GeneMark

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

PROGRAM INFORMATION

```
Sequence         :  Mycobacterium phage ZoeJ complete sequence, 57315 bp including 11-base 3' overhang (CCTCGCG
Analysis Date    :  3/29/24 at 10:13:53
Pages            :  29
Sequence Length  :  57315 bp
GC Content       :   68.52%

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

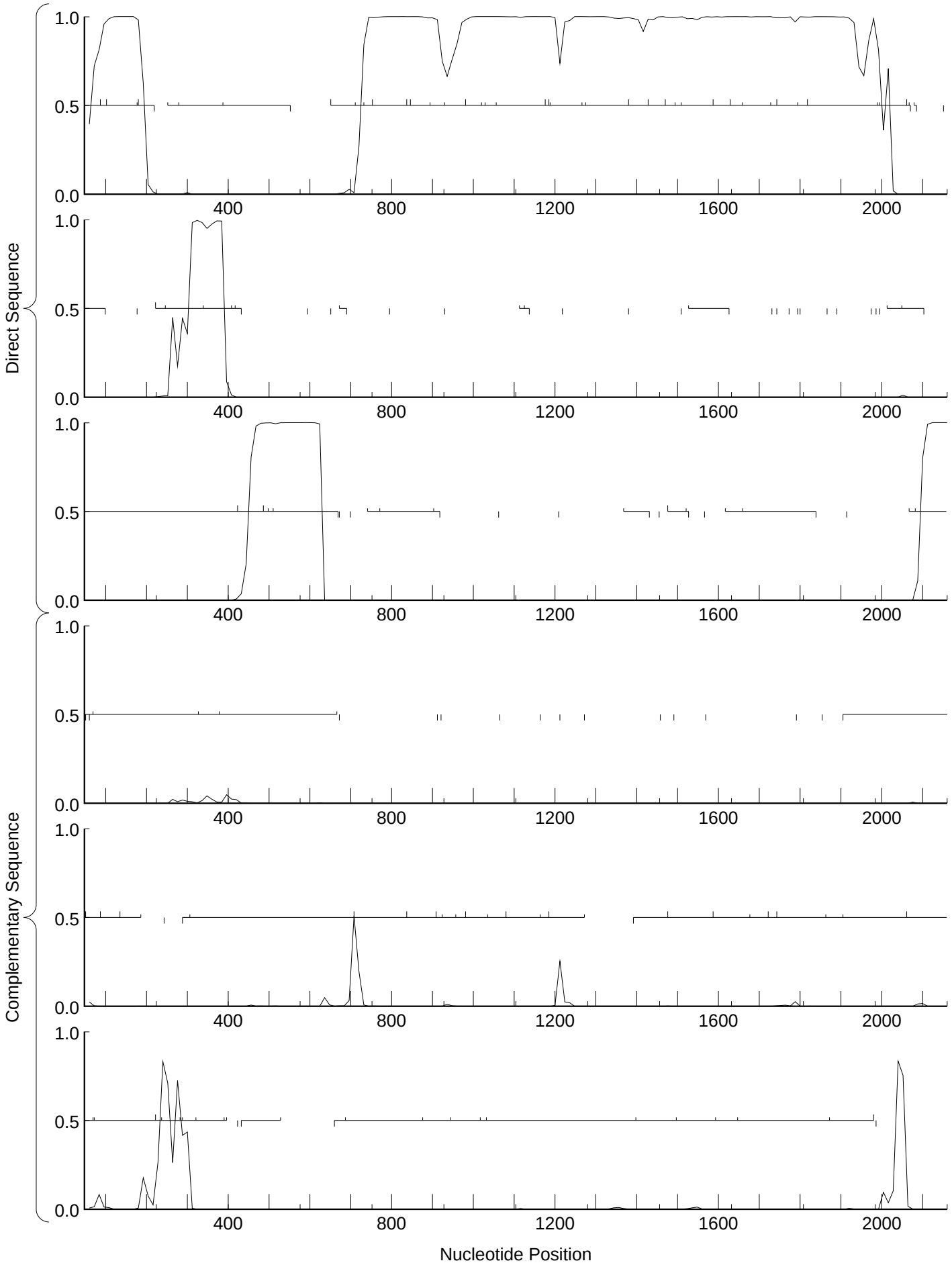

  Send questions / comments to:
      Dr. M. Borodovsky
      Georgia Institute of Technology
      School of Biology
      Atlanta, GA  30332-0230
```

Matrix notes & comments

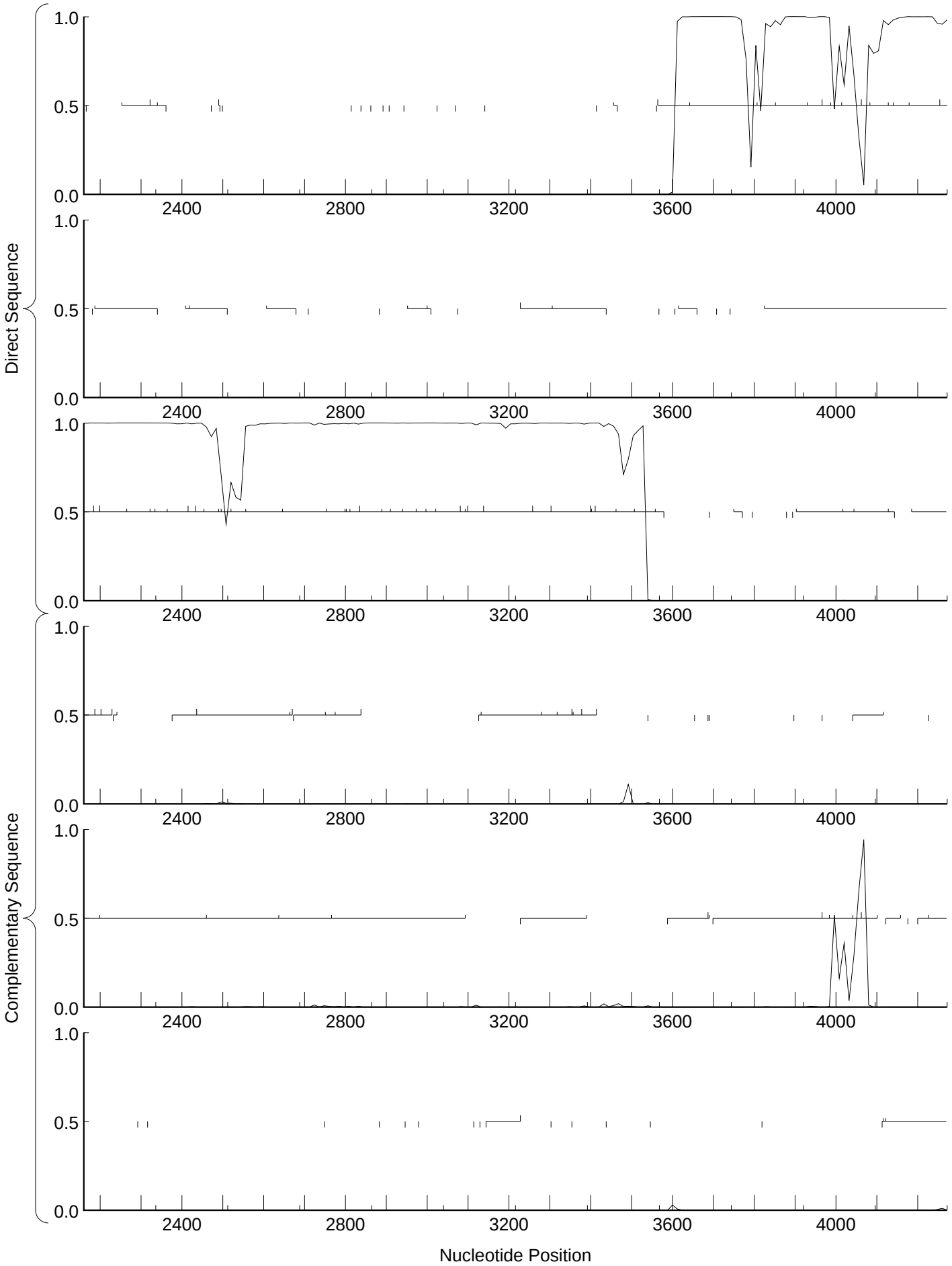
Training set derived by GeneMarkS, 4.27 September 2014
Tue Sep 23 15:14:37 2014

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

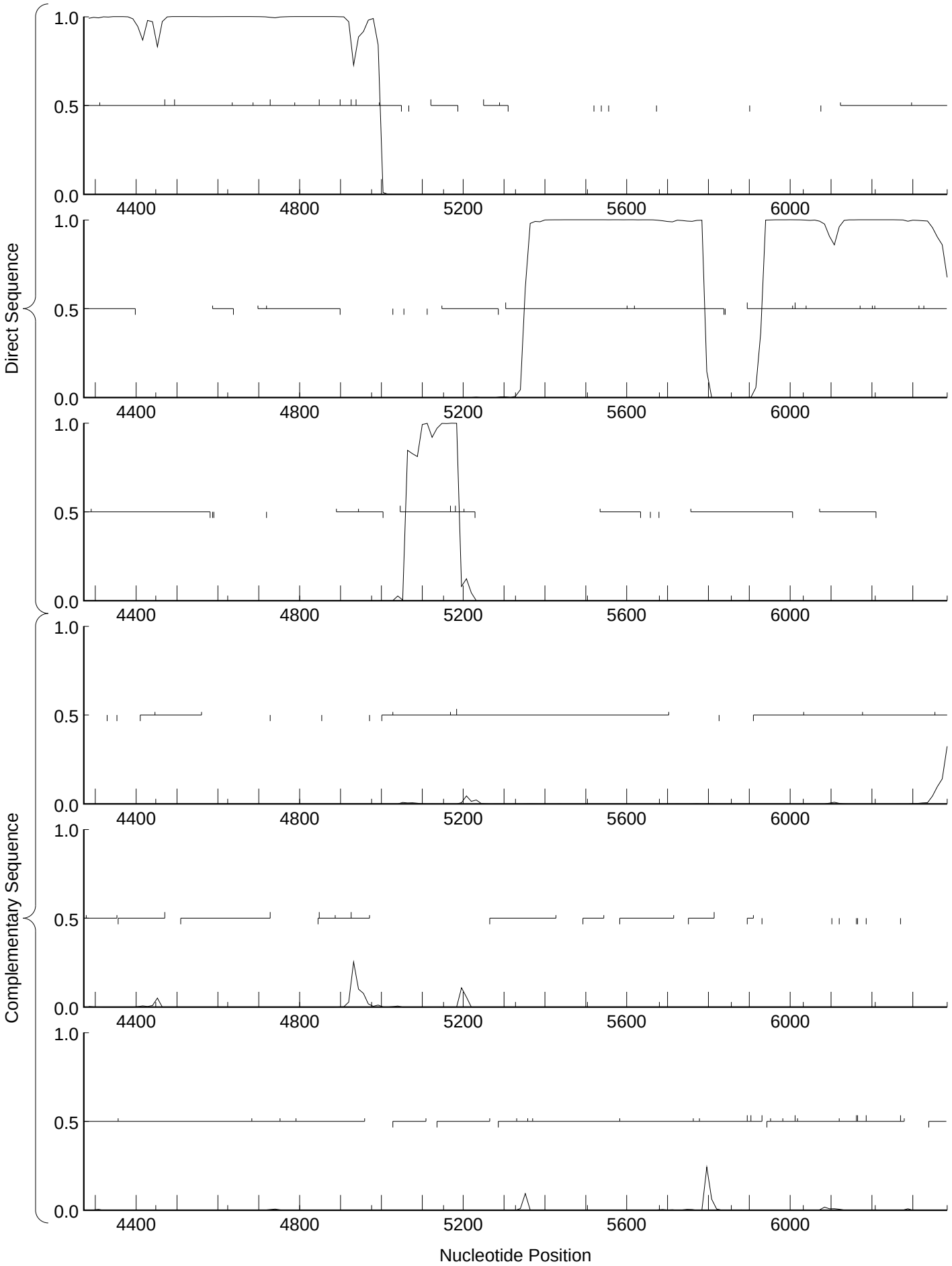
complete sequence, 57315 bp including 11-base 3’ overhang (CCTCGCGGCAT), Cluster K2, Order 4, Window 96, Step 12, 2/29



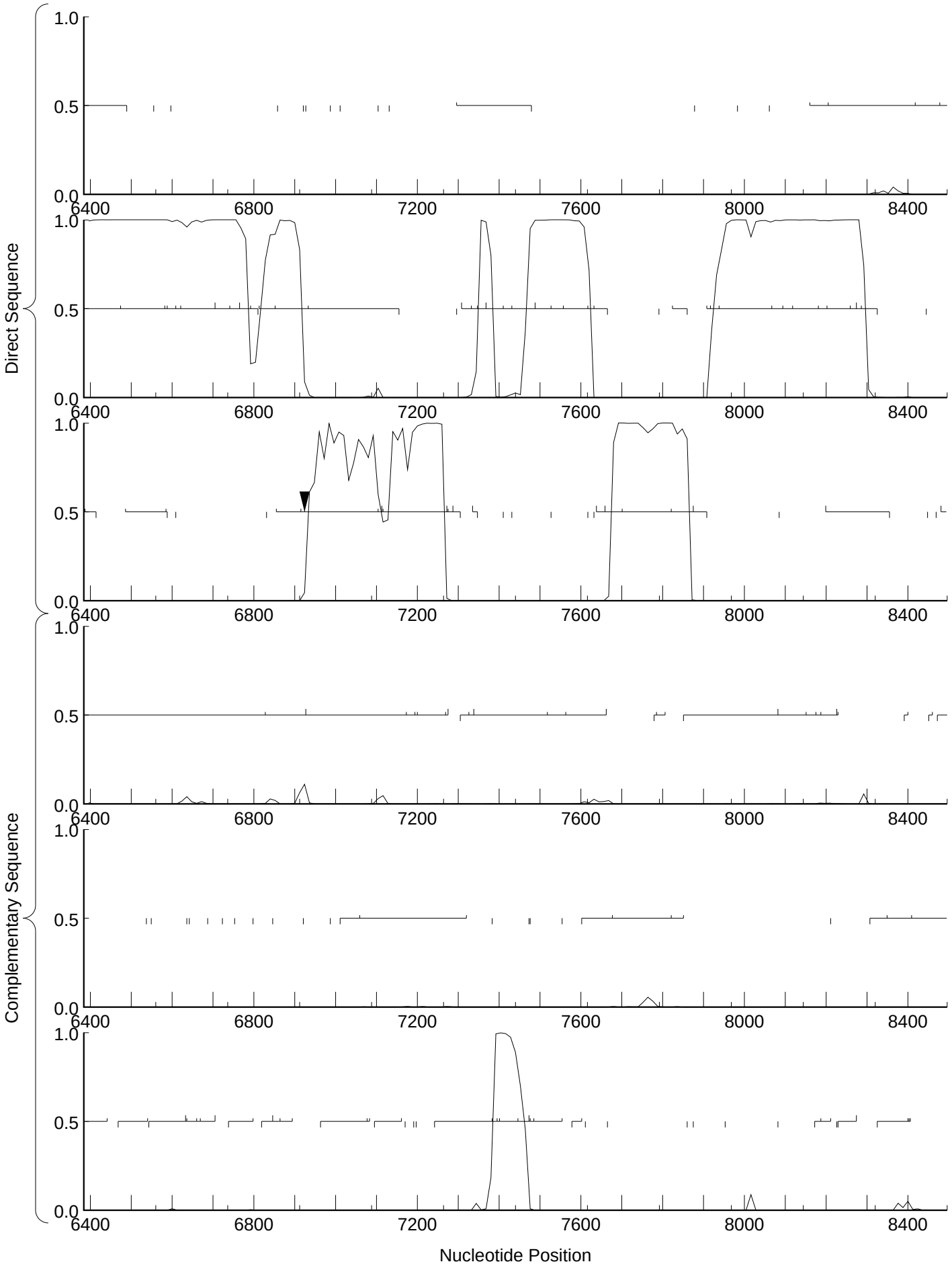
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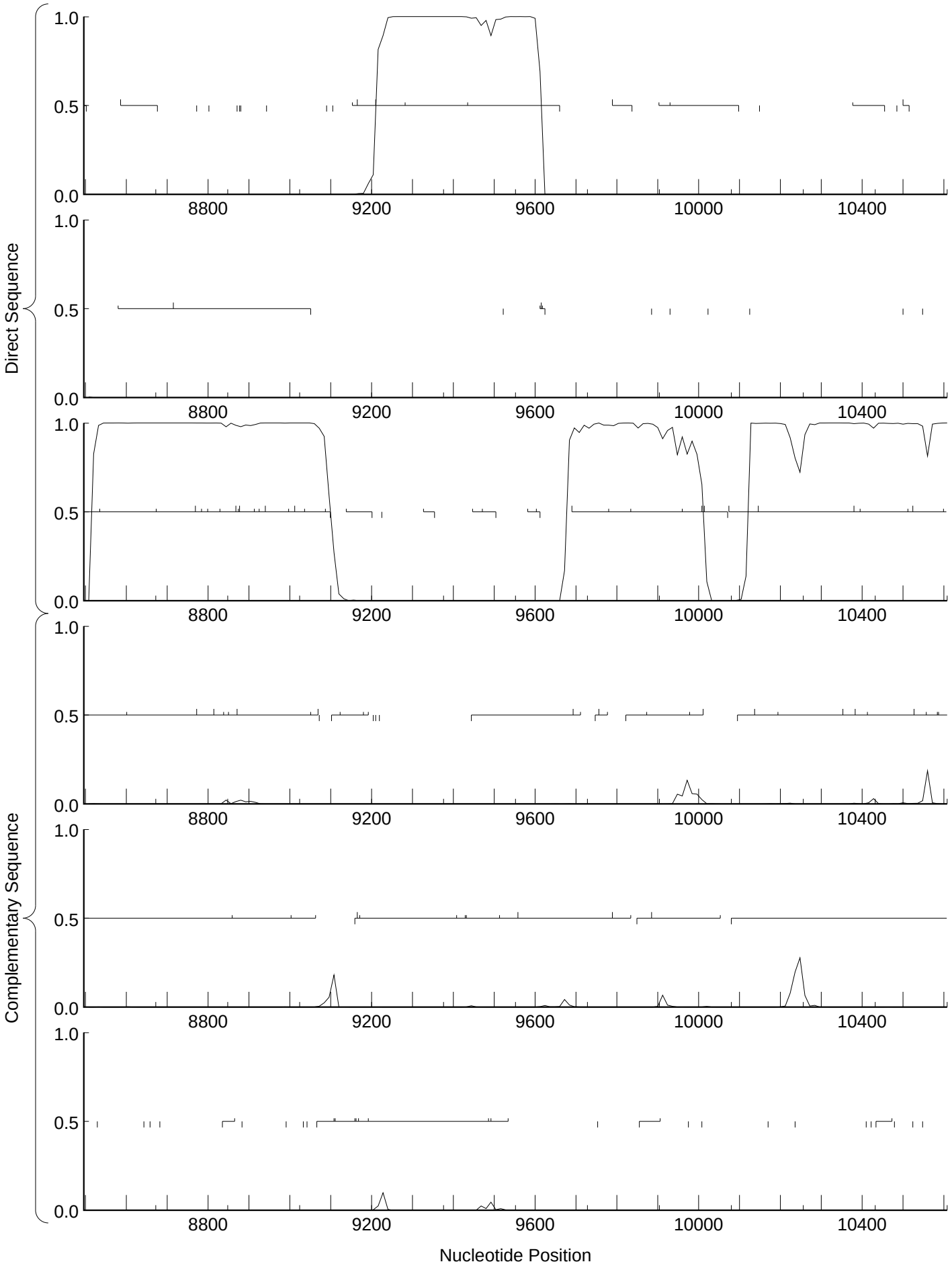
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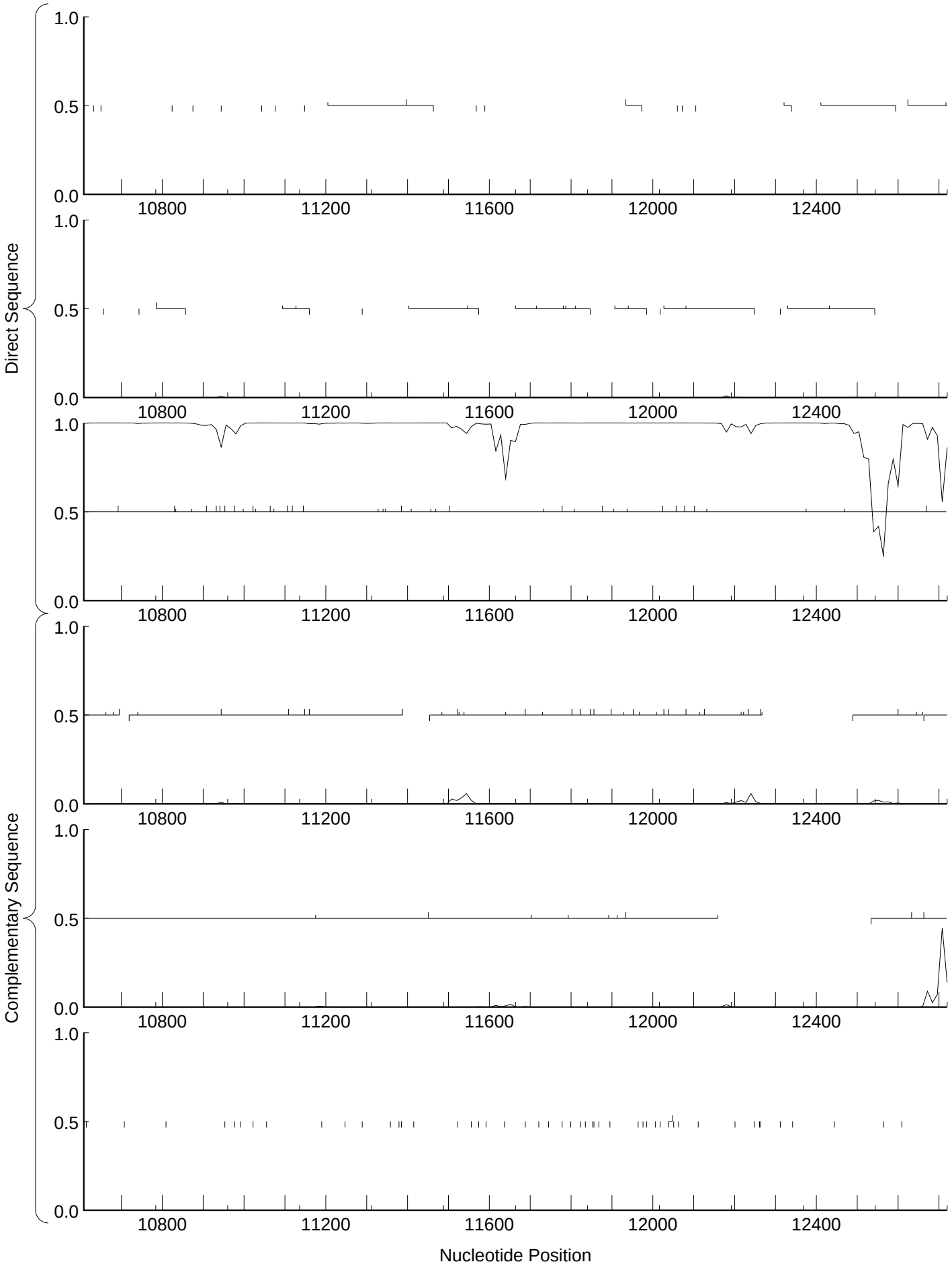
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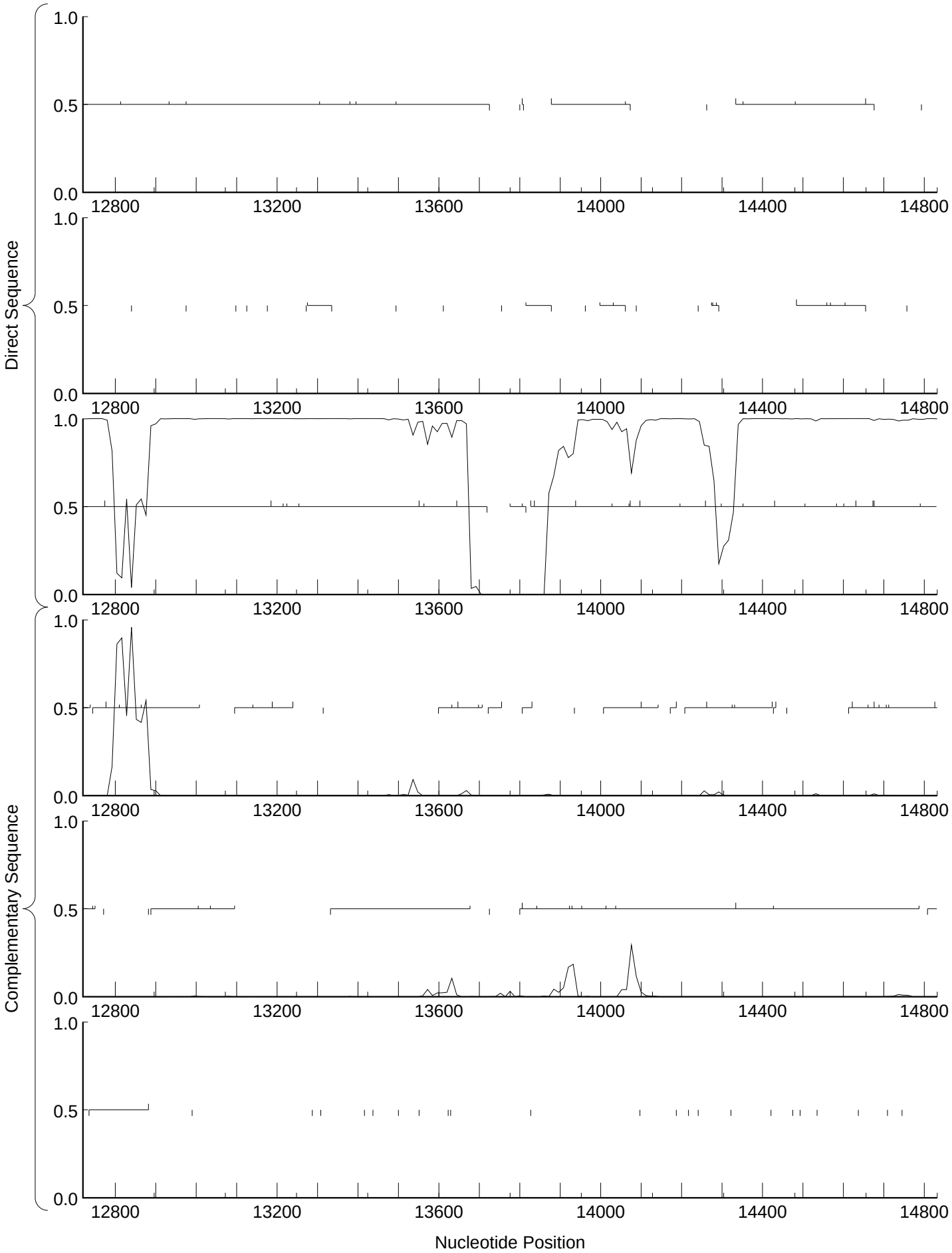
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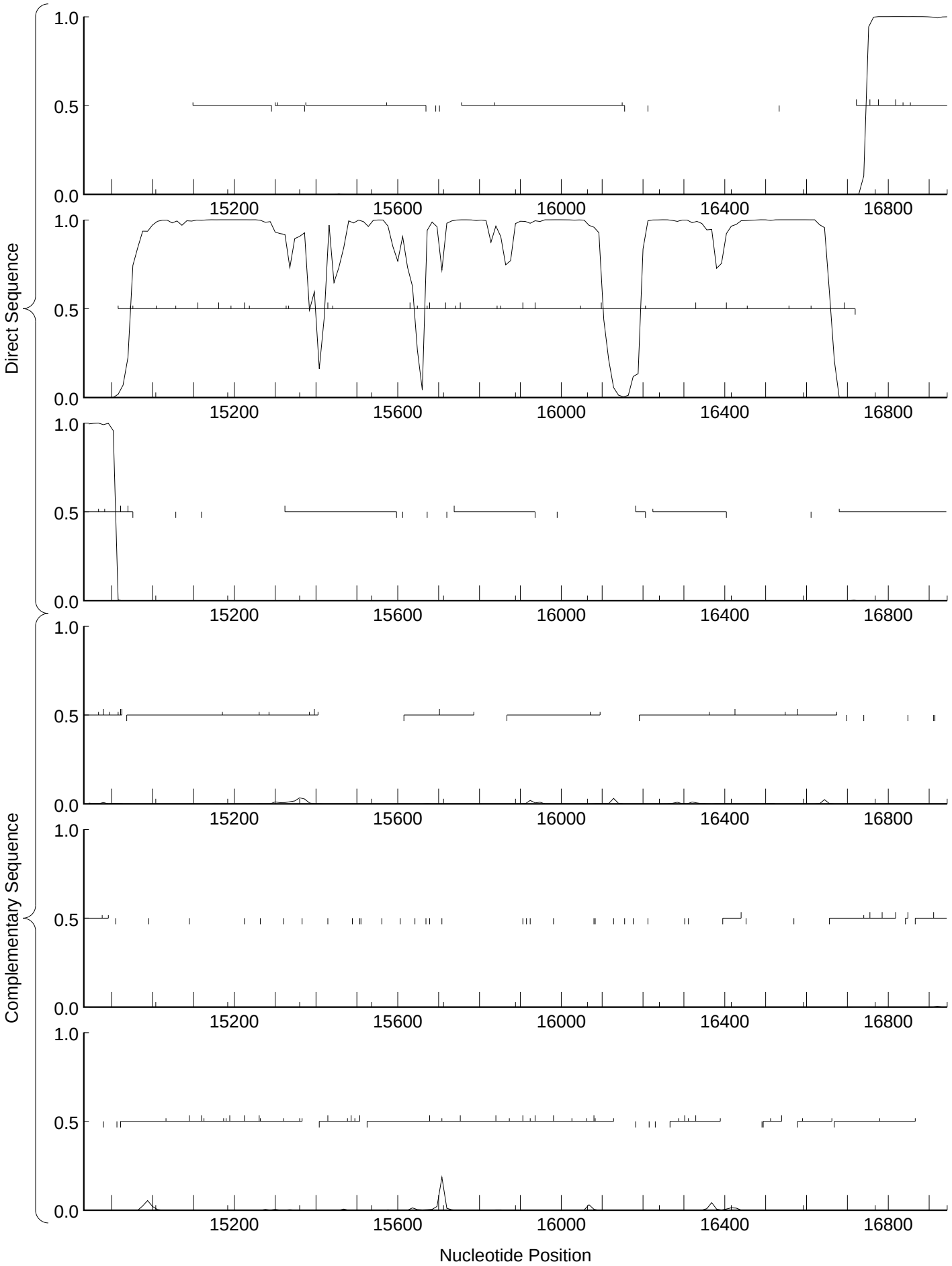
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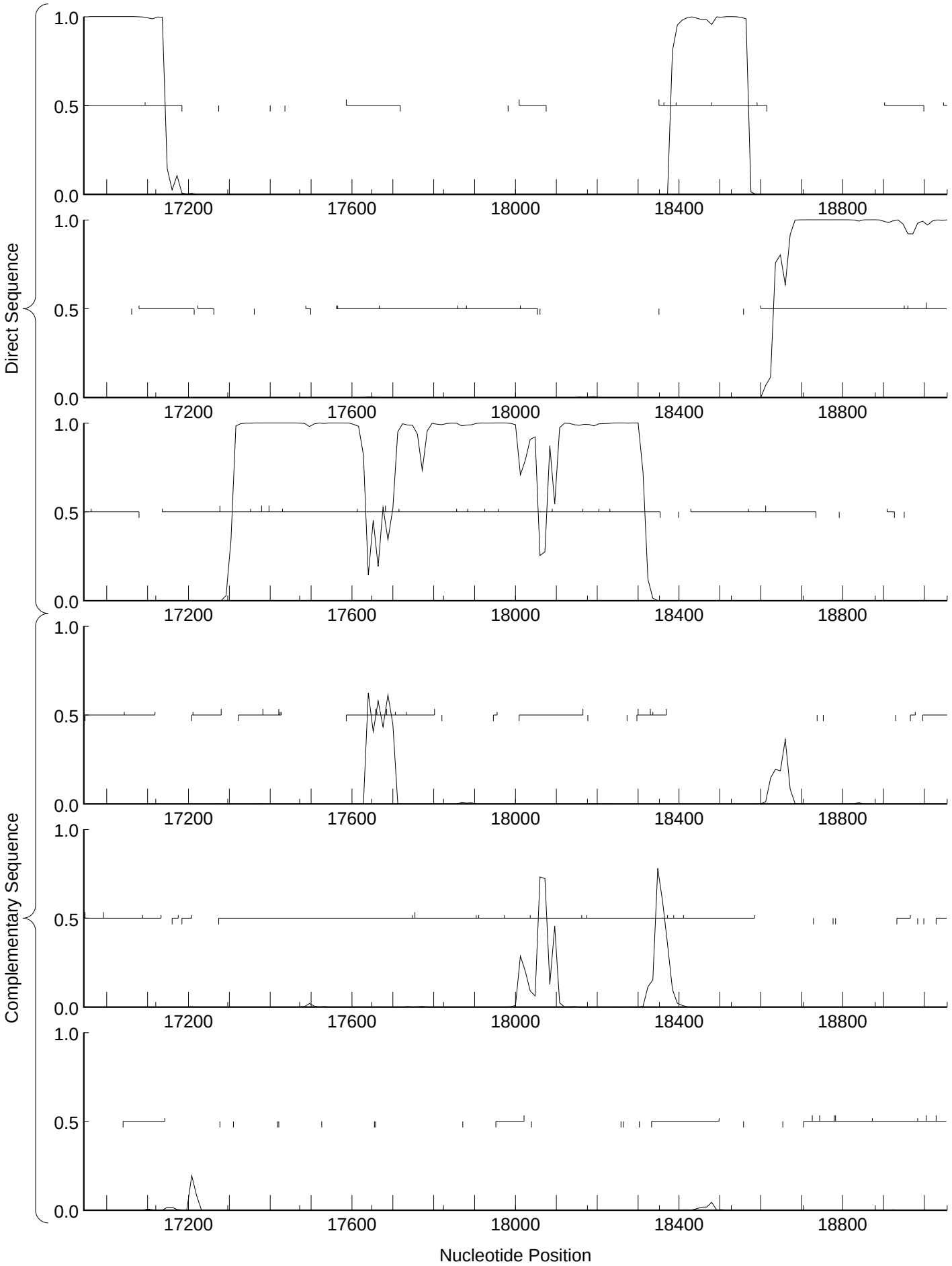
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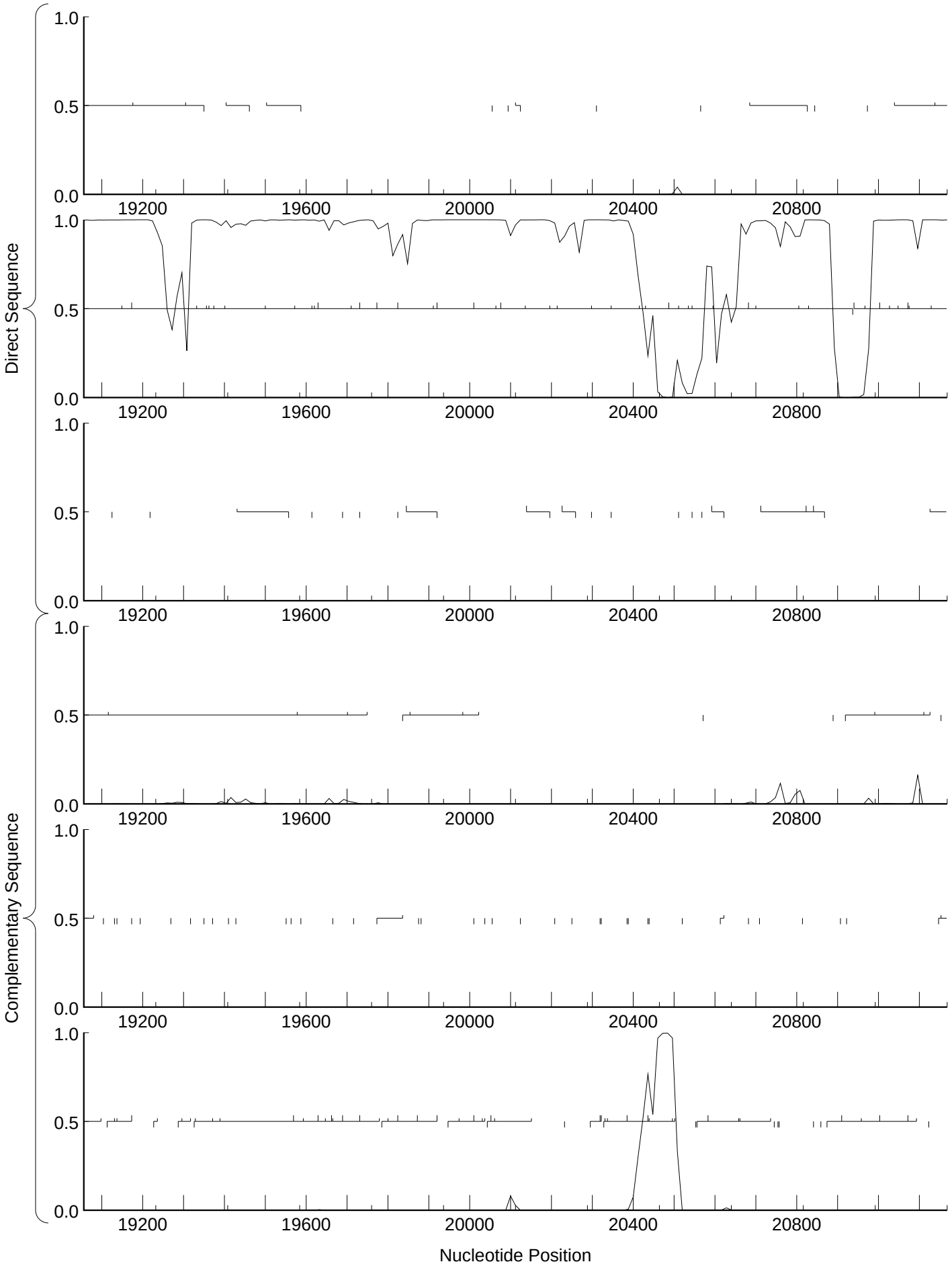
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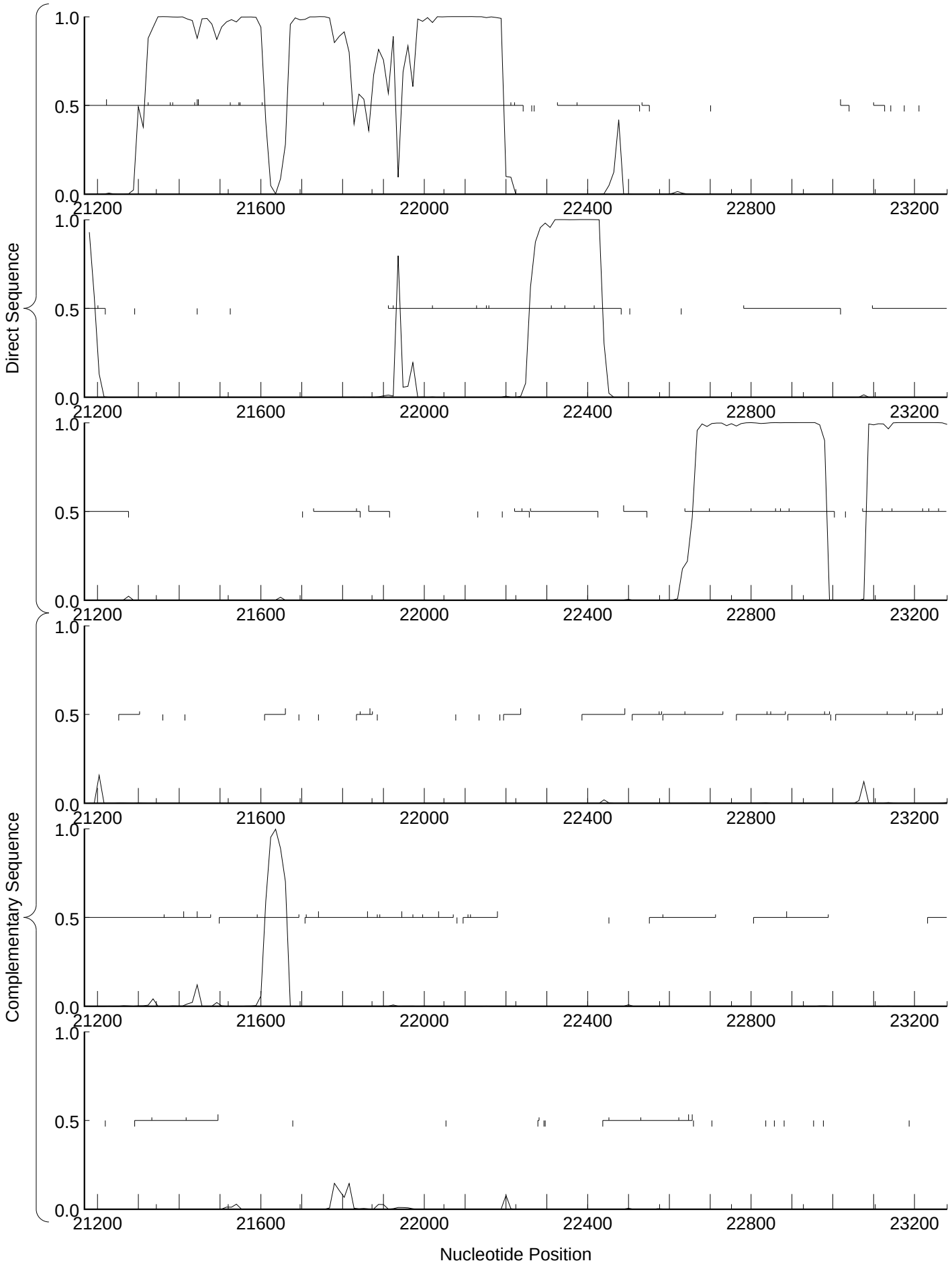
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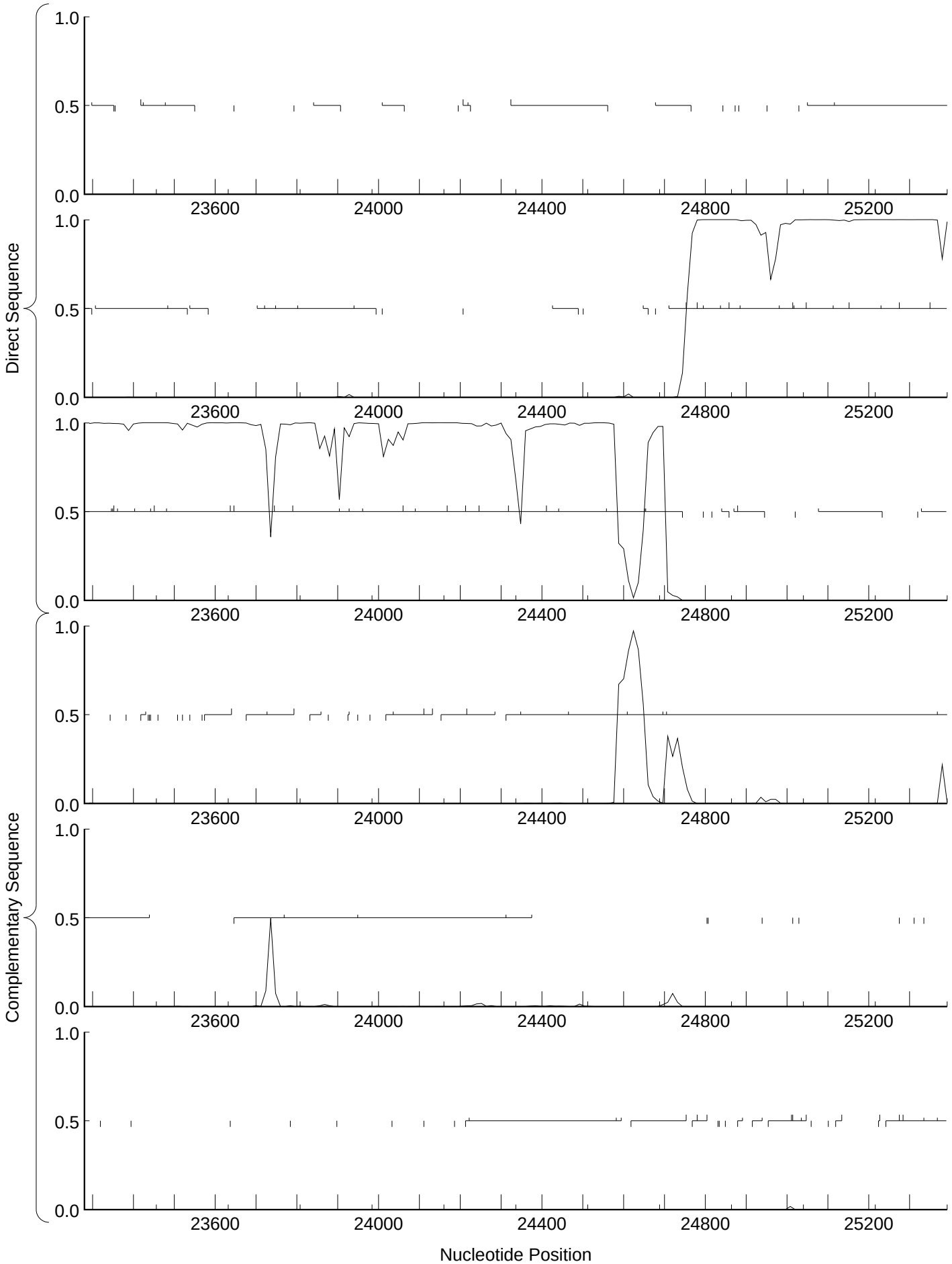
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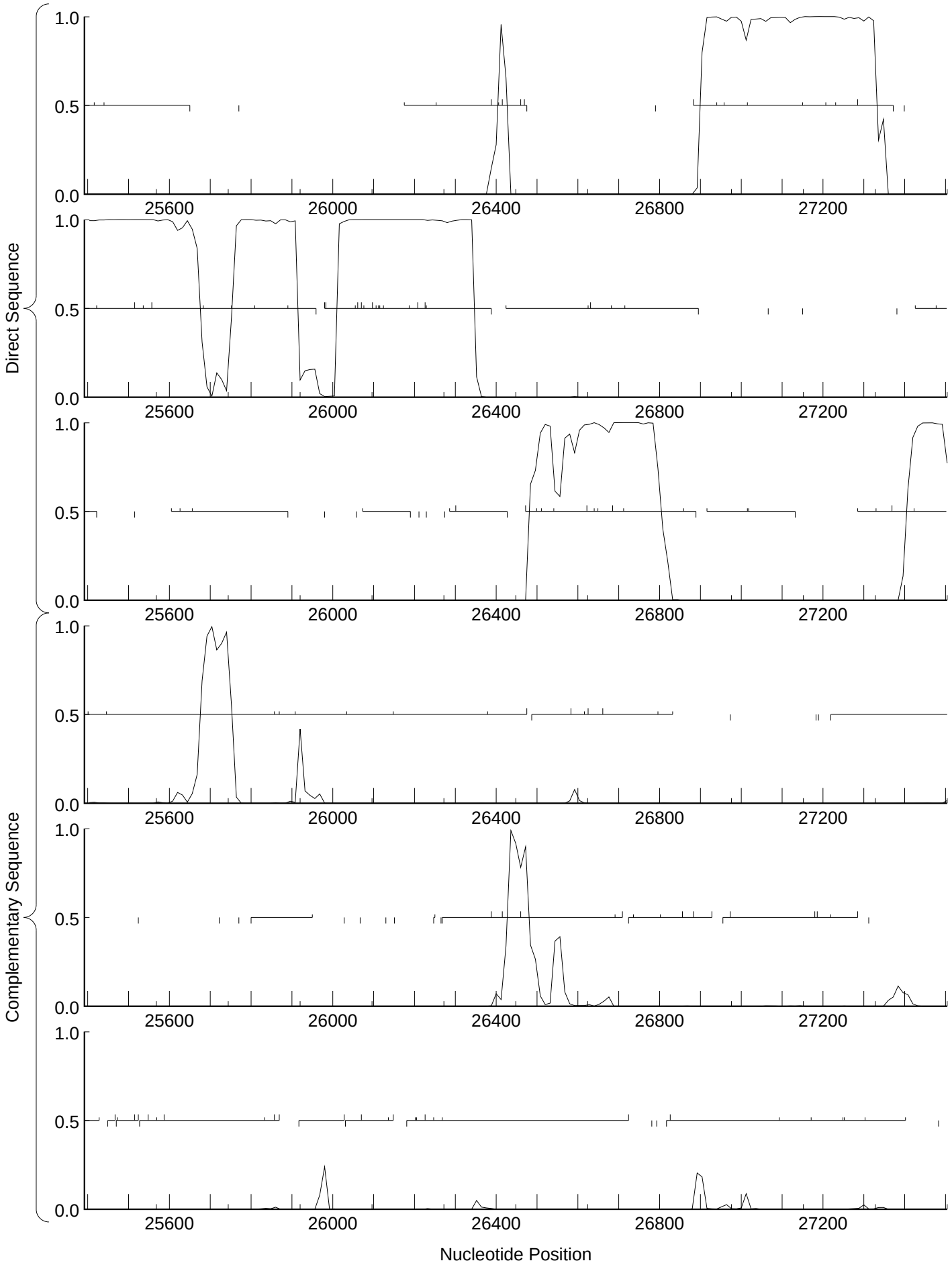
complete sequence, 57315 bp including 11-base 3’ overhang (CCTCGCGGCAT), Cluster K2, Order 4, Window 96, Step 12, 12/29



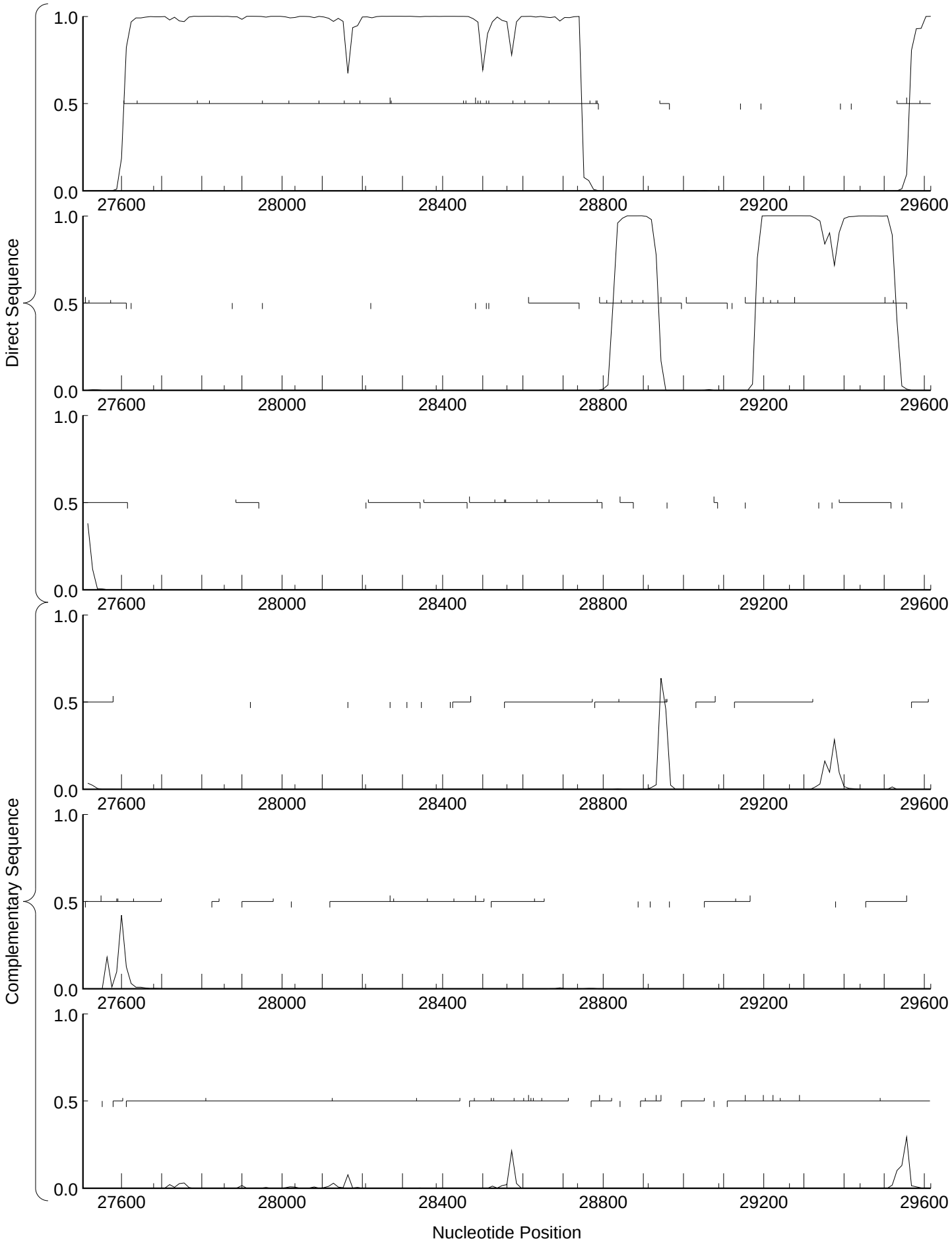
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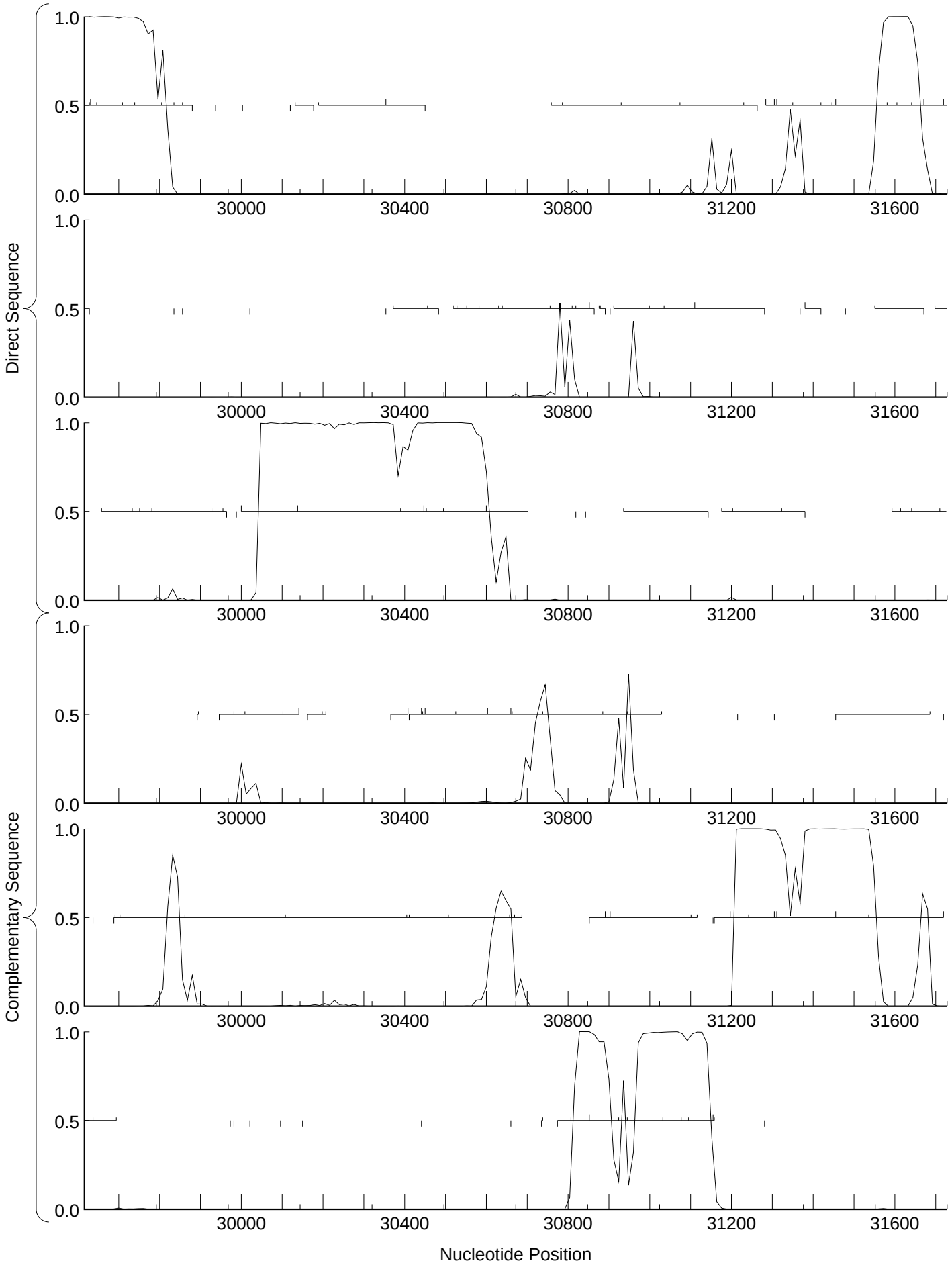
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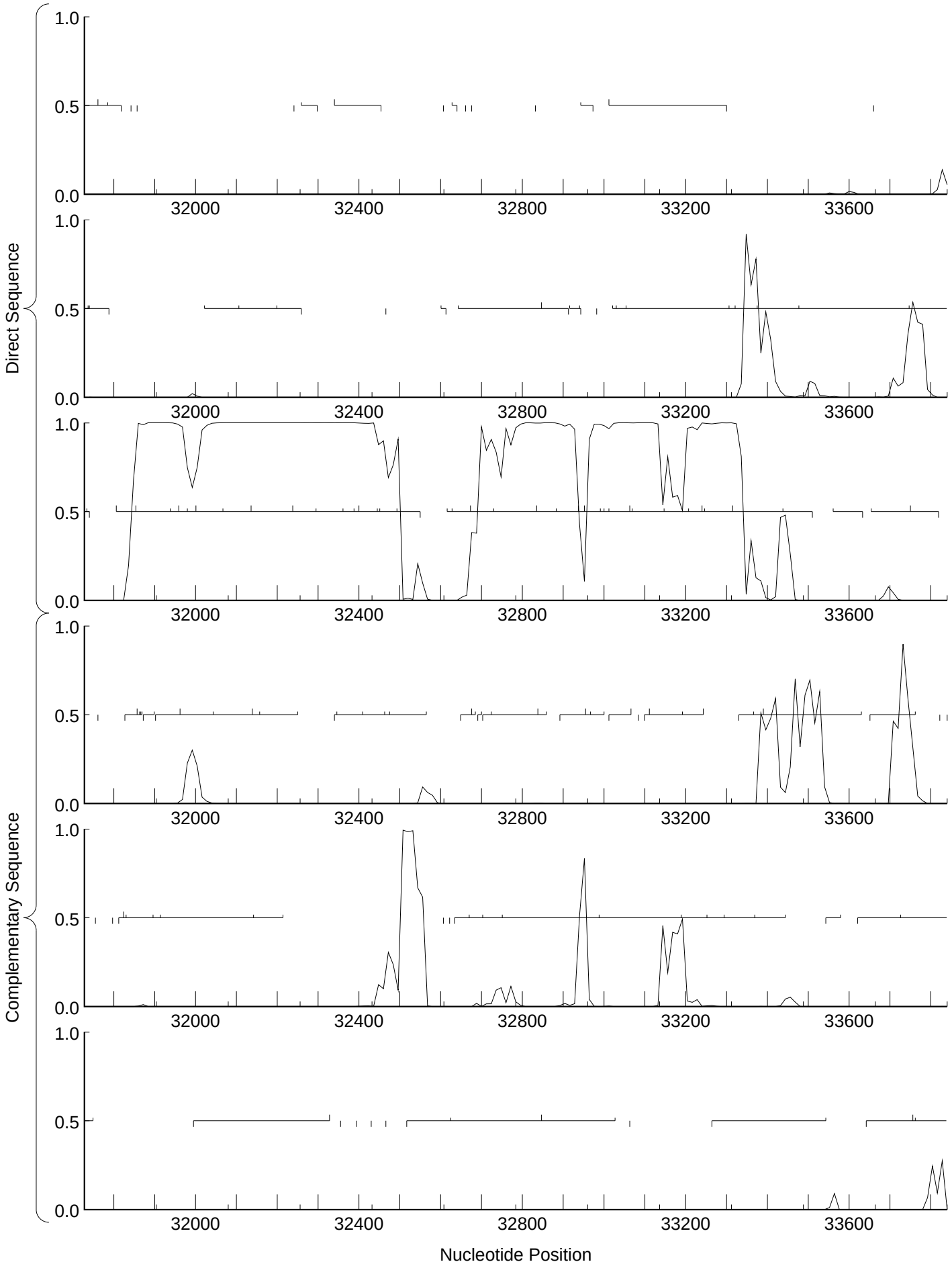
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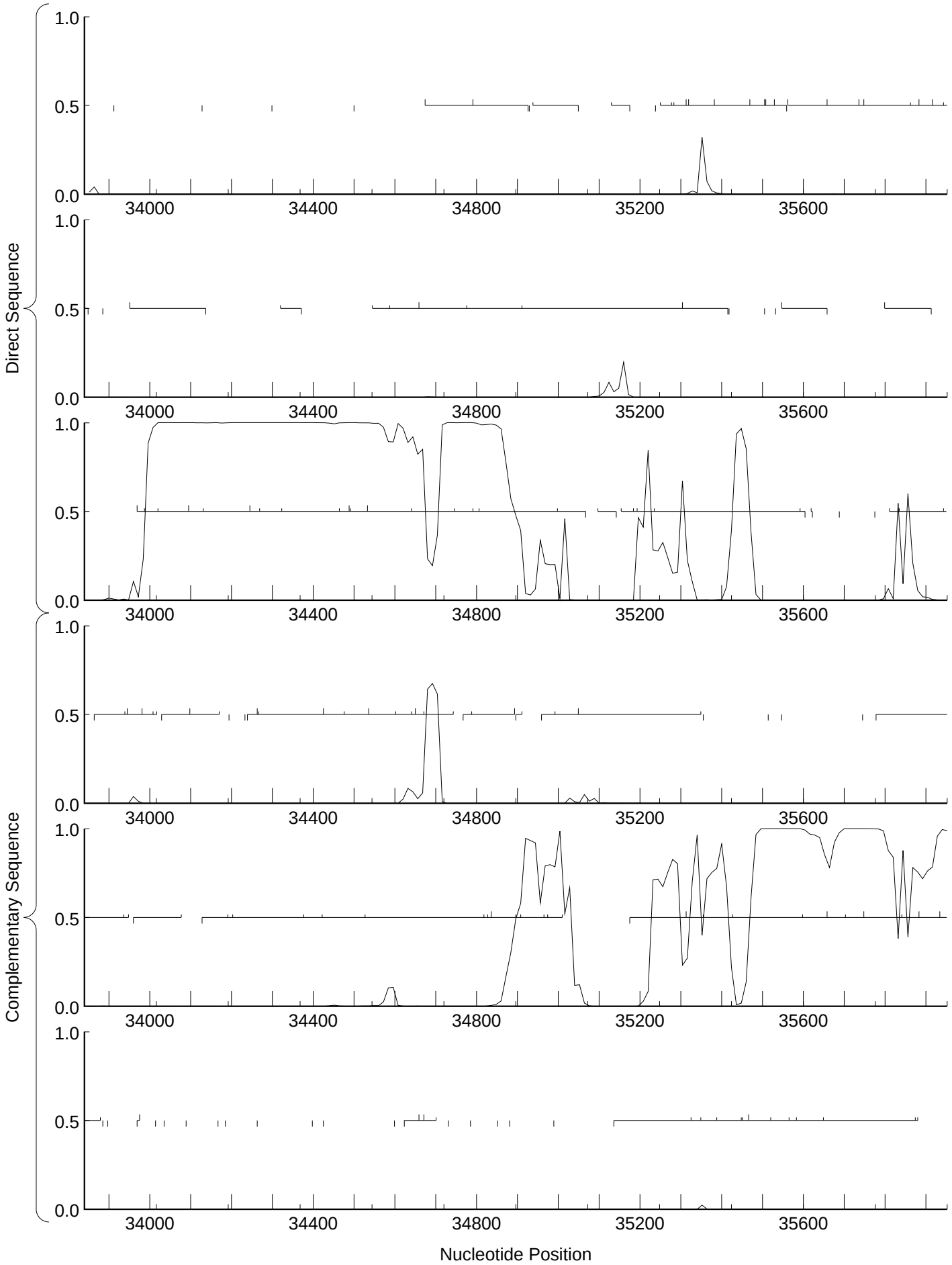


complete sequence, 57315 bp including 11-base 3’ overhang (CCTCGCGGCAT), Cluster K2, Order 4, Window 96, Step 12, 16/29

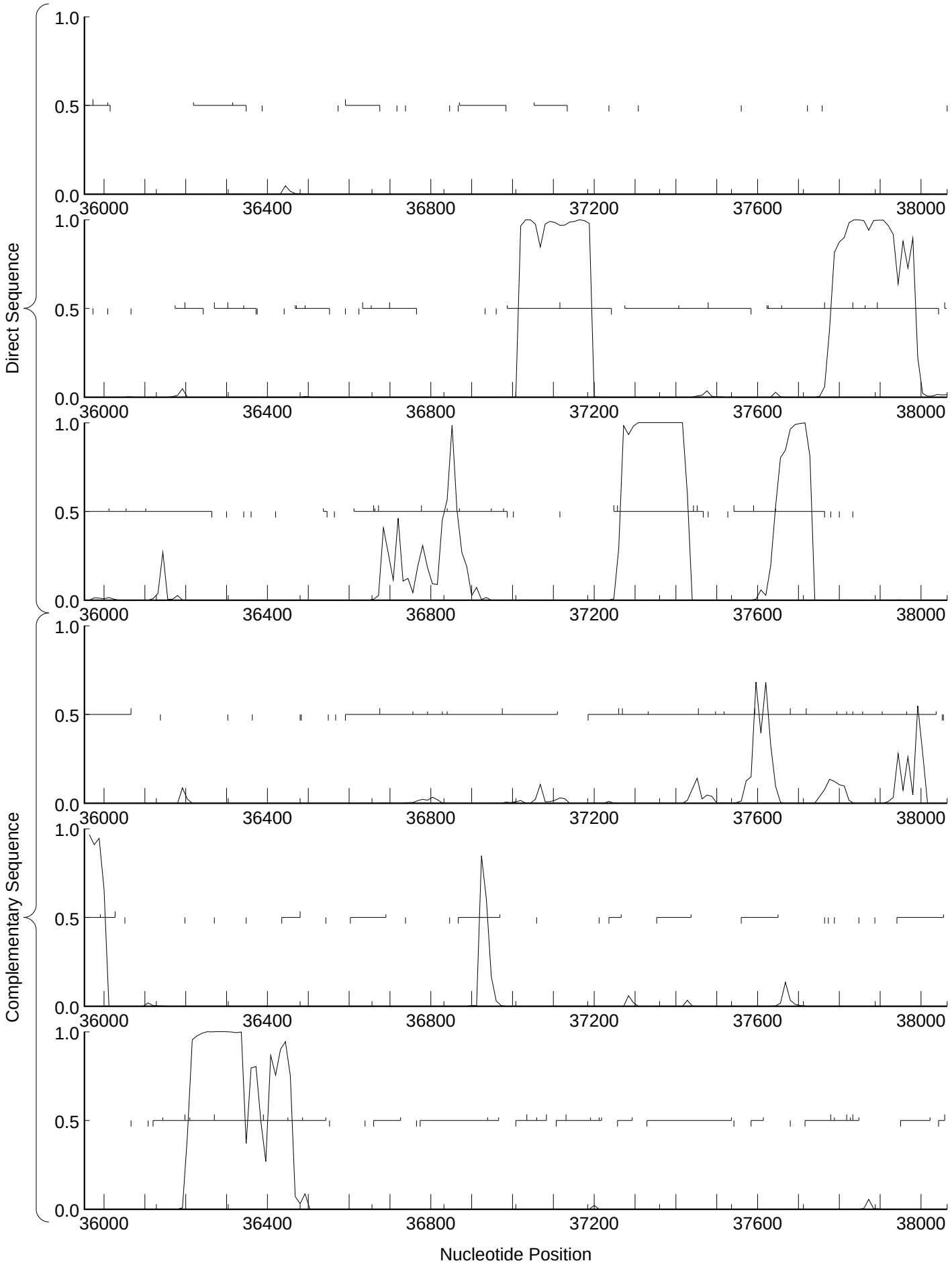


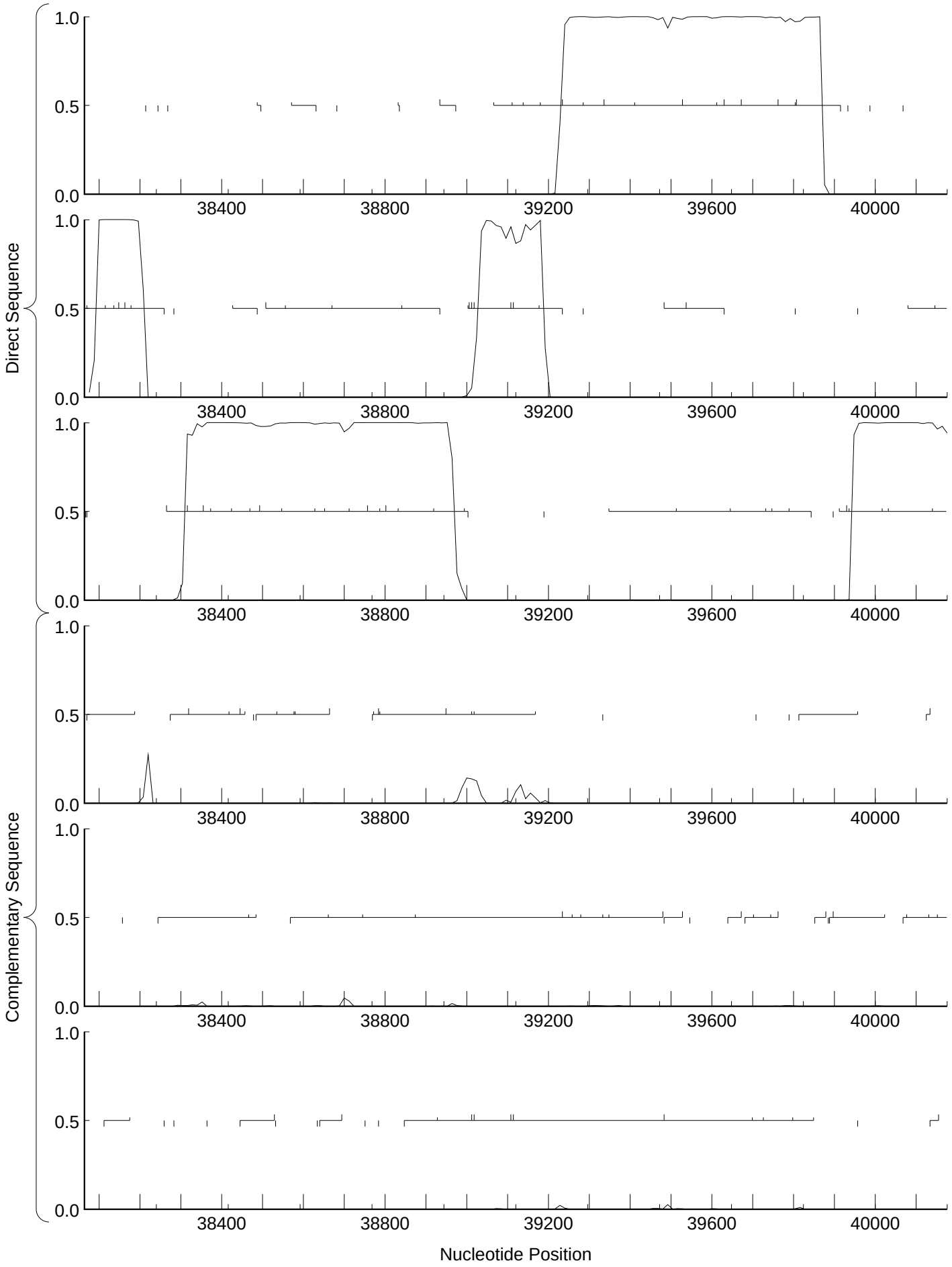
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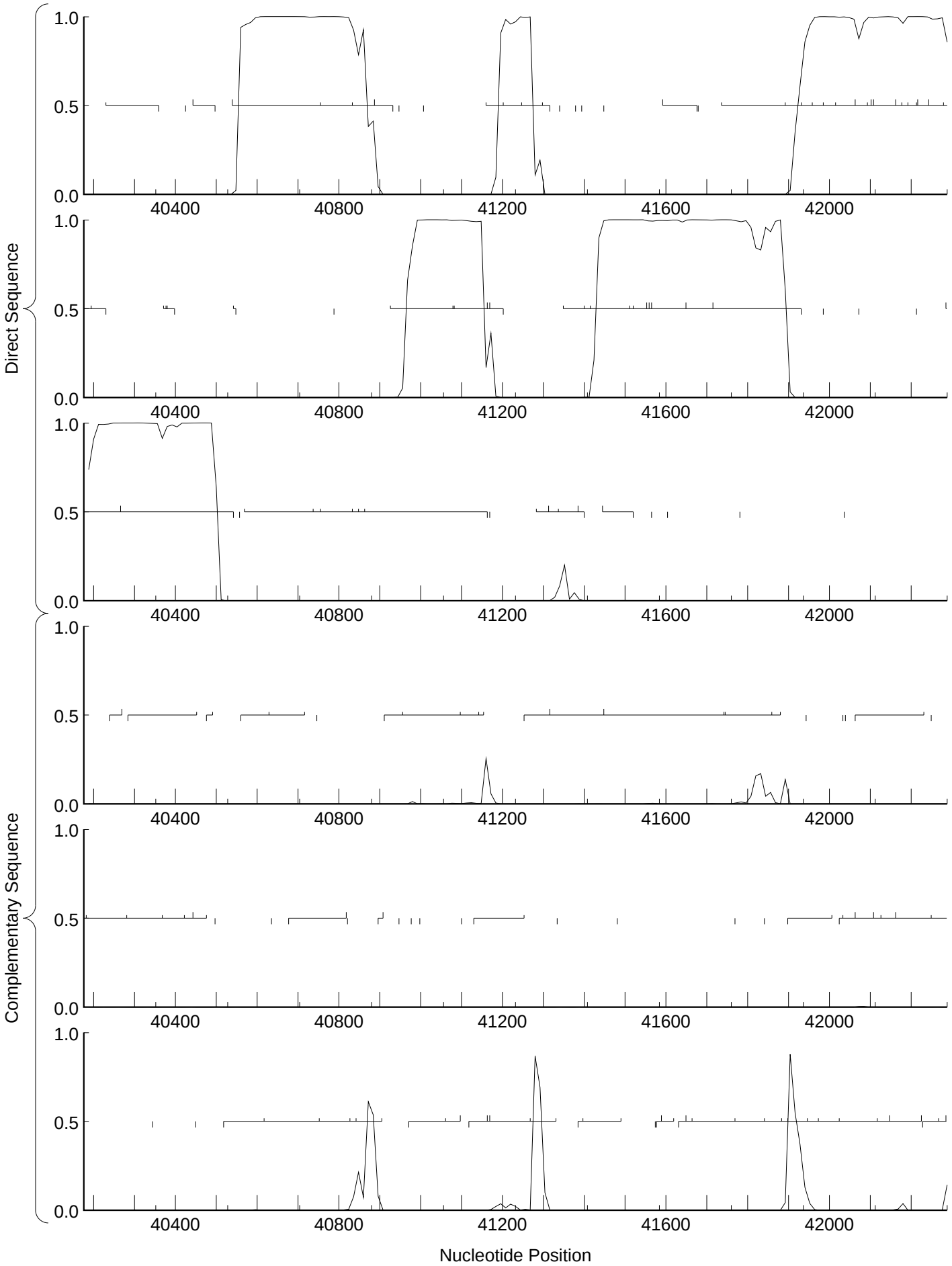

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
34000
34400
34800
35200
35600
Nucleotide Position

complete sequence, 57315 bp including 11-base 3' overhang (CCTCGCGGCAT), Cluster K2, Order 4, Window 96, Step 12, 19/29

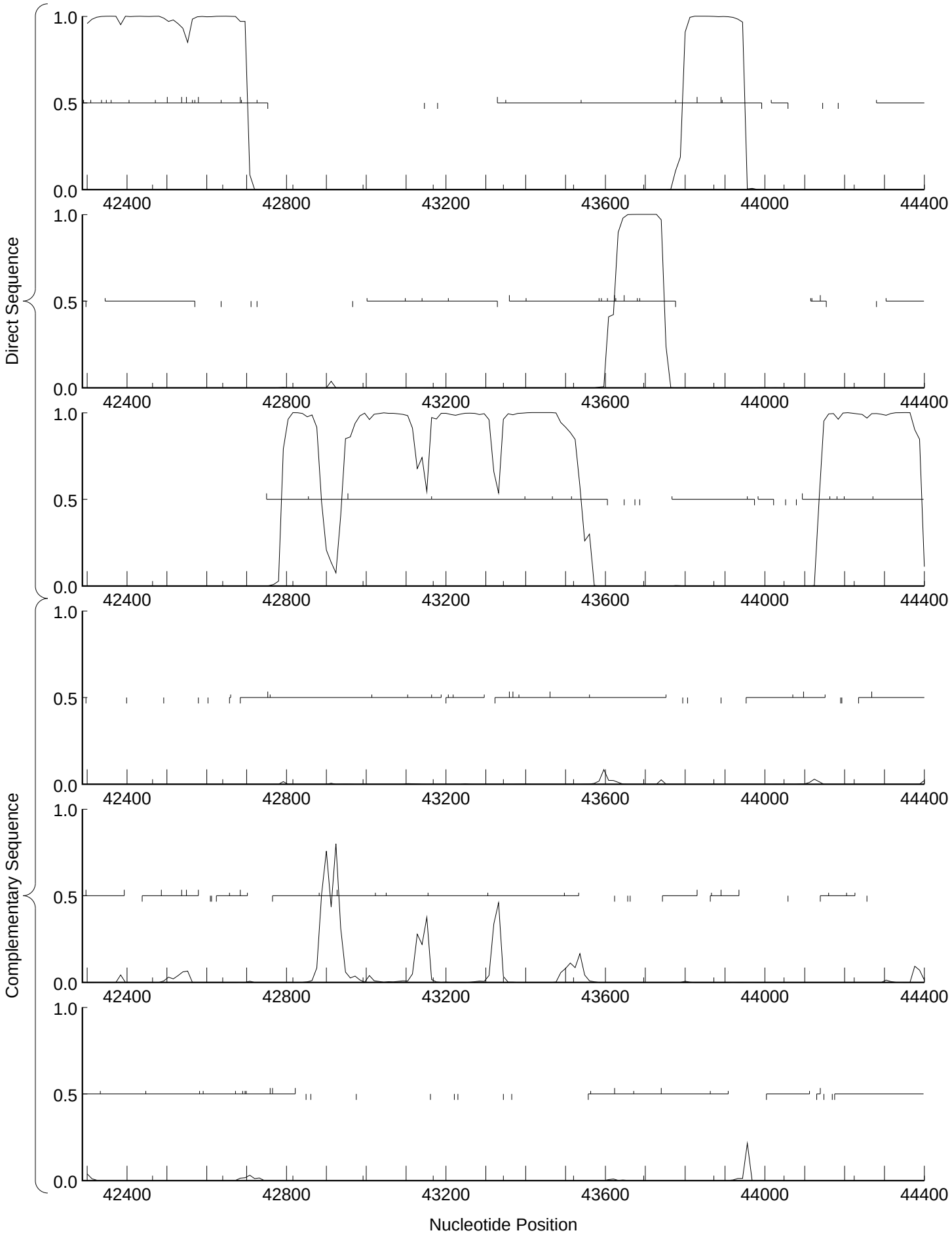



Direct Sequence
Complementary Sequence
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0.5
0.0
38400
38800
39200
39600
40000
Nucleotide Position

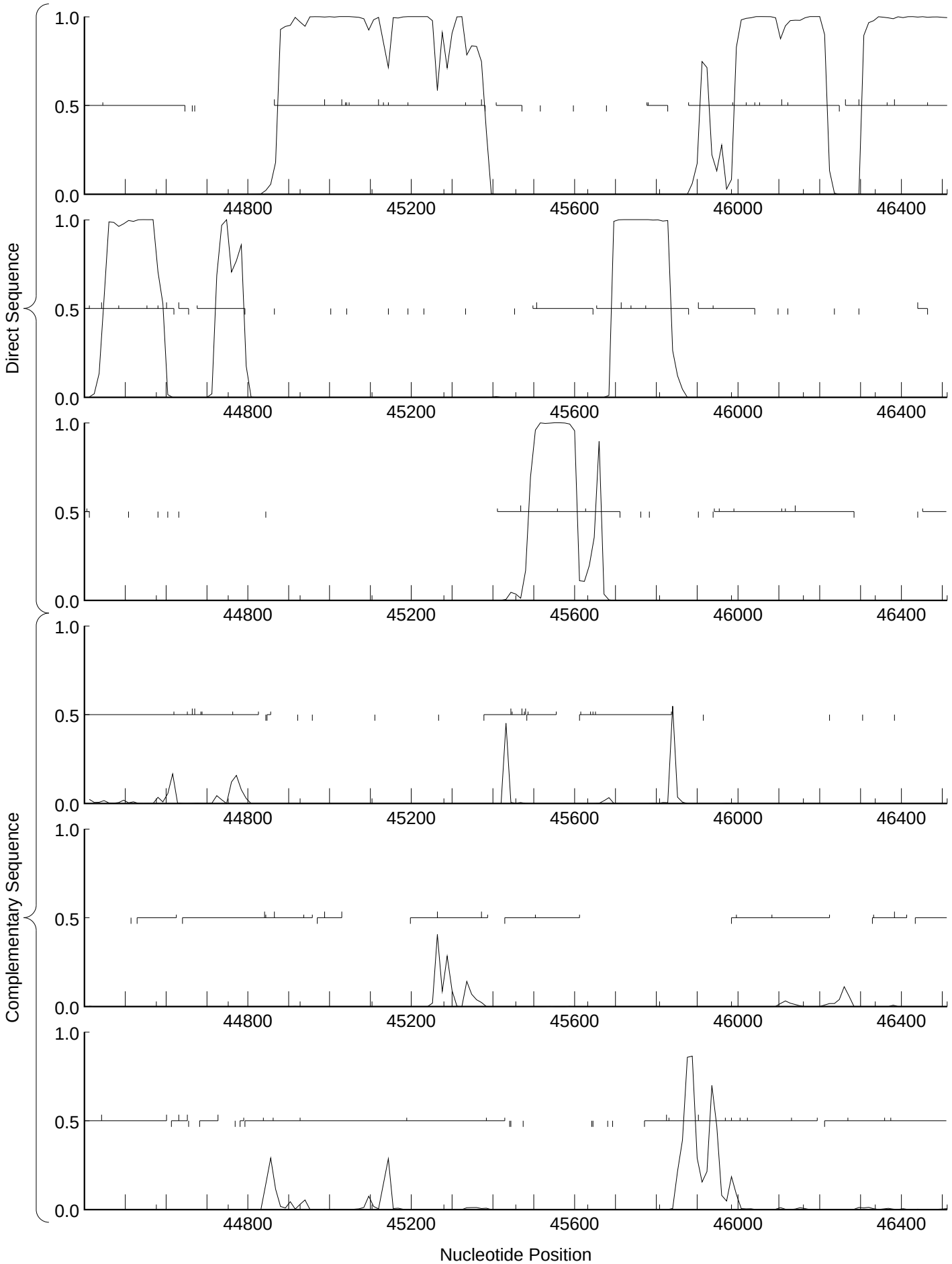
complete sequence, 57315 bp including 11-base 3' overhang (CCTCGCGGCAT), Cluster K2, Order 4, Window 96, Step 12, 21/29

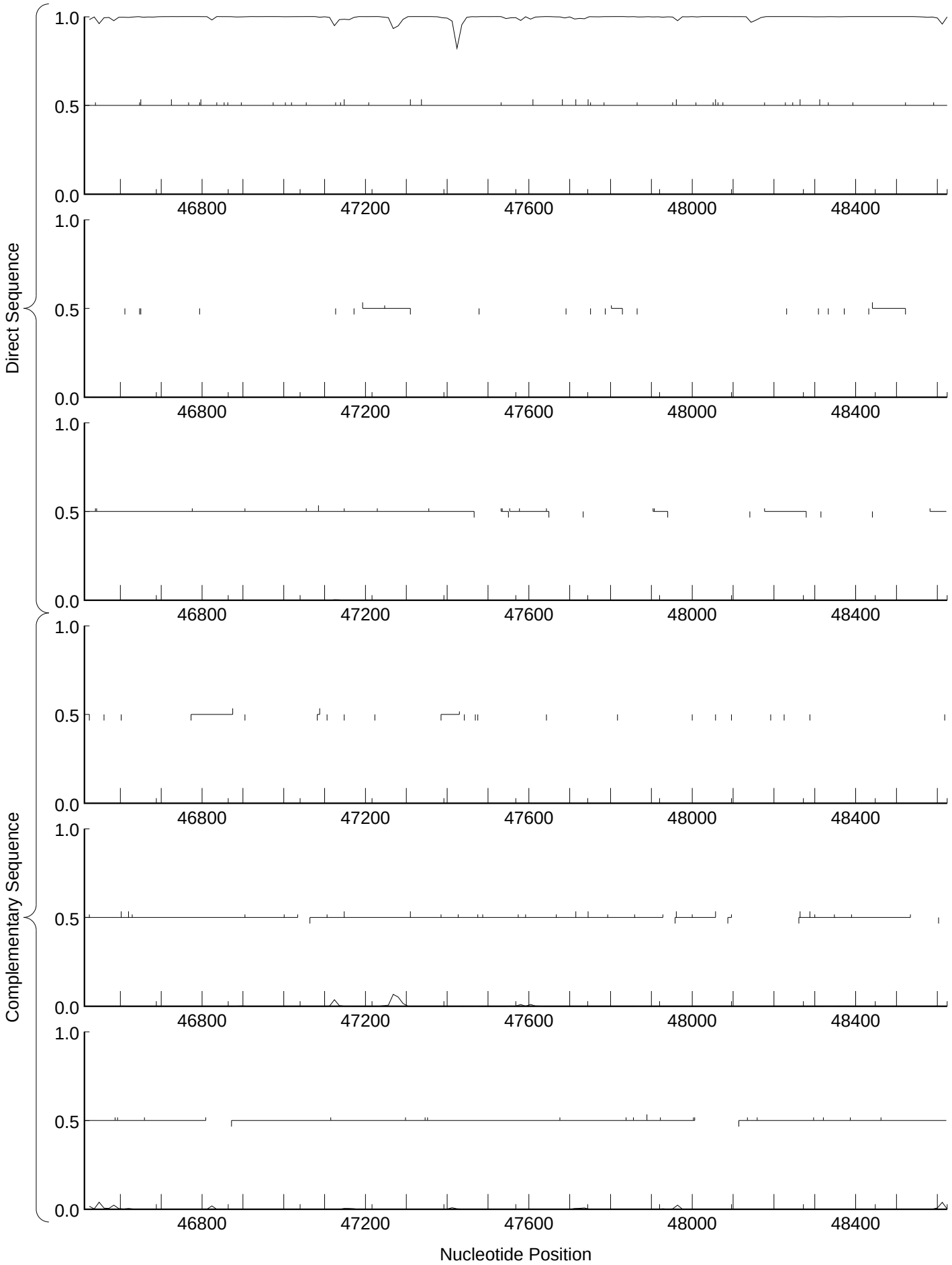


complete sequence, 57315 bp including 11-base 3’ overhang (CCTCGCGGCAT), Cluster K2, Order 4, Window 96, Step 12, 22/29

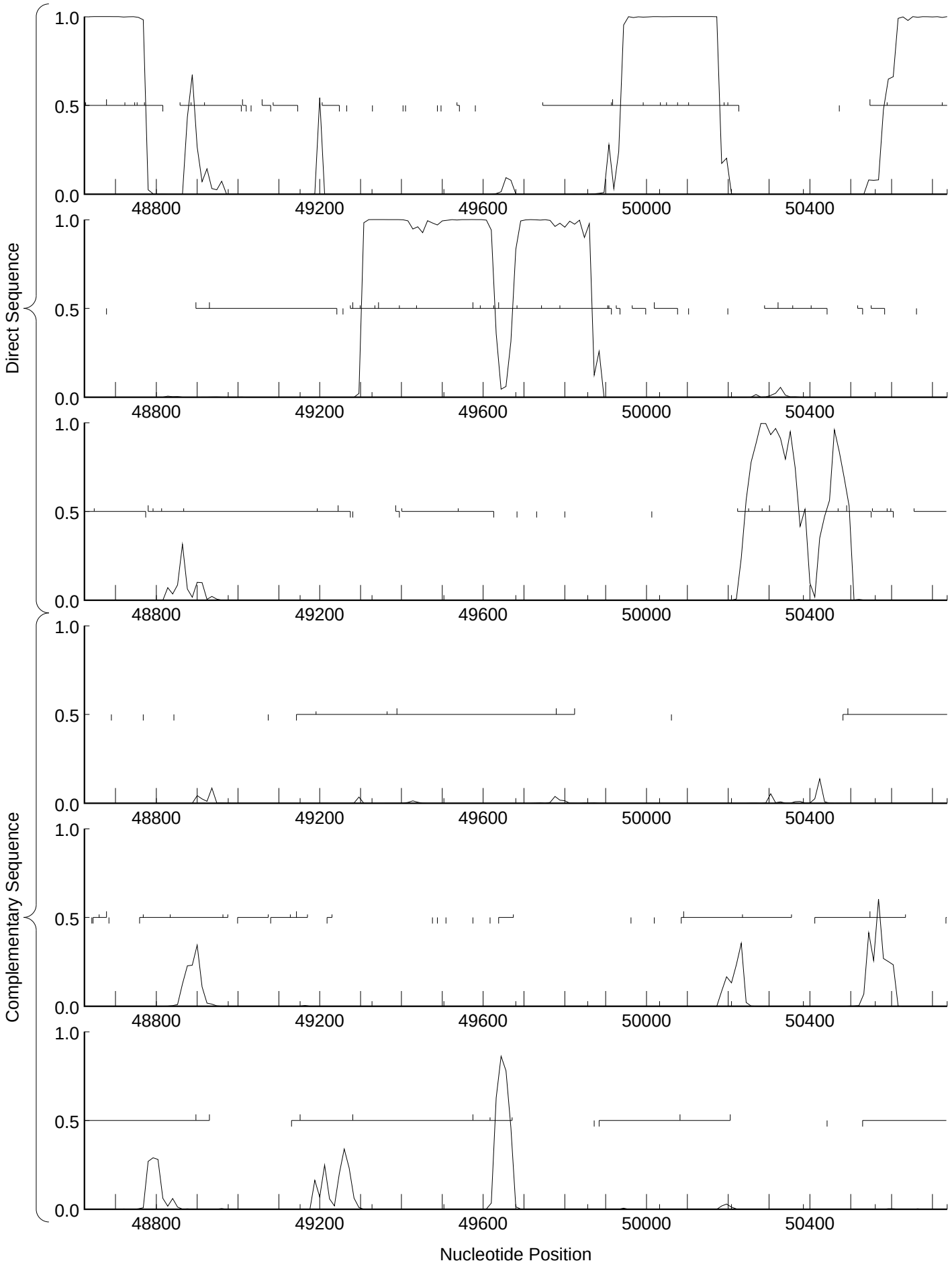


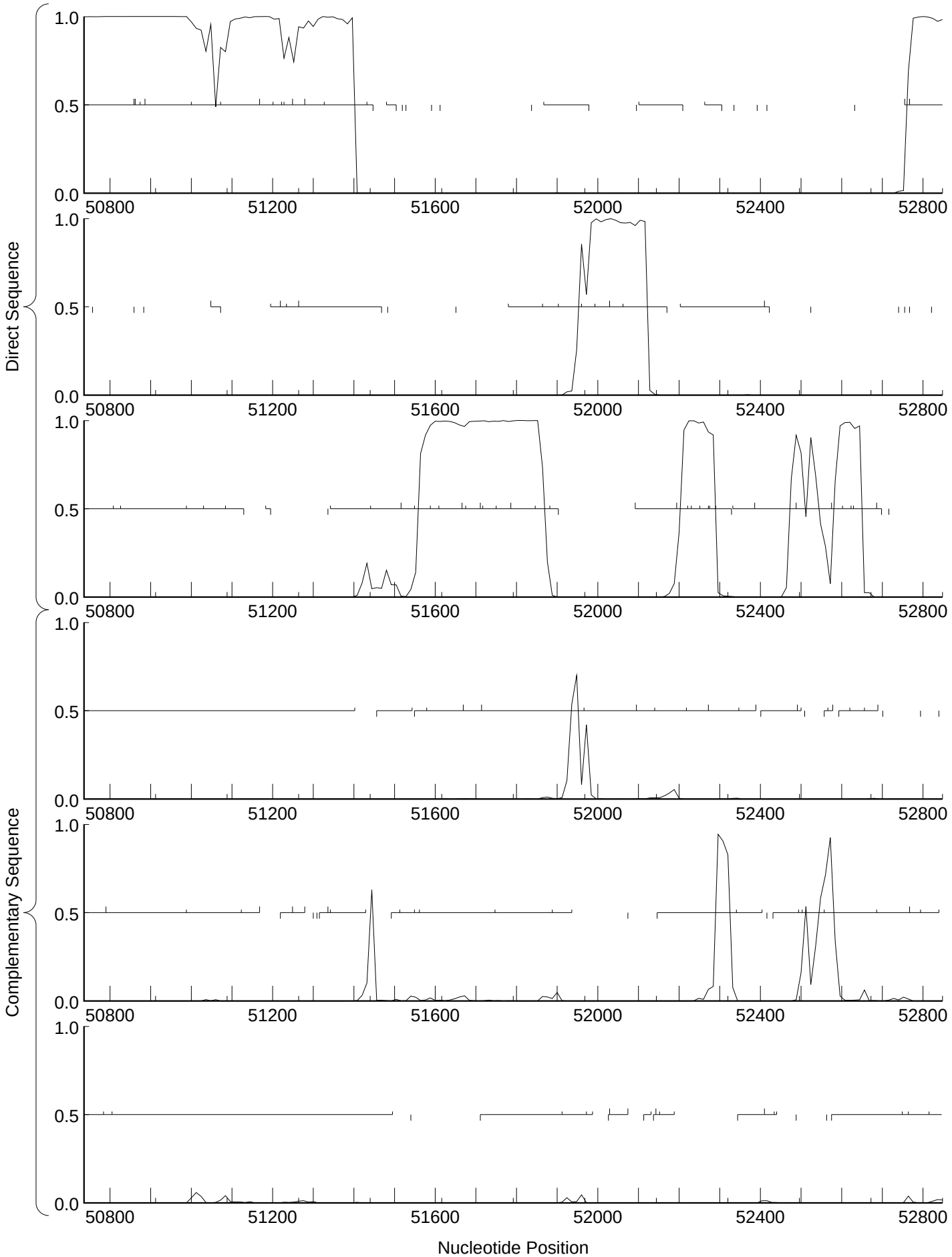
complete sequence, 57315 bp including 11-base 3' overhang (CCTCGCGGCAT), Cluster K2, Order 4, Window 96, Step 12, 23/29



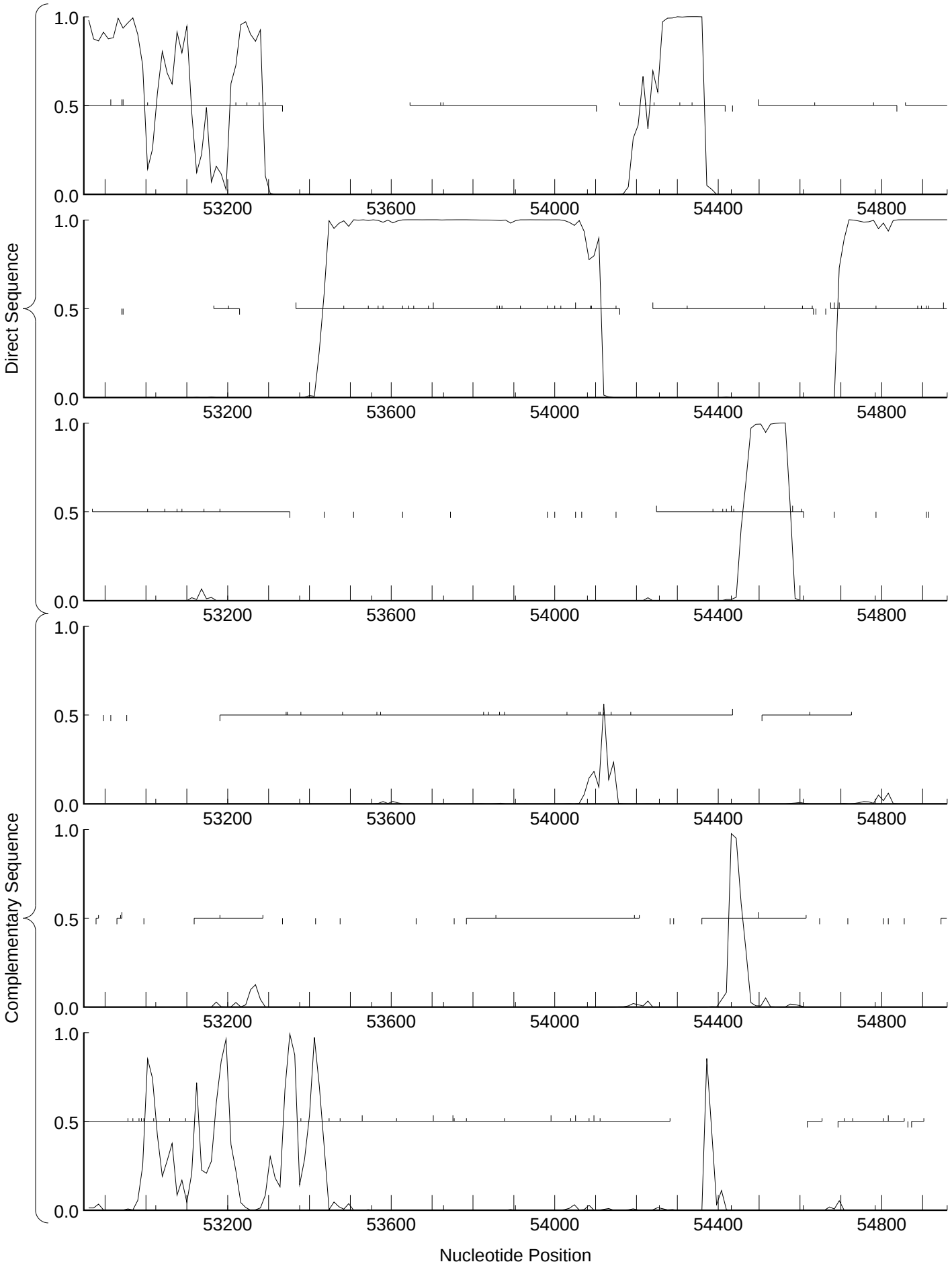

Direct Sequence
Complementary Sequence
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0.5
0.0
46800
47200
47600
48000
48400
Nucleotide Position

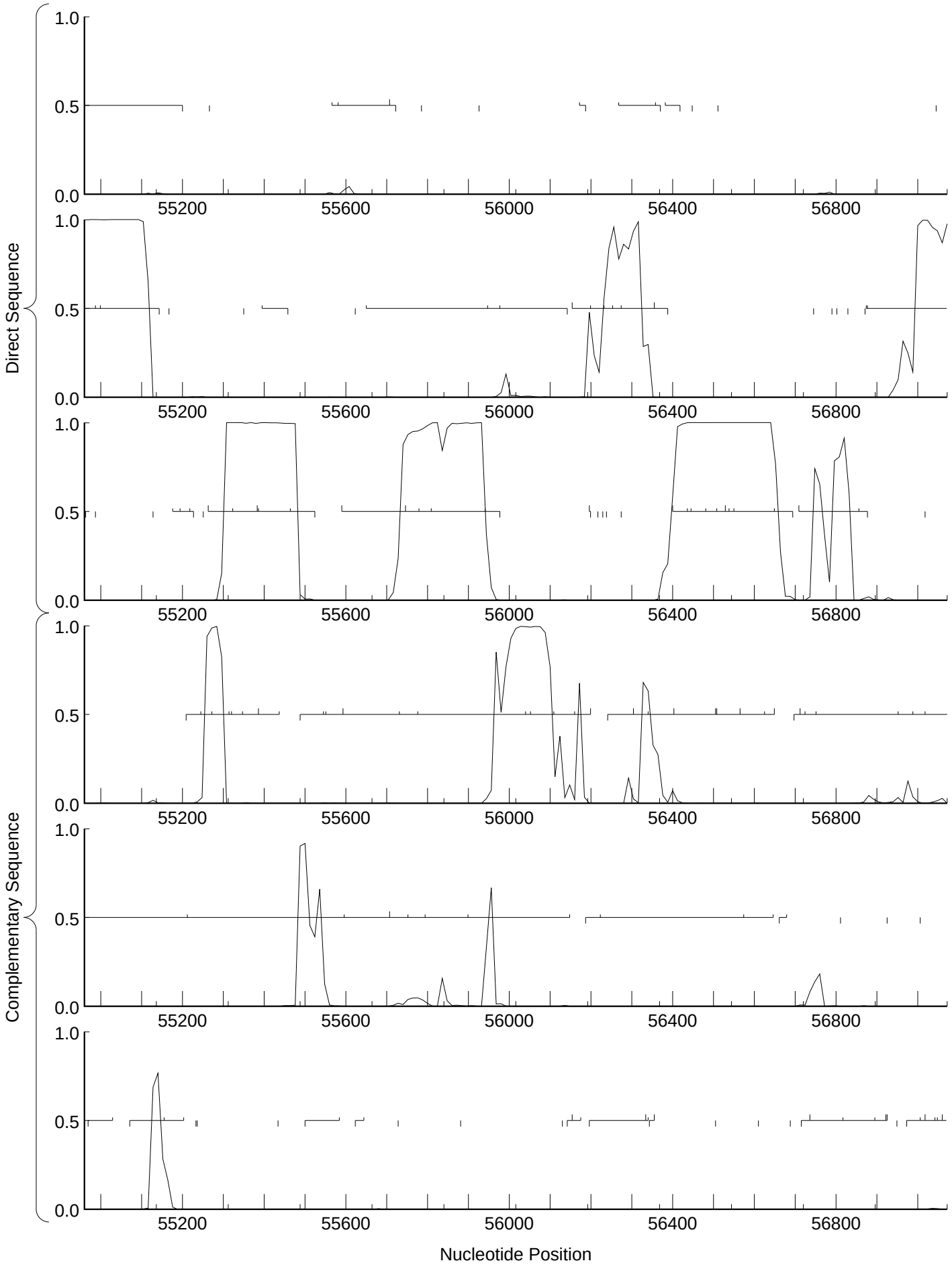
complete sequence, 57315 bp including 11-base 3’ overhang (CCTCGCGGCAT), Cluster K2, Order 4, Window 96, Step 12, 25/29




Direct Sequence
Complementary Sequence
1.0
0.5
0.0
50800
51200
51600
52000
52400
52800
Nucleotide Position

complete sequence, 57315 bp including 11-base 3' overhang (CCTCGCGGCAT), Cluster K2, Order 4, Window 96, Step 12, 27/29




Direct Sequence
Complementary Sequence
1.0
0.5
0.0
55200
55600
56000
56400
56800
Nucleotide Position

complete sequence, 57315 bp including 11-base 3’ overhang (CCTCGCGGCAT), Cluster K2, Order 4, Window 96, Step 12, 29/29

