GeneMark

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

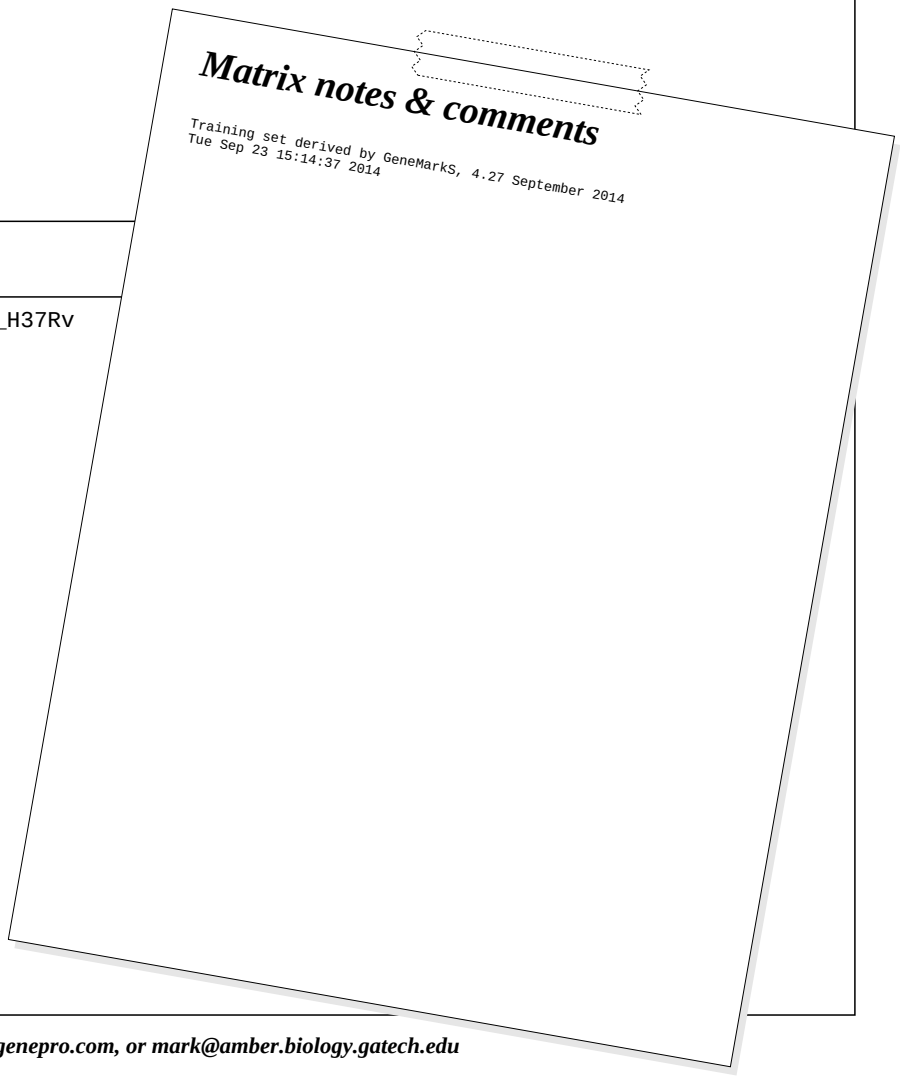
PROGRAM INFORMATION

```
Sequence         :  Mycobacterium phage Beakin complete sequence, 54926 bp including 10-base 3' overhang (CCGAC
Analysis Date    :  3/29/24 at 2:08:05
Pages            :  28
Sequence Length  :  54926 bp
GC Content       :   61.25%

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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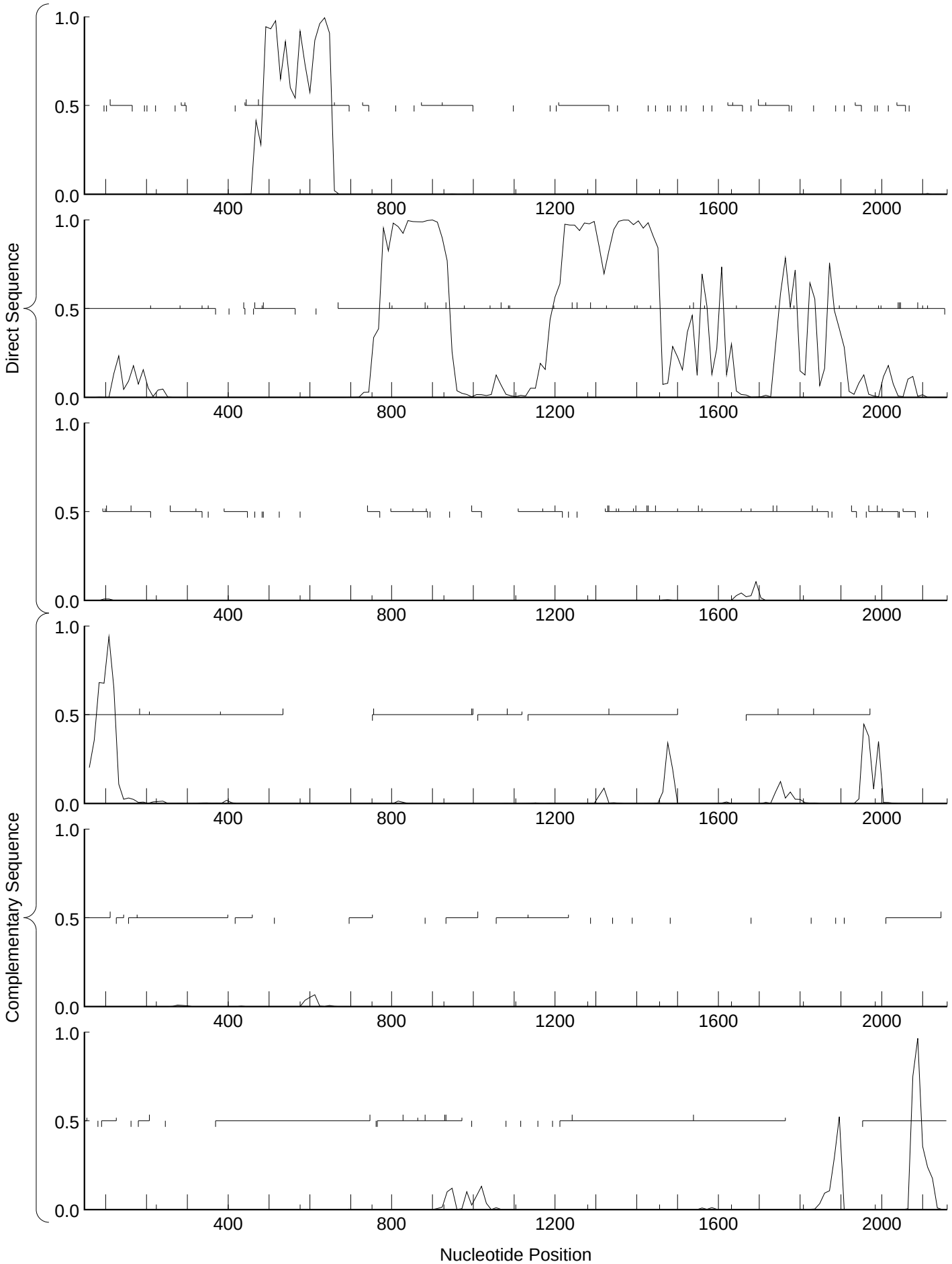
MATRIX INFORMATION

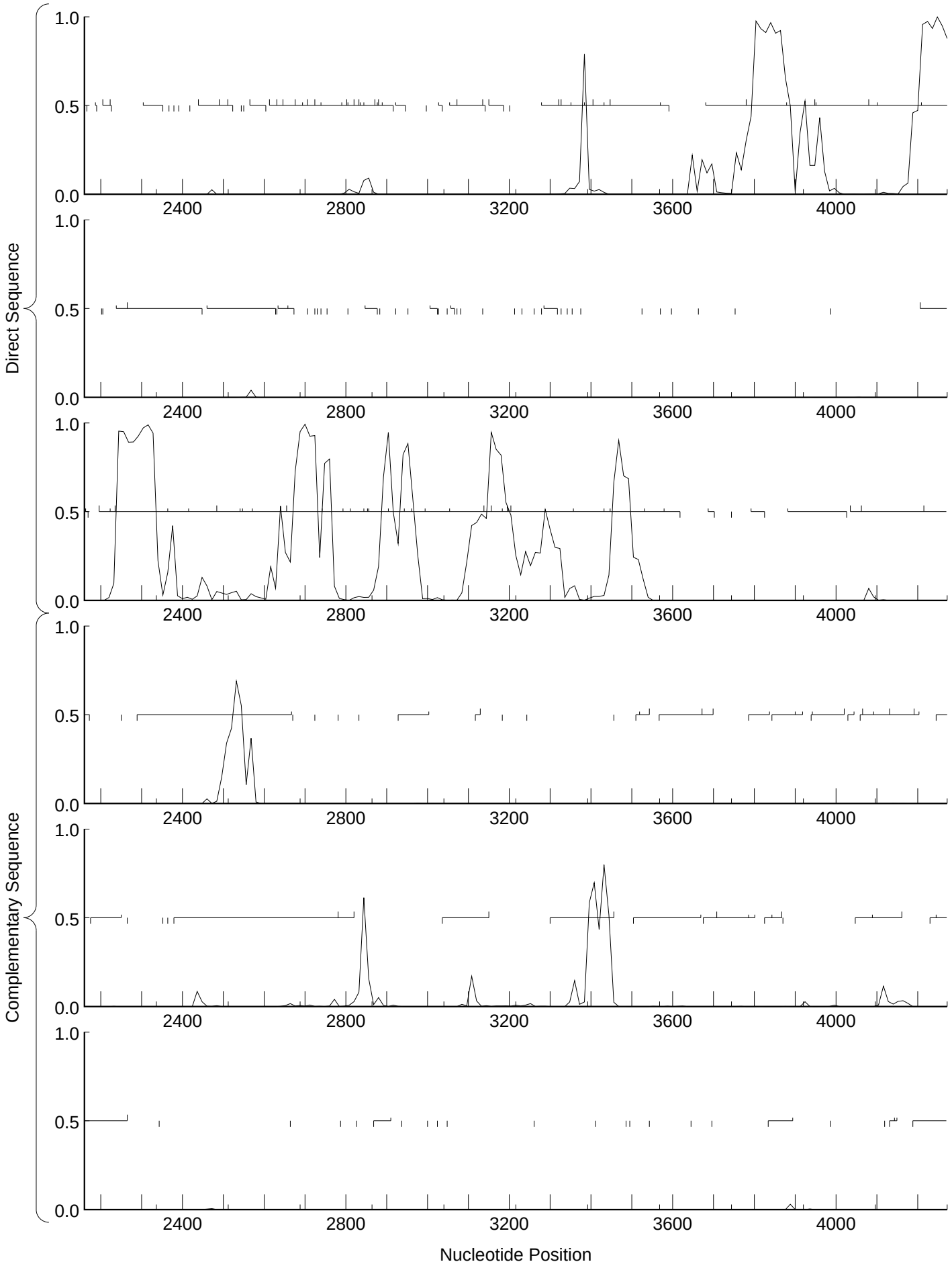
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Matrix     :  Mycobacterium_tuberculosis_H37Rv
Author     :  -

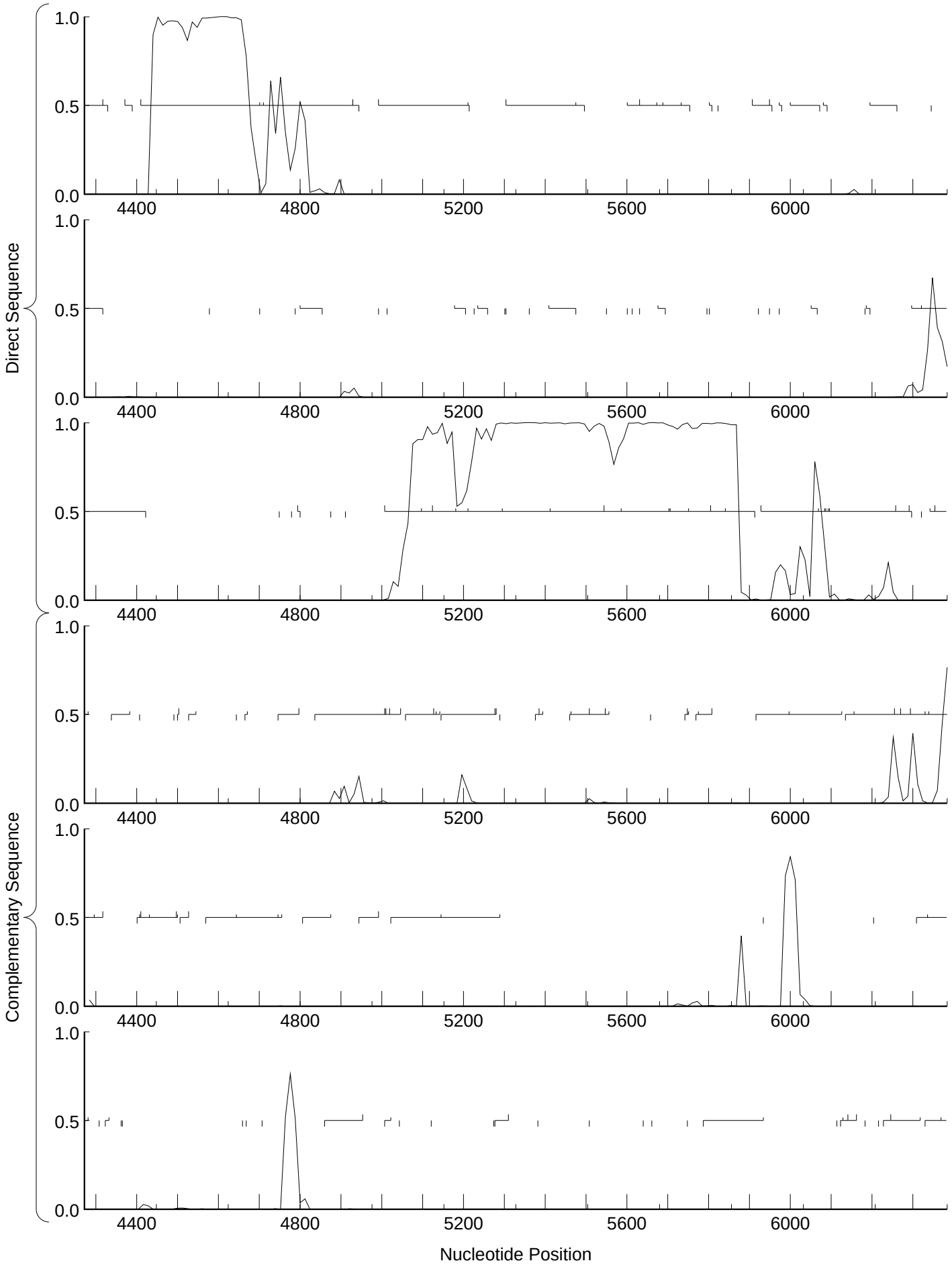
Order      :  4
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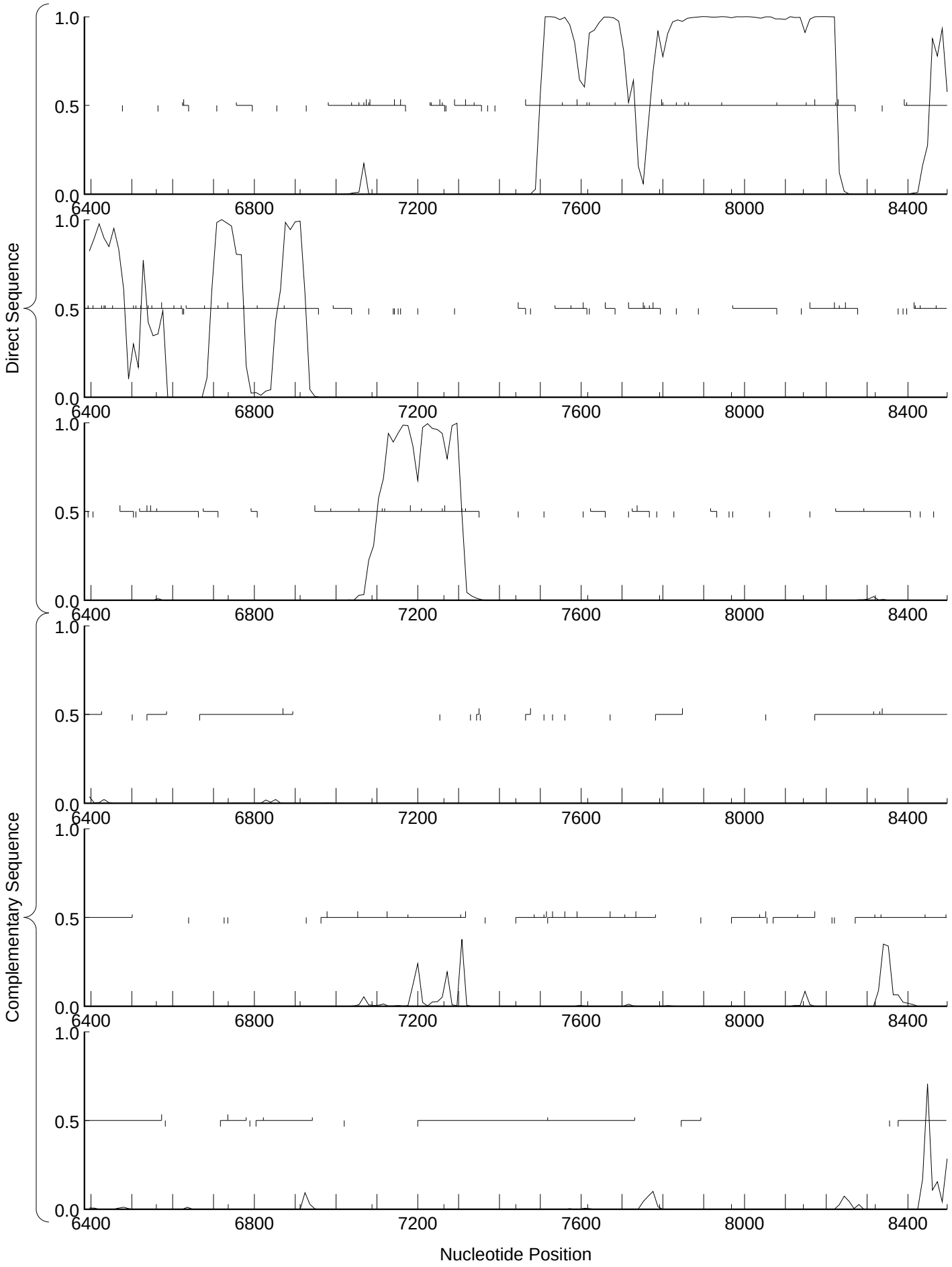

```
  Send questions / comments to:
      Dr. M. Borodovsky
      Georgia Institute of Technology
      School of Biology
      Atlanta, GA  30332-0230
```

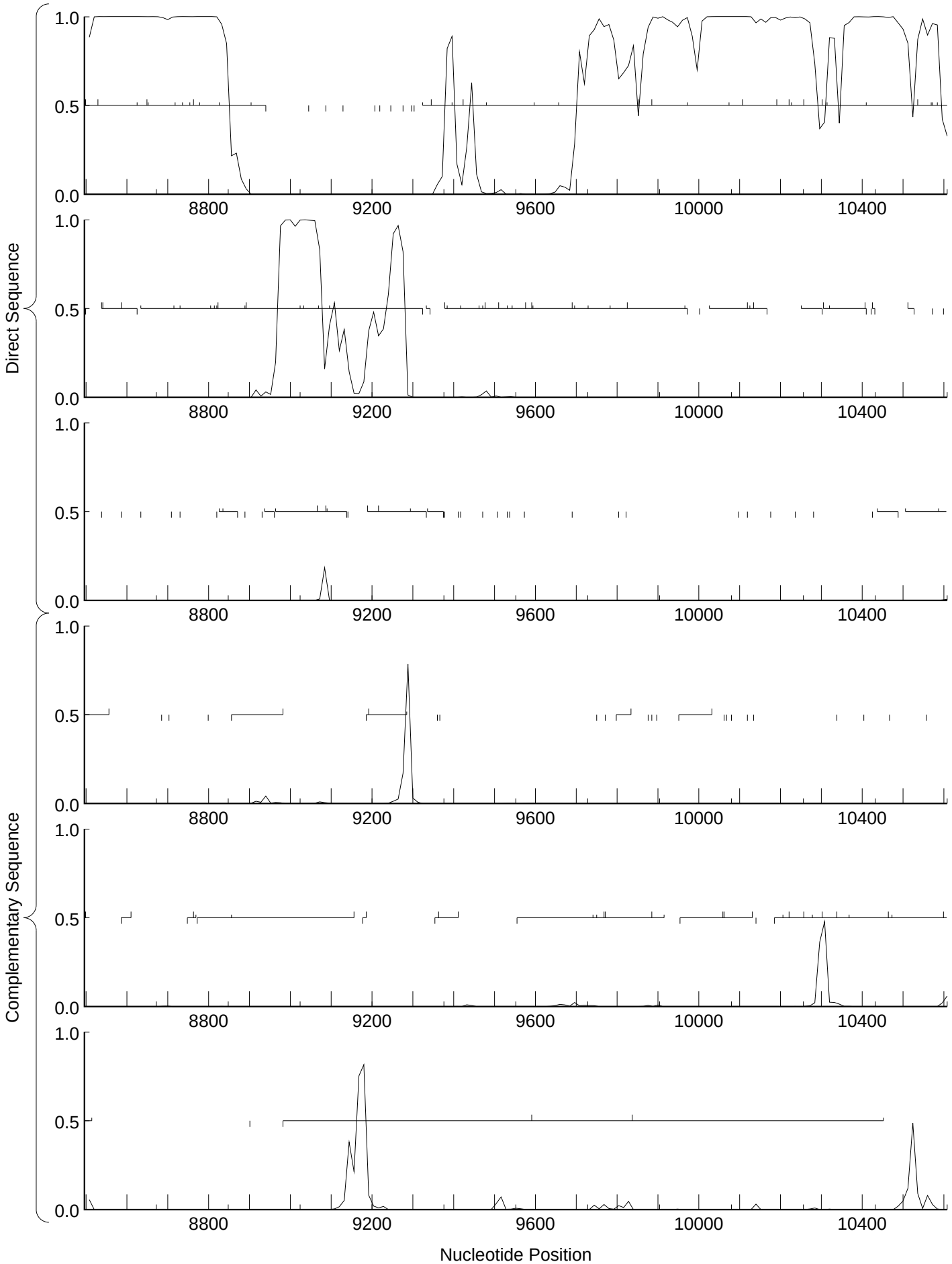

For help or information, send electronic mail to: custserv@genepro.com, or mark@amber.biology.gatech.edu

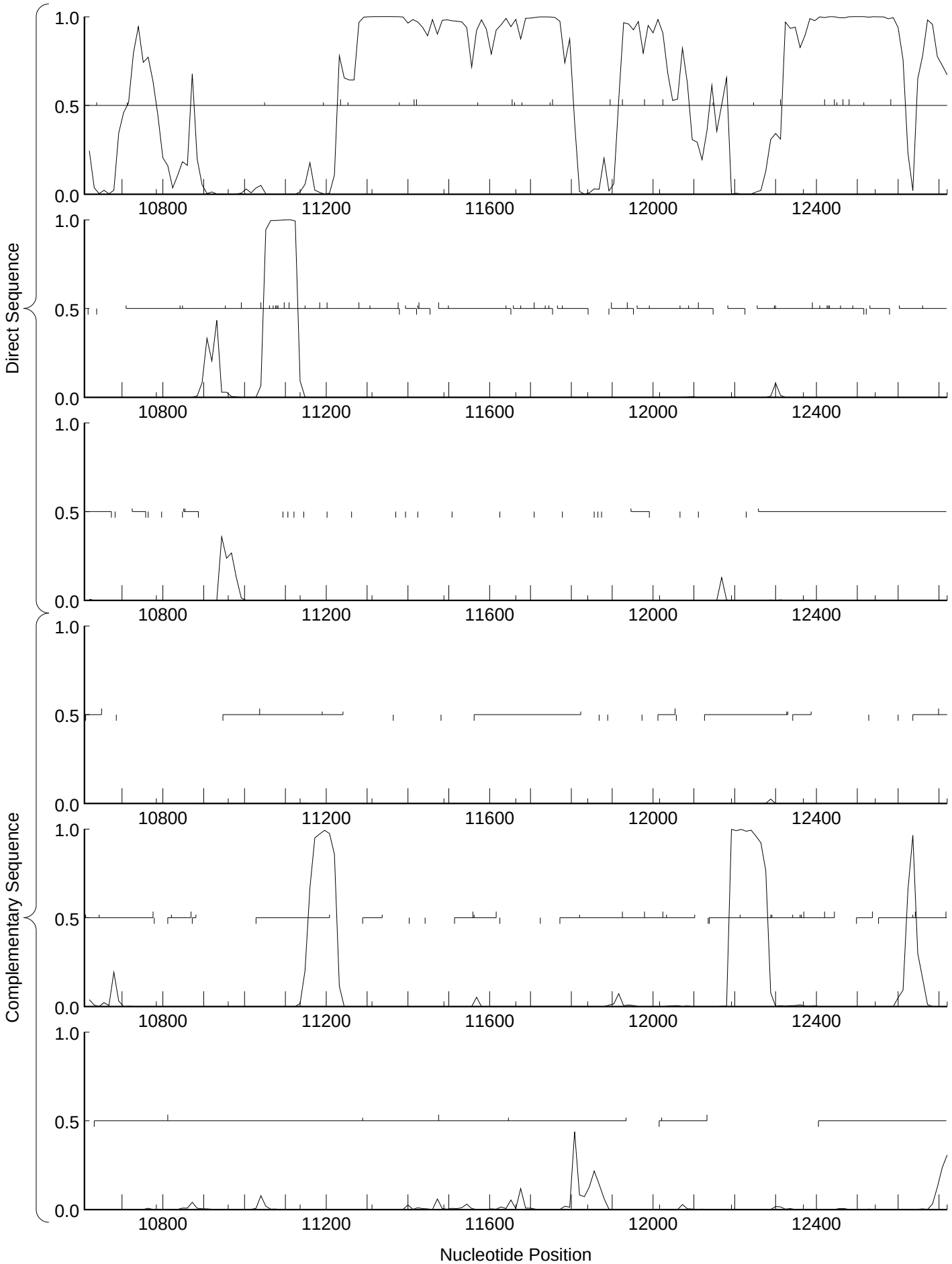

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
400
800
1200
1600
2000
Nucleotide Position

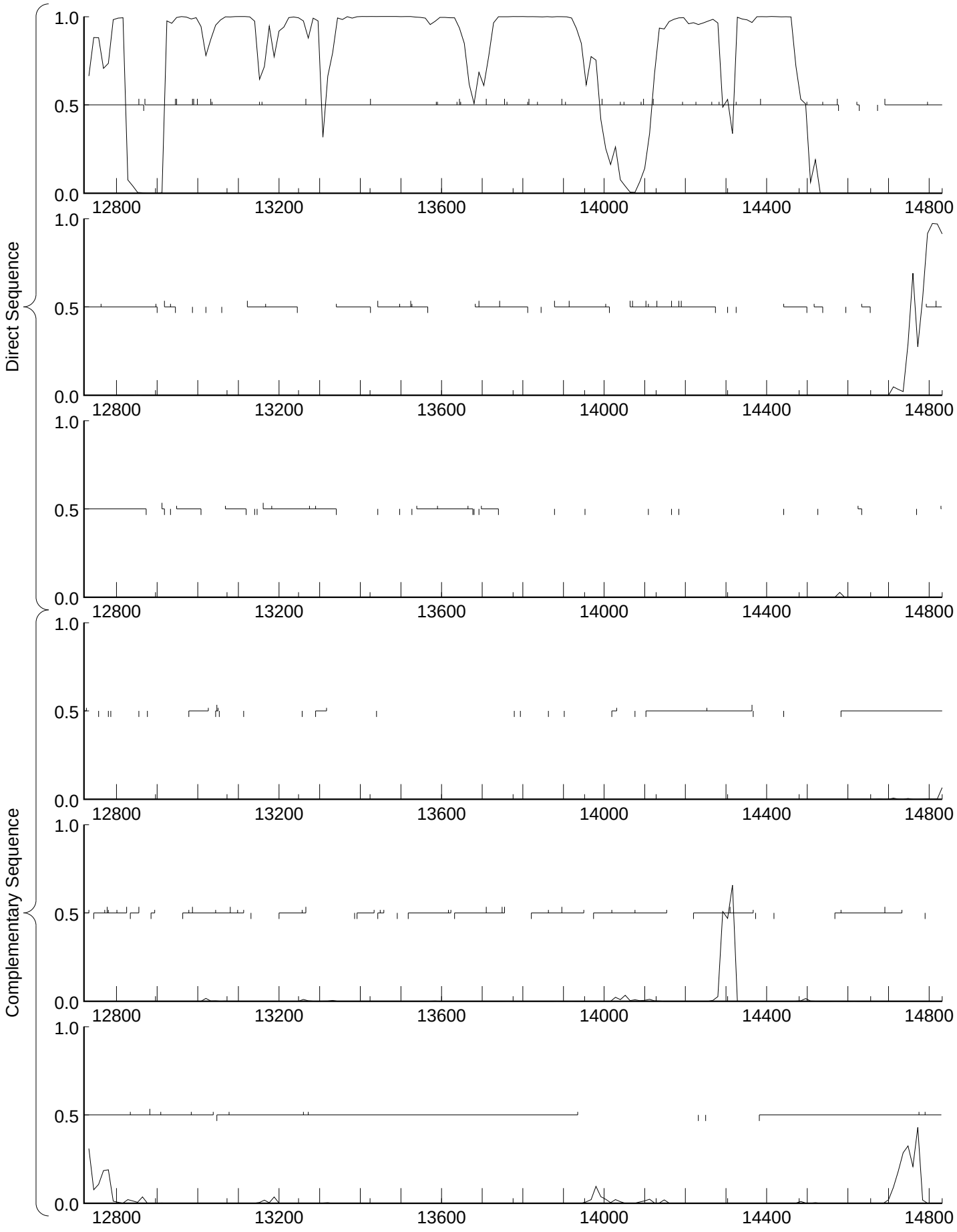

Direct Sequence
Complementary Sequence
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0.5
0.0
2400
2800
3200
3600
4000
Nucleotide Position

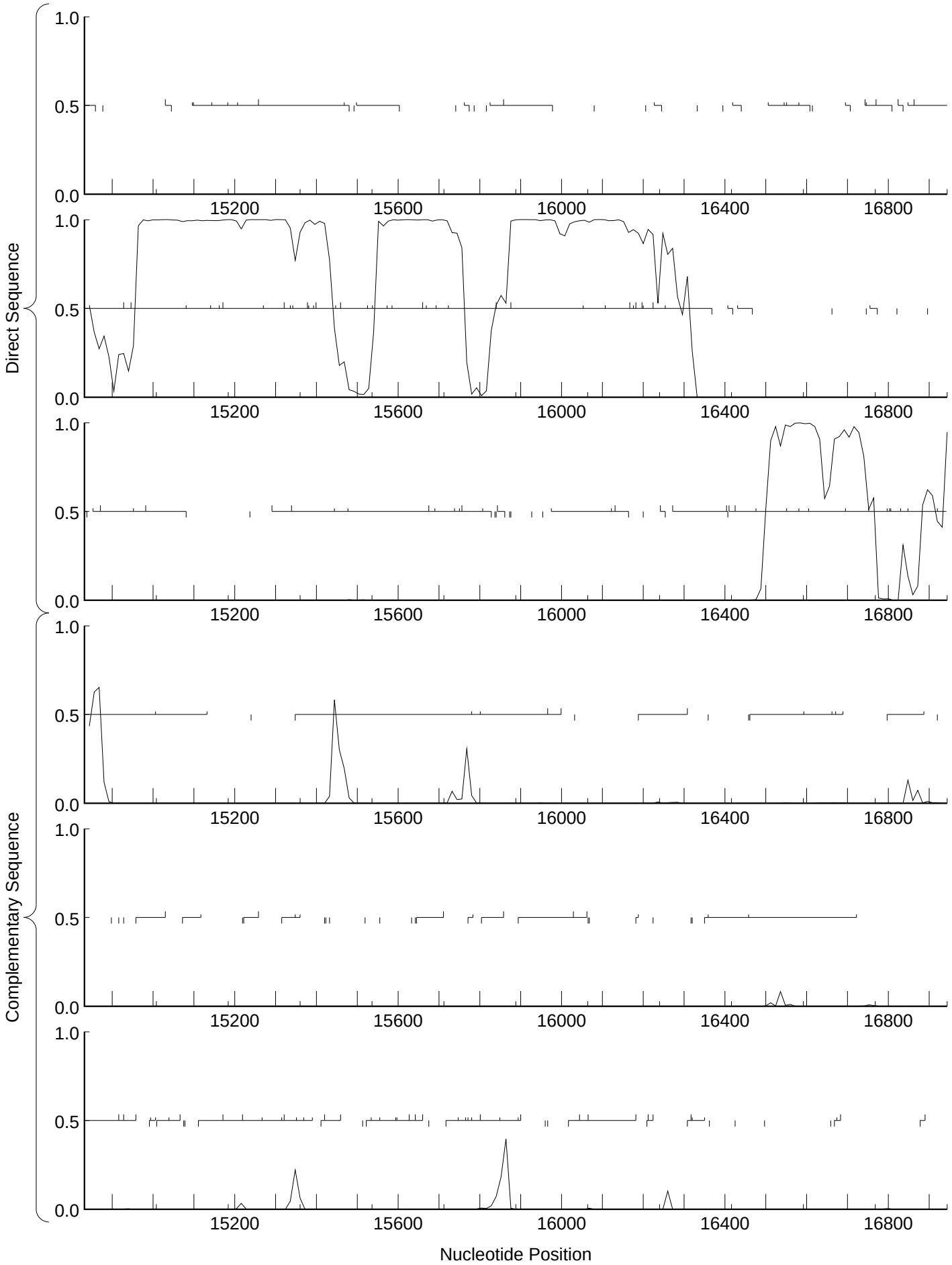

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
4400
4800
5200
5600
6000
Nucleotide Position


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
6400
6800
7200
7600
8000
8400
Nucleotide Position

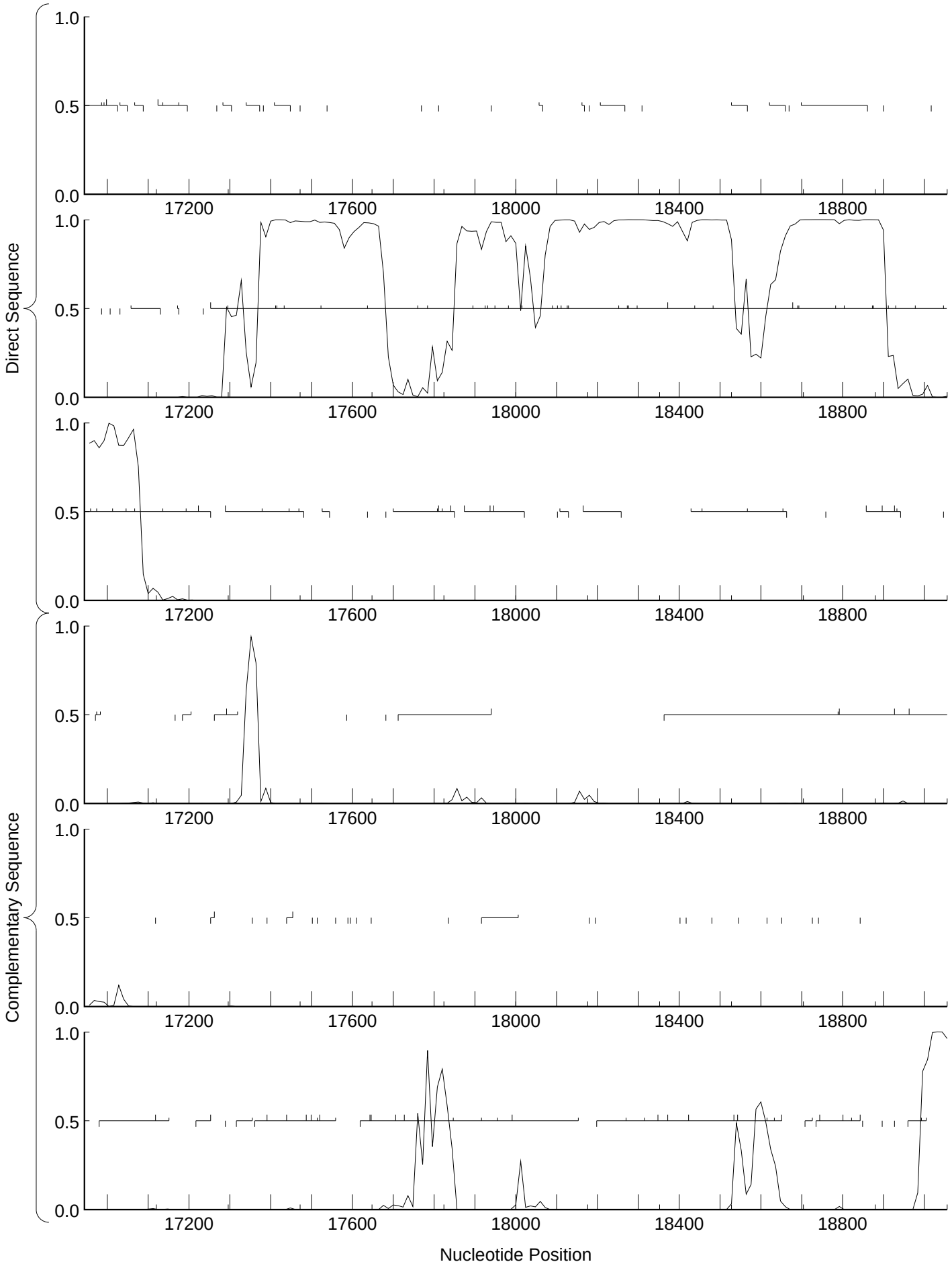

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Complementary Sequence
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0.0
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9600
10000
10400
Nucleotide Position

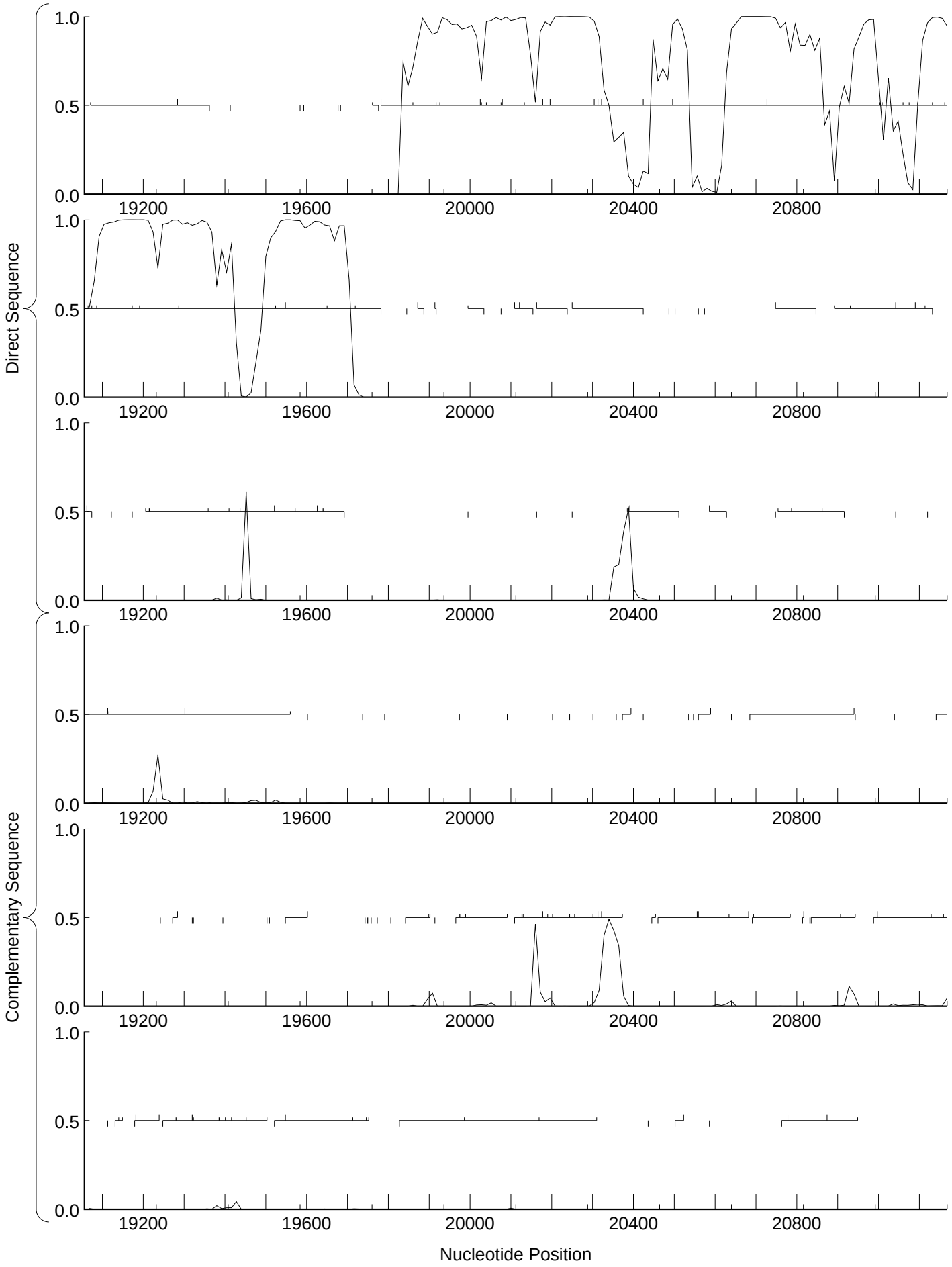

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
10800
11200
11600
12000
12400
Nucleotide Position


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

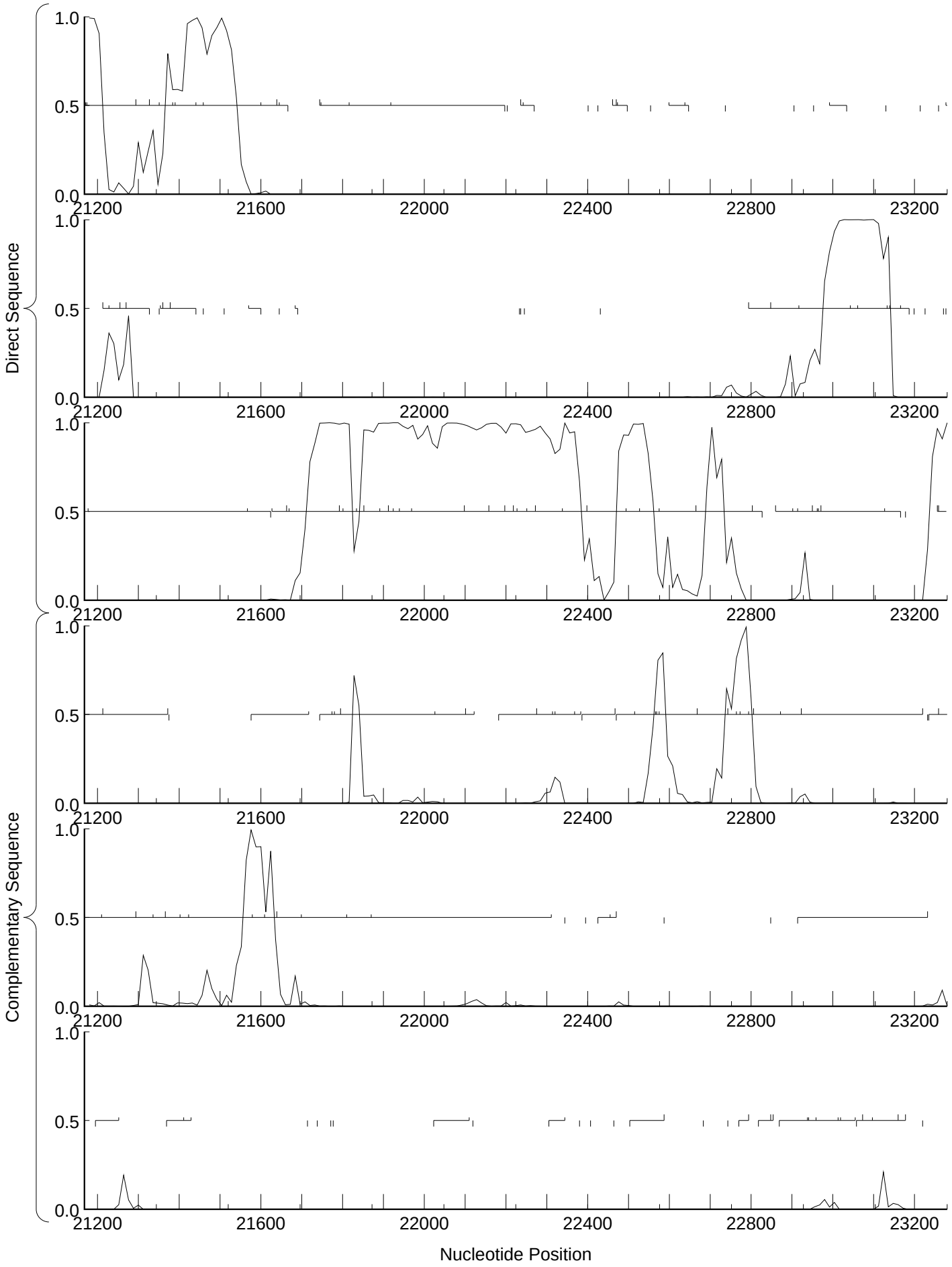

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
15200
15600
16000
16400
16800
Nucleotide Position

nage Beakin complete sequence, 54926 bp including 10-base 3’ overhang (CCGACGGCAT), Order 4, Window 96, Step 12, 10/28

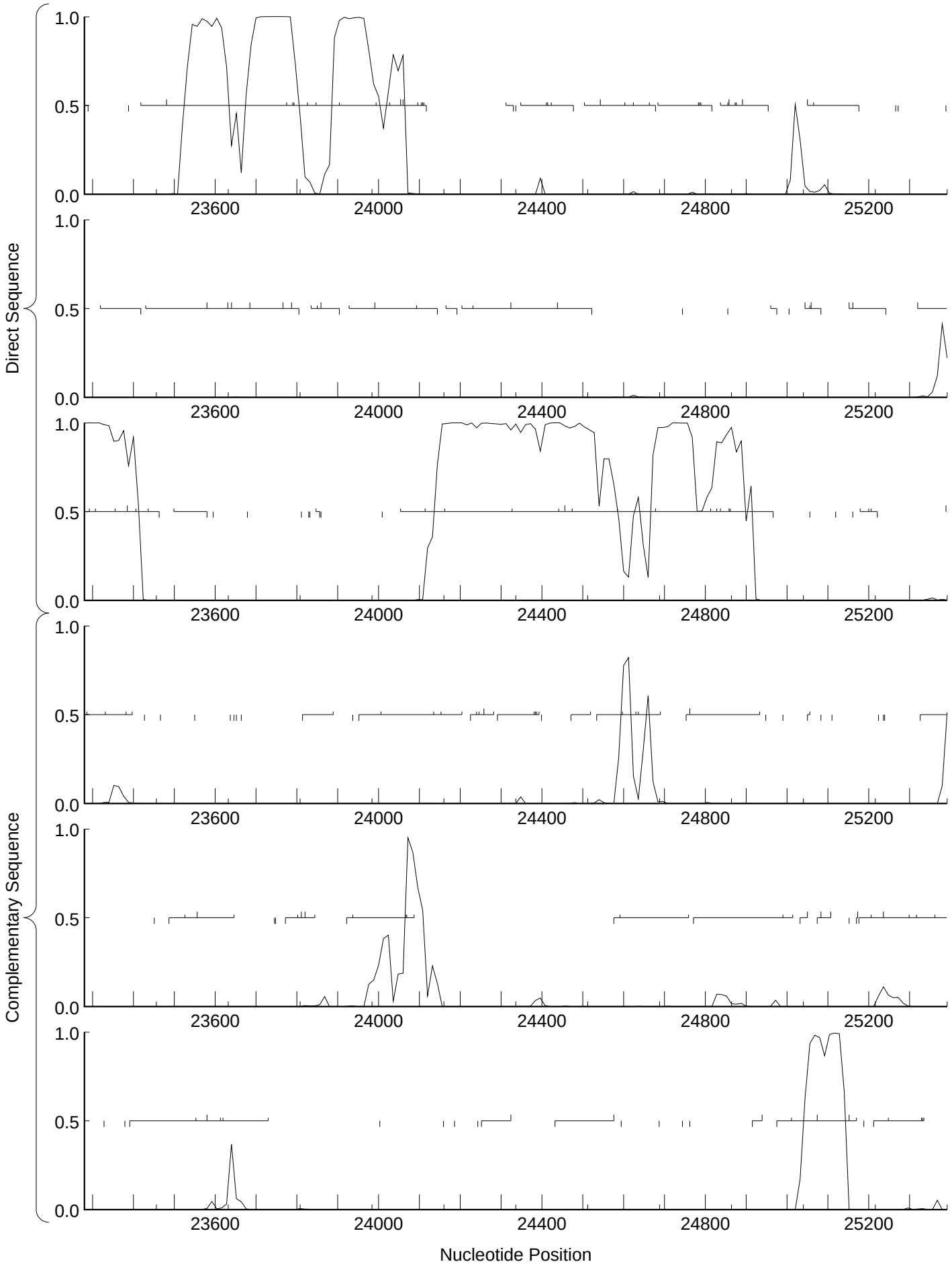



Direct Sequence
Complementary Sequence
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0.5
0.0
19200
19600
20000
20400
20800
Nucleotide Position

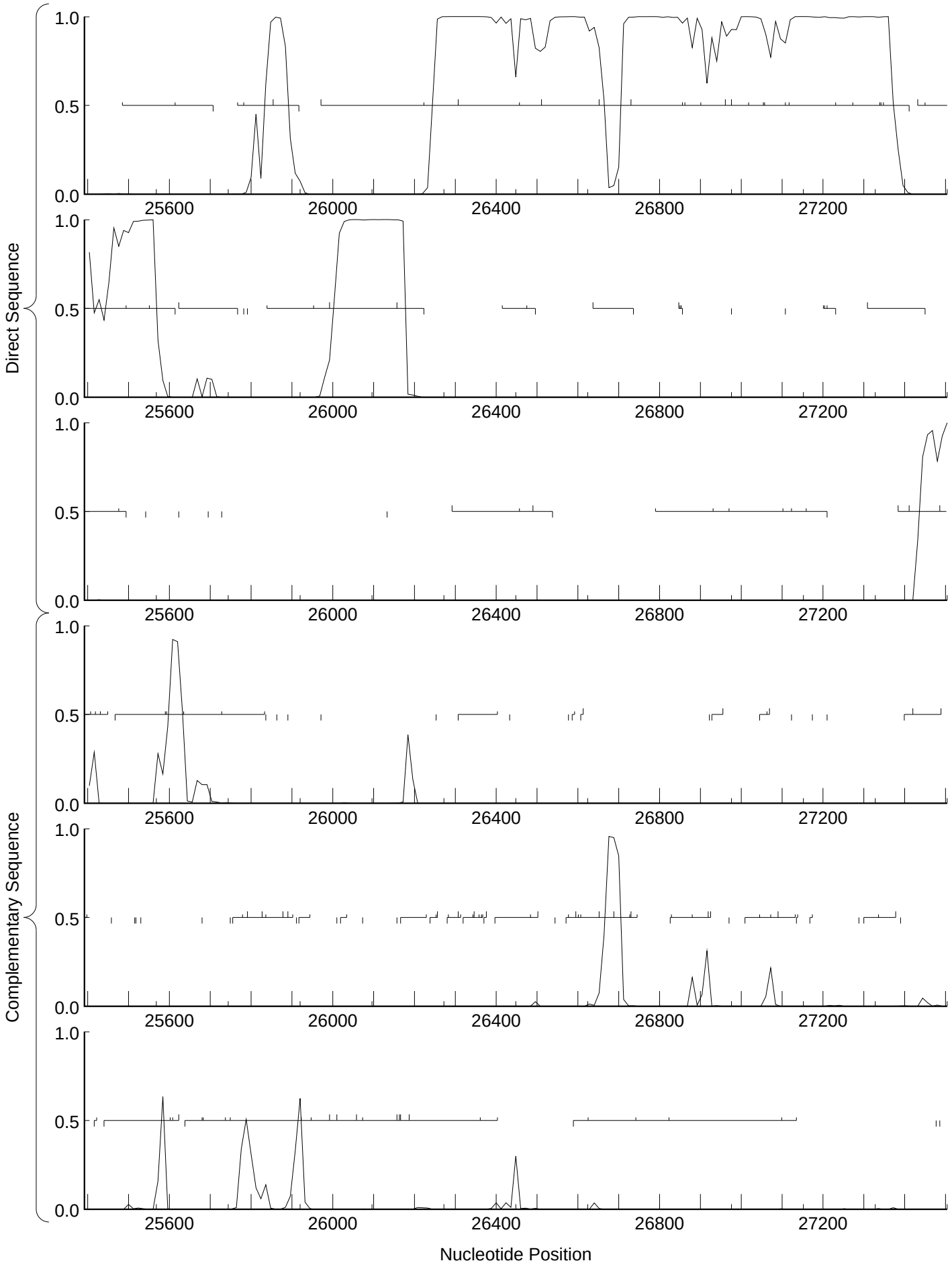
nage Beakin complete sequence, 54926 bp including 10-base 3’ overhang (CCGACGGCAT), Order 4, Window 96, Step 12, 12/28

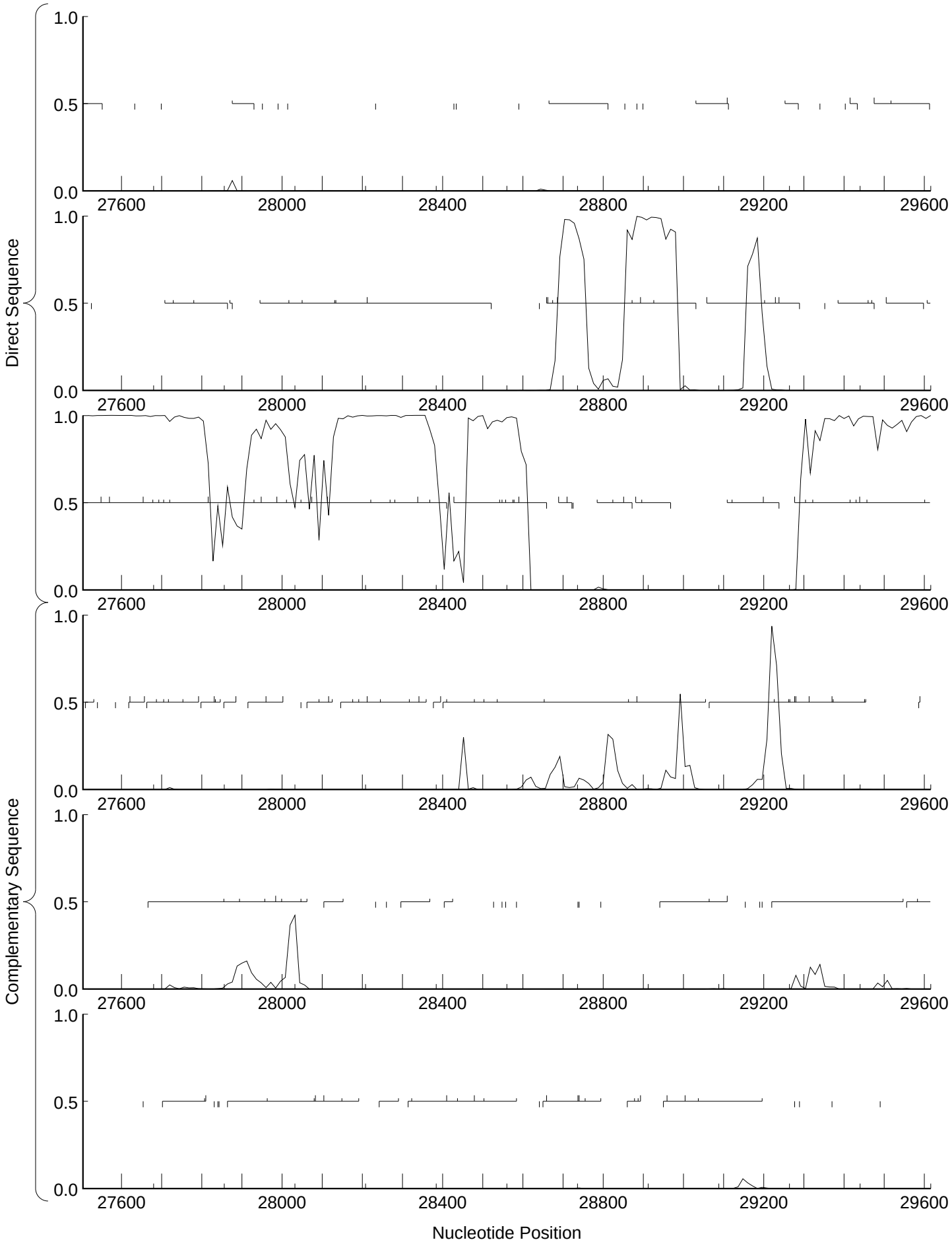


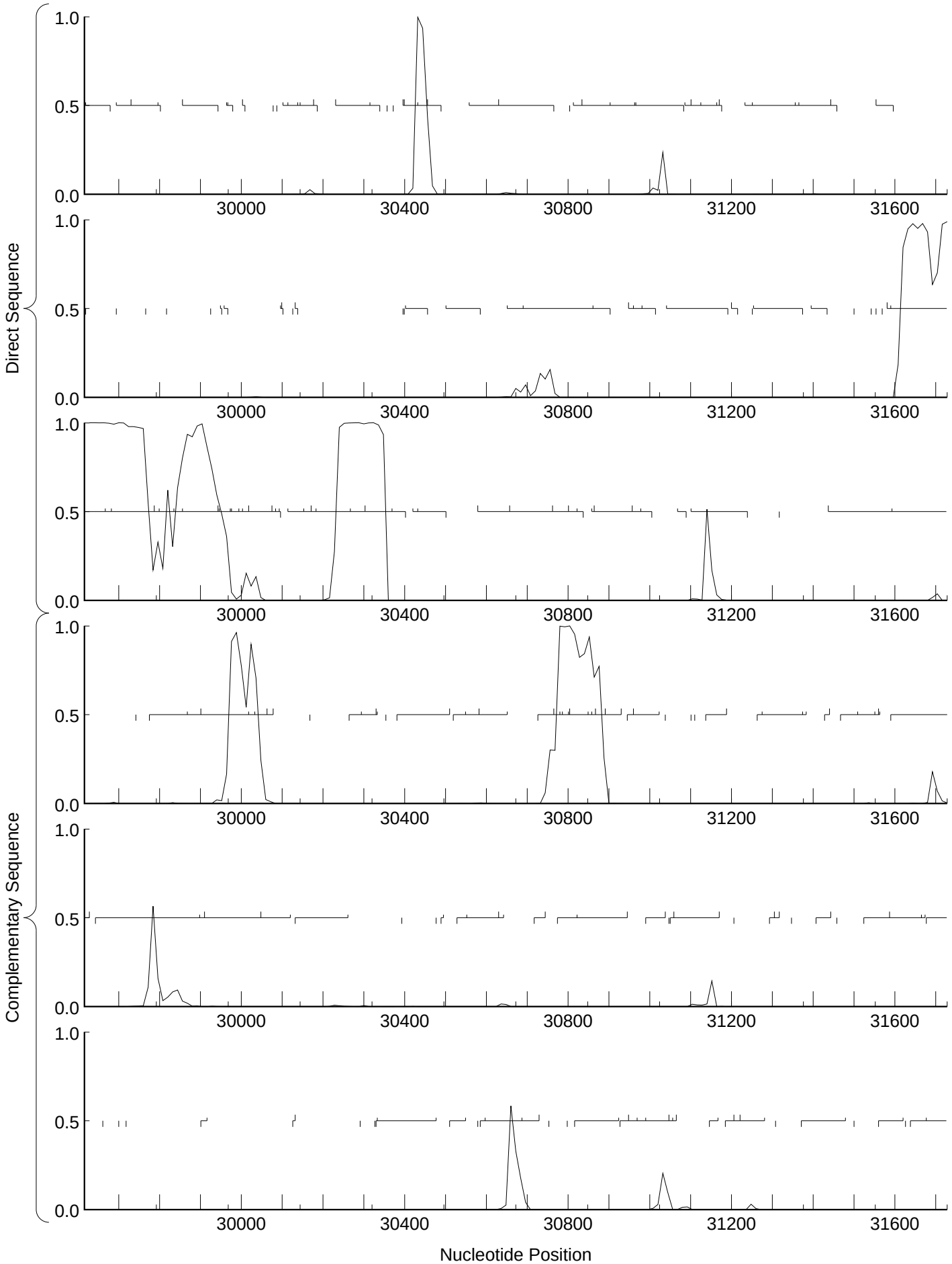
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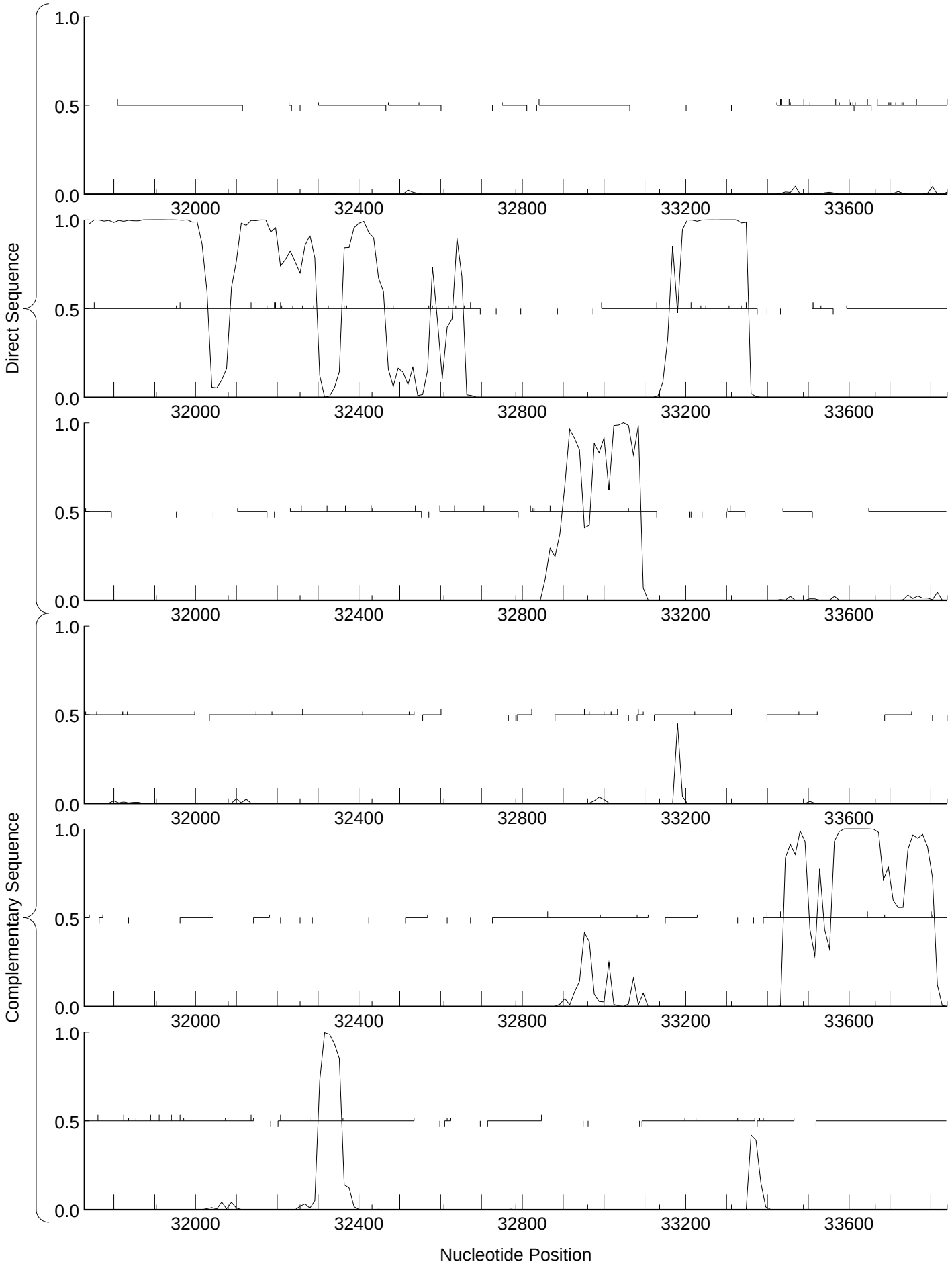


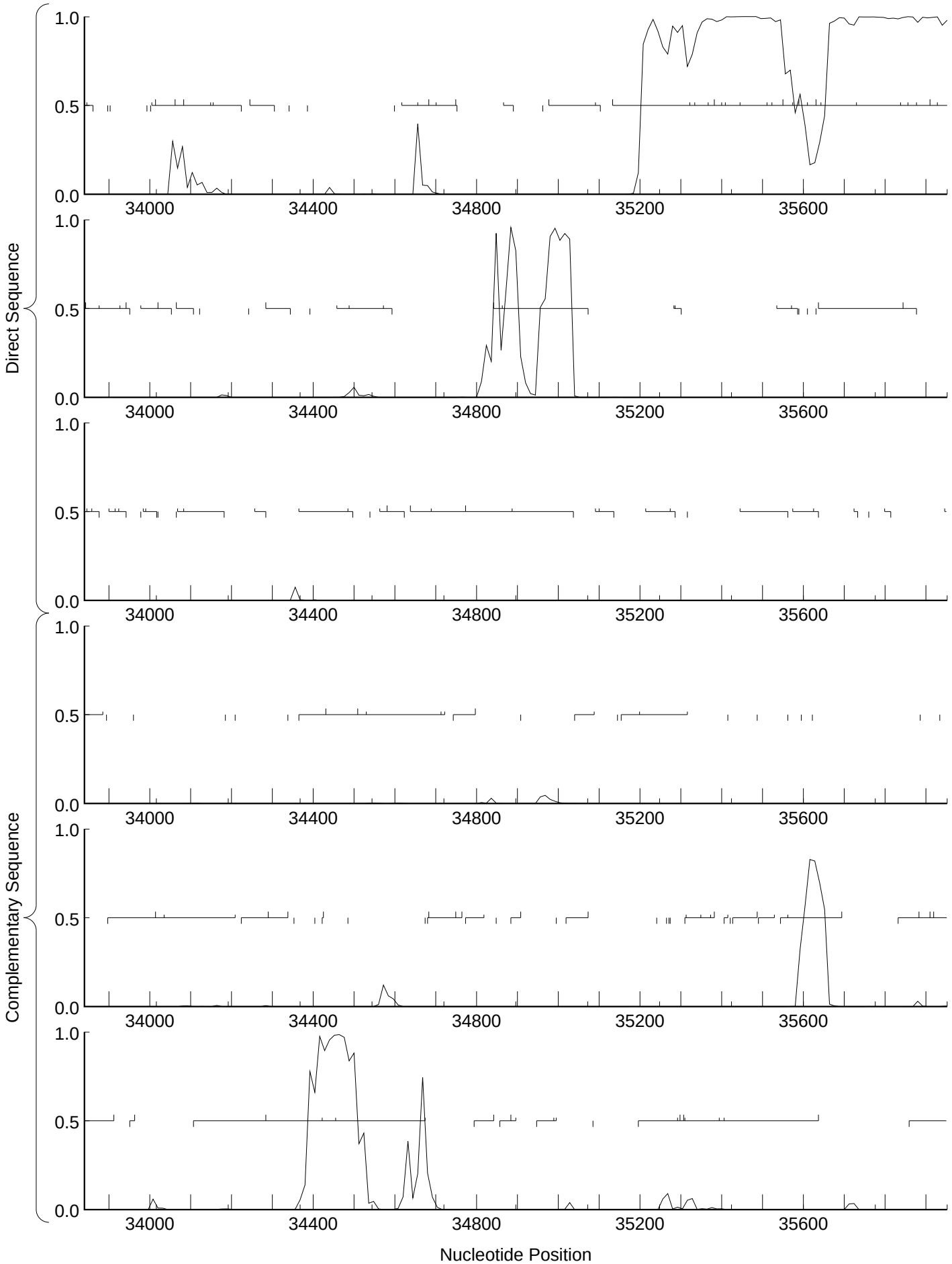
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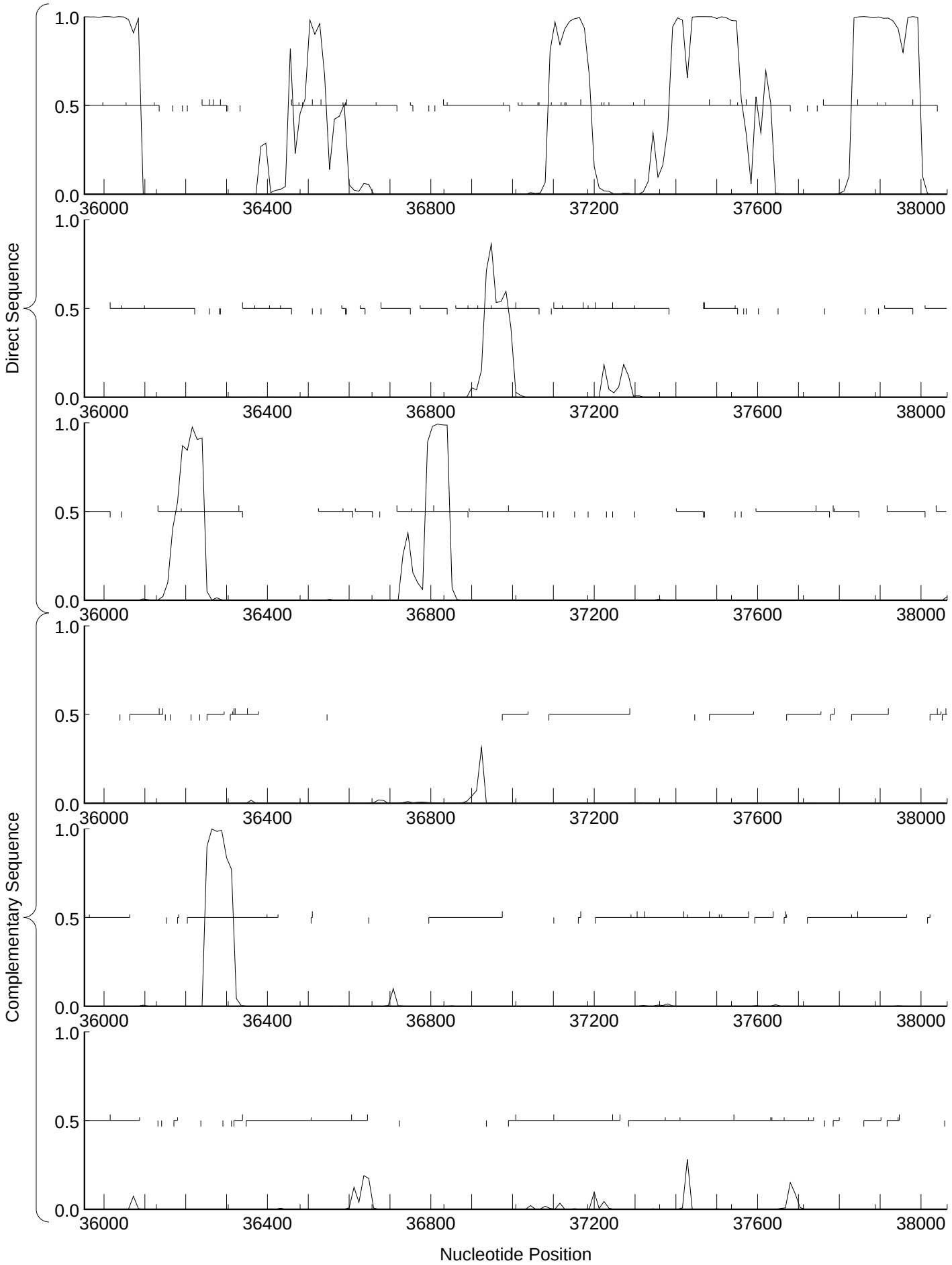


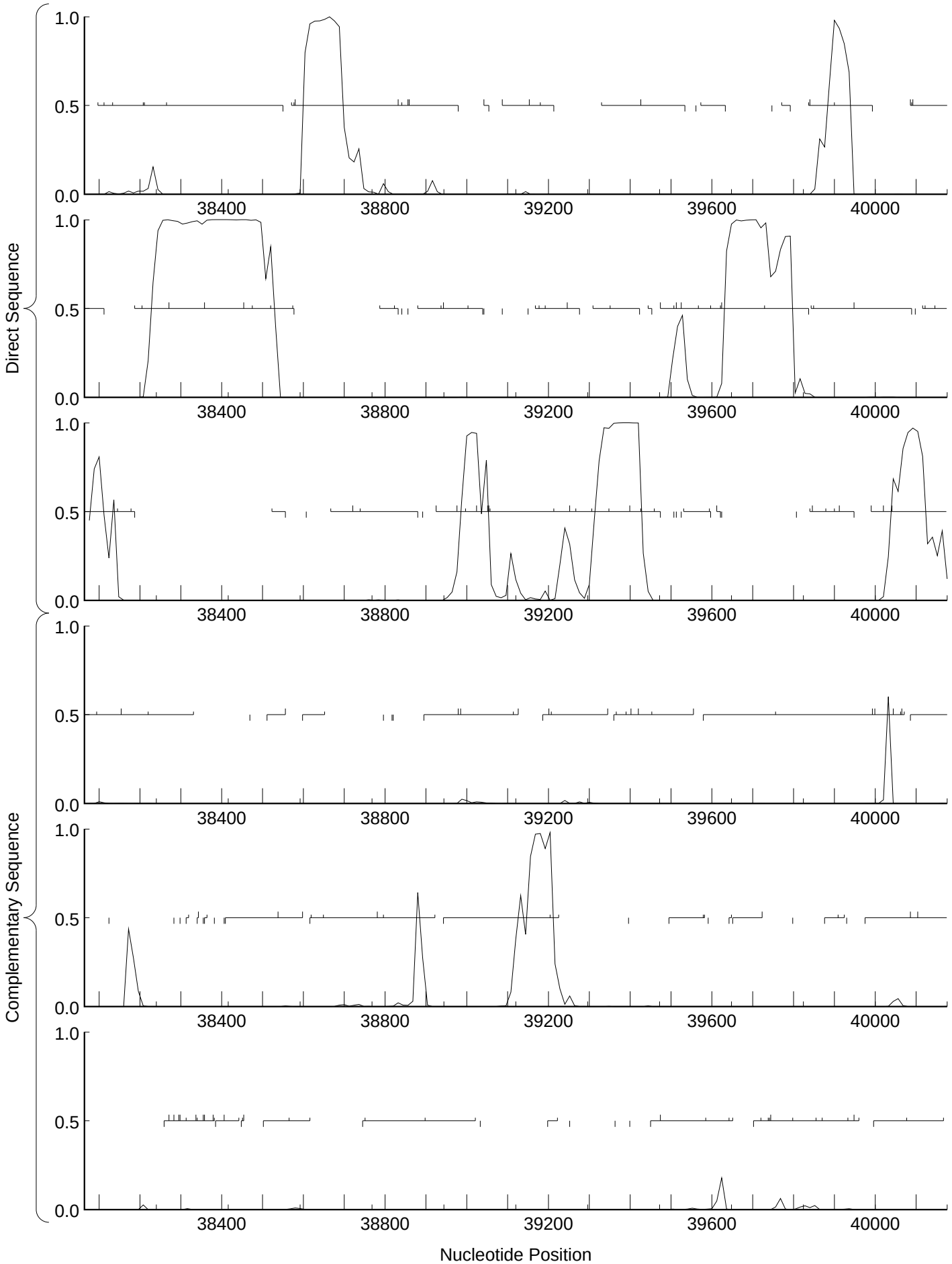

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
27600
28000
28400
28800
29200
29600
Nucleotide Position


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

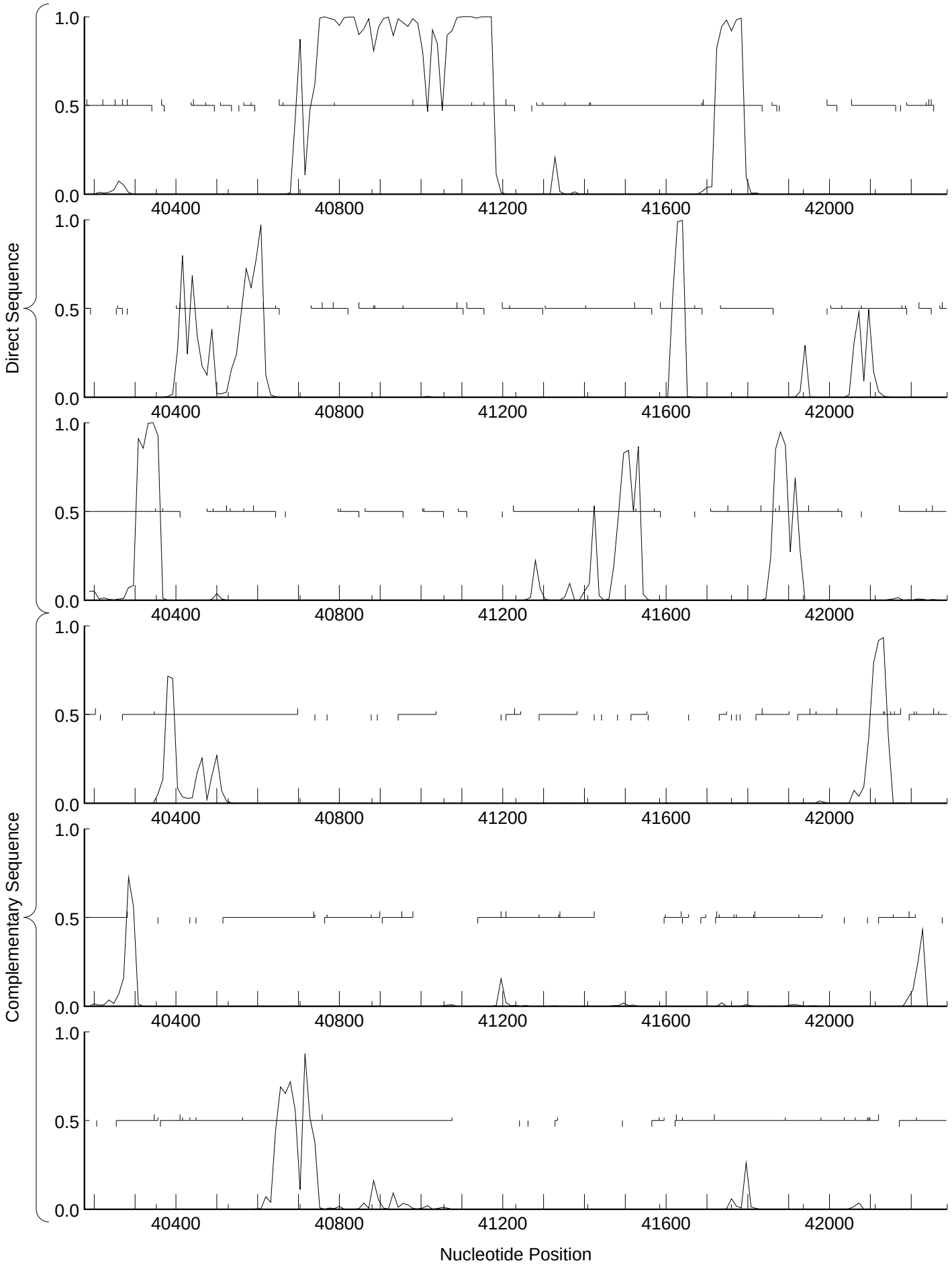

Direct Sequence
Complementary Sequence
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0.5
0.0
32000
32400
32800
33200
33600
Nucleotide Position

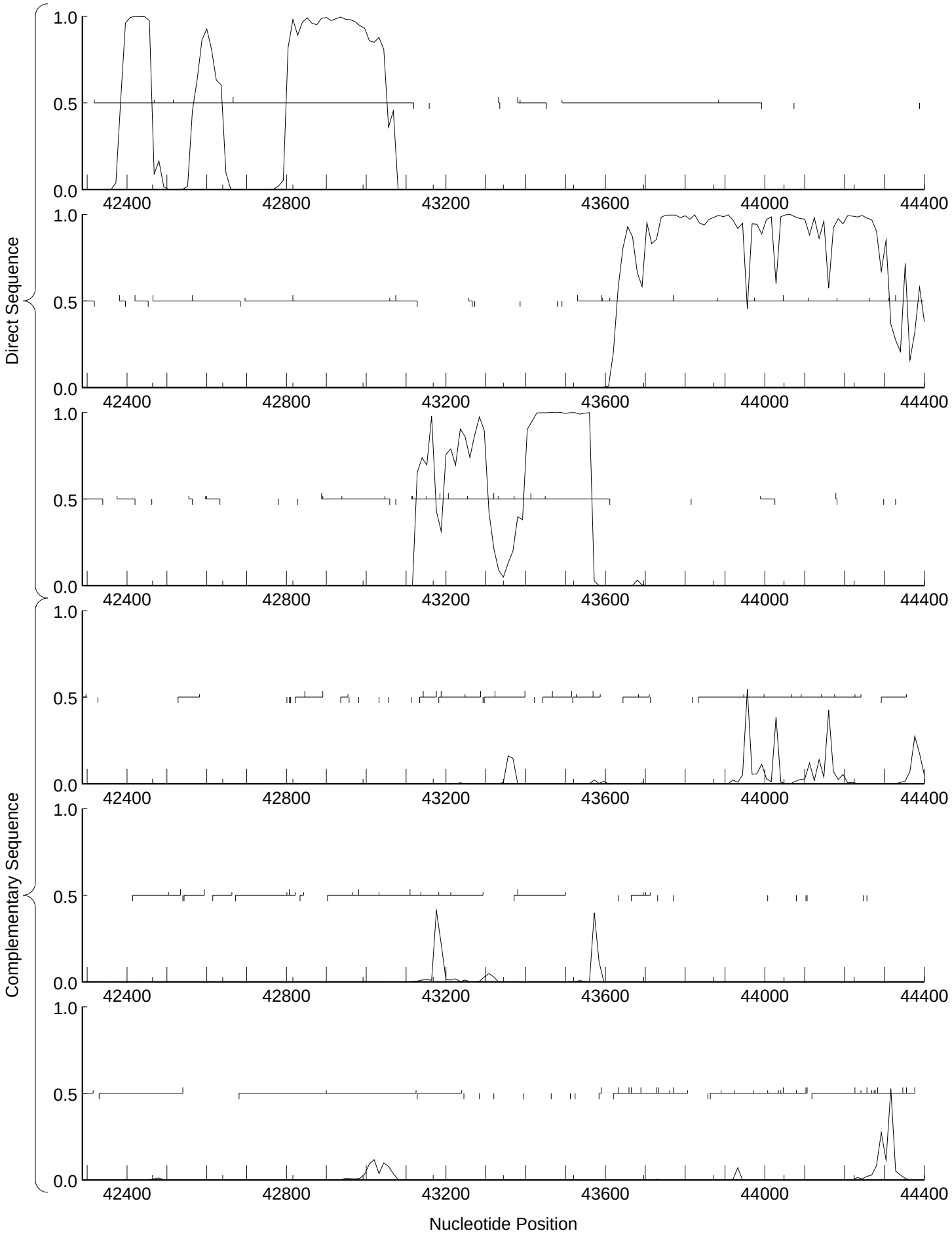

Direct Sequence
Complementary Sequence
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0.5
0.0
34000
34400
34800
35200
35600
Nucleotide Position

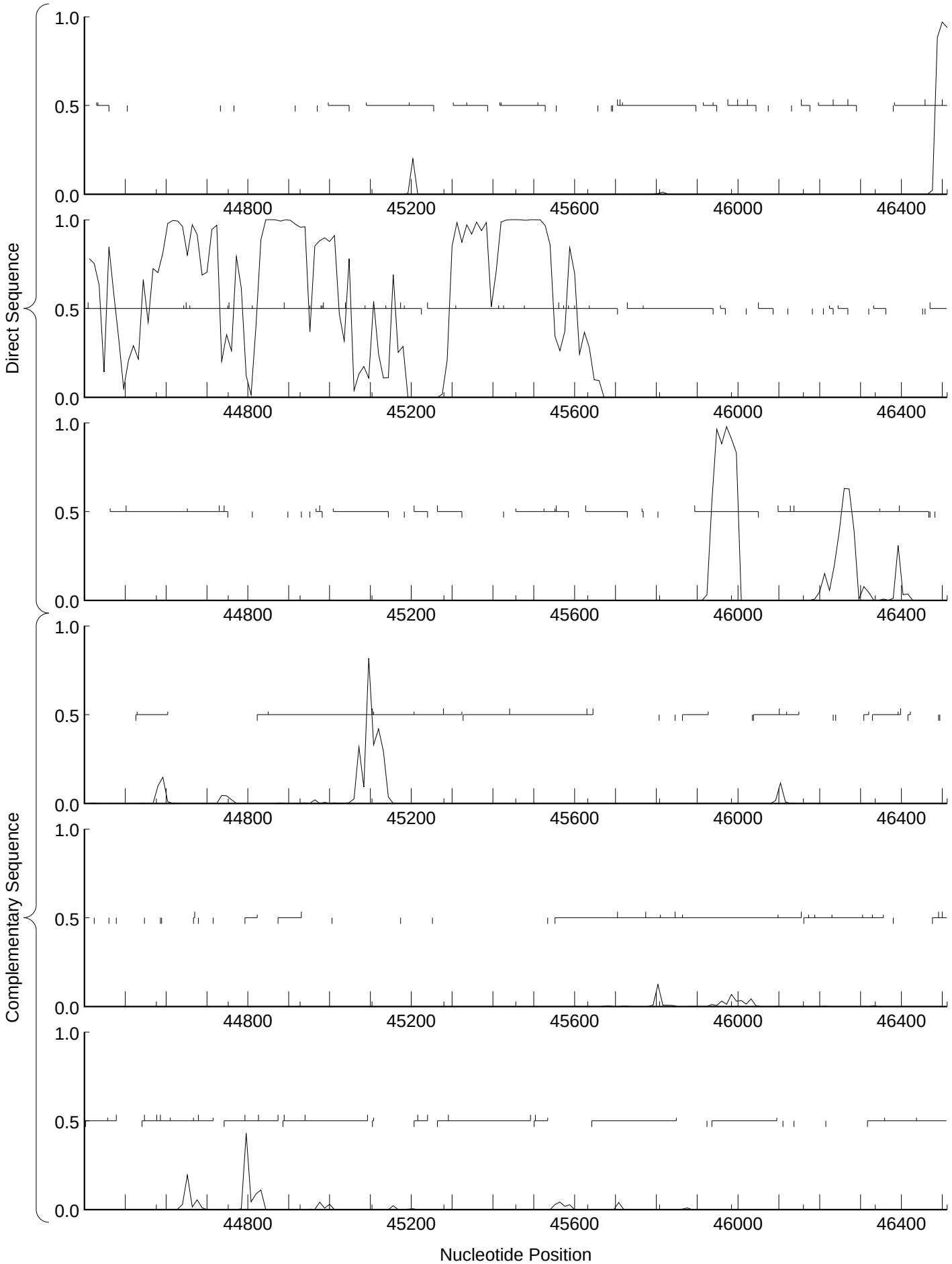

Direct Sequence
Complementary Sequence
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0.5
0.0
36000
36400
36800
37200
37600
38000
Nucleotide Position

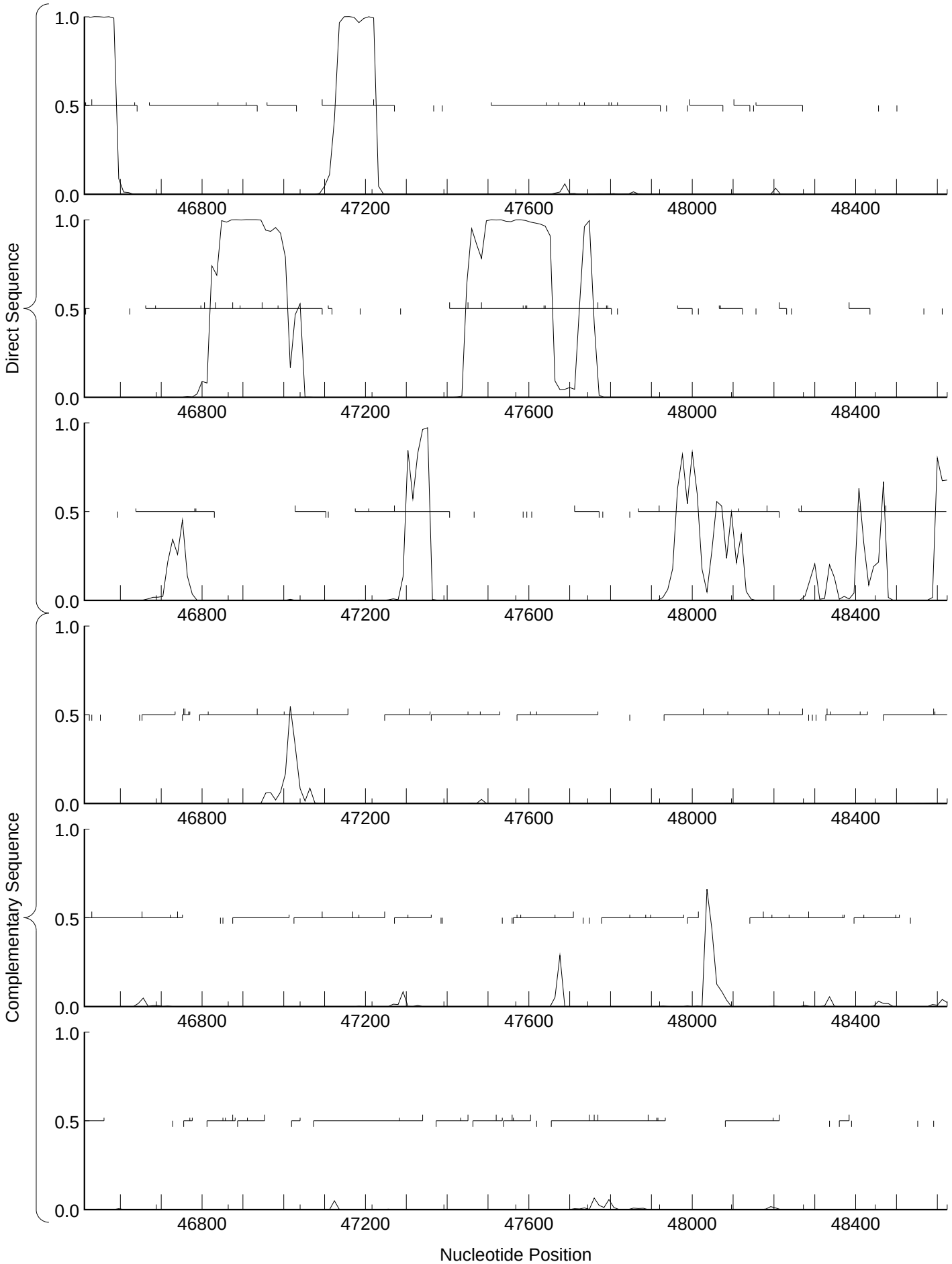

Direct Sequence
Complementary Sequence
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0.5
0.0
38400
38800
39200
39600
40000
Nucleotide Position

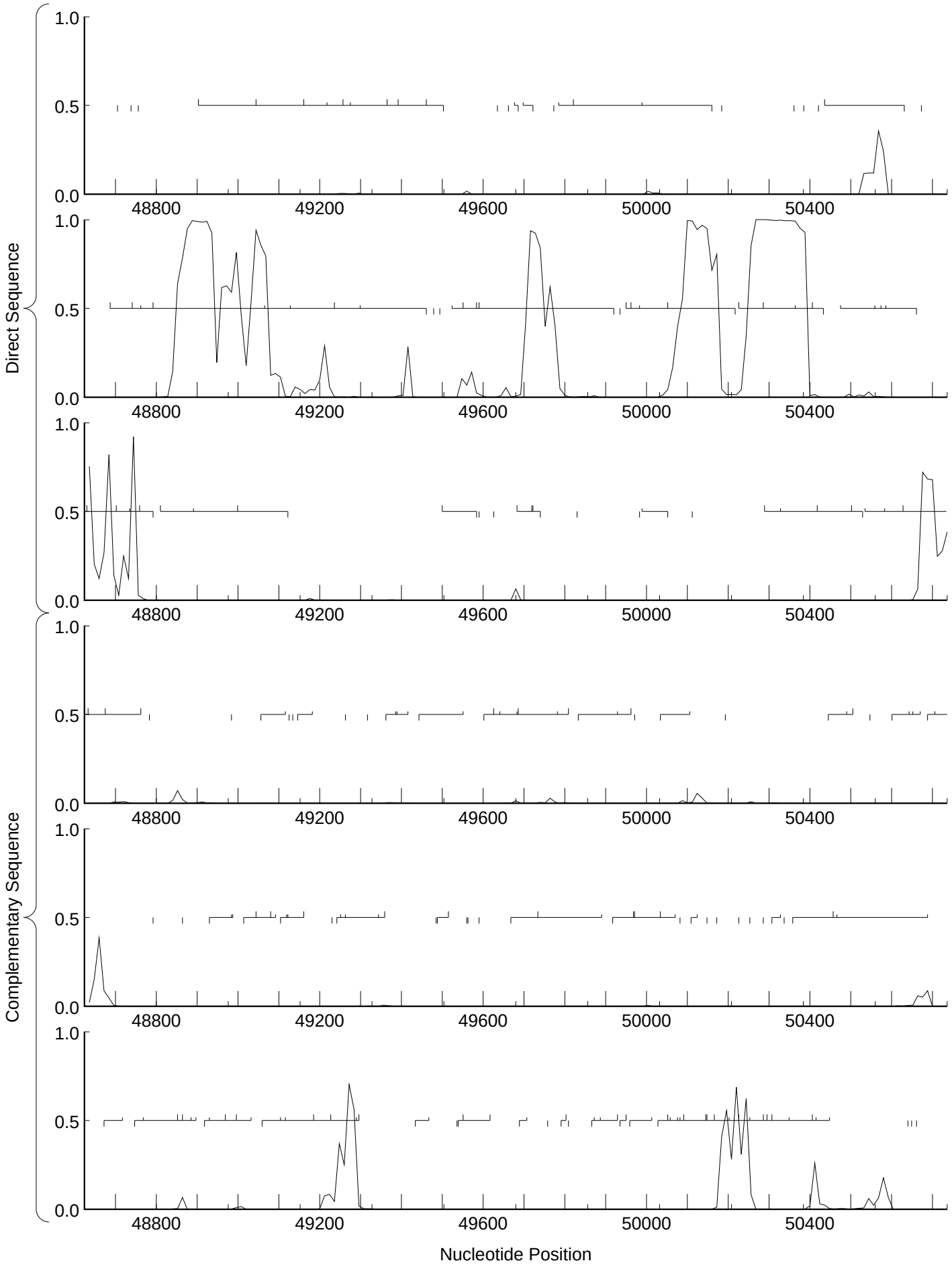
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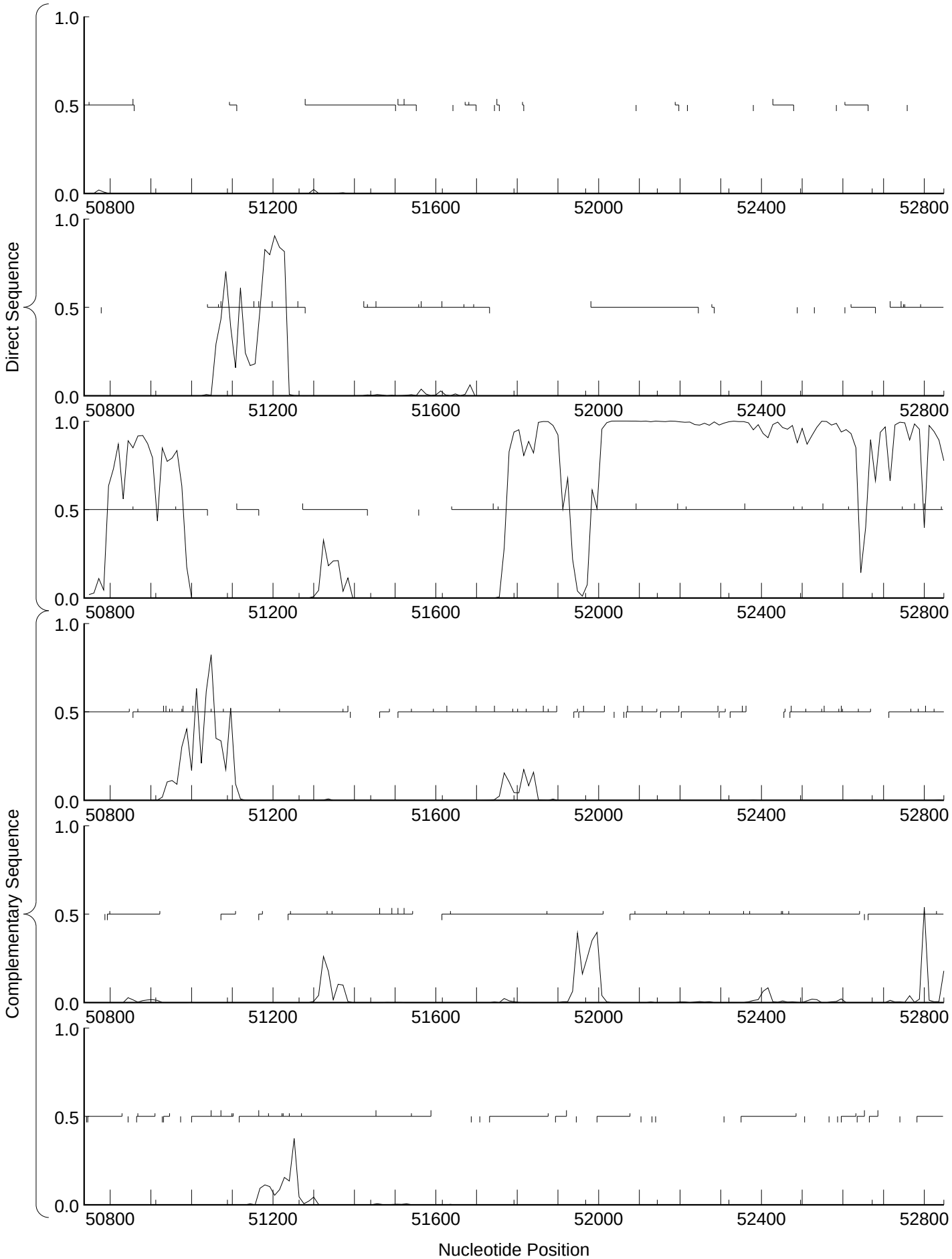



Direct Sequence
Complementary Sequence
1.0
0.5
0.0
42400
42800
43200
43600
44000
44400
Nucleotide Position


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


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
48800
49200
49600
50000
50400
Nucleotide Position


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
50800
51200
51600
52000
52400
52800
Nucleotide Position

nage Beakin complete sequence, 54926 bp including 10-base 3’ overhang (CCGACGGCAT), Order 4, Window 96, Step 12, 27/28

