

GeneMark

Version 2.5p (09.08.06)

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PROGRAM INFORMATION

Sequence : Microbacterium phage Balsa complete sequence, 41862 bp, circularly permuted, Cluster EAI
Analysis Date : 3/17/18 at 16:21:16
Pages : 21
Sequence Length : 41862 bp
GC Content : 63.38%

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,

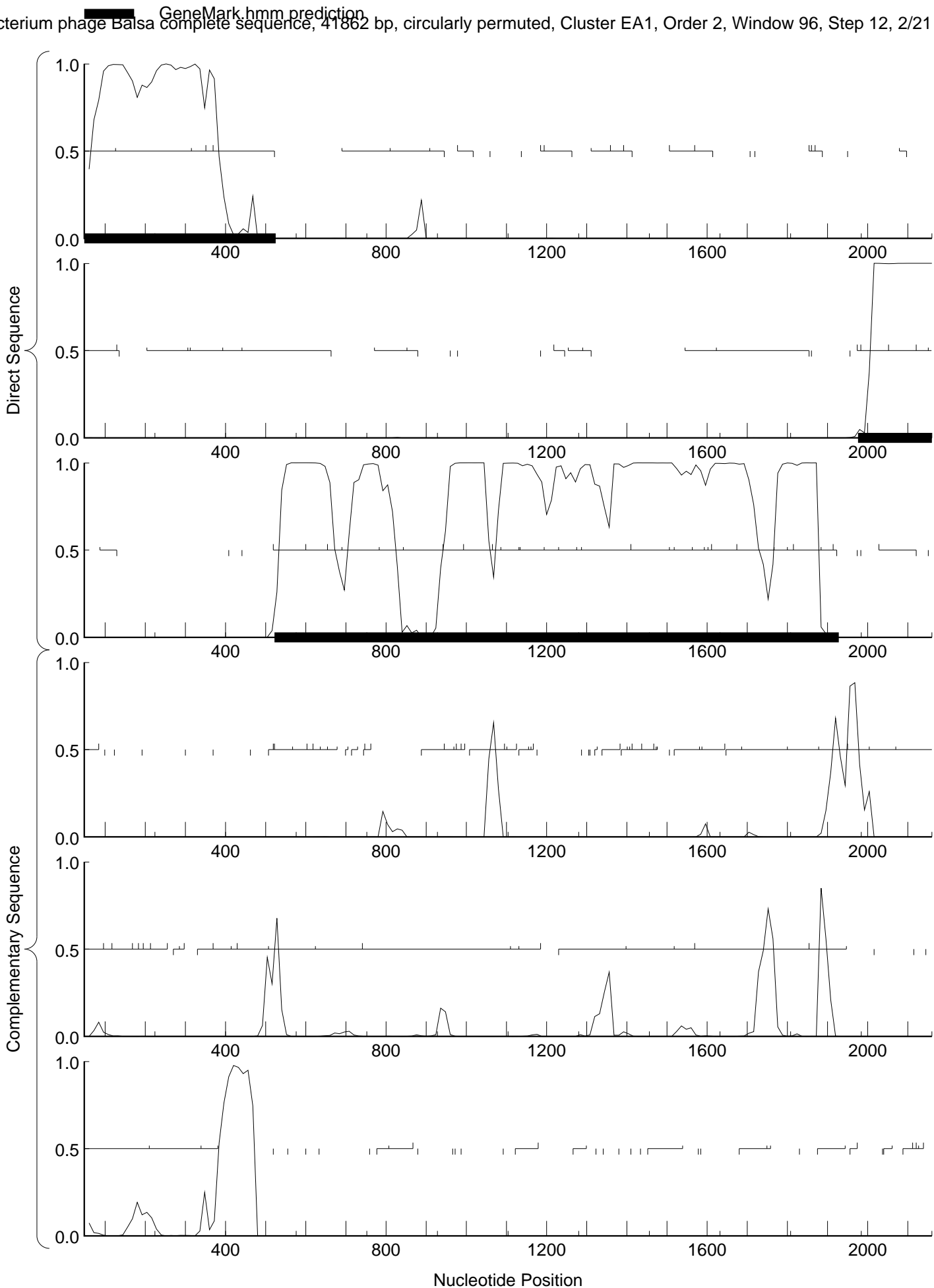
MATRIX INFORMATION

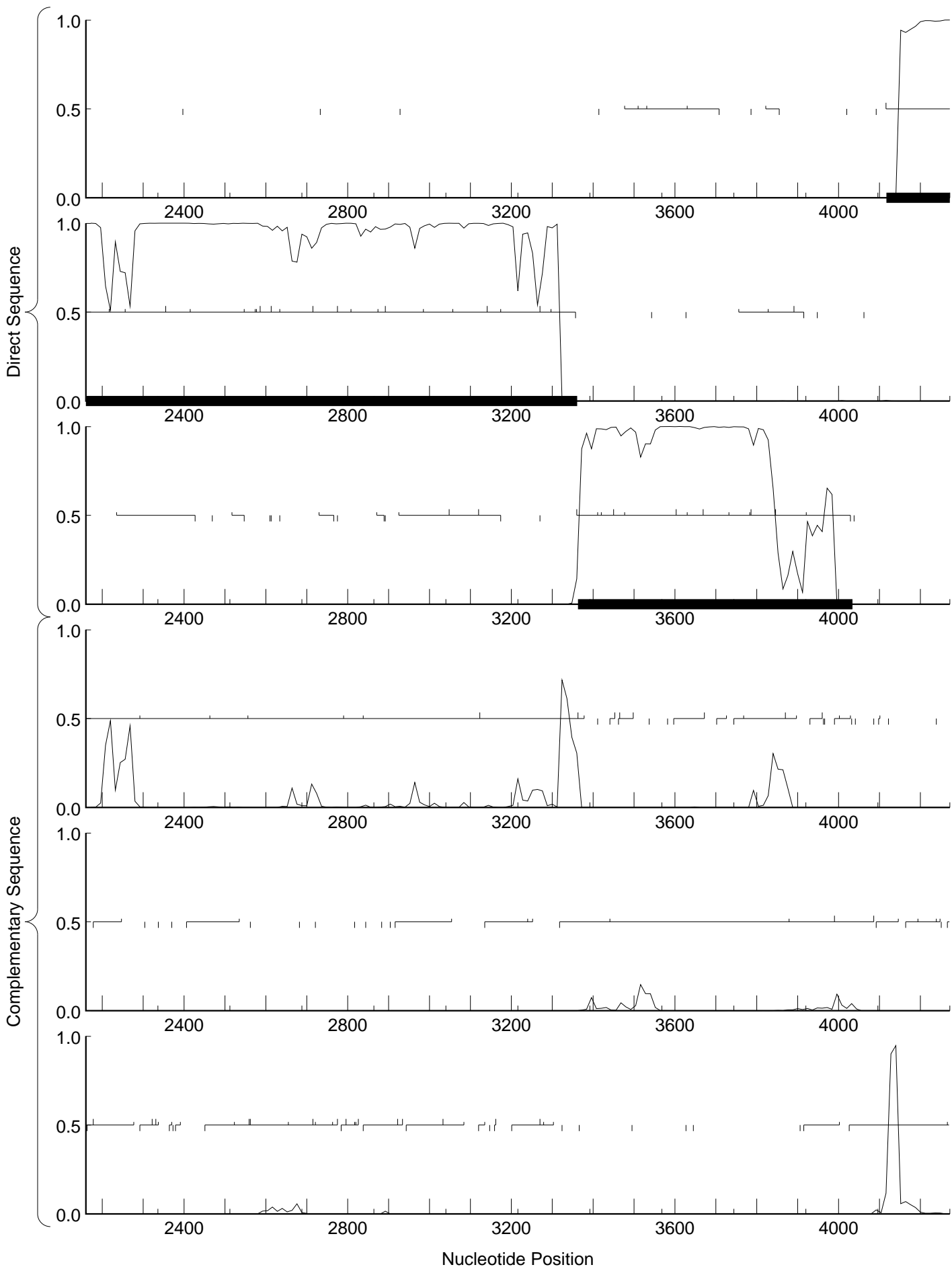
Matrix : Heuristic, GC = 63
Author : Borodovsky Laboratory - Georgia Tech
Order : 2

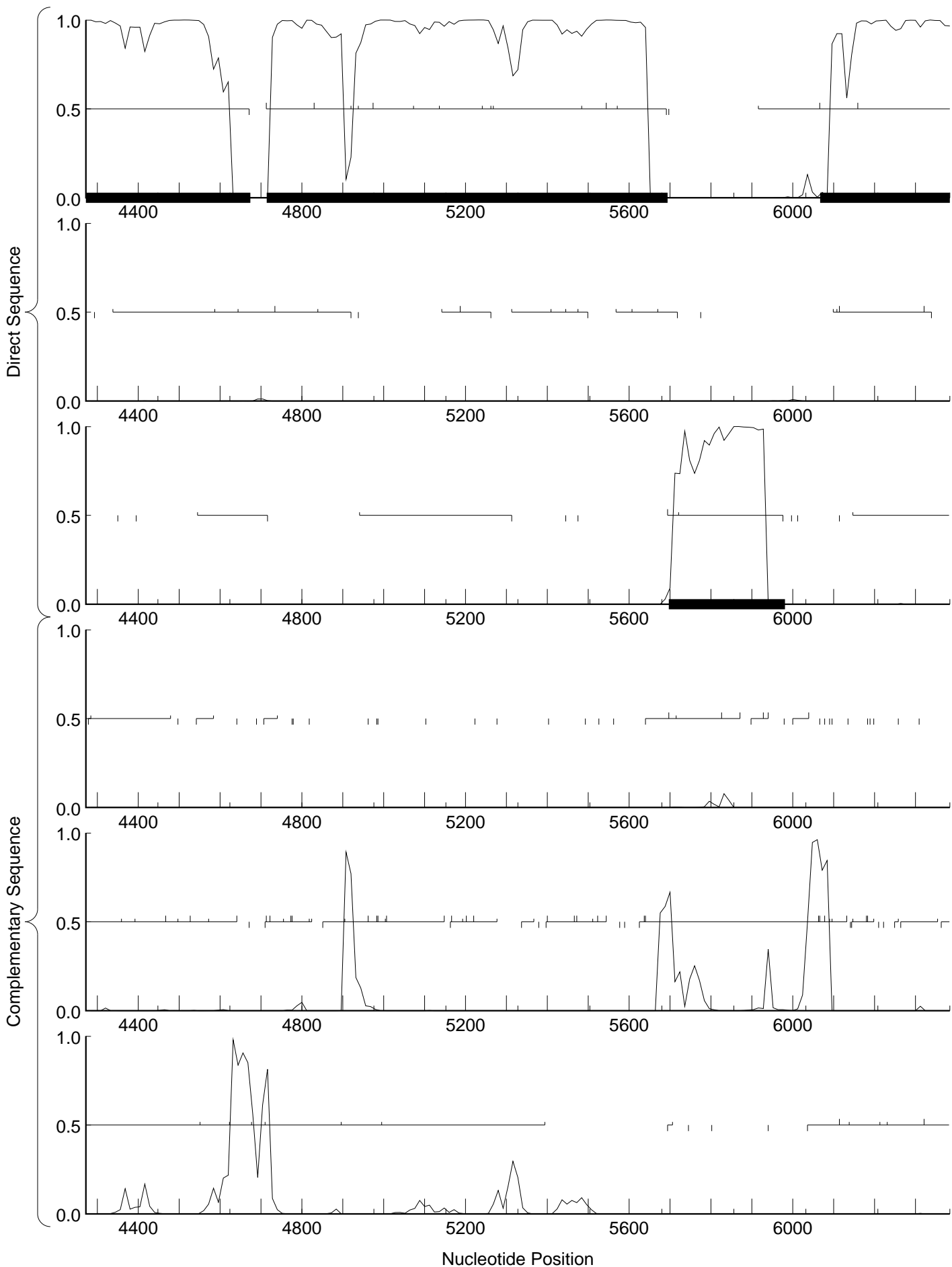
Send questions / comments to:
Dr. M. Borodovsky
Georgia Institute of Technology
School of Biology
Atlanta, GA 30332-0230

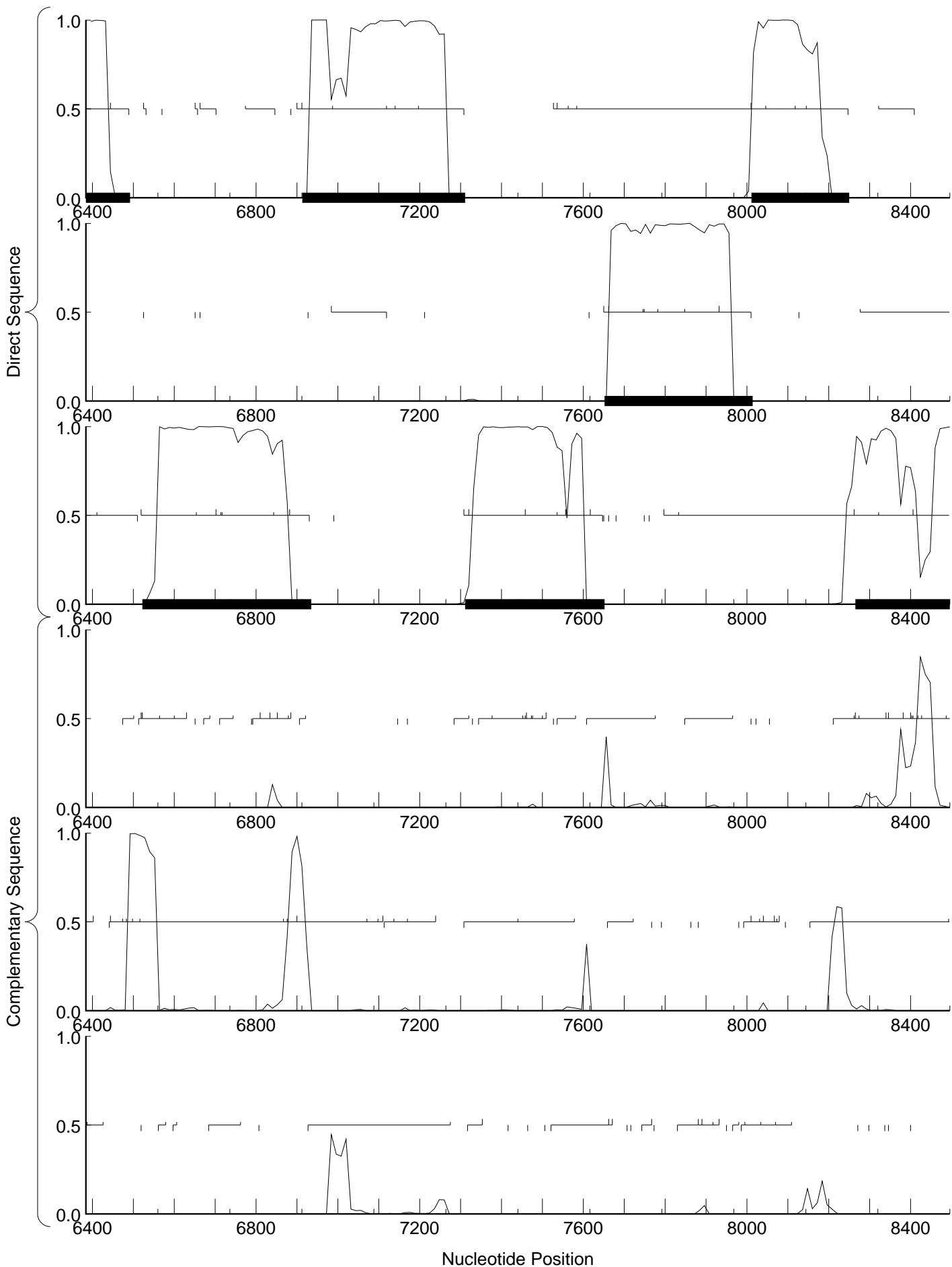
Matrix notes & comments

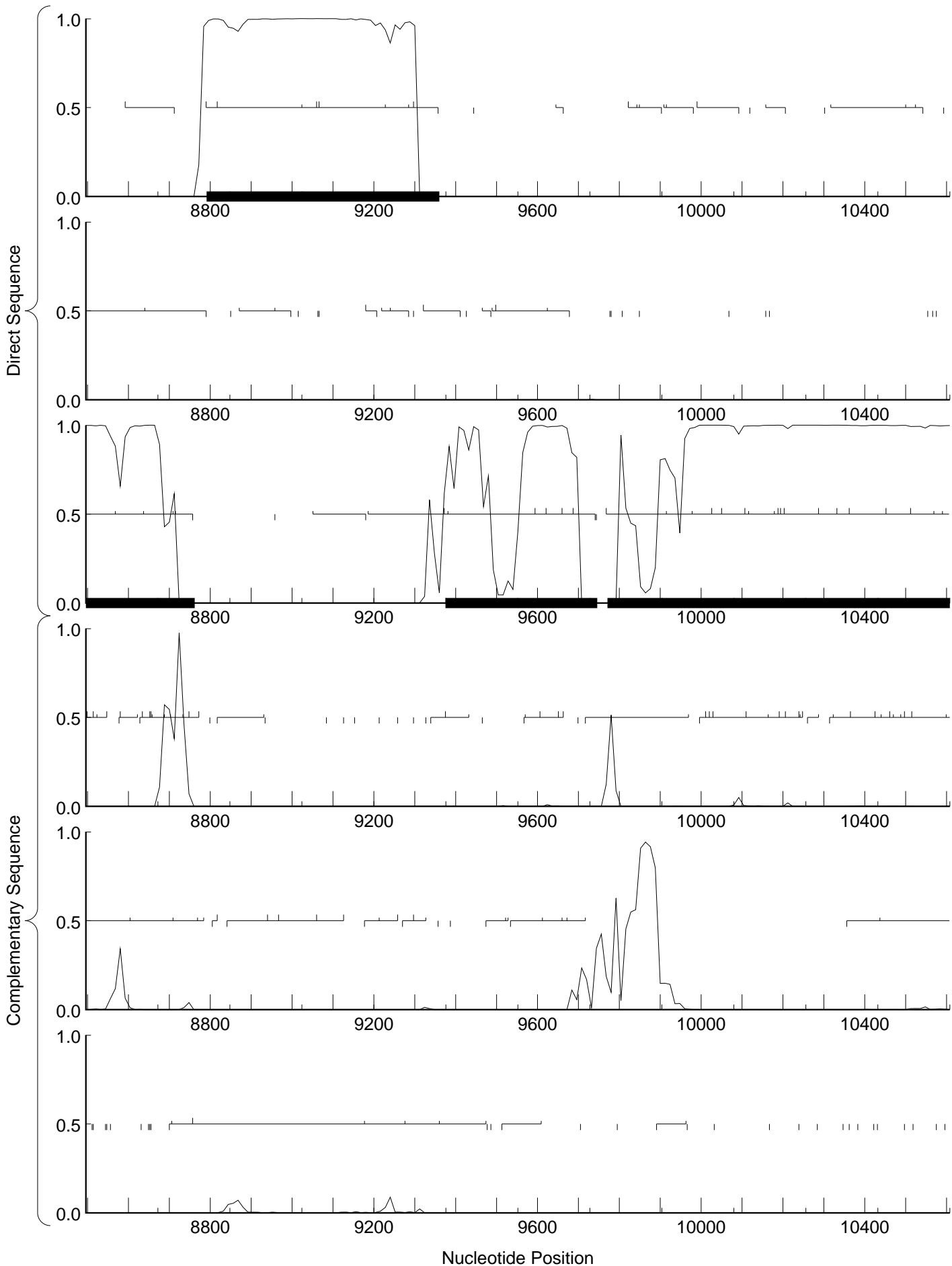
For details on the model building procedure see:
Besemer J. and Borodovsky M.
"Heuristic approach to deriving models for gene finding"
NAR, 1999, Vol. 27, No. 19, pp. 3911-3920

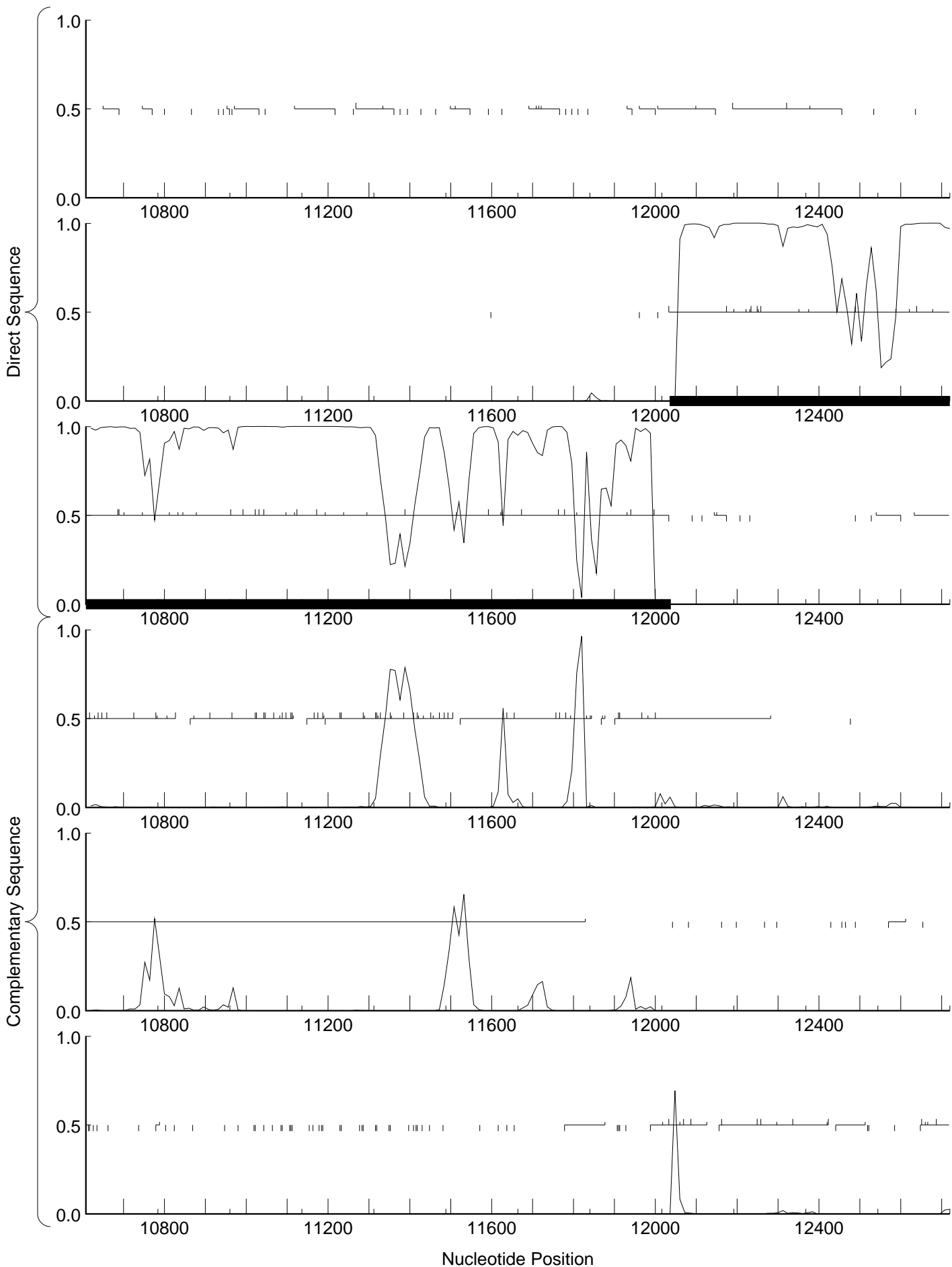


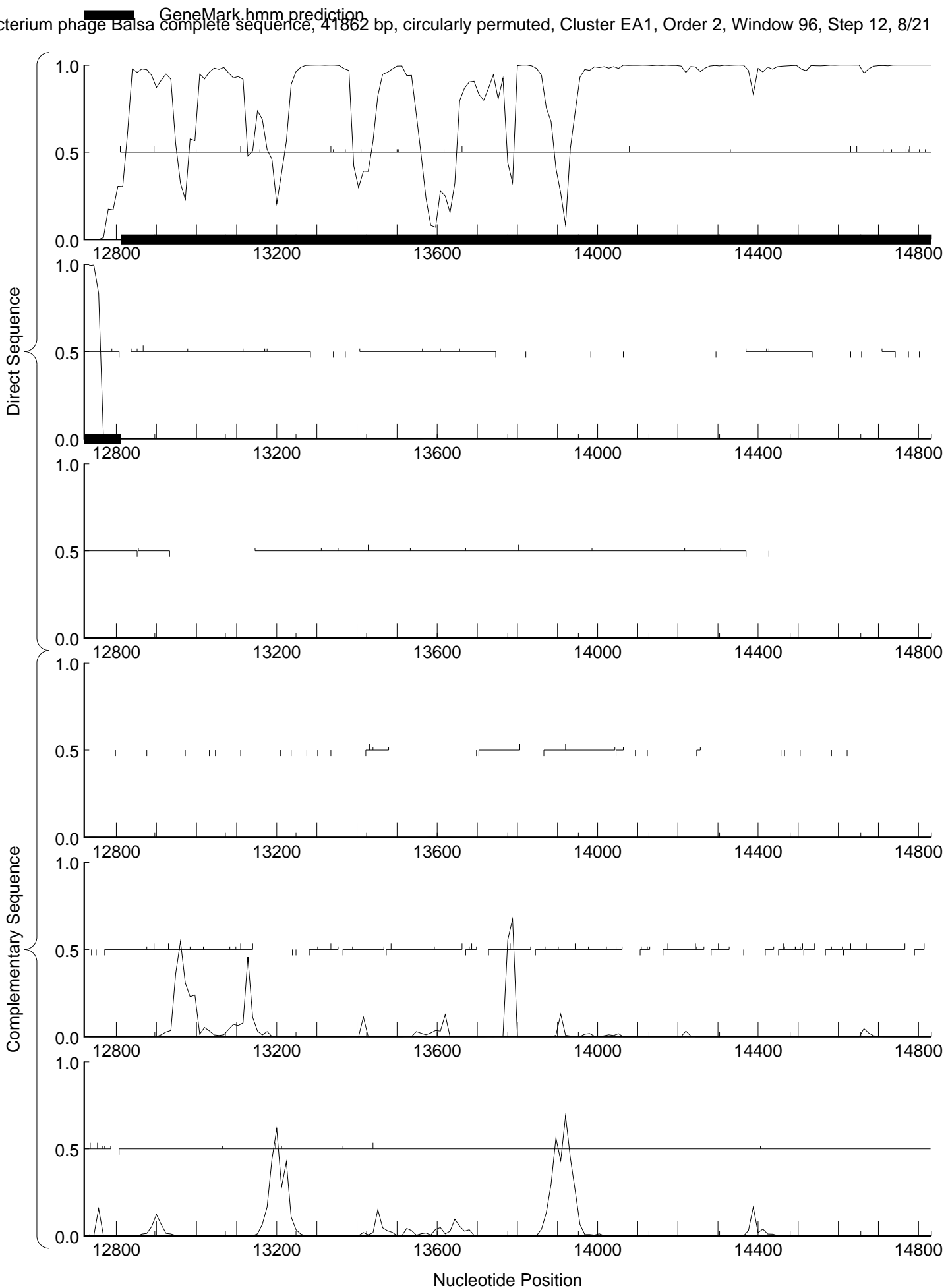


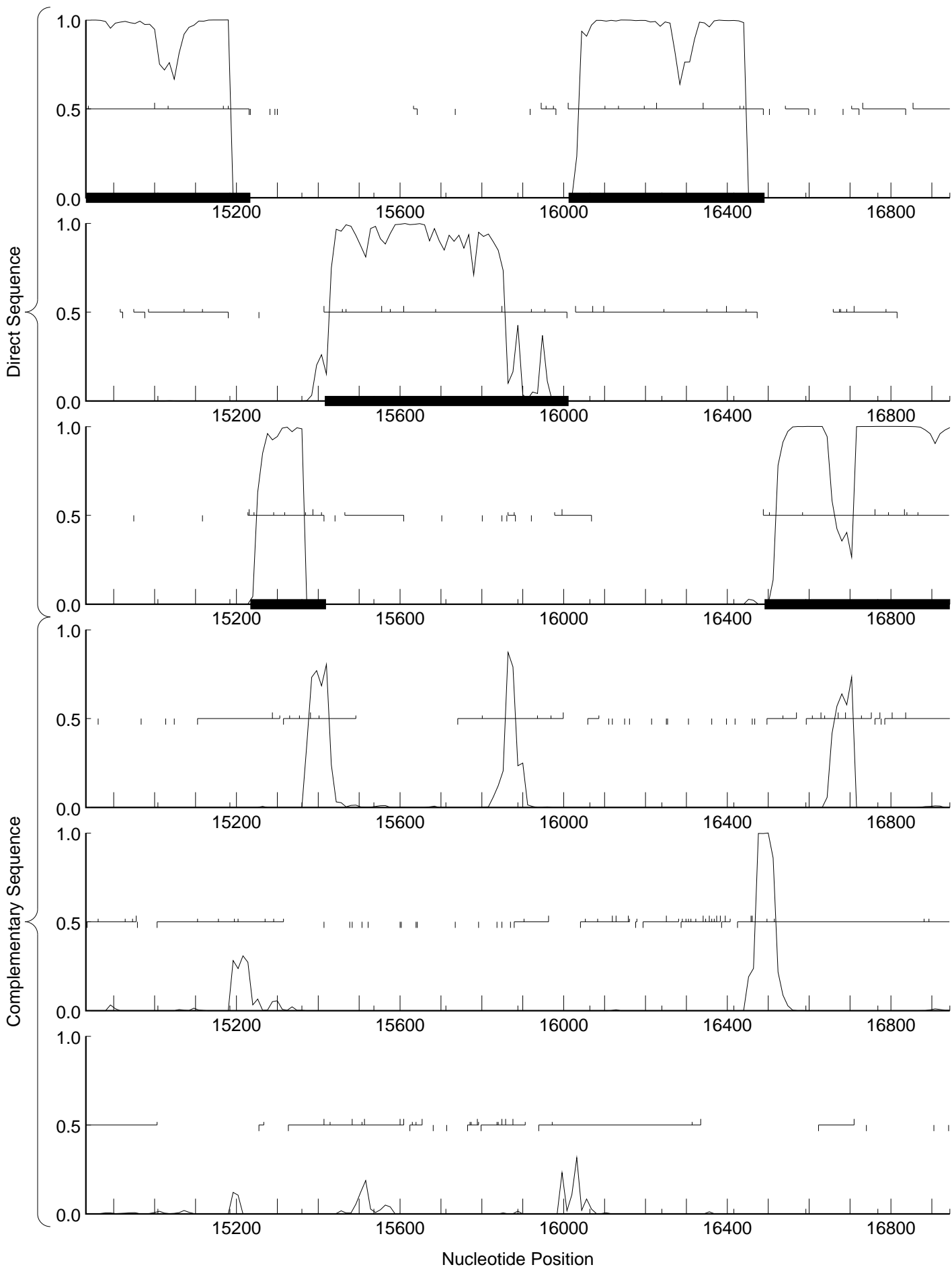


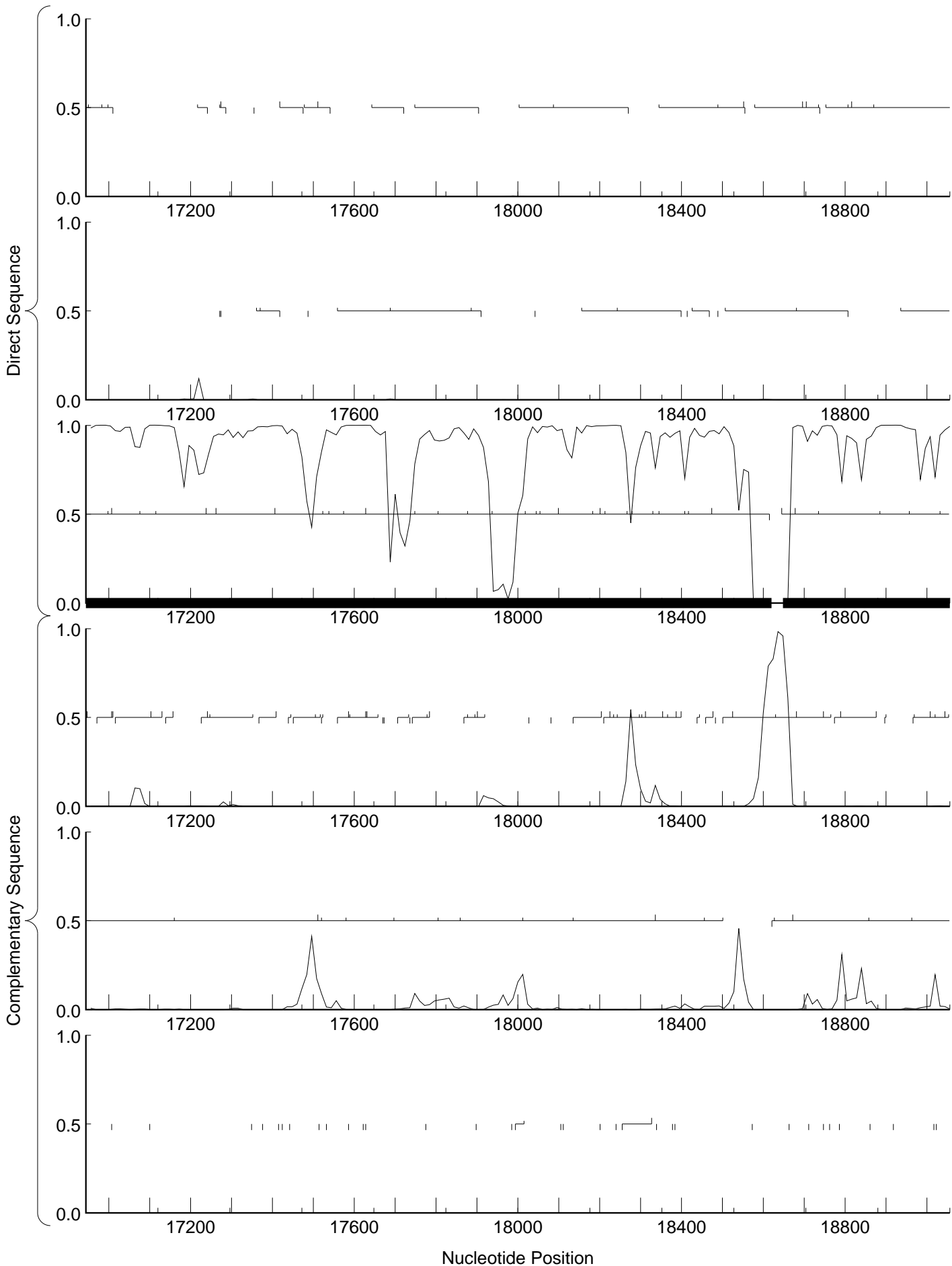


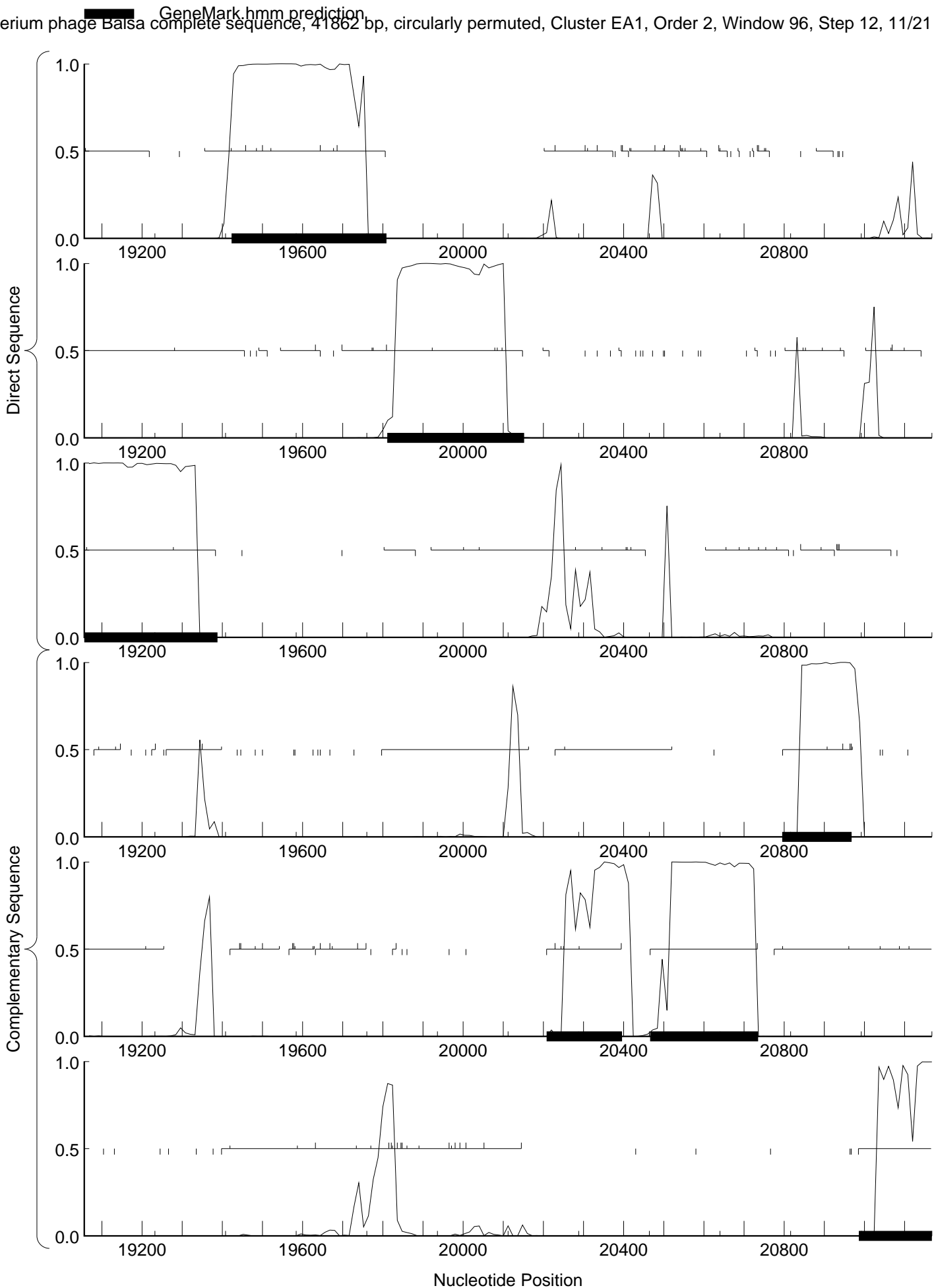


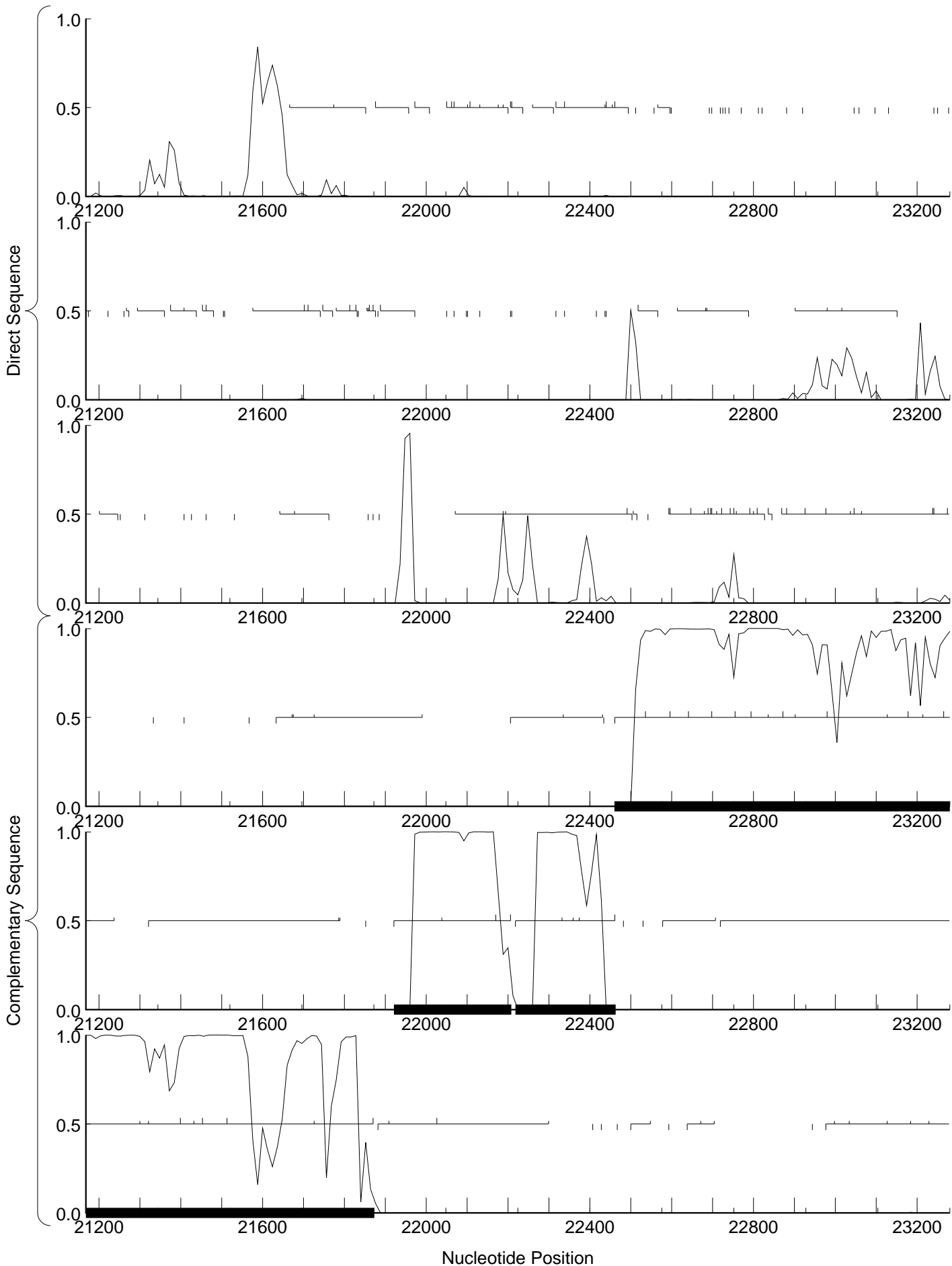


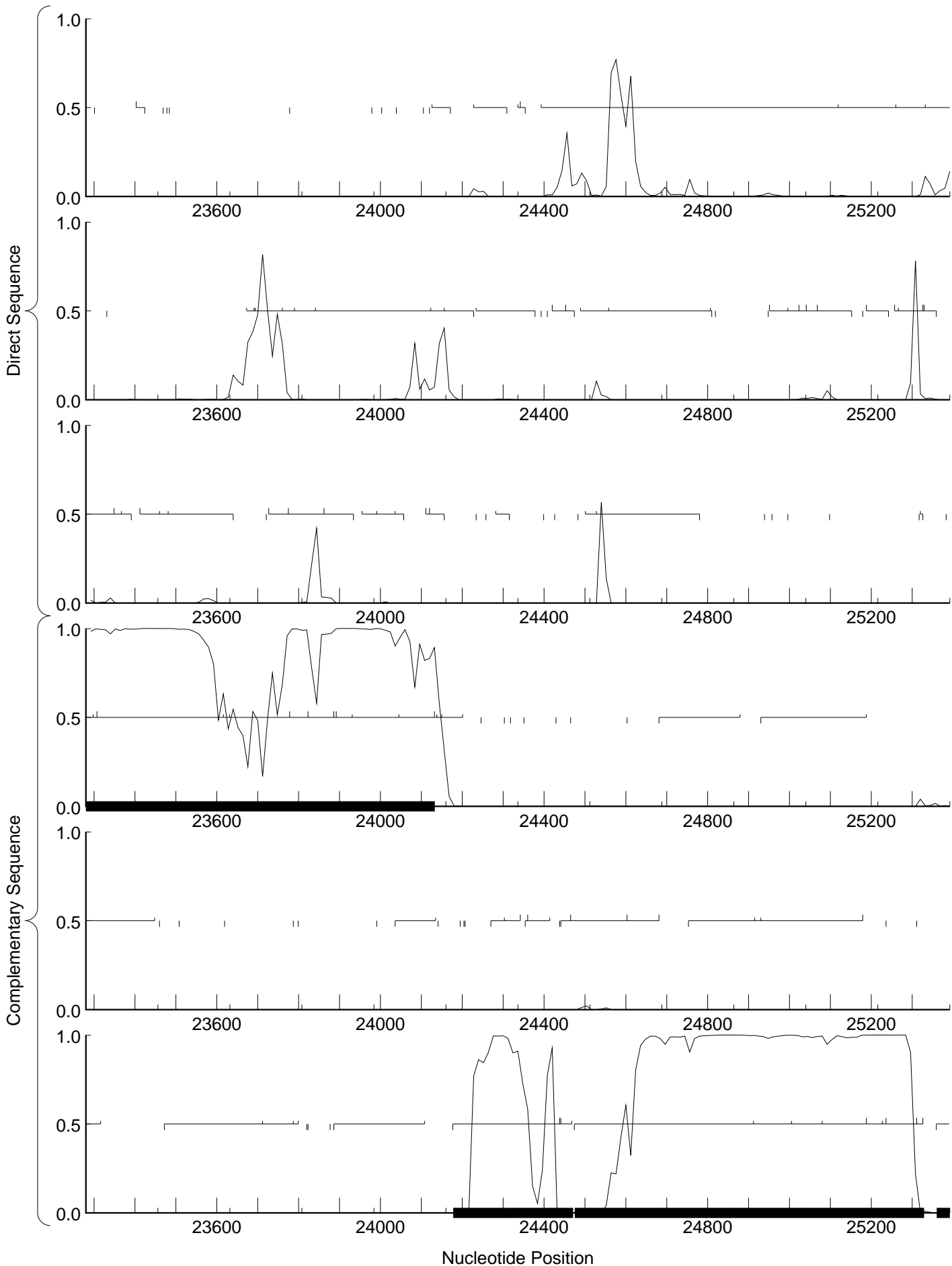


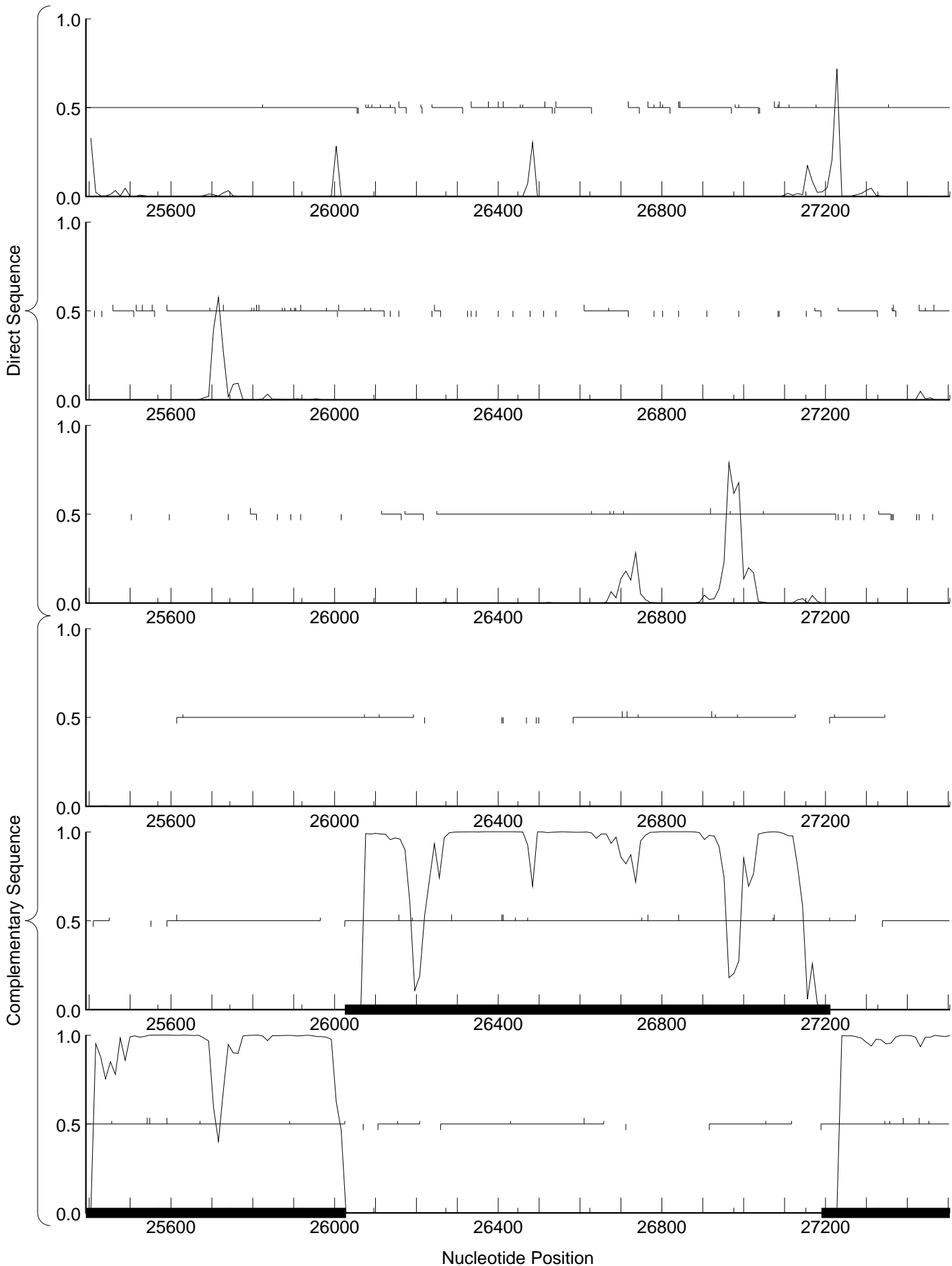


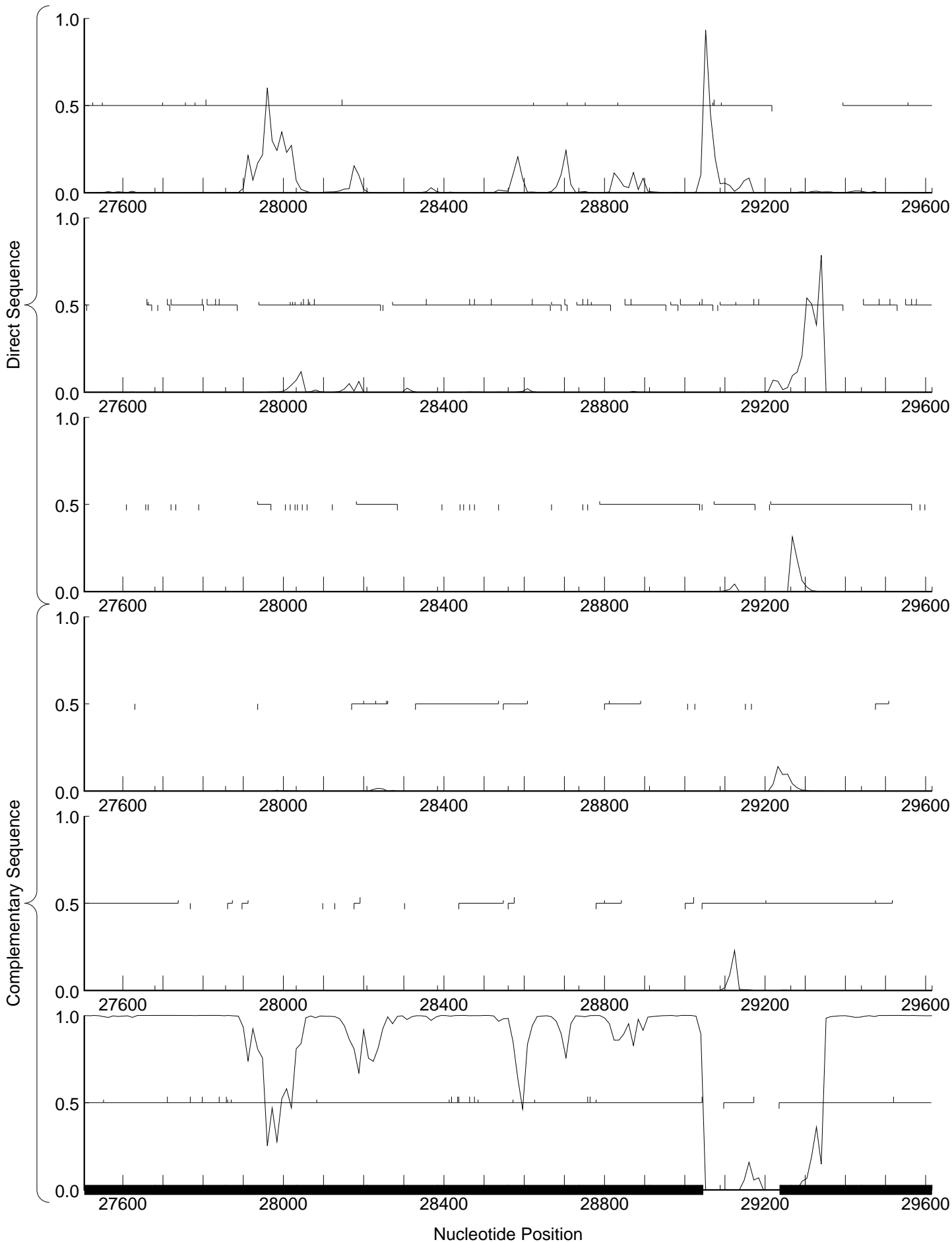


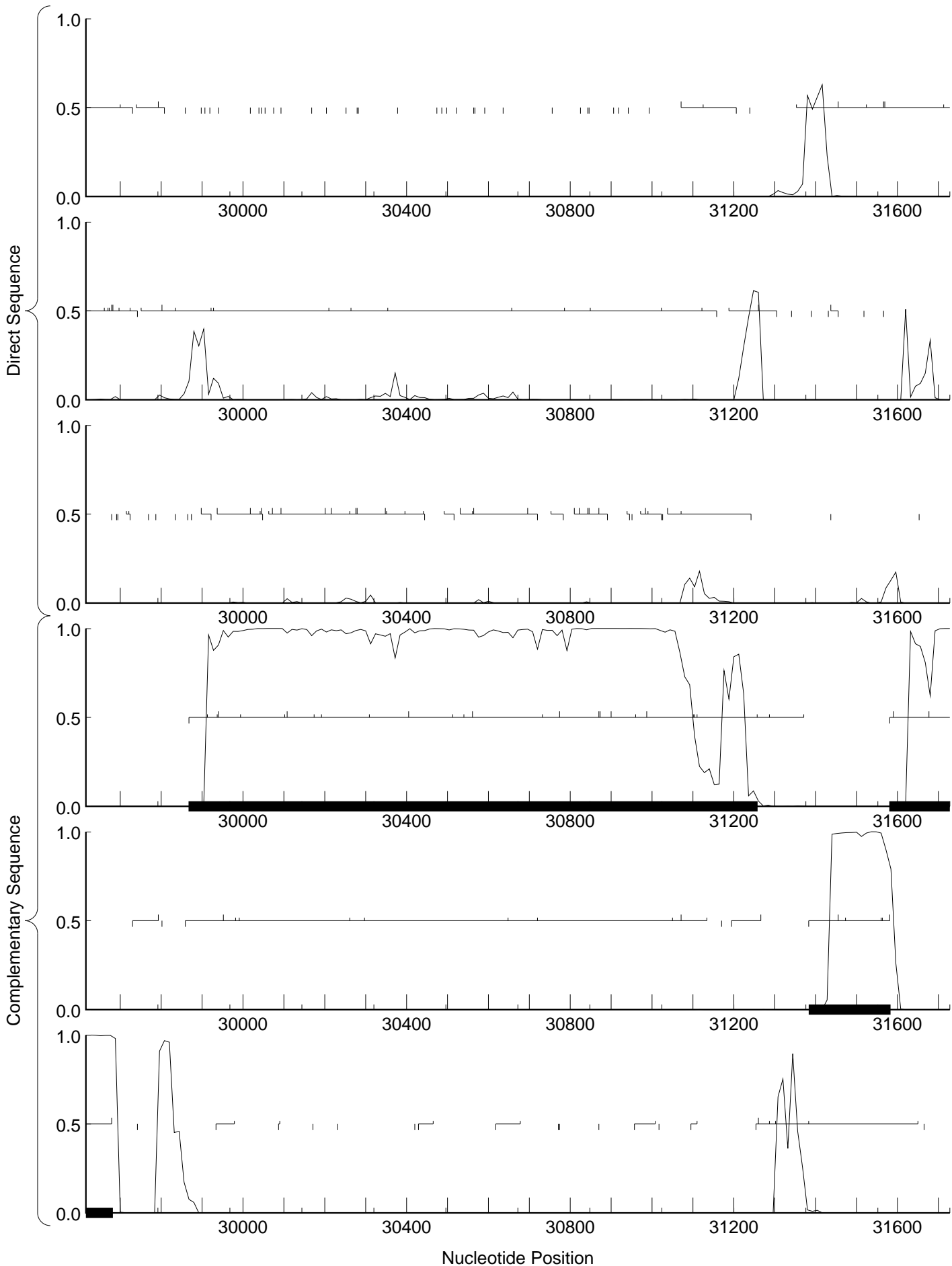


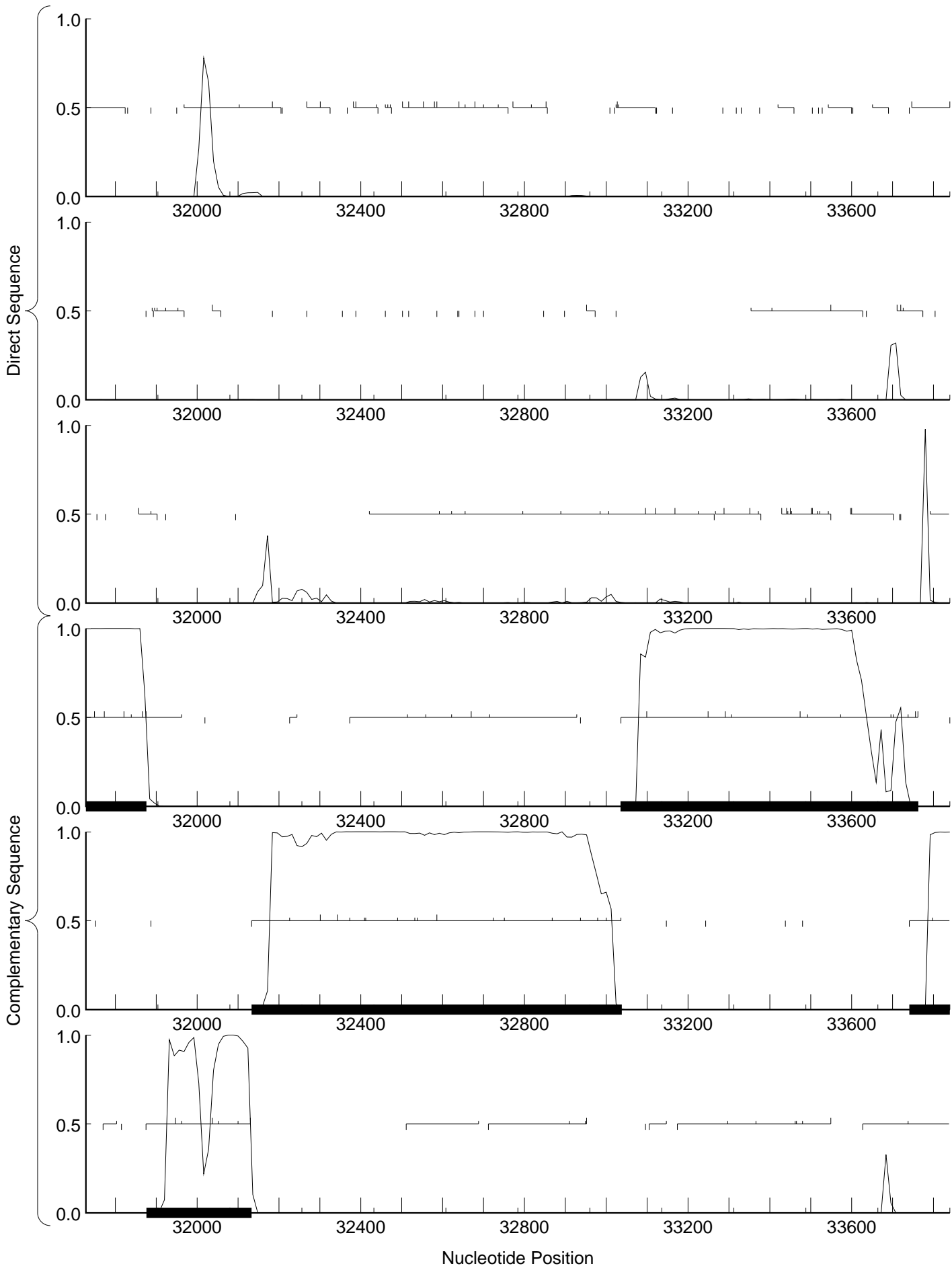


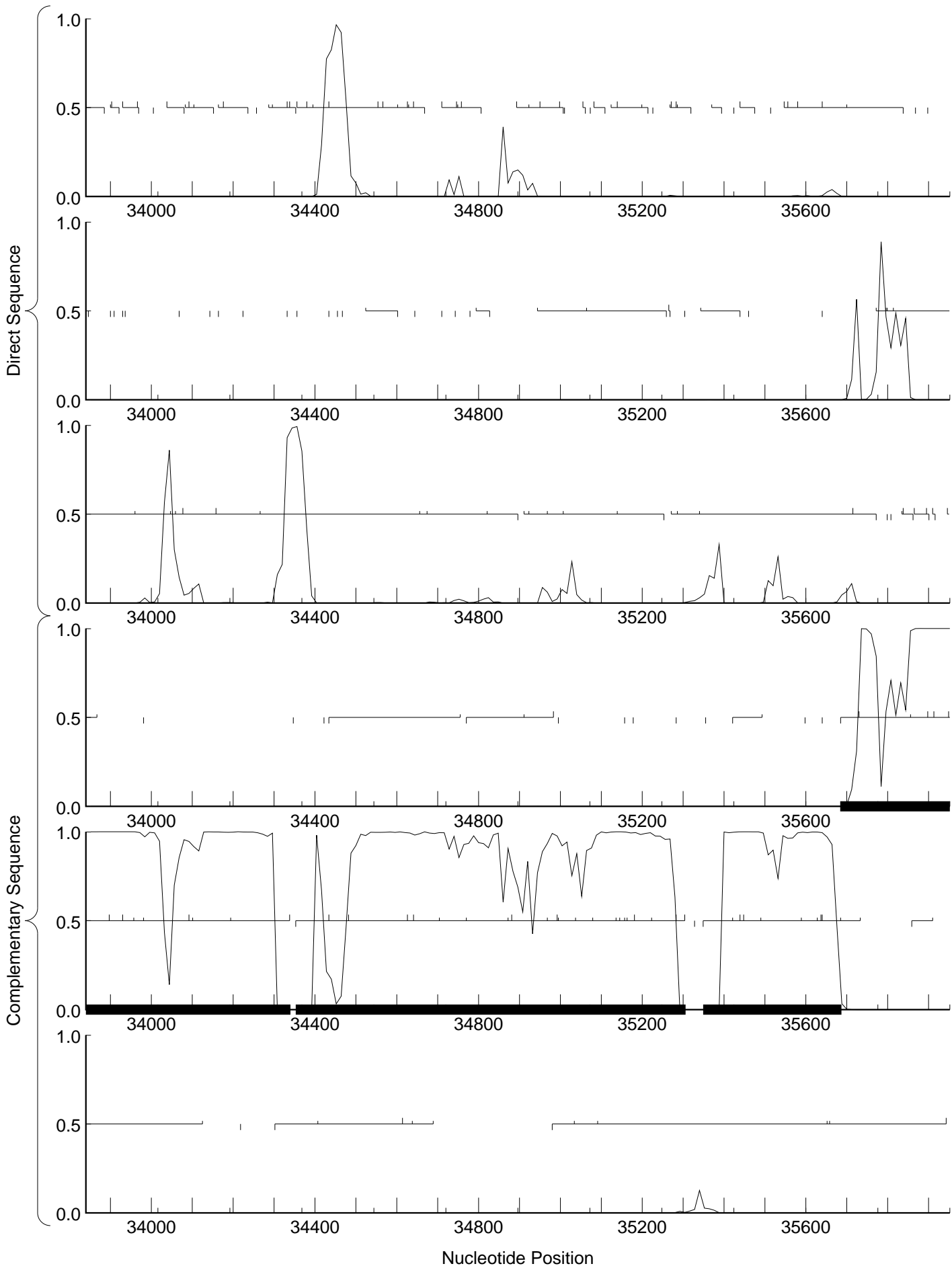


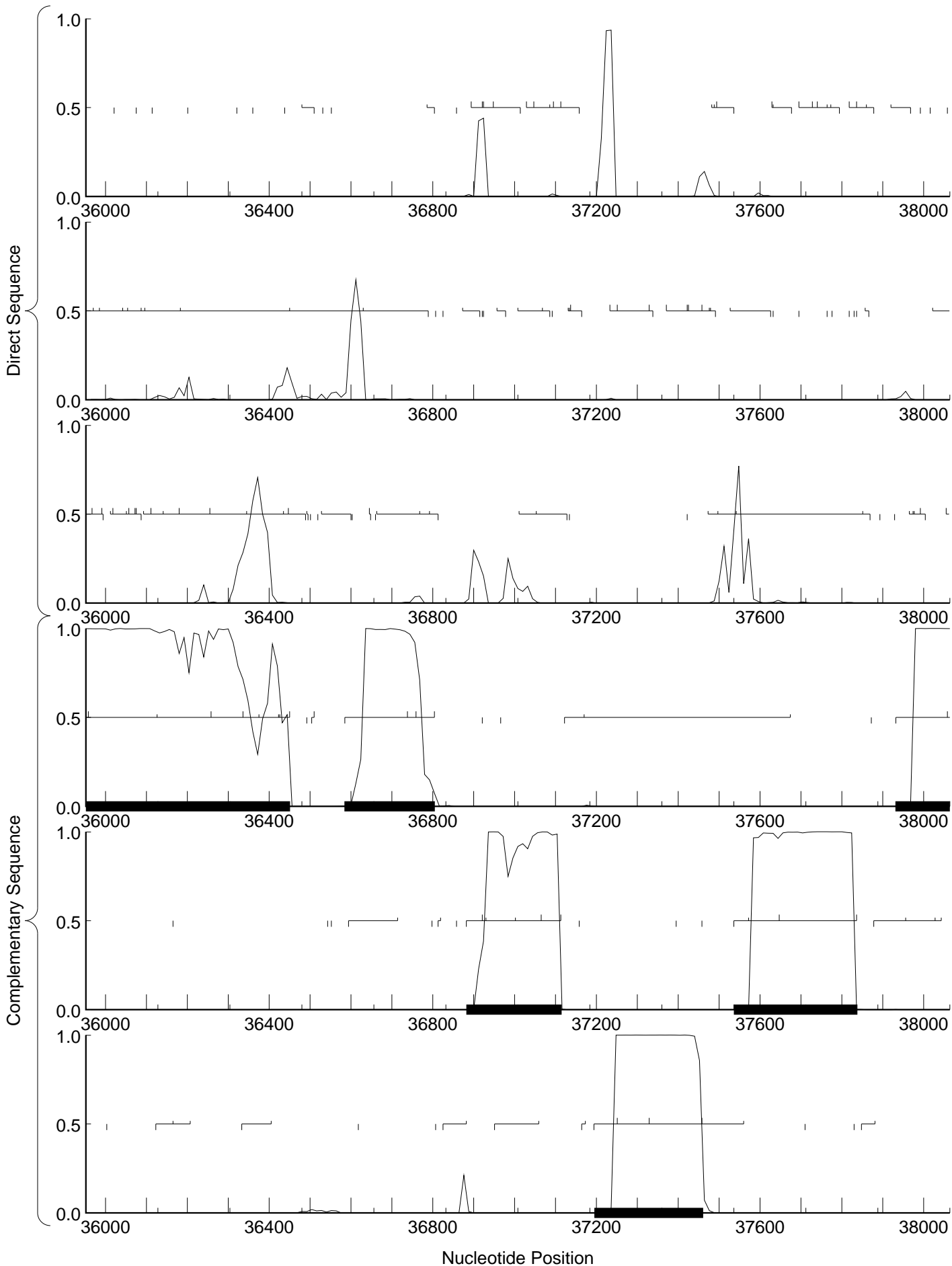


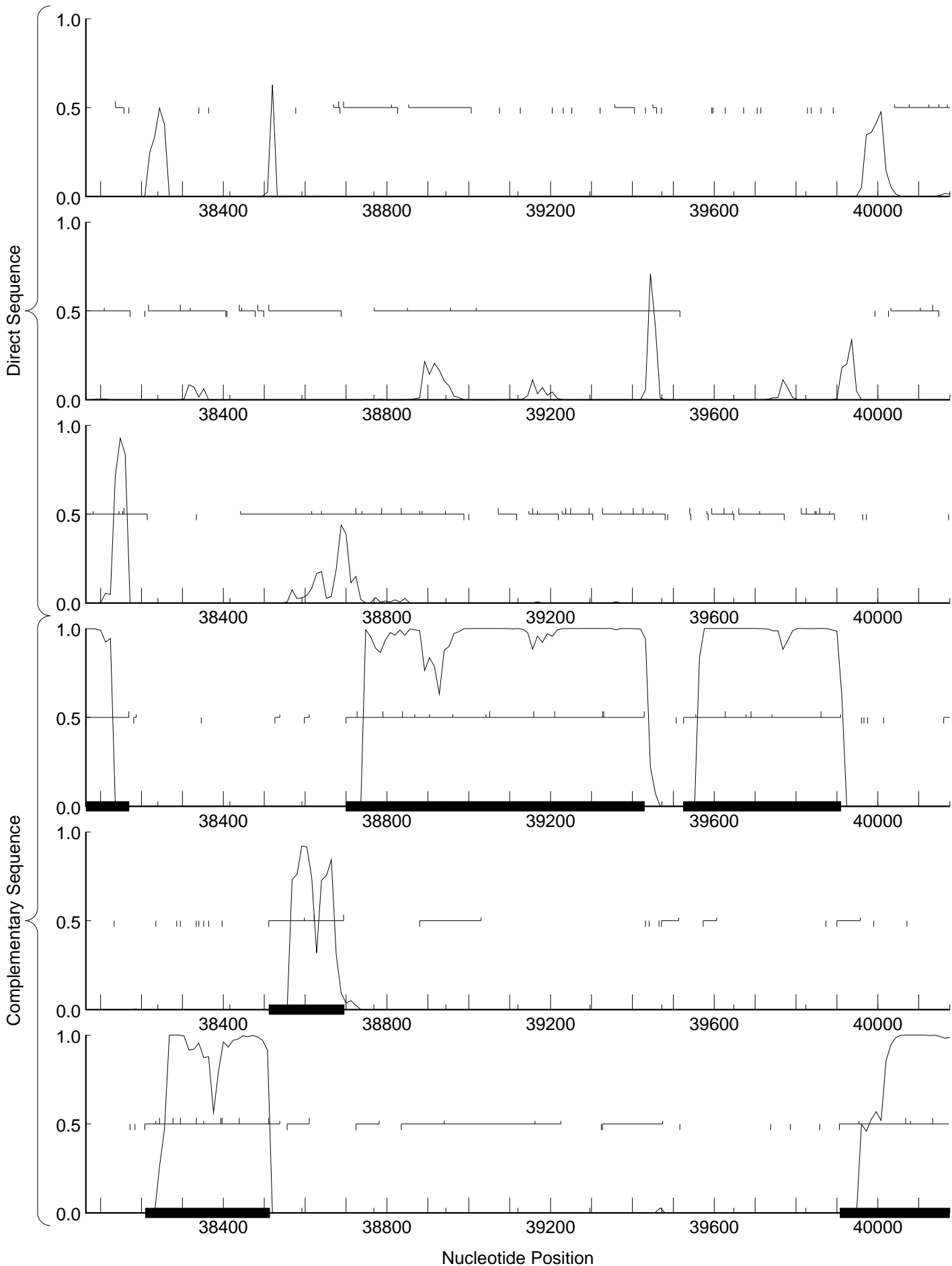












GeneMark.hmm prediction

