

# GeneMark

Version 2.5p (09.08.06)

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## PROGRAM INFORMATION

Sequence : Mycobacterium phage Kasen3 complete sequence, 41890 bp including 11-base 3' overhang (CCCCA  
Analysis Date : 6/22/18 at 13:16:05  
Pages : 21  
Sequence Length : 41890 bp  
GC Content : 66.58%

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,

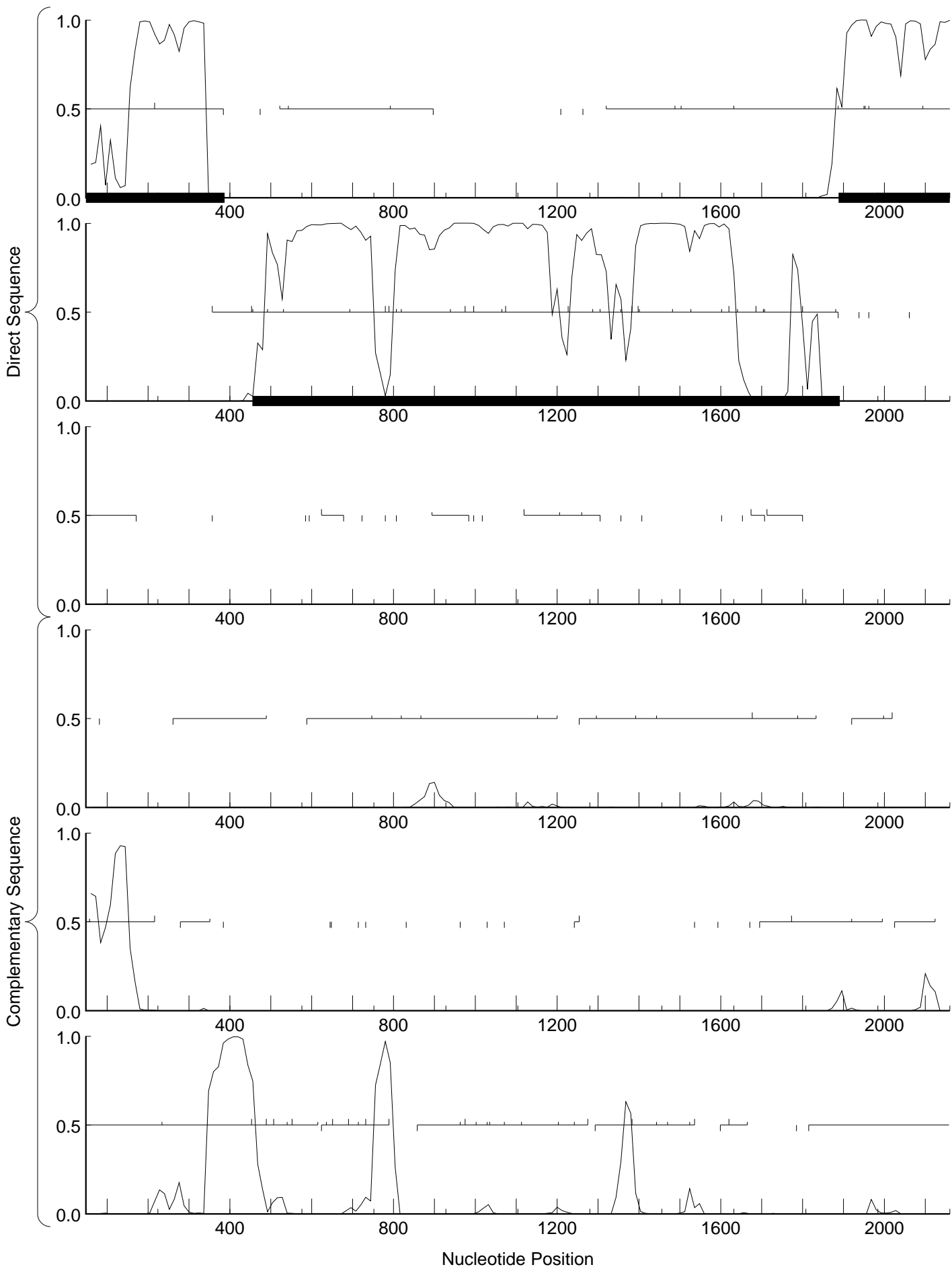
## Matrix notes & comments

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

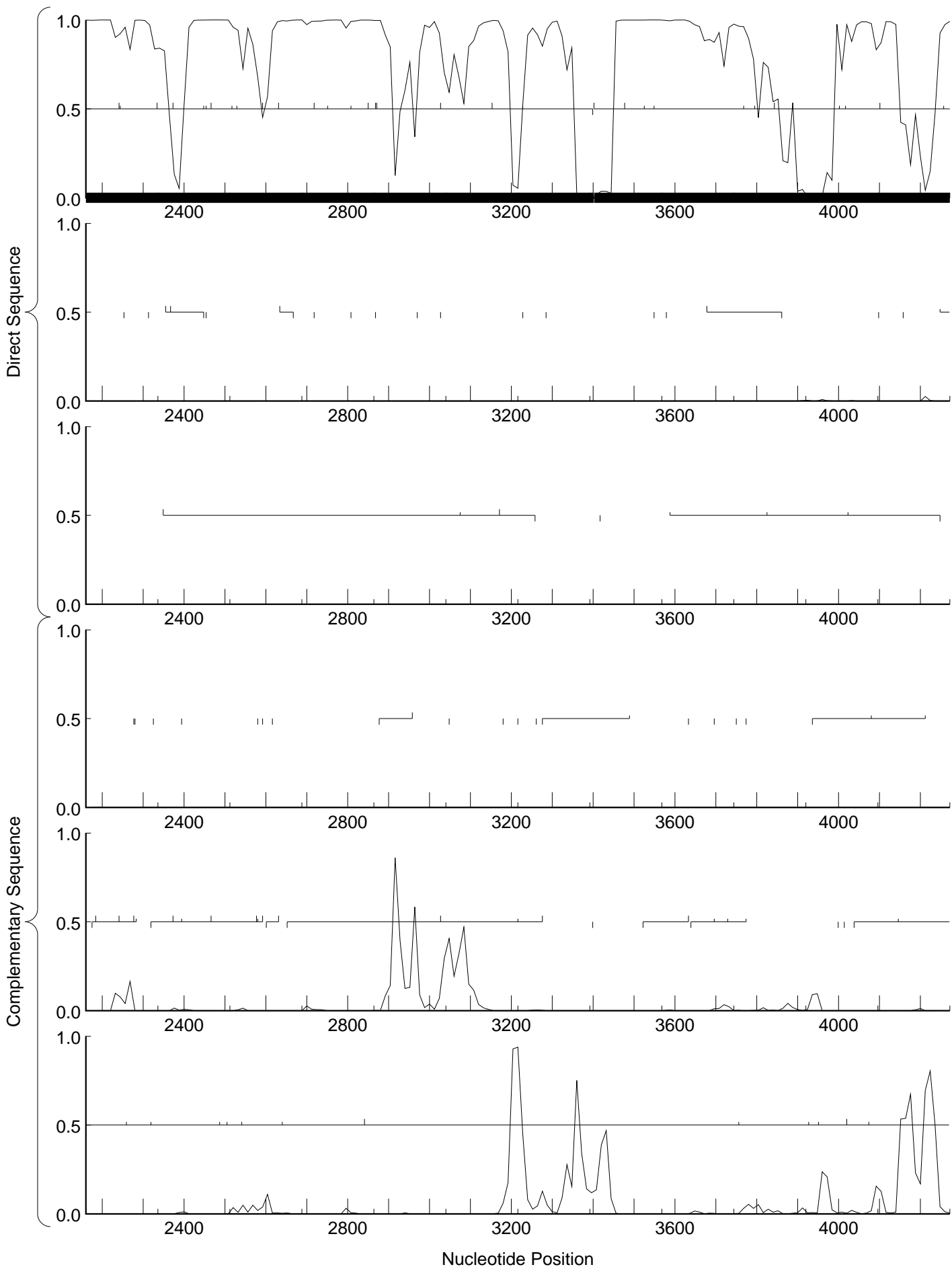
## MATRIX INFORMATION

Matrix : Heuristic, GC = 67  
Author : Borodovsky Laboratory - Georgia Tech  
Order : 2

Send questions / comments to:  
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Atlanta, GA 30332-0230

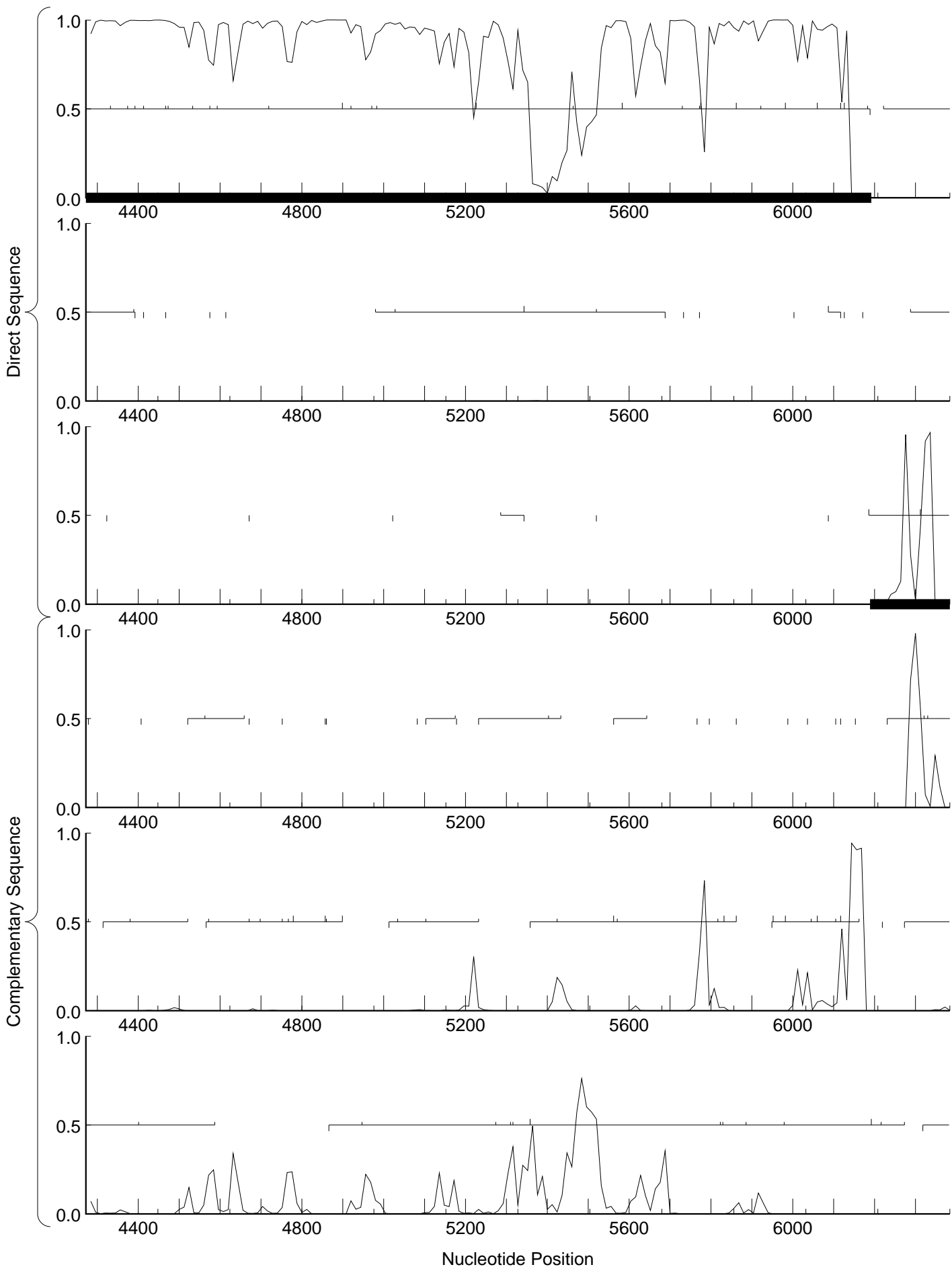


complete sequence, 41890 bp including 11-base 3' overhang (CCCCATGGCAT), Cluster G1, Order 2, Window 96, Step 12, 3/21

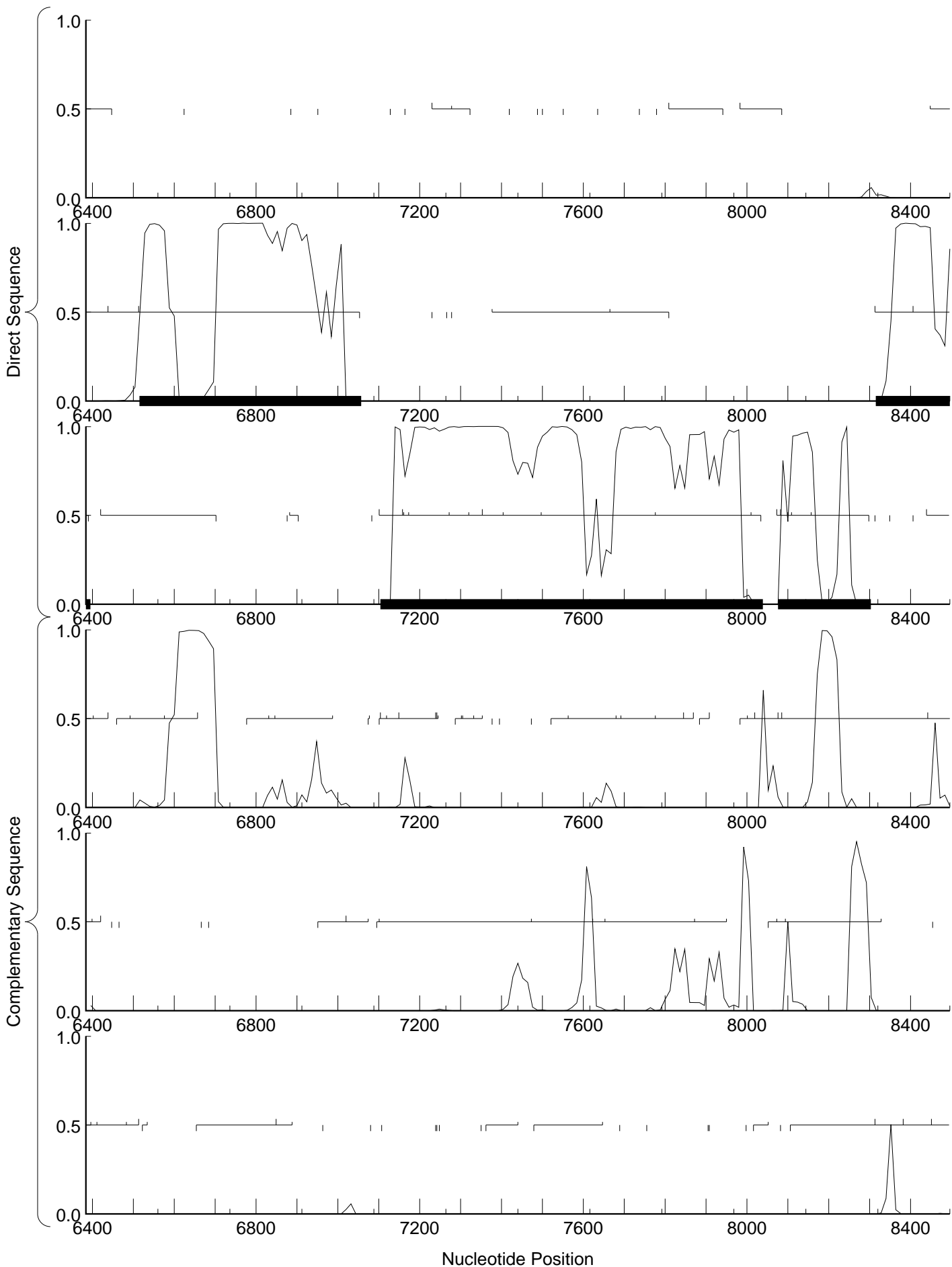


██████████

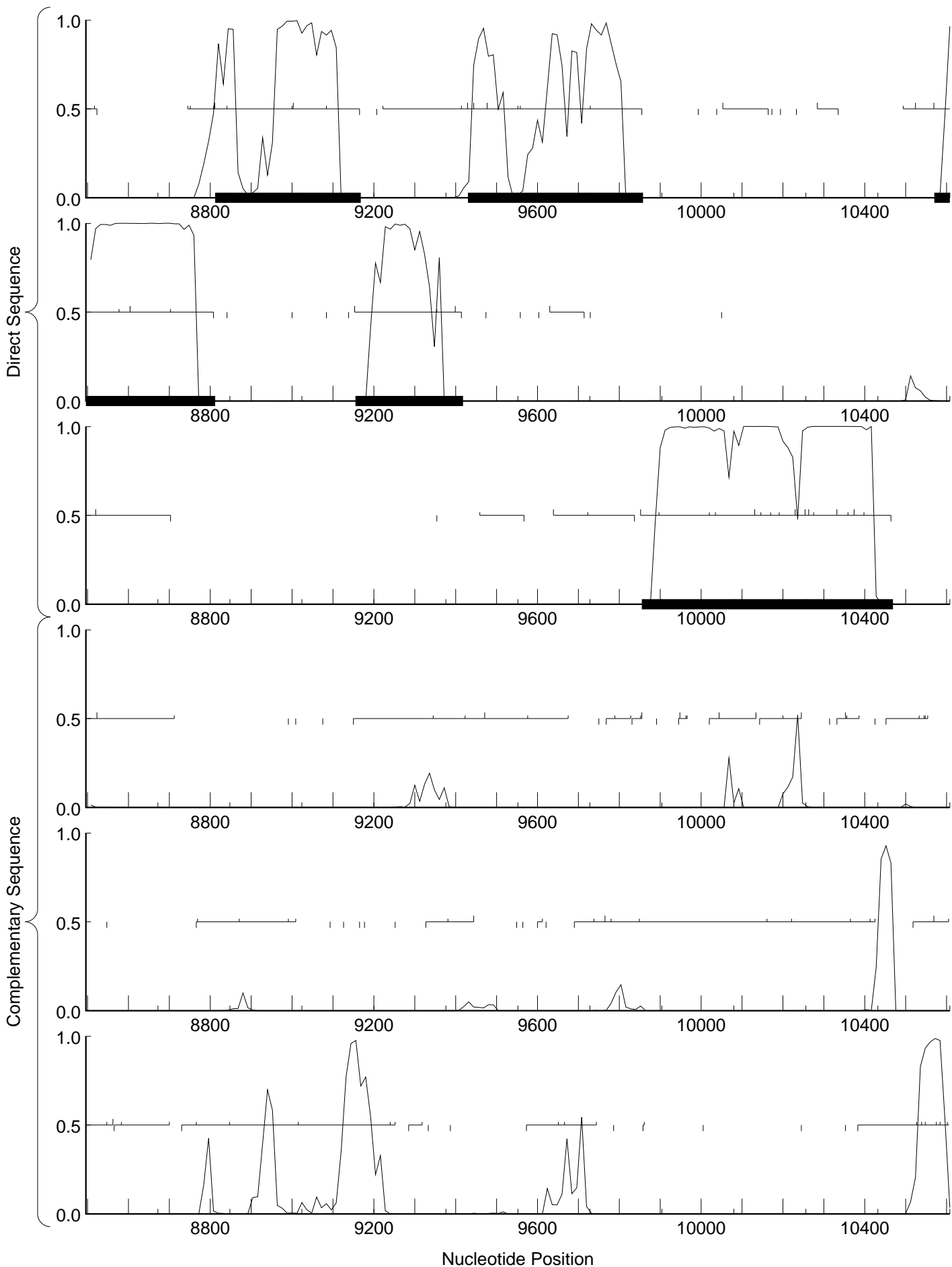
GeneMark.hmm prediction



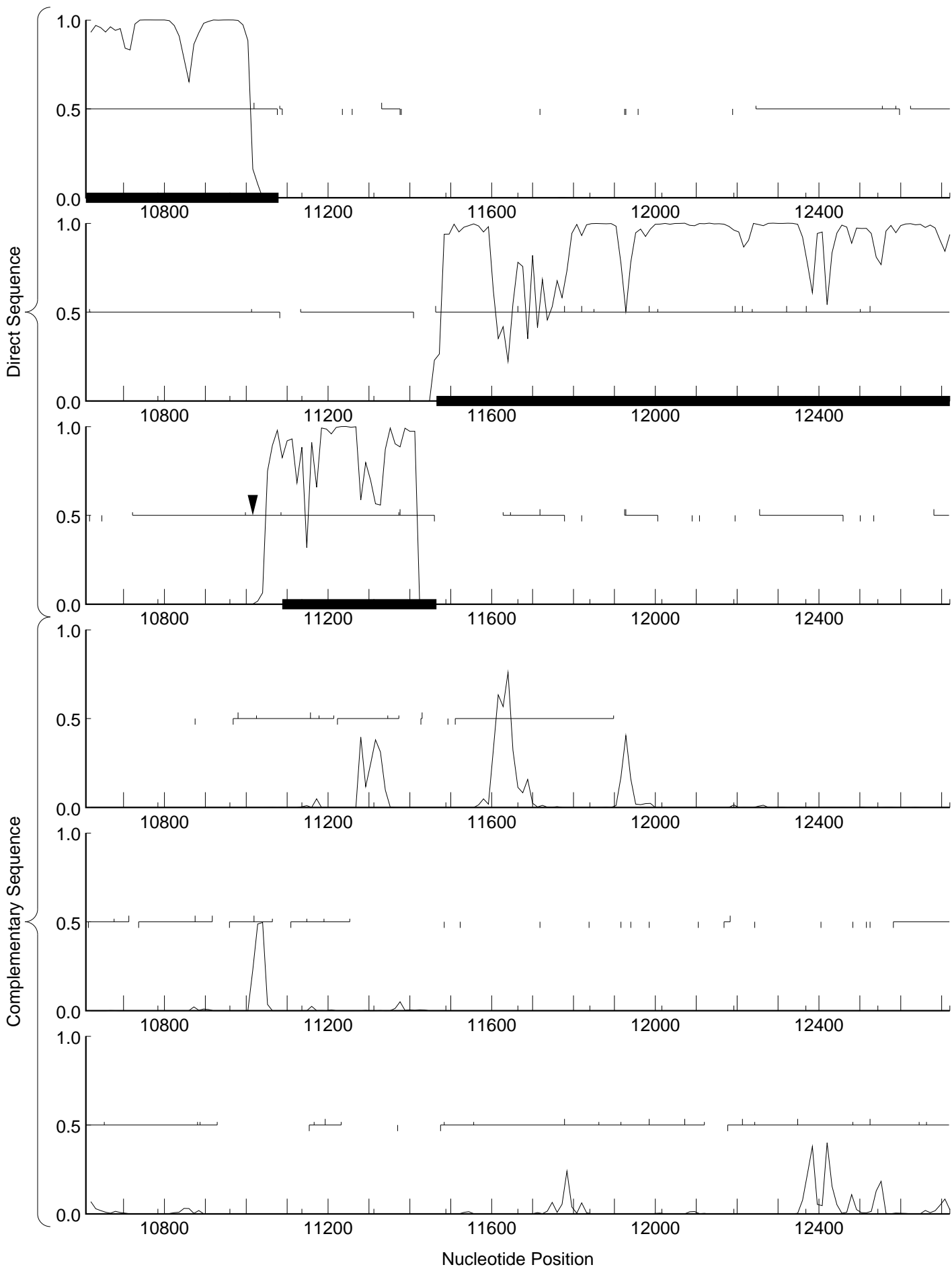
GeneMark.hmm prediction

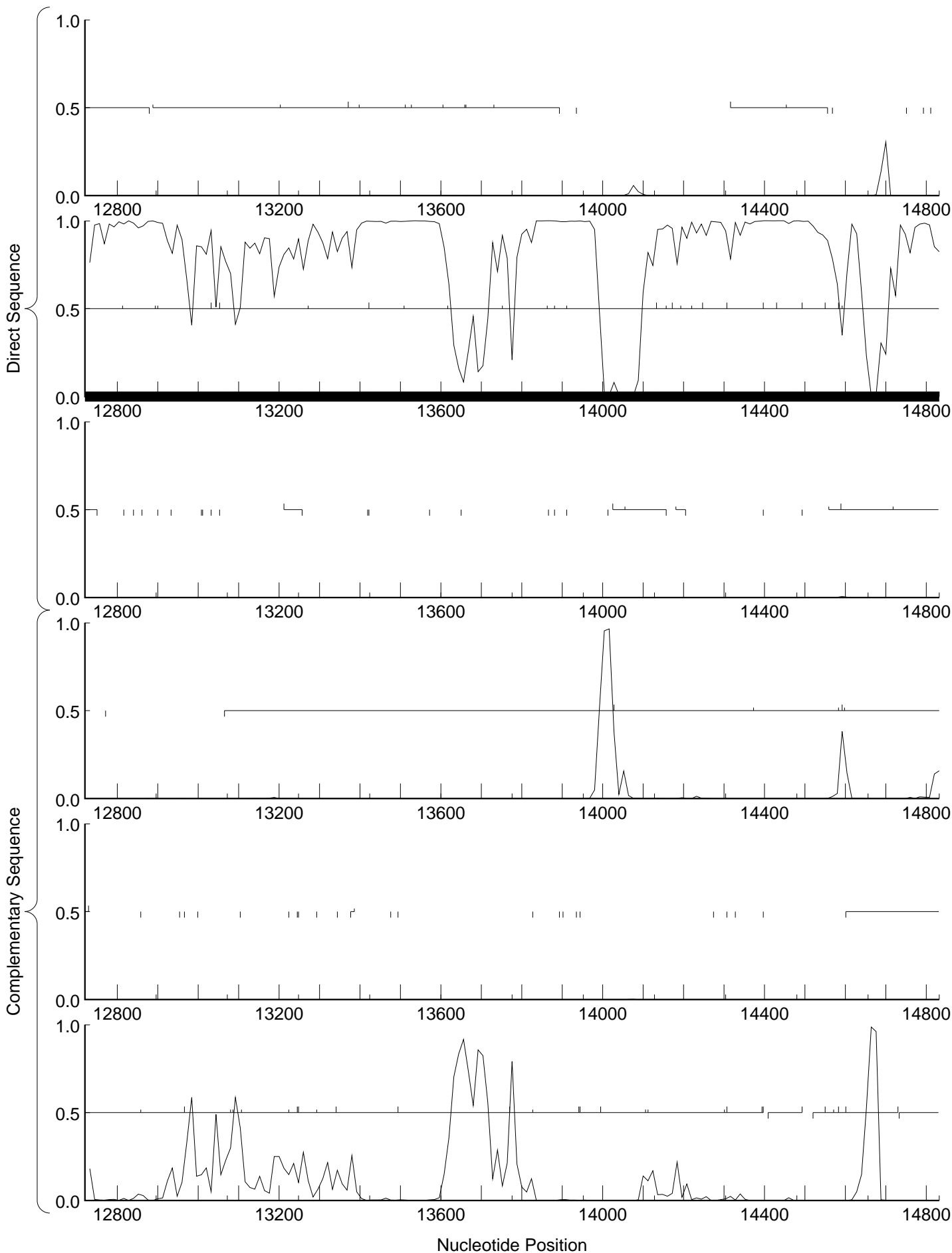


complete sequence, 41890 bp including 11-base 3' overhang (CCCCATGGCAT), Cluster G1, Order 2, Window 96, Step 12, 6/21



GeneMark.hmm prediction

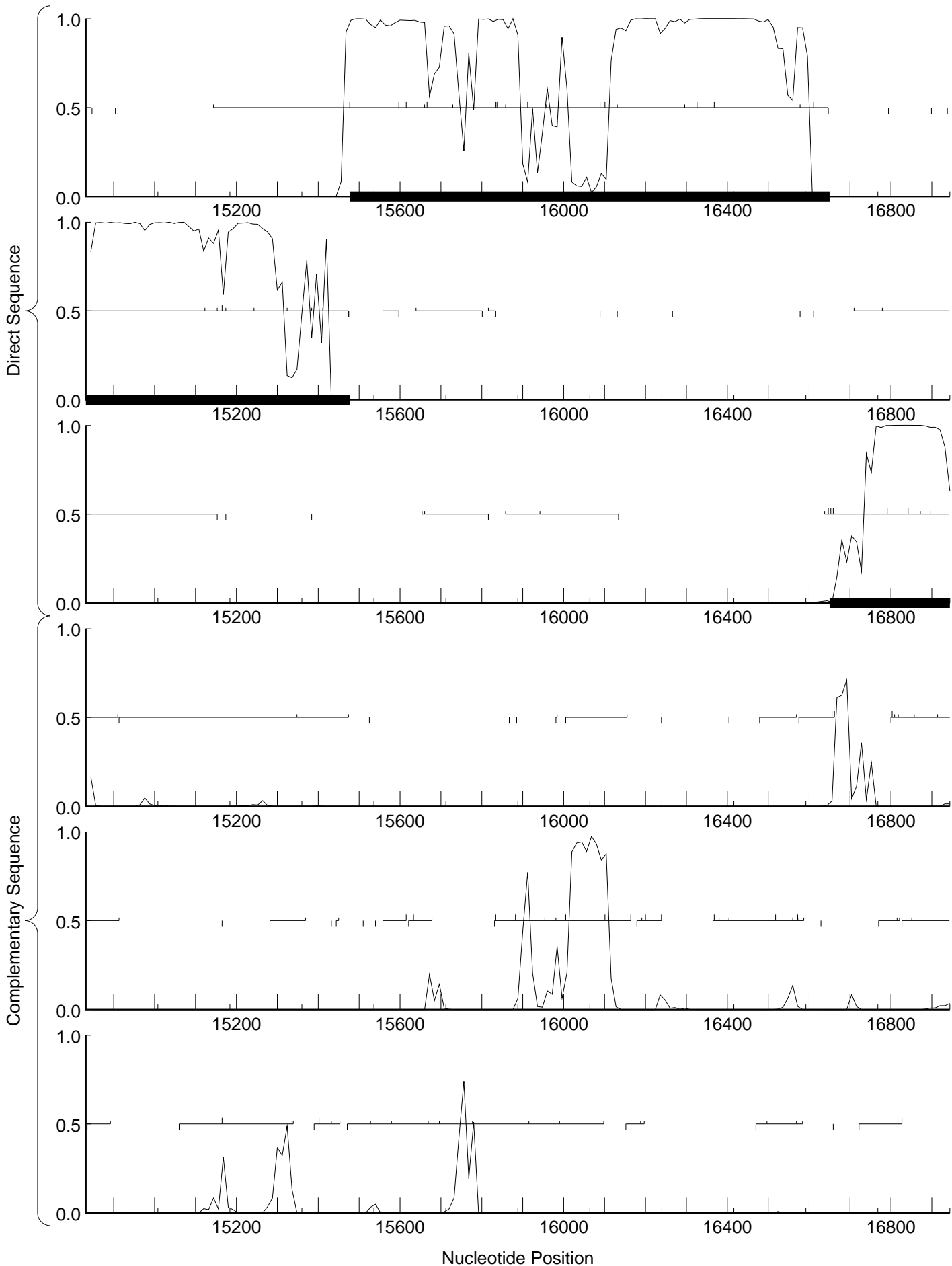




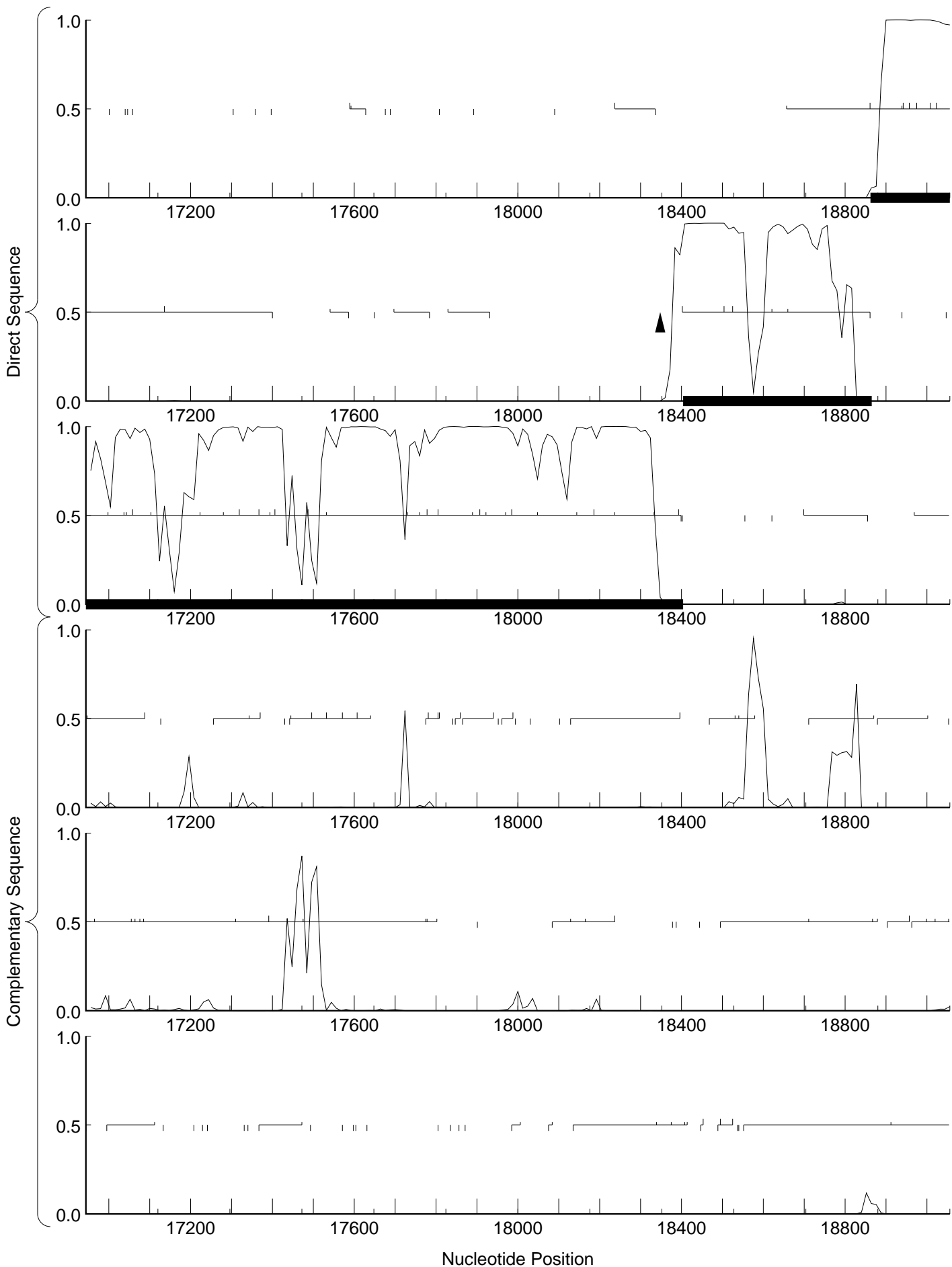


██████████

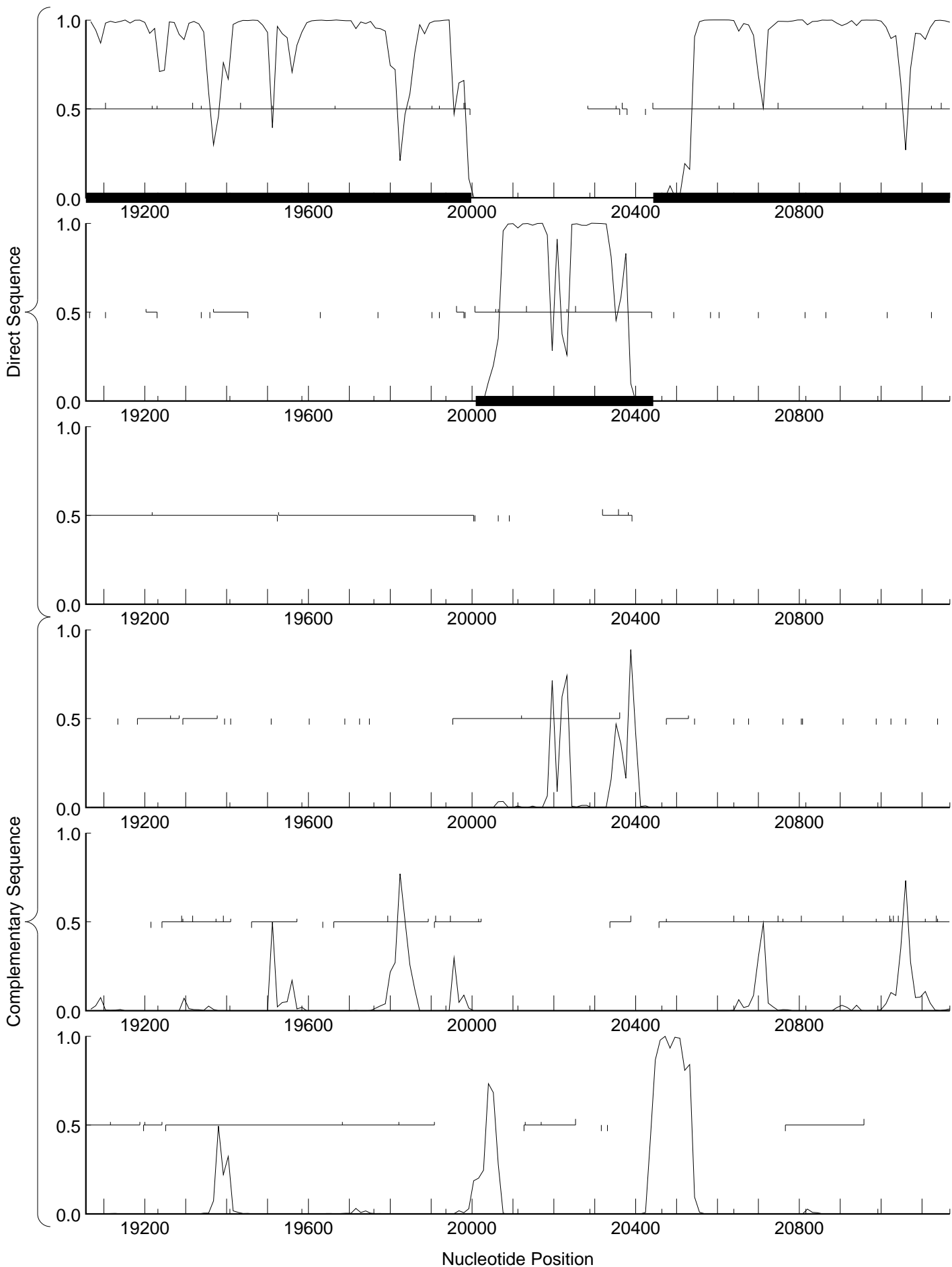
GeneMark.hmm prediction



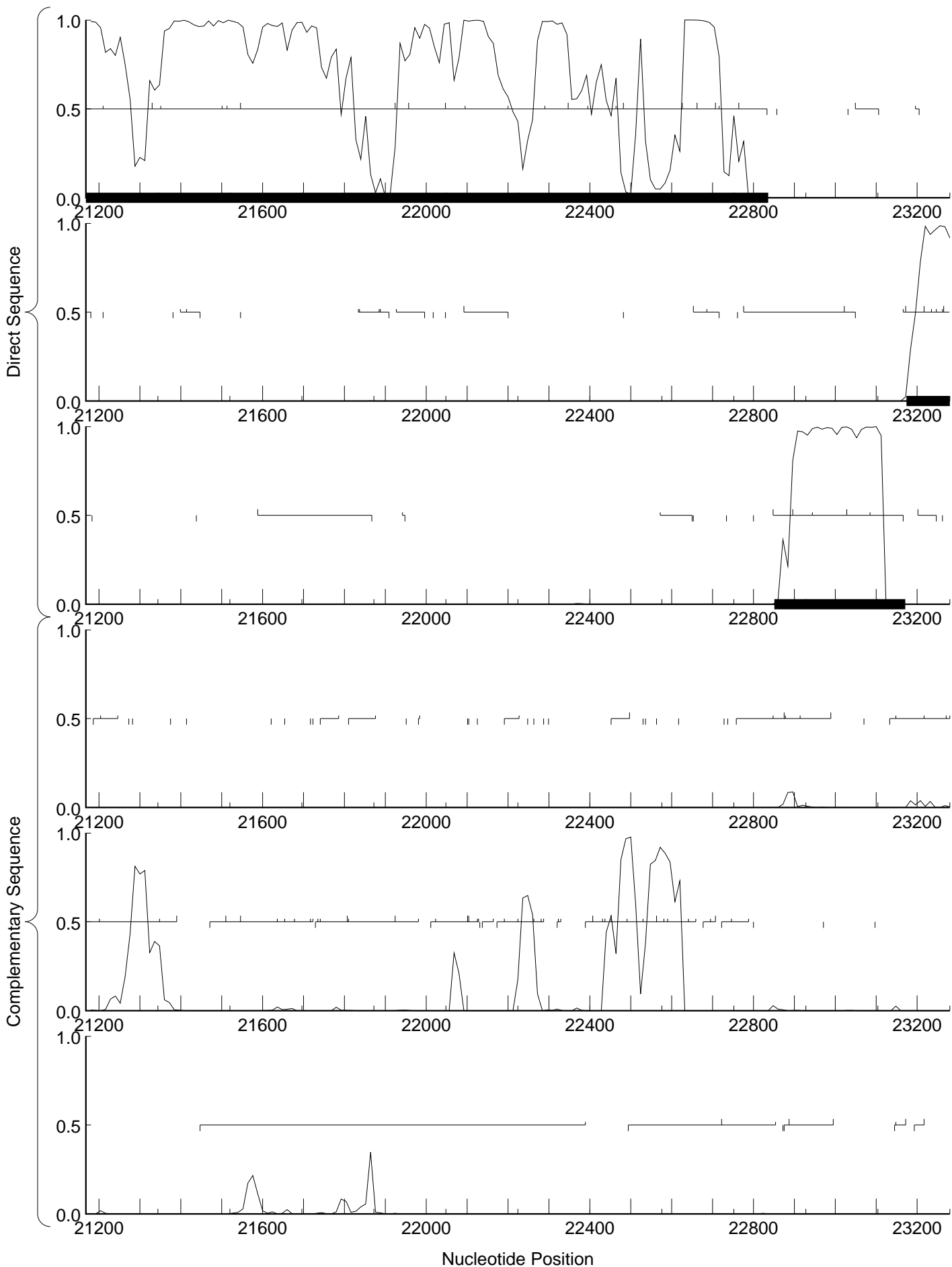
GeneMark.hmm prediction



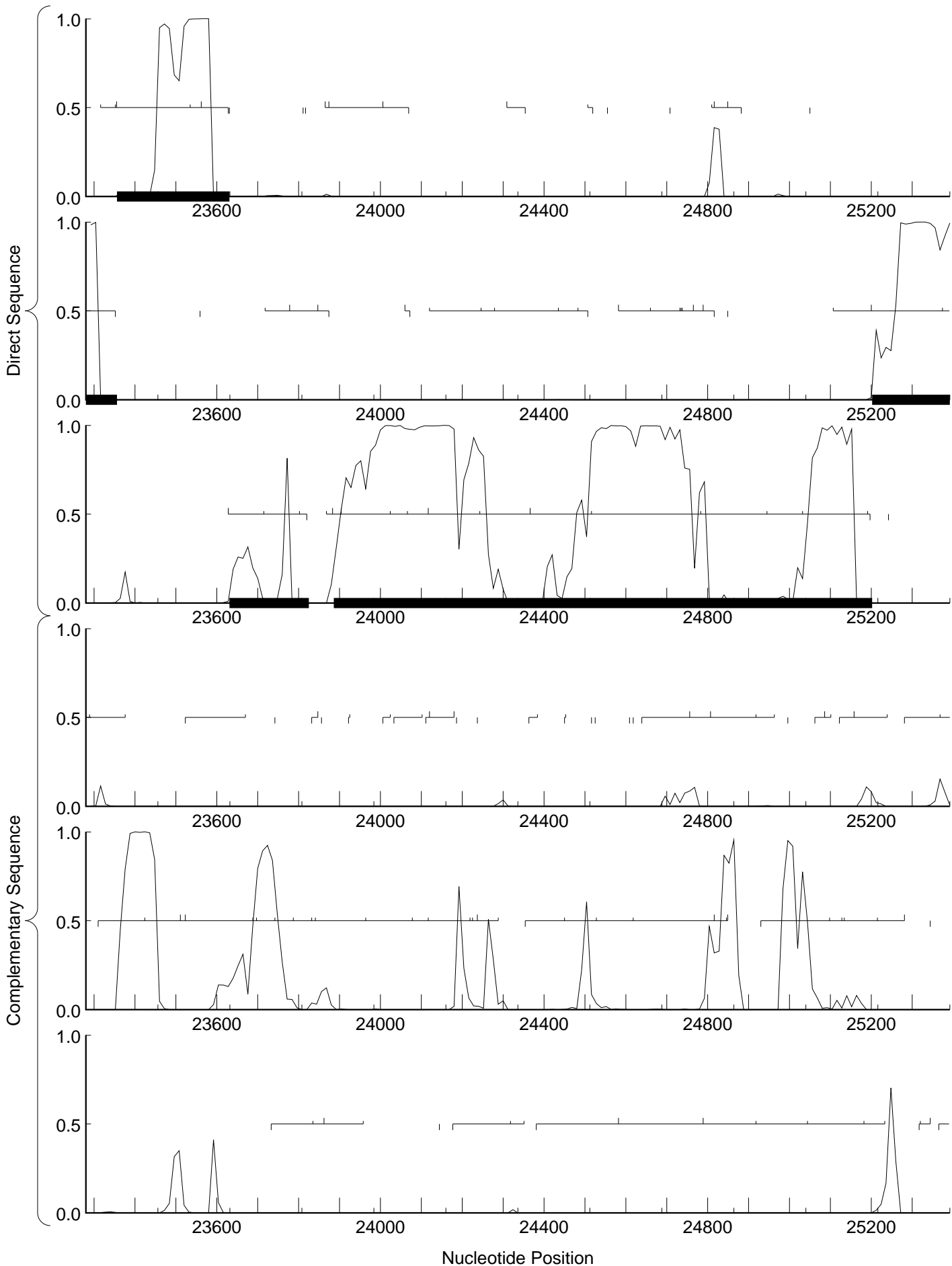
GeneMark.hmm prediction



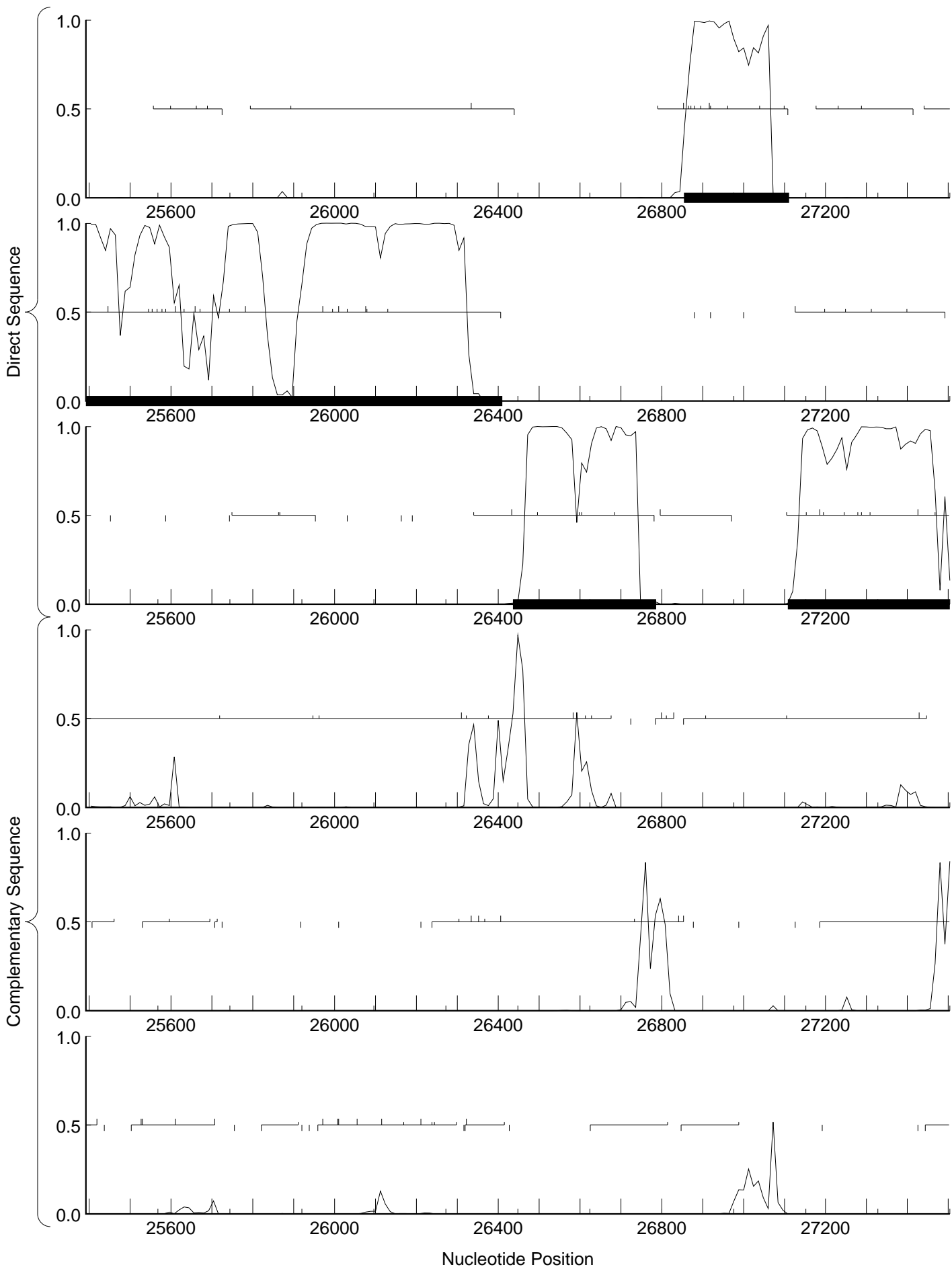
GeneMark.hmm prediction



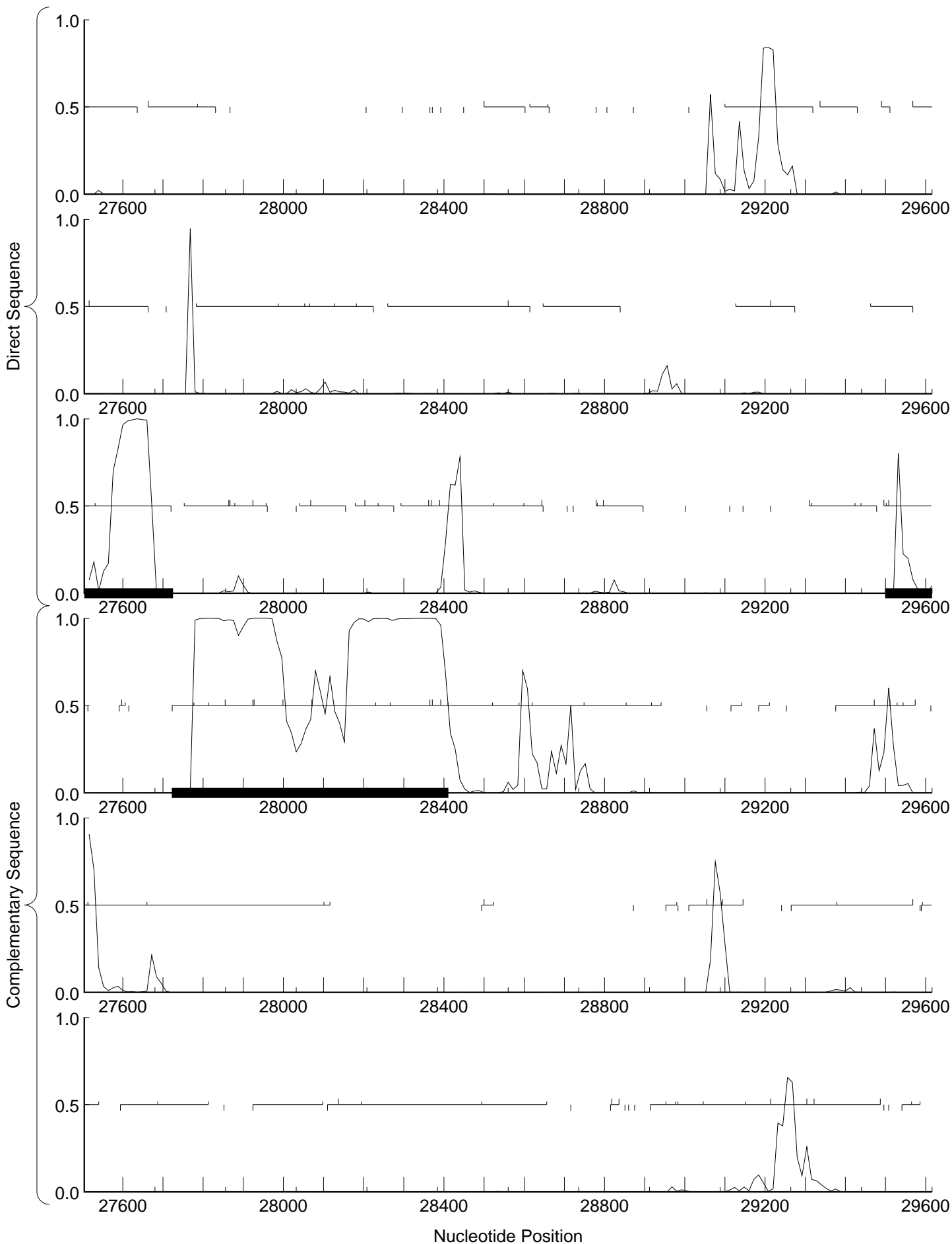
GeneMark.hmm prediction



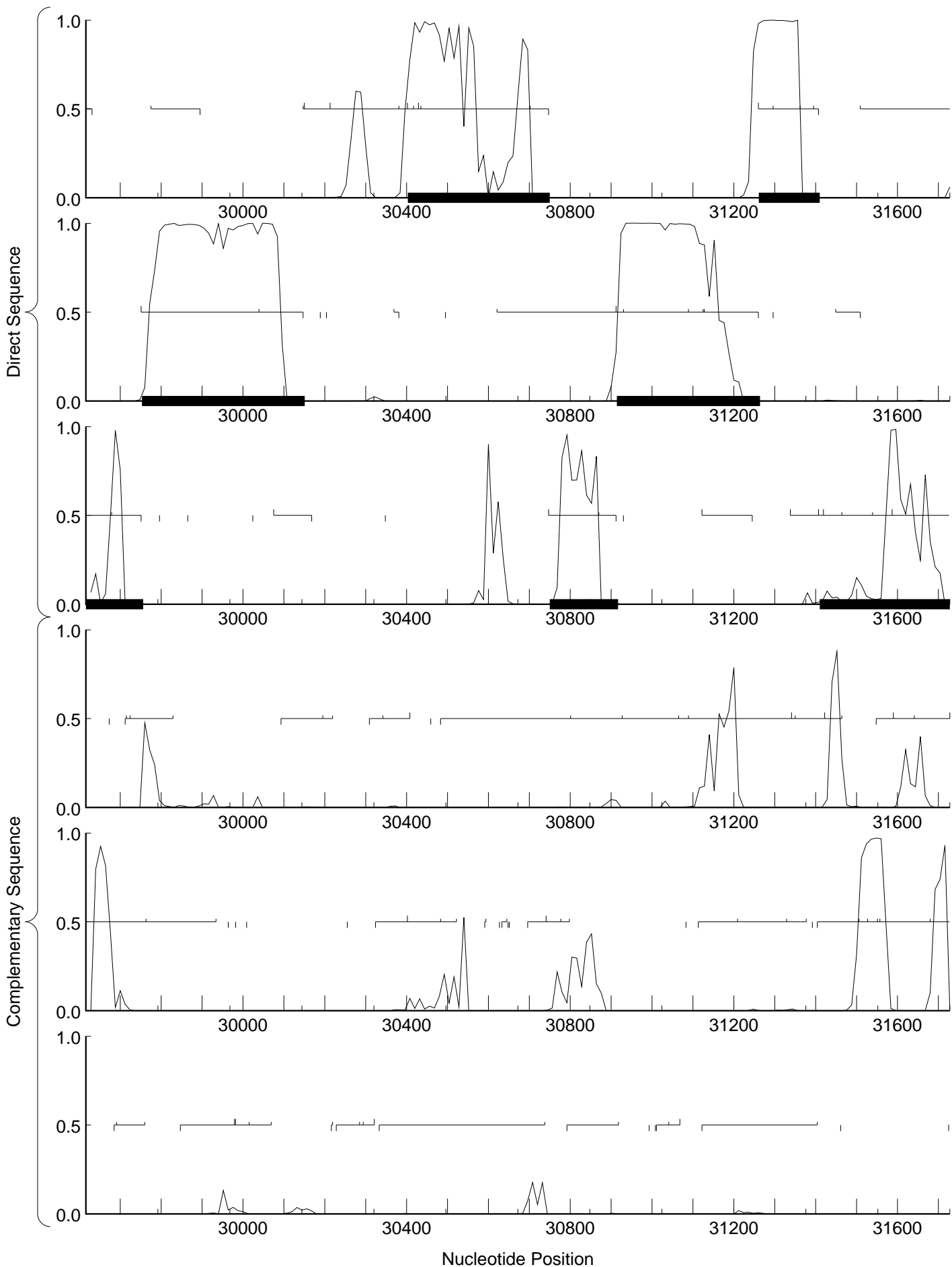
GeneMark.hmm prediction



GeneMark.hmm prediction

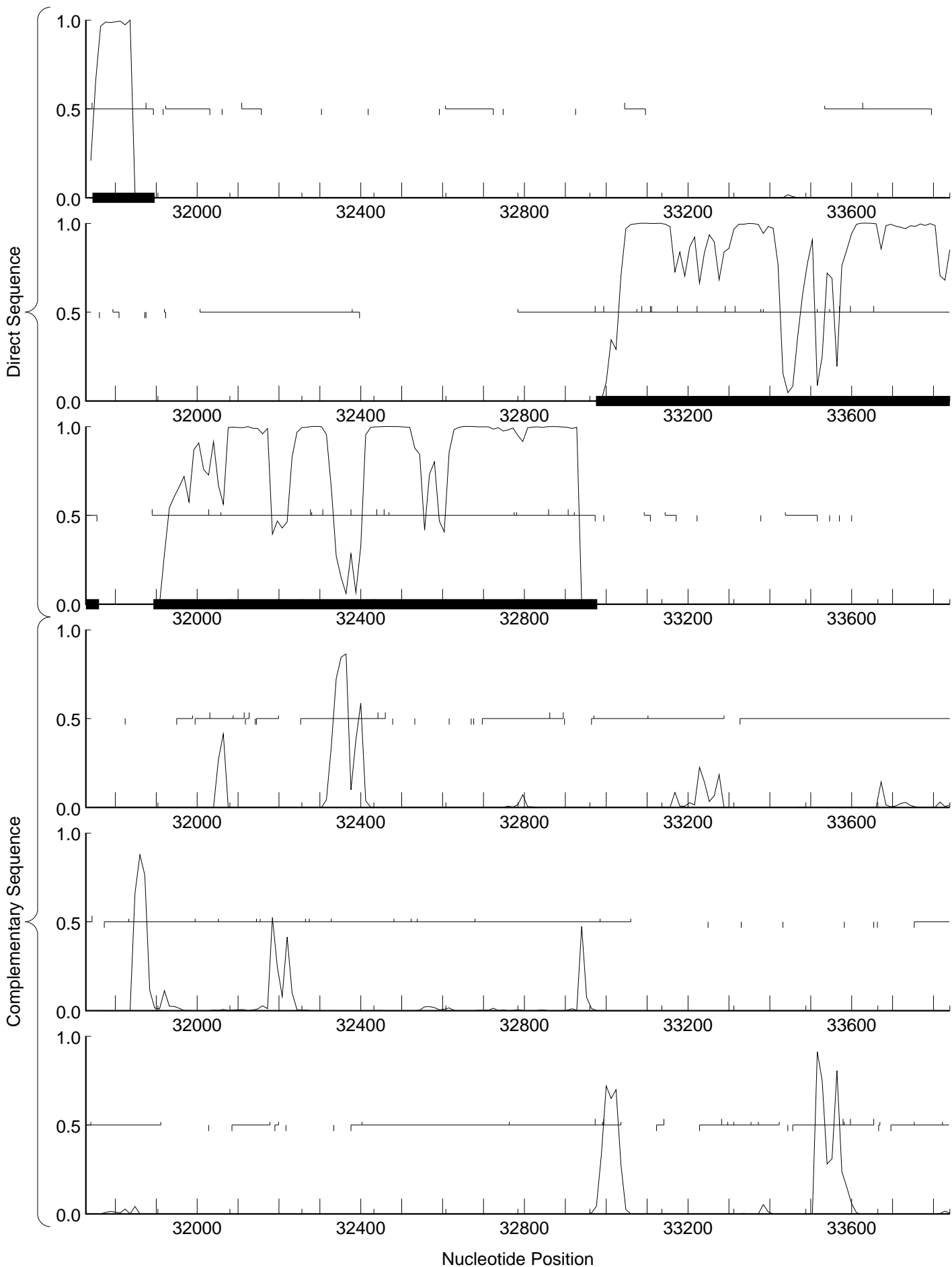


GeneMark.hmm prediction

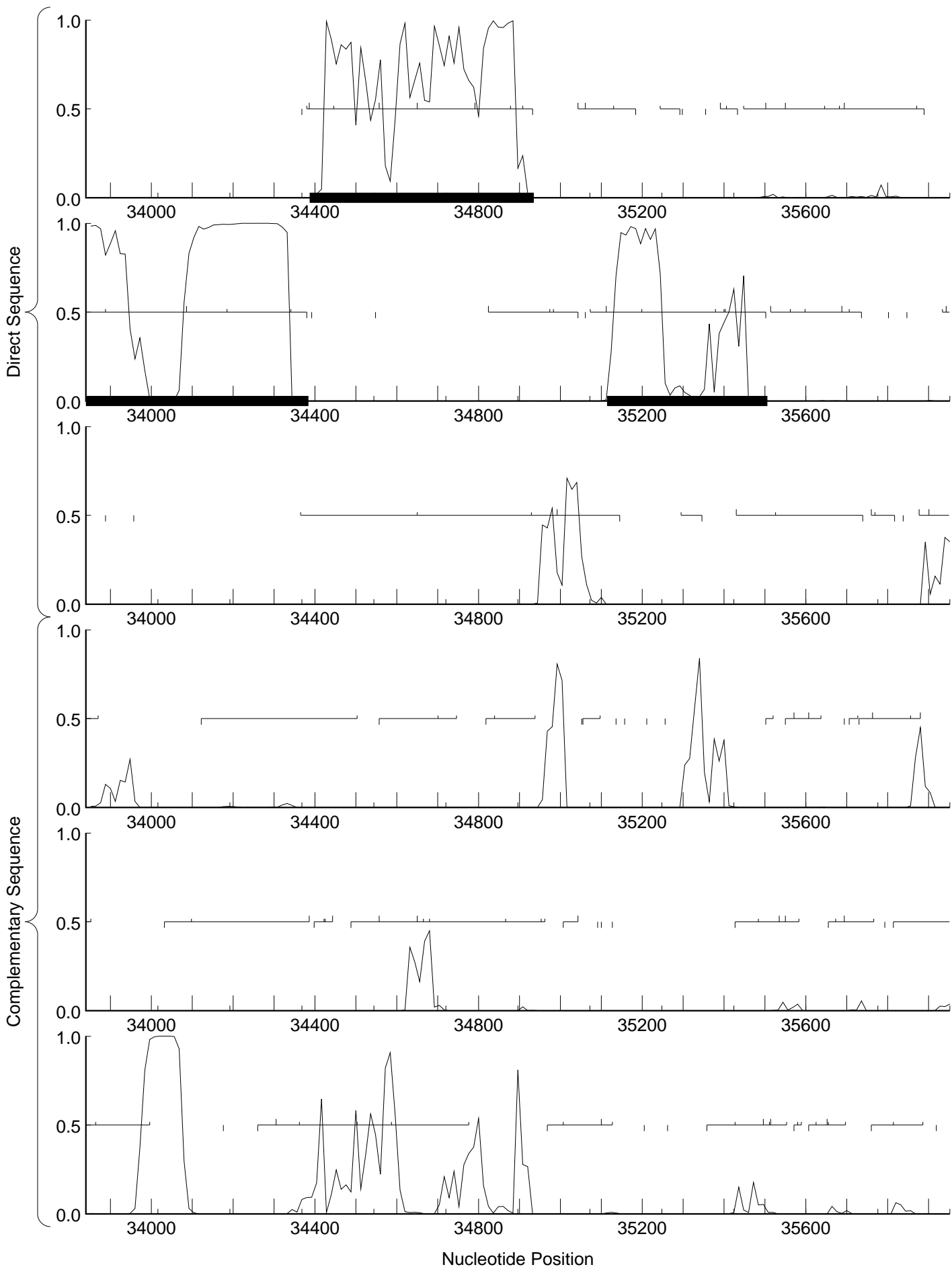


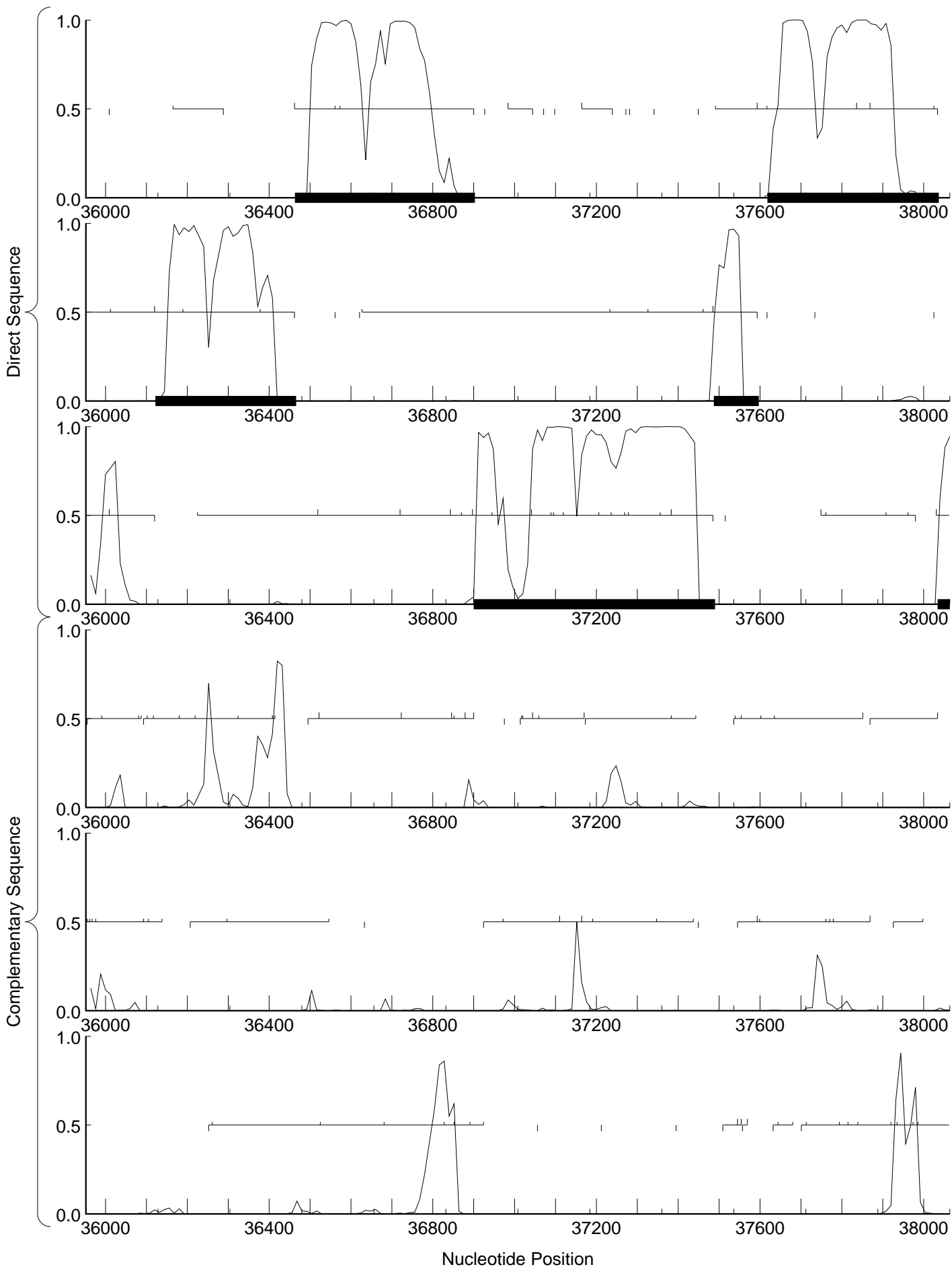


GeneMark.hmm prediction

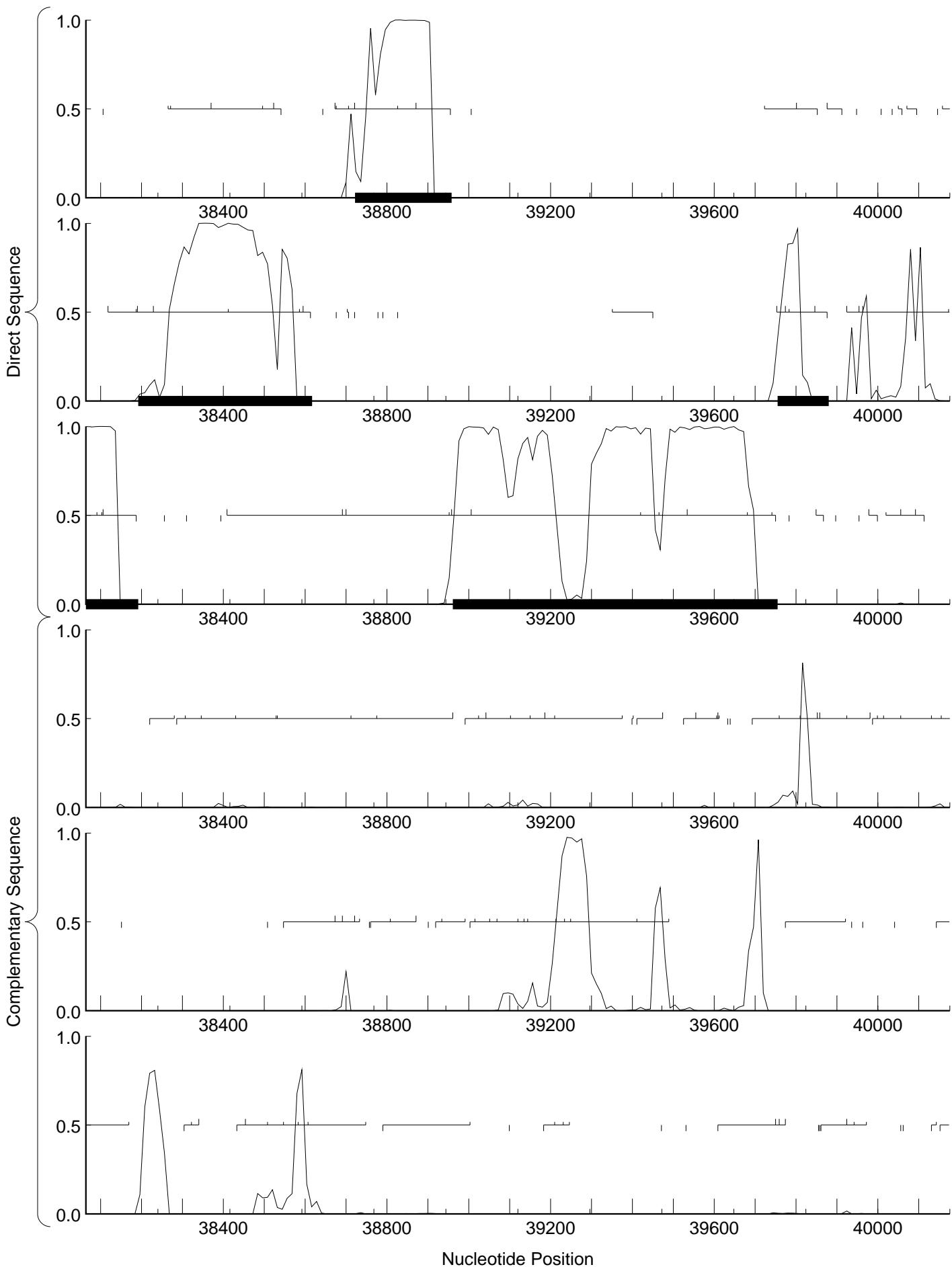


GeneMark.hmm prediction





GeneMark.hmm prediction



GeneMark.hmm prediction

