

# GeneMark

Version 2.5p (09.08.06)

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## PROGRAM INFORMATION

Sequence : Streptomyces phage Nerdos complete sequence, 49557 bp including 11-base 3' overhang (CGGGCA  
Analysis Date : 11/23/17 at 6:12:28  
Pages : 25  
Sequence Length : 49557 bp  
GC Content : 66.22%

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,

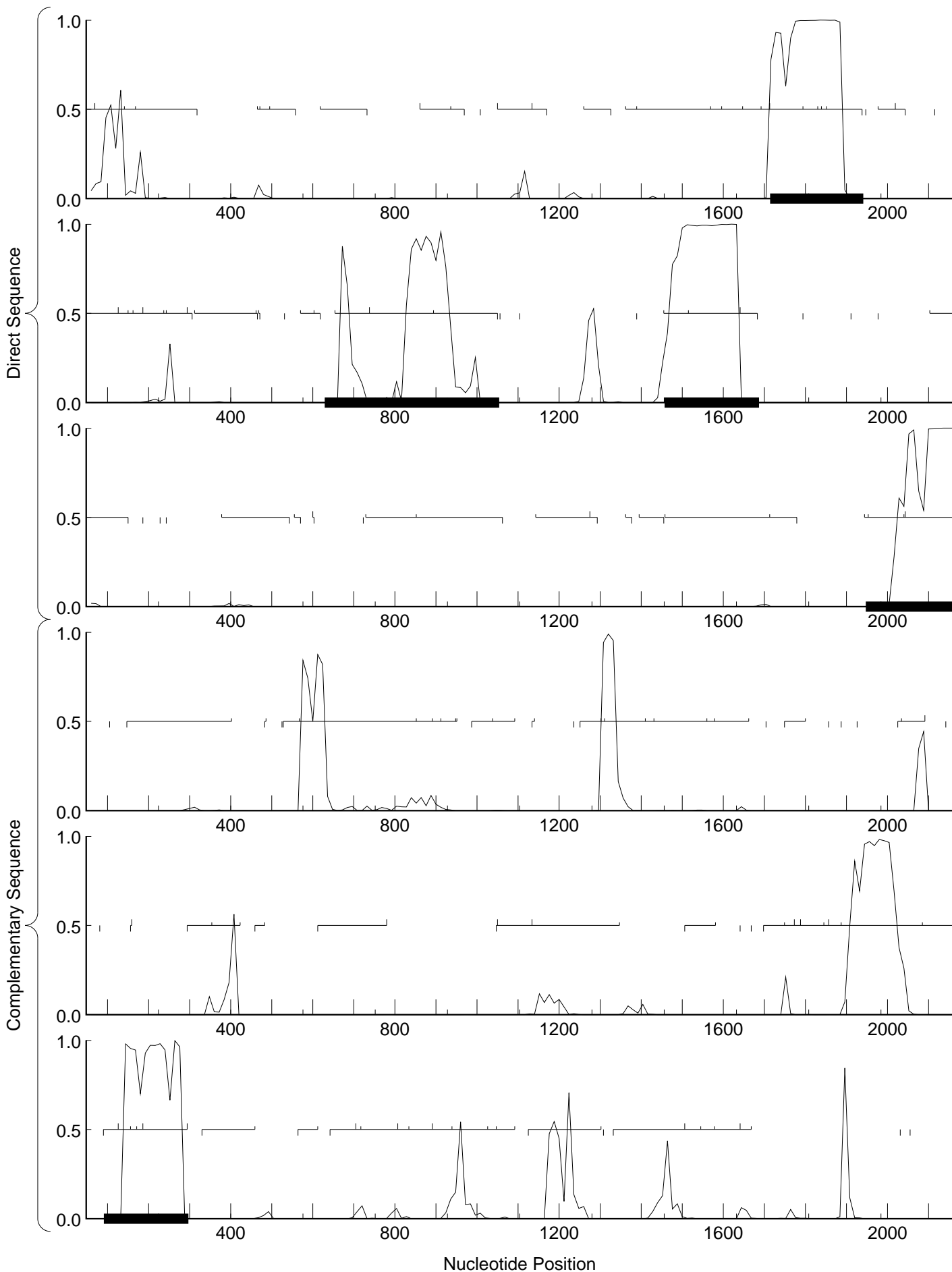
## MATRIX INFORMATION

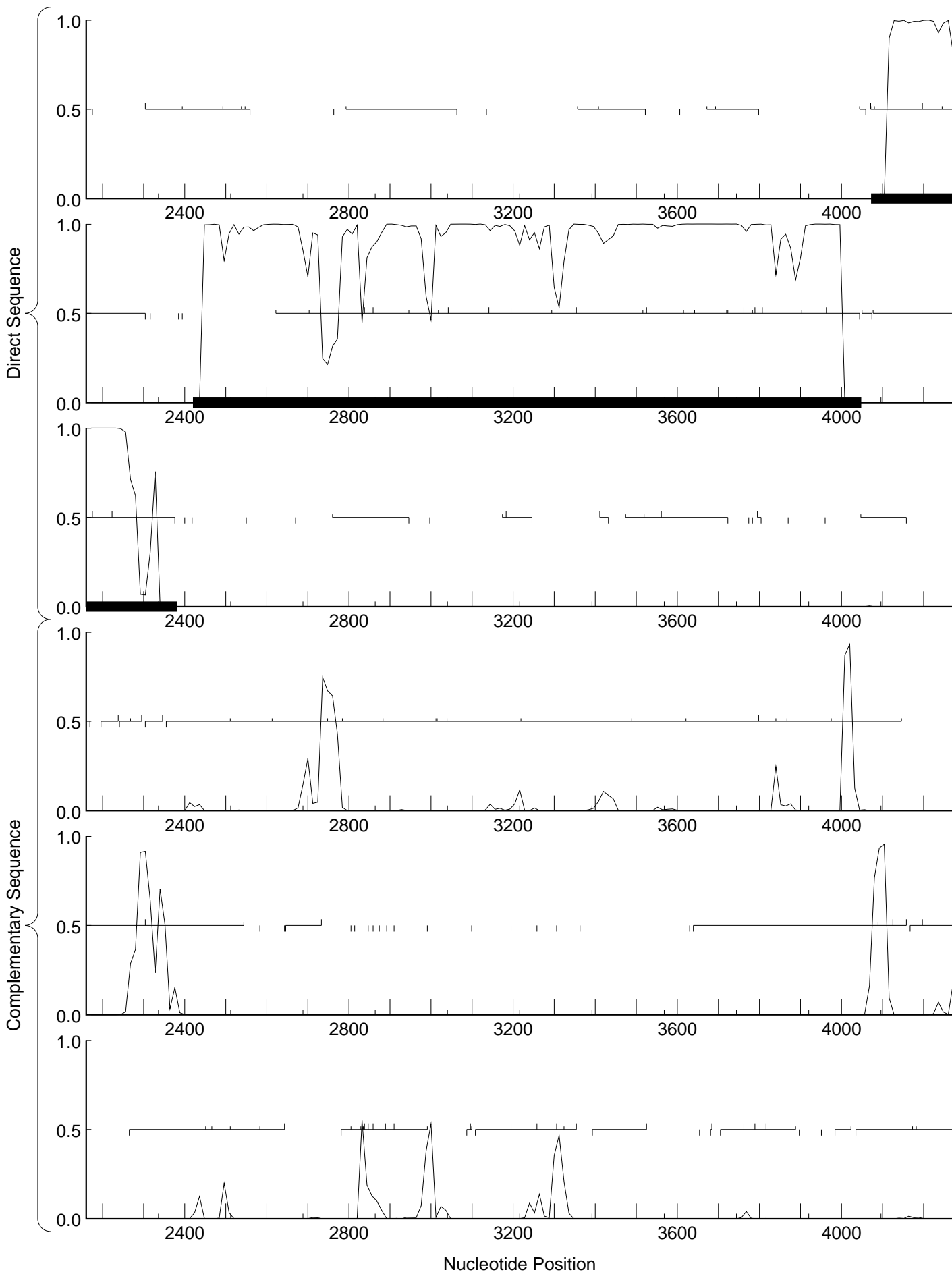
Matrix : Heuristic, GC = 66  
Author : Borodovsky Laboratory - Georgia Tech  
Order : 2

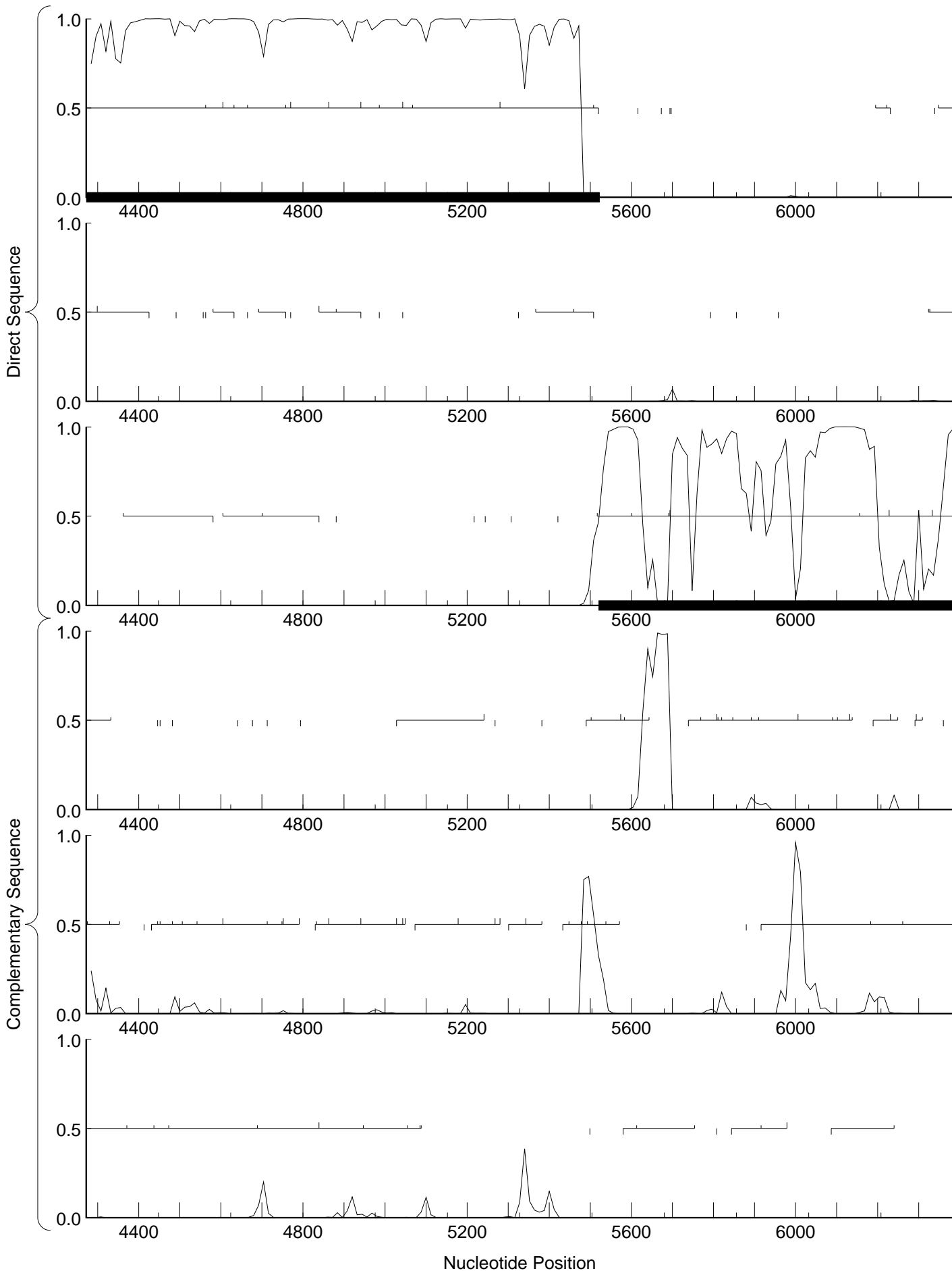
Send questions / comments to:  
Dr. M. Borodovsky  
Georgia Institute of Technology  
School of Biology  
Atlanta, GA 30332-0230

### Matrix notes & comments

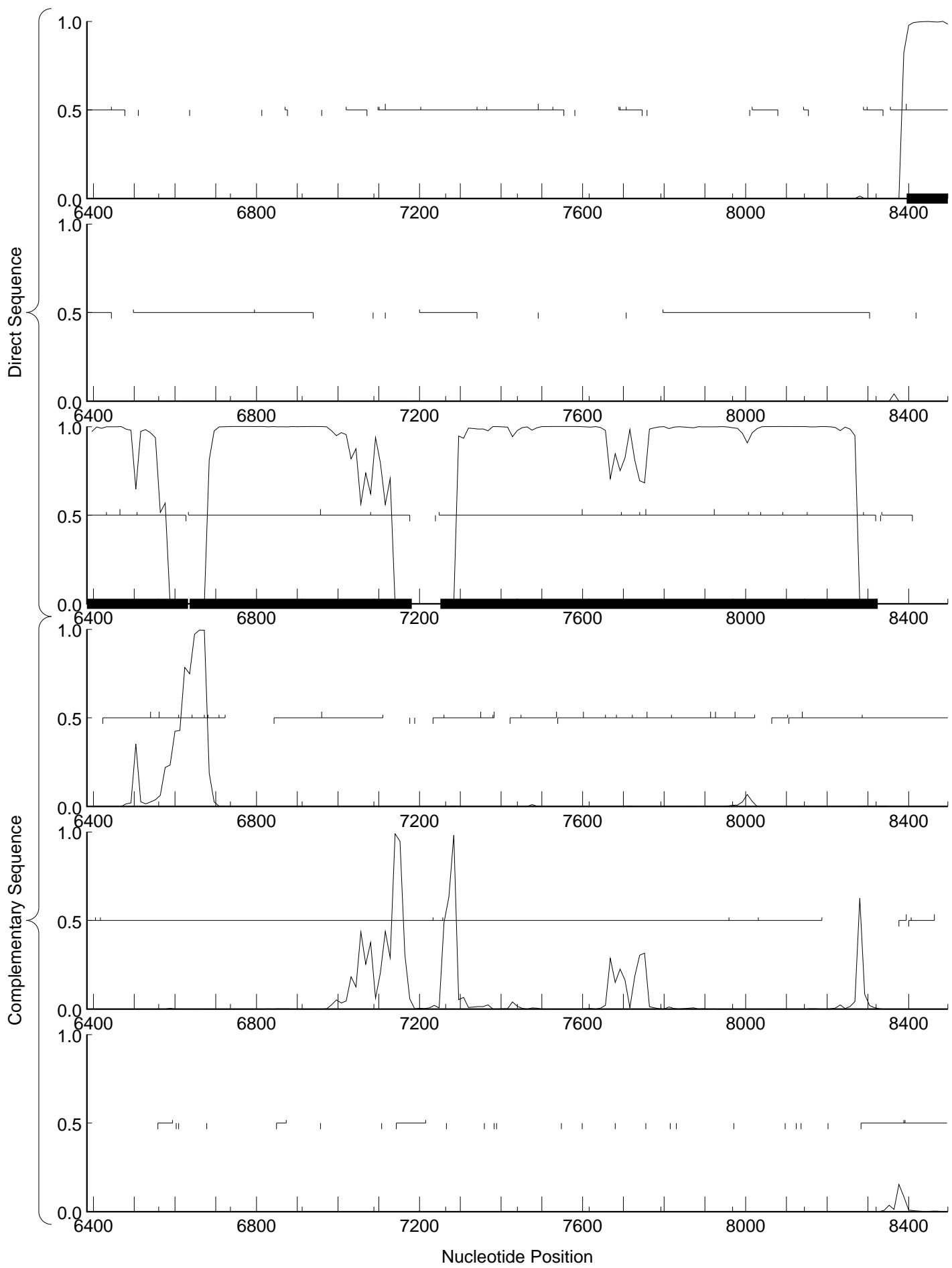
For details on the model building procedure see:  
Besemer J. and Borodovsky M.  
"Heuristic approach to deriving models for gene finding"  
NAR, 1999, Vol. 27, No. 19, pp. 3911-3920





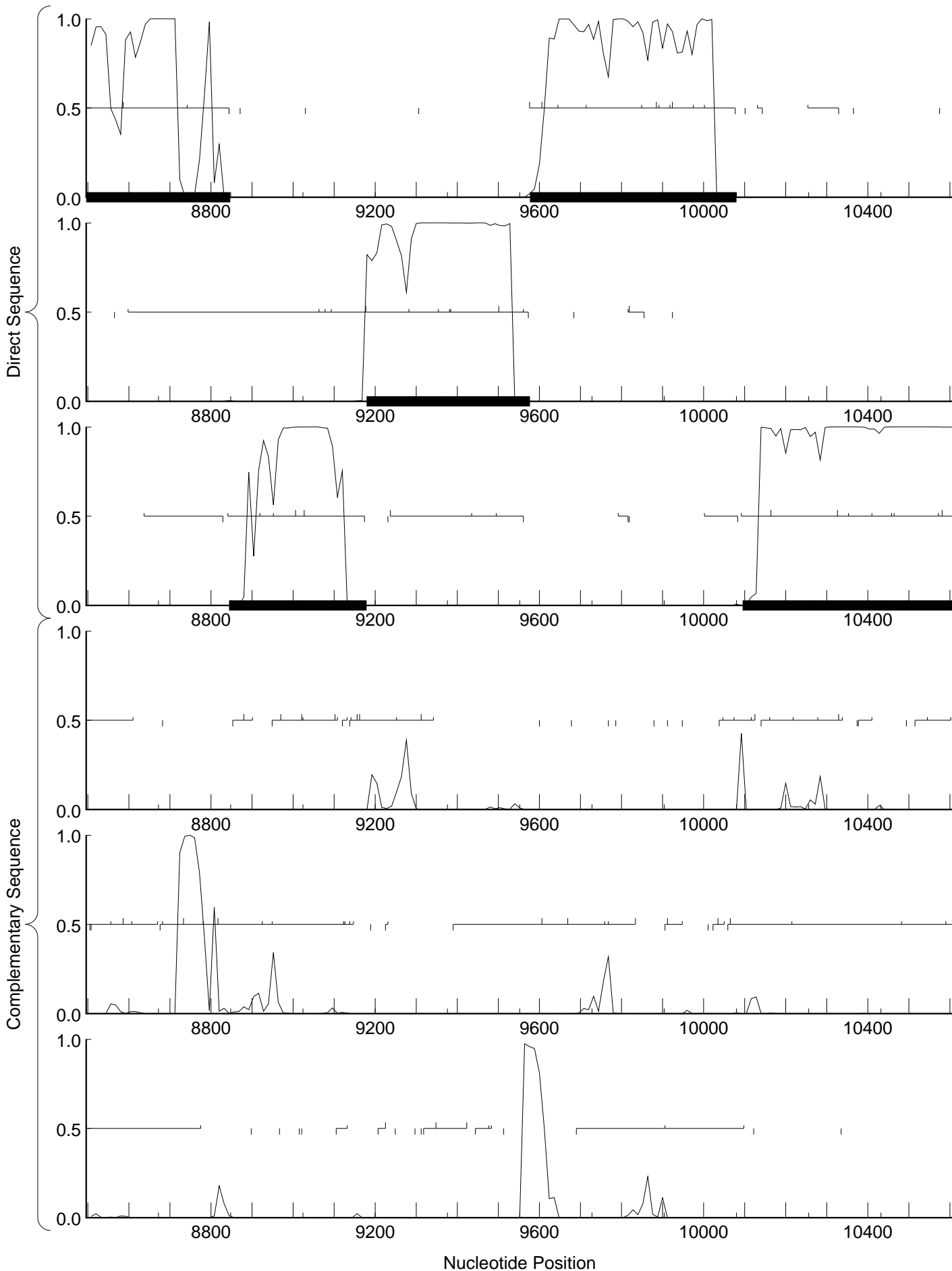


GeneMark, hmm prediction

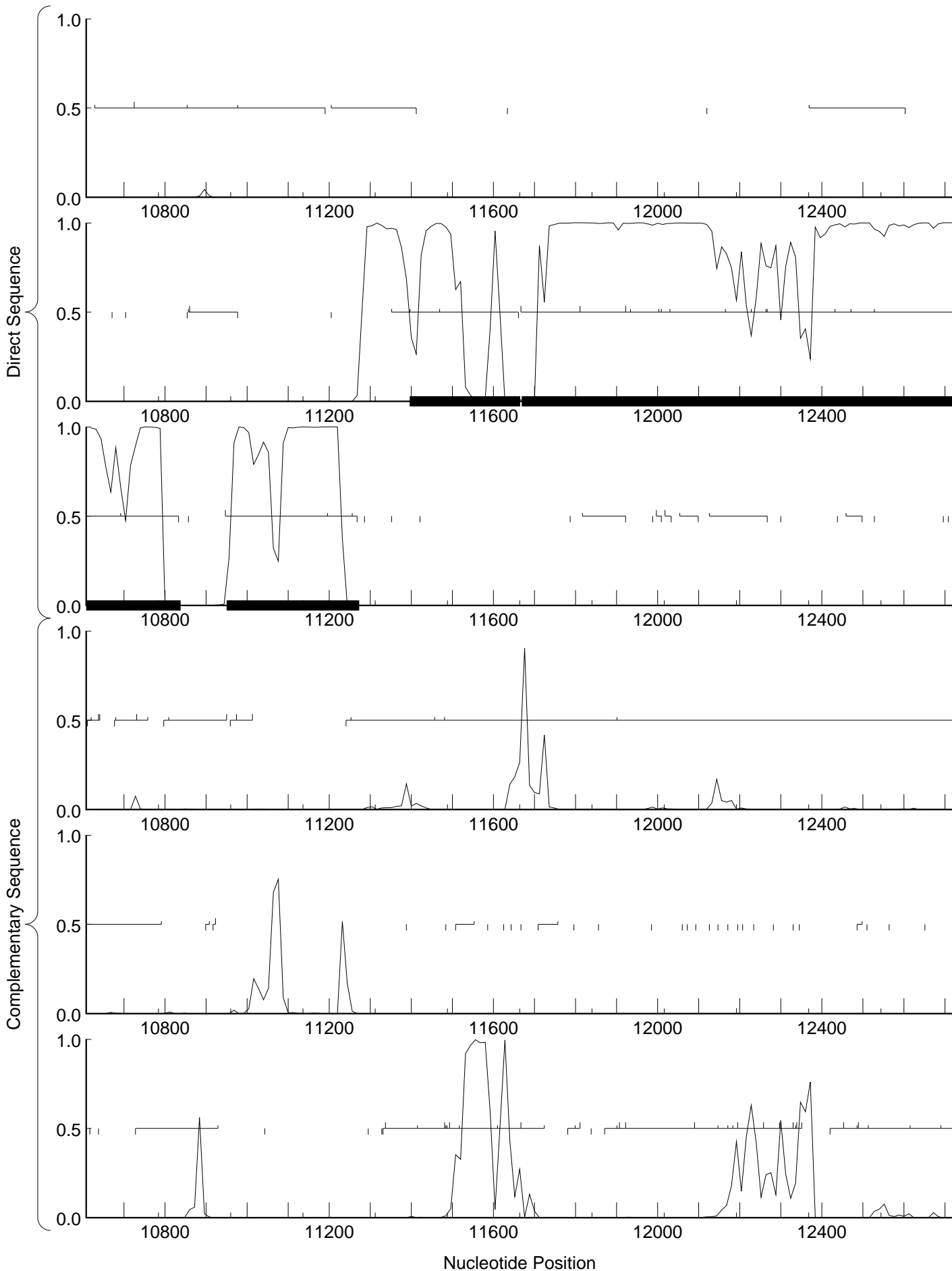


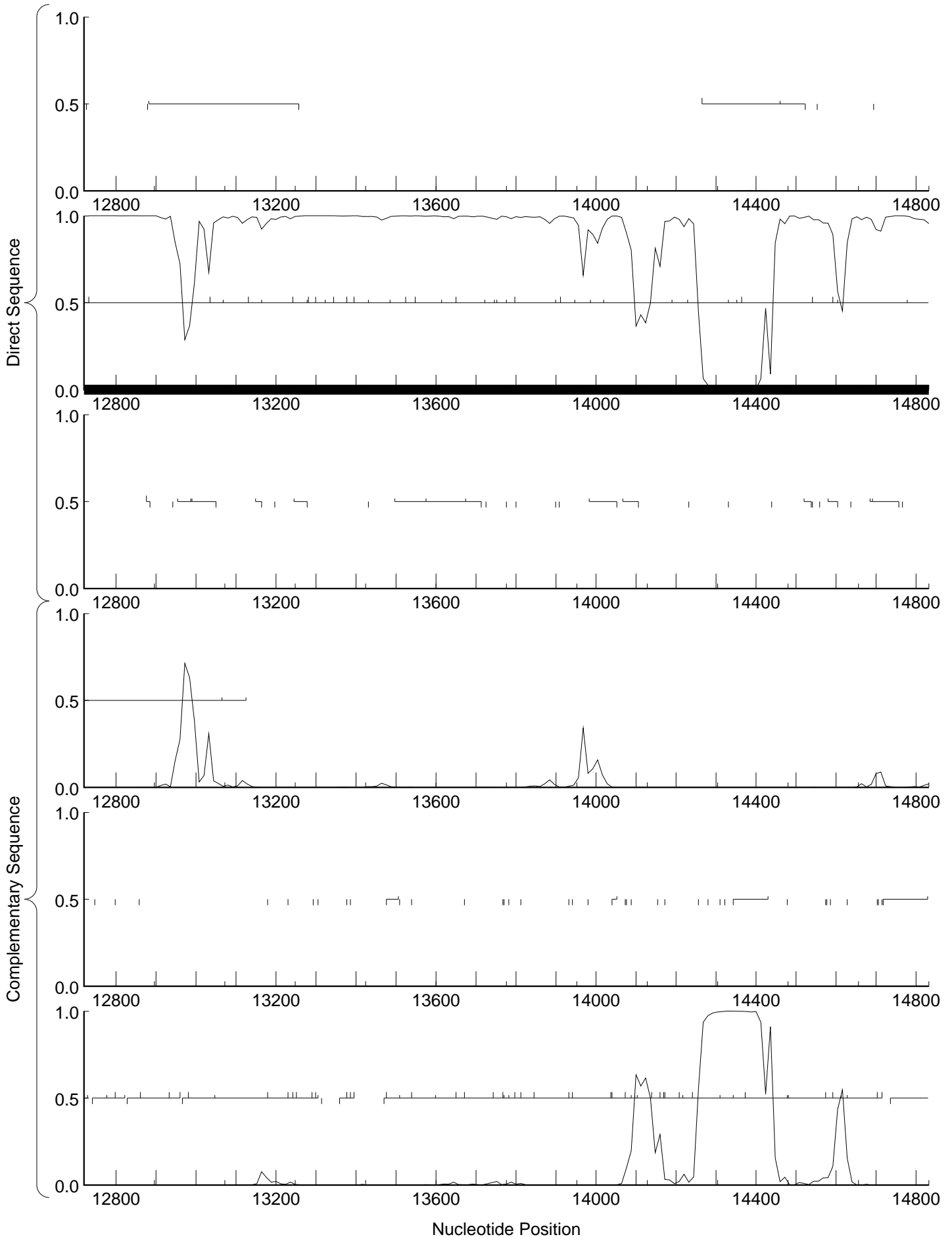
Nucleotide Position

GeneMark, hmm prediction



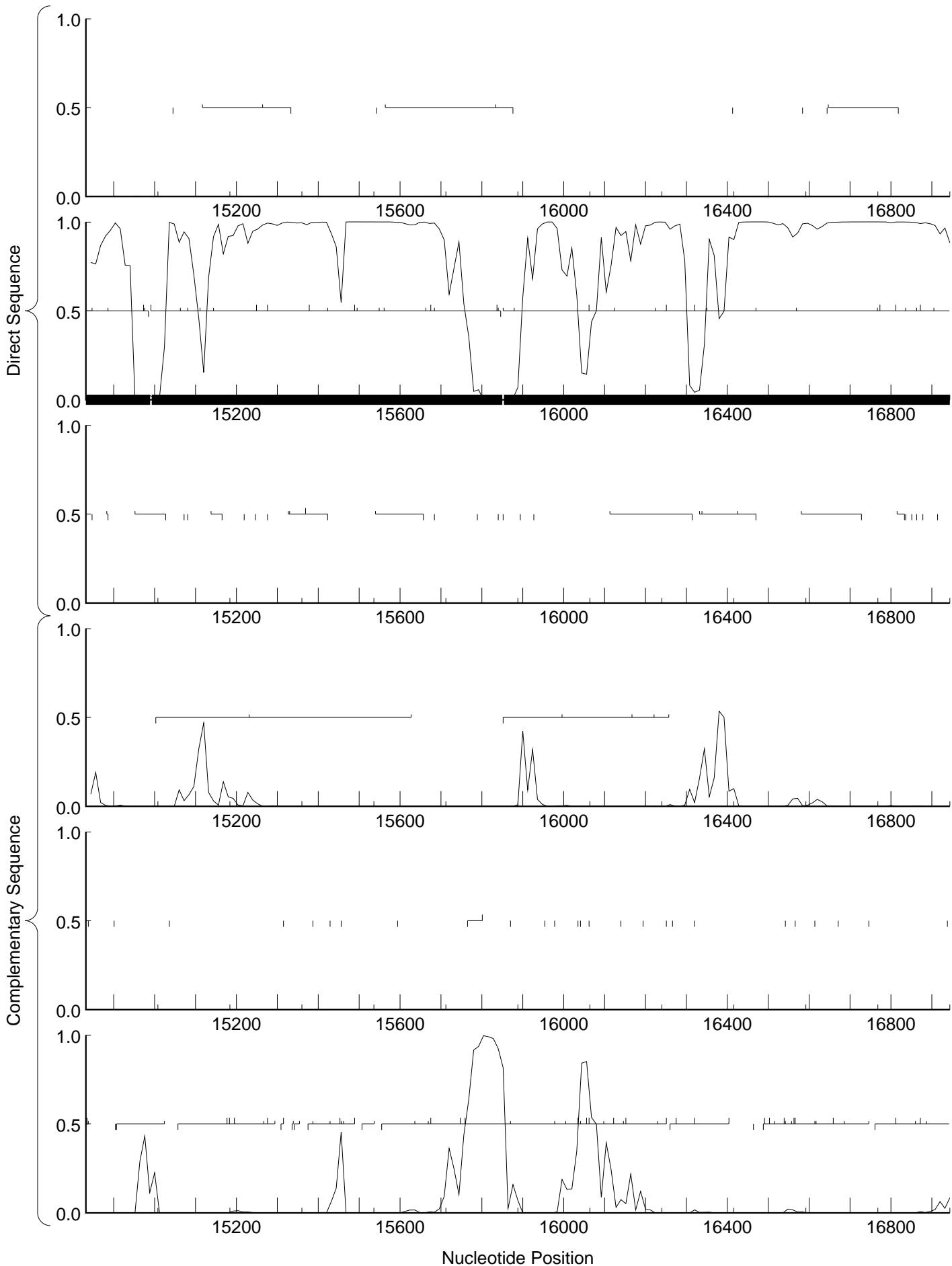
GeneMark, hmm prediction

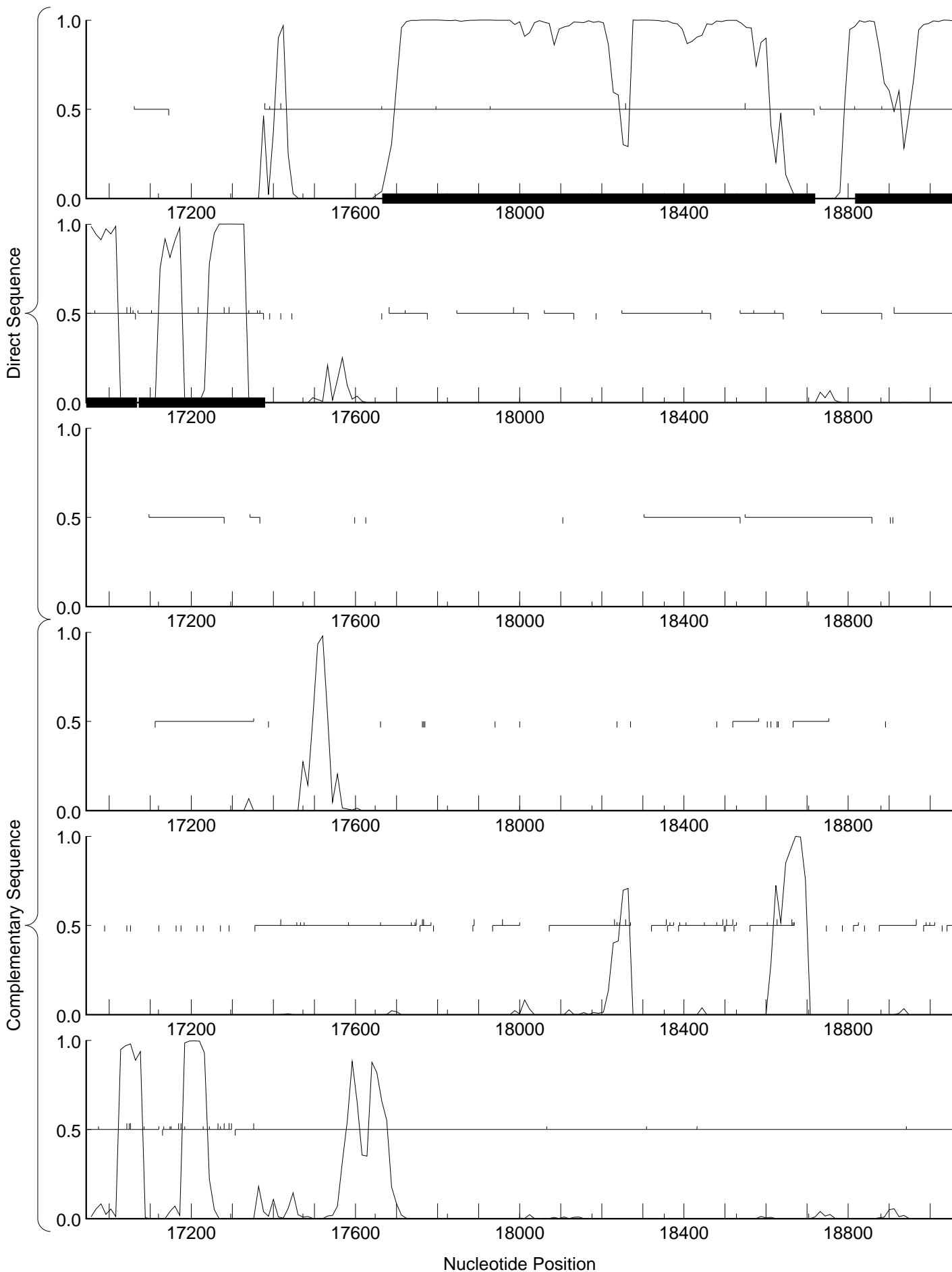




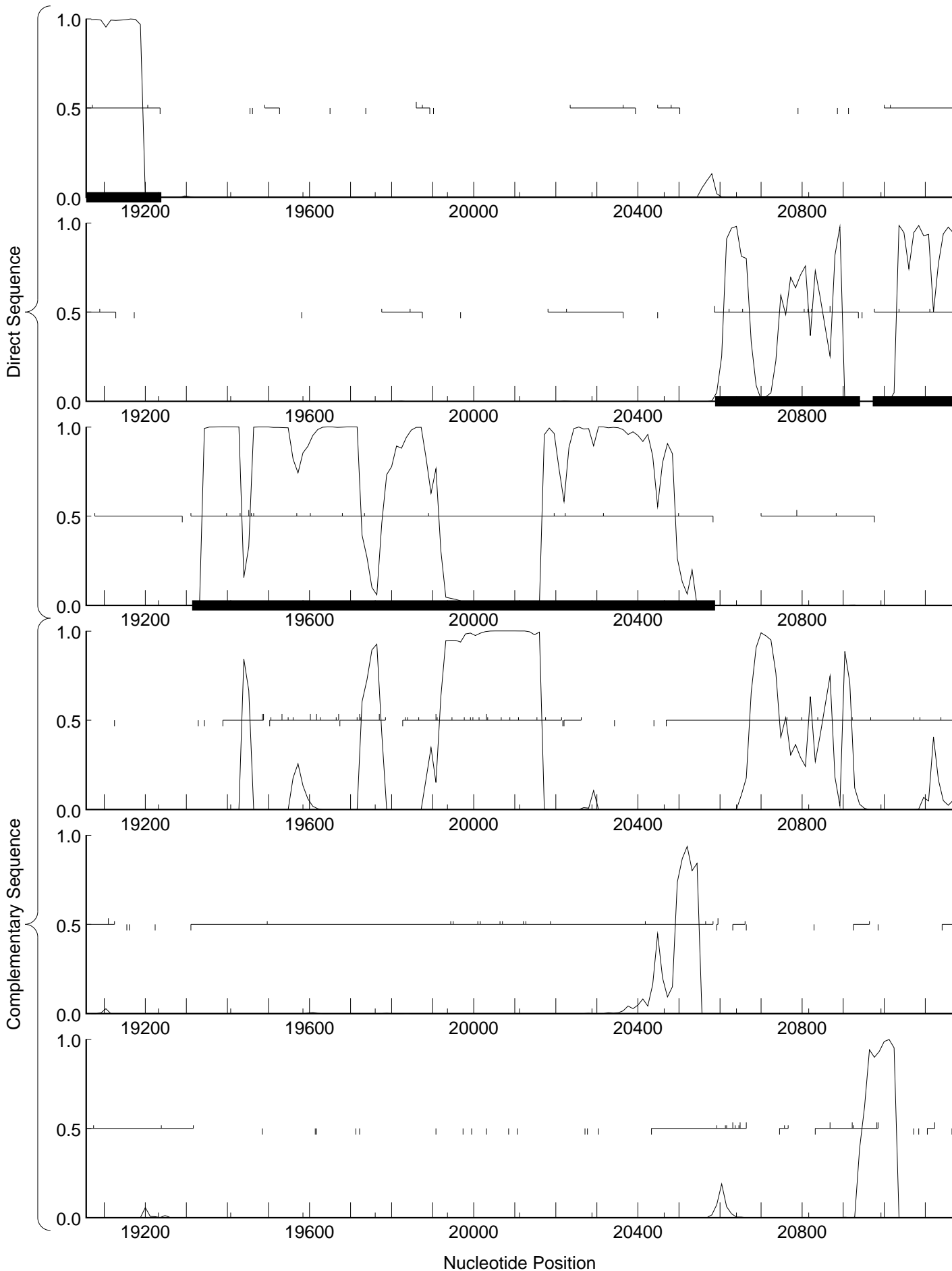


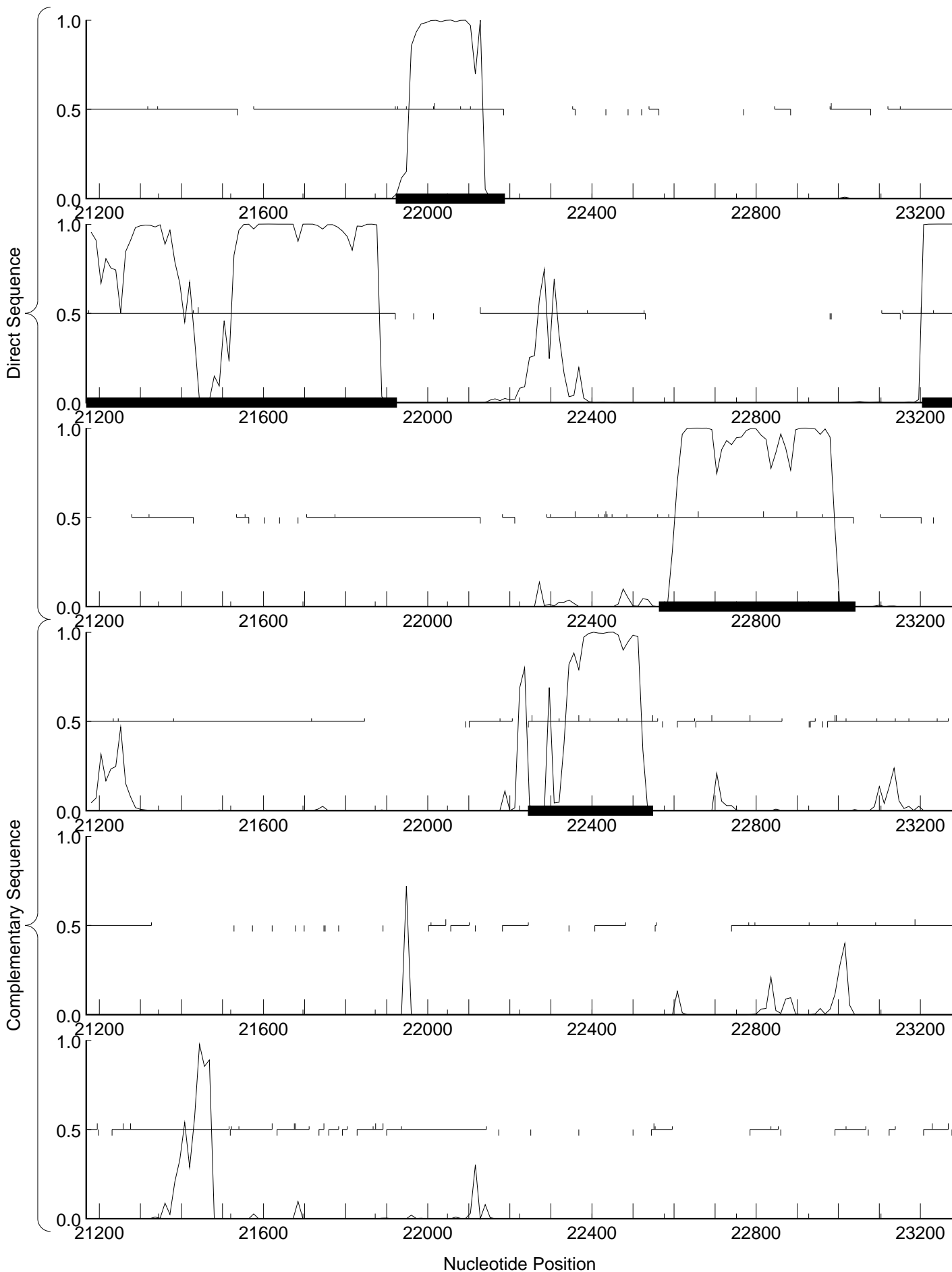
GeneMark, hmm prediction





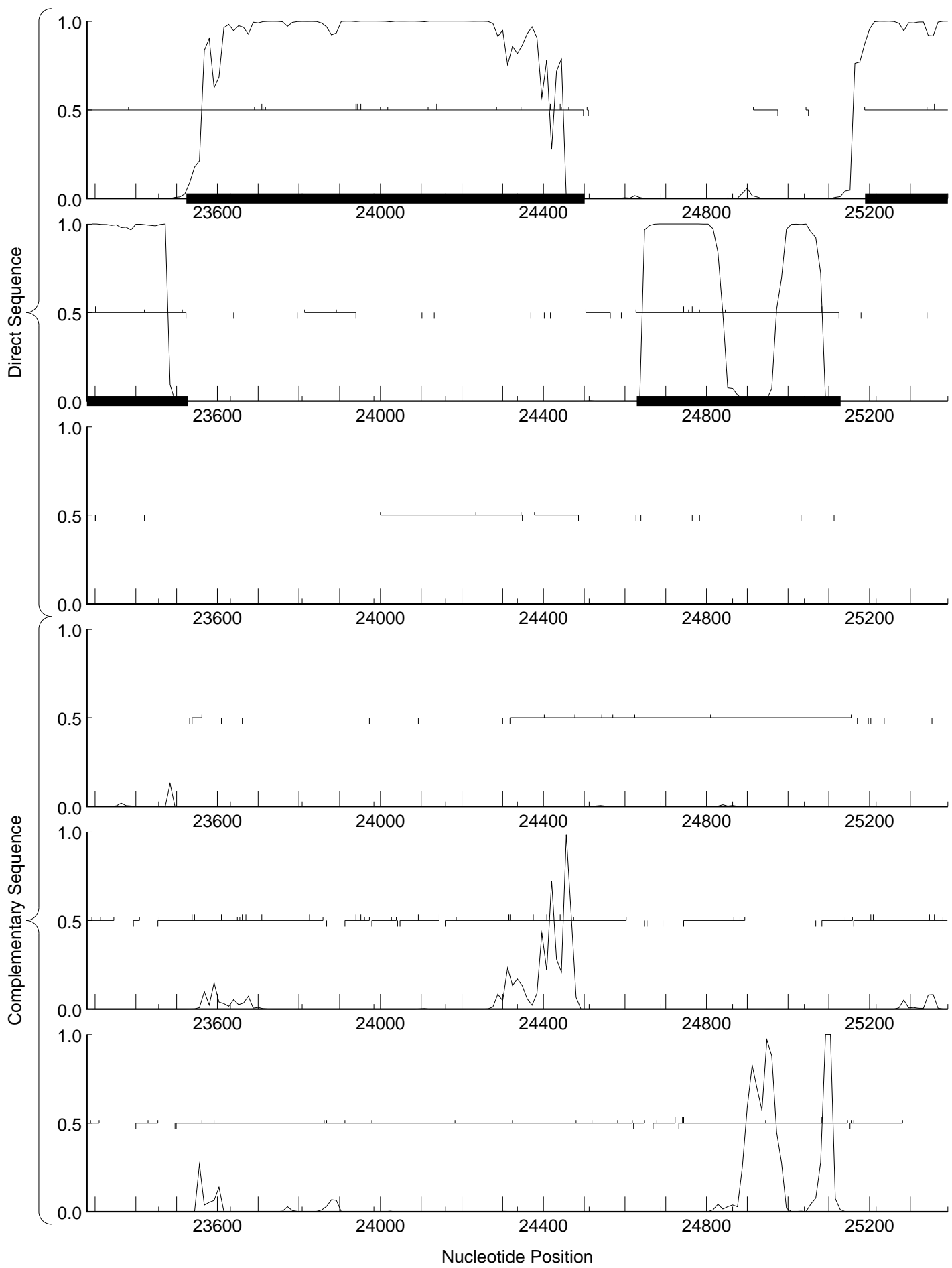
GeneMark, hmm prediction



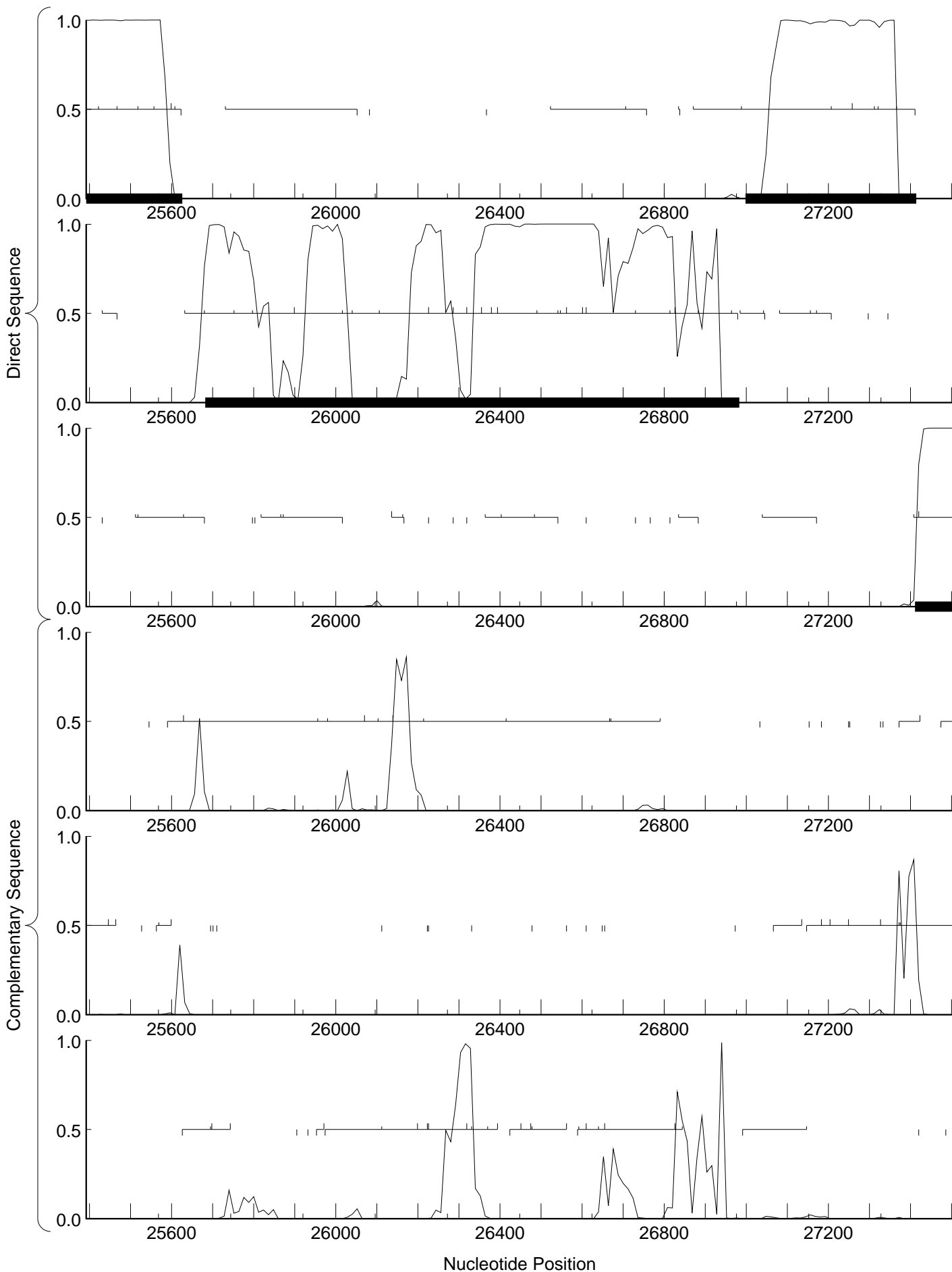


complete sequence, 49557 bp including 11-base 3' overhang (CGGGCAGTGAT), Cluster BD1, Order 2, Window 96, Step 12, 13/25

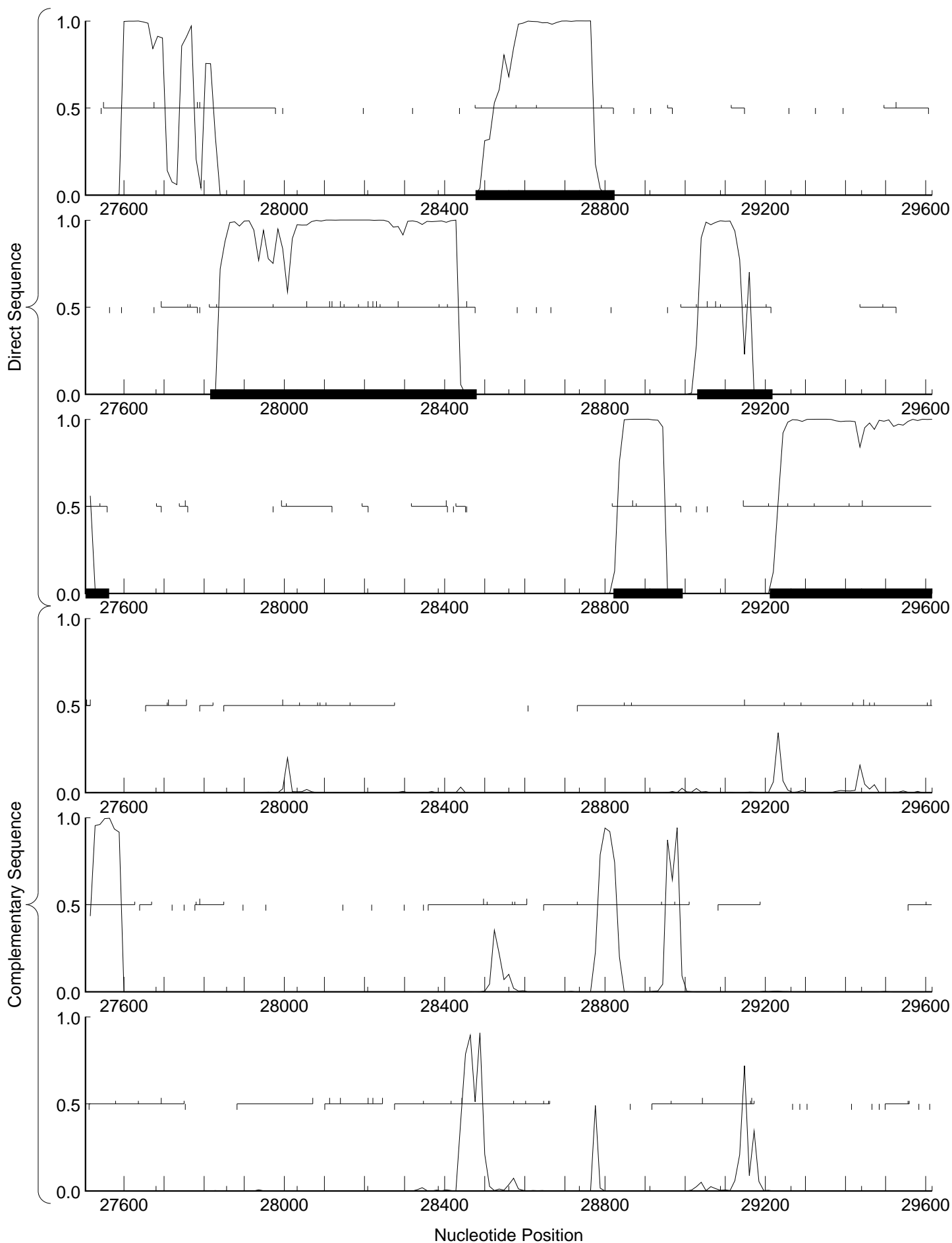
GeneMark, hmm prediction



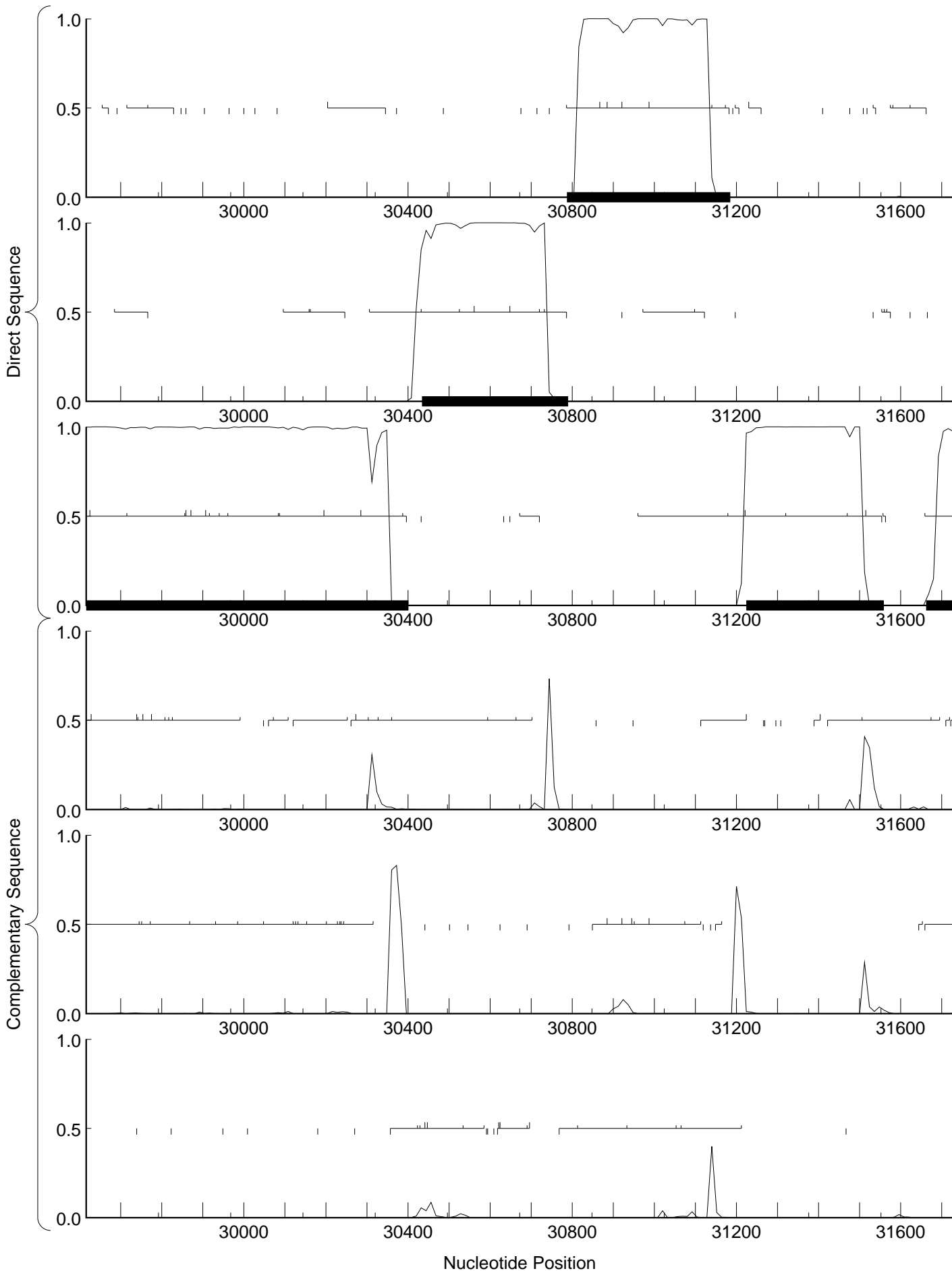
GeneMark, hmm prediction



GeneMark, hmm prediction

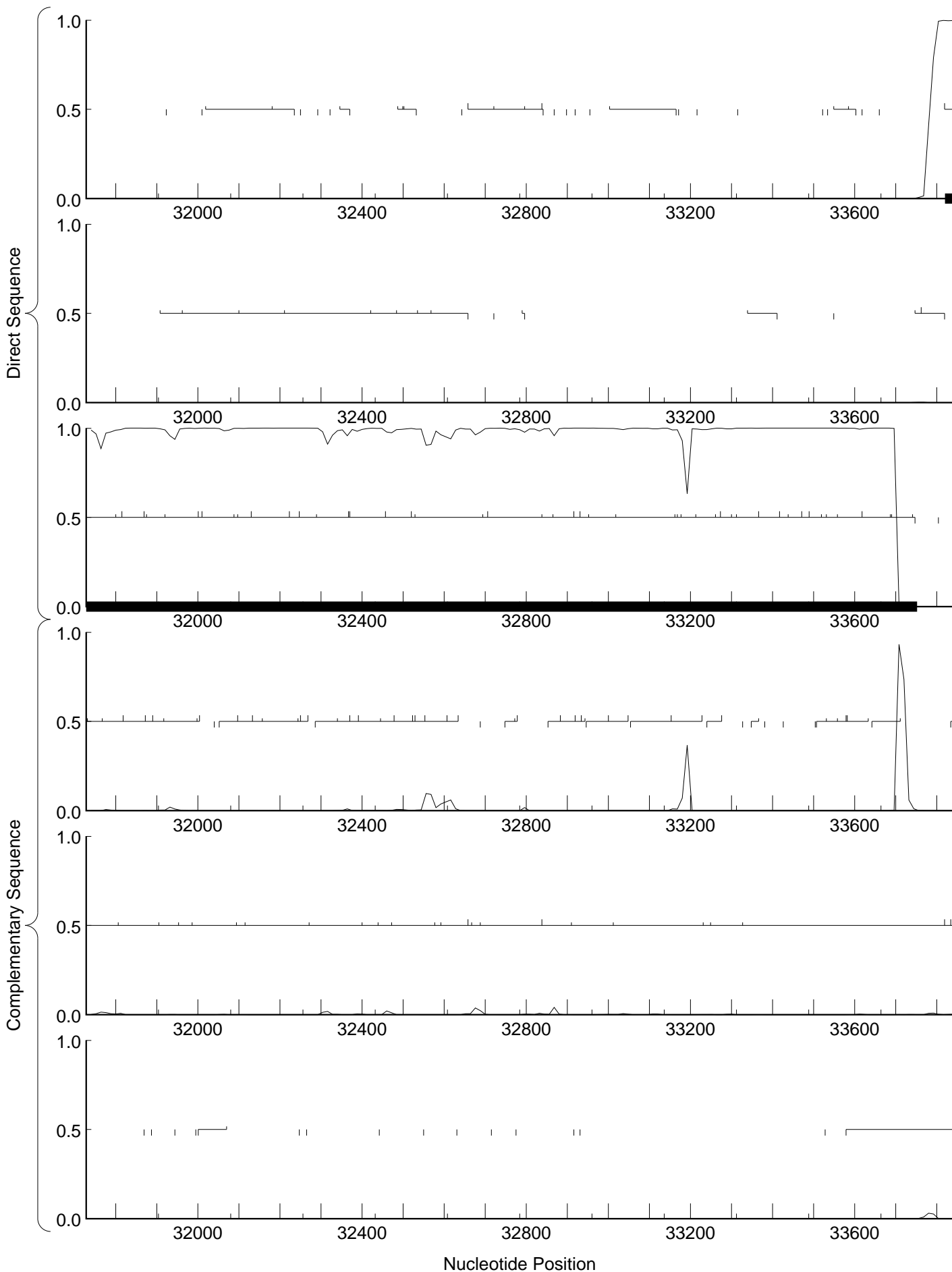


GeneMark, hmm prediction

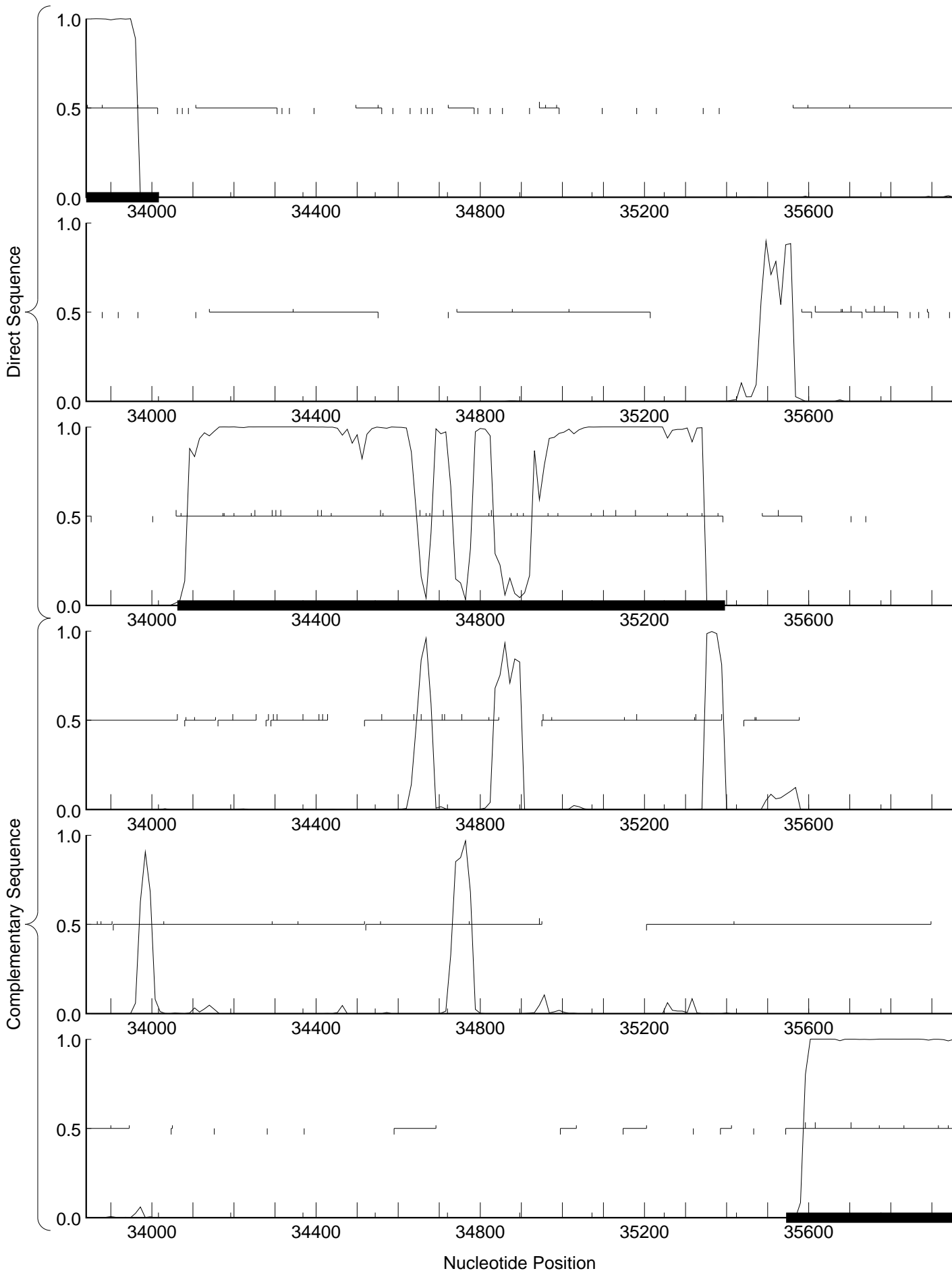




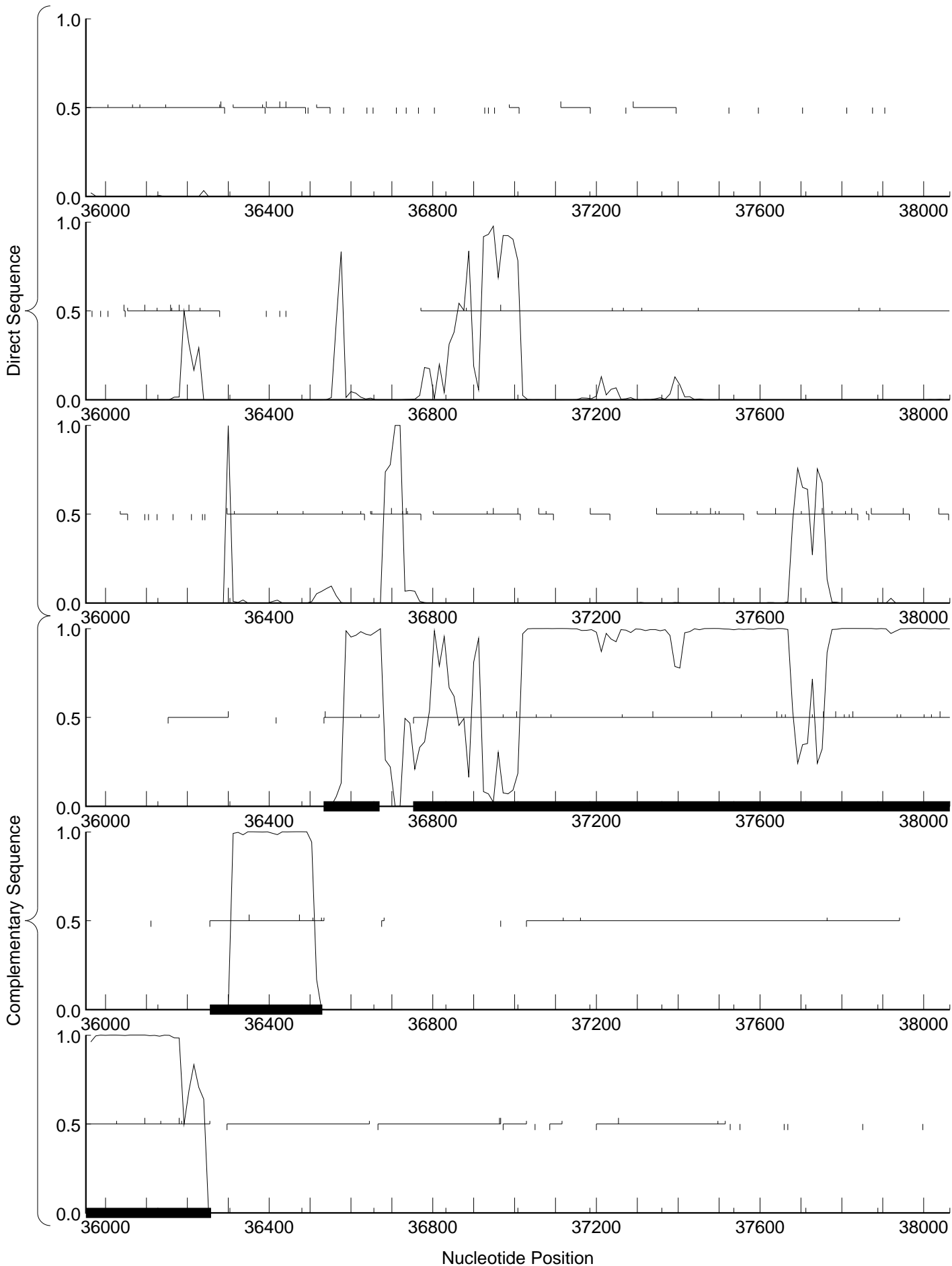
GeneMark, hmm prediction



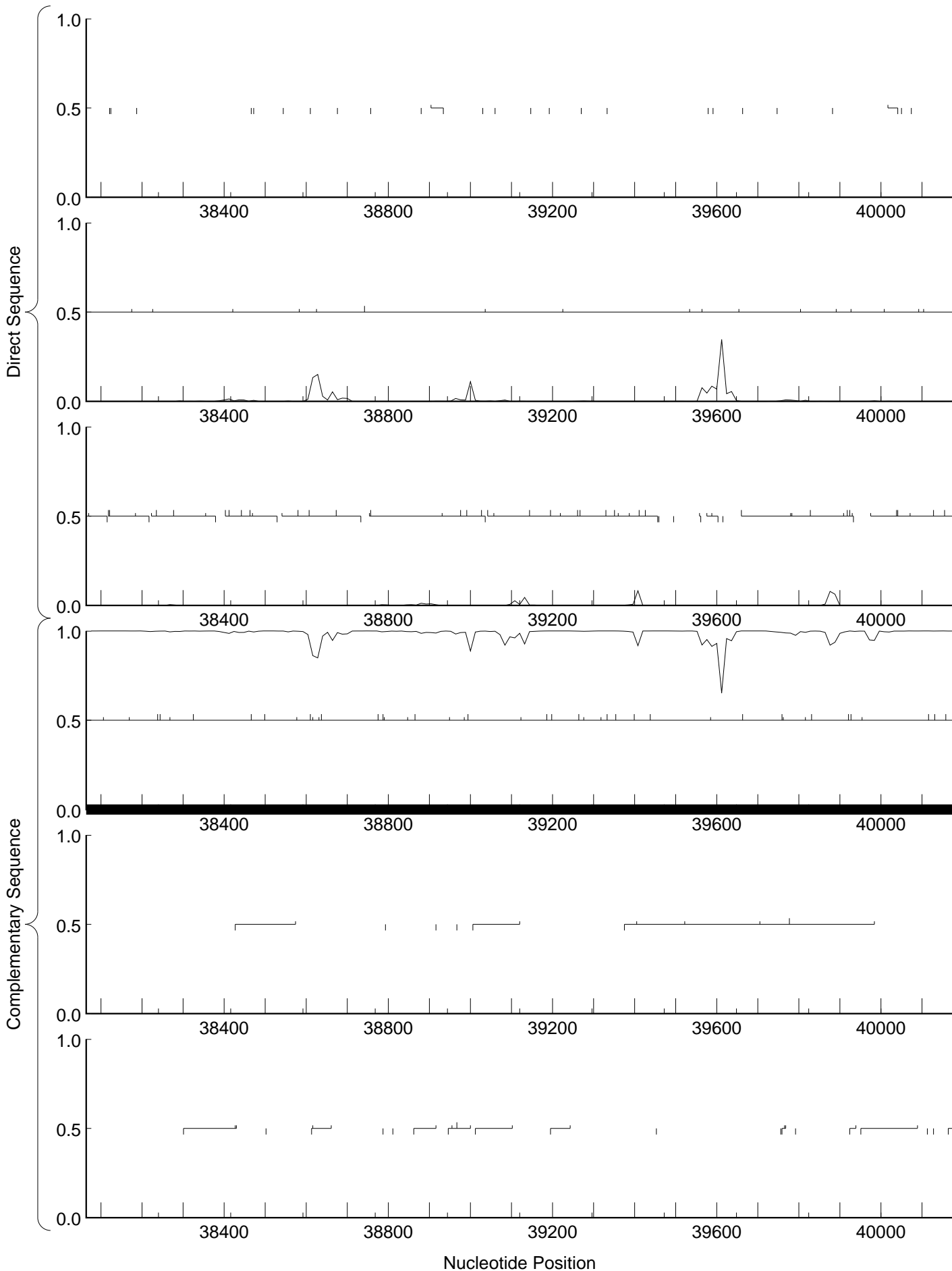
GeneMark, hmm prediction



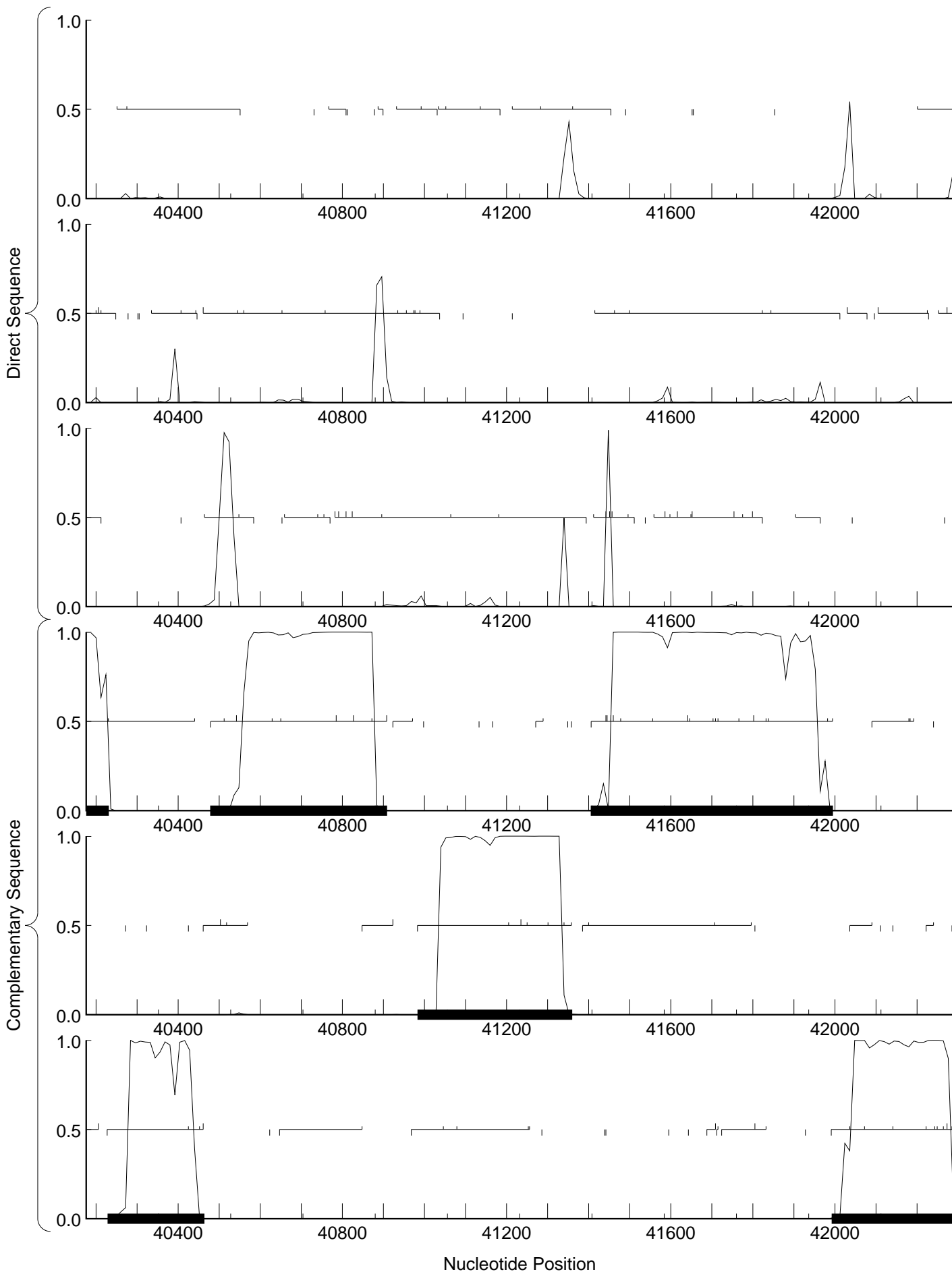
GeneMark, hmm prediction



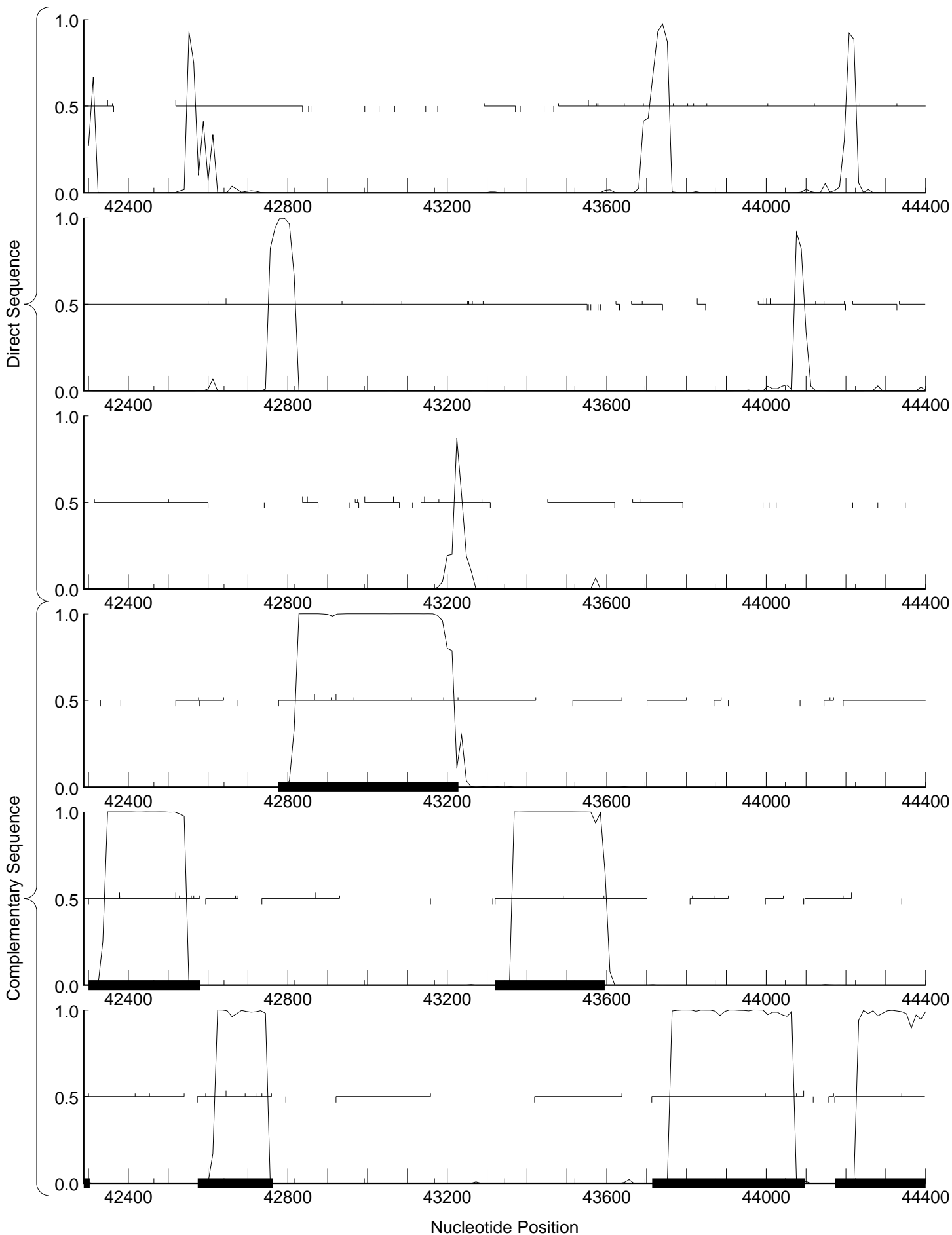
GeneMark, hmm prediction



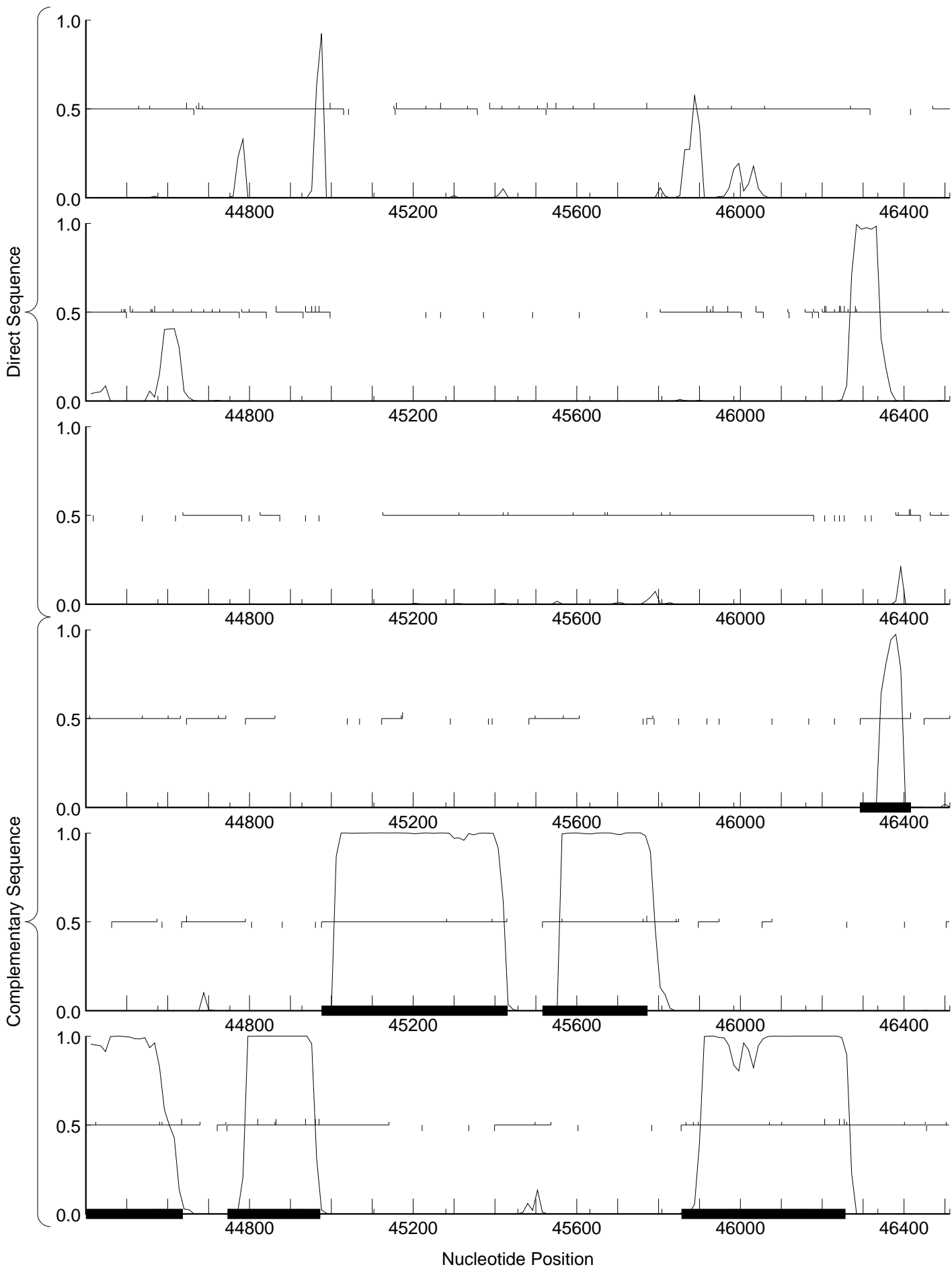
GeneMark, hmm prediction



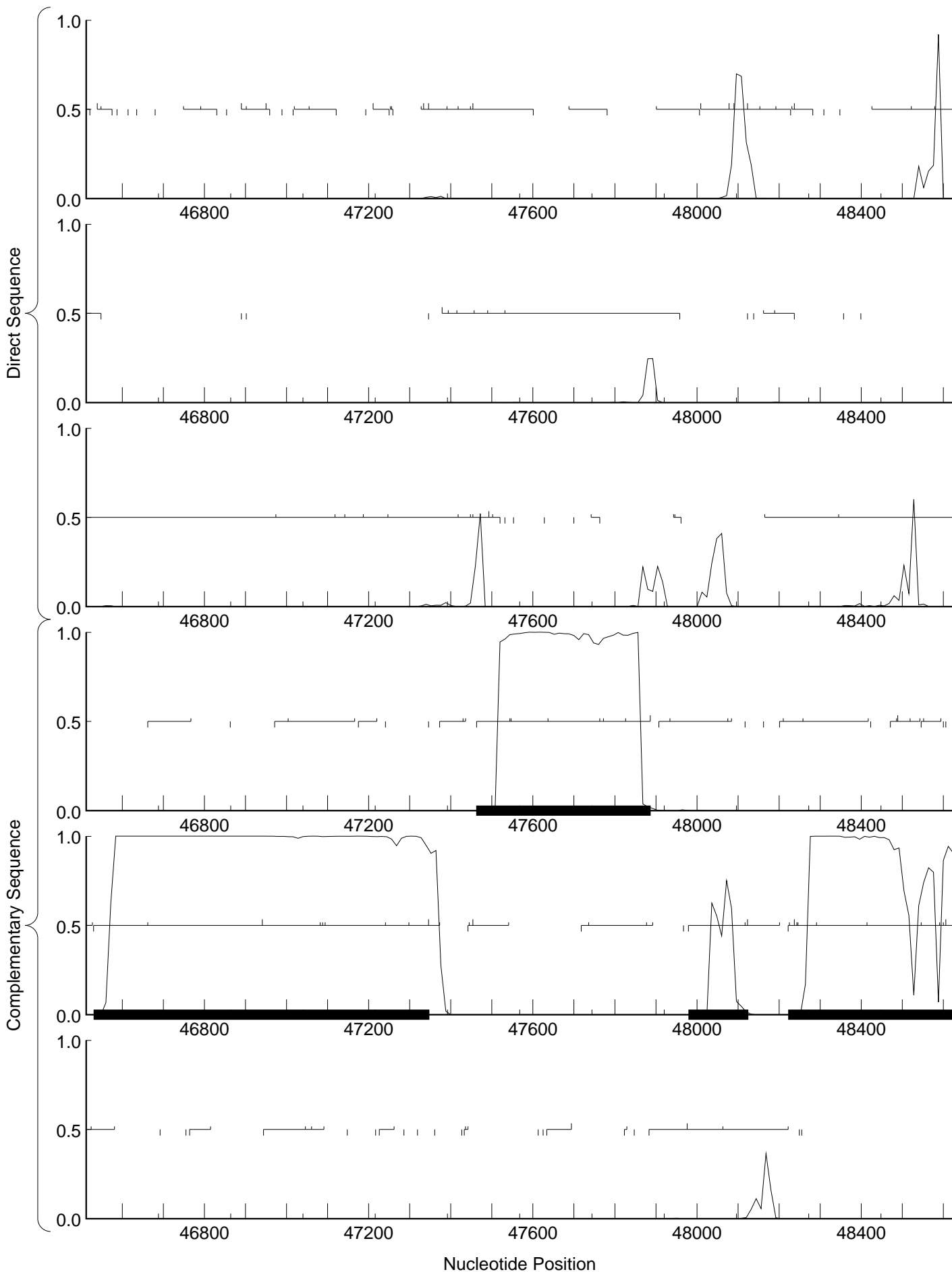
GeneMark, hmm prediction



GeneMark.hmm prediction



GeneMark, hmm prediction





GeneMark, hmm prediction

