GeneMark

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

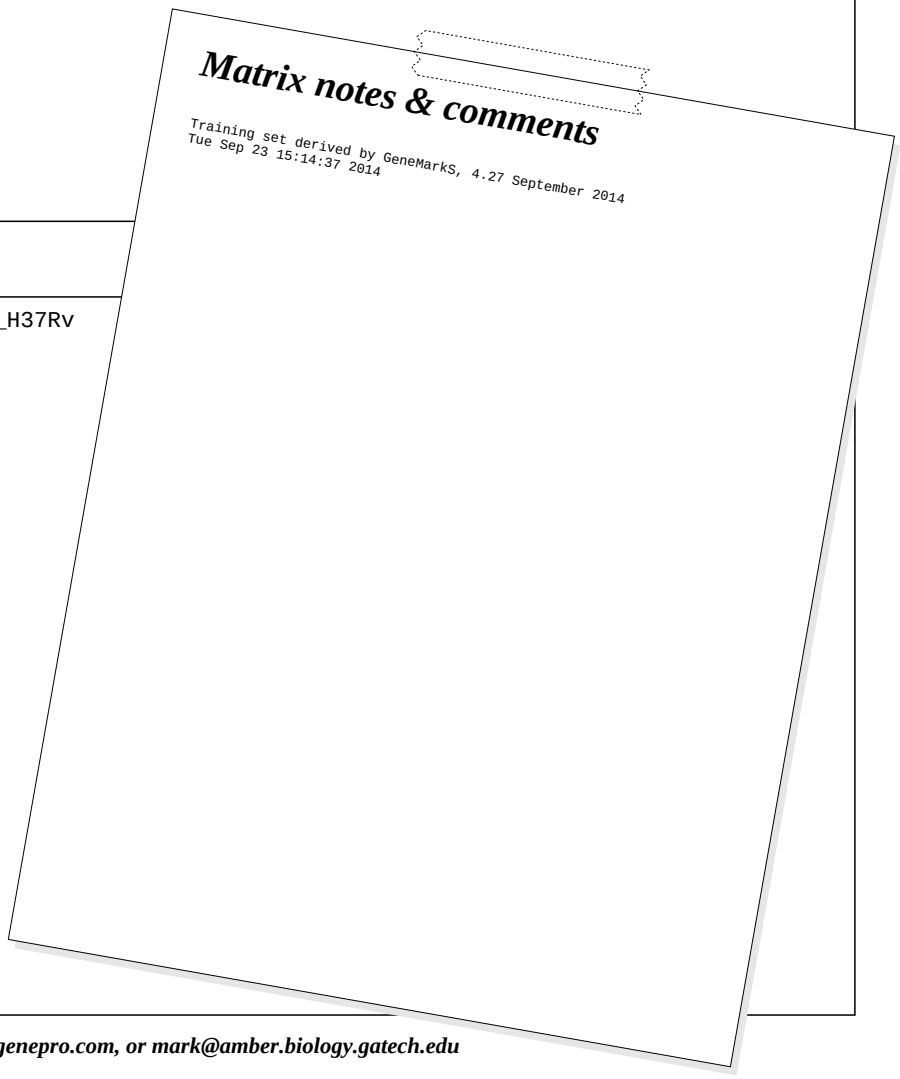
PROGRAM INFORMATION

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Analysis Date    :  3/29/24 at 8:22:26
Pages            :  52
Sequence Length  :  106327 bp
GC Content       :   60.79%

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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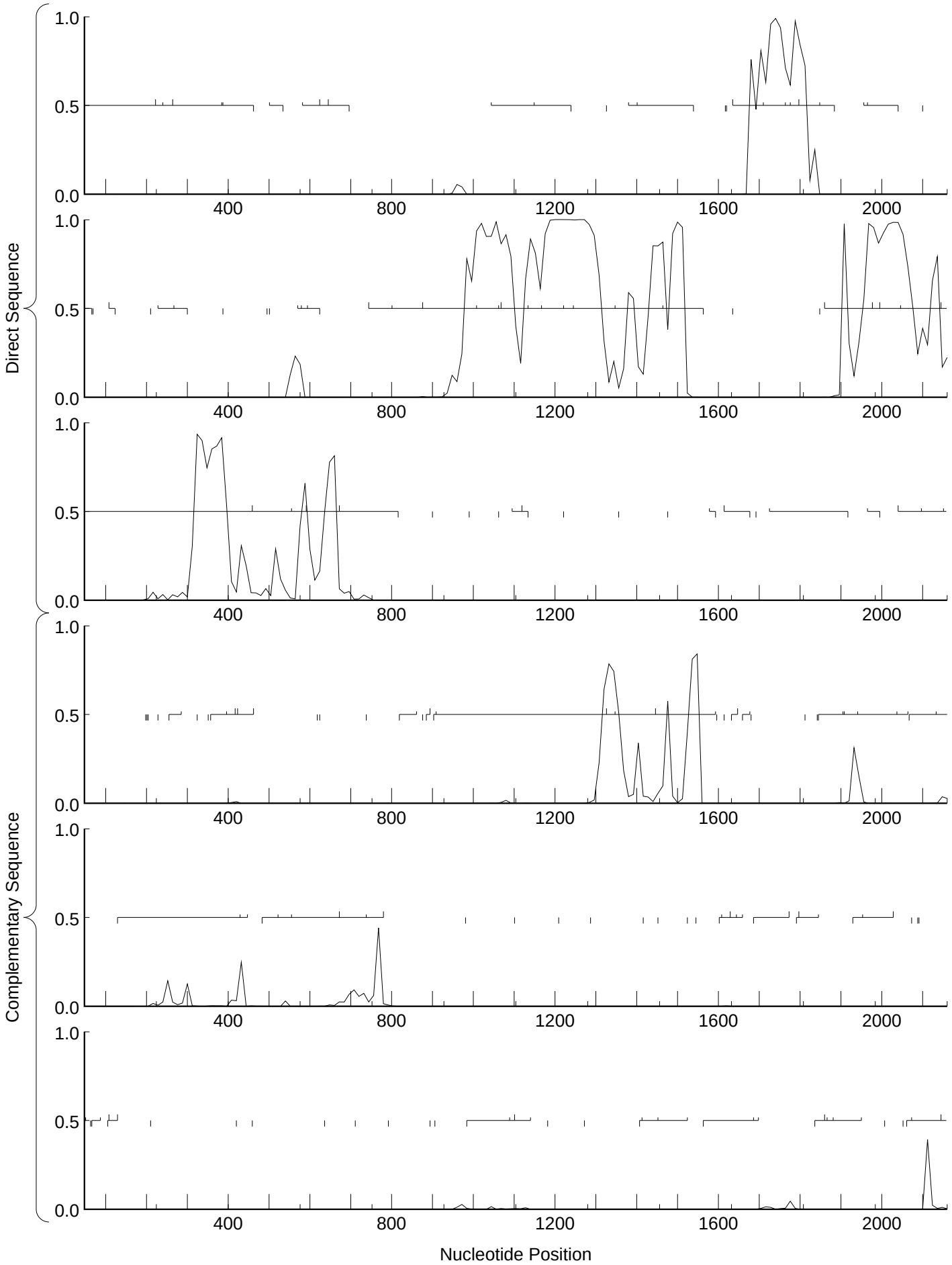
MATRIX INFORMATION

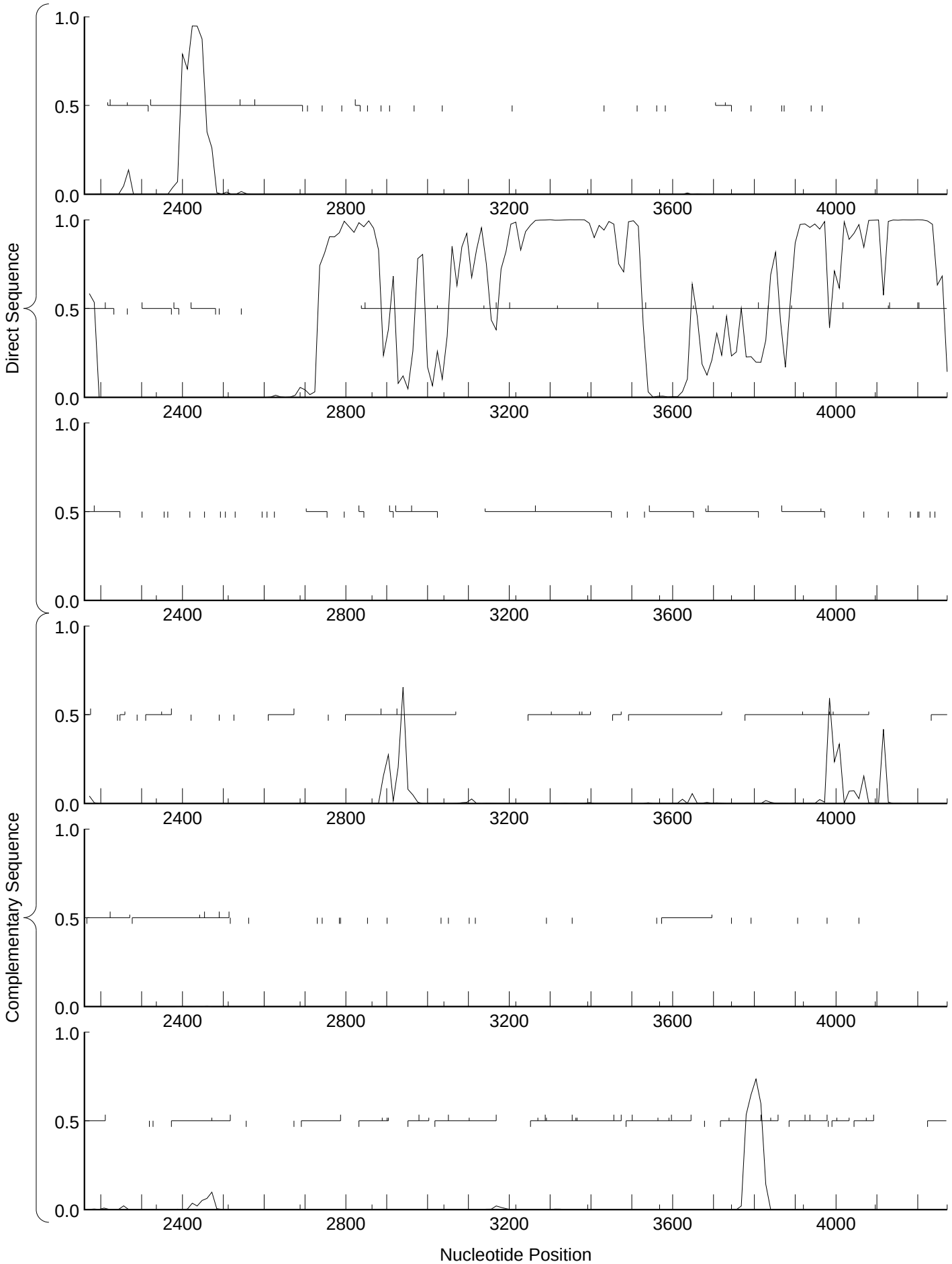
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Matrix     :  Mycobacterium_tuberculosis_H37Rv
Author     :  -

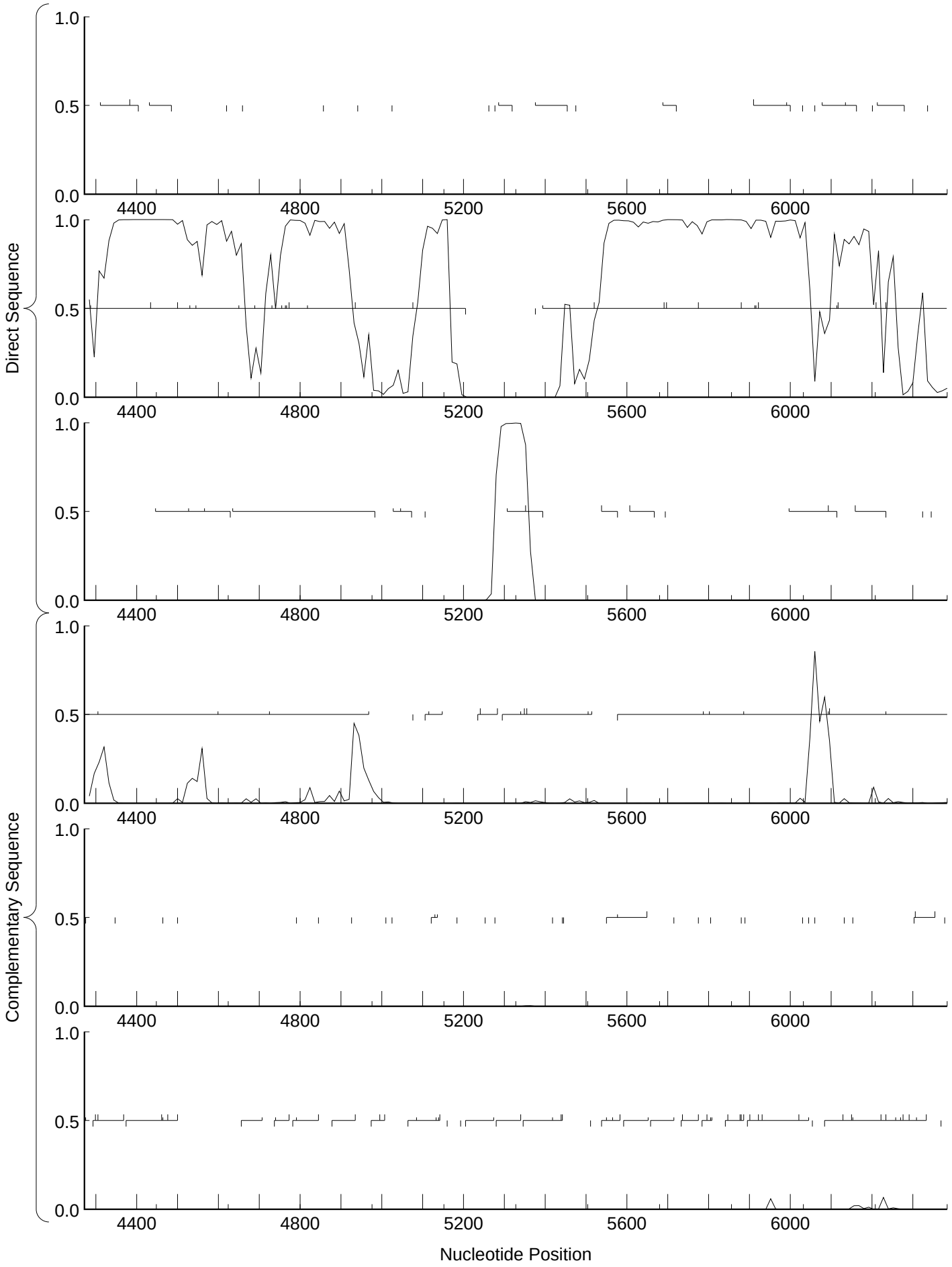
Order      :  4
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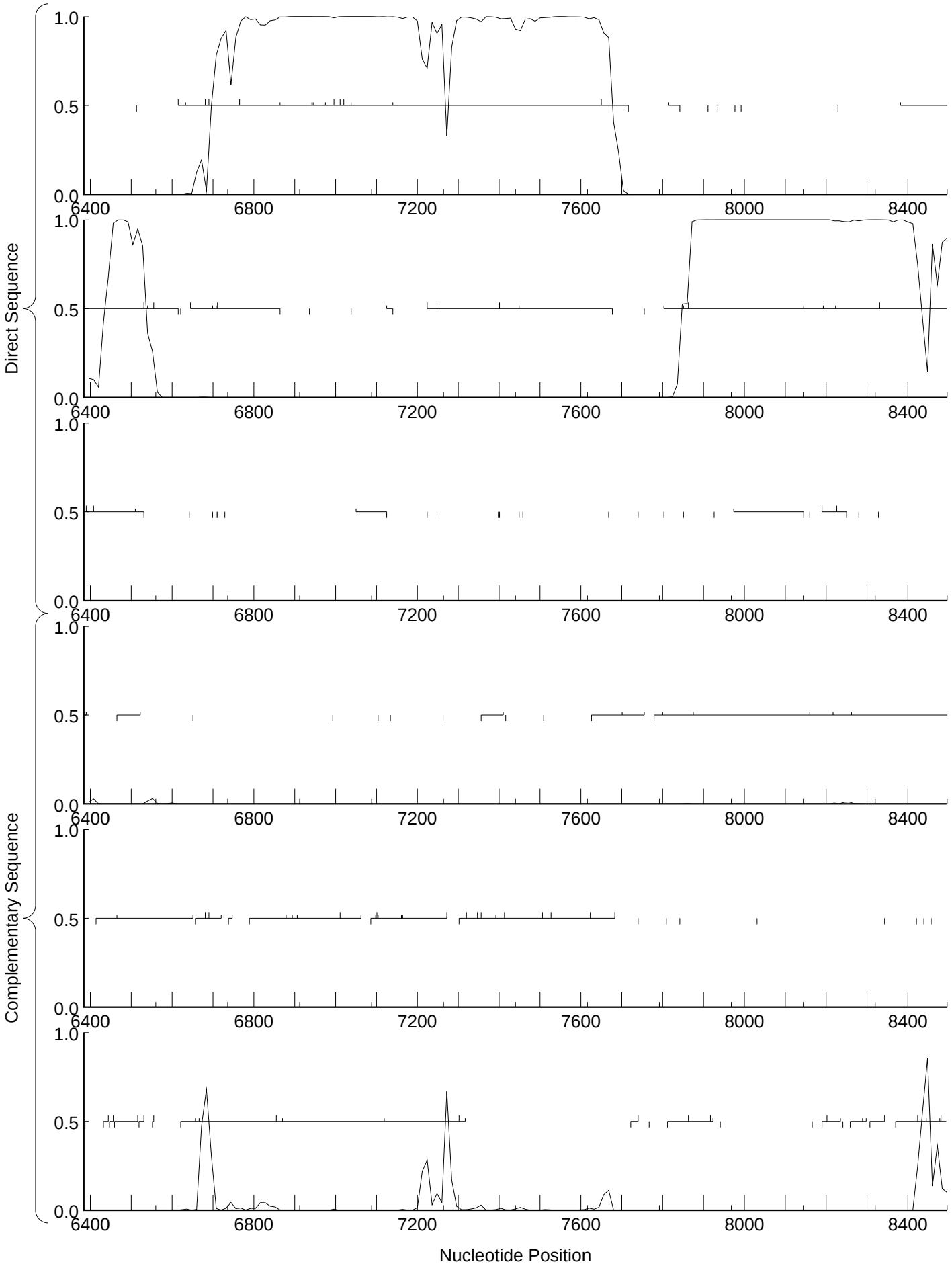

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  Send questions / comments to:
      Dr. M. Borodovsky
      Georgia Institute of Technology
      School of Biology
      Atlanta, GA  30332-0230
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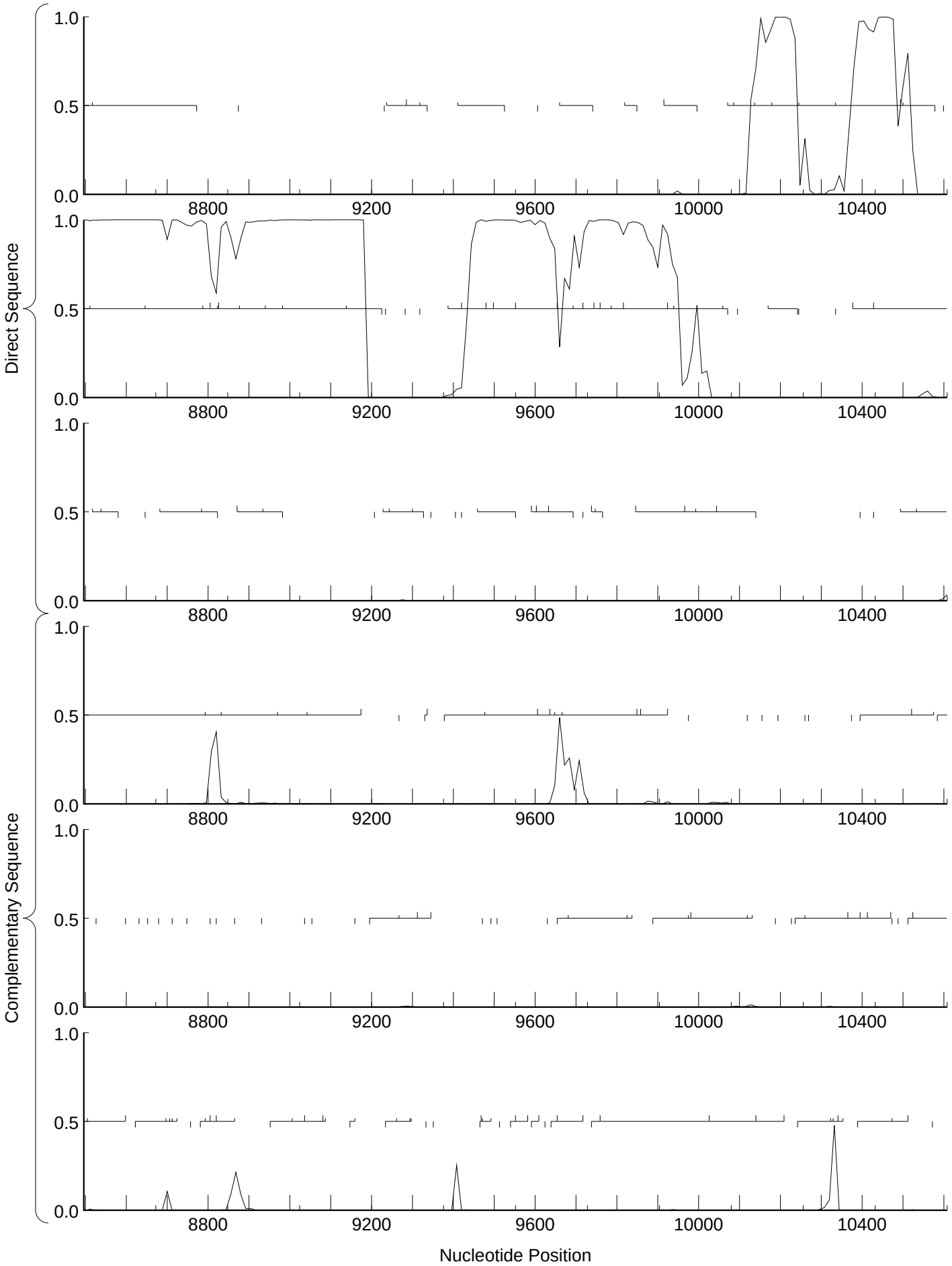

For help or information, send electronic mail to: custserv@genepro.com, or mark@amber.biology.gatech.edu

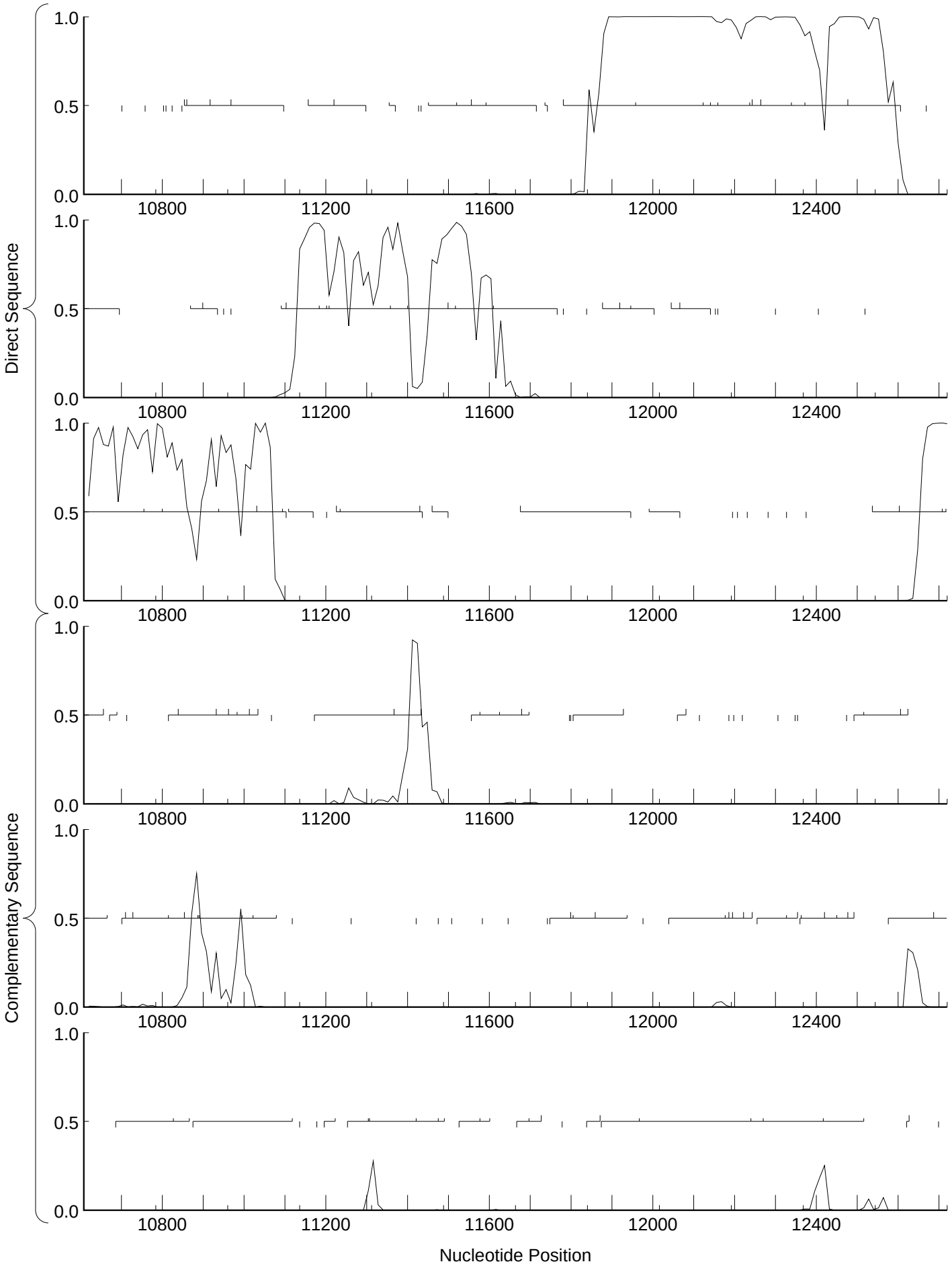

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Nucleotide Position

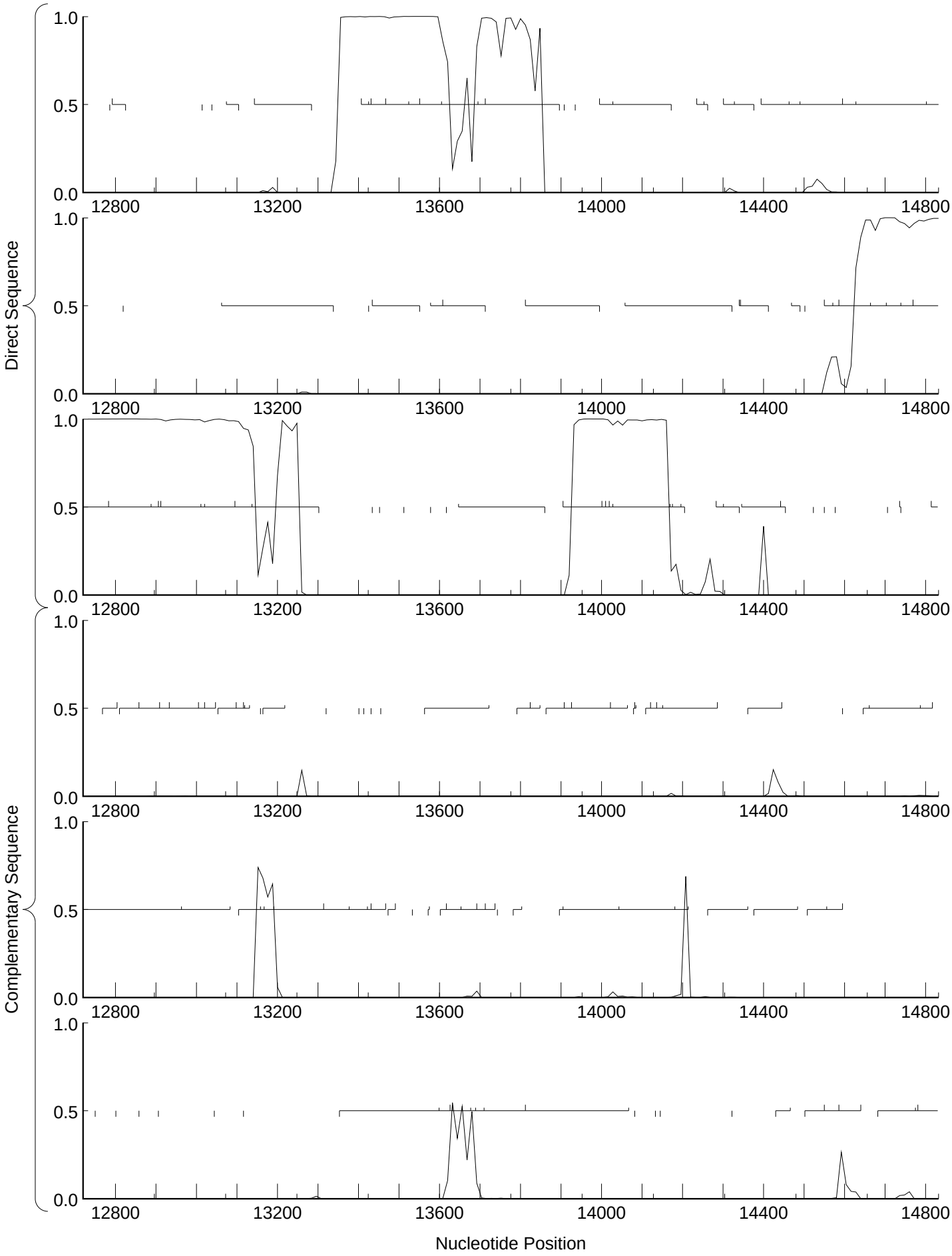

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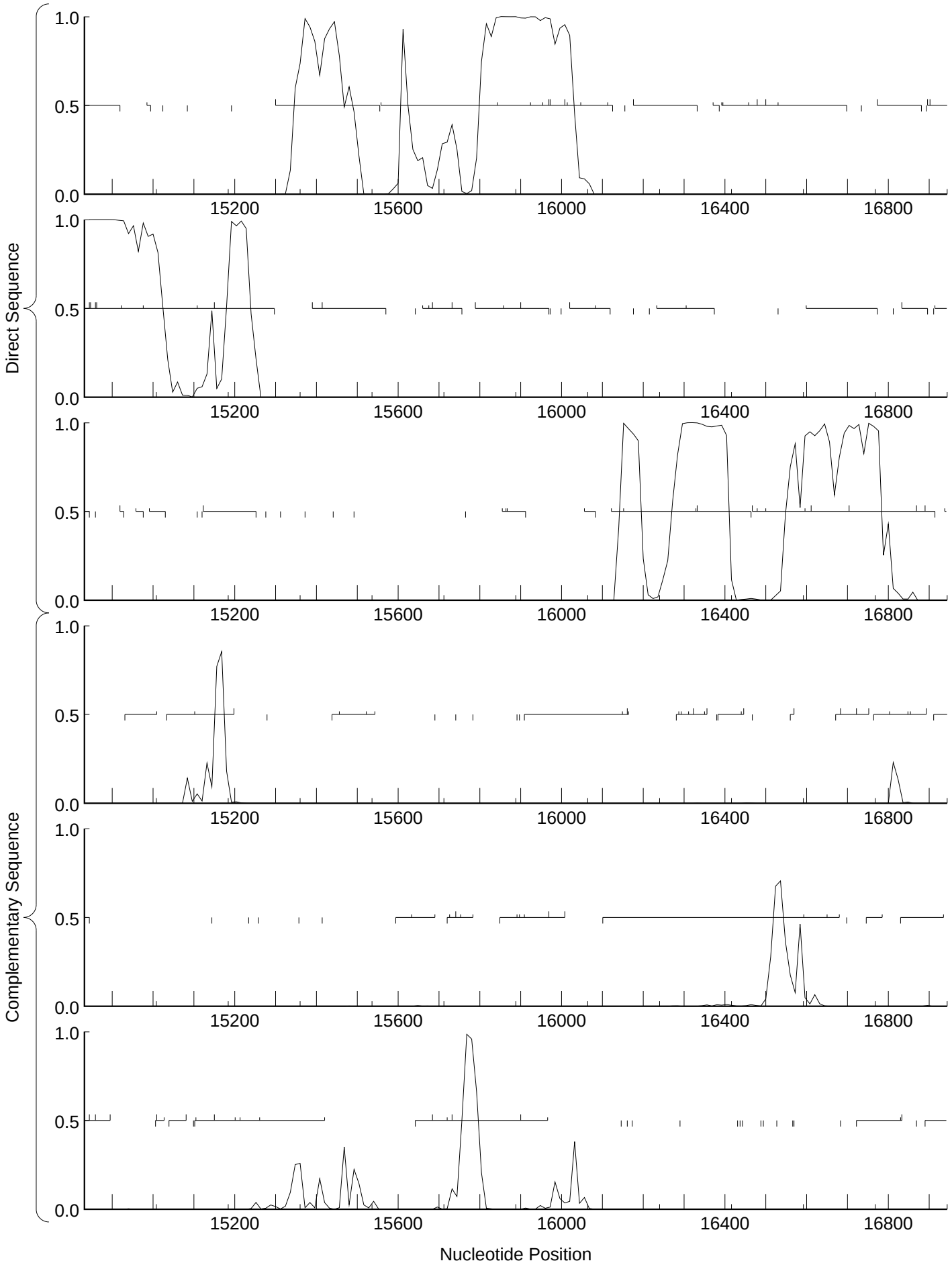

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5600
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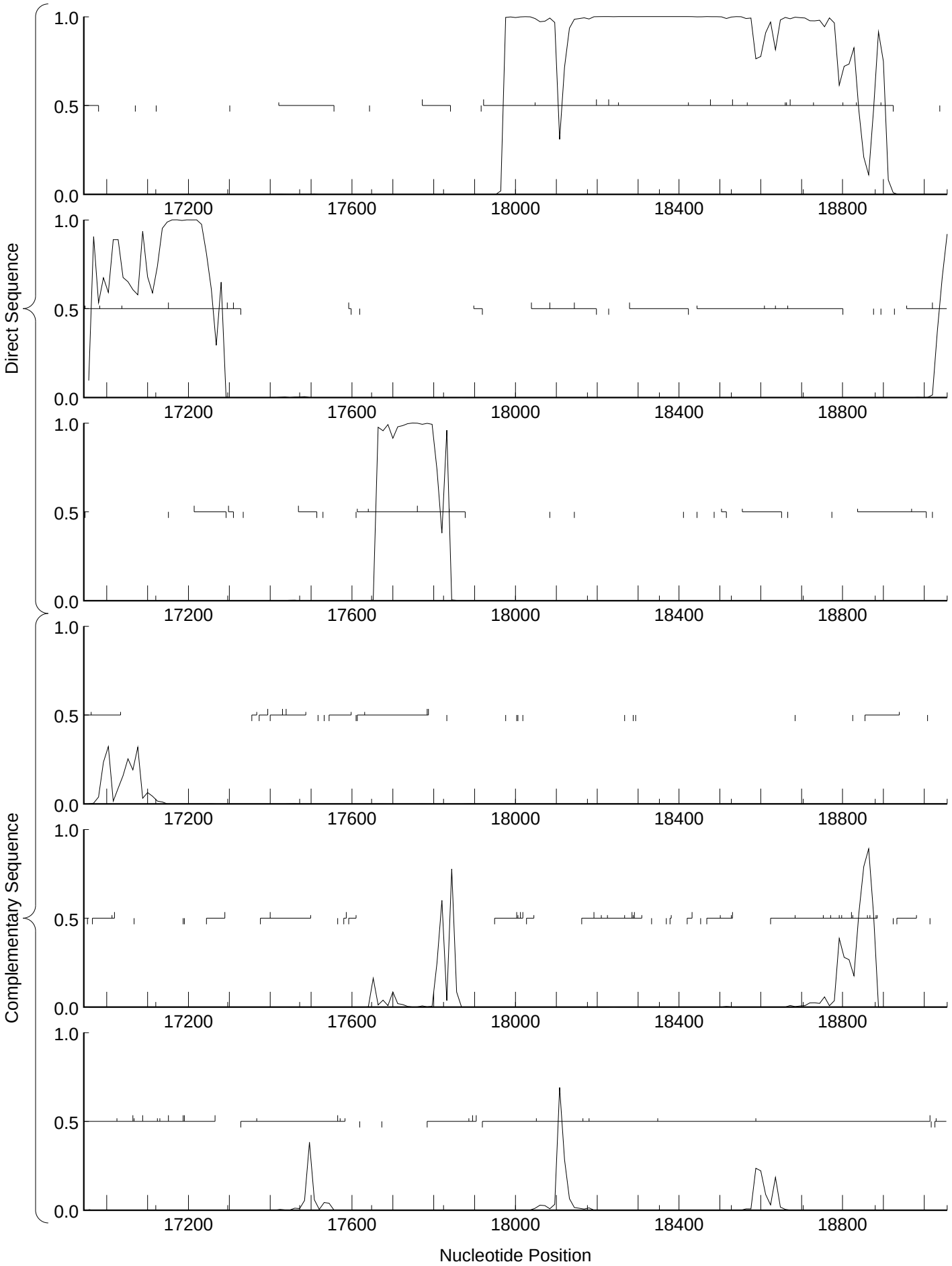

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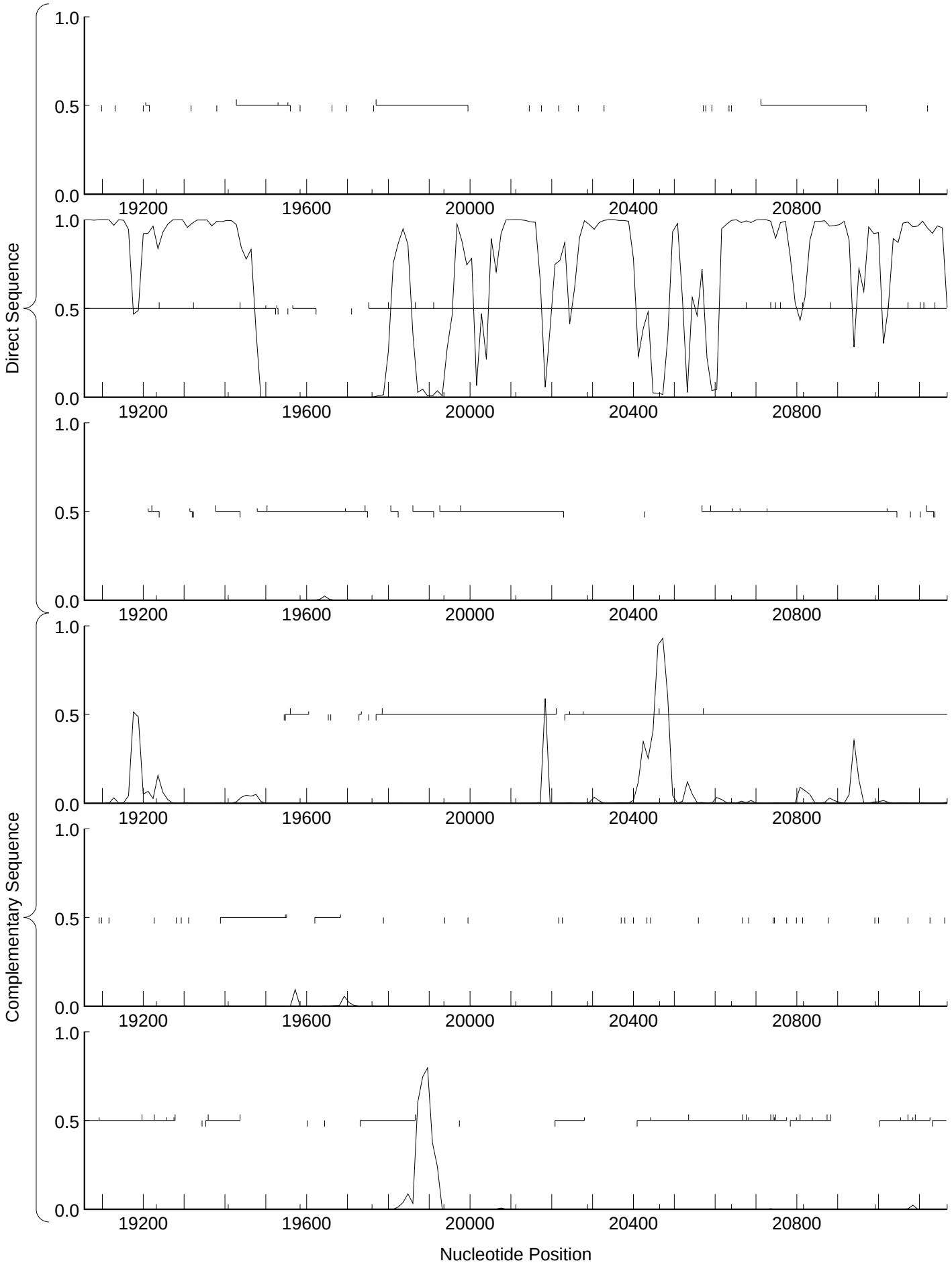

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Nucleotide Position

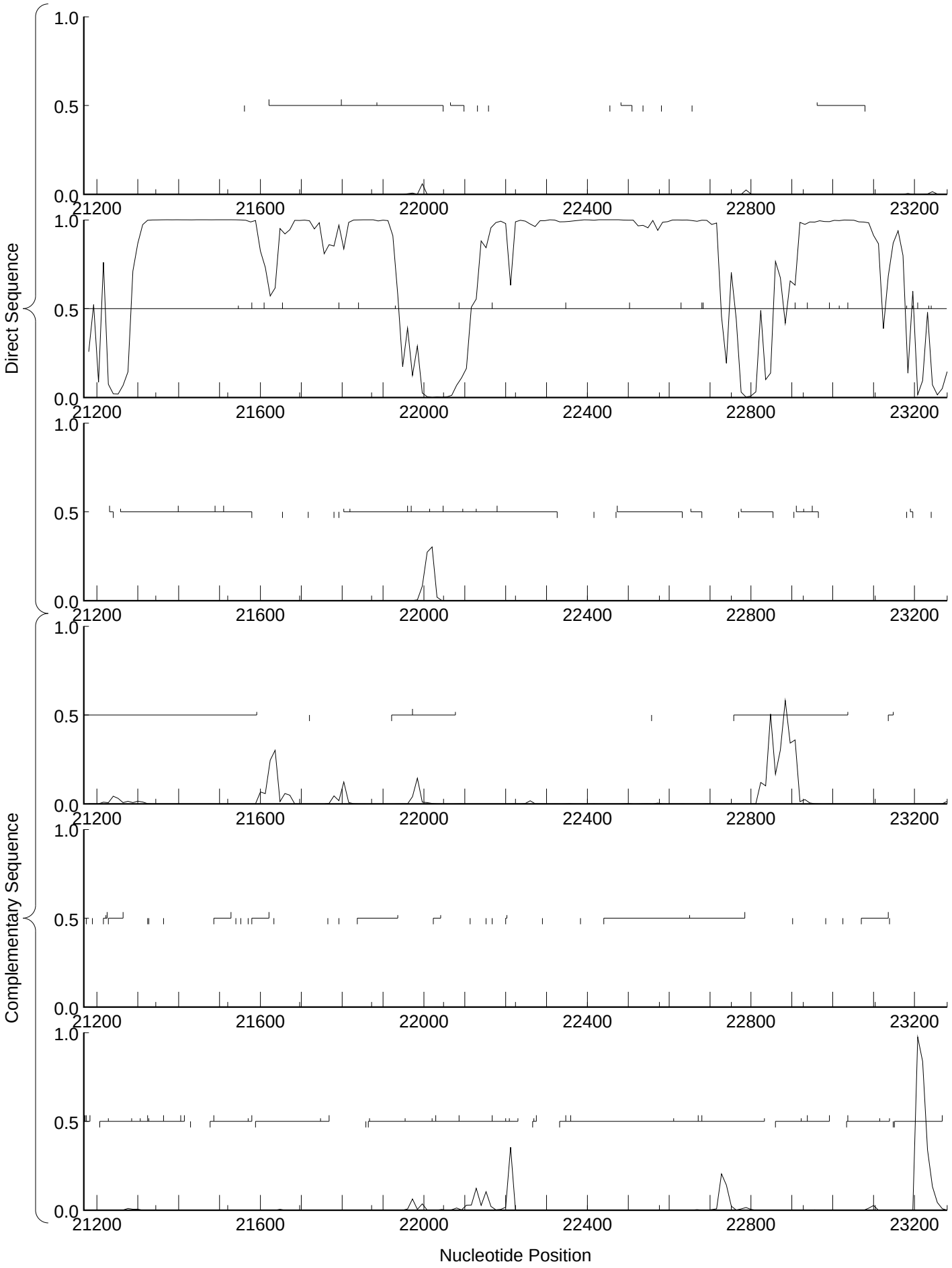

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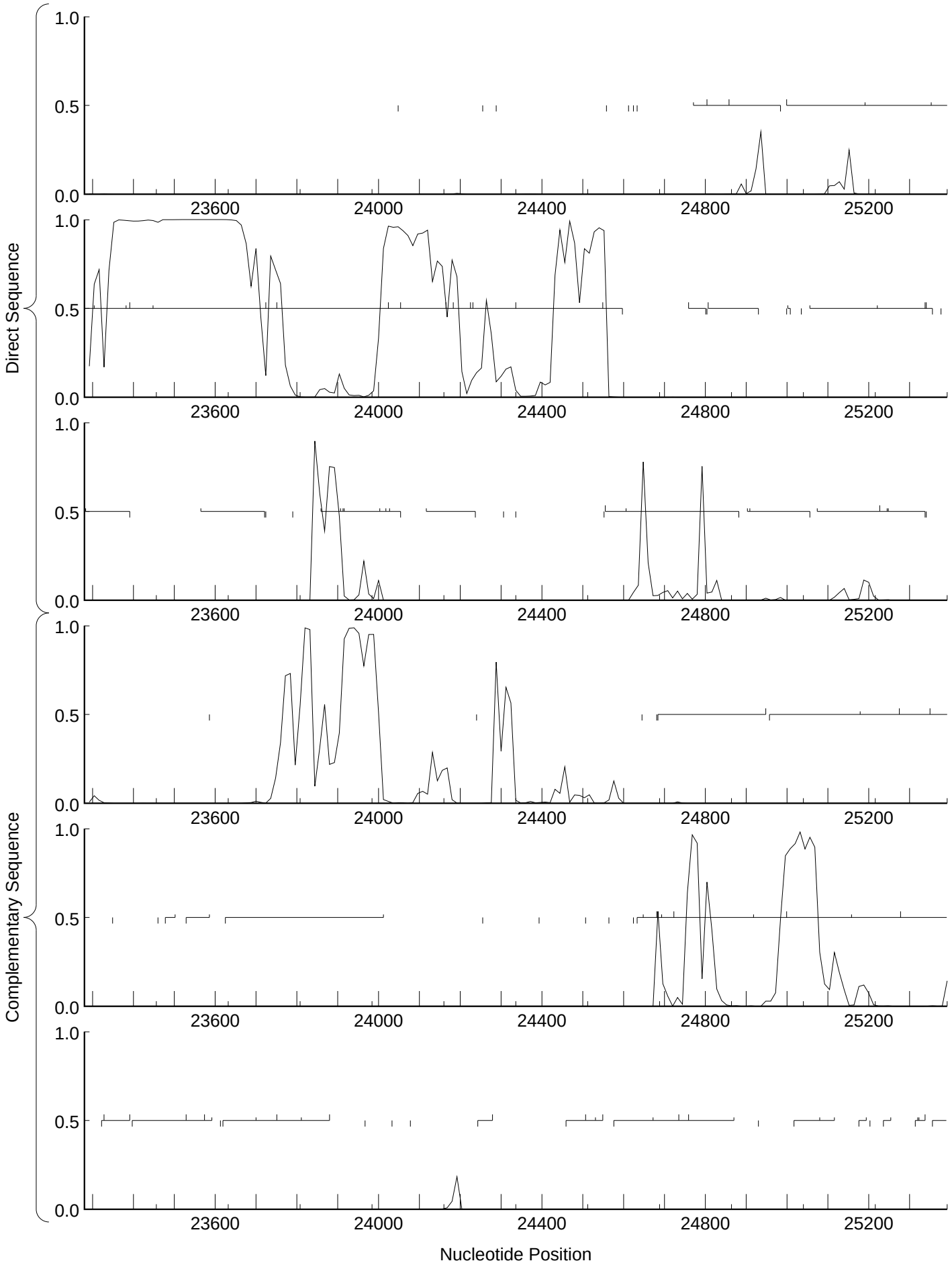
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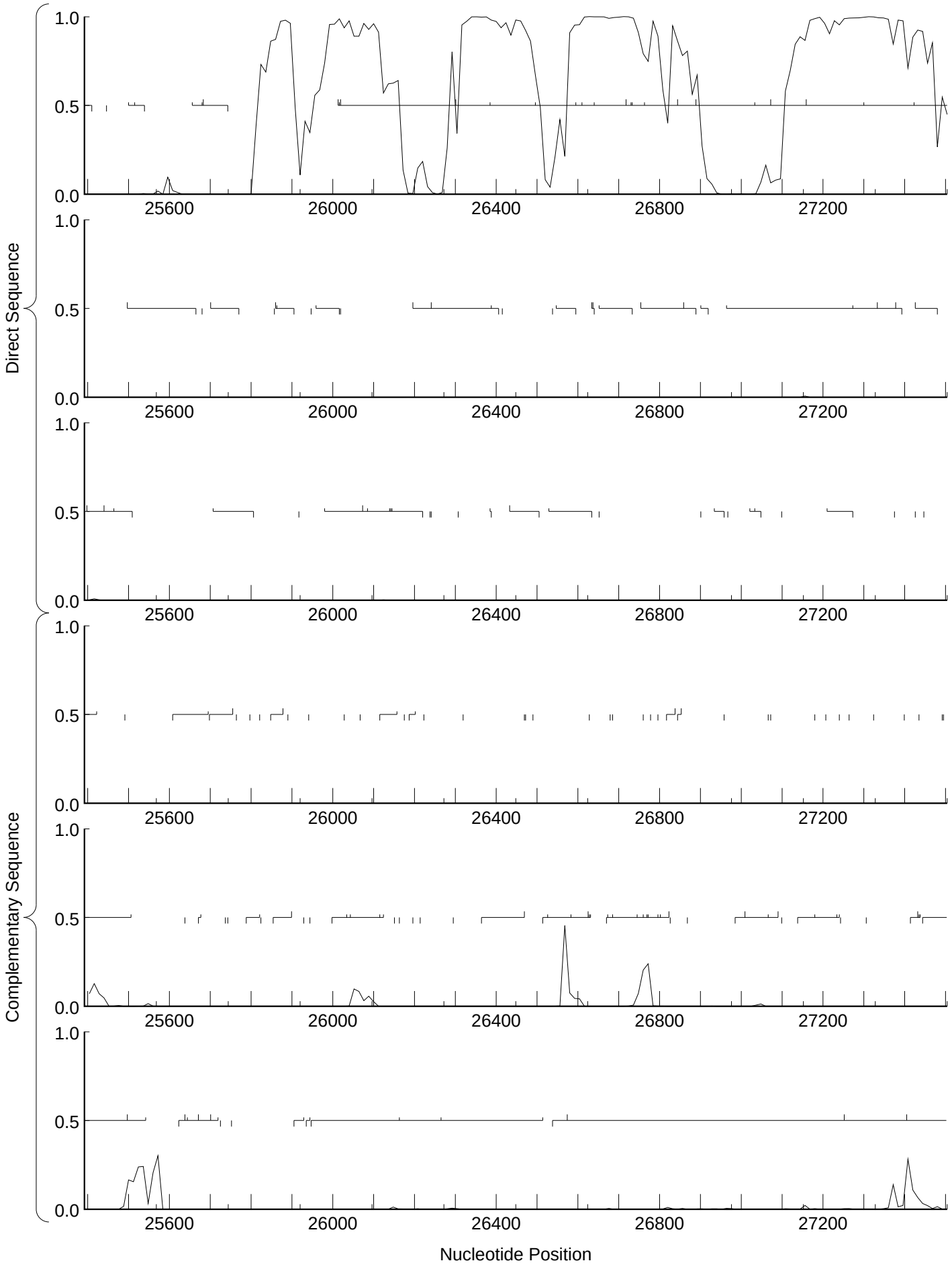



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Nucleotide Position

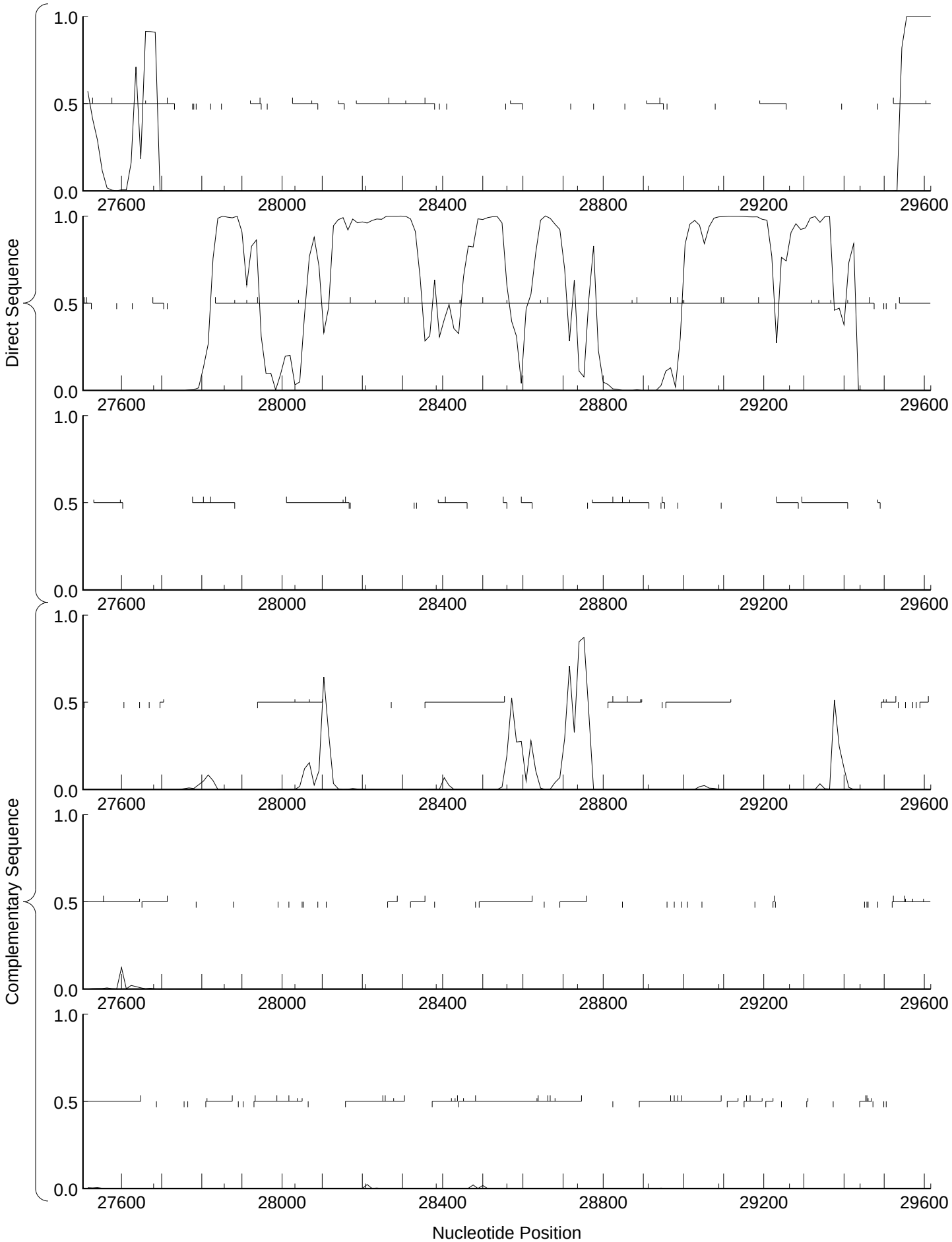
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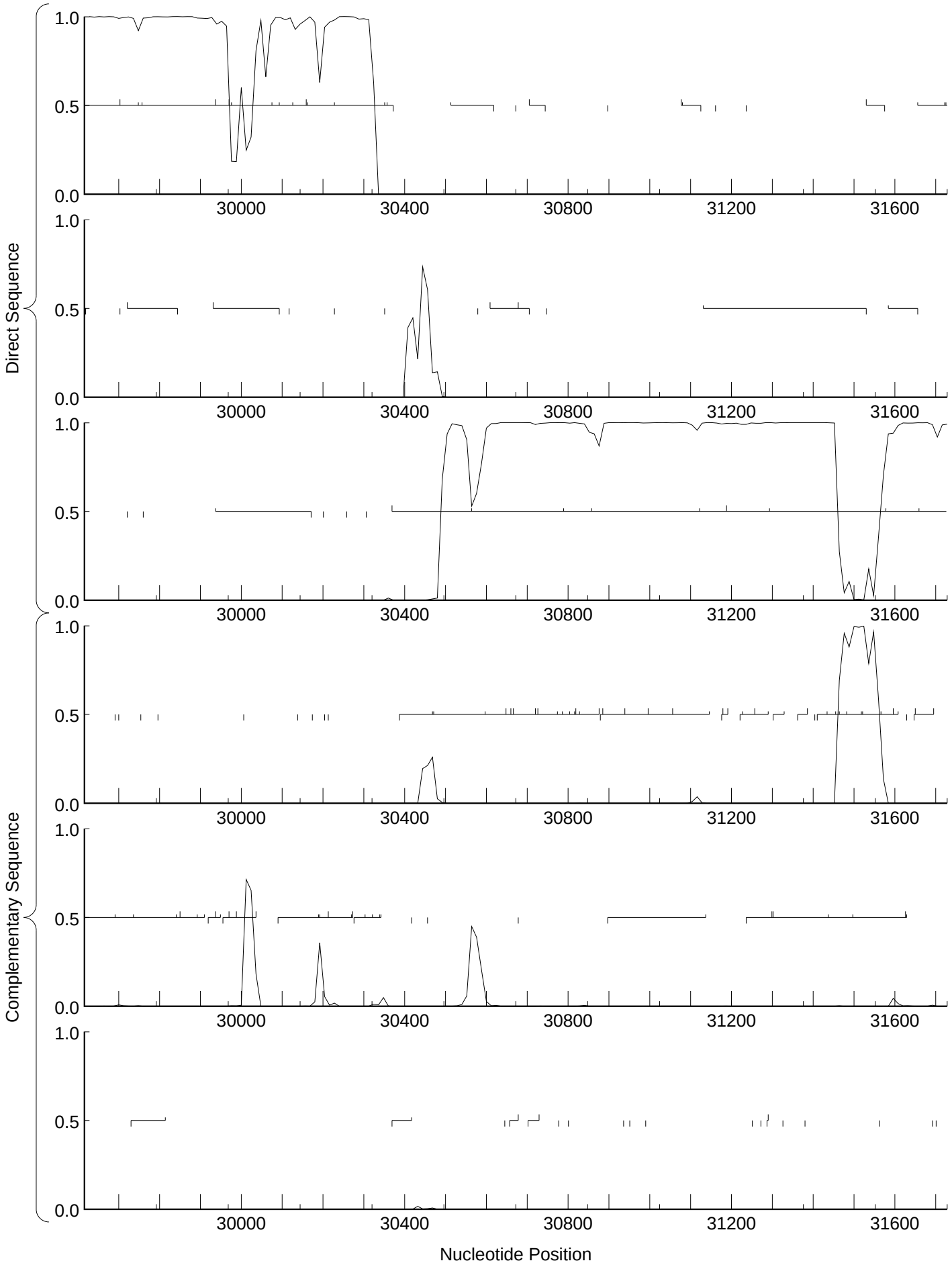


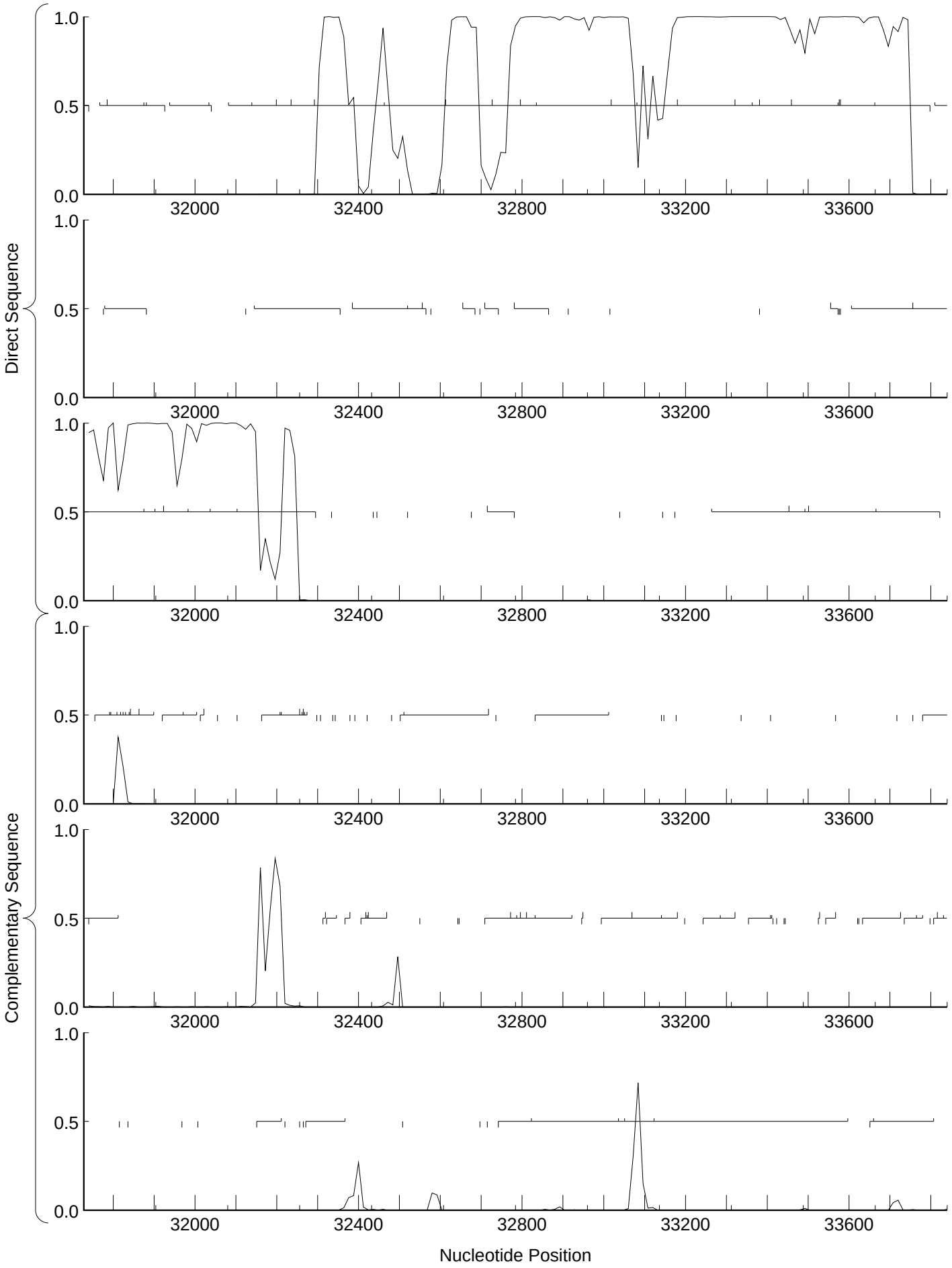

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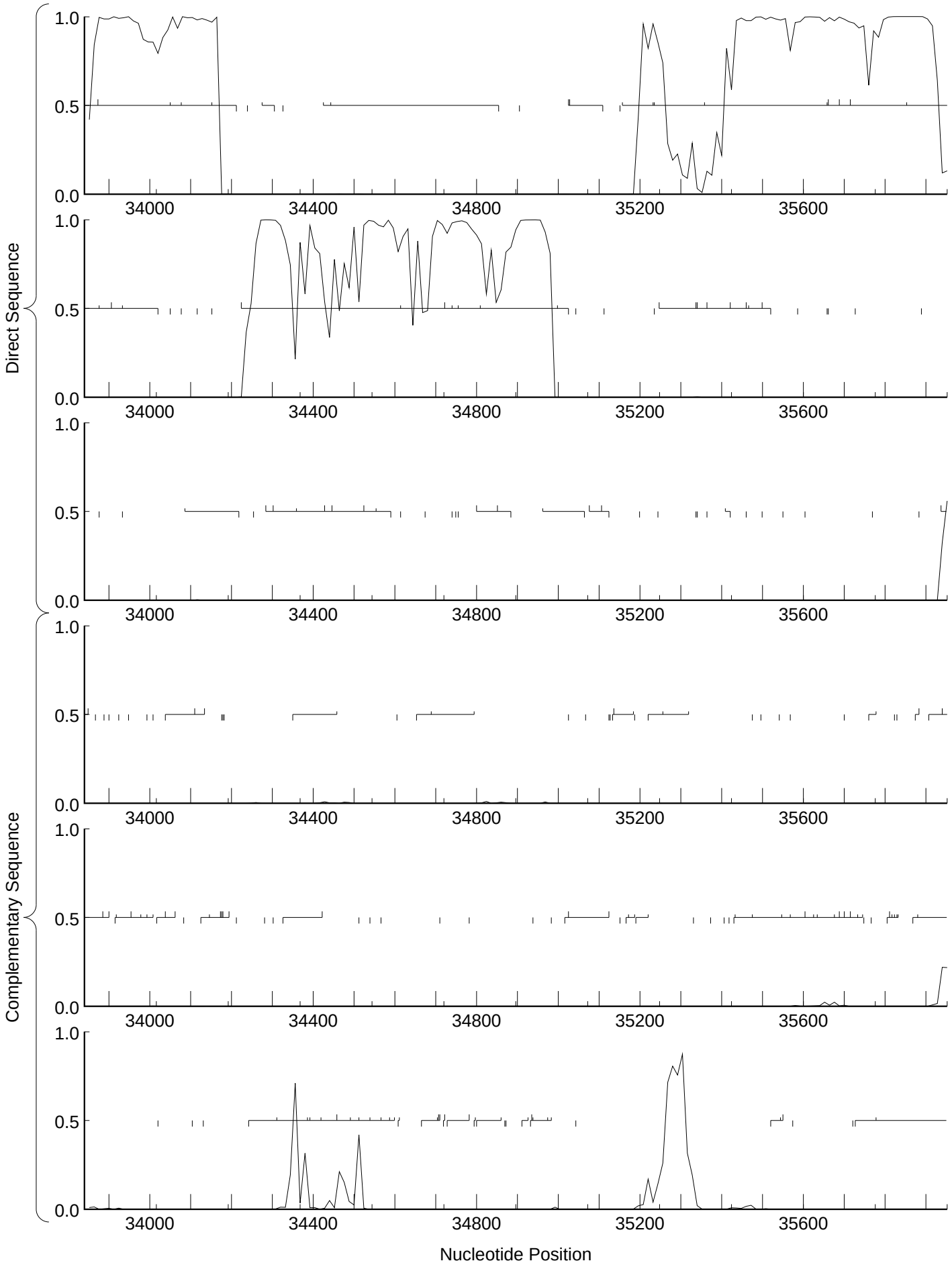

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Complementary Sequence
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Nucleotide Position

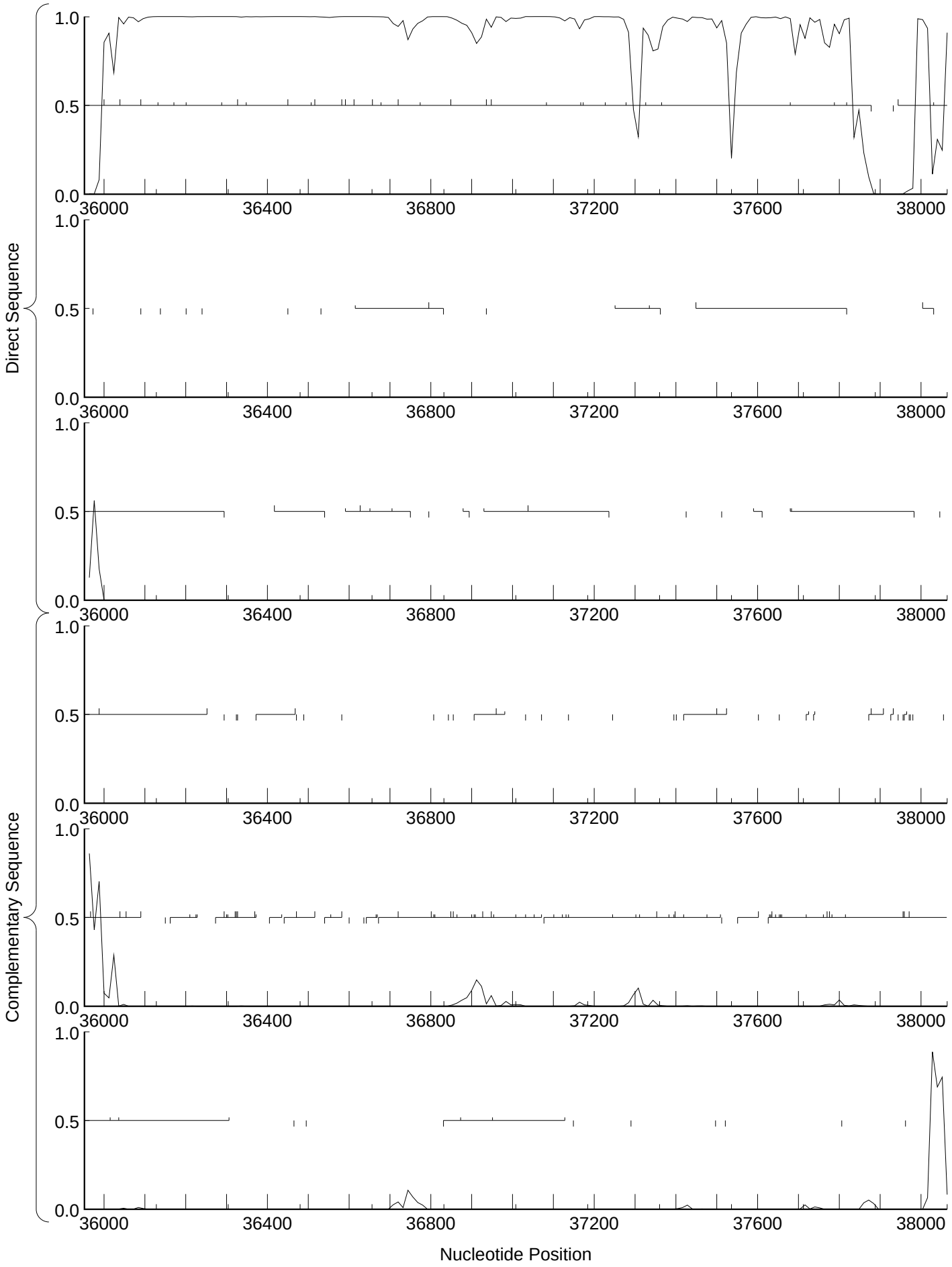
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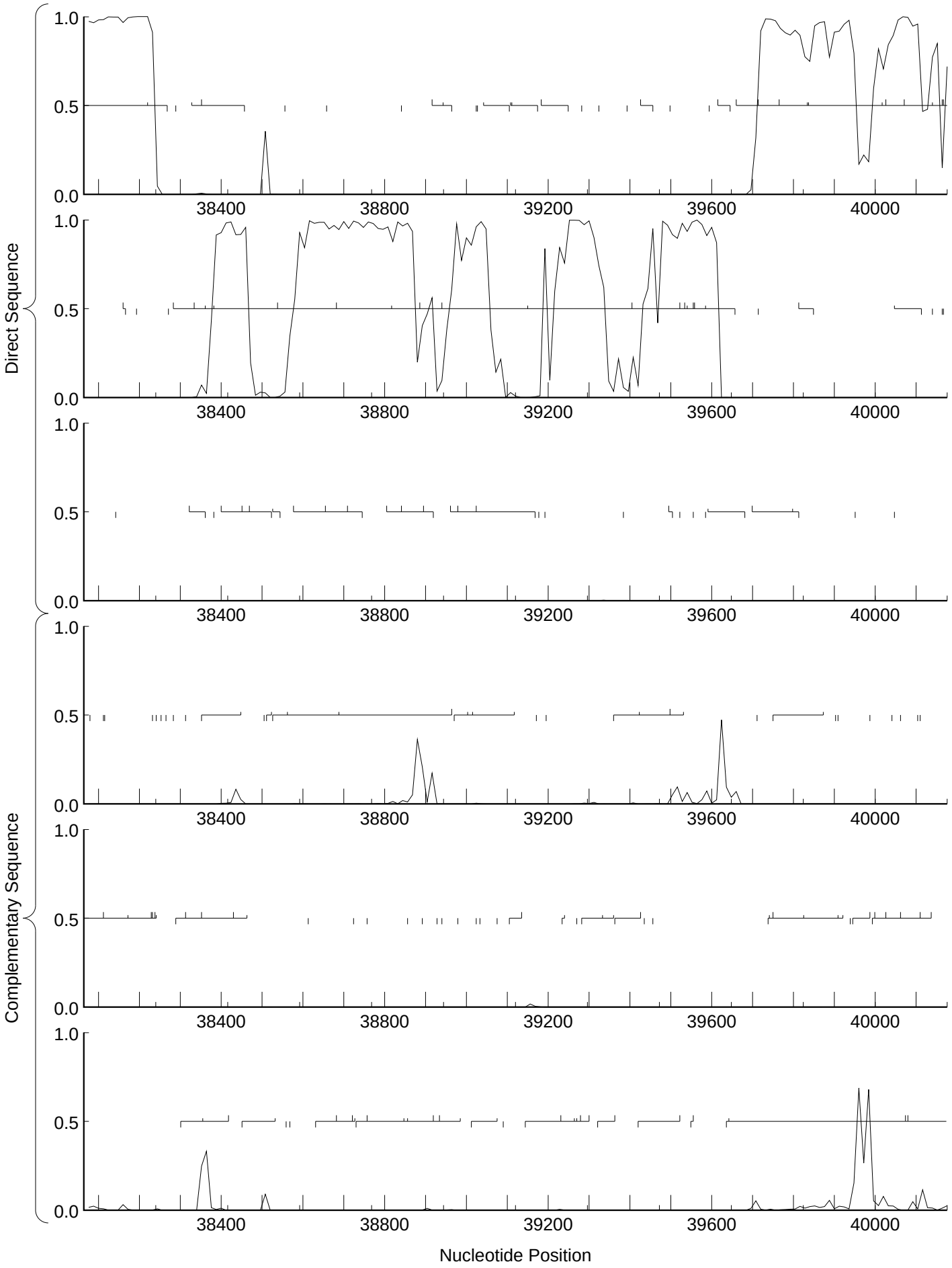


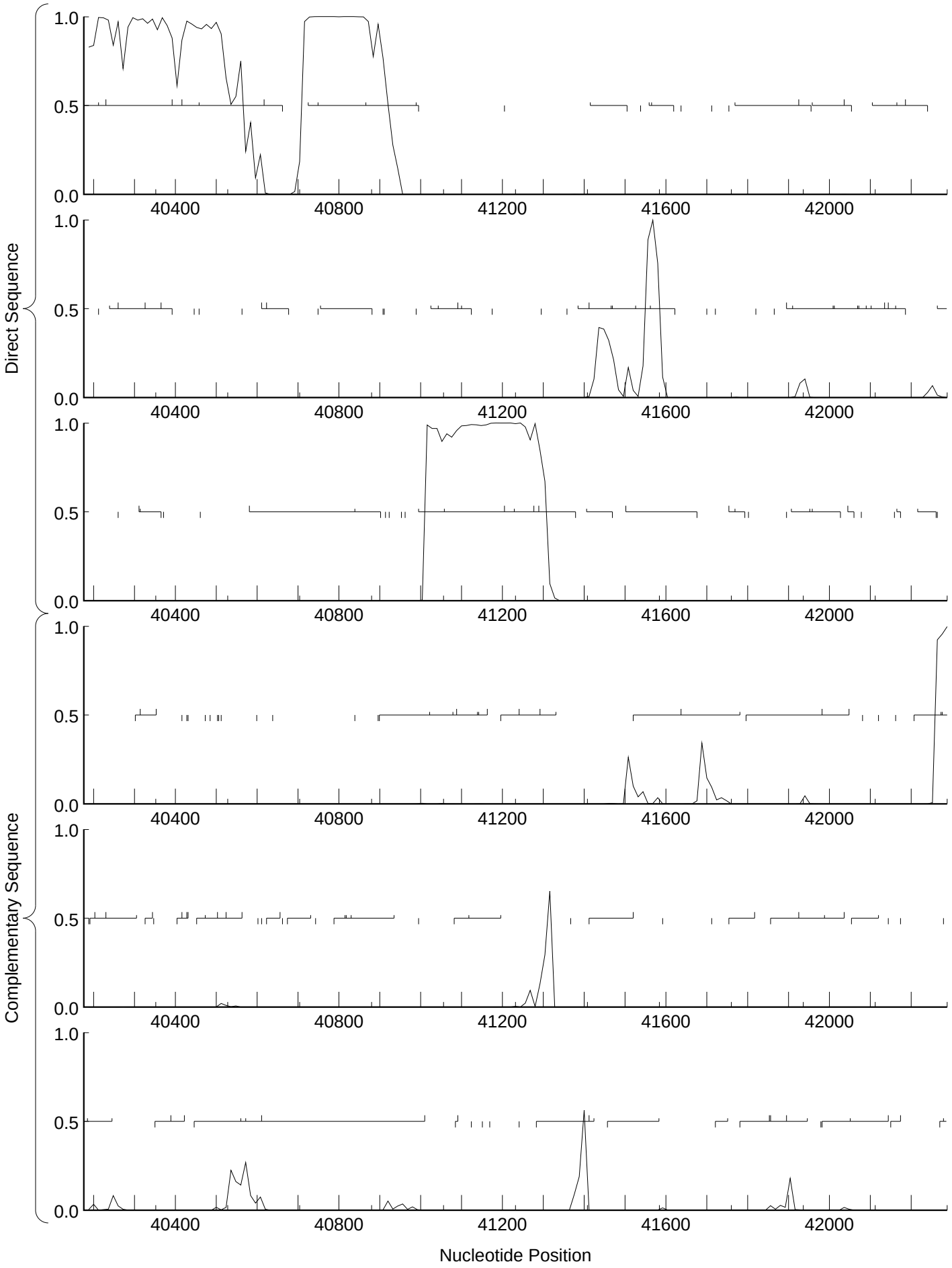

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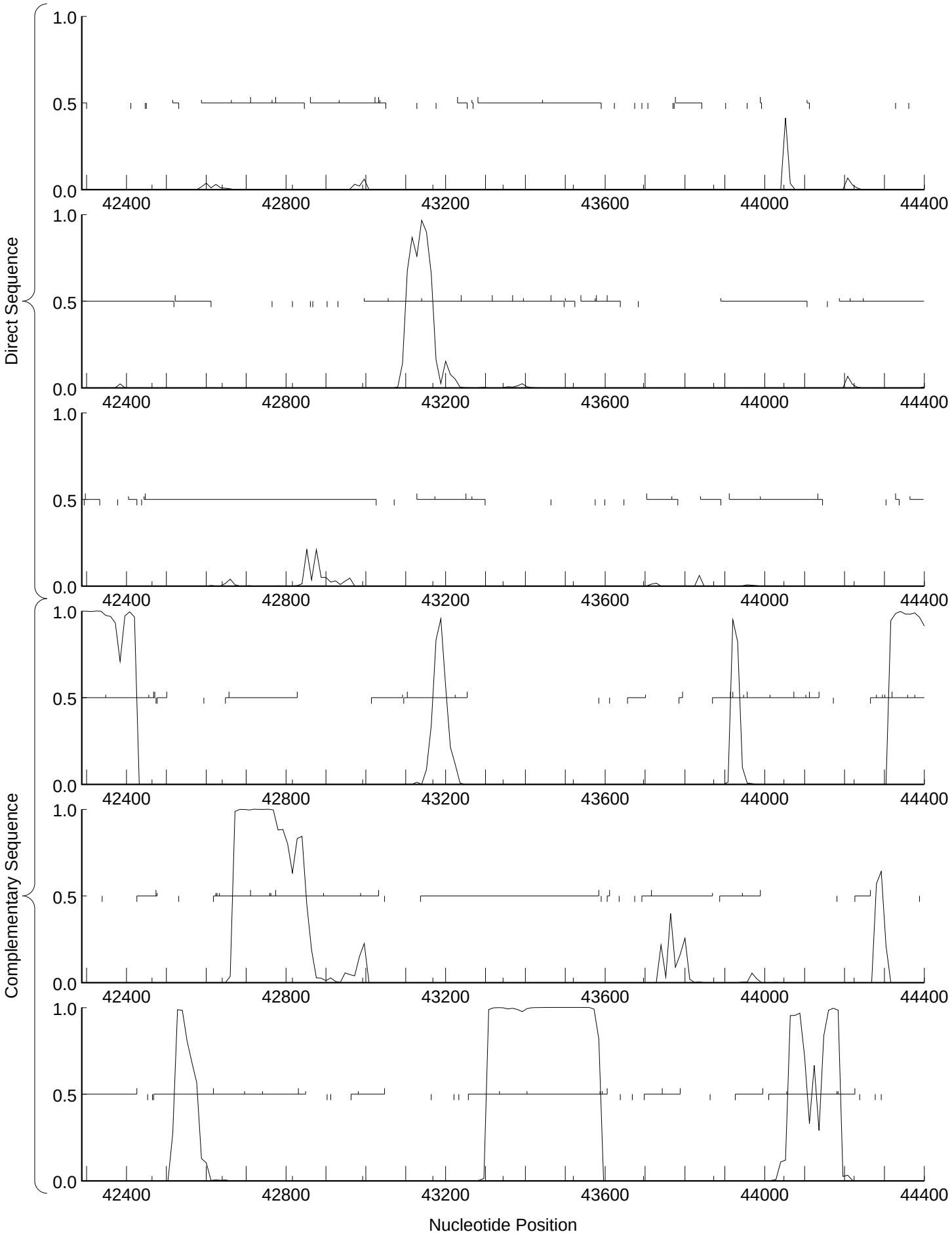

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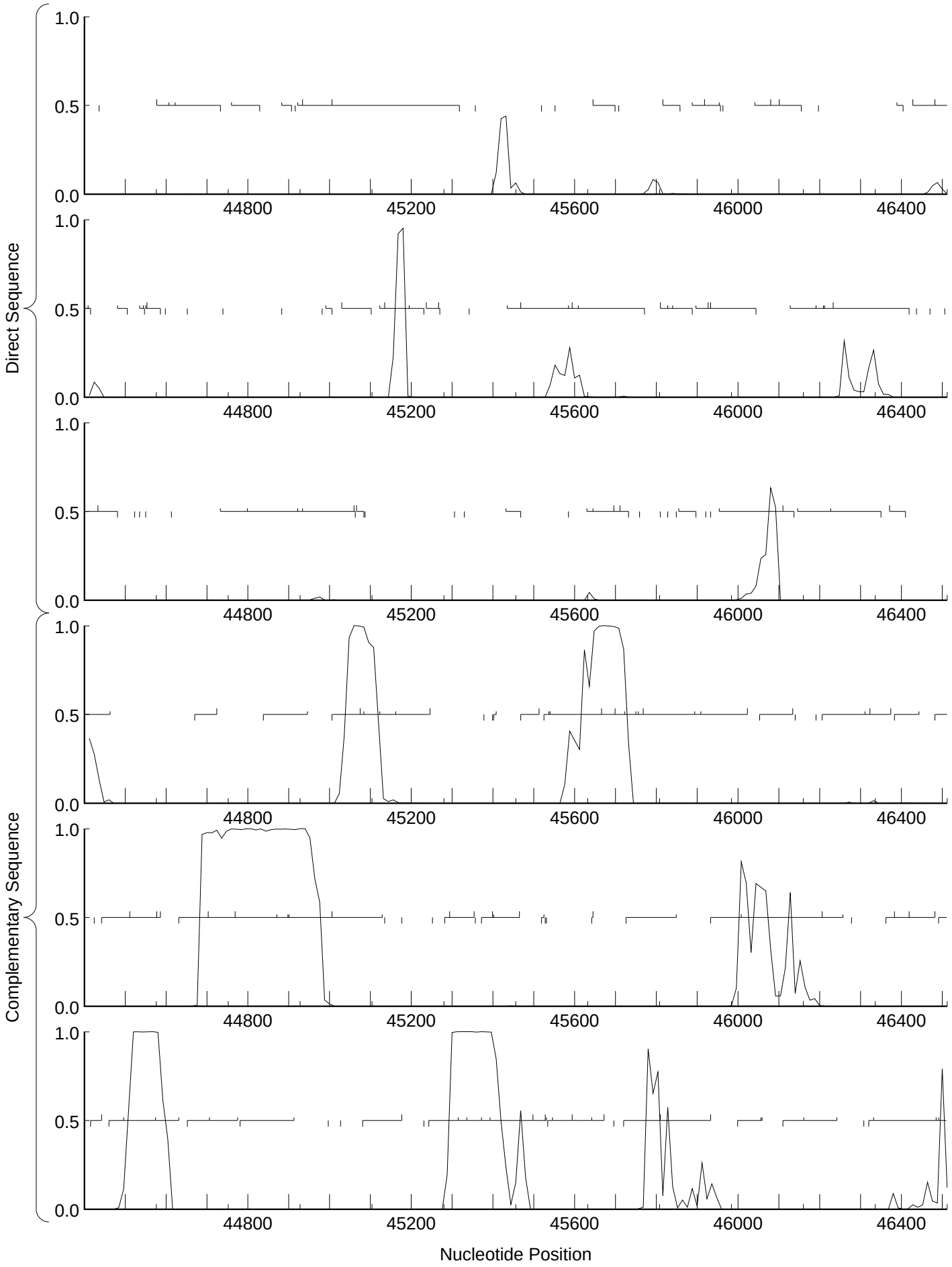

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Nucleotide Position

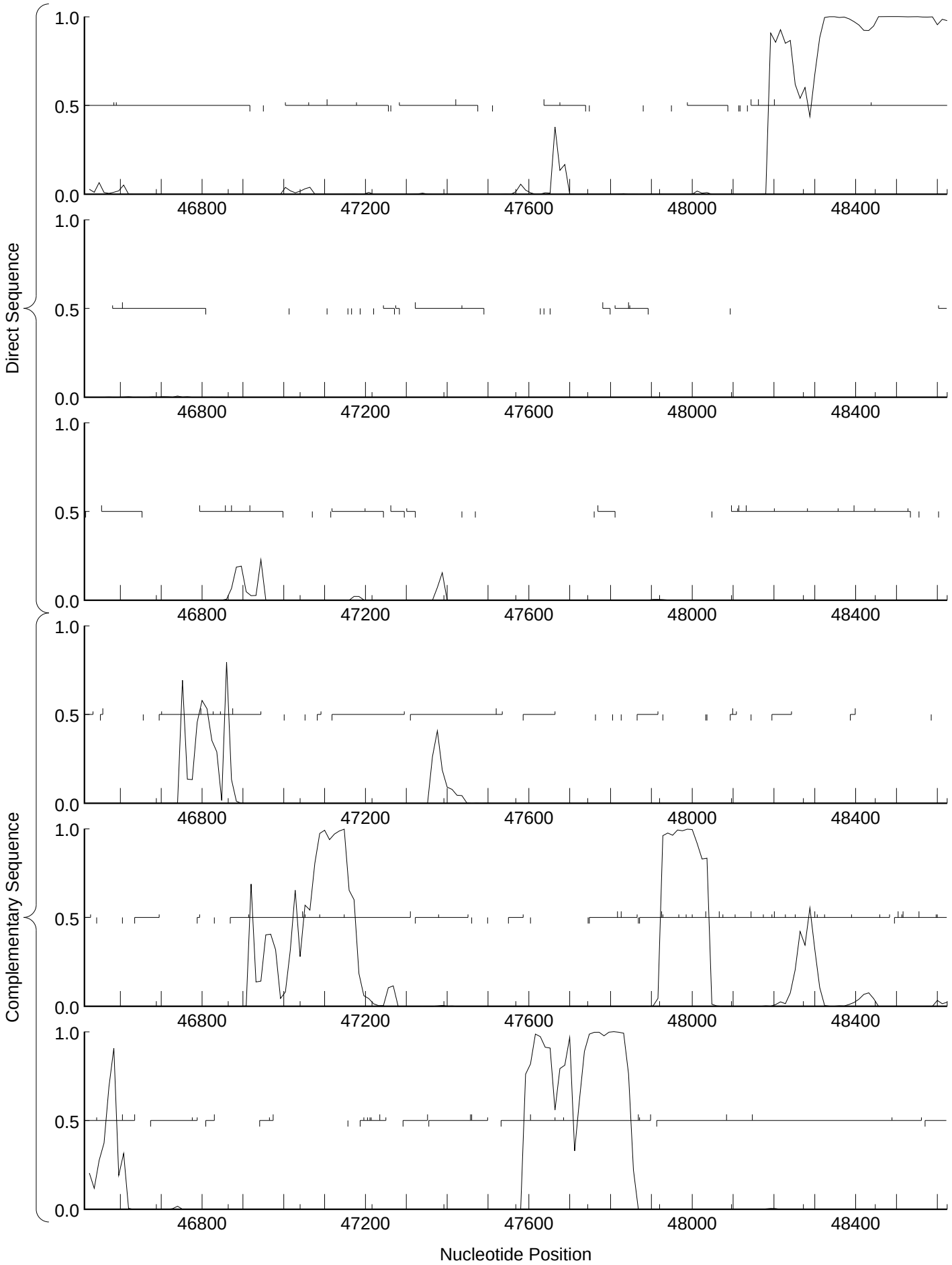

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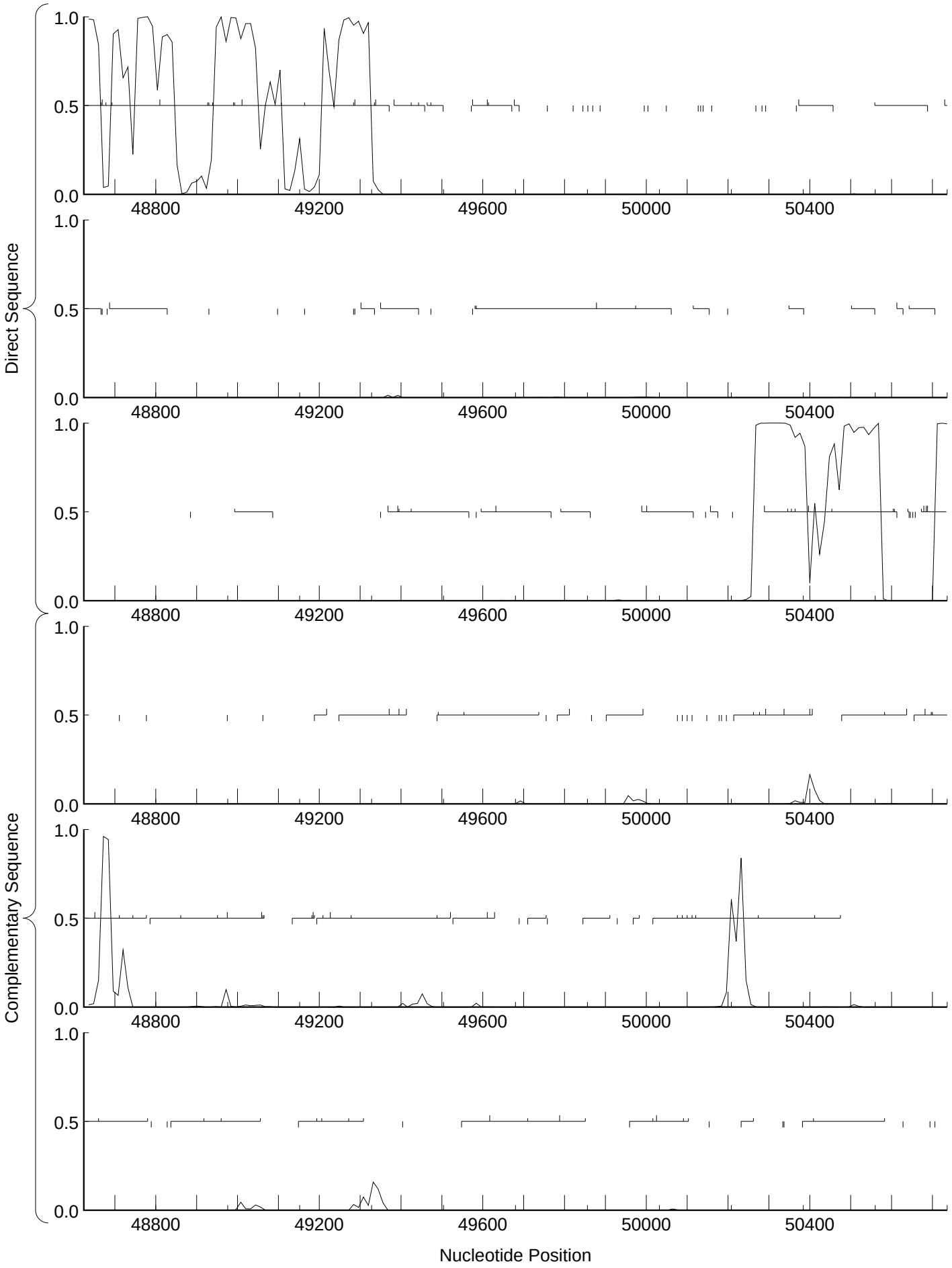

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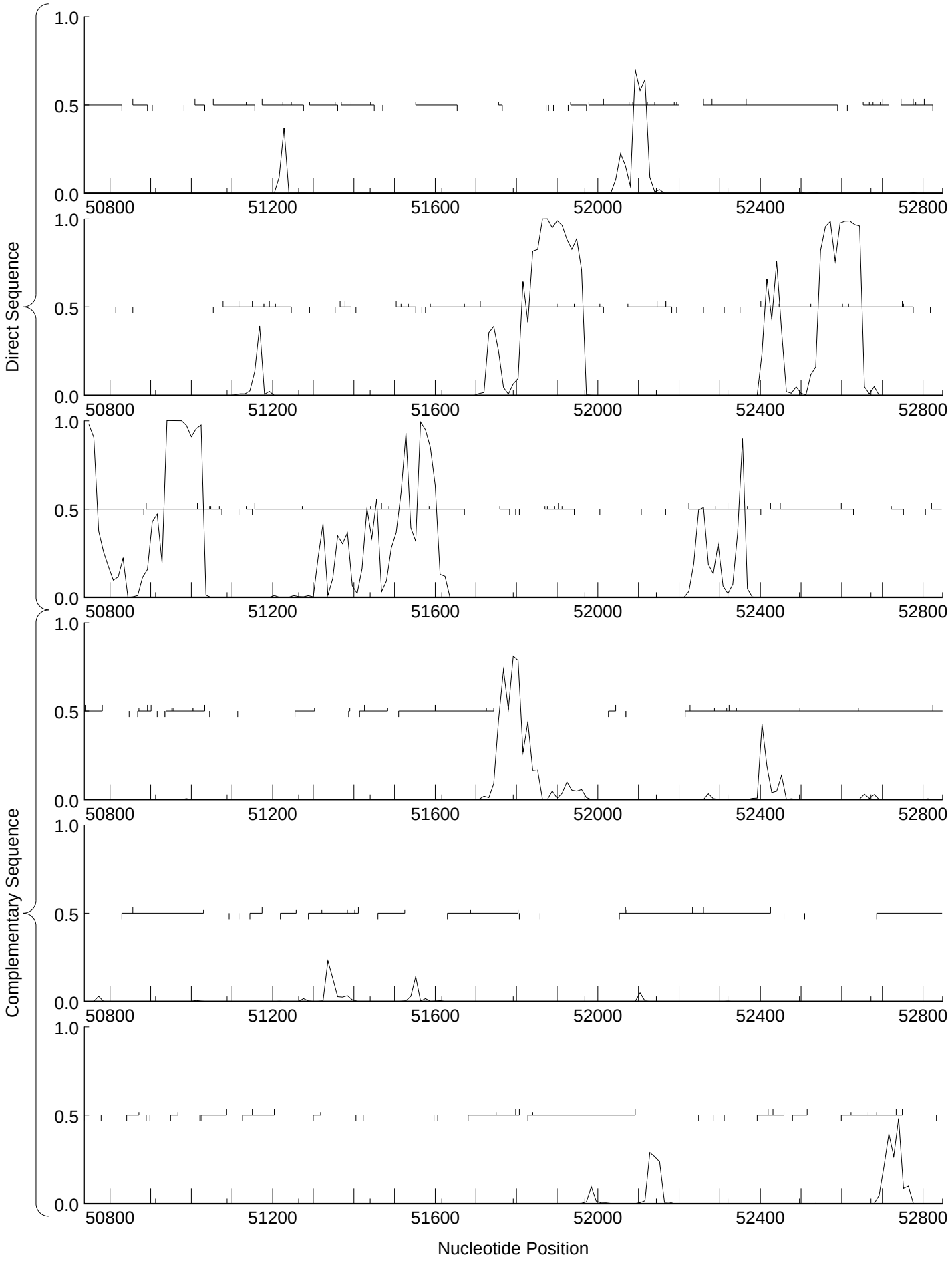

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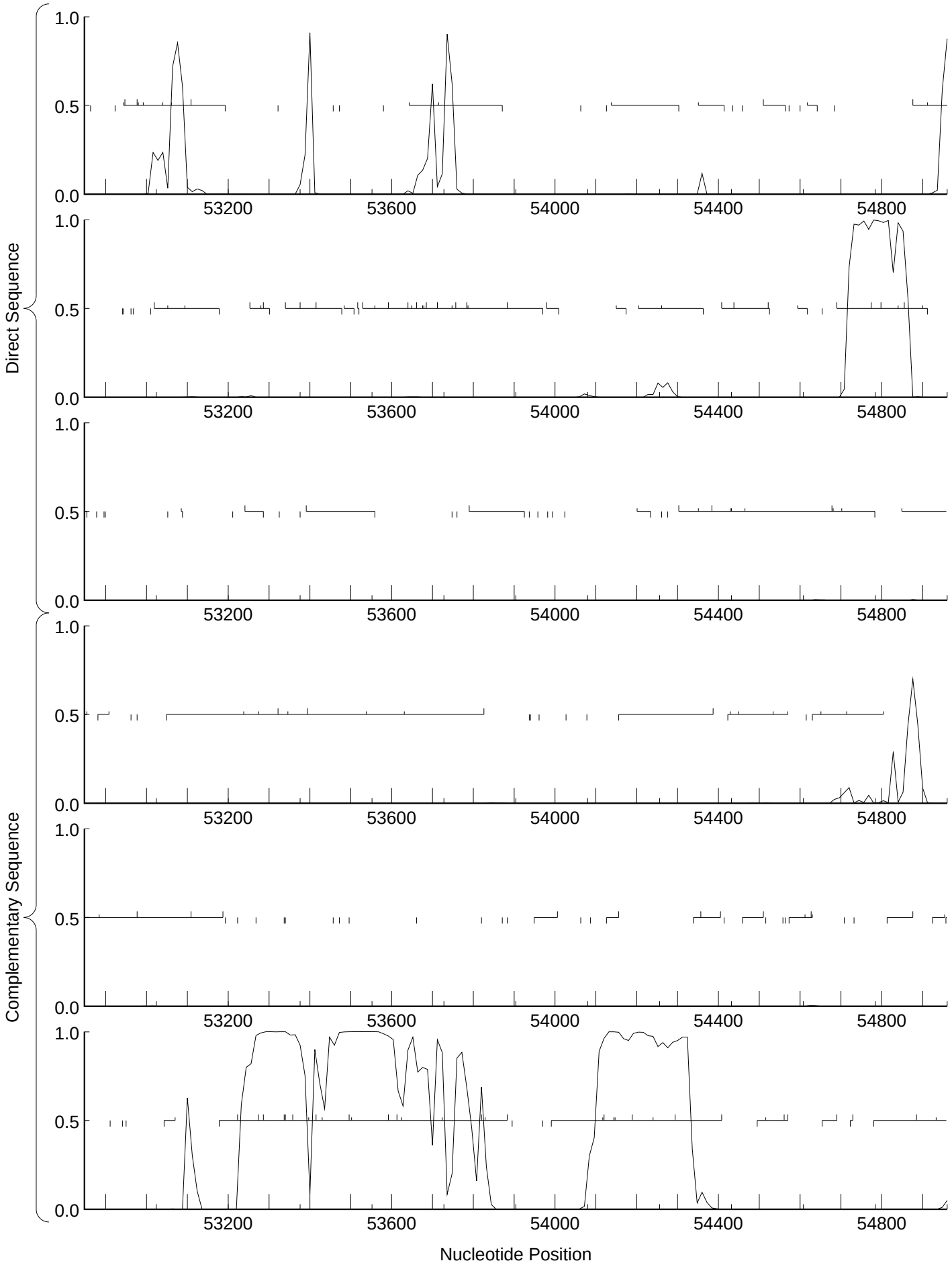
ge Thibault Complete Sequence, 106327 bp including 4-base 3’ overhang (ATCC), Cluster J, Order 4, Window 96, Step 12, 24/52

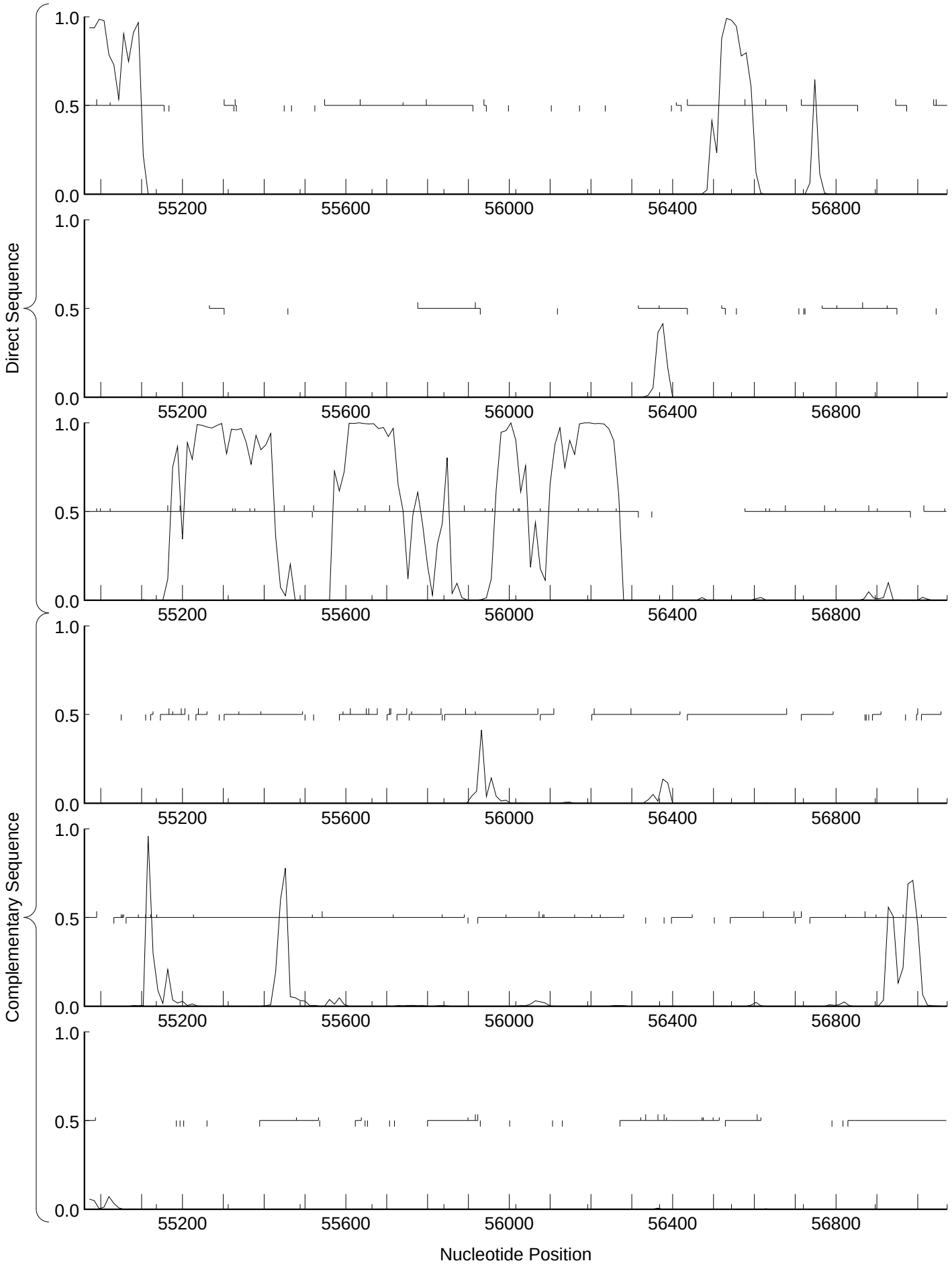


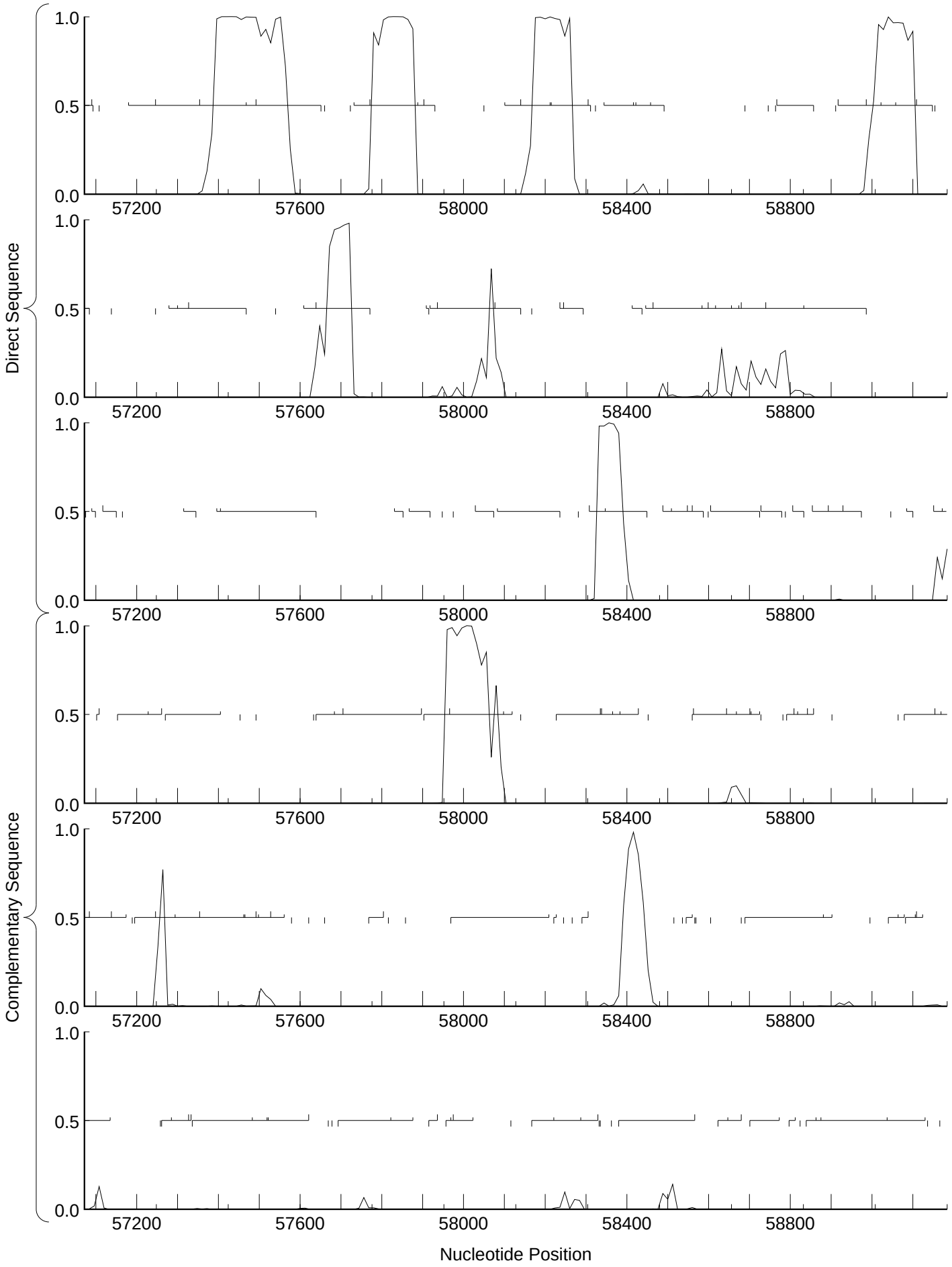

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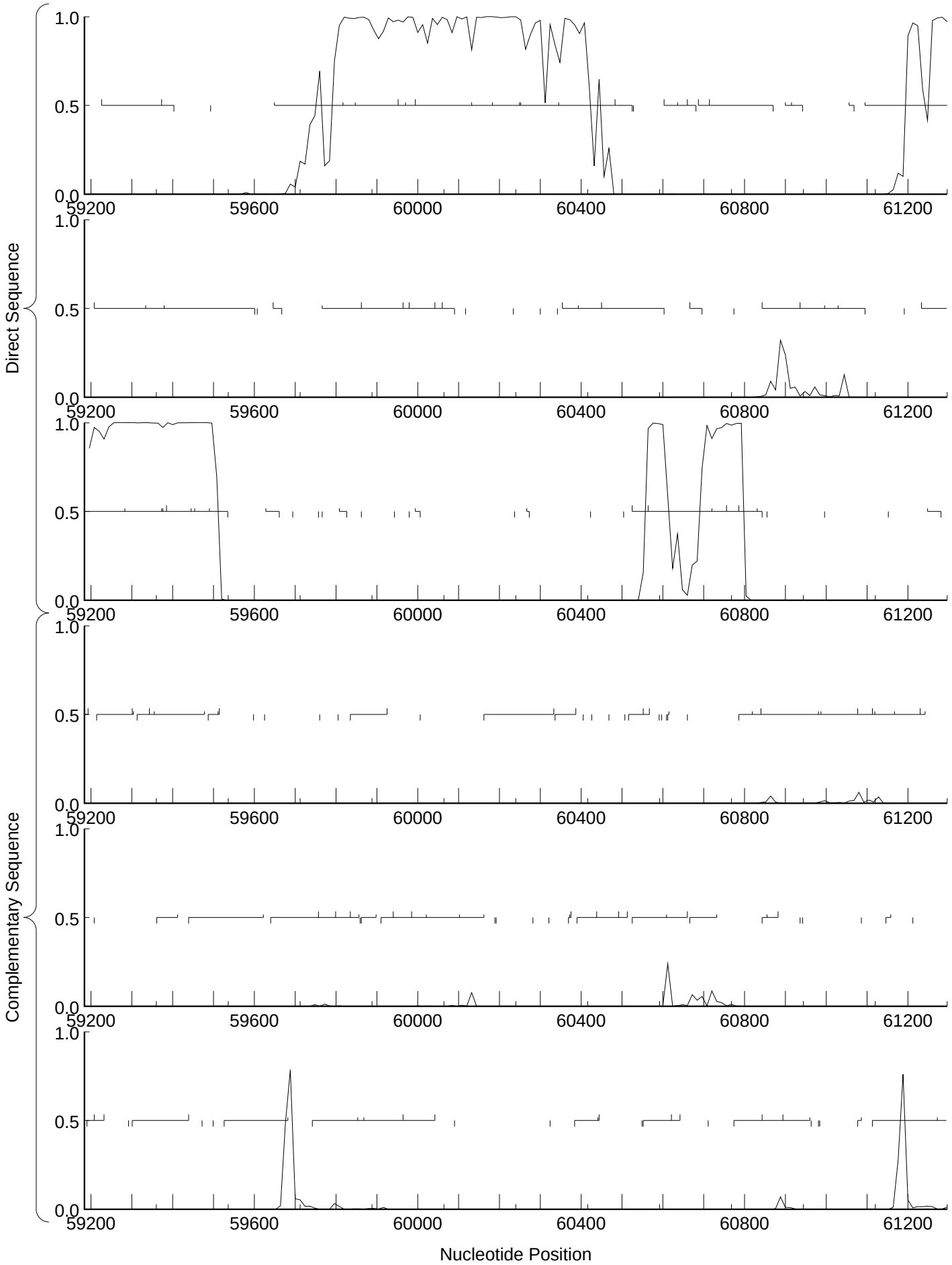
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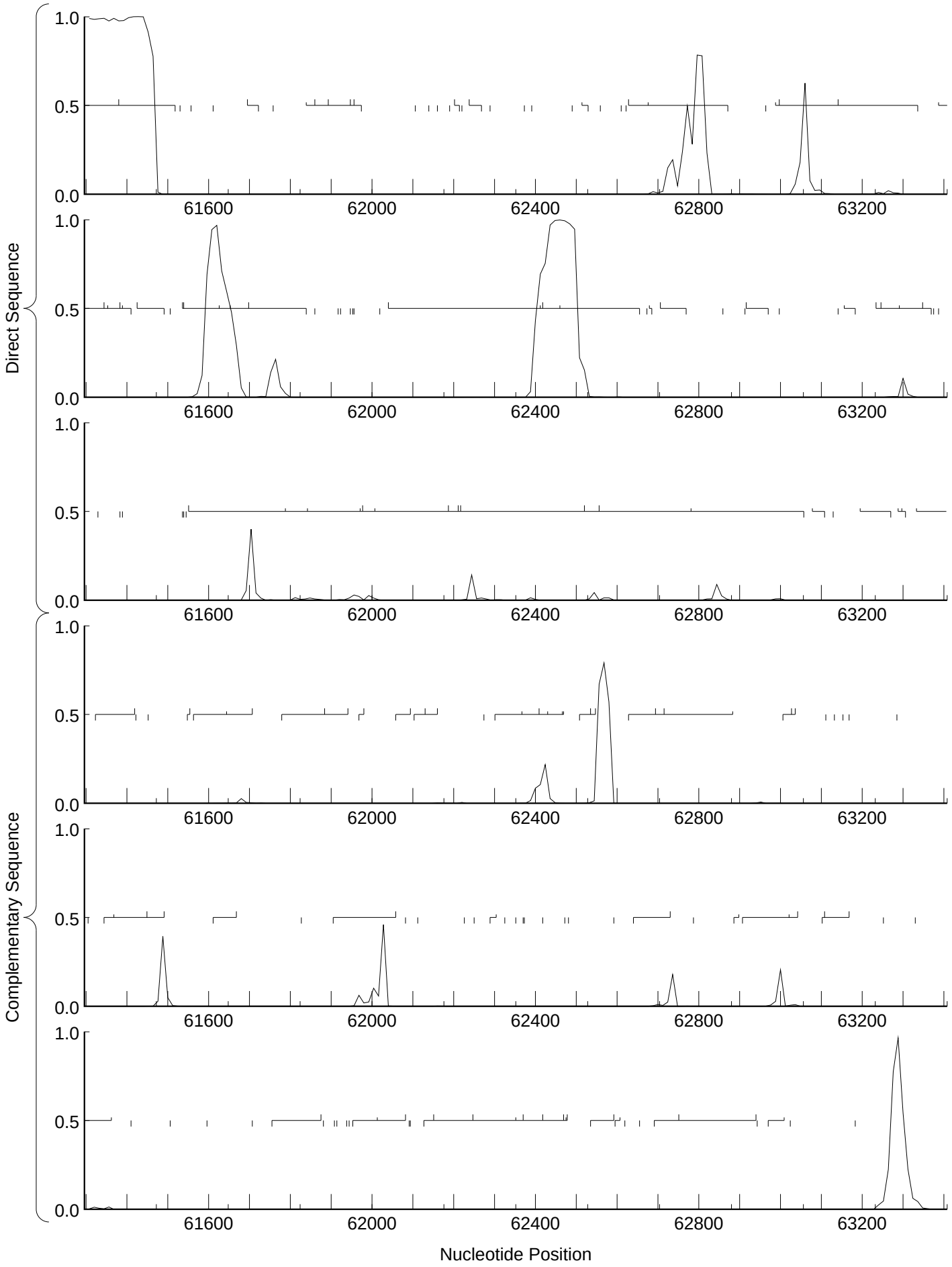


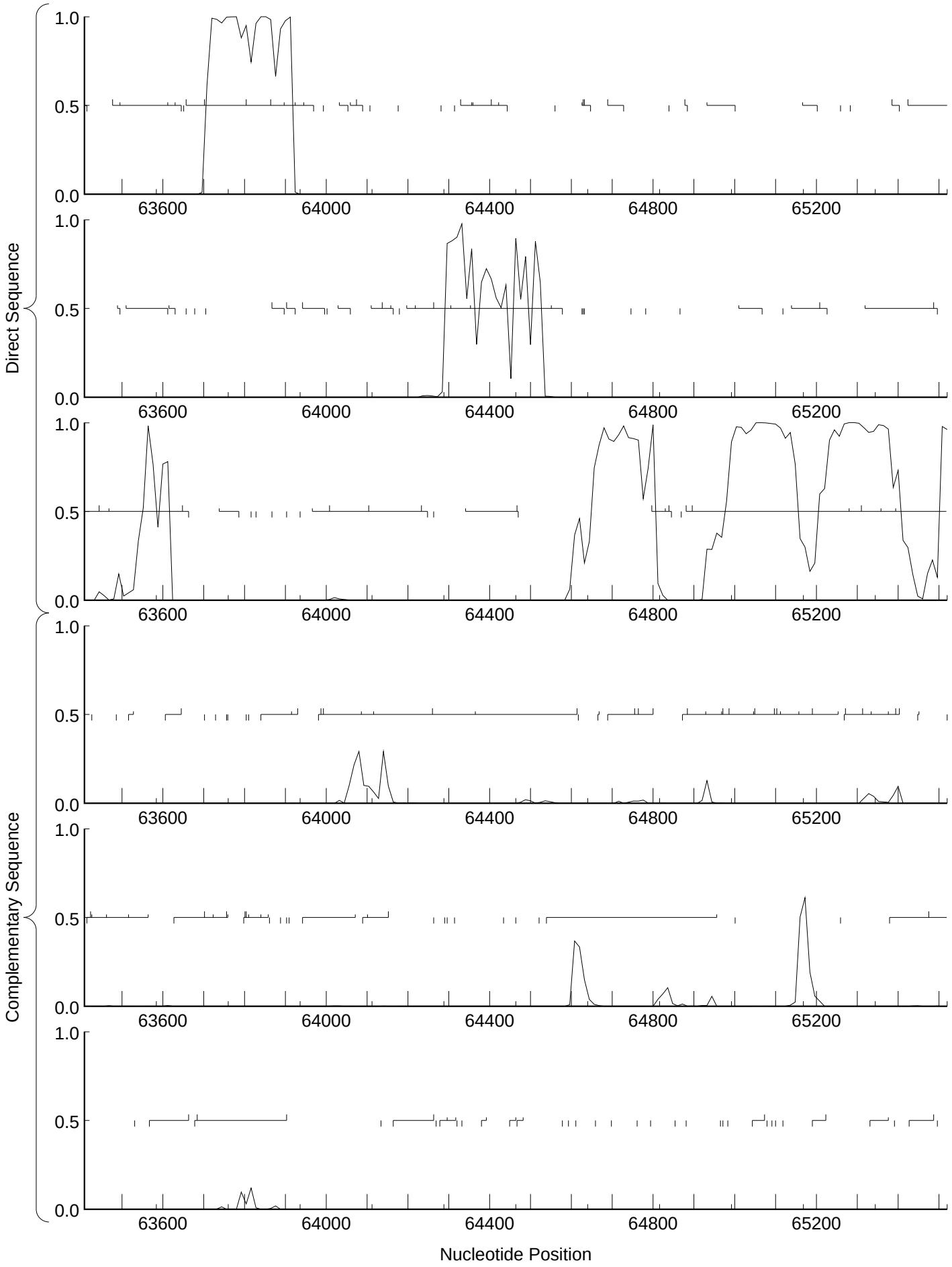

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Nucleotide Position

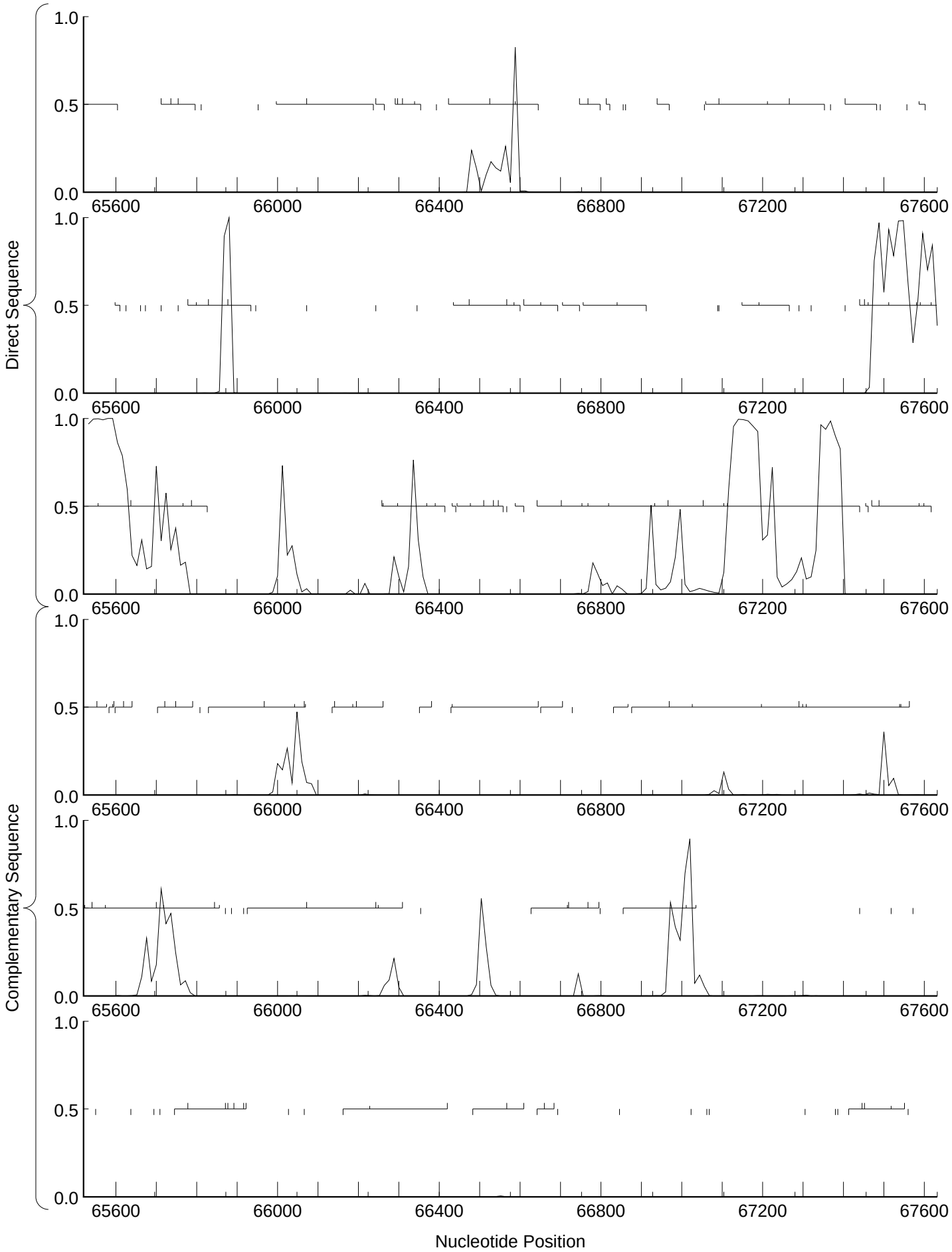

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Complementary Sequence
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58800
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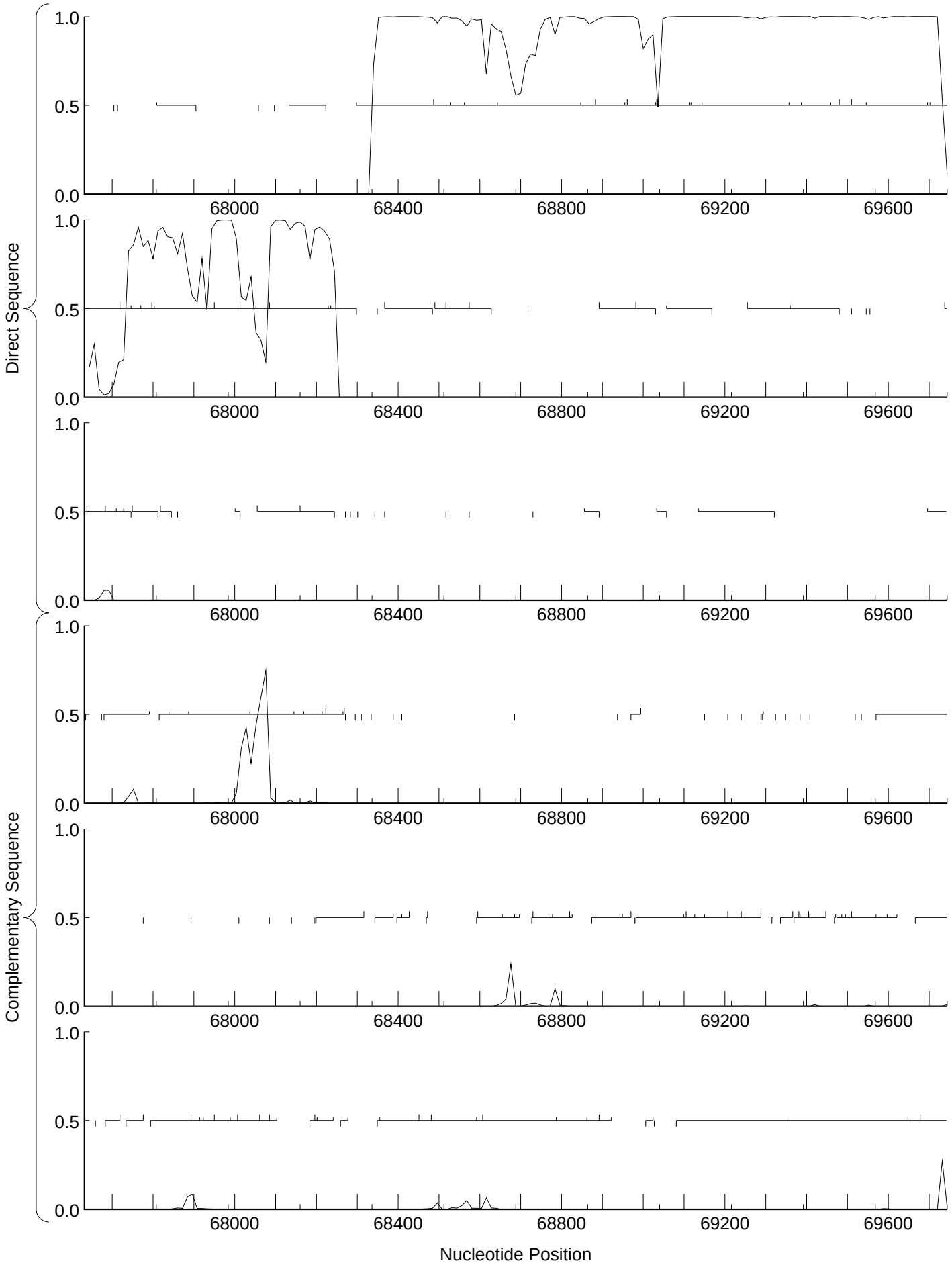



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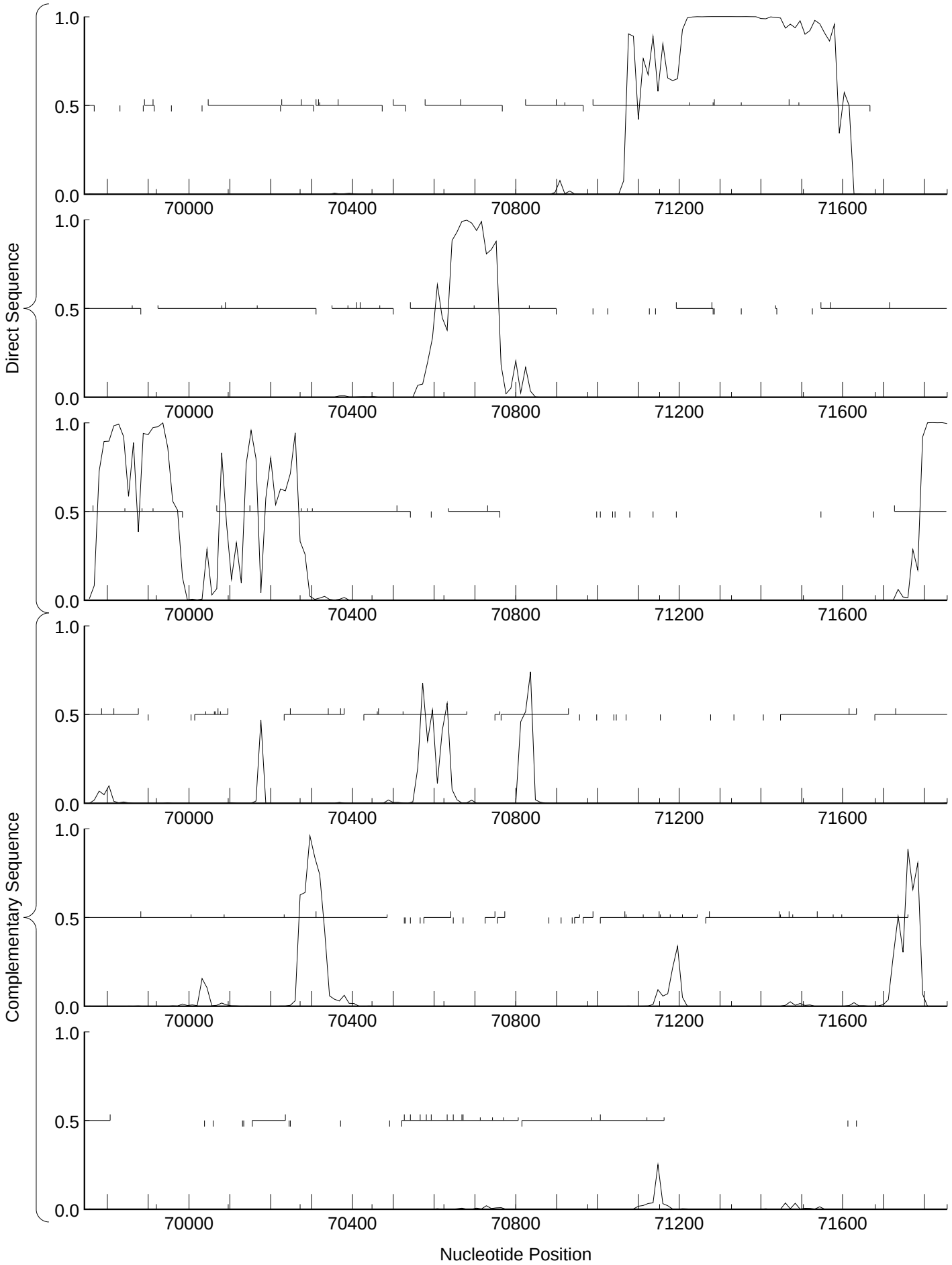

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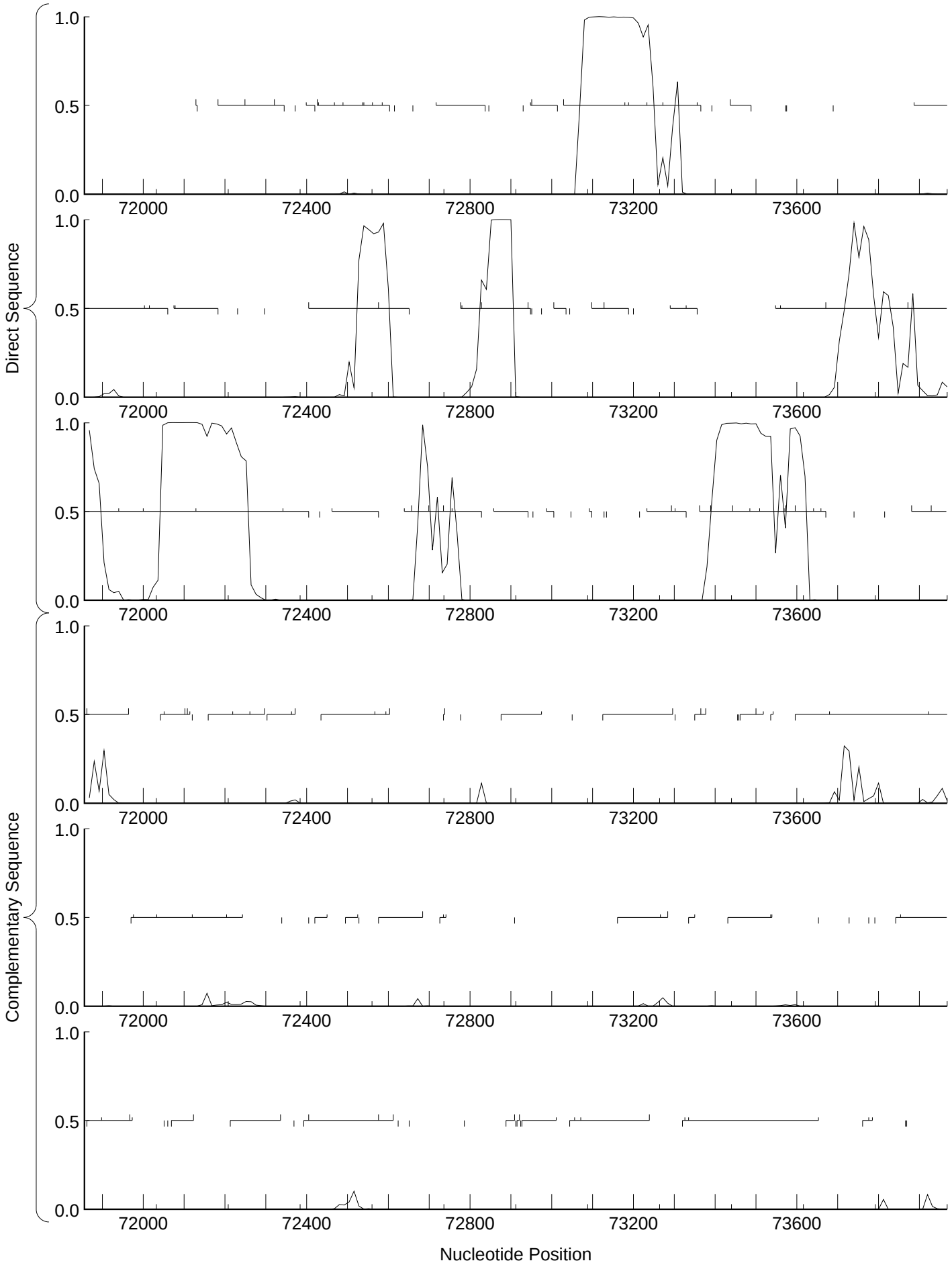

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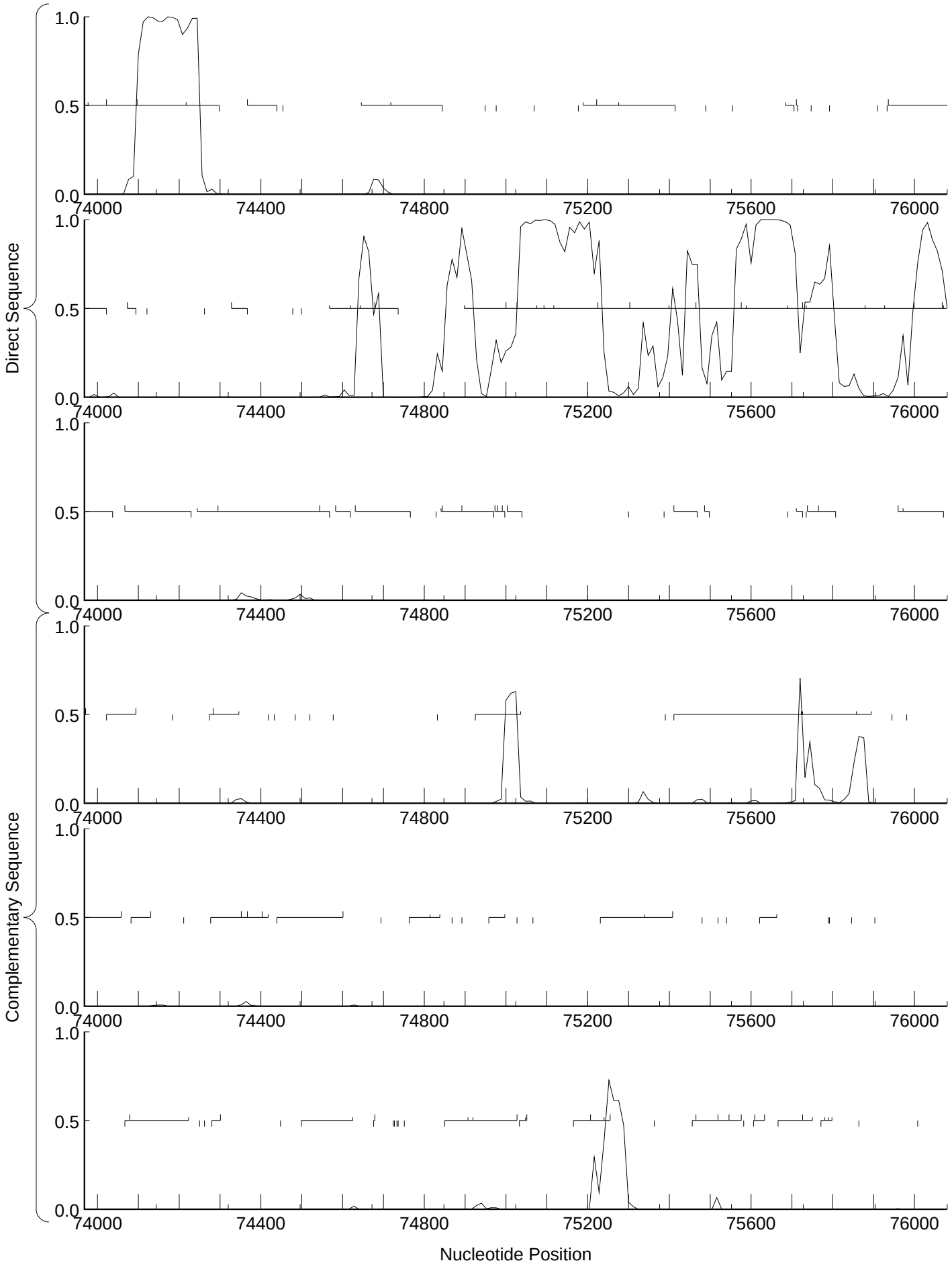


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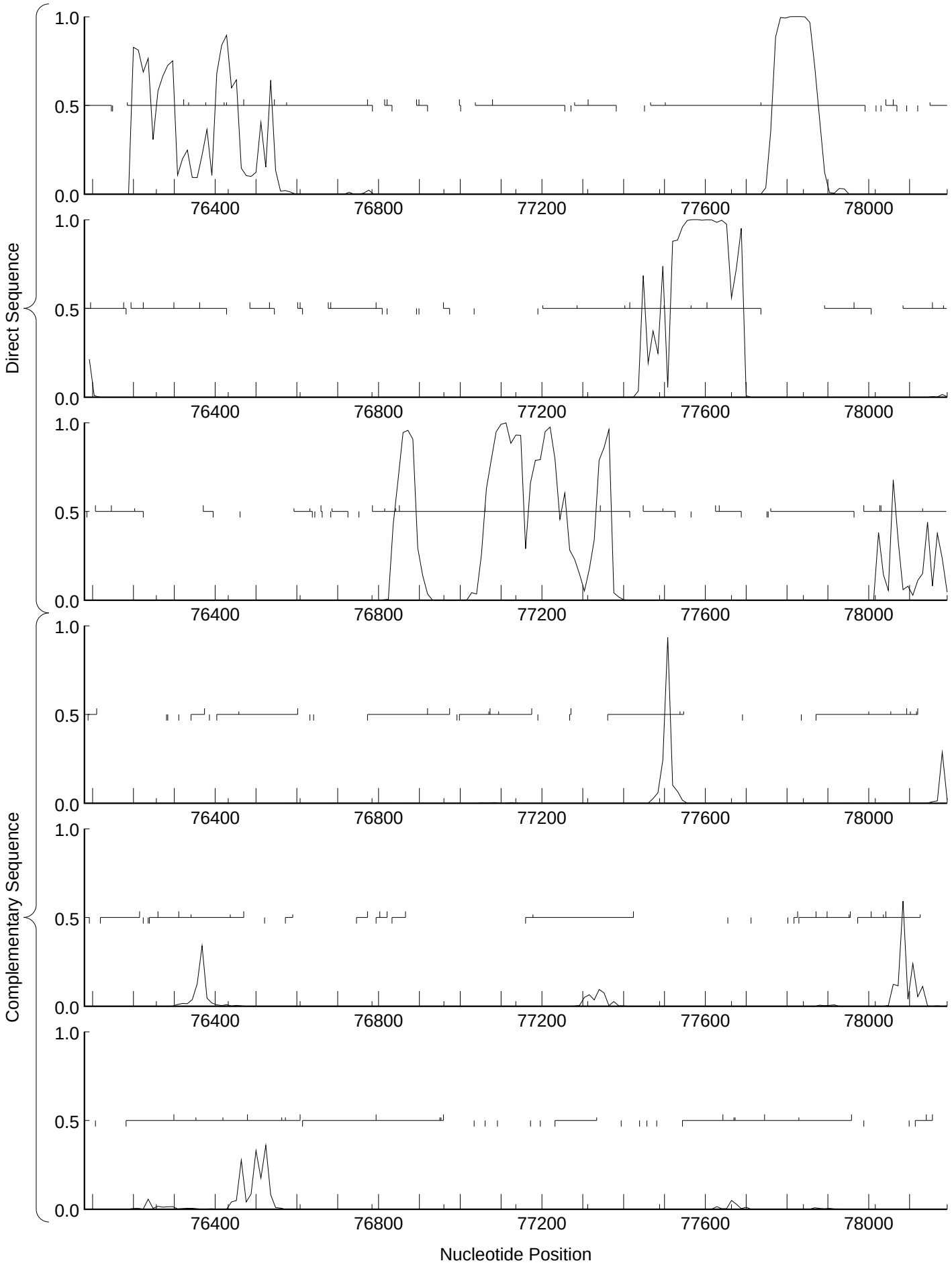


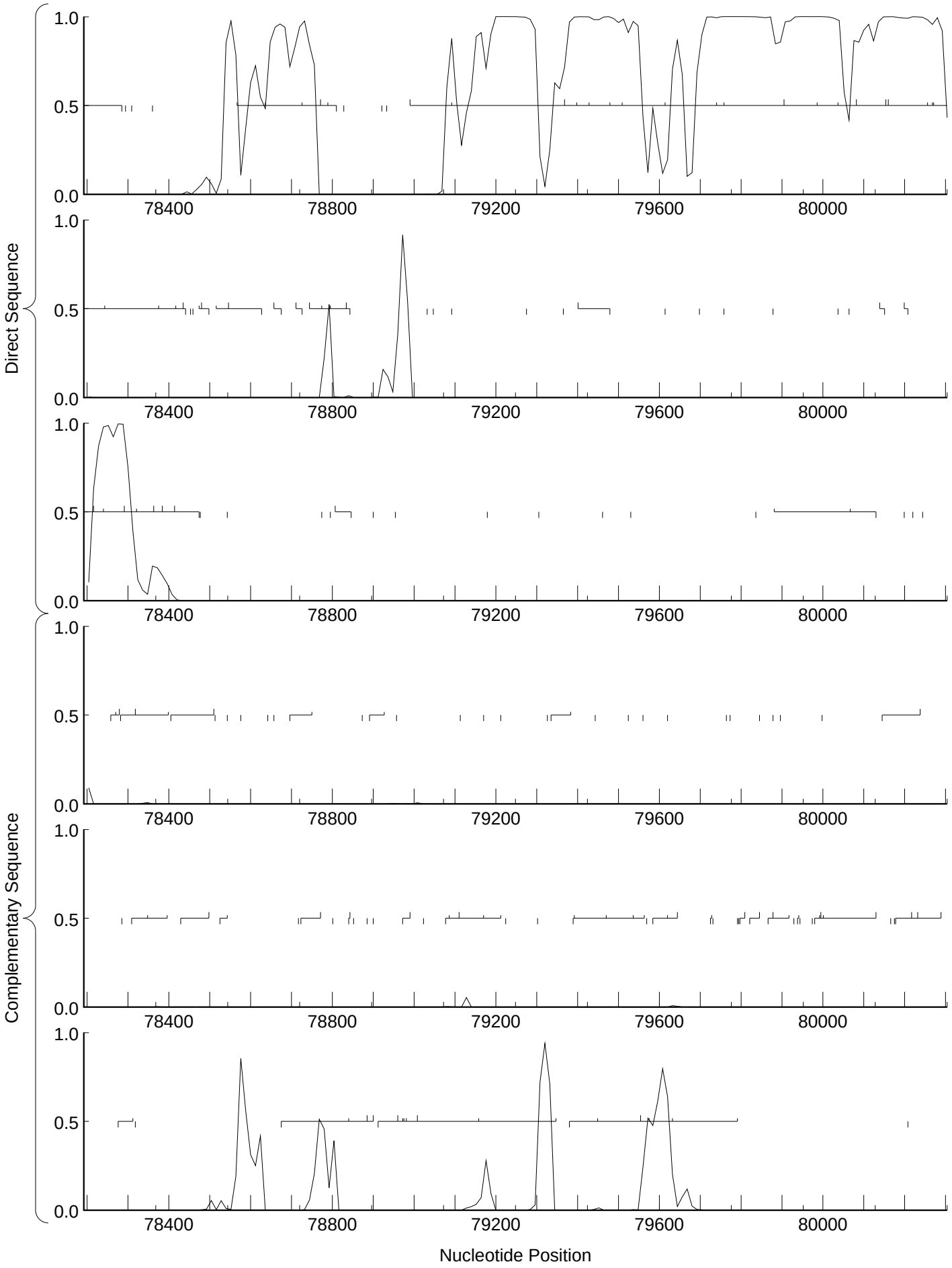

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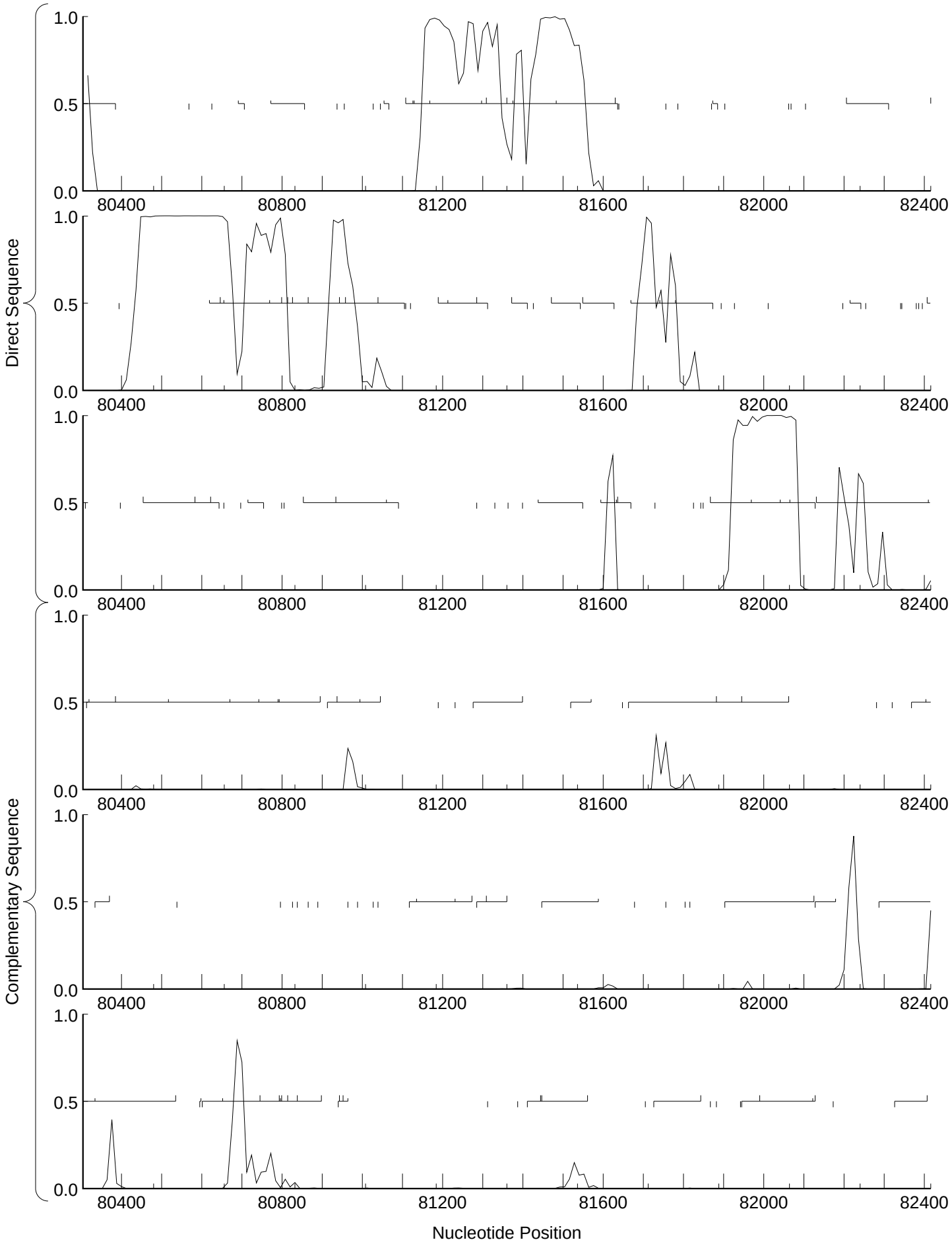
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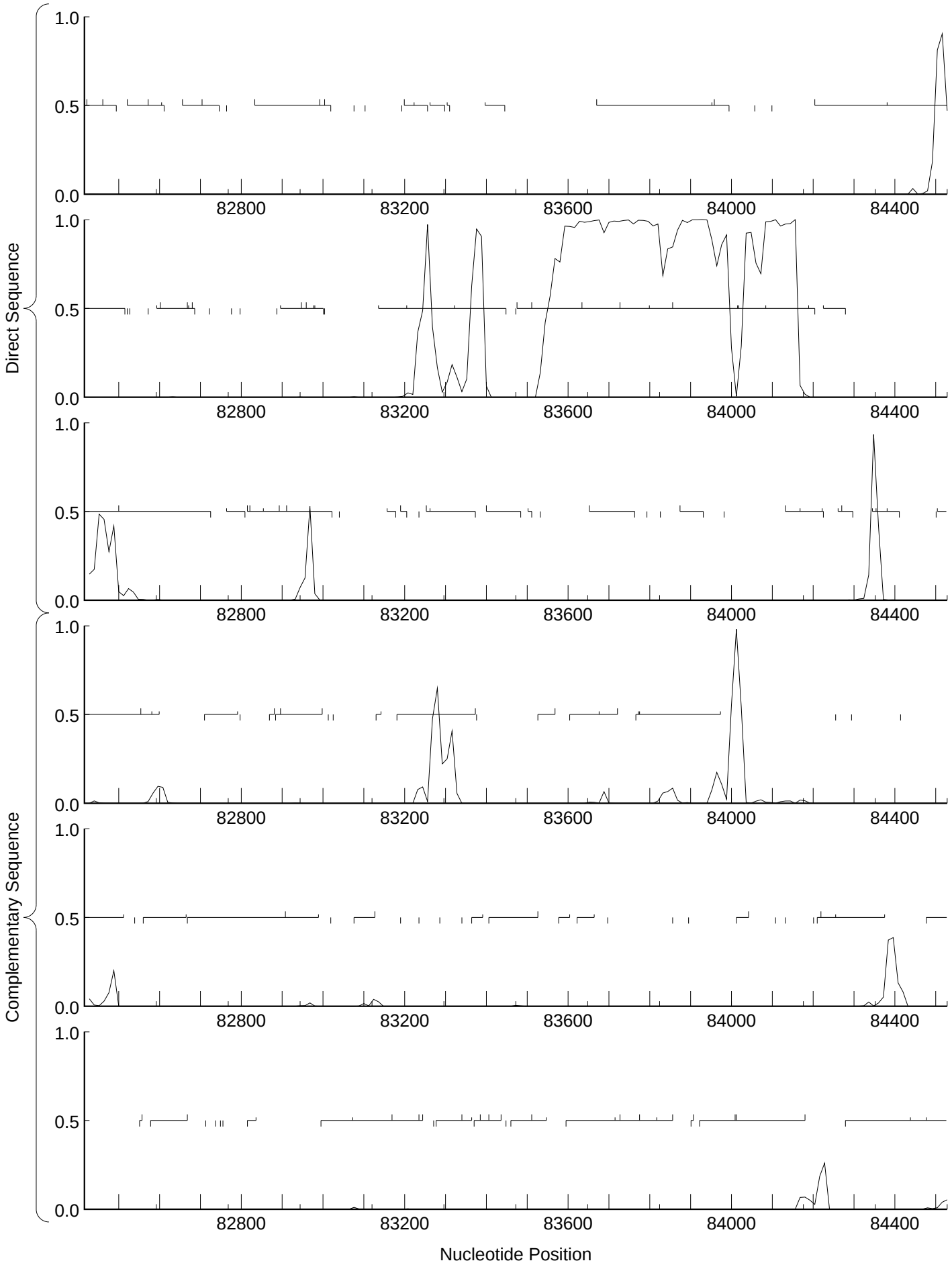


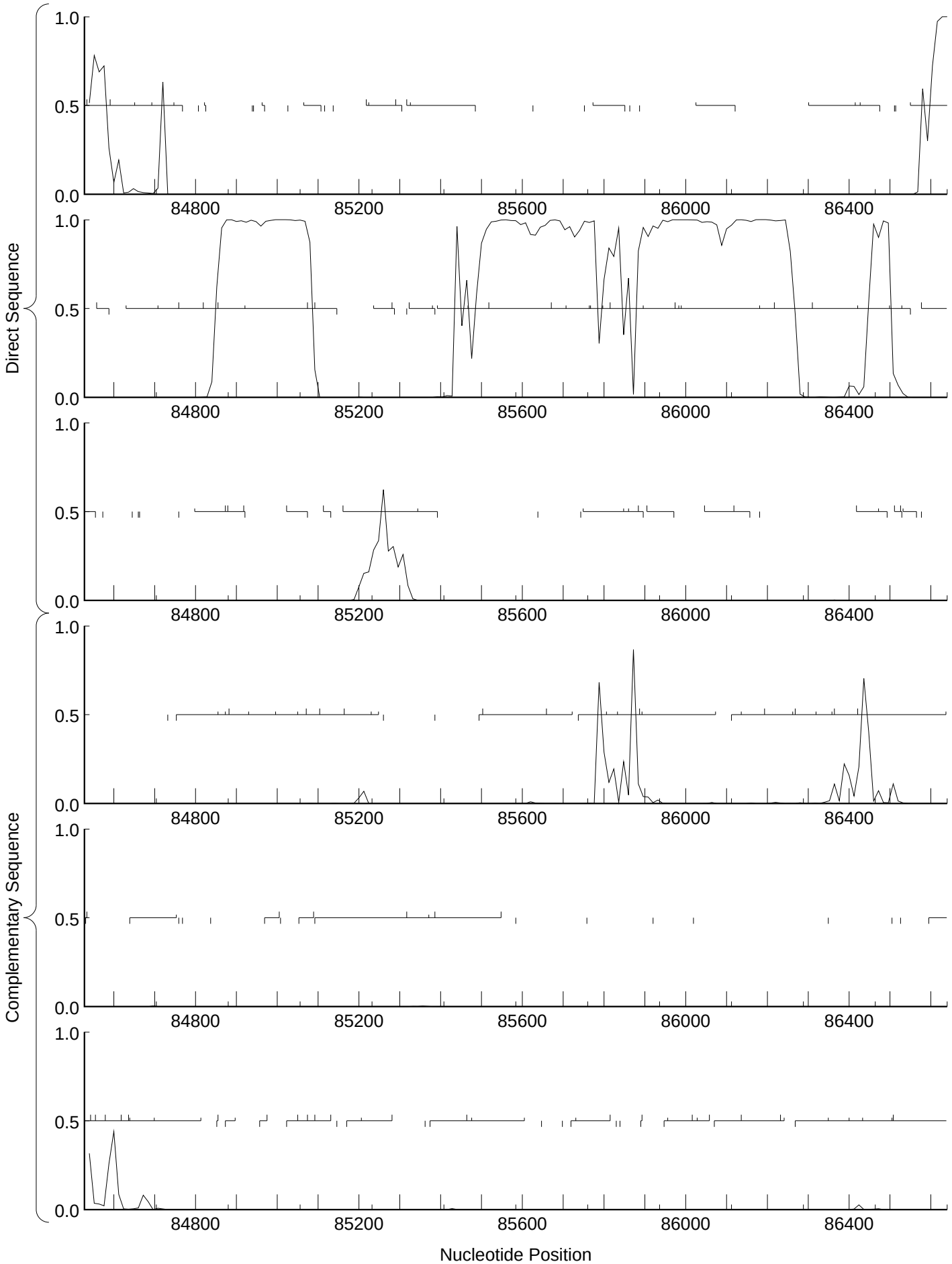
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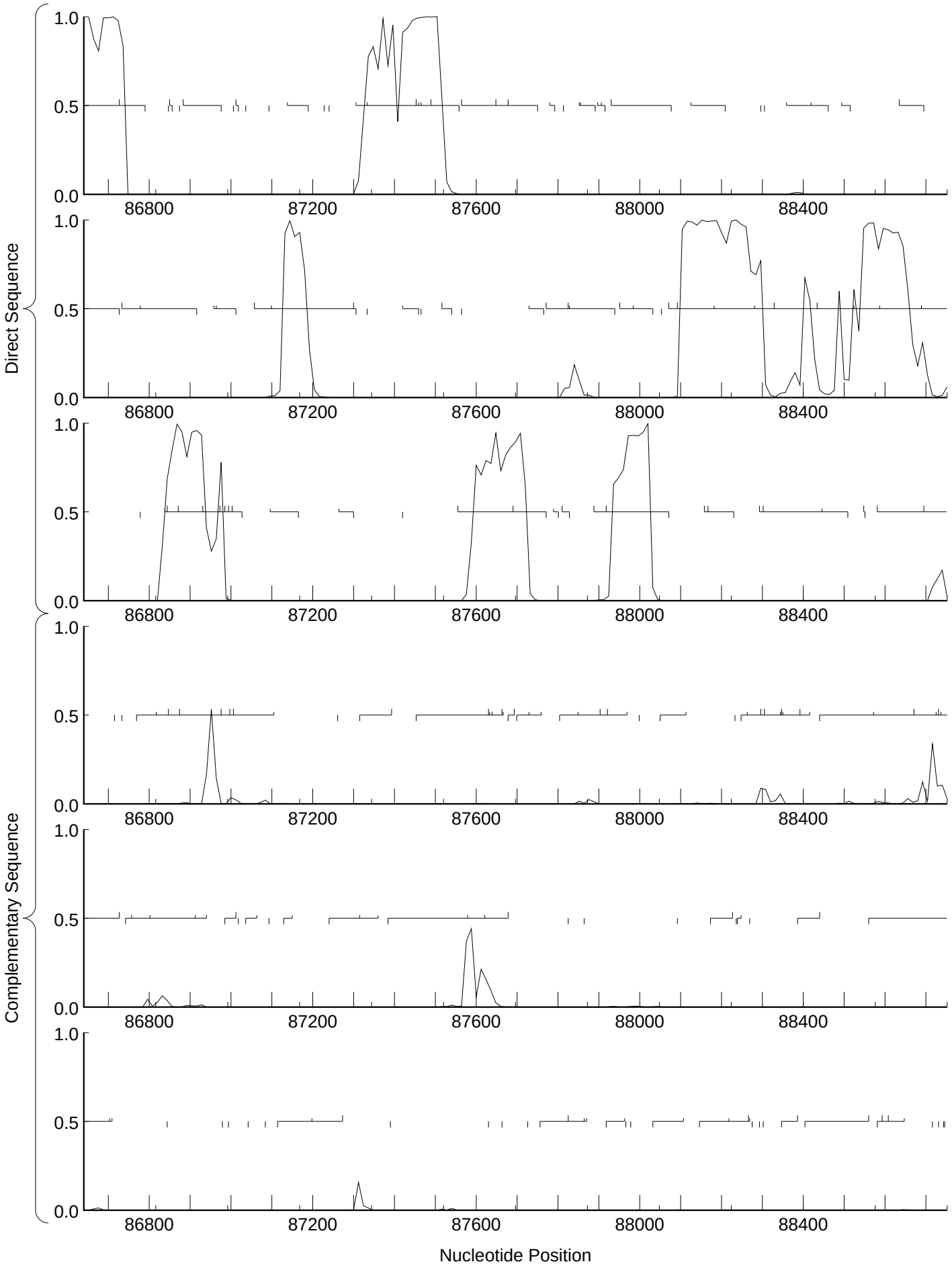


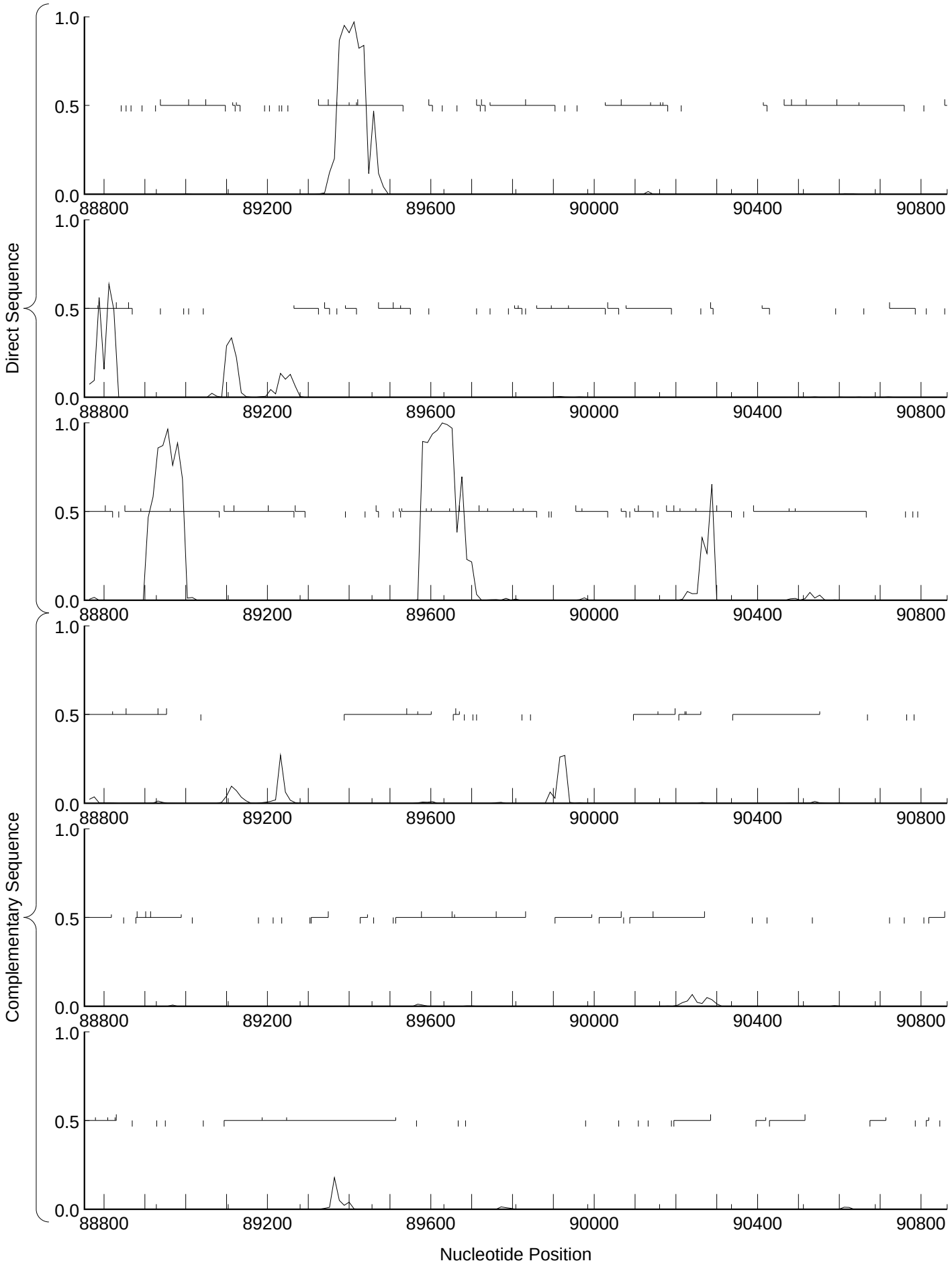

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Complementary Sequence
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79200
79600
80000
Nucleotide Position

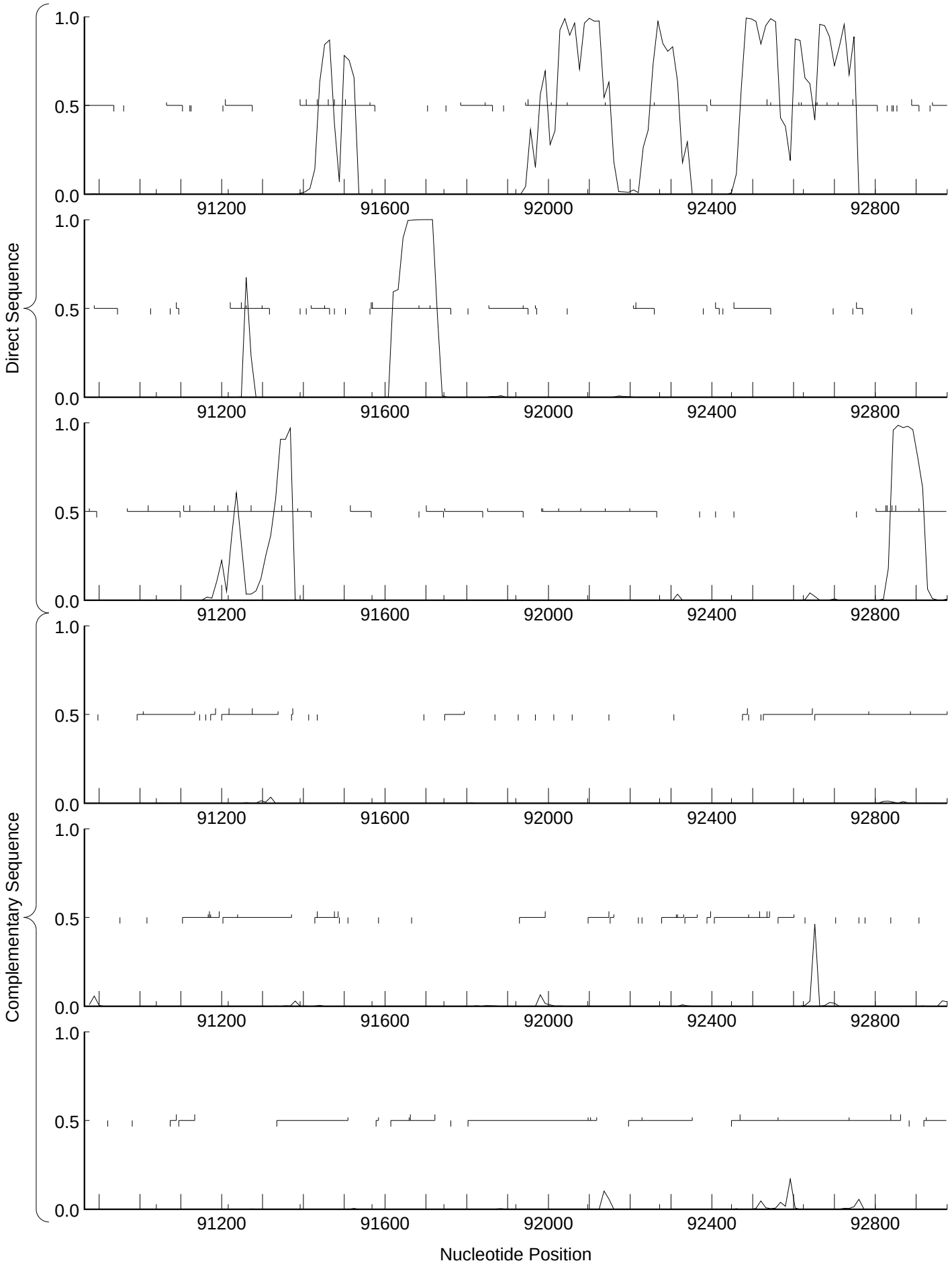

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
80400
80800
81200
81600
82000
82400
Nucleotide Position

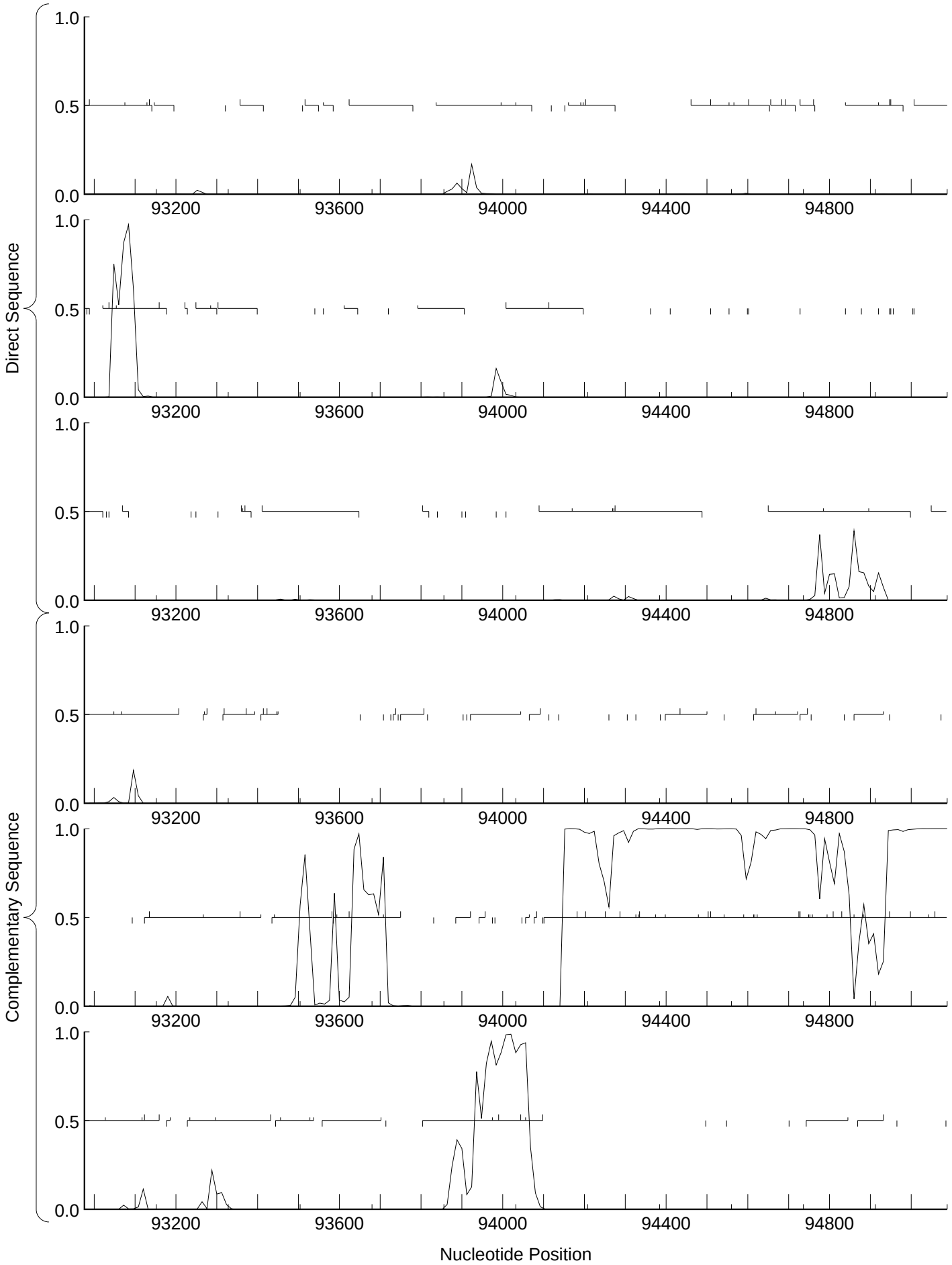

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
82800
83200
83600
84000
84400
Nucleotide Position

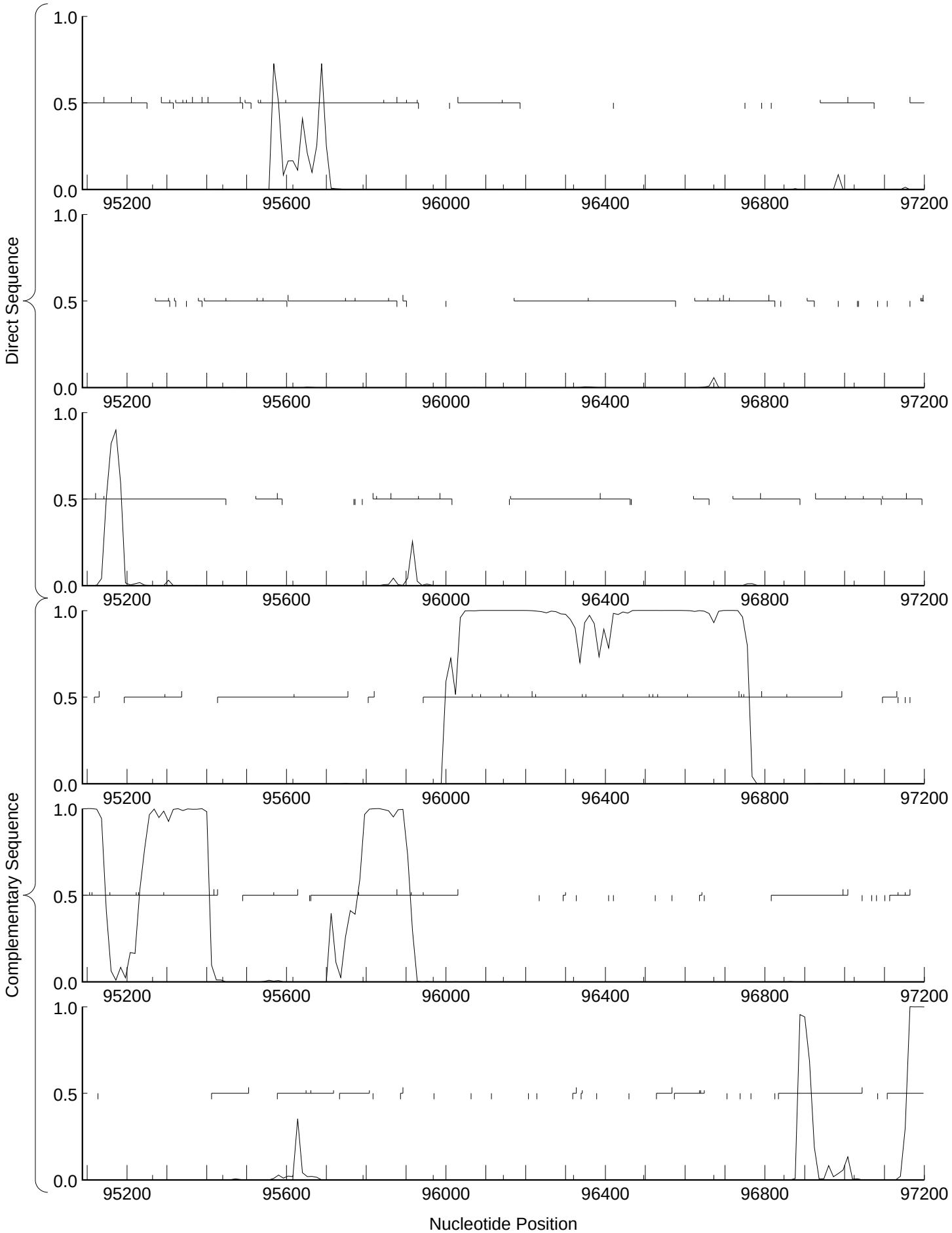

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
84800
85200
85600
86000
86400
Nucleotide Position

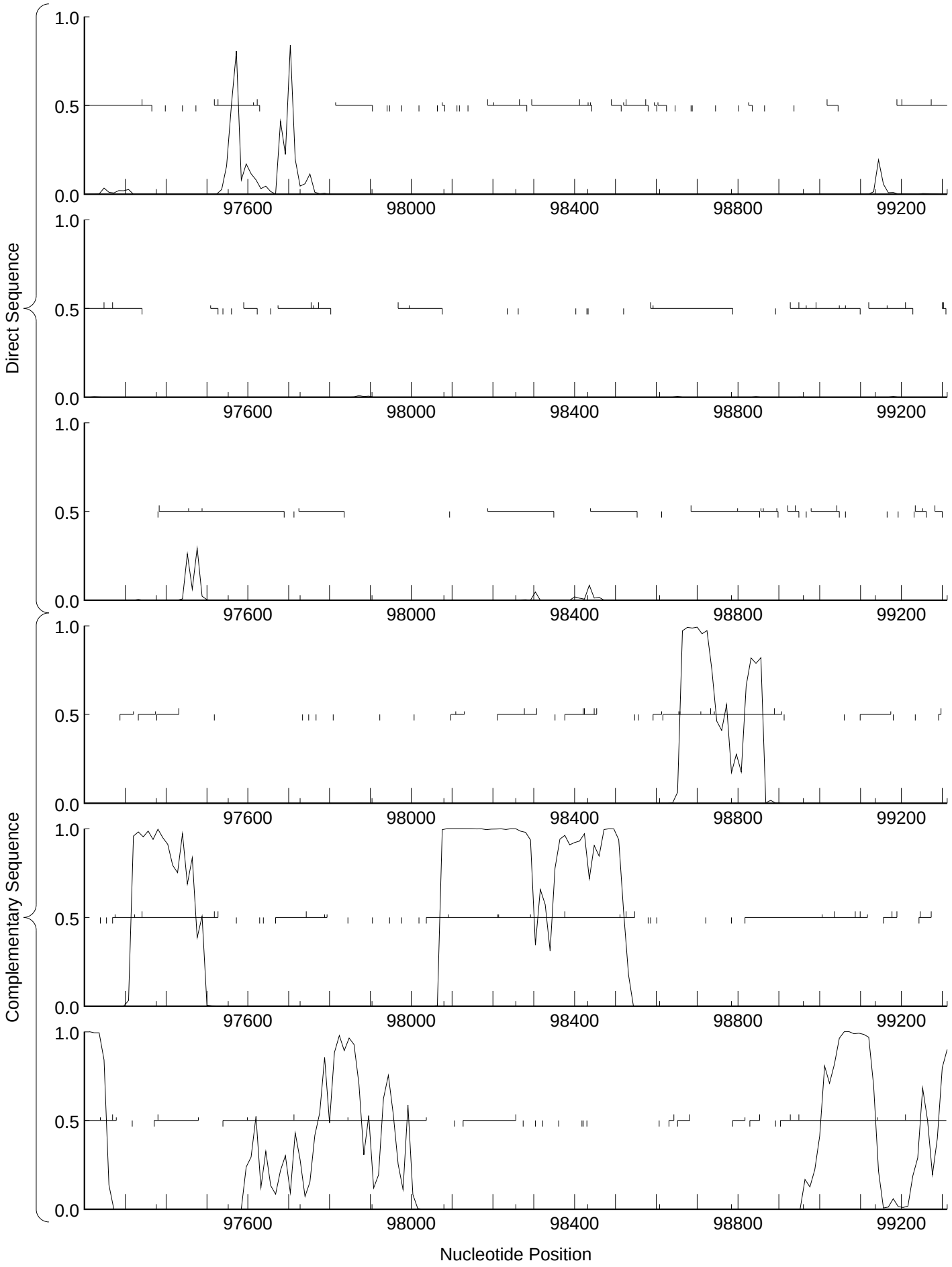

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
86800
87200
87600
88000
88400
Nucleotide Position

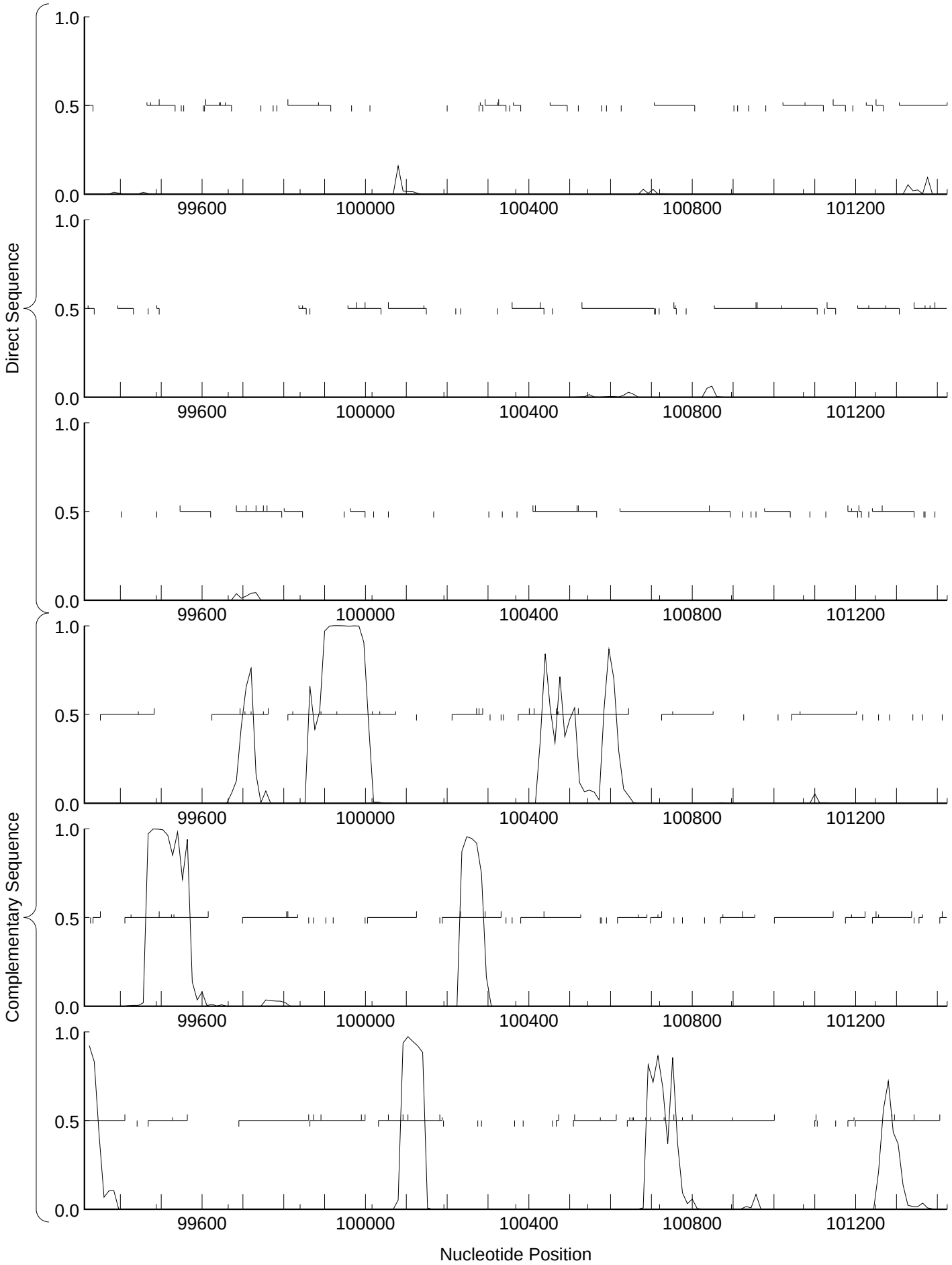

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
88800
89200
89600
90000
90400
90800
Nucleotide Position


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

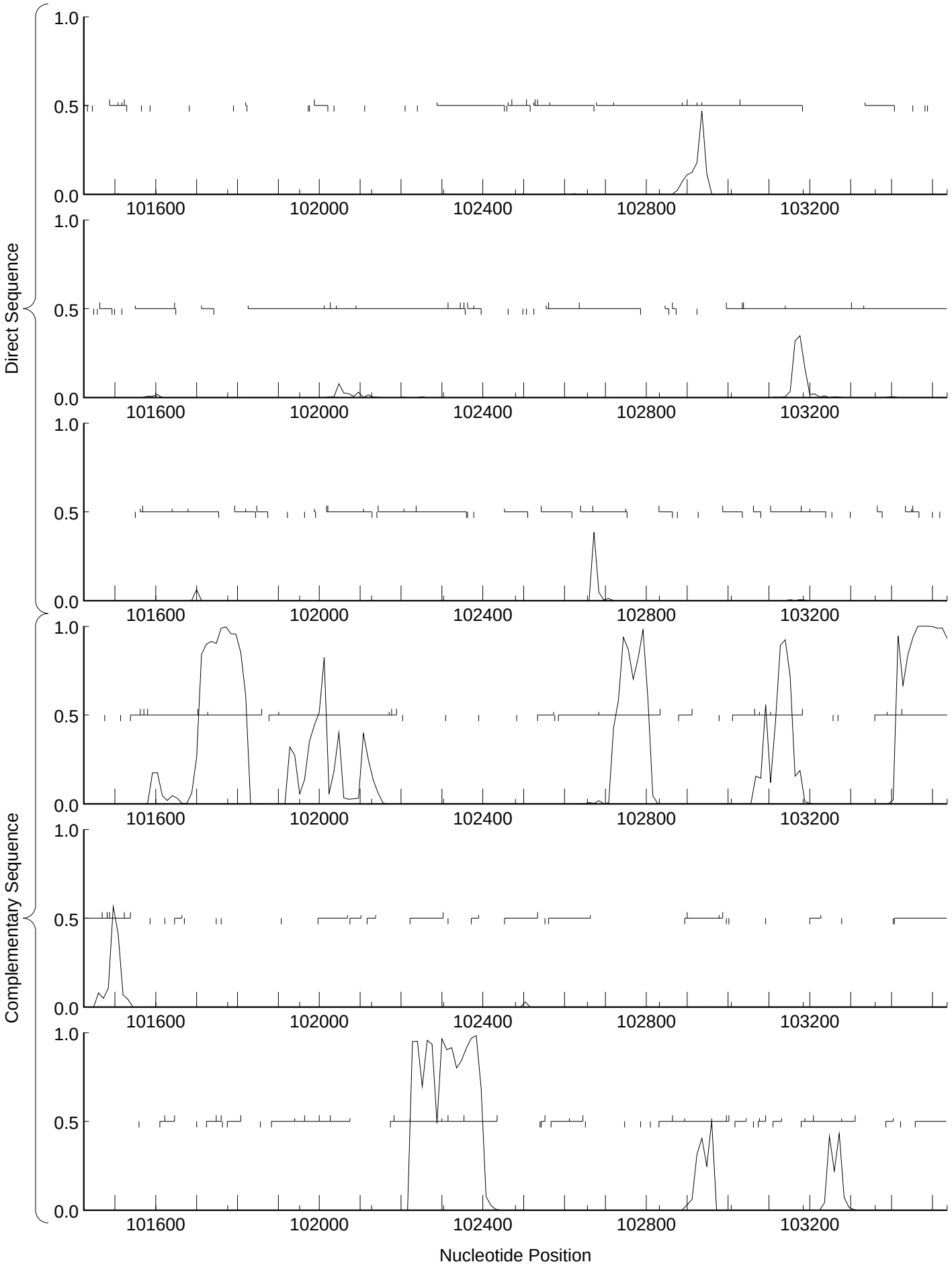

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
93200
93600
94000
94400
94800
Nucleotide Position

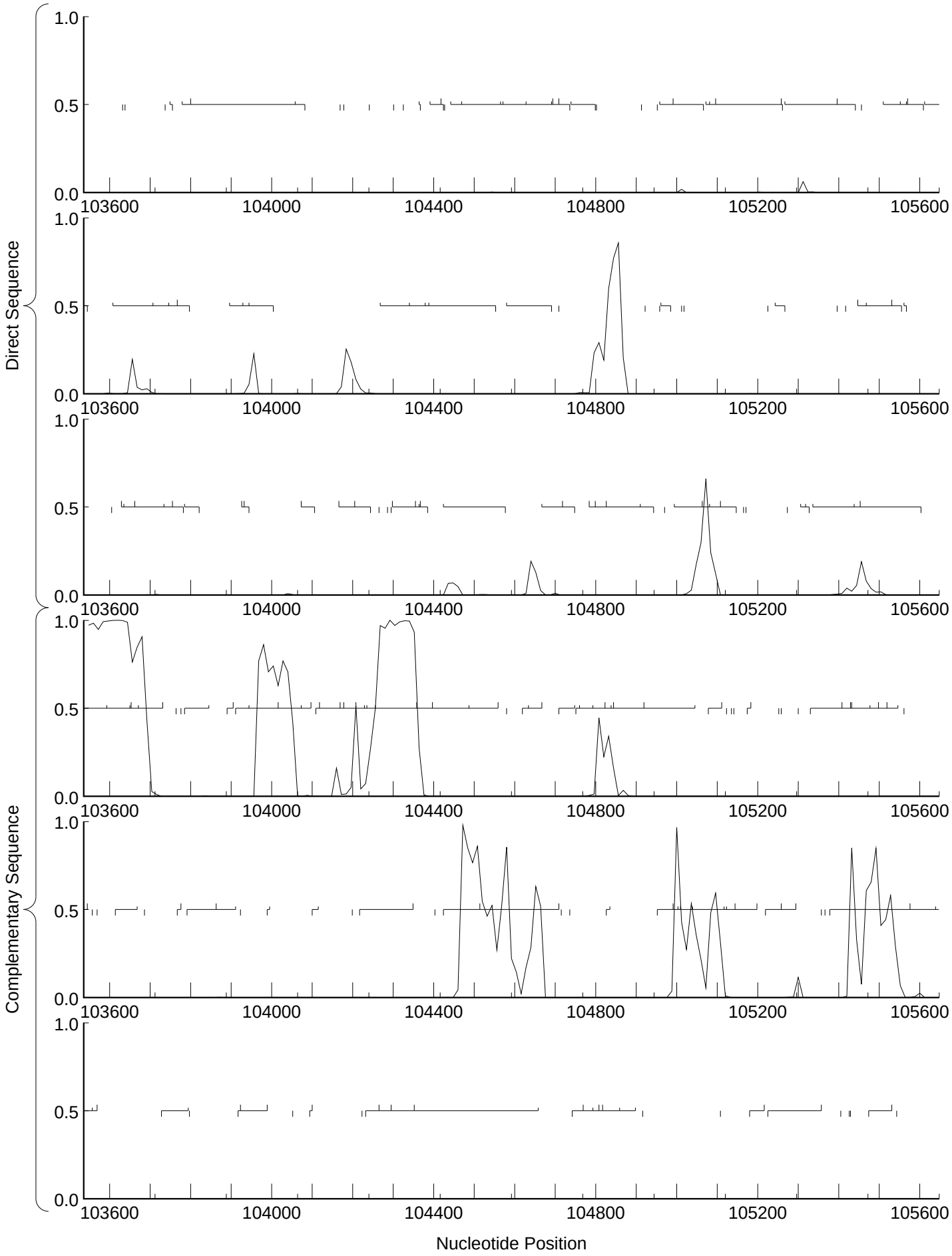

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
95200
95600
96000
96400
96800
97200
Nucleotide Position


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


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
99600
100000
100400
100800
101200
Nucleotide Position

ge Thibault Complete Sequence, 106327 bp including 4-base 3’ overhang (ATCC), Cluster J, Order 4, Window 96, Step 12, 50/52




Direct Sequence
Complementary Sequence
1.0
0.5
0.0
103600
104000
104400
104800
105200
105600
Nucleotide Position

ge Thibault Complete Sequence, 106327 bp including 4-base 3’ overhang (ATCC), Cluster J, Order 4, Window 96, Step 12, 52/52

