GeneMark

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

PROGRAM INFORMATION

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Sequence         :  Mycobacterium phage AlishaPH complete sequence, 57034 bp including 11-base 3' overhang (CTC
Analysis Date    :  3/28/24 at 17:31:45
Pages            :  29
Sequence Length  :  57034 bp
GC Content       :   66.61%

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

PS-Version       :  1.2

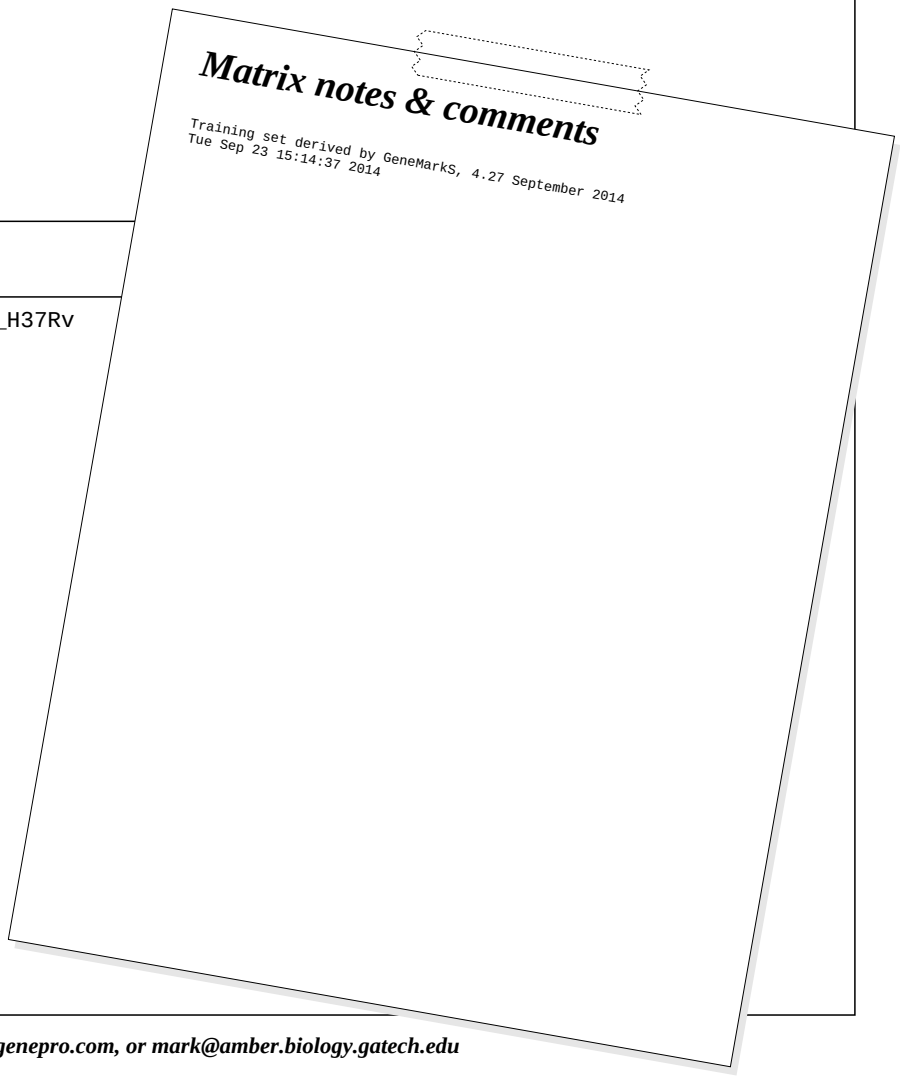
GeneMark Options :  PostScript graph,
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MATRIX INFORMATION

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Author     :  -

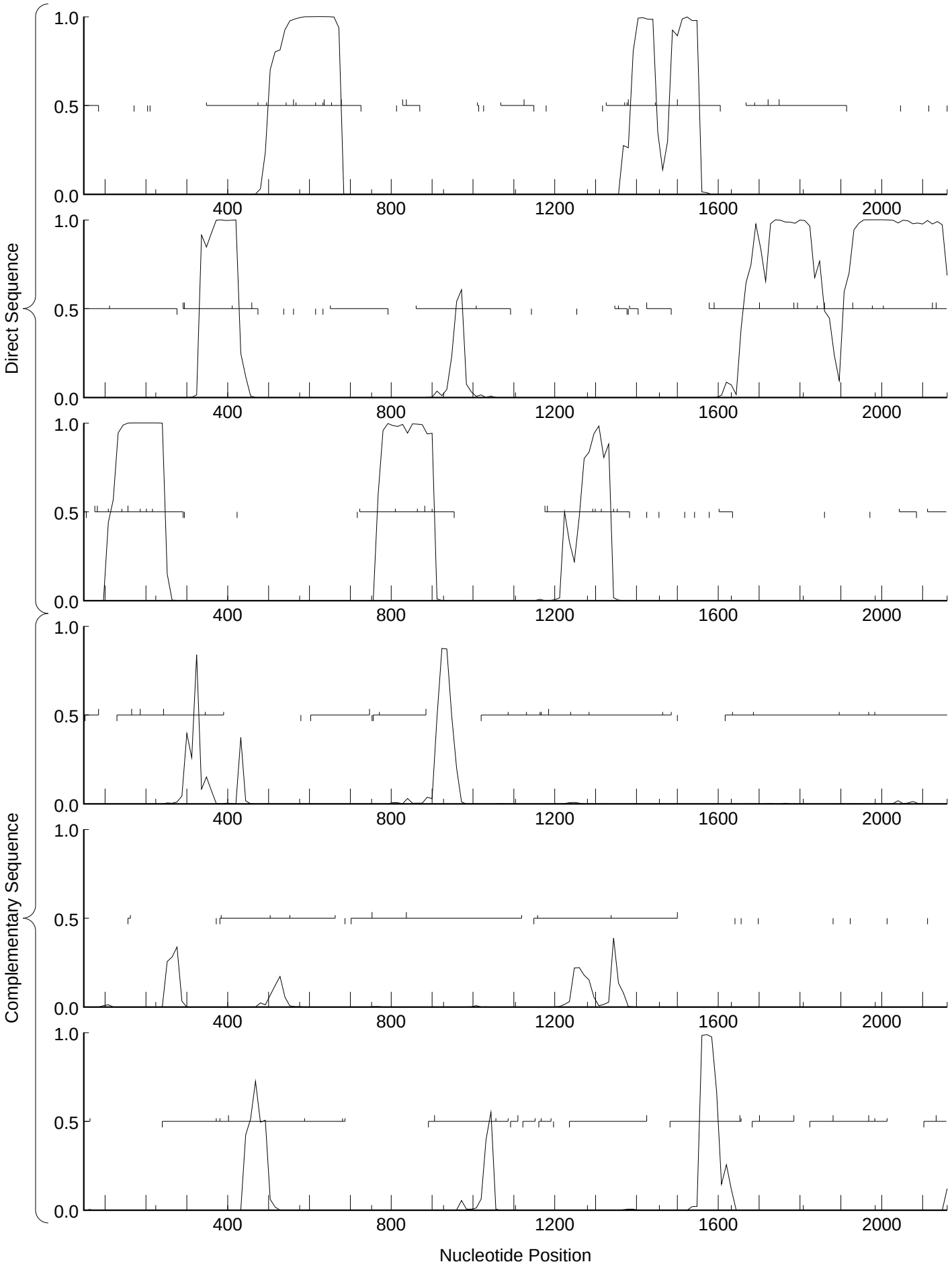
Order      :  4


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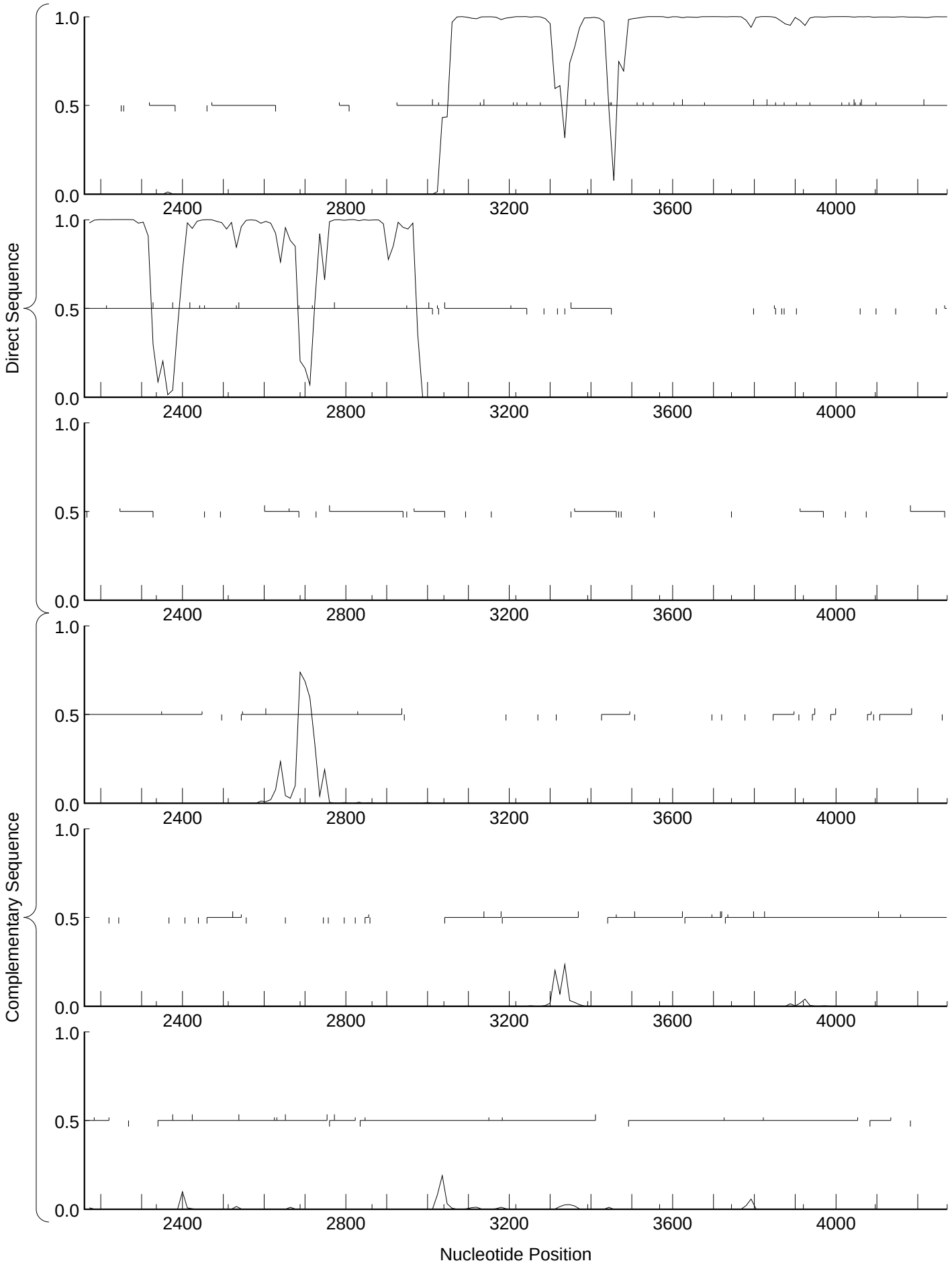


For help or information, send electronic mail to: custserv@genepro.com, or mark@amber.biology.gatech.edu

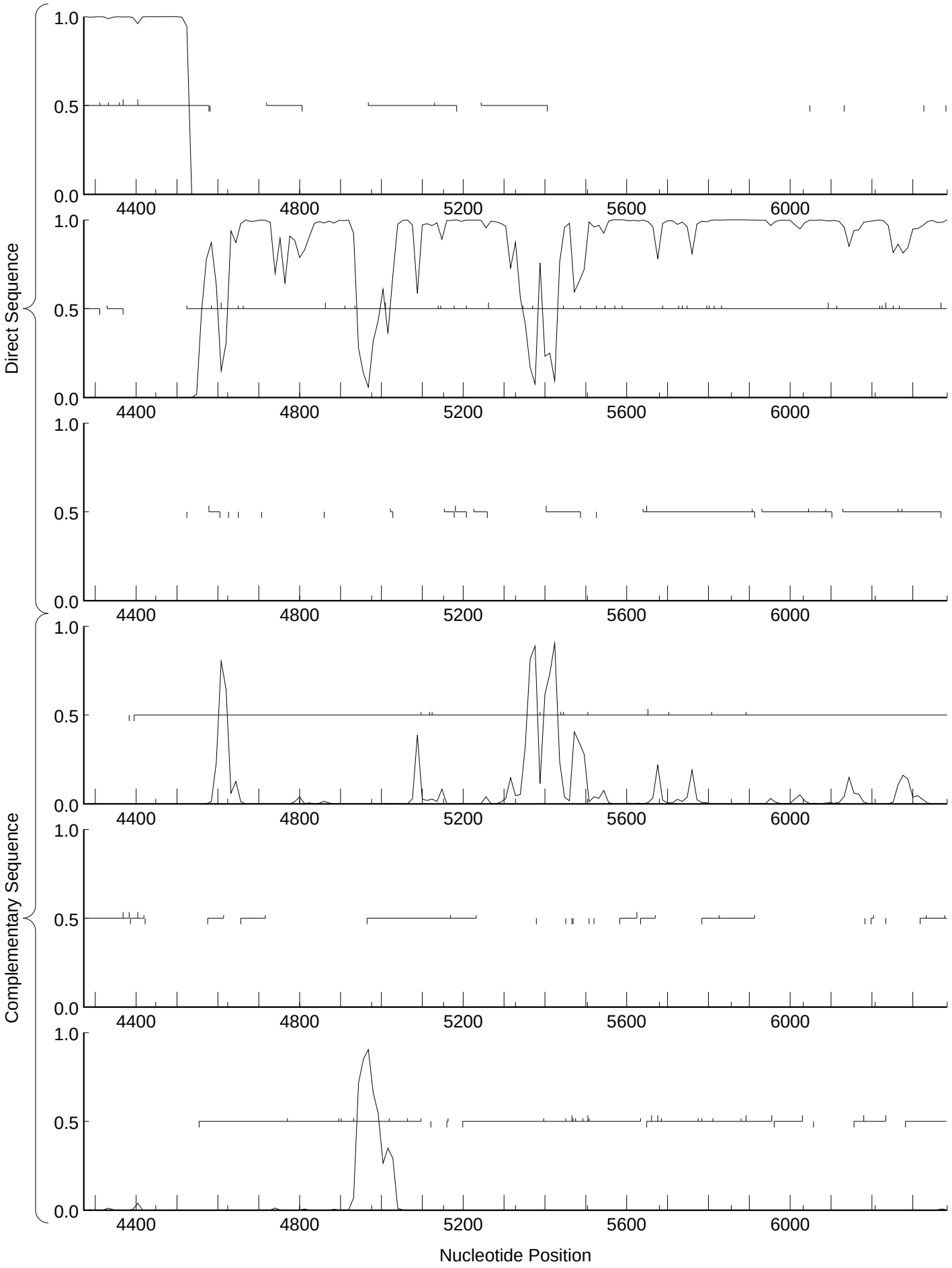
complete sequence, 57034 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K1, Order 4, Window 96, Step 12, 2/29



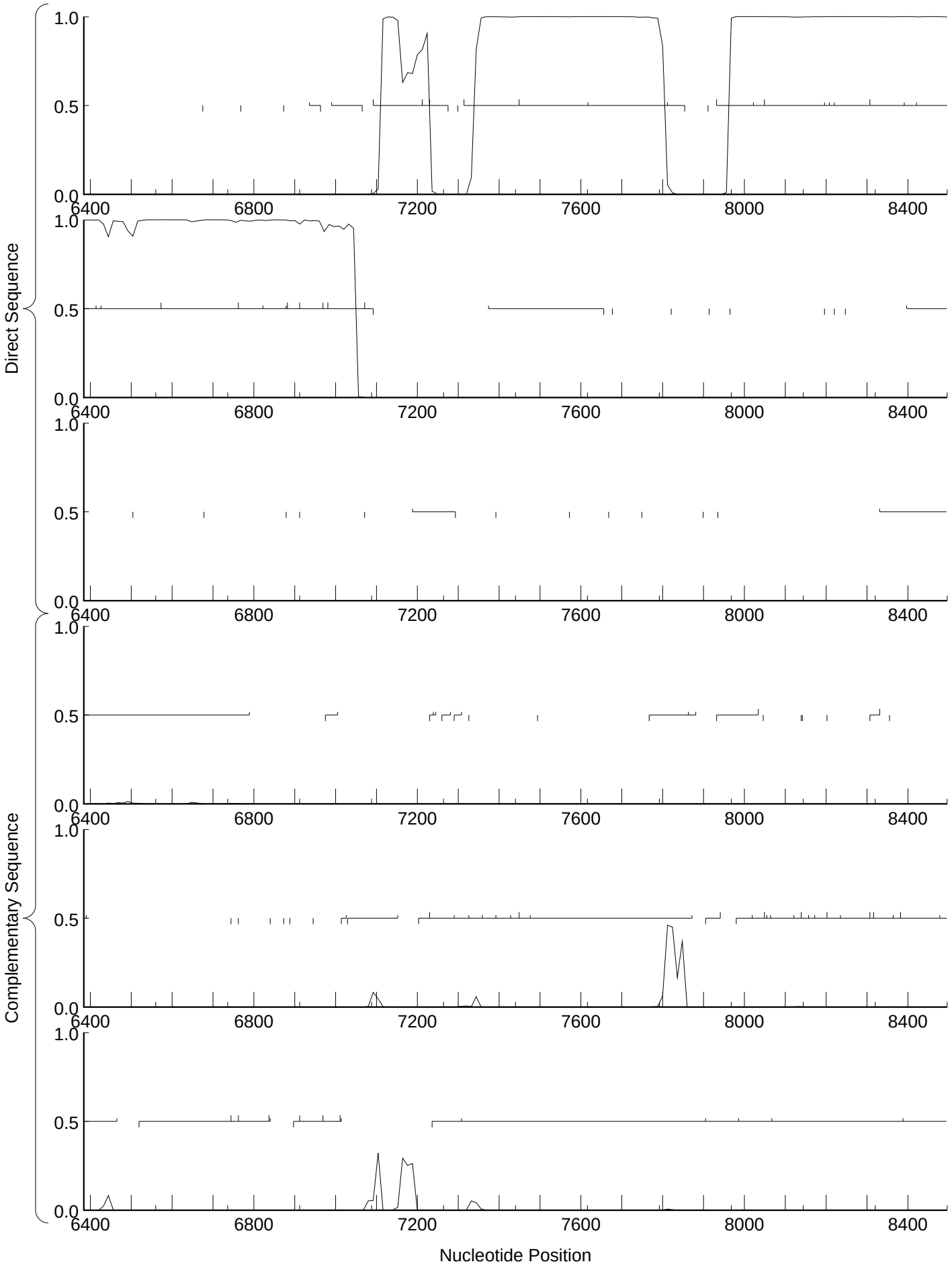
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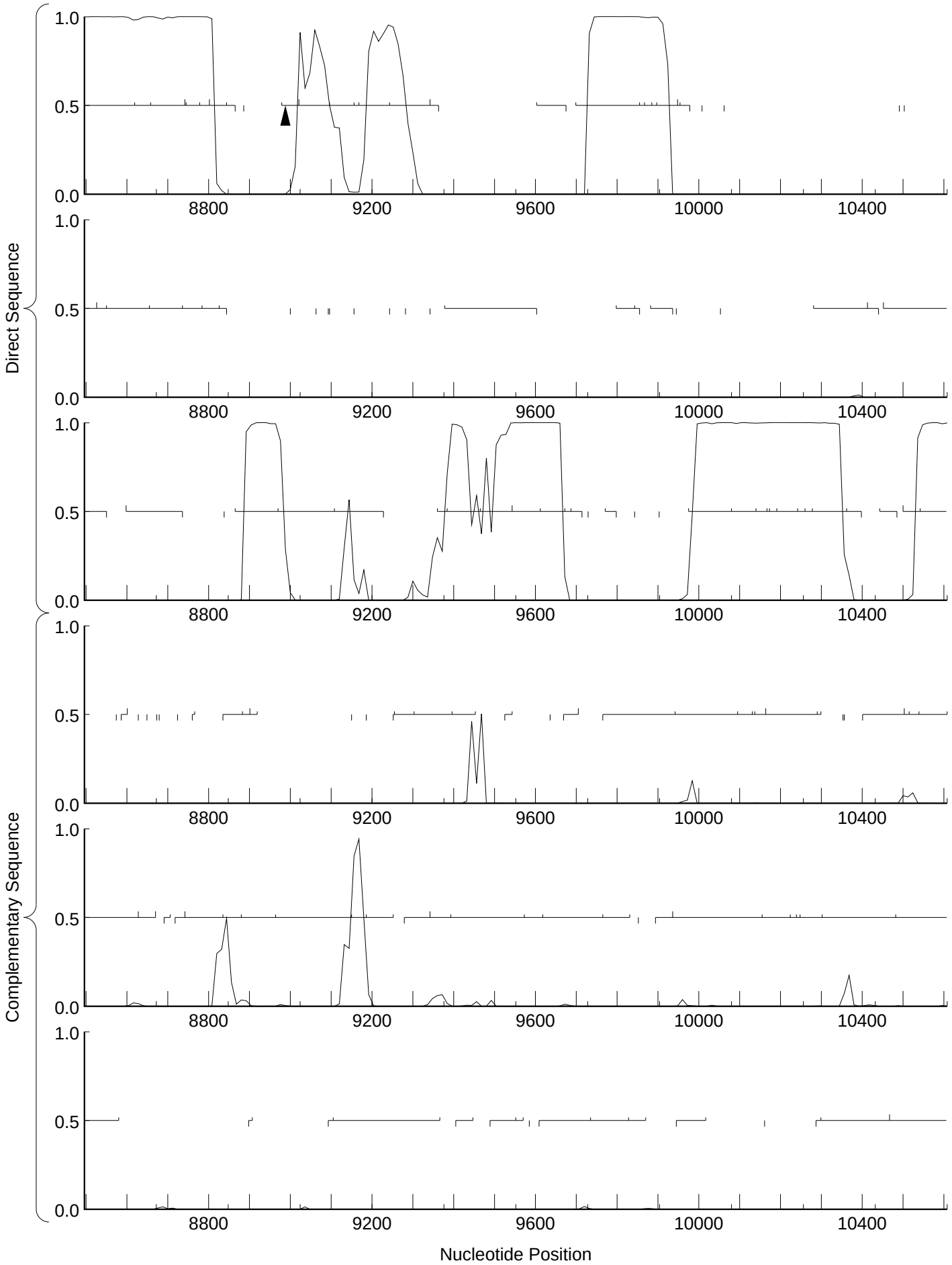
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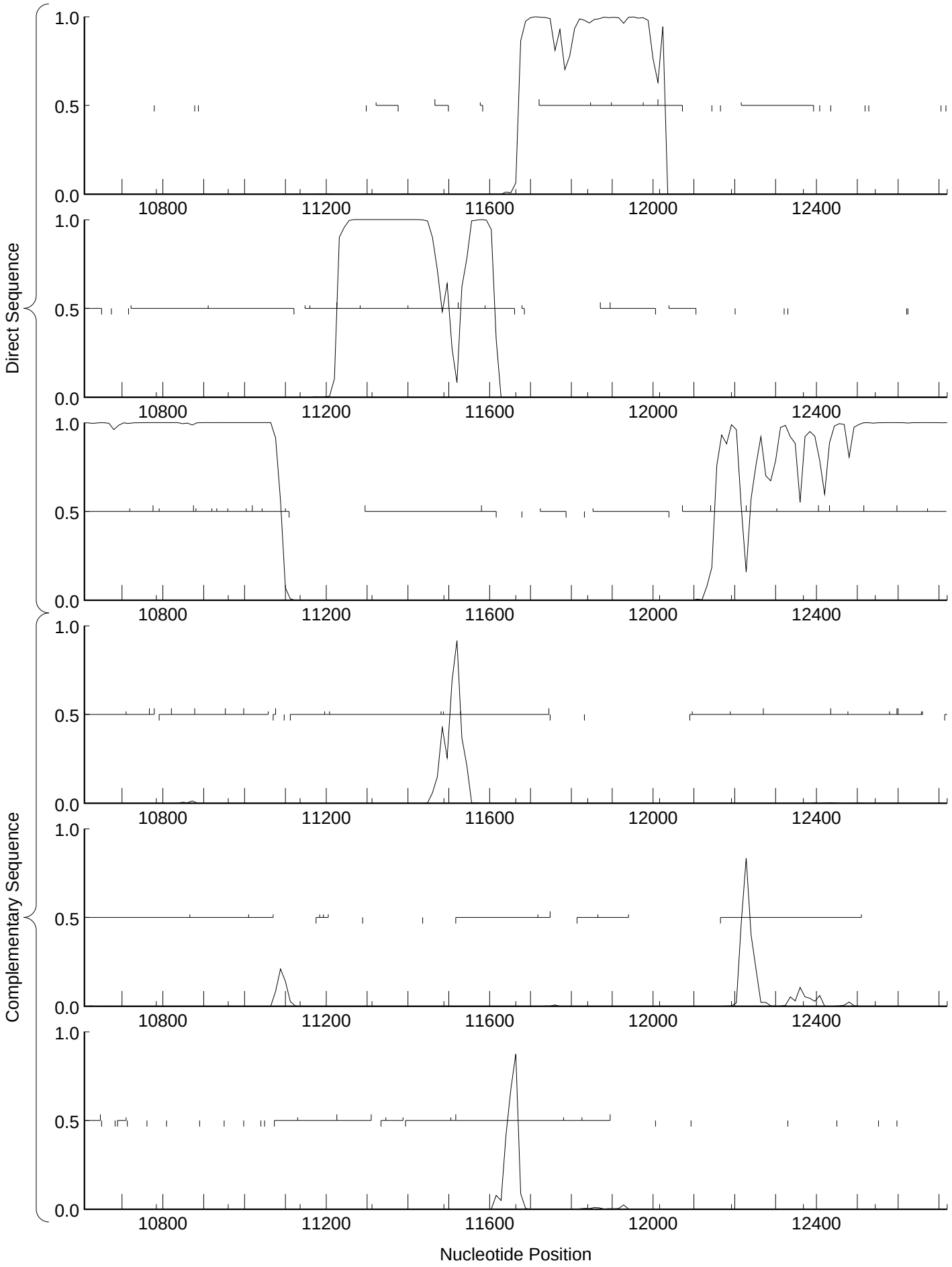
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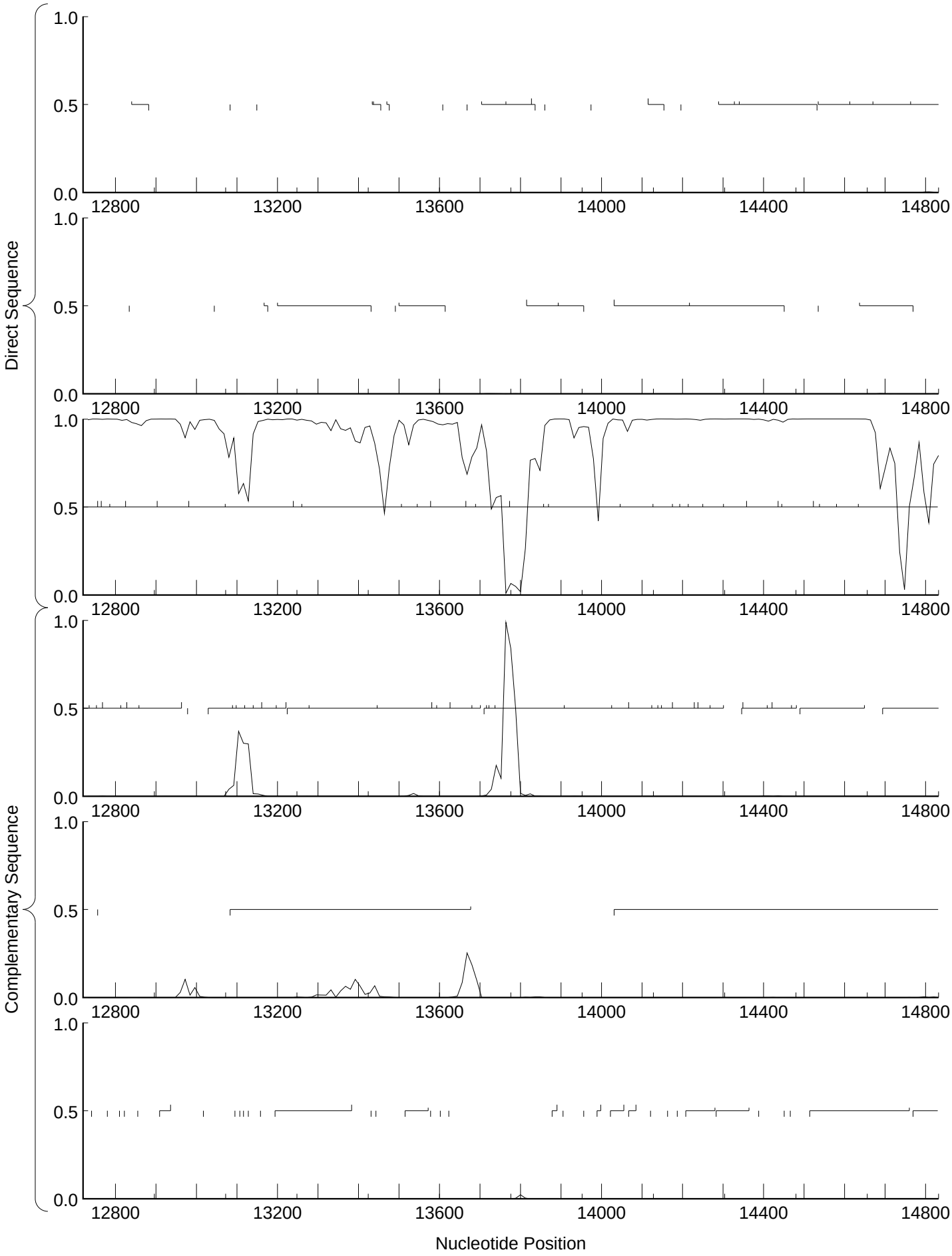
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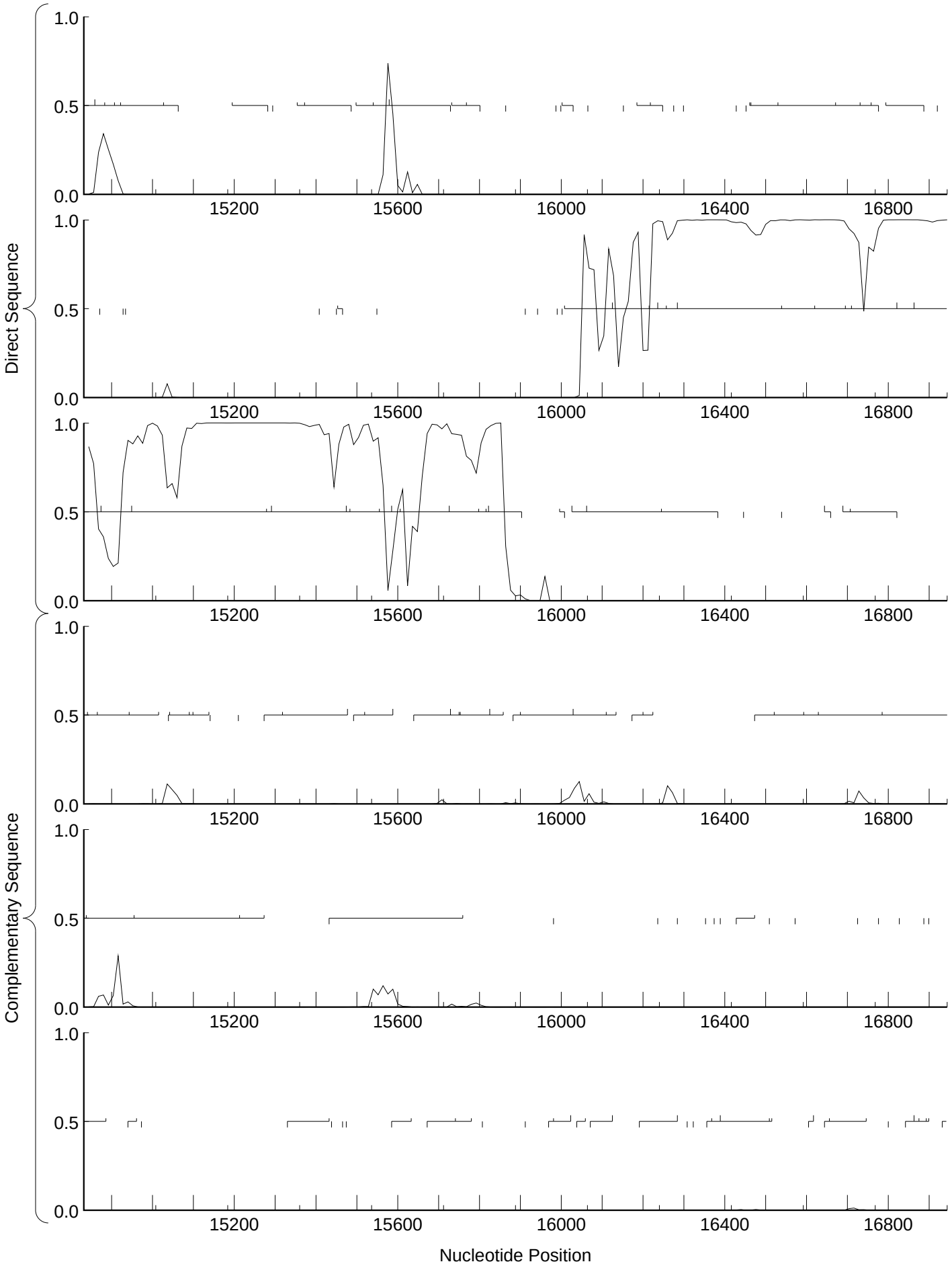
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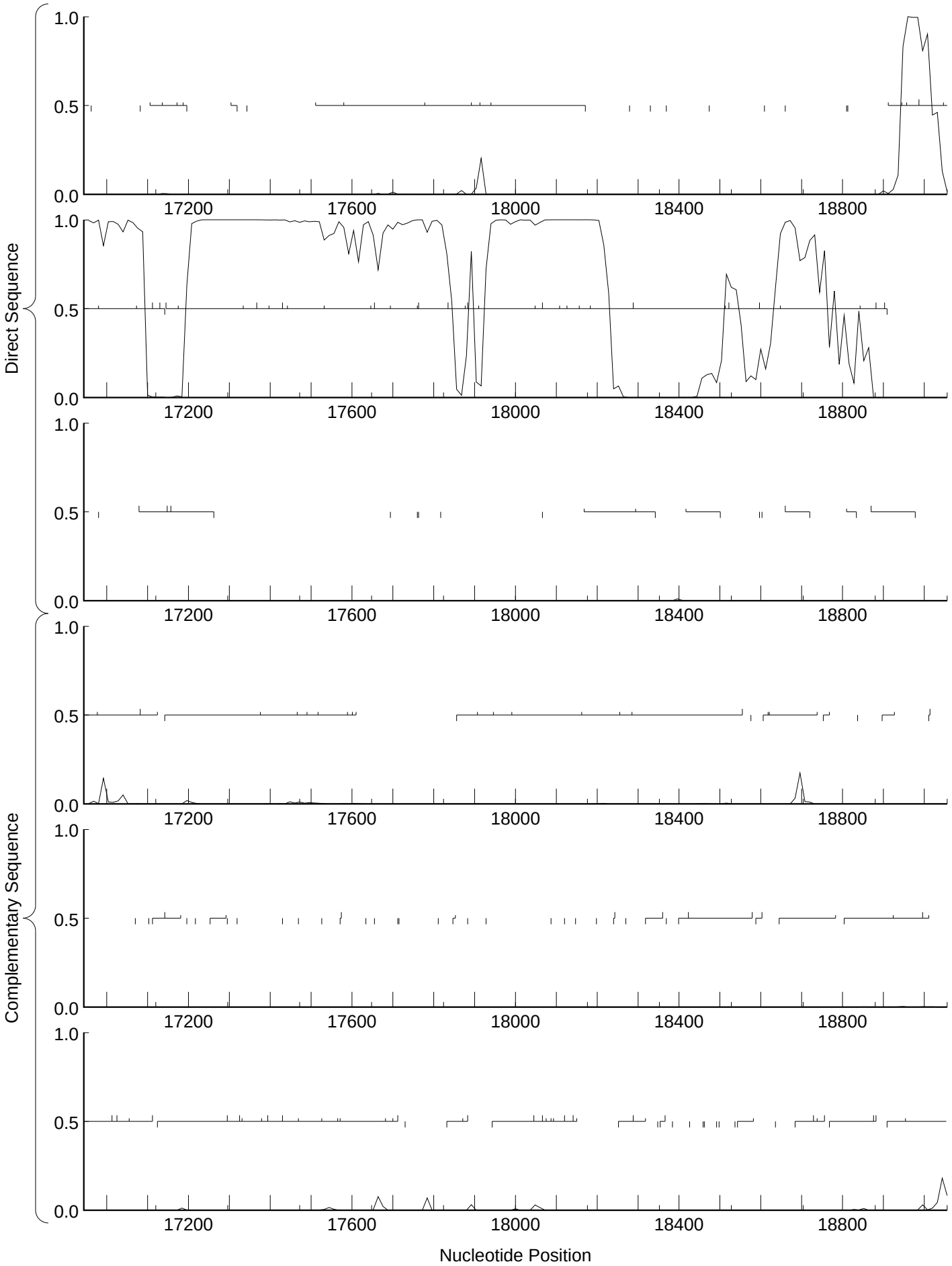
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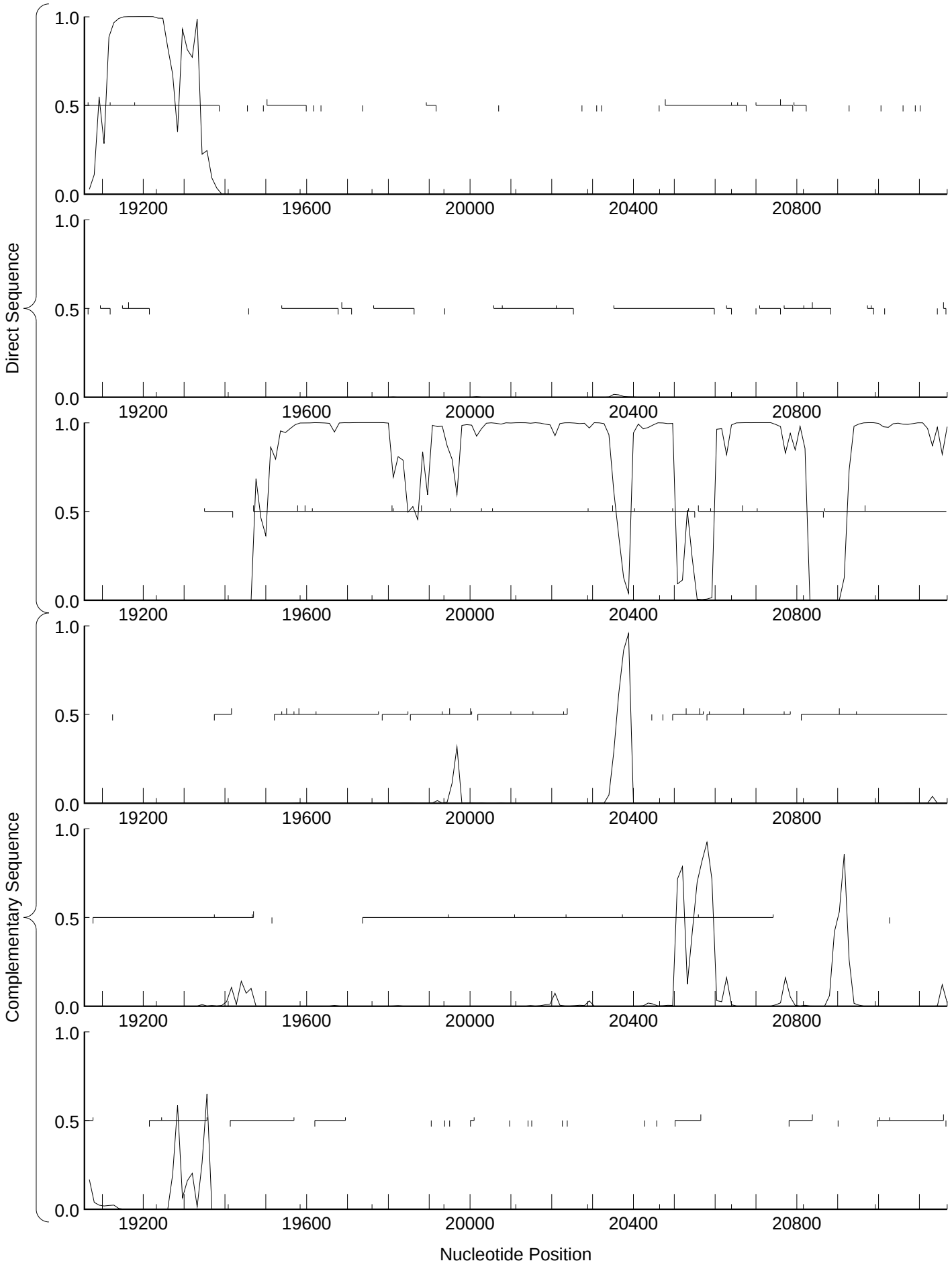
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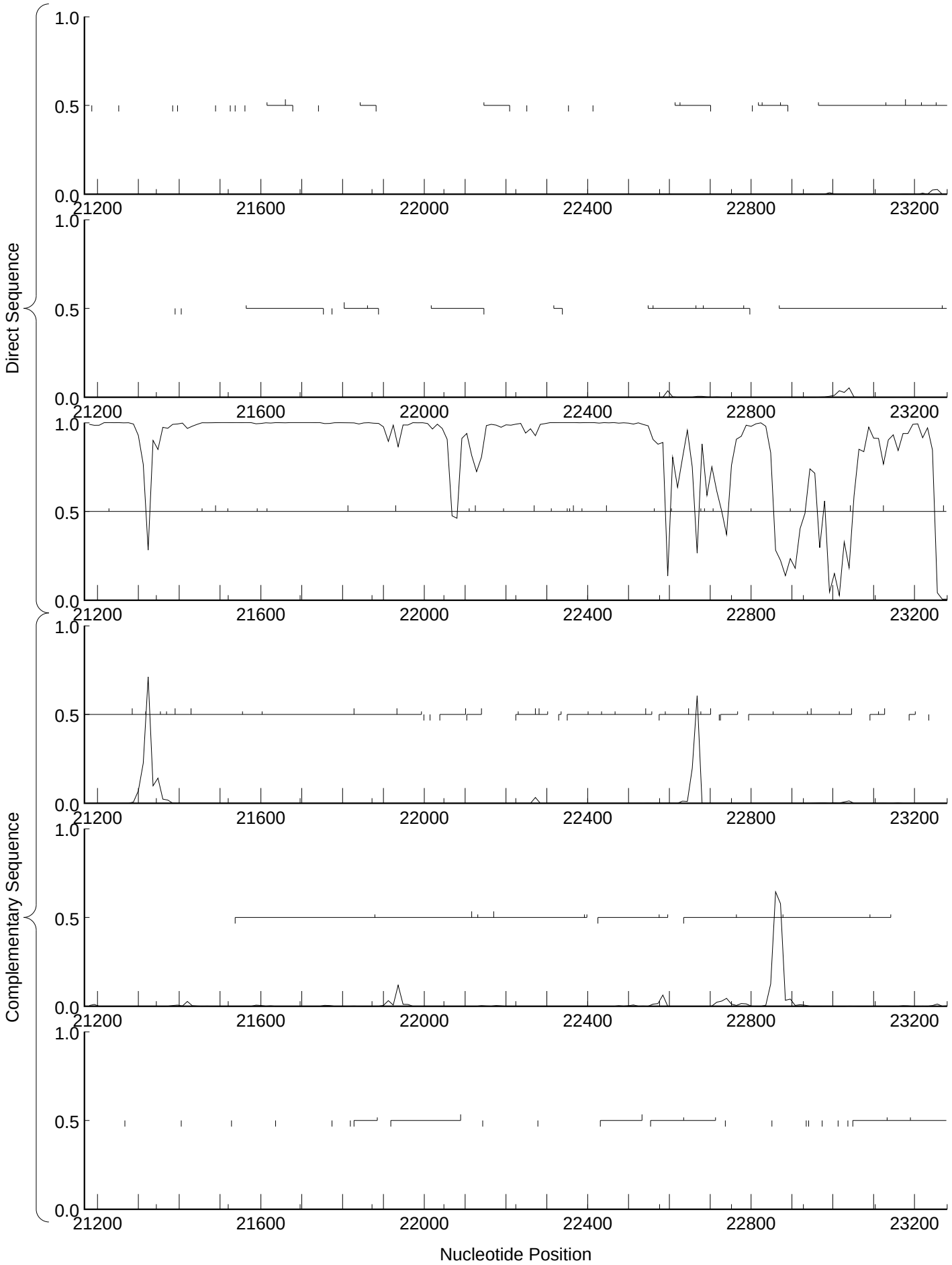
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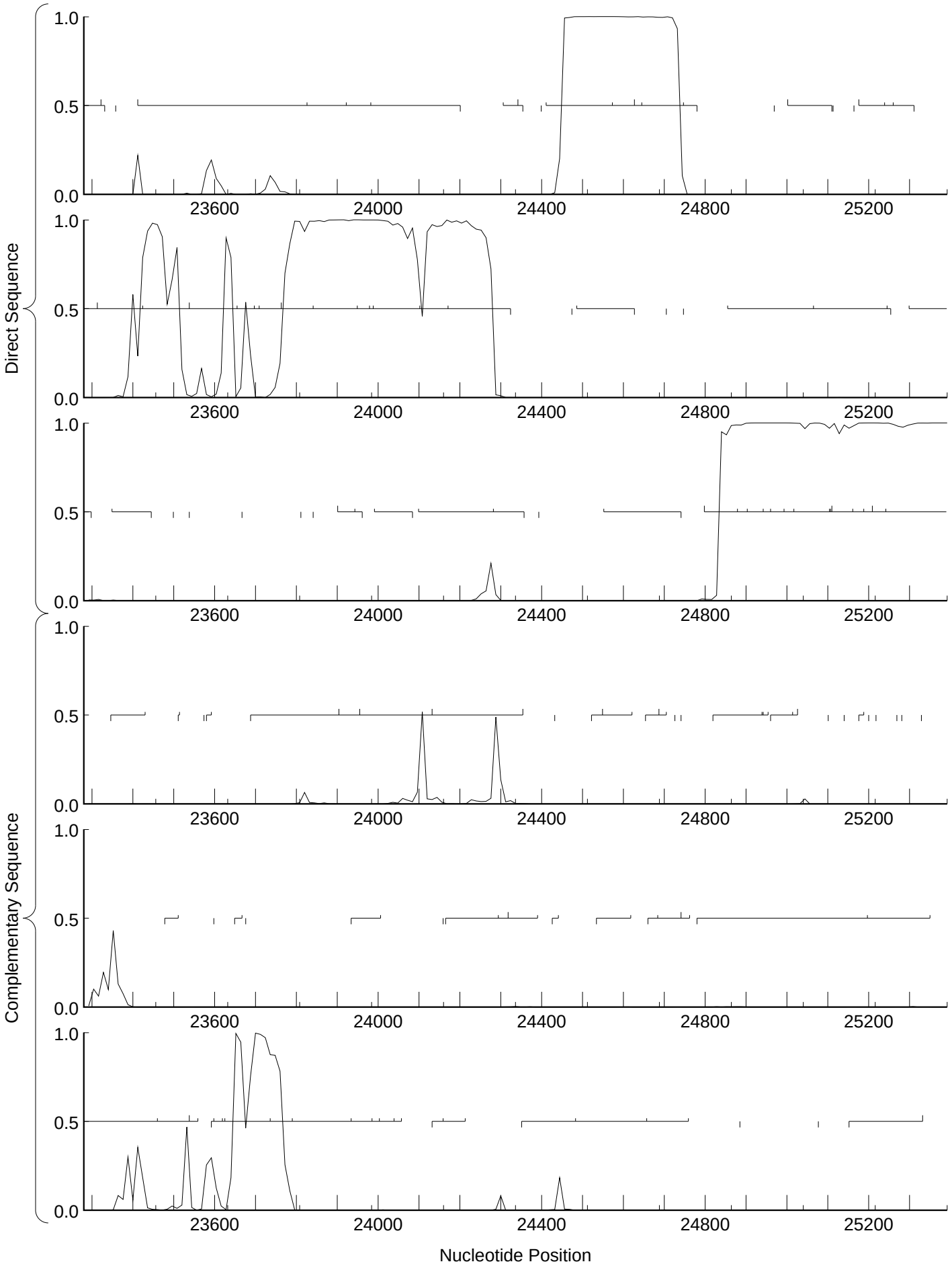
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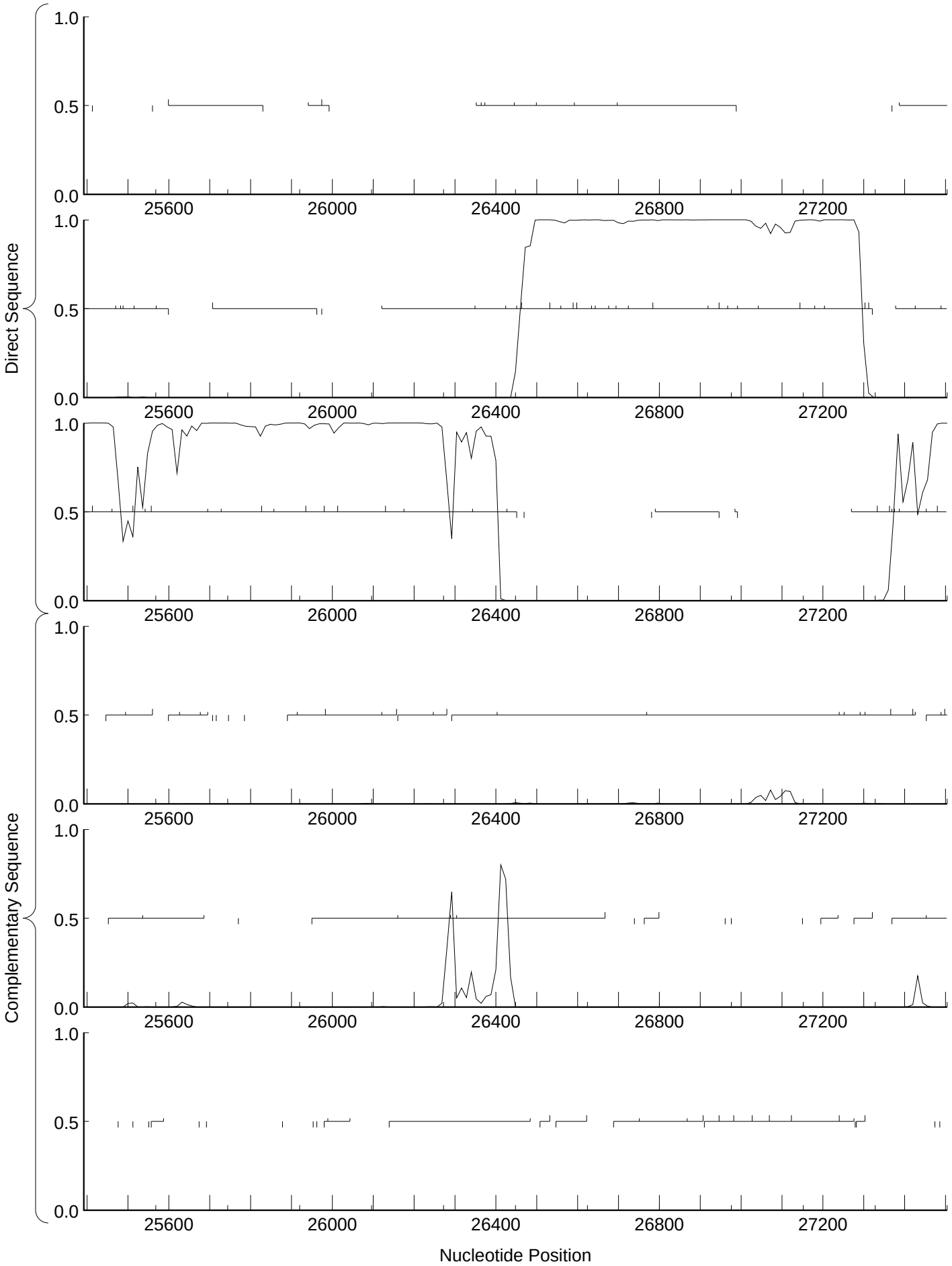


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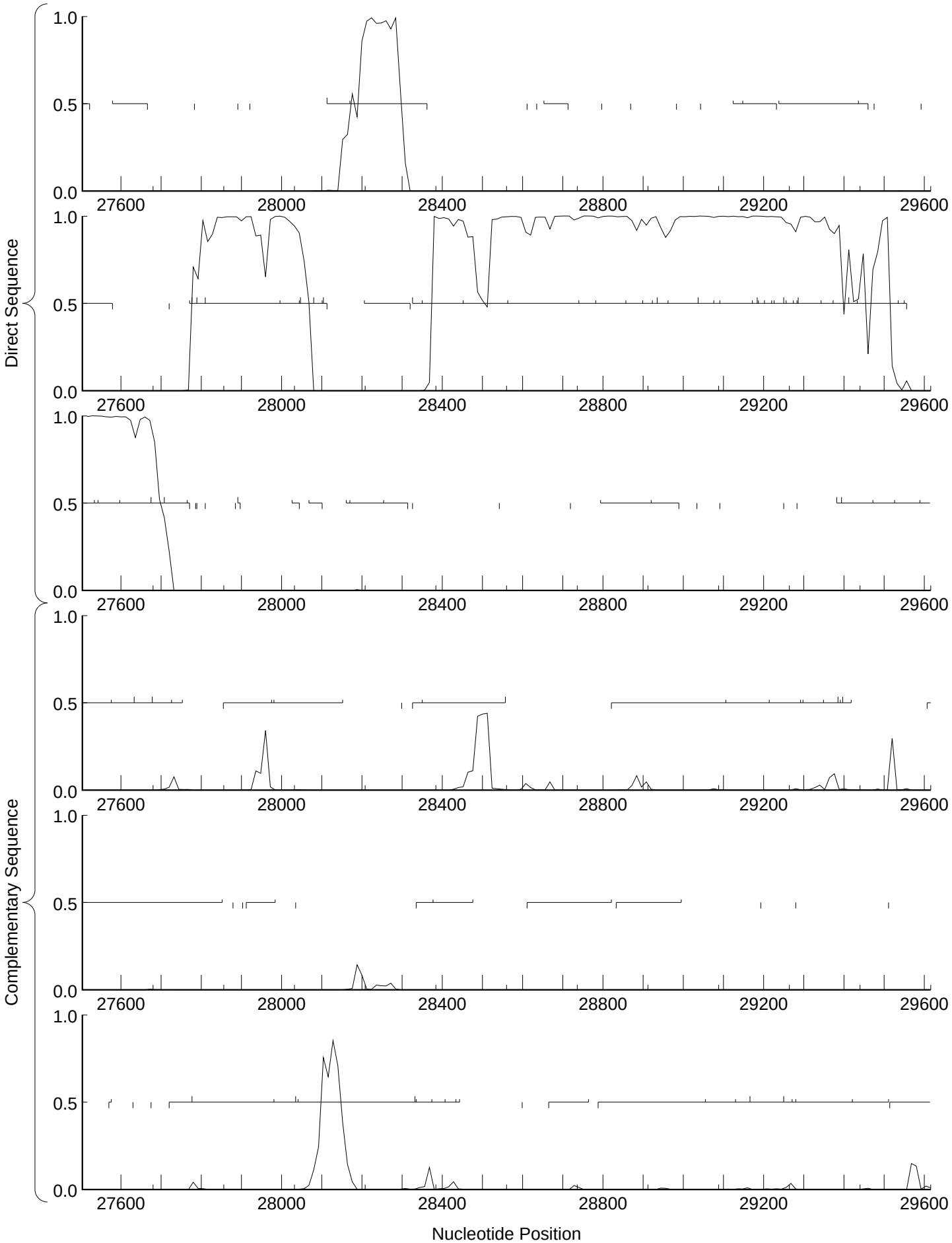


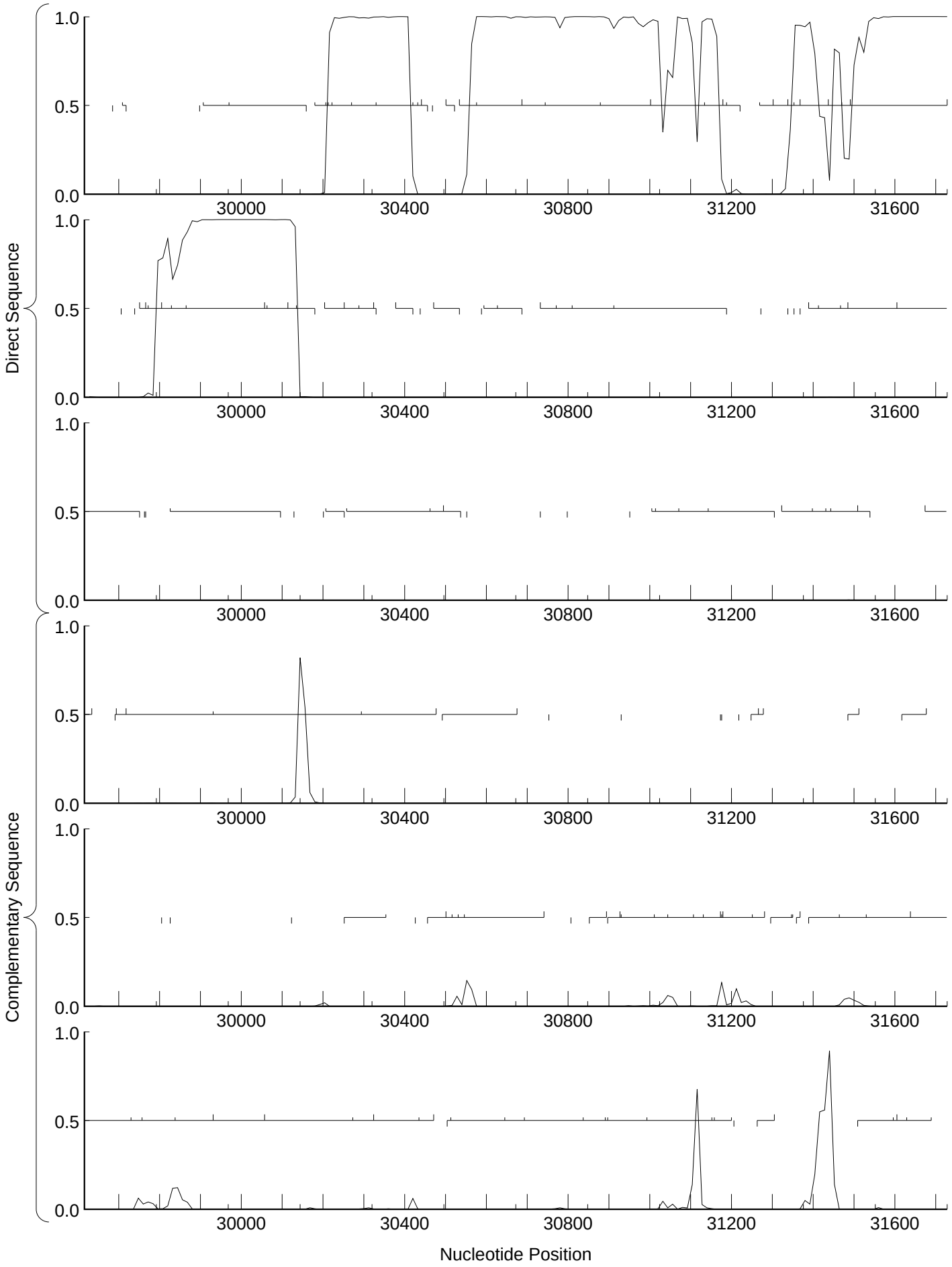
complete sequence, 57034 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K1, Order 4, Window 96, Step 12, 13/29



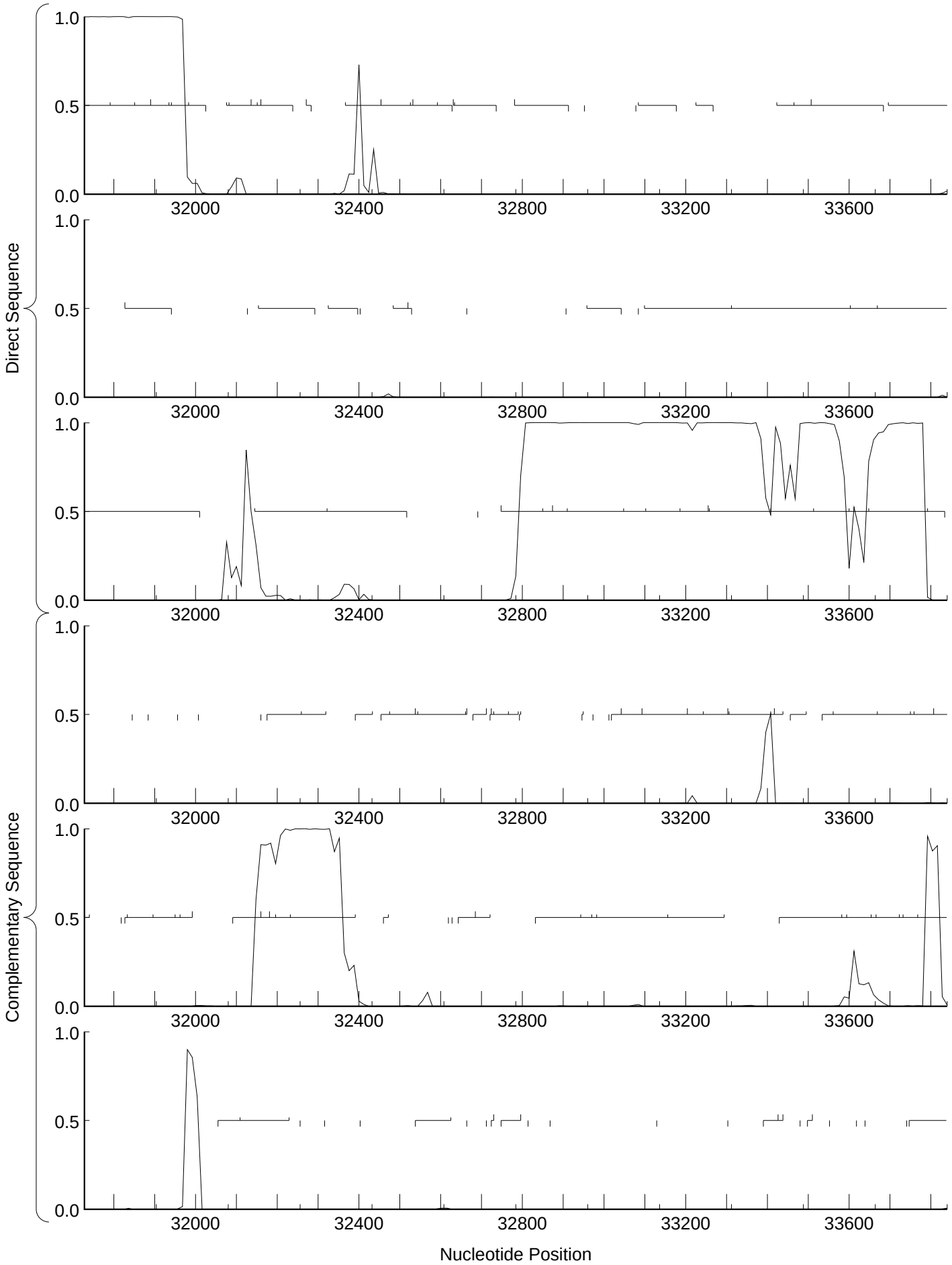

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
25600
26000
26400
26800
27200
Nucleotide Position

complete sequence, 57034 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K1, Order 4, Window 96, Step 12, 15/29

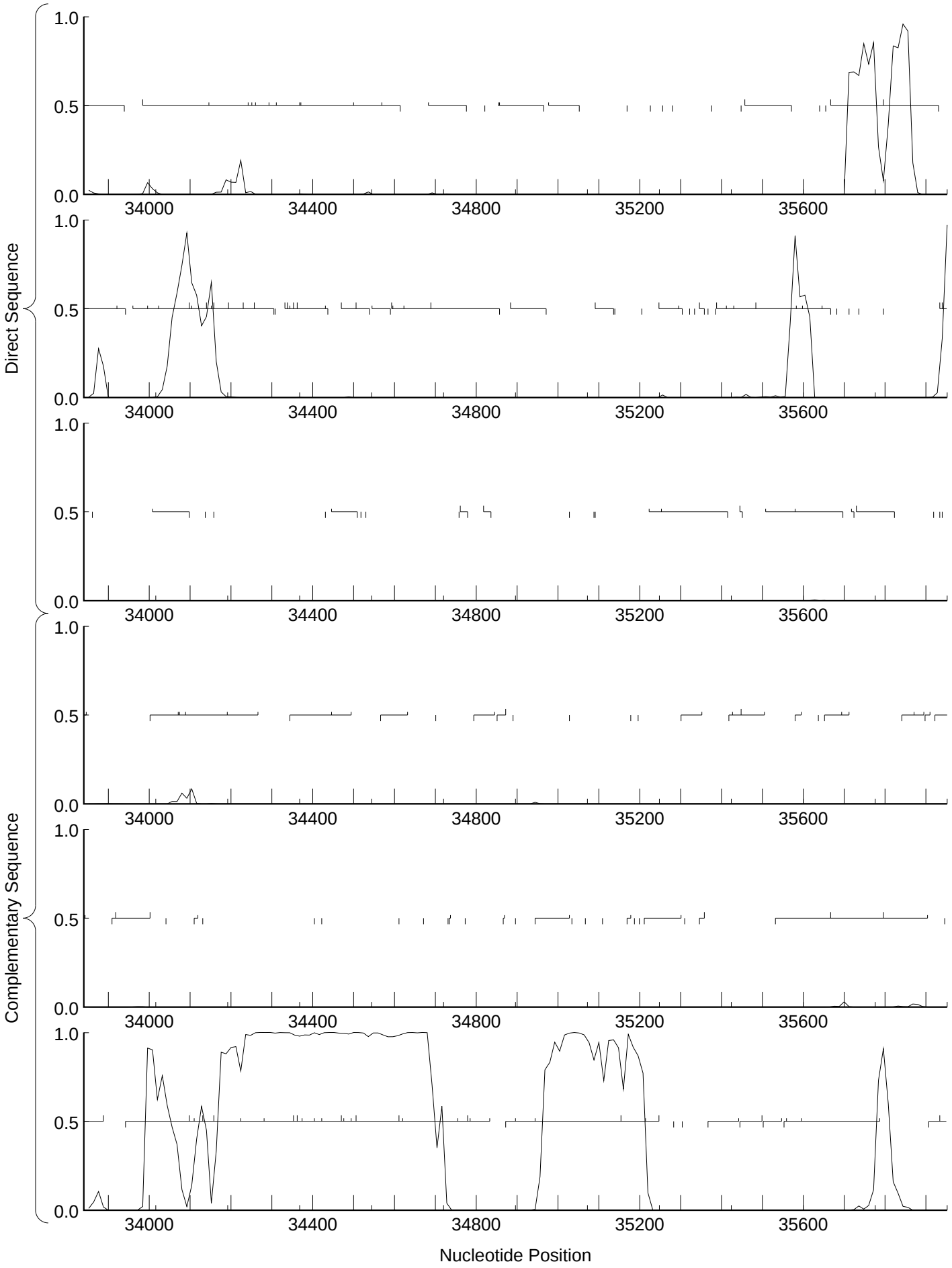



Direct Sequence
Complementary Sequence
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0.5
0.0
30000
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30800
31200
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Nucleotide Position

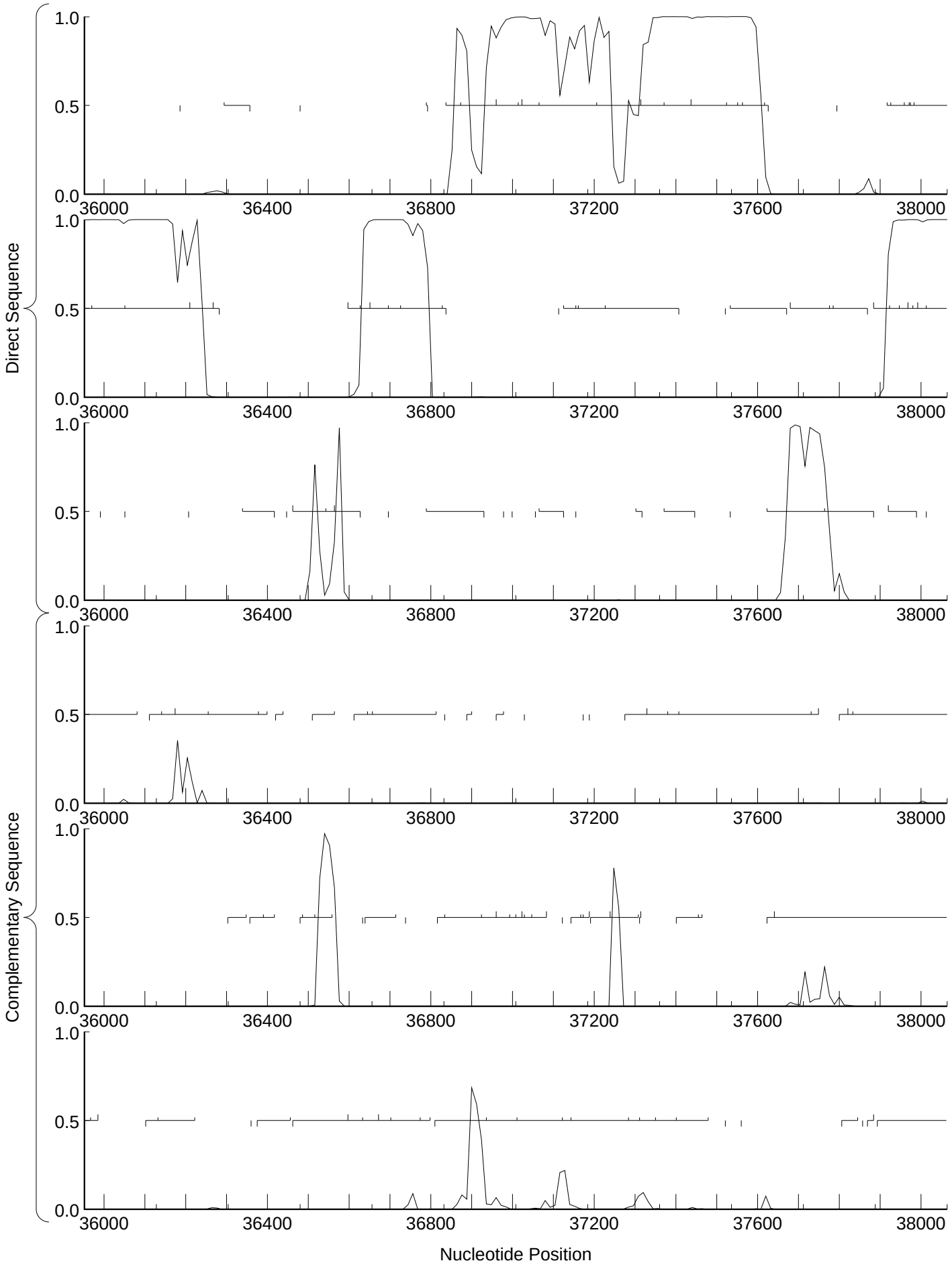
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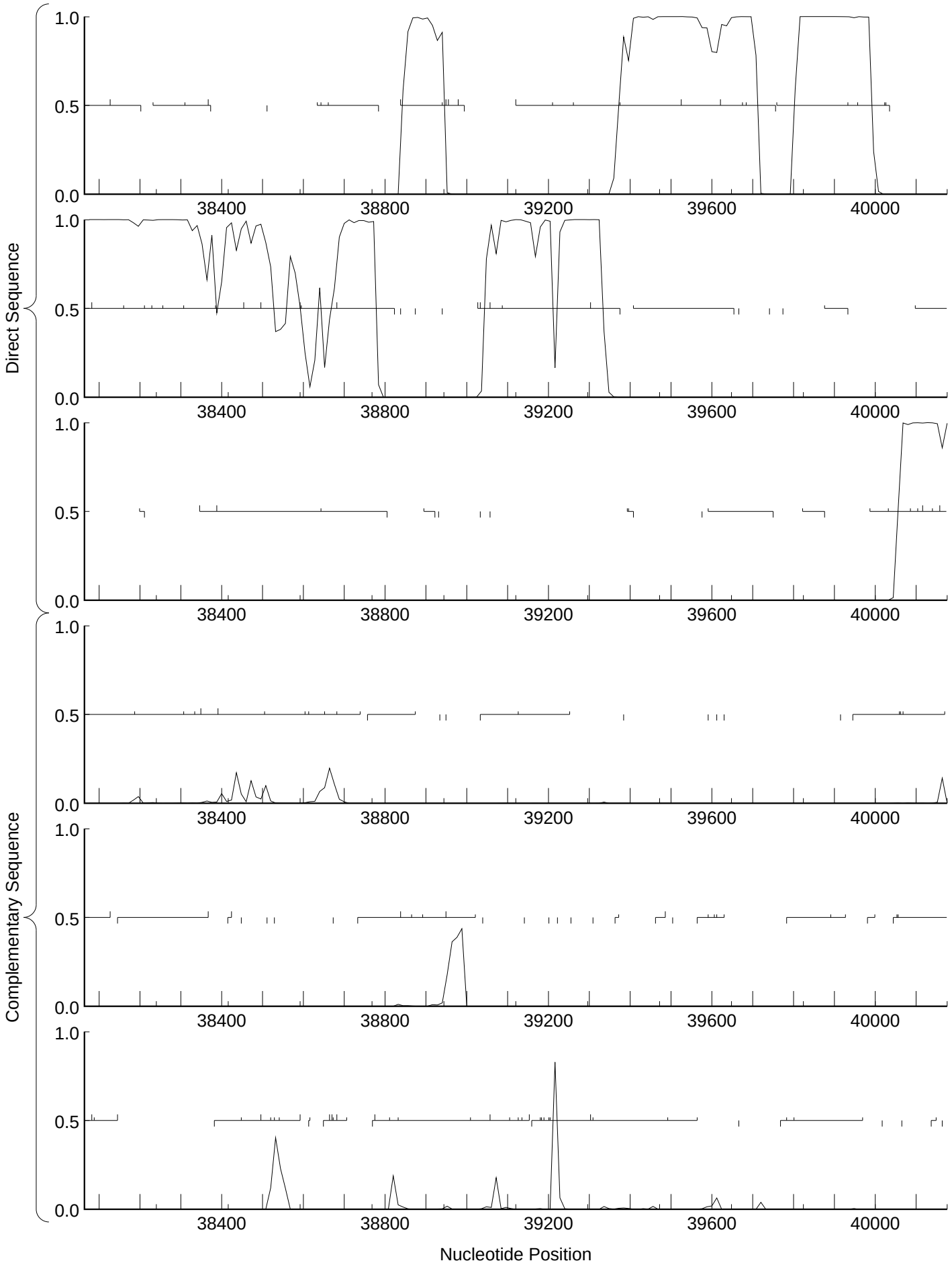
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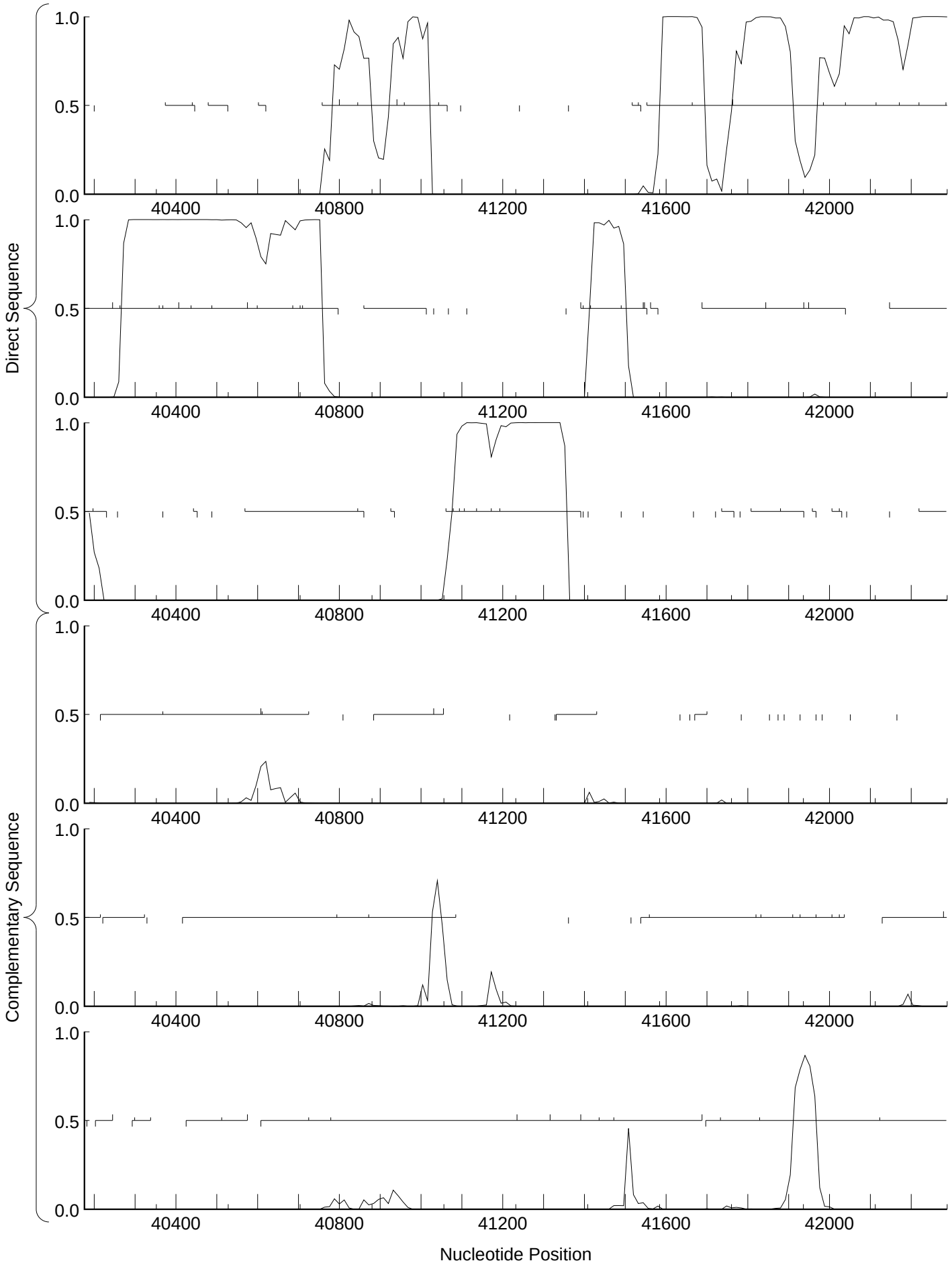
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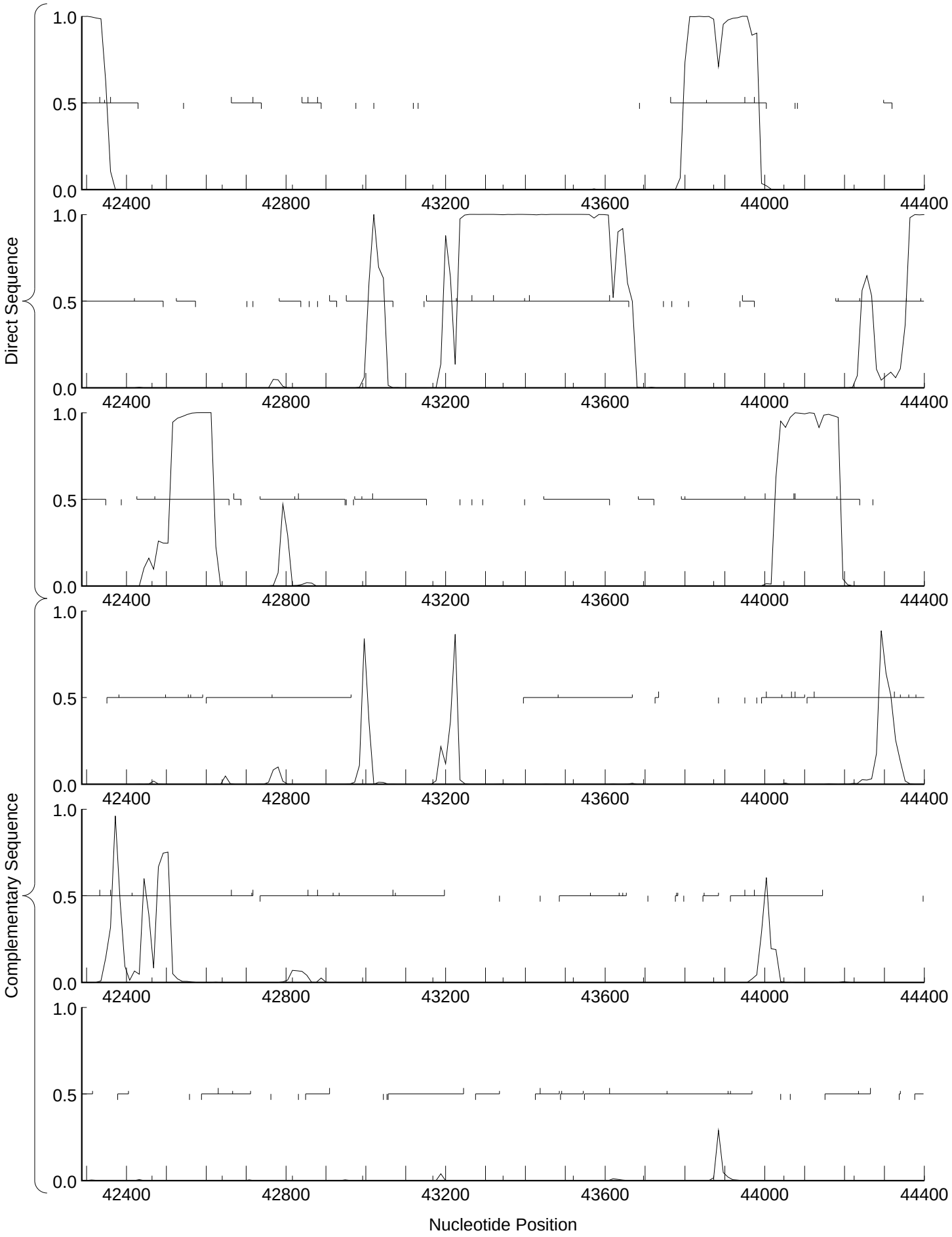
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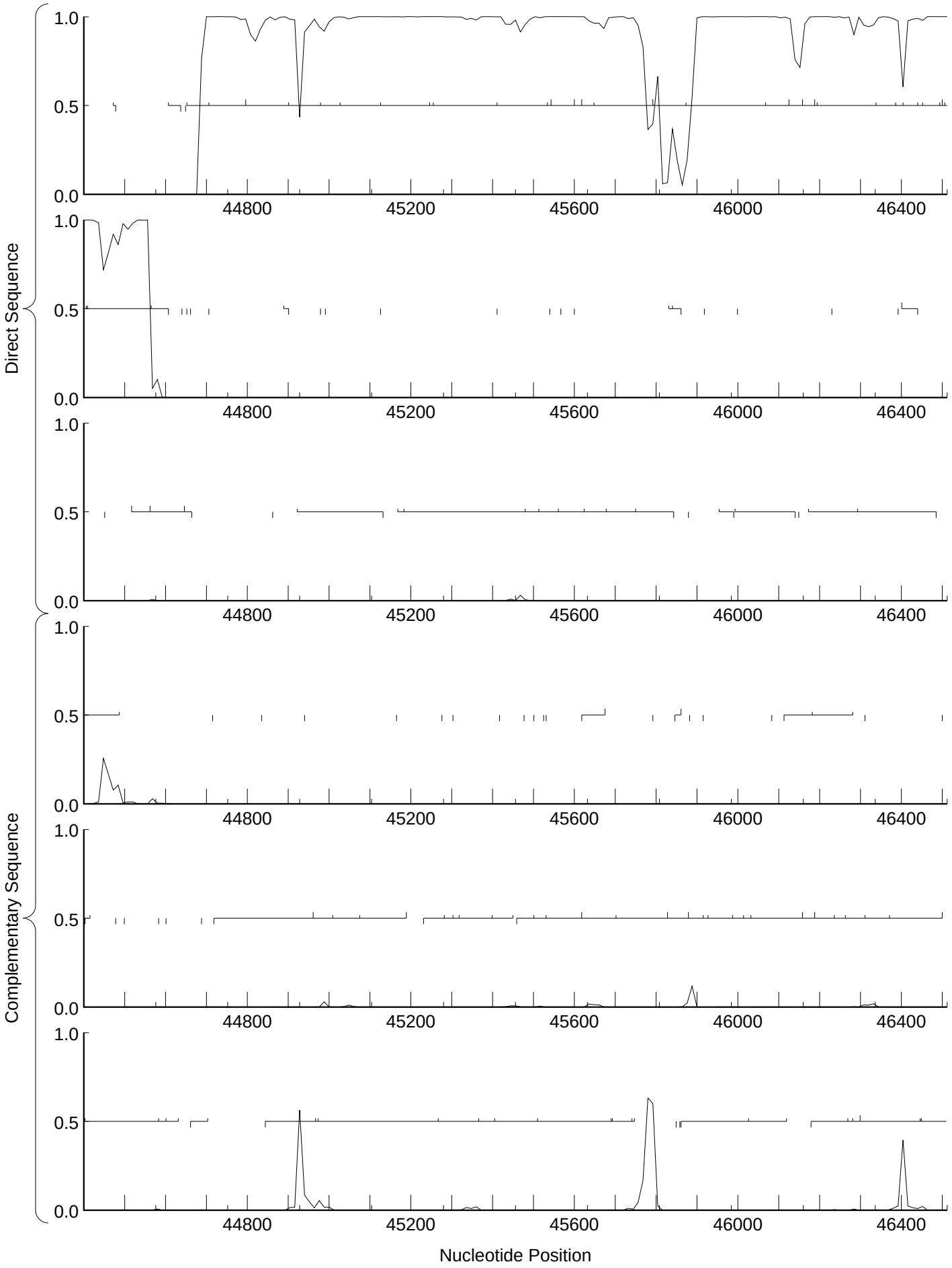
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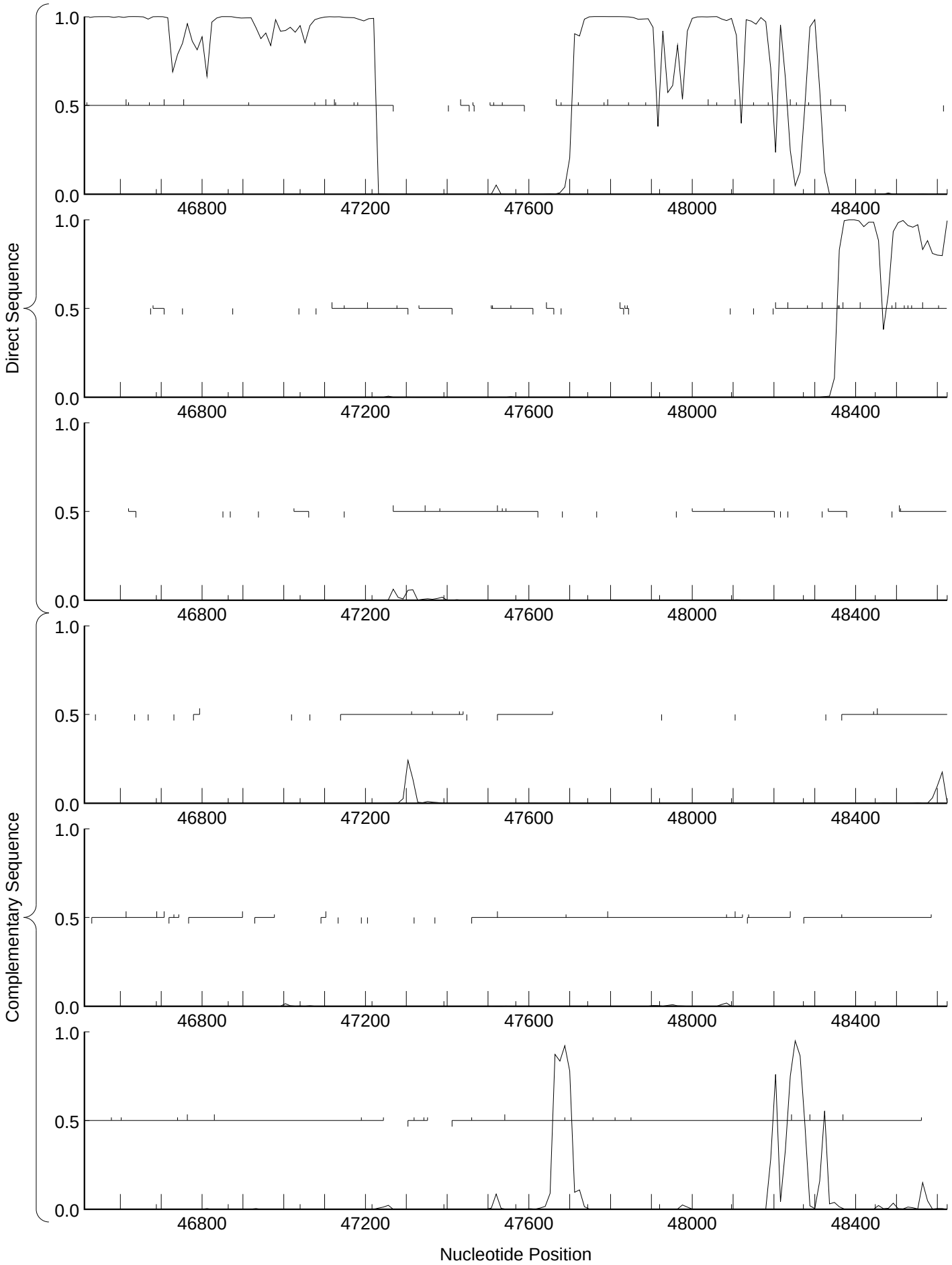
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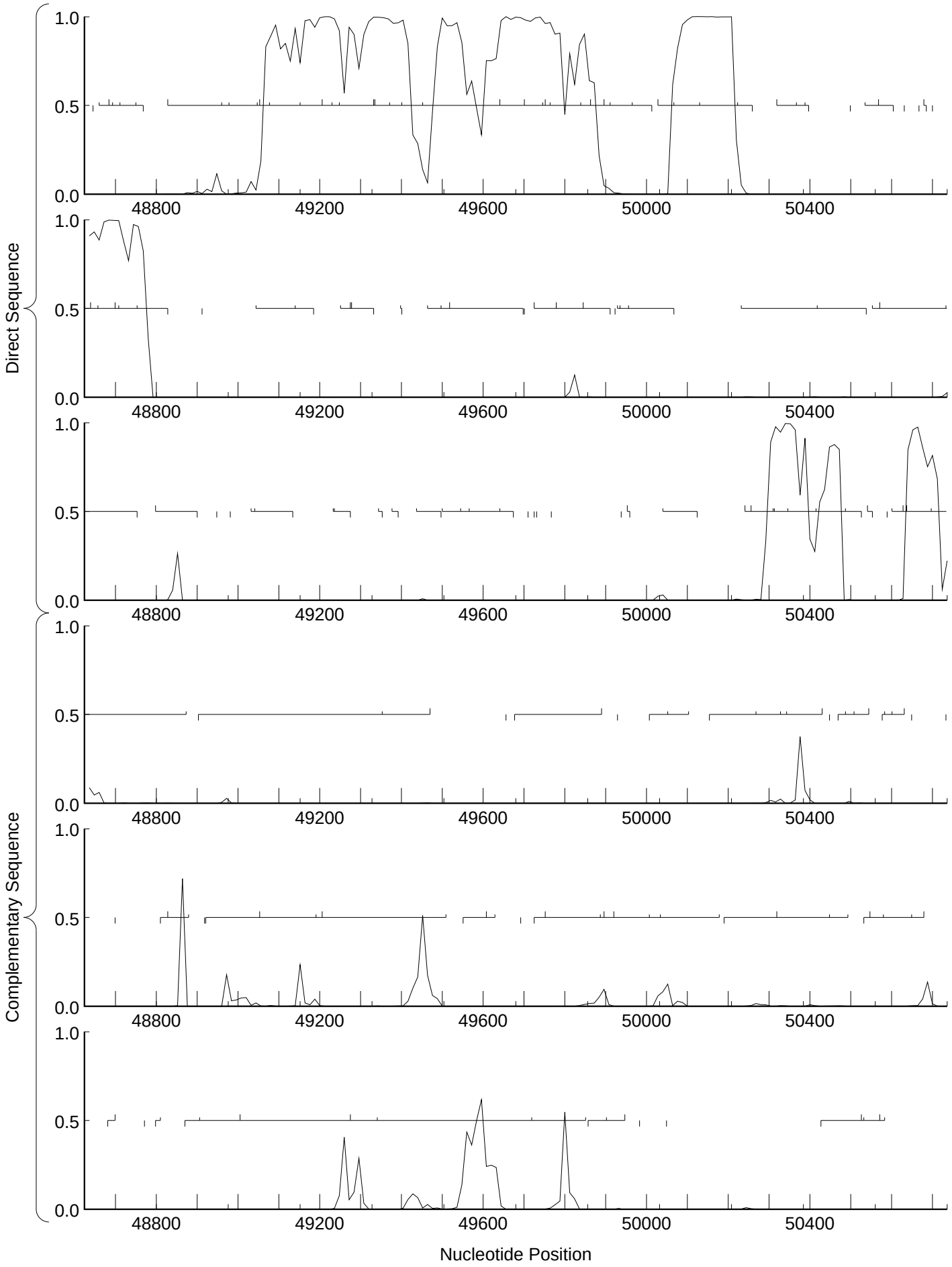
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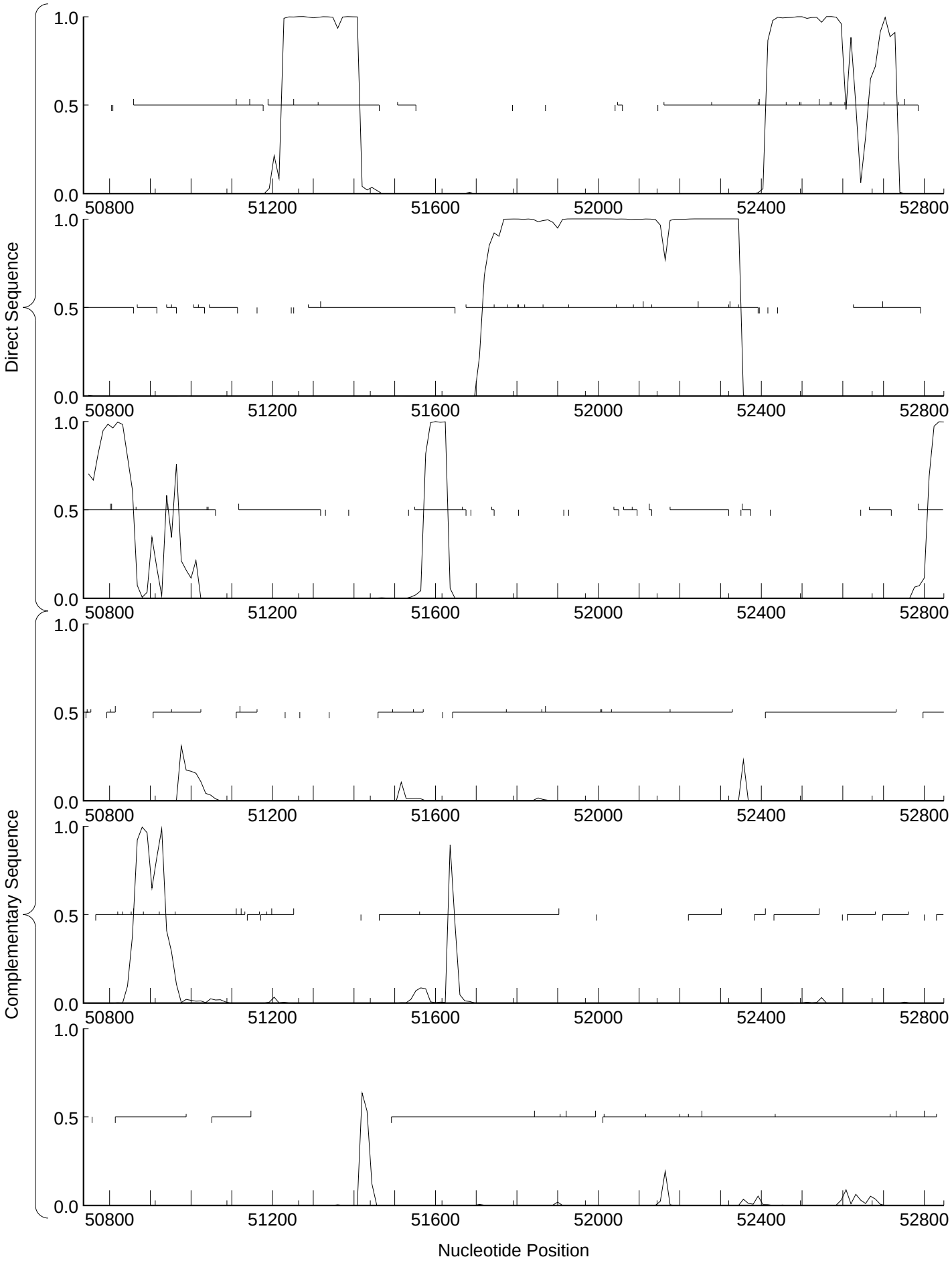
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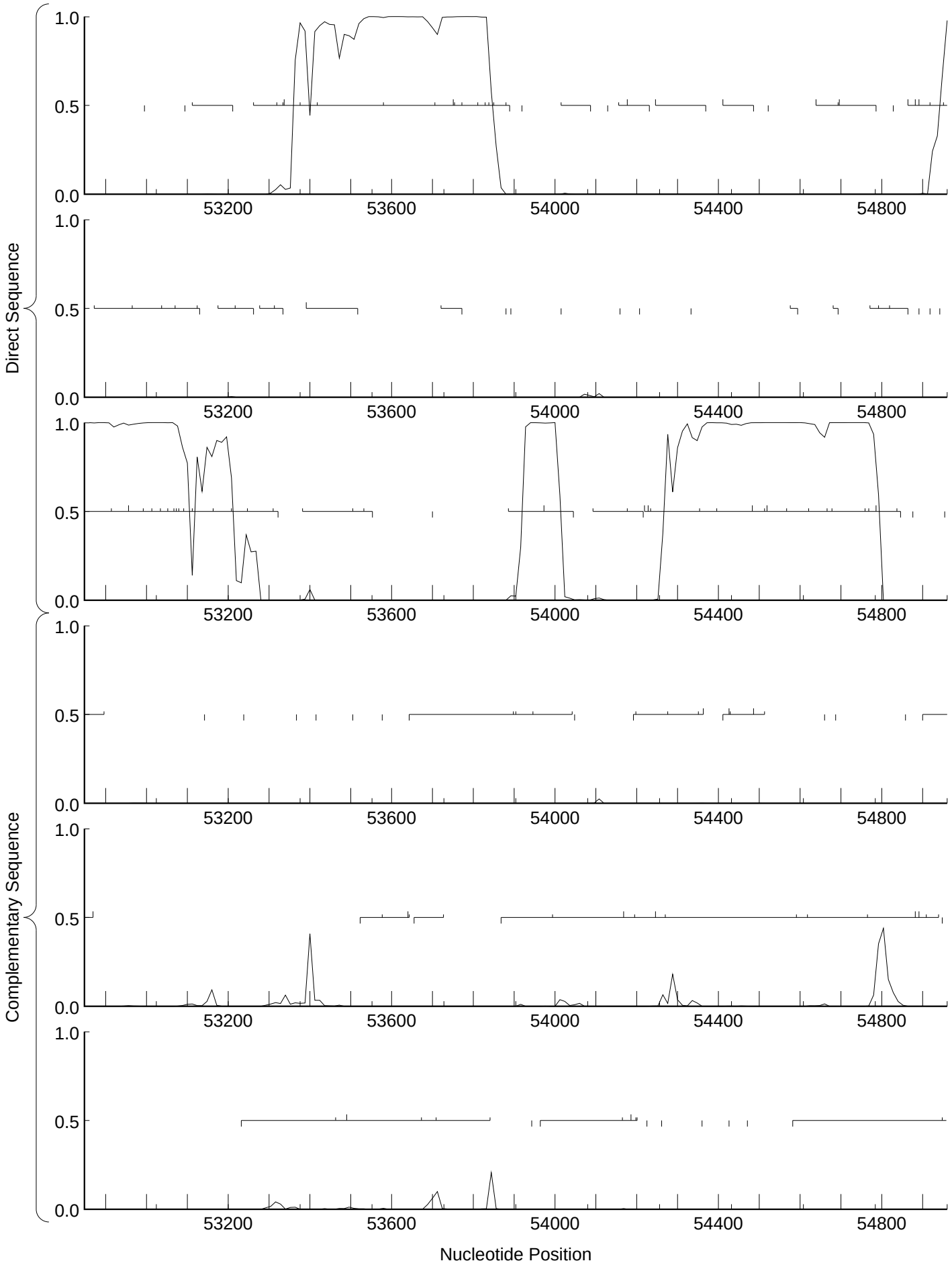
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complete sequence, 57034 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K1, Order 4, Window 96, Step 12, 26/29



complete sequence, 57034 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K1, Order 4, Window 96, Step 12, 27/29



complete sequence, 57034 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K1, Order 4, Window 96, Step 12, 28/29

