

# GeneMark

Version 2.5p (09.08.06)

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## PROGRAM INFORMATION

Sequence : Mycobacterium phage Tyson complete sequence, 74429 bp including 10-base 3' overhang (TCGAAC  
Analysis Date : 2/8/23 at 5:47:42  
Pages : 37  
Sequence Length : 74429 bp  
GC Content : 58.72%

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,

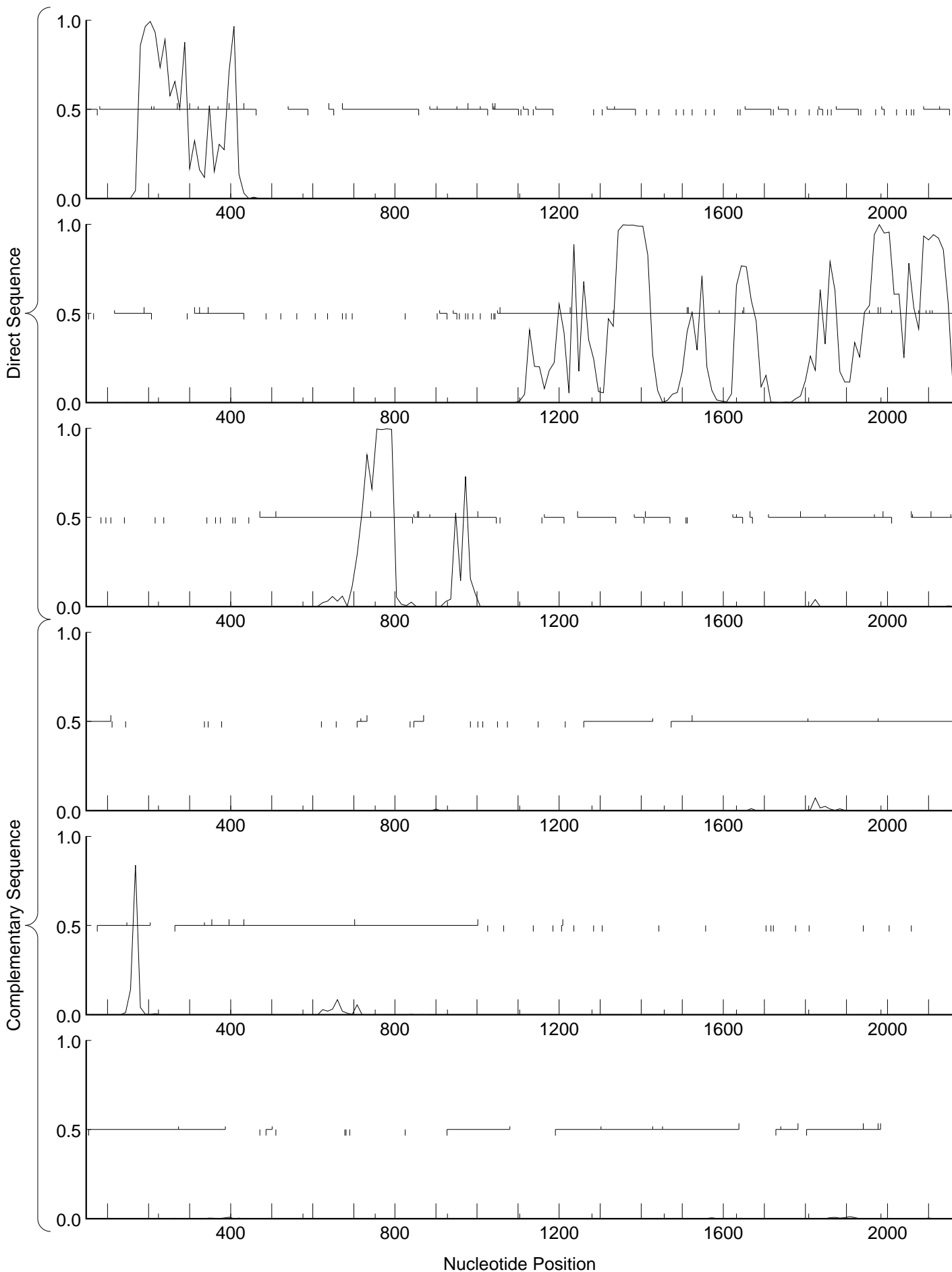
## Matrix notes & comments

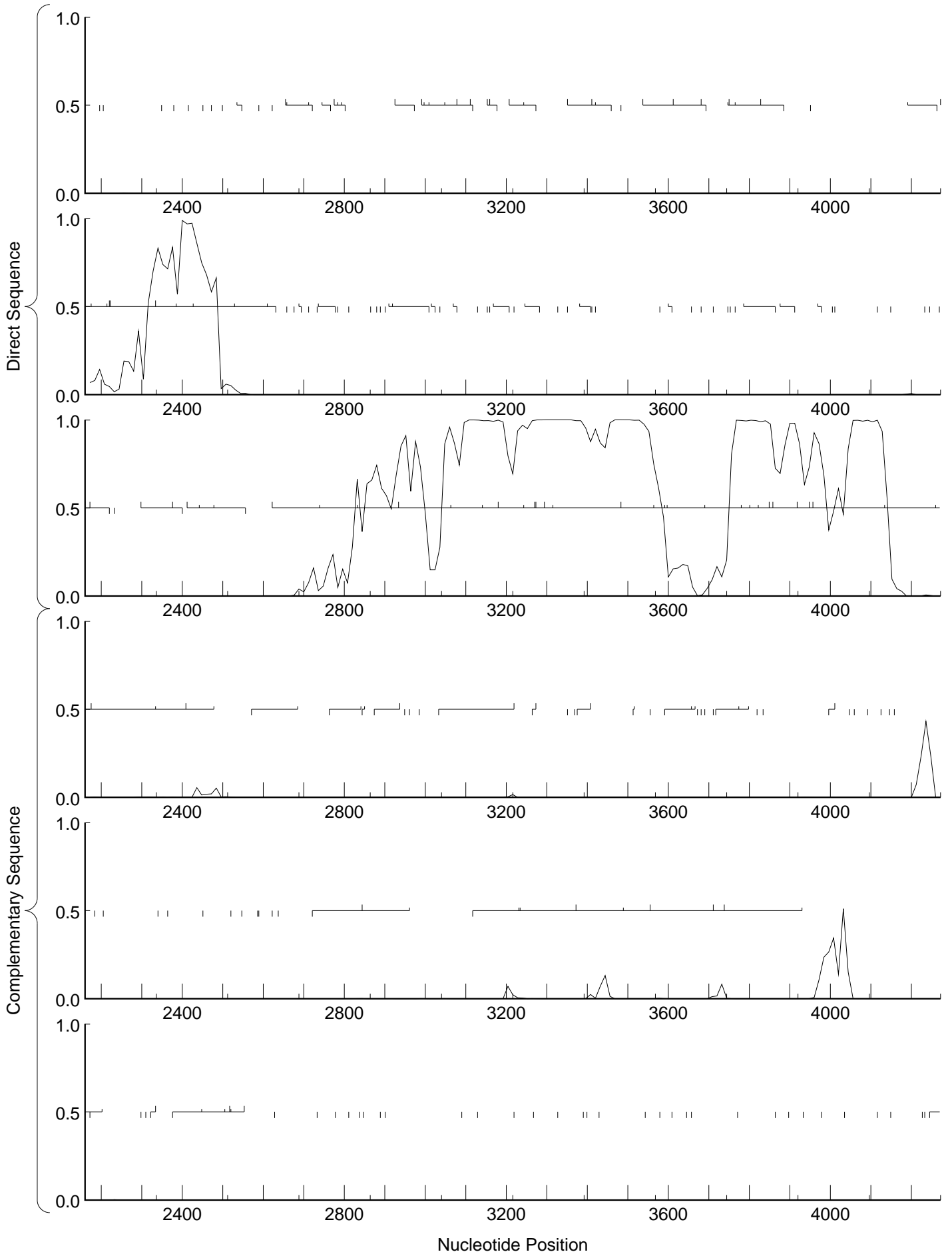
Training set derived by GeneMarkS, 4.27 September 2014  
Tue Sep 23 15:14:37 2014

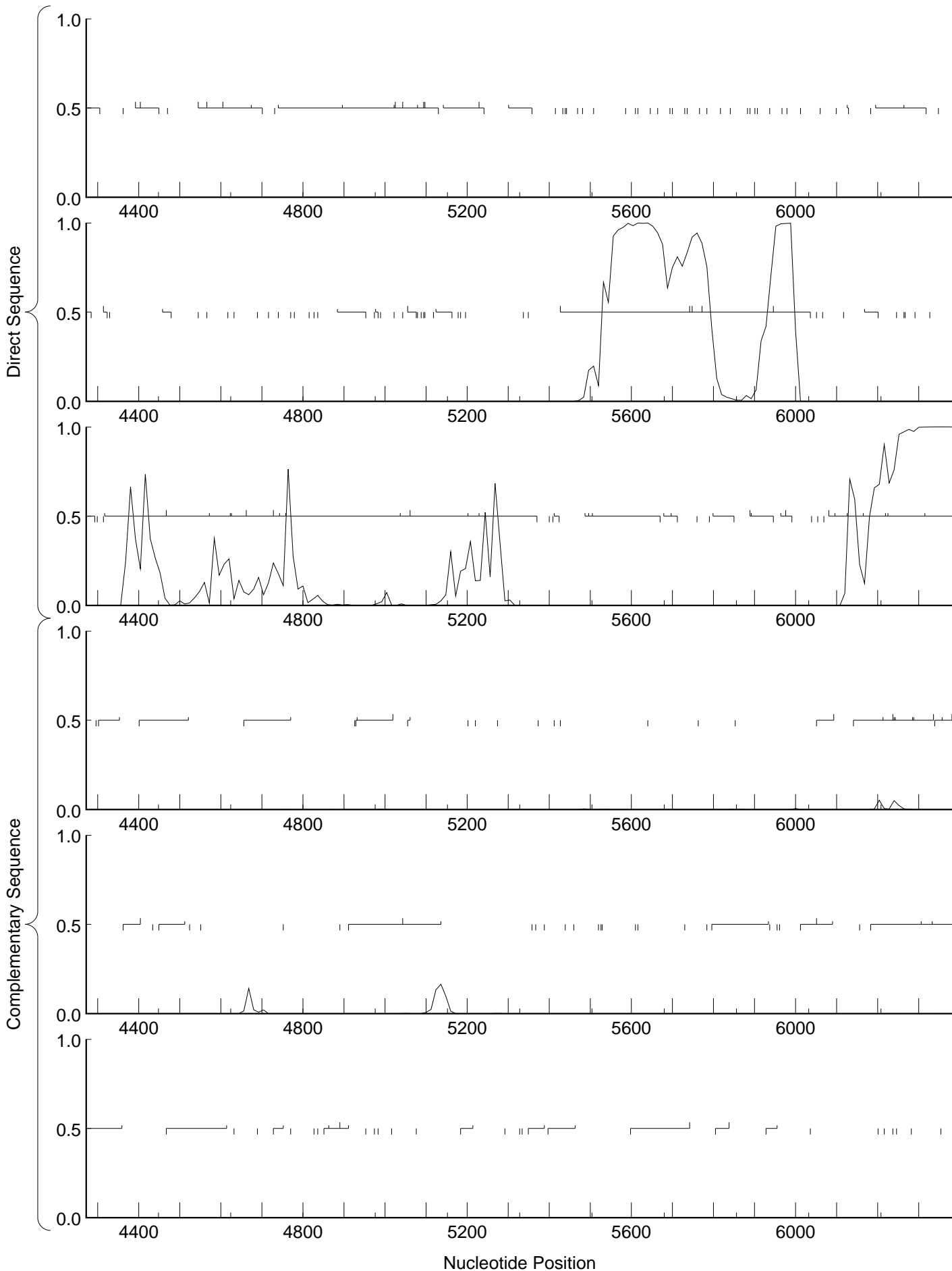
## MATRIX INFORMATION

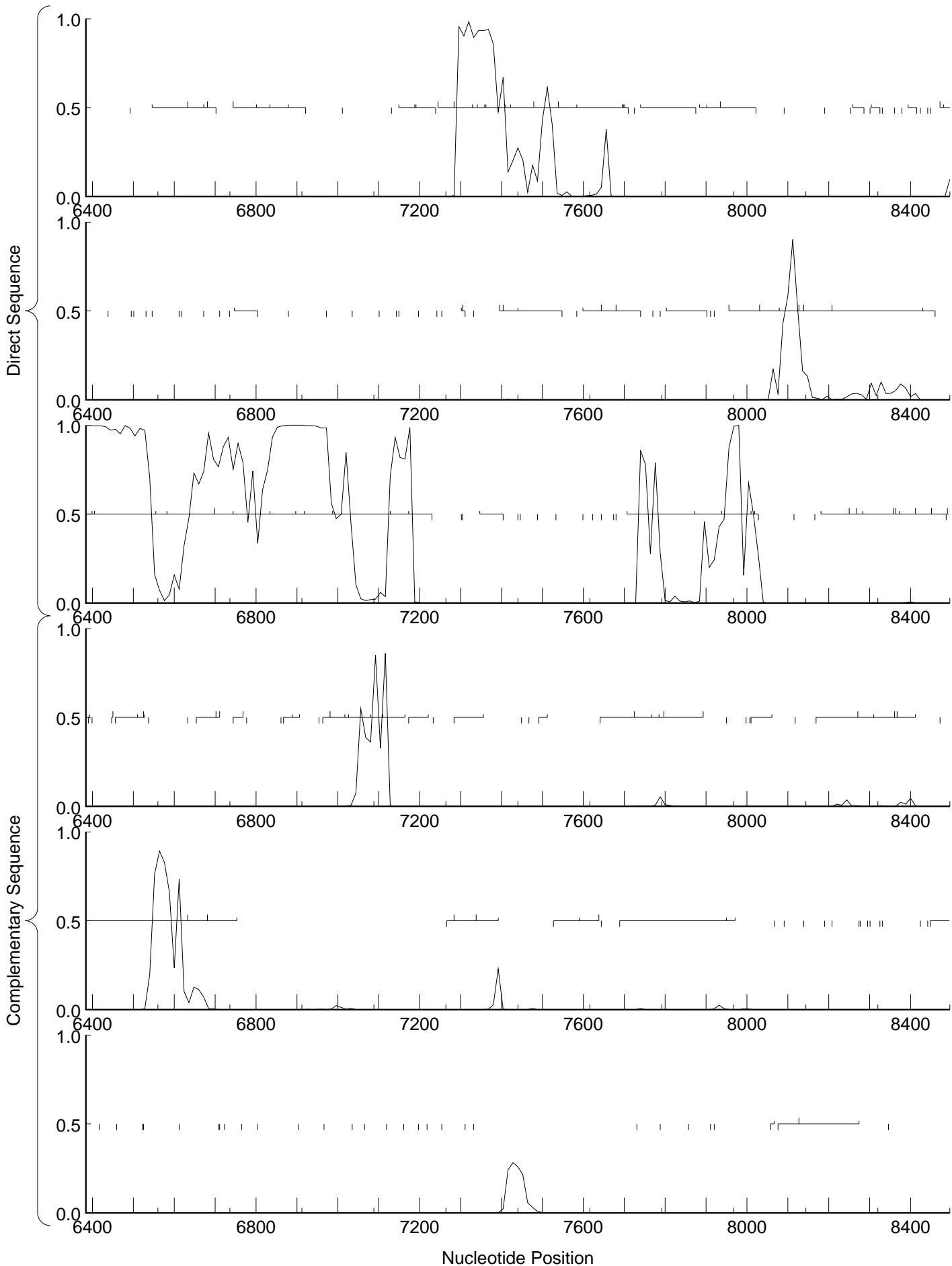
Matrix : Mycobacterium\_tuberculosis\_H37Rv  
Author : -  
Order : 4

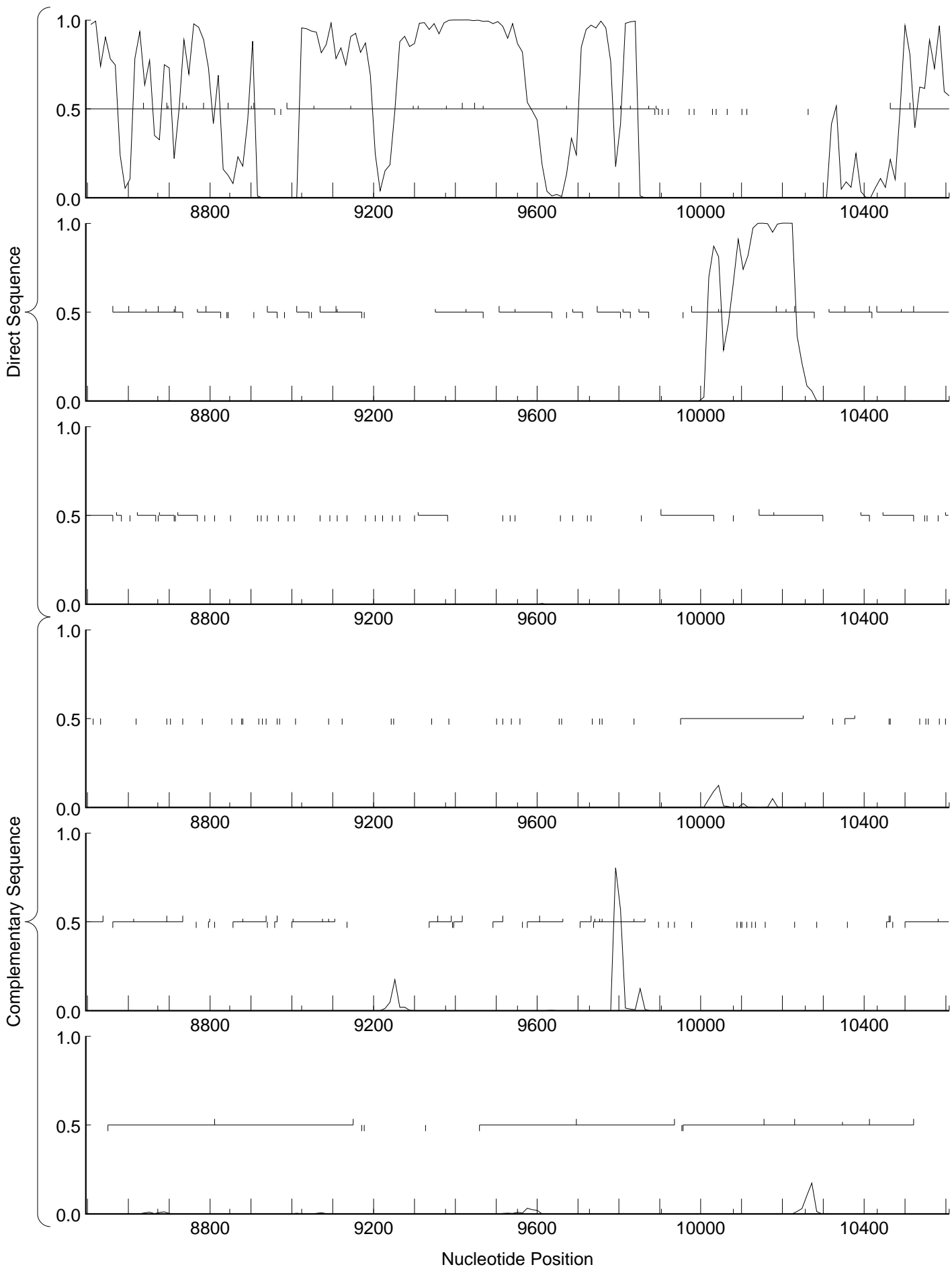
Send questions / comments to:  
Dr. M. Borodovsky  
Georgia Institute of Technology  
School of Biology  
Atlanta, GA 30332-0230

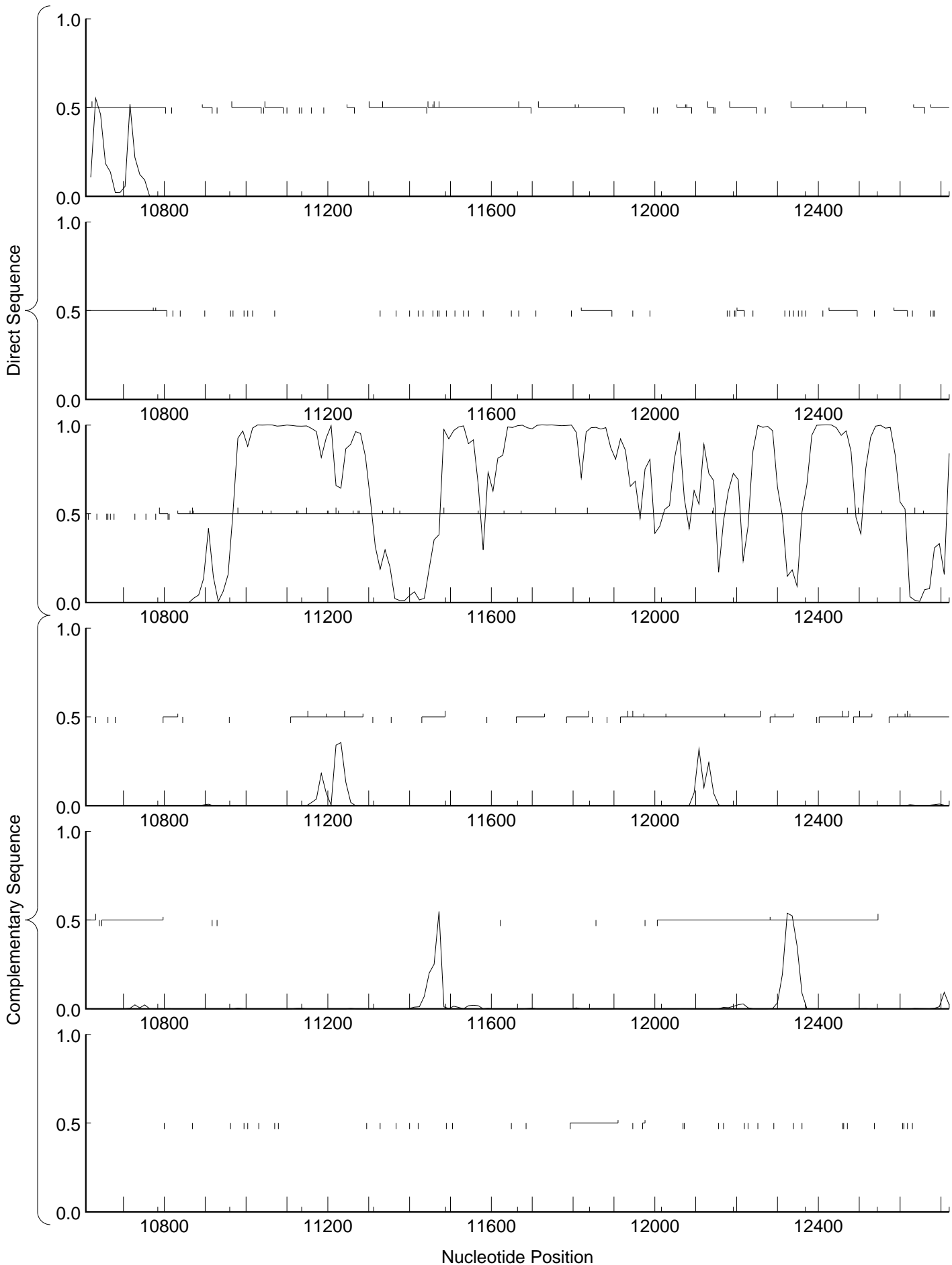


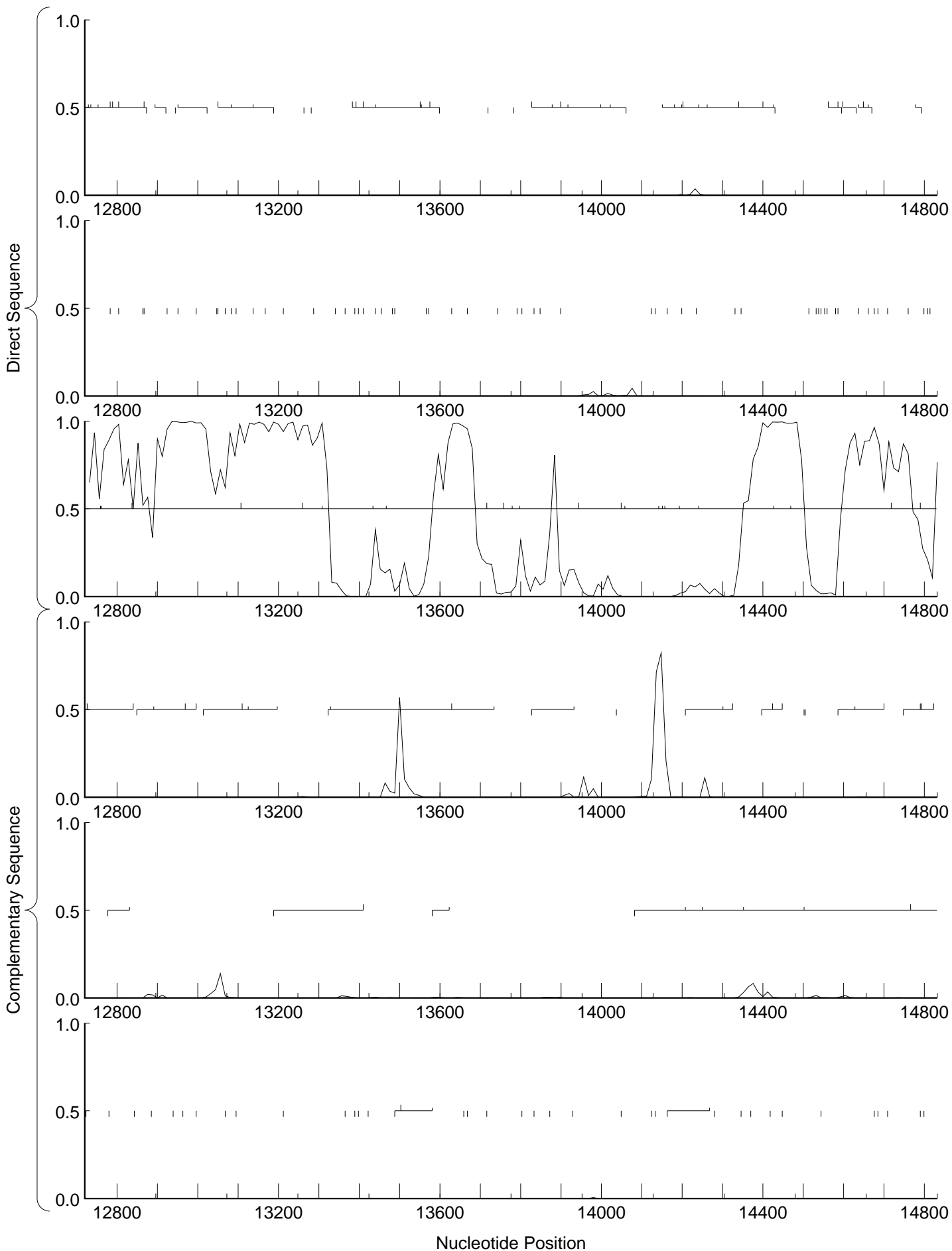




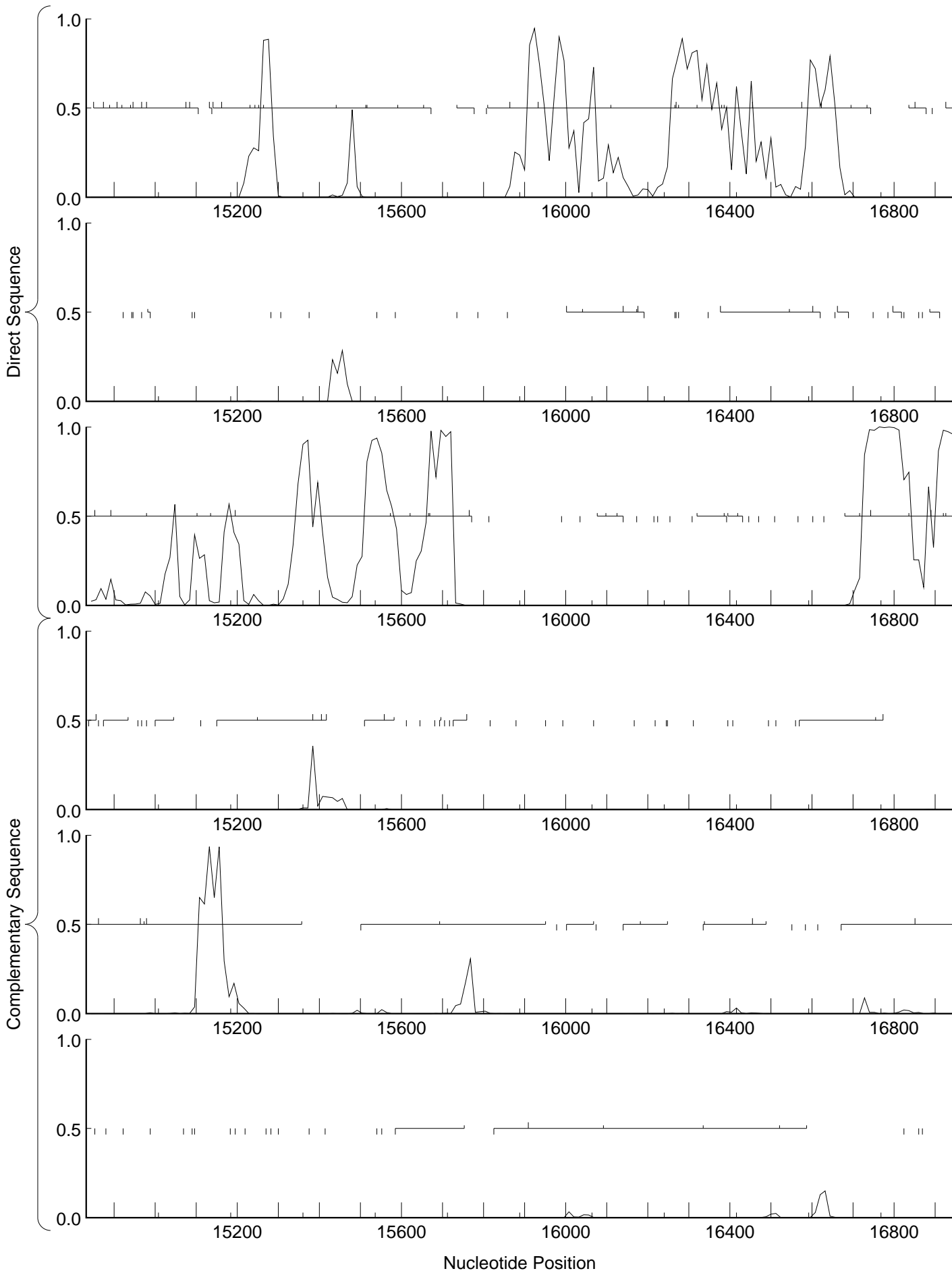


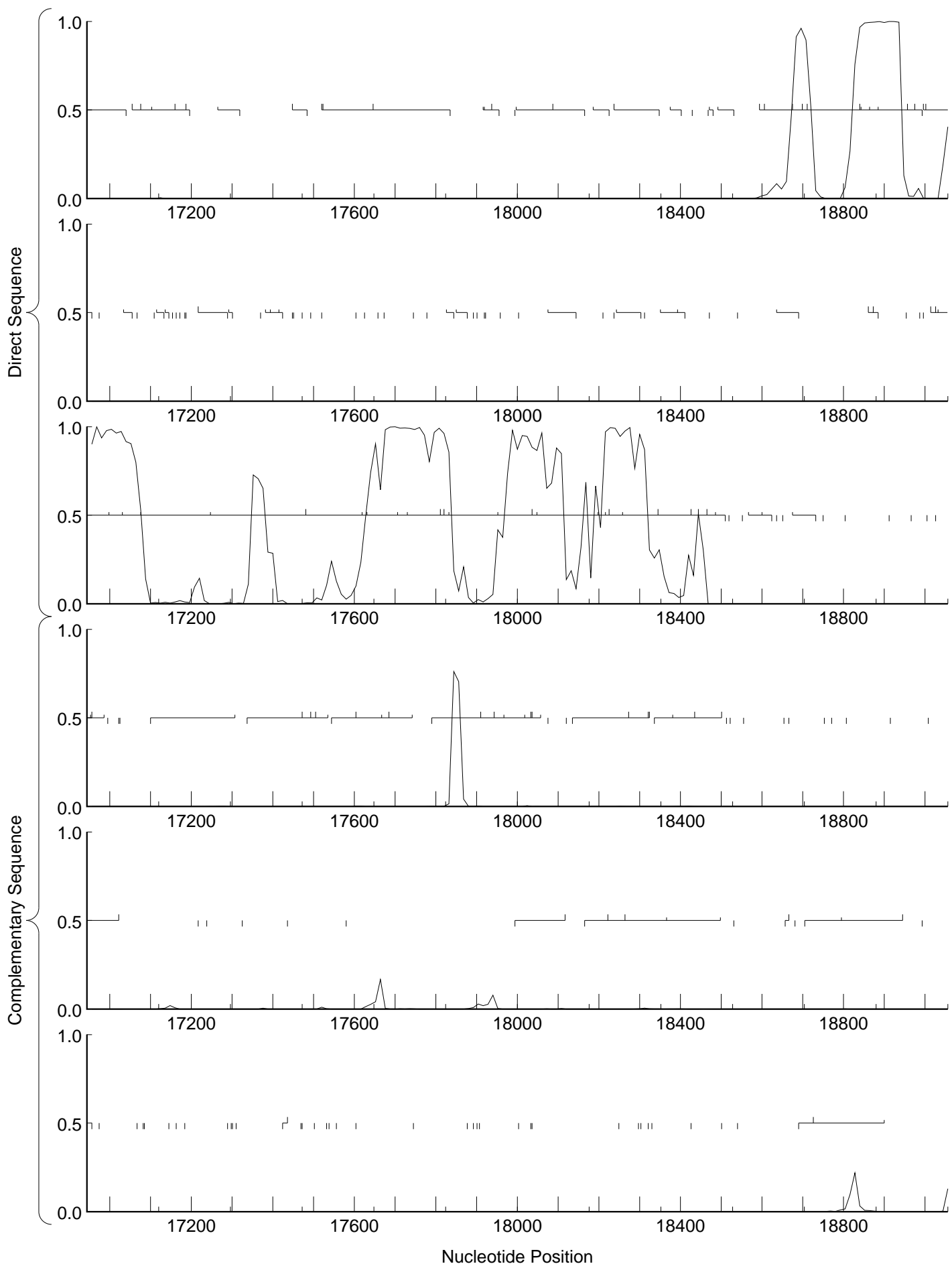




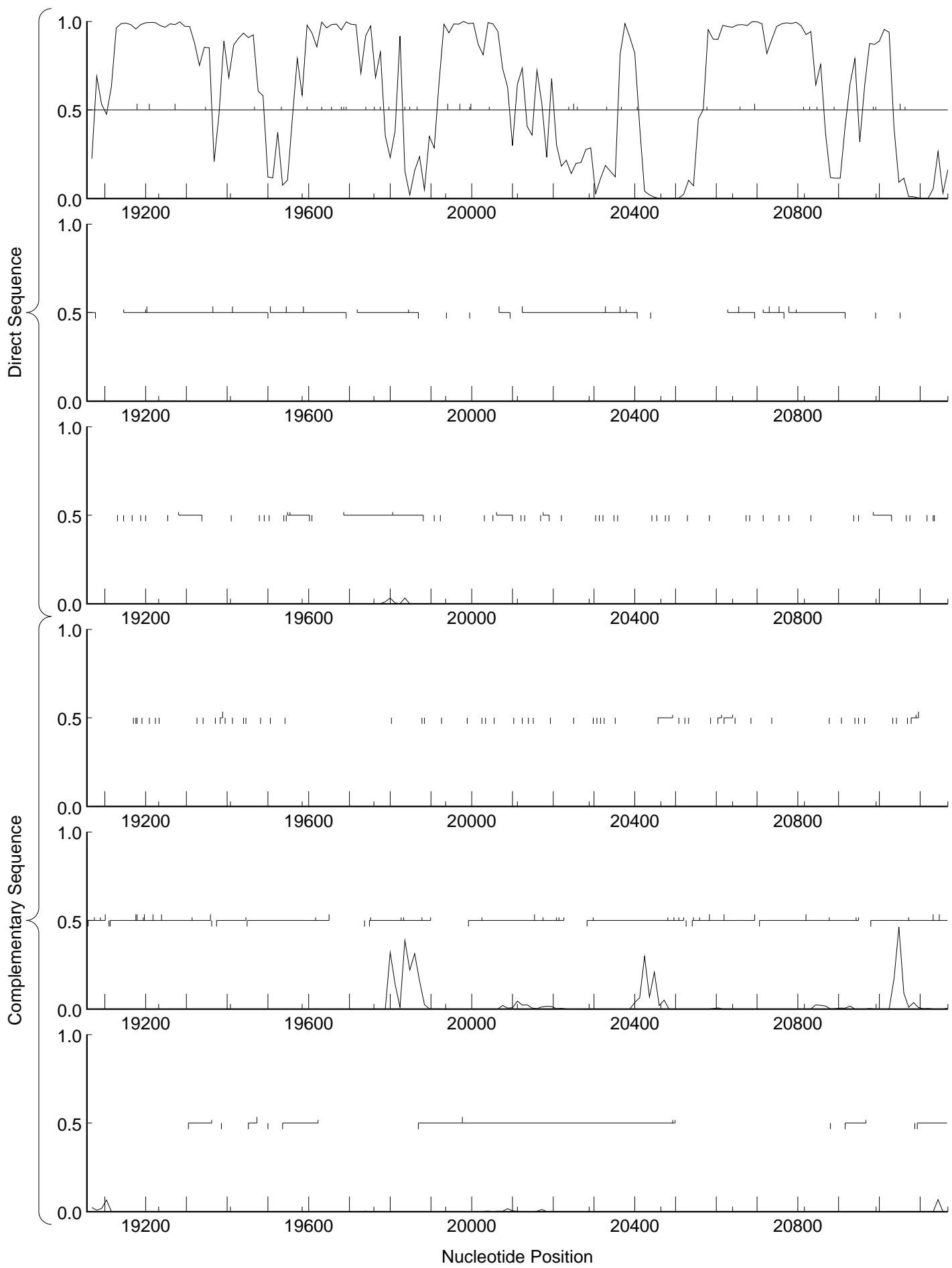


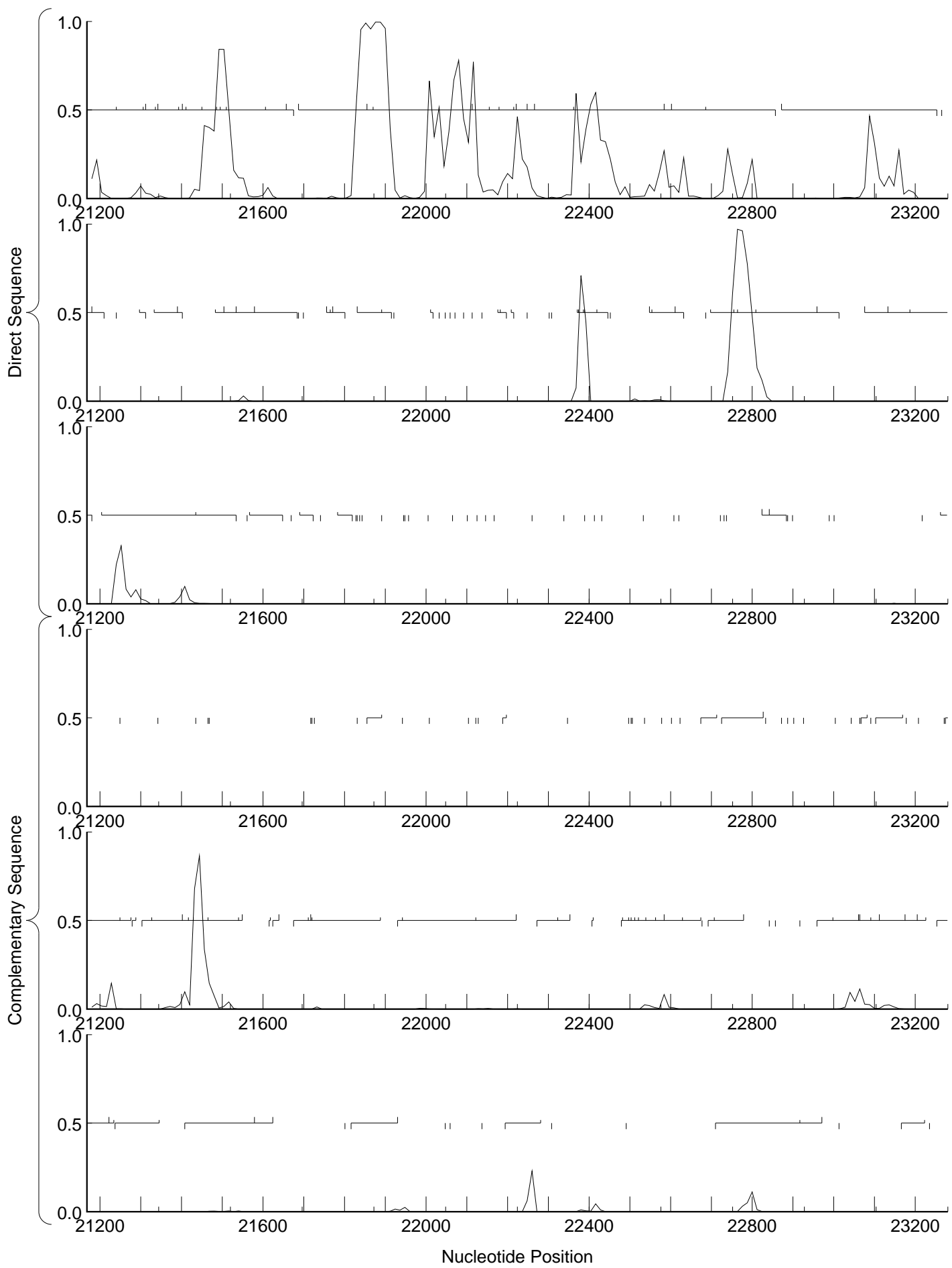


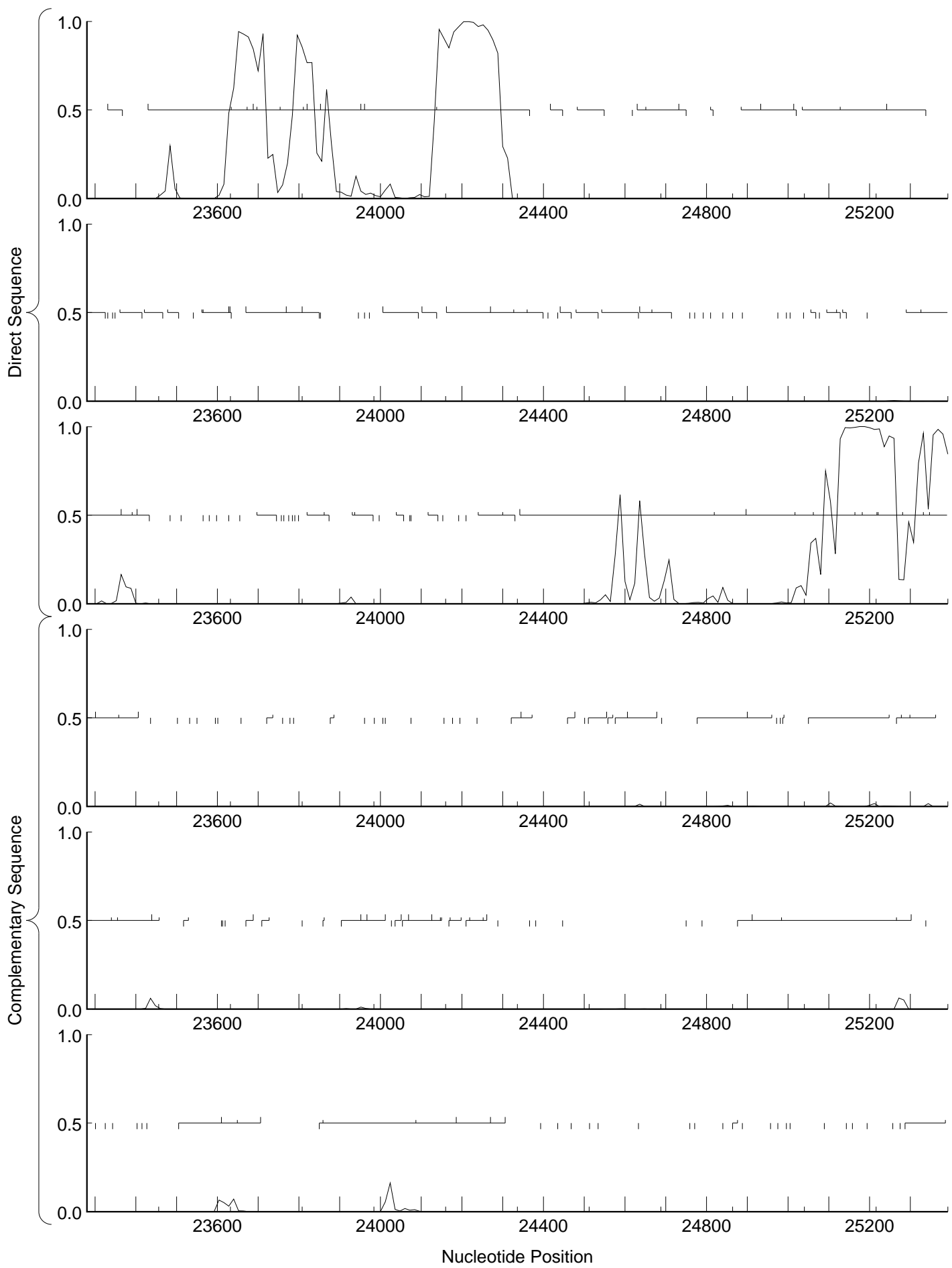


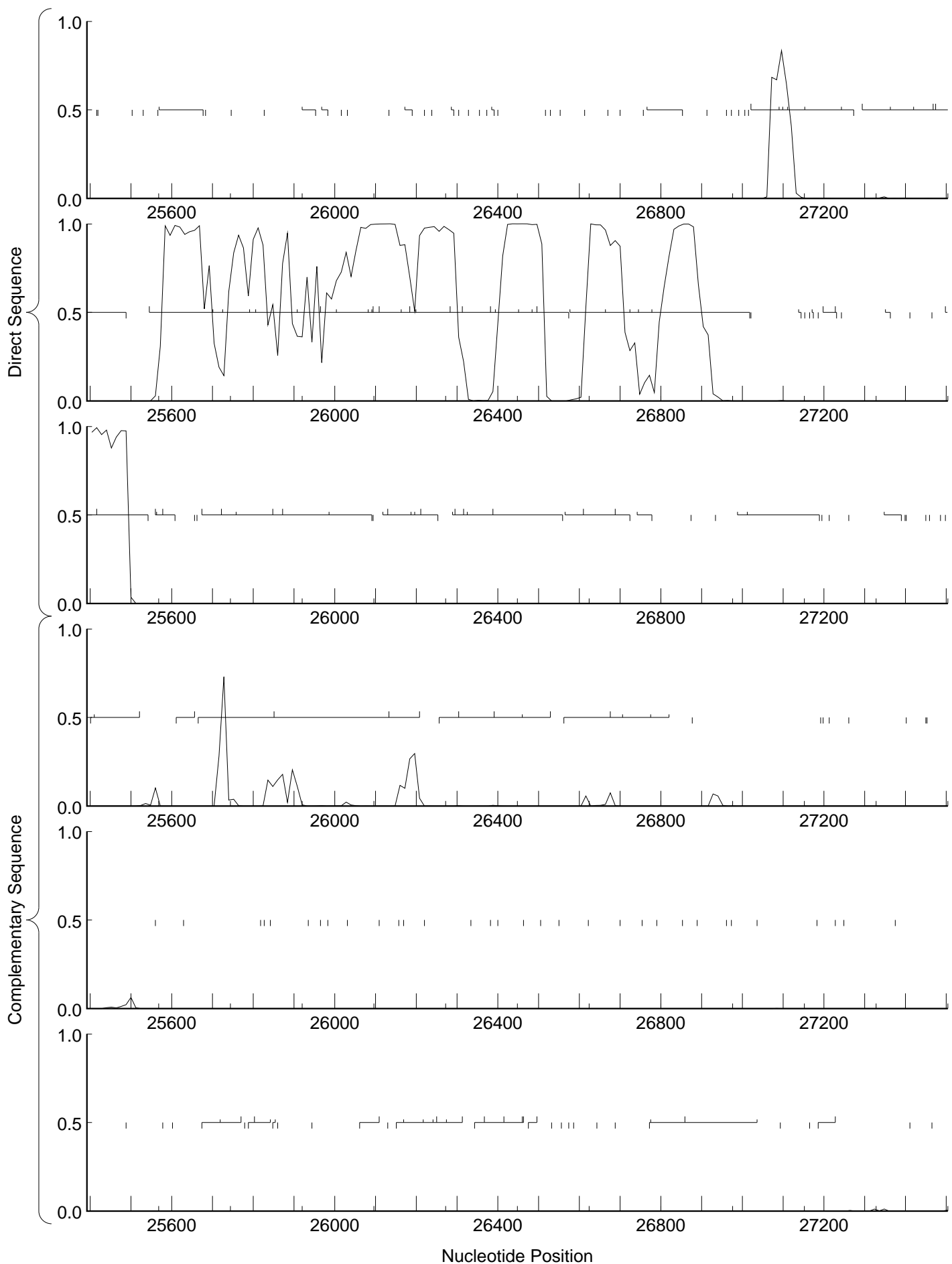


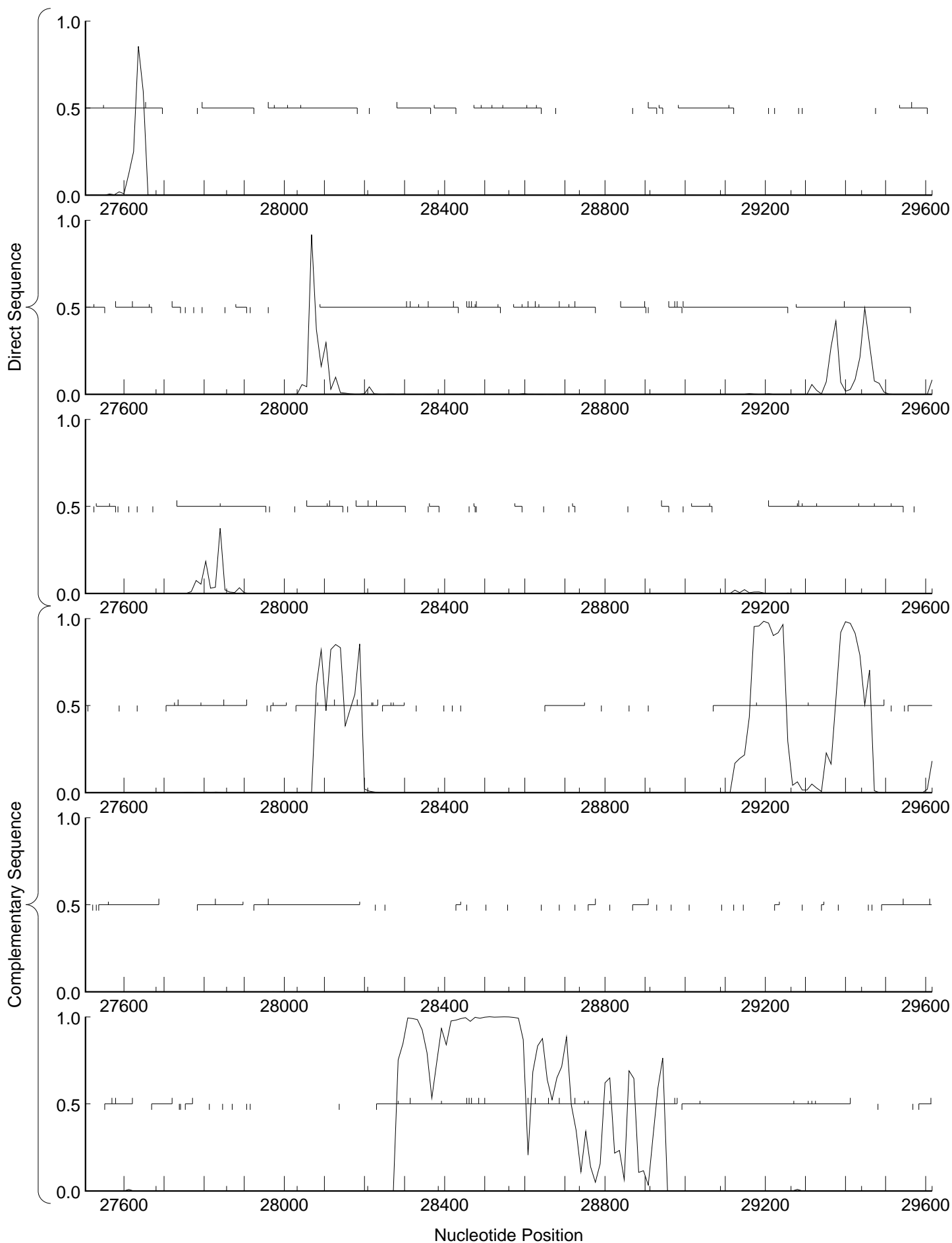
complete sequence, 74429 bp including 10-base 3' overhang (TCGAACGGCC), Cluster L1, Order 4, Window 96, Step 12, 11/37



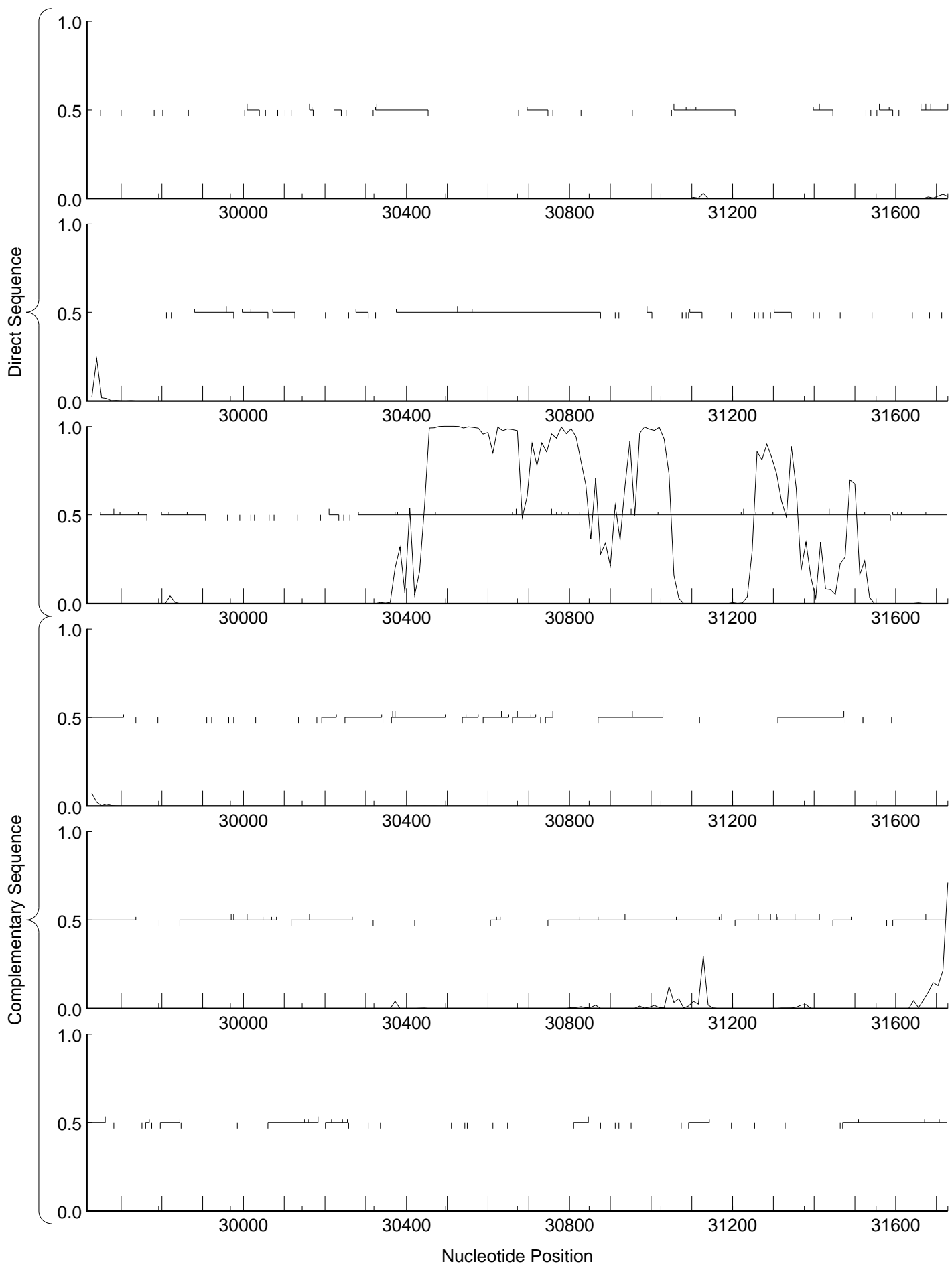




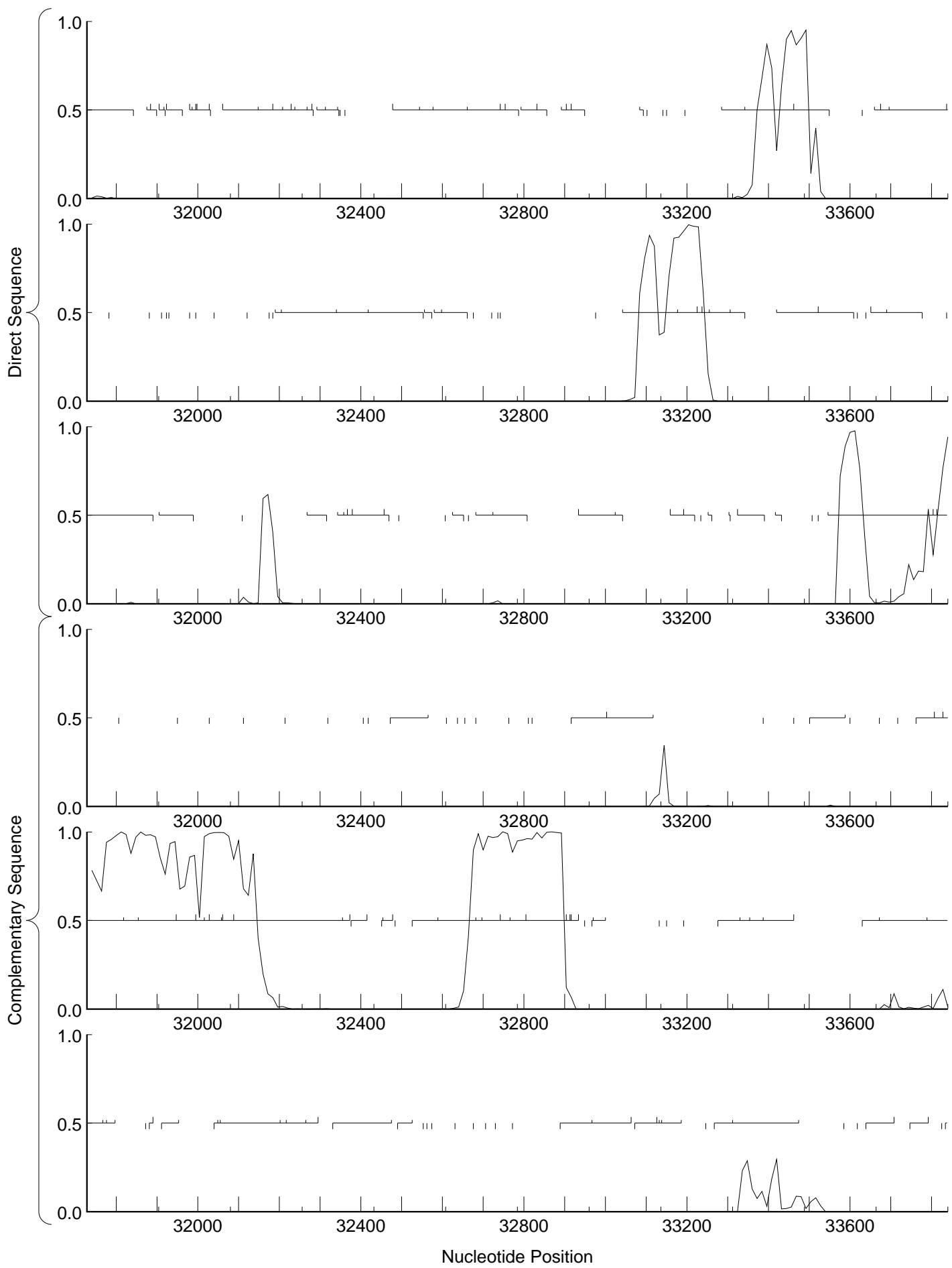


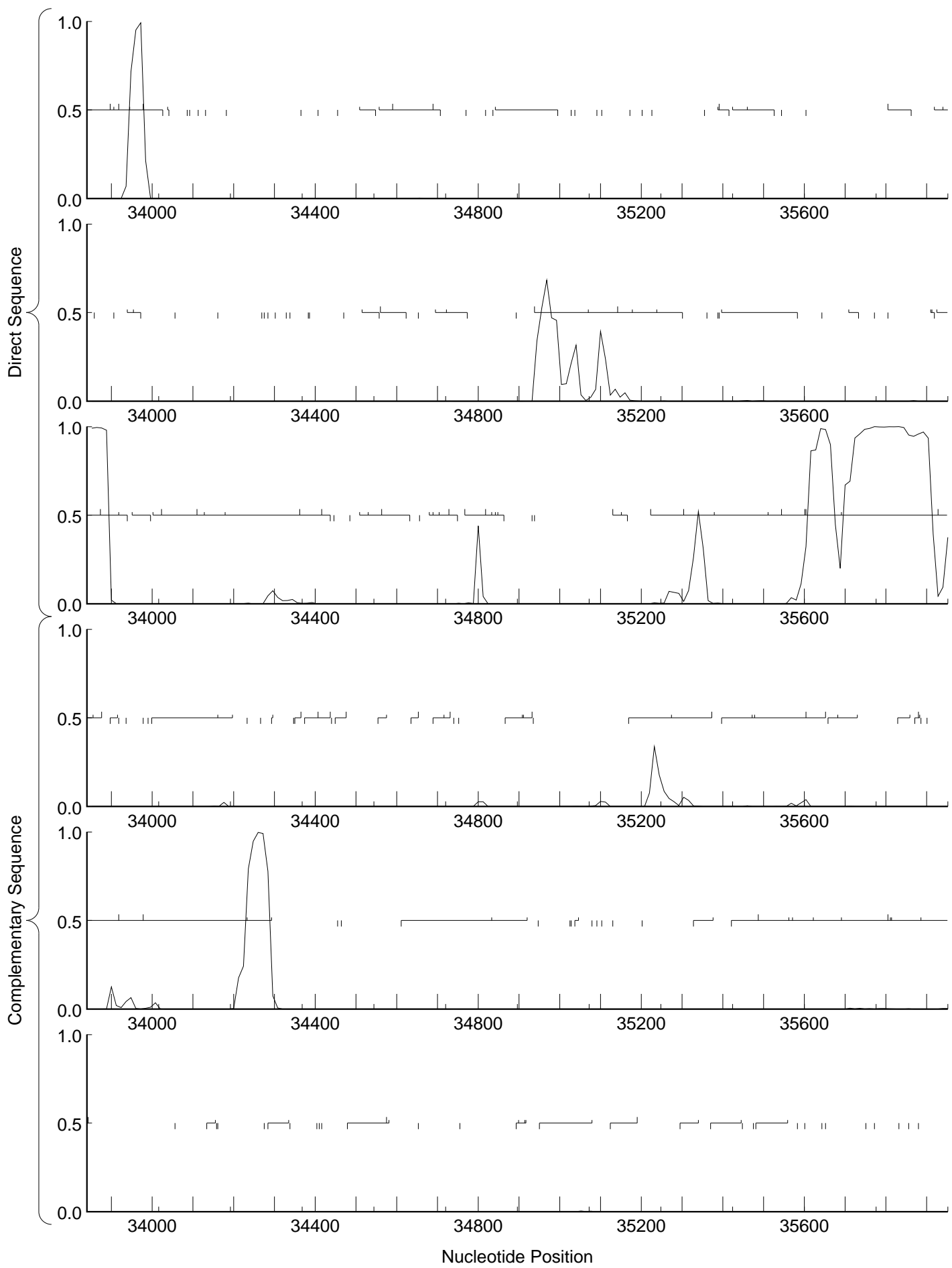


complete sequence, 74429 bp including 10-base 3' overhang (TCGAACGGCC), Cluster L1, Order 4, Window 96, Step 12, 16/37

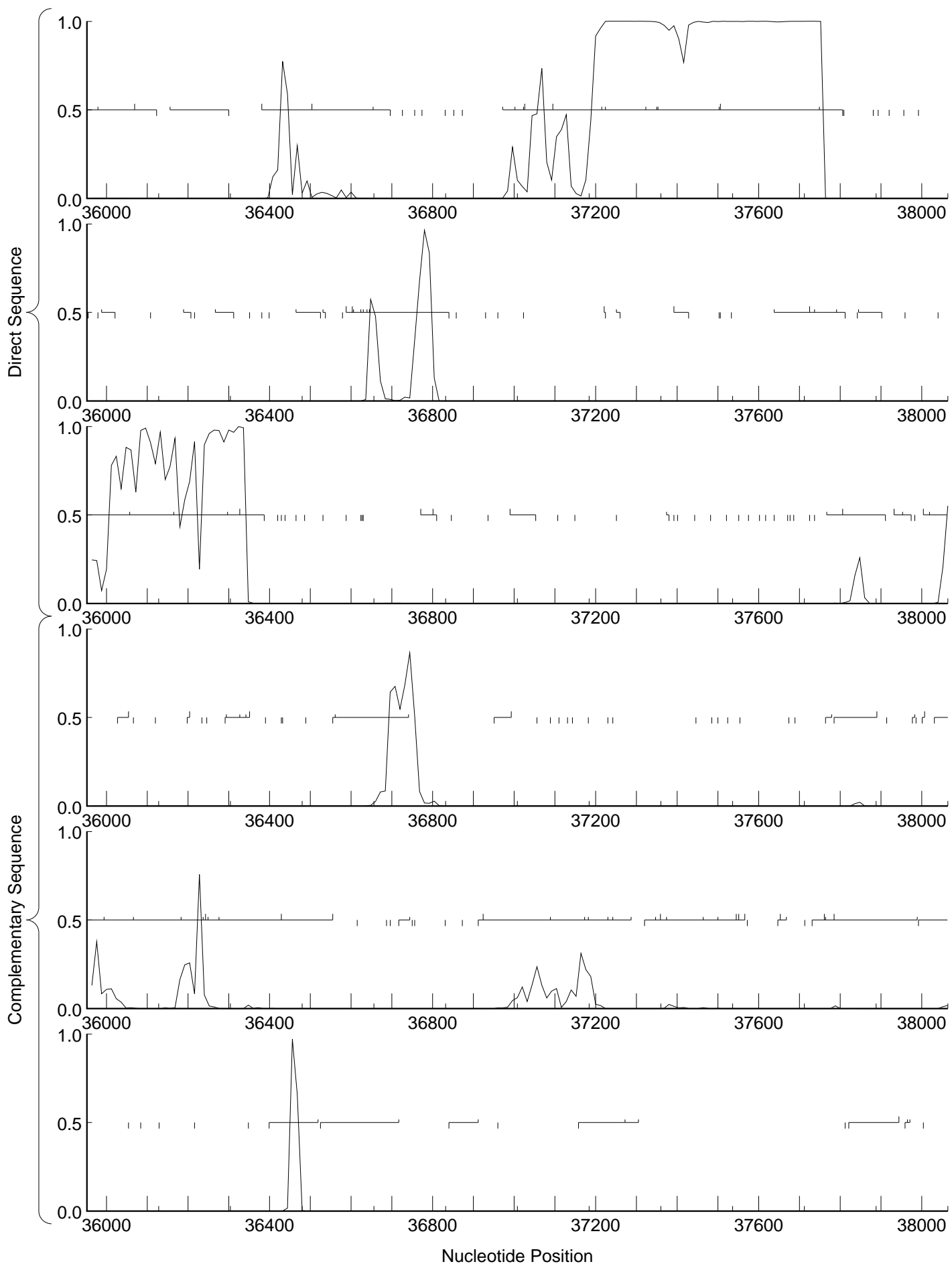


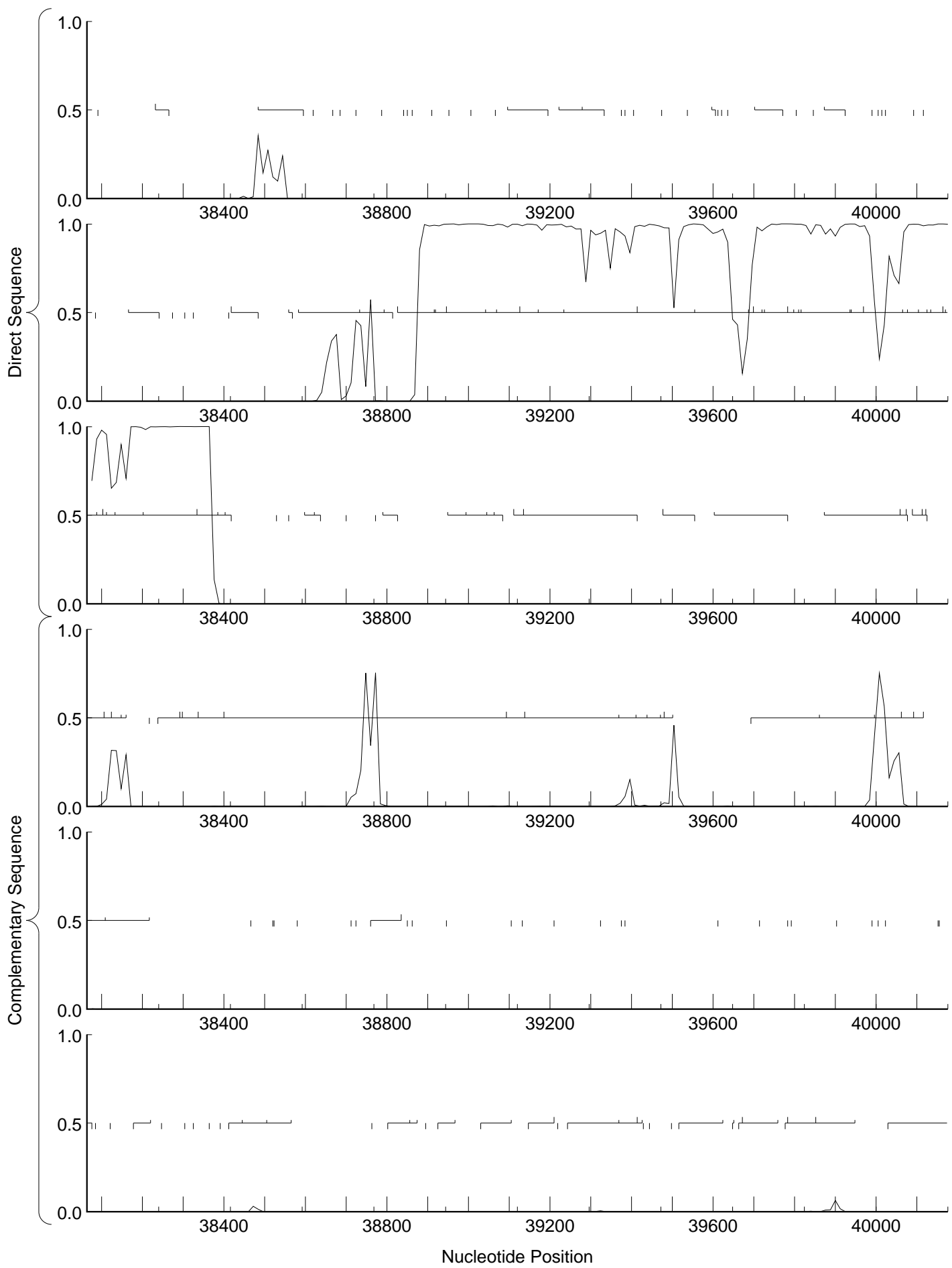




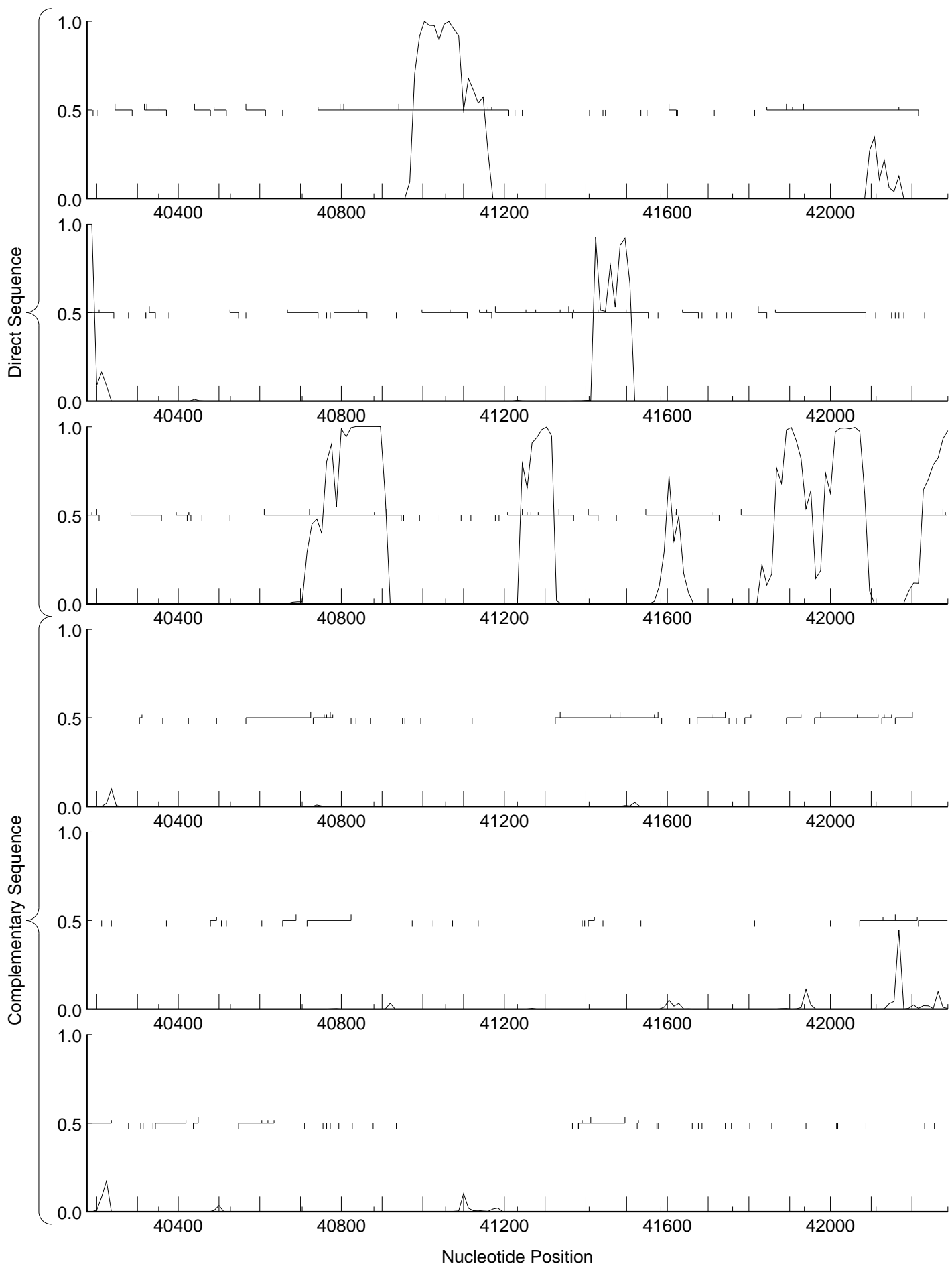


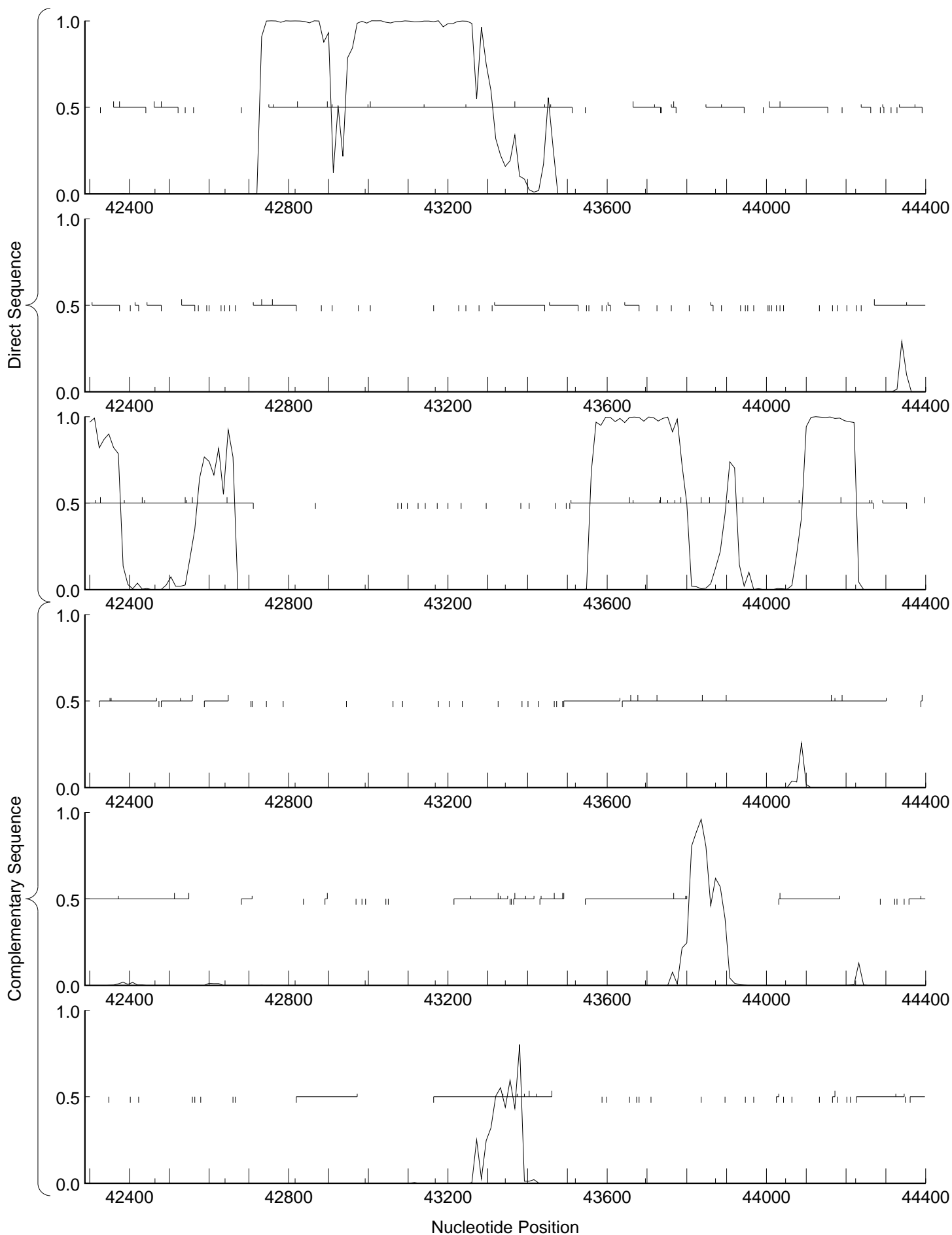
complete sequence, 74429 bp including 10-base 3' overhang (TCGAACGGCC), Cluster L1, Order 4, Window 96, Step 12, 19/37



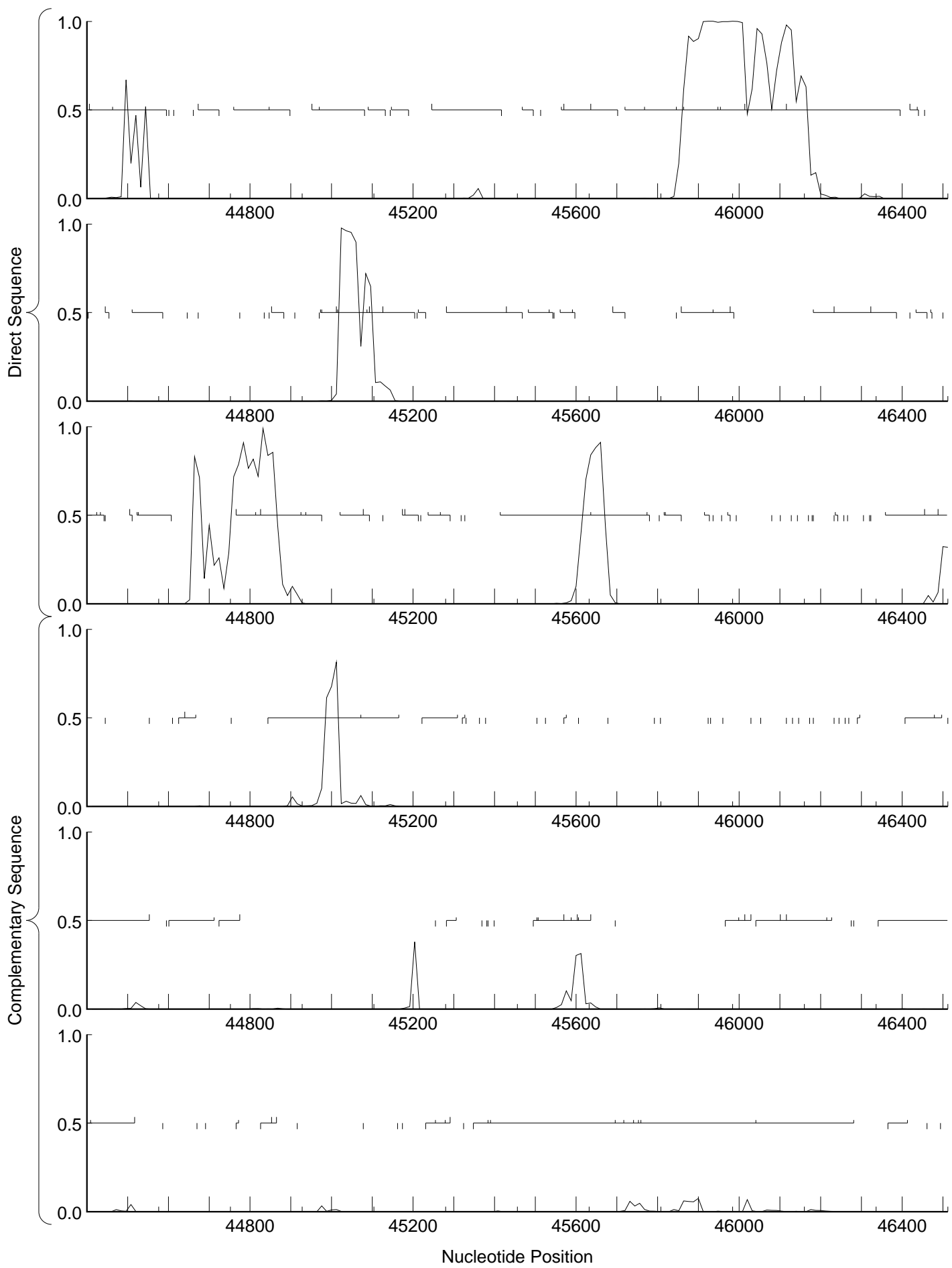


complete sequence, 74429 bp including 10-base 3' overhang (TCGAACGGCC), Cluster L1, Order 4, Window 96, Step 12, 21/37

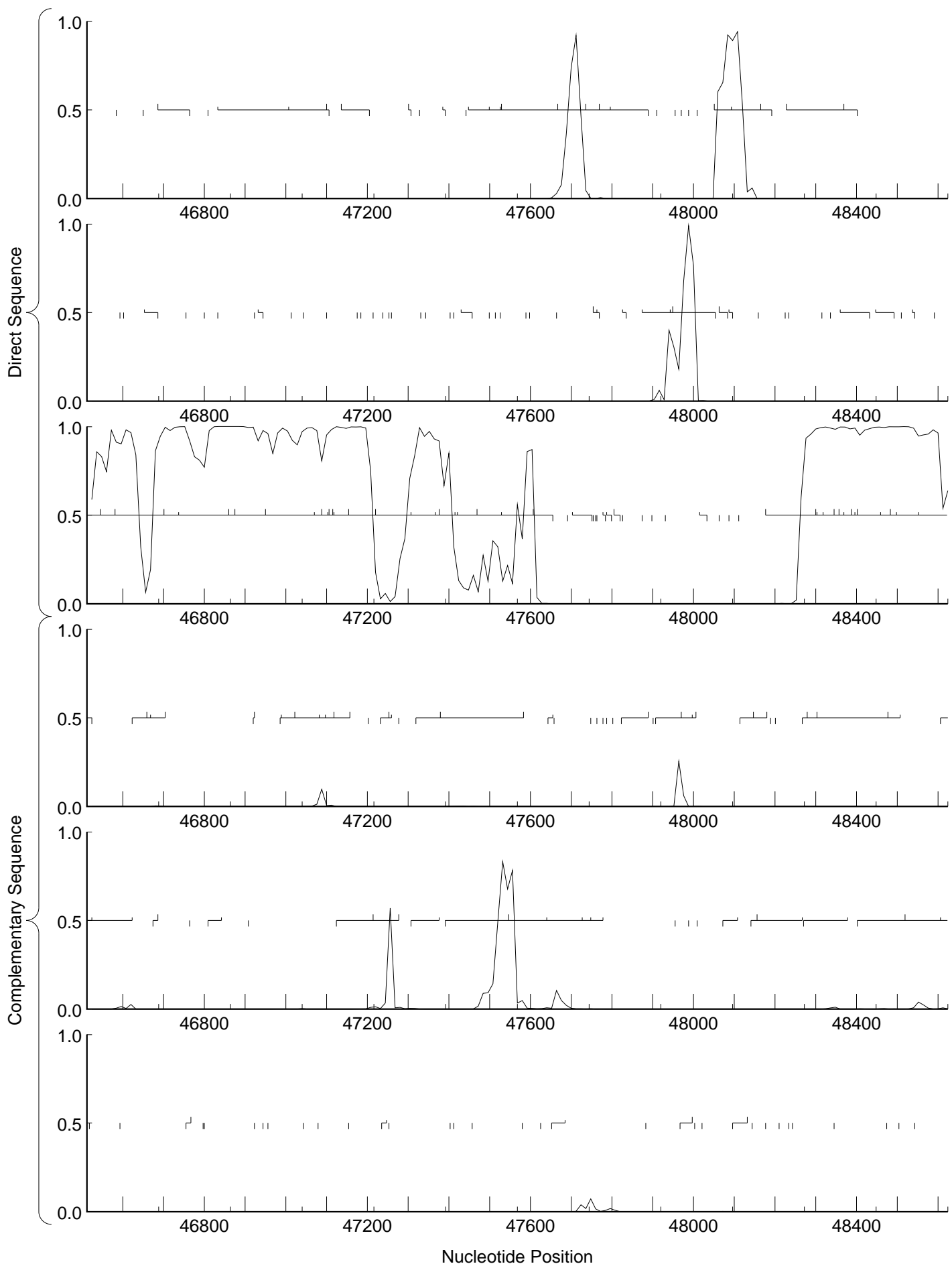




complete sequence, 74429 bp including 10-base 3' overhang (TCGAACGGCC), Cluster L1, Order 4, Window 96, Step 12, 23/37

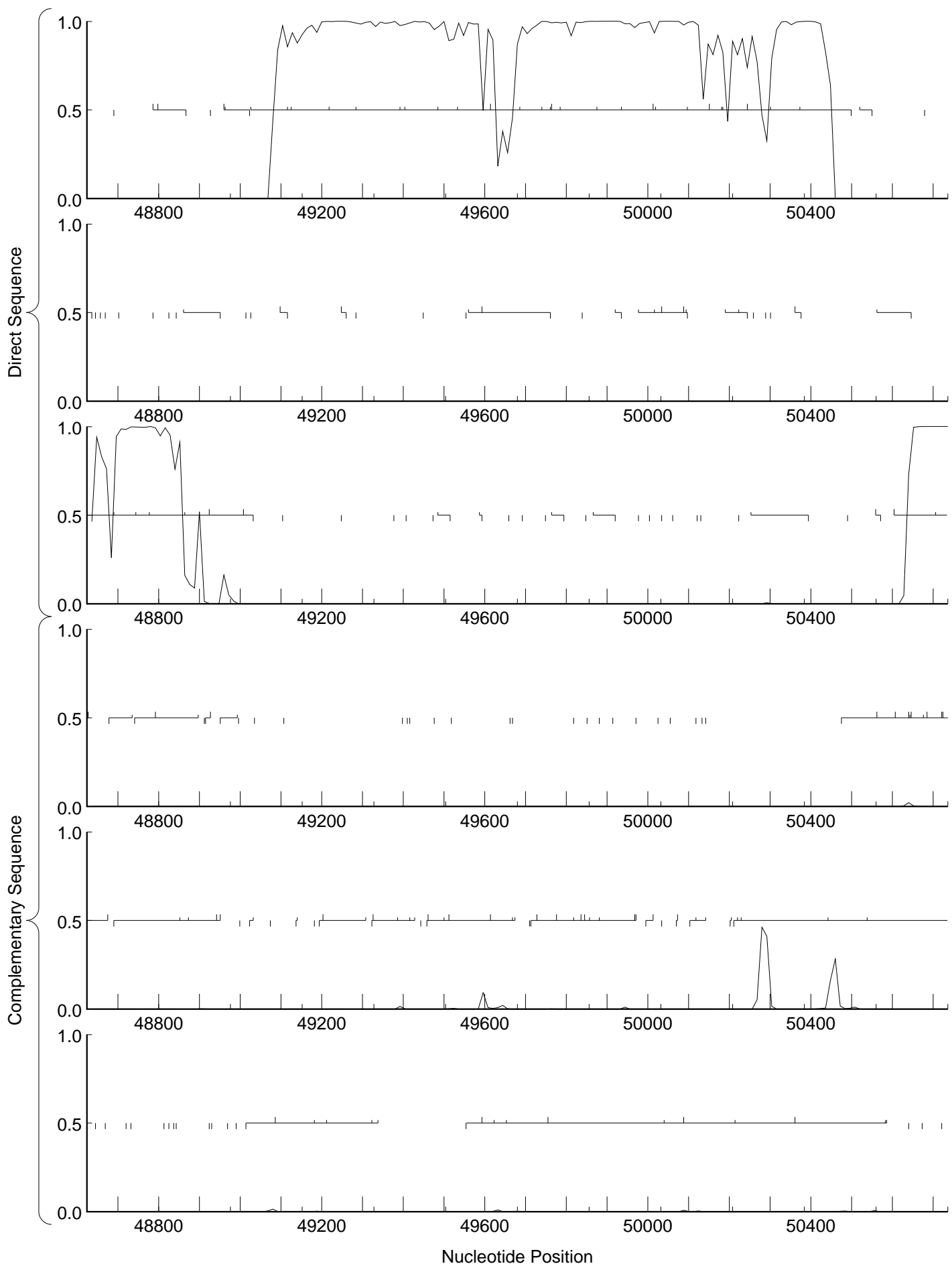


complete sequence, 74429 bp including 10-base 3' overhang (TCGAACGGCC), Cluster L1, Order 4, Window 96, Step 12, 24/37

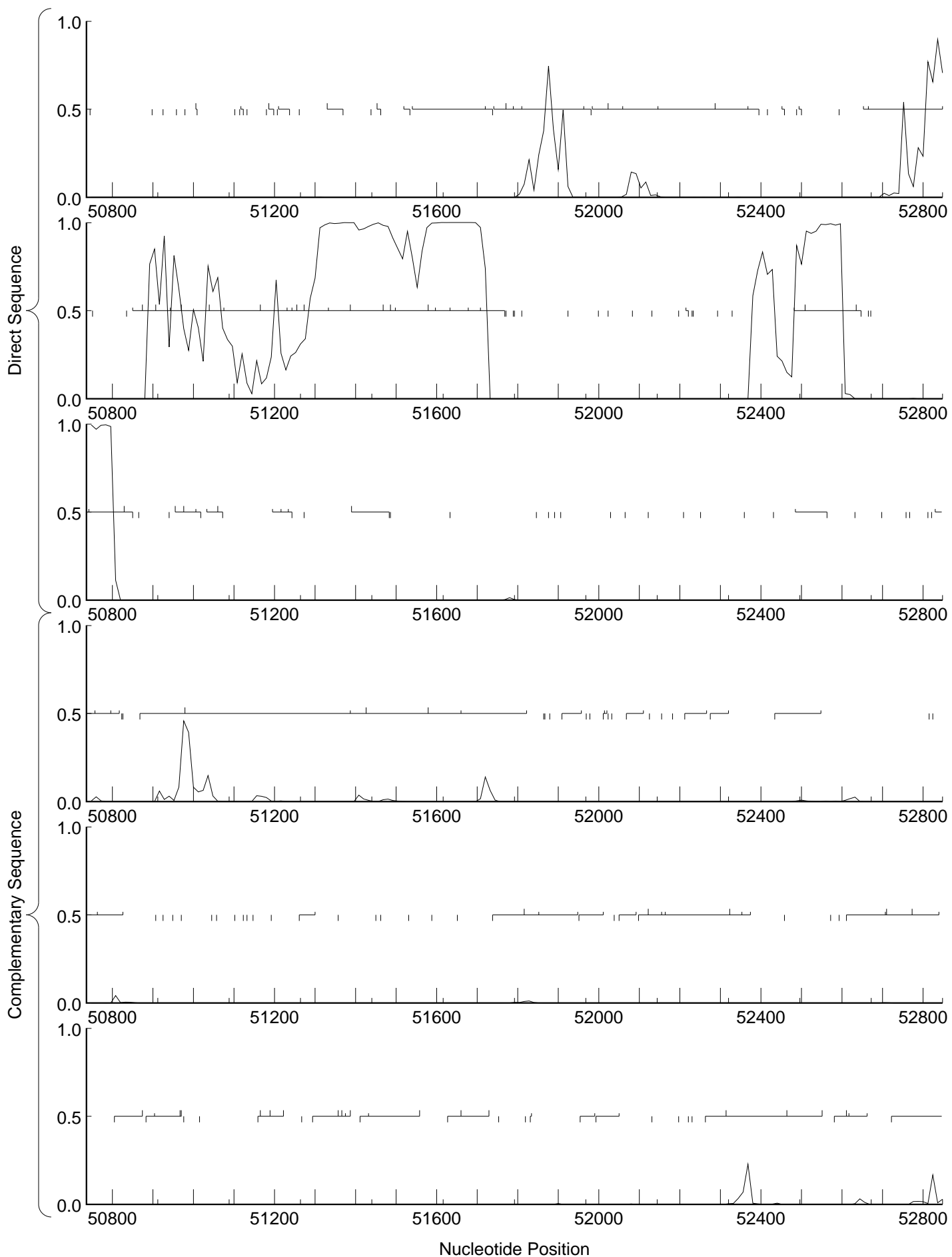




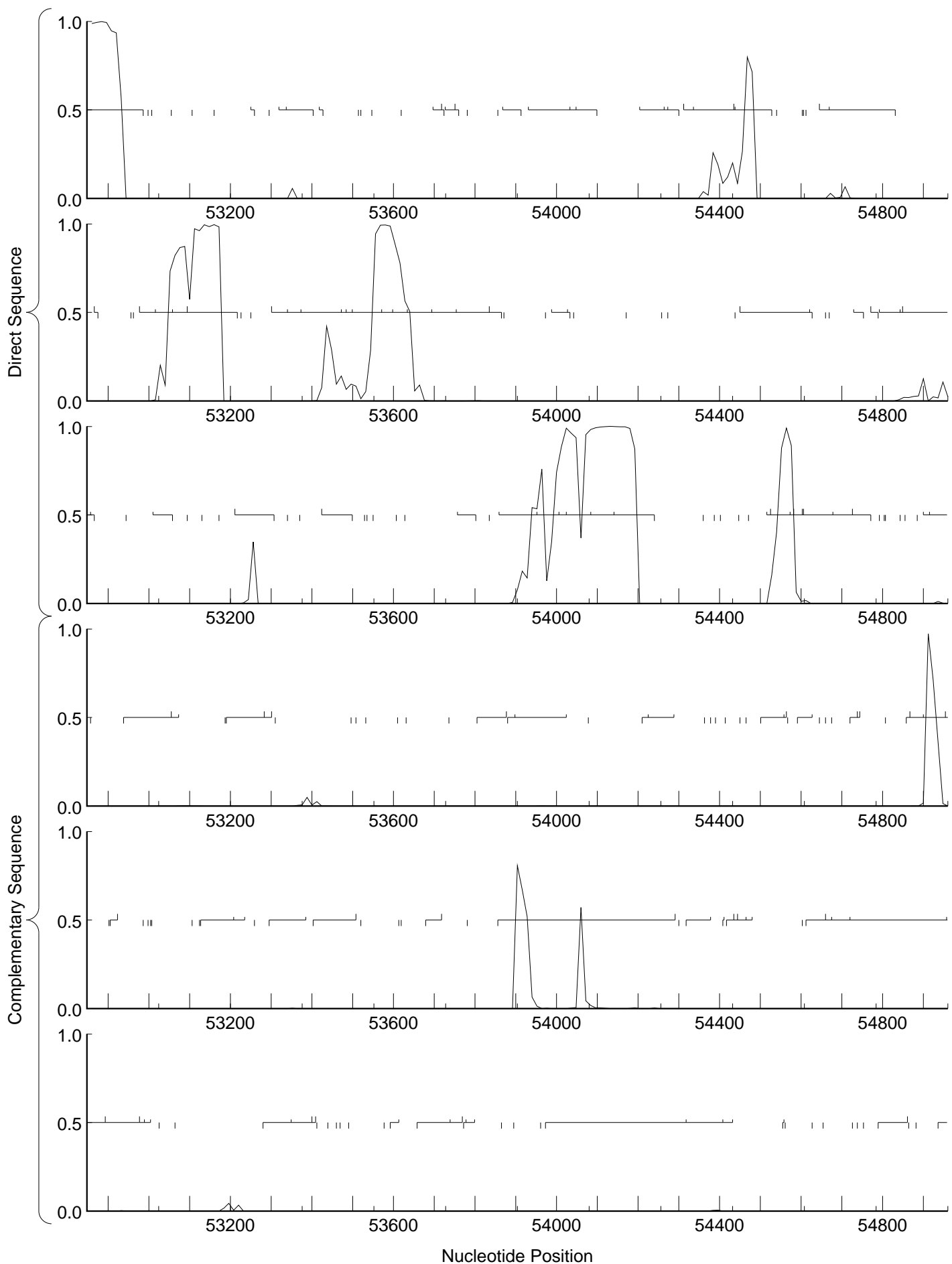
complete sequence, 74429 bp including 10-base 3' overhang (TCGAACGGCC), Cluster L1, Order 4, Window 96, Step 12, 25/37



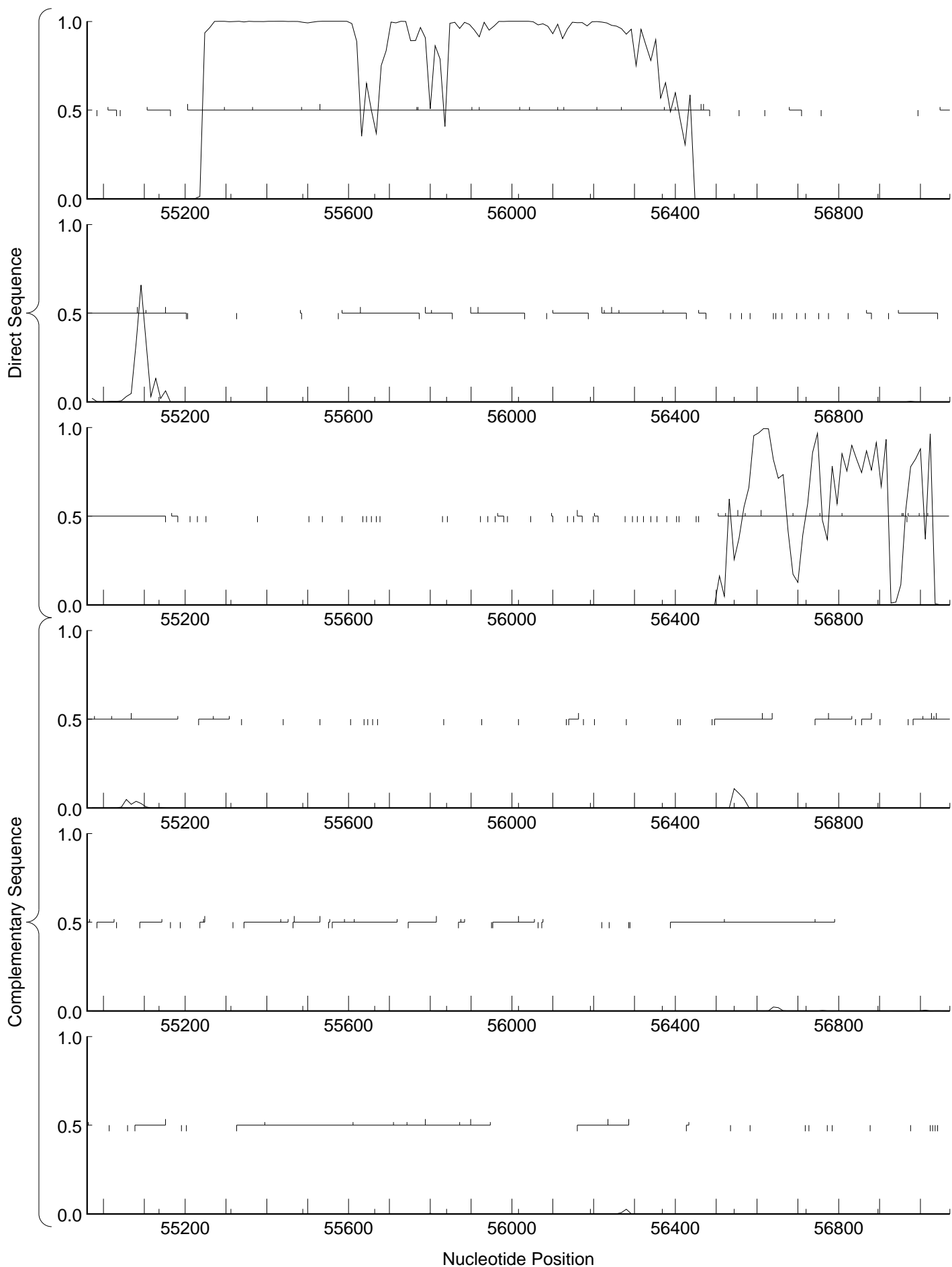
complete sequence, 74429 bp including 10-base 3' overhang (TCGAACGGCC), Cluster L1, Order 4, Window 96, Step 12, 26/37

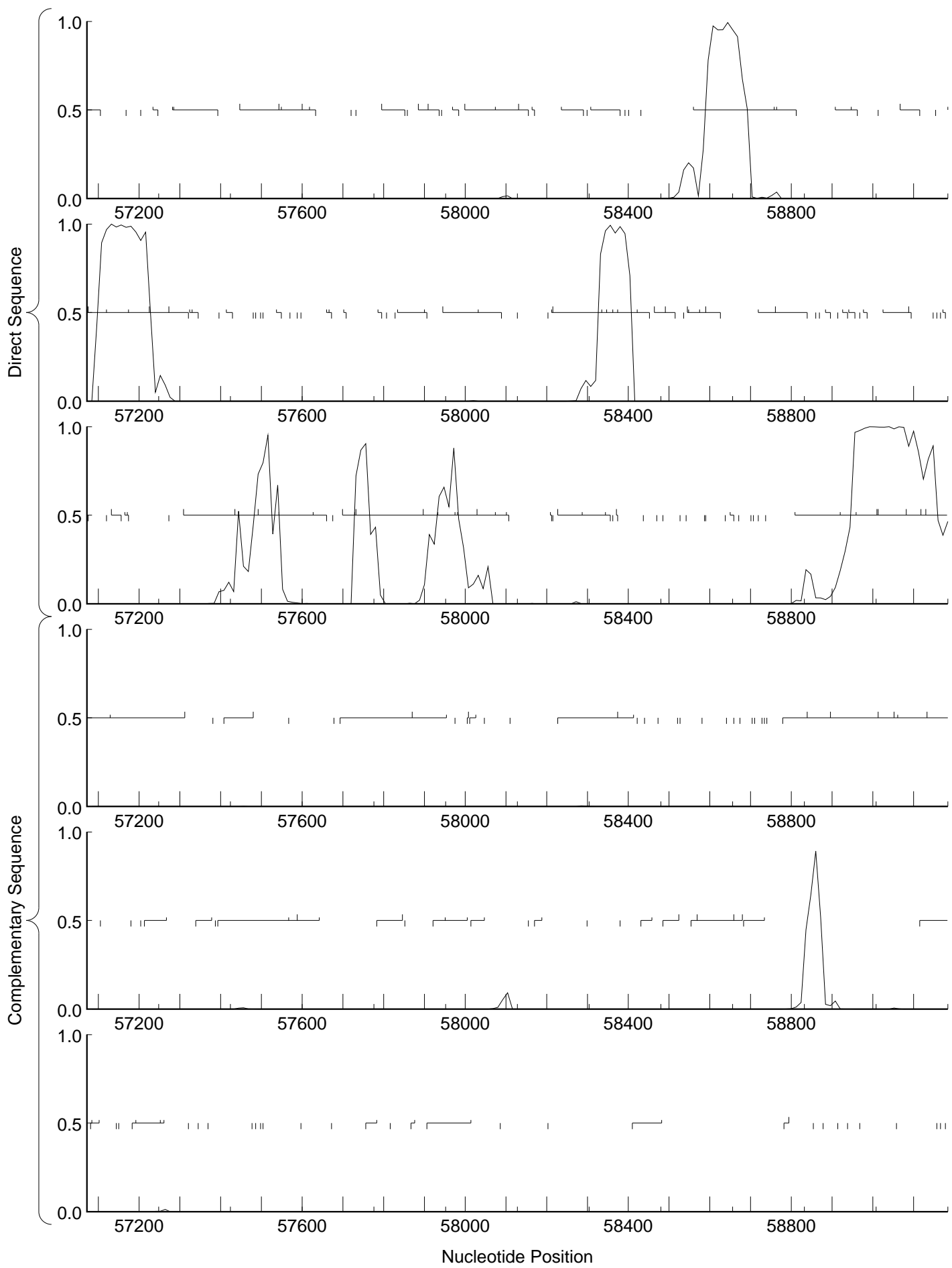


complete sequence, 74429 bp including 10-base 3' overhang (TCGAACGGCC), Cluster L1, Order 4, Window 96, Step 12, 27/37

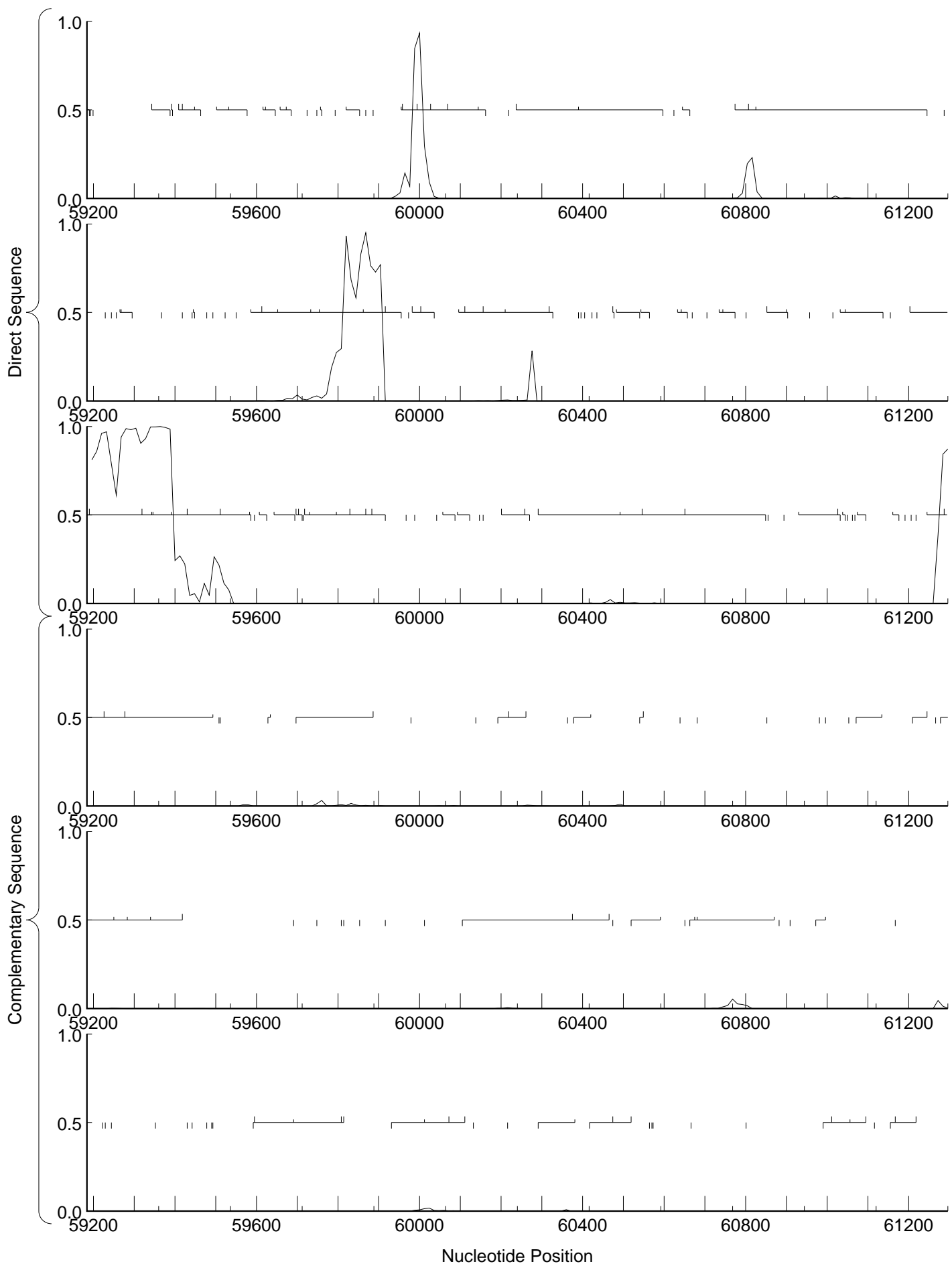


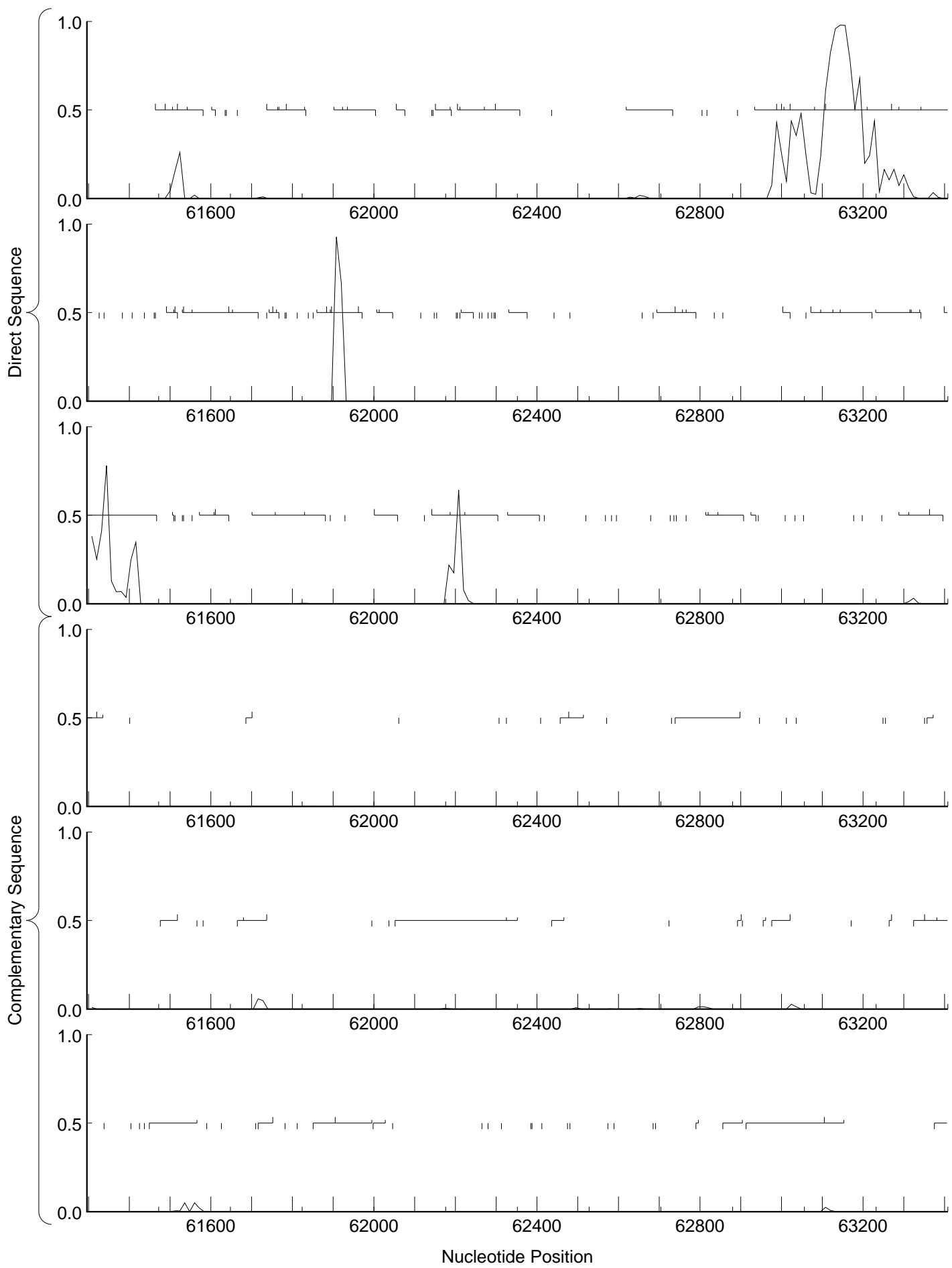
complete sequence, 74429 bp including 10-base 3' overhang (TCGAACGGCC), Cluster L1, Order 4, Window 96, Step 12, 28/37



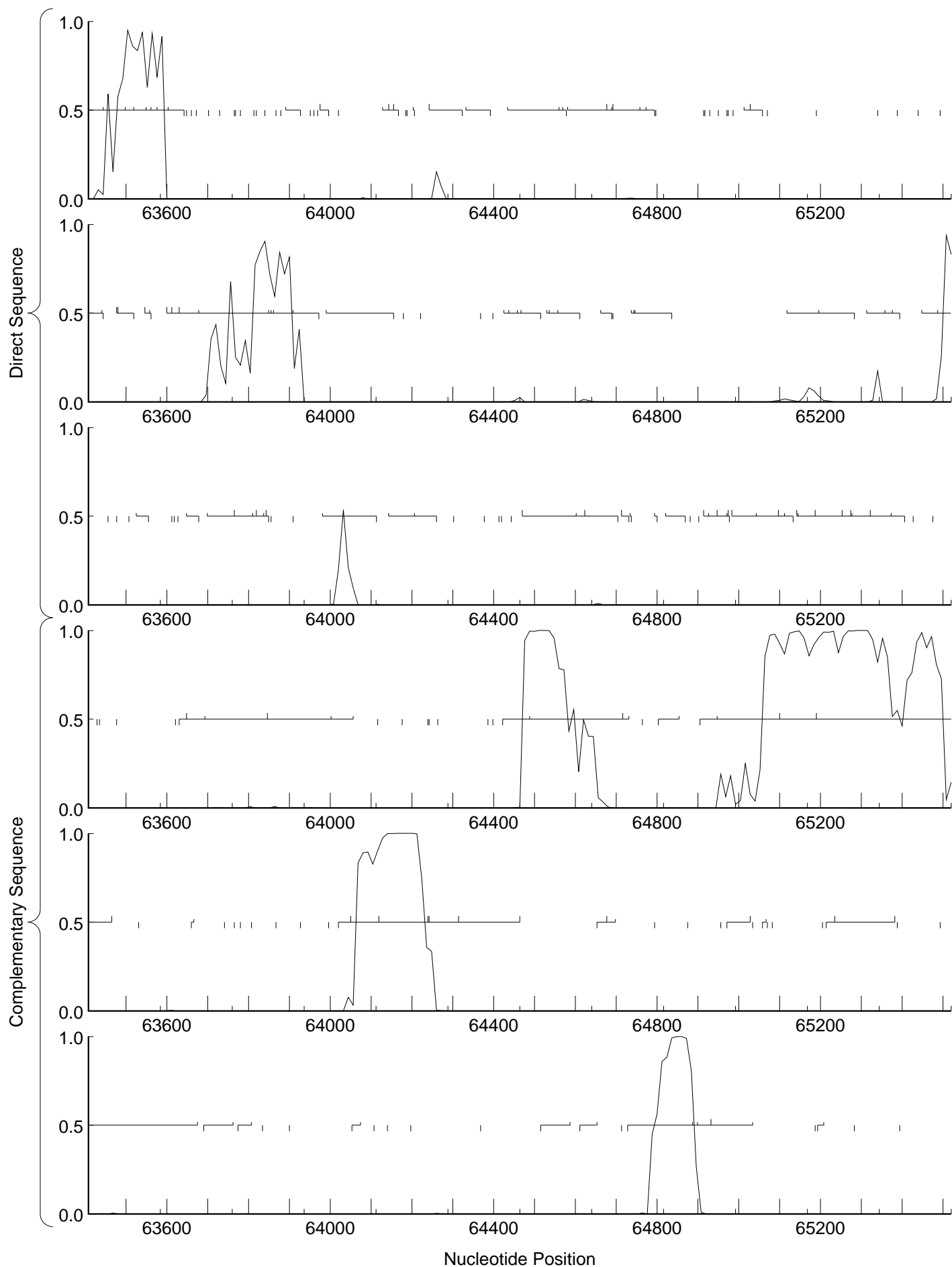


complete sequence, 74429 bp including 10-base 3' overhang (TCGAACGGCC), Cluster L1, Order 4, Window 96, Step 12, 30/37

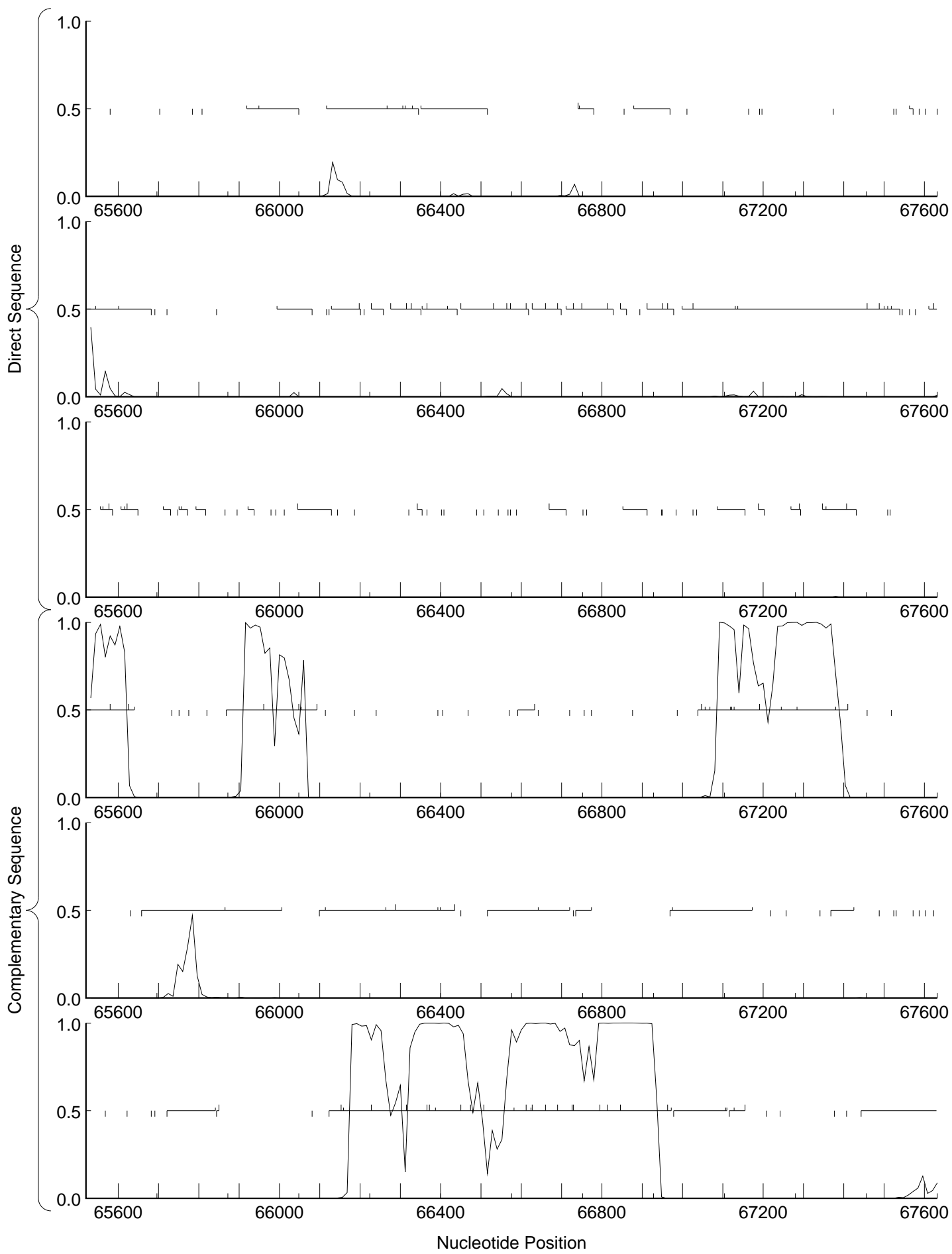


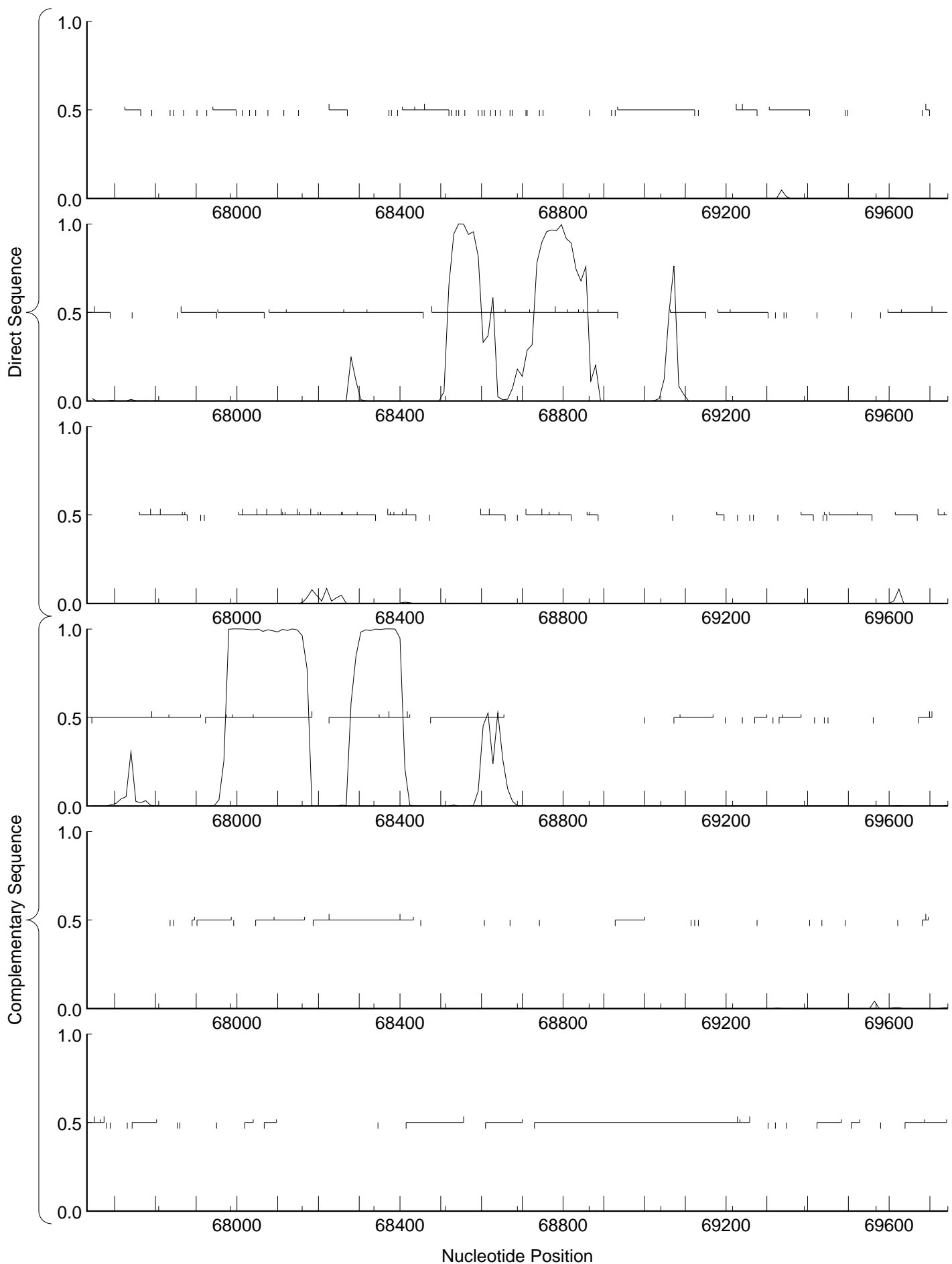


complete sequence, 74429 bp including 10-base 3' overhang (TCGAACGGCC), Cluster L1, Order 4, Window 96, Step 12, 32/37









complete sequence, 74429 bp including 10-base 3' overhang (TCGAACGGCC), Cluster L1, Order 4, Window 96, Step 12, 35/37

