

# GeneMark

Version 2.5p (09.08.06)

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## PROGRAM INFORMATION

Sequence : Mycobacterium phage Lorde complete sequence, 53852 bp including 10-base 3' overhang (CCGATG  
Analysis Date : 5/26/18 at 8:07:36  
Pages : 27  
Sequence Length : 53852 bp  
GC Content : 61.20%

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,

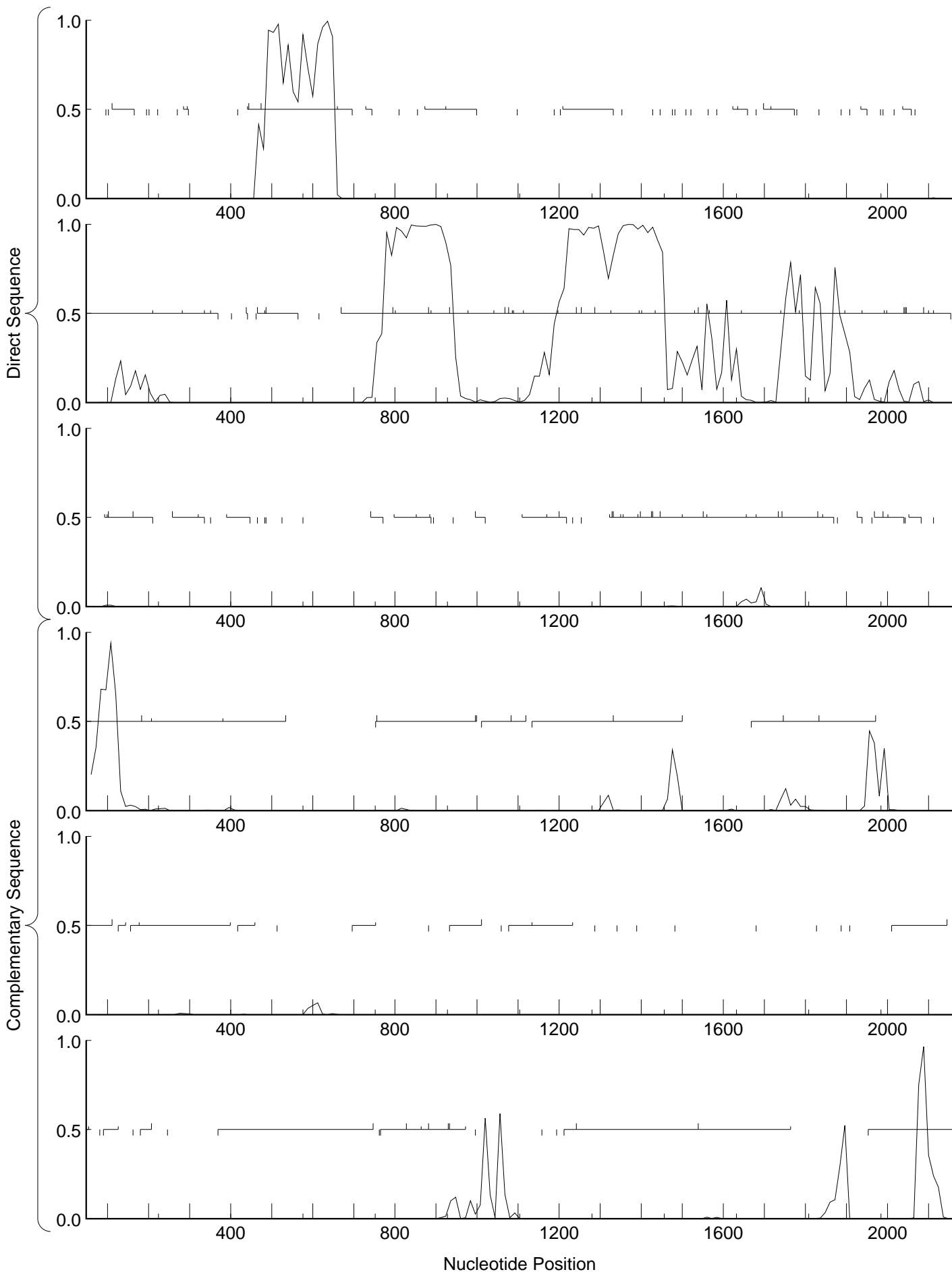
## Matrix notes & comments

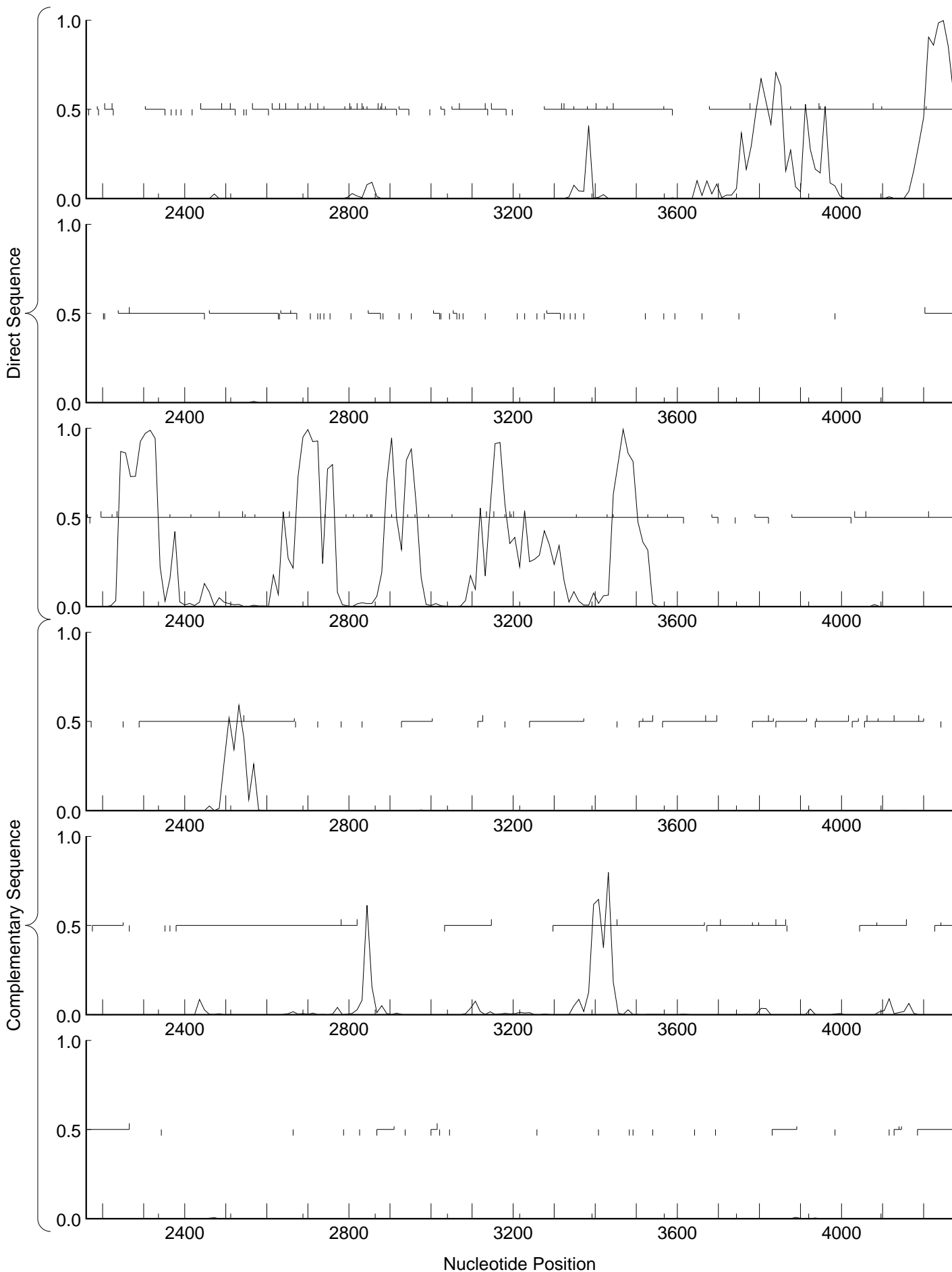
Training set derived by GeneMarkS, 4.27 September 2014  
Tue Sep 23 15:14:37 2014

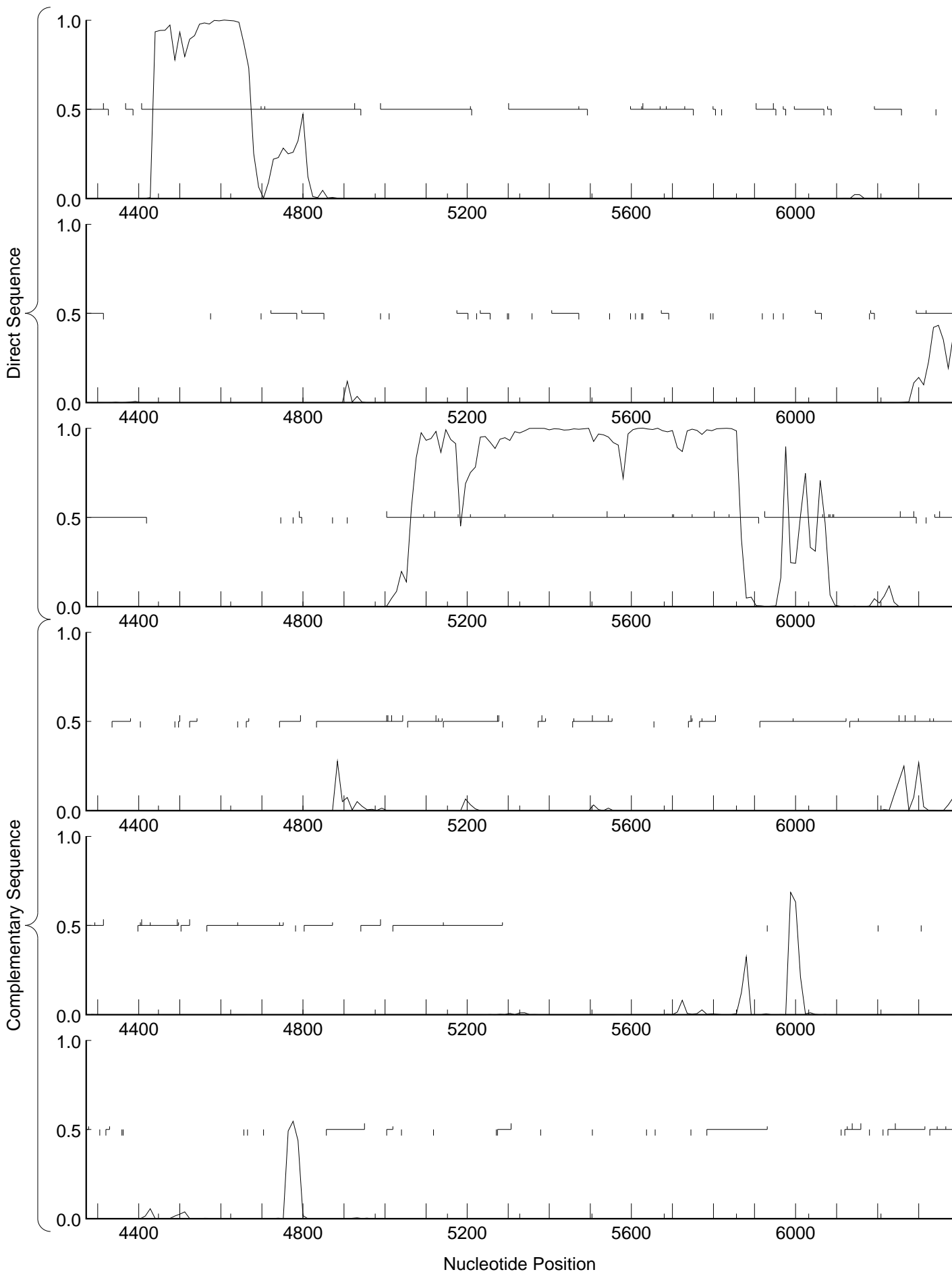
## MATRIX INFORMATION

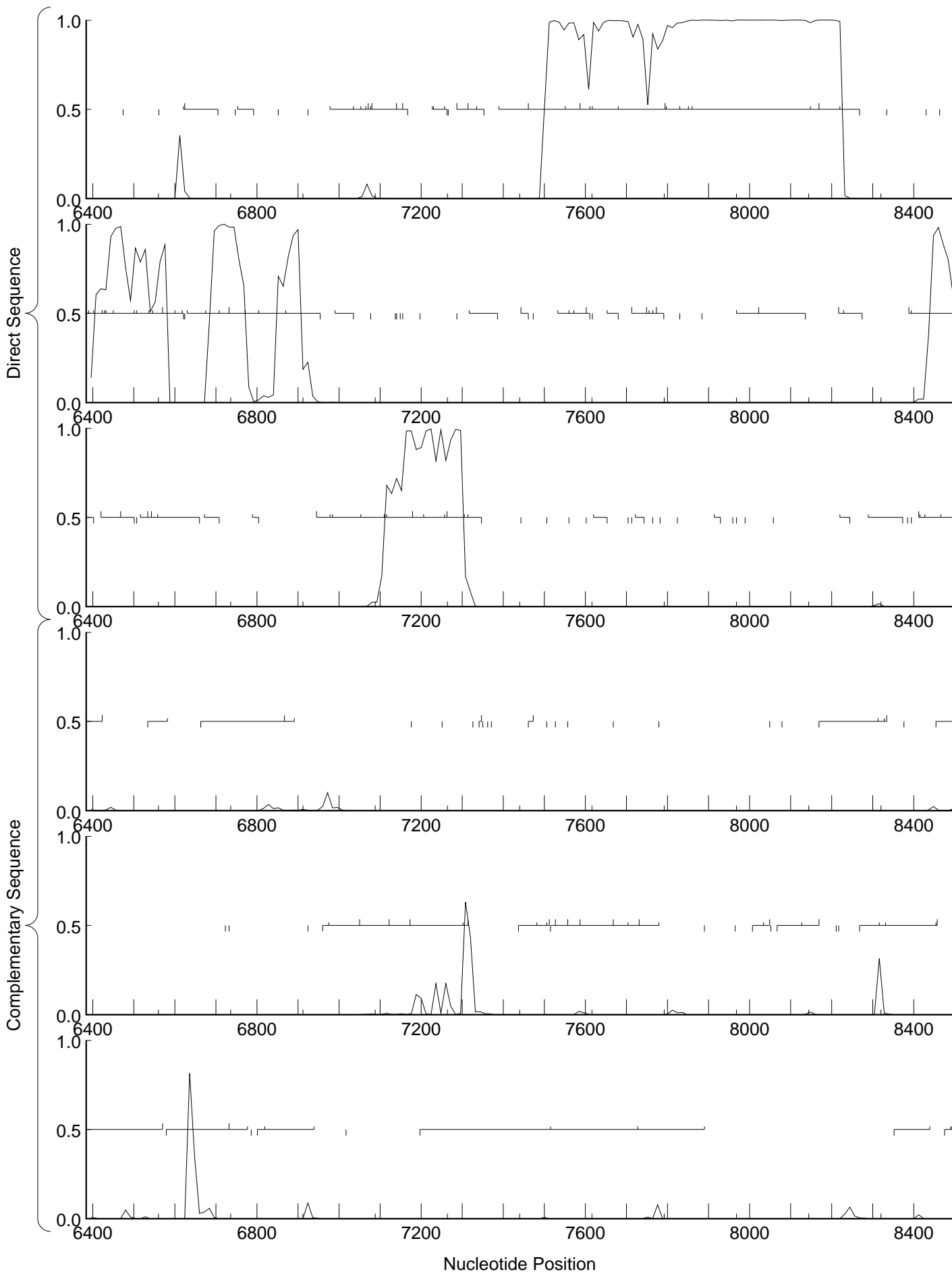
Matrix : Mycobacterium\_tuberculosis\_H37Rv  
Author : -  
Order : 4

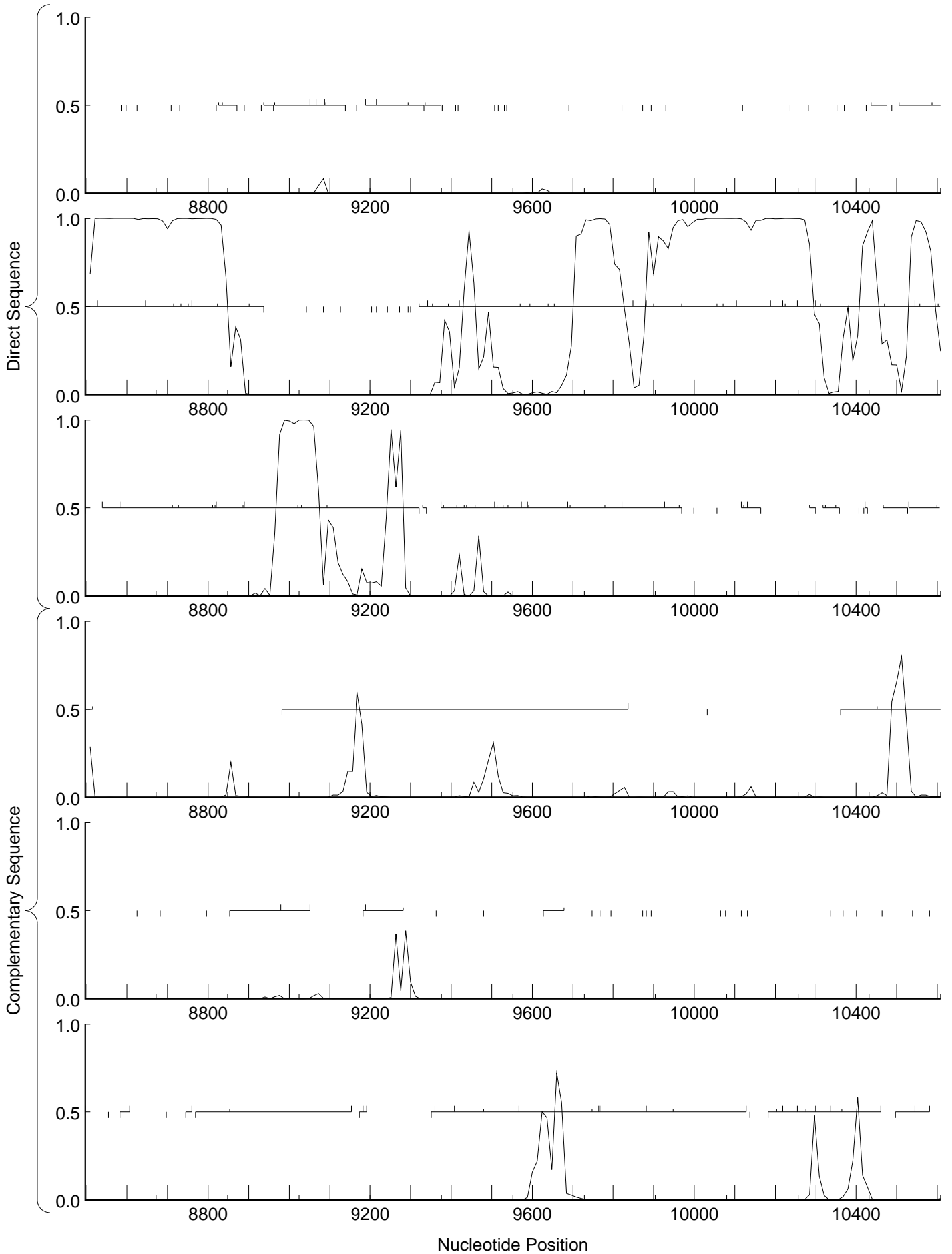
Send questions / comments to:  
Dr. M. Borodovsky  
Georgia Institute of Technology  
School of Biology  
Atlanta, GA 30332-0230

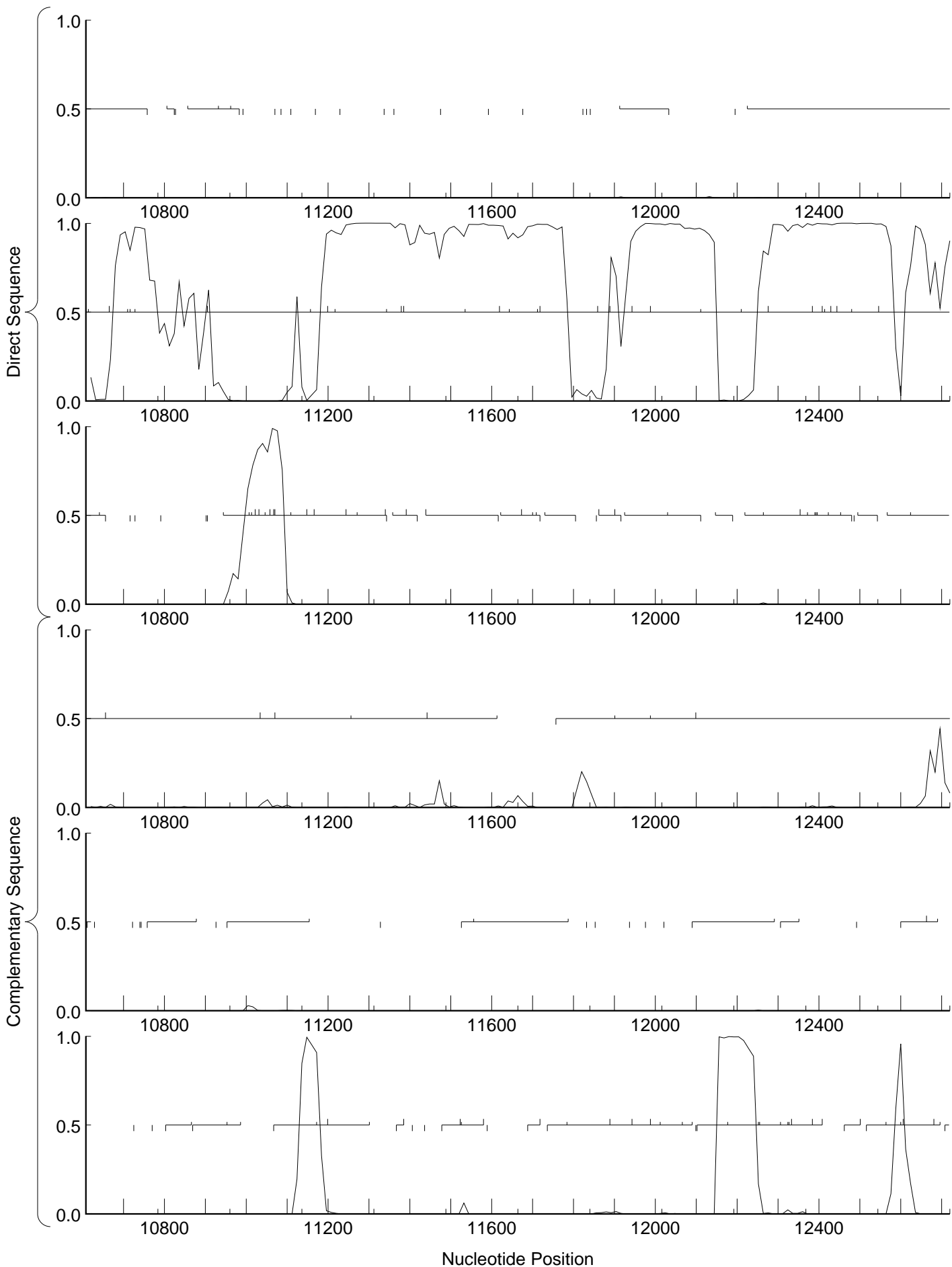


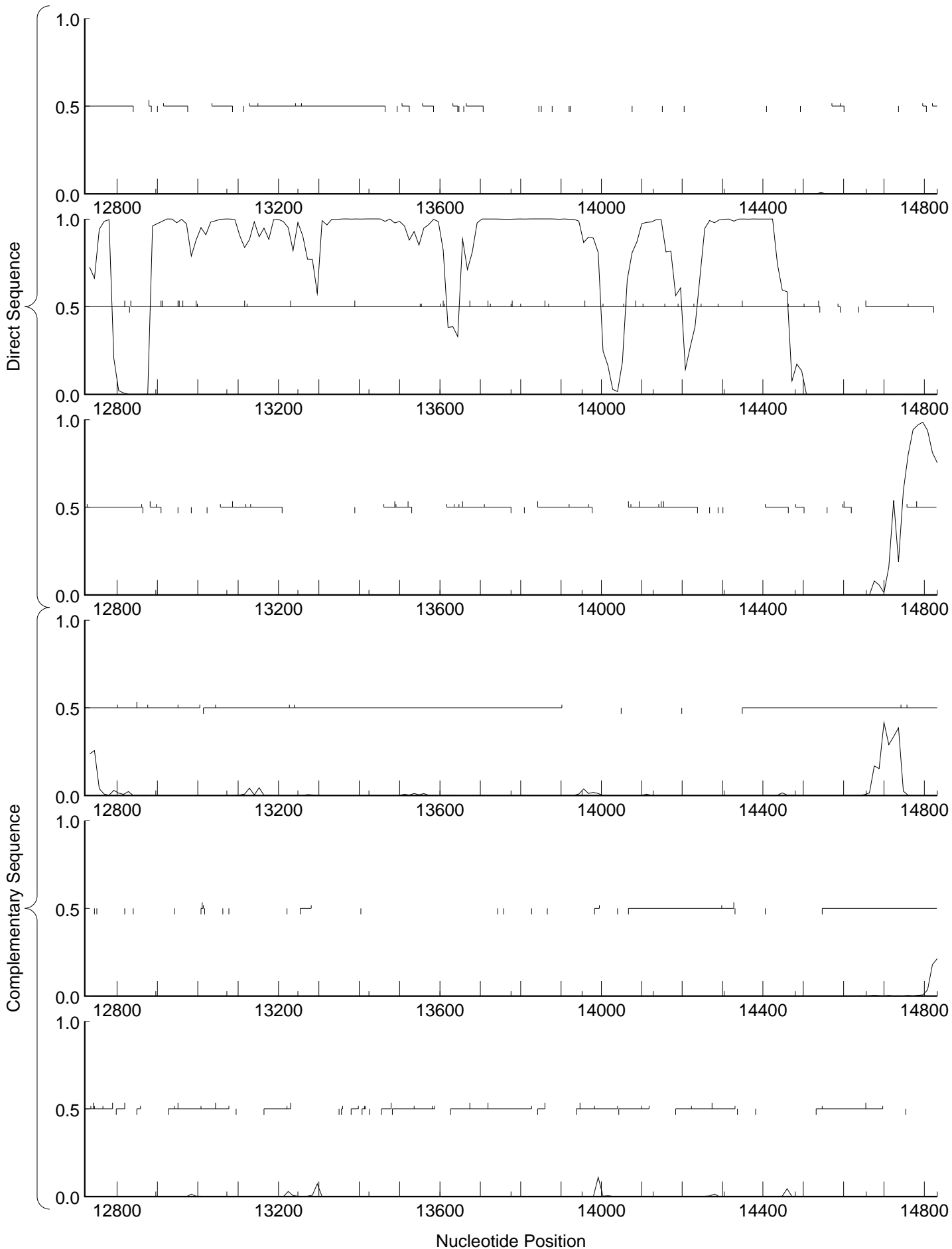




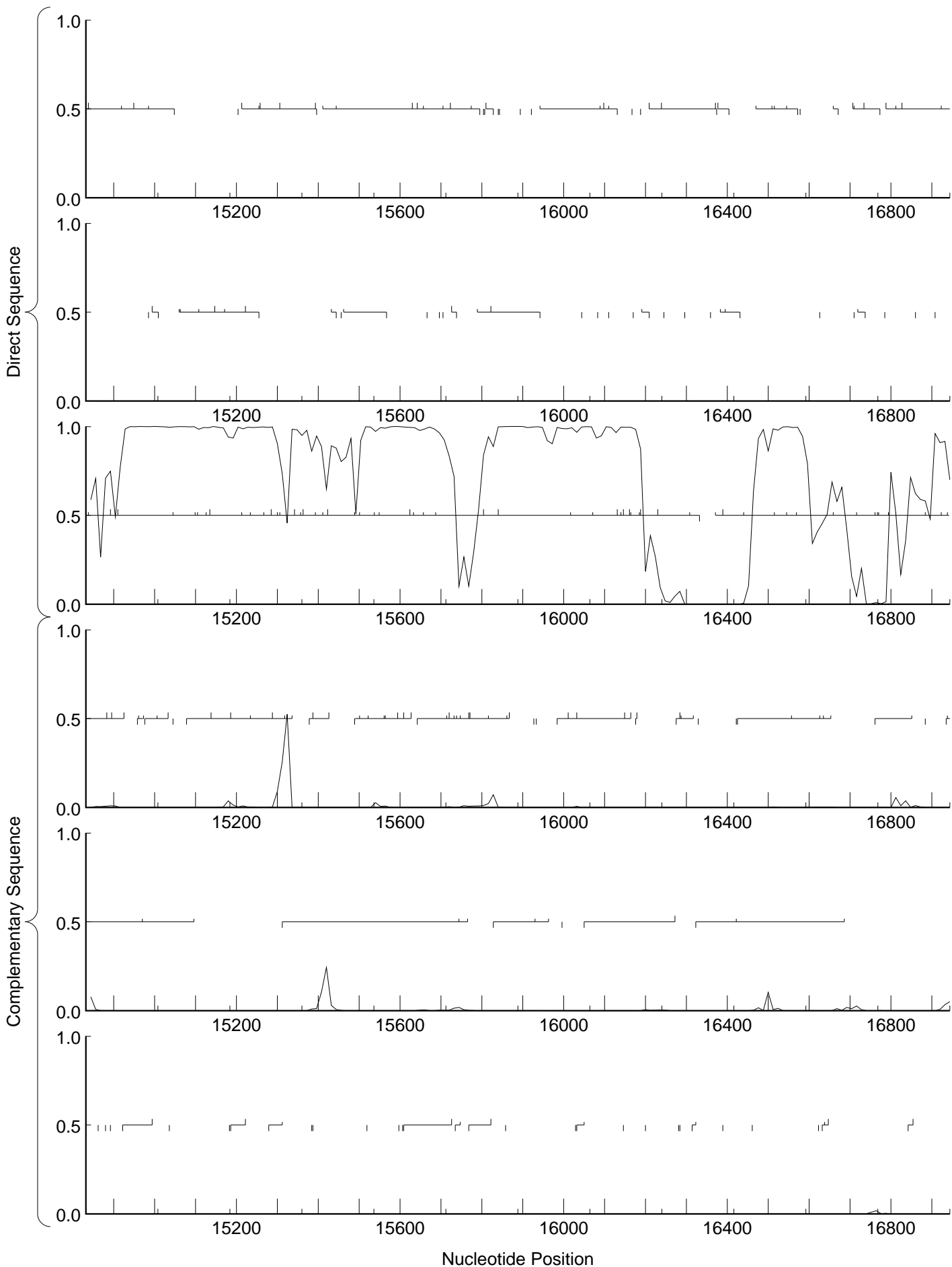


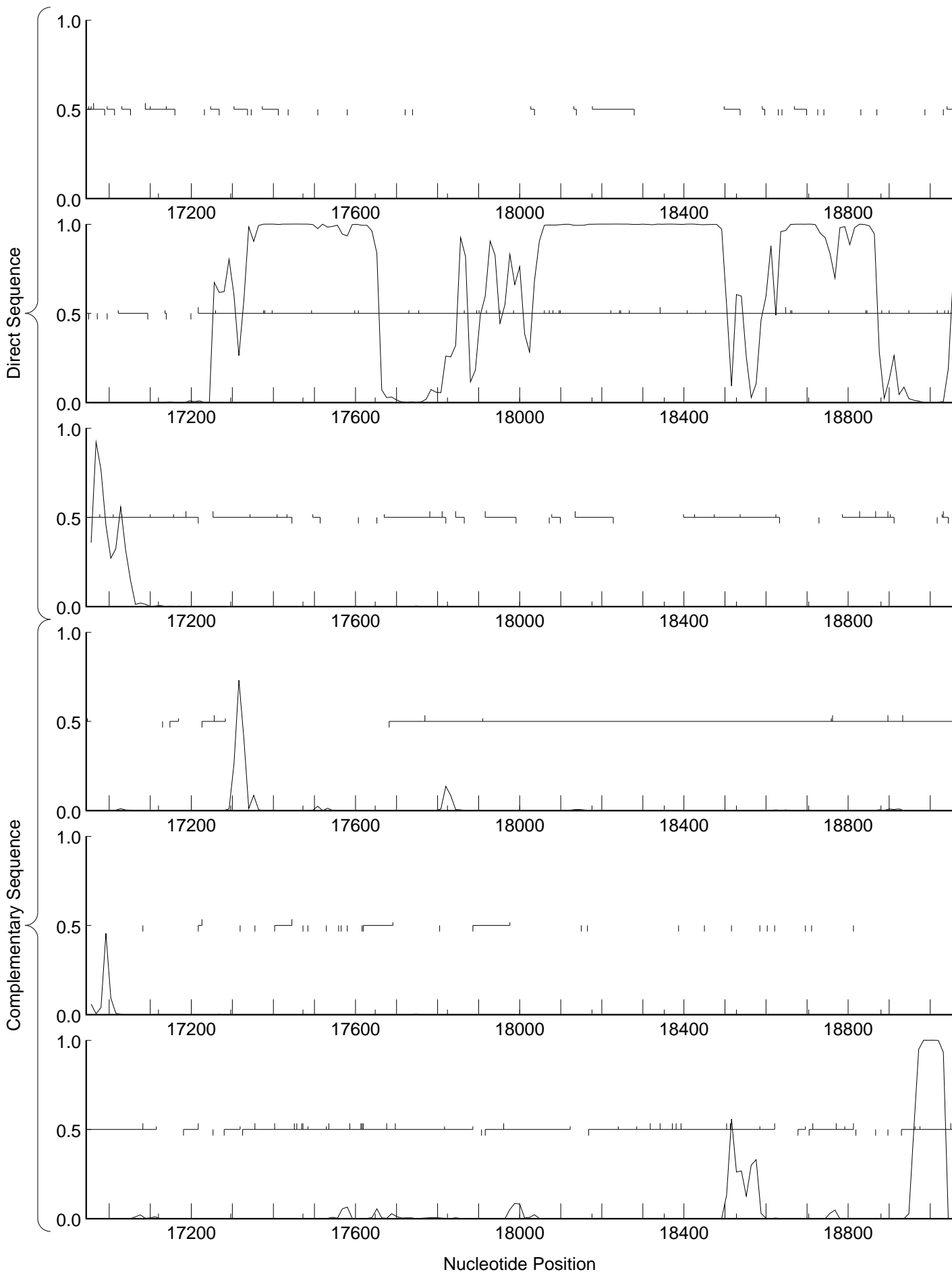




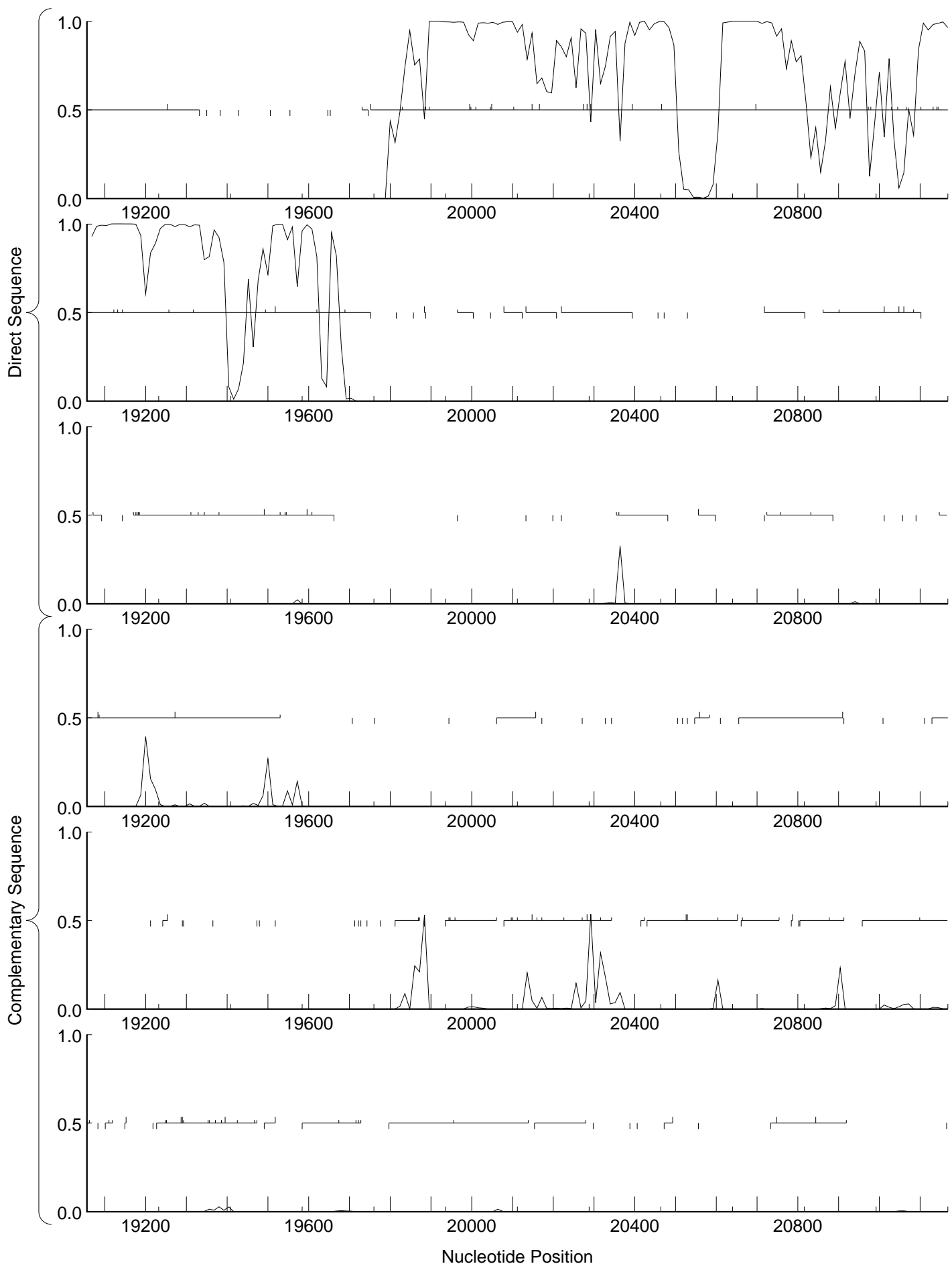


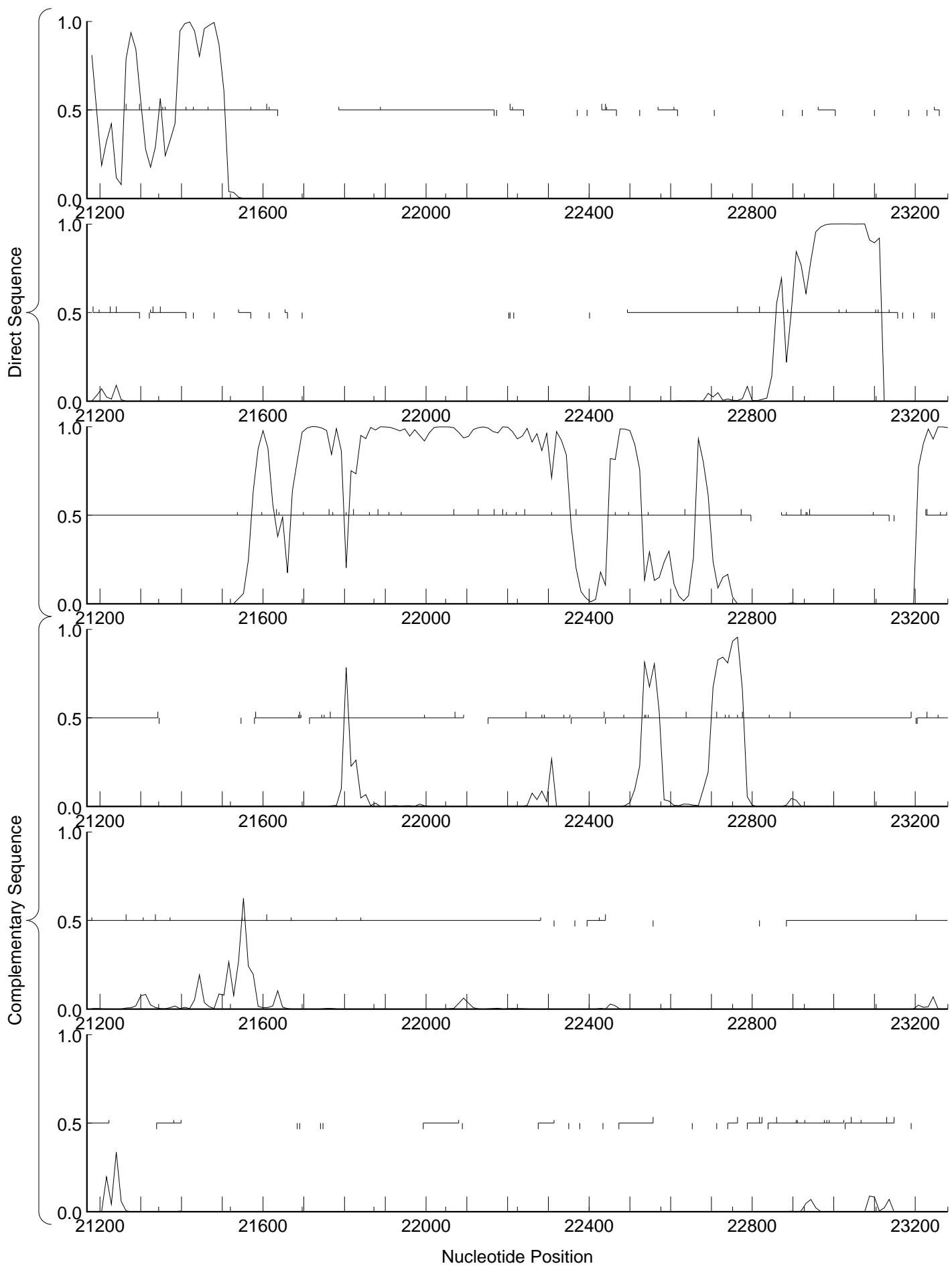


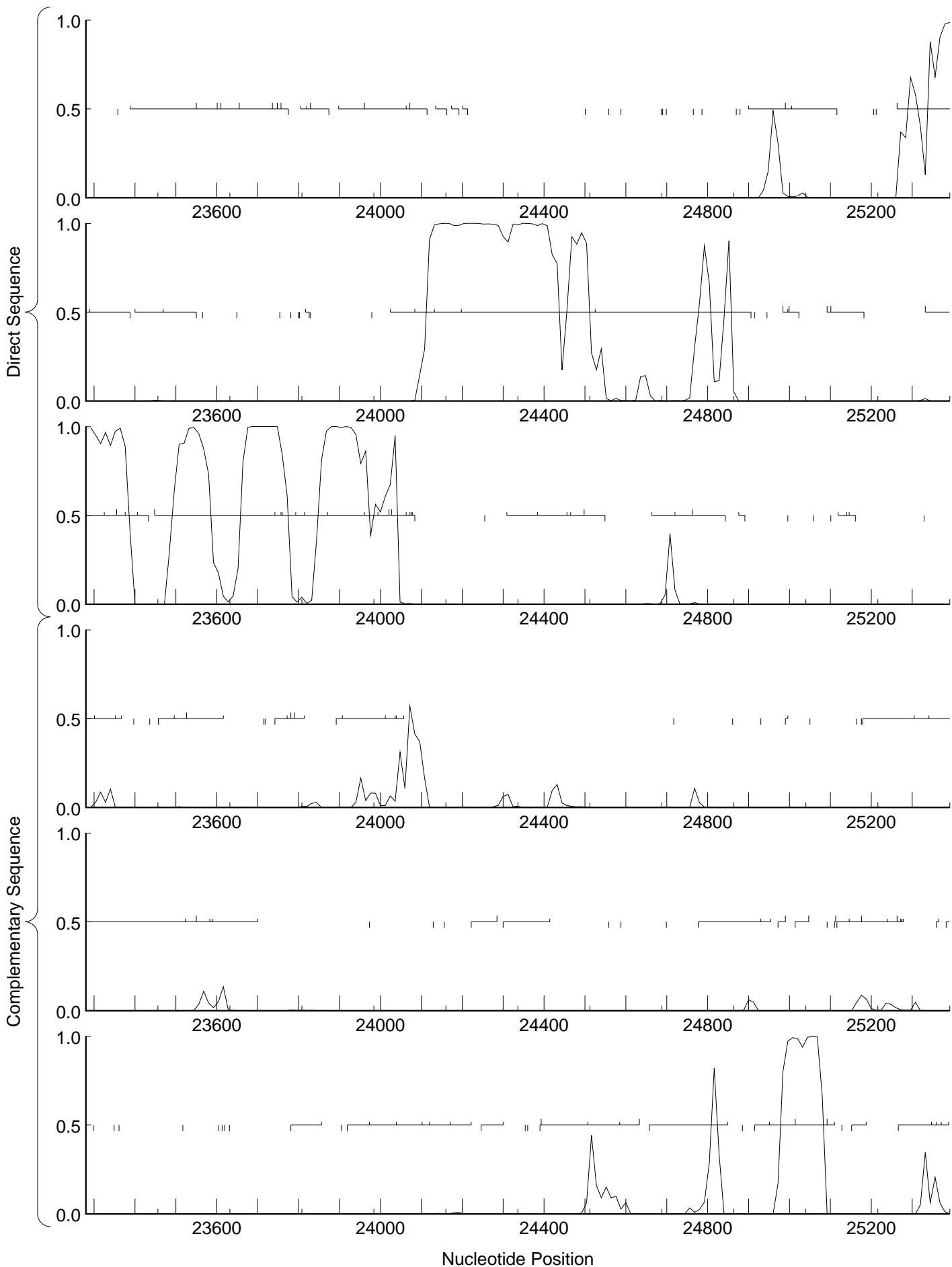


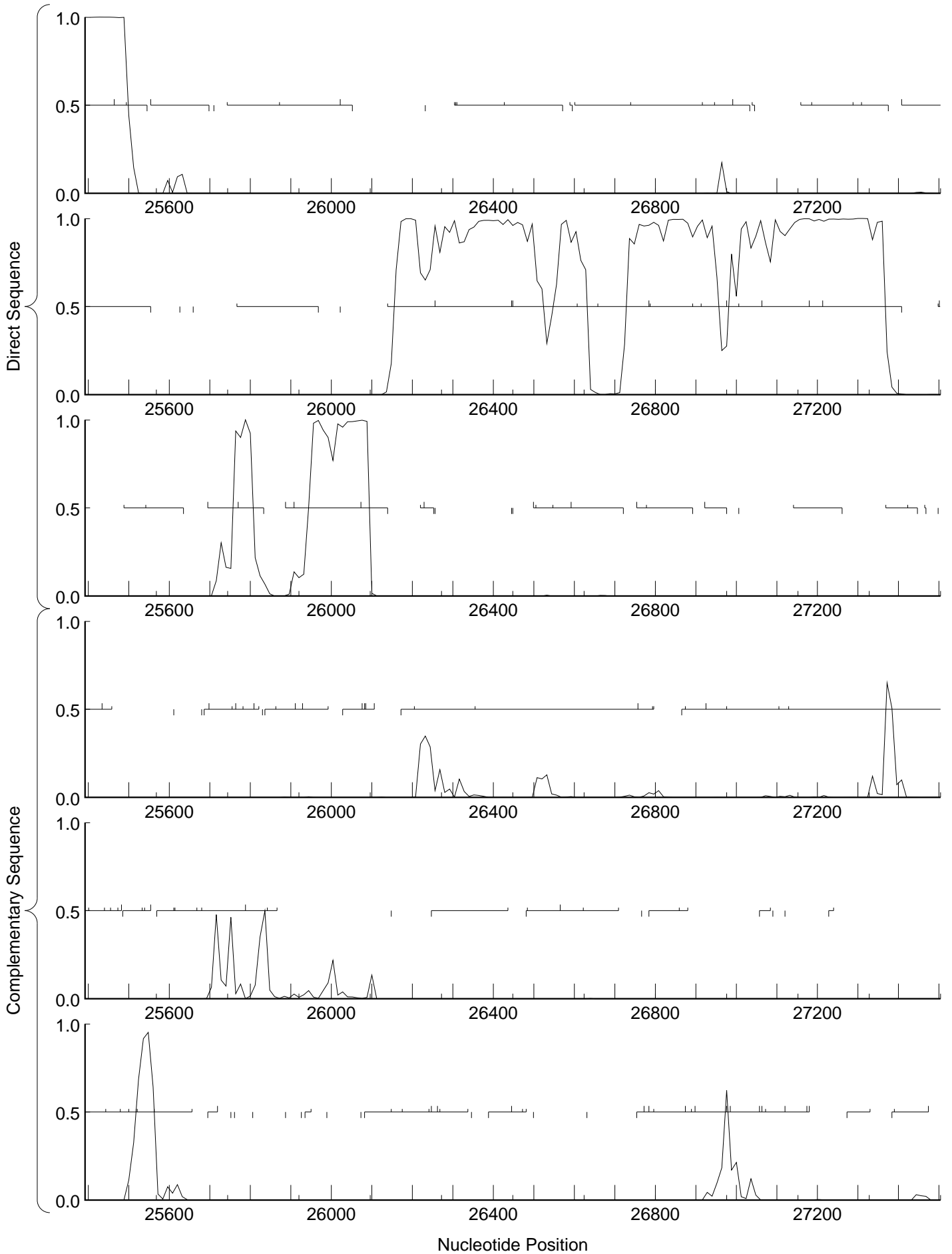


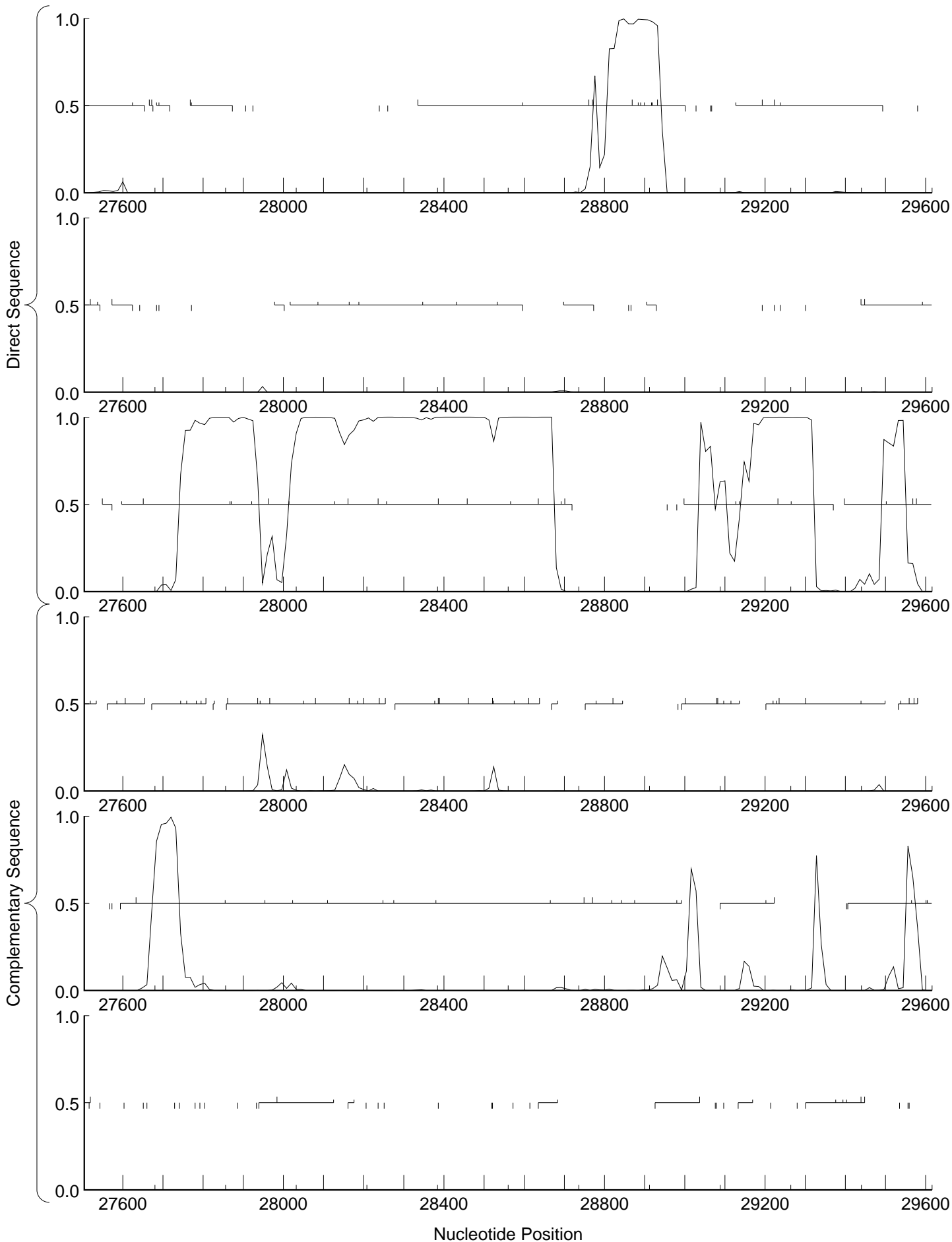
complete sequence, 53852 bp including 10-base 3' overhang (CCGATGGCAT), Cluster F1, Order 4, Window 96, Step 12, 11/27

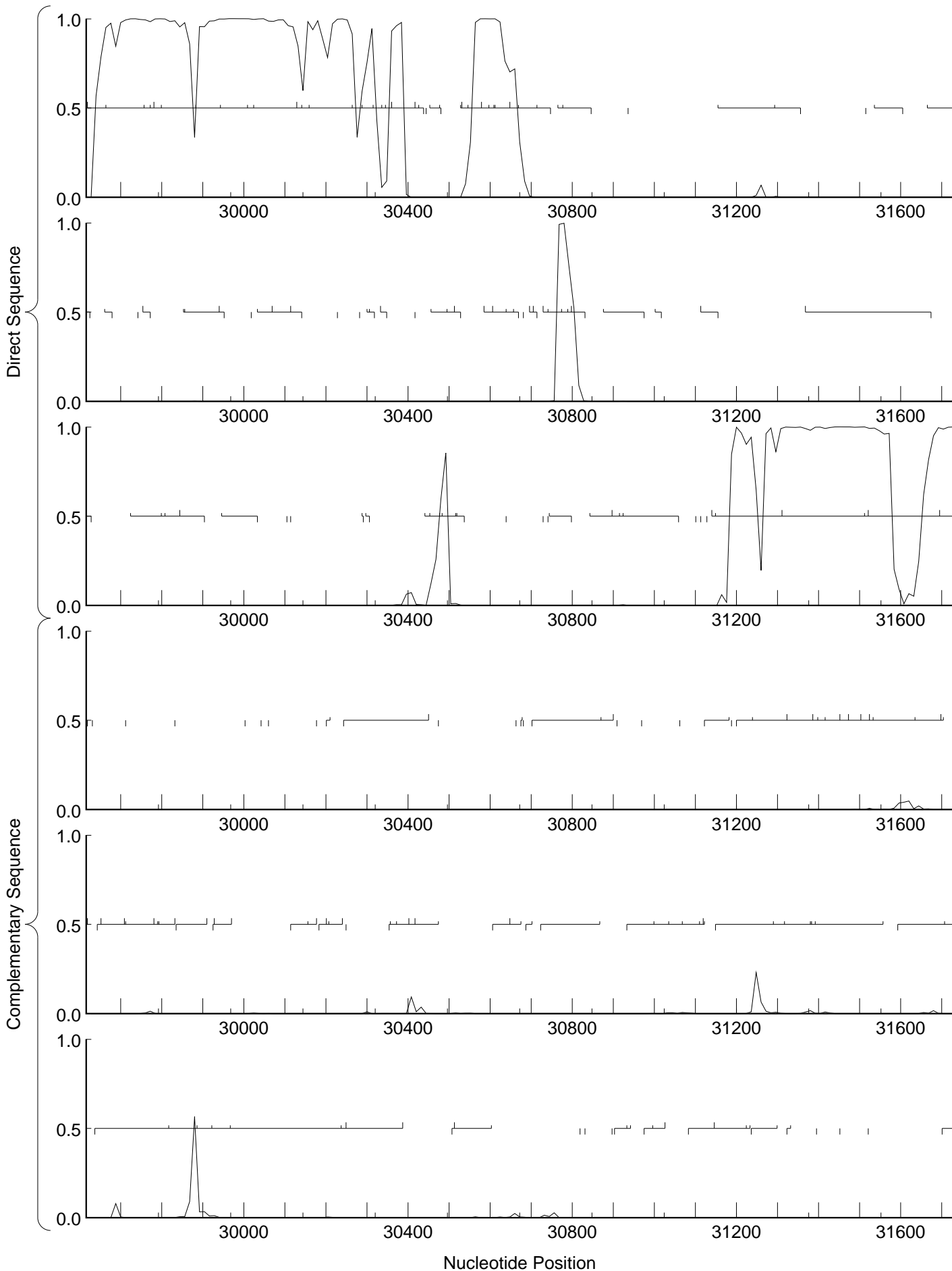




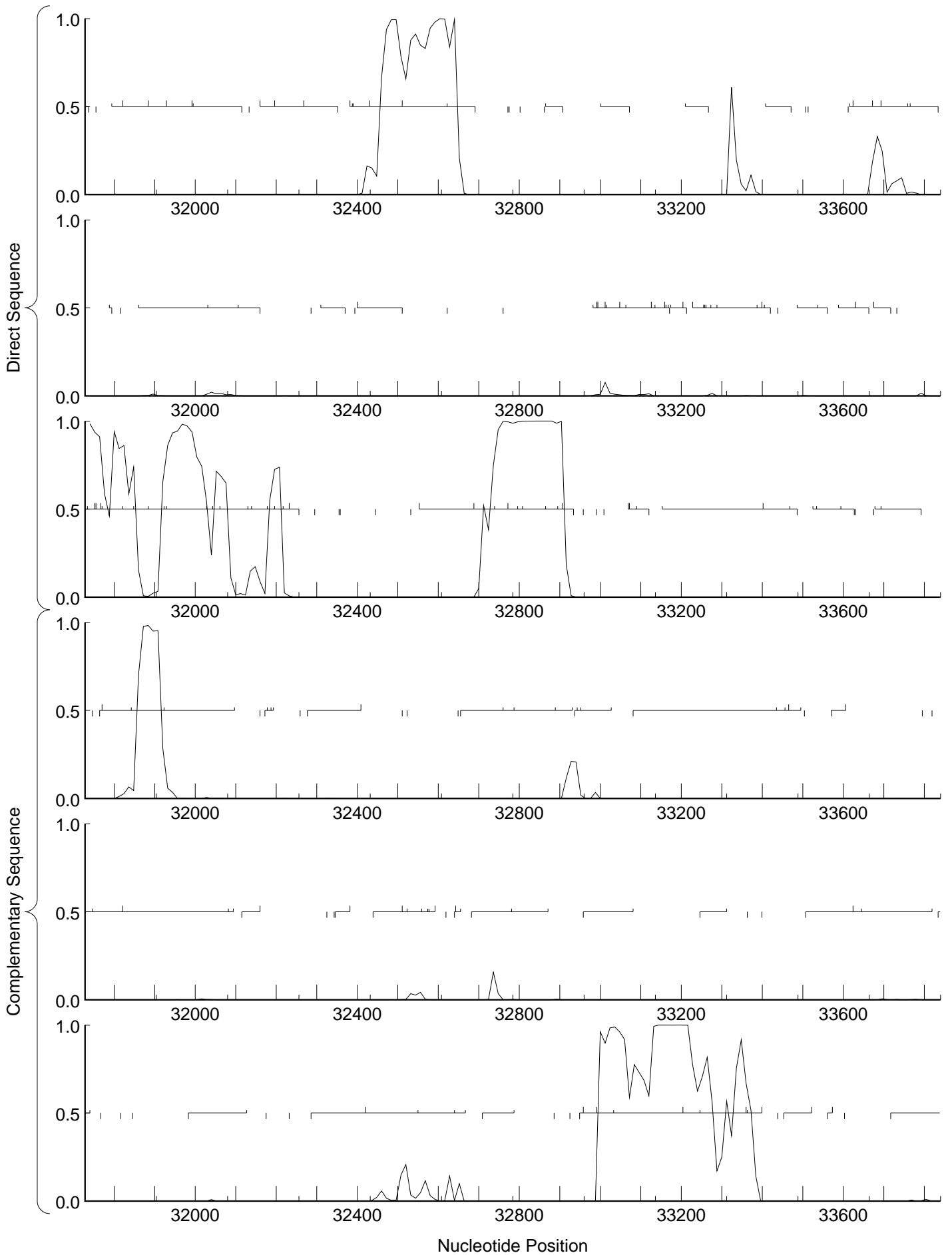


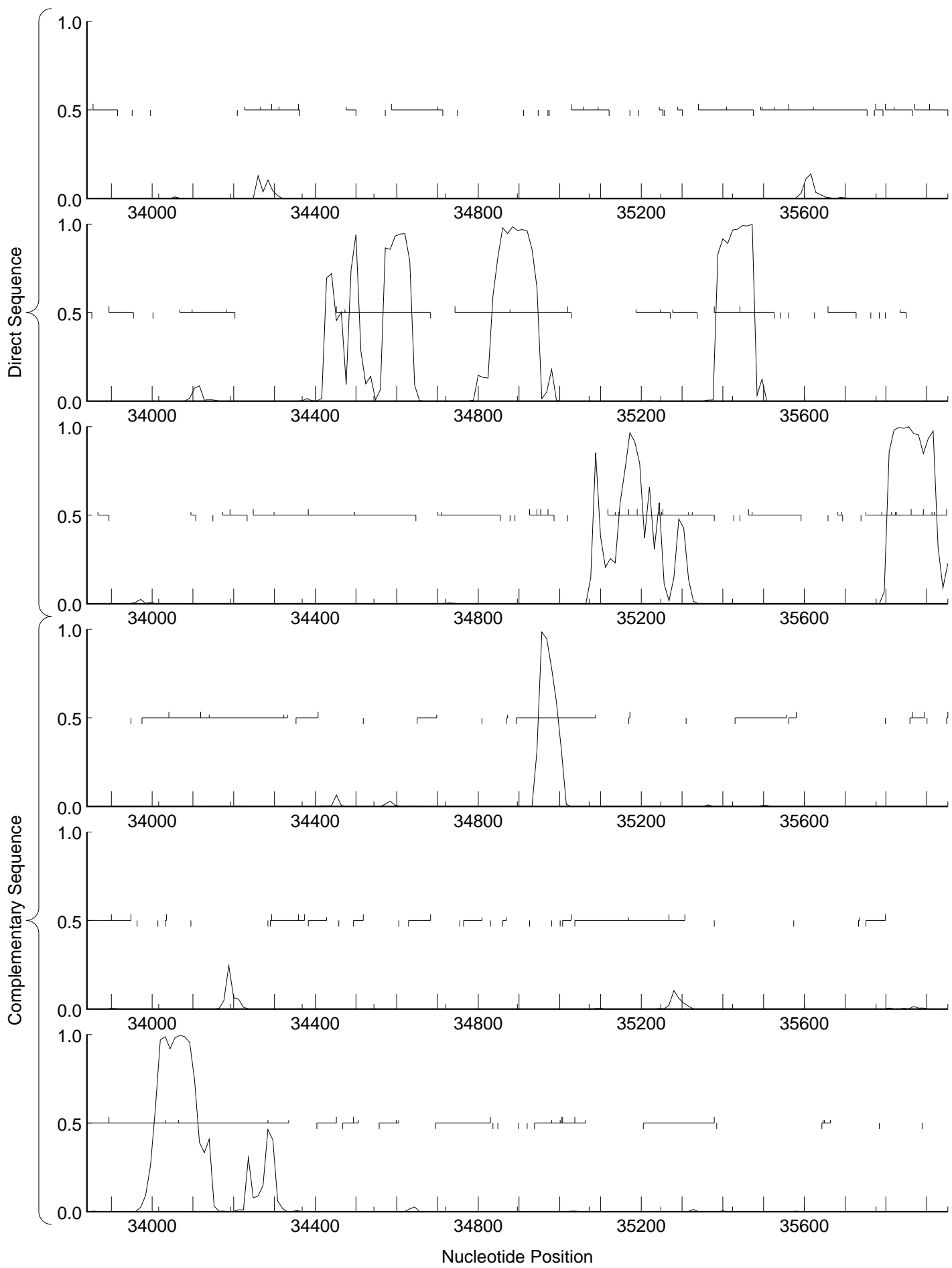


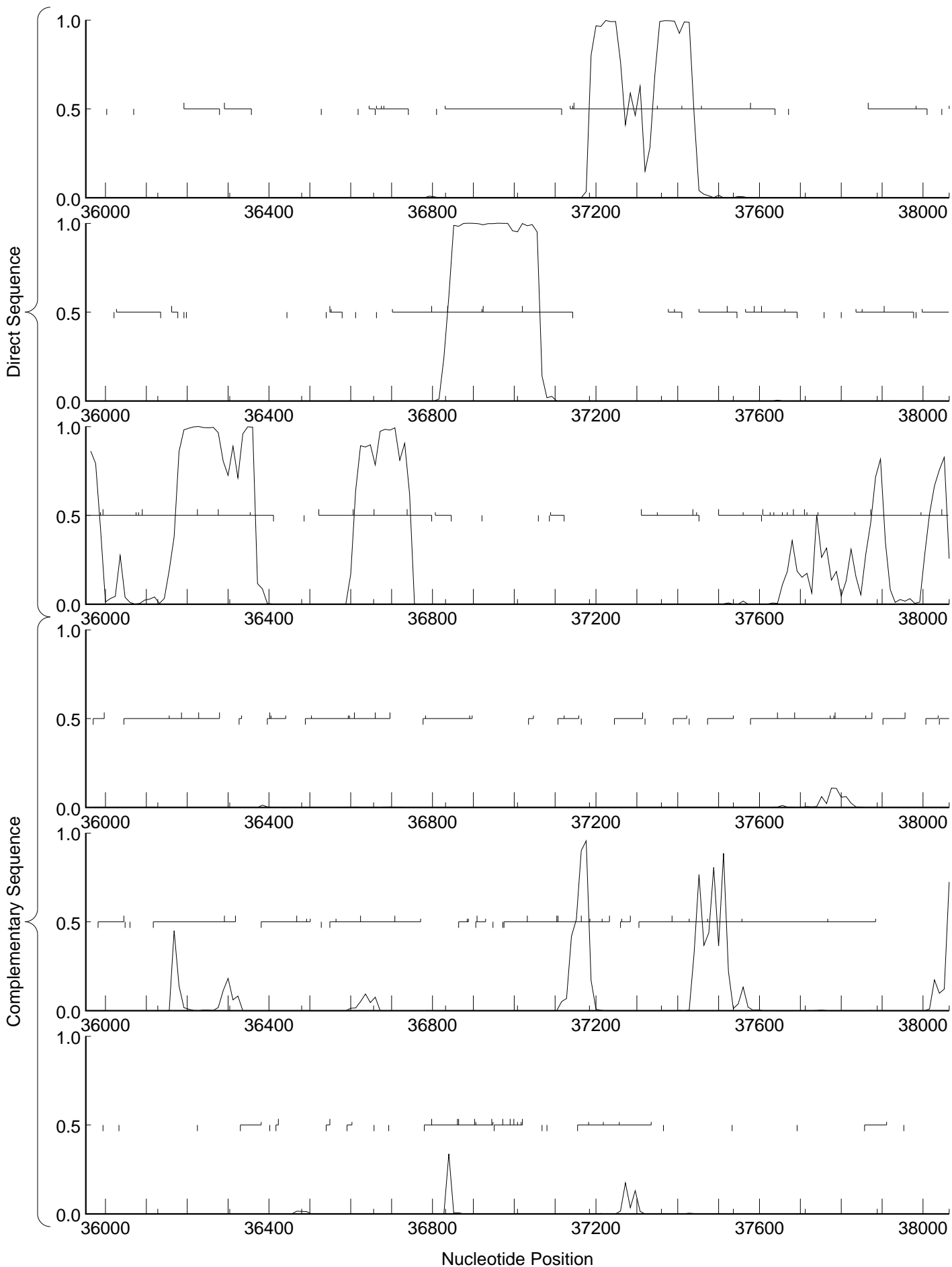


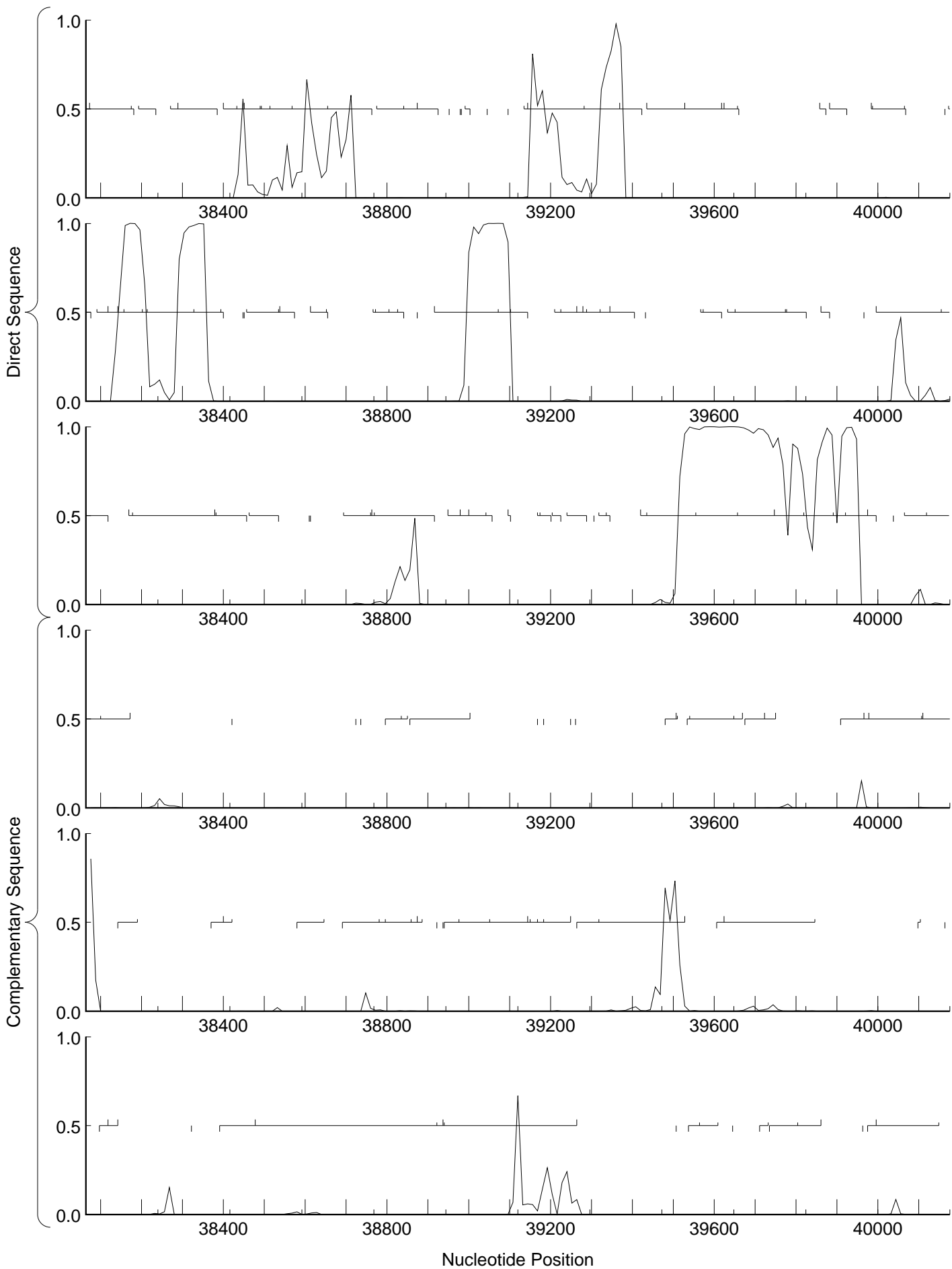


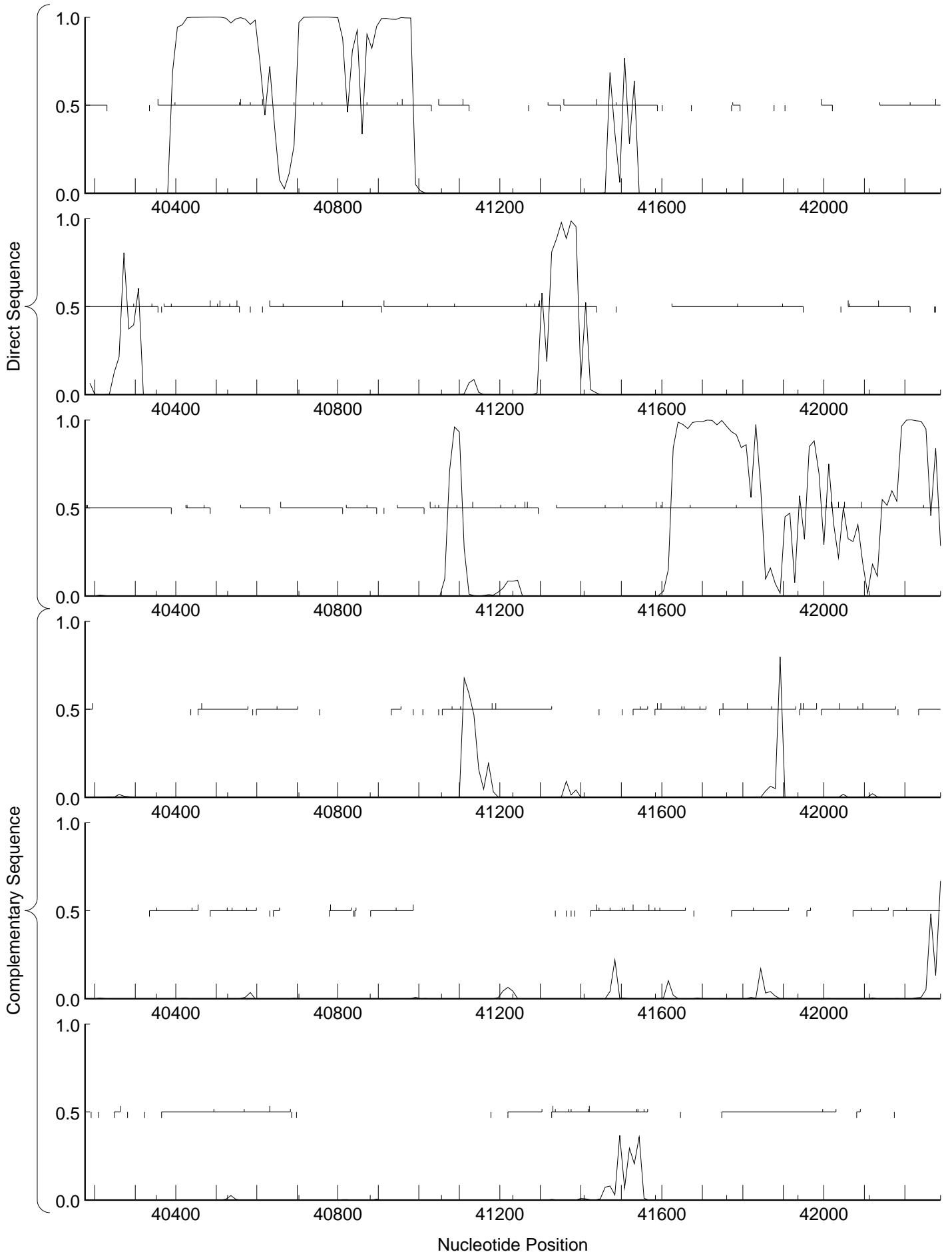












complete sequence, 53852 bp including 10-base 3' overhang (CCGATGGCAT), Cluster F1, Order 4, Window 96, Step 12, 22/27

