GeneMark

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

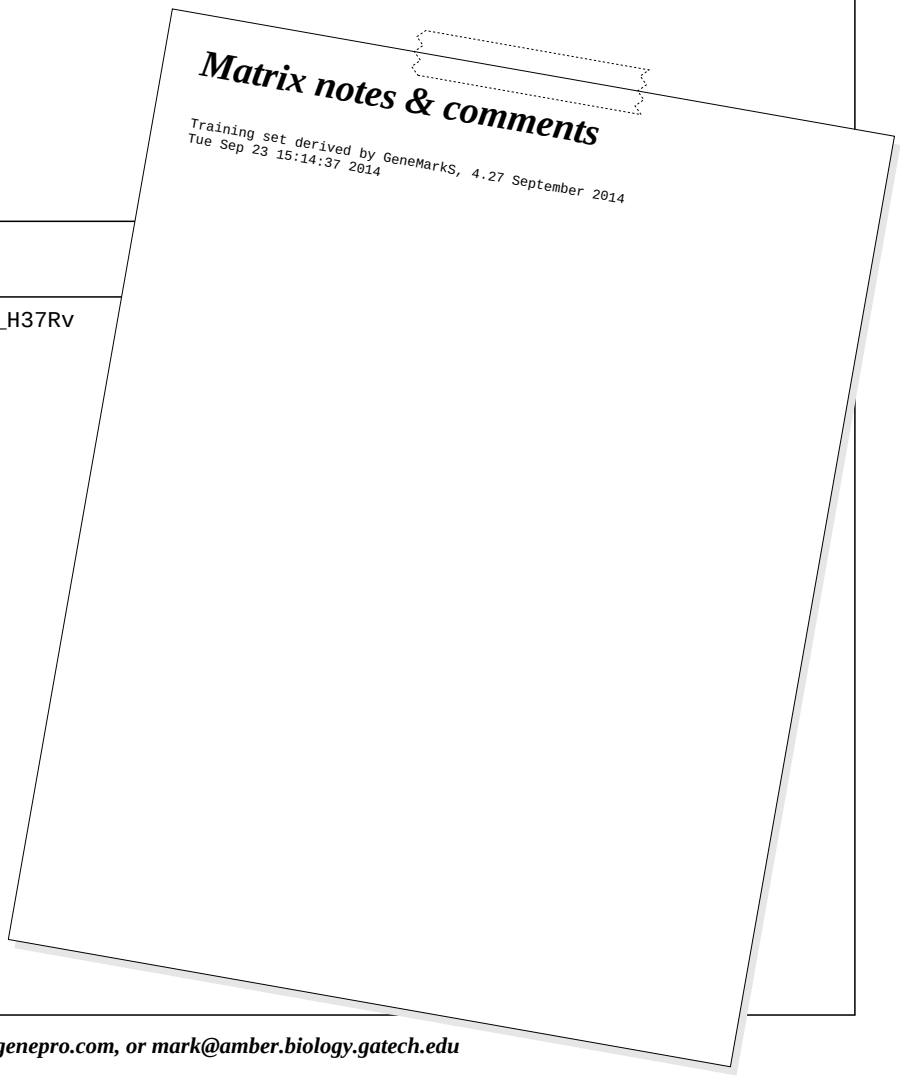
PROGRAM INFORMATION

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Sequence         :  Mycobacterium phage Refuge complete sequence, 53594 bp including 10-base 3' overhang (CGGGA
Analysis Date    :  3/29/24 at 11:08:04
Pages            :  27
Sequence Length  :  53594 bp
GC Content       :   63.55%

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

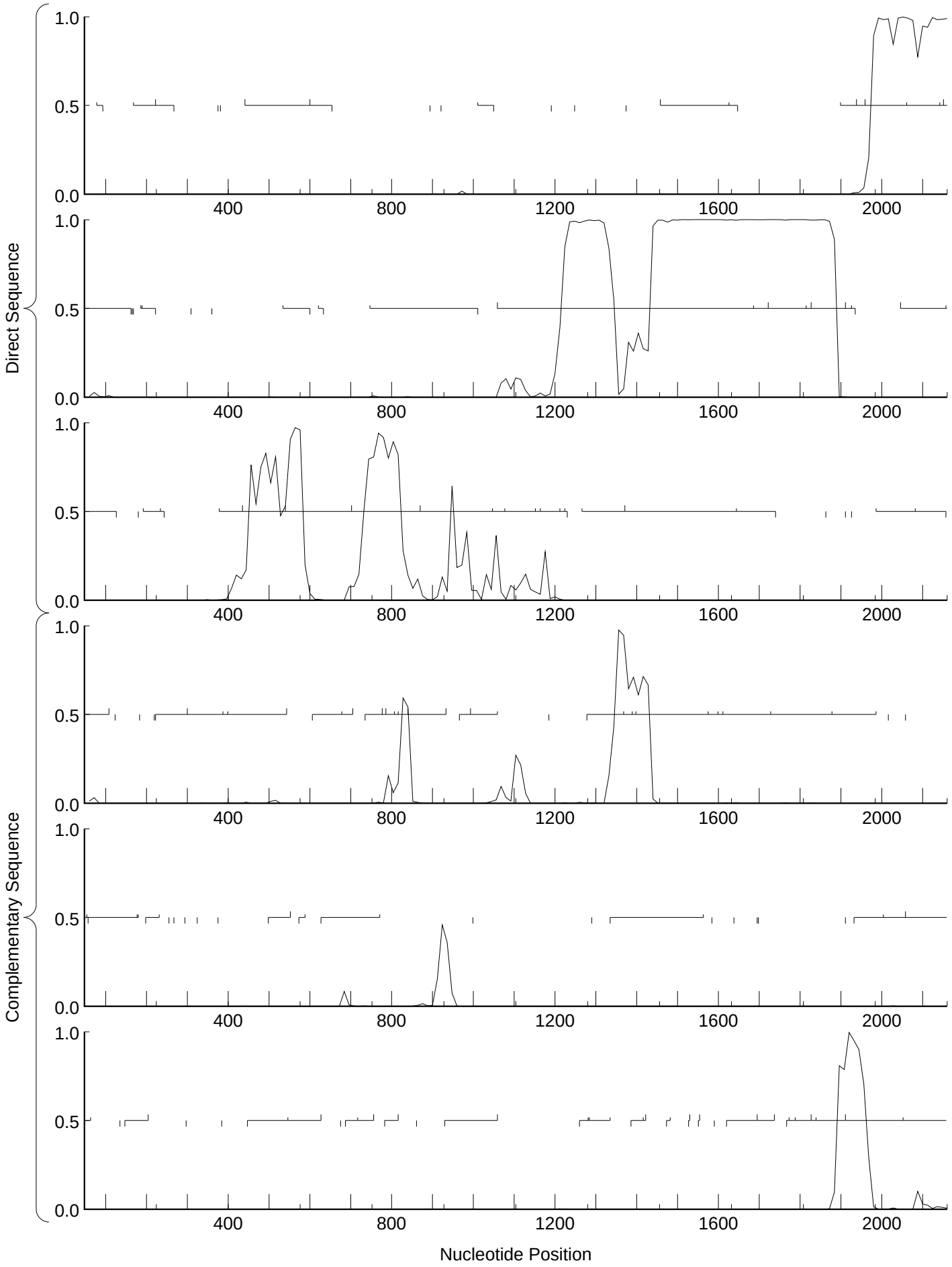
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Matrix     :  Mycobacterium_tuberculosis_H37Rv
Author     :  -

Order      :  4
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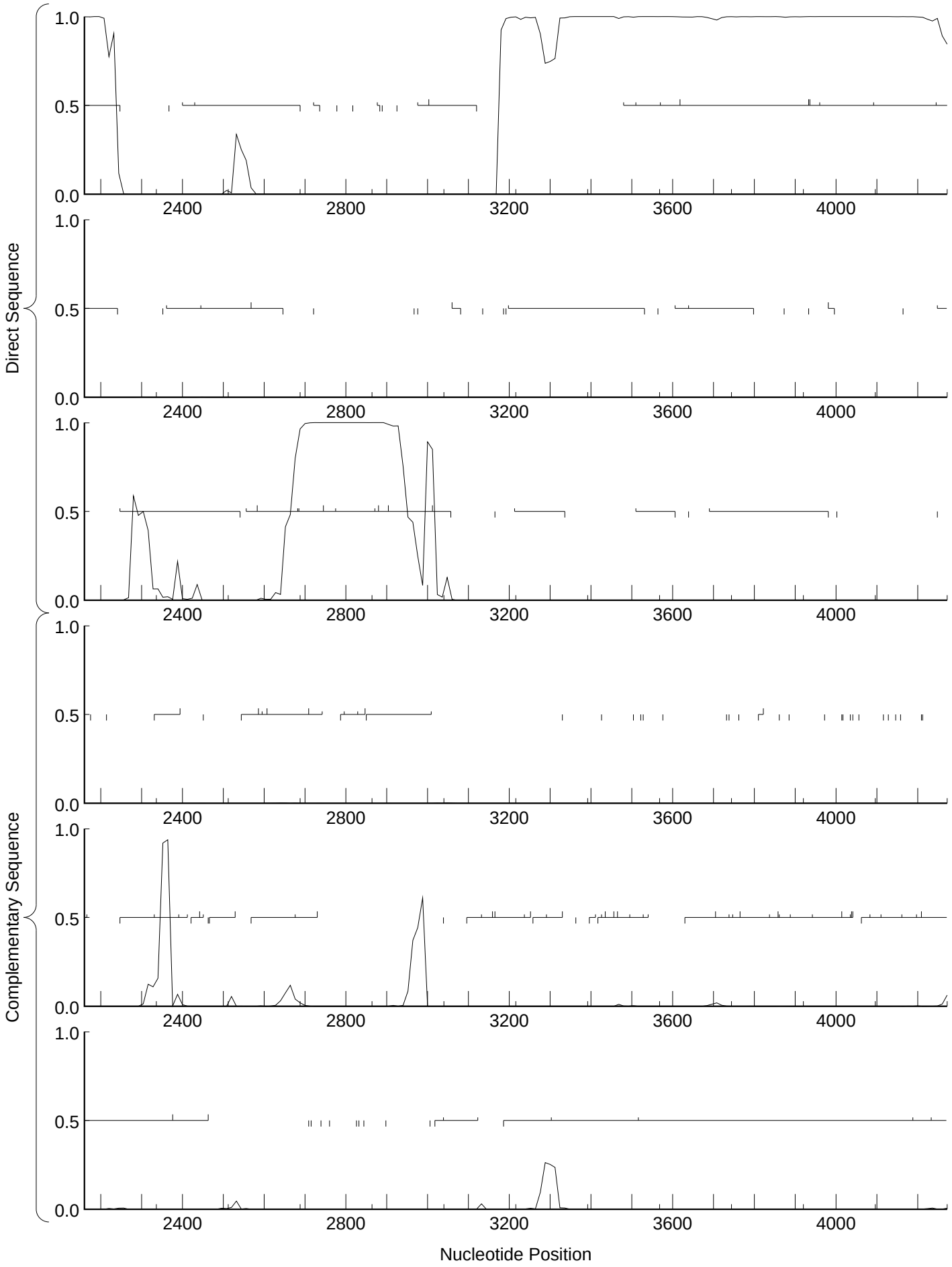

```
  Send questions / comments to:
      Dr. M. Borodovsky
      Georgia Institute of Technology
      School of Biology
      Atlanta, GA  30332-0230
```


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

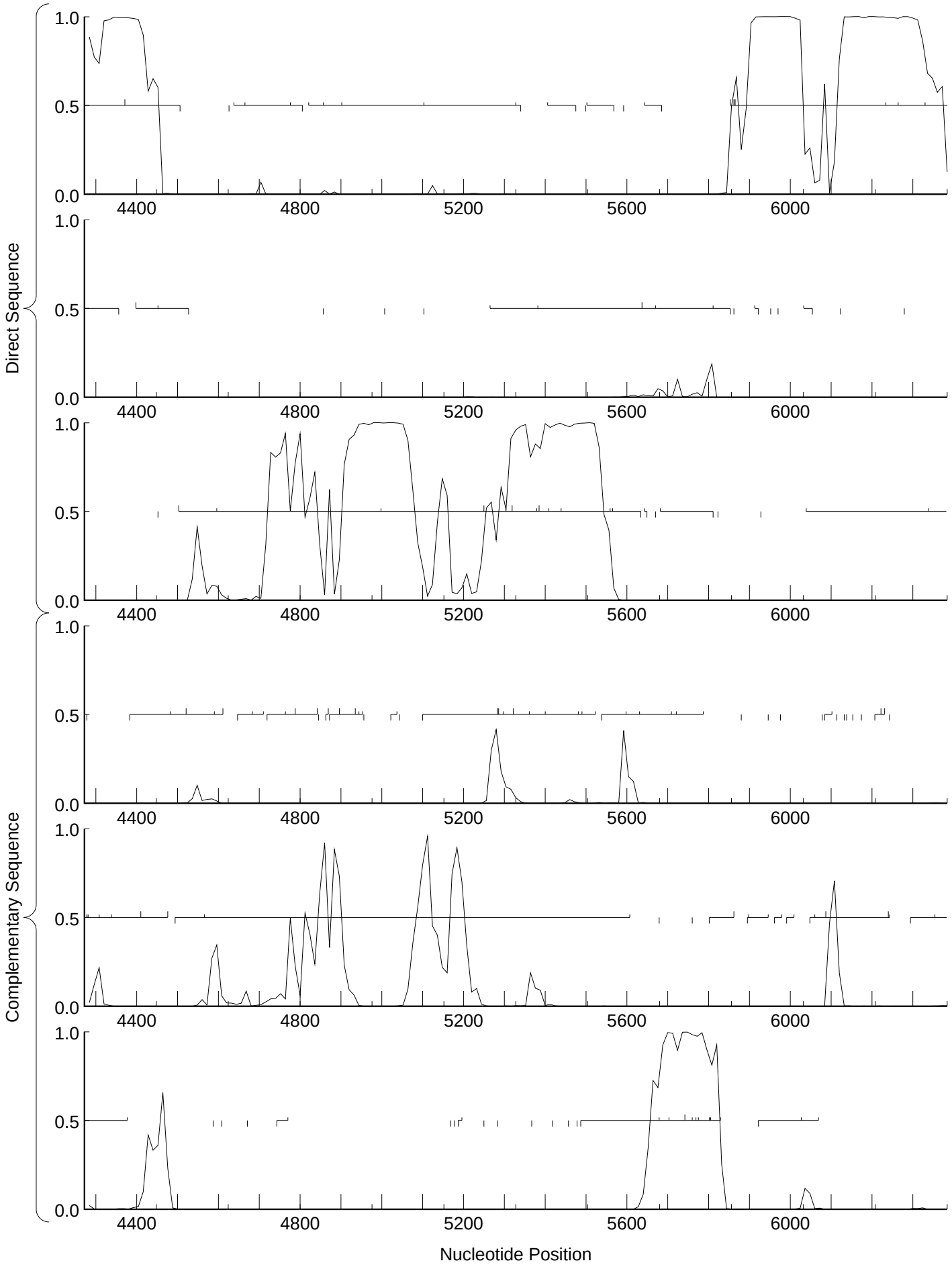
complete sequence, 53594 bp including 10-base 3’ overhang (CGGGACGTAA), Cluster A12, Order 4, Window 96, Step 12, 2/27



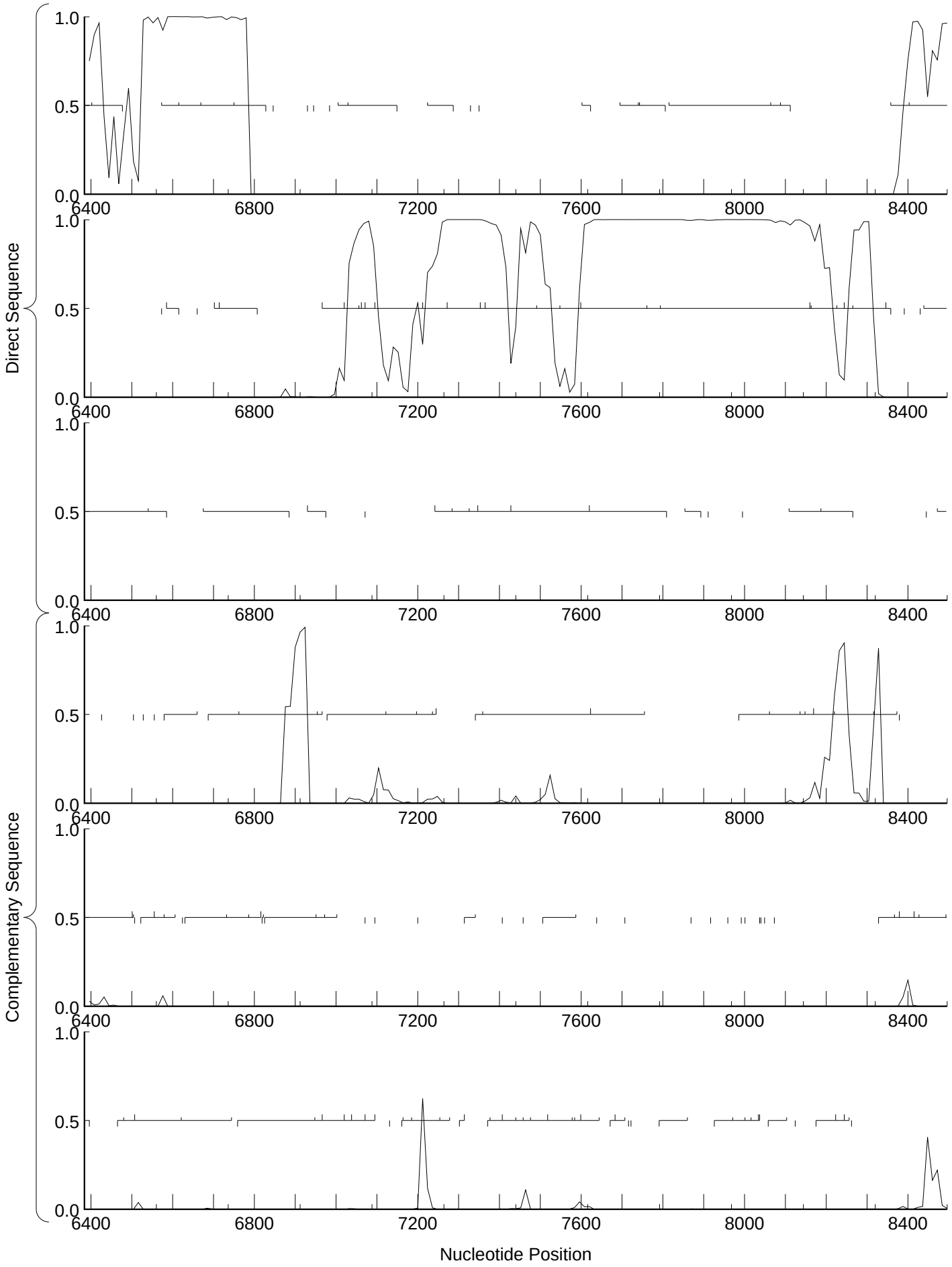
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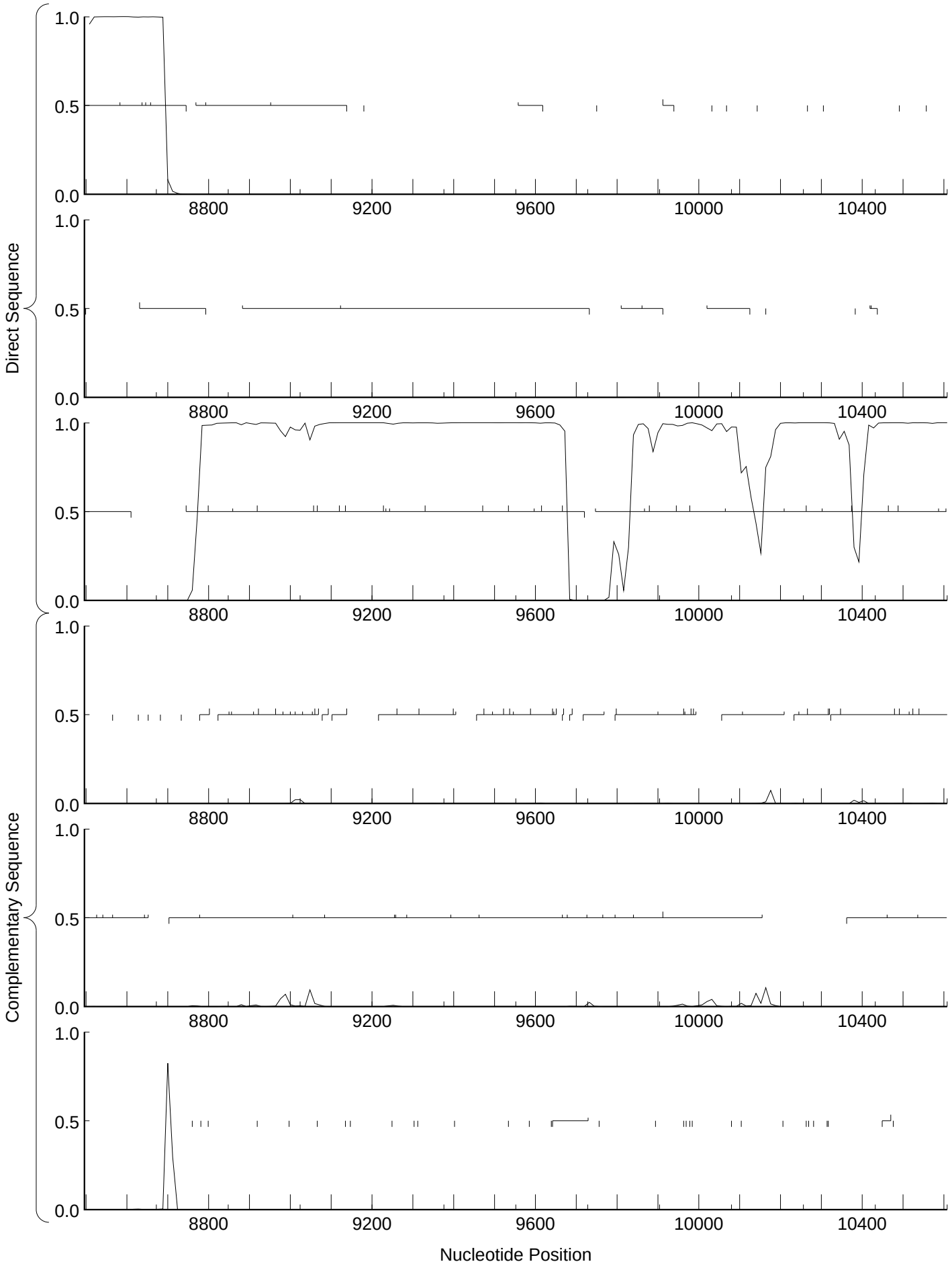
complete sequence, 53594 bp including 10-base 3’ overhang (CGGGACGTAA), Cluster A12, Order 4, Window 96, Step 12, 4/27



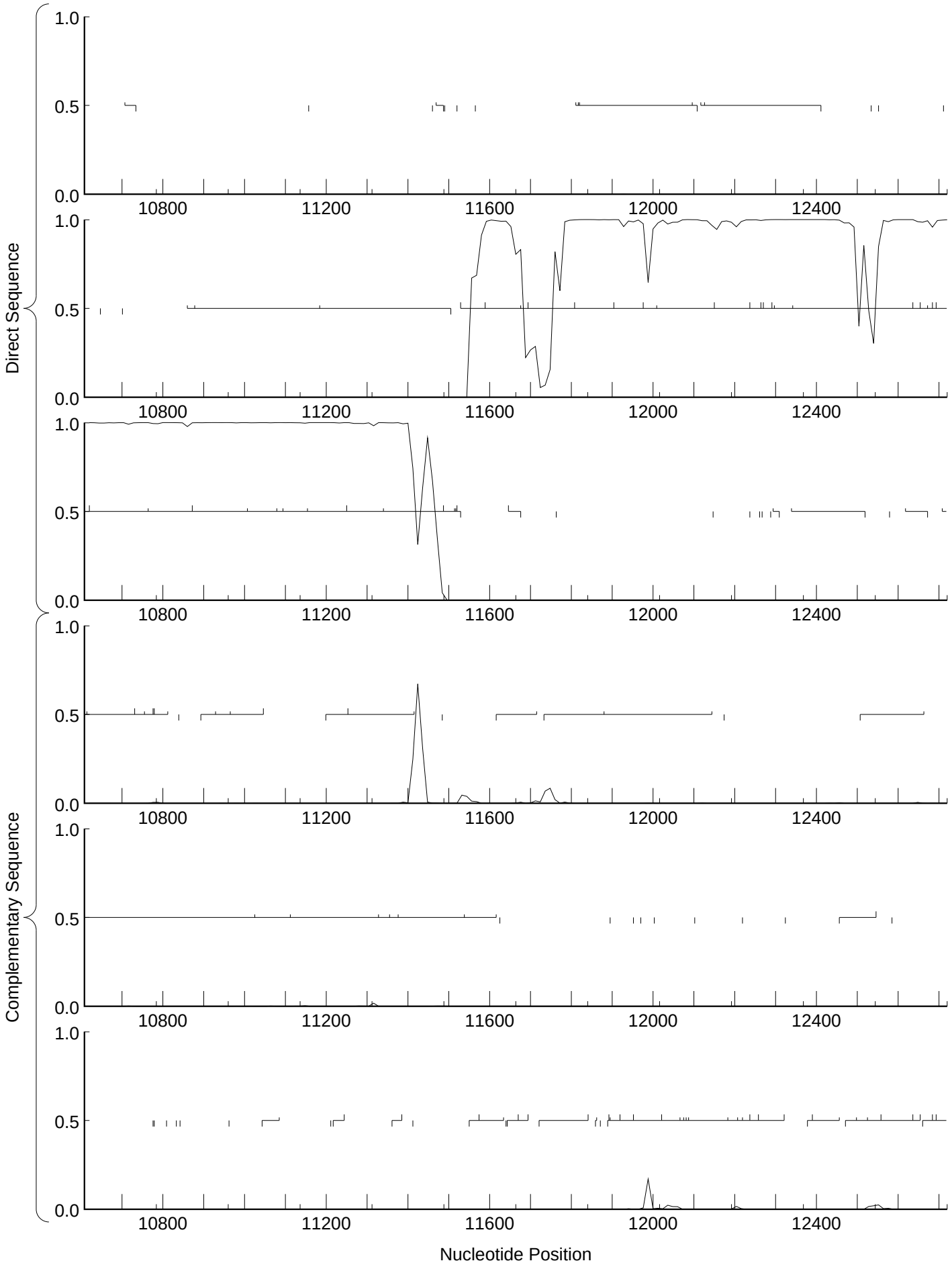
complete sequence, 53594 bp including 10-base 3’ overhang (CGGGACGTAA), Cluster A12, Order 4, Window 96, Step 12, 5/27



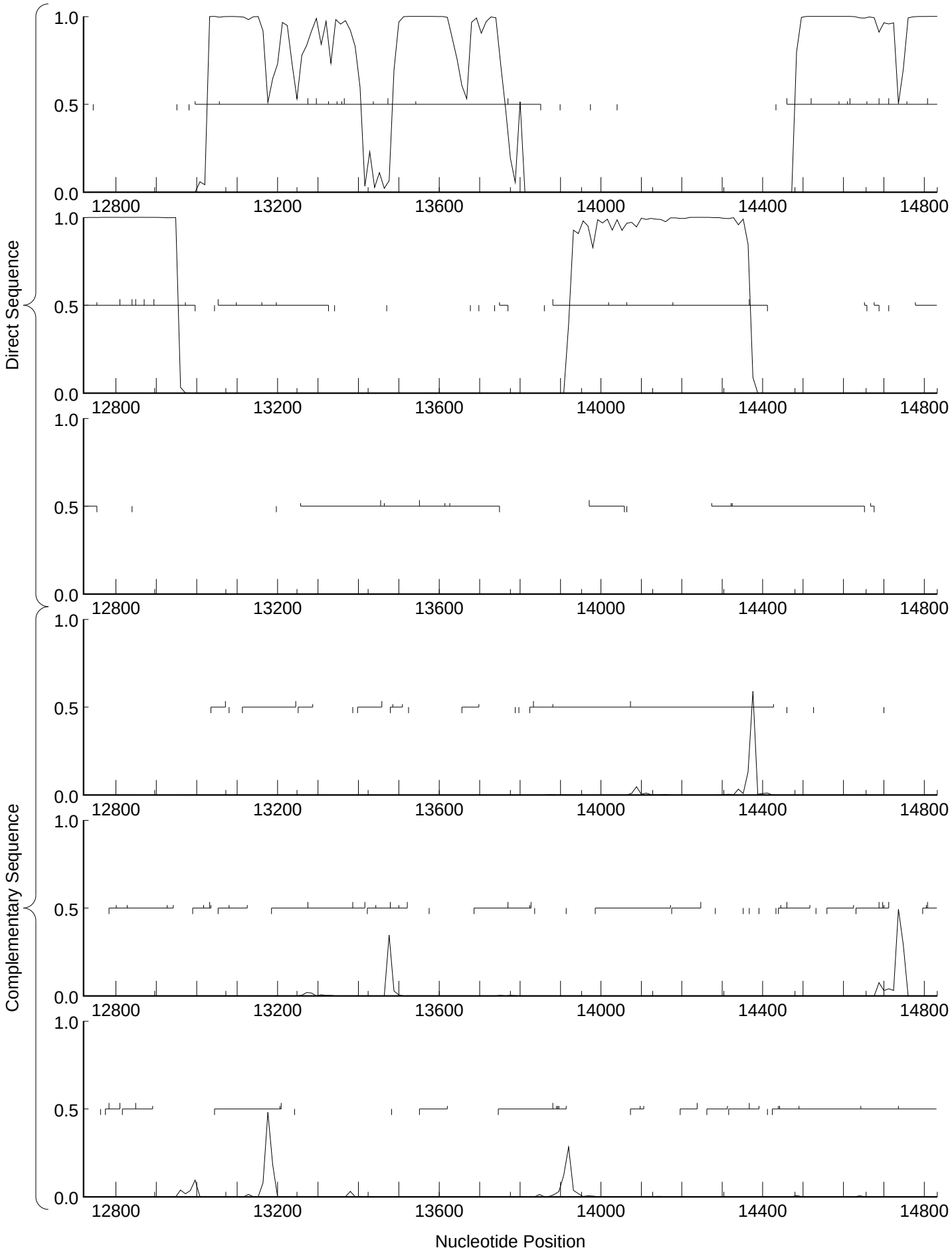
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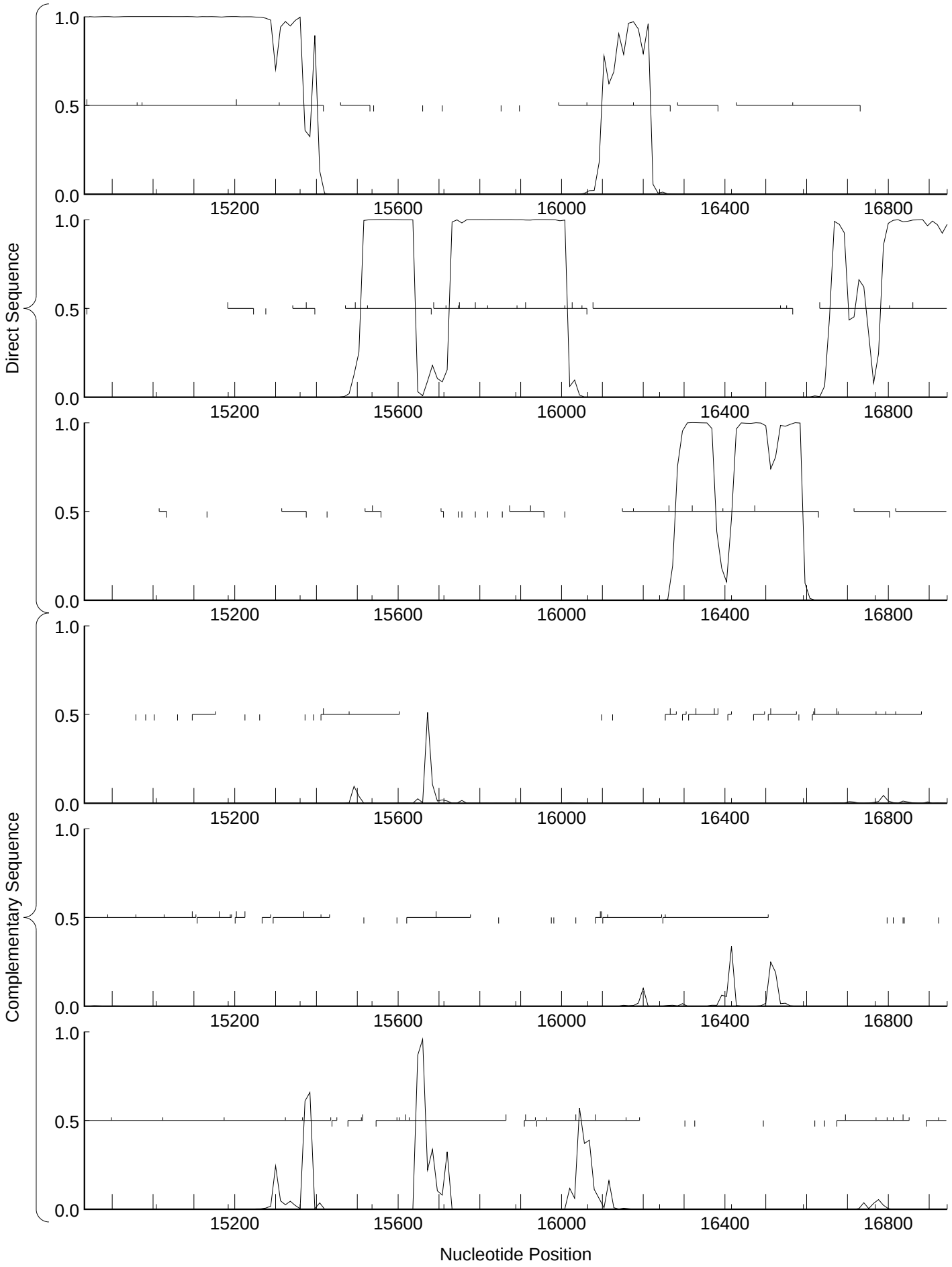
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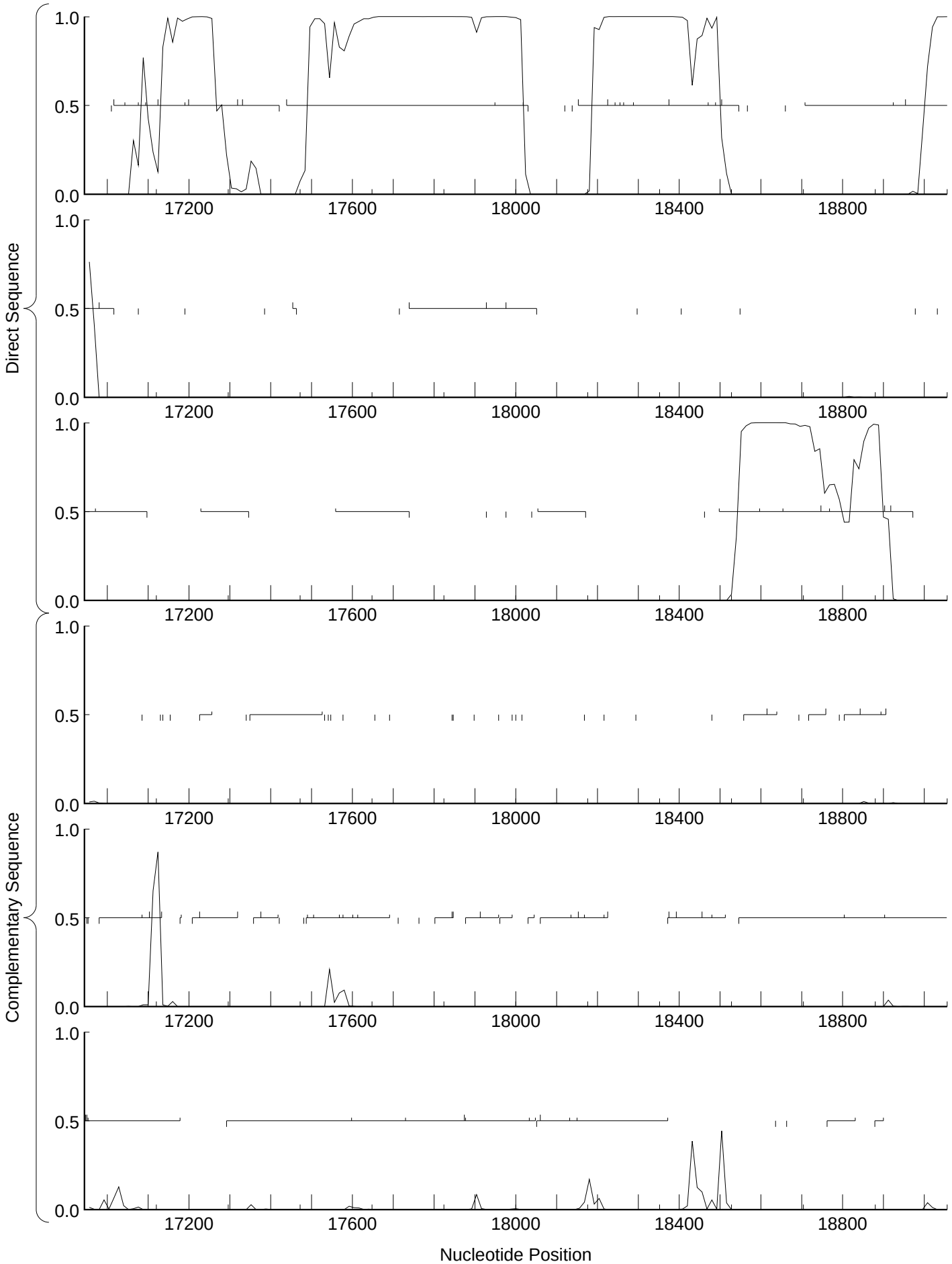
complete sequence, 53594 bp including 10-base 3’ overhang (CGGGACGTAA), Cluster A12, Order 4, Window 96, Step 12, 8/27



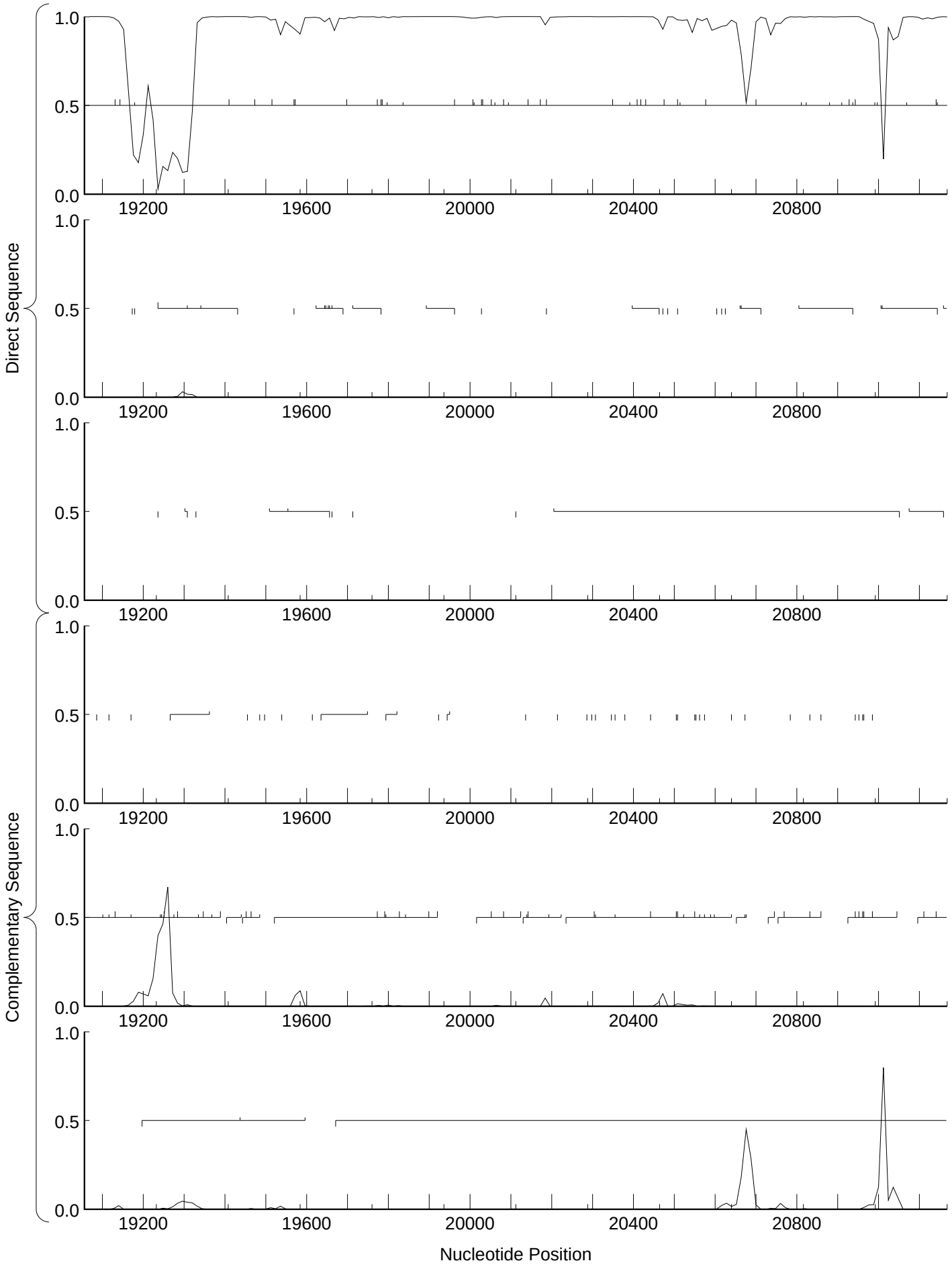
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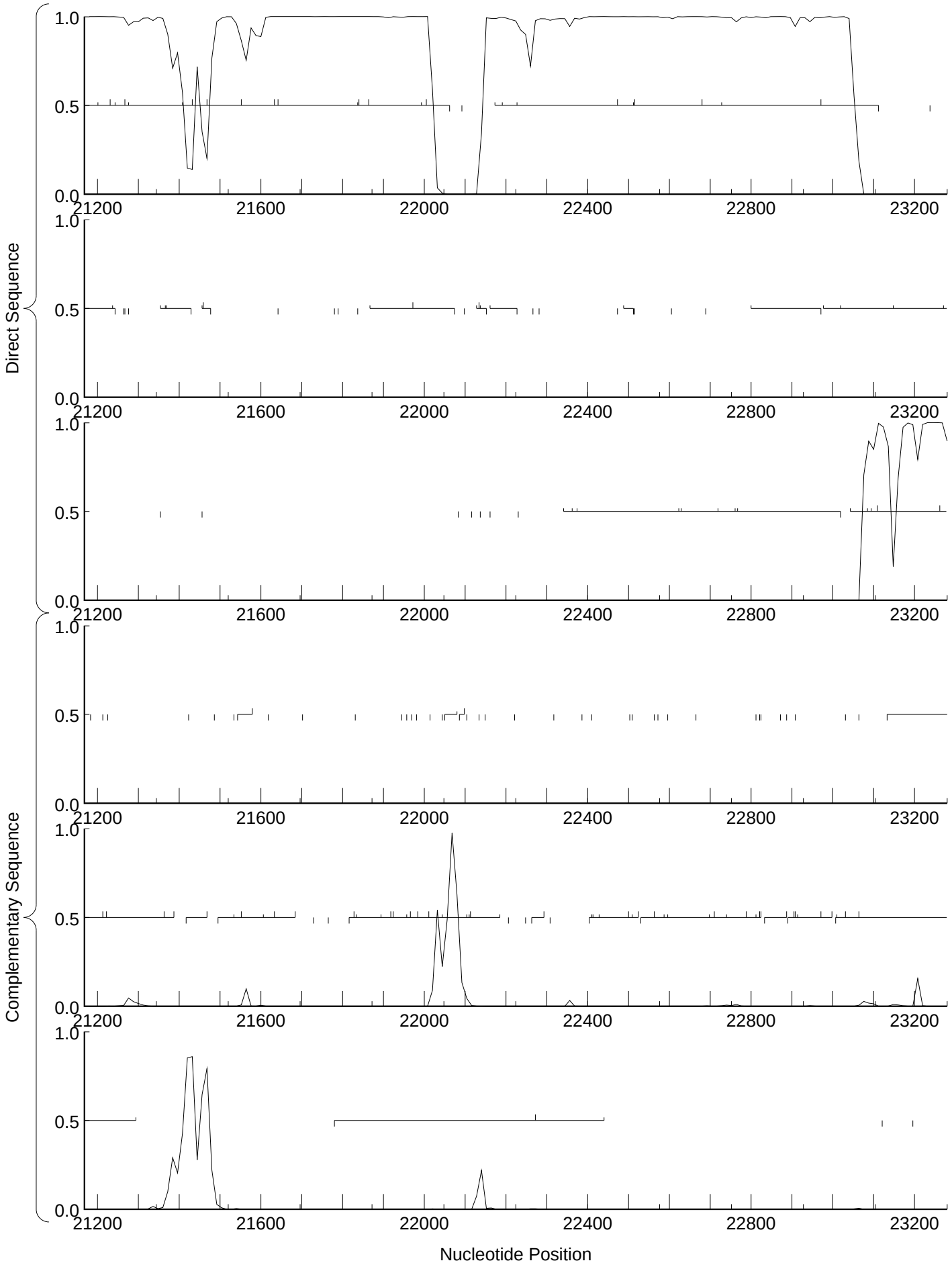
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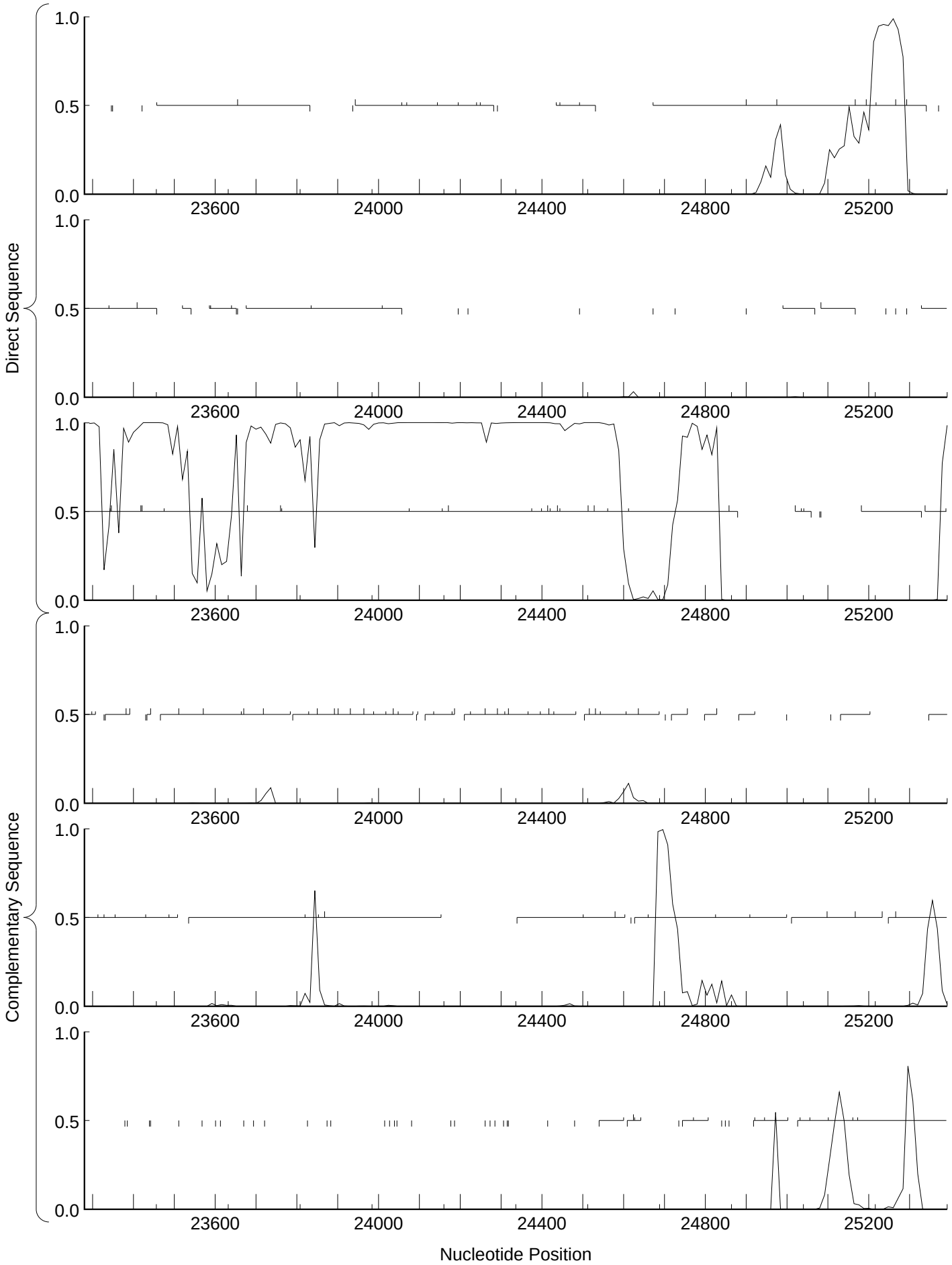
complete sequence, 53594 bp including 10-base 3' overhang (CGGGACGTAA), Cluster A12, Order 4, Window 96, Step 12, 11/27



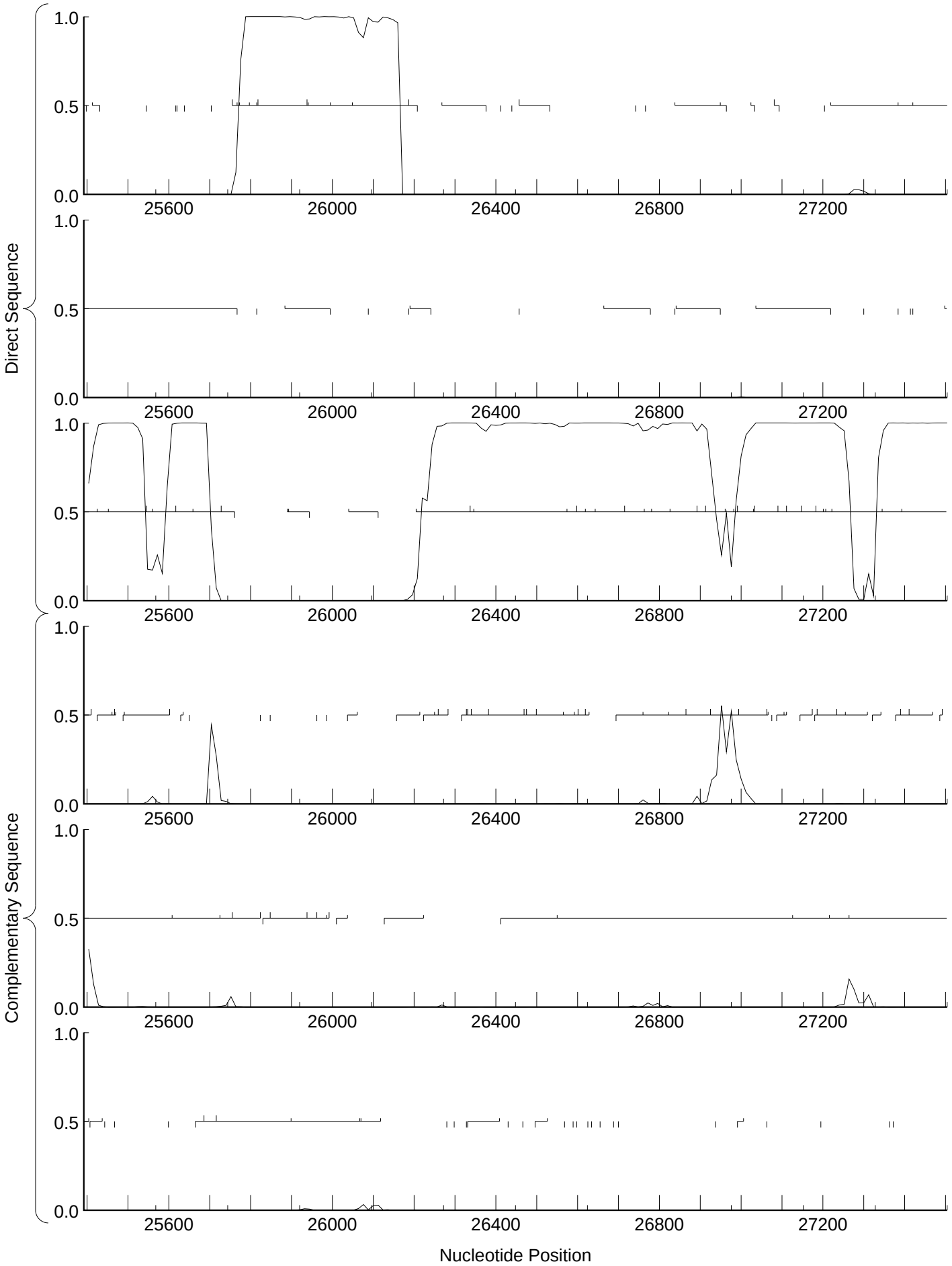
complete sequence, 53594 bp including 10-base 3’ overhang (CGGGACGTAA), Cluster A12, Order 4, Window 96, Step 12, 12/27



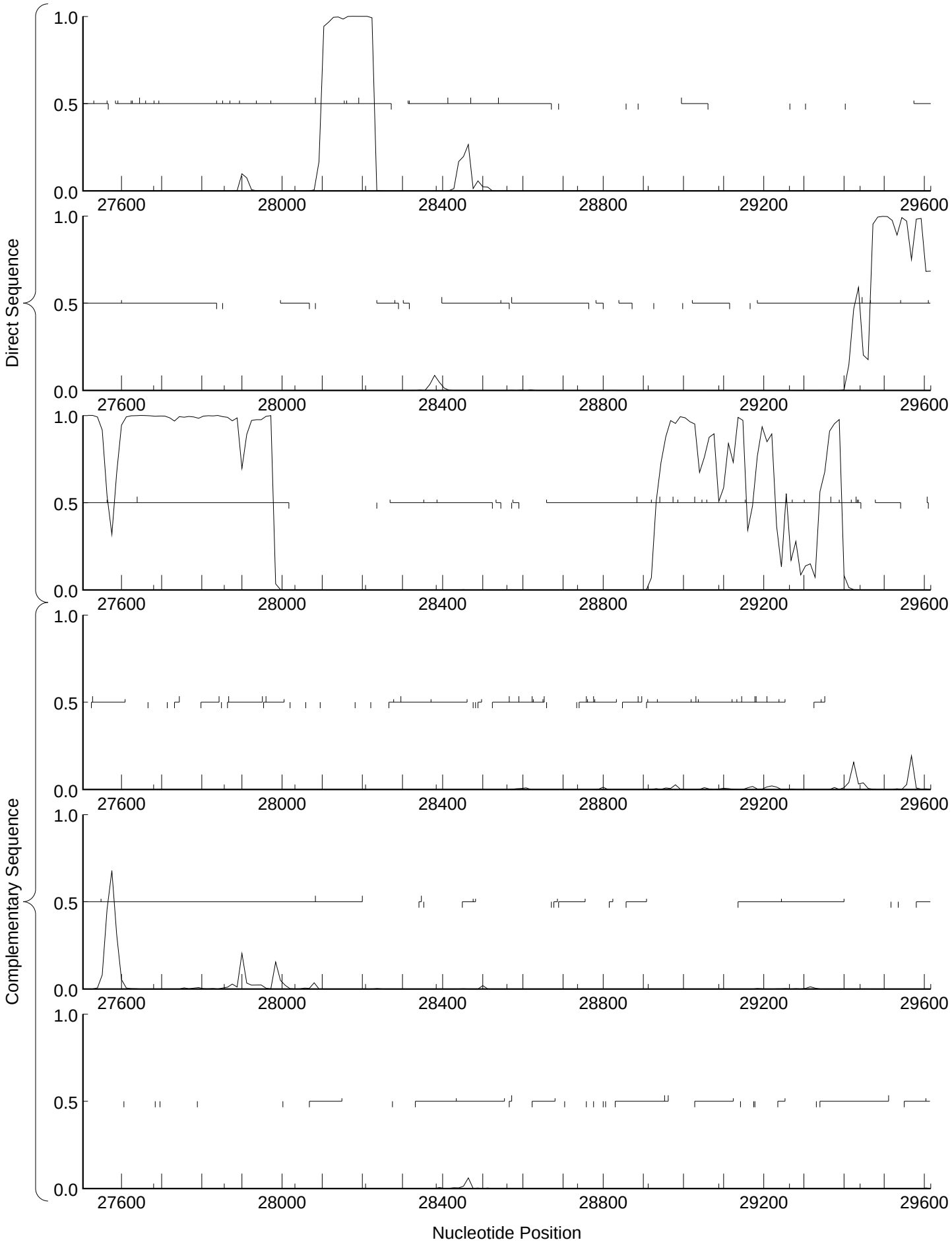
complete sequence, 53594 bp including 10-base 3’ overhang (CGGGACGTAA), Cluster A12, Order 4, Window 96, Step 12, 13/27



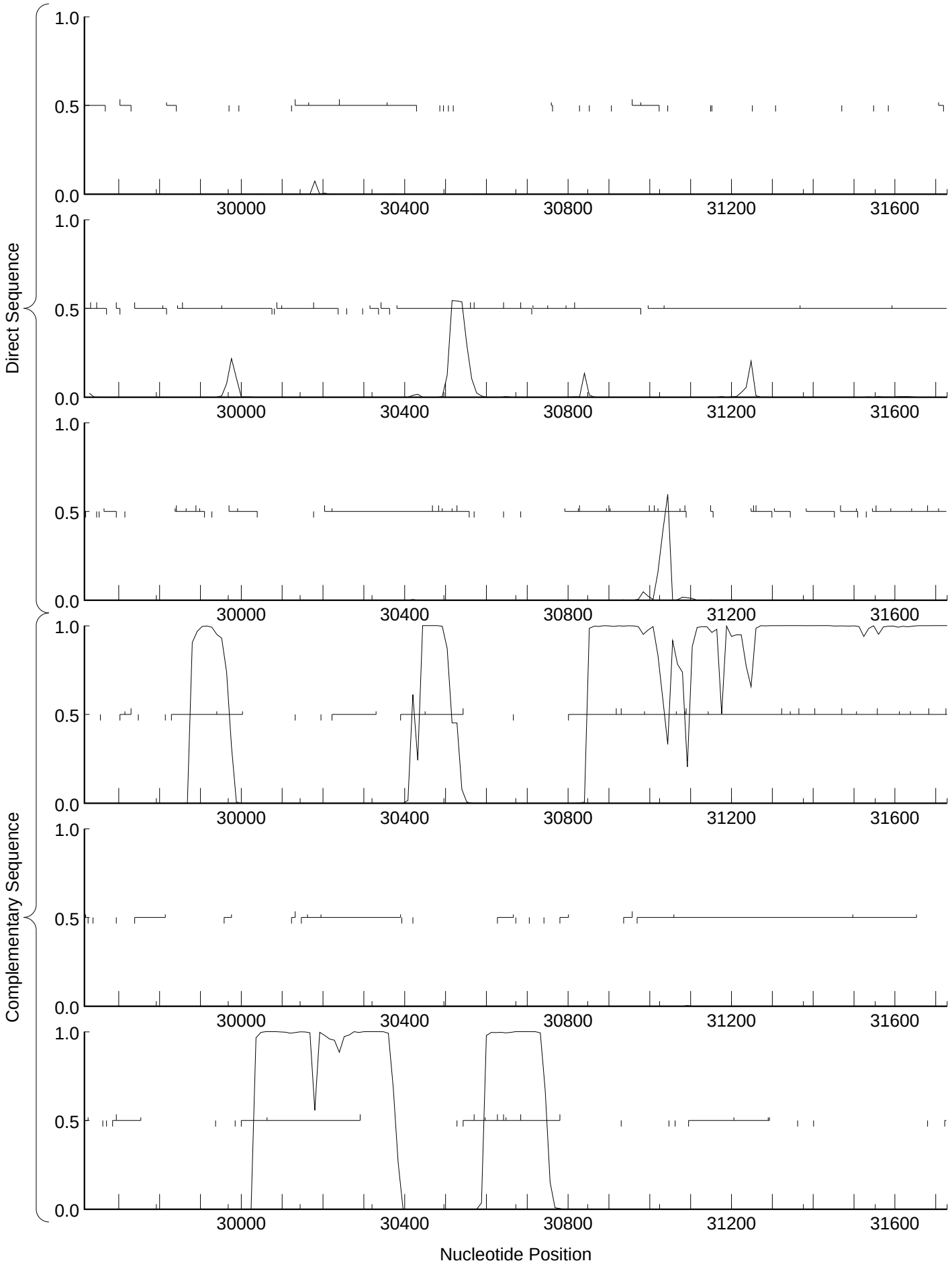
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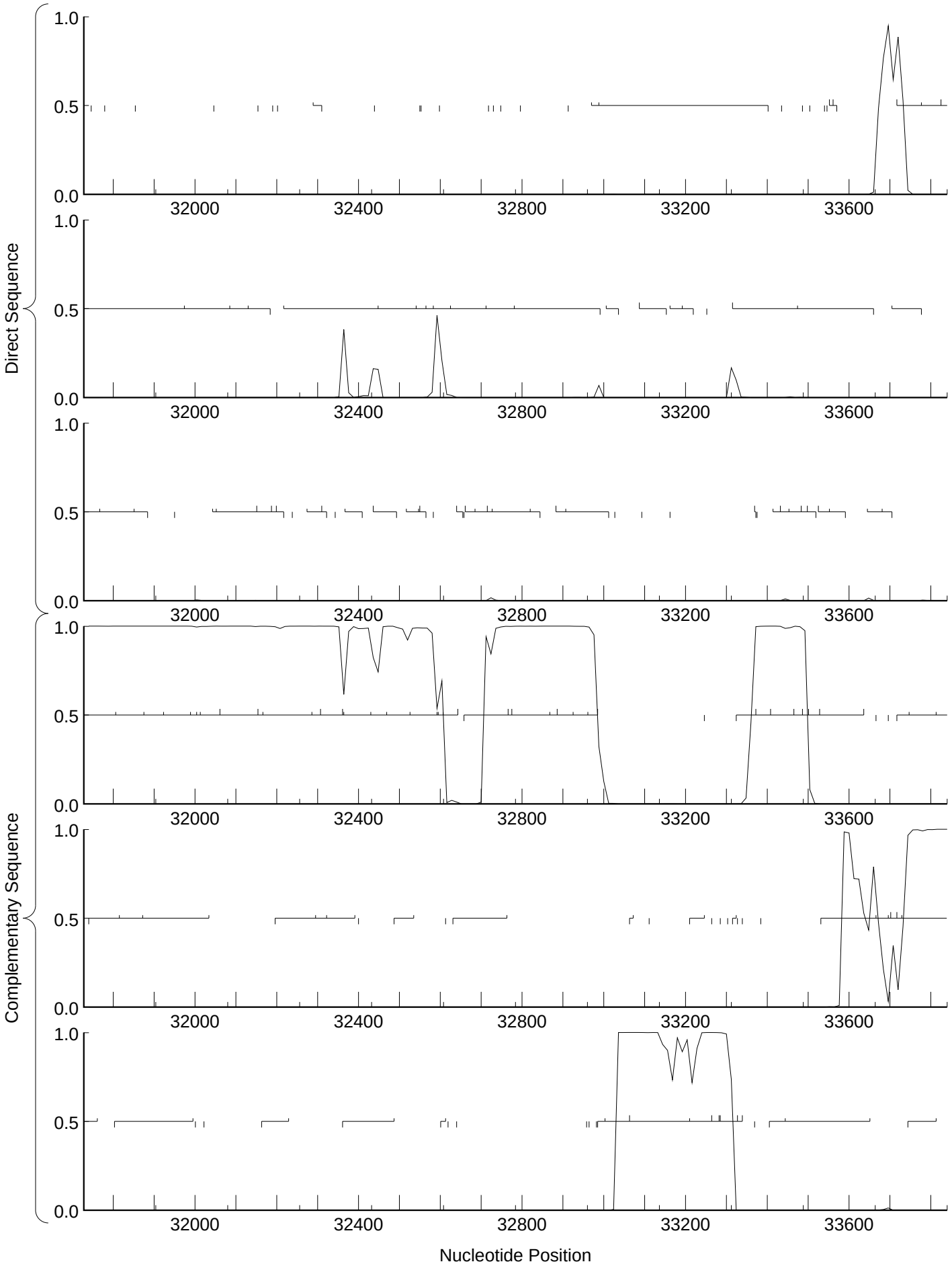
complete sequence, 53594 bp including 10-base 3’ overhang (CGGGACGTAA), Cluster A12, Order 4, Window 96, Step 12, 15/27



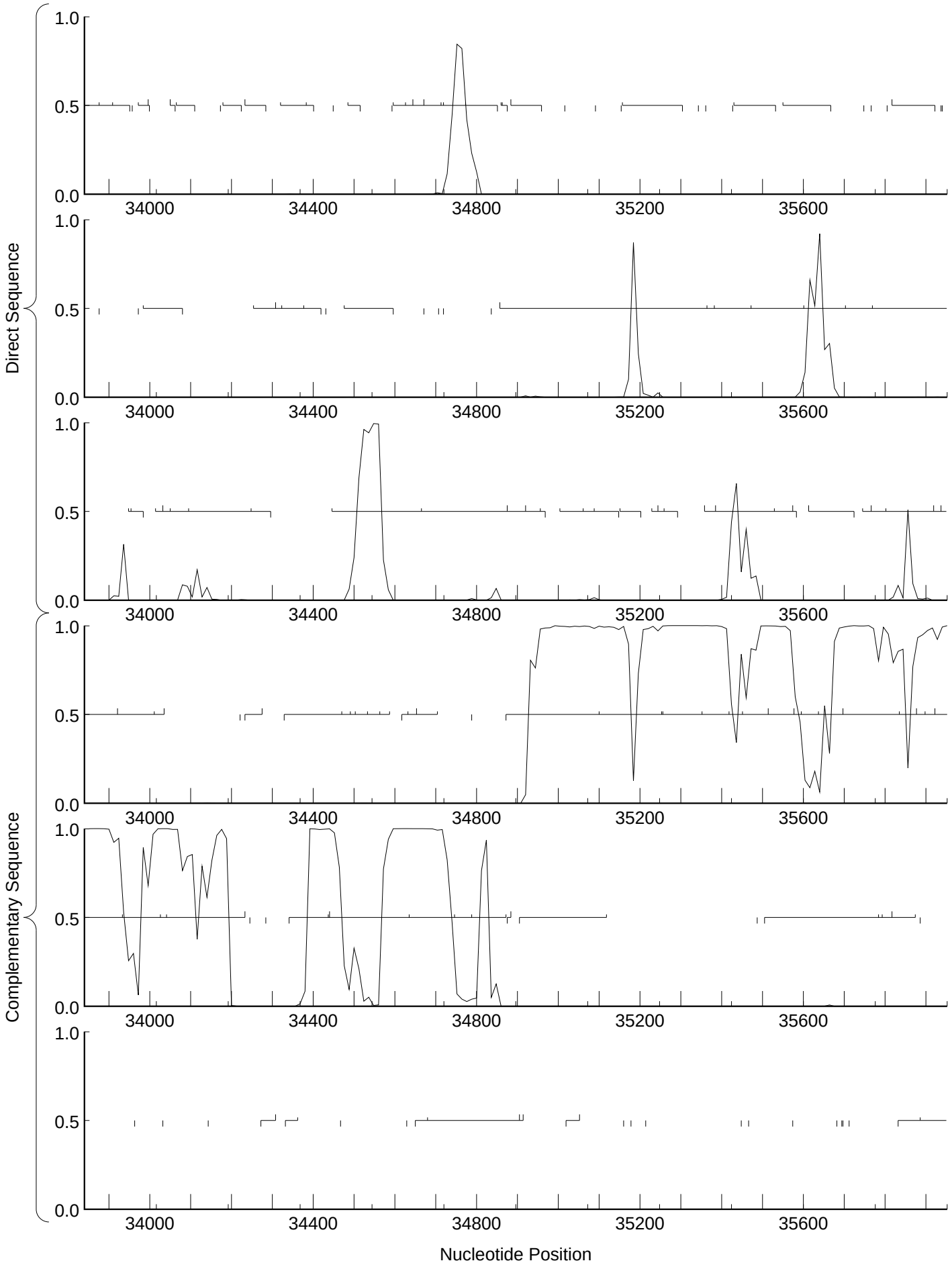
complete sequence, 53594 bp including 10-base 3’ overhang (CGGGACGTAA), Cluster A12, Order 4, Window 96, Step 12, 16/27



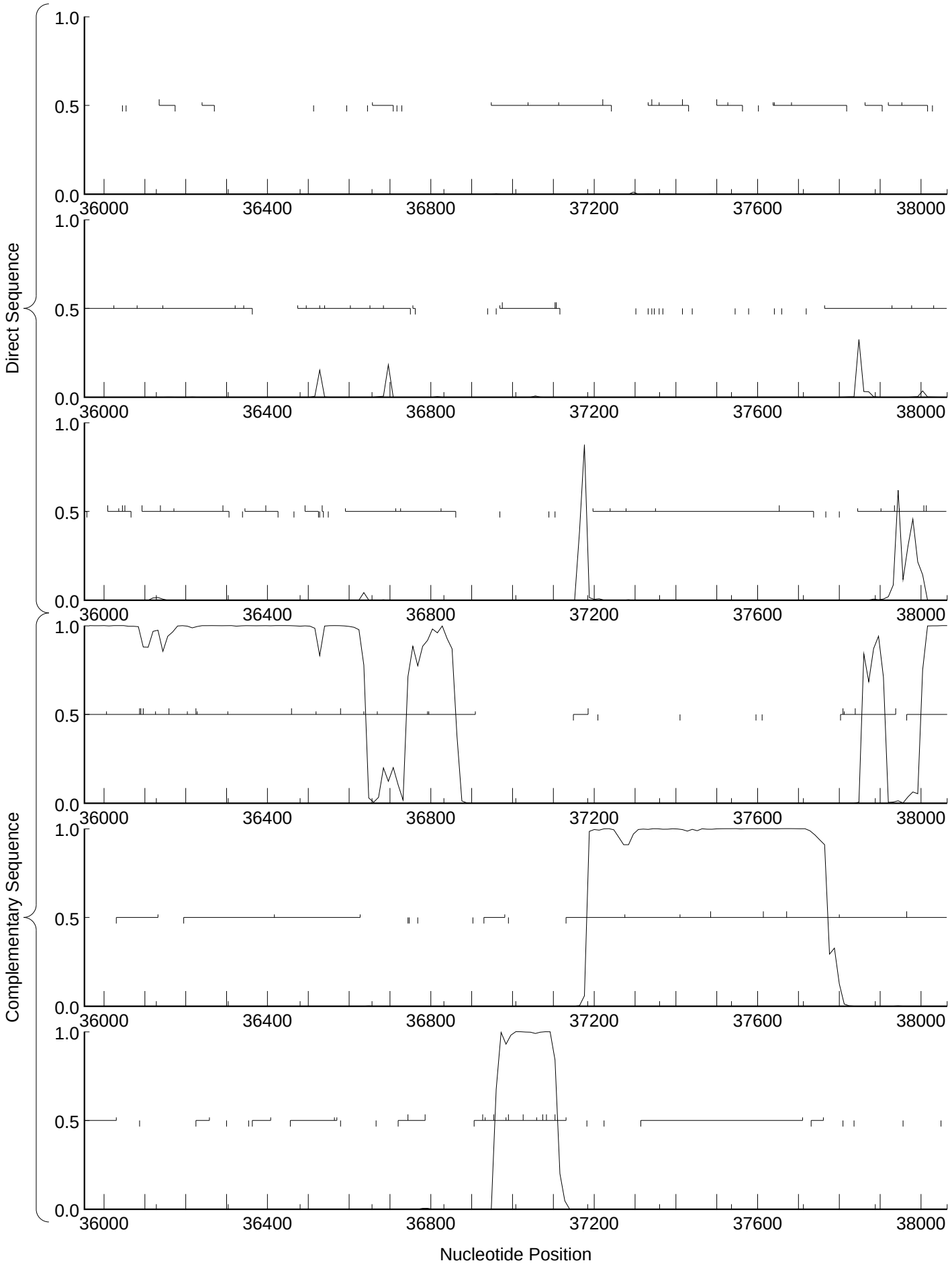
complete sequence, 53594 bp including 10-base 3’ overhang (CGGGACGTAA), Cluster A12, Order 4, Window 96, Step 12, 17/27

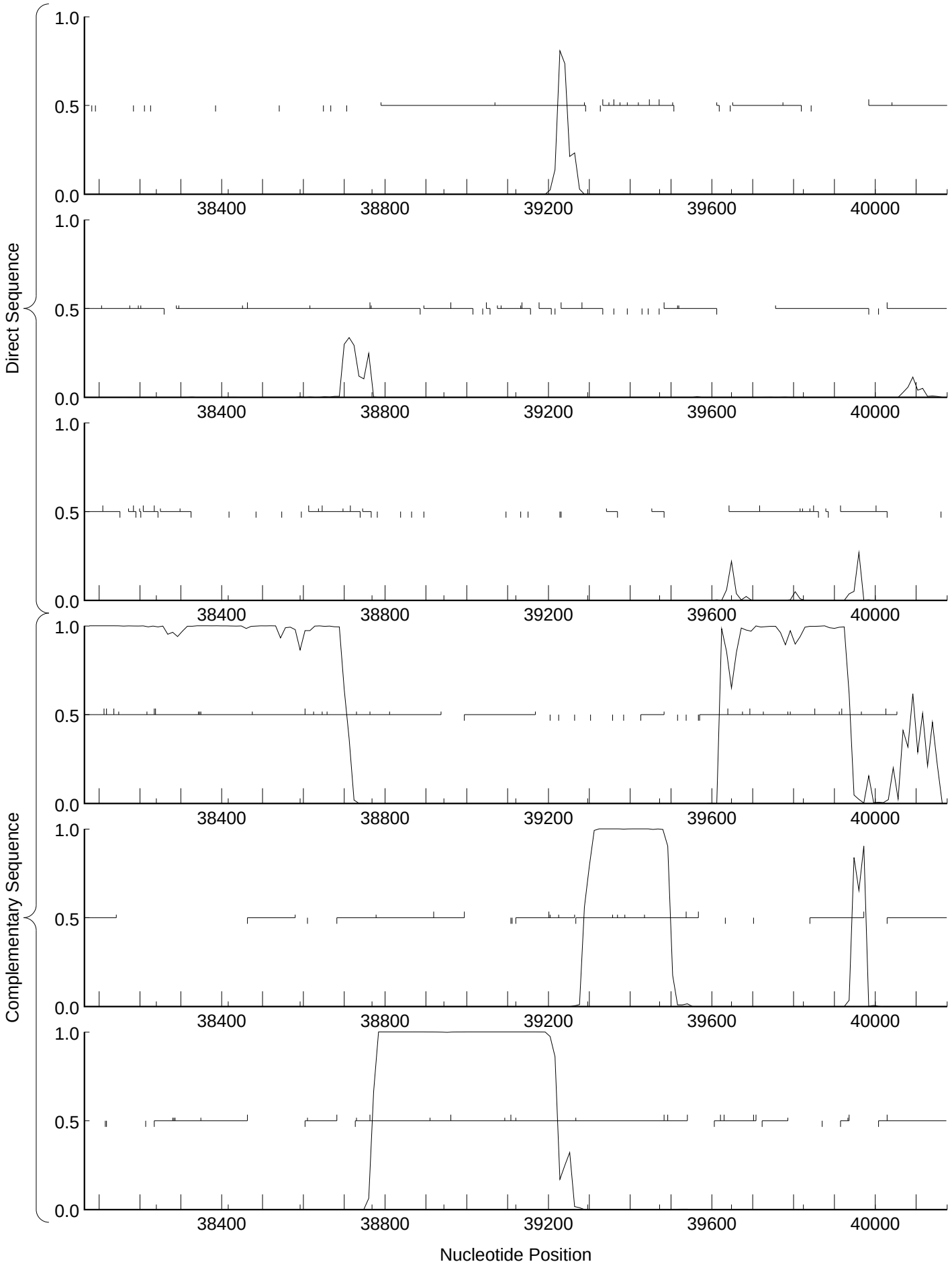


complete sequence, 53594 bp including 10-base 3’ overhang (CGGGACGTAA), Cluster A12, Order 4, Window 96, Step 12, 18/27

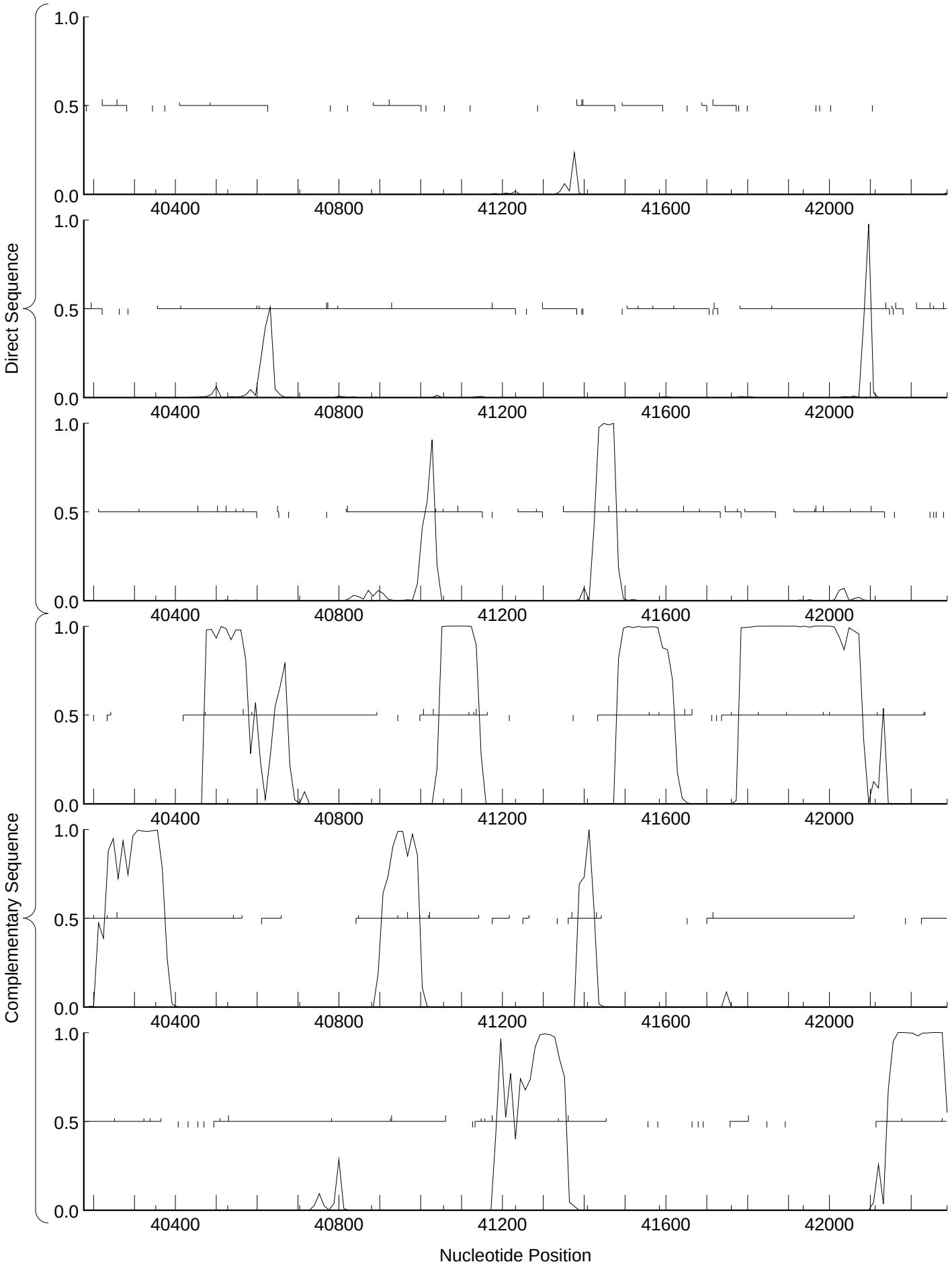


complete sequence, 53594 bp including 10-base 3’ overhang (CGGGACGTAA), Cluster A12, Order 4, Window 96, Step 12, 19/27

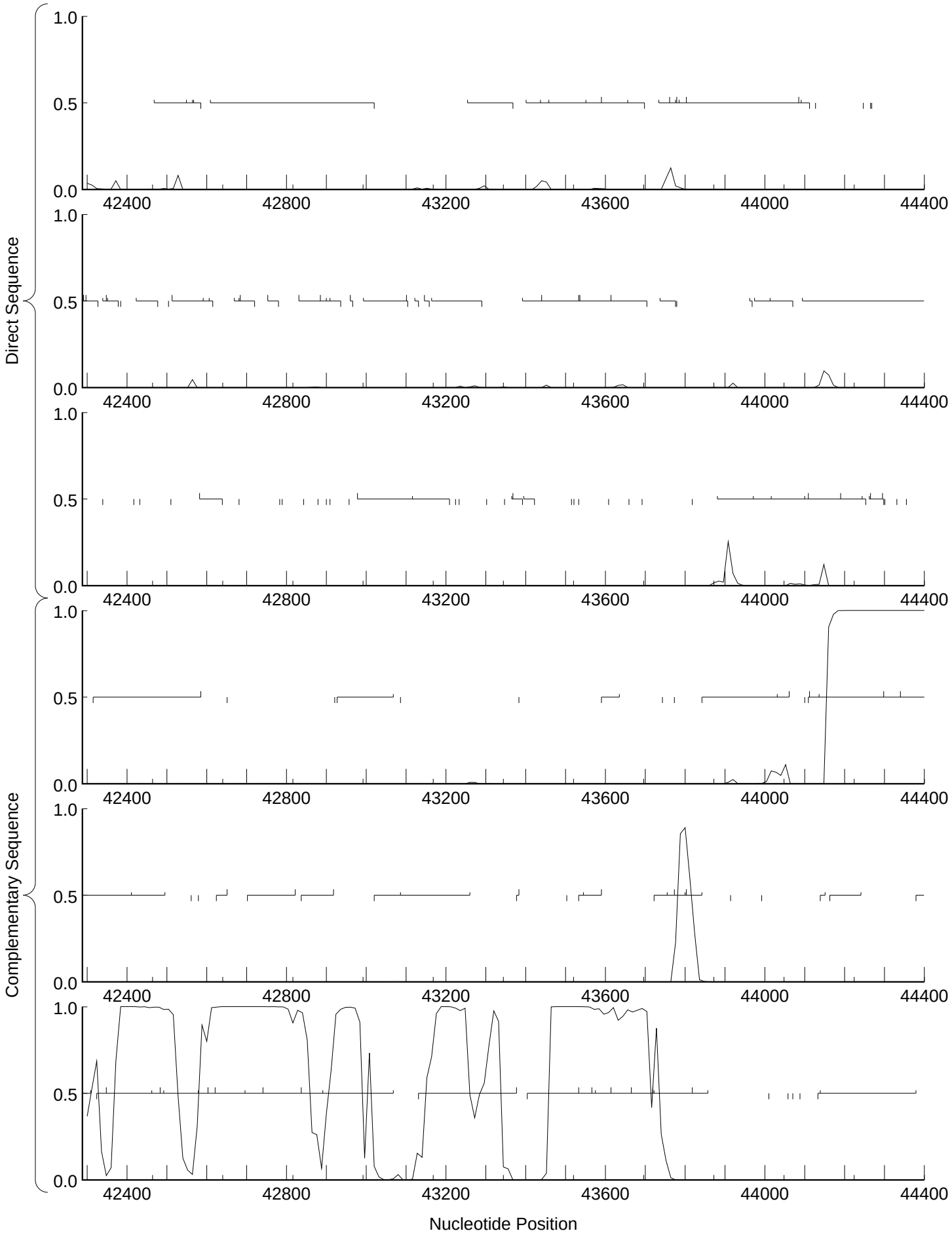



Direct Sequence
Complementary Sequence
1.0
0.5
0.0
38400
38800
39200
39600
40000
Nucleotide Position

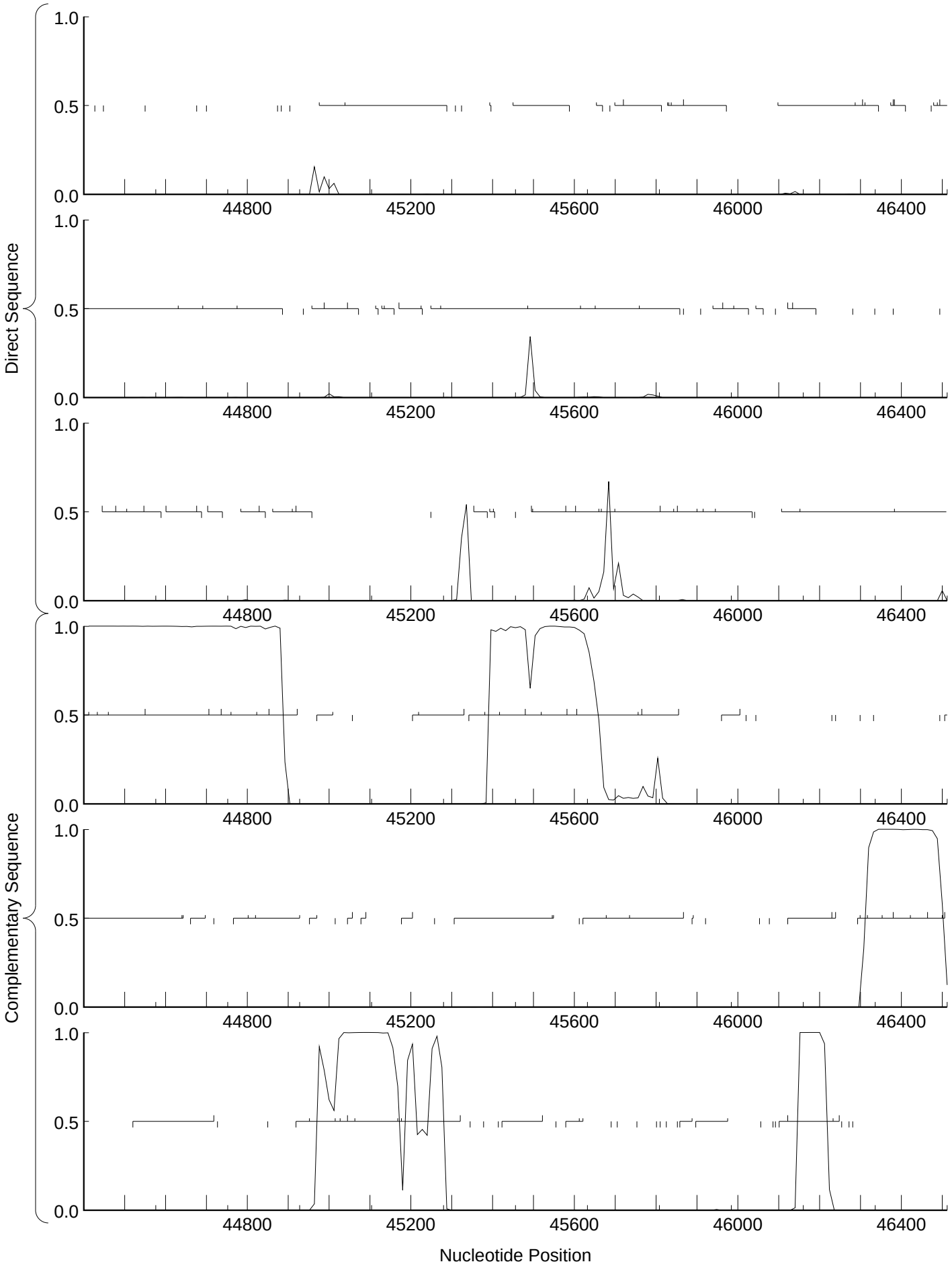
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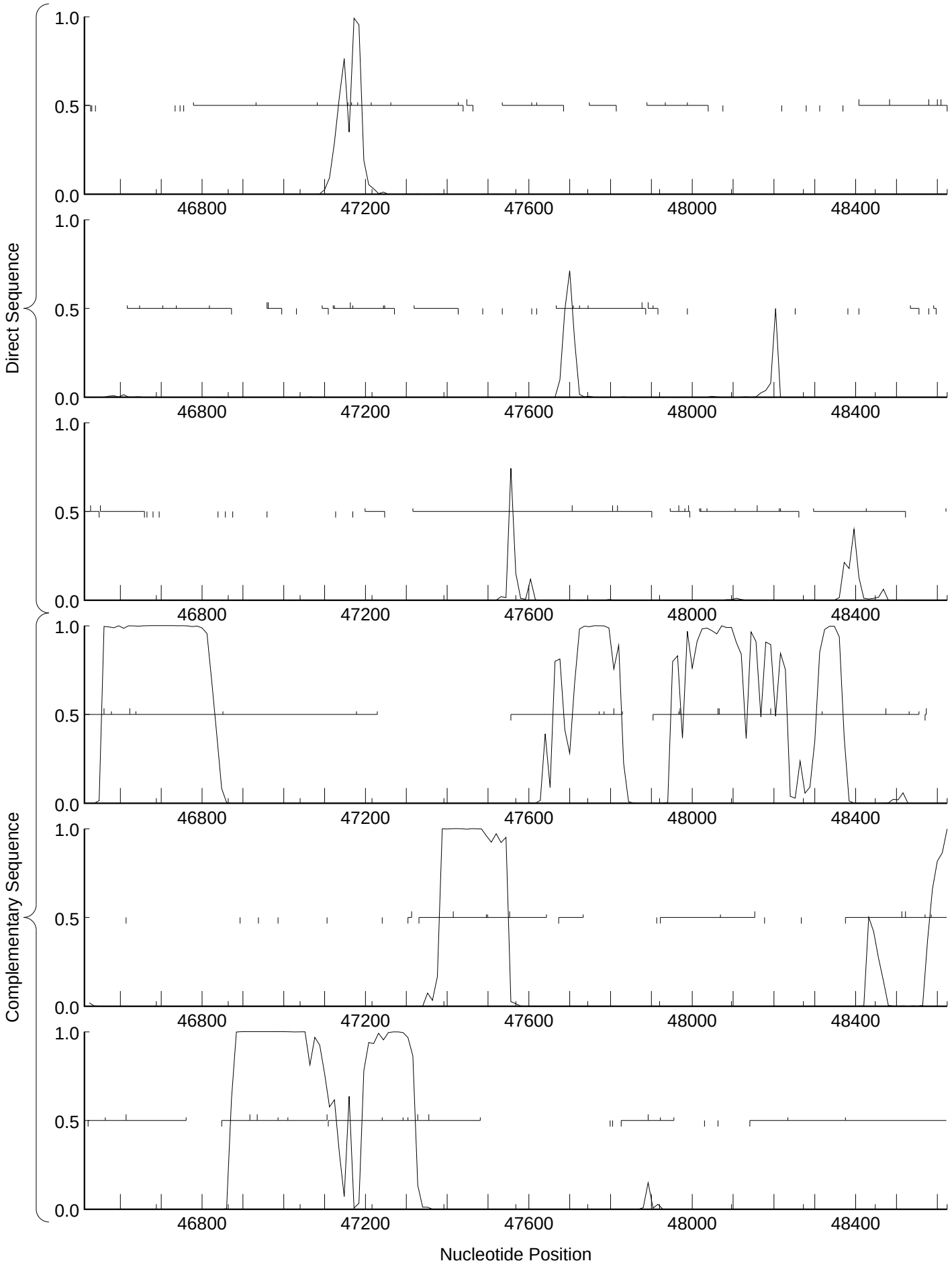
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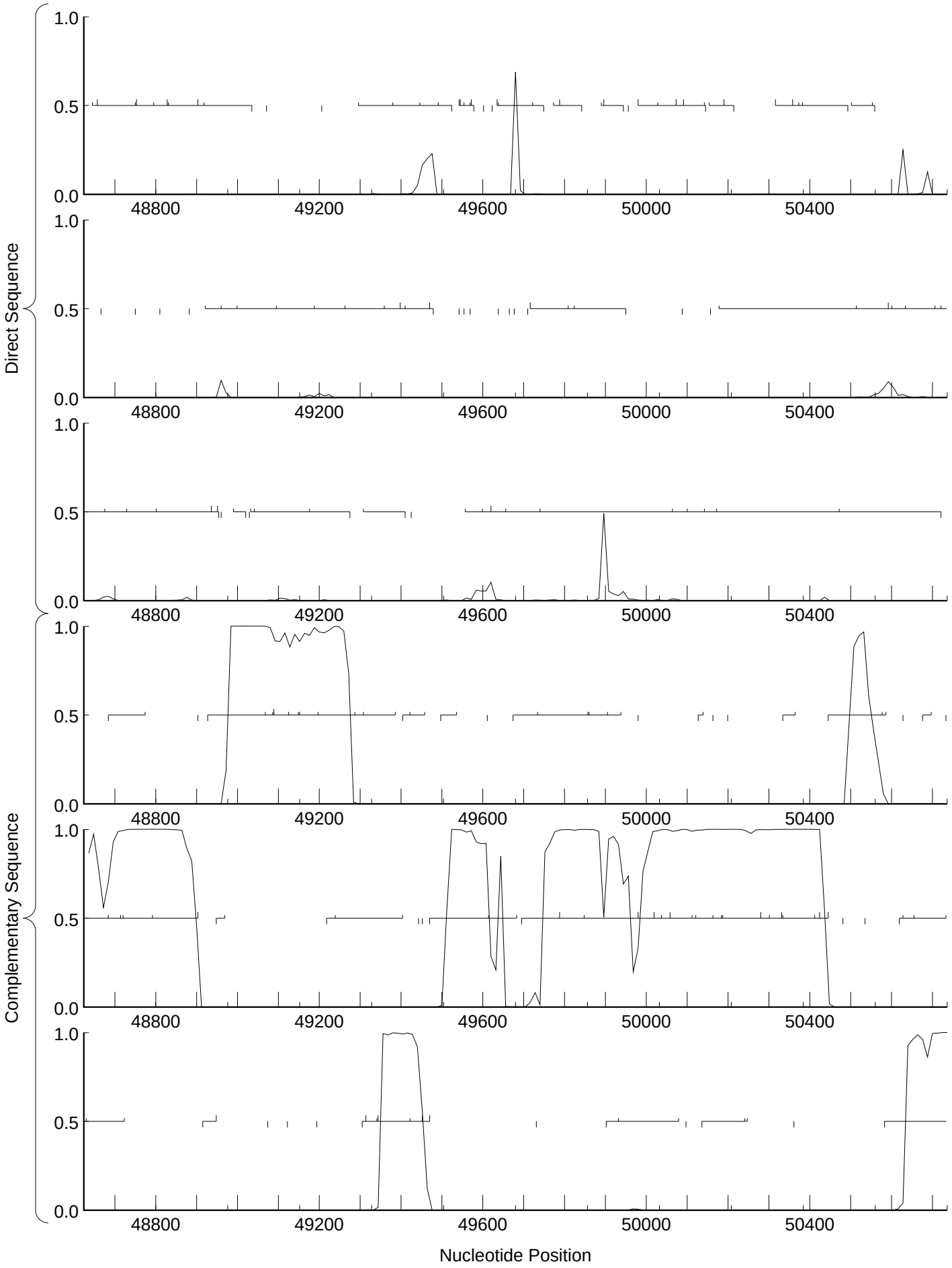
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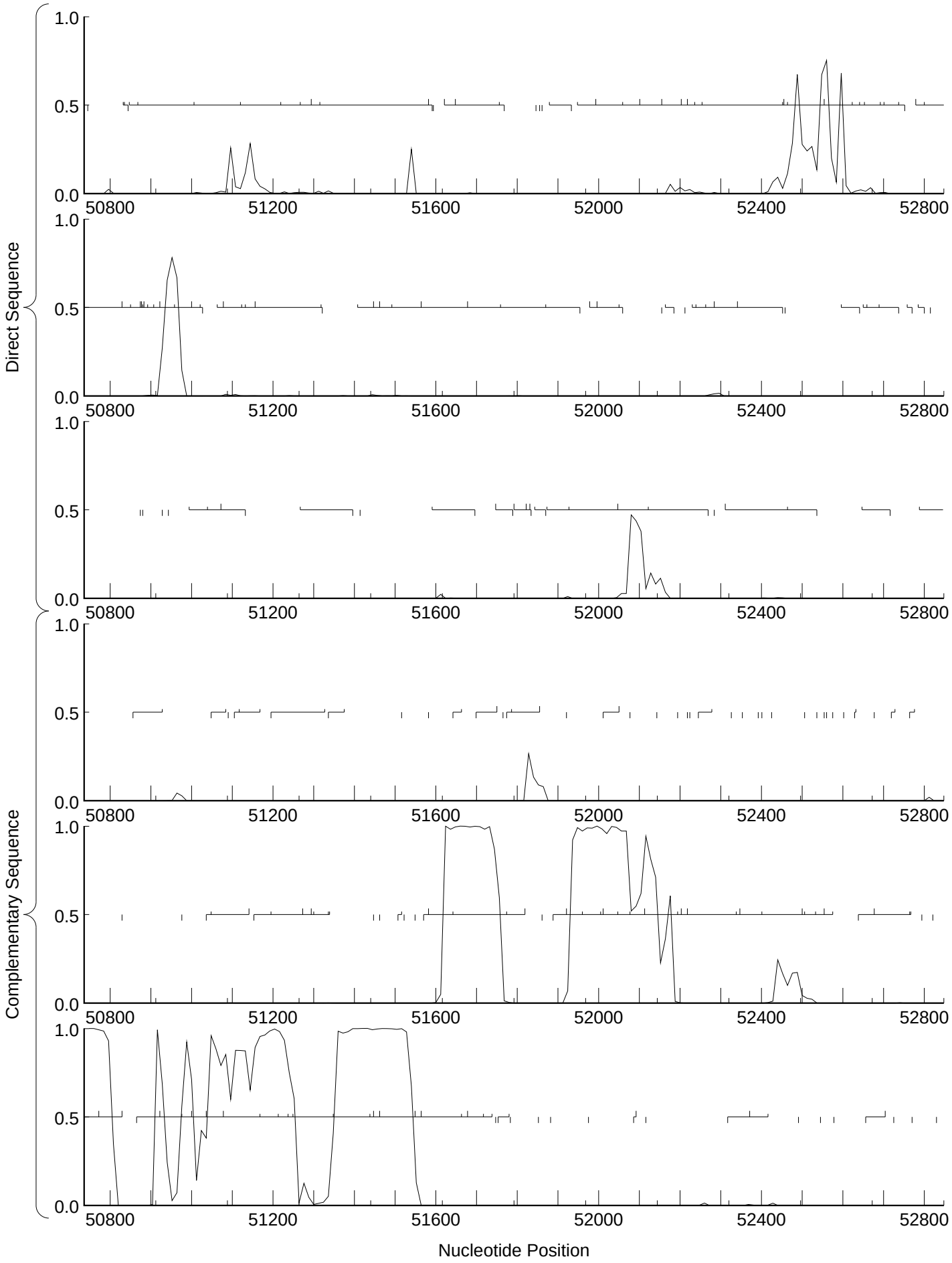
complete sequence, 53594 bp including 10-base 3’ overhang (CGGGACGTAA), Cluster A12, Order 4, Window 96, Step 12, 24/27



complete sequence, 53594 bp including 10-base 3’ overhang (CGGGACGTAA), Cluster A12, Order 4, Window 96, Step 12, 25/27



complete sequence, 53594 bp including 10-base 3’ overhang (CGGGACGTAA), Cluster A12, Order 4, Window 96, Step 12, 26/27



complete sequence, 53594 bp including 10-base 3’ overhang (CGGGACGTAA), Cluster A12, Order 4, Window 96, Step 12, 27/27

