

# GeneMark

Version 2.5p (09.08.06)

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## PROGRAM INFORMATION

Sequence : Mycobacterium phage PSullivan complete sequence, 49990 bp including 10-base 3' overhang (CG  
Analysis Date : 3/21/20 at 15:56:07  
Pages : 25  
Sequence Length : 49990 bp  
GC Content : 63.43%

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,

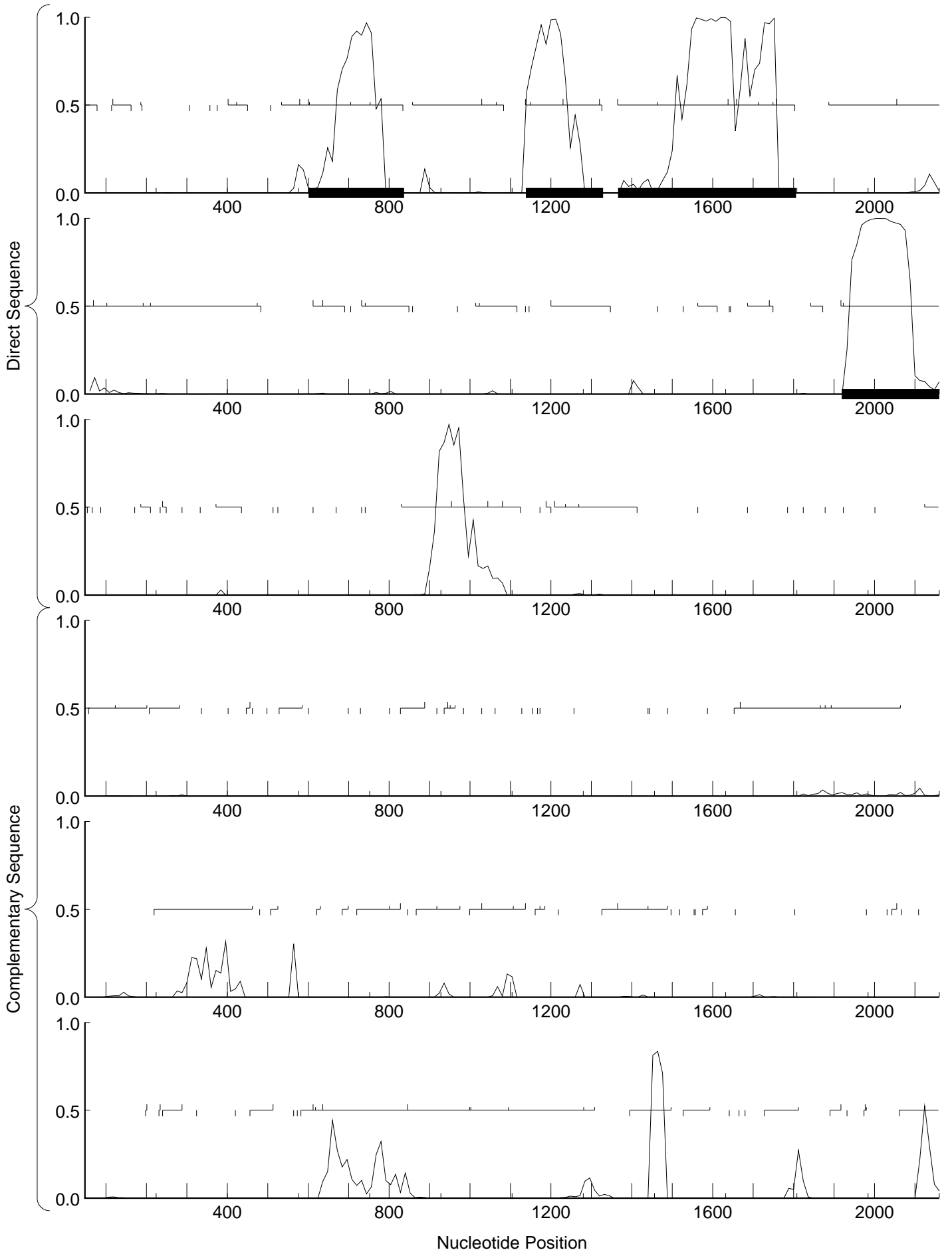
## Matrix notes & comments

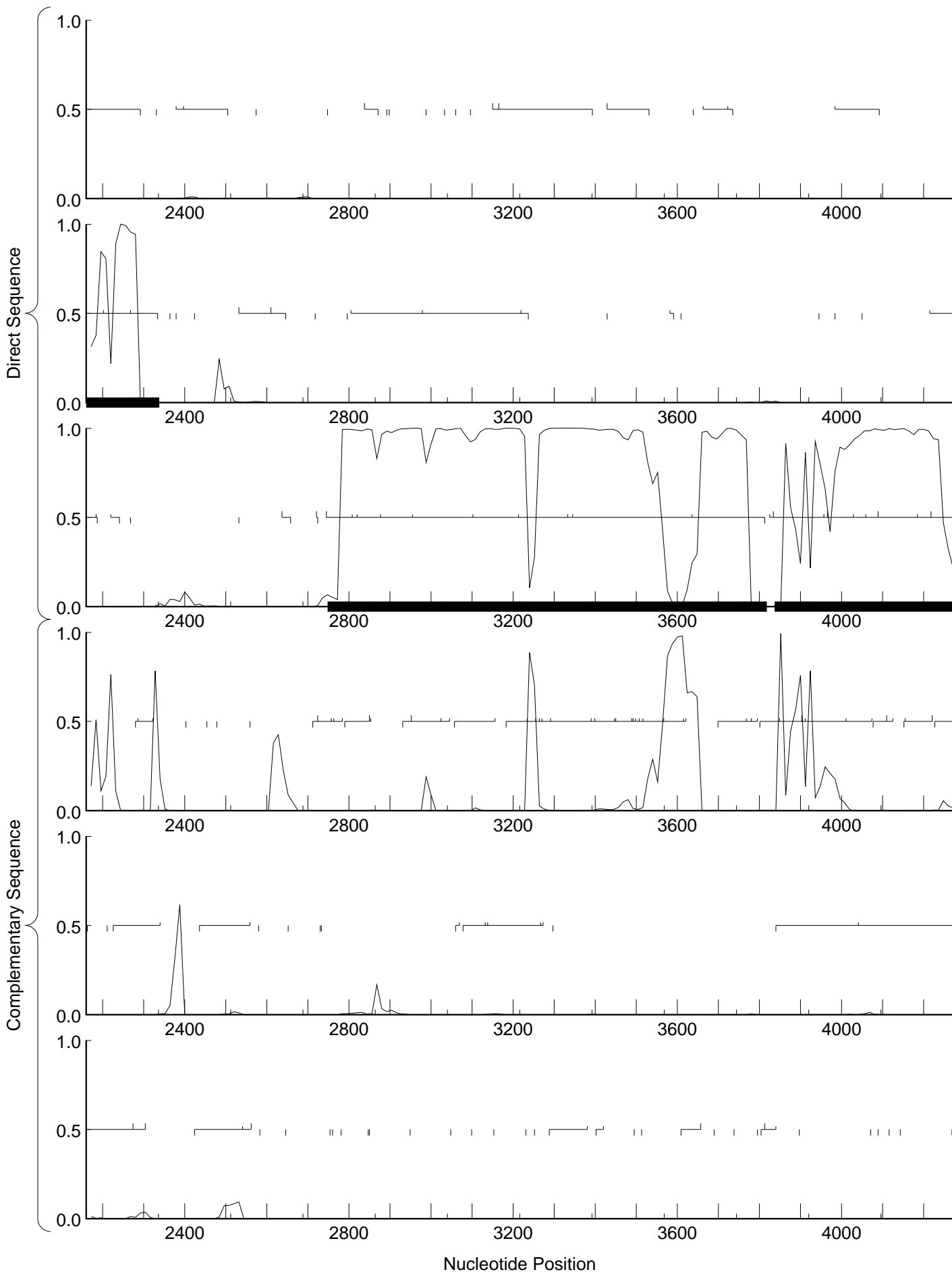
For details on the model building procedure see:  
Besemer J. and Borodovsky M.  
"Heuristic approach to deriving models for gene finding"  
NAR, 1999, Vol. 27, No. 19, pp. 3911-3920

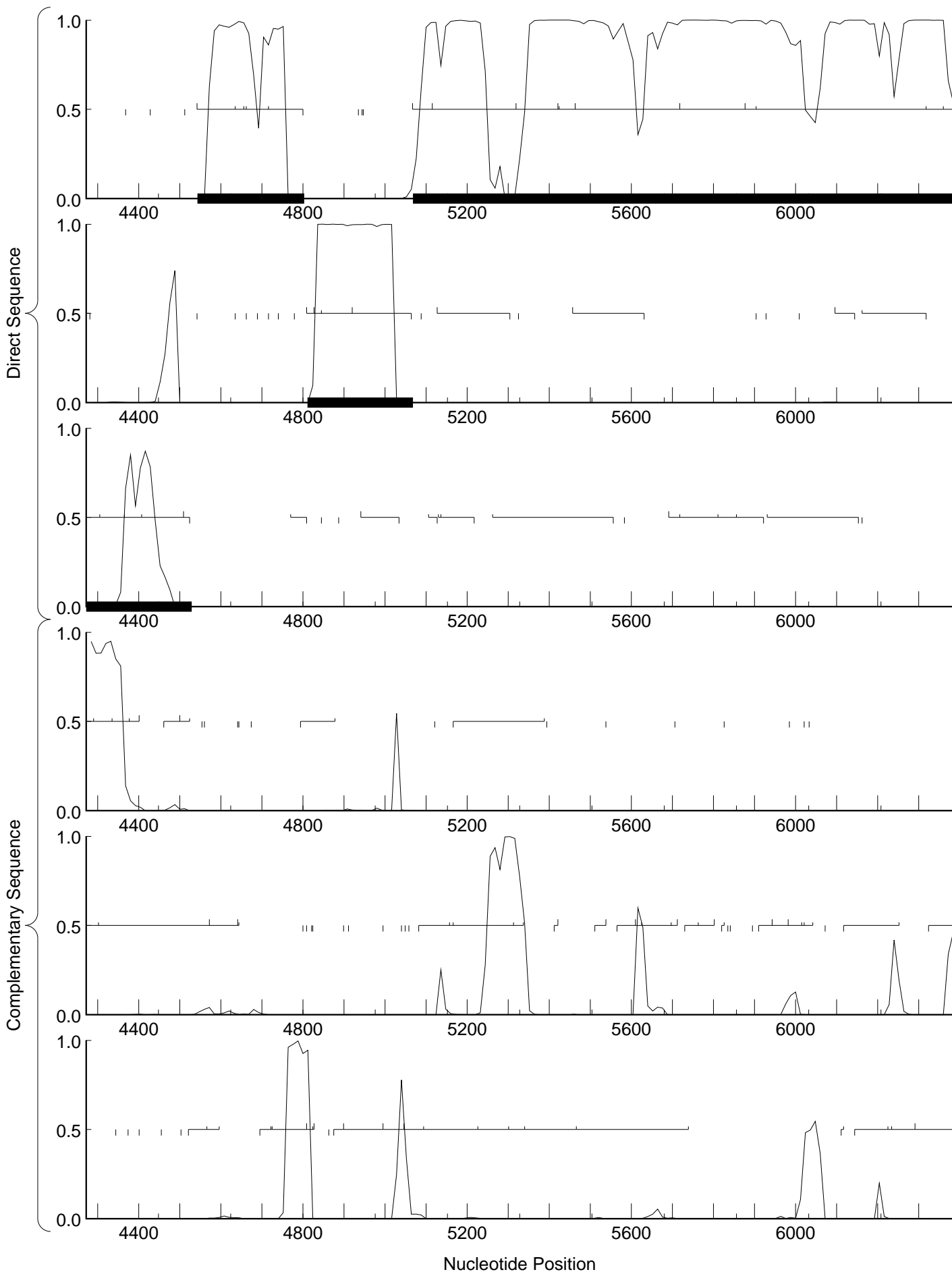
## MATRIX INFORMATION

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

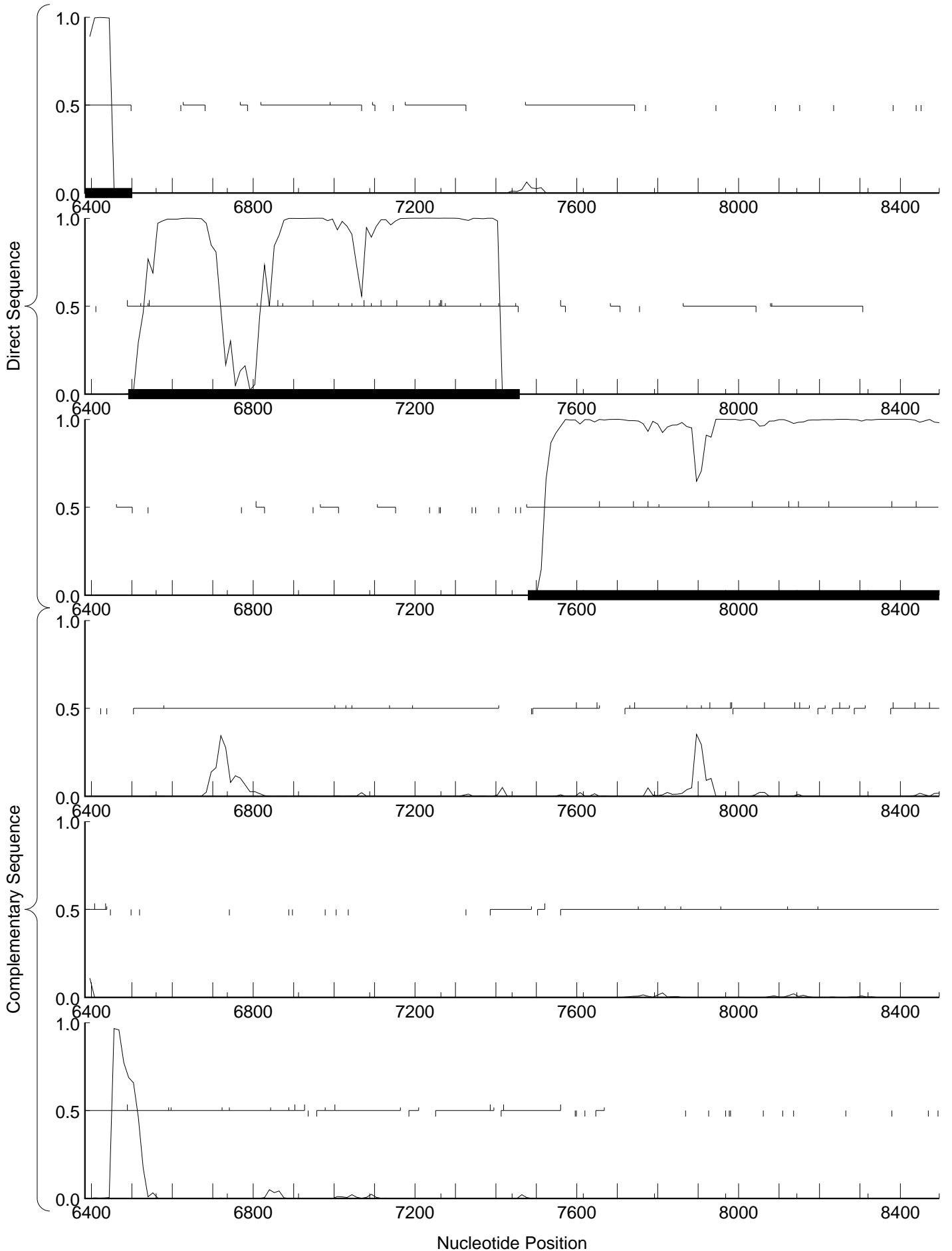
Send questions / comments to:  
Dr. M. Borodovsky  
Georgia Institute of Technology  
School of Biology  
Atlanta, GA 30332-0230

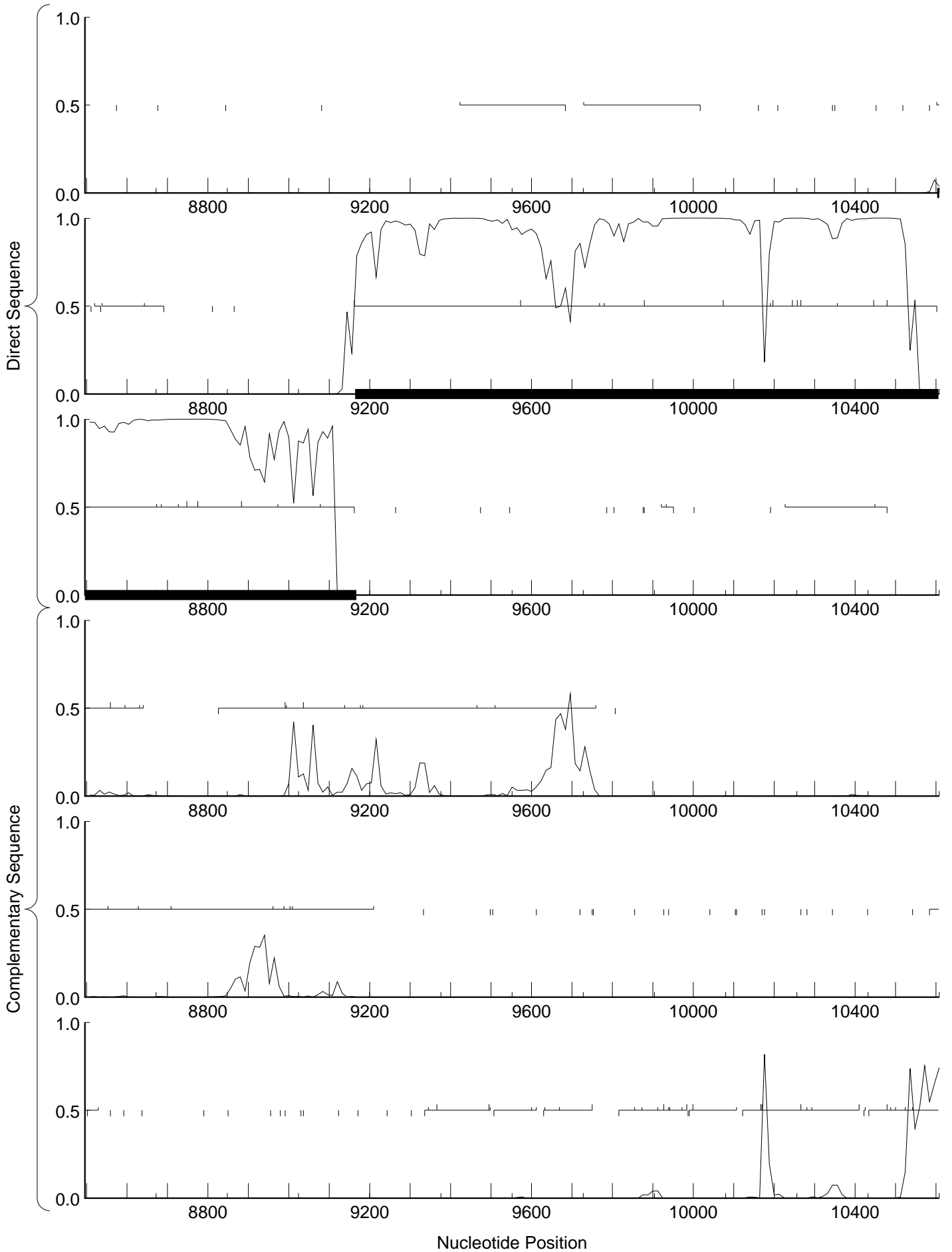


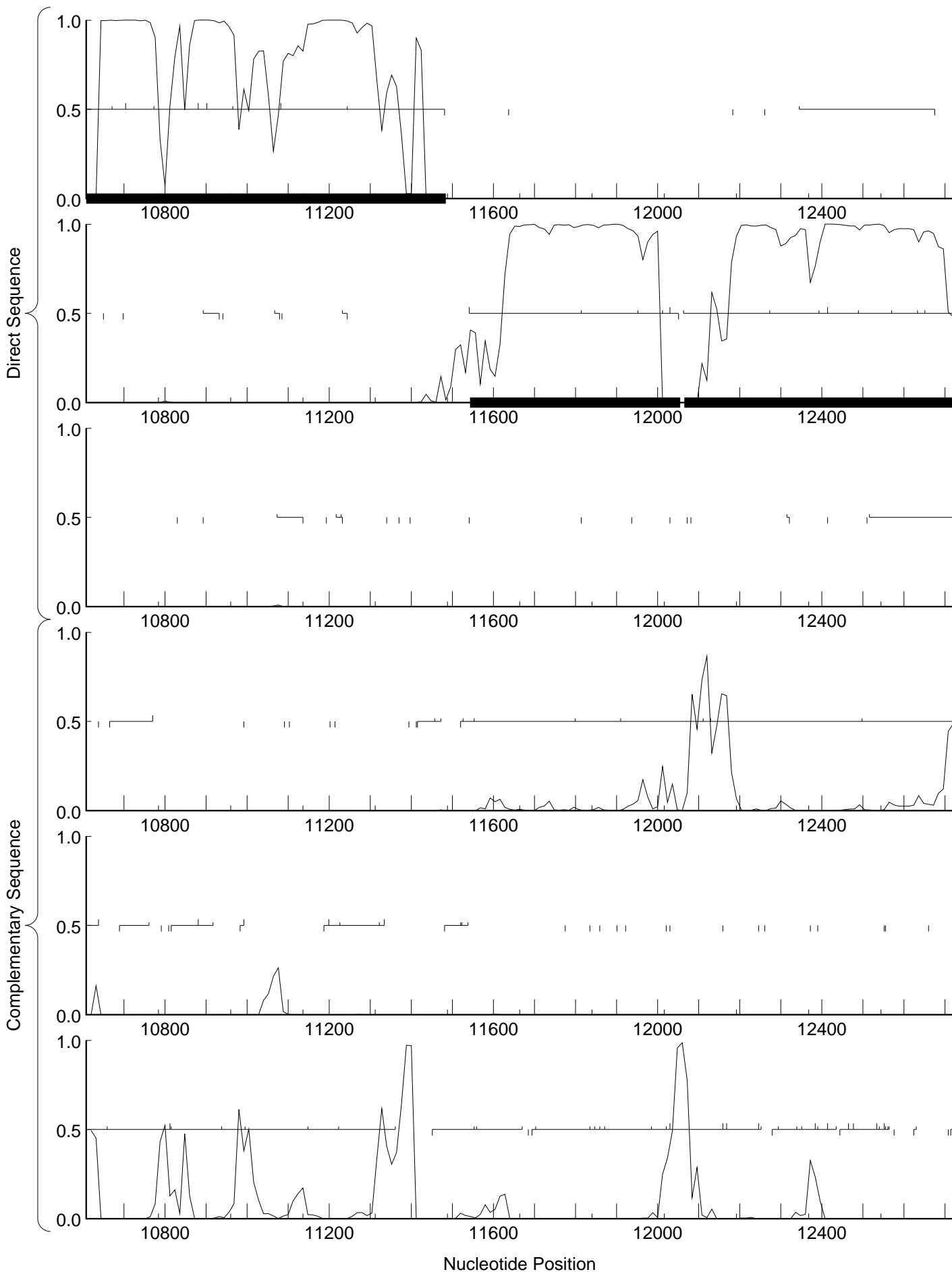


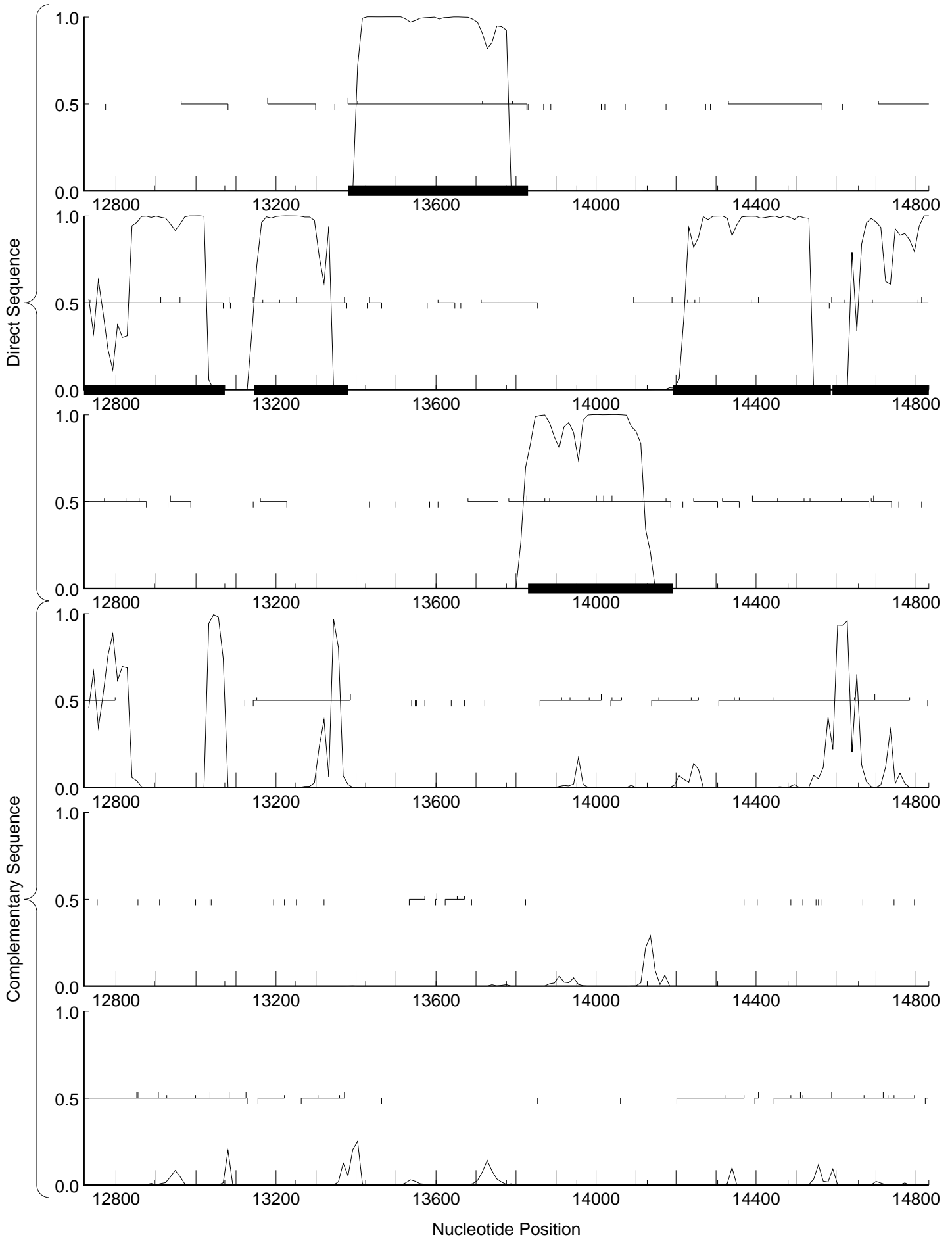


GeneMark.hmm prediction

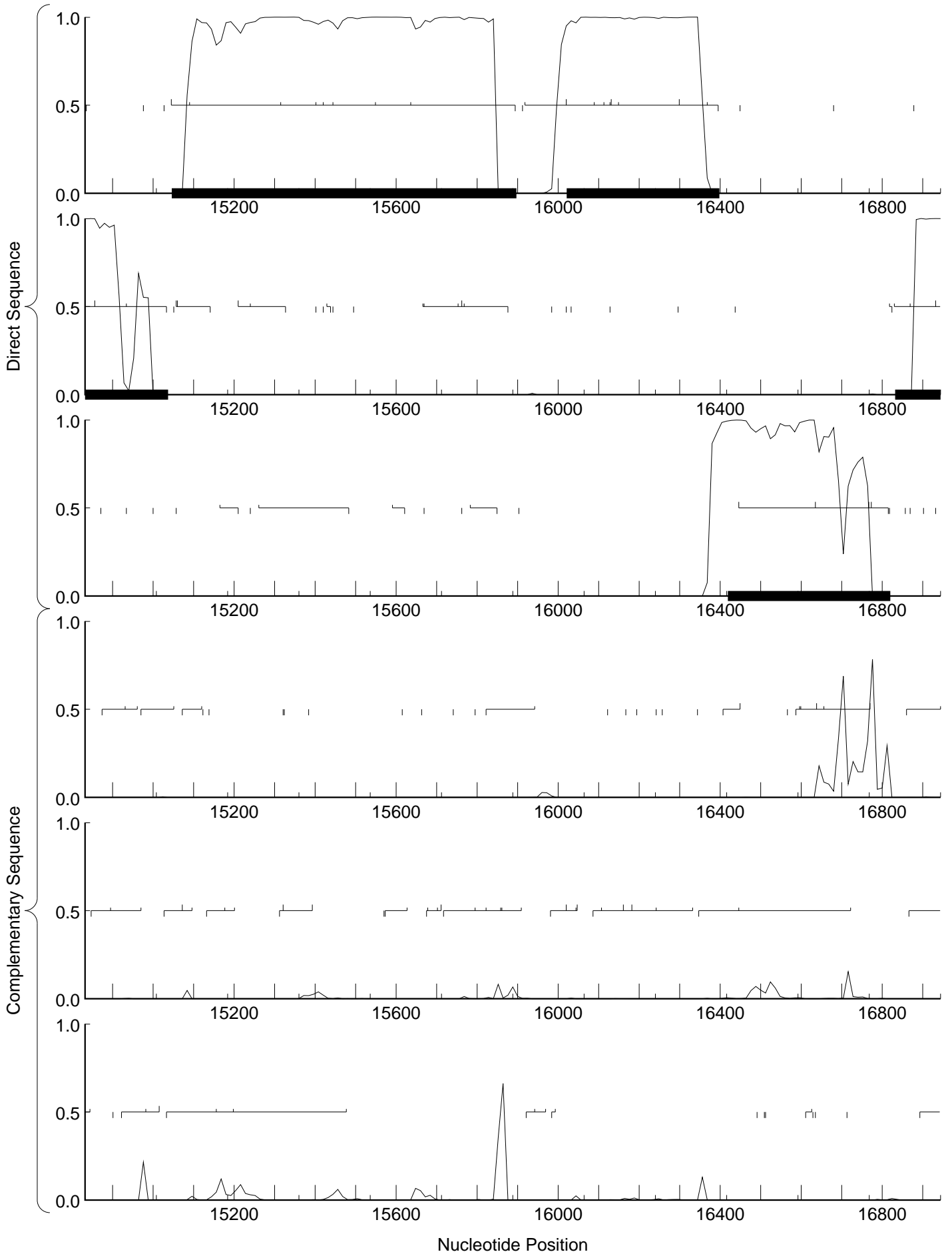




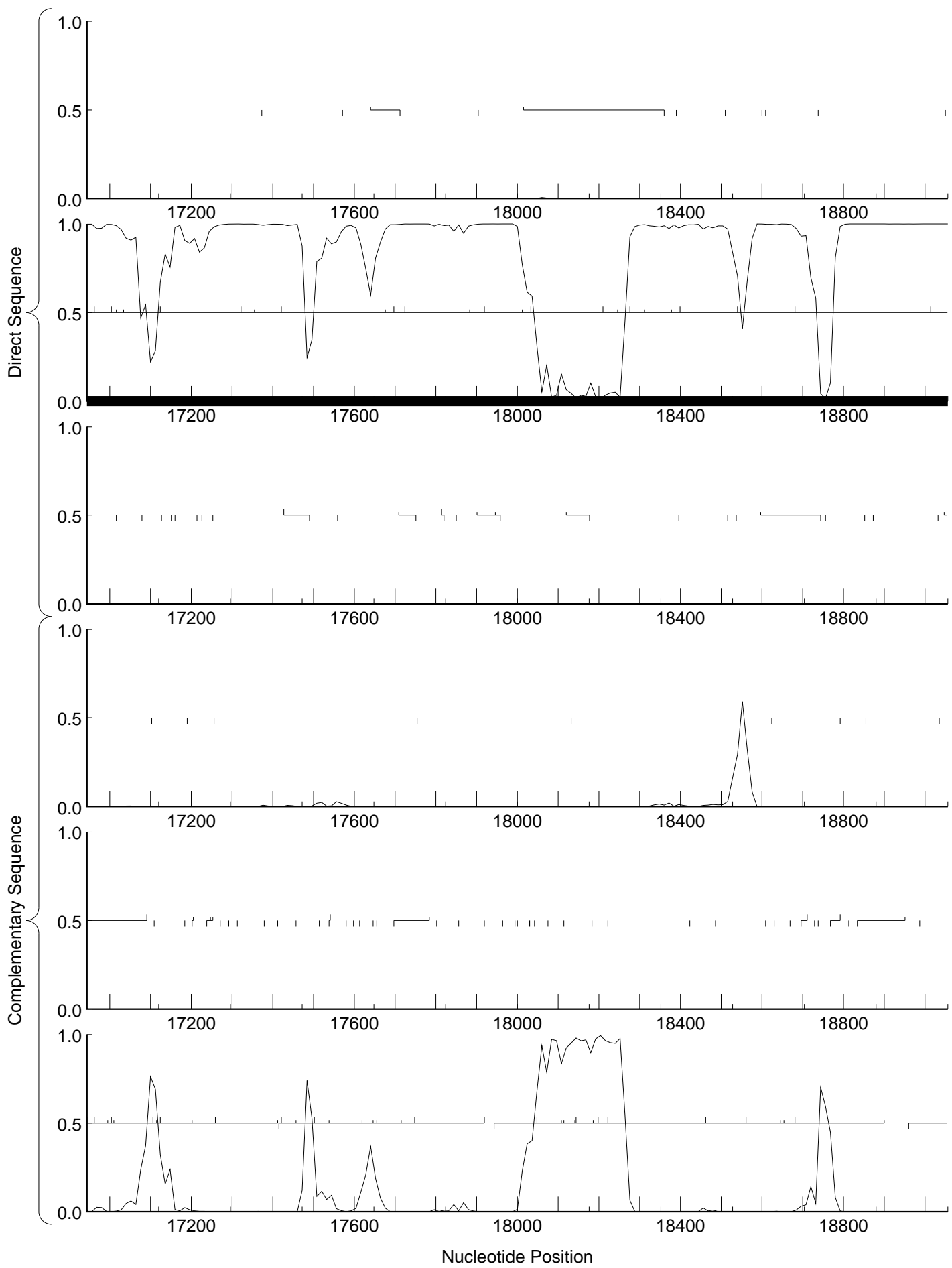


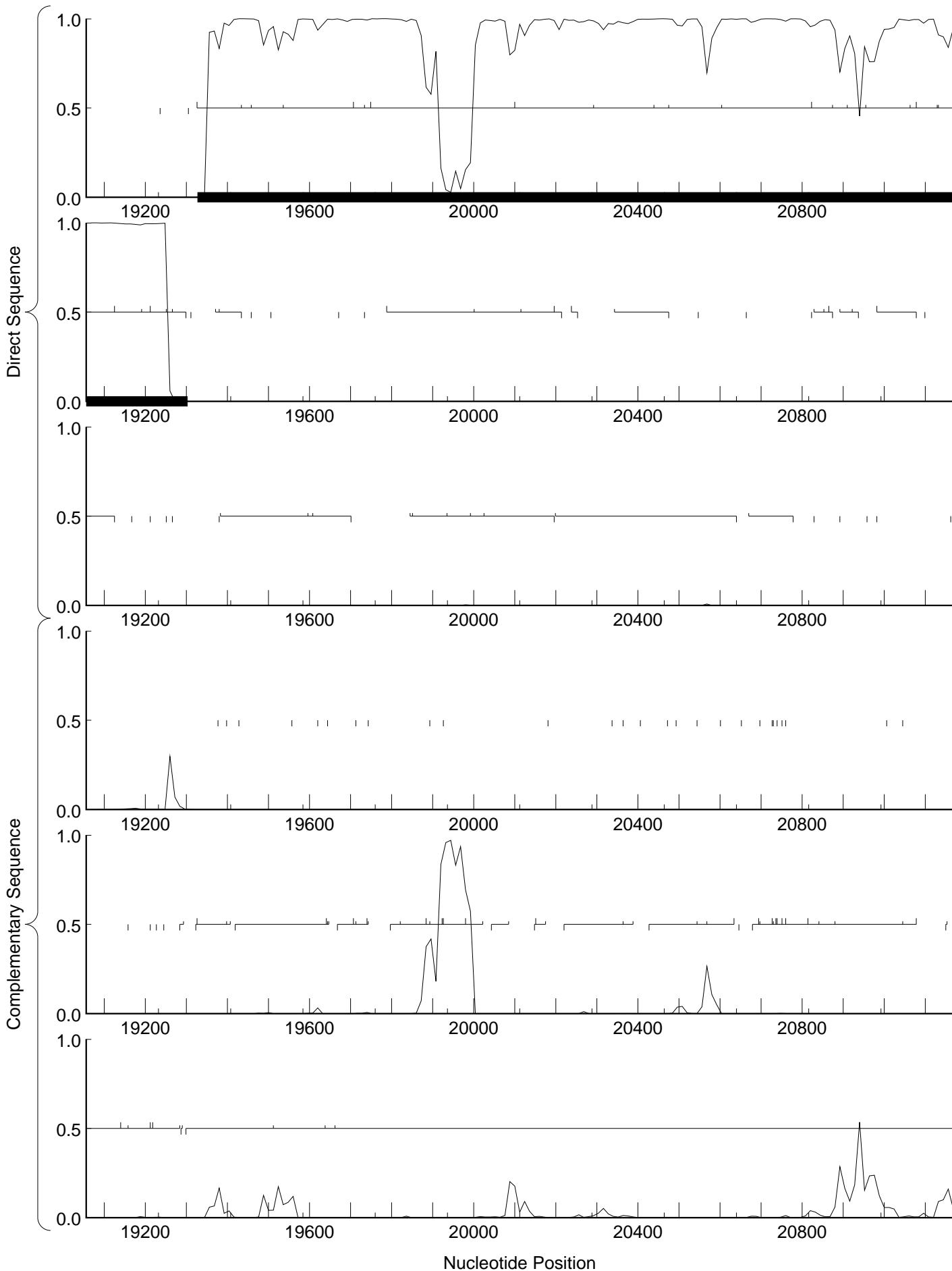




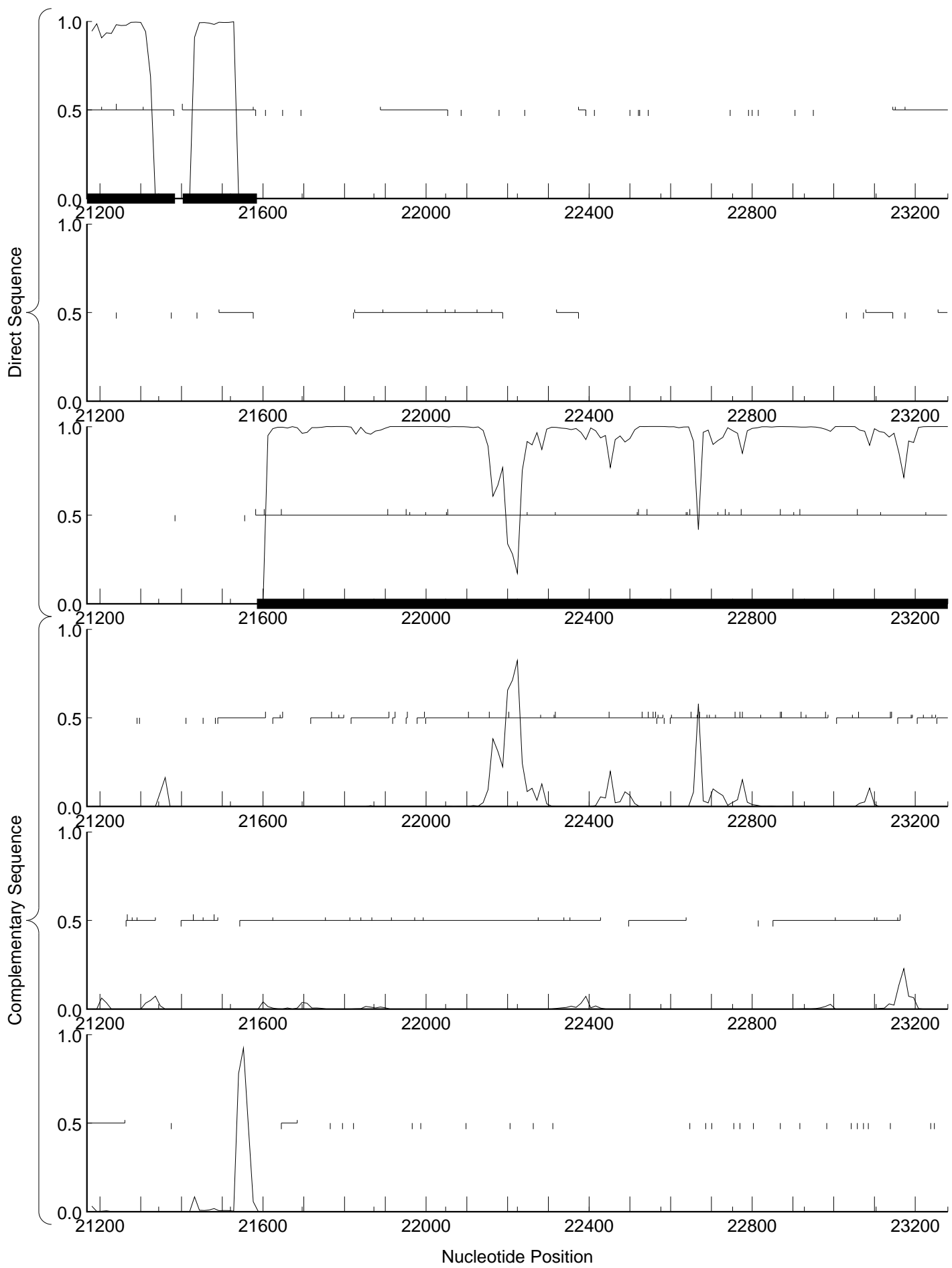


GeneMark.hmm prediction

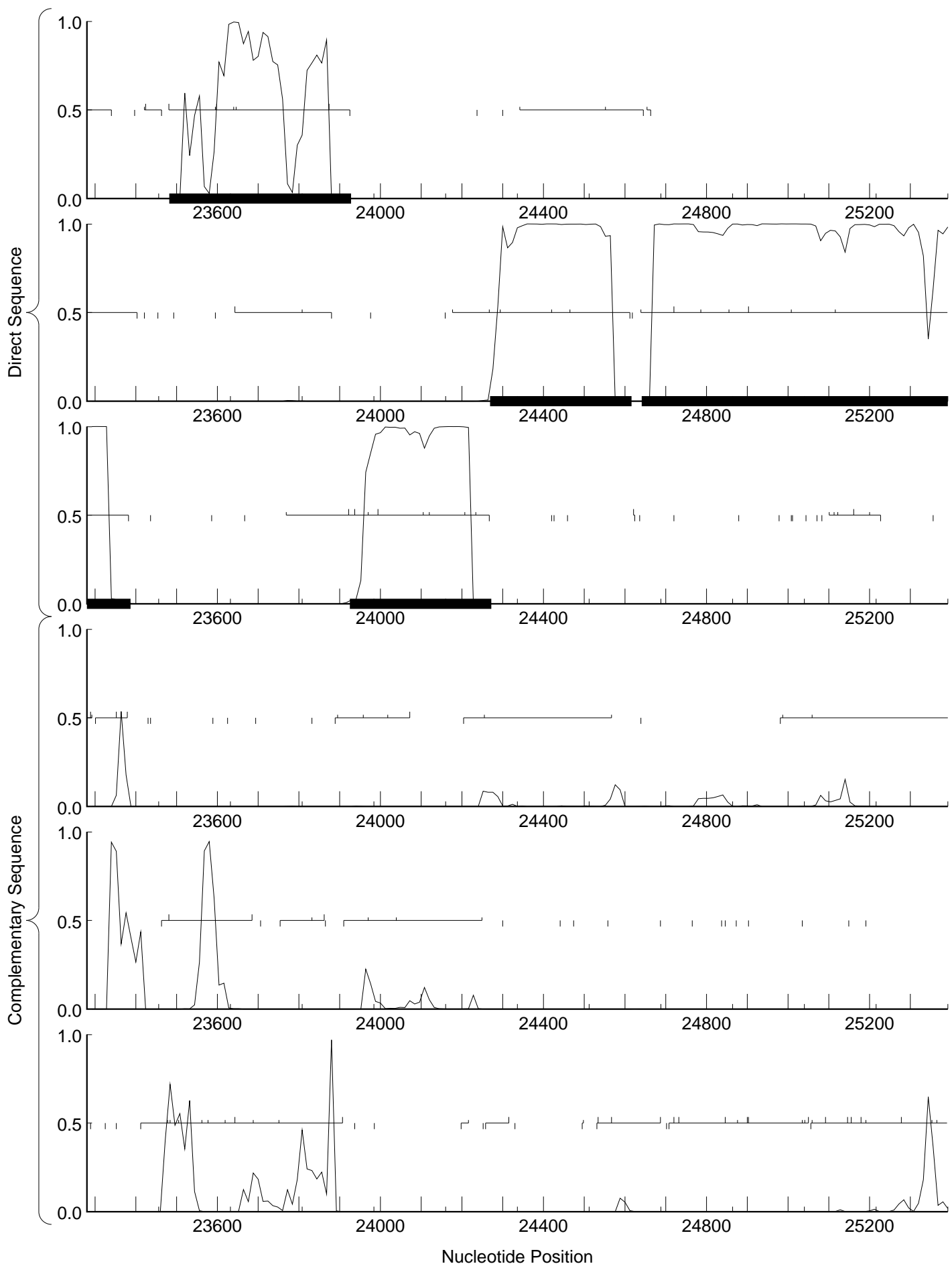




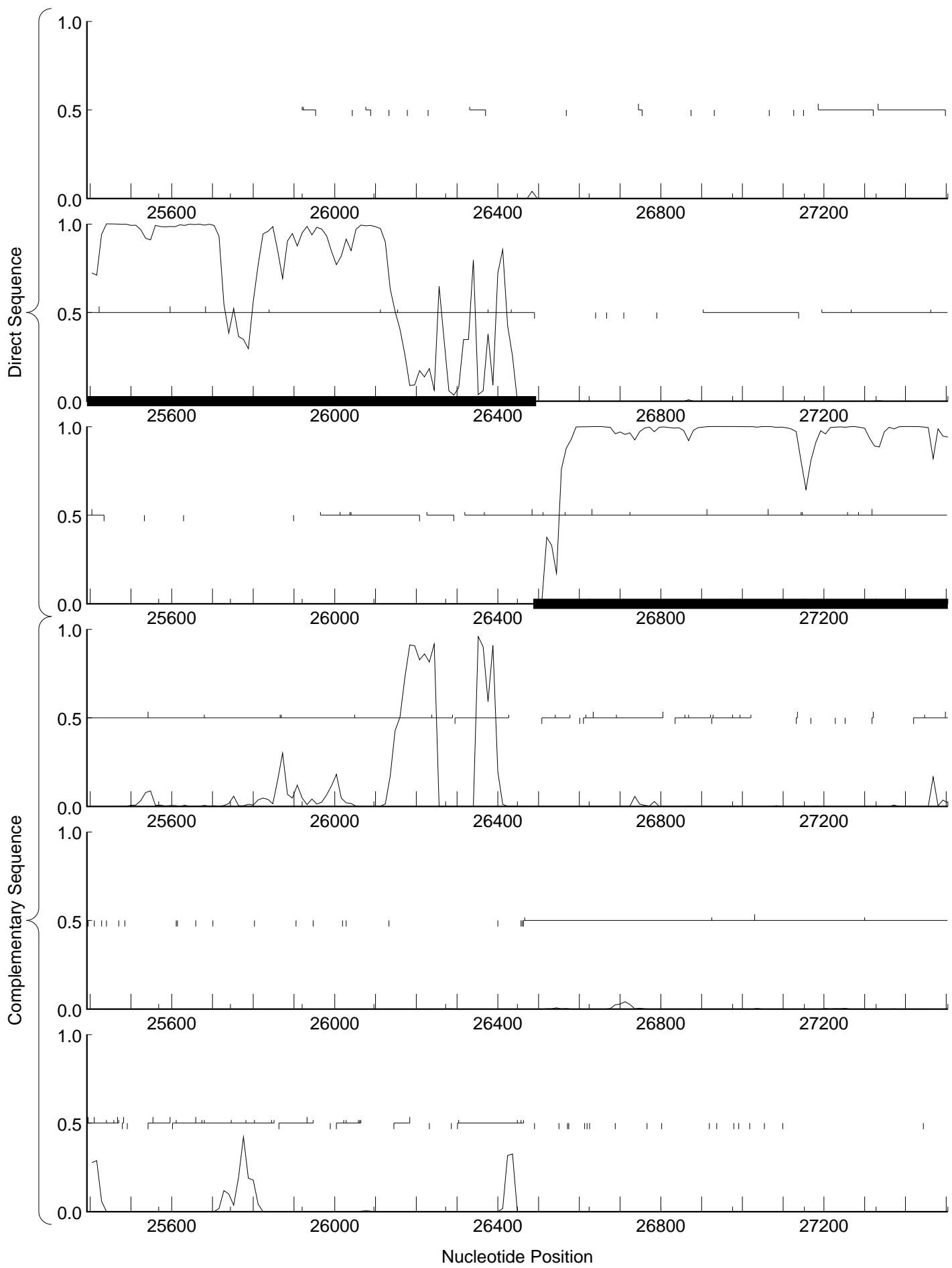
GeneMark.hmm prediction



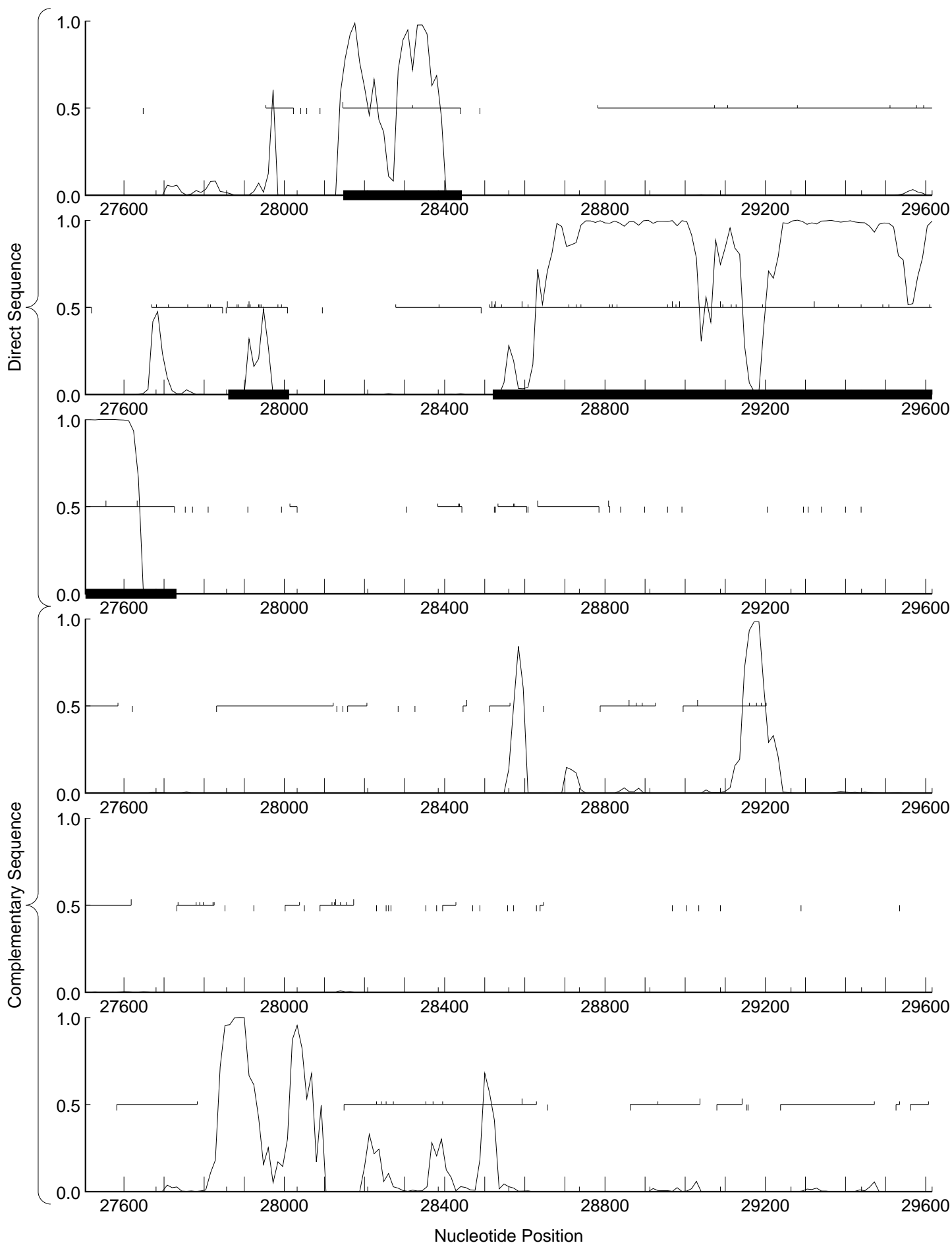
GeneMark.hmm prediction



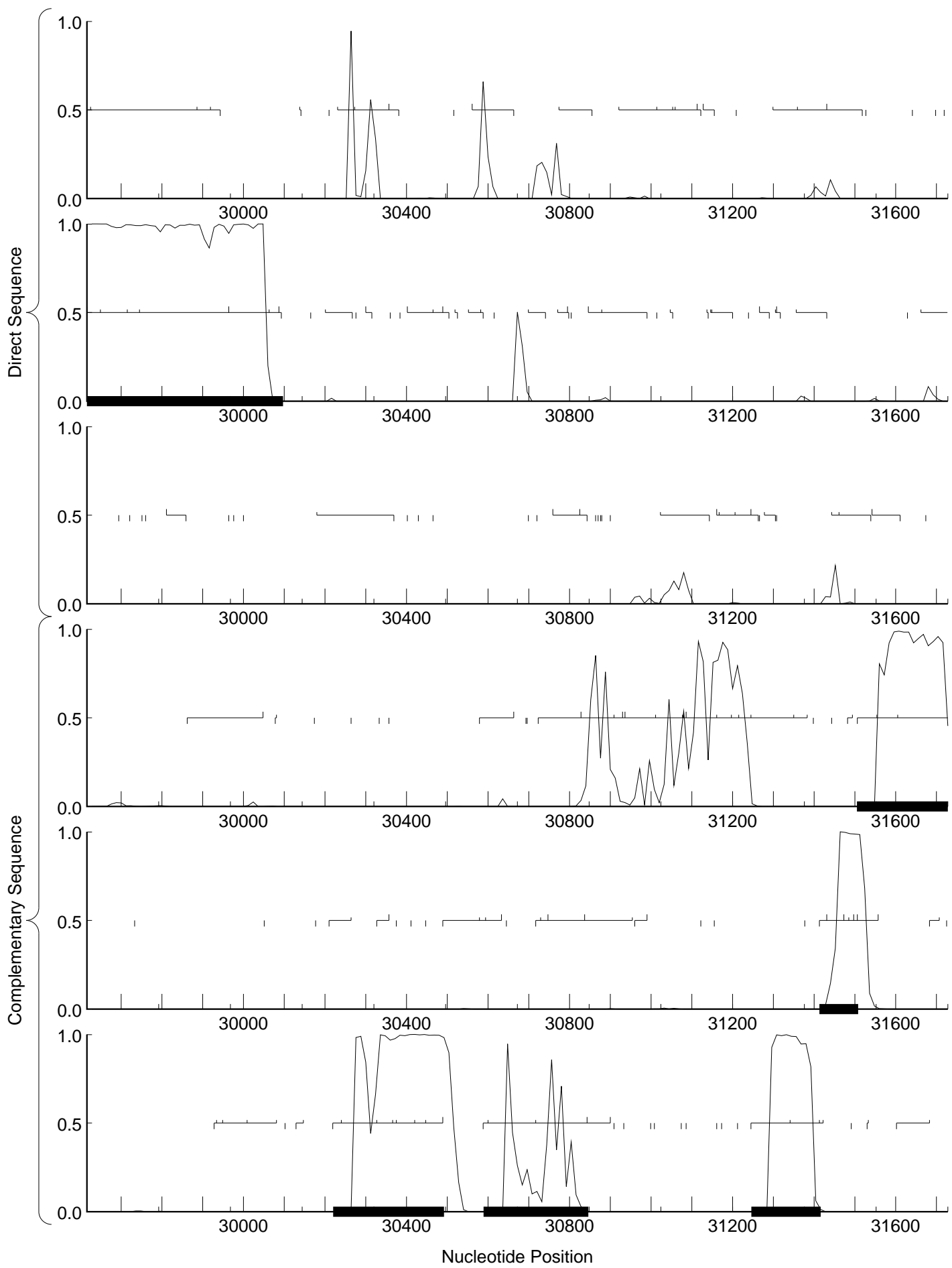
GeneMark.hmm prediction



GeneMark.hmm prediction

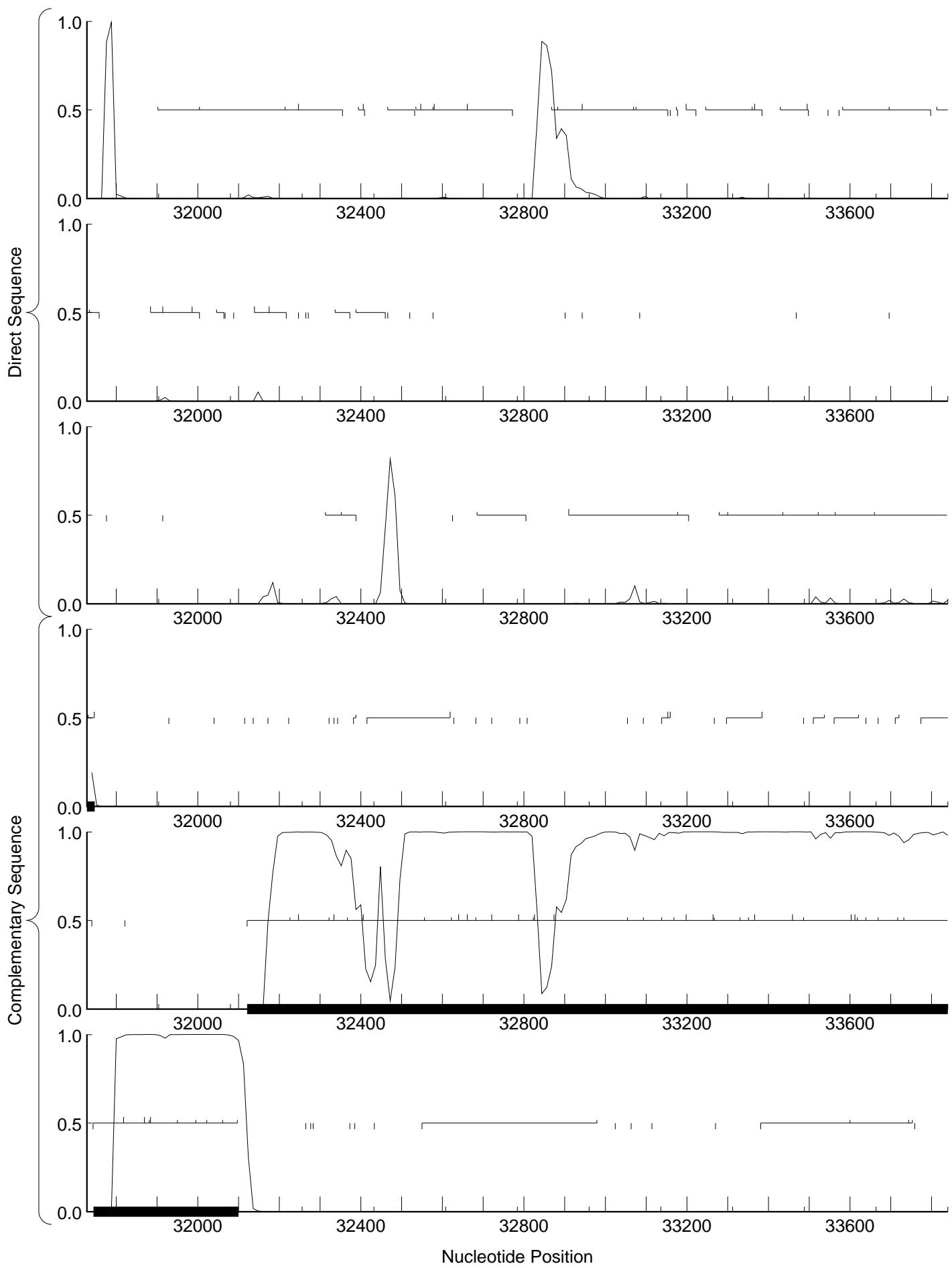


GeneMark.hmm prediction

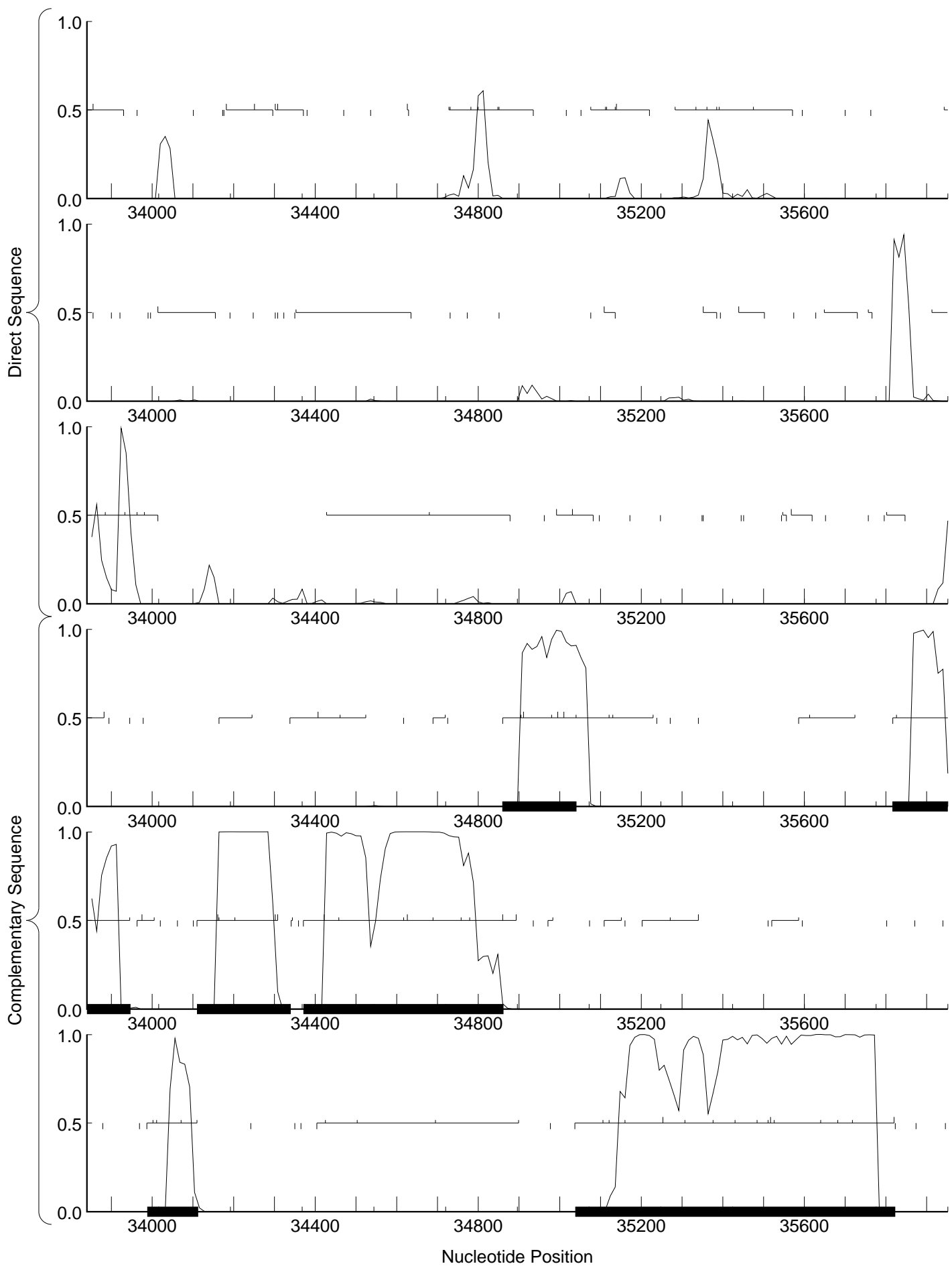




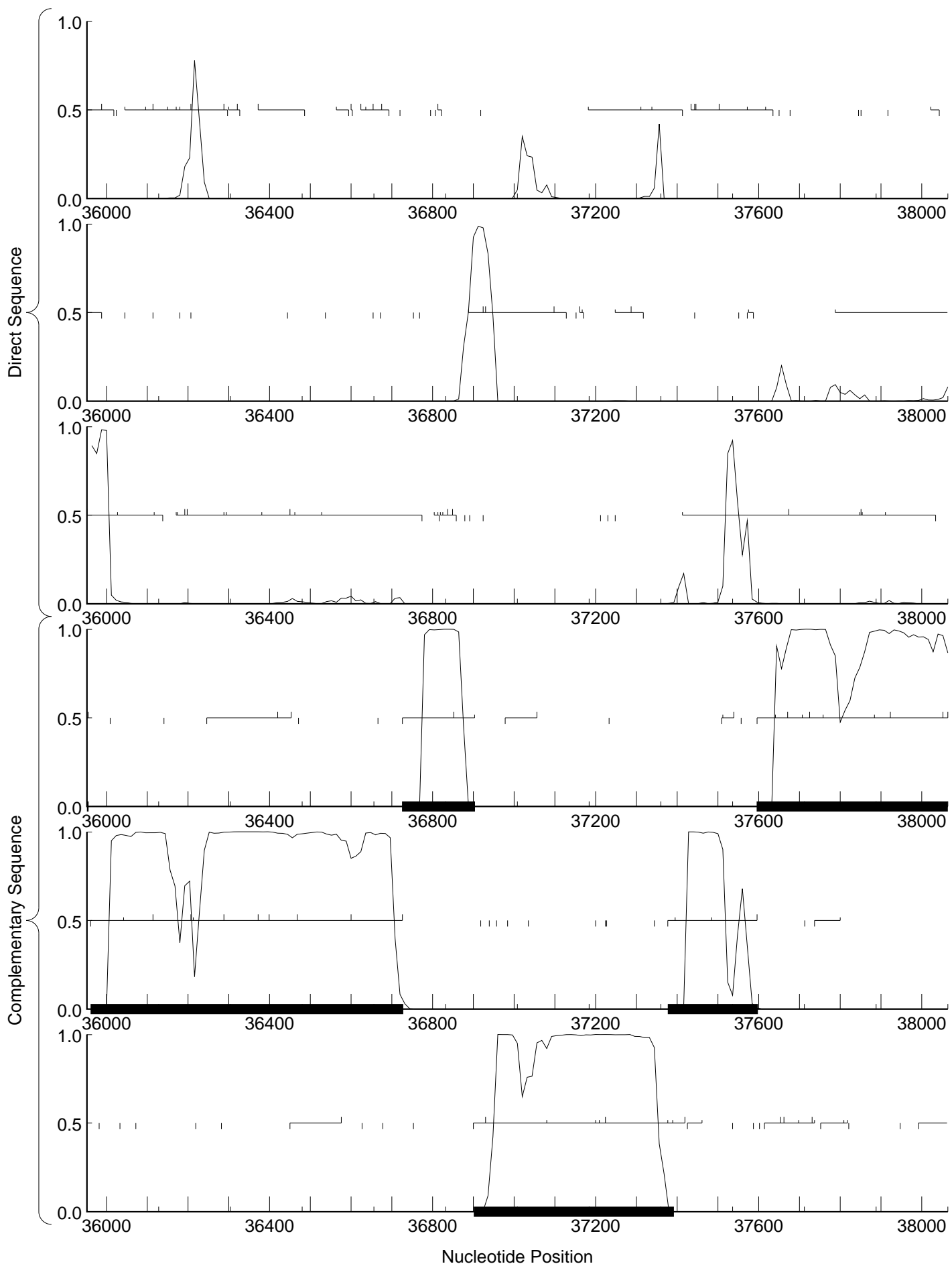
GeneMark.hmm prediction



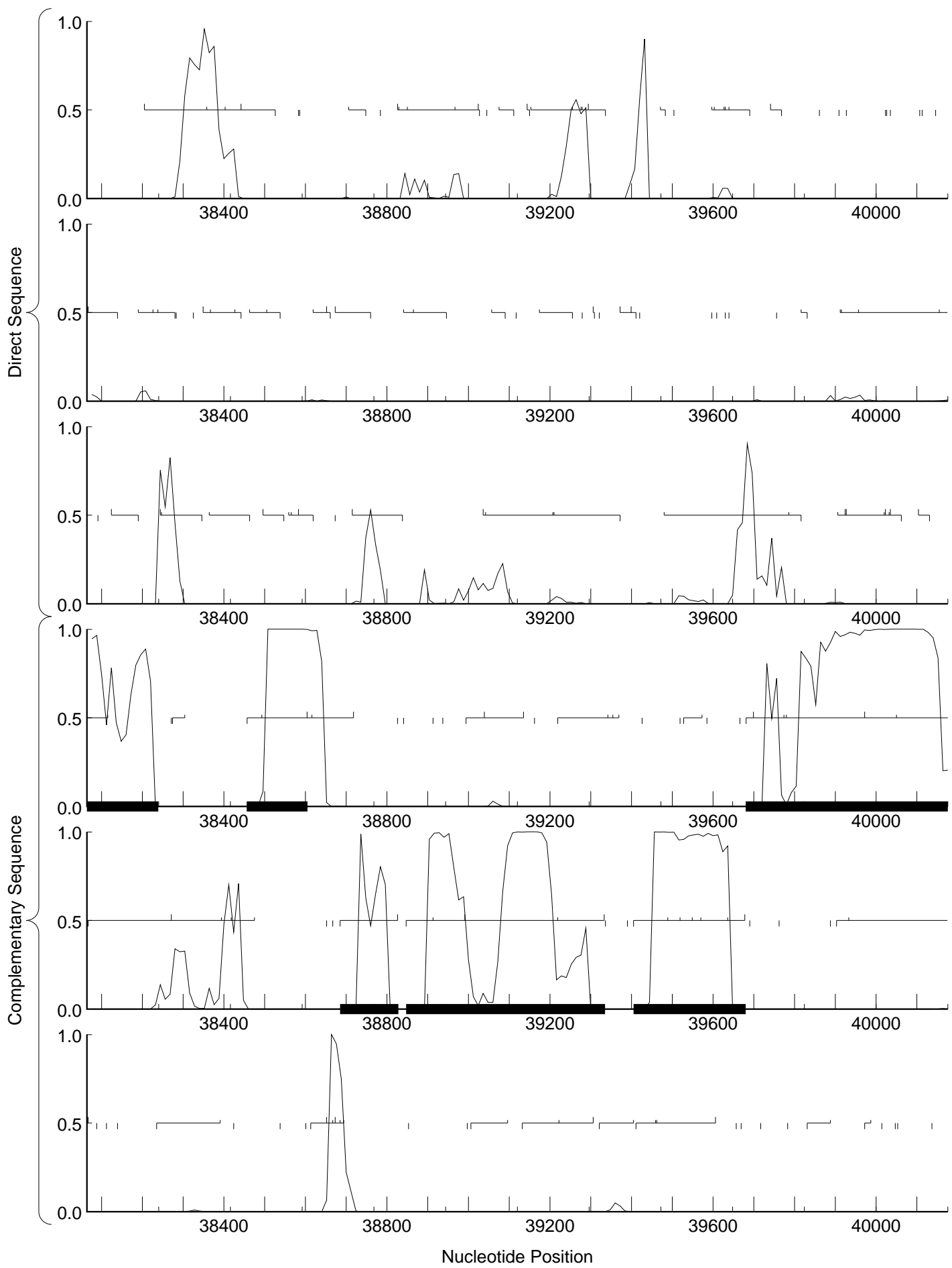
GeneMark.hmm prediction



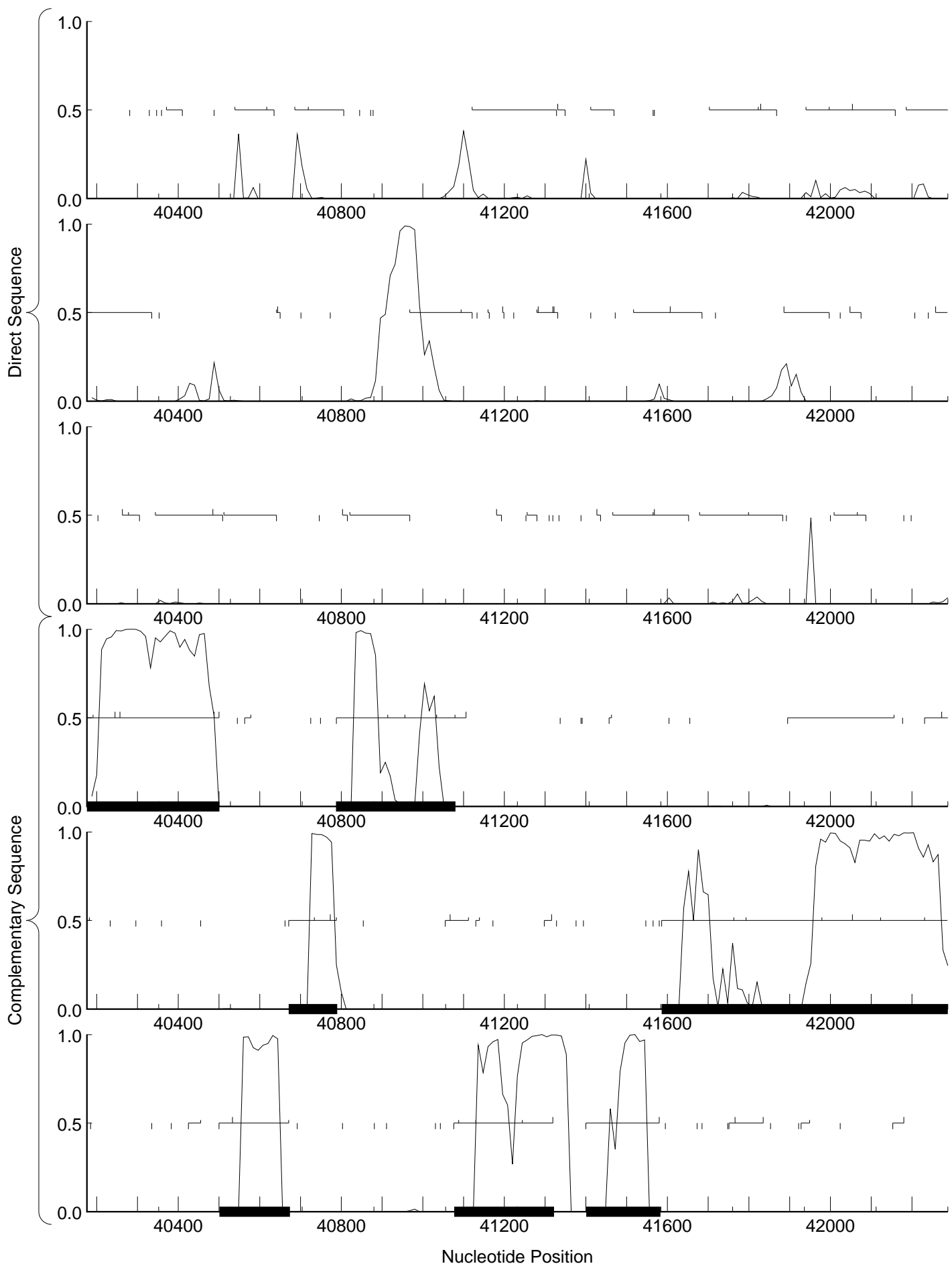
GeneMark.hmm prediction



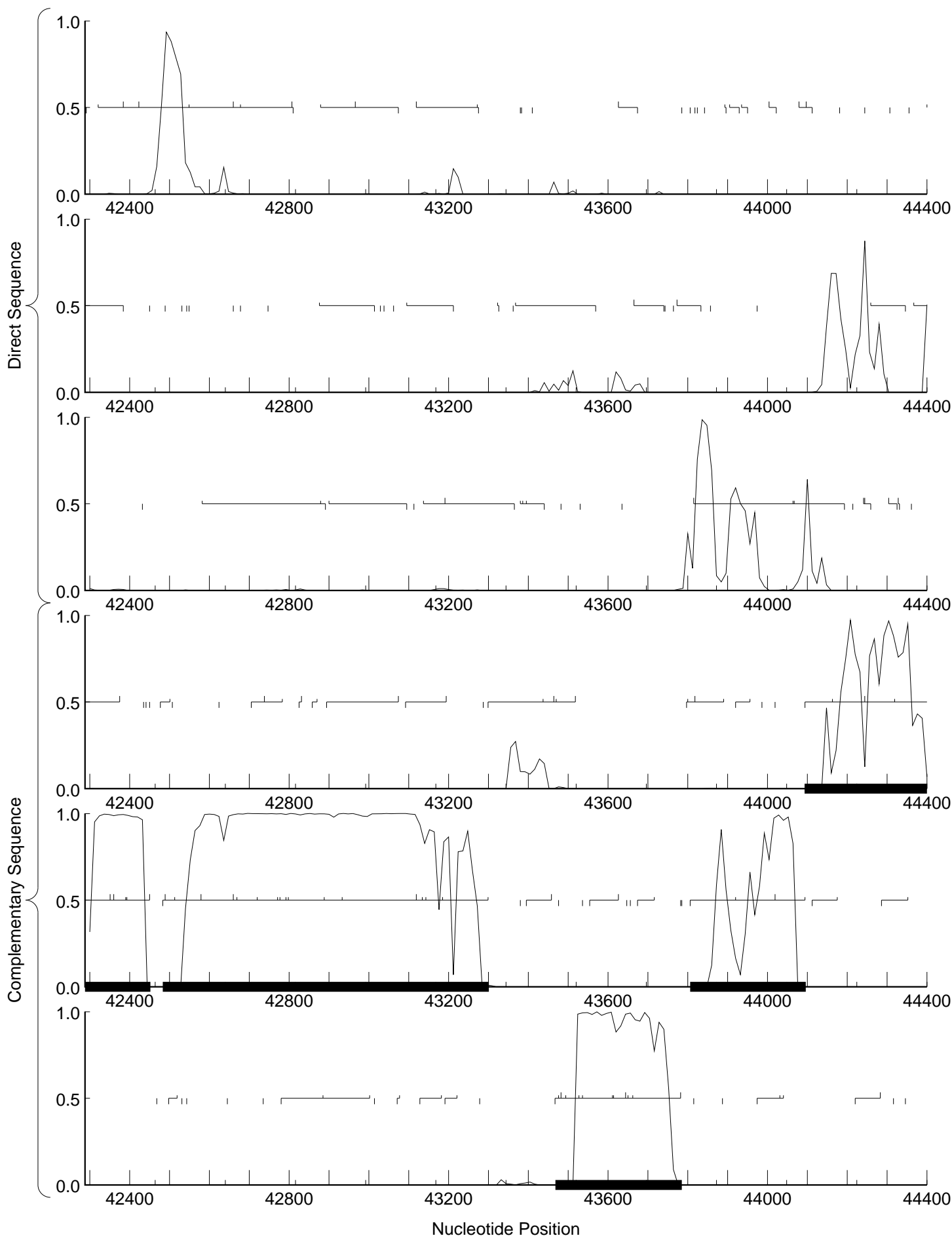
GeneMark.hmm prediction



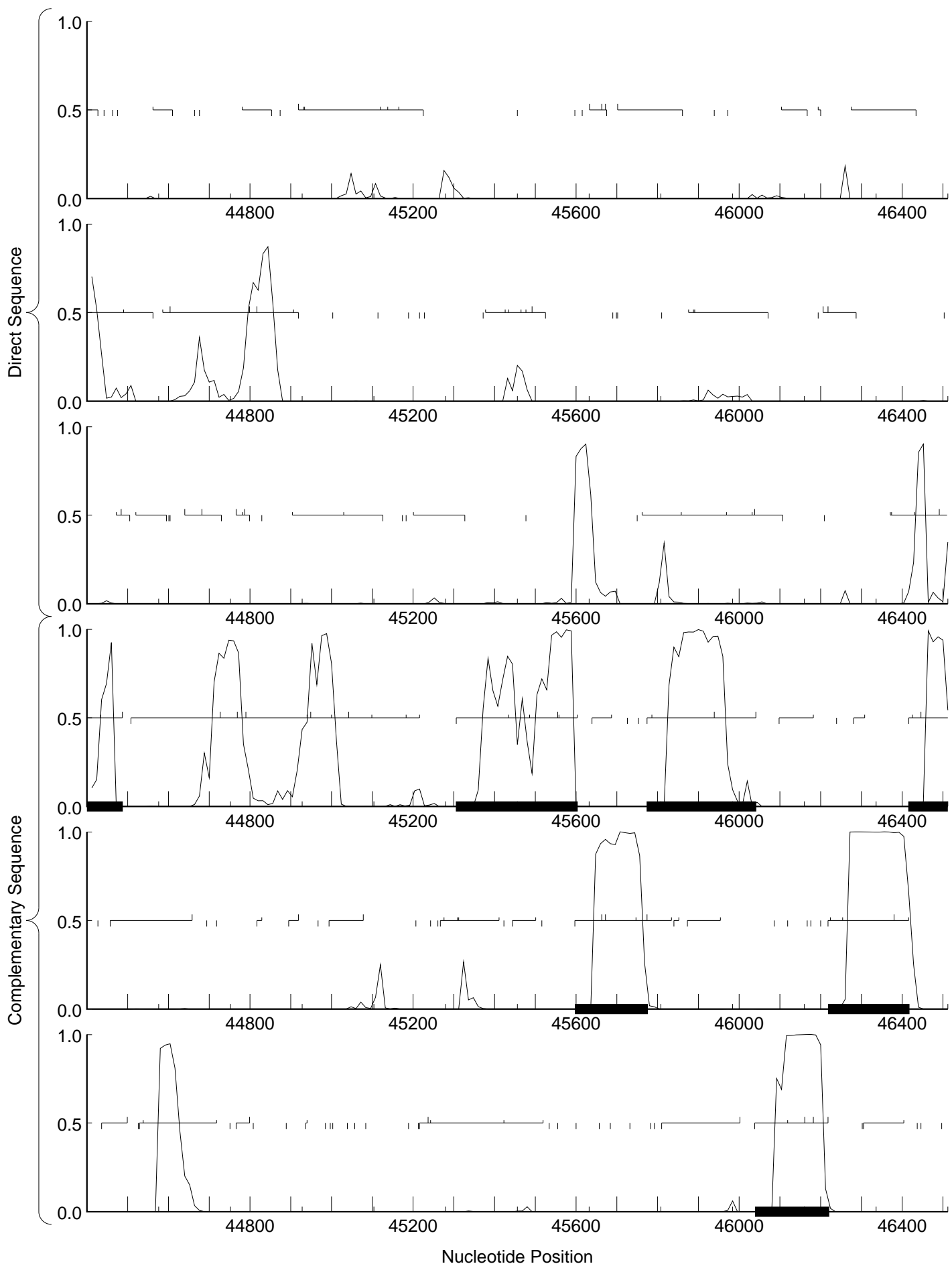
GeneMark.hmm prediction



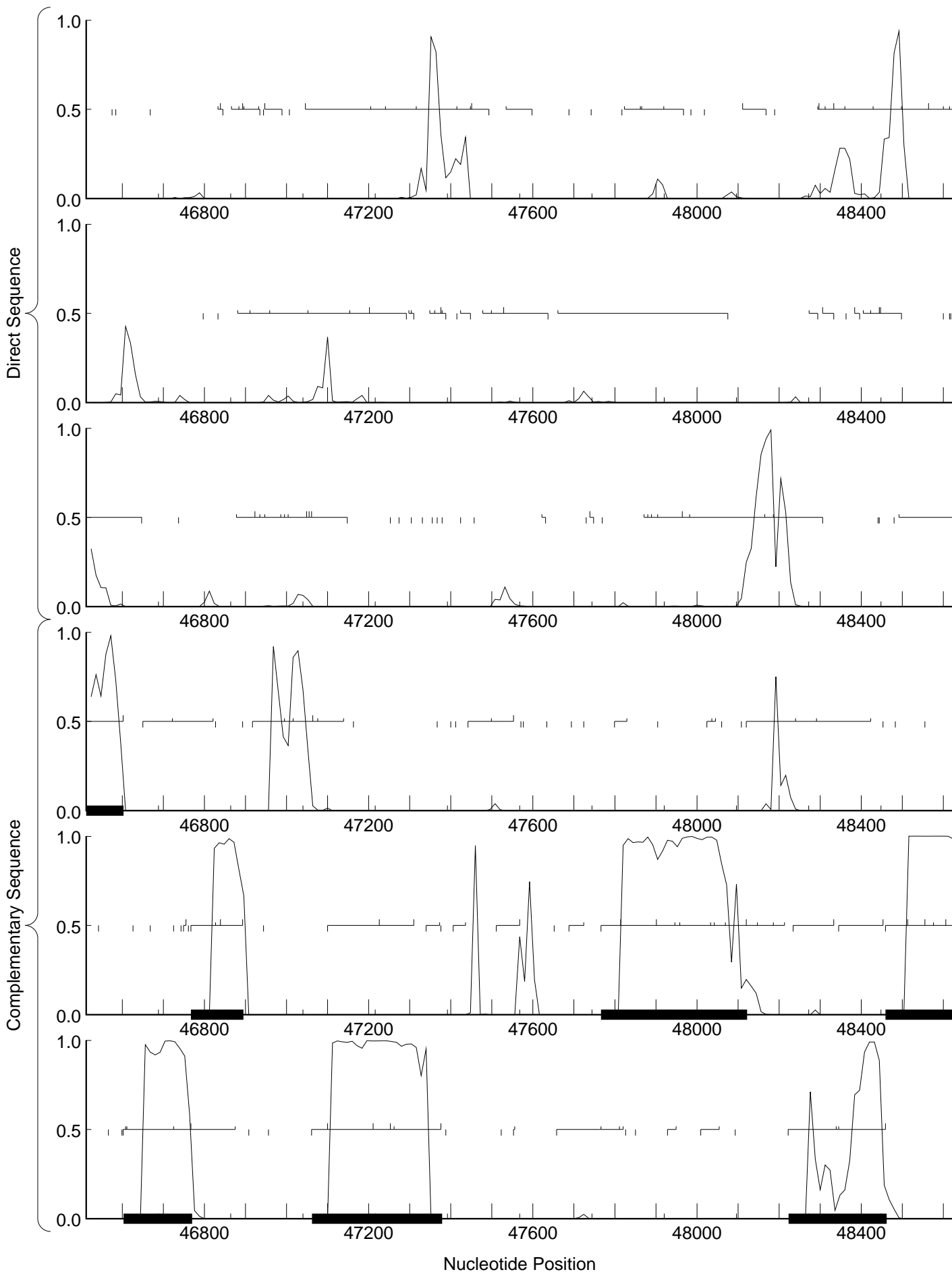
GeneMark.hmm prediction



GeneMark.hmm prediction



Nucleotide Position





GeneMark.hmm prediction

