

# GeneMark

Version 2.5p (09.08.06)

Copyright 1993 - M. Borodovsky, J. McIninch

## PROGRAM INFORMATION

Sequence : Streptomyces phage ZooBear complete sequence, 46135 bp including 274 bp terminal repeat, Cl  
Analysis Date : 6/23/18 at 8:24:39  
Pages : 23  
Sequence Length : 46135 bp  
GC Content : 59.65%

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

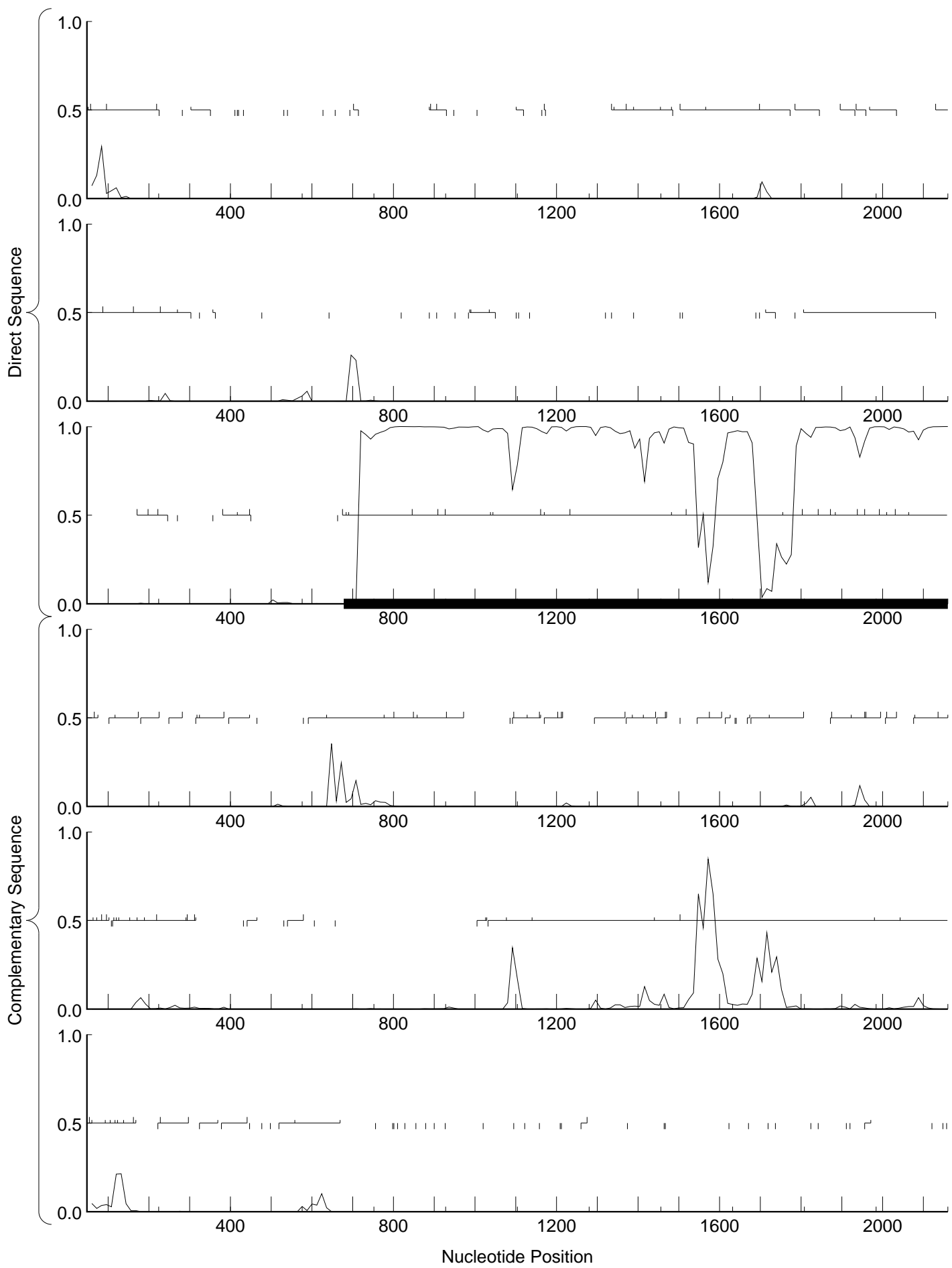
For details on the model building procedure see:  
Besemer J. and Borodovsky M.  
"Heuristic approach to deriving models for gene finding"  
NAR, 1999, Vol. 27, No. 19, pp. 3911-3920

## MATRIX INFORMATION

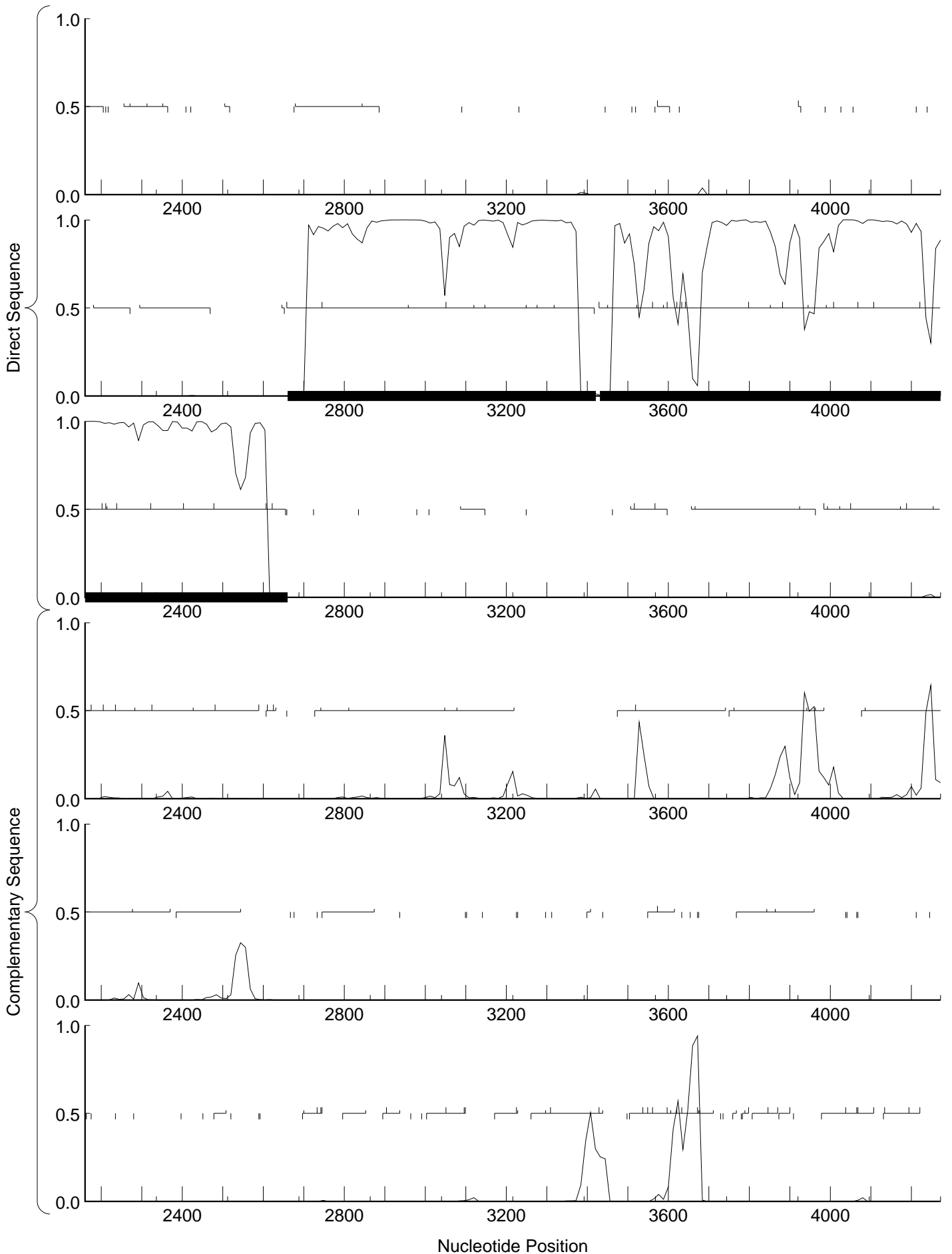
Matrix : Heuristic, GC = 60  
Author : Borodovsky Laboratory - Georgia Tech  
Order : 2

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

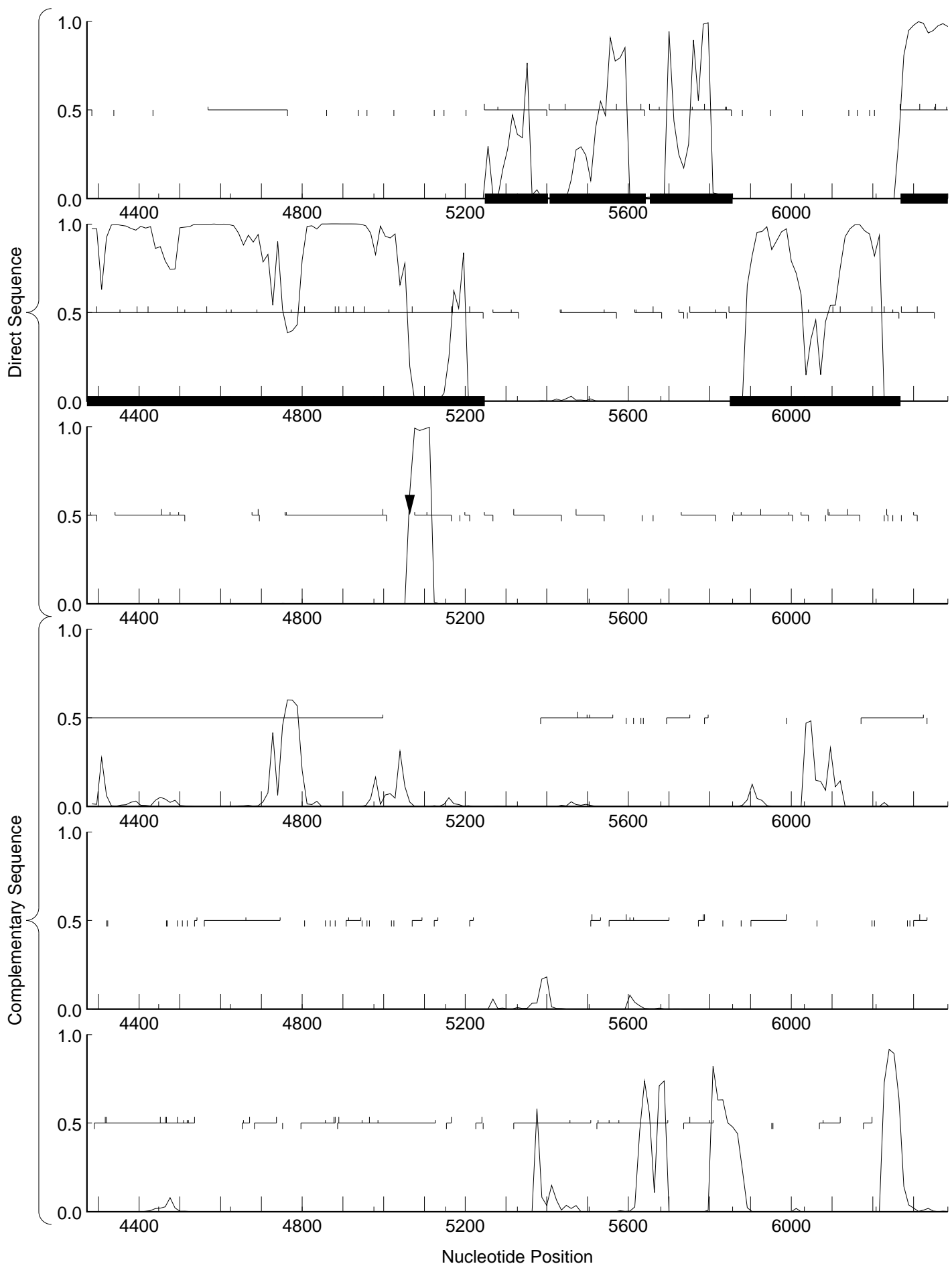
GeneMark\_hmm prediction



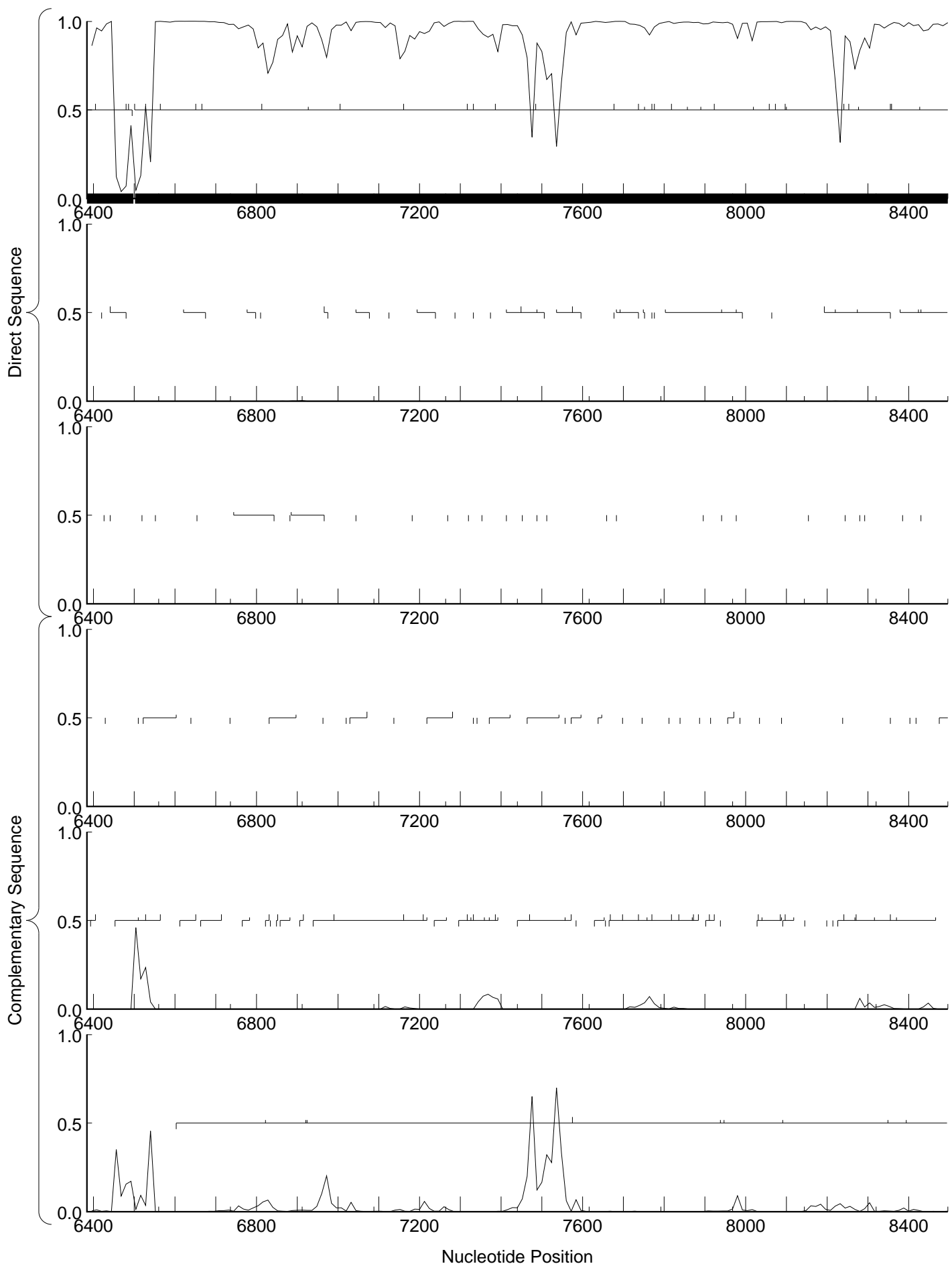
GeneMark\_hmm prediction



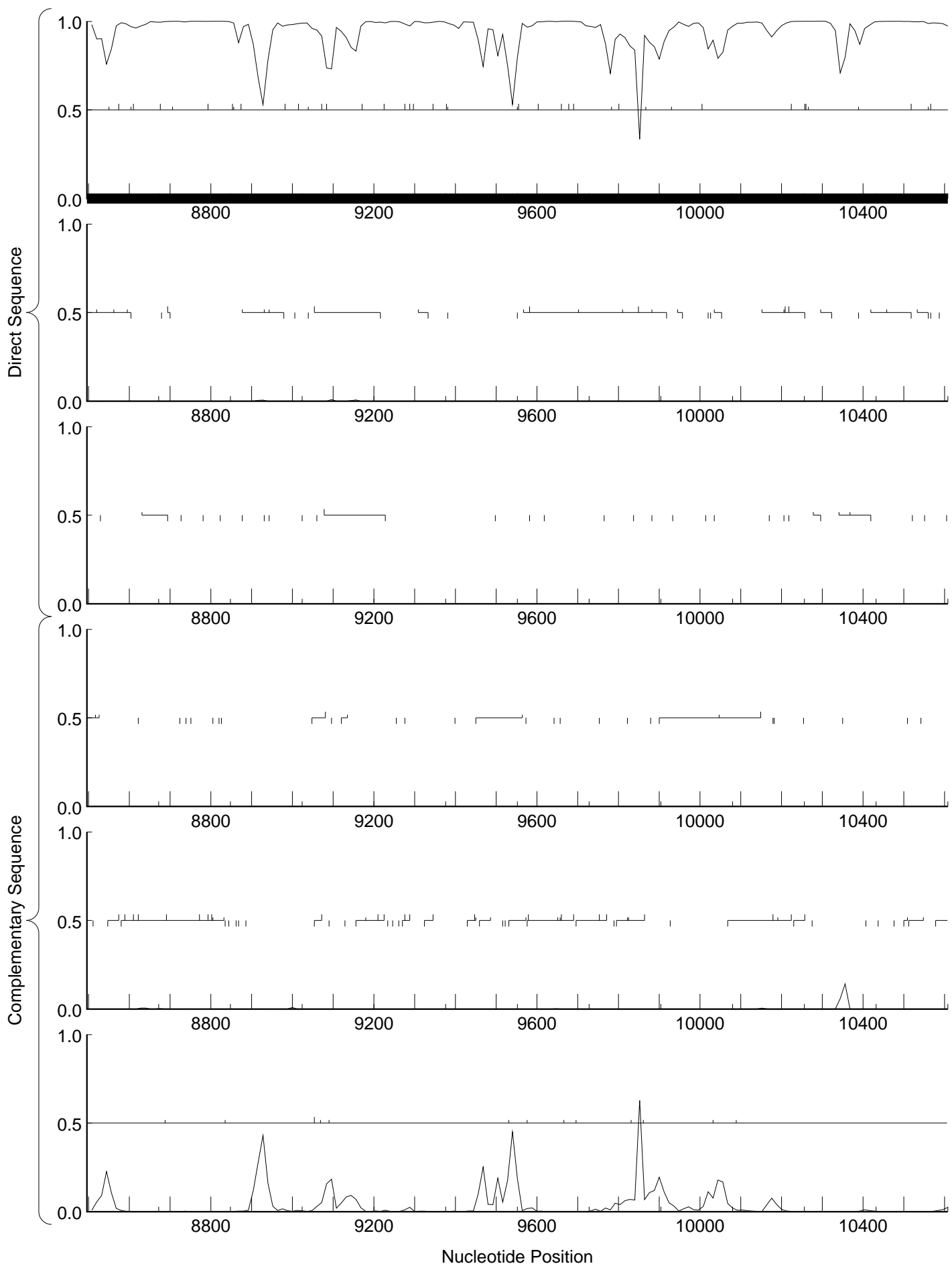
GeneMark, hmm prediction



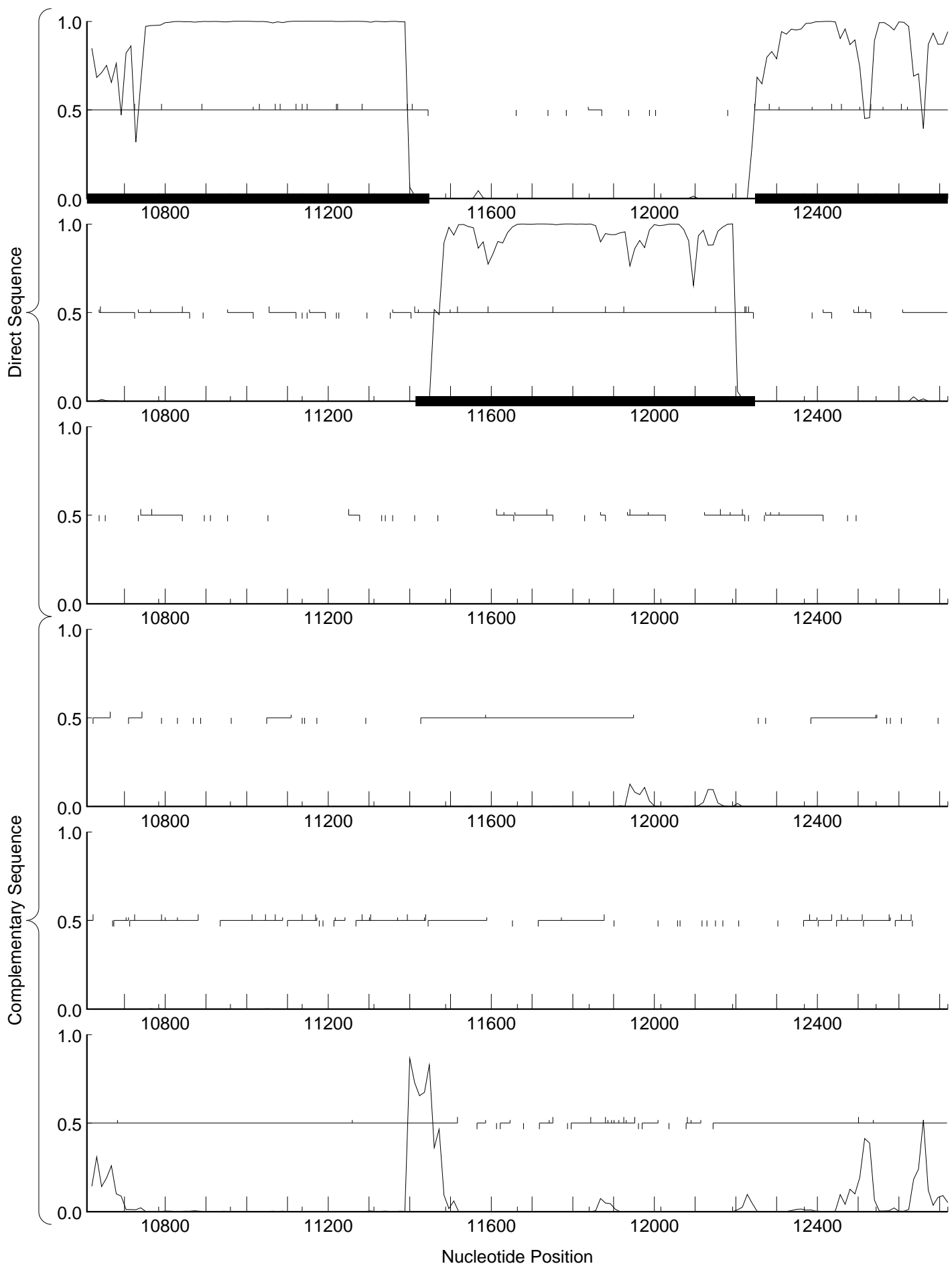
GeneMark\_hmm prediction



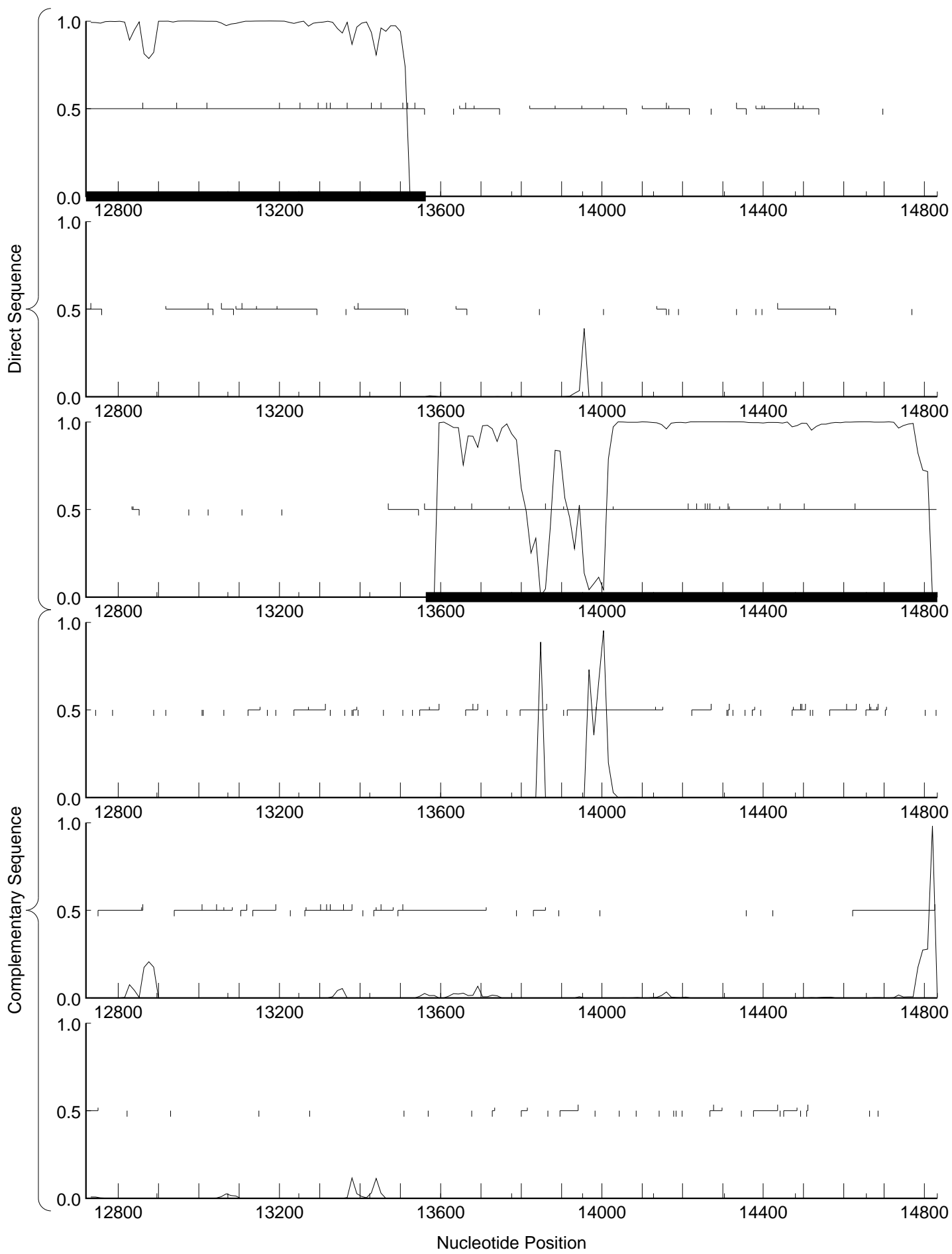
GeneMark, hmm prediction



GeneMark, hmm prediction

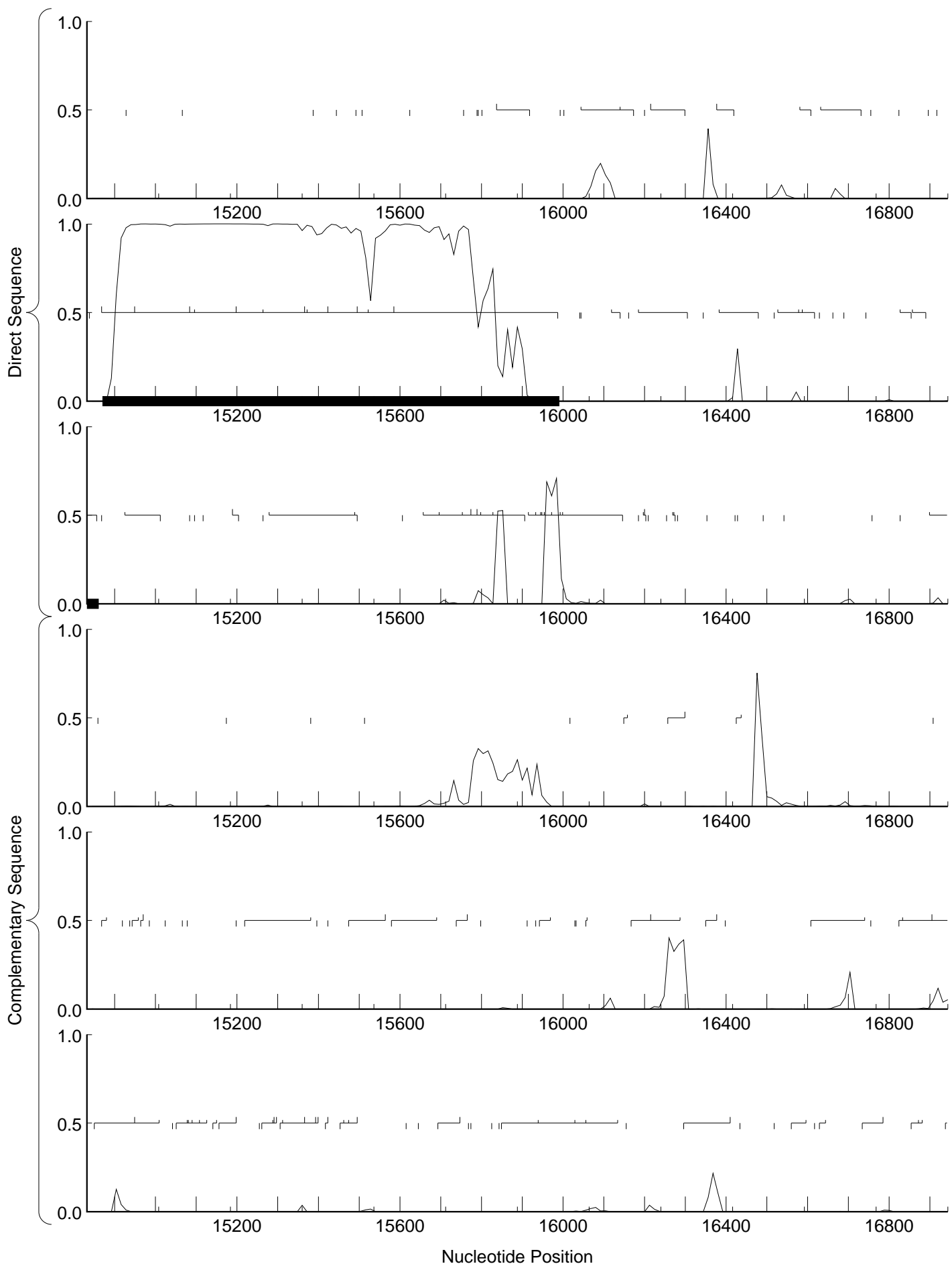


GeneMark, hmm prediction

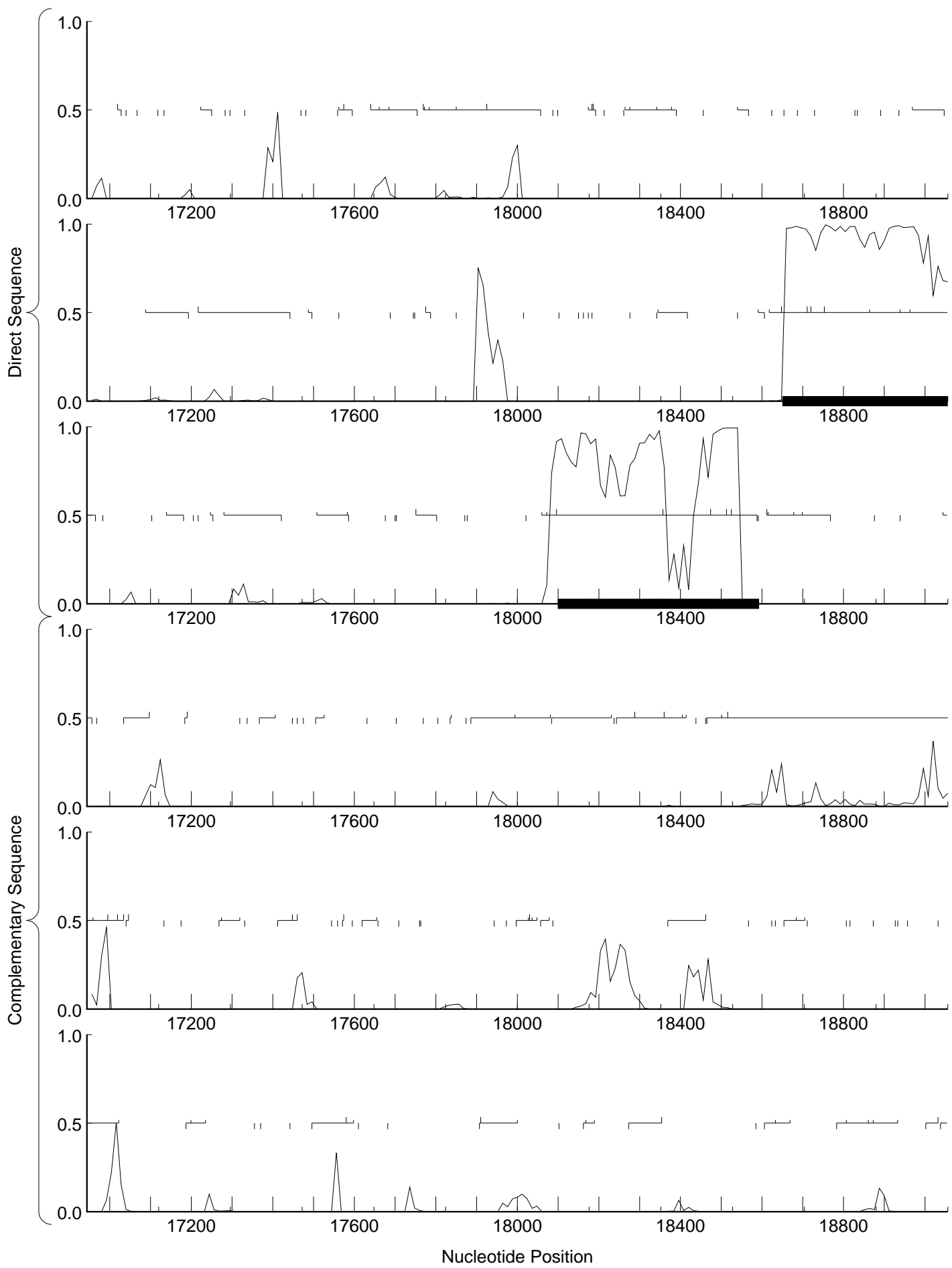




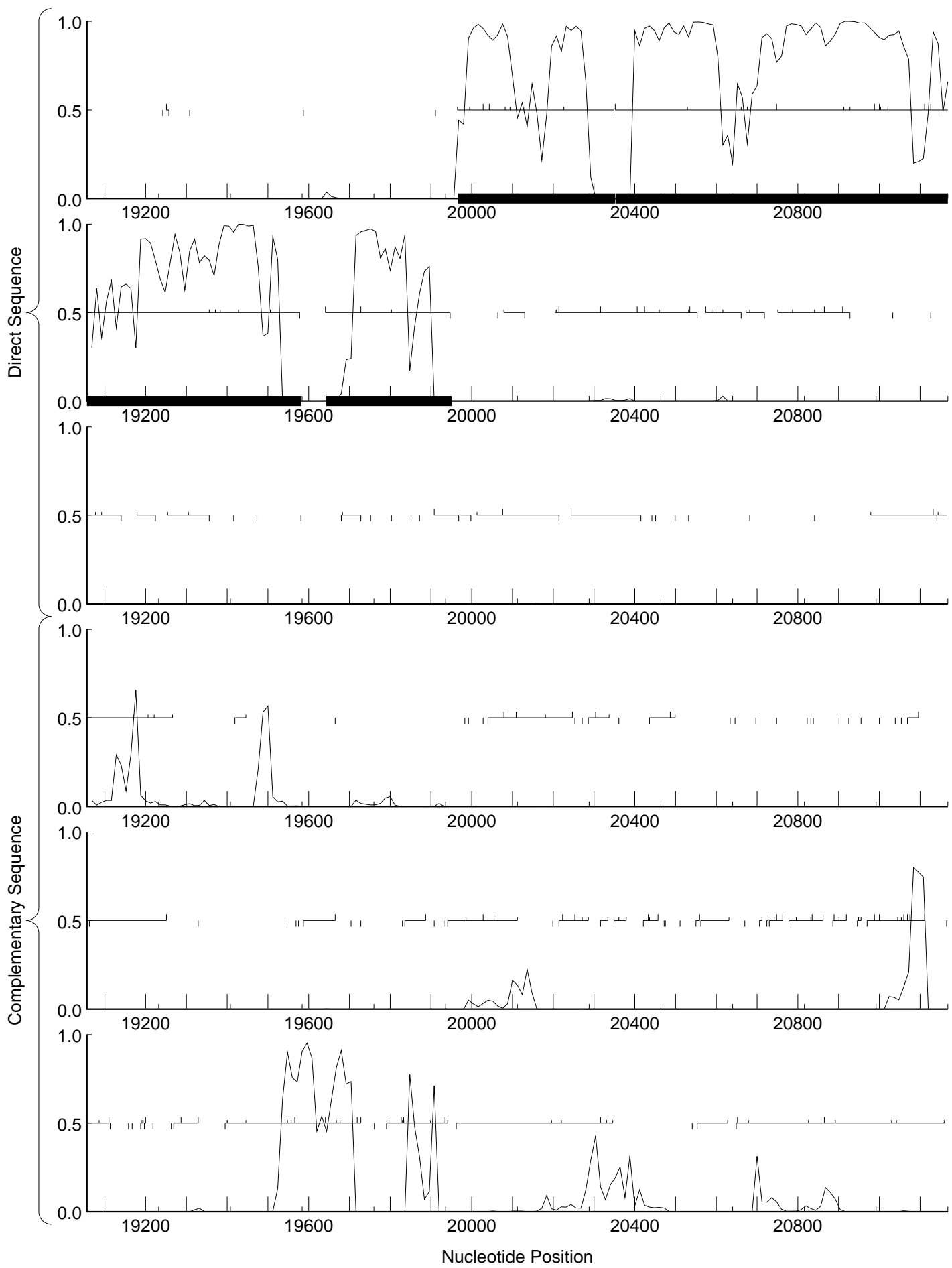
GeneMark, hmm prediction



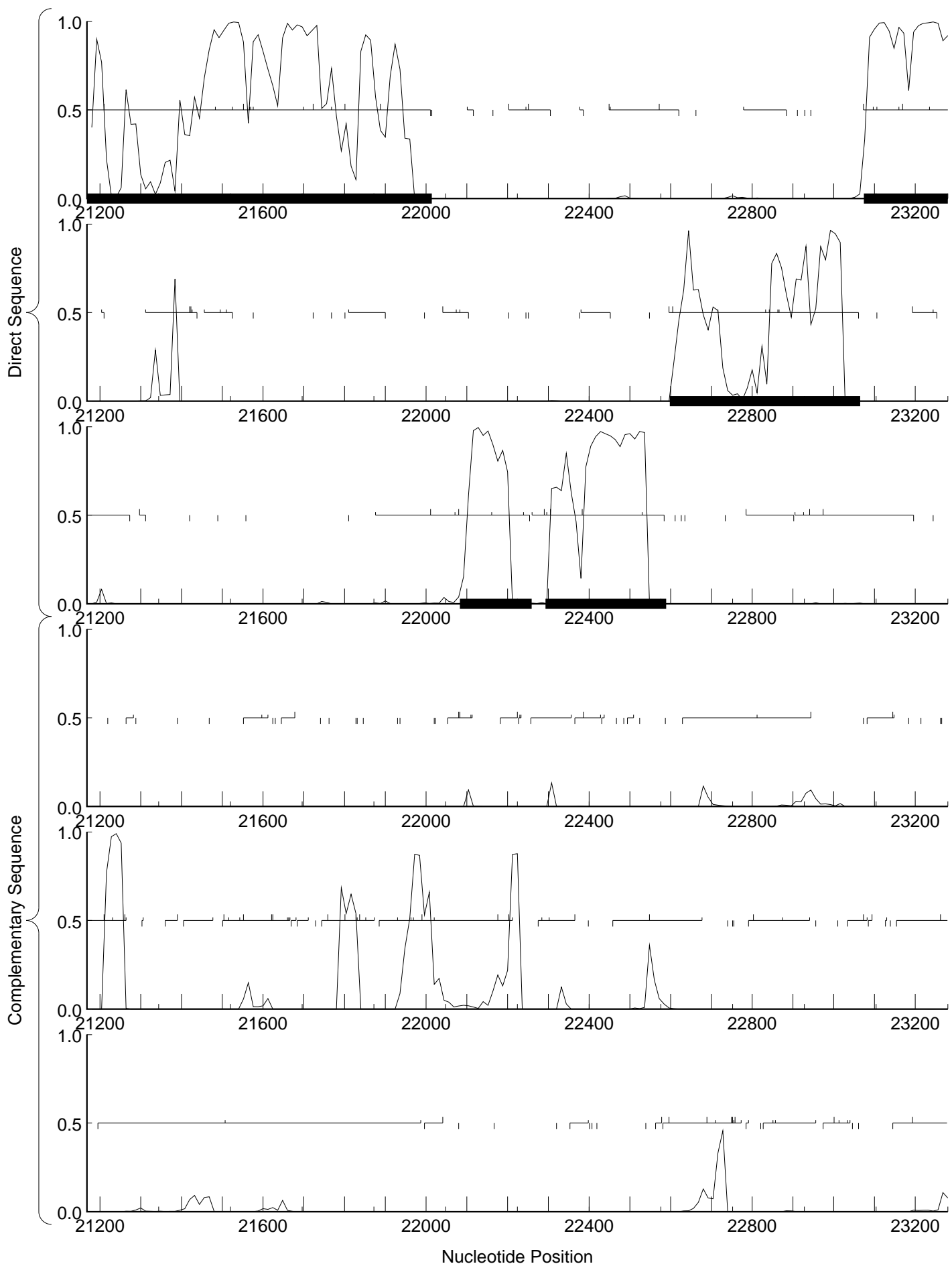
GeneMark.hmm prediction



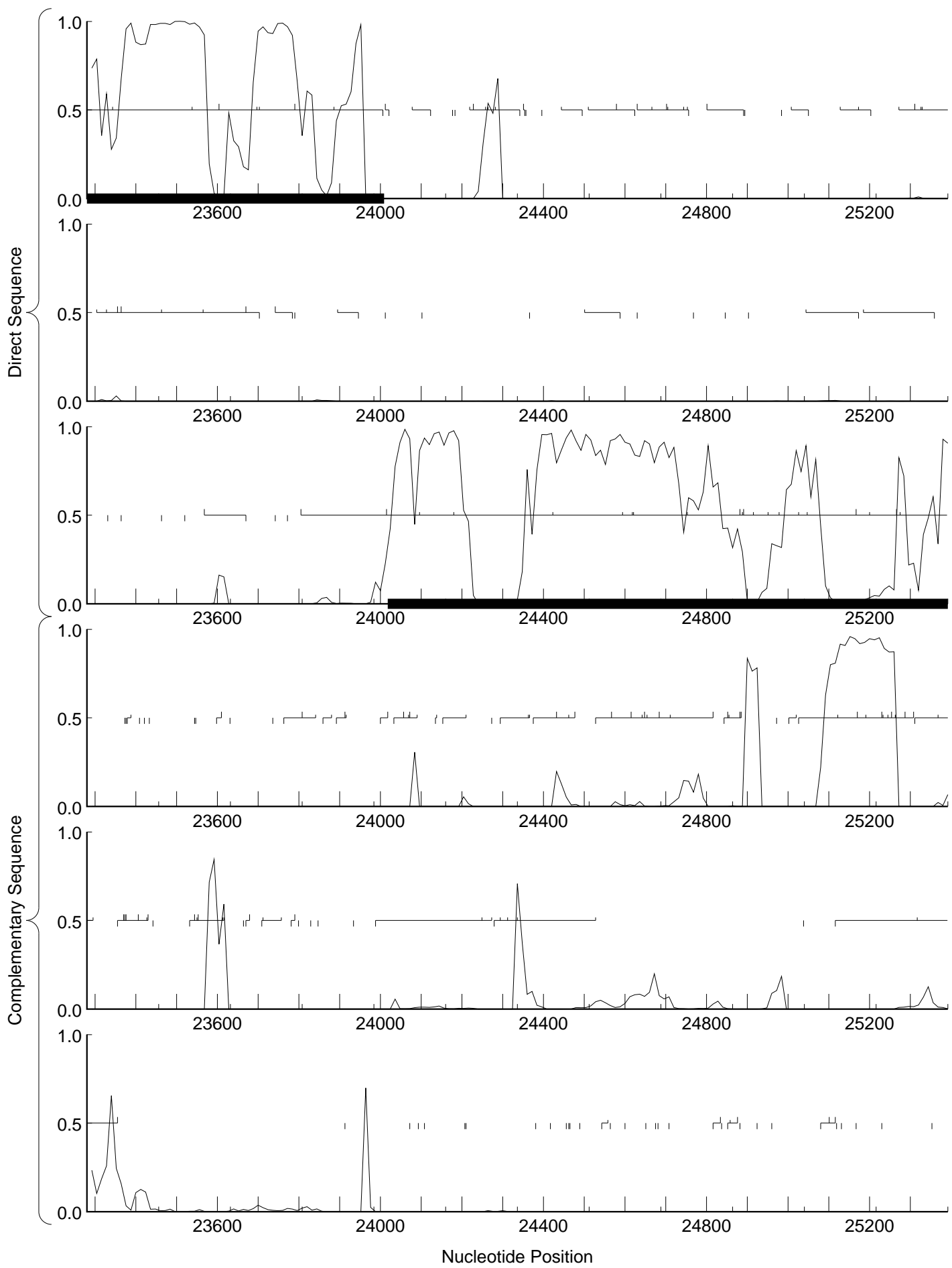
GeneMark\_hmm prediction



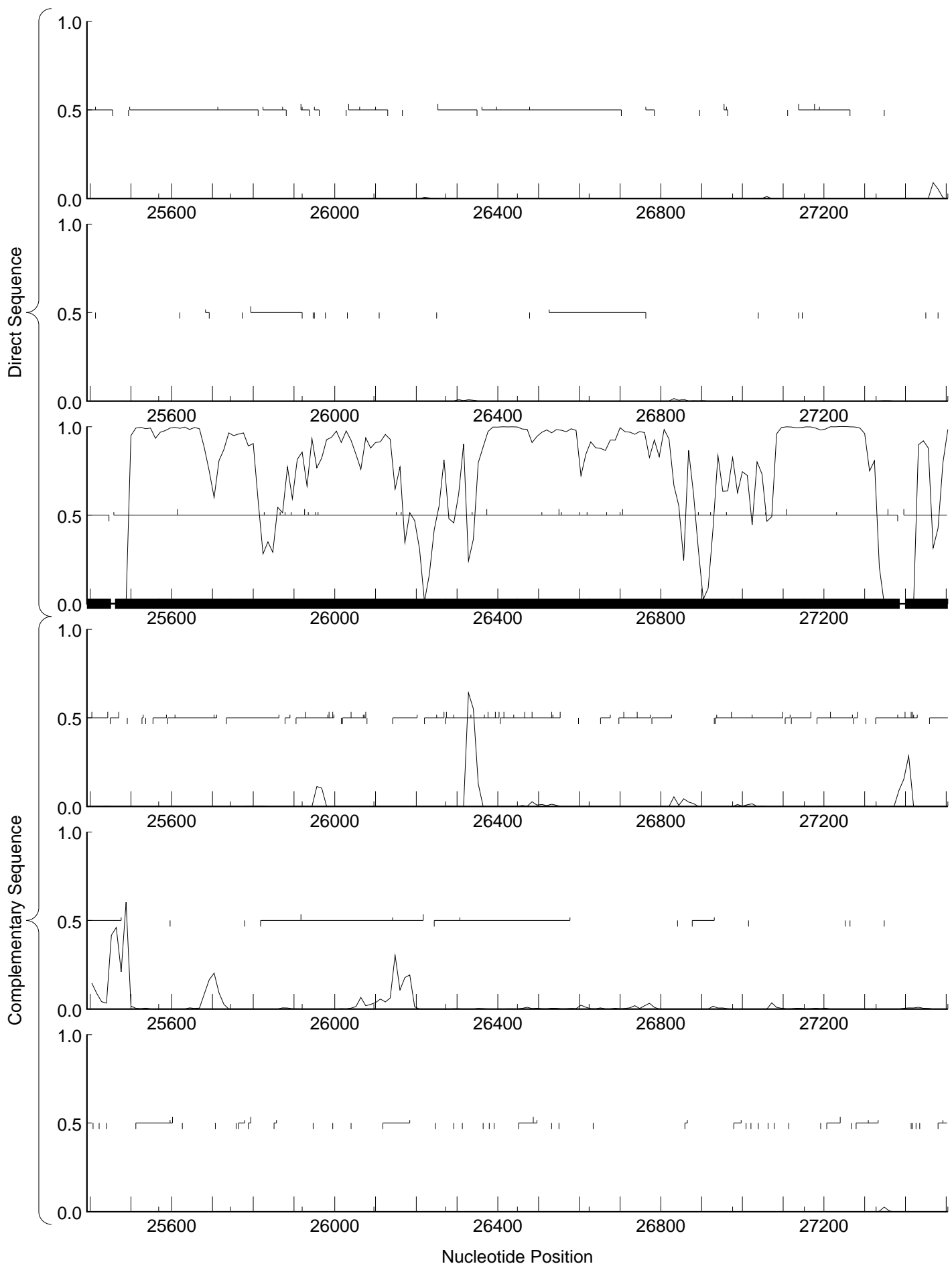
GeneMark.hmm prediction



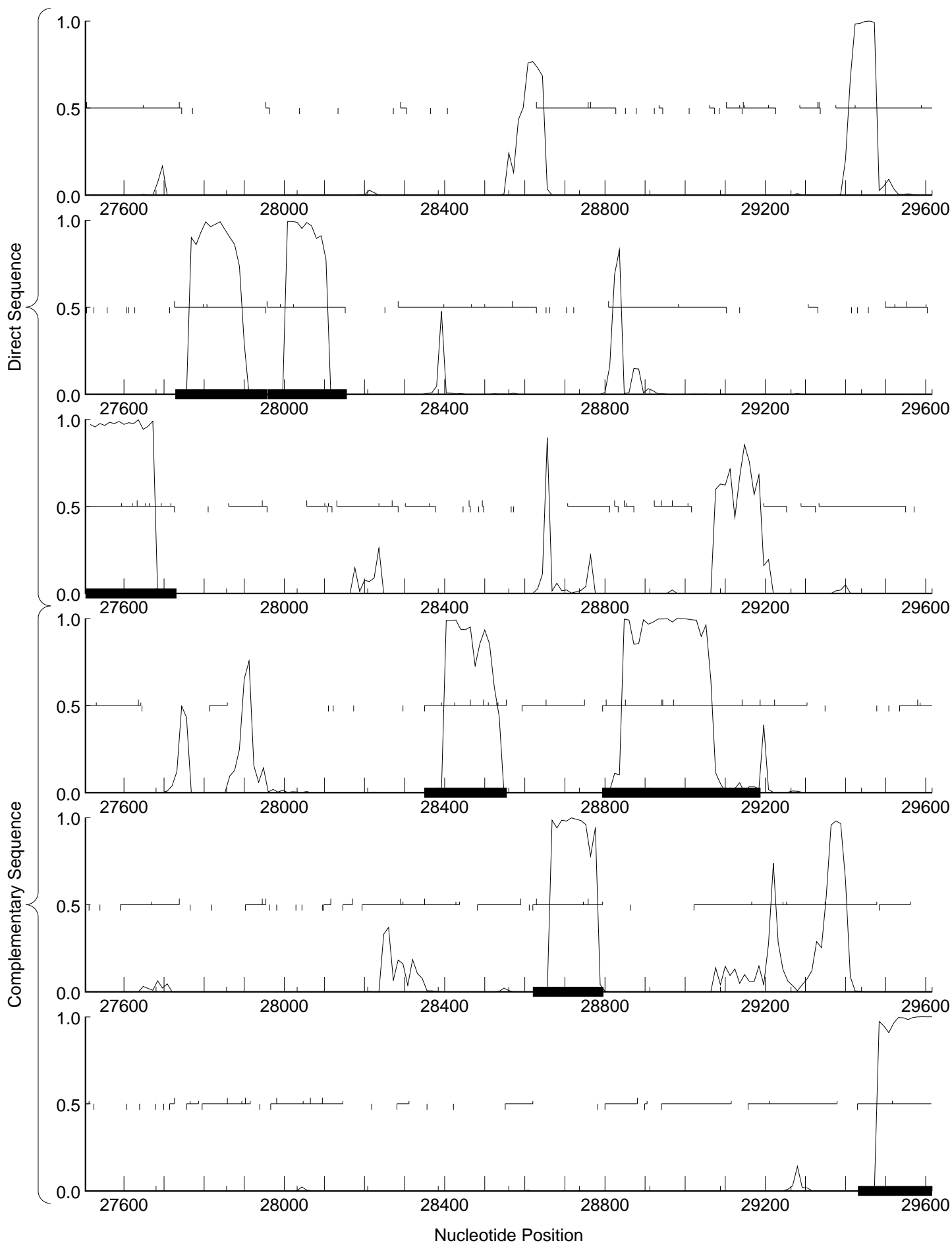
GeneMark.hmm prediction



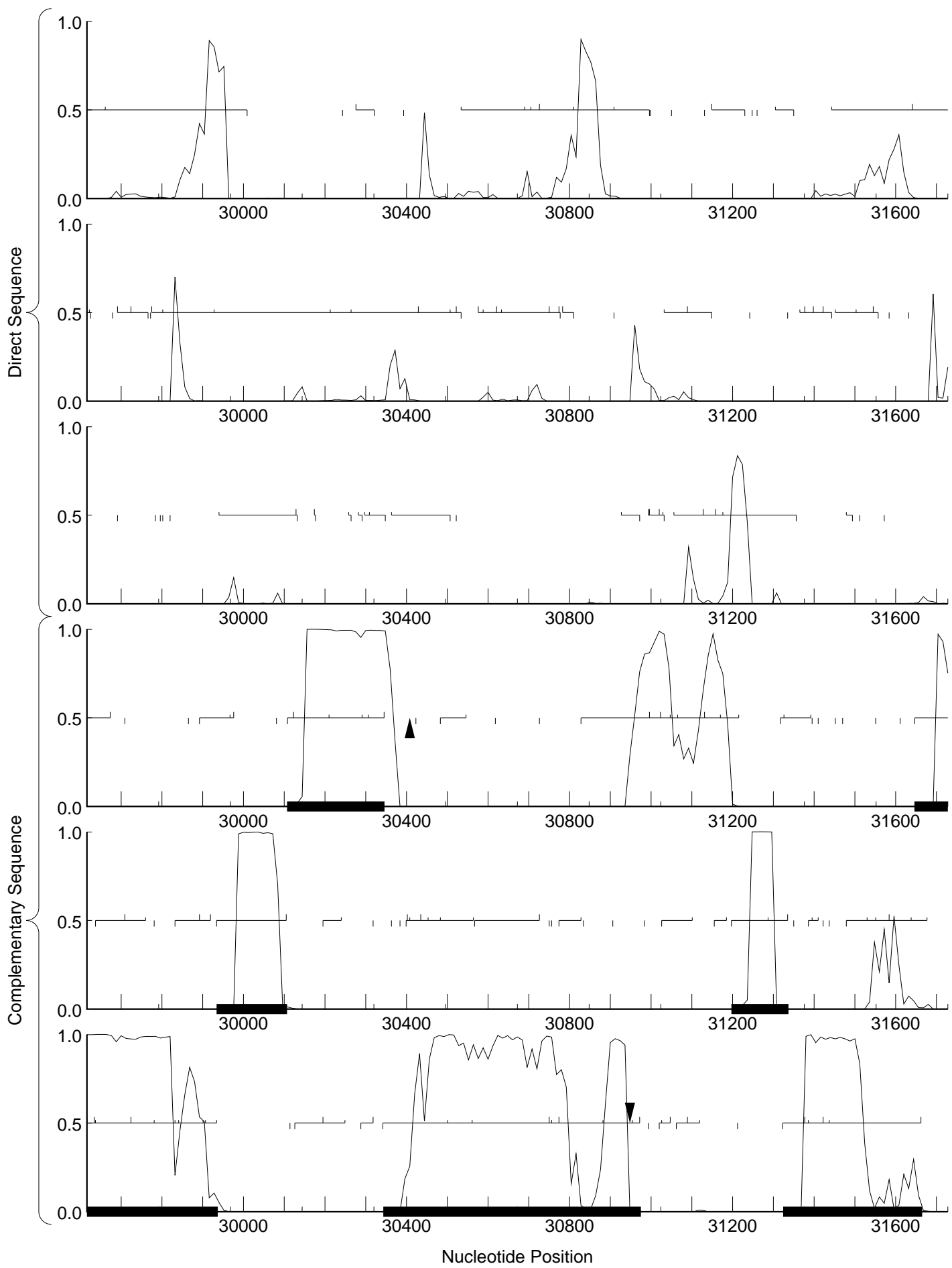
GeneMark.hmm prediction



GeneMark.hmm prediction

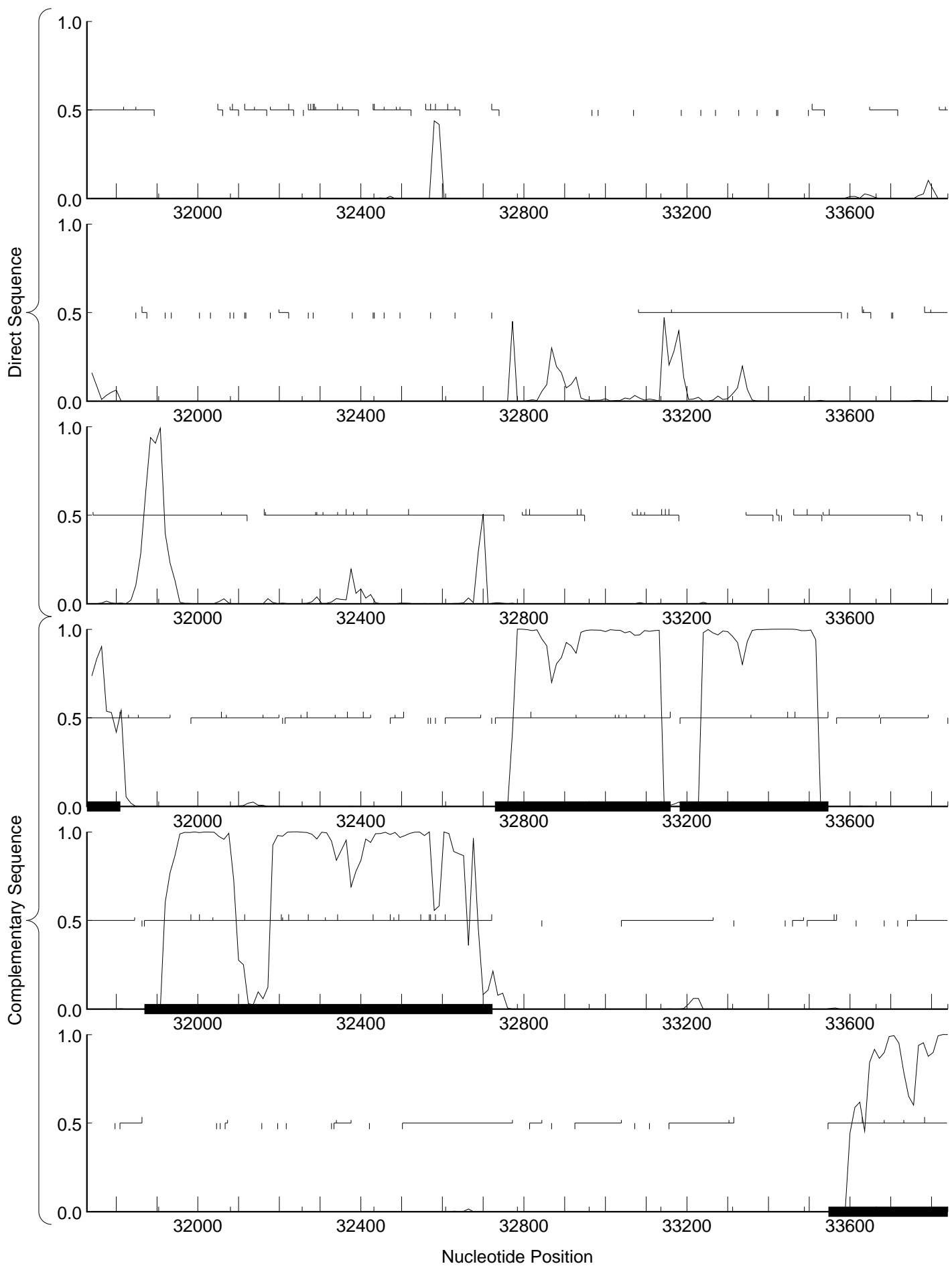


GeneMark\_hmm prediction

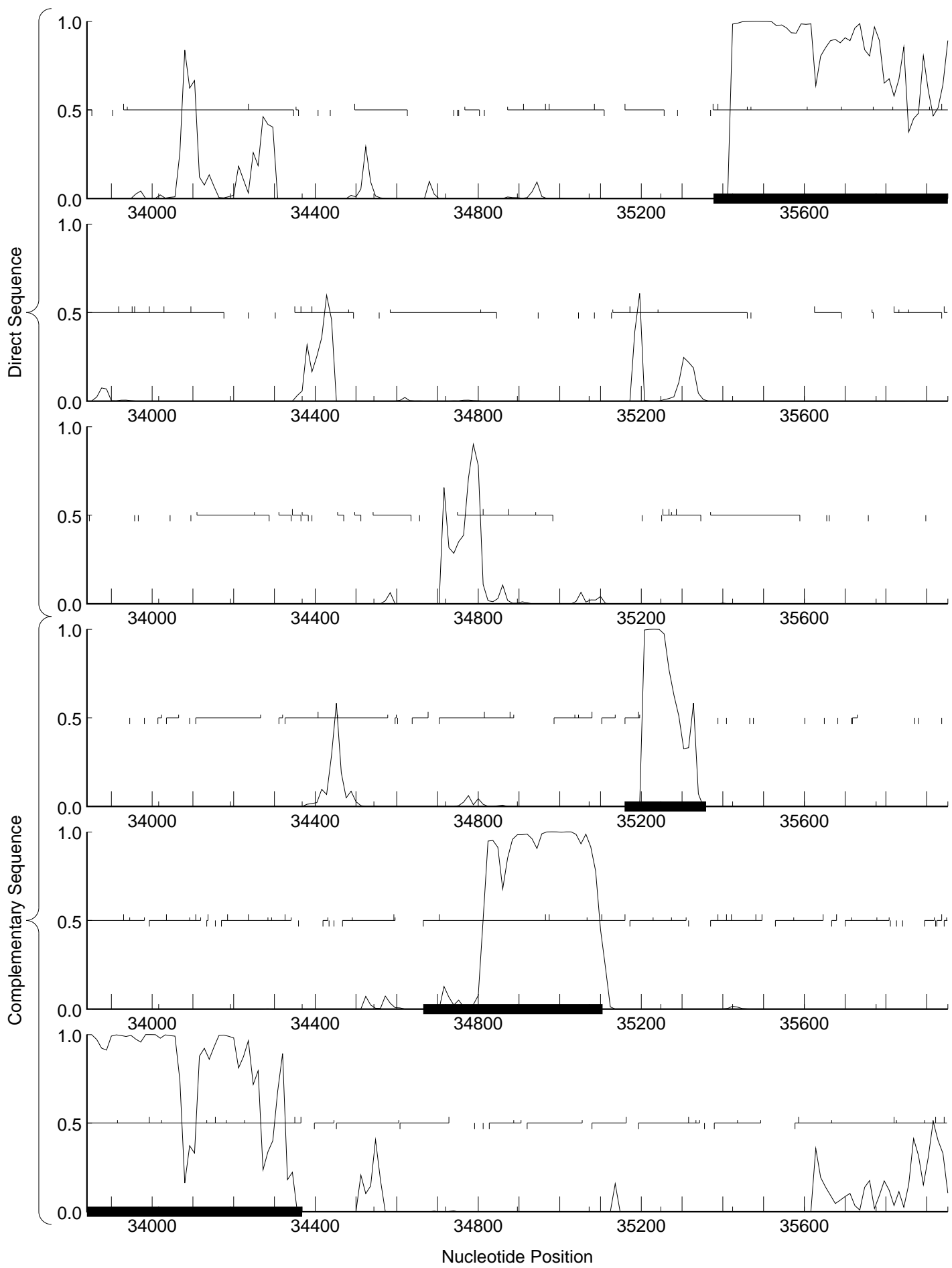




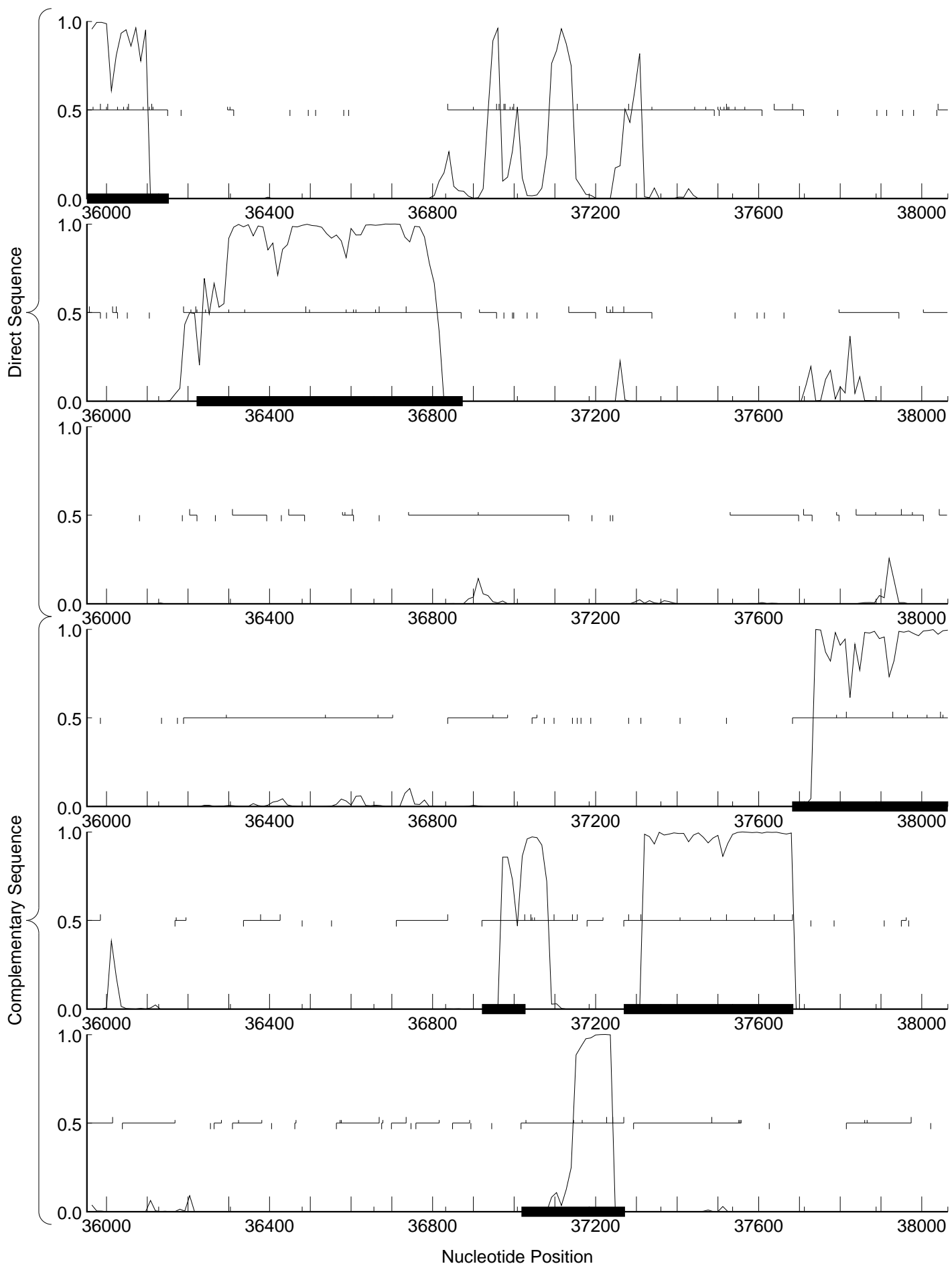
GeneMark.hmm prediction



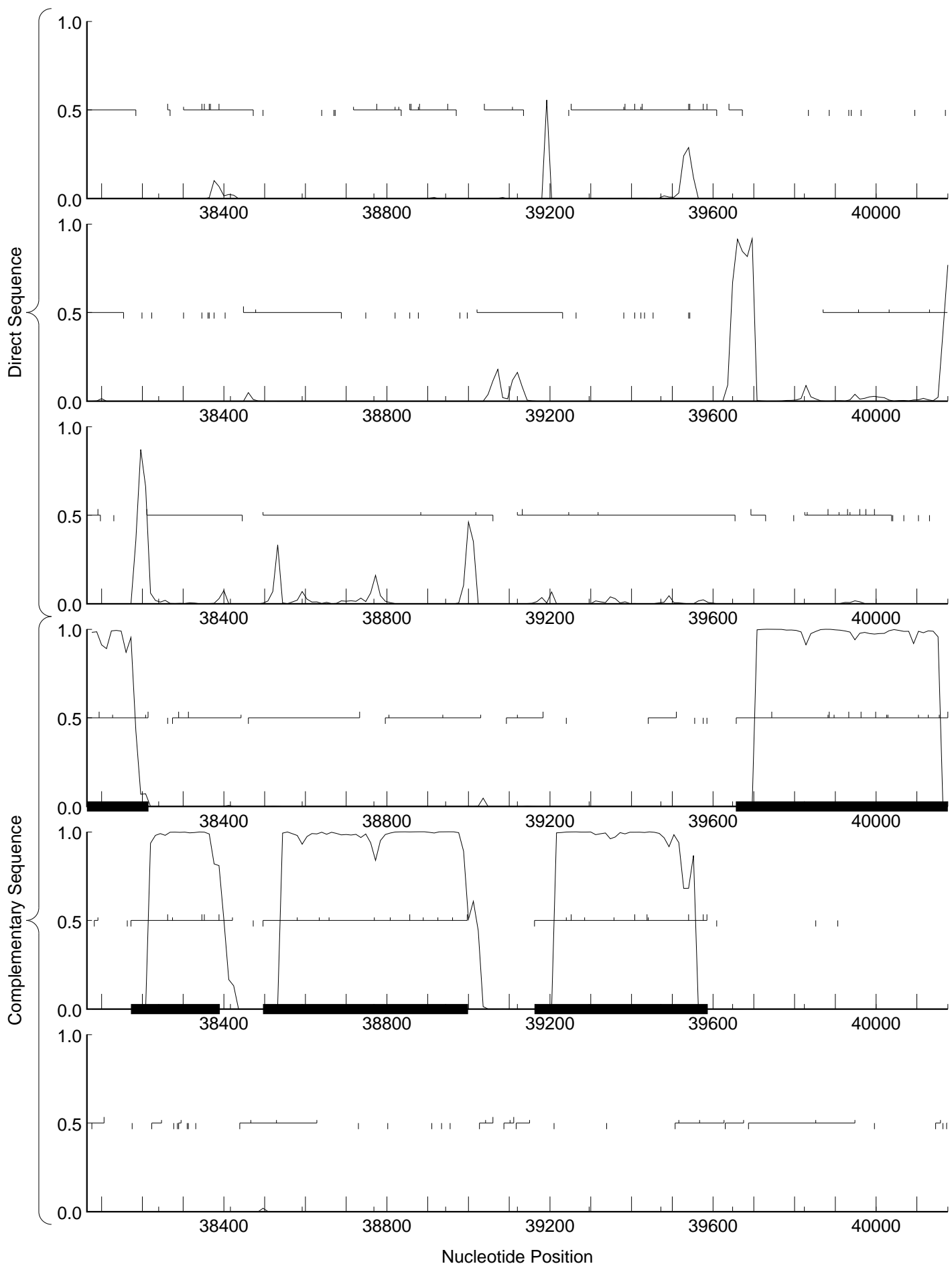
GeneMark.hmm prediction



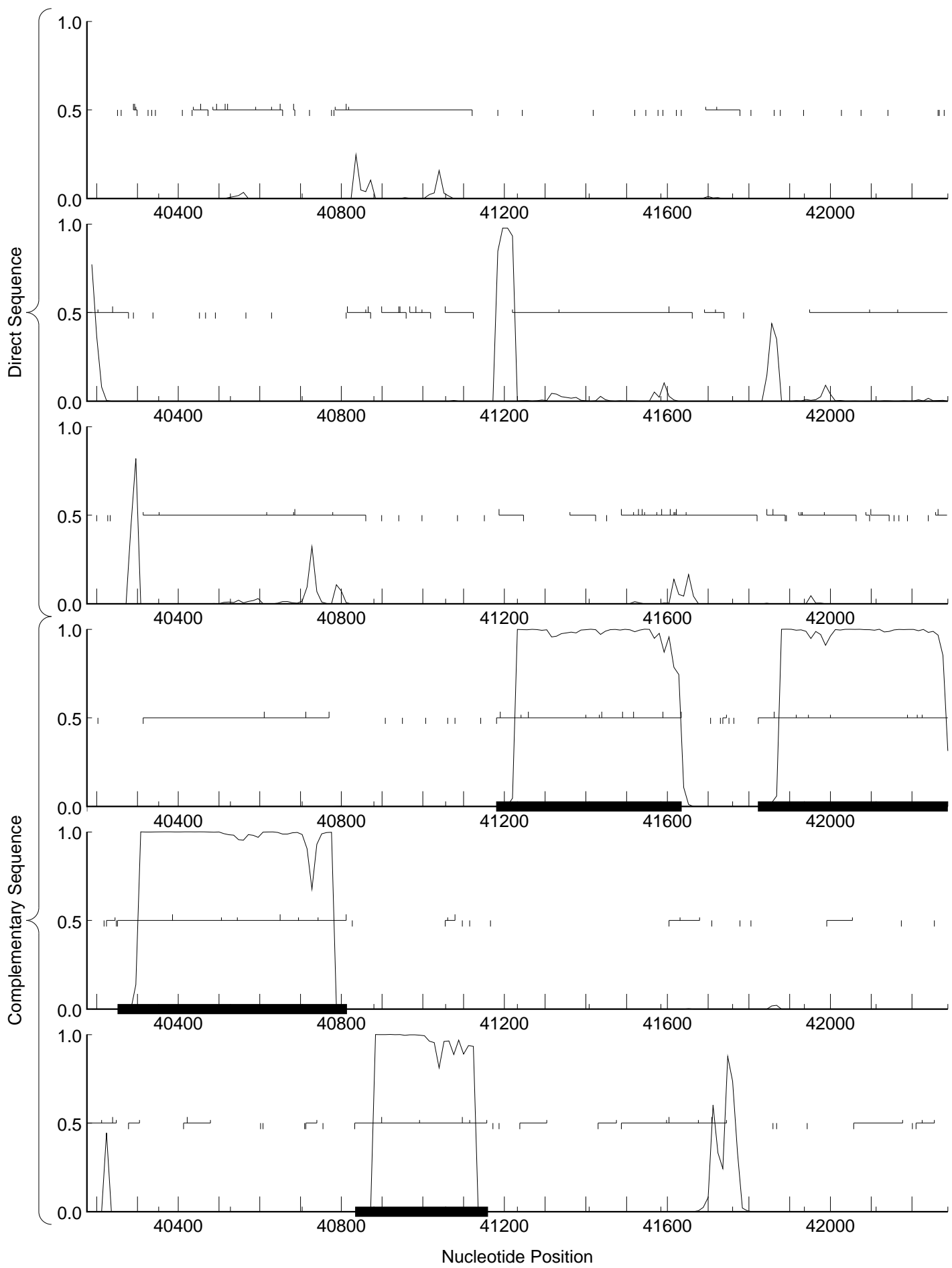
GeneMark\_hmm prediction



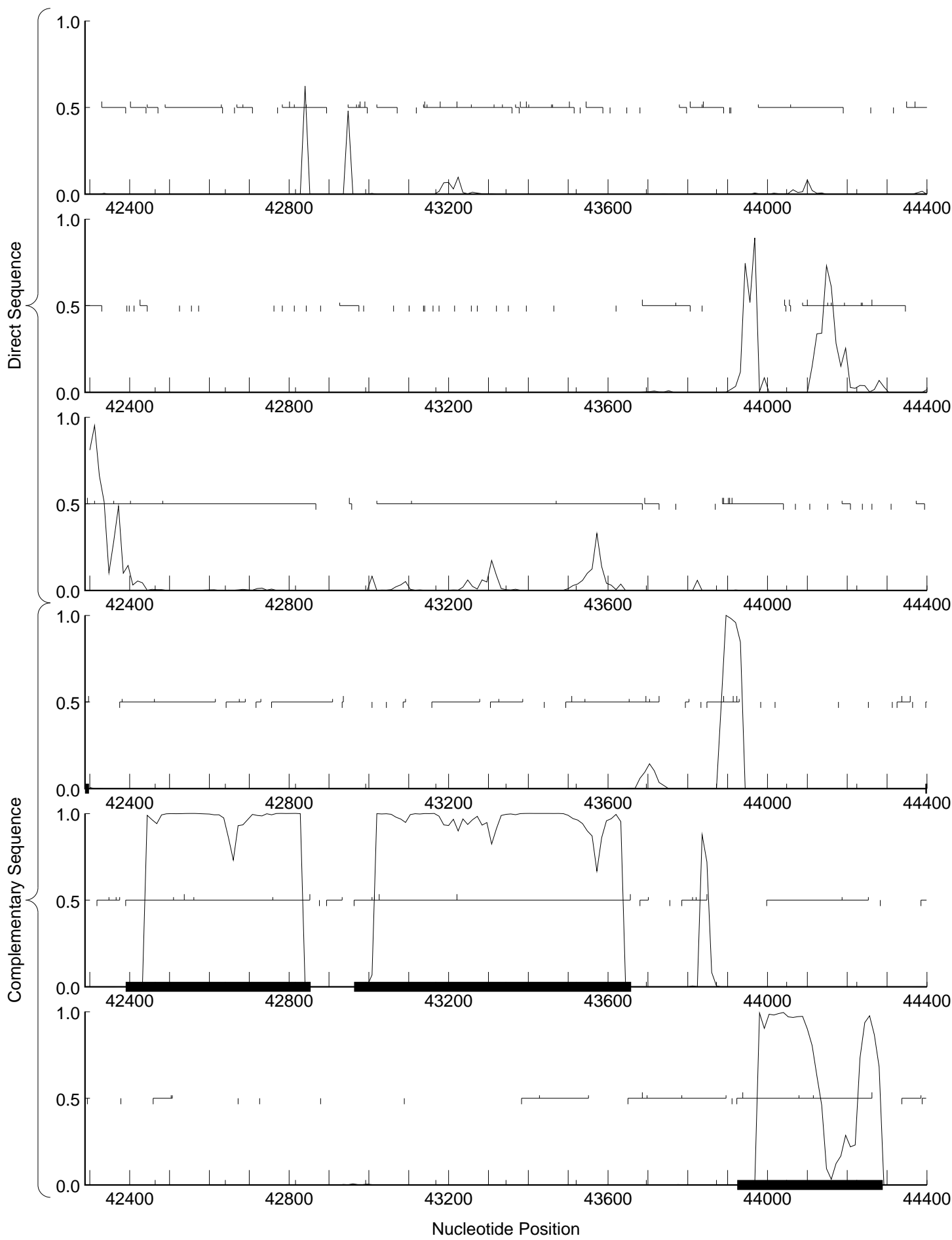
GeneMark.hmm prediction



GeneMark.hmm prediction



GeneMark\_hmm prediction



GeneMark\_hmm prediction

