GeneMark

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

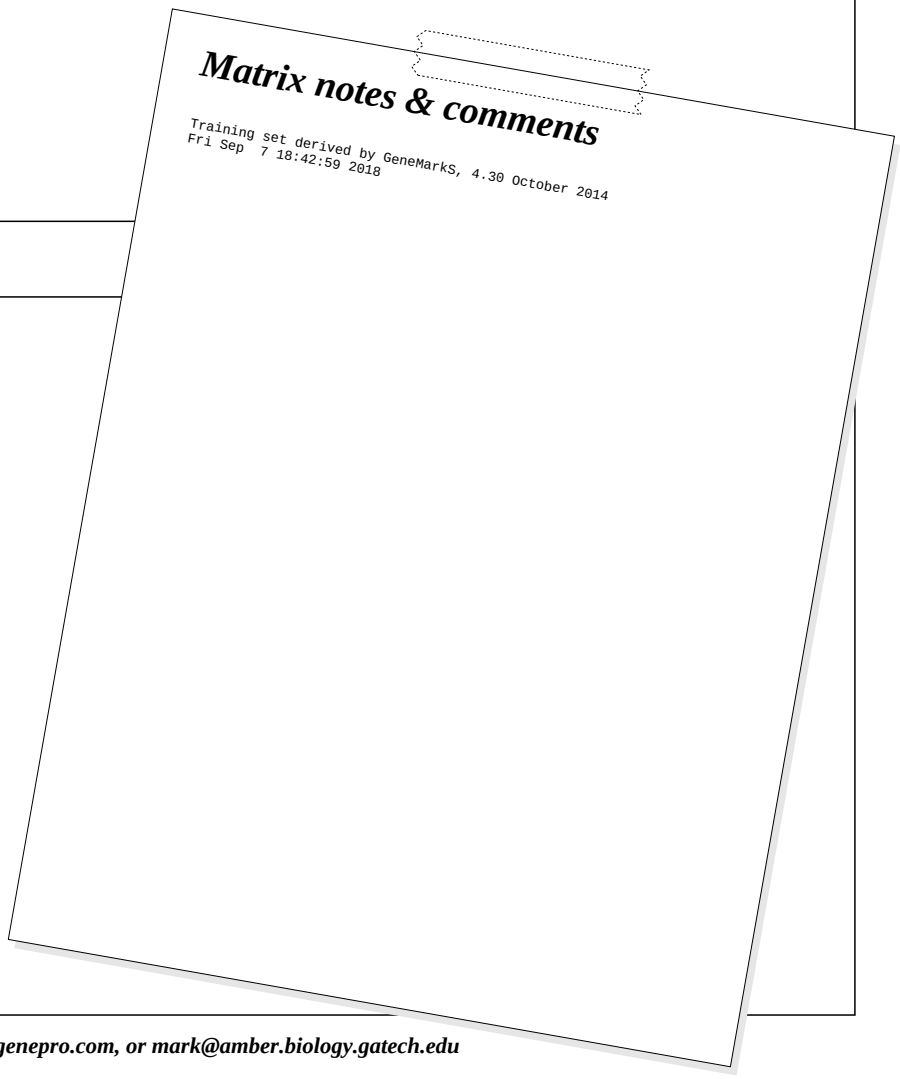
PROGRAM INFORMATION

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Sequence         :  Microbacterium phage Hiddenleaf complete sequence, 56082 bp, circularly permuted, Cluster E
Analysis Date    :  3/28/24 at 14:14:15
Pages            :  28
Sequence Length  :  56082 bp
GC Content       :   63.66%

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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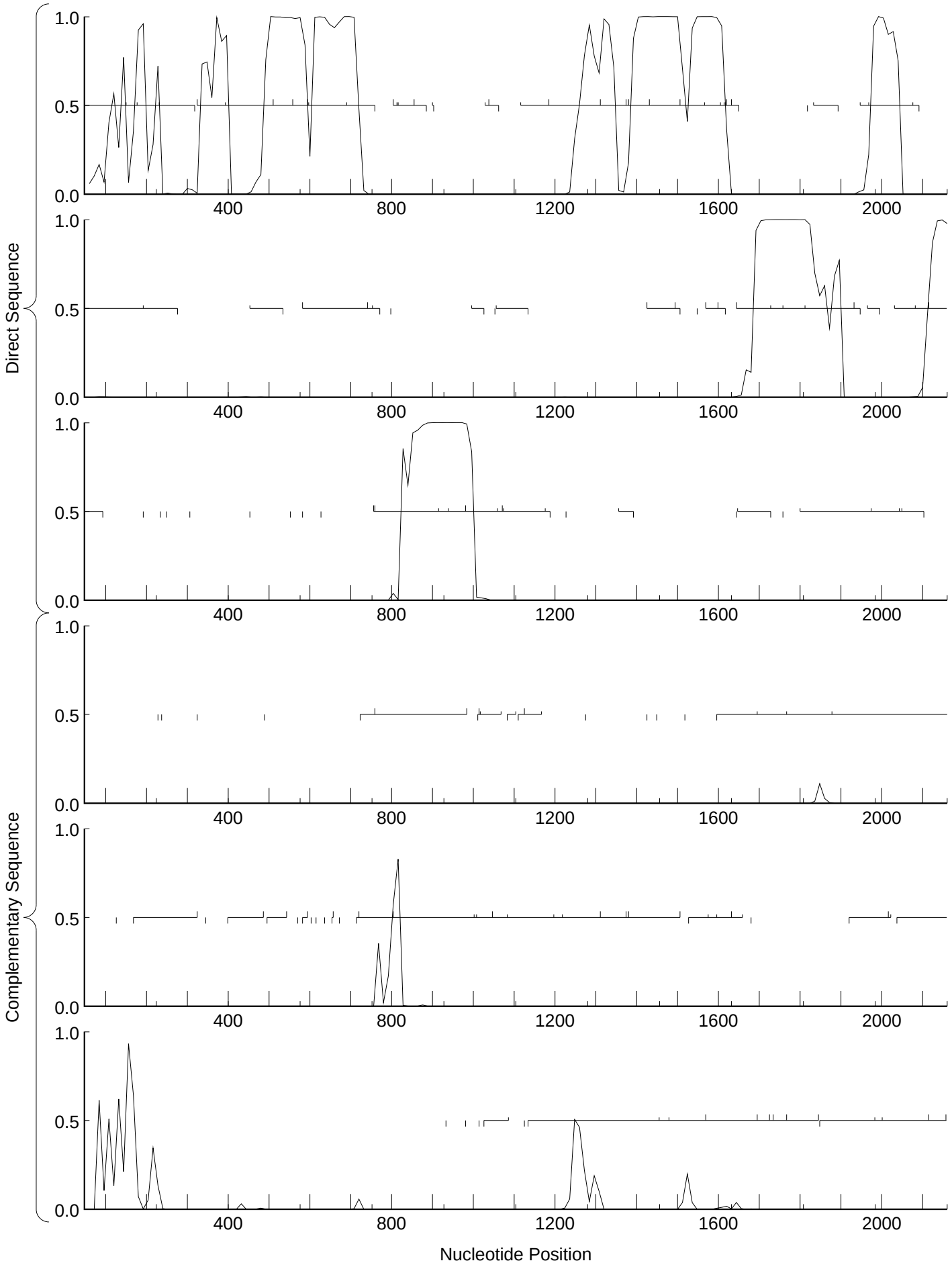
MATRIX INFORMATION

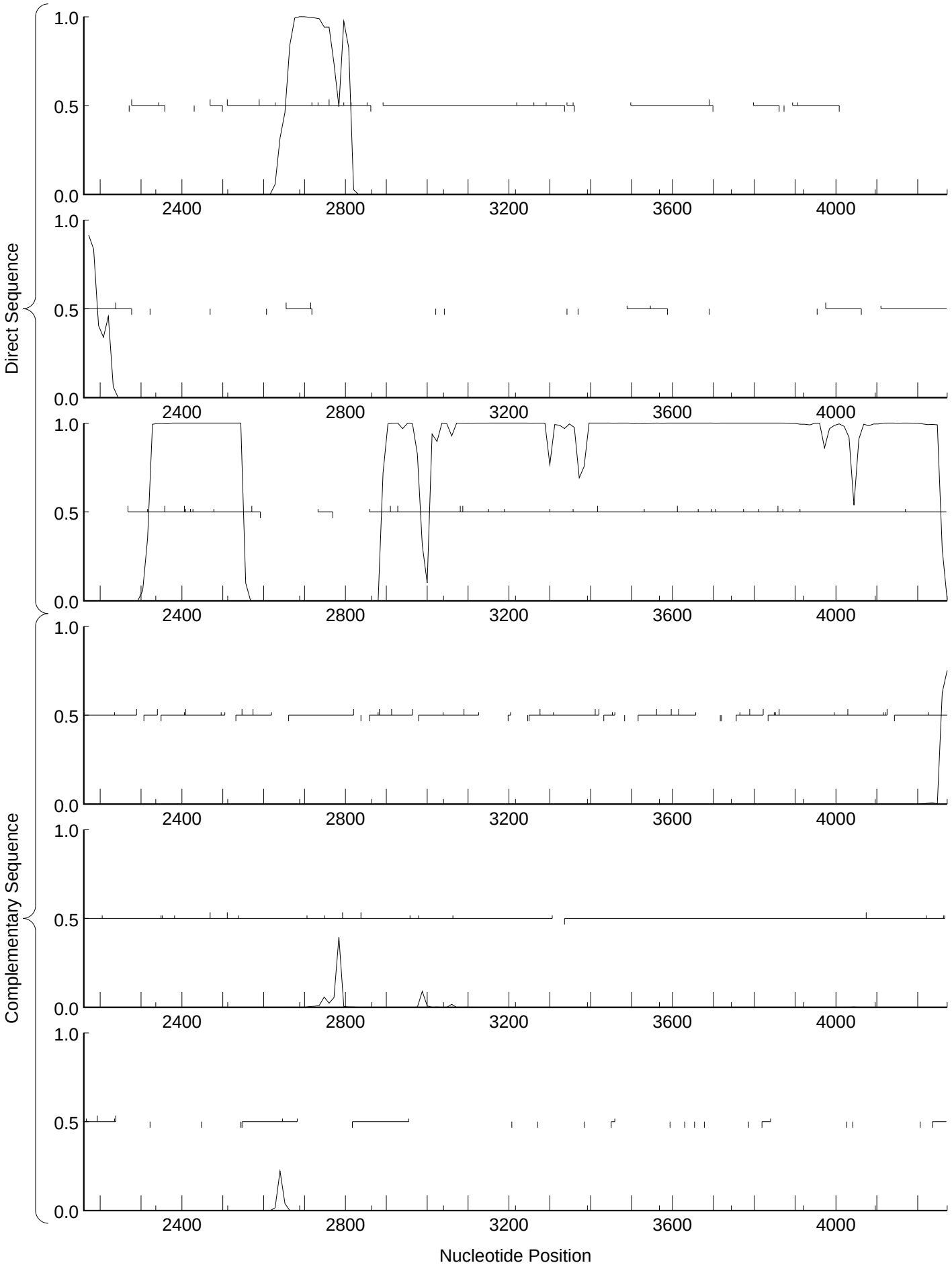
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Matrix     :  -
Author     :  -

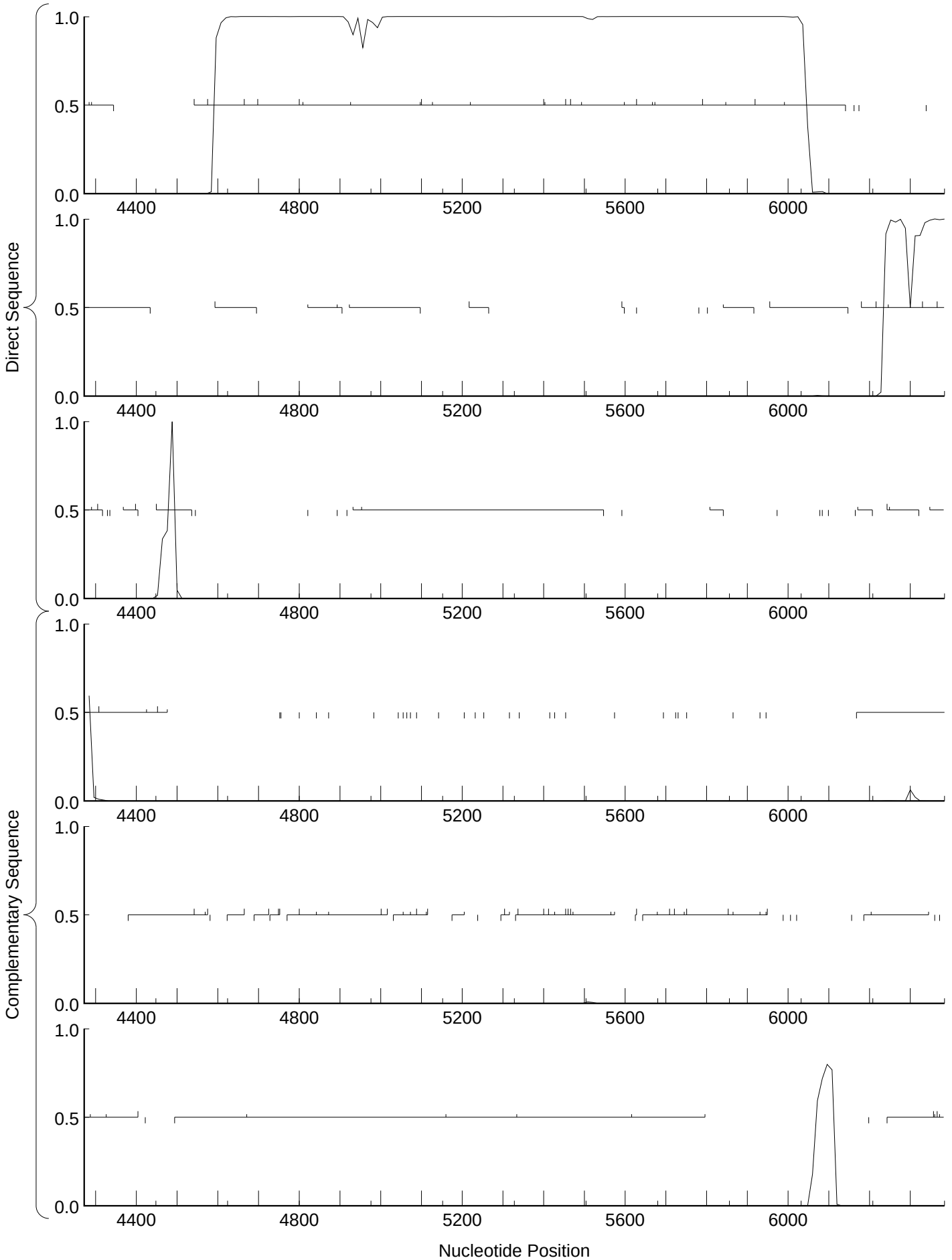
Order      :  4
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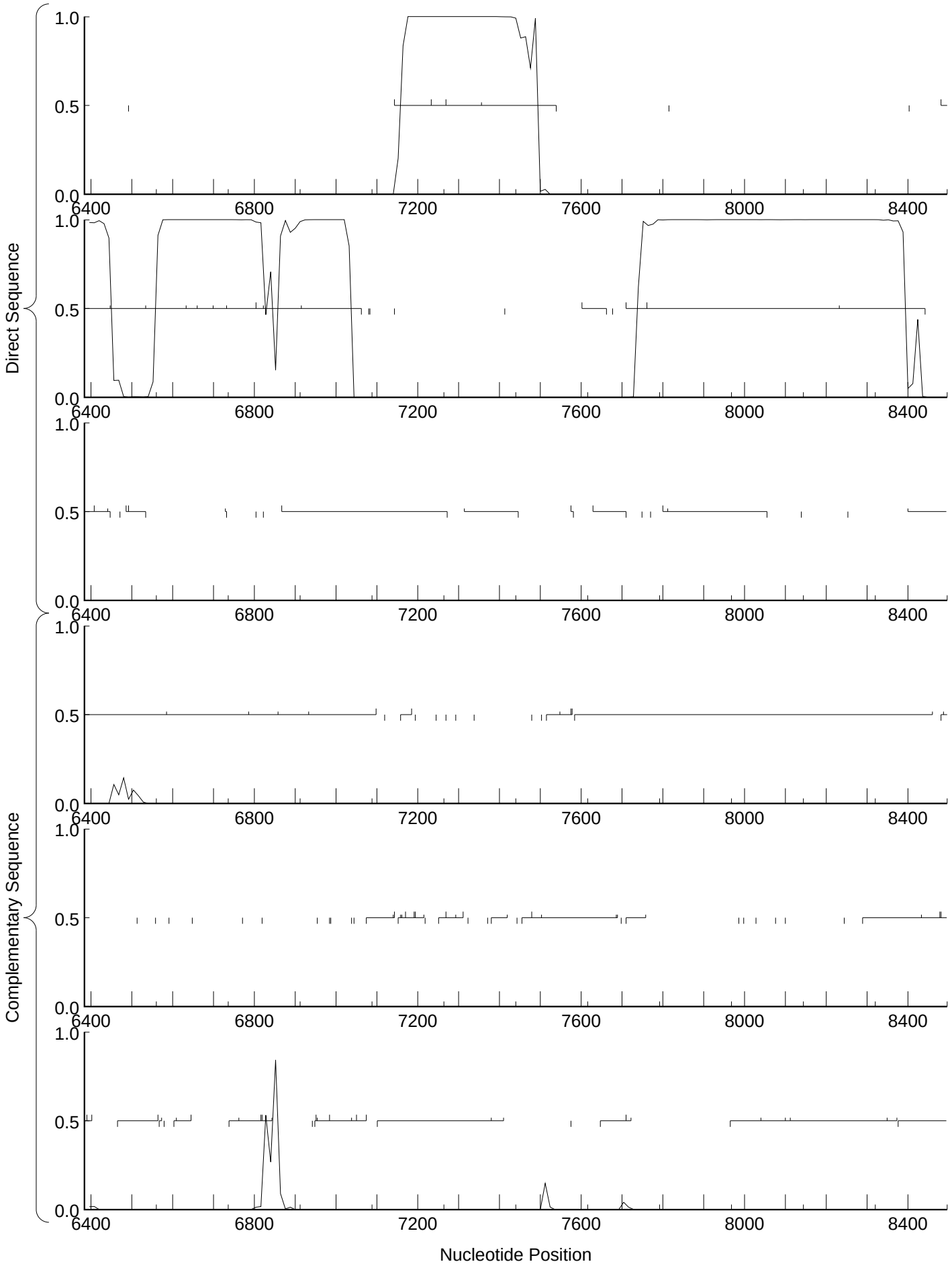

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  Send questions / comments to:
      Dr. M. Borodovsky
      Georgia Institute of Technology
      School of Biology
      Atlanta, GA  30332-0230
```

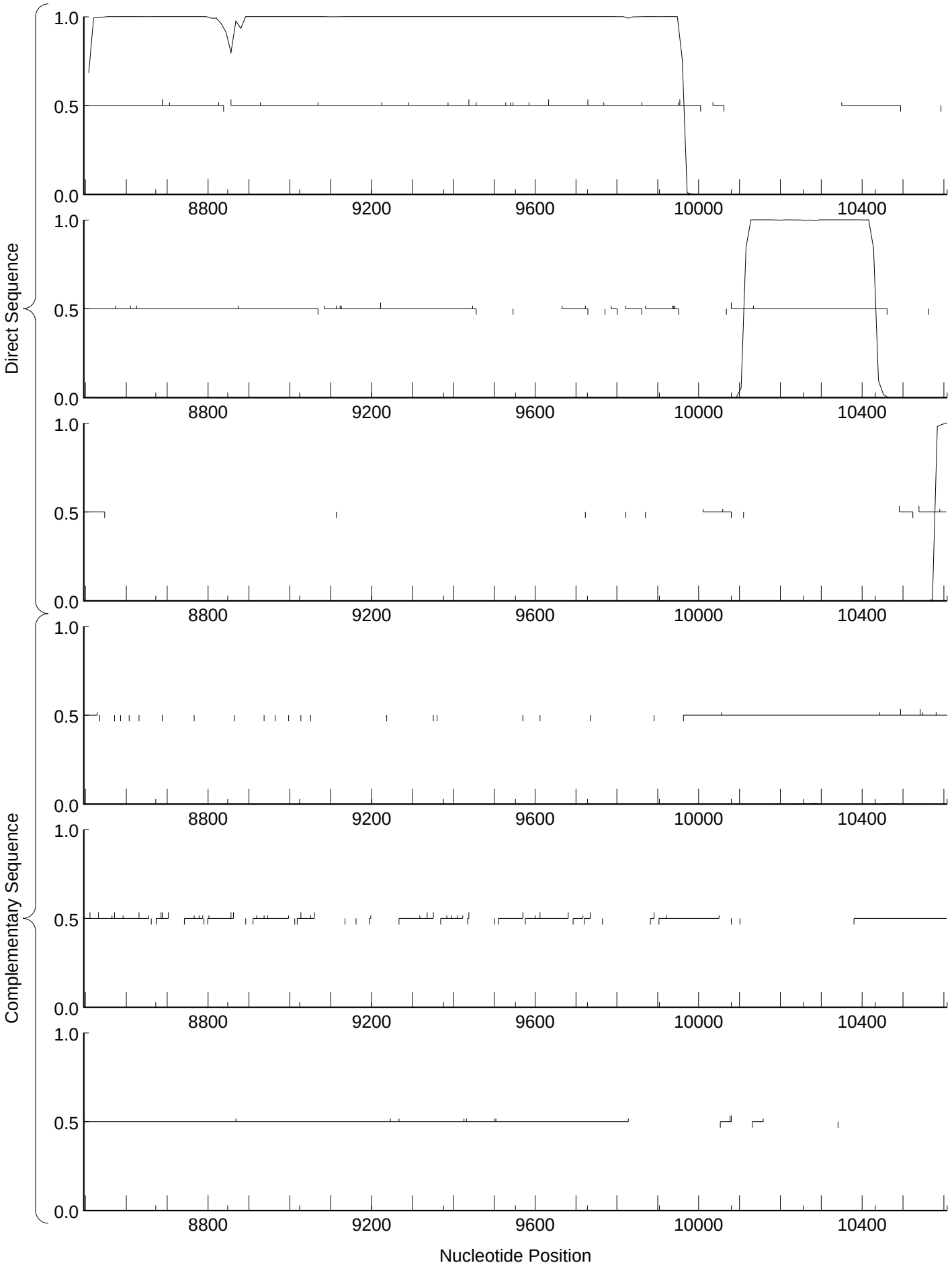

For help or information, send electronic mail to: custserv@genepro.com, or mark@amber.biology.gatech.edu

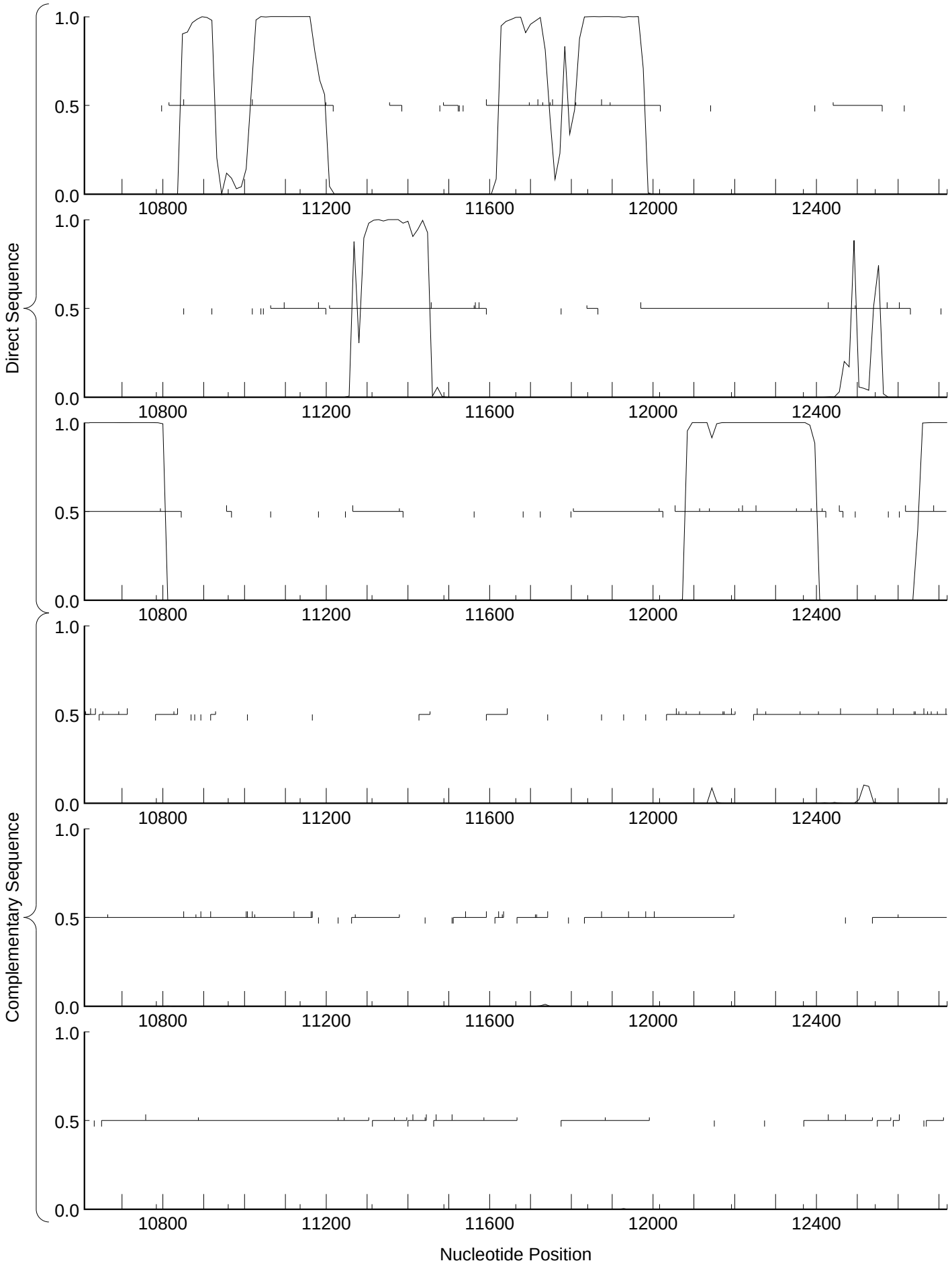

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
400
800
1200
1600
2000
Nucleotide Position

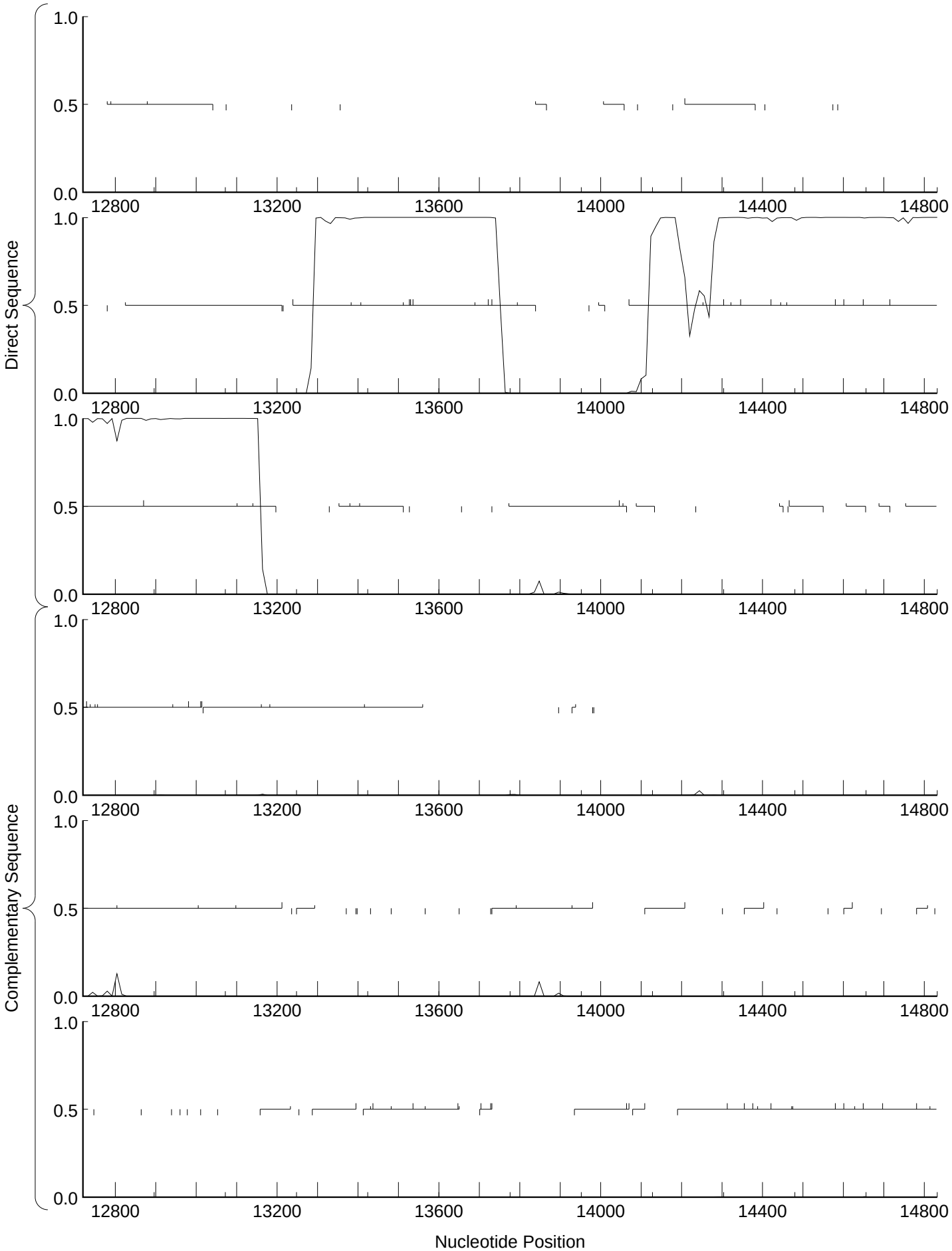

Direct Sequence
Complementary Sequence
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0.5
0.0
2400
2800
3200
3600
4000
Nucleotide Position

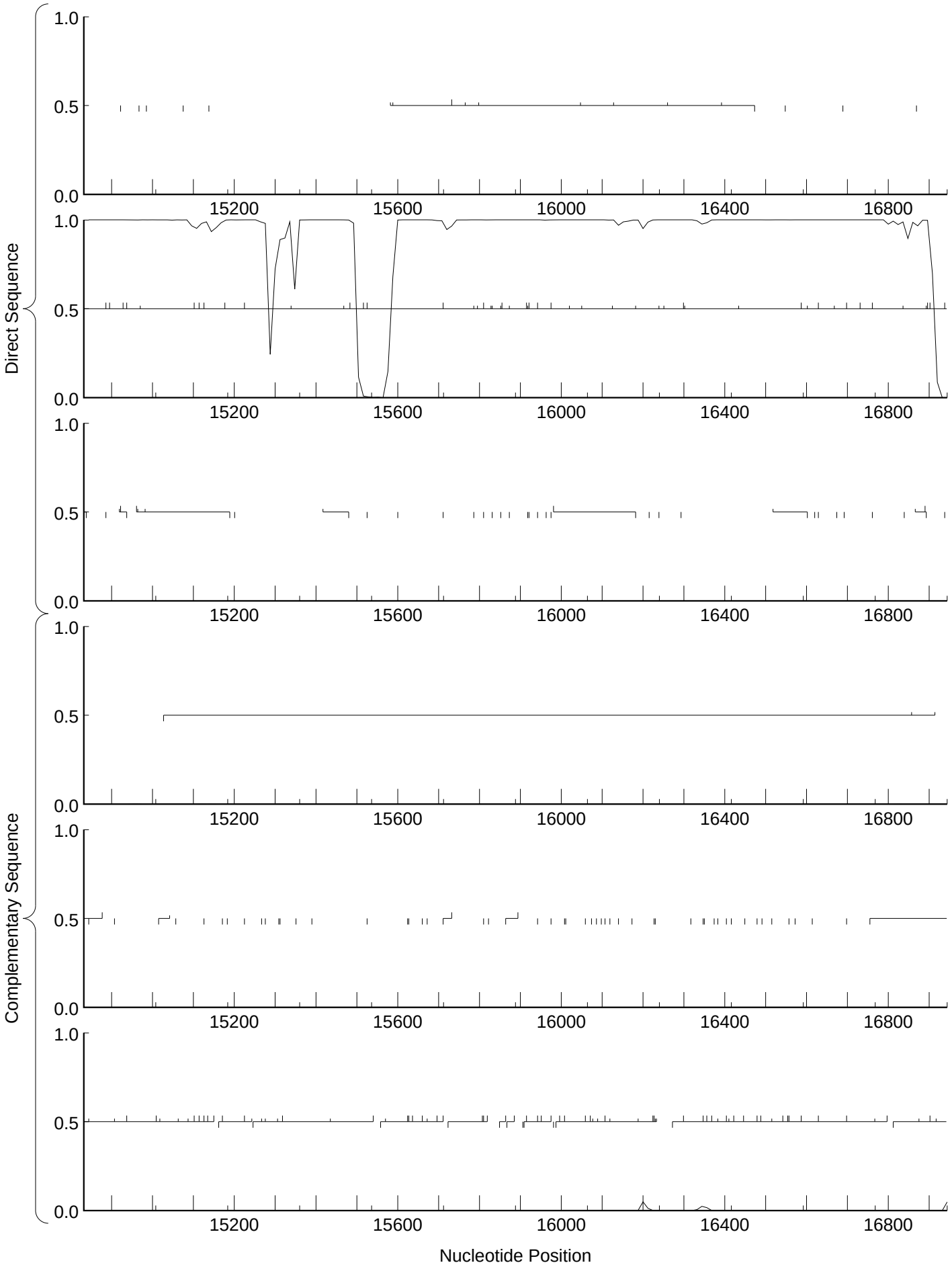

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
4400
4800
5200
5600
6000
Nucleotide Position


Direct Sequence
Complementary Sequence
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0.5
0.0
6400
6800
7200
7600
8000
8400
Nucleotide Position

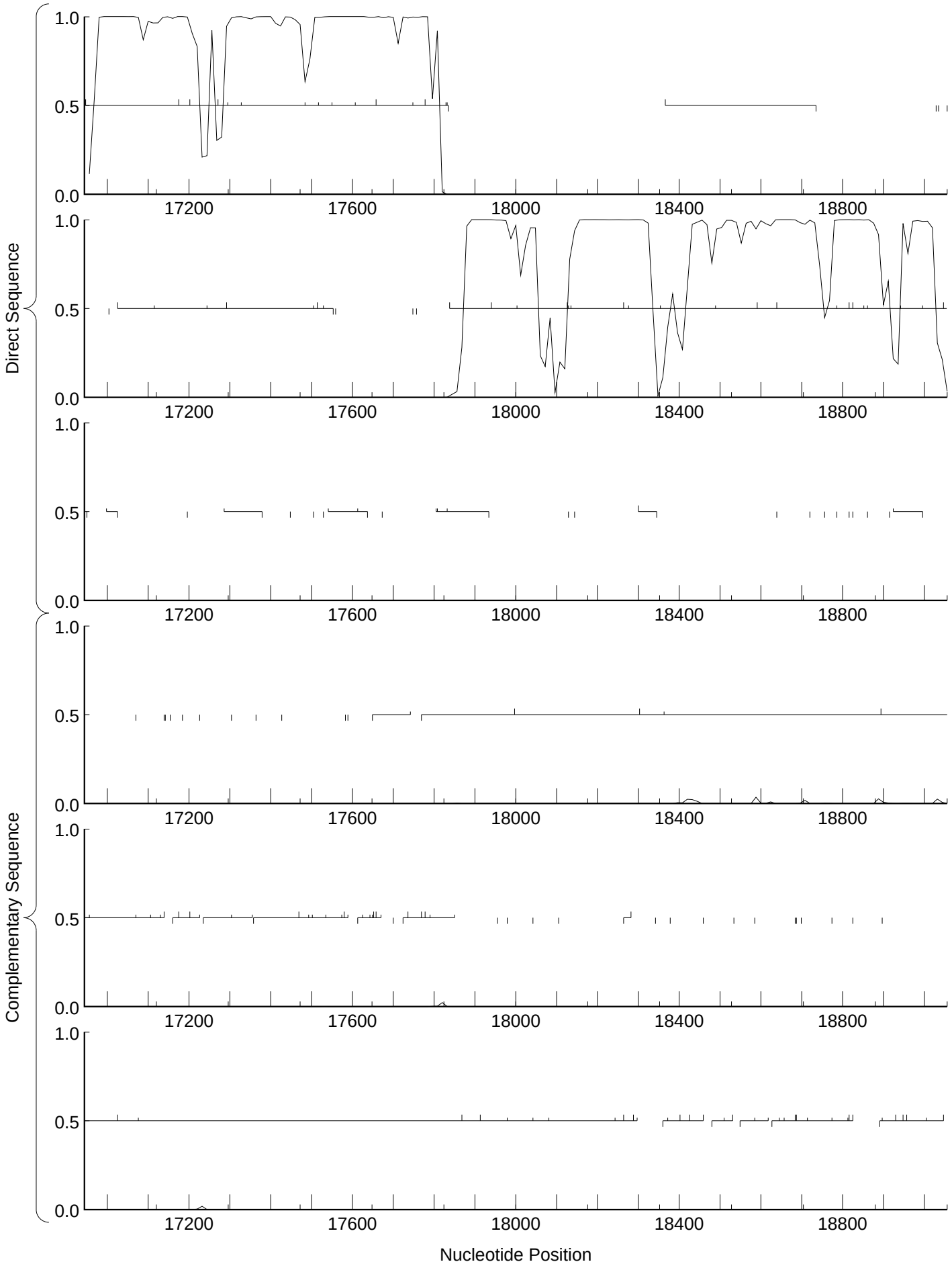

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
8800
9200
9600
10000
10400
Nucleotide Position


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

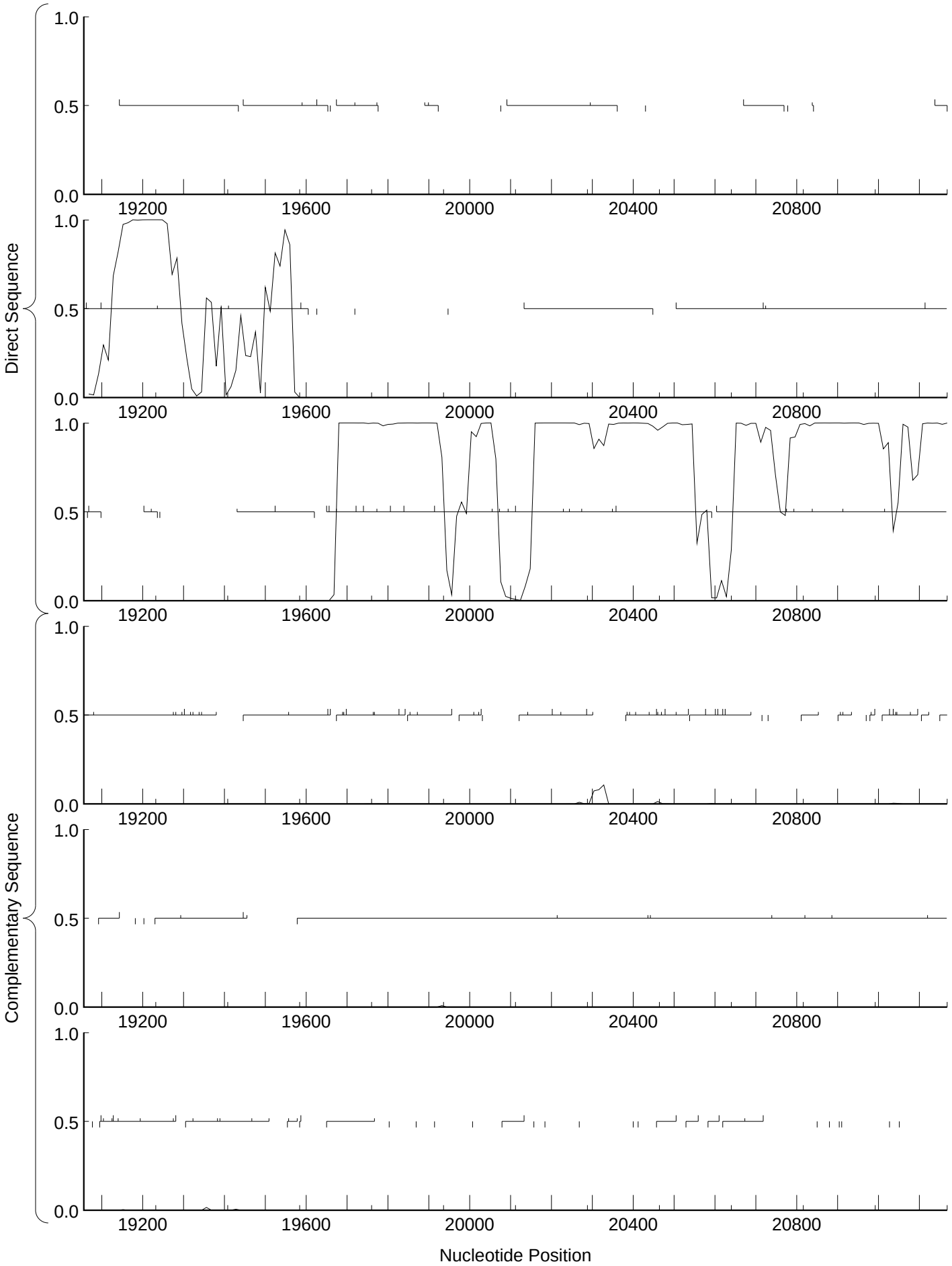

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
12800
13200
13600
14000
14400
14800
Nucleotide Position


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

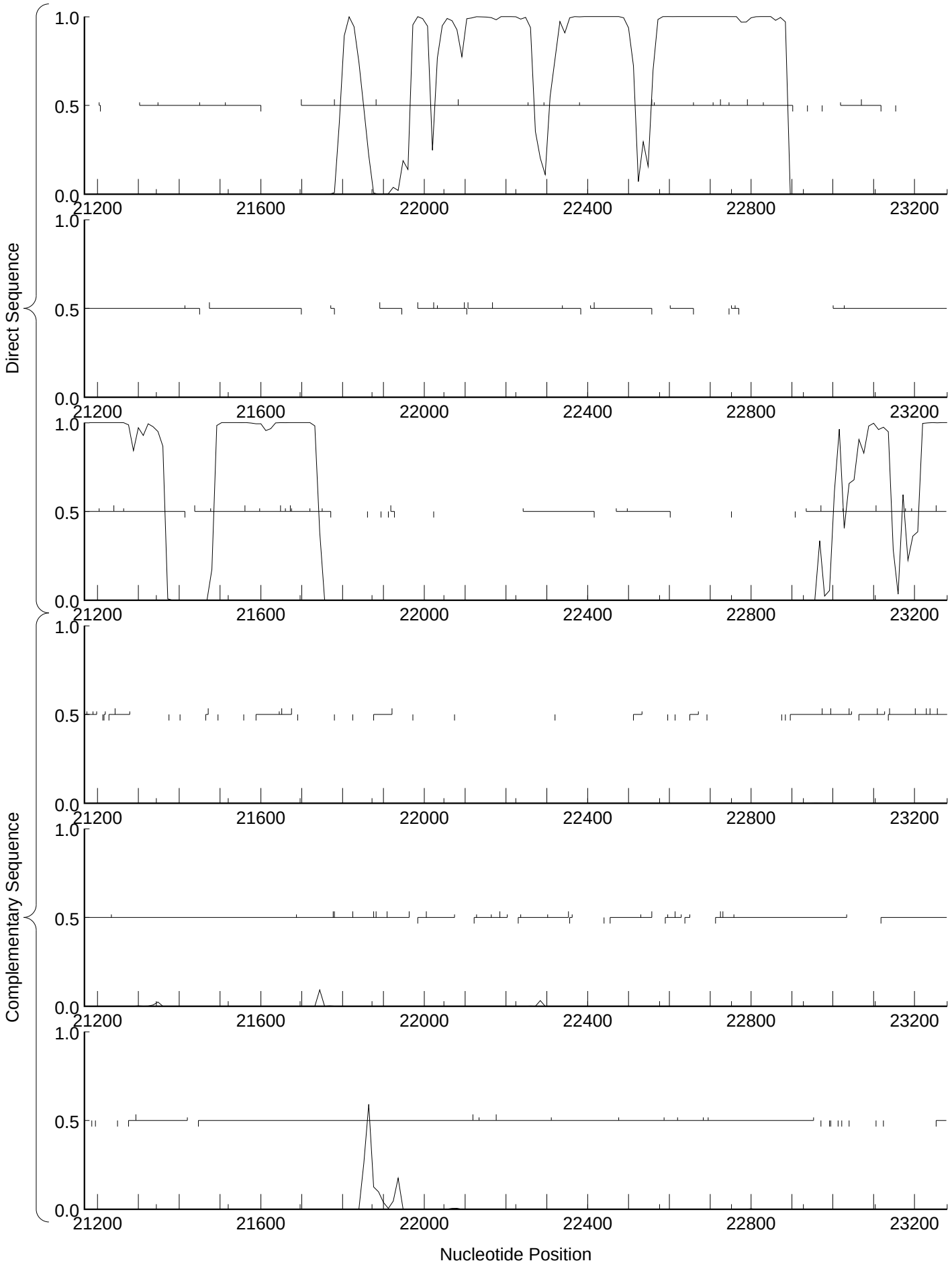
obacterium phage Hiddenleaf complete sequence, 56082 bp, circularly permuted, Cluster EF, Order 4, Window 96, Step 12, 10/28



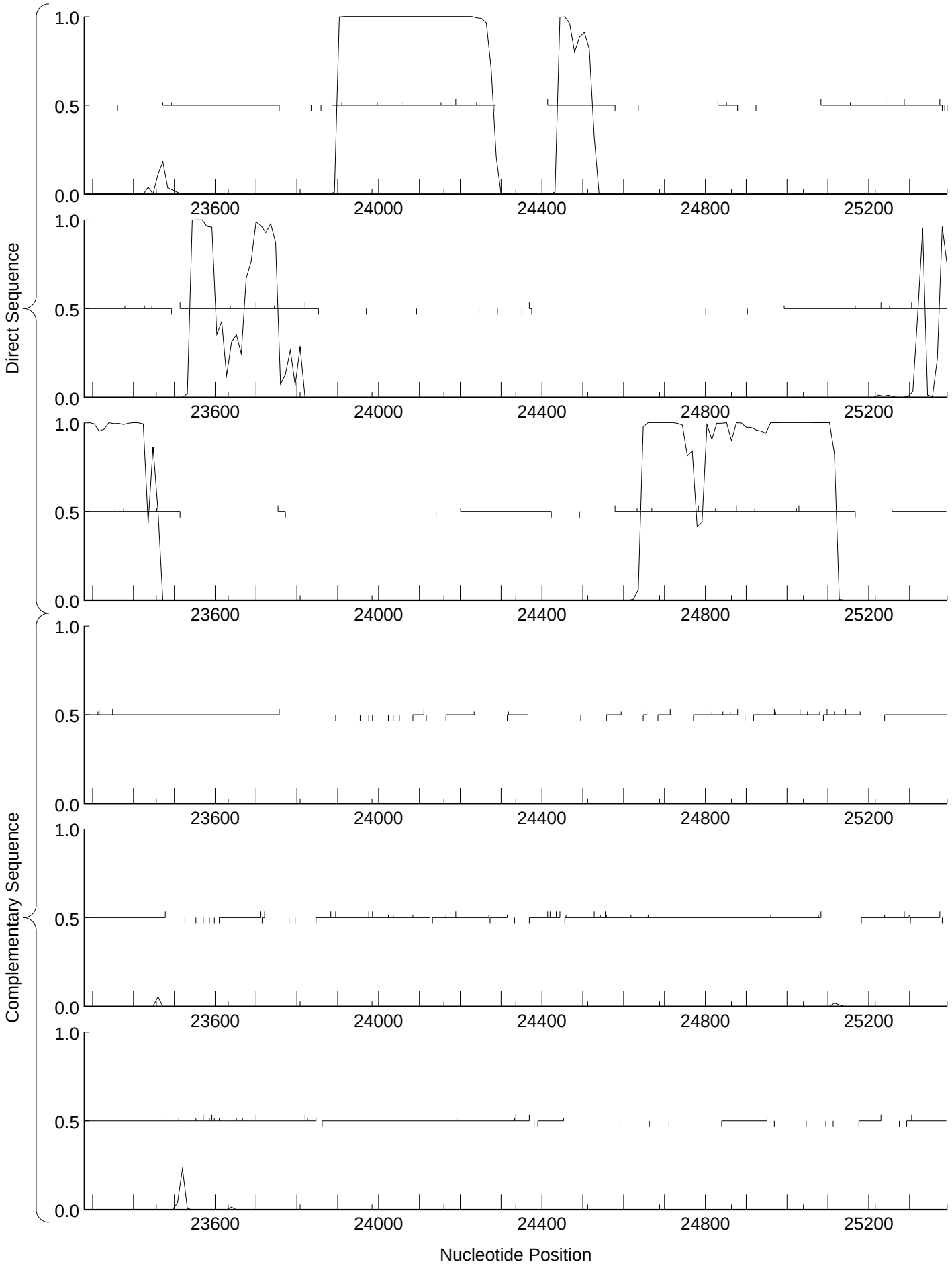
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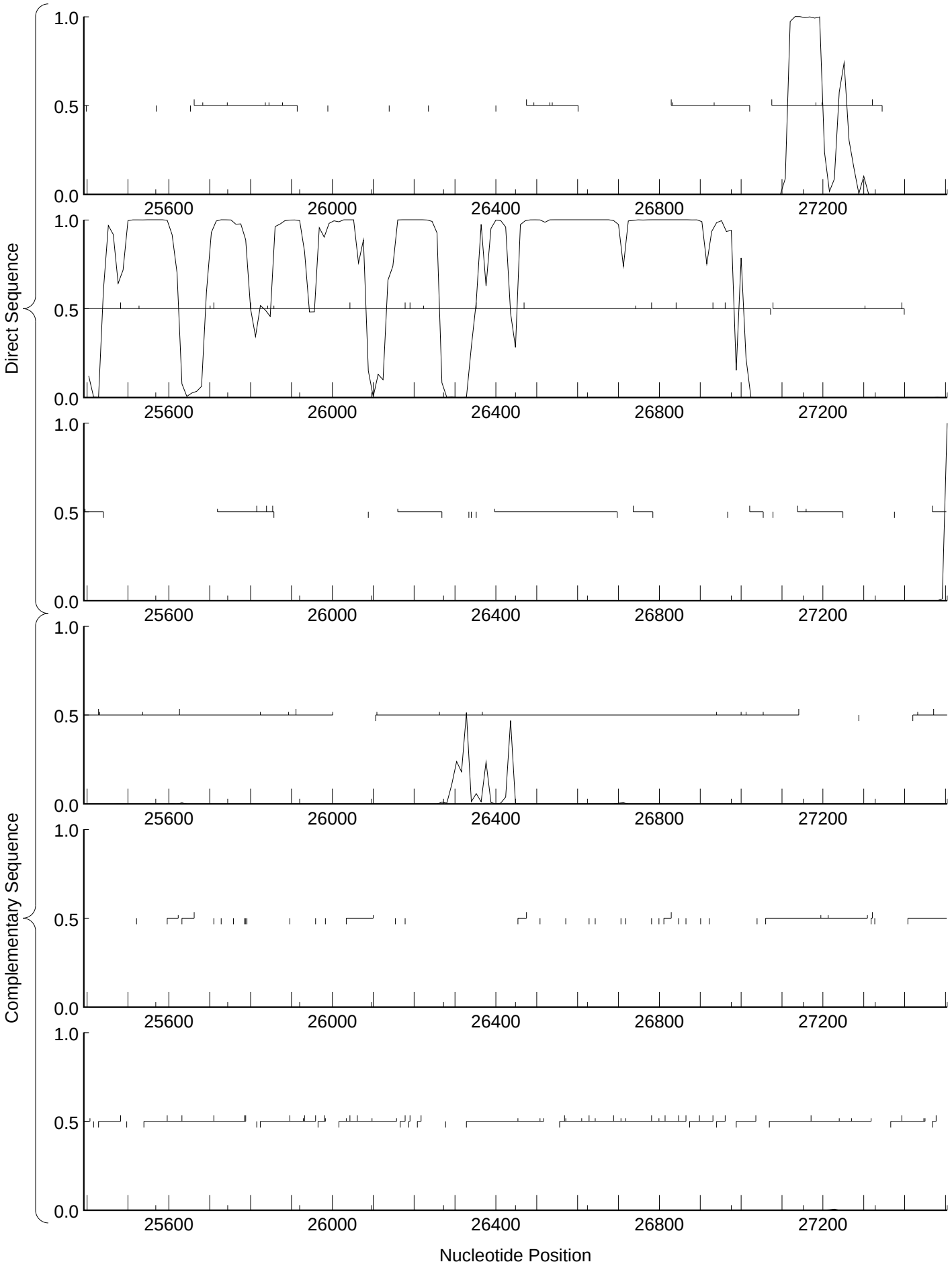
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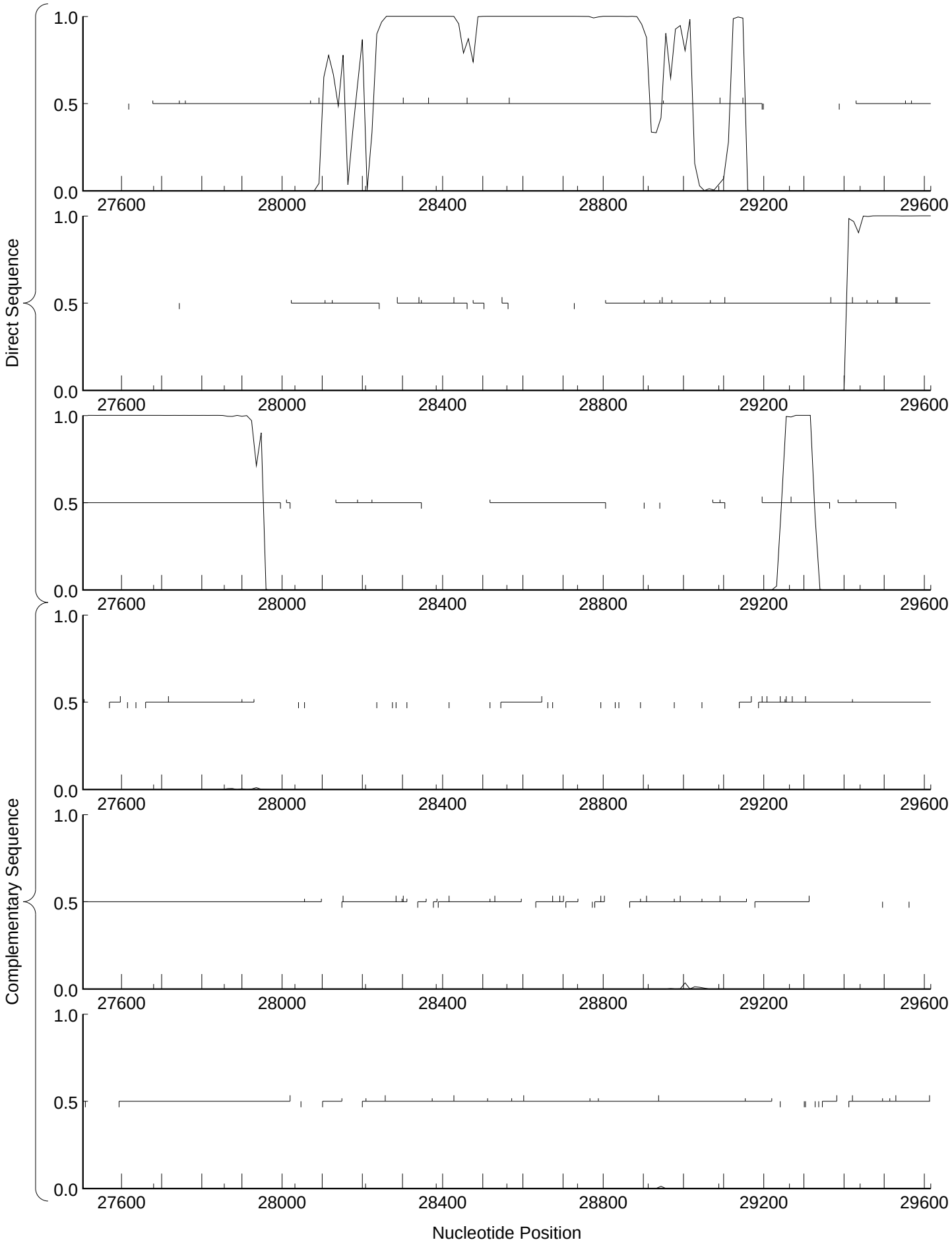
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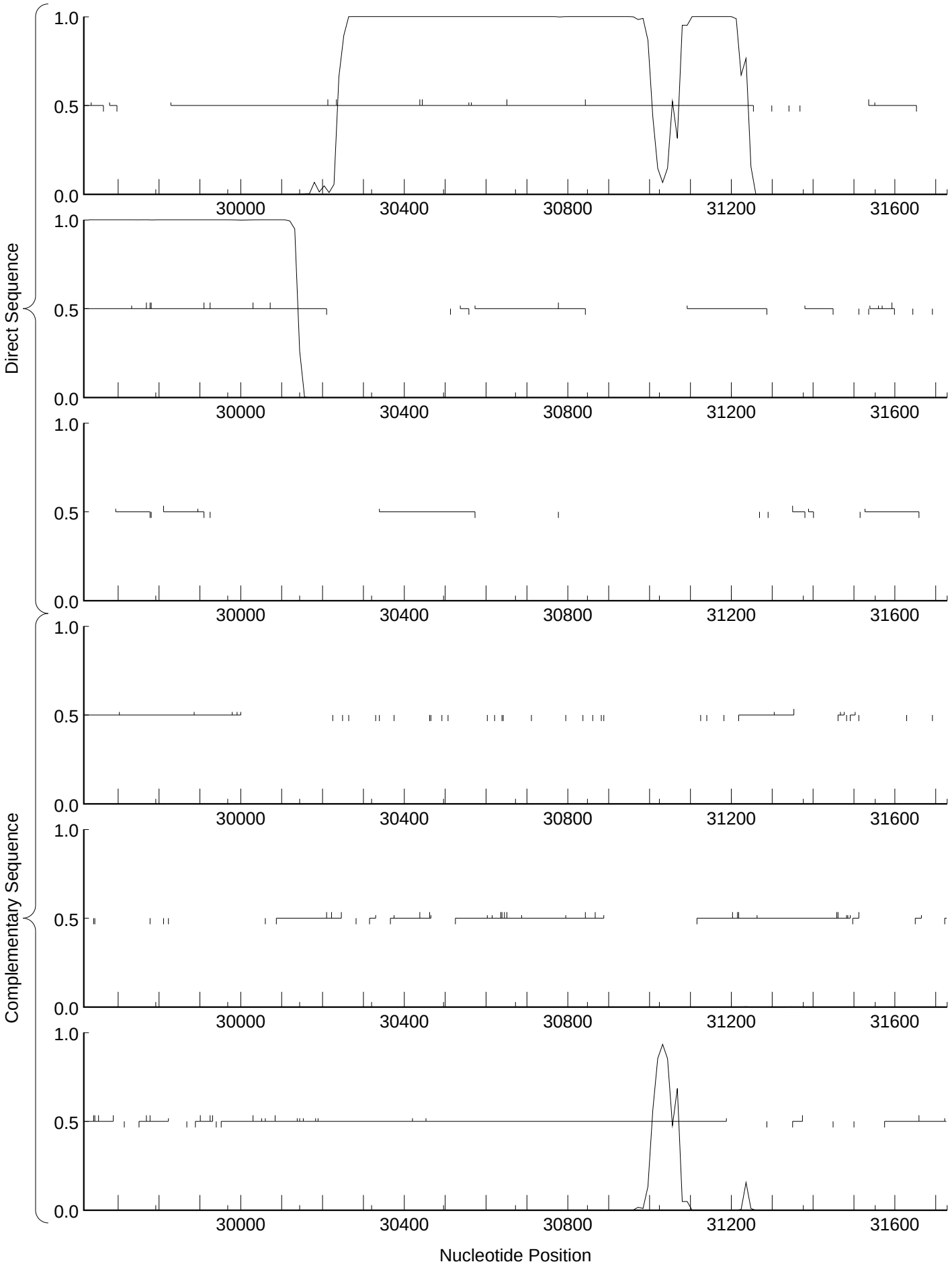
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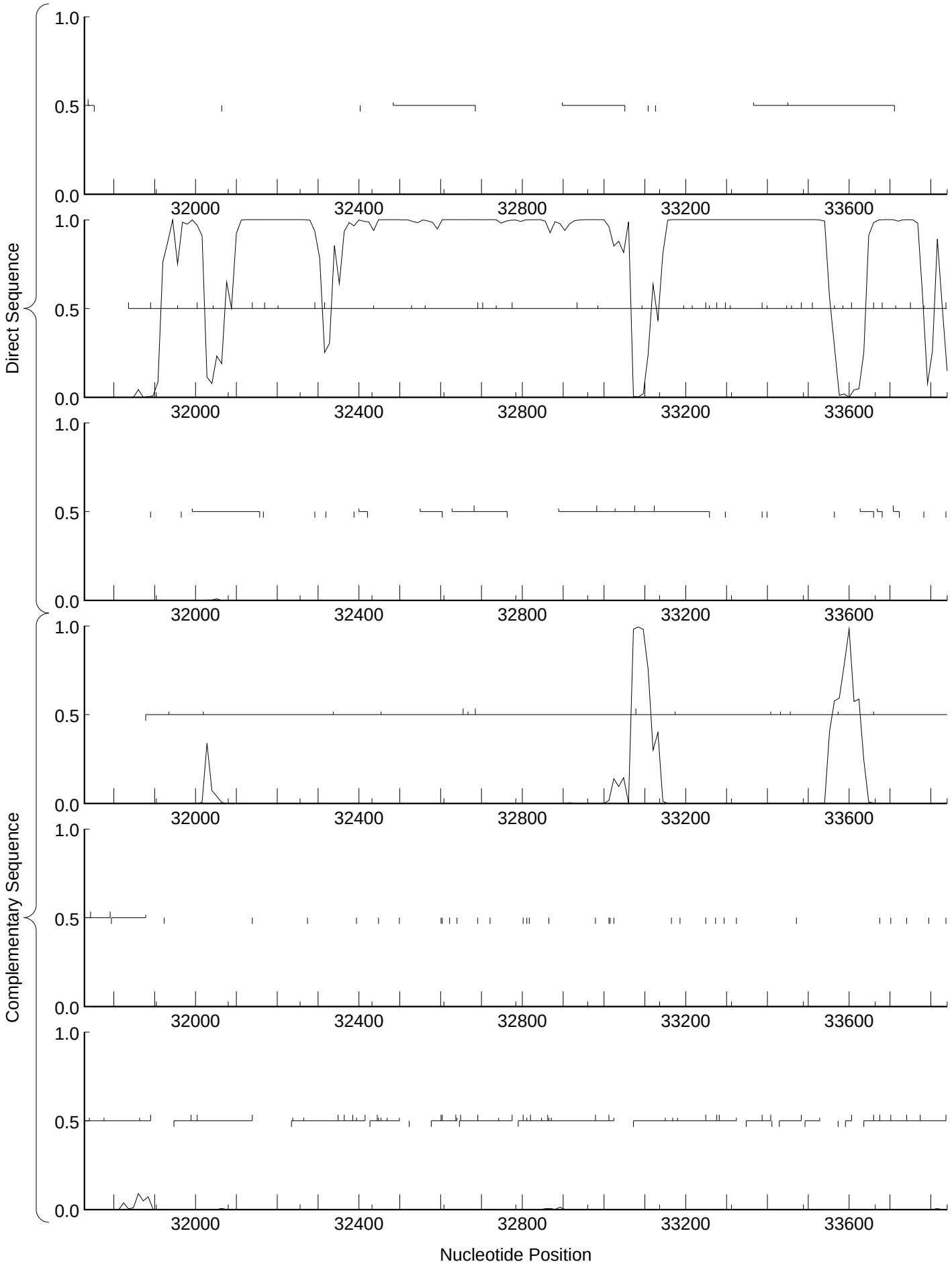
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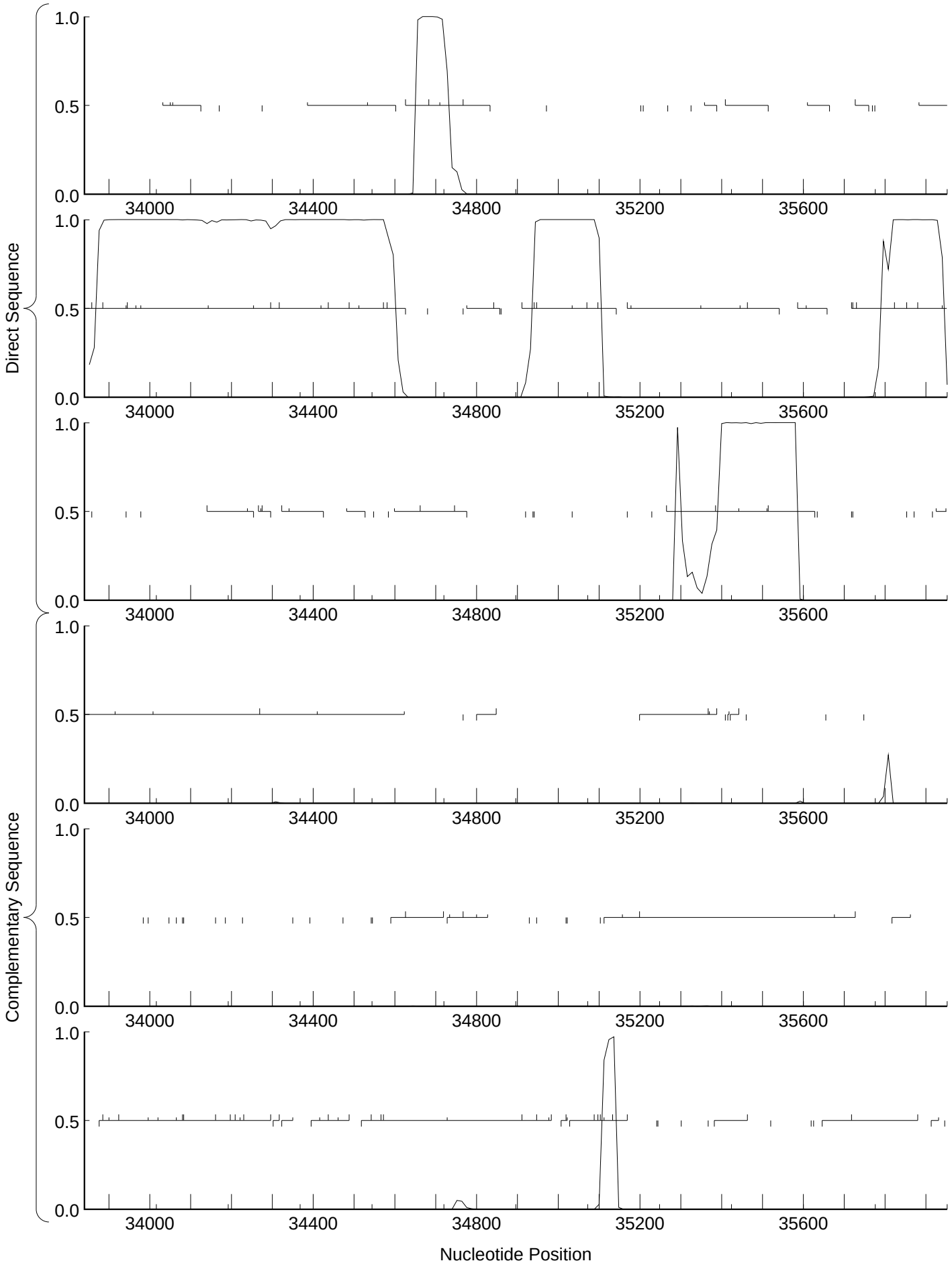
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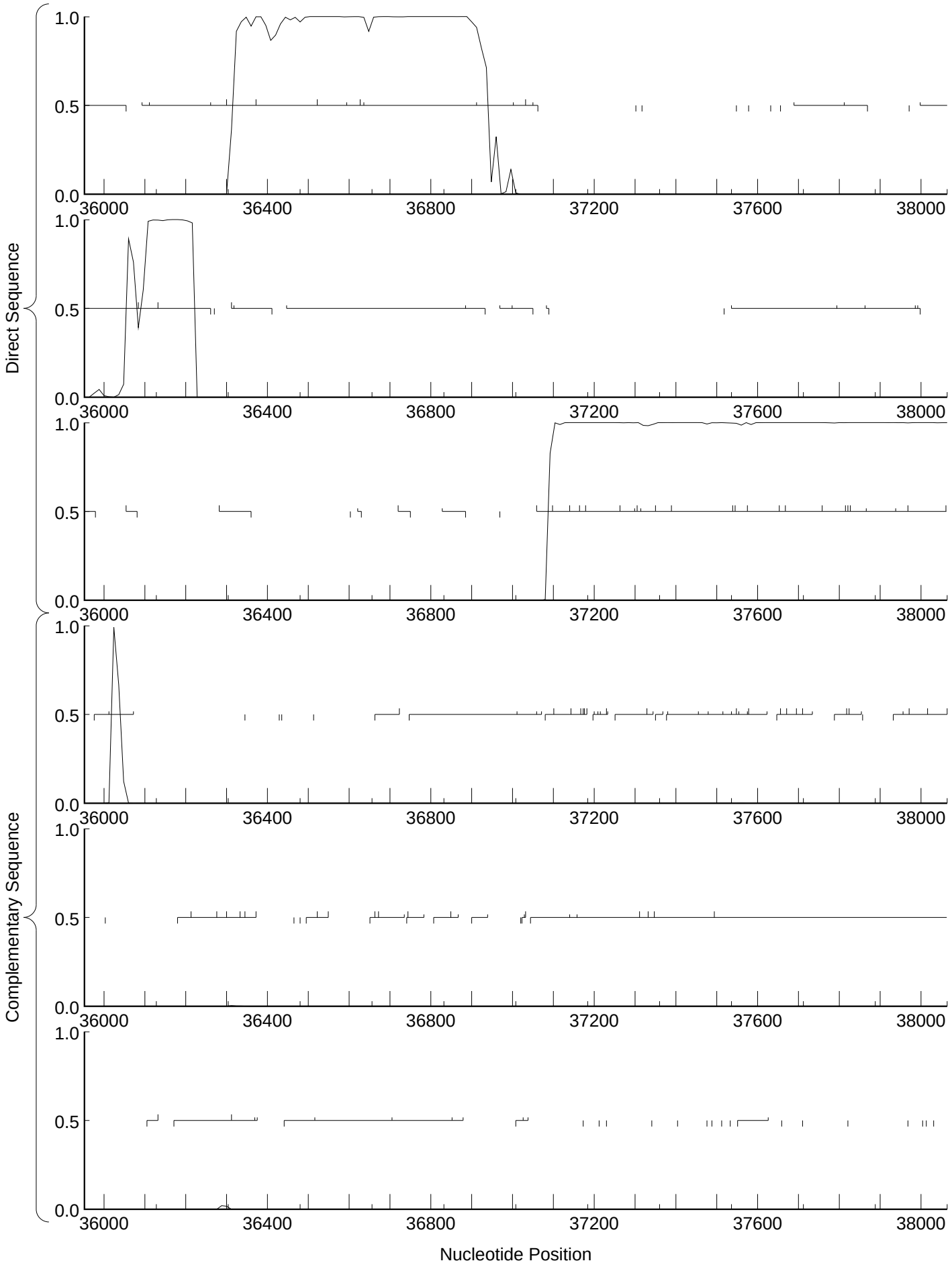
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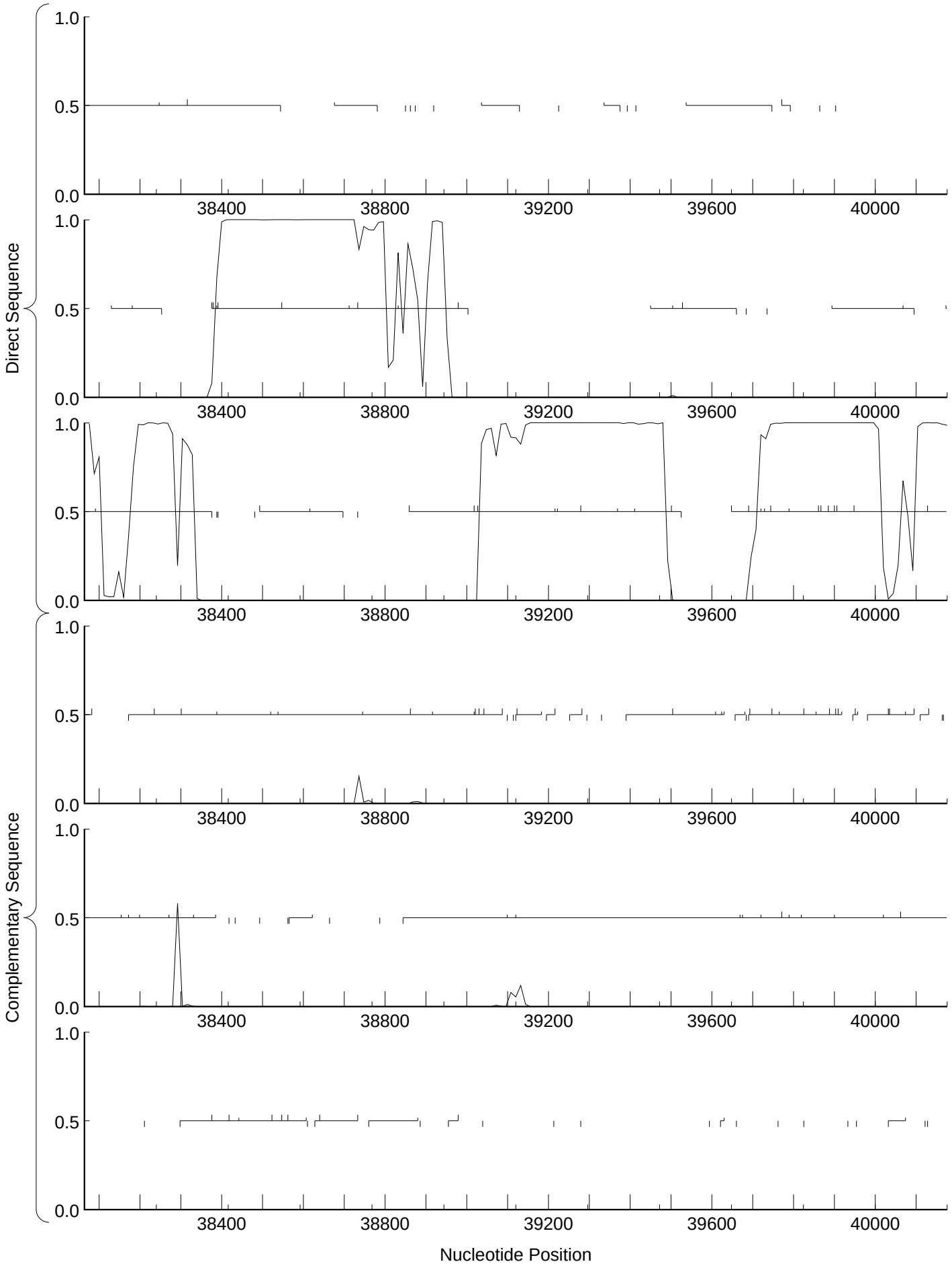
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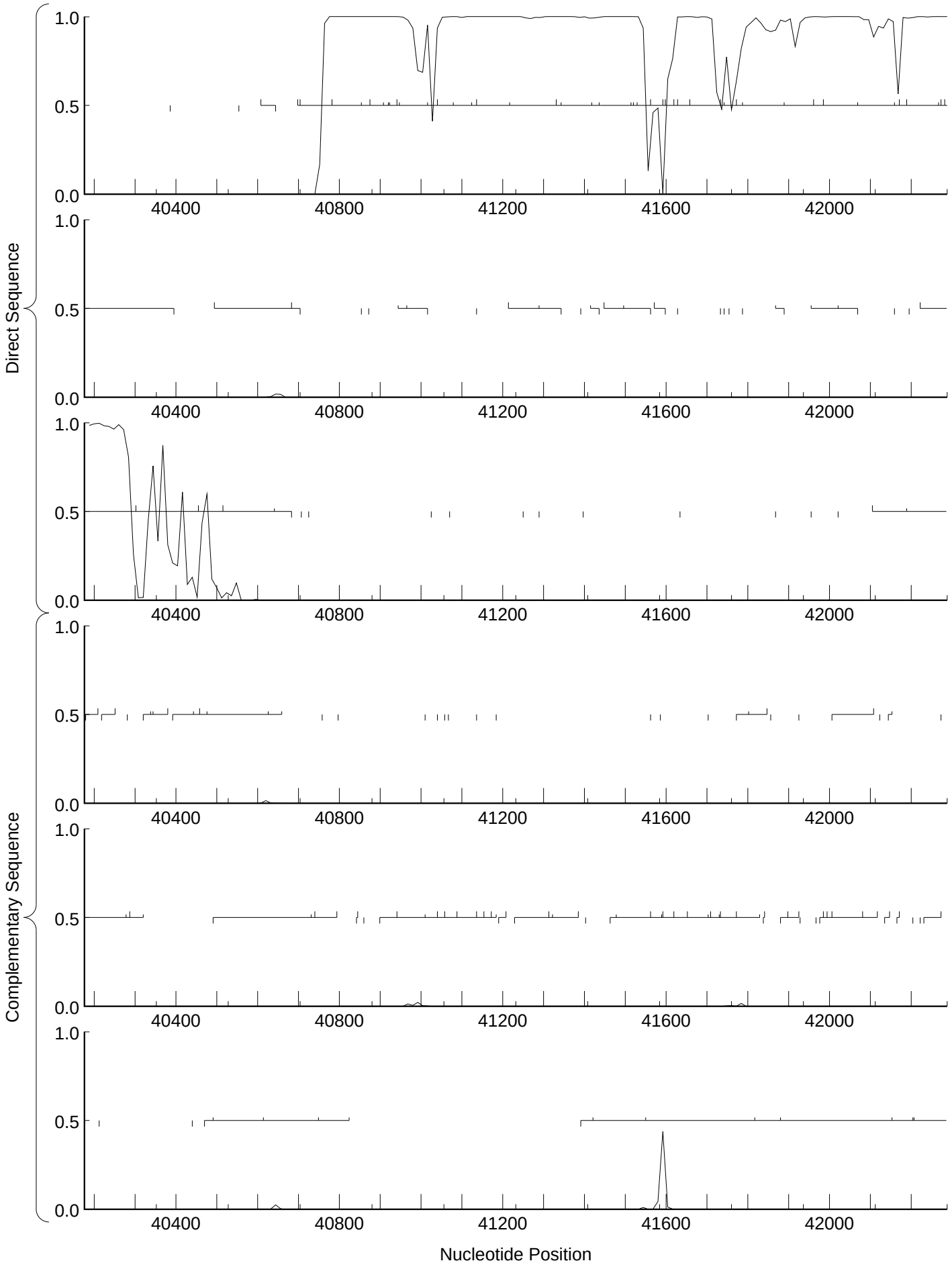
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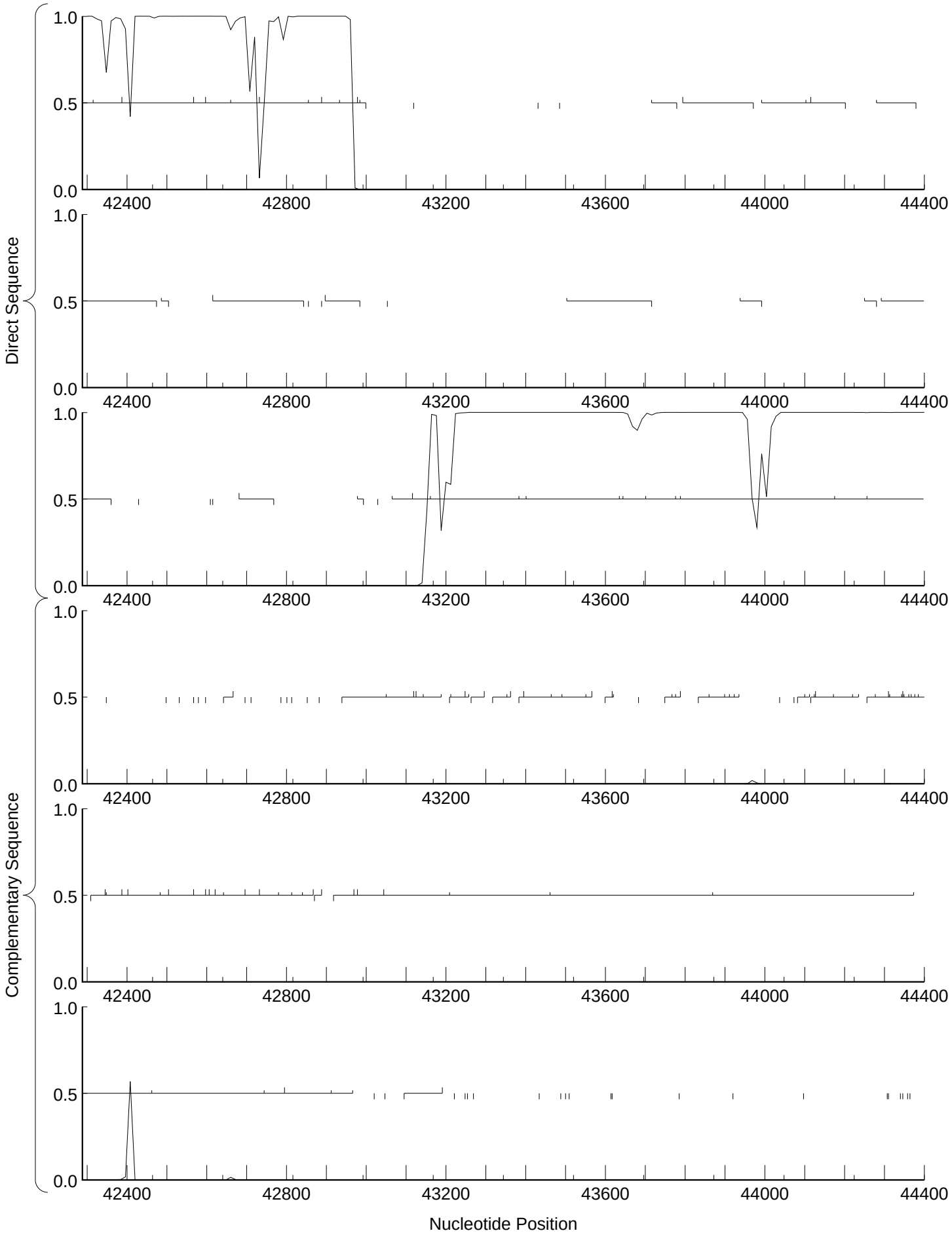
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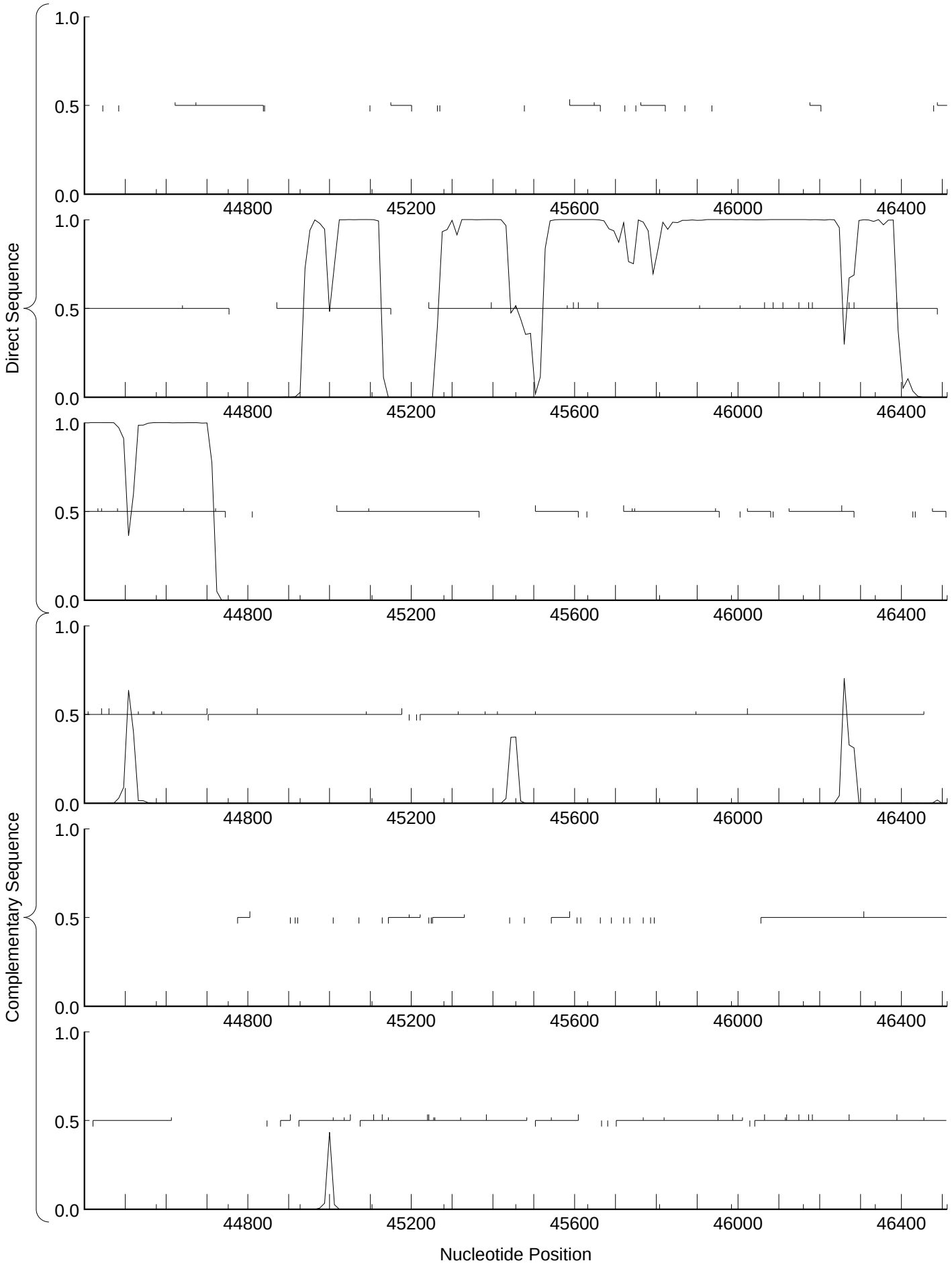
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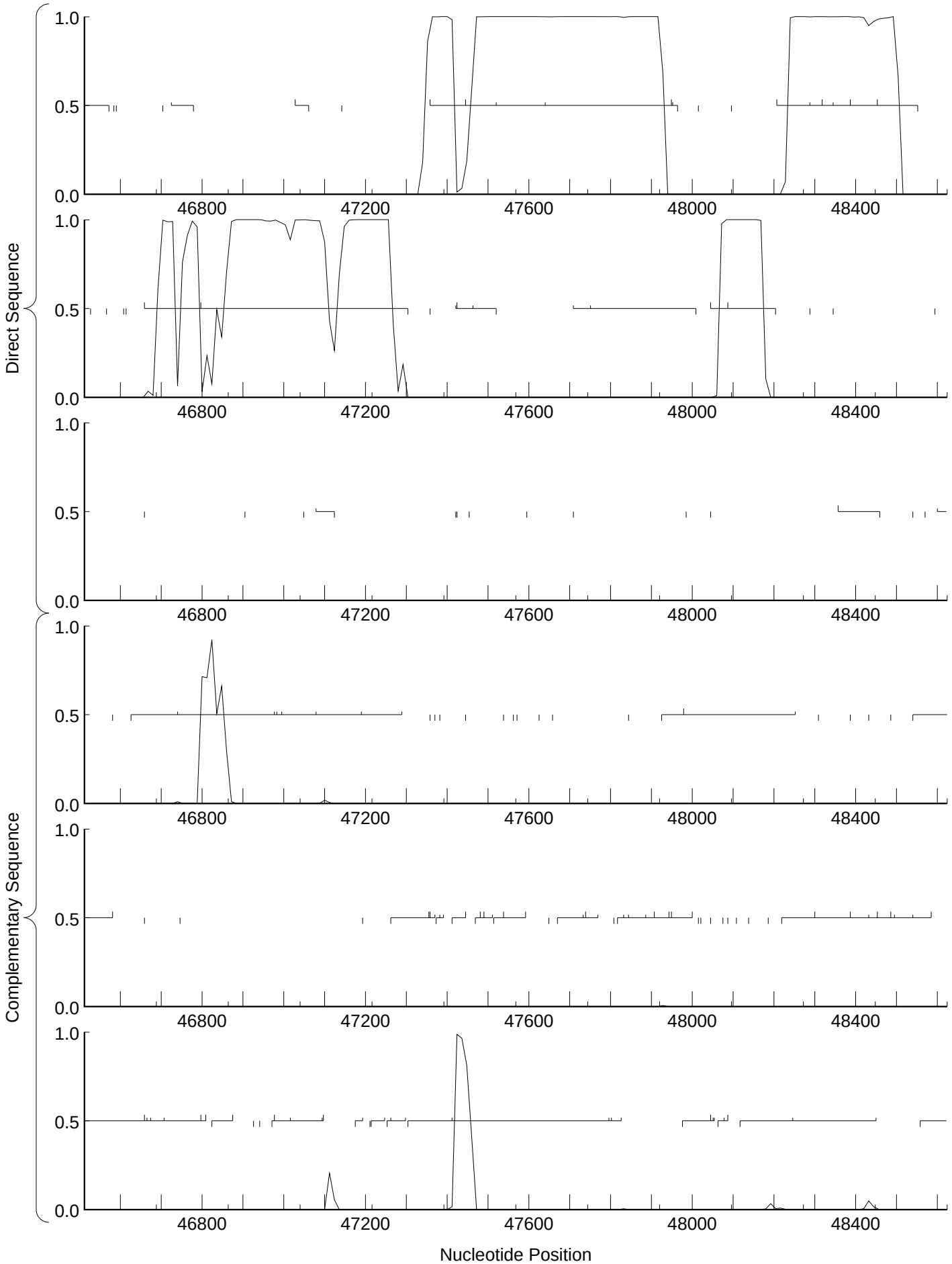
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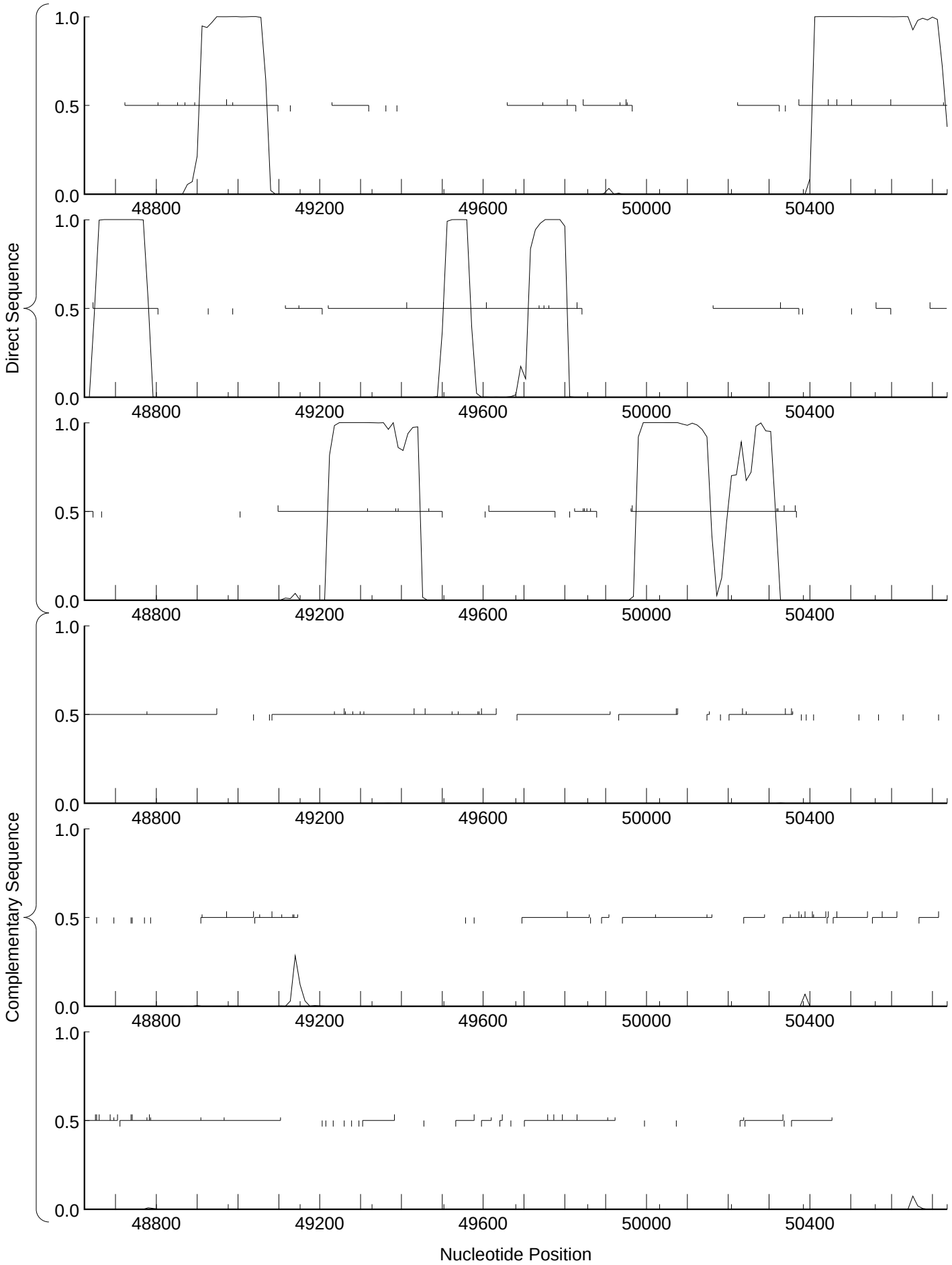
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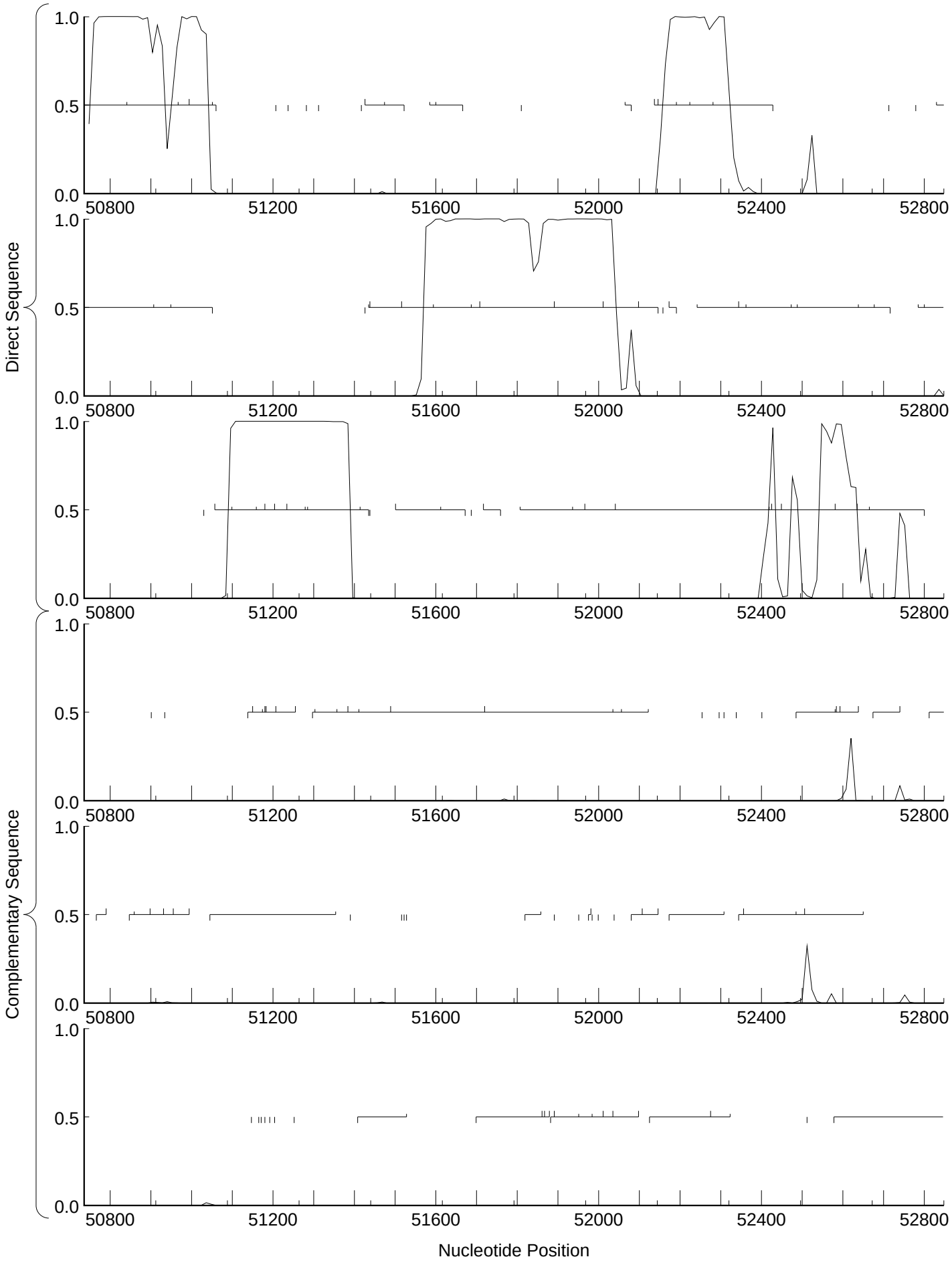
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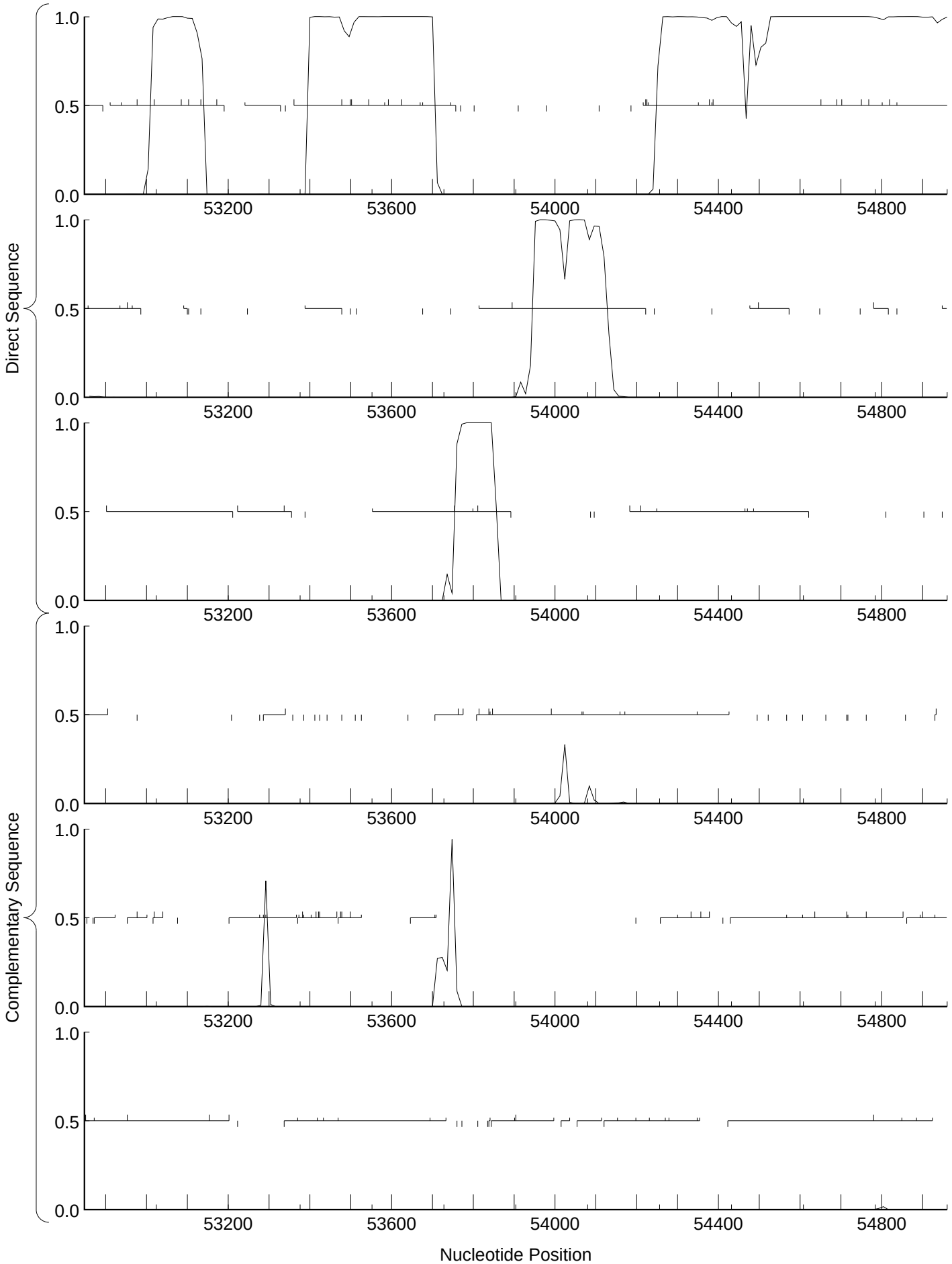
obacterium phage Hiddenleaf complete sequence, 56082 bp, circularly permuted, Cluster EF, Order 4, Window 96, Step 12, 25/28



obacterium phage Hiddenleaf complete sequence, 56082 bp, circularly permuted, Cluster EF, Order 4, Window 96, Step 12, 26/28



obacterium phage Hiddenleaf complete sequence, 56082 bp, circularly permuted, Cluster EF, Order 4, Window 96, Step 12, 27/28



obacterium phage Hiddenleaf complete sequence, 56082 bp, circularly permuted, Cluster EF, Order 4, Window 96, Step 12, 28/28

