GeneMark

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

PROGRAM INFORMATION

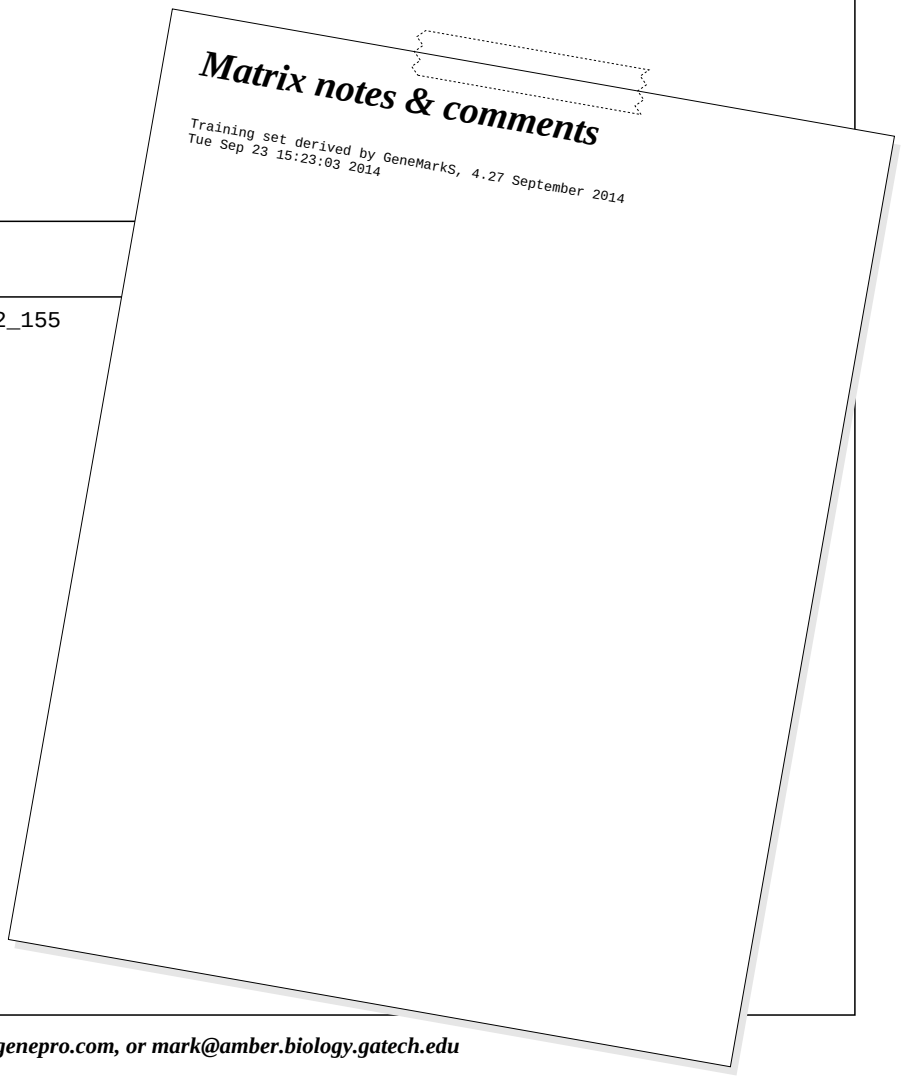
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Sequence         :  Mycobacterium phage LilHazelnut complete sequence, 53746 bp including 14-base 3’ overhang (

Analysis Date    :  3/28/24 at 17:30:14
Pages            :  27
Sequence Length  :  53746 bp
GC Content       :   67.45%

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

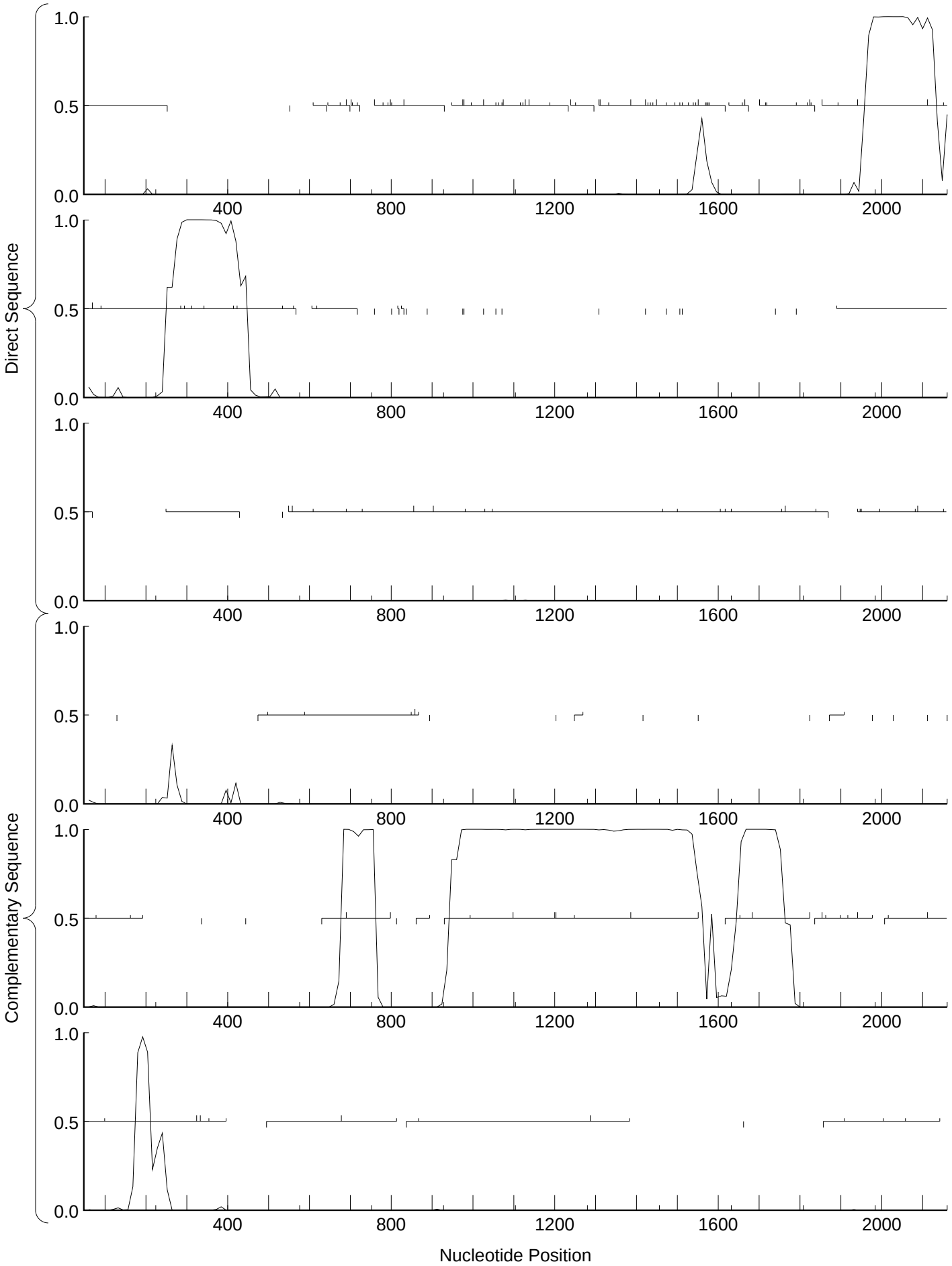
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Matrix     :  Mycobacterium_smegmatis_MC2_155
Author     :  -

Order      :  4
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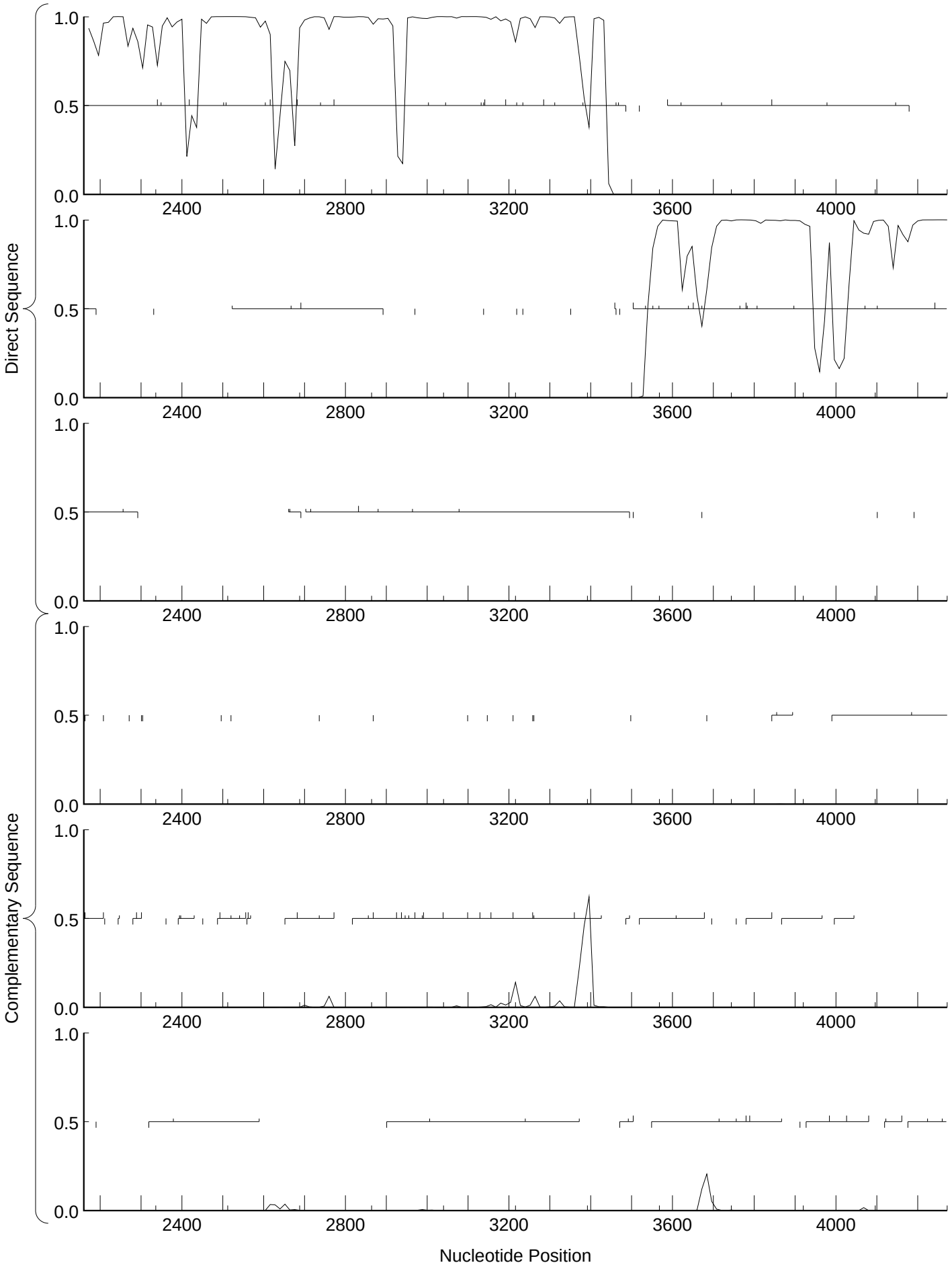

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  Send questions / comments to:
      Dr. M. Borodovsky
      Georgia Institute of Technology
      School of Biology
      Atlanta, GA  30332-0230
```


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

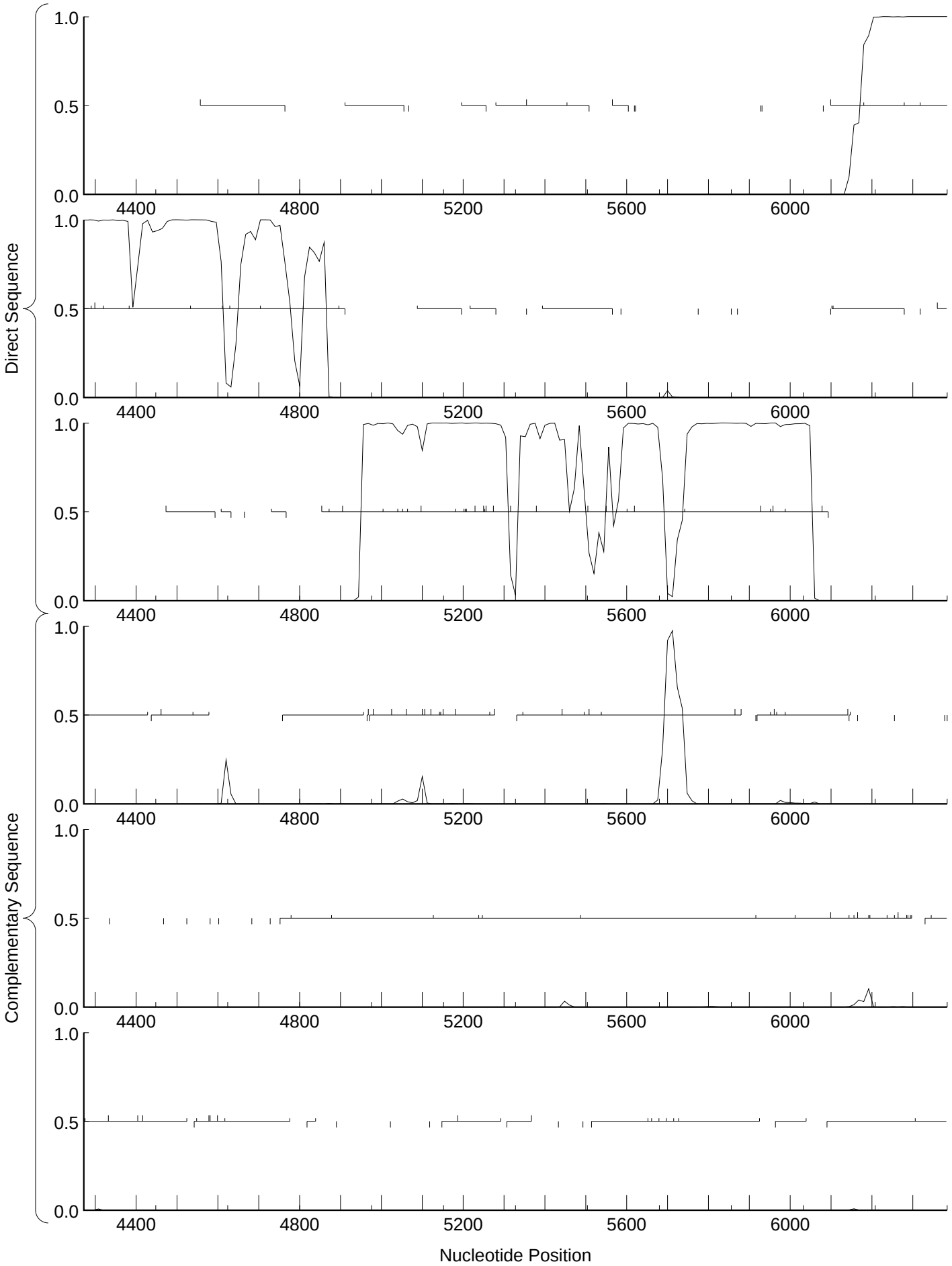
mplete sequence, 53746 bp including 14-base 3’ overhang (TAAGCCGCGCGGTA), Cluster Q, Order 4, Window 96, Step 12, 2/27



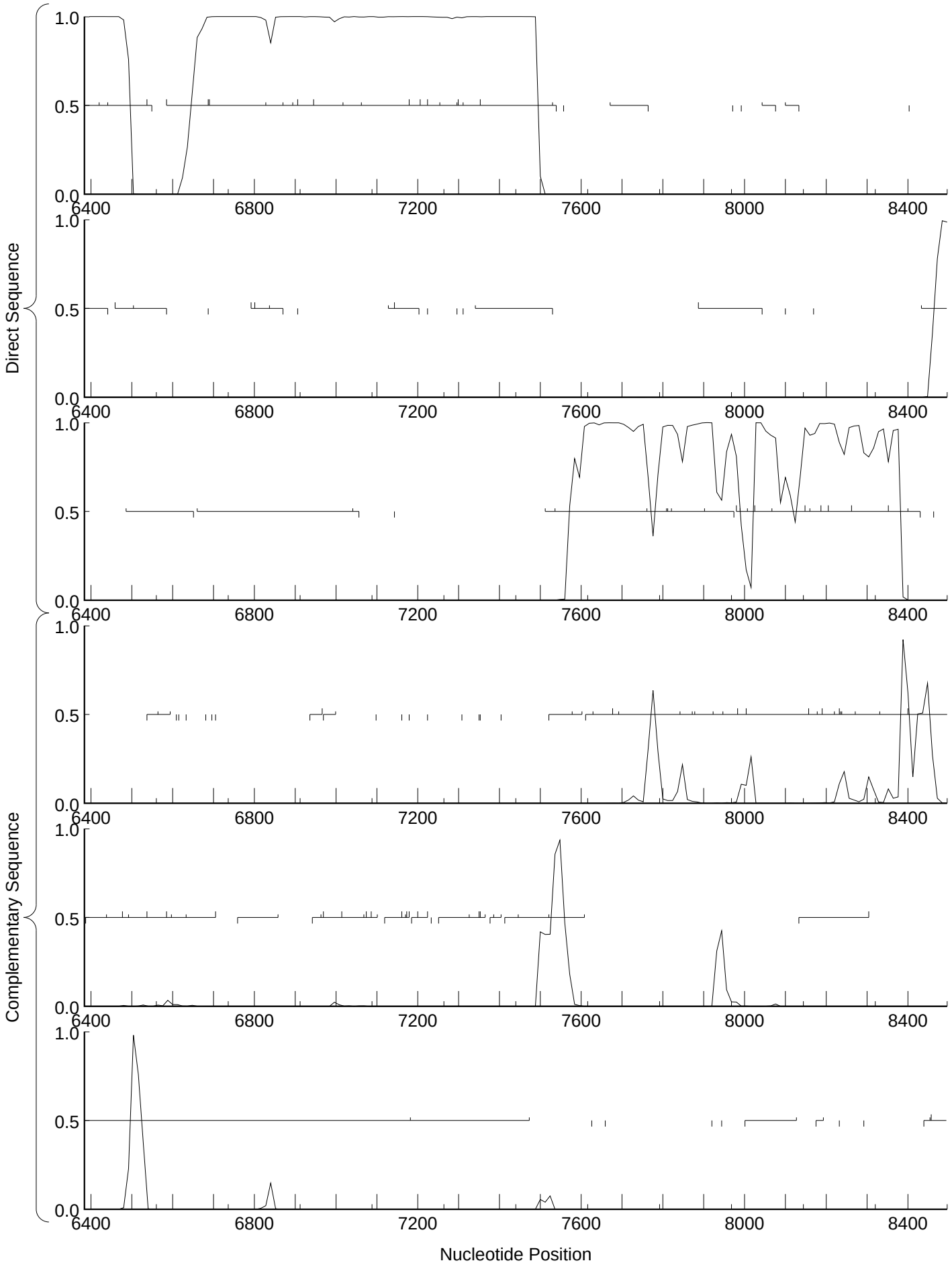
mplete sequence, 53746 bp including 14-base 3' overhang (TAAGCCGCGCGGTA), Cluster Q, Order 4, Window 96, Step 12, 3/27



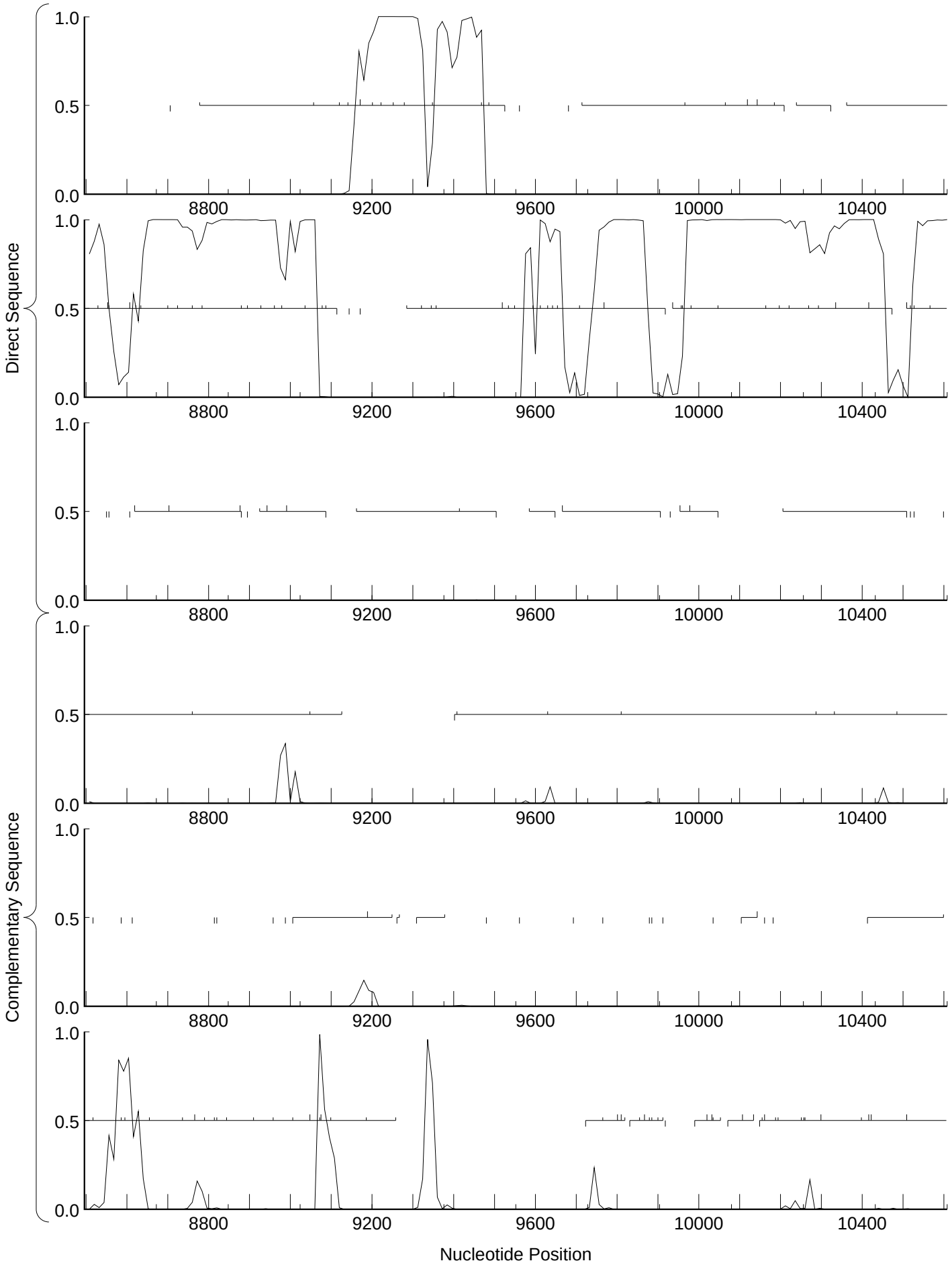
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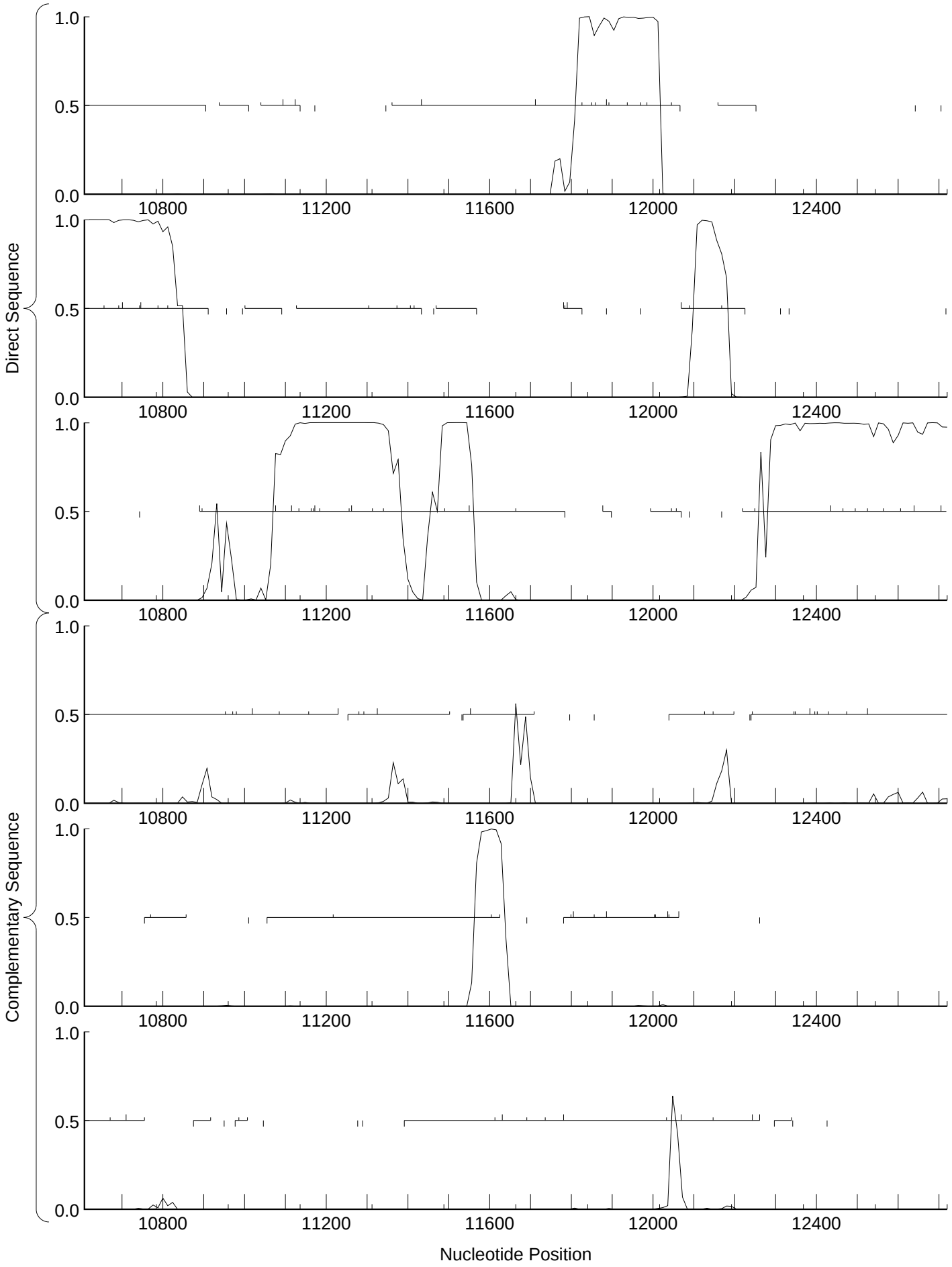
mplete sequence, 53746 bp including 14-base 3' overhang (TAAGCCGCGCGGTA), Cluster Q, Order 4, Window 96, Step 12, 5/27



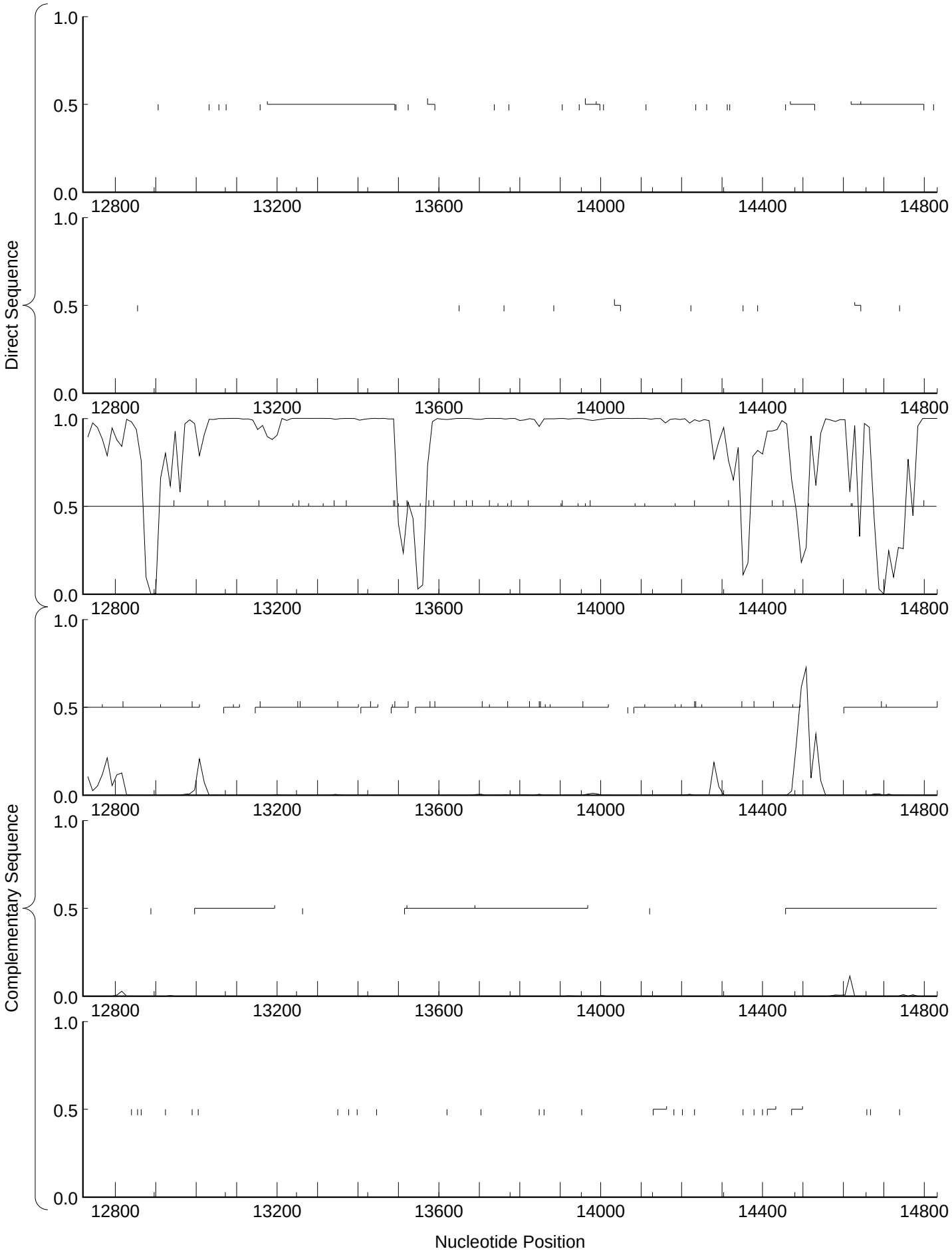
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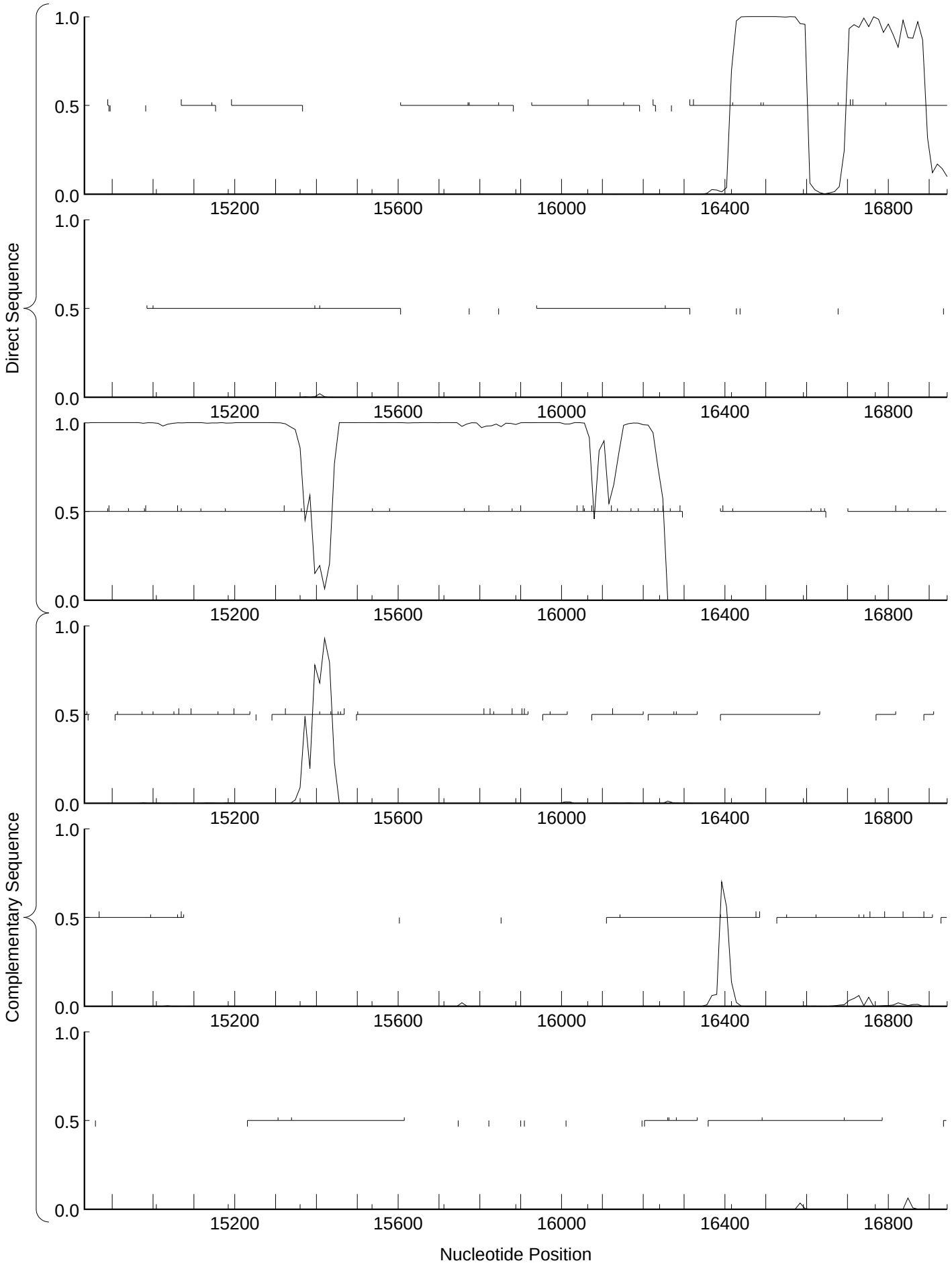
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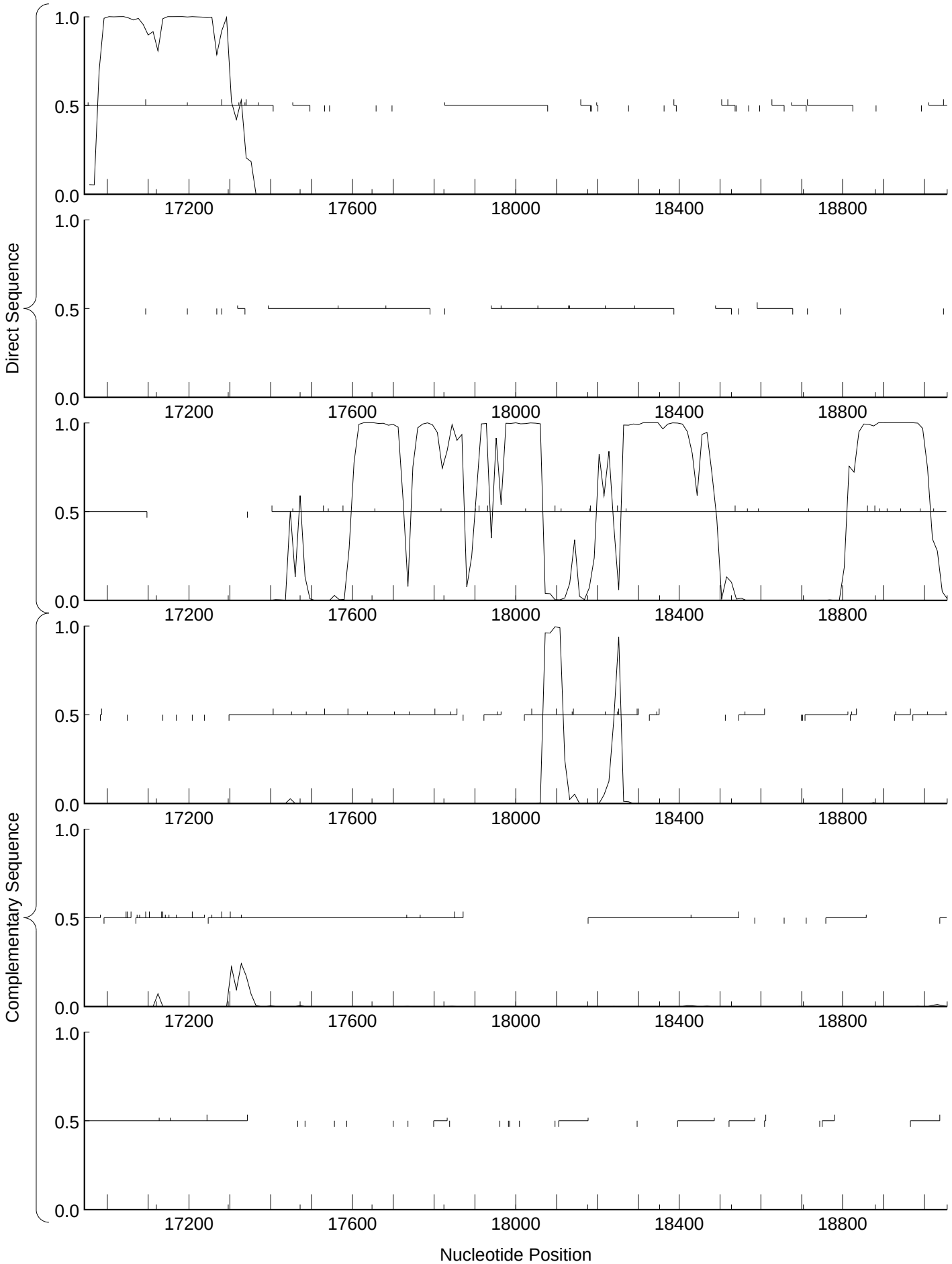
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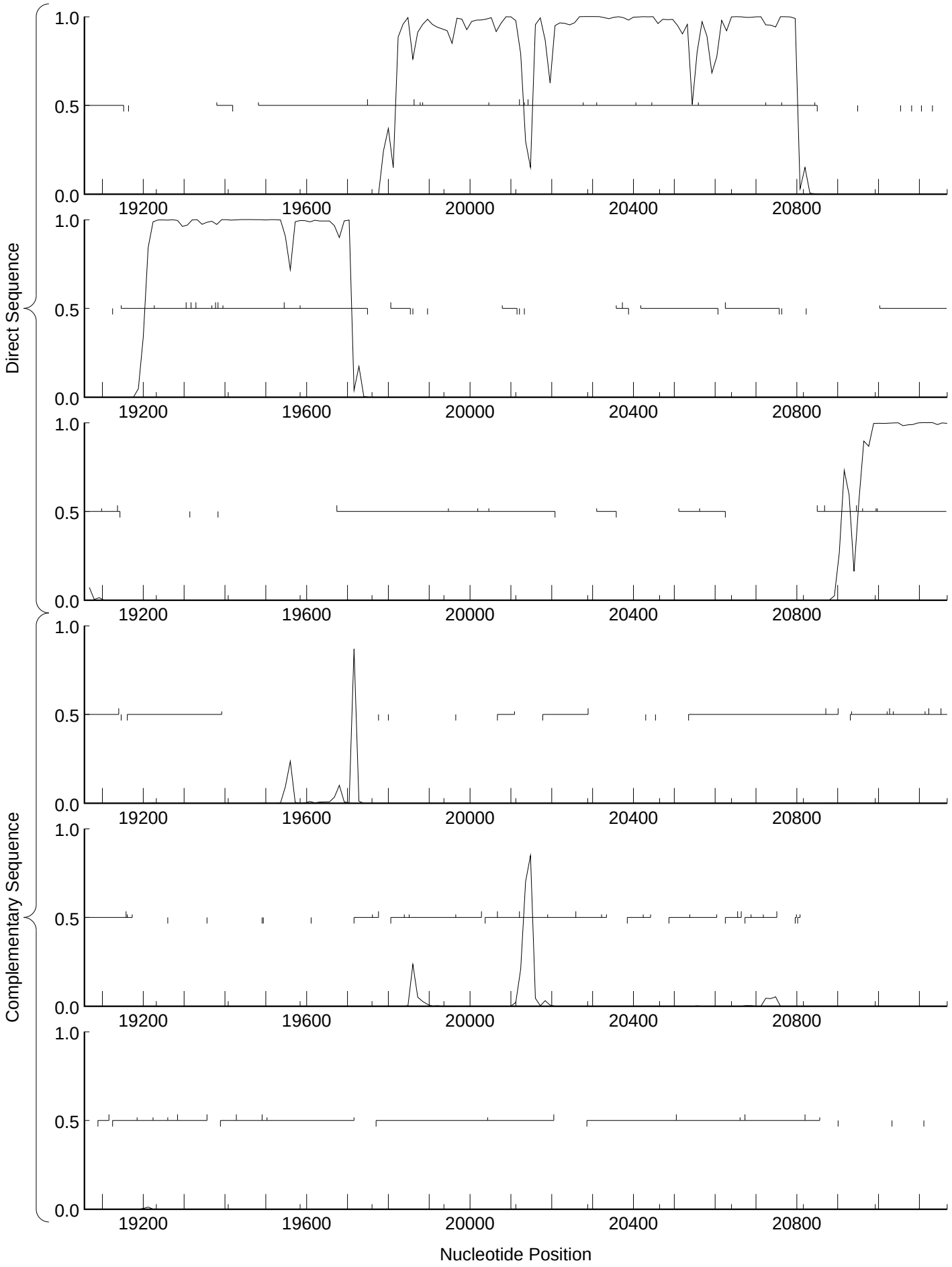
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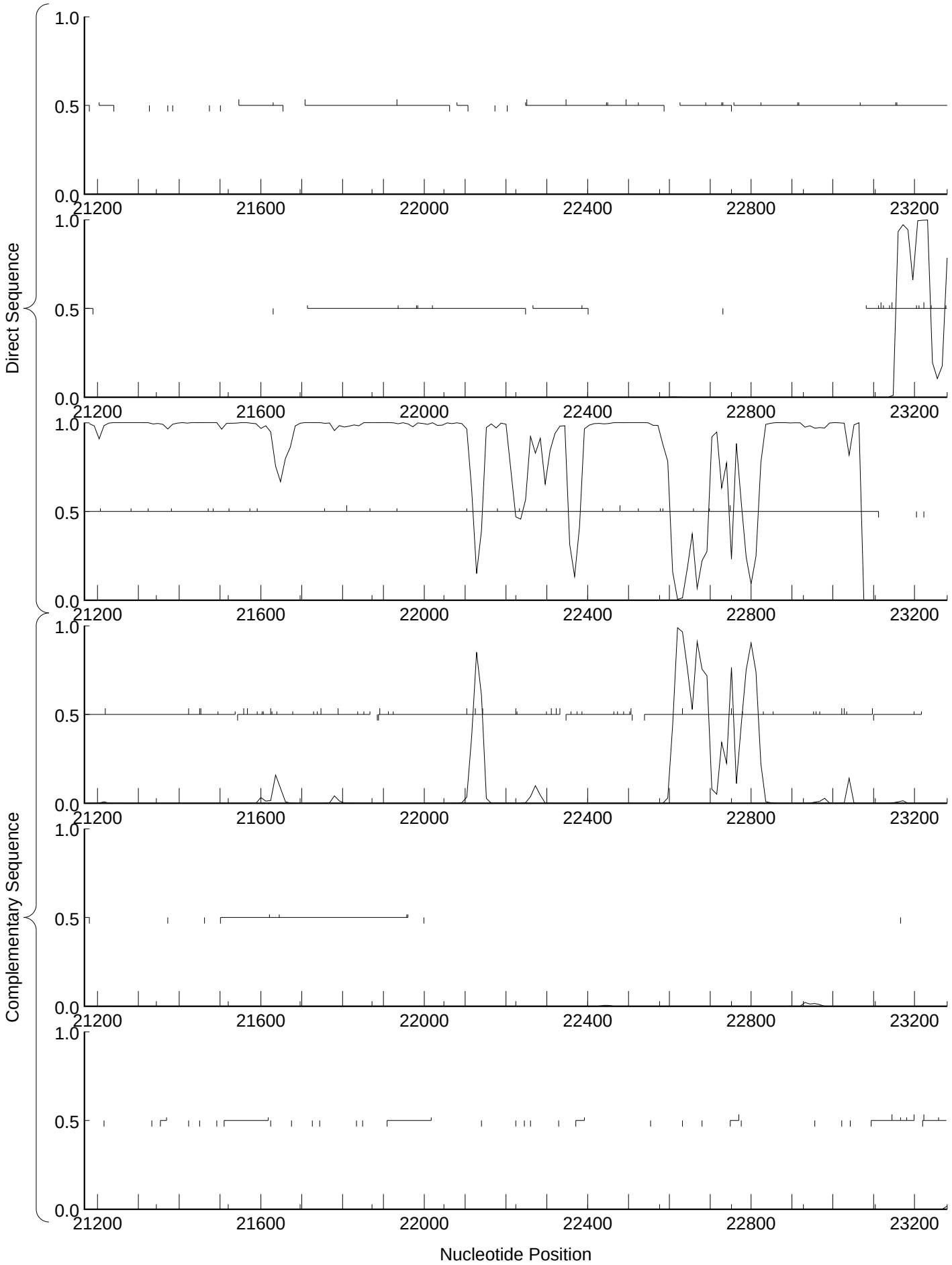


plete sequence, 53746 bp including 14-base 3’ overhang (TAAGCCGCGCGGTA), Cluster Q, Order 4, Window 96, Step 12, 10/27

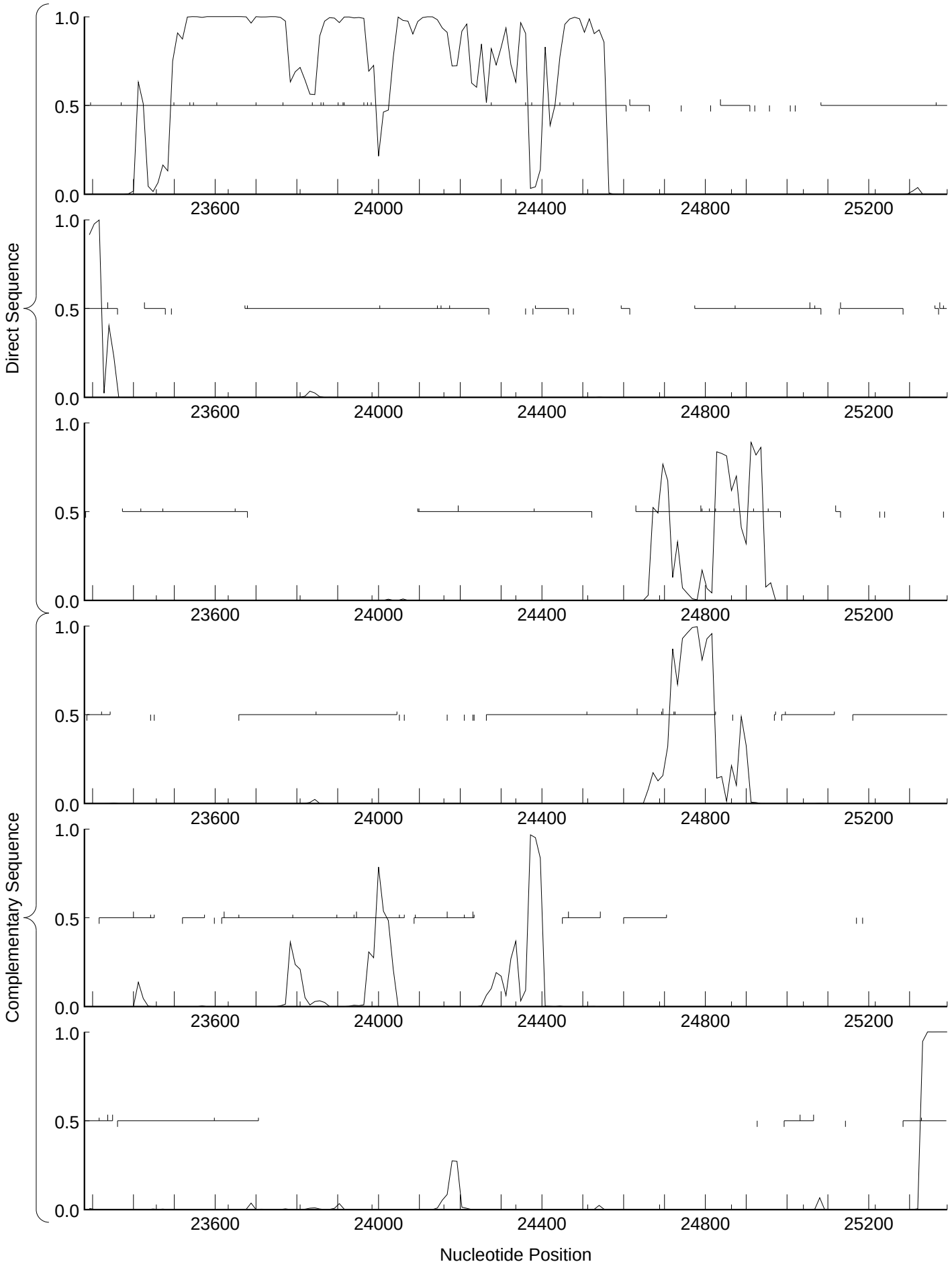


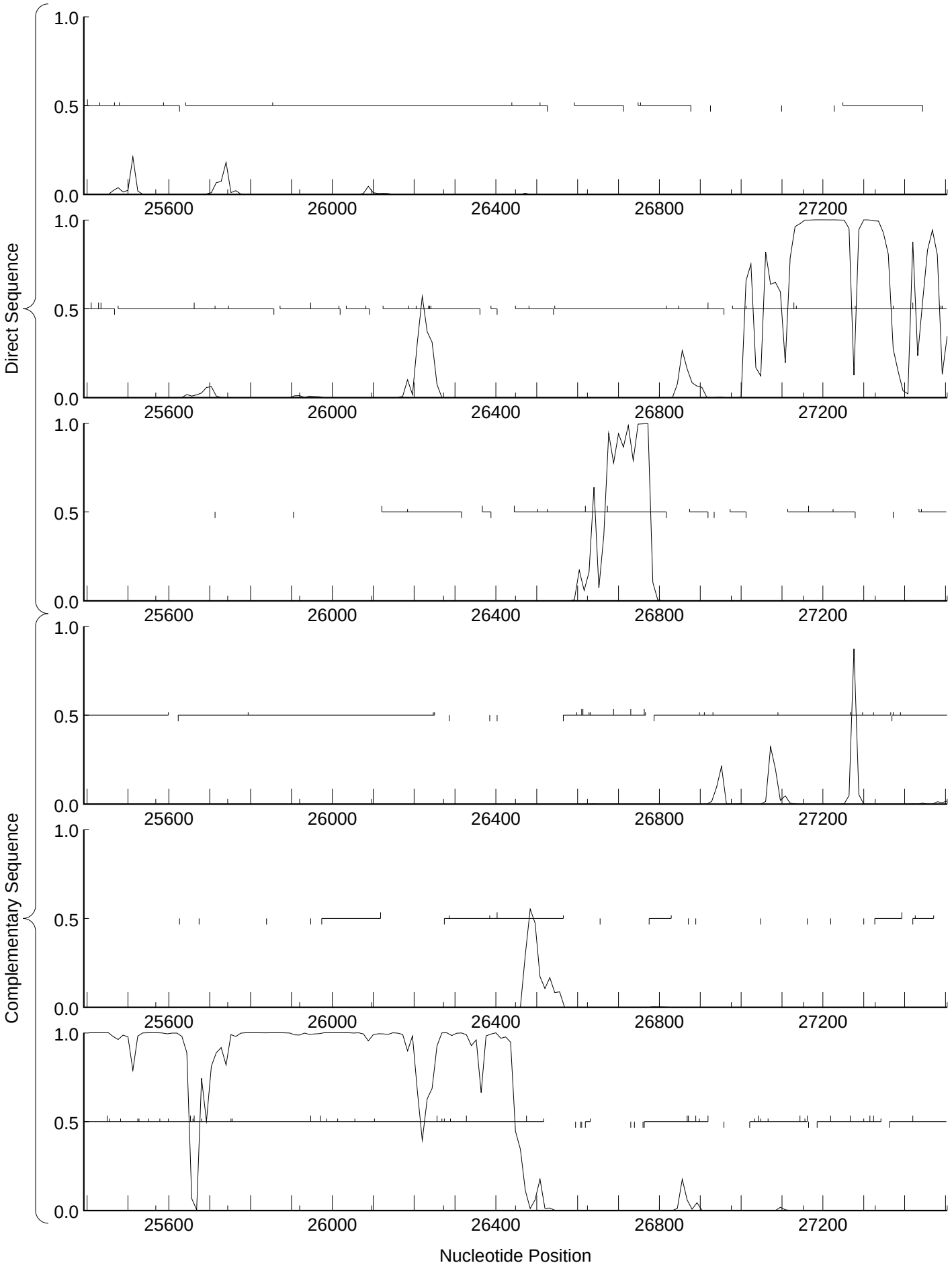
plete sequence, 53746 bp including 14-base 3’ overhang (TAAGCCGCGCGGTA), Cluster Q, Order 4, Window 96, Step 12, 11/27



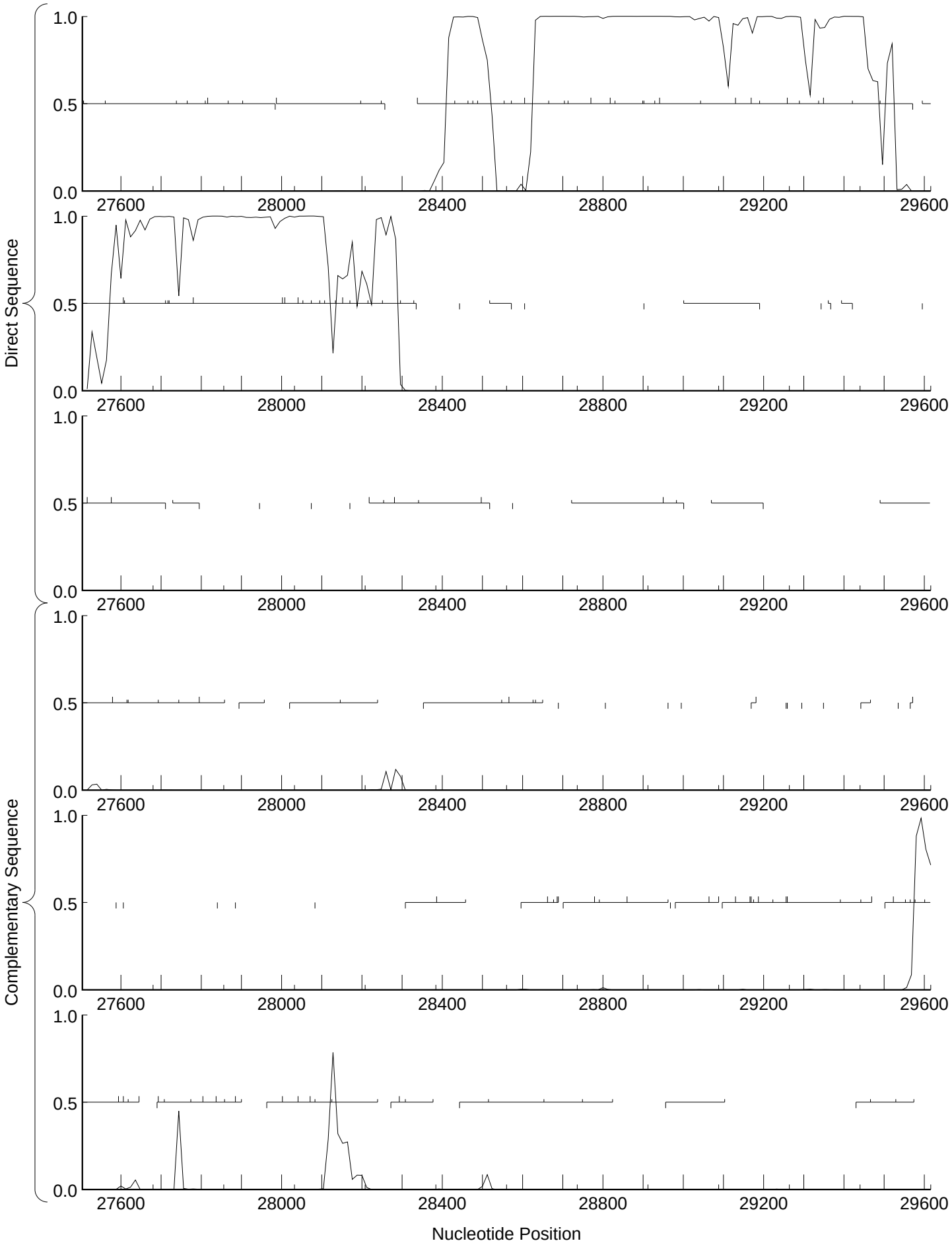

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
21200
21600
22000
22400
22800
23200
Nucleotide Position

plete sequence, 53746 bp including 14-base 3’ overhang (TAAGCCGCGCGGTA), Cluster Q, Order 4, Window 96, Step 12, 13/27

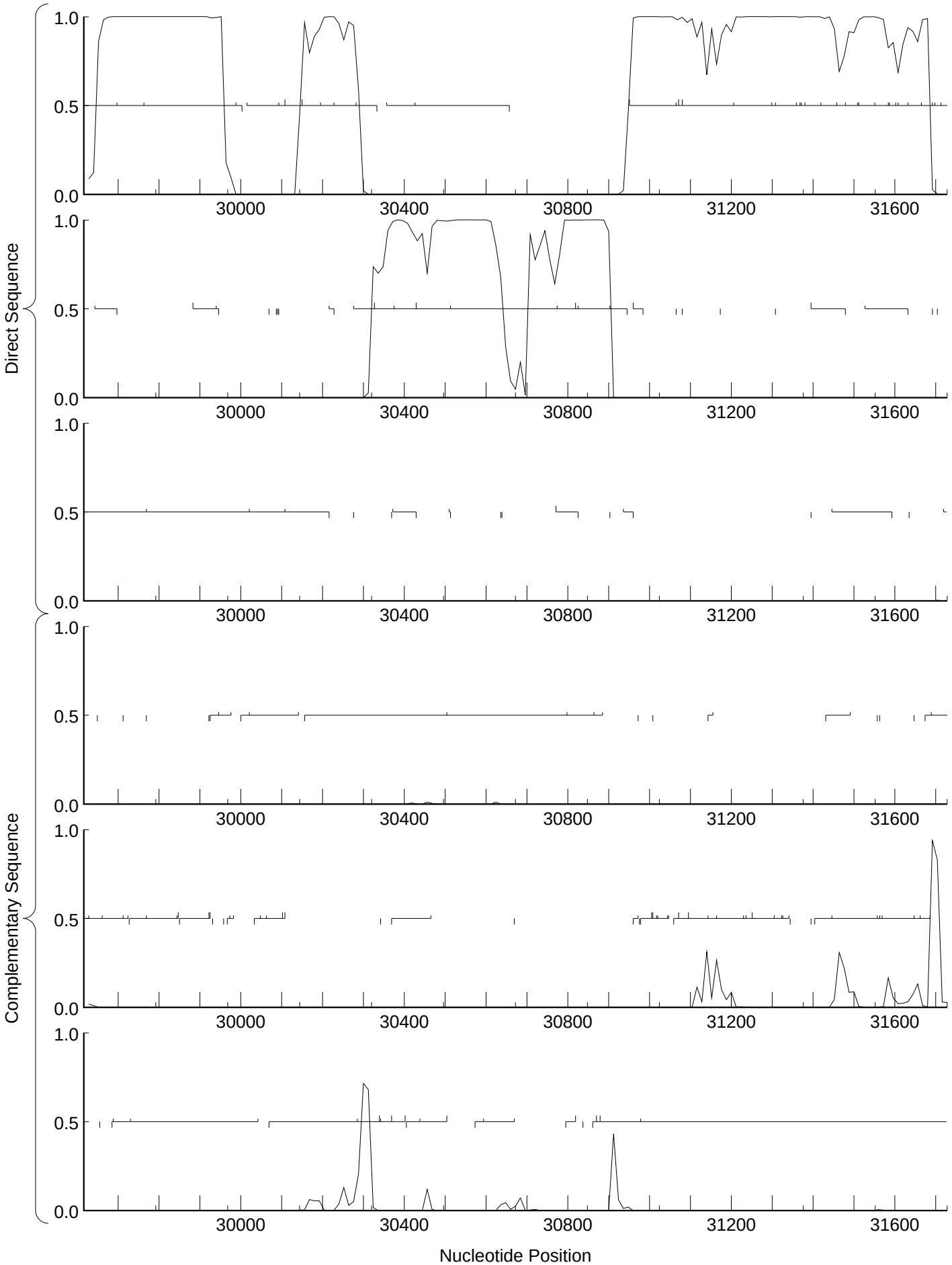


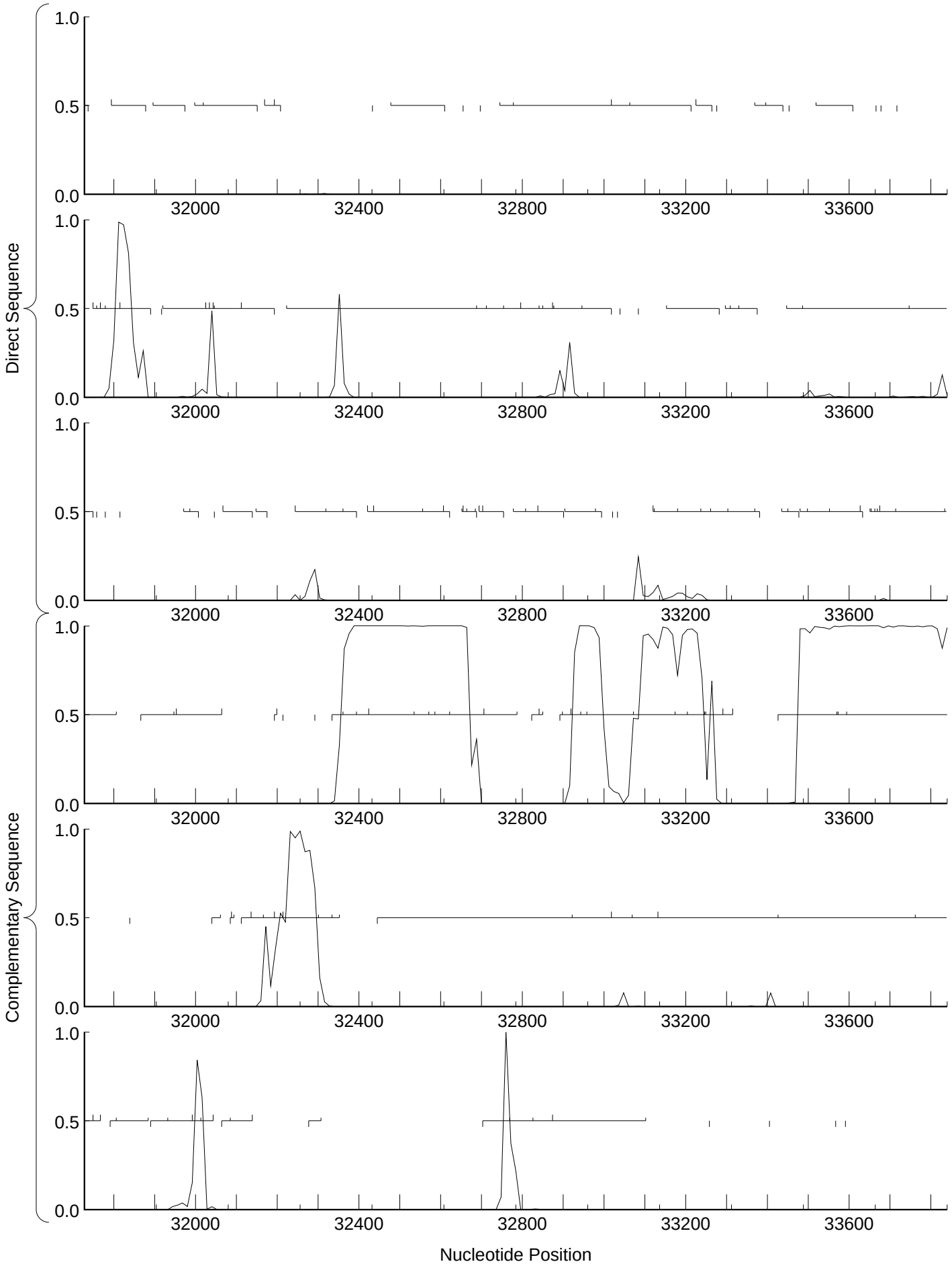

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
25600
26000
26400
26800
27200
Nucleotide Position

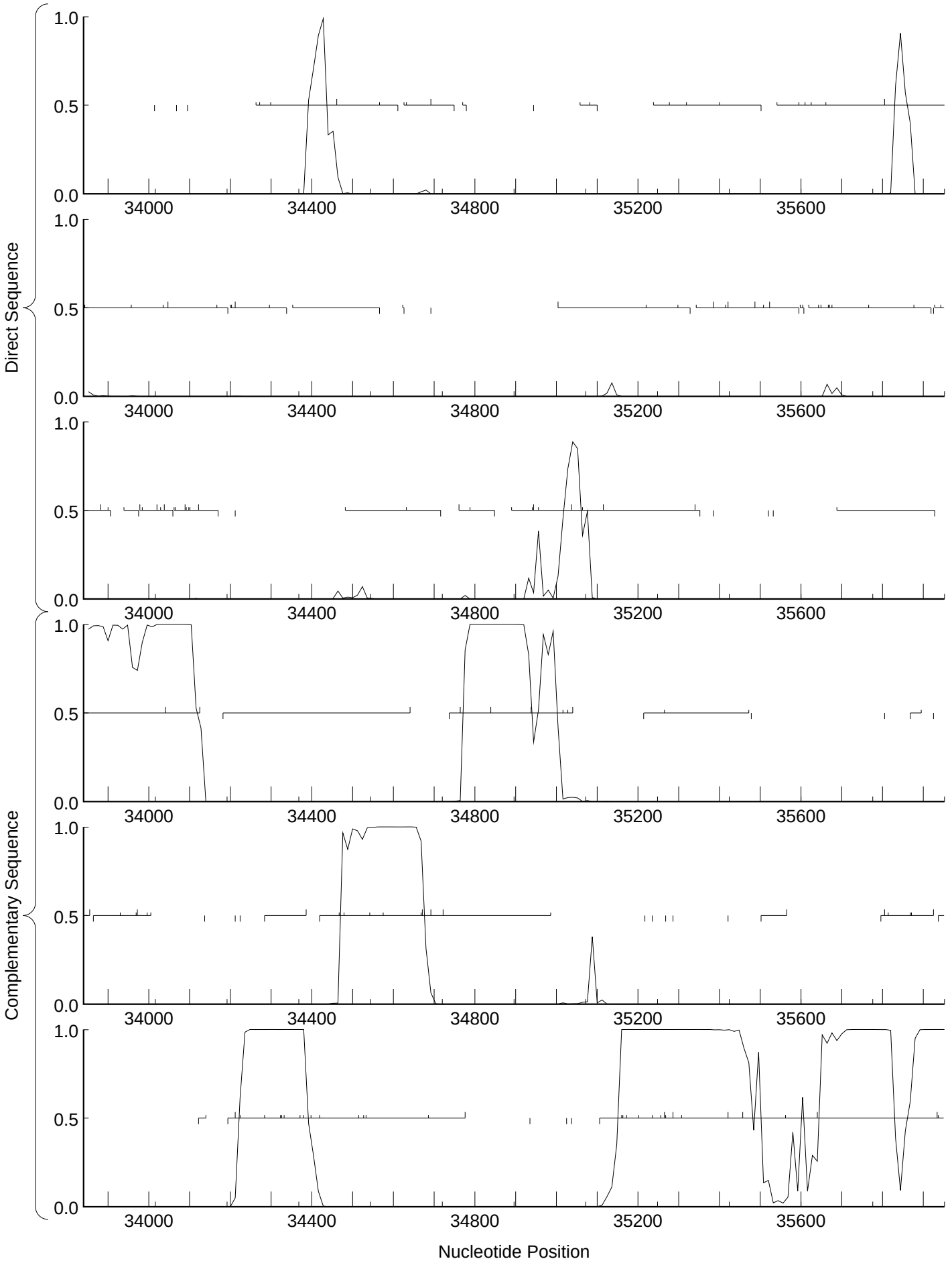
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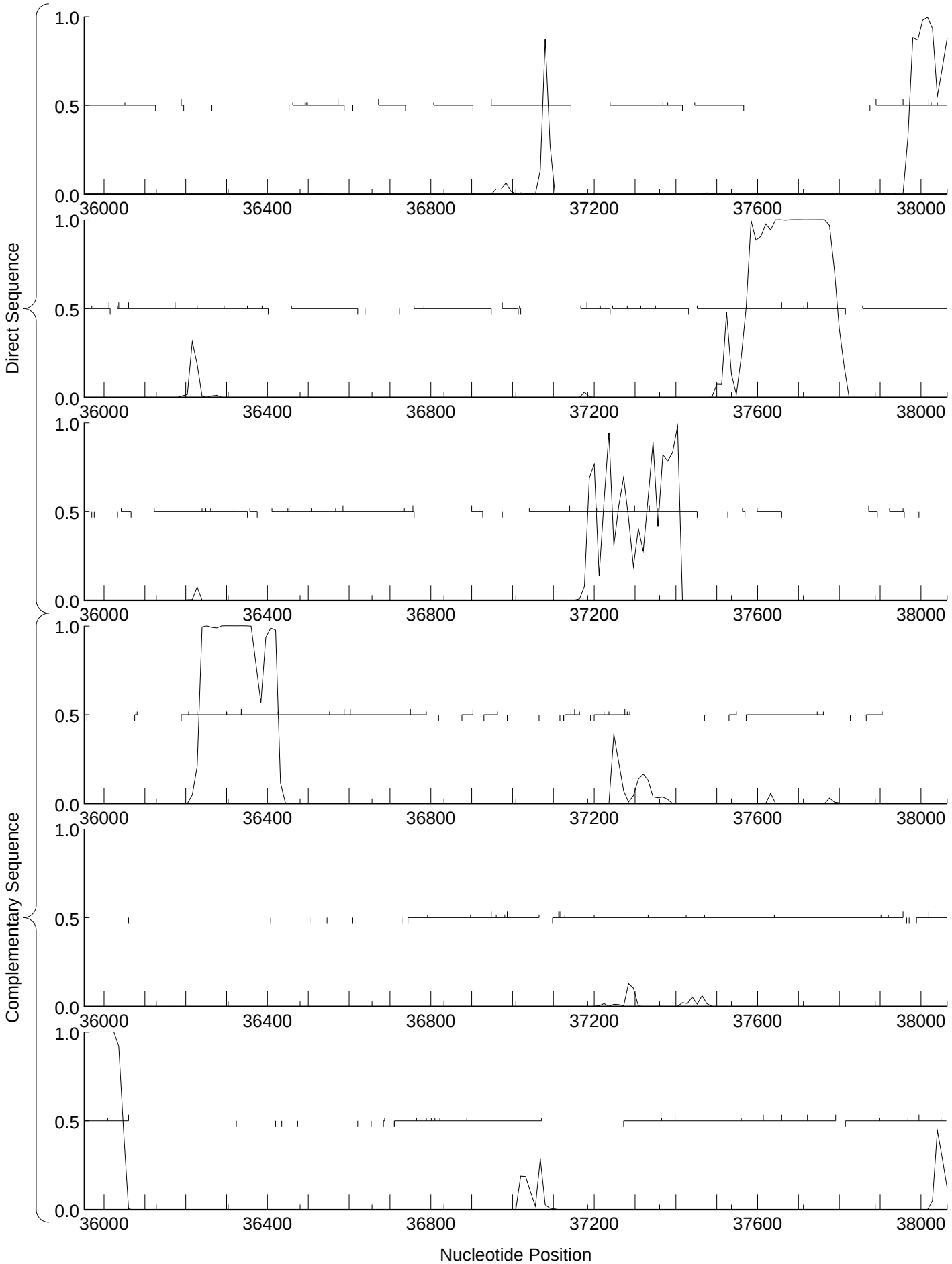


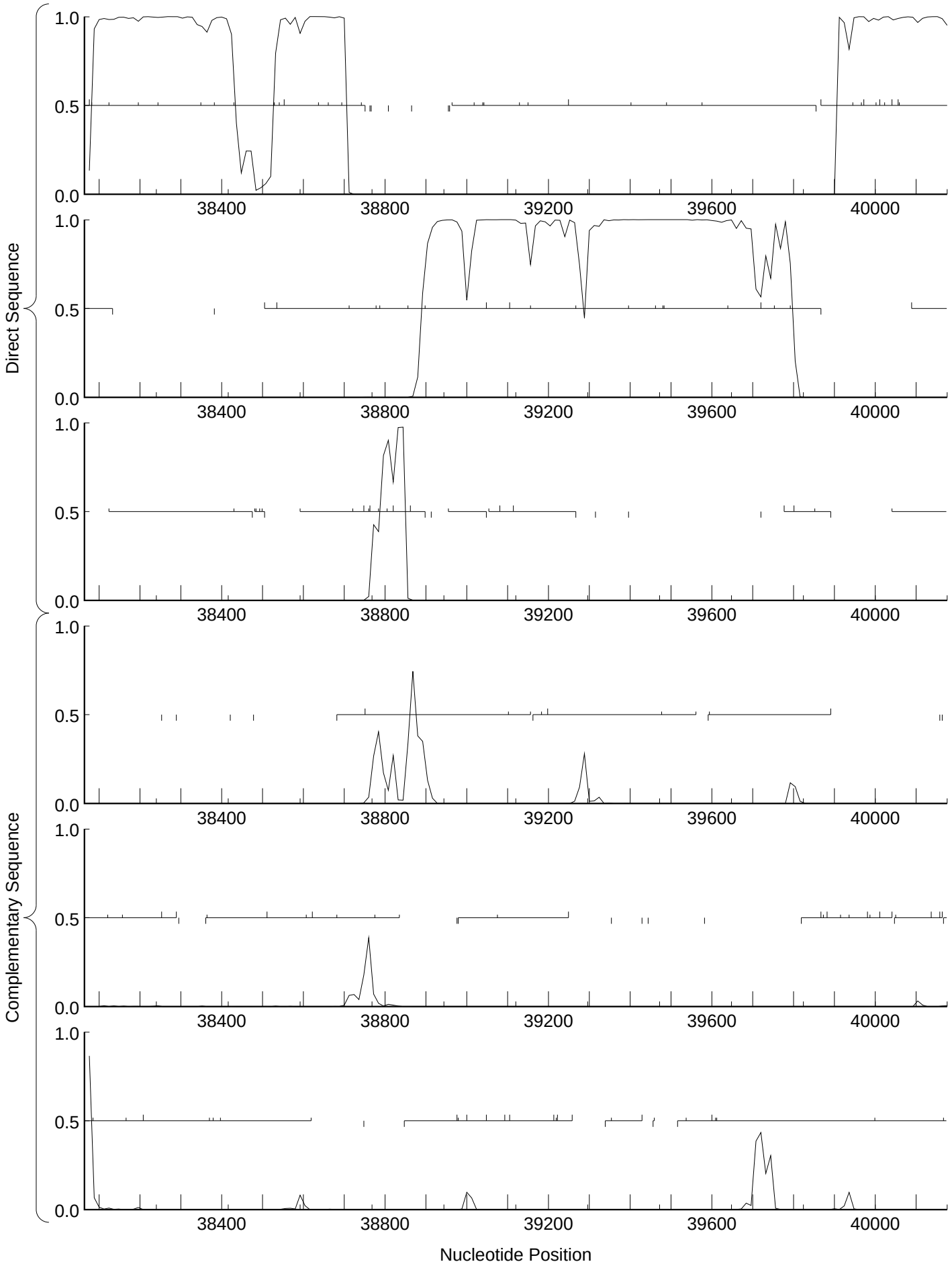
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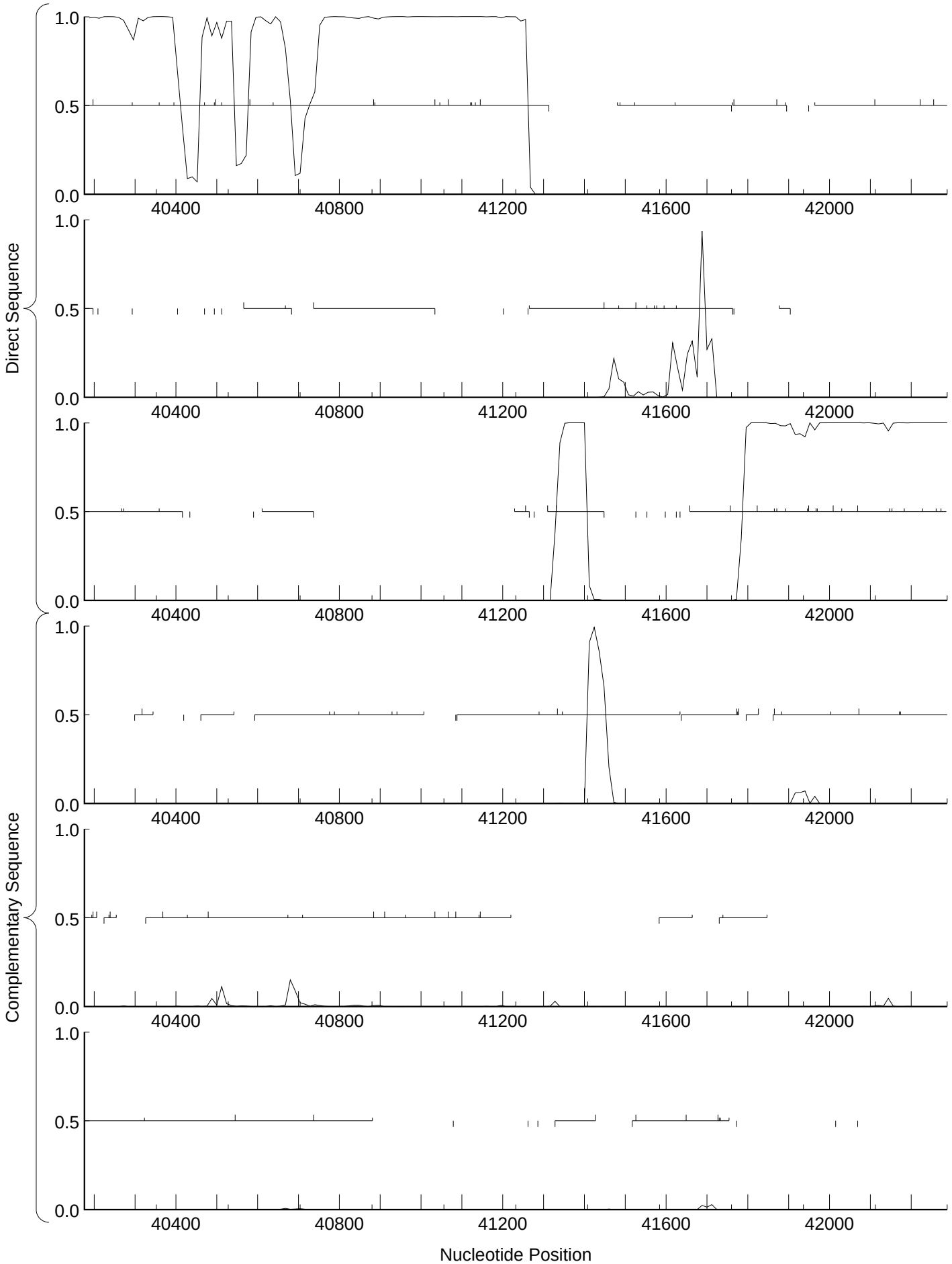

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
32000
32400
32800
33200
33600
Nucleotide Position

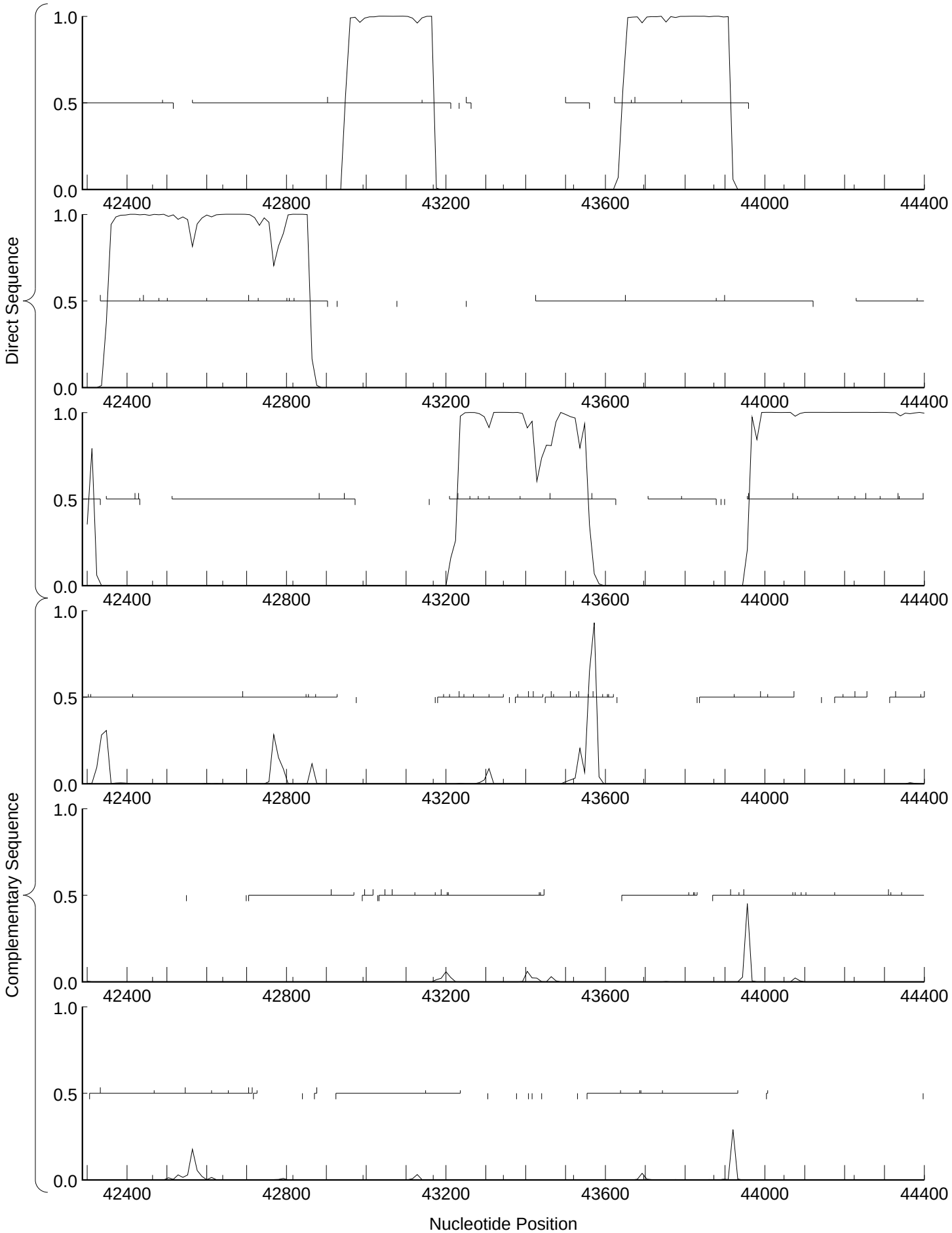

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
34000
34400
34800
35200
35600
Nucleotide Position


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
36000
36400
36800
37200
37600
38000
Nucleotide Position

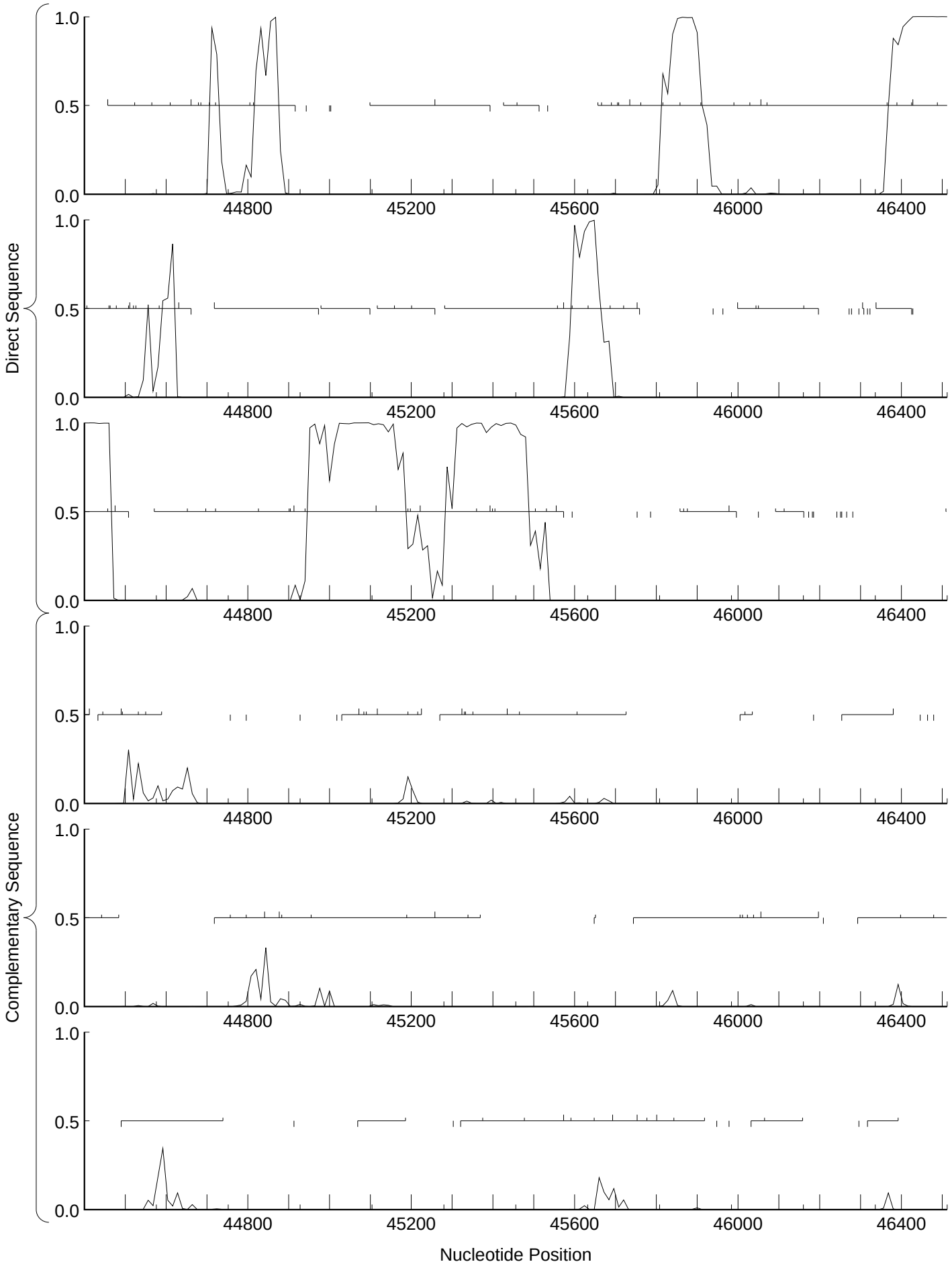

Direct Sequence
Complementary Sequence
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0.5
0.0
38400
38800
39200
39600
40000
Nucleotide Position

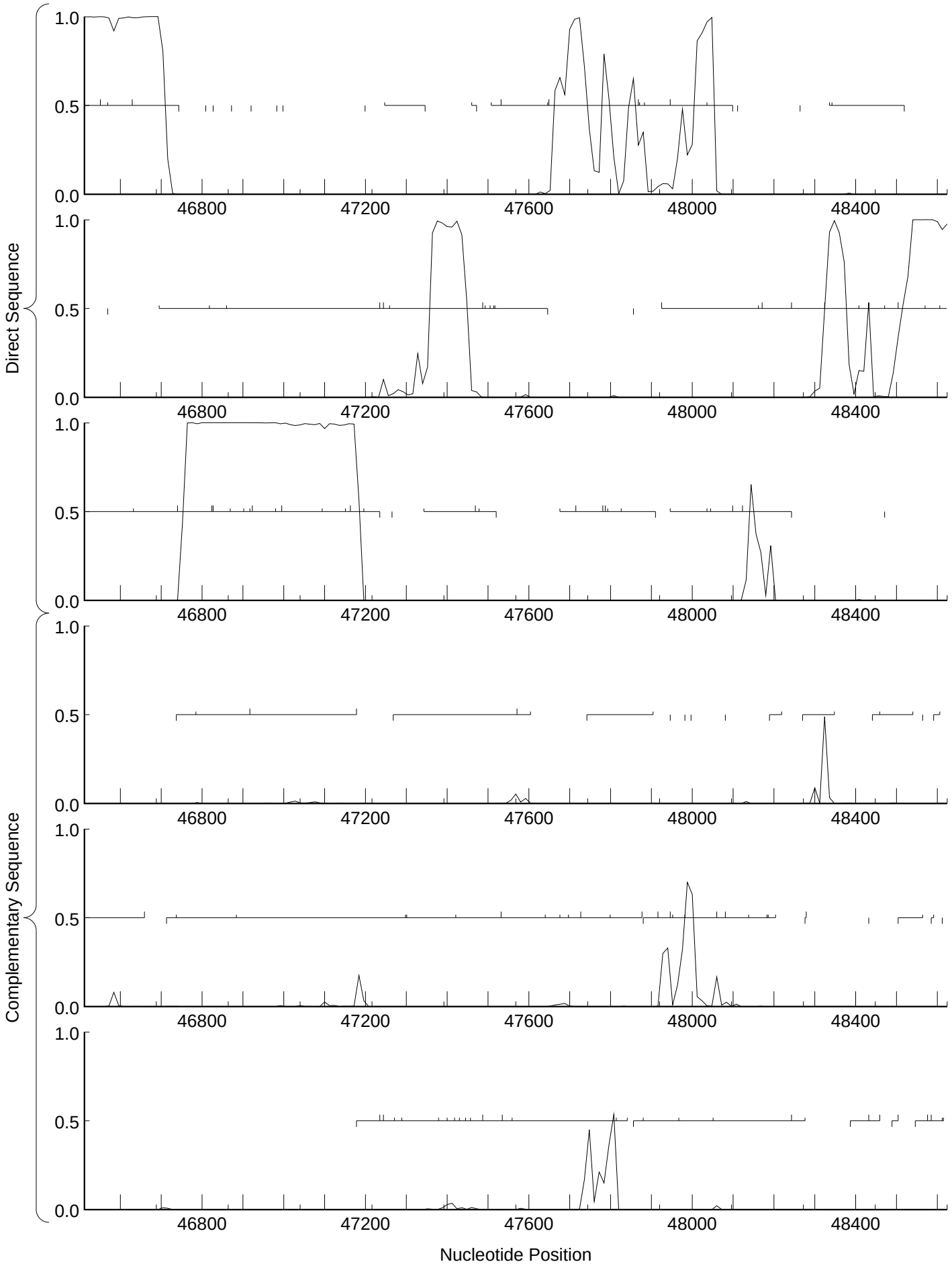
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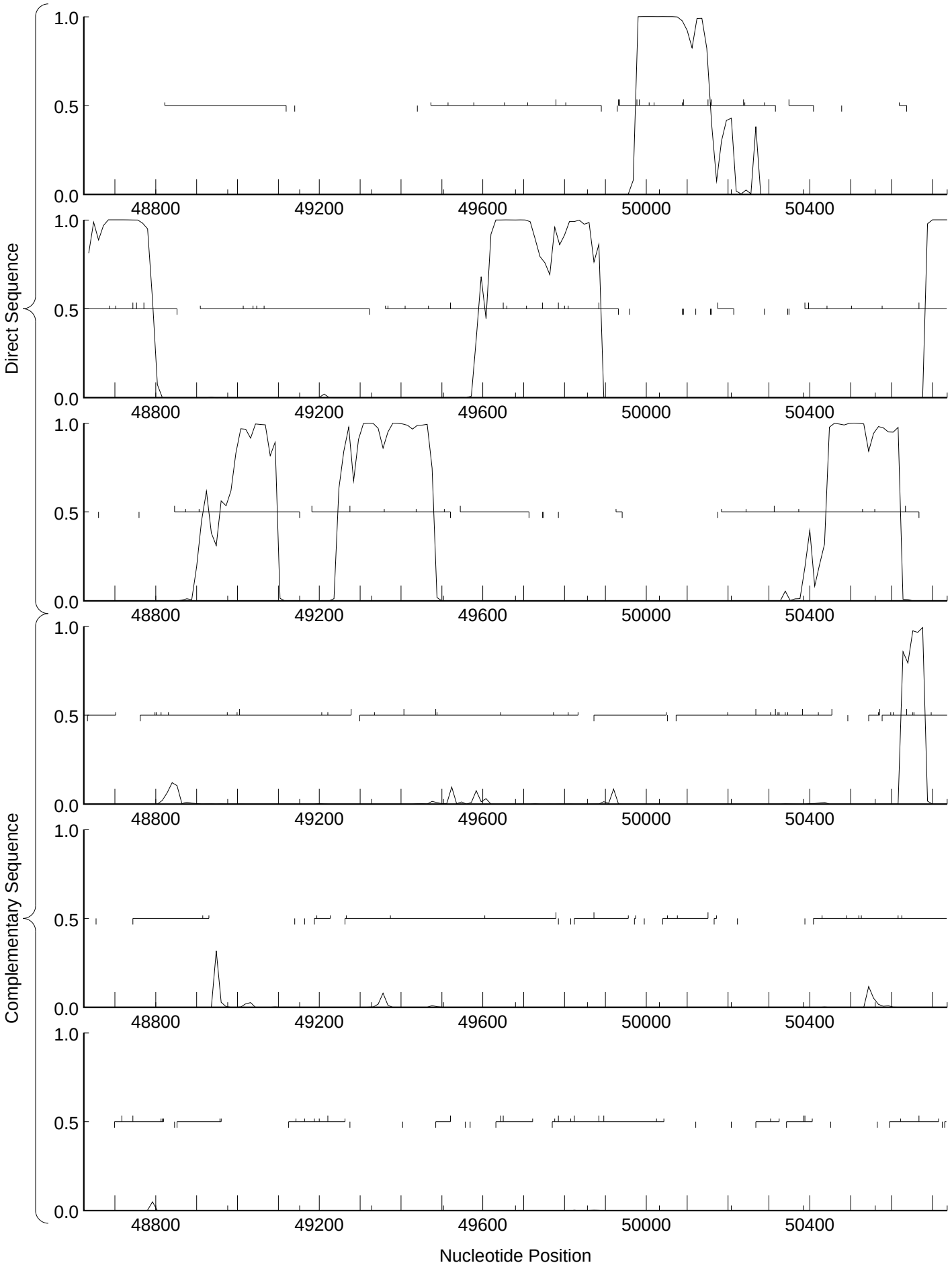



Direct Sequence
Complementary Sequence
1.0
0.5
0.0
42400
42800
43200
43600
44000
44400
Nucleotide Position

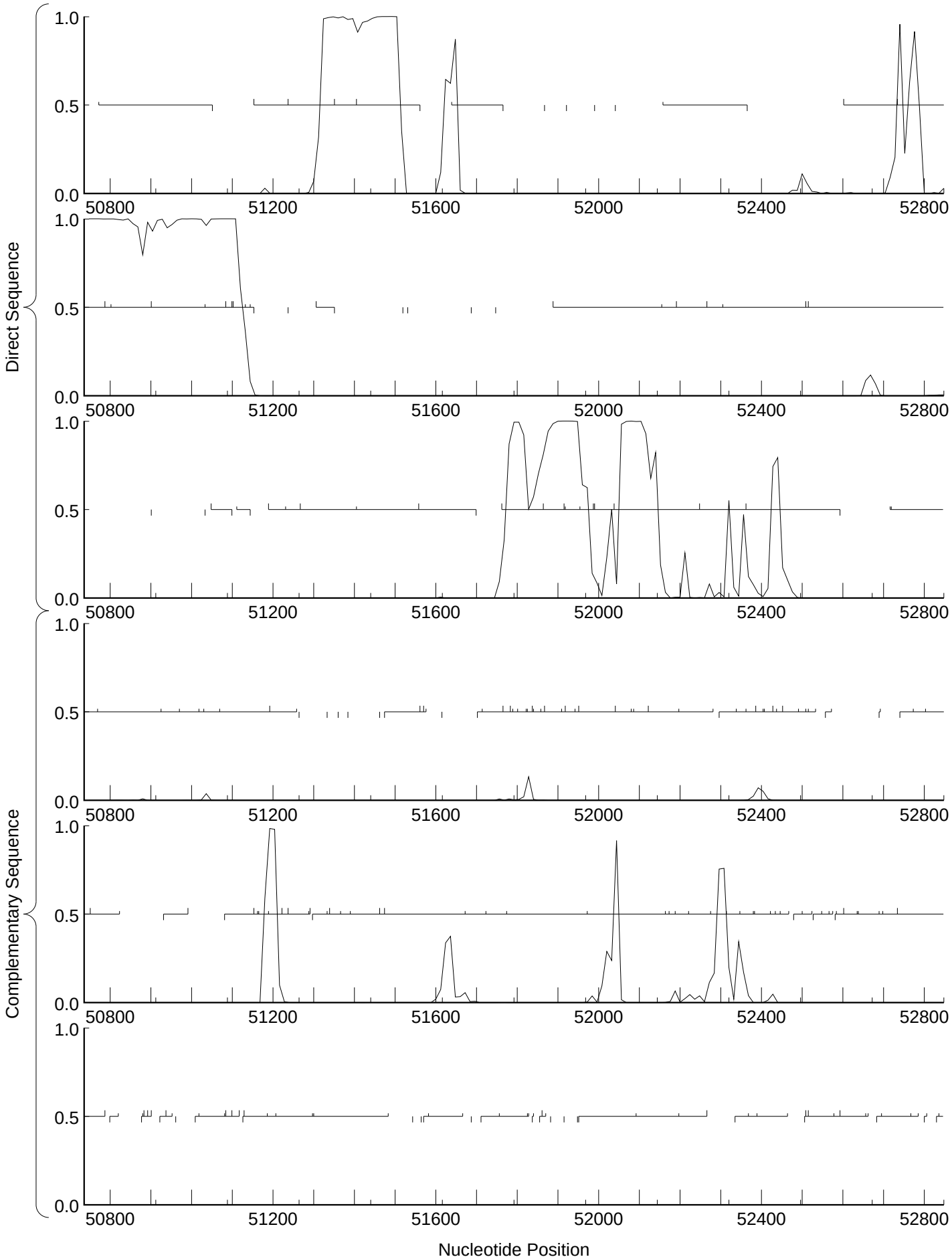
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Direct Sequence
Complementary Sequence
1.0
0.5
0.0
46800
47200
47600
48000
48400
Nucleotide Position


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
48800
49200
49600
50000
50400
Nucleotide Position

plete sequence, 53746 bp including 14-base 3’ overhang (TAAGCCGCGCGGTA), Cluster Q, Order 4, Window 96, Step 12, 26/27



plete sequence, 53746 bp including 14-base 3’ overhang (TAAGCCGCGCGGTA), Cluster Q, Order 4, Window 96, Step 12, 27/27

