# GeneMark

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

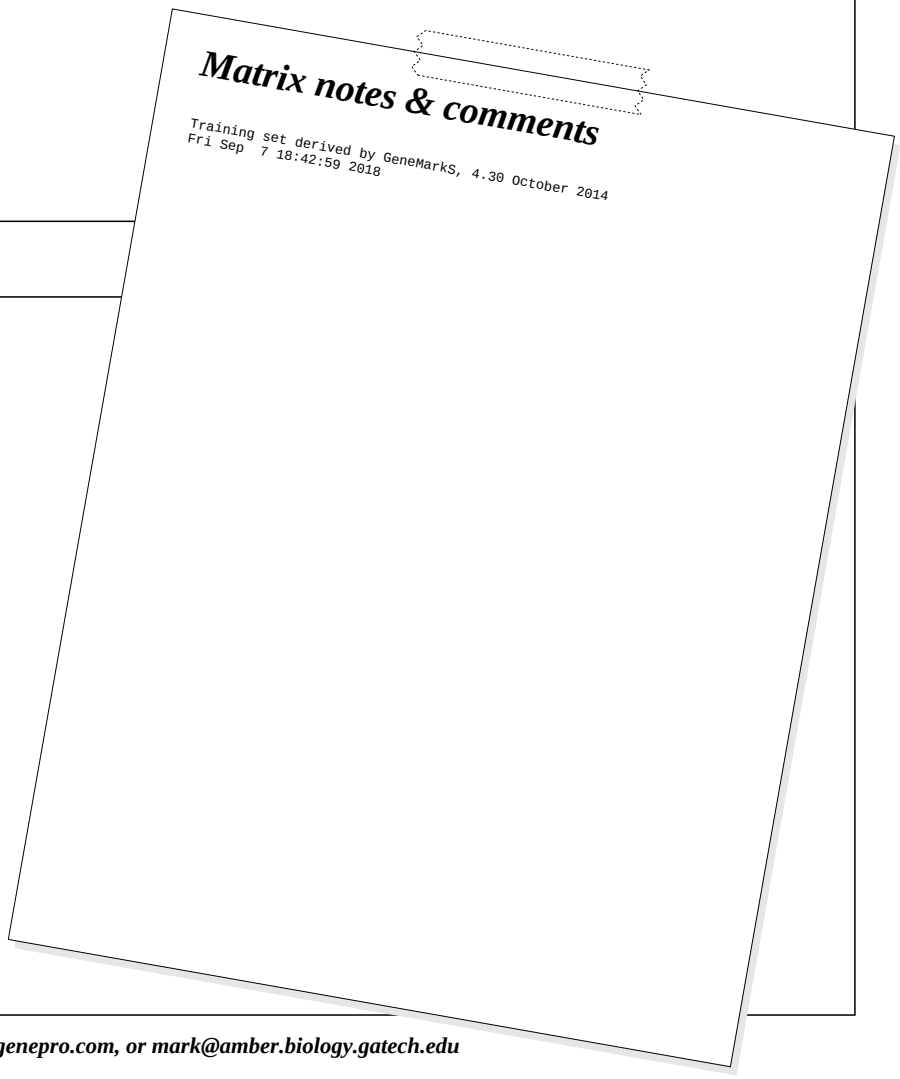
## PROGRAM INFORMATION

```
Sequence         :  Microbacterium phage Hortus1 complete sequence, 63119 bp including 3159 bp terminal repeat,
Analysis Date    :  3/29/24 at 2:18:44
Pages            :  31
Sequence Length  :  63119 bp
GC Content       :   64.59%

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,
```




## MATRIX INFORMATION

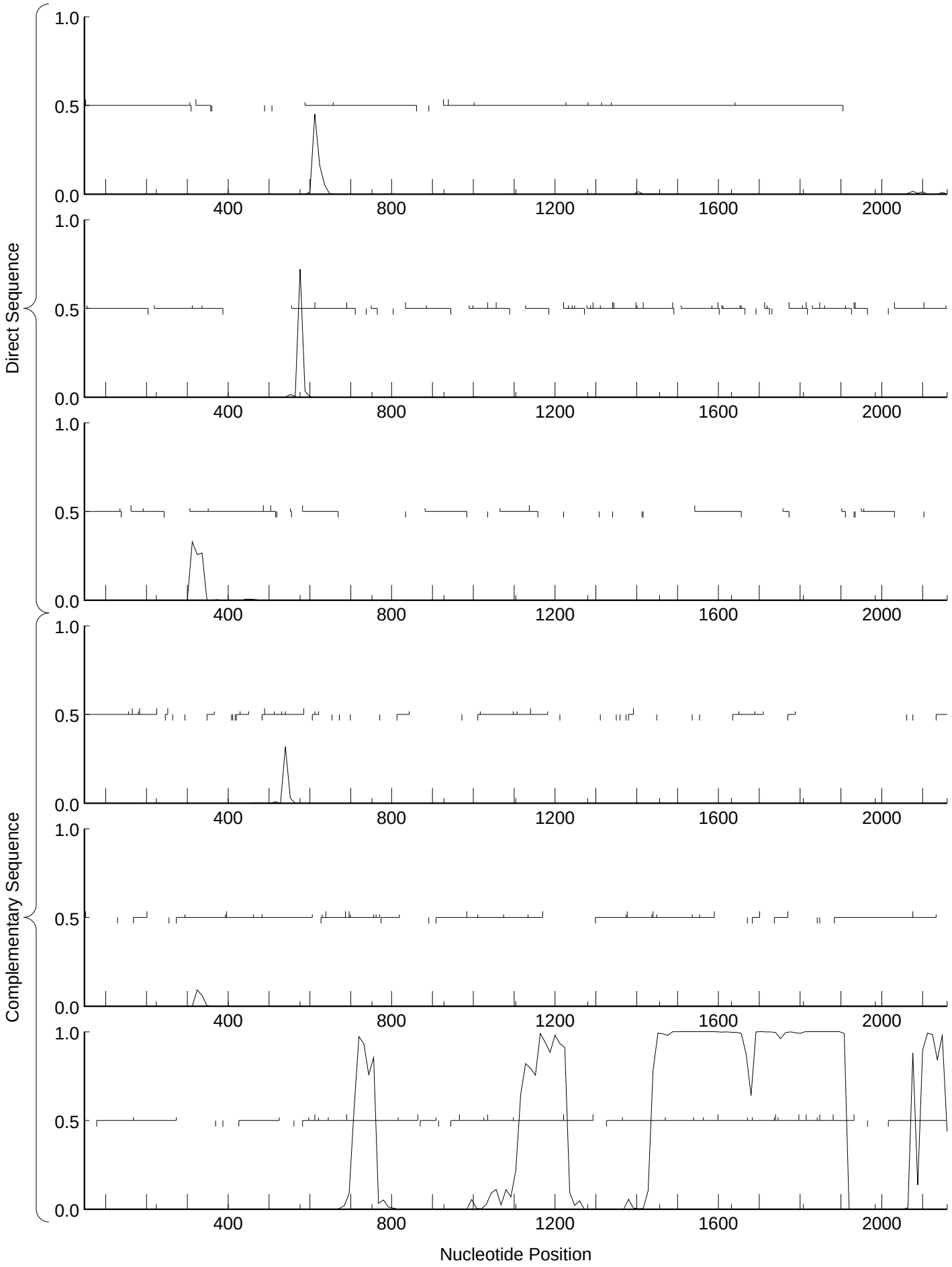
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Matrix     :  -
Author     :  -

Order      :  4
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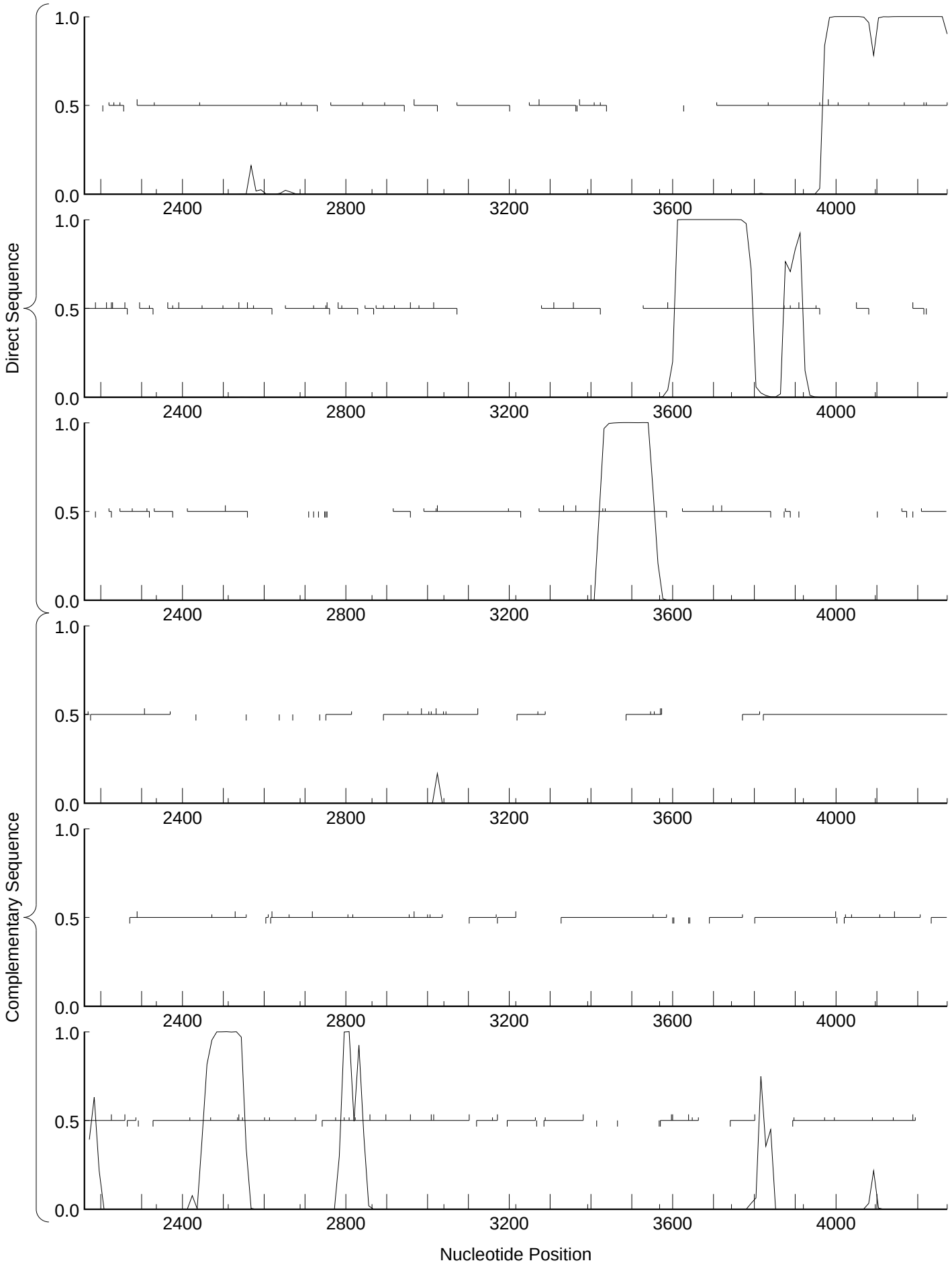

Send questions / comments to:
Dr. M. Borodovsky
Georgia Institute of Technology
School of Biology
Atlanta, GA 30332-0230


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

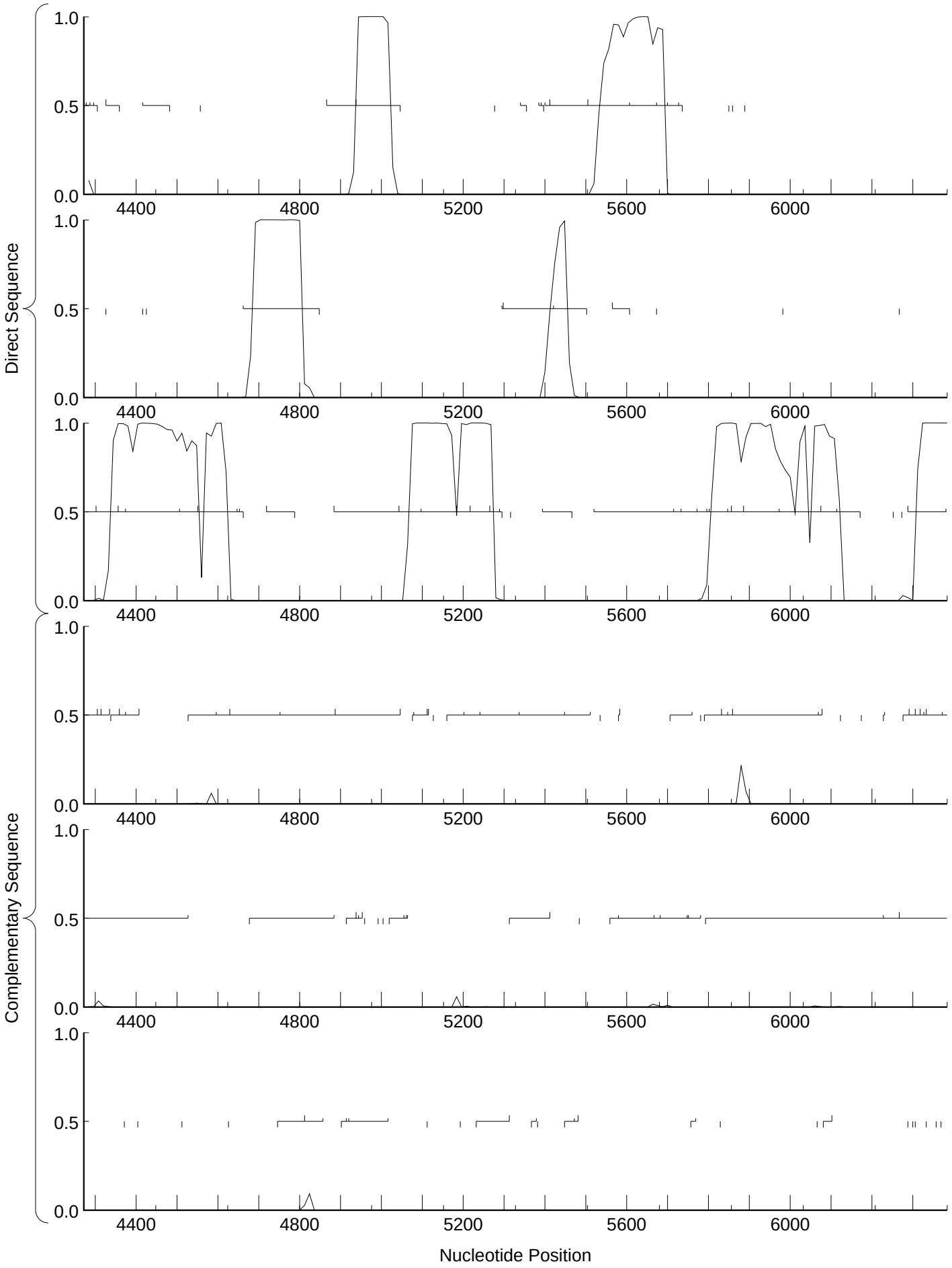
n phage Hortus1 complete sequence, 63119 bp including 3159 bp terminal repeat, Cluster ED, Order 4, Window 96, Step 12, 2/31

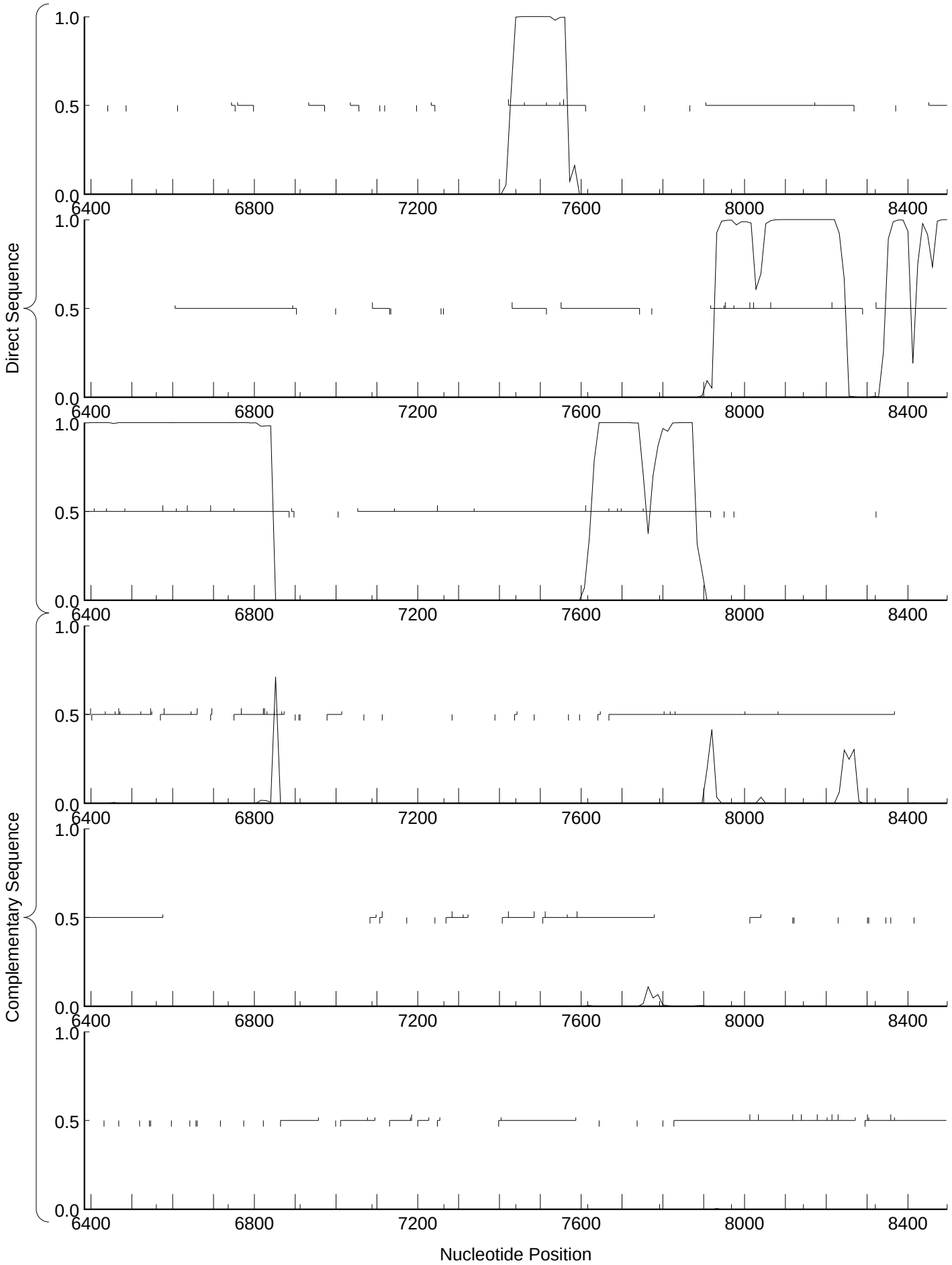


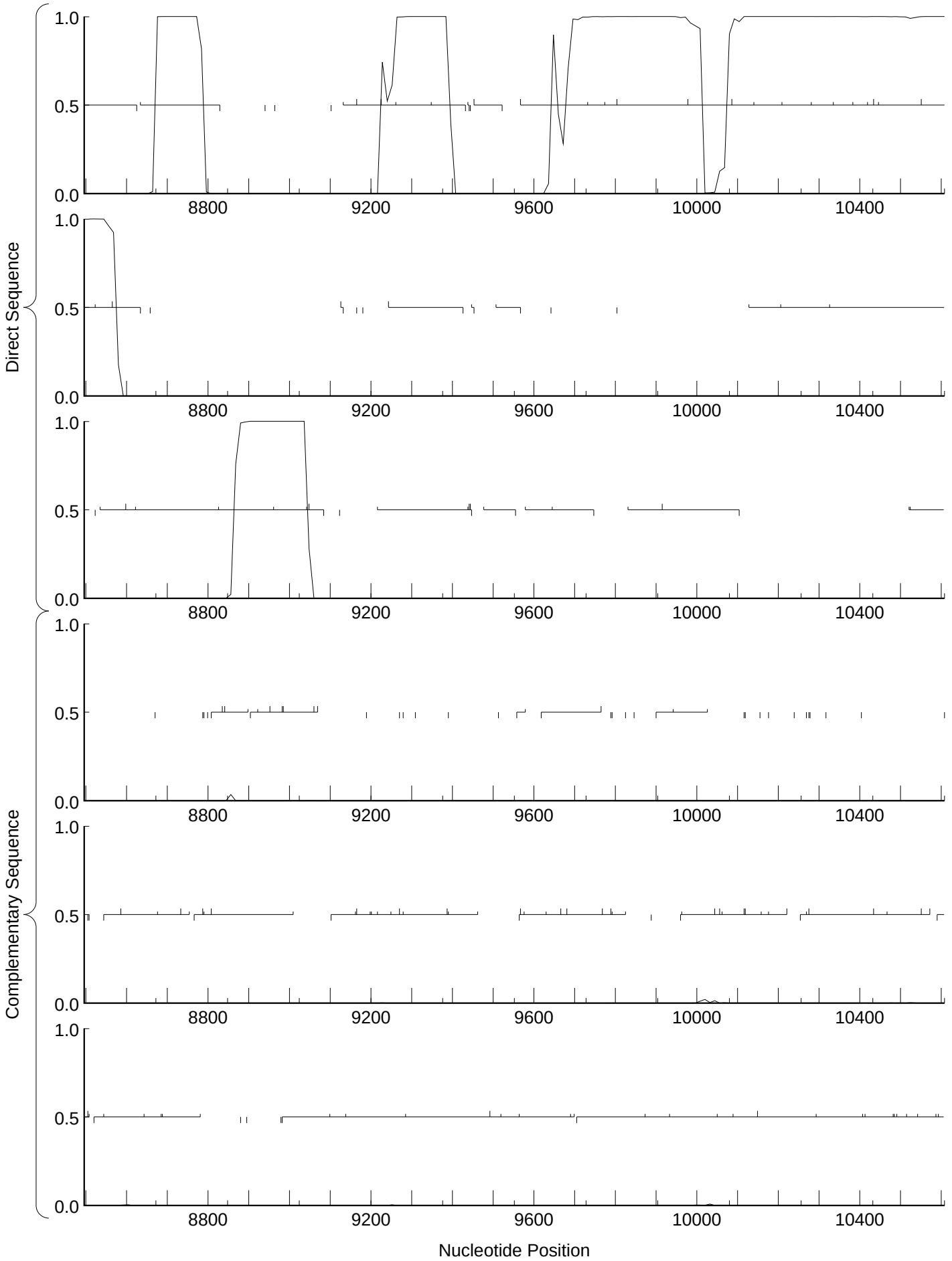
n phage Hortus1 complete sequence, 63119 bp including 3159 bp terminal repeat, Cluster ED, Order 4, Window 96, Step 12, 3/31

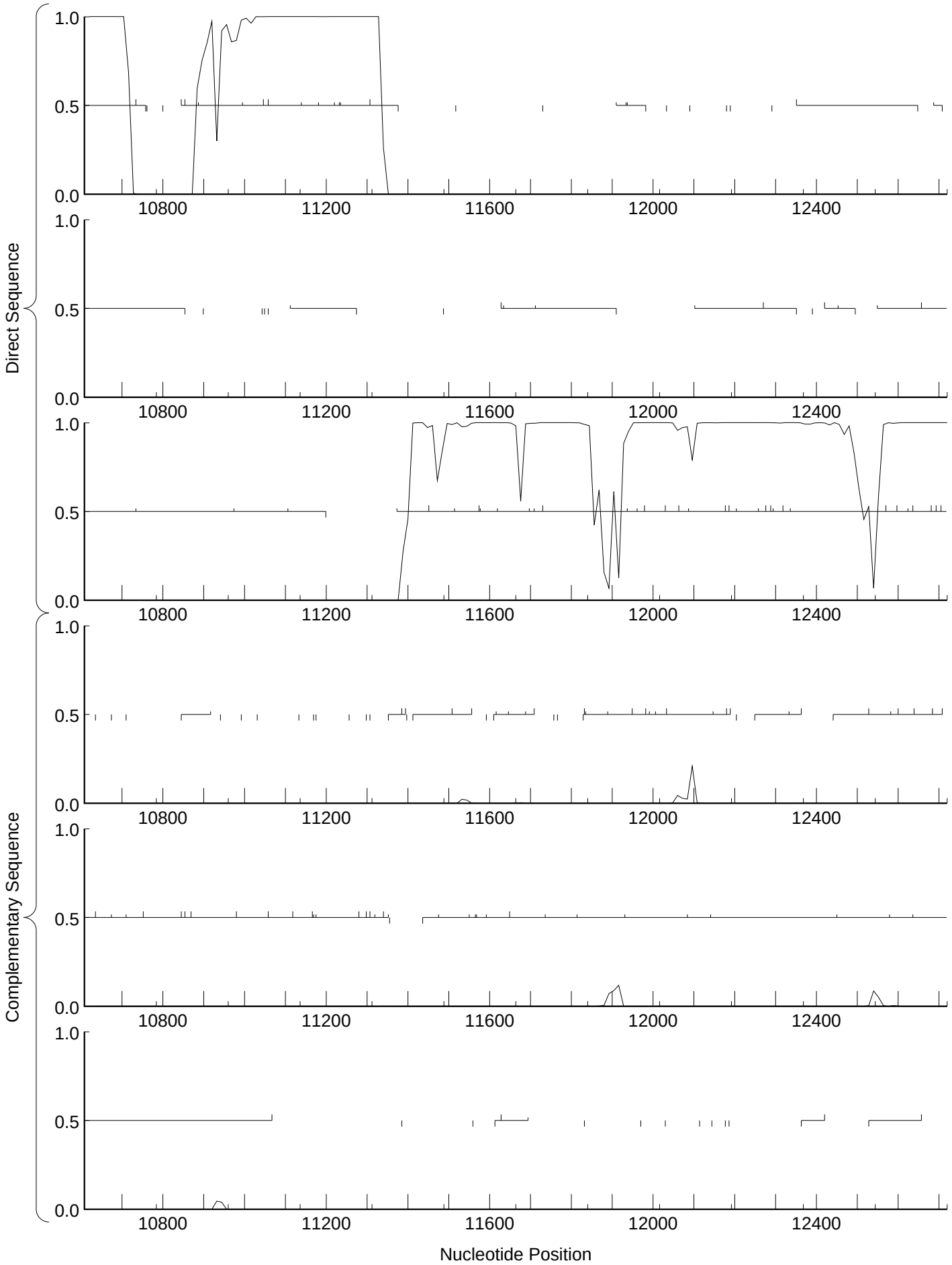


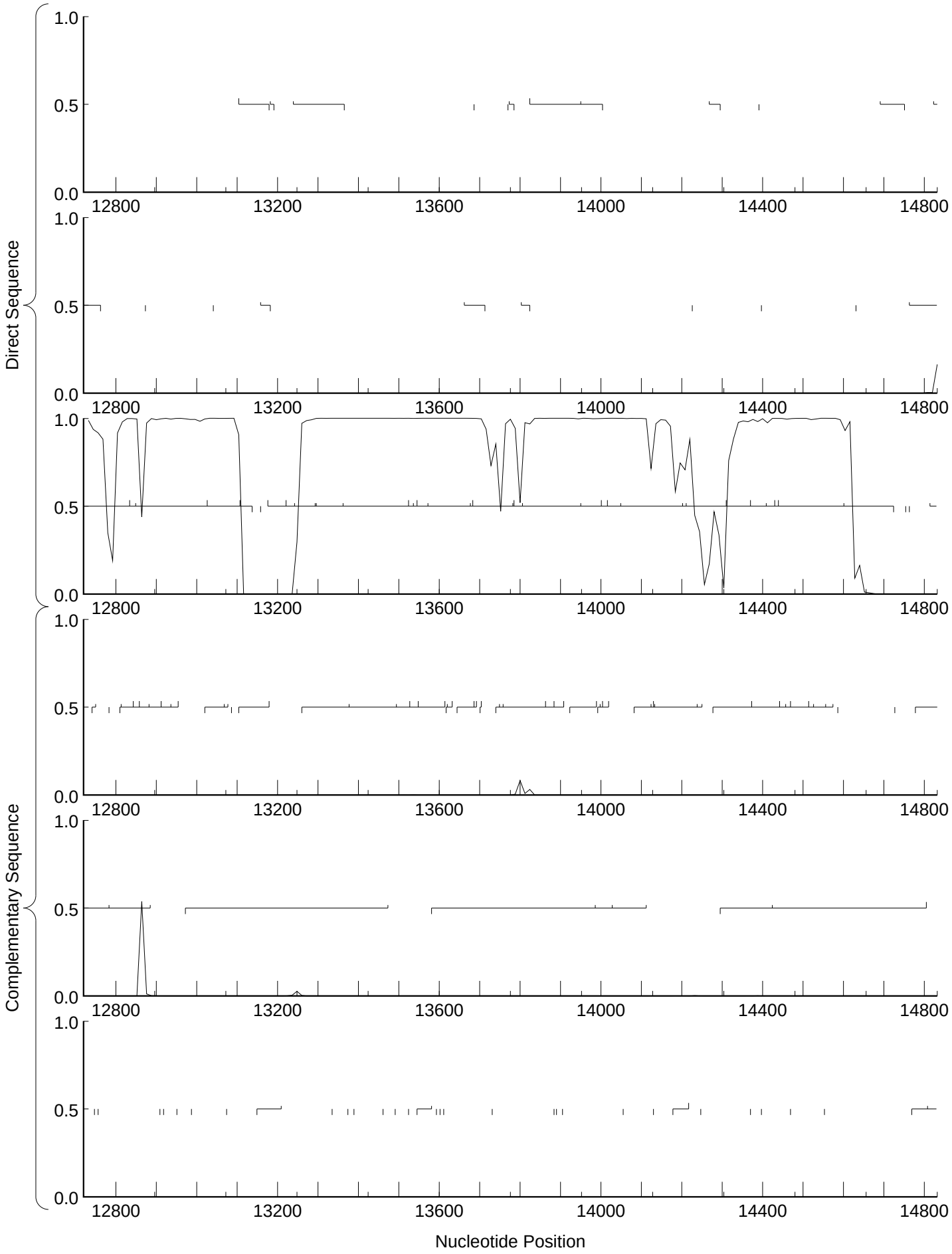
n phage Hortus1 complete sequence, 63119 bp including 3159 bp terminal repeat, Cluster ED, Order 4, Window 96, Step 12, 4/31

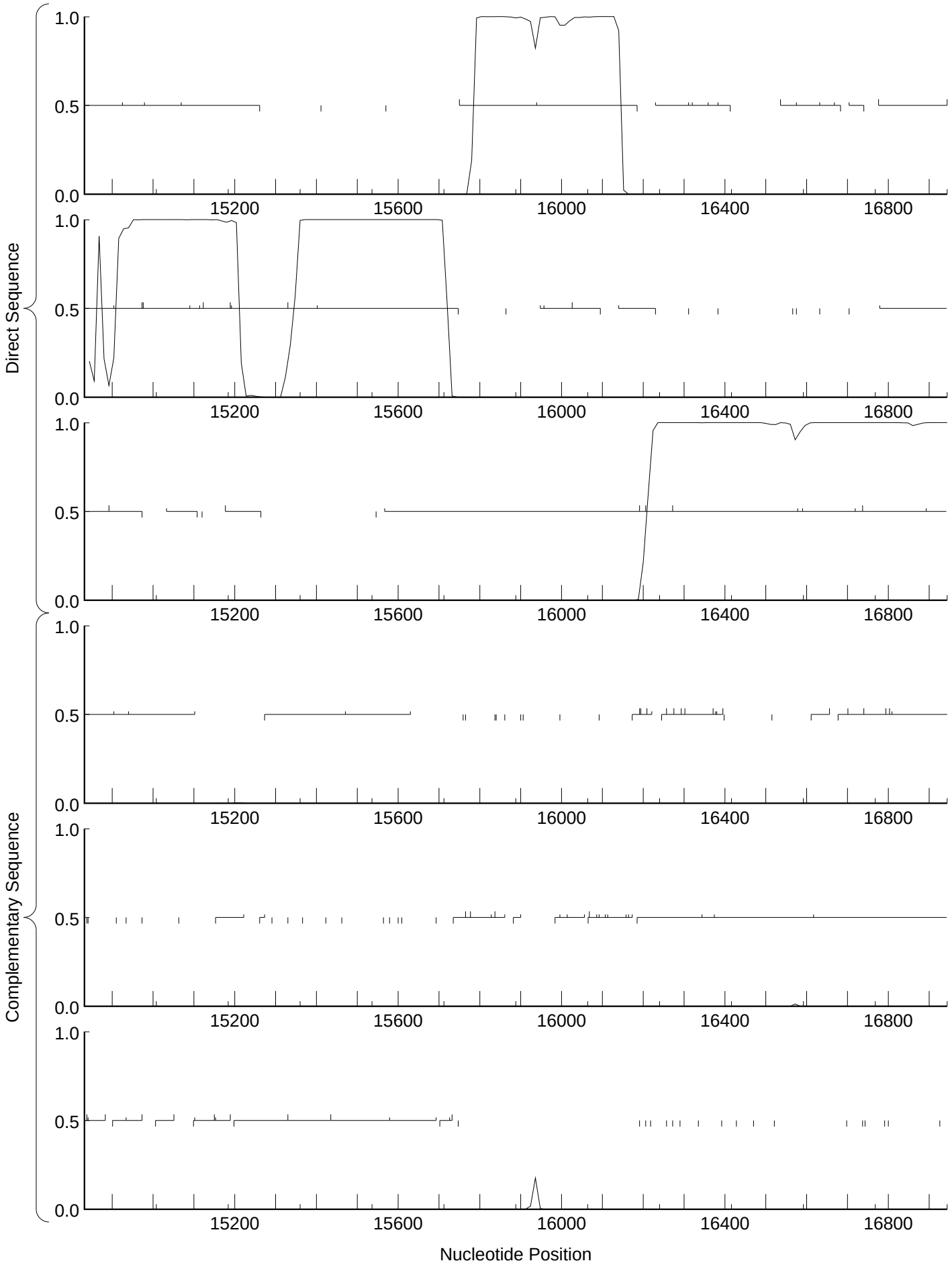



Direct Sequence
Complementary Sequence
1.0
0.5
0.0
6400
6800
7200
7600
8000
8400
Nucleotide Position

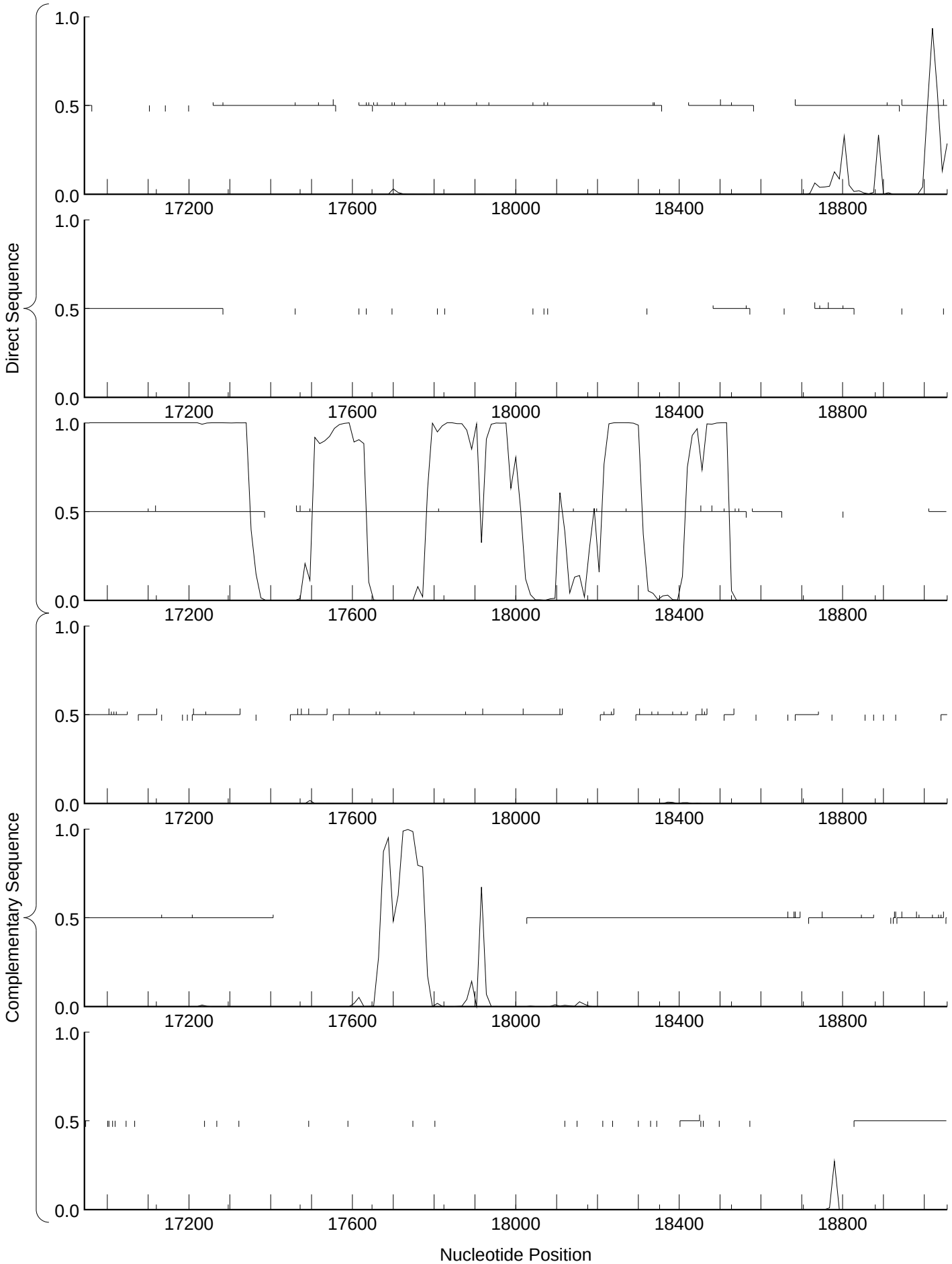

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
8800
9200
9600
10000
10400
Nucleotide Position


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
10800
11200
11600
12000
12400
Nucleotide Position

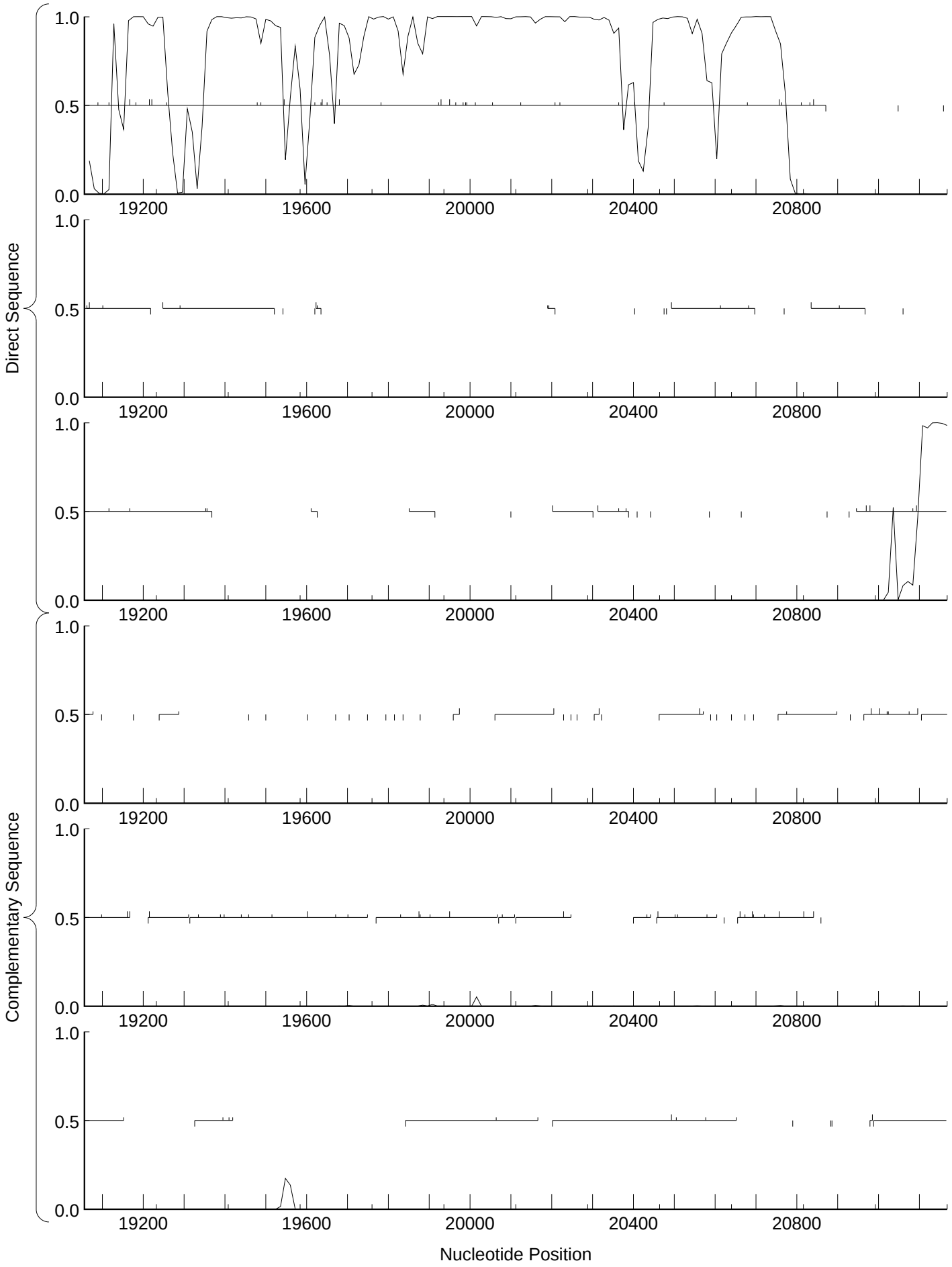

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
12800
13200
13600
14000
14400
14800
Nucleotide Position


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
15200
15600
16000
16400
16800
Nucleotide Position

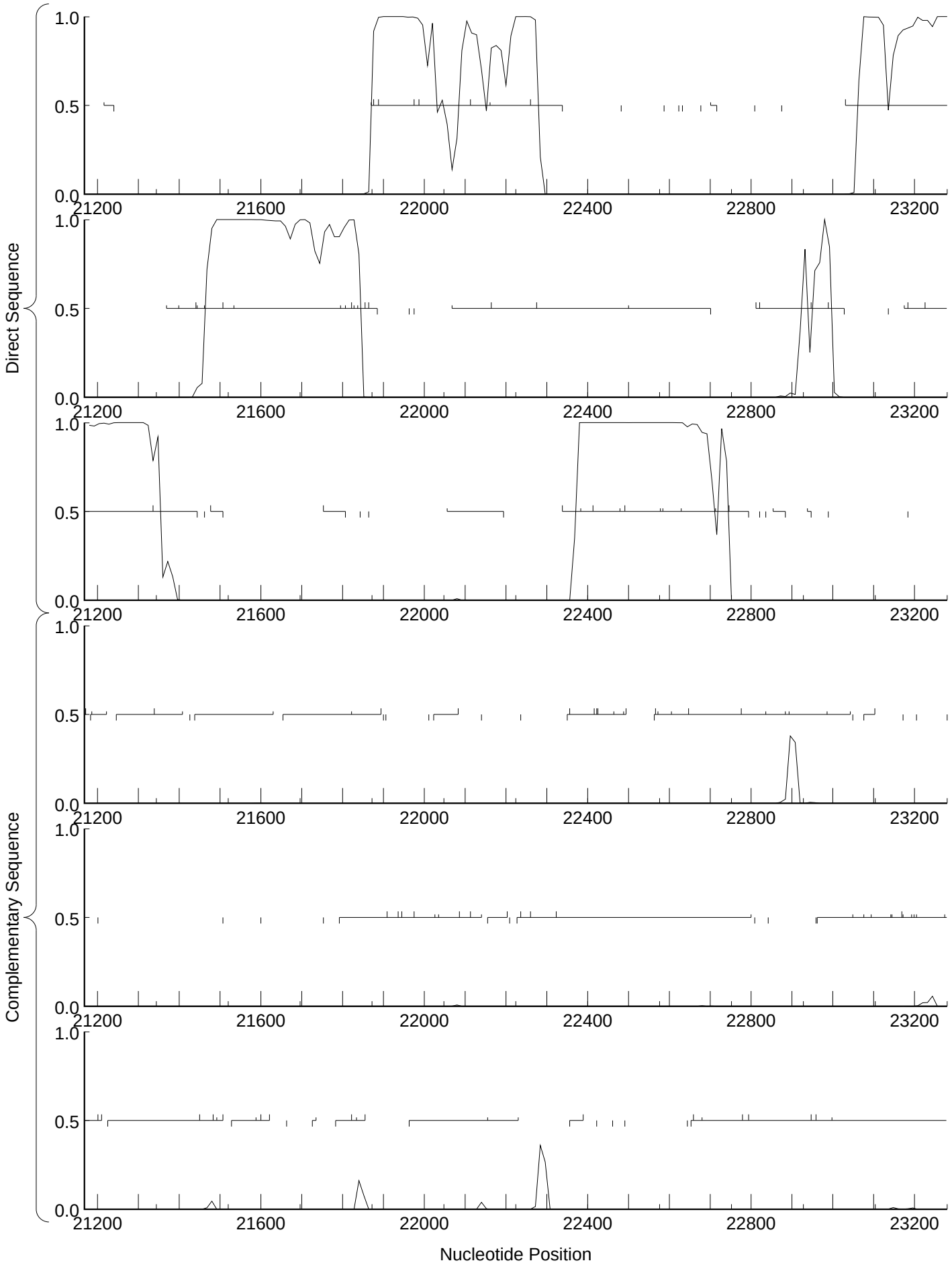
phage Hortus1 complete sequence, 63119 bp including 3159 bp terminal repeat, Cluster ED, Order 4, Window 96, Step 12, 10/31



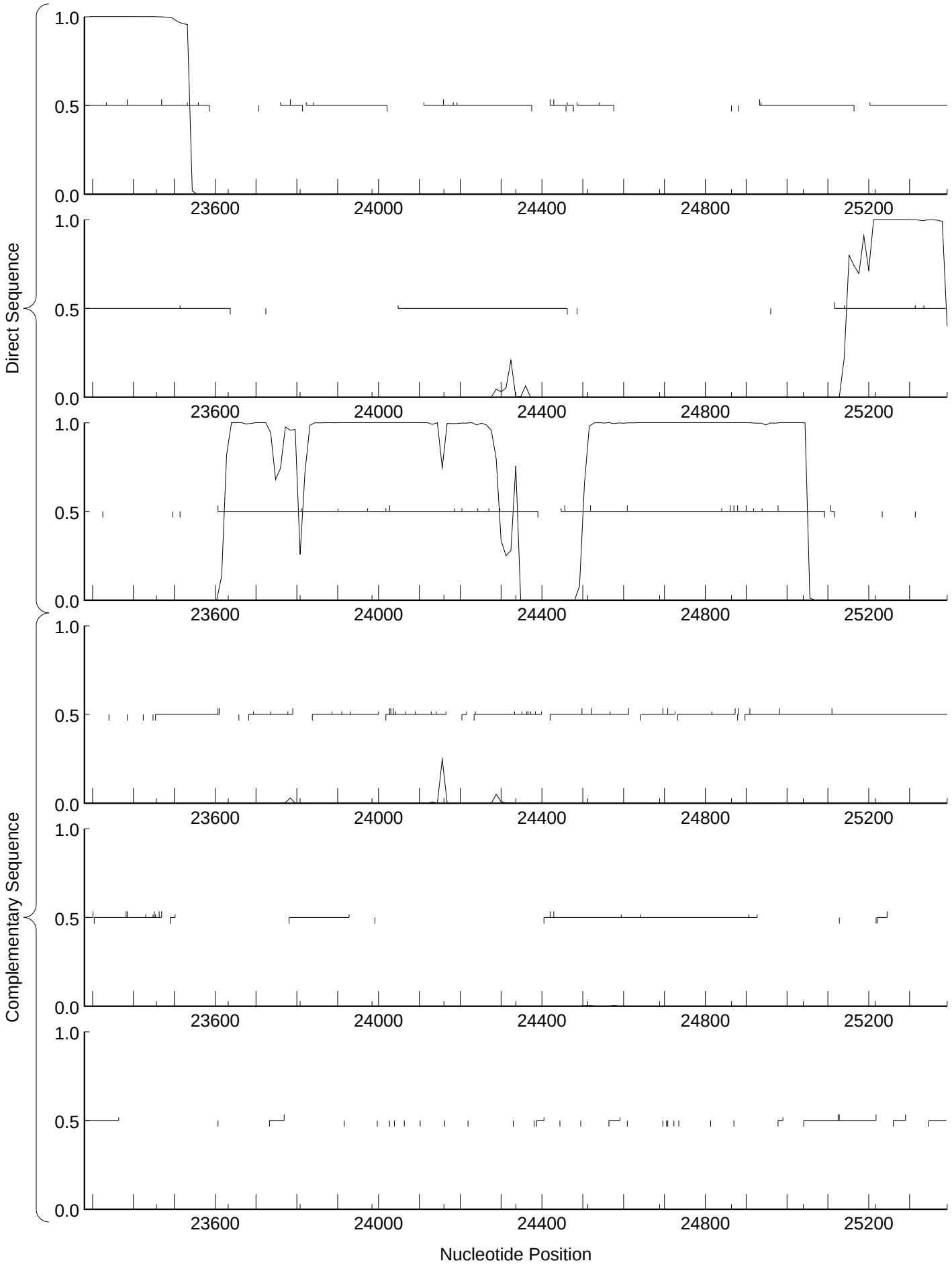
phage Hortus1 complete sequence, 63119 bp including 3159 bp terminal repeat, Cluster ED, Order 4, Window 96, Step 12, 11/31

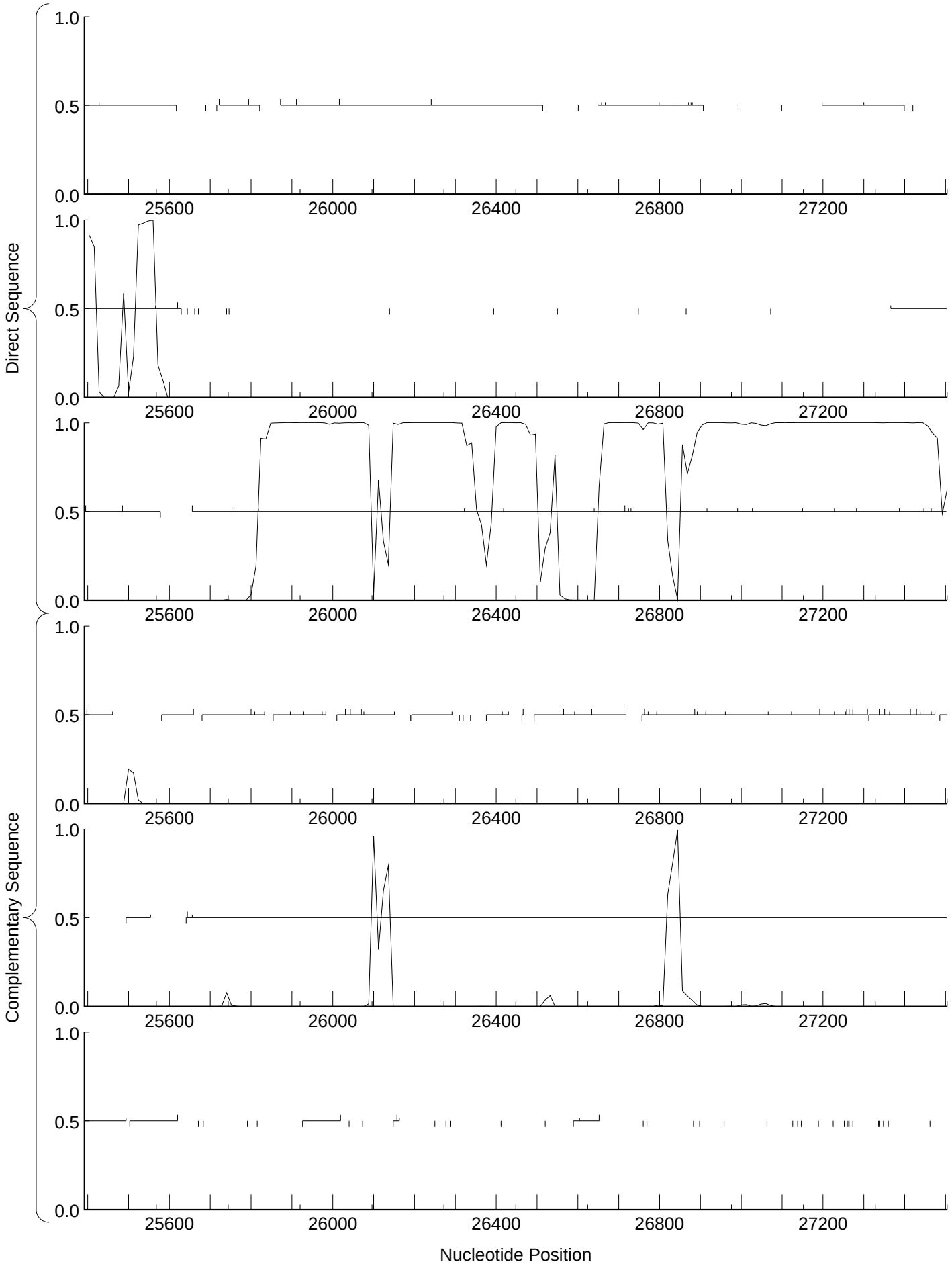


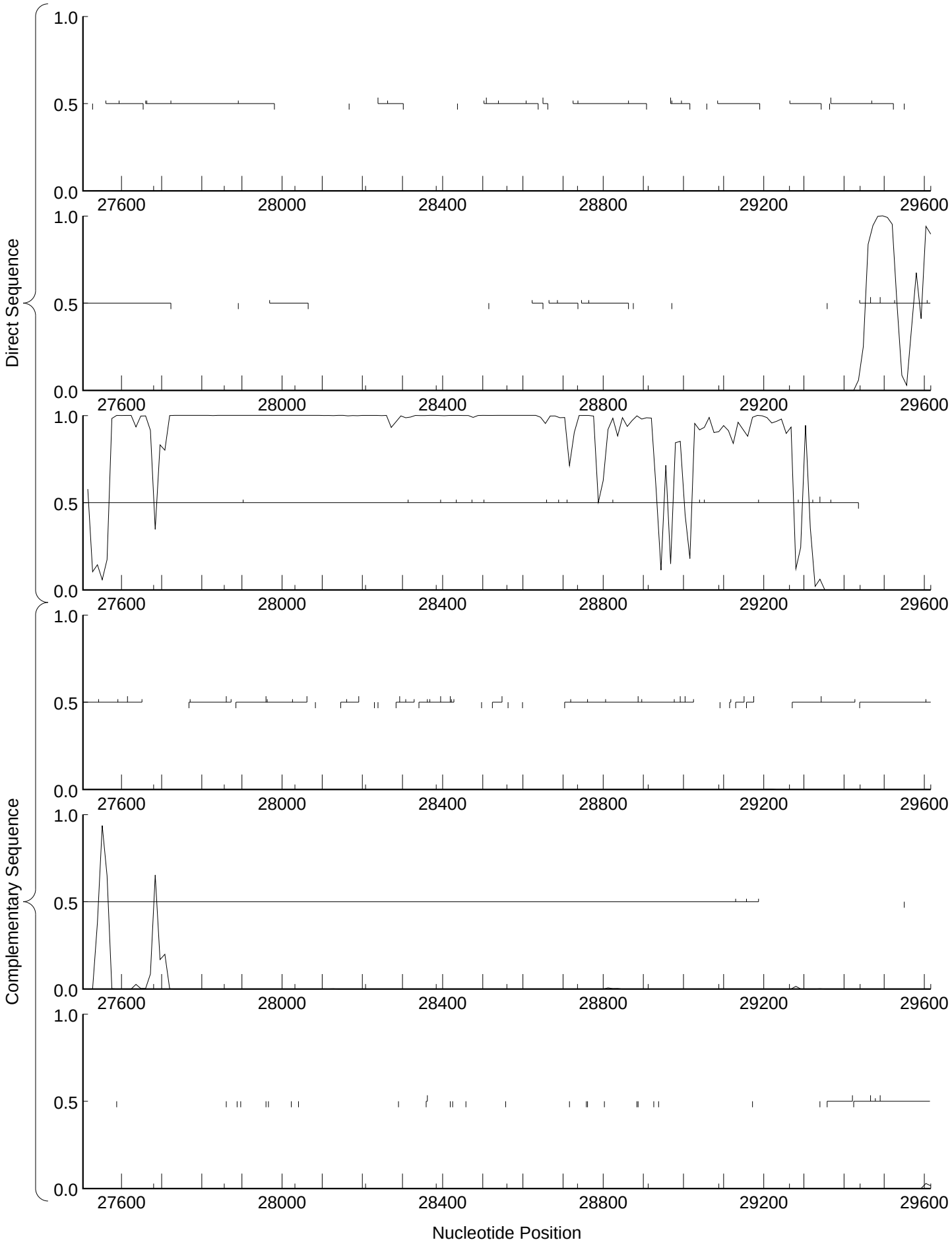
phage Hortus1 complete sequence, 63119 bp including 3159 bp terminal repeat, Cluster ED, Order 4, Window 96, Step 12, 12/31

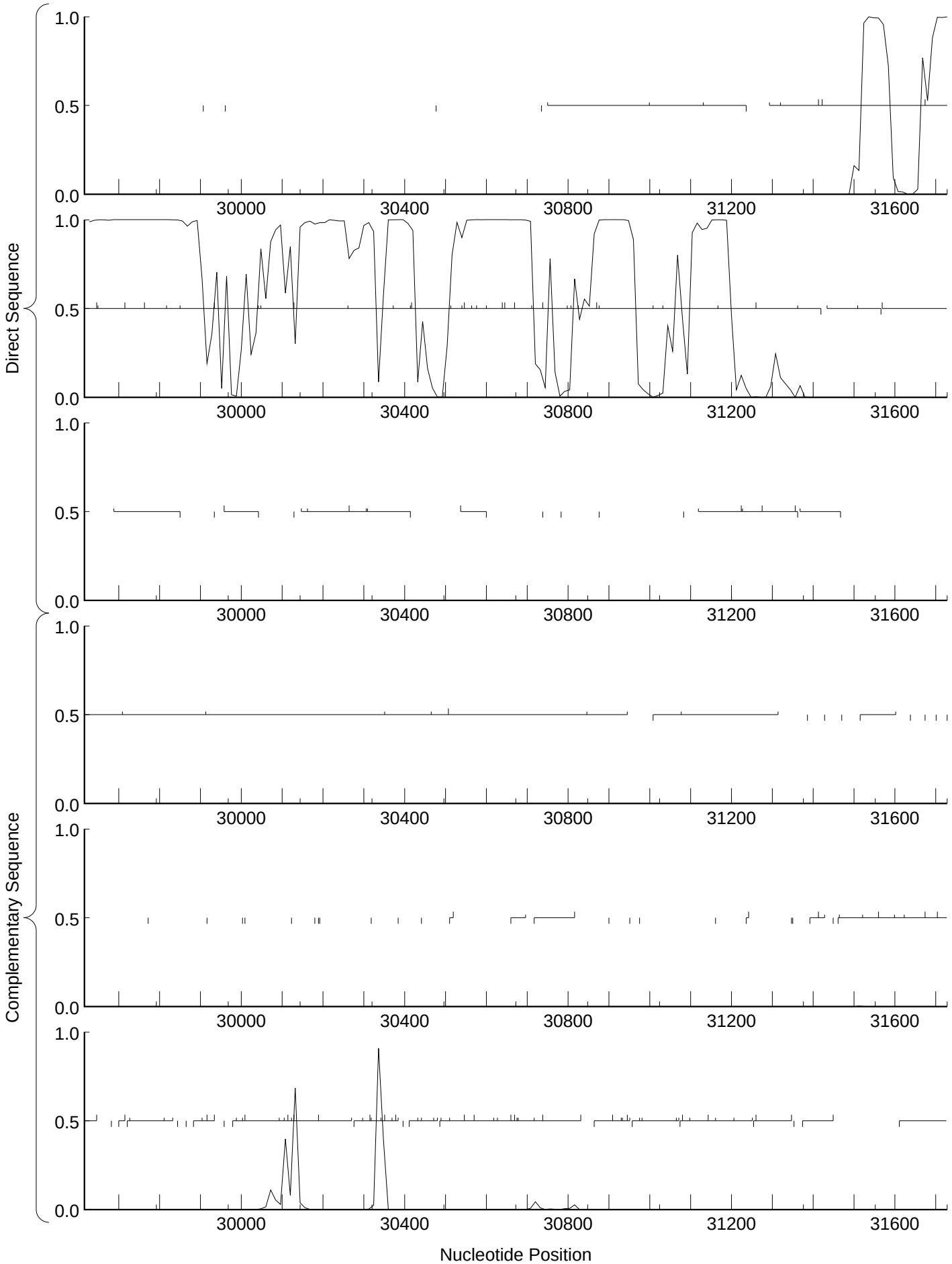


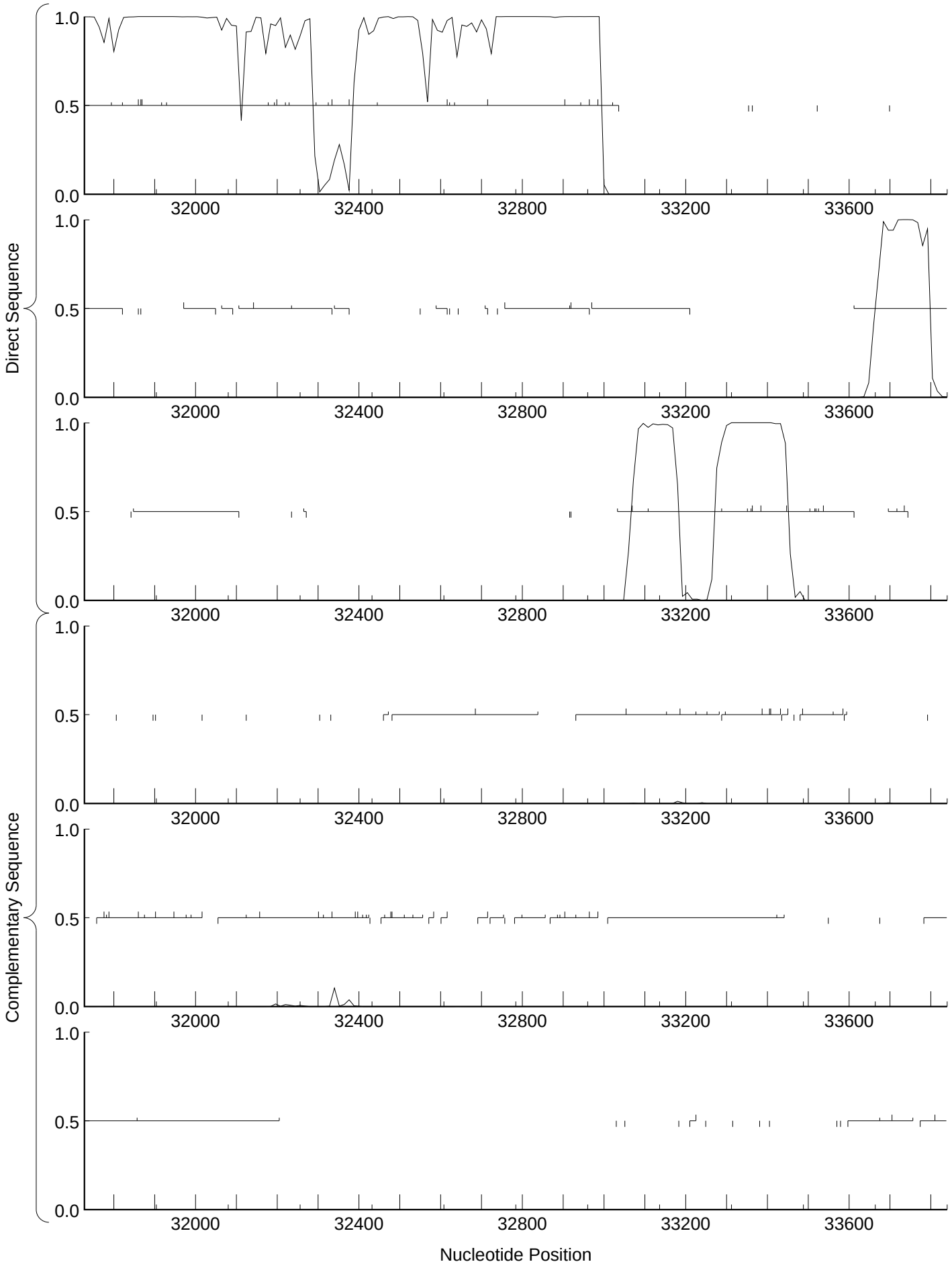
phage Hortus1 complete sequence, 63119 bp including 3159 bp terminal repeat, Cluster ED, Order 4, Window 96, Step 12, 13/31

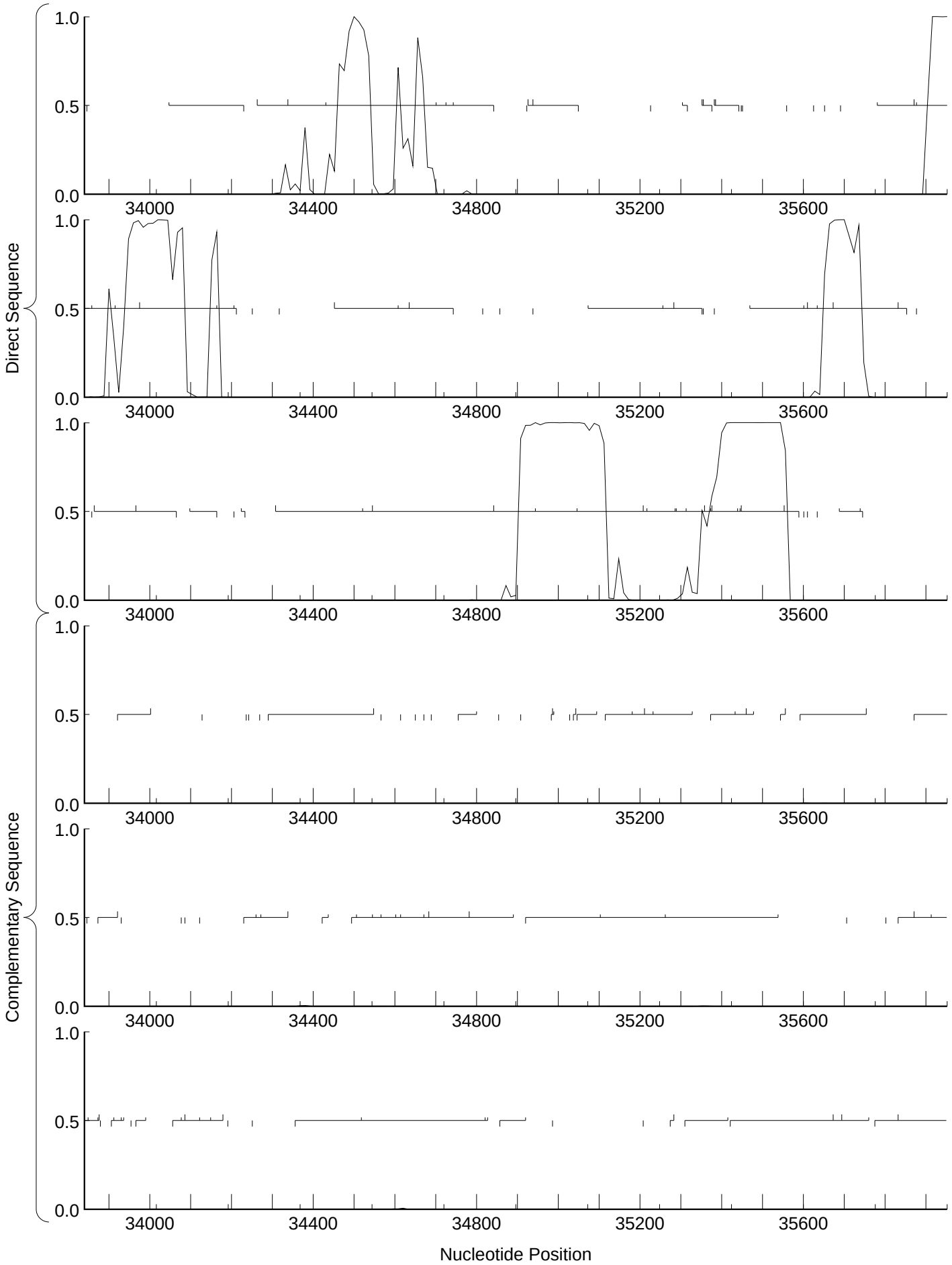


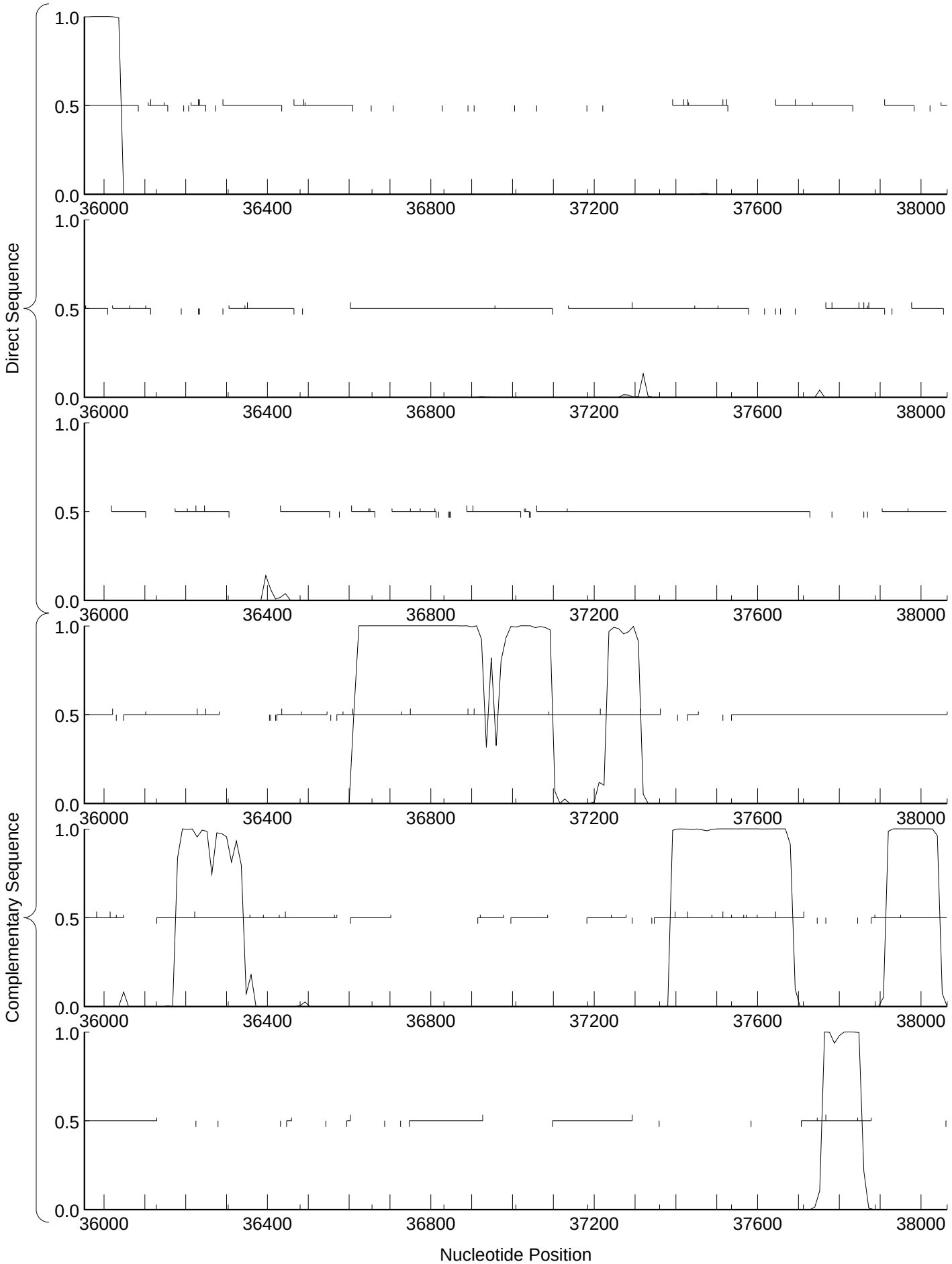

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
25600
26000
26400
26800
27200
Nucleotide Position

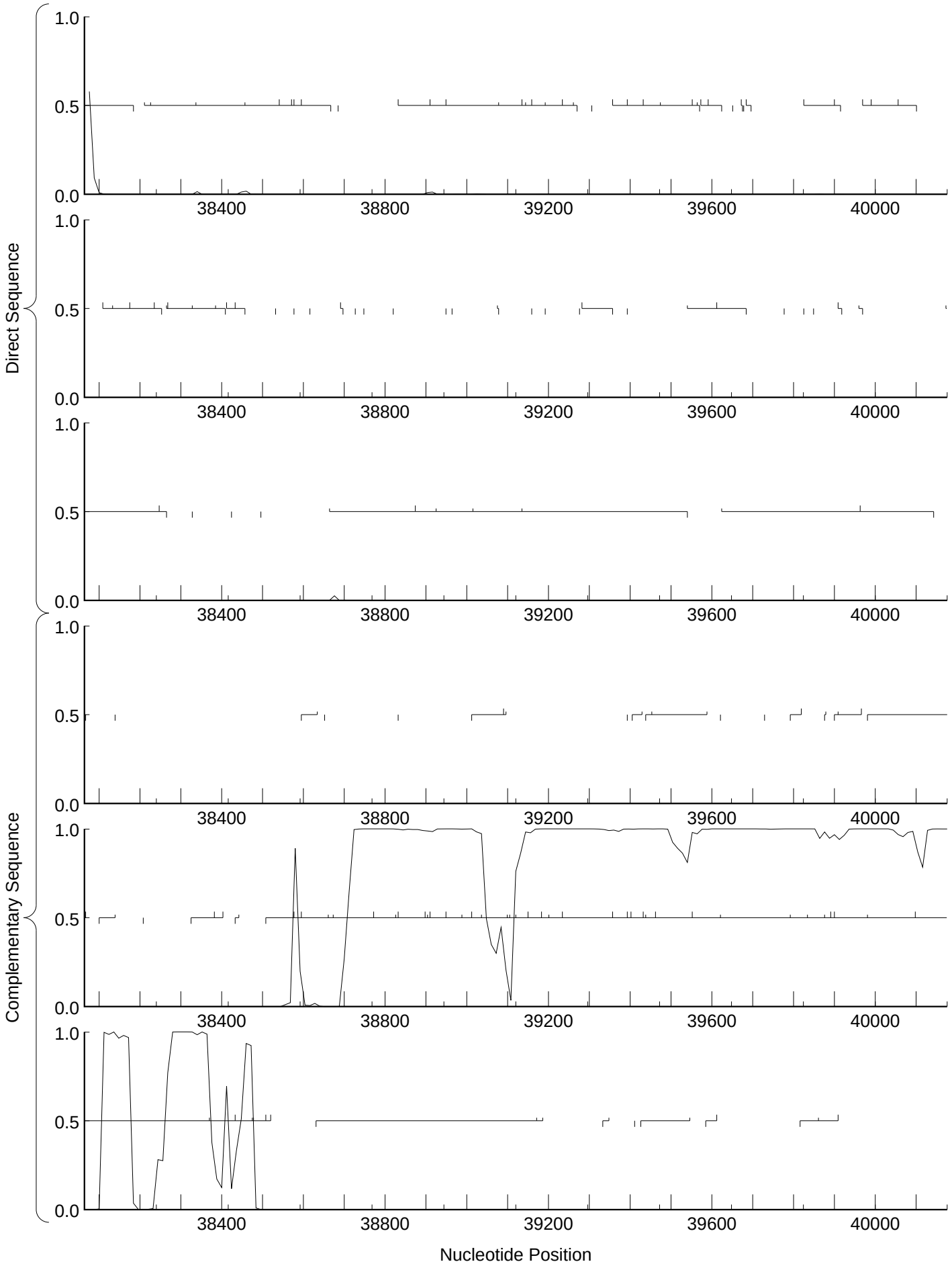

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
27600
28000
28400
28800
29200
29600
Nucleotide Position


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

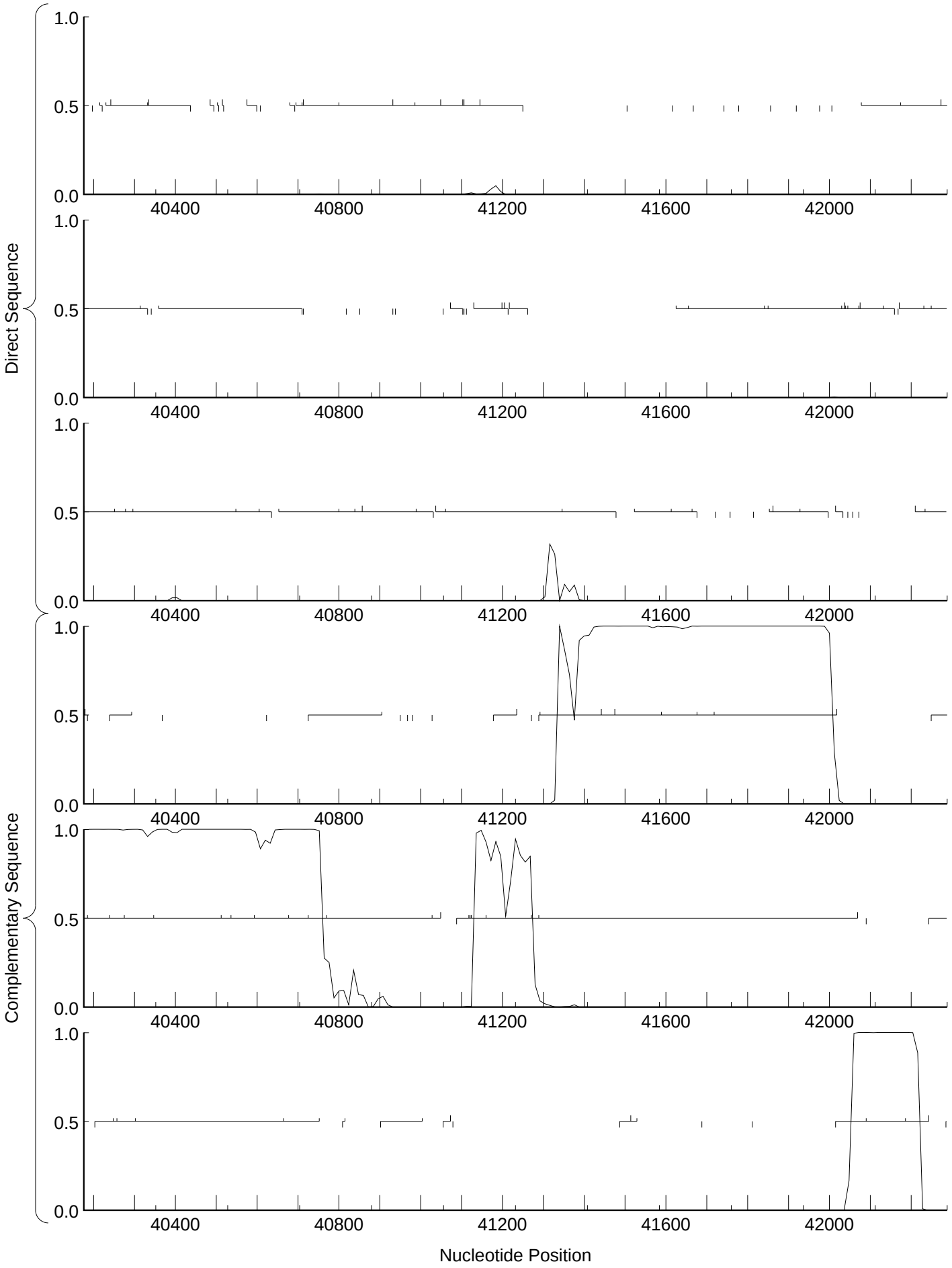

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
32000
32400
32800
33200
33600
Nucleotide Position

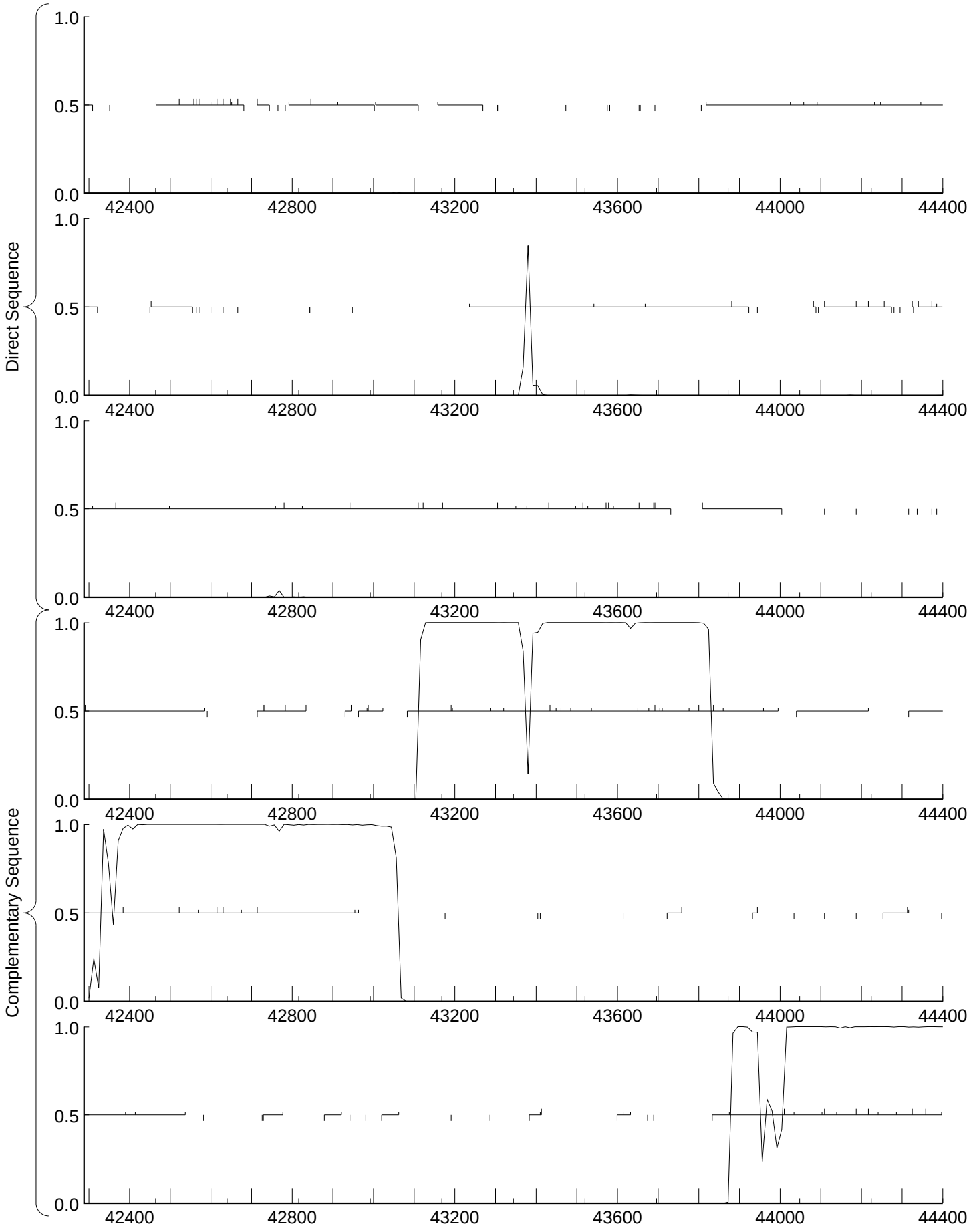

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
34000
34400
34800
35200
35600
Nucleotide Position

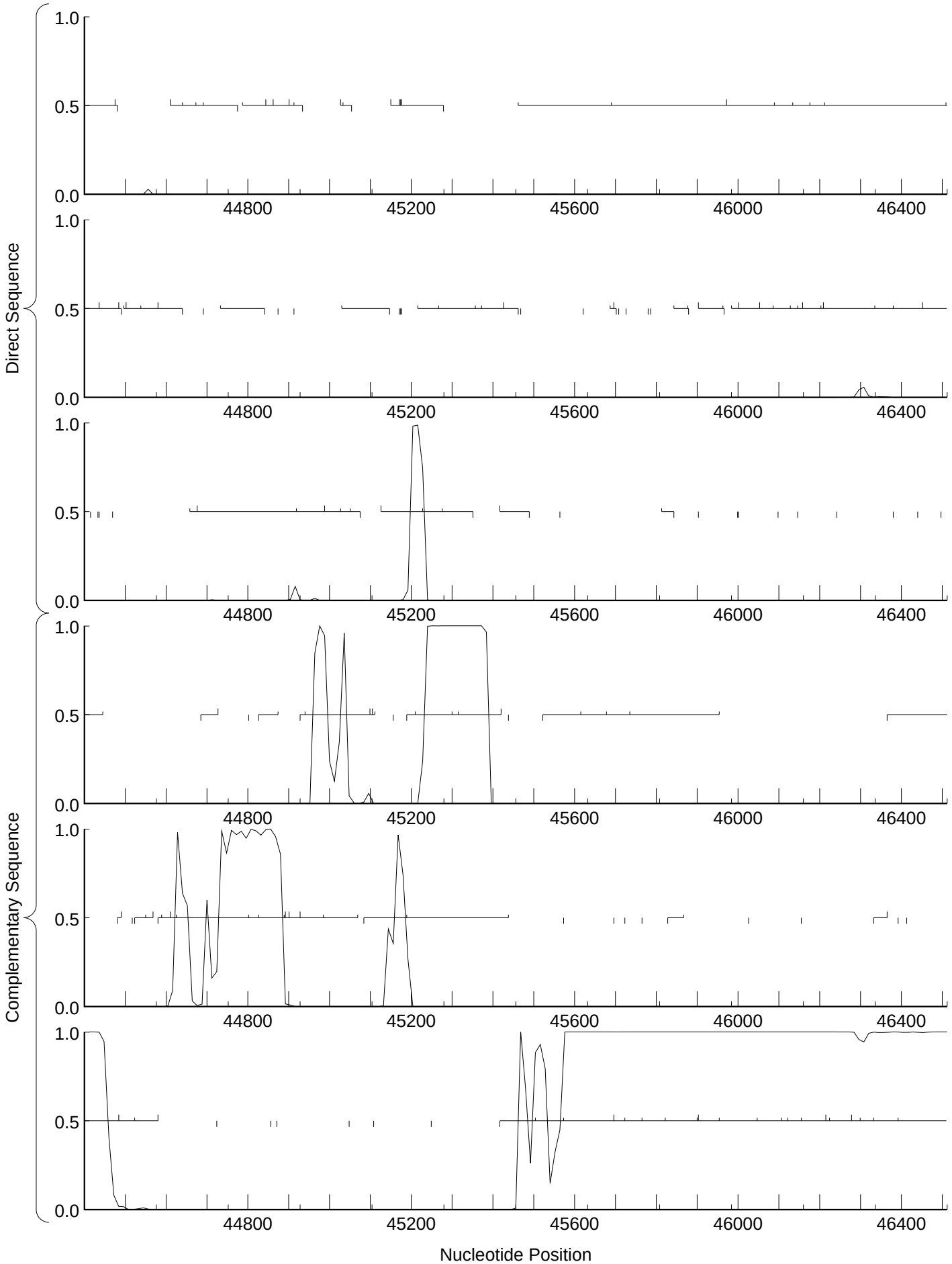

Direct Sequence
Complementary Sequence
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0.5
0.0
36000
36400
36800
37200
37600
38000
Nucleotide Position

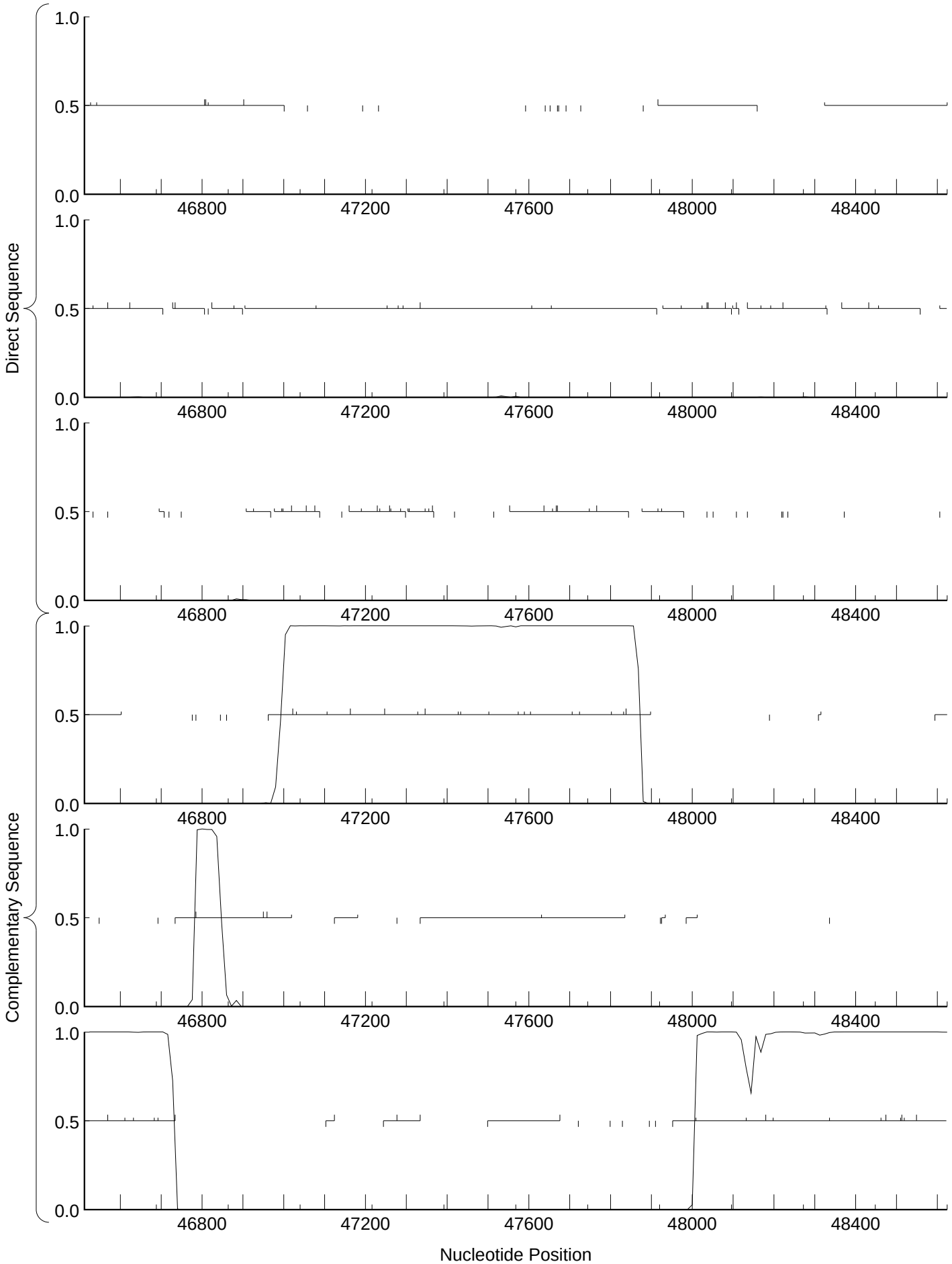

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
38400
38800
39200
39600
40000
Nucleotide Position

phage Hortus1 complete sequence, 63119 bp including 3159 bp terminal repeat, Cluster ED, Order 4, Window 96, Step 12, 21/31

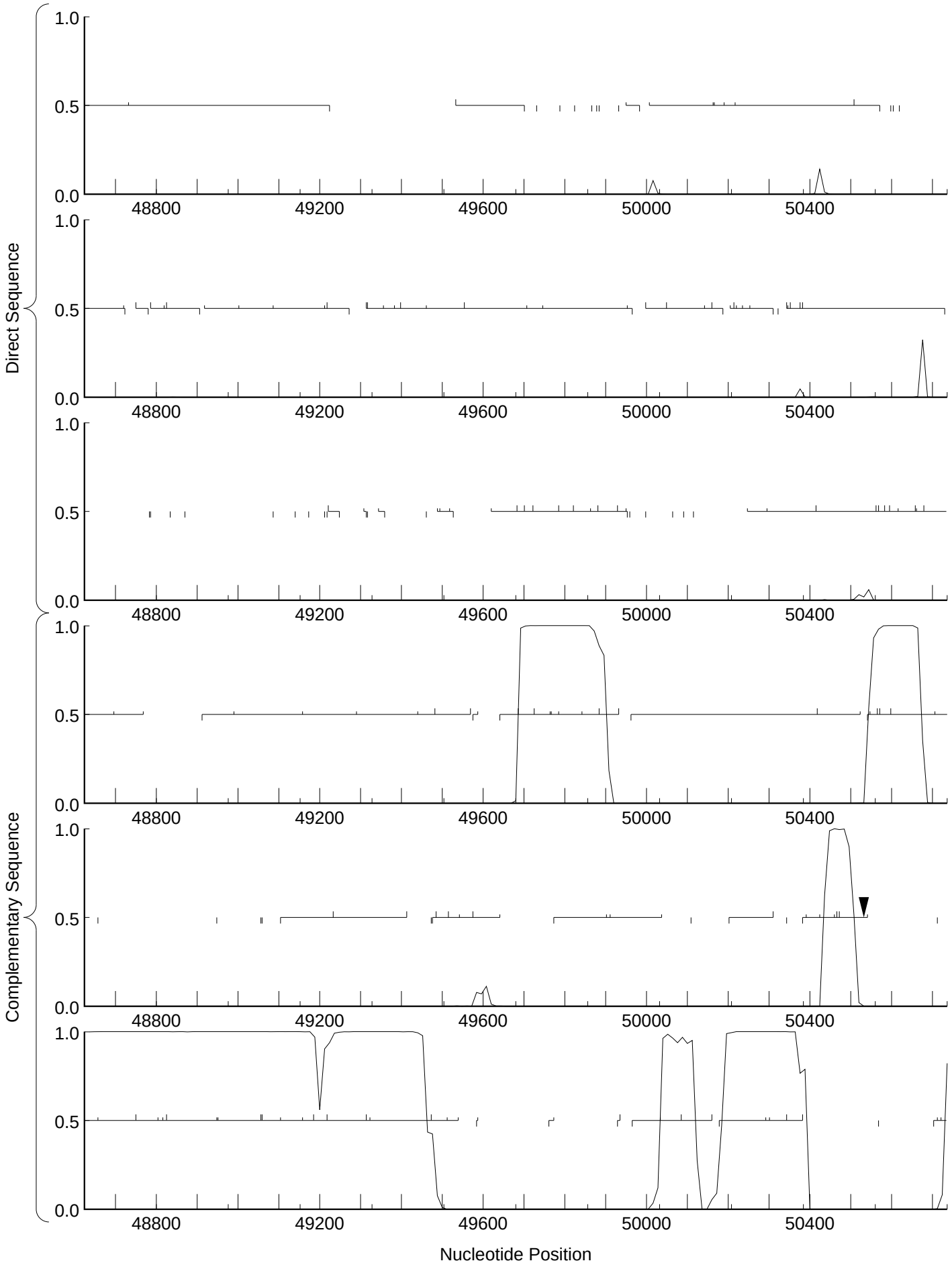


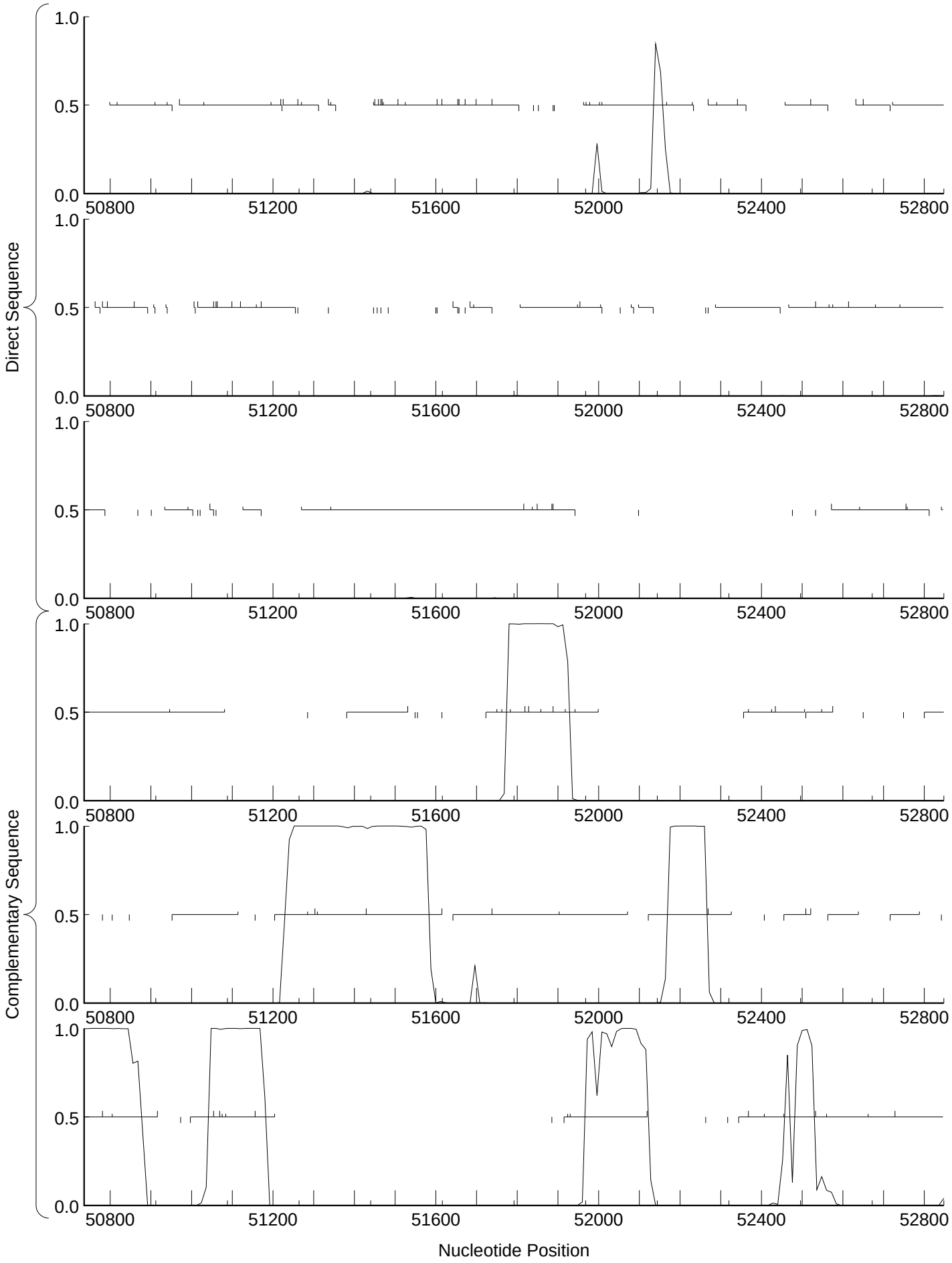

Direct Sequence
Complementary Sequence
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0.5
0.0
42400
42800
43200
43600
44000
44400
Nucleotide Position

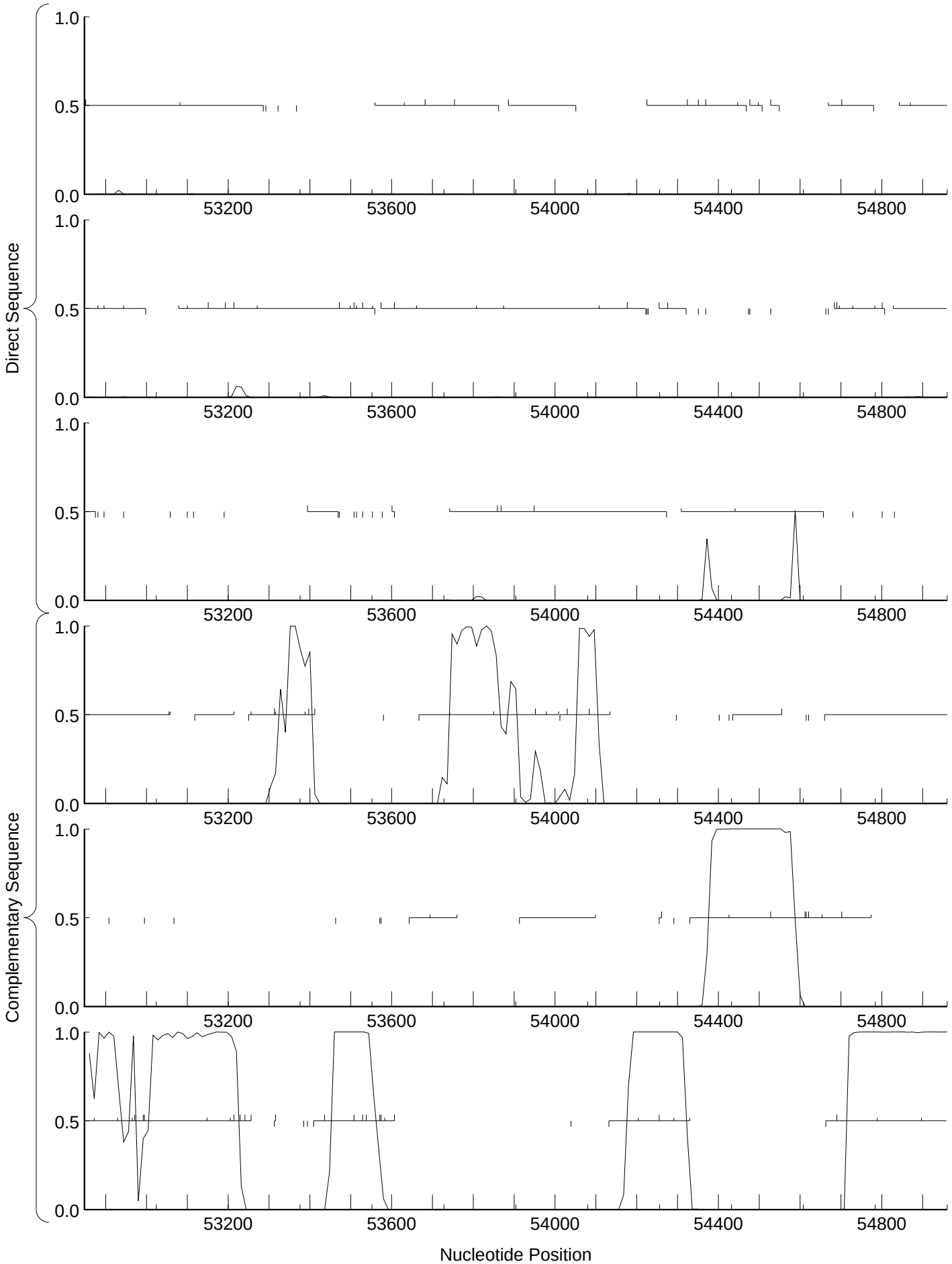

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
44800
45200
45600
46000
46400
Nucleotide Position

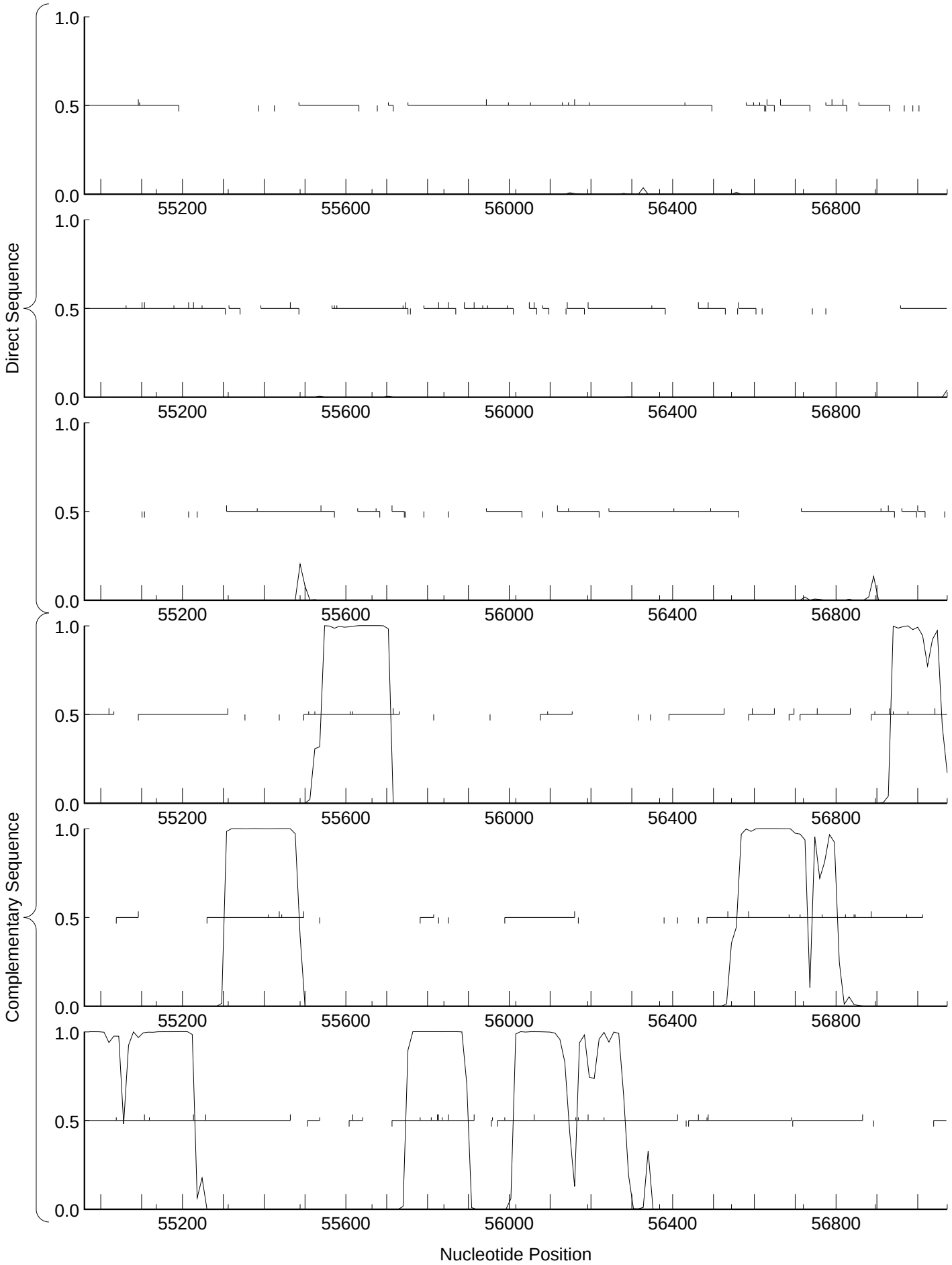

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
46800
47200
47600
48000
48400
Nucleotide Position

phage Hortus1 complete sequence, 63119 bp including 3159 bp terminal repeat, Cluster ED, Order 4, Window 96, Step 12, 25/31

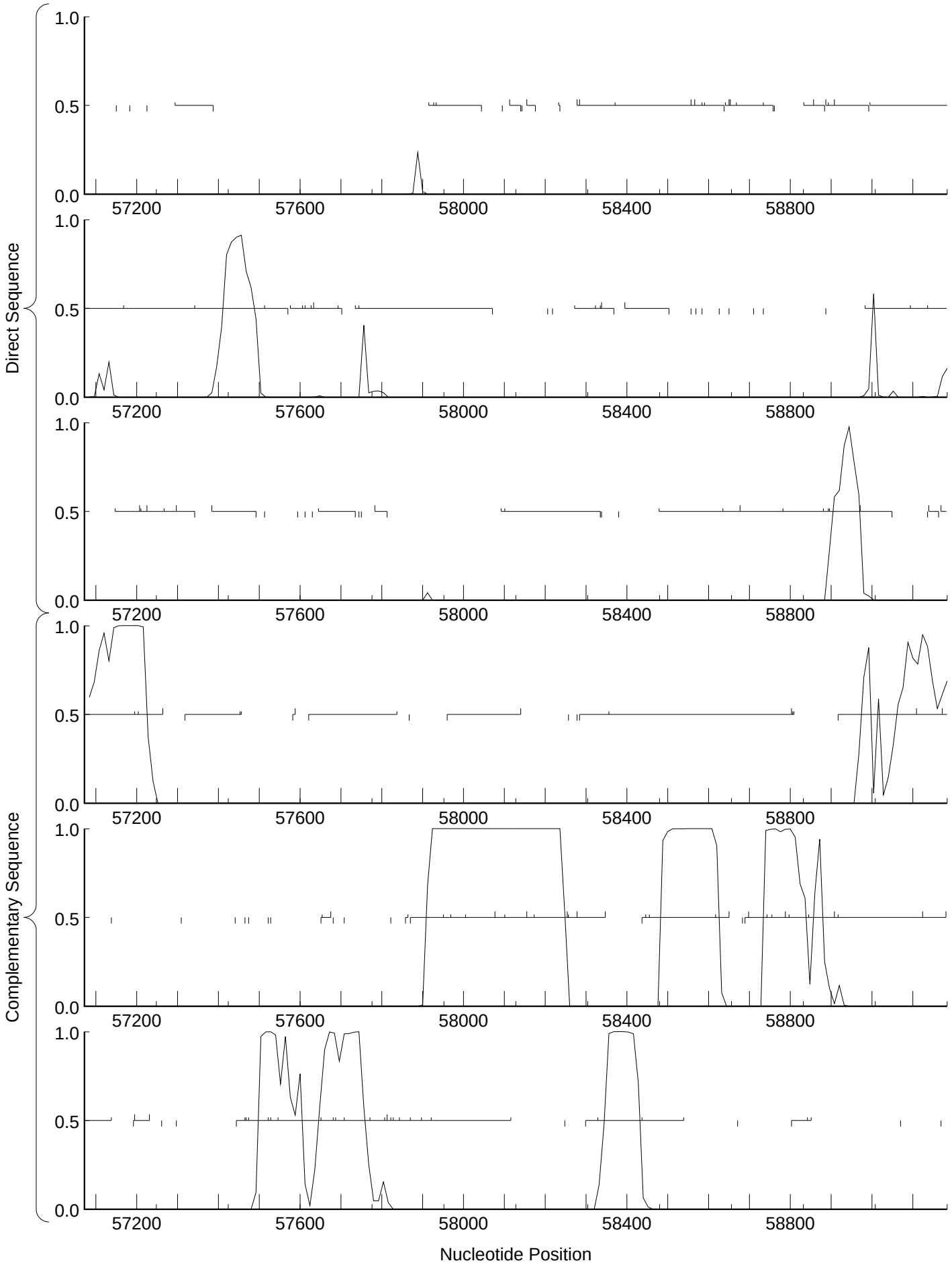



Direct Sequence
Complementary Sequence
1.0
0.5
0.0
50800
51200
51600
52000
52400
52800
Nucleotide Position

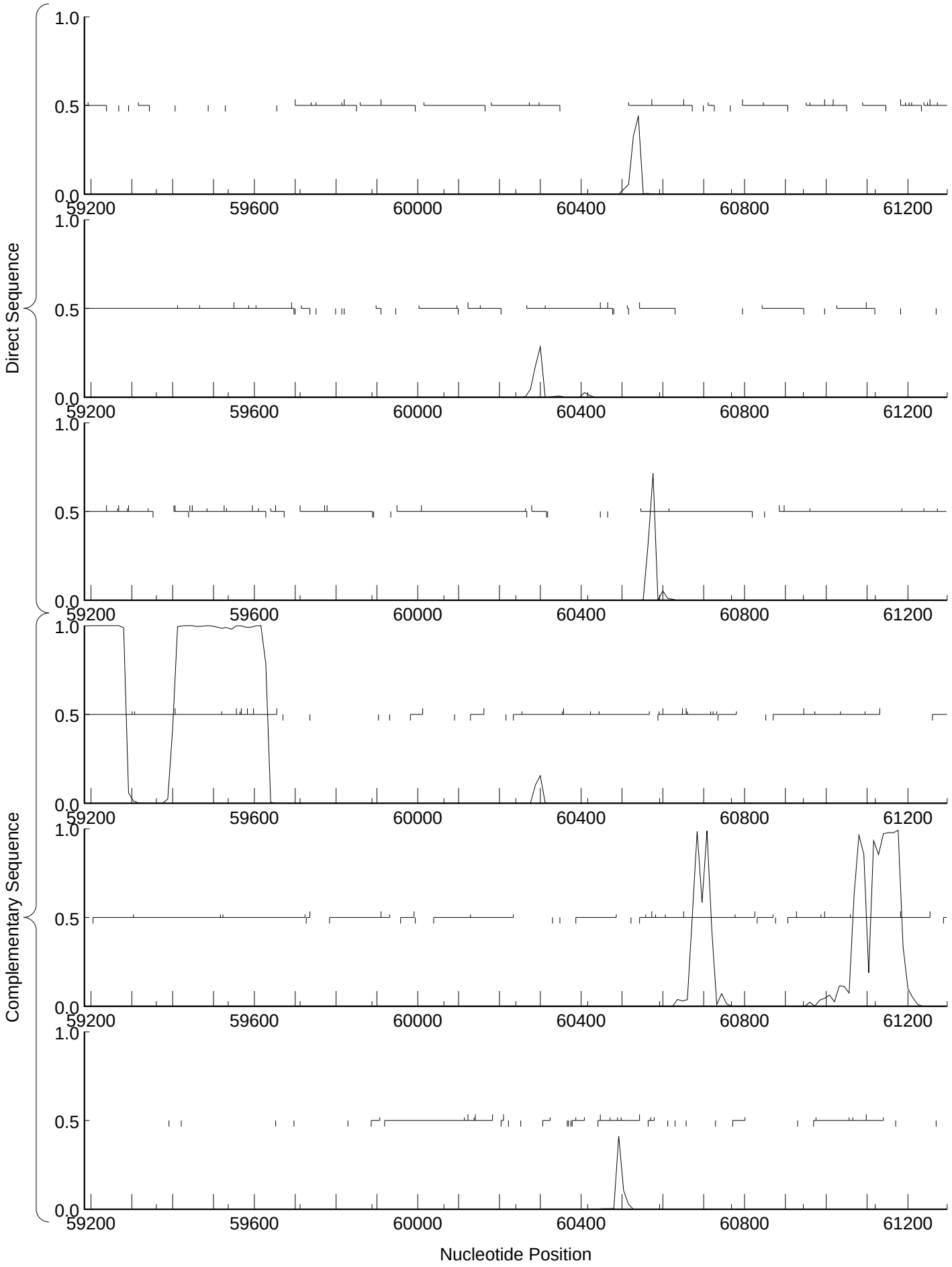

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
53200
53600
54000
54400
54800
Nucleotide Position


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

phage Hortus1 complete sequence, 63119 bp including 3159 bp terminal repeat, Cluster ED, Order 4, Window 96, Step 12, 29/31



phage Hortus1 complete sequence, 63119 bp including 3159 bp terminal repeat, Cluster ED, Order 4, Window 96, Step 12, 30/31



phage Hortus1 complete sequence, 63119 bp including 3159 bp terminal repeat, Cluster ED, Order 4, Window 96, Step 12, 31/31

