GeneMark

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

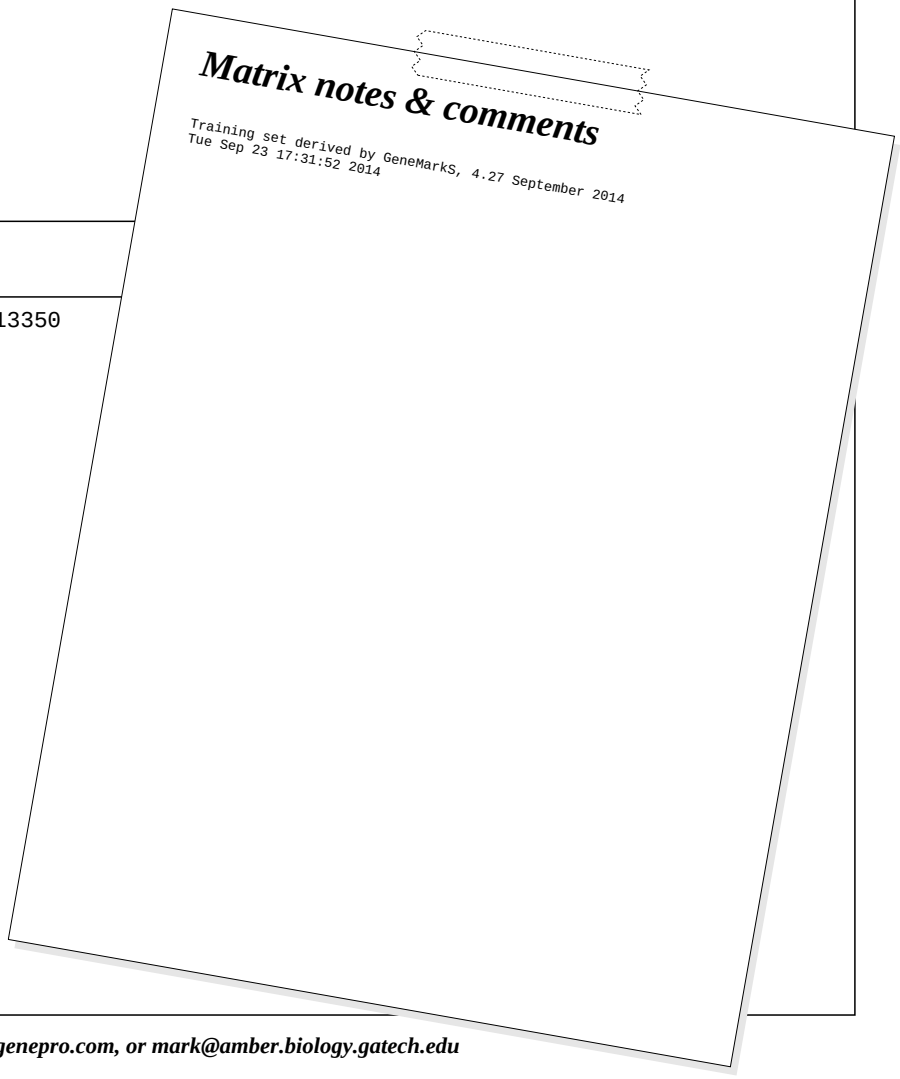
PROGRAM INFORMATION

```
Sequence         :  Streptomyces phage Battuta complete sequence, 130734 bp including 12579 bp terminal repeat,
Analysis Date    :  3/28/24 at 9:04:28
Pages            :  63
Sequence Length  :  130734 bp
GC Content       :   49.51%

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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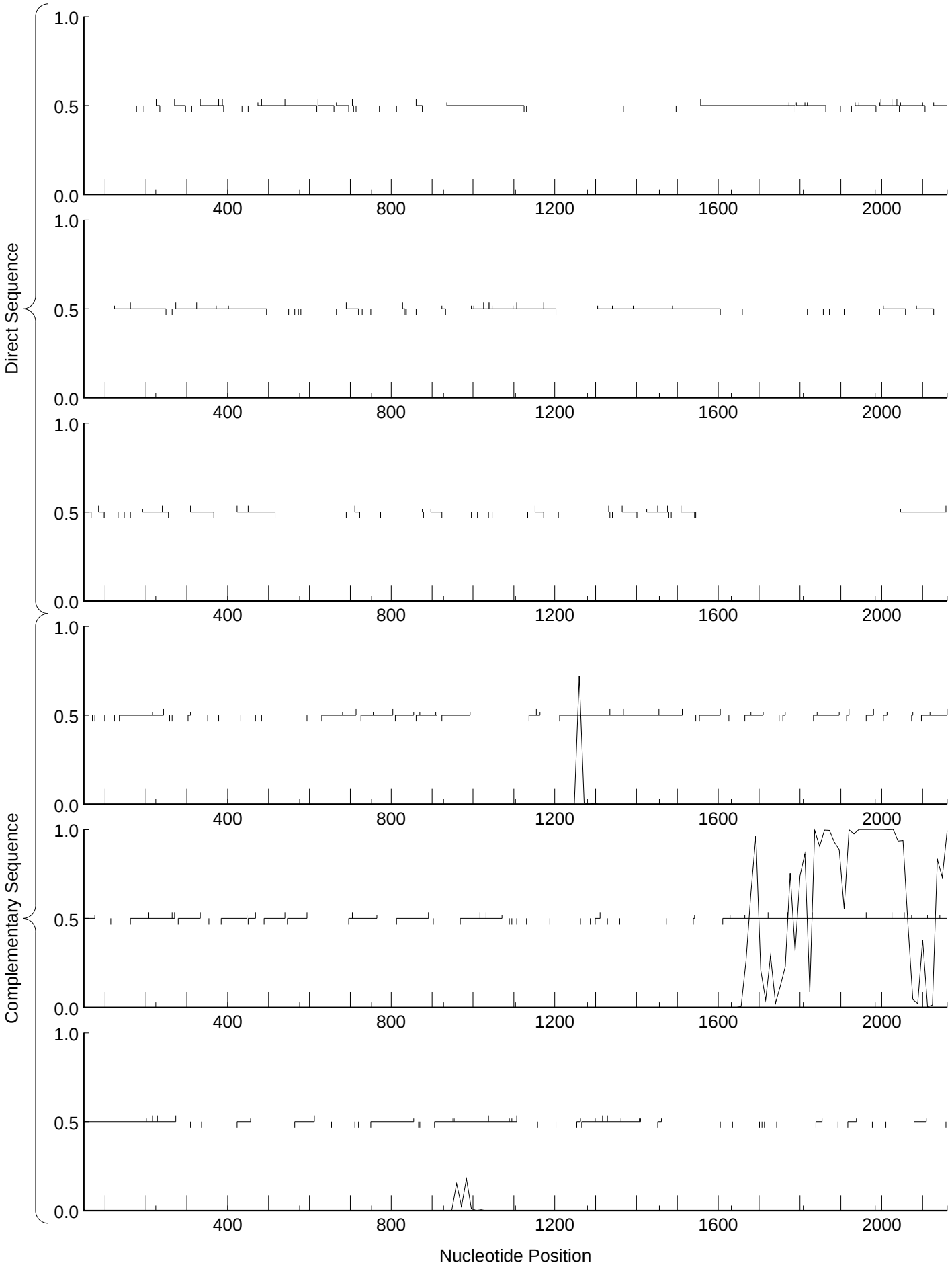
MATRIX INFORMATION

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Author     :  -

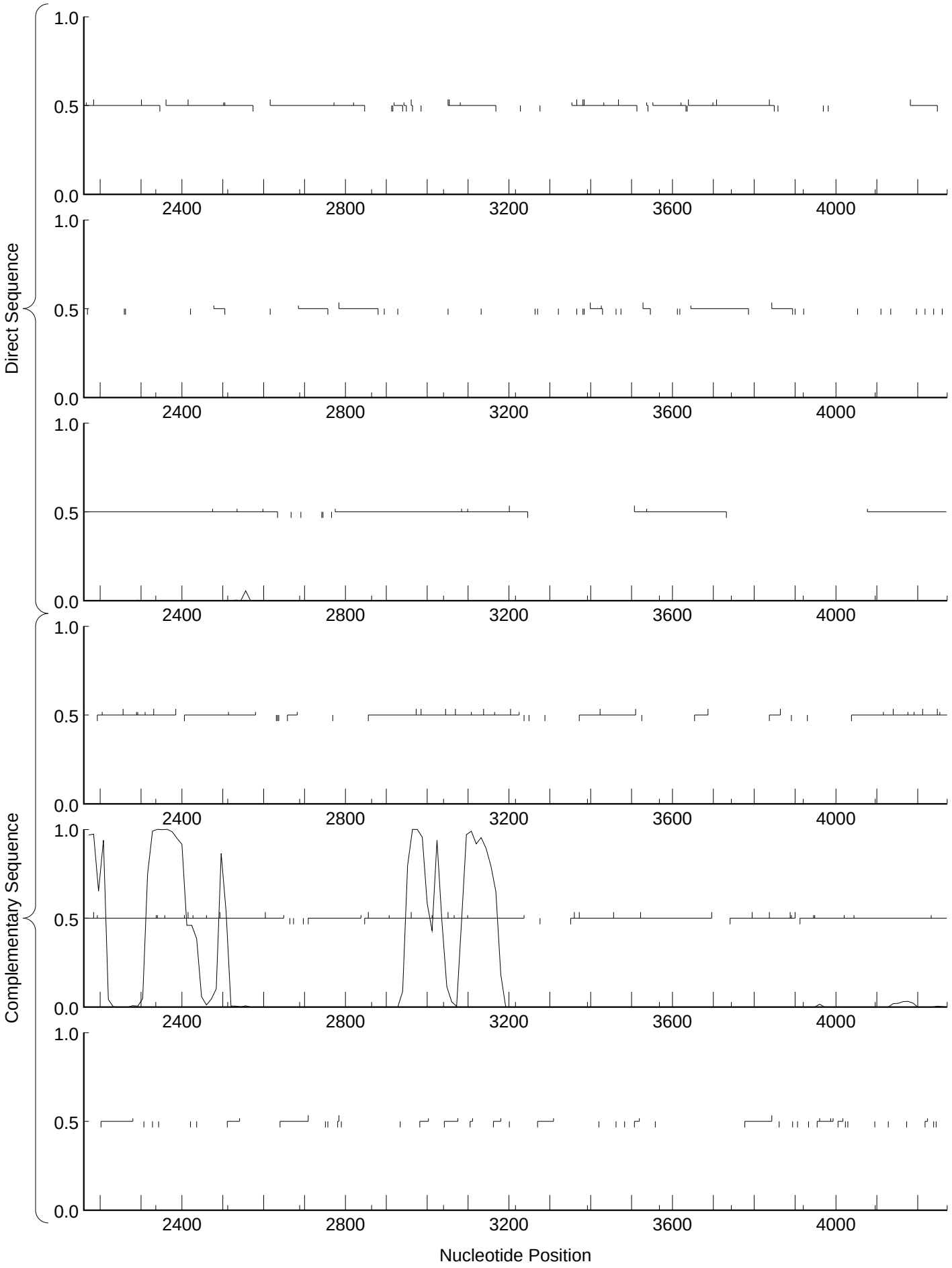
Order      :  4
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  Send questions / comments to:
      Dr. M. Borodovsky
      Georgia Institute of Technology
      School of Biology
      Atlanta, GA  30332-0230
```

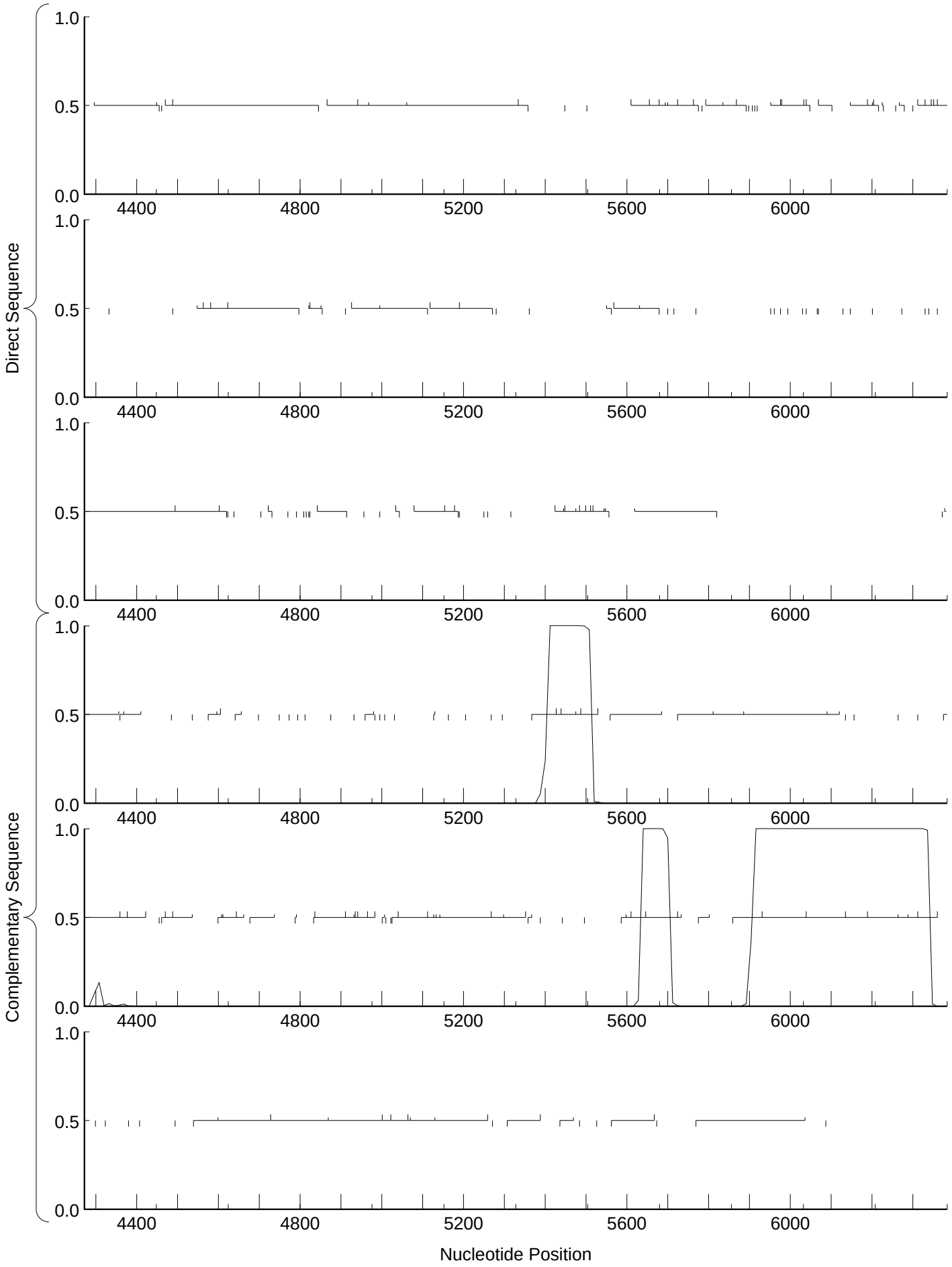

For help or information, send electronic mail to: custserv@genepro.com, or mark@amber.biology.gatech.edu


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
400
800
1200
1600
2000
Nucleotide Position

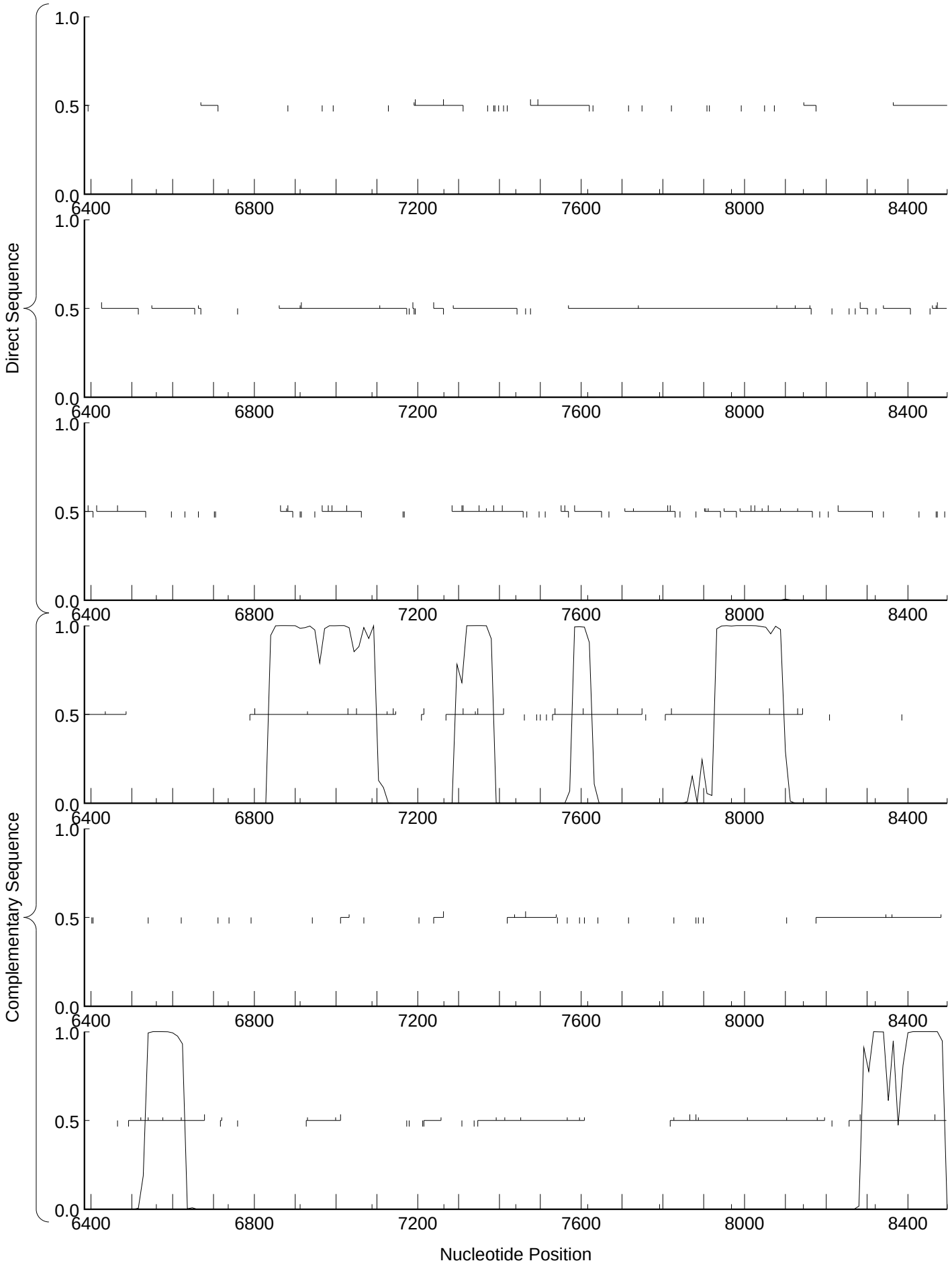
nage Battuta complete sequence, 130734 bp including 12579 bp terminal repeat, Cluster BE2, Order 4, Window 96, Step 12, 3/63



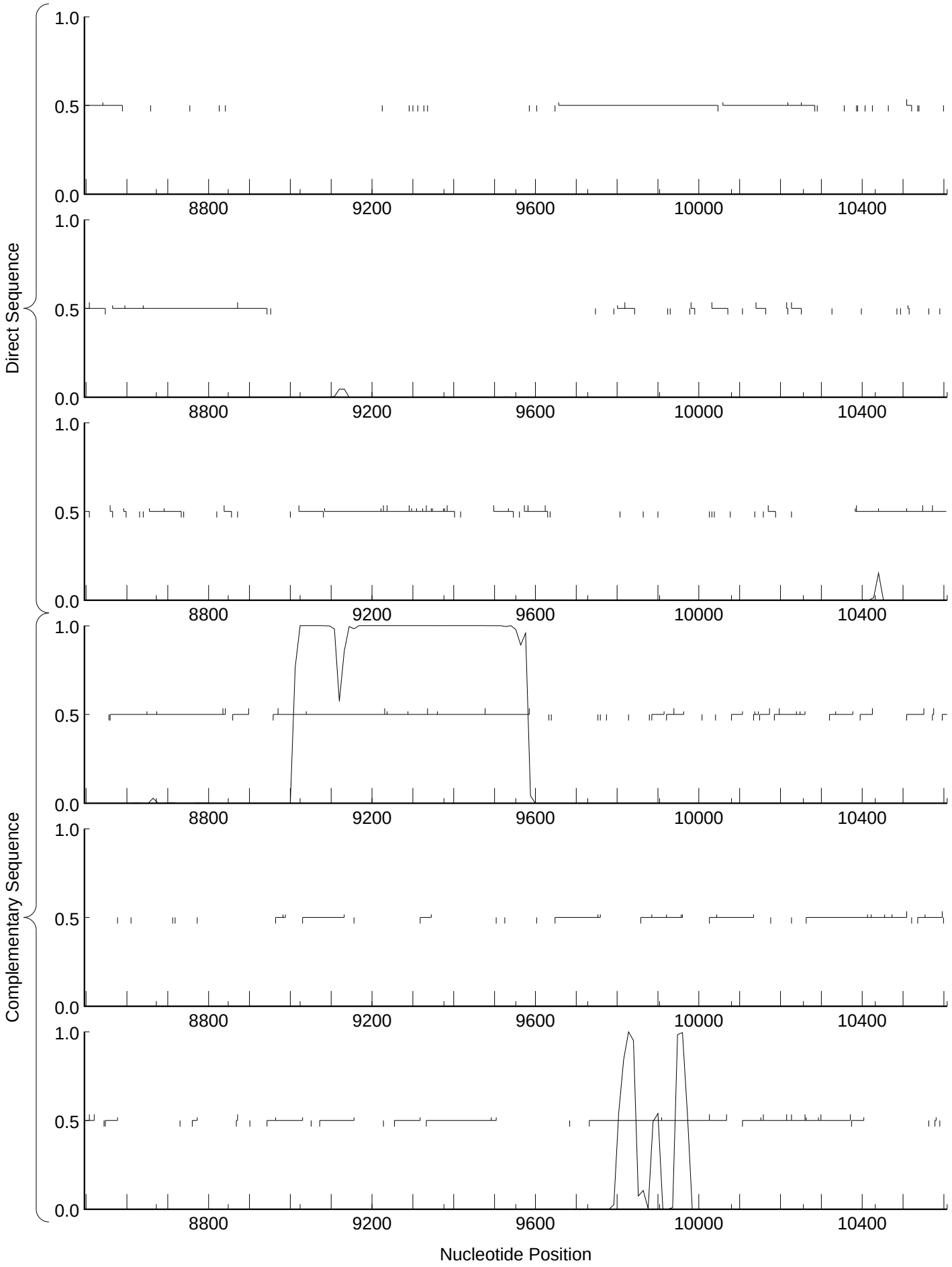
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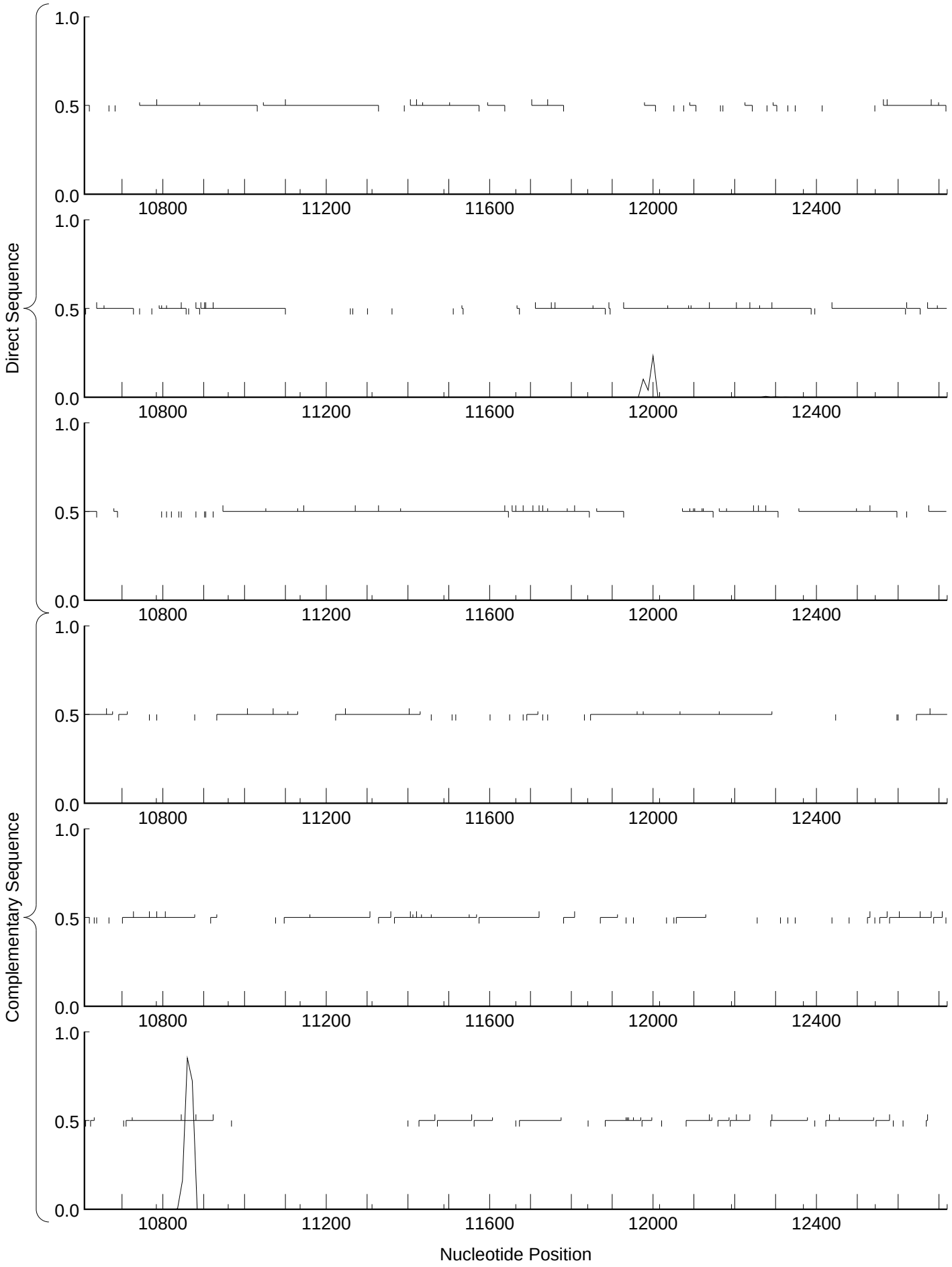
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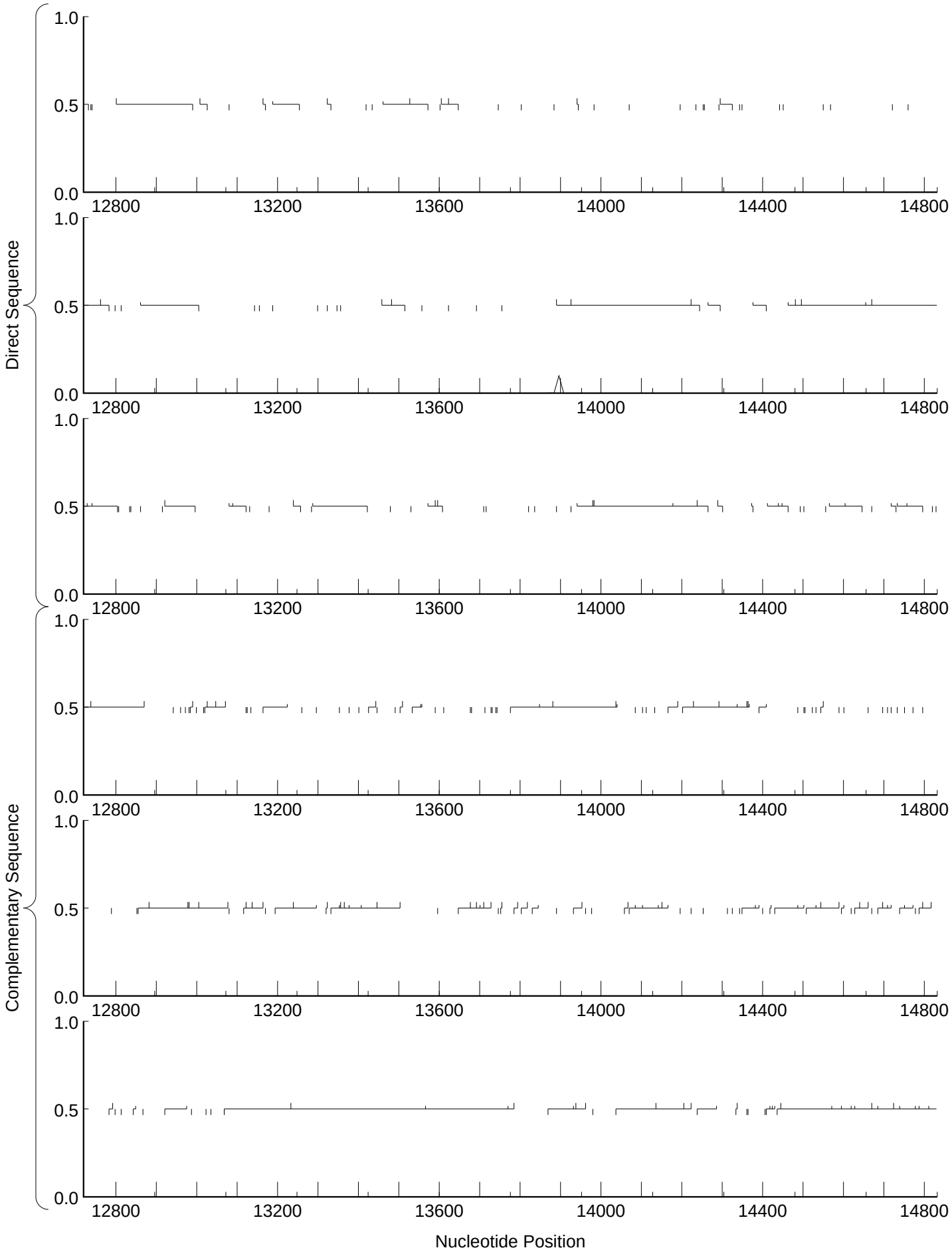
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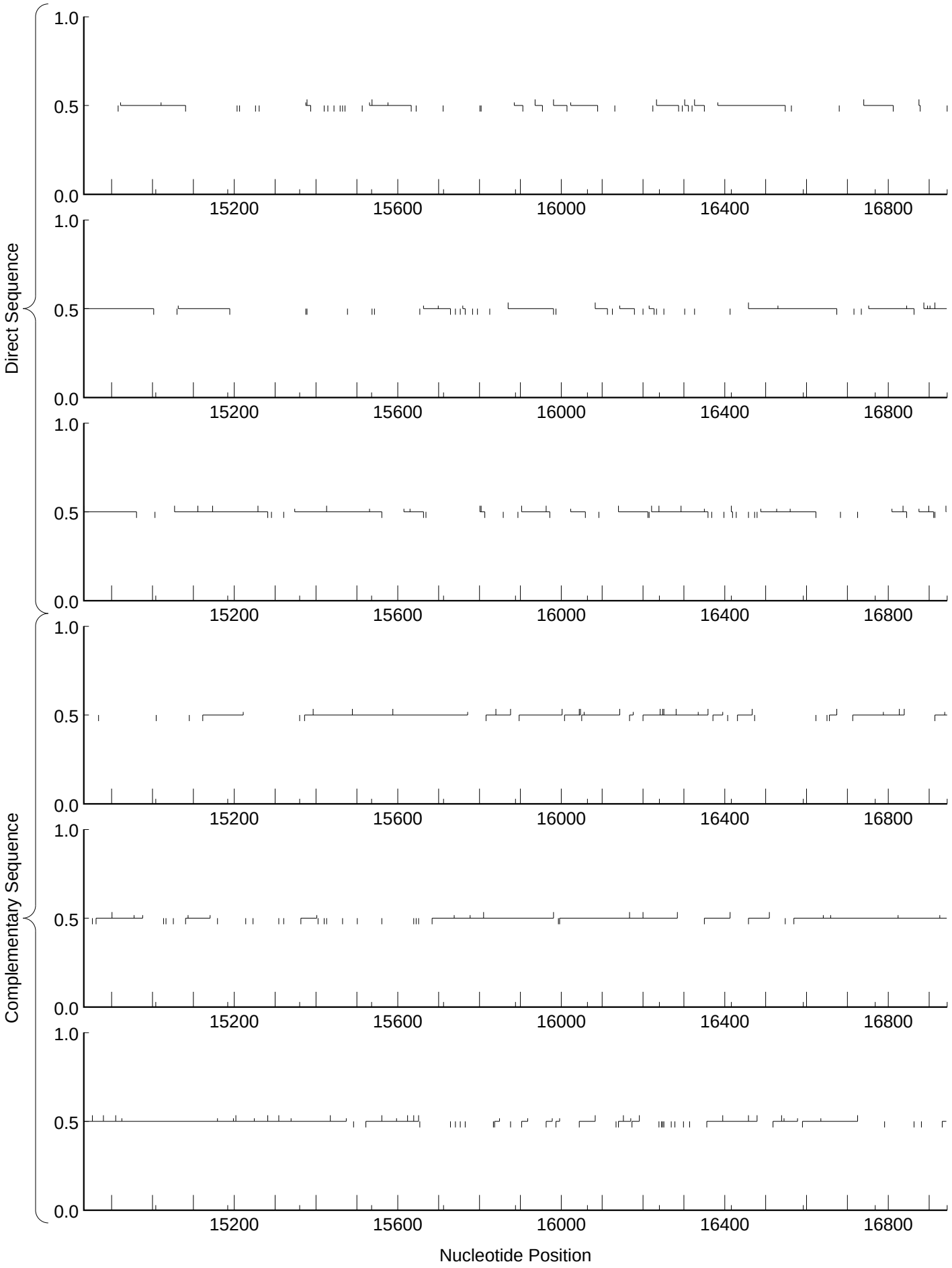
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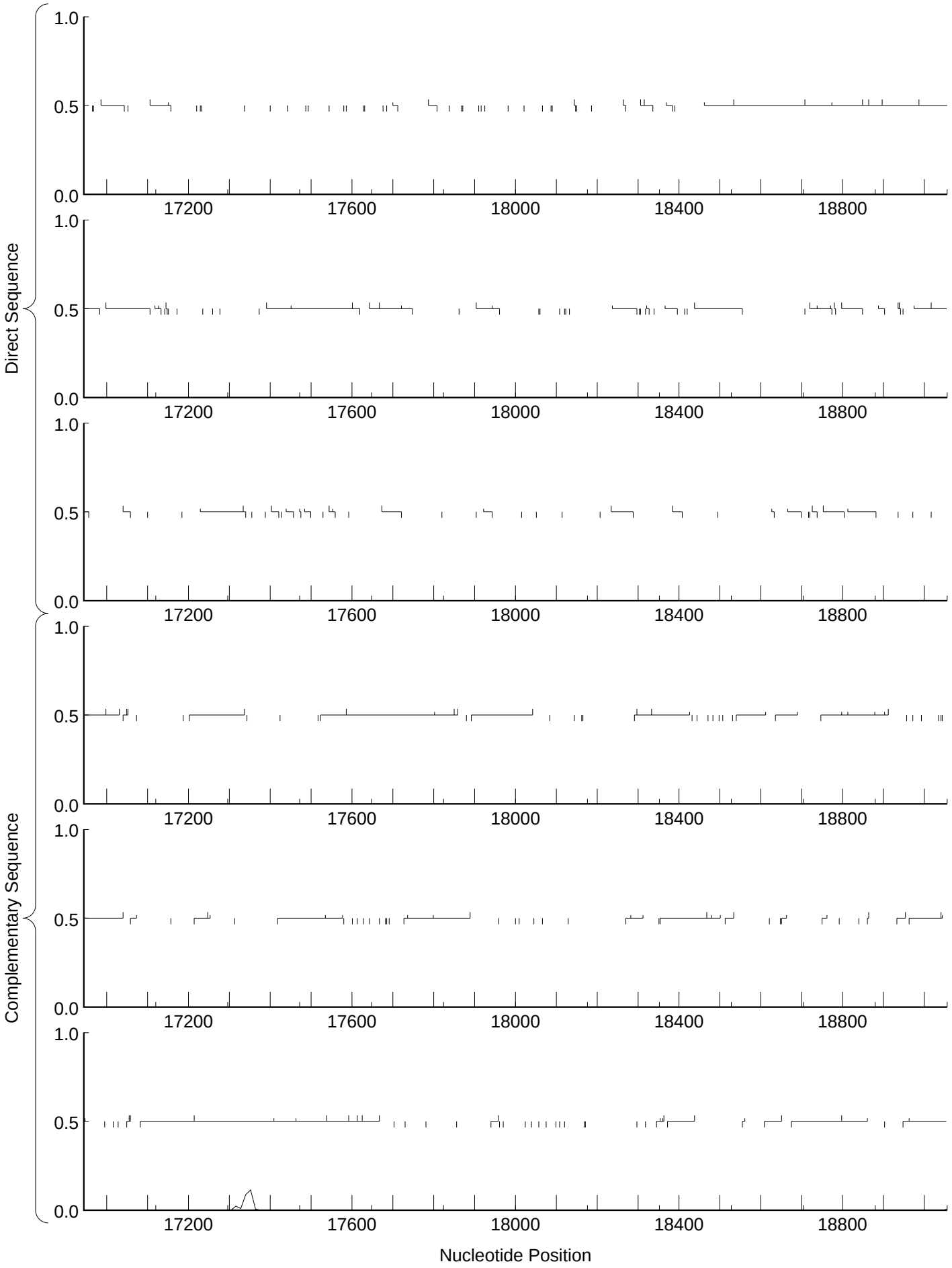
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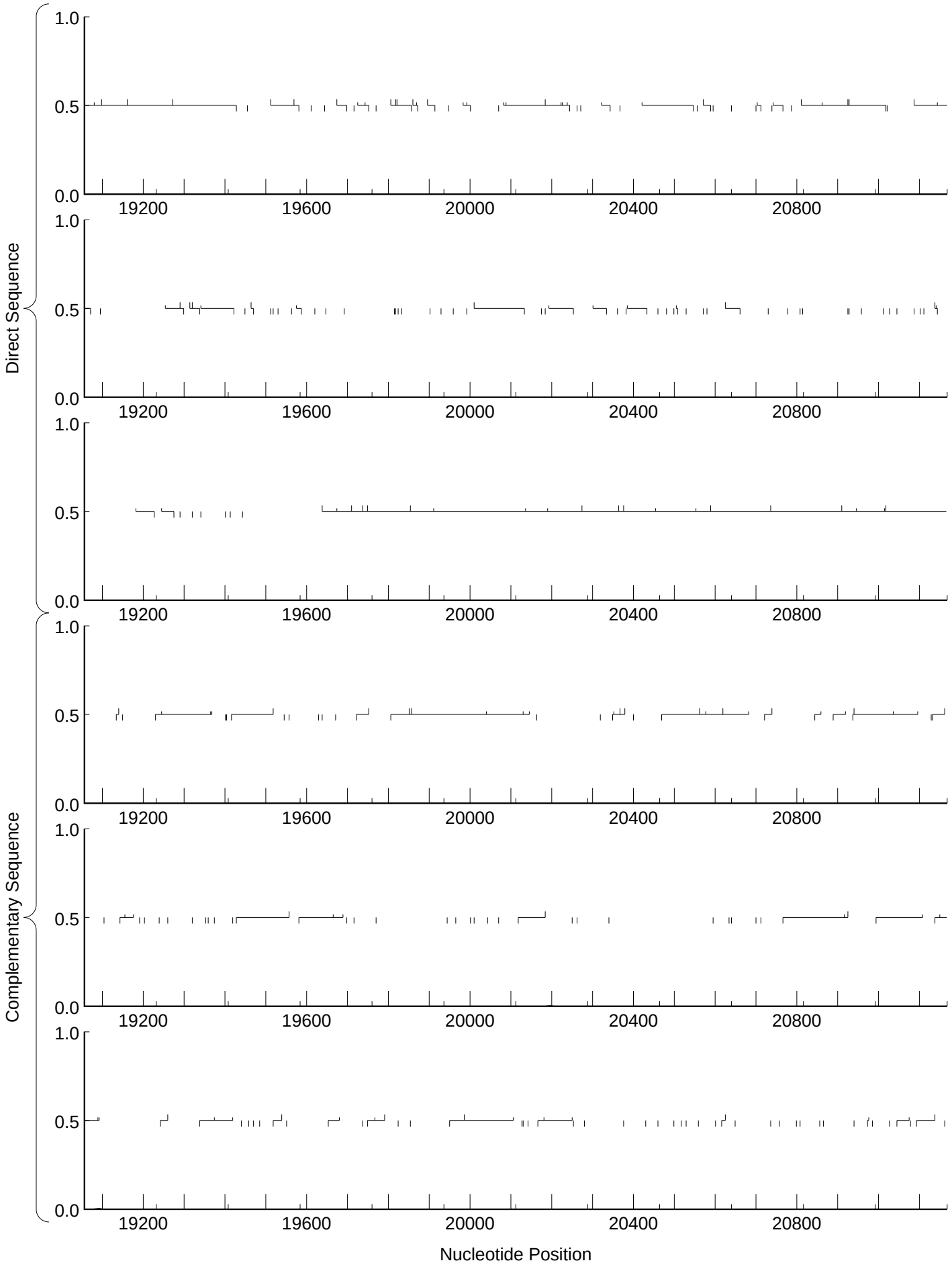


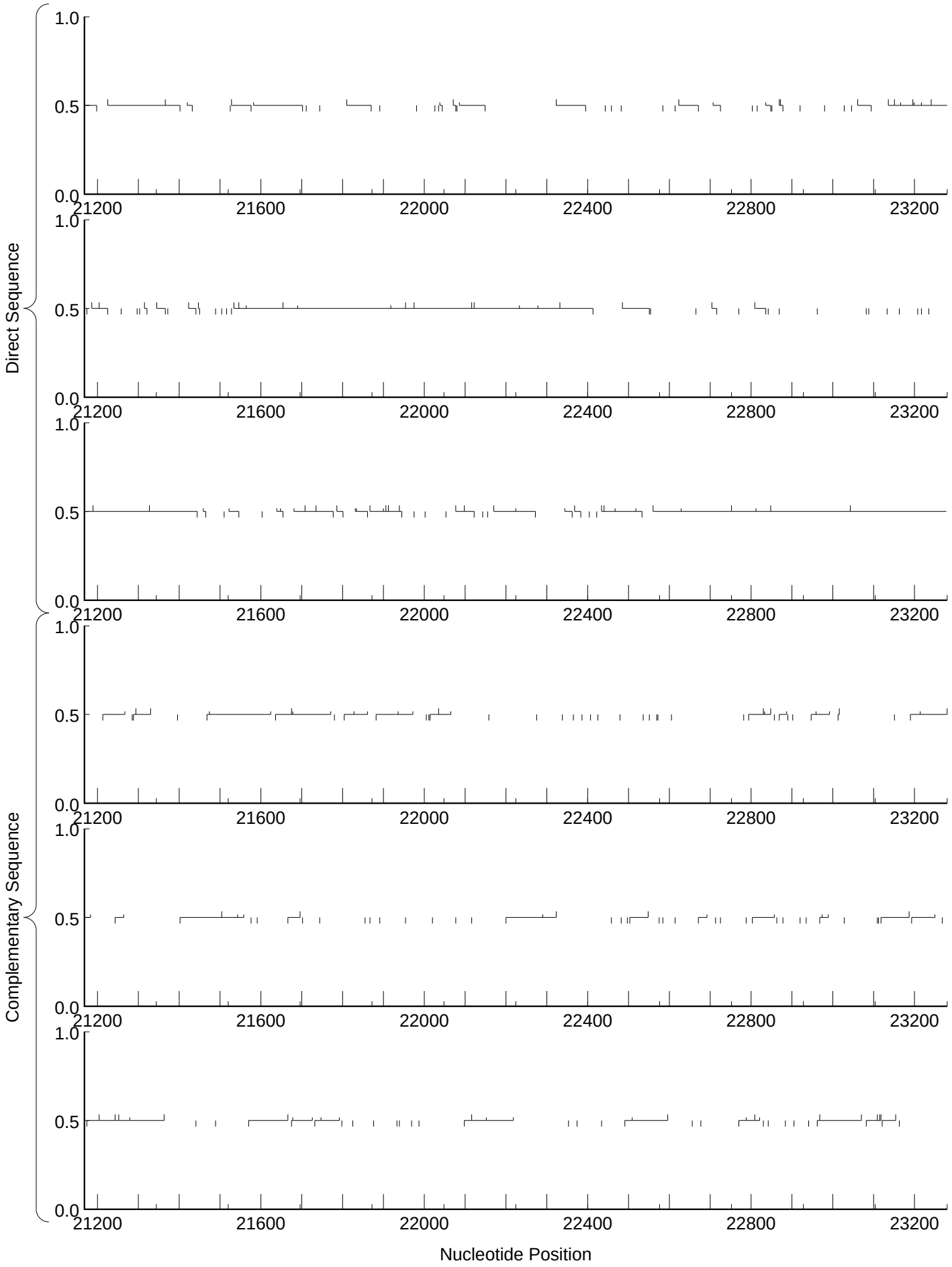
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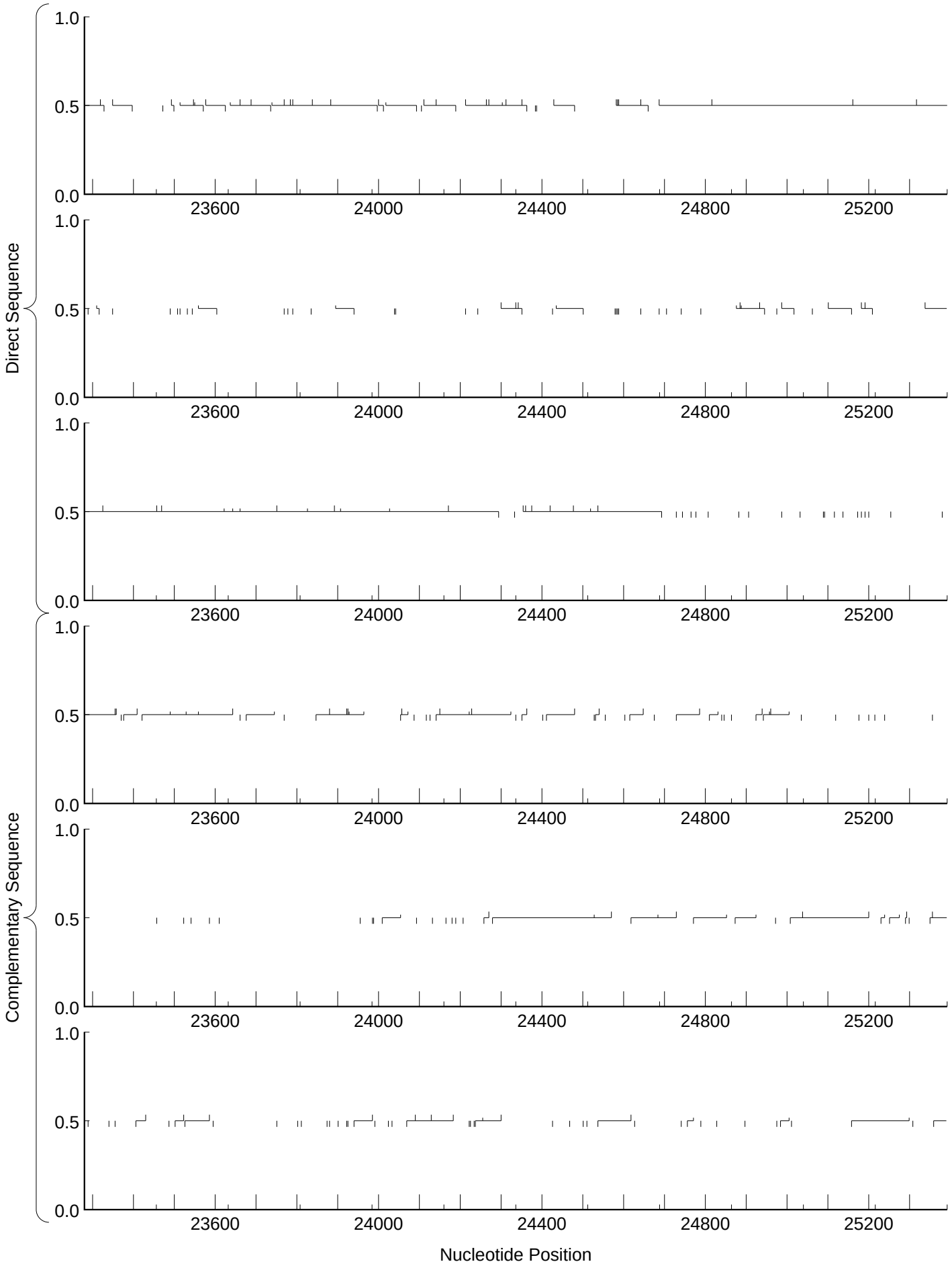


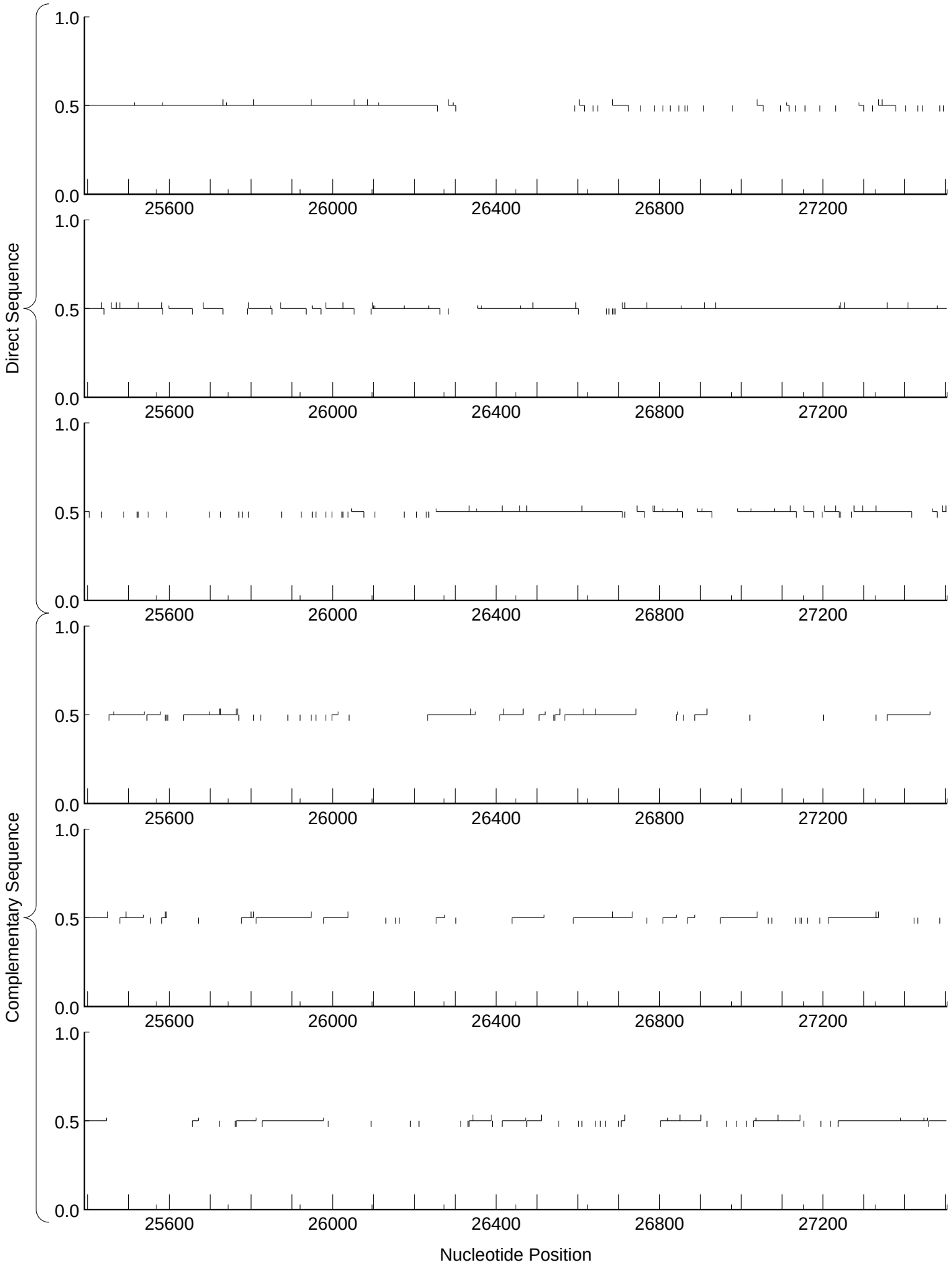
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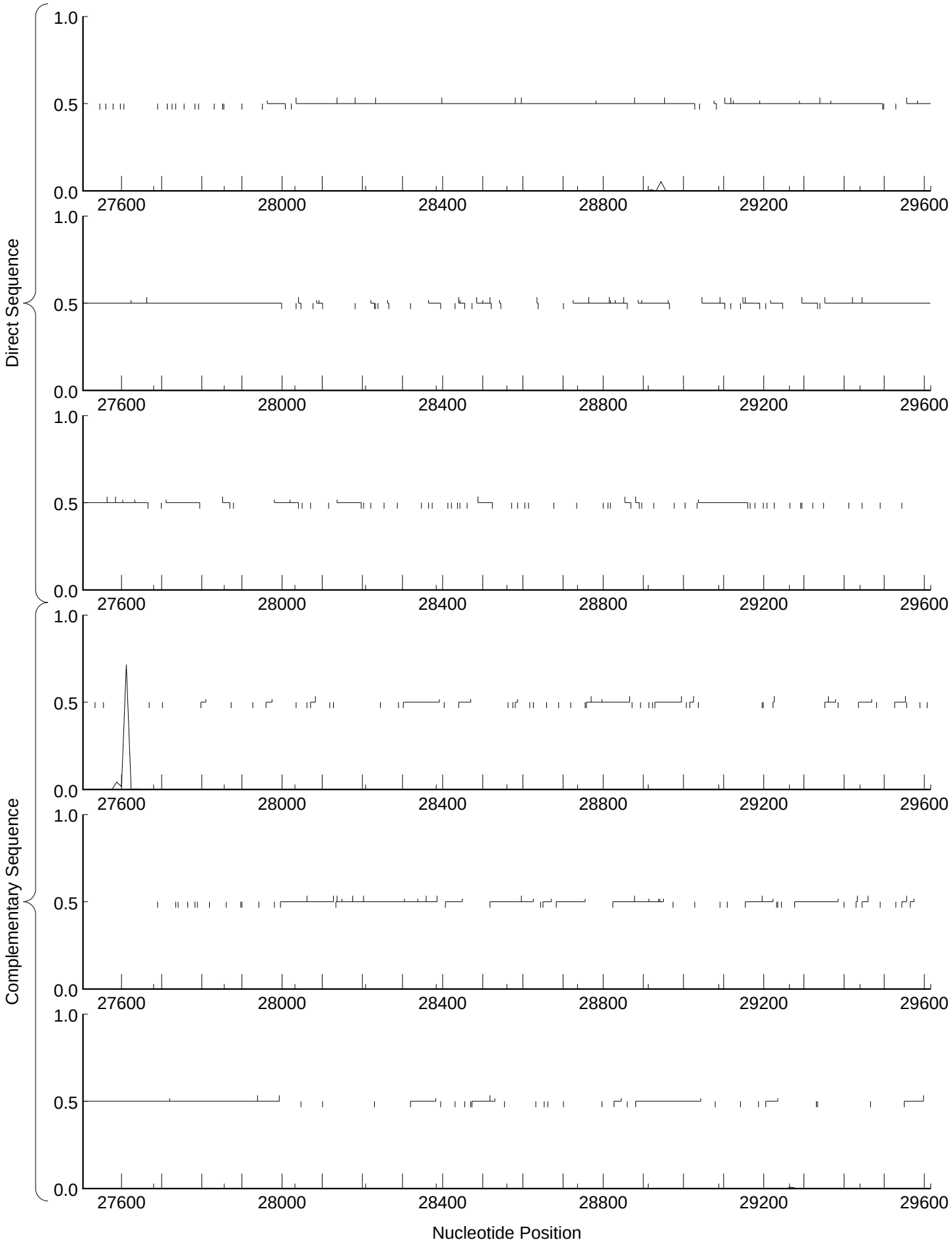

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Complementary Sequence
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20800
Nucleotide Position

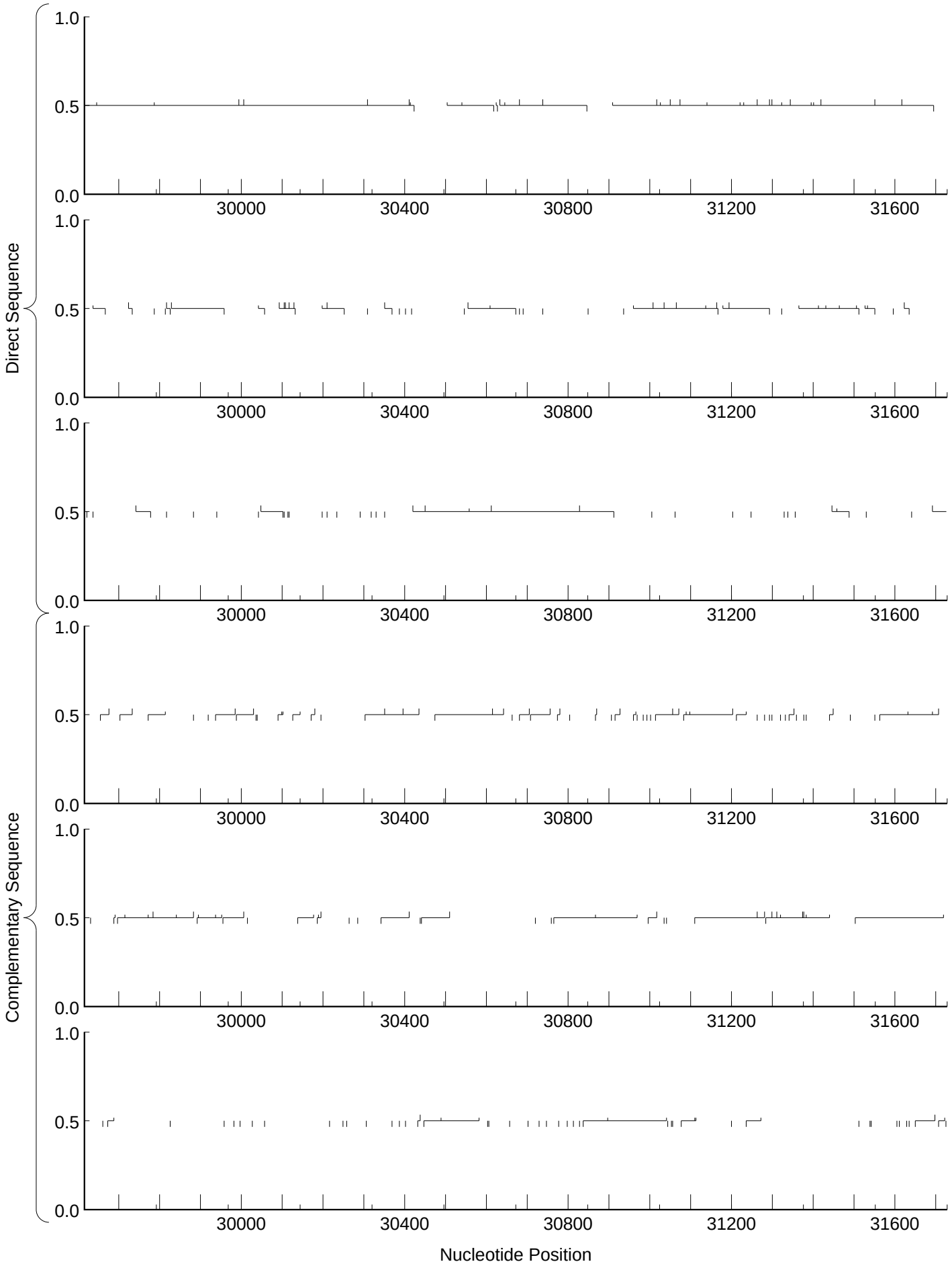

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Complementary Sequence
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22000
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22800
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Nucleotide Position

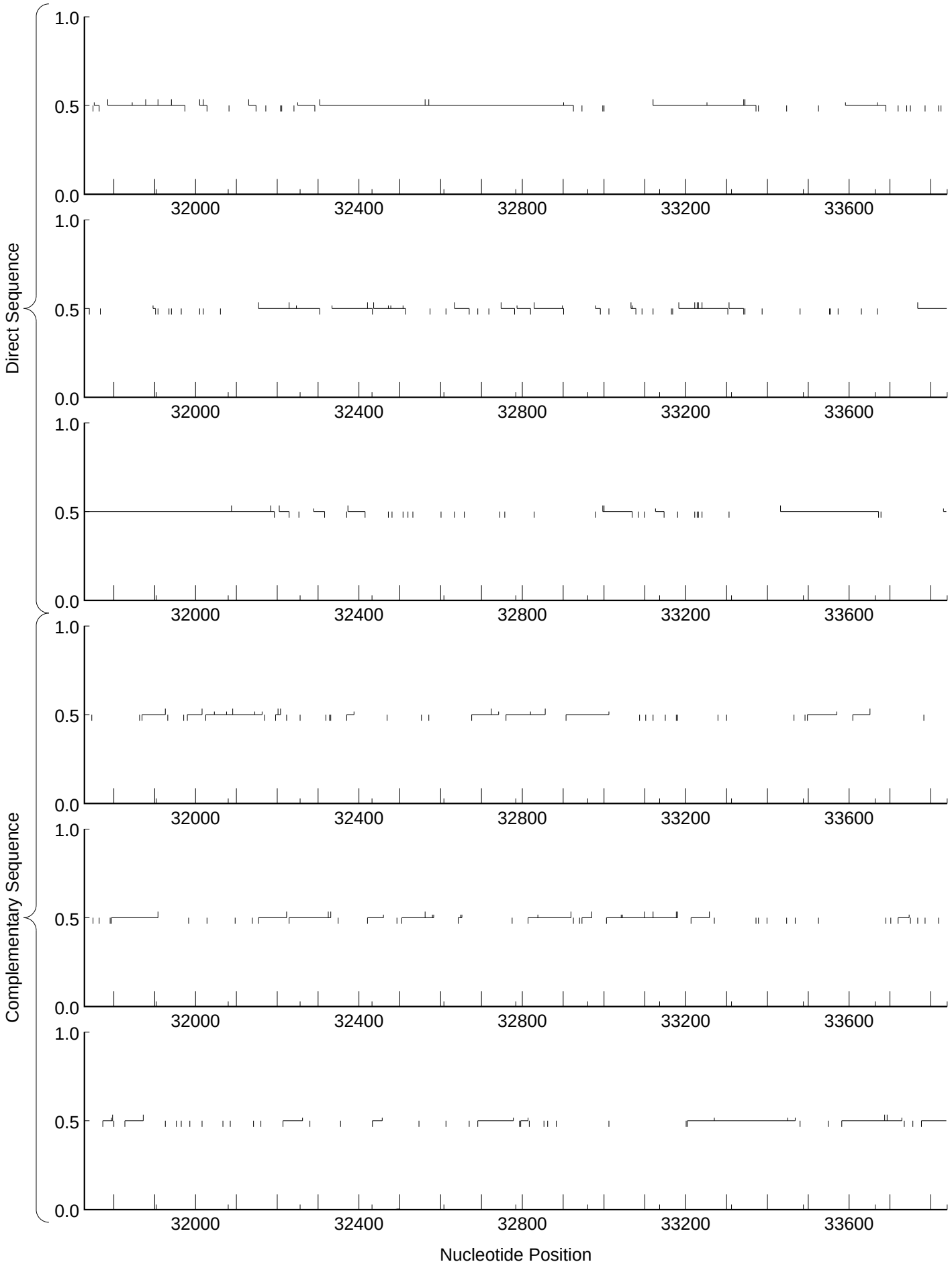

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Complementary Sequence
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Nucleotide Position

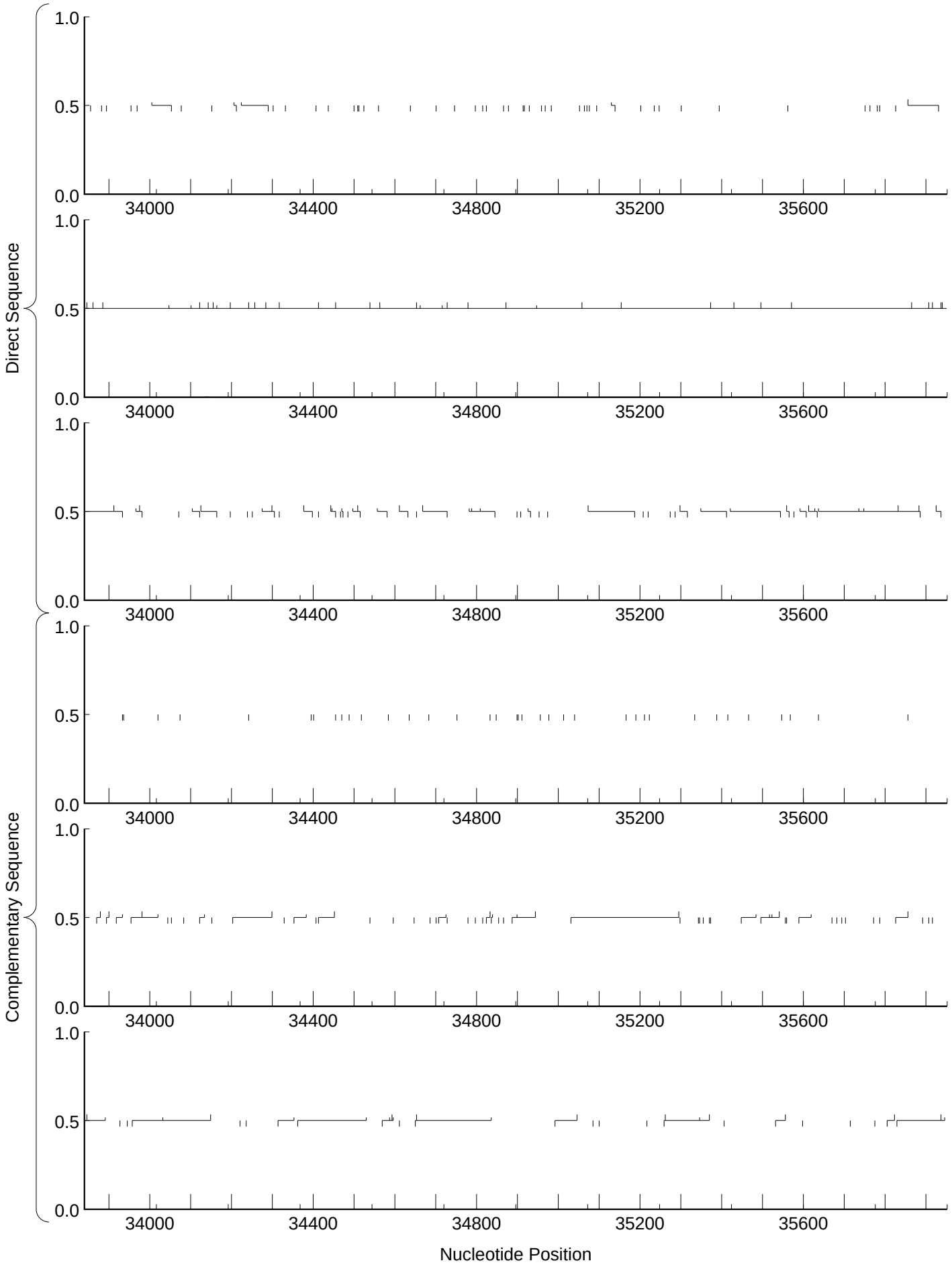

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Complementary Sequence
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Nucleotide Position

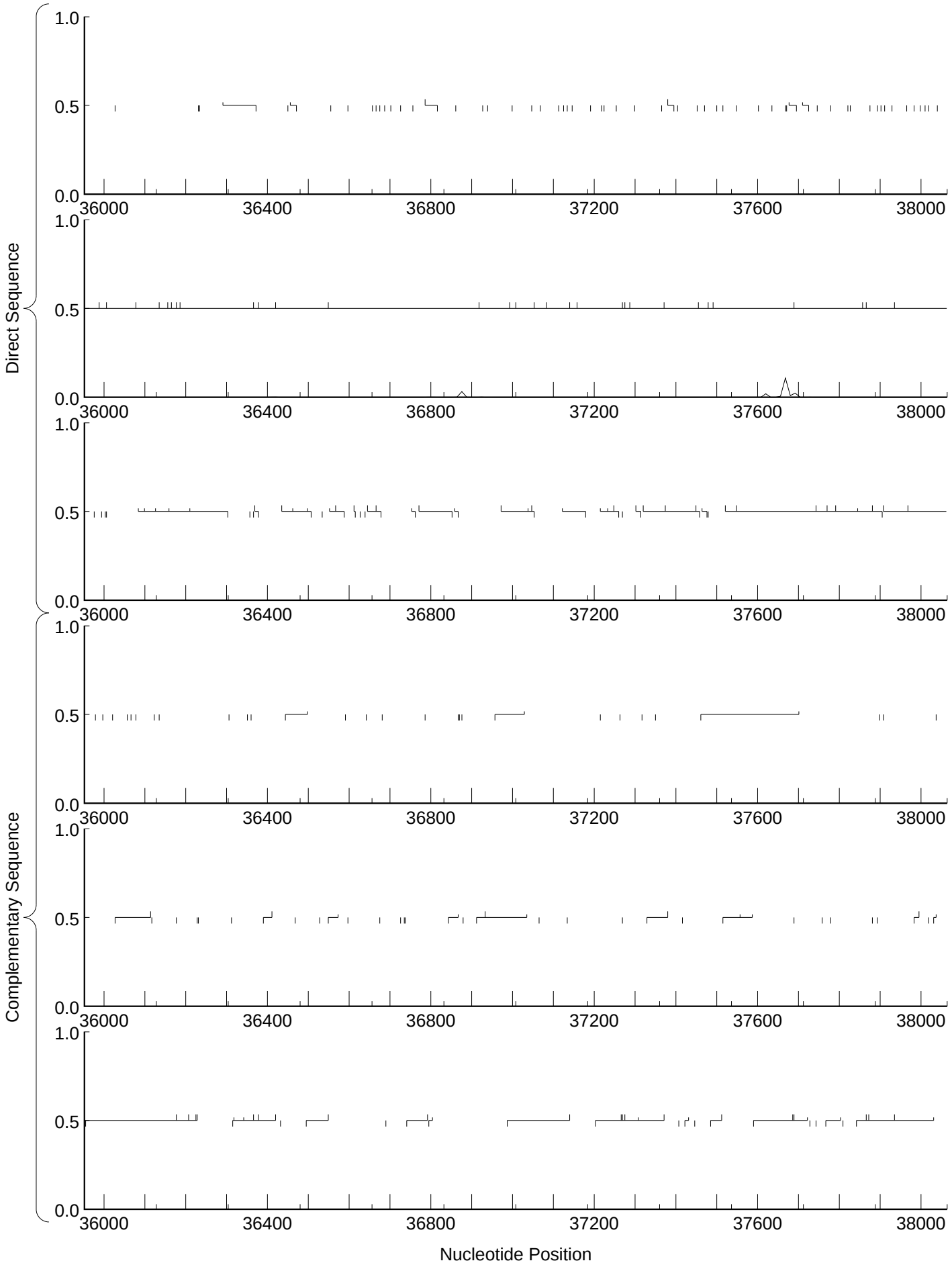
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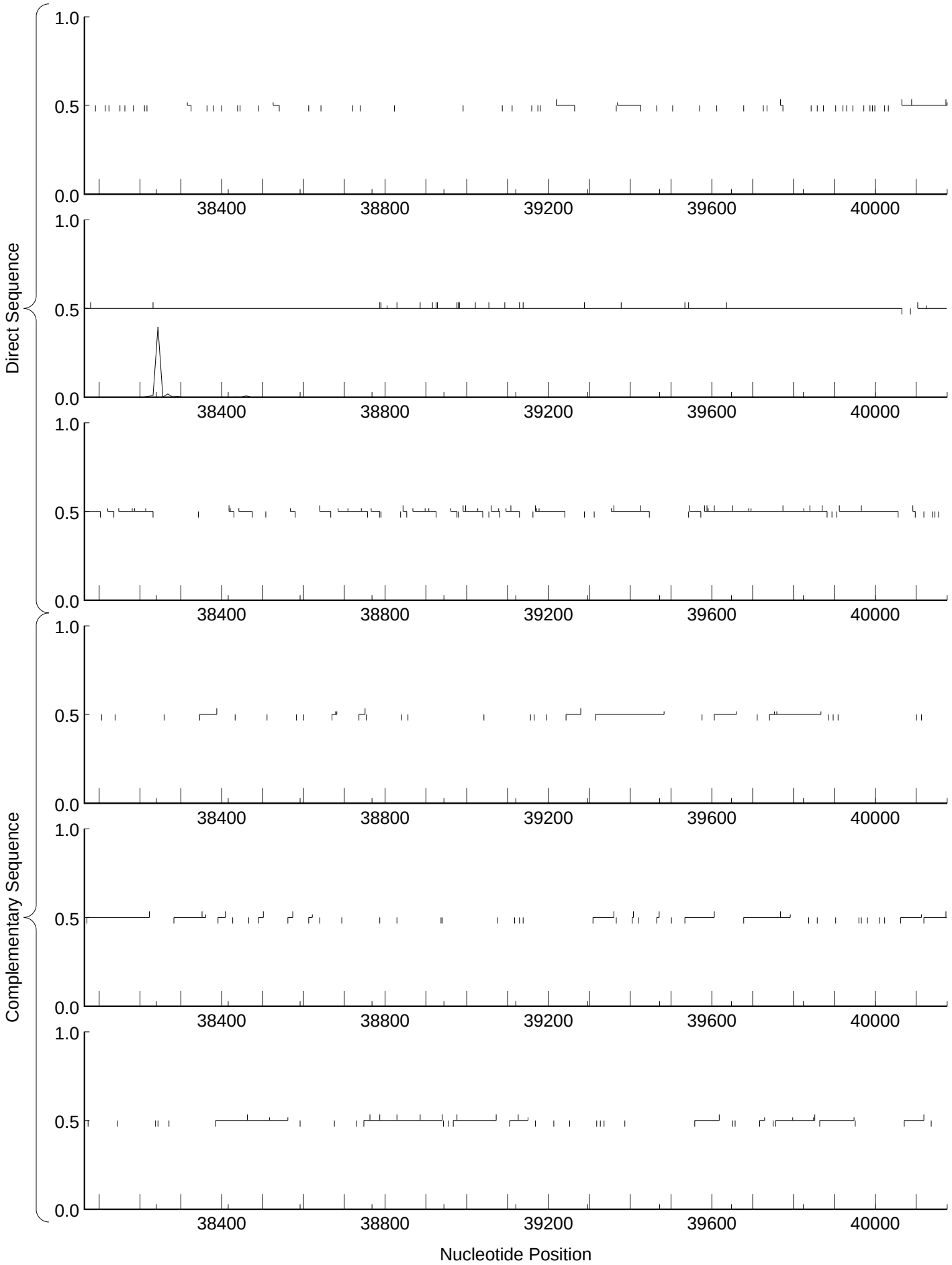


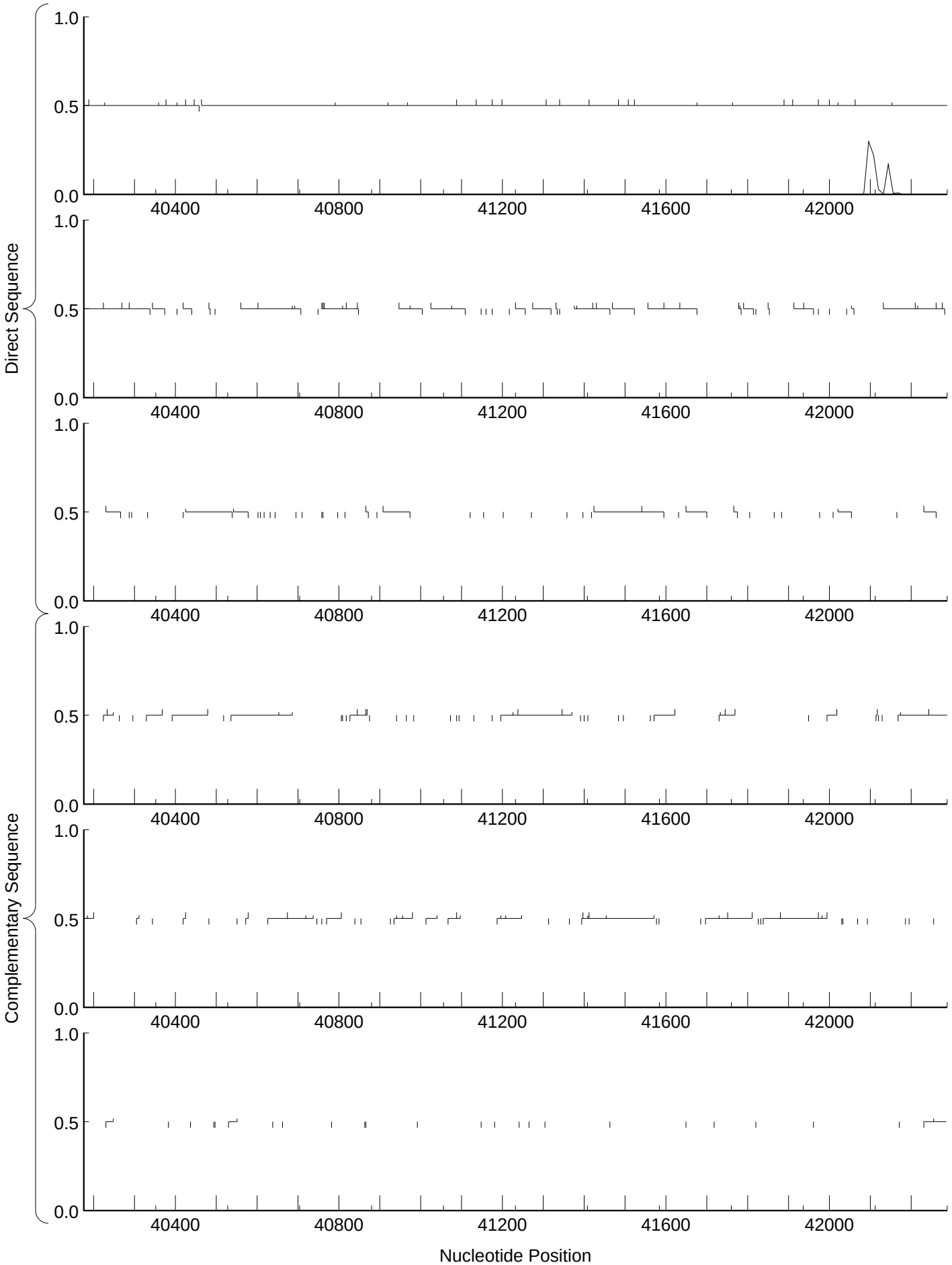

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Complementary Sequence
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Nucleotide Position

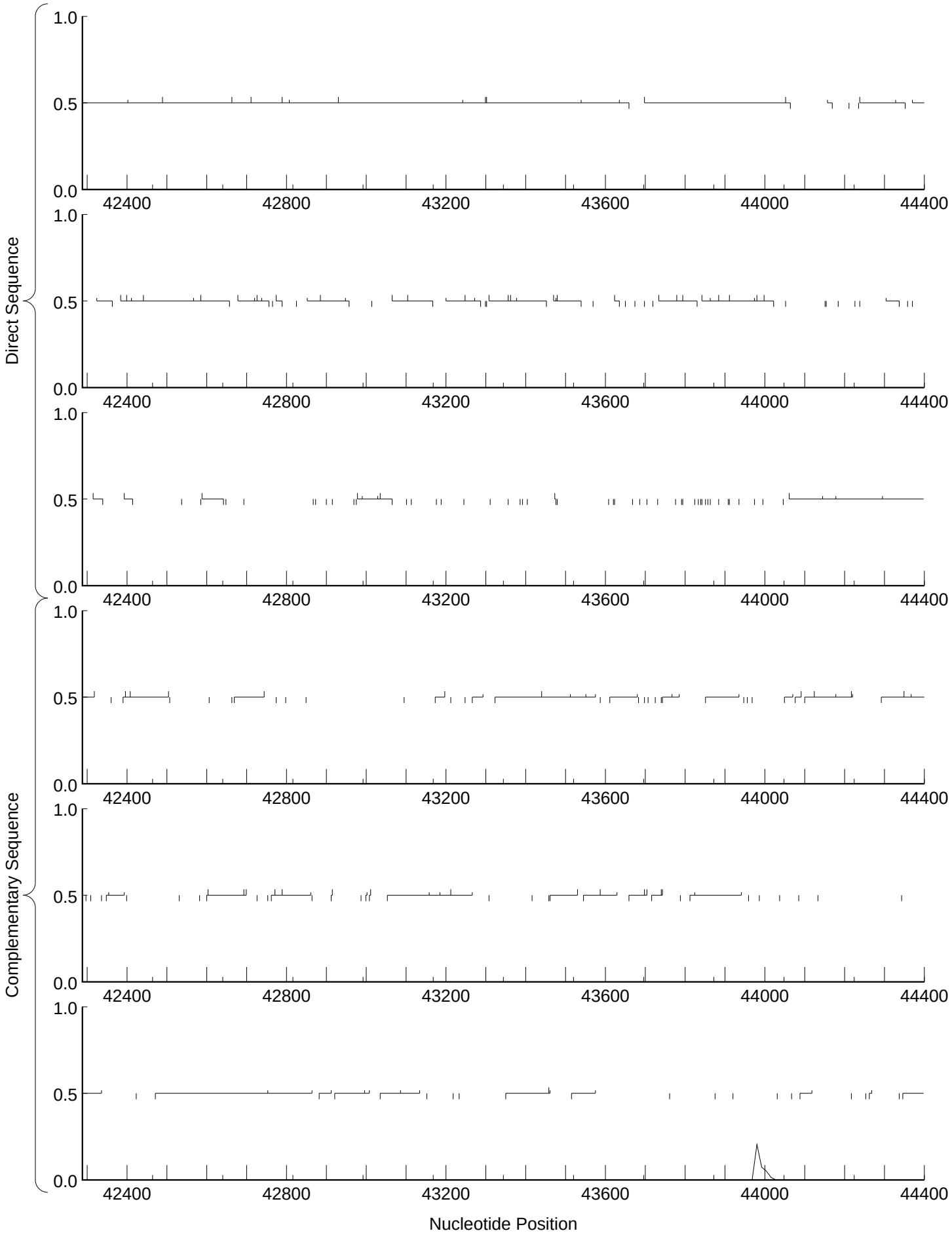

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Complementary Sequence
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33200
33600
Nucleotide Position

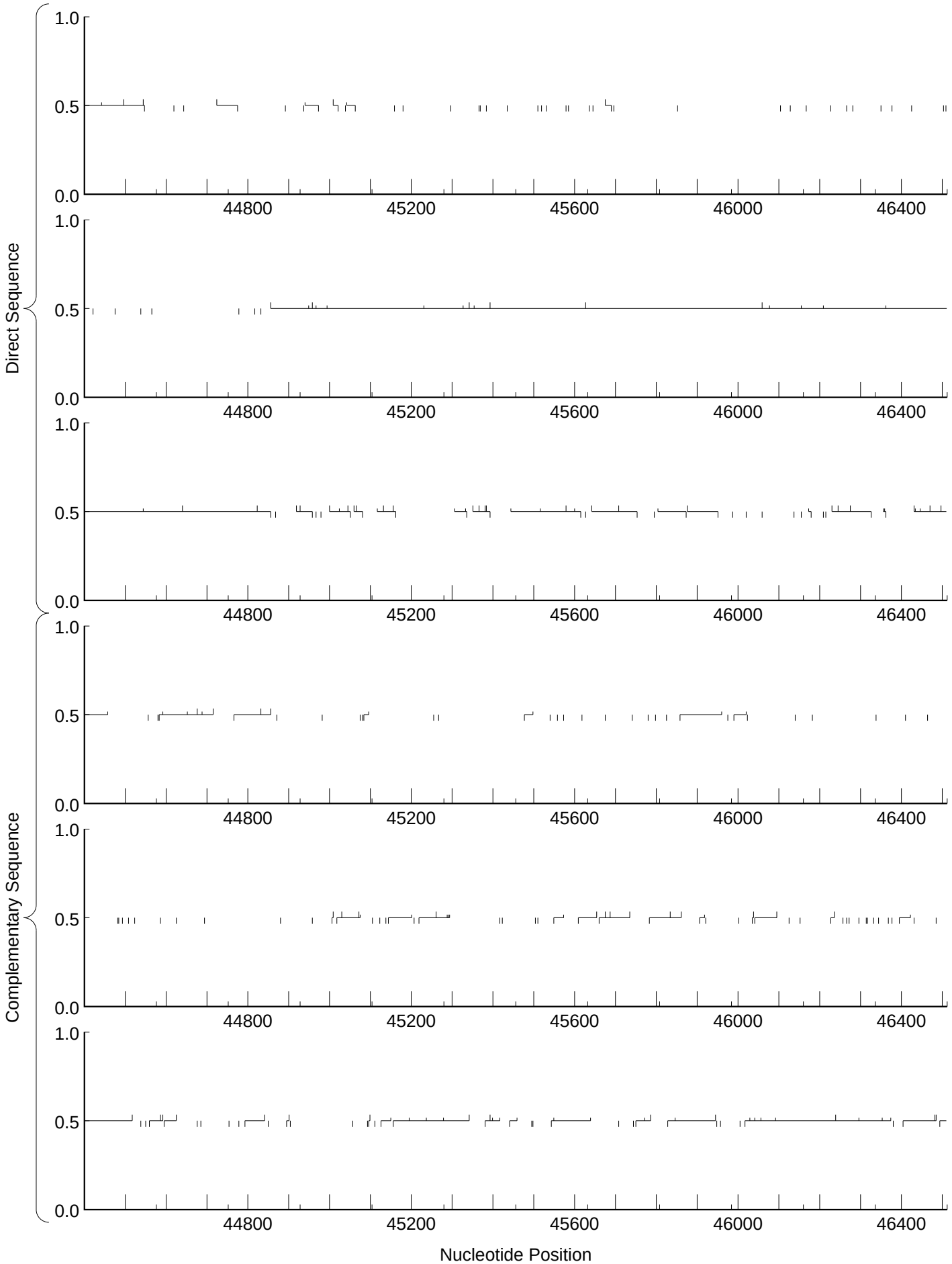

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Complementary Sequence
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35200
35600
Nucleotide Position

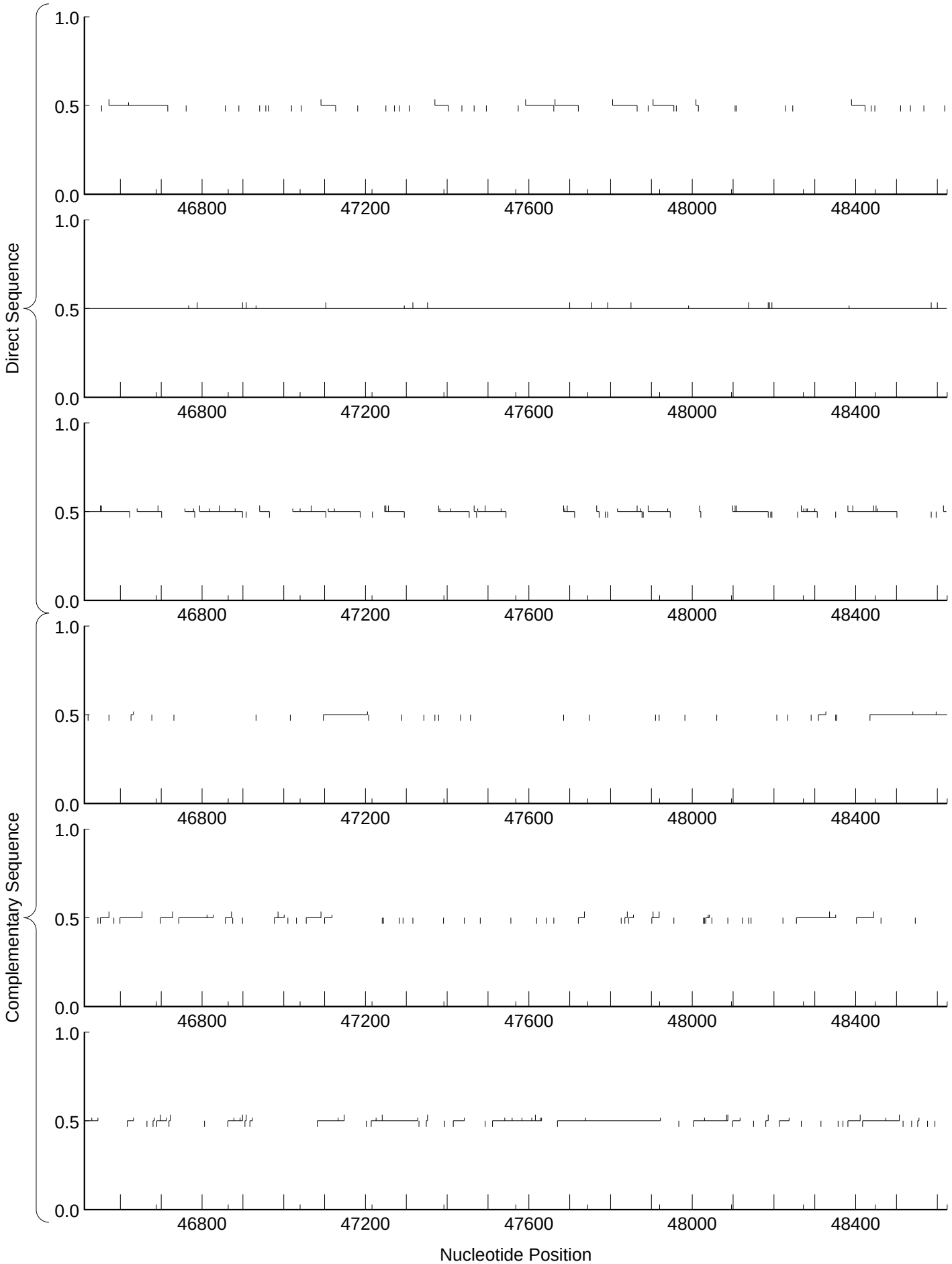

Direct Sequence
Complementary Sequence
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36800
37200
37600
38000
Nucleotide Position


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

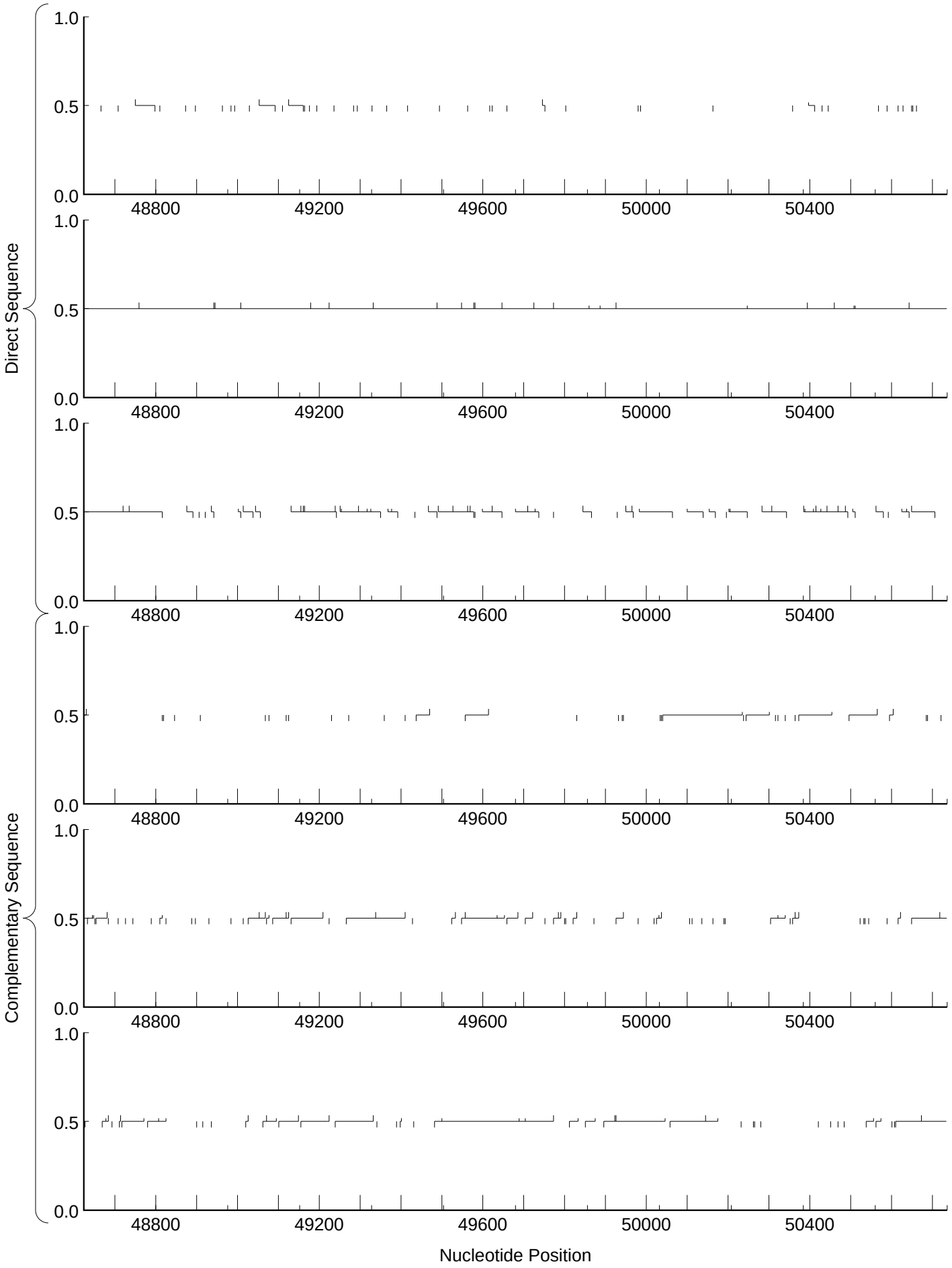

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Complementary Sequence
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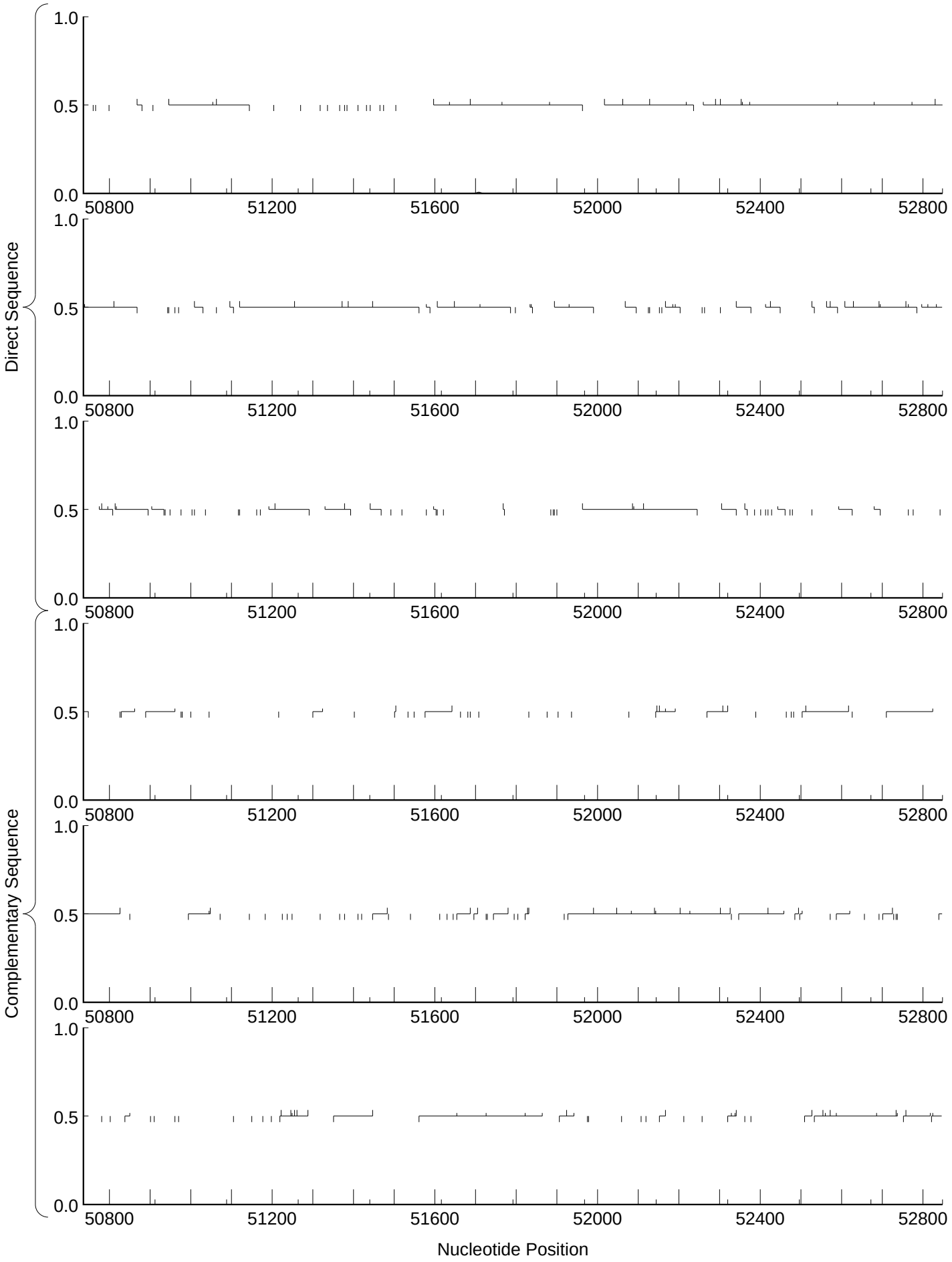

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Nucleotide Position

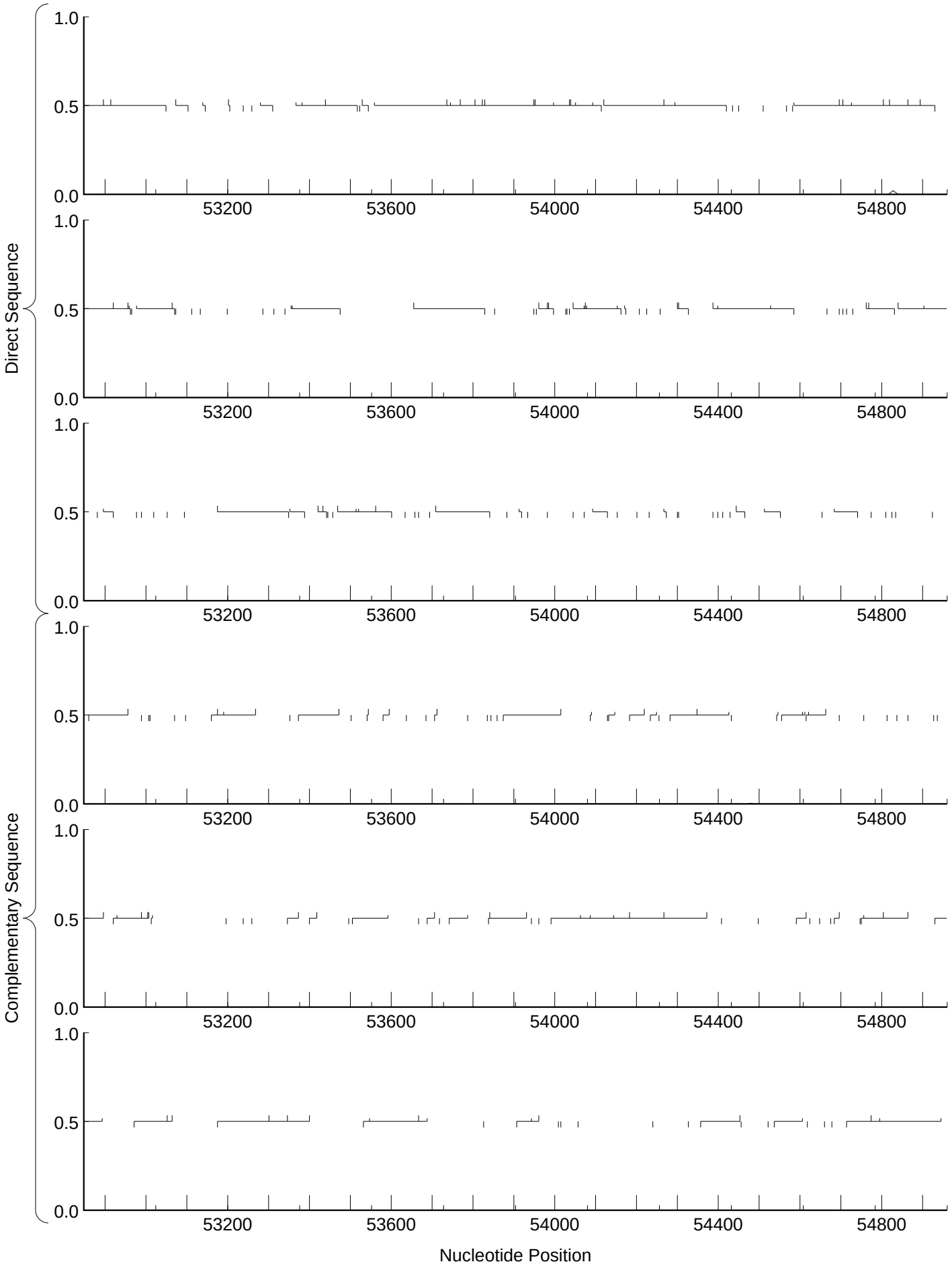

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Complementary Sequence
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46000
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Nucleotide Position

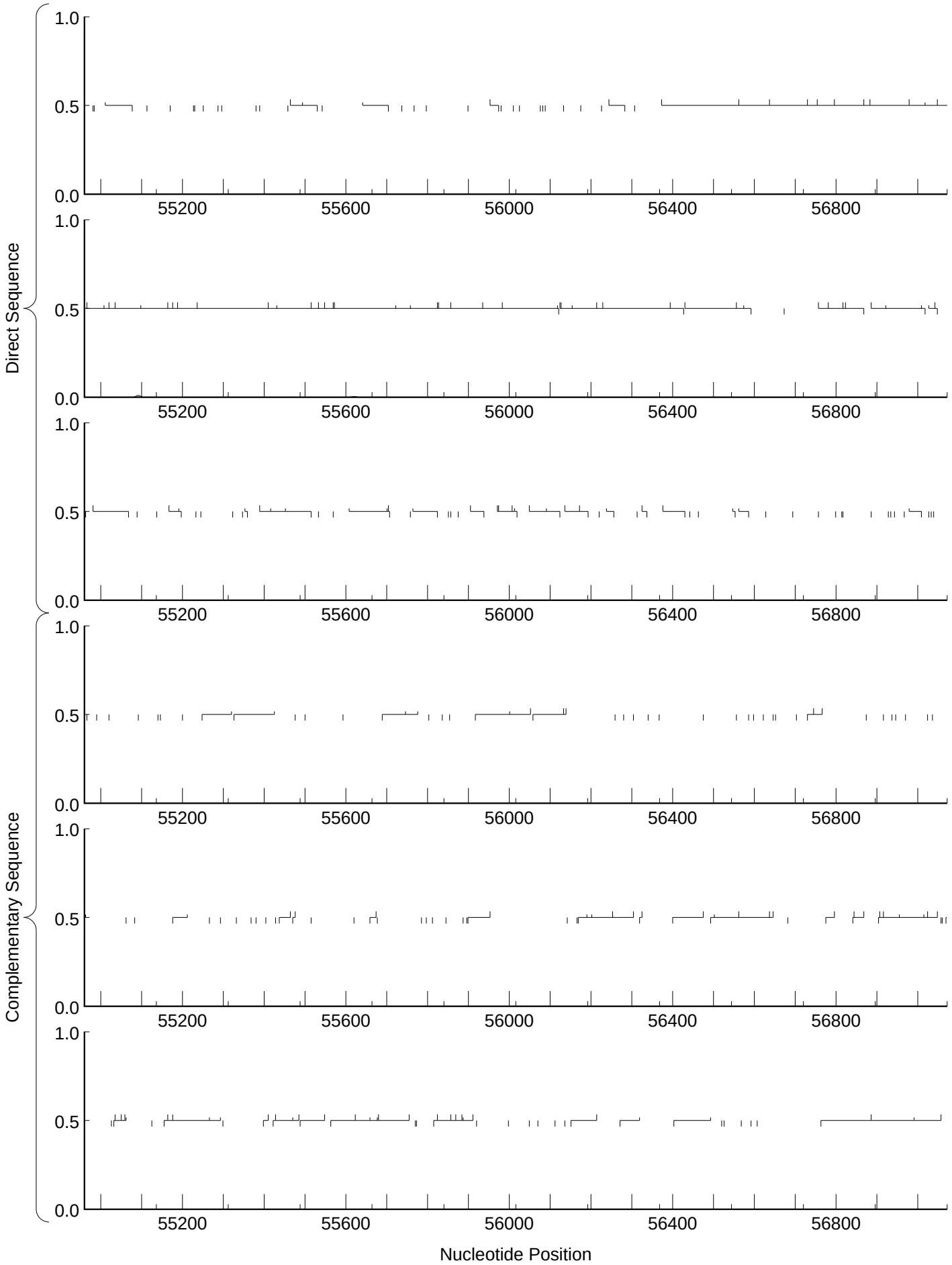

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48000
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Nucleotide Position

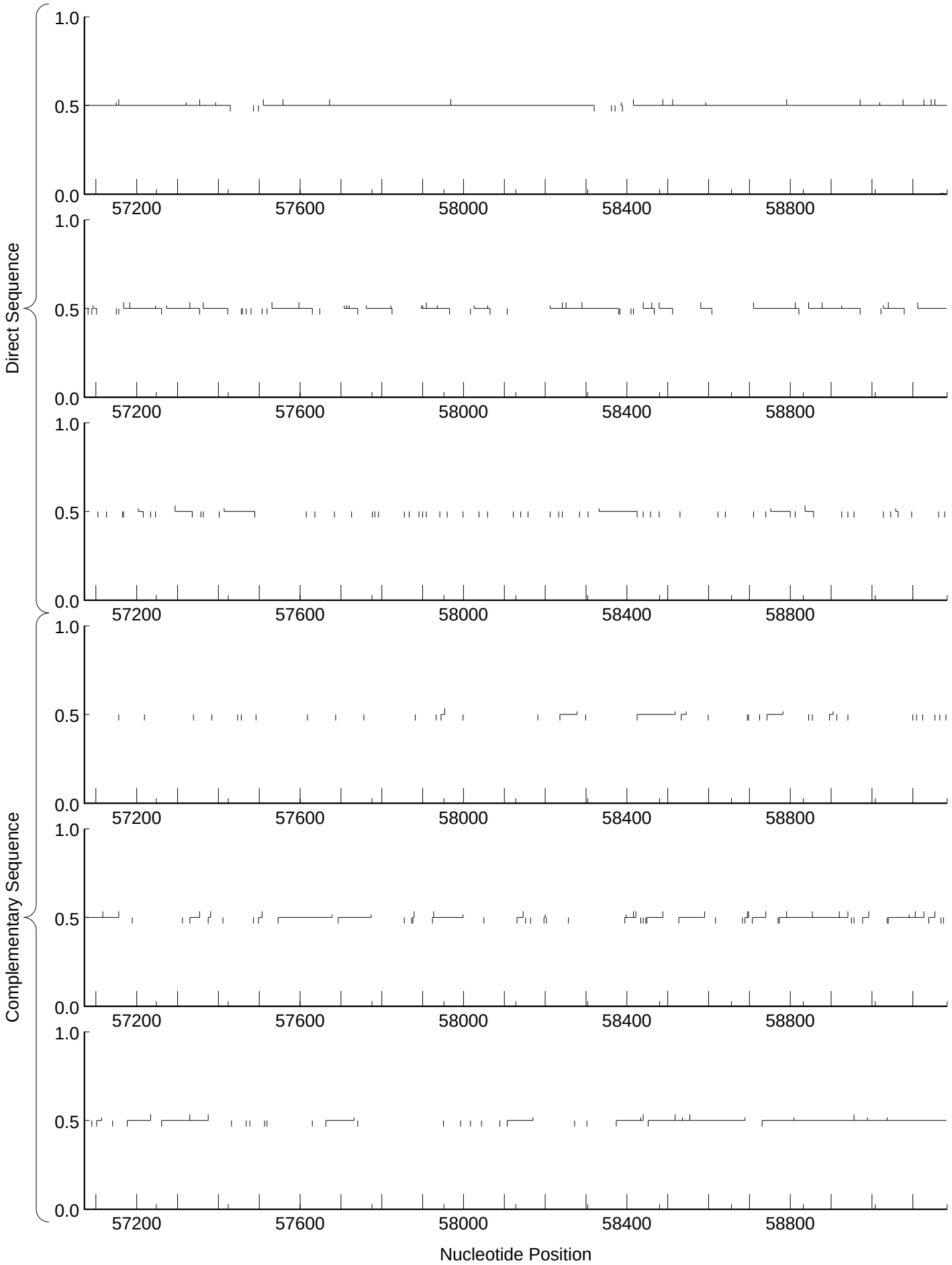
age Battuta complete sequence, 130734 bp including 12579 bp terminal repeat, Cluster BE2, Order 4, Window 96, Step 12, 25/63

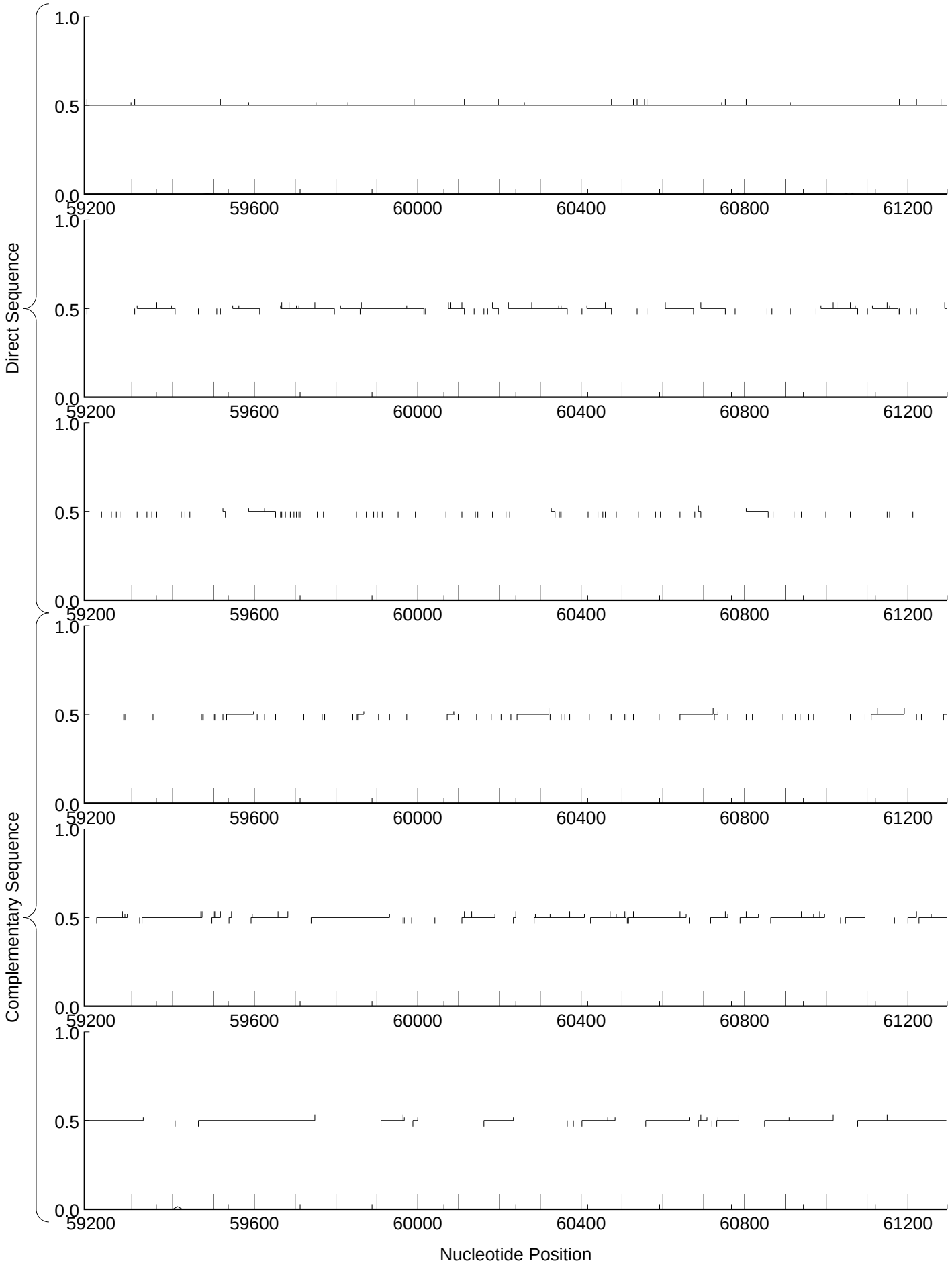


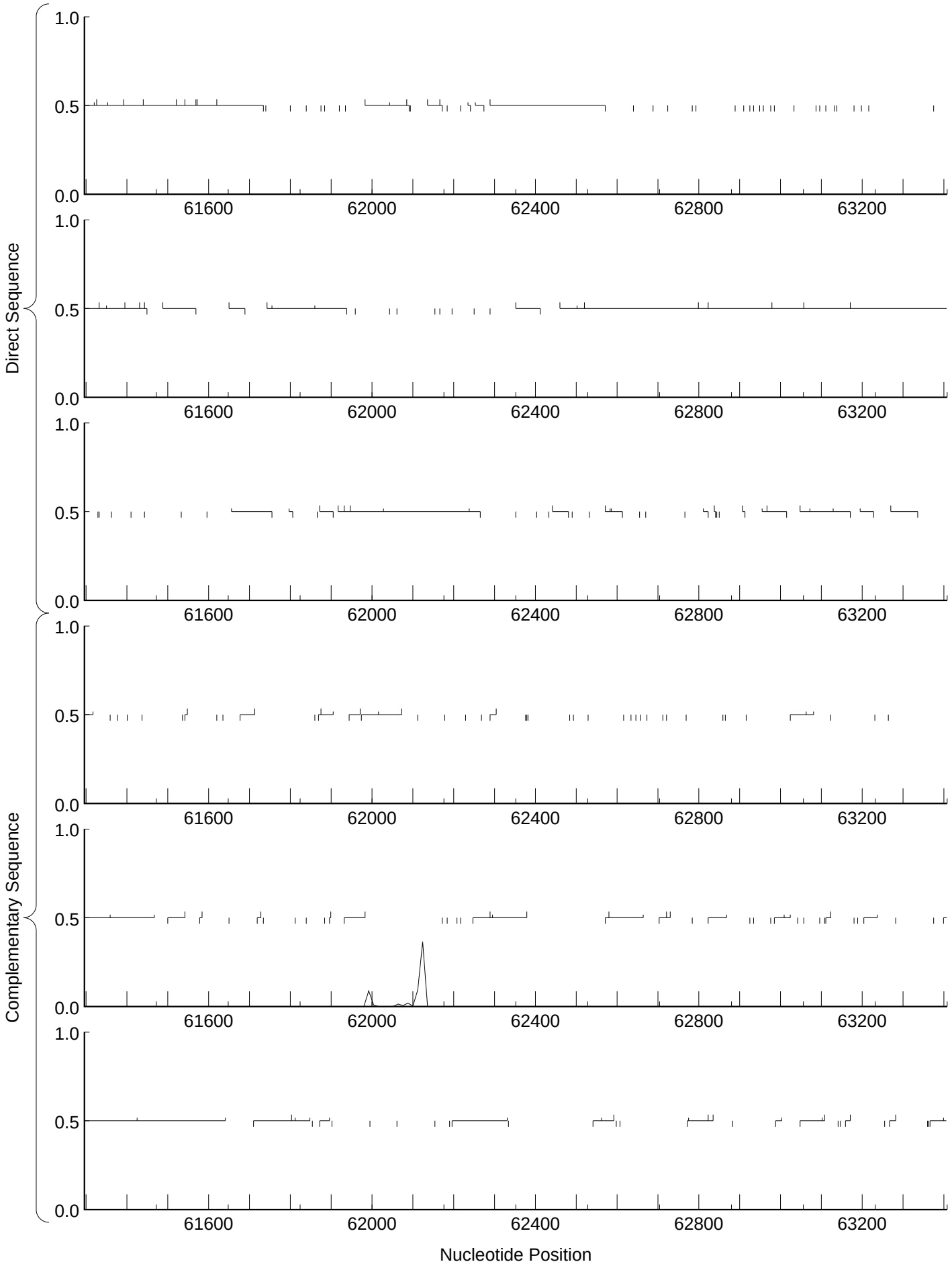

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Nucleotide Position

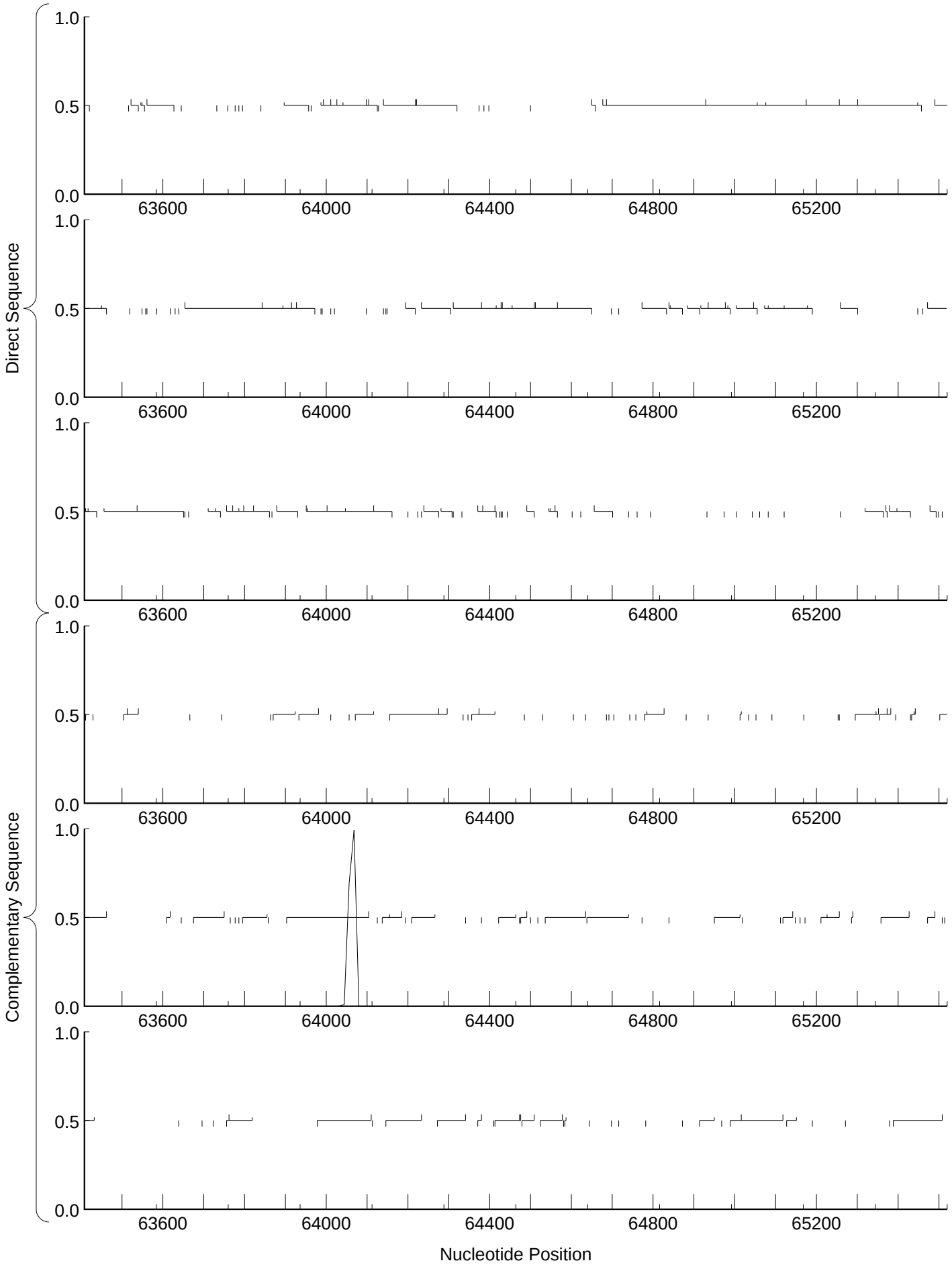

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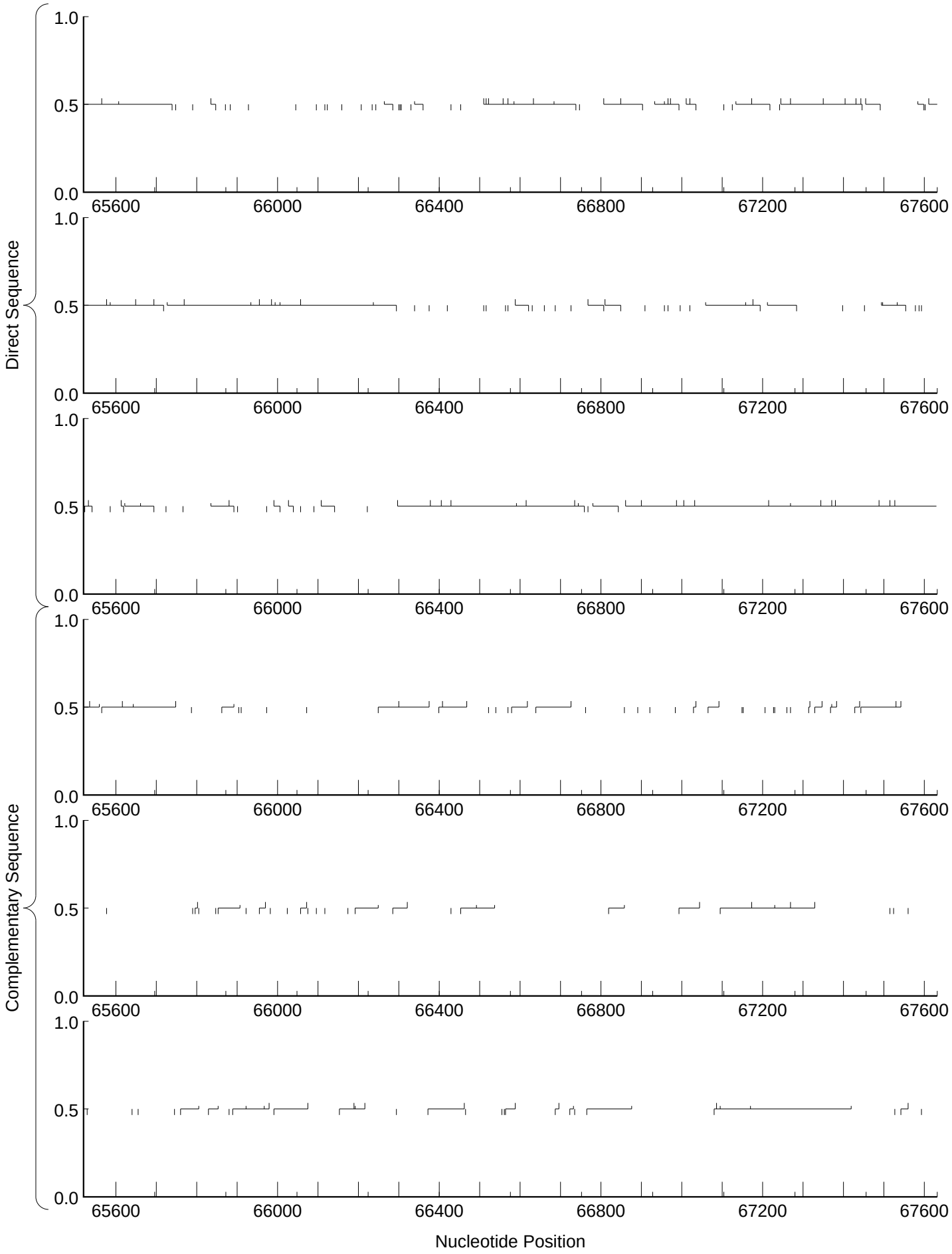

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Nucleotide Position

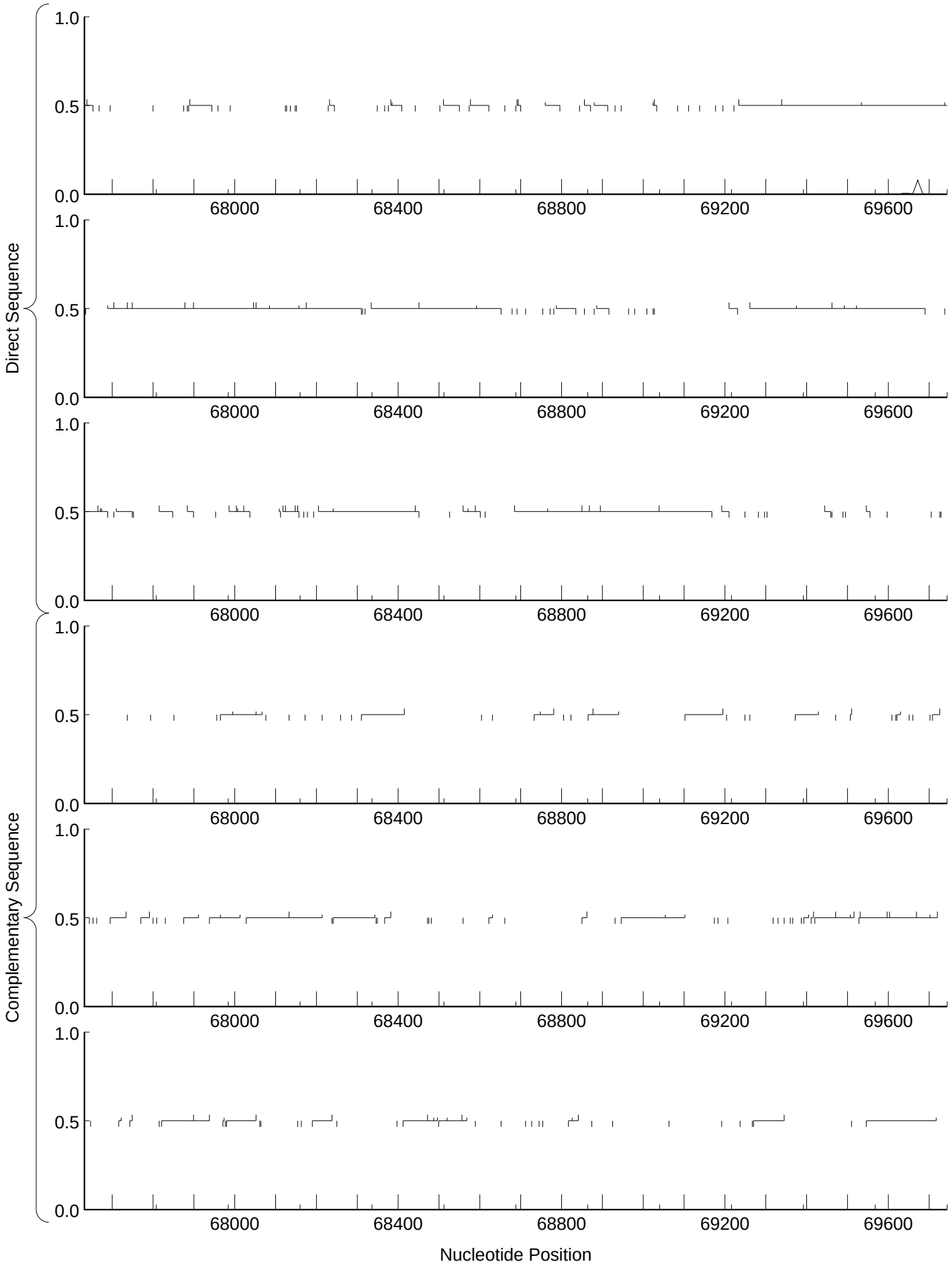

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Nucleotide Position

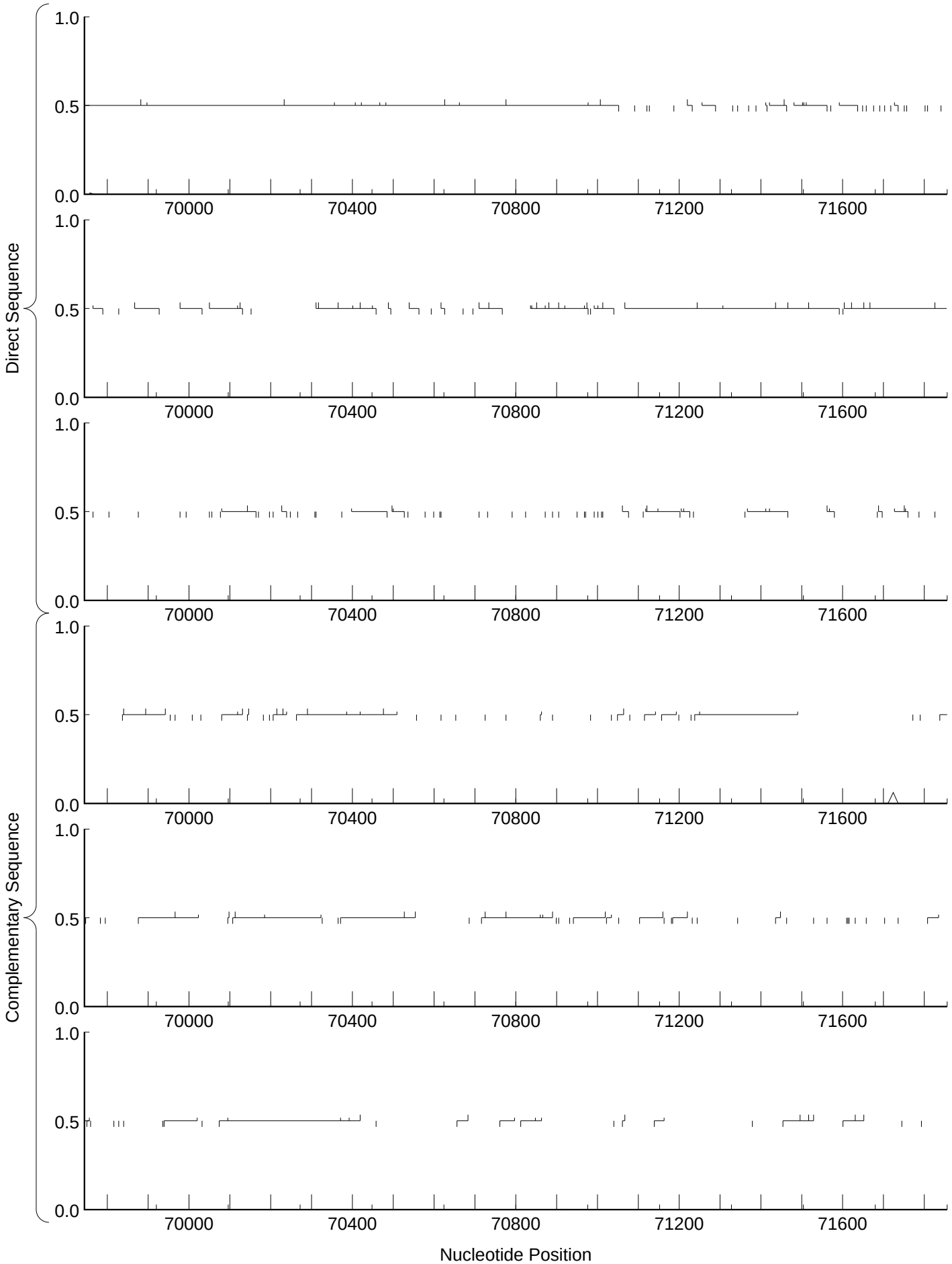

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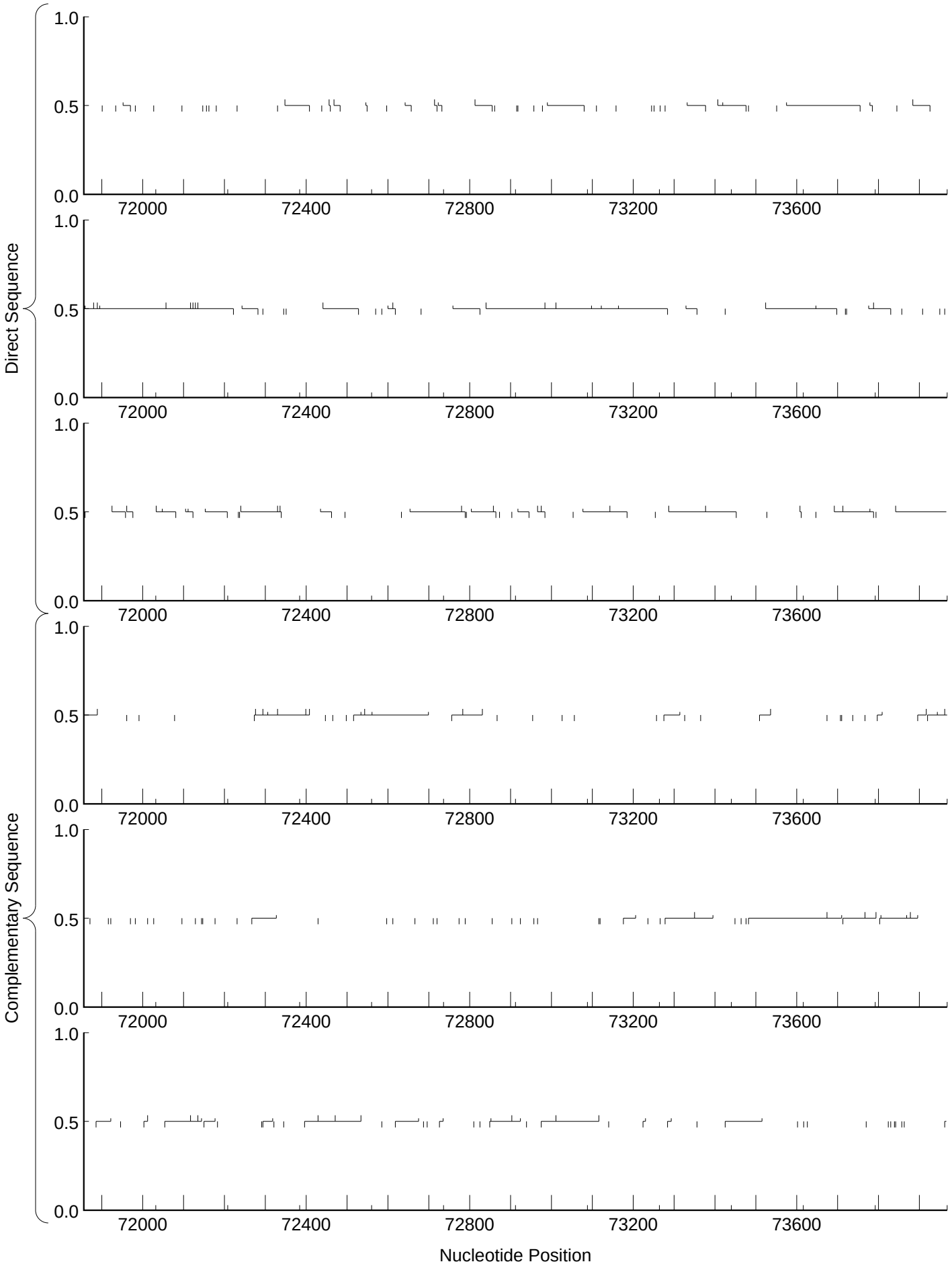

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Complementary Sequence
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Nucleotide Position

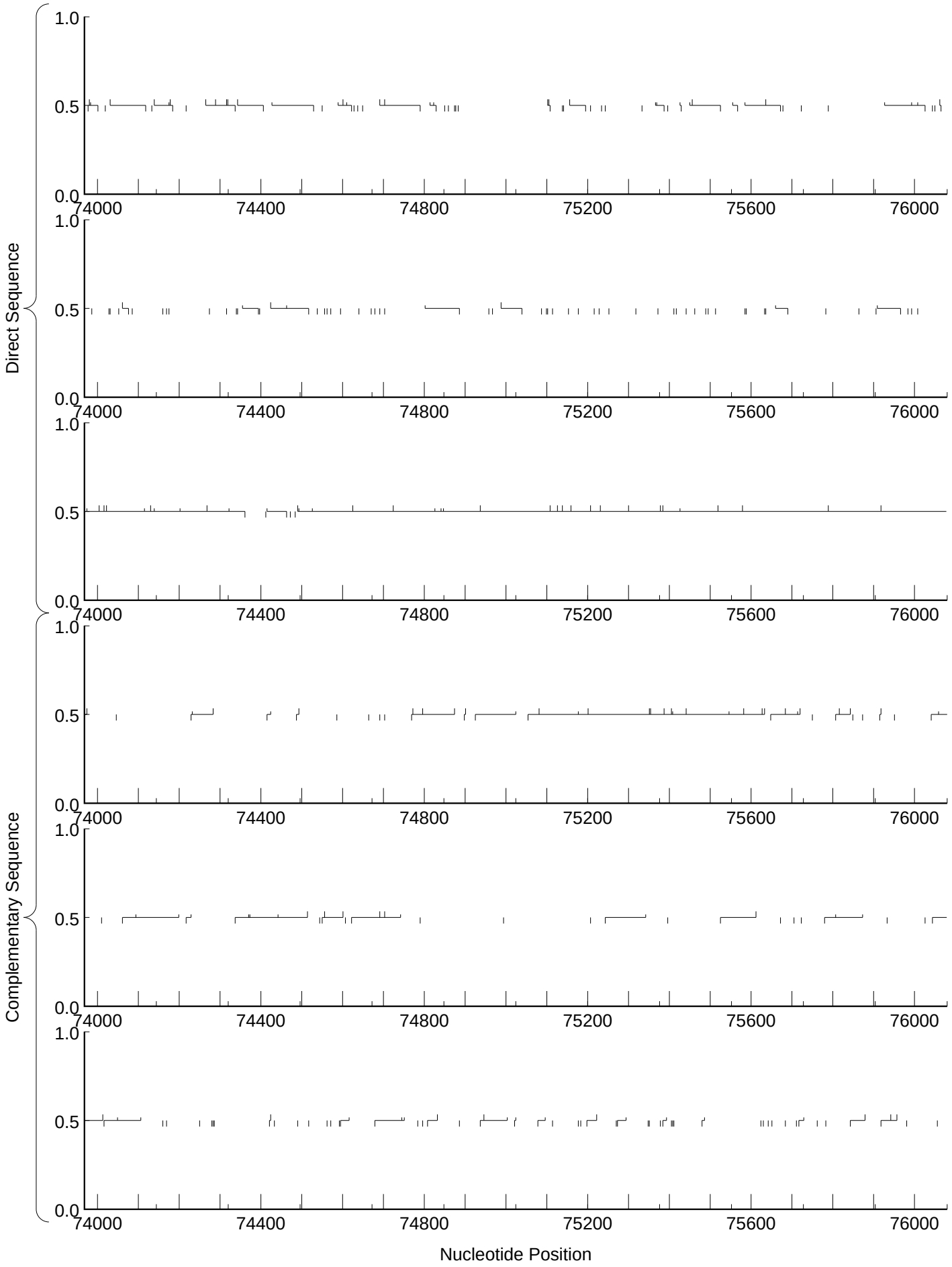

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Nucleotide Position

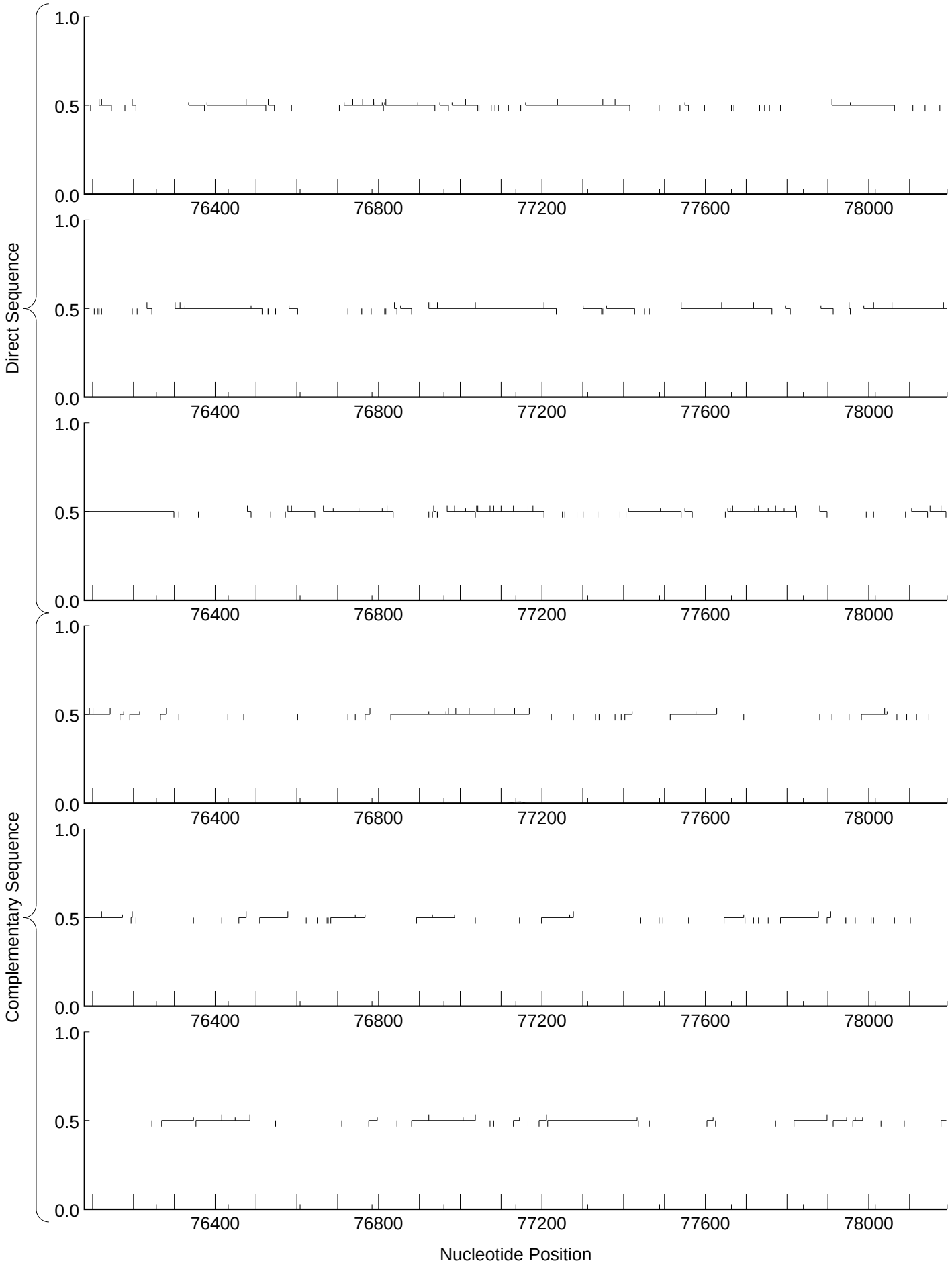

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Nucleotide Position

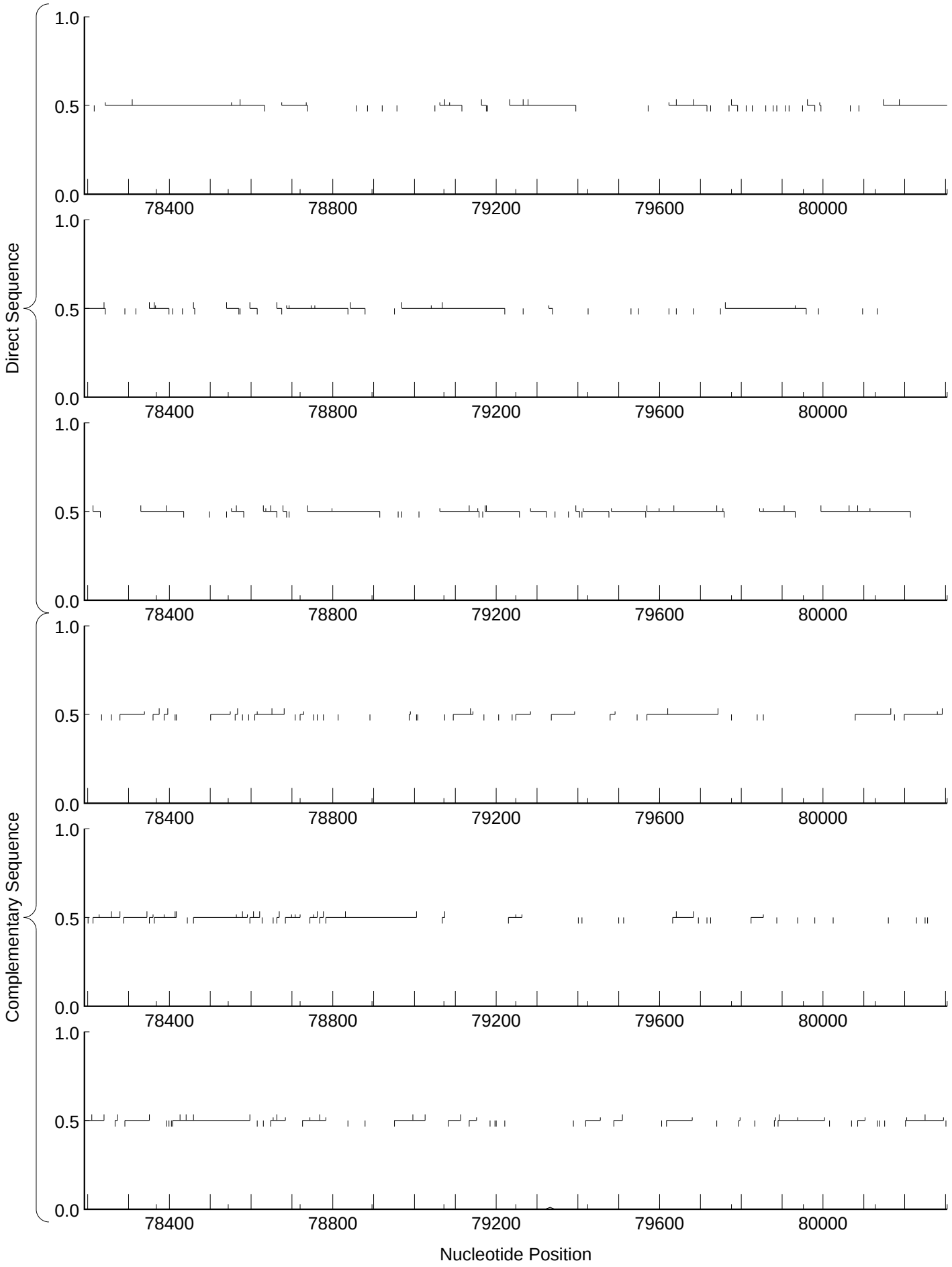

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Nucleotide Position

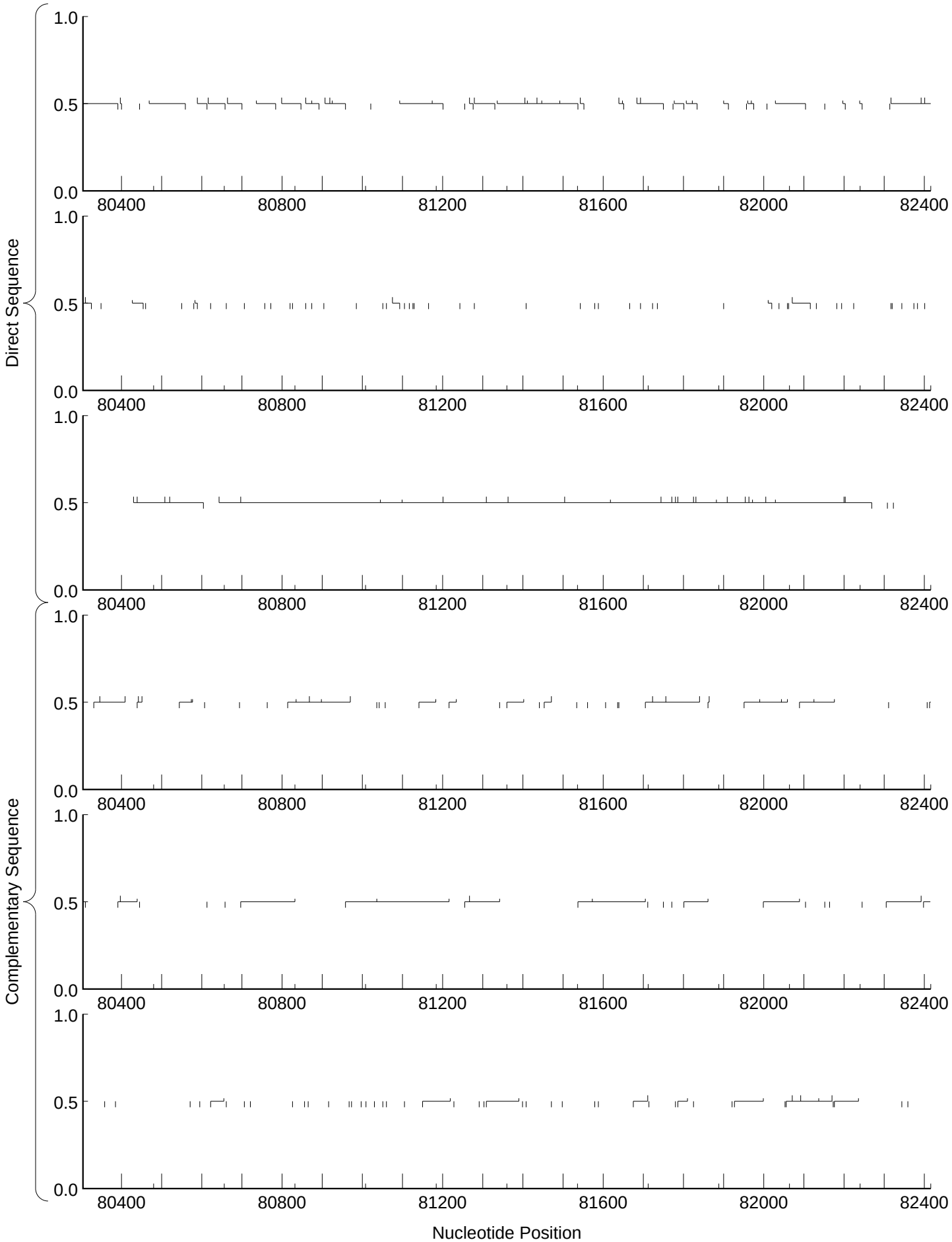

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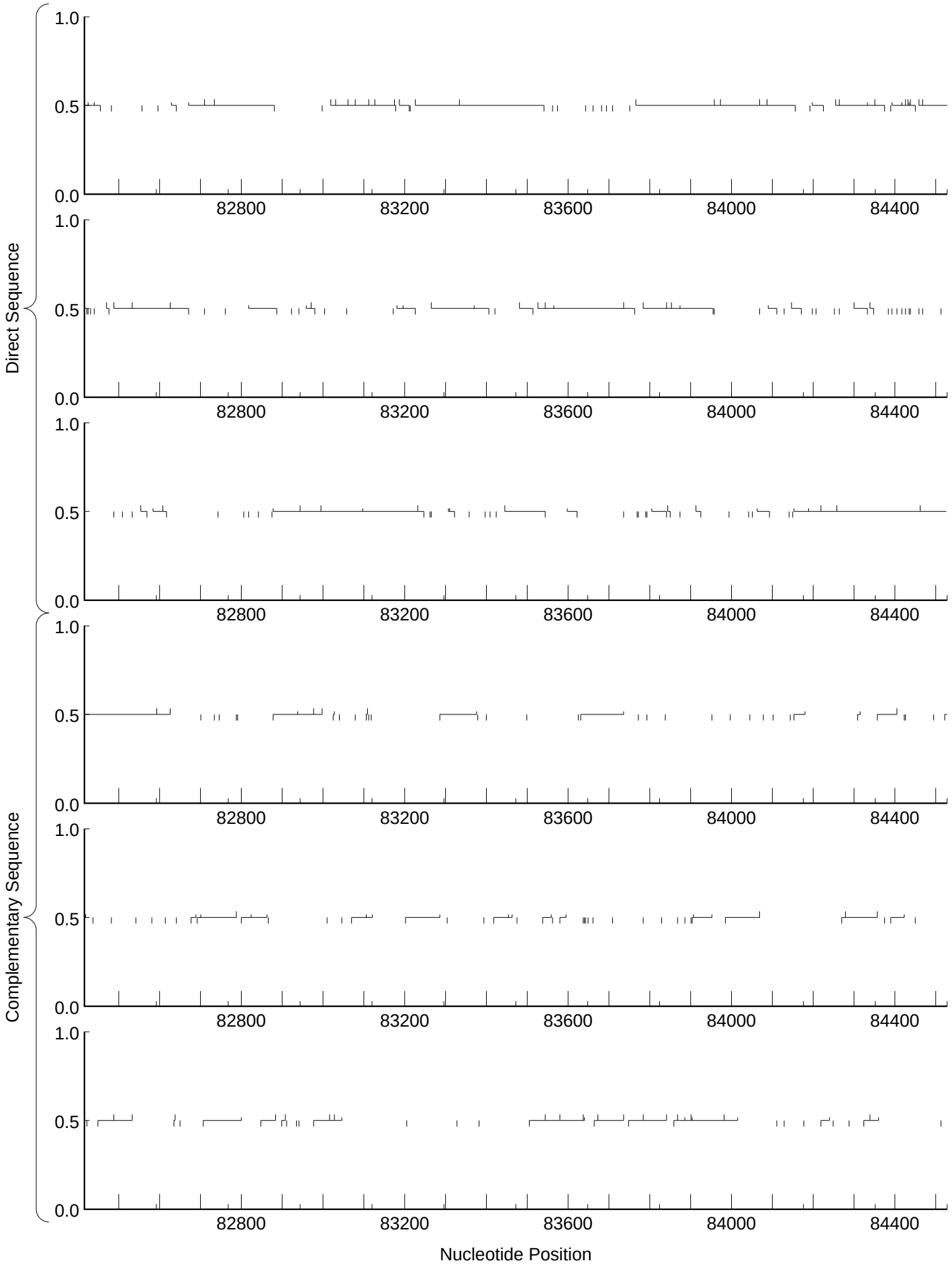

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Nucleotide Position

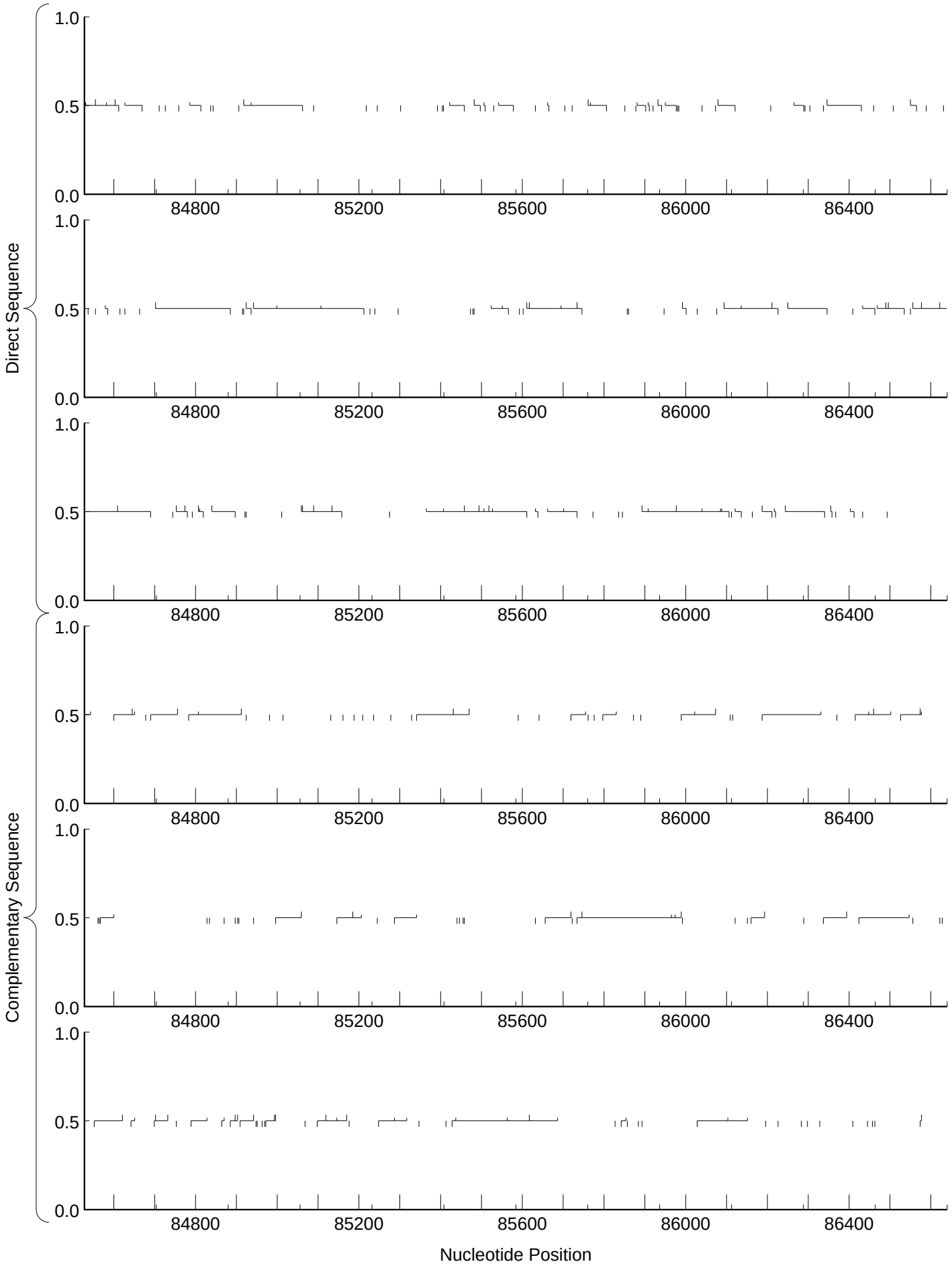

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Complementary Sequence
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74400
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Nucleotide Position

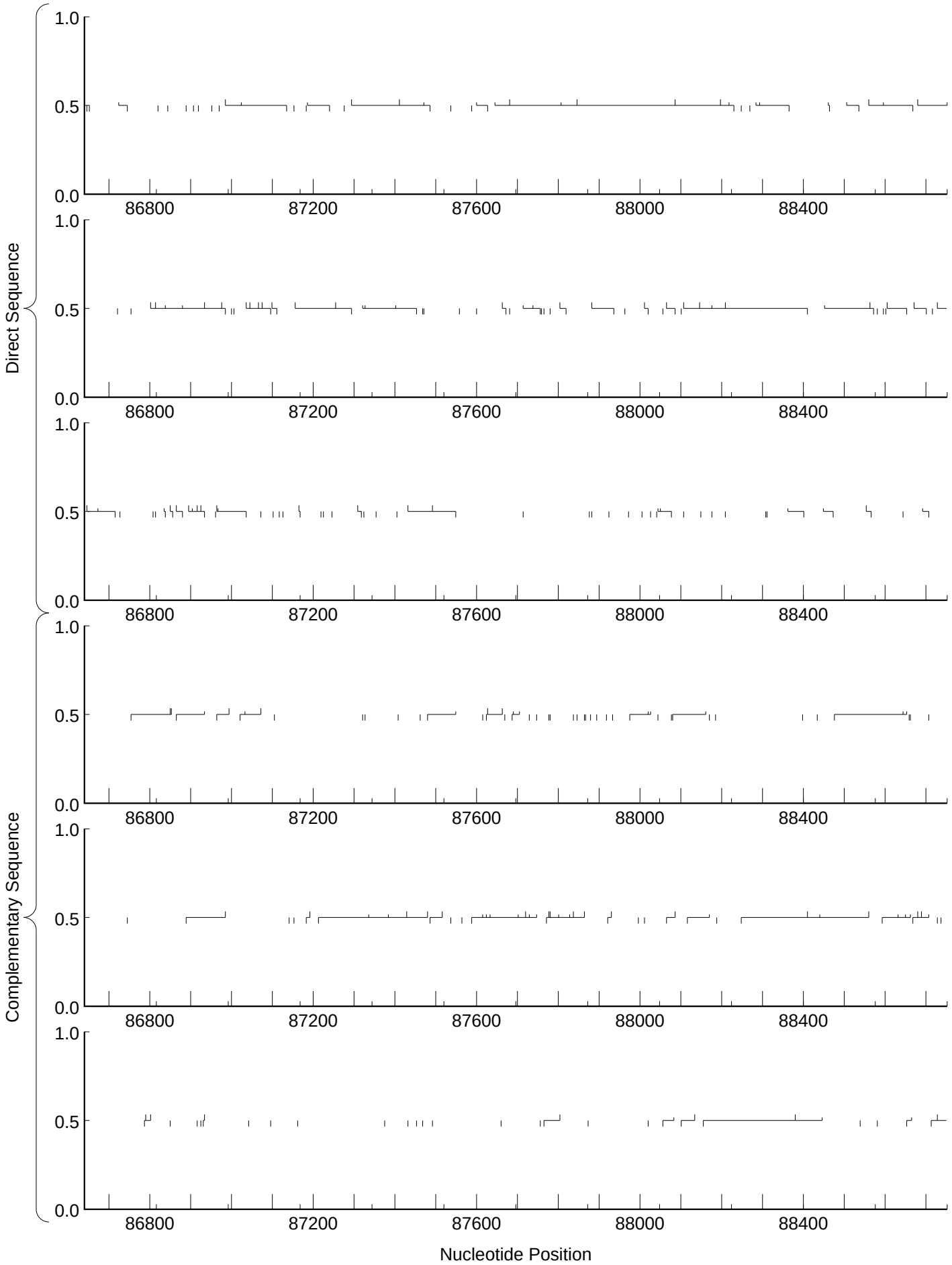

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Nucleotide Position

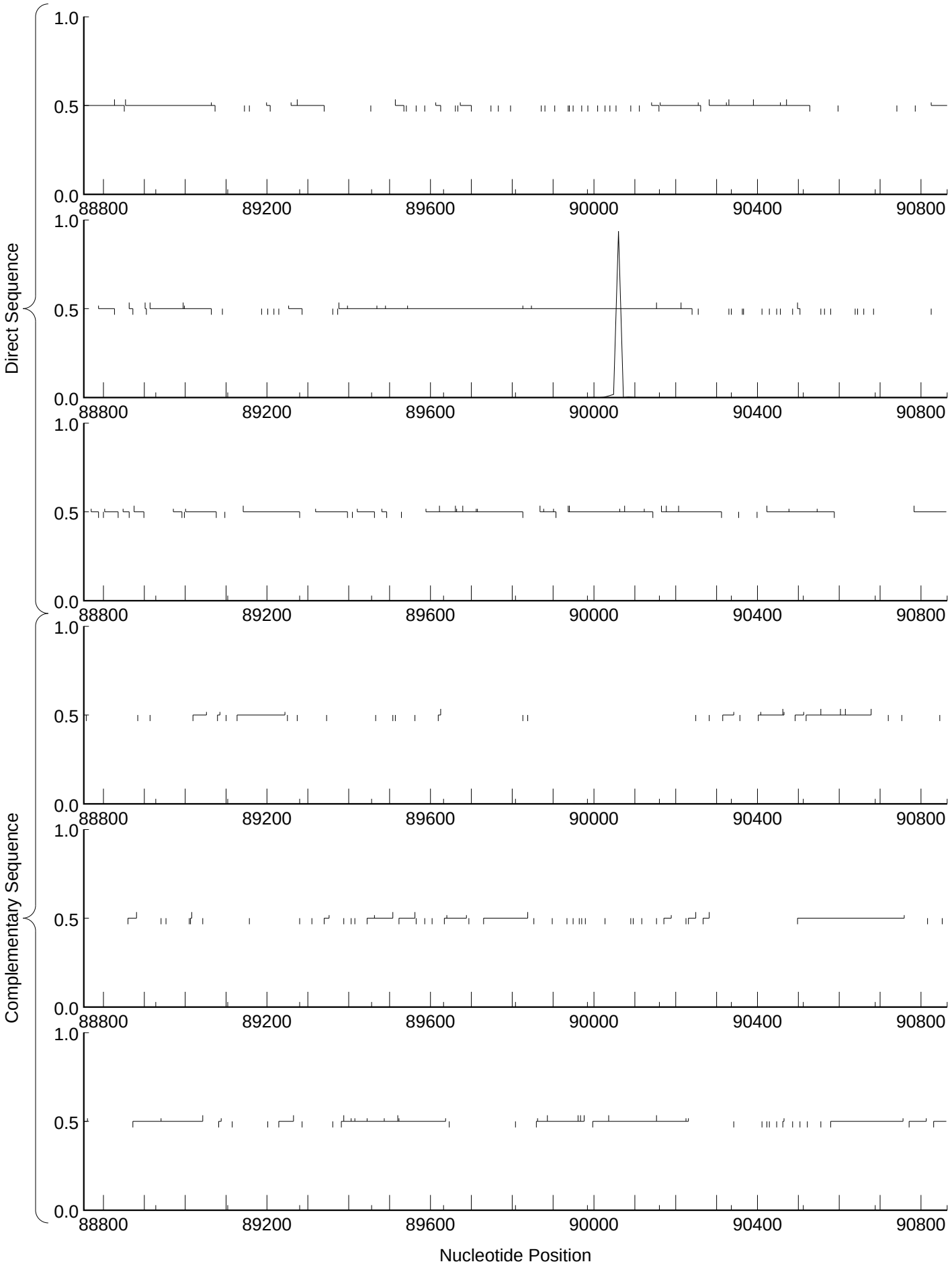

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Complementary Sequence
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80000
Nucleotide Position

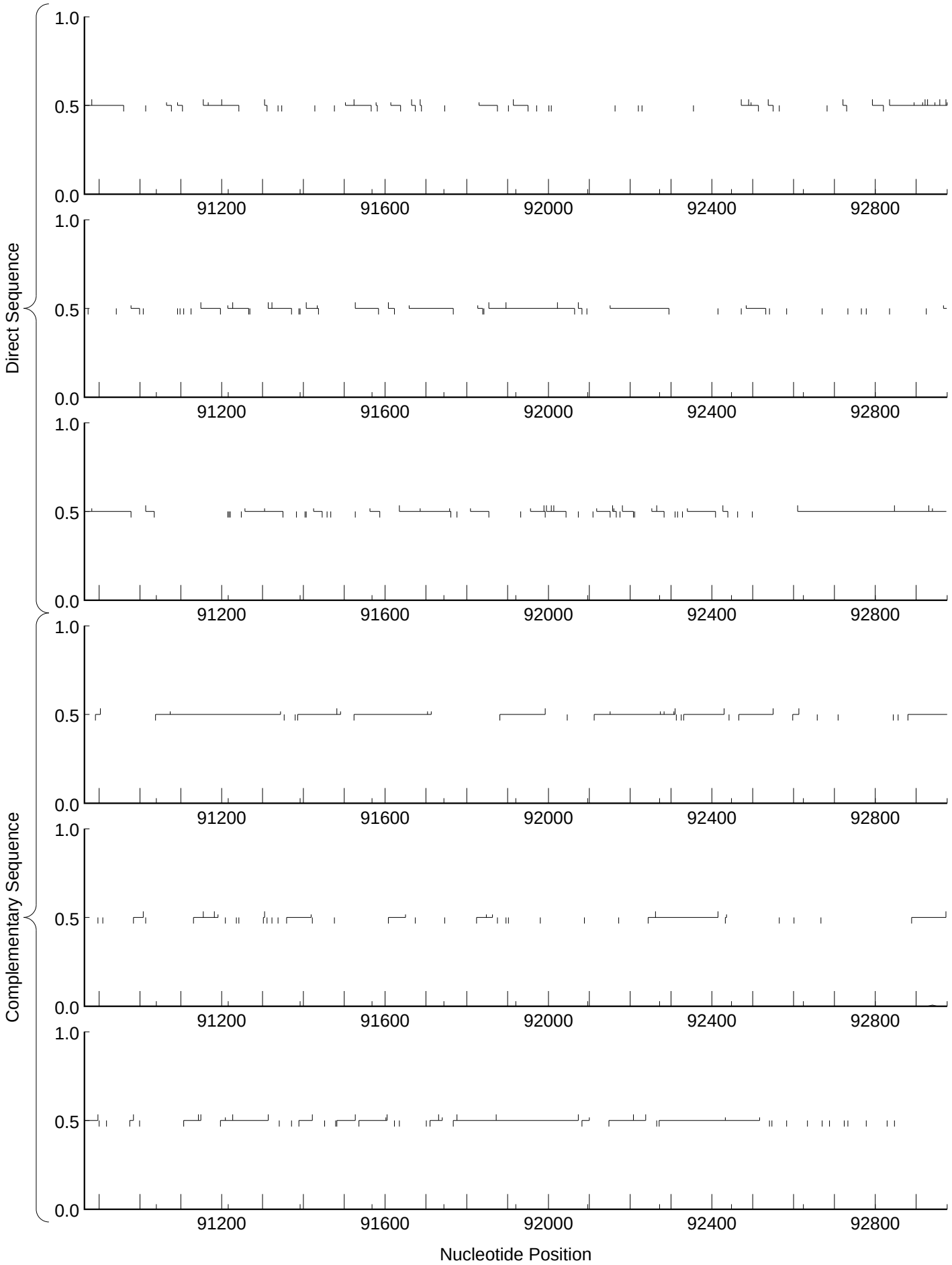

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
80400
80800
81200
81600
82000
82400
Nucleotide Position

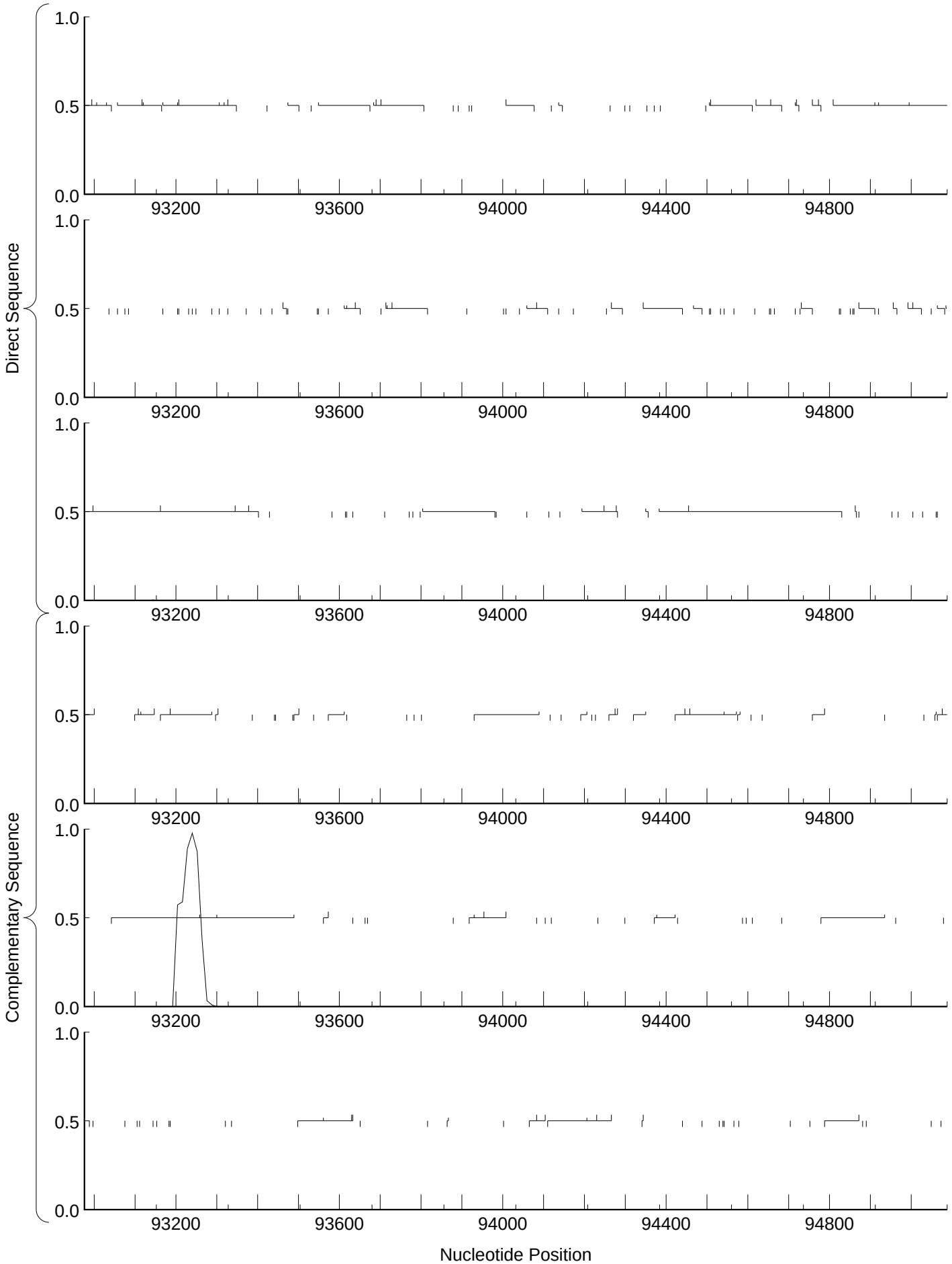

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
82800
83200
83600
84000
84400
Nucleotide Position

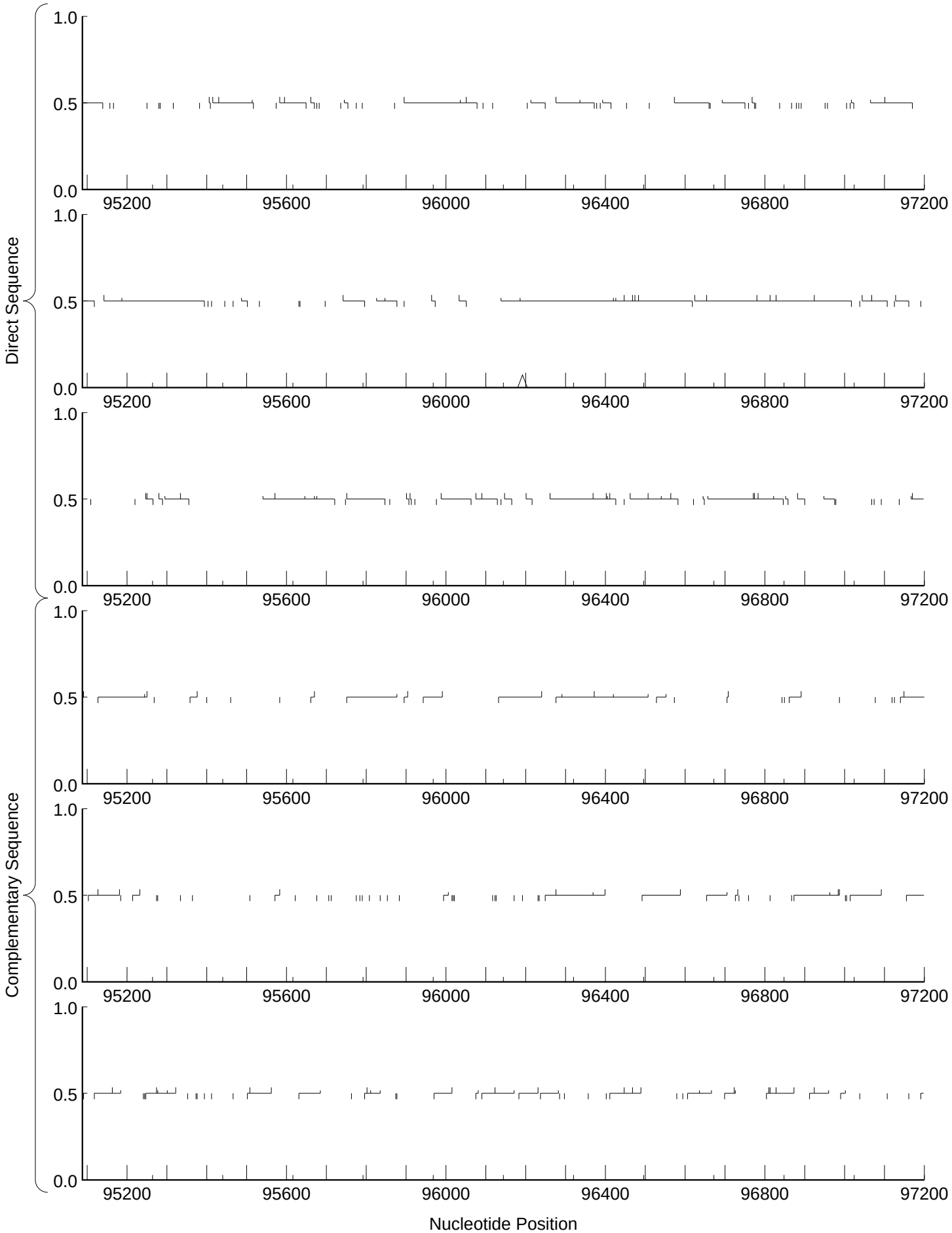

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
84800
85200
85600
86000
86400
Nucleotide Position

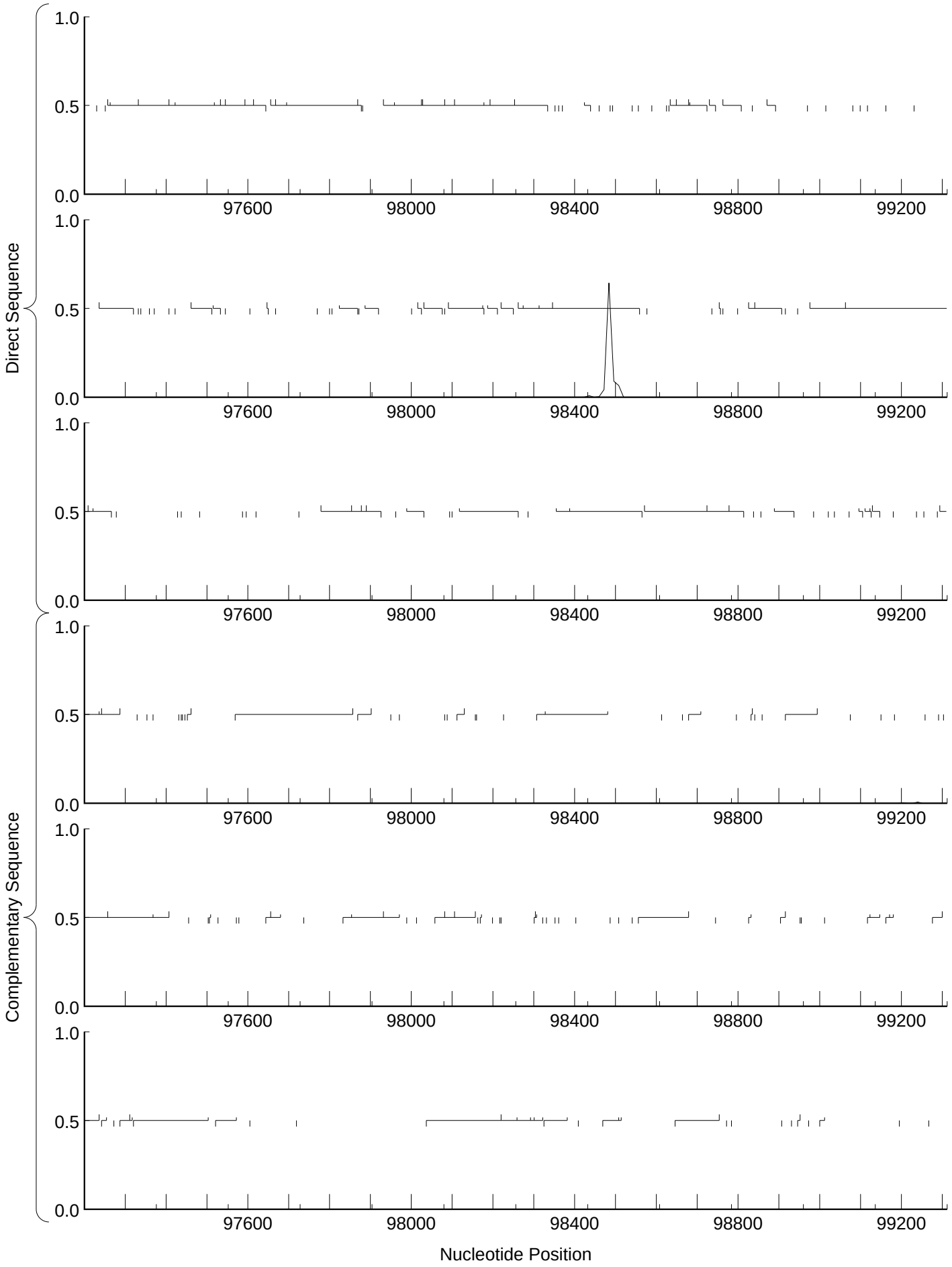

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
86800
87200
87600
88000
88400
Nucleotide Position

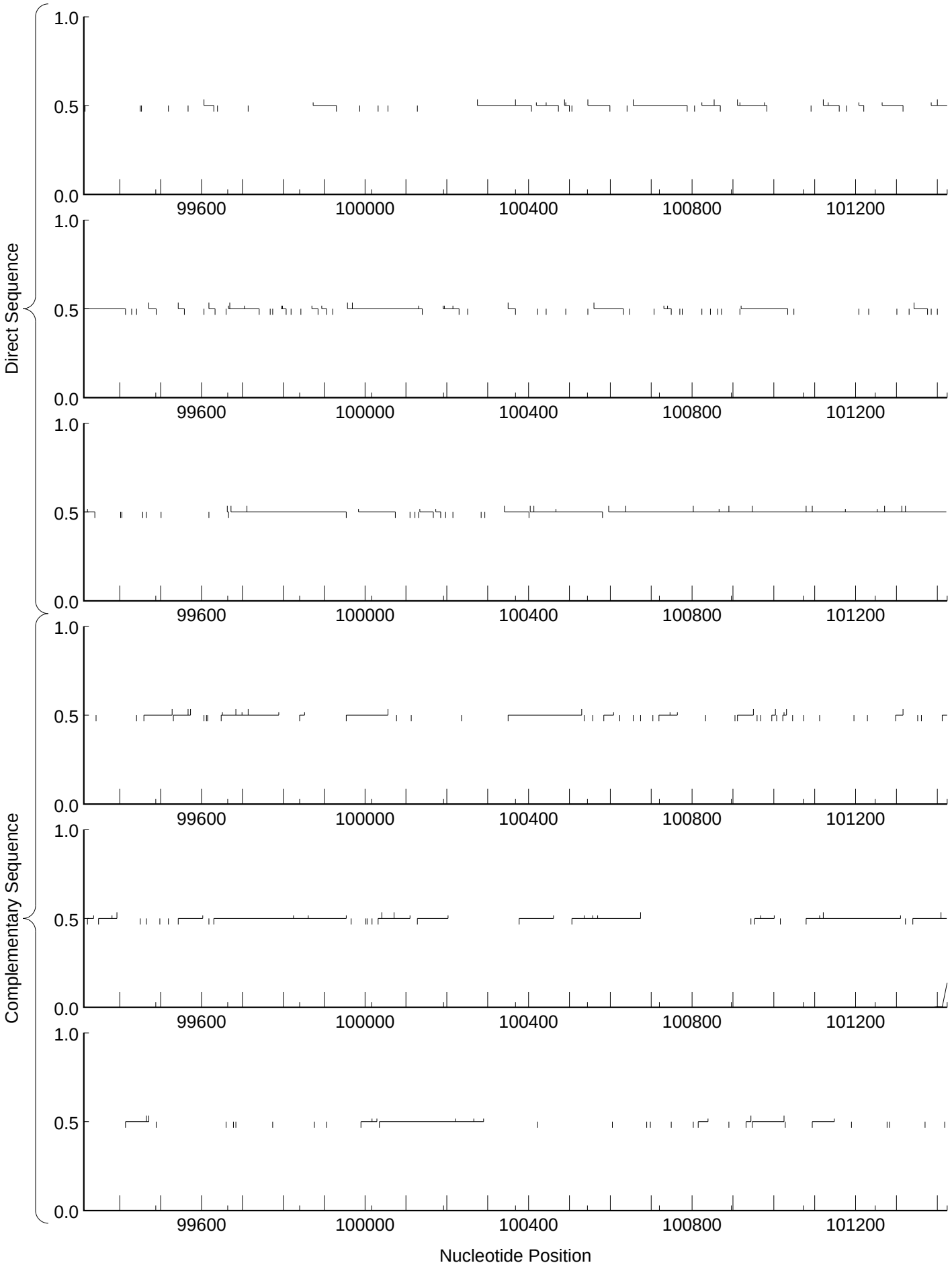

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
88800
89200
89600
90000
90400
90800
Nucleotide Position

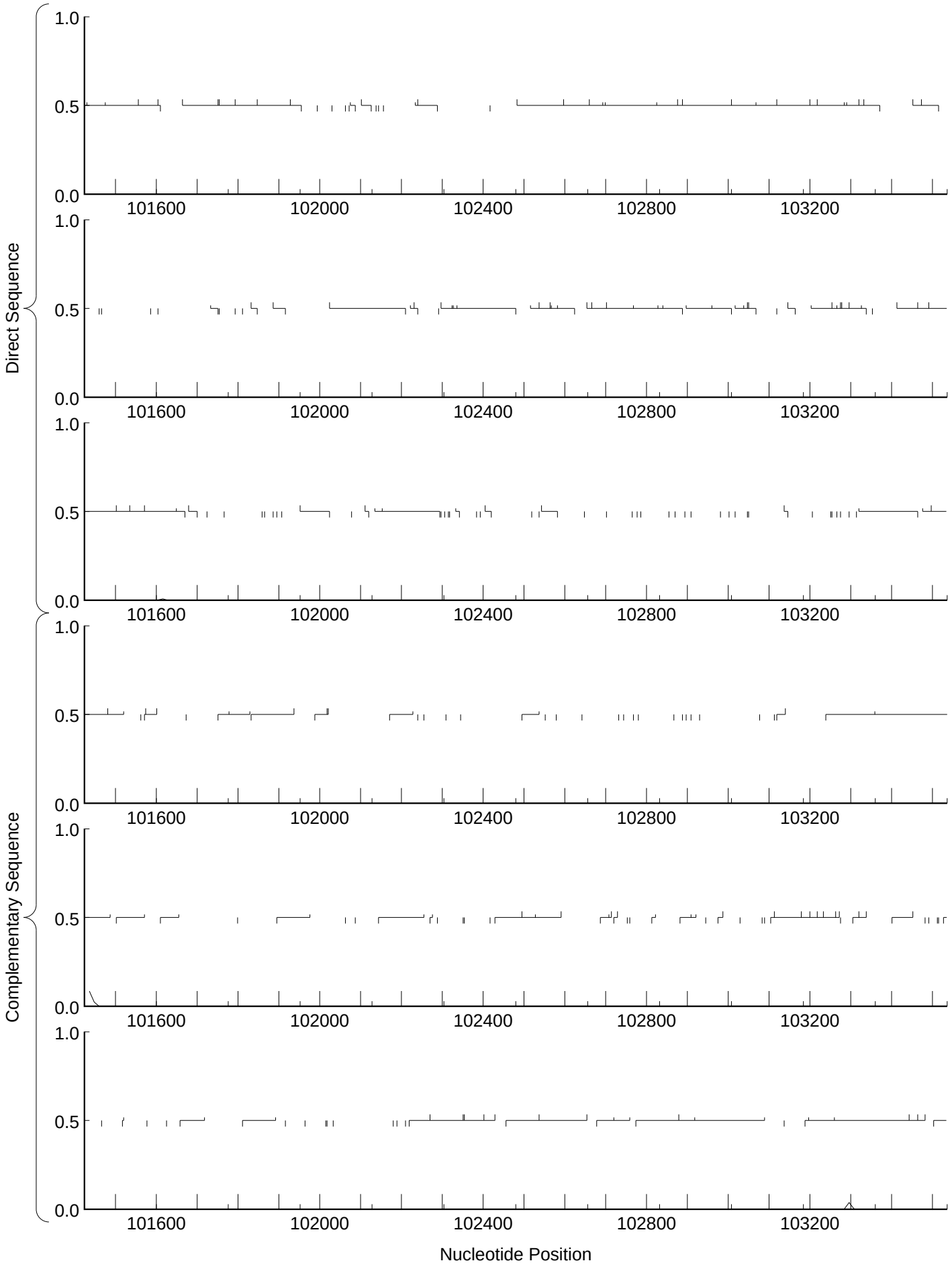

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
91200
91600
92000
92400
92800
Nucleotide Position

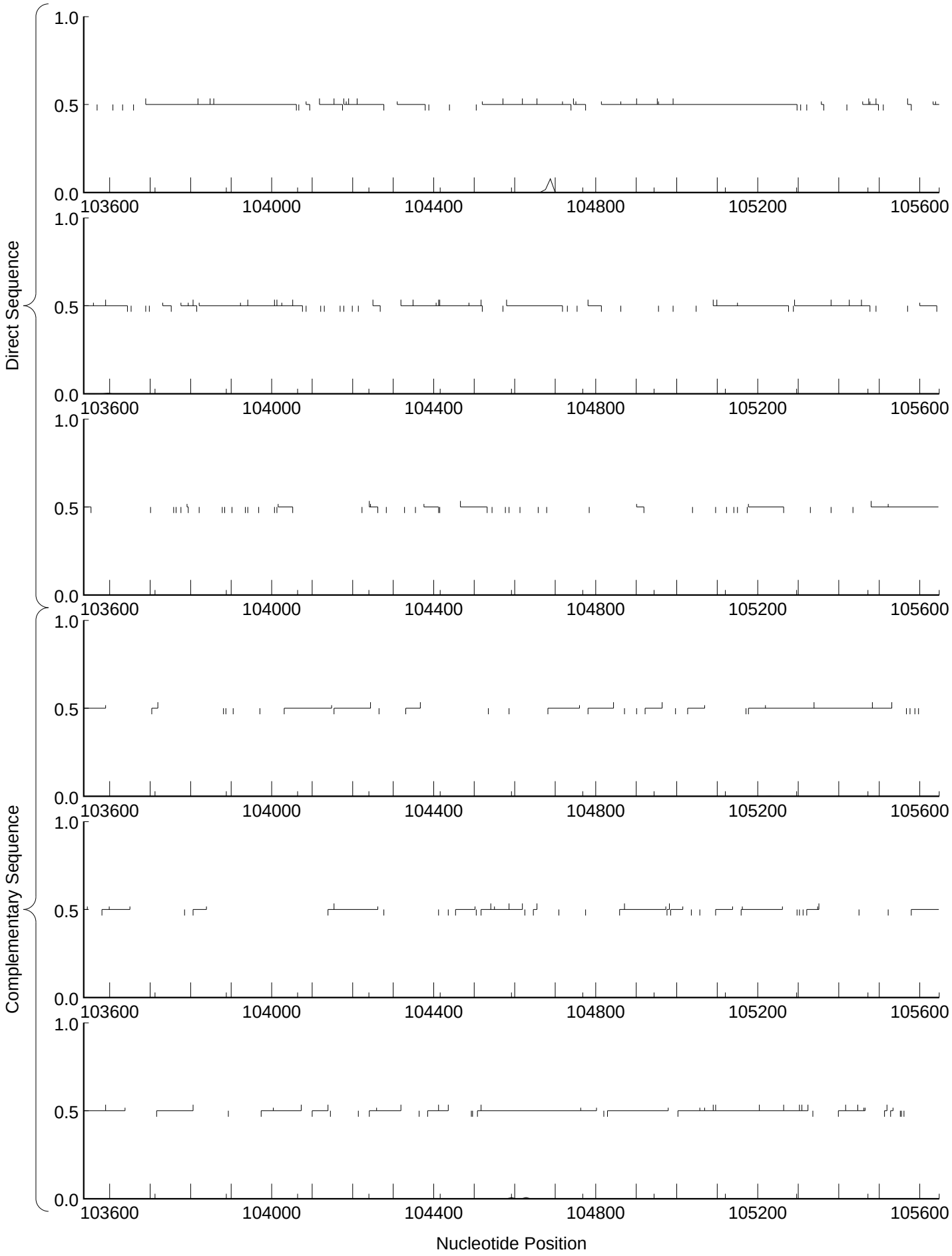

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
93200
93600
94000
94400
94800
Nucleotide Position

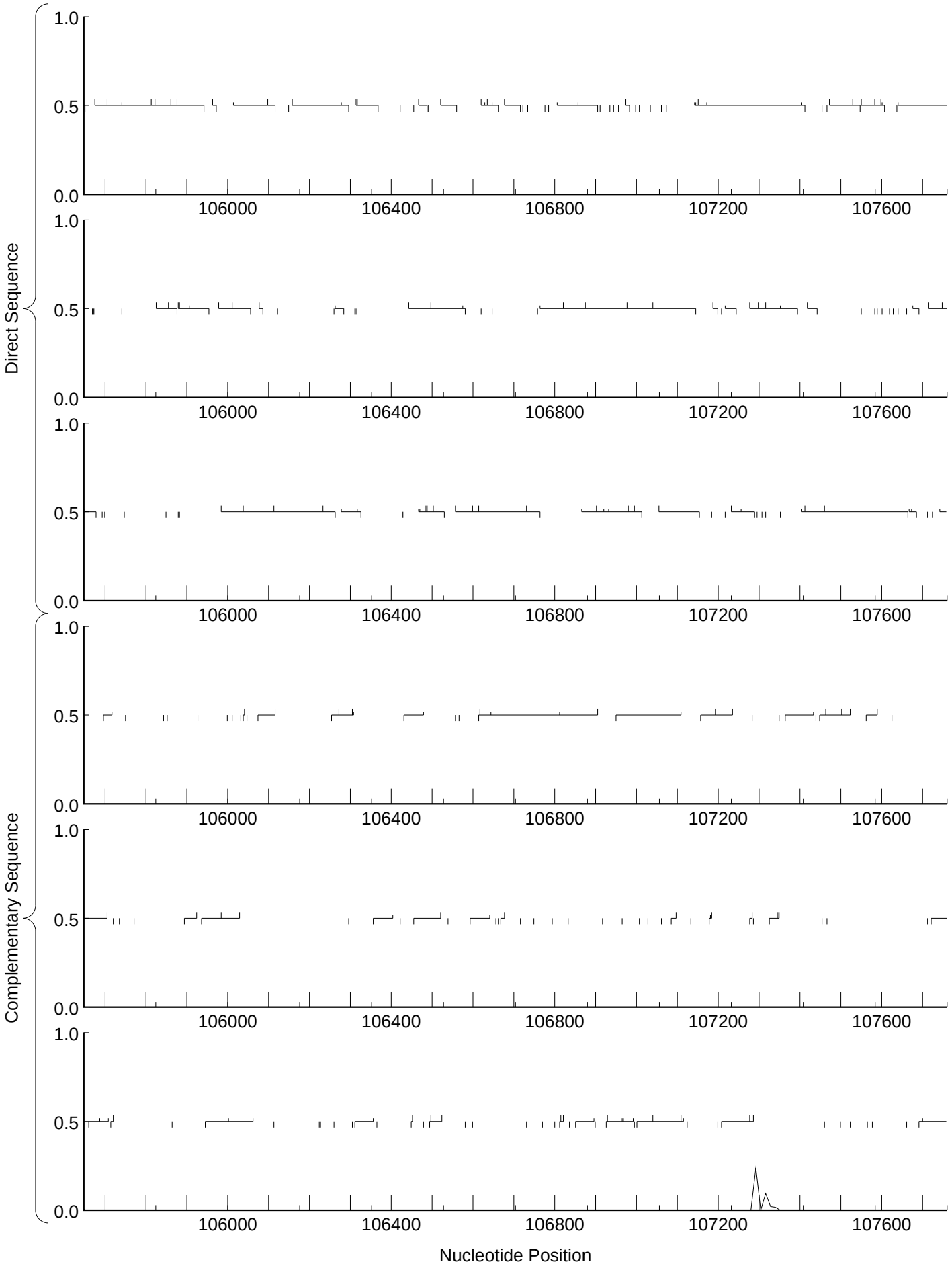

Direct Sequence
Complementary Sequence
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0.5
0.0
95200
95600
96000
96400
96800
97200
Nucleotide Position

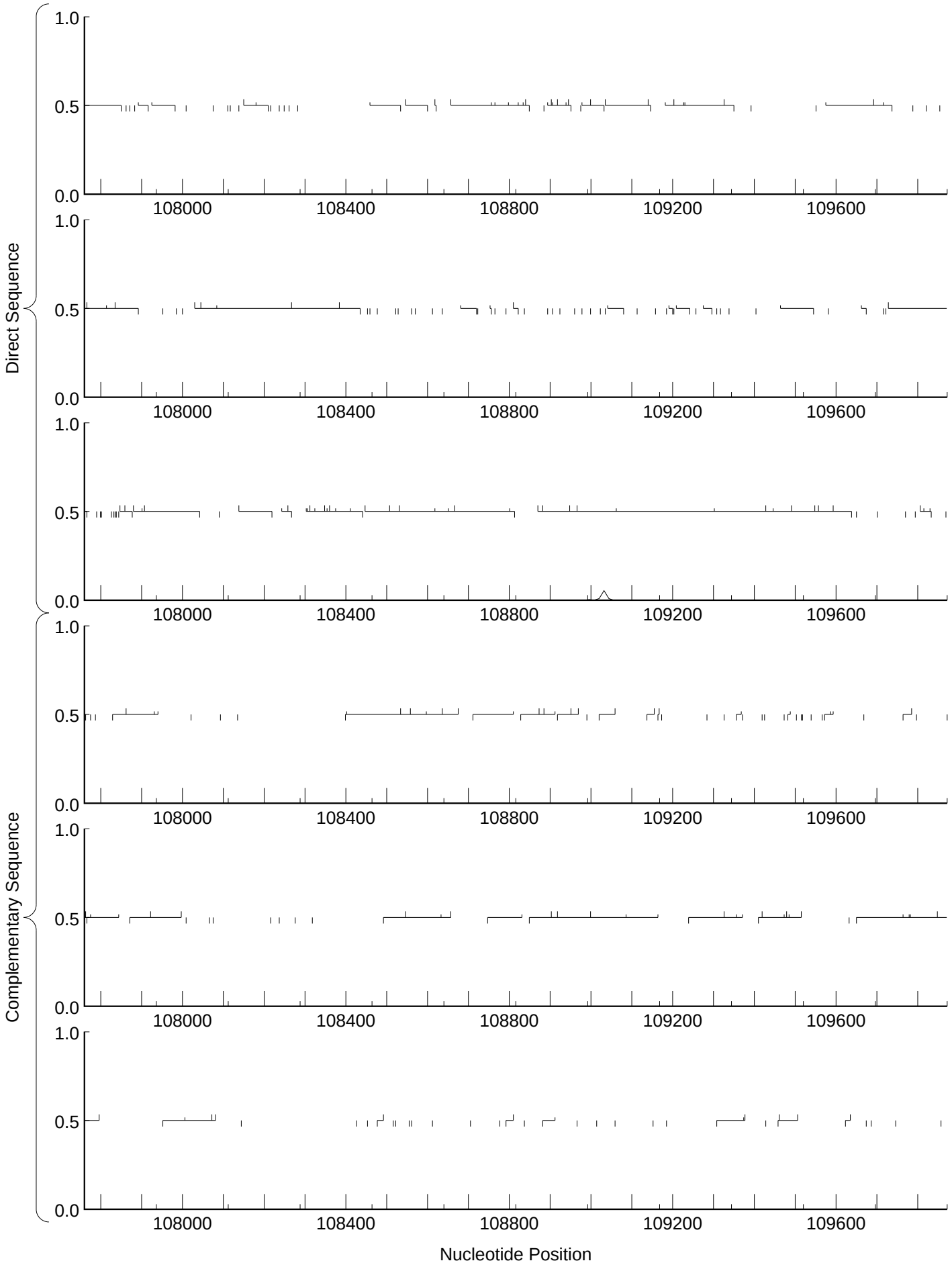

Direct Sequence
Complementary Sequence
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0.5
0.0
97600
98000
98400
98800
99200
Nucleotide Position

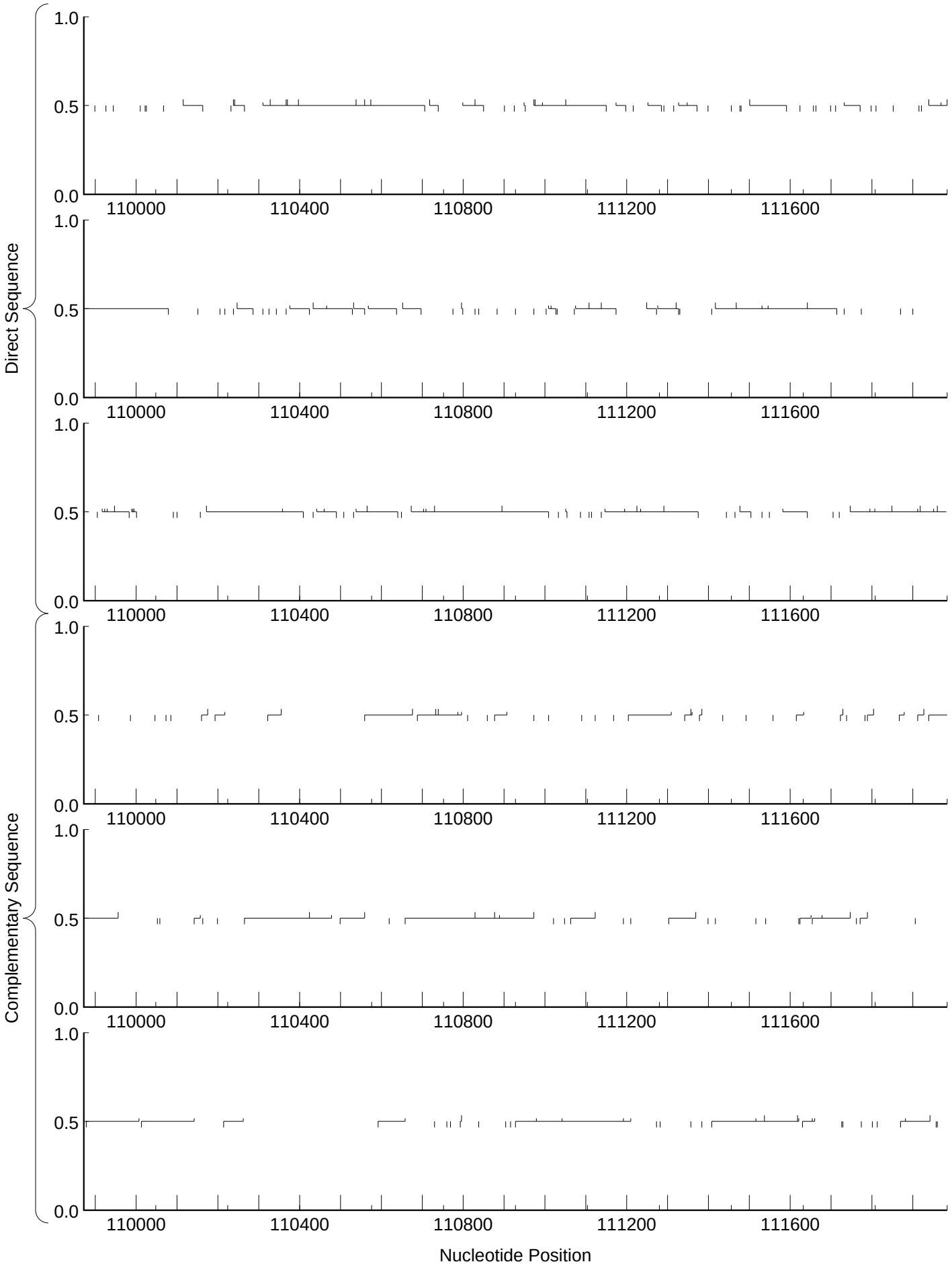

Direct Sequence
Complementary Sequence
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0.5
0.0
99600
100000
100400
100800
101200
Nucleotide Position

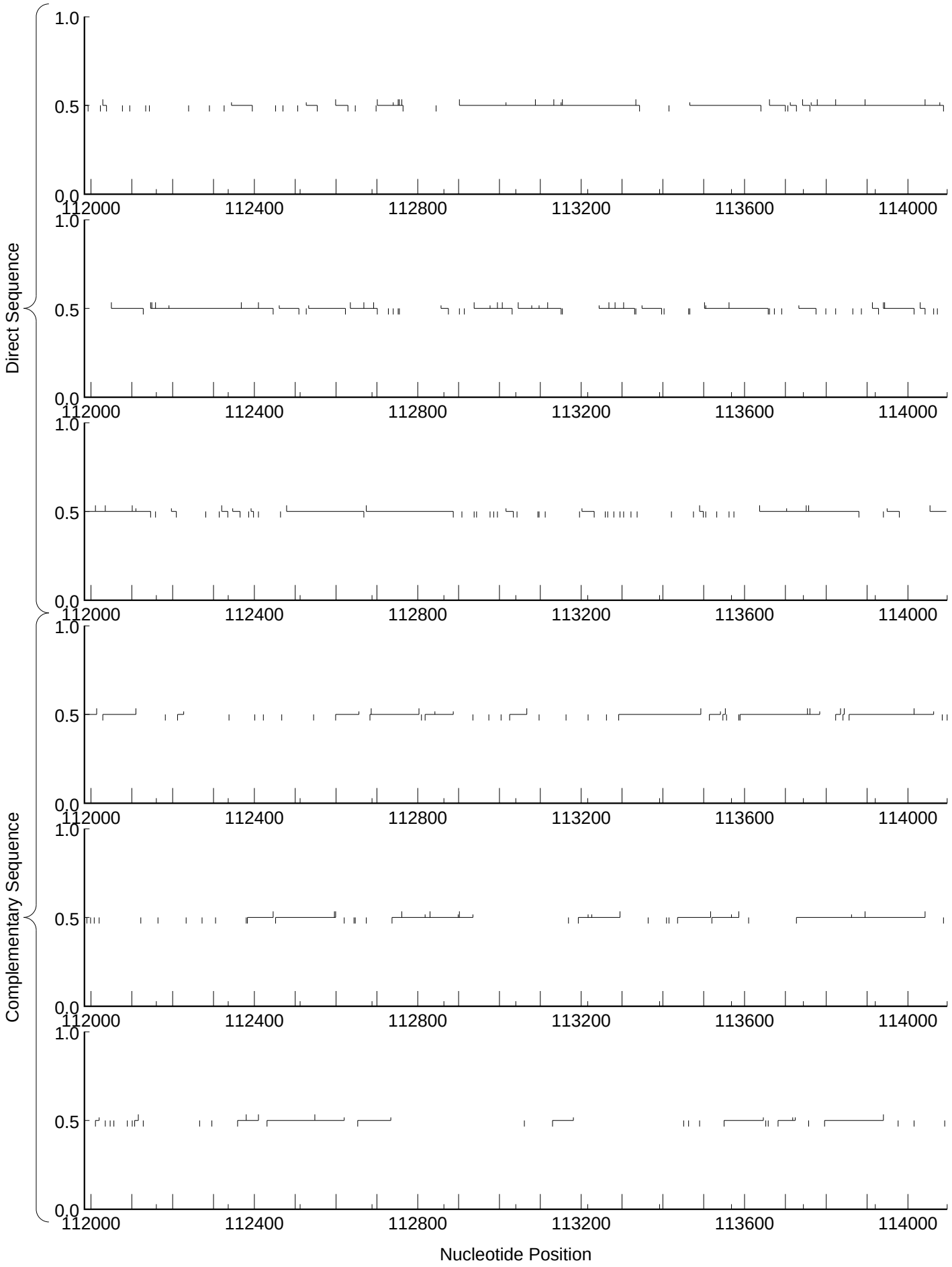

Direct Sequence
Complementary Sequence
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0.5
0.0
101600
102000
102400
102800
103200
Nucleotide Position

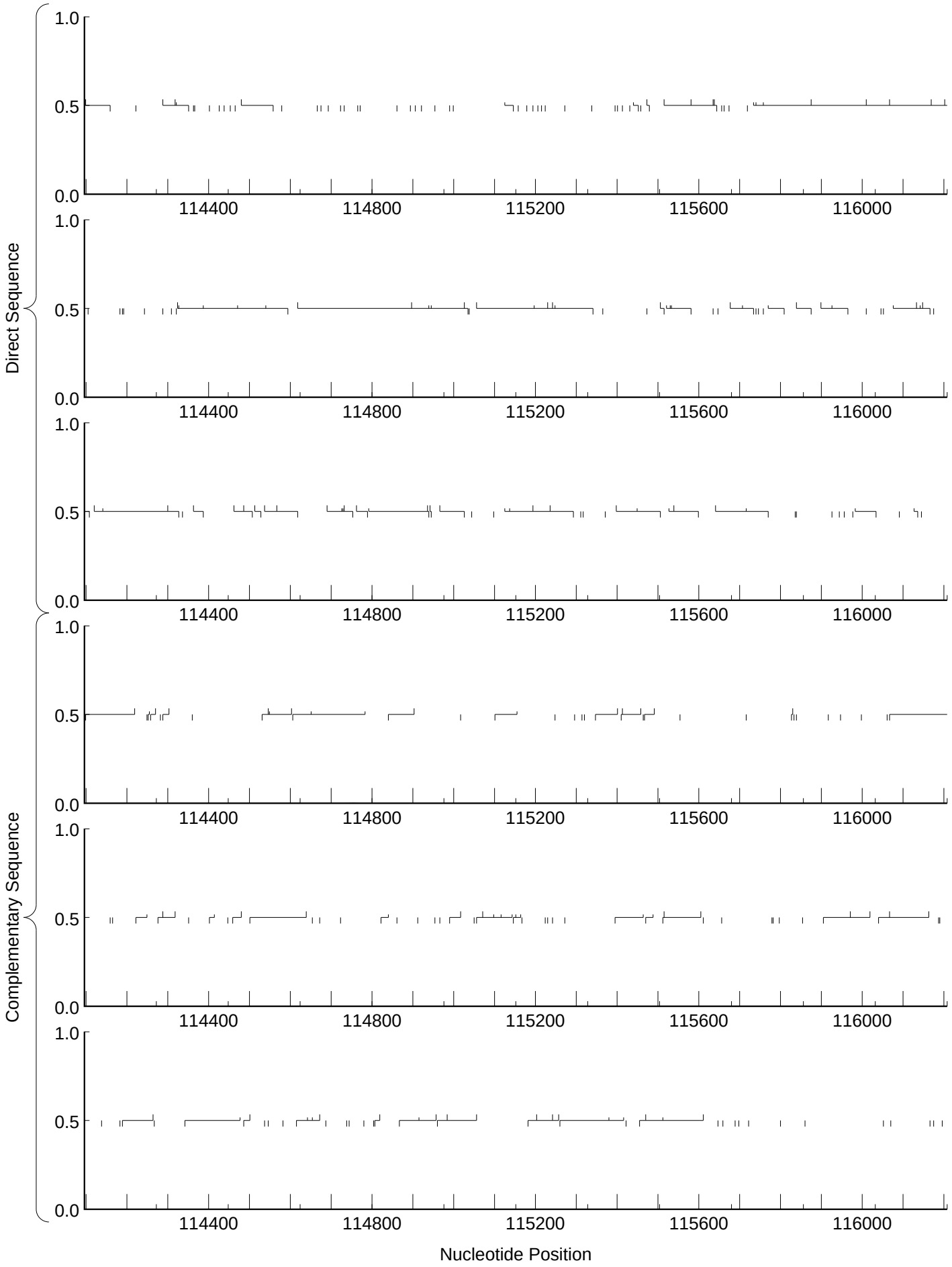

Direct Sequence
Complementary Sequence
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0.5
0.0
103600
104000
104400
104800
105200
105600
Nucleotide Position

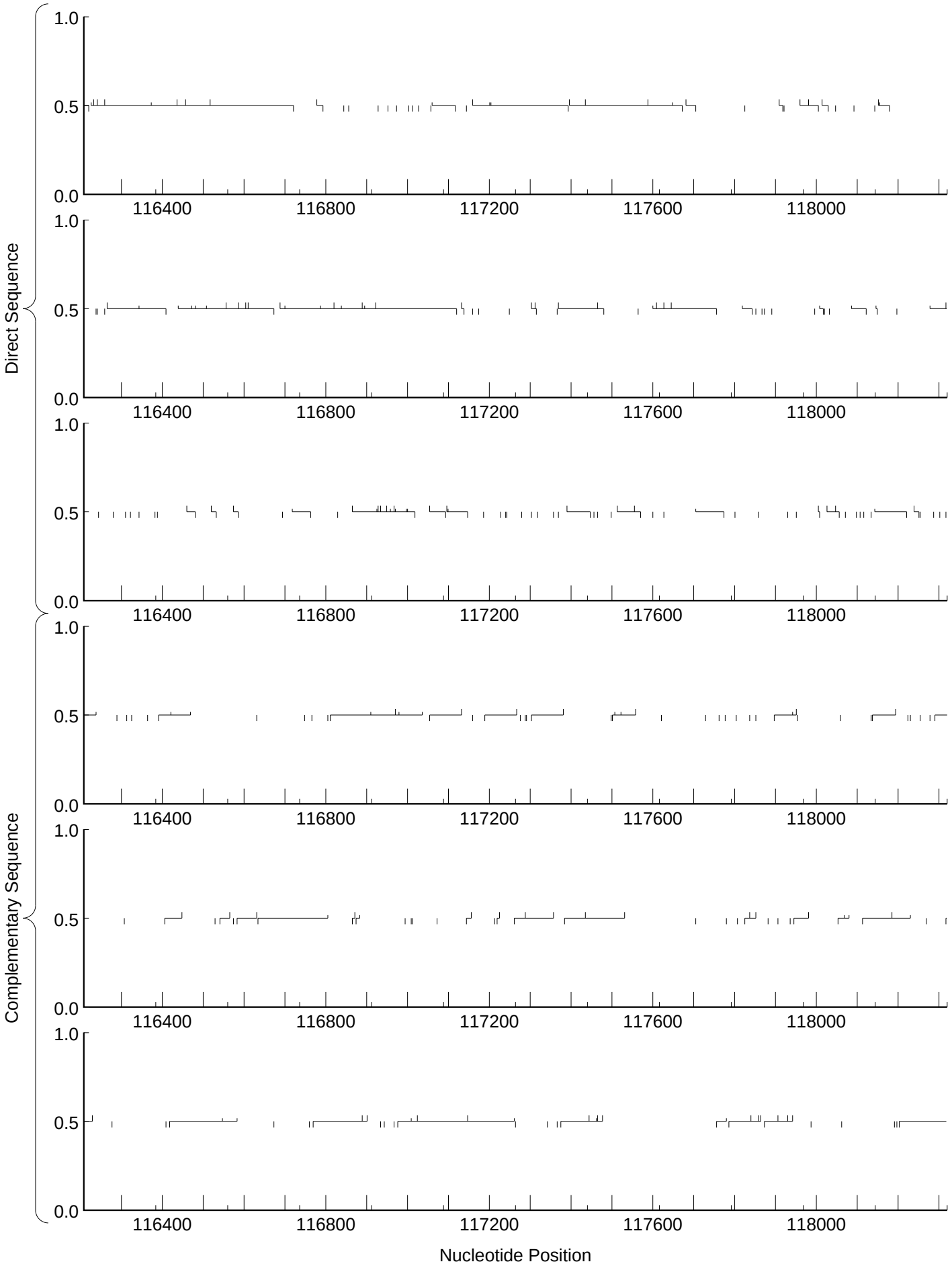

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
106000
106400
106800
107200
107600
Nucleotide Position

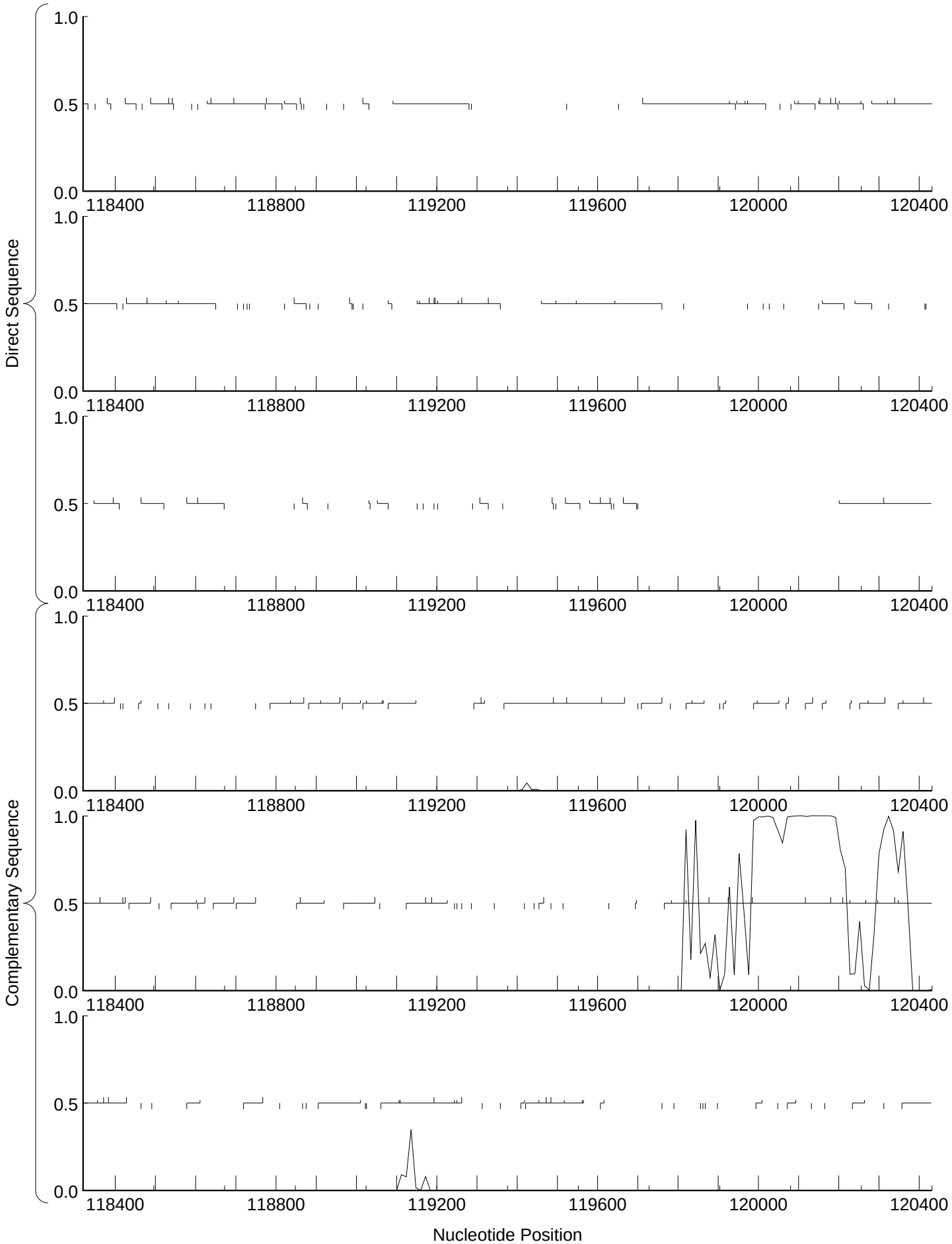

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
108000
108400
108800
109200
109600
Nucleotide Position

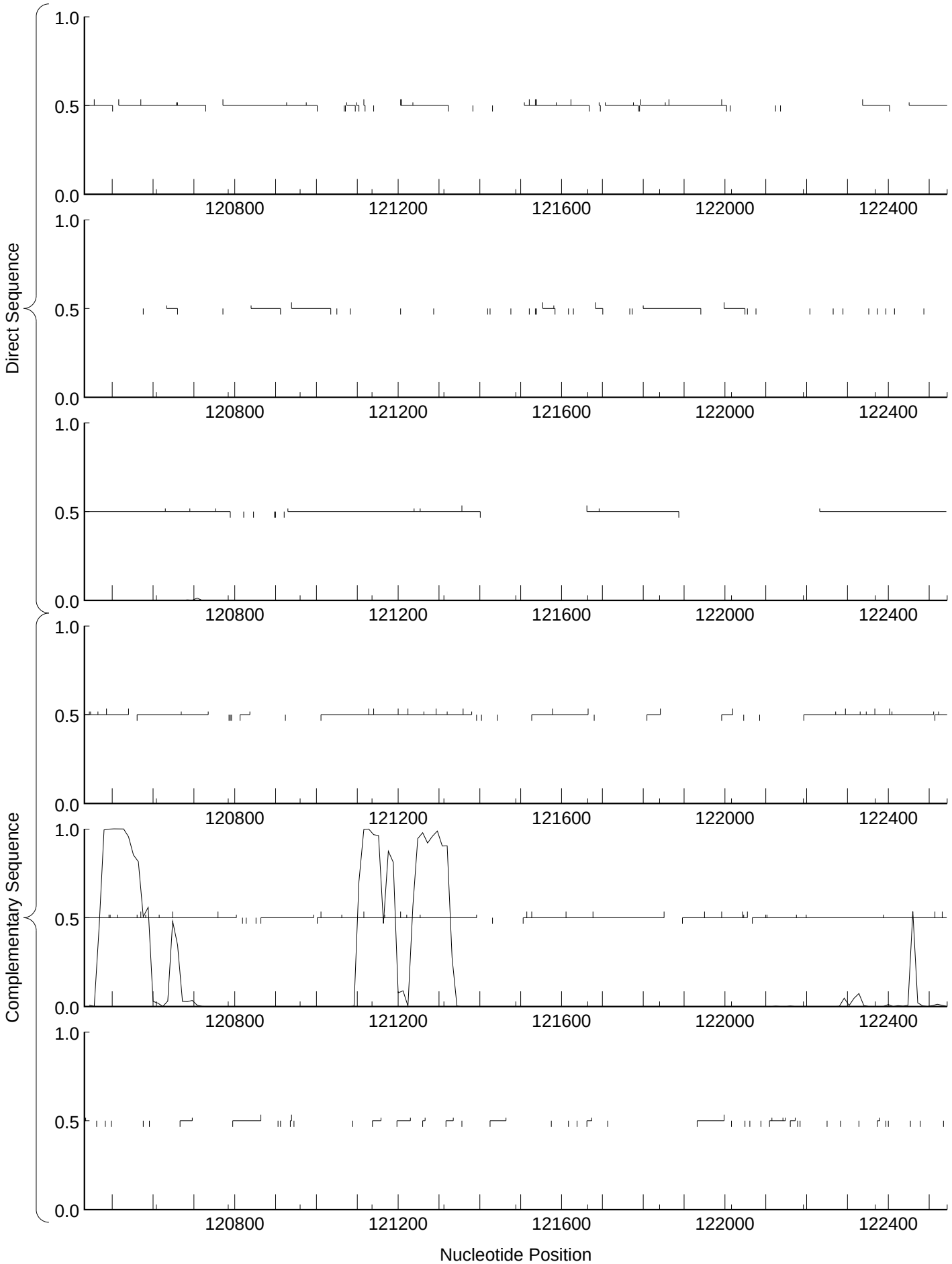

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
110000
110400
110800
111200
111600
Nucleotide Position

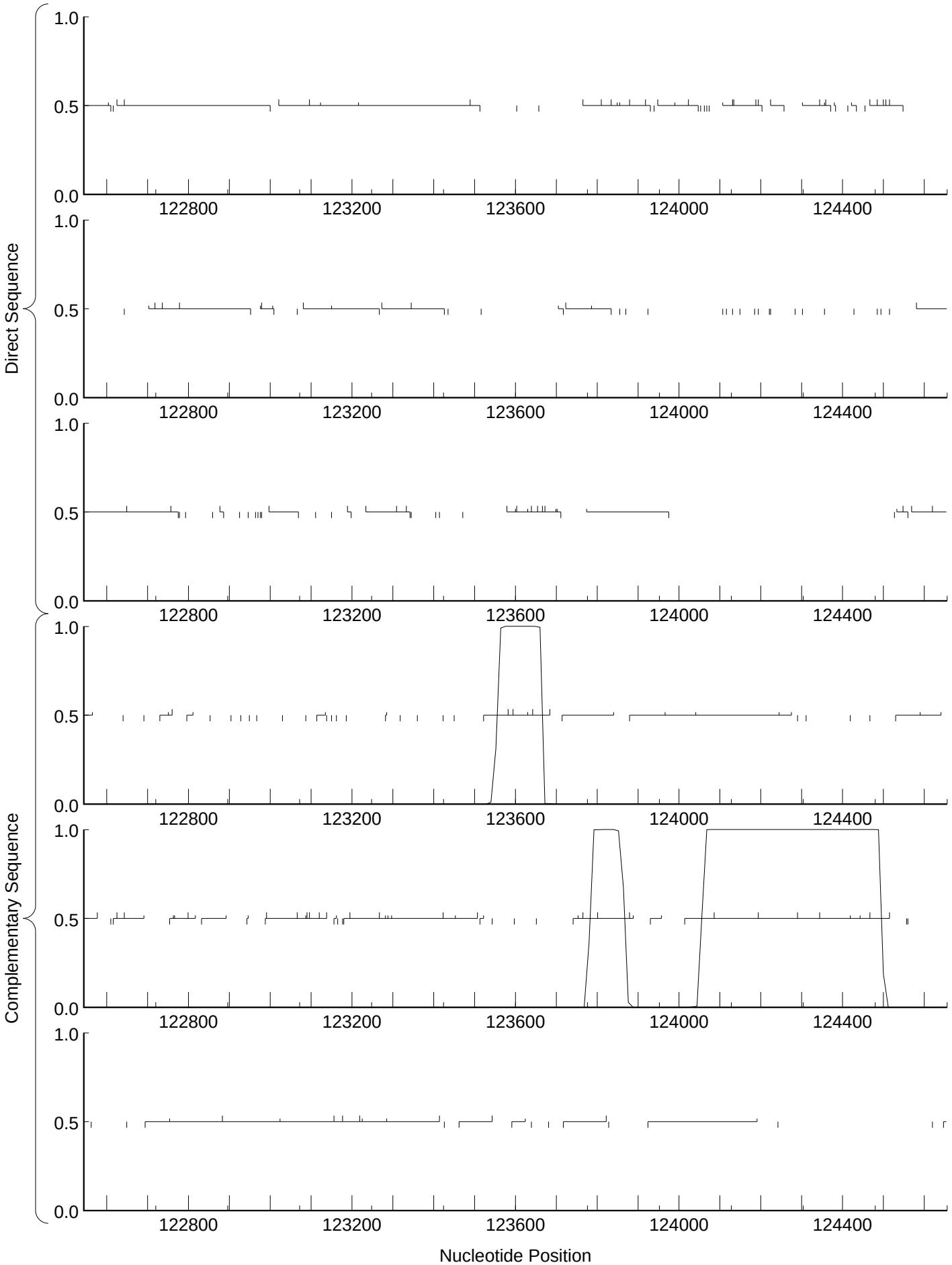

Direct Sequence
Complementary Sequence
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0.5
0.0
112000
112400
112800
113200
113600
114000
Nucleotide Position

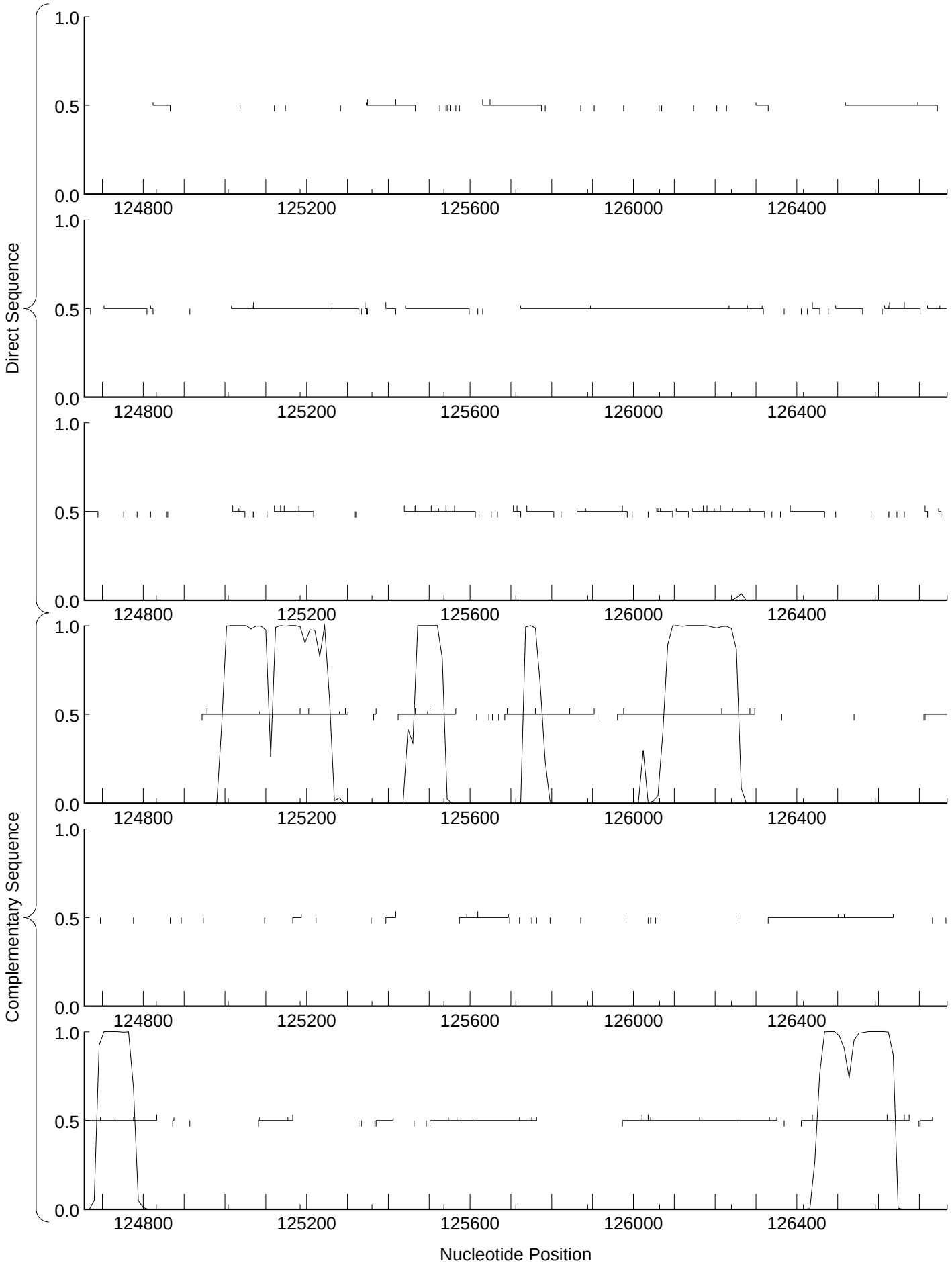

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
114400
114800
115200
115600
116000
Nucleotide Position

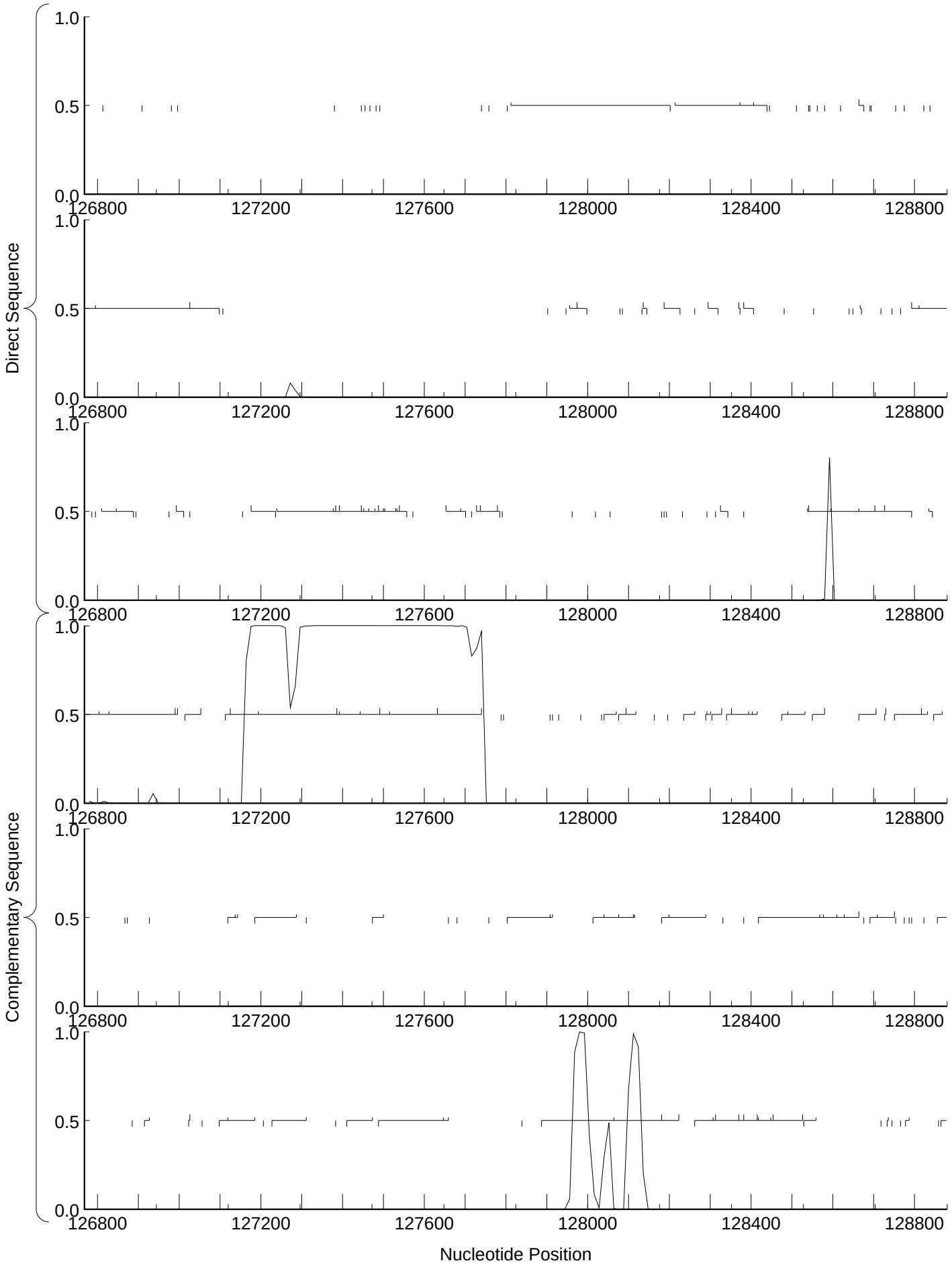

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
116400
116800
117200
117600
118000
Nucleotide Position

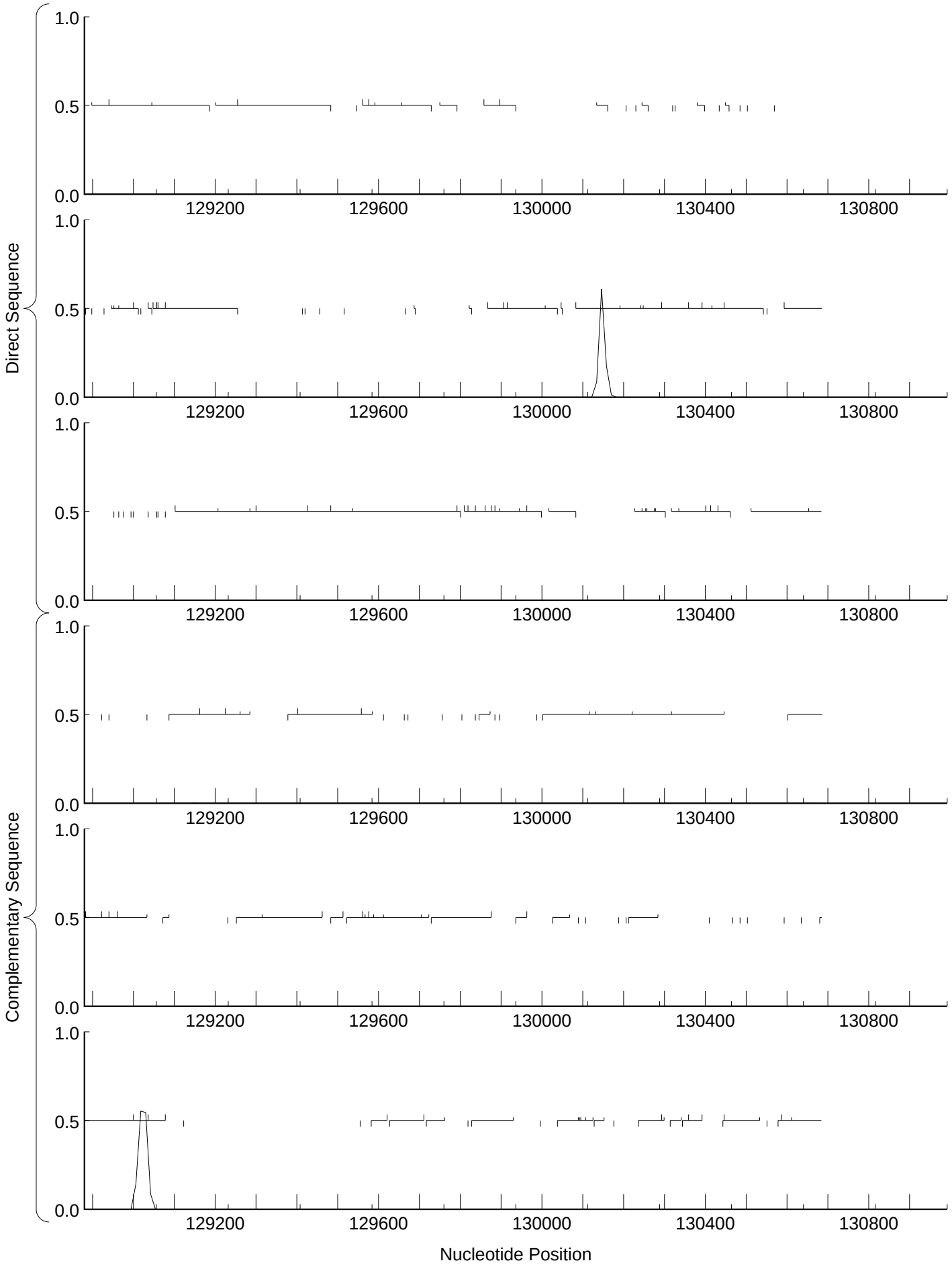

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
118400
118800
119200
119600
120000
120400
Nucleotide Position


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