GeneMark

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

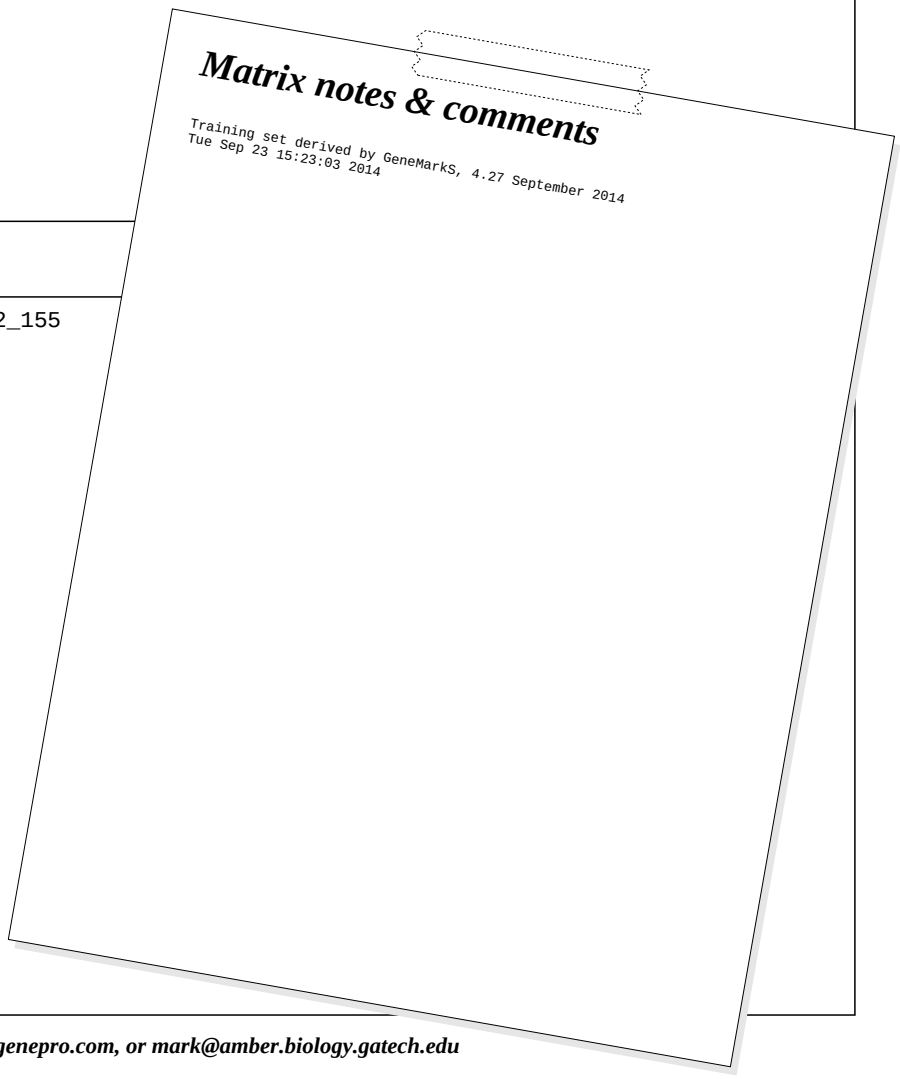
PROGRAM INFORMATION

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Sequence         :  Mycobacterium phage Nivrat complete sequence, 58009 bp including 10-base 3' overhang (CGGAA
Analysis Date    :  3/28/24 at 8:47:14
Pages            :  29
Sequence Length  :  58009 bp
GC Content       :   61.45%

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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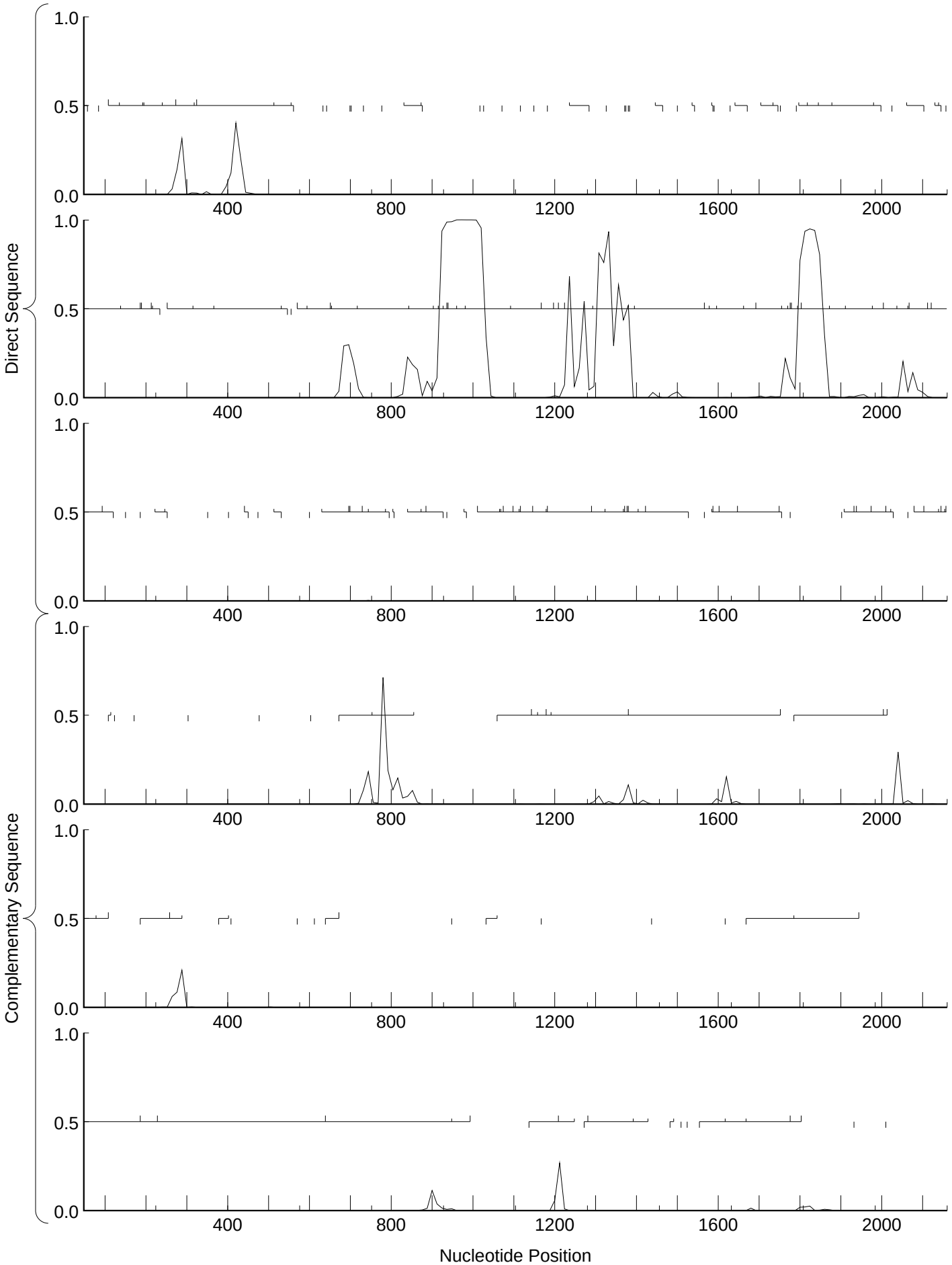
MATRIX INFORMATION

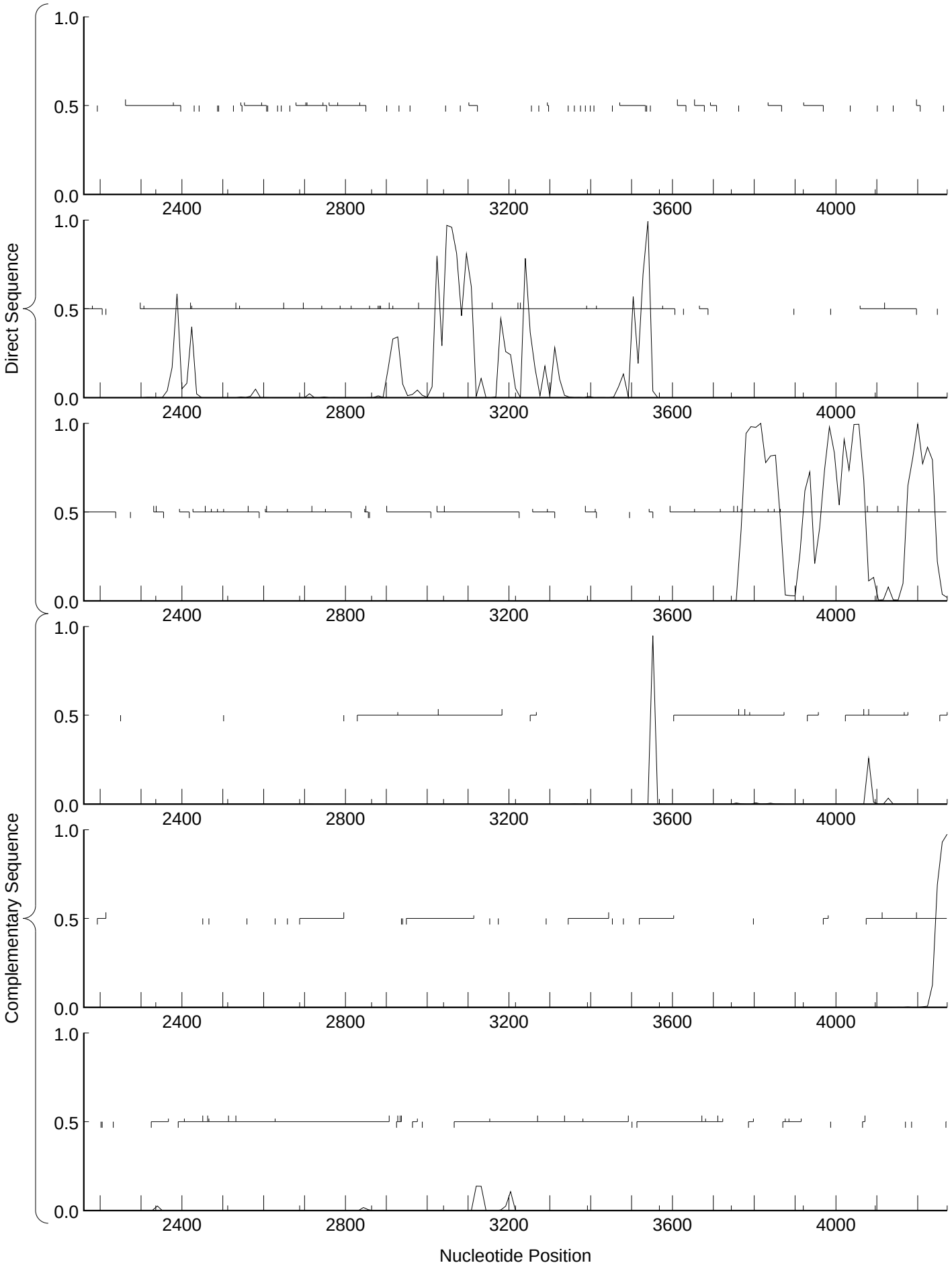
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Matrix     :  Mycobacterium_smegmatis_MC2_155
Author     :  -

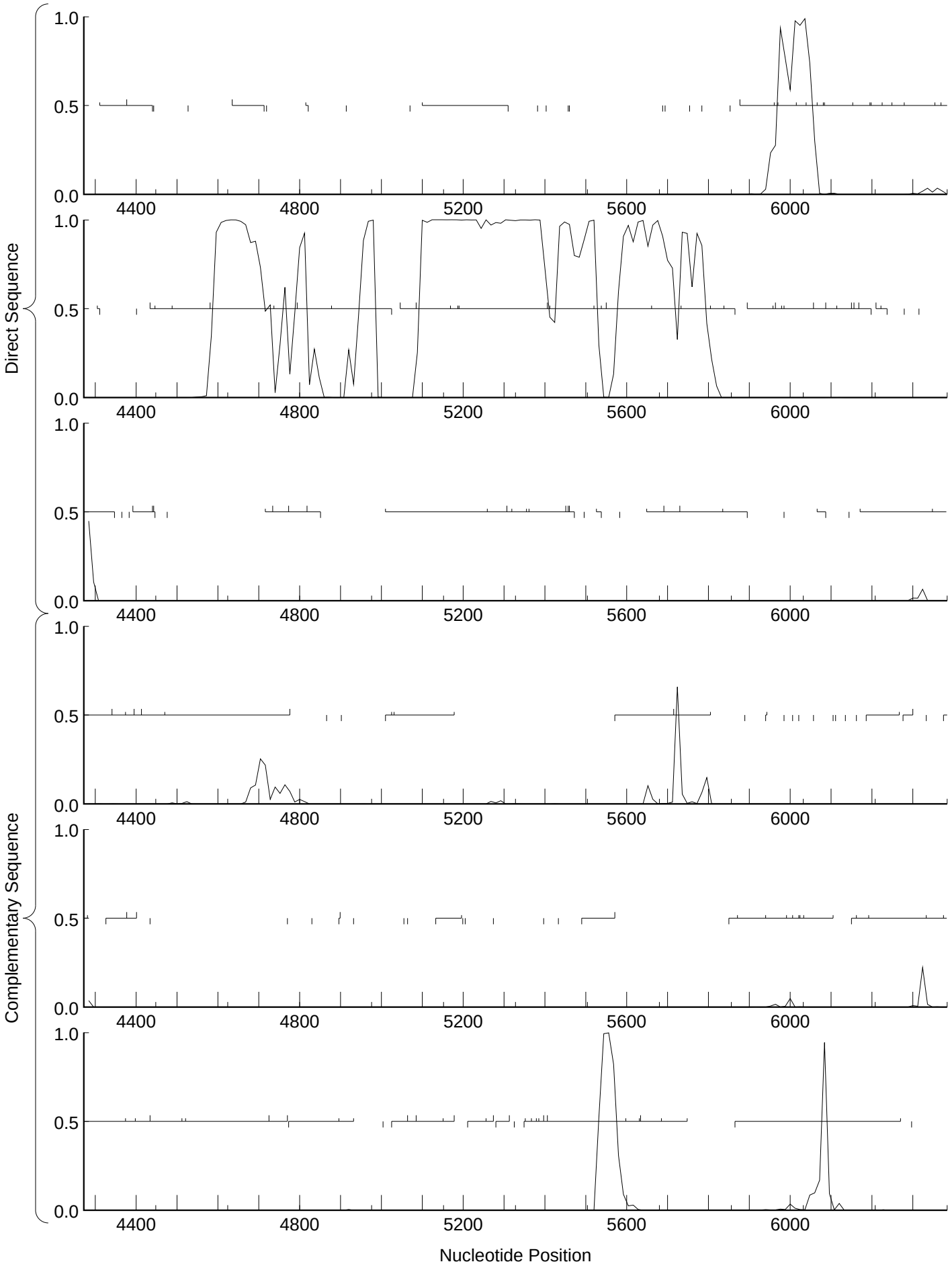
Order      :  4
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  Send questions / comments to:
      Dr. M. Borodovsky
      Georgia Institute of Technology
      School of Biology
      Atlanta, GA  30332-0230
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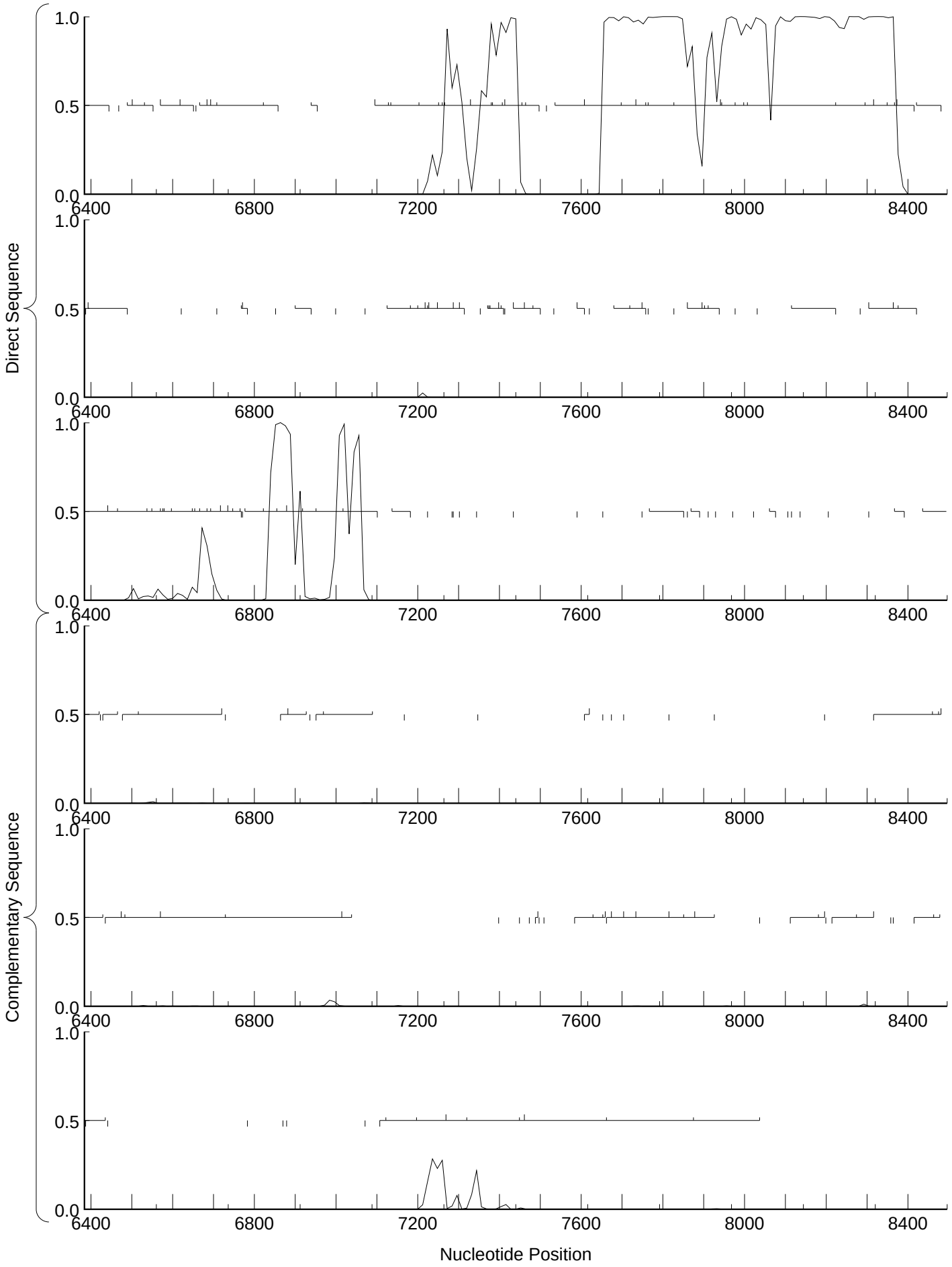

For help or information, send electronic mail to: custserv@genepro.com, or mark@amber.biology.gatech.edu

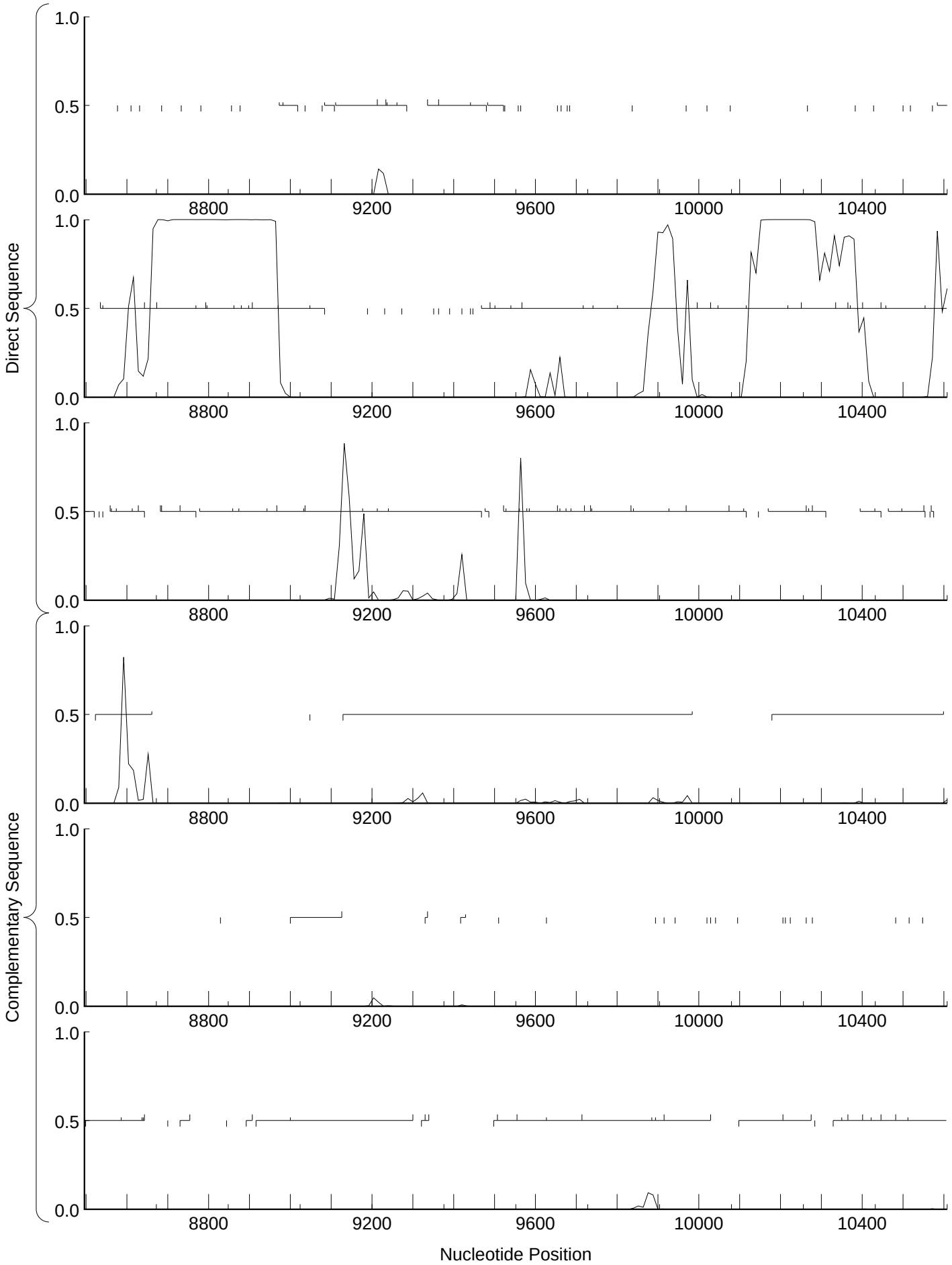

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
400
800
1200
1600
2000
Nucleotide Position

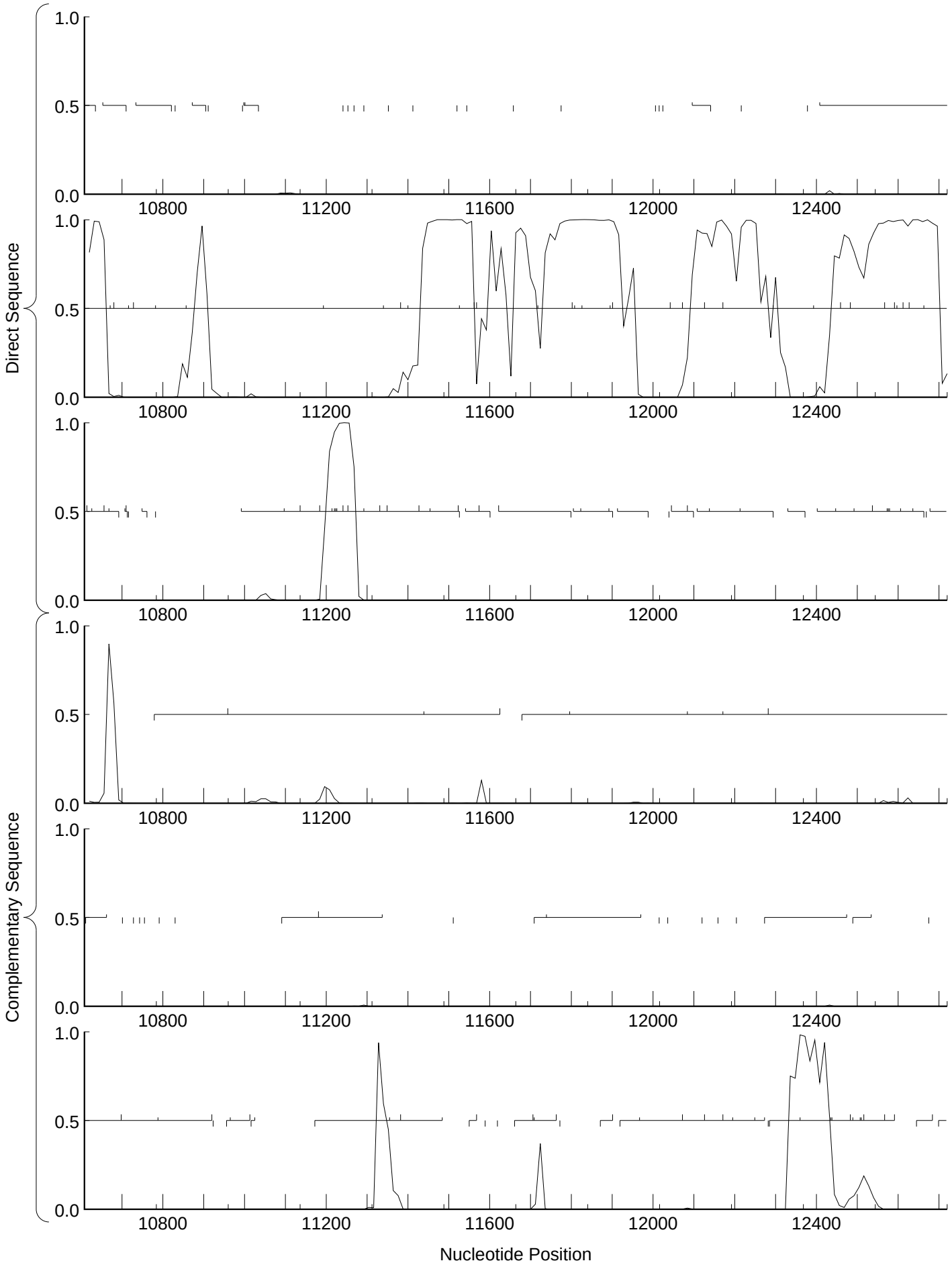

Direct Sequence
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0.0
2400
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3200
3600
4000
Nucleotide Position

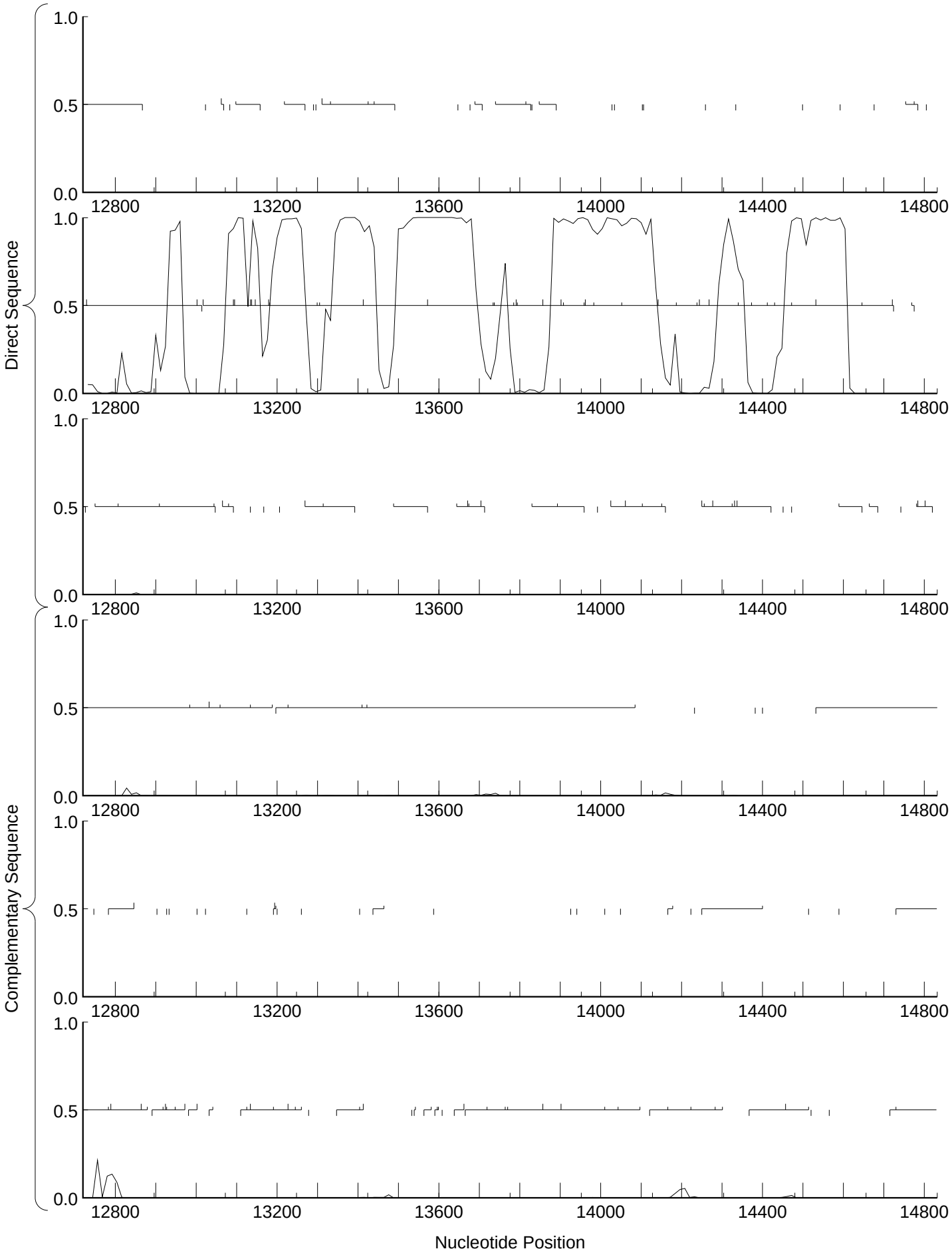

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5200
5600
6000
Nucleotide Position

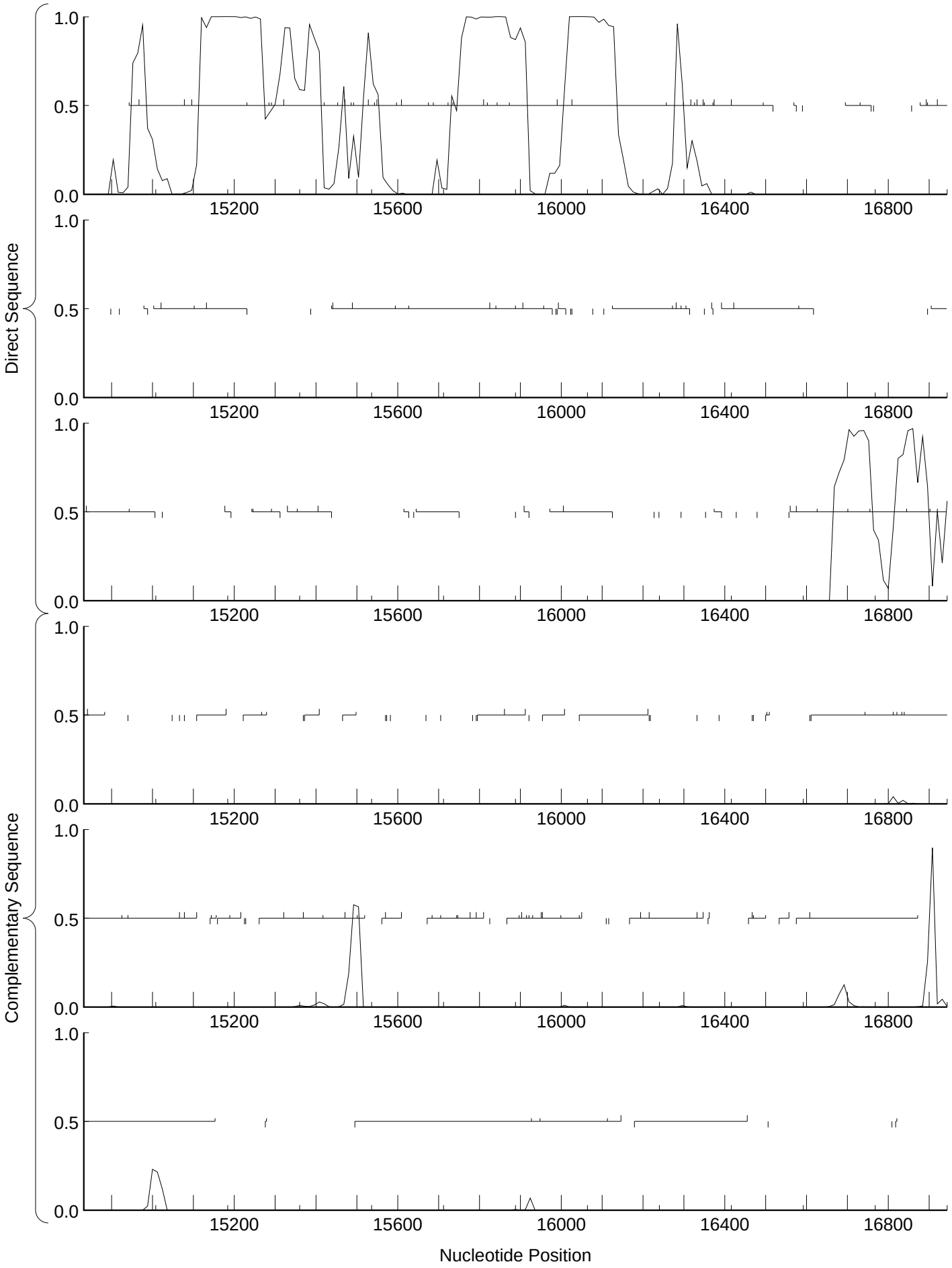
at complete sequence, 58009 bp including 10-base 3’ overhang (CGGAAGGCGC), Cluster F1, Order 4, Window 96, Step 12, 5/29



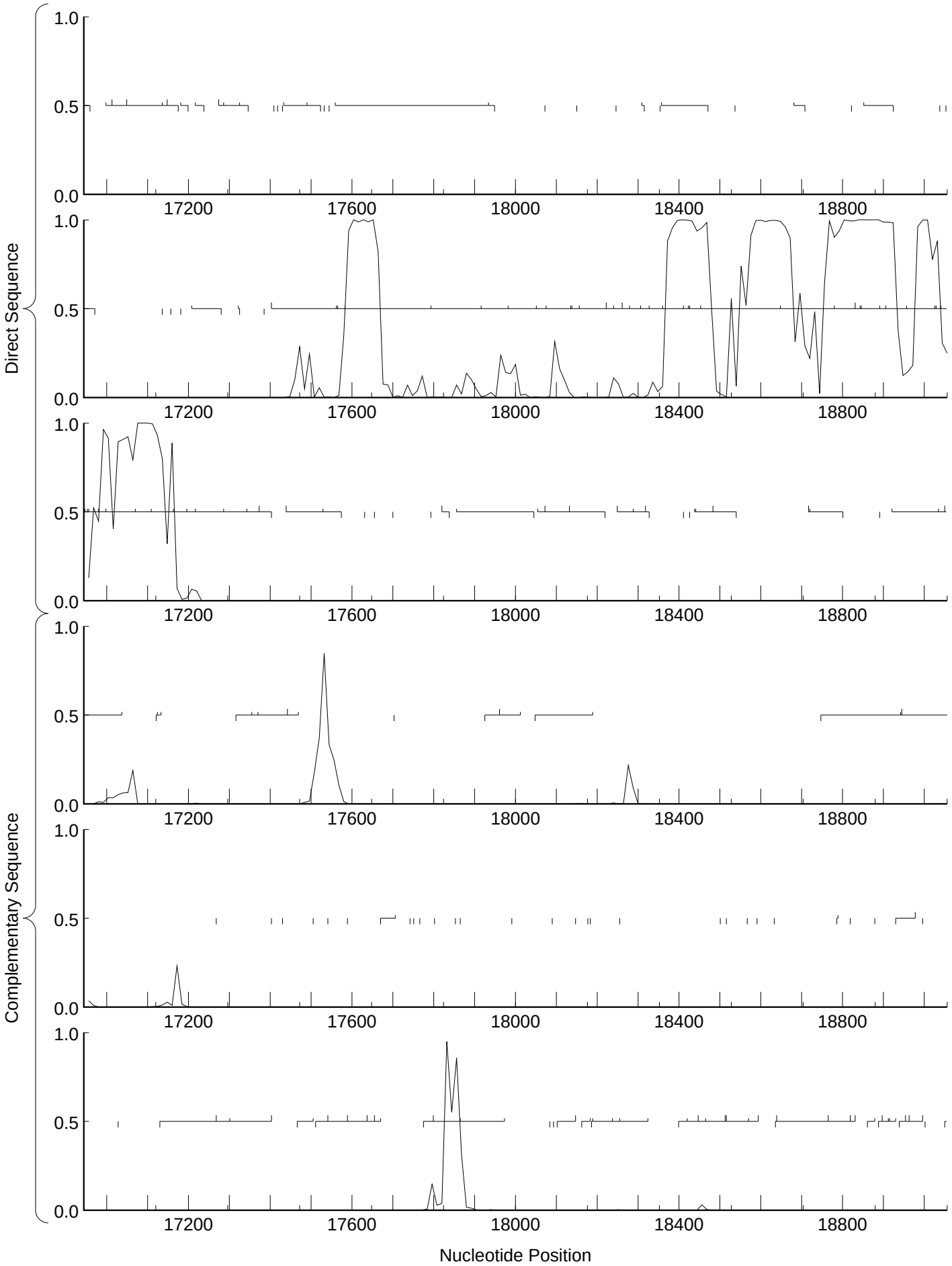

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
8800
9200
9600
10000
10400
Nucleotide Position


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

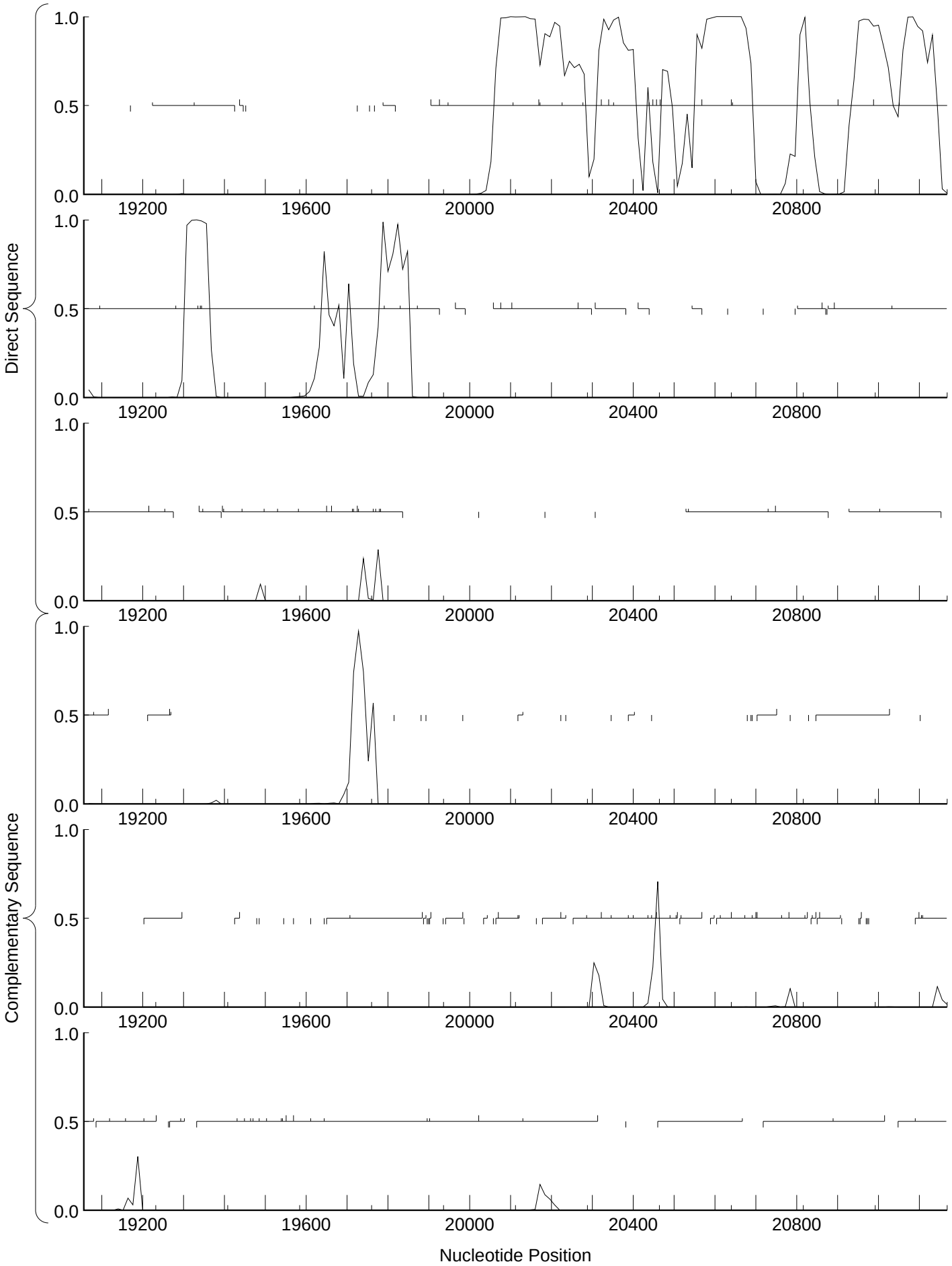

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
12800
13200
13600
14000
14400
14800
Nucleotide Position


Direct Sequence
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0.0
15200
15600
16000
16400
16800
Nucleotide Position

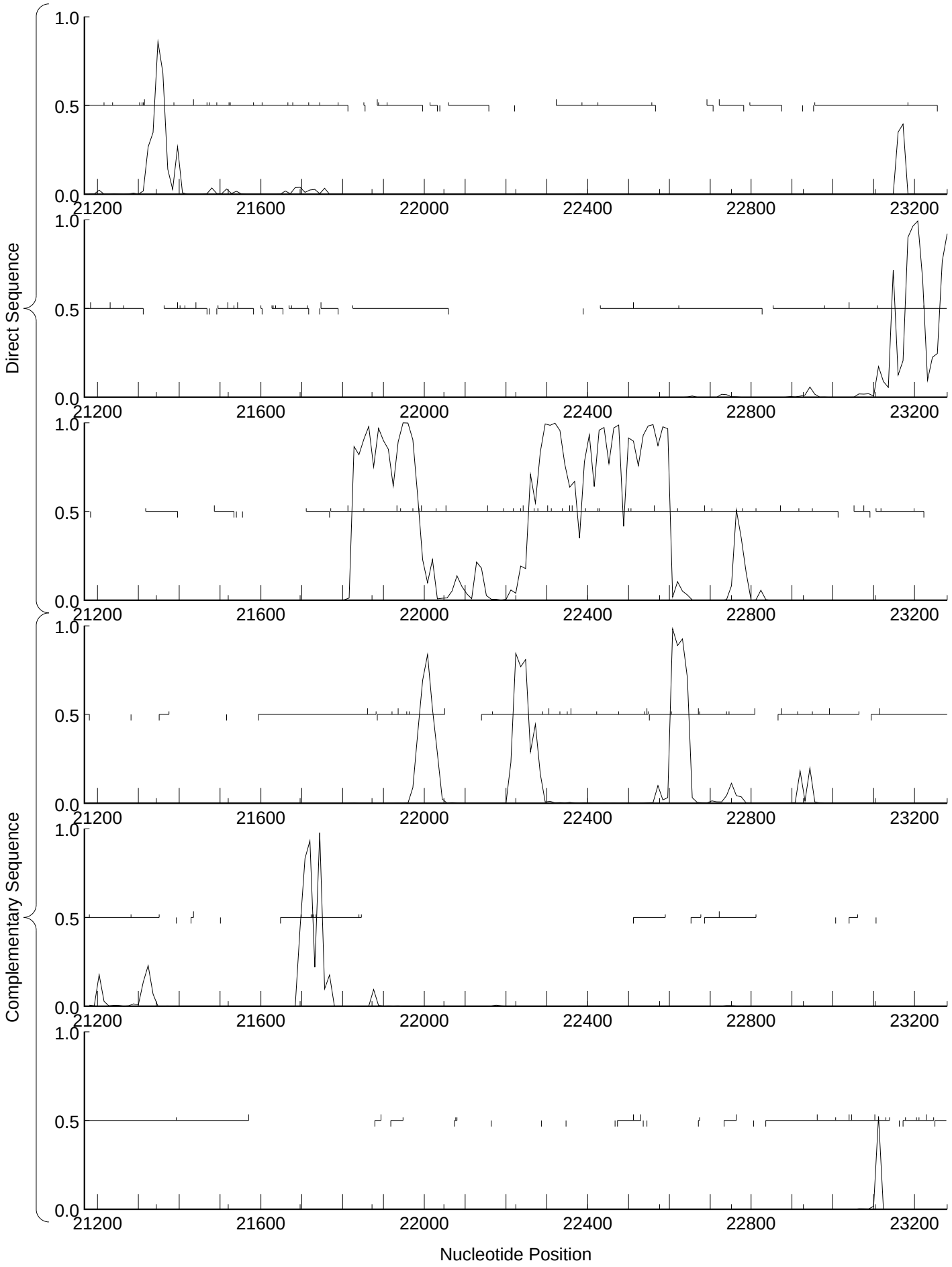
complete sequence, 58009 bp including 10-base 3’ overhang (CGGAAGGCGC), Cluster F1, Order 4, Window 96, Step 12, 10/29



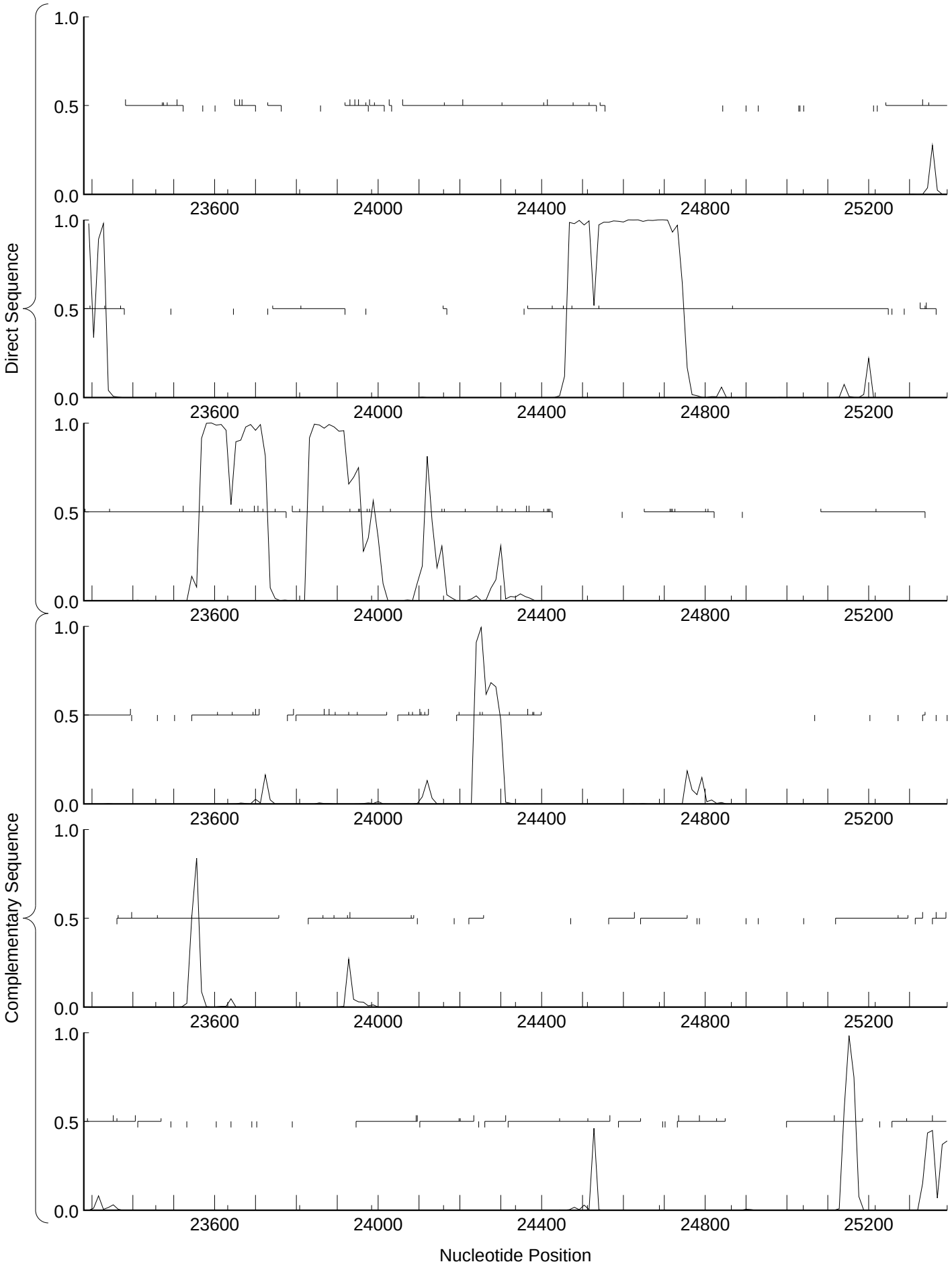
complete sequence, 58009 bp including 10-base 3’ overhang (CGGAAGGCGC), Cluster F1, Order 4, Window 96, Step 12, 11/29



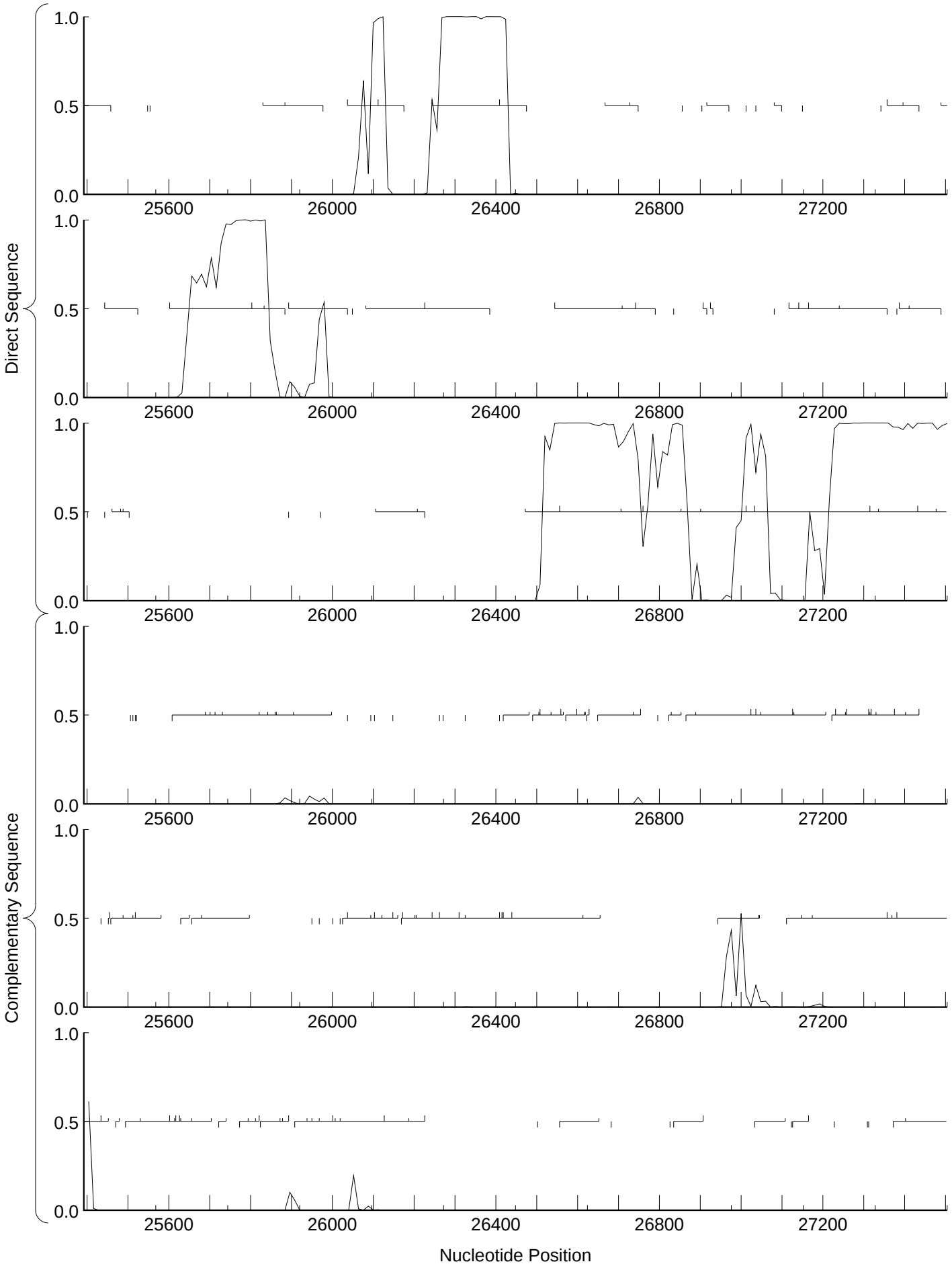
complete sequence, 58009 bp including 10-base 3’ overhang (CGGAAGGCGC), Cluster F1, Order 4, Window 96, Step 12, 12/29



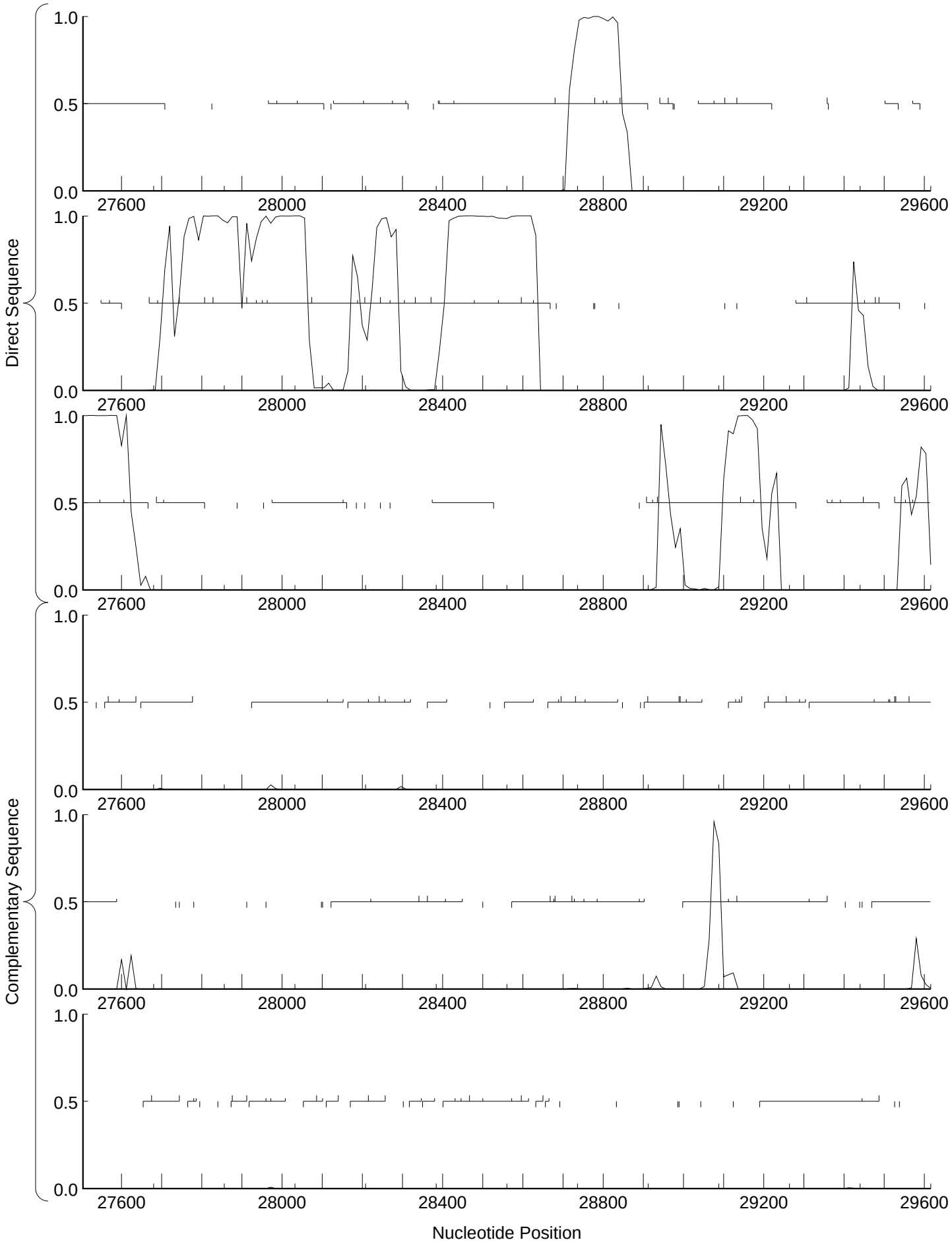
complete sequence, 58009 bp including 10-base 3’ overhang (CGGAAGGCGC), Cluster F1, Order 4, Window 96, Step 12, 13/29



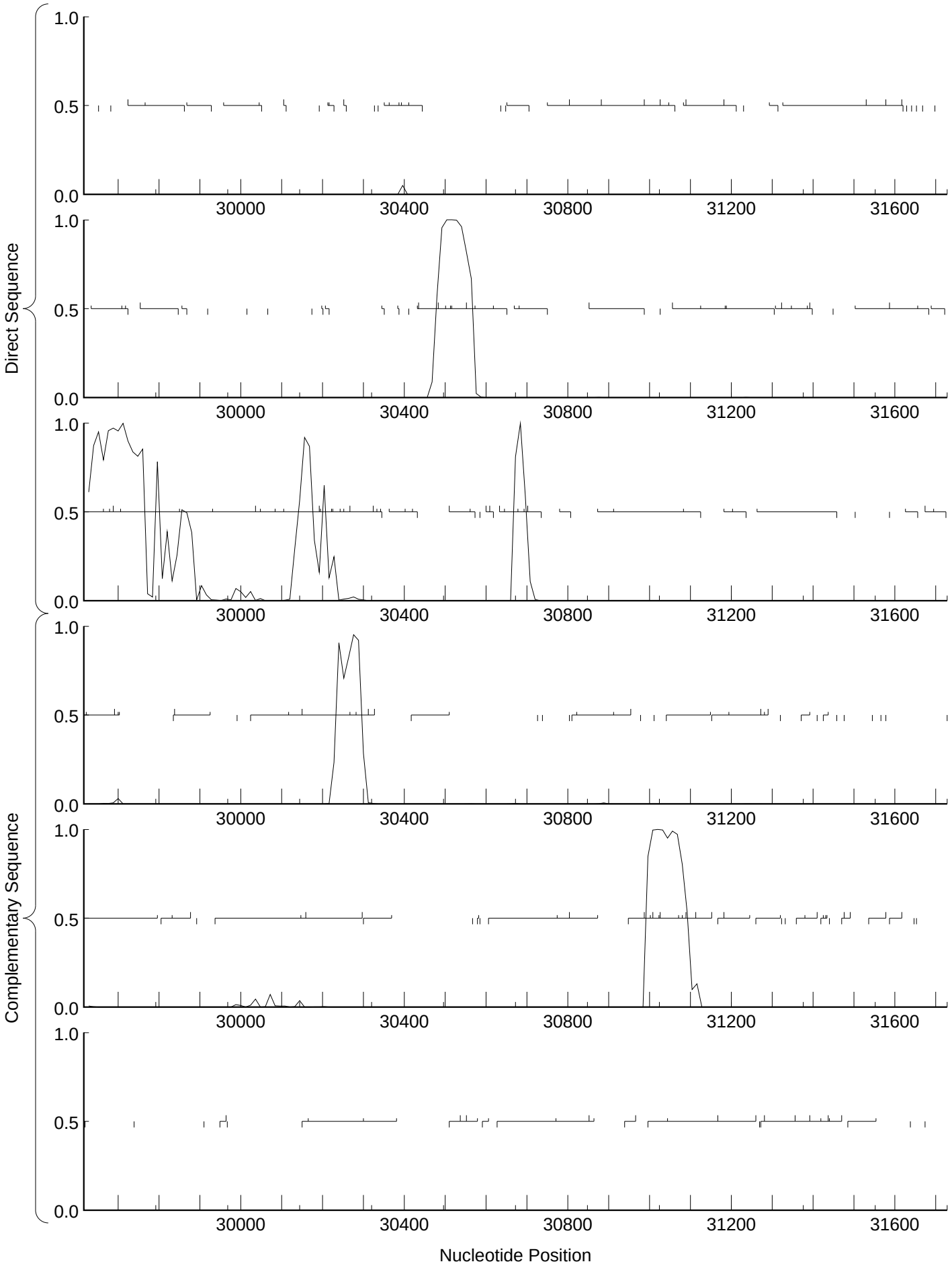
complete sequence, 58009 bp including 10-base 3’ overhang (CGGAAGGCGC), Cluster F1, Order 4, Window 96, Step 12, 14/29



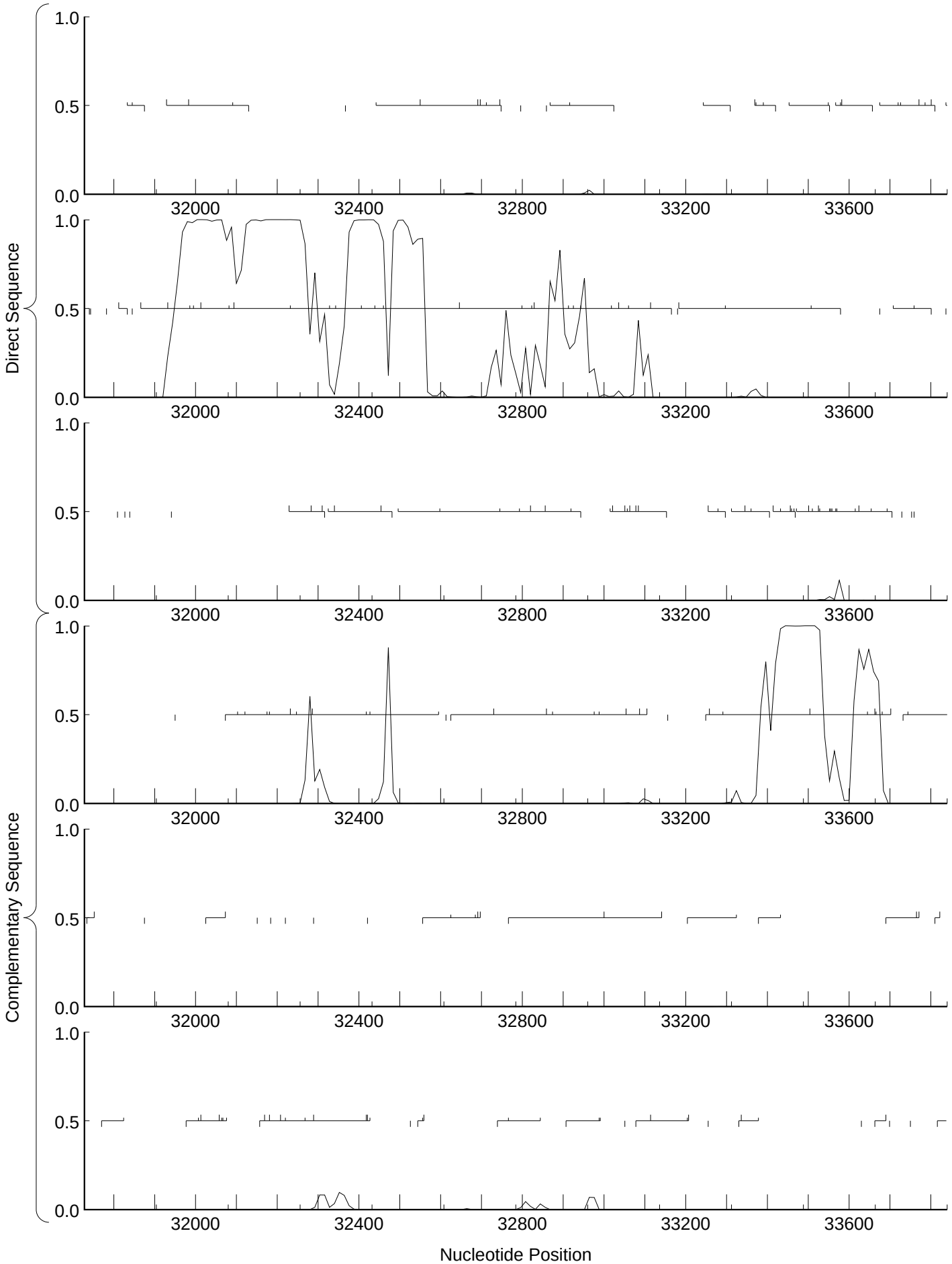
complete sequence, 58009 bp including 10-base 3’ overhang (CGGAAGGCGC), Cluster F1, Order 4, Window 96, Step 12, 15/29



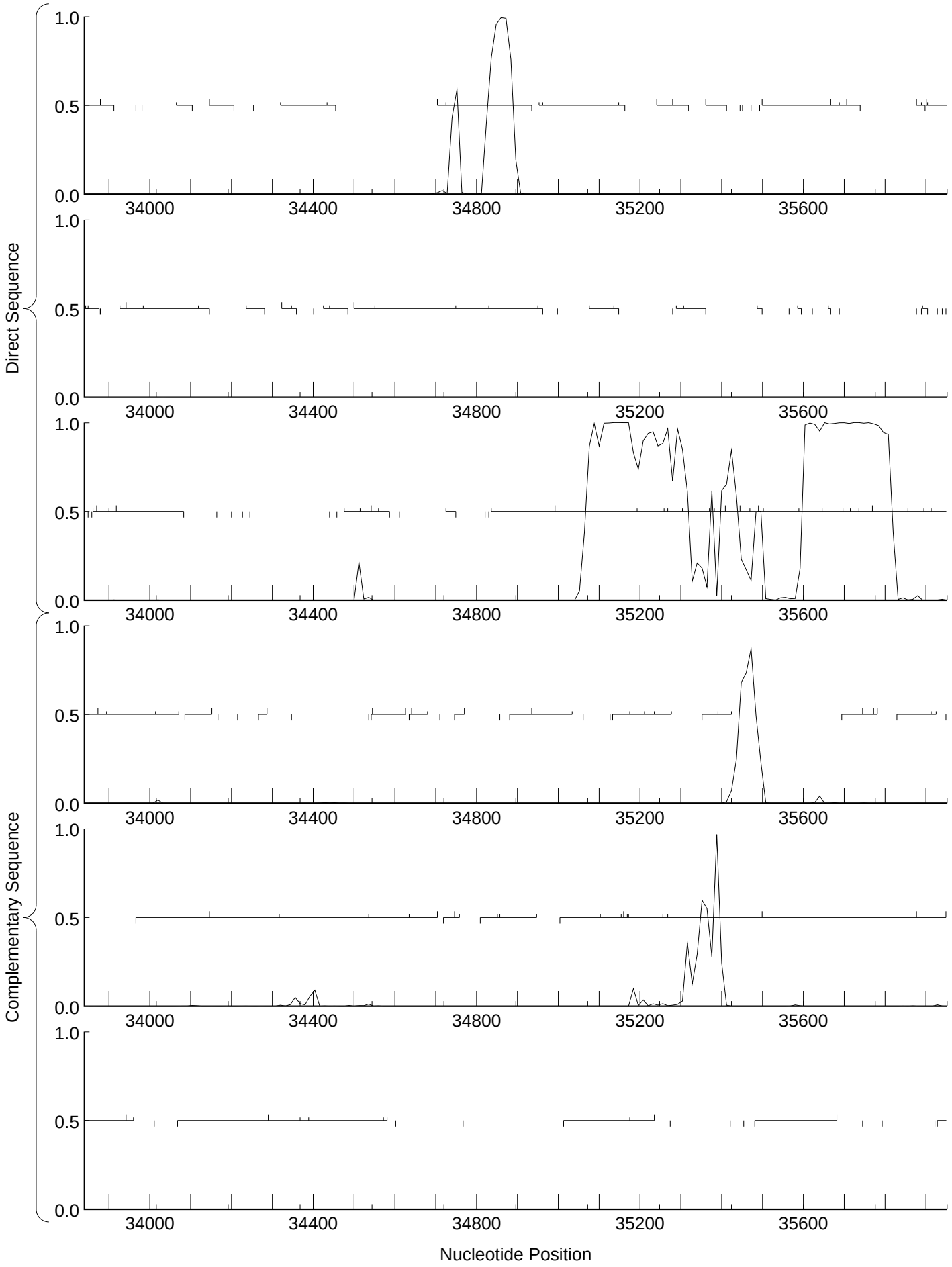
complete sequence, 58009 bp including 10-base 3’ overhang (CGGAAGGCGC), Cluster F1, Order 4, Window 96, Step 12, 16/29



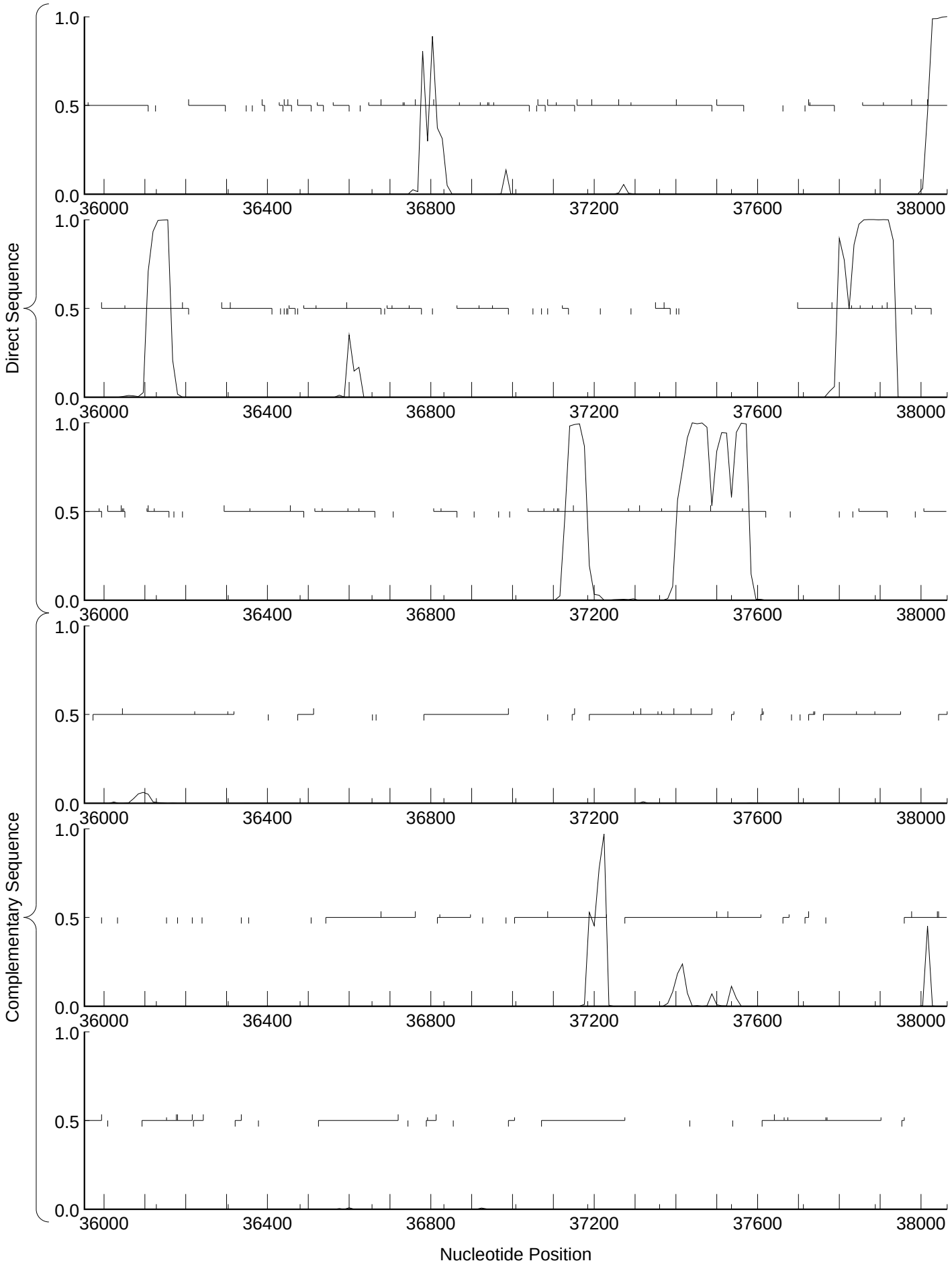
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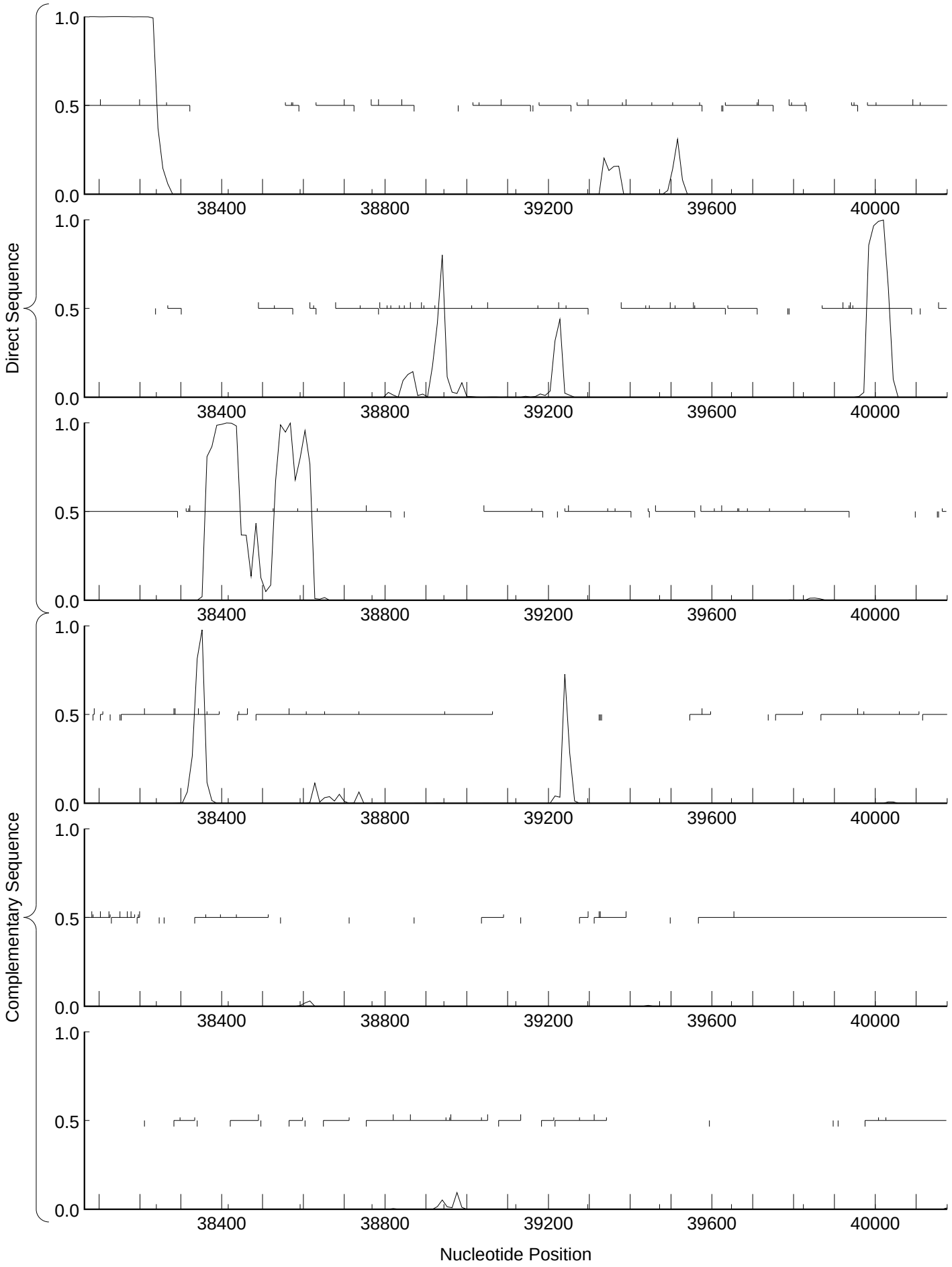
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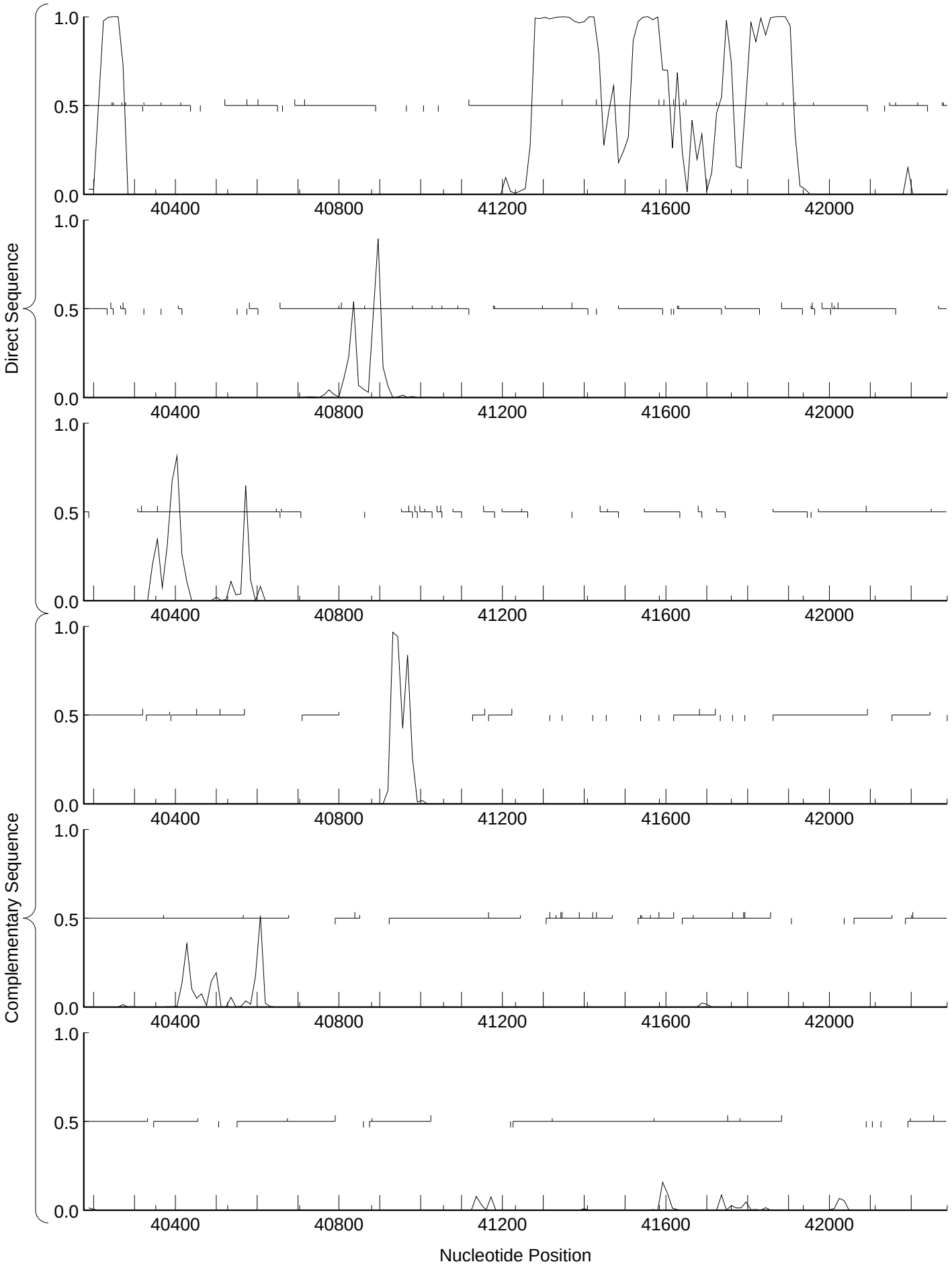
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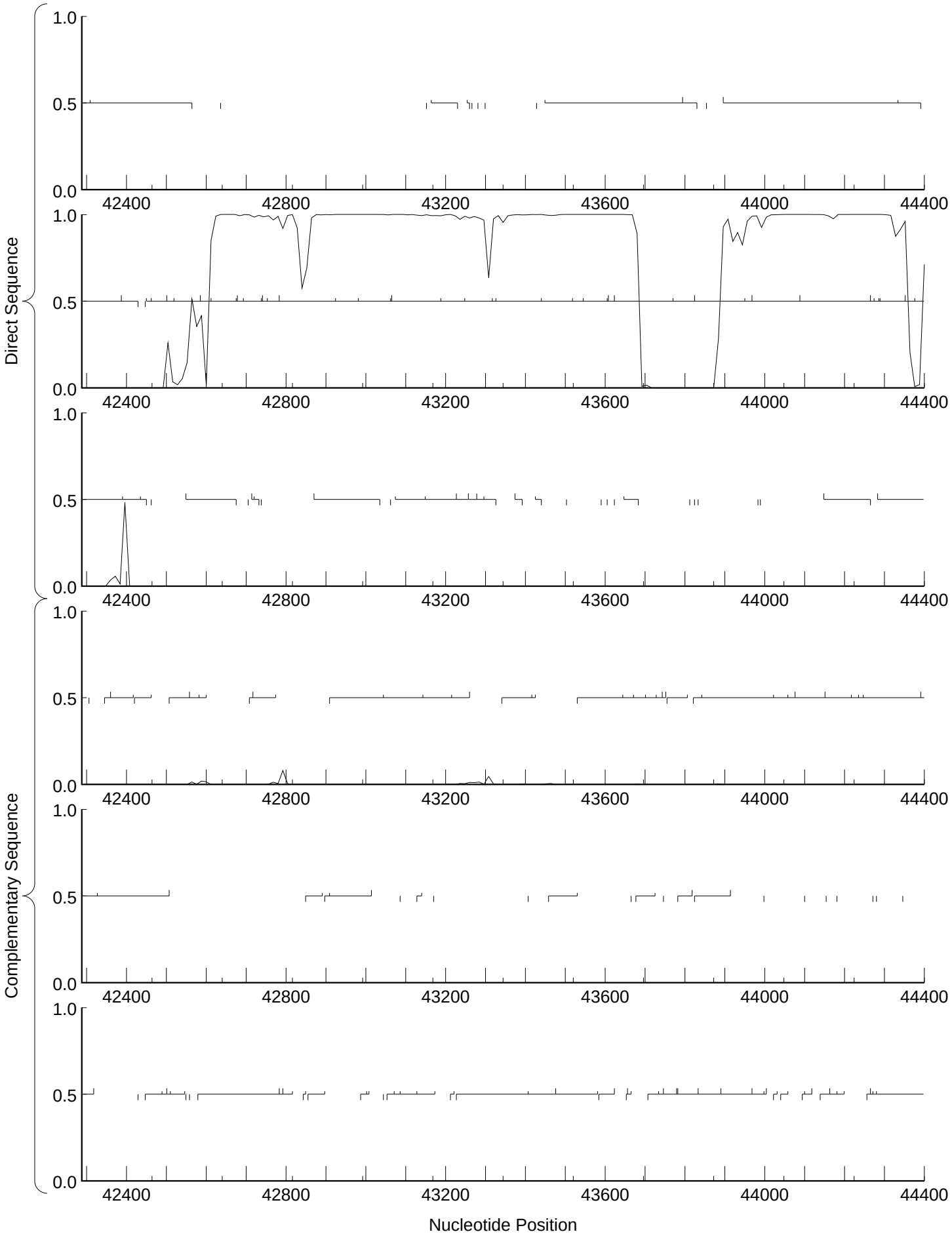
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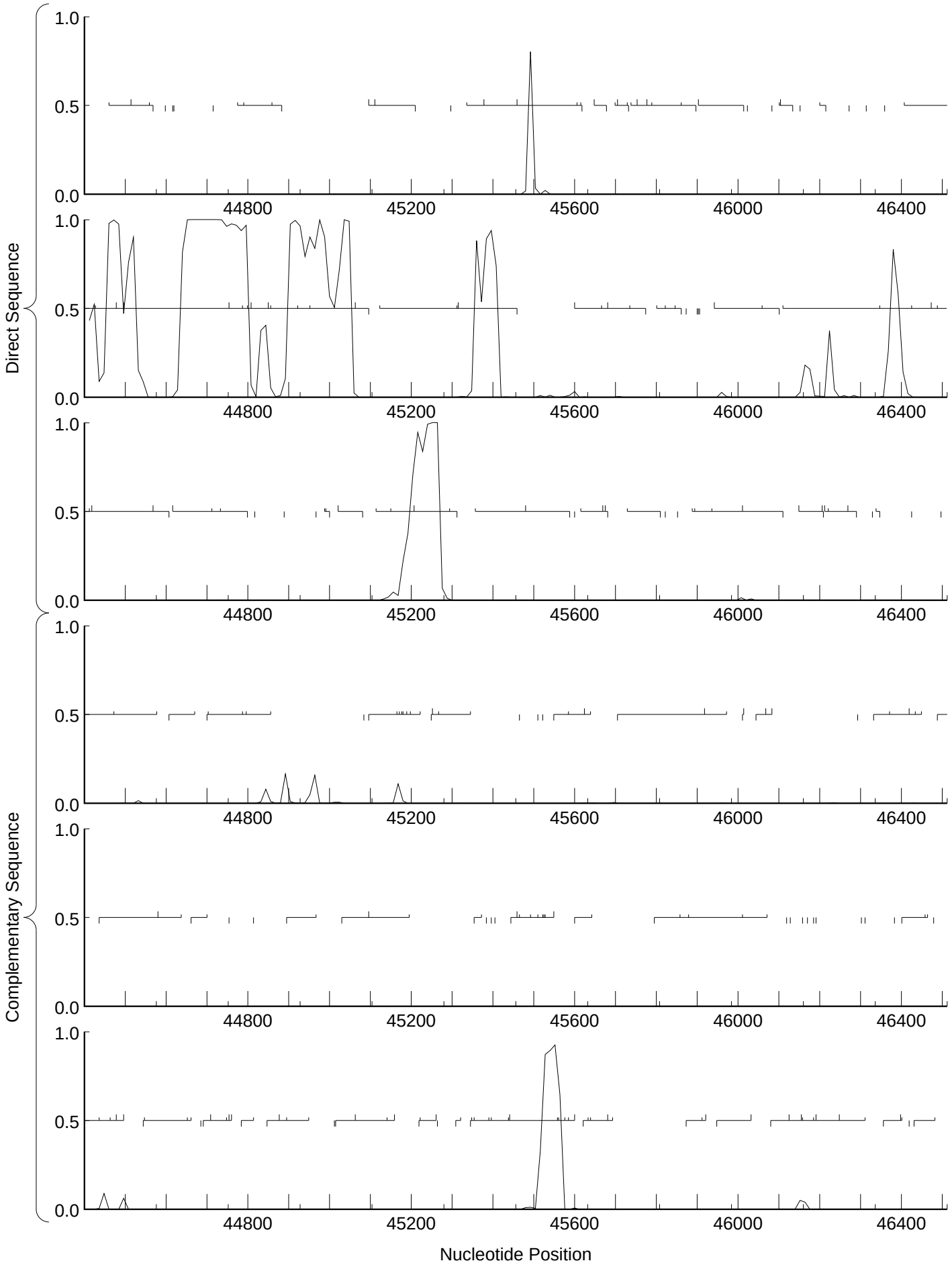
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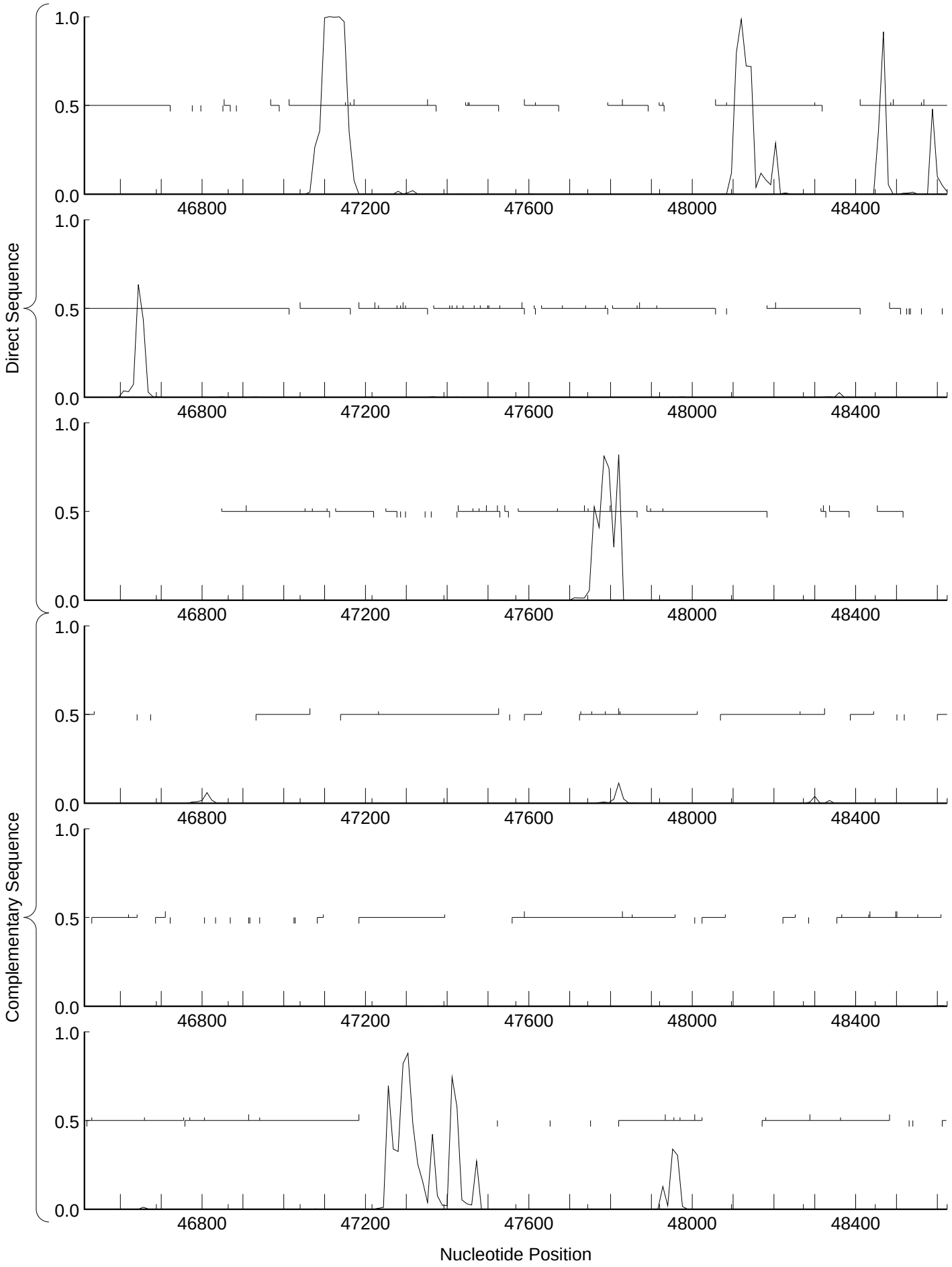
complete sequence, 58009 bp including 10-base 3’ overhang (CGGAAGGCGC), Cluster F1, Order 4, Window 96, Step 12, 22/29



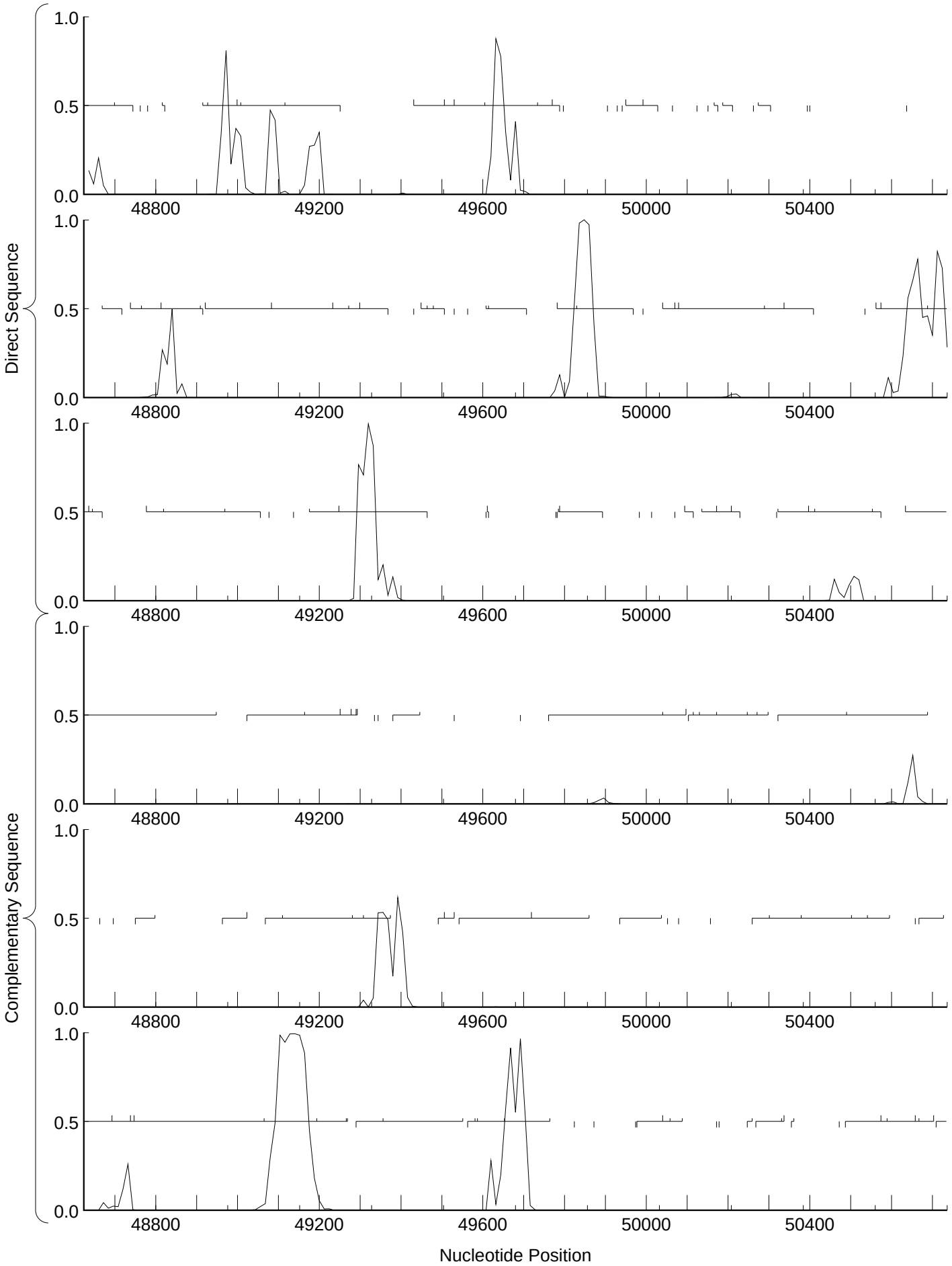
complete sequence, 58009 bp including 10-base 3’ overhang (CGGAAGGCGC), Cluster F1, Order 4, Window 96, Step 12, 23/29



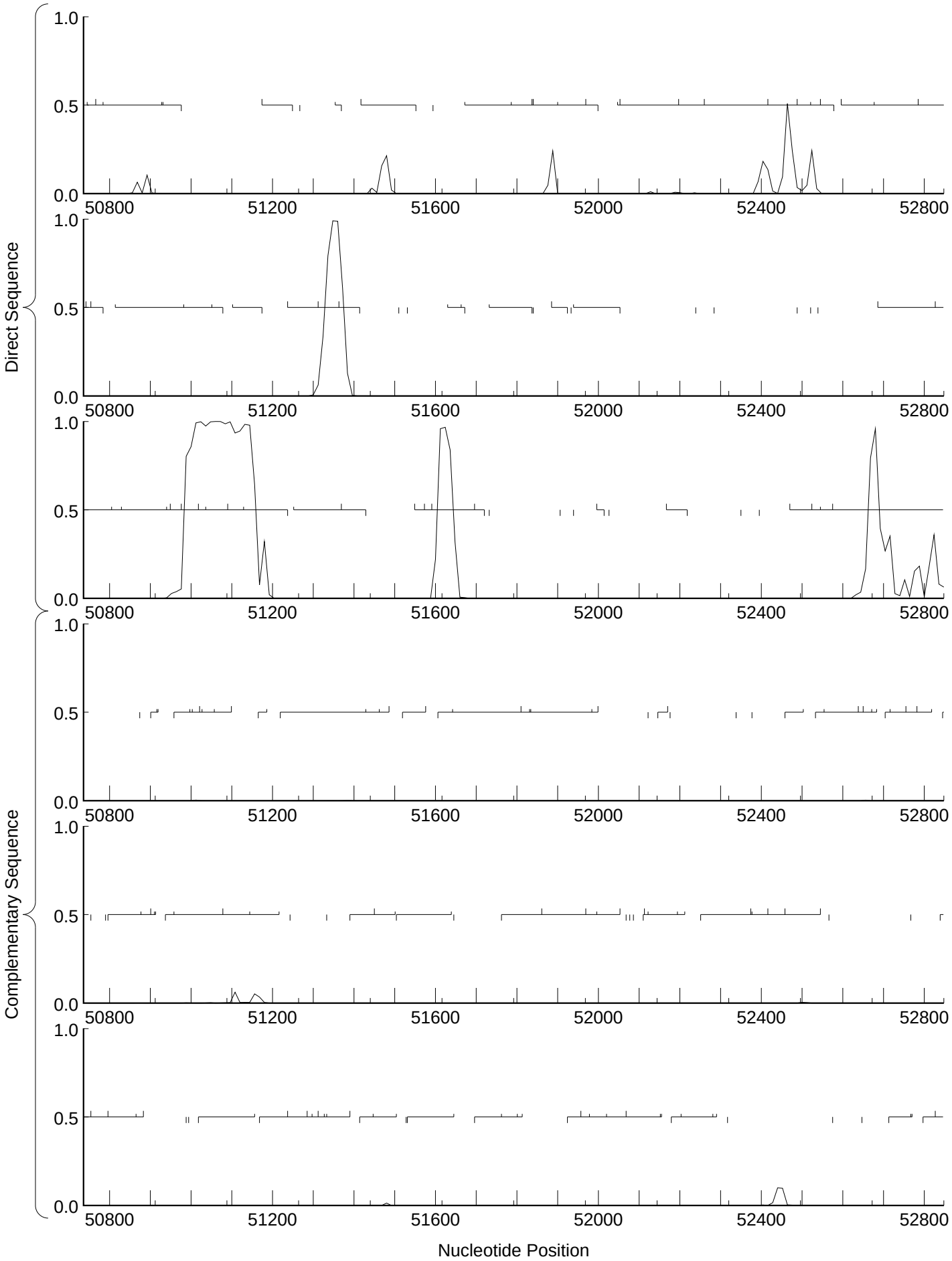
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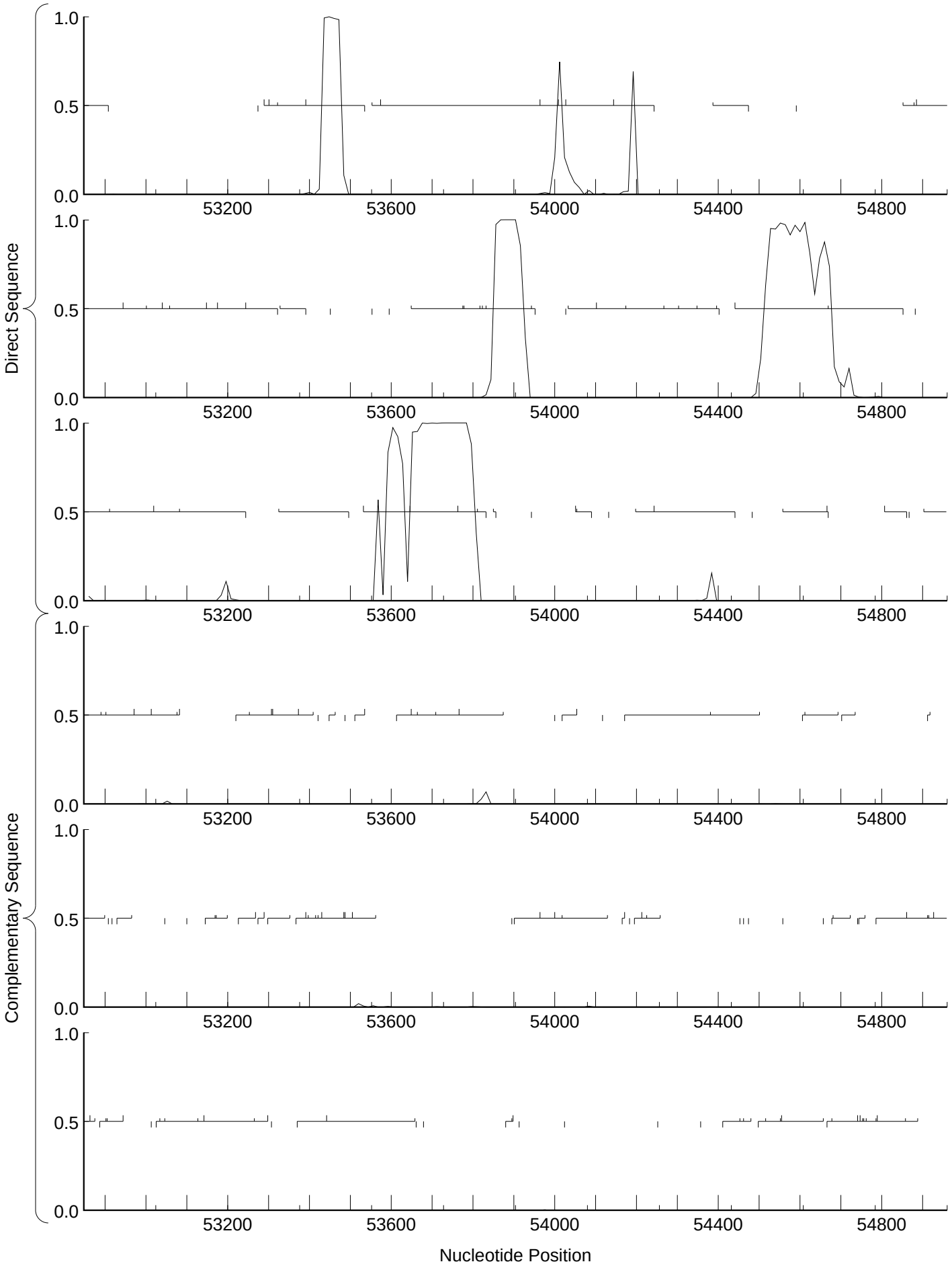
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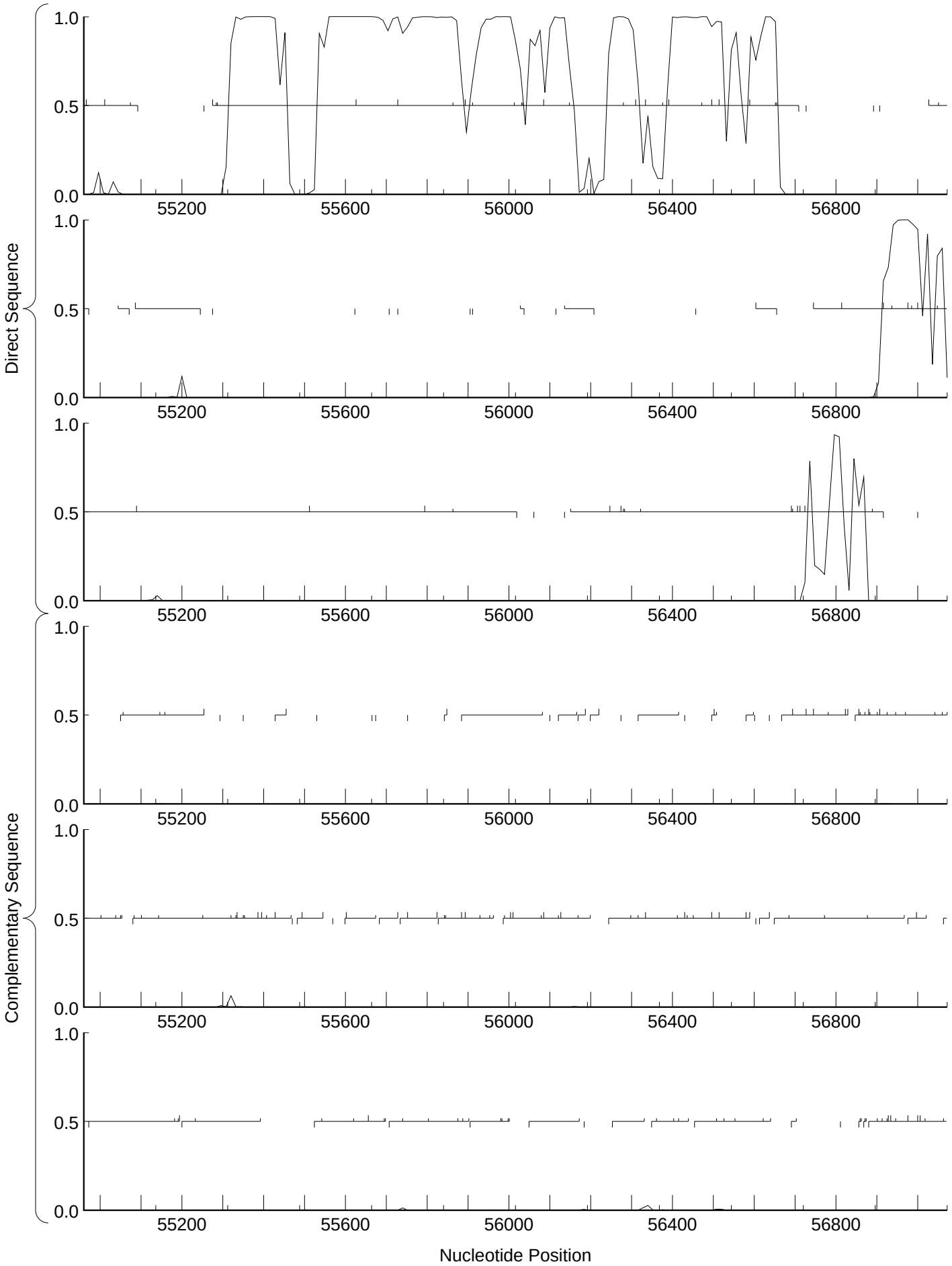
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complete sequence, 58009 bp including 10-base 3’ overhang (CGGAAGGCGC), Cluster F1, Order 4, Window 96, Step 12, 27/29



complete sequence, 58009 bp including 10-base 3’ overhang (CGGAAGGCGC), Cluster F1, Order 4, Window 96, Step 12, 28/29



complete sequence, 58009 bp including 10-base 3’ overhang (CGGAAGGCGC), Cluster F1, Order 4, Window 96, Step 12, 29/29

