GeneMark

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

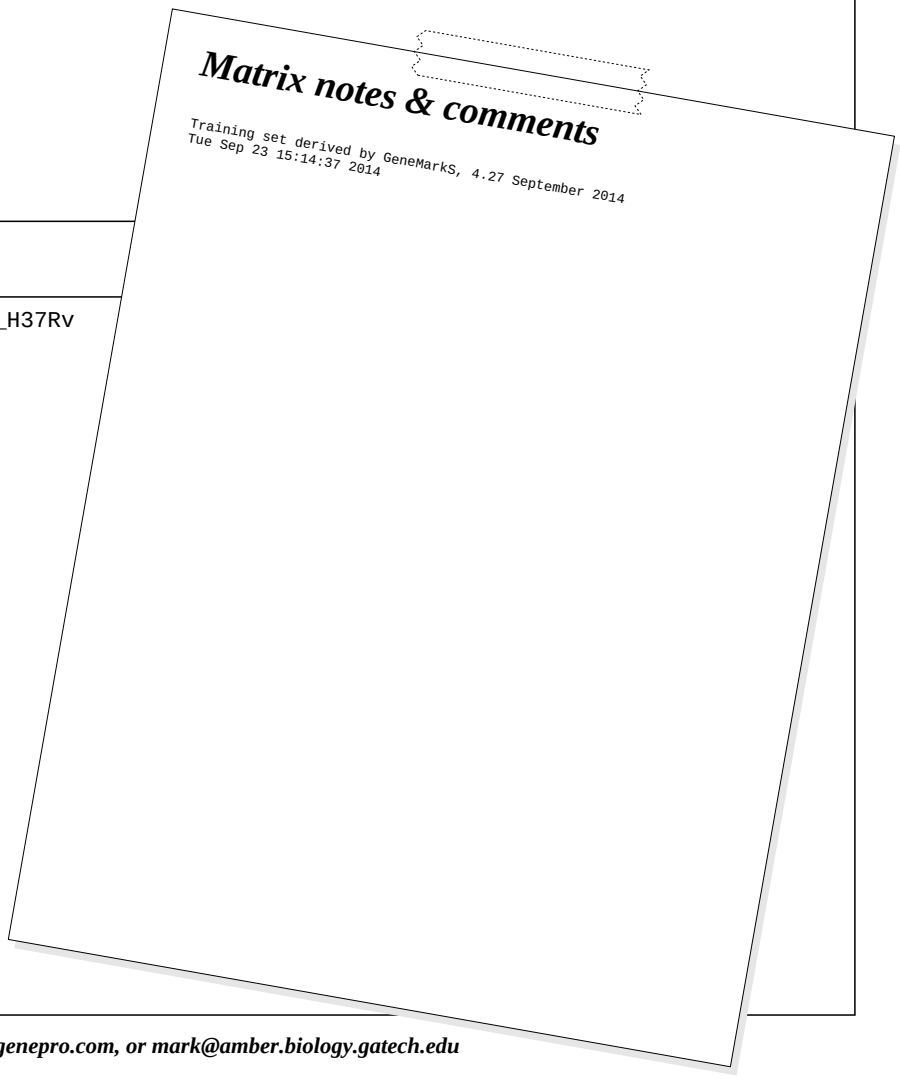
PROGRAM INFORMATION

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Sequence         :  Mycobacterium phage Zaka complete sequence, 52122 bp including 10-base 3' overhang (CGGTCGG
Analysis Date    :  3/28/24 at 10:13:36
Pages            :  26
Sequence Length  :  52122 bp
GC Content       :   61.50%

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

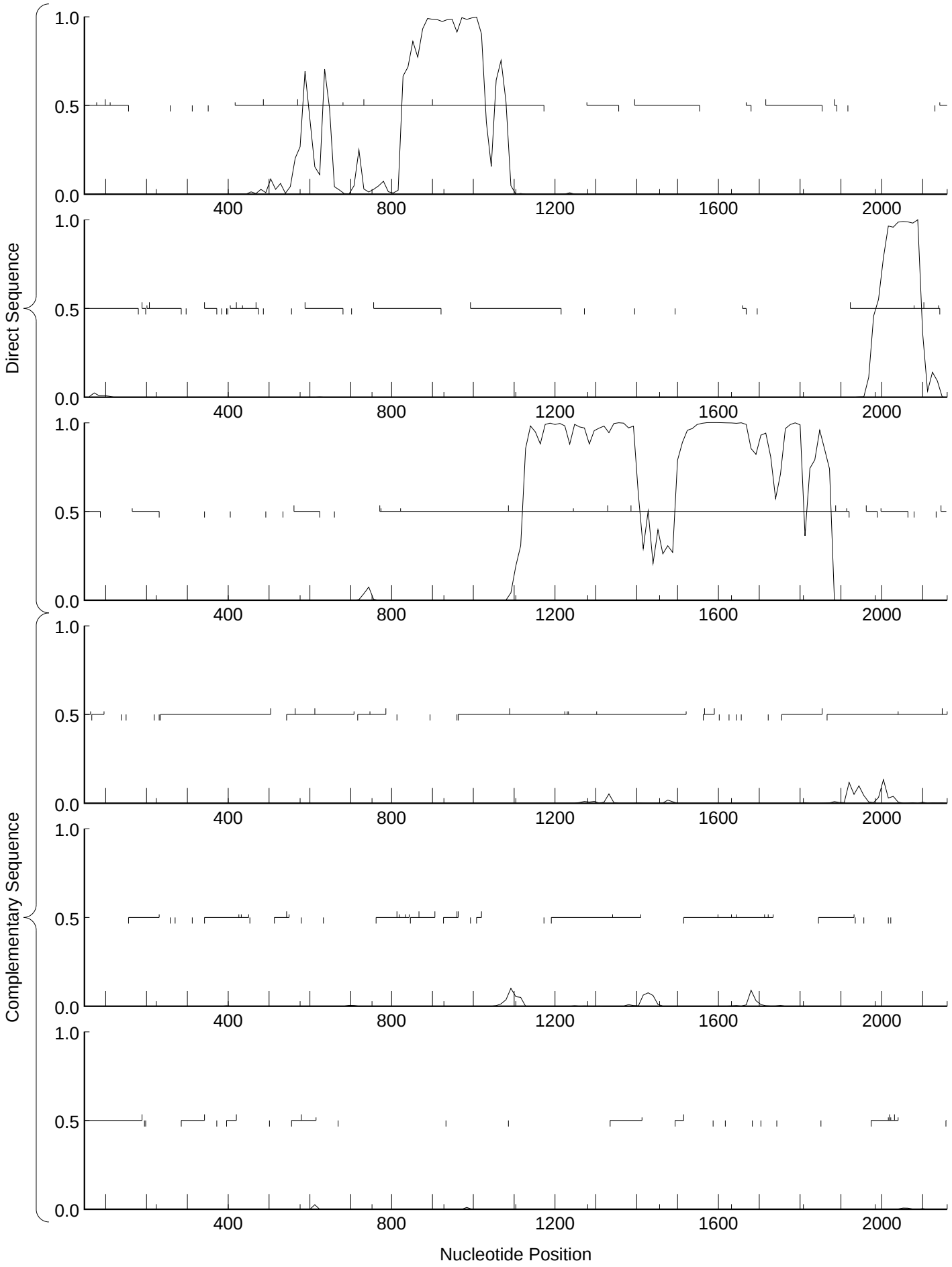
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Matrix     :  Mycobacterium_tuberculosis_H37Rv
Author     :  -

Order      :  4

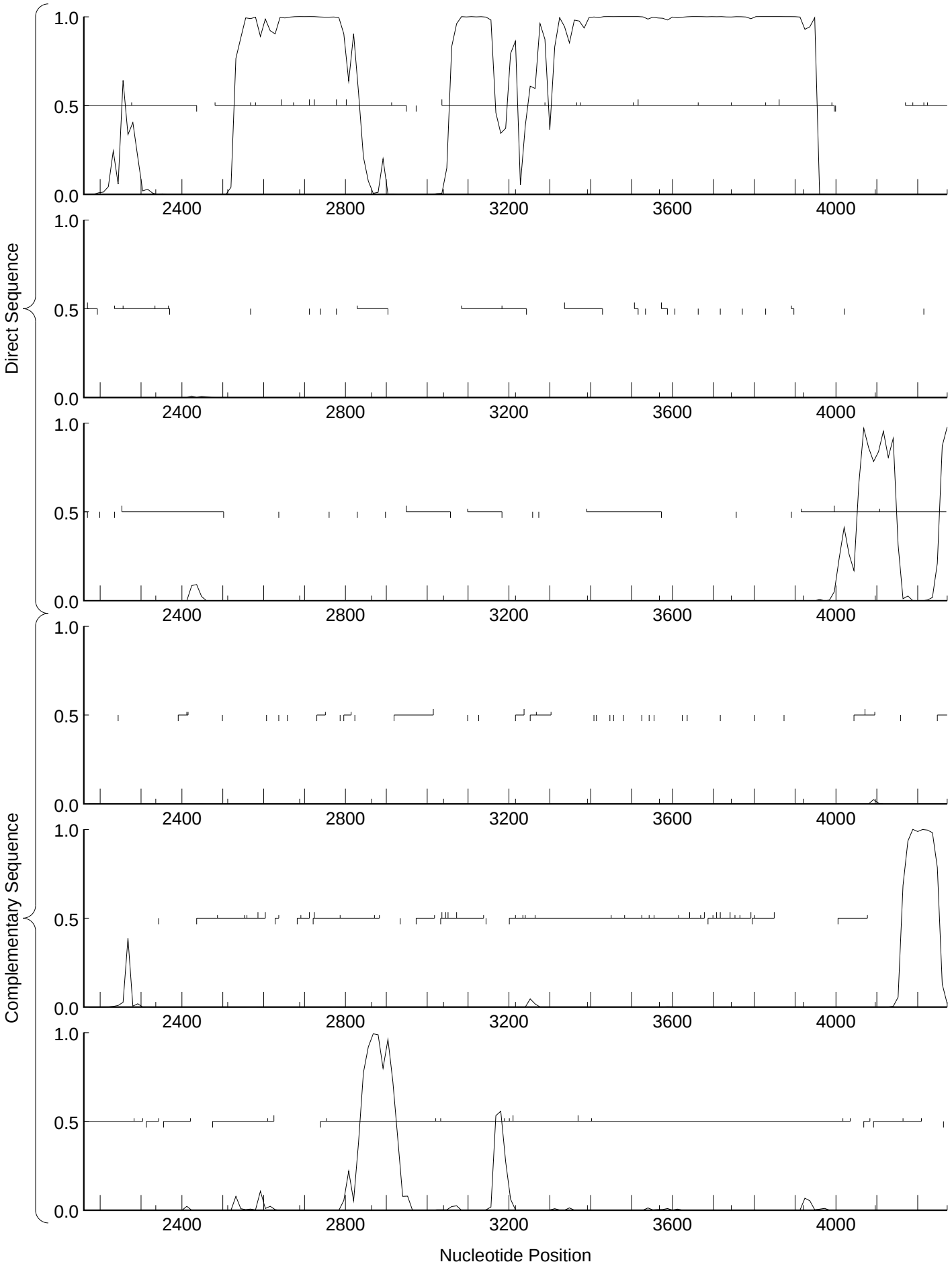

  Send questions / comments to:
      Dr. M. Borodovsky
      Georgia Institute of Technology
      School of Biology
      Atlanta, GA  30332-0230
```

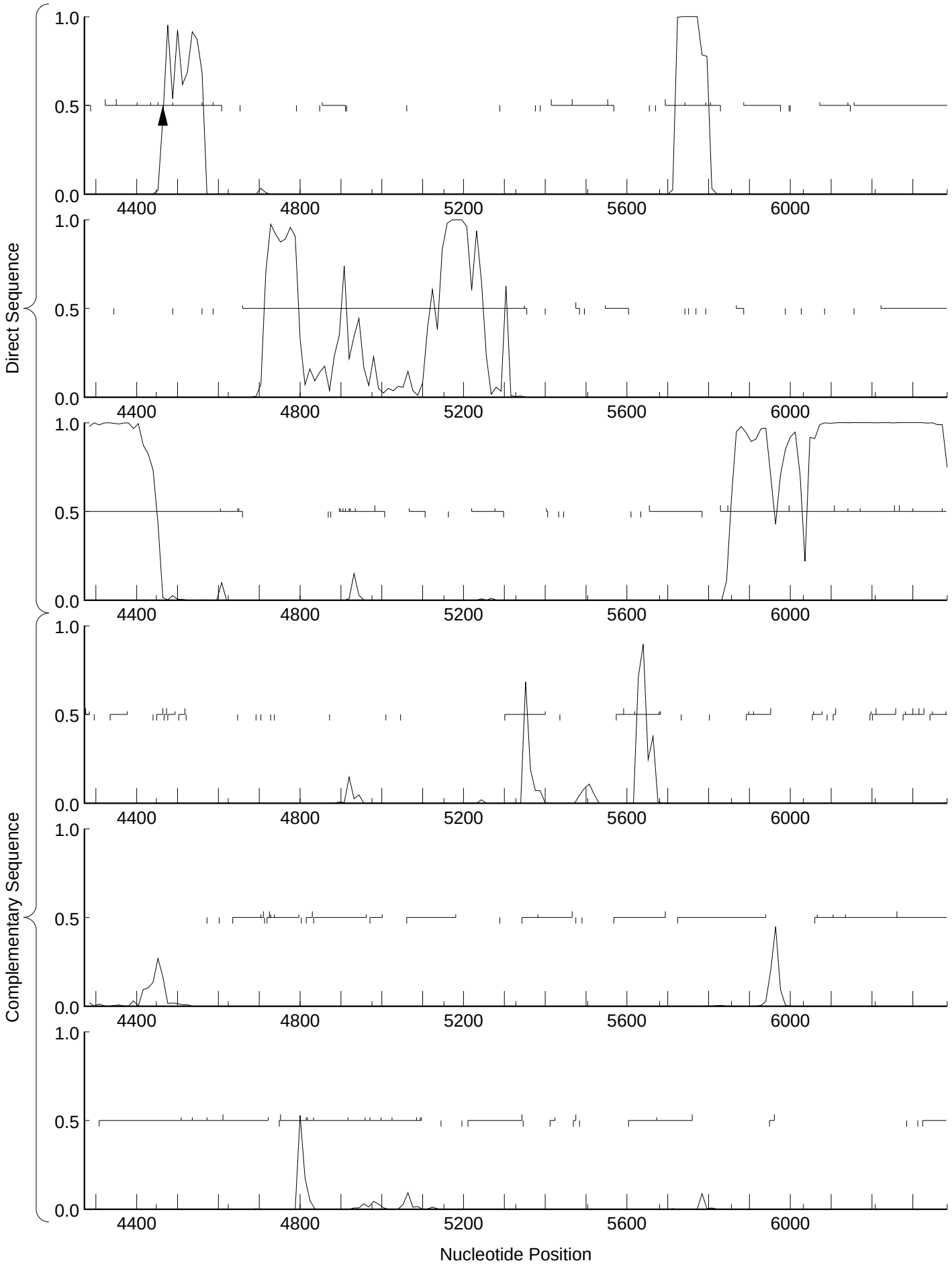
For help or information, send electronic mail to: custserv@genepro.com, or mark@amber.biology.gatech.edu

ka complete sequence, 52122 bp including 10-base 3’ overhang (CGGTCGGTAA), Cluster A6, Order 4, Window 96, Step 12, 2/26

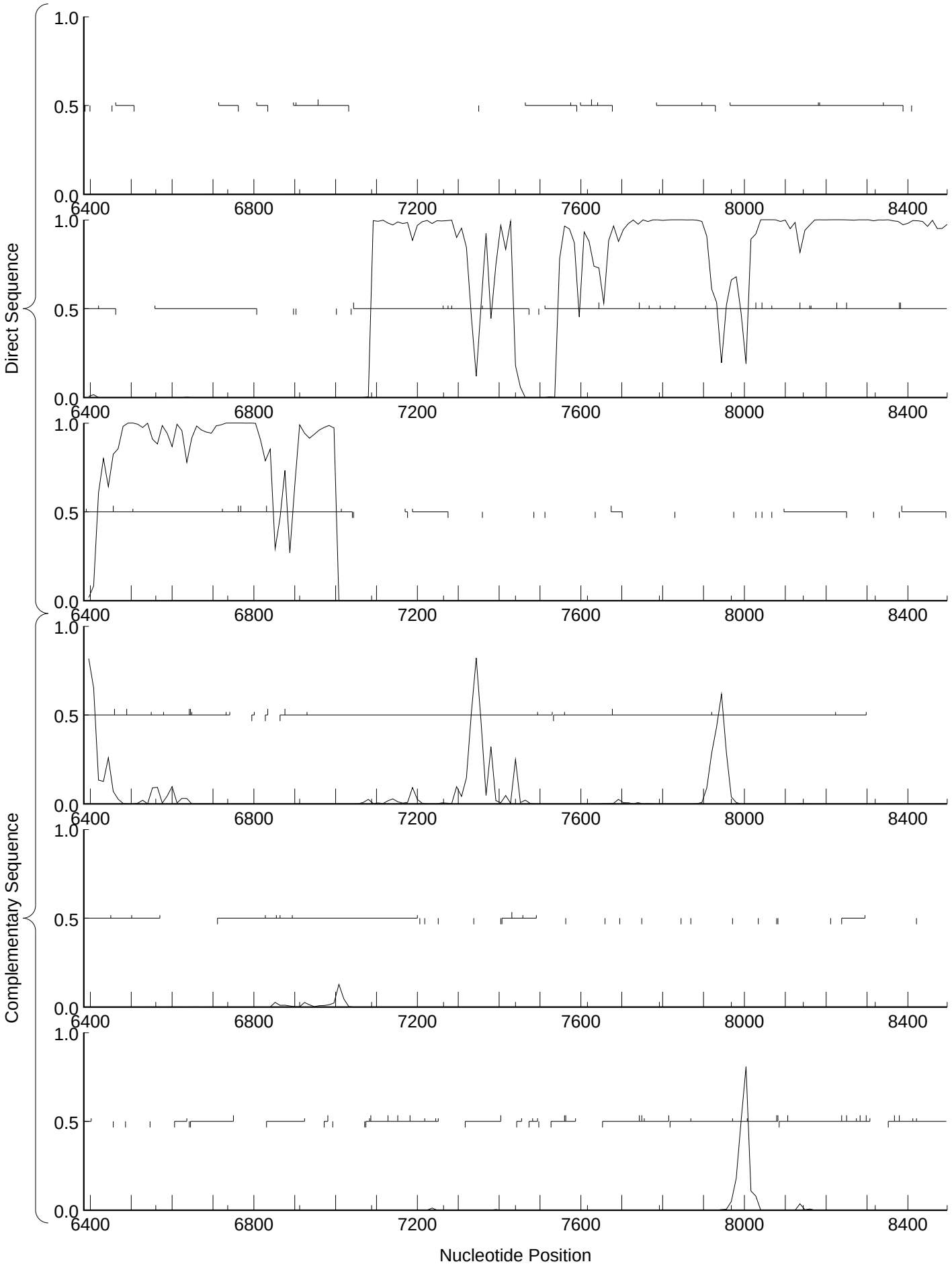


ka complete sequence, 52122 bp including 10-base 3’ overhang (CGGTCGGTAA), Cluster A6, Order 4, Window 96, Step 12, 3/26

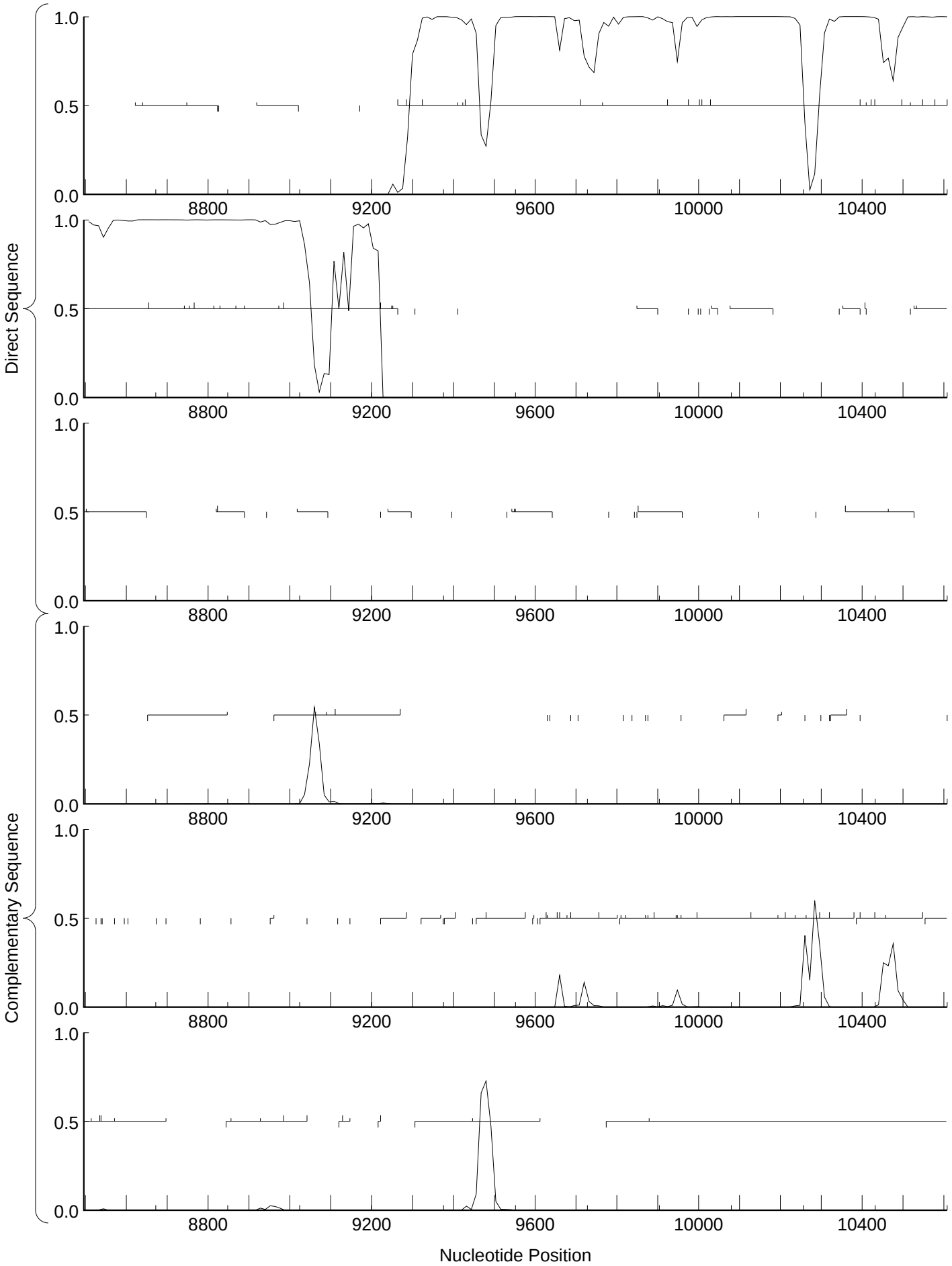



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Complementary Sequence
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0.0
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5600
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Nucleotide Position

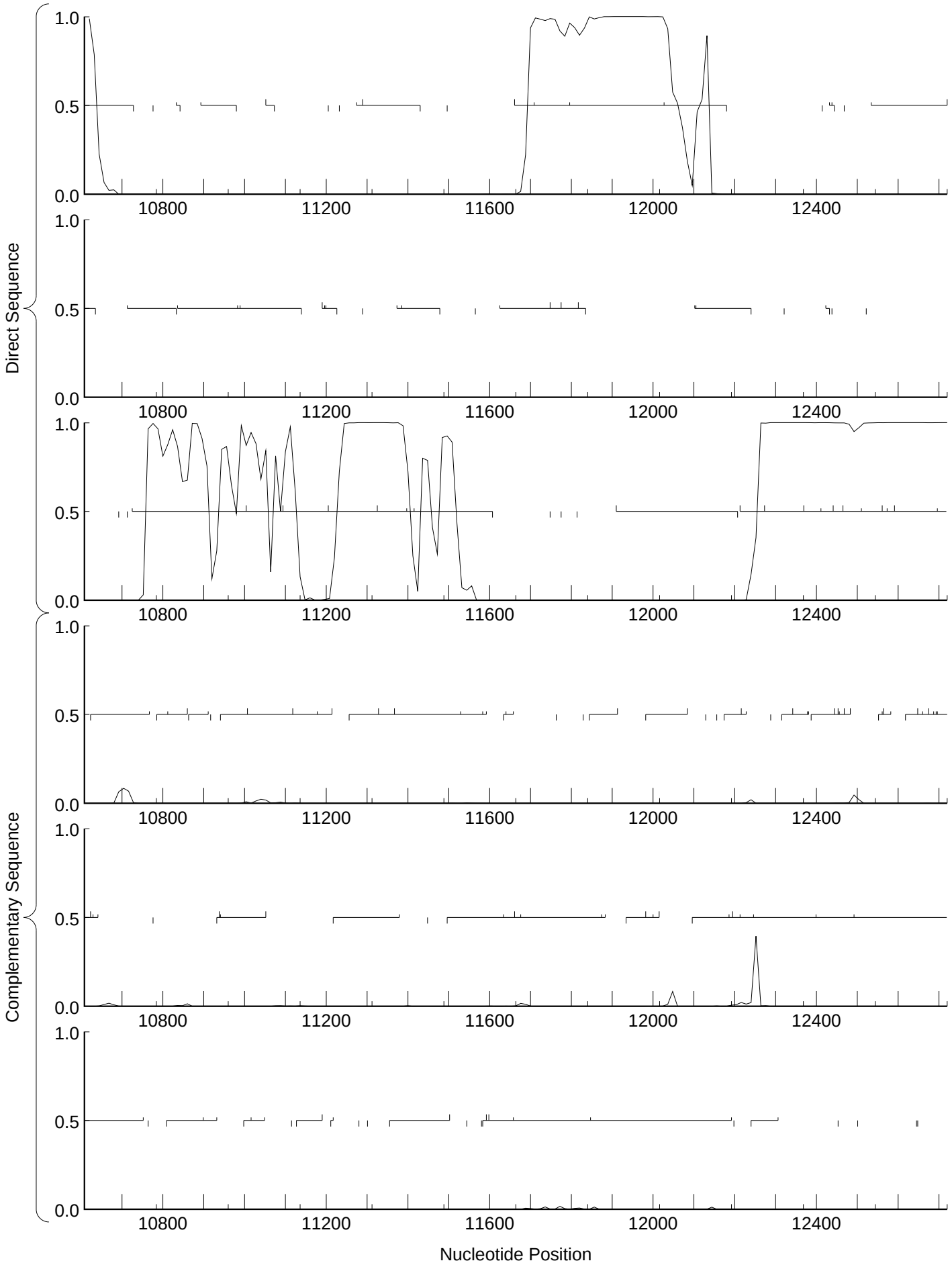
a complete sequence, 52122 bp including 10-base 3’ overhang (CGGTCGGTAA), Cluster A6, Order 4, Window 96, Step 12, 5/26



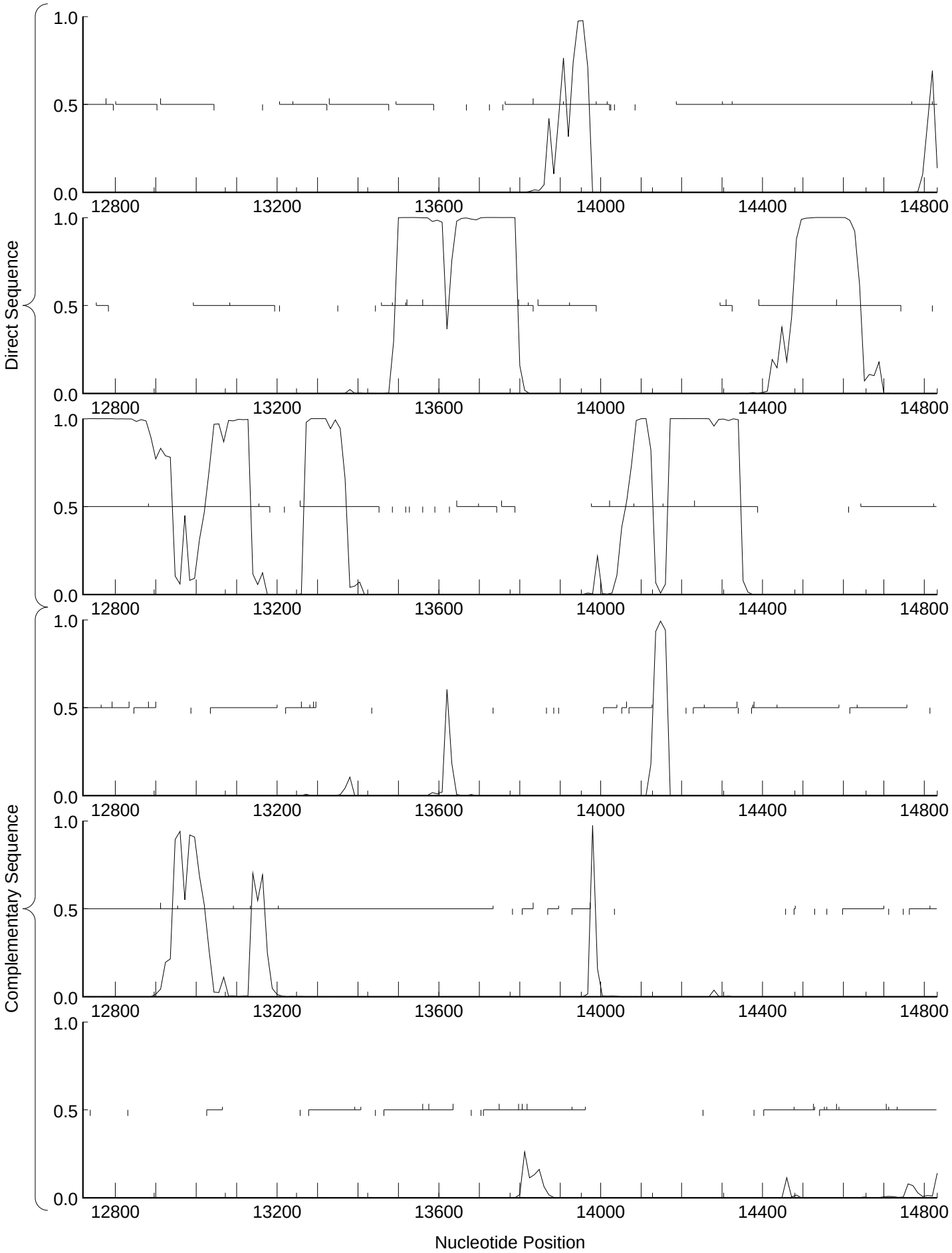
a complete sequence, 52122 bp including 10-base 3’ overhang (CGGTCGGTAA), Cluster A6, Order 4, Window 96, Step 12, 6/26



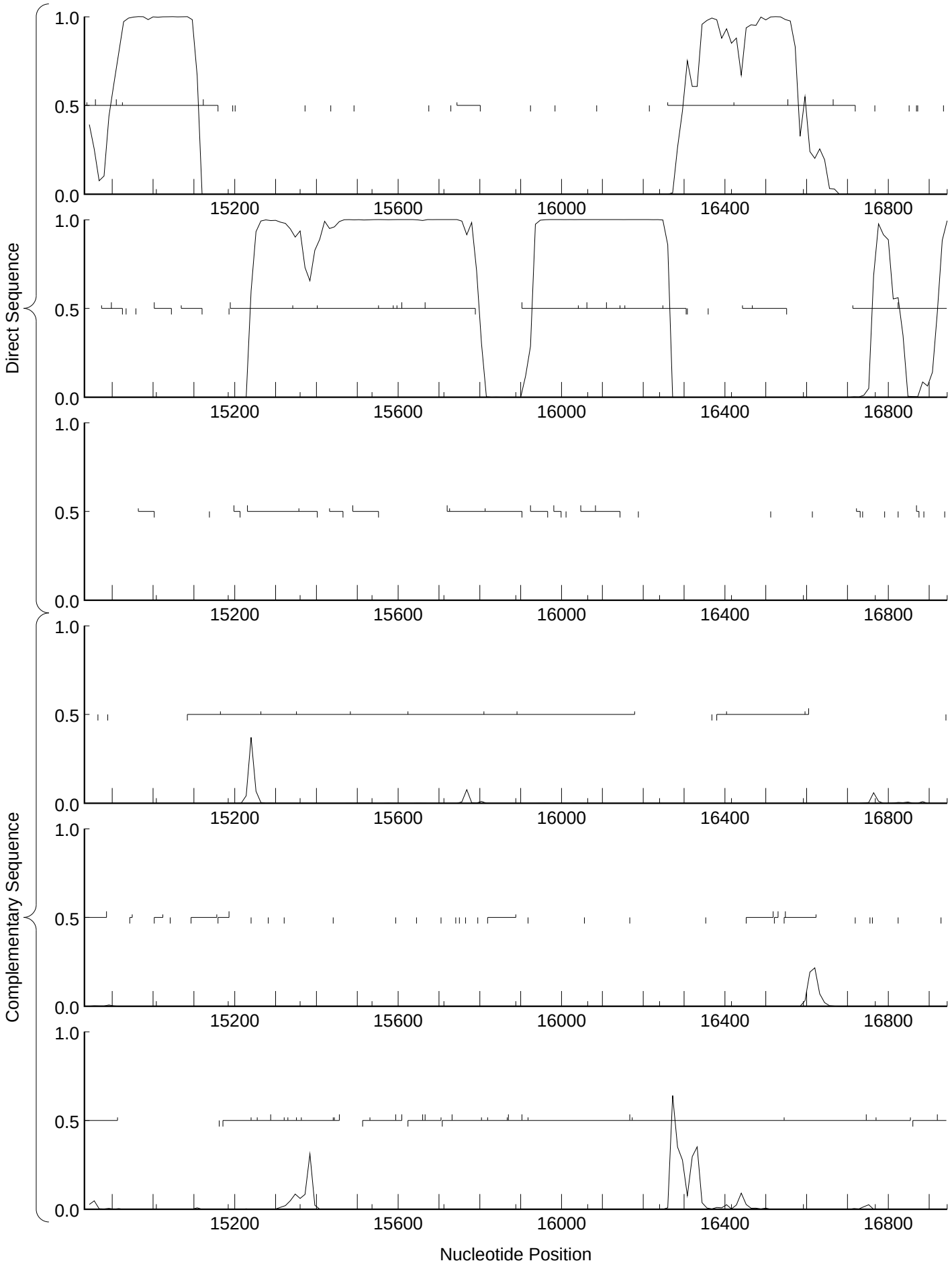
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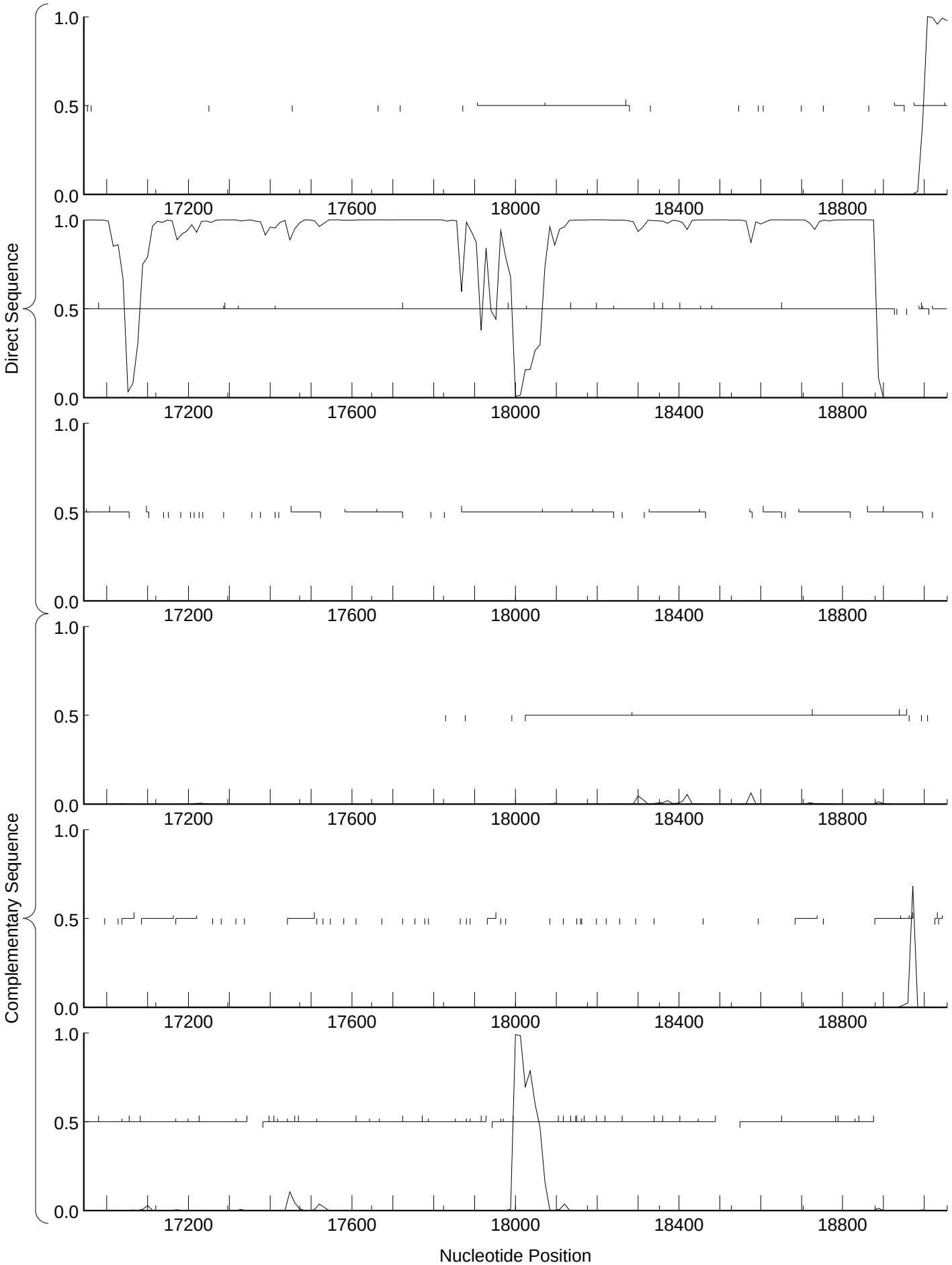
ka complete sequence, 52122 bp including 10-base 3’ overhang (CGGTCGGTAA), Cluster A6, Order 4, Window 96, Step 12, 8/26



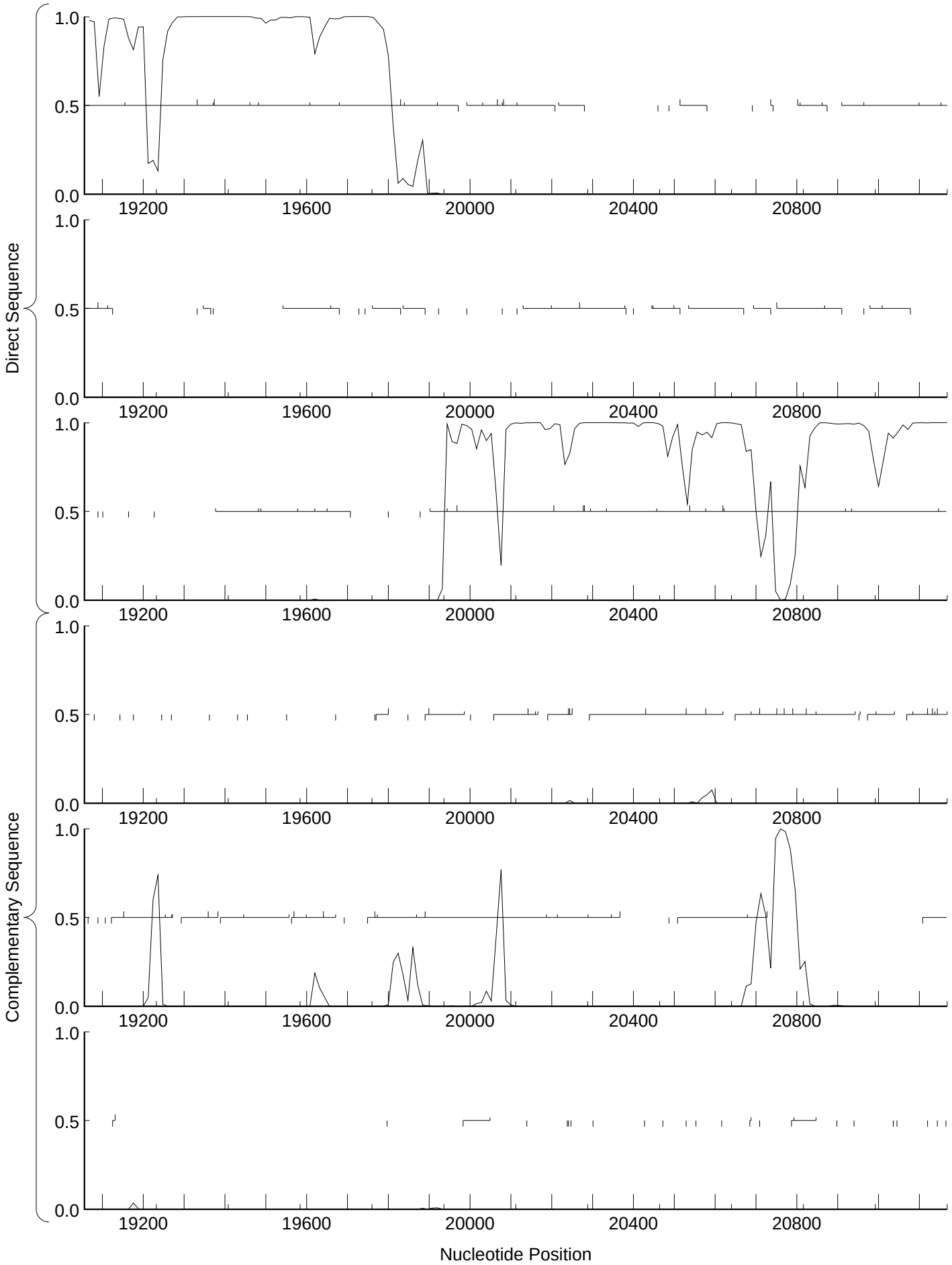
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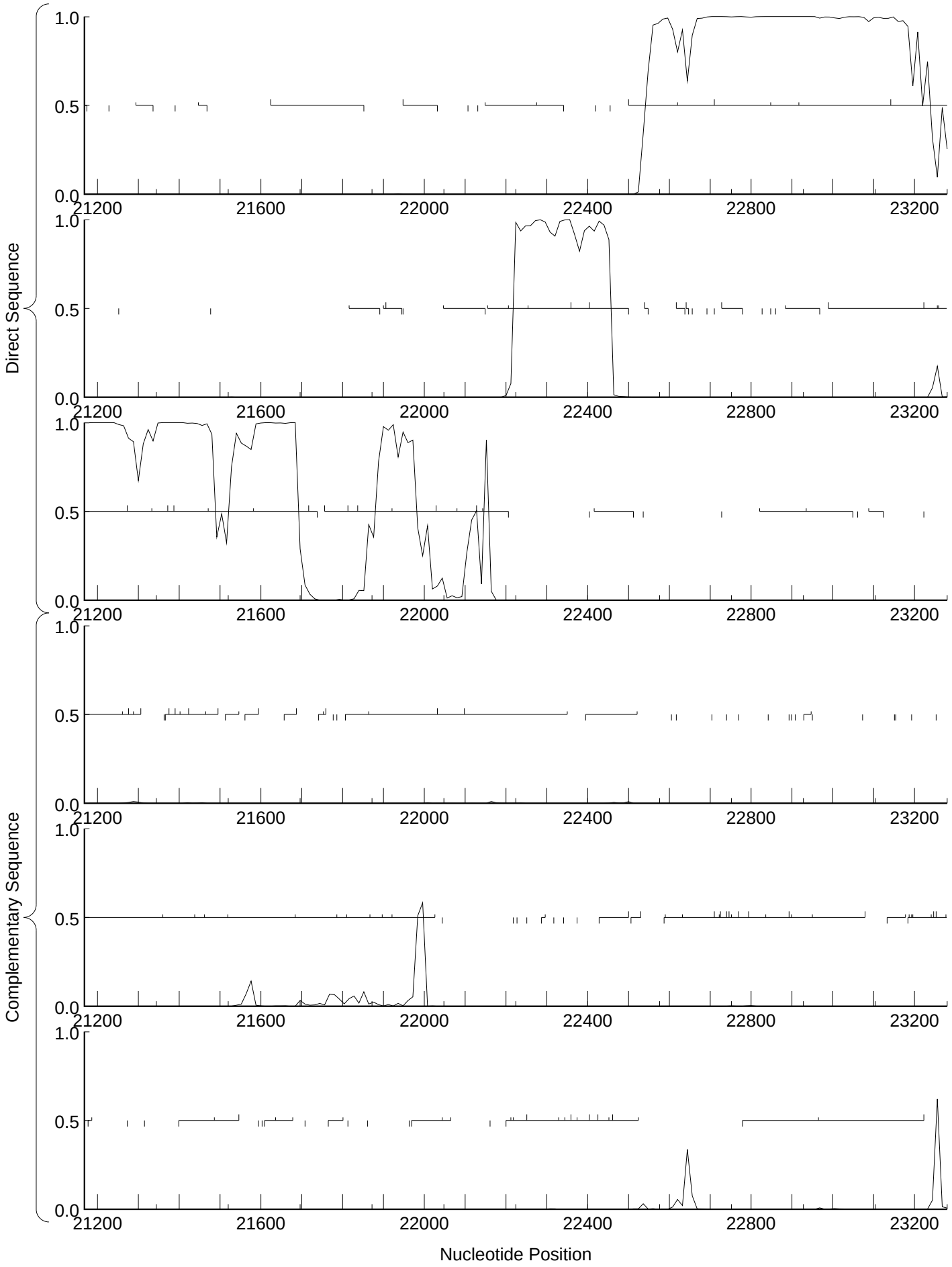
complete sequence, 52122 bp including 10-base 3’ overhang (CGGTCGGTAA), Cluster A6, Order 4, Window 96, Step 12, 10/26



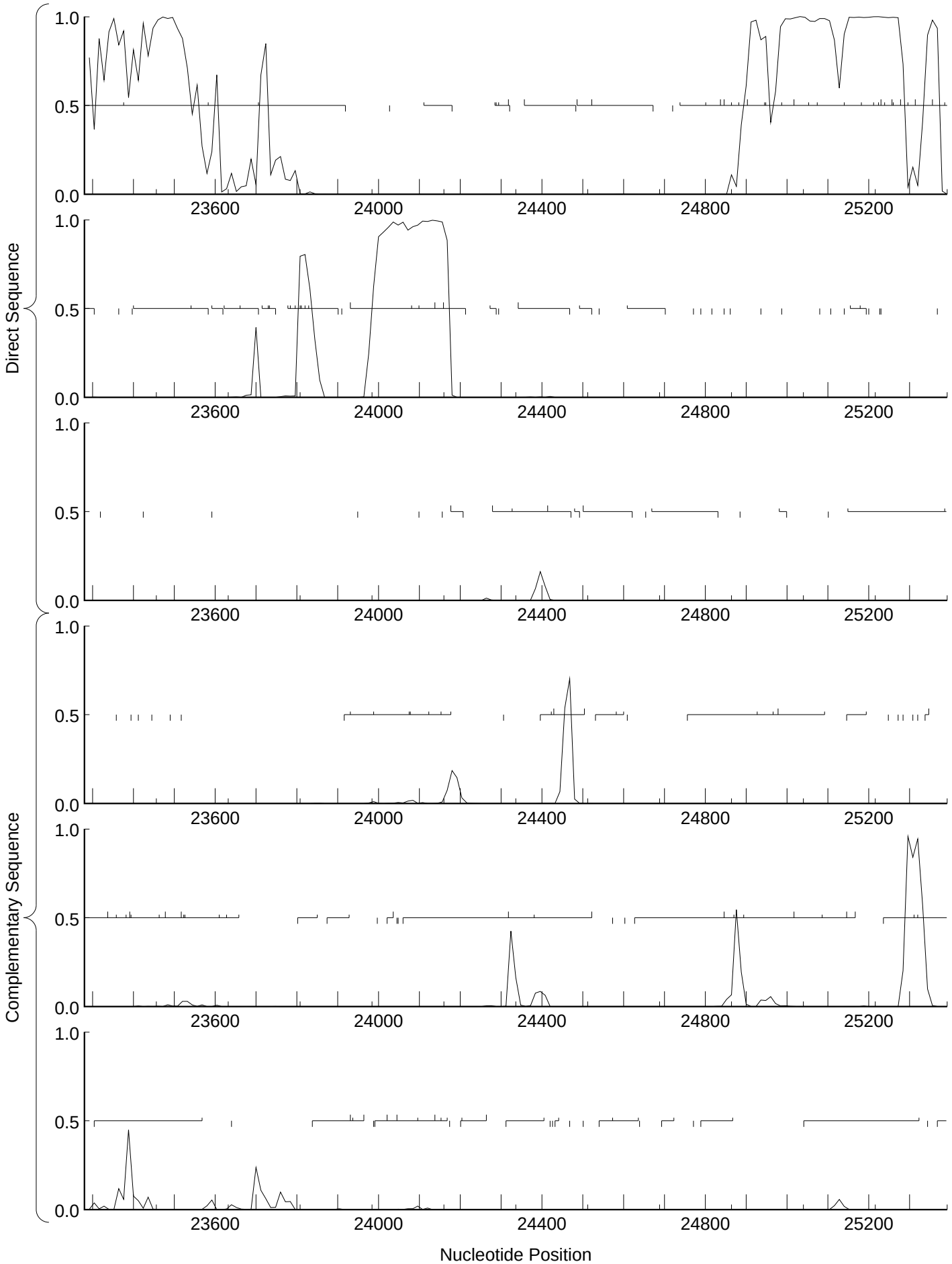
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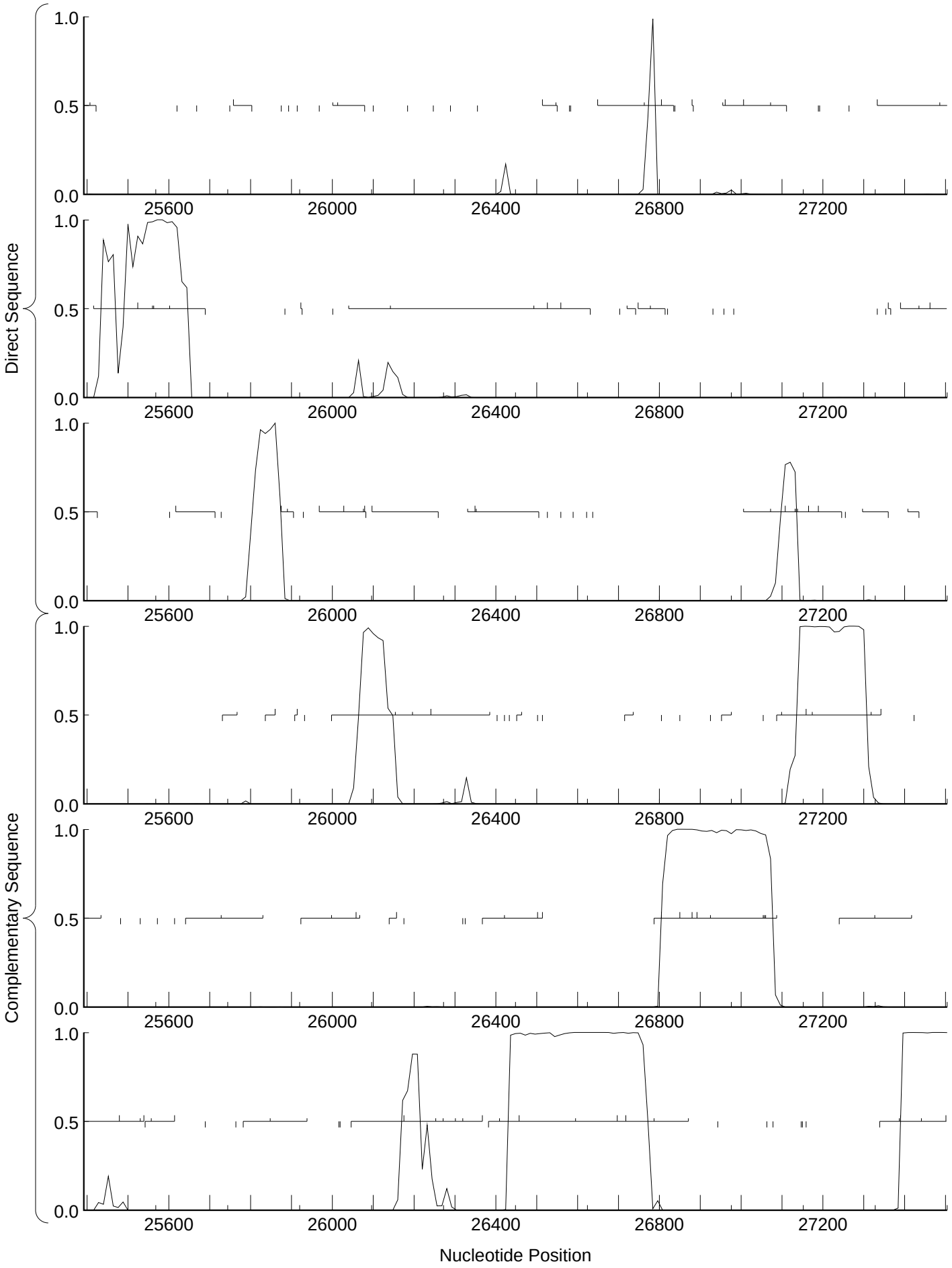
complete sequence, 52122 bp including 10-base 3’ overhang (CGGTCGGTAA), Cluster A6, Order 4, Window 96, Step 12, 12/26

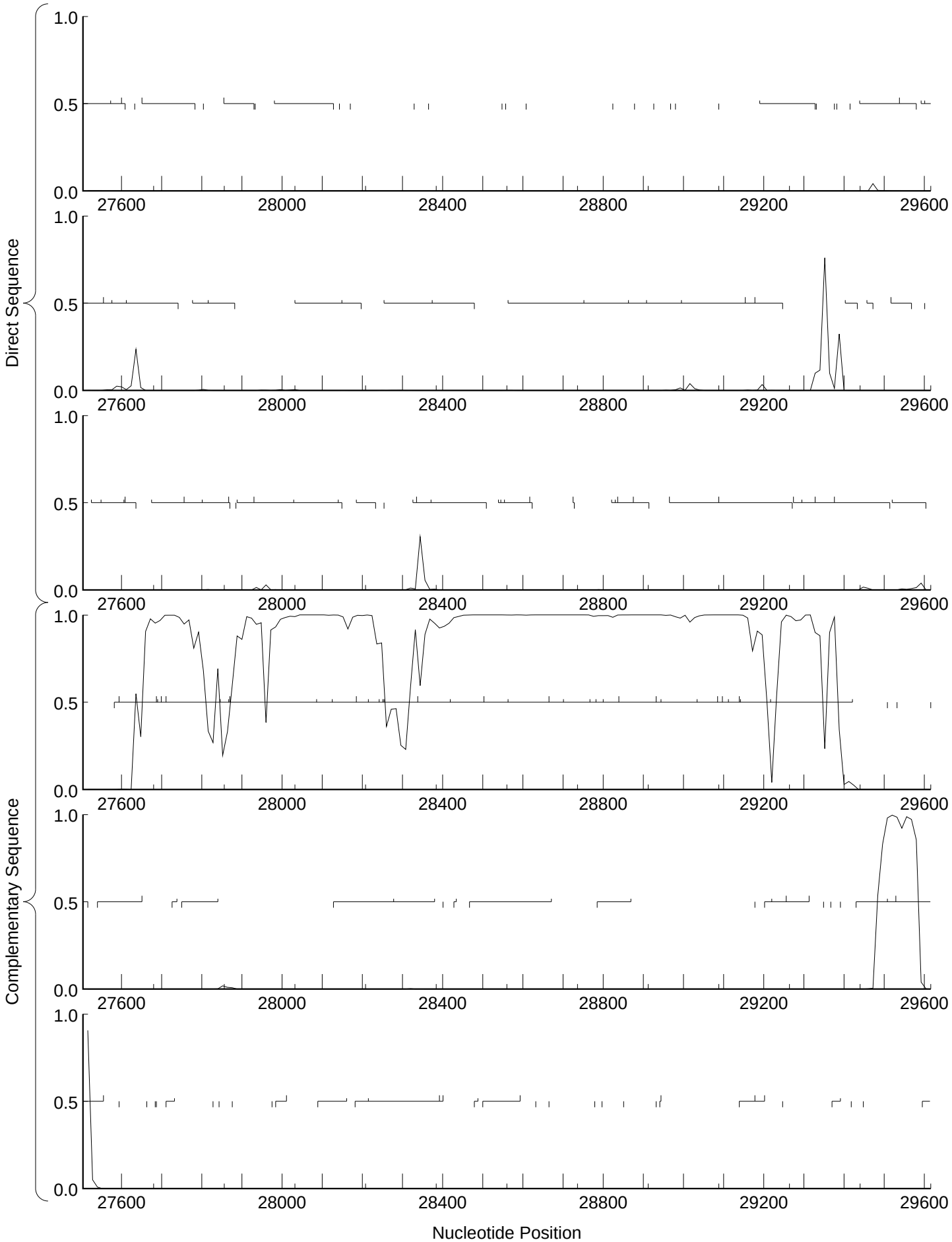


complete sequence, 52122 bp including 10-base 3’ overhang (CGGTCGGTAA), Cluster A6, Order 4, Window 96, Step 12, 13/26

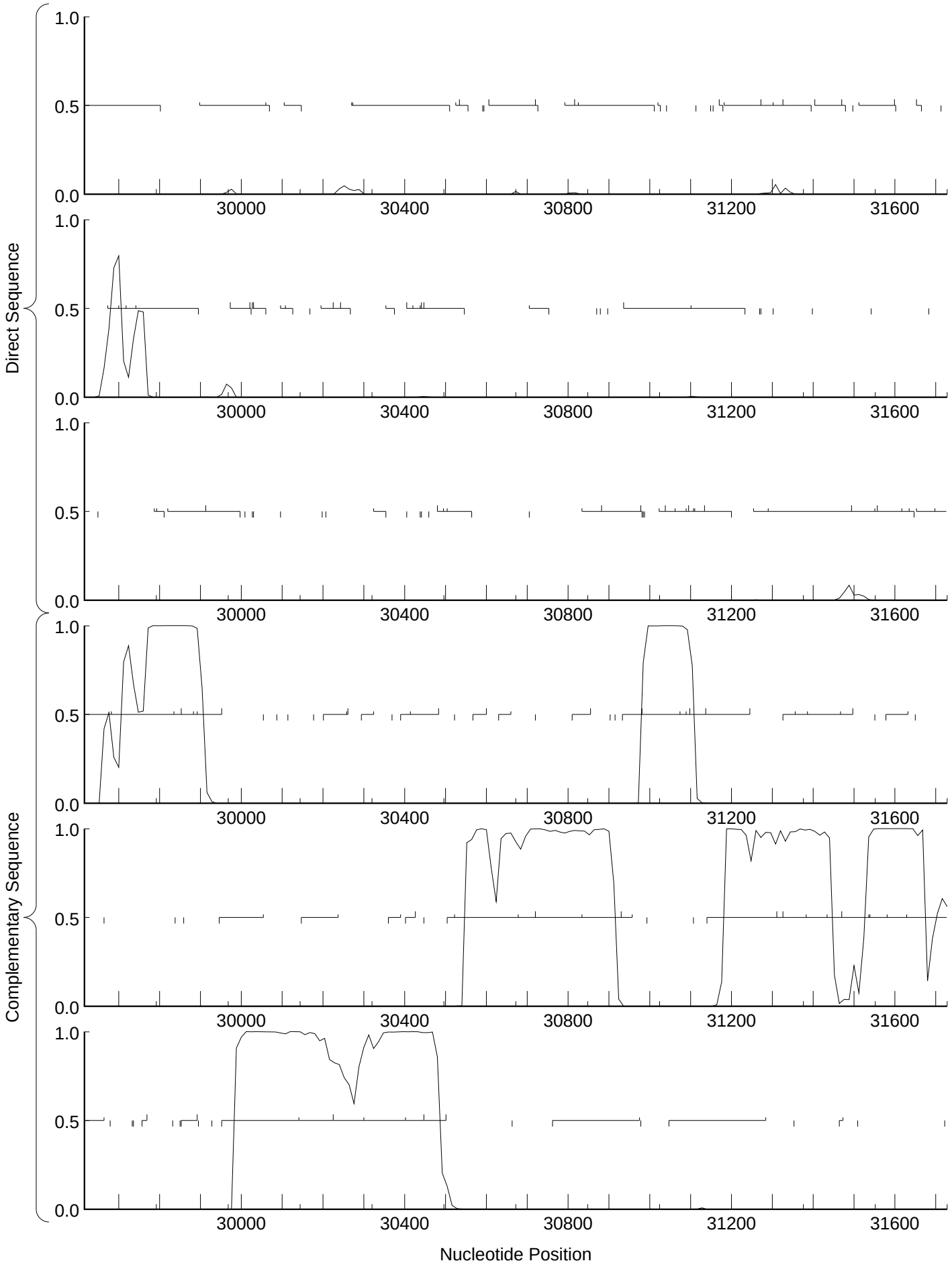


complete sequence, 52122 bp including 10-base 3’ overhang (CGGTCGGTAA), Cluster A6, Order 4, Window 96, Step 12, 14/26

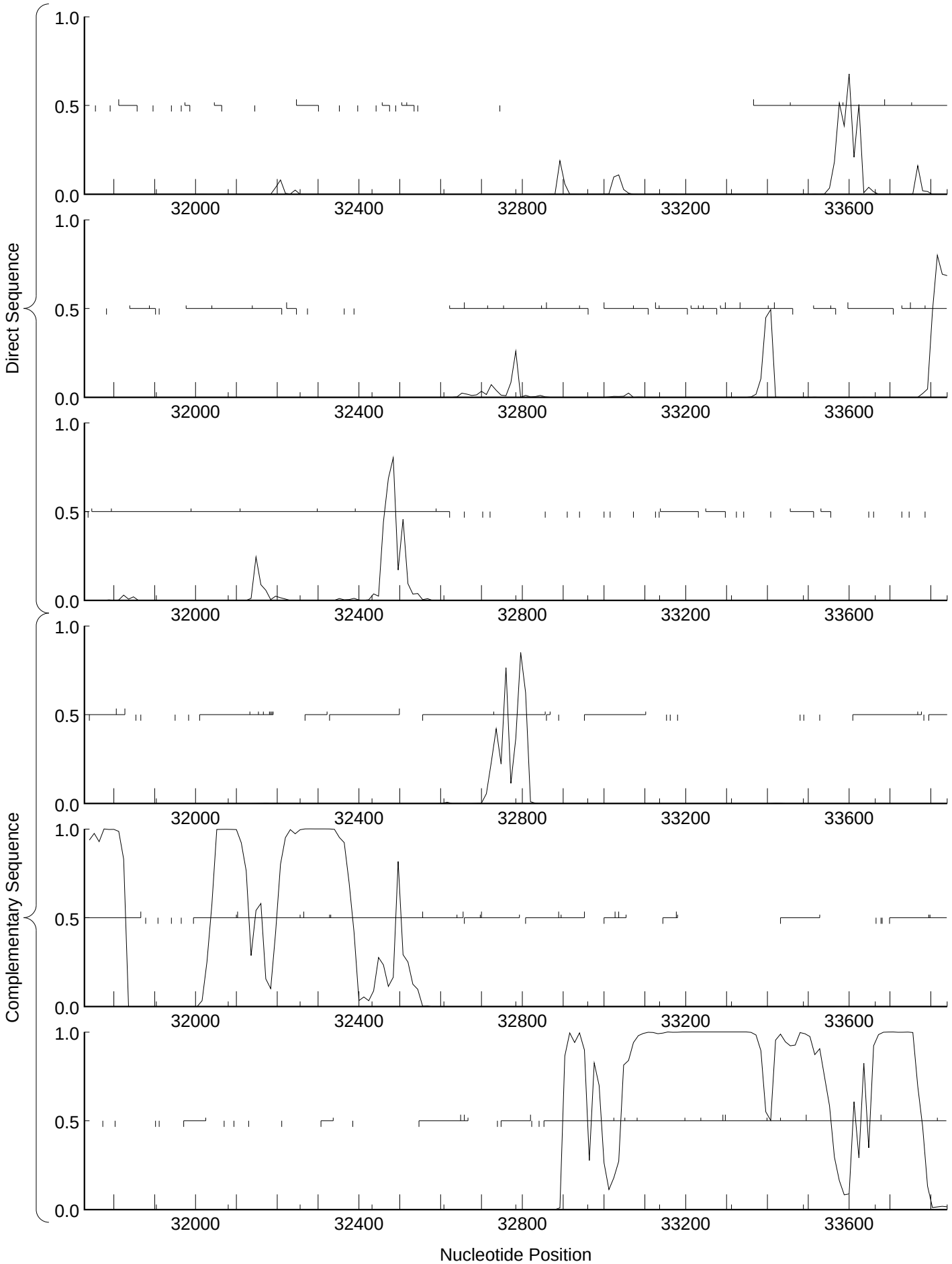



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Complementary Sequence
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28000
28400
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29200
29600
Nucleotide Position

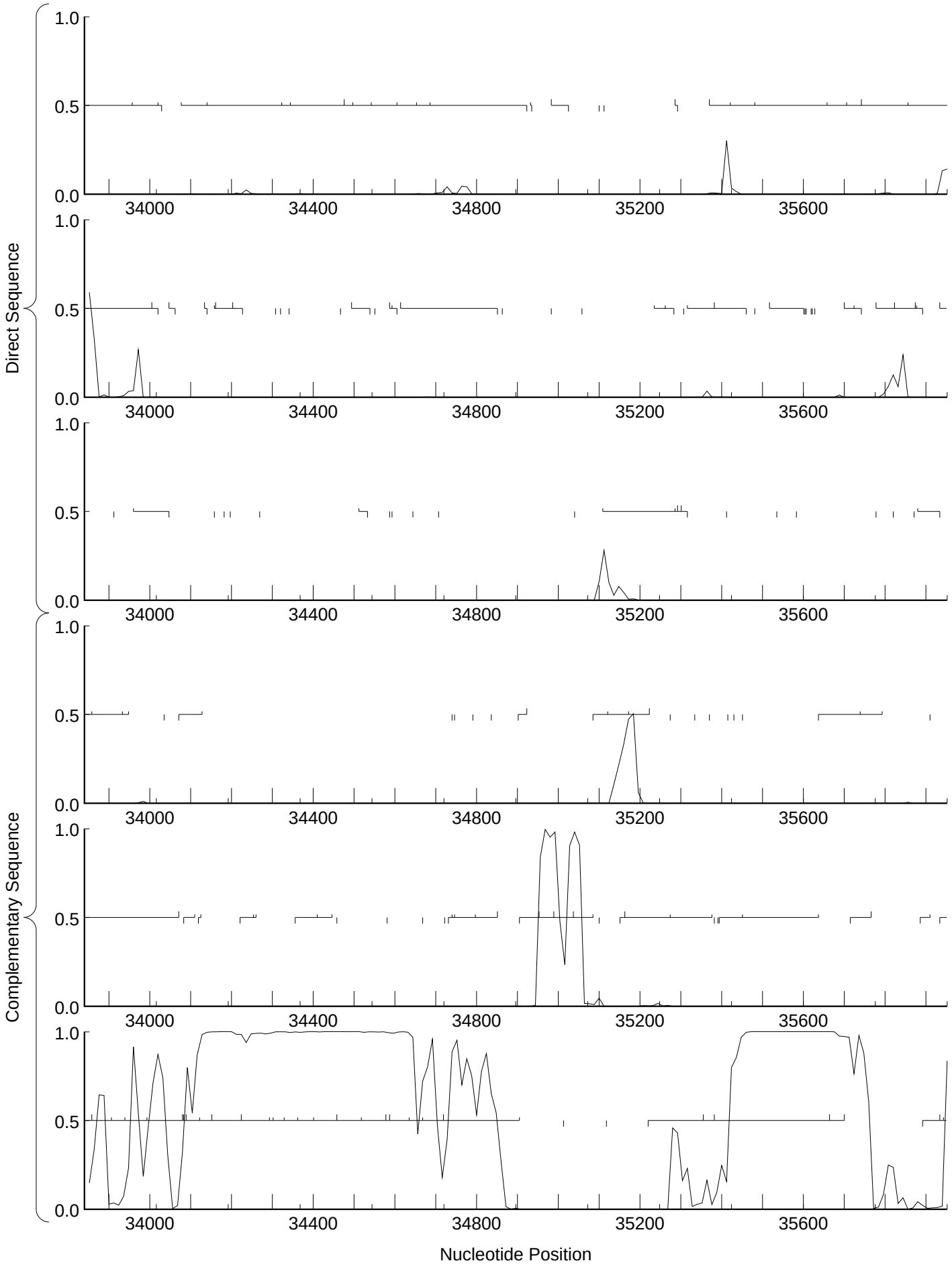
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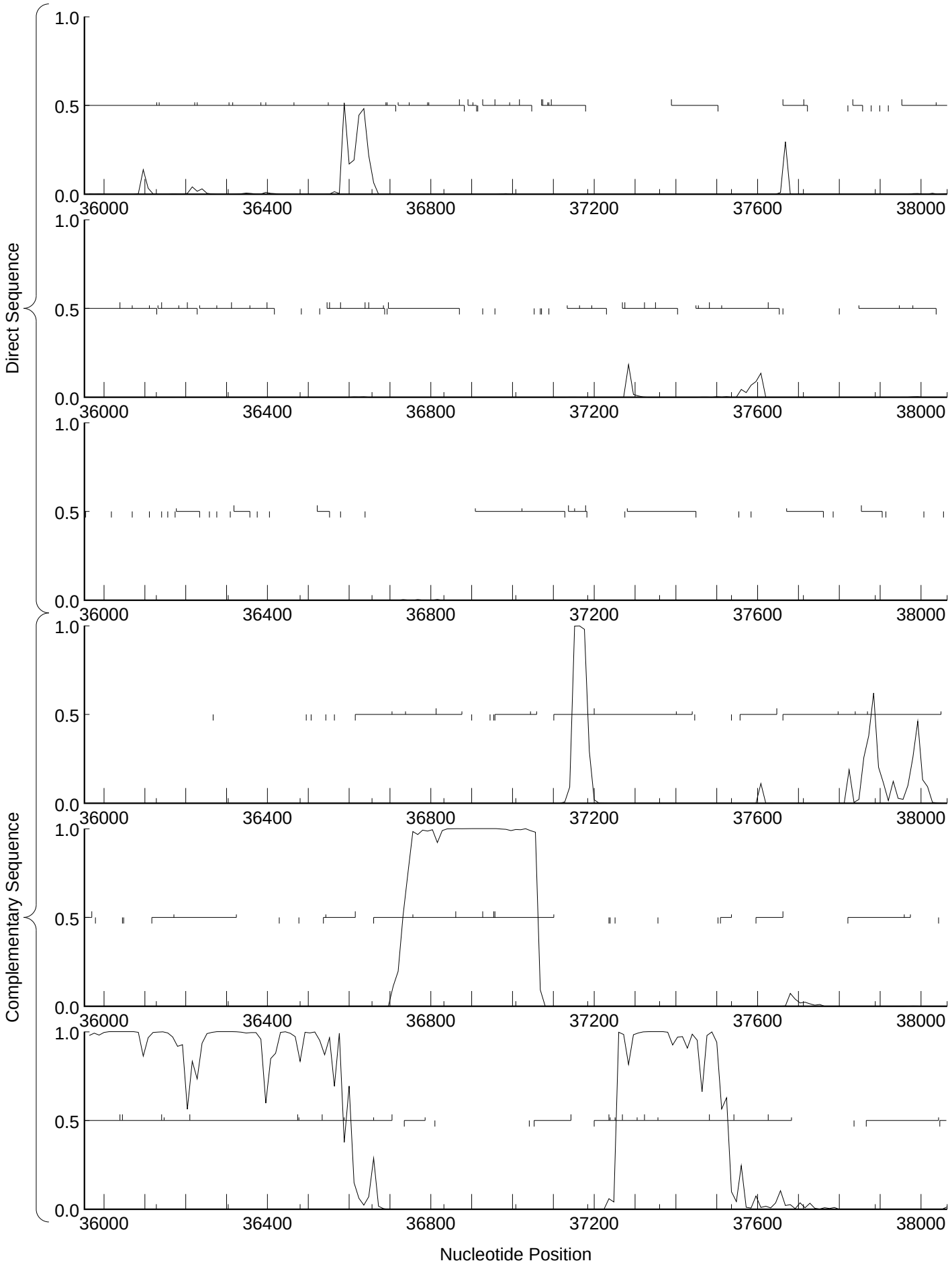
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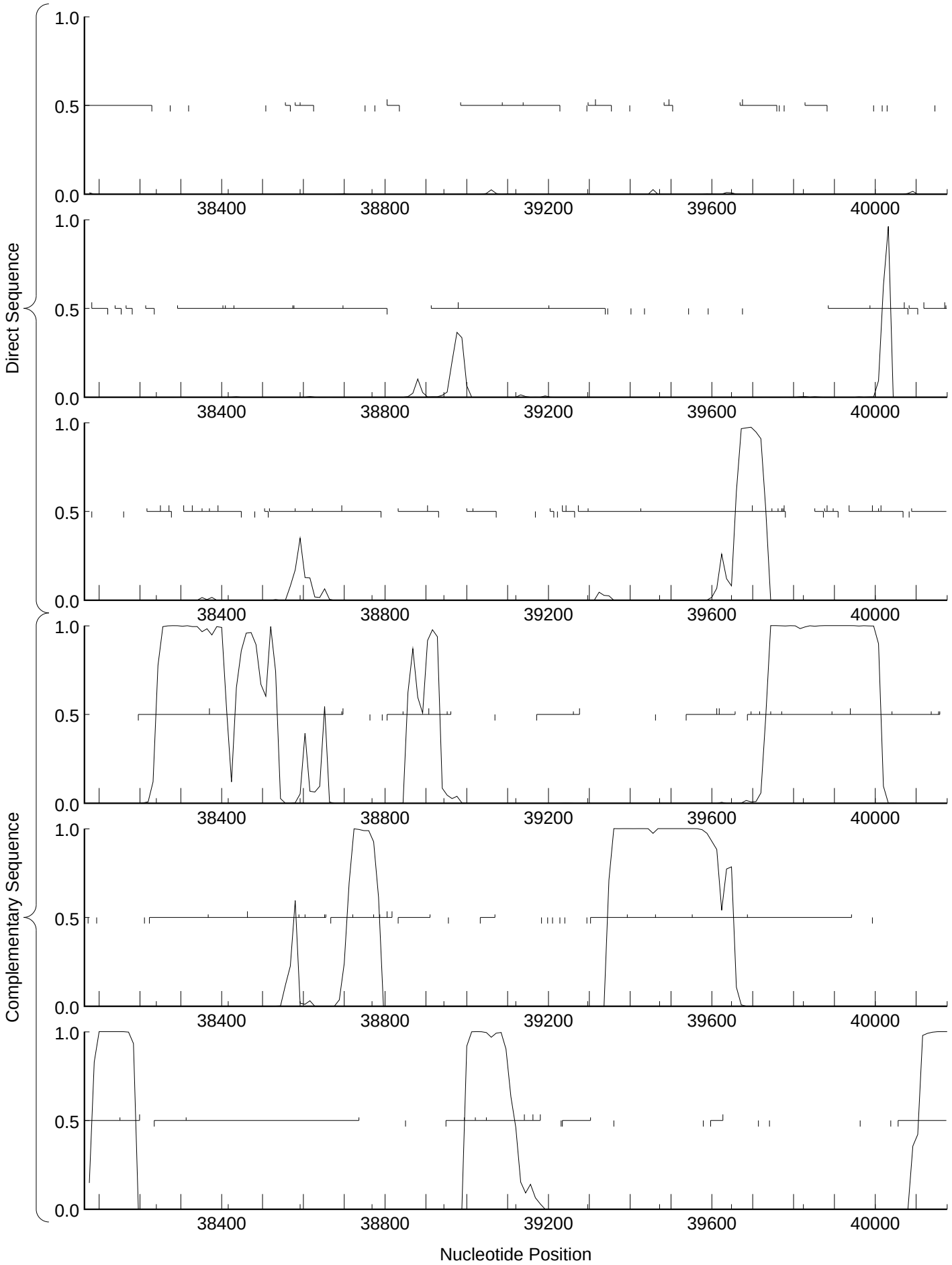
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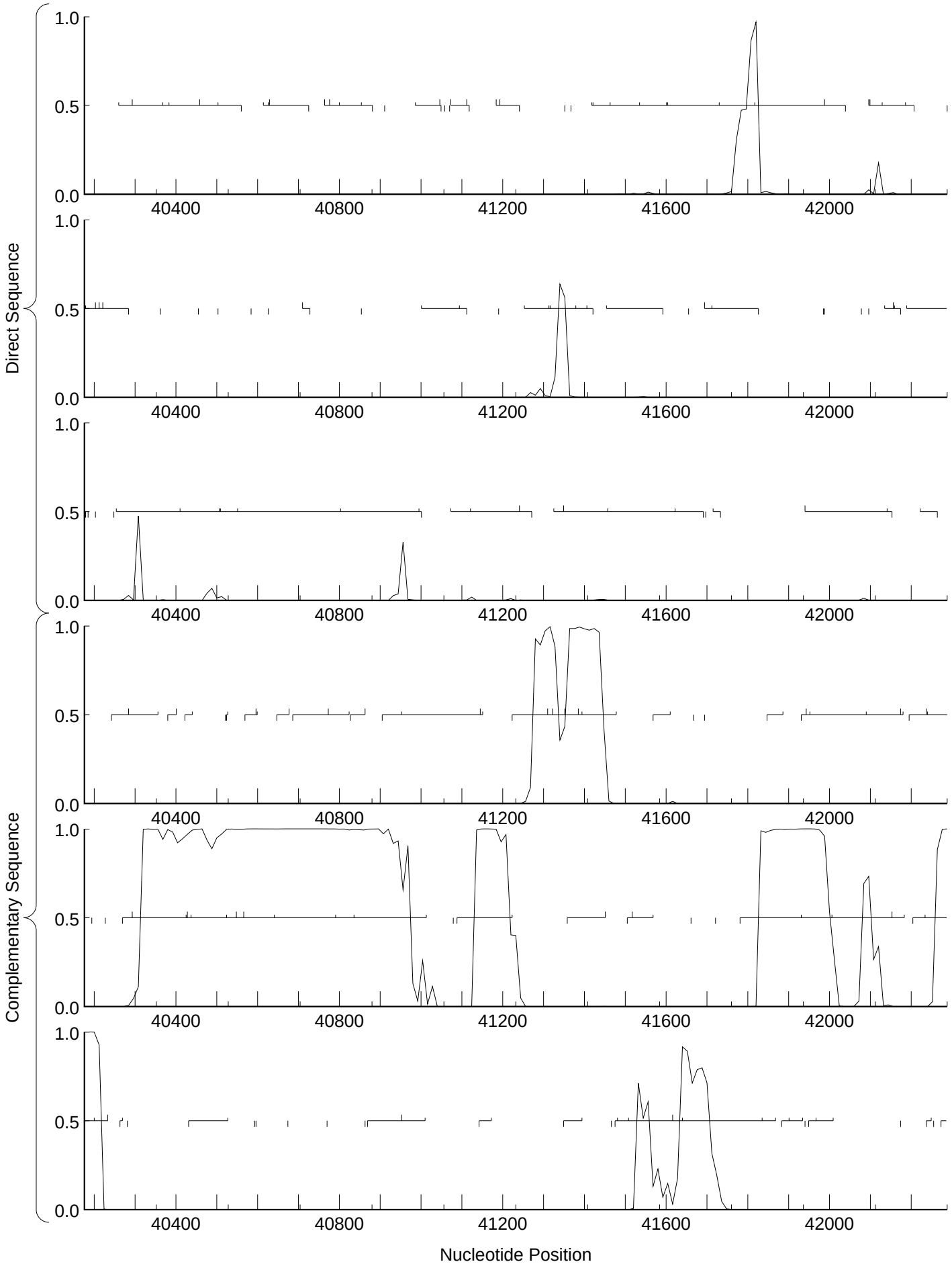
complete sequence, 52122 bp including 10-base 3’ overhang (CGGTCGGTAA), Cluster A6, Order 4, Window 96, Step 12, 19/26

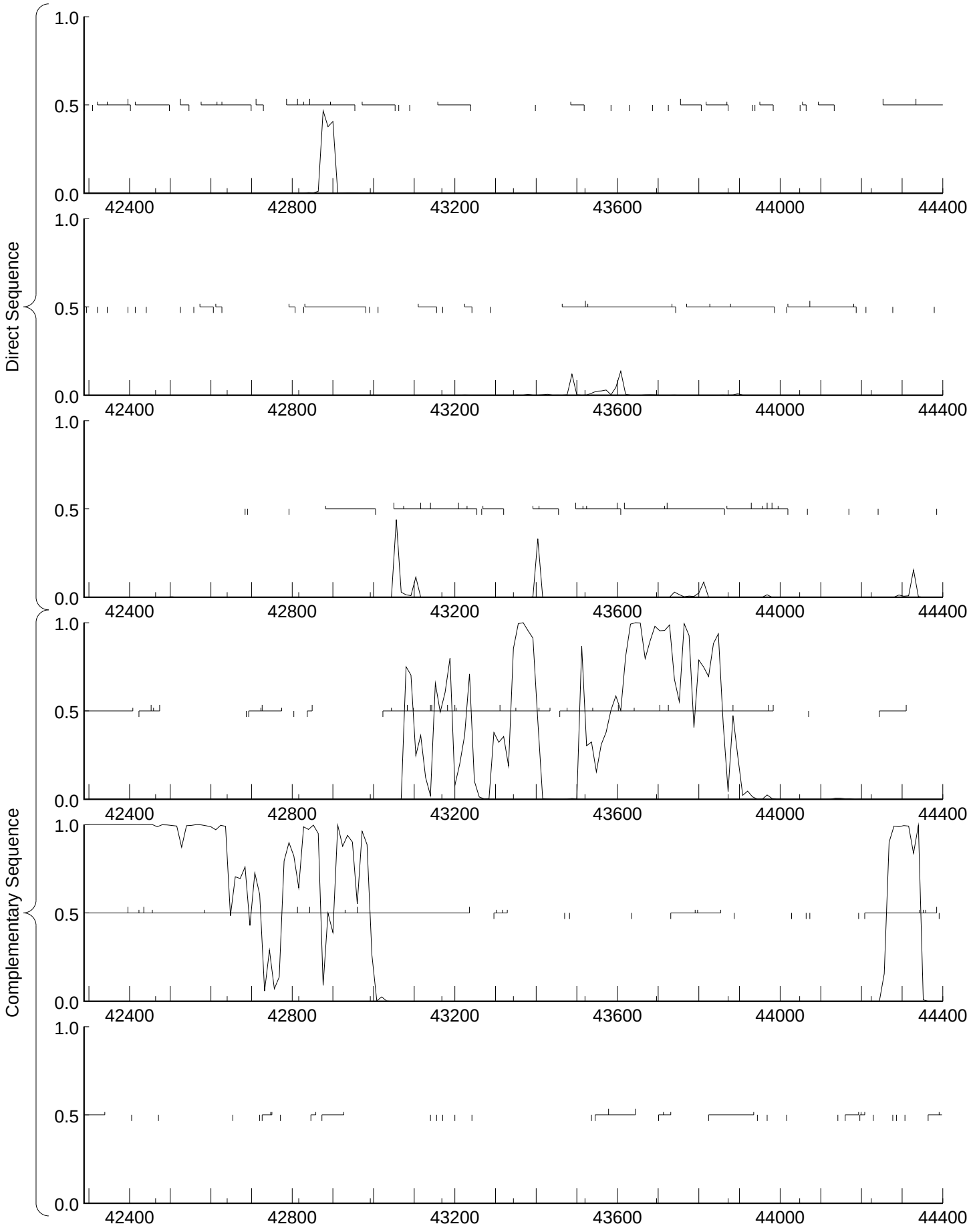


complete sequence, 52122 bp including 10-base 3’ overhang (CGGTCGGTAA), Cluster A6, Order 4, Window 96, Step 12, 20/26

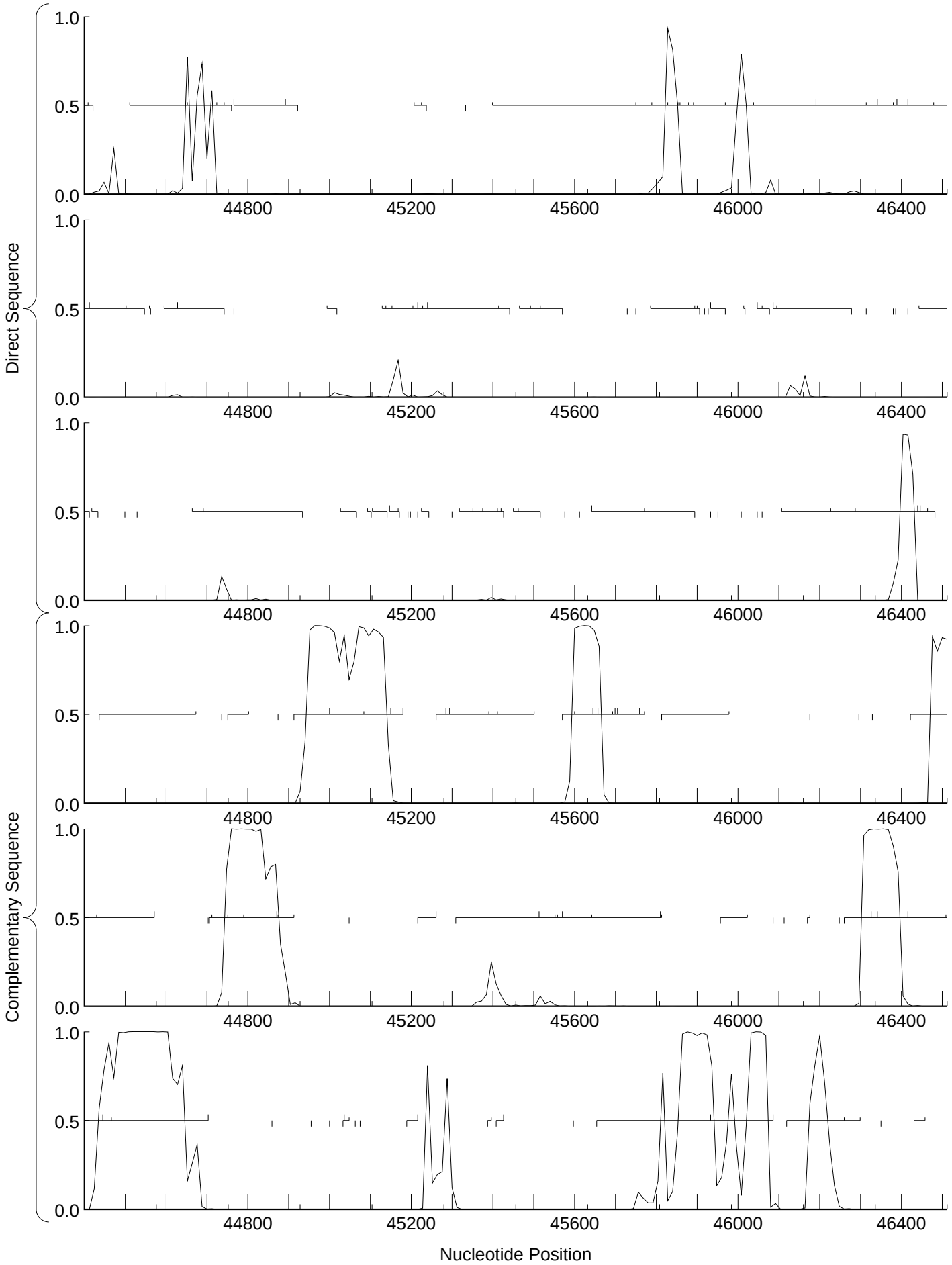


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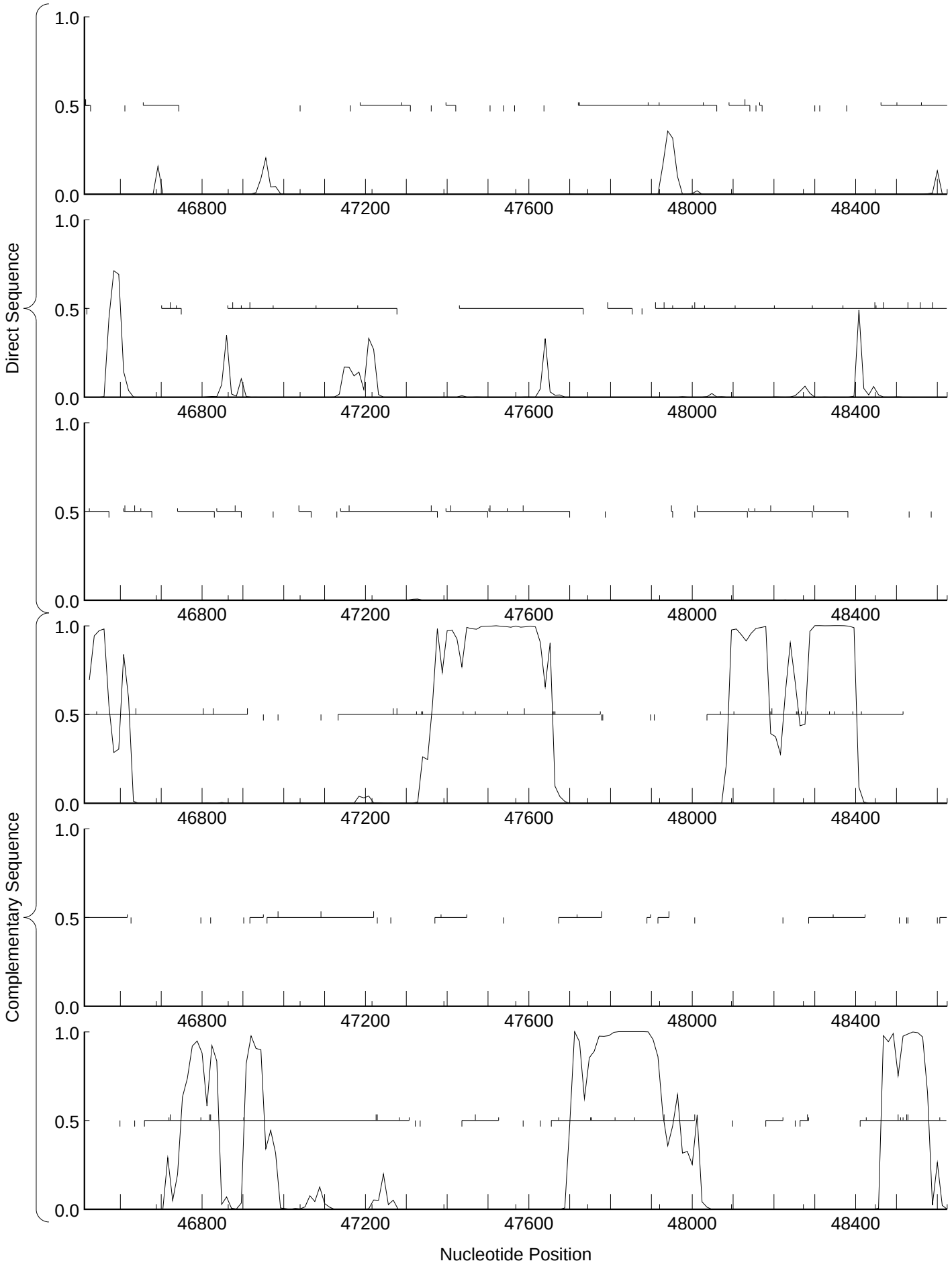



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Complementary Sequence
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0.0
42400
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Nucleotide Position

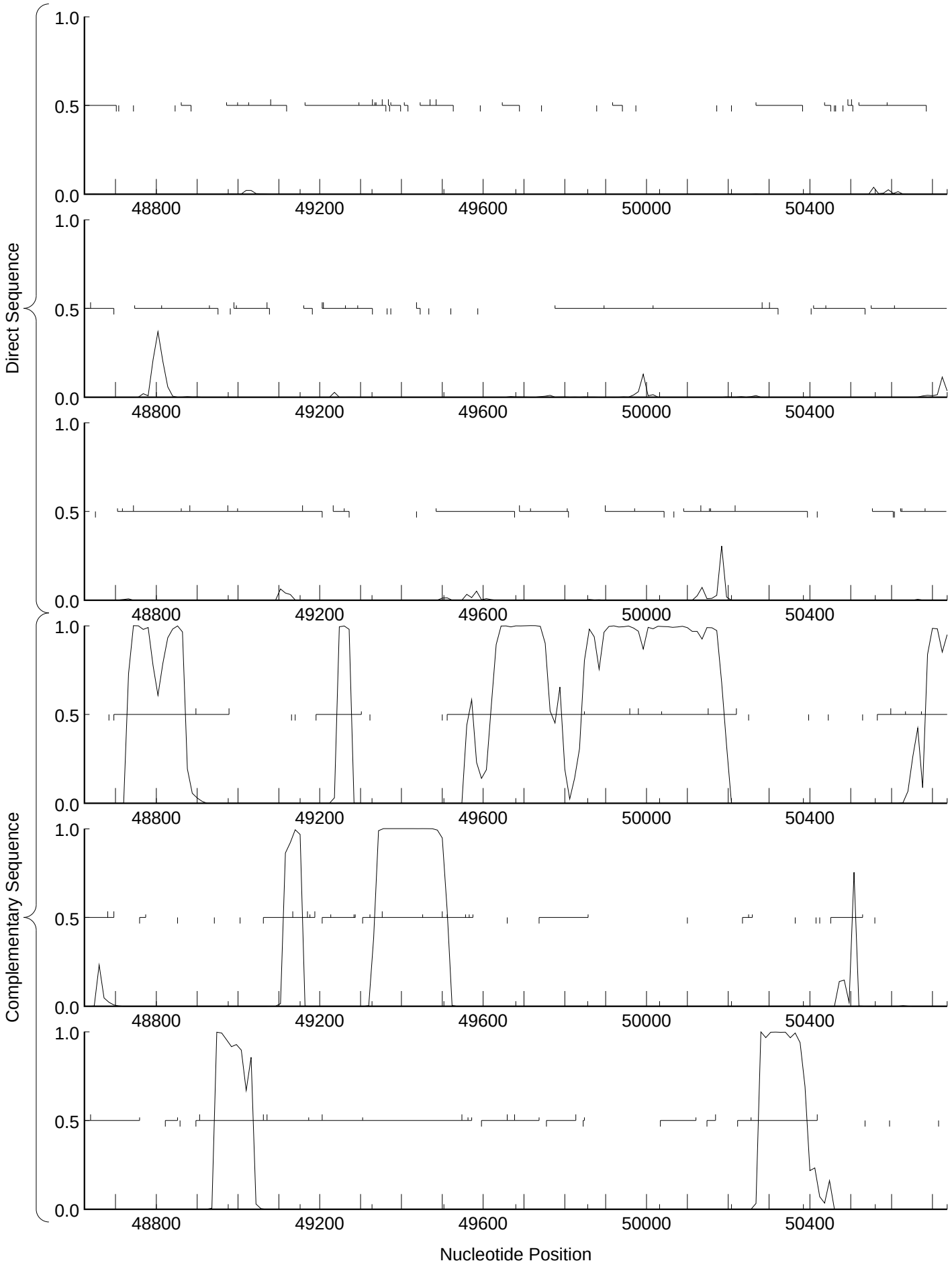
complete sequence, 52122 bp including 10-base 3’ overhang (CGGTCGGTAA), Cluster A6, Order 4, Window 96, Step 12, 23/26



complete sequence, 52122 bp including 10-base 3’ overhang (CGGTCGGTAA), Cluster A6, Order 4, Window 96, Step 12, 24/26



complete sequence, 52122 bp including 10-base 3’ overhang (CGGTCGGTAA), Cluster A6, Order 4, Window 96, Step 12, 25/26



complete sequence, 52122 bp including 10-base 3’ overhang (CGGTCGGTAA), Cluster A6, Order 4, Window 96, Step 12, 26/26

