GeneMark

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

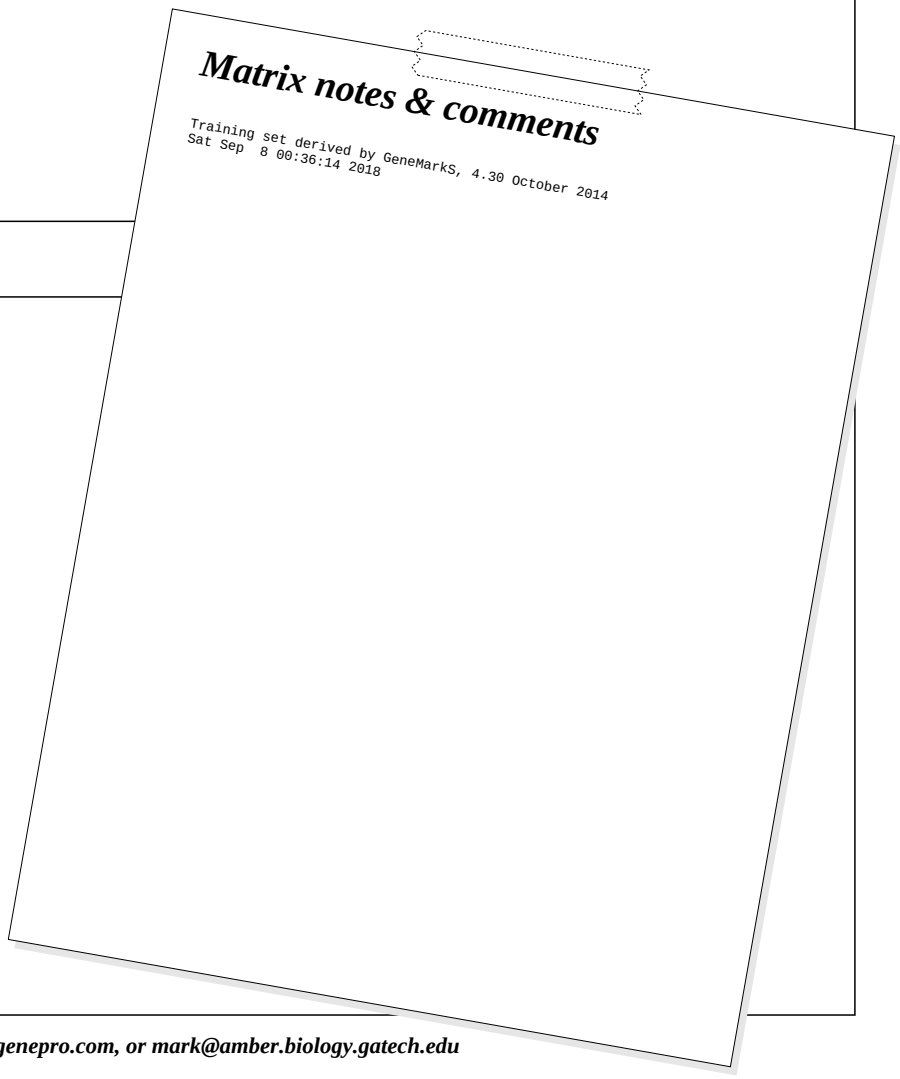
PROGRAM INFORMATION

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Sequence         :  Gordonia phage Harambe complete sequence, 73511 bp including 184 bp terminal repeat, Cluste
Analysis Date    :  3/29/24 at 7:56:01
Pages            :  36
Sequence Length  :  73511 bp
GC Content       :   59.17%

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

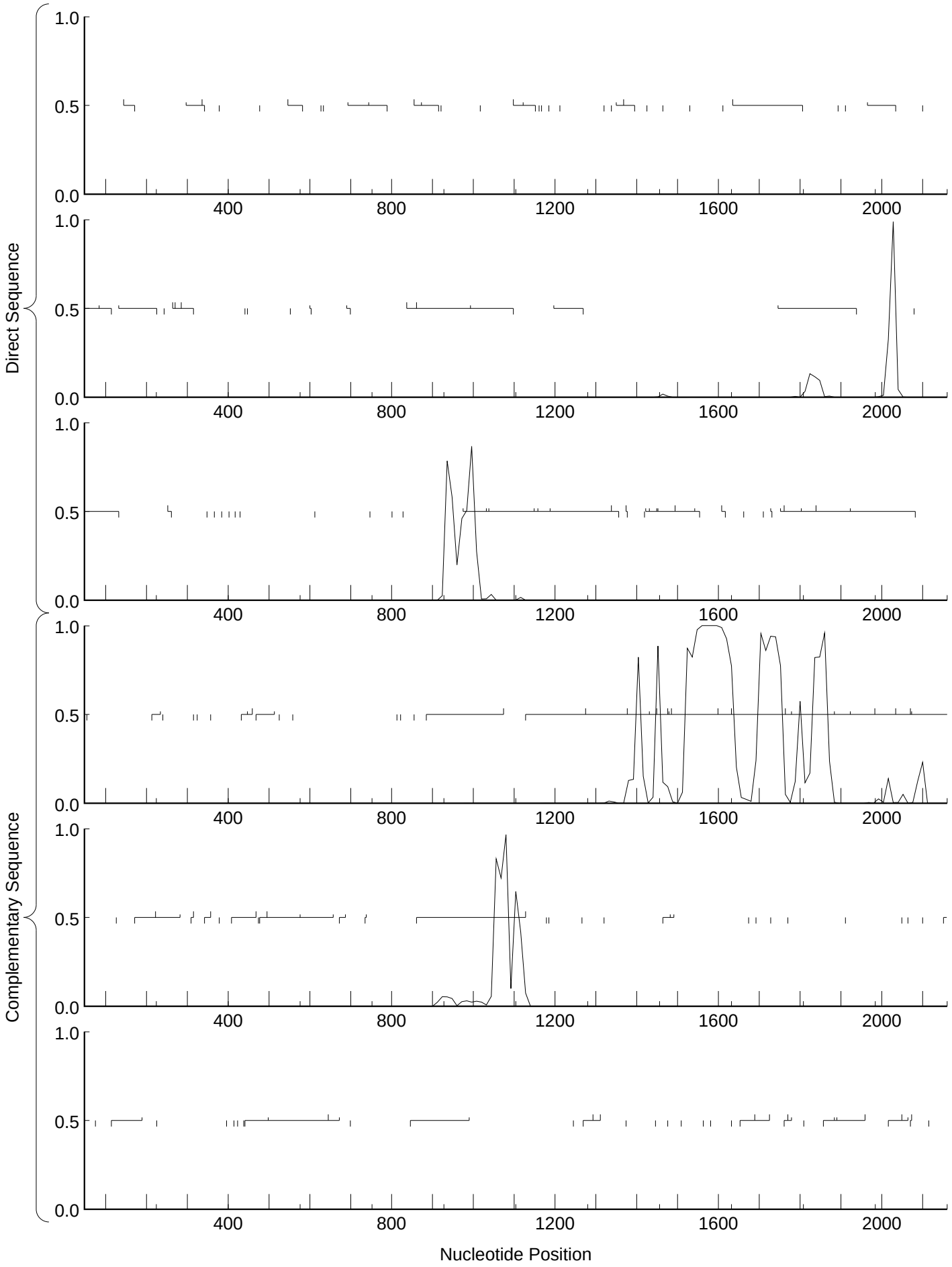
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Matrix     :  -
Author     :  -

Order      :  4
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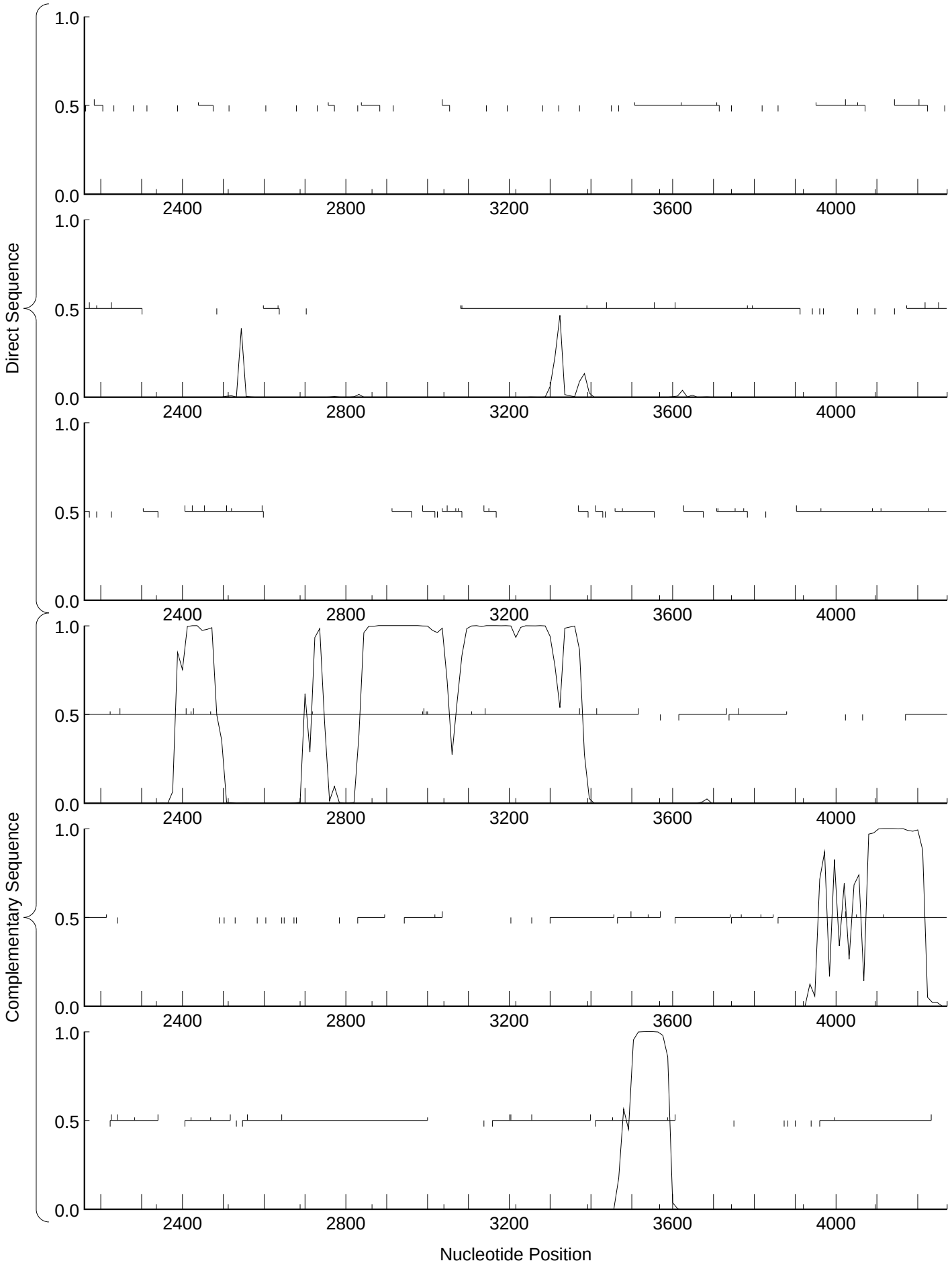

```
  Send questions / comments to:
      Dr. M. Borodovsky
      Georgia Institute of Technology
      School of Biology
      Atlanta, GA  30332-0230
```


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

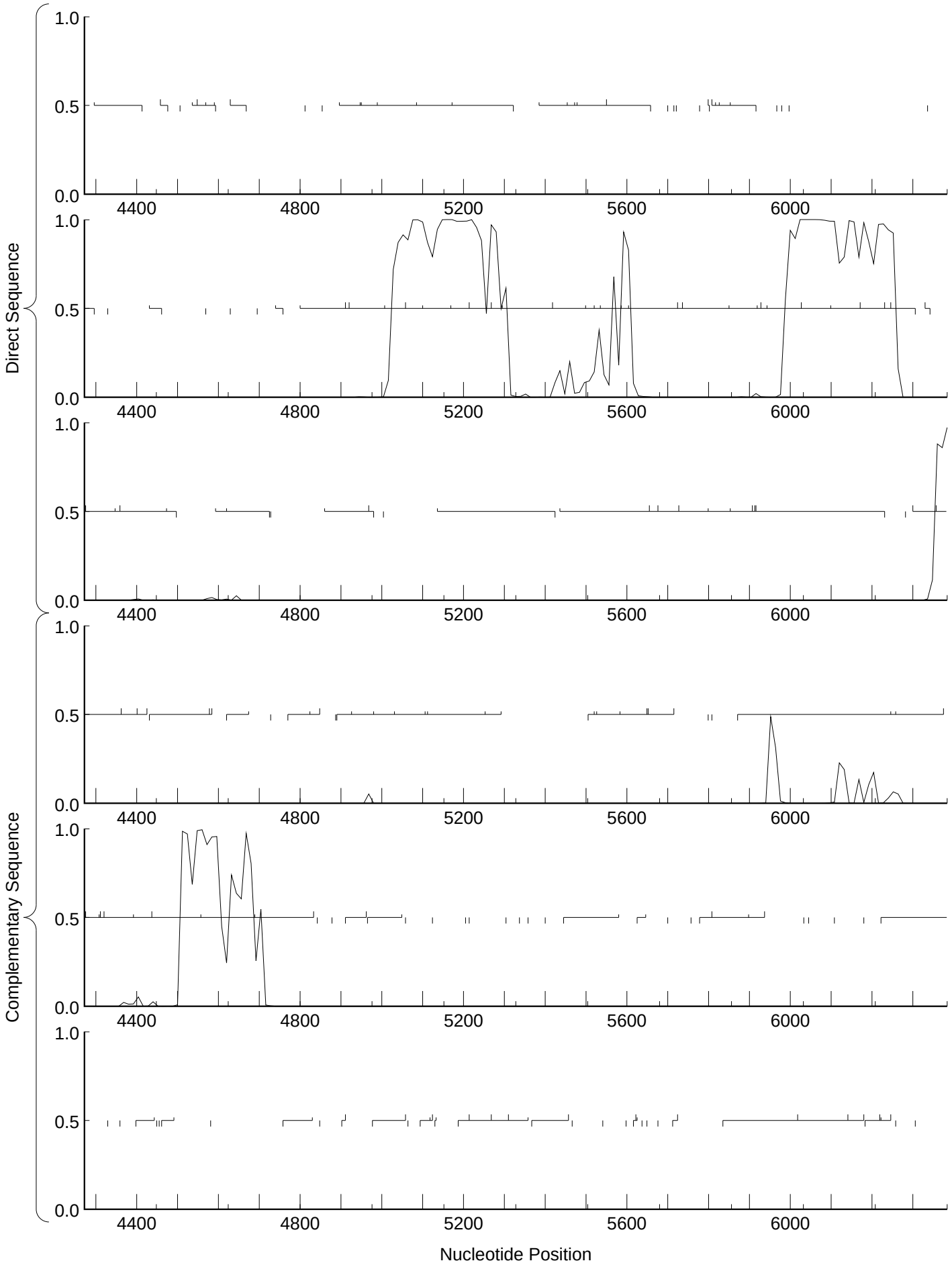
a phage Harambe complete sequence, 73511 bp including 184 bp terminal repeat, Cluster CS, Order 4, Window 96, Step 12, 2/36



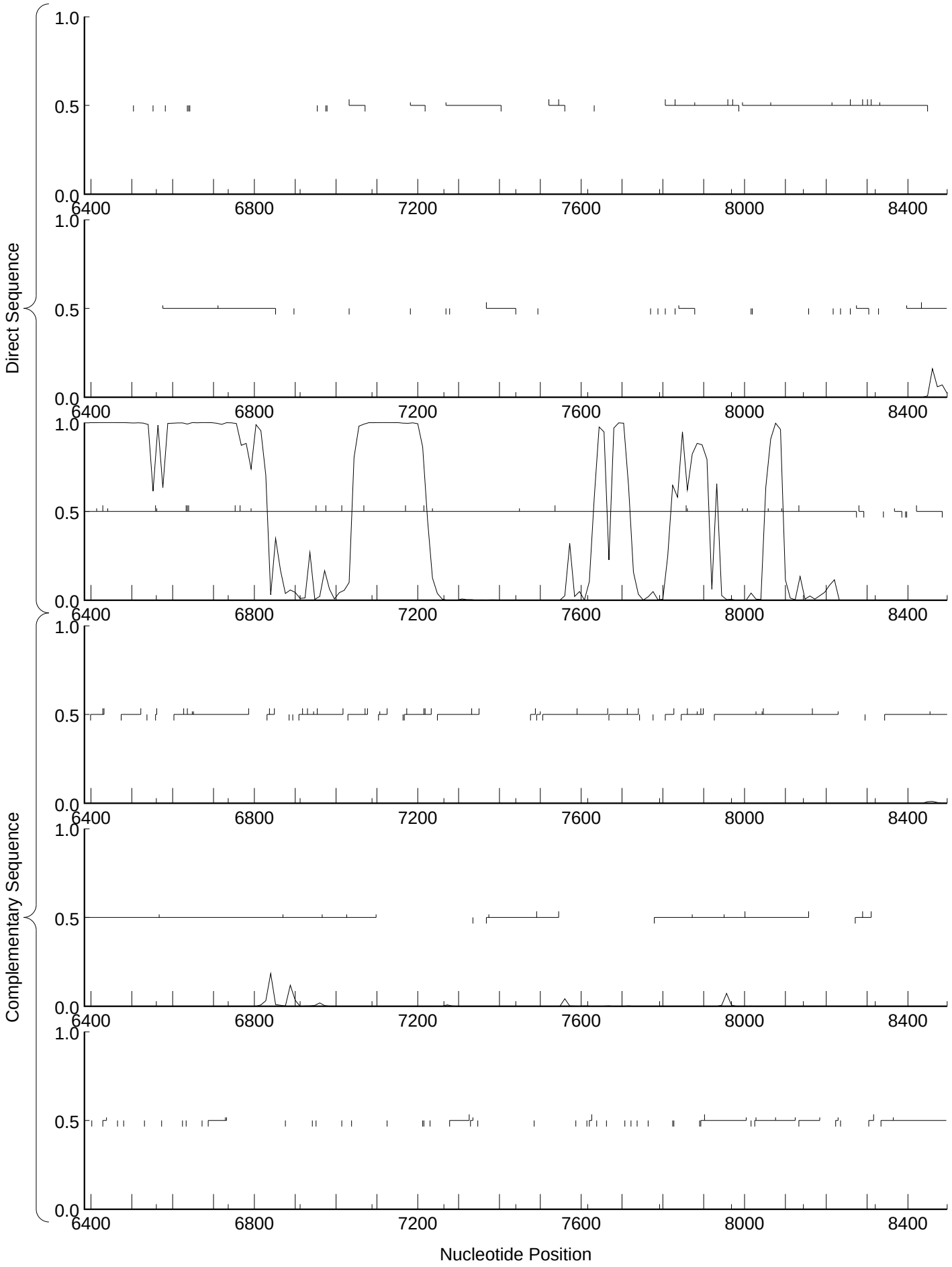
a phage Harambe complete sequence, 73511 bp including 184 bp terminal repeat, Cluster CS, Order 4, Window 96, Step 12, 3/36



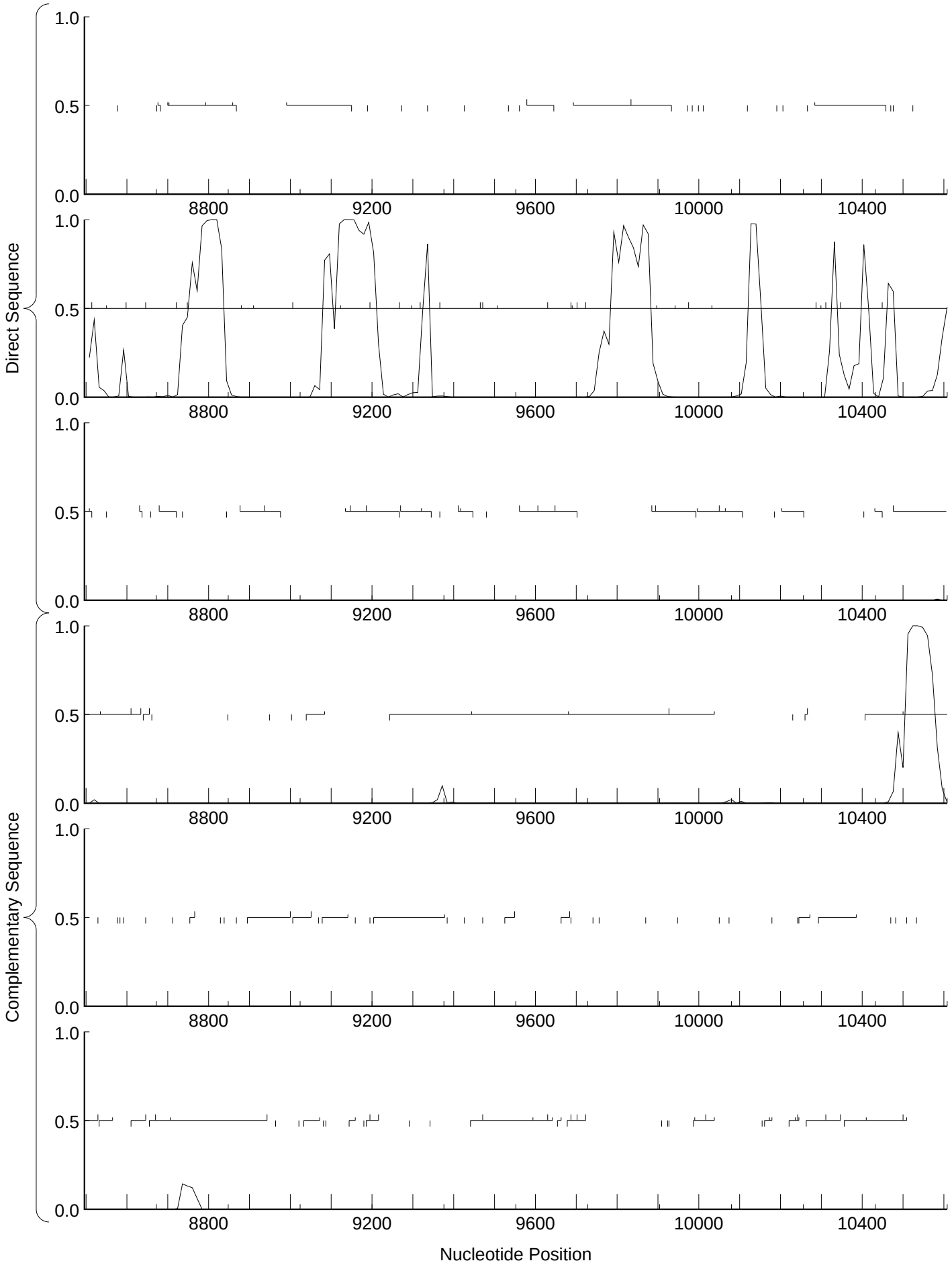
a phage Harambe complete sequence, 73511 bp including 184 bp terminal repeat, Cluster CS, Order 4, Window 96, Step 12, 4/36



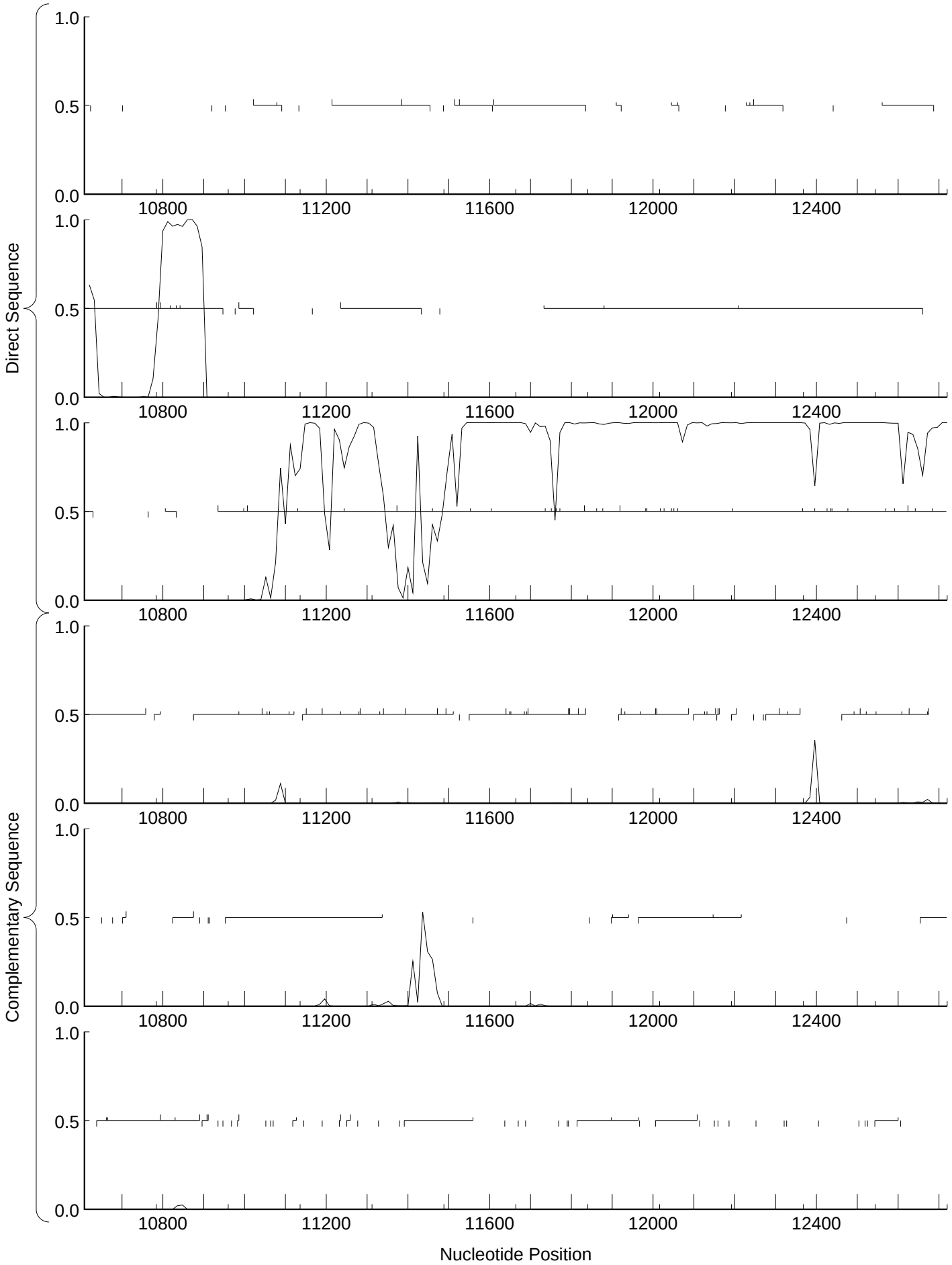
a phage Harambe complete sequence, 73511 bp including 184 bp terminal repeat, Cluster CS, Order 4, Window 96, Step 12, 5/36



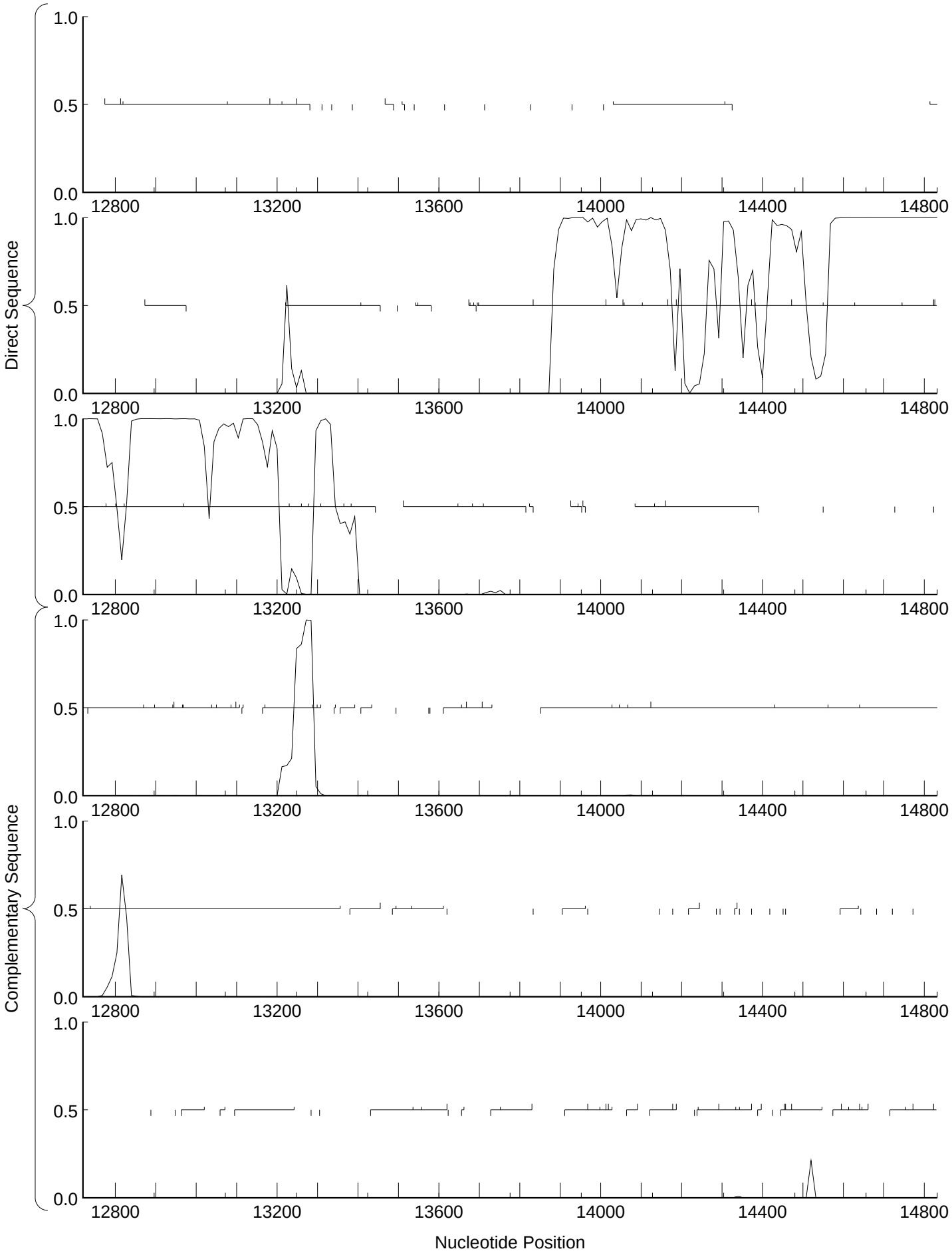
a phage Harambe complete sequence, 73511 bp including 184 bp terminal repeat, Cluster CS, Order 4, Window 96, Step 12, 6/36



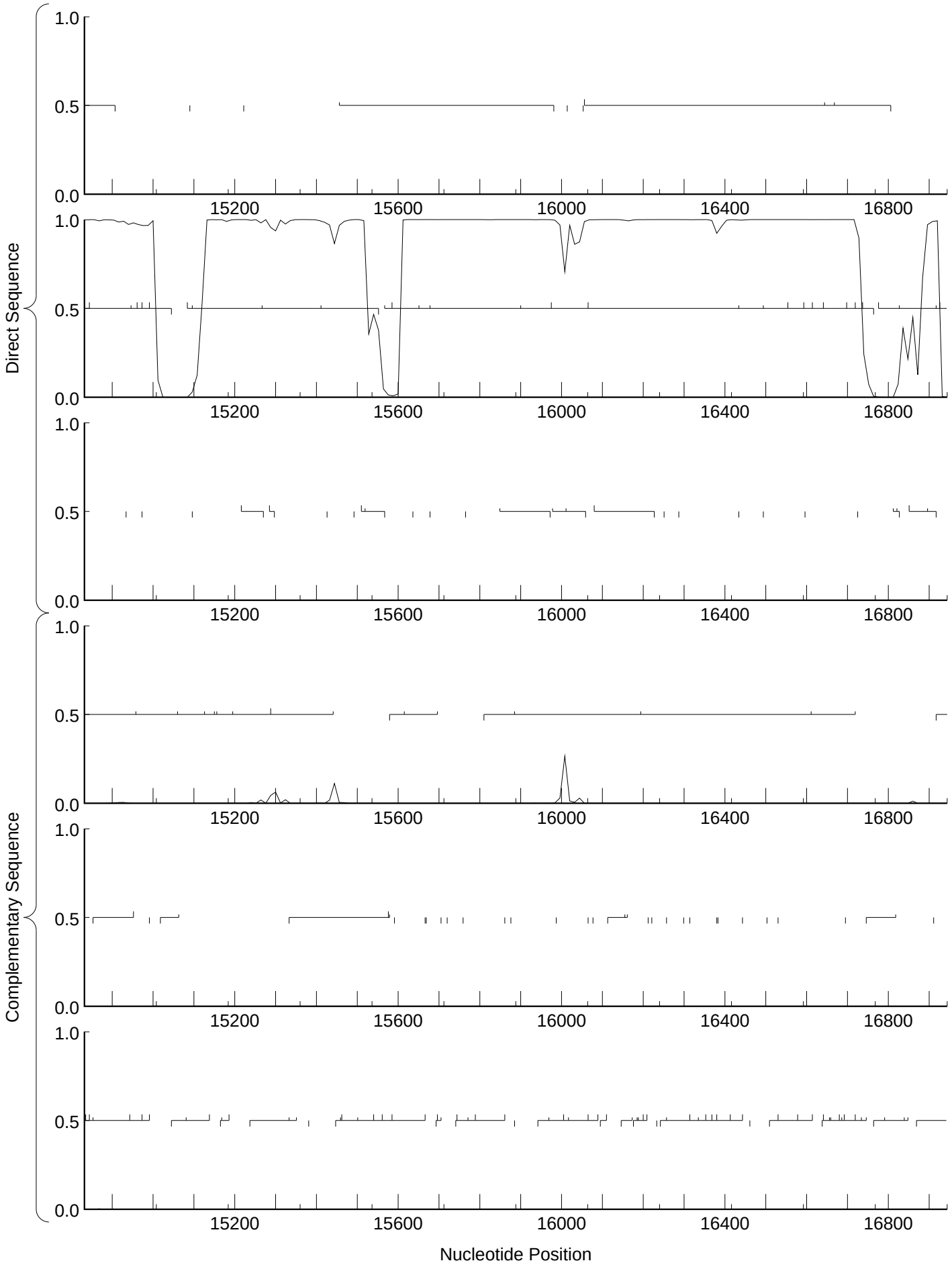
a phage Harambe complete sequence, 73511 bp including 184 bp terminal repeat, Cluster CS, Order 4, Window 96, Step 12, 7/36



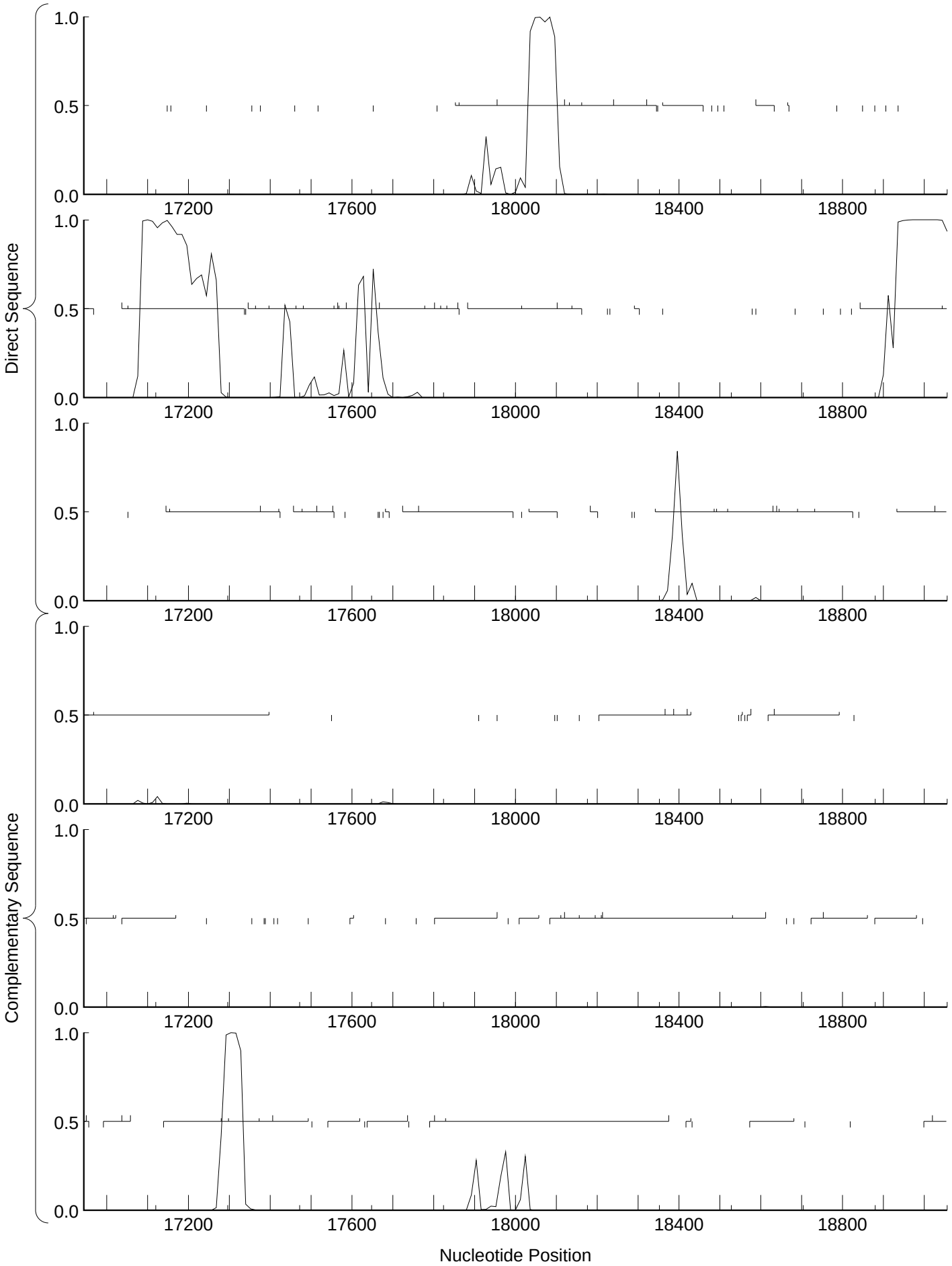
a phage Harambe complete sequence, 73511 bp including 184 bp terminal repeat, Cluster CS, Order 4, Window 96, Step 12, 8/36

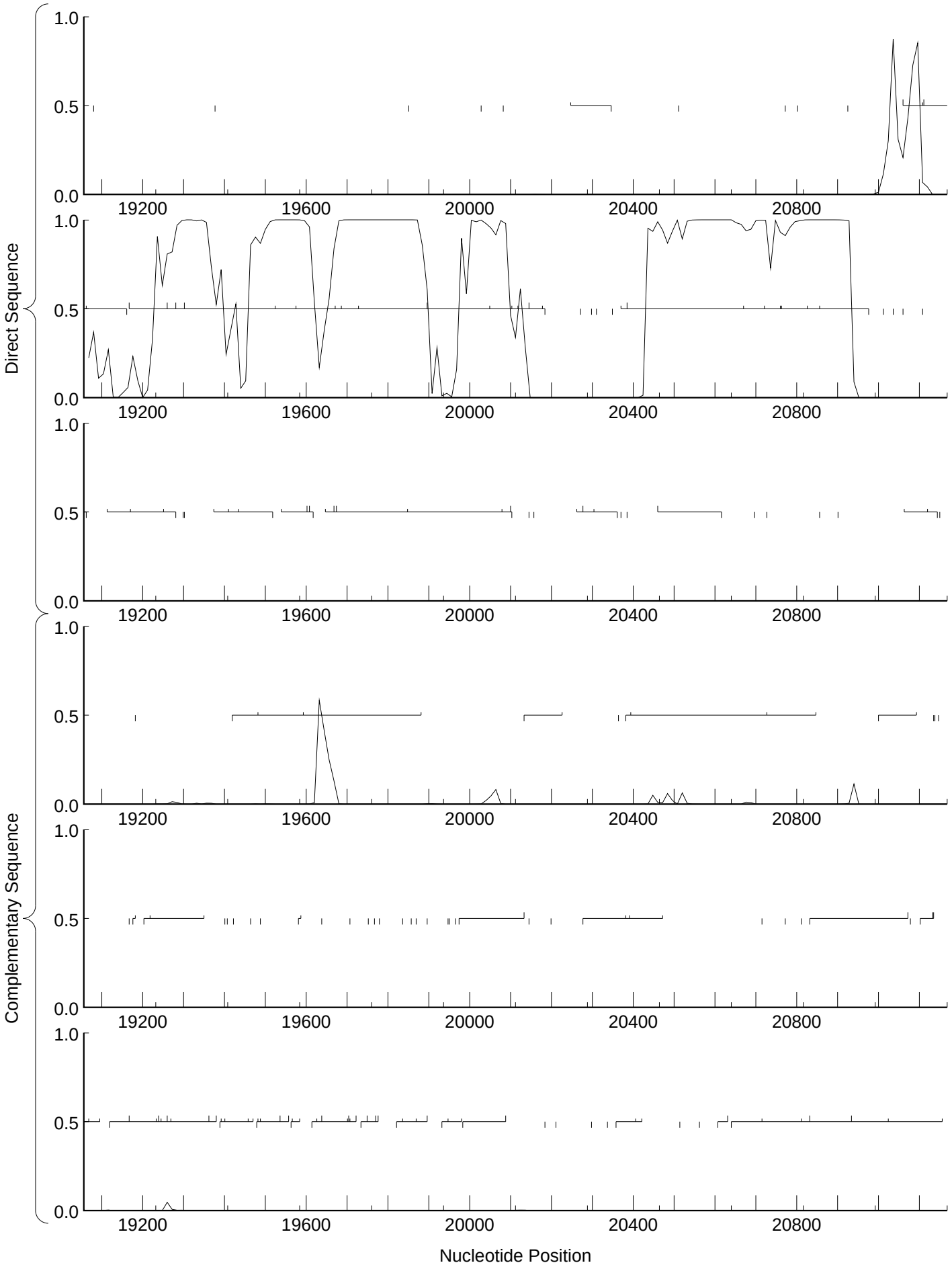


a phage Harambe complete sequence, 73511 bp including 184 bp terminal repeat, Cluster CS, Order 4, Window 96, Step 12, 9/36

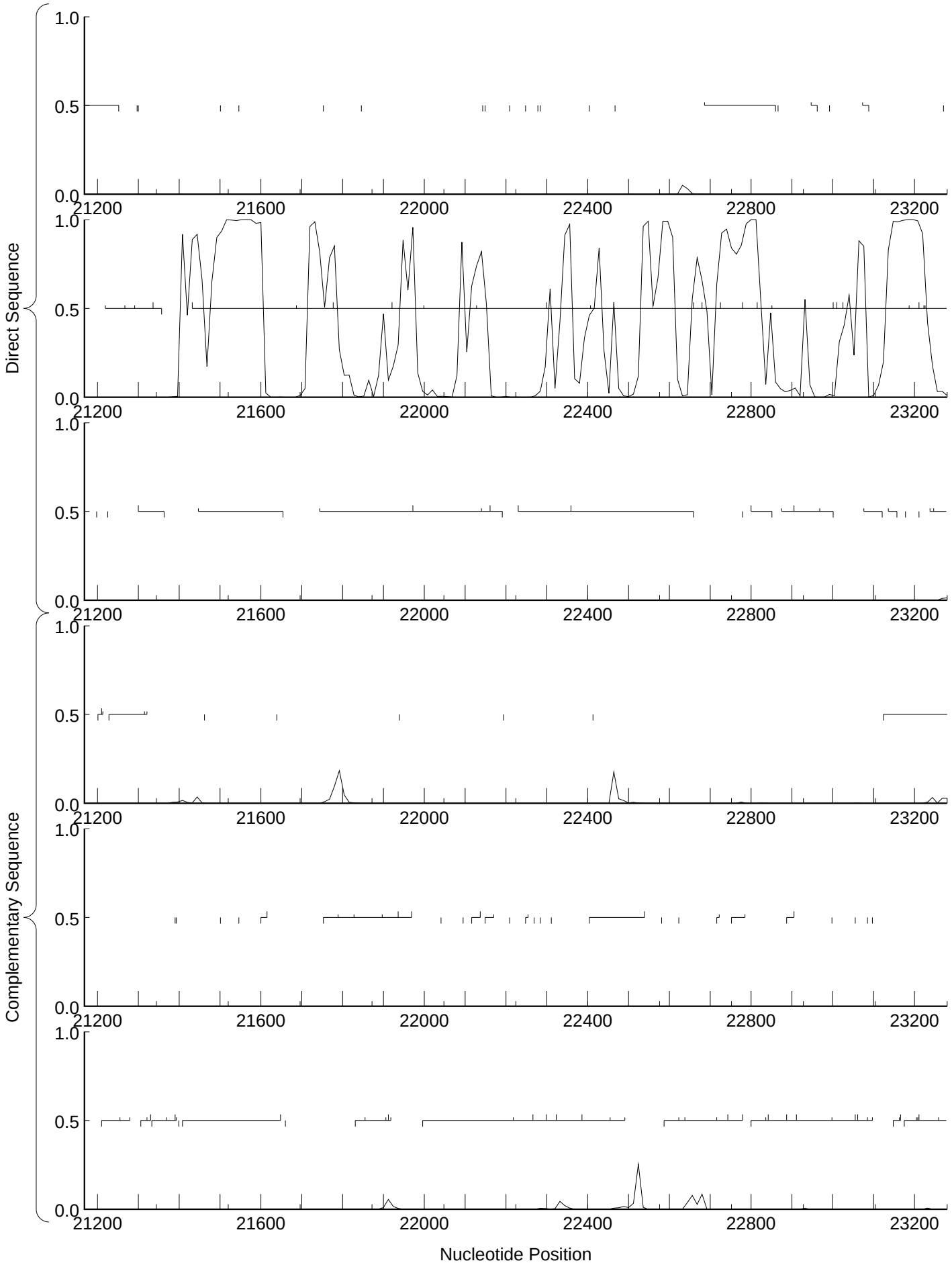


phage Harambe complete sequence, 73511 bp including 184 bp terminal repeat, Cluster CS, Order 4, Window 96, Step 12, 10/36

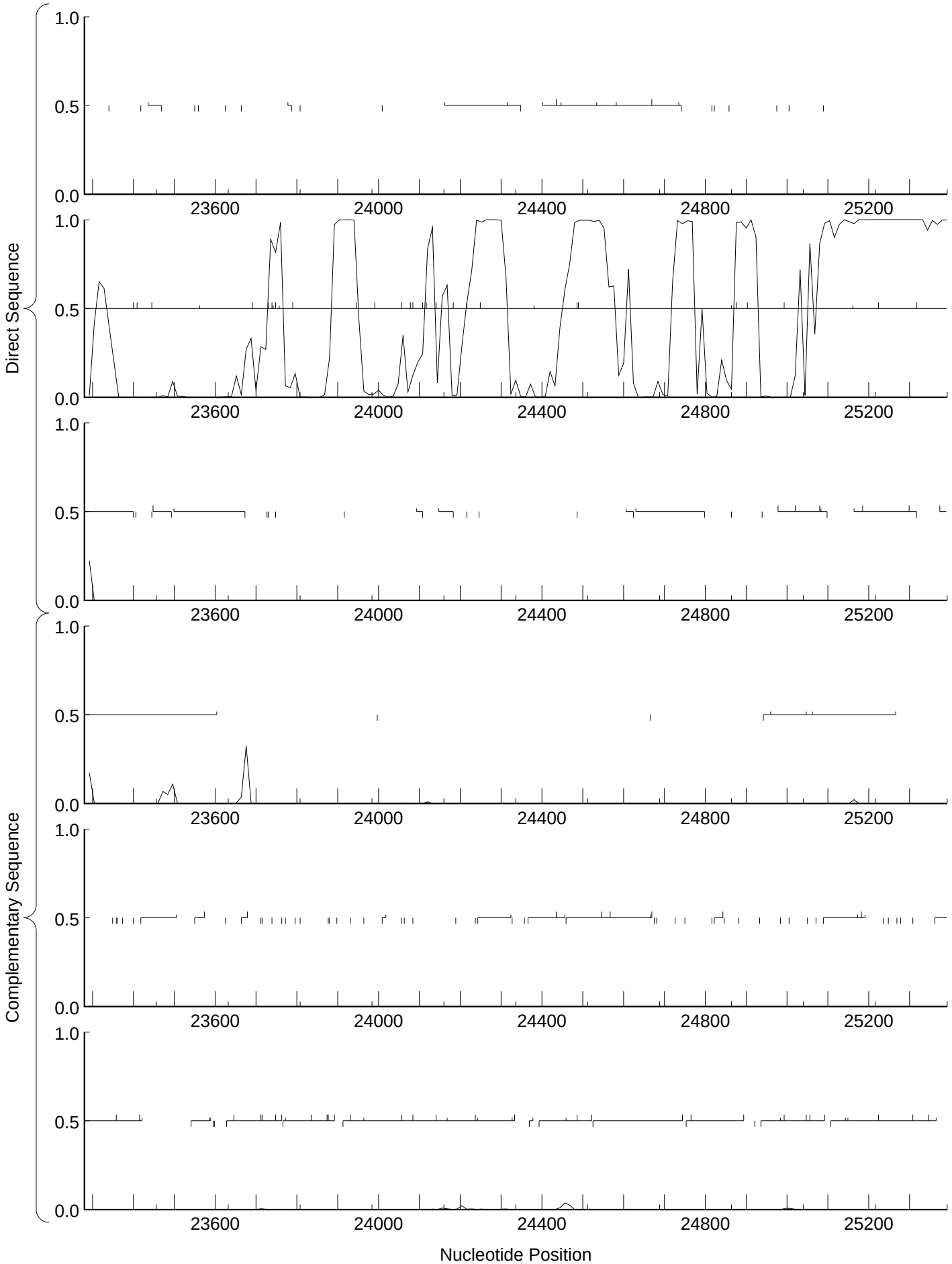


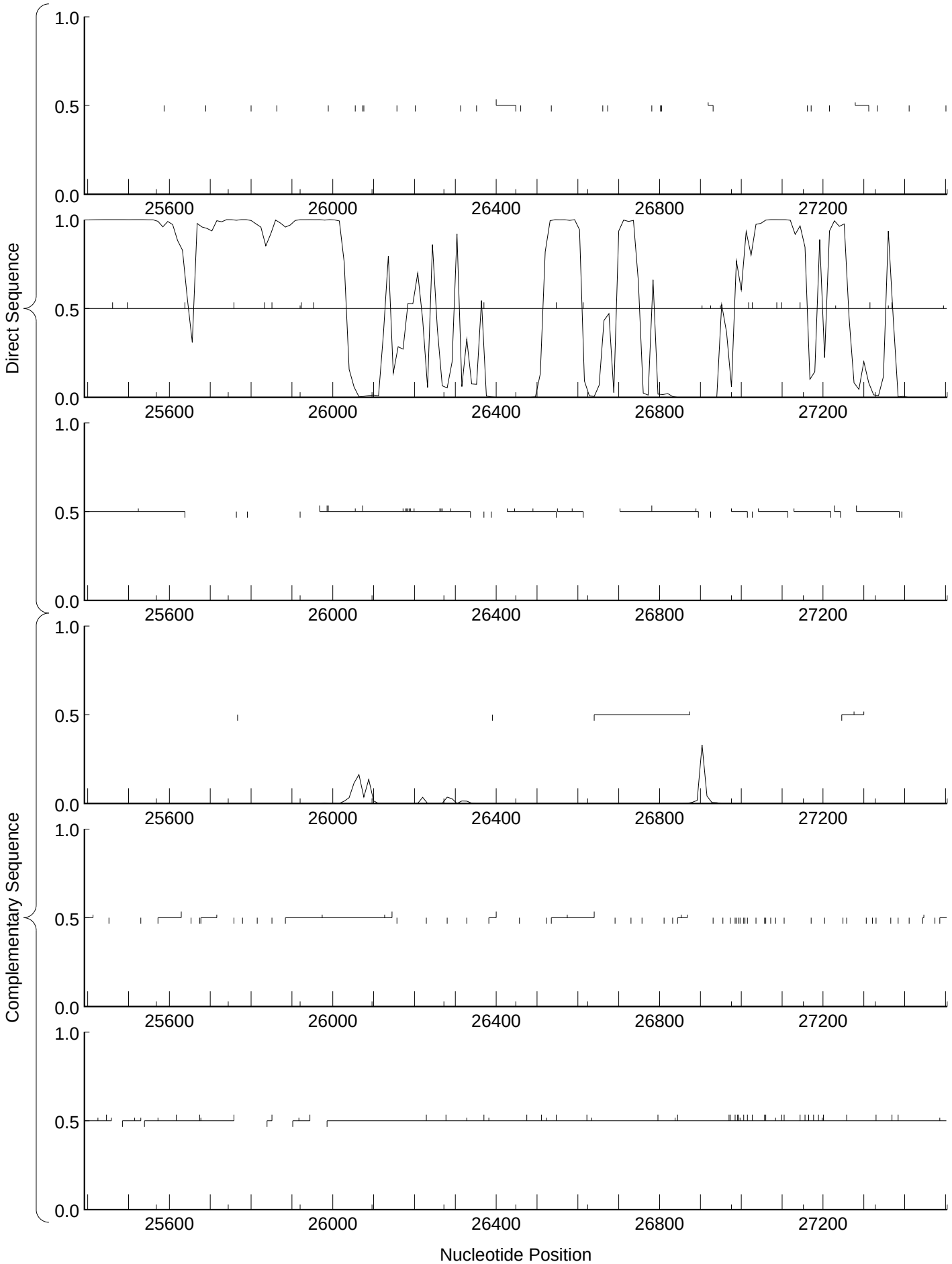

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
19200
19600
20000
20400
20800
Nucleotide Position

phage Harambe complete sequence, 73511 bp including 184 bp terminal repeat, Cluster CS, Order 4, Window 96, Step 12, 12/36

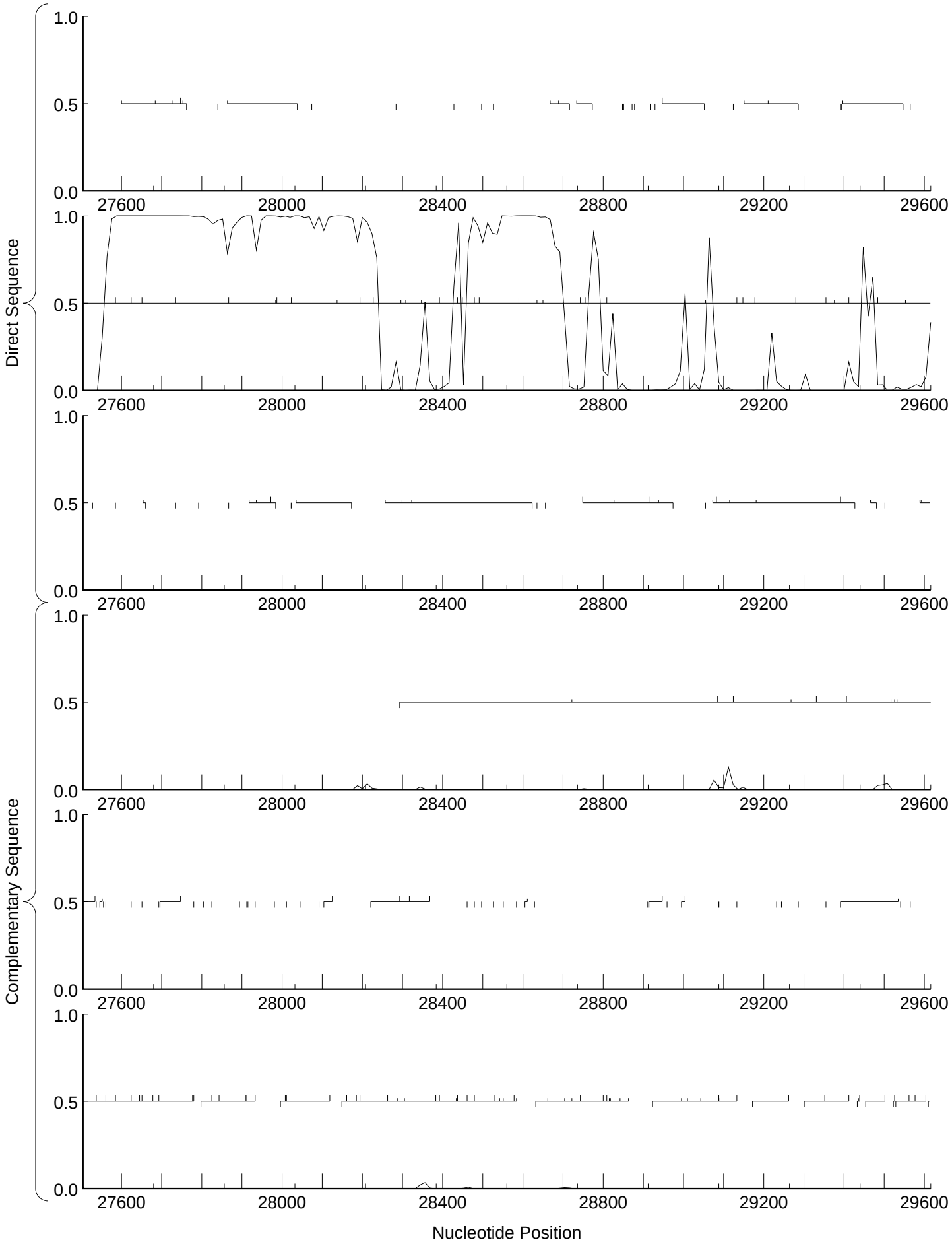


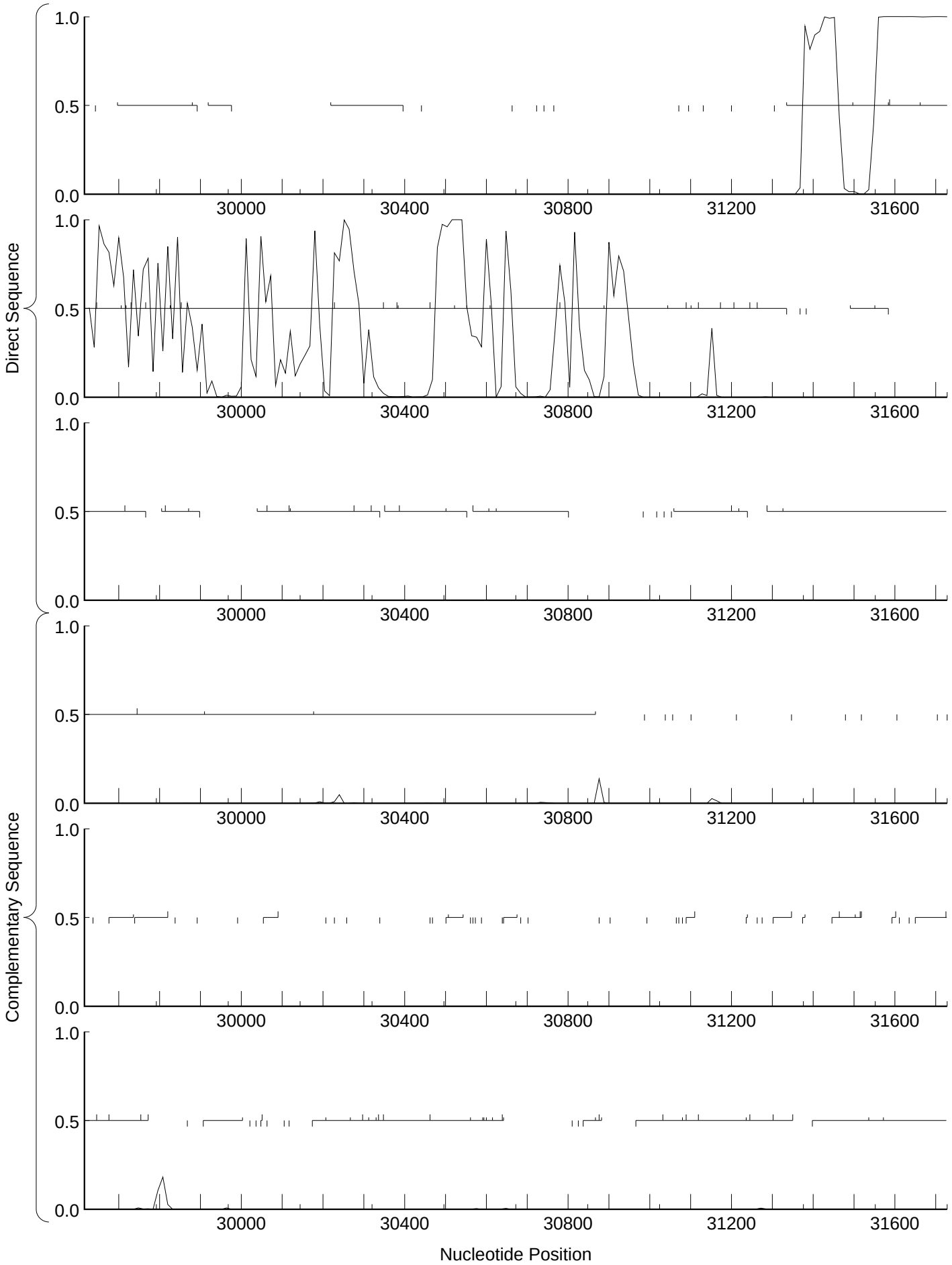
phage Harambe complete sequence, 73511 bp including 184 bp terminal repeat, Cluster CS, Order 4, Window 96, Step 12, 13/36



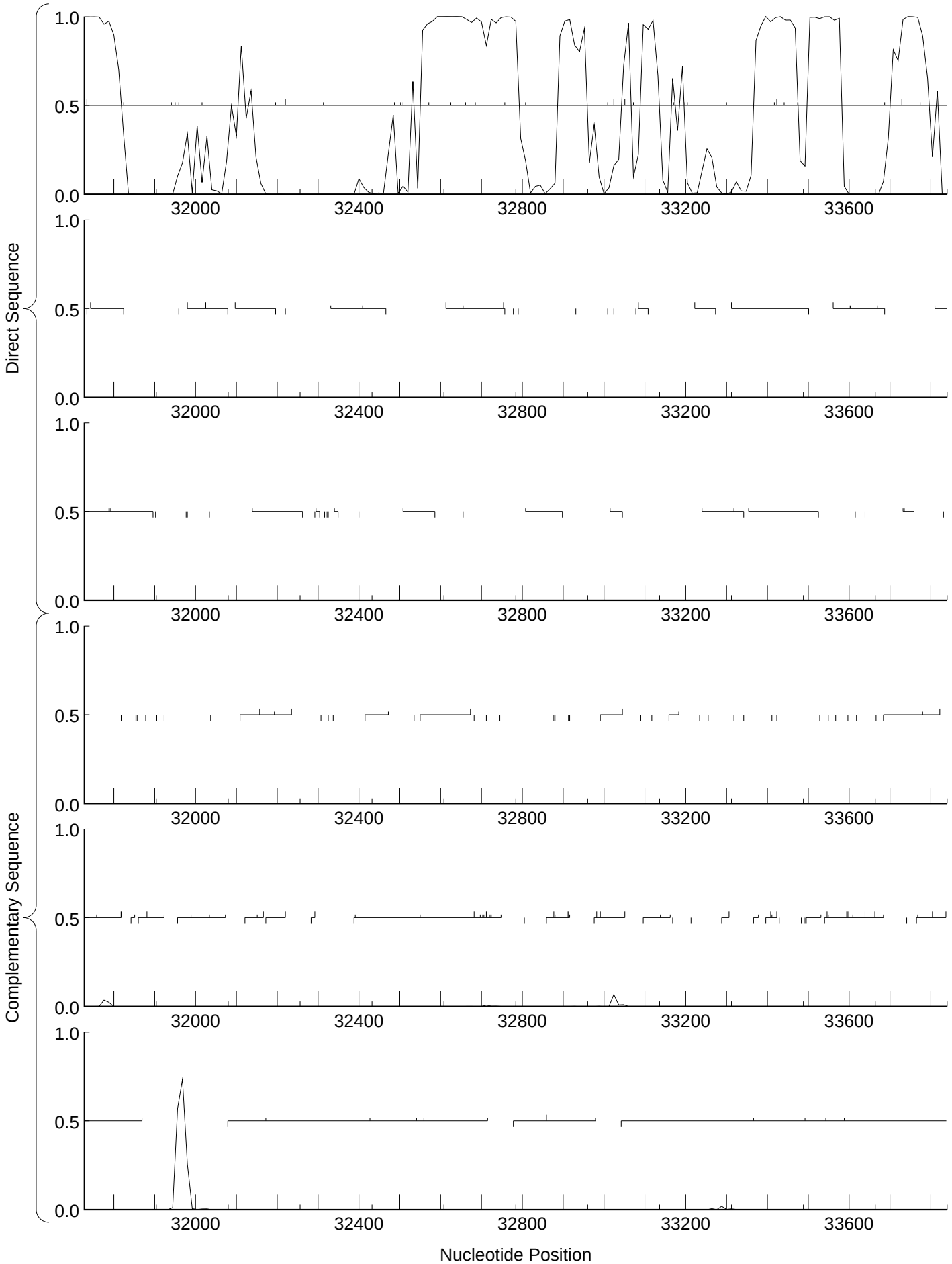

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
25600
26000
26400
26800
27200
Nucleotide Position

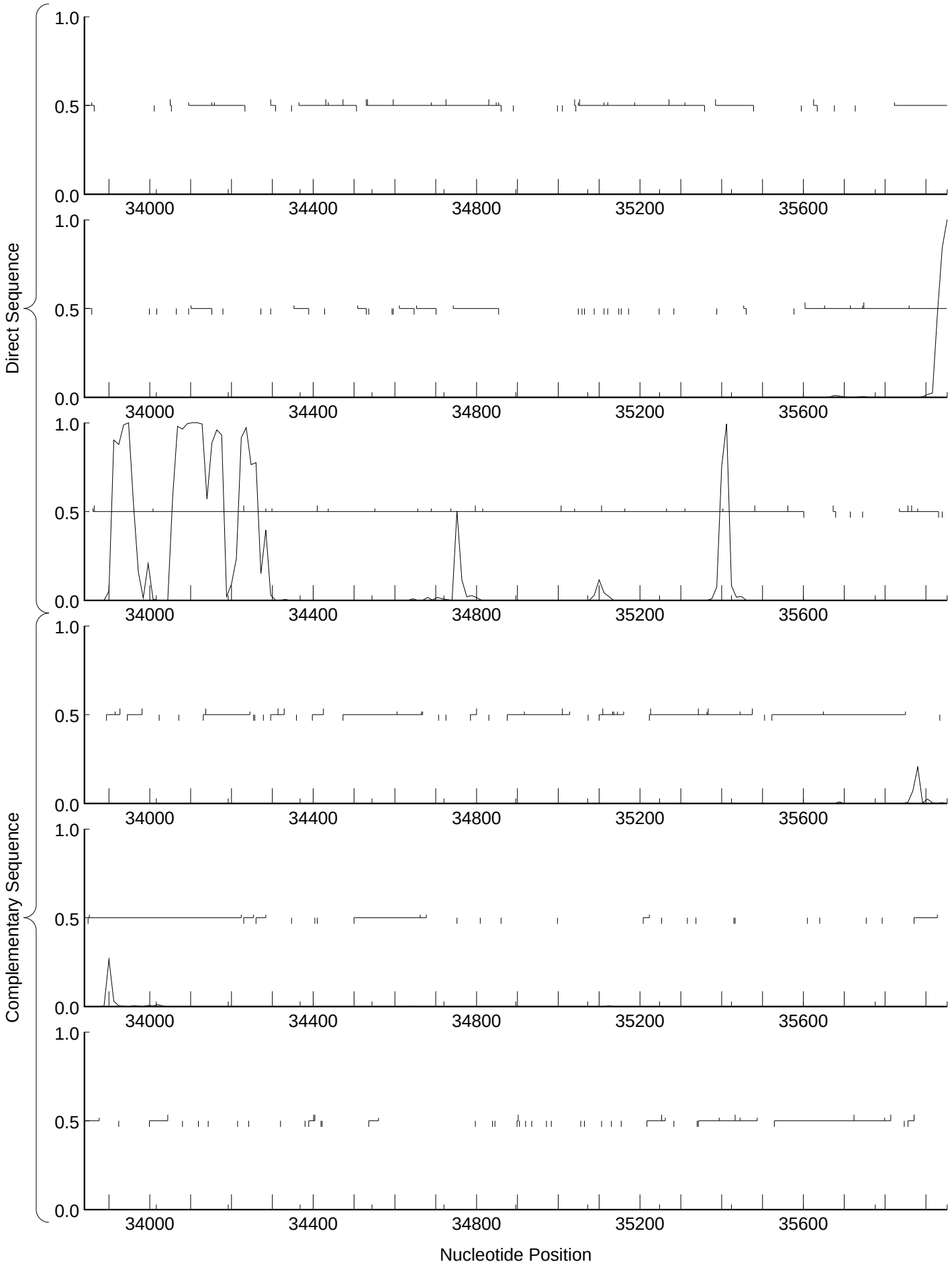
phage Harambe complete sequence, 73511 bp including 184 bp terminal repeat, Cluster CS, Order 4, Window 96, Step 12, 15/36

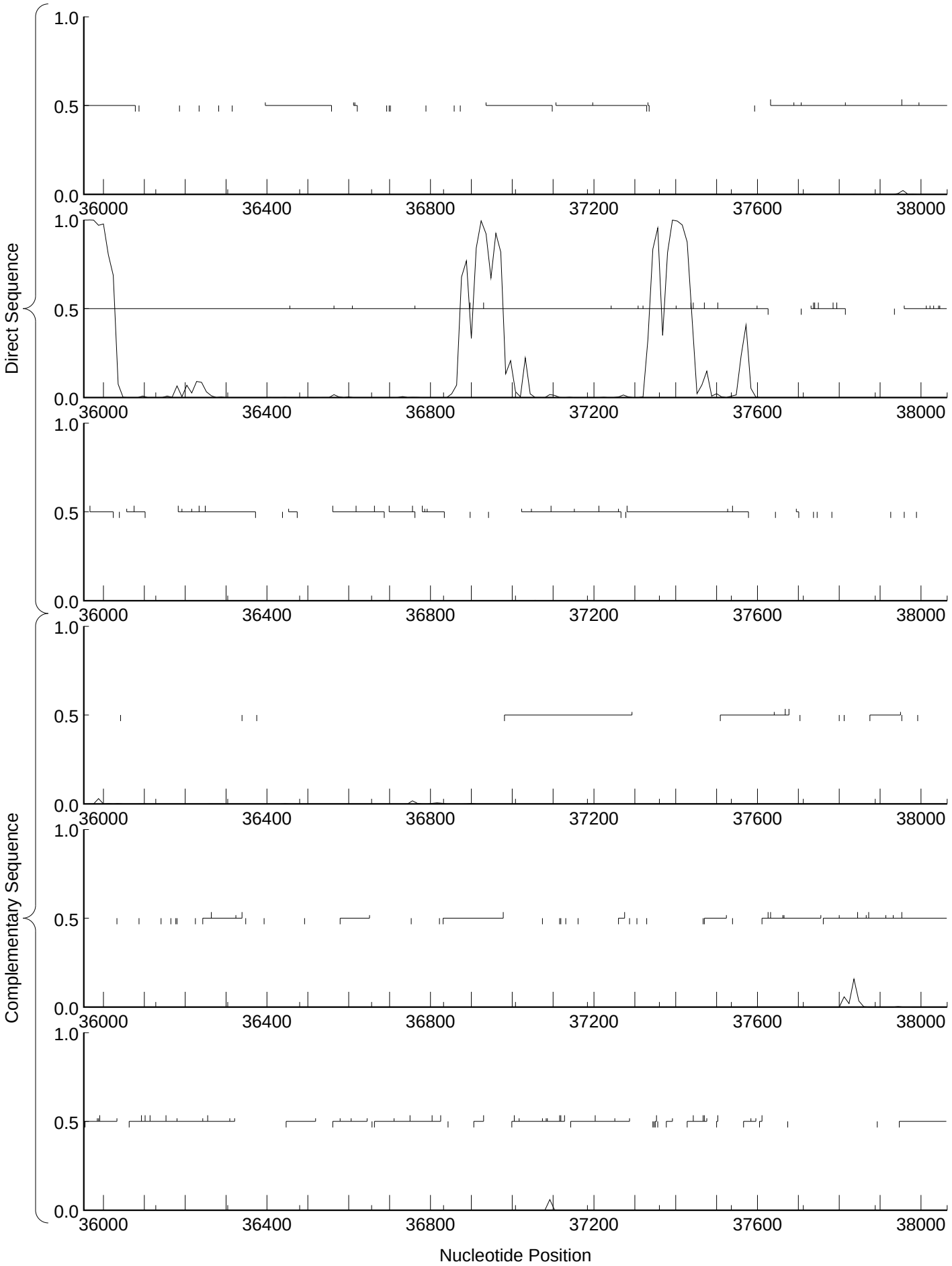


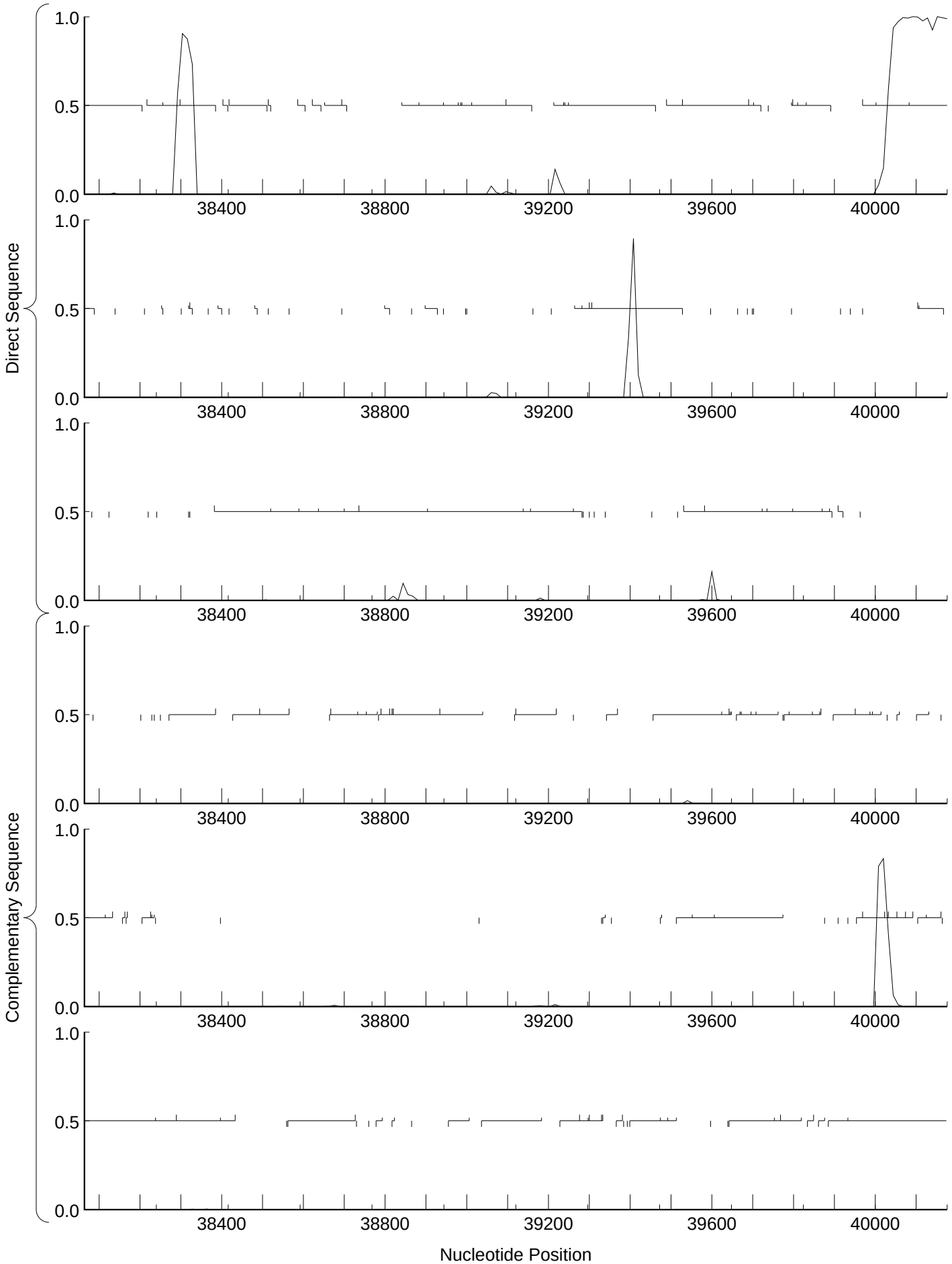

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
30000
30400
30800
31200
31600
Nucleotide Position

phage Harambe complete sequence, 73511 bp including 184 bp terminal repeat, Cluster CS, Order 4, Window 96, Step 12, 17/36

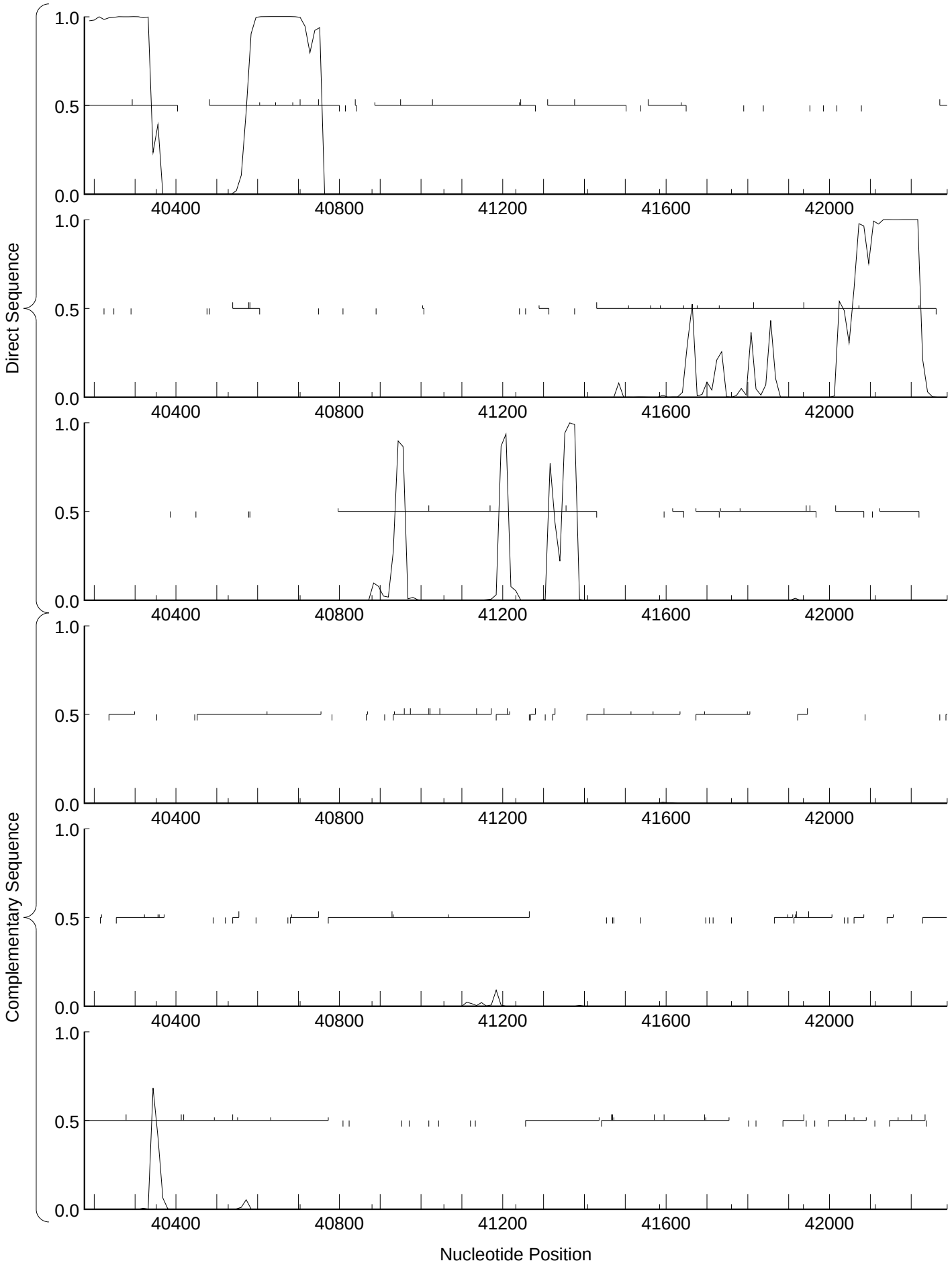



Direct Sequence
Complementary Sequence
1.0
0.5
0.0
34000
34400
34800
35200
35600
Nucleotide Position

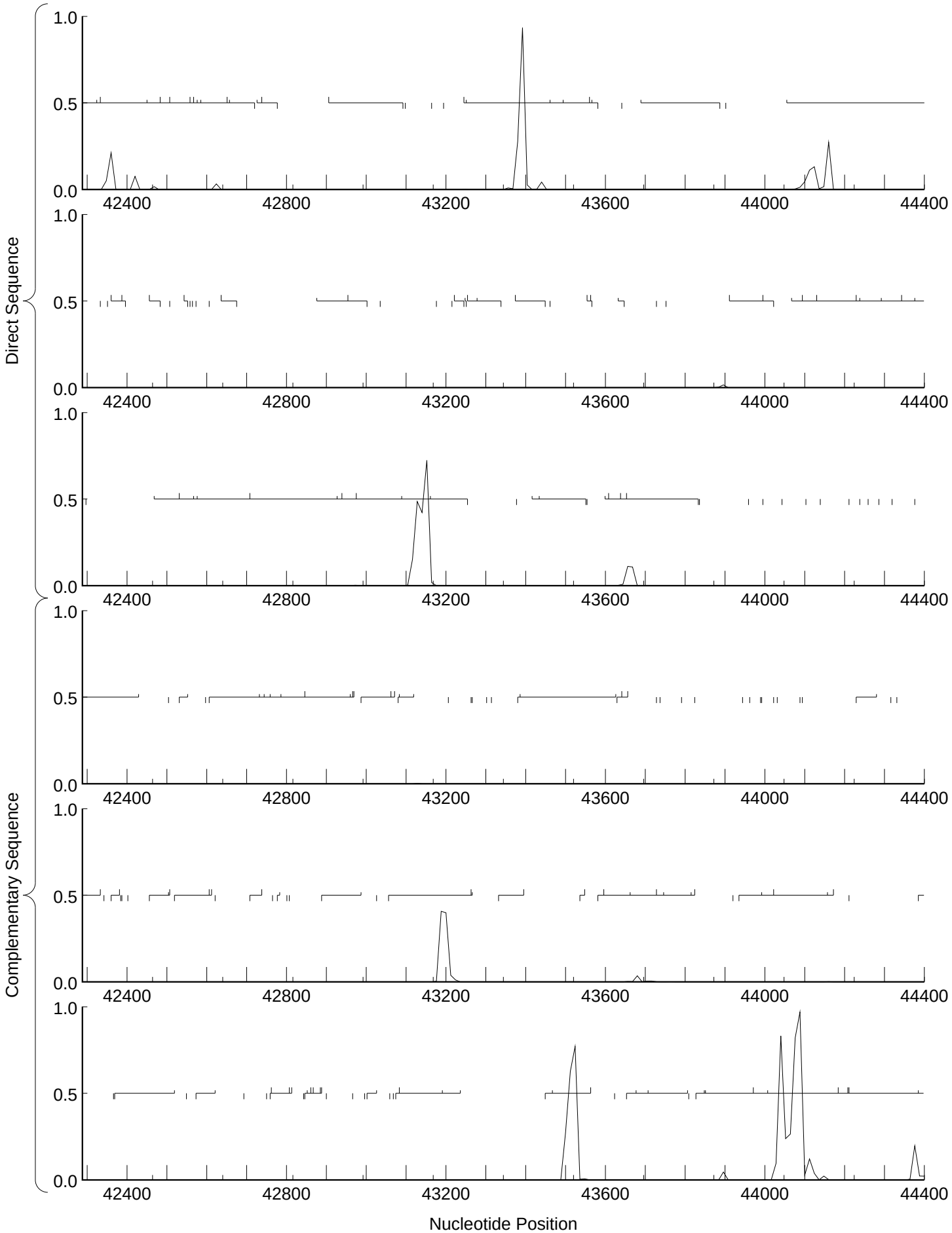

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
36000
36400
36800
37200
37600
38000
Nucleotide Position

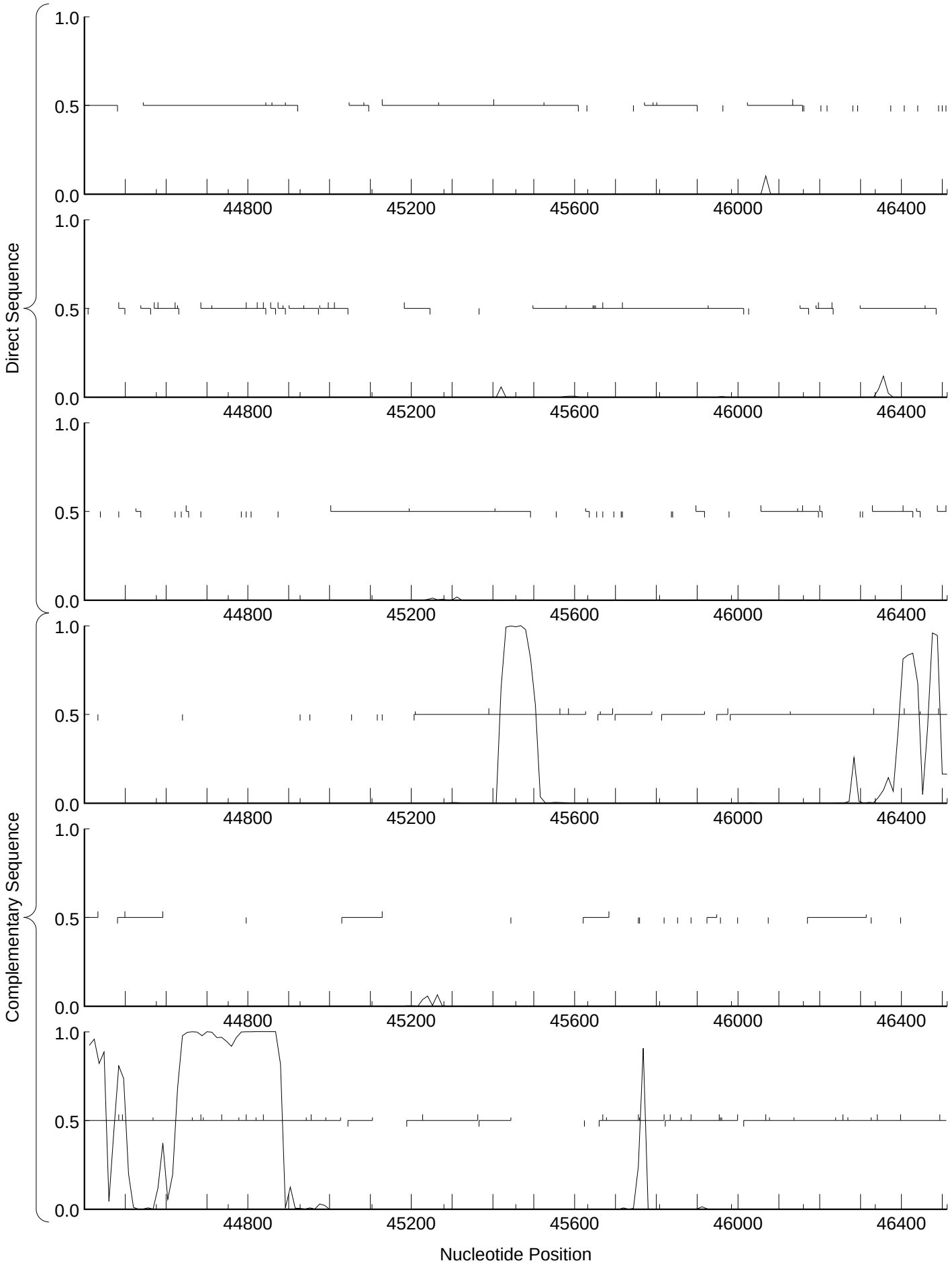

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
38400
38800
39200
39600
40000
Nucleotide Position

phage Harambe complete sequence, 73511 bp including 184 bp terminal repeat, Cluster CS, Order 4, Window 96, Step 12, 21/36

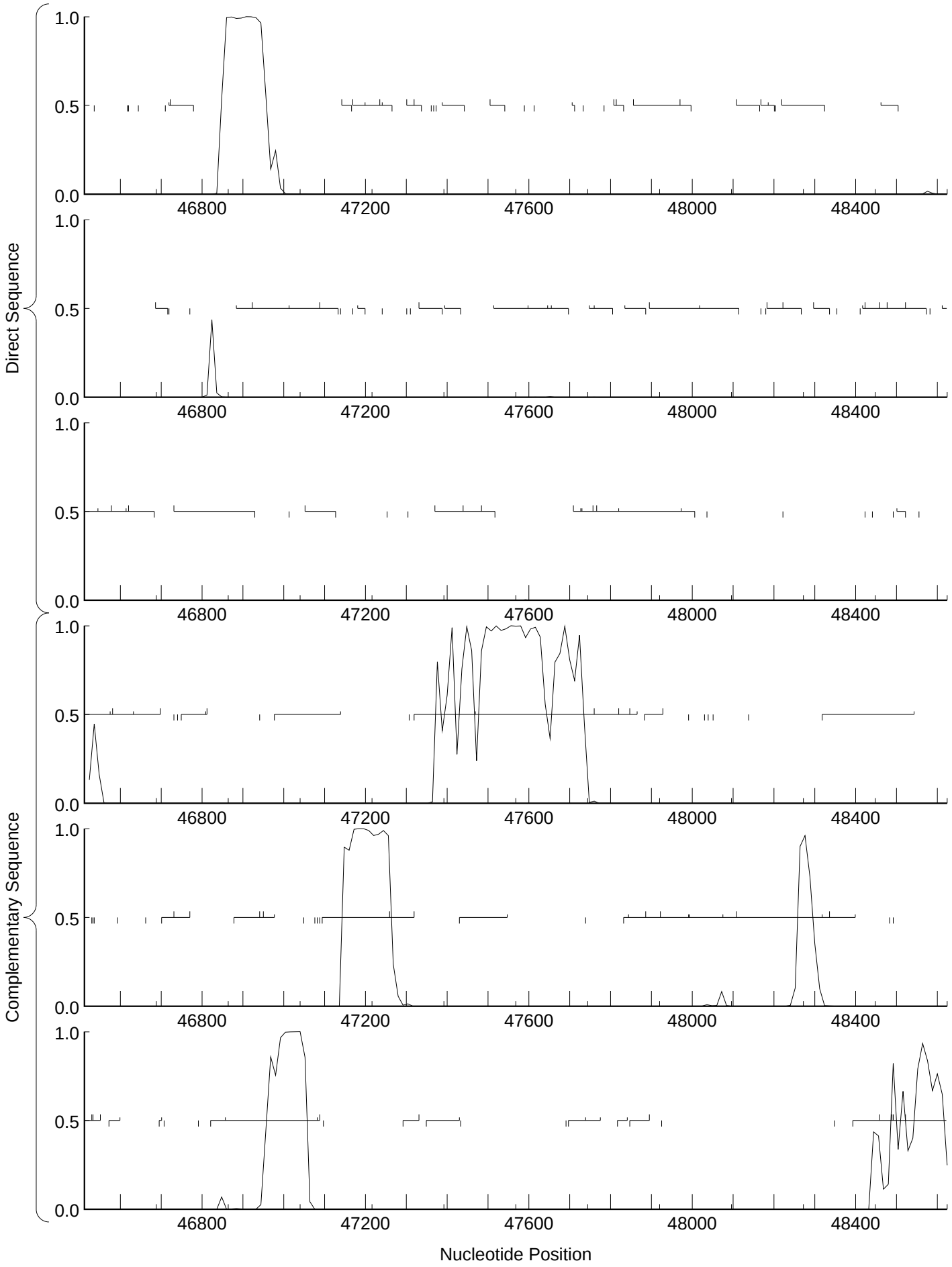


phage Harambe complete sequence, 73511 bp including 184 bp terminal repeat, Cluster CS, Order 4, Window 96, Step 12, 22/36

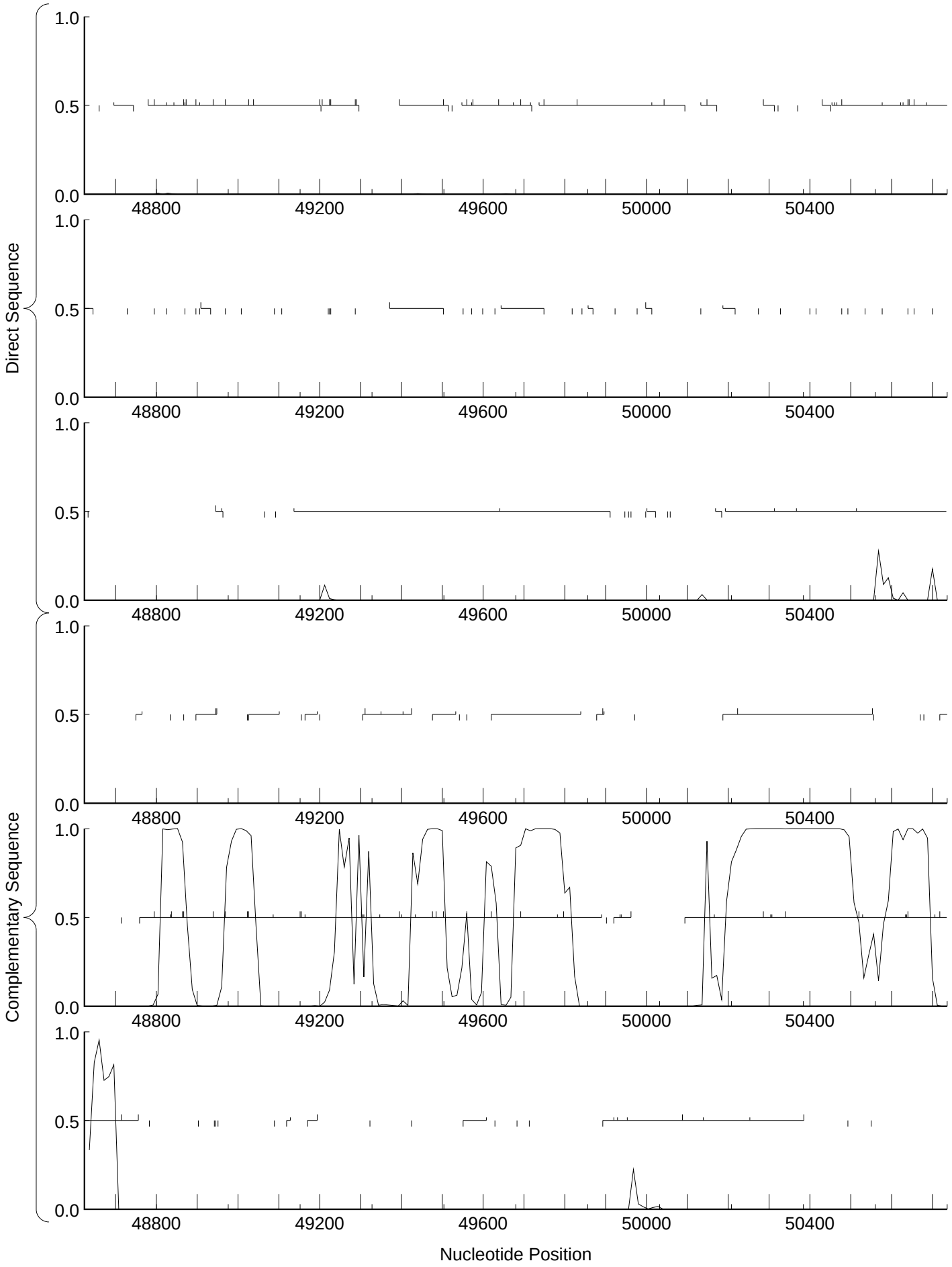


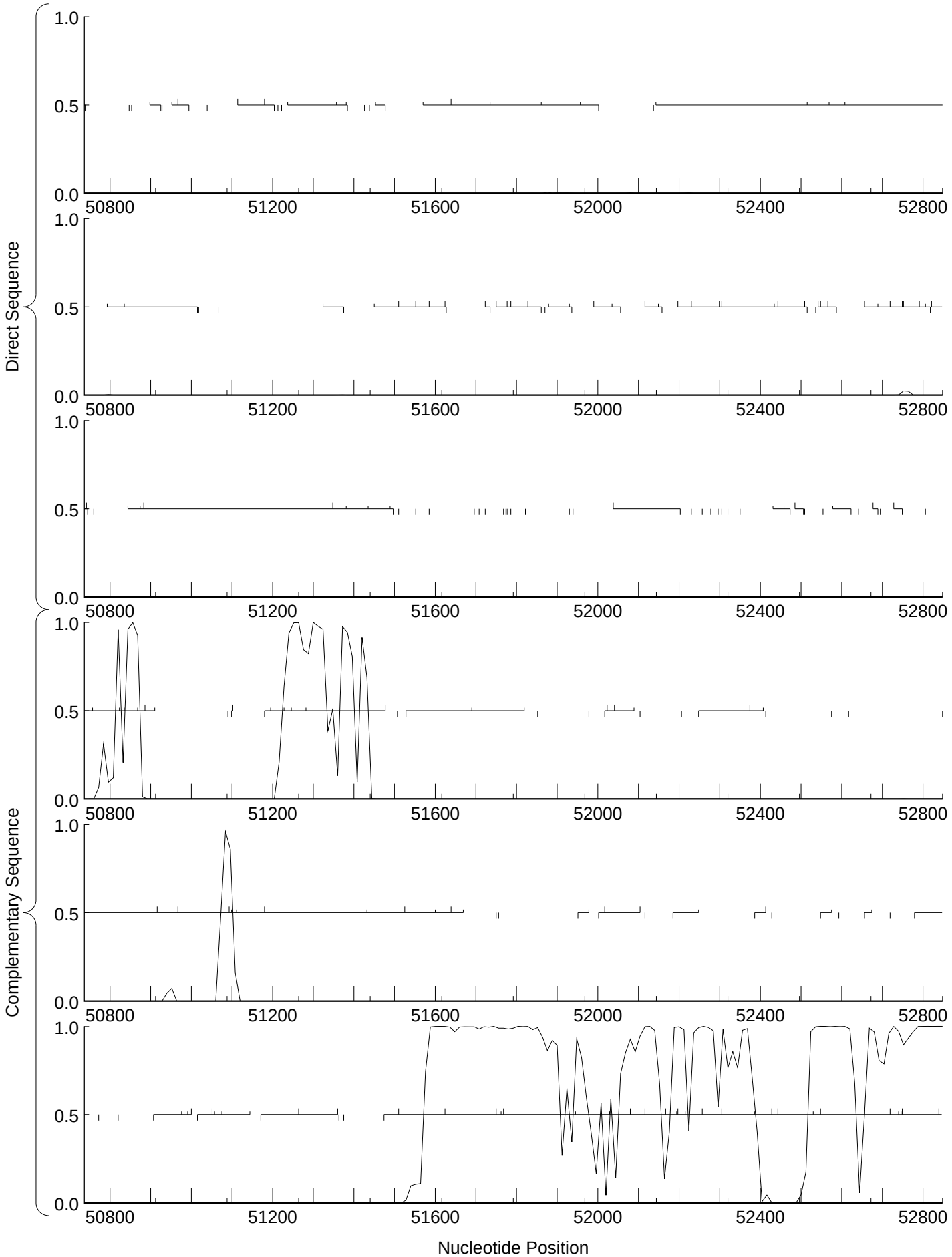

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
44800
45200
45600
46000
46400
Nucleotide Position

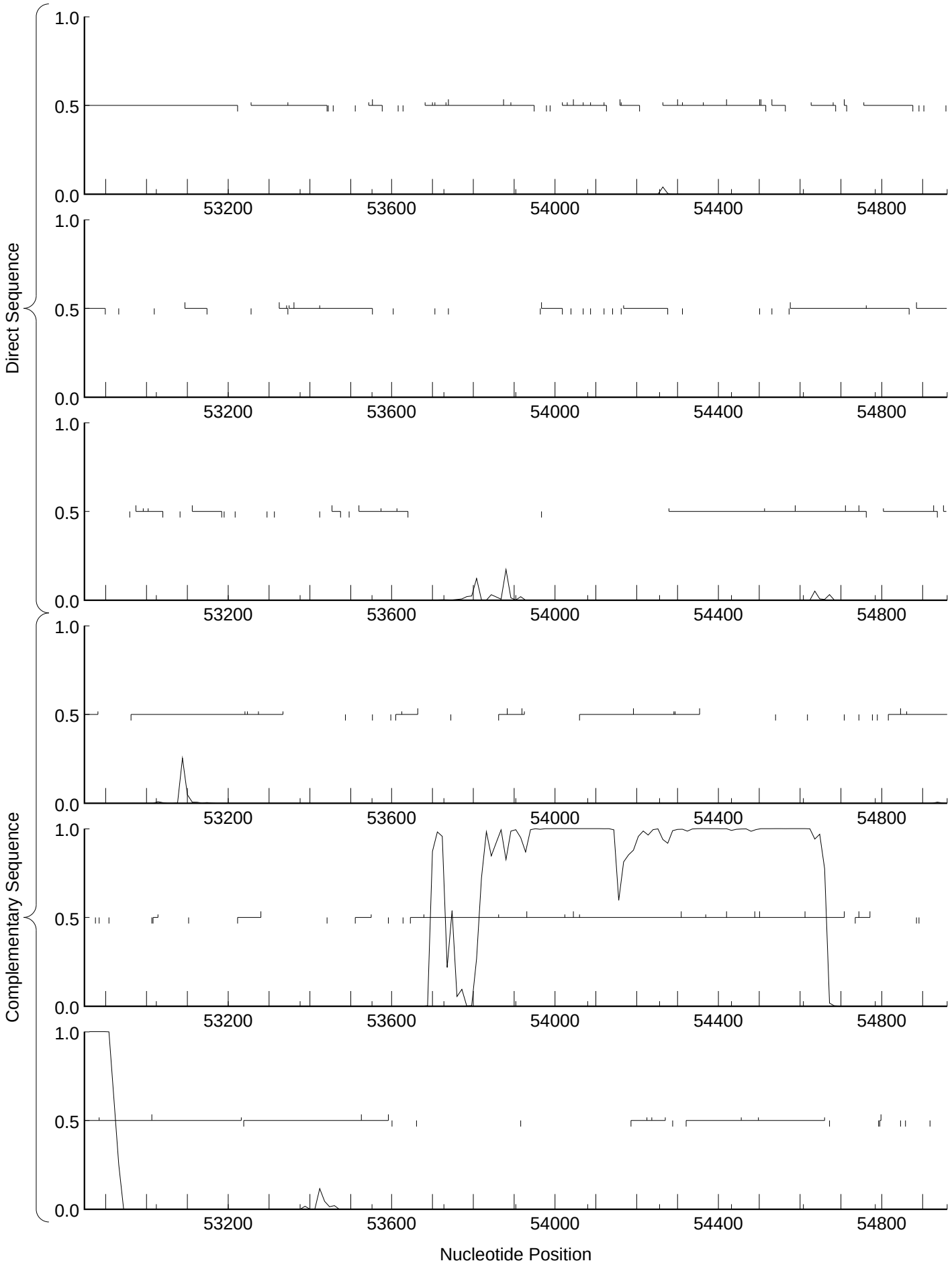
phage Harambe complete sequence, 73511 bp including 184 bp terminal repeat, Cluster CS, Order 4, Window 96, Step 12, 24/36

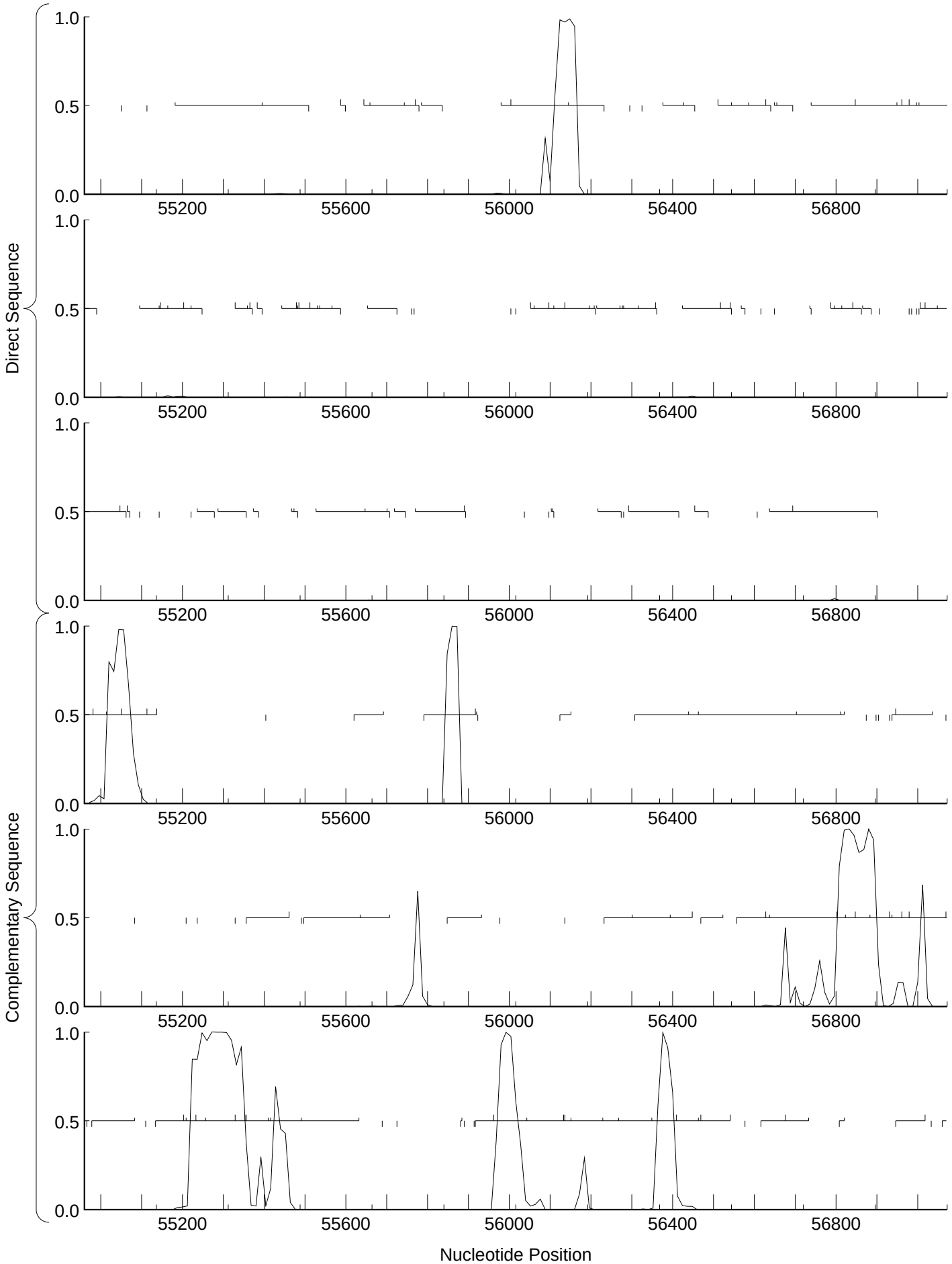


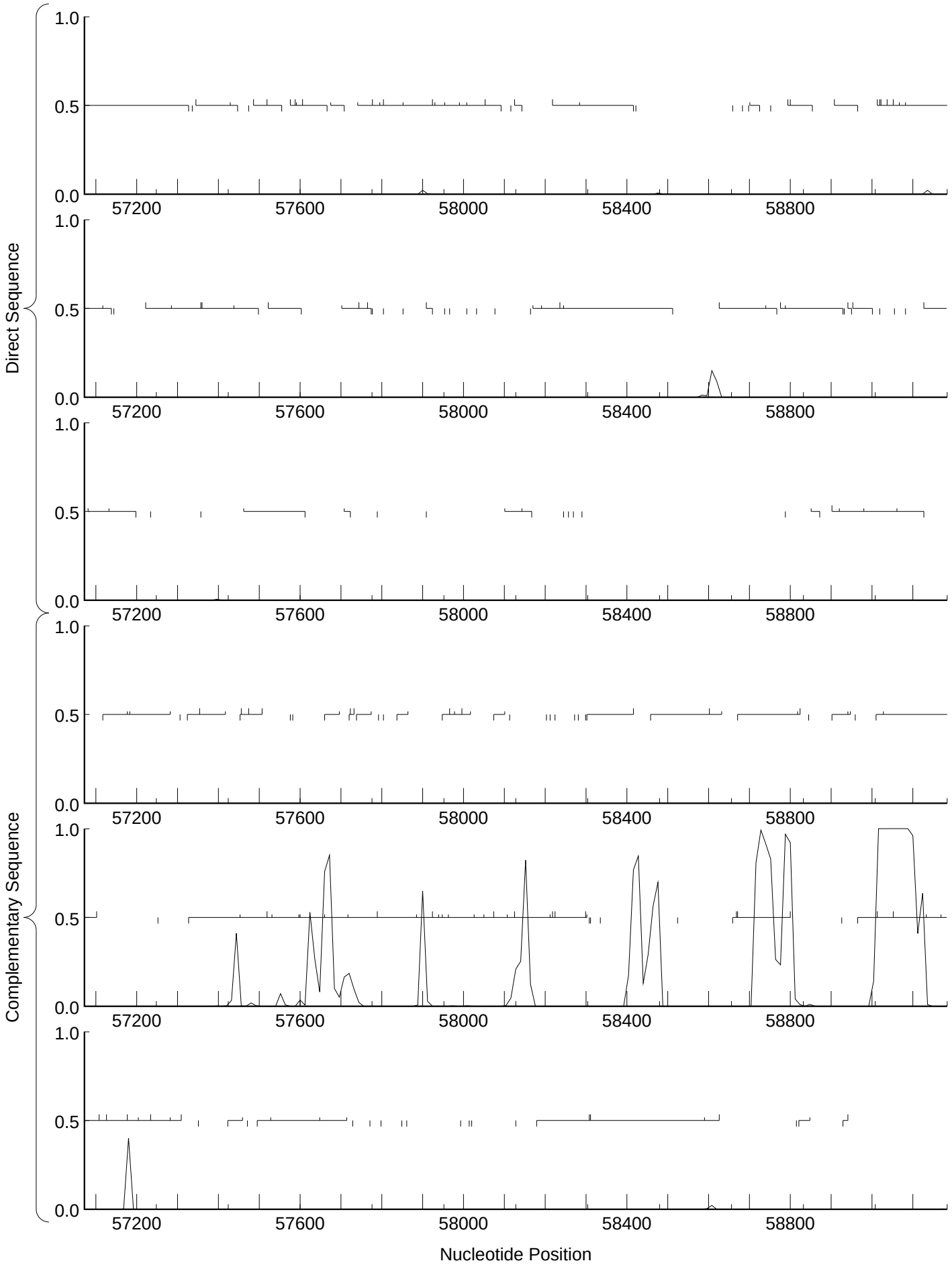
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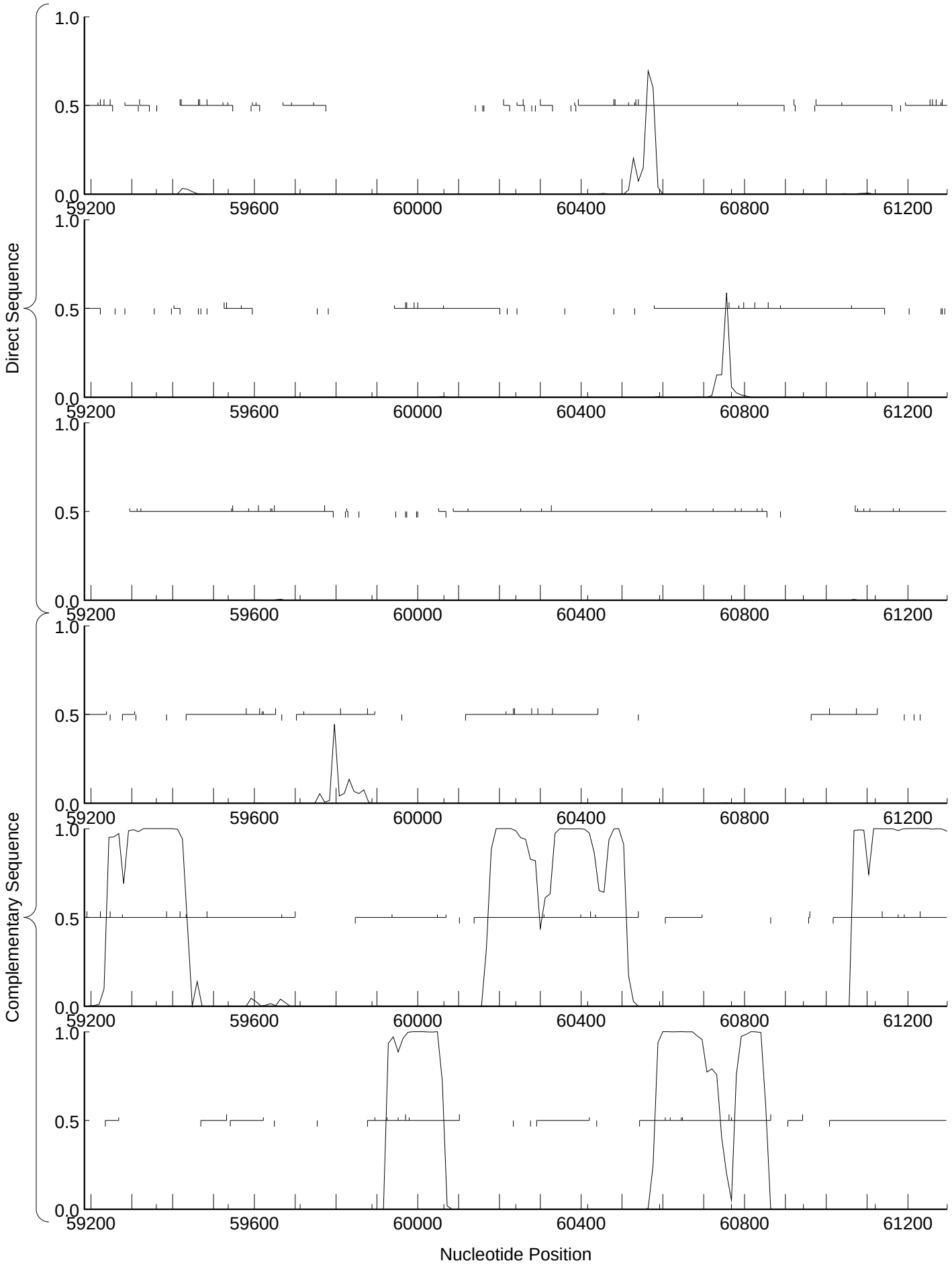



Direct Sequence
Complementary Sequence
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0.5
0.0
50800
51200
51600
52000
52400
52800
Nucleotide Position

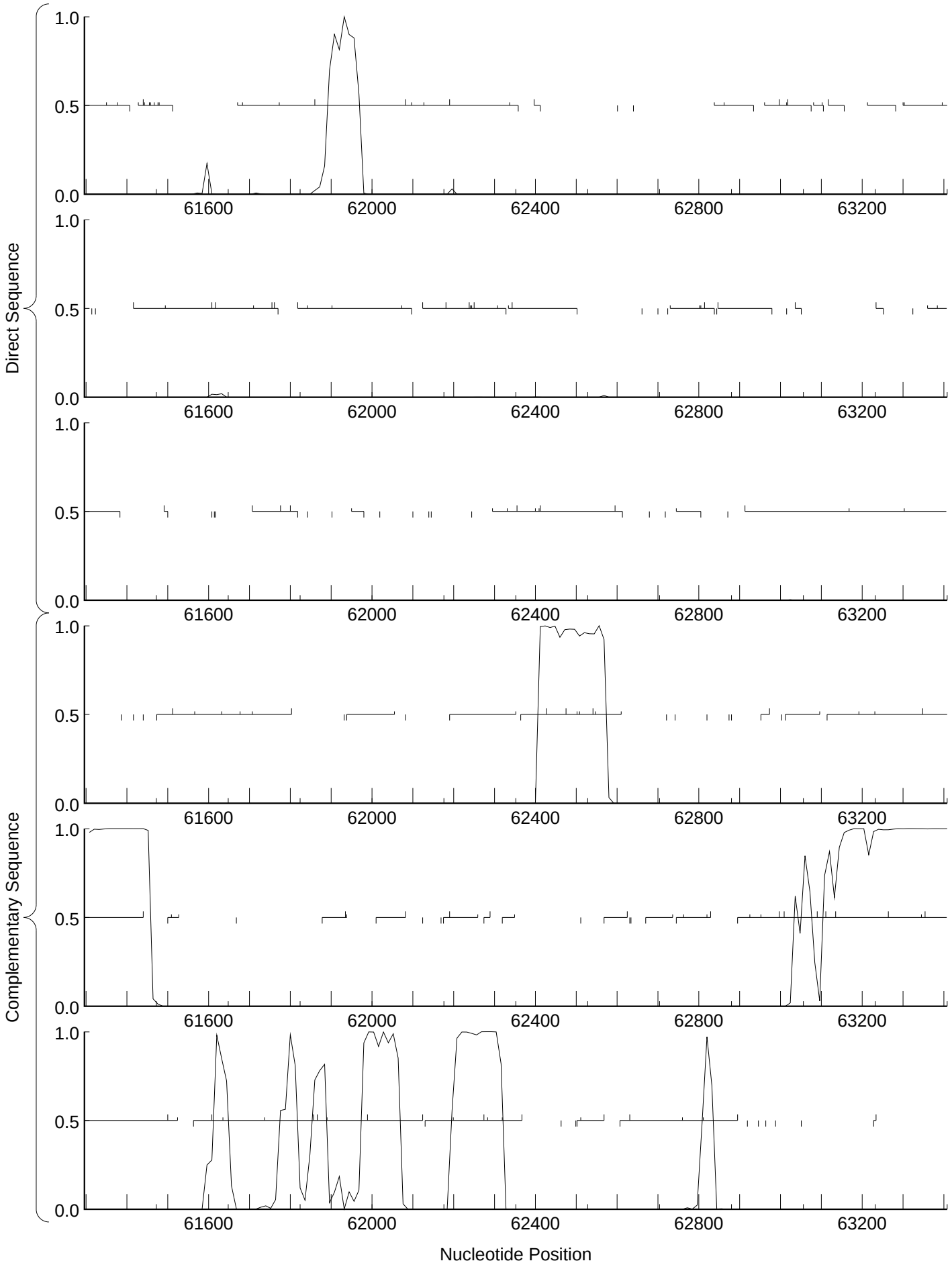

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
53200
53600
54000
54400
54800
Nucleotide Position


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

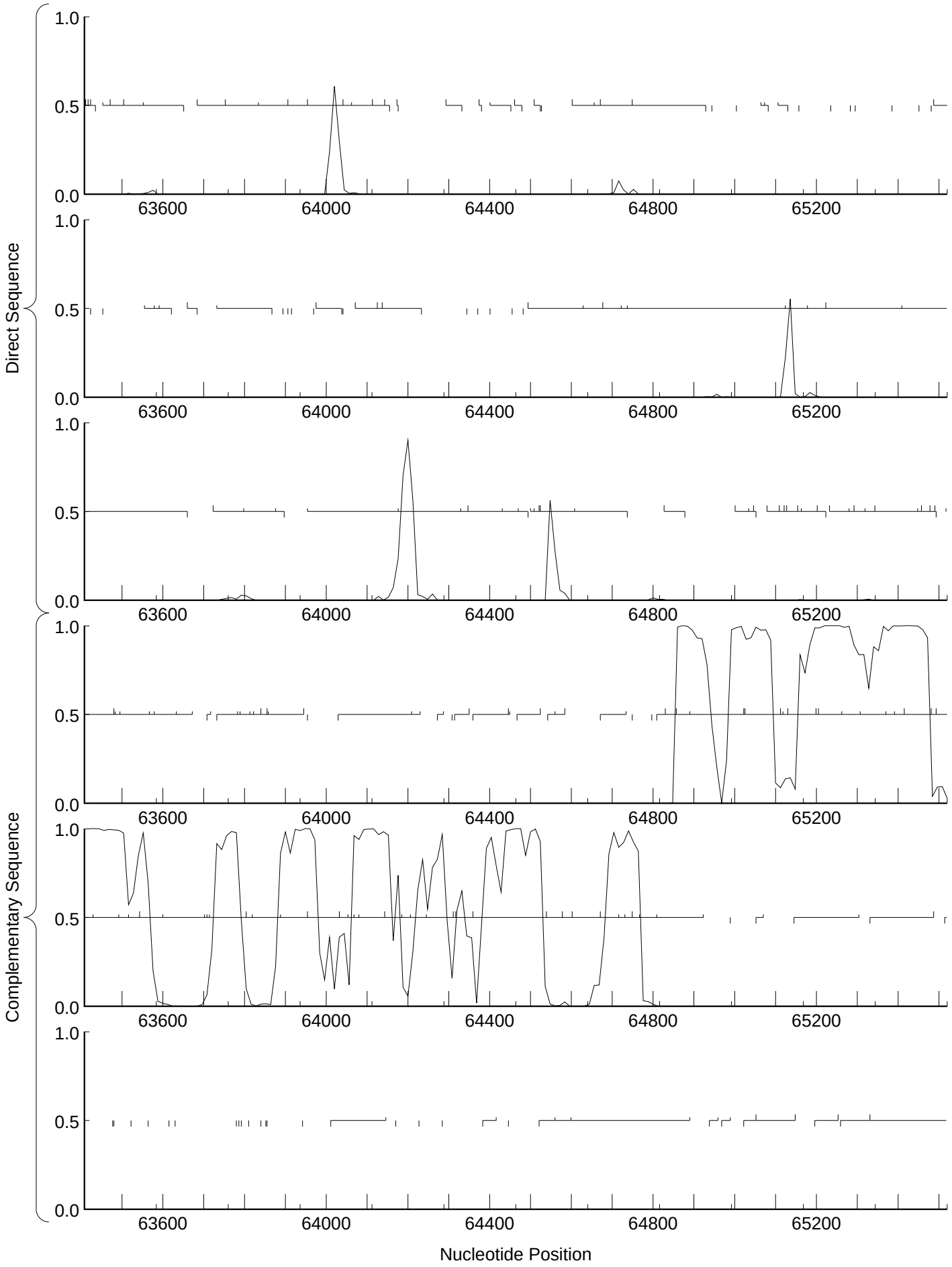

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
57200
57600
58000
58400
58800
Nucleotide Position


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

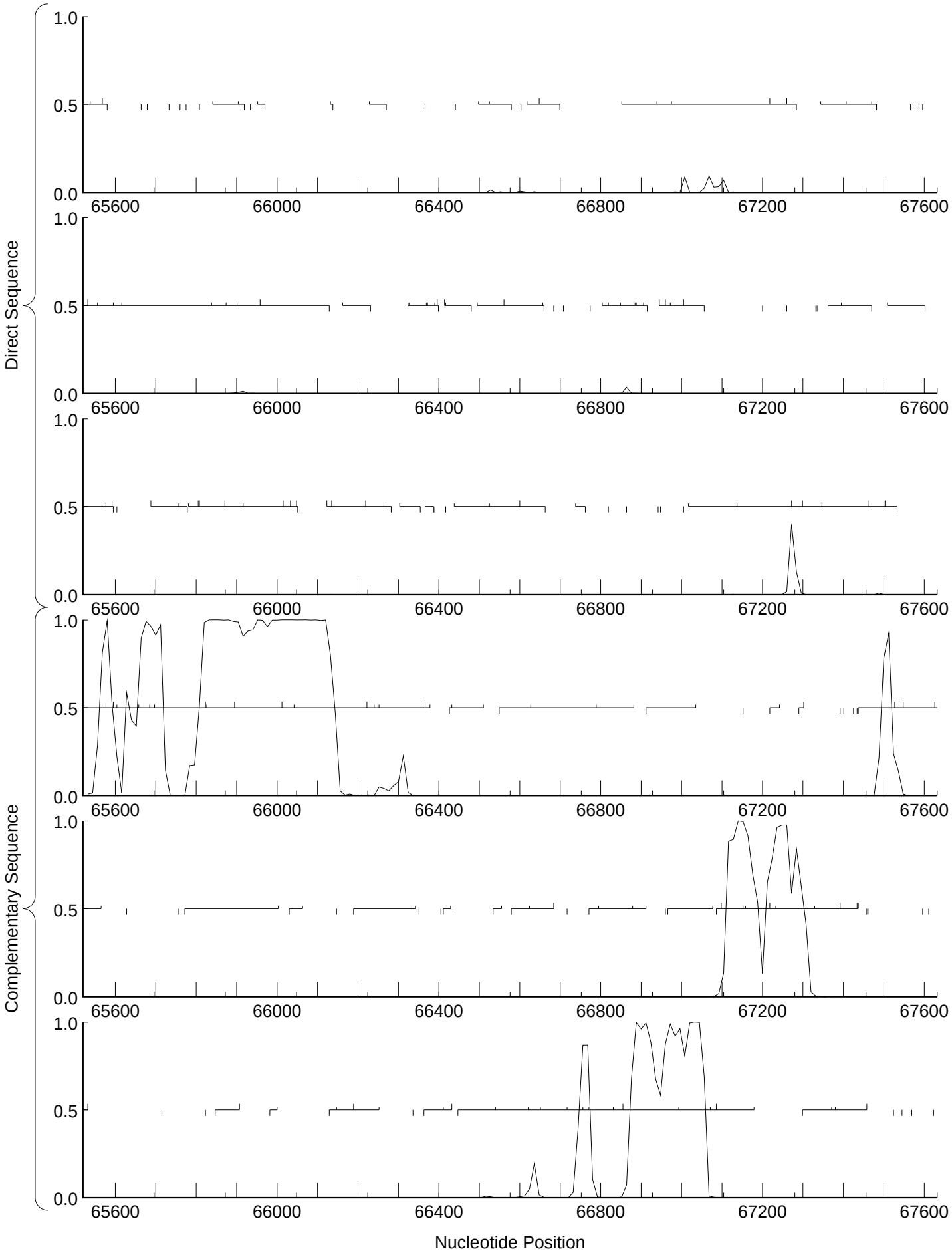
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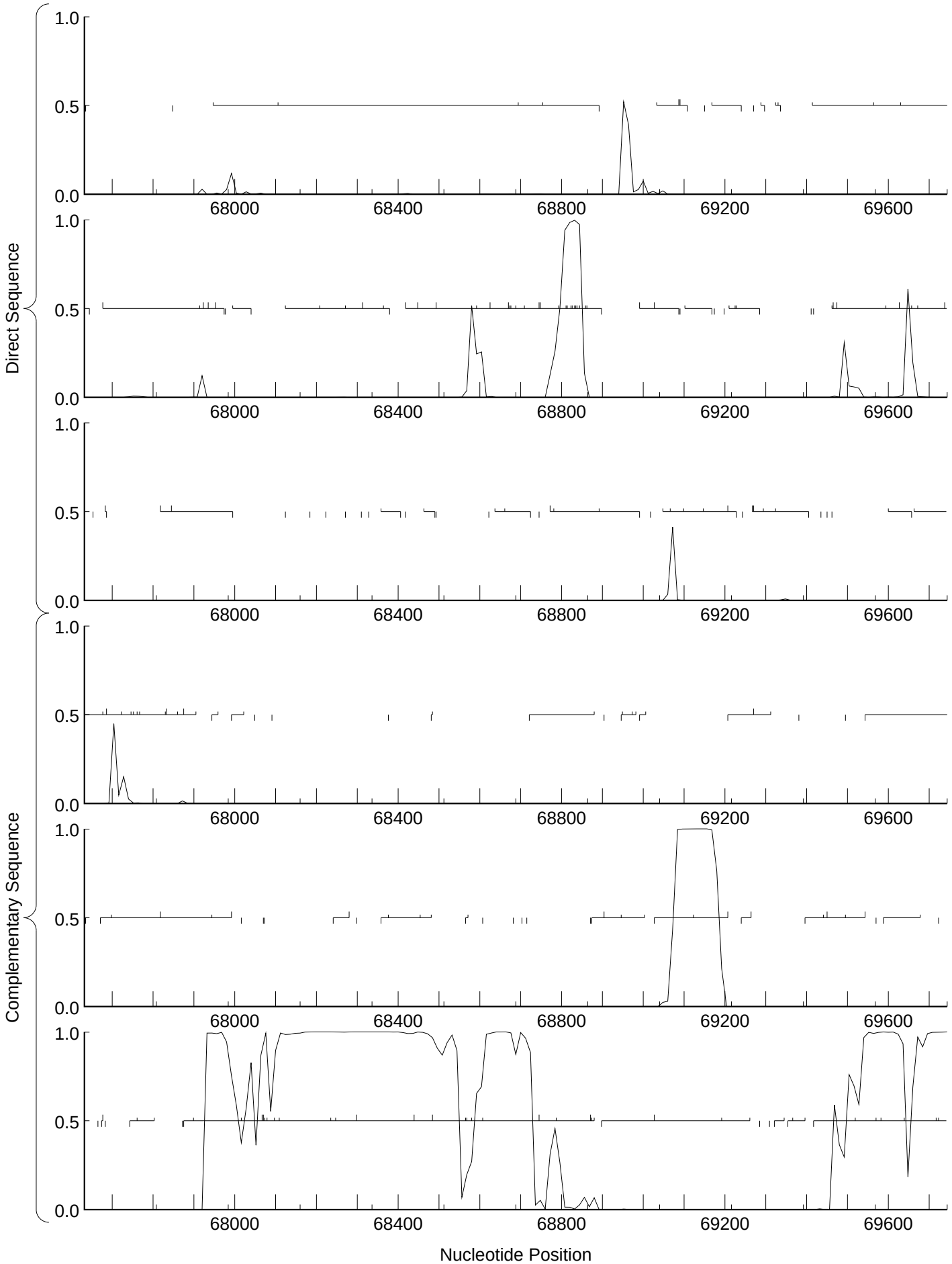


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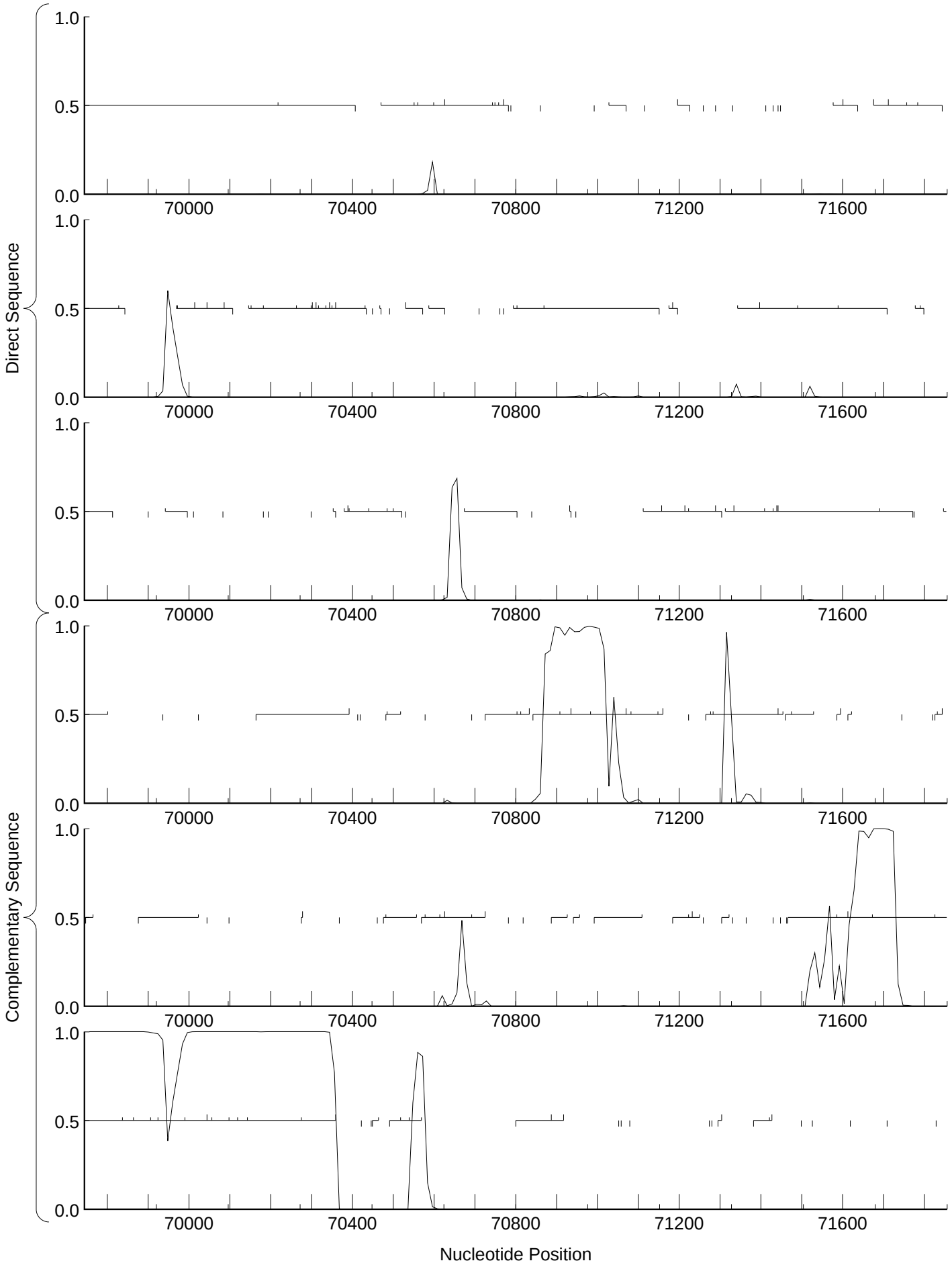


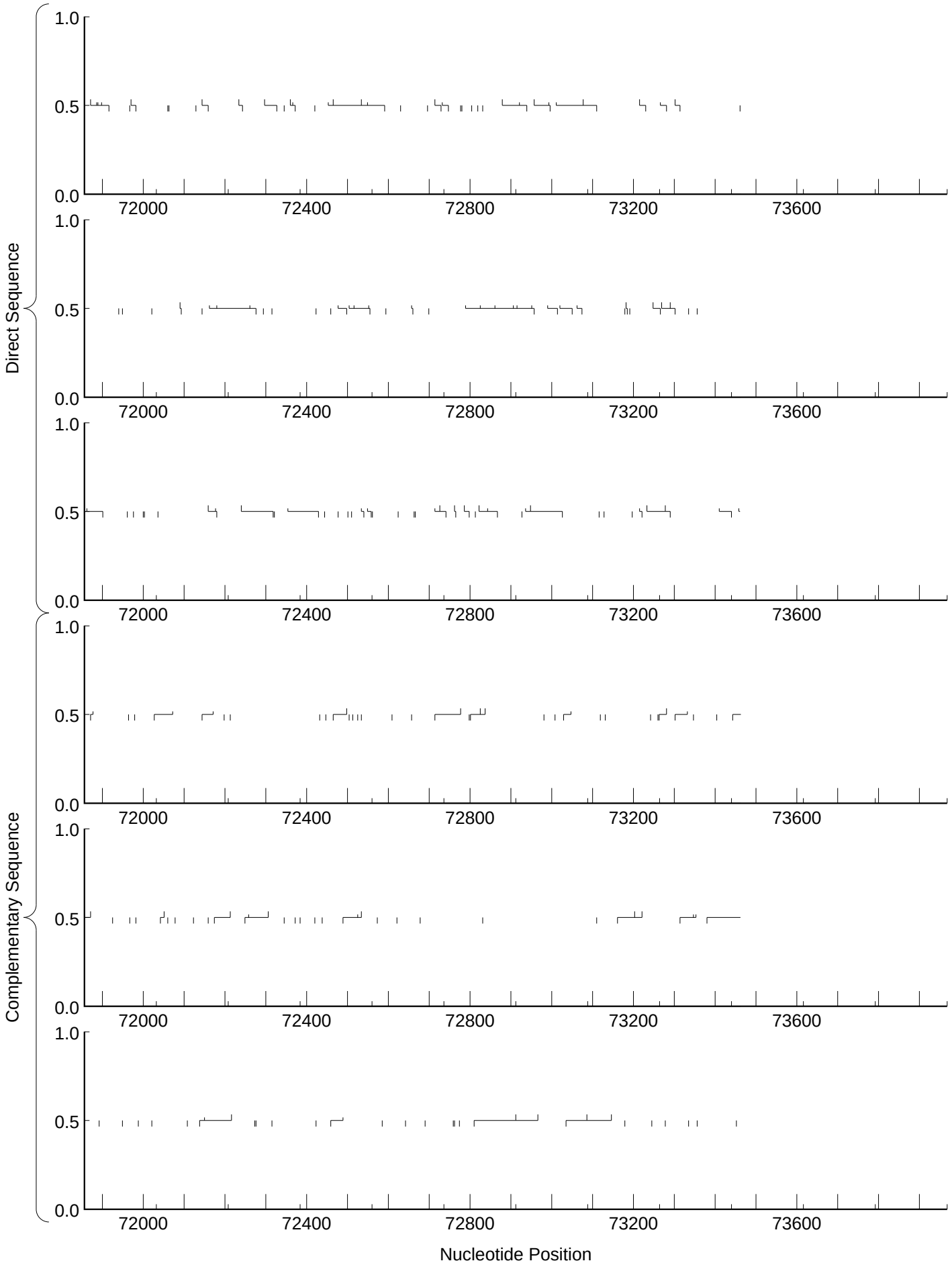
phage Harambe complete sequence, 73511 bp including 184 bp terminal repeat, Cluster CS, Order 4, Window 96, Step 12, 33/36




Direct Sequence
Complementary Sequence
1.0
0.5
0.0
68000
68400
68800
69200
69600
Nucleotide Position

phage Harambe complete sequence, 73511 bp including 184 bp terminal repeat, Cluster CS, 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