GeneMark

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

PROGRAM INFORMATION

```
Sequence         :  Streptomyces phage Wipeout complete sequence, 132935 bp including 12204 bp terminal repeat,
Analysis Date    :  3/29/24 at 1:45:26
Pages            :  64
Sequence Length  :  132935 bp
GC Content       :   49.34%

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

PS-Version       :  1.2

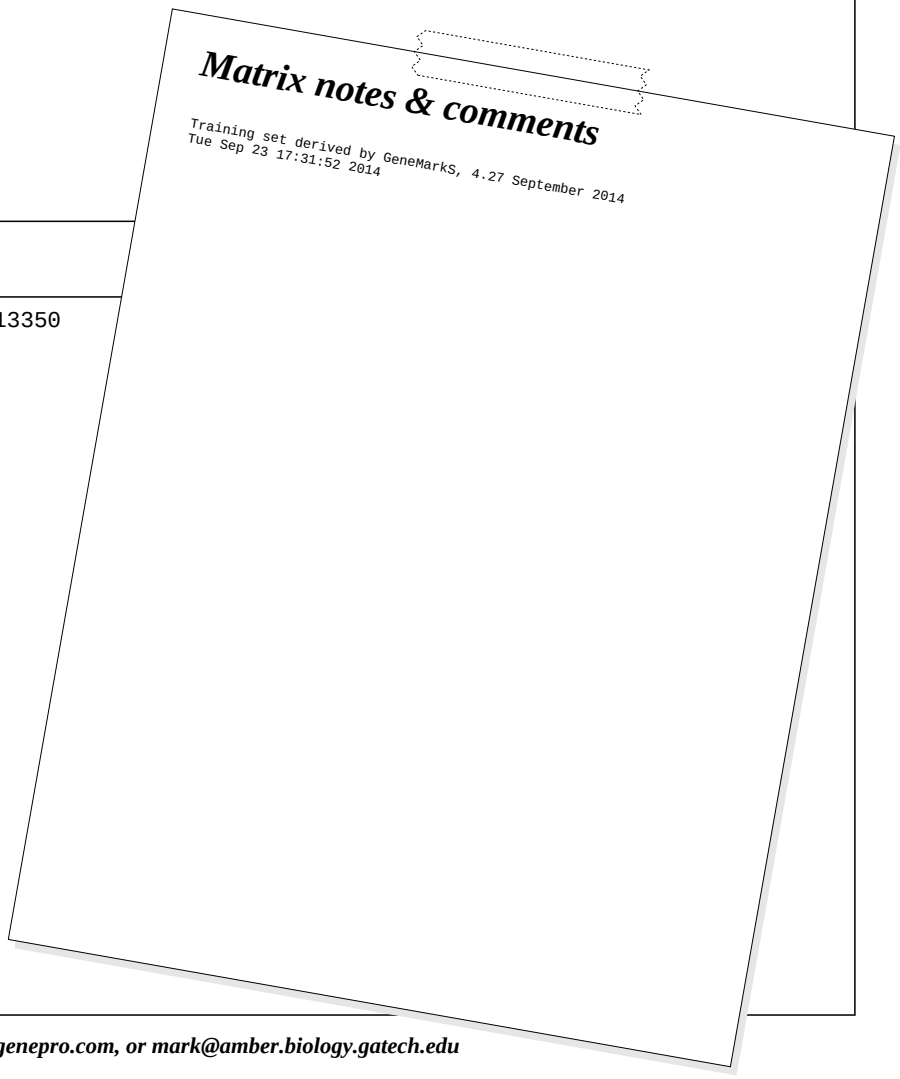
GeneMark Options :  PostScript graph,
                    Mark ORFs / splice sites,
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                    List regions and/or splice sites,
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MATRIX INFORMATION

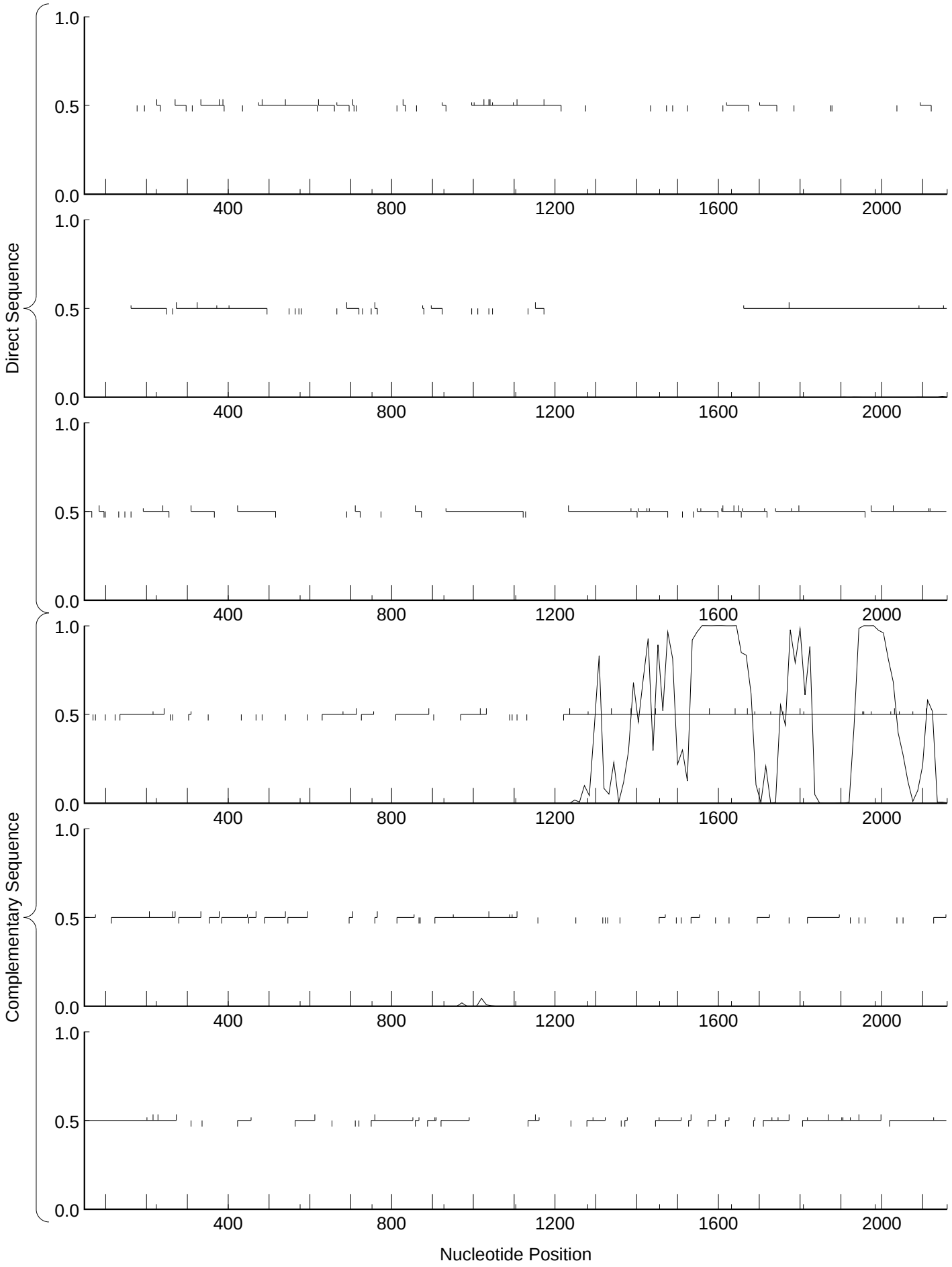
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Matrix     :  Streptomyces_griseus_NBRC_13350
Author     :  -

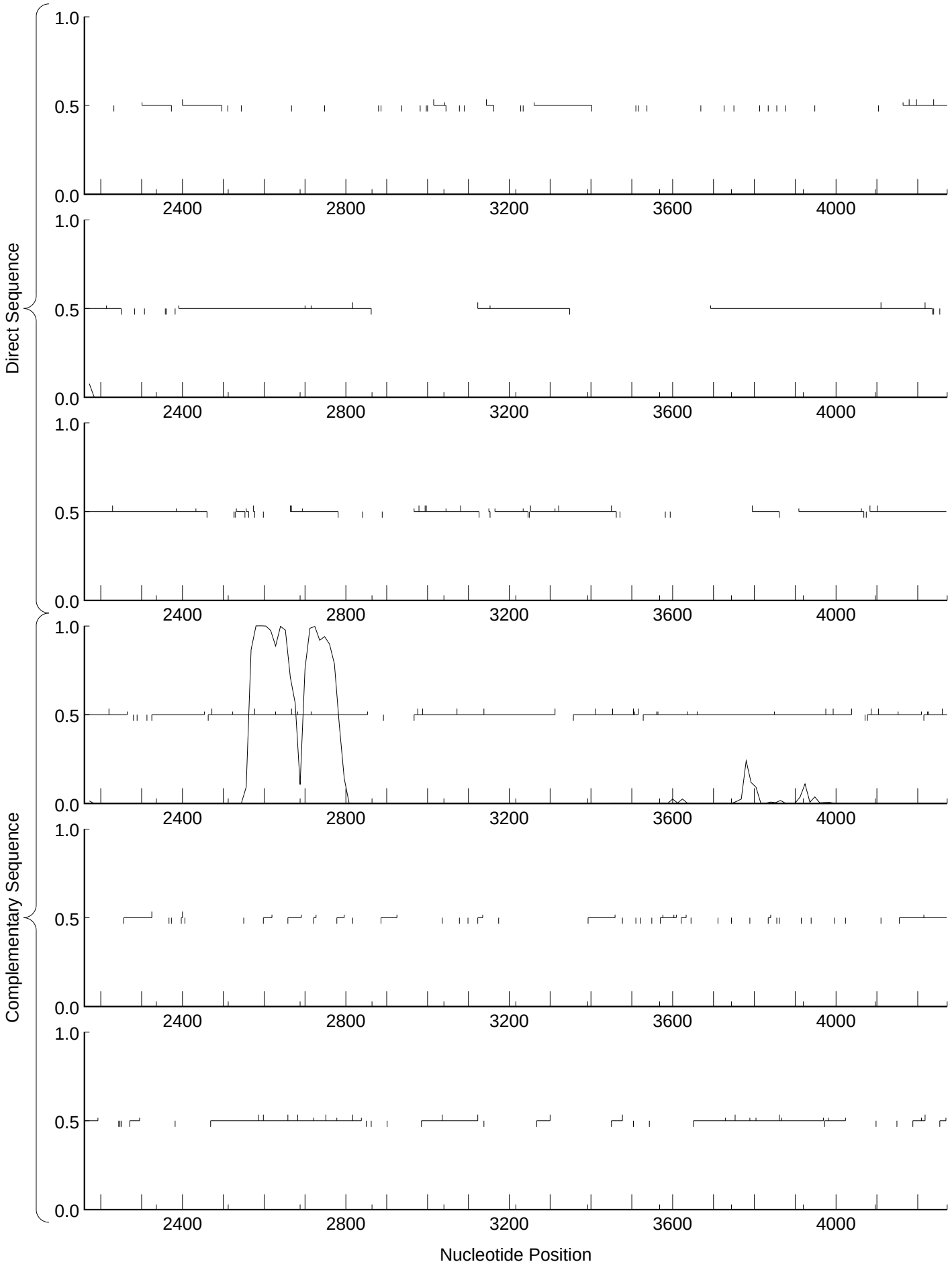
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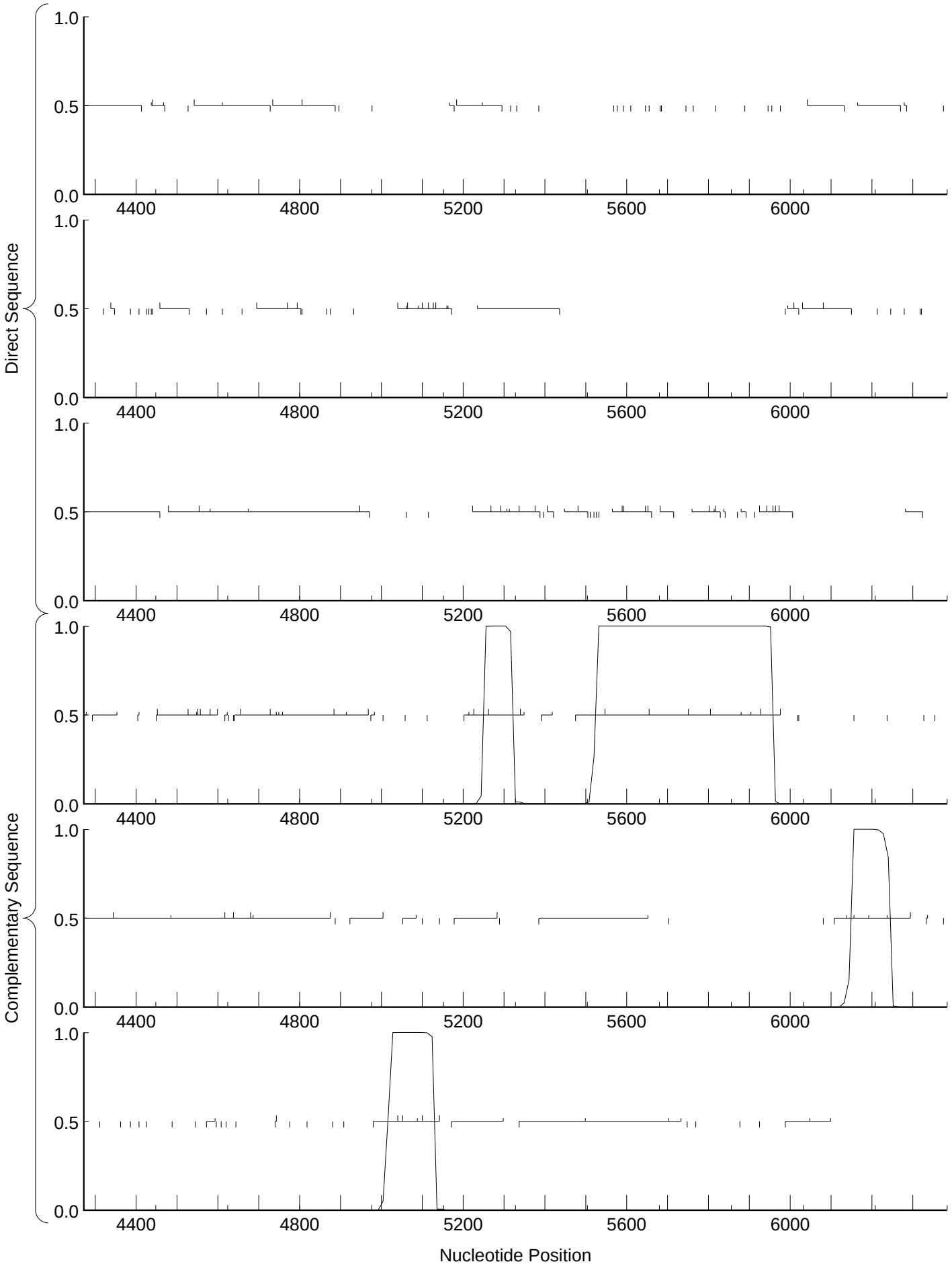

  Send questions / comments to:
      Dr. M. Borodovsky
      Georgia Institute of Technology
      School of Biology
      Atlanta, GA  30332-0230
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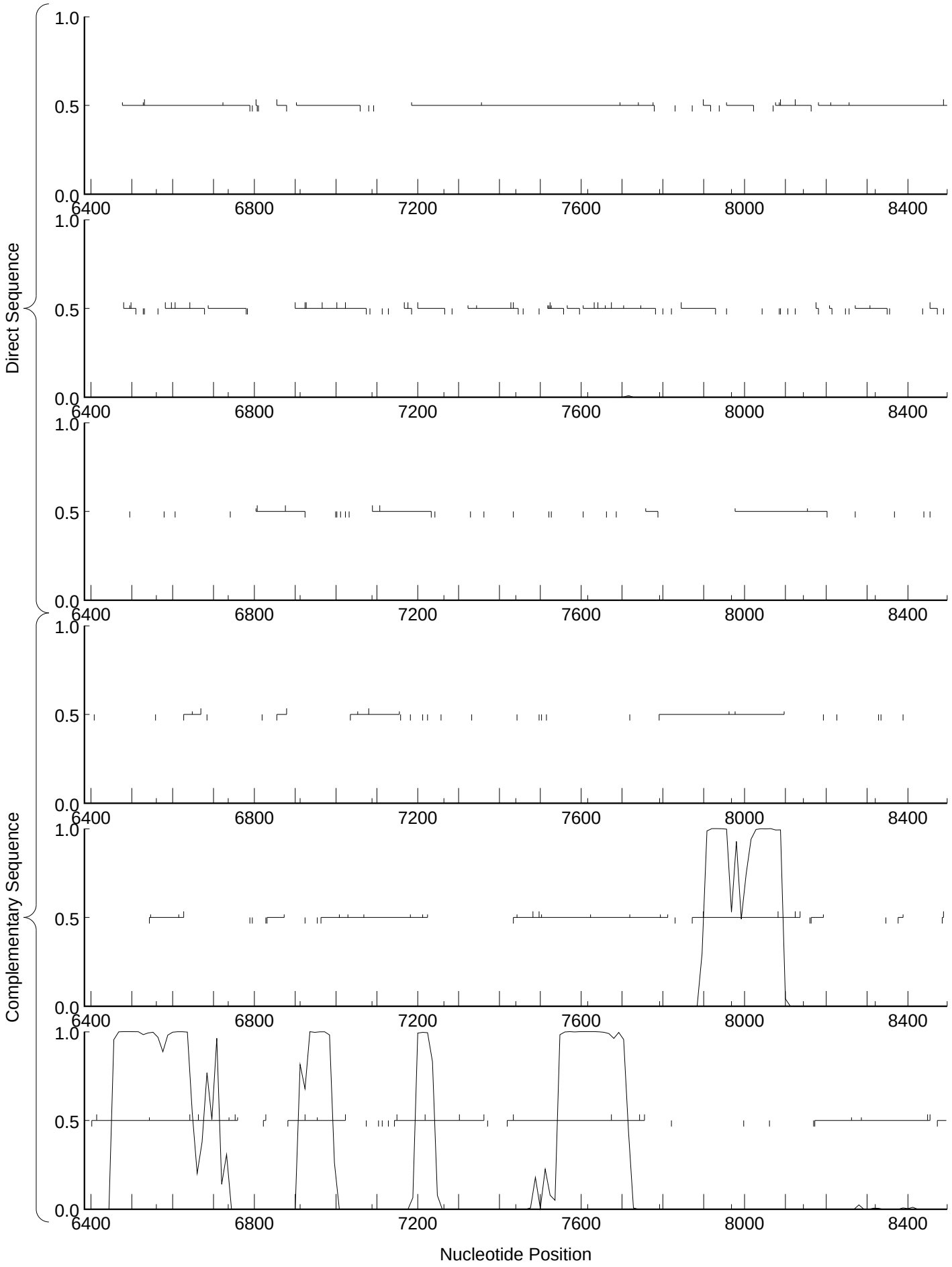


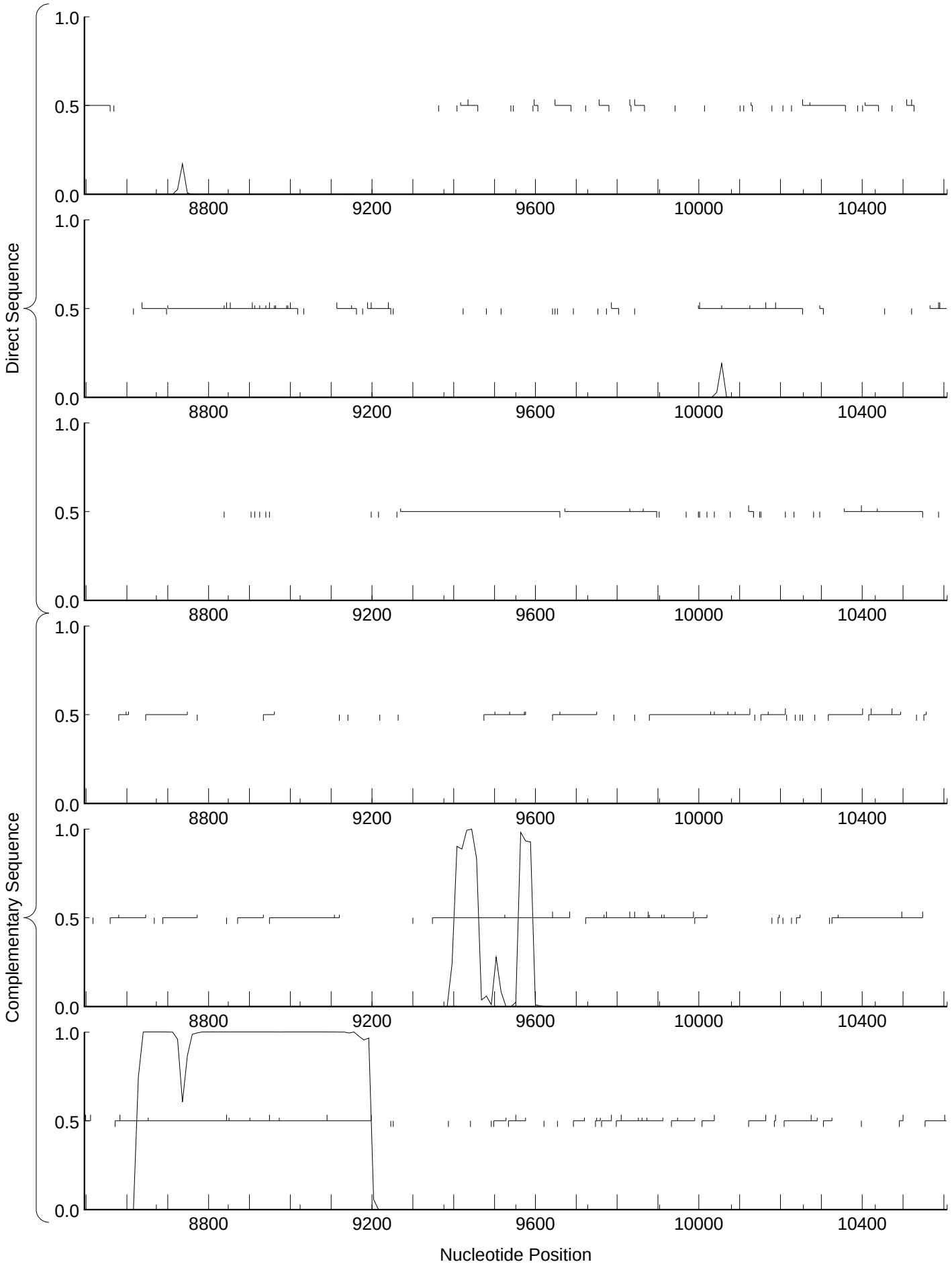
For help or information, send electronic mail to: custserv@genepro.com, or mark@amber.biology.gatech.edu

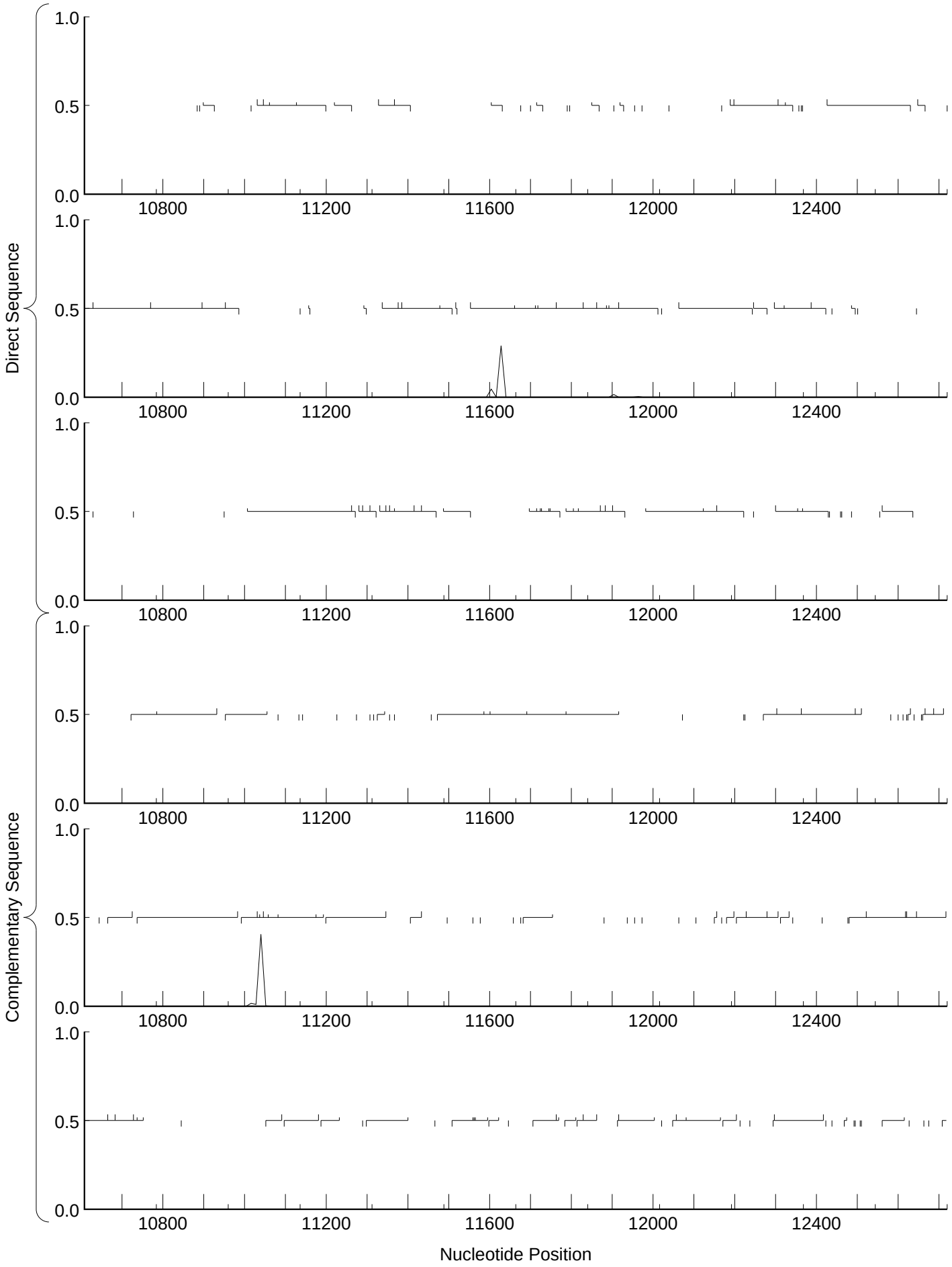

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800
1200
1600
2000
Nucleotide Position

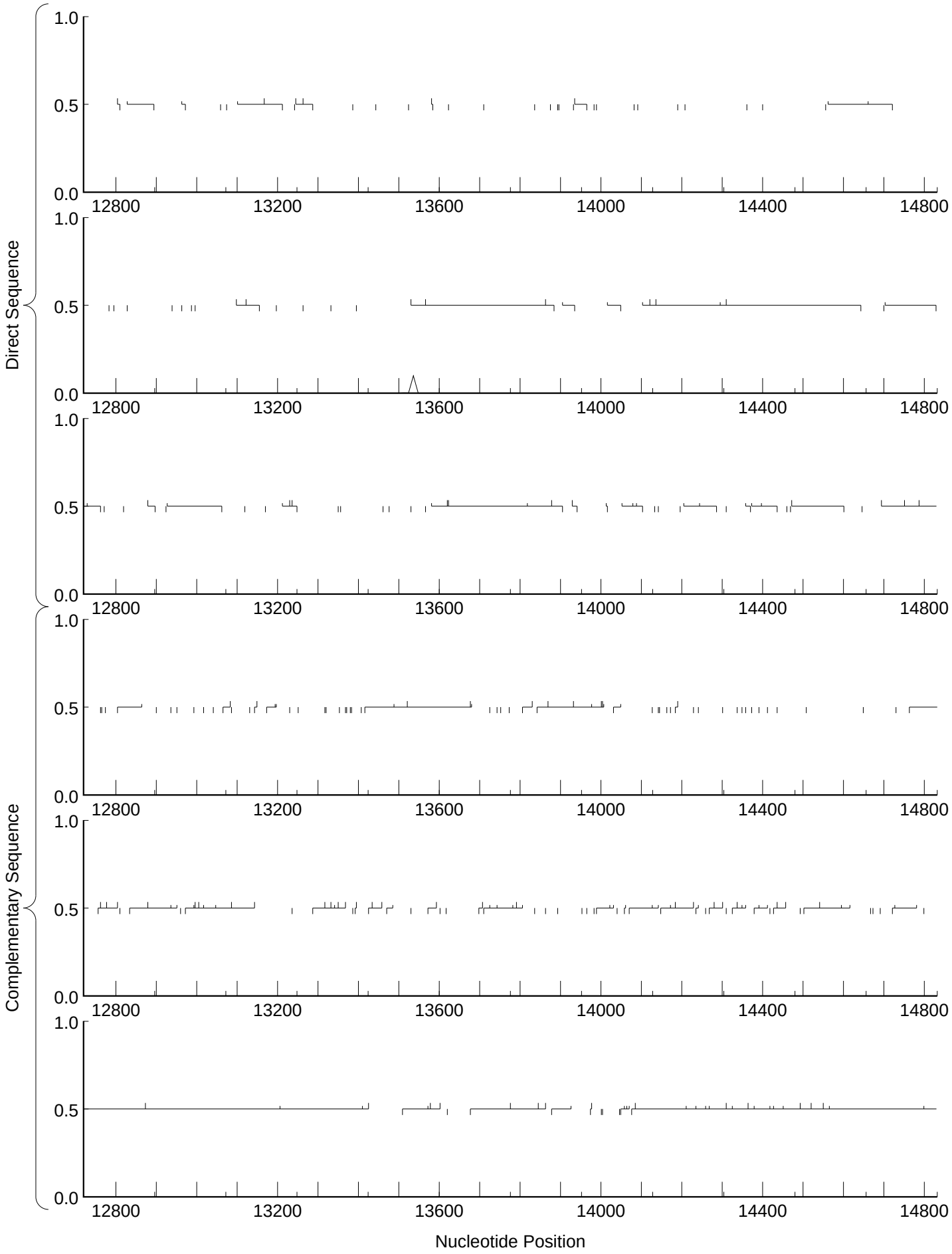

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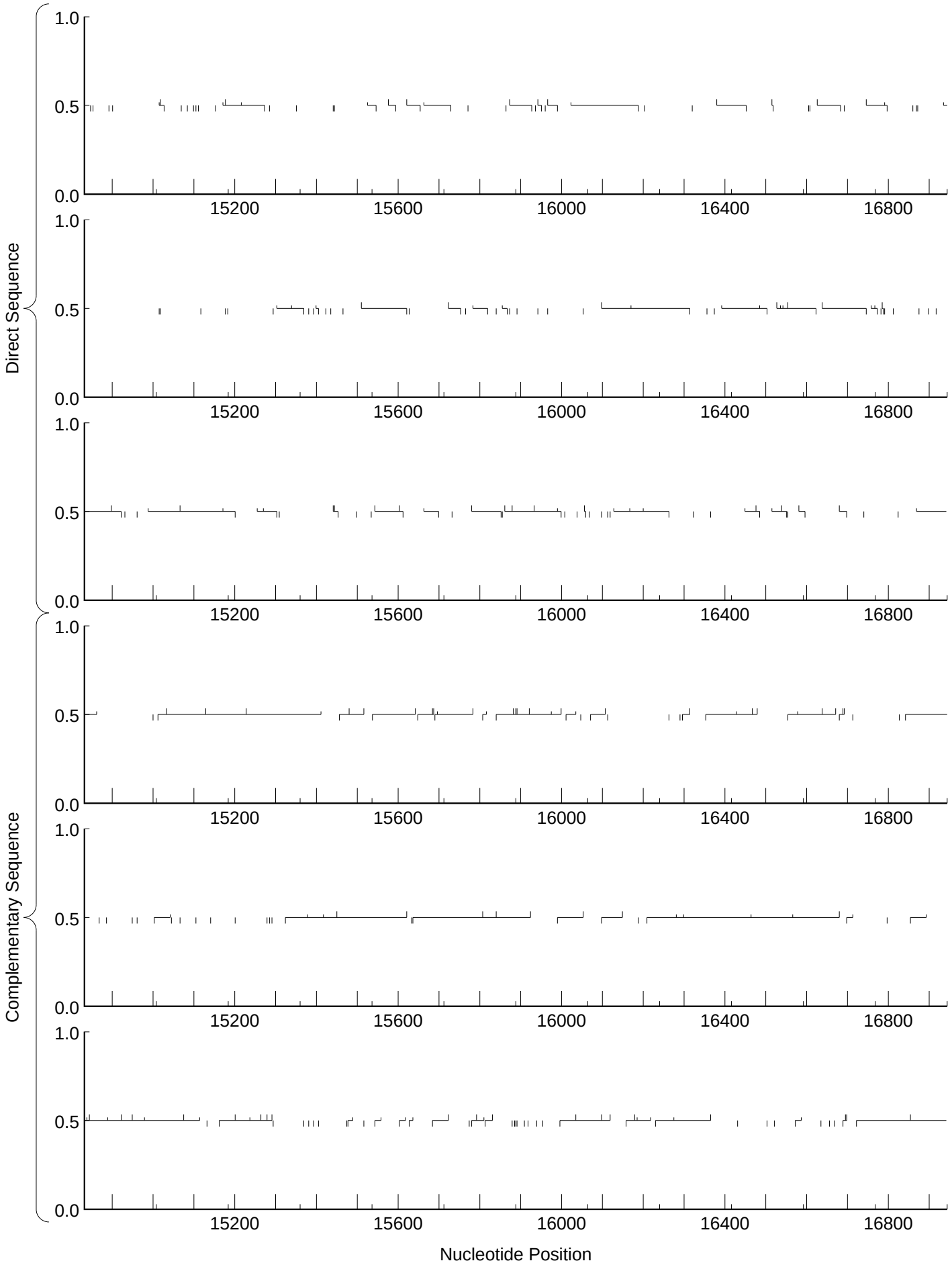

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Complementary Sequence
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5600
6000
Nucleotide Position

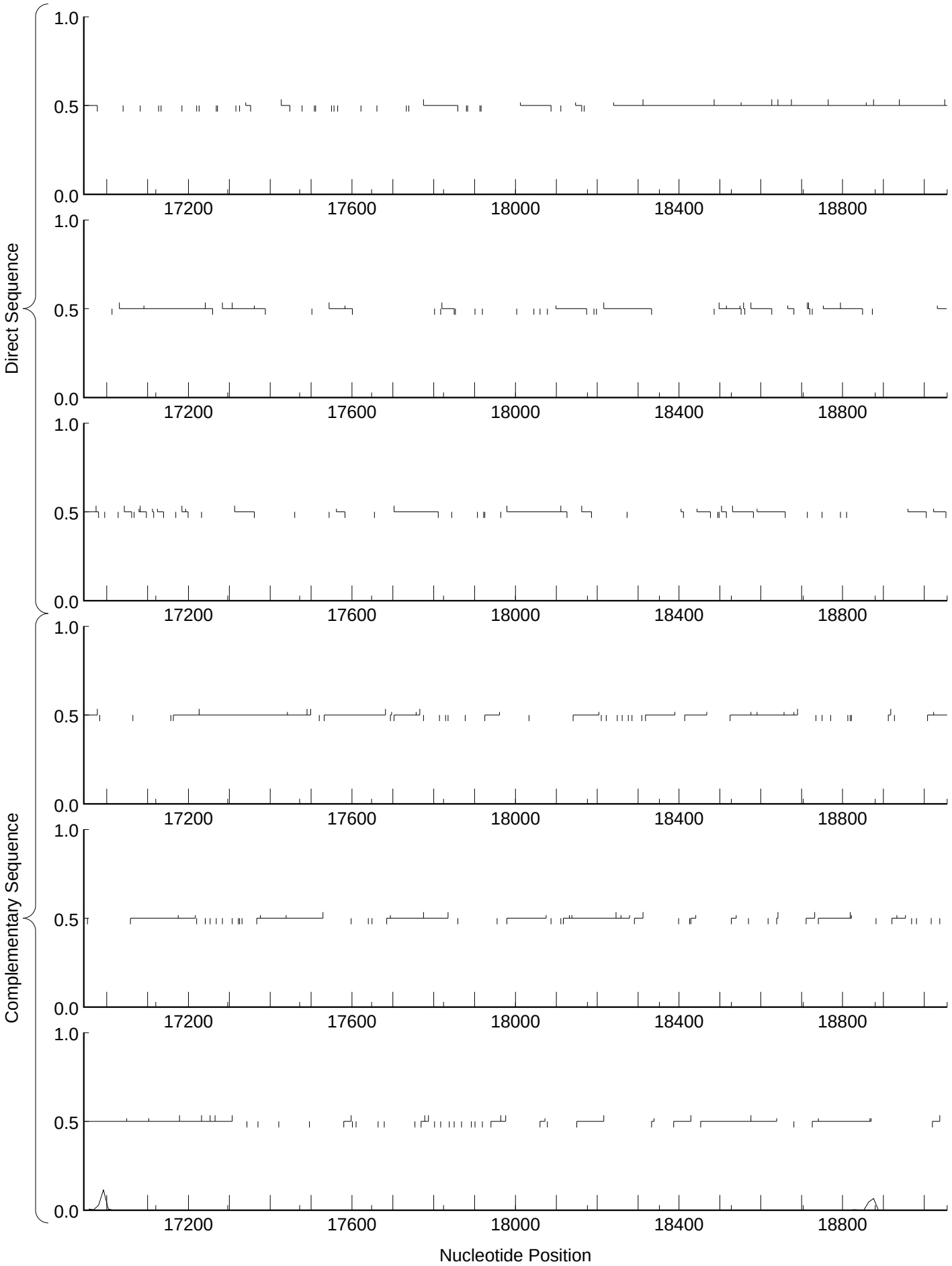

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Complementary Sequence
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0.5
0.0
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6800
7200
7600
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Direct Sequence
Complementary Sequence
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8800
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10000
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Nucleotide Position

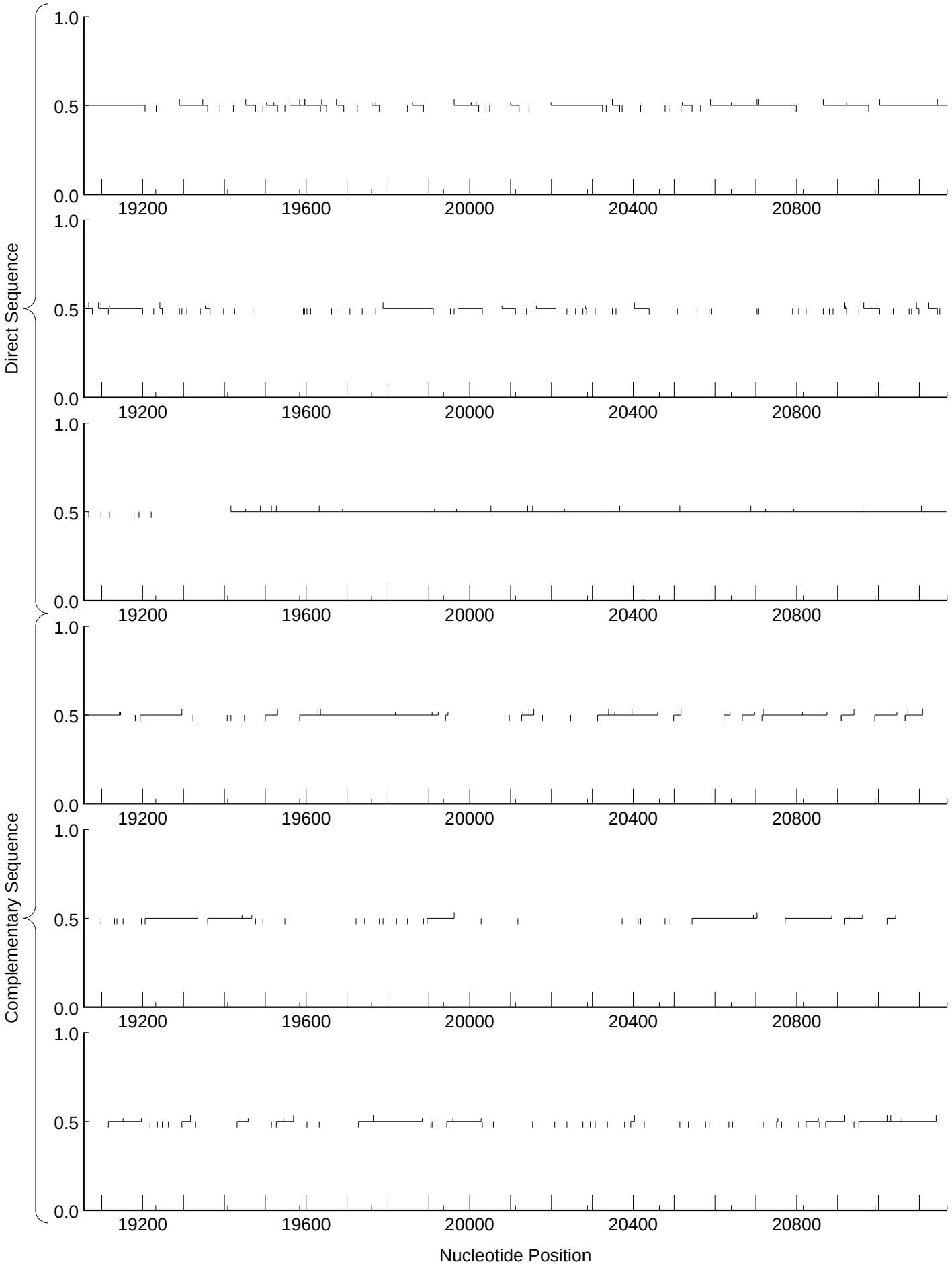

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Complementary Sequence
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Nucleotide Position

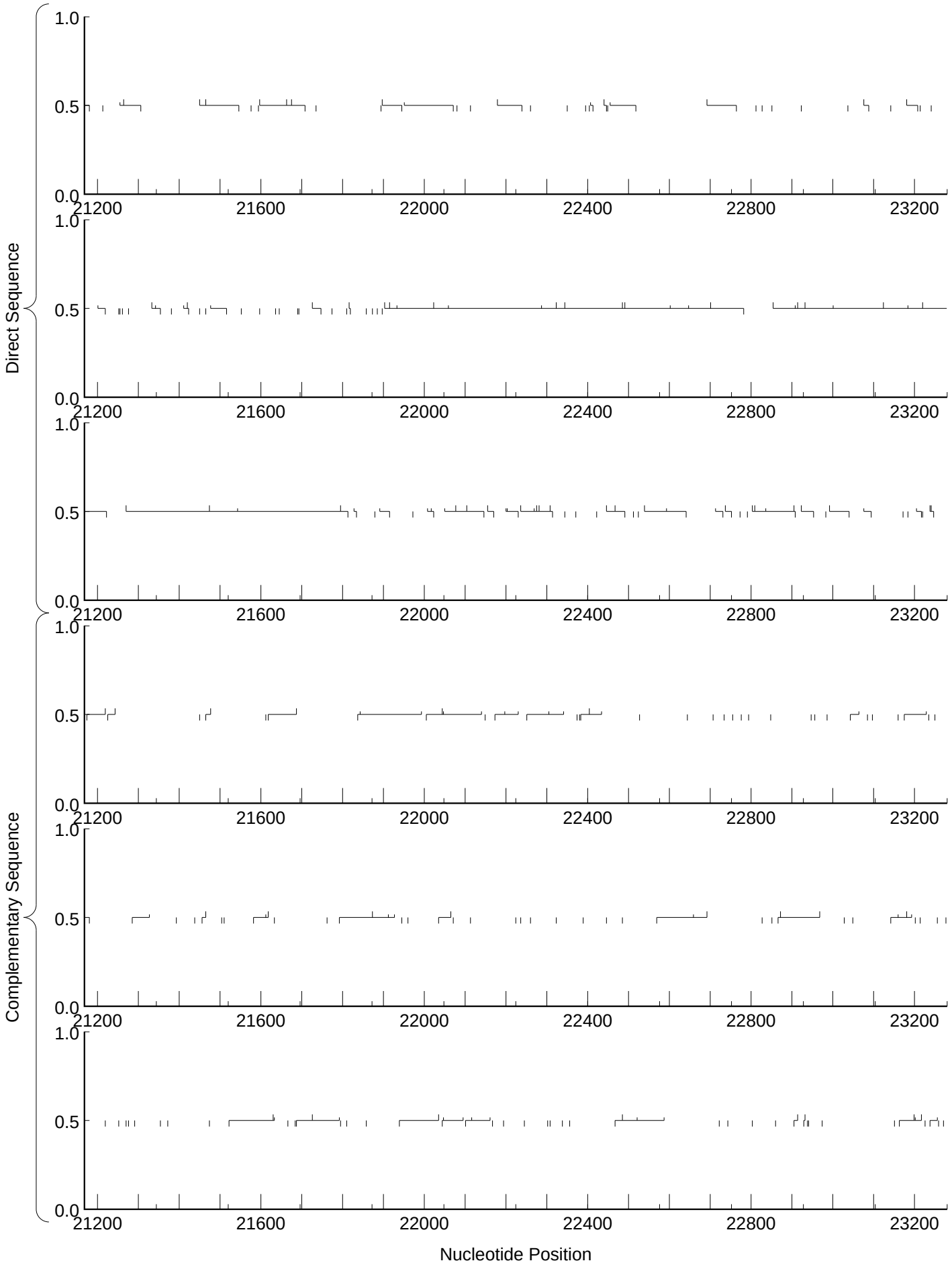

Direct Sequence
Complementary Sequence
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0.5
0.0
12800
13200
13600
14000
14400
14800
Nucleotide Position


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

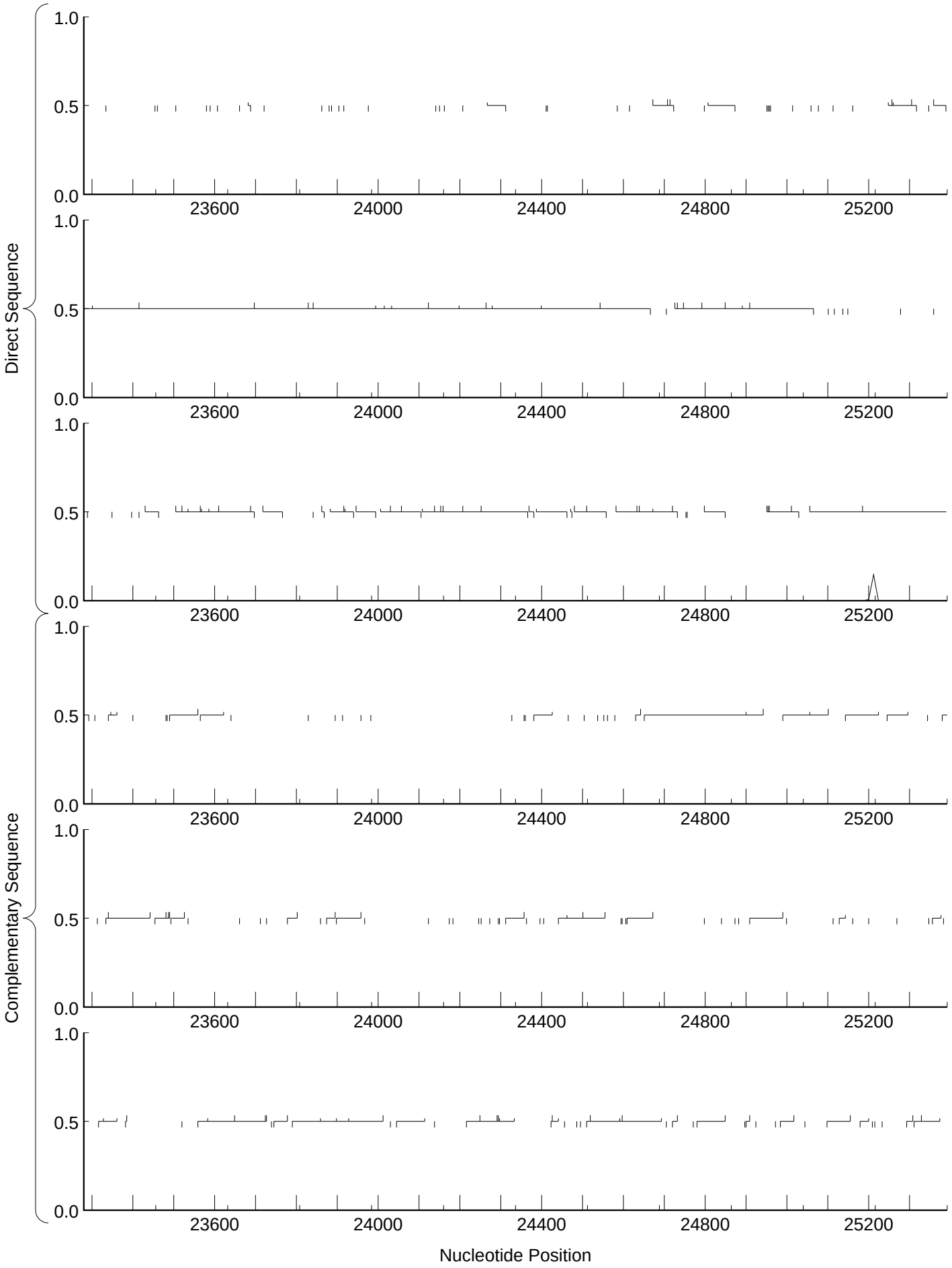

Direct Sequence
Complementary Sequence
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0.5
0.0
17200
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18400
18800
Nucleotide Position

ge Wipeout complete sequence, 132935 bp including 12204 bp terminal repeat, Cluster BE2, Order 4, Window 96, Step 12, 11/64

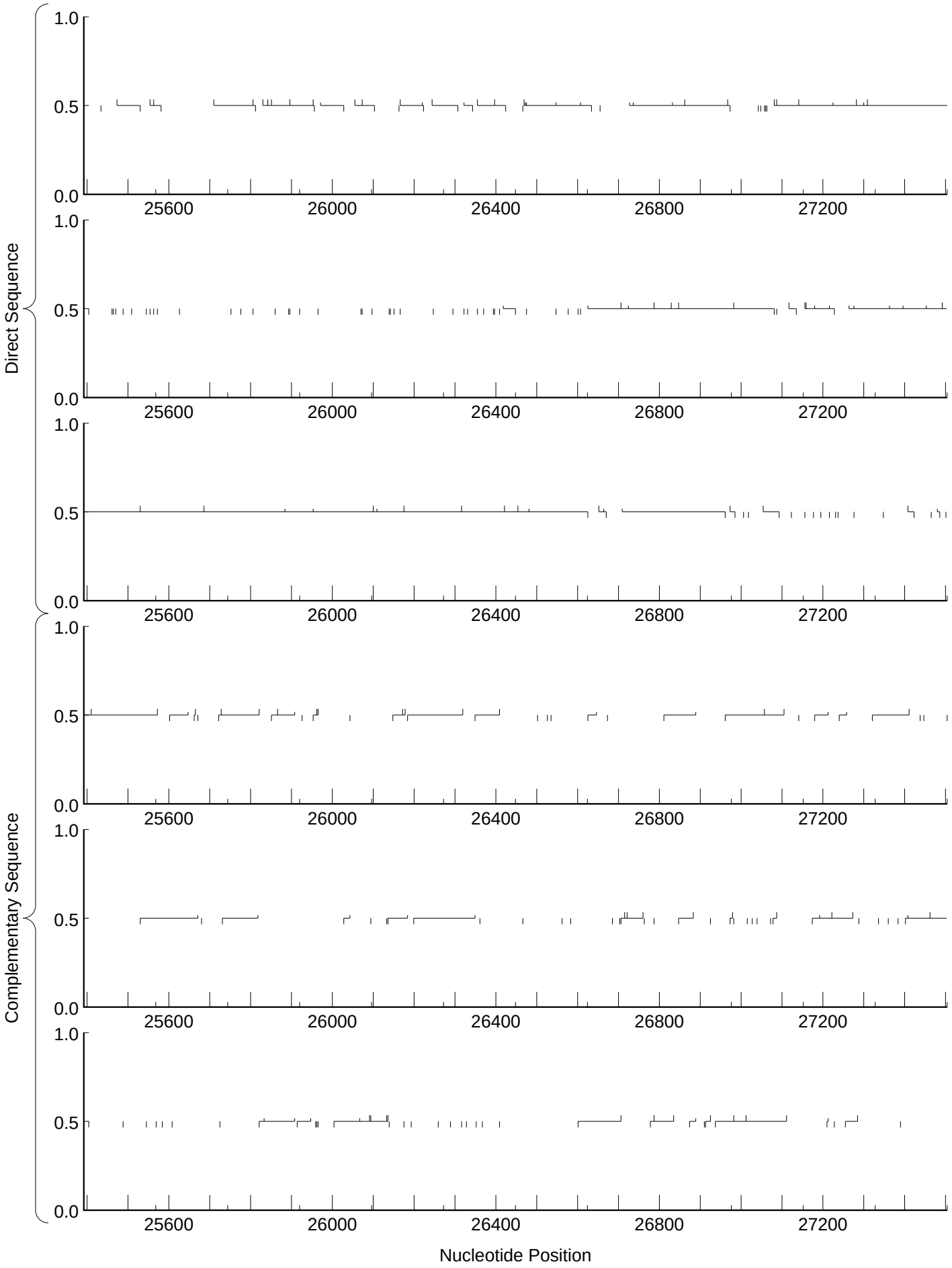


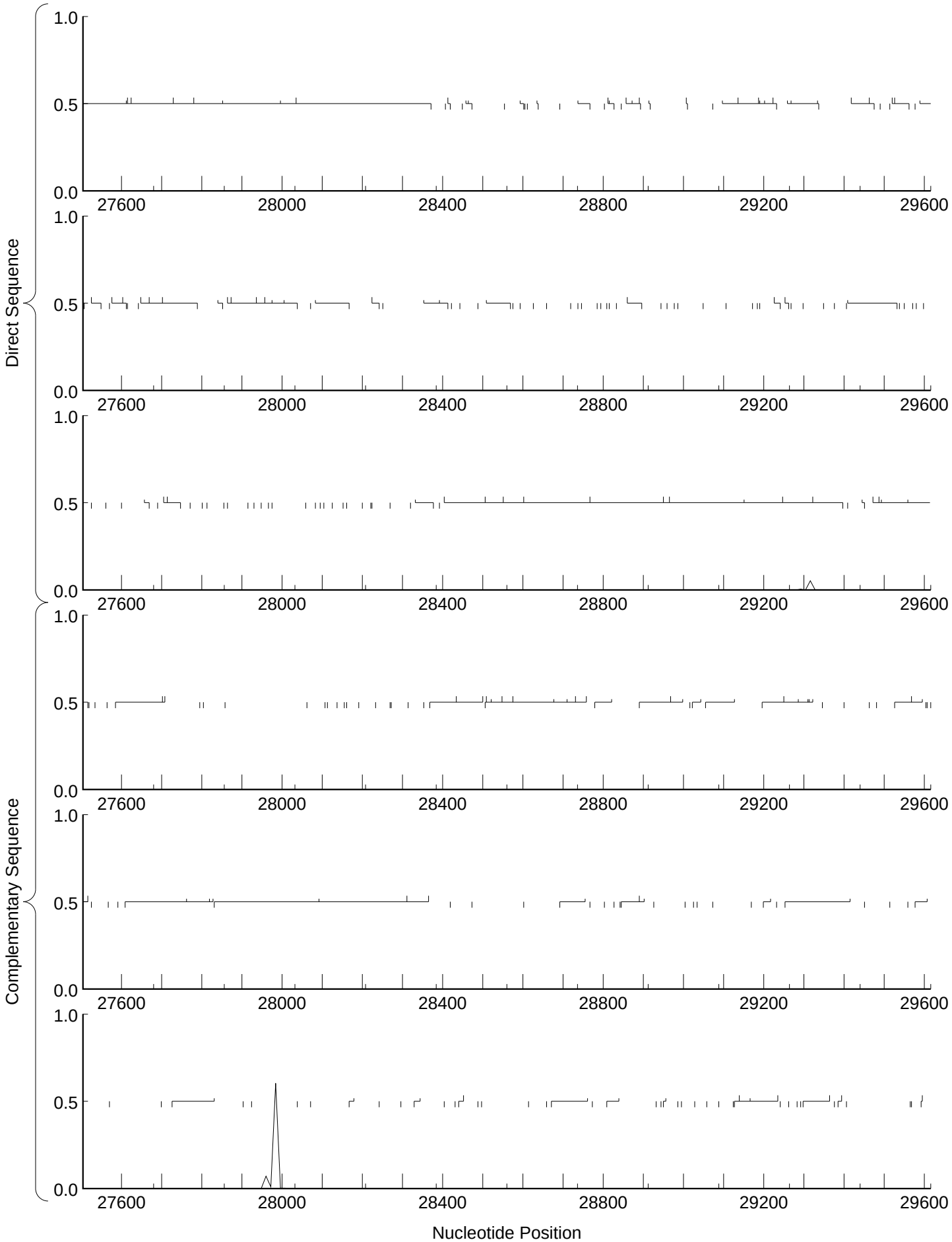

Direct Sequence
Complementary Sequence
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0.5
0.0
21200
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22800
23200
Nucleotide Position

ge Wipeout complete sequence, 132935 bp including 12204 bp terminal repeat, Cluster BE2, Order 4, Window 96, Step 12, 13/64

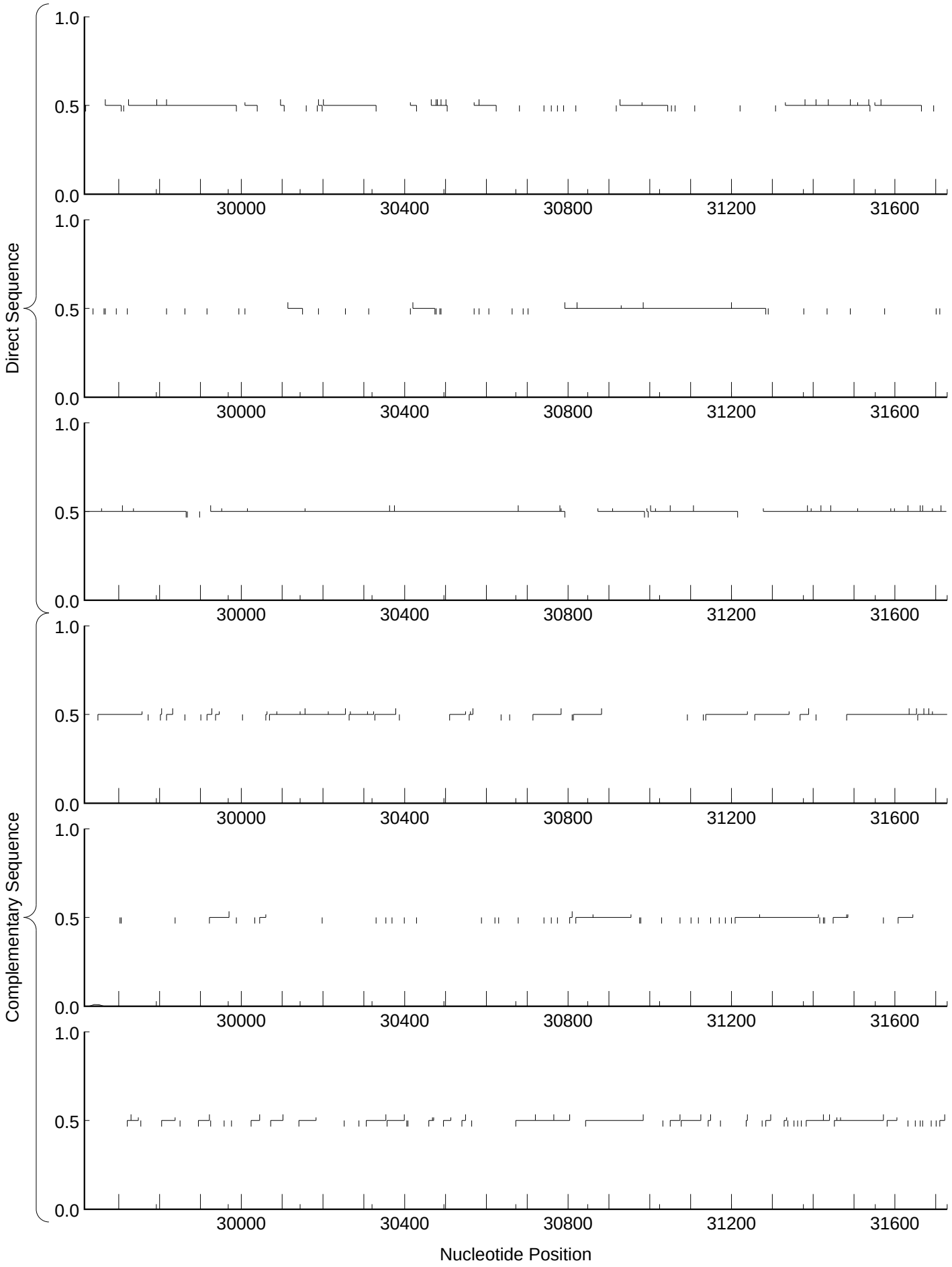


ge Wipeout complete sequence, 132935 bp including 12204 bp terminal repeat, Cluster BE2, Order 4, Window 96, Step 12, 14/64

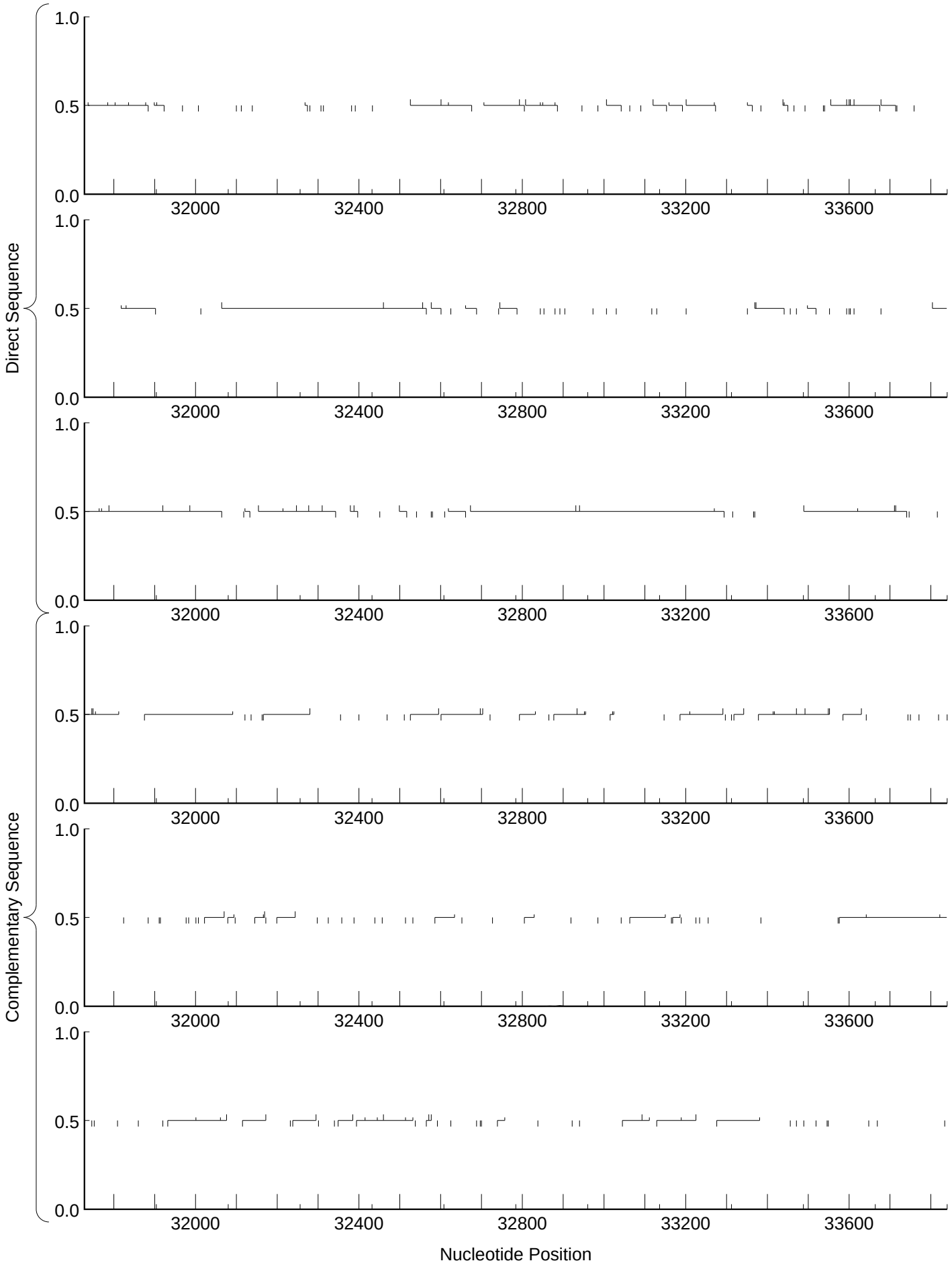


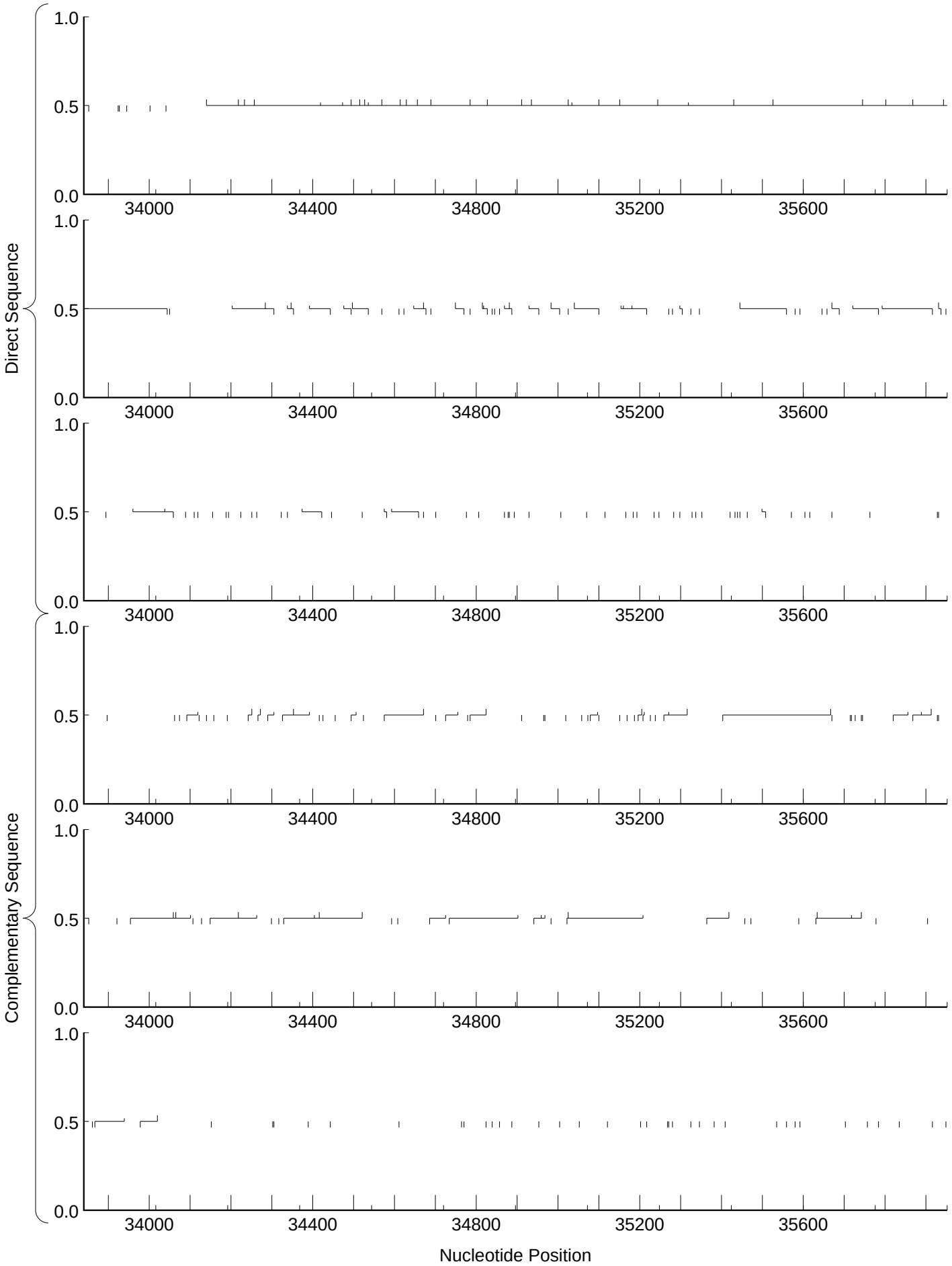

Direct Sequence
Complementary Sequence
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0.0
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28800
29200
29600
Nucleotide Position

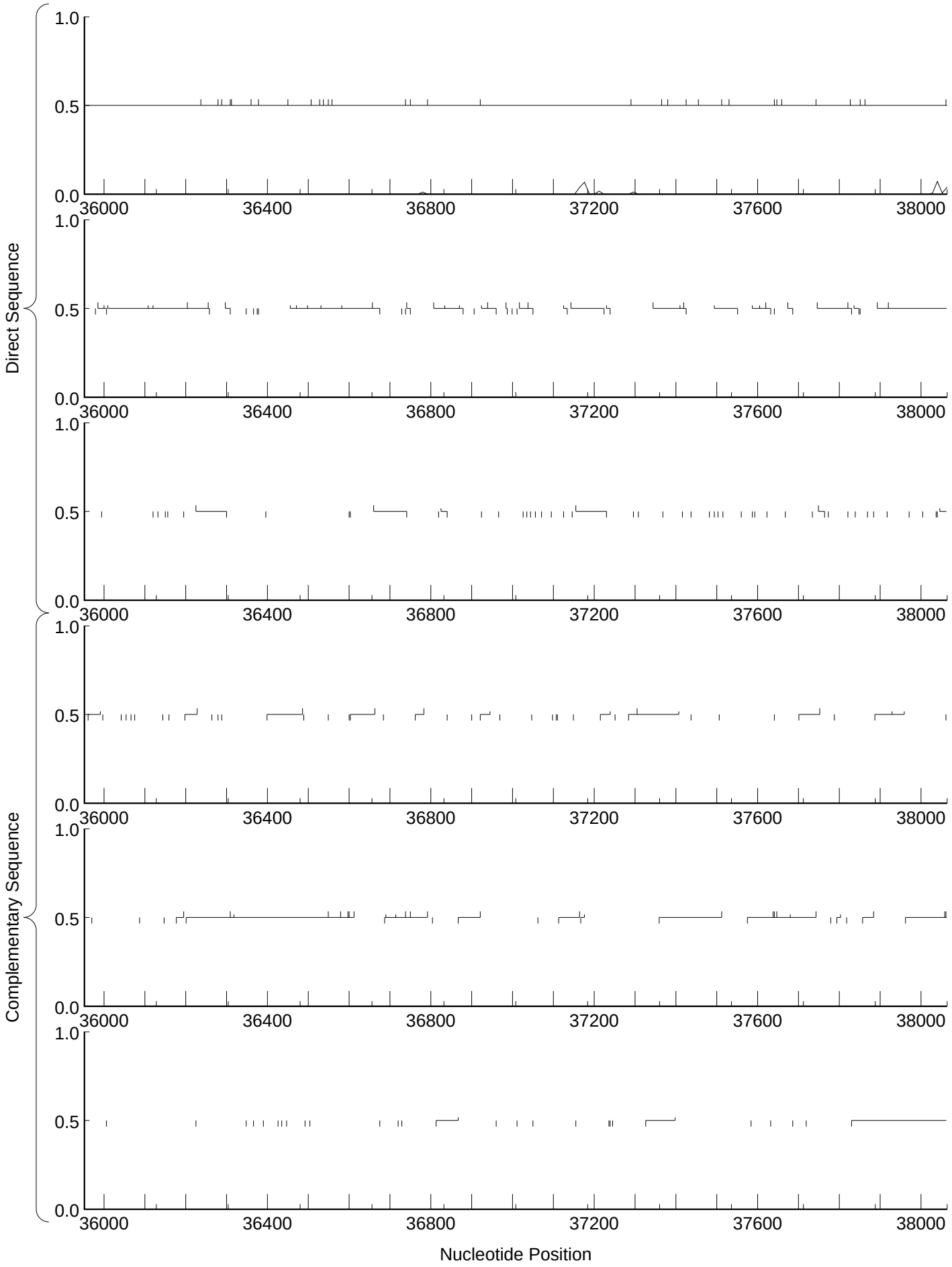
ge Wipeout complete sequence, 132935 bp including 12204 bp terminal repeat, Cluster BE2, Order 4, Window 96, Step 12, 16/64

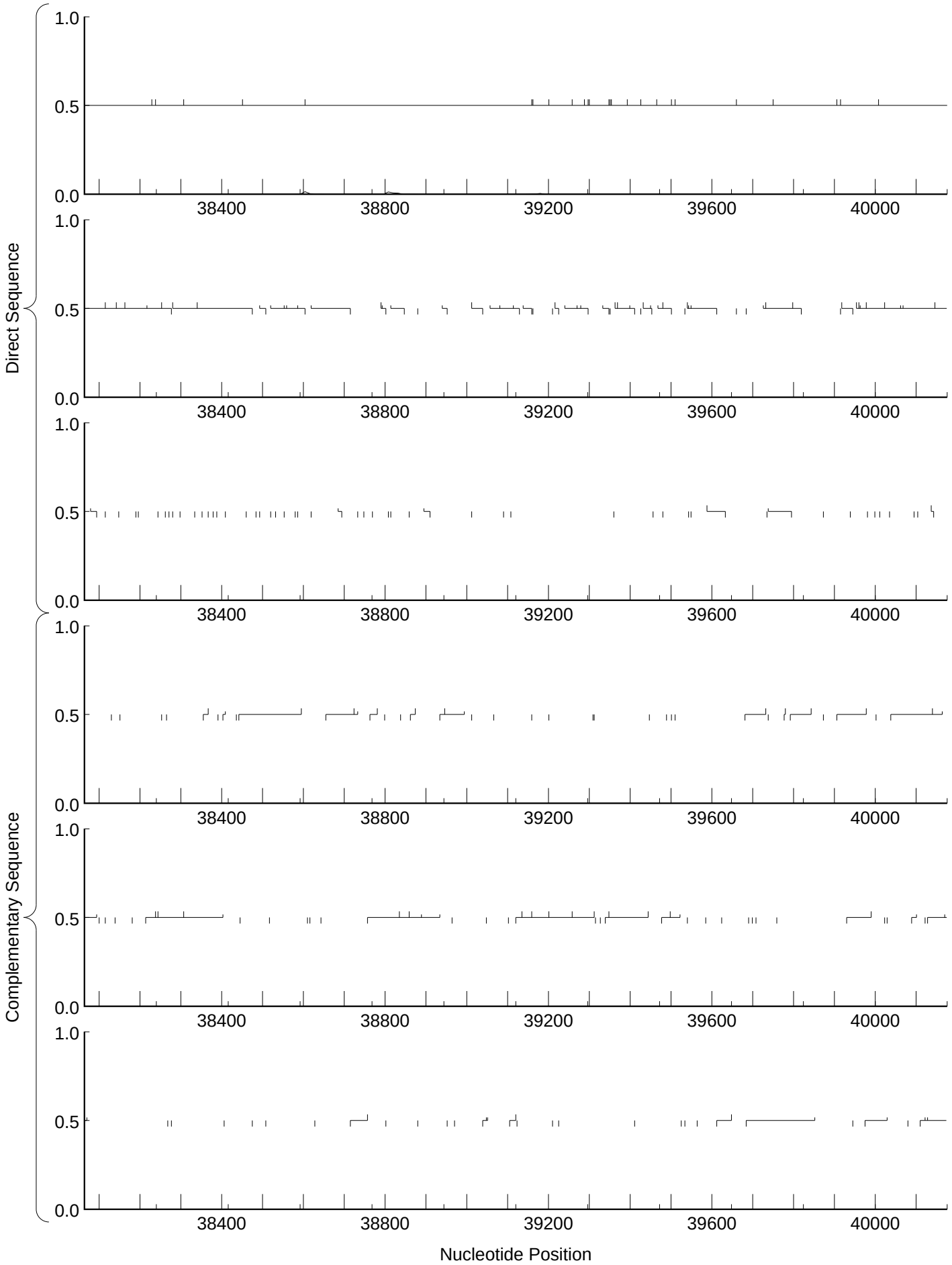


ge Wipeout complete sequence, 132935 bp including 12204 bp terminal repeat, Cluster BE2, Order 4, Window 96, Step 12, 17/64

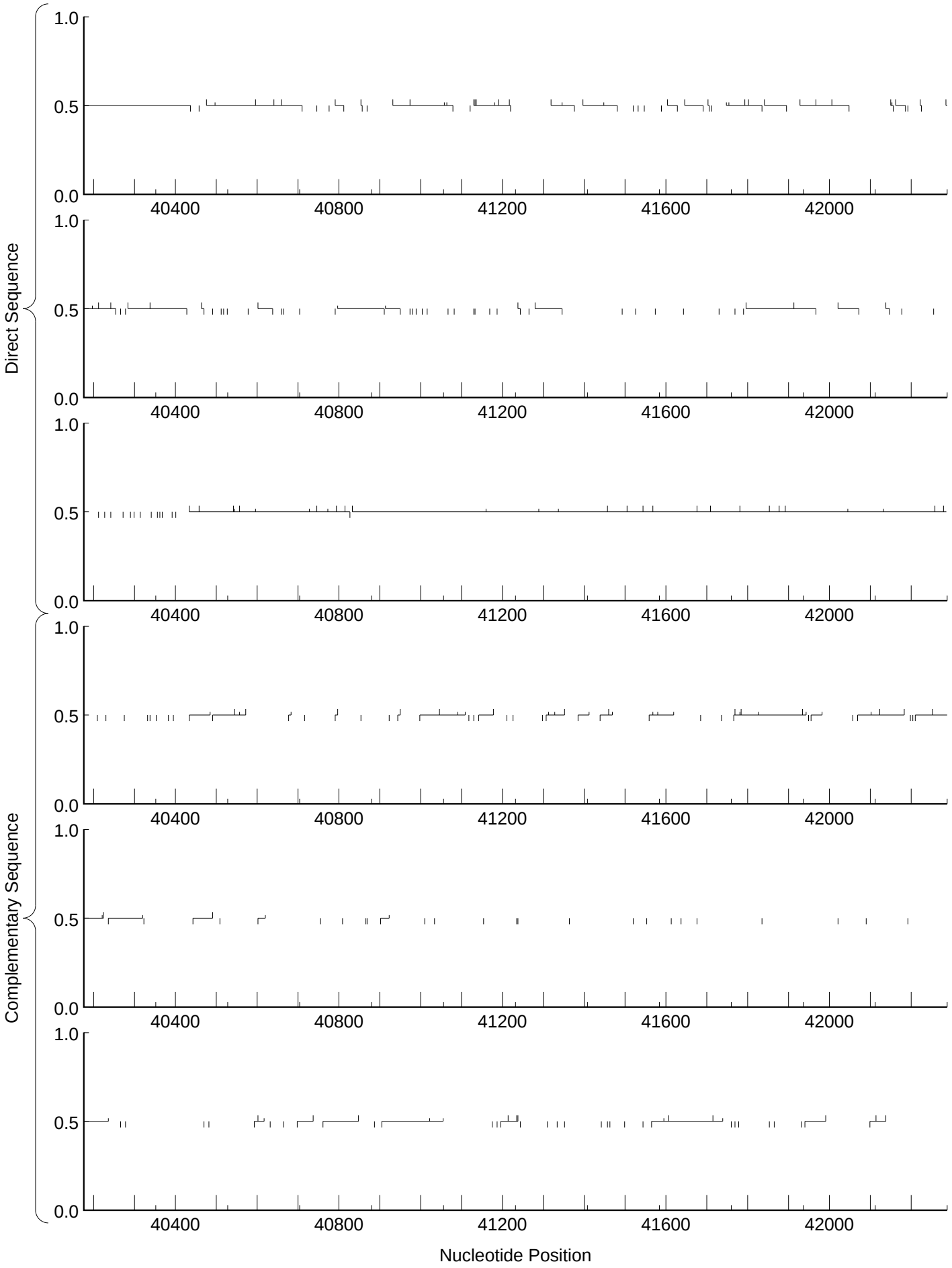



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Complementary Sequence
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34800
35200
35600
Nucleotide Position

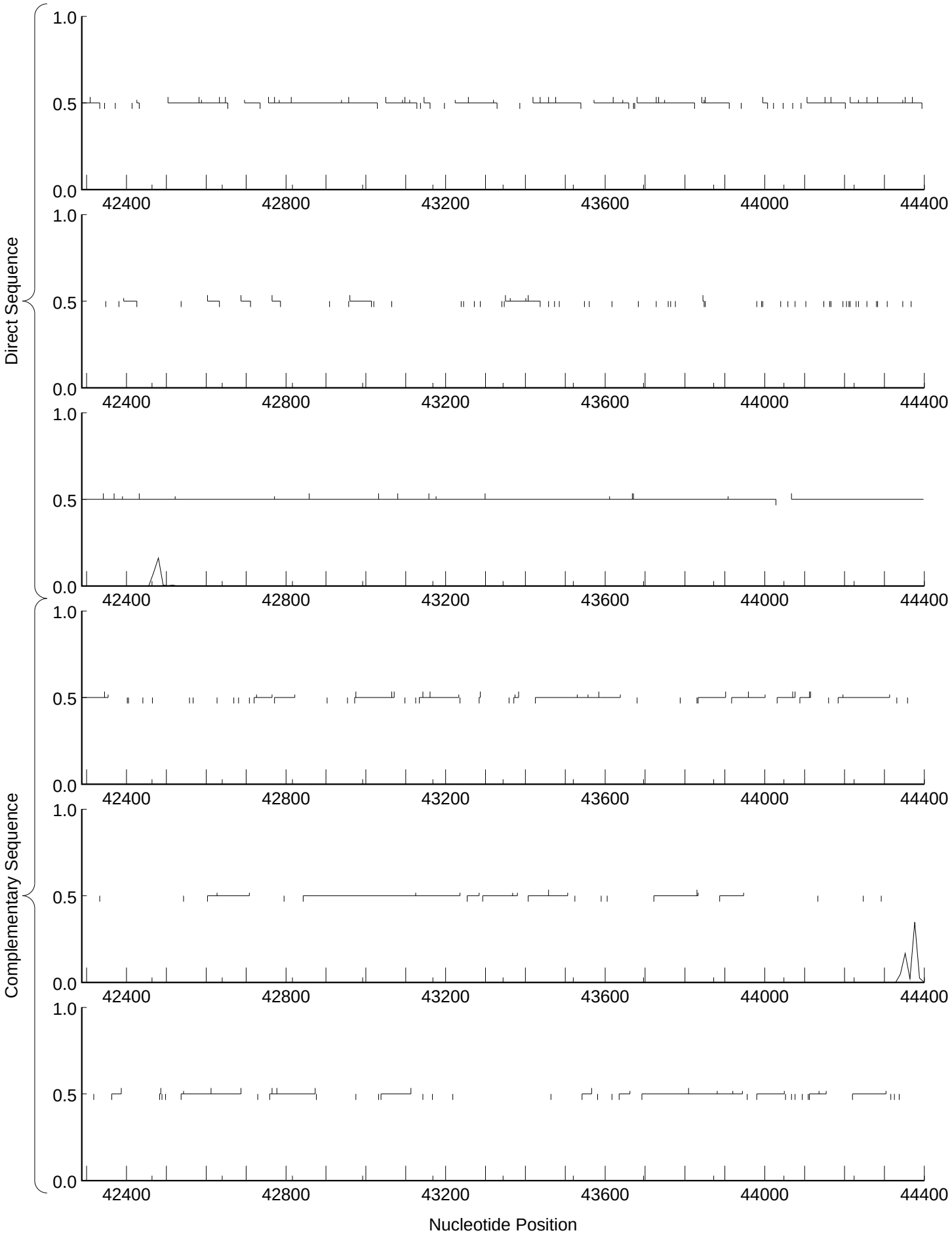

Direct Sequence
Complementary Sequence
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0.0
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36400
36800
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37600
38000
Nucleotide Position

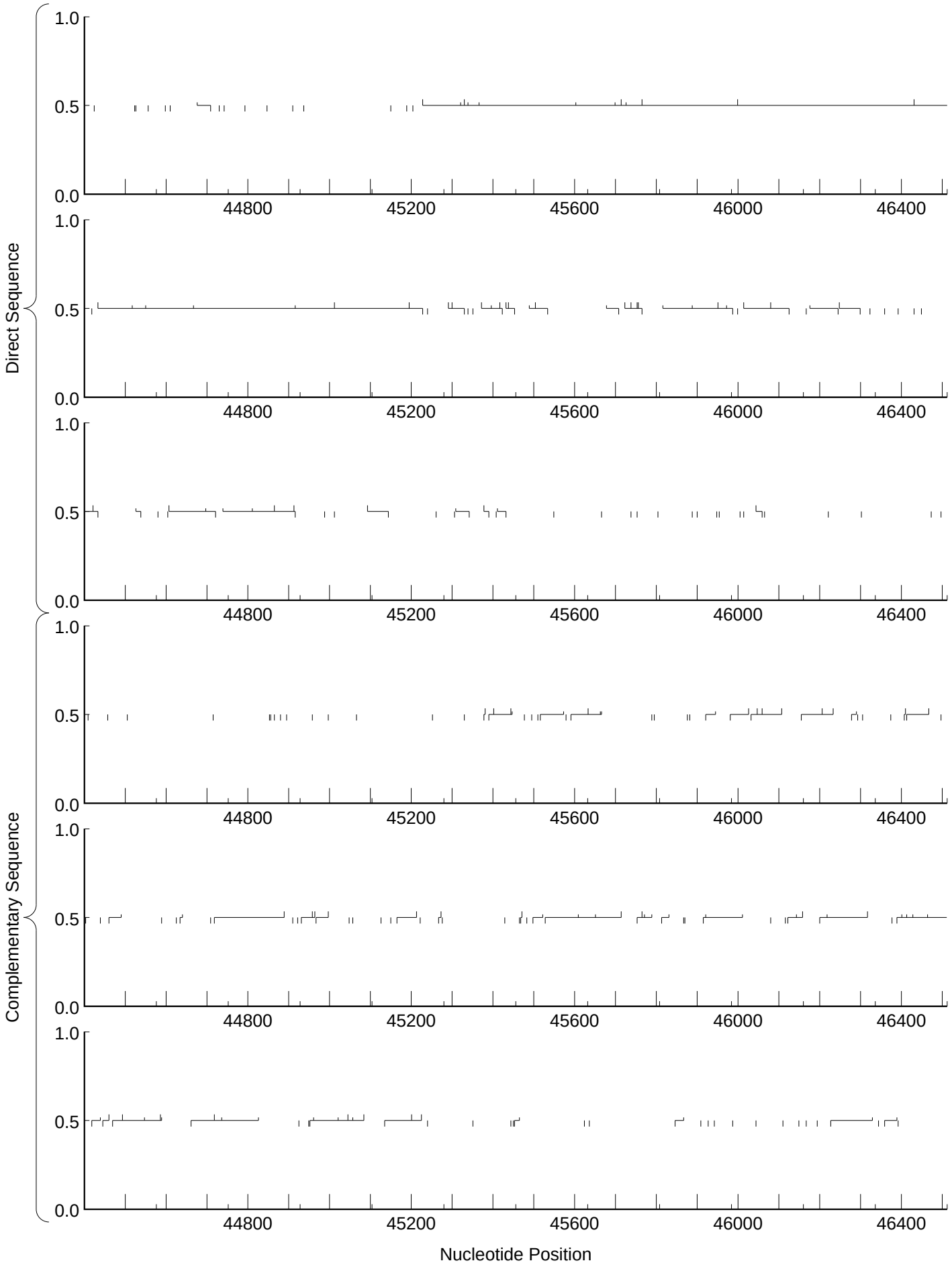

Direct Sequence
Complementary Sequence
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0.0
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39600
40000
Nucleotide Position

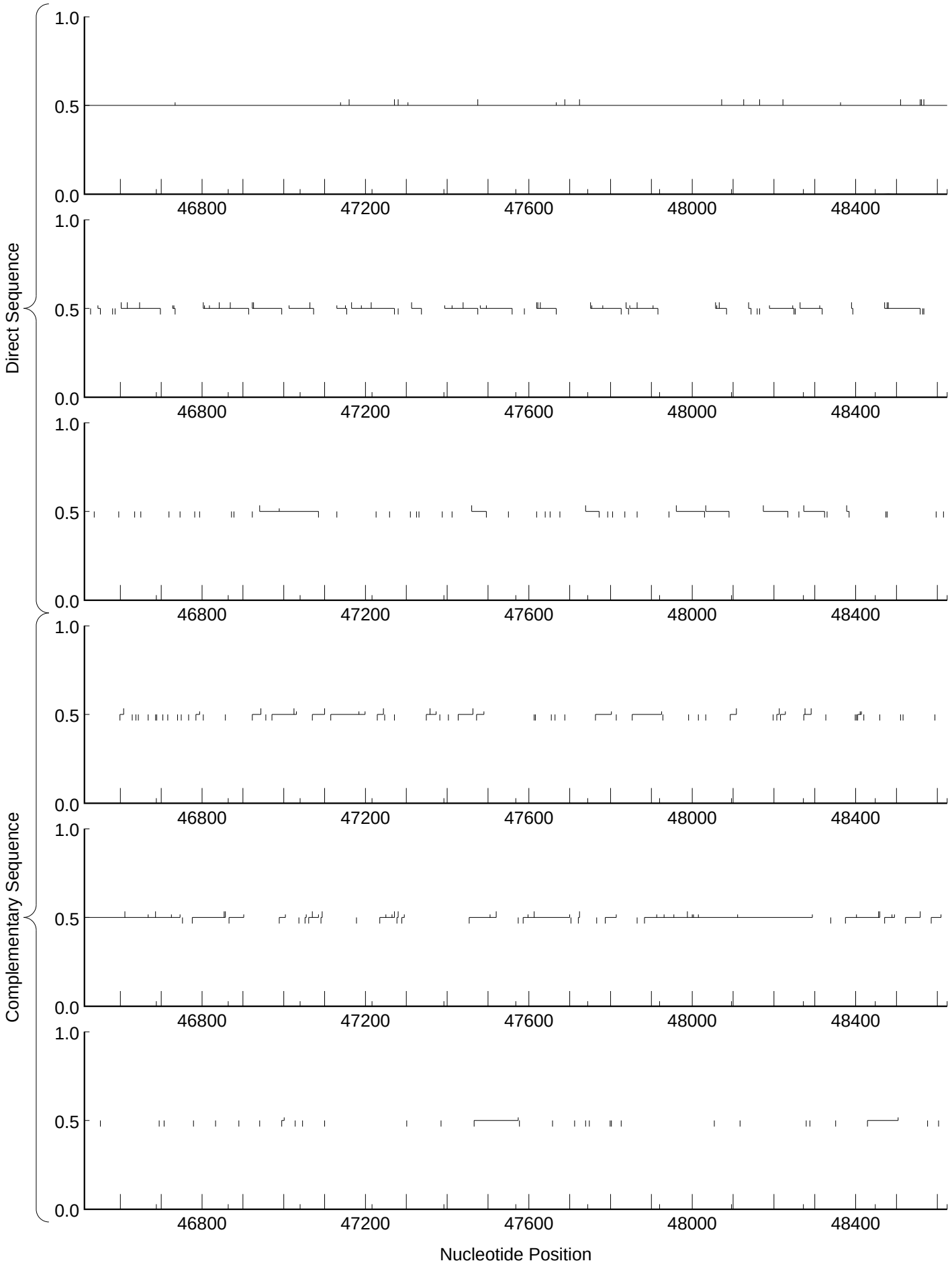
ge Wipeout complete sequence, 132935 bp including 12204 bp terminal repeat, Cluster BE2, Order 4, Window 96, Step 12, 21/64



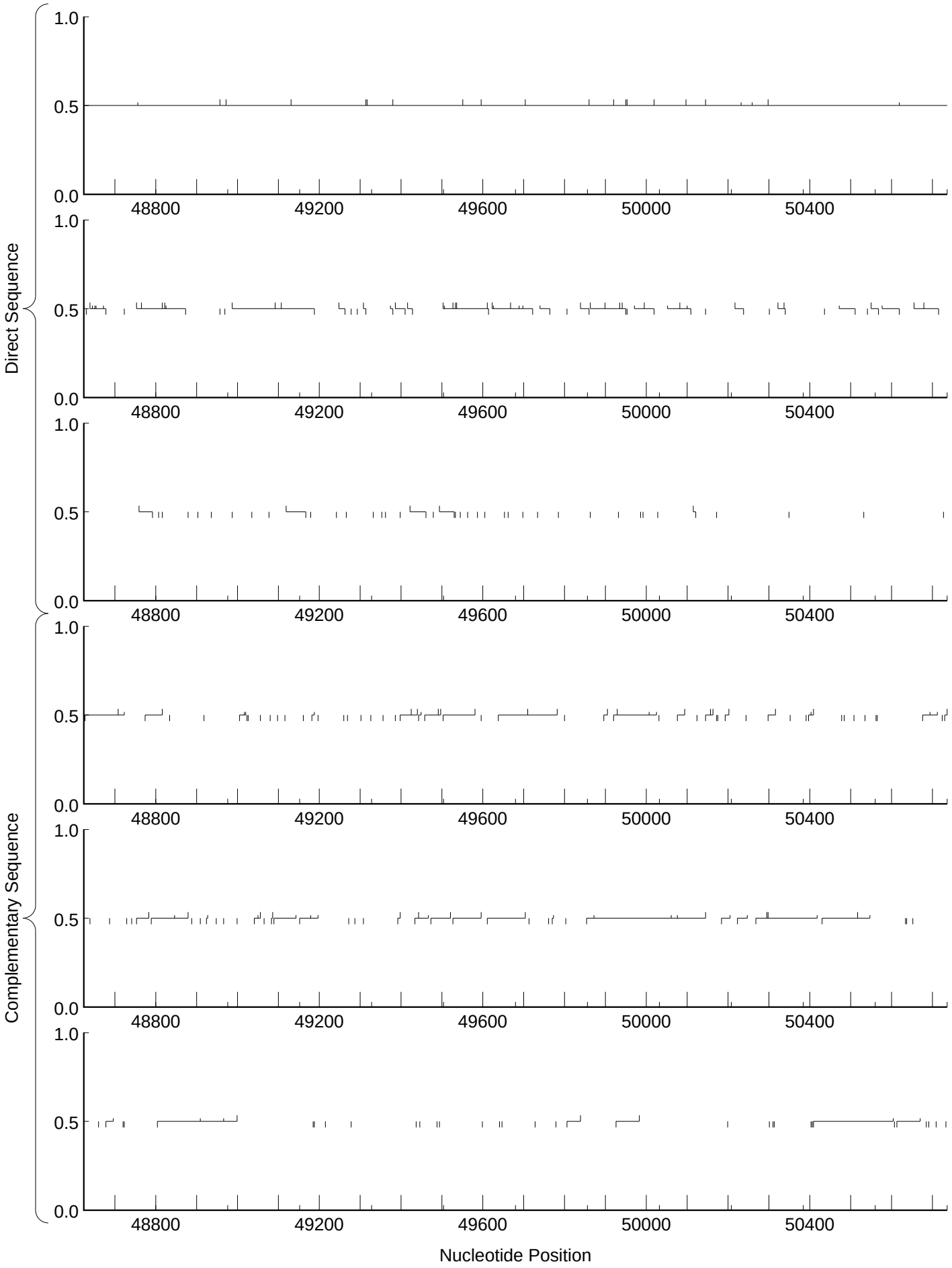
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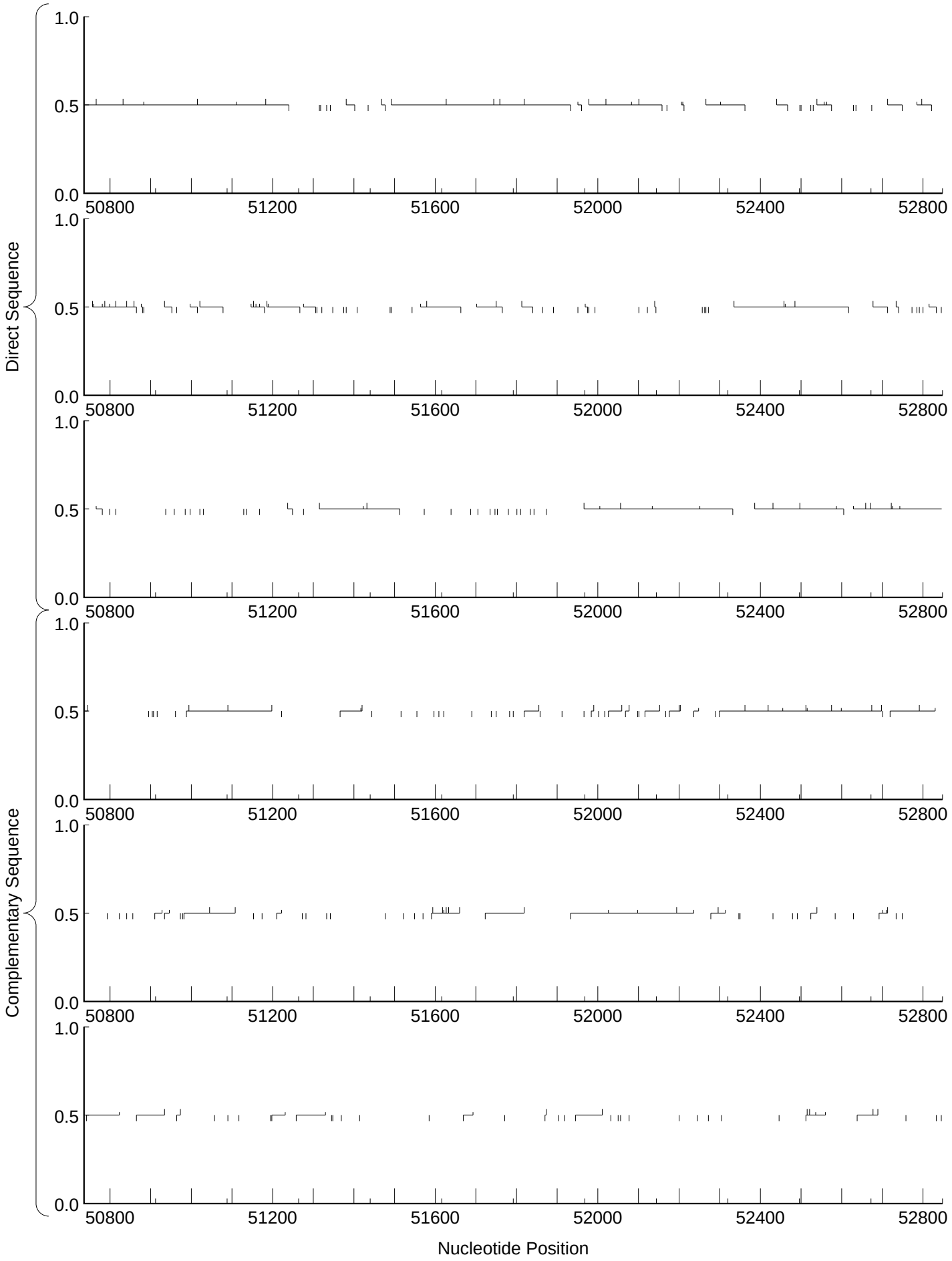



Direct Sequence
Complementary Sequence
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0.0
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45200
45600
46000
46400
Nucleotide Position

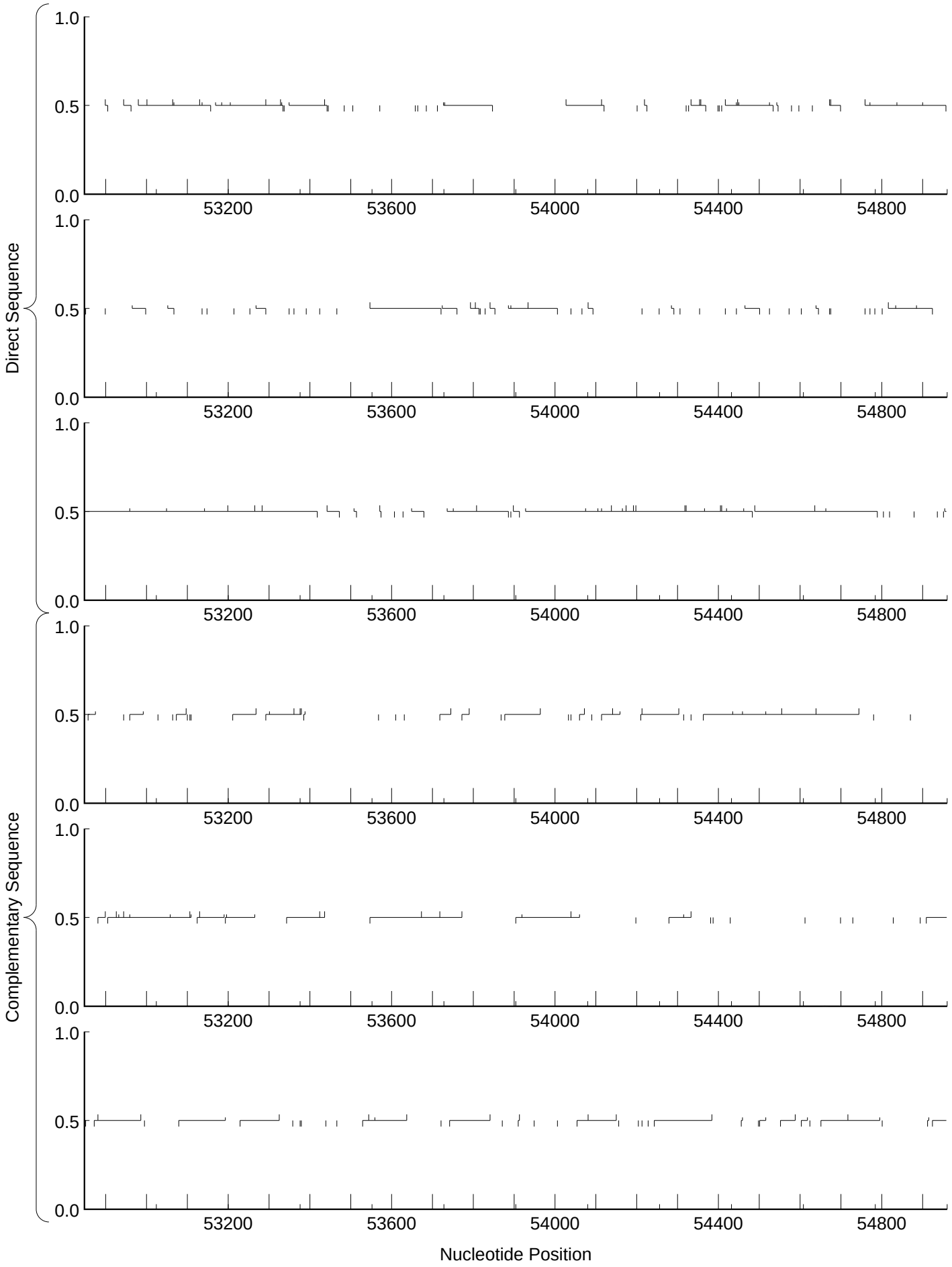

Direct Sequence
Complementary Sequence
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0.0
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48400
Nucleotide Position

ge Wipeout complete sequence, 132935 bp including 12204 bp terminal repeat, Cluster BE2, Order 4, Window 96, Step 12, 25/64

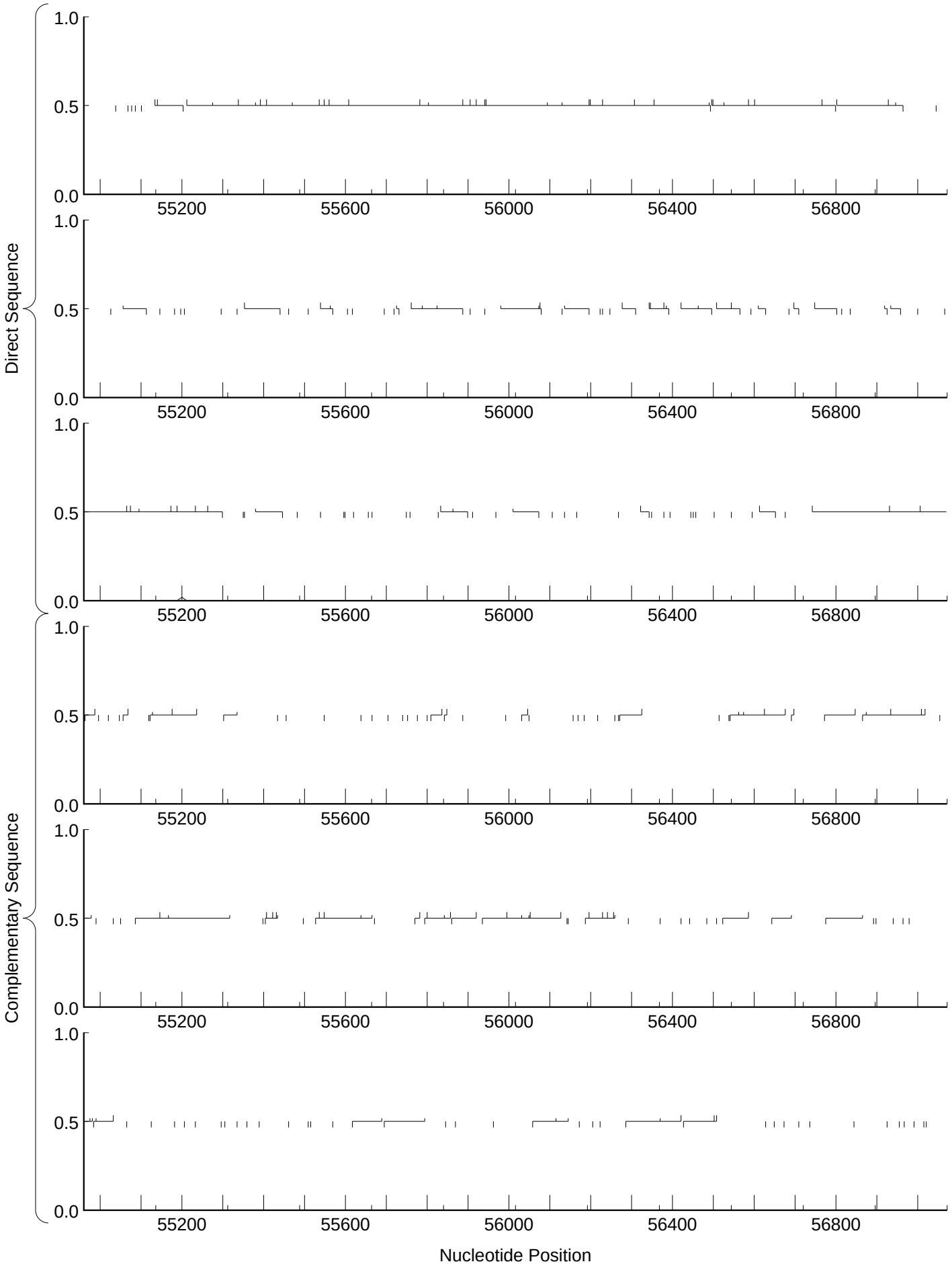



Direct Sequence
Complementary Sequence
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52000
52400
52800
Nucleotide Position

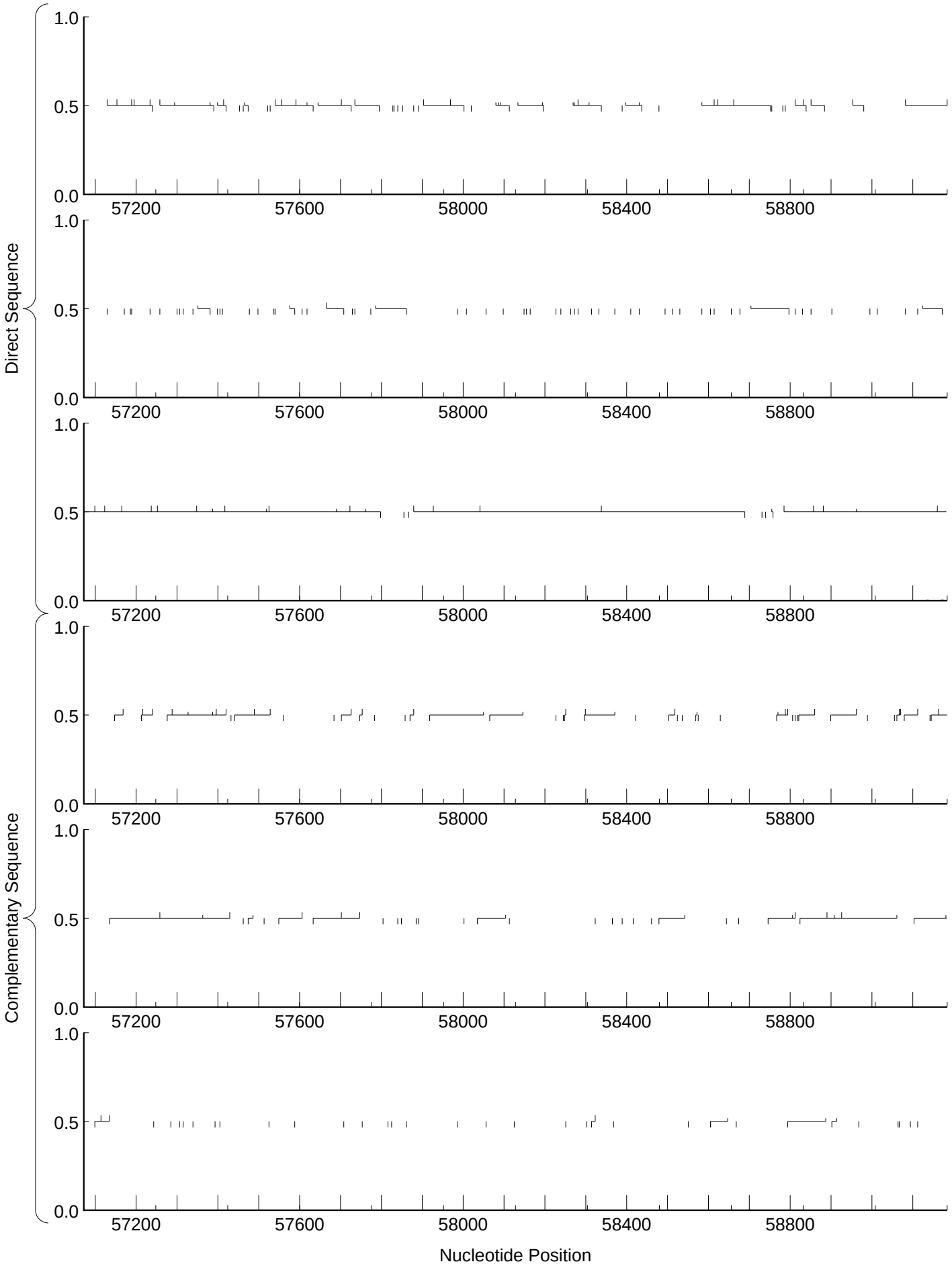
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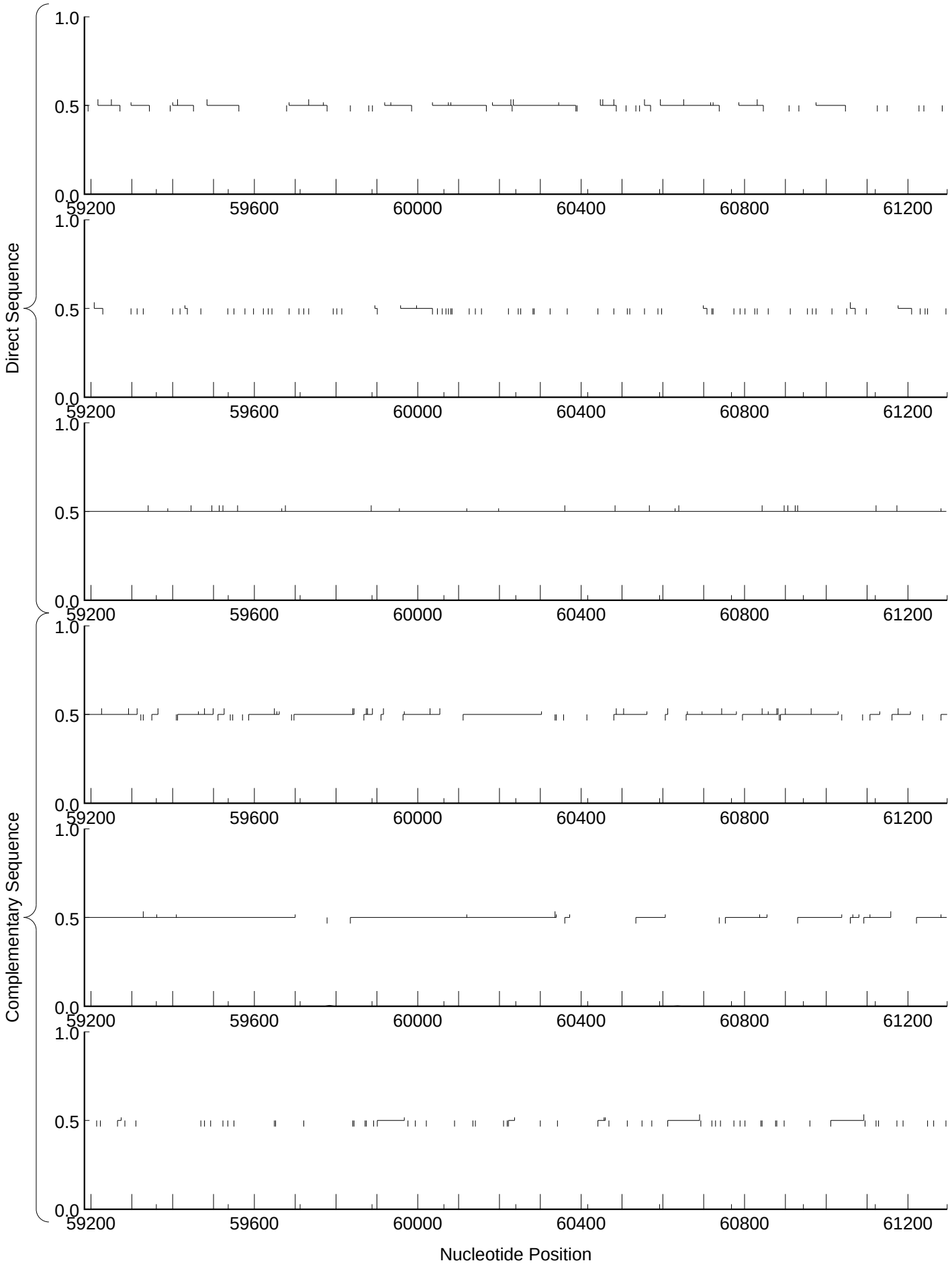


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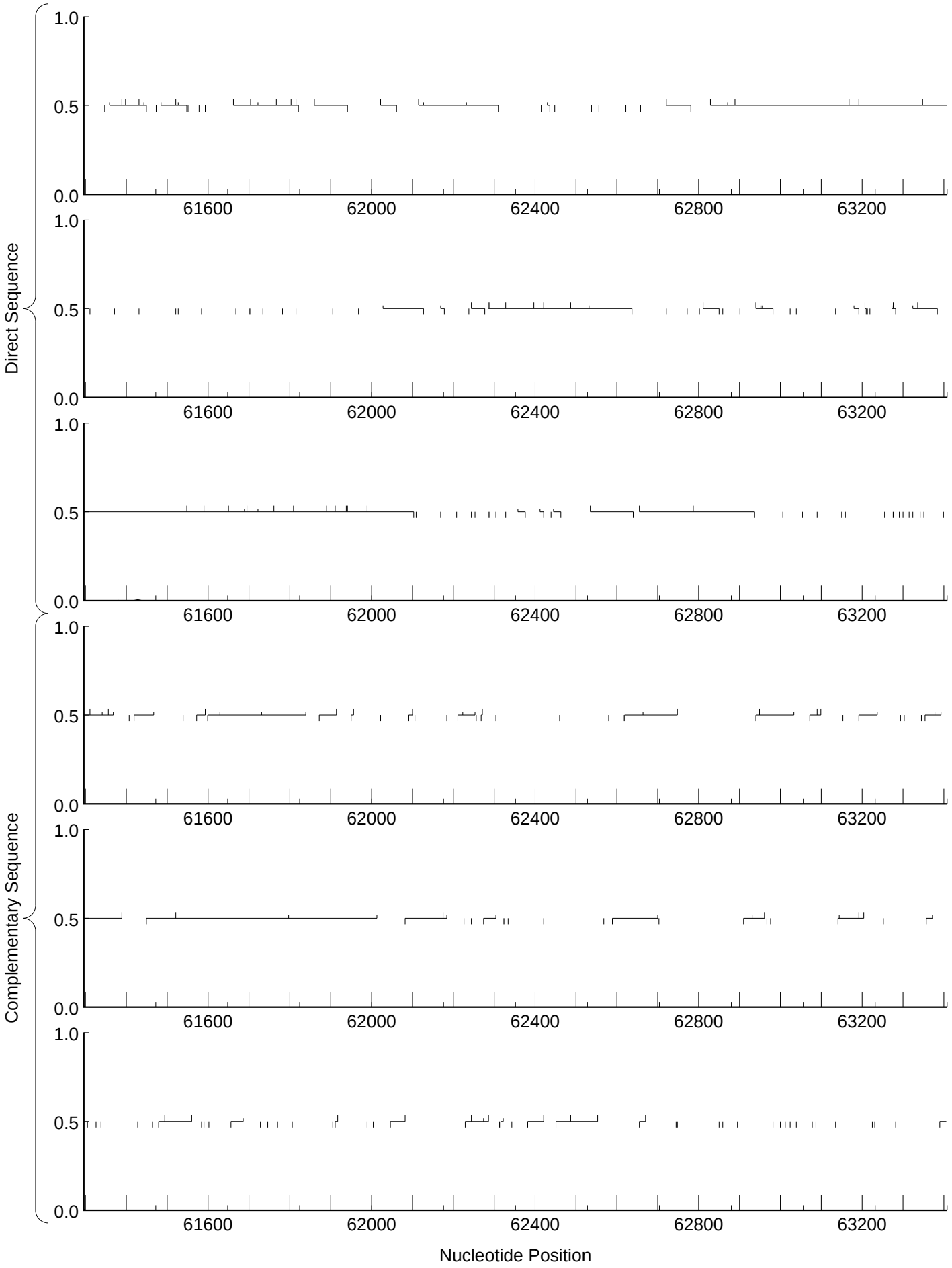


ge Wipeout complete sequence, 132935 bp including 12204 bp terminal repeat, Cluster BE2, Order 4, Window 96, Step 12, 29/64

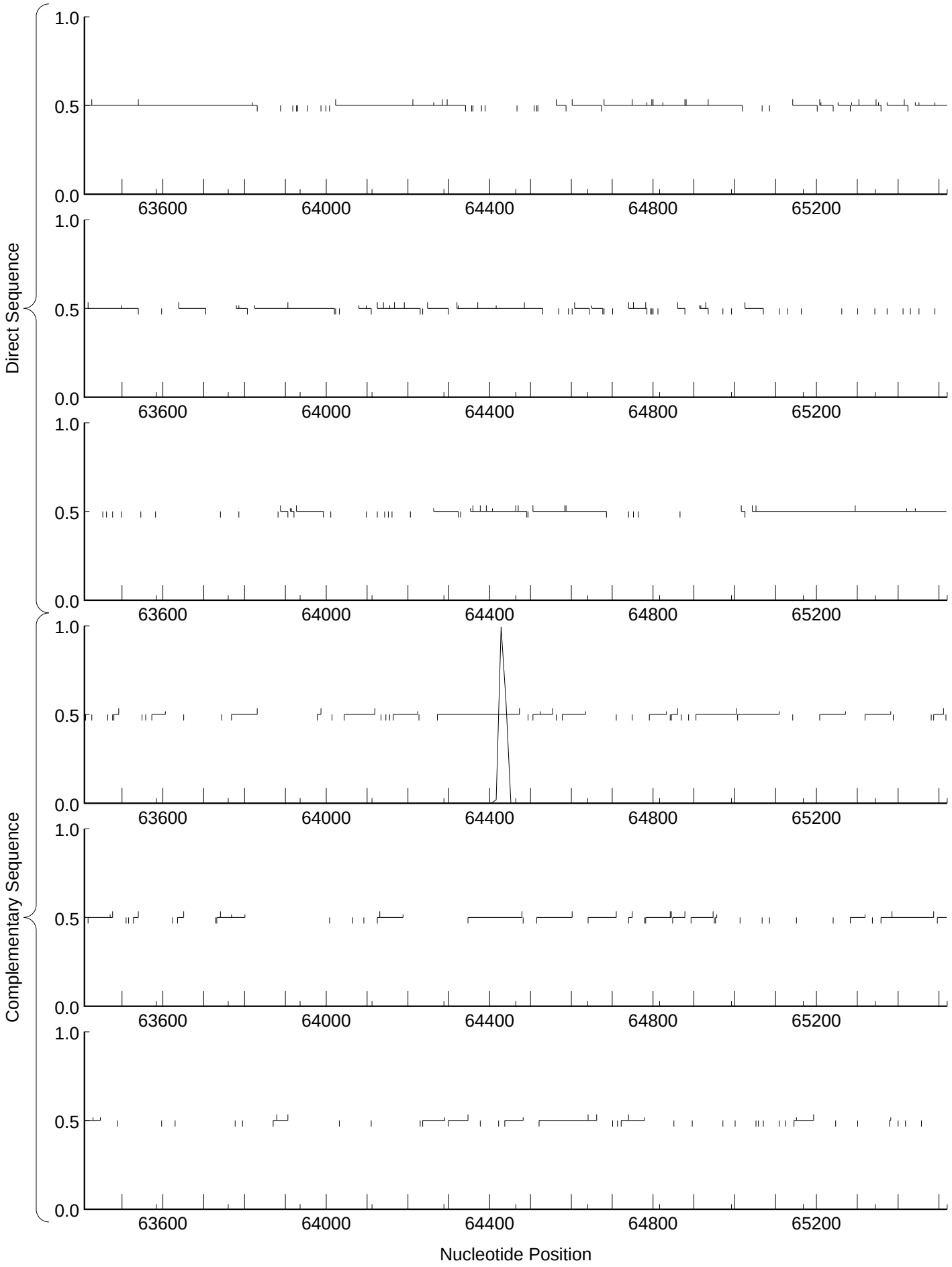


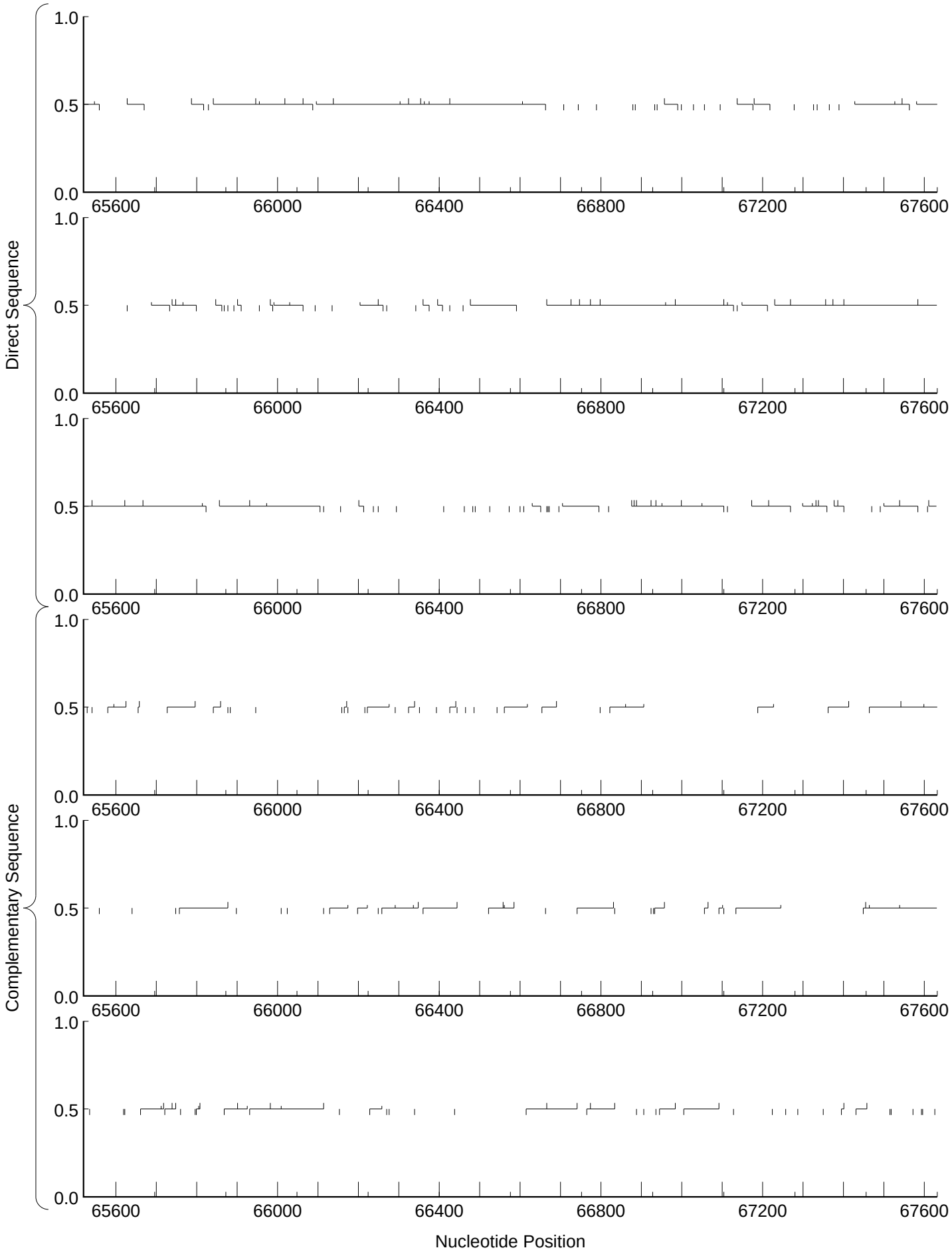

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
59200
59600
60000
60400
60800
61200
Nucleotide Position

ge Wipeout complete sequence, 132935 bp including 12204 bp terminal repeat, Cluster BE2, Order 4, Window 96, Step 12, 31/64

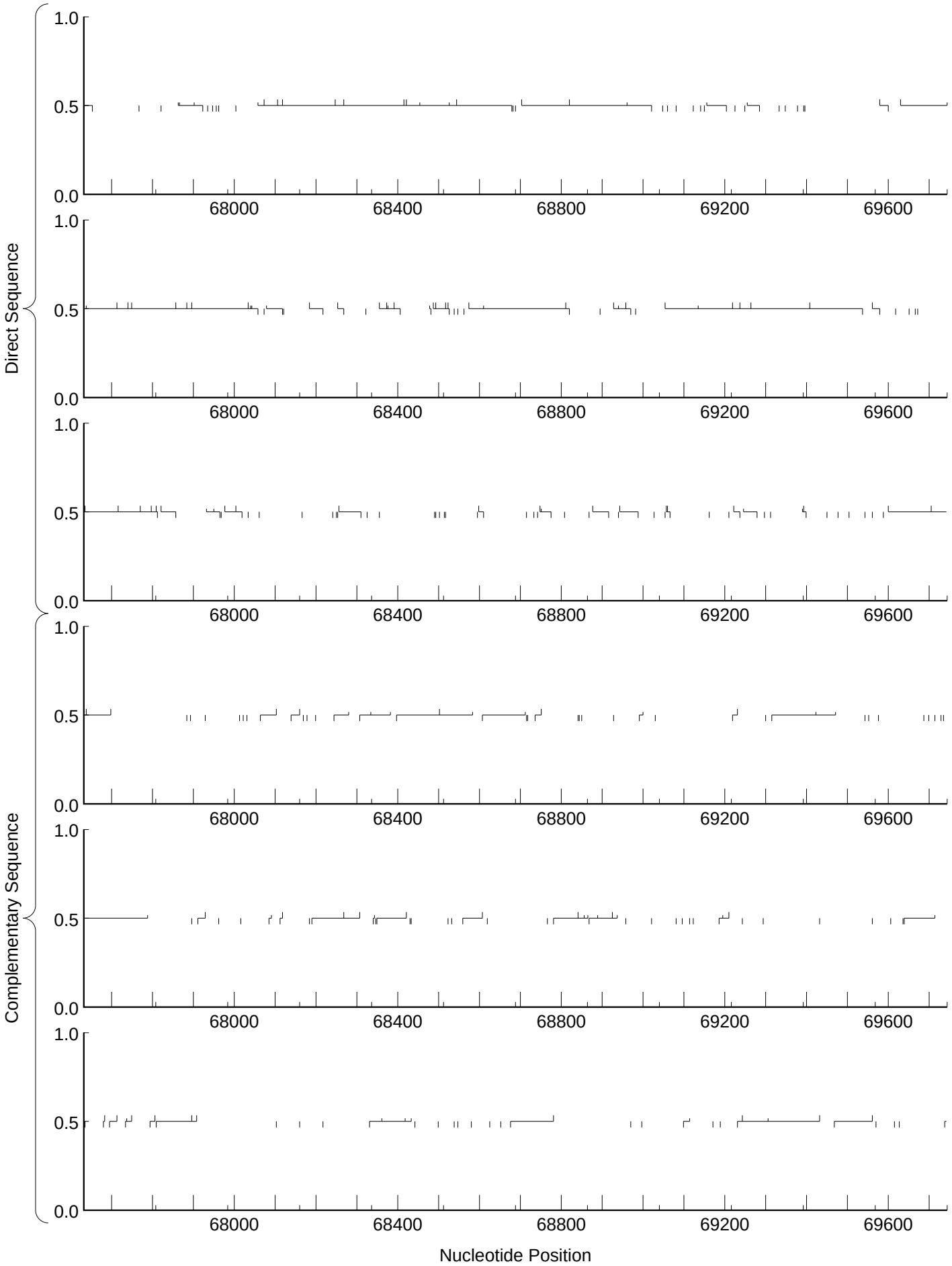


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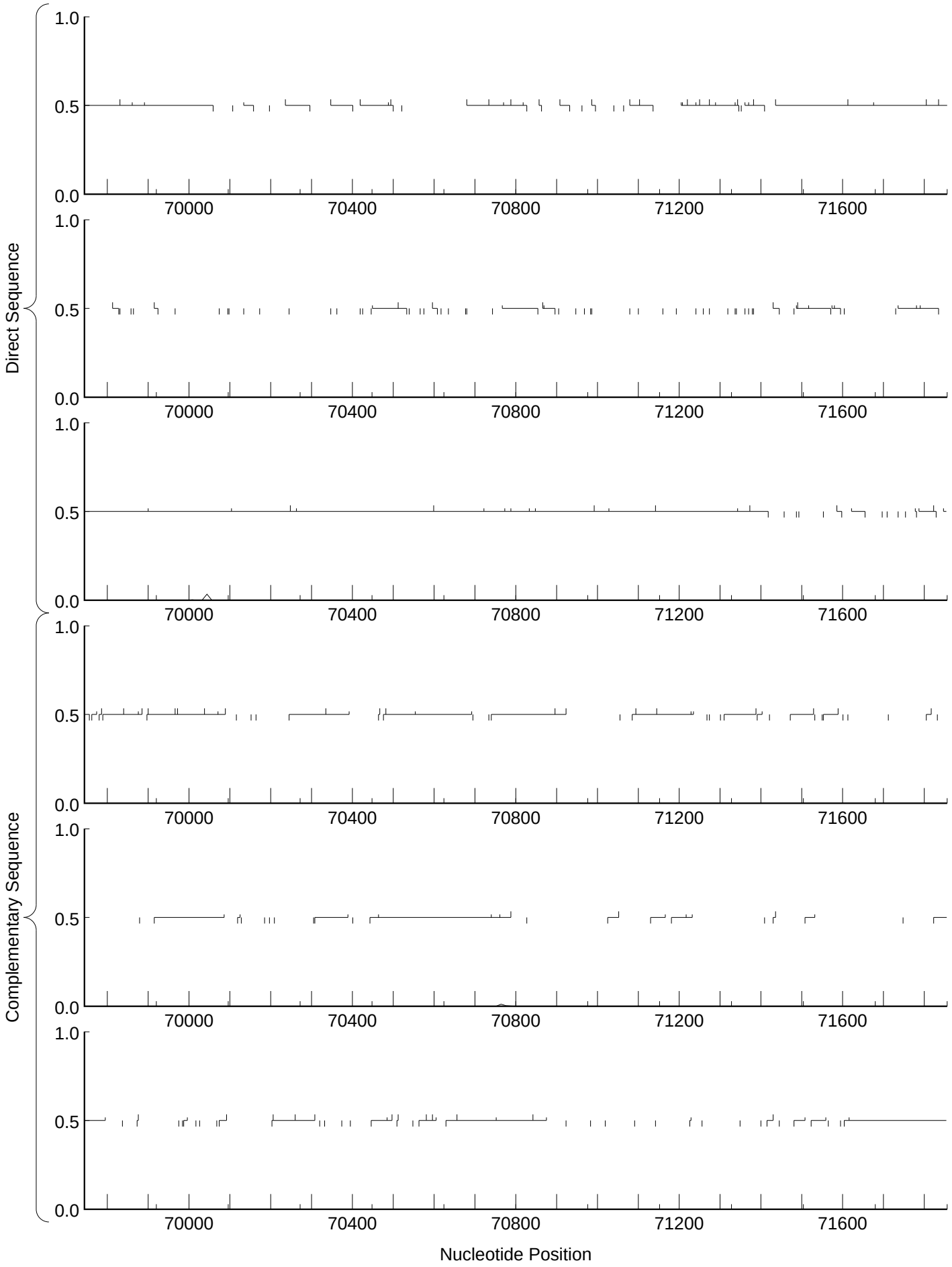


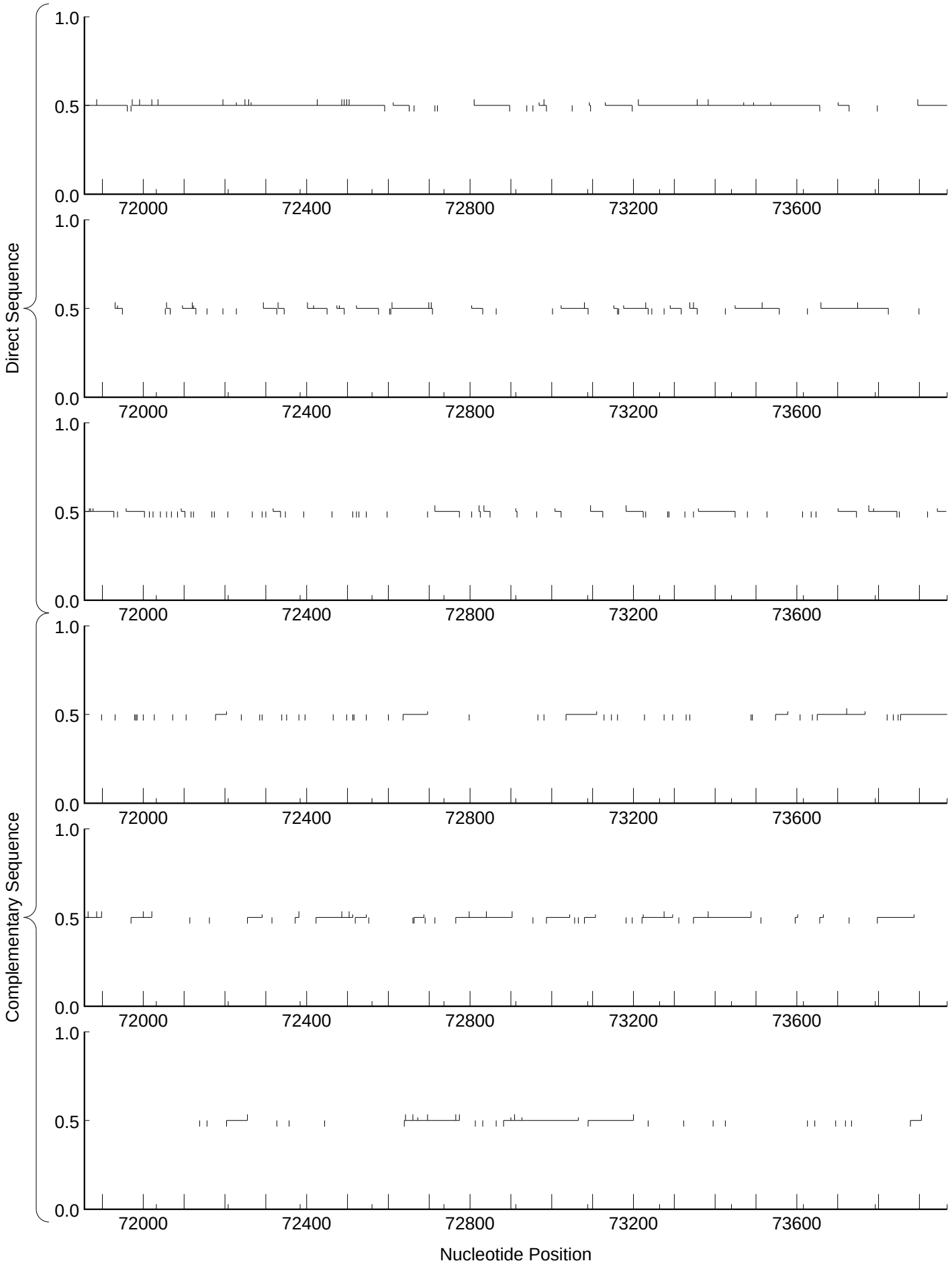

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Complementary Sequence
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67600
Nucleotide Position

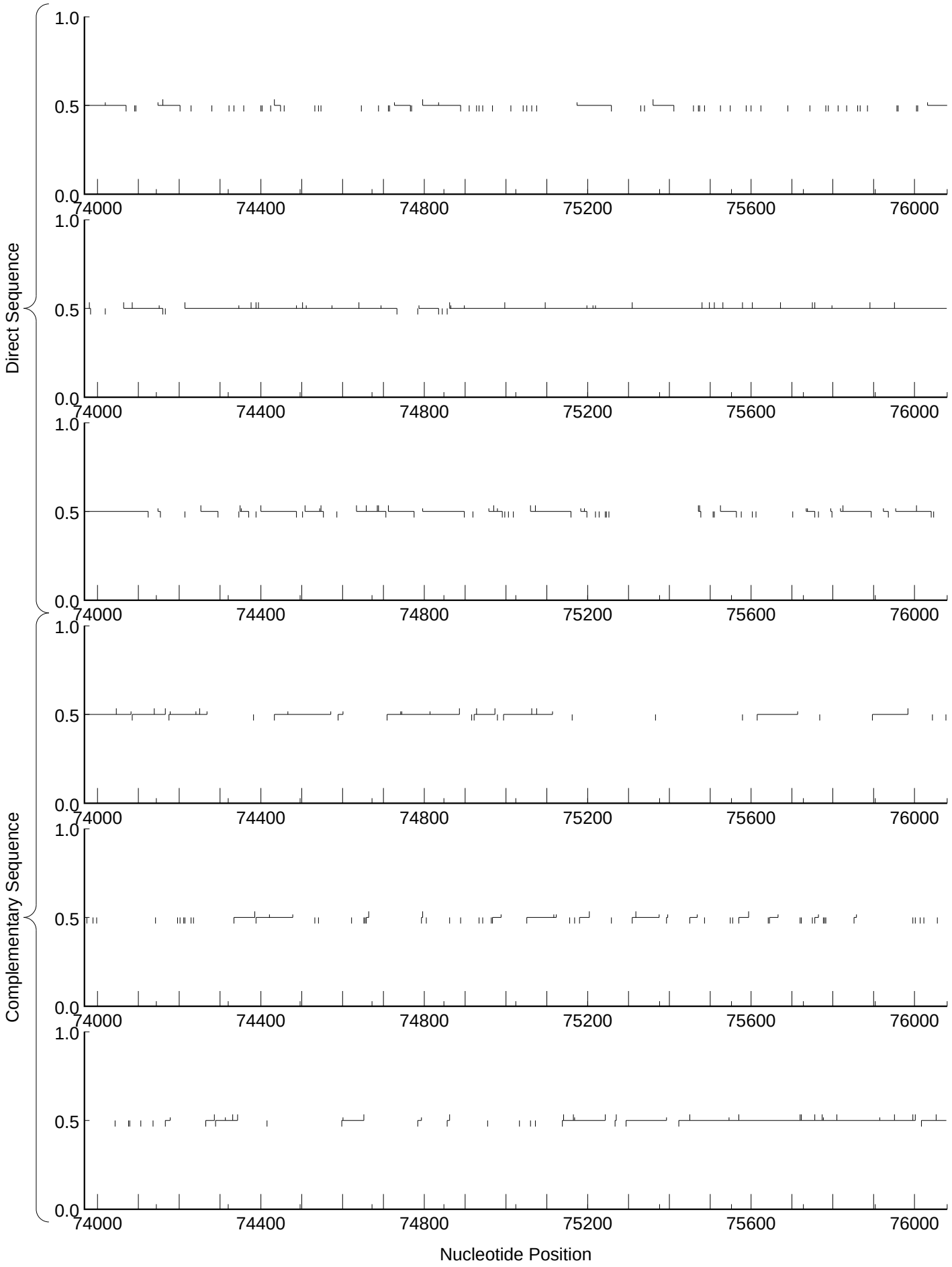
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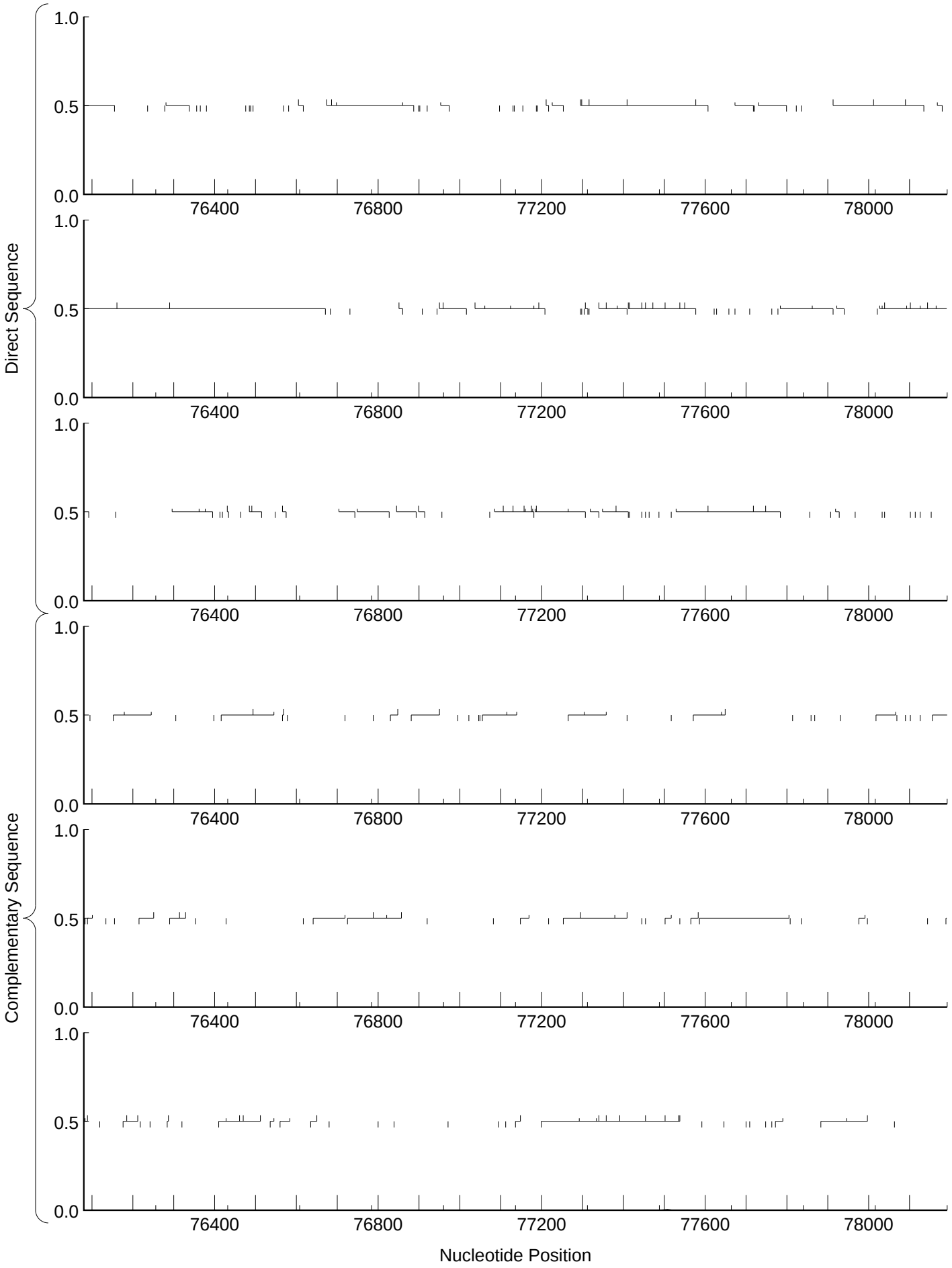
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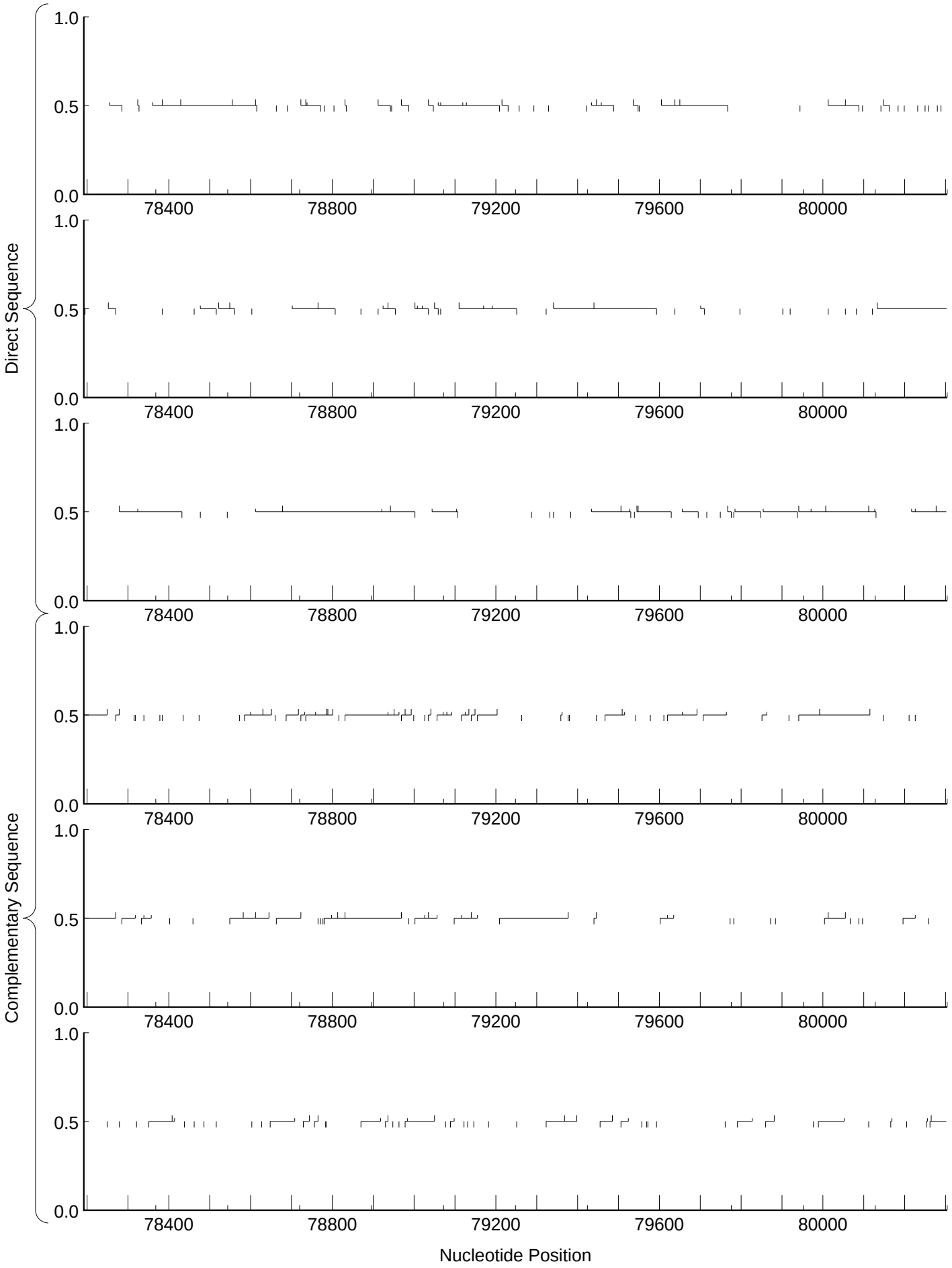


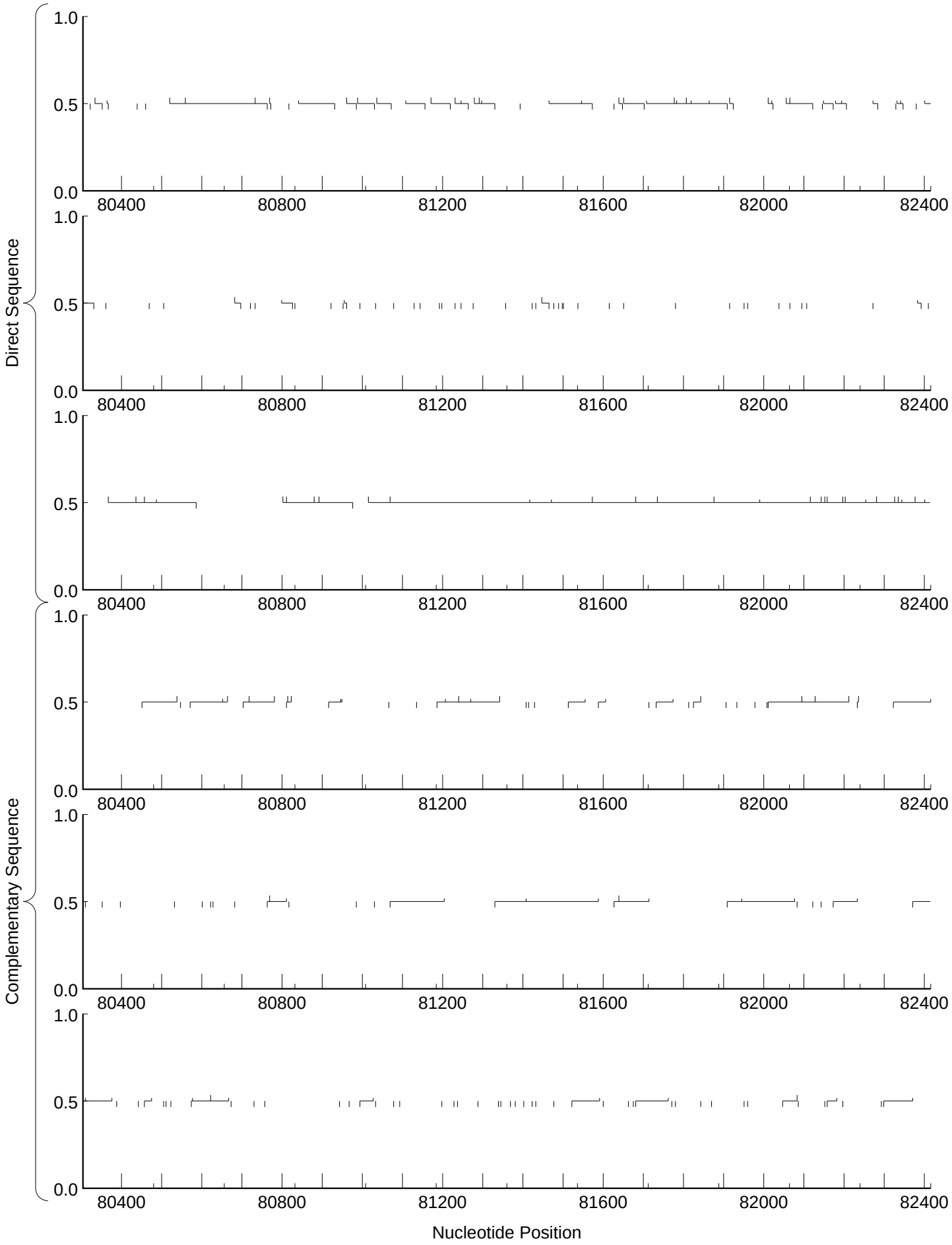

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Complementary Sequence
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73200
73600
Nucleotide Position

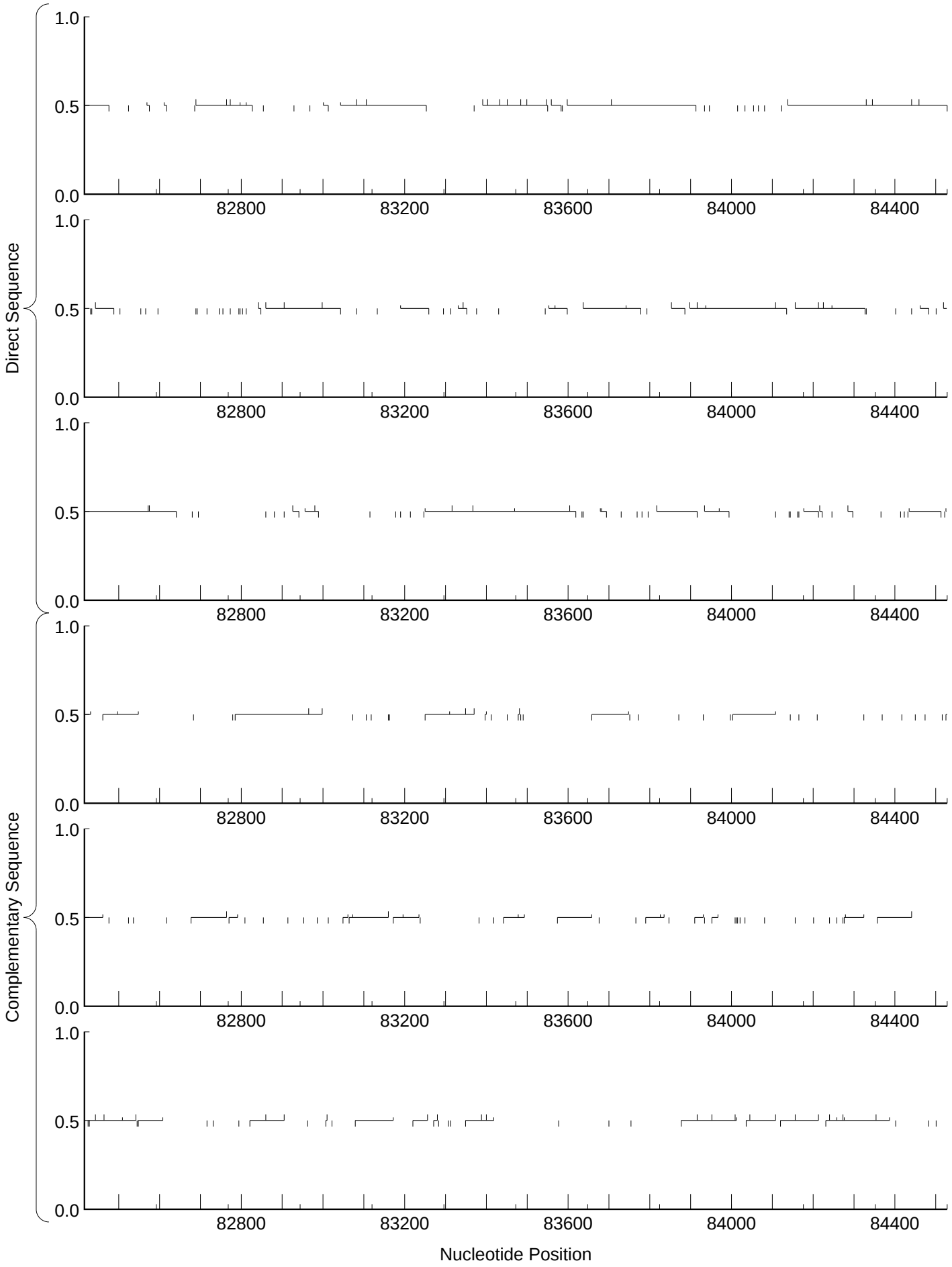

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Complementary Sequence
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0.5
0.0
74000
74400
74800
75200
75600
76000
Nucleotide Position

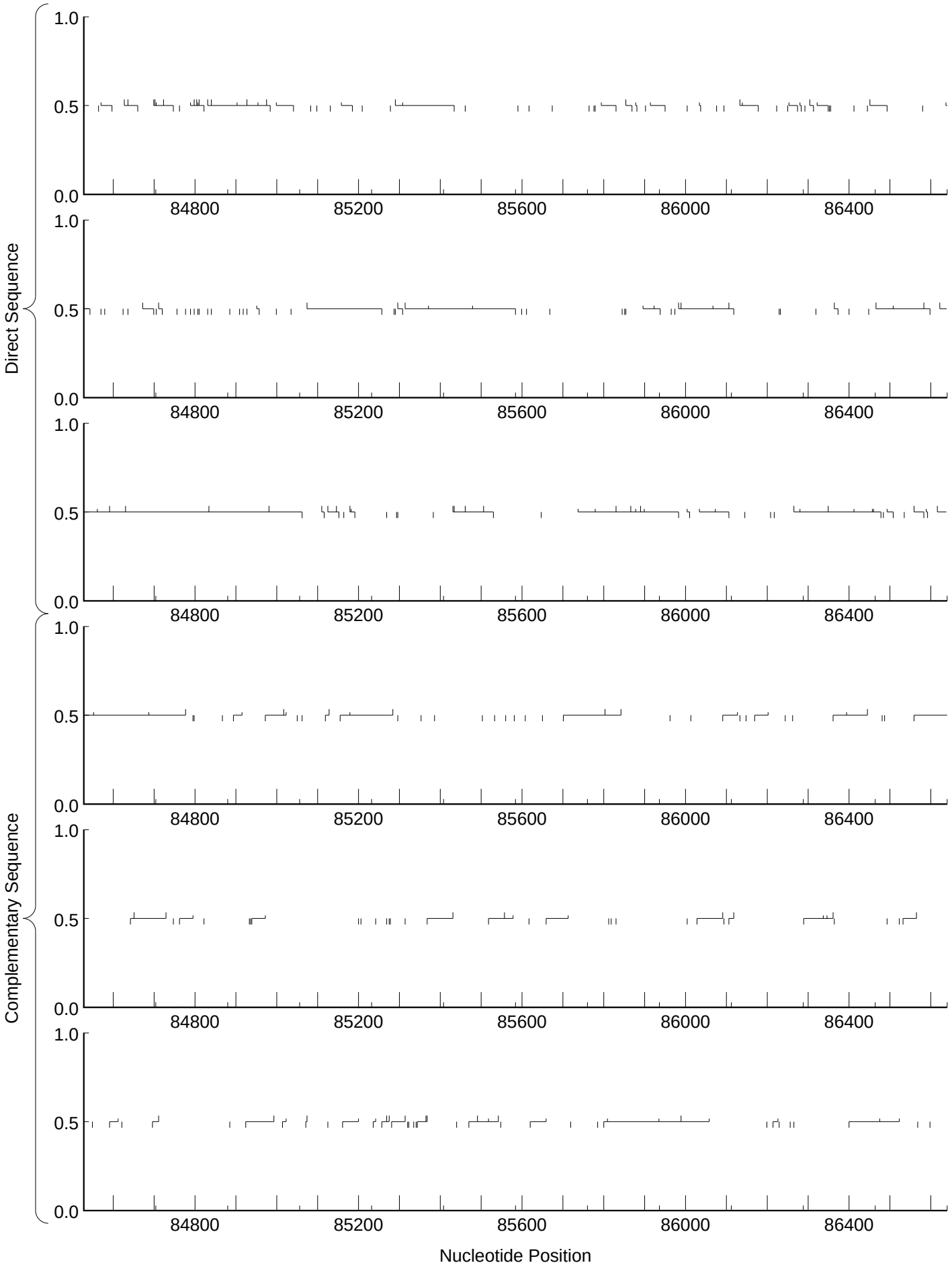
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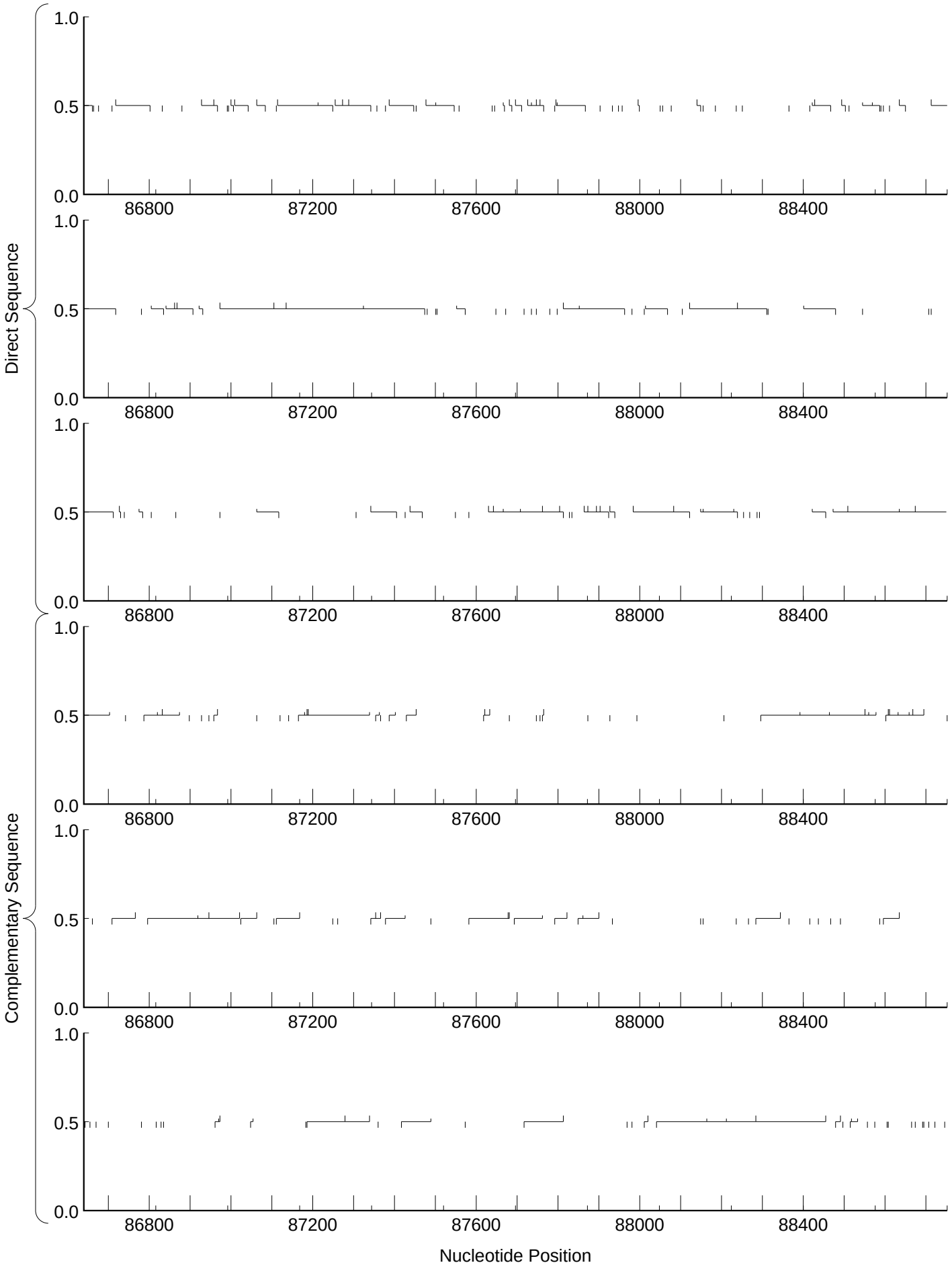


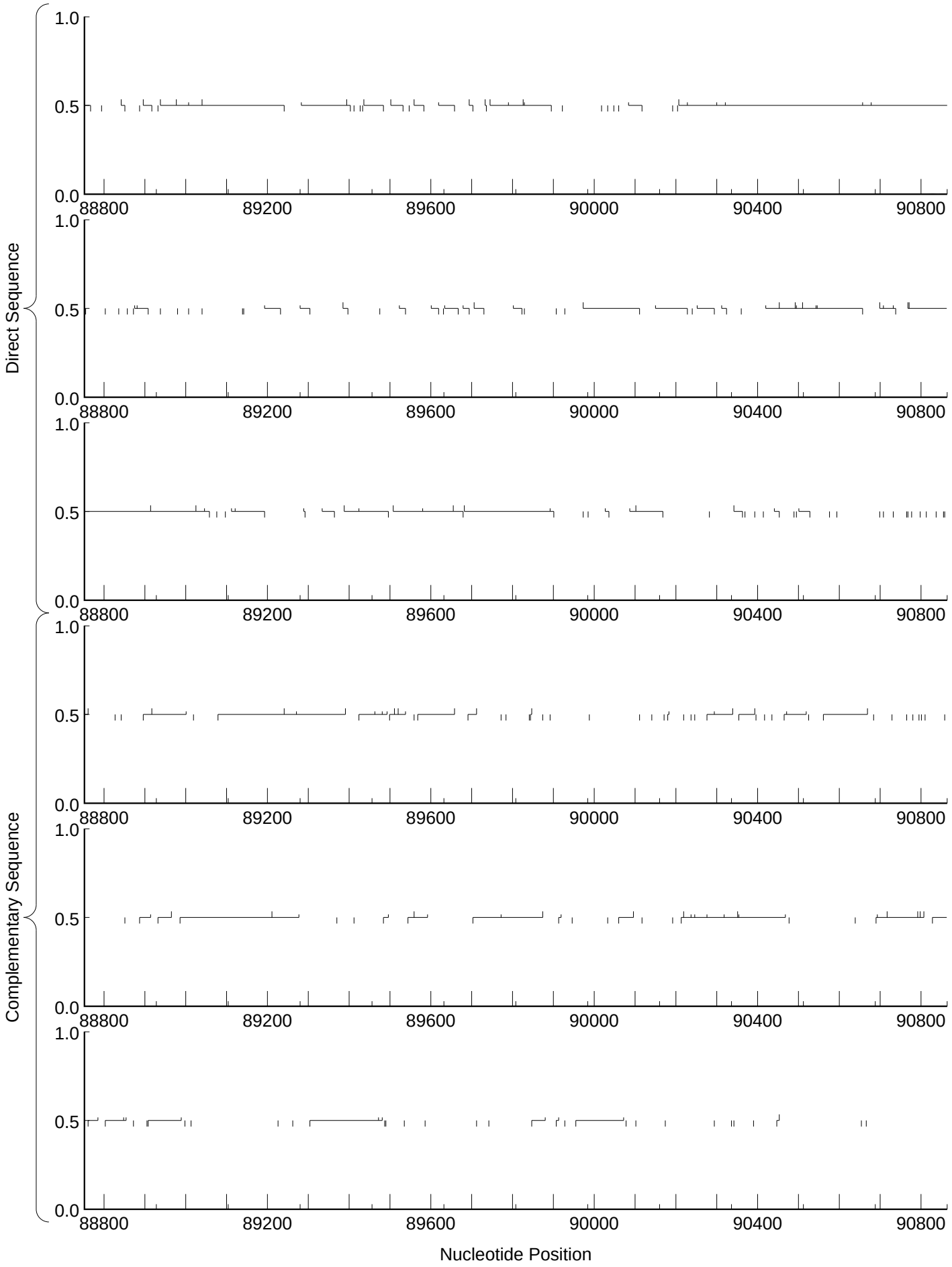

Direct Sequence
Complementary Sequence
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0.5
0.0
78400
78800
79200
79600
80000
Nucleotide Position

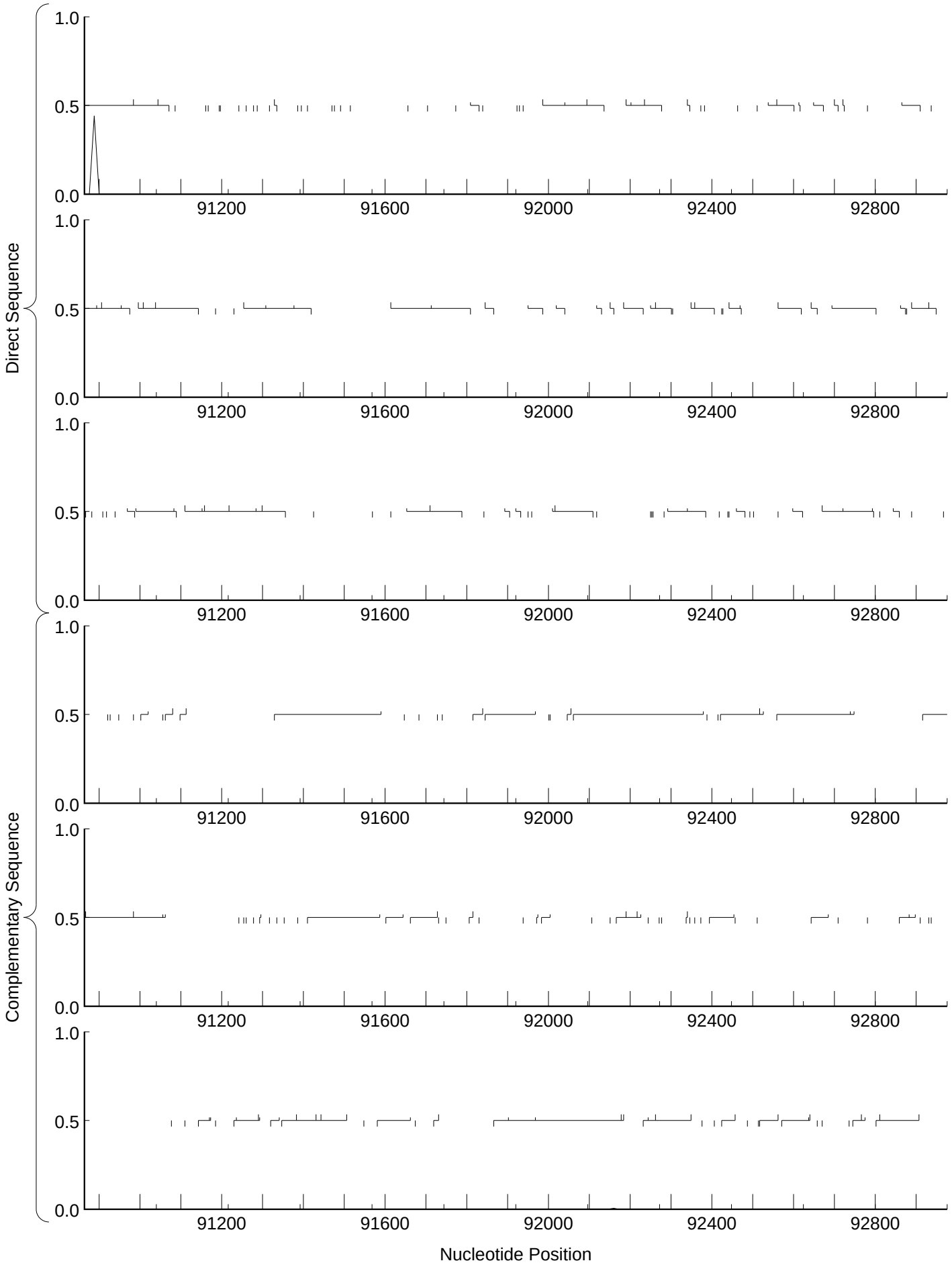

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
80400
80800
81200
81600
82000
82400
Nucleotide Position

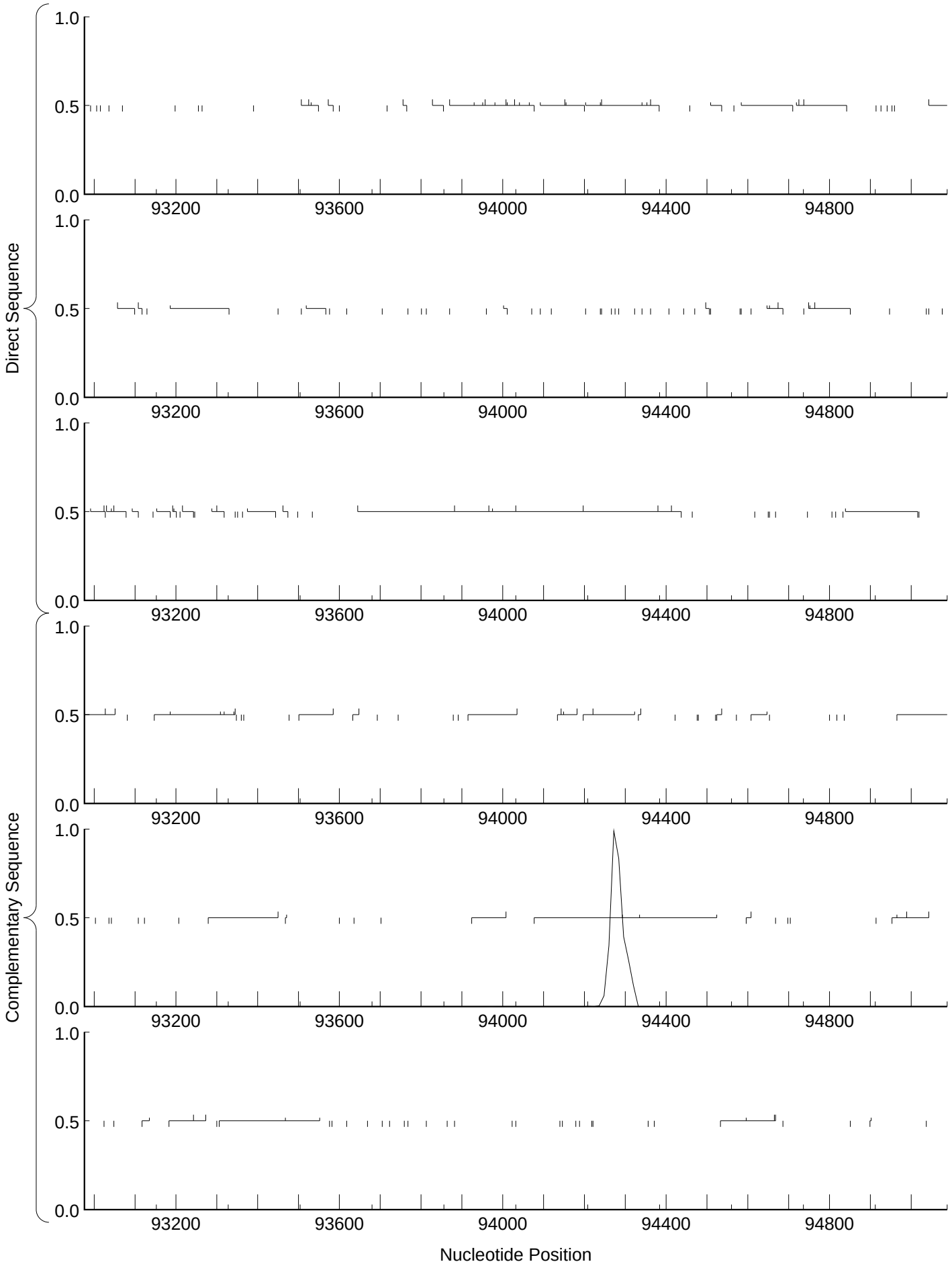

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
82800
83200
83600
84000
84400
Nucleotide Position

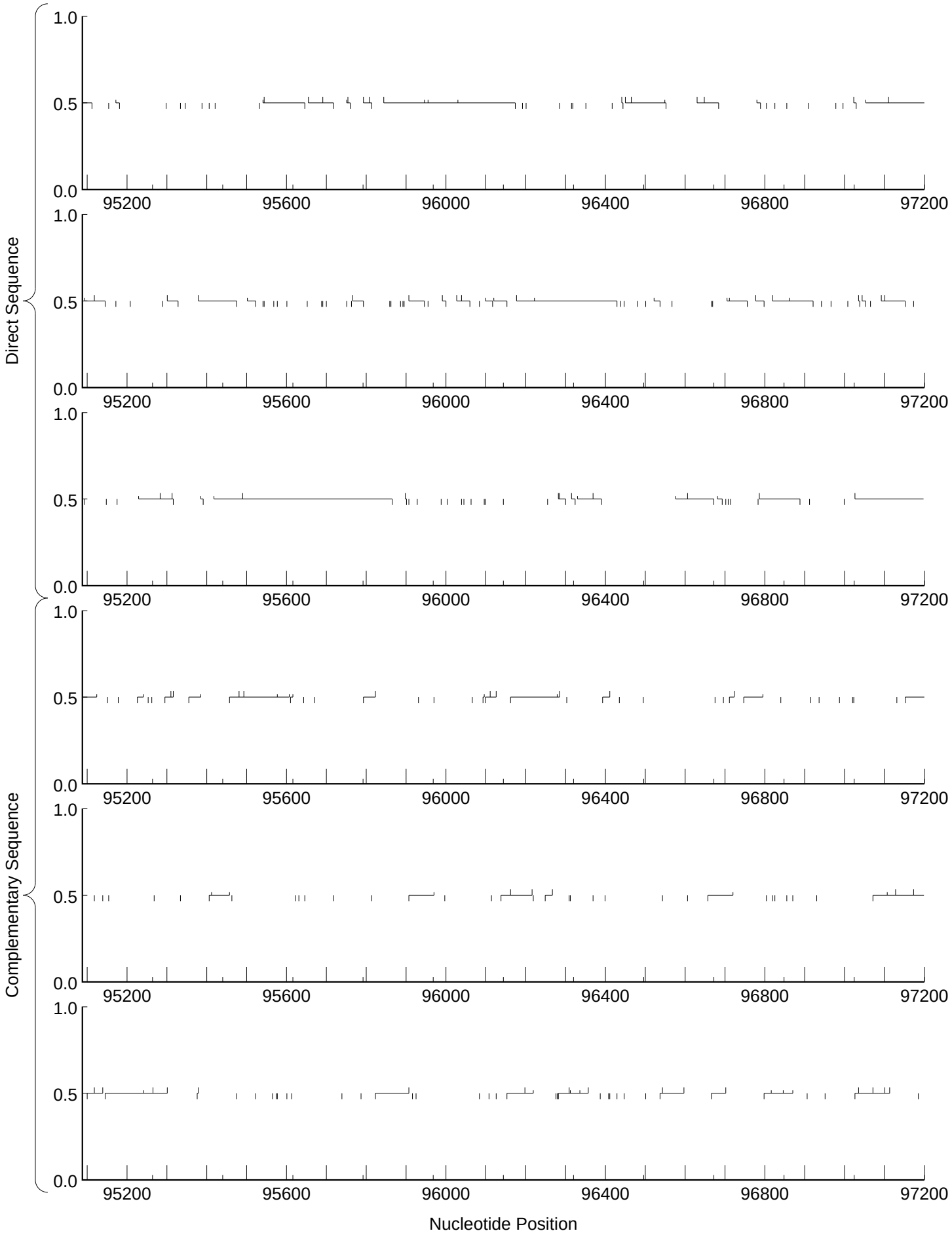

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
84800
85200
85600
86000
86400
Nucleotide Position

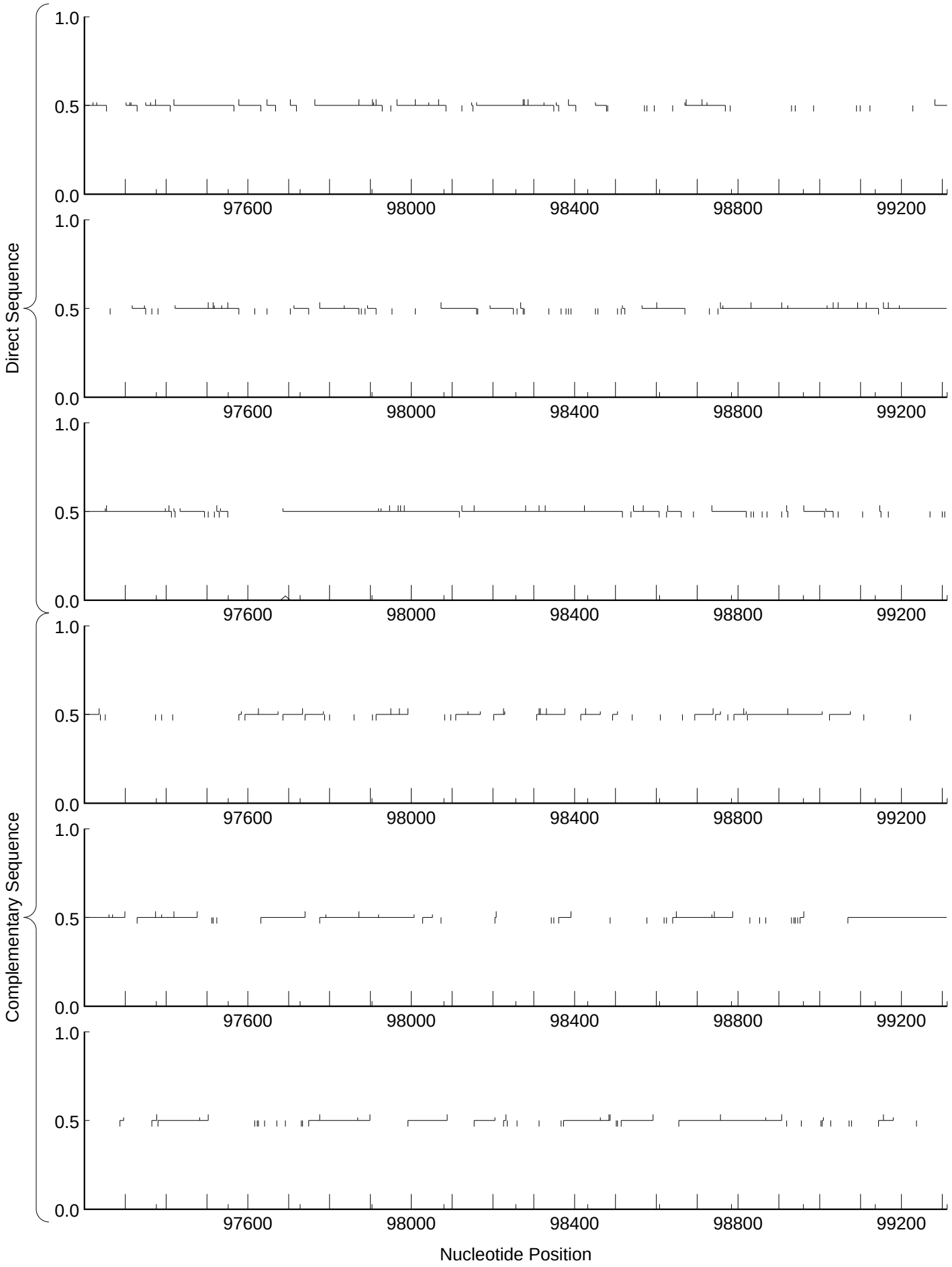

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
86800
87200
87600
88000
88400
Nucleotide Position

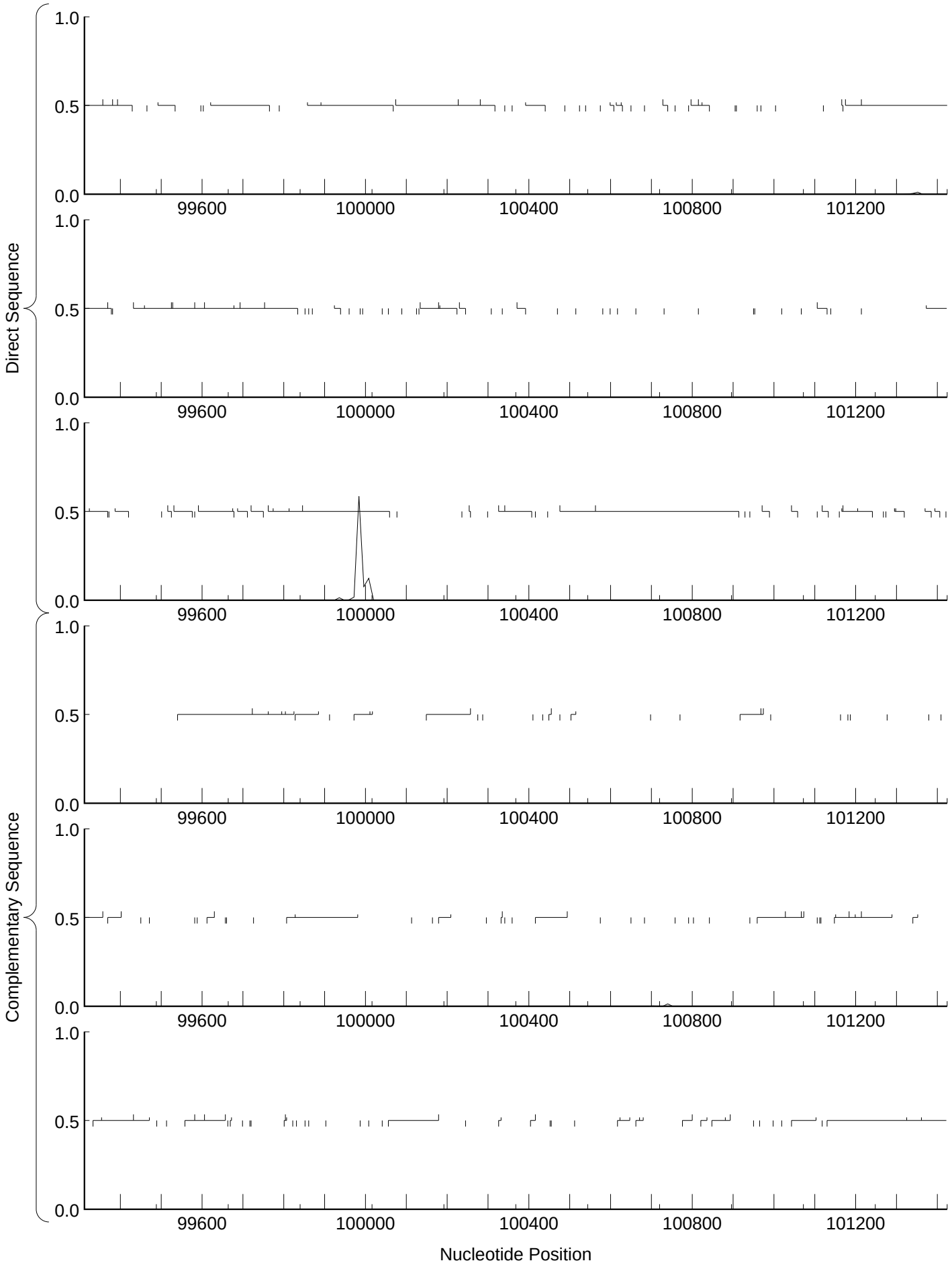

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
88800
89200
89600
90000
90400
90800
Nucleotide Position

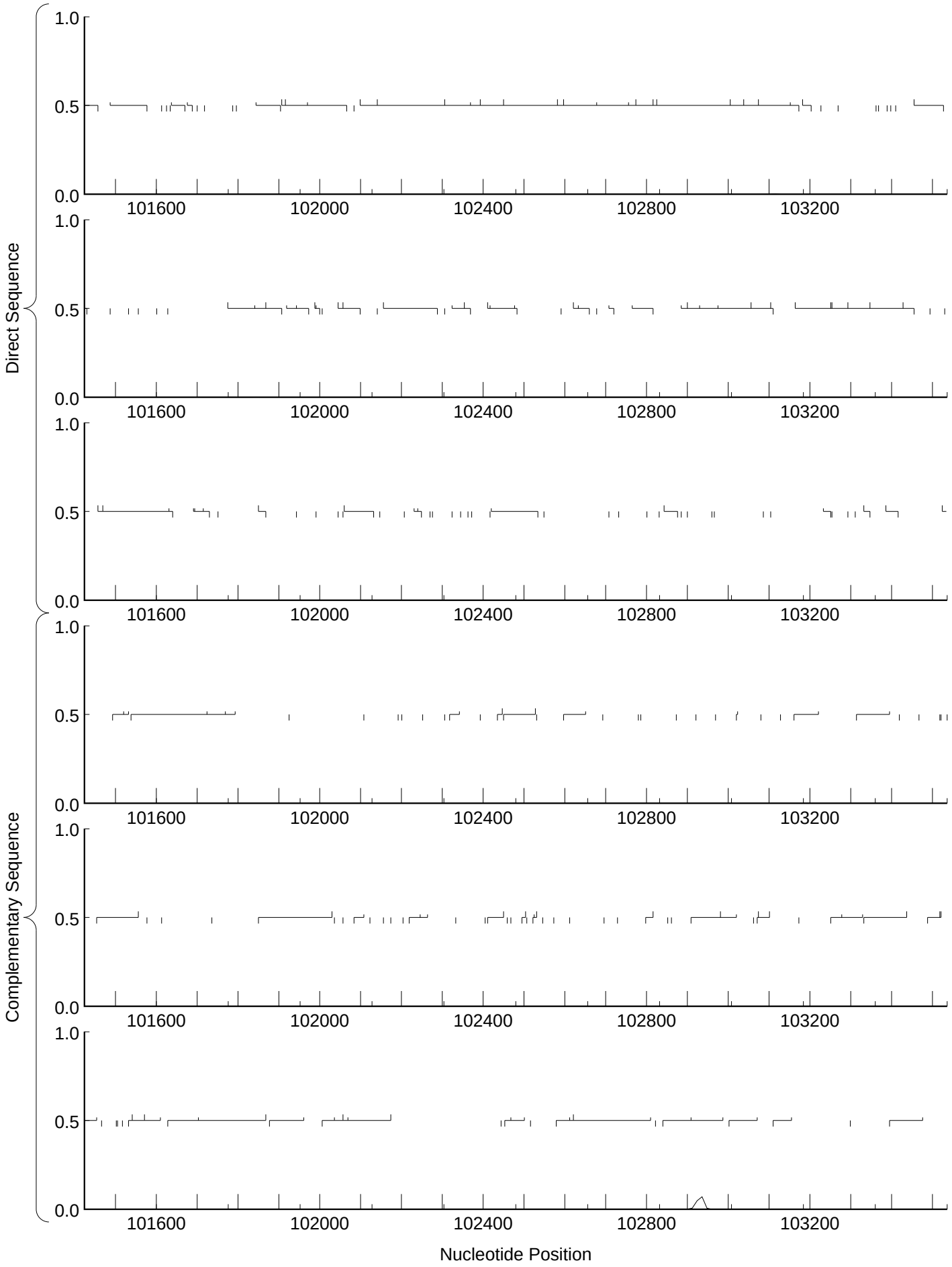

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
91200
91600
92000
92400
92800
Nucleotide Position


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
93200
93600
94000
94400
94800
Nucleotide Position

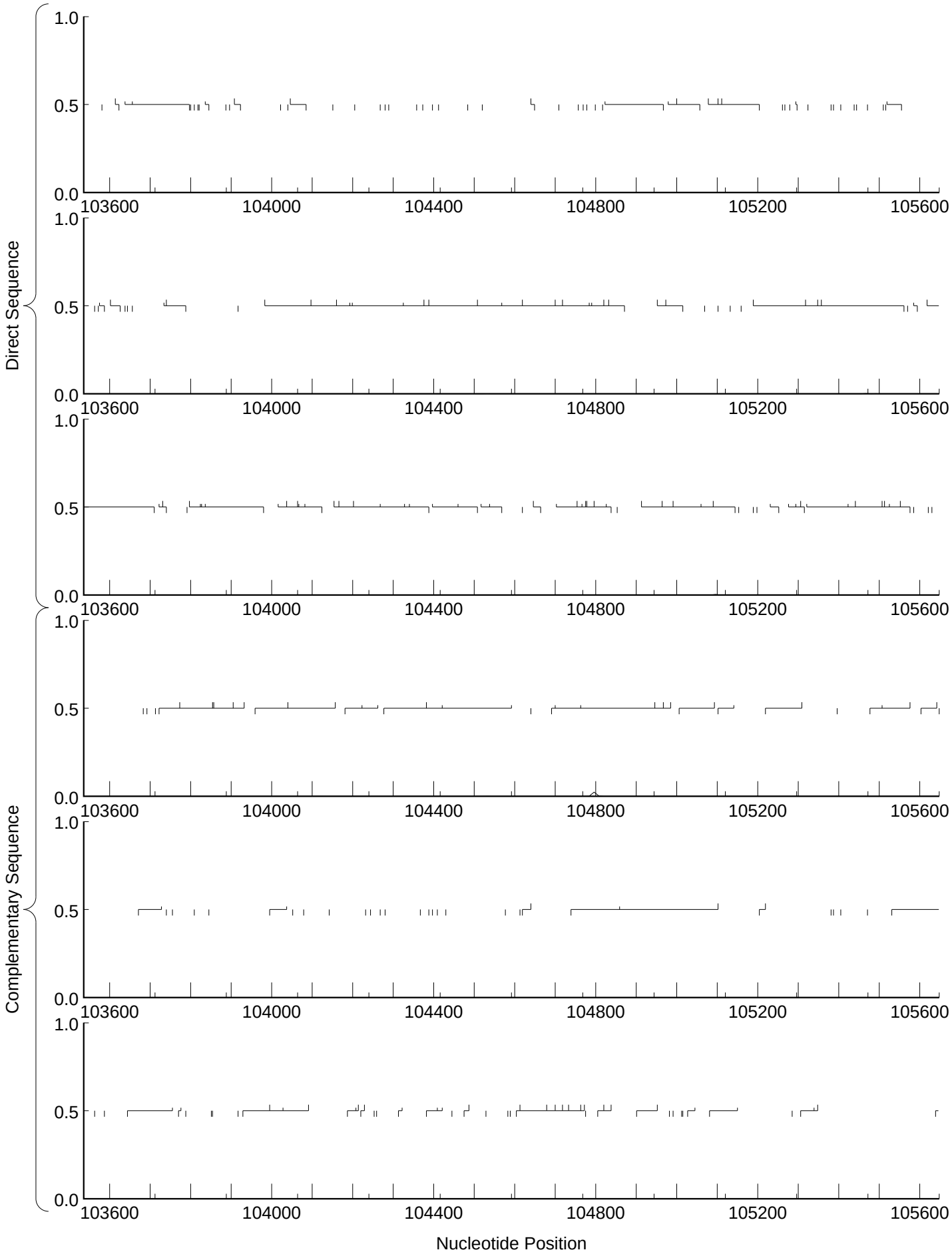

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
95200
95600
96000
96400
96800
97200
Nucleotide Position


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
97600
98000
98400
98800
99200
Nucleotide Position

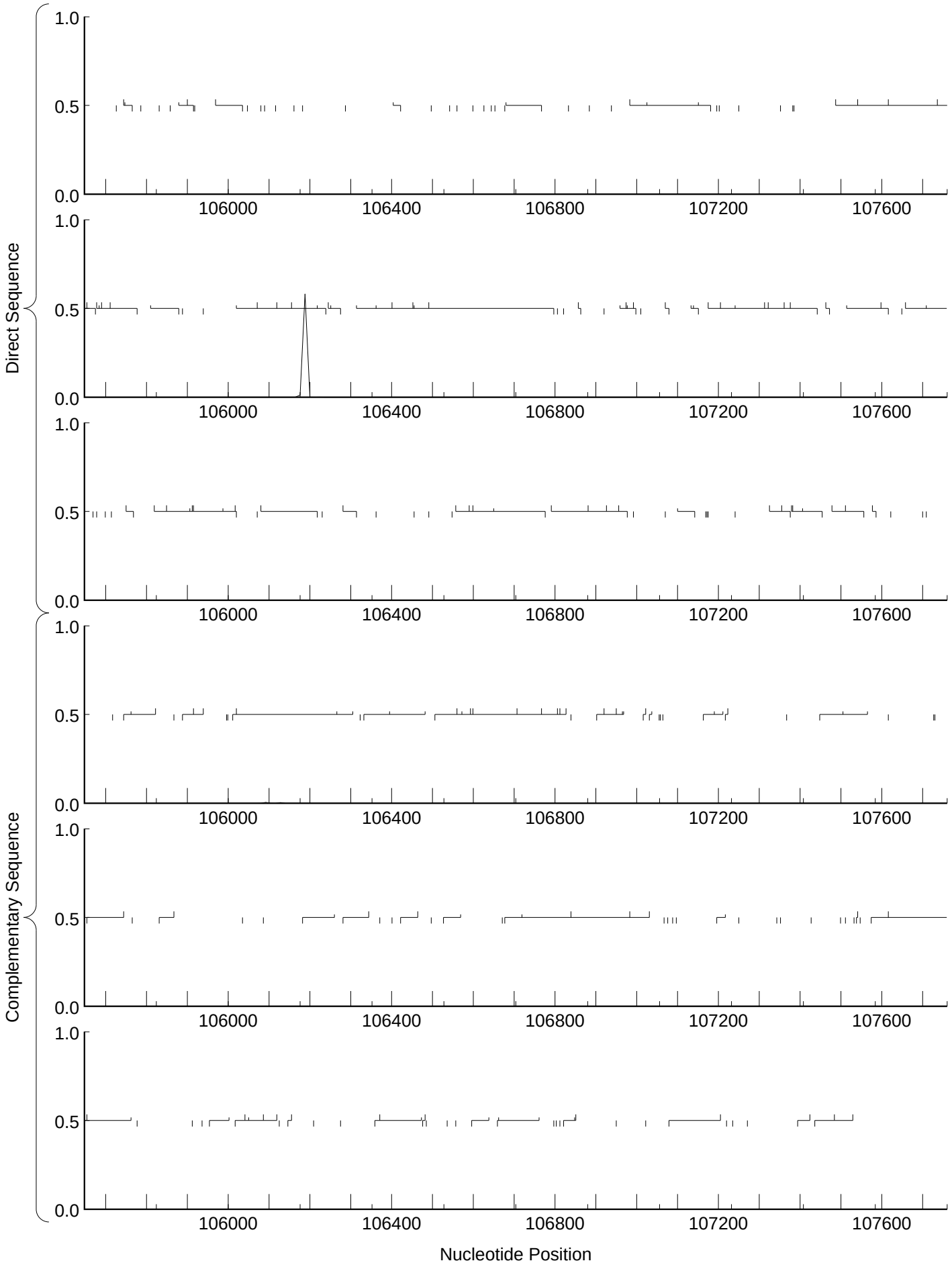

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
99600
100000
100400
100800
101200
Nucleotide Position


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
101600
102000
102400
102800
103200
Nucleotide Position

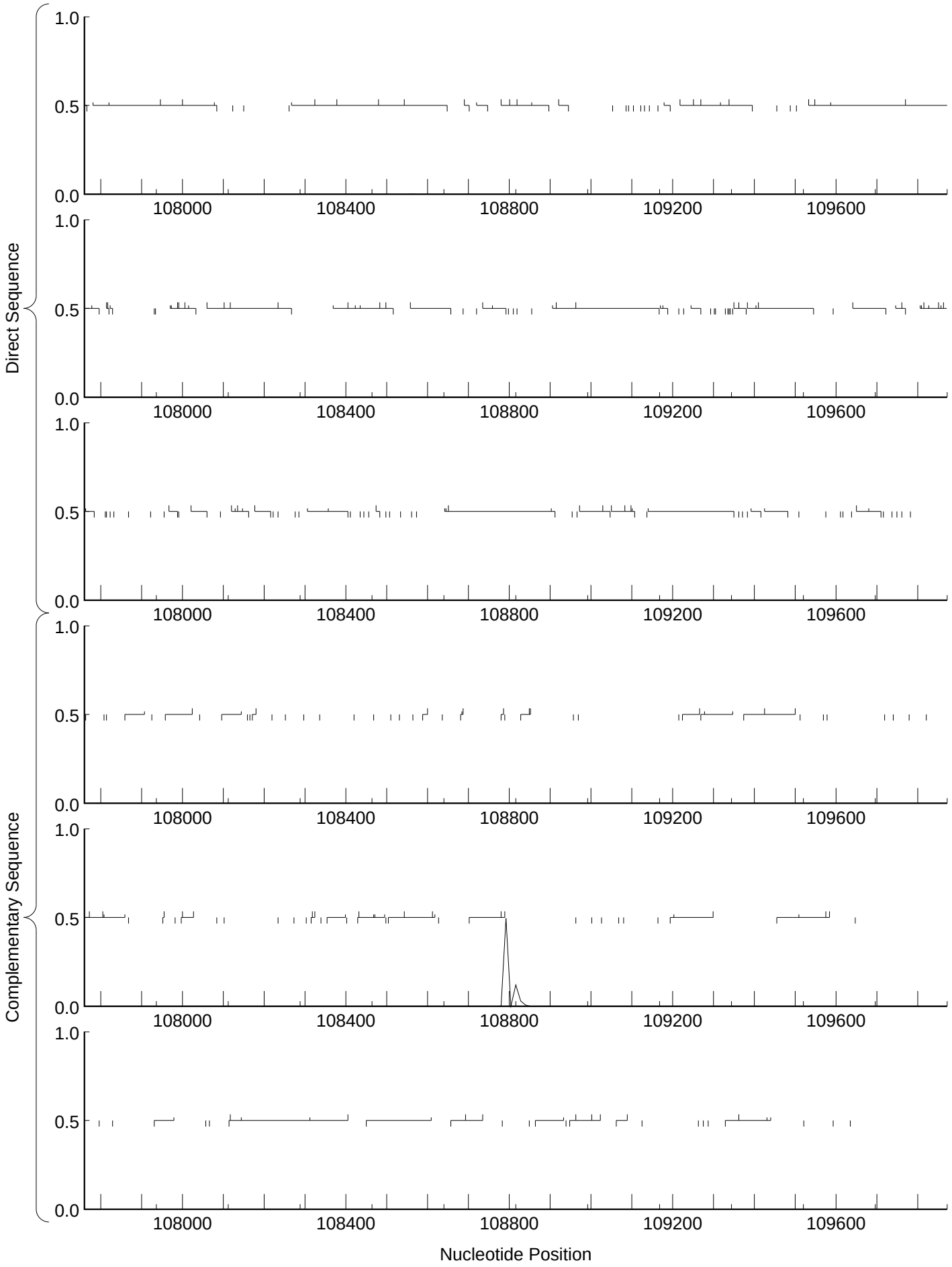
ge Wipeout complete sequence, 132935 bp including 12204 bp terminal repeat, Cluster BE2, Order 4, Window 96, Step 12, 51/64



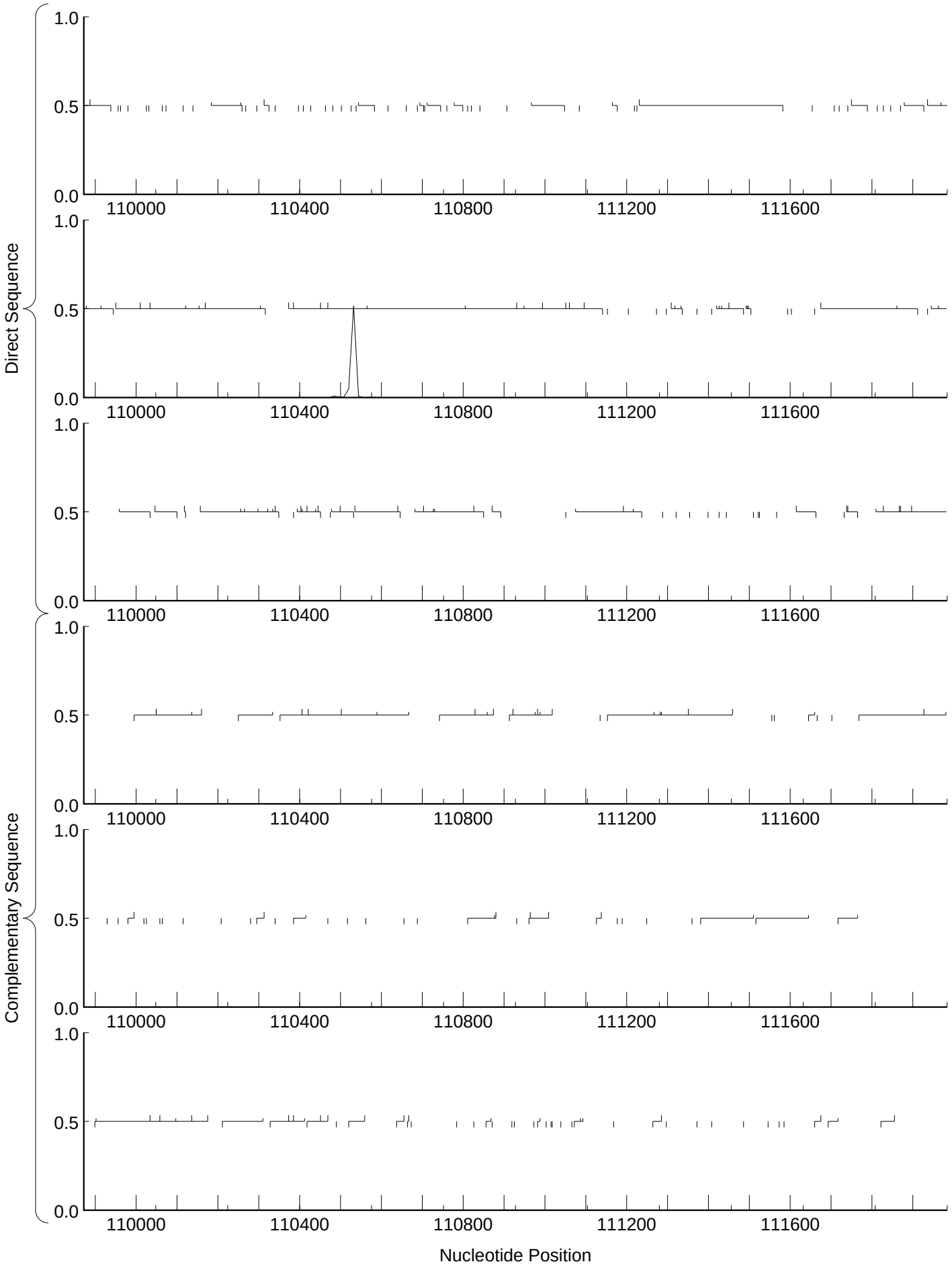
ge Wipeout complete sequence, 132935 bp including 12204 bp terminal repeat, Cluster BE2, Order 4, Window 96, Step 12, 52/64

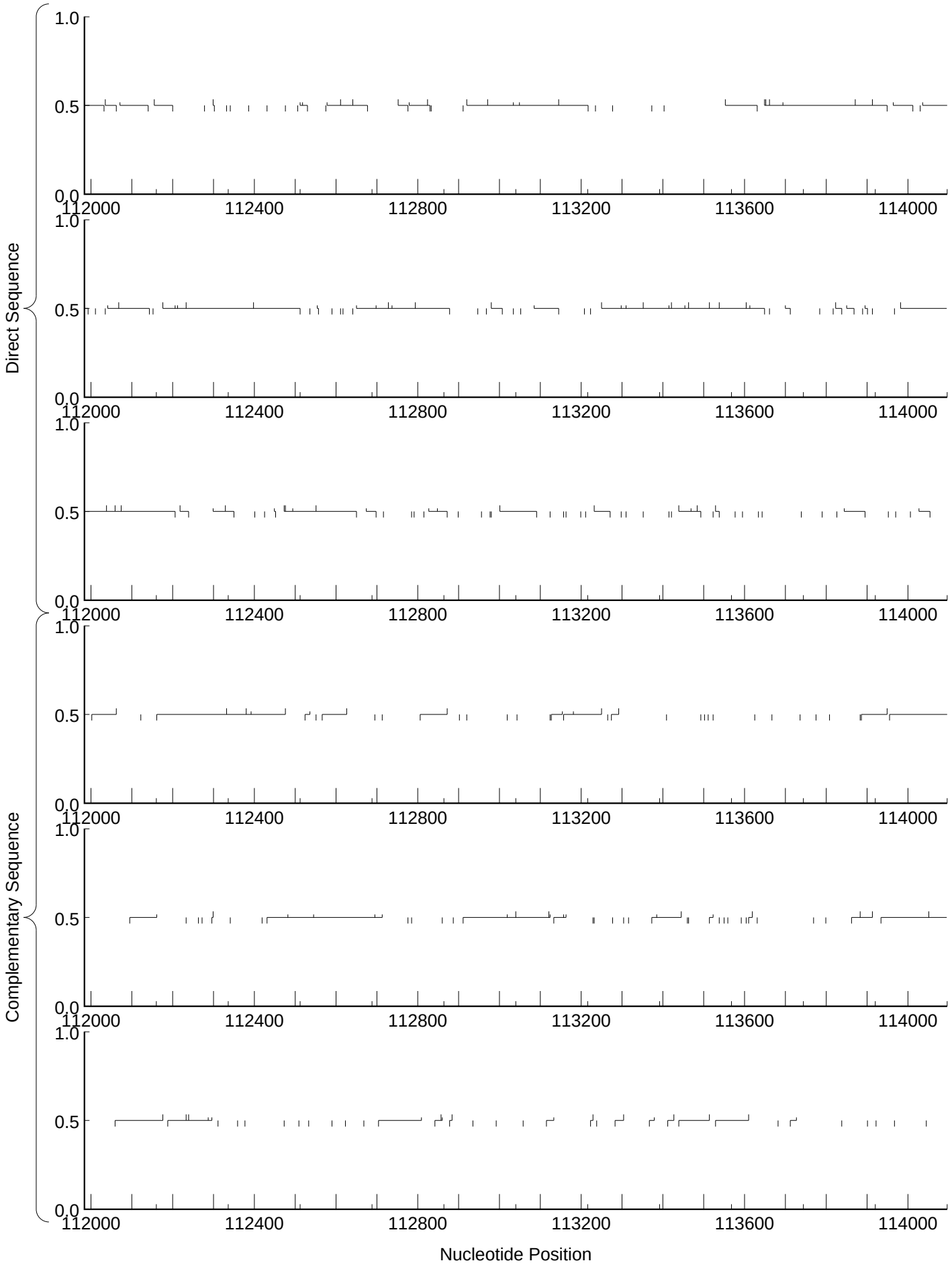


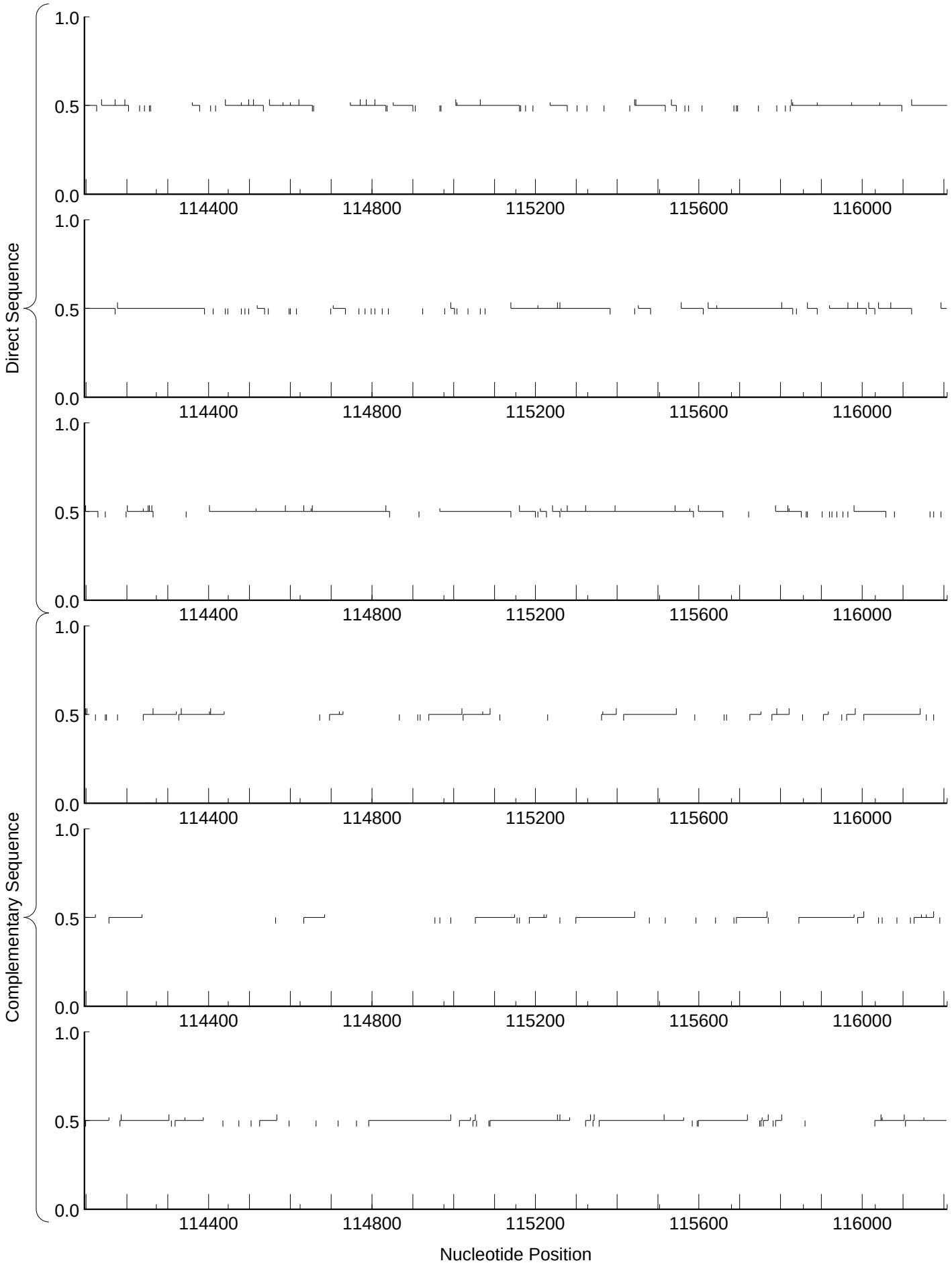
ge Wipeout complete sequence, 132935 bp including 12204 bp terminal repeat, Cluster BE2, Order 4, Window 96, Step 12, 53/64

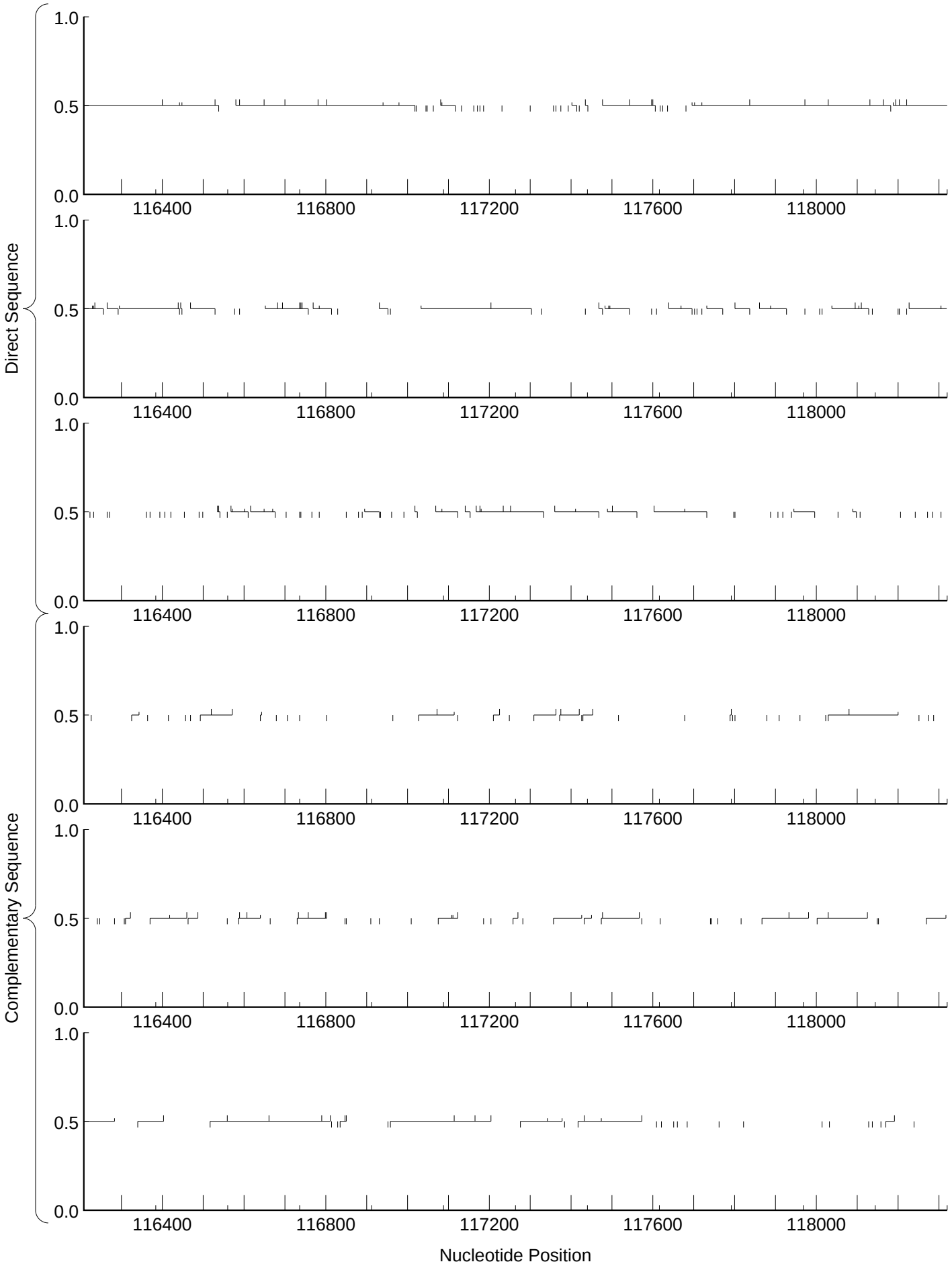


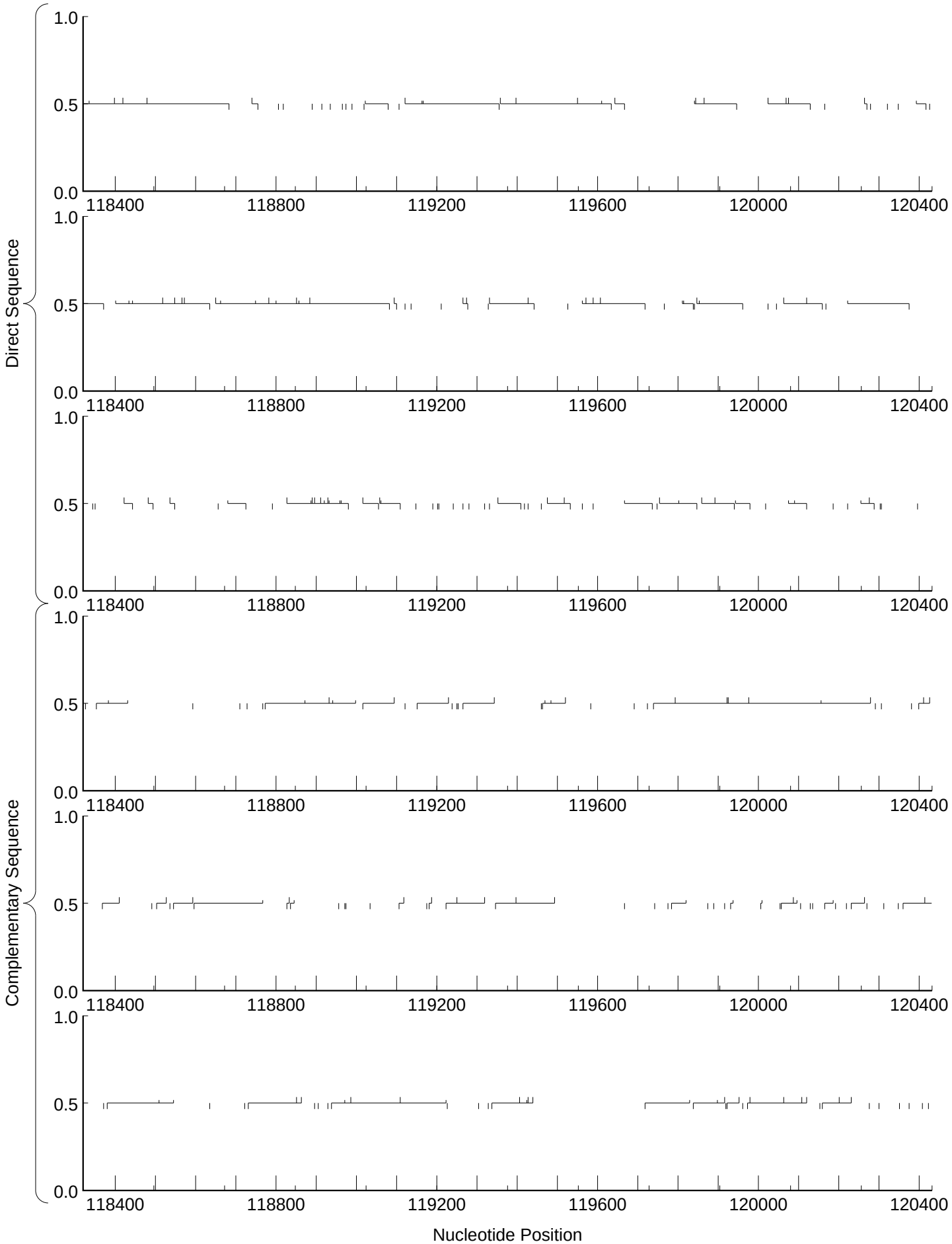
ge Wipeout complete sequence, 132935 bp including 12204 bp terminal repeat, Cluster BE2, Order 4, Window 96, Step 12, 54/64

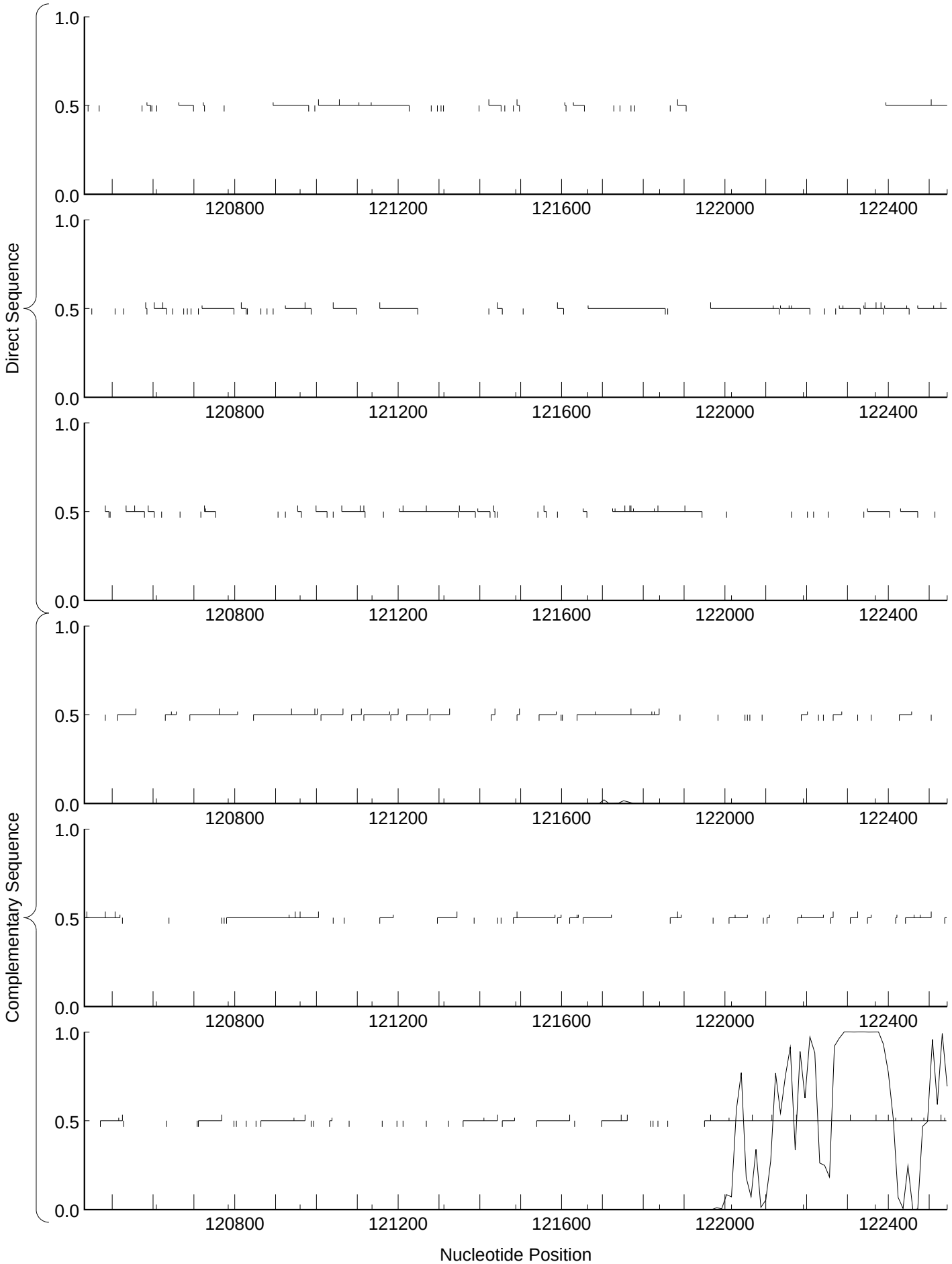


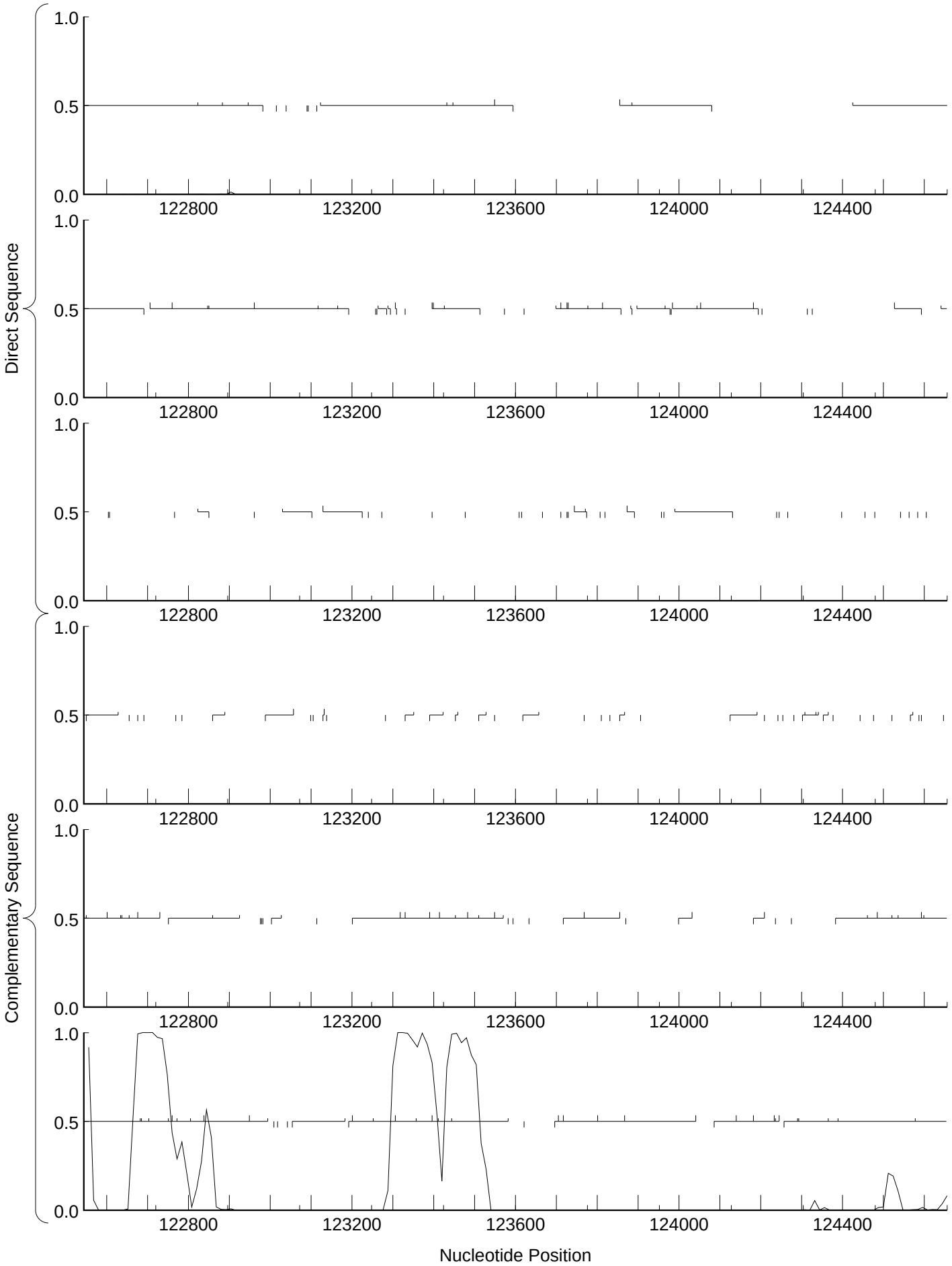

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
112000
112400
112800
113200
113600
114000
Nucleotide Position


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
114400
114800
115200
115600
116000
Nucleotide Position

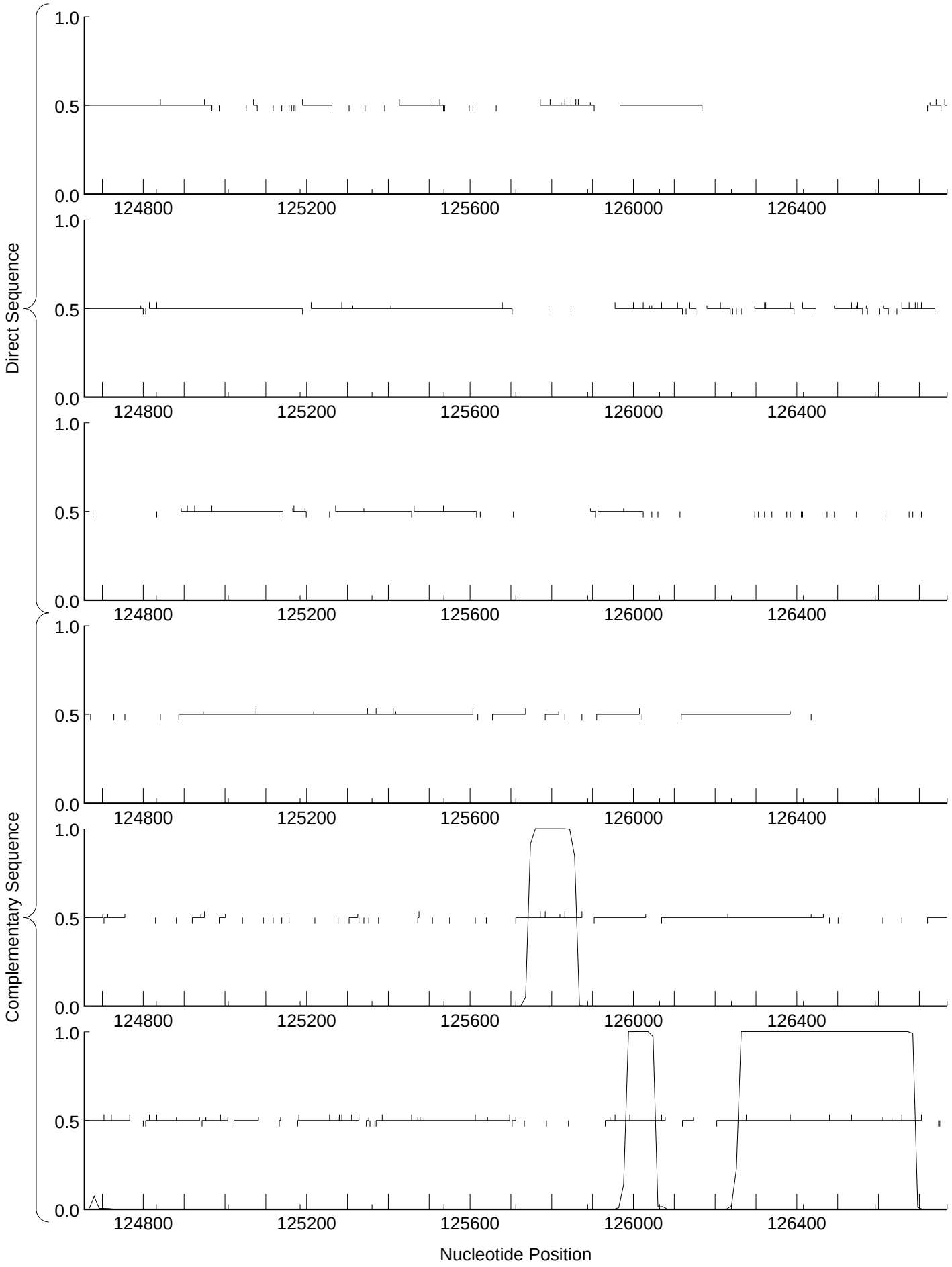

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
116400
116800
117200
117600
118000
Nucleotide Position


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
118400
118800
119200
119600
120000
120400
Nucleotide Position

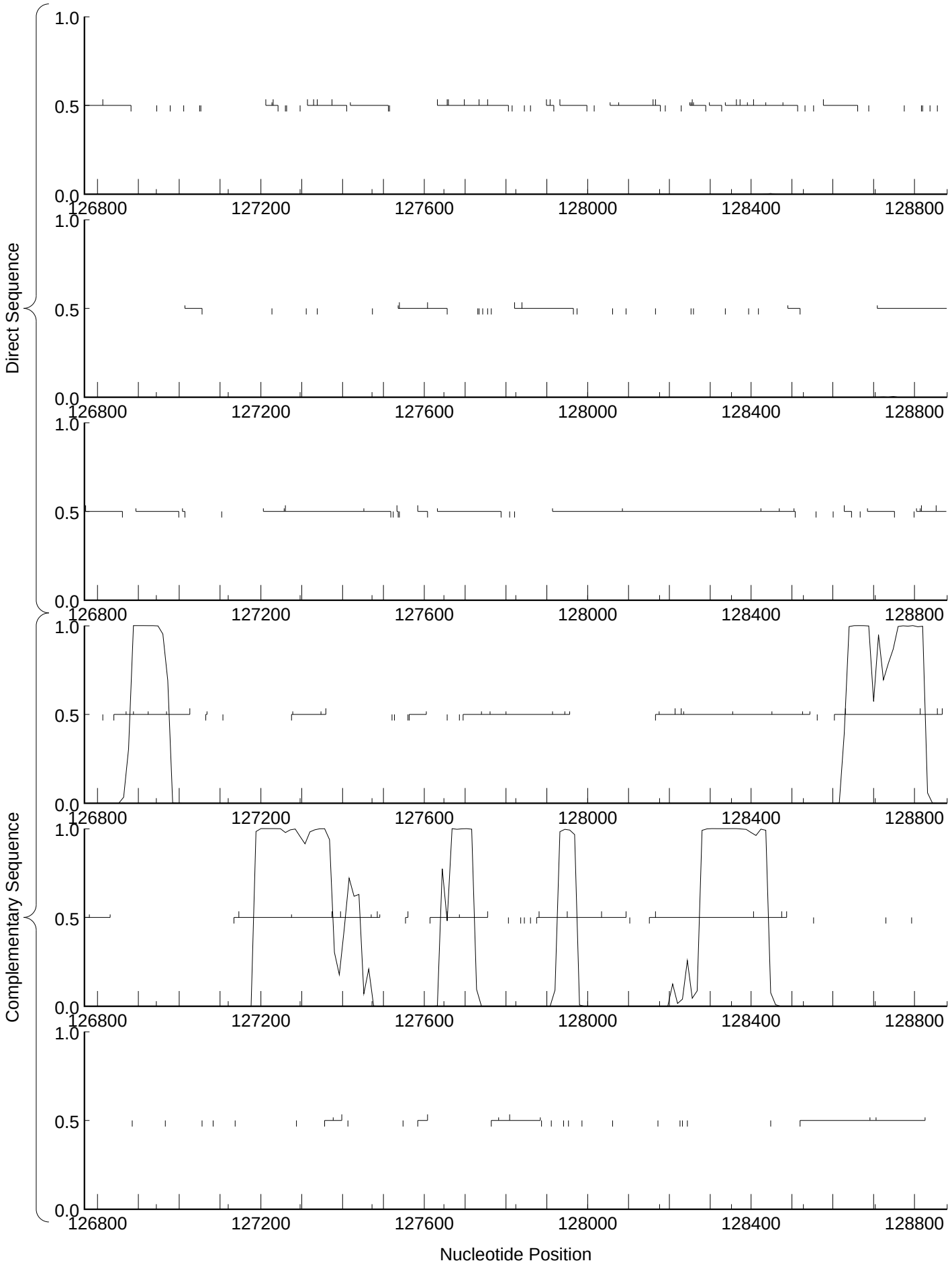

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
120800
121200
121600
122000
122400
Nucleotide Position


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
122800
123200
123600
124000
124400
Nucleotide Position

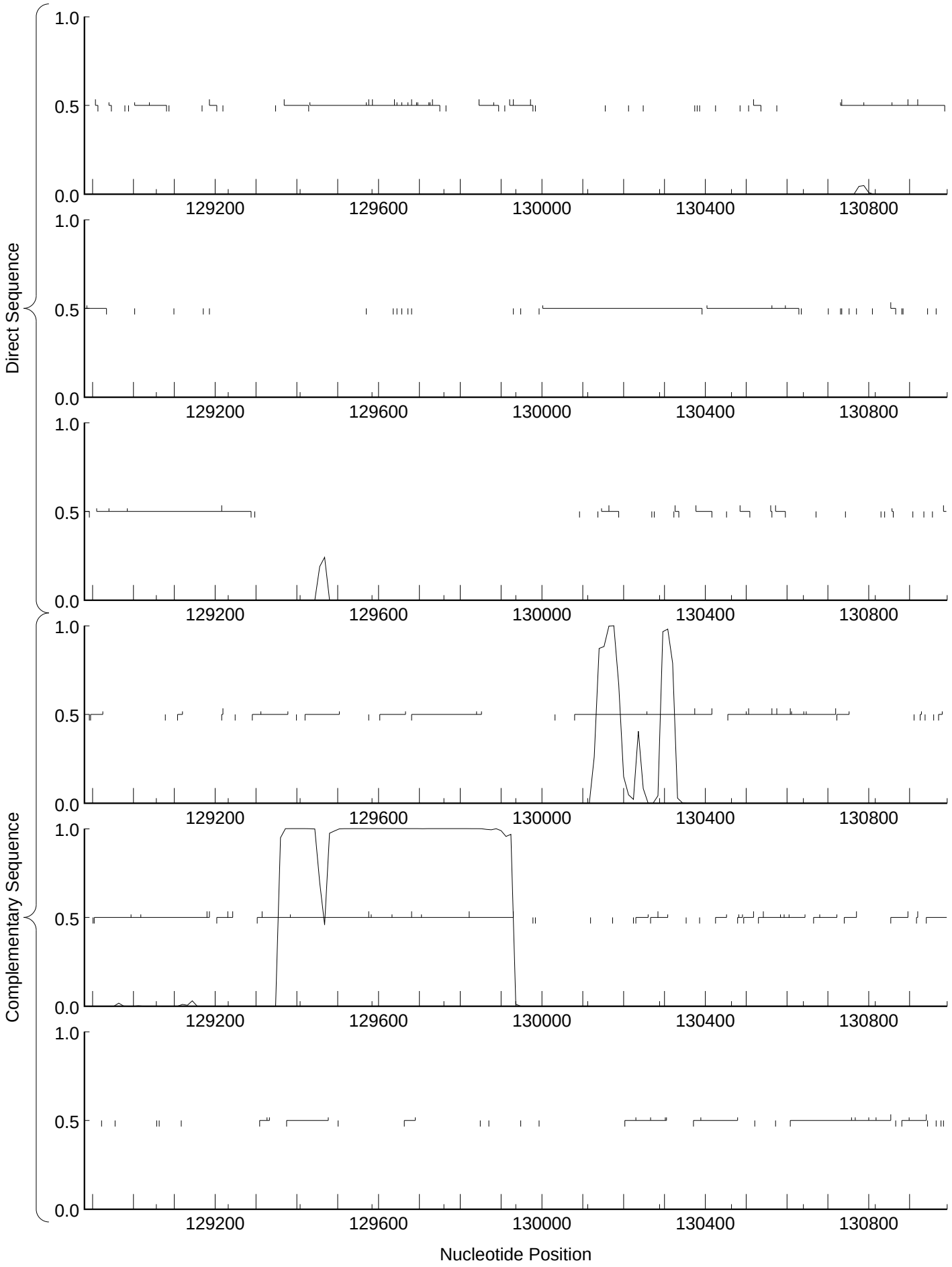
ge Wipeout complete sequence, 132935 bp including 12204 bp terminal repeat, Cluster BE2, Order 4, Window 96, Step 12, 61/64

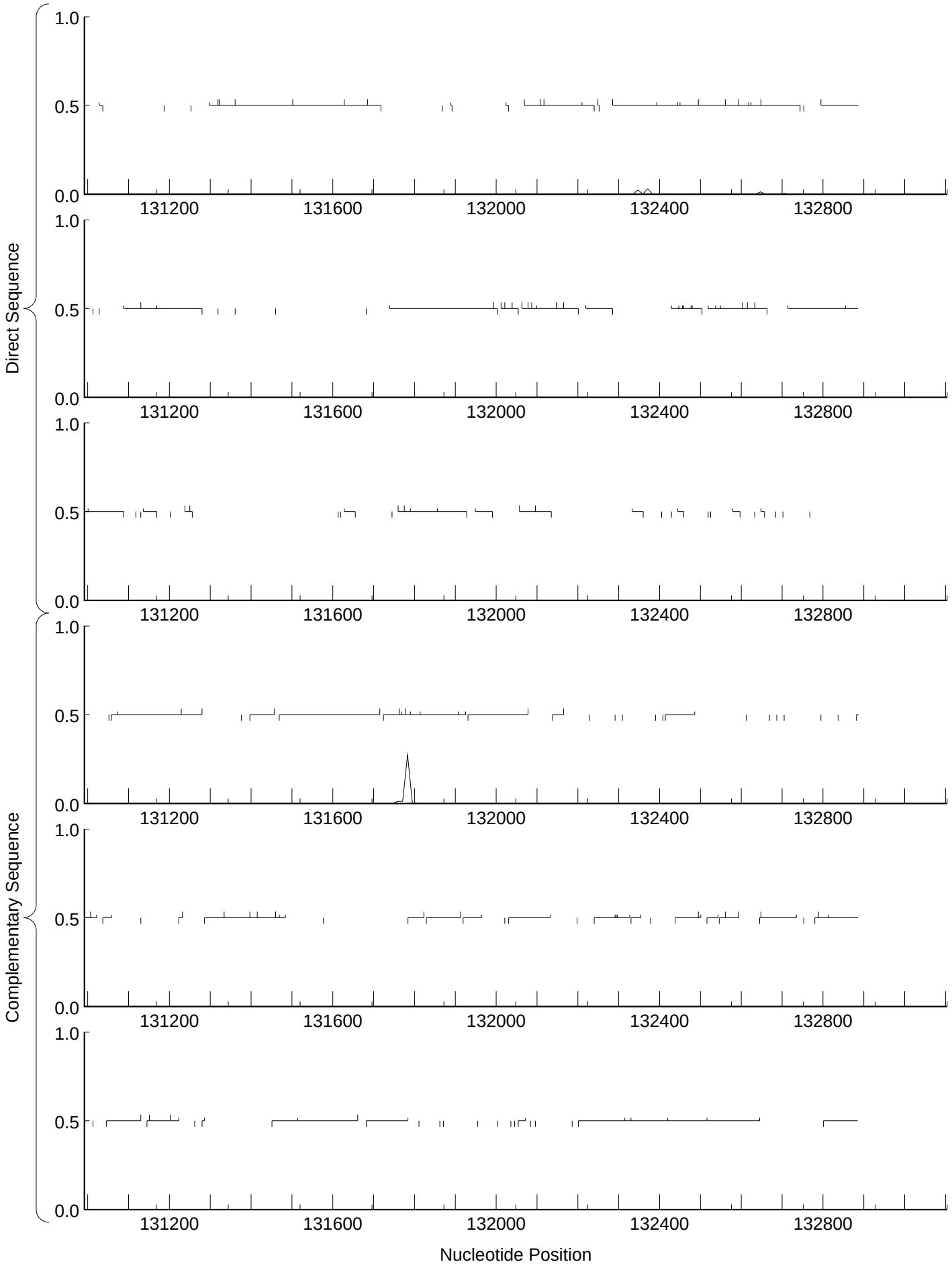


ge Wipeout complete sequence, 132935 bp including 12204 bp terminal repeat, Cluster BE2, Order 4, Window 96, Step 12, 62/64



ge Wipeout complete sequence, 132935 bp including 12204 bp terminal repeat, Cluster BE2, Order 4, Window 96, Step 12, 63/64




Direct Sequence
Complementary Sequence
1.0
0.5
0.0
131200
131600
132000
132400
132800
Nucleotide Position