GeneMark

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

PROGRAM INFORMATION

```
Sequence         :  Mycobacterium phage Rapunzel97 complete sequence, 59687 bp including 11-base 3’ overhang (C
Analysis Date    :  3/29/24 at 6:48:21
Pages            :  30
Sequence Length  :  59687 bp
GC Content       :   66.60%

Window Length    :  96 bp
Window Step      :  12 bp
Threshold Value  :  0.500

PS-Version       :  1.2

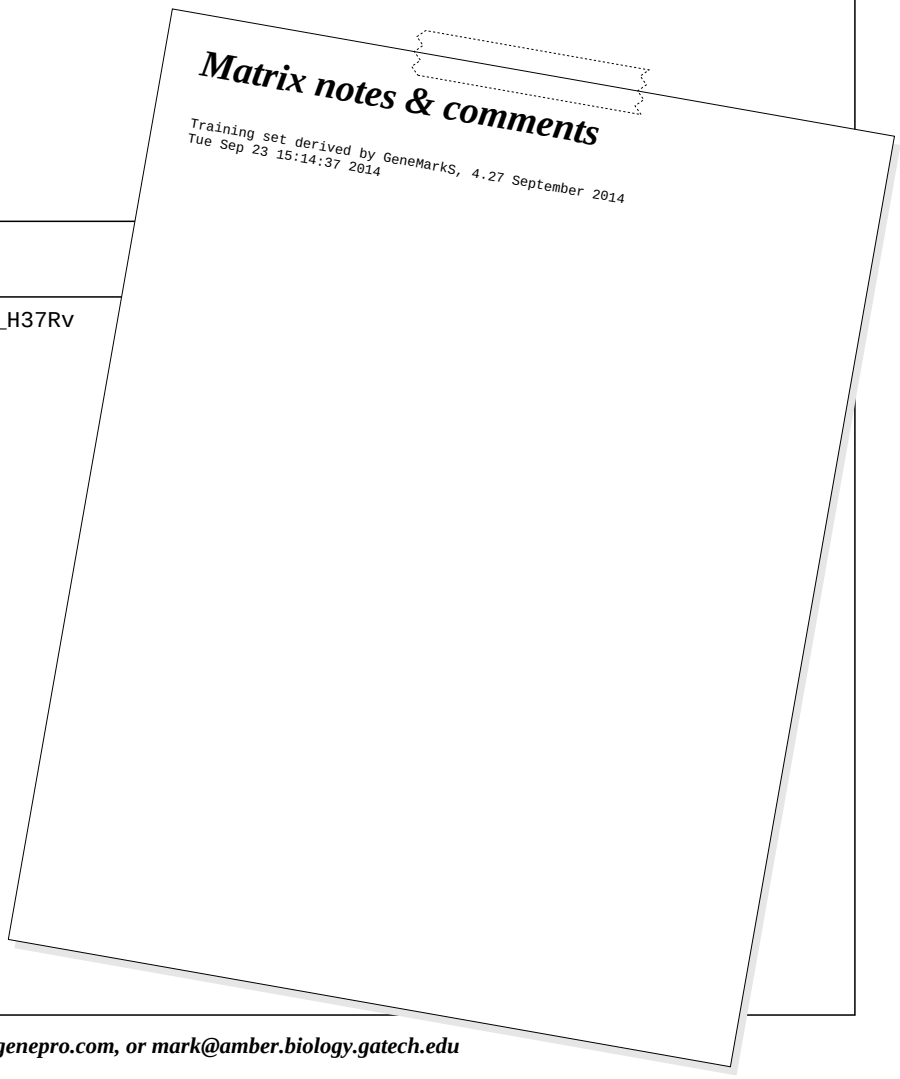
GeneMark Options :  PostScript graph,
                    Mark ORFs / splice sites,
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MATRIX INFORMATION

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Author     :  -

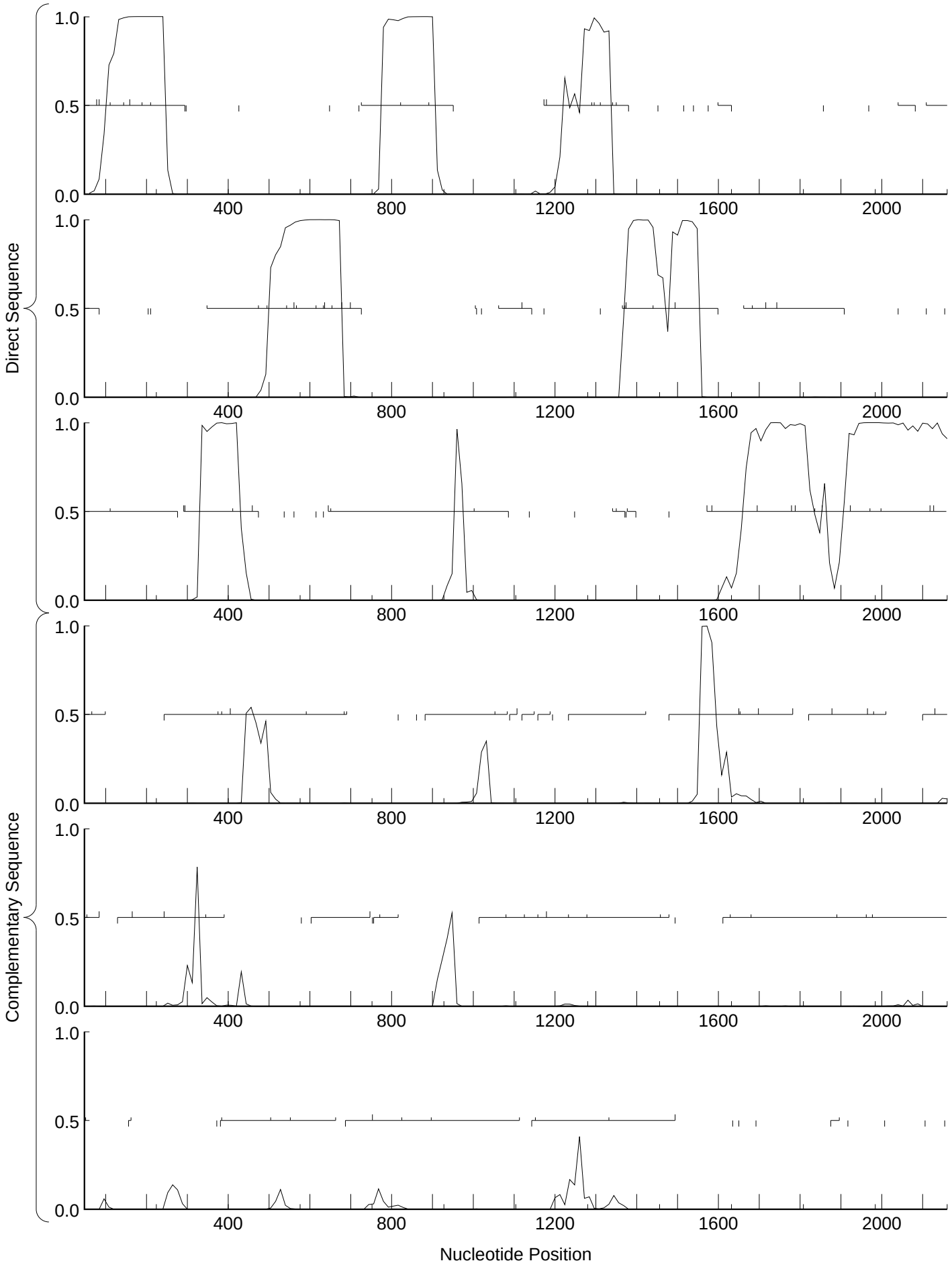
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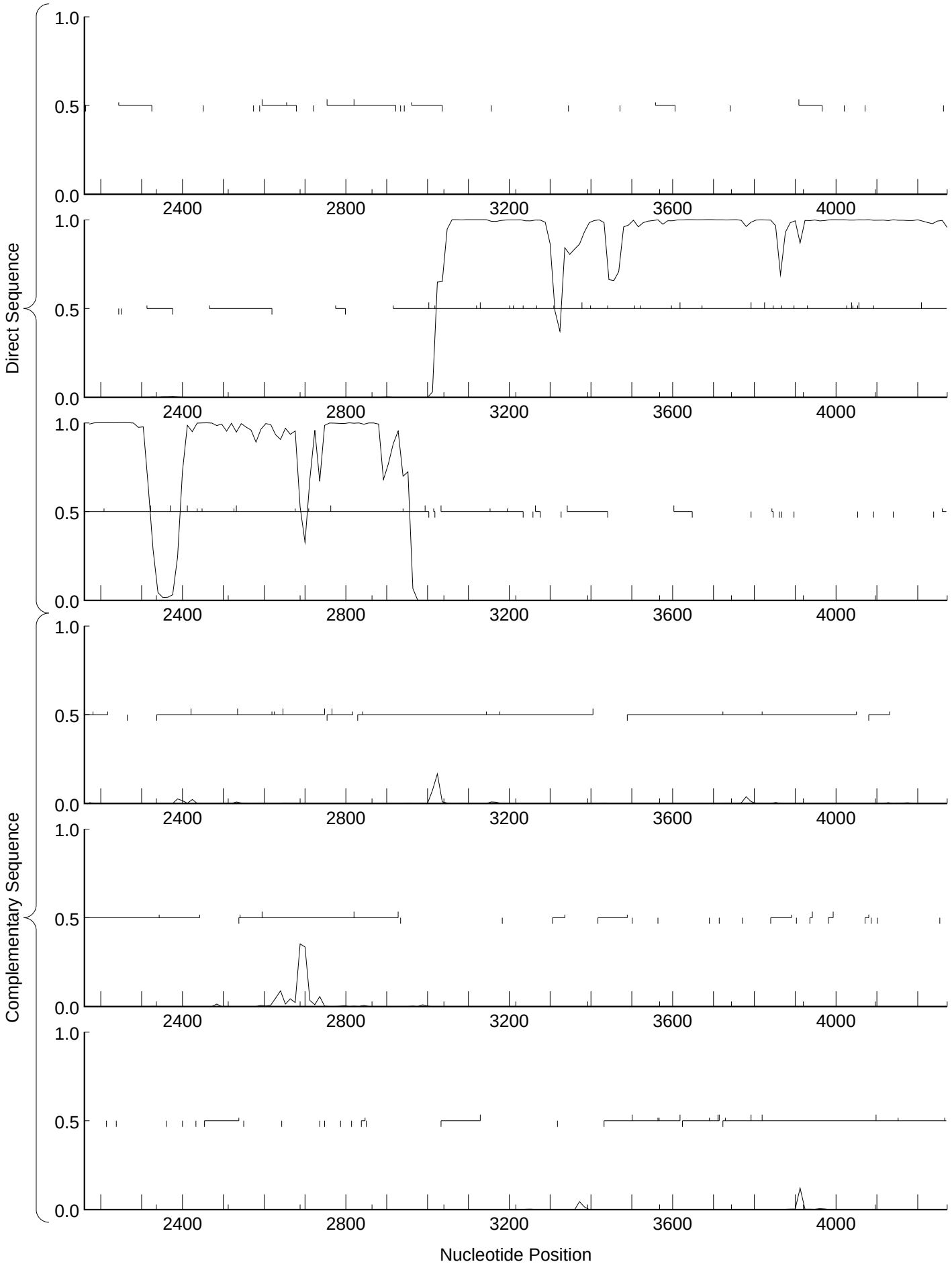

  Send questions / comments to:
      Dr. M. Borodovsky
      Georgia Institute of Technology
      School of Biology
      Atlanta, GA  30332-0230
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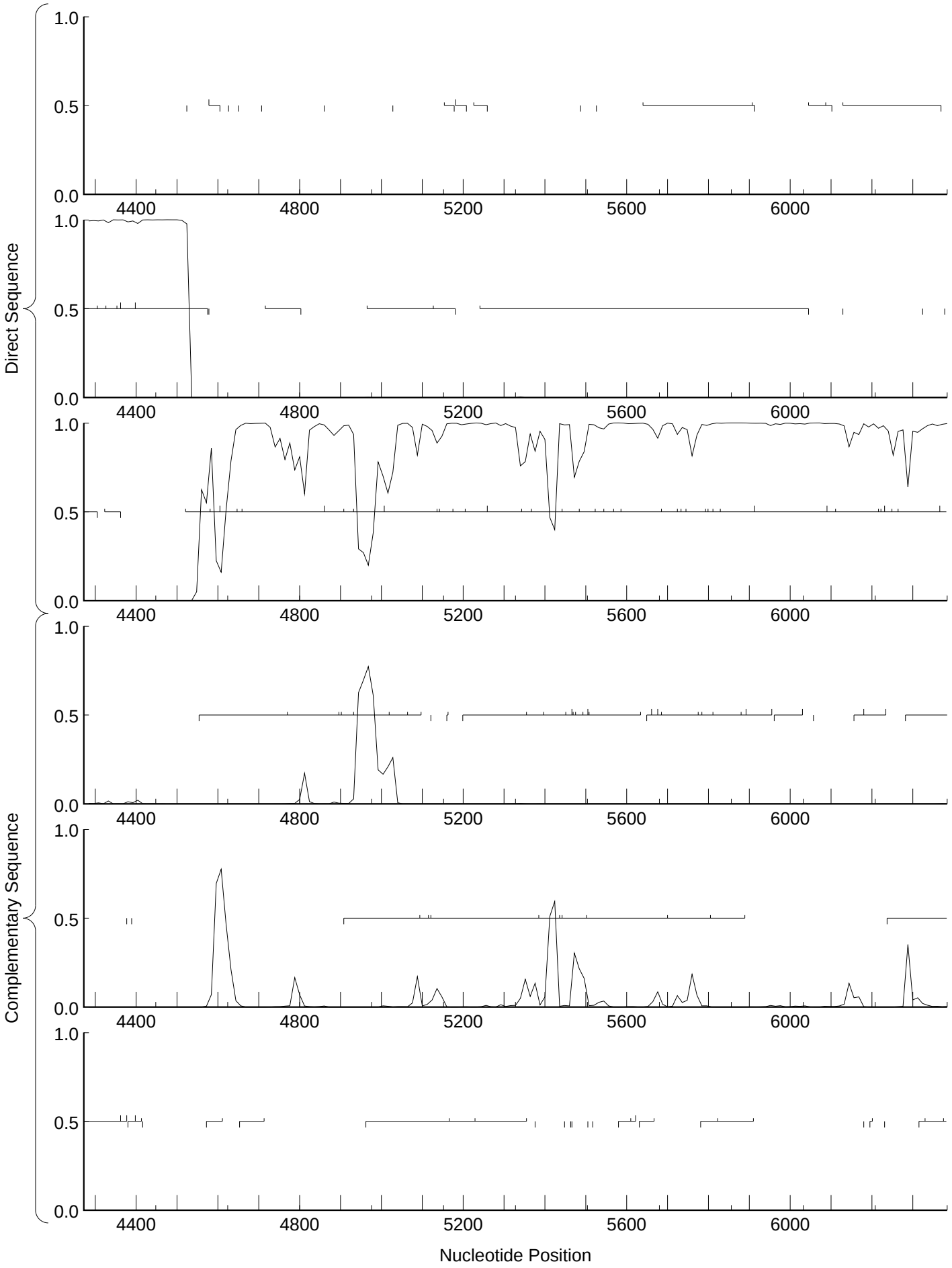


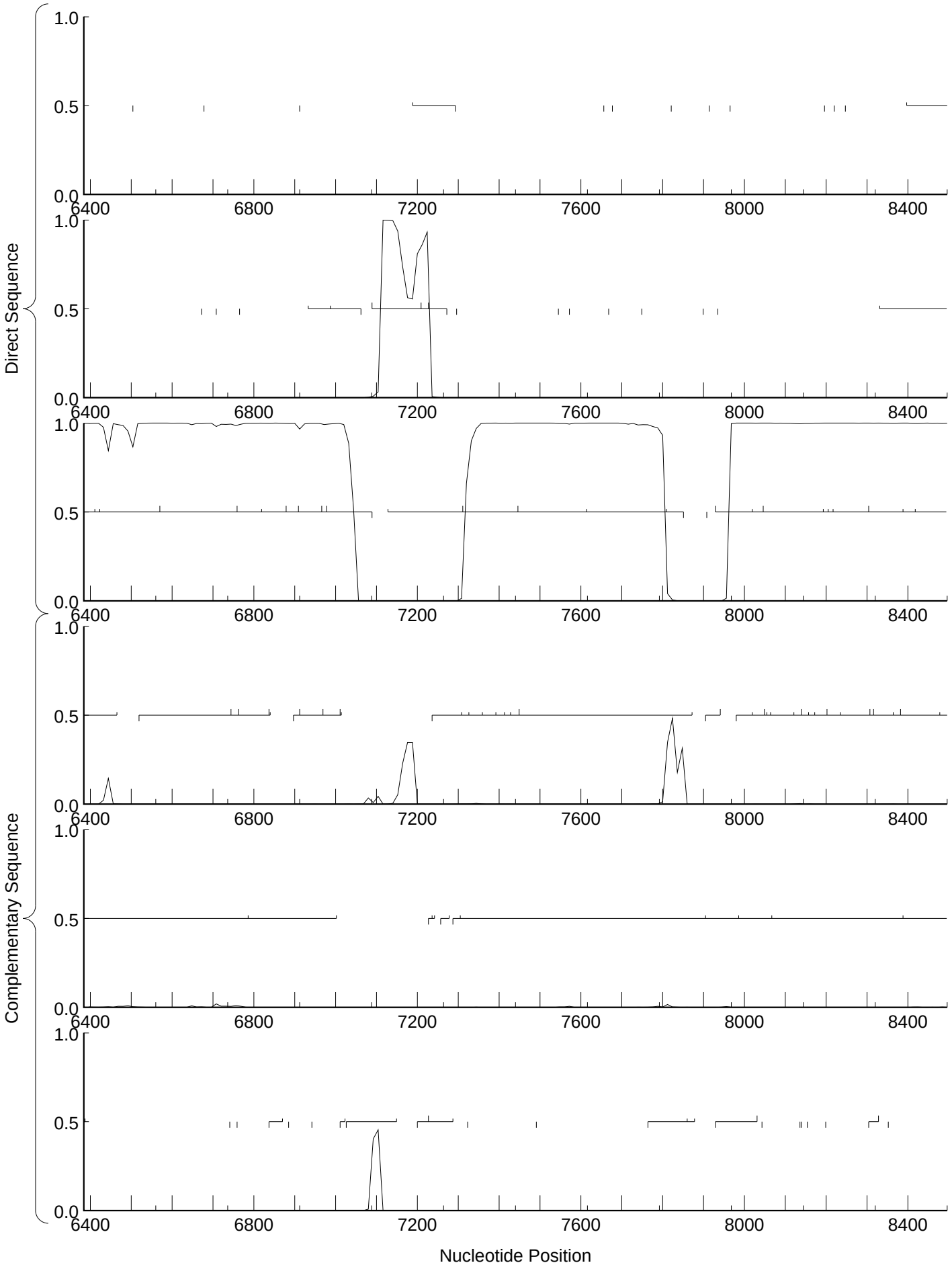
For help or information, send electronic mail to: custserv@genepro.com, or mark@amber.biology.gatech.edu

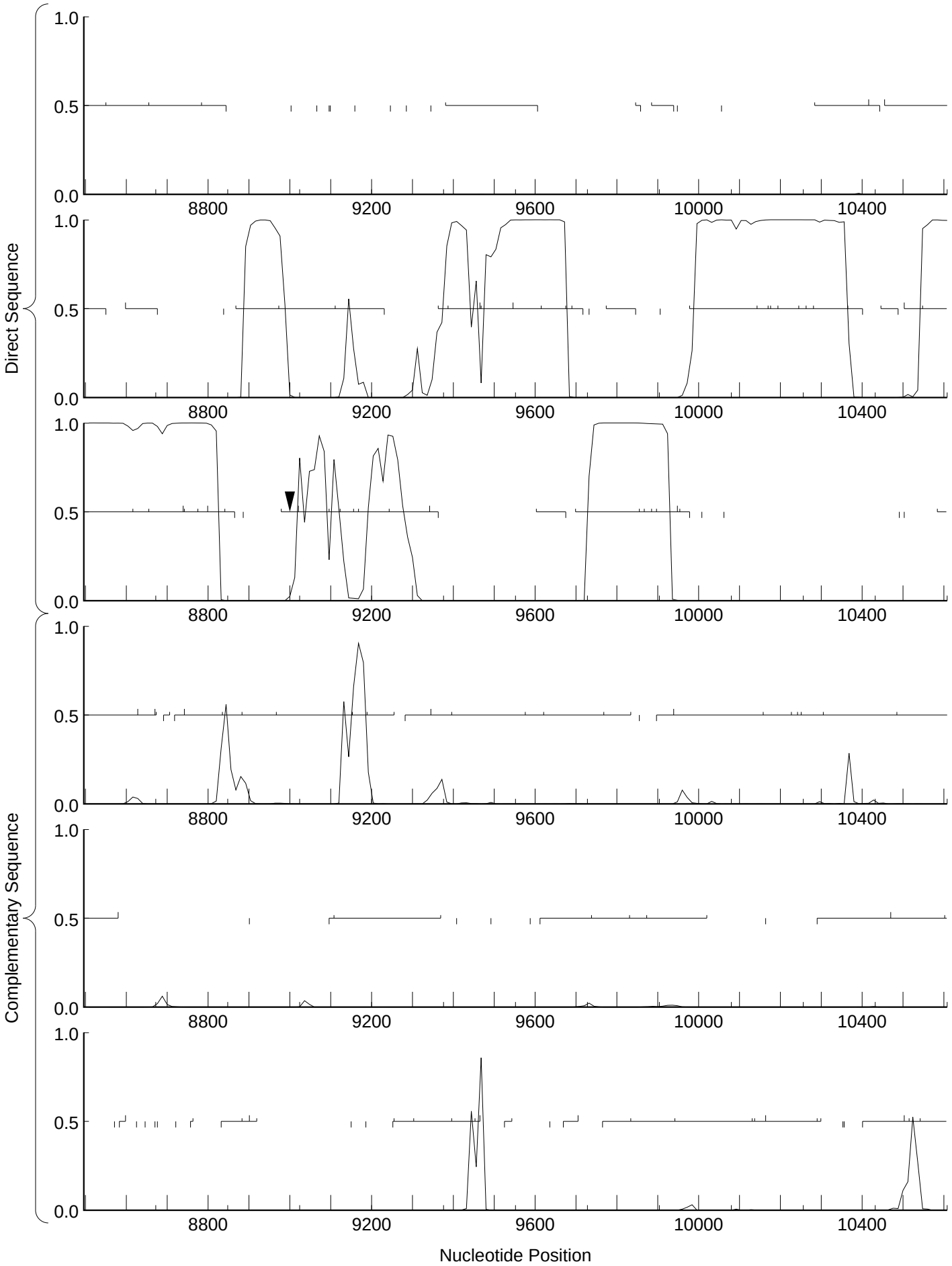
' complete sequence, 59687 bp including 11-base 3' overhang (CTCGTAGGCAT), Cluster K1, Order 4, Window 96, Step 12, 2/30

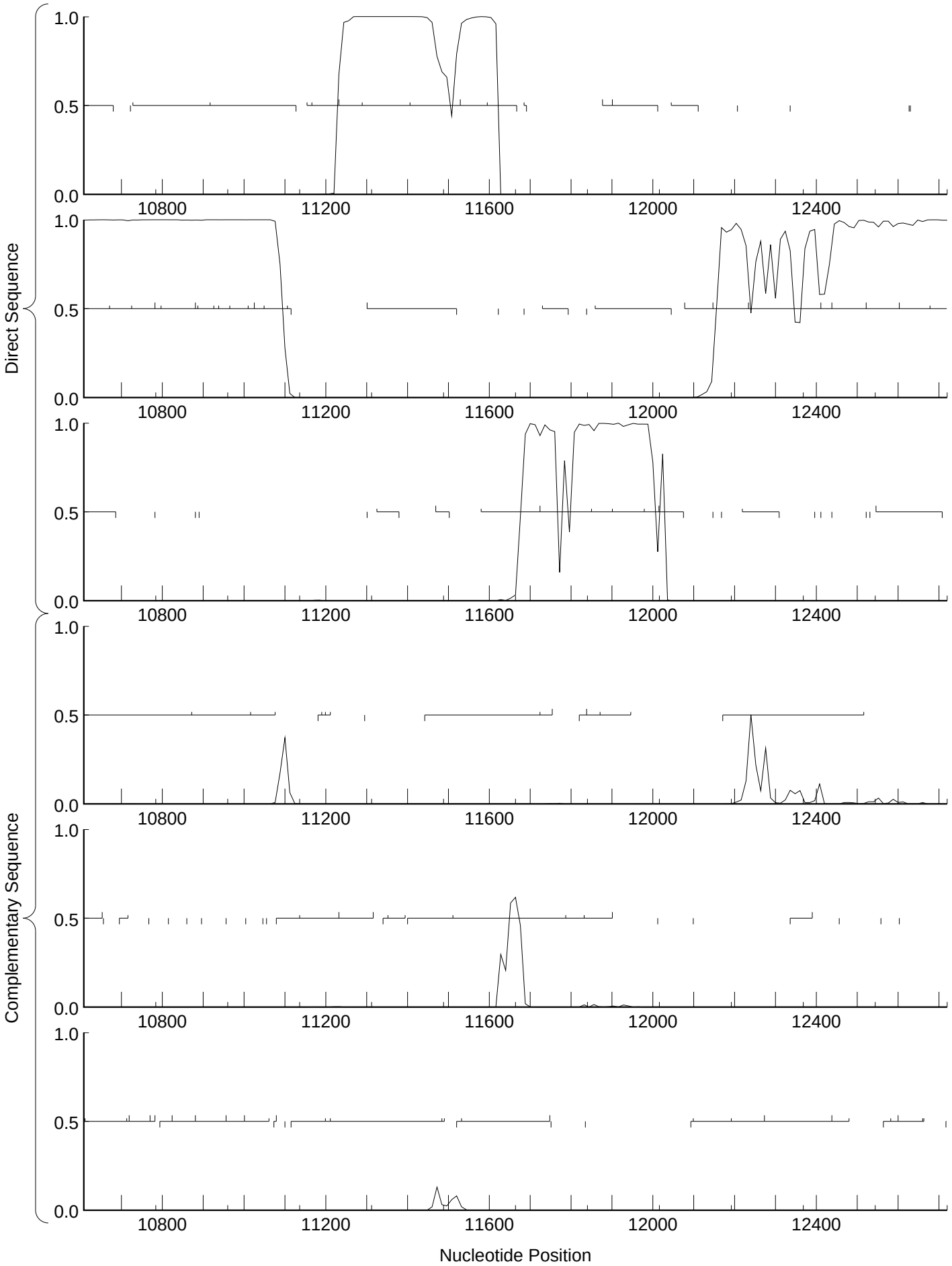


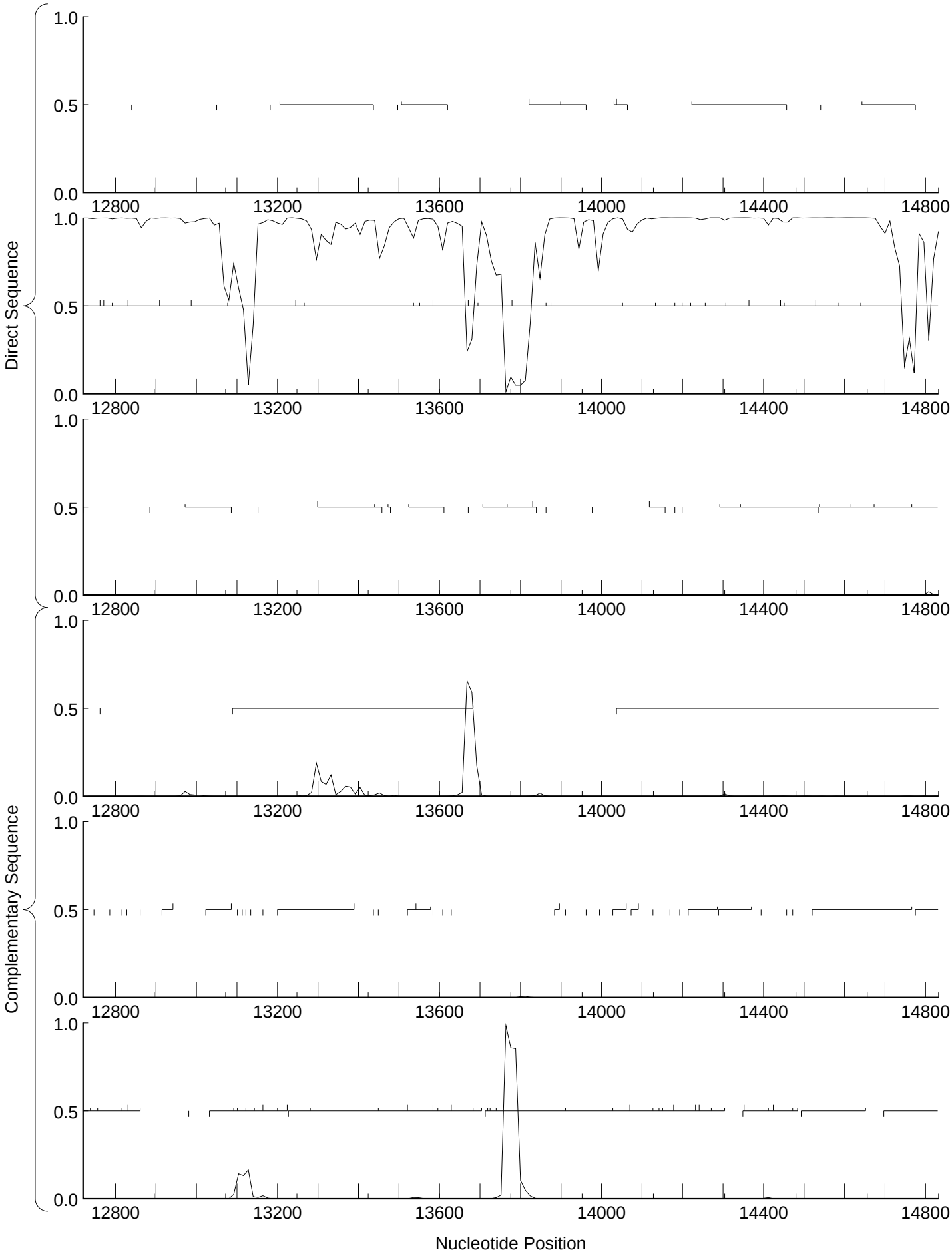

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2800
3200
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Nucleotide Position


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Nucleotide Position

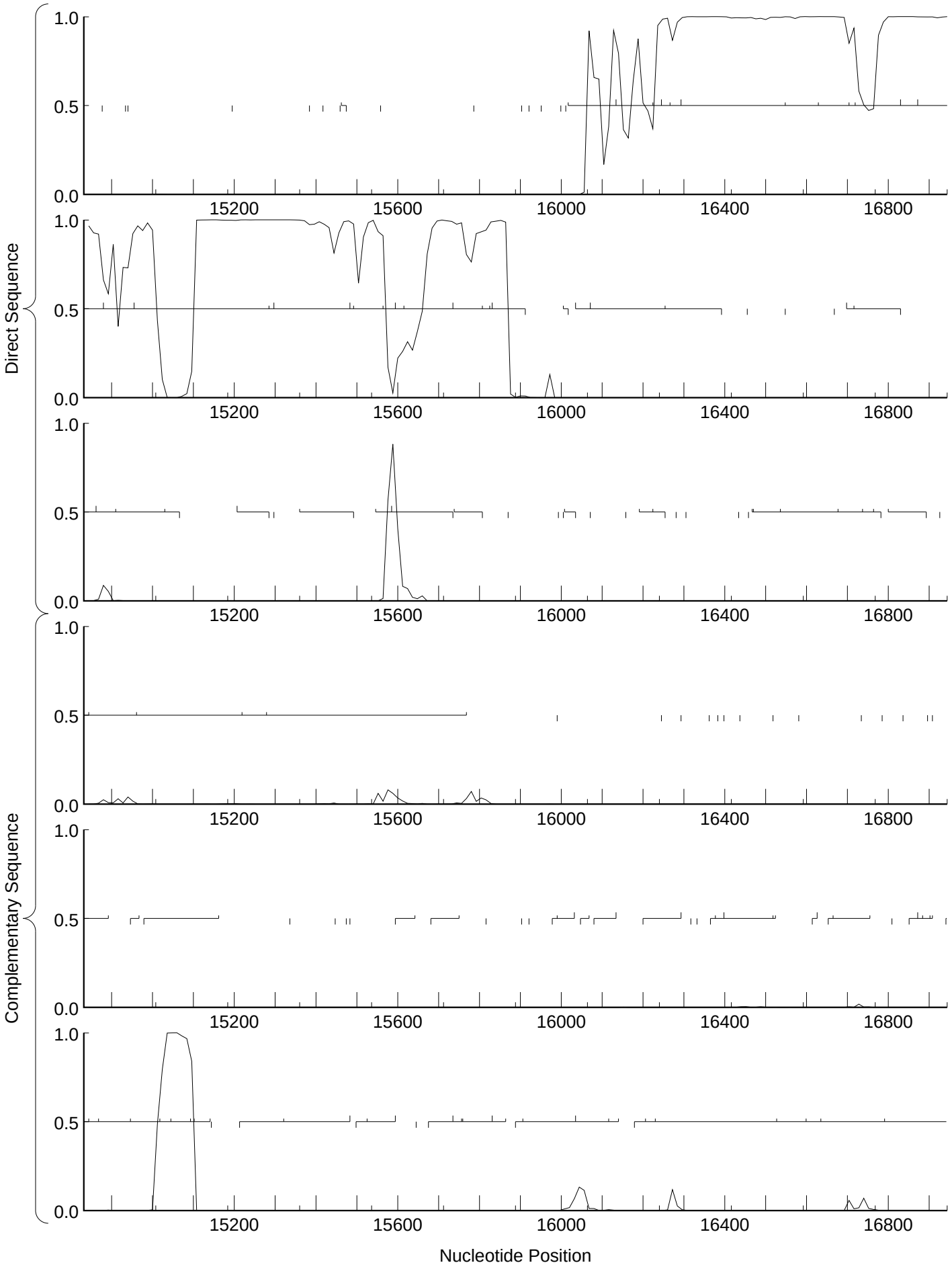

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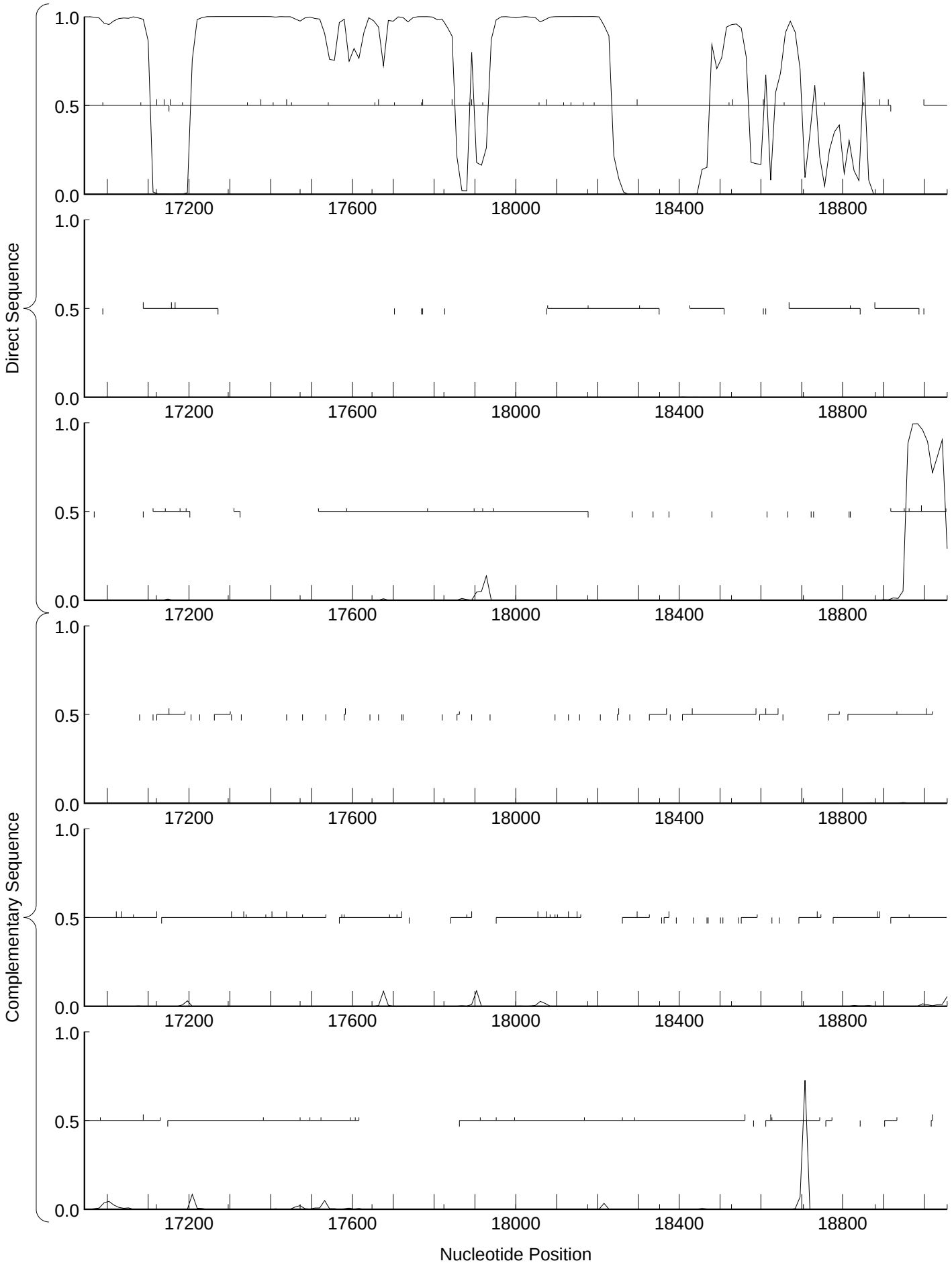

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Nucleotide Position

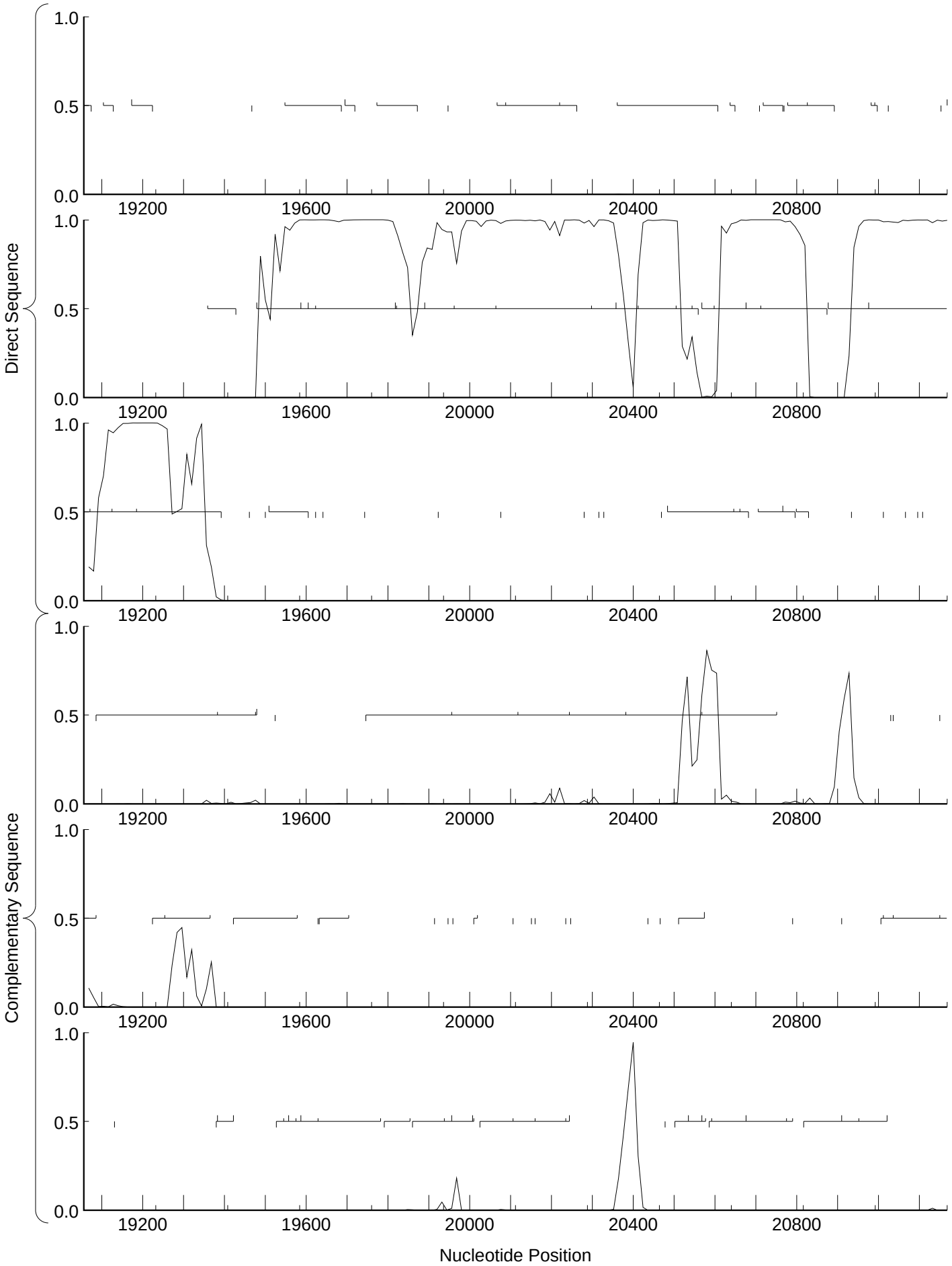
' complete sequence, 59687 bp including 11-base 3' overhang (CTCGTAGGCAT), Cluster K1, Order 4, Window 96, Step 12, 9/30



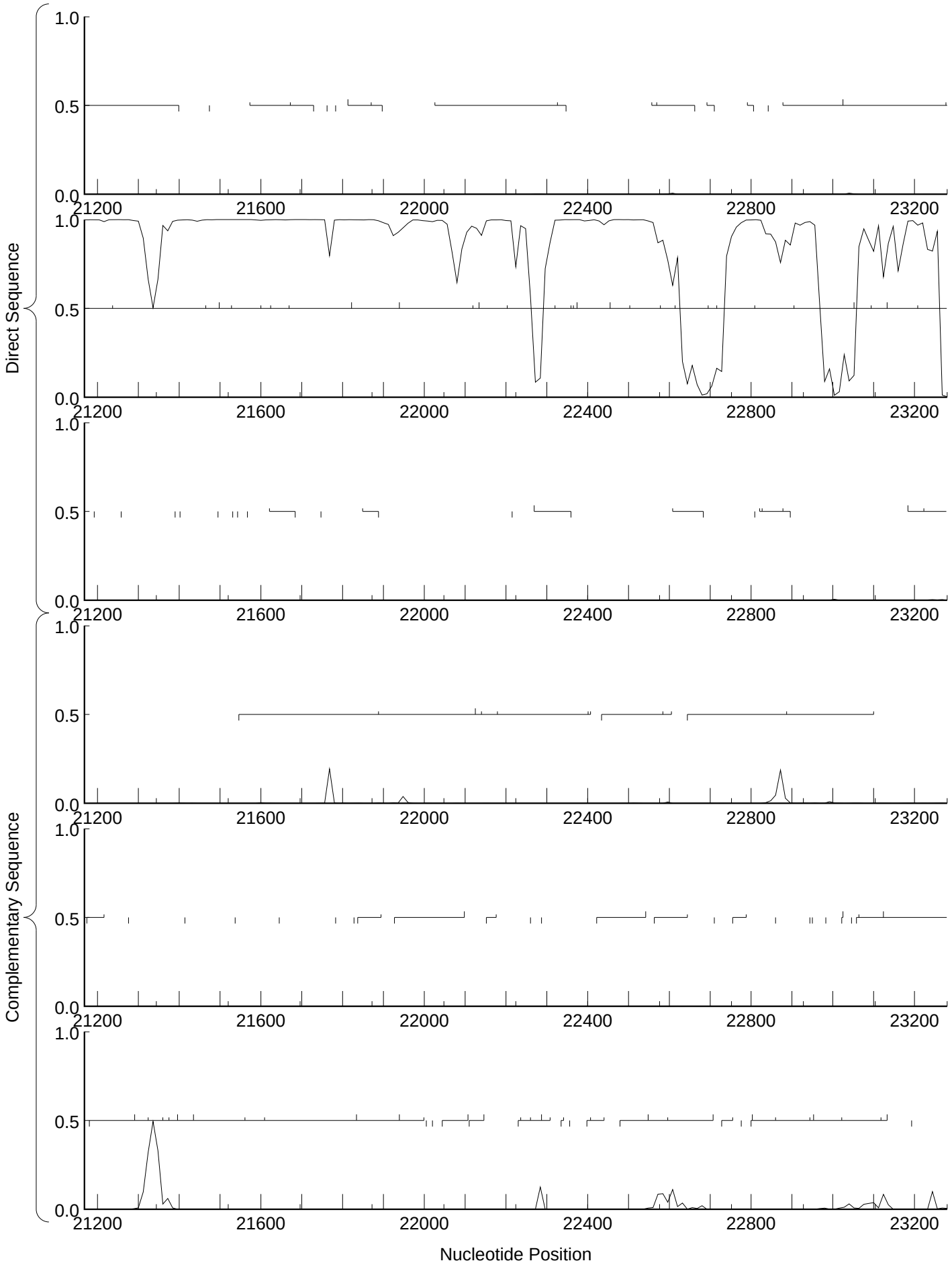
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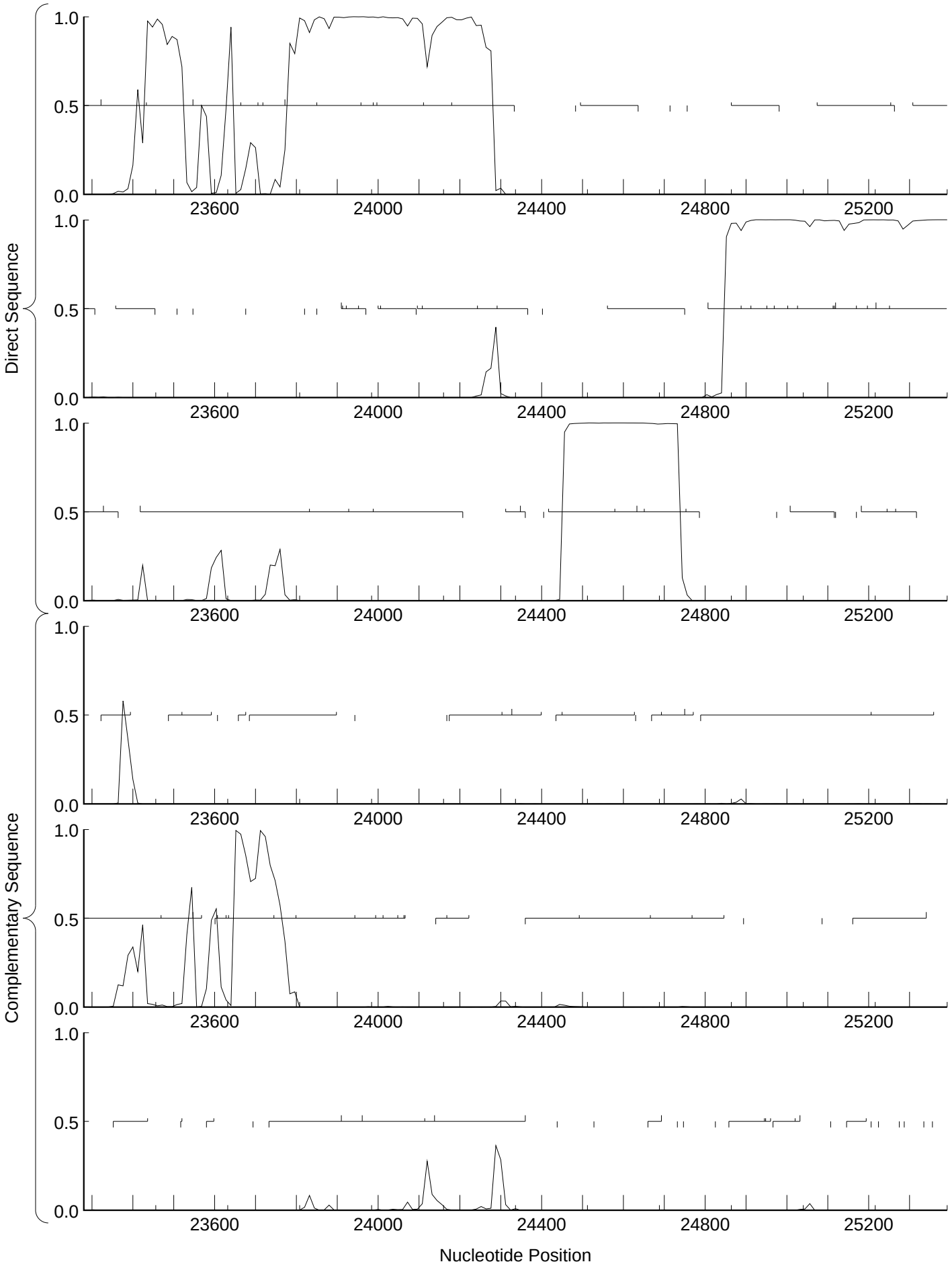
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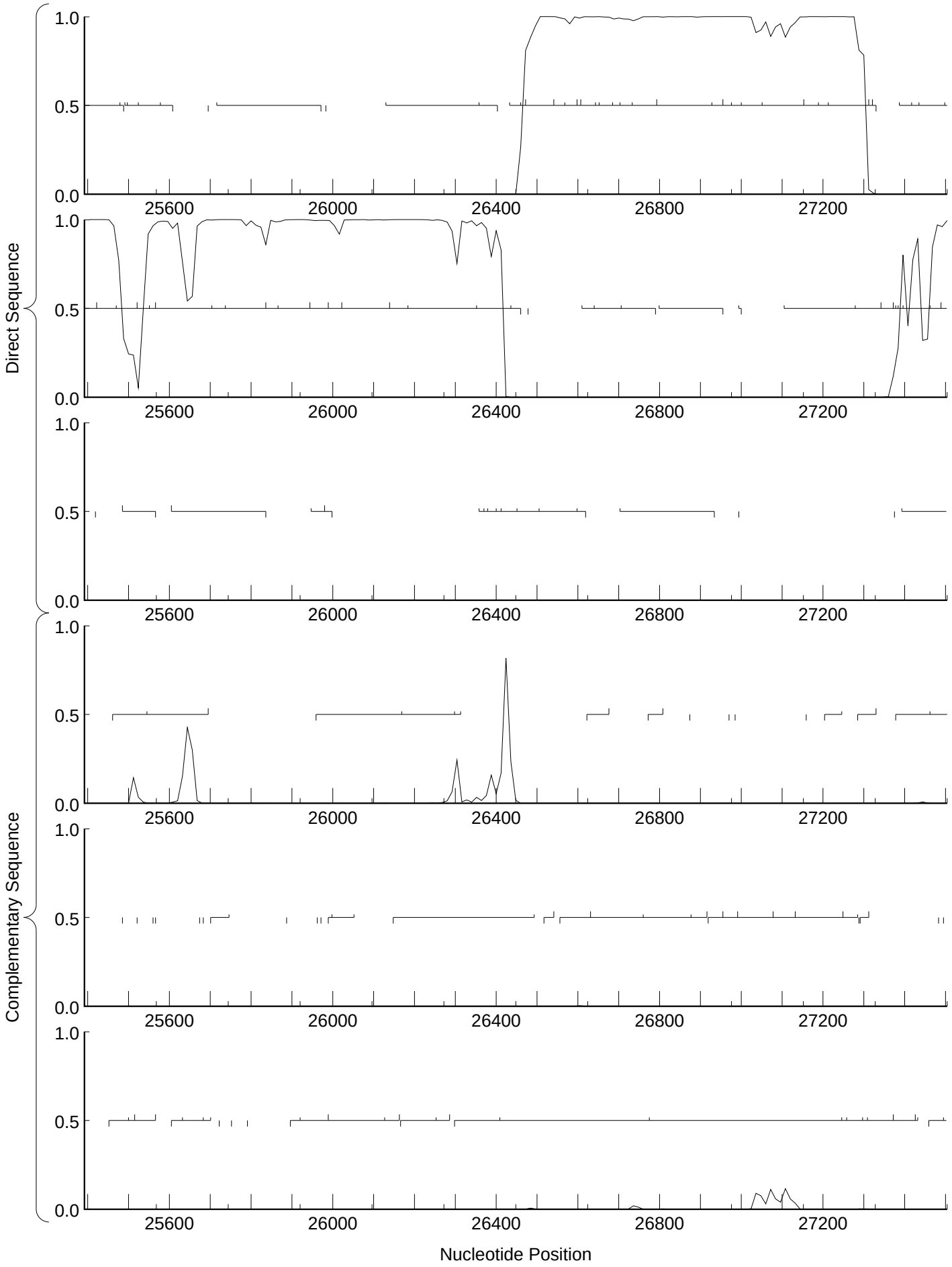
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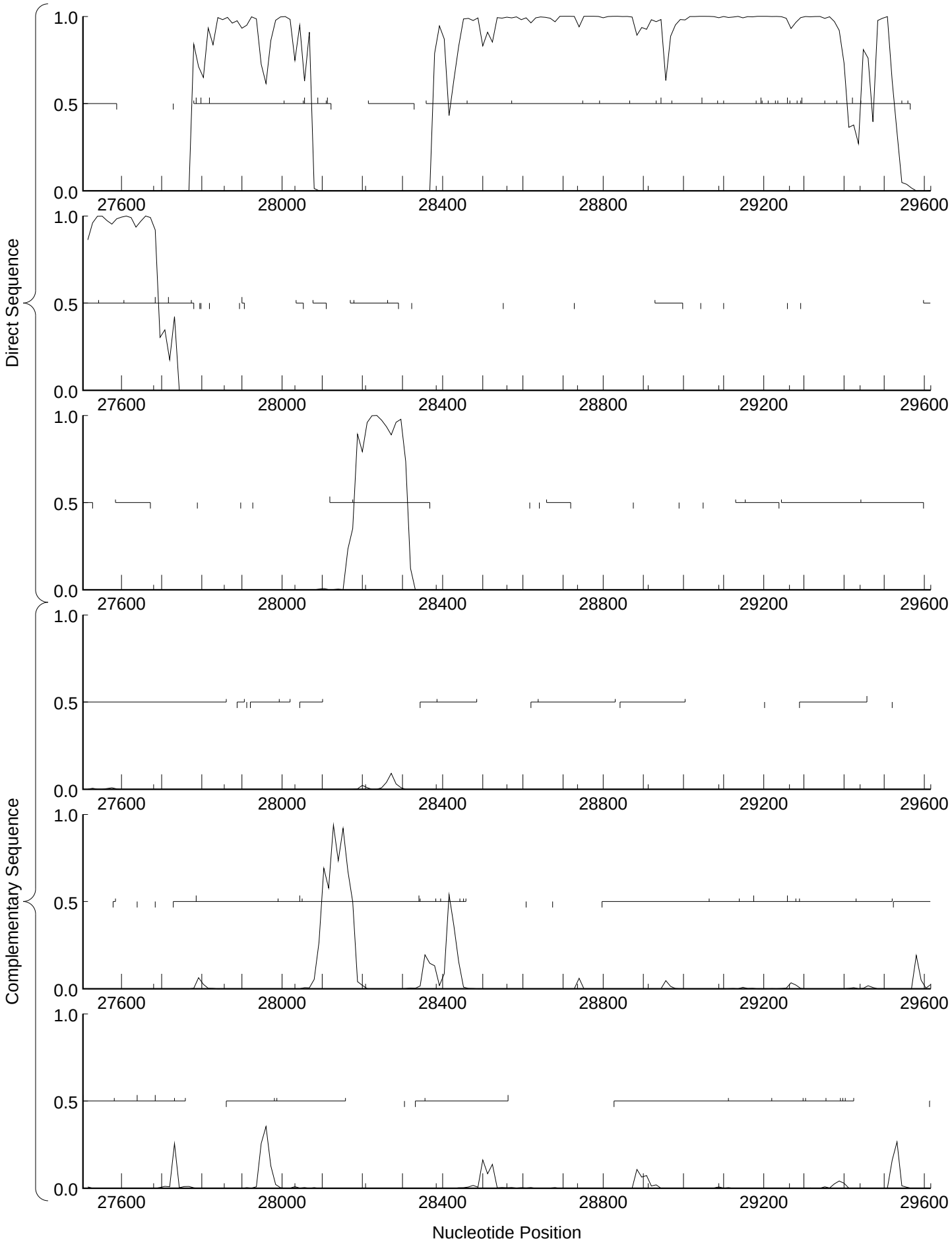
complete sequence, 59687 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K1, Order 4, Window 96, Step 12, 13/30



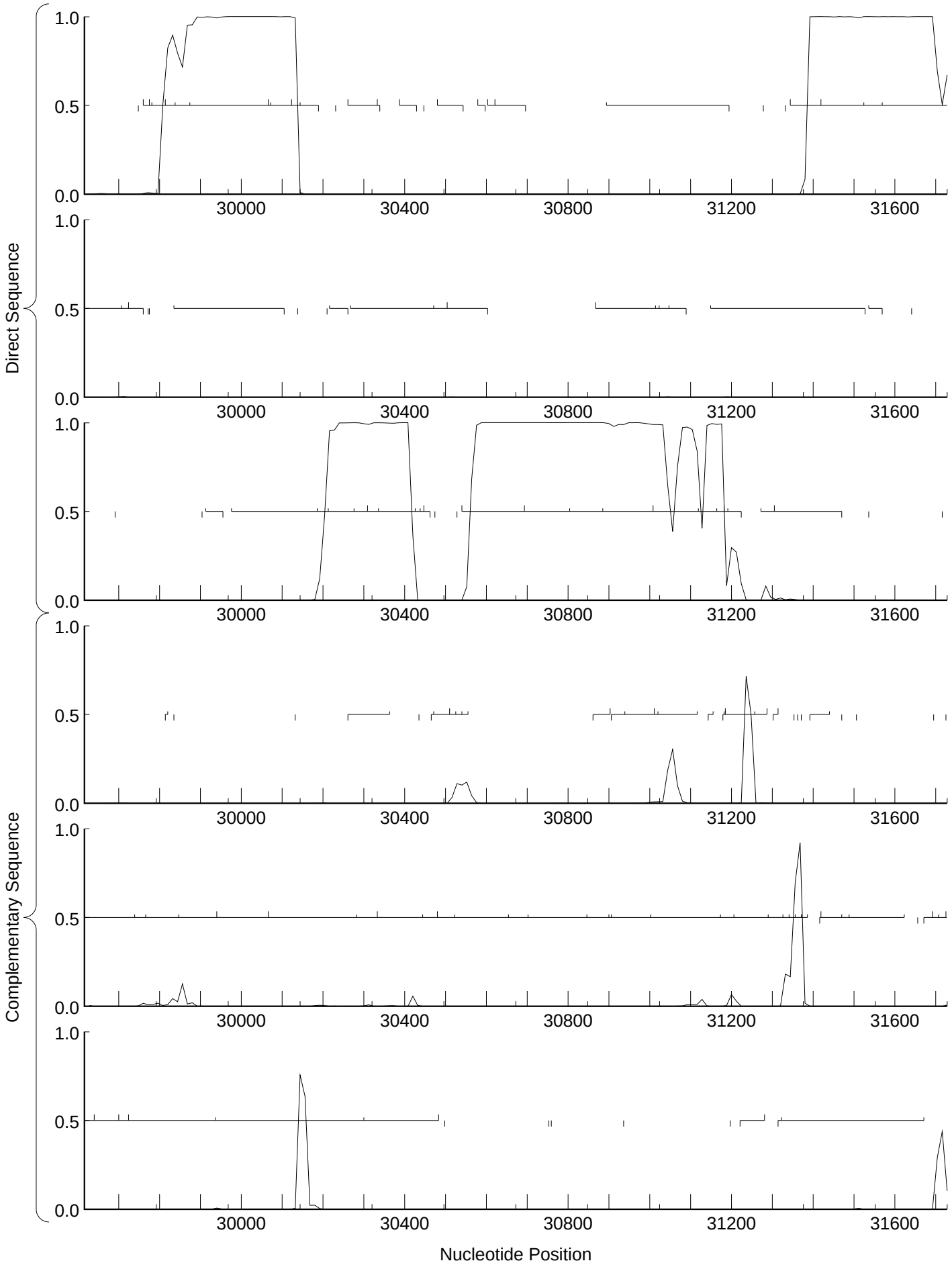
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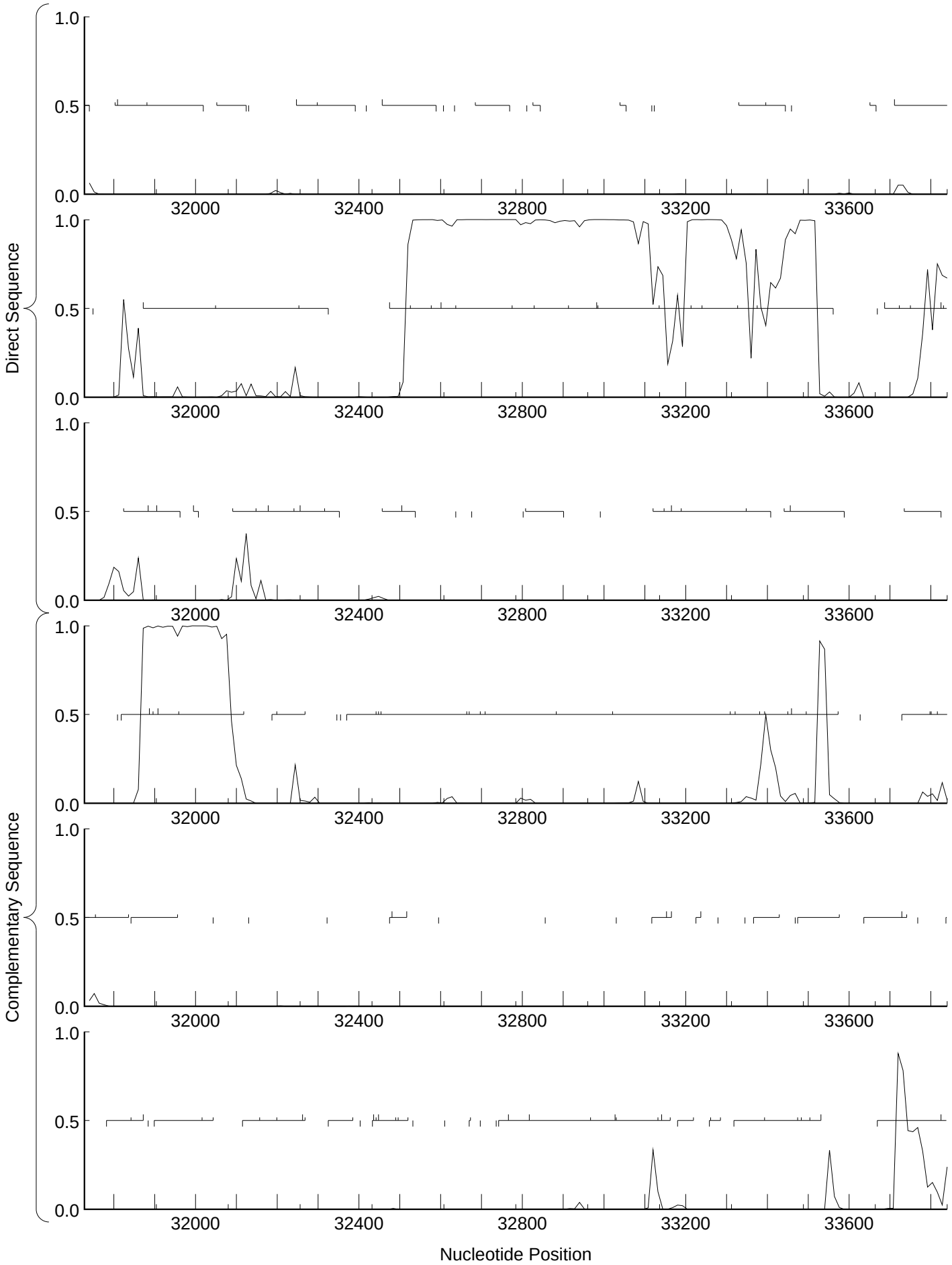
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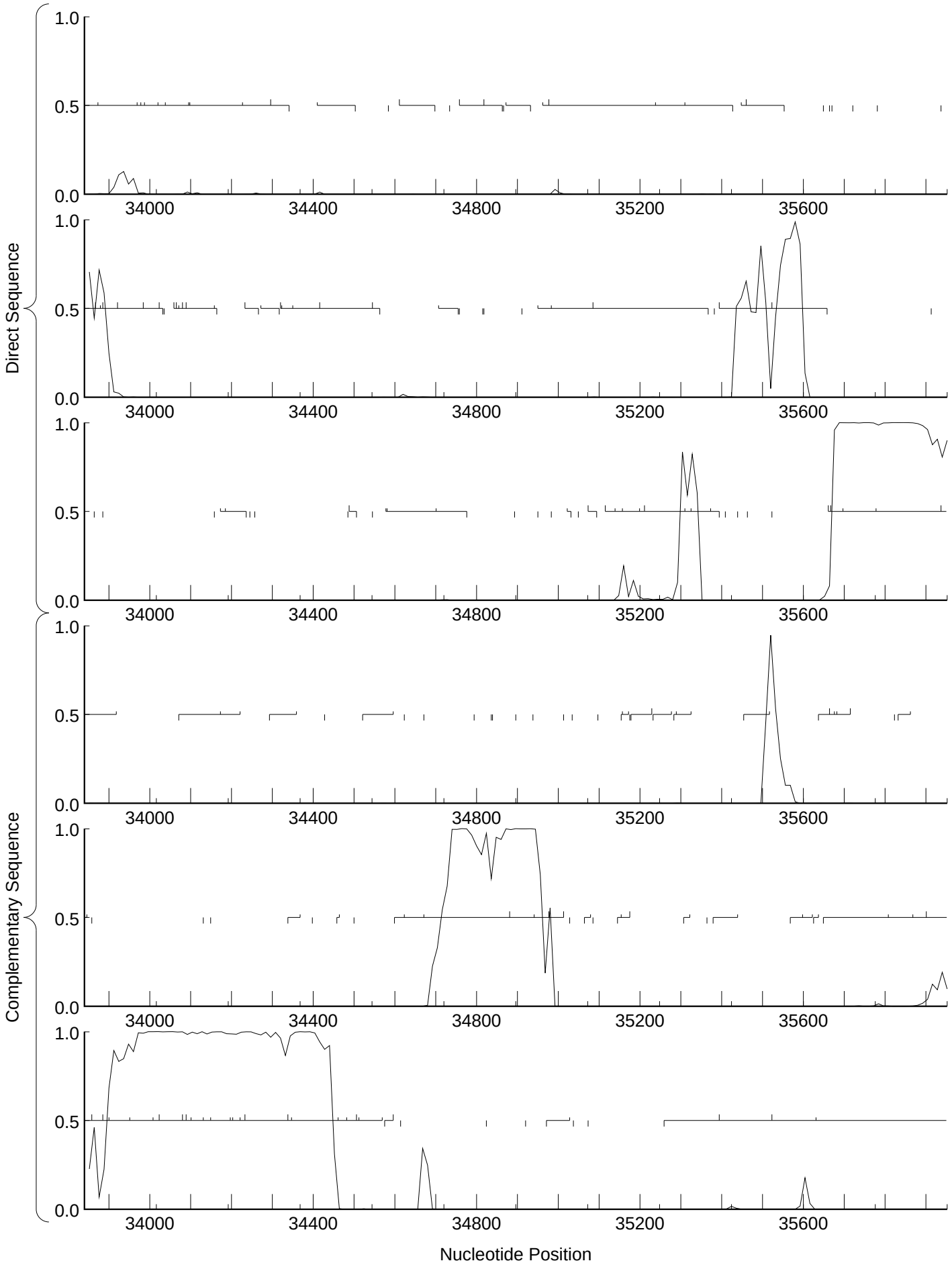
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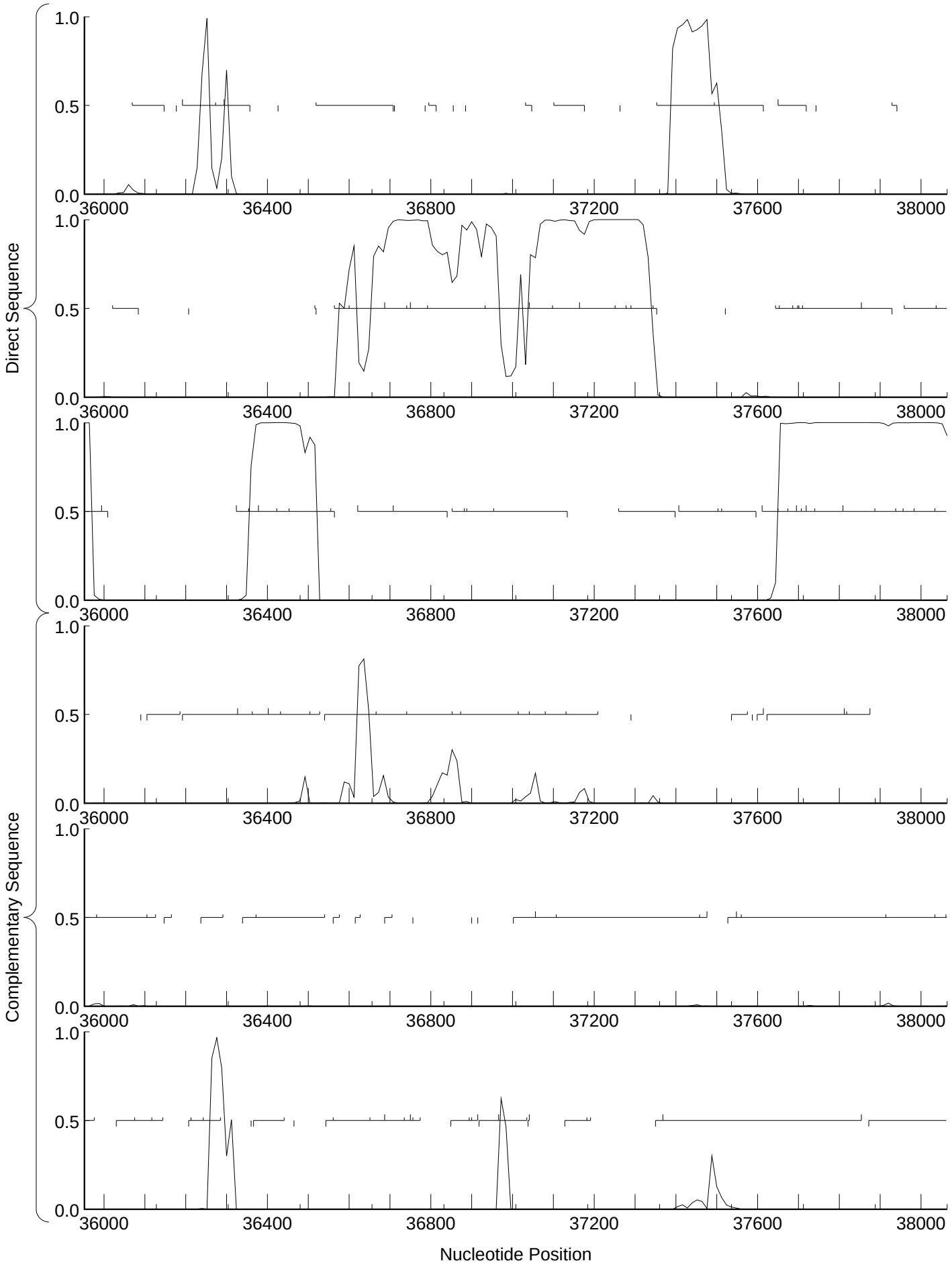
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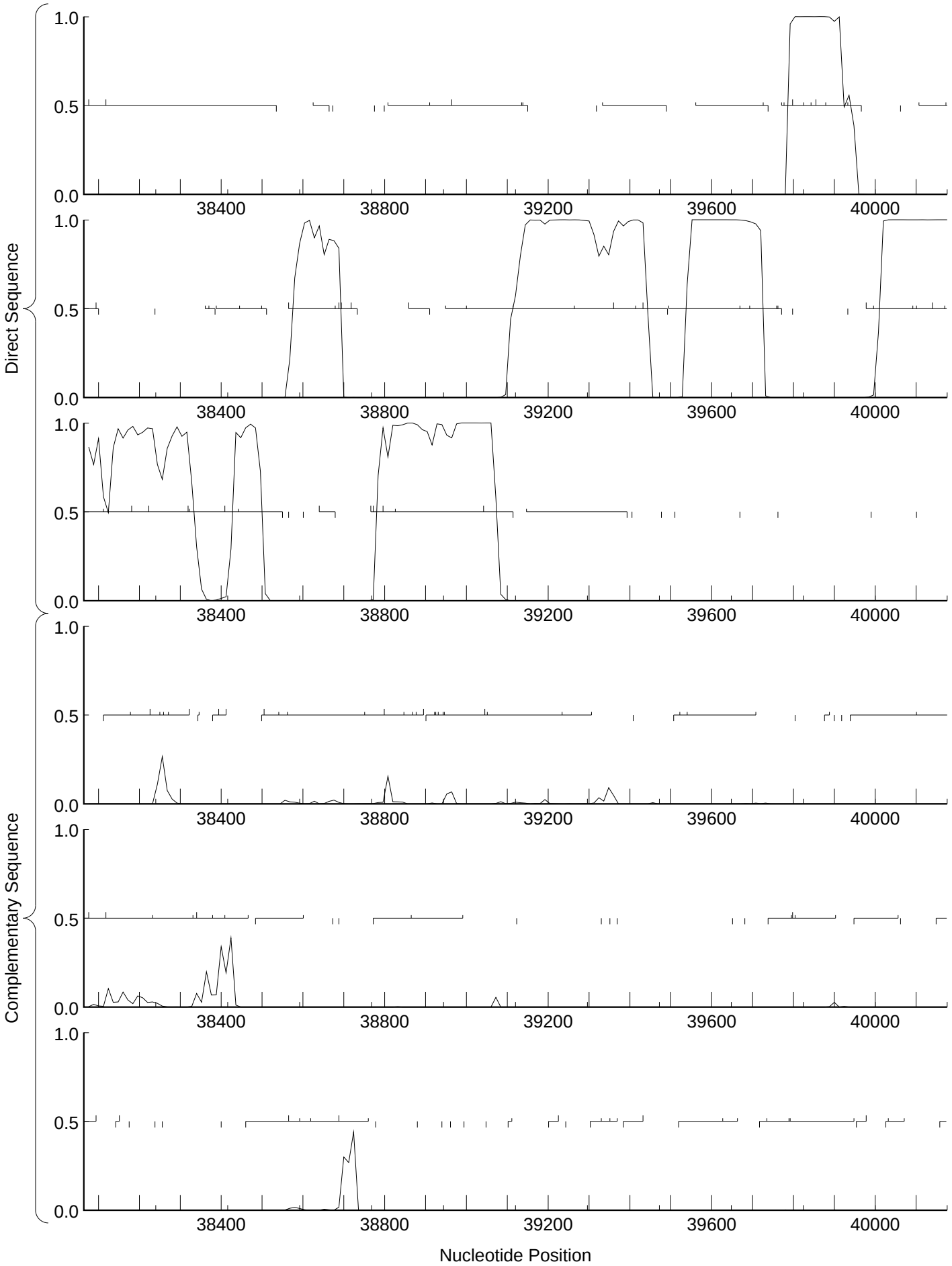
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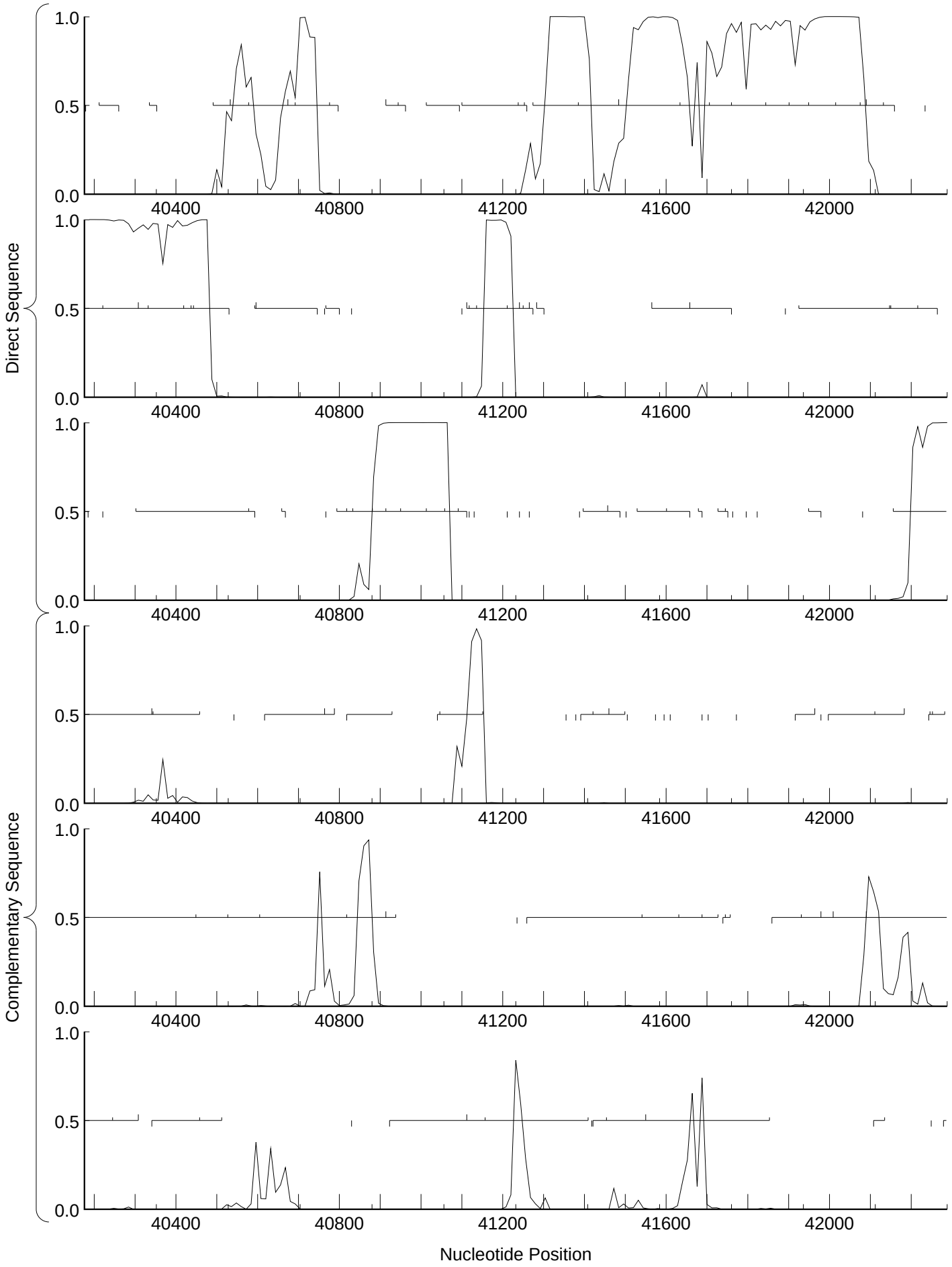
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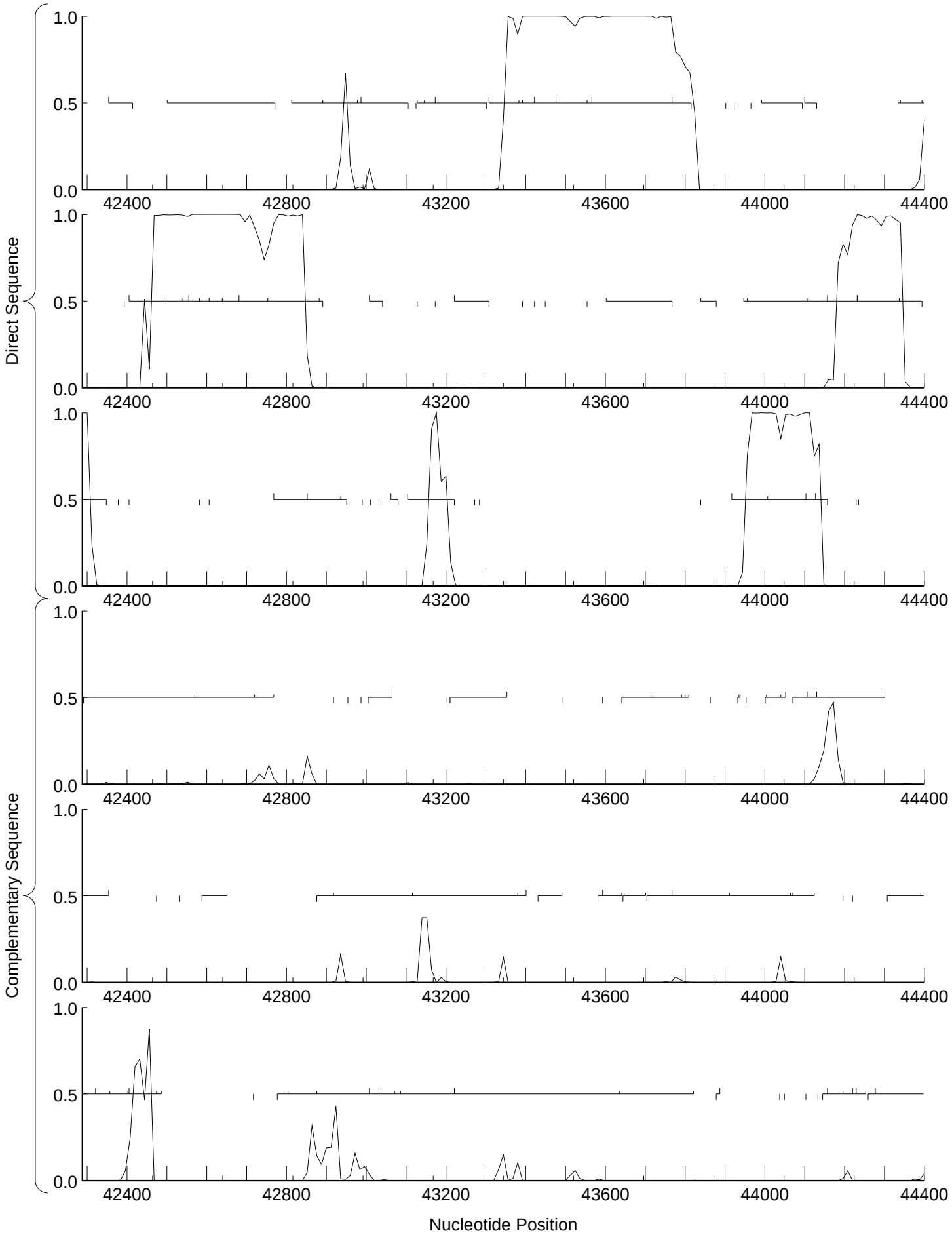
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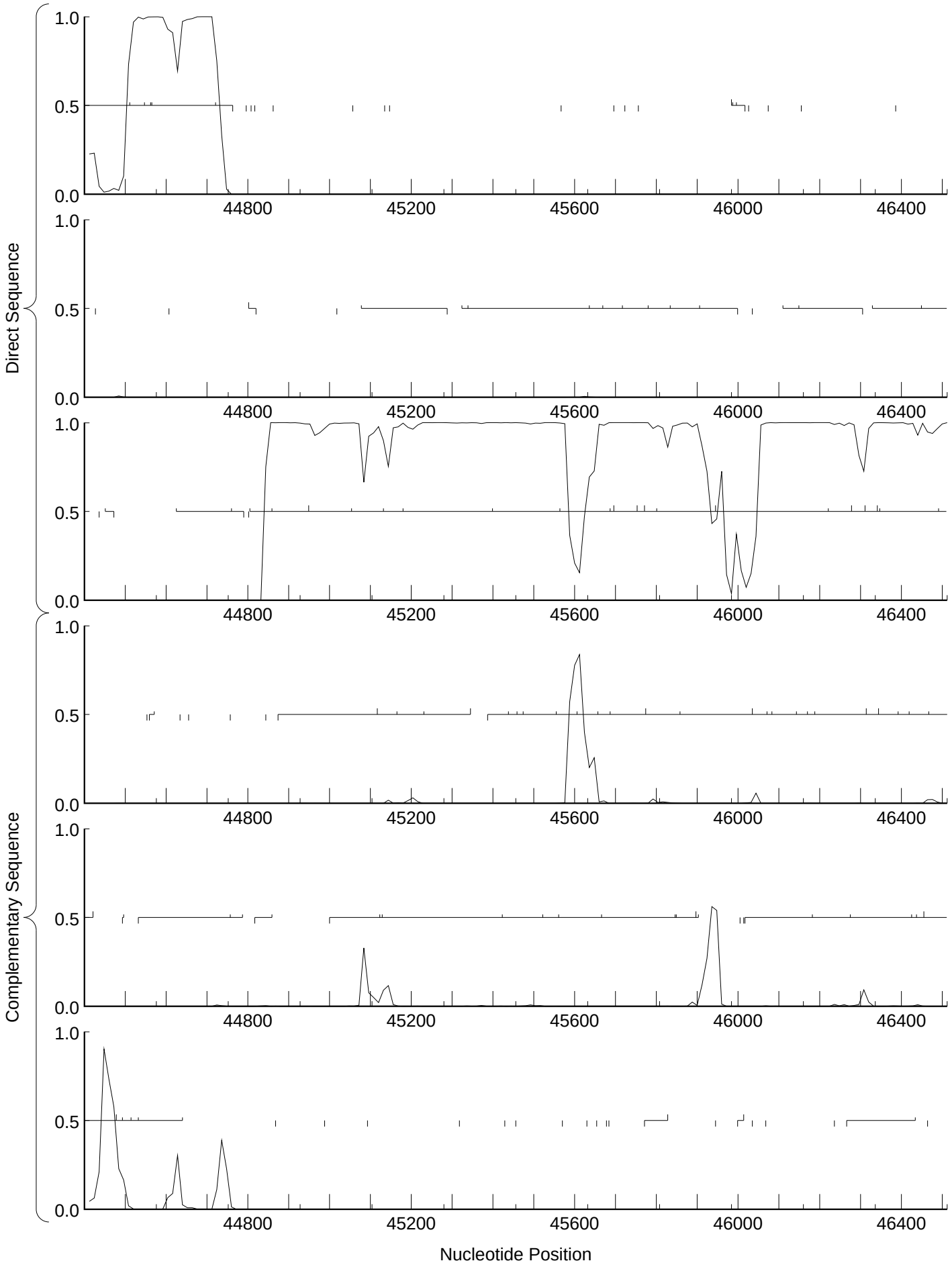
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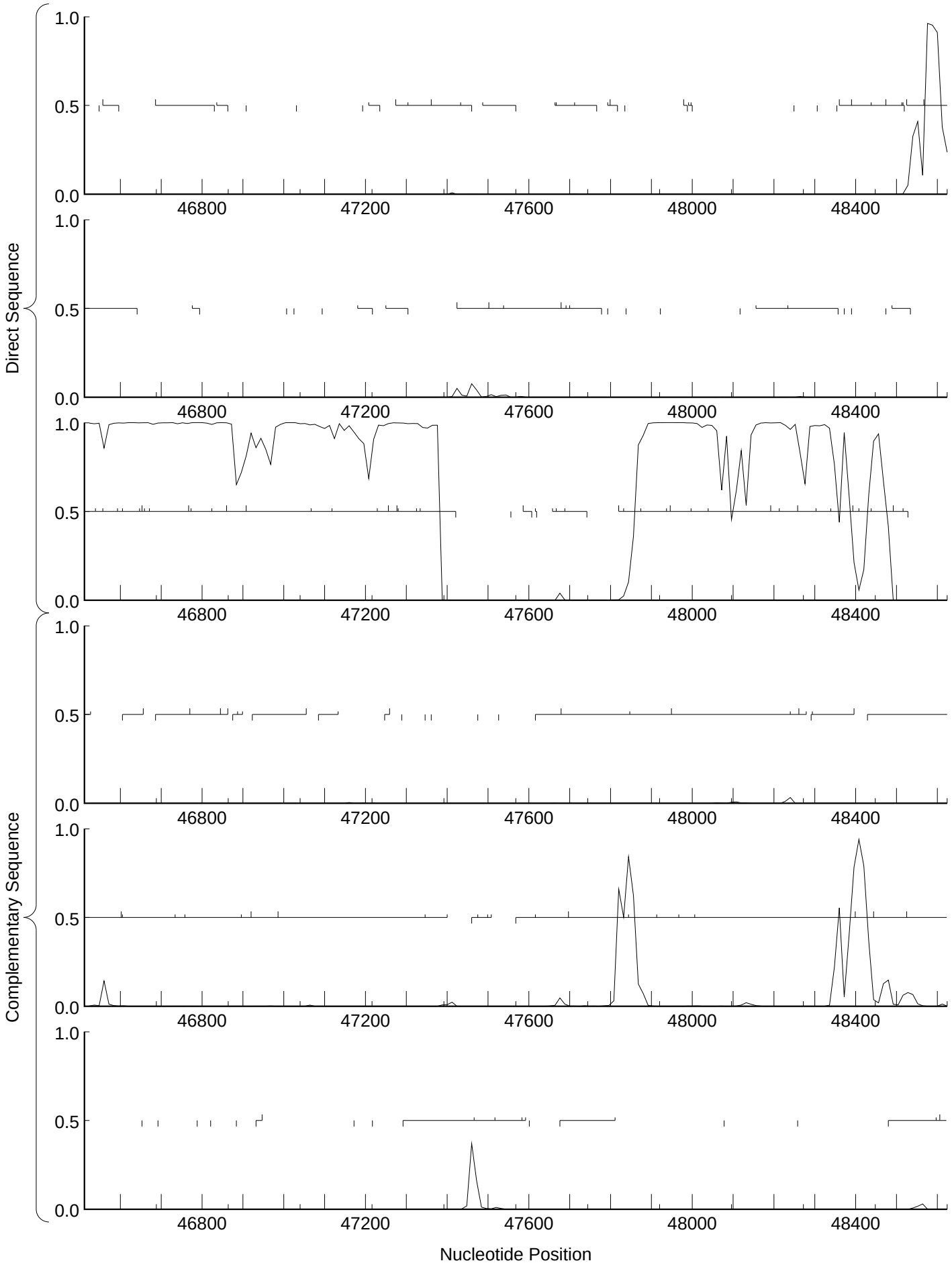
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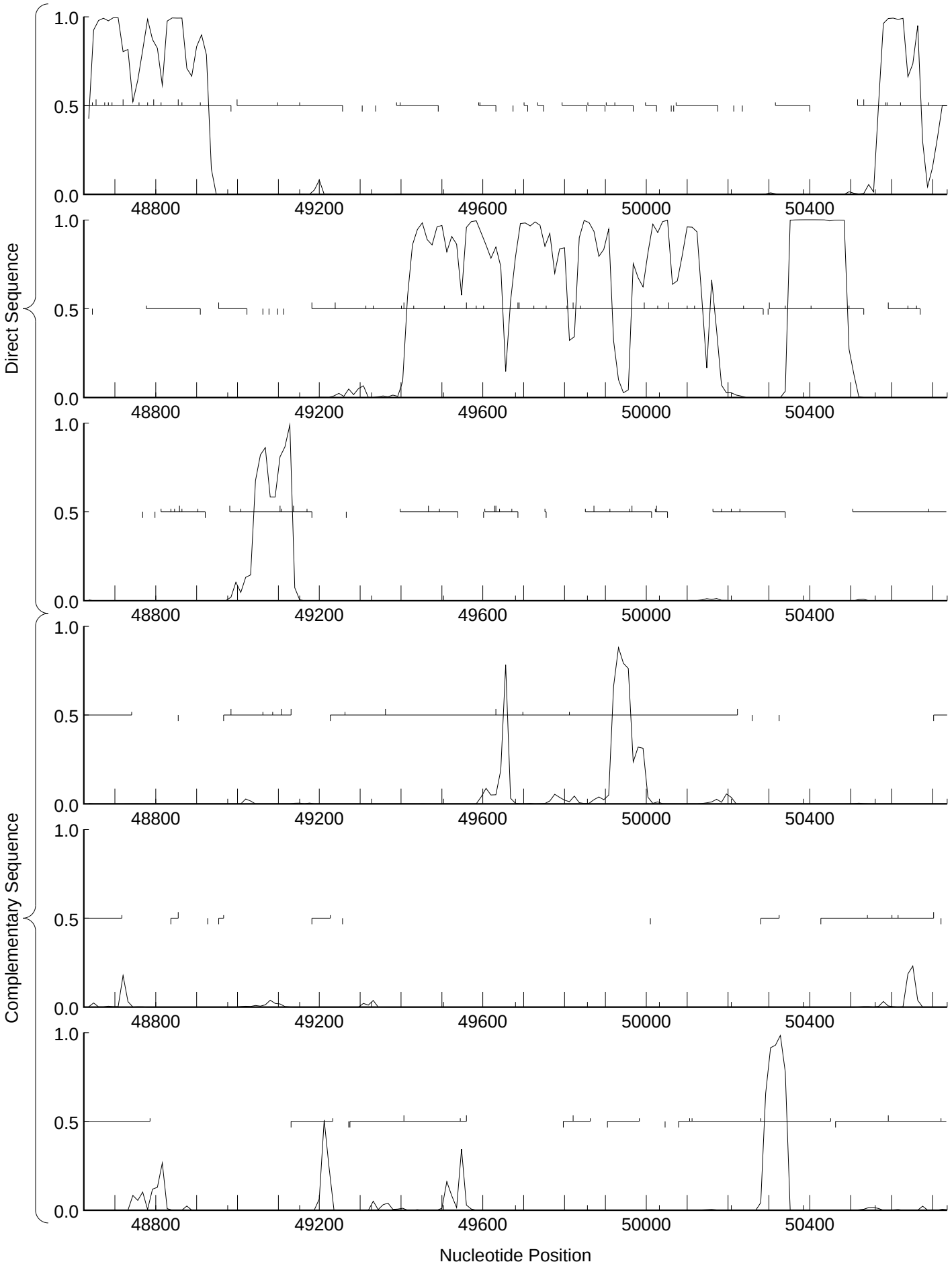
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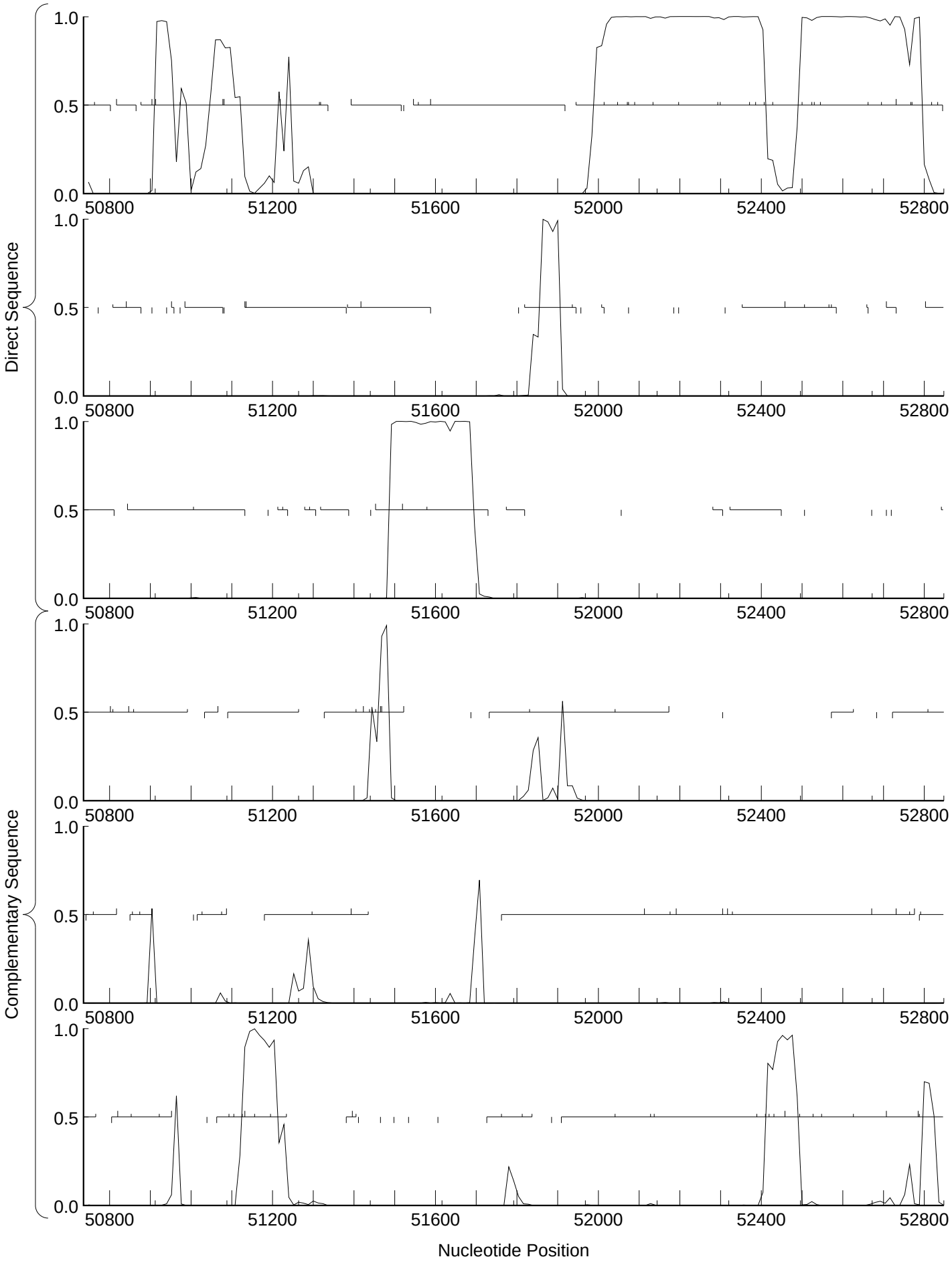
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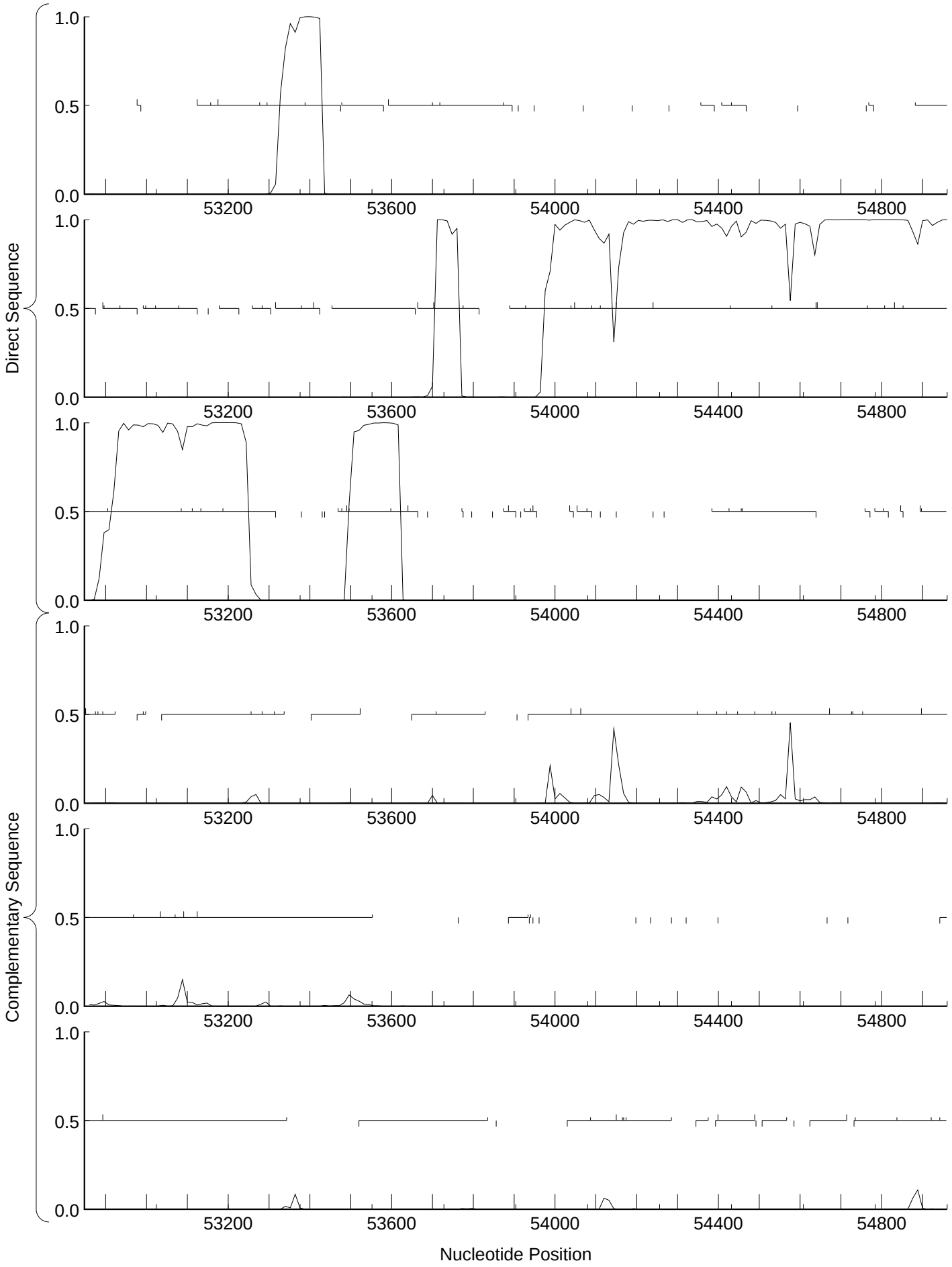
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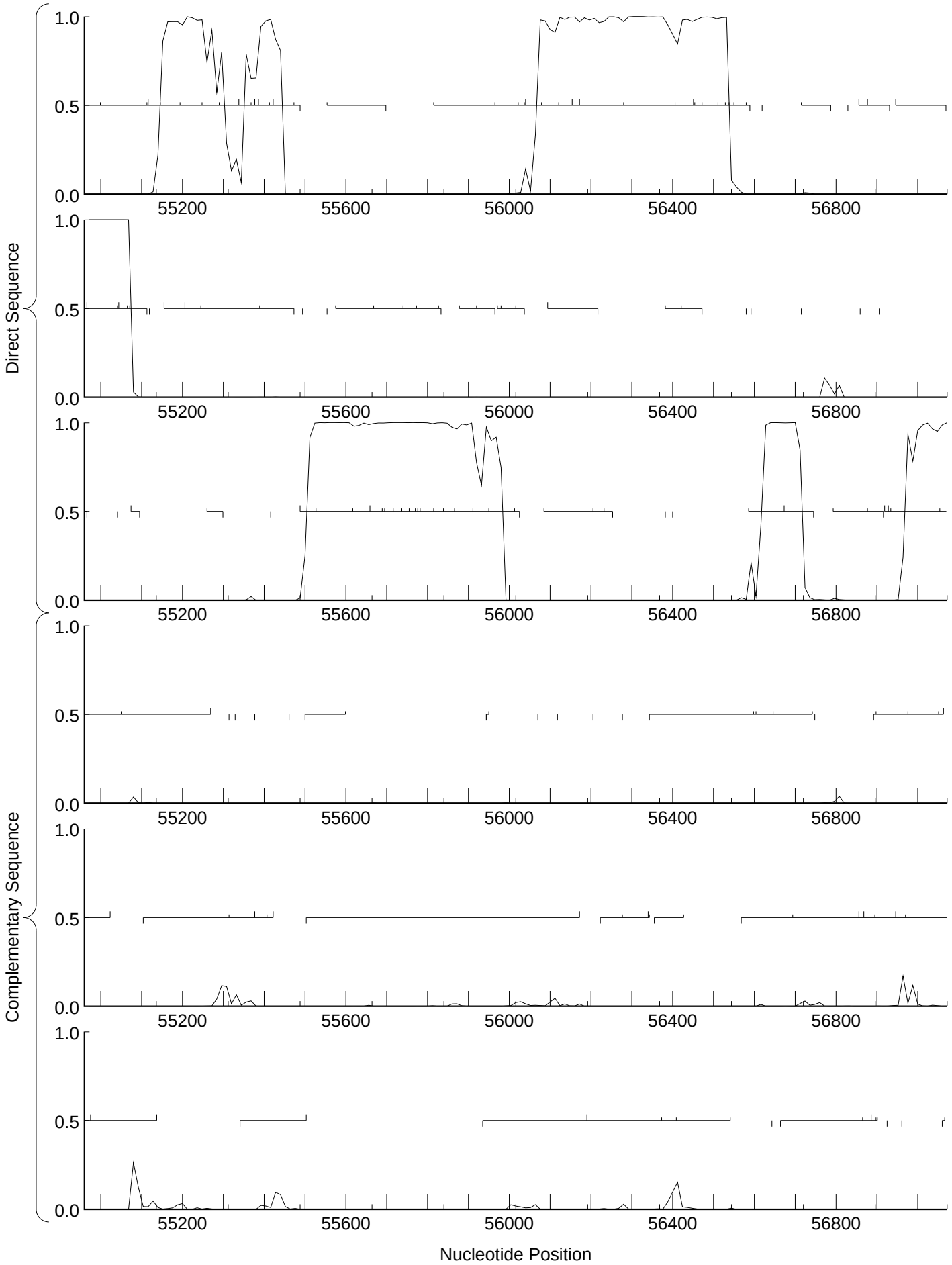


complete sequence, 59687 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K1, Order 4, Window 96, Step 12, 26/30

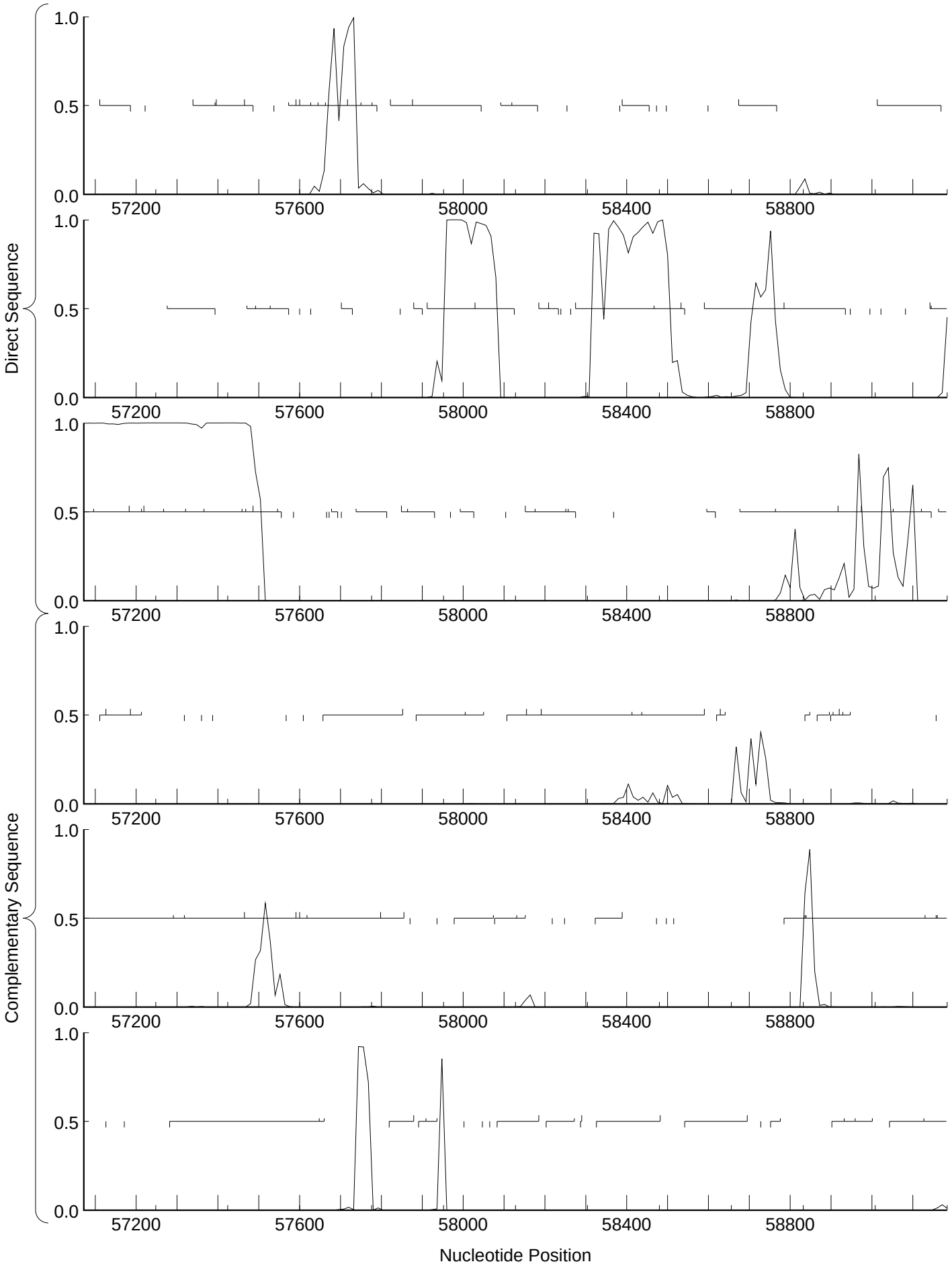


complete sequence, 59687 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K1, Order 4, Window 96, Step 12, 27/30




Direct Sequence
Complementary Sequence
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0.5
0.0
55200
55600
56000
56400
56800
Nucleotide Position

complete sequence, 59687 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K1, Order 4, Window 96, Step 12, 29/30



complete sequence, 59687 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K1, Order 4, Window 96, Step 12, 30/30

