GeneMark

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

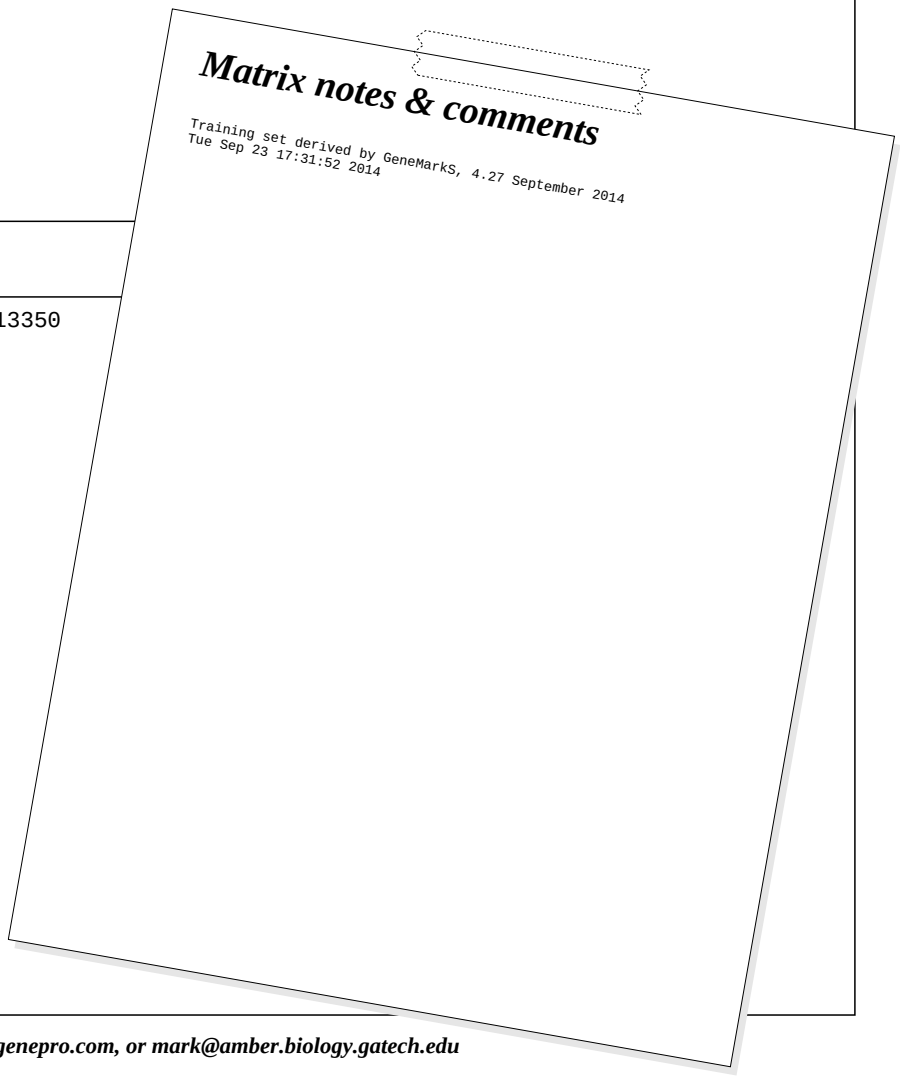
PROGRAM INFORMATION

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Sequence         :  Streptomyces phage Yaboi complete sequence, 131250 bp including 12433 bp terminal repeat, C
Analysis Date    :  3/29/24 at 5:41:59
Pages            :  64
Sequence Length  :  131250 bp
GC Content       :   49.30%

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

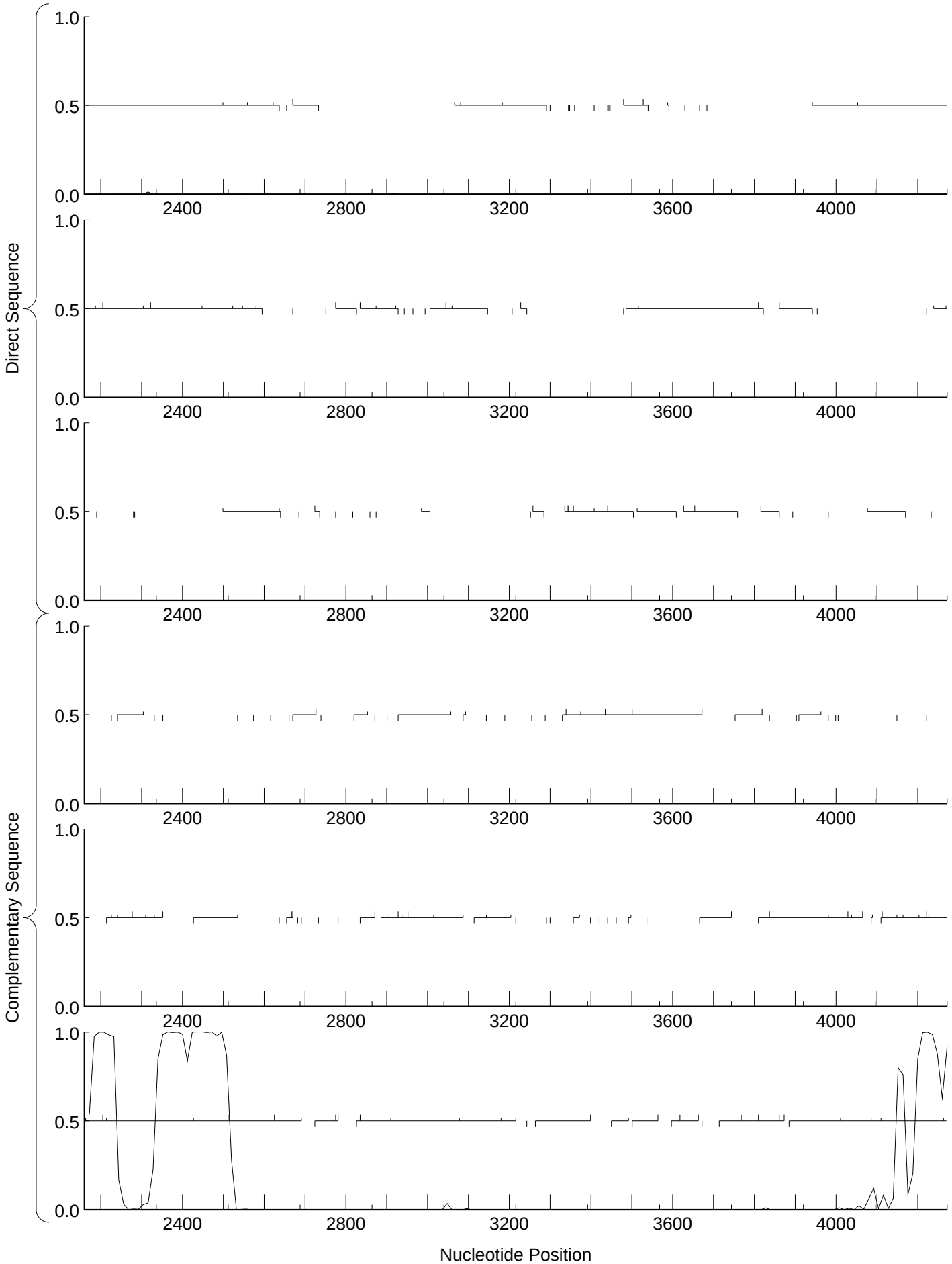
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Matrix     :  Streptomyces_griseus_NBRC_13350
Author     :  -

Order      :  4
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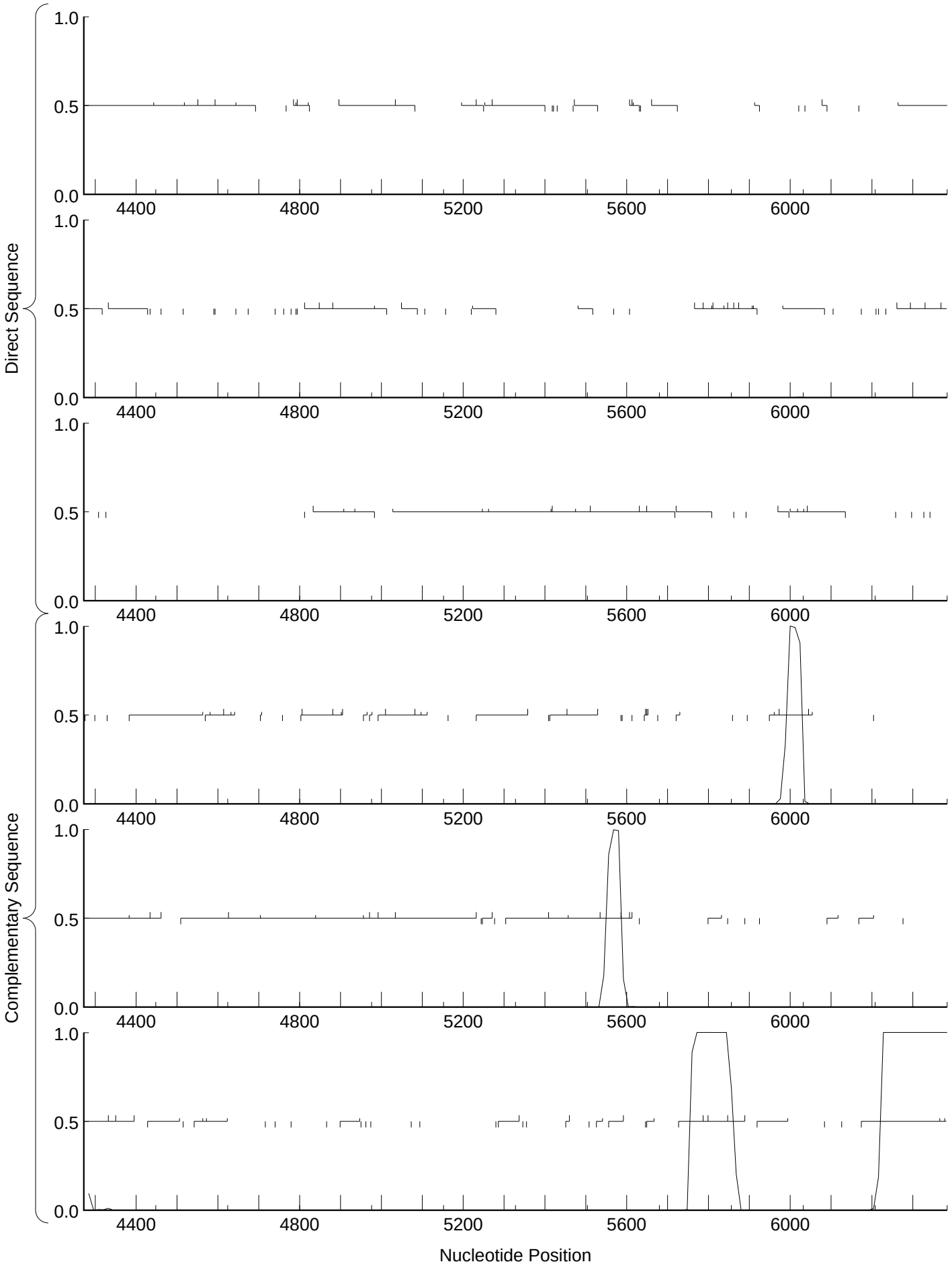

```
  Send questions / comments to:
      Dr. M. Borodovsky
      Georgia Institute of Technology
      School of Biology
      Atlanta, GA  30332-0230
```


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

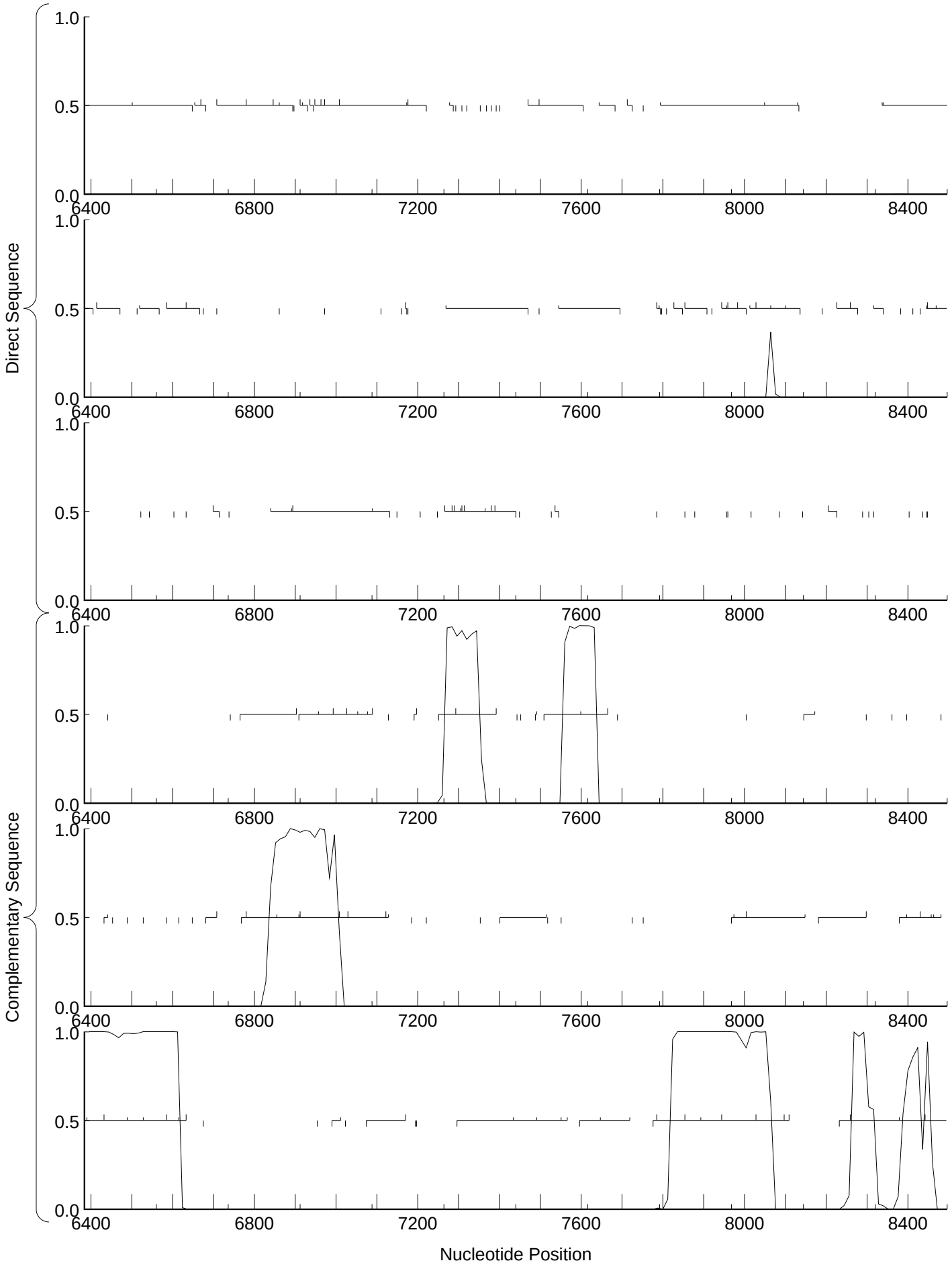
phage Yaboi complete sequence, 131250 bp including 12433 bp terminal repeat, Cluster BE2, Order 4, Window 96, Step 12, 2/64
Direct Sequence
Complementary Sequence
1.0
0.5
0.0
400
800
1200
1600
2000
Nucleotide Position


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
2400
2800
3200
3600
4000
Nucleotide Position

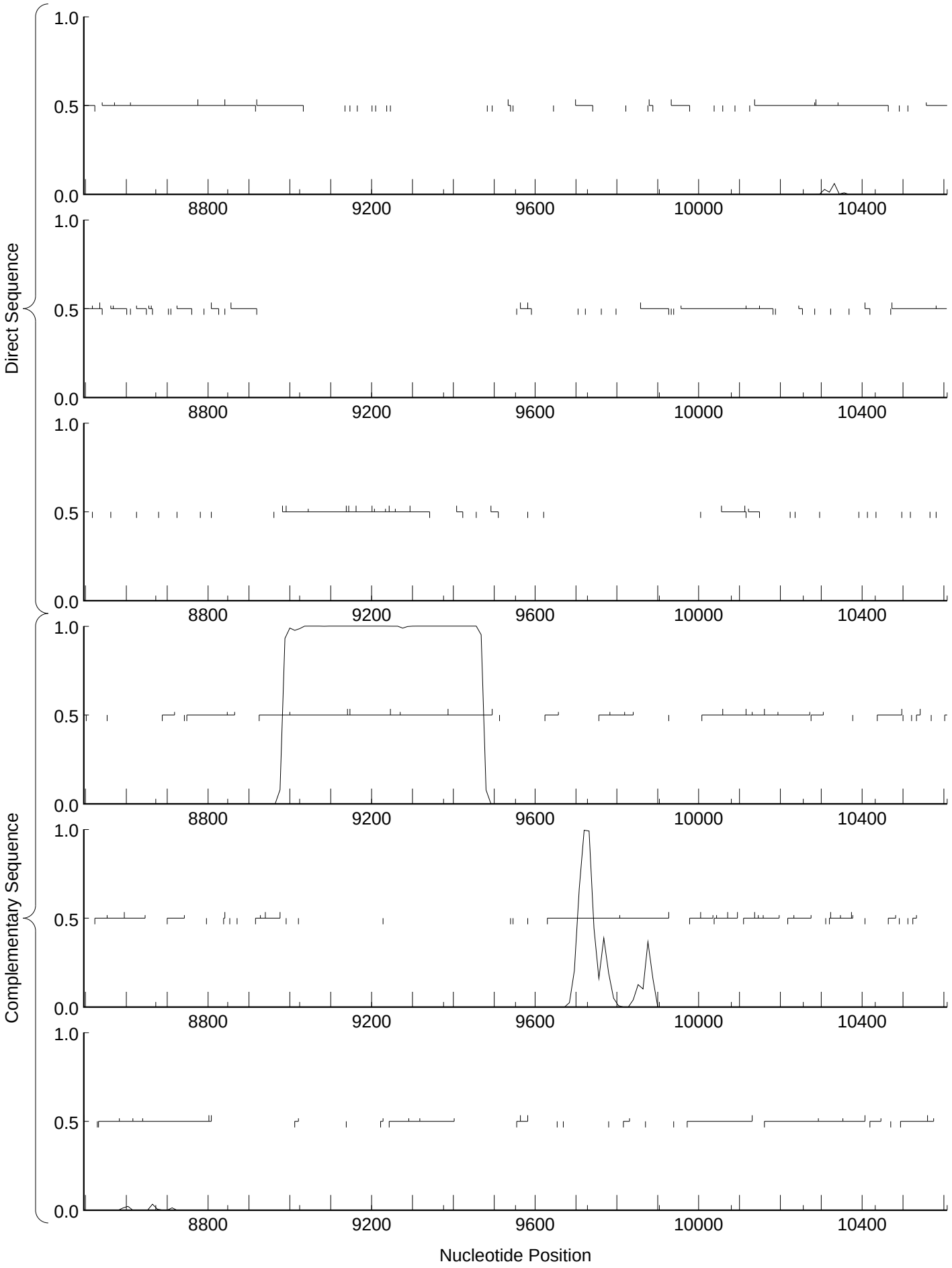
phage Yaboi complete sequence, 131250 bp including 12433 bp terminal repeat, Cluster BE2, Order 4, Window 96, Step 12, 4/64

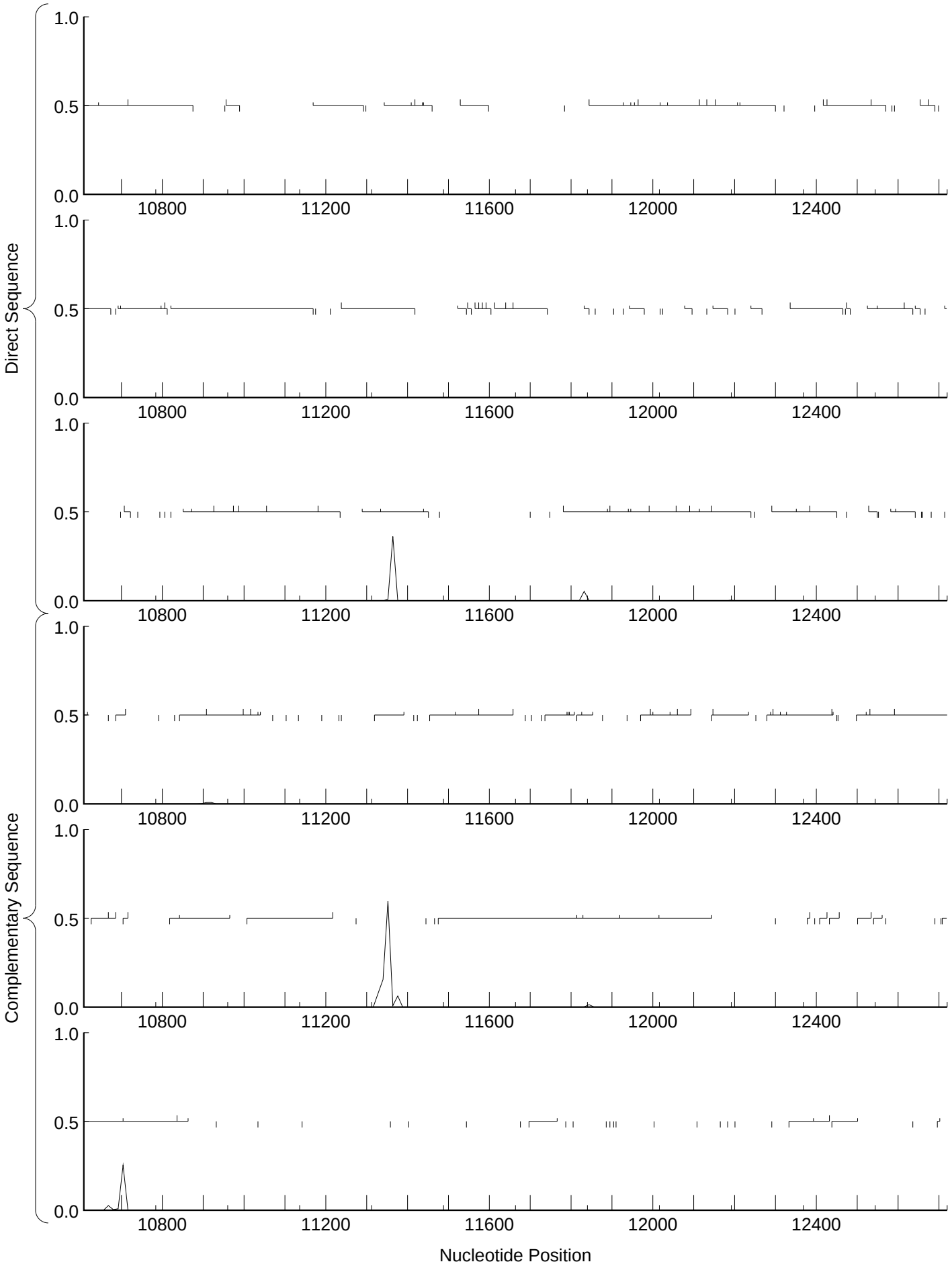


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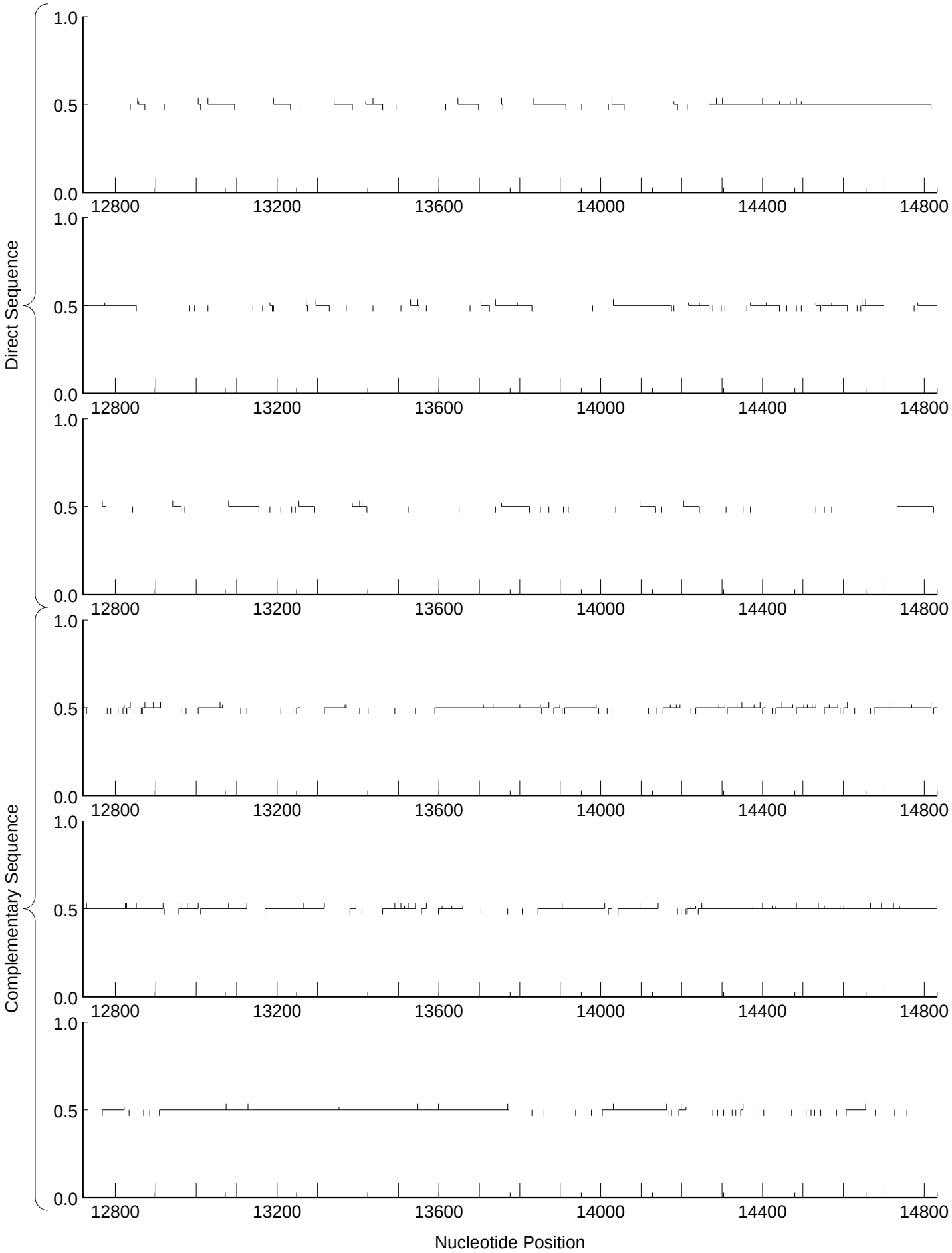


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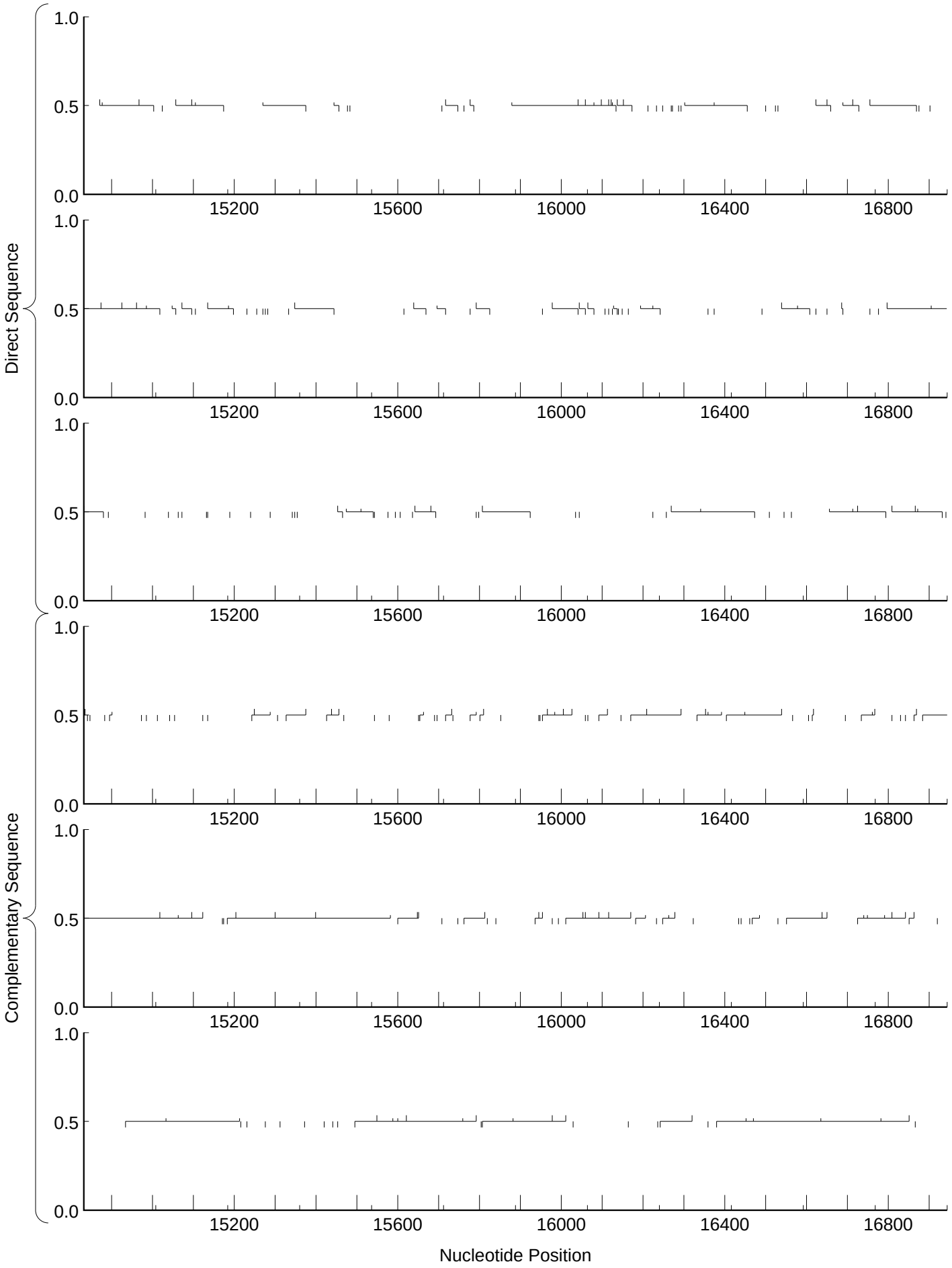


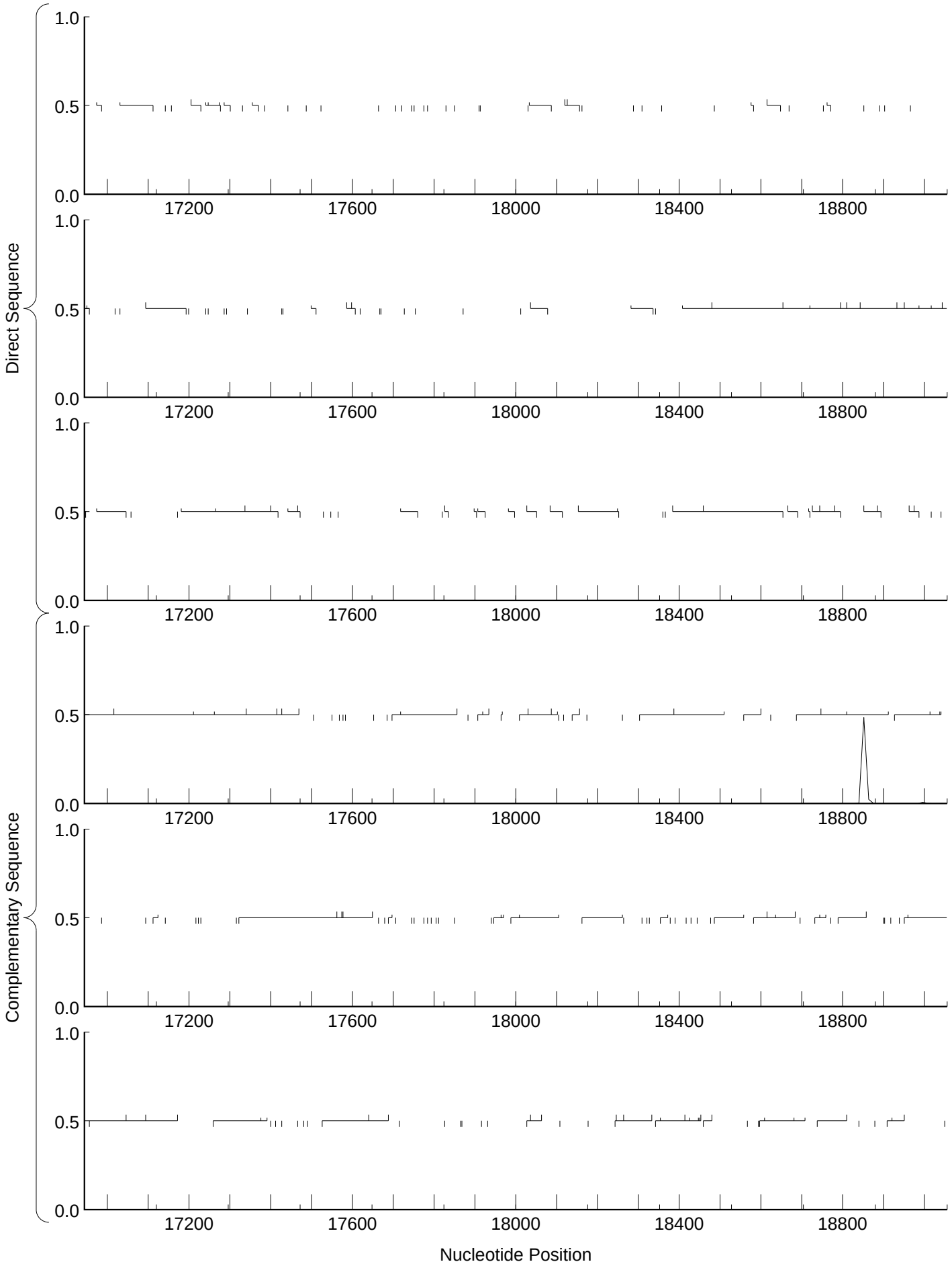

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
10800
11200
11600
12000
12400
Nucleotide Position

phage Yaboi complete sequence, 131250 bp including 12433 bp terminal repeat, Cluster BE2, Order 4, Window 96, Step 12, 8/64

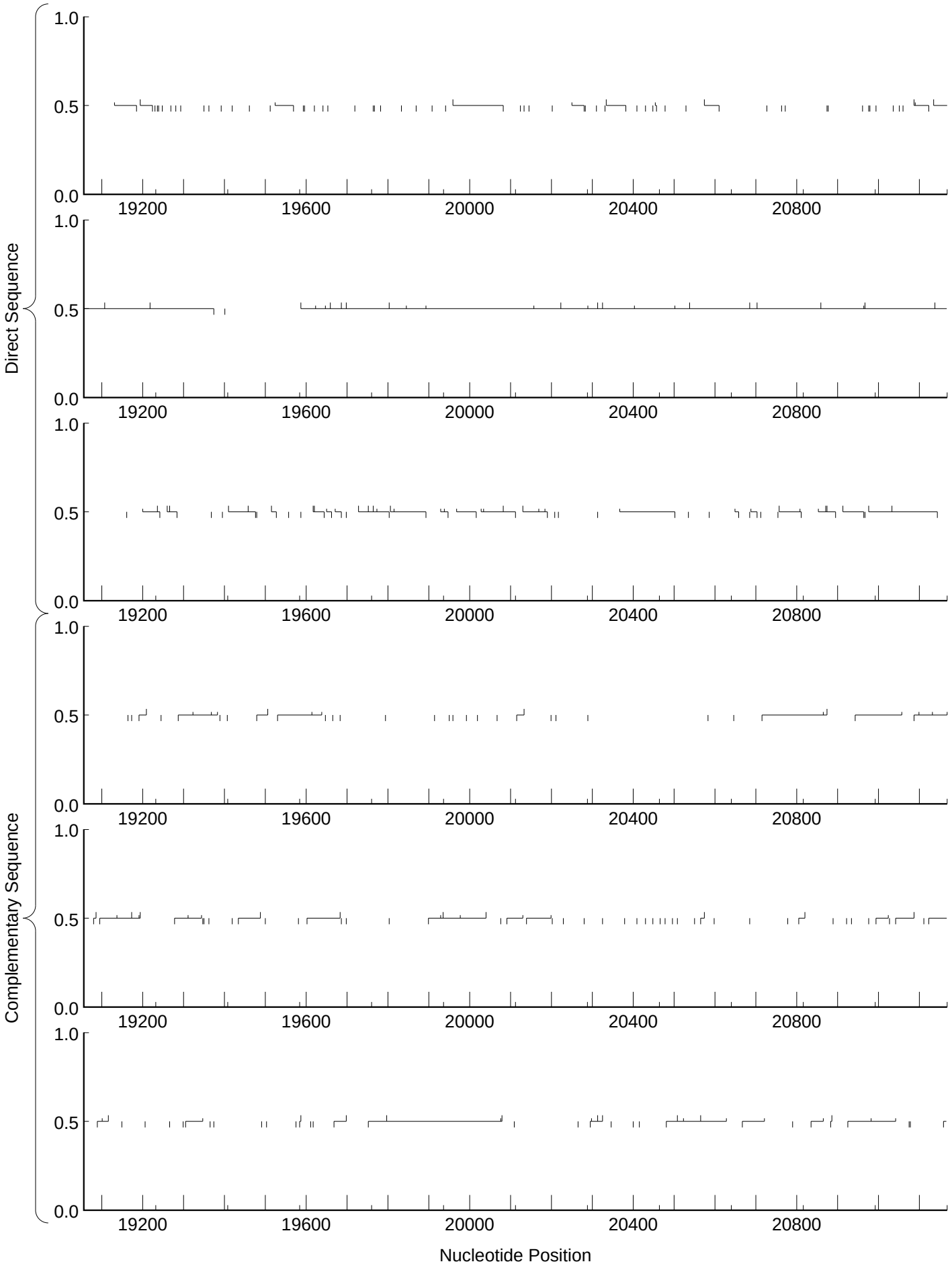


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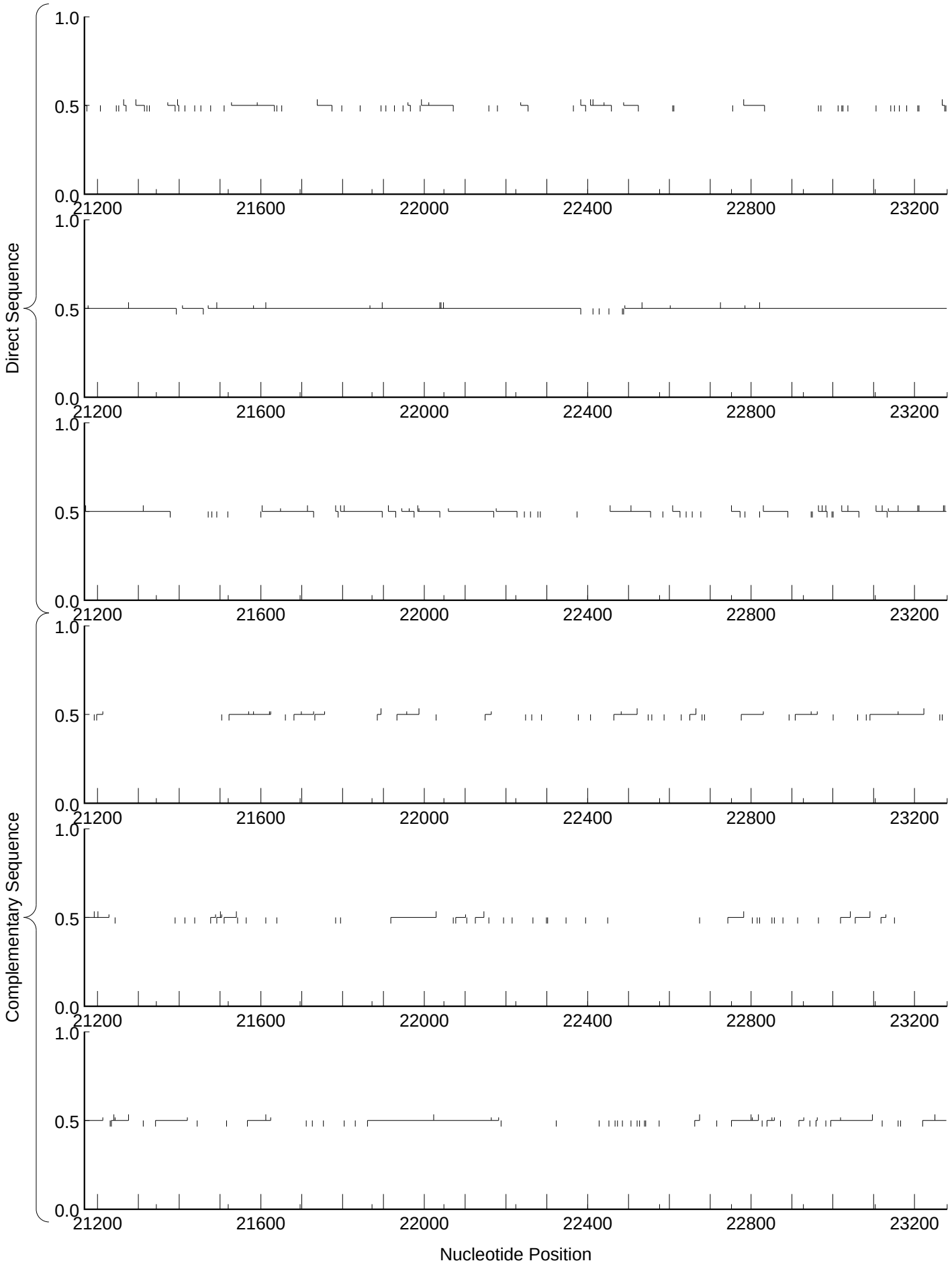


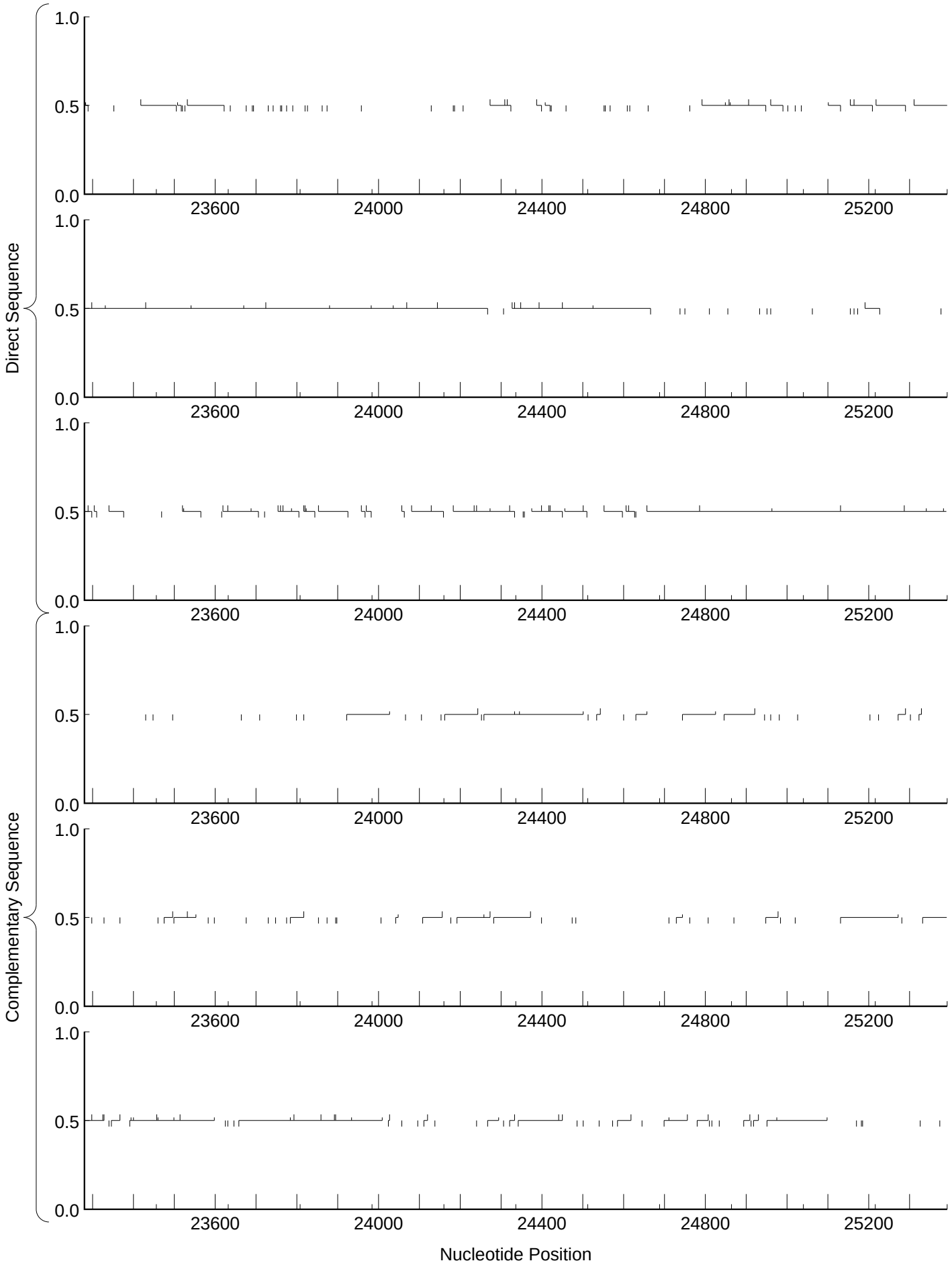

Direct Sequence
Complementary Sequence
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0.5
0.0
17200
17600
18000
18400
18800
Nucleotide Position

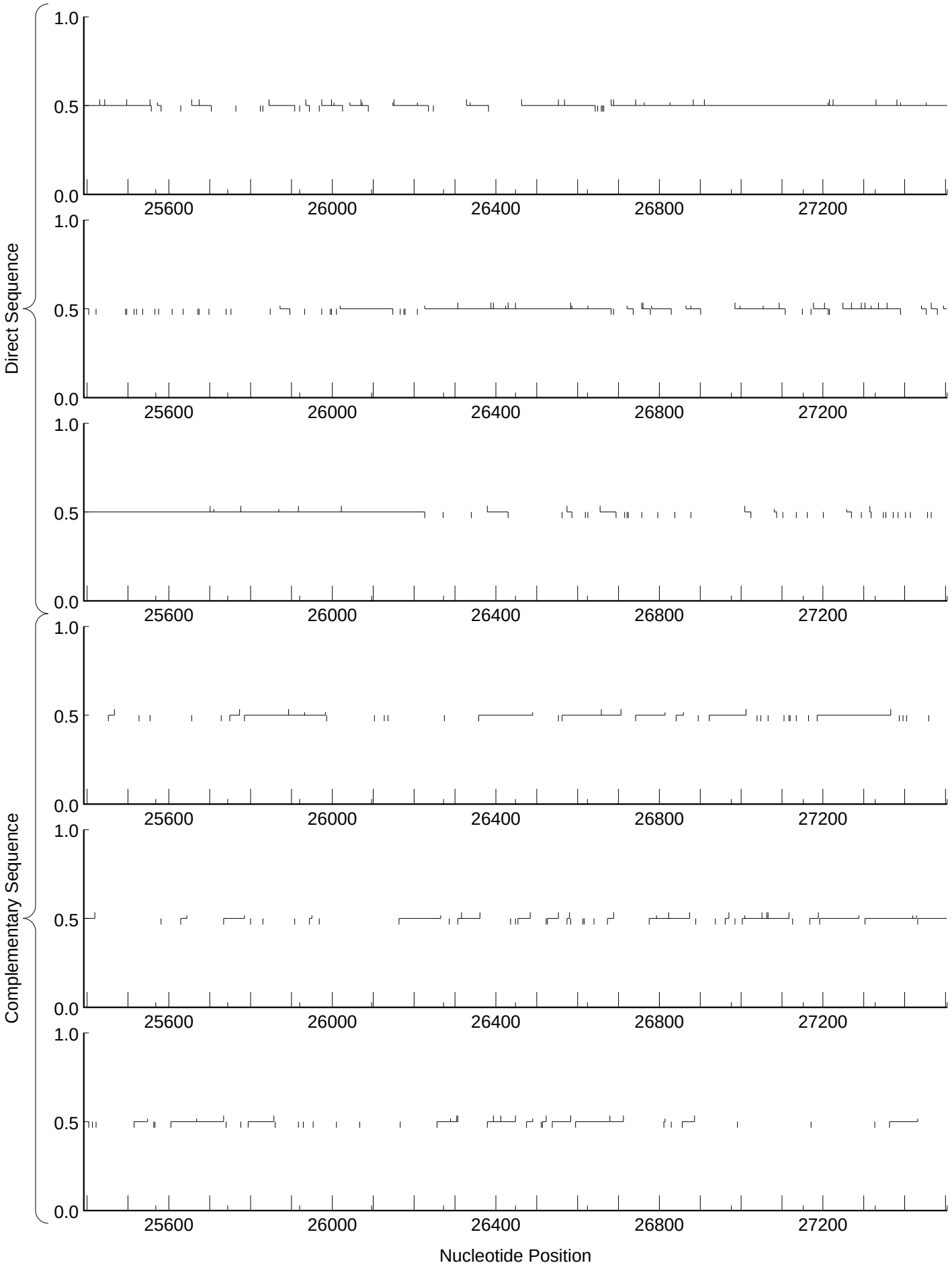
hage Yaboi complete sequence, 131250 bp including 12433 bp terminal repeat, Cluster BE2, Order 4, Window 96, Step 12, 11/64



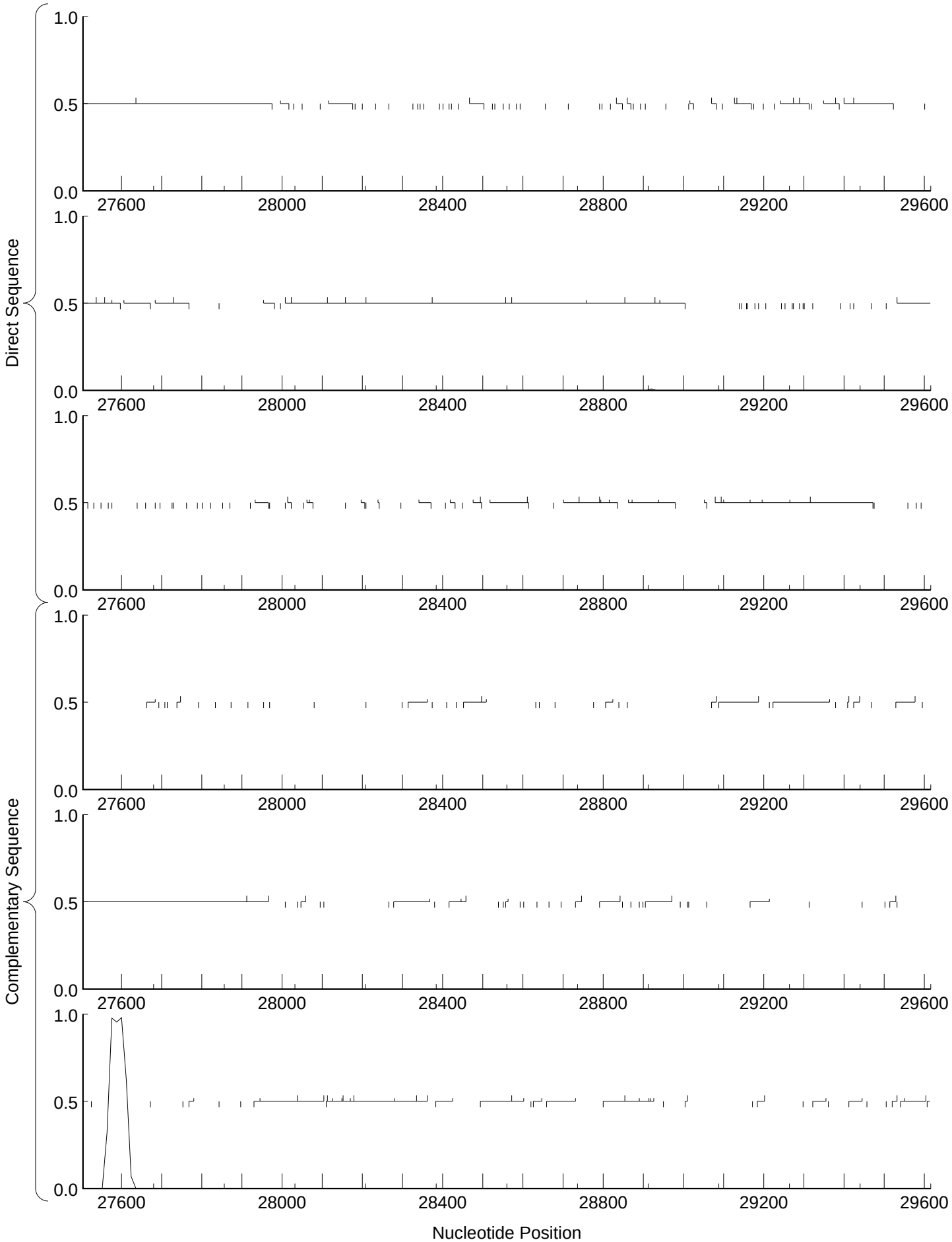
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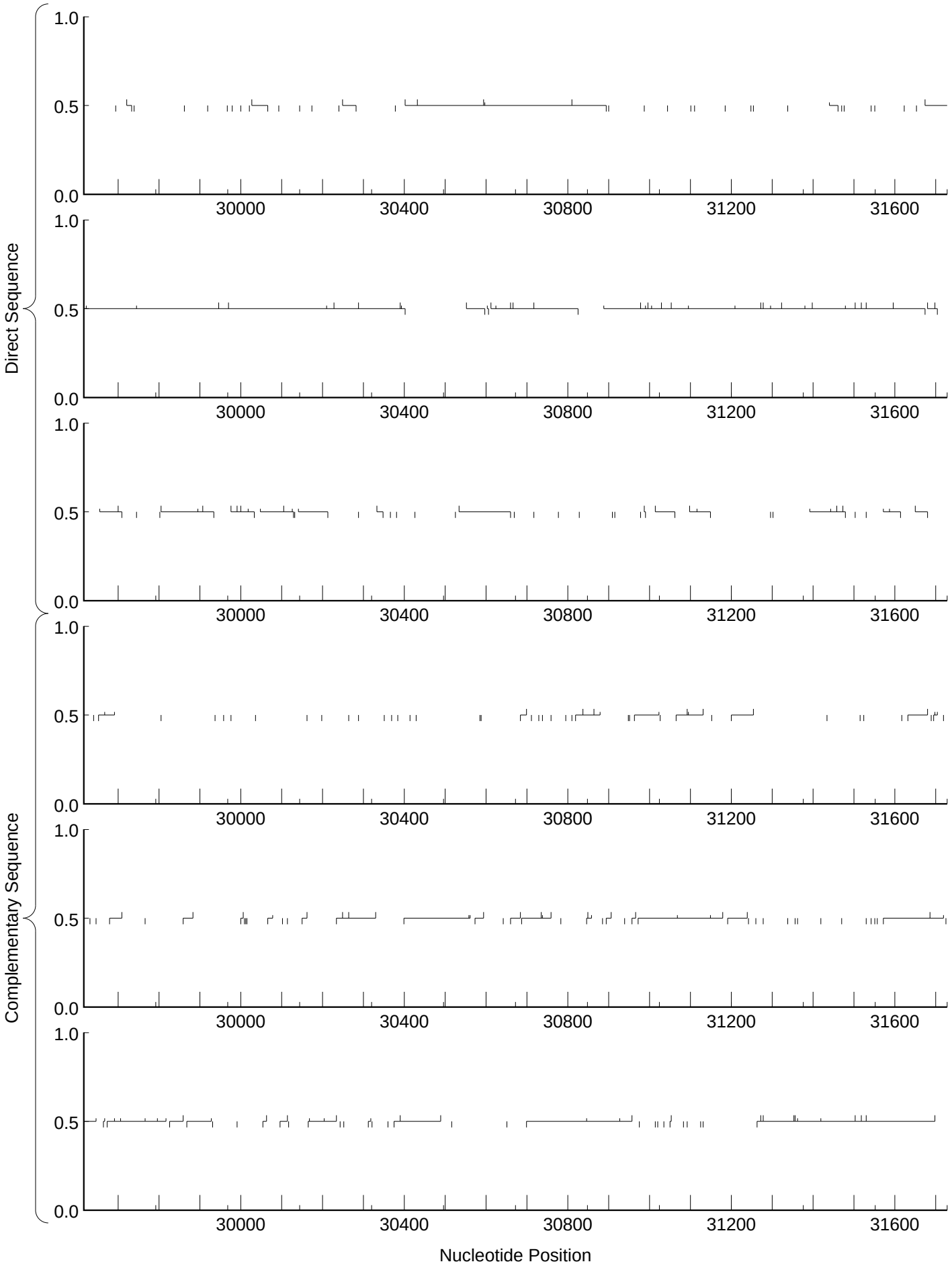


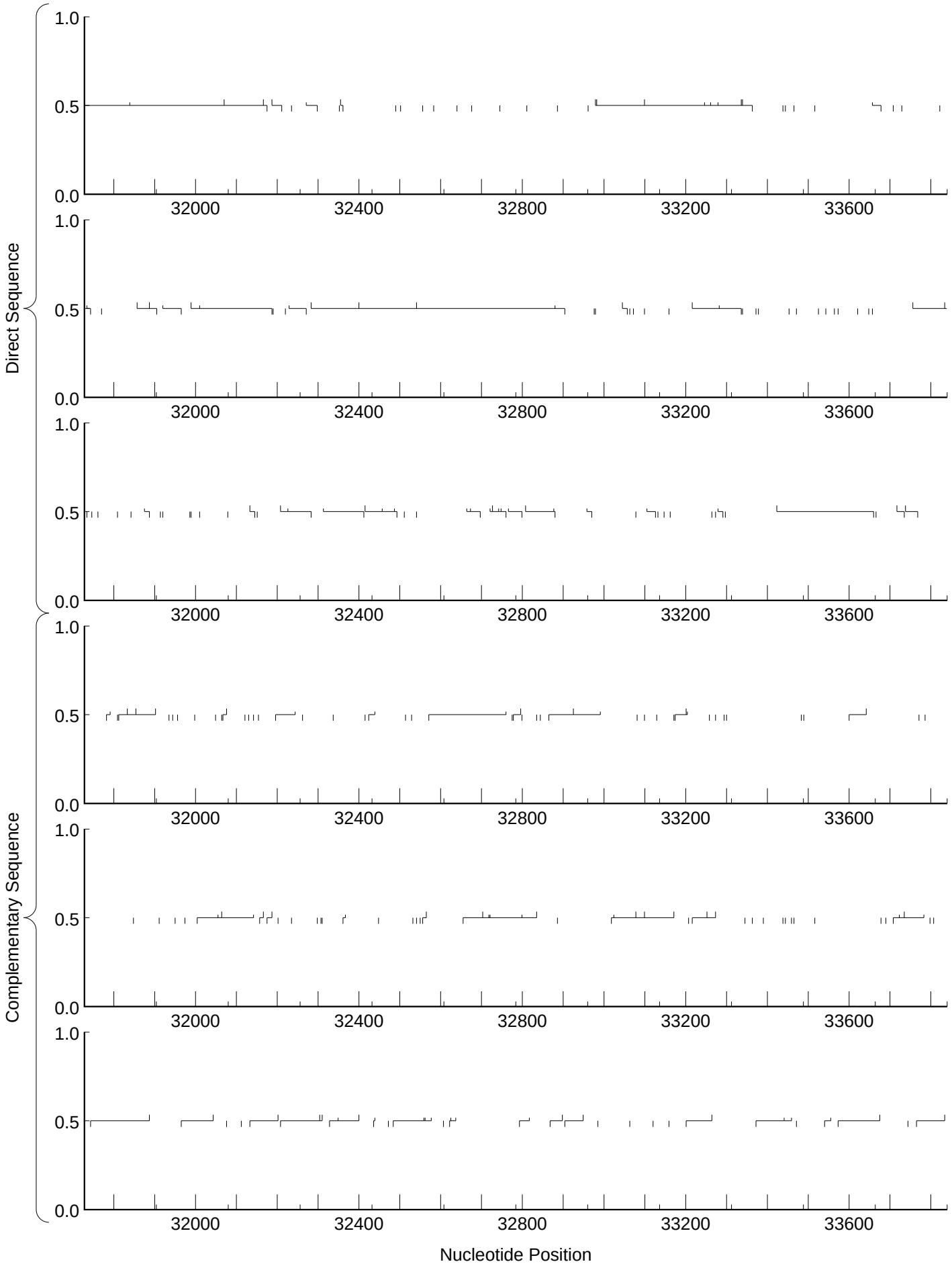

Direct Sequence
Complementary Sequence
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0.0
23600
24000
24400
24800
25200
Nucleotide Position

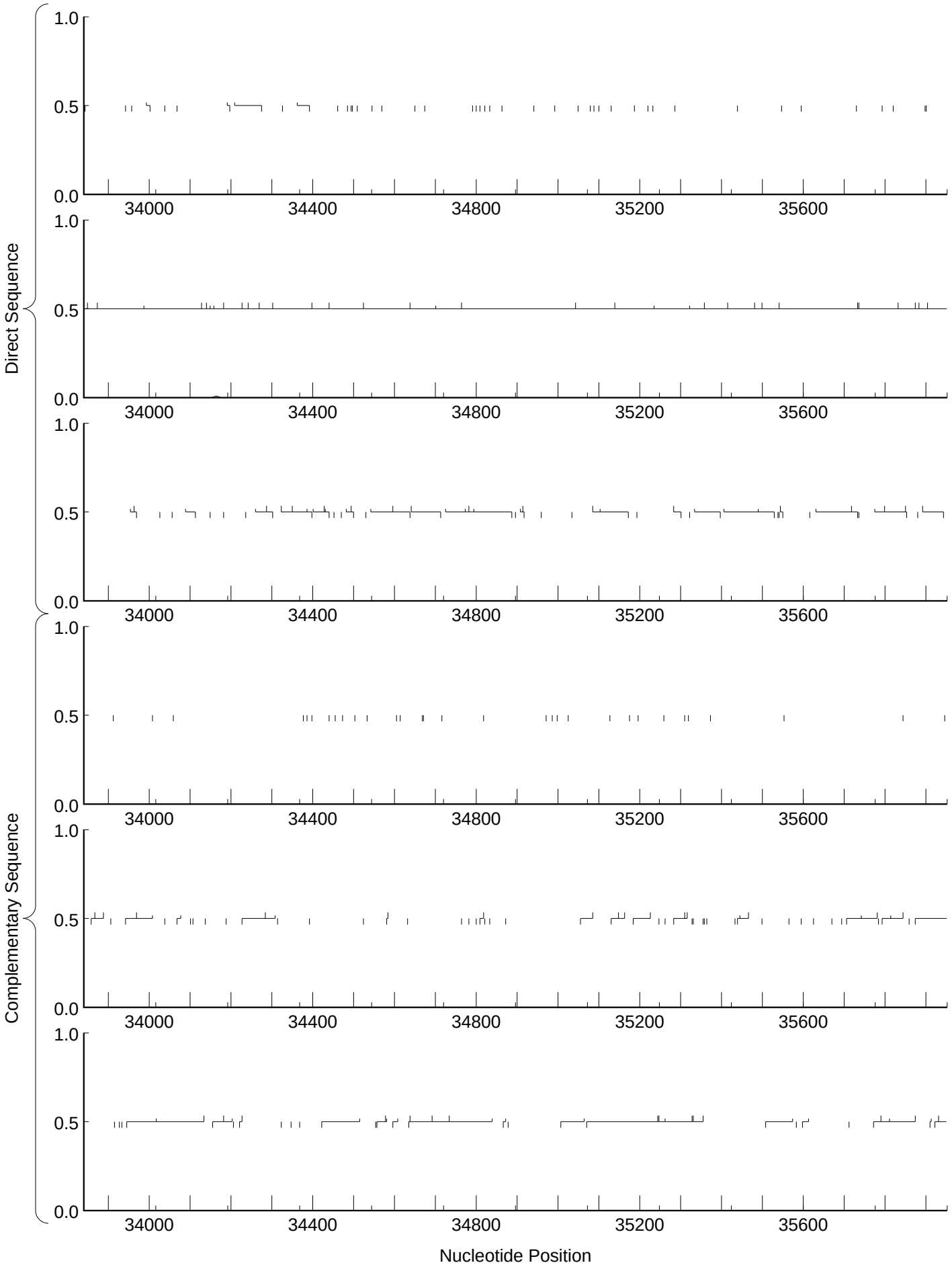

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
25600
26000
26400
26800
27200
Nucleotide Position

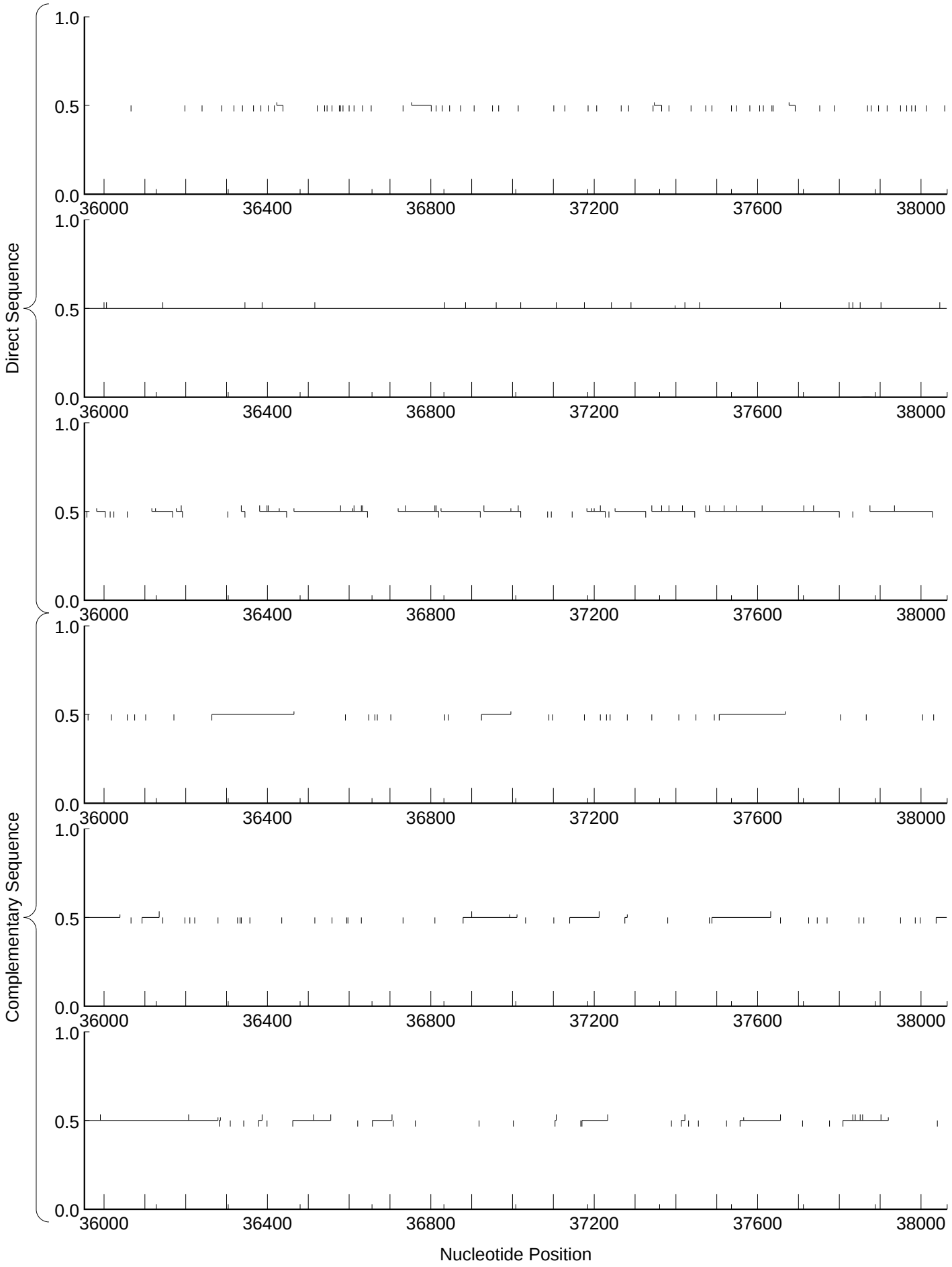
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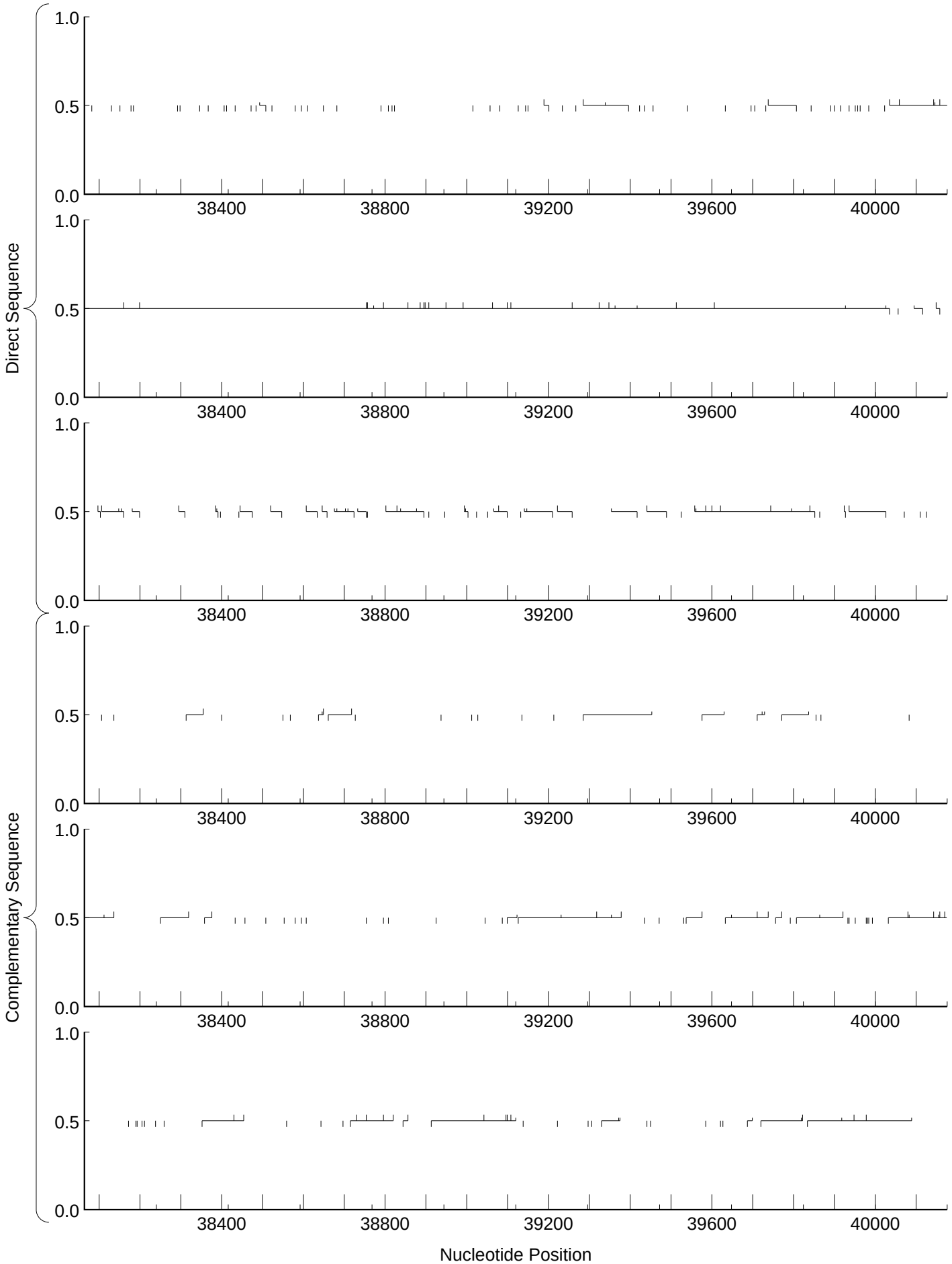



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Complementary Sequence
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0.5
0.0
30000
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30800
31200
31600
Nucleotide Position

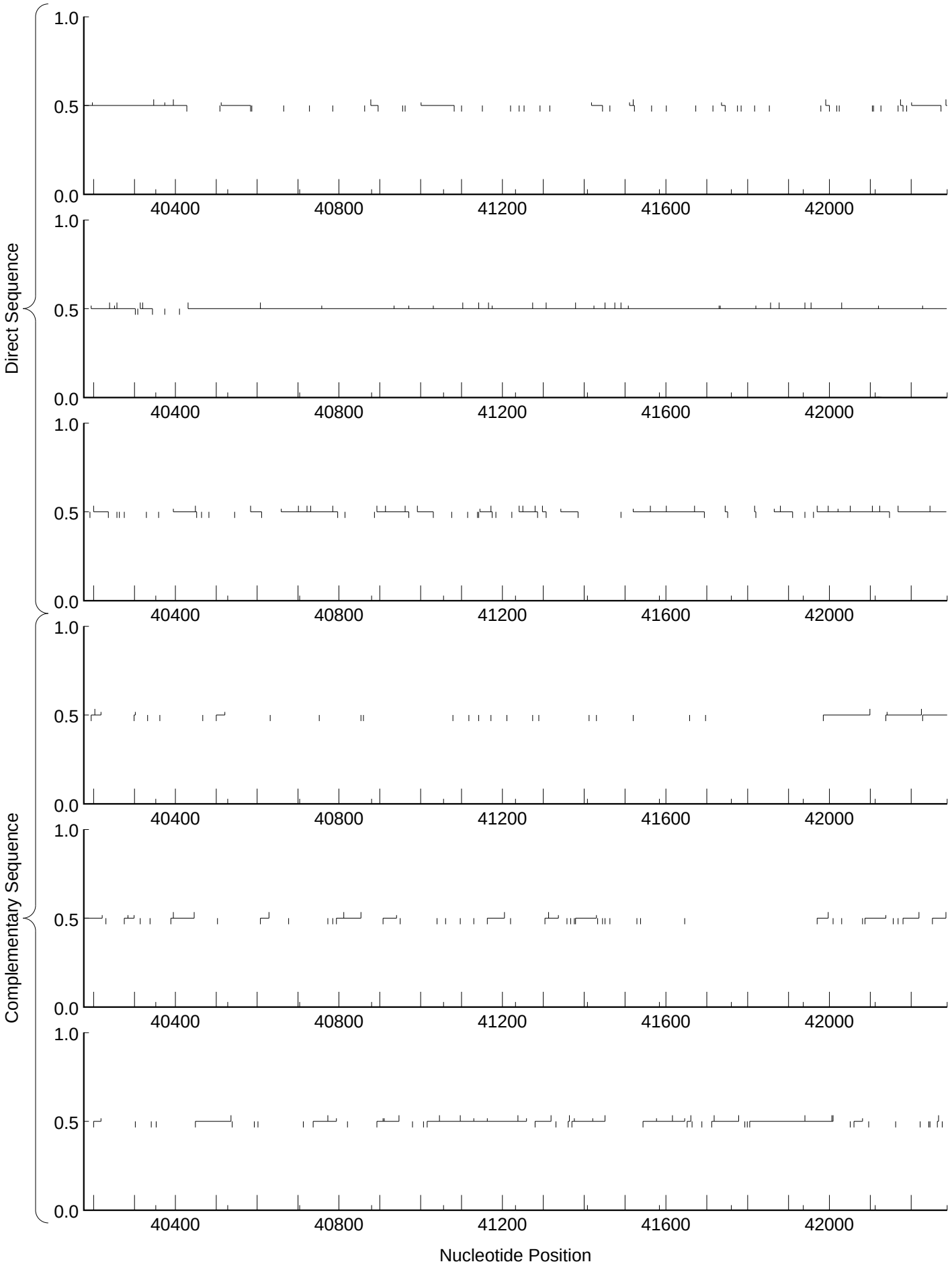

Direct Sequence
Complementary Sequence
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0.5
0.0
32000
32400
32800
33200
33600
Nucleotide Position

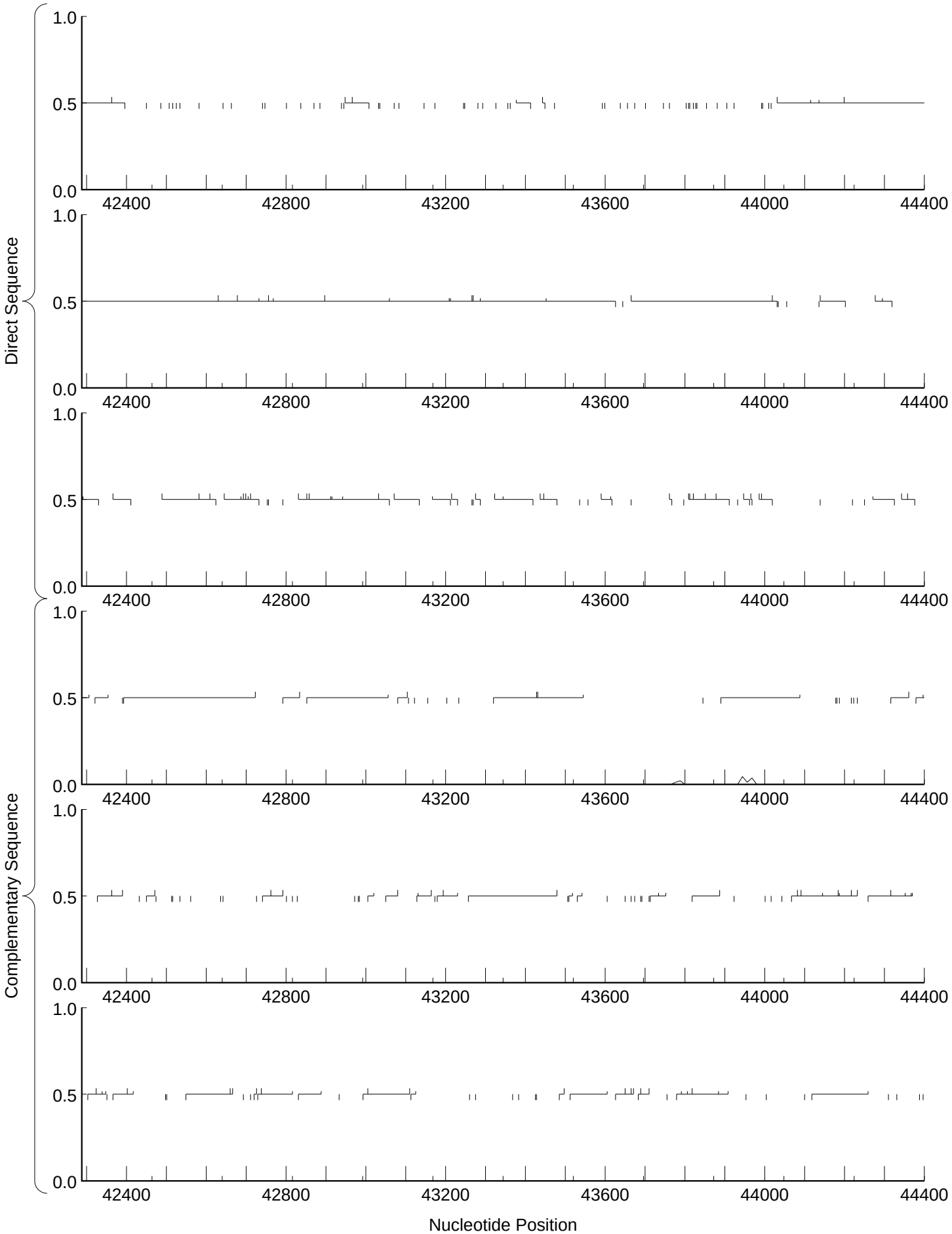

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Complementary Sequence
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0.0
34000
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34800
35200
35600
Nucleotide Position

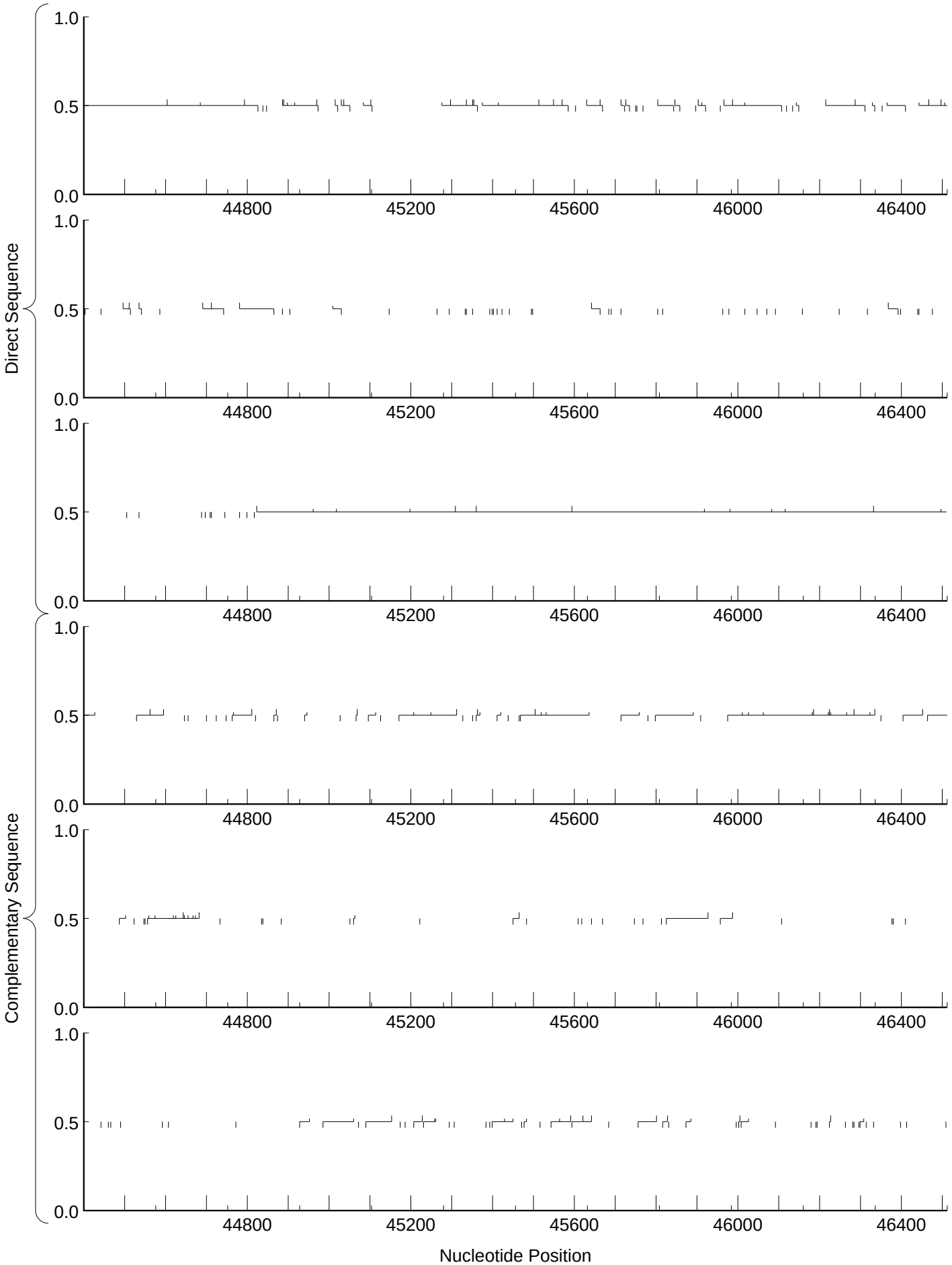

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Complementary Sequence
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0.0
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36400
36800
37200
37600
38000
Nucleotide Position

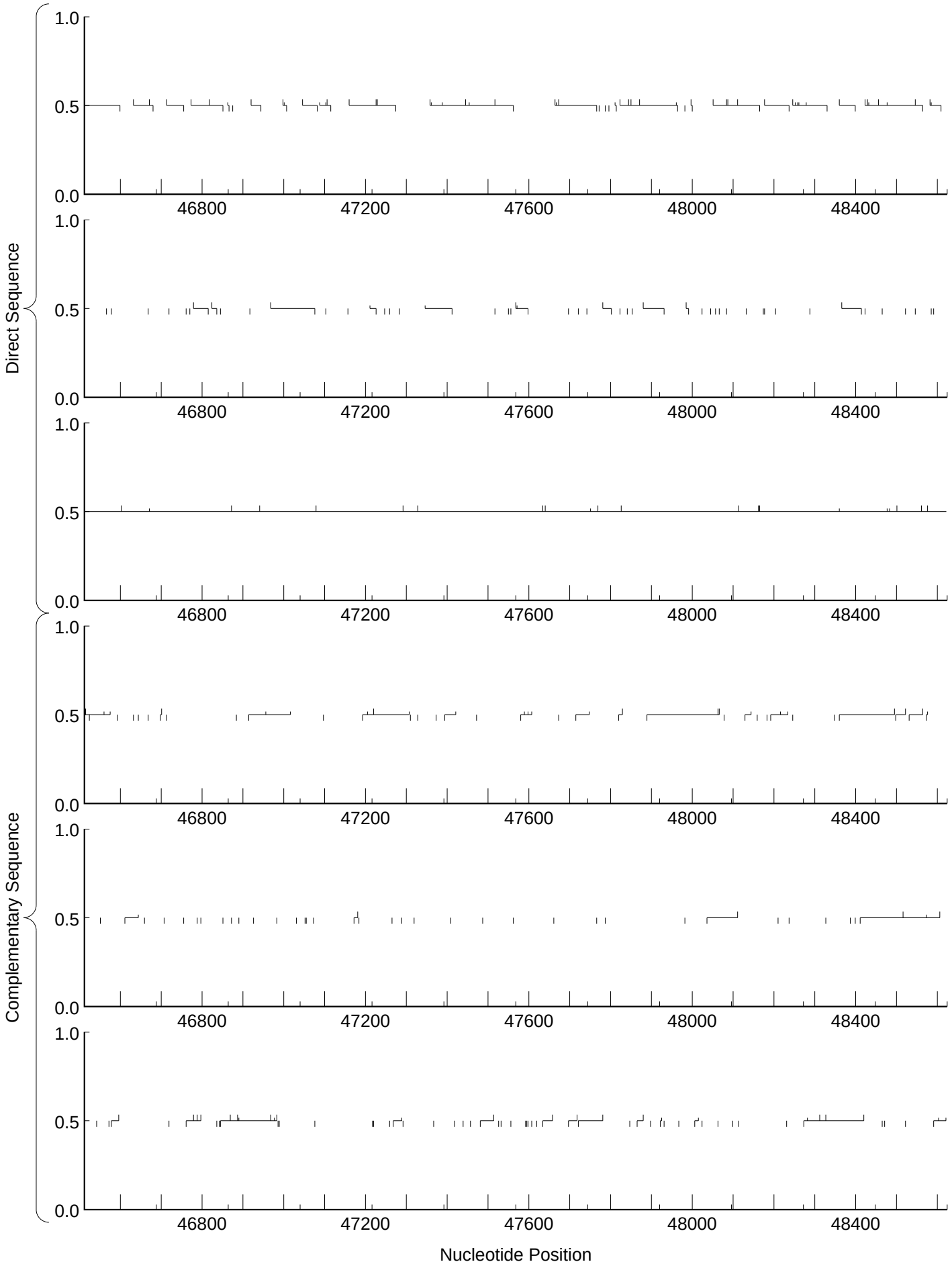

Direct Sequence
Complementary Sequence
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0.0
38400
38800
39200
39600
40000
Nucleotide Position

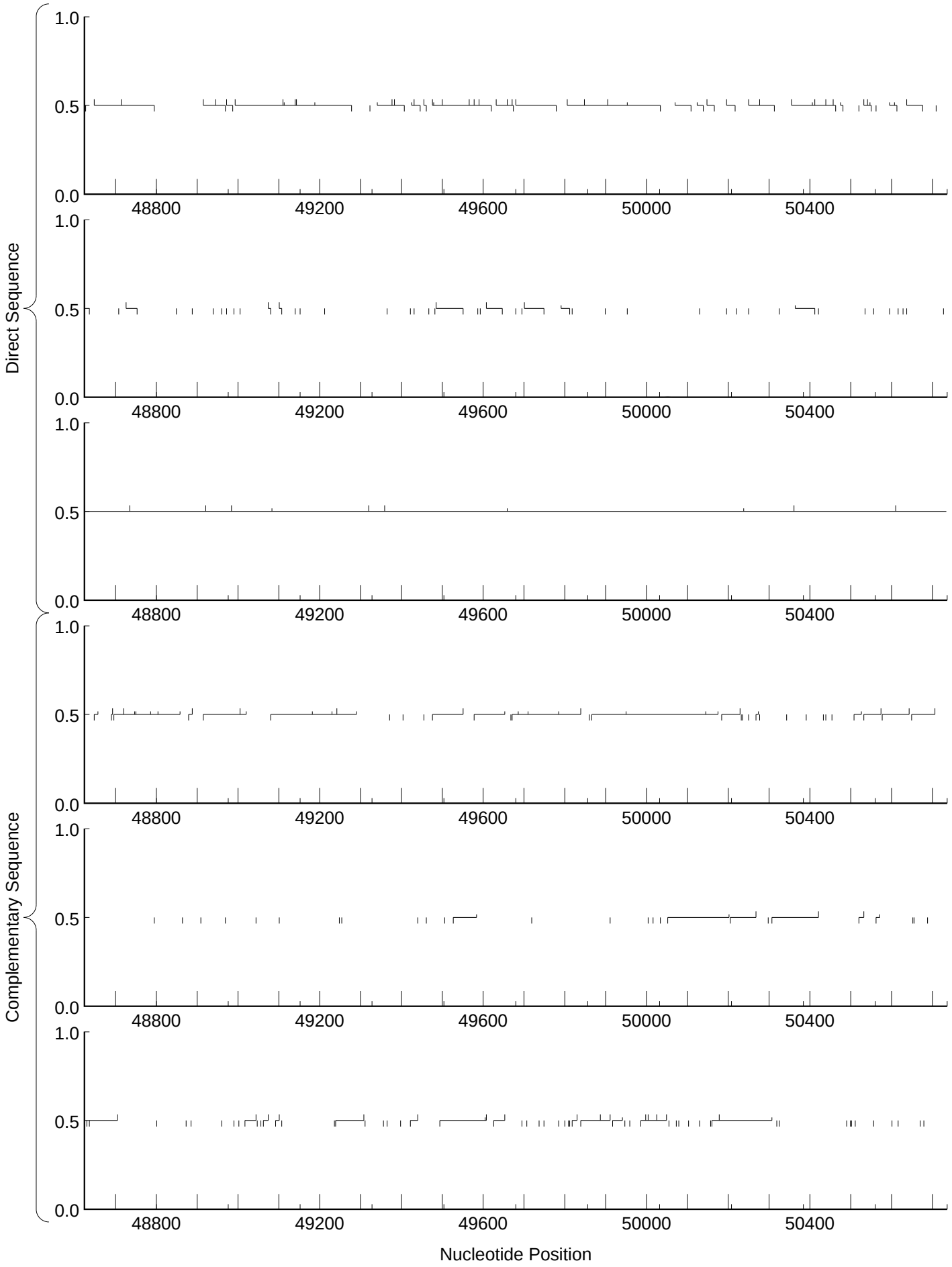
nage Yaboi complete sequence, 131250 bp including 12433 bp terminal repeat, Cluster BE2, Order 4, Window 96, Step 12, 21/64

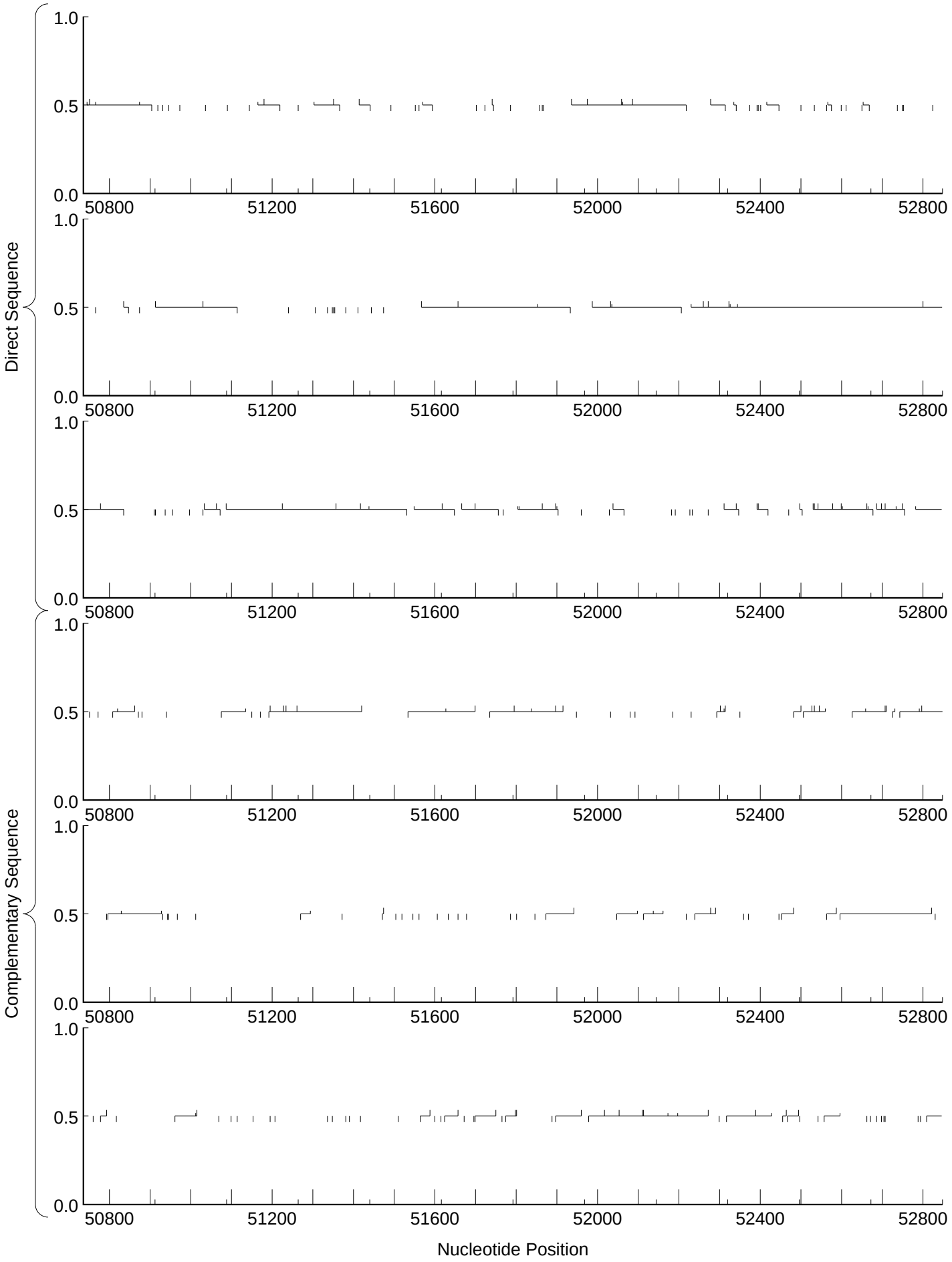


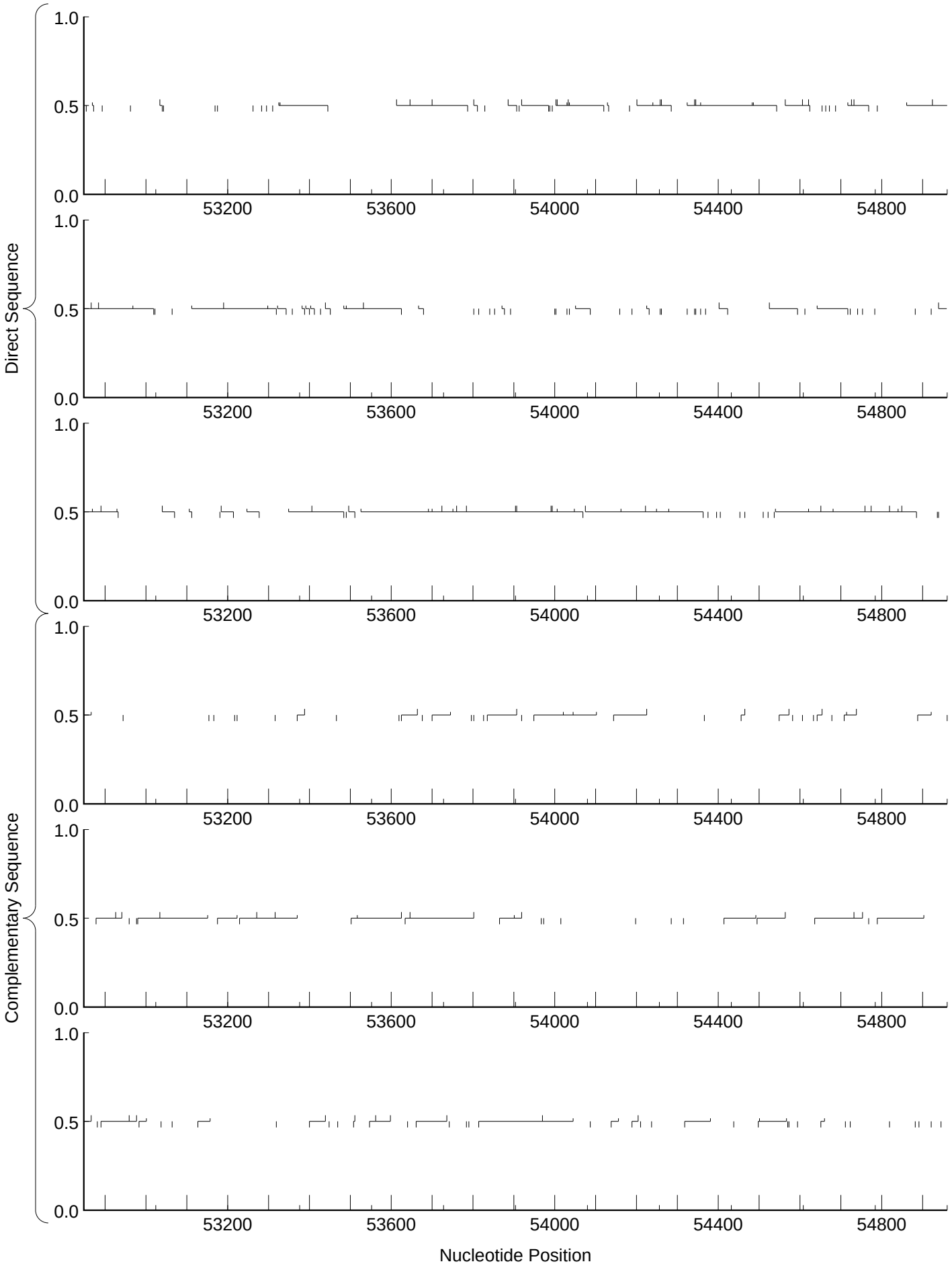

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Complementary Sequence
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42800
43200
43600
44000
44400
Nucleotide Position

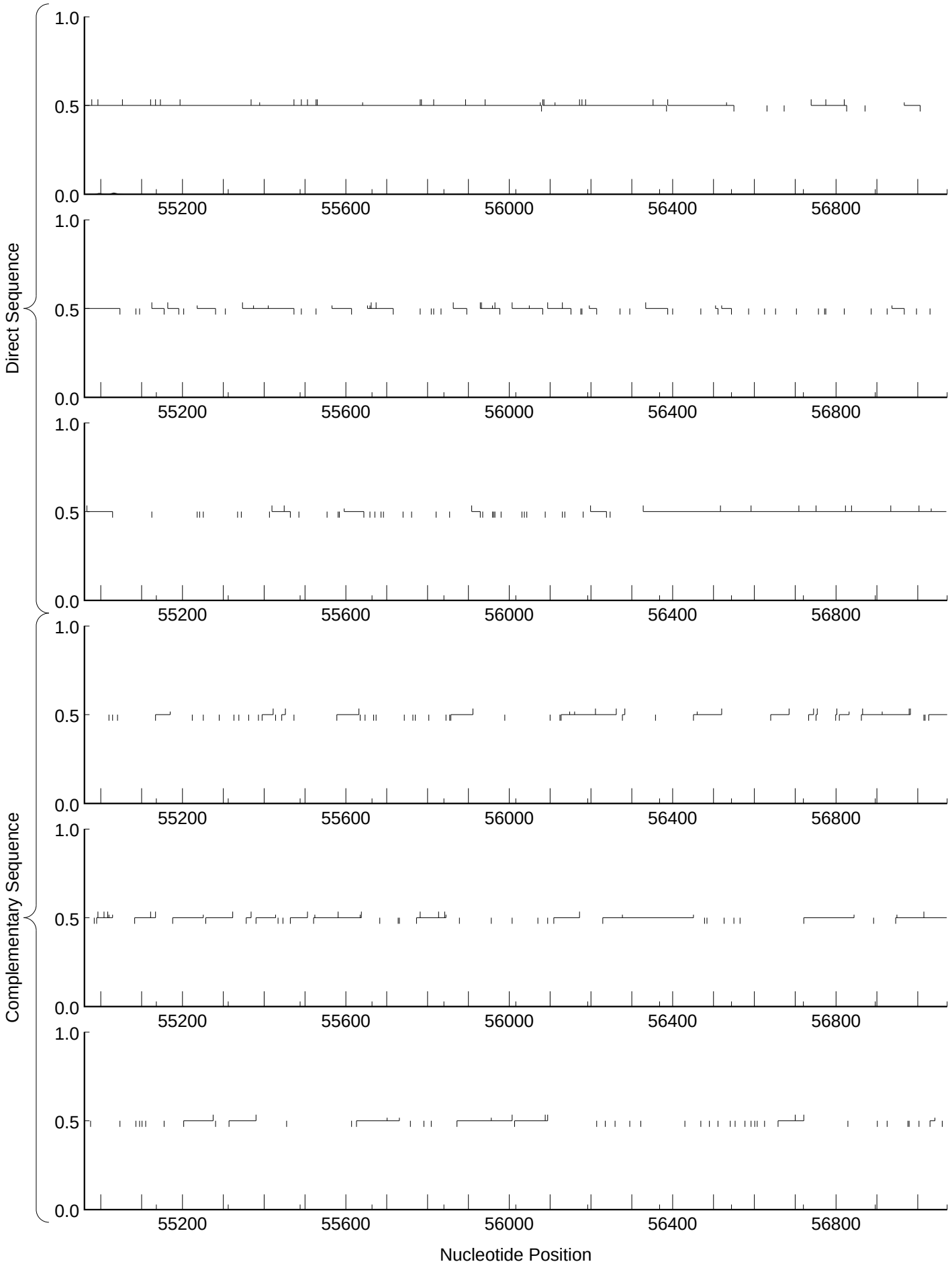

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Complementary Sequence
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45600
46000
46400
Nucleotide Position

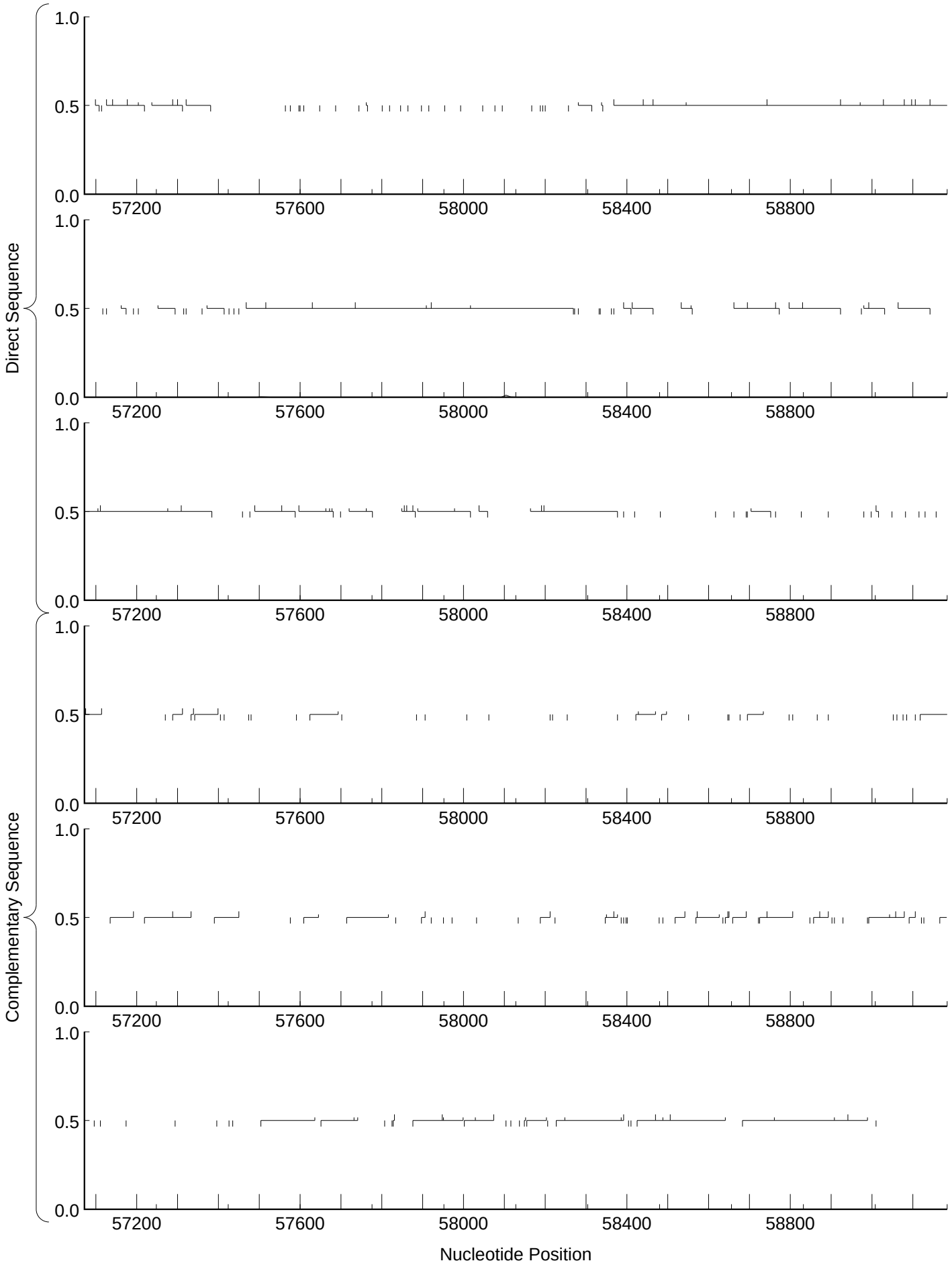

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Complementary Sequence
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0.0
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47600
48000
48400
Nucleotide Position

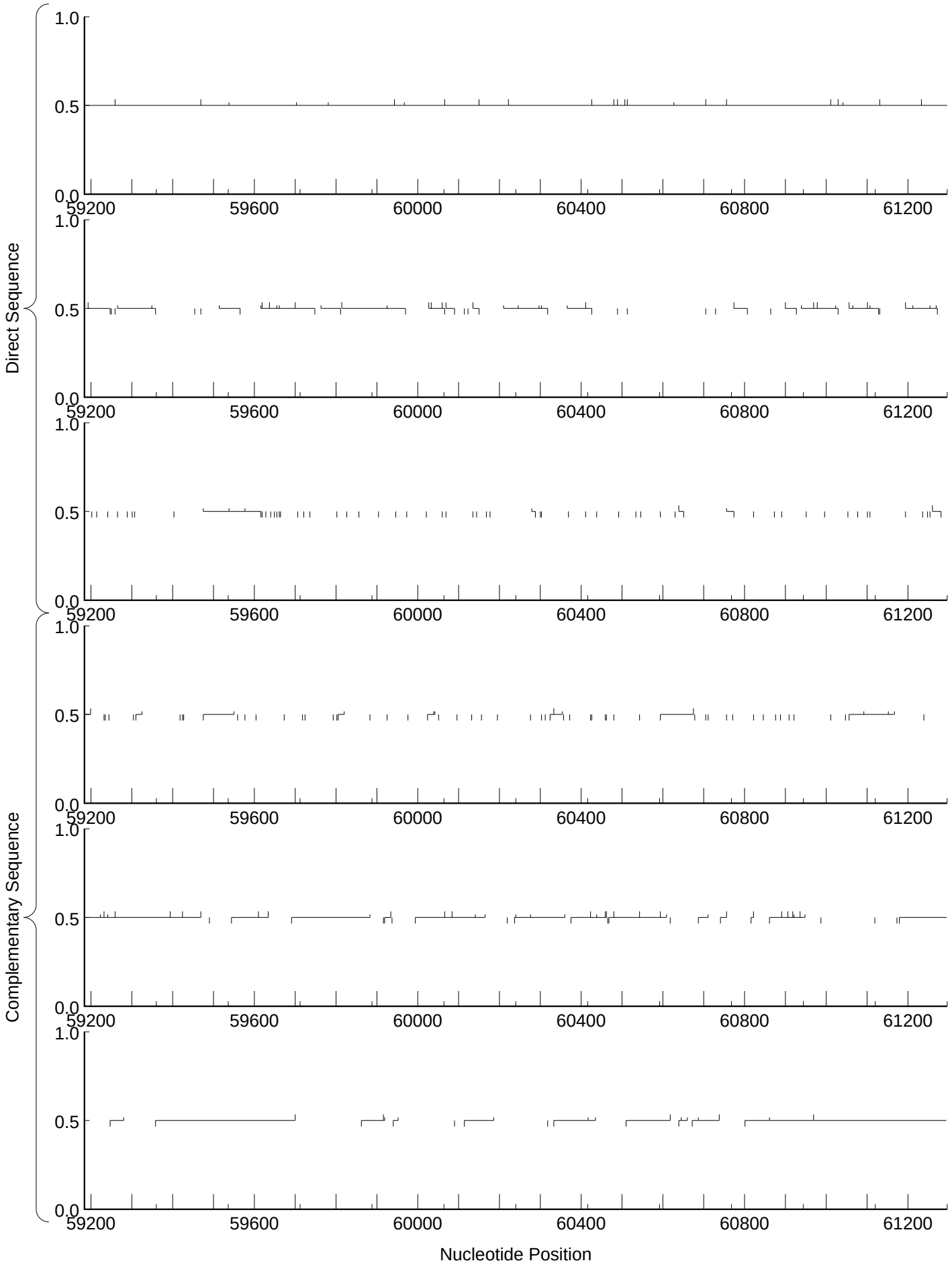

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49600
50000
50400
Nucleotide Position

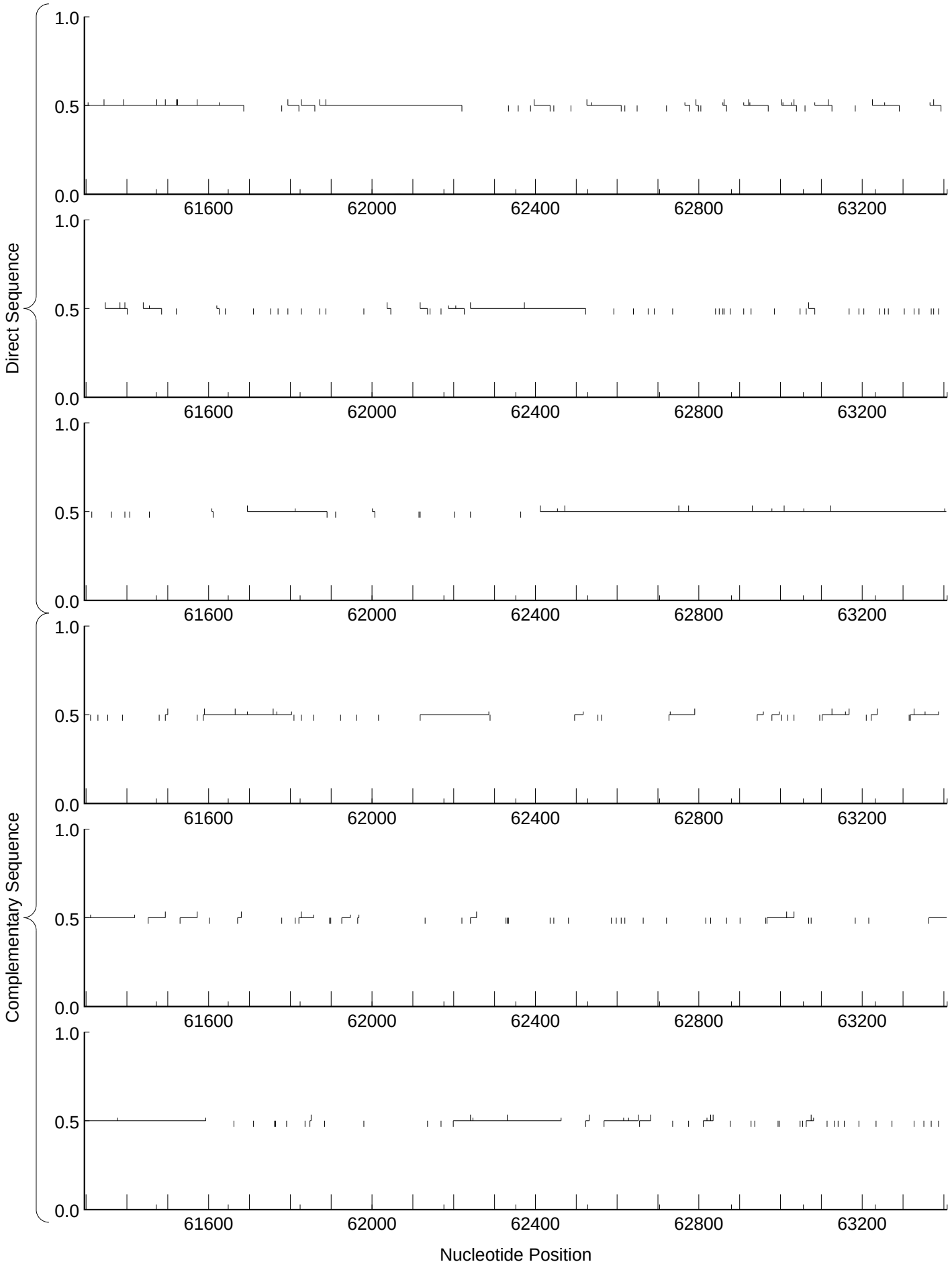

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Complementary Sequence
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52000
52400
52800
Nucleotide Position

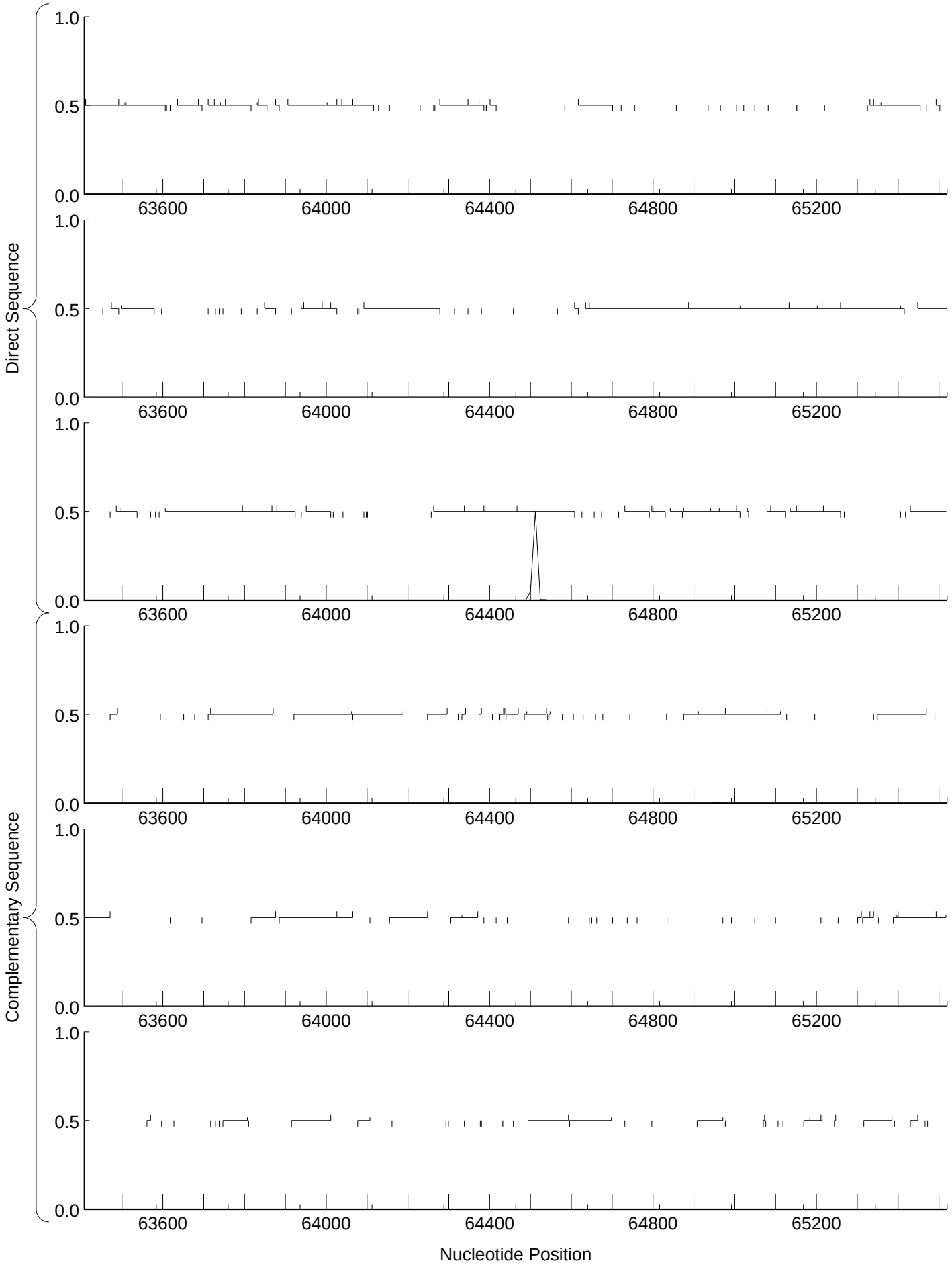

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Complementary Sequence
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54400
54800
Nucleotide Position

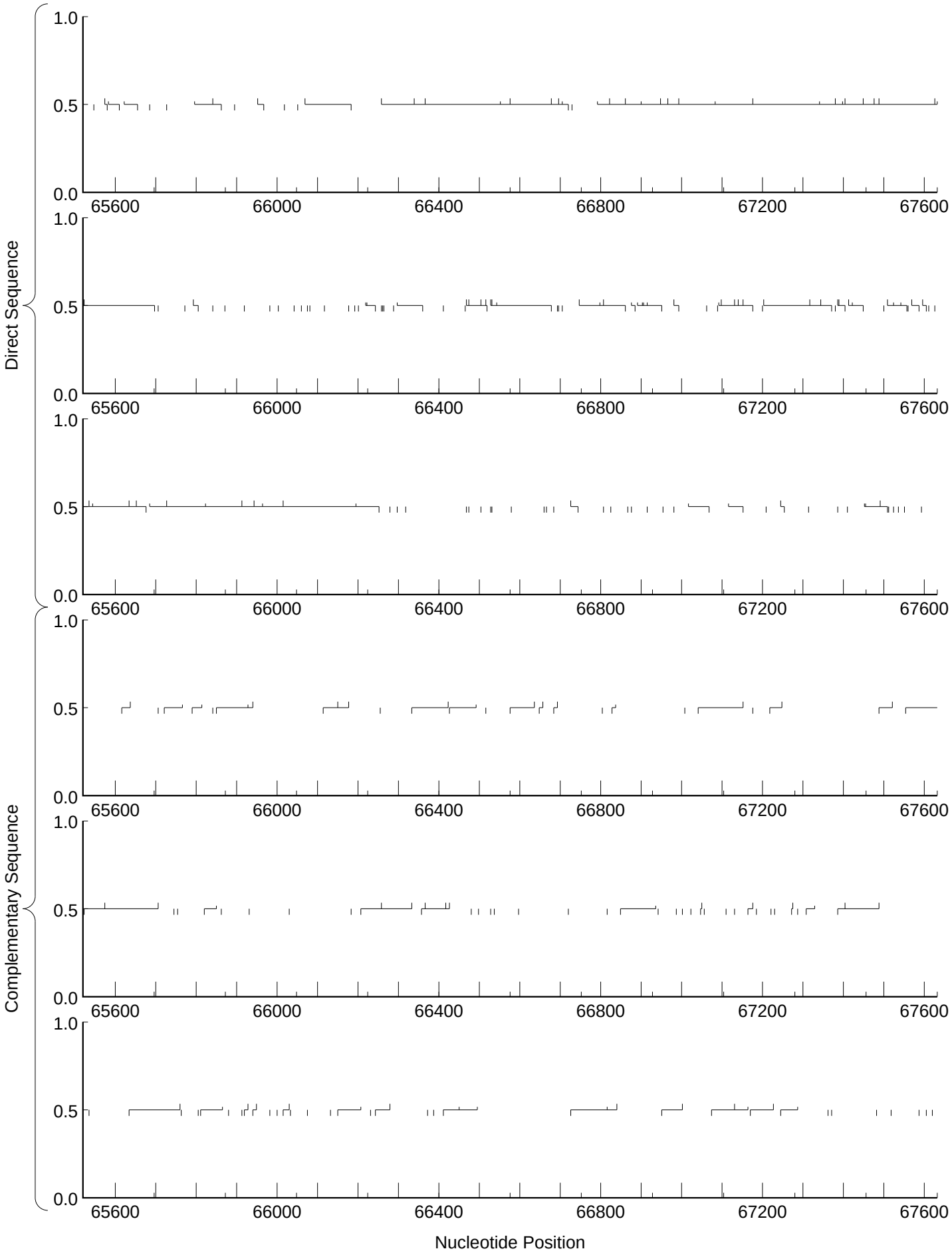

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Complementary Sequence
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56000
56400
56800
Nucleotide Position

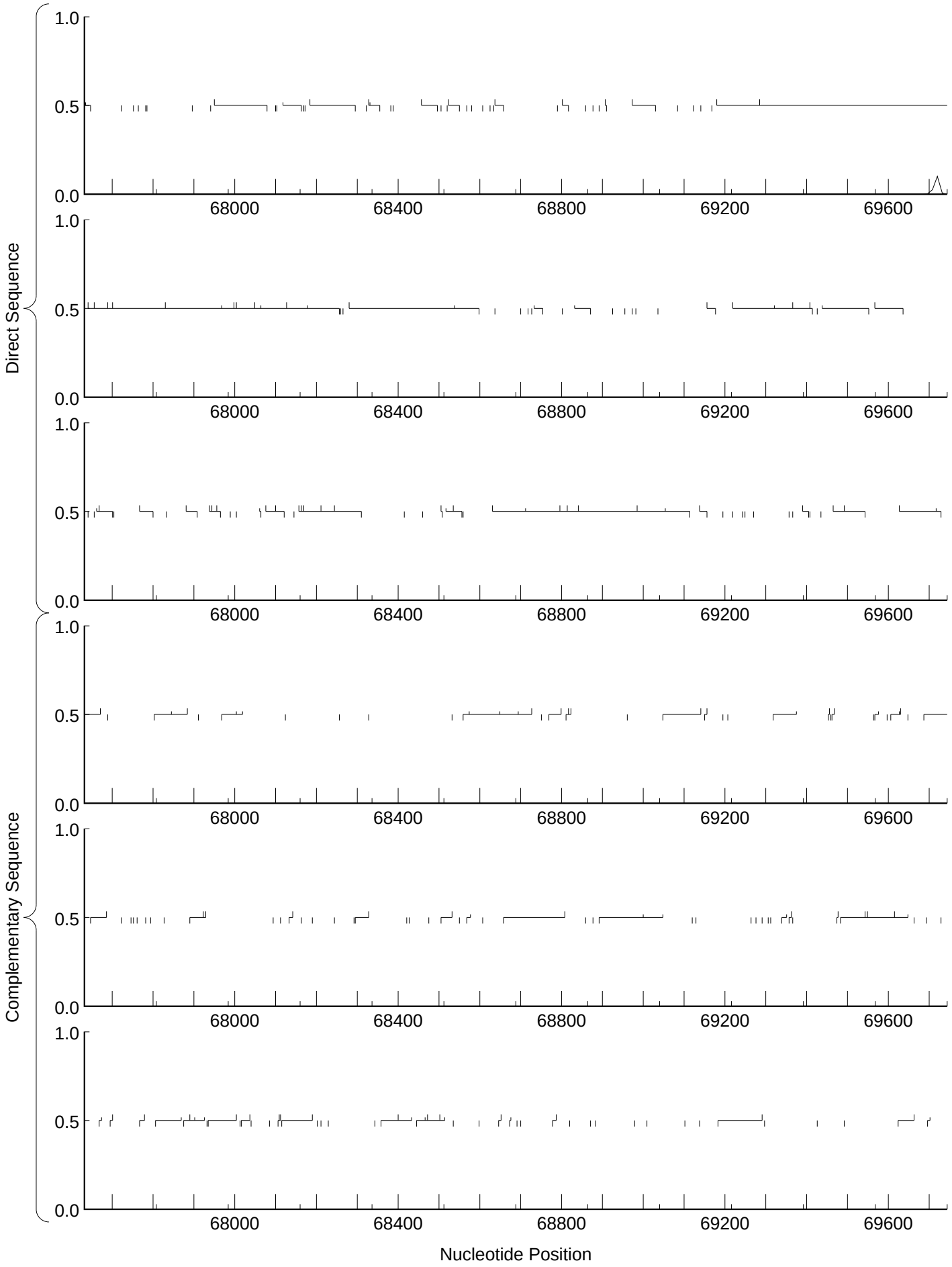

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Complementary Sequence
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0.0
57200
57600
58000
58400
58800
Nucleotide Position

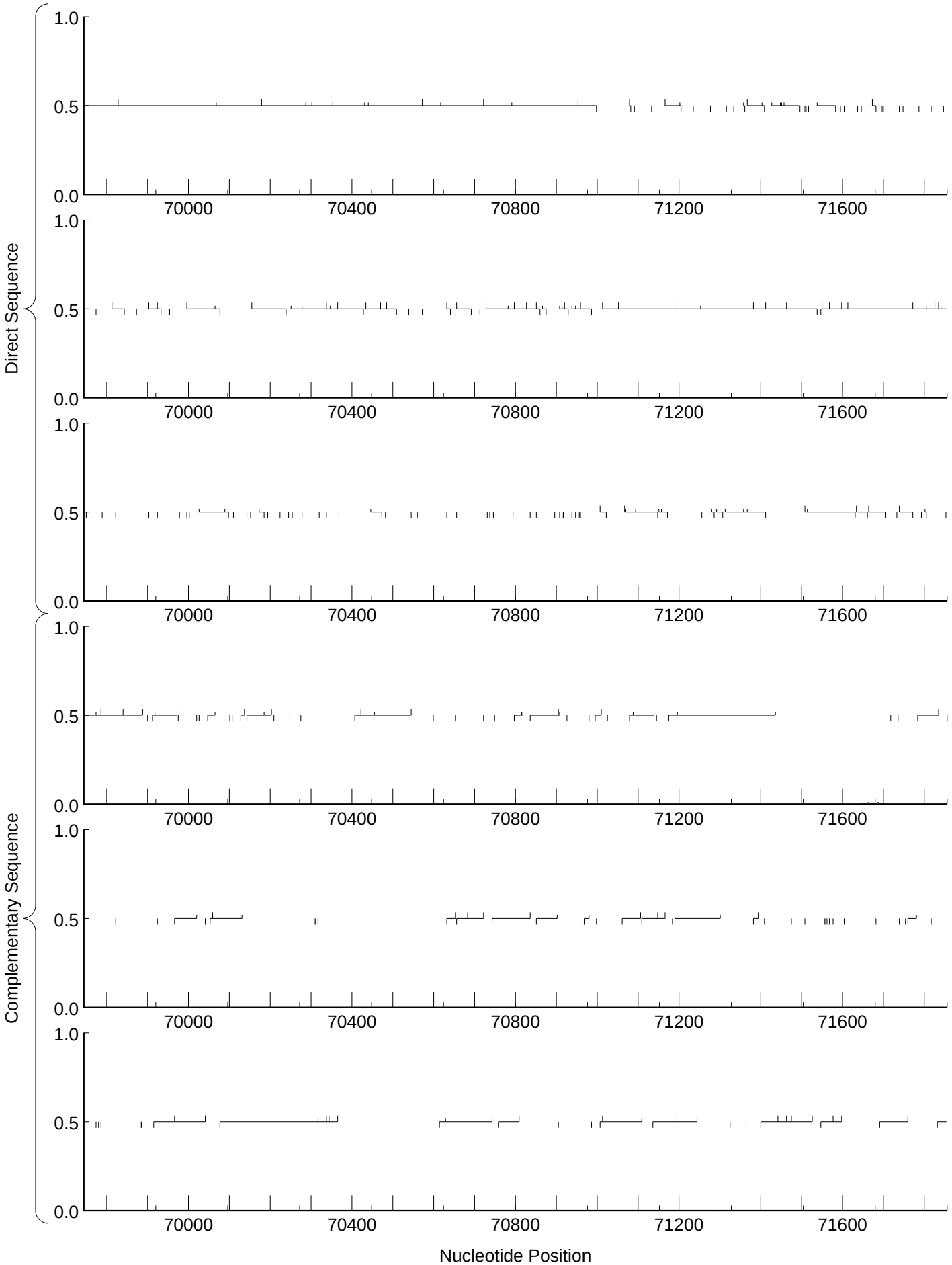

Direct Sequence
Complementary Sequence
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59600
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60400
60800
61200
Nucleotide Position

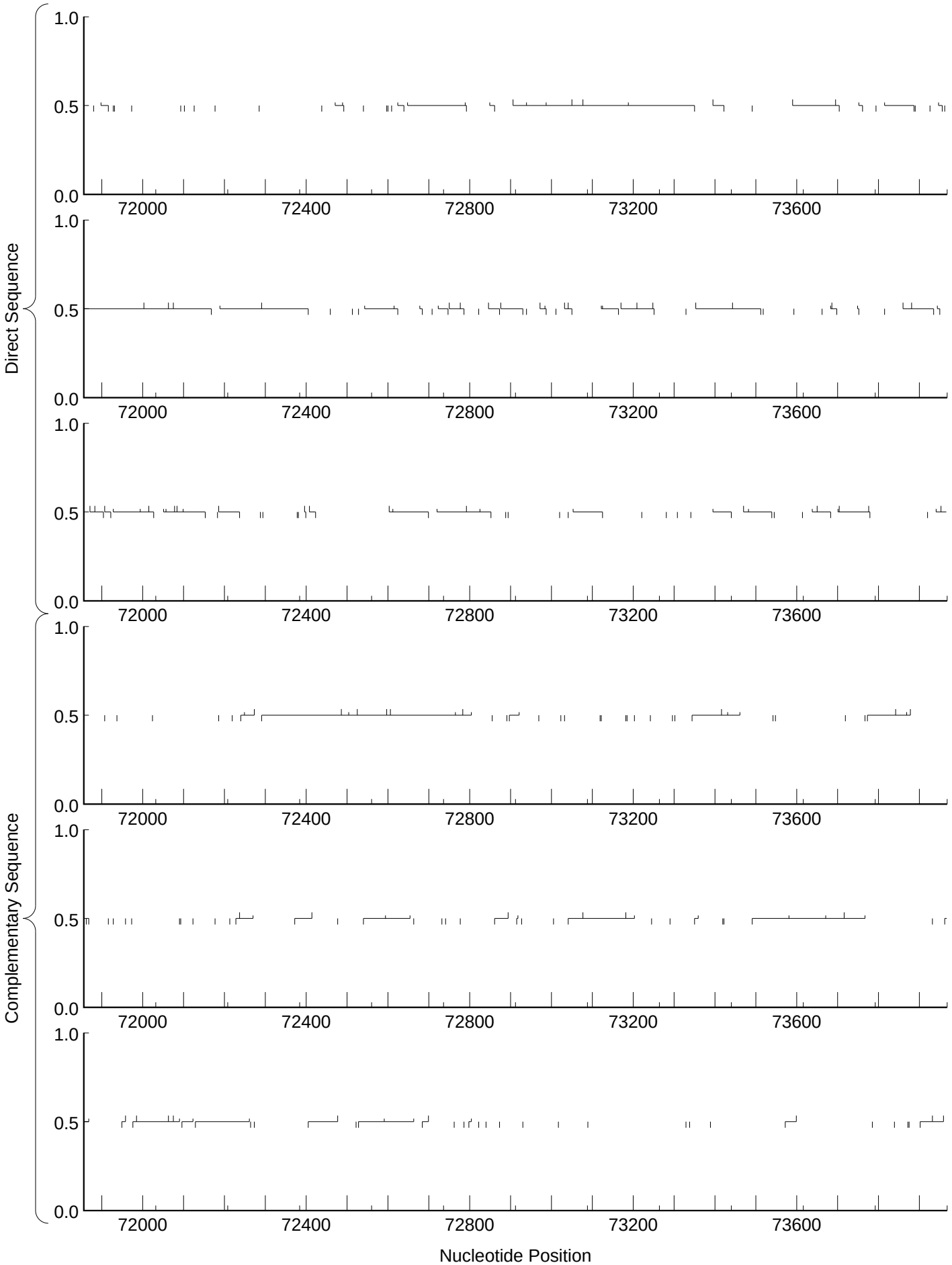

Direct Sequence
Complementary Sequence
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62400
62800
63200
Nucleotide Position

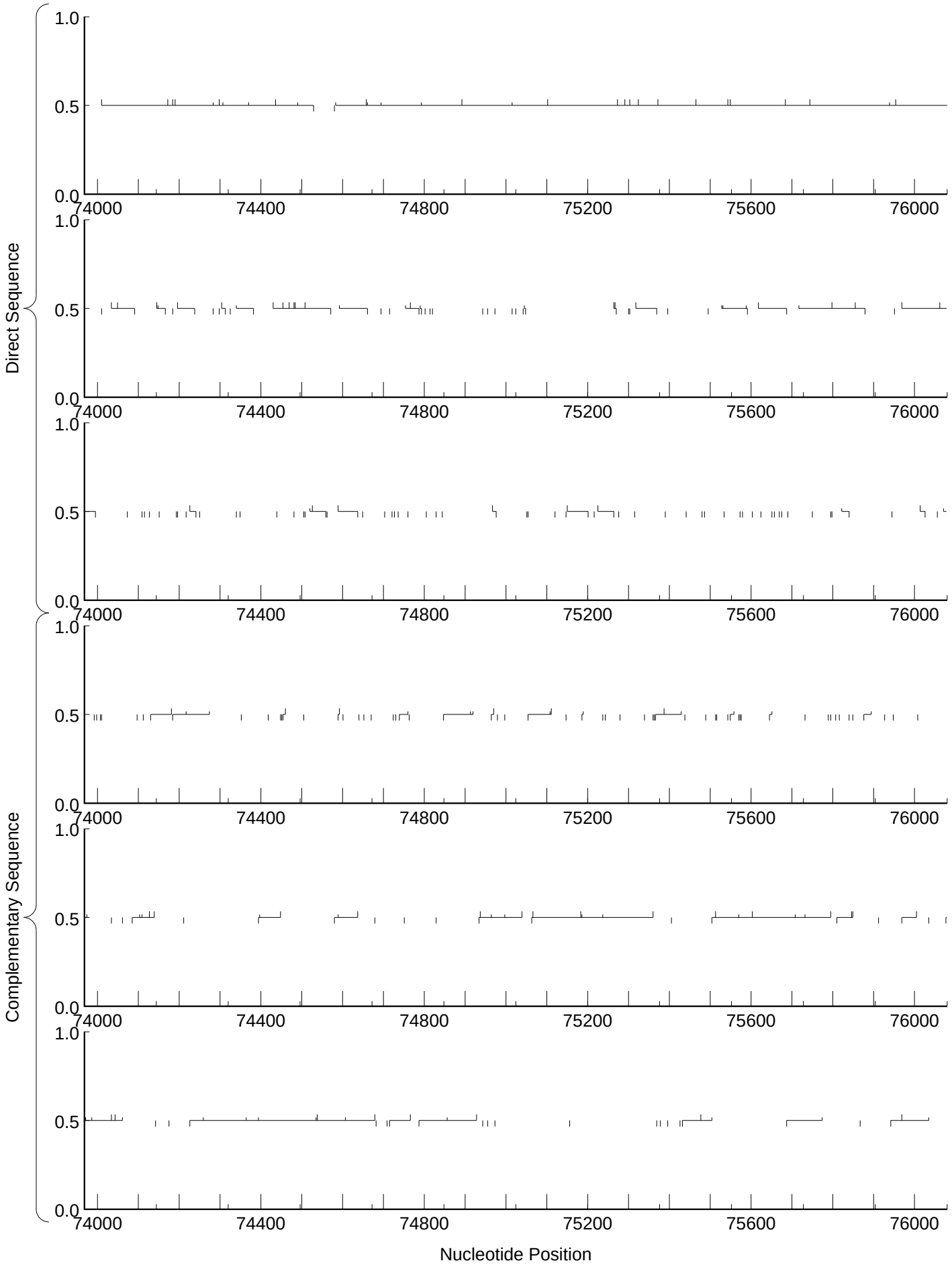

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64000
64400
64800
65200
Nucleotide Position

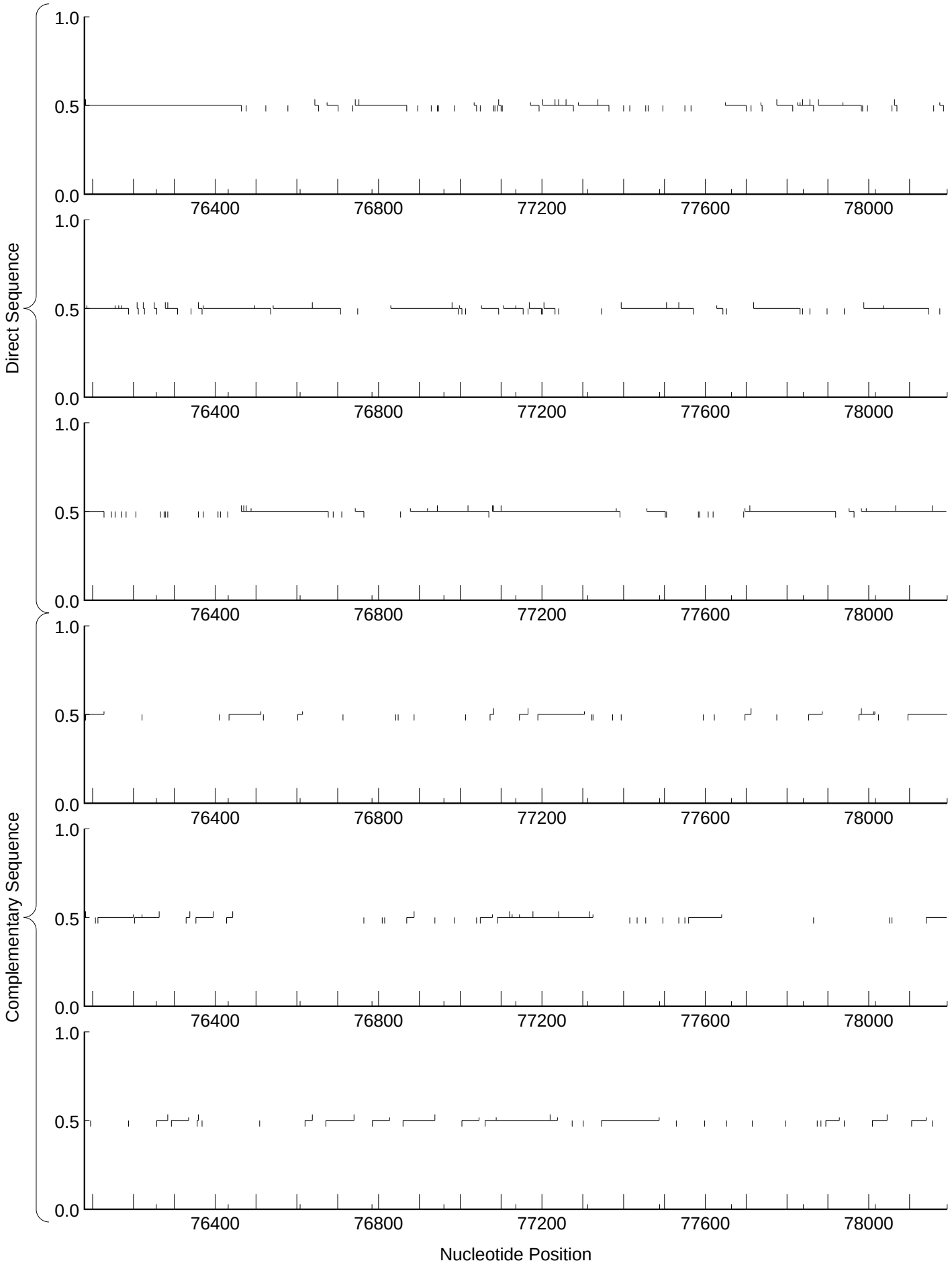

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66800
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Nucleotide Position

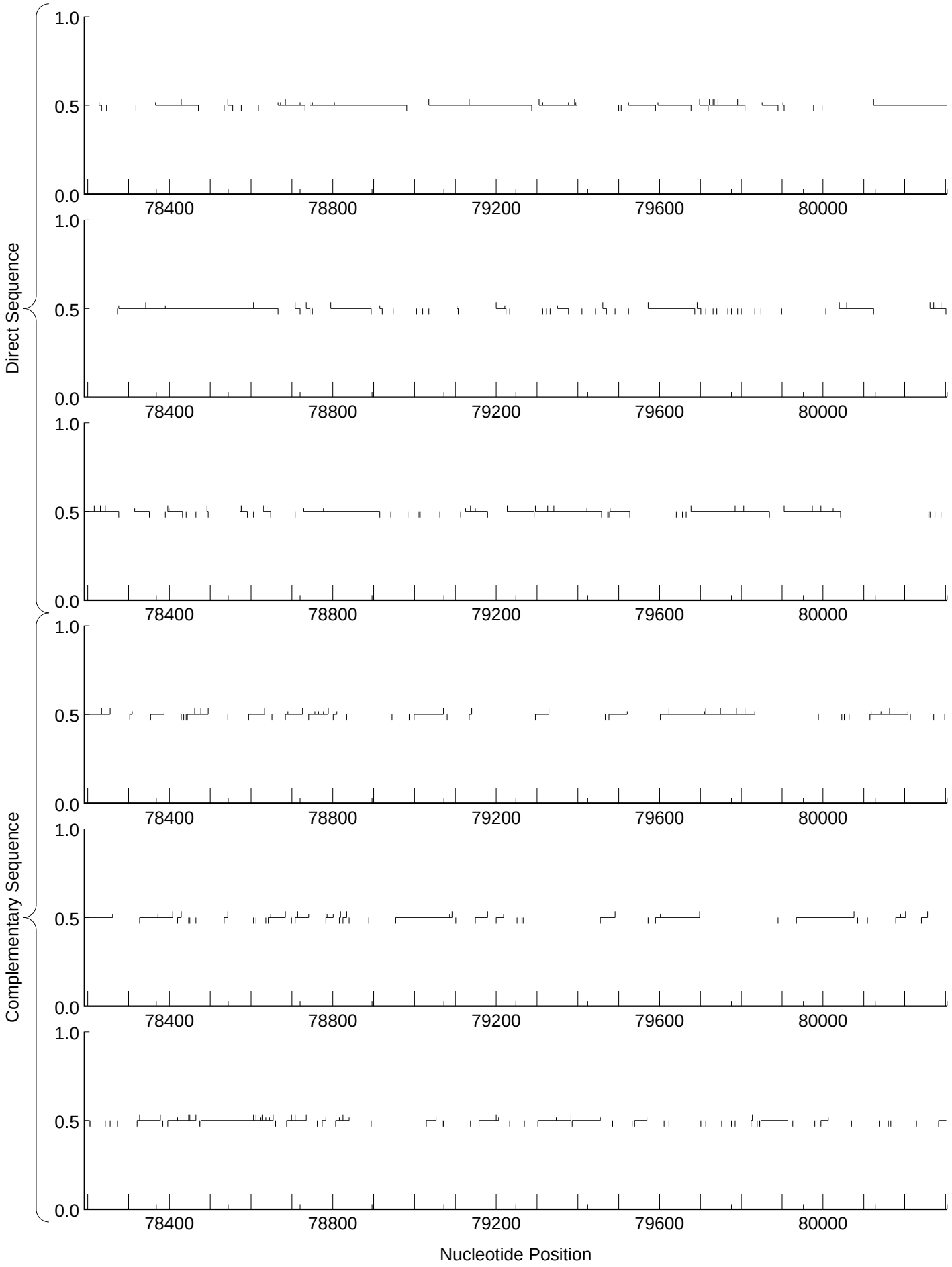

Direct Sequence
Complementary Sequence
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0.5
0.0
68000
68400
68800
69200
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Nucleotide Position


Direct Sequence
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70400
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Nucleotide Position

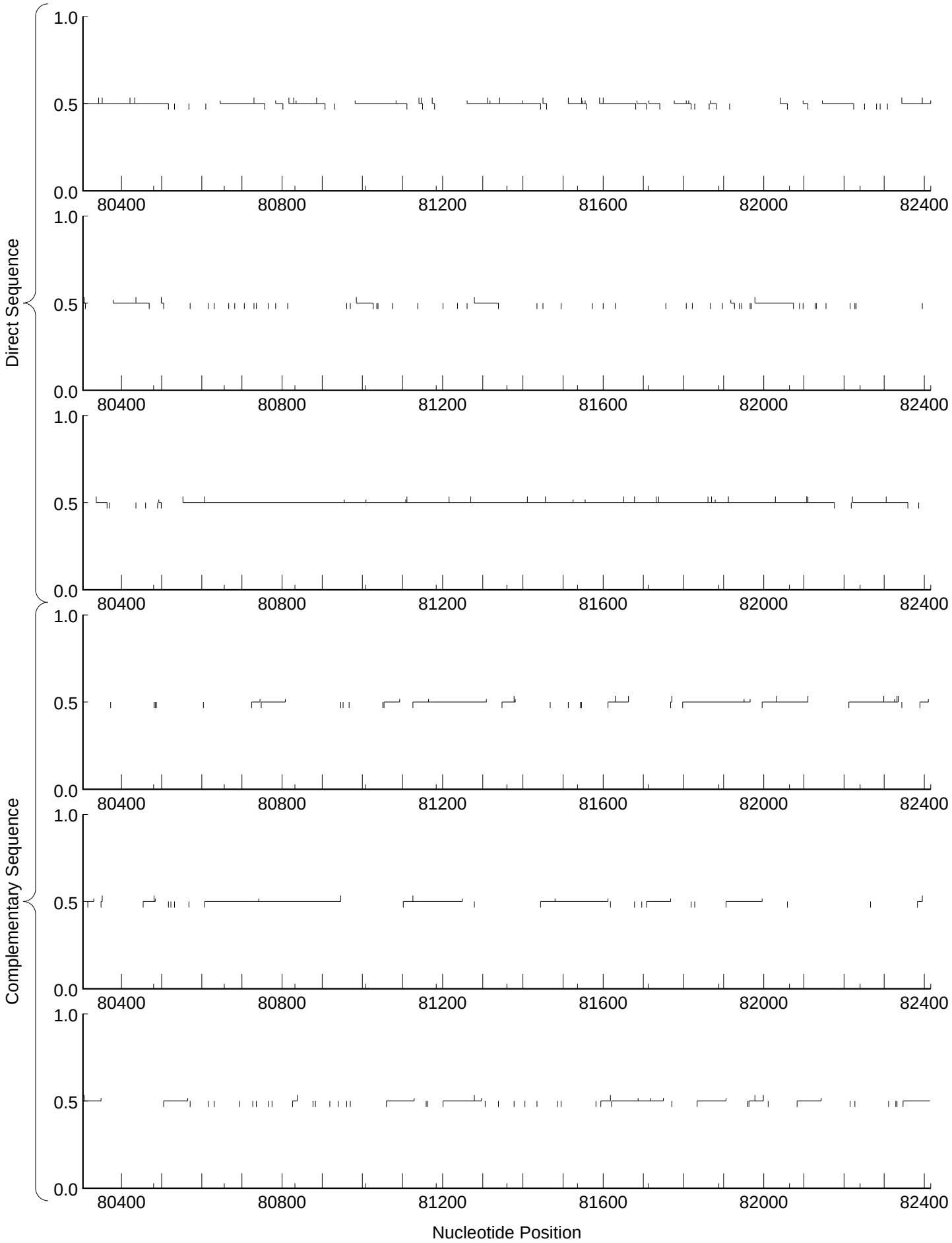

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73200
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Nucleotide Position

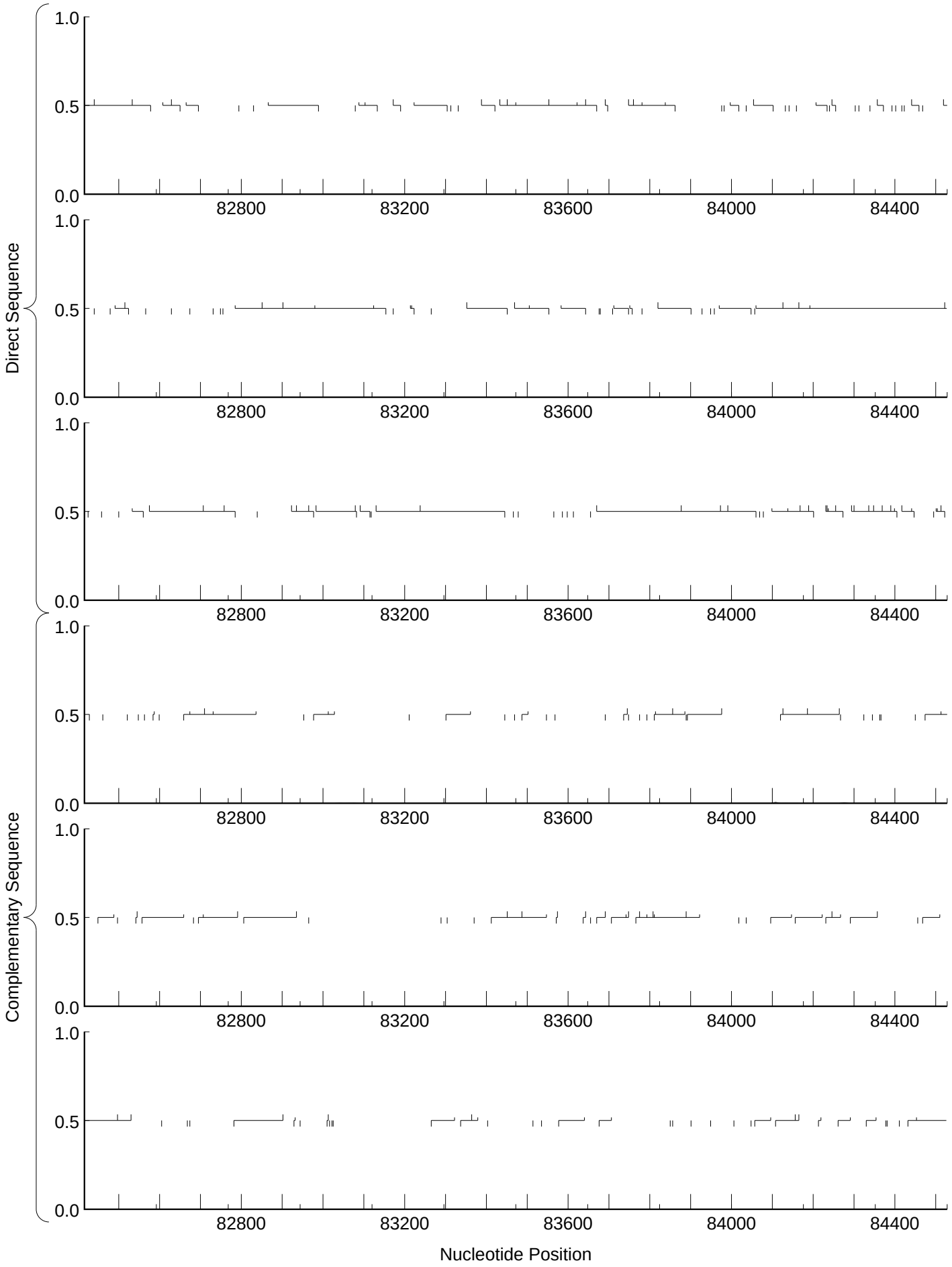

Direct Sequence
Complementary Sequence
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0.0
74000
74400
74800
75200
75600
76000
Nucleotide Position

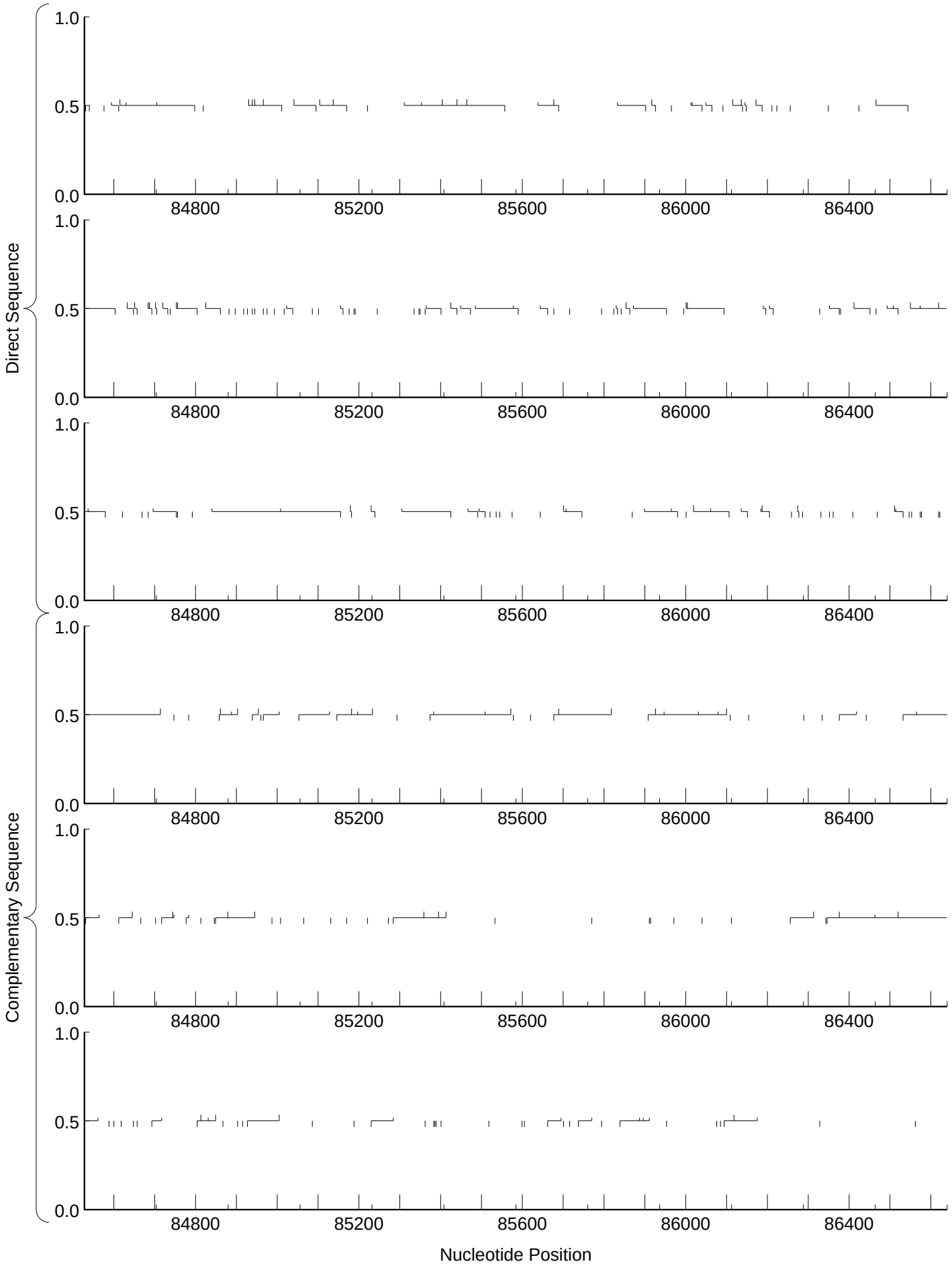

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Complementary Sequence
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0.5
0.0
76400
76800
77200
77600
78000
Nucleotide Position

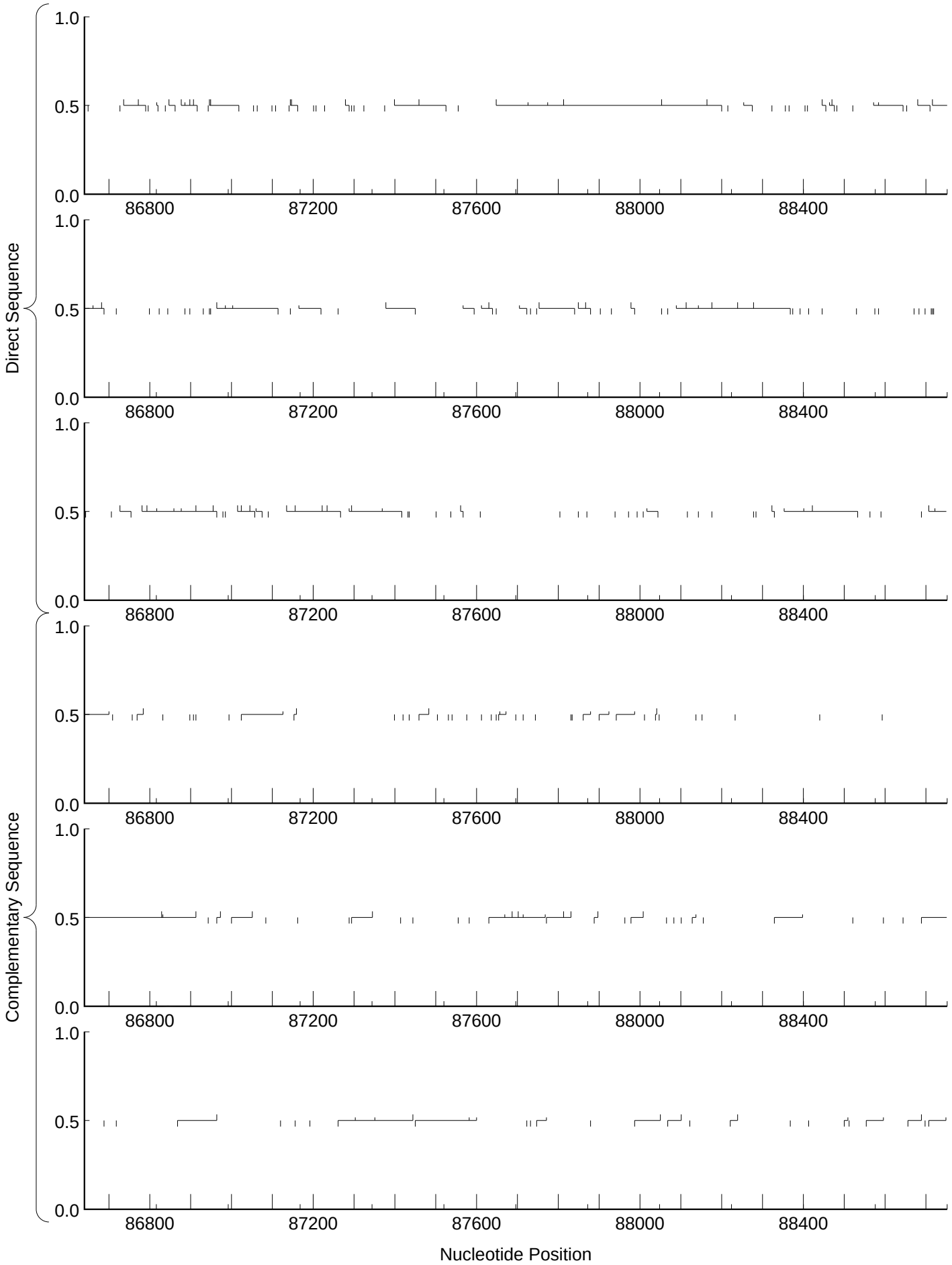

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Complementary Sequence
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0.5
0.0
78400
78800
79200
79600
80000
Nucleotide Position

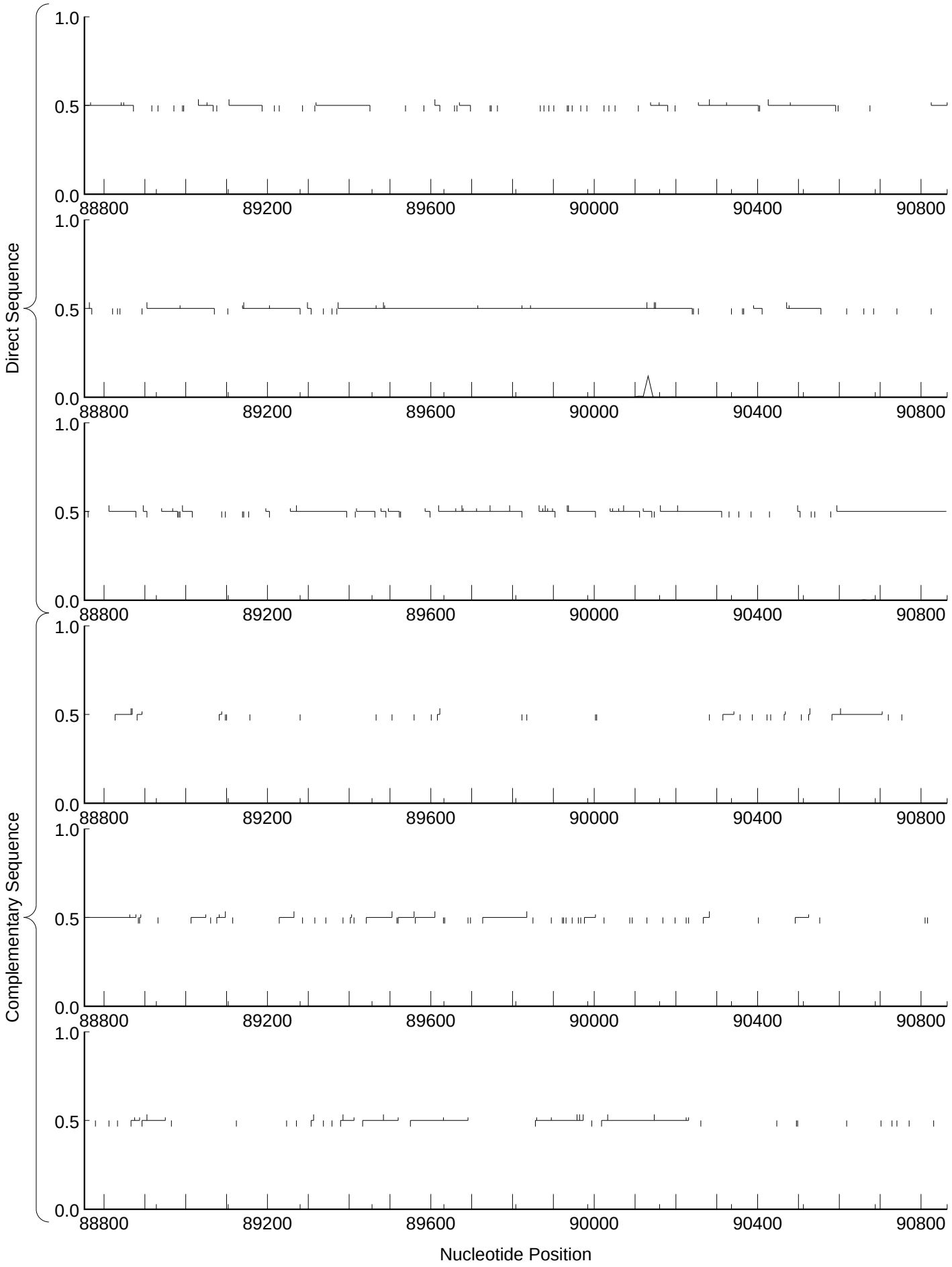
hage Yaboi complete sequence, 131250 bp including 12433 bp terminal repeat, Cluster BE2, Order 4, Window 96, Step 12, 40/64

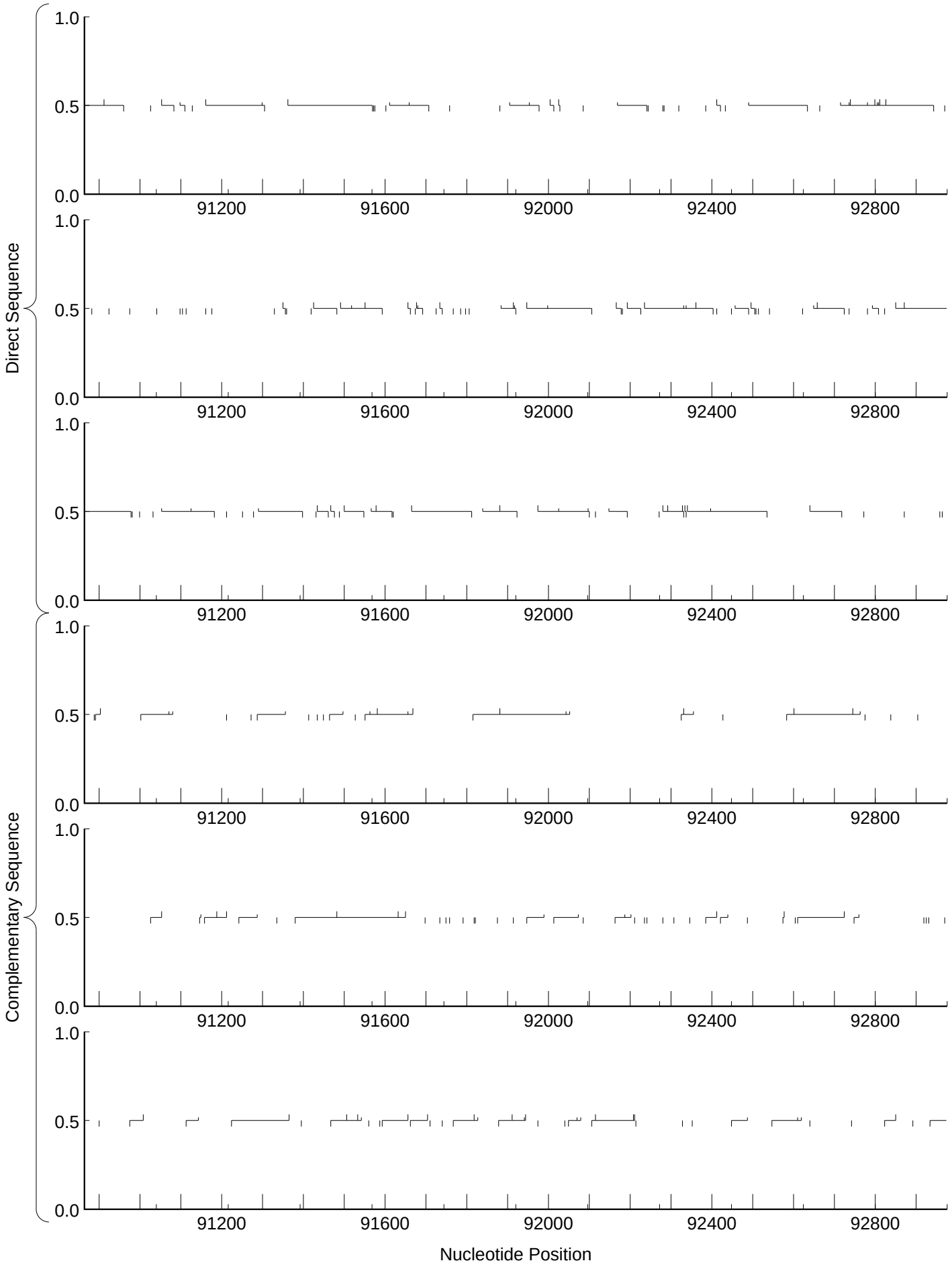


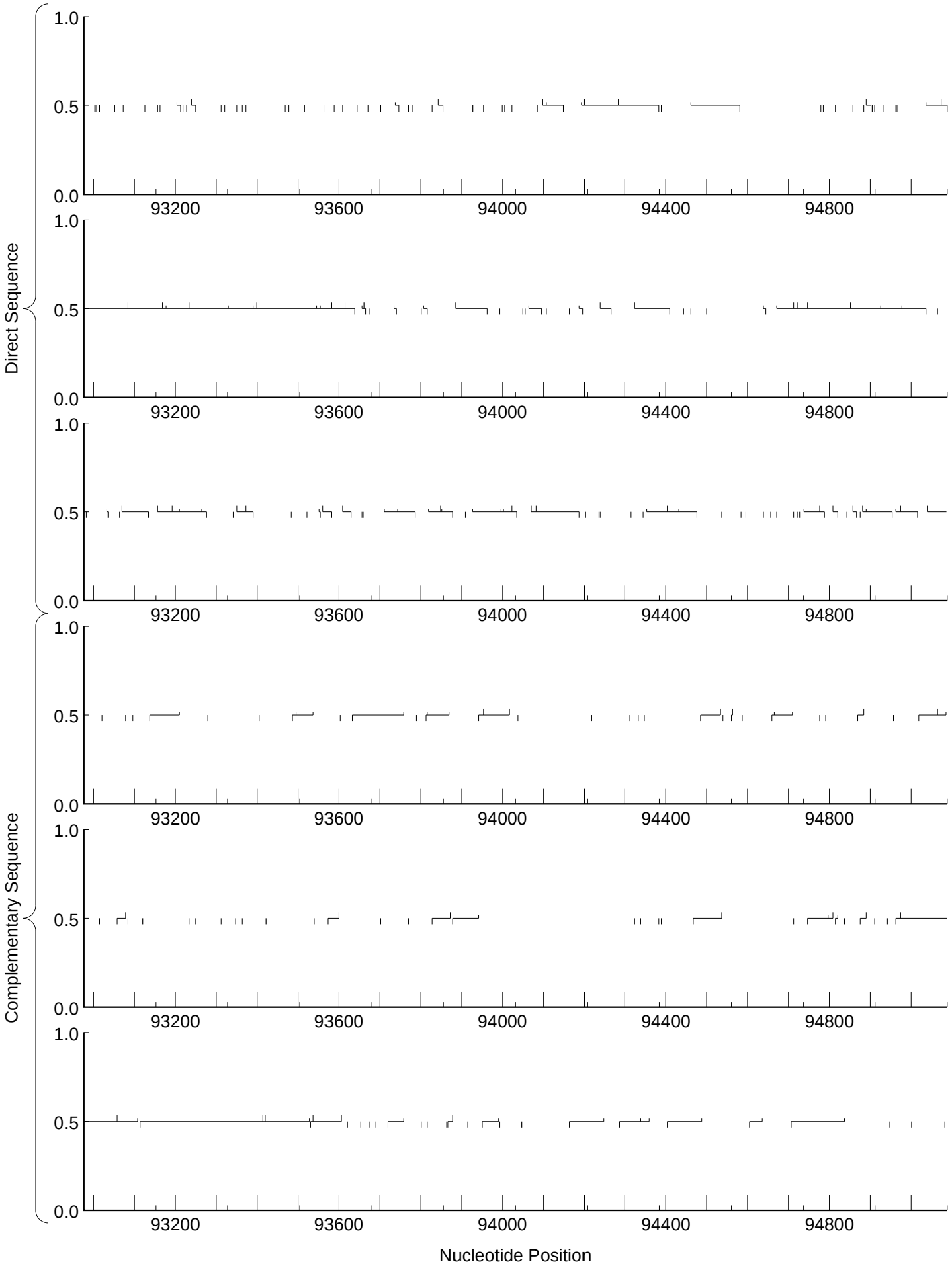

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
82800
83200
83600
84000
84400
Nucleotide Position

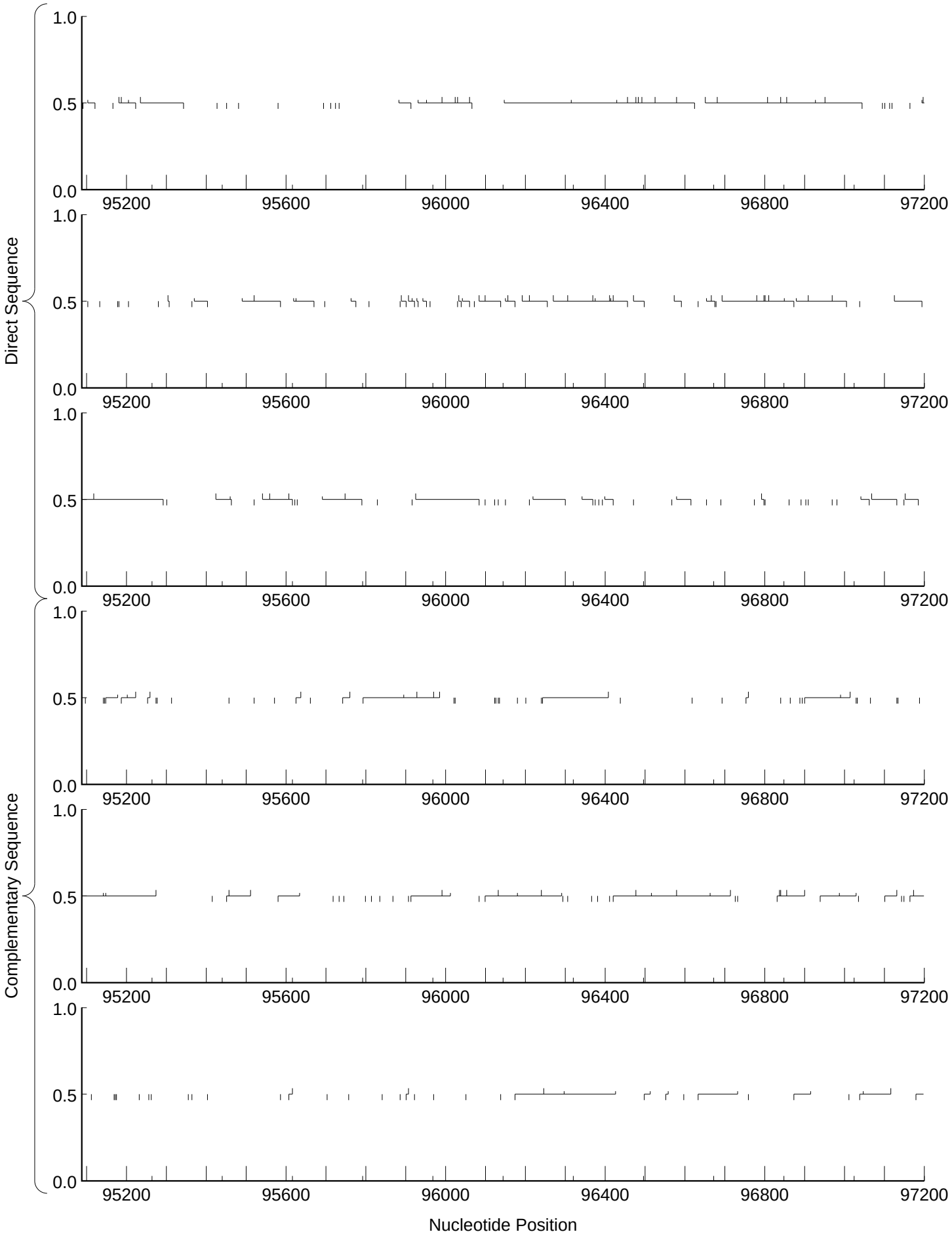

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
84800
85200
85600
86000
86400
Nucleotide Position

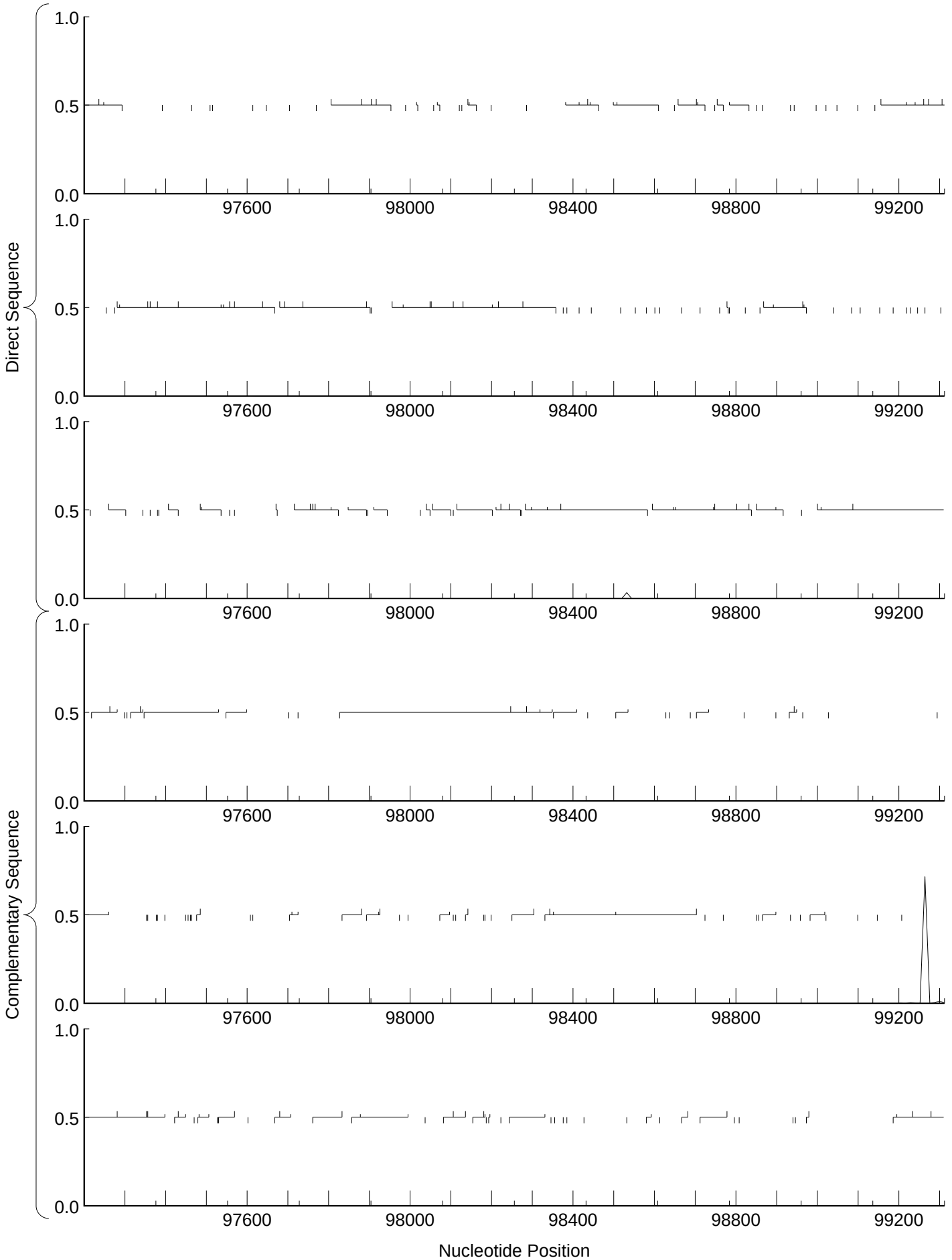

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
86800
87200
87600
88000
88400
Nucleotide Position


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

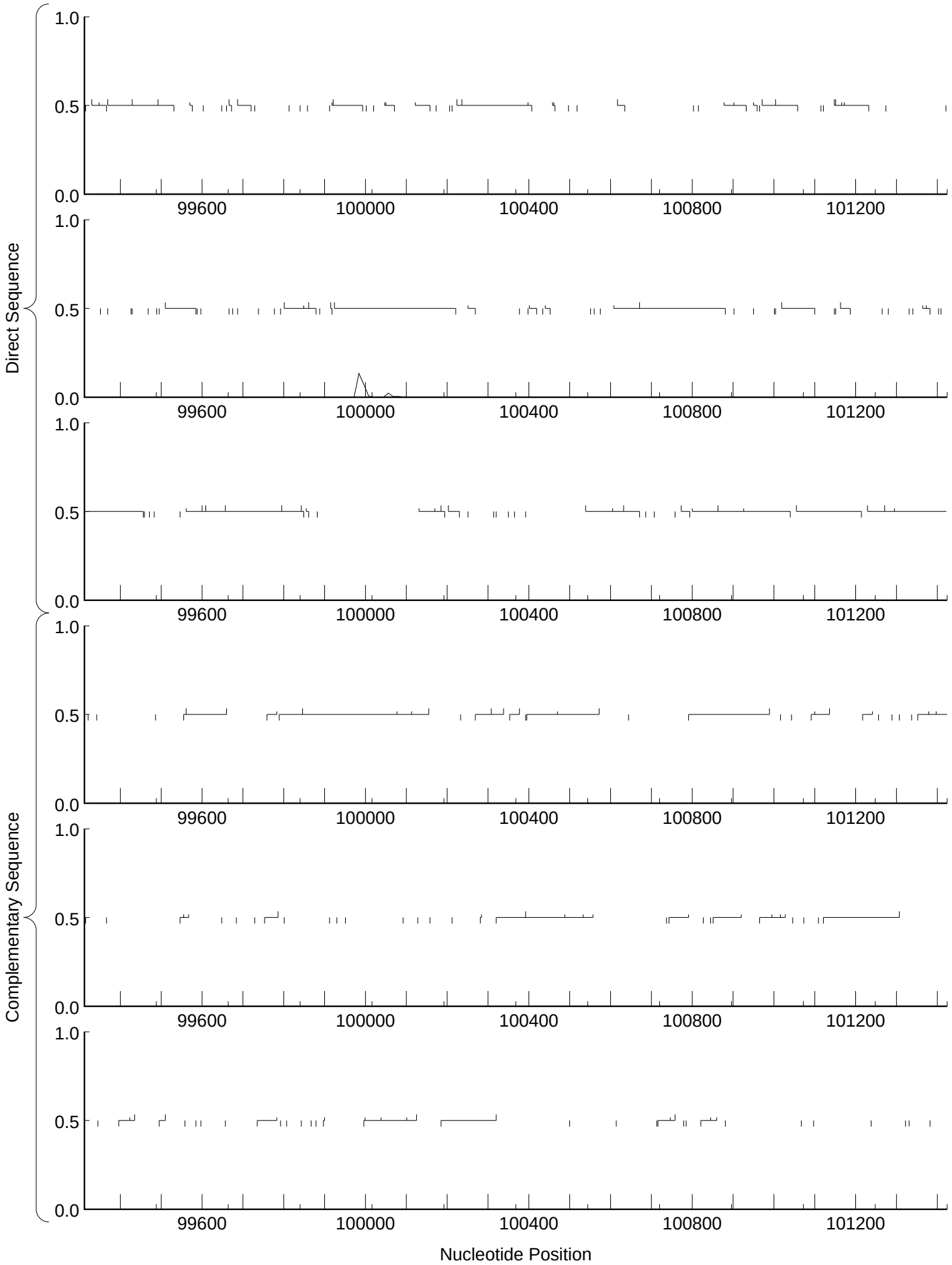

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
91200
91600
92000
92400
92800
Nucleotide Position

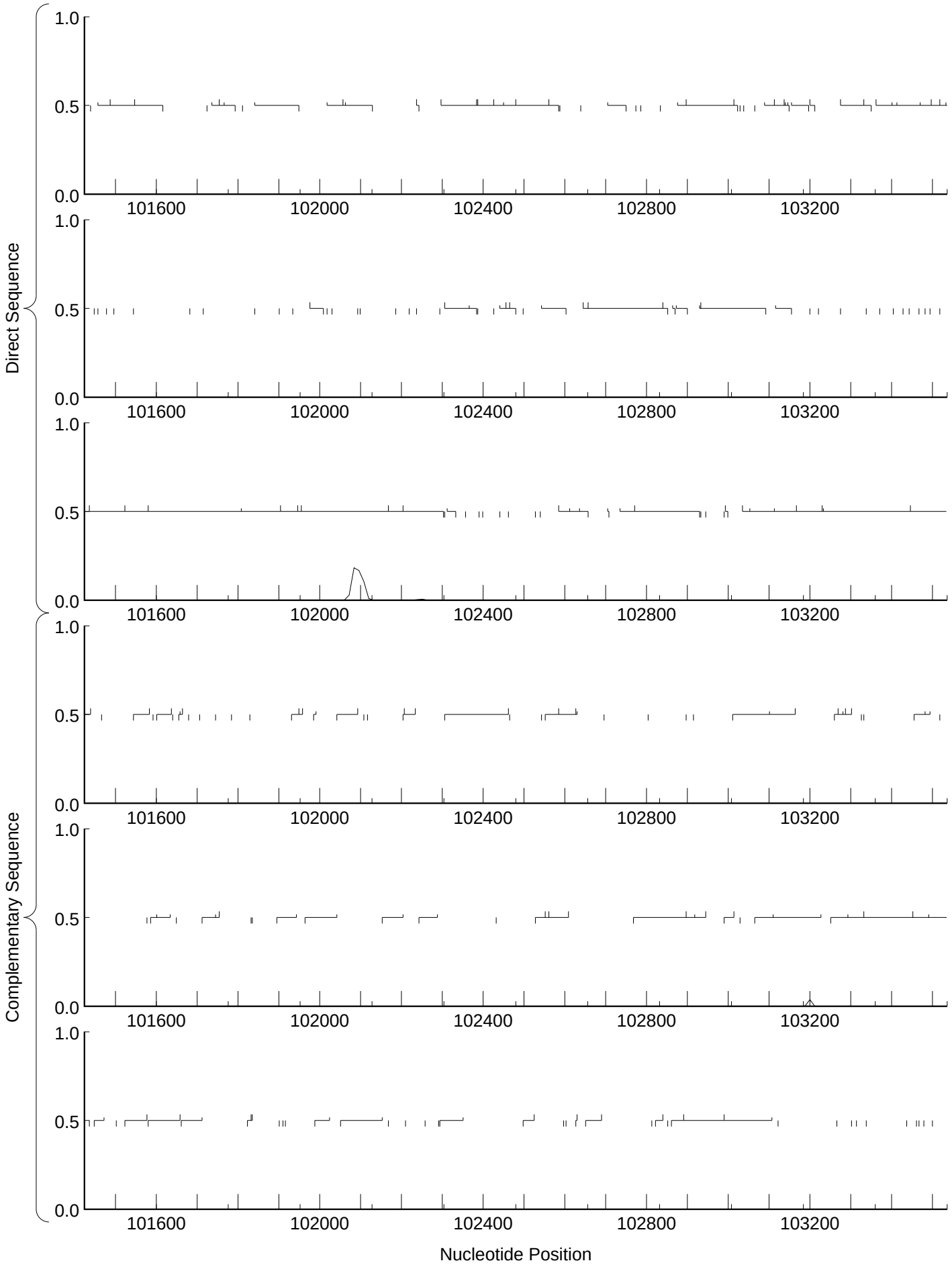

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
93200
93600
94000
94400
94800
Nucleotide Position


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

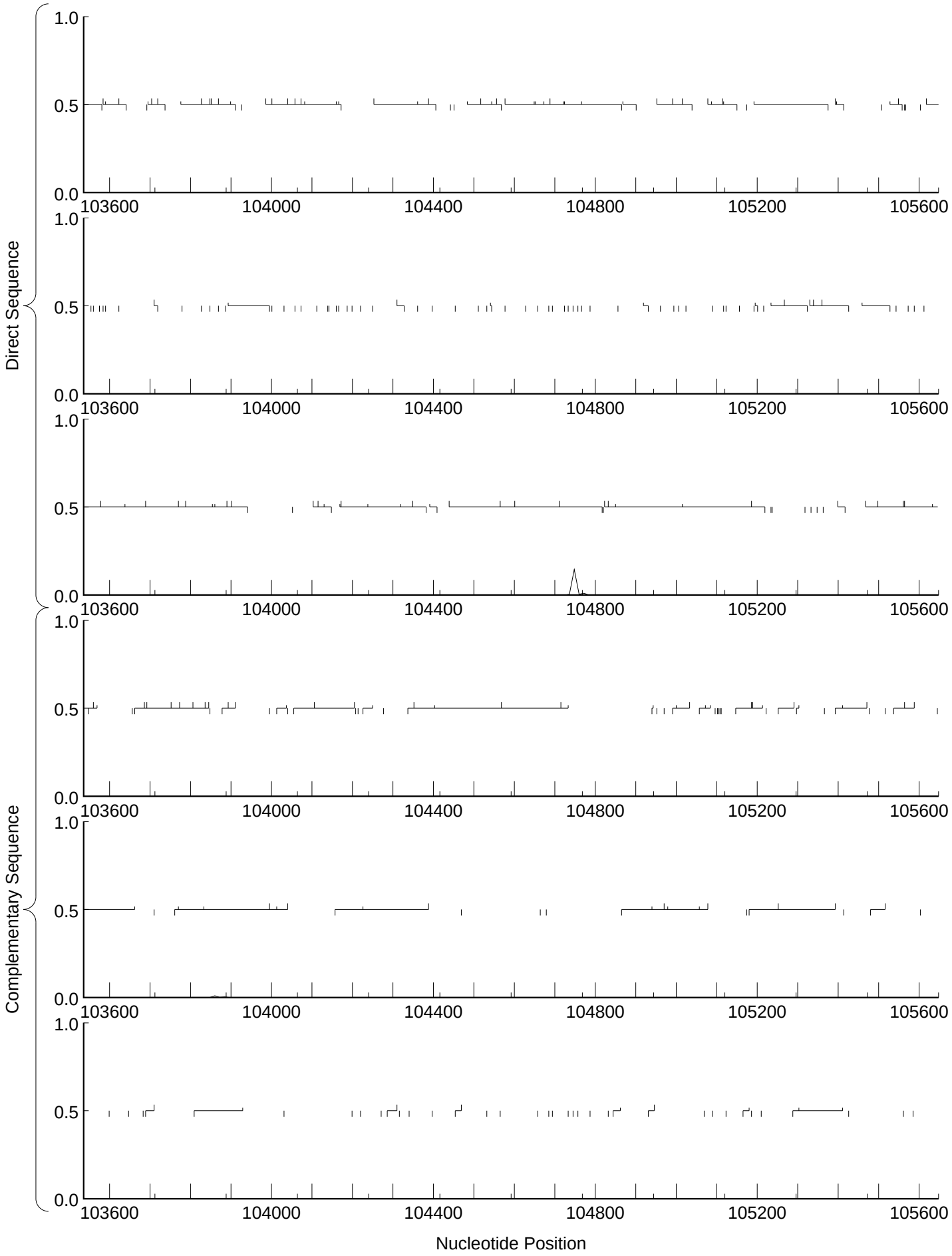

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
97600
98000
98400
98800
99200
Nucleotide Position

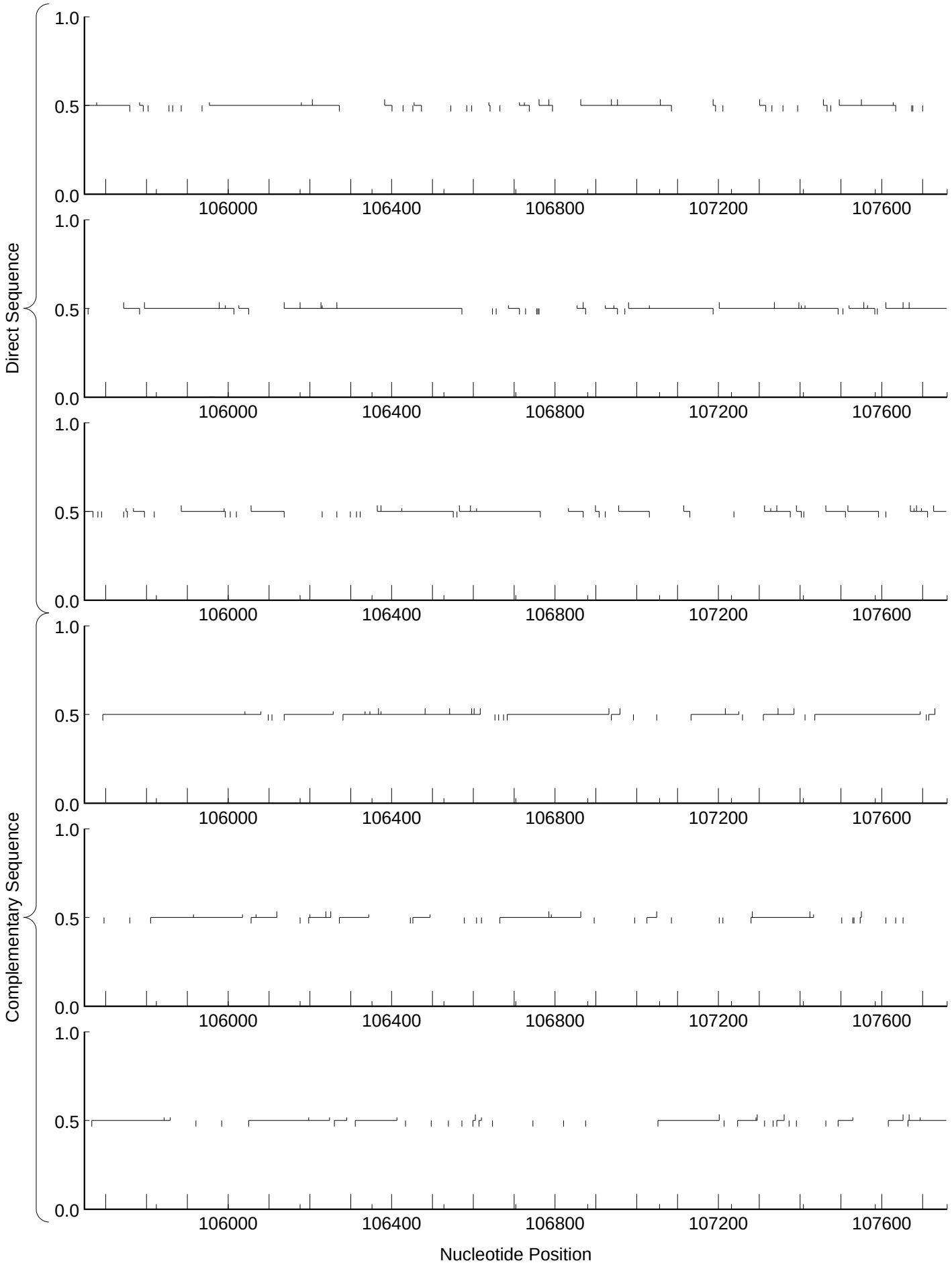
hage Yaboi complete sequence, 131250 bp including 12433 bp terminal repeat, Cluster BE2, Order 4, Window 96, Step 12, 49/64



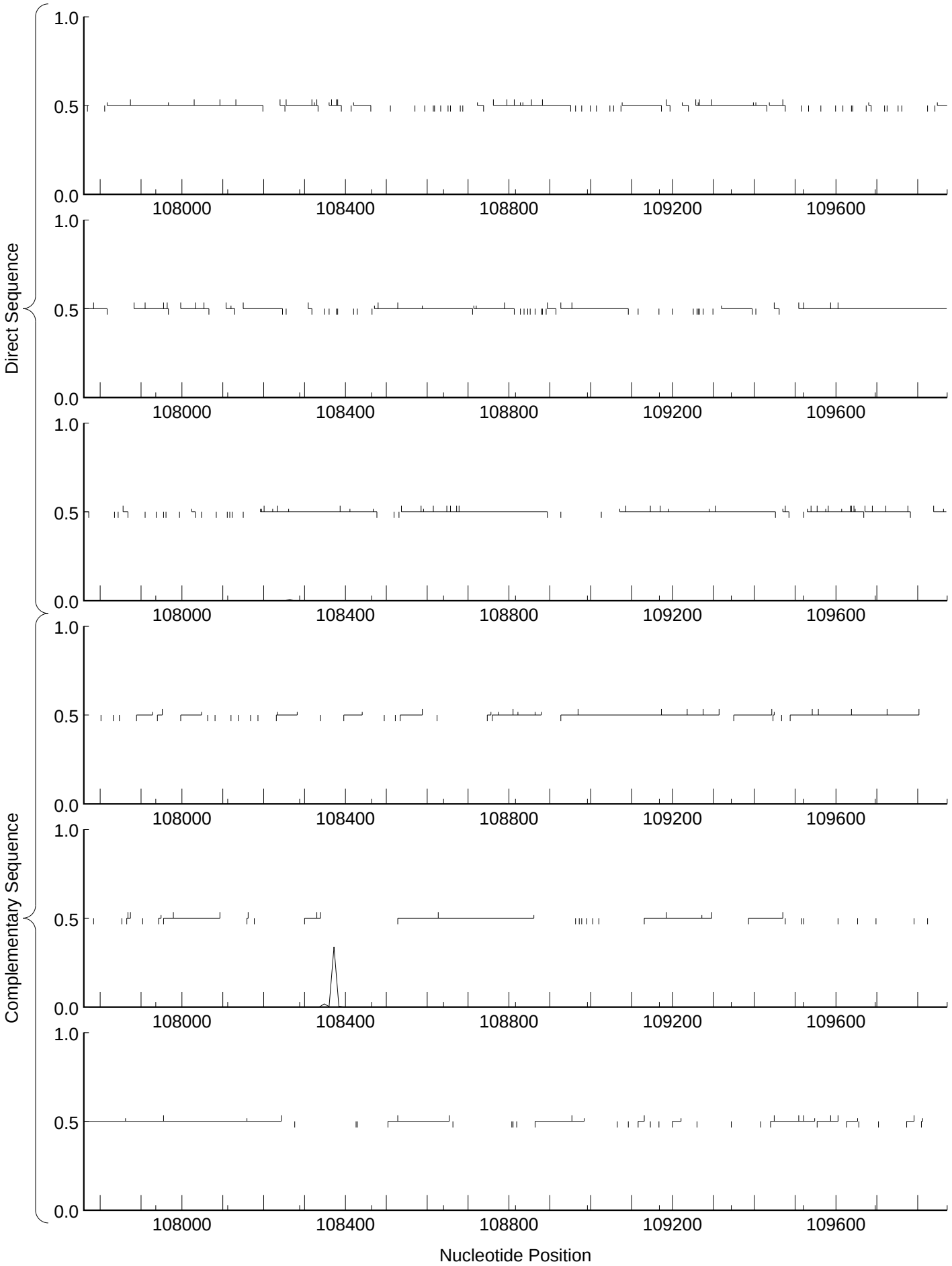

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
101600
102000
102400
102800
103200
Nucleotide Position

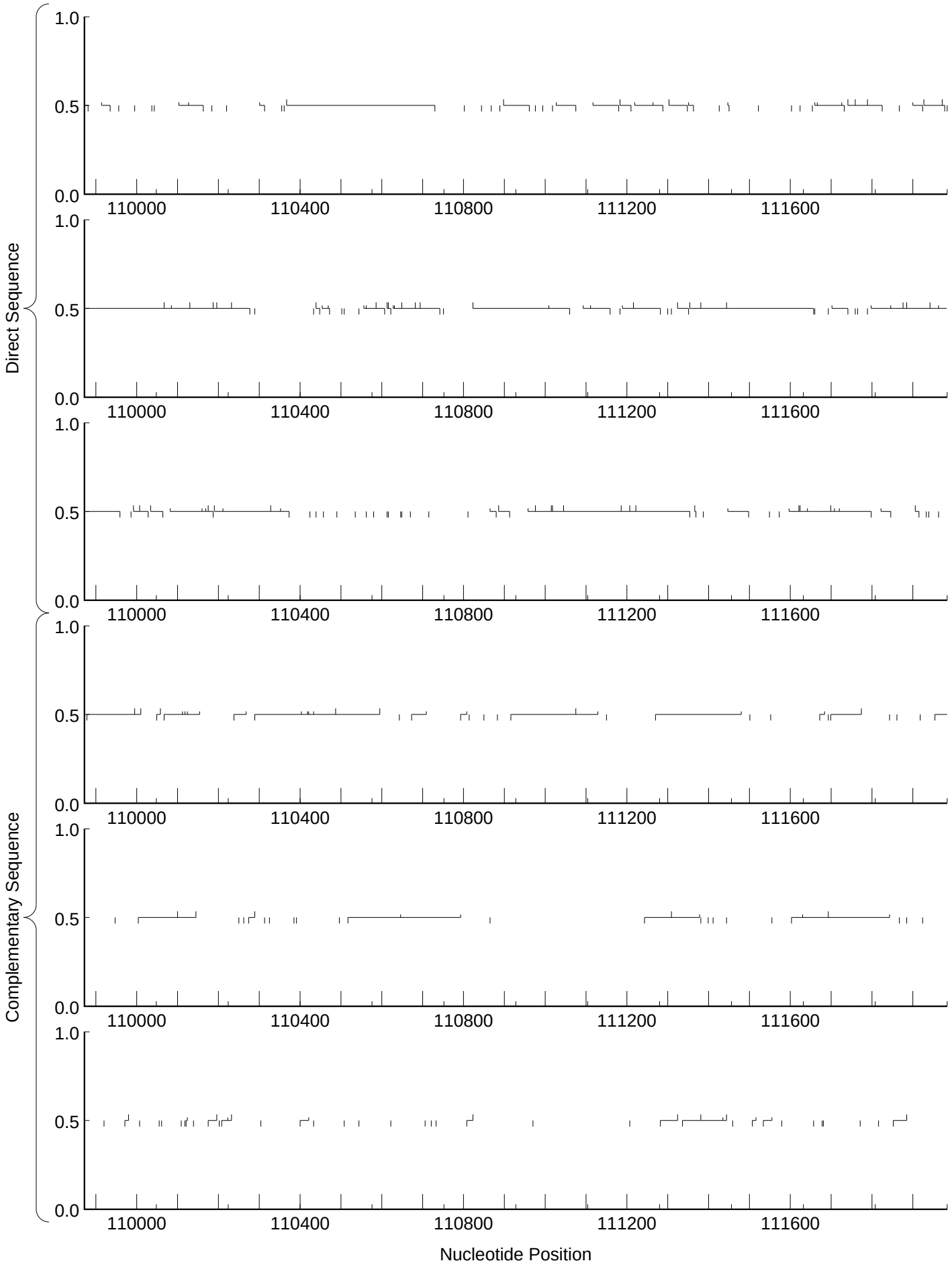
hage Yaboi complete sequence, 131250 bp including 12433 bp terminal repeat, Cluster BE2, Order 4, Window 96, Step 12, 51/64

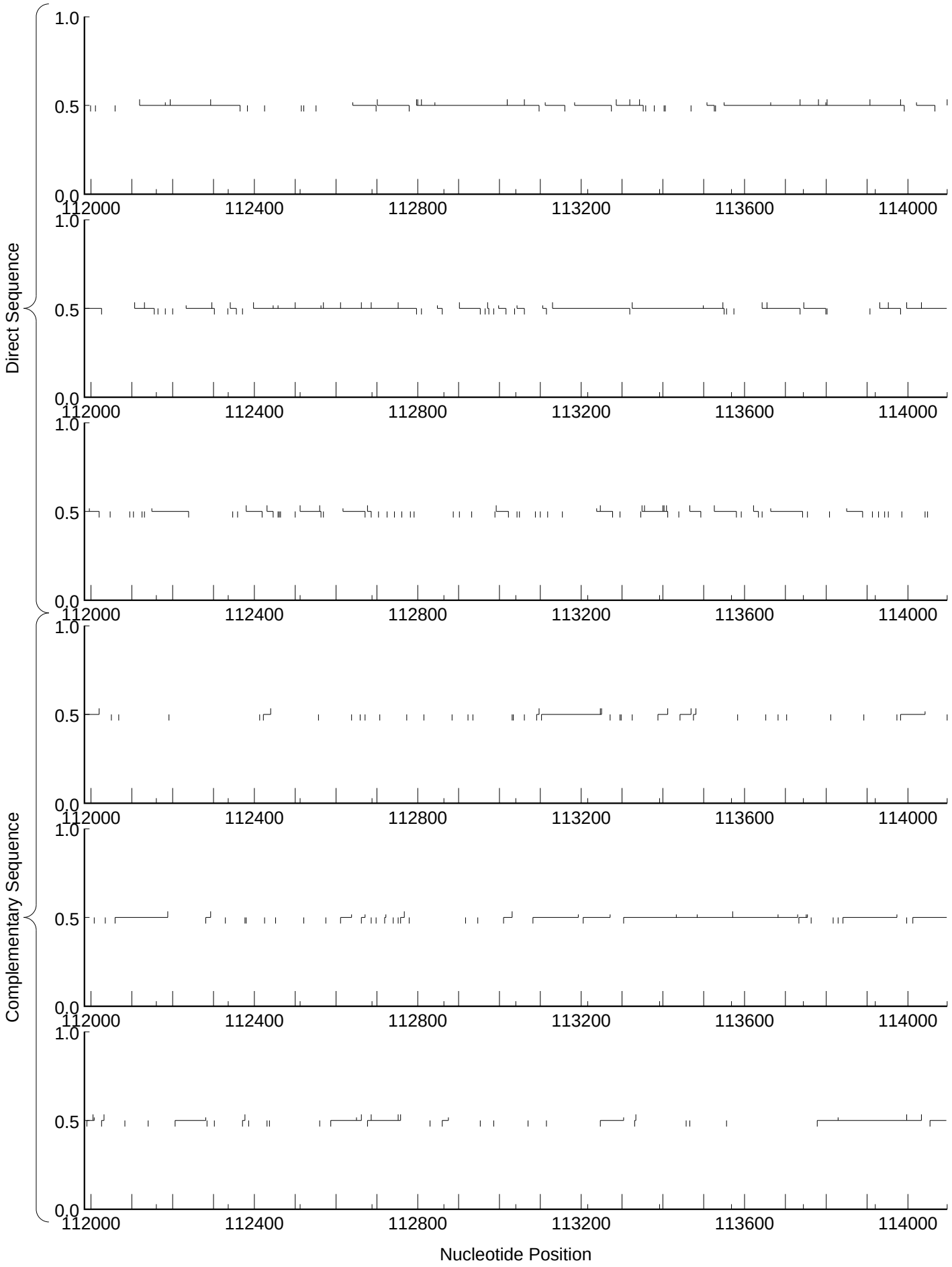


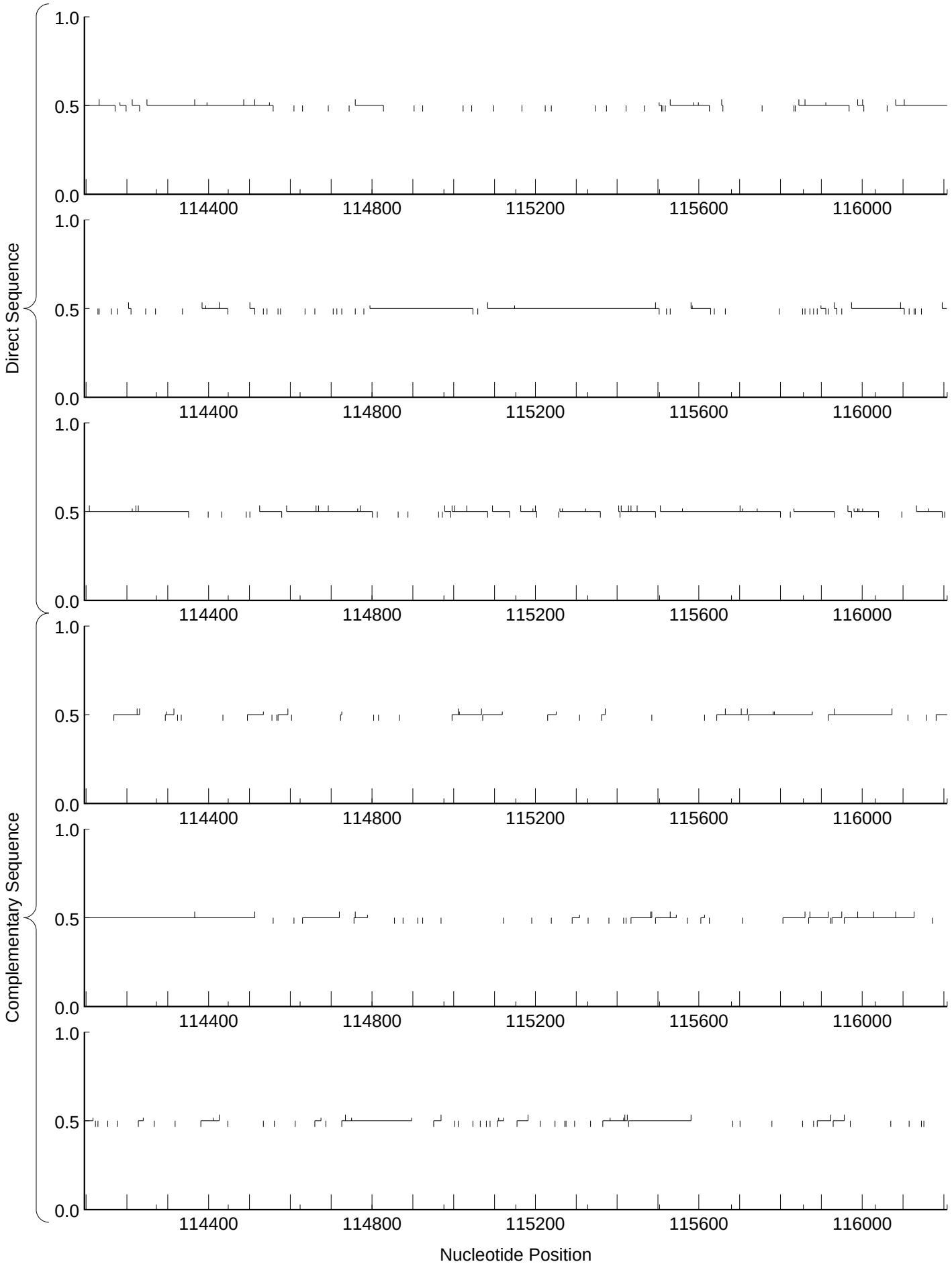

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
106000
106400
106800
107200
107600
Nucleotide Position

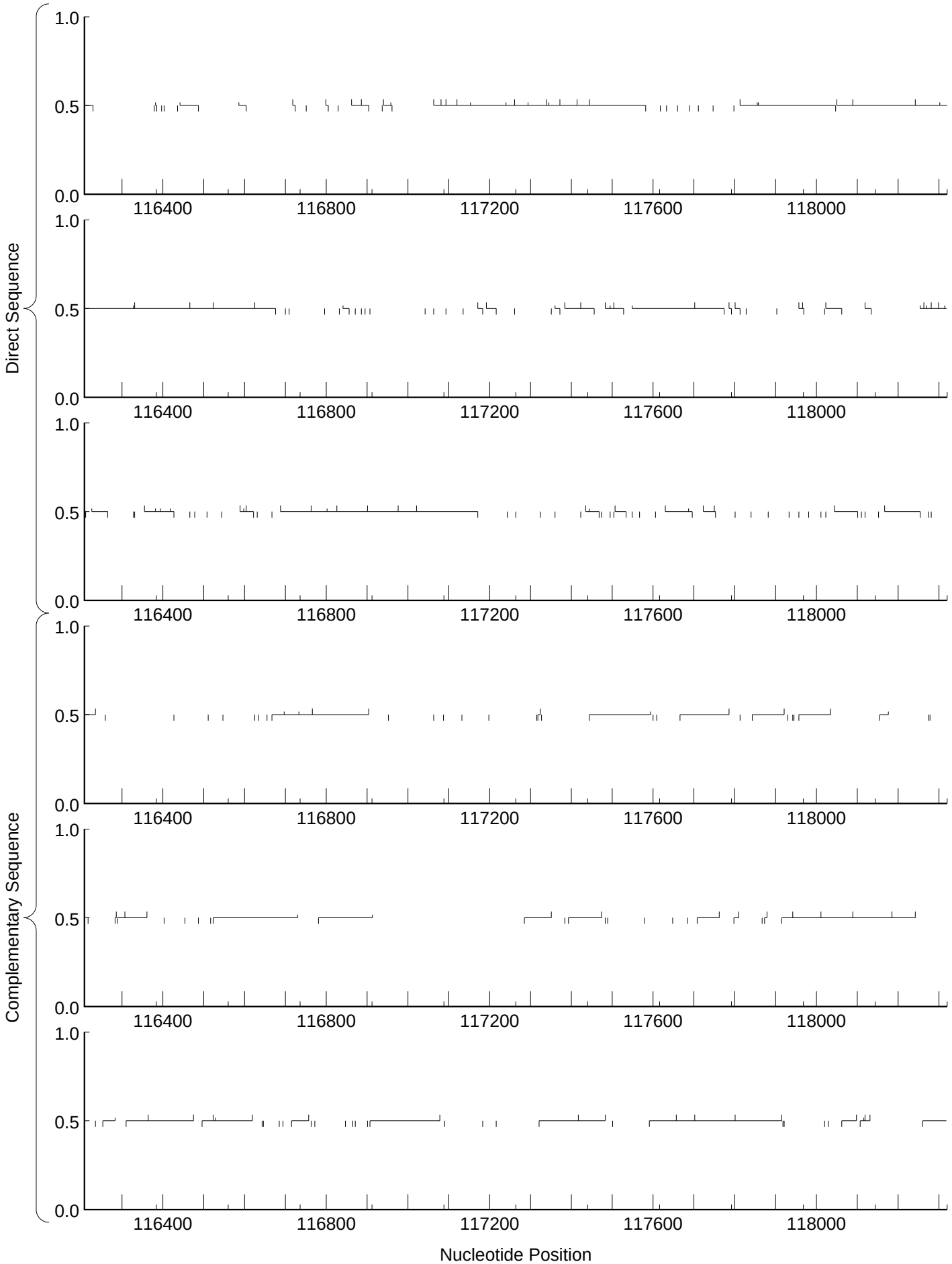
hage Yaboi complete sequence, 131250 bp including 12433 bp terminal repeat, Cluster BE2, Order 4, Window 96, Step 12, 53/64

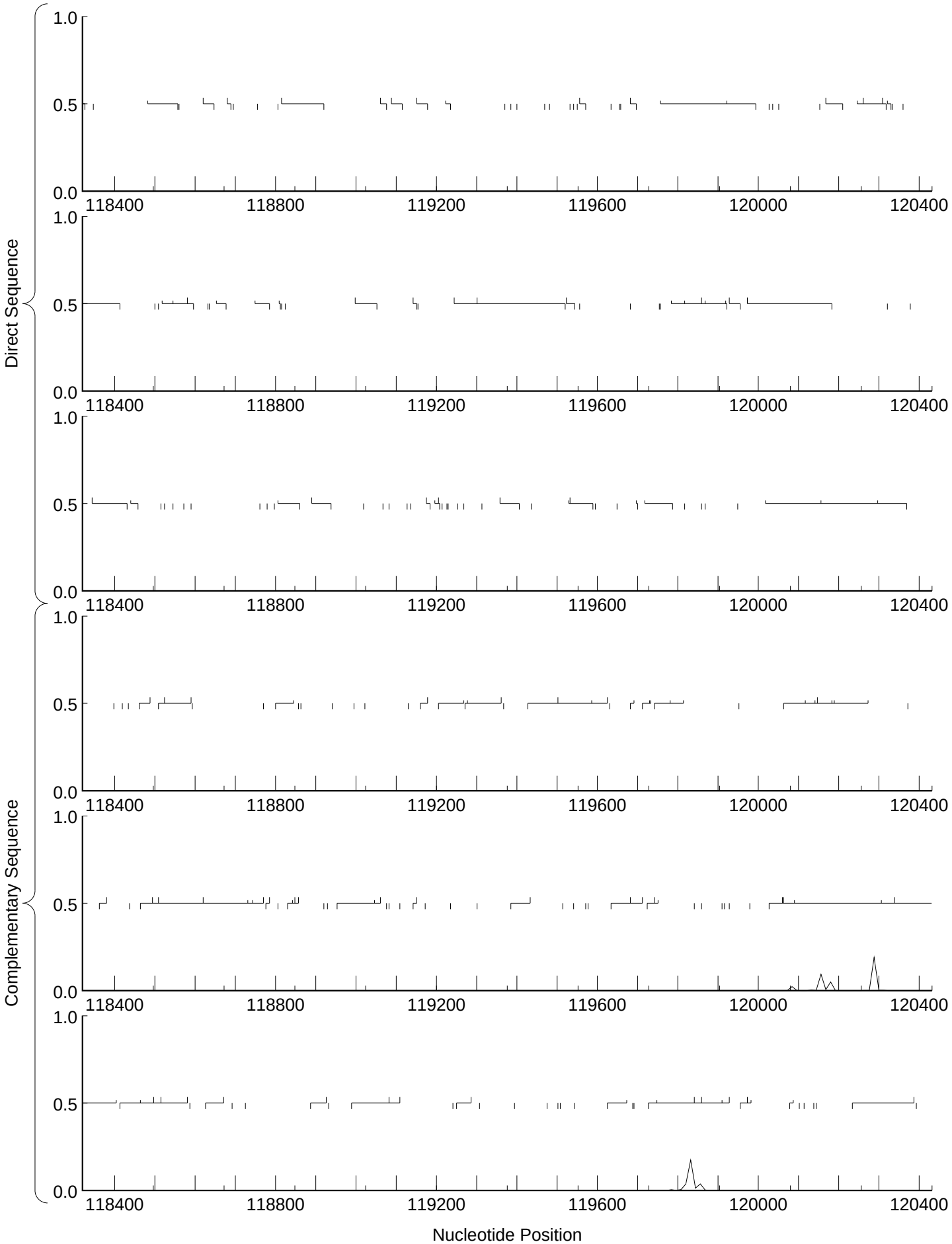


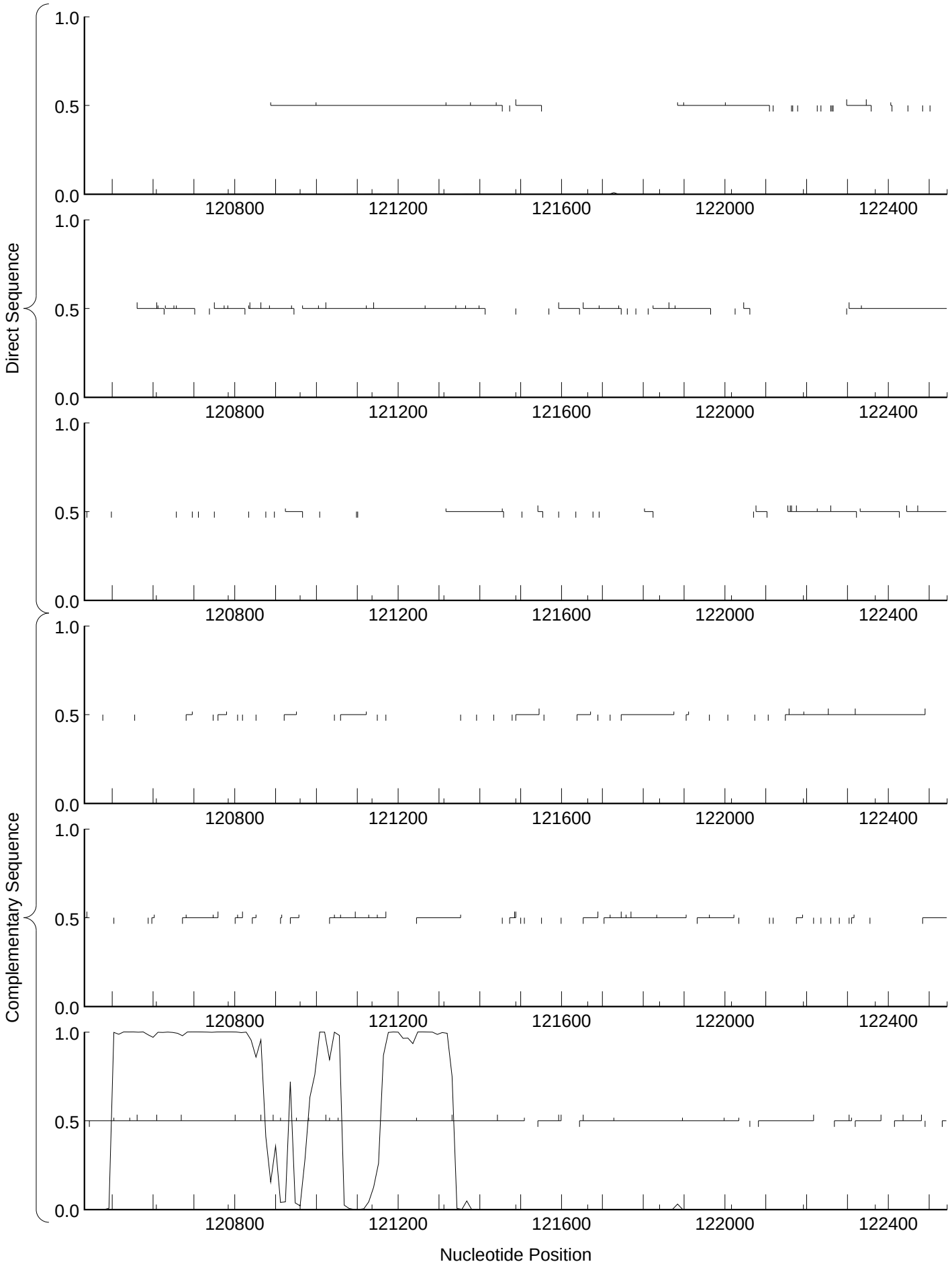

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
110000
110400
110800
111200
111600
Nucleotide Position

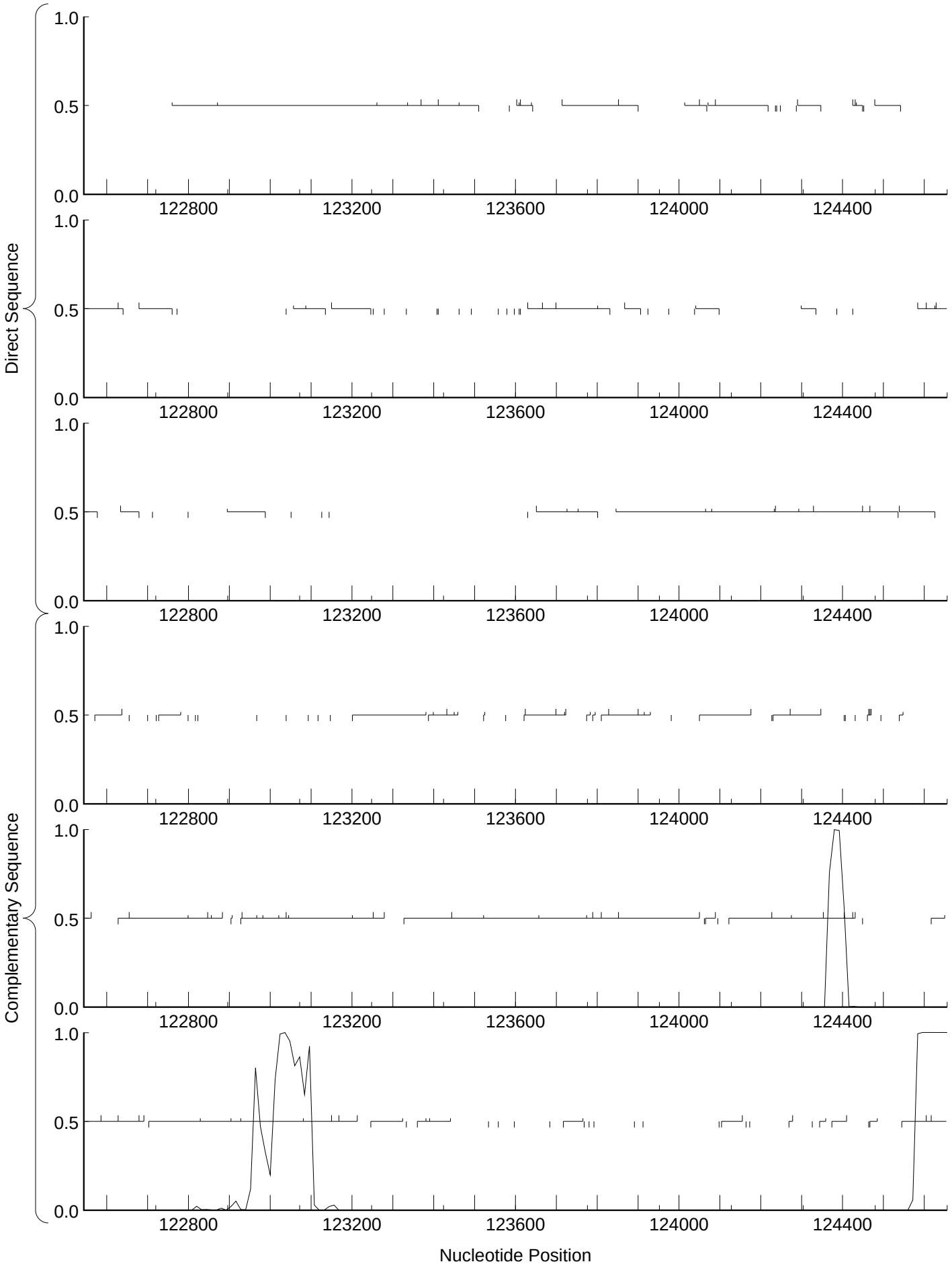

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
112000
112400
112800
113200
113600
114000
Nucleotide Position

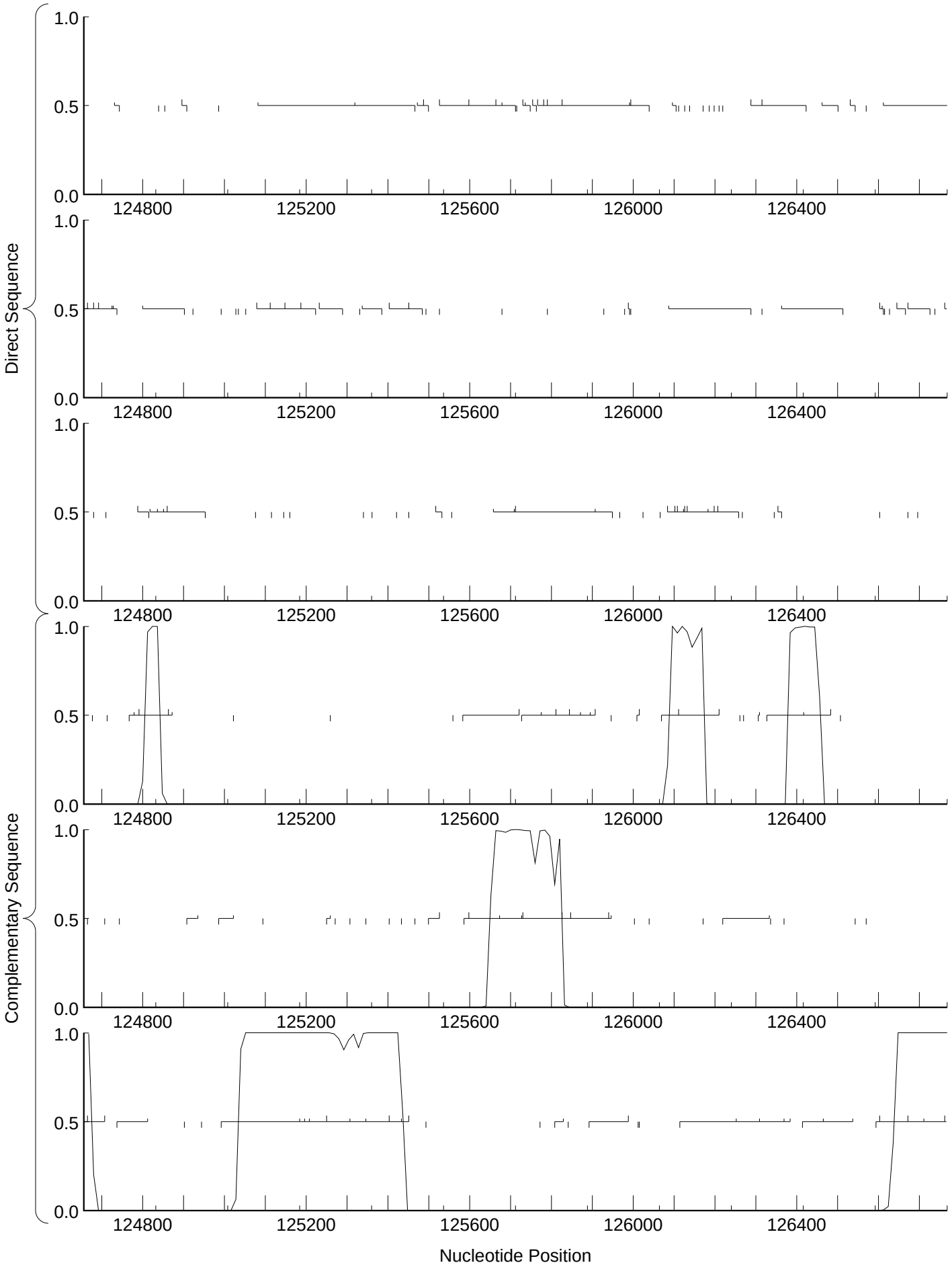

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
114400
114800
115200
115600
116000
Nucleotide Position

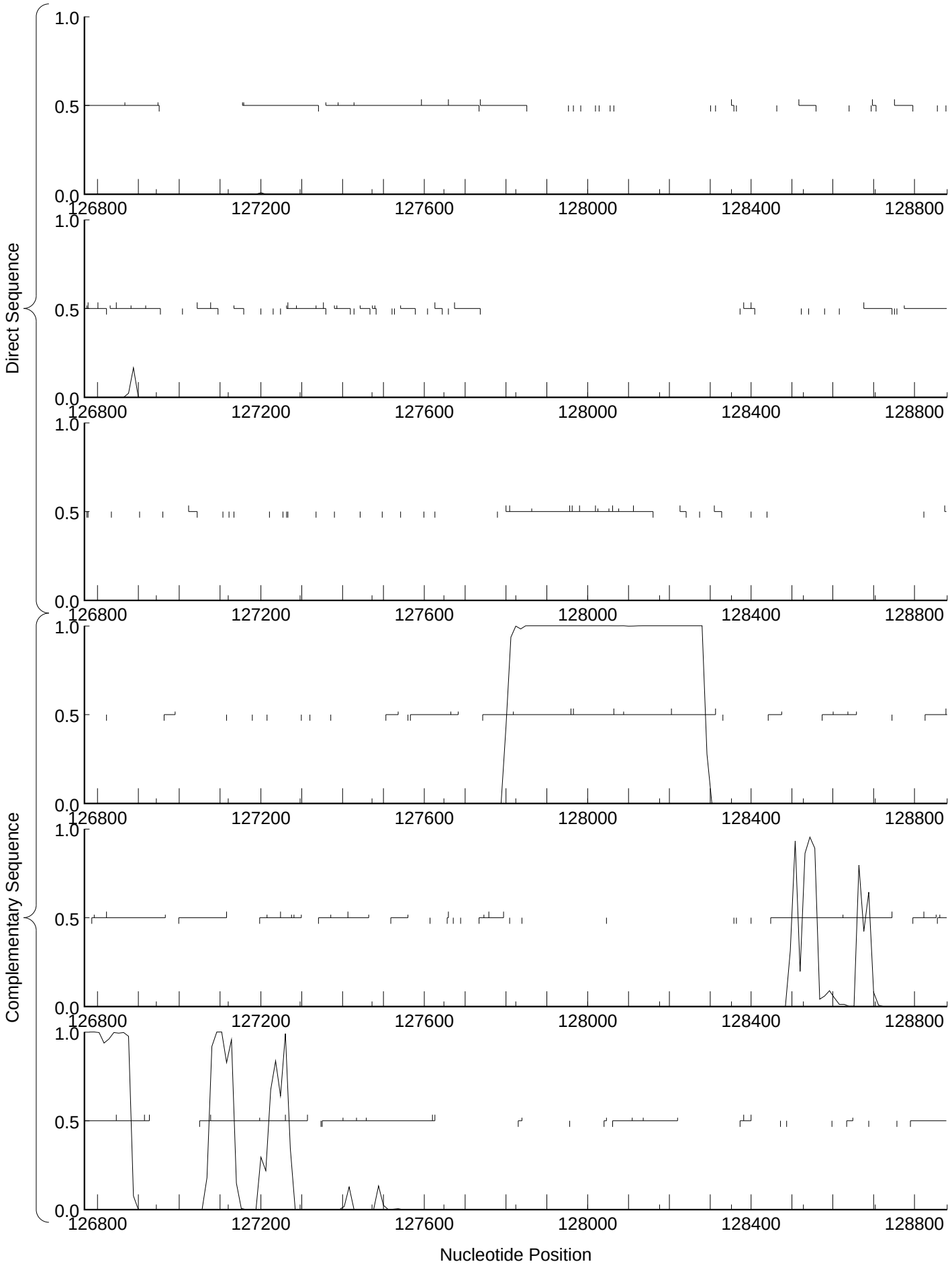

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
116400
116800
117200
117600
118000
Nucleotide Position

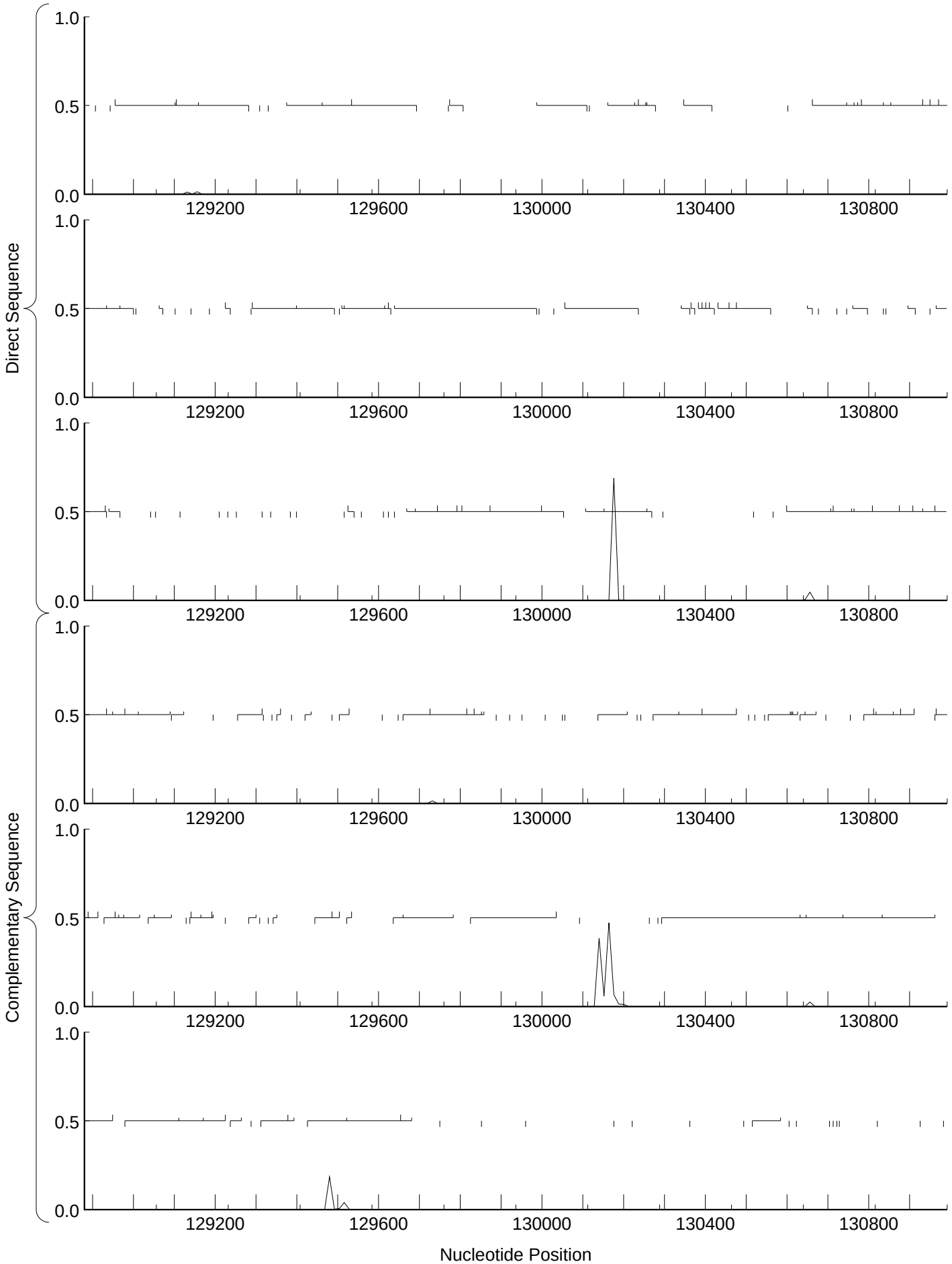

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
118400
118800
119200
119600
120000
120400
Nucleotide Position


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


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
124800
125200
125600
126000
126400
Nucleotide Position


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
126800
127200
127600
128000
128400
128800
Nucleotide Position


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
129200
129600
130000
130400
130800
Nucleotide Position

nage Yaboi complete sequence, 131250 bp including 12433 bp terminal repeat, Cluster BE2, Order 4, Window 96, Step 12, 64/64

