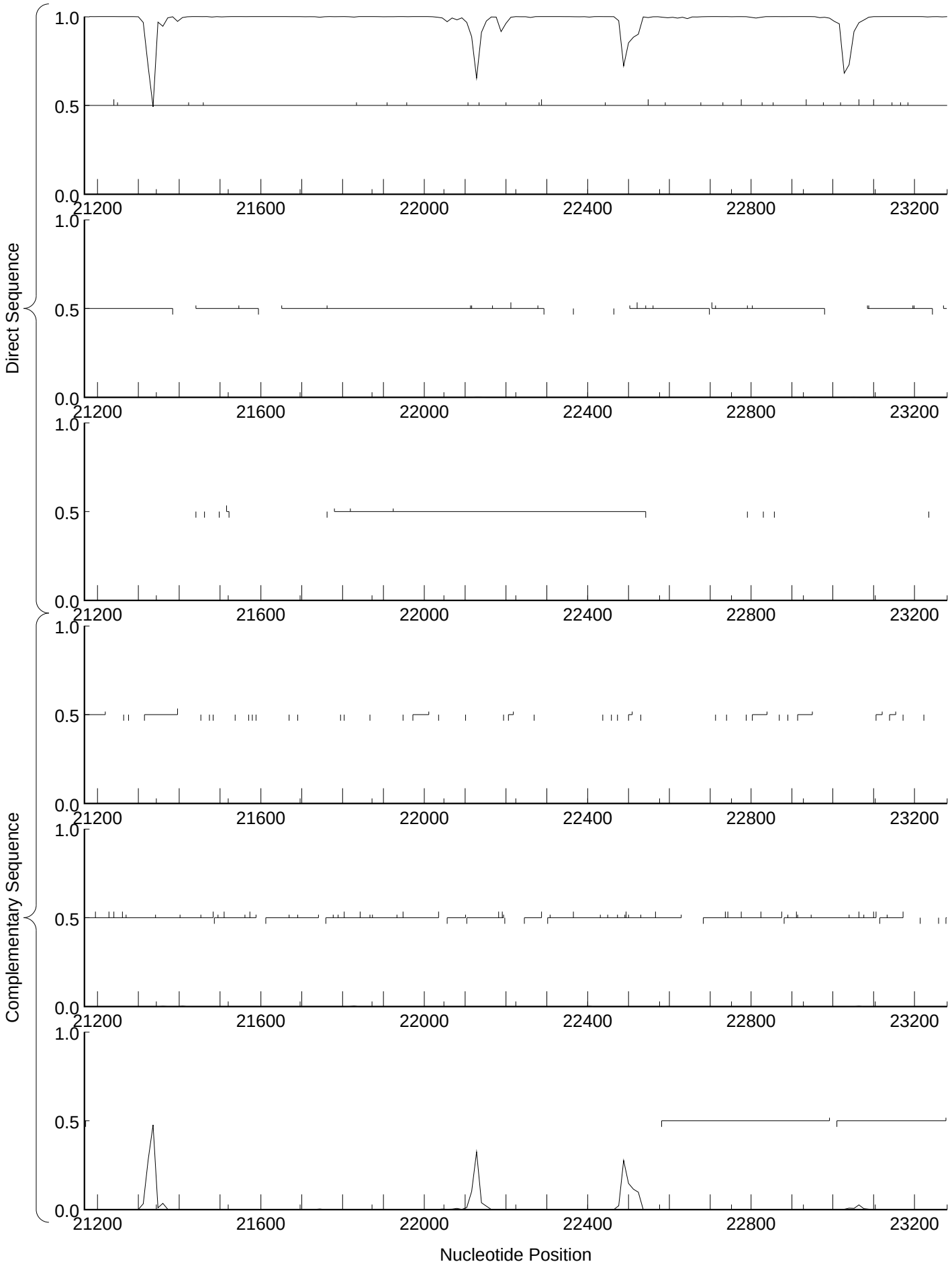


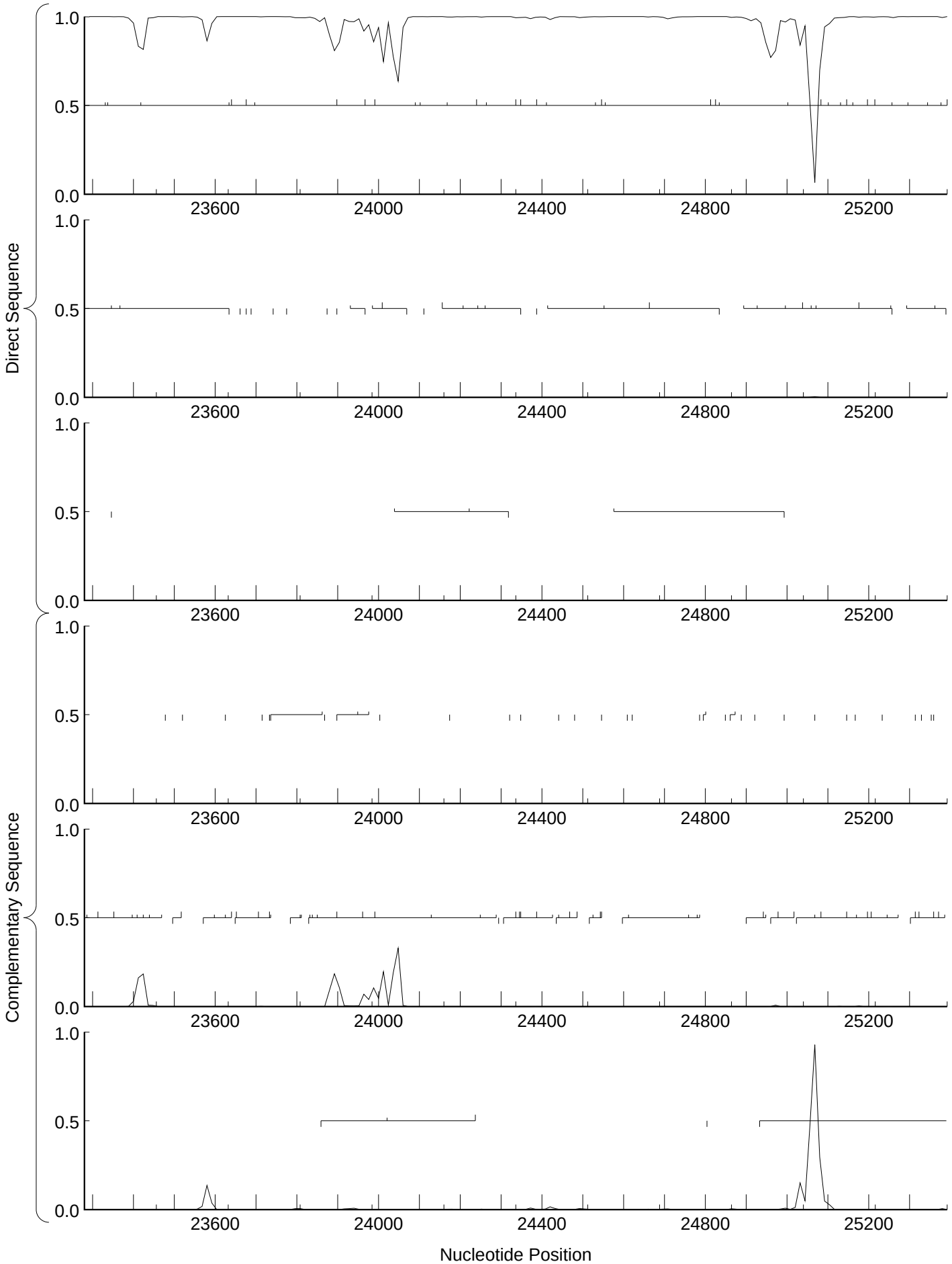
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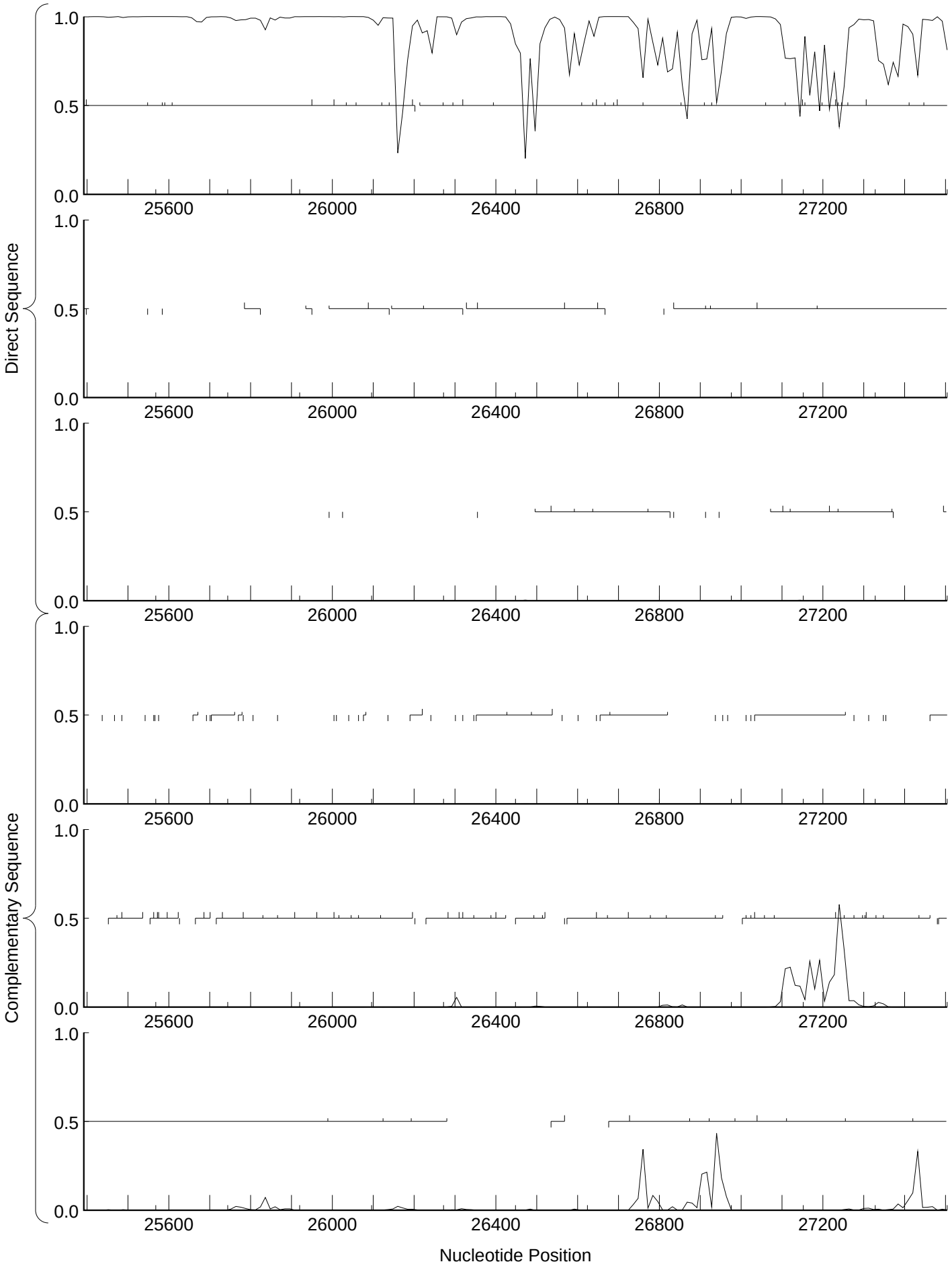
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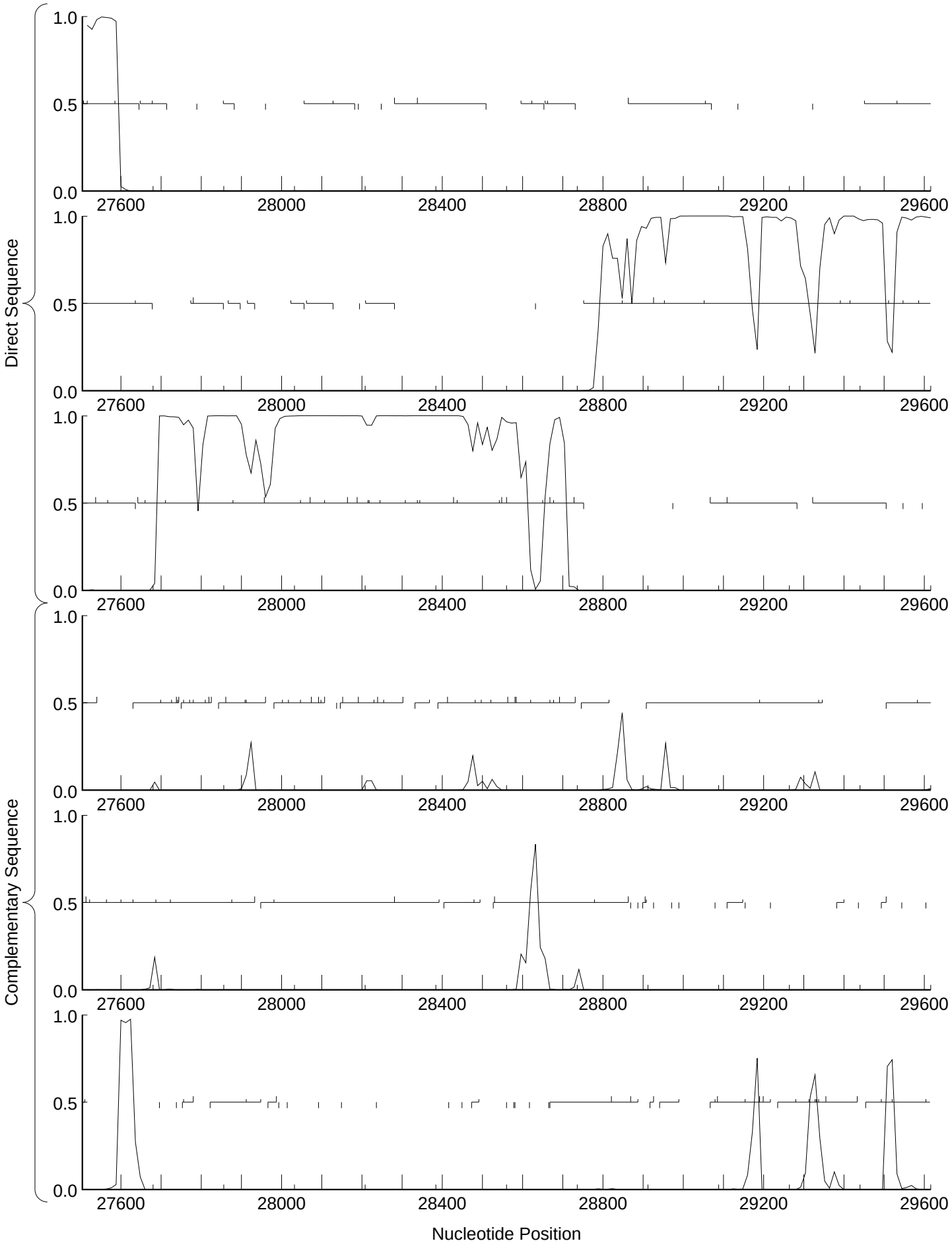

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
21200
21600
22000
22400
22800
23200
Nucleotide Position


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
23600
24000
24400
24800
25200
Nucleotide Position

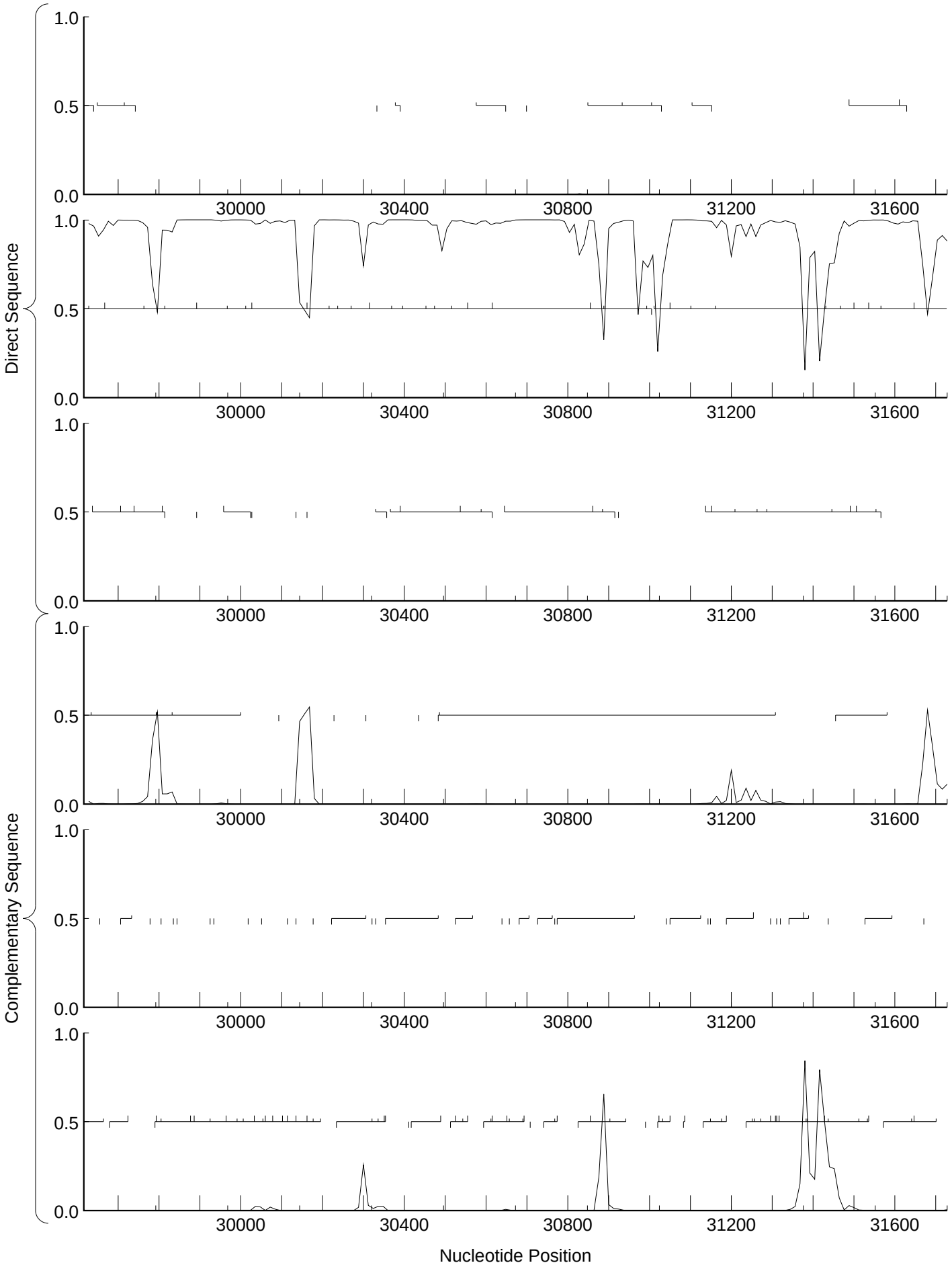
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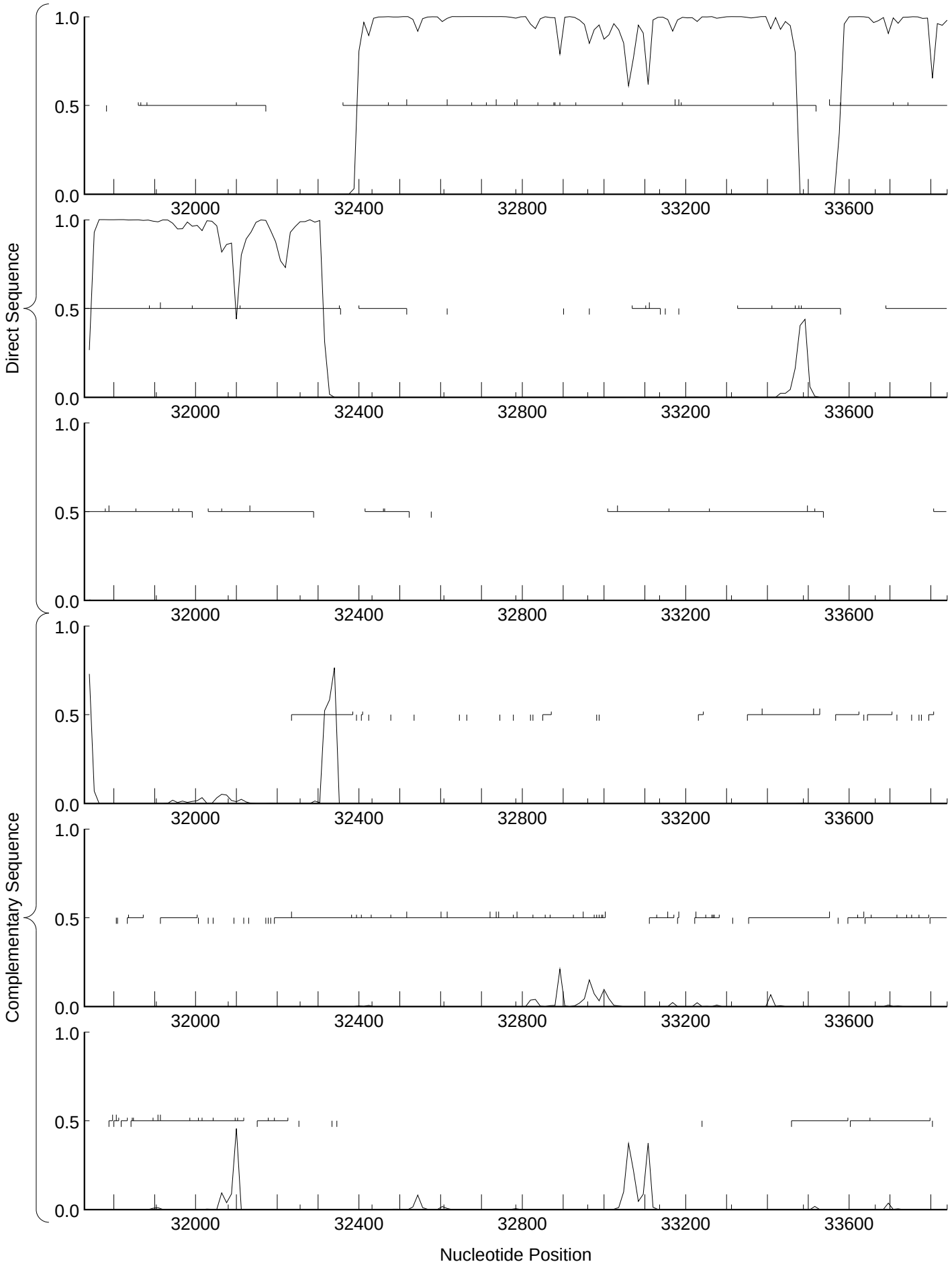
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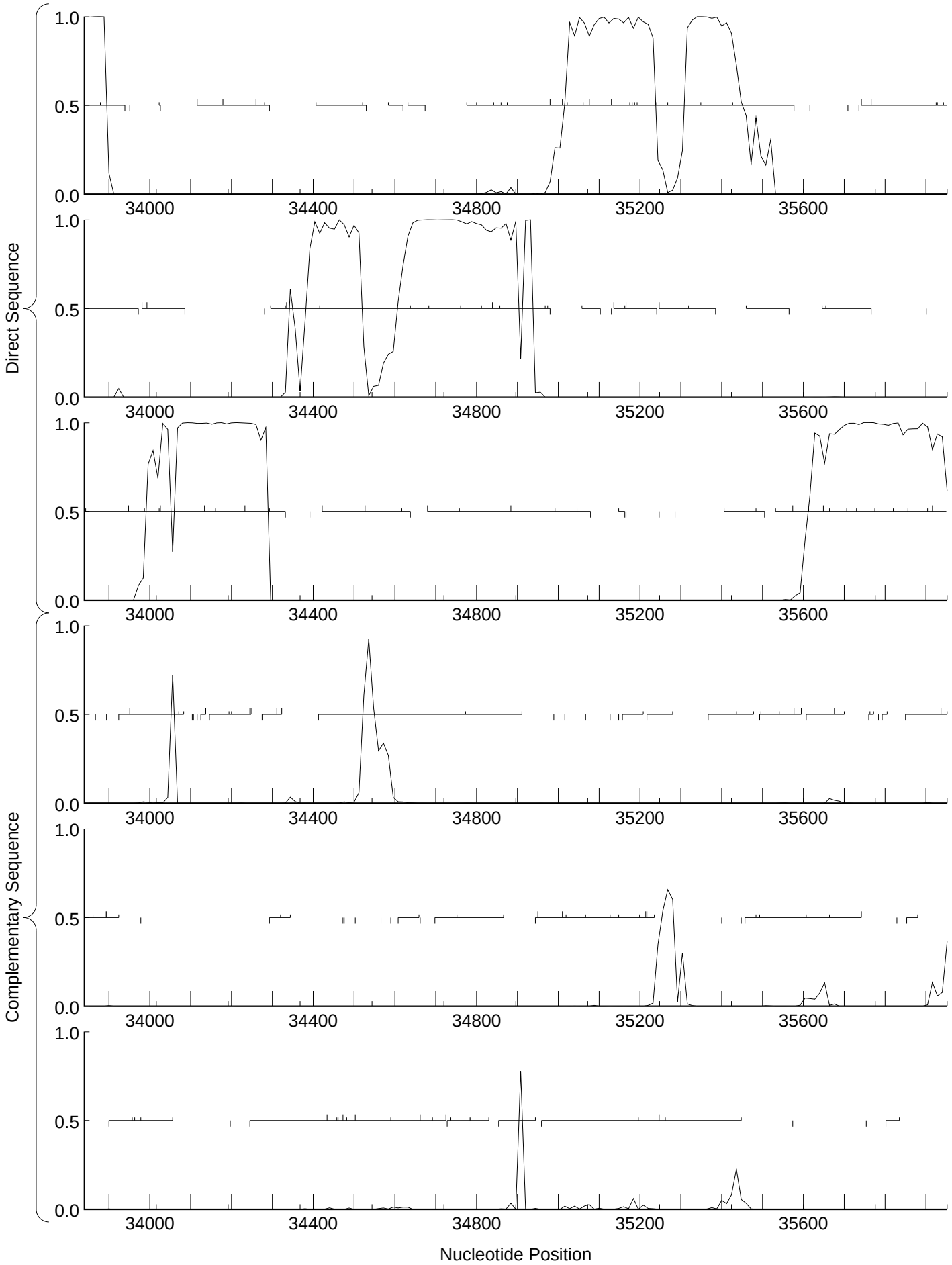
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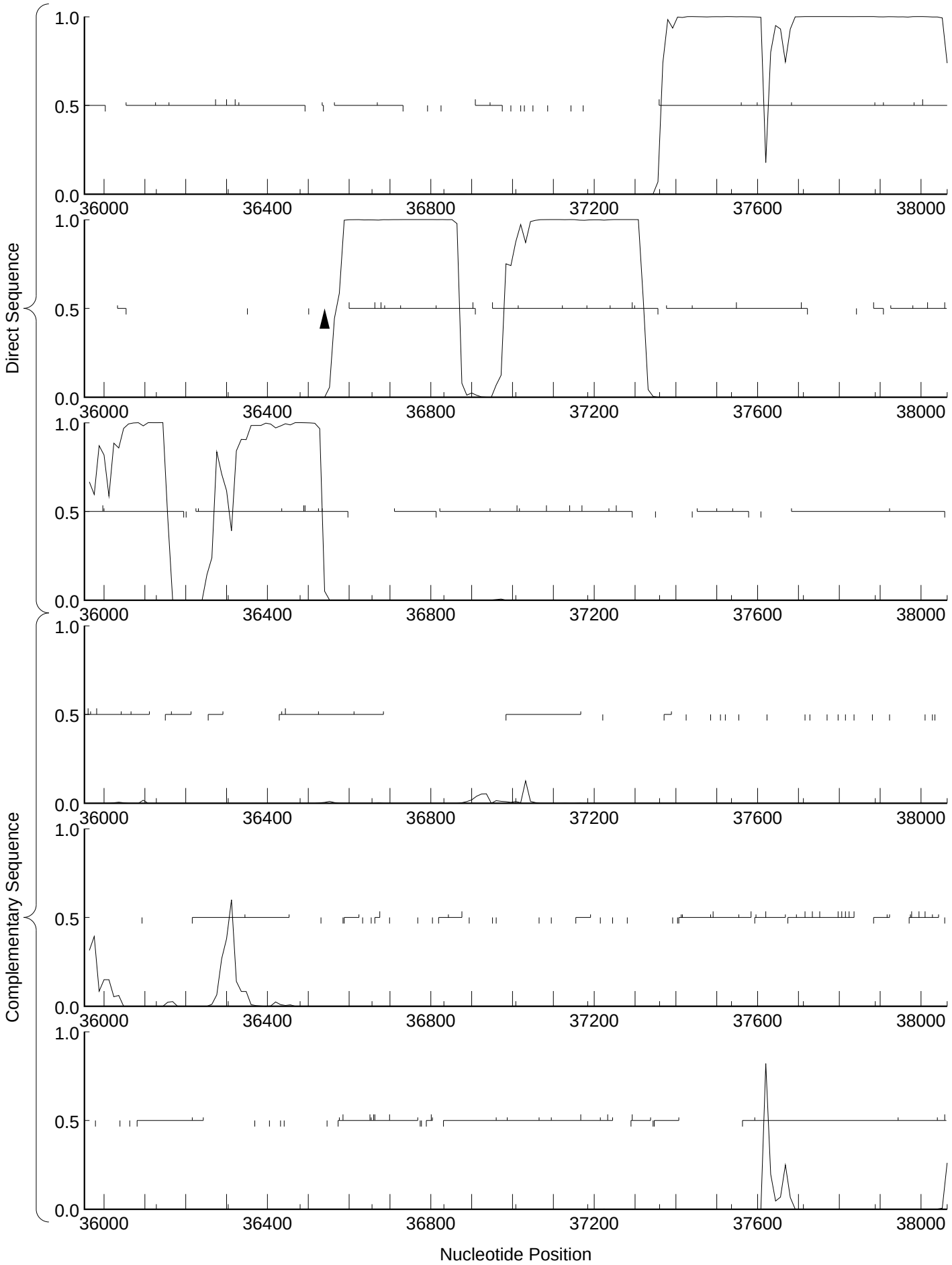


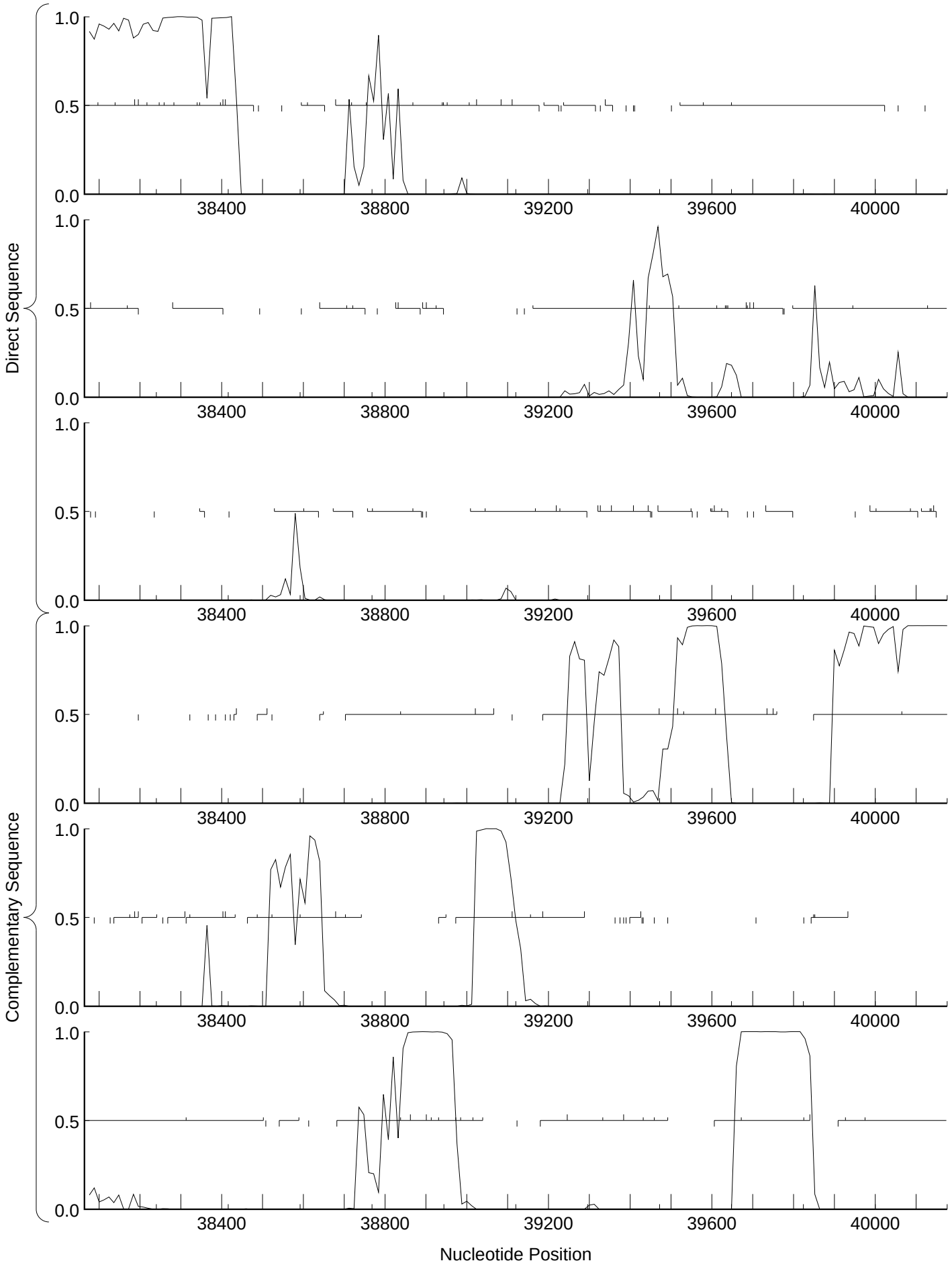
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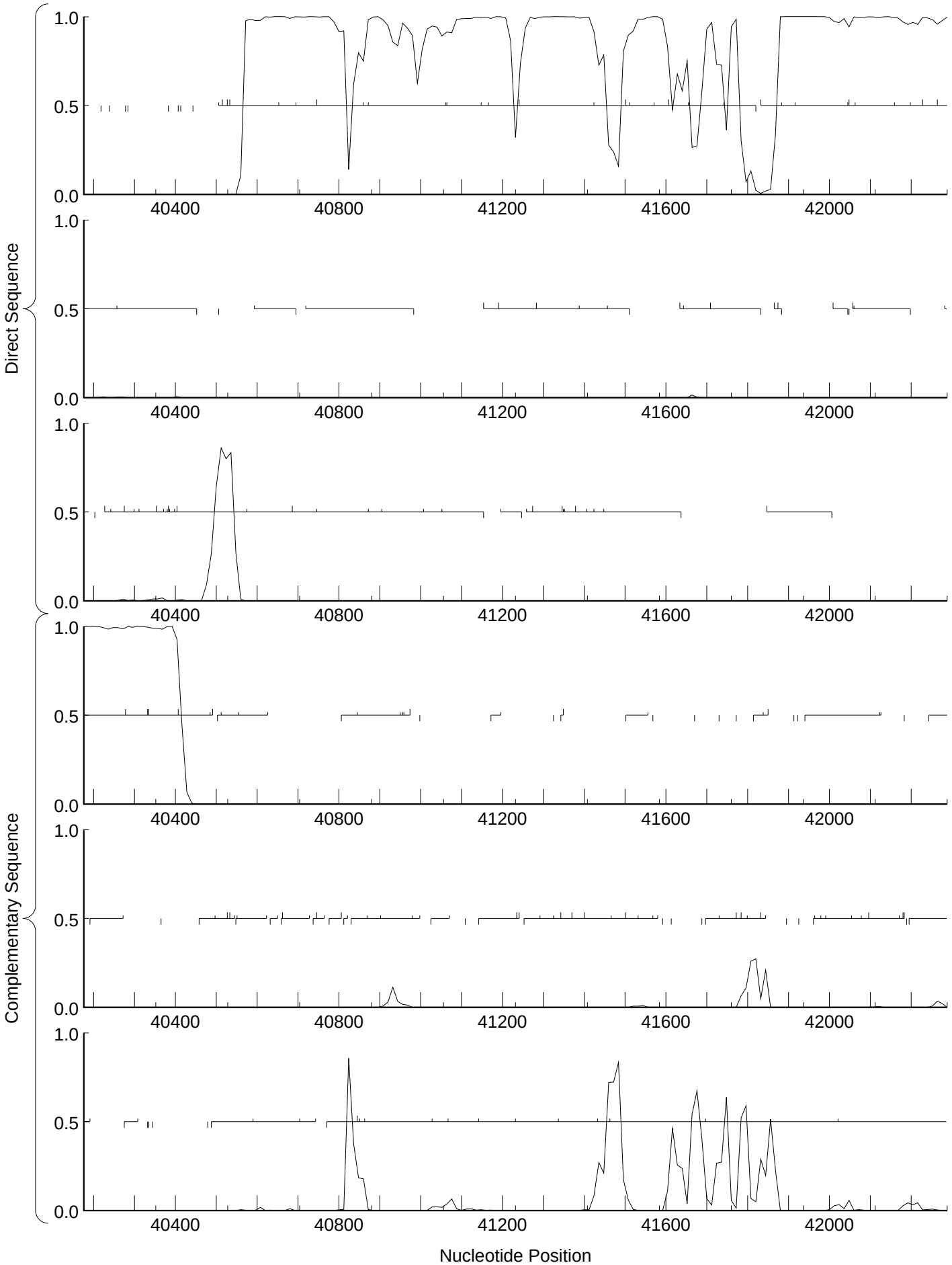


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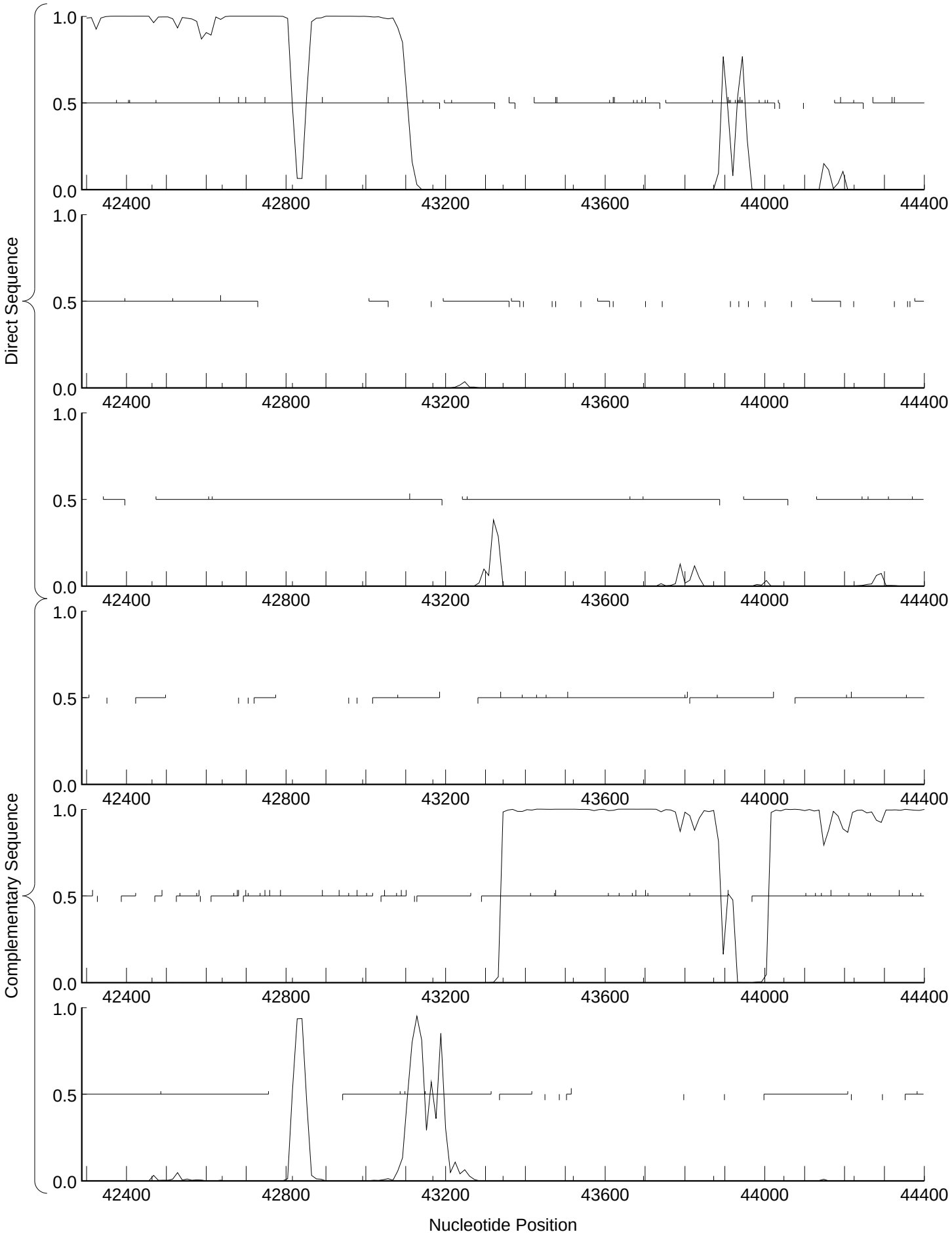



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Complementary Sequence
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0.5
0.0
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36400
36800
37200
37600
38000
Nucleotide Position

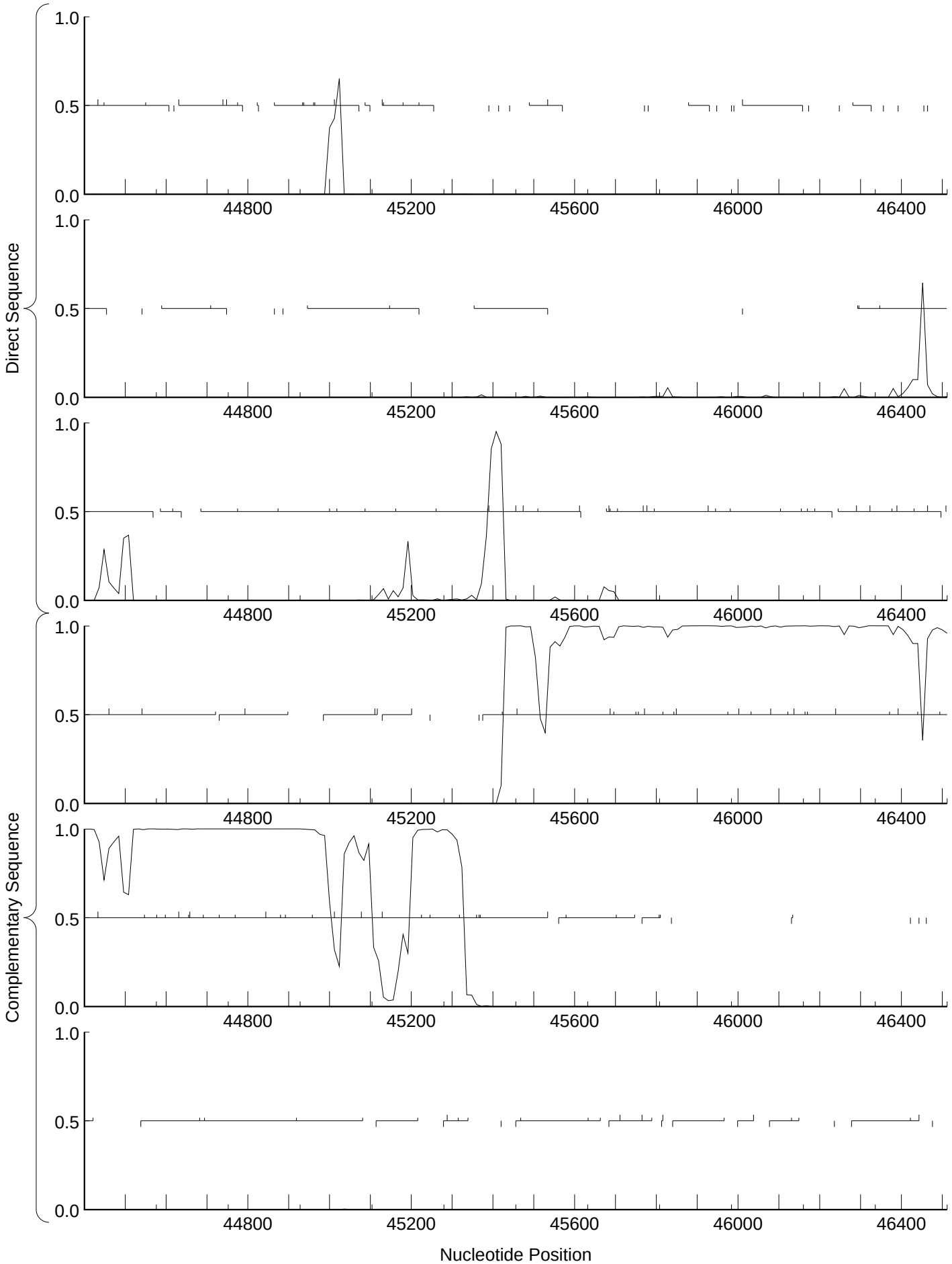

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
38400
38800
39200
39600
40000
Nucleotide Position


Direct Sequence
Complementary Sequence
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0.0
40400
40800
41200
41600
42000
Nucleotide Position

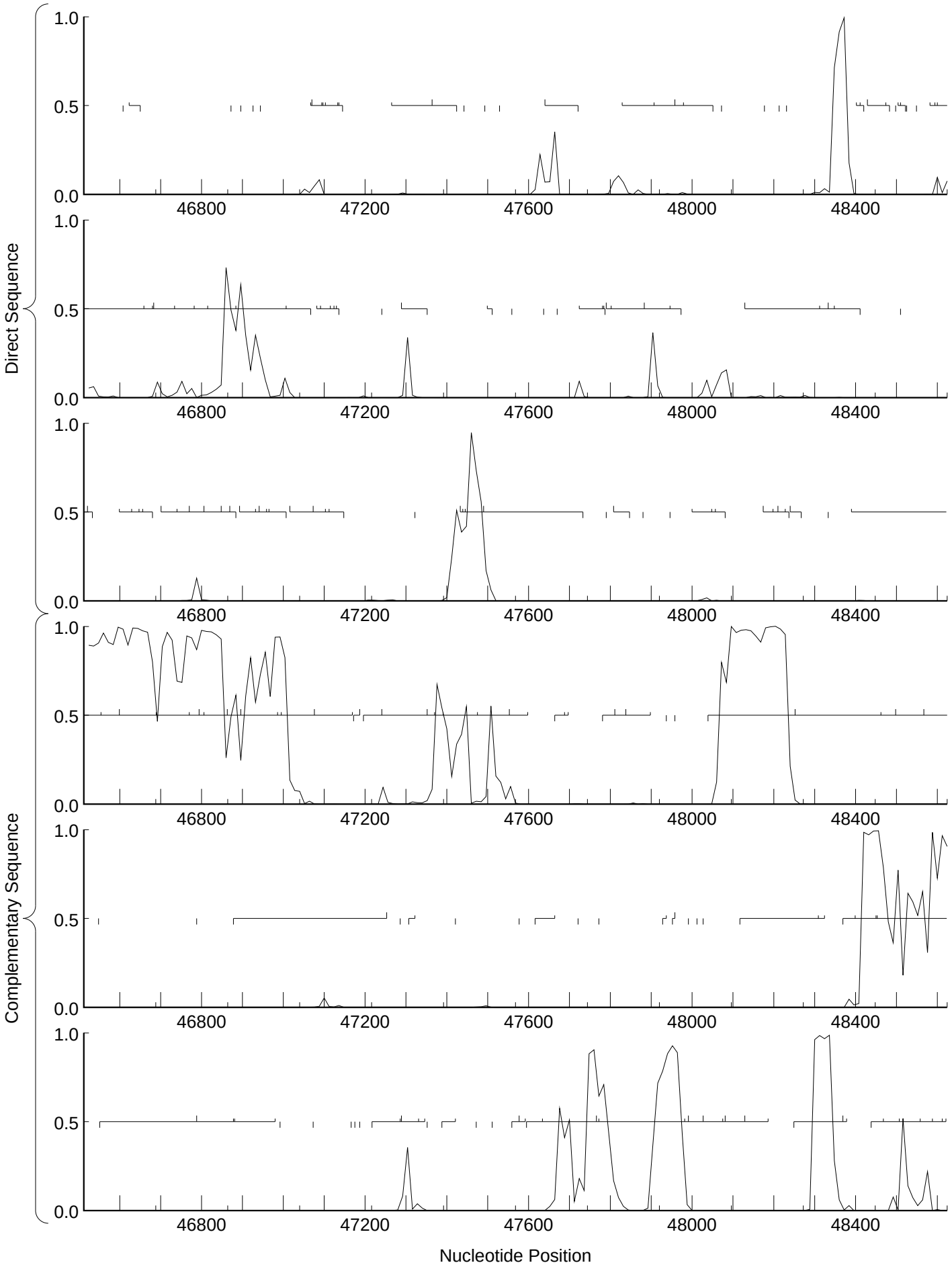
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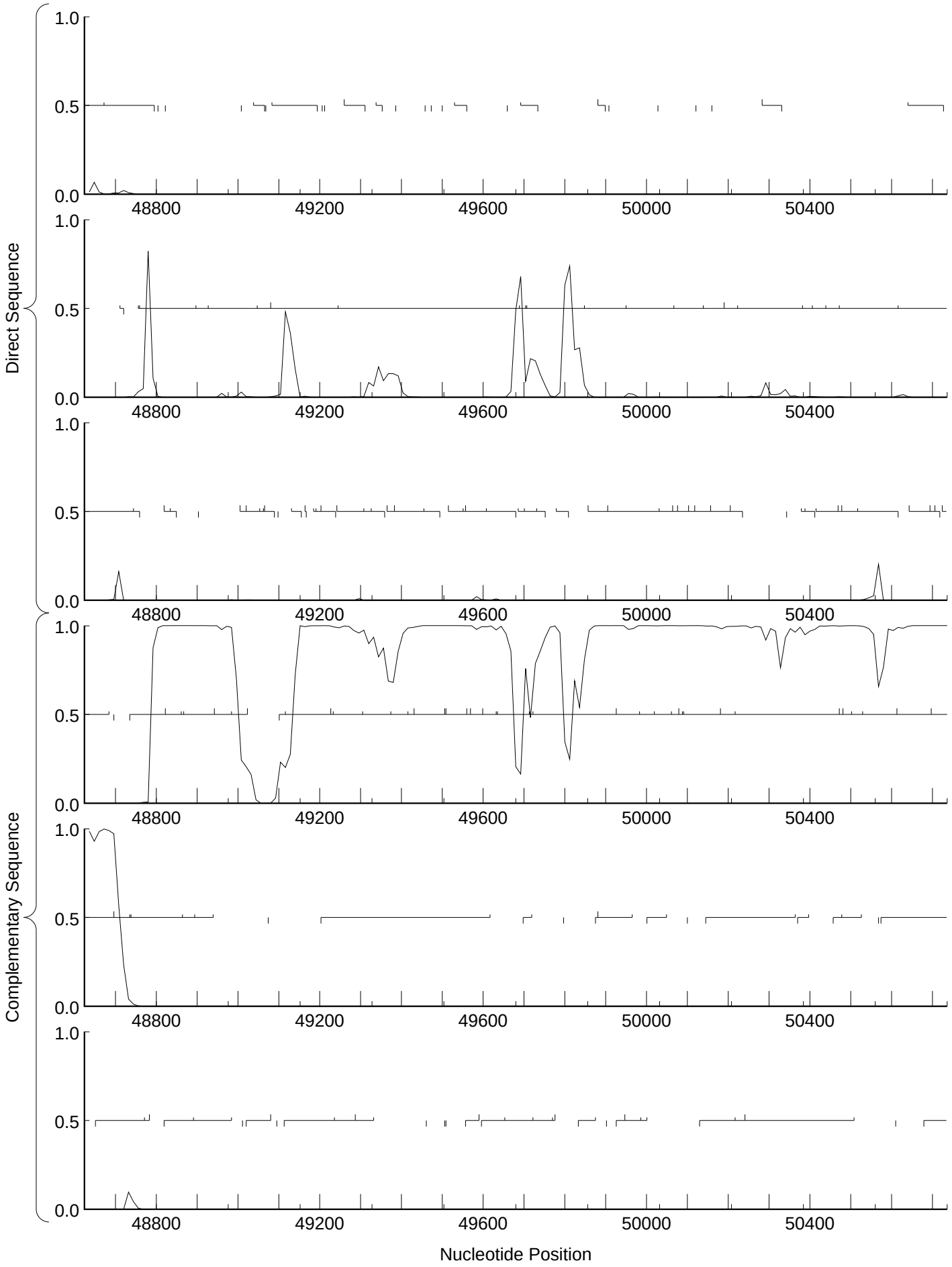
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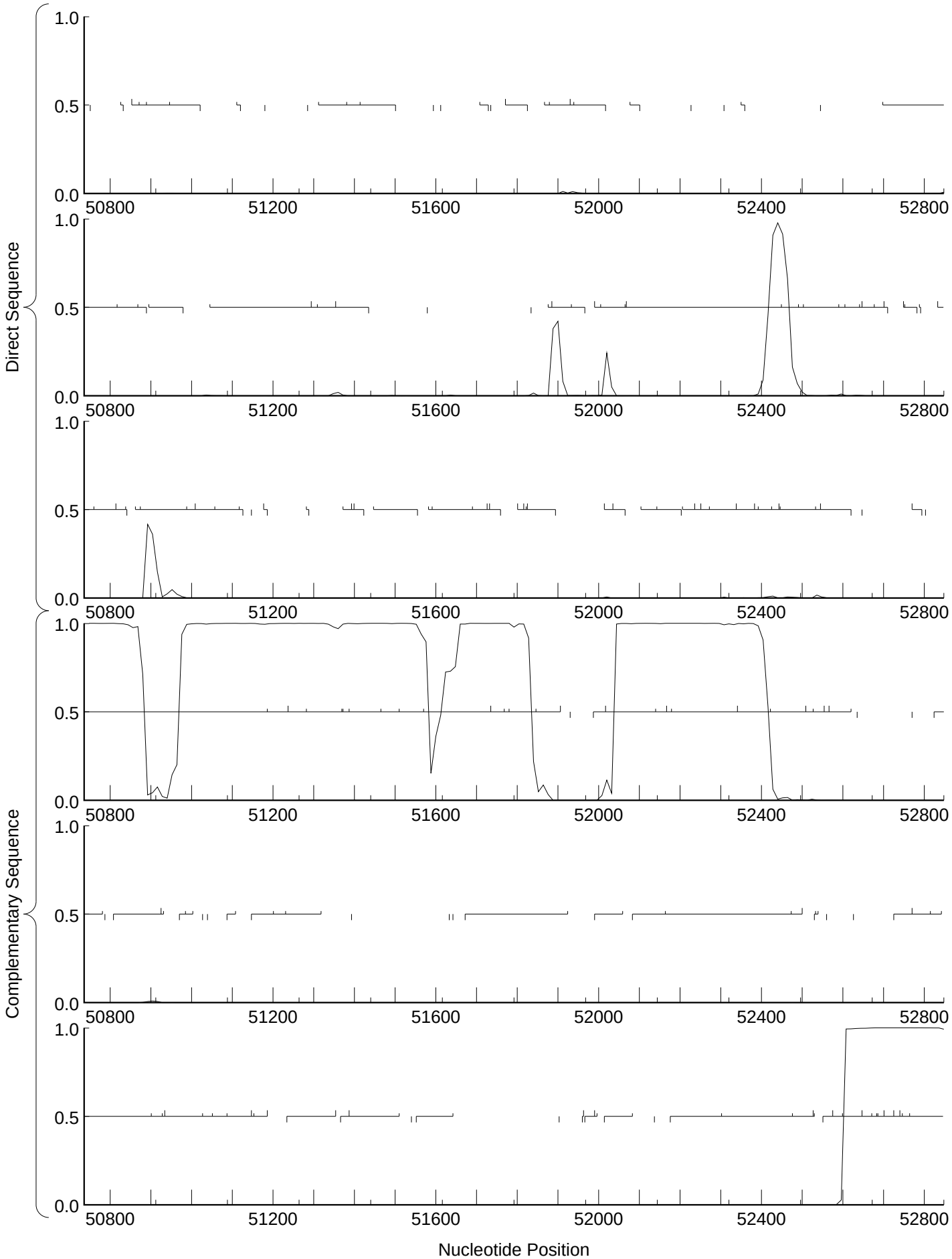


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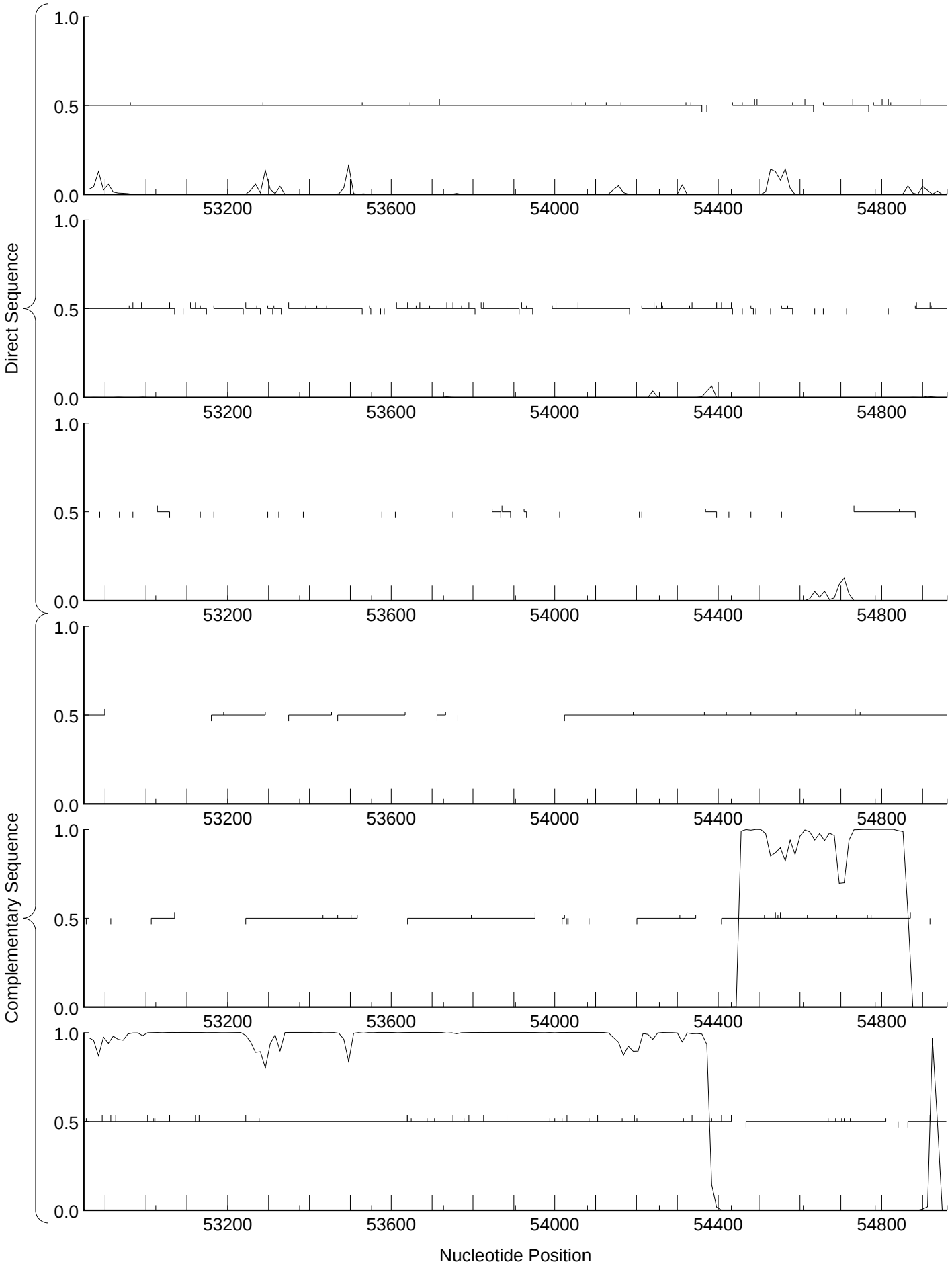


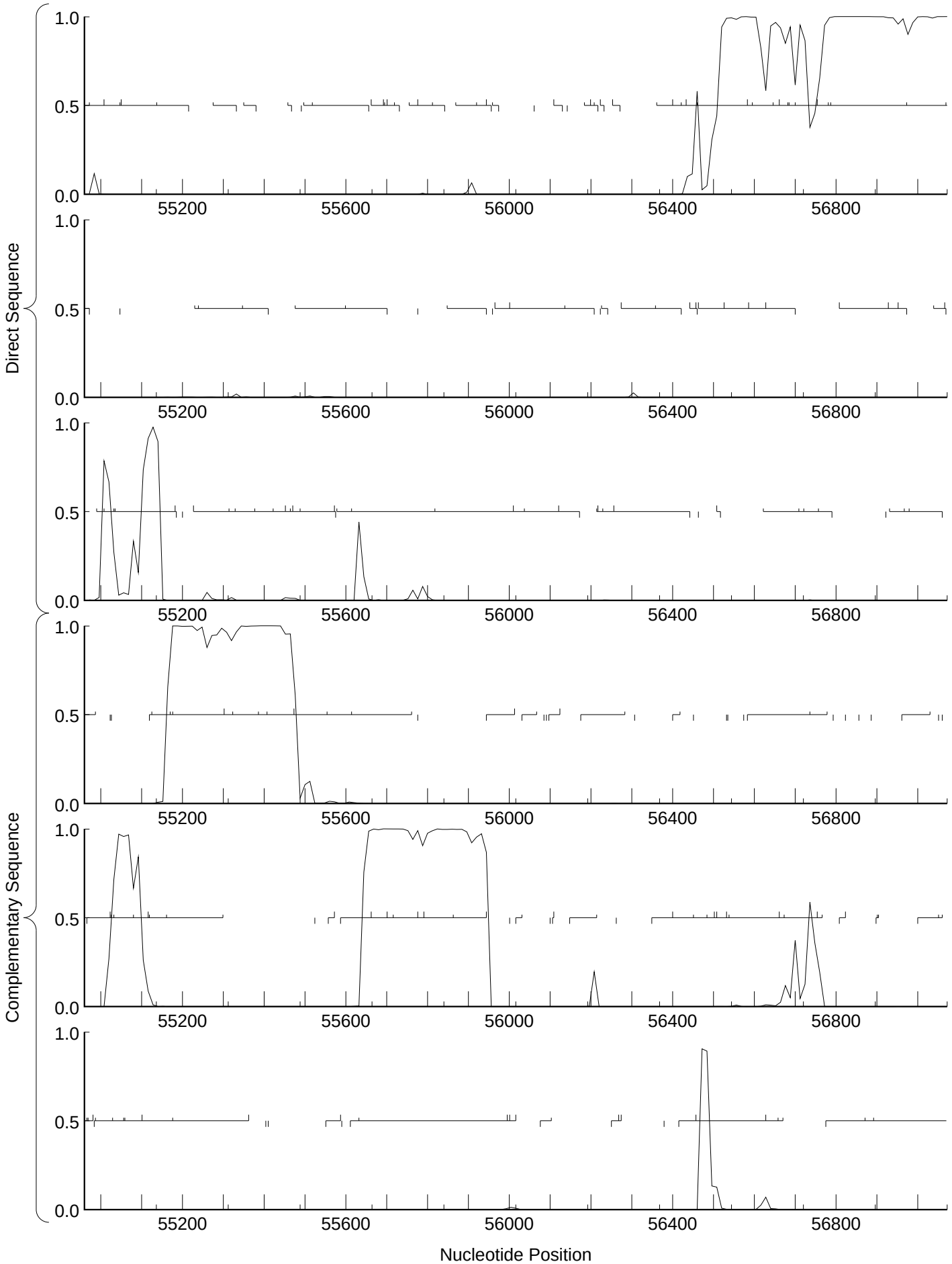
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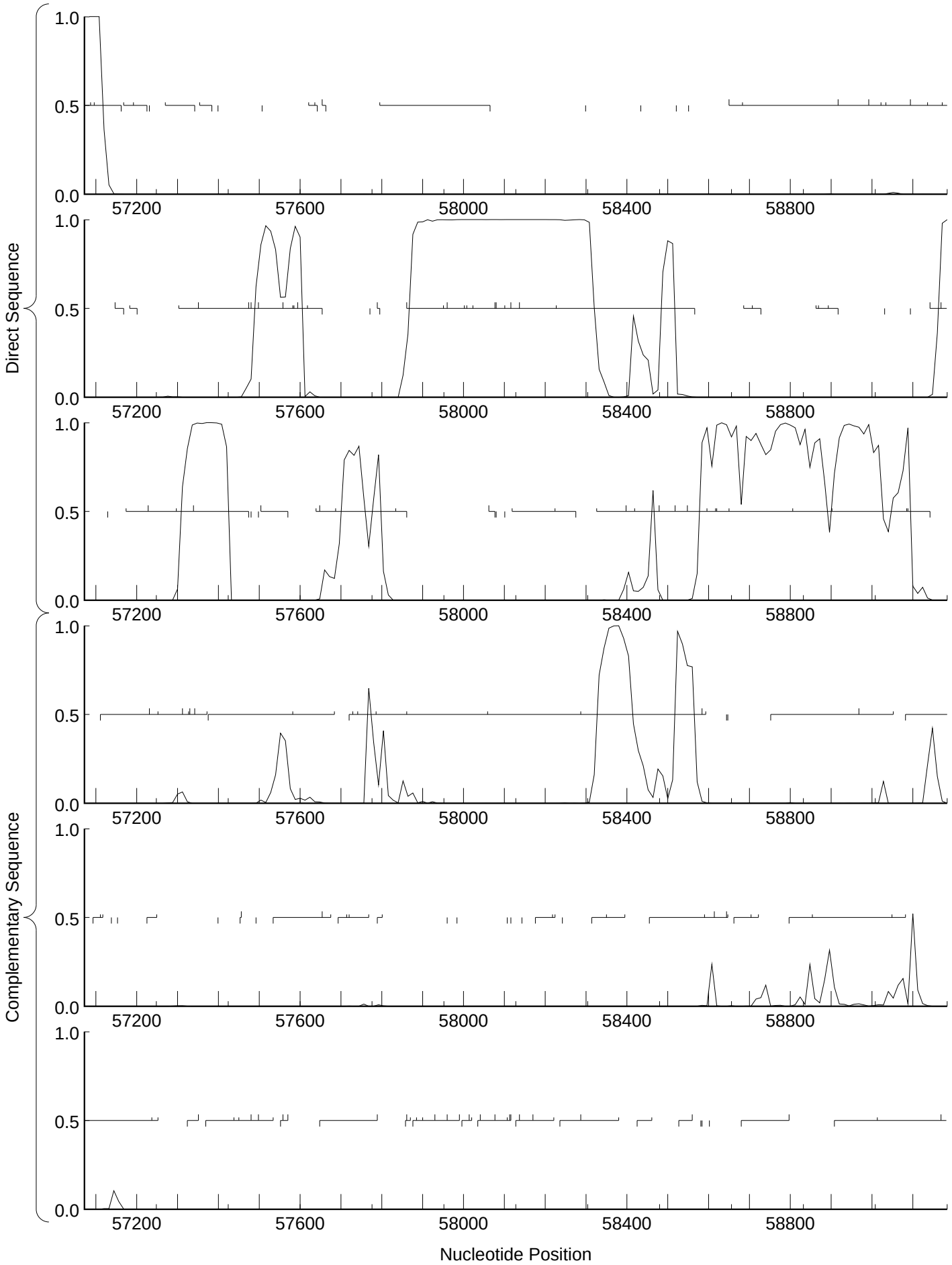

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
50800
51200
51600
52000
52400
52800
Nucleotide Position

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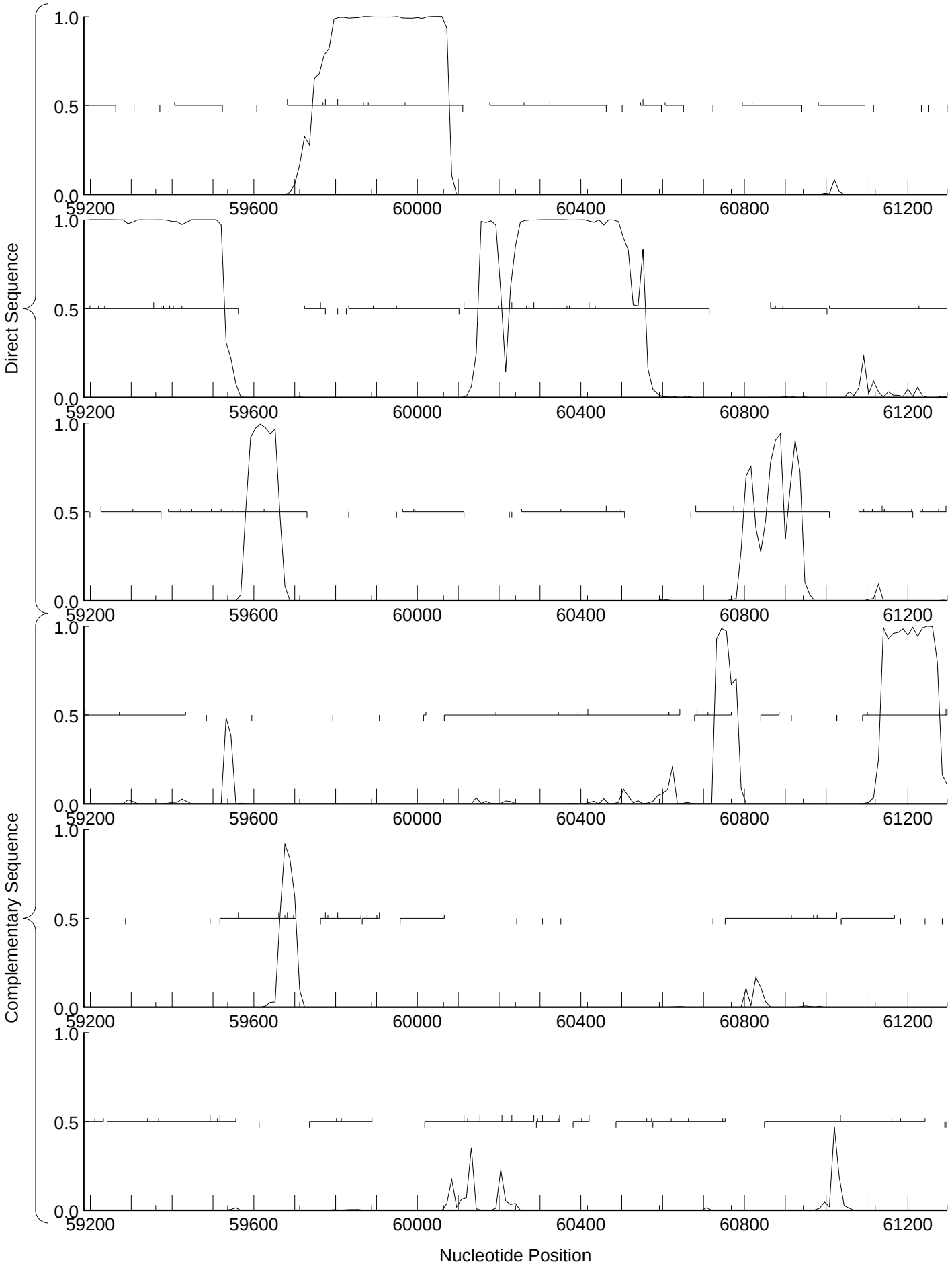



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Complementary Sequence
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56000
56400
56800
Nucleotide Position

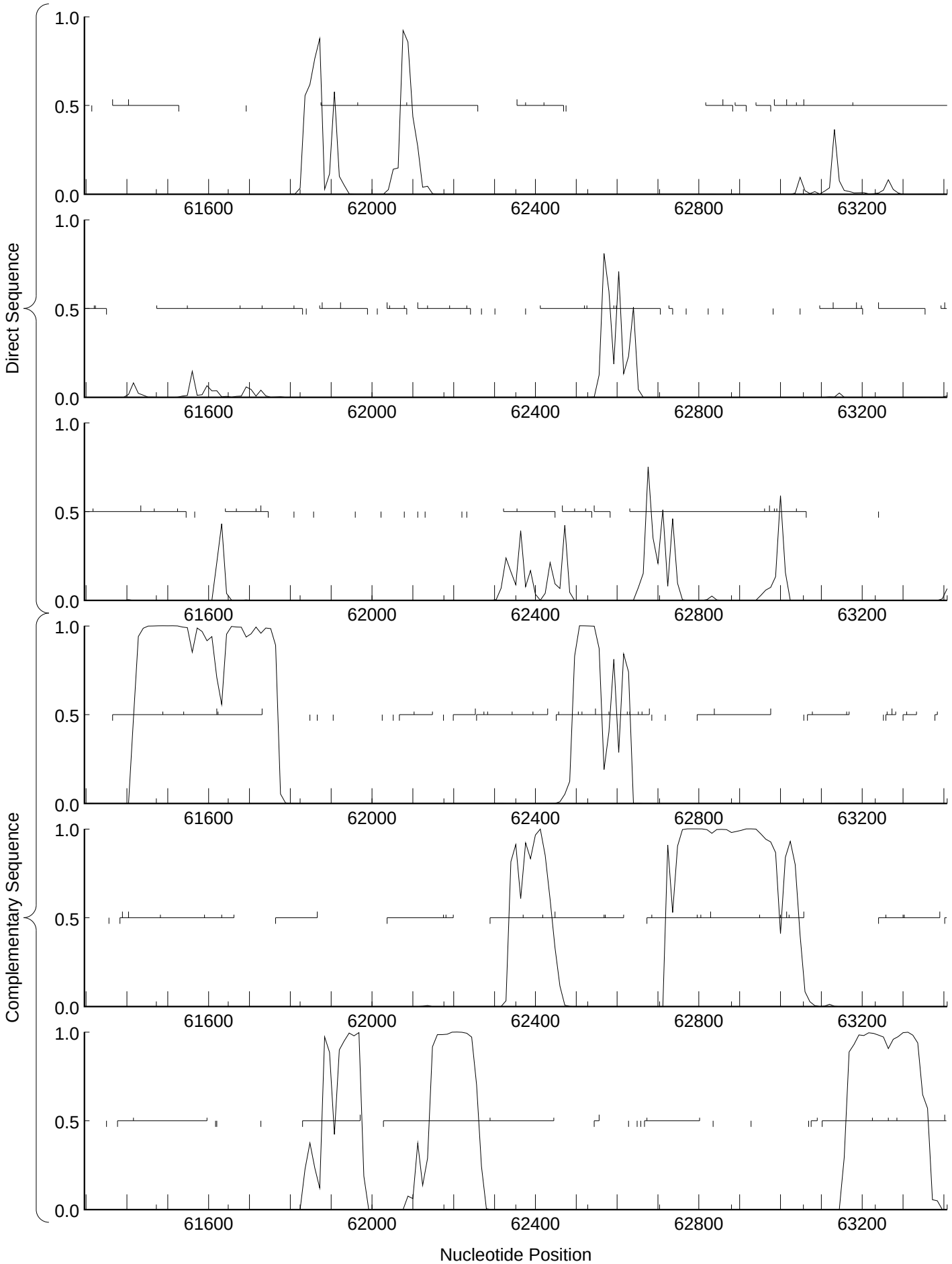
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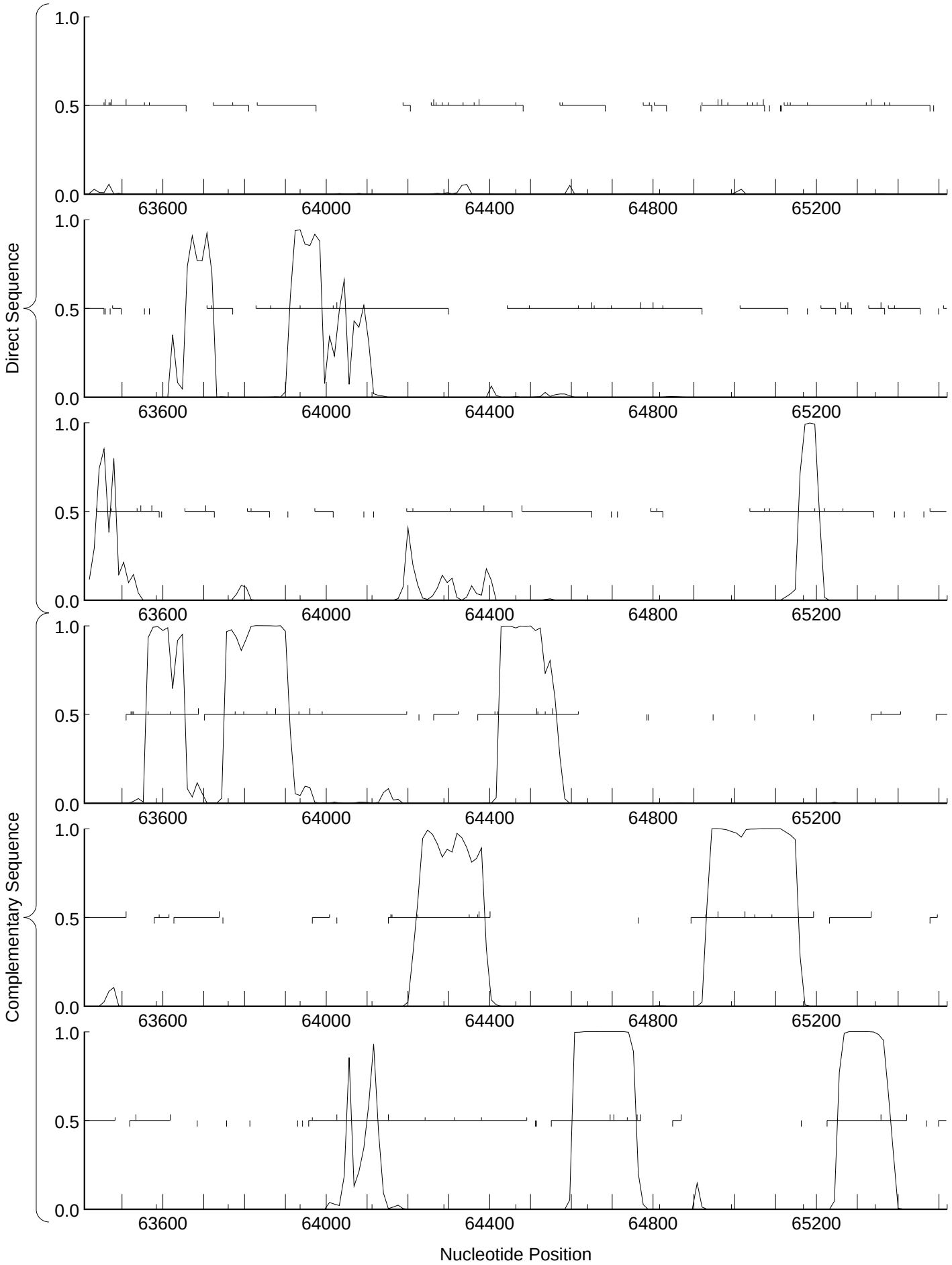
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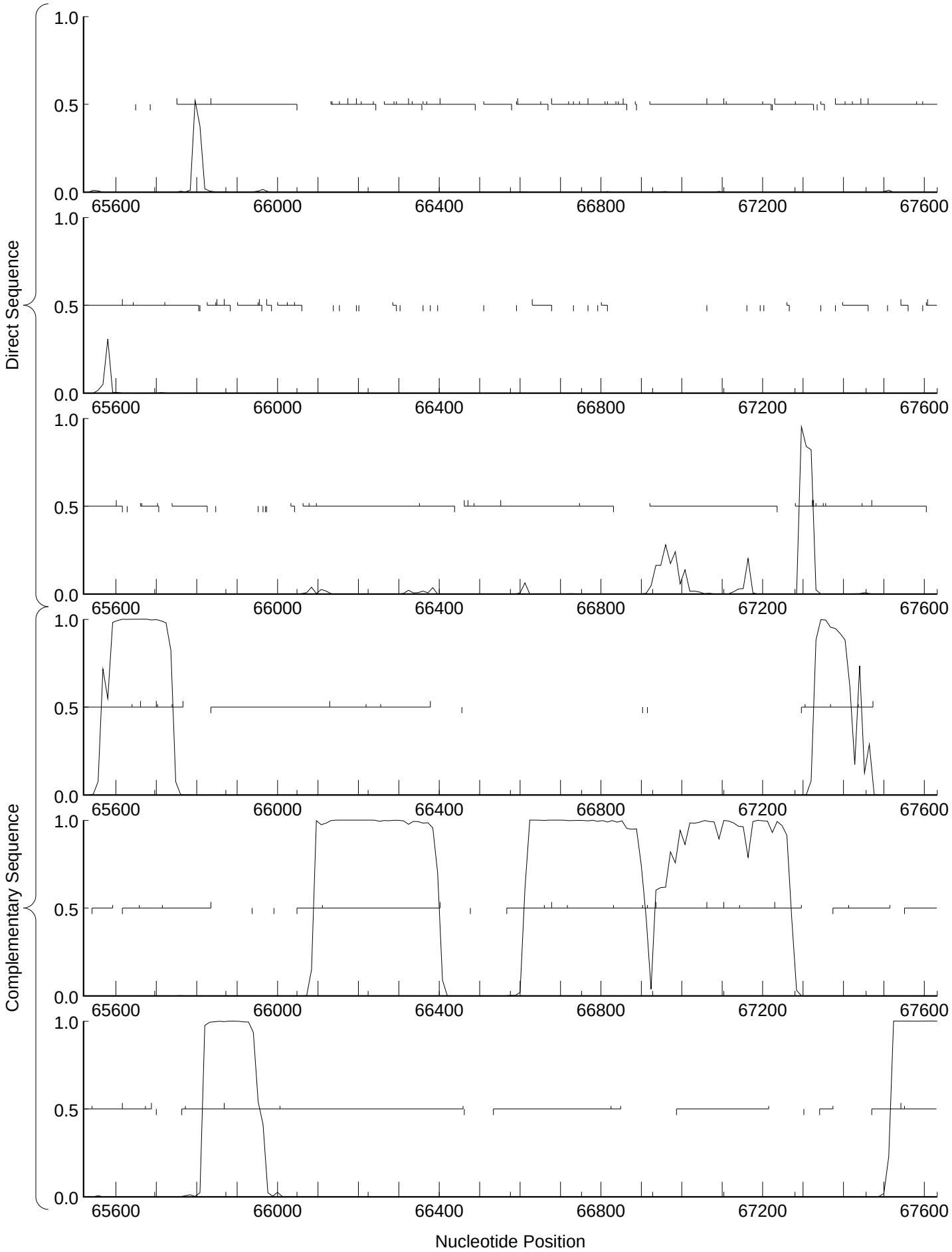
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erium phage PhrodoBaggins complete sequence, 68873 bp, circularly permuted, Cluster B1, Order 4, Window 96, Step 12, 32/34



erium phage PhrodoBaggins complete sequence, 68873 bp, circularly permuted, Cluster B1, Order 4, Window 96, Step 12, 33/34



erium phage PhrodoBaggins complete sequence, 68873 bp, circurlarly permuted, Cluster B1, Order 4, Window 96, Step 12, 34/34

