GeneMark

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

PROGRAM INFORMATION

```
Sequence         :  Mycobacterium phage ElTiger69 Complete Sequence, 51505 bp including 10-base 3’ overhang (CG
Analysis Date    :  3/29/24 at 8:32:04
Pages            :  26
Sequence Length  :  51505 bp
GC Content       :   59.78%

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

PS-Version       :  1.2

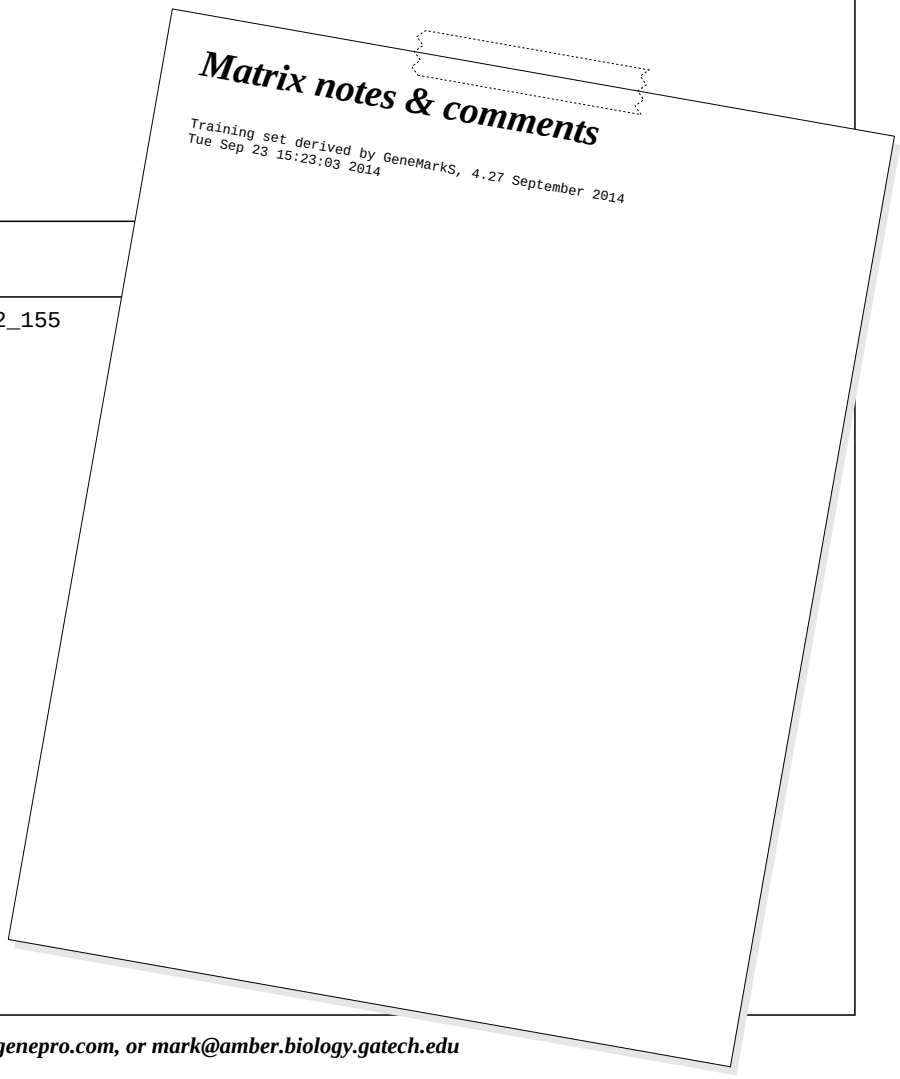
GeneMark Options :  PostScript graph,
                    Mark ORFs / splice sites,
                    List ORFs,
                    List regions and/or splice sites,
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MATRIX INFORMATION

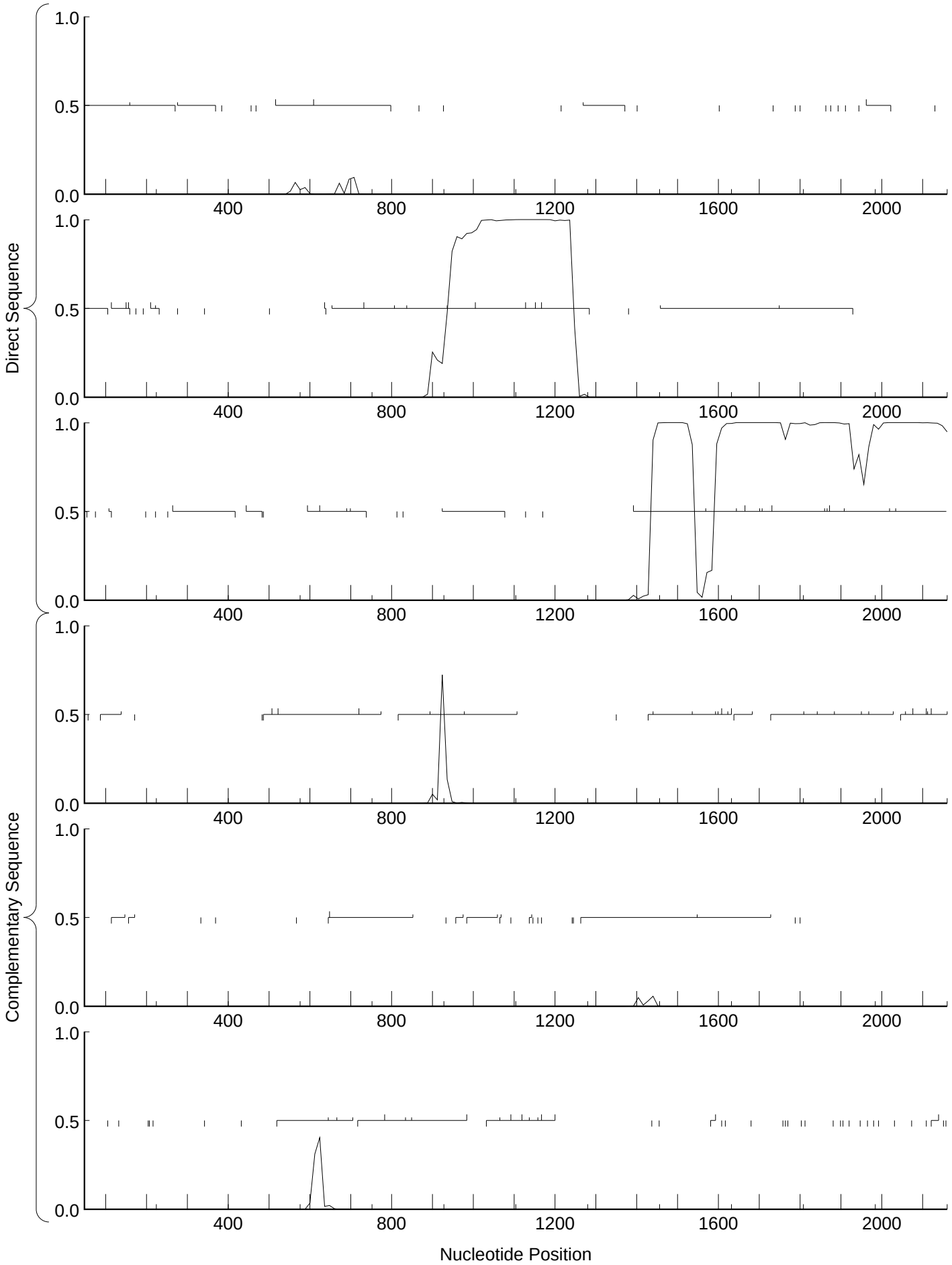
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Matrix     :  Mycobacterium_smegmatis_MC2_155
Author     :  -

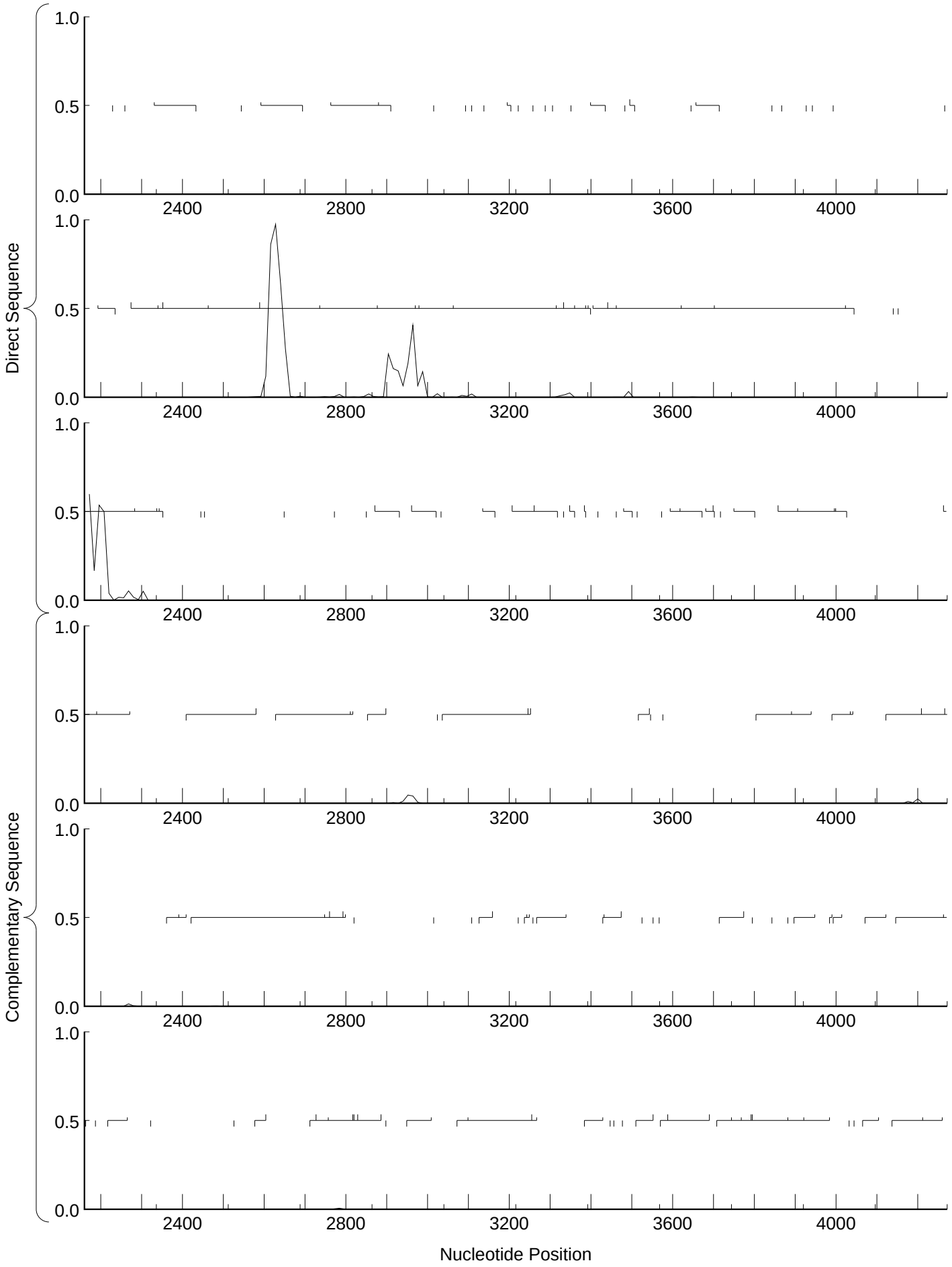
Order      :  4

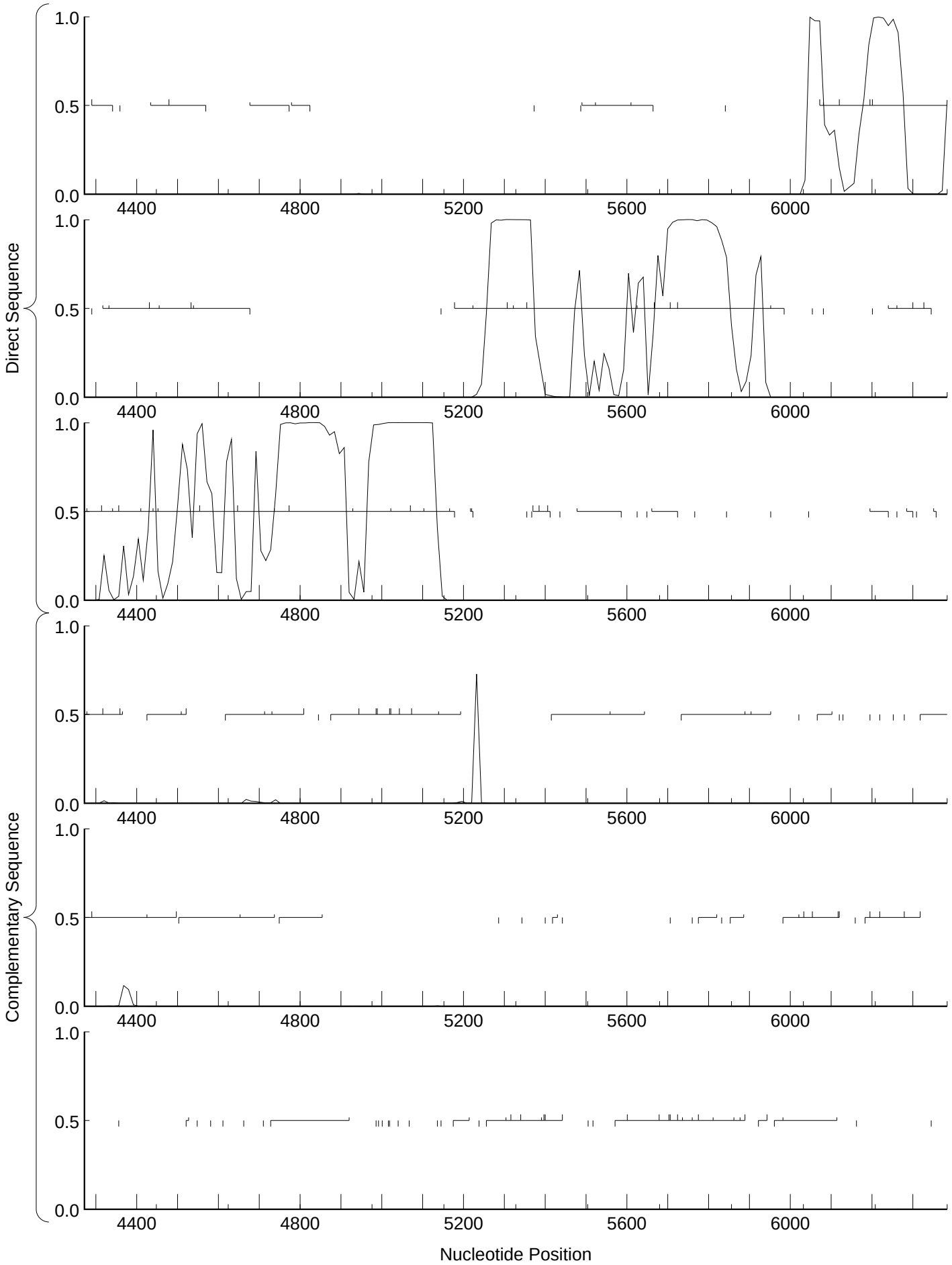

  Send questions / comments to:
      Dr. M. Borodovsky
      Georgia Institute of Technology
      School of Biology
      Atlanta, GA  30332-0230
```

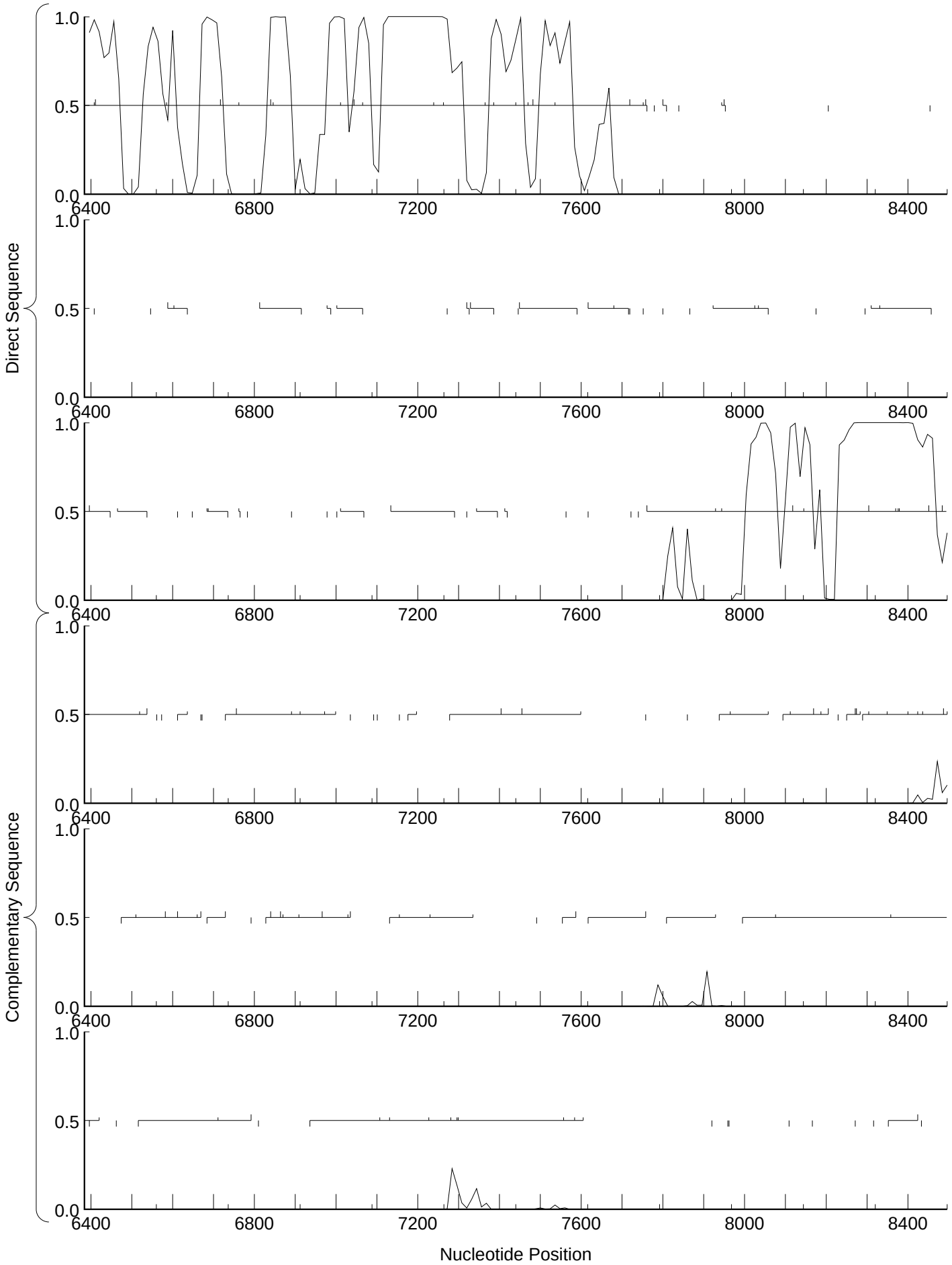


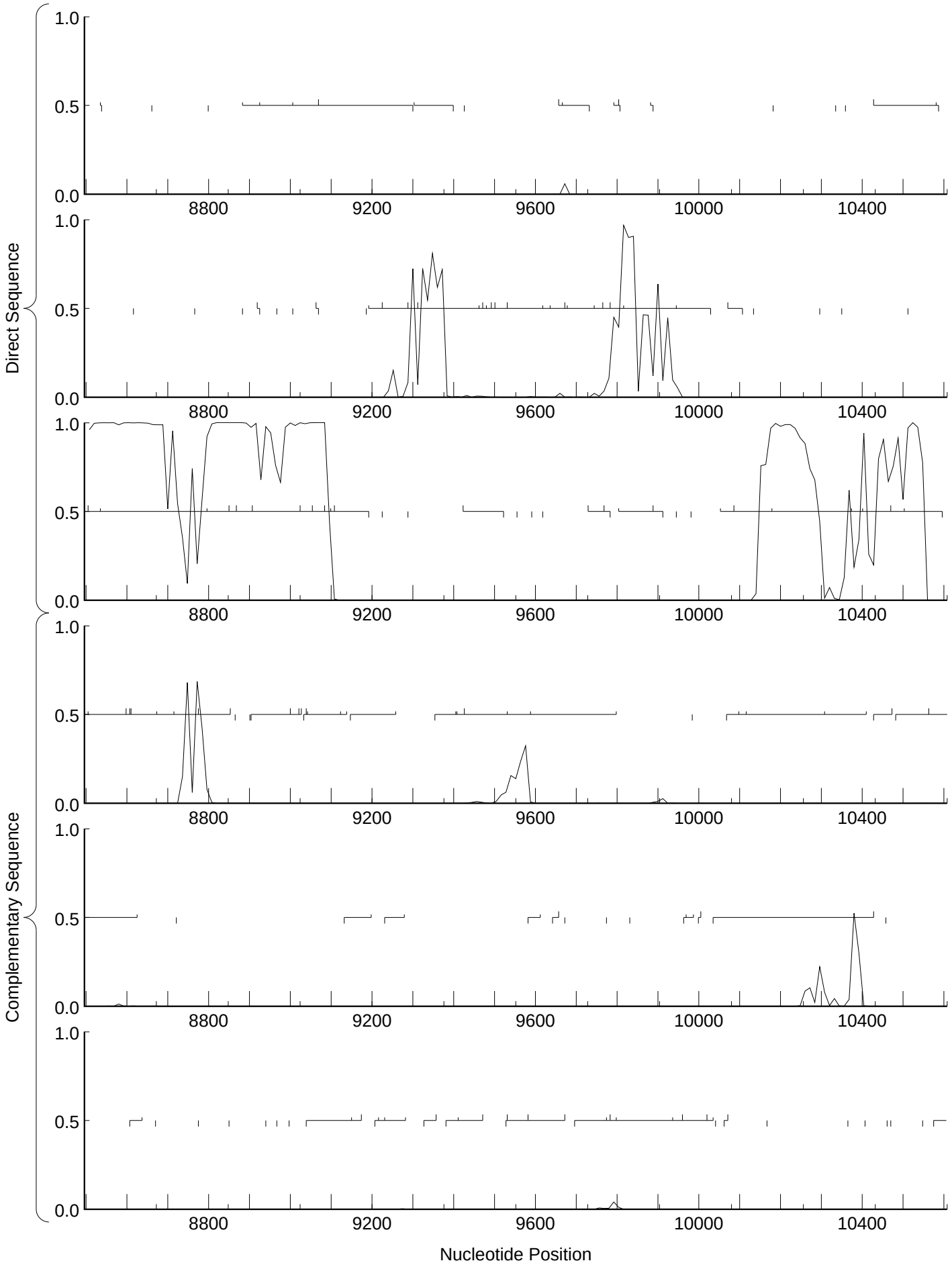
For help or information, send electronic mail to: custserv@genepro.com, or mark@amber.biology.gatech.edu

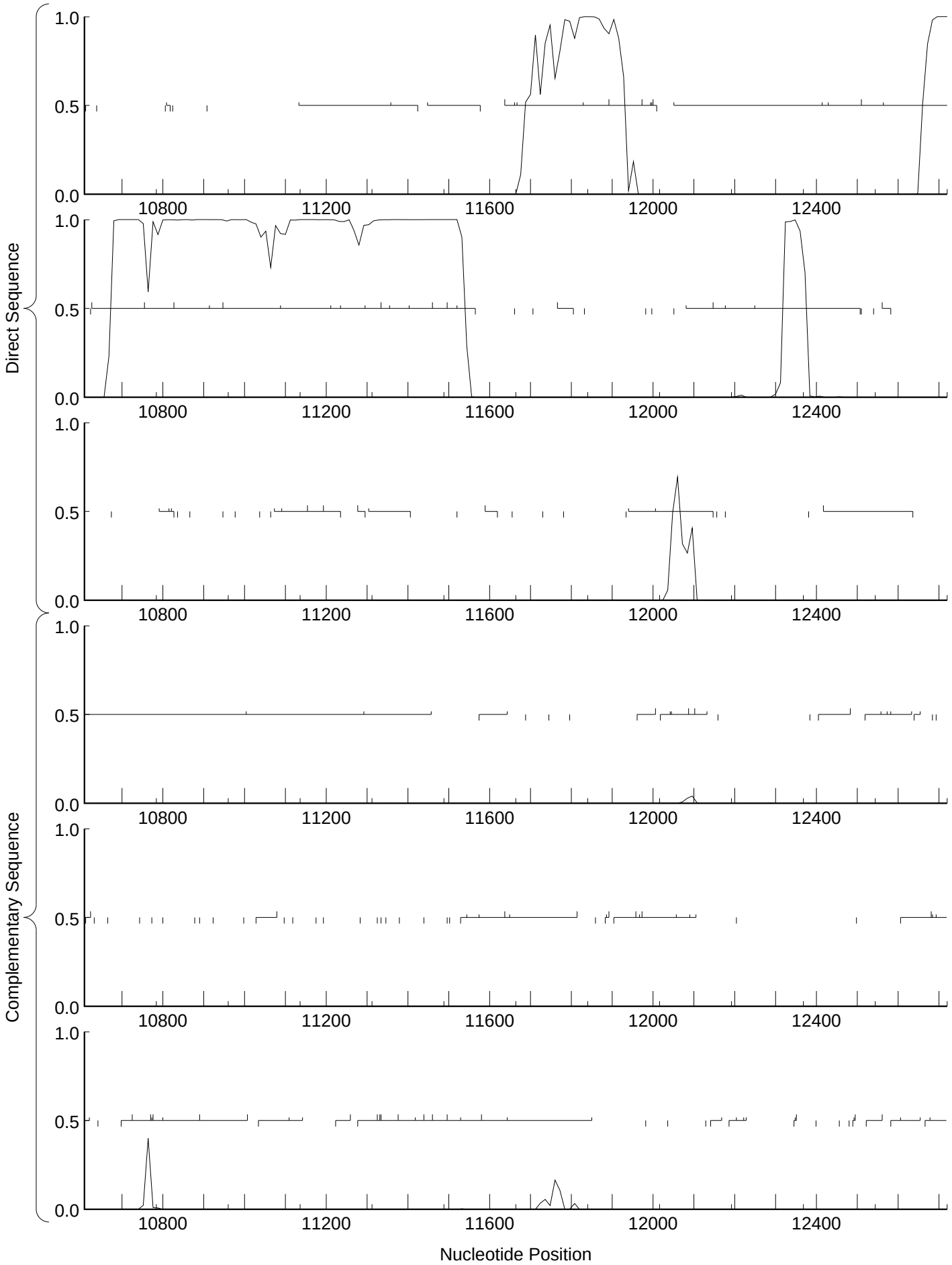

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Complementary Sequence
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0.5
0.0
400
800
1200
1600
2000
Nucleotide Position

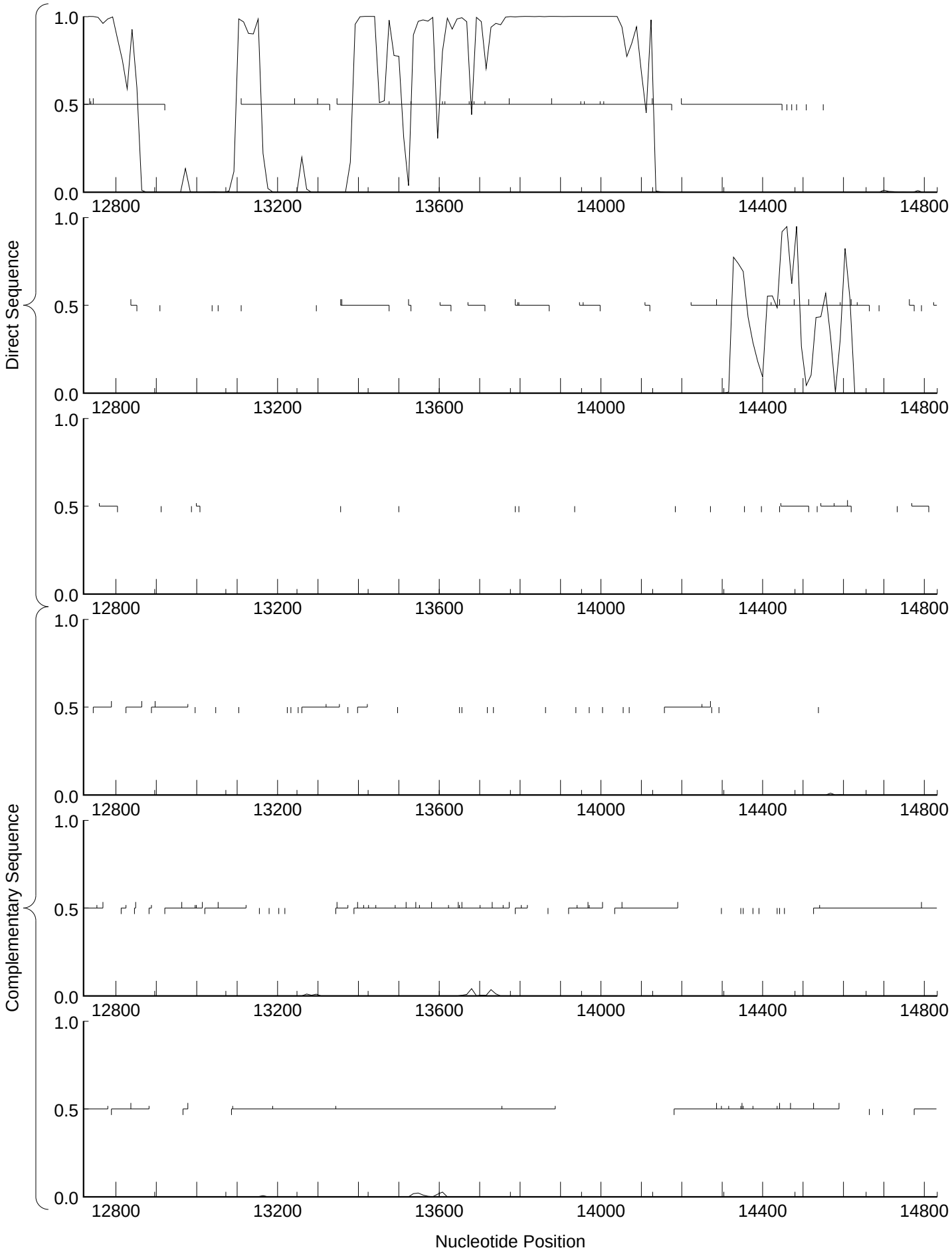

Direct Sequence
Complementary Sequence
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0.5
0.0
2400
2800
3200
3600
4000
Nucleotide Position

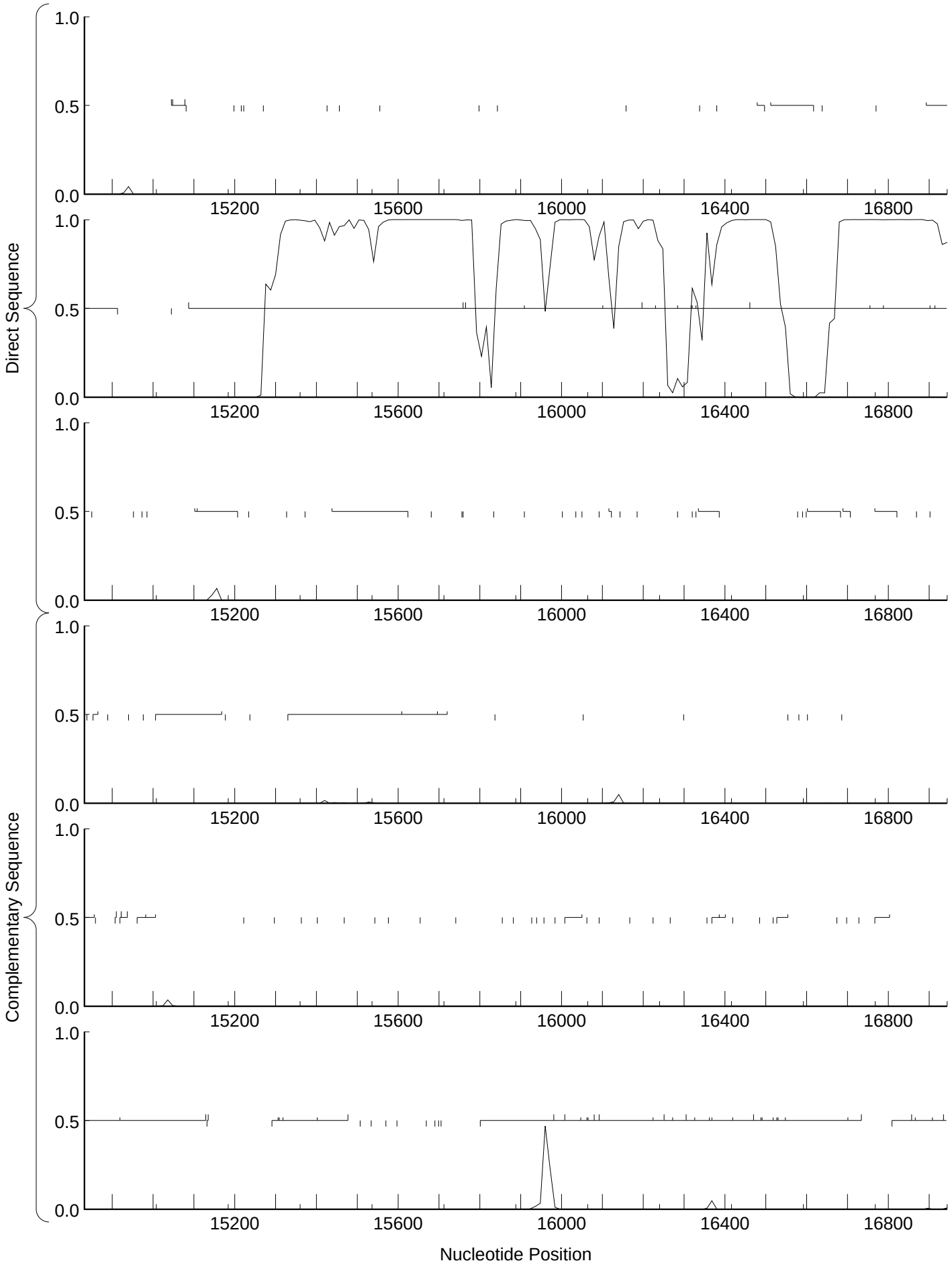

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
4400
4800
5200
5600
6000
Nucleotide Position


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

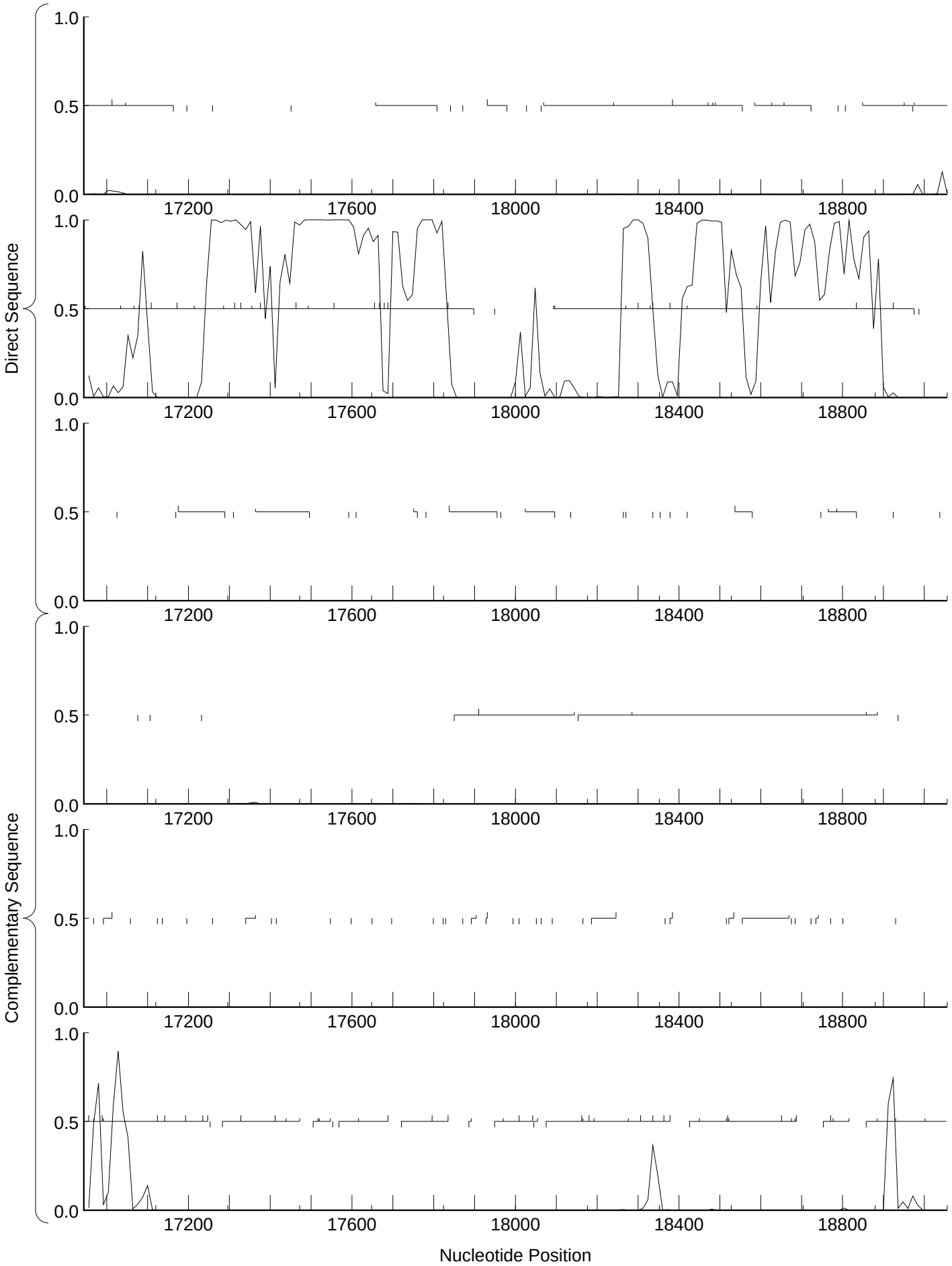

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
8800
9200
9600
10000
10400
Nucleotide Position


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

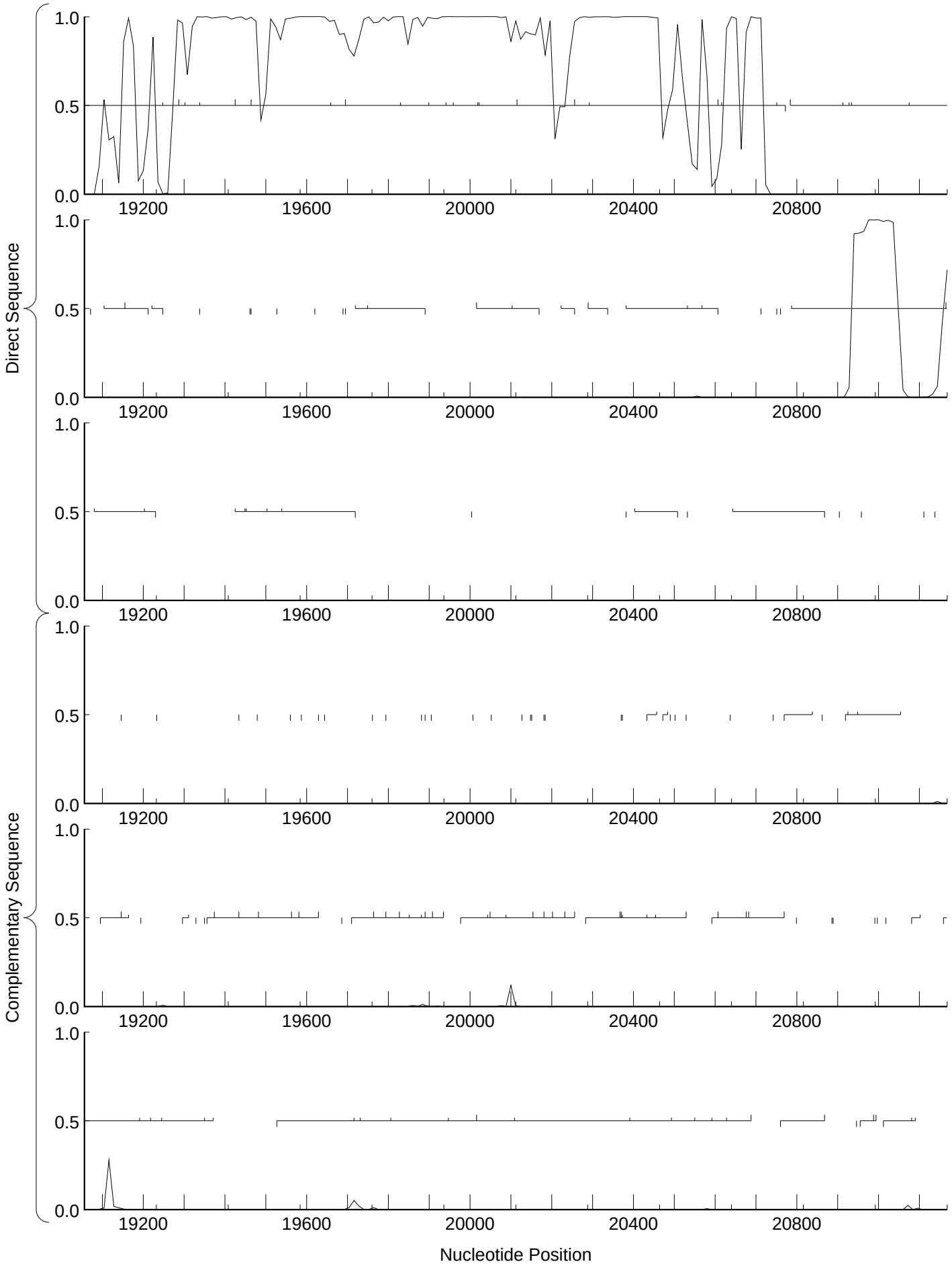

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
12800
13200
13600
14000
14400
14800
Nucleotide Position


Direct Sequence
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16000
16400
16800
Nucleotide Position

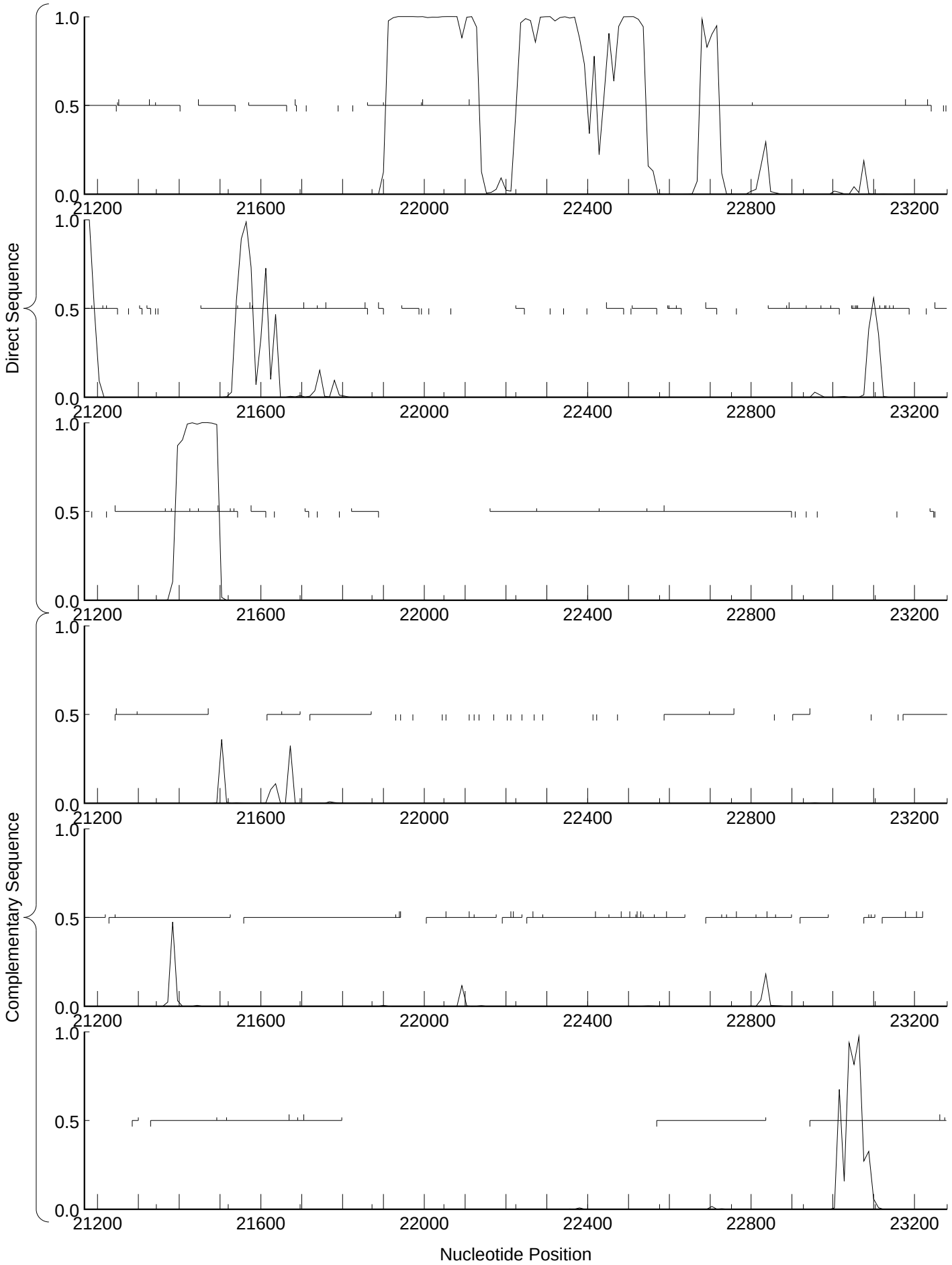
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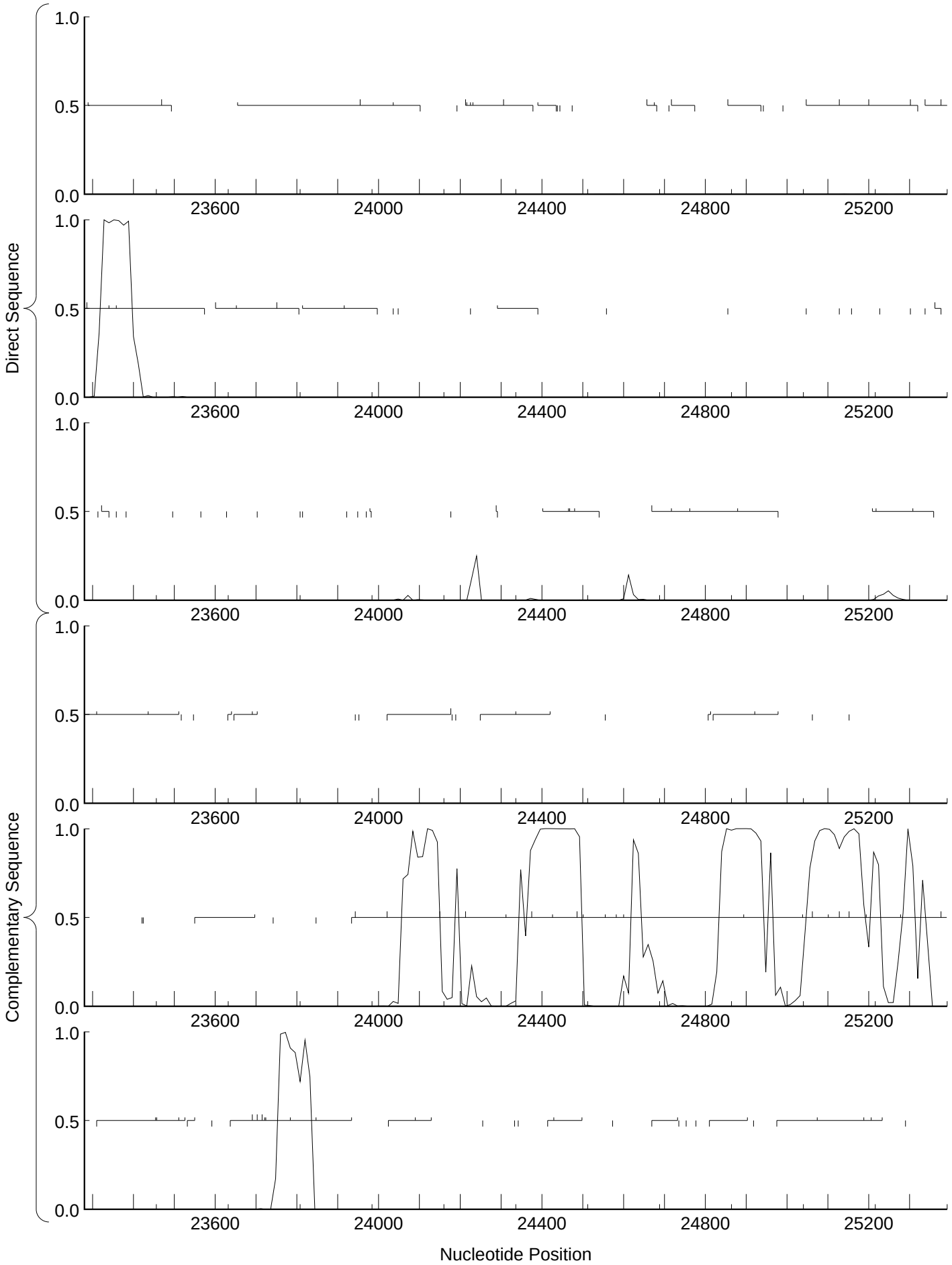
e ElTiger69 Complete Sequence, 51505 bp including 10-base 3’ overhang (CGGGAGGTAA), Order 4, Window 96, Step 12, 11/26

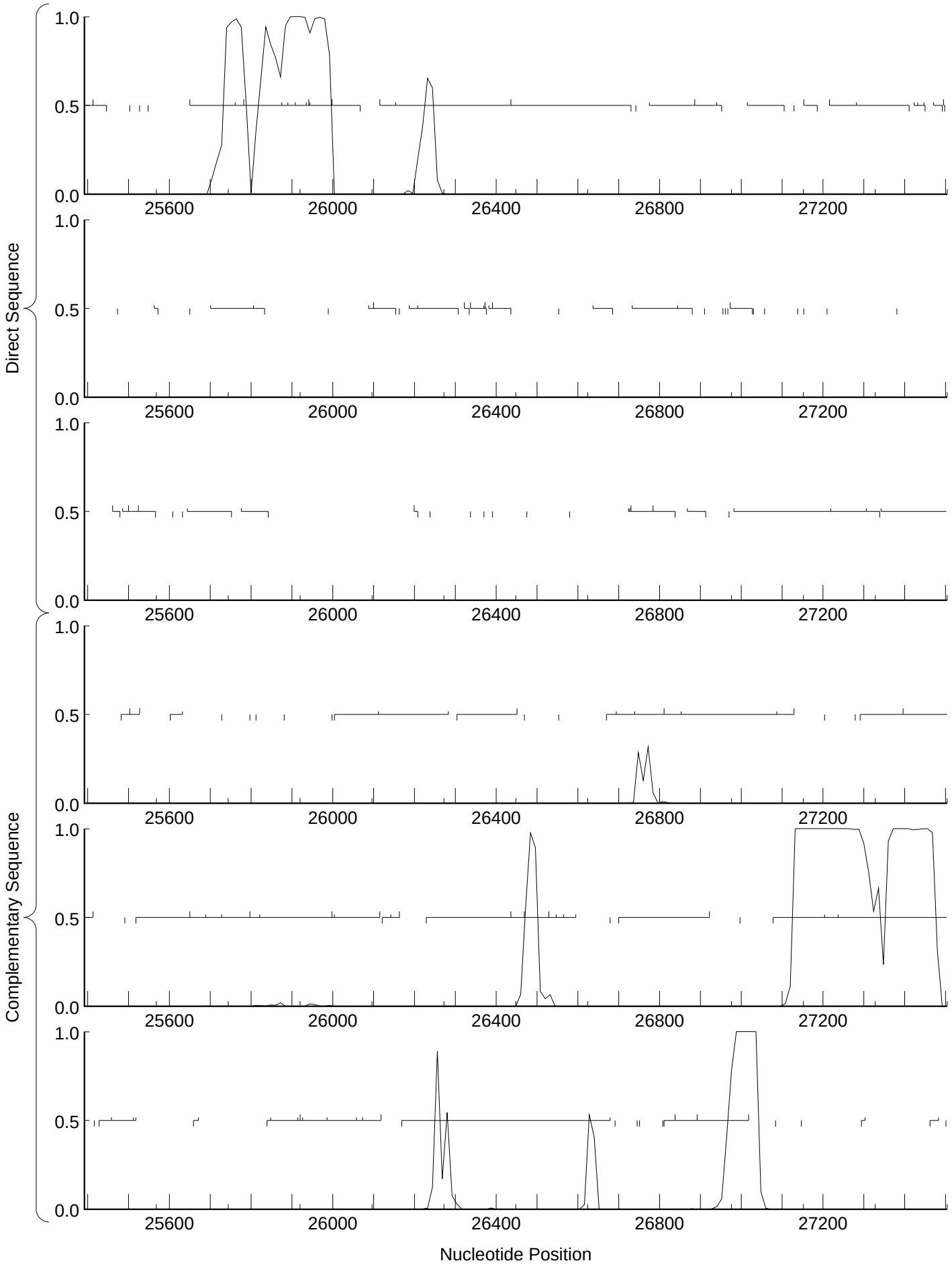


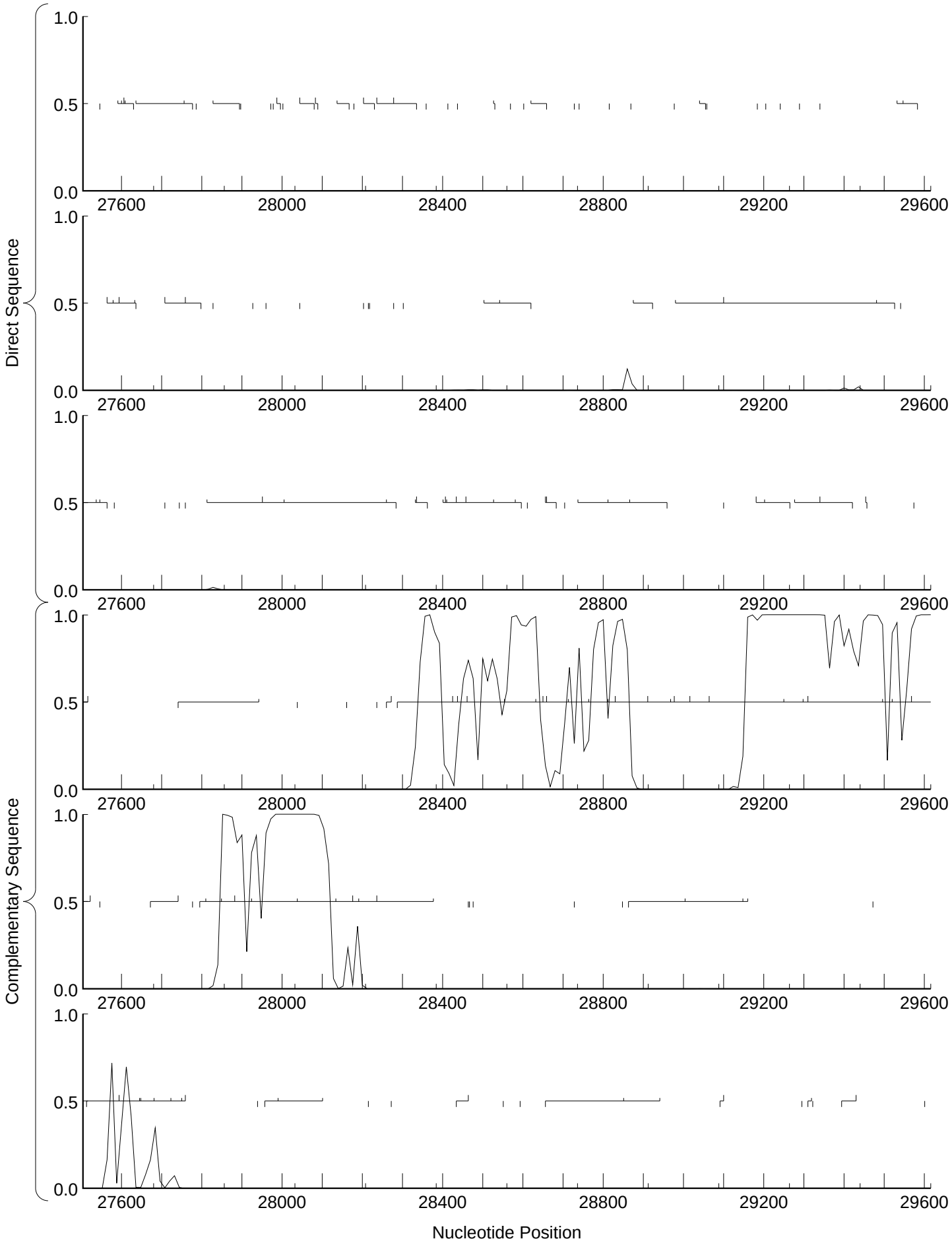
e ElTiger69 Complete Sequence, 51505 bp including 10-base 3’ overhang (CGGGAGGTAA), Order 4, Window 96, Step 12, 12/26



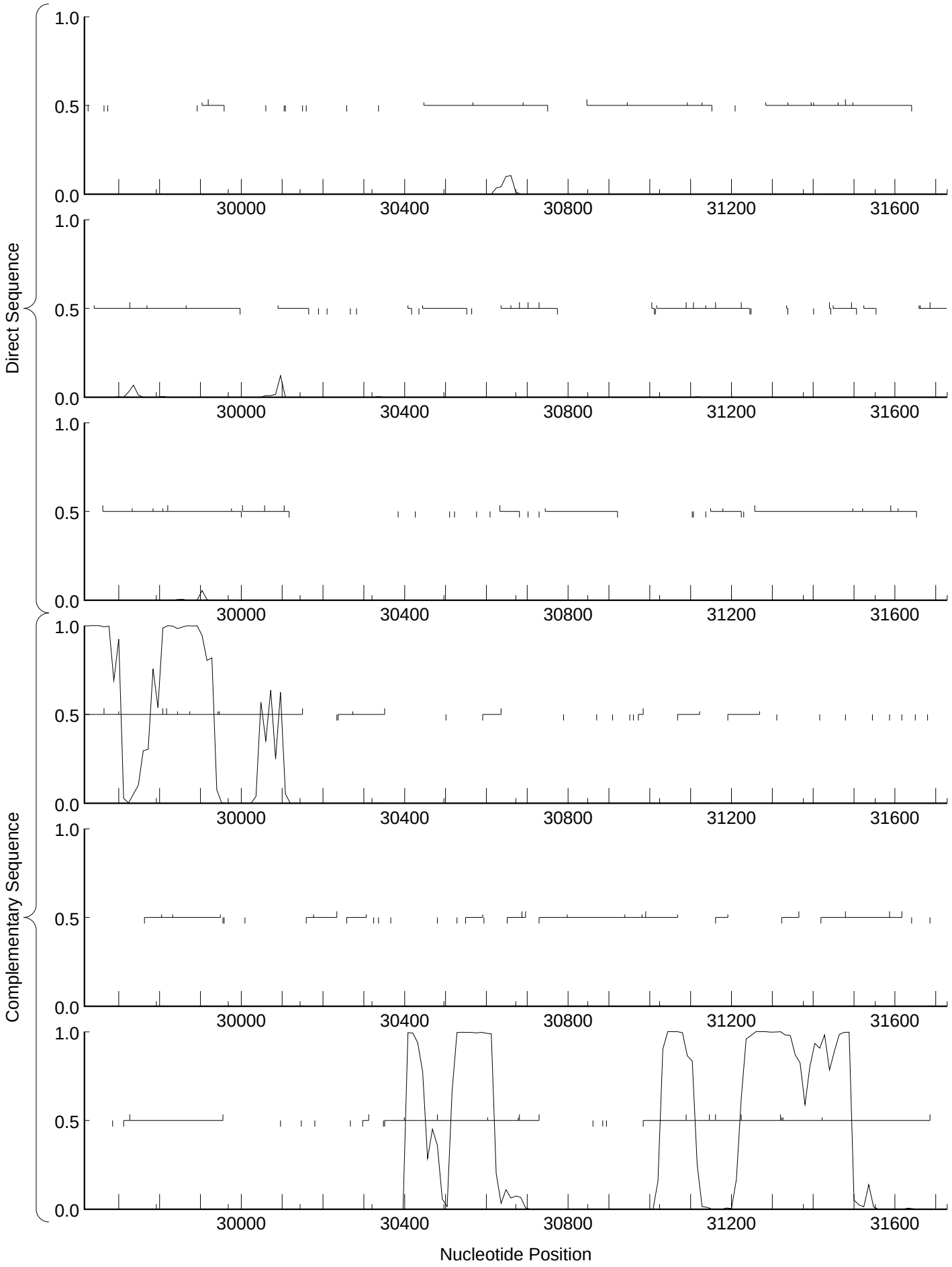
e ElTiger69 Complete Sequence, 51505 bp including 10-base 3’ overhang (CGGGAGGTAA), Order 4, Window 96, Step 12, 13/26

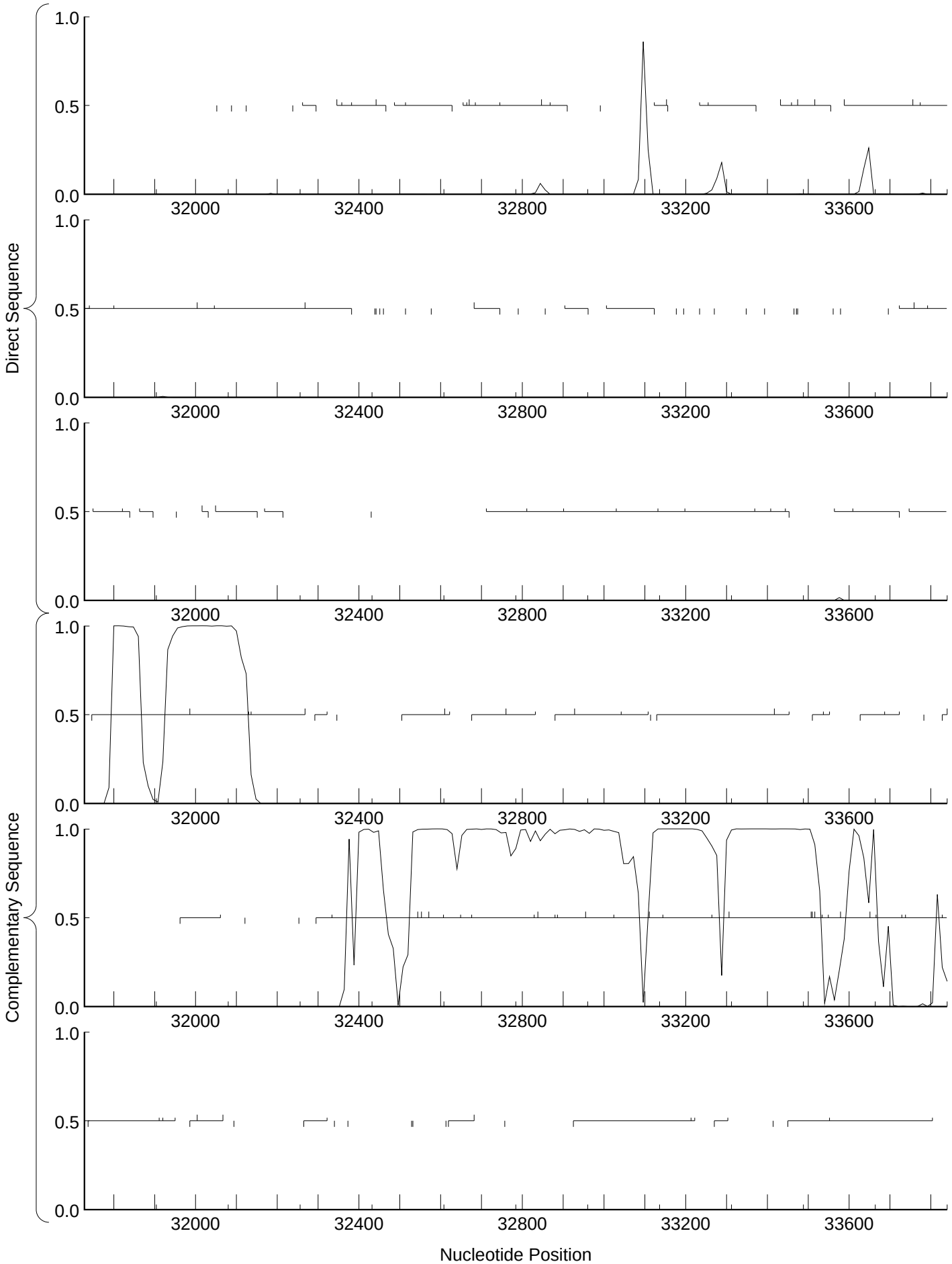


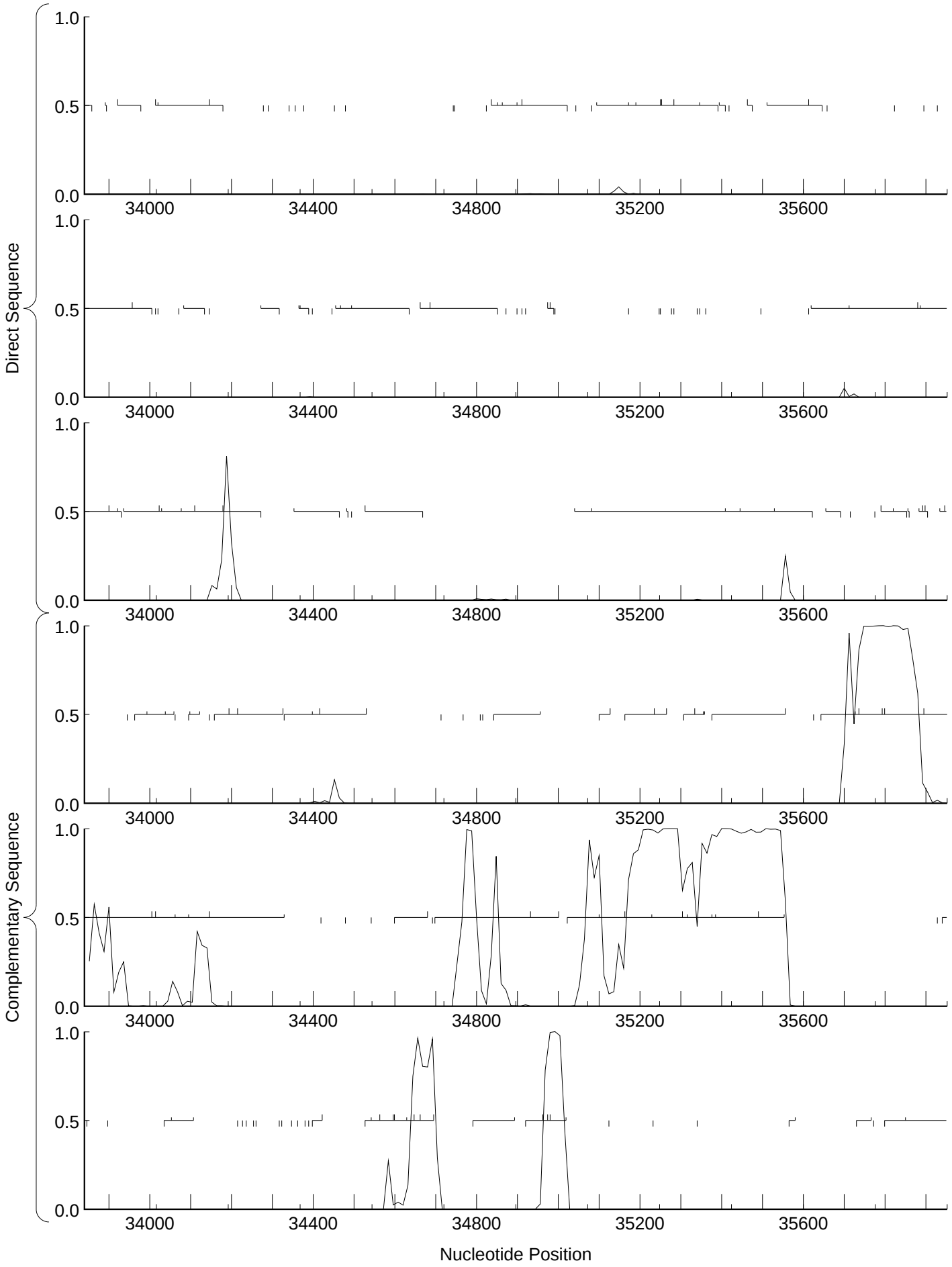

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
25600
26000
26400
26800
27200
Nucleotide Position


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

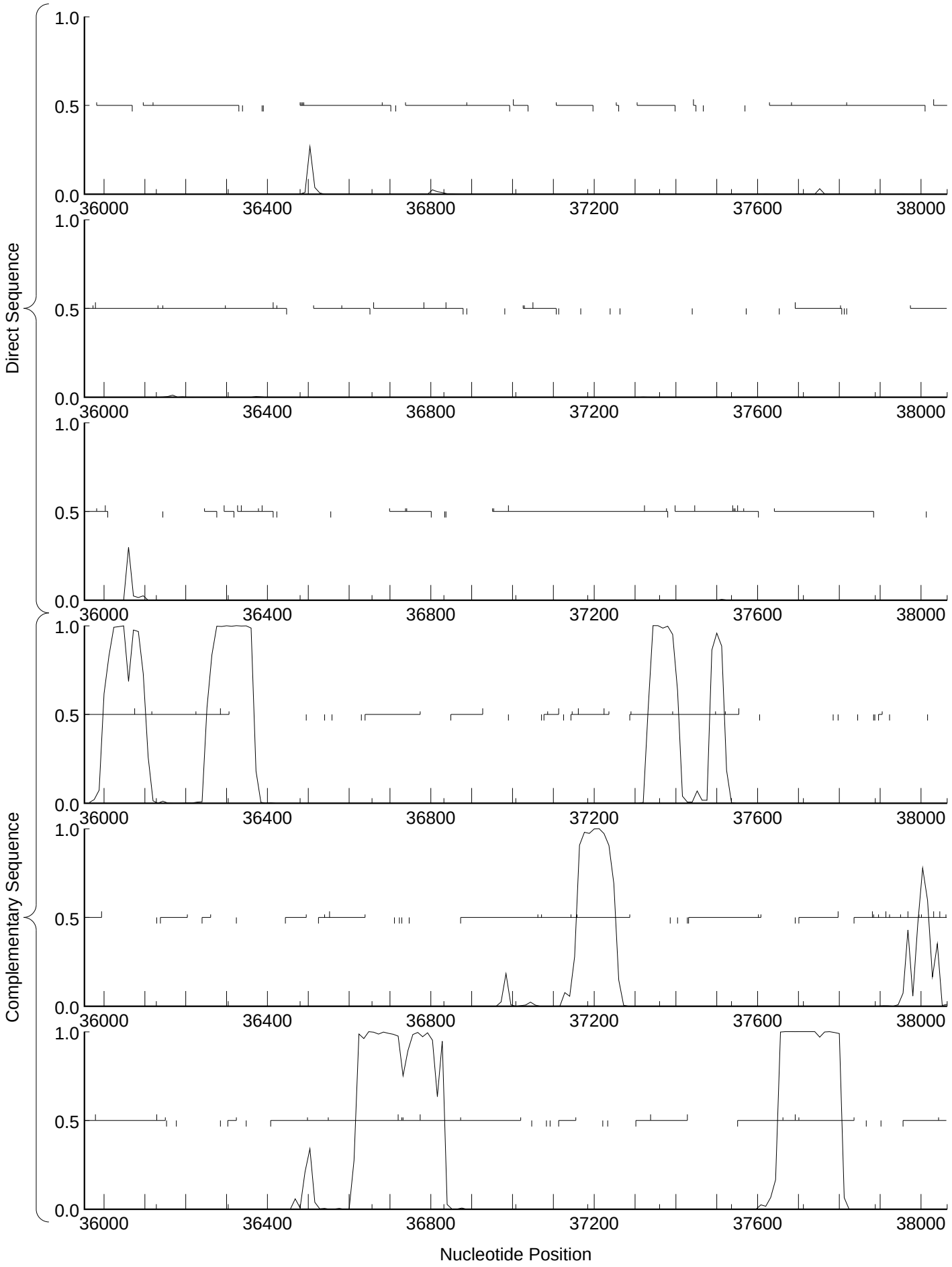
e ElTiger69 Complete Sequence, 51505 bp including 10-base 3’ overhang (CGGGAGGTAA), Order 4, Window 96, Step 12, 16/26



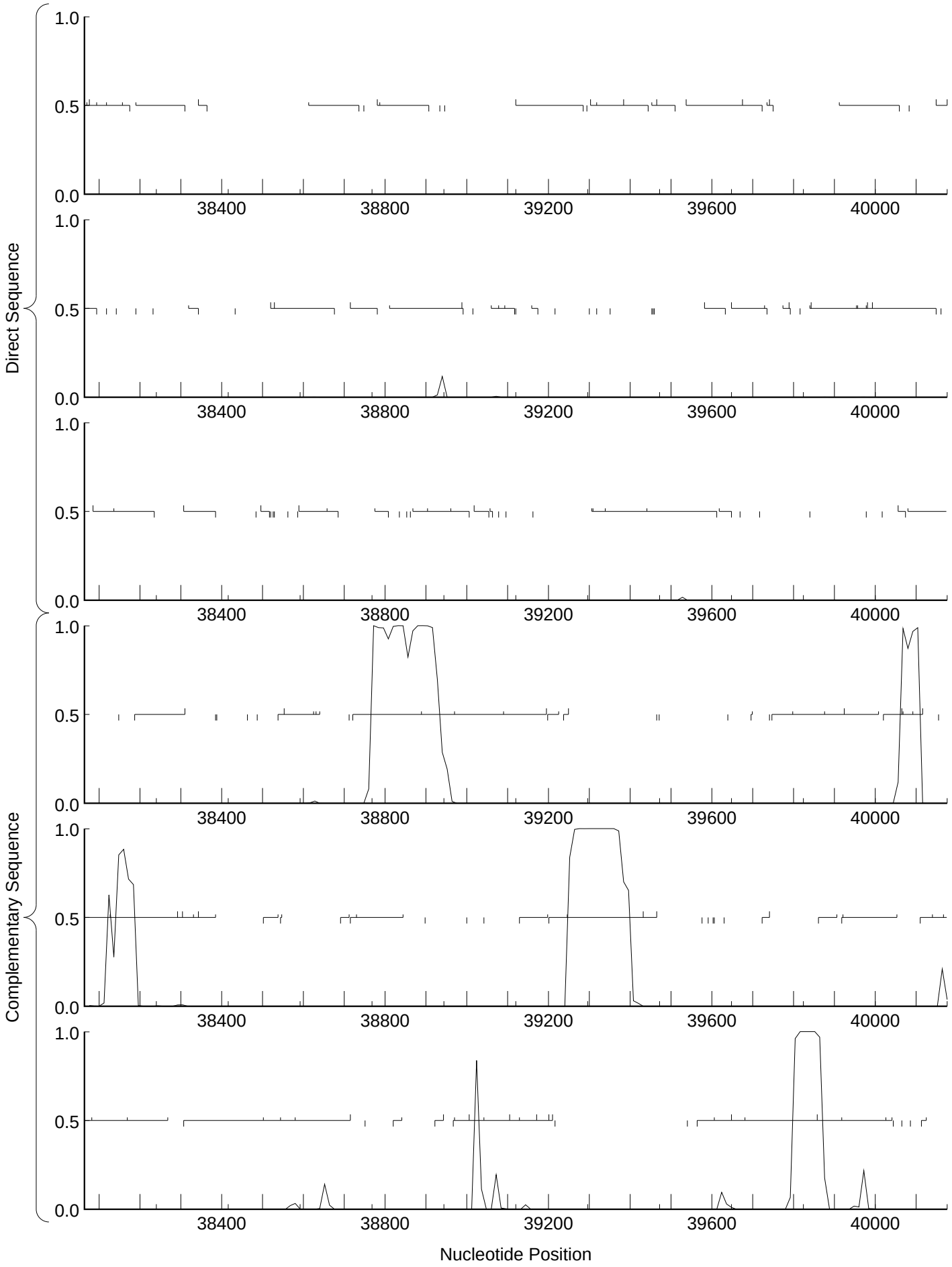

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
32000
32400
32800
33200
33600
Nucleotide Position


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

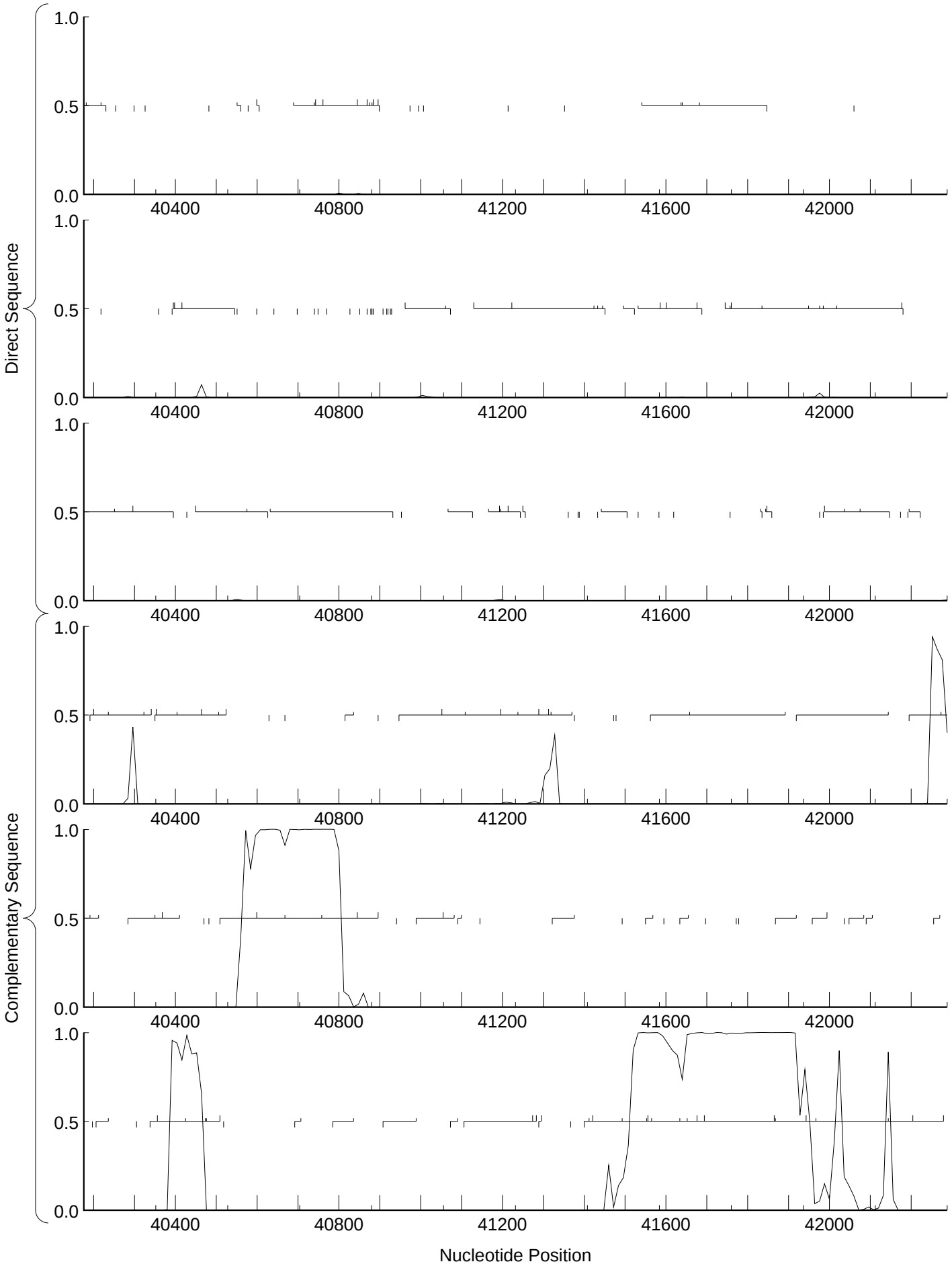
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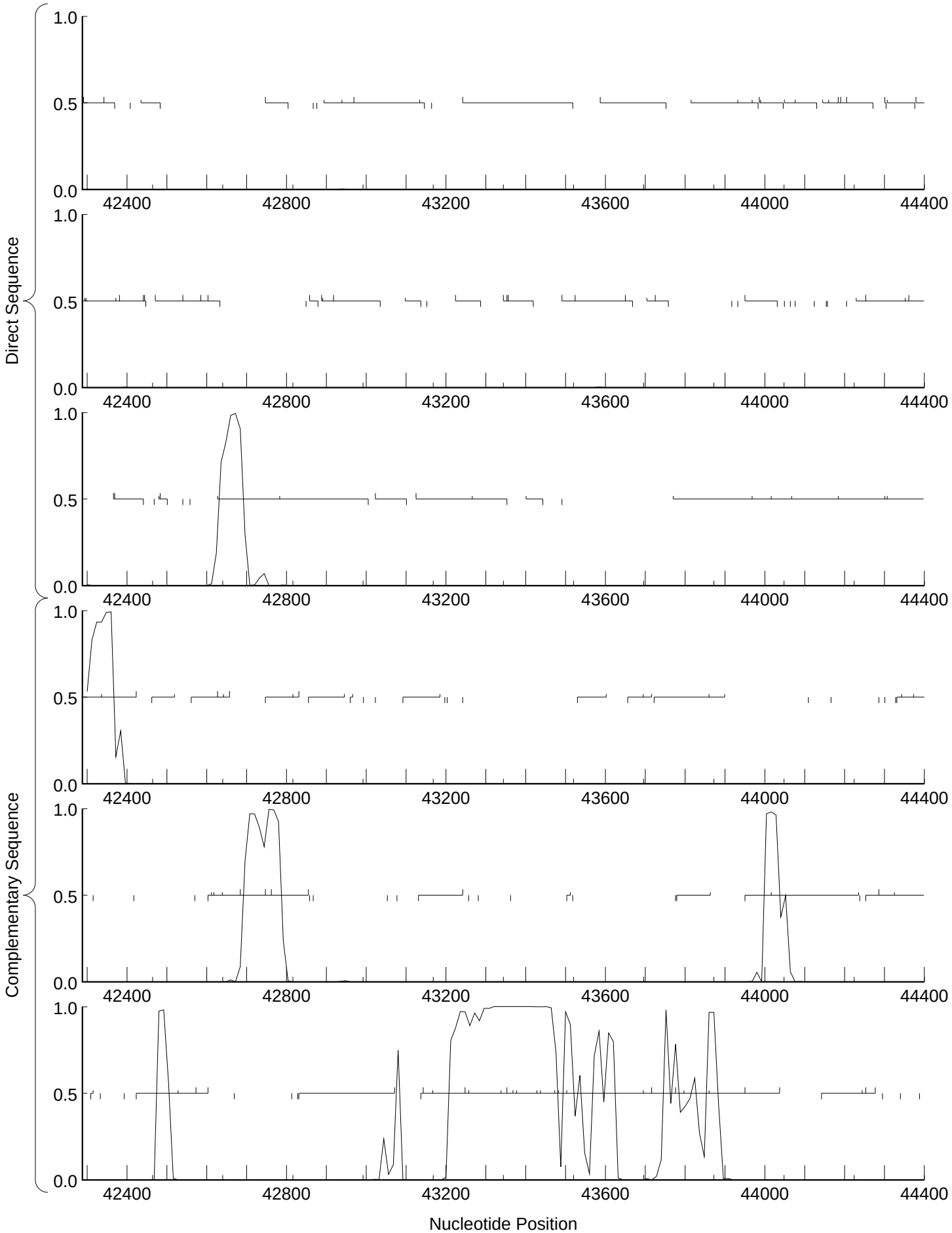


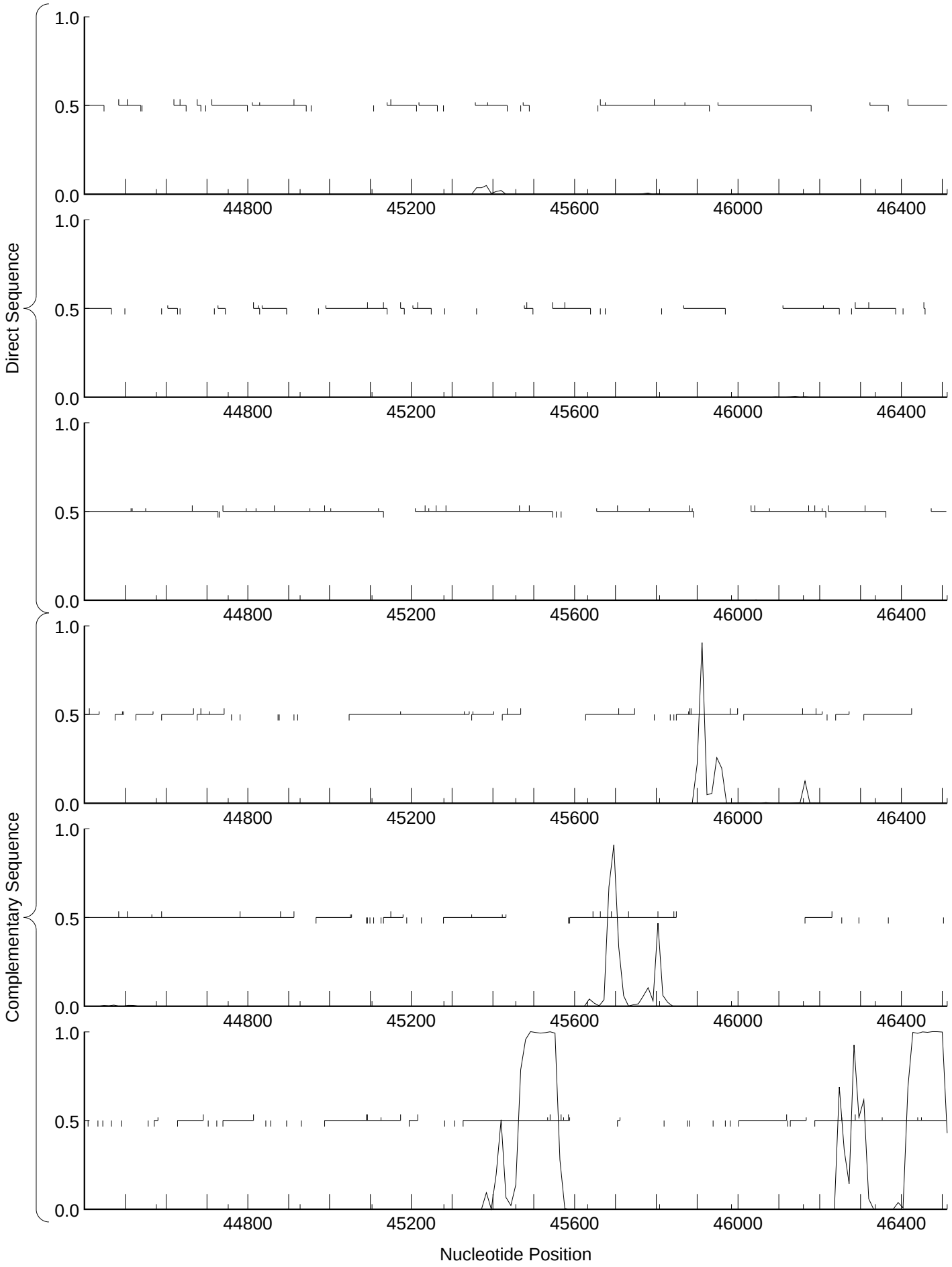
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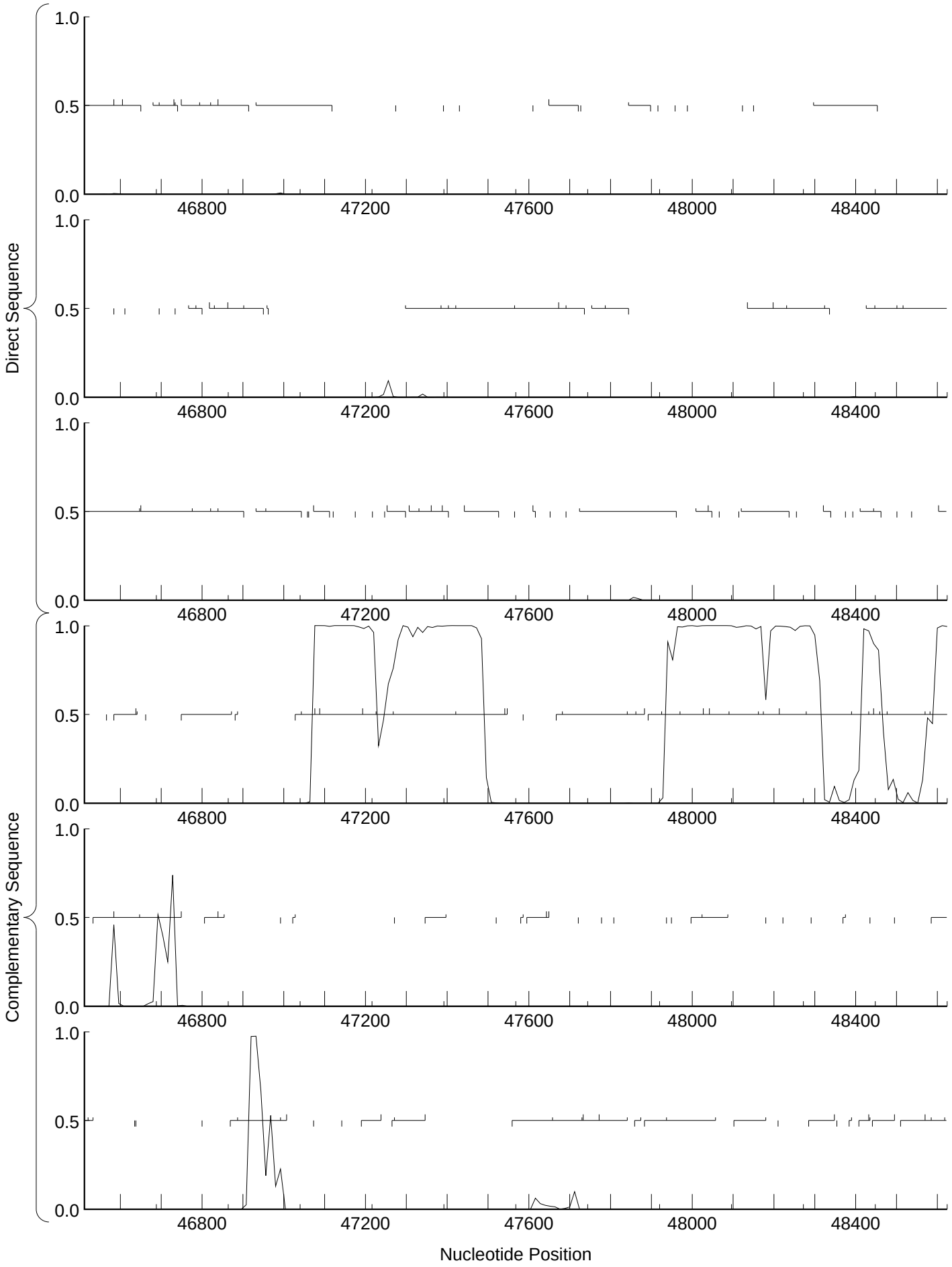


e ElTiger69 Complete Sequence, 51505 bp including 10-base 3’ overhang (CGGGAGGTAA), Order 4, Window 96, Step 12, 21/26

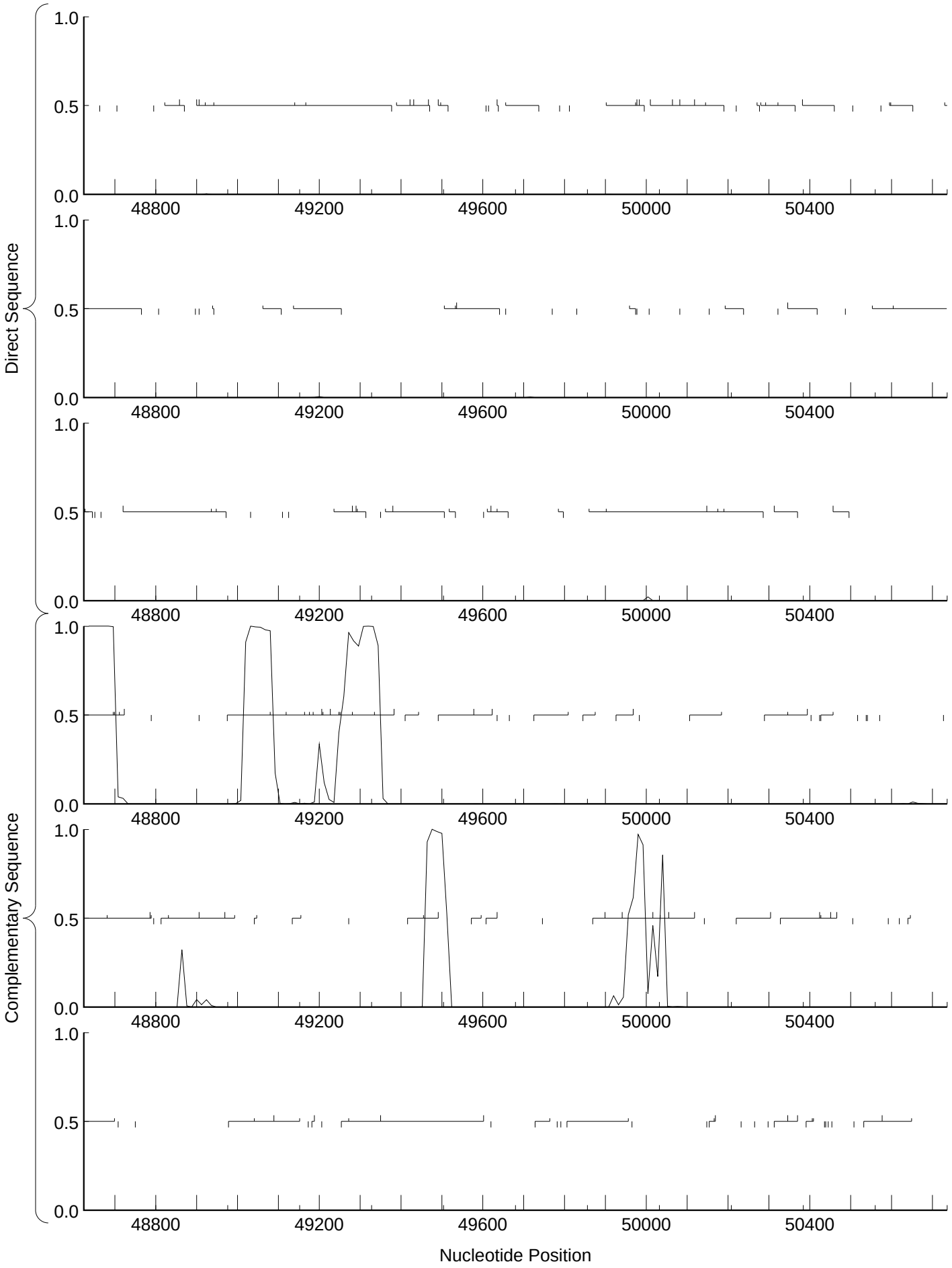



Direct Sequence
Complementary Sequence
1.0
0.5
0.0
42400
42800
43200
43600
44000
44400
Nucleotide Position


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

e ElTiger69 Complete Sequence, 51505 bp including 10-base 3’ overhang (CGGGAGGTAA), Order 4, Window 96, Step 12, 25/26



e ElTiger69 Complete Sequence, 51505 bp including 10-base 3’ overhang (CGGGAGGTAA), Order 4, Window 96, Step 12, 26/26

