

GeneMark

Version 2.5p (09.08.06)

Copyright 1993 - M. Borodovsky, J. McIninch

PROGRAM INFORMATION

Sequence : Microbacterium phage Golden complete sequence, 39640 bp, circularly permuted, Cluster EA4
Analysis Date : 11/23/17 at 8:11:29
Pages : 20
Sequence Length : 39640 bp
GC Content : 64.08%

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,

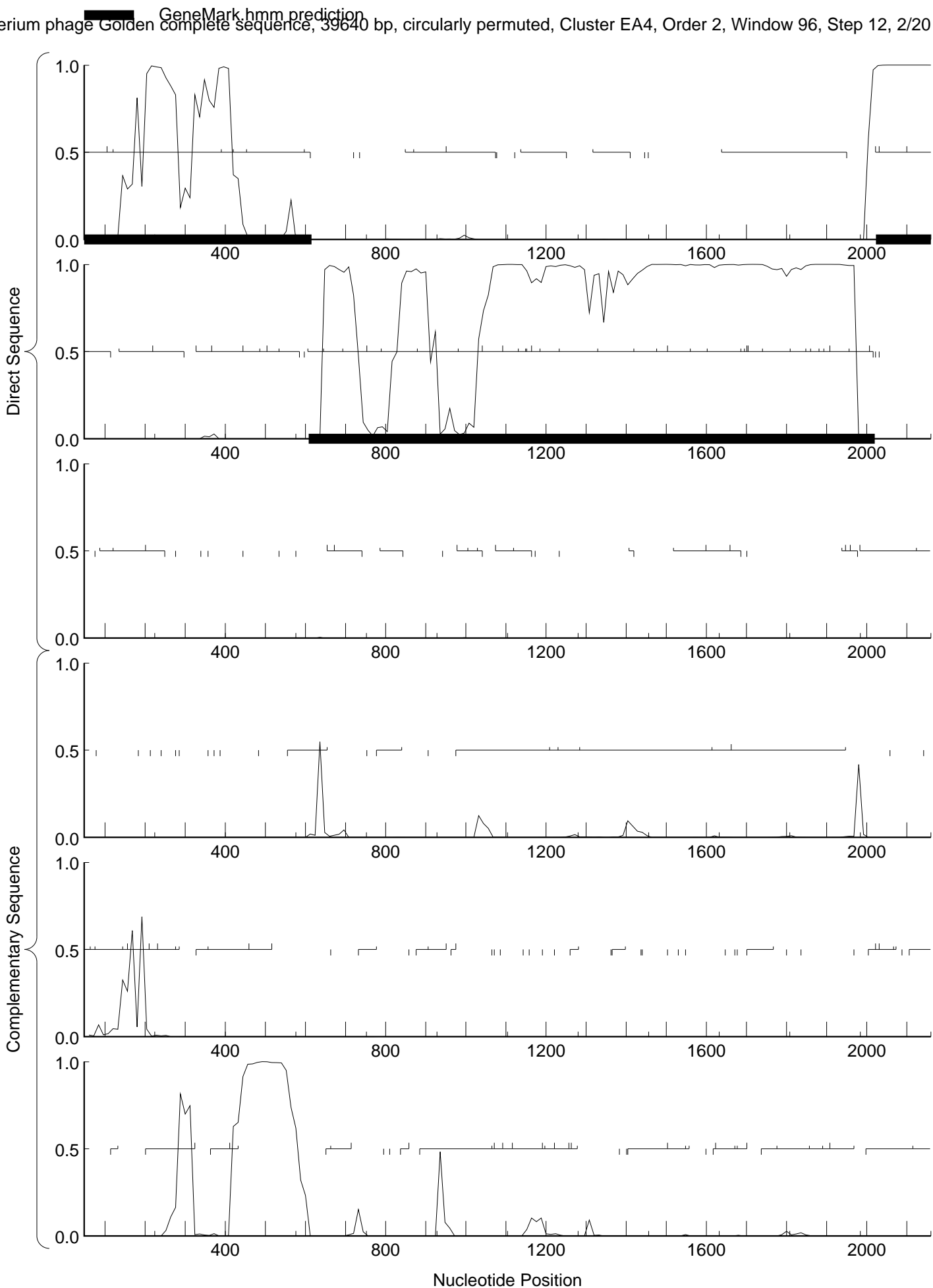
Matrix notes & comments

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

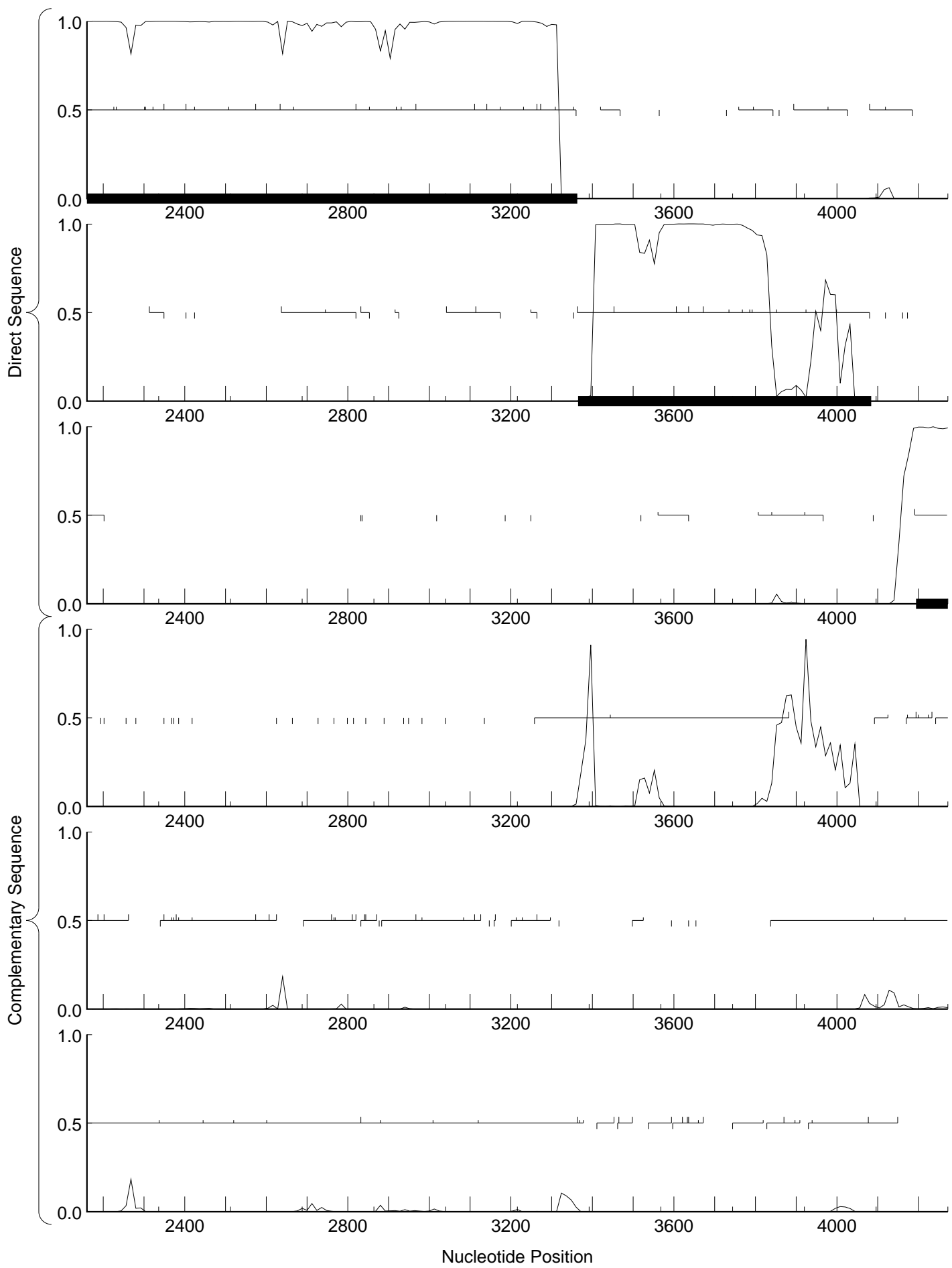
MATRIX INFORMATION

Matrix : Heuristic, GC = 64
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

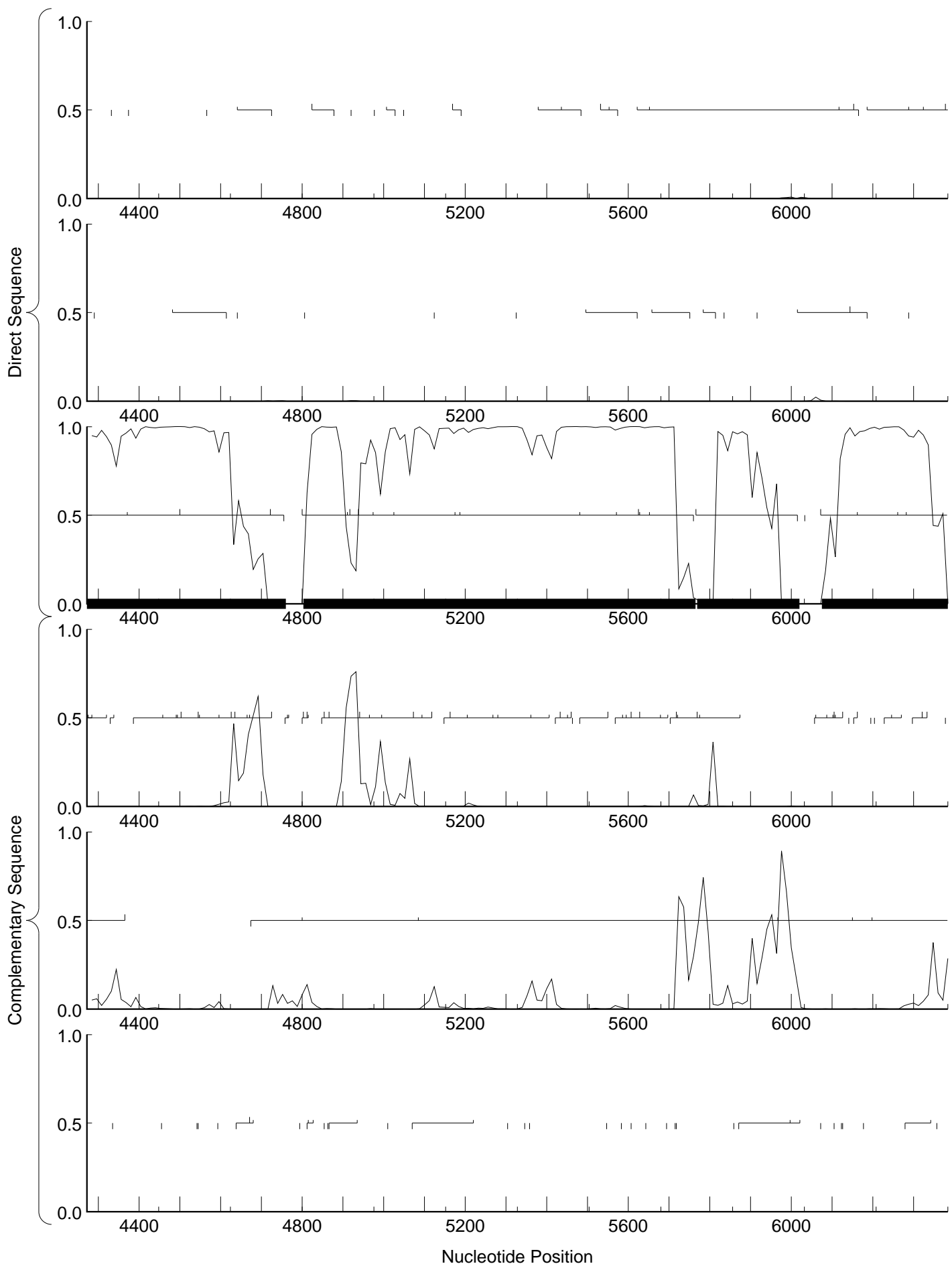


GeneMark.hmm prediction

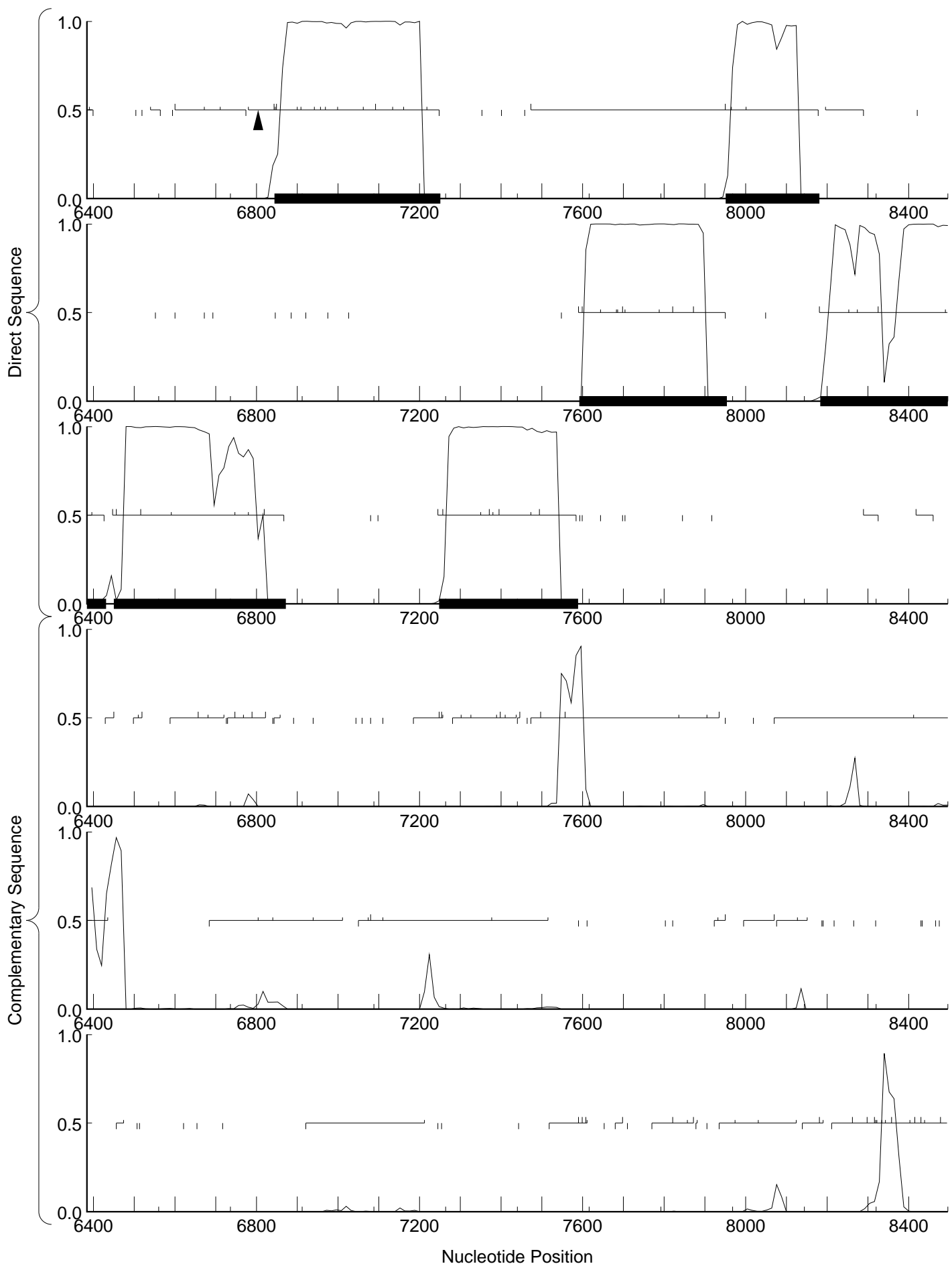


Nucleotide Position

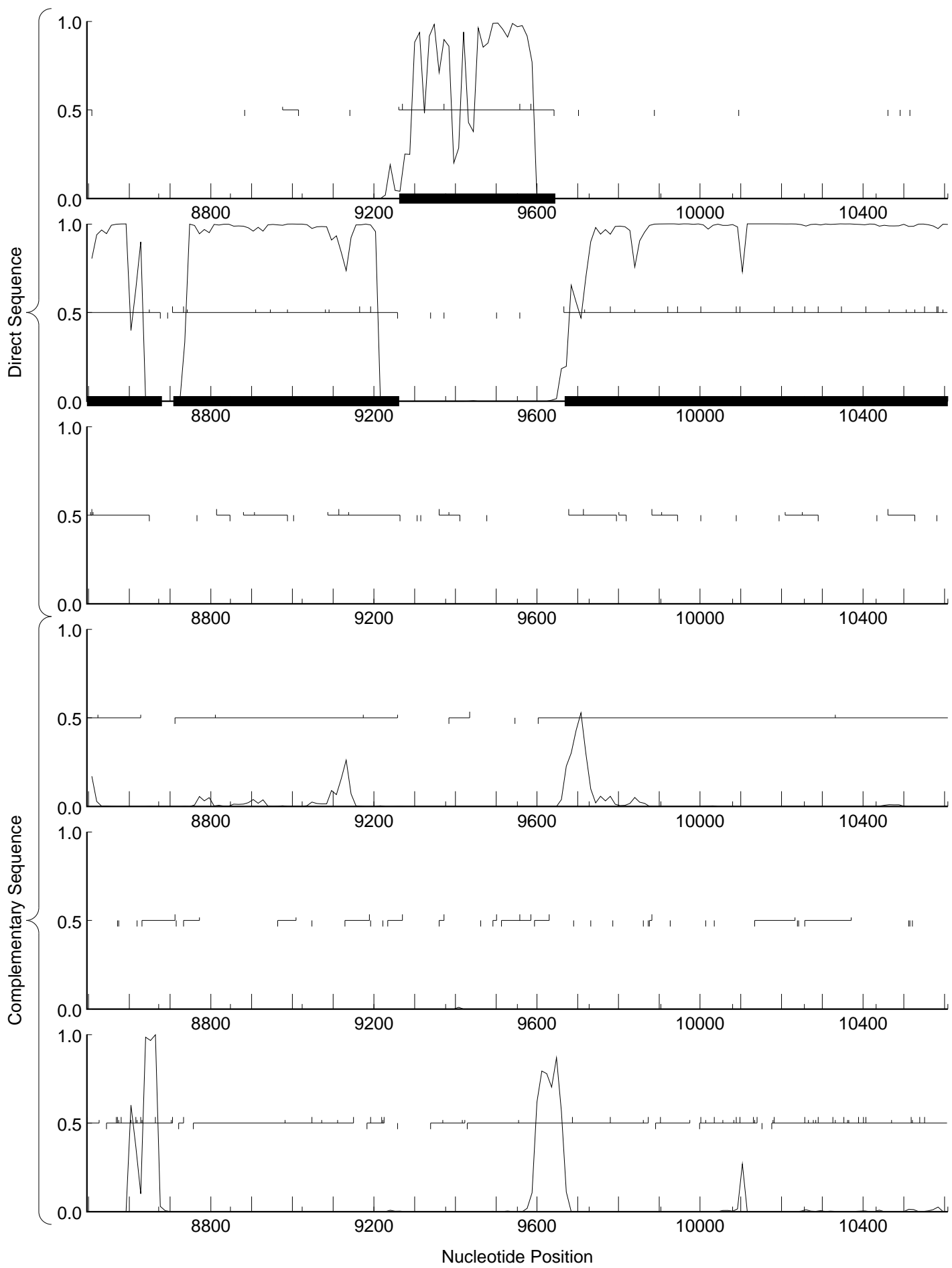
GeneMark.hmm prediction



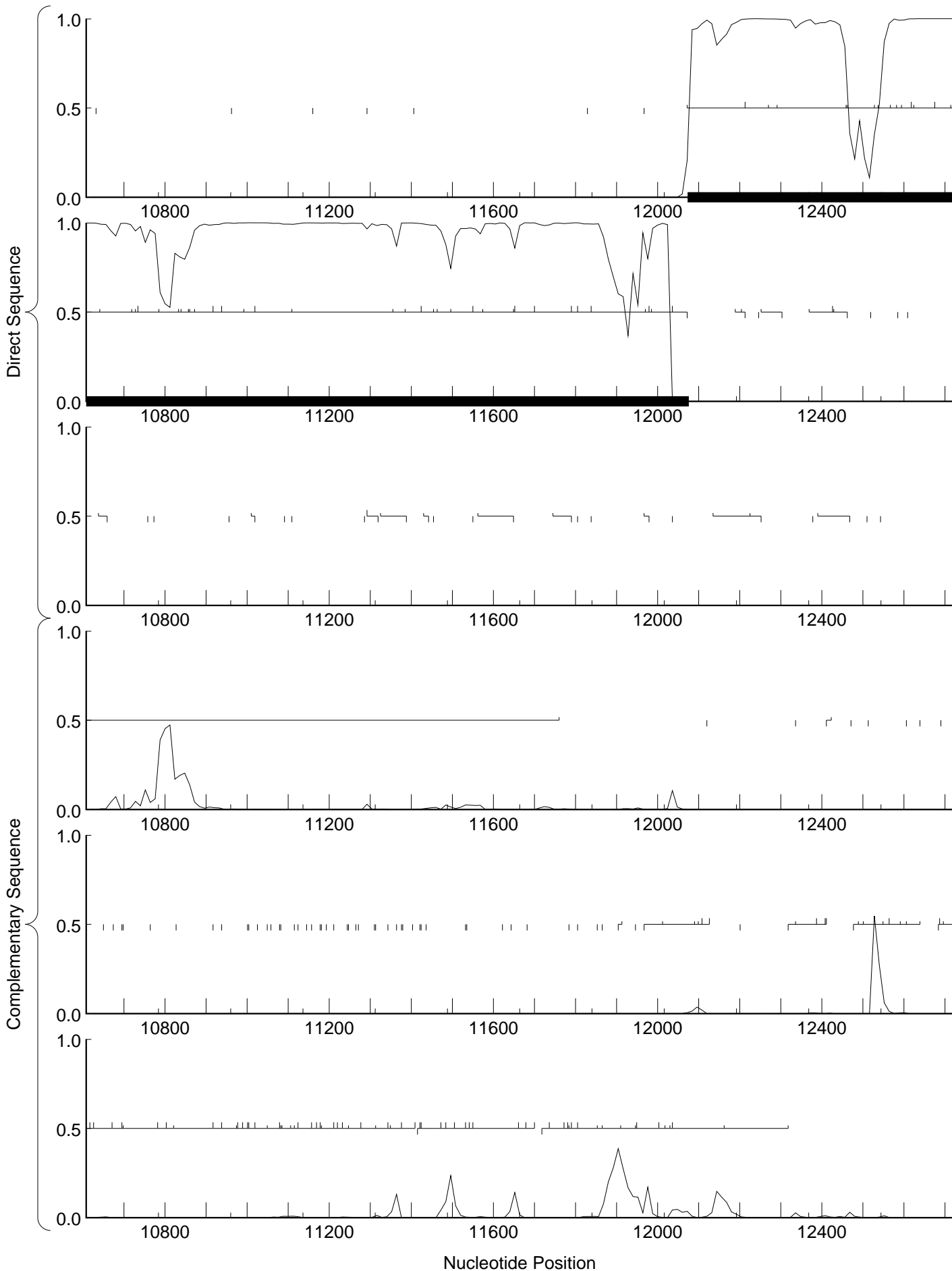
GeneMark.hmm prediction

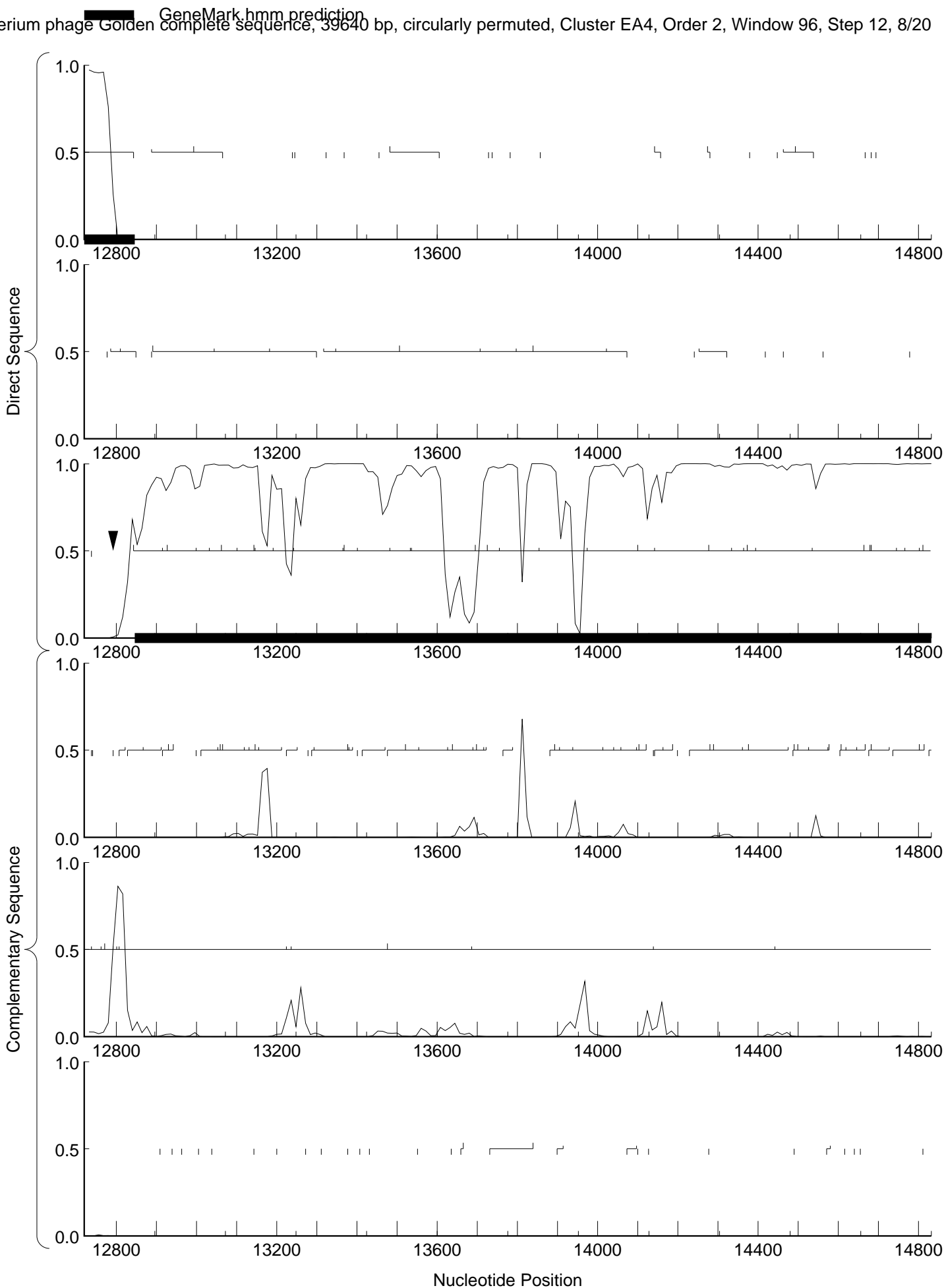


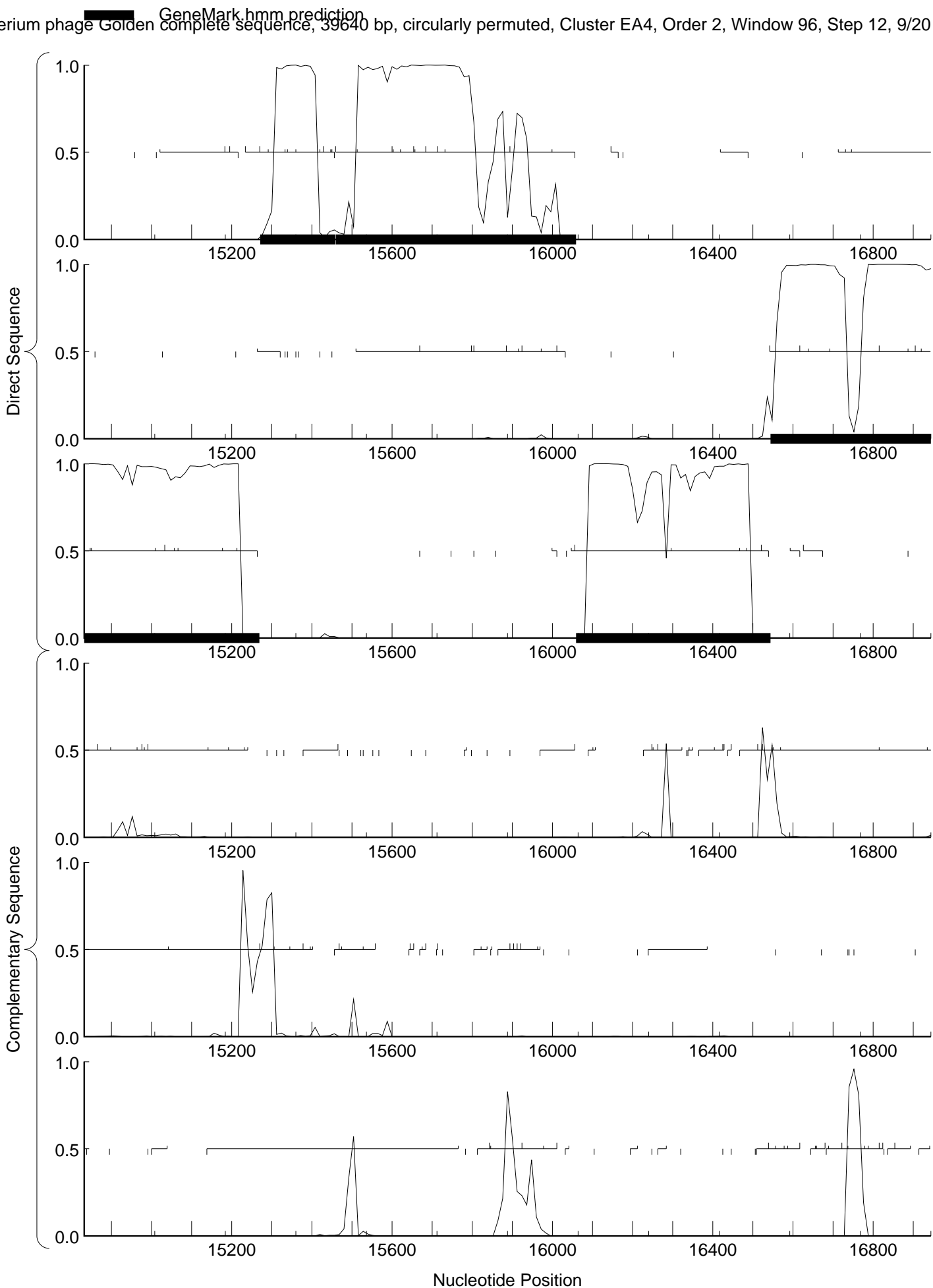
GeneMark.hmm prediction

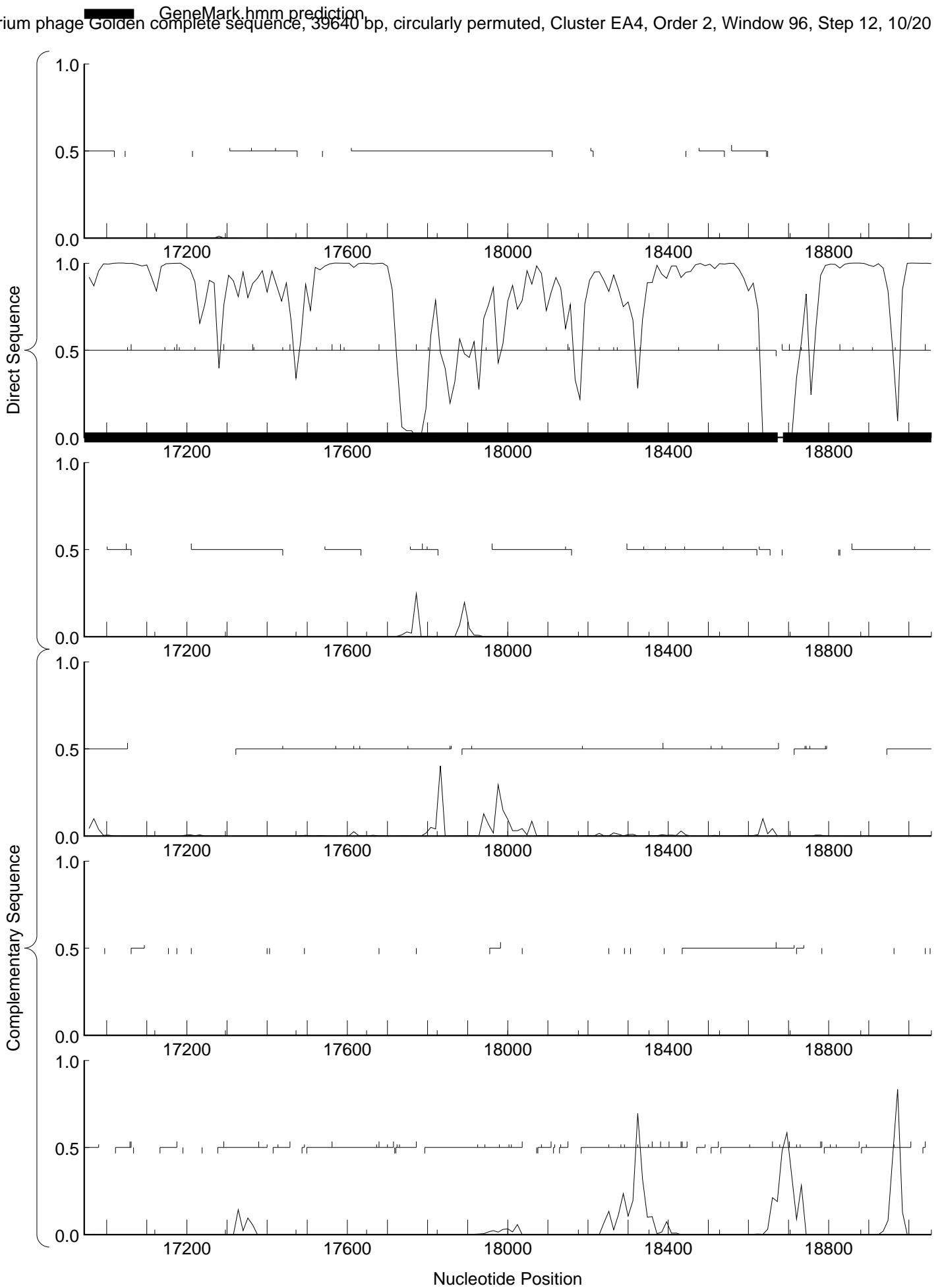


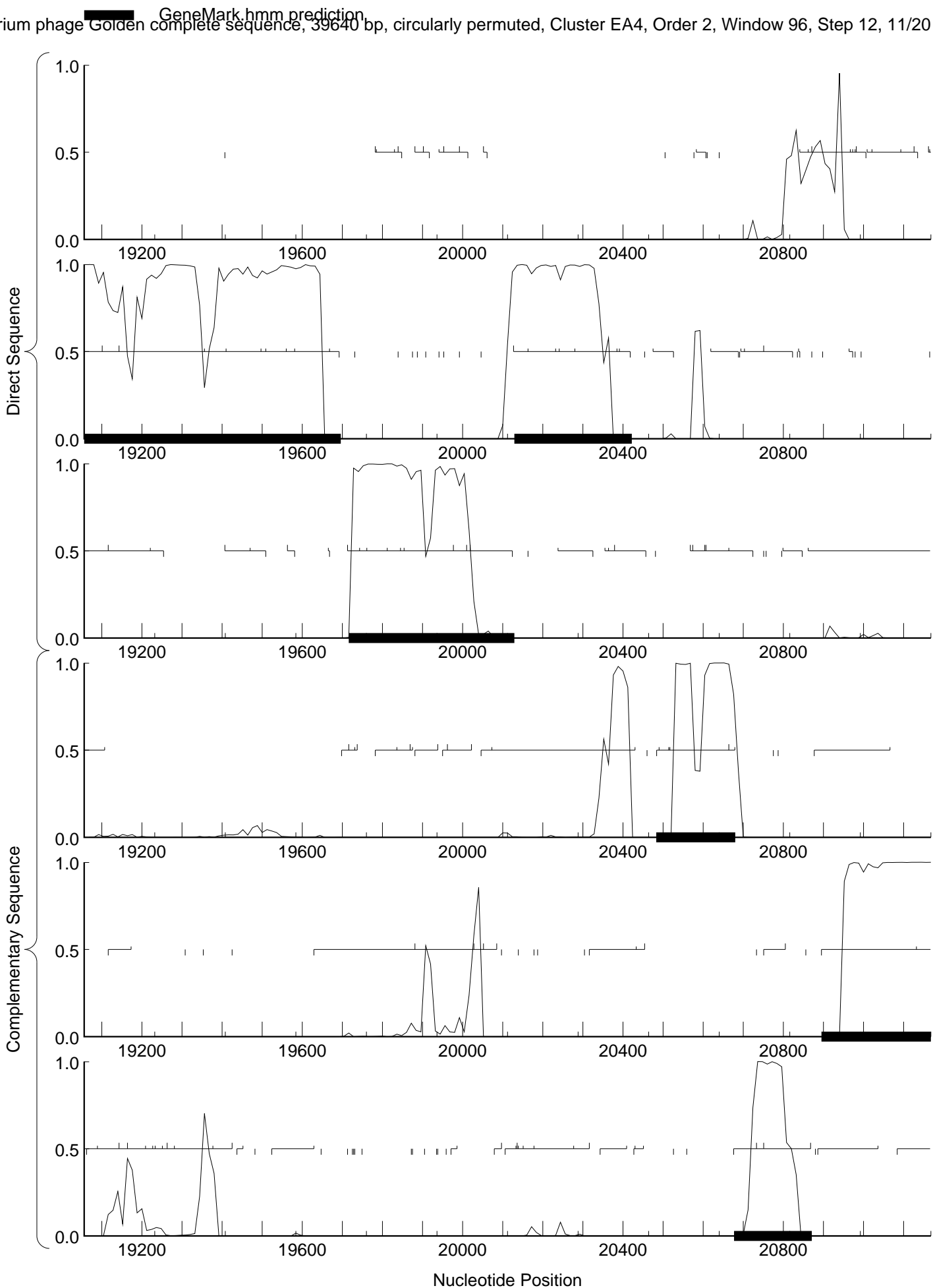
GeneMark.hmm prediction

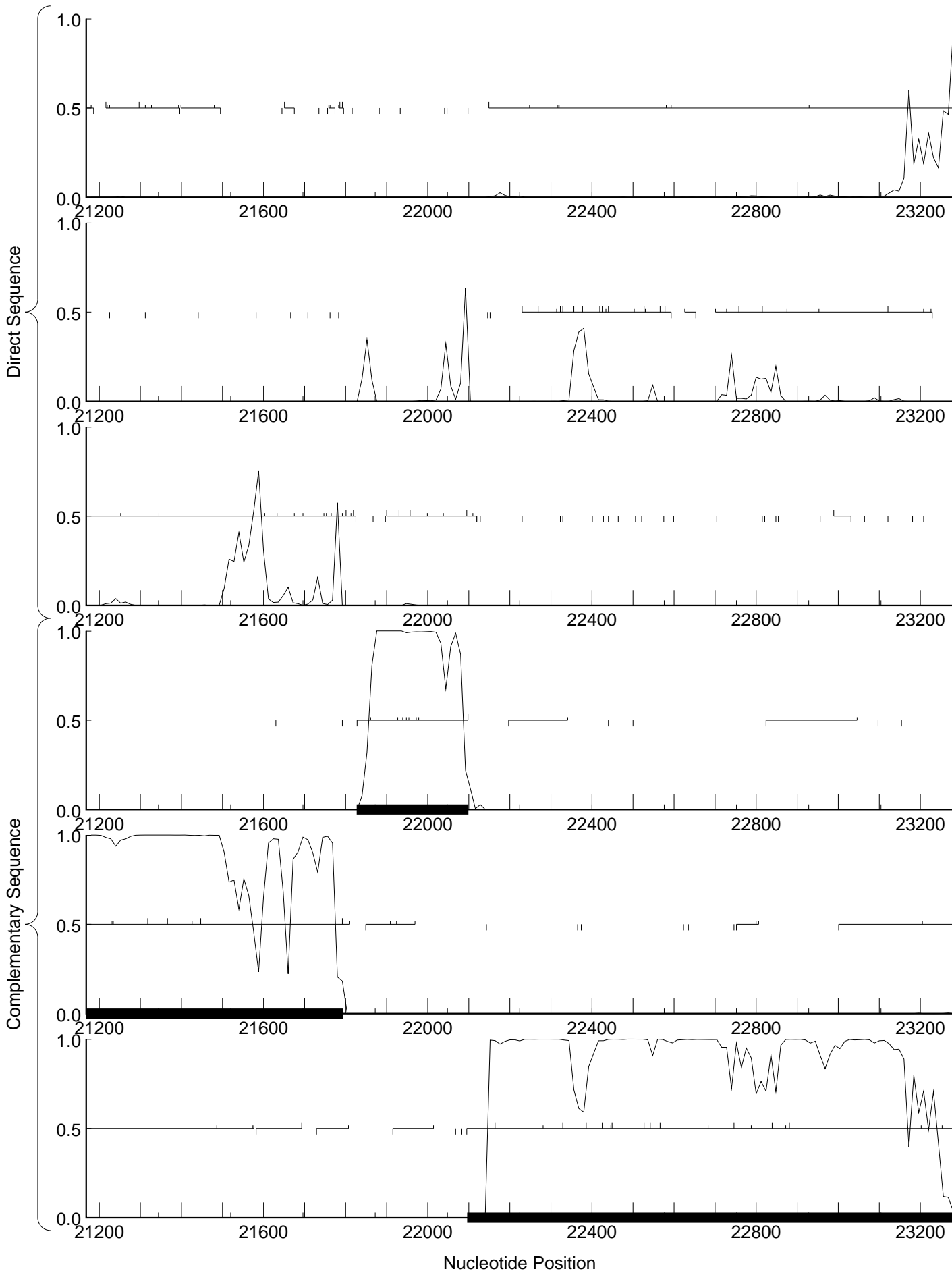


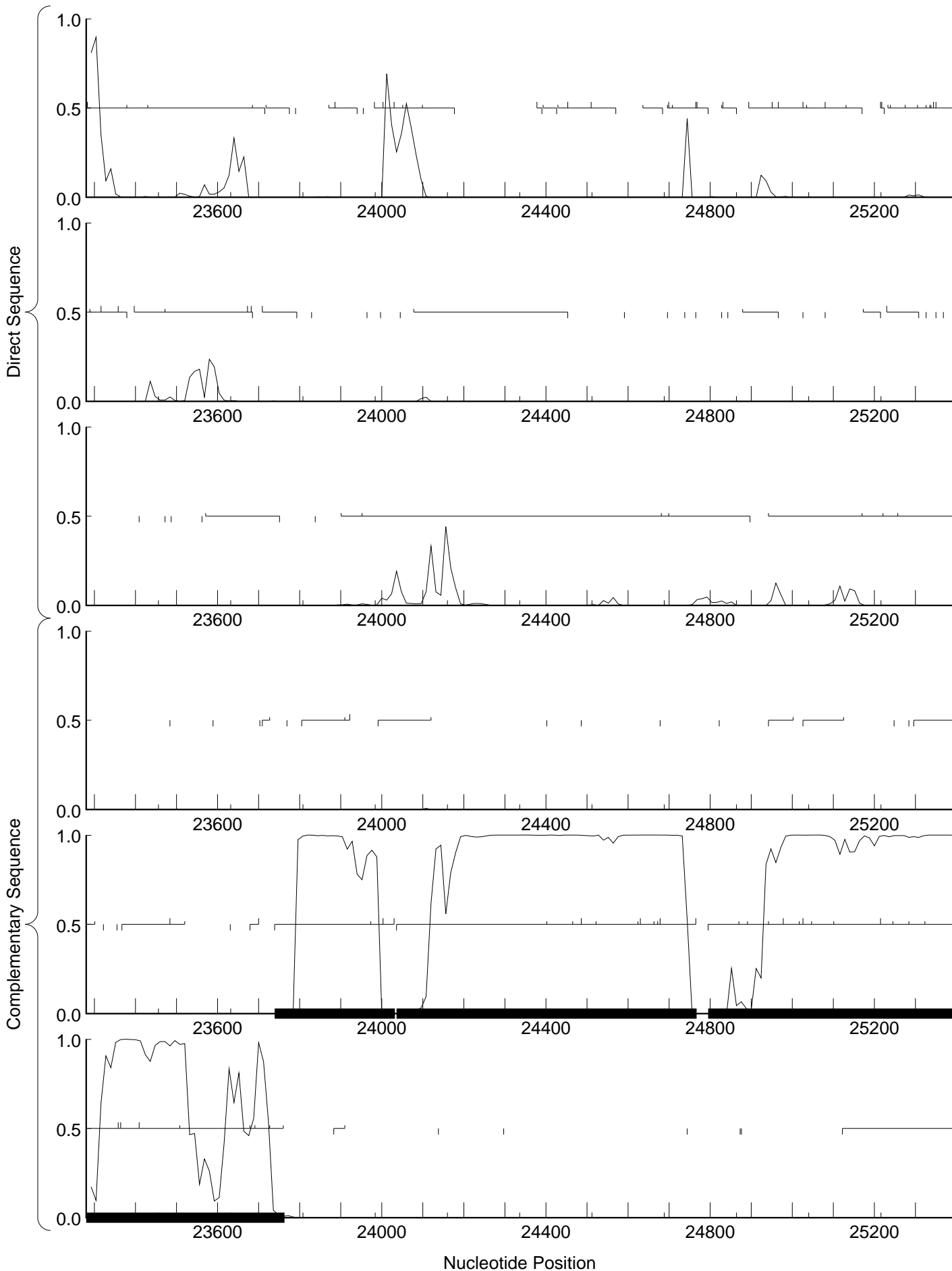


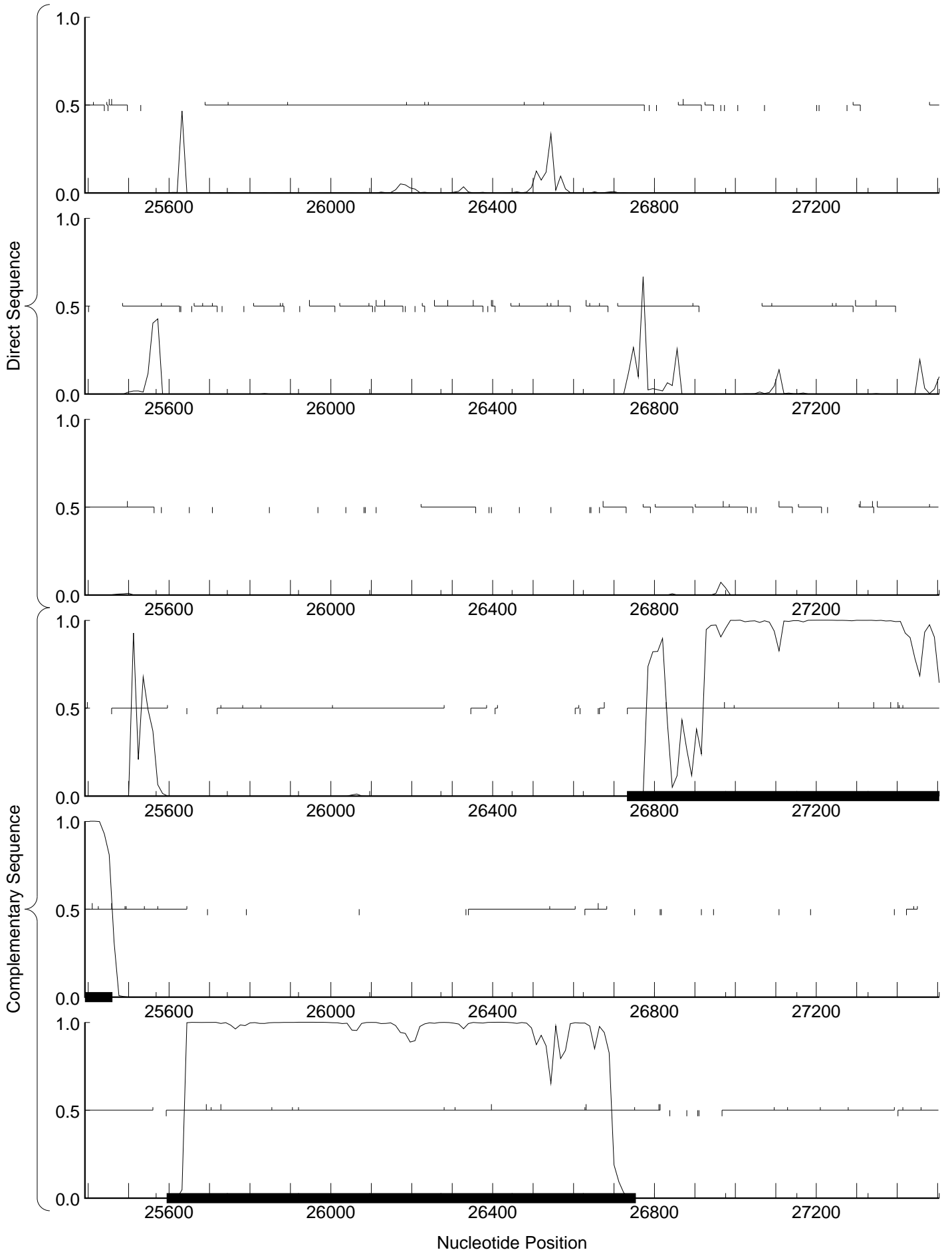


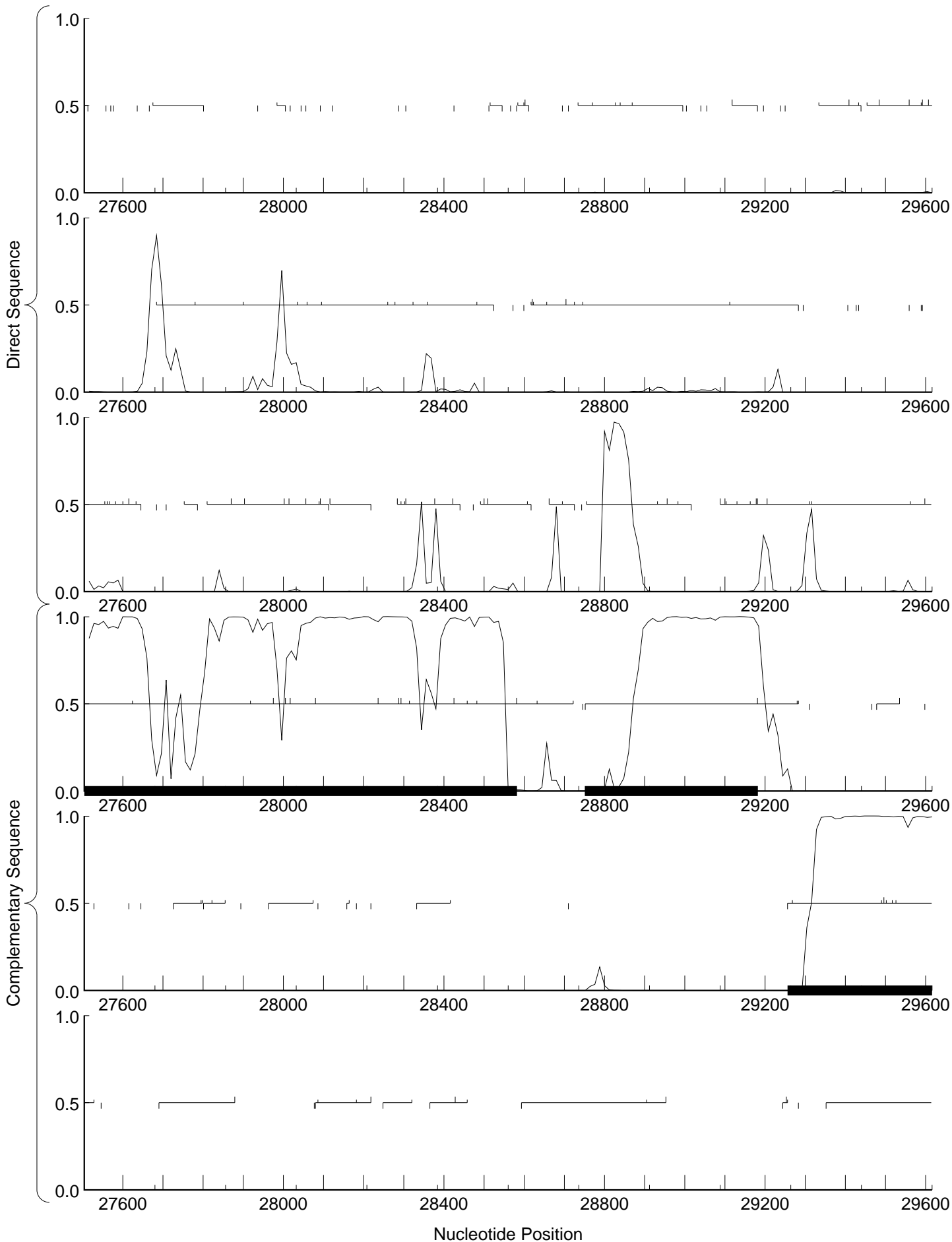


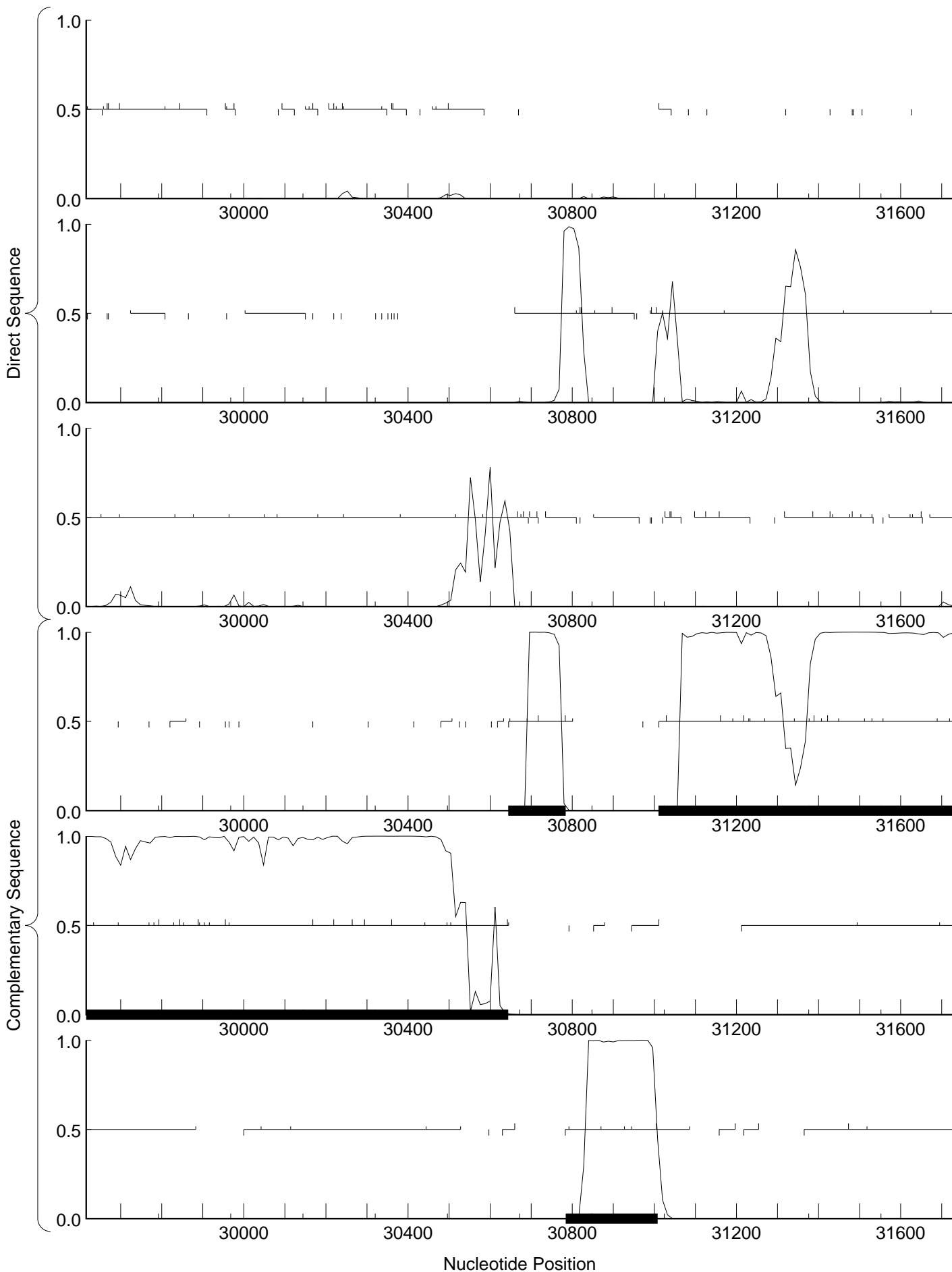


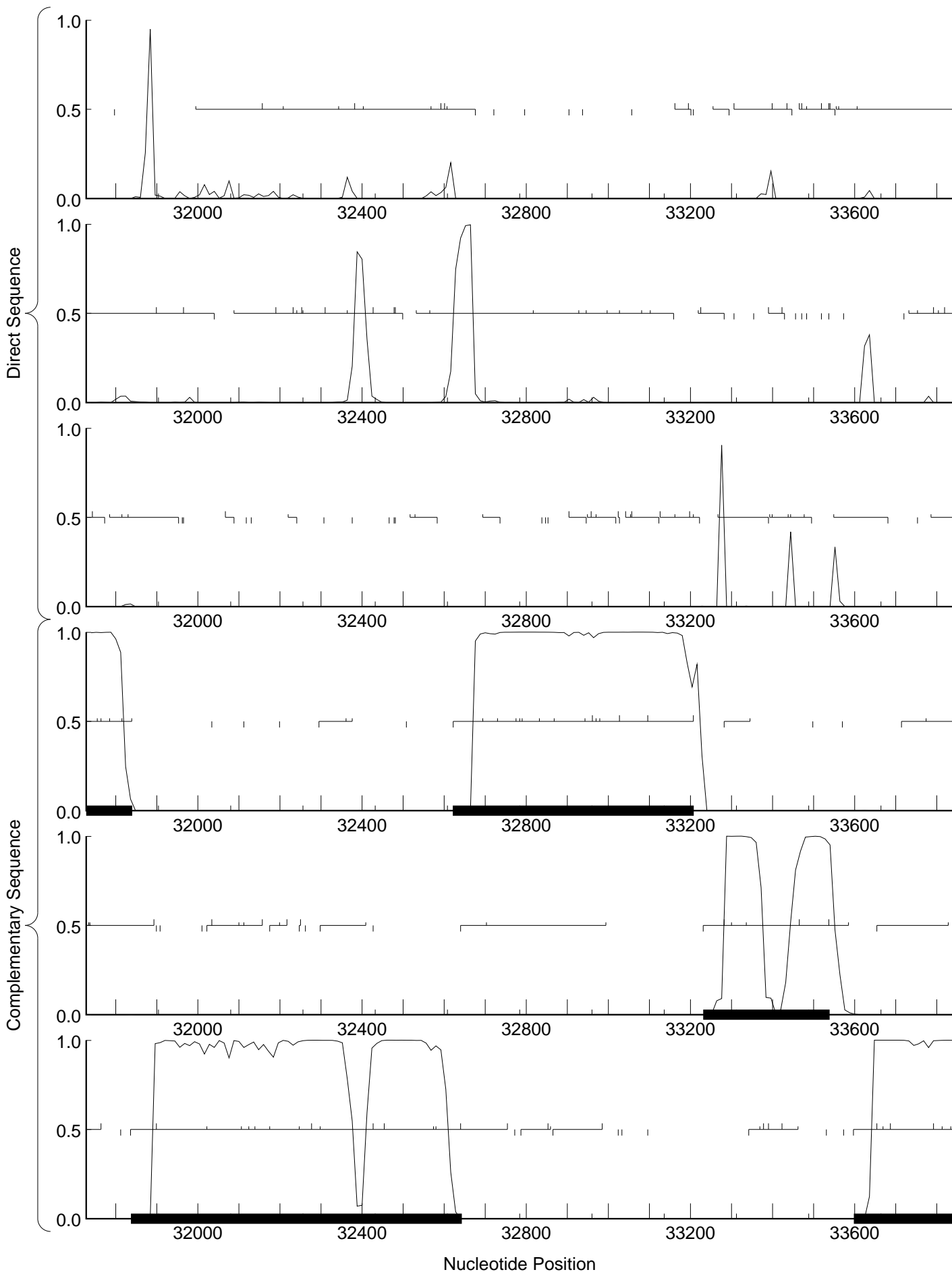


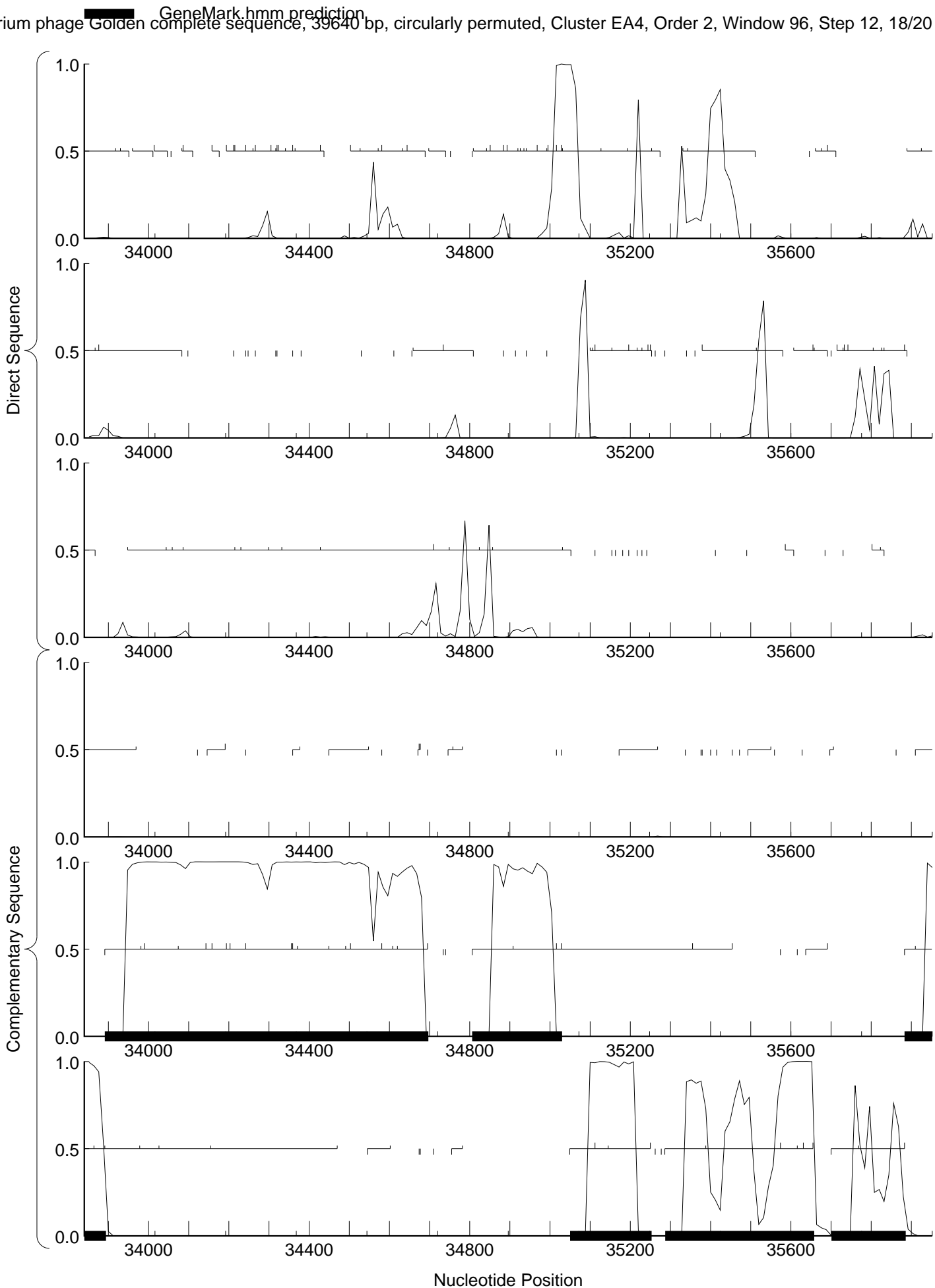


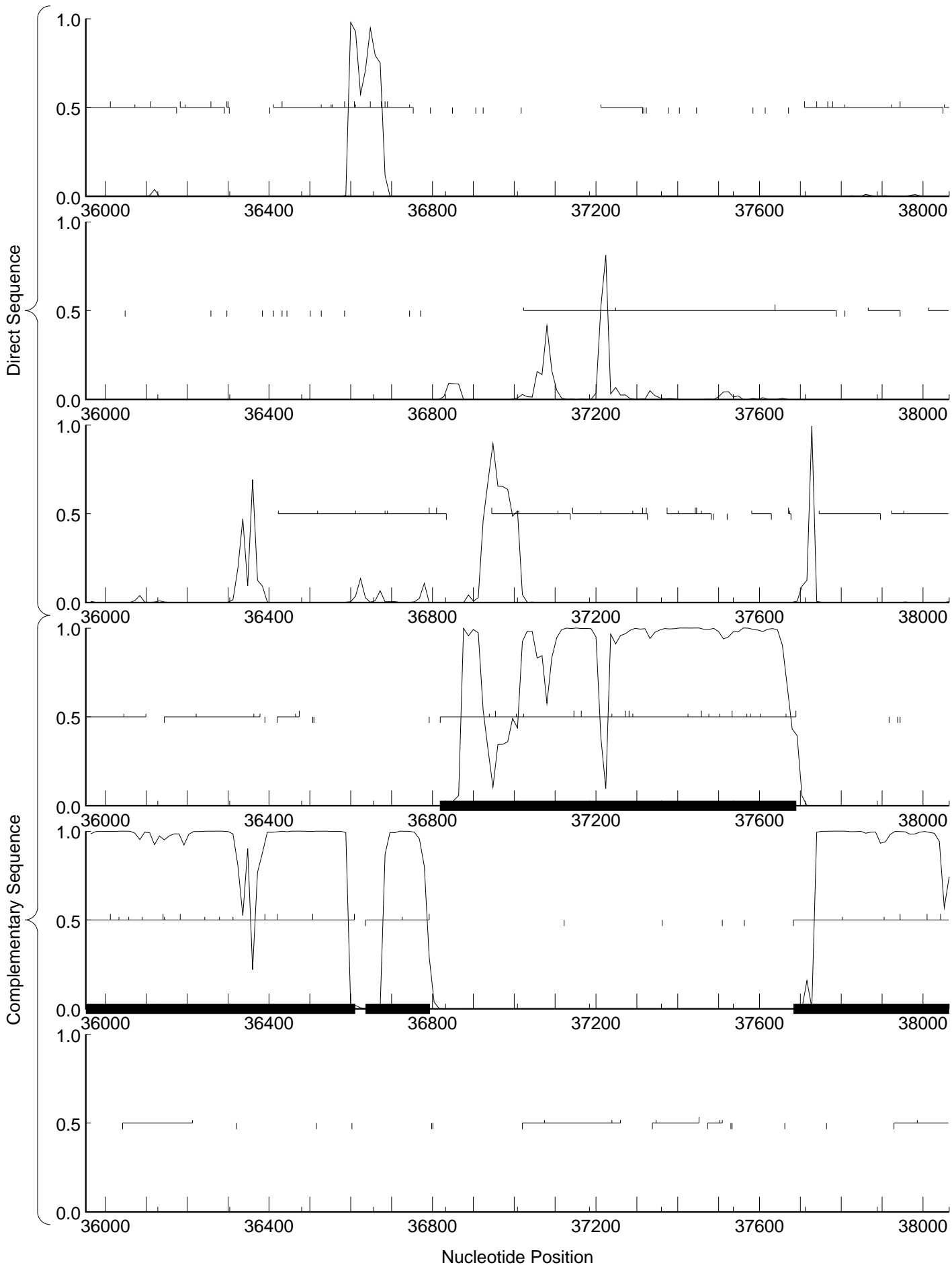












GeneMark.hmm prediction

