GeneMark

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

PROGRAM INFORMATION

```
Sequence         :  Mycobacterium phage Guanica15 complete sequence, 60974 bp including 11-base 3’ overhang (CT
Analysis Date    :  3/28/24 at 9:52:23
Pages            :  30
Sequence Length  :  60974 bp
GC Content       :   66.58%

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

PS-Version       :  1.2

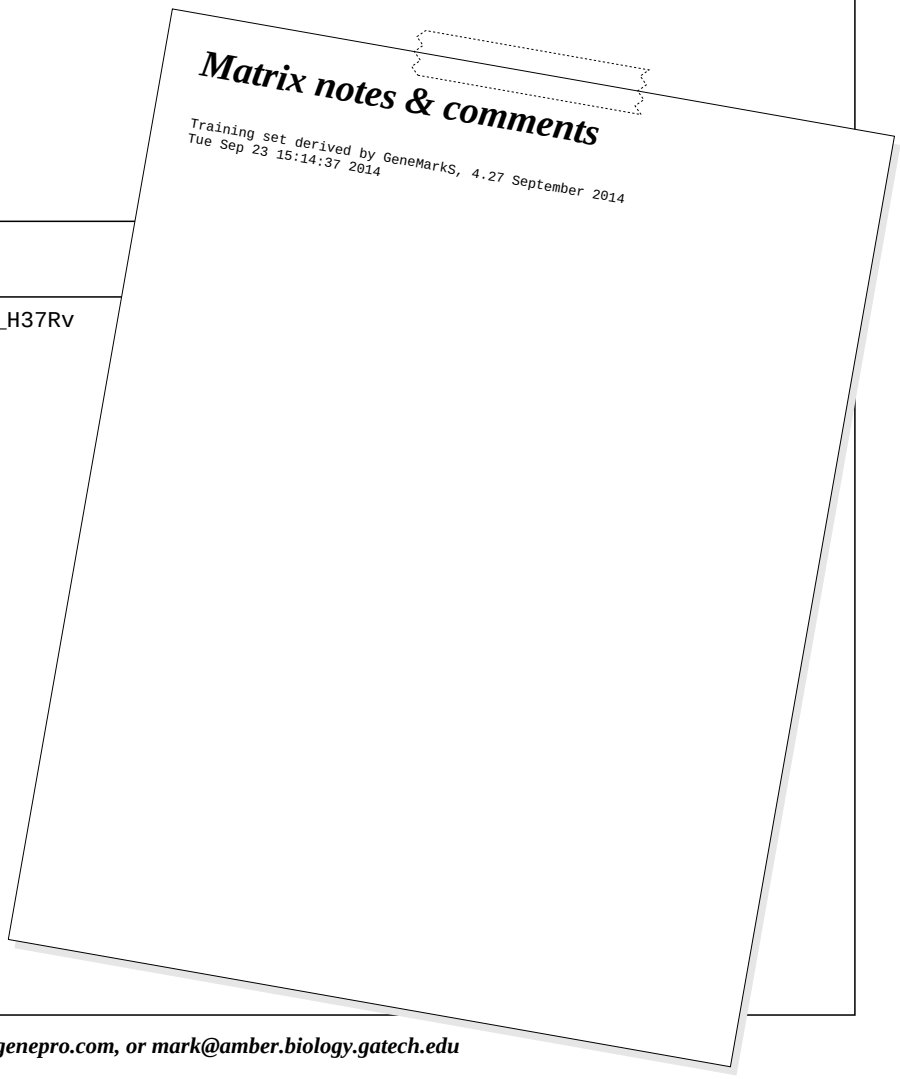
GeneMark Options :  PostScript graph,
                    Mark ORFs / splice sites,
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MATRIX INFORMATION

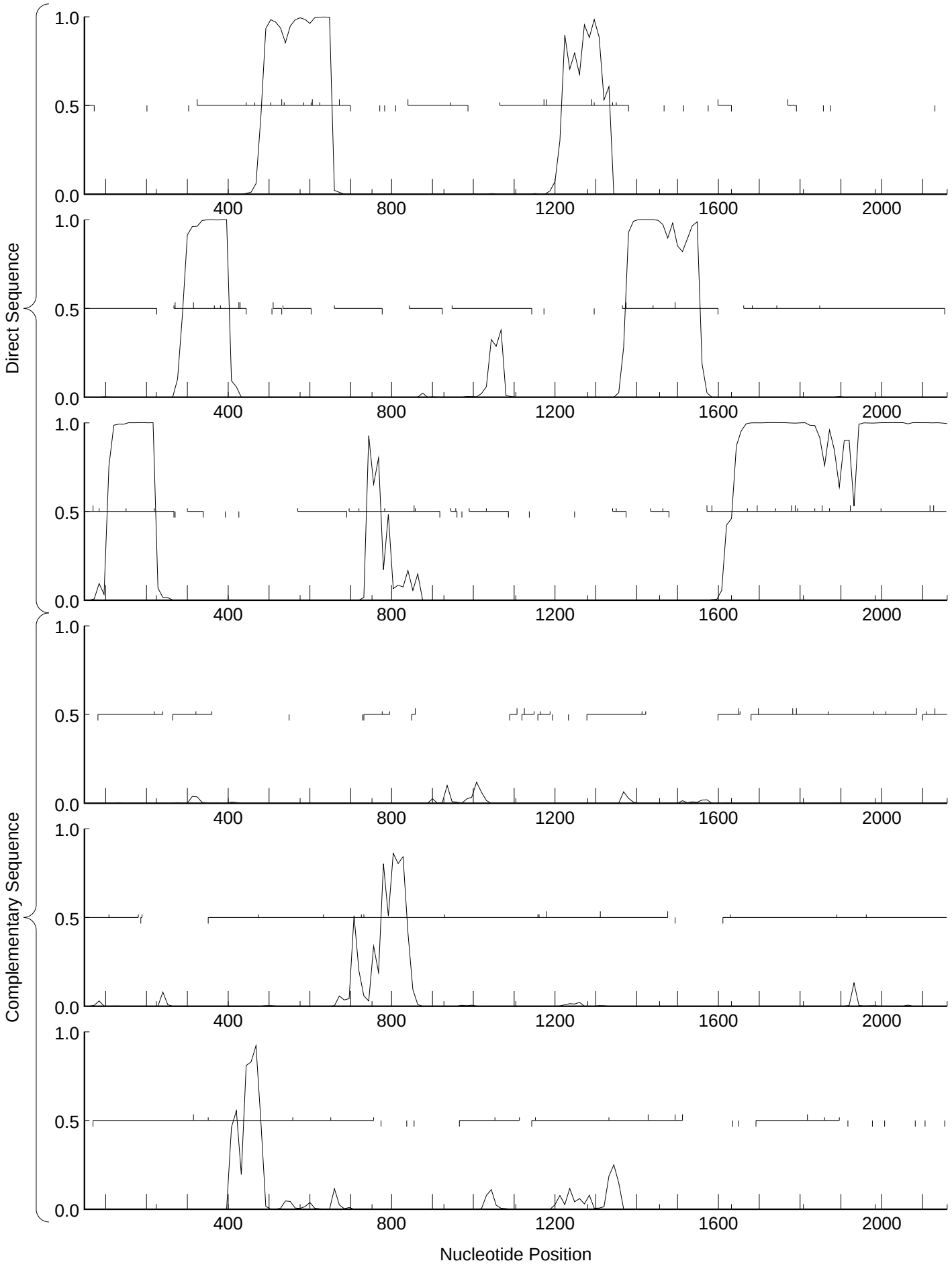
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Matrix     :  Mycobacterium_tuberculosis_H37Rv
Author     :  -

Order      :  4

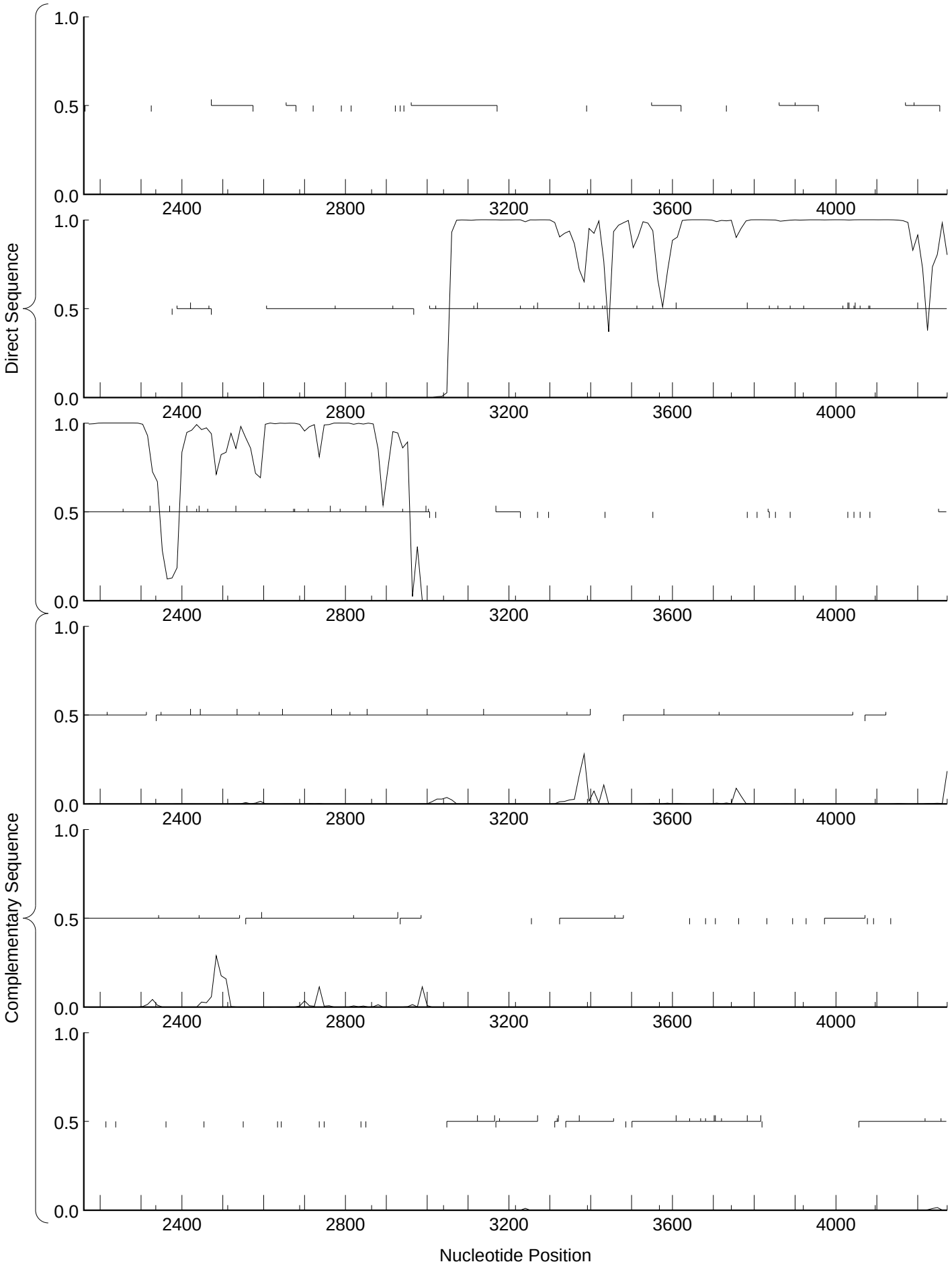

  Send questions / comments to:
      Dr. M. Borodovsky
      Georgia Institute of Technology
      School of Biology
      Atlanta, GA  30332-0230
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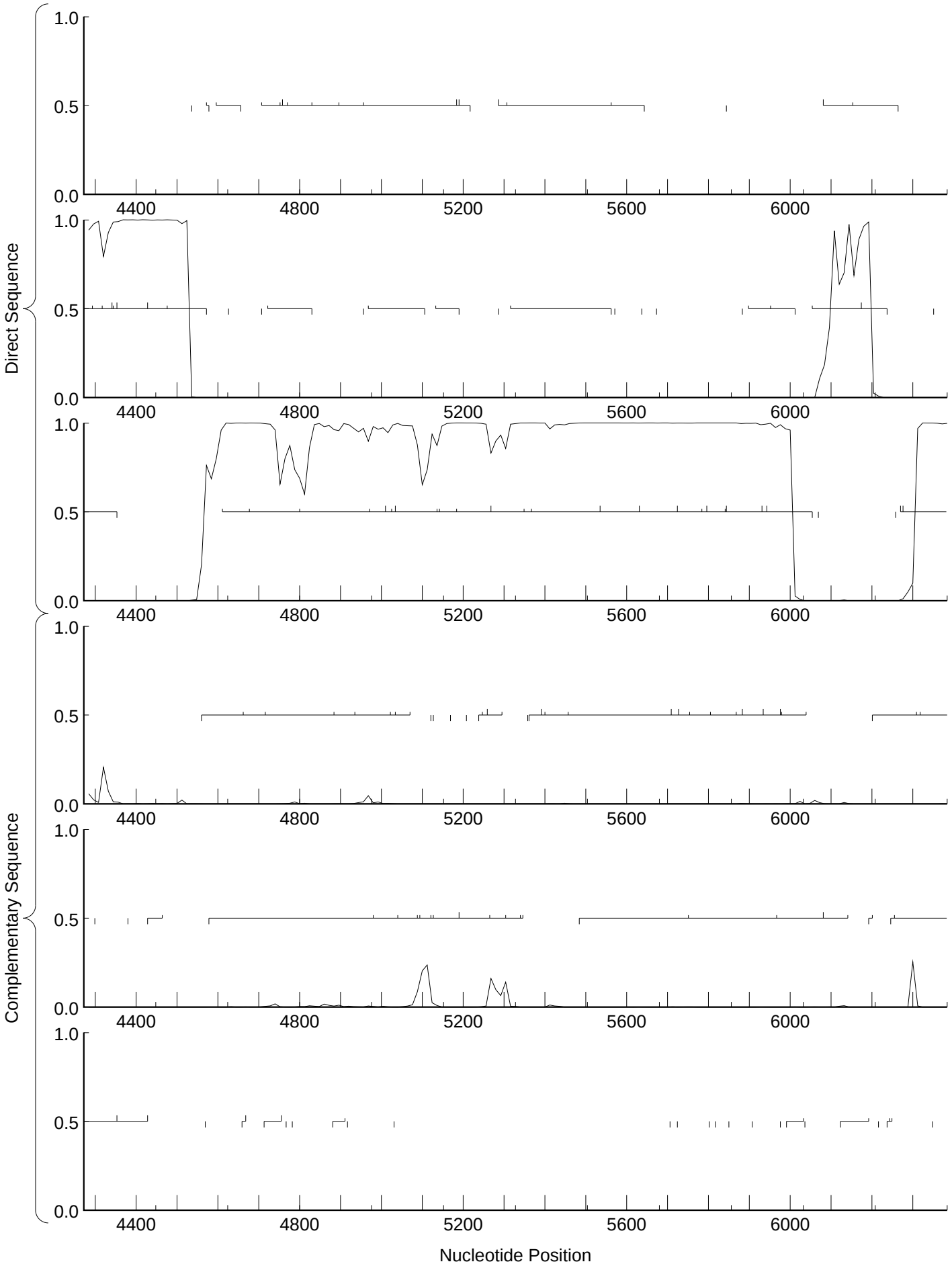


For help or information, send electronic mail to: custserv@genepro.com, or mark@amber.biology.gatech.edu

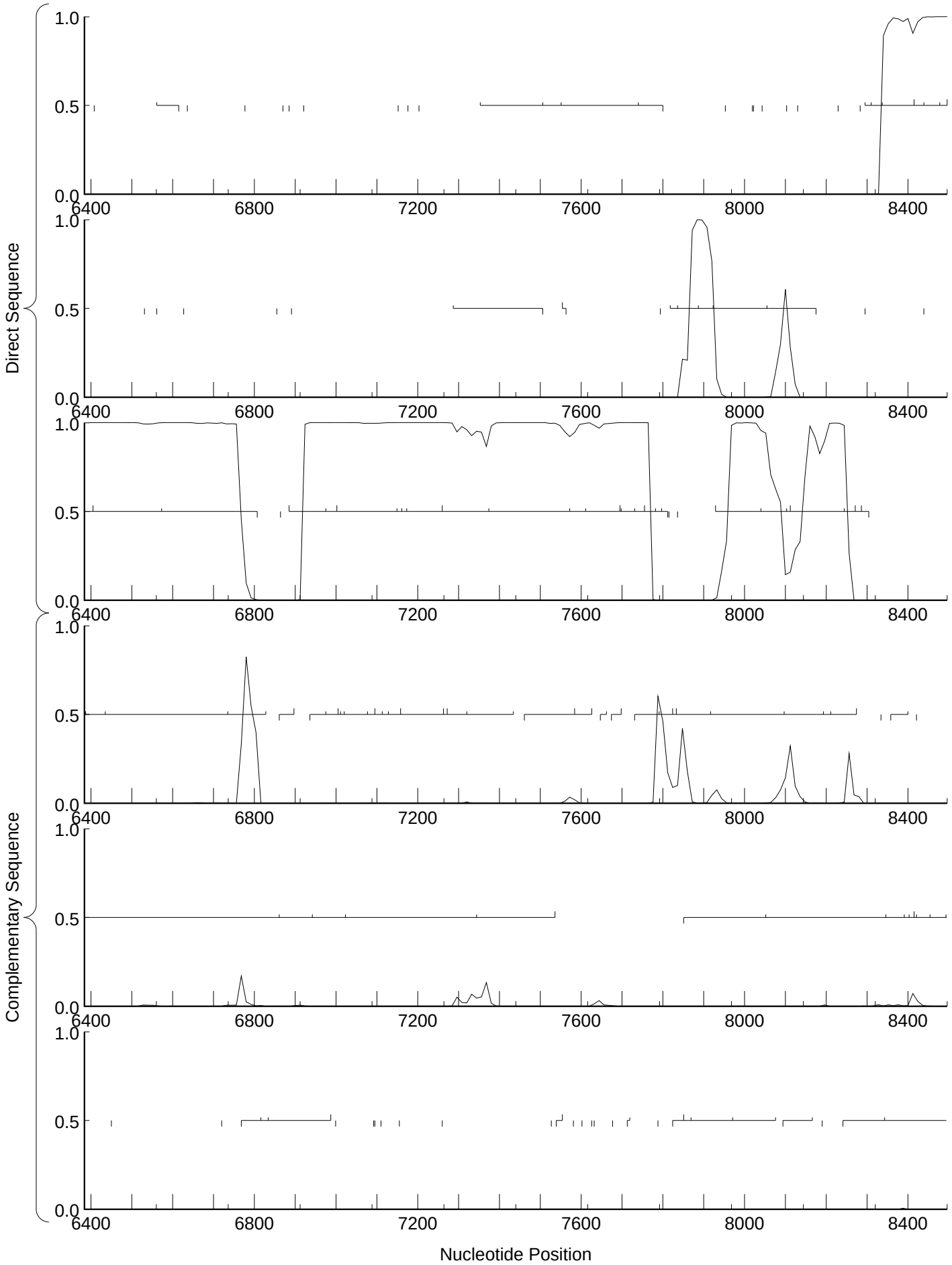

Direct Sequence
Complementary Sequence
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0.5
0.0
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1200
1600
2000
Nucleotide Position

complete sequence, 60974 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K1, Order 4, Window 96, Step 12, 3/30

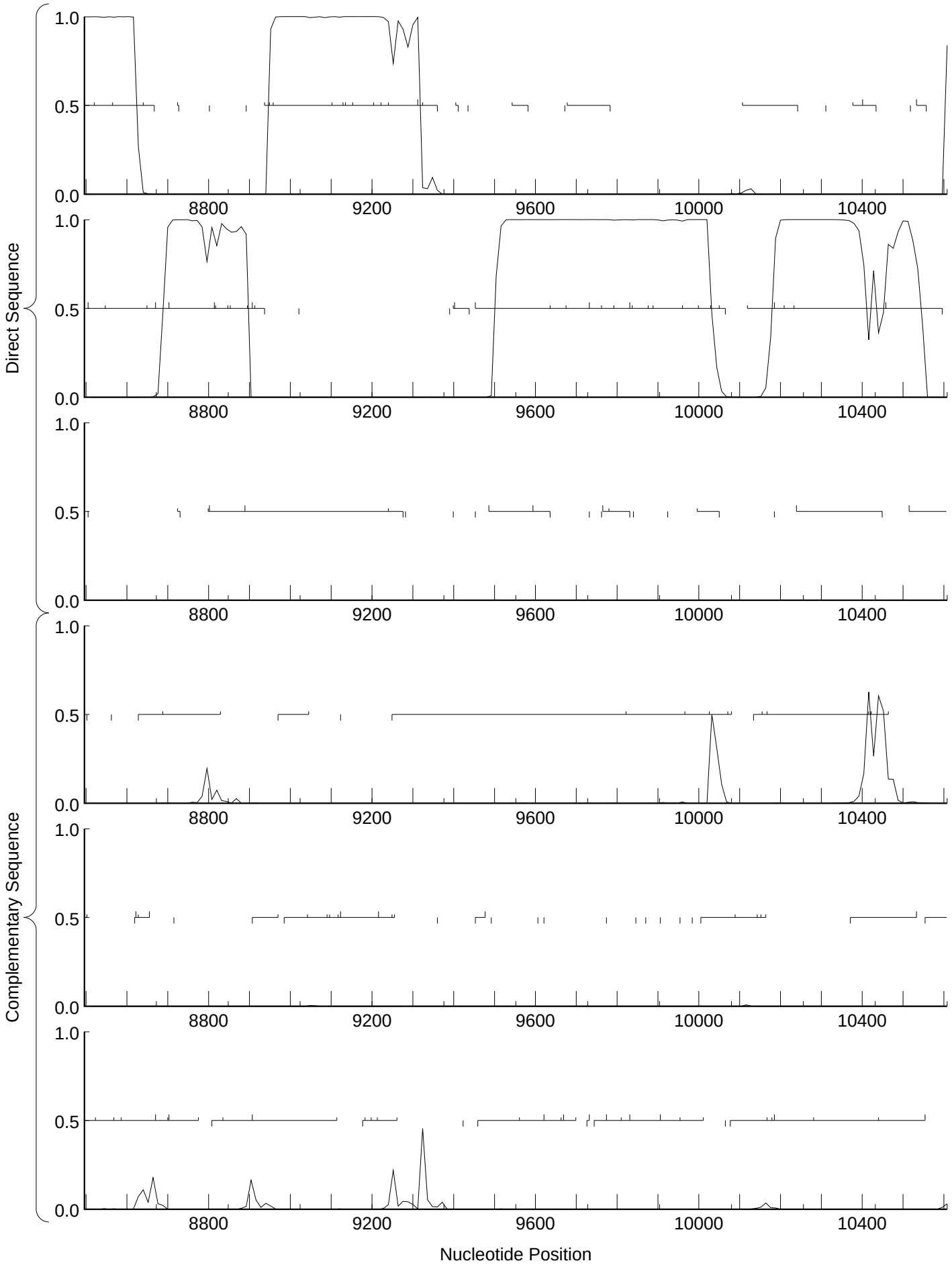



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5200
5600
6000
Nucleotide Position

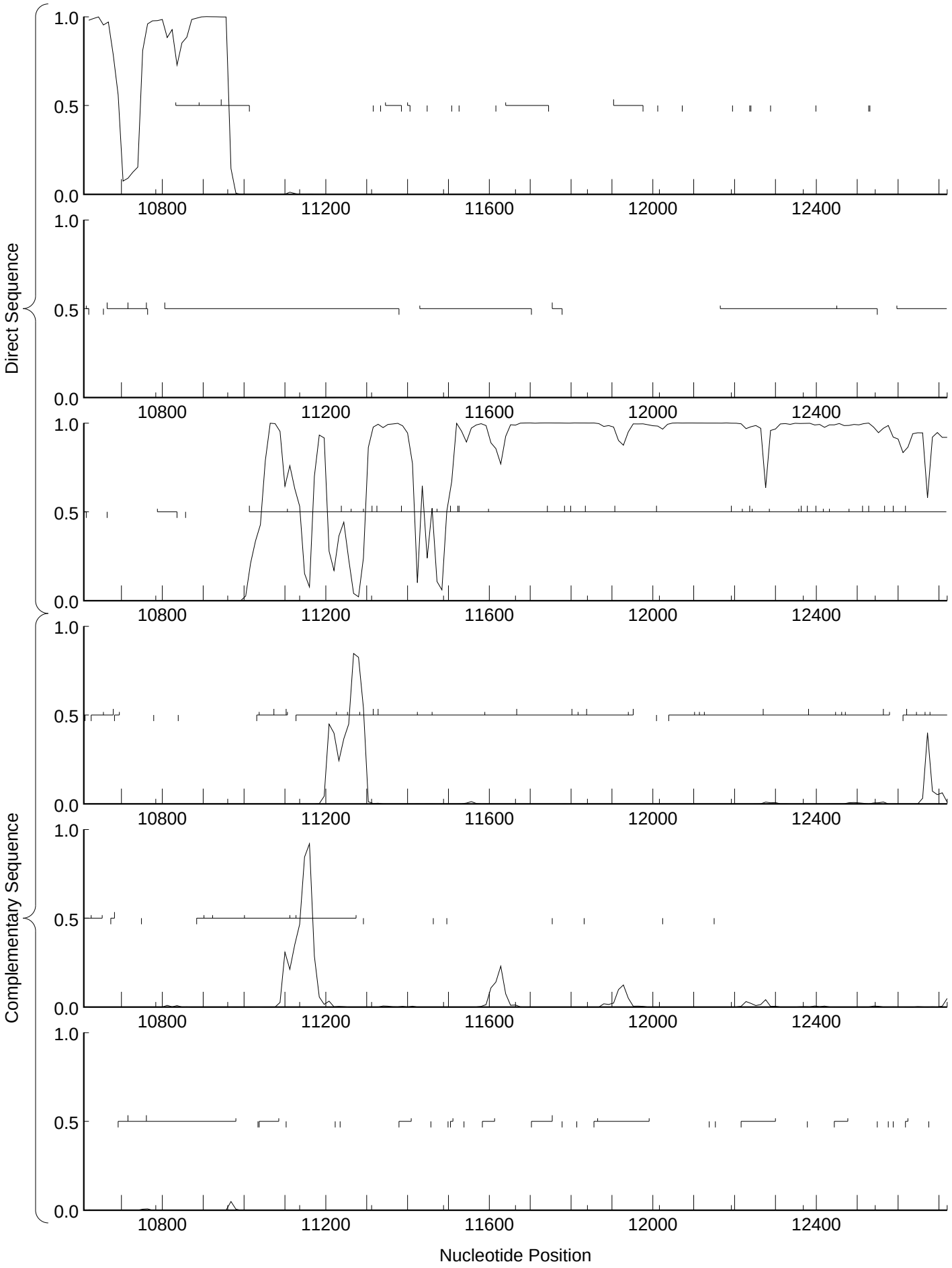
complete sequence, 60974 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K1, Order 4, Window 96, Step 12, 5/30

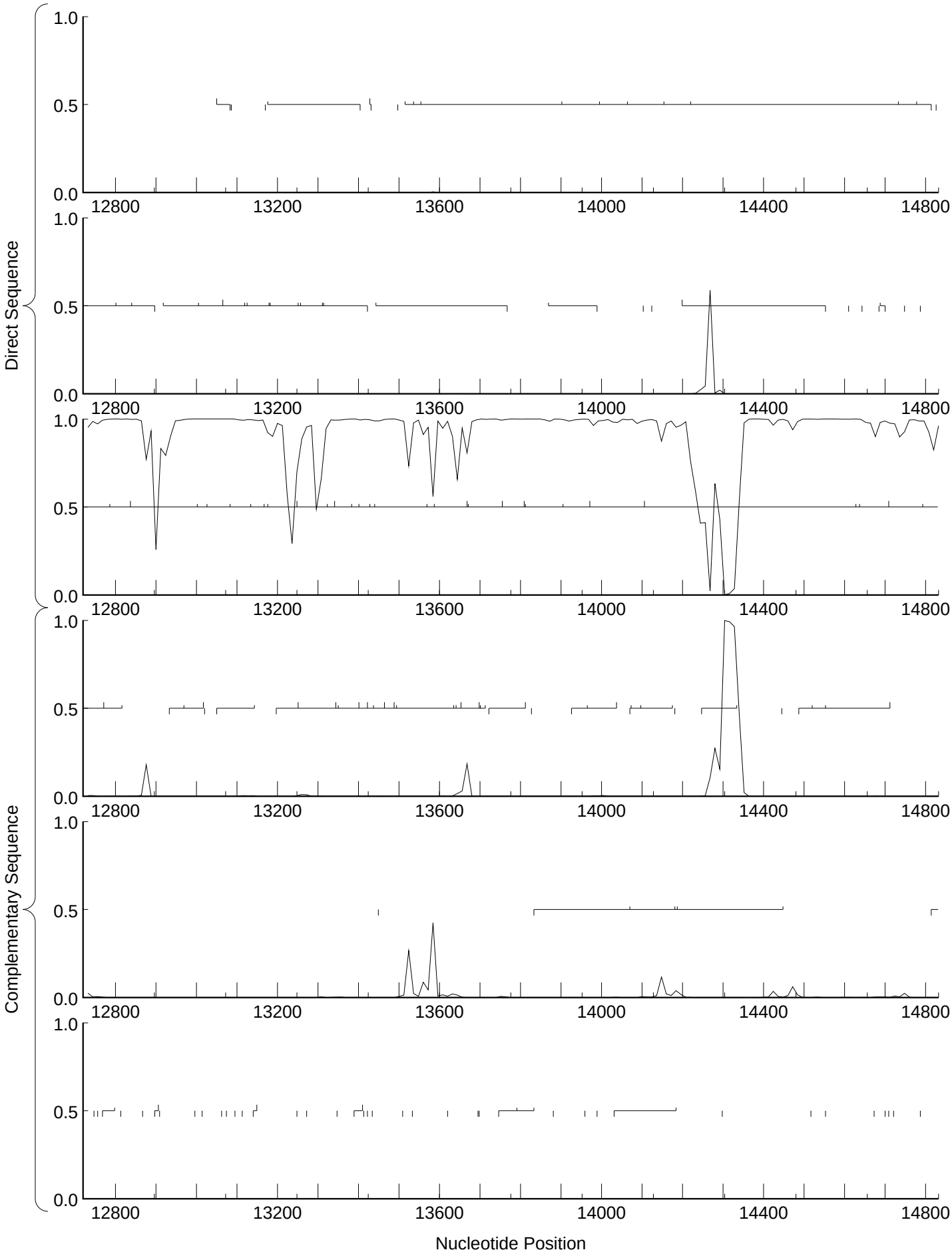


complete sequence, 60974 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K1, Order 4, Window 96, Step 12, 6/30

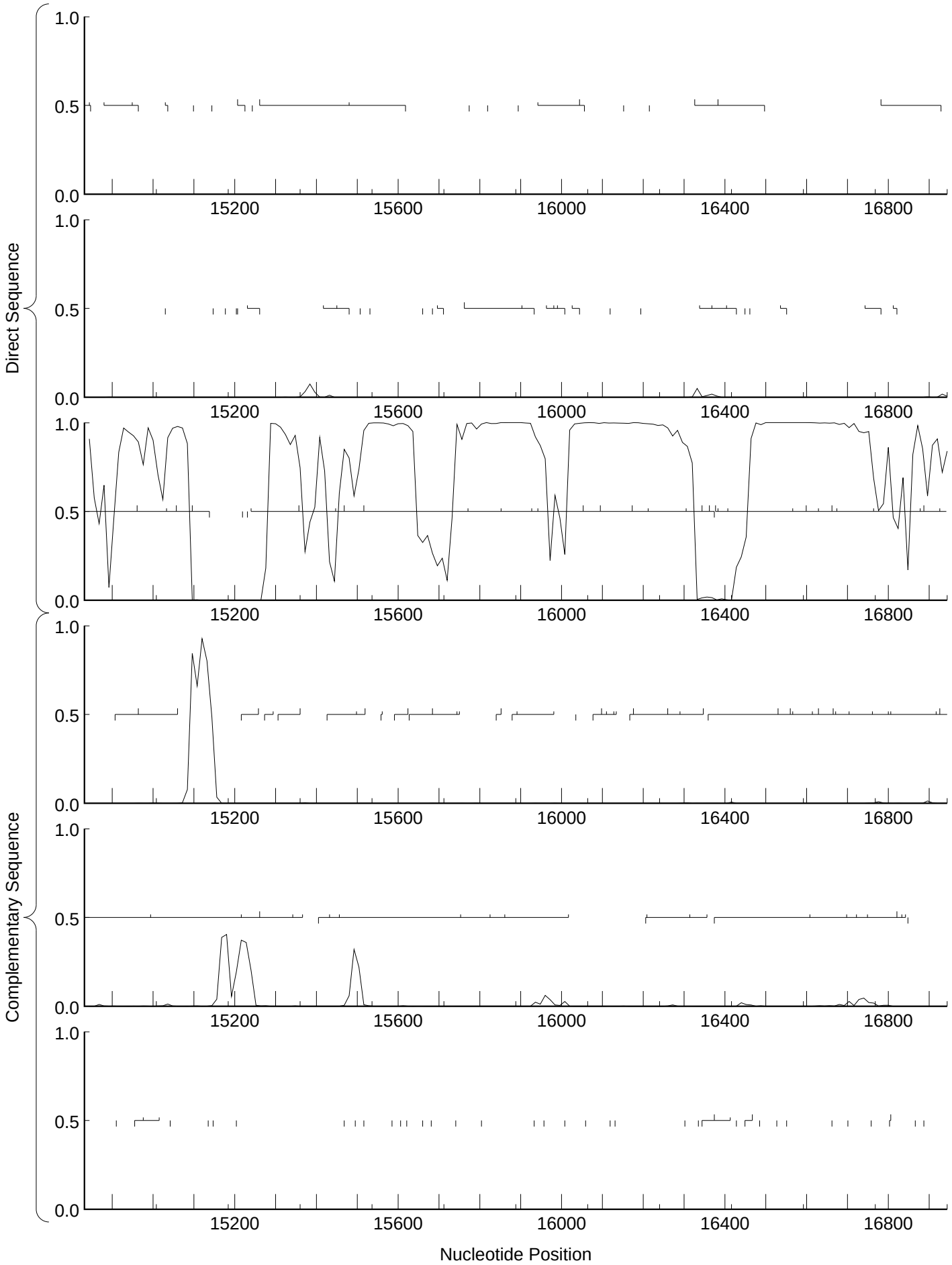


complete sequence, 60974 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K1, Order 4, Window 96, Step 12, 7/30

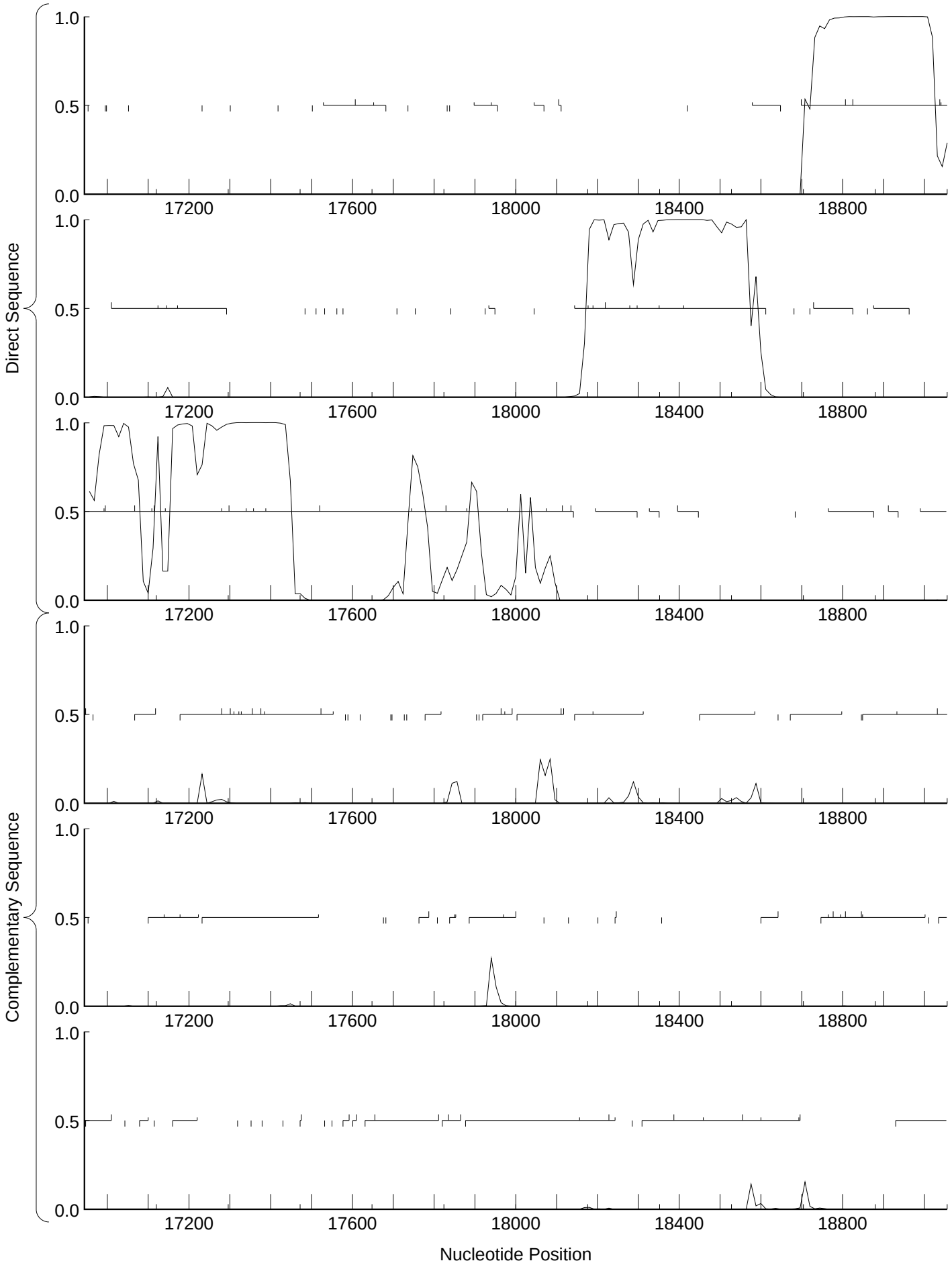



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Complementary Sequence
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14000
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Nucleotide Position

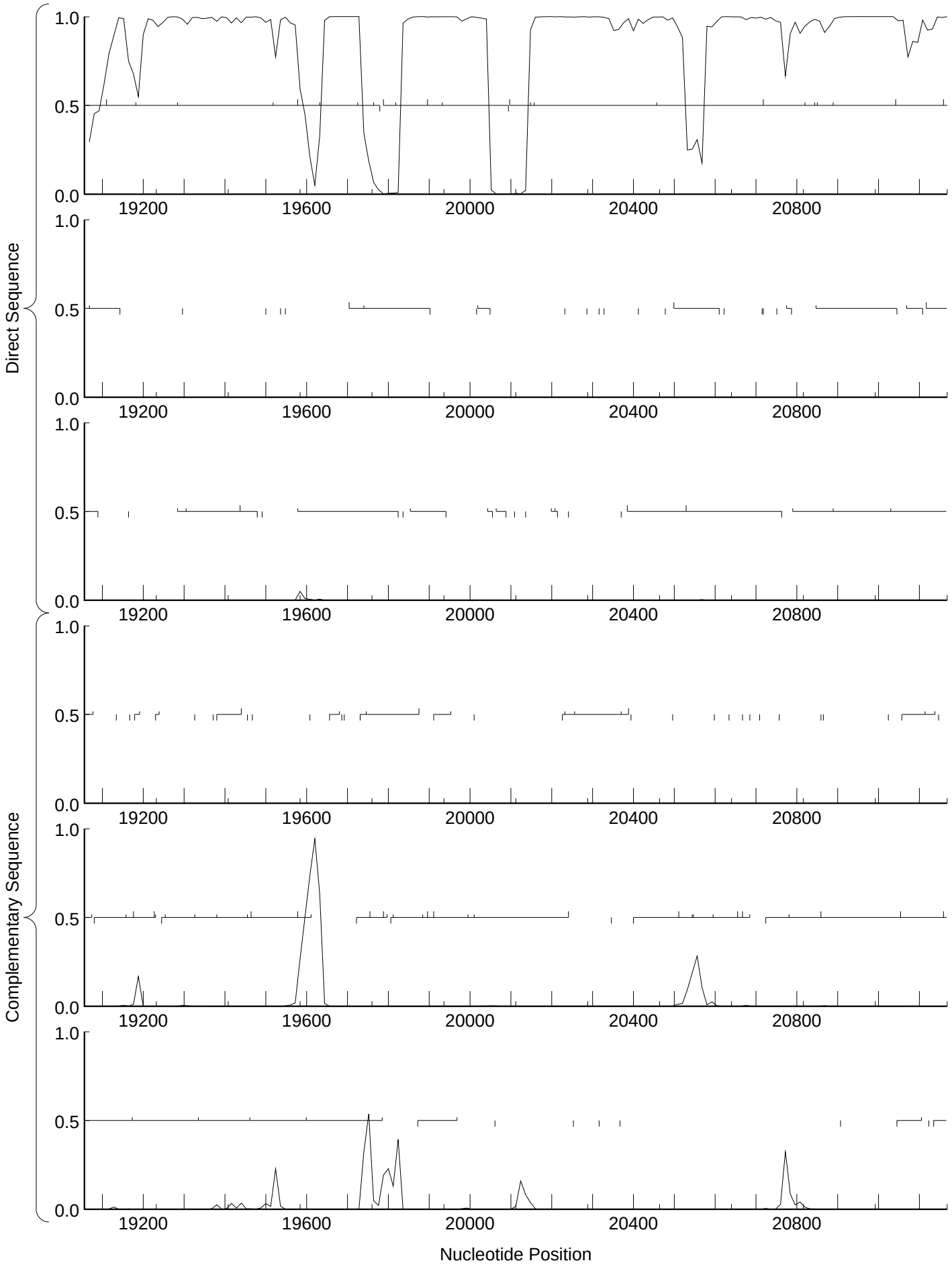
complete sequence, 60974 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K1, Order 4, Window 96, Step 12, 9/30



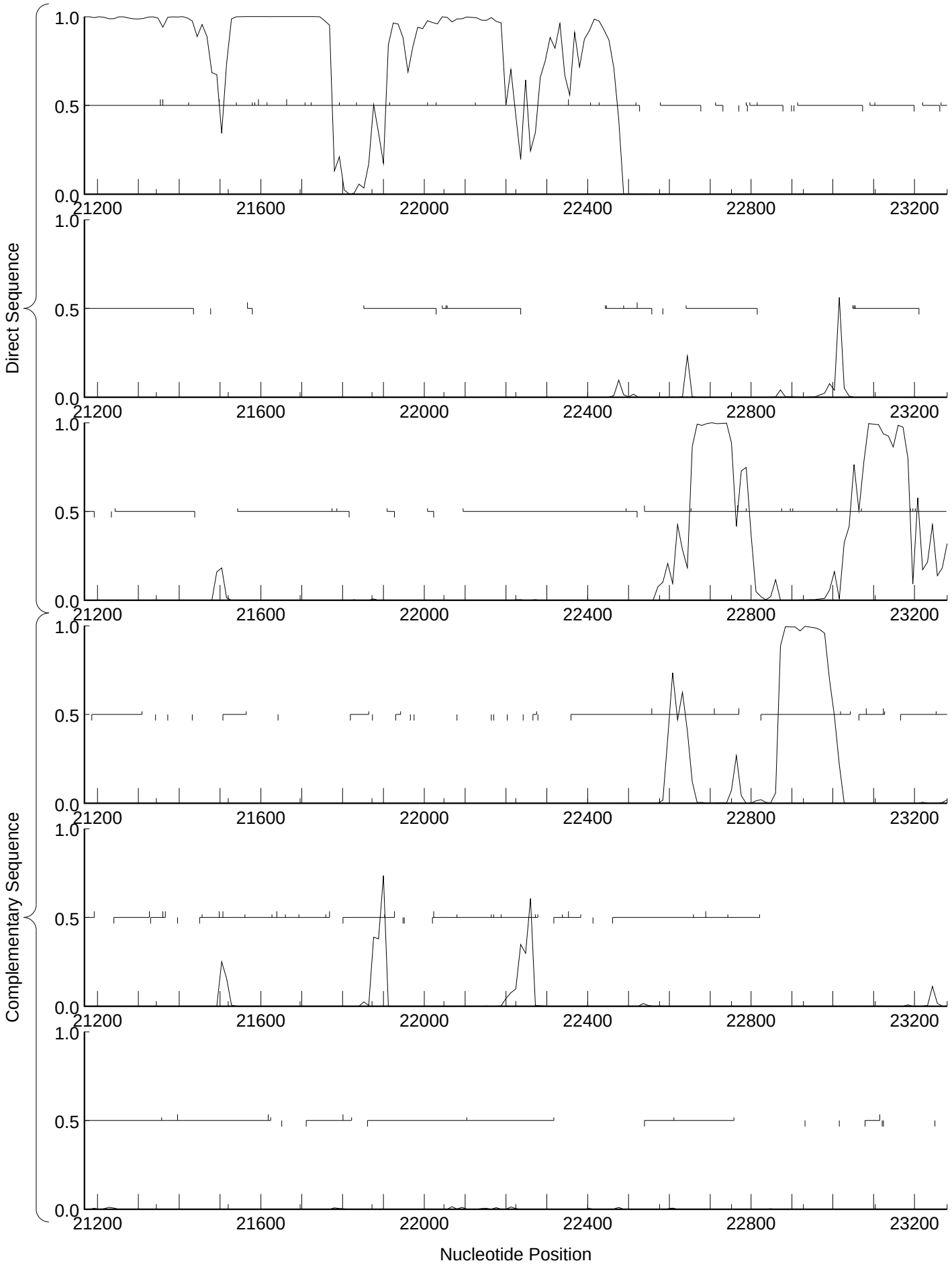
complete sequence, 60974 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K1, Order 4, Window 96, Step 12, 10/30



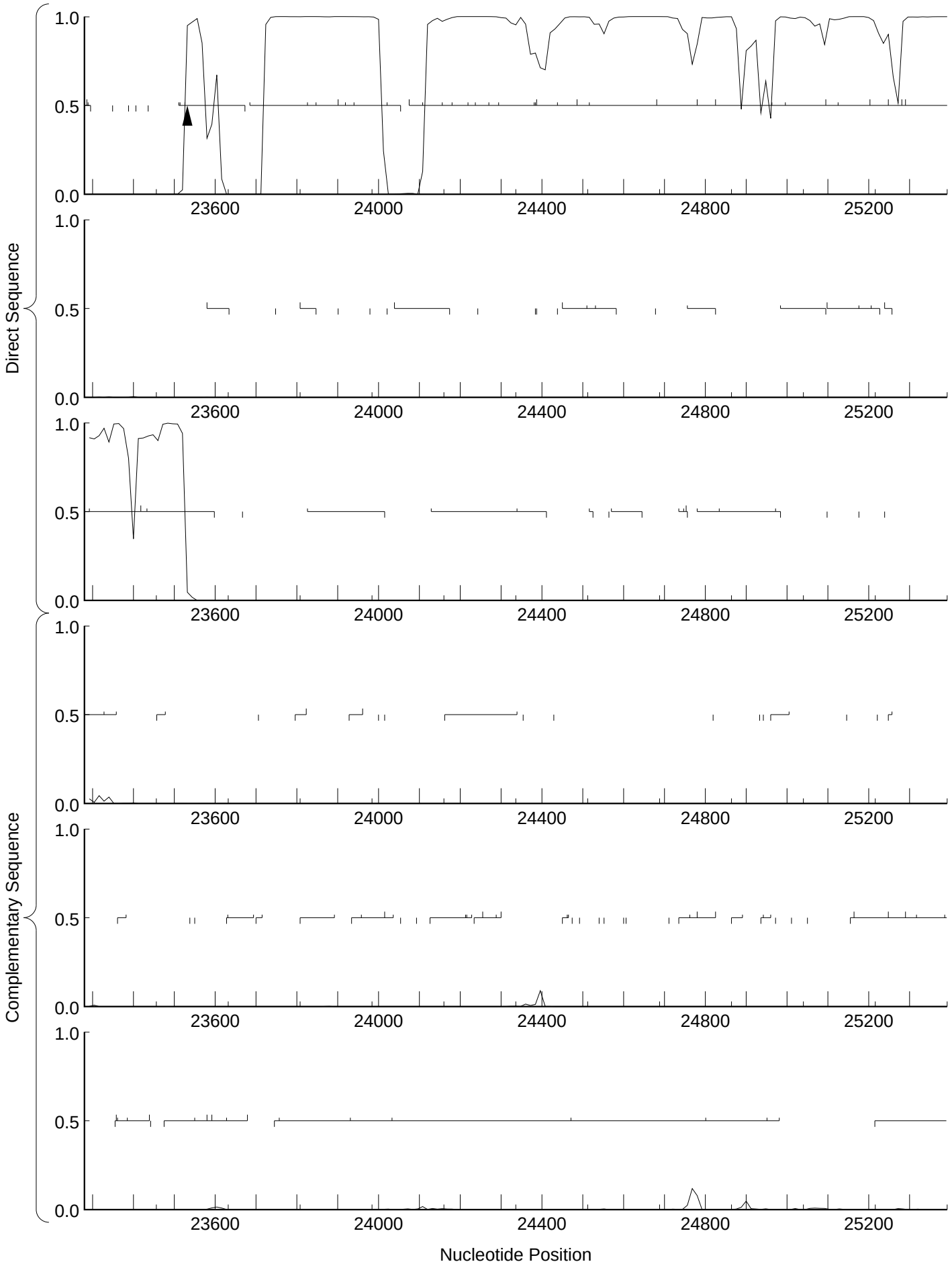
complete sequence, 60974 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K1, Order 4, Window 96, Step 12, 11/30



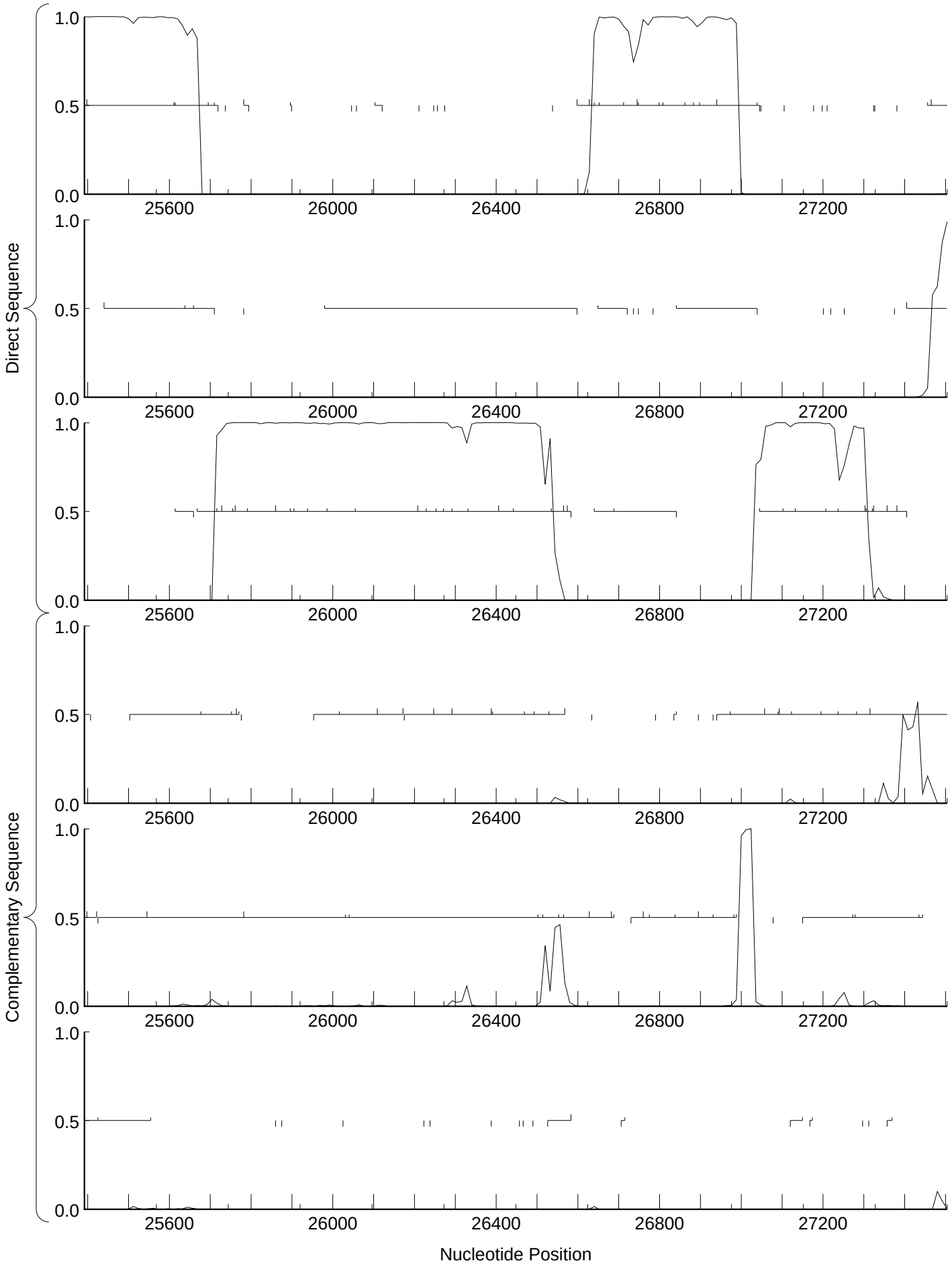
complete sequence, 60974 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K1, Order 4, Window 96, Step 12, 12/30



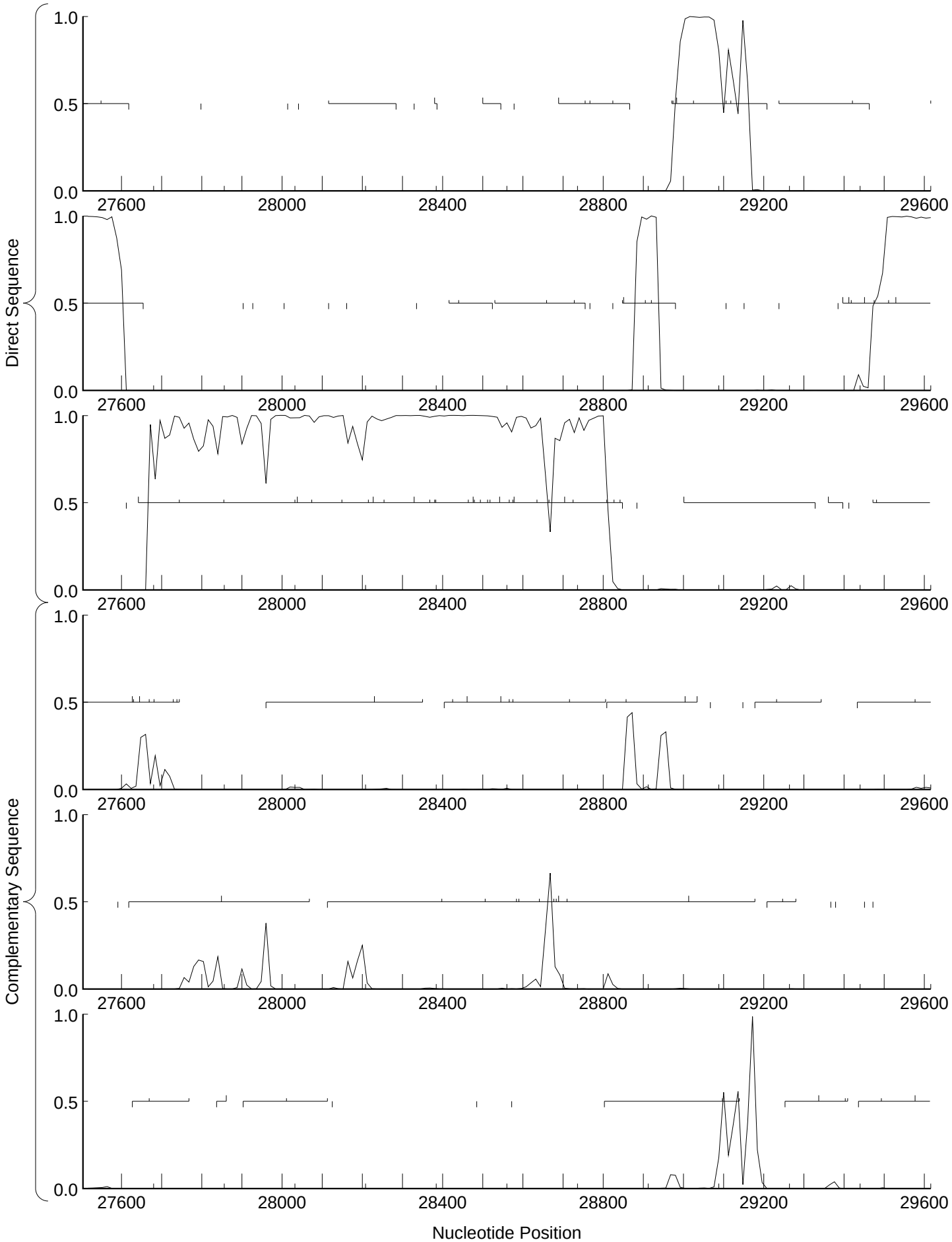
complete sequence, 60974 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K1, Order 4, Window 96, Step 12, 13/30



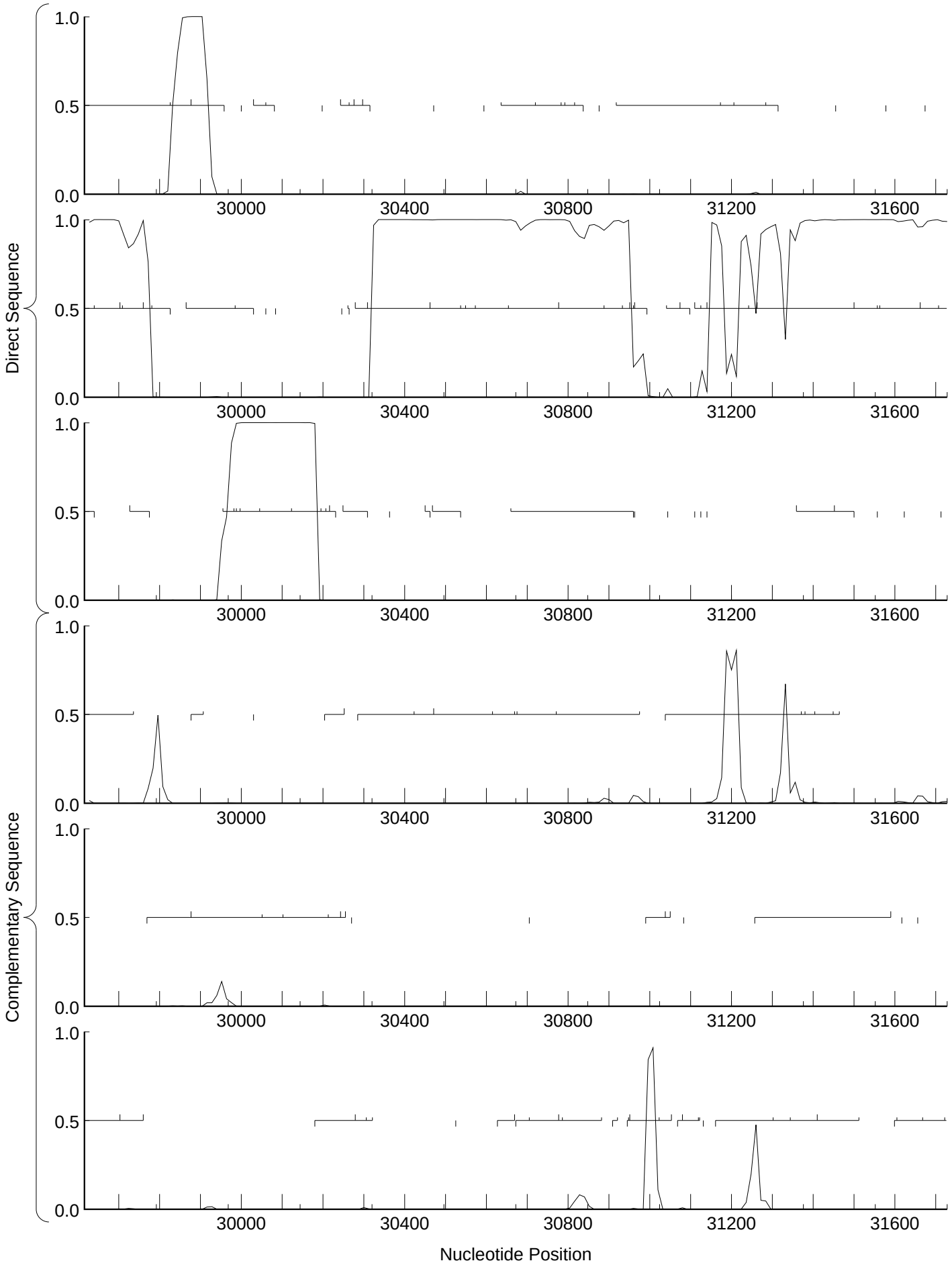
complete sequence, 60974 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K1, Order 4, Window 96, Step 12, 14/30



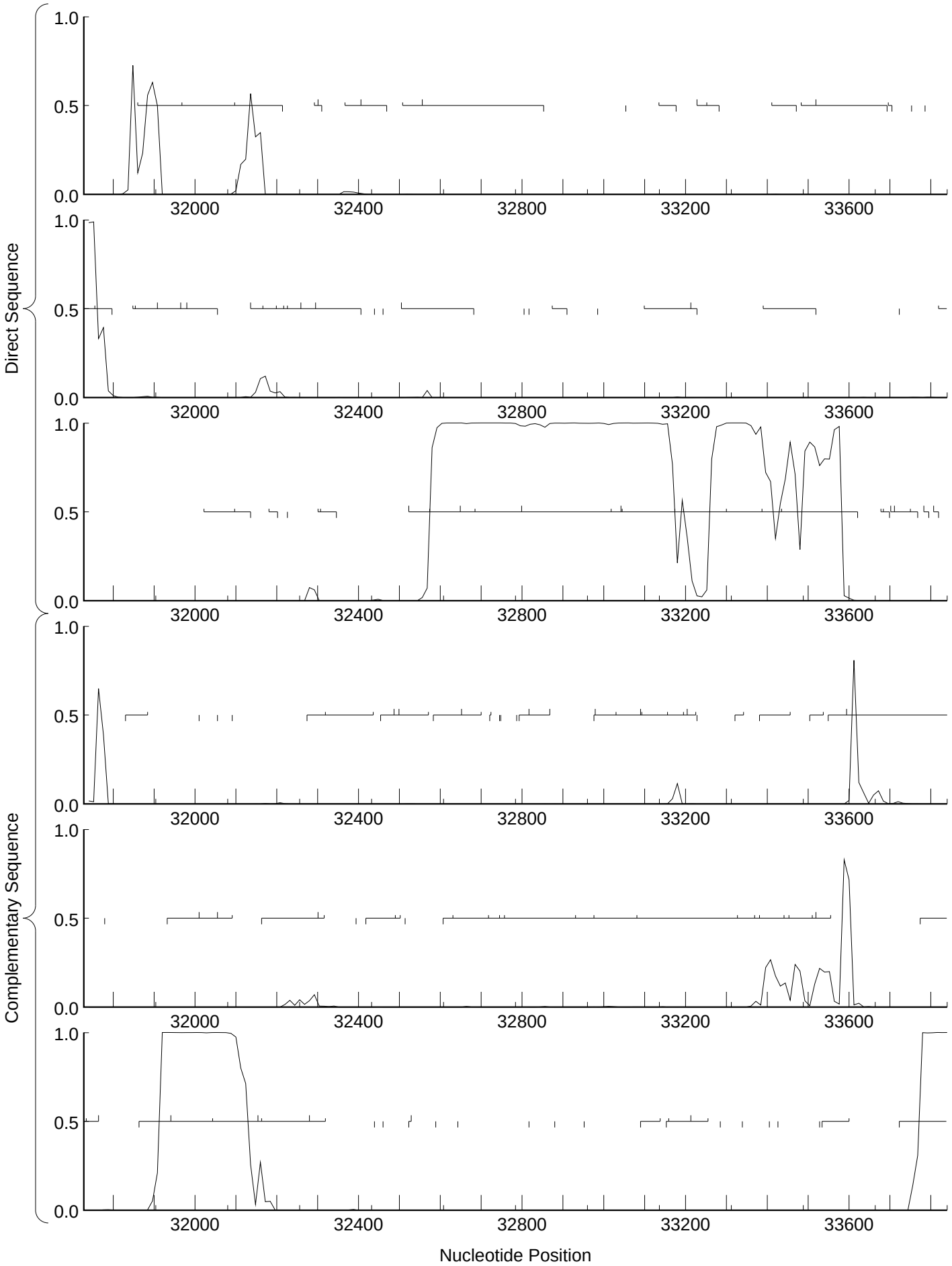
complete sequence, 60974 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K1, Order 4, Window 96, Step 12, 15/30

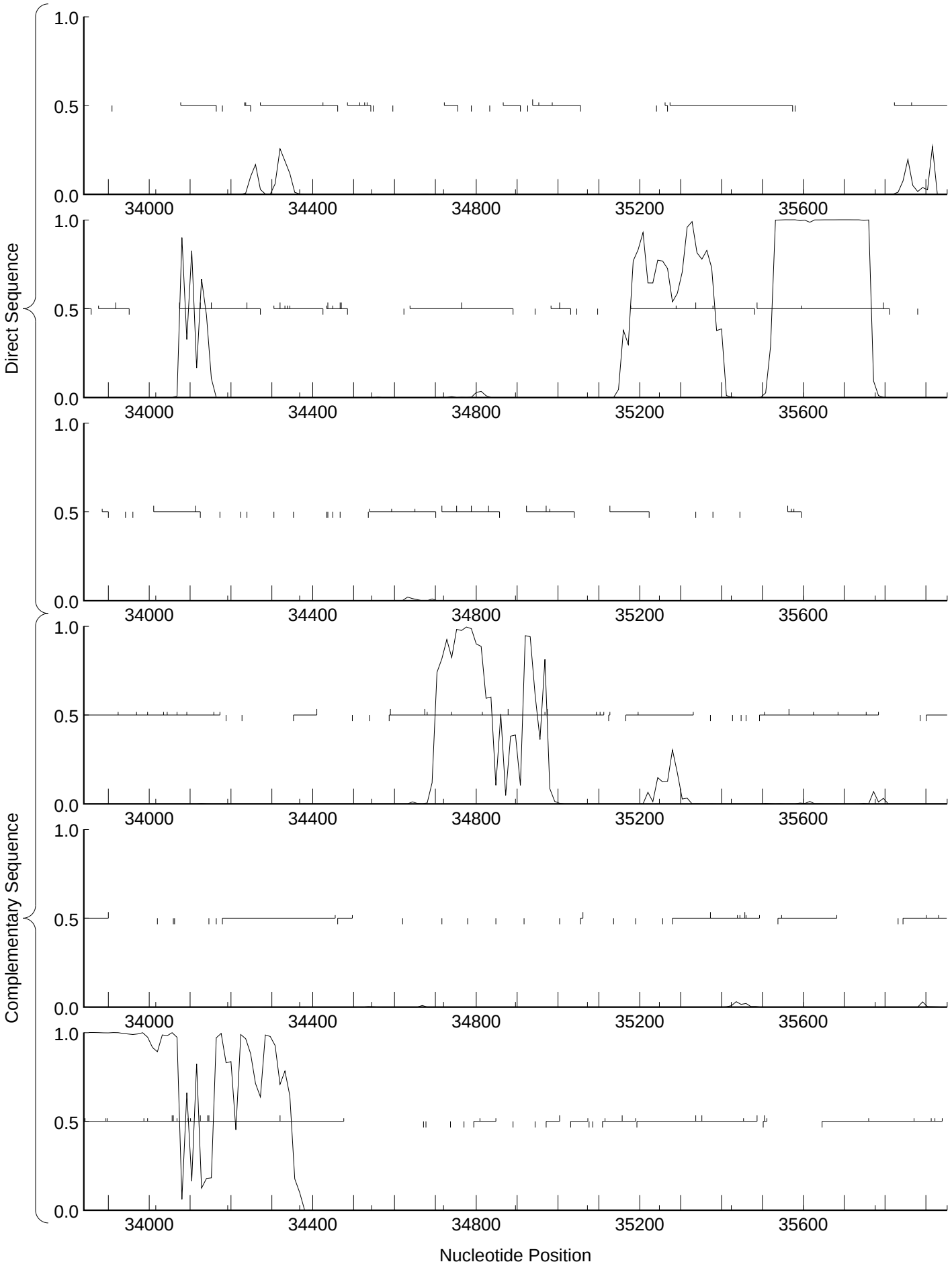


complete sequence, 60974 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K1, Order 4, Window 96, Step 12, 16/30

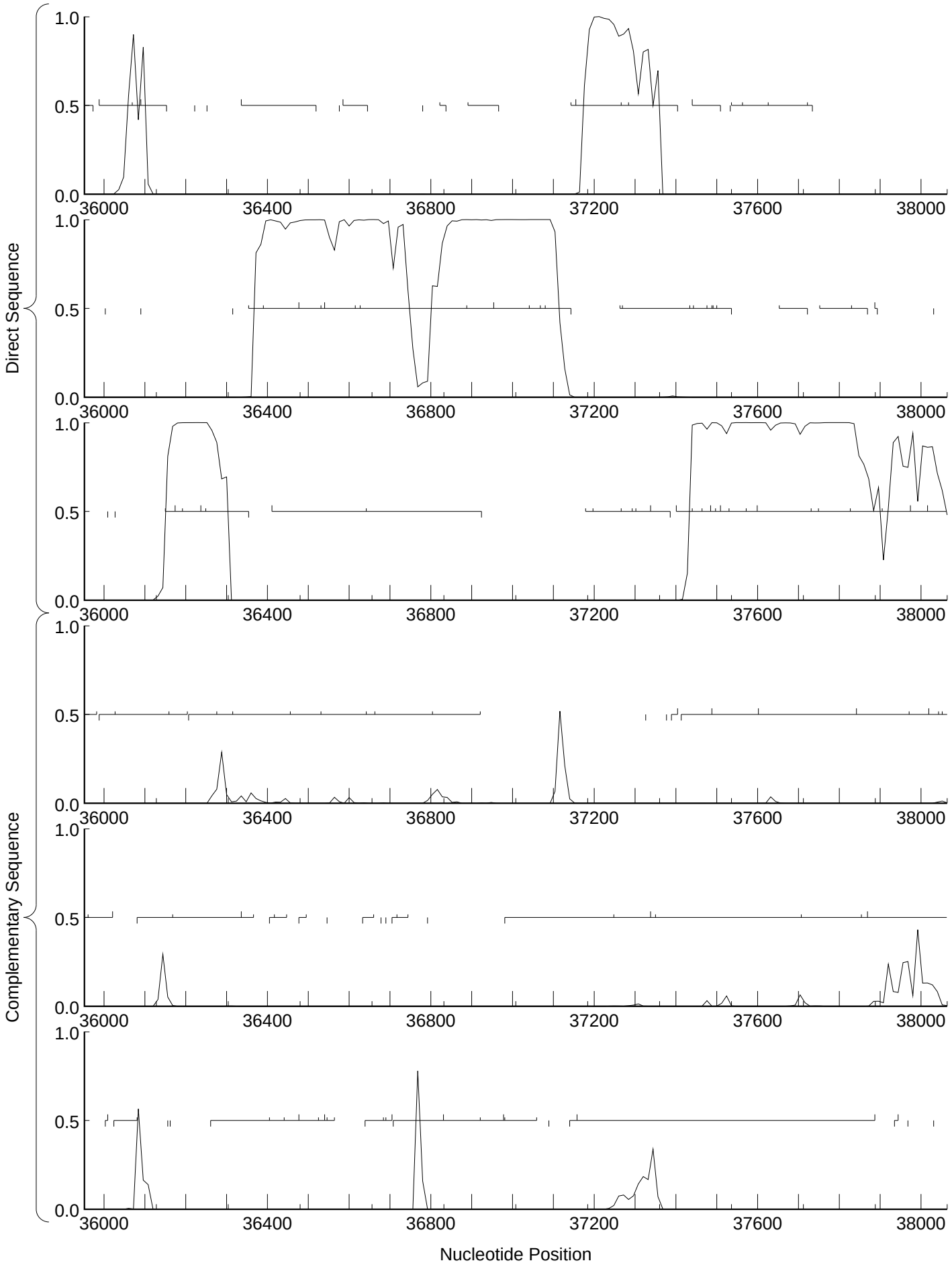


complete sequence, 60974 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K1, Order 4, Window 96, Step 12, 17/30

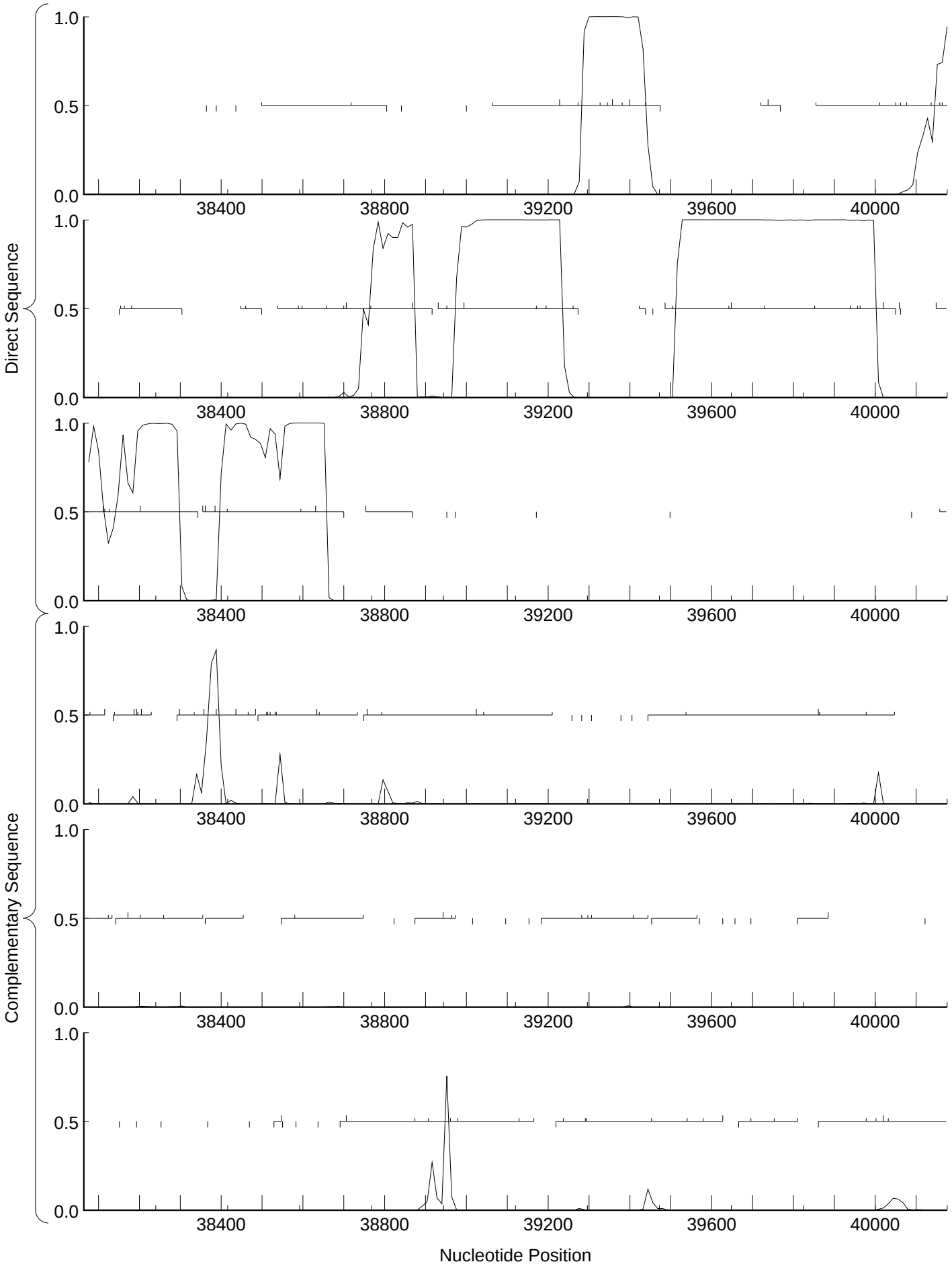



Direct Sequence
Complementary Sequence
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0.5
0.0
34000
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34800
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35600
Nucleotide Position

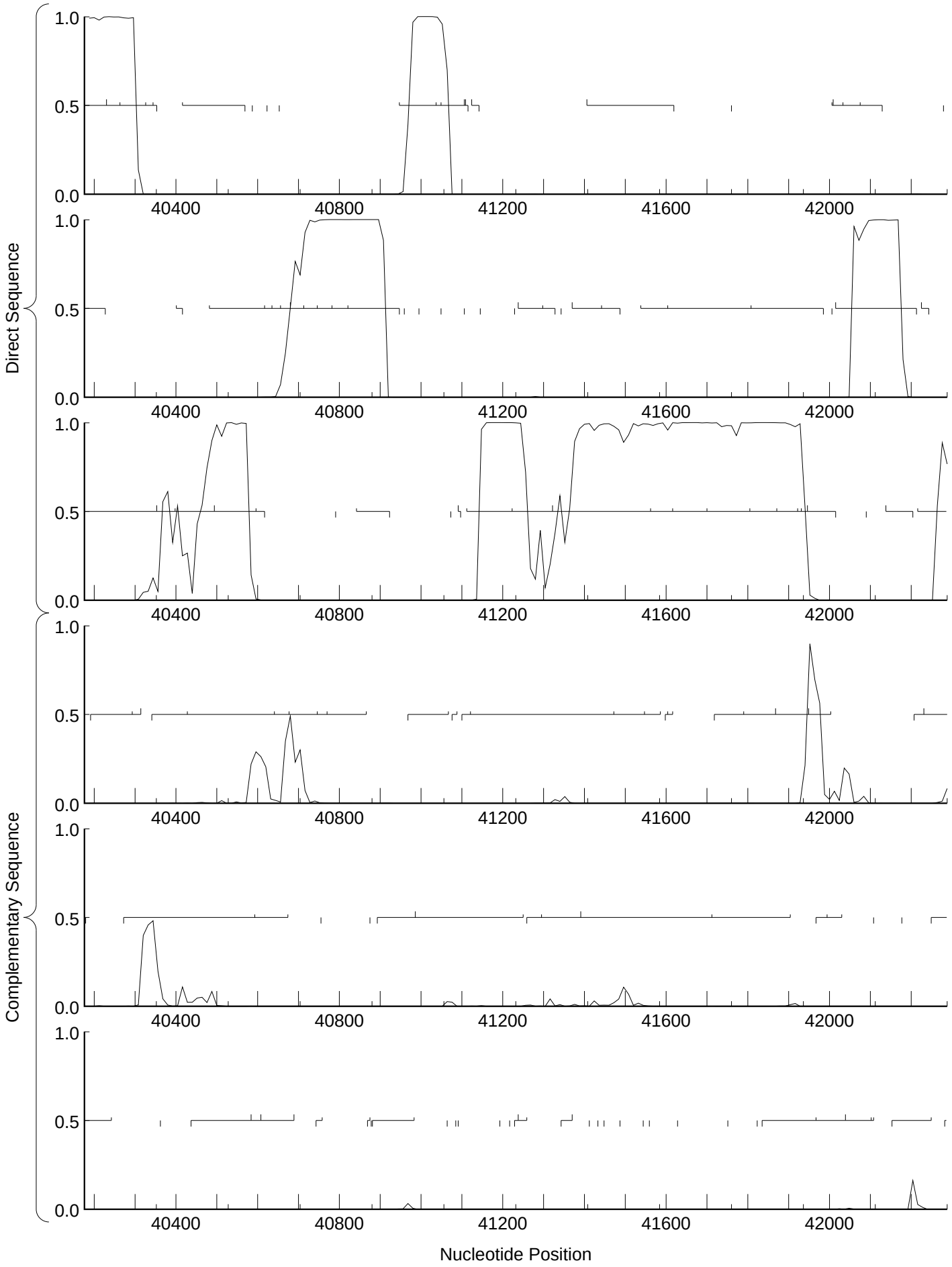
complete sequence, 60974 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K1, Order 4, Window 96, Step 12, 19/30

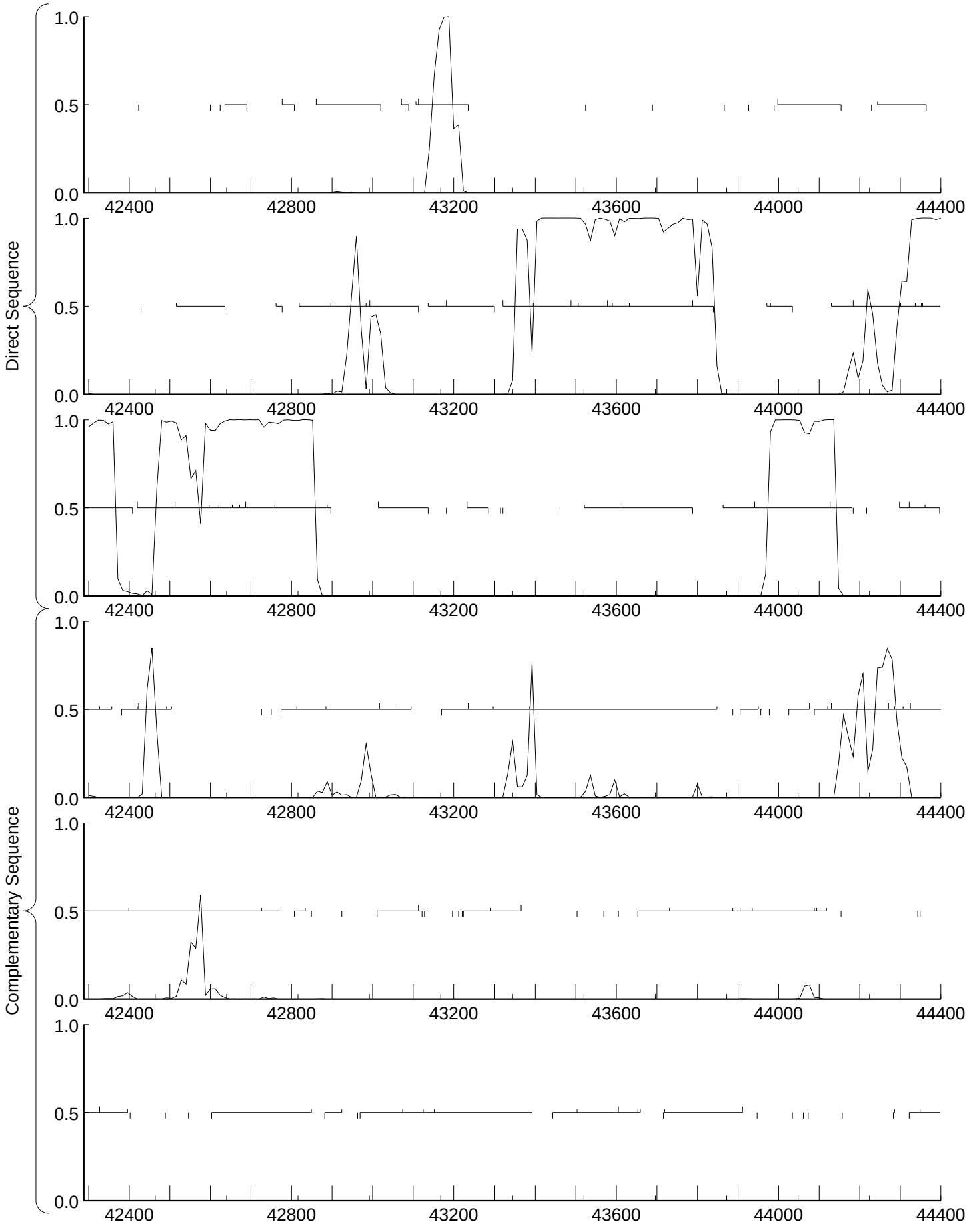


complete sequence, 60974 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K1, Order 4, Window 96, Step 12, 20/30

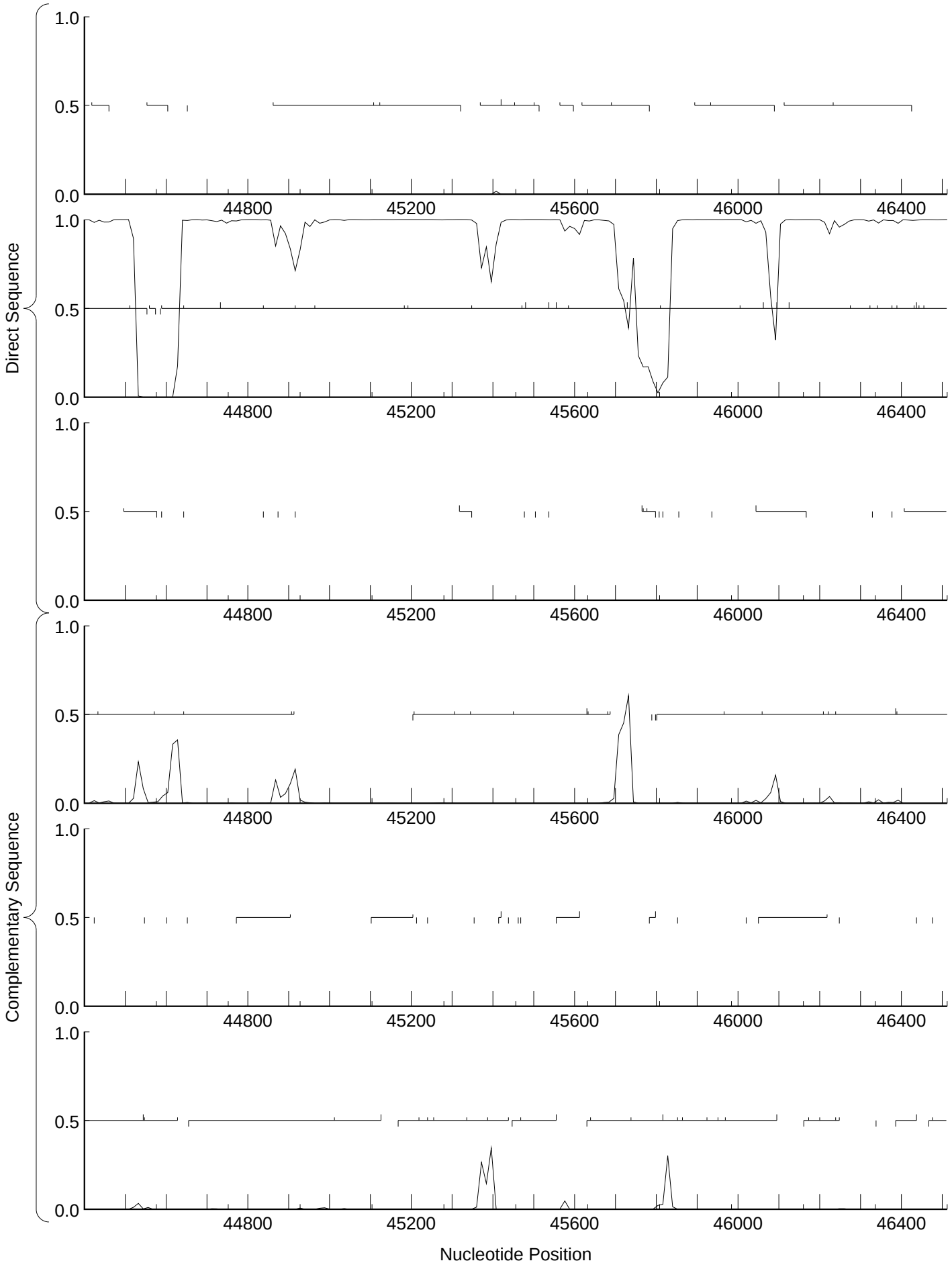


complete sequence, 60974 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K1, Order 4, Window 96, Step 12, 21/30

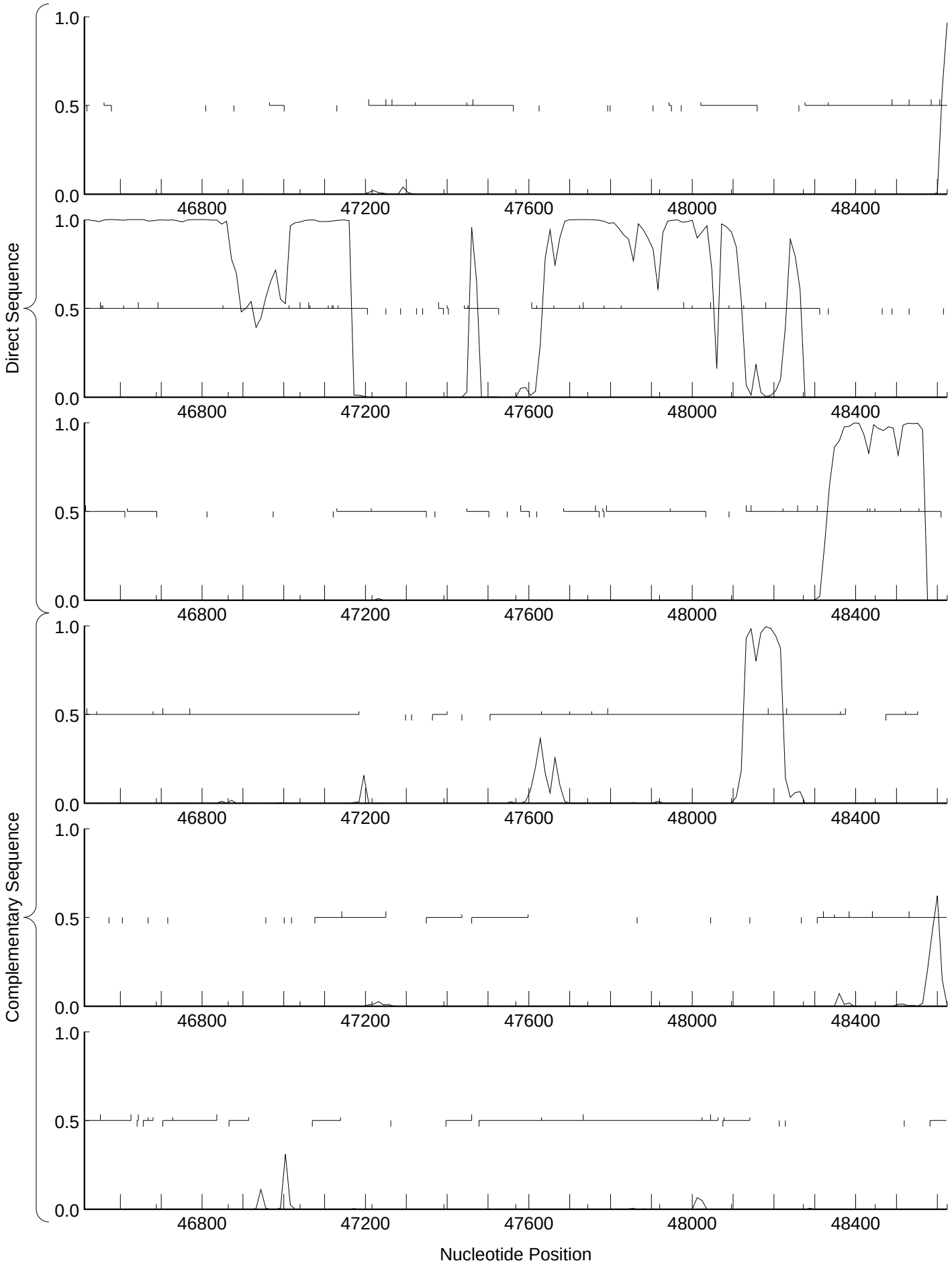



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Complementary Sequence
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43600
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Nucleotide Position

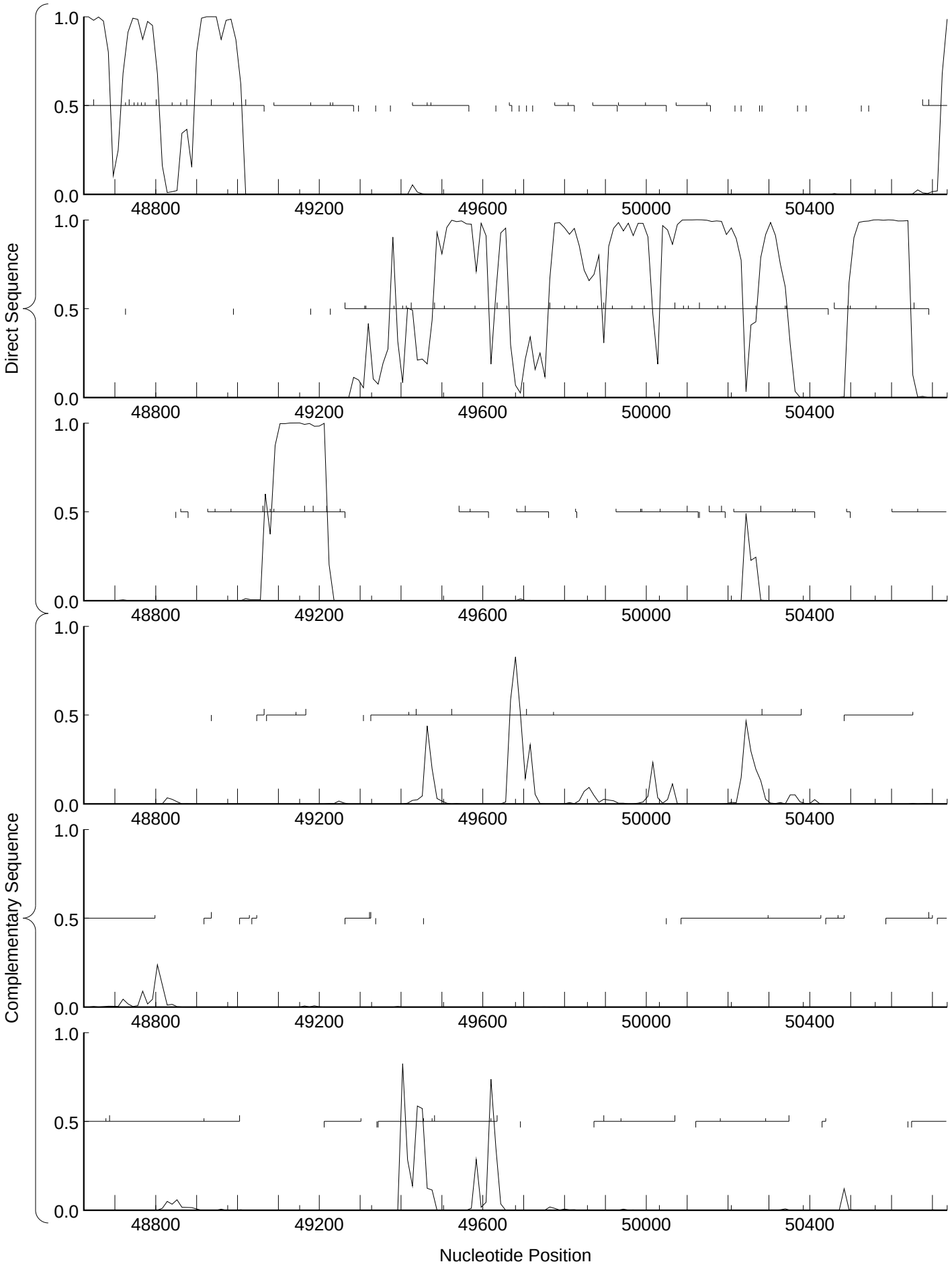
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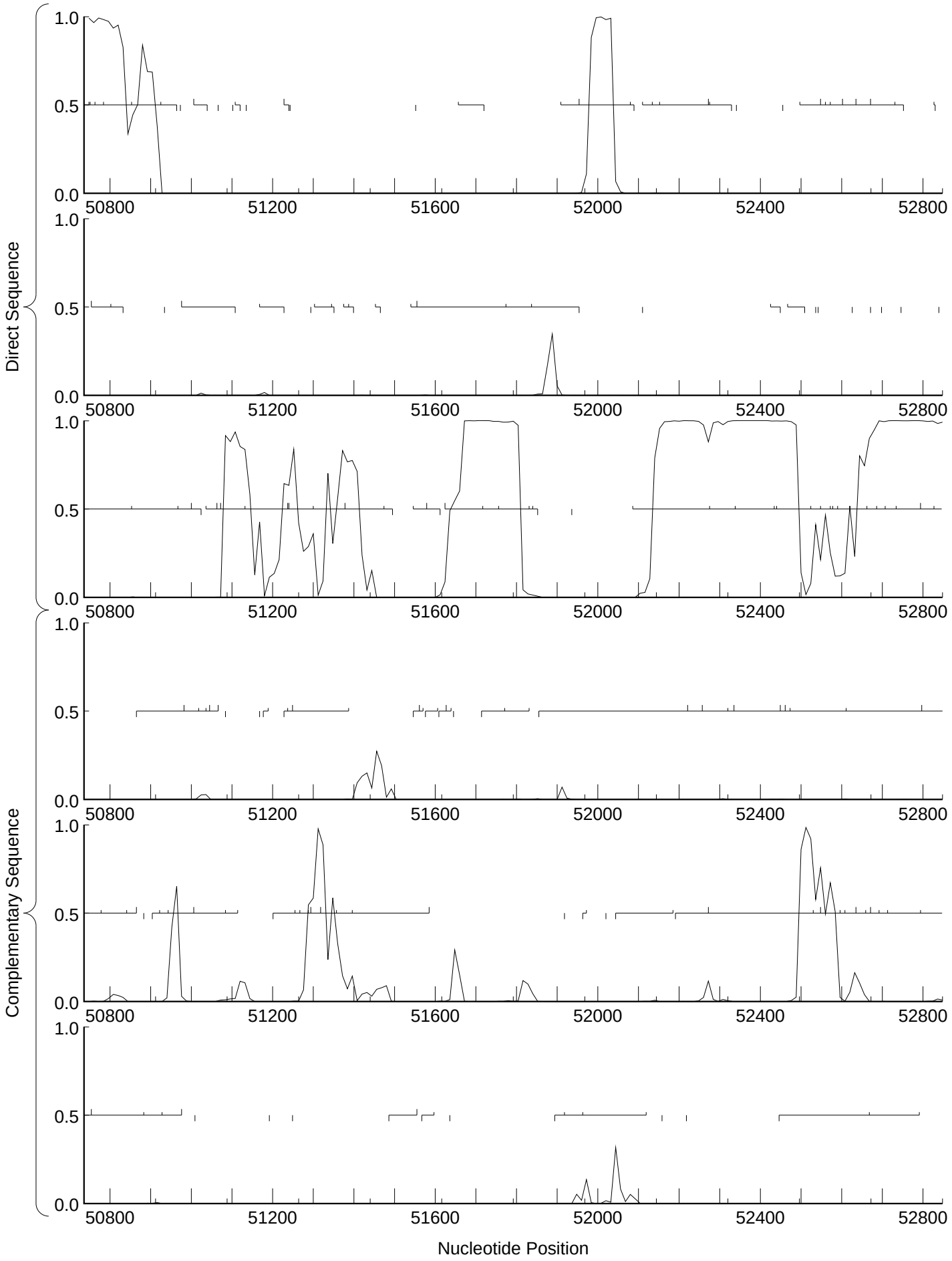


complete sequence, 60974 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K1, Order 4, Window 96, Step 12, 24/30

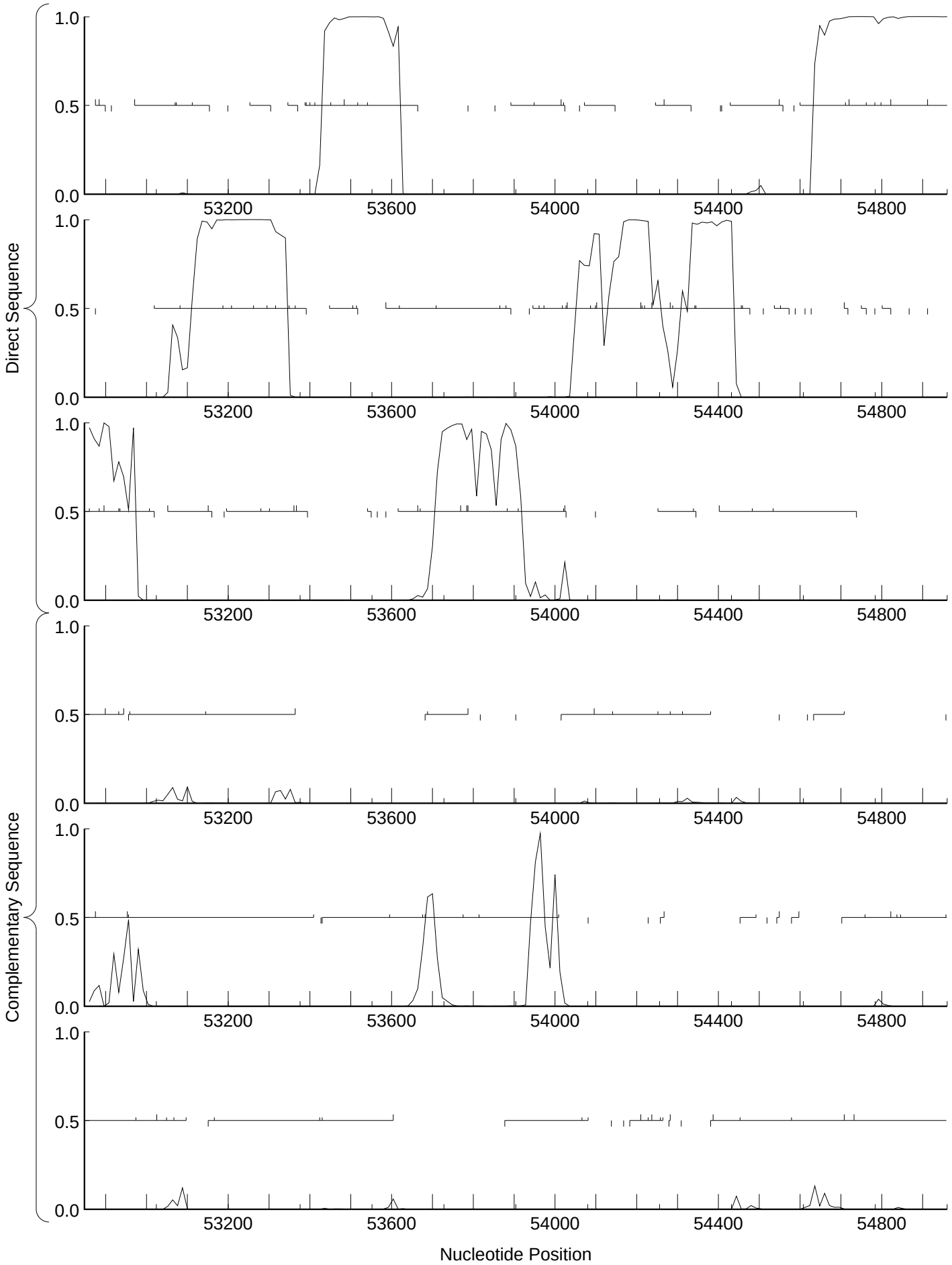


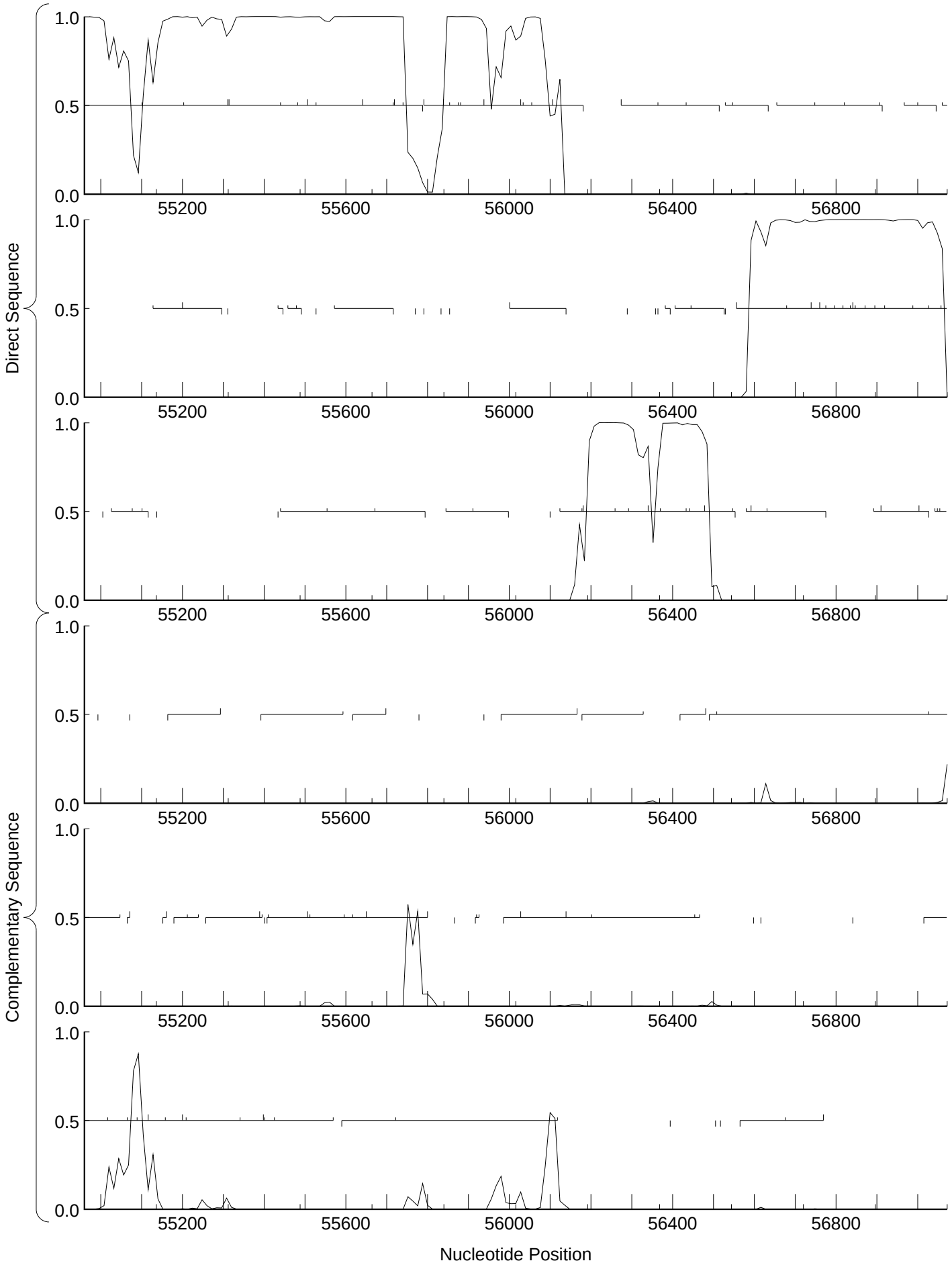
complete sequence, 60974 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K1, Order 4, Window 96, Step 12, 25/30



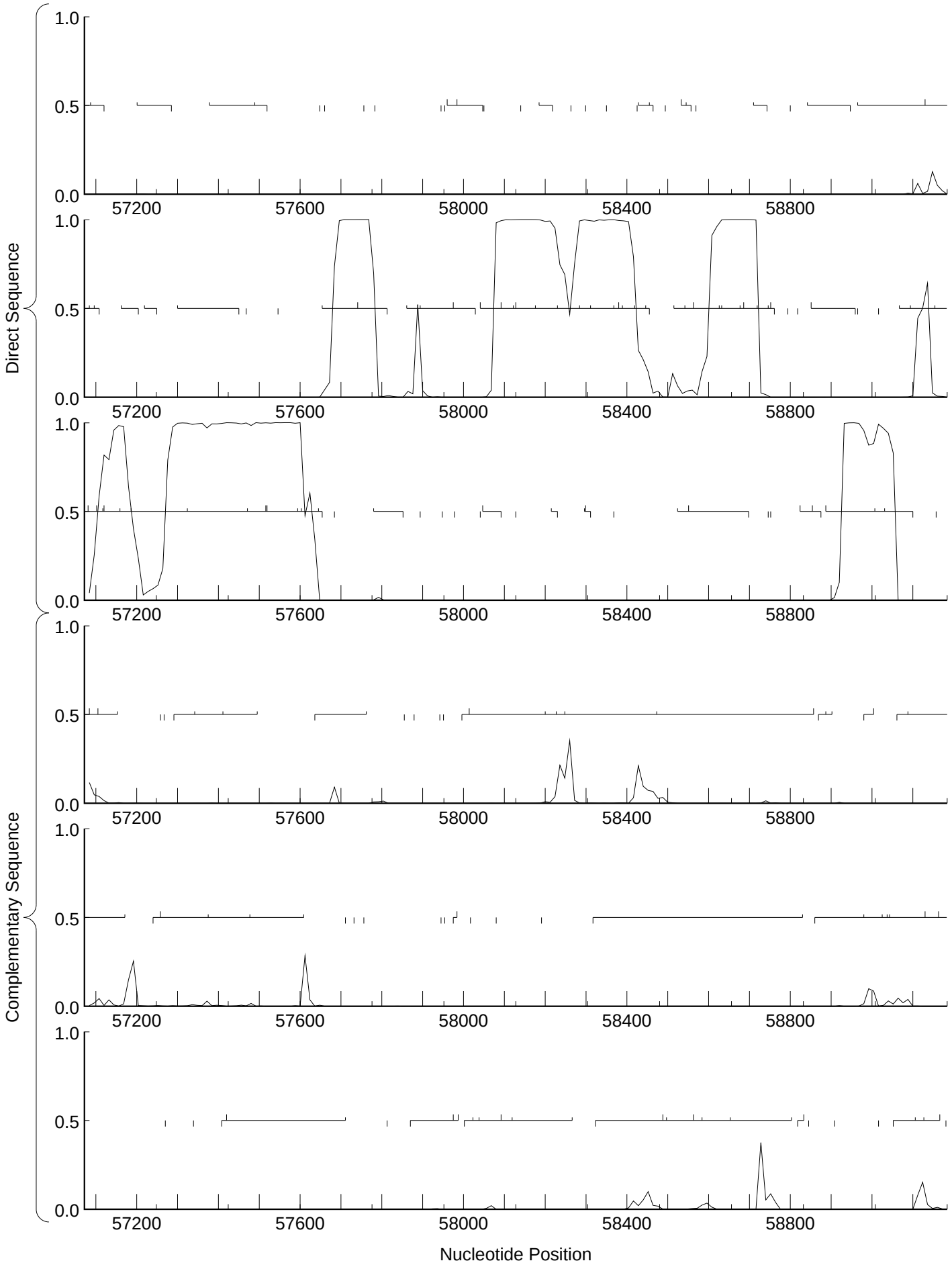

Direct Sequence
Complementary Sequence
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0.0
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51600
52000
52400
52800
Nucleotide Position

complete sequence, 60974 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K1, Order 4, Window 96, Step 12, 27/30




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

complete sequence, 60974 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K1, Order 4, Window 96, Step 12, 29/30



complete sequence, 60974 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K1, Order 4, Window 96, Step 12, 30/30

