GeneMark

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

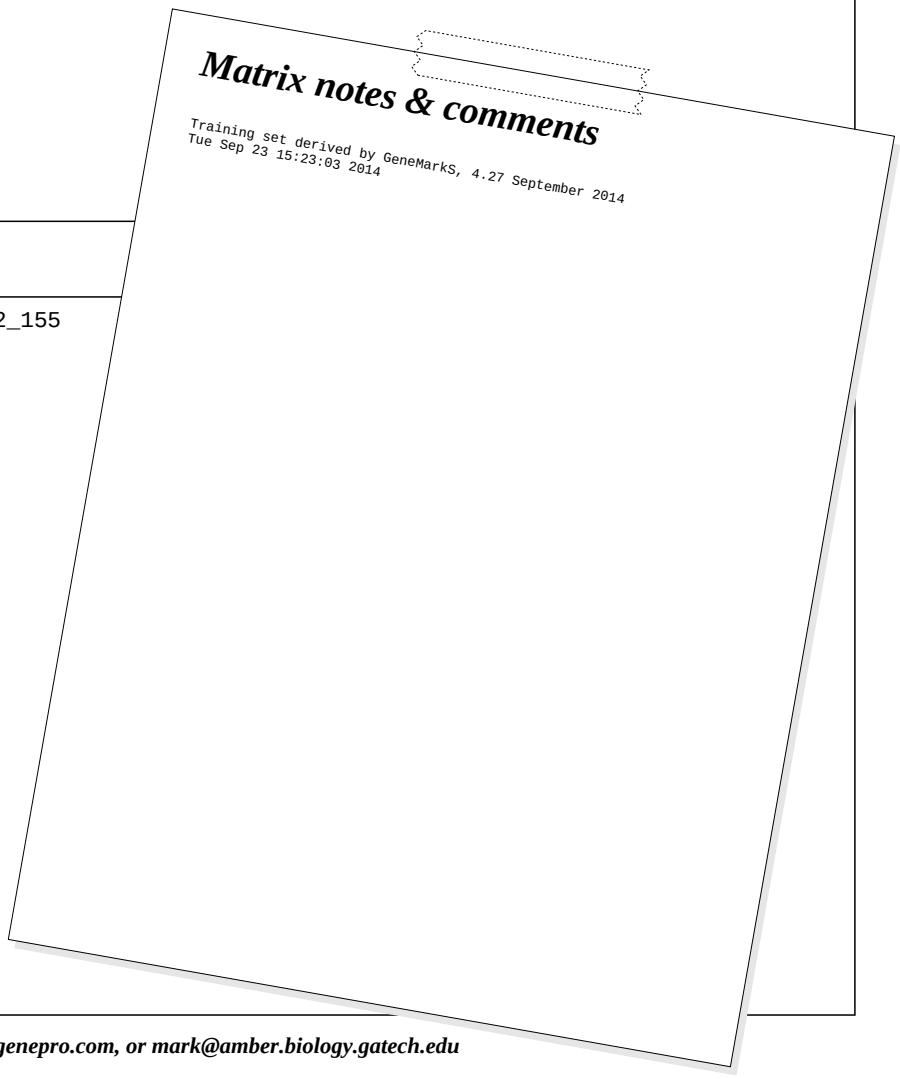
PROGRAM INFORMATION

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Sequence         :  Mycobacterium phage DarthP complete sequence, 61594 bp including 11-base 3' overhang (CTCGT
Analysis Date    :  3/28/24 at 4:13:33
Pages            :  31
Sequence Length  :  61594 bp
GC Content       :   67.24%

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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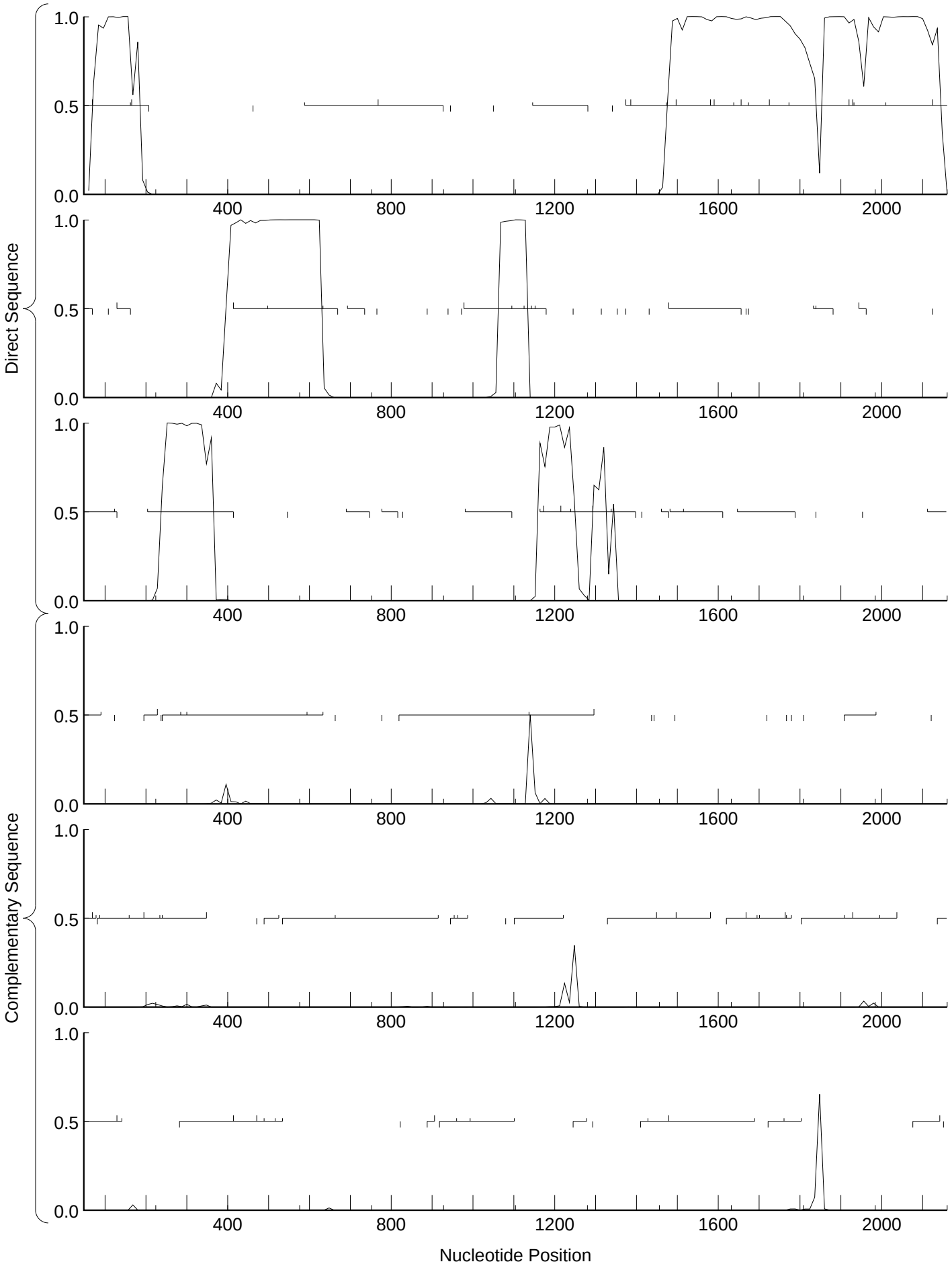
MATRIX INFORMATION

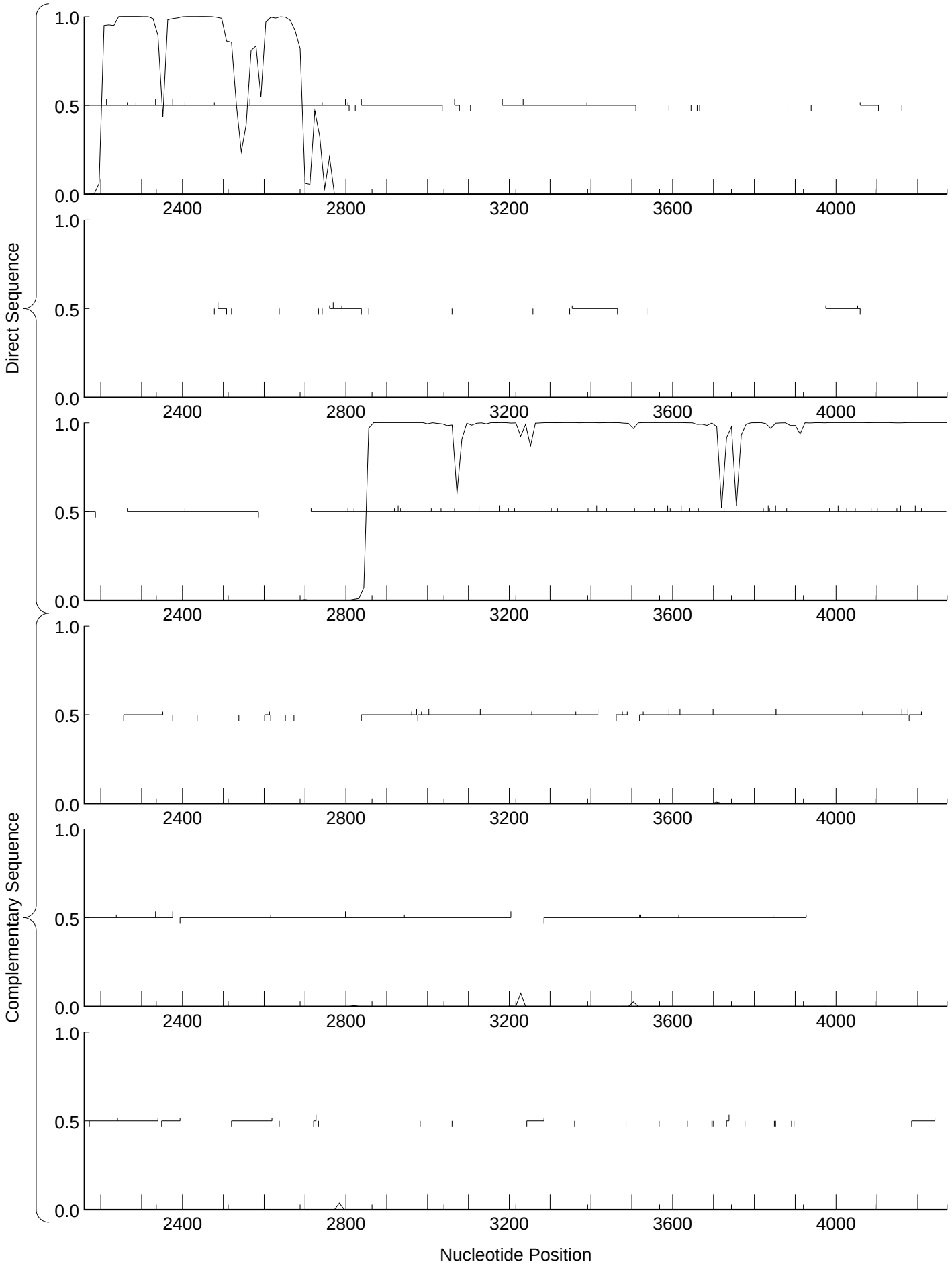
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Matrix     :  Mycobacterium_smegmatis_MC2_155
Author     :  -

Order      :  4
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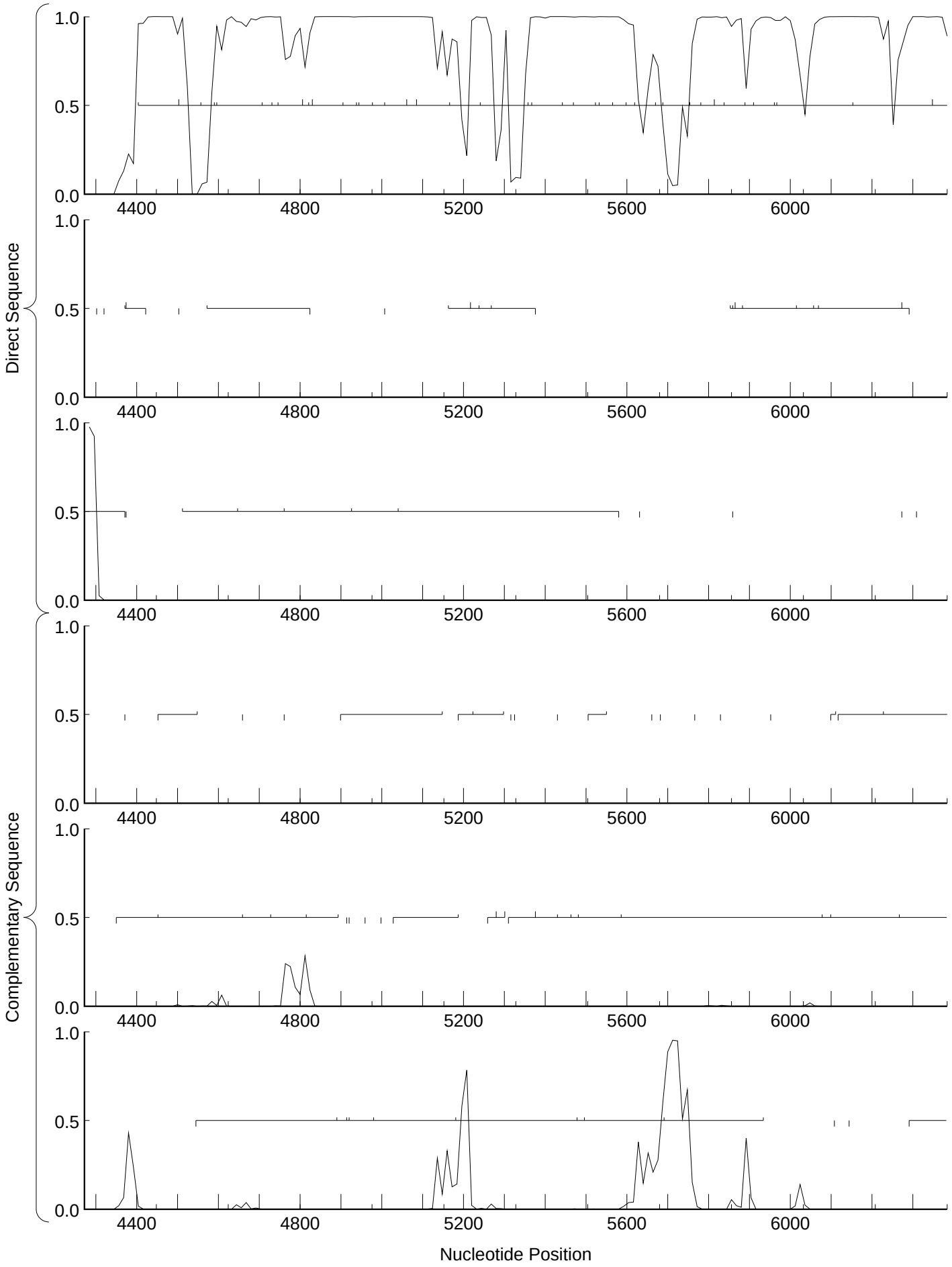

```
  Send questions / comments to:
      Dr. M. Borodovsky
      Georgia Institute of Technology
      School of Biology
      Atlanta, GA  30332-0230
```


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

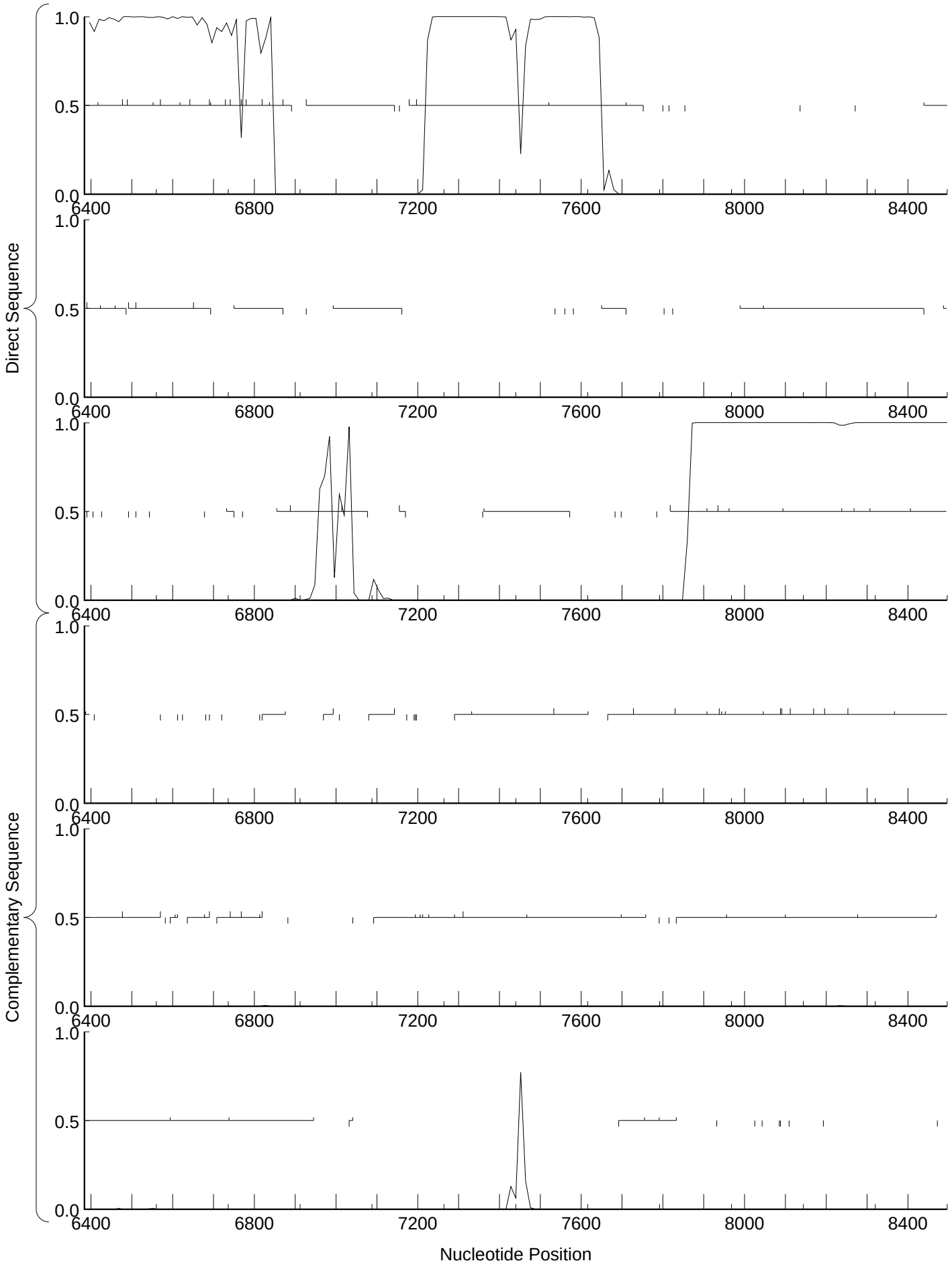

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
400
800
1200
1600
2000
Nucleotide Position


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
2400
2800
3200
3600
4000
Nucleotide Position

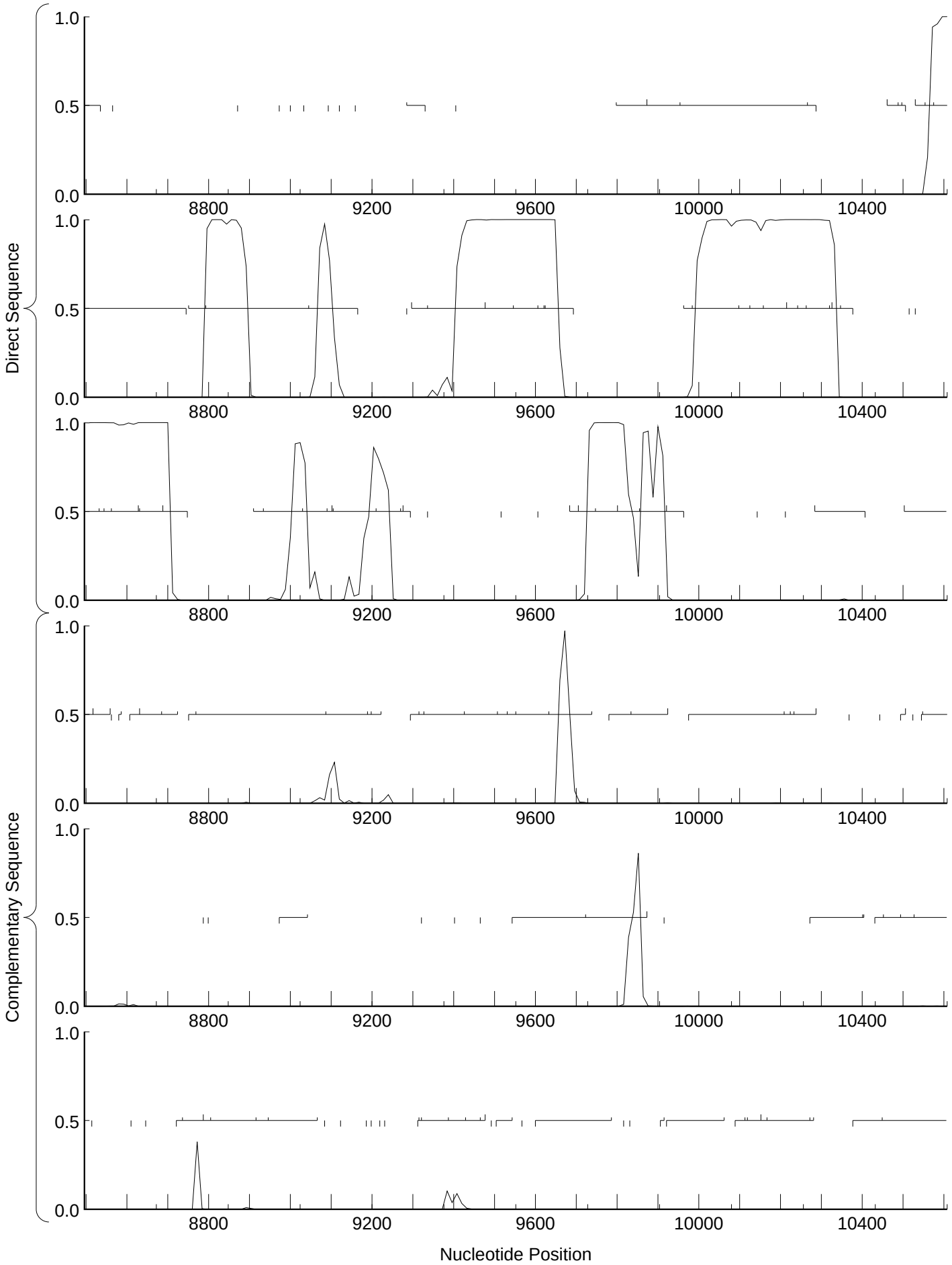
complete sequence, 61594 bp including 11-base 3' overhang (CTCGTAGGCAT), Cluster K6, Order 4, Window 96, Step 12, 4/31



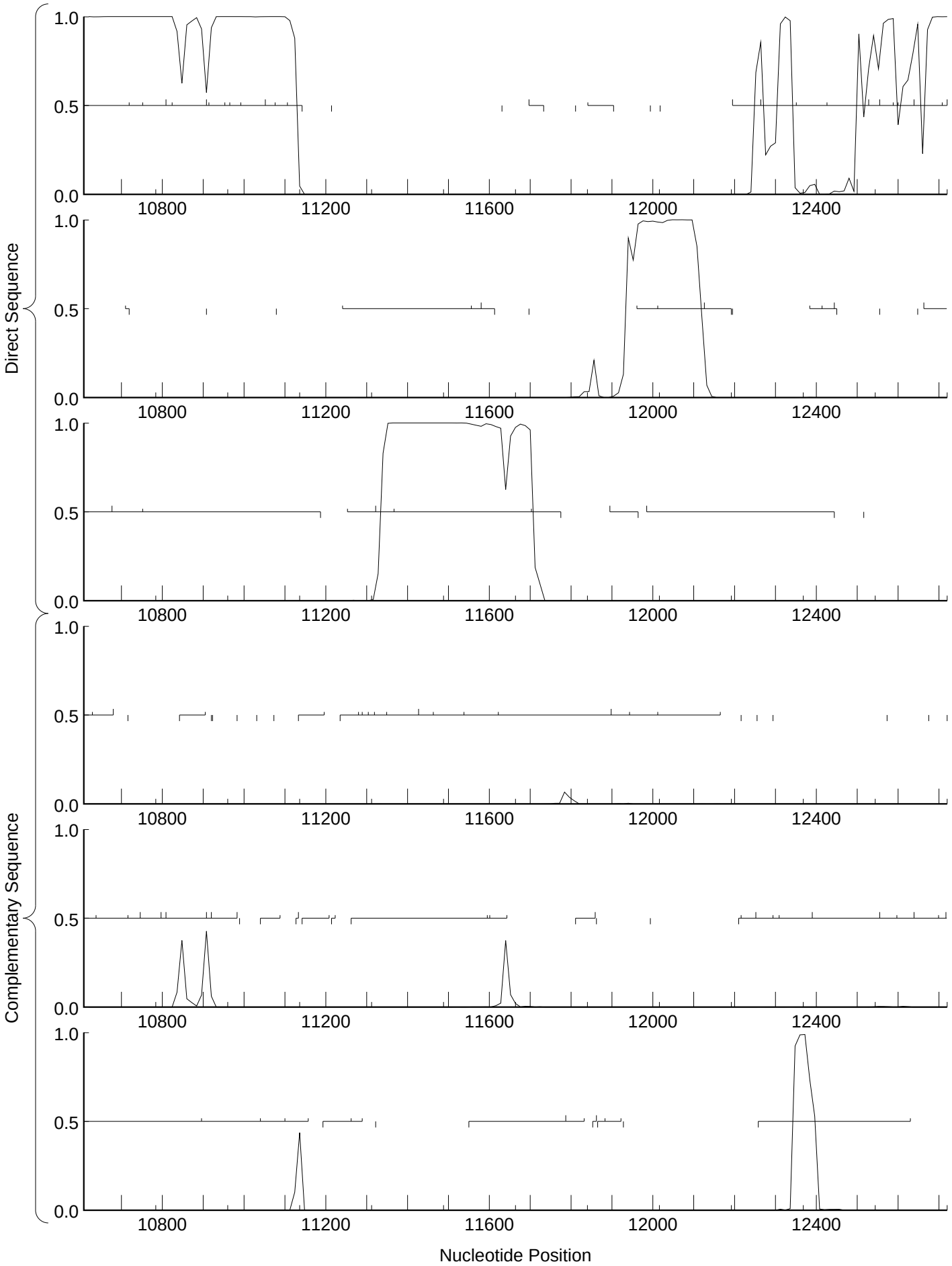
complete sequence, 61594 bp including 11-base 3' overhang (CTCGTAGGCAT), Cluster K6, Order 4, Window 96, Step 12, 5/31

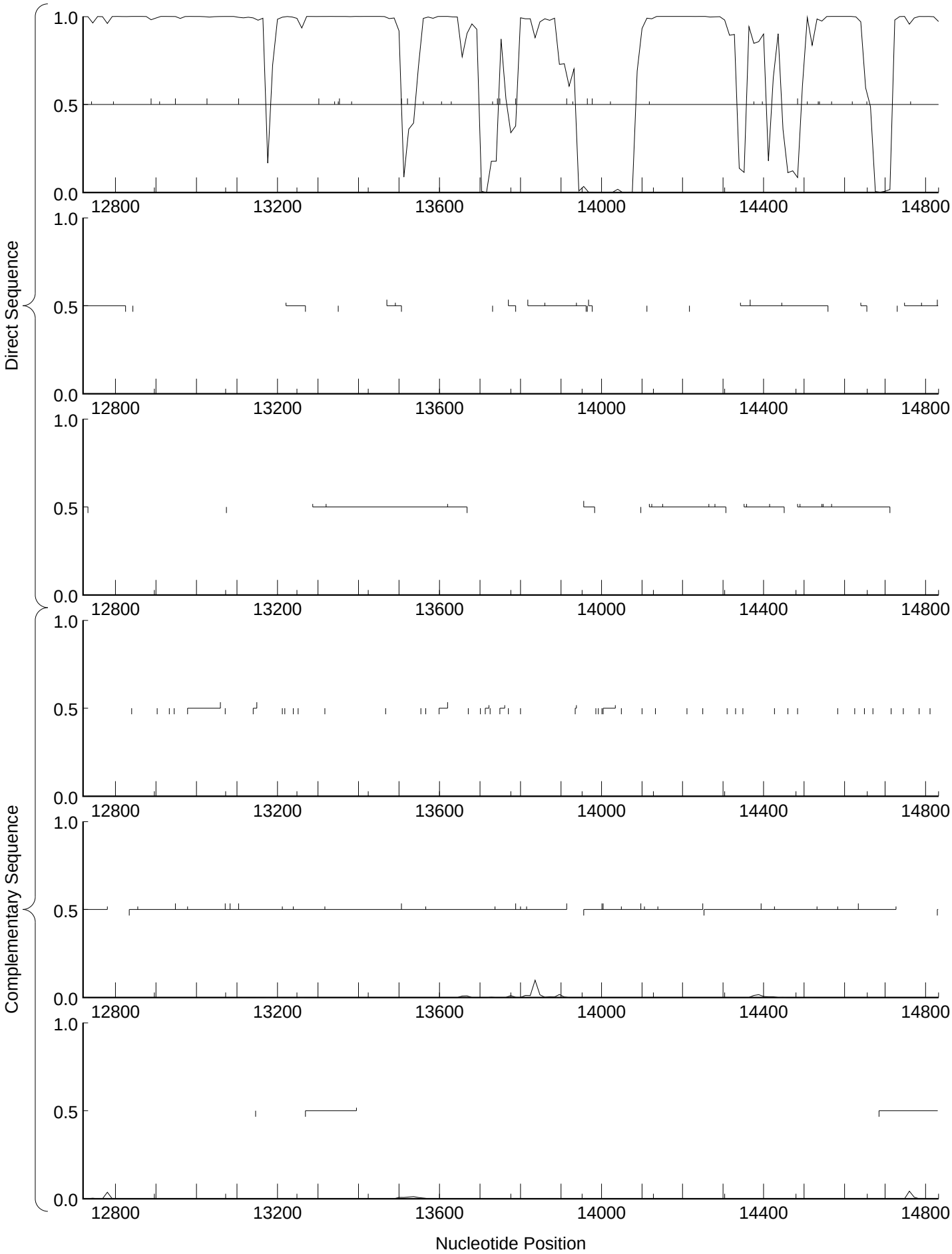


complete sequence, 61594 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K6, Order 4, Window 96, Step 12, 6/31

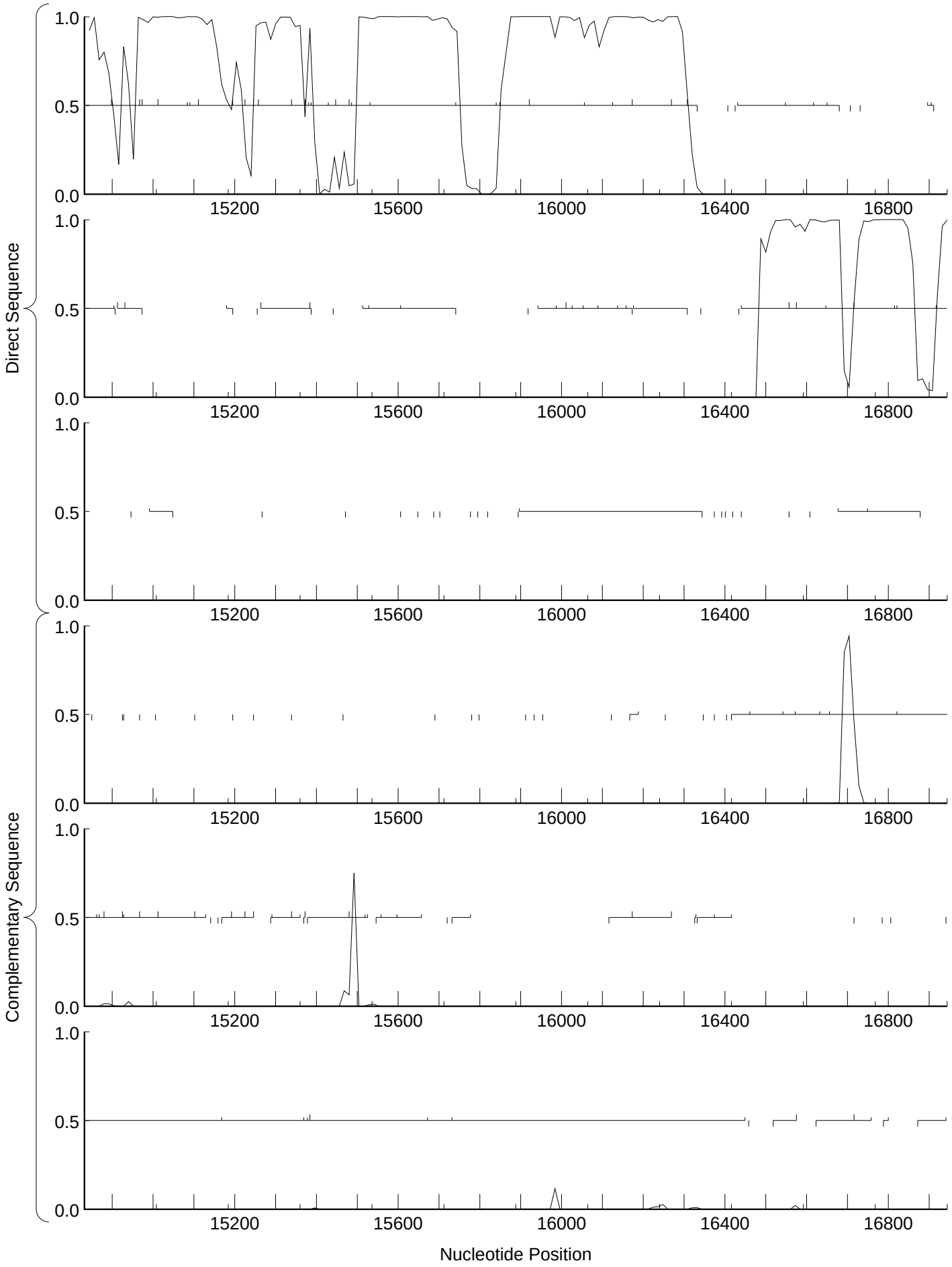


complete sequence, 61594 bp including 11-base 3' overhang (CTCGTAGGCAT), Cluster K6, Order 4, Window 96, Step 12, 7/31

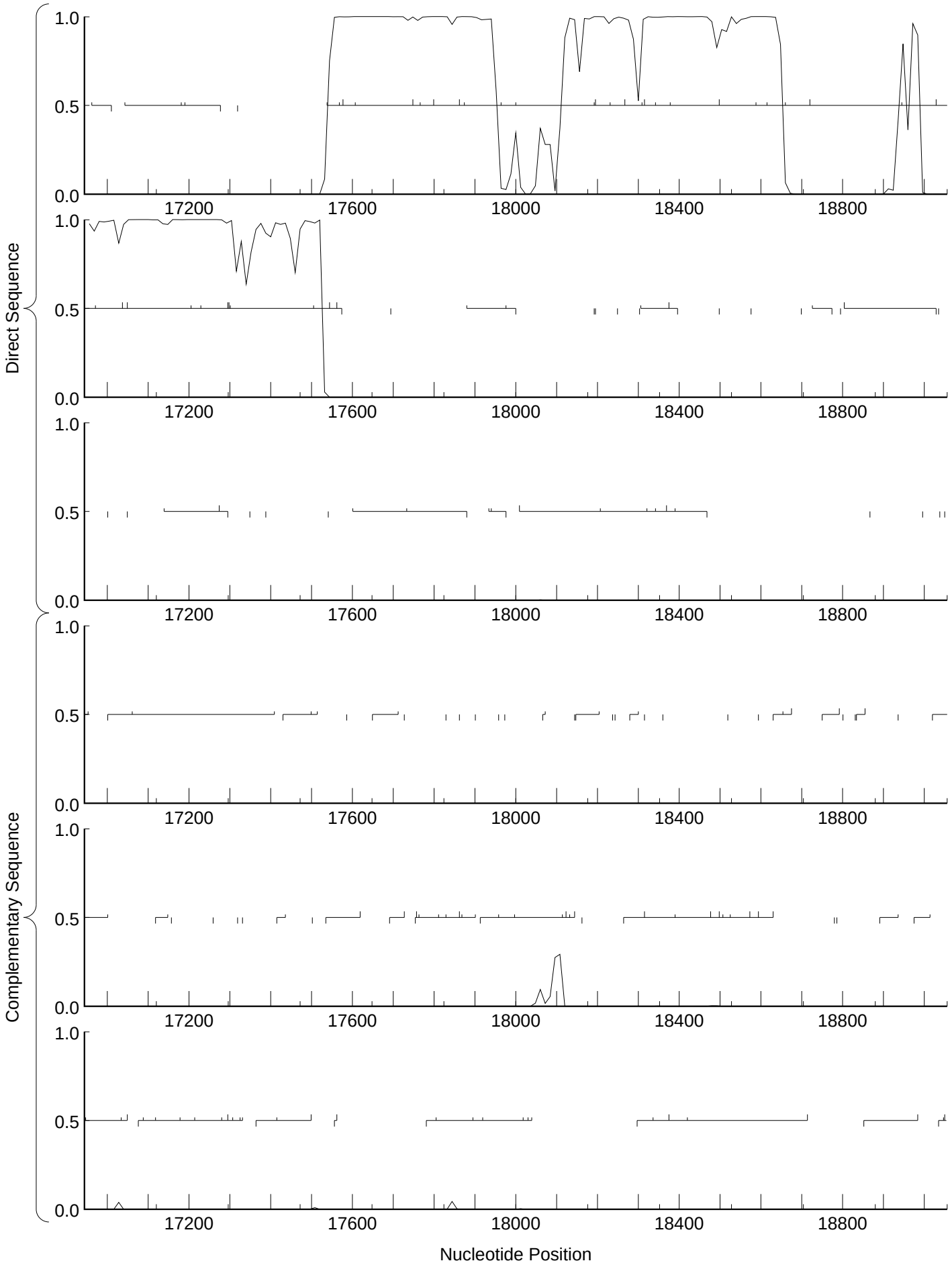



Direct Sequence
Complementary Sequence
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0.5
0.0
12800
13200
13600
14000
14400
14800
Nucleotide Position

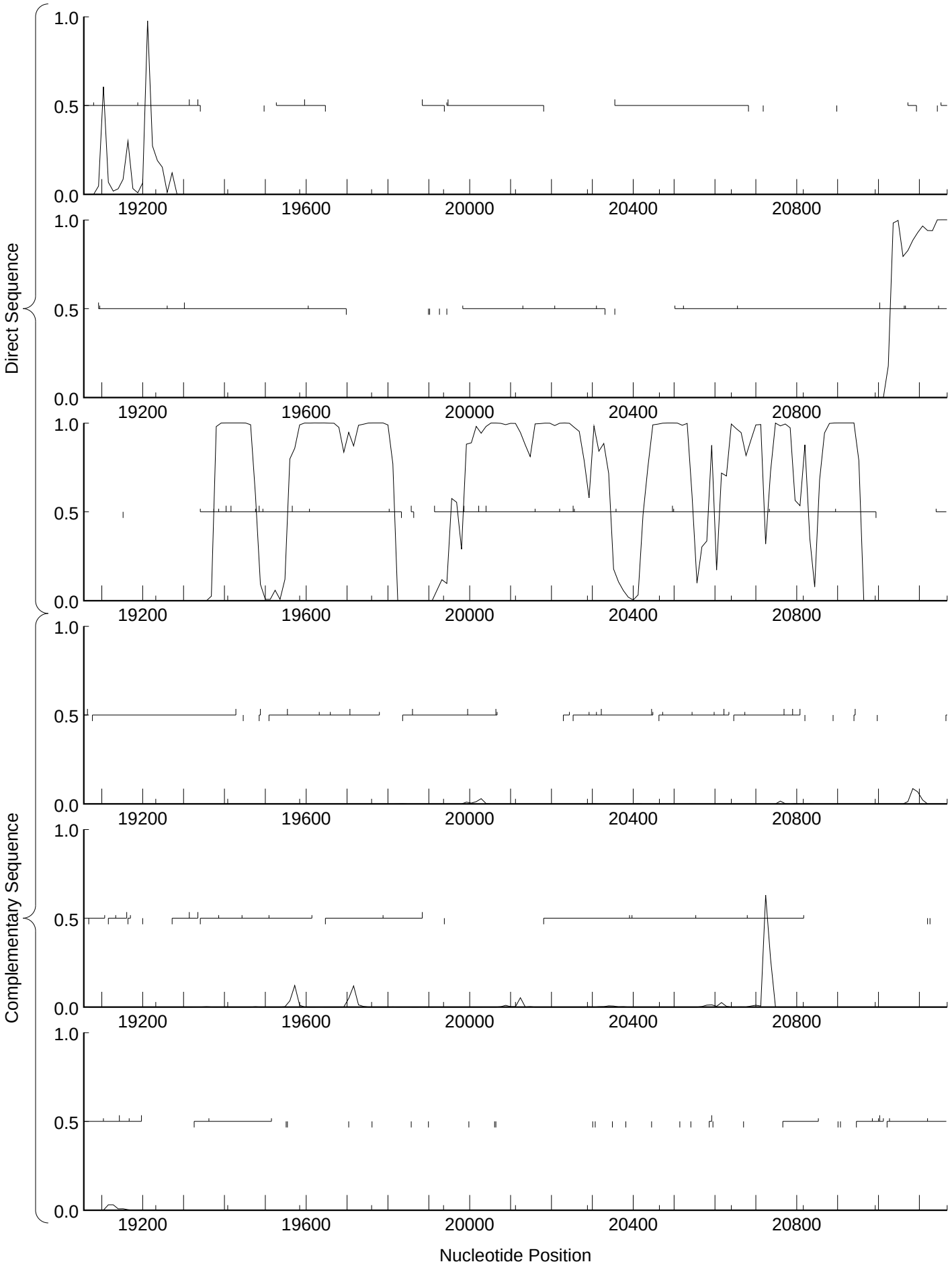
complete sequence, 61594 bp including 11-base 3' overhang (CTCGTAGGCAT), Cluster K6, Order 4, Window 96, Step 12, 9/31



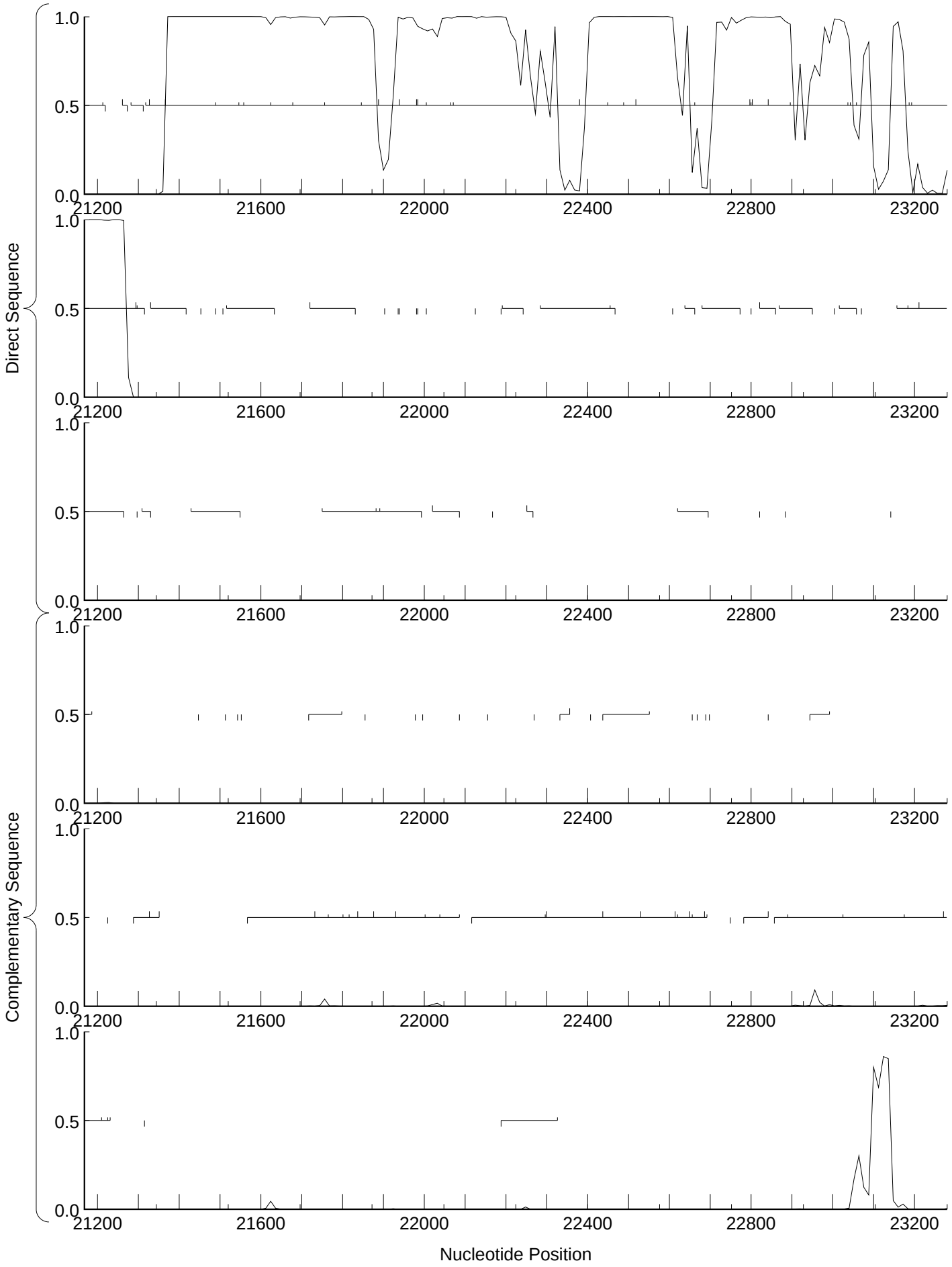
complete sequence, 61594 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K6, Order 4, Window 96, Step 12, 10/31



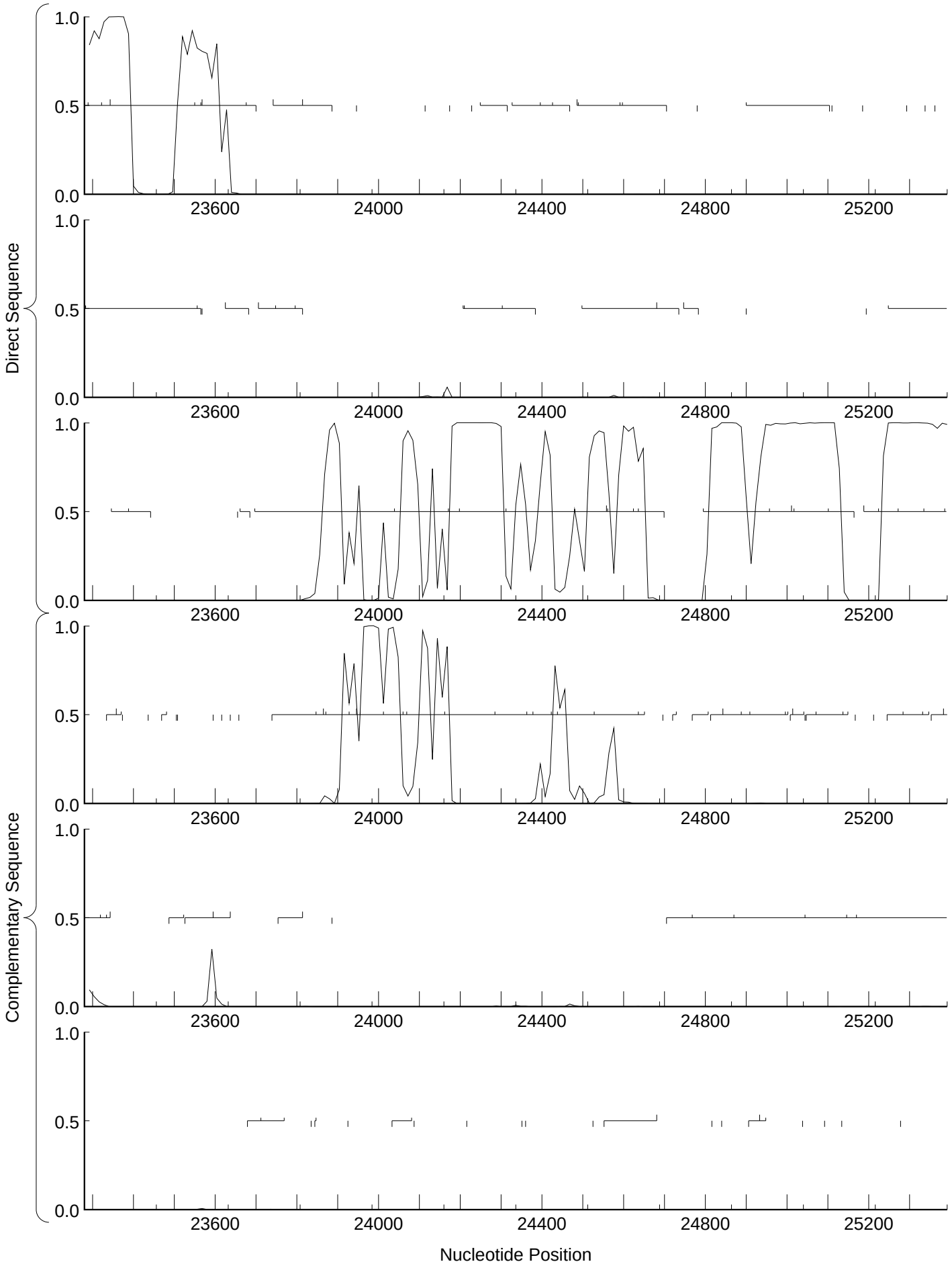
complete sequence, 61594 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K6, Order 4, Window 96, Step 12, 11/31



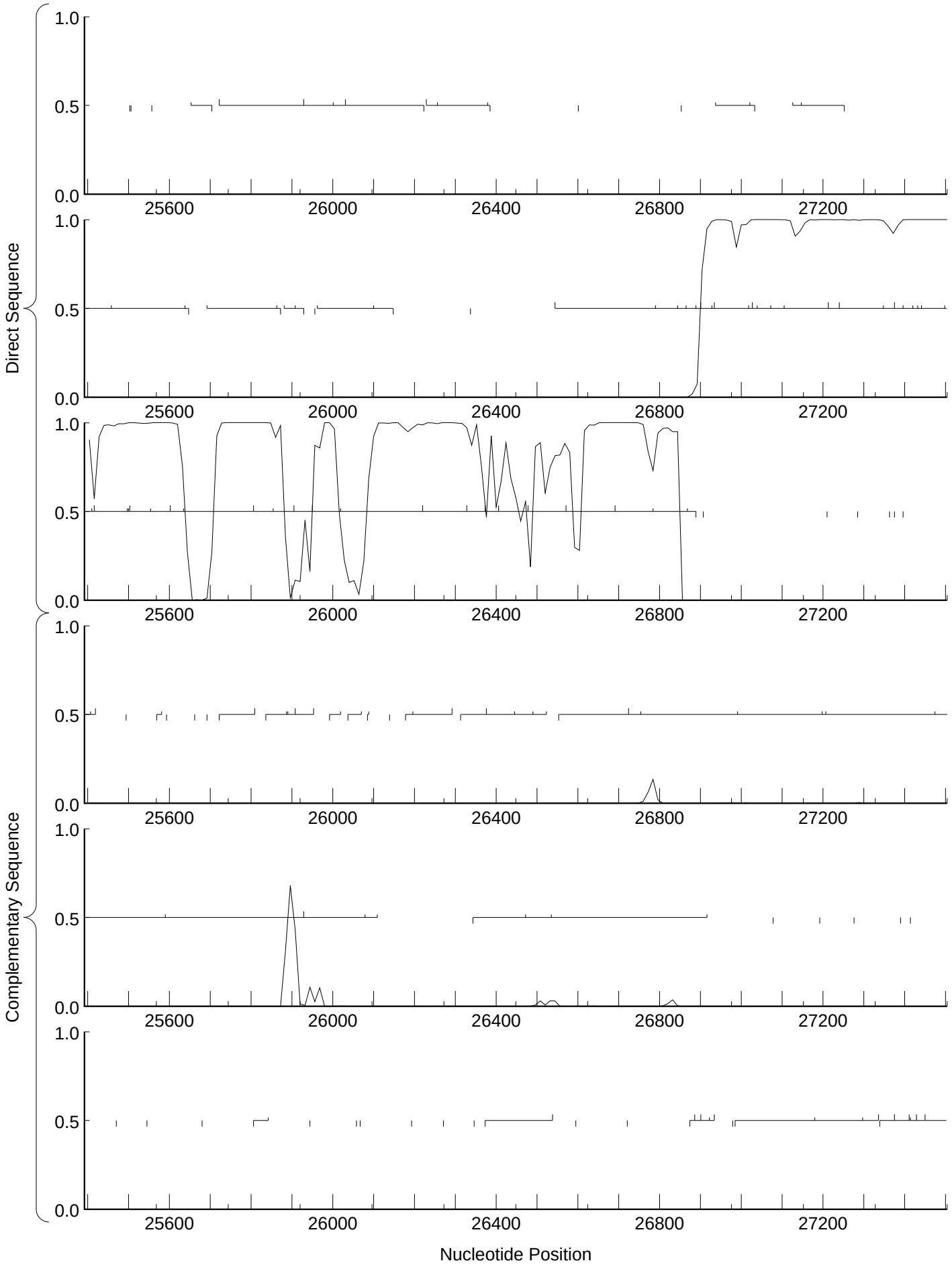
complete sequence, 61594 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K6, Order 4, Window 96, Step 12, 12/31



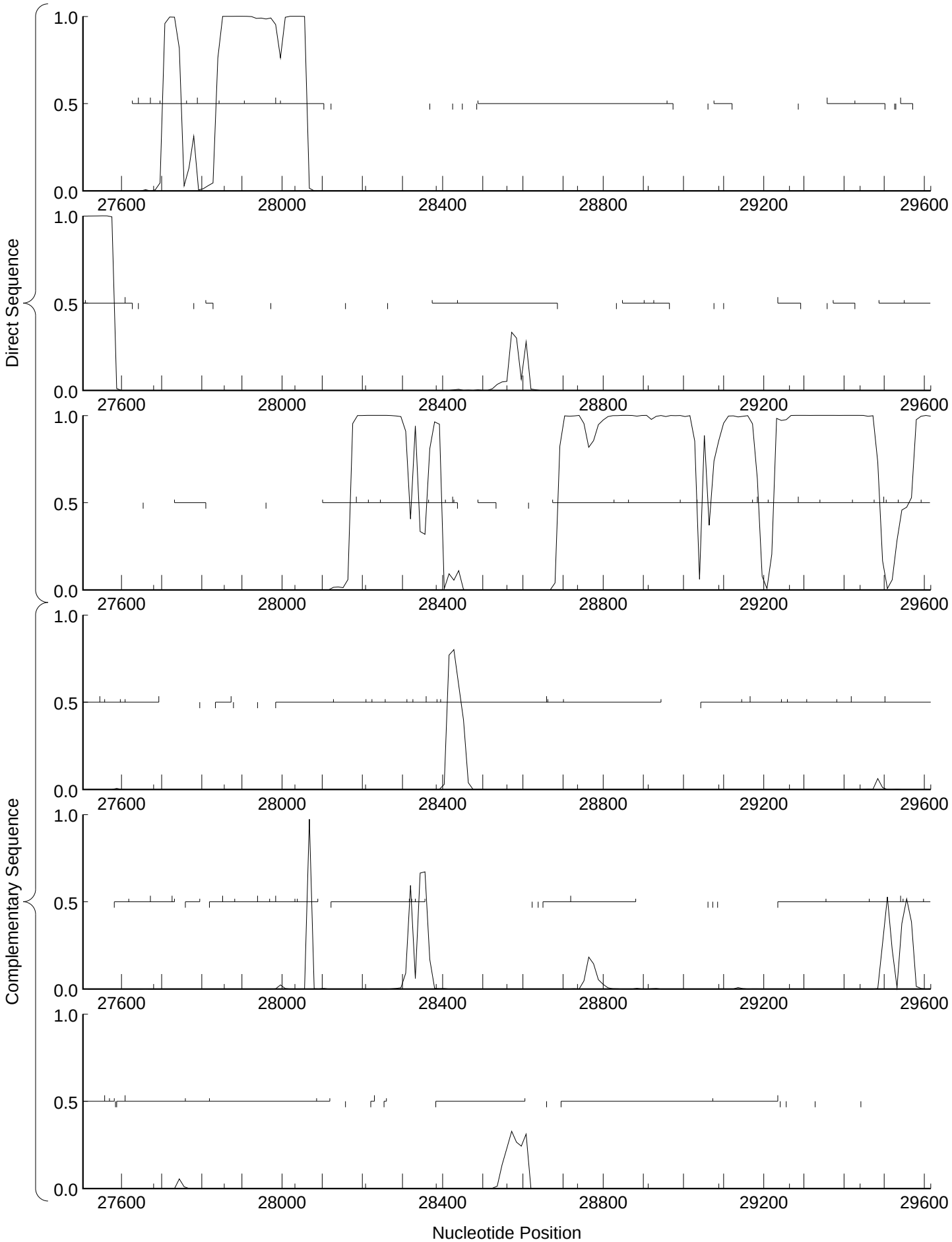
complete sequence, 61594 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K6, Order 4, Window 96, Step 12, 13/31



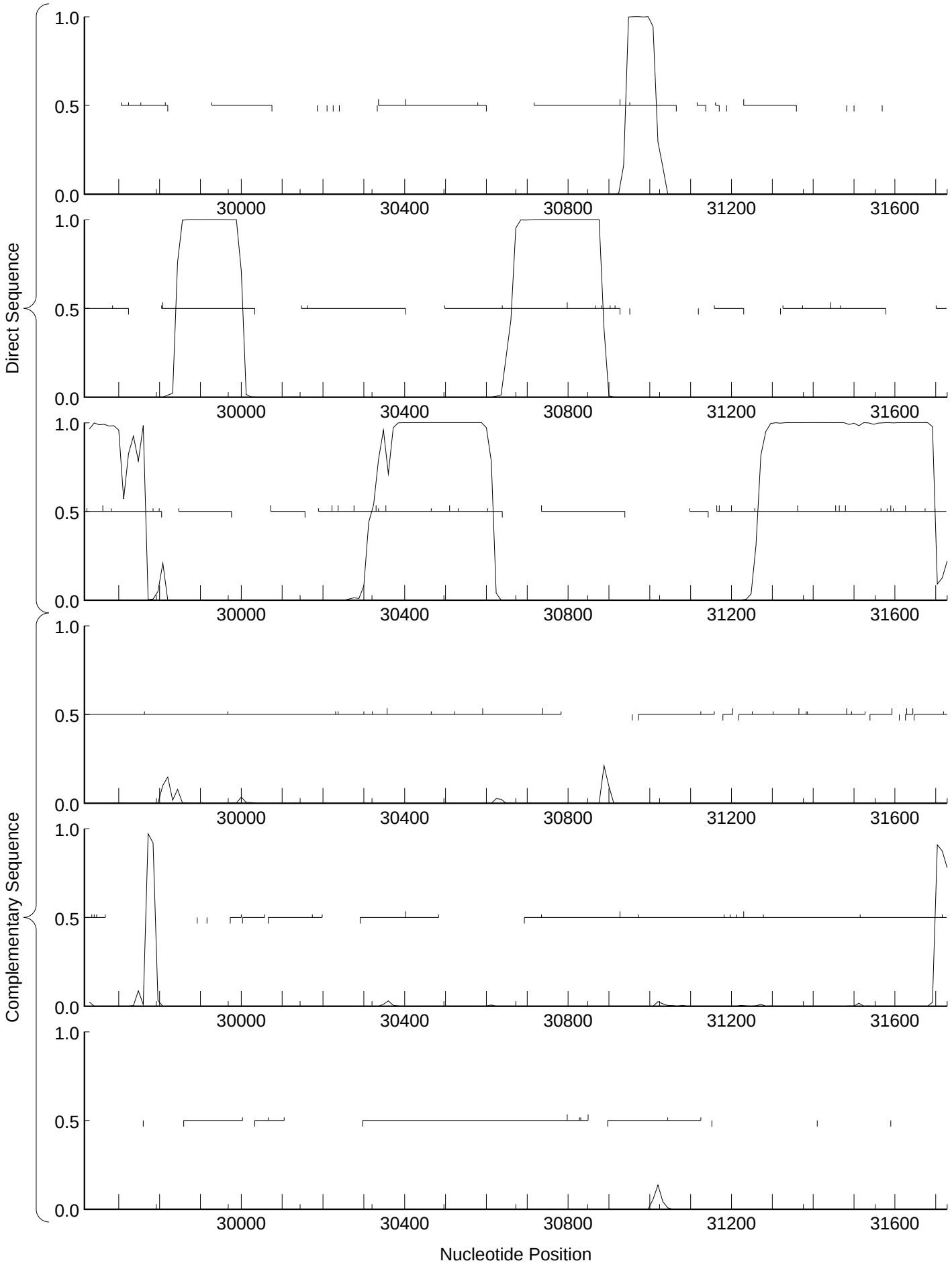
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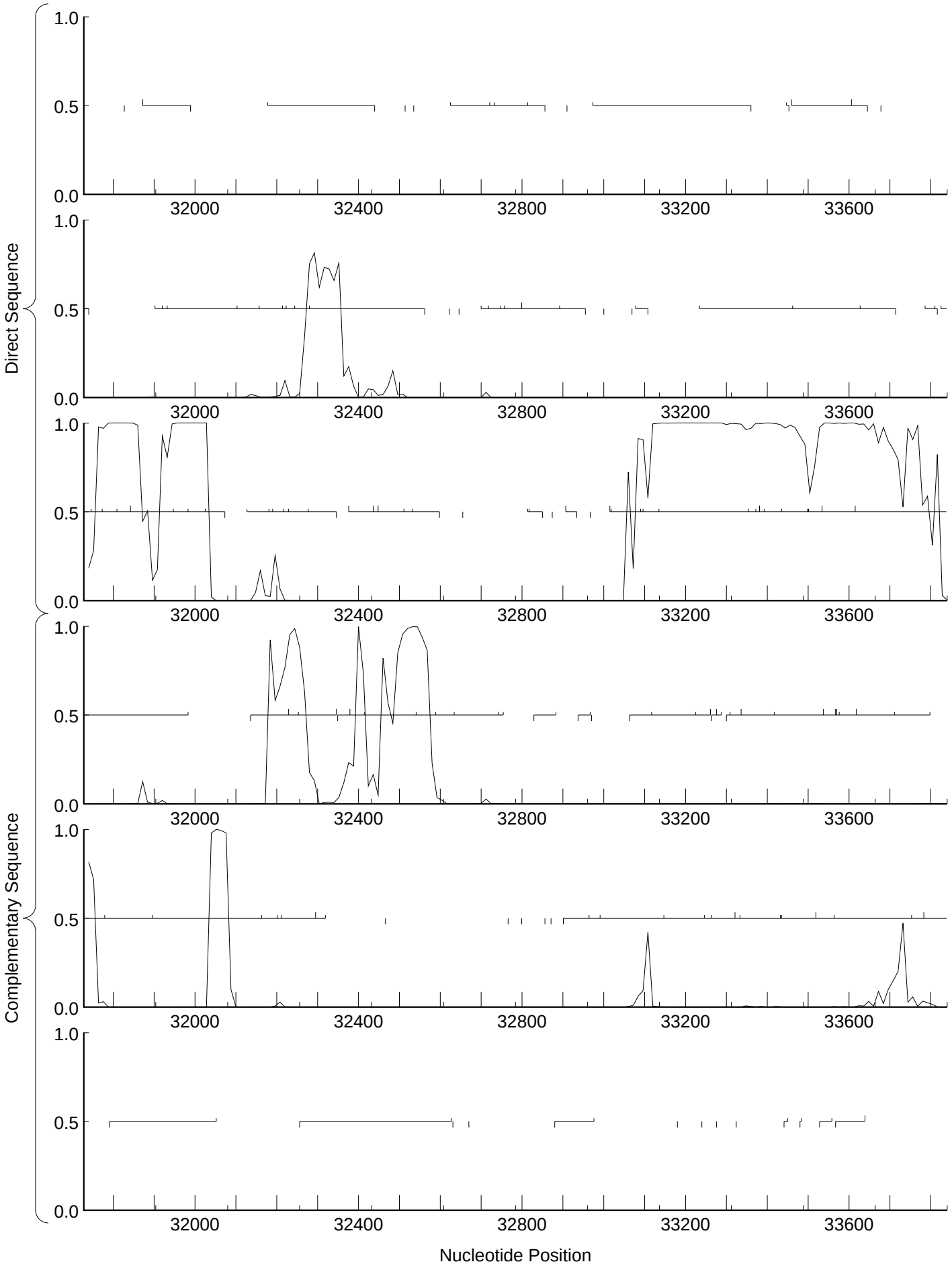
complete sequence, 61594 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K6, Order 4, Window 96, Step 12, 15/31



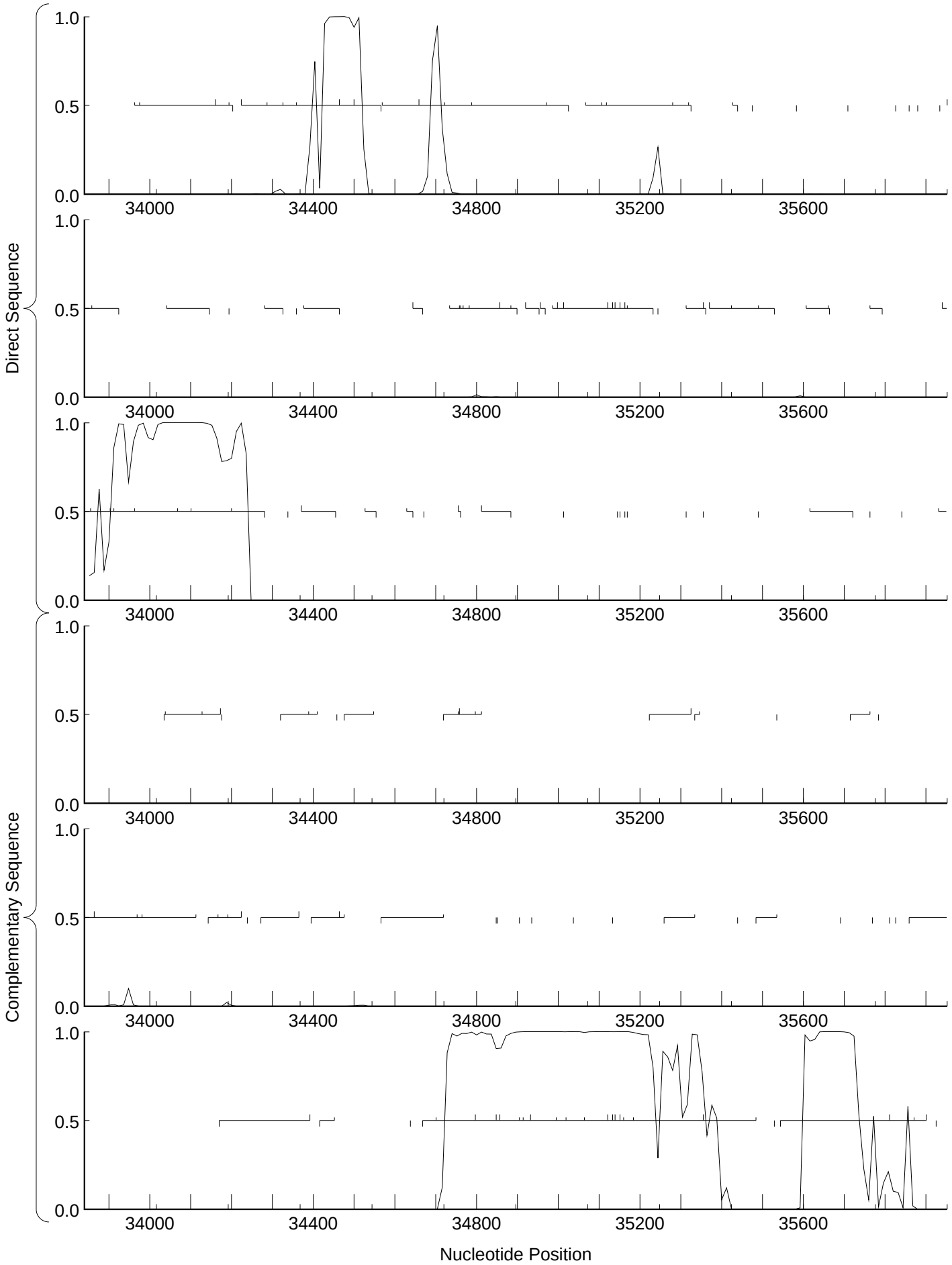
complete sequence, 61594 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K6, Order 4, Window 96, Step 12, 16/31



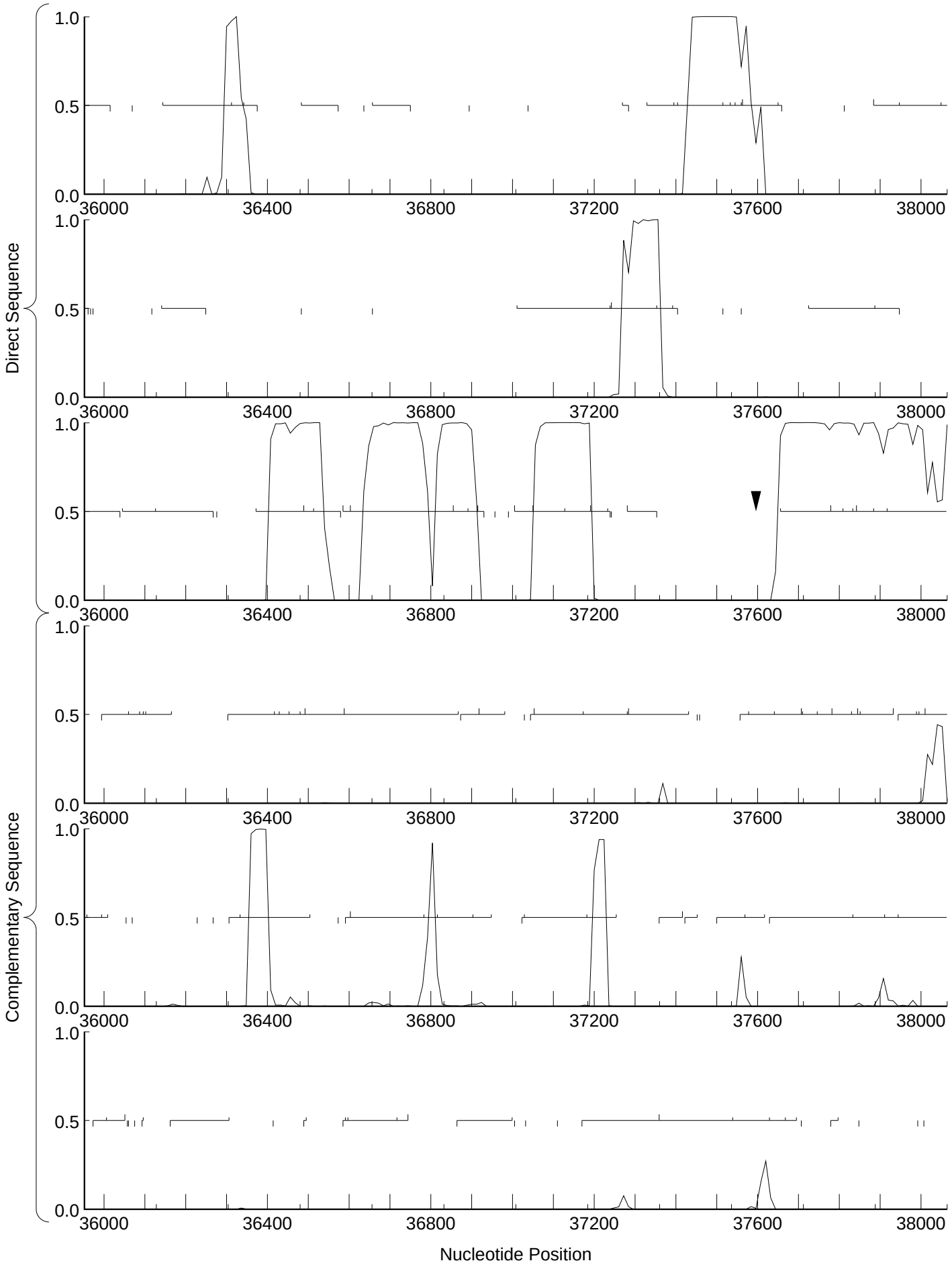
complete sequence, 61594 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K6, Order 4, Window 96, Step 12, 17/31



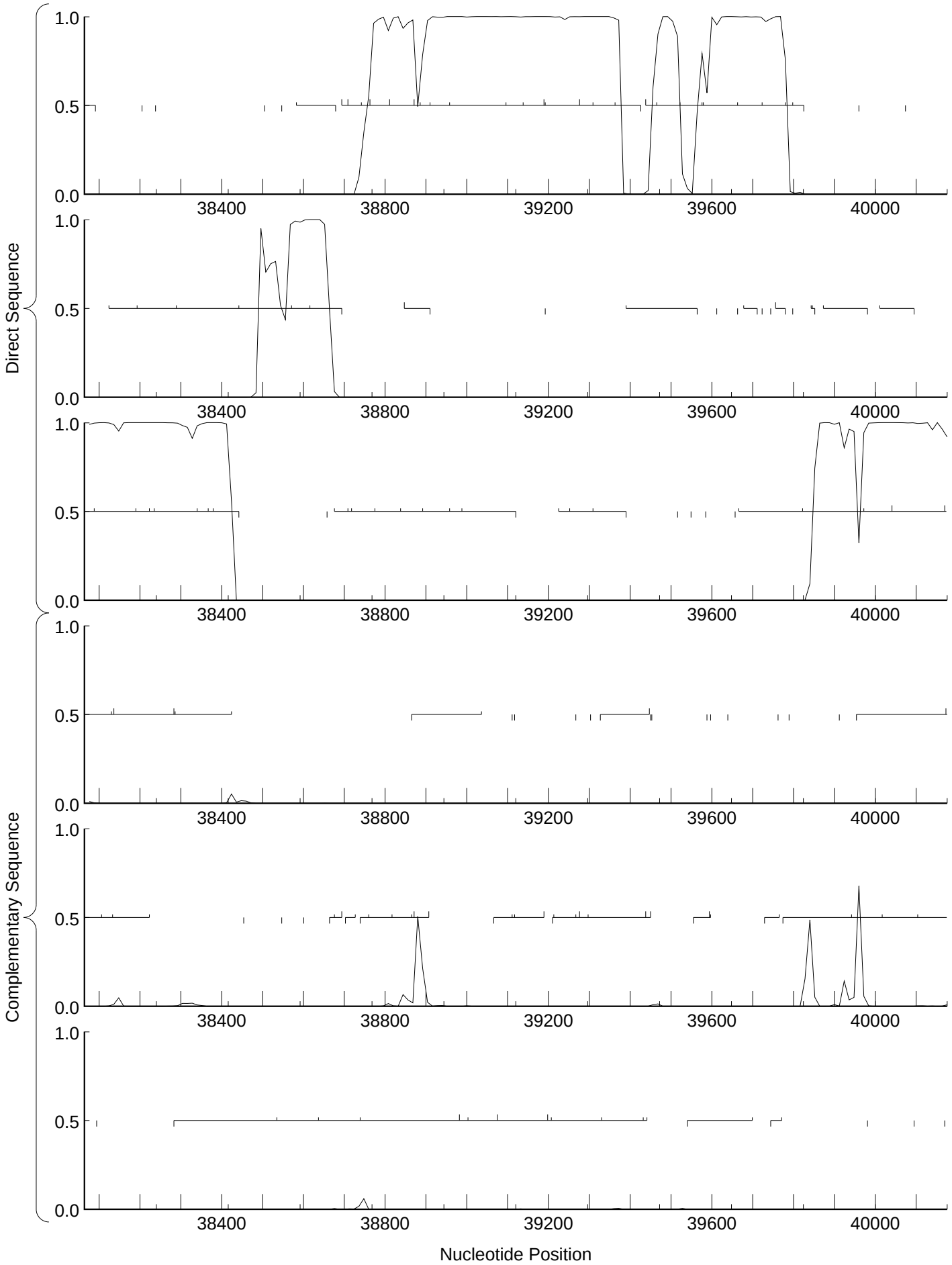
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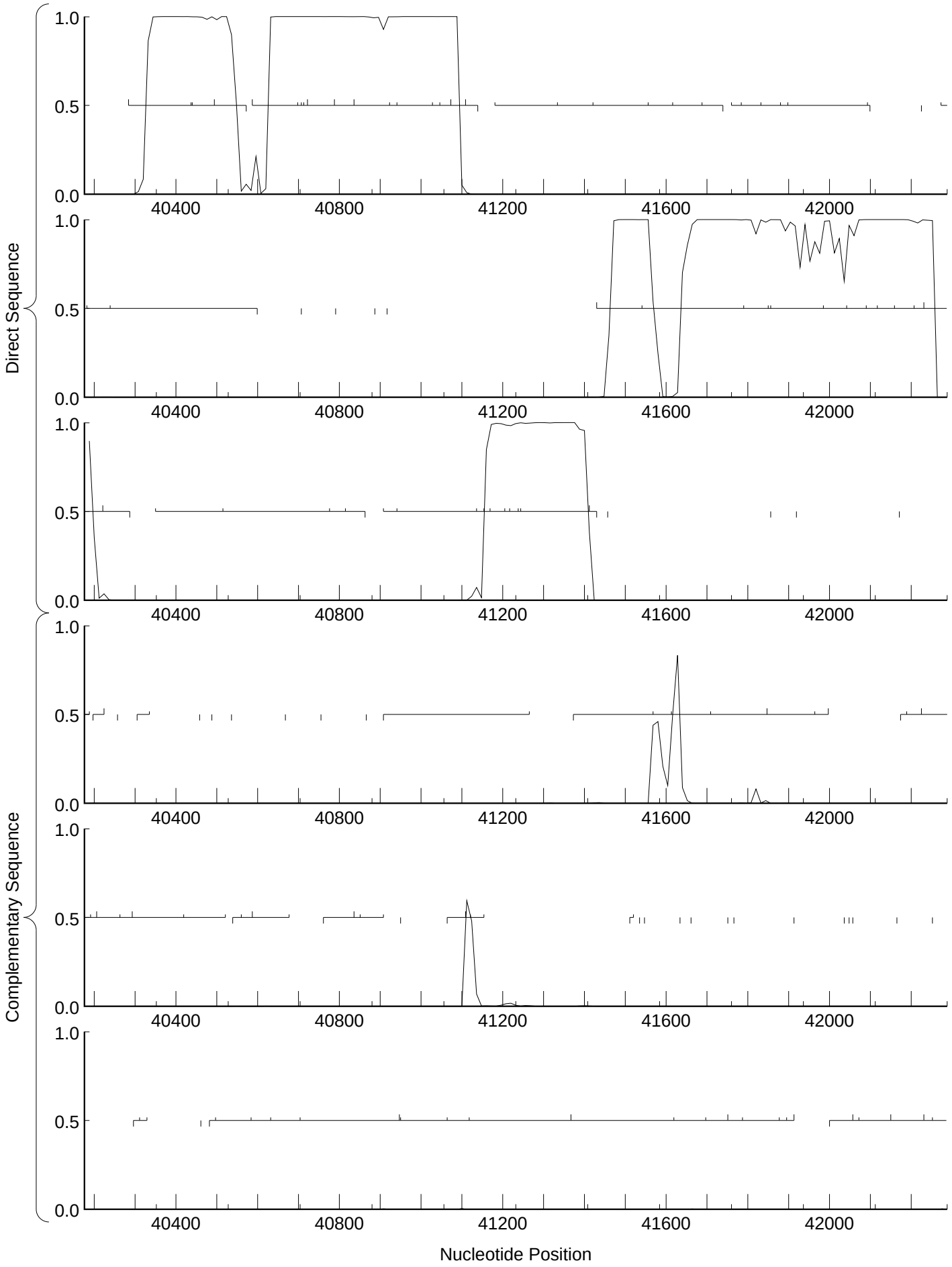
complete sequence, 61594 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K6, Order 4, Window 96, Step 12, 19/31

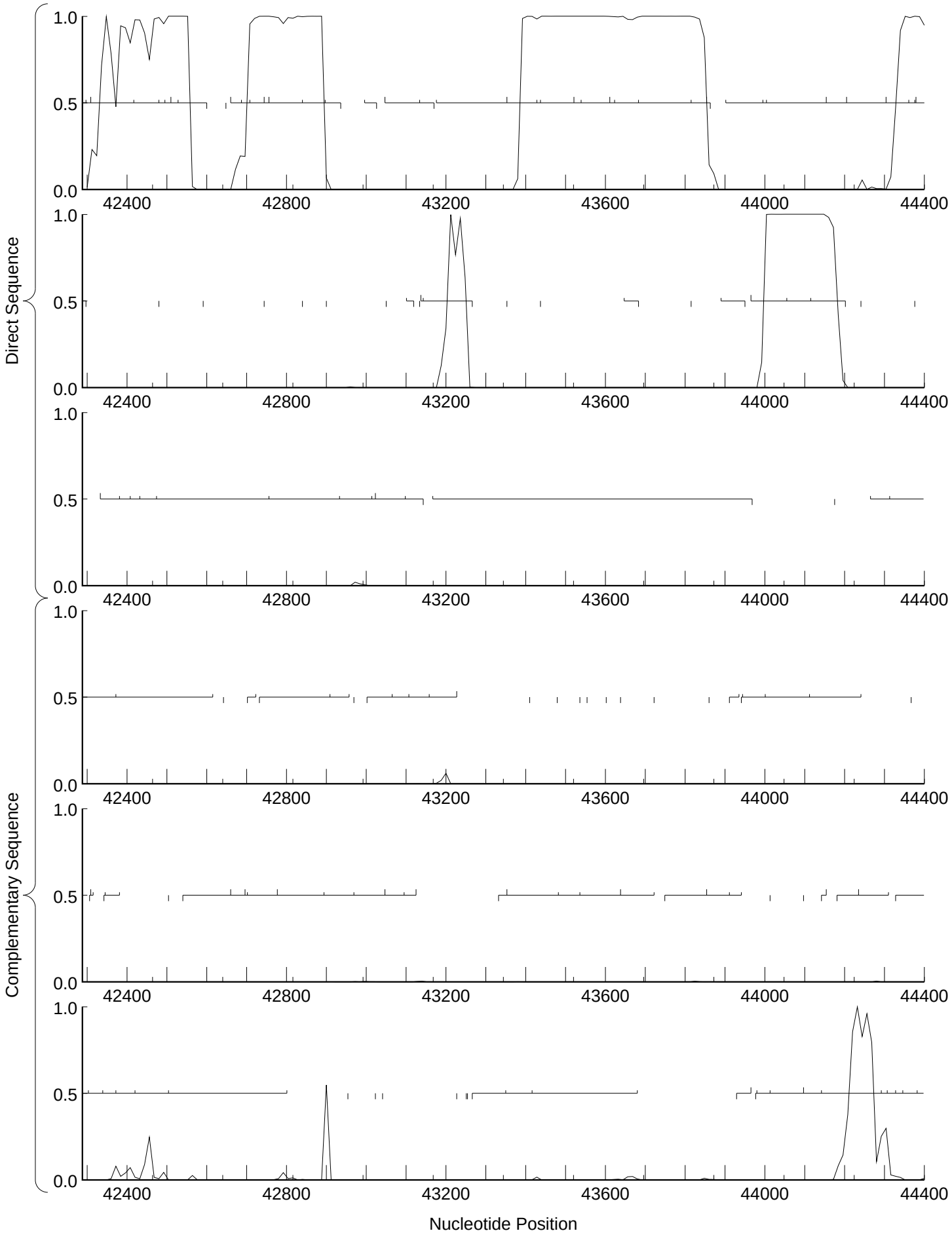


complete sequence, 61594 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K6, Order 4, Window 96, Step 12, 20/31

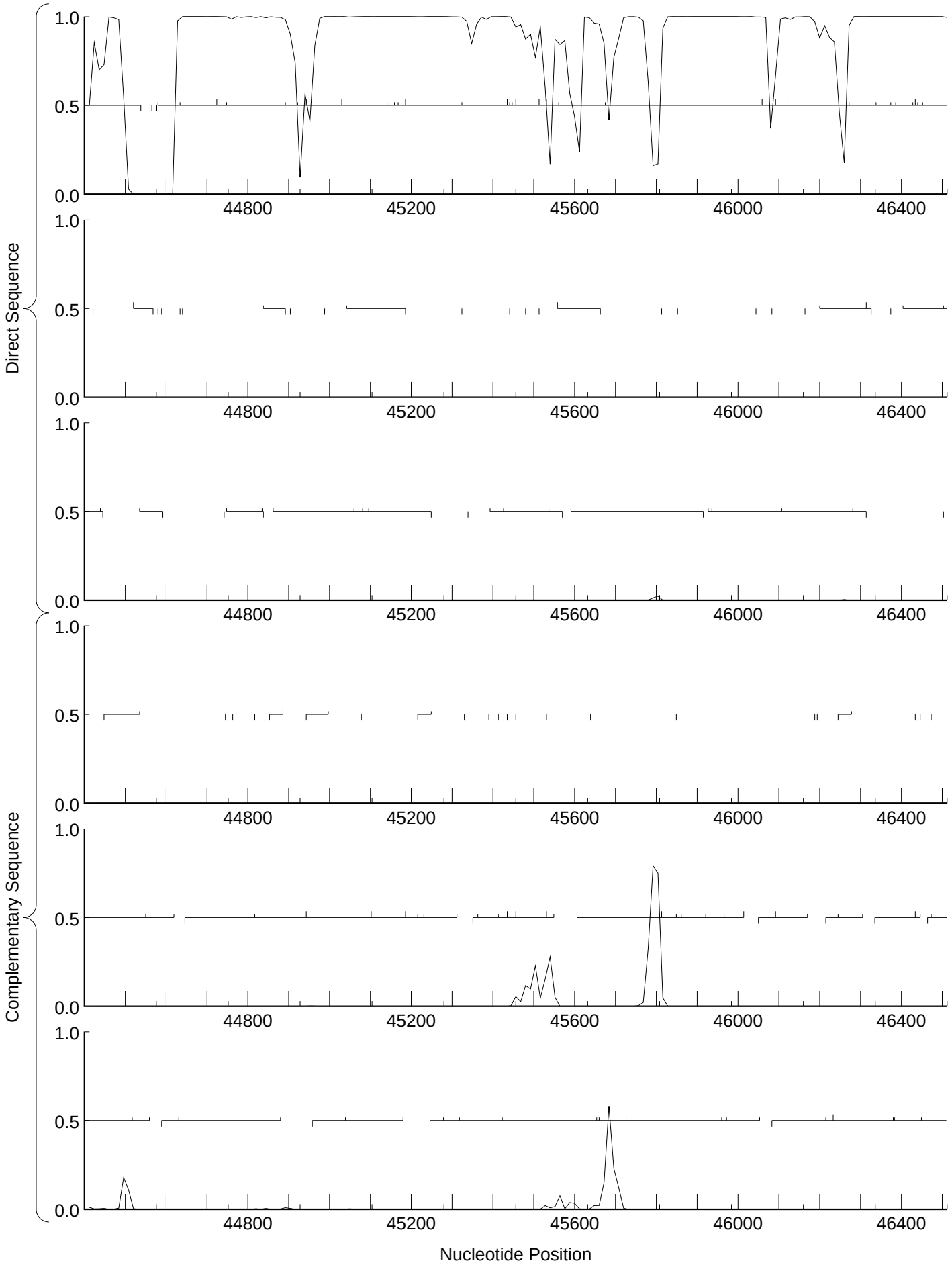


complete sequence, 61594 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K6, Order 4, Window 96, Step 12, 21/31

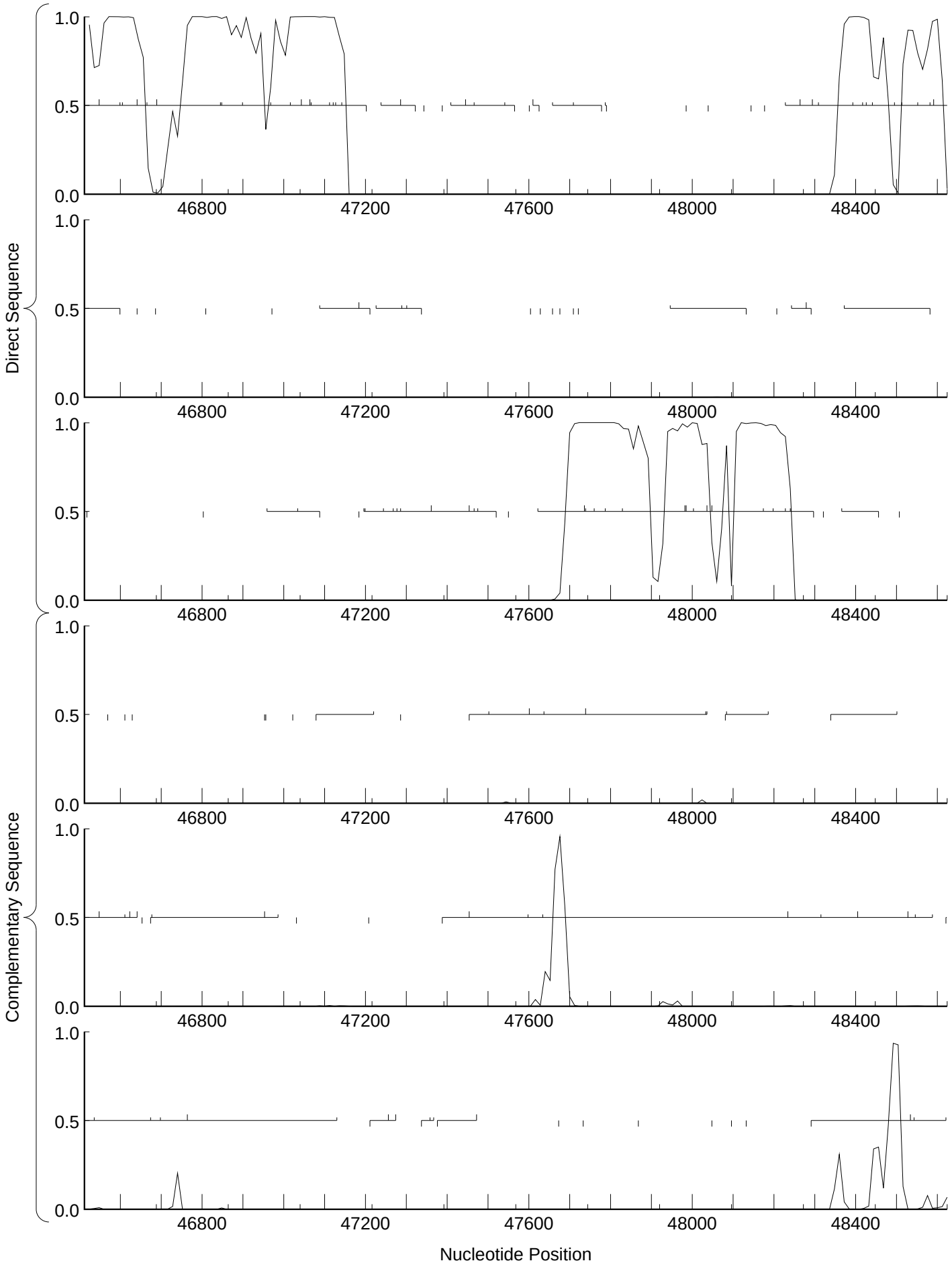



Direct Sequence
Complementary Sequence
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0.5
0.0
42400
42800
43200
43600
44000
44400
Nucleotide Position

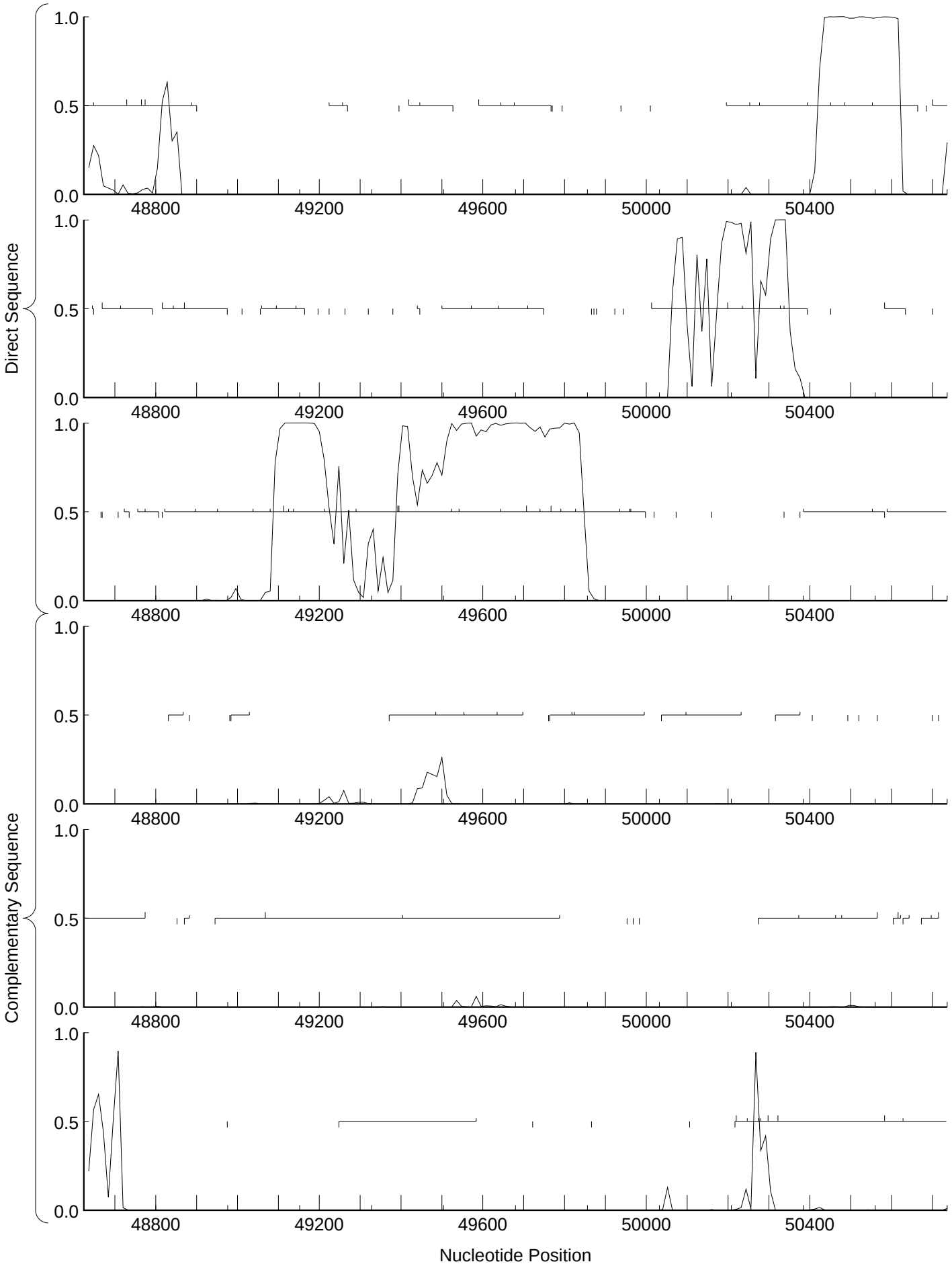
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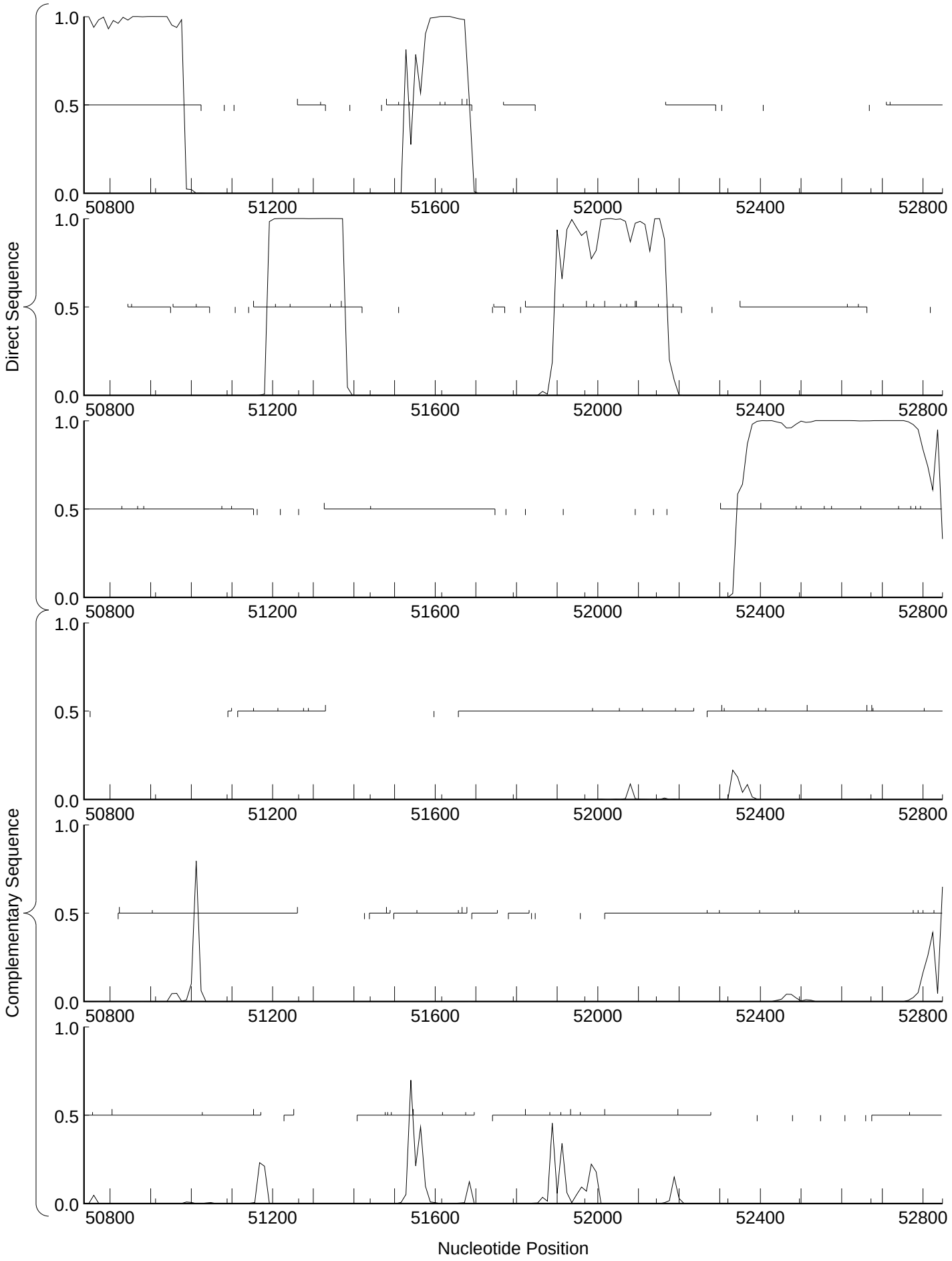
complete sequence, 61594 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K6, Order 4, Window 96, Step 12, 24/31



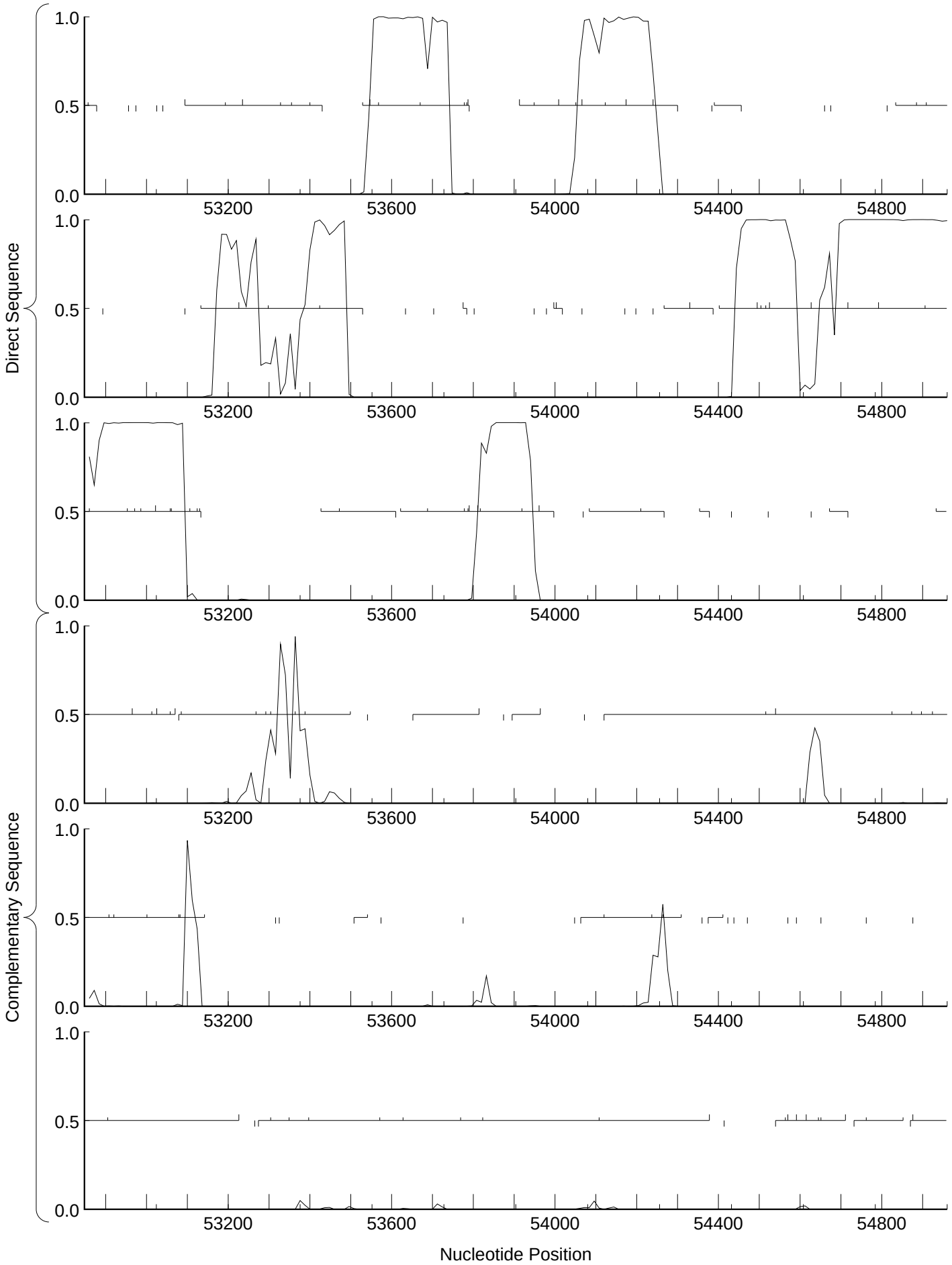
complete sequence, 61594 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K6, Order 4, Window 96, Step 12, 25/31



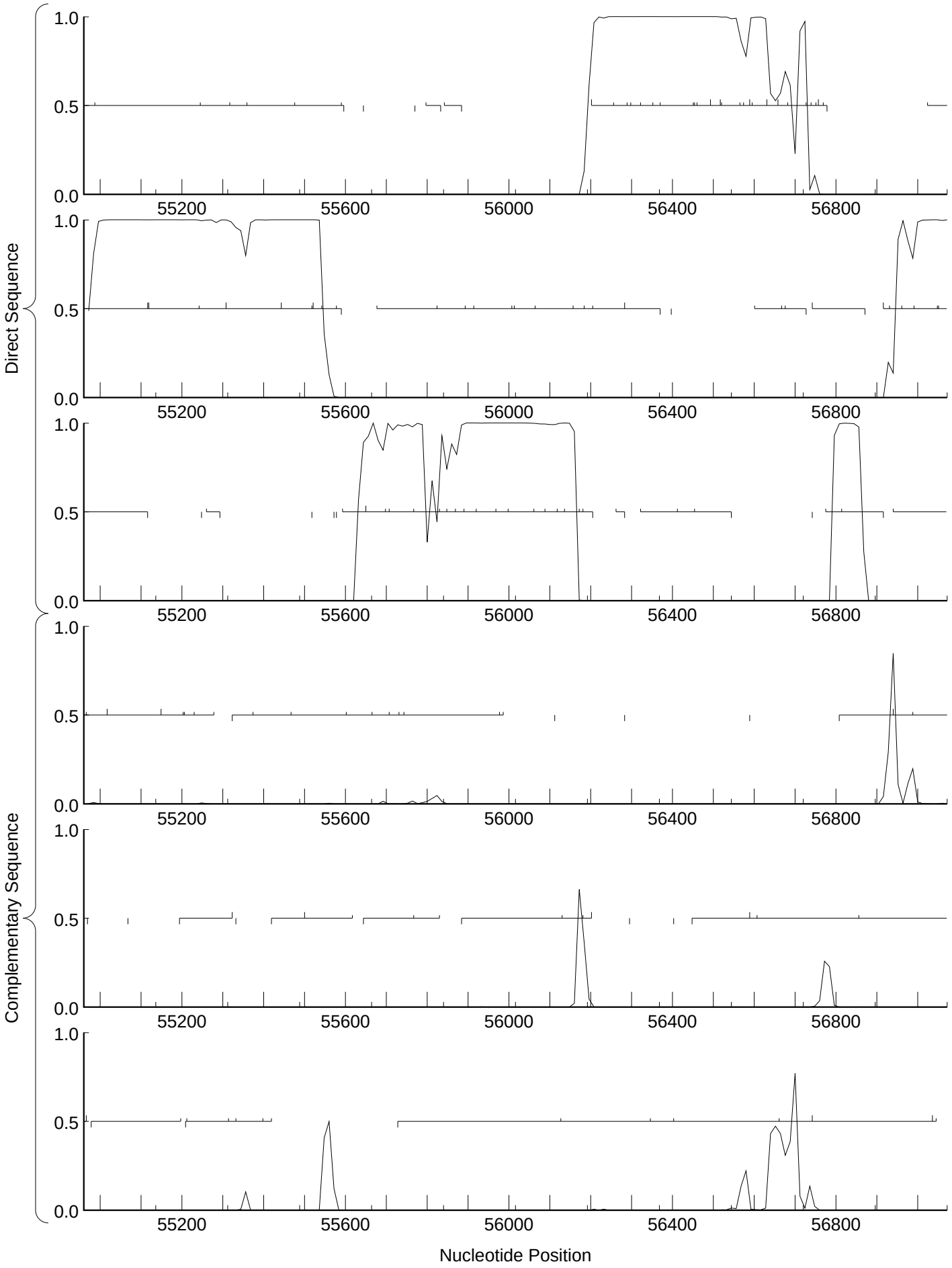
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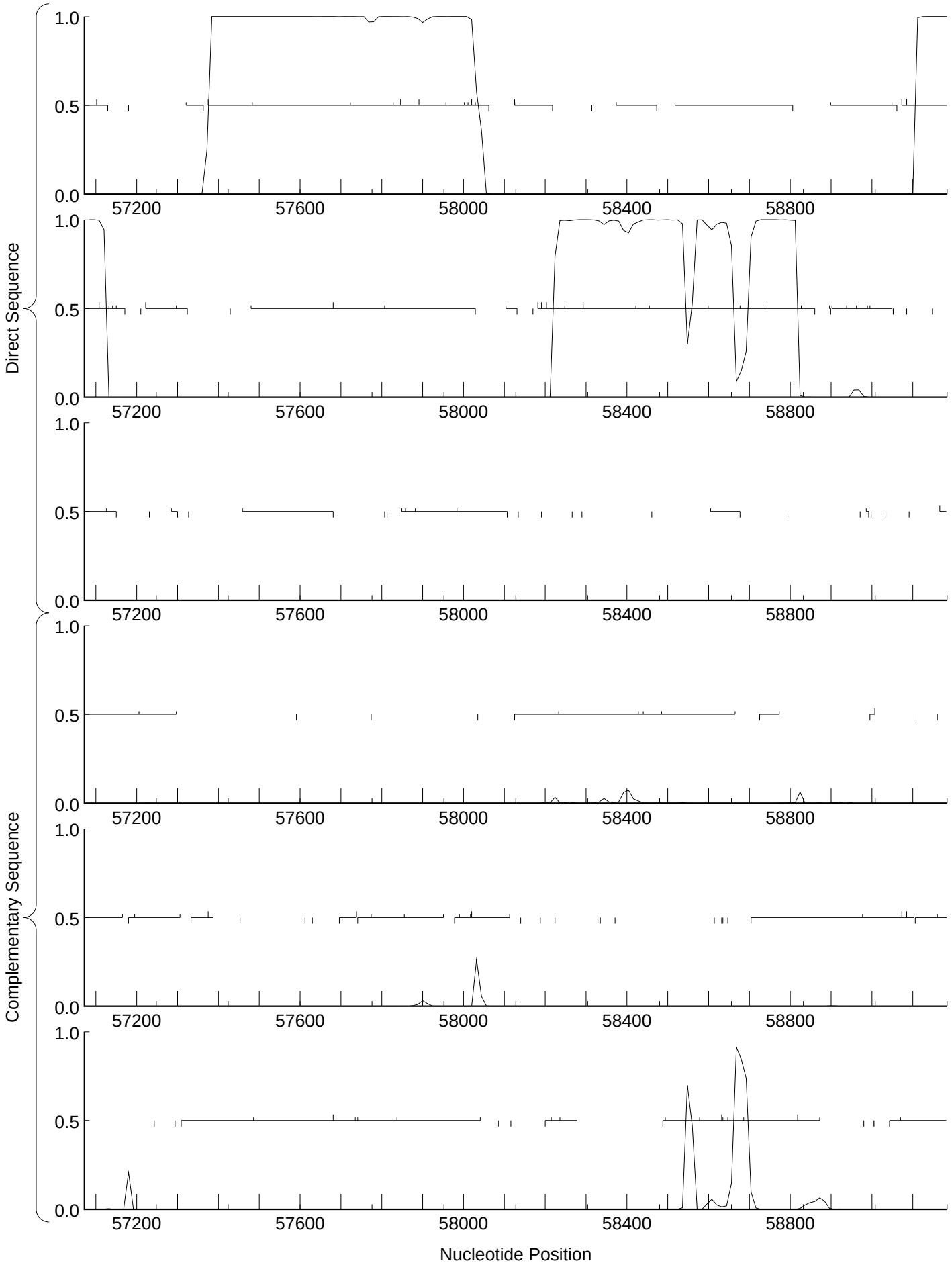
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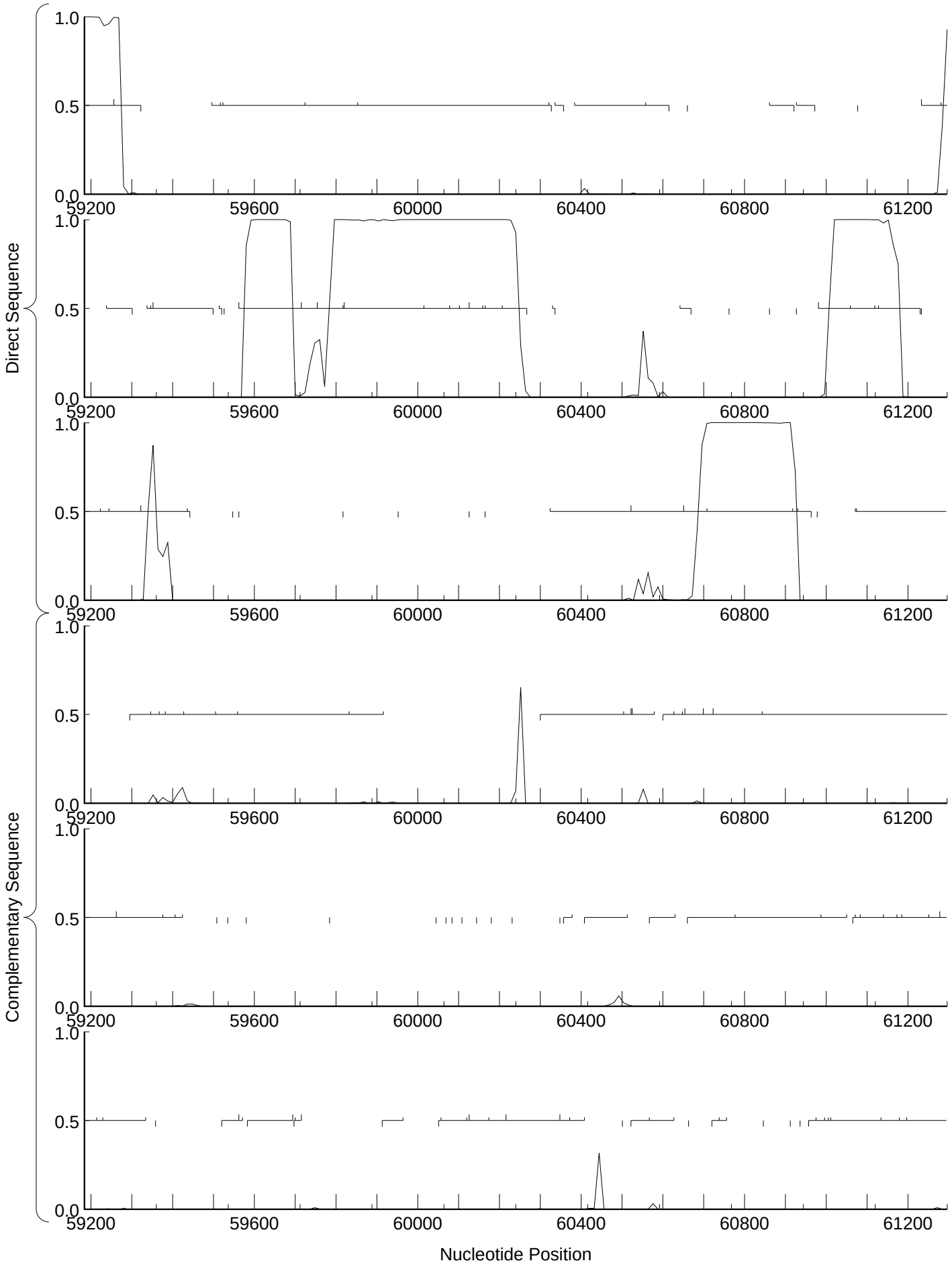
complete sequence, 61594 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K6, Order 4, Window 96, Step 12, 28/31



complete sequence, 61594 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K6, Order 4, Window 96, Step 12, 29/31



complete sequence, 61594 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K6, Order 4, Window 96, Step 12, 30/31



complete sequence, 61594 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K6, Order 4, Window 96, Step 12, 31/31

