GeneMark

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

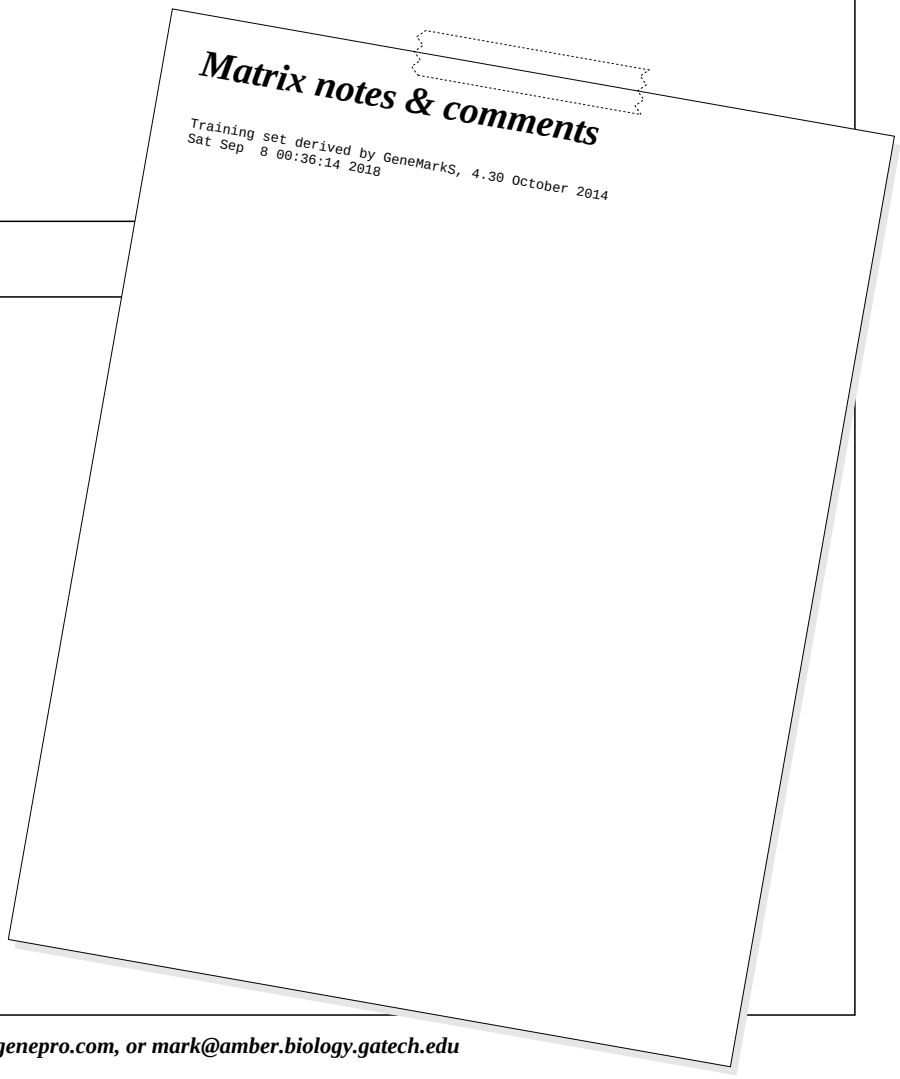
PROGRAM INFORMATION

```
Sequence         :  Gordonia phage Luker complete sequence, 73453 bp including 161 bp terminal repeat, Cluster
Analysis Date    :  3/29/24 at 10:58:13
Pages            :  36
Sequence Length  :  73453 bp
GC Content       :   58.99%

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

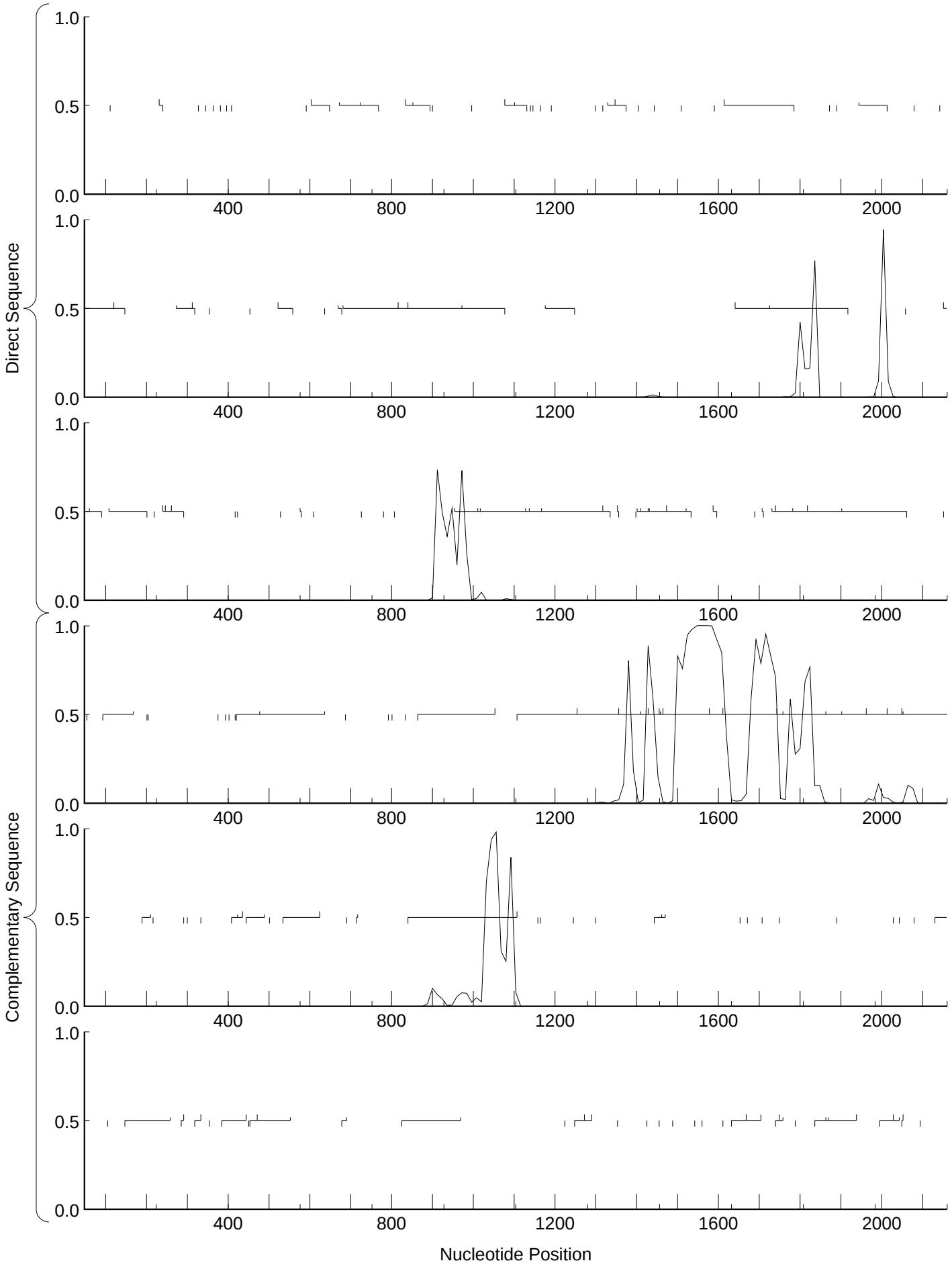
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Matrix     :  -
Author     :  -

Order      :  4
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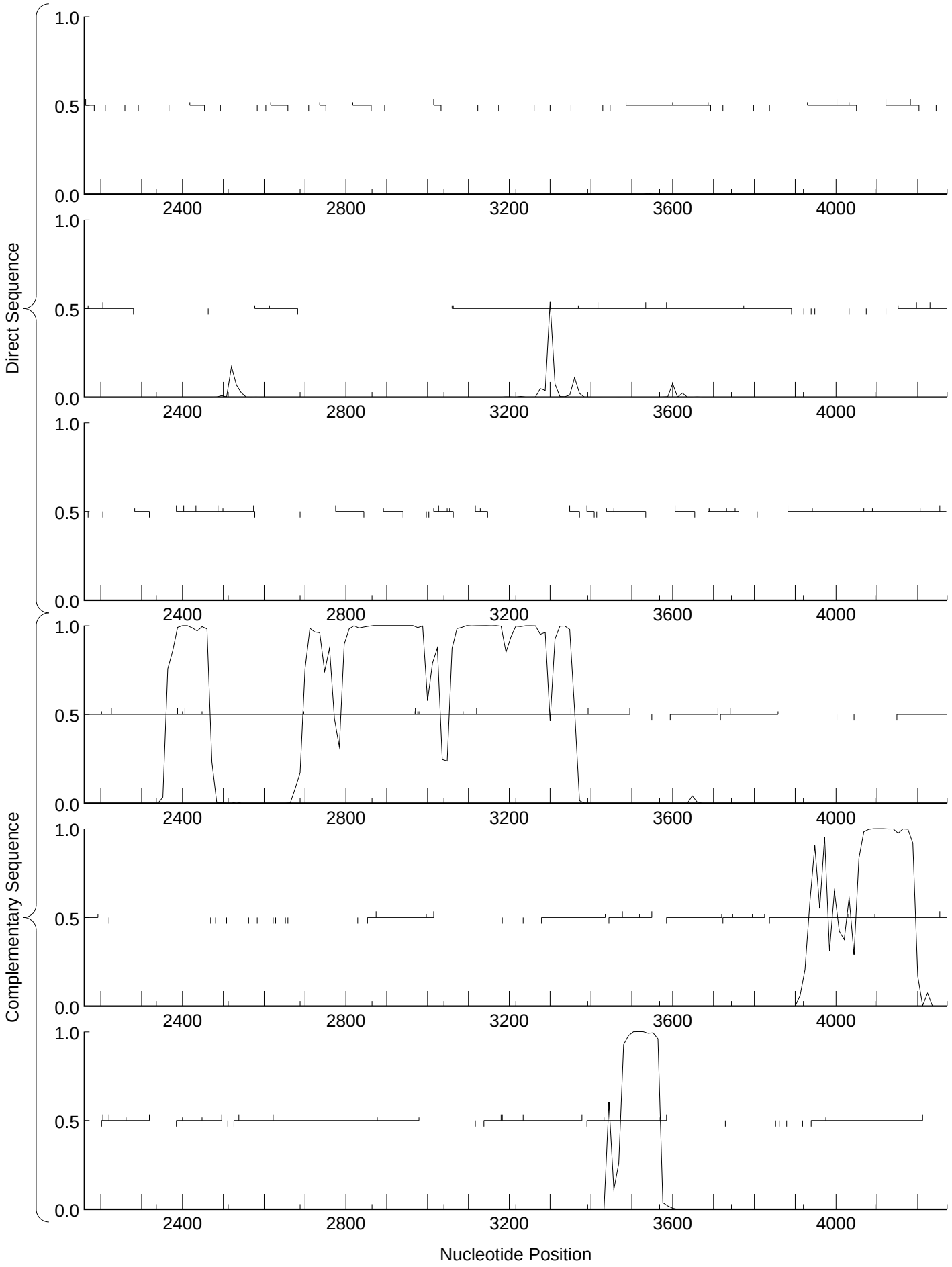

```
  Send questions / comments to:
      Dr. M. Borodovsky
      Georgia Institute of Technology
      School of Biology
      Atlanta, GA  30332-0230
```


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

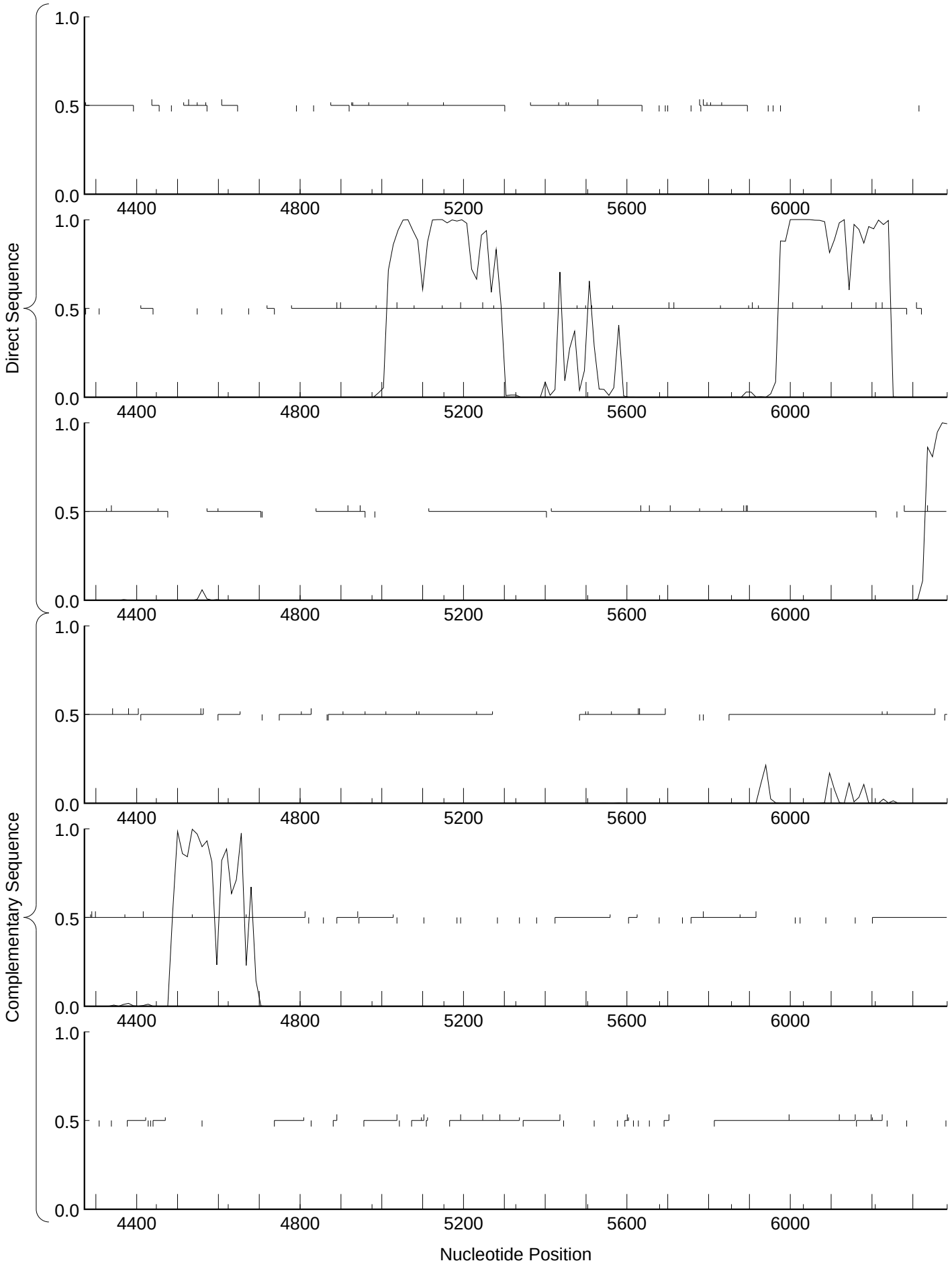
nia phage Luker complete sequence, 73453 bp including 161 bp terminal repeat, Cluster CS3, Order 4, Window 96, Step 12, 2/36



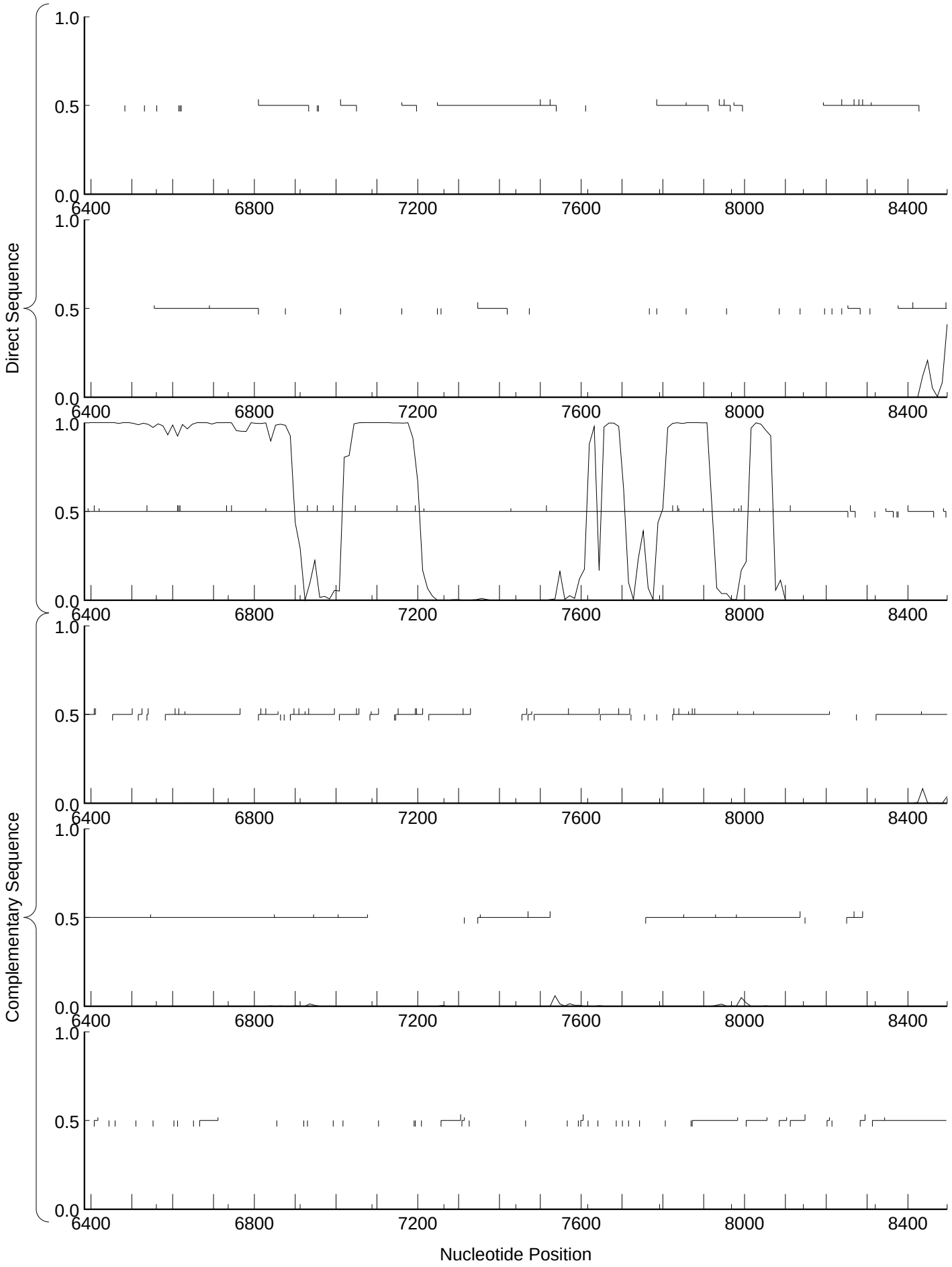
nia phage Luker complete sequence, 73453 bp including 161 bp terminal repeat, Cluster CS3, Order 4, Window 96, Step 12, 3/36



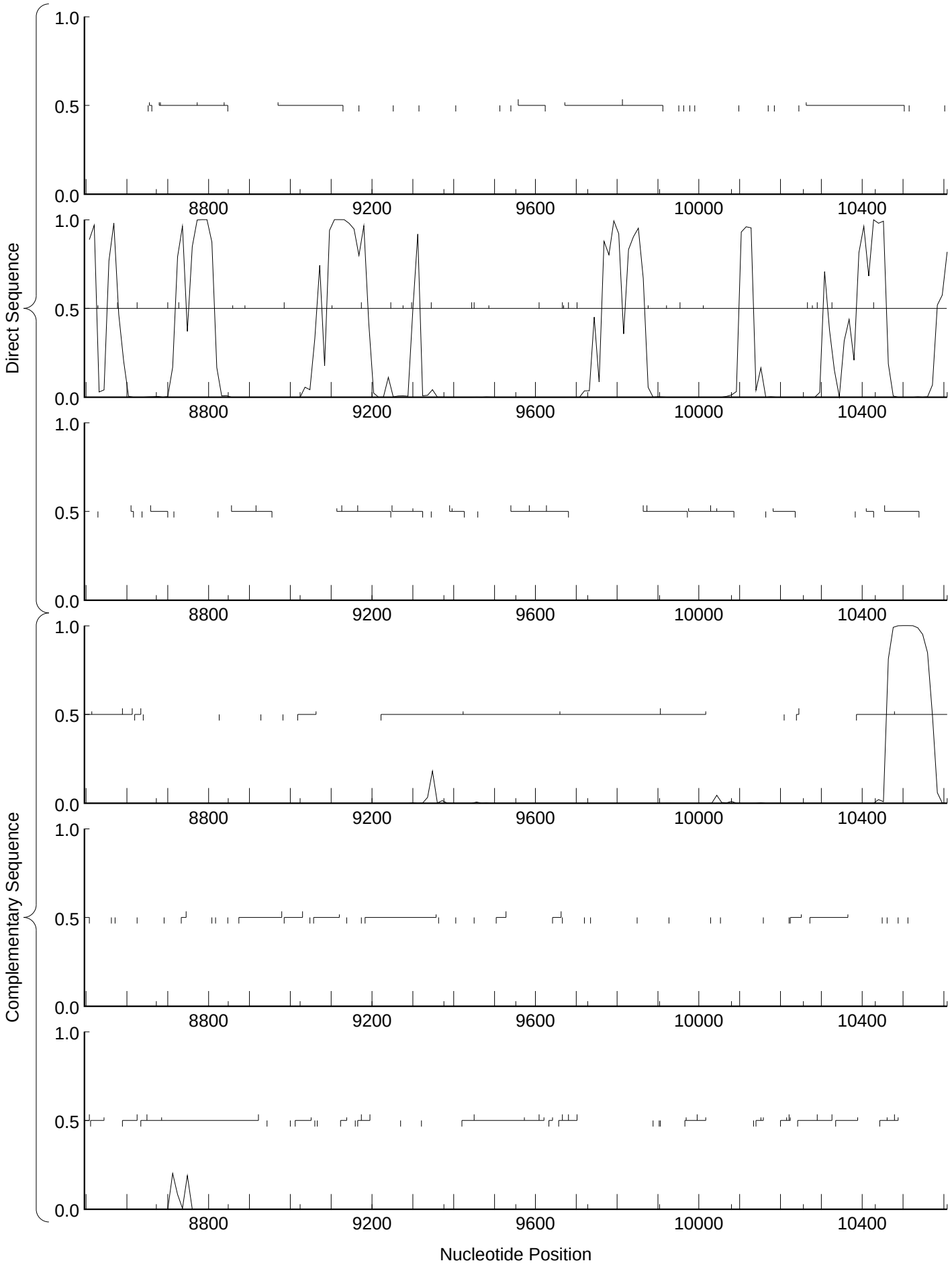
nia phage Luker complete sequence, 73453 bp including 161 bp terminal repeat, Cluster CS3, Order 4, Window 96, Step 12, 4/36



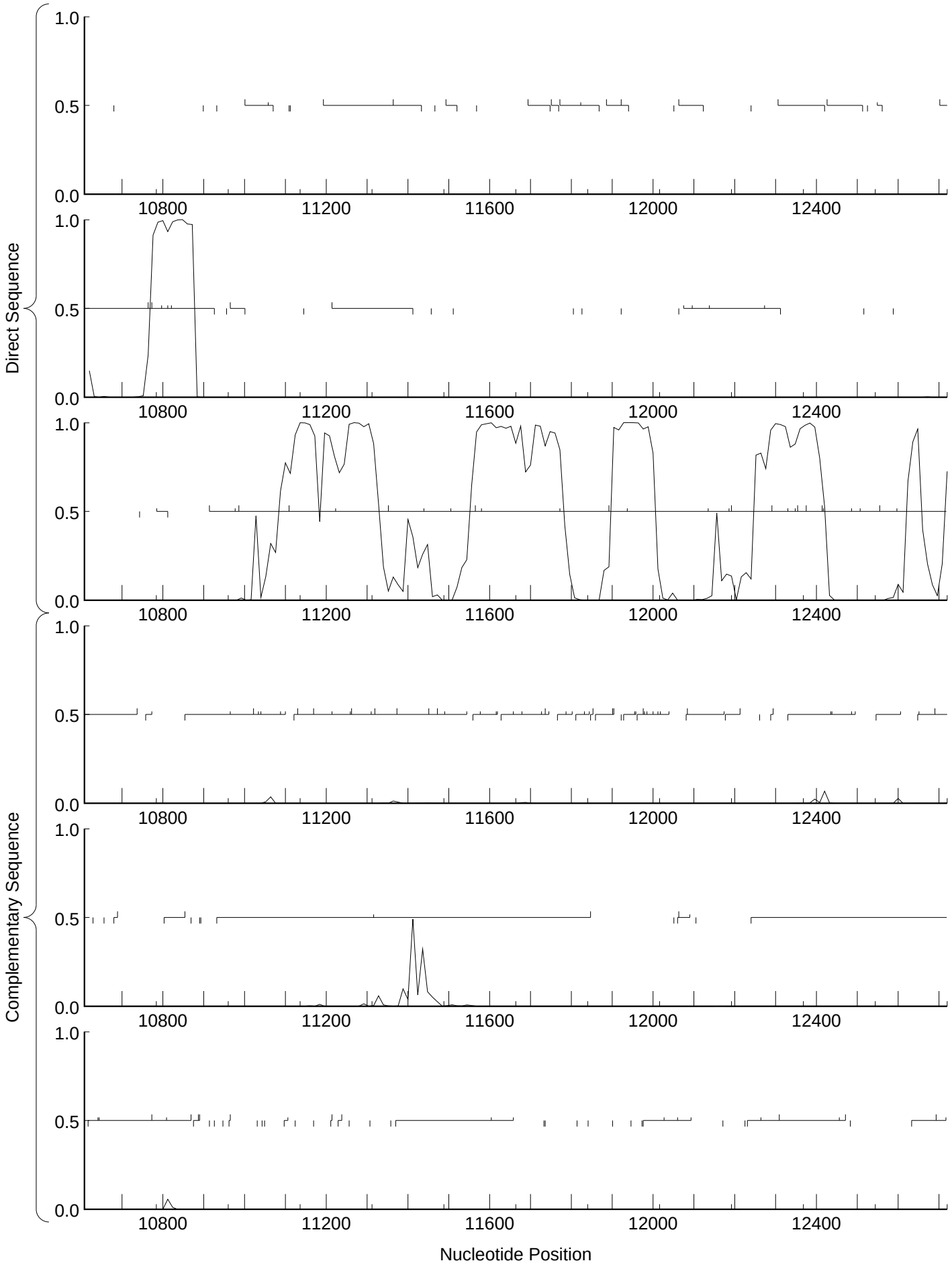
nia phage Luker complete sequence, 73453 bp including 161 bp terminal repeat, Cluster CS3, Order 4, Window 96, Step 12, 5/36



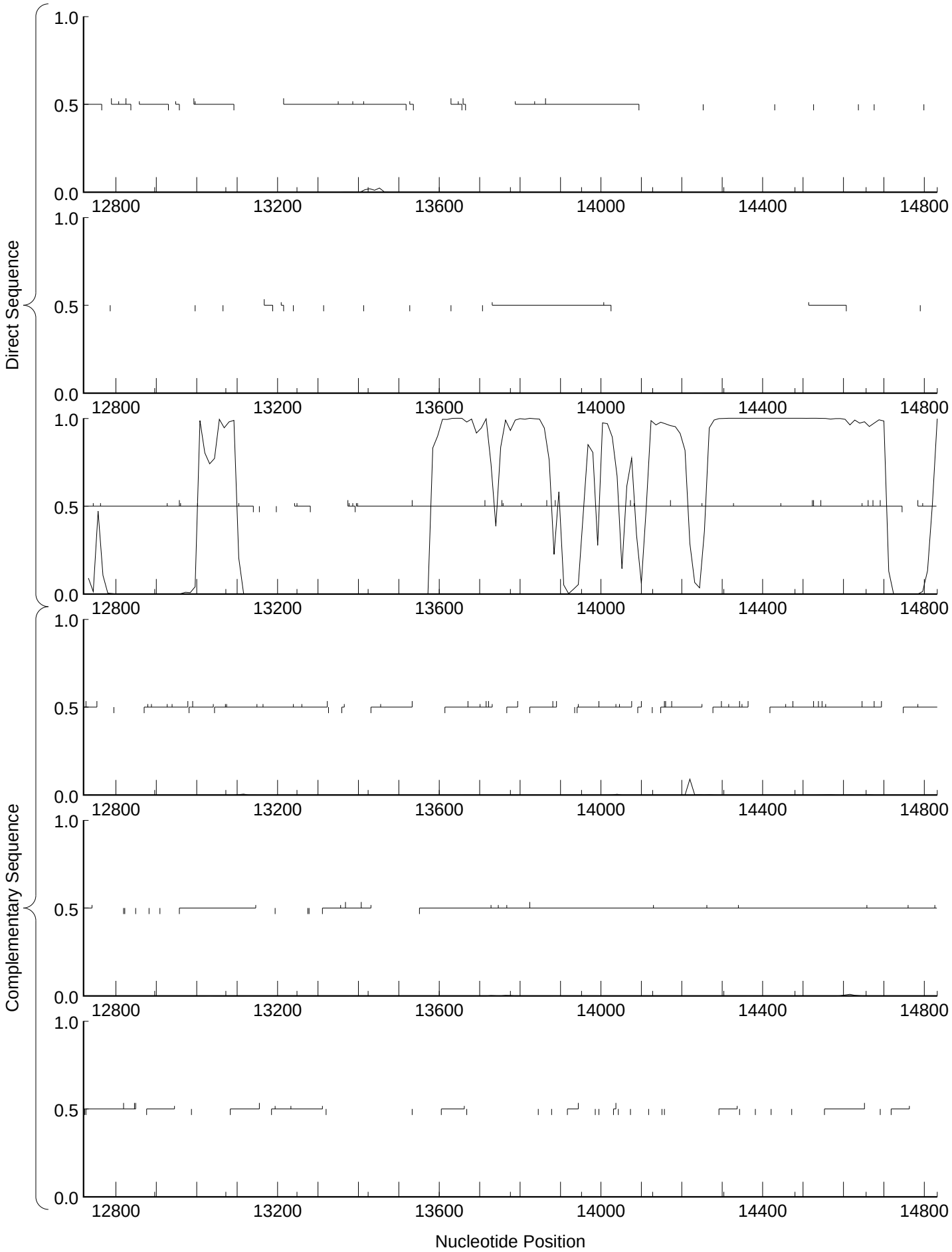
nia phage Luker complete sequence, 73453 bp including 161 bp terminal repeat, Cluster CS3, Order 4, Window 96, Step 12, 6/36



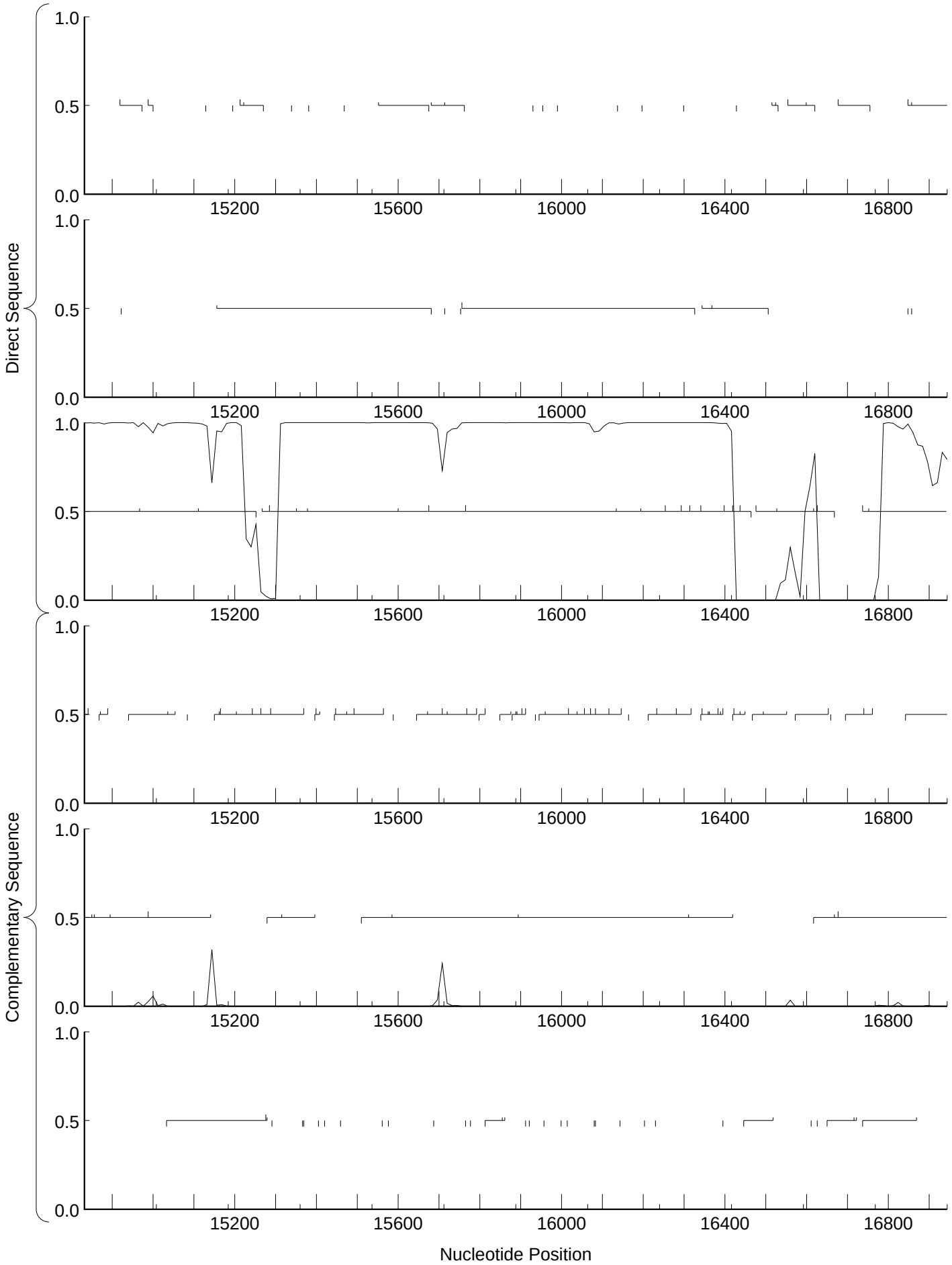
nia phage Luker complete sequence, 73453 bp including 161 bp terminal repeat, Cluster CS3, Order 4, Window 96, Step 12, 7/36

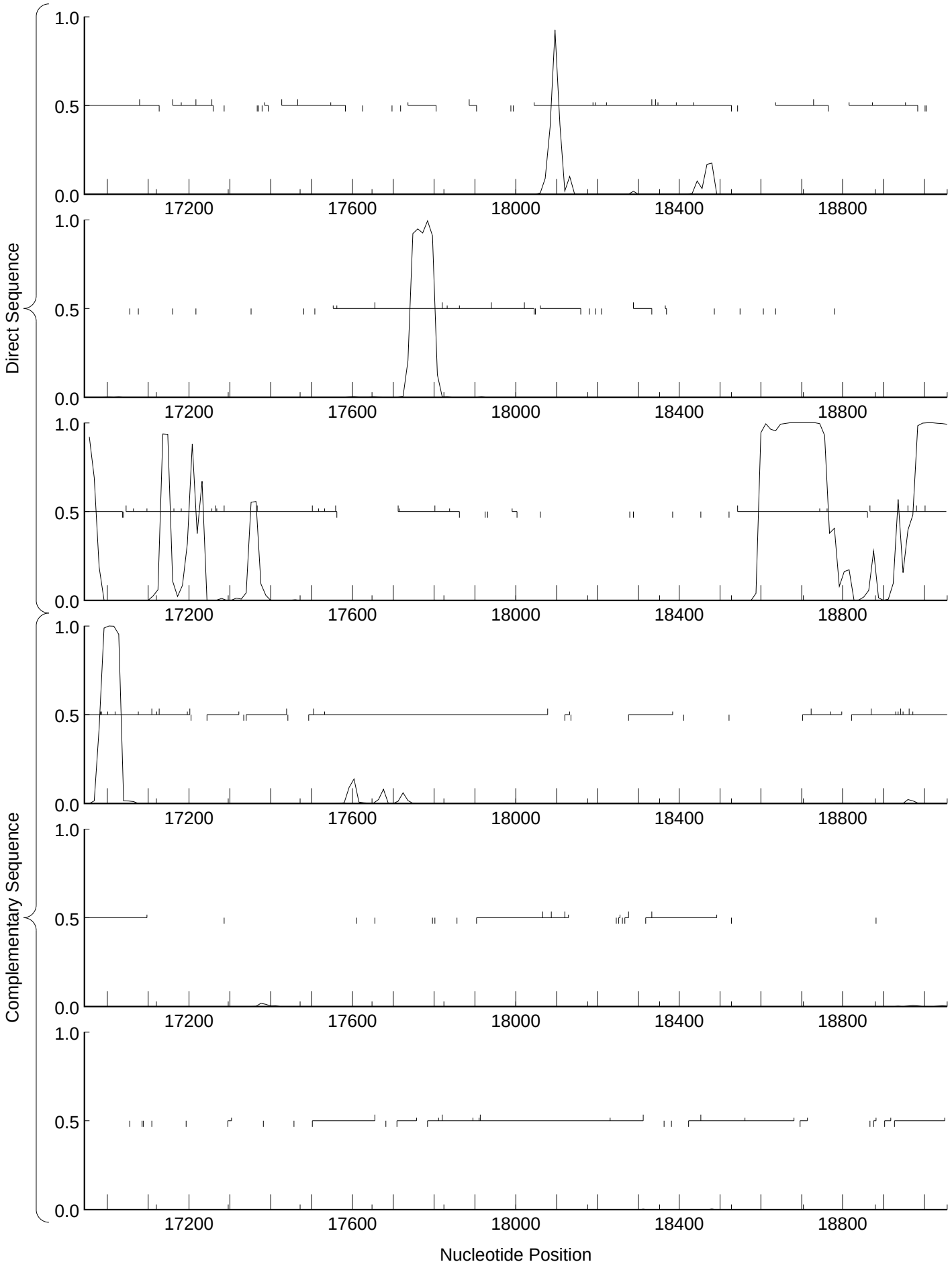


nia phage Luker complete sequence, 73453 bp including 161 bp terminal repeat, Cluster CS3, Order 4, Window 96, Step 12, 8/36

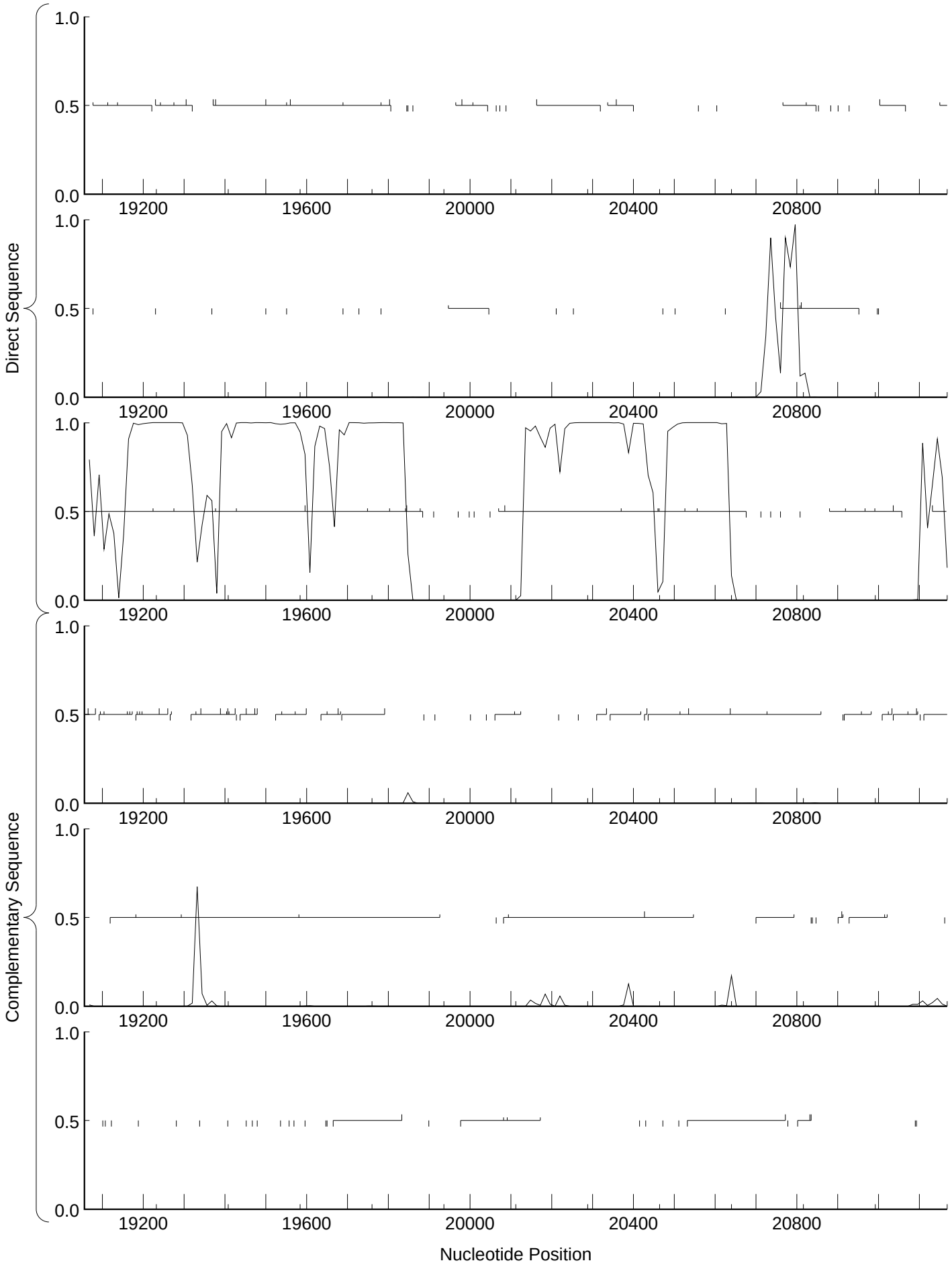


nia phage Luker complete sequence, 73453 bp including 161 bp terminal repeat, Cluster CS3, Order 4, Window 96, Step 12, 9/36

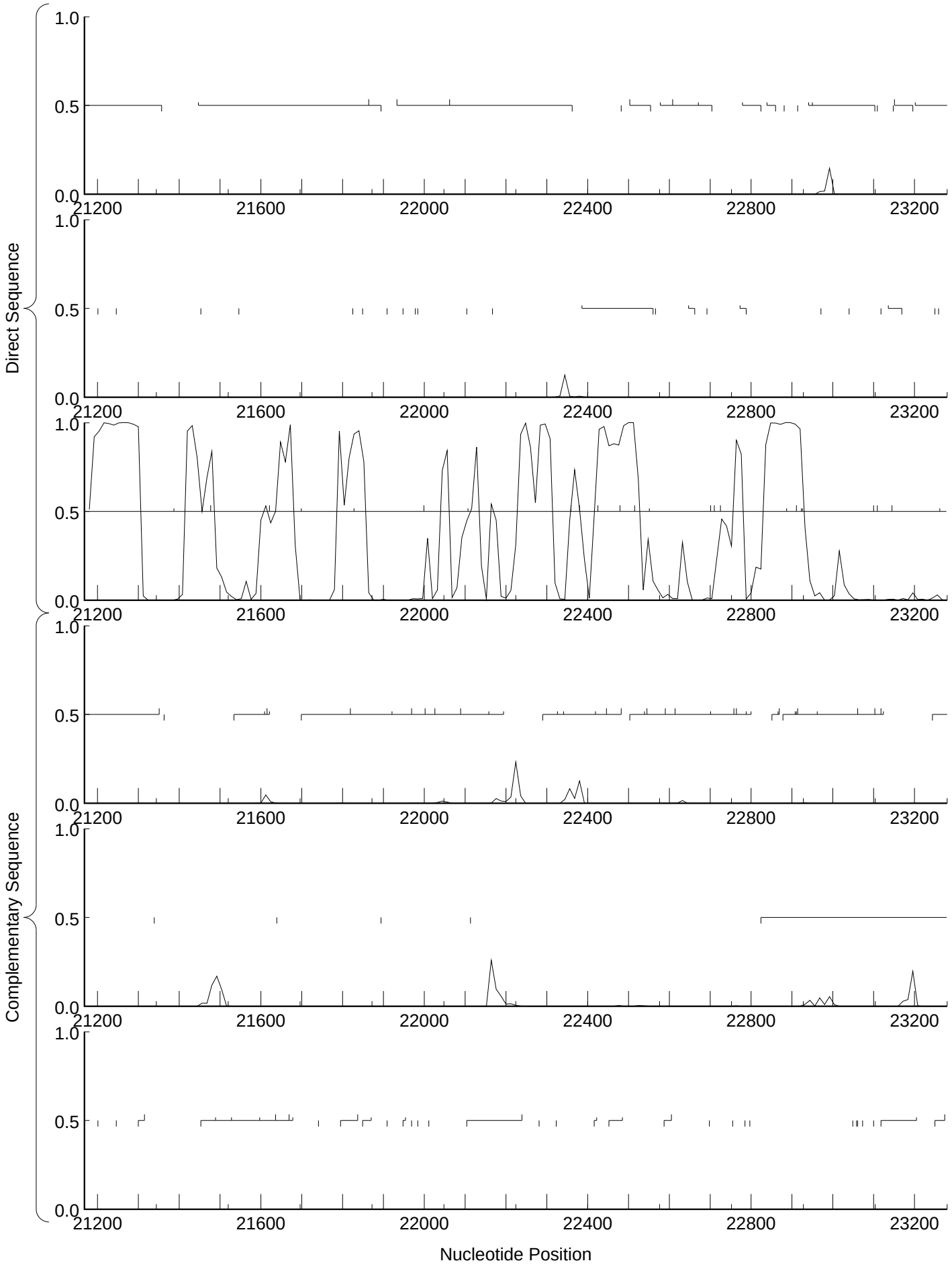



Direct Sequence
Complementary Sequence
1.0
0.5
0.0
17200
17600
18000
18400
18800
Nucleotide Position

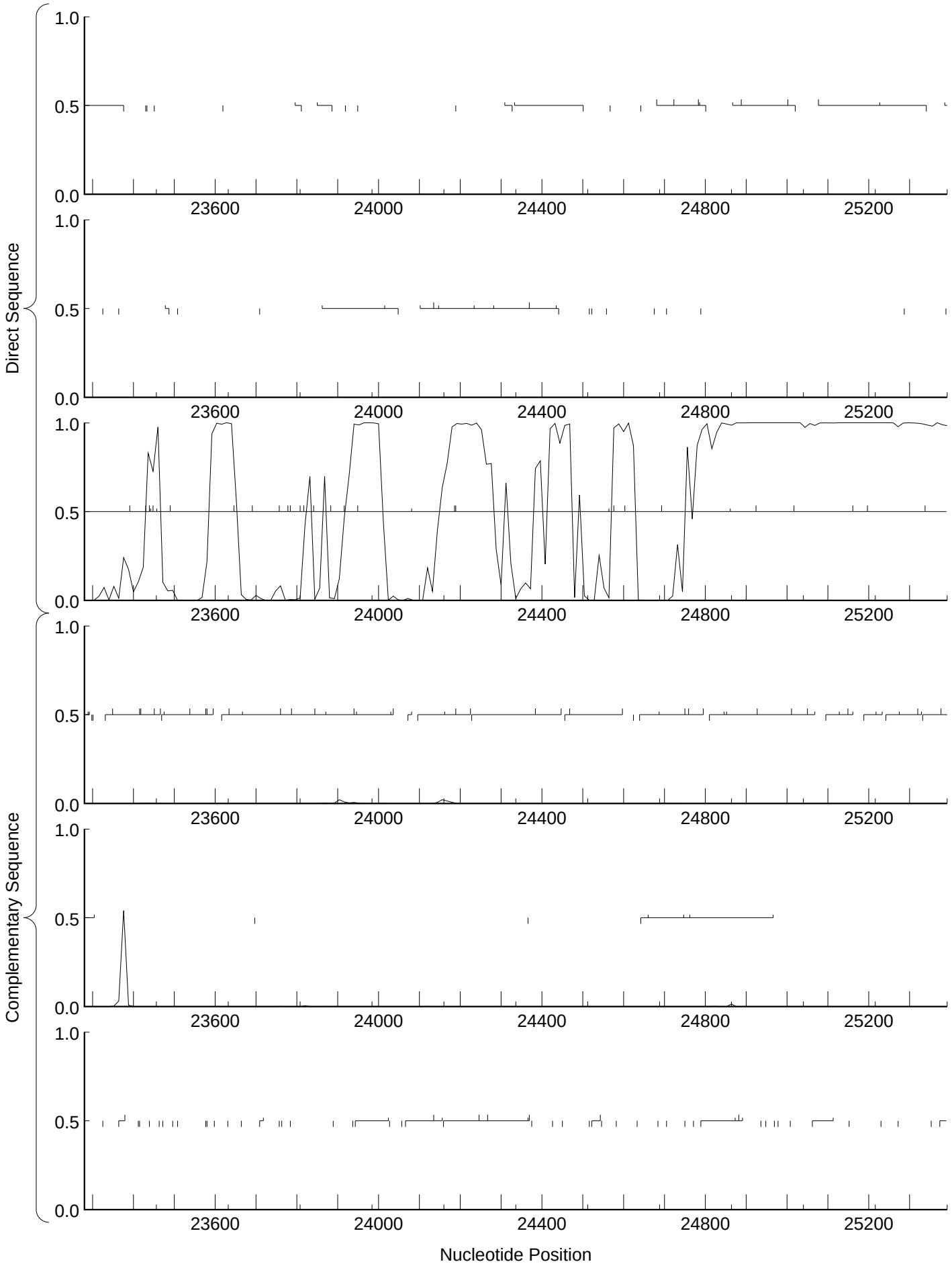
ia phage Luker complete sequence, 73453 bp including 161 bp terminal repeat, Cluster CS3, Order 4, Window 96, Step 12, 11/36



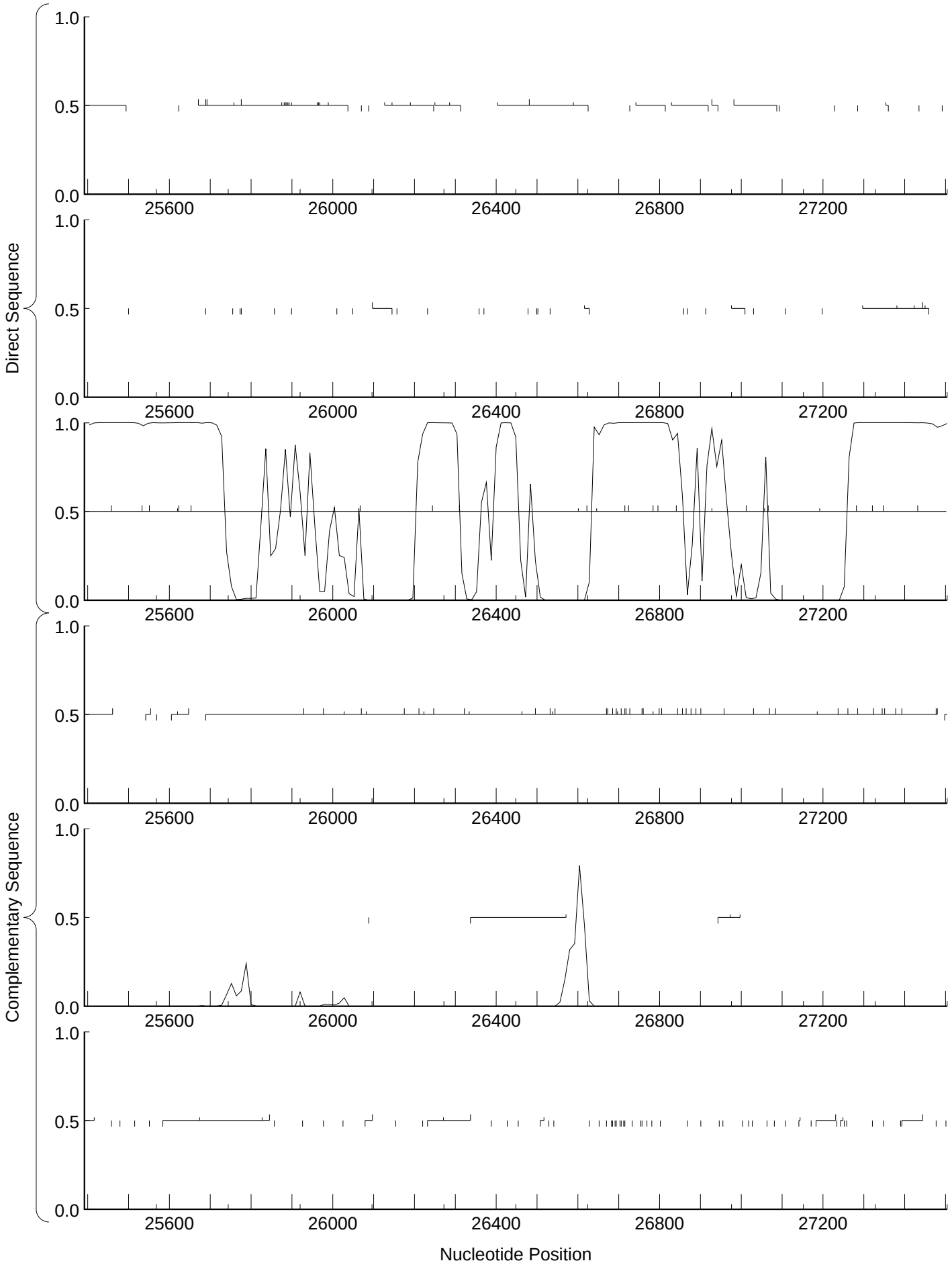
ia phage Luker complete sequence, 73453 bp including 161 bp terminal repeat, Cluster CS3, Order 4, Window 96, Step 12, 12/36



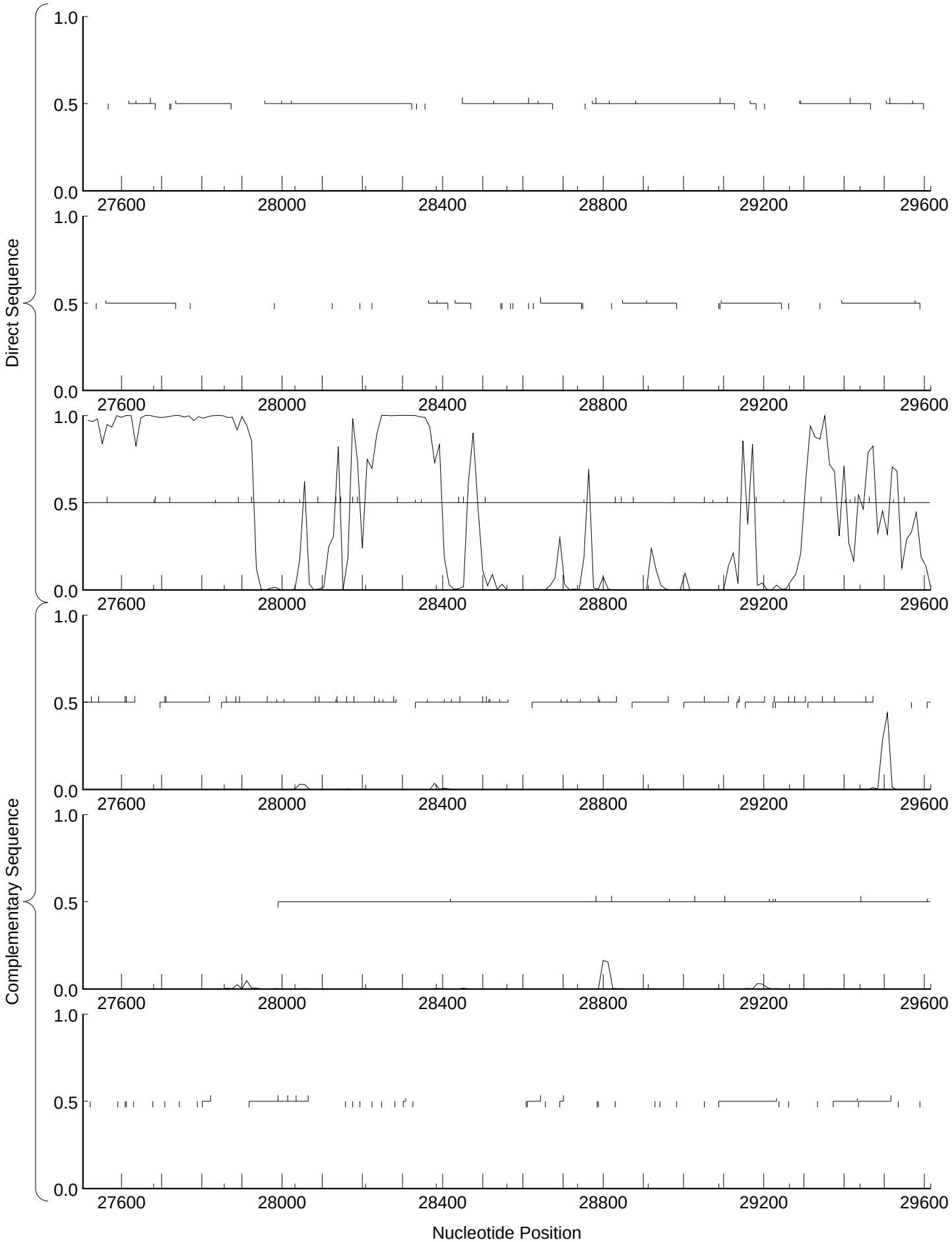
ia phage Luker complete sequence, 73453 bp including 161 bp terminal repeat, Cluster CS3, Order 4, Window 96, Step 12, 13/36

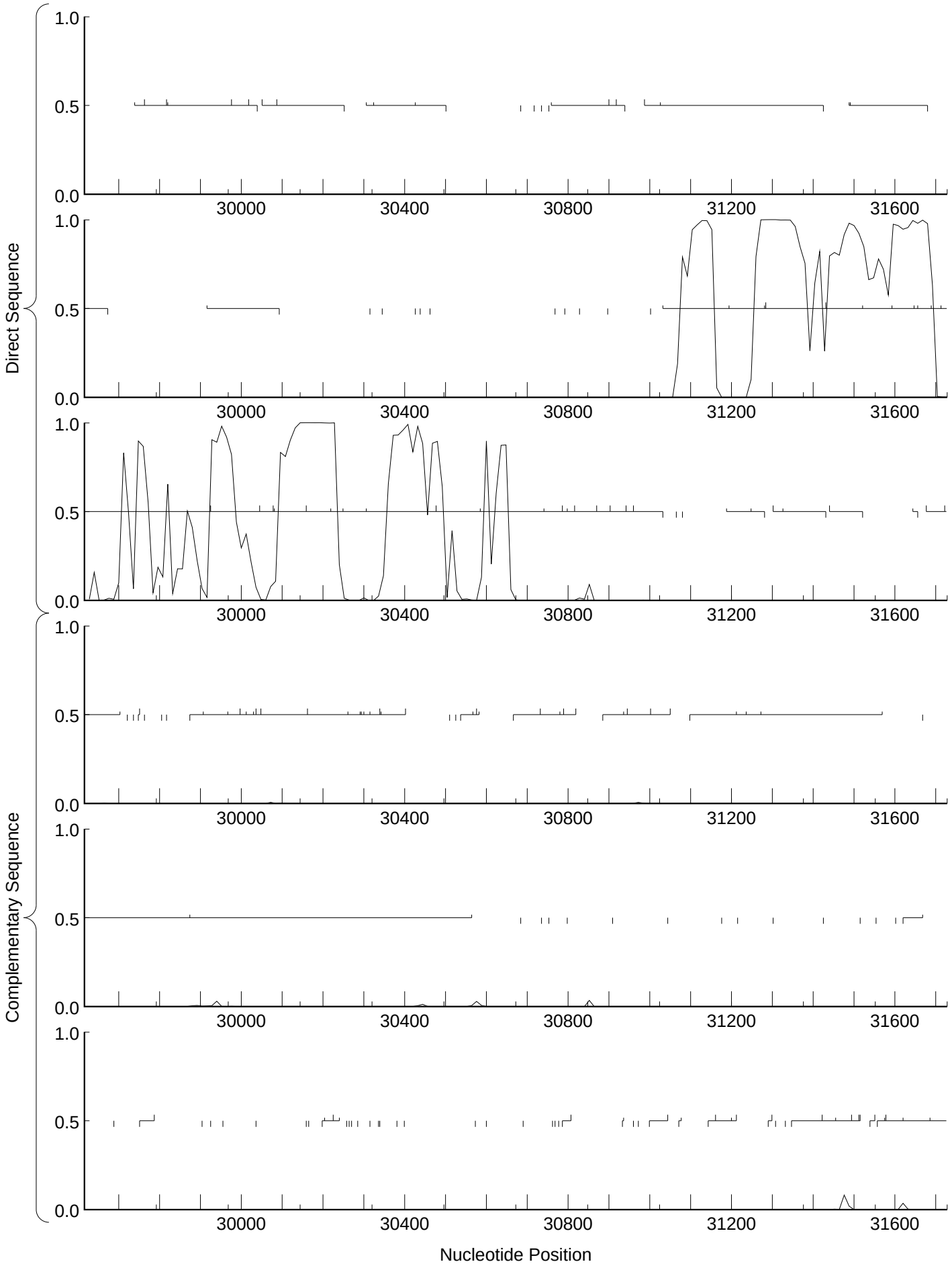


ia phage Luker complete sequence, 73453 bp including 161 bp terminal repeat, Cluster CS3, Order 4, Window 96, Step 12, 14/36

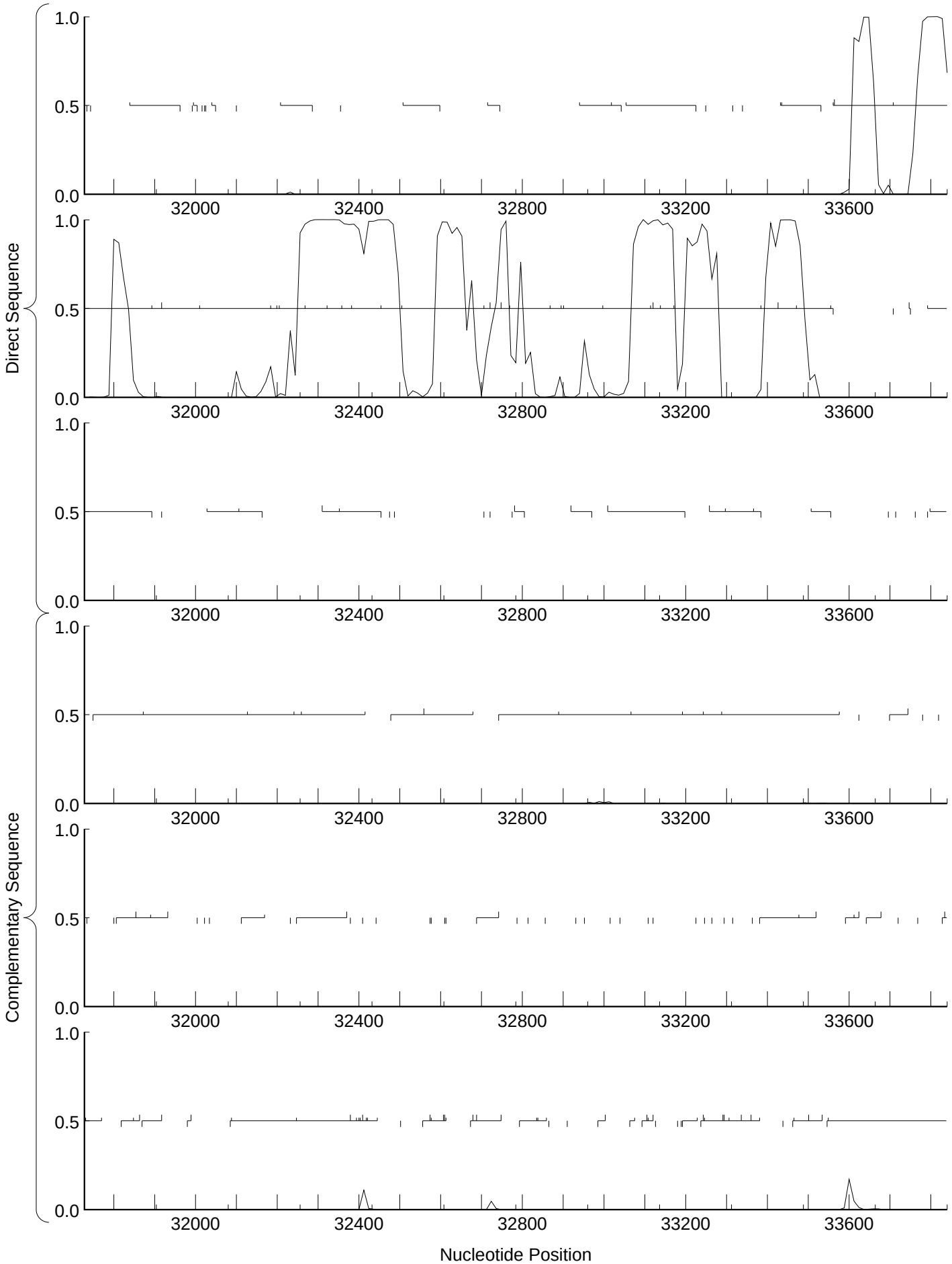


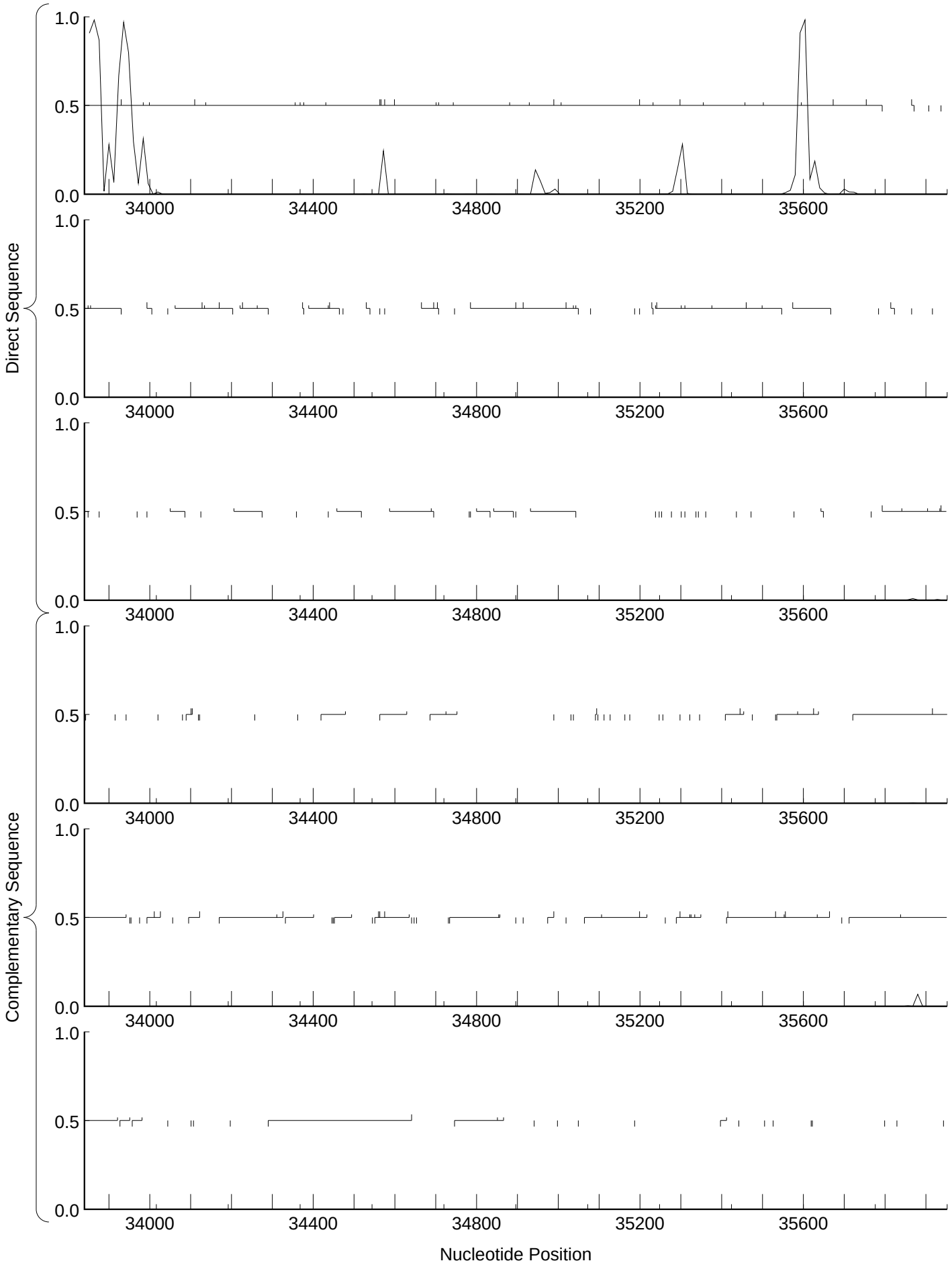
ia phage Luker complete sequence, 73453 bp including 161 bp terminal repeat, Cluster CS3, Order 4, Window 96, Step 12, 15/36



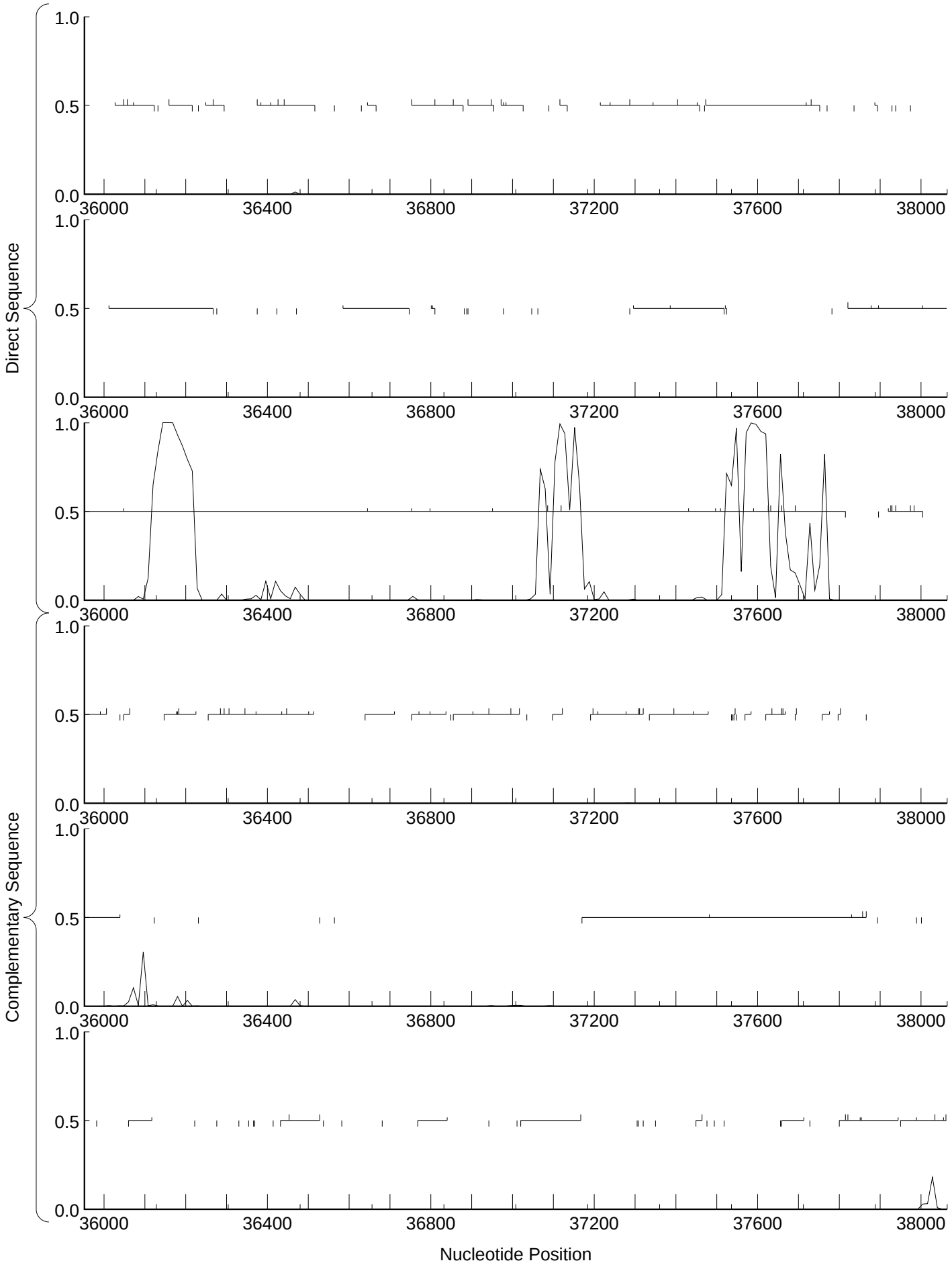

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
30000
30400
30800
31200
31600
Nucleotide Position

ia phage Luker complete sequence, 73453 bp including 161 bp terminal repeat, Cluster CS3, Order 4, Window 96, Step 12, 17/36

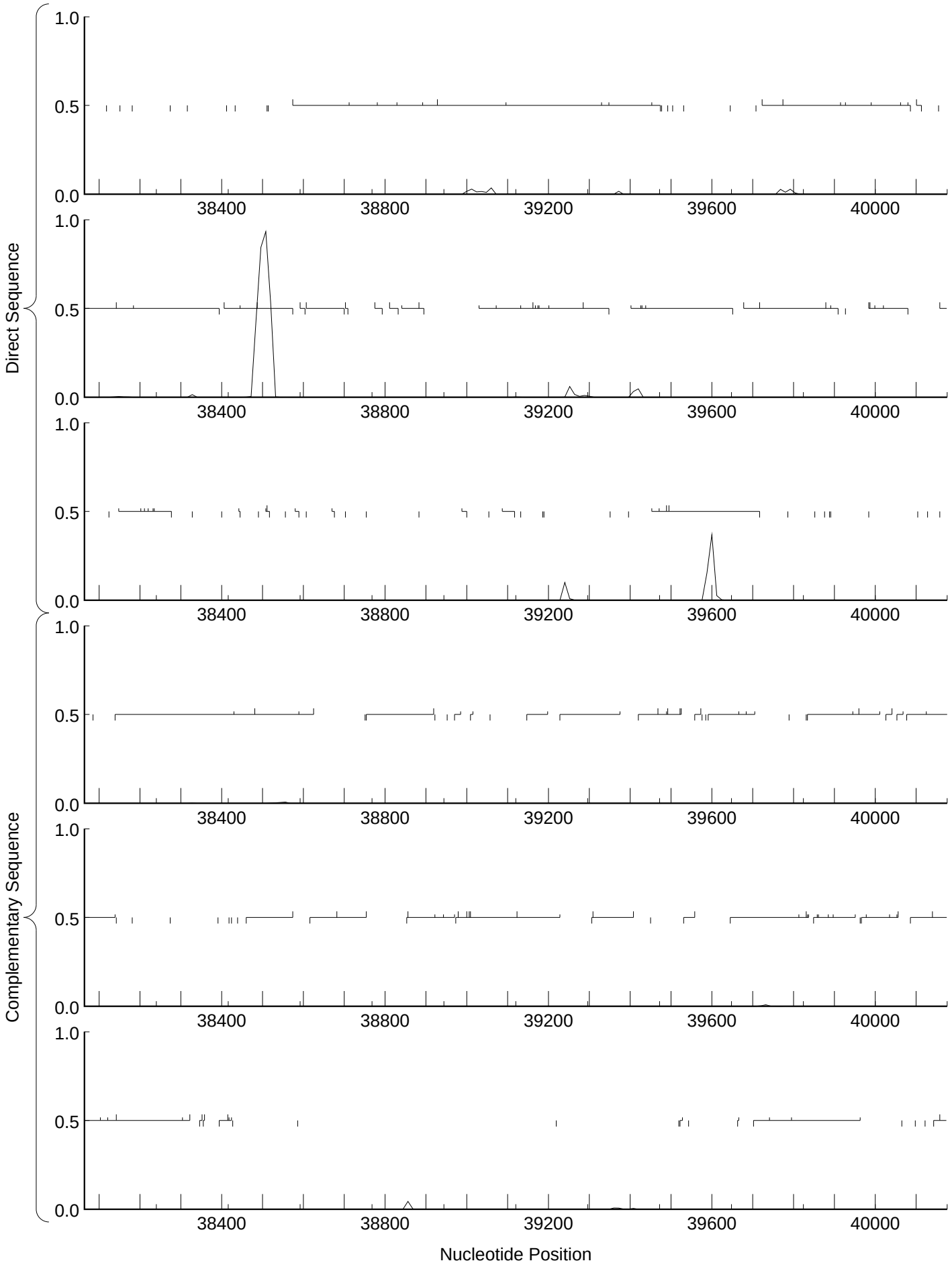


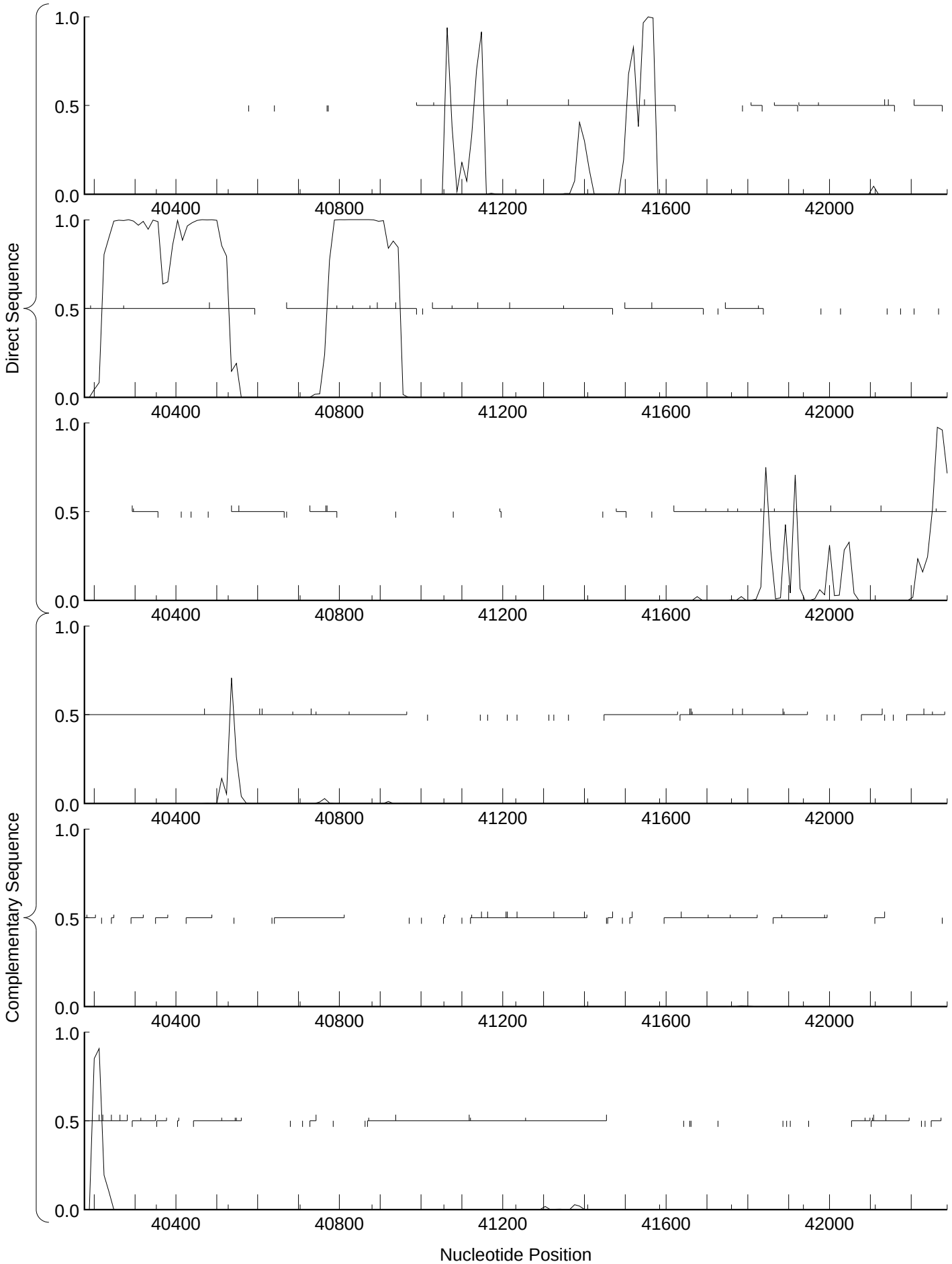

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
34000
34400
34800
35200
35600
Nucleotide Position

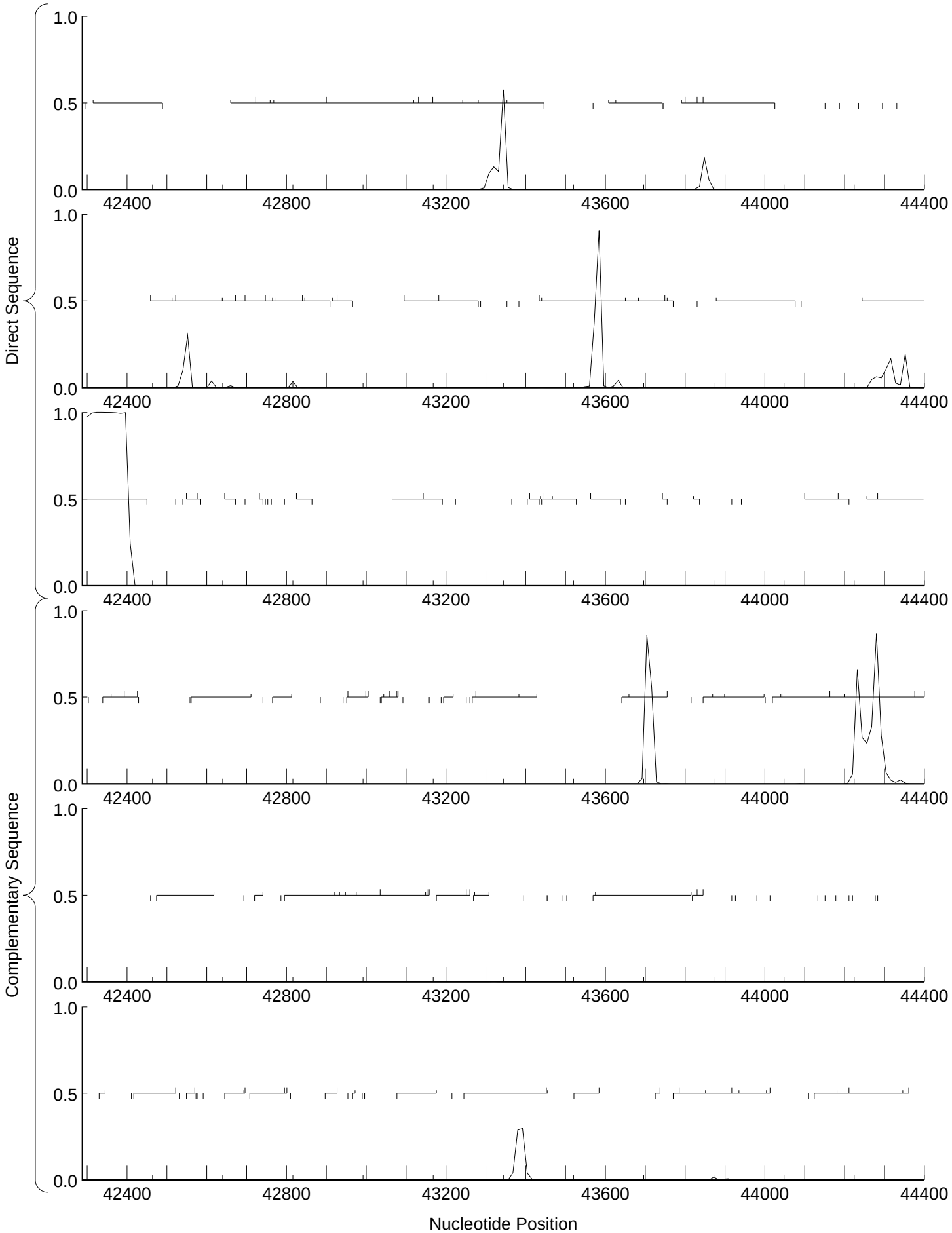
ia phage Luker complete sequence, 73453 bp including 161 bp terminal repeat, Cluster CS3, Order 4, Window 96, Step 12, 19/36

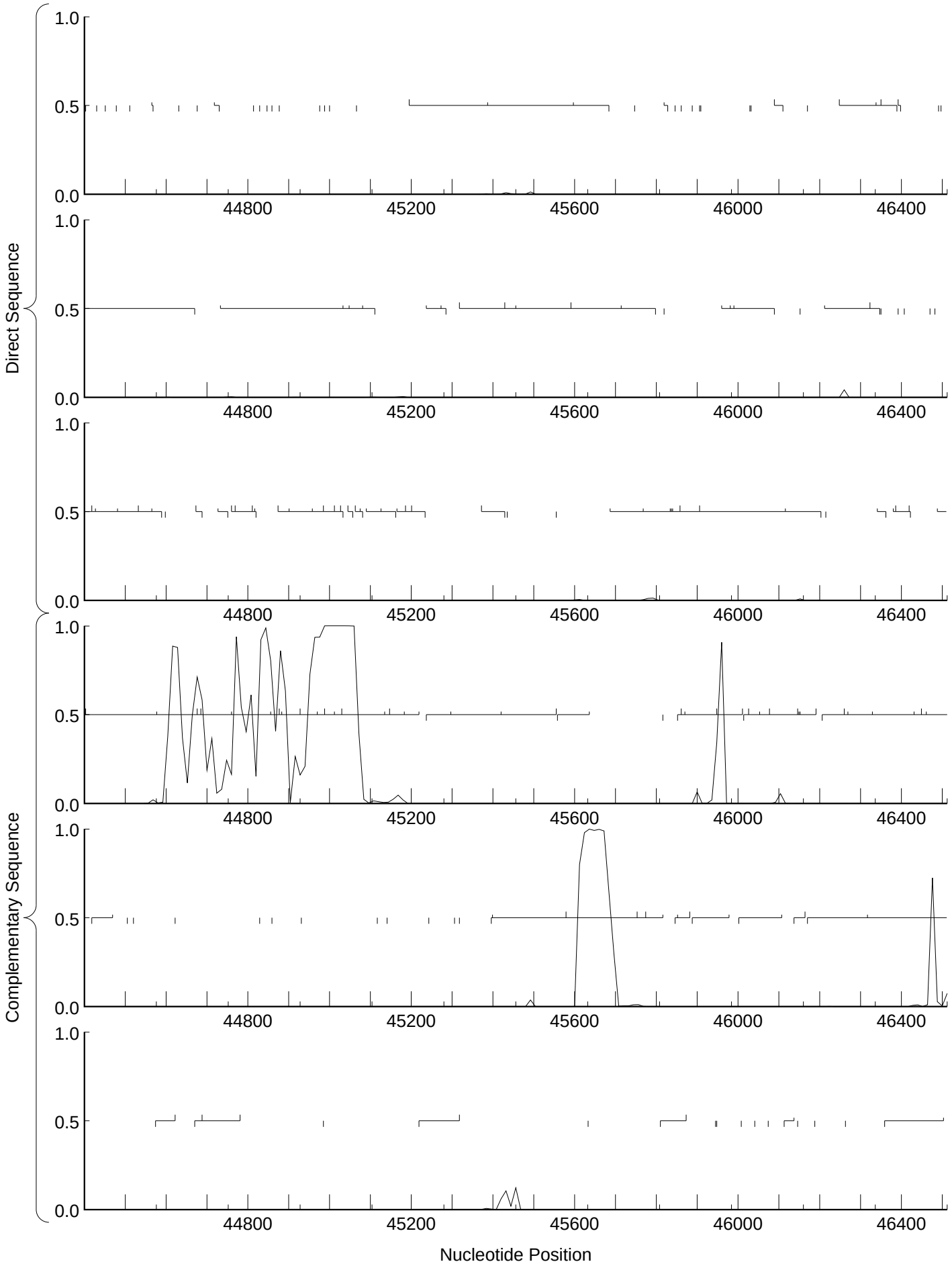


ia phage Luker complete sequence, 73453 bp including 161 bp terminal repeat, Cluster CS3, Order 4, Window 96, Step 12, 20/36

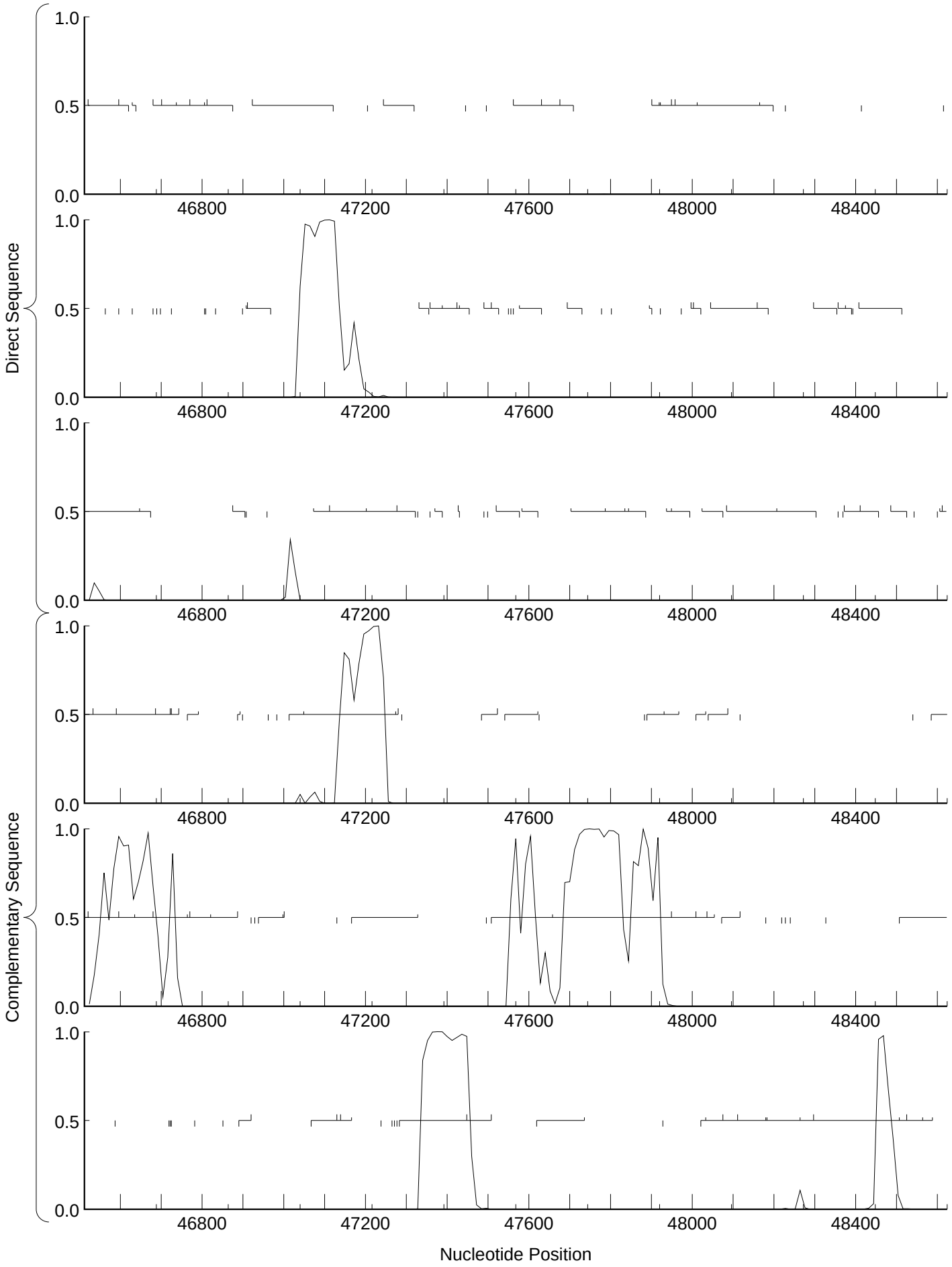


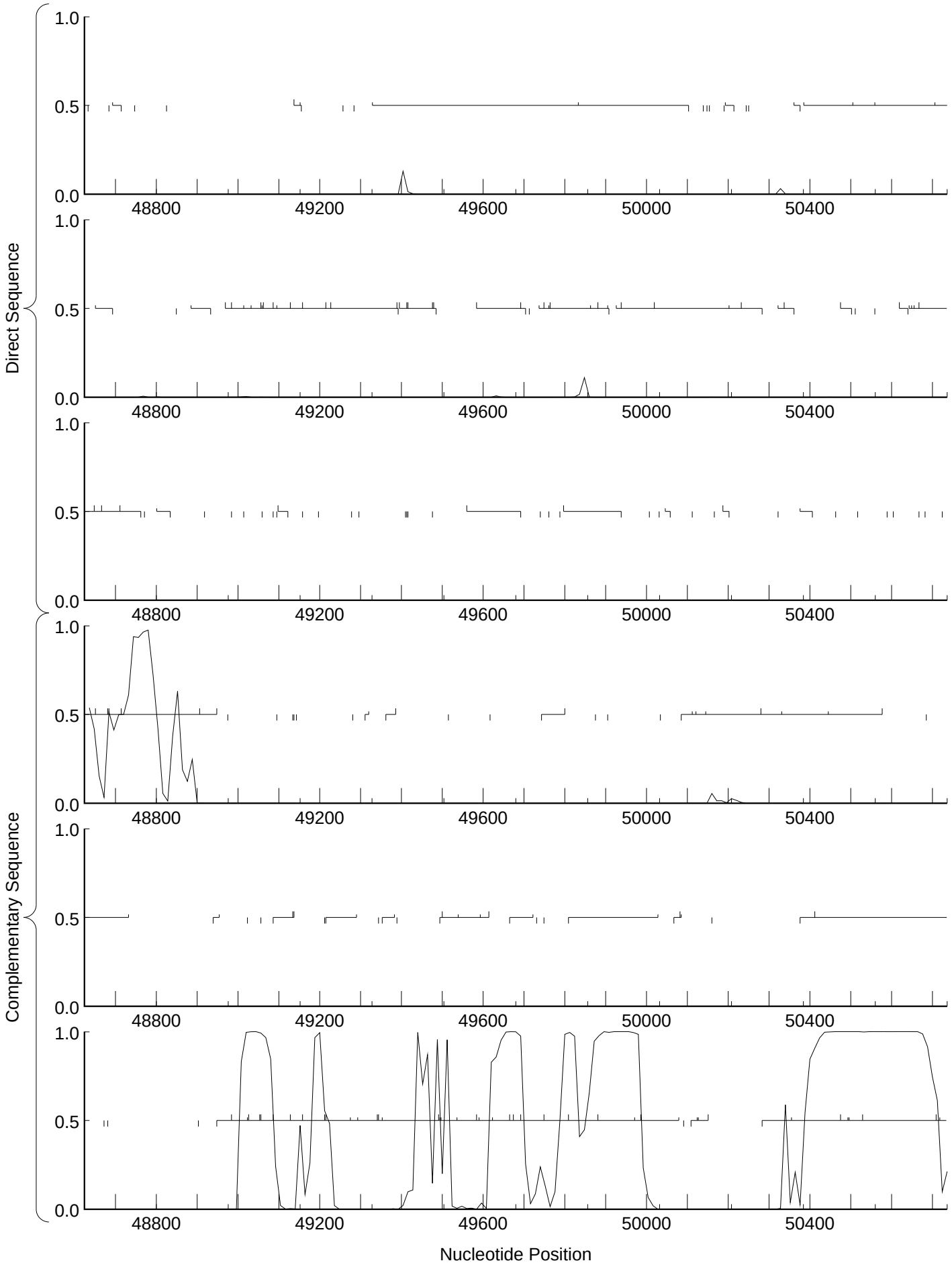

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
40400
40800
41200
41600
42000
Nucleotide Position

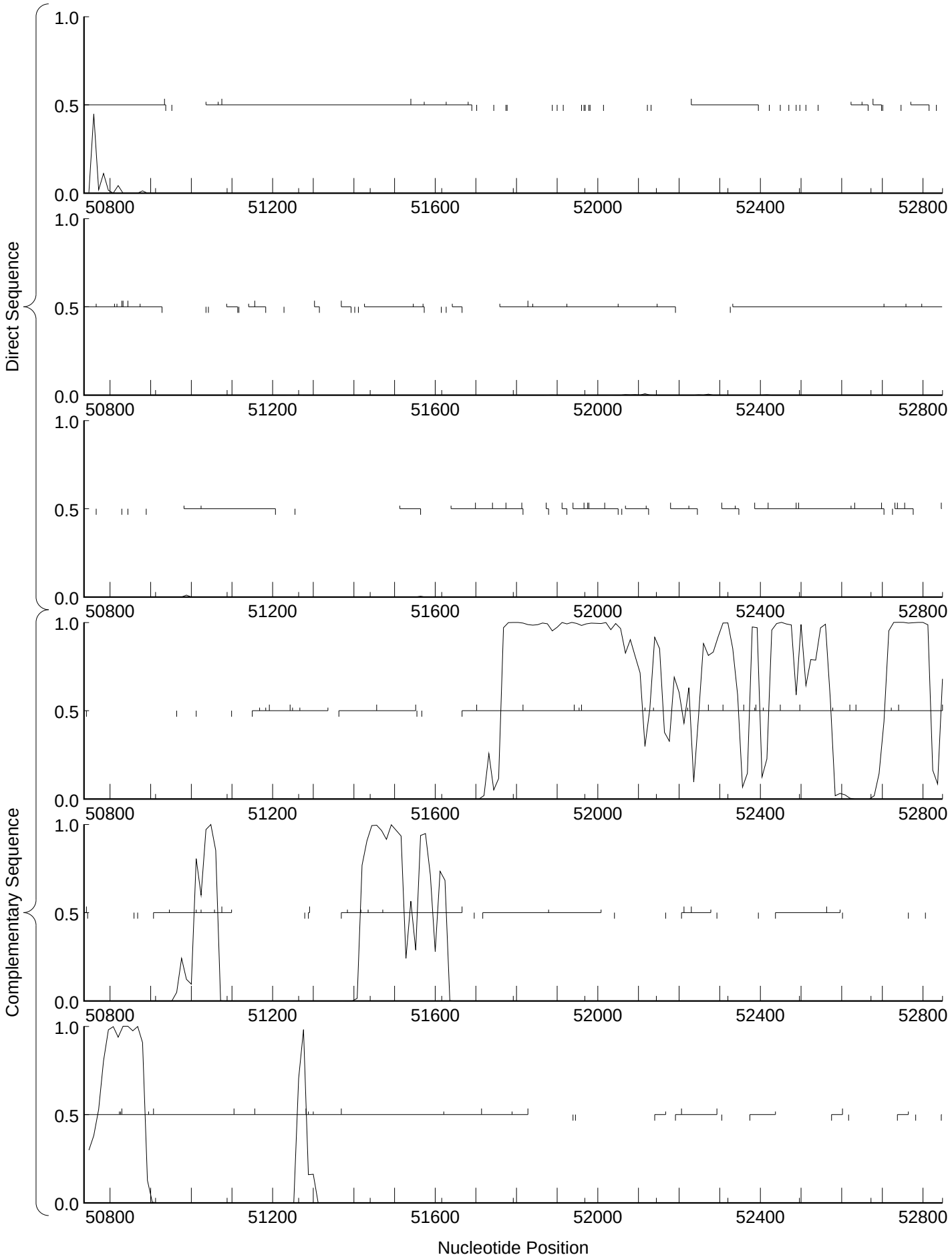

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
42400
42800
43200
43600
44000
44400
Nucleotide Position


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
44800
45200
45600
46000
46400
Nucleotide Position

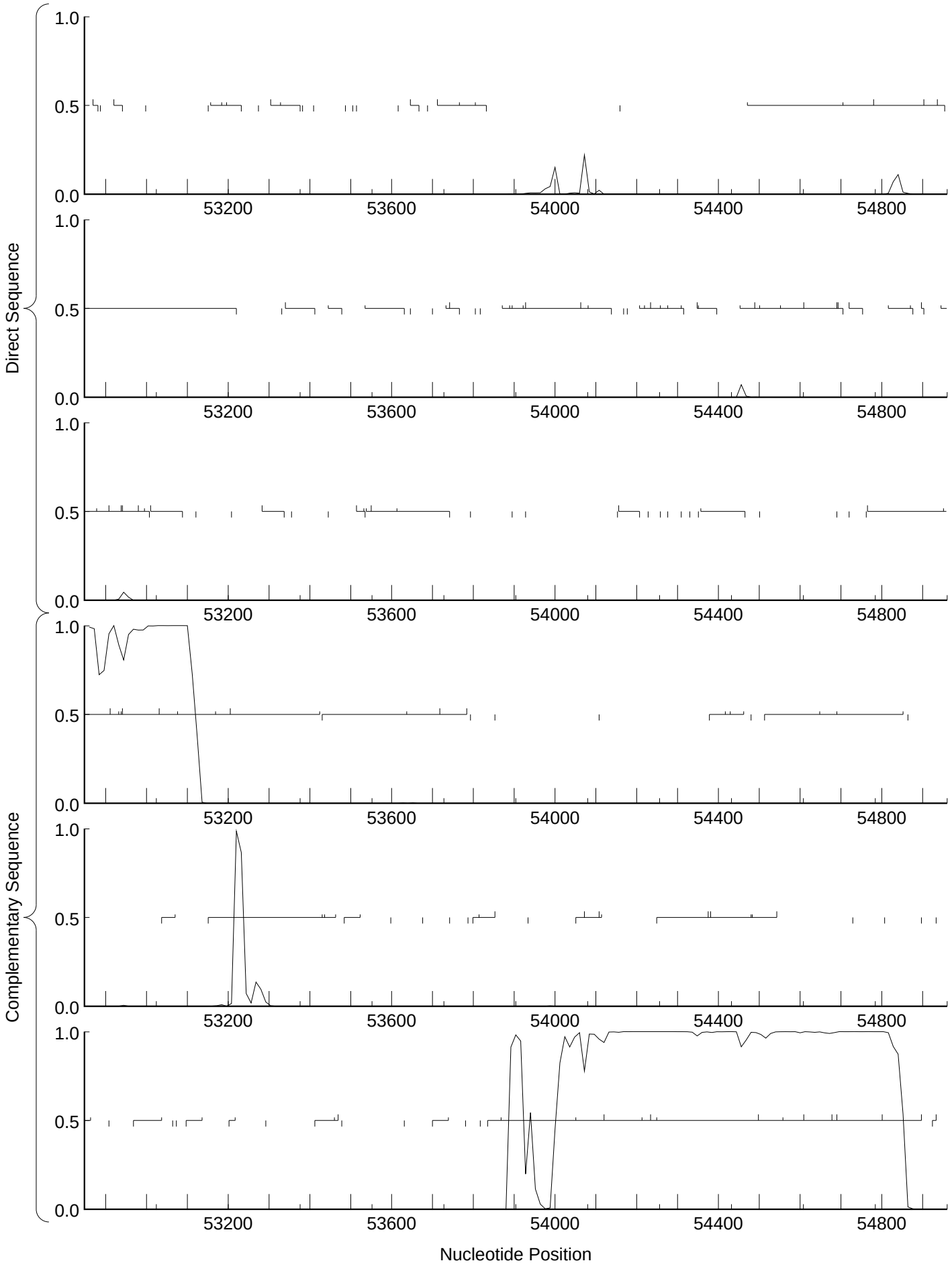
ia phage Luker complete sequence, 73453 bp including 161 bp terminal repeat, Cluster CS3, Order 4, Window 96, Step 12, 24/36

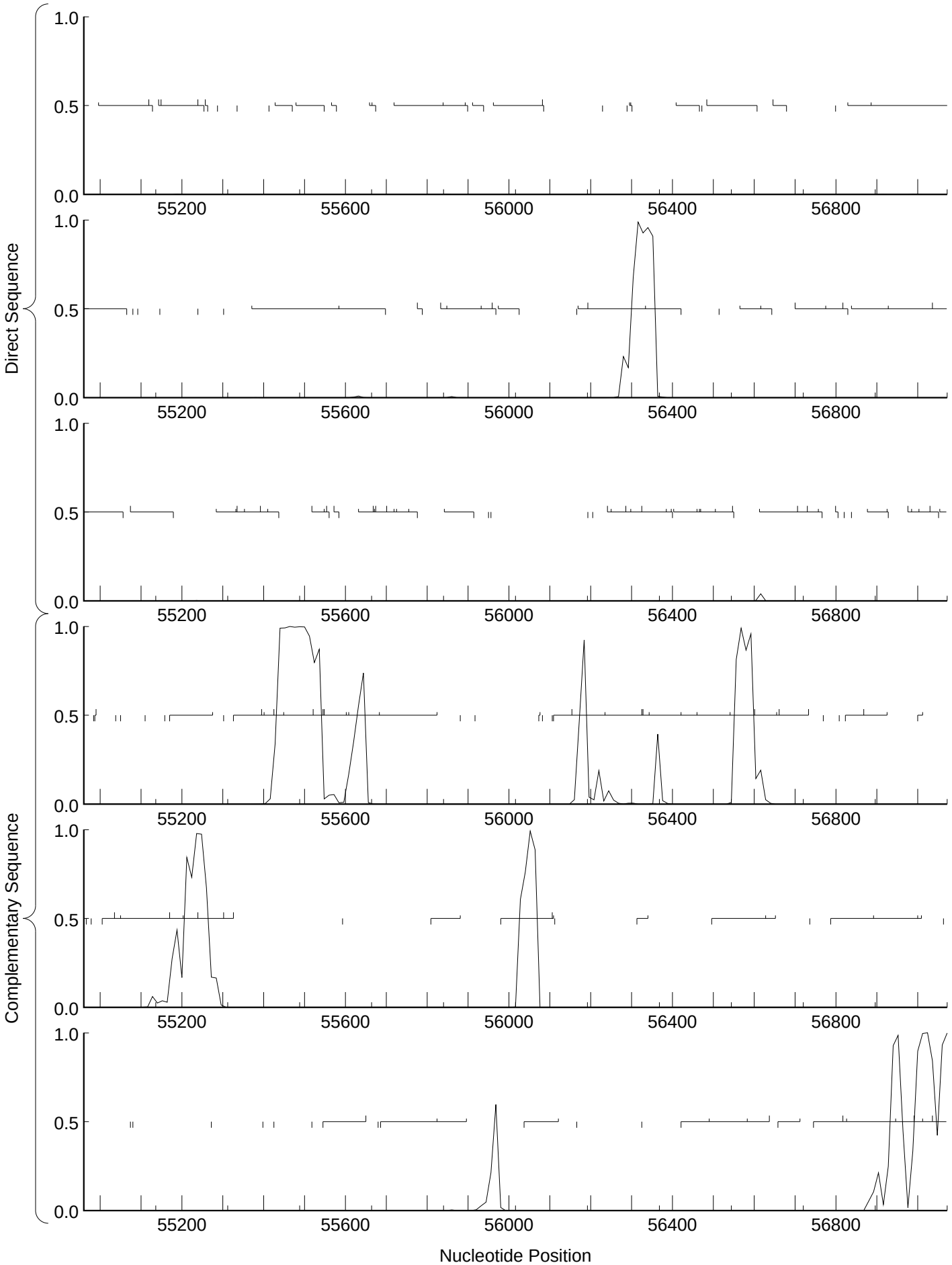


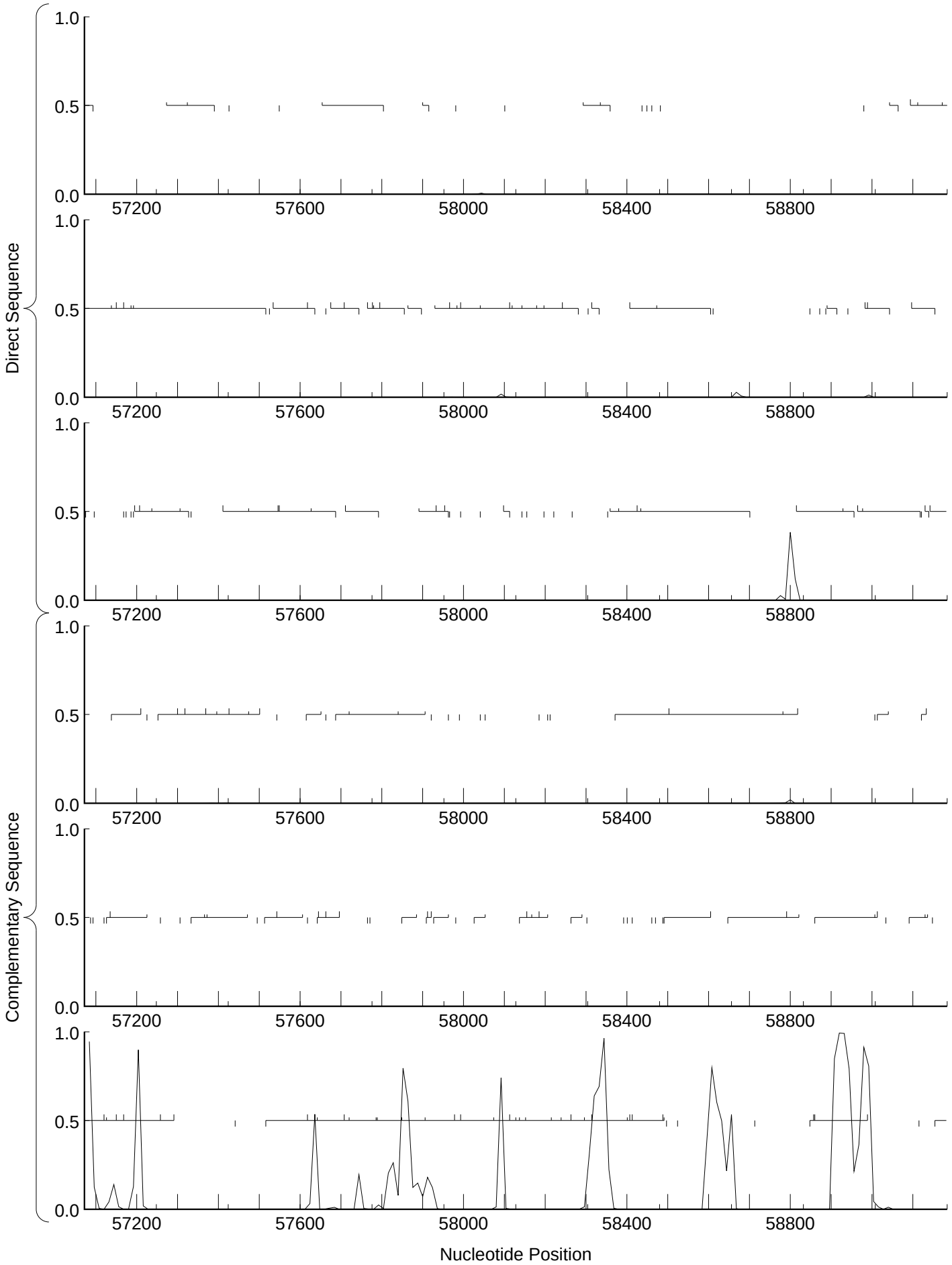

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
48800
49200
49600
50000
50400
Nucleotide Position

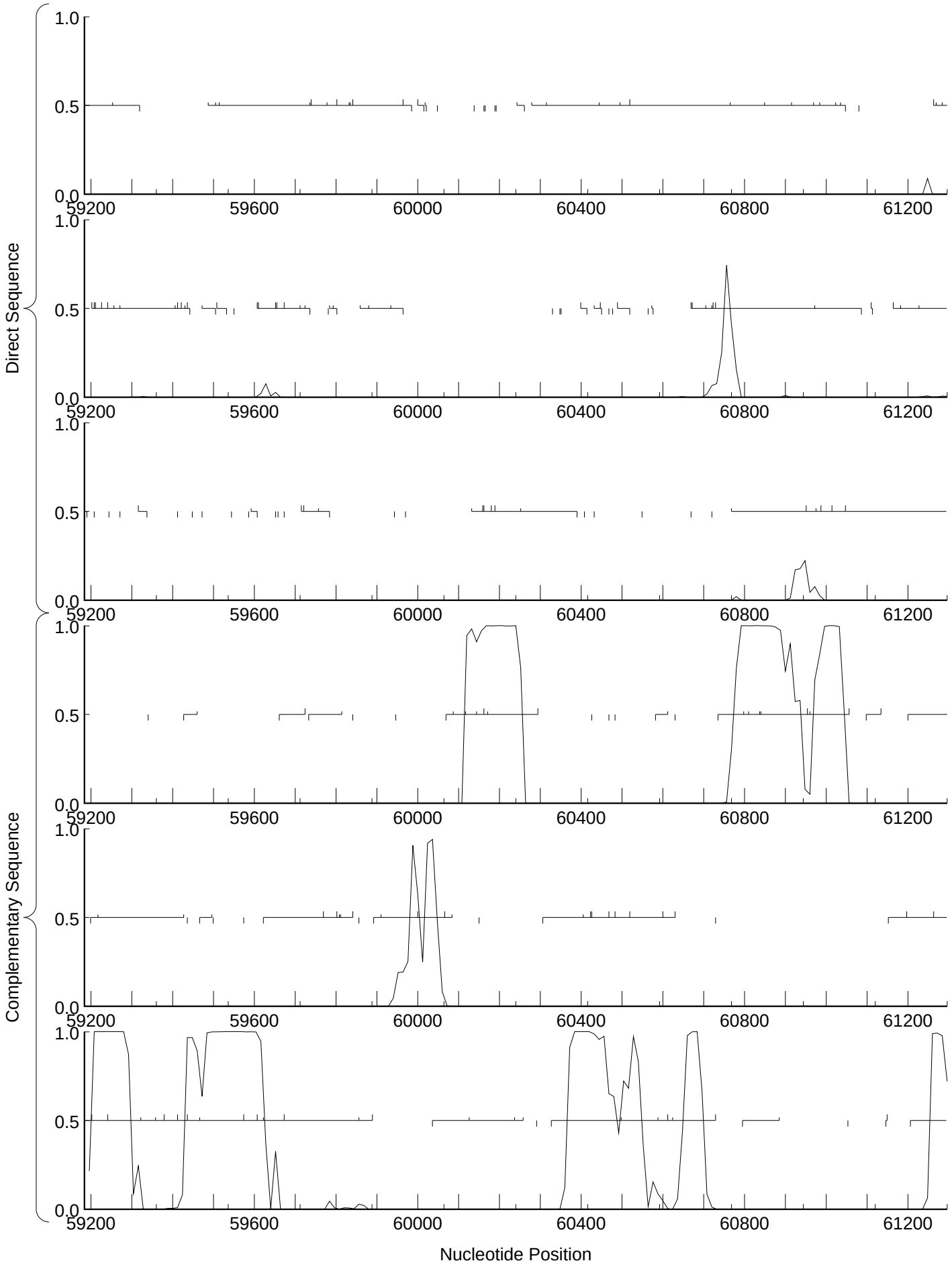

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
50800
51200
51600
52000
52400
52800
Nucleotide Position

ia phage Luker complete sequence, 73453 bp including 161 bp terminal repeat, Cluster CS3, Order 4, Window 96, Step 12, 27/36

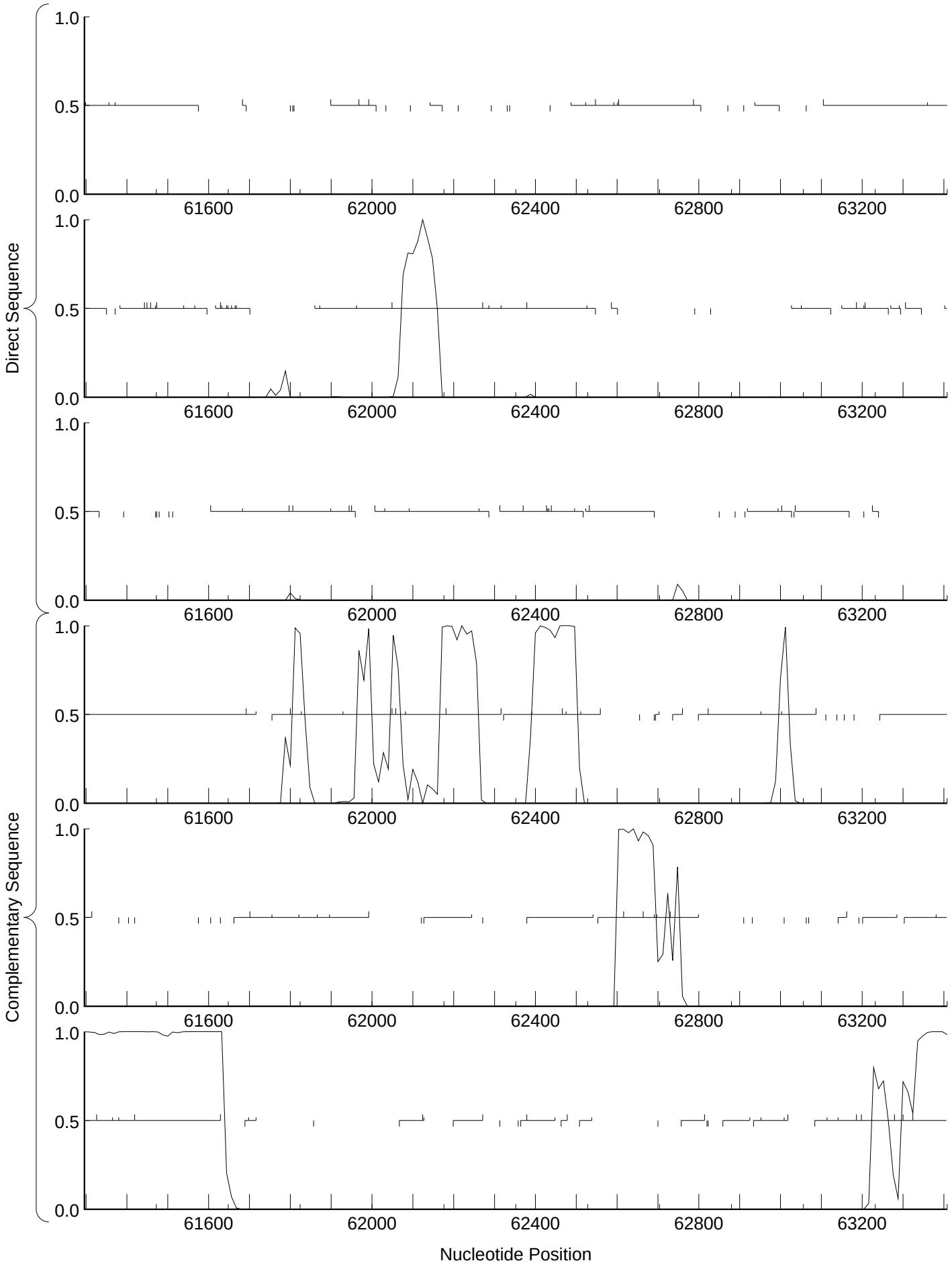


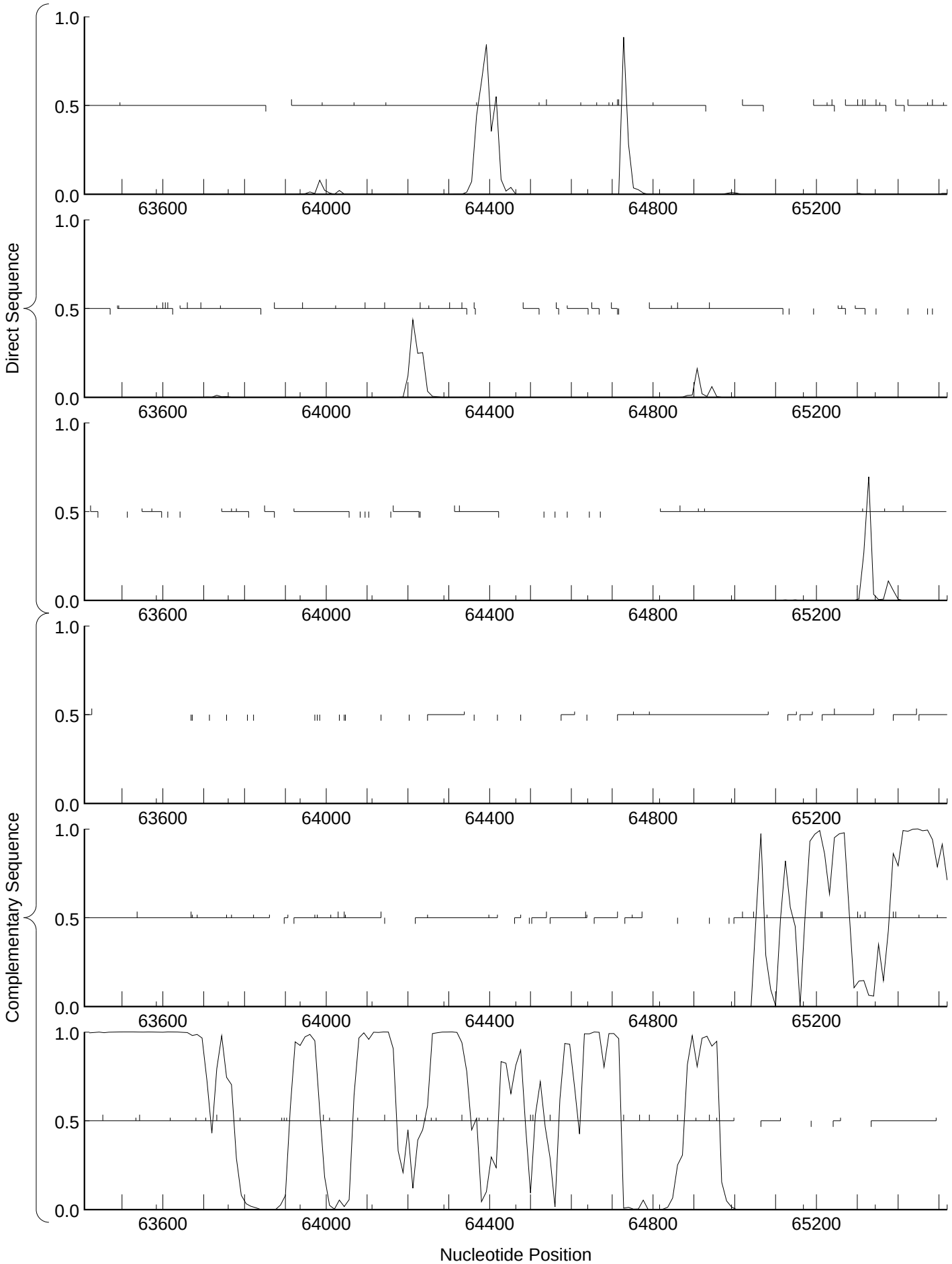

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
55200
55600
56000
56400
56800
Nucleotide Position

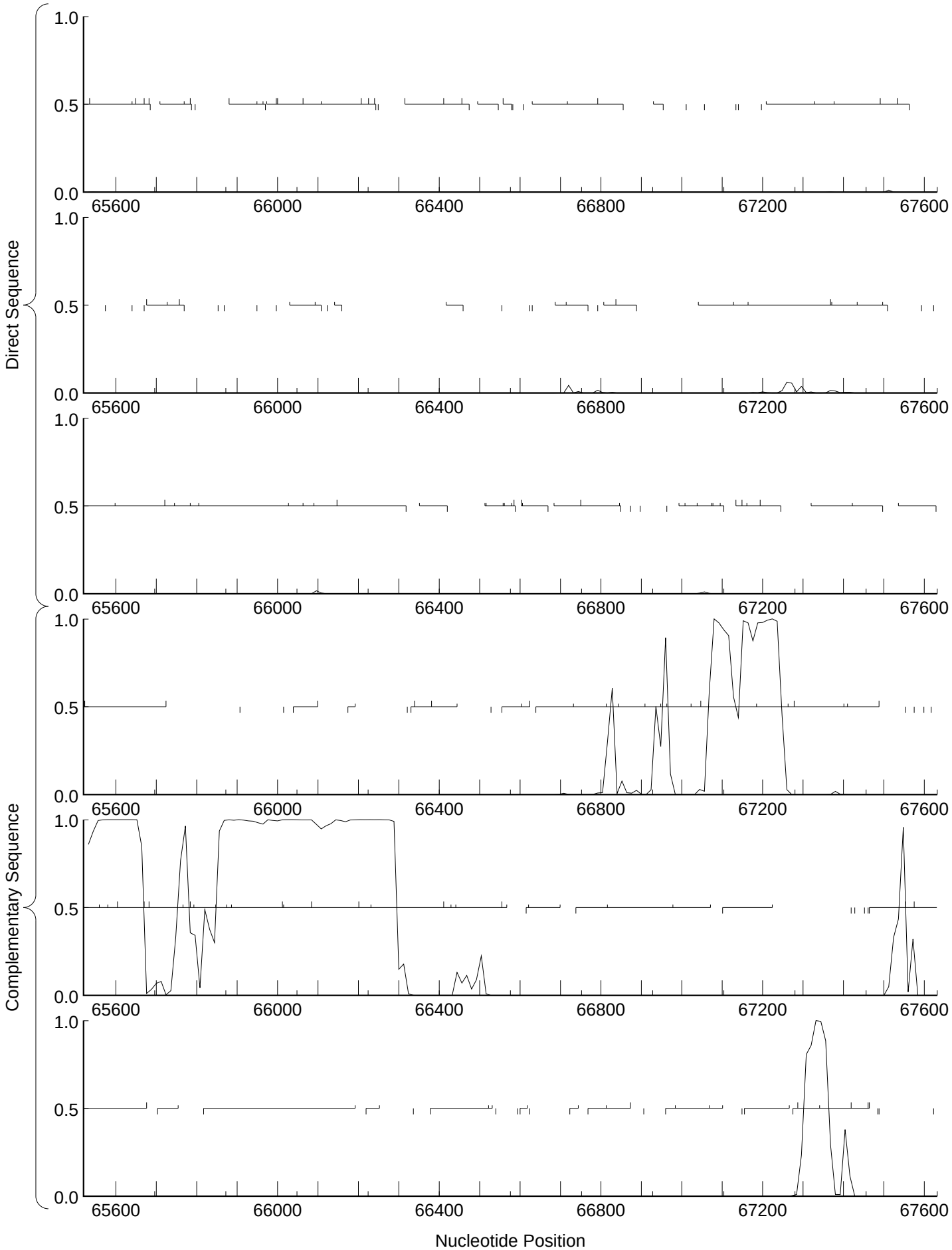

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
57200
57600
58000
58400
58800
Nucleotide Position


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
59200
59600
60000
60400
60800
61200
Nucleotide Position

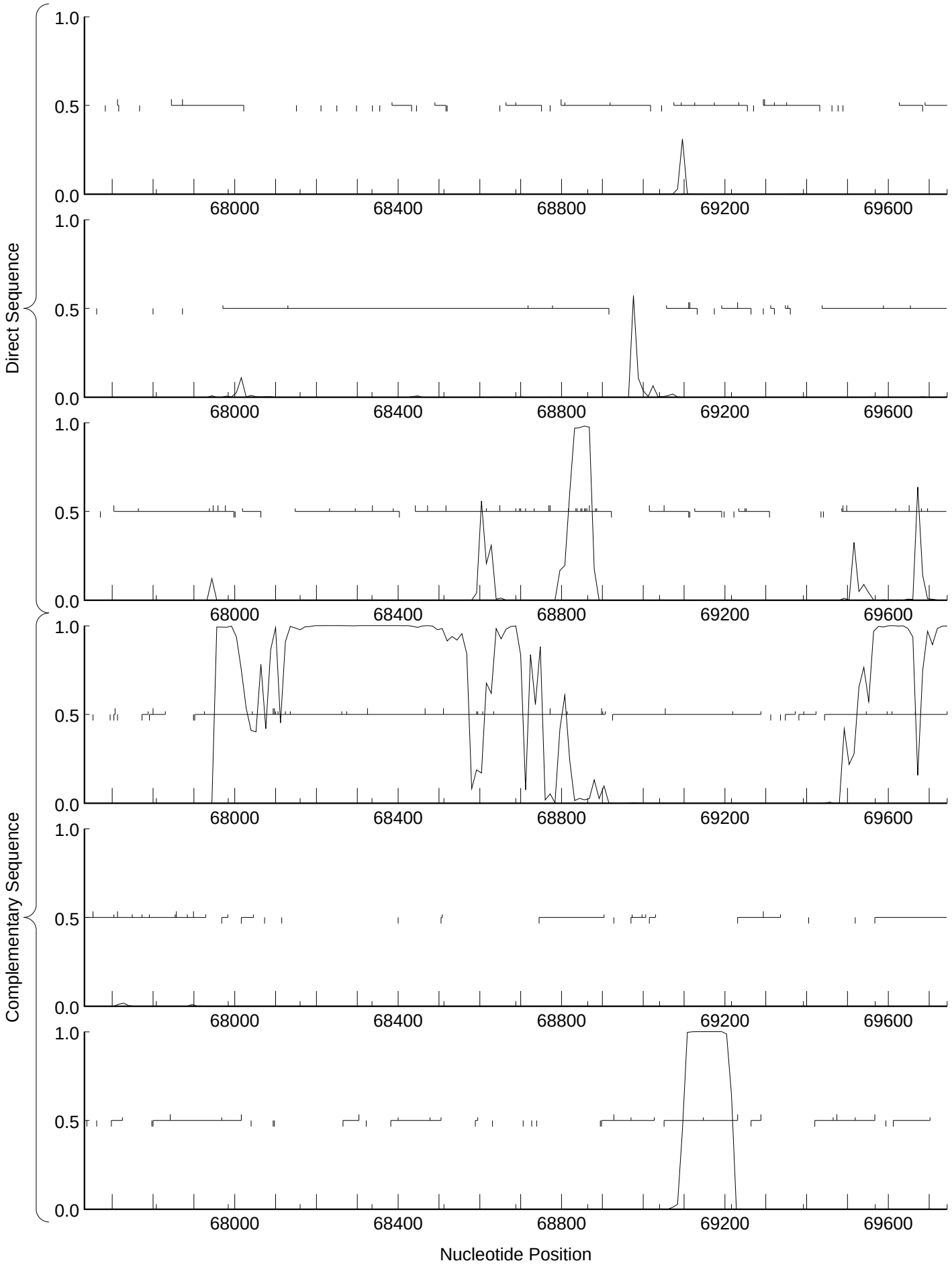
ia phage Luker complete sequence, 73453 bp including 161 bp terminal repeat, Cluster CS3, Order 4, Window 96, Step 12, 31/36



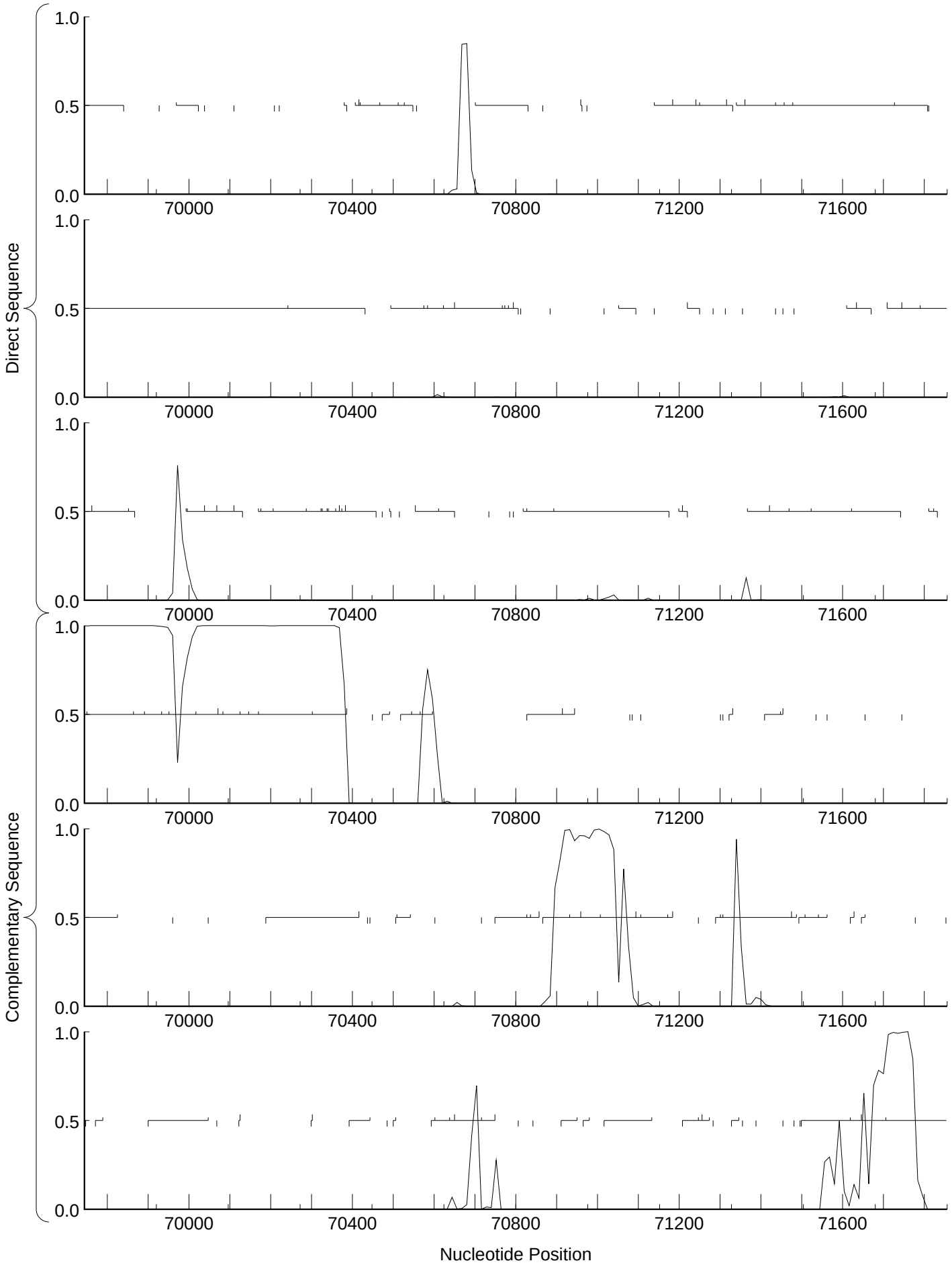

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
63600
64000
64400
64800
65200
Nucleotide Position

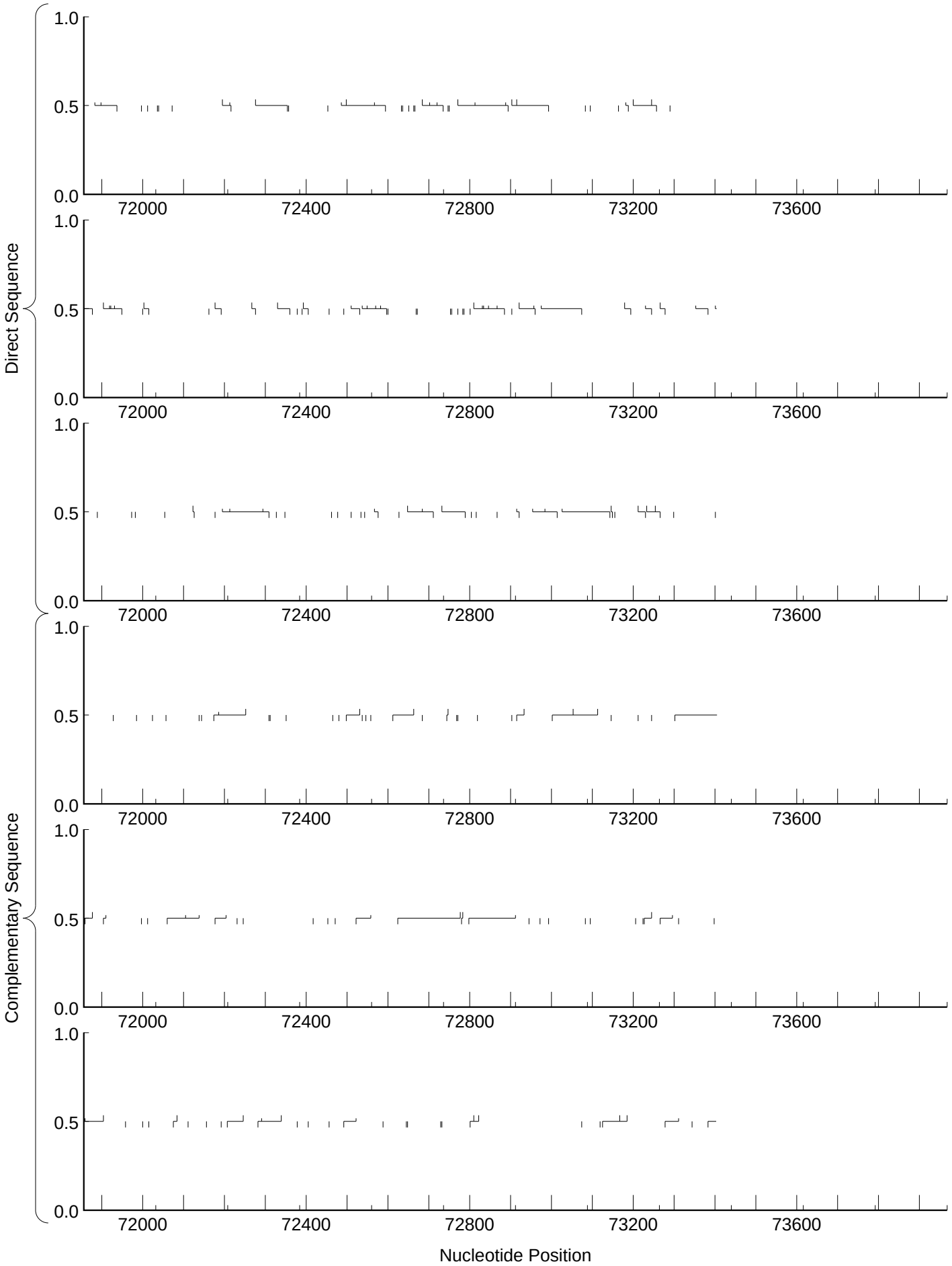

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
65600
66000
66400
66800
67200
67600
Nucleotide Position

ia phage Luker complete sequence, 73453 bp including 161 bp terminal repeat, Cluster CS3, Order 4, Window 96, Step 12, 34/36



ia phage Luker complete sequence, 73453 bp including 161 bp terminal repeat, Cluster CS3, Order 4, Window 96, Step 12, 35/36




Direct Sequence
Complementary Sequence
1.0
0.5
0.0
72000
72400
72800
73200
73600
Nucleotide Position