

GeneMark

Version 2.5p (09.08.06)

Copyright 1993 - M. Borodovsky, J. McIninch

PROGRAM INFORMATION

Sequence : Mycobacterium phage DismalStressor complete sequence, 58129 bp including 10-base 3' overhang
Analysis Date : 5/27/18 at 11:42:27
Pages : 29
Sequence Length : 58129 bp
GC Content : 68.25%

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,

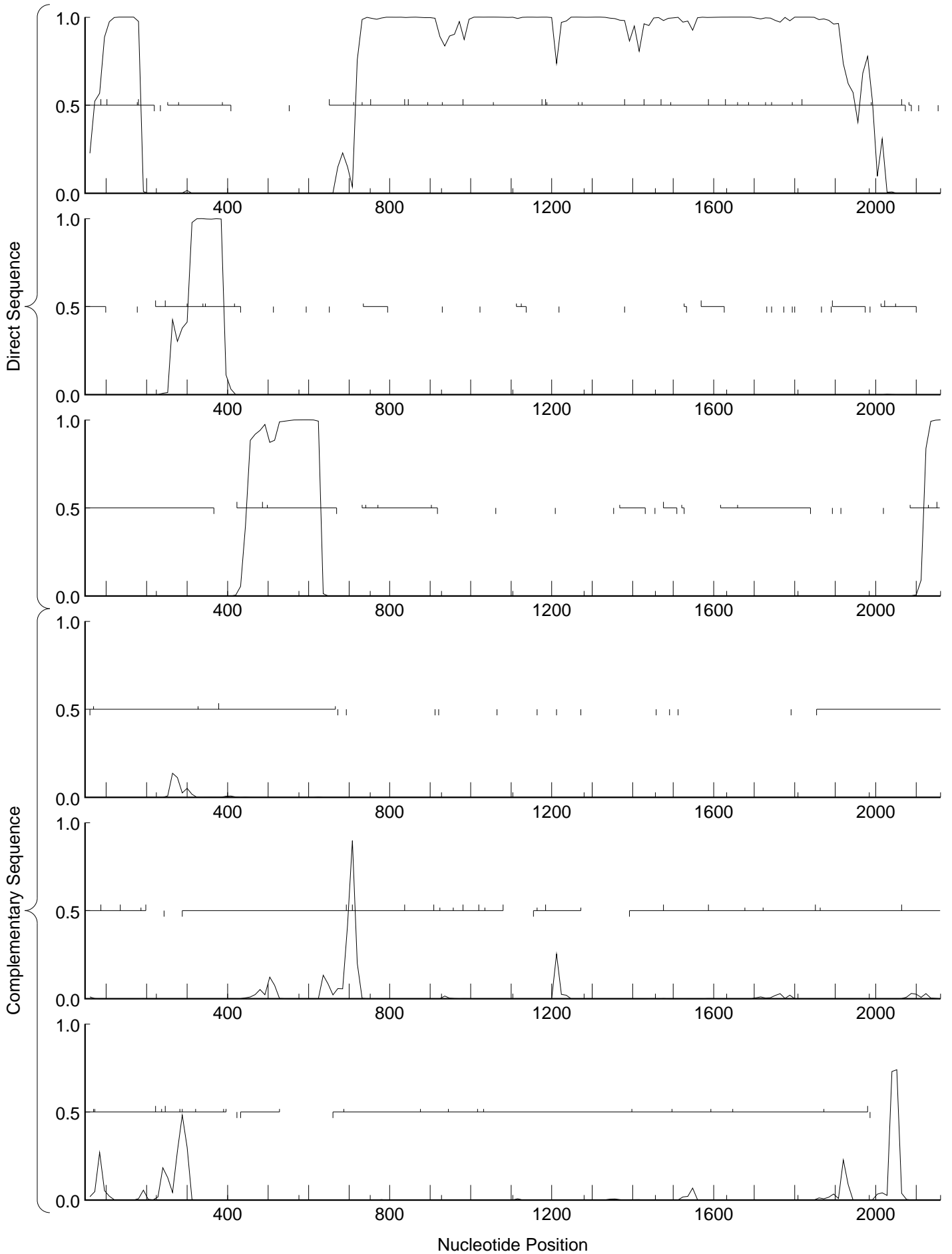
Matrix notes & comments

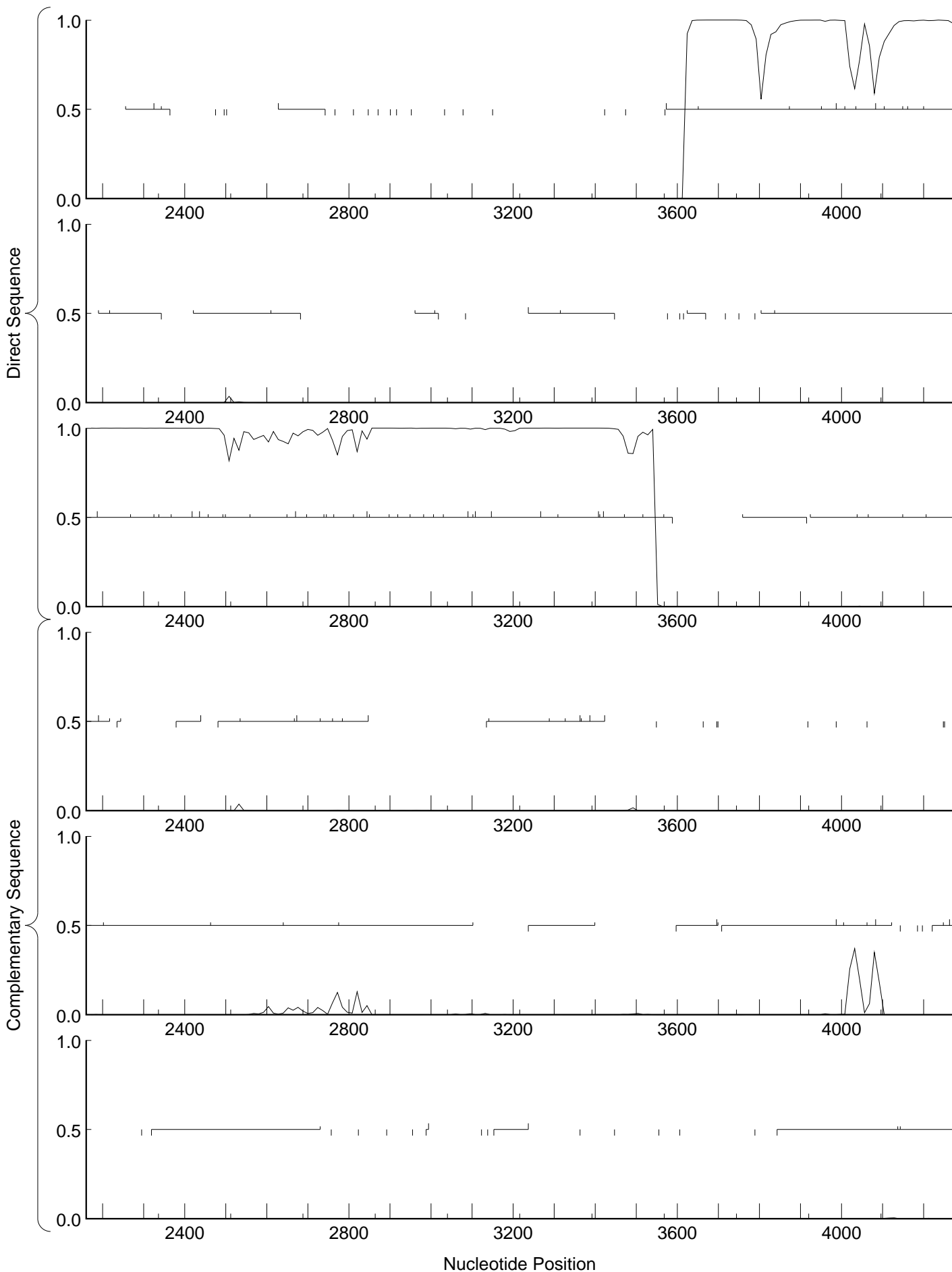
Training set derived by GeneMarkS, 4.27 September 2014
Tue Sep 23 15:14:37 2014

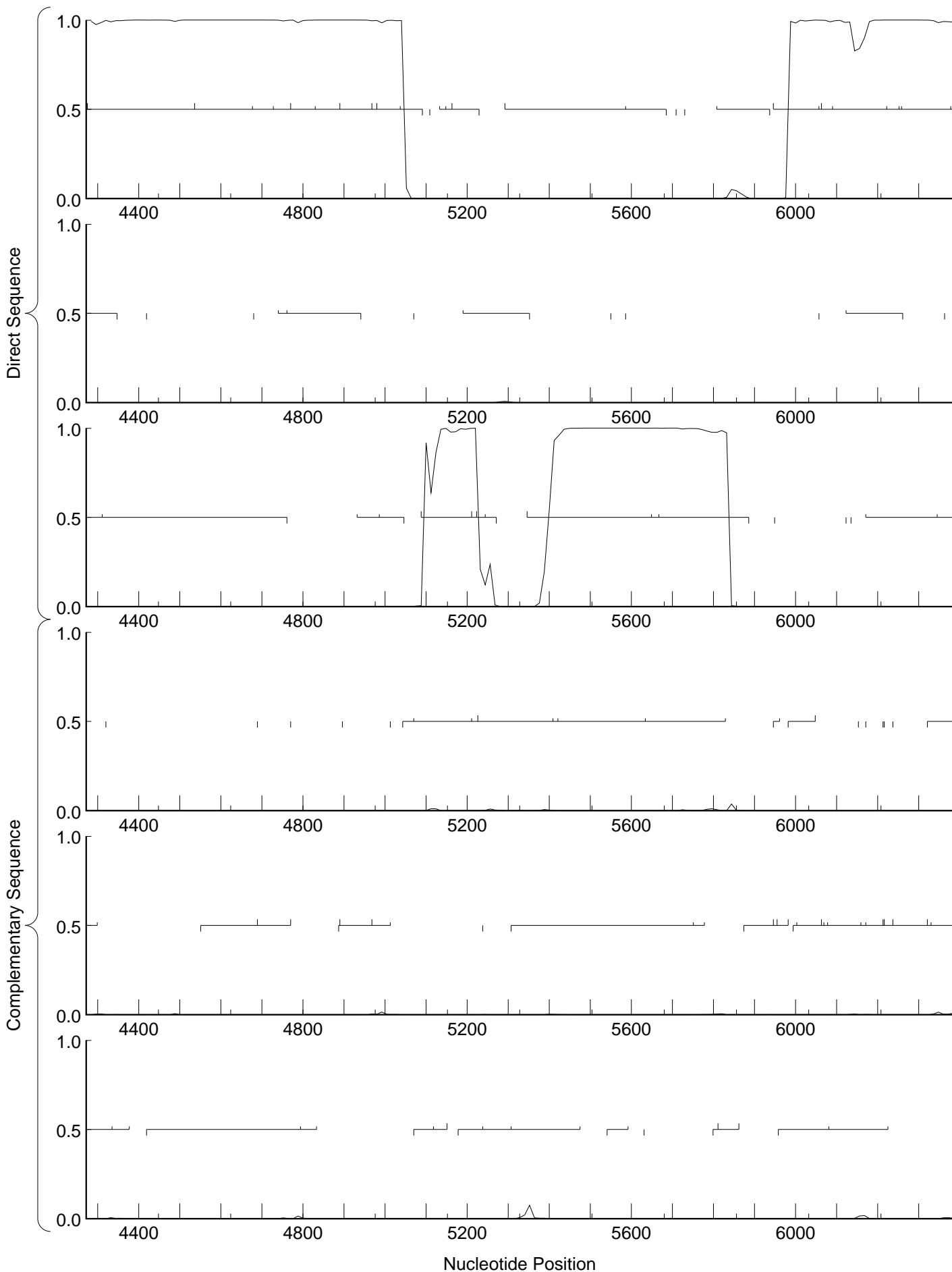
MATRIX INFORMATION

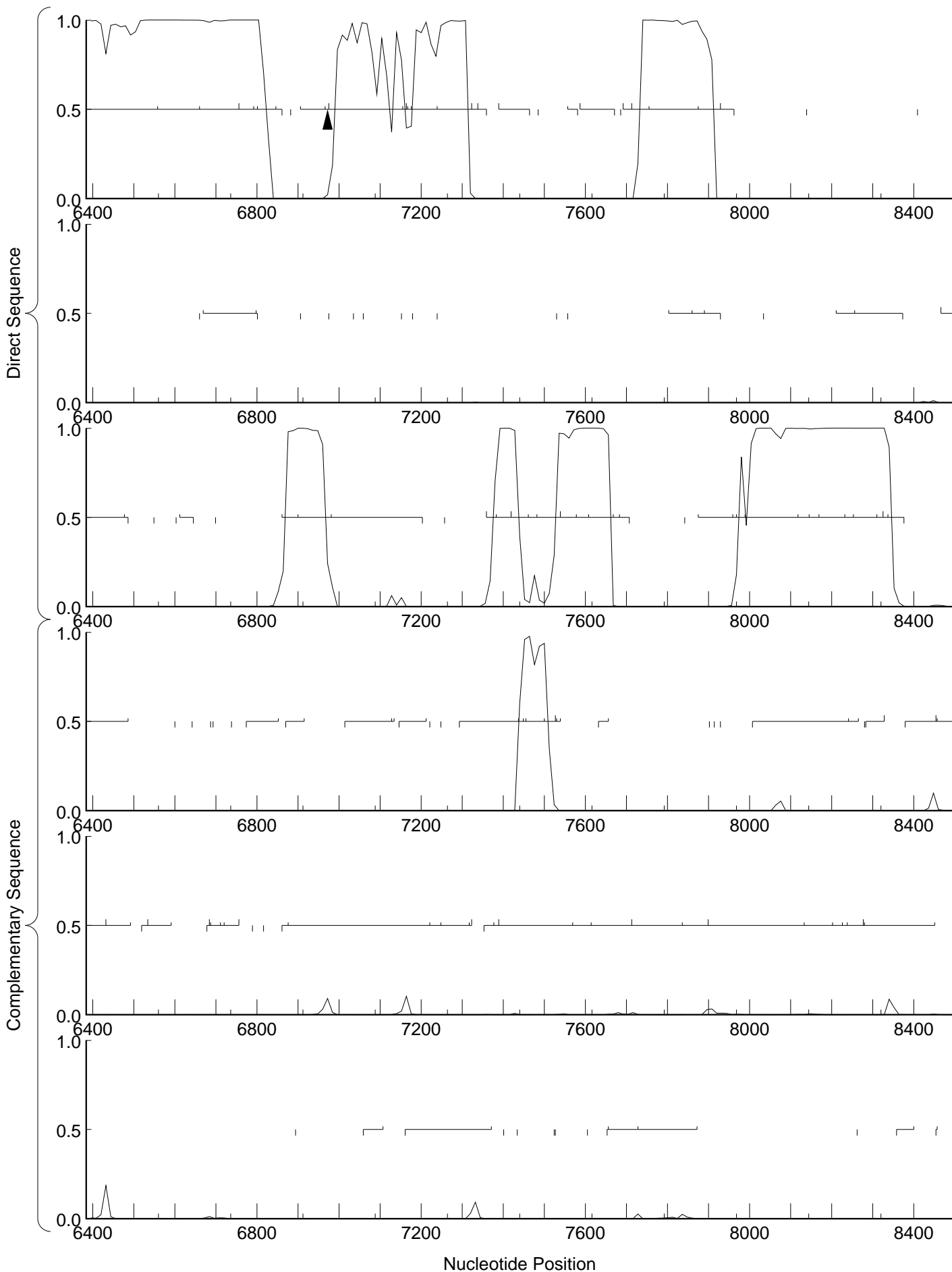
Matrix : Mycobacterium_tuberculosis_H37Rv
Author : -
Order : 4

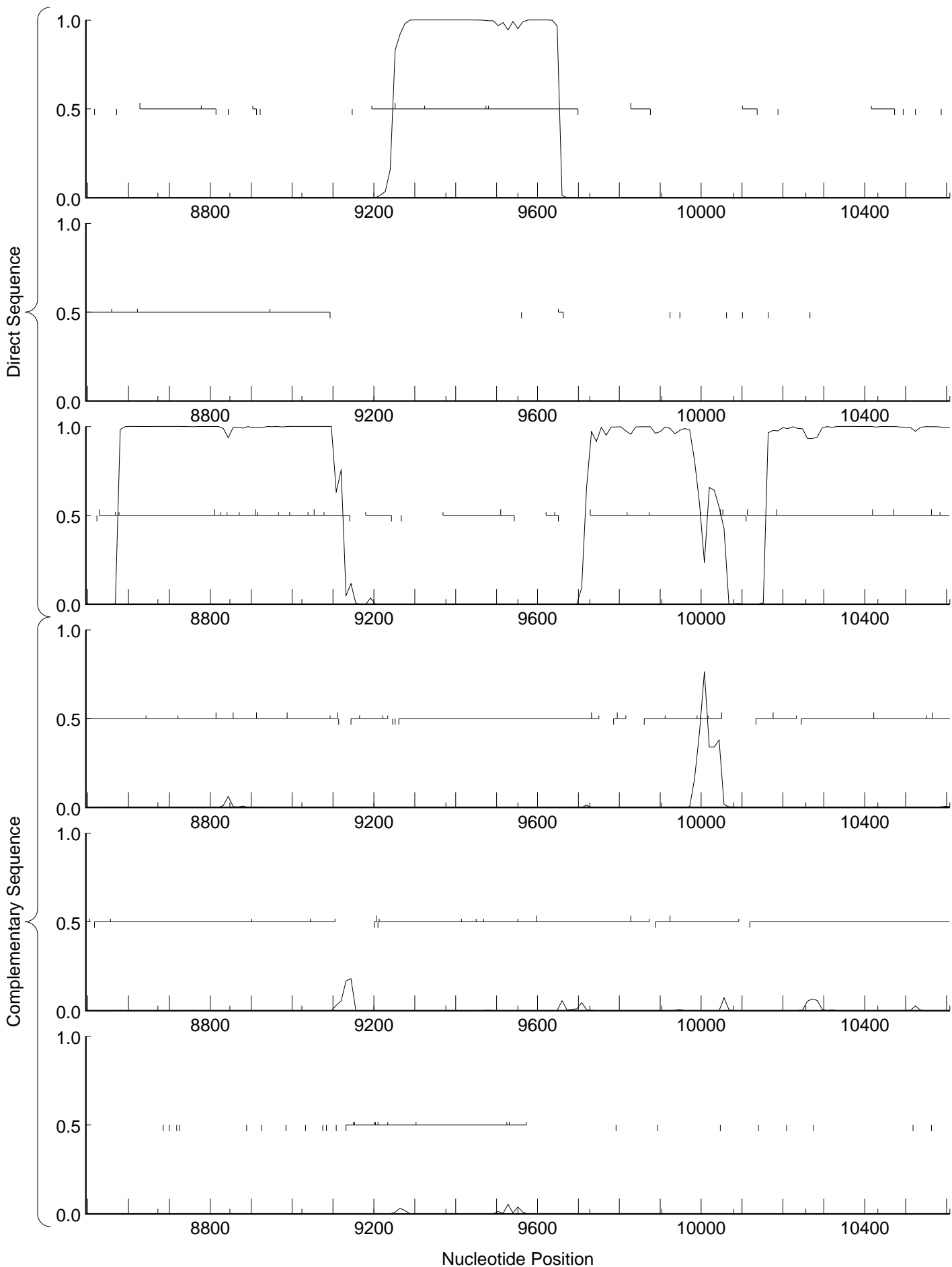
Send questions / comments to:
Dr. M. Borodovsky
Georgia Institute of Technology
School of Biology
Atlanta, GA 30332-0230

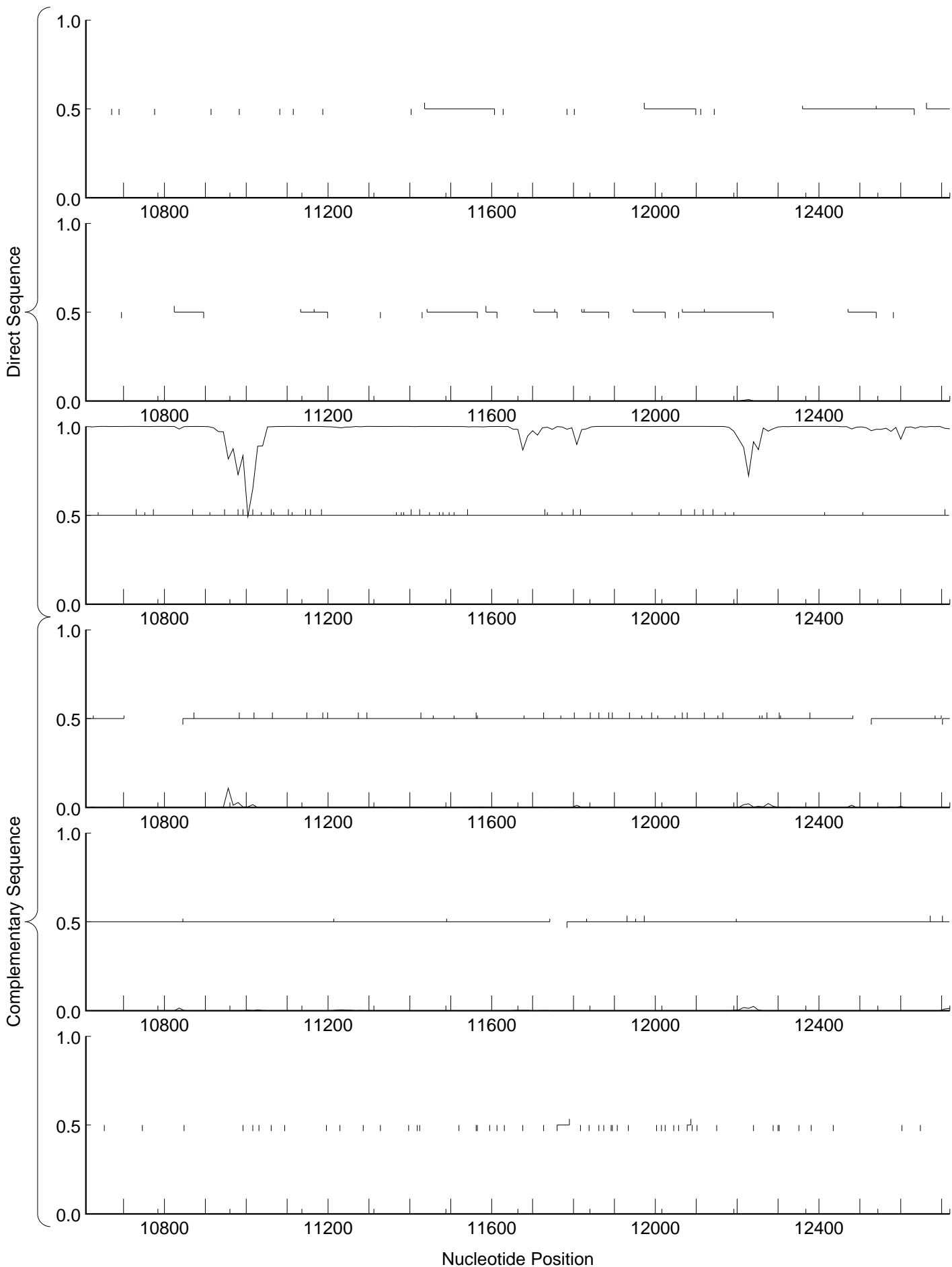


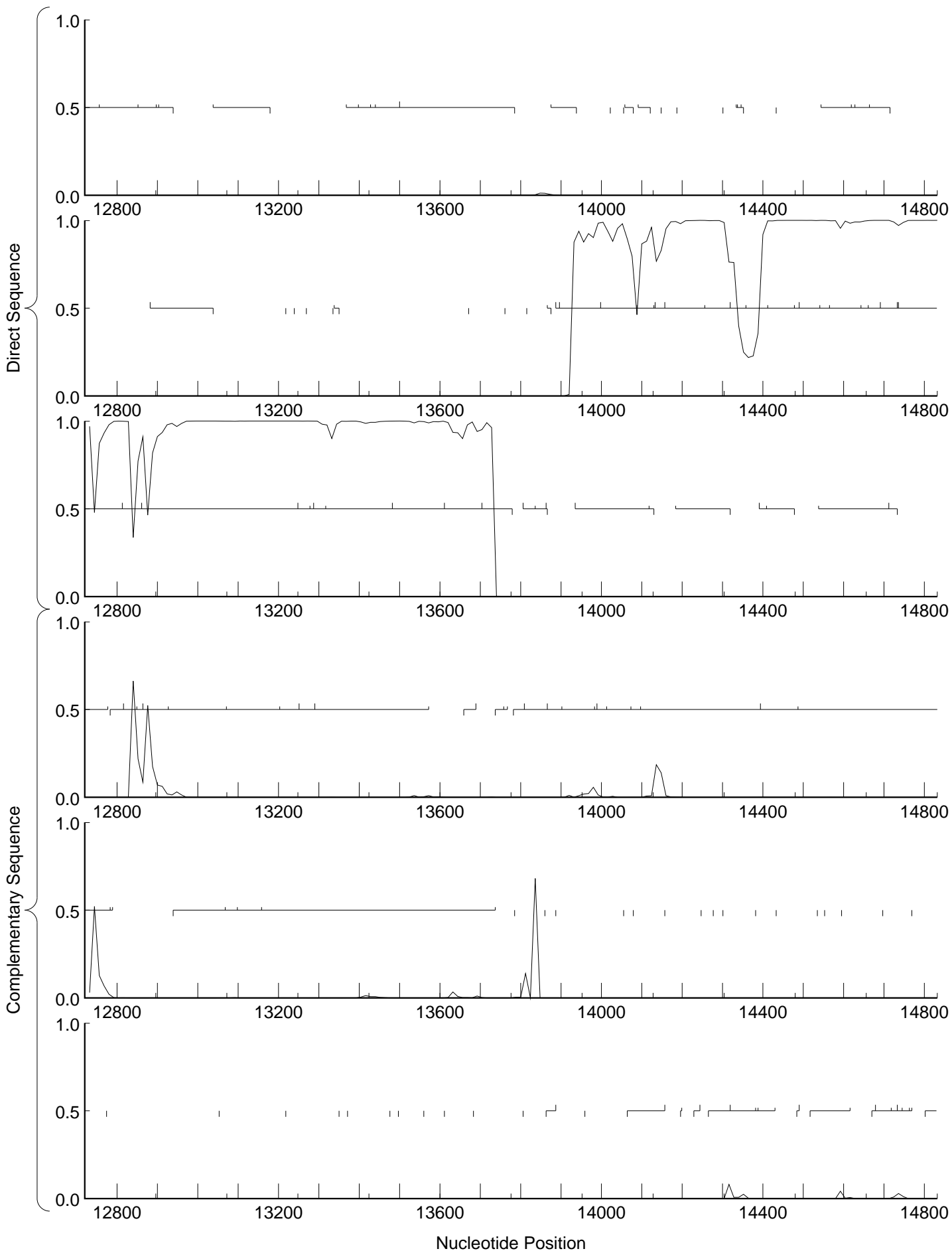


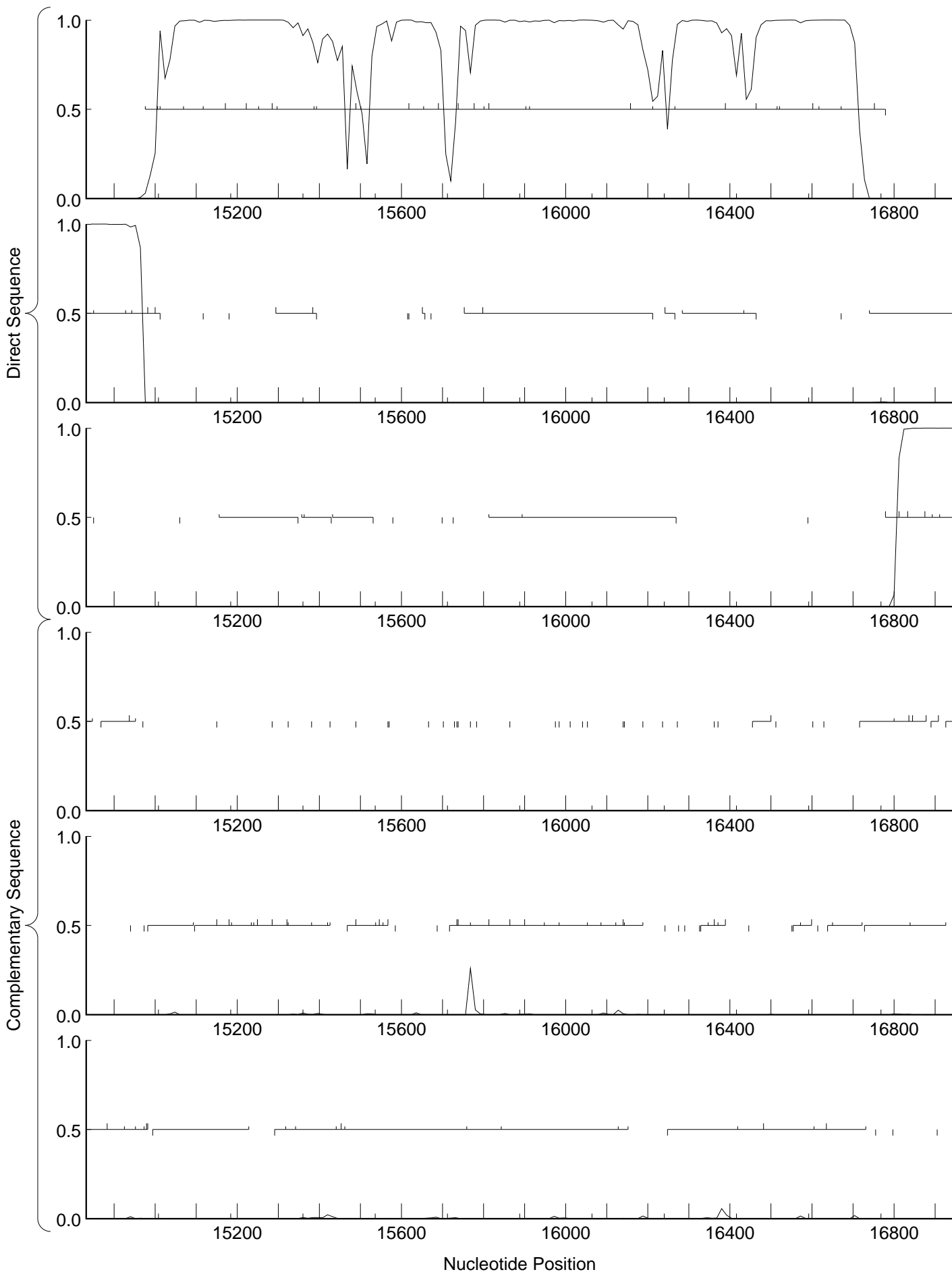


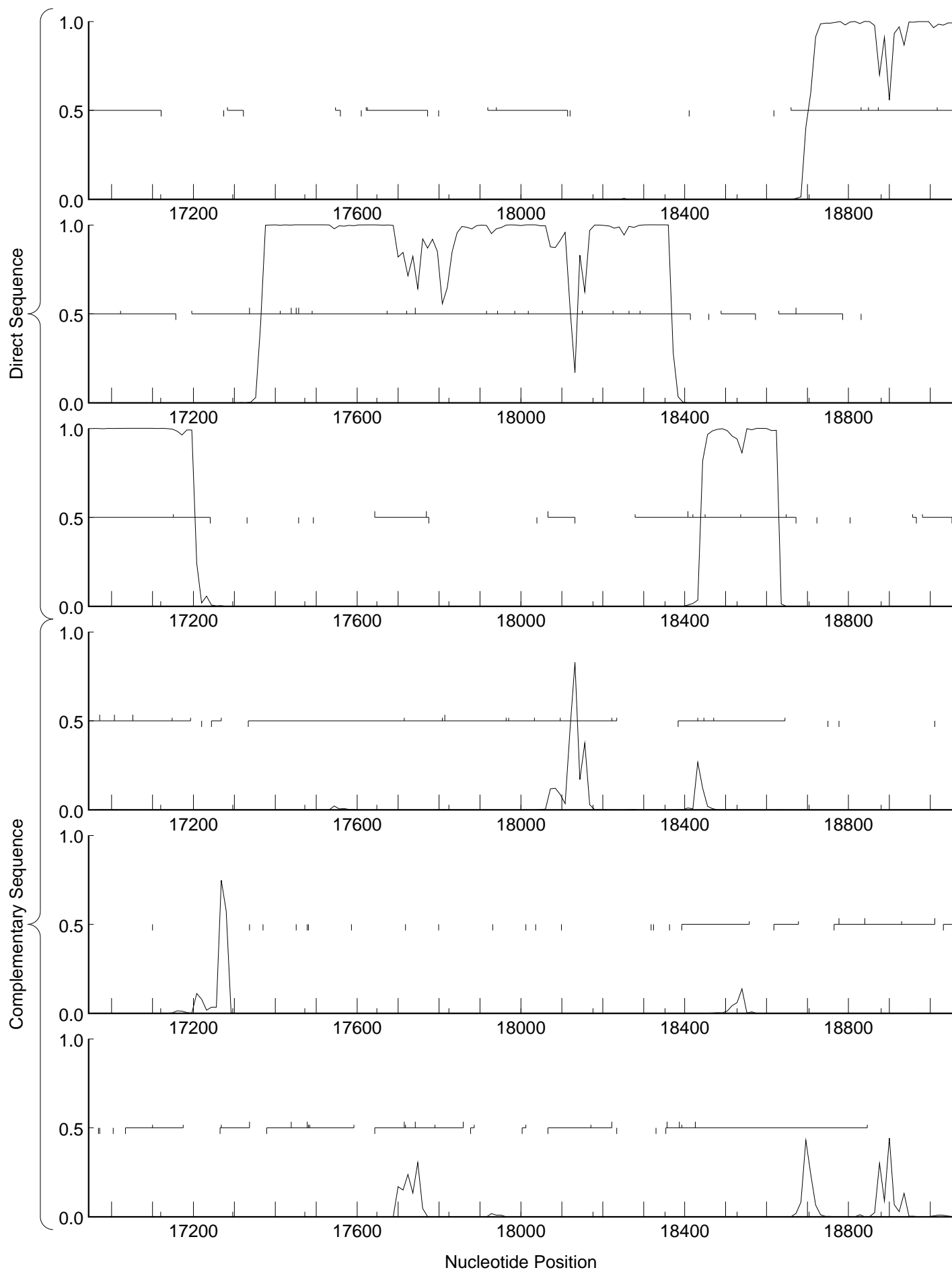




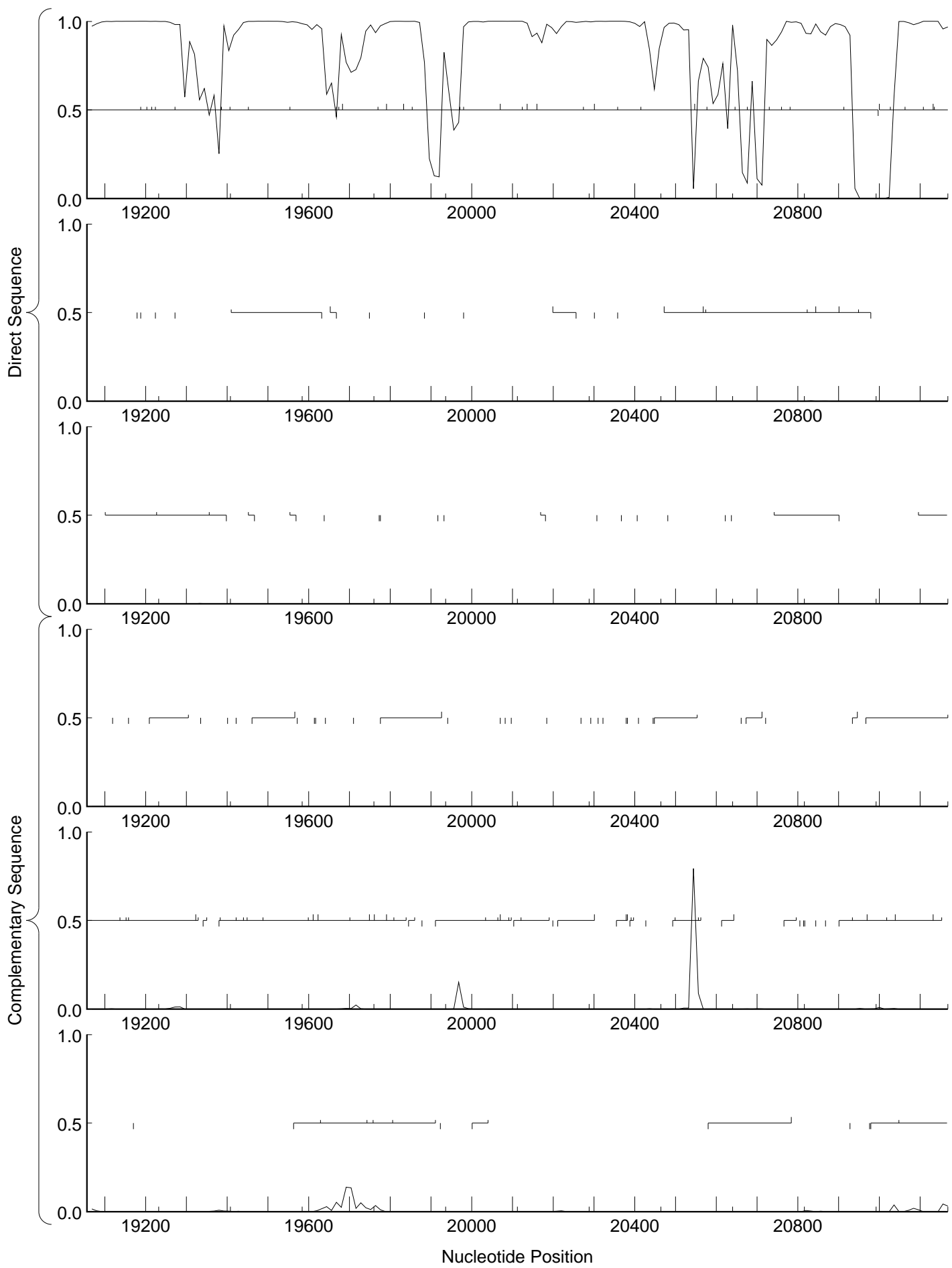


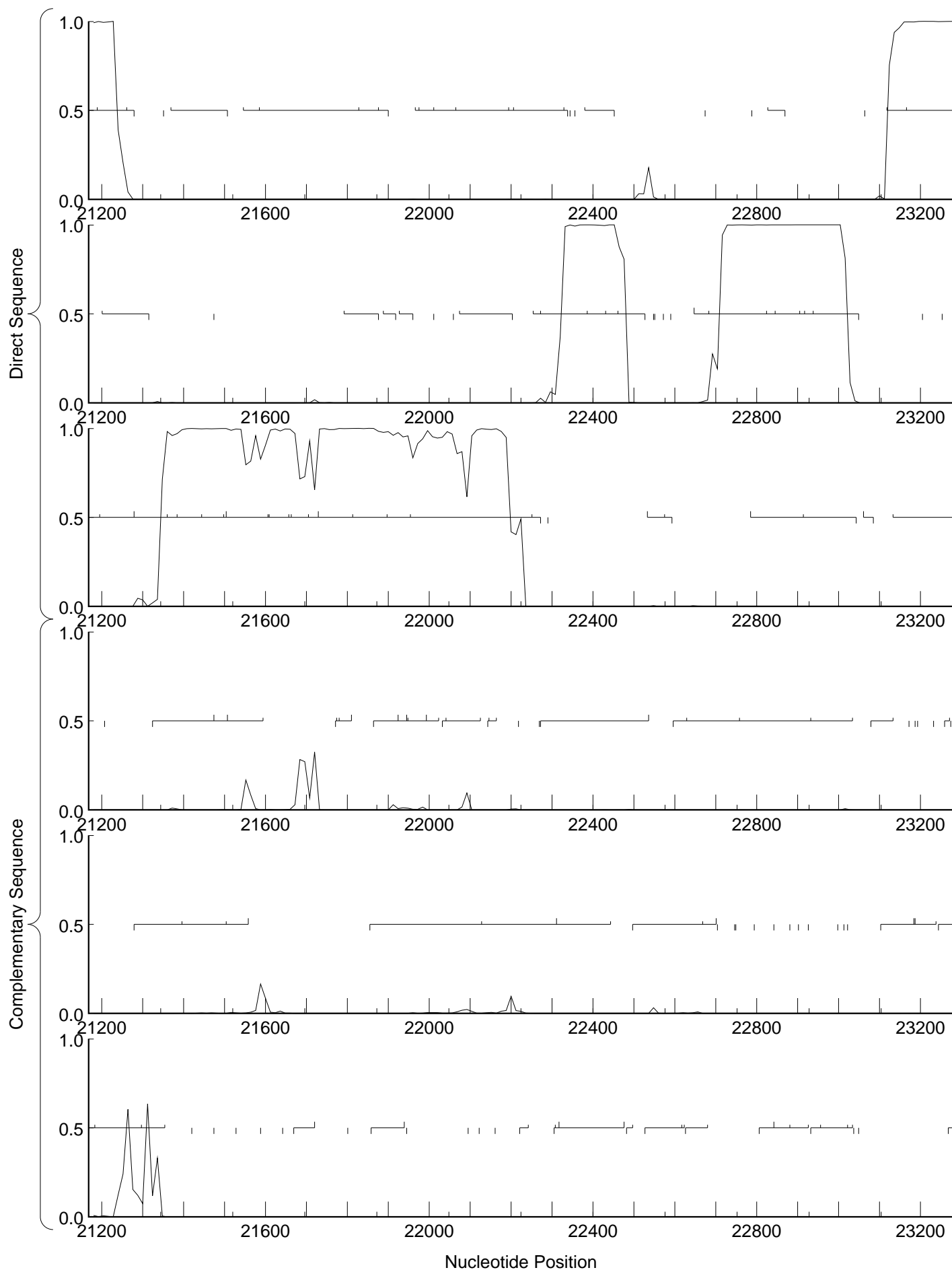


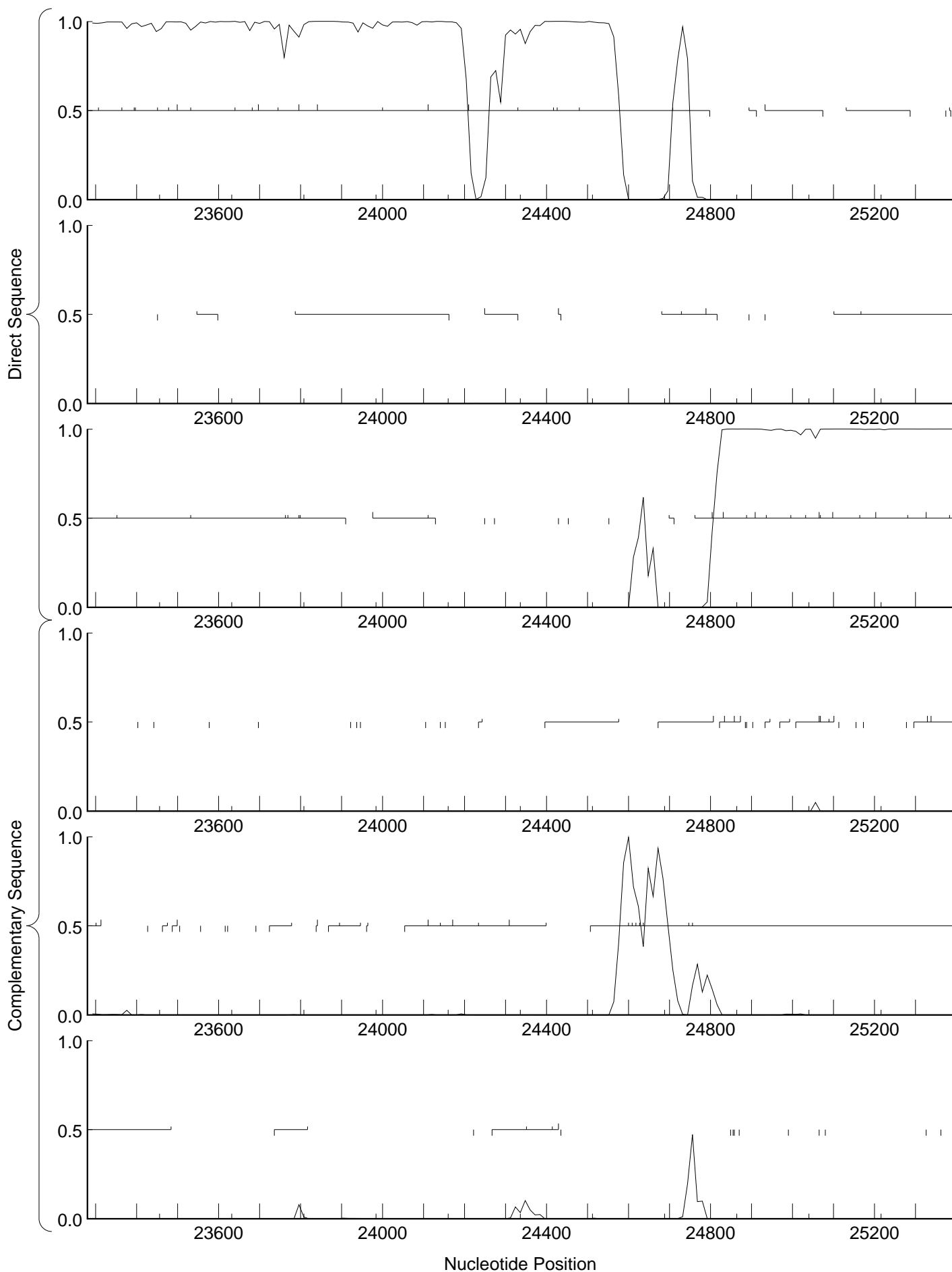


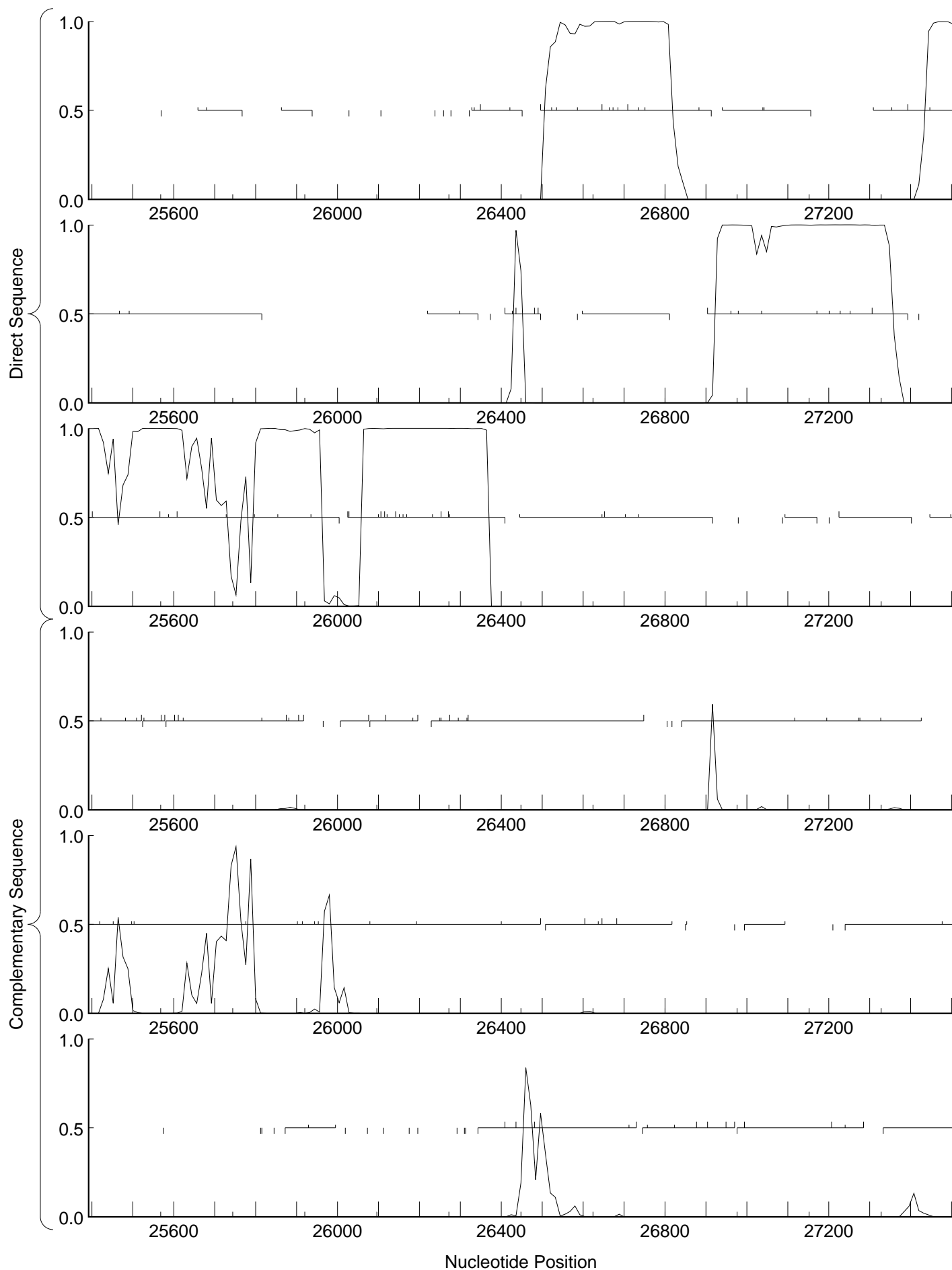


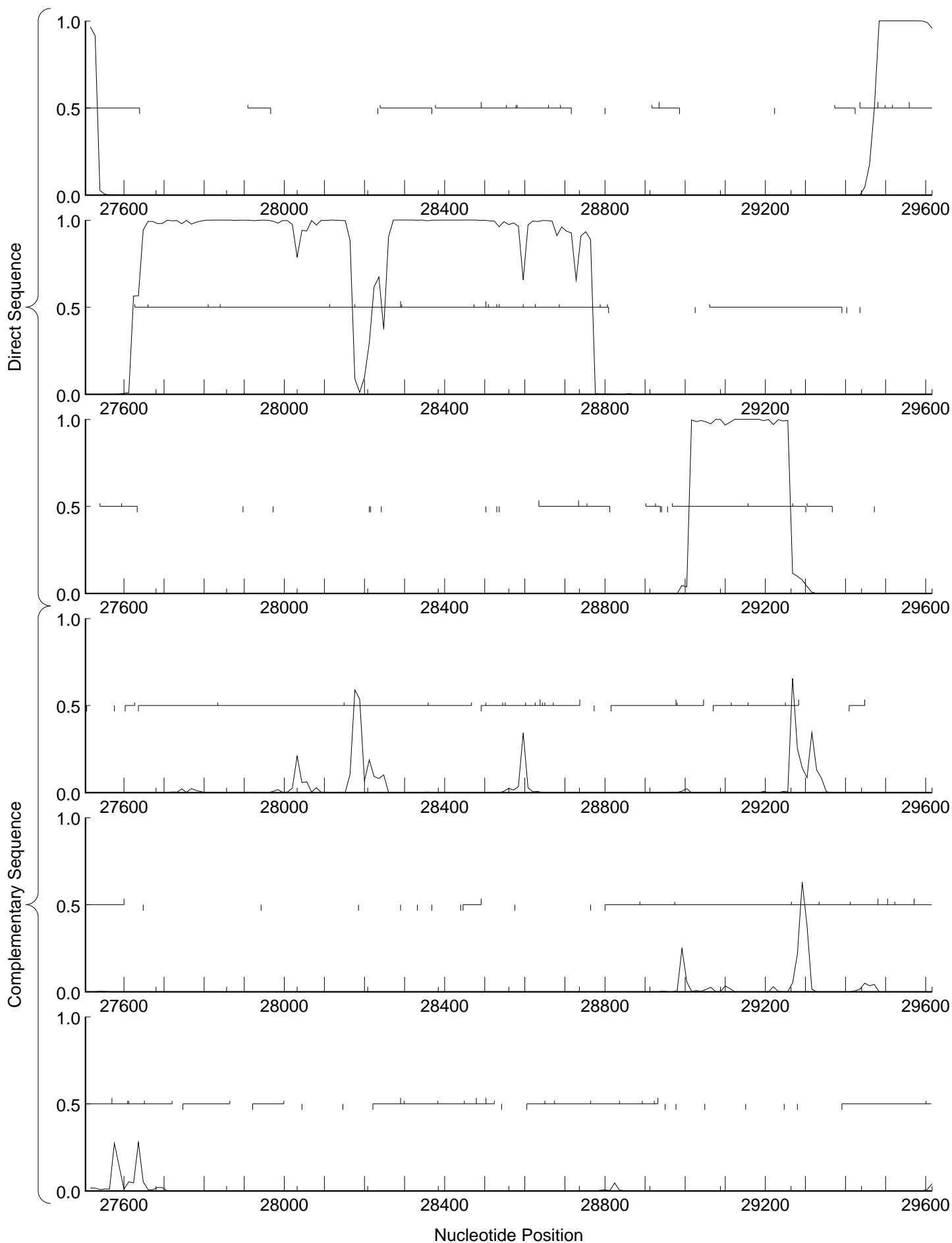
complete sequence, 58129 bp including 10-base 3' overhang (CTCGCGGCAT), Cluster K2, Order 4, Window 96, Step 12, 11/29

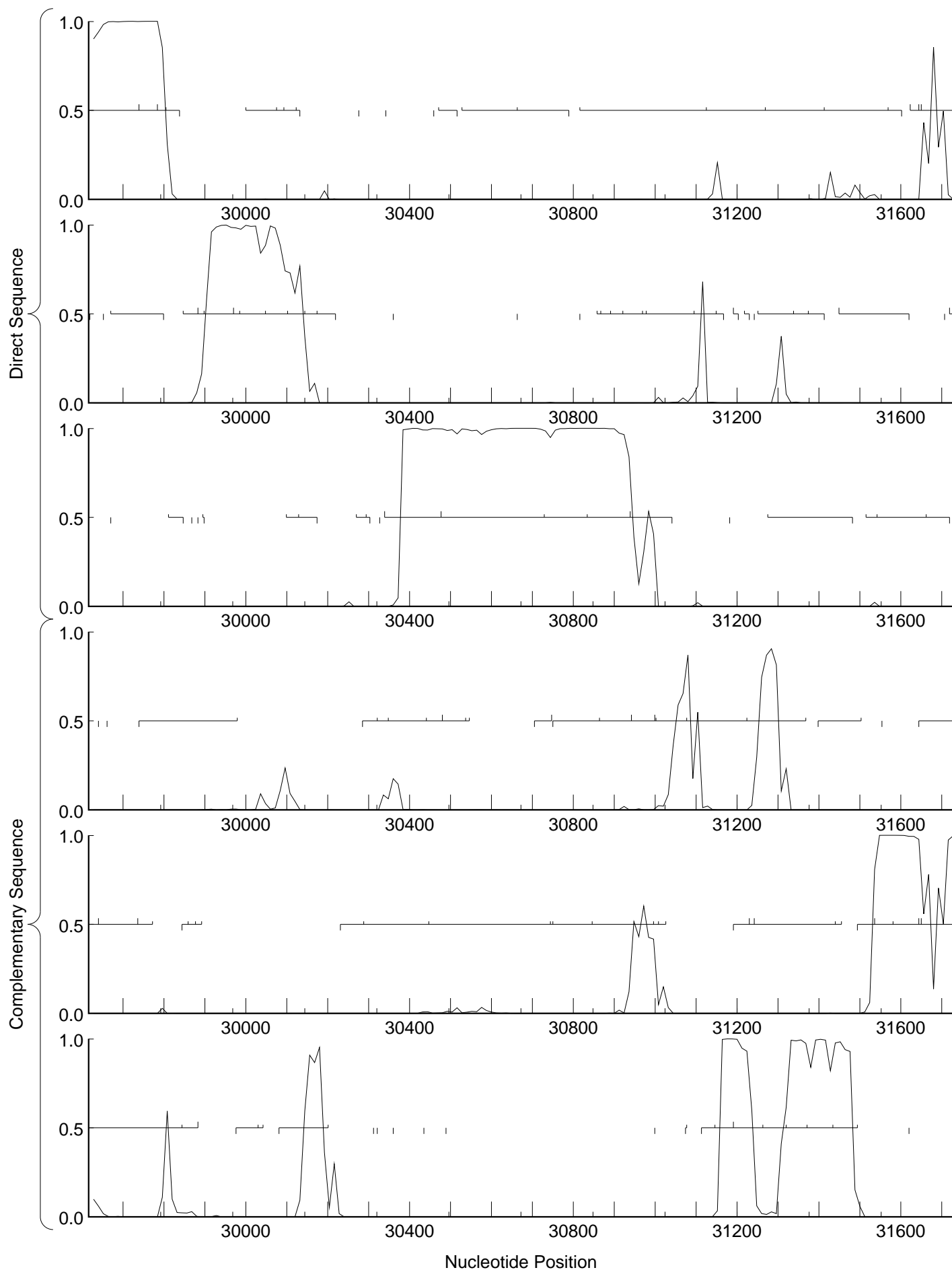


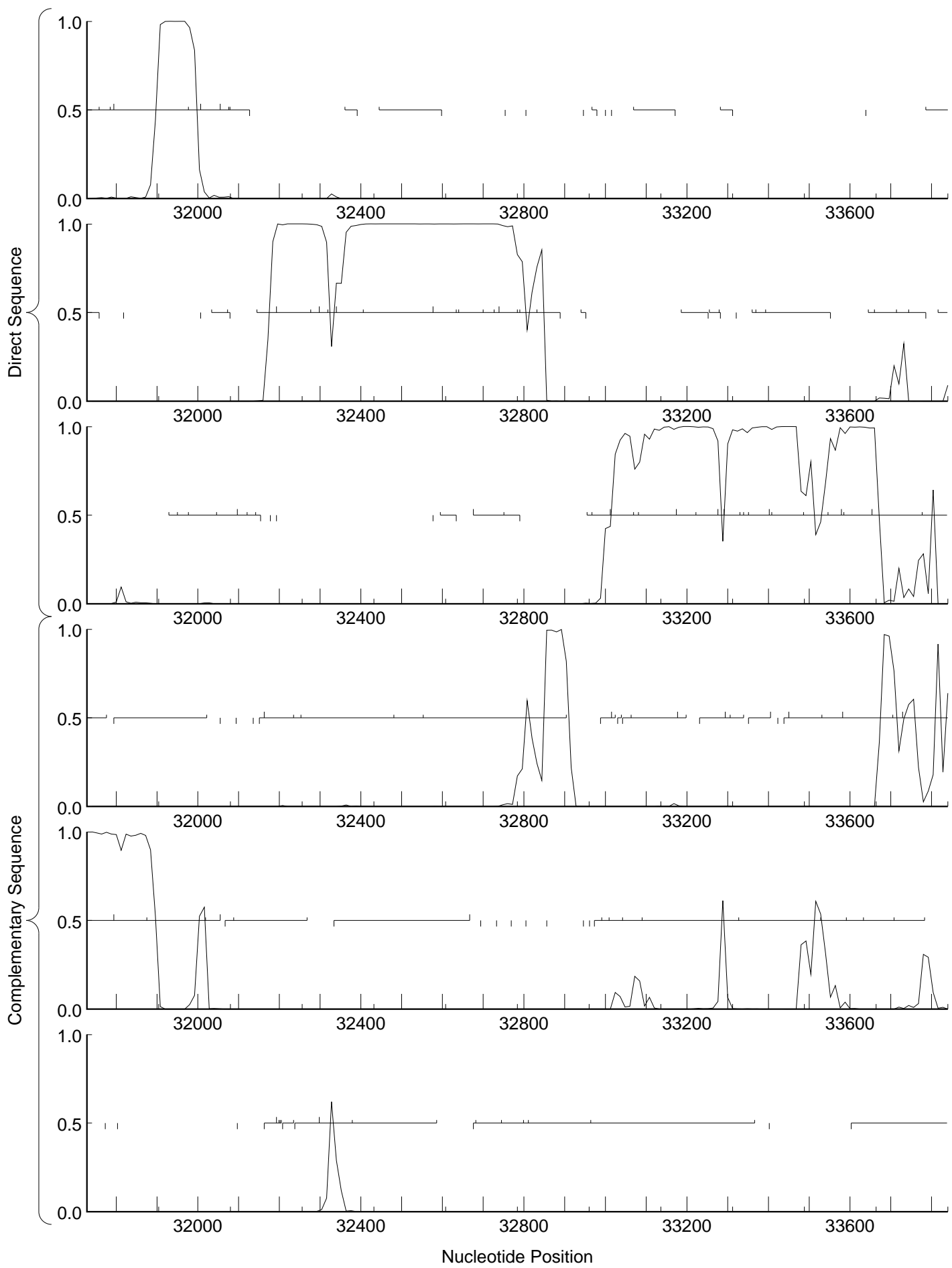


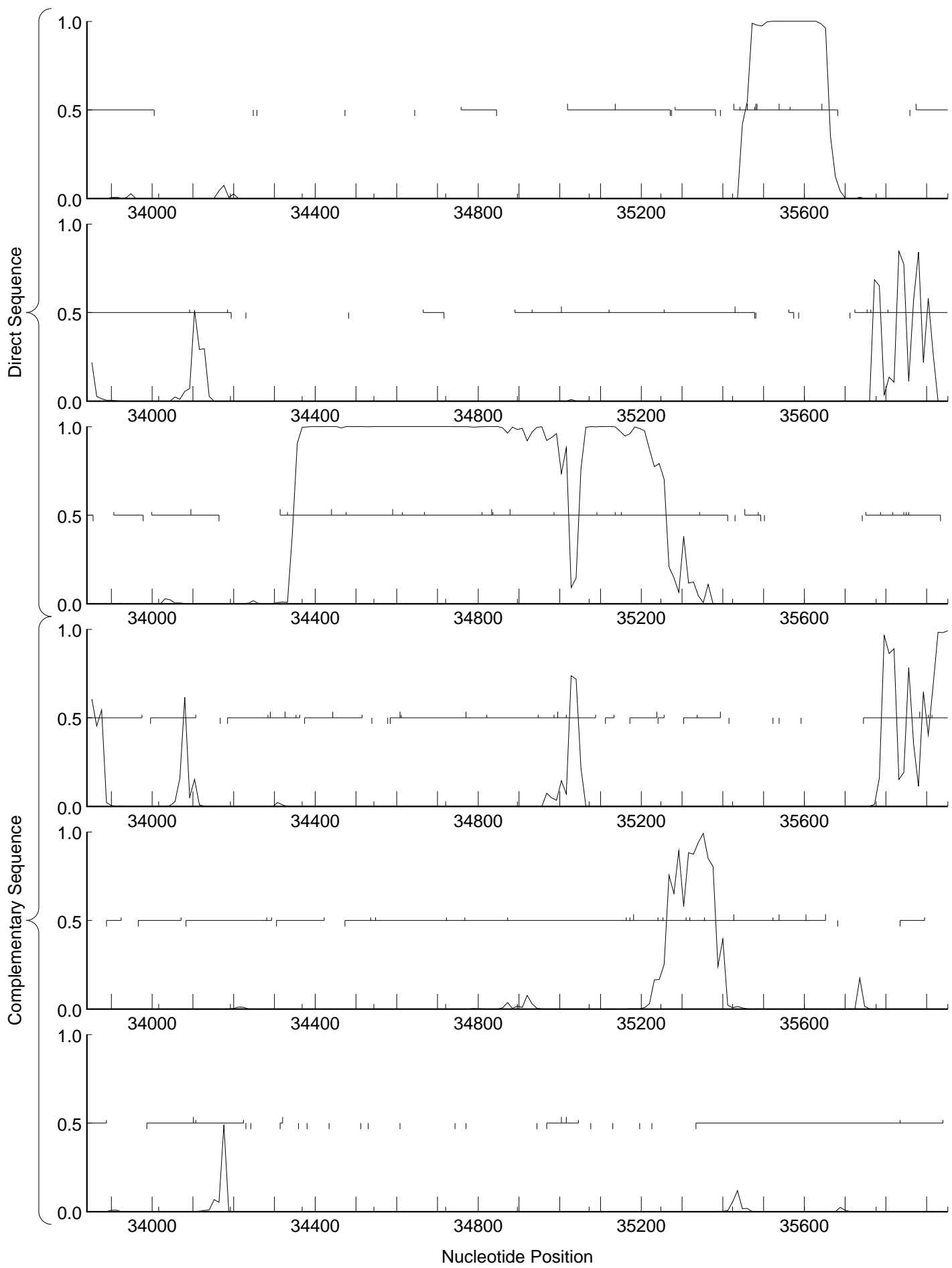


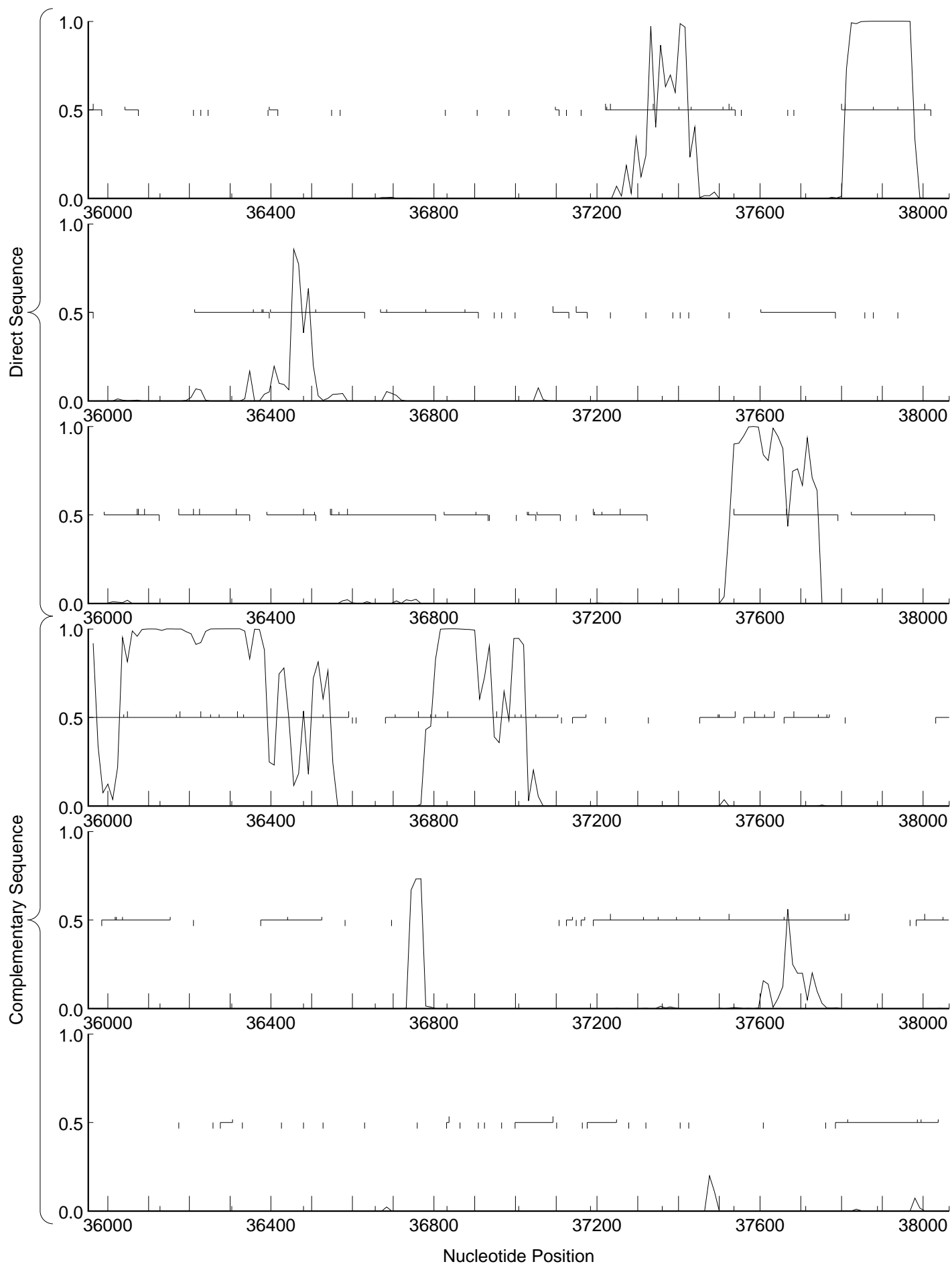


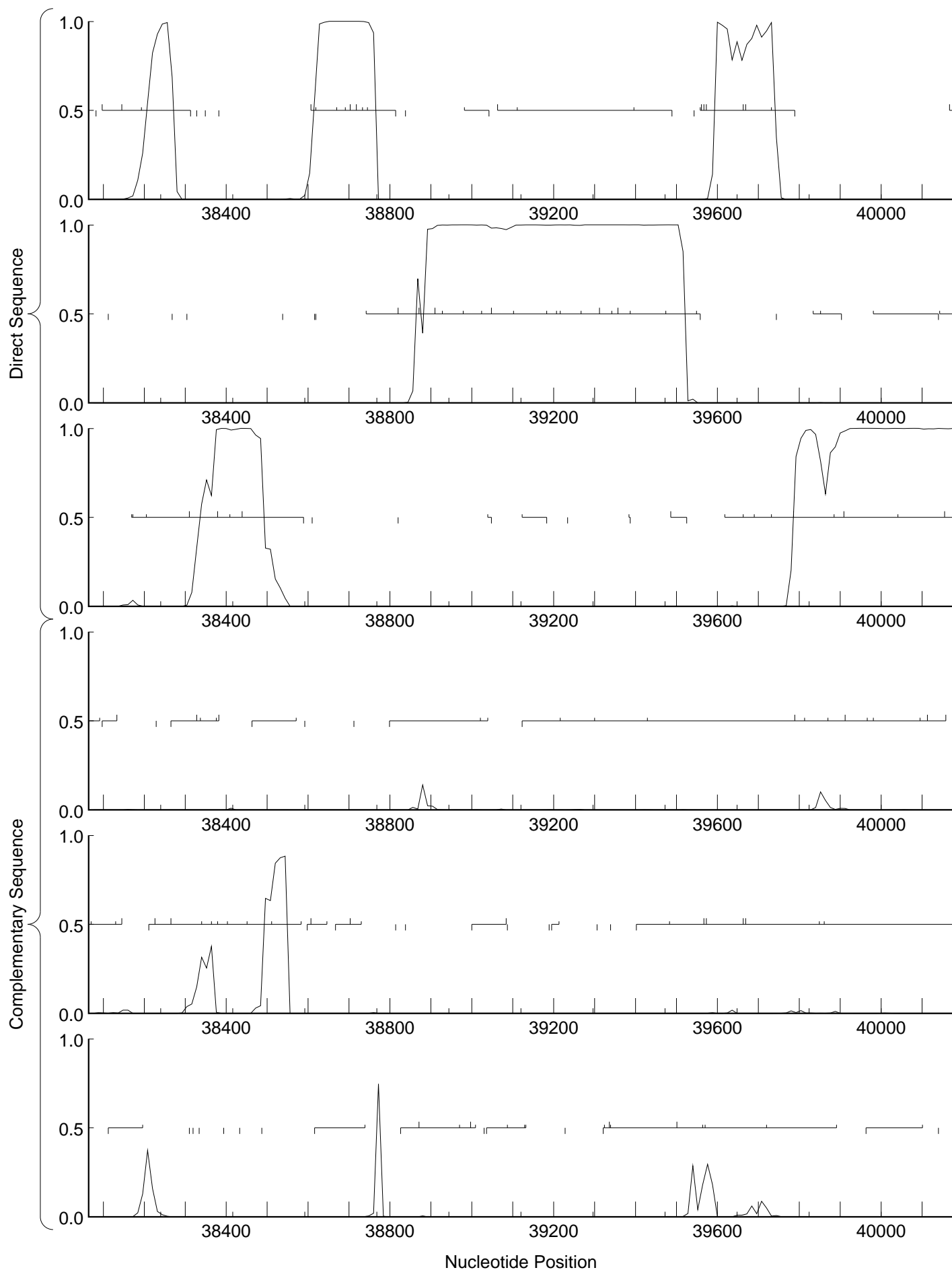


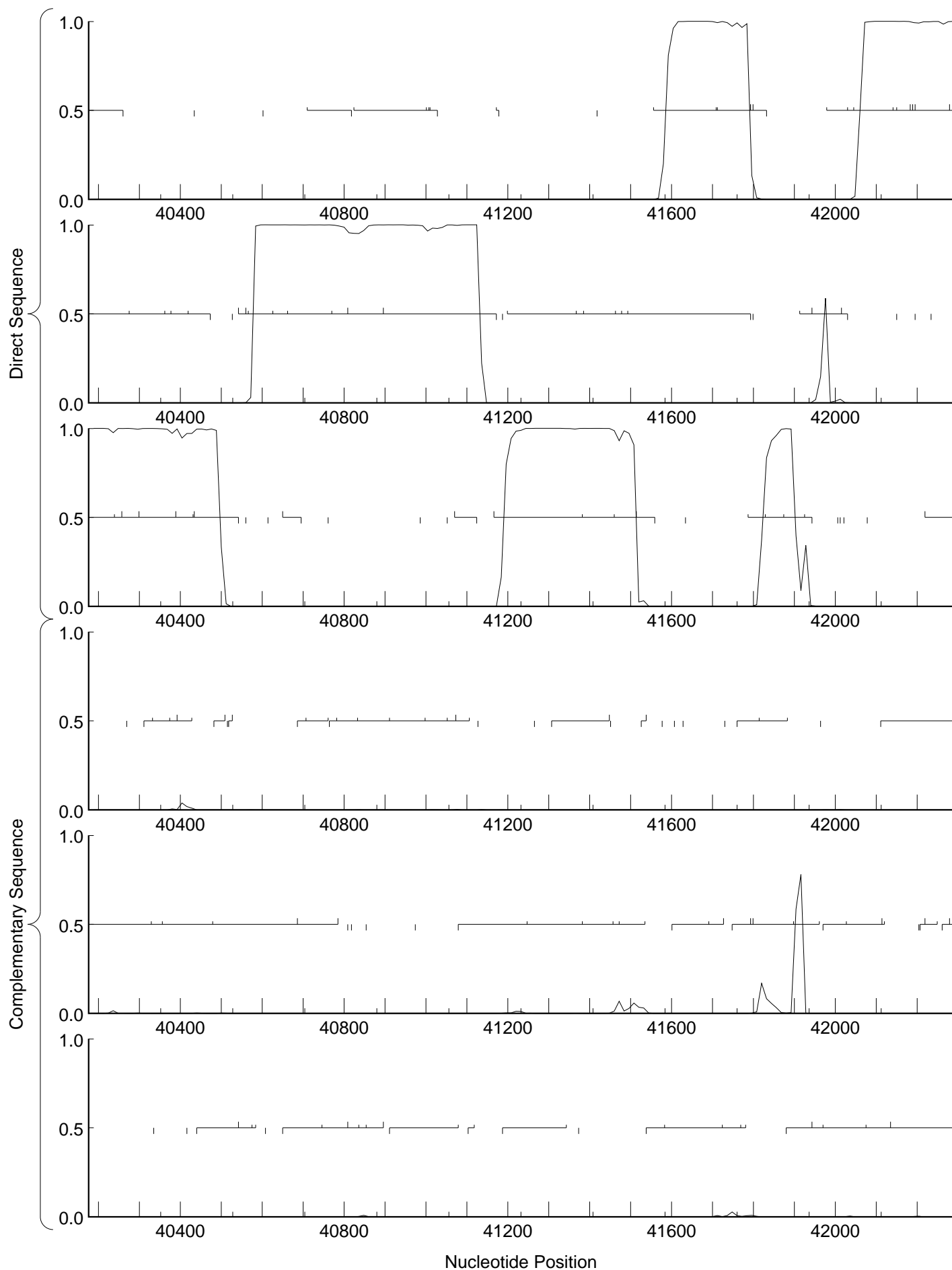












complete sequence, 58129 bp including 10-base 3' overhang (CTCGCGGCAT), Cluster K2, Order 4, Window 96, Step 12, 22/29

