GeneMark

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

PROGRAM INFORMATION

```
Sequence         :  Microbacterium phage Lyell complete sequence, 62716 bp including 3549 bp terminal repeat, C
Analysis Date    :  3/29/24 at 5:57:57
Pages            :  31
Sequence Length  :  62716 bp
GC Content       :   61.60%

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     :  -

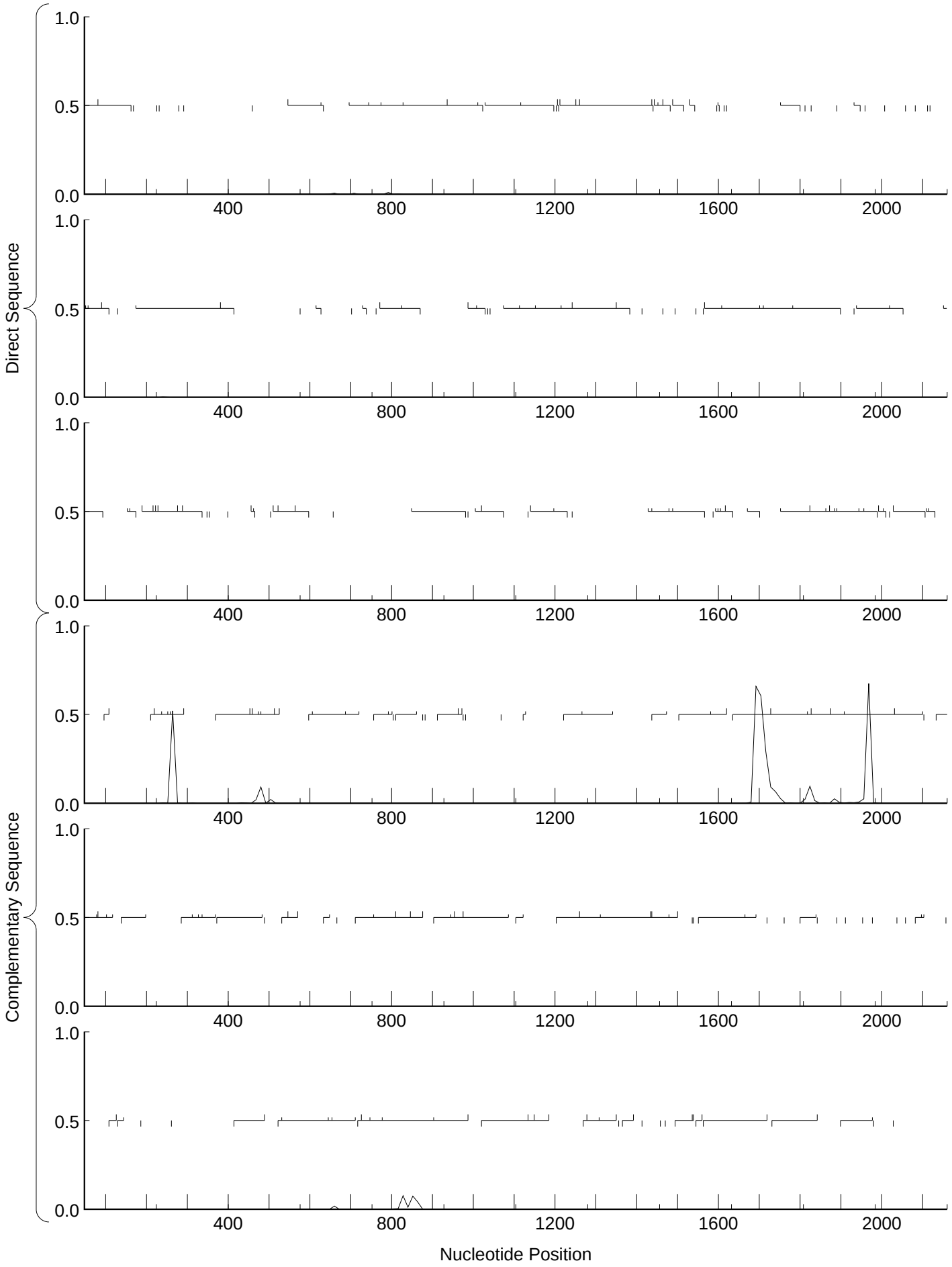
Order      :  4


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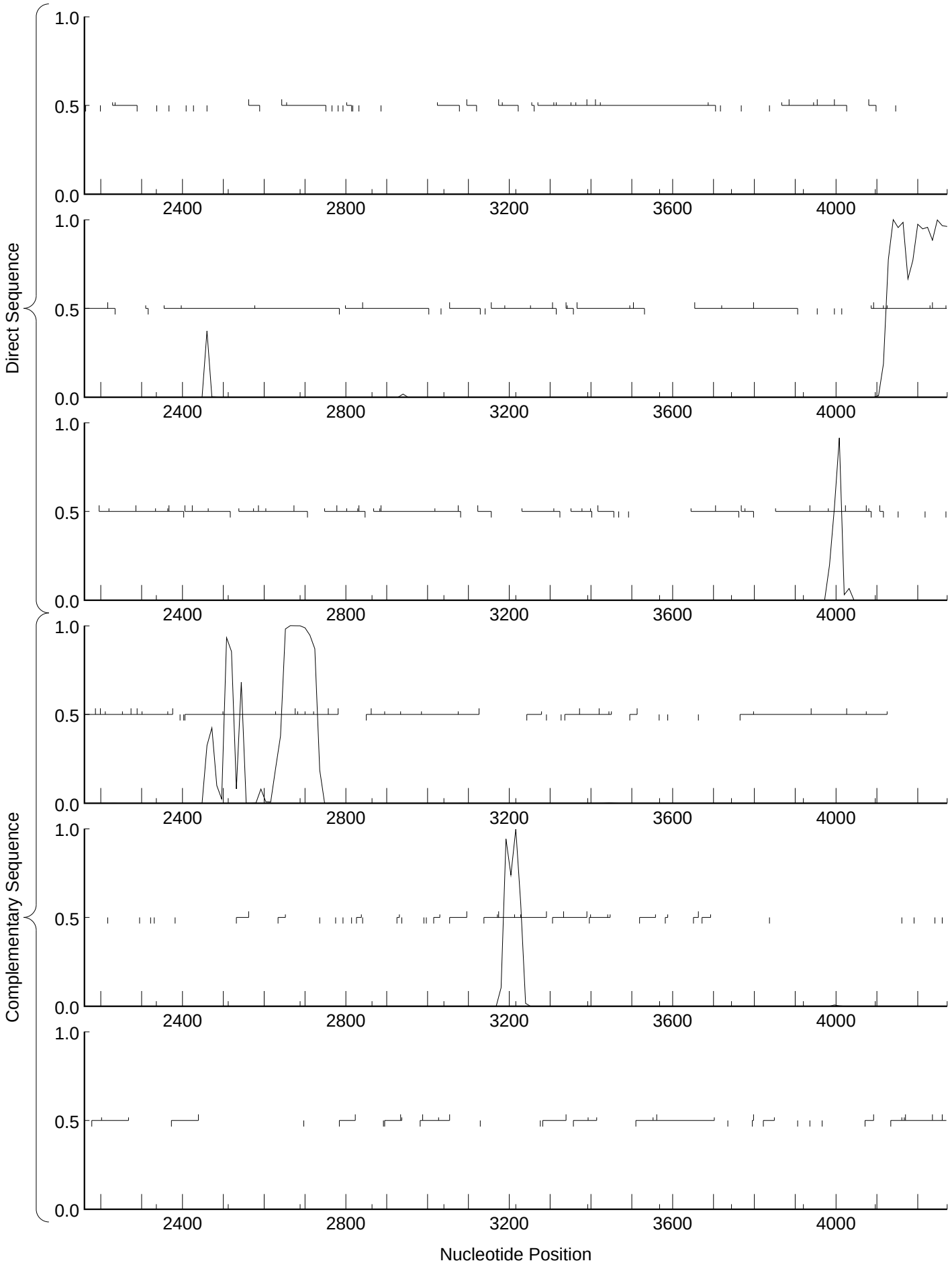
Matrix notes & comments

Training set derived by GeneMarkS, 4.30 October 2014
Fri Sep 7 18:42:59 2018

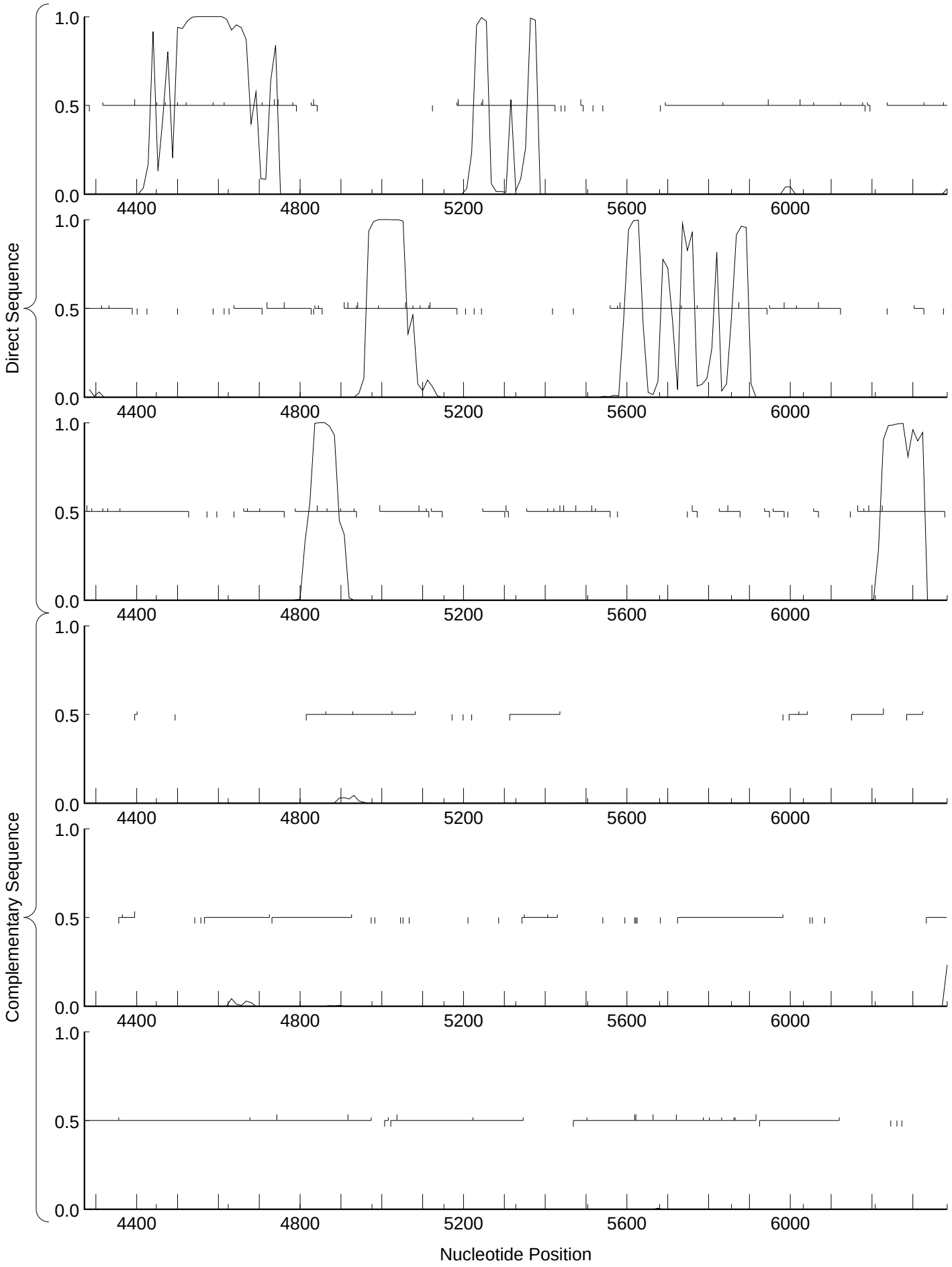
For help or information, send electronic mail to: custserv@genepro.com, or mark@amber.biology.gatech.edu


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

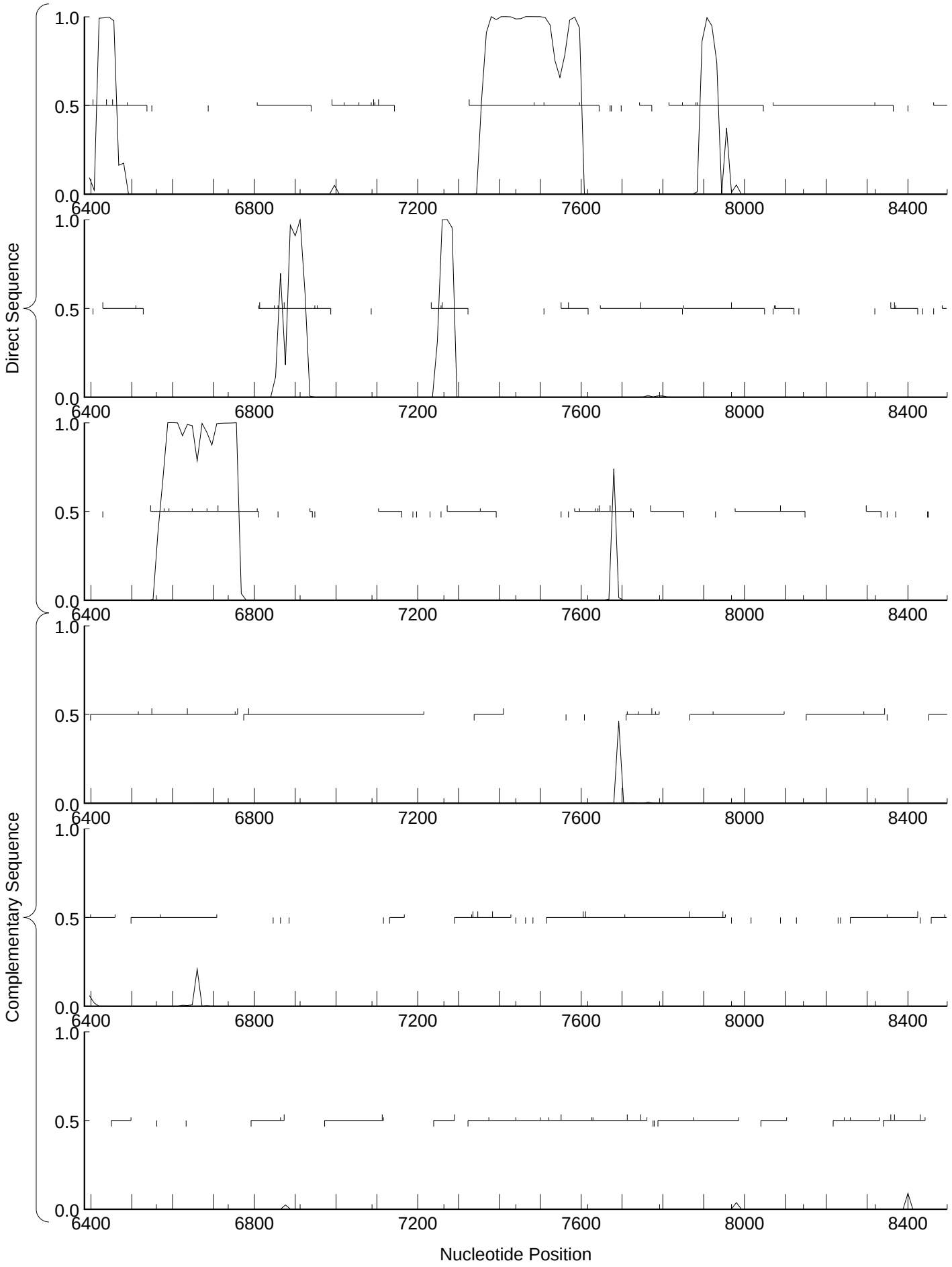
um phage Lyell complete sequence, 62716 bp including 3549 bp terminal repeat, Cluster ED2, Order 4, Window 96, Step 12, 3/31



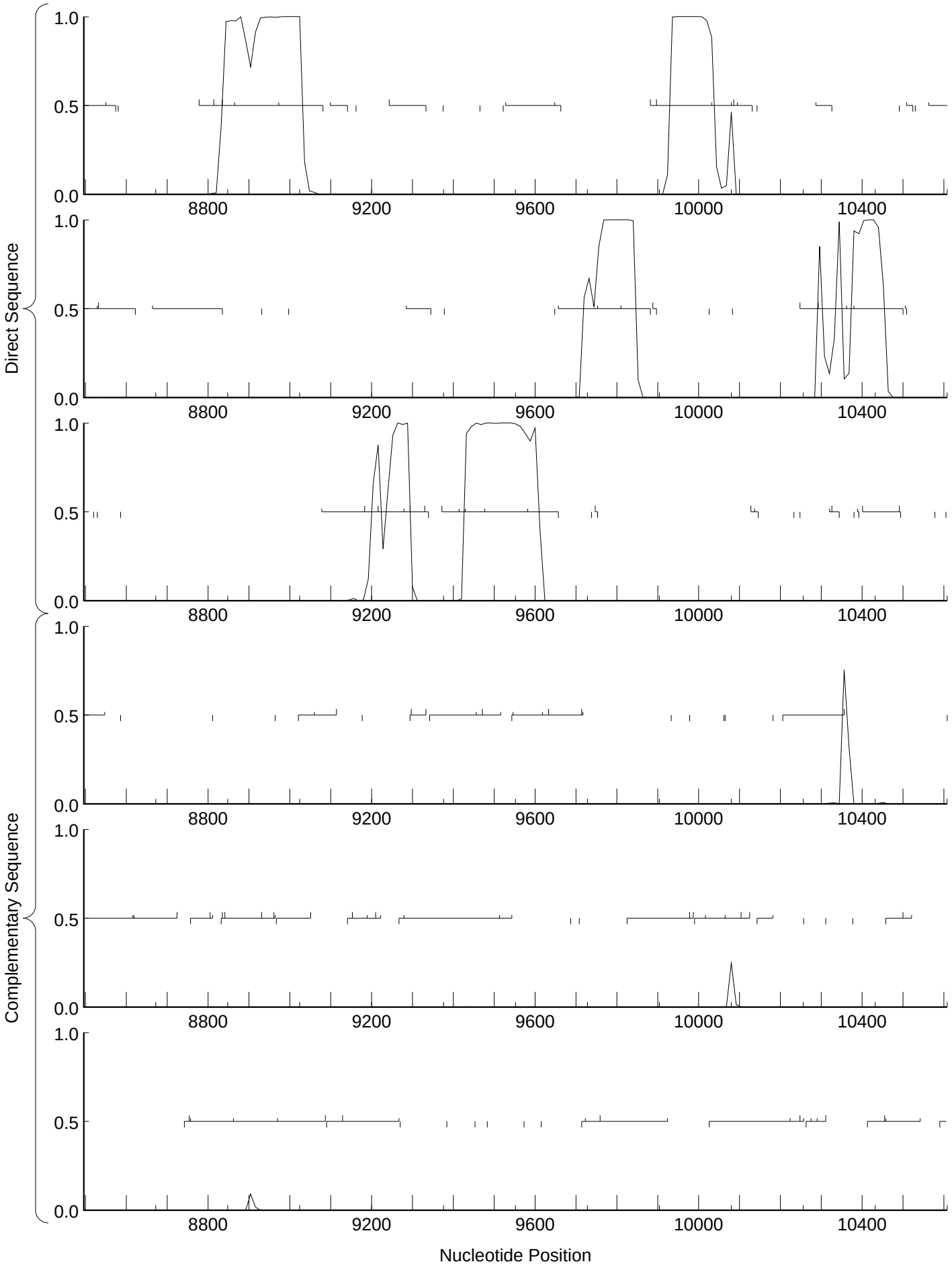
um phage Lyell complete sequence, 62716 bp including 3549 bp terminal repeat, Cluster ED2, Order 4, Window 96, Step 12, 4/31



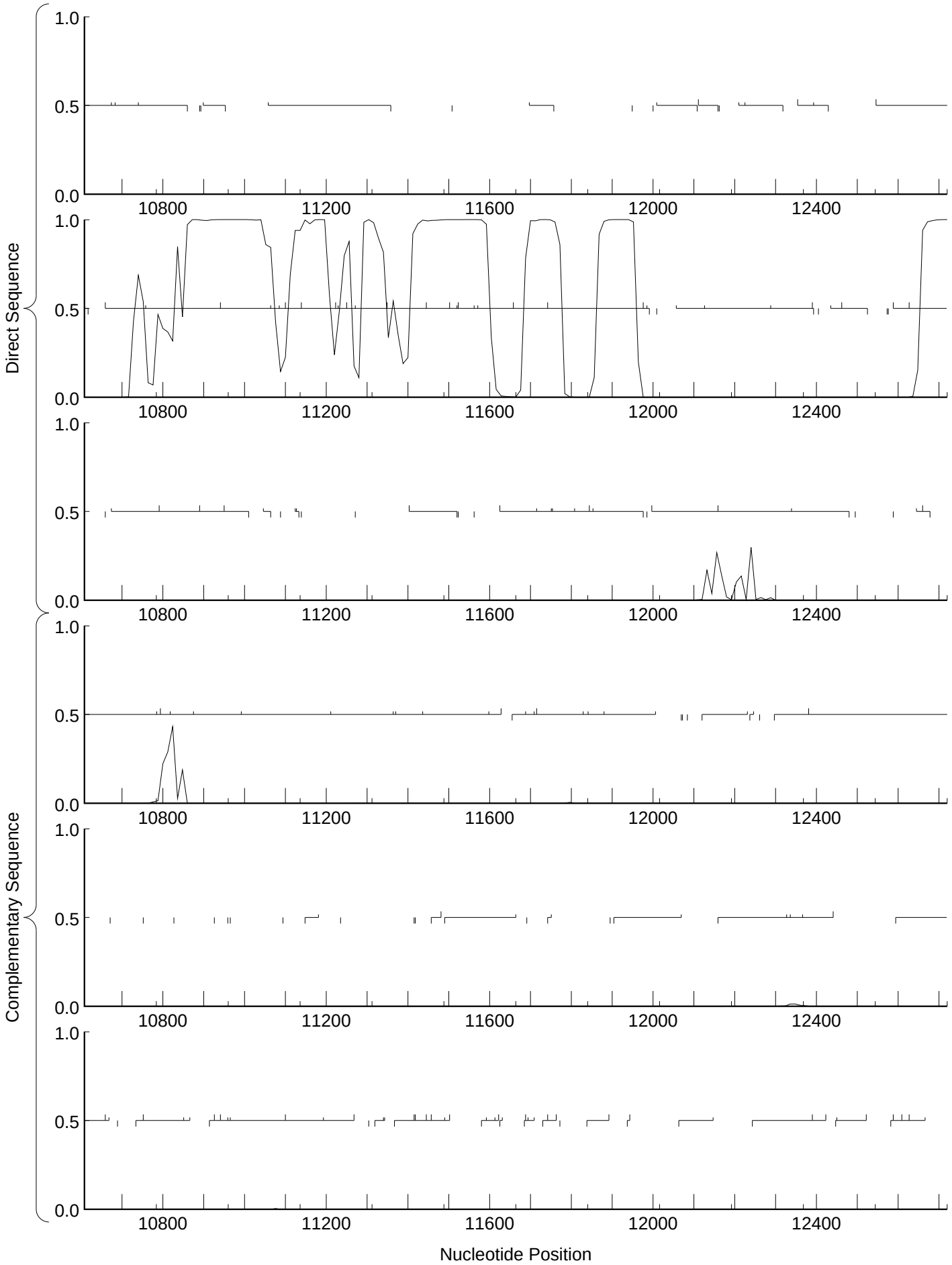
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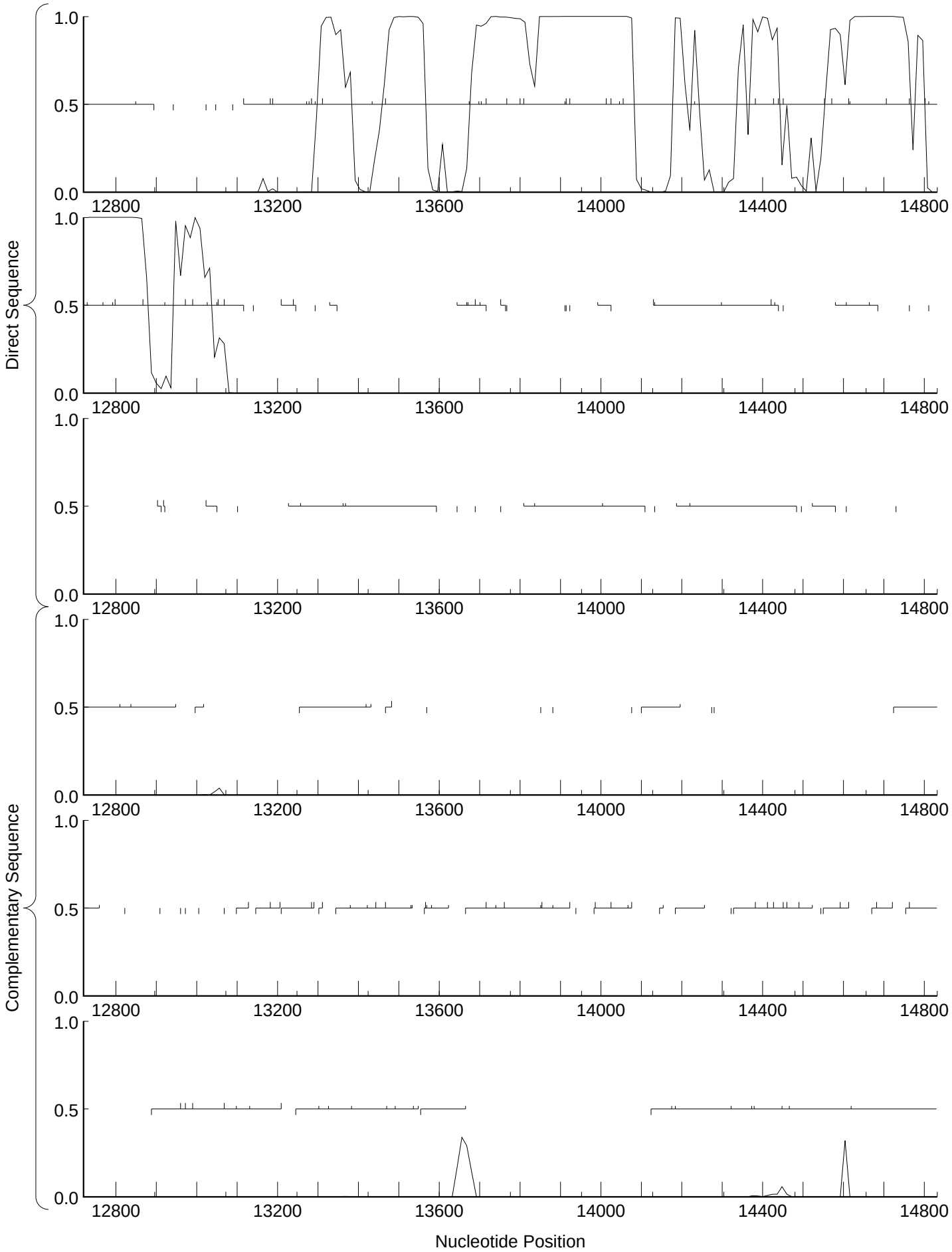
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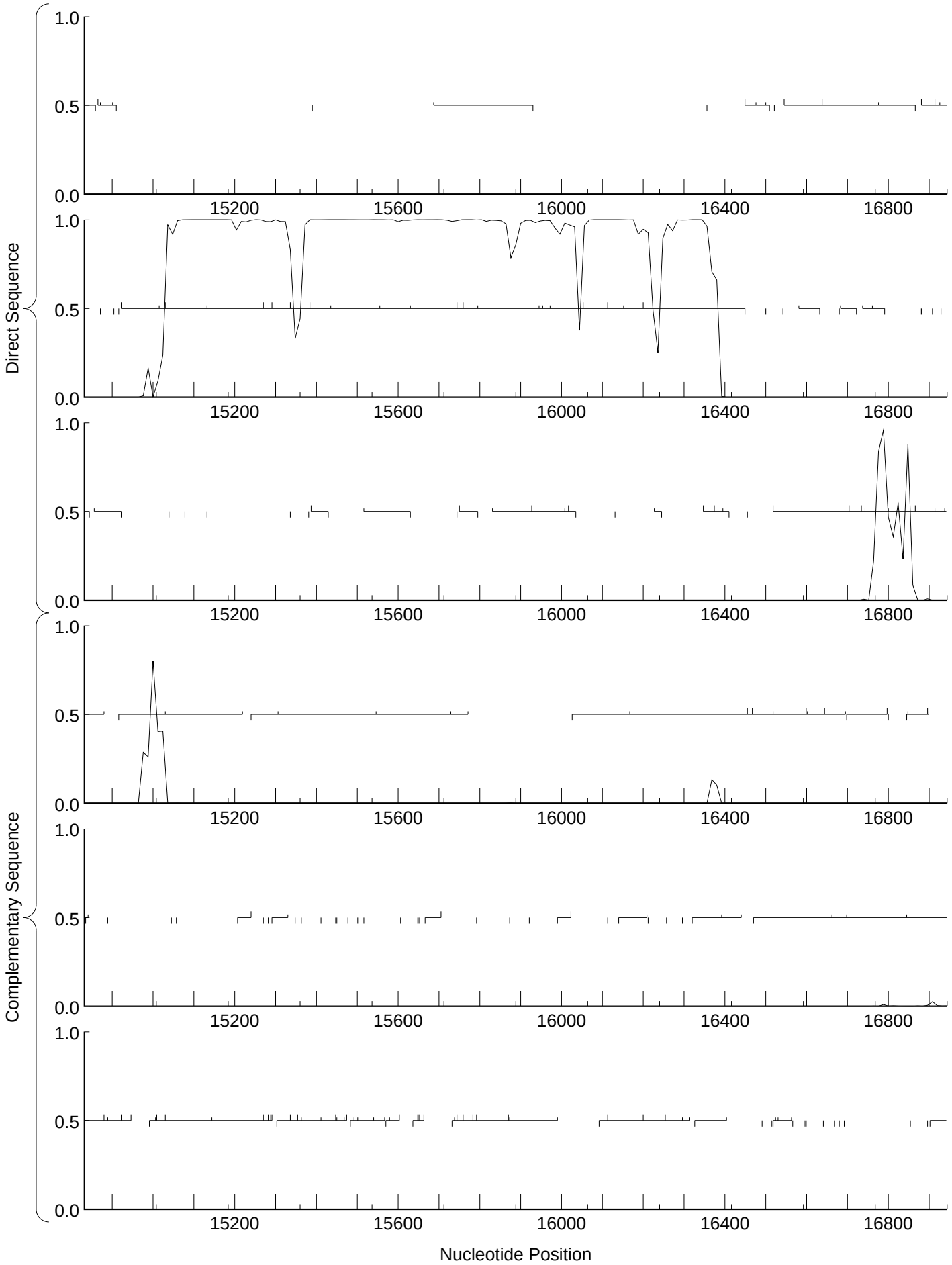
um phage Lyell complete sequence, 62716 bp including 3549 bp terminal repeat, Cluster ED2, Order 4, Window 96, Step 12, 7/31



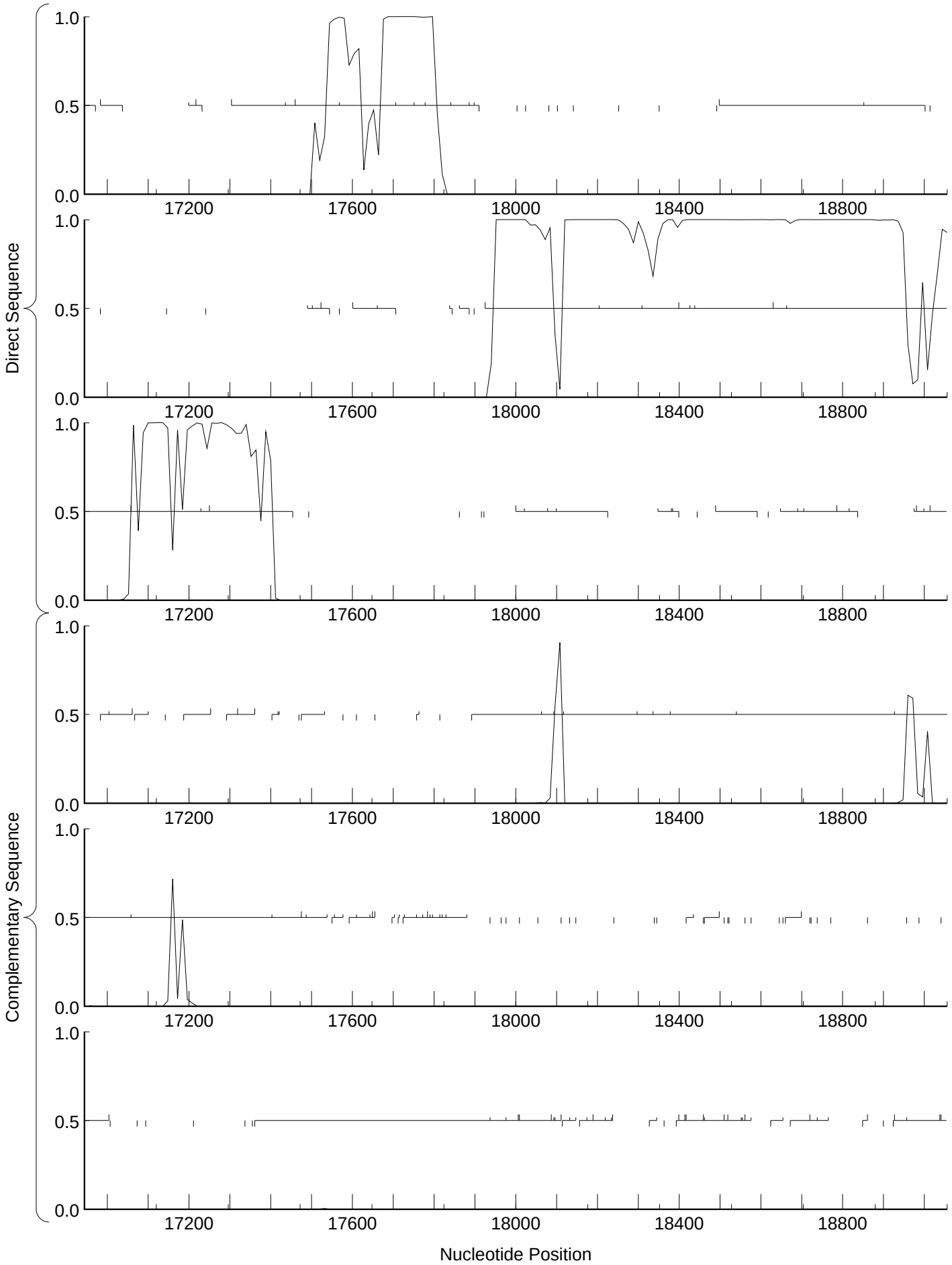
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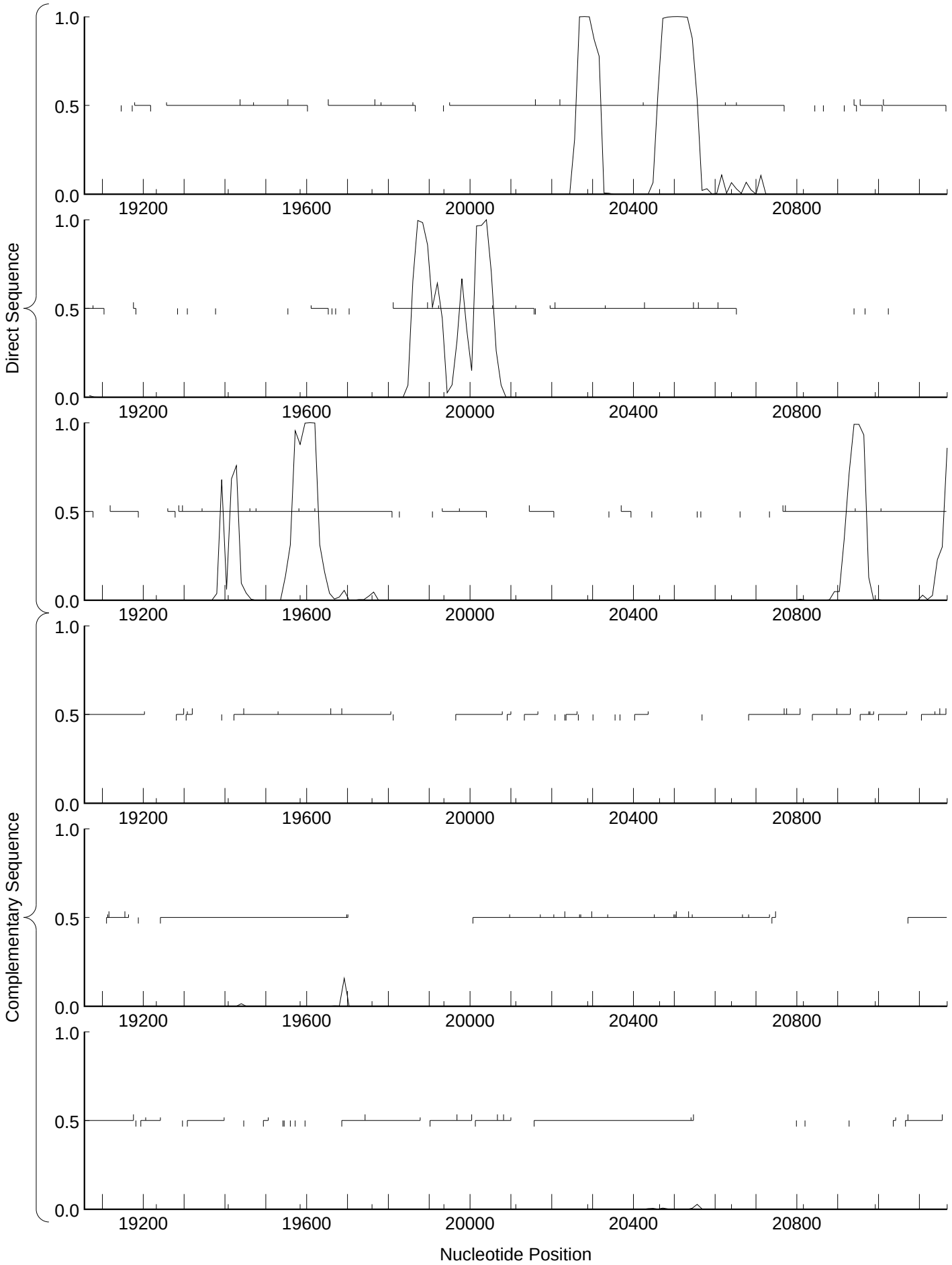
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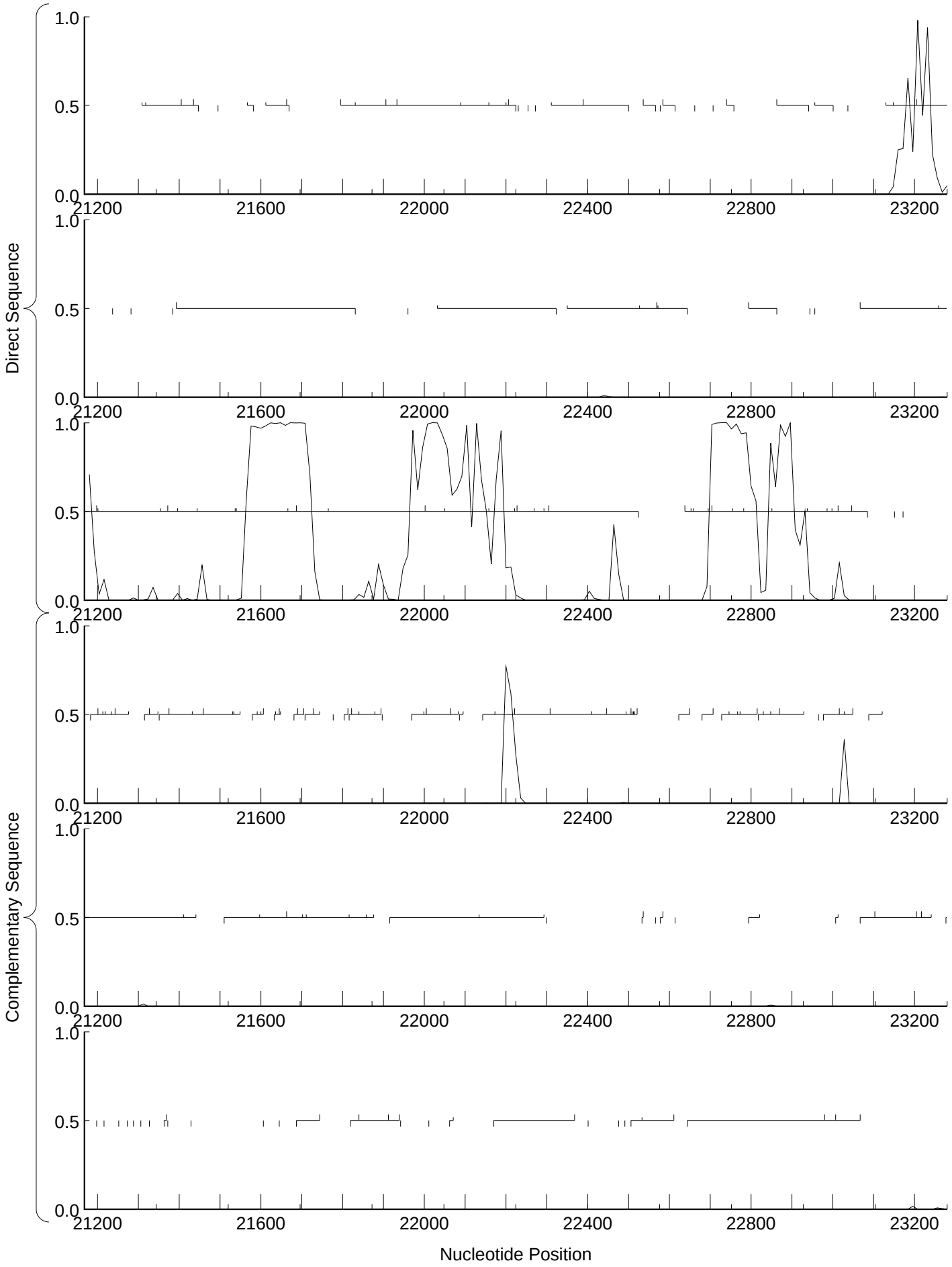
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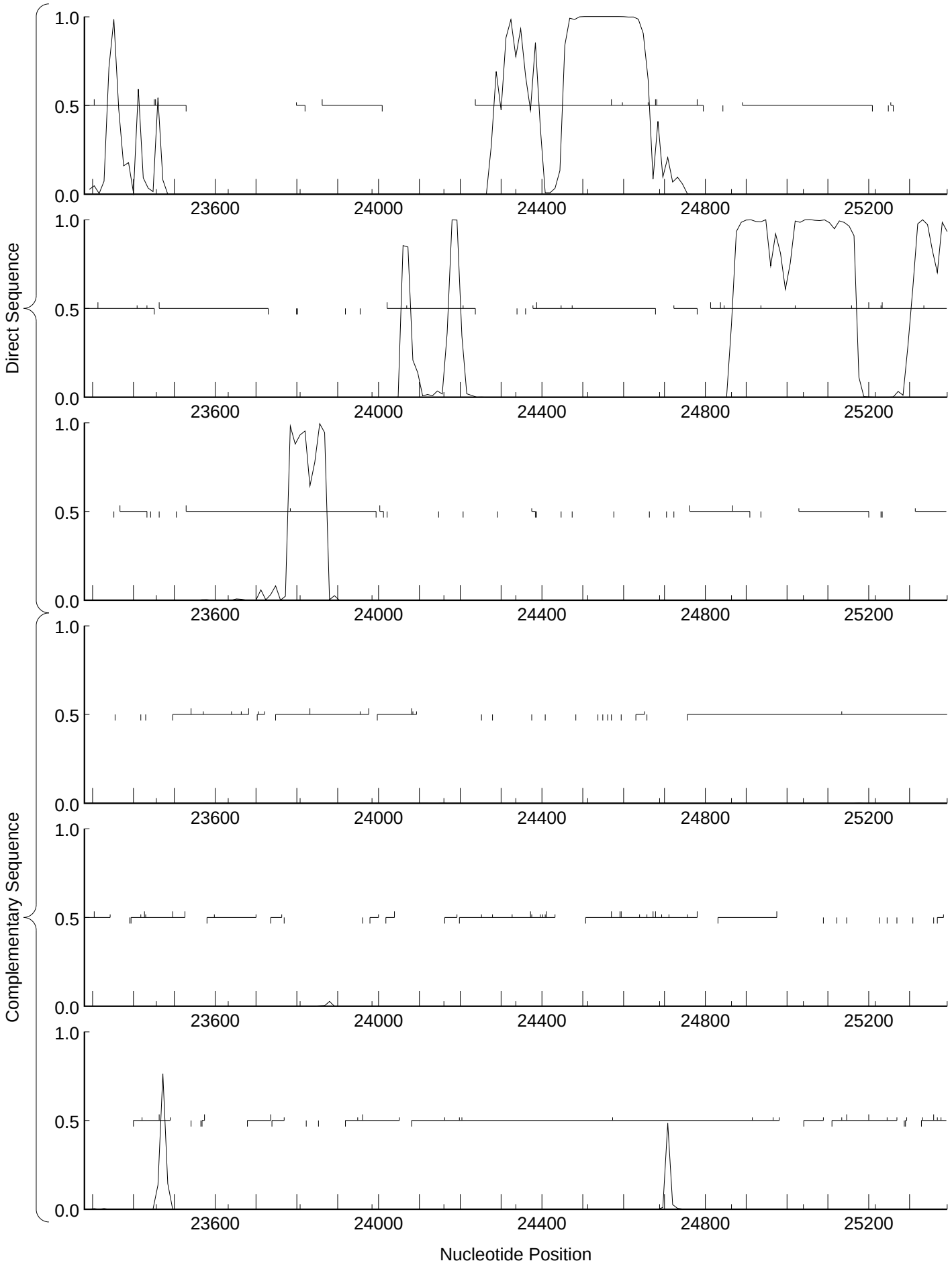
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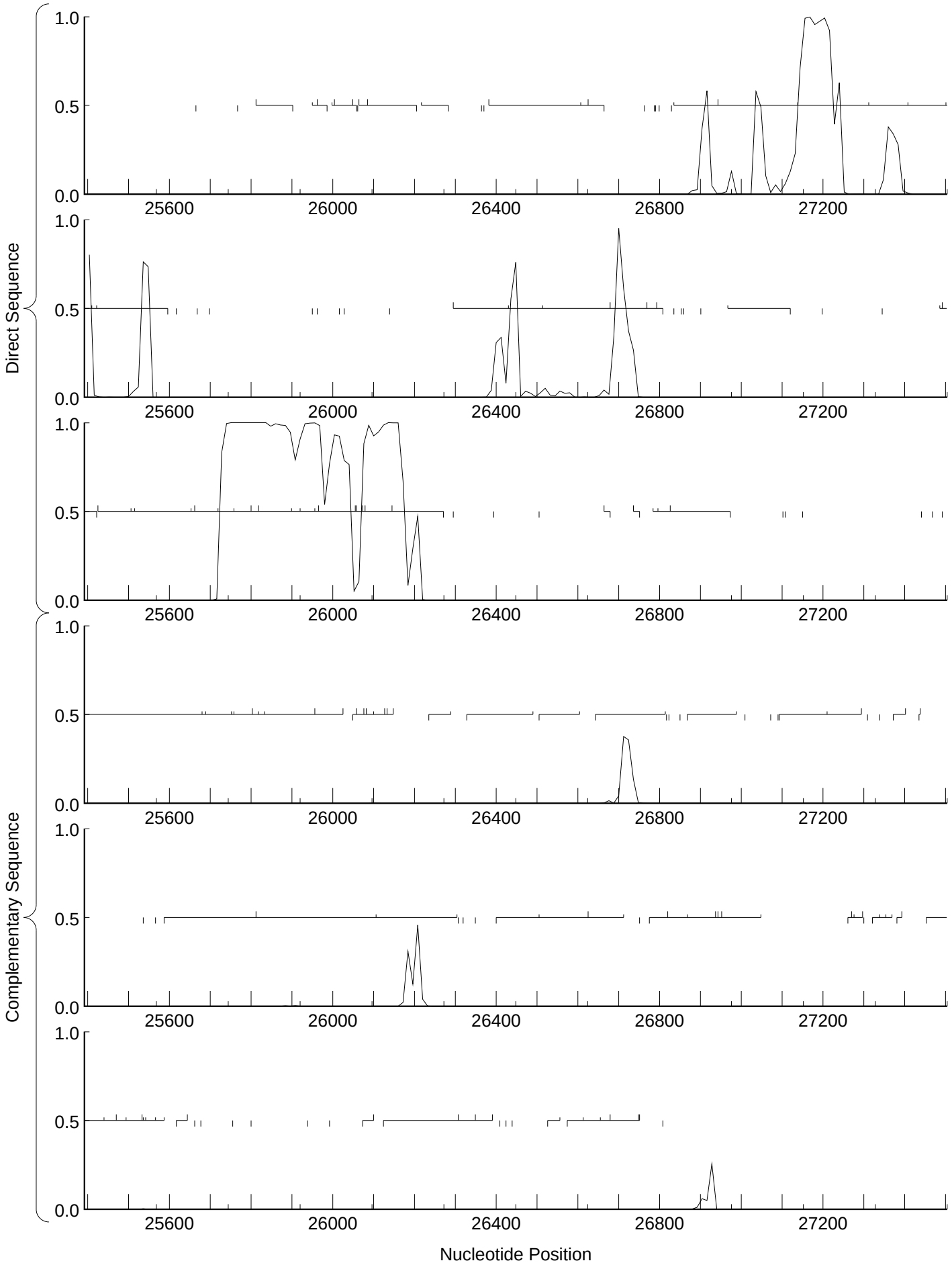


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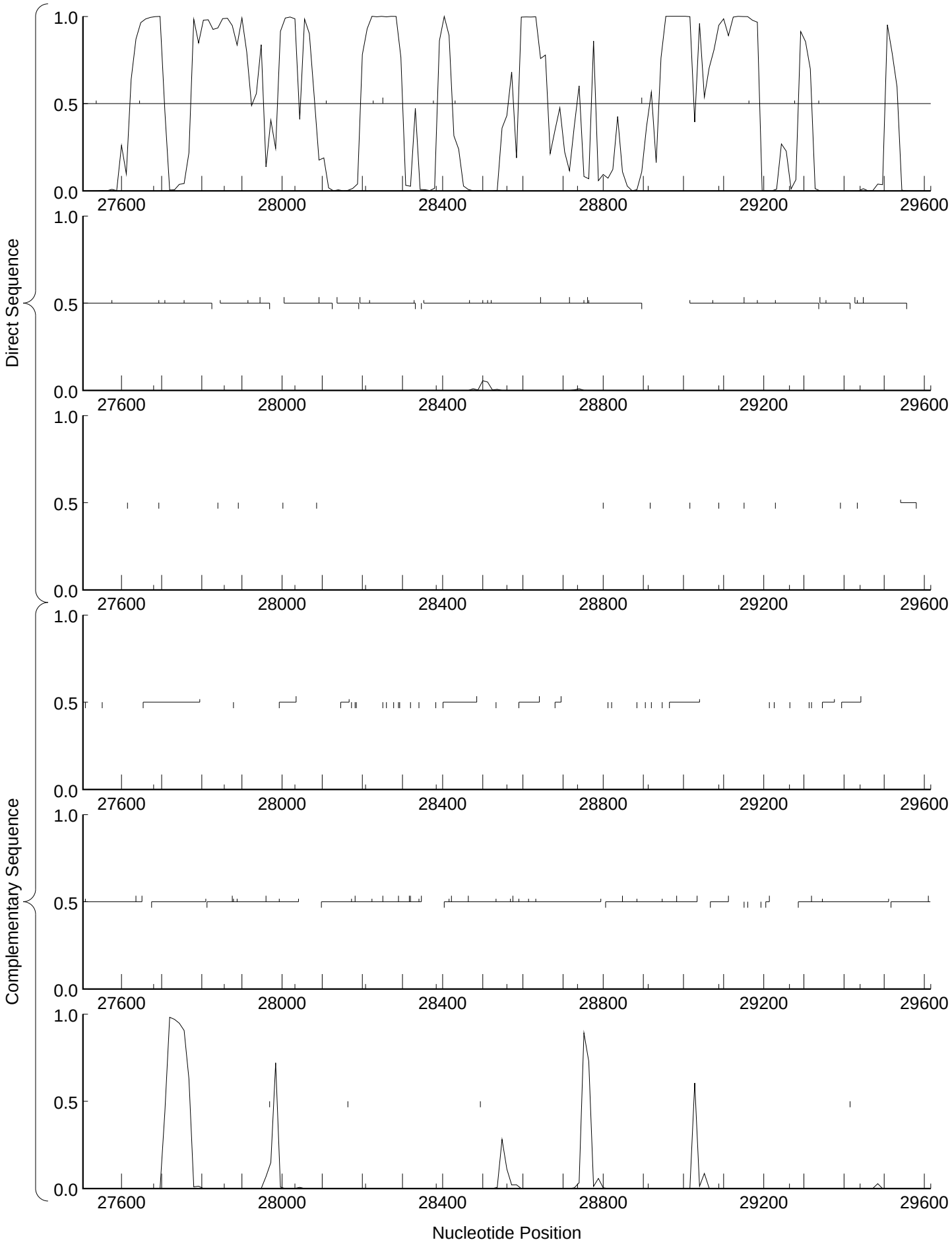


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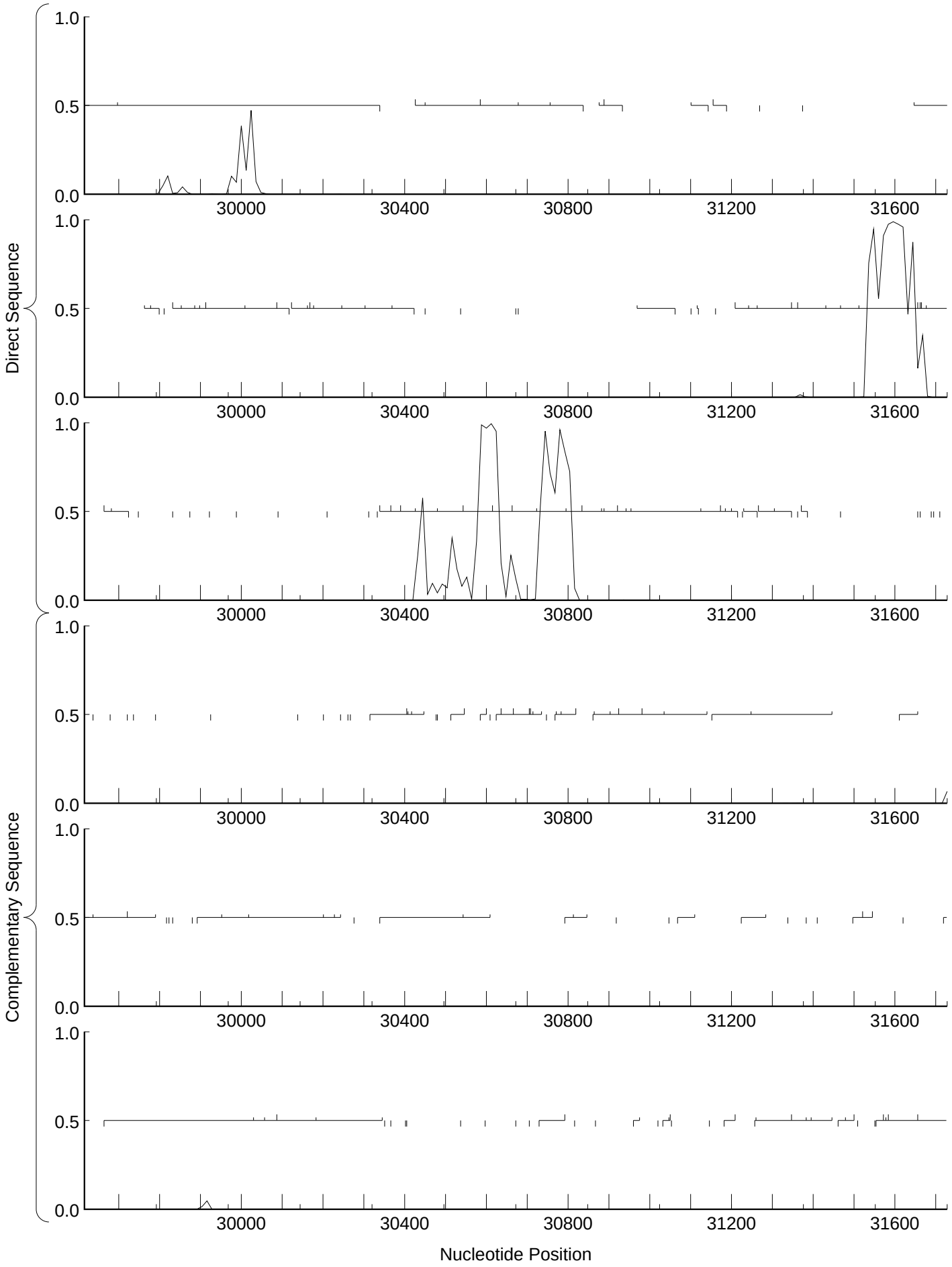



Direct Sequence
Complementary Sequence
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0.5
0.0
25600
26000
26400
26800
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Nucleotide Position

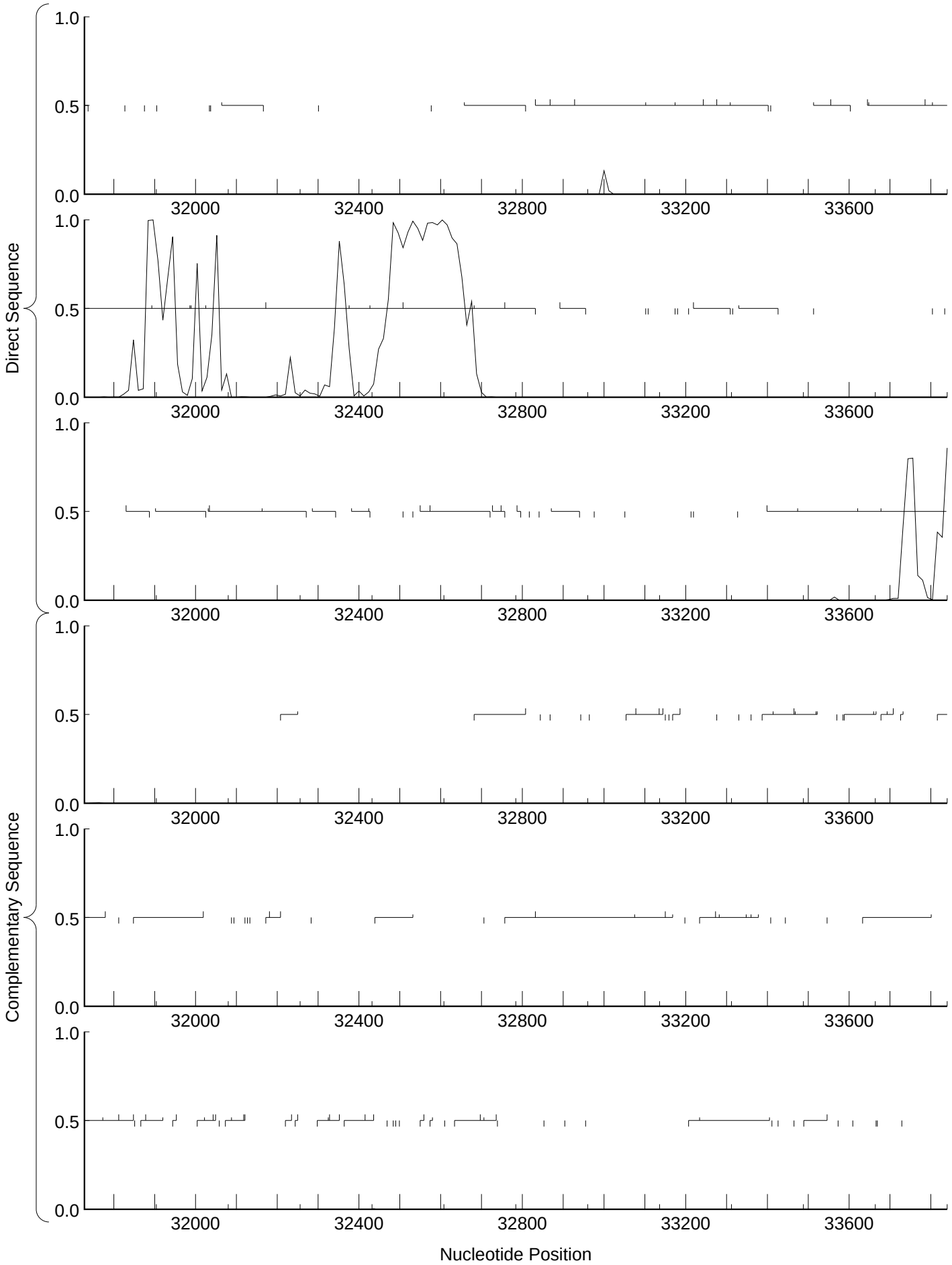
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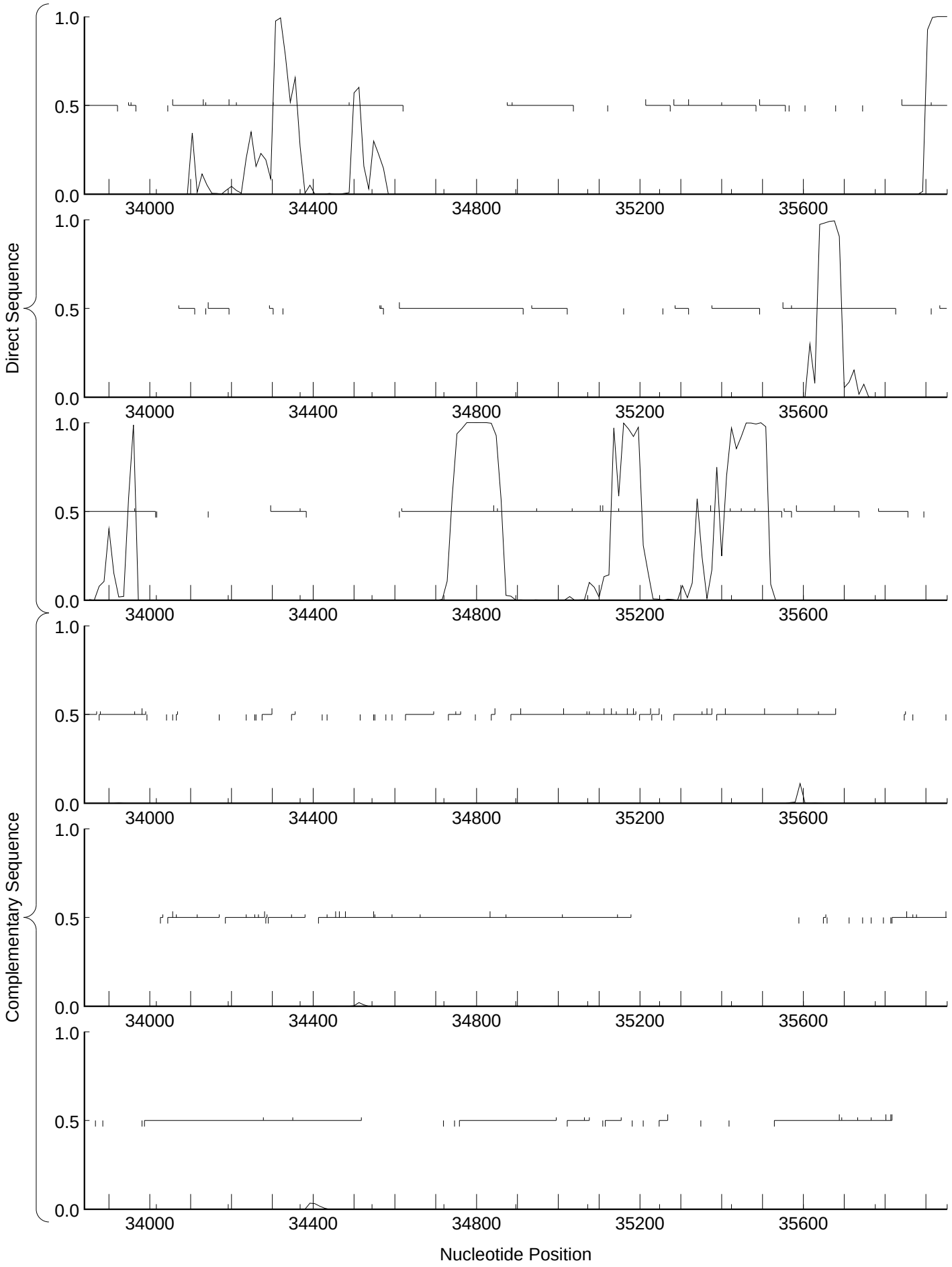
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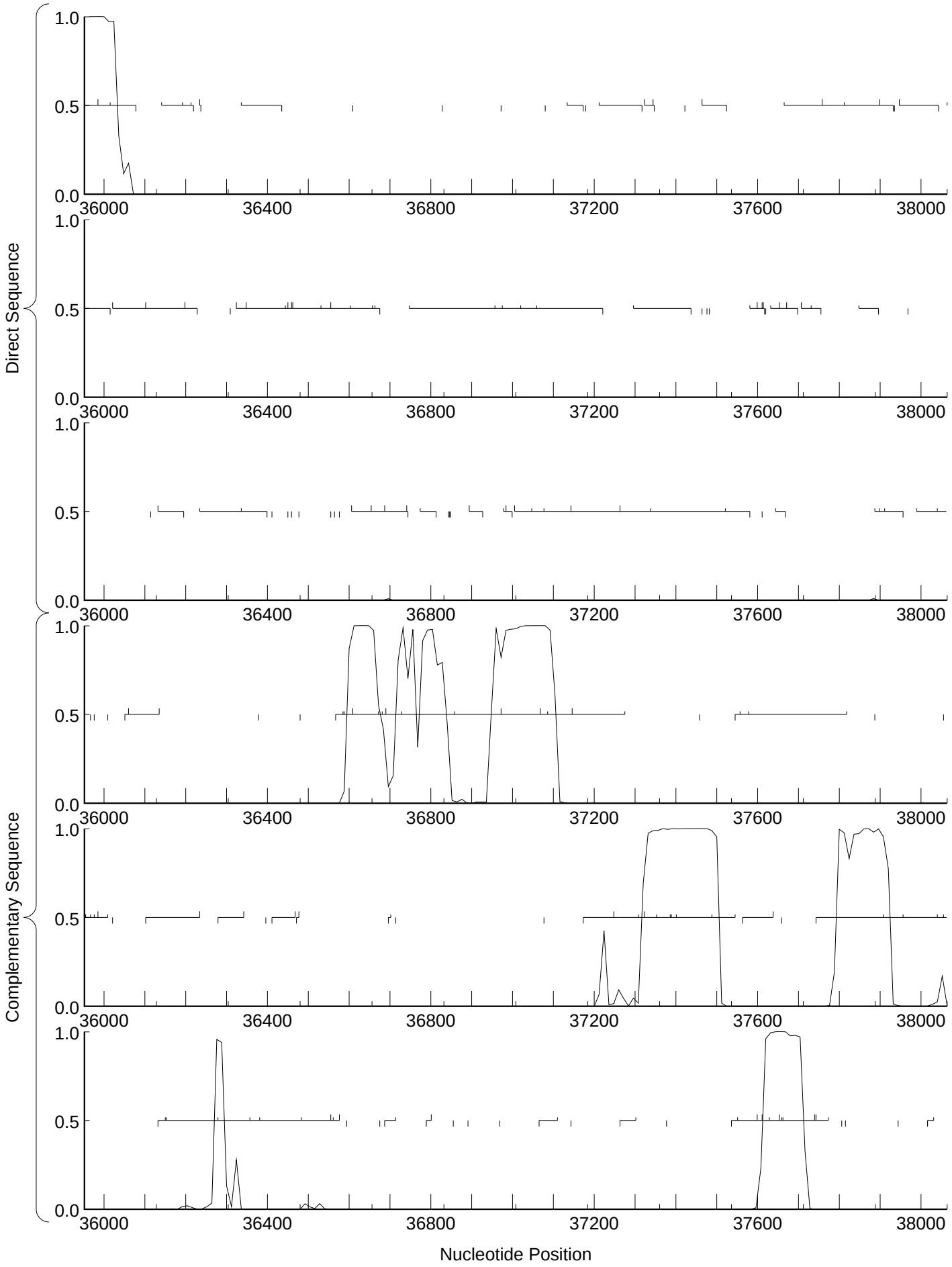
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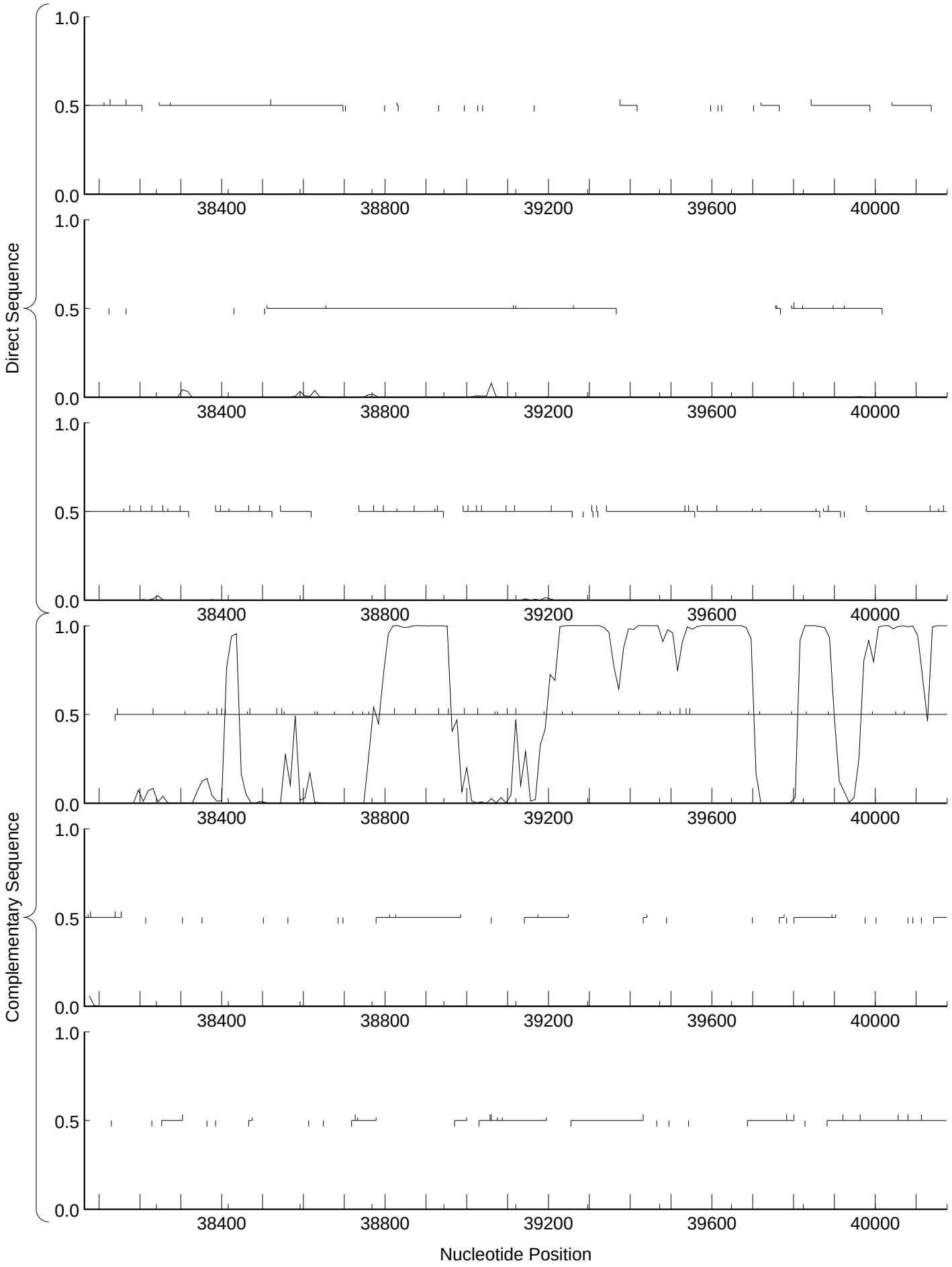
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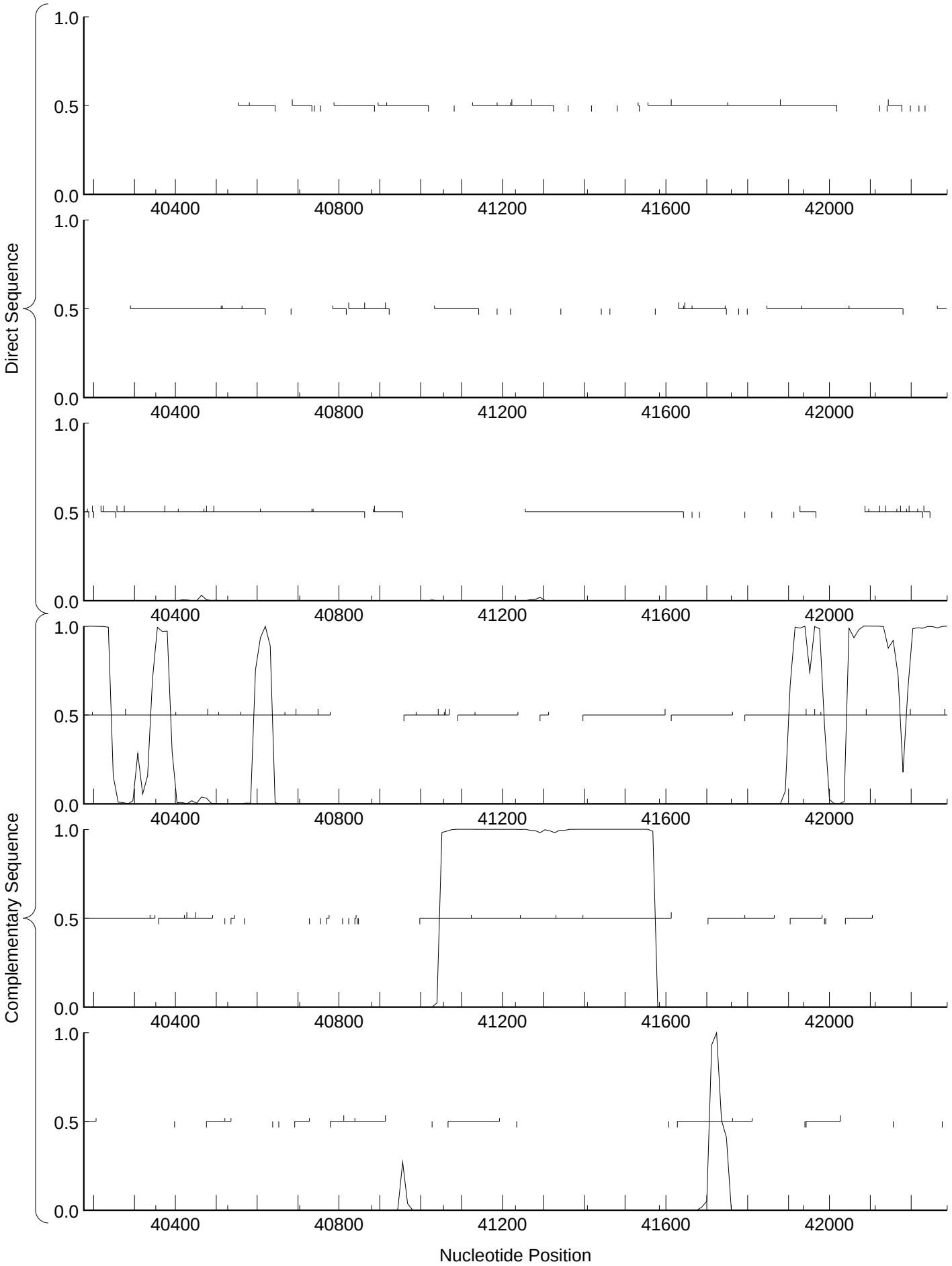


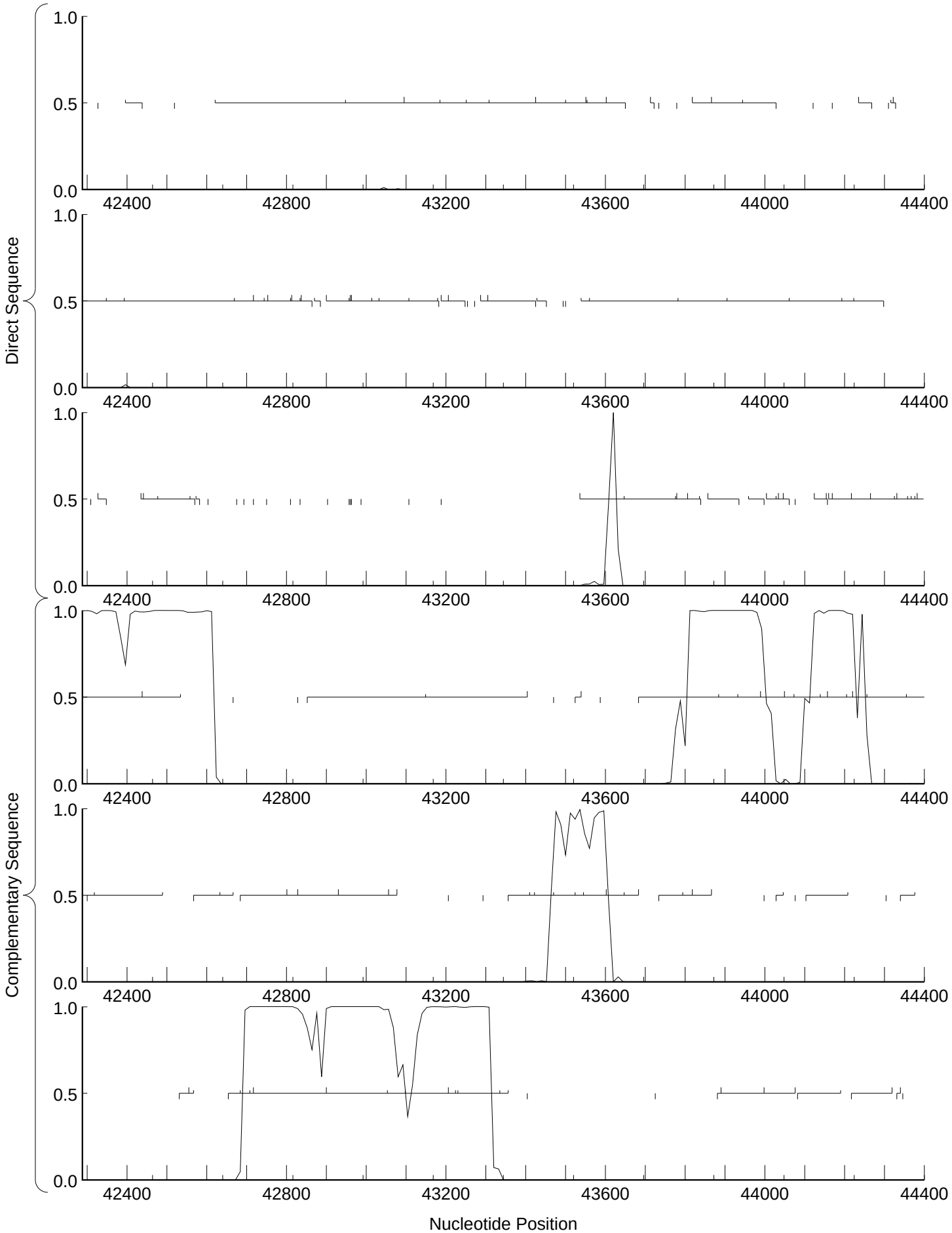
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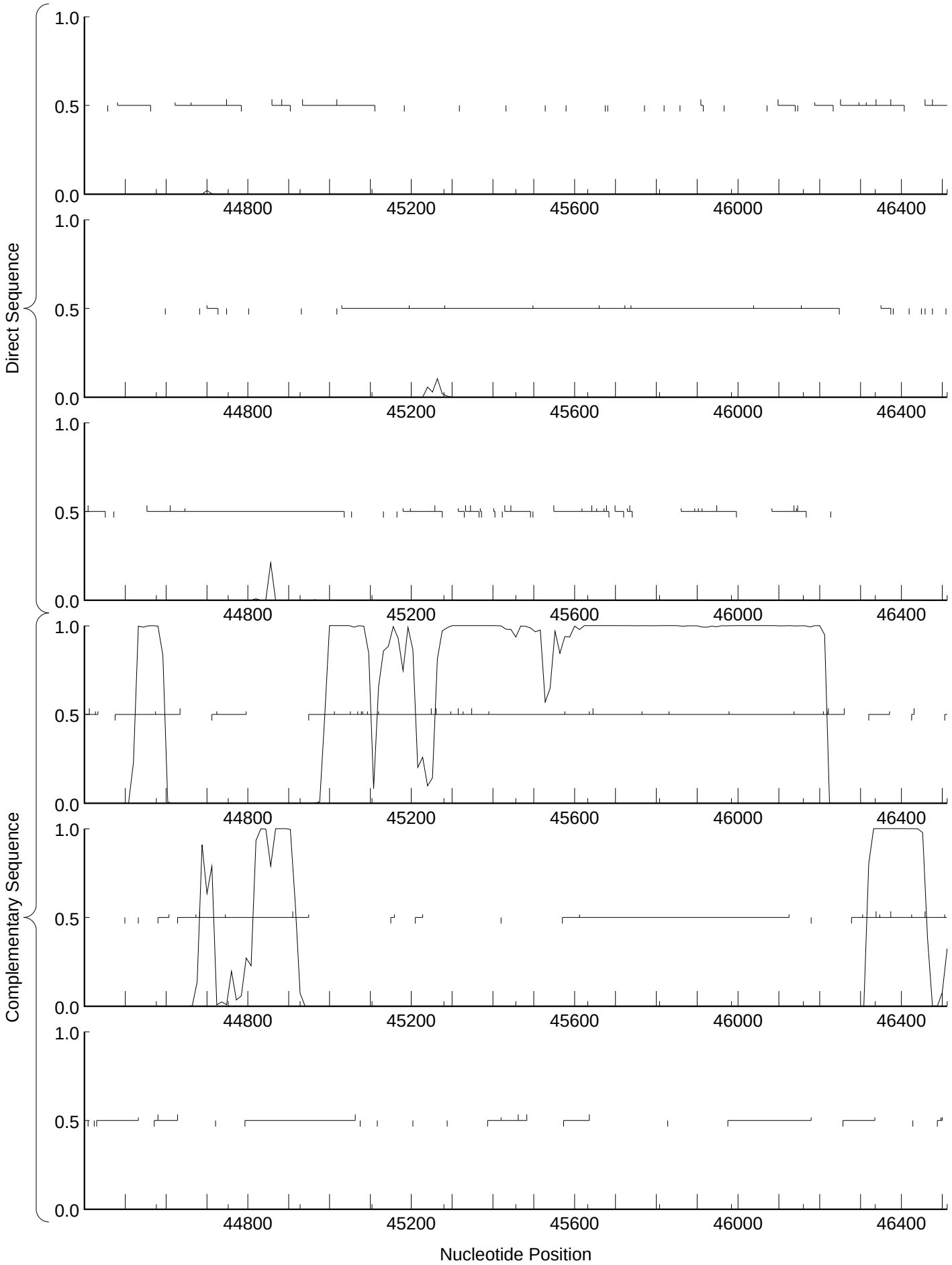
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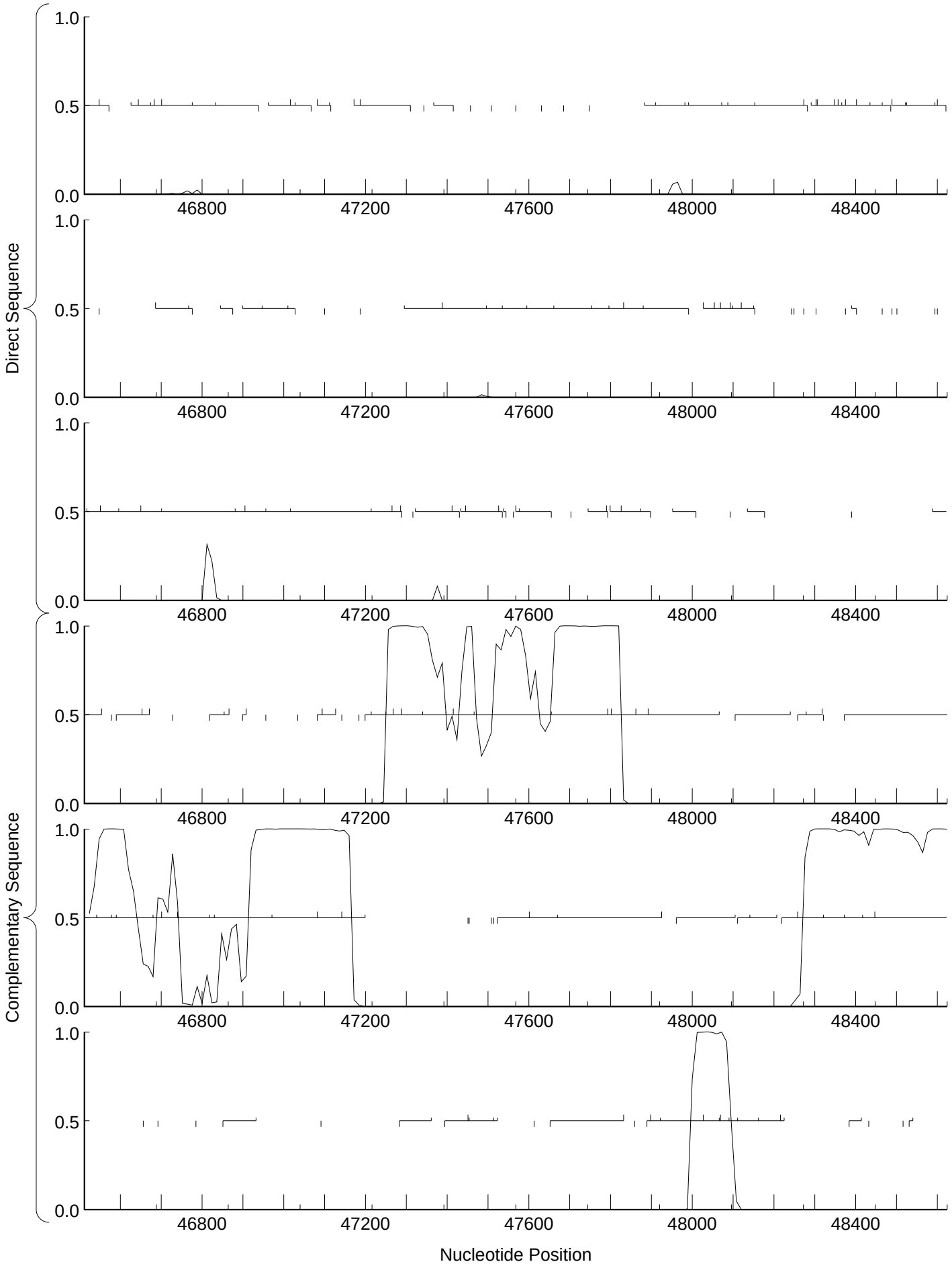



Direct Sequence
Complementary Sequence
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0.5
0.0
40400
40800
41200
41600
42000
Nucleotide Position

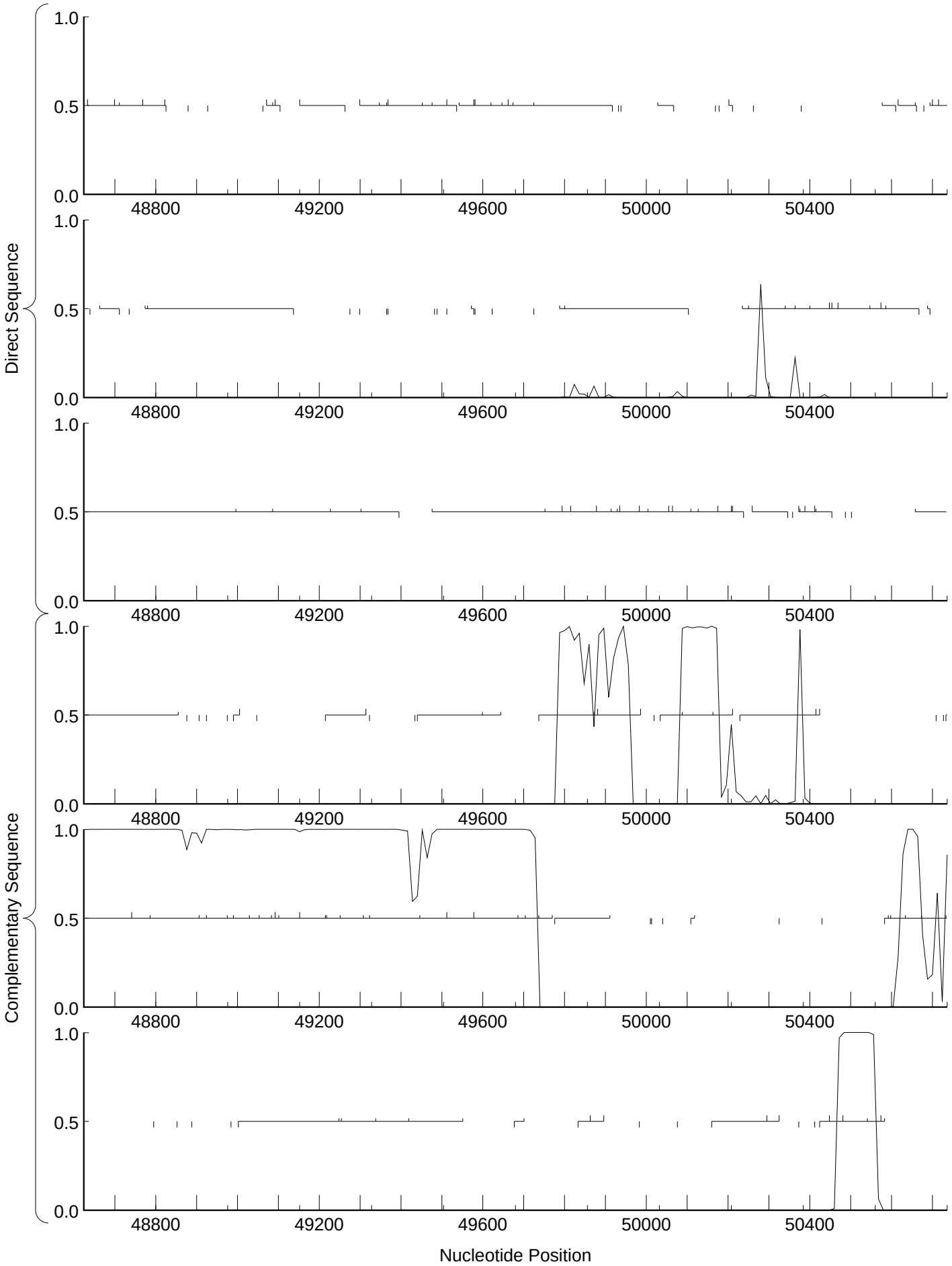

Direct Sequence
Complementary Sequence
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0.0
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43600
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44400
Nucleotide Position

m phage Lyell complete sequence, 62716 bp including 3549 bp terminal repeat, Cluster ED2, Order 4, Window 96, Step 12, 23/31

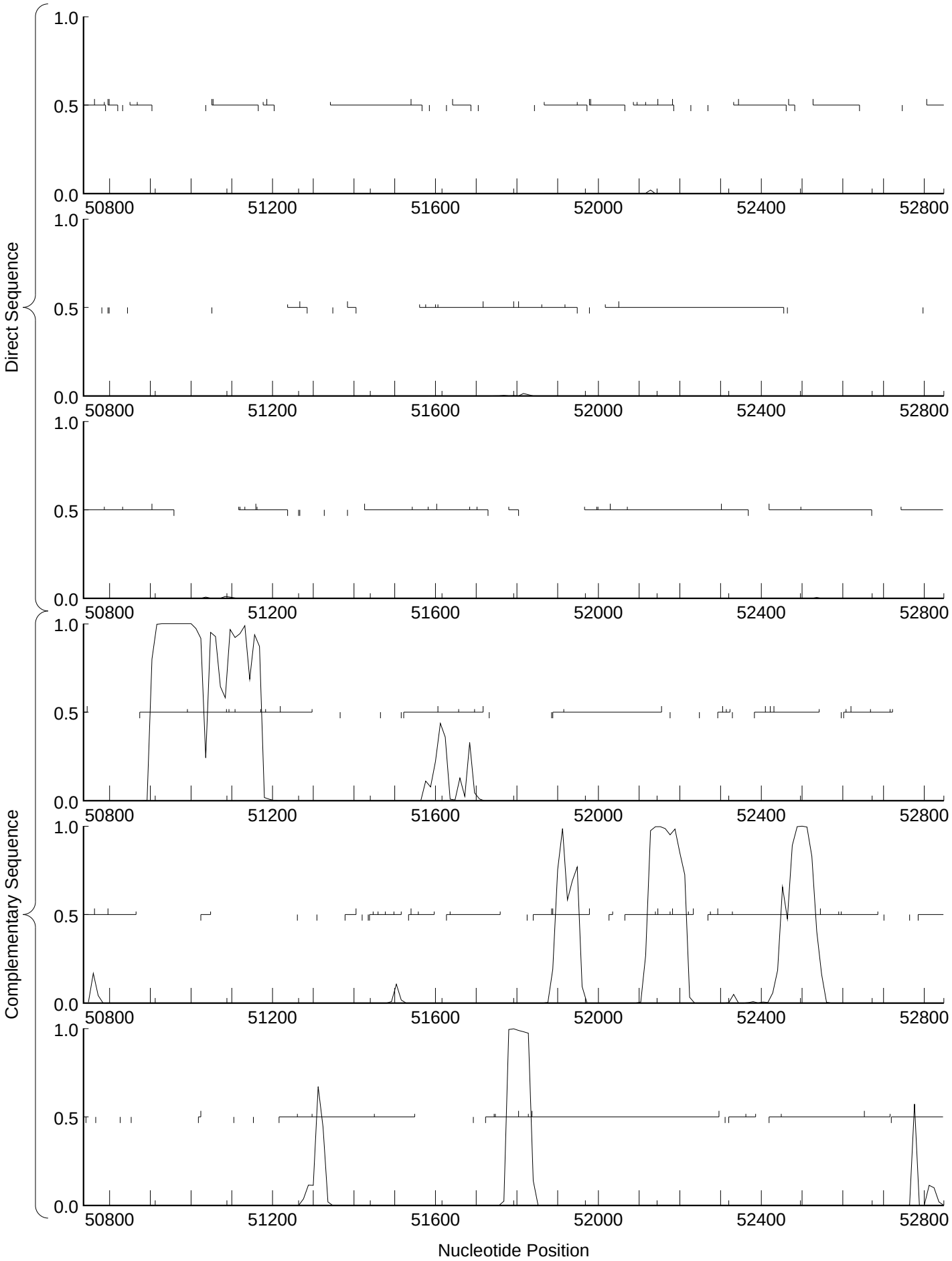



Direct Sequence
Complementary Sequence
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0.5
0.0
46800
47200
47600
48000
48400
Nucleotide Position

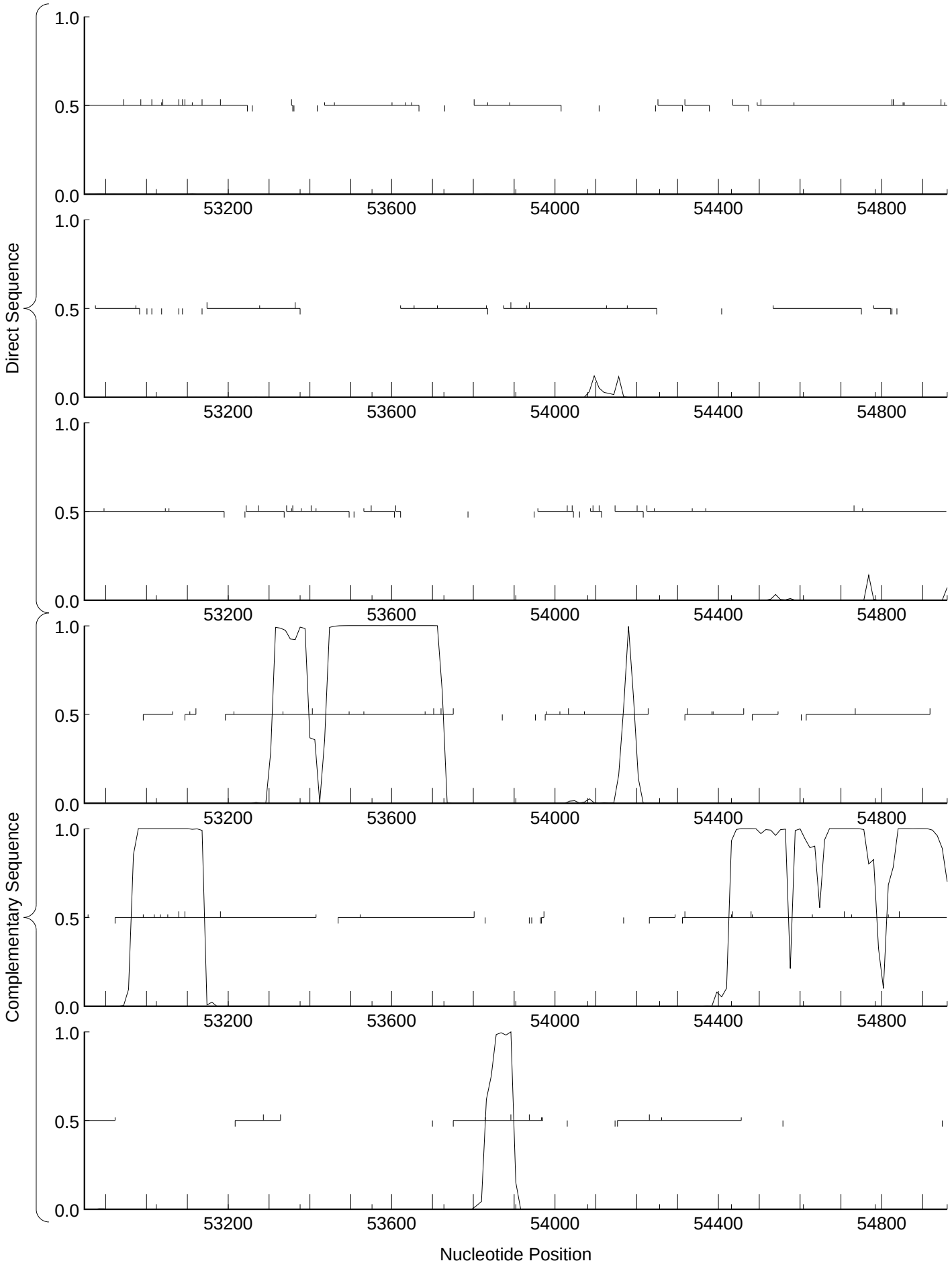
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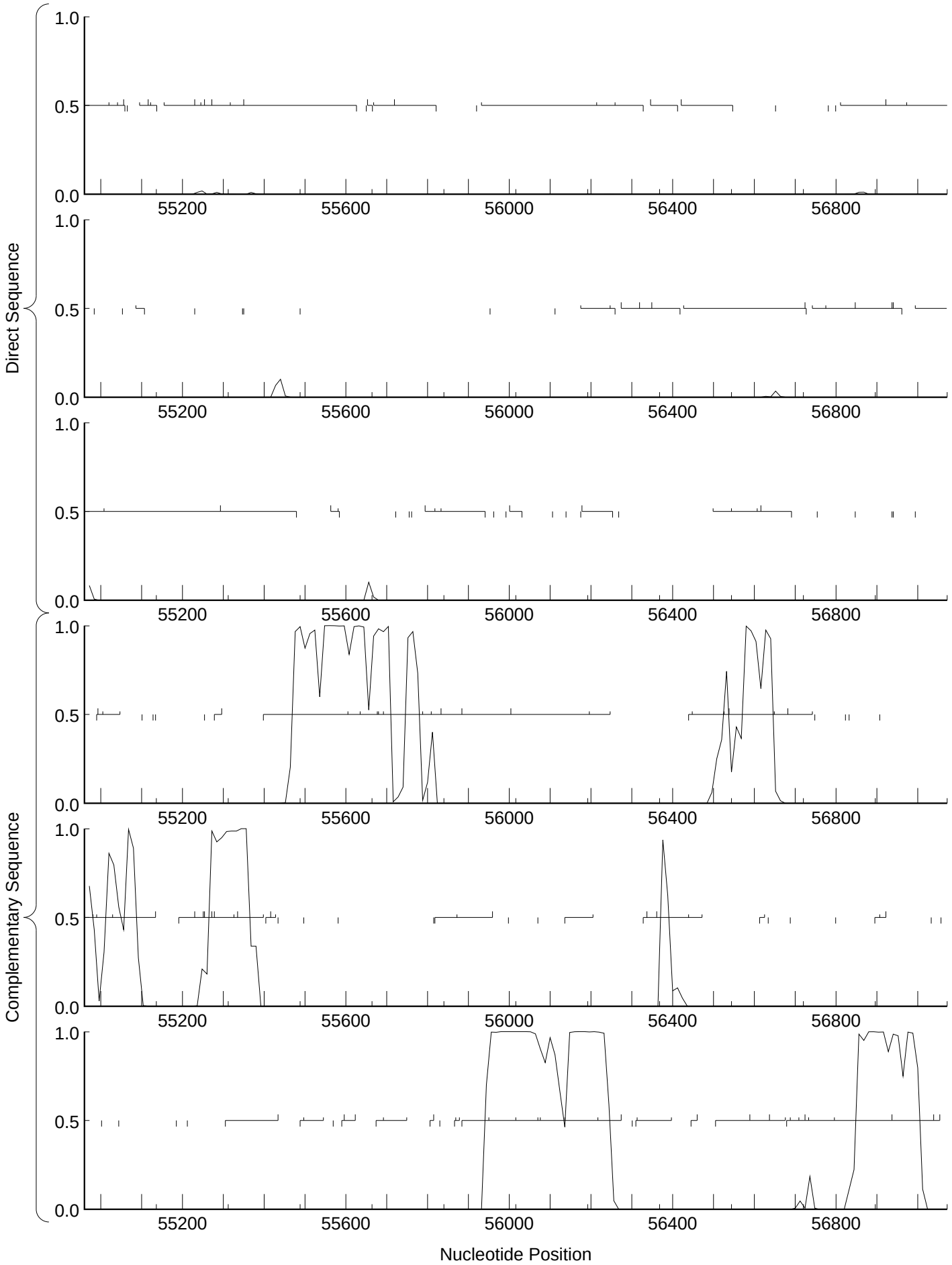
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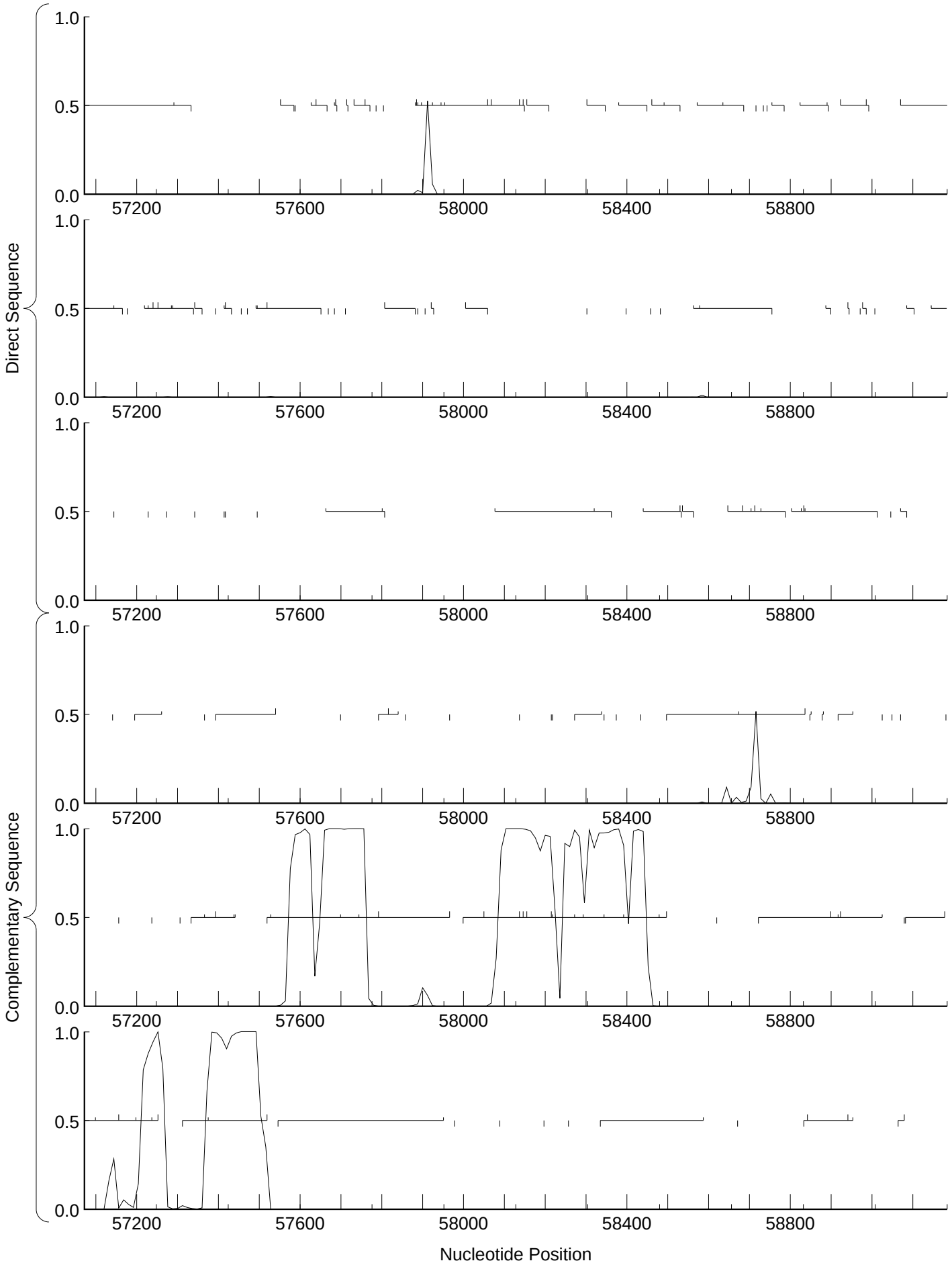
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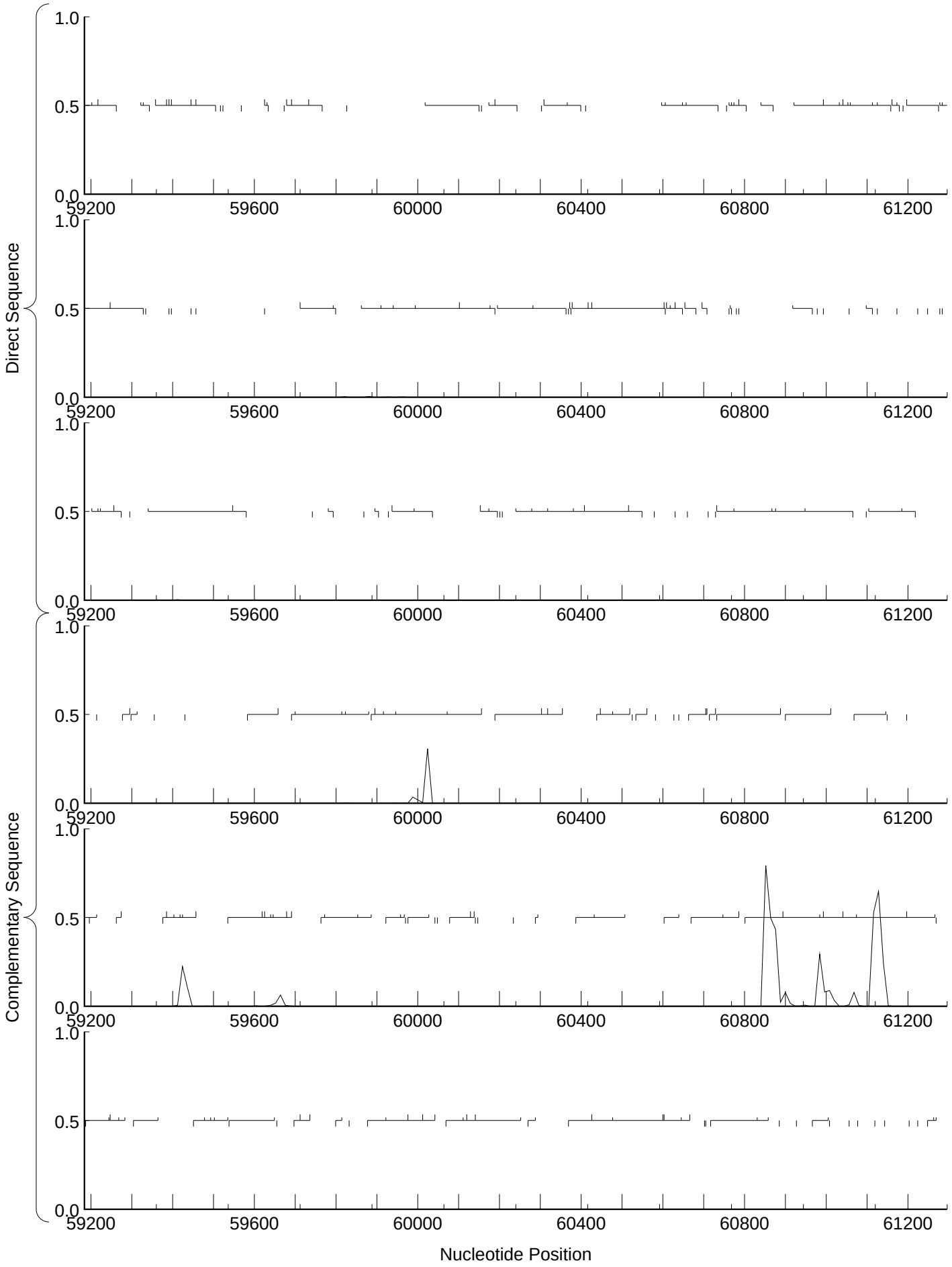
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m phage Lyell complete sequence, 62716 bp including 3549 bp terminal repeat, Cluster ED2, Order 4, Window 96, Step 12, 29/31



m phage Lyell complete sequence, 62716 bp including 3549 bp terminal repeat, Cluster ED2, Order 4, Window 96, Step 12, 30/31



m phage Lyell complete sequence, 62716 bp including 3549 bp terminal repeat, Cluster ED2, Order 4, Window 96, Step 12, 31/31

