

# GeneMark

Version 2.5p (09.08.06)

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## PROGRAM INFORMATION

Sequence : Mycobacterium phage Chewbacca complete sequence 43575 bp including 13-base 3' overhang (CC  
Analysis Date : 5/24/18 at 4:03:25  
Pages : 22  
Sequence Length : 43575 bp  
GC Content : 66.19%

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

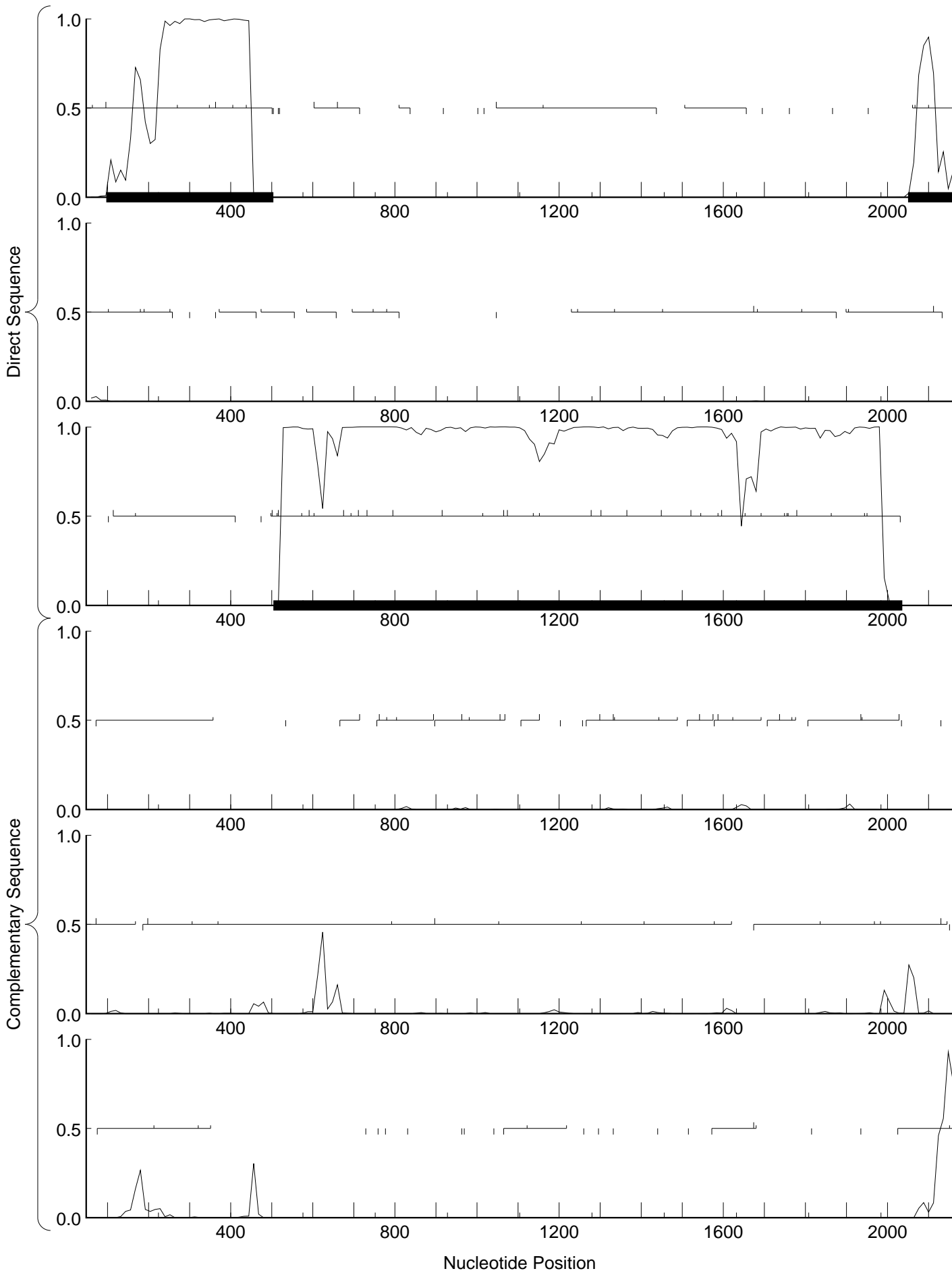
Send questions / comments to:  
Dr. M. Borodovsky  
Georgia Institute of Technology  
School of Biology  
Atlanta, GA 30332-0230

### Matrix notes & comments

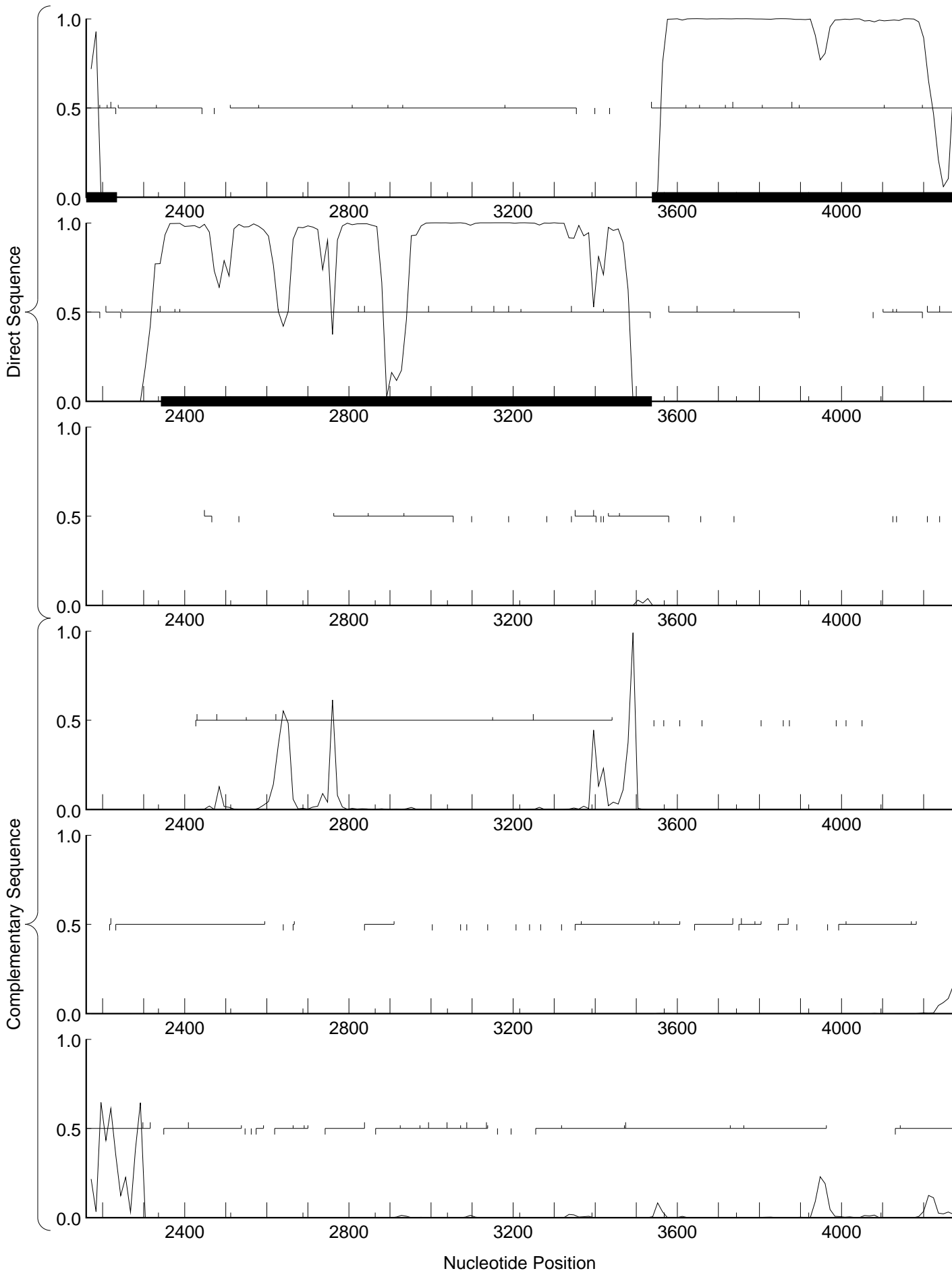
For details on the model building procedure see:  
Besemer J. and Borodovsky M.  
"Heuristic approach to deriving models for gene finding"  
NAR, 1999, Vol. 27, No. 19, pp. 3911-3920

complete sequence 43575 bp including 13-base 3' overhang (CCCGCCGCAATGG), Cluster N, Order 2, Window 96, Step 12, 2/22

GeneMark.hmm prediction

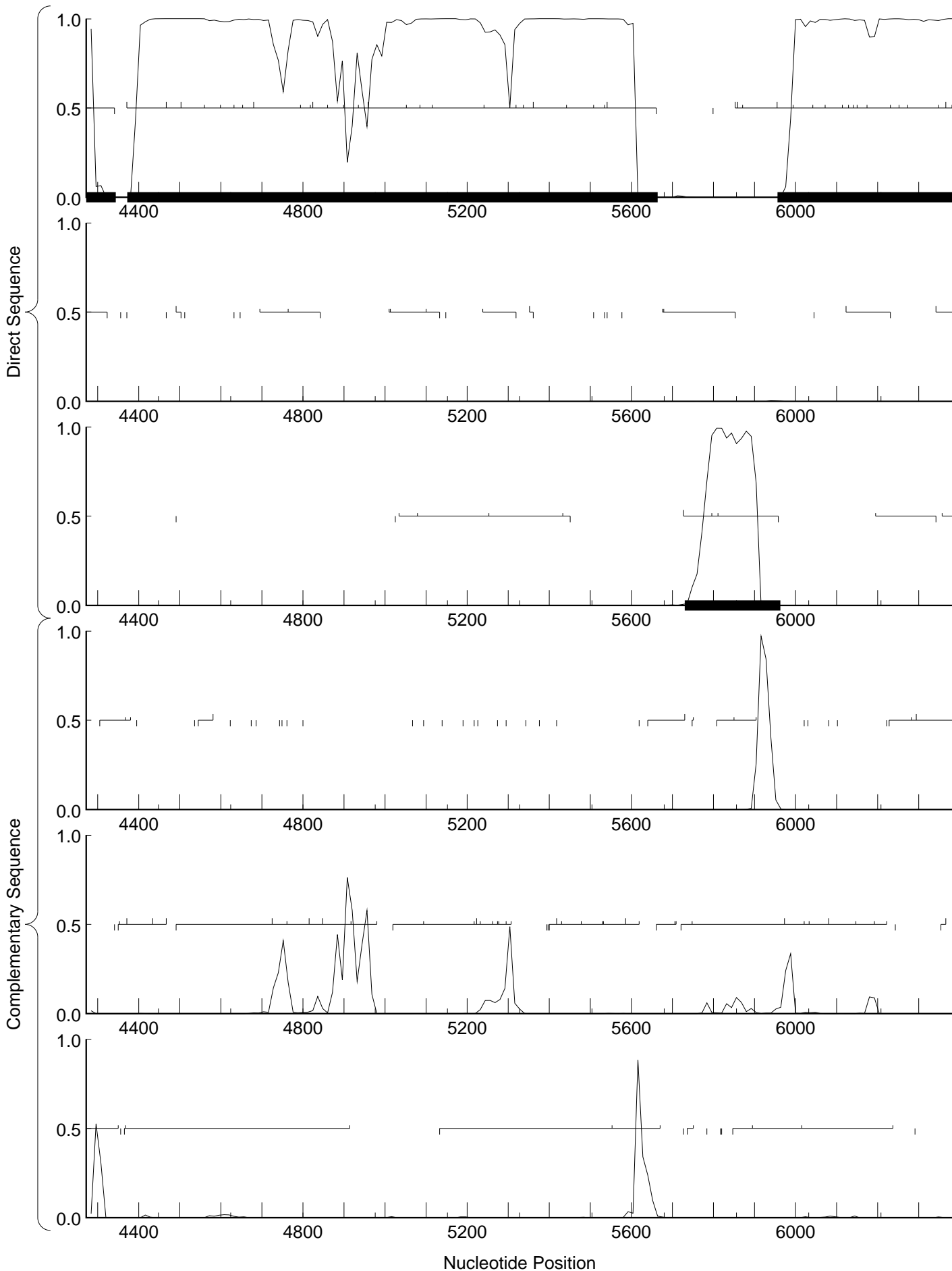


complete sequence 43575 bp including 13-base 3' overhang (CCGCCGCAATGG), Cluster N, Order 2, Window 96, Step 12, 3/22

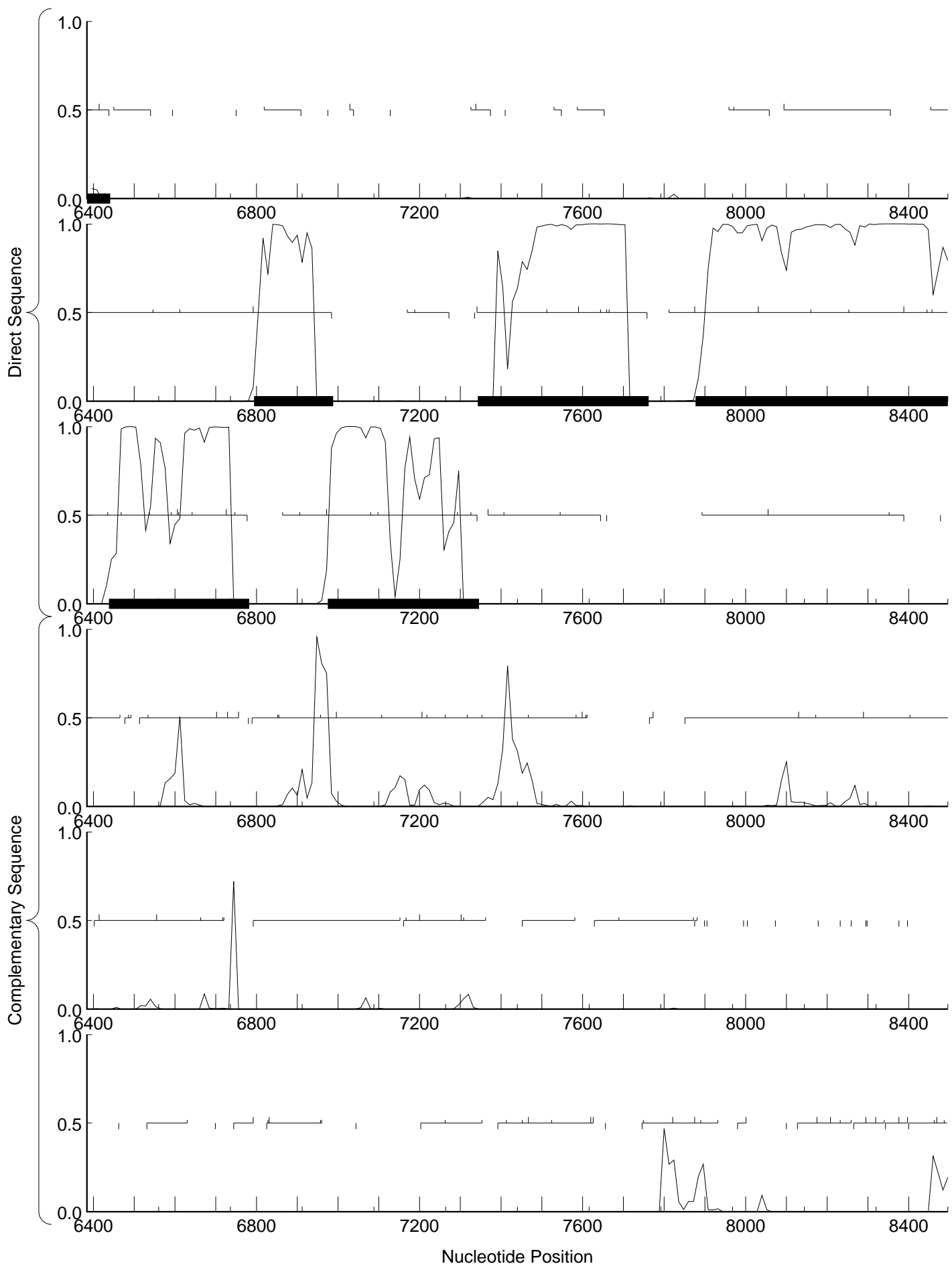


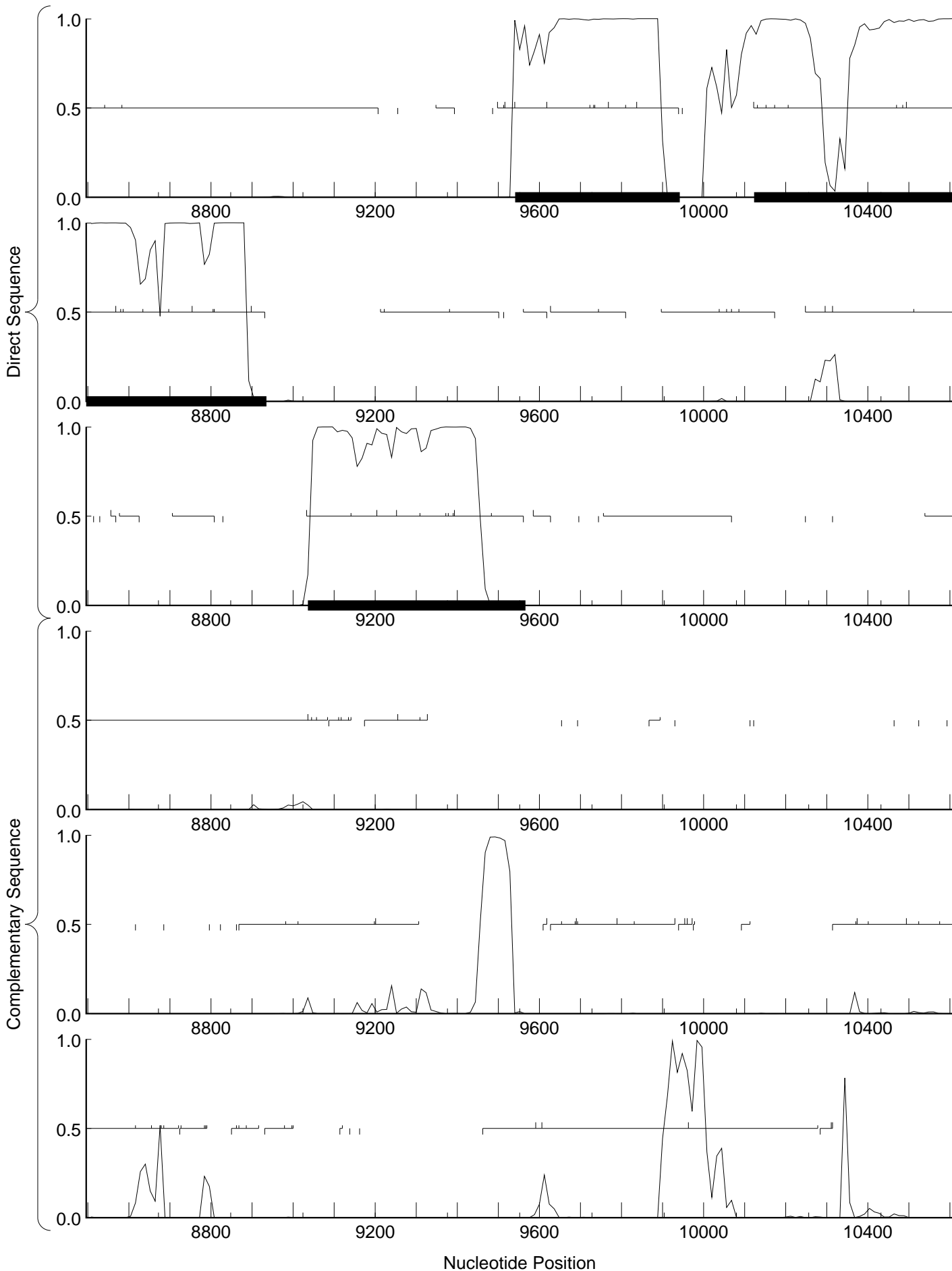
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GeneMark.hmm prediction



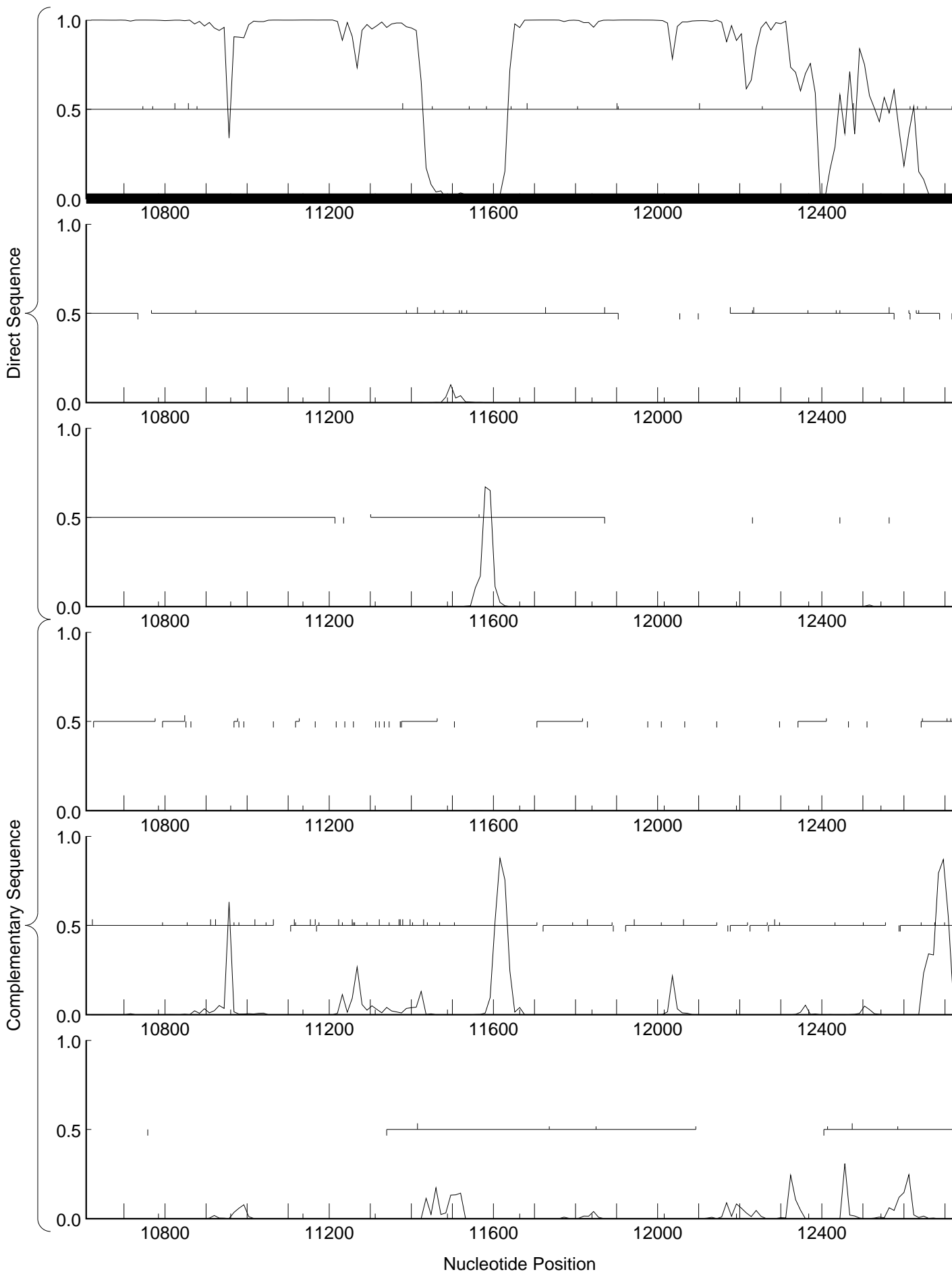
GeneMark.hmm prediction





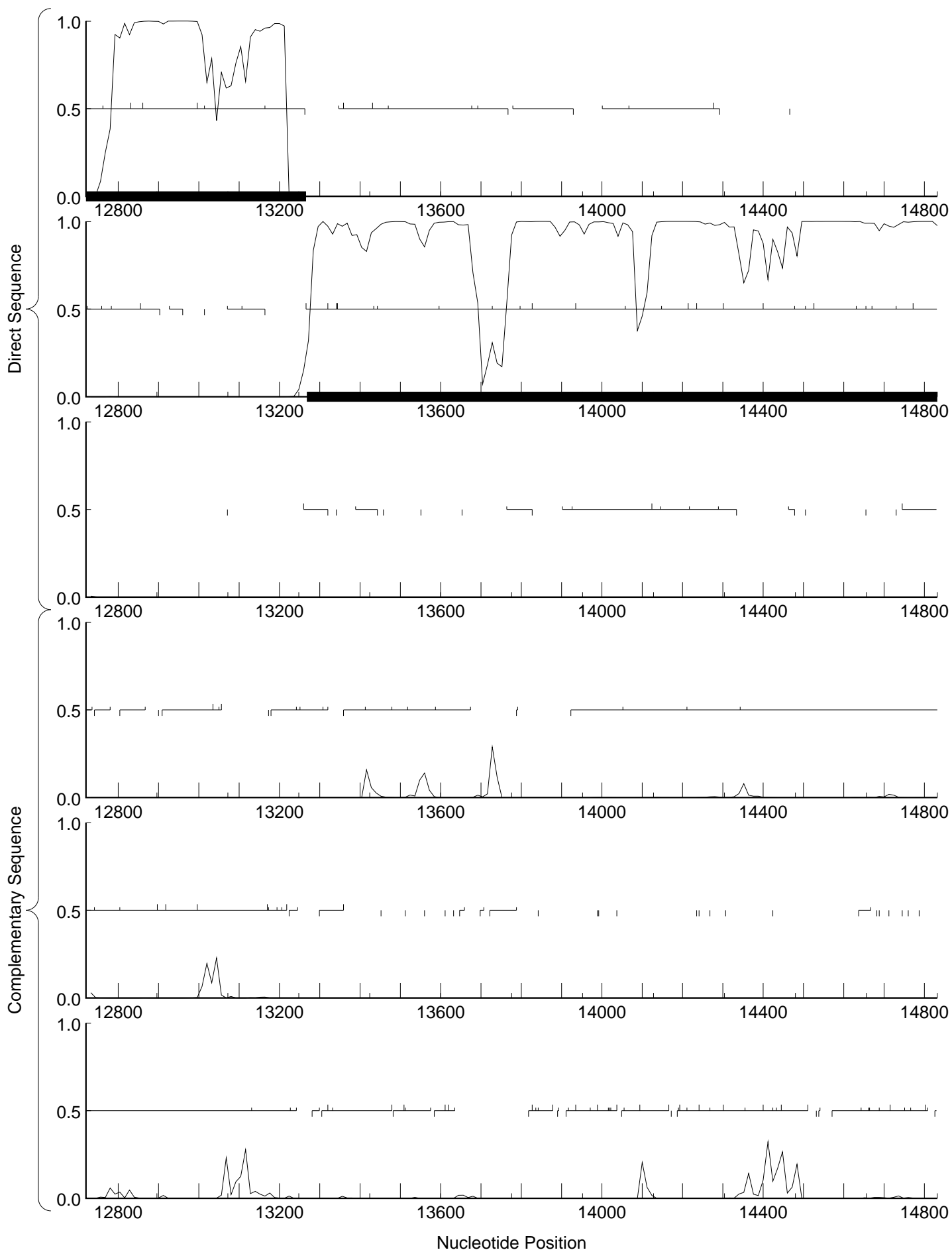
complete sequence 43575 bp including 13-base 3' overhang (CCGCCGCAATGG), Cluster N, Order 2, Window 96, Step 12, 7/22

GeneMark.hmm prediction



complete sequence 43575 bp including 13-base 3' overhang (CCGCCGCAATGG), Cluster N, Order 2, Window 96, Step 12, 8/22

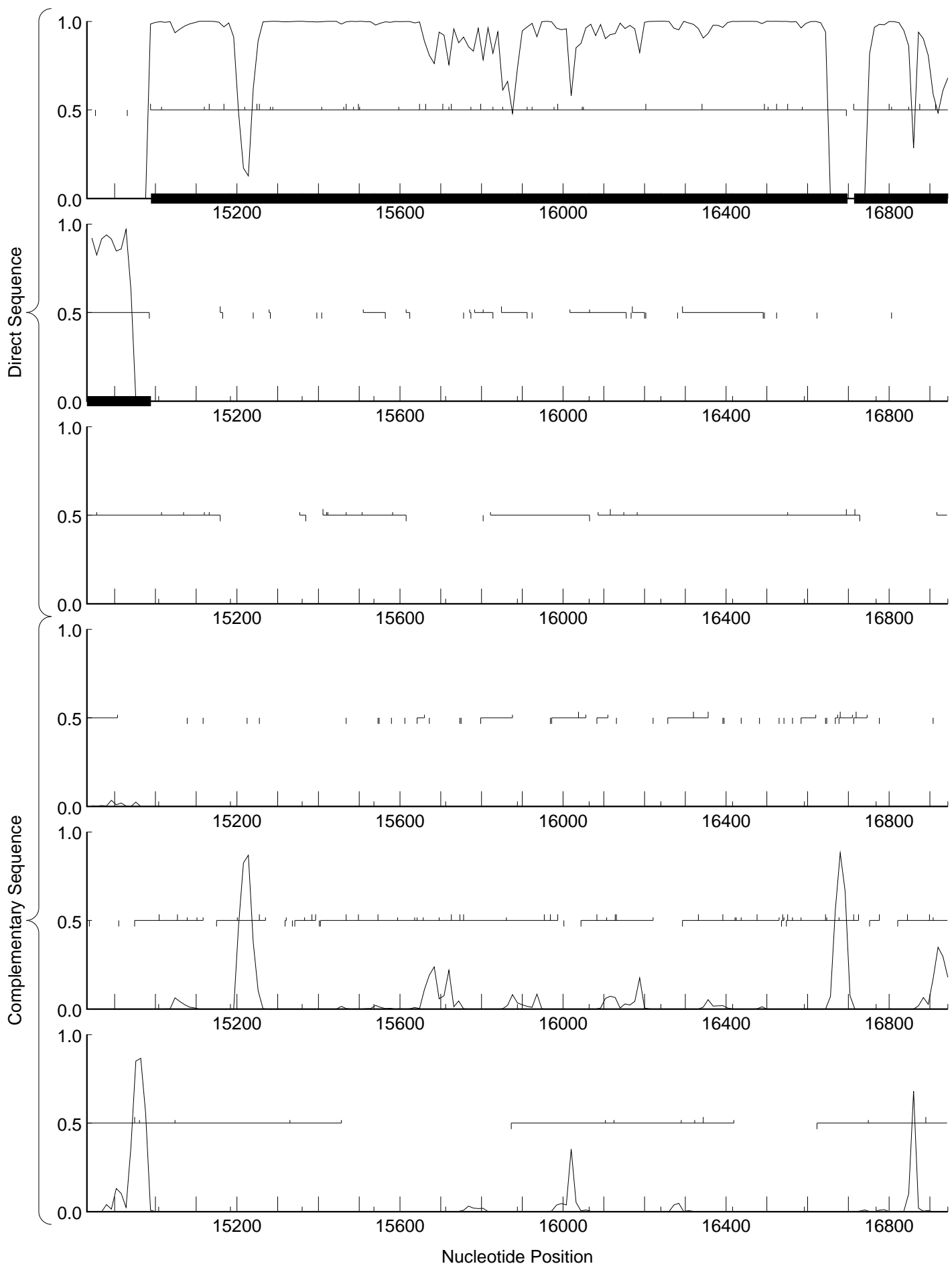
GeneMark.hmm prediction



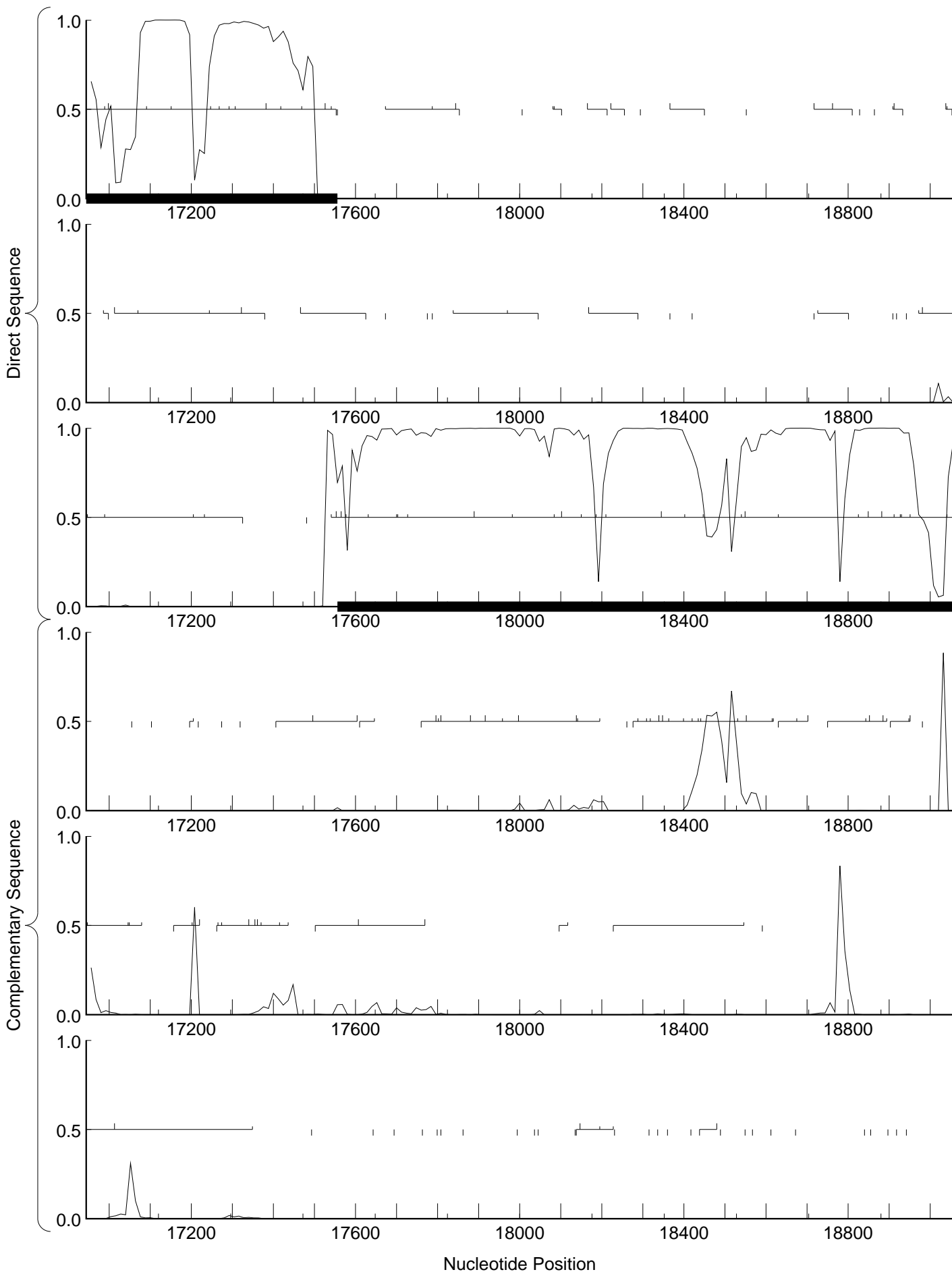


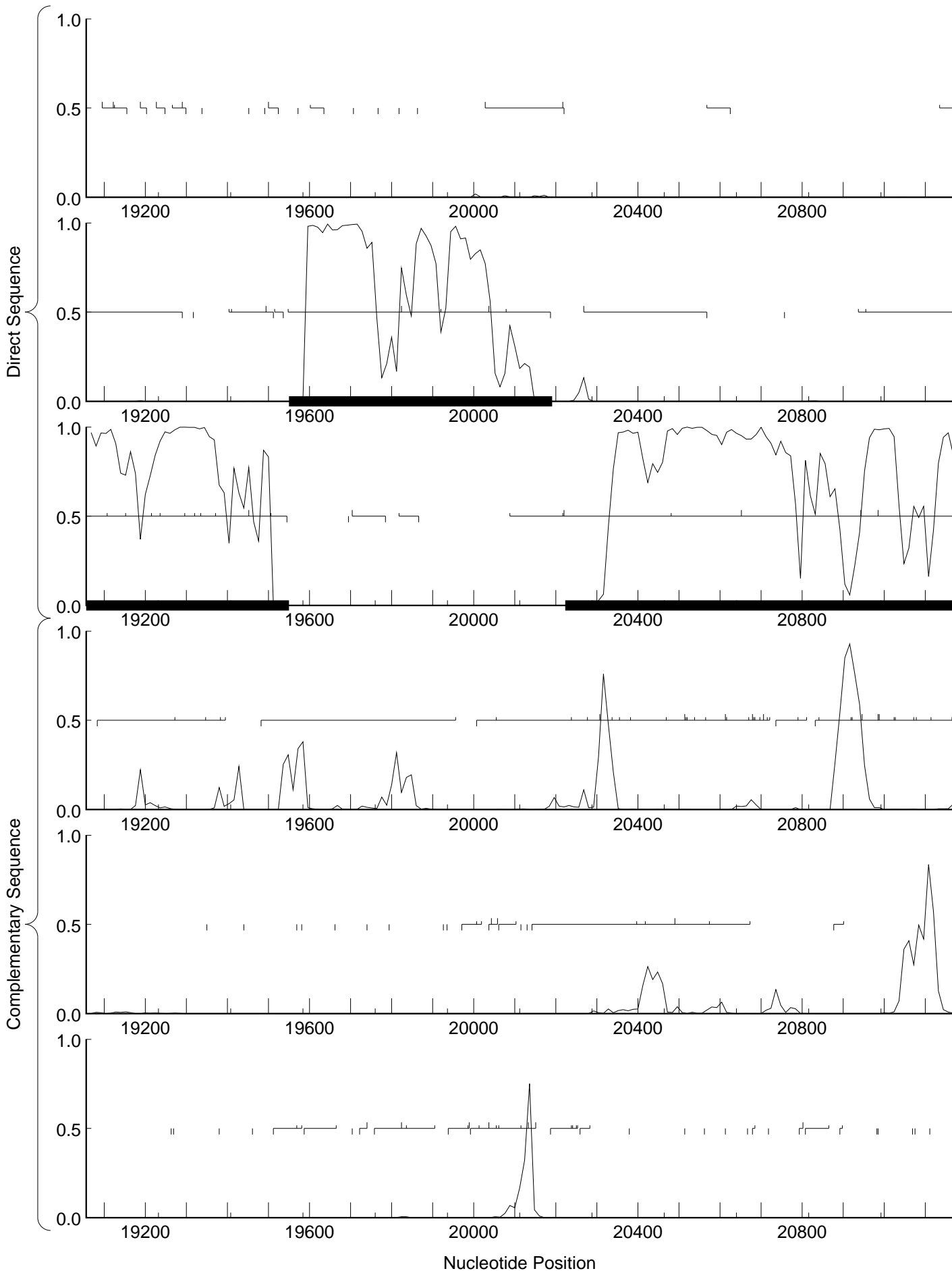
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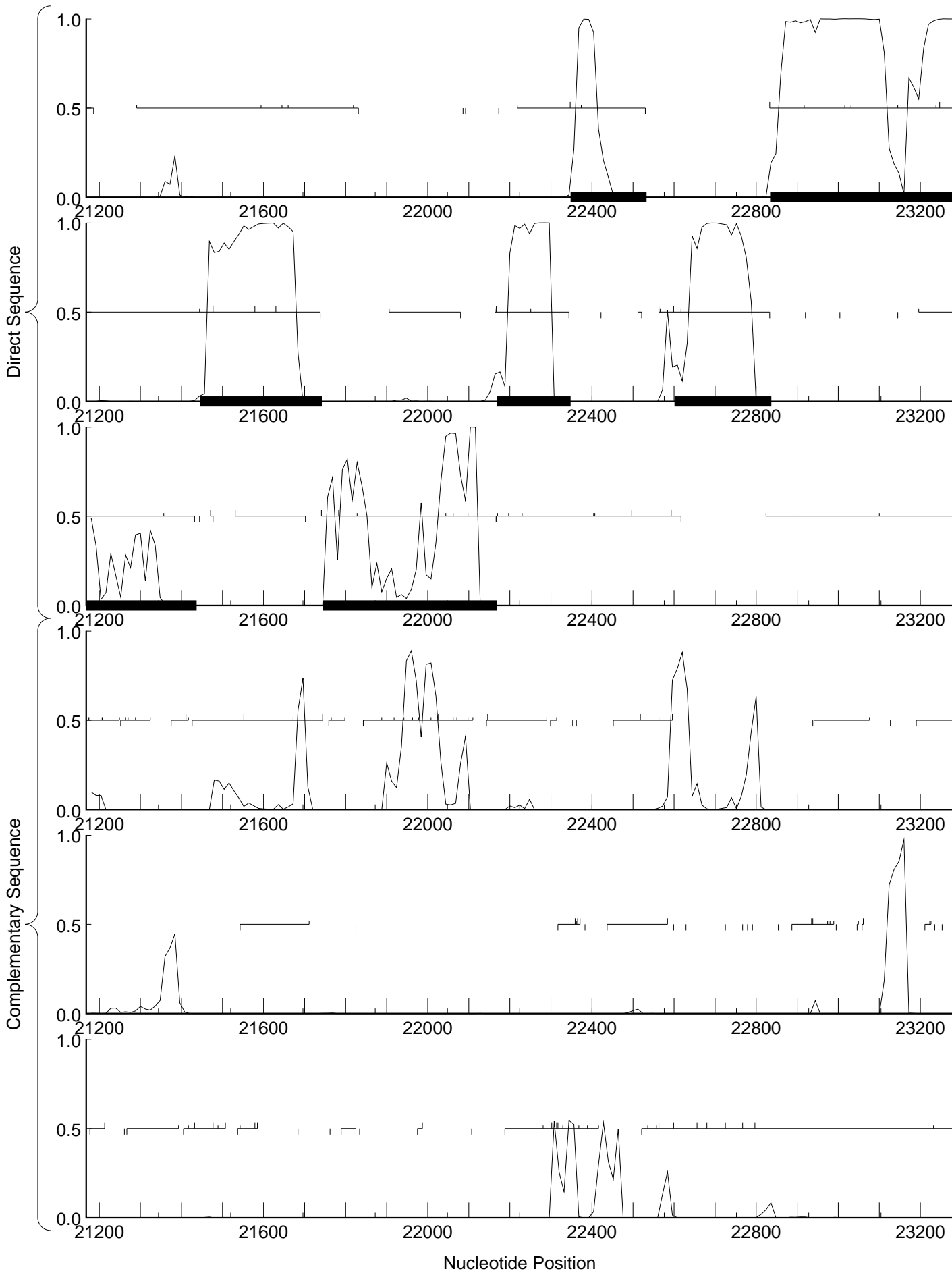
GeneMark.hmm prediction



GeneMark.hmm prediction

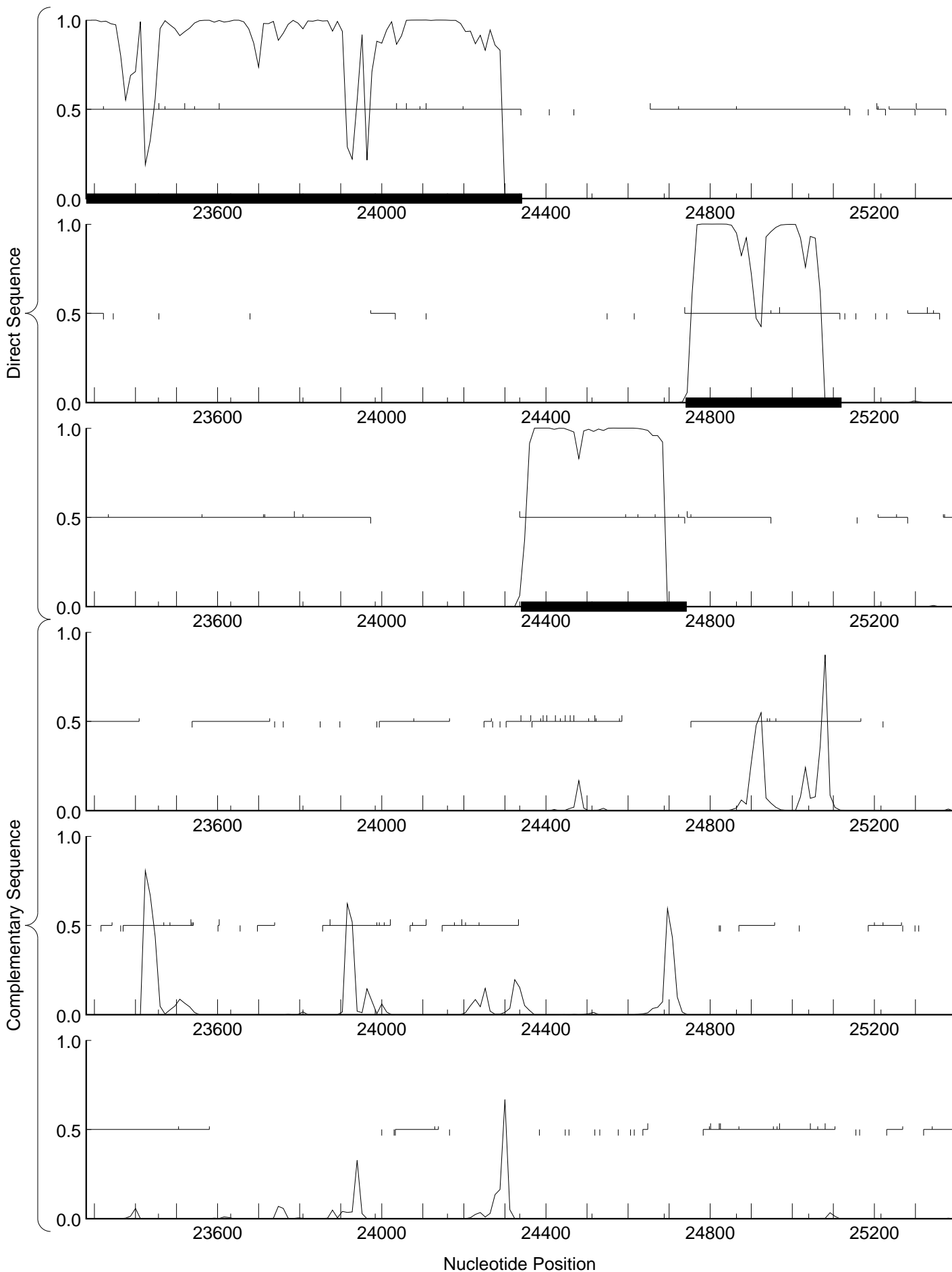


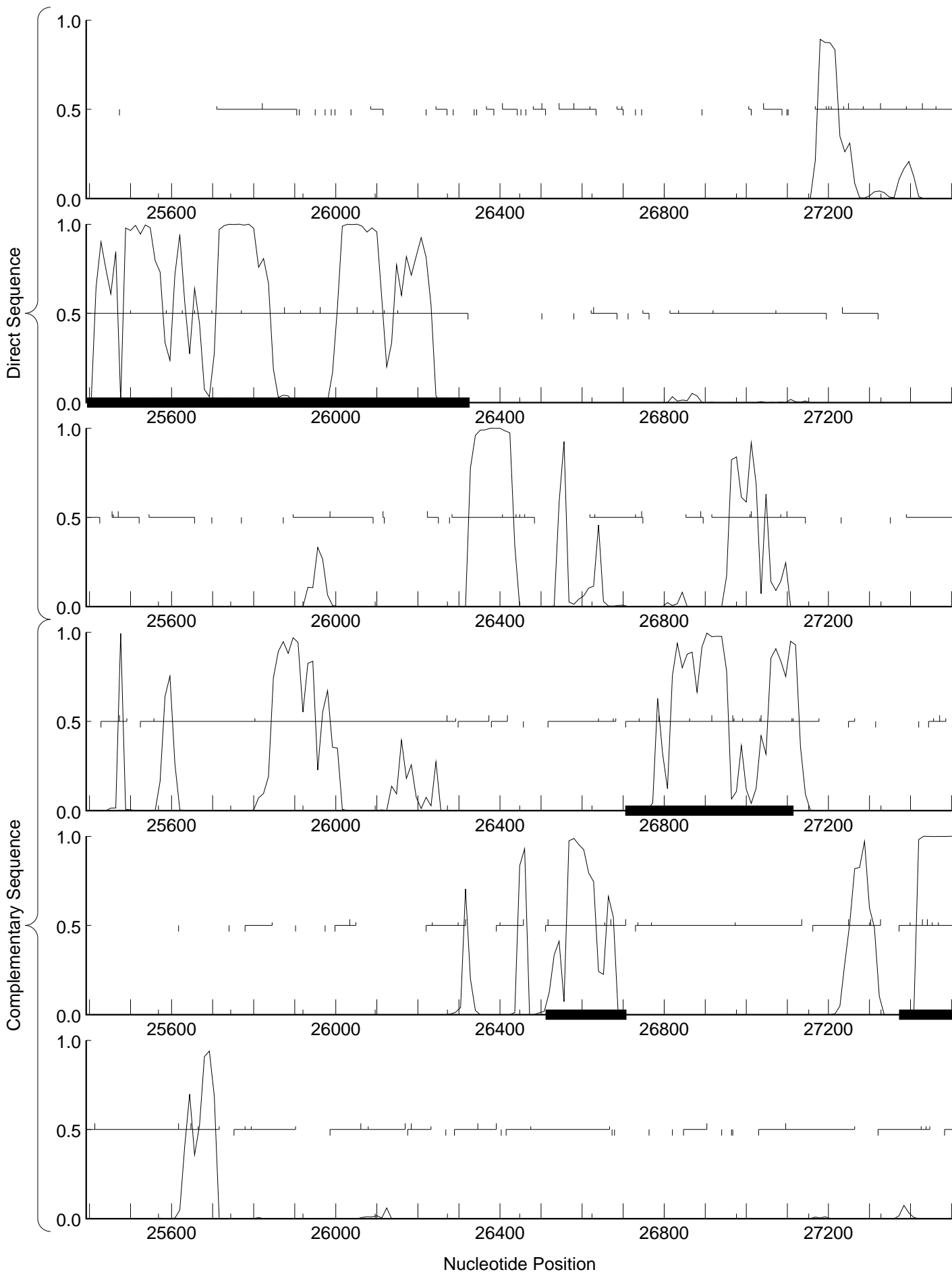




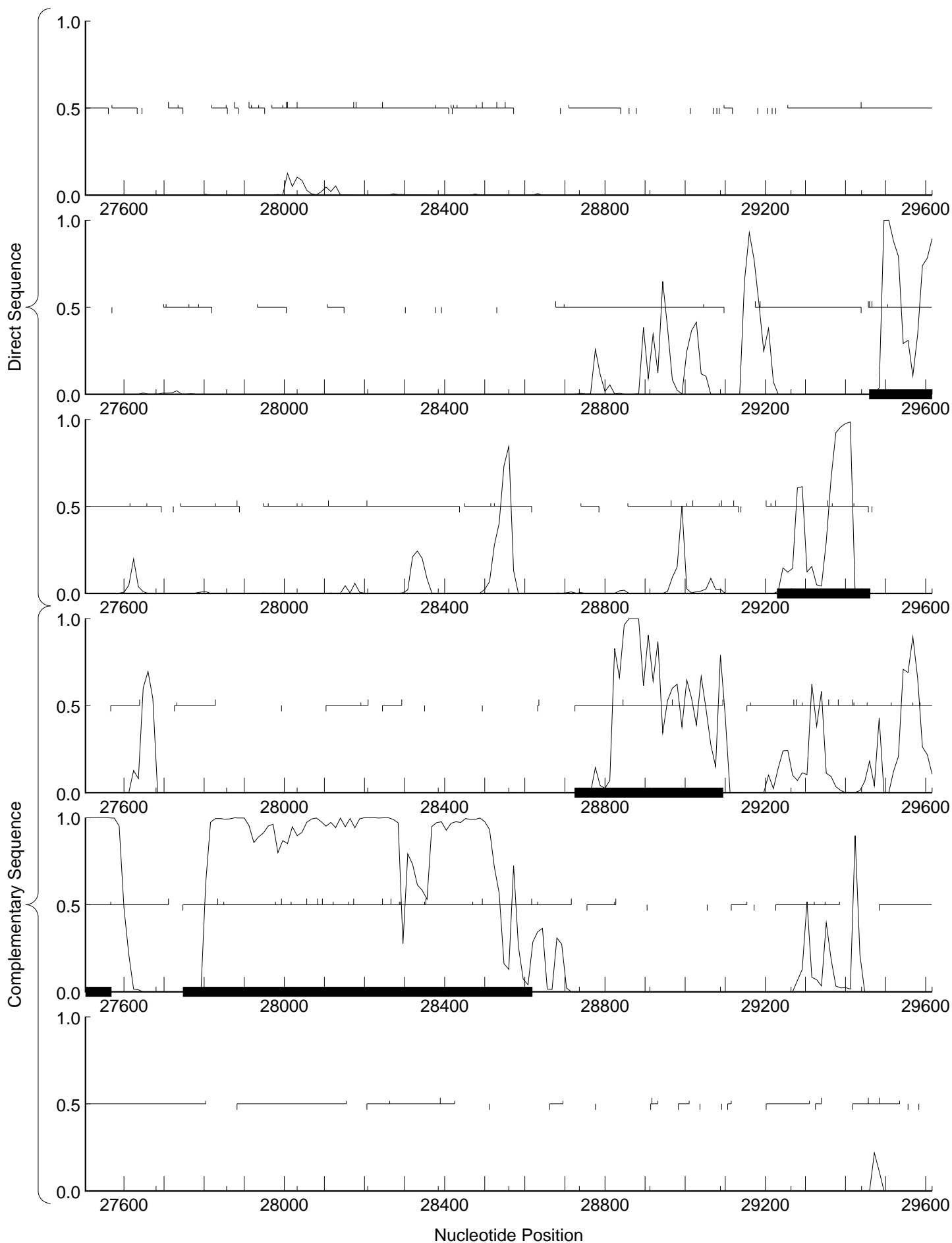
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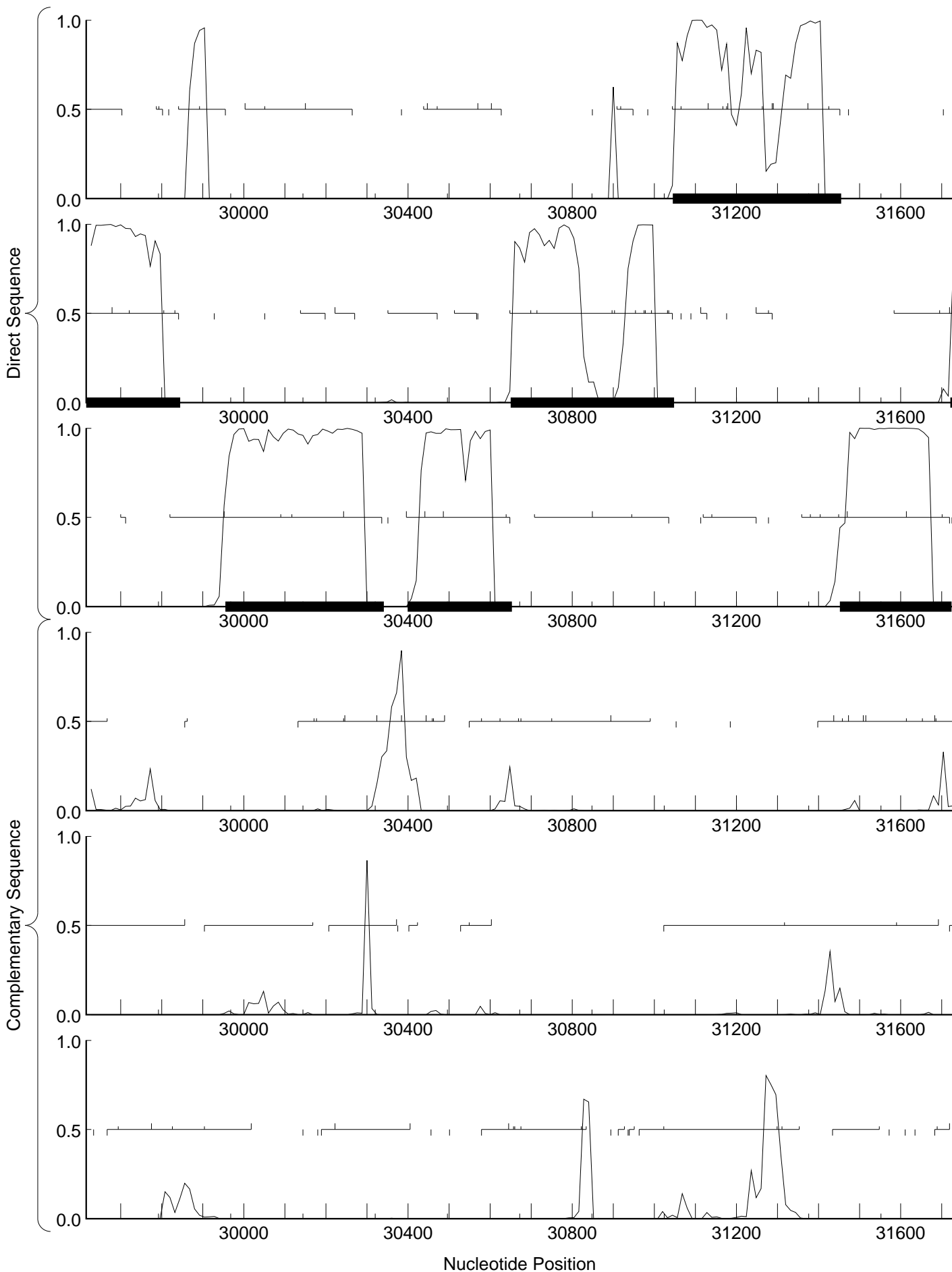
GeneMark.hmm prediction



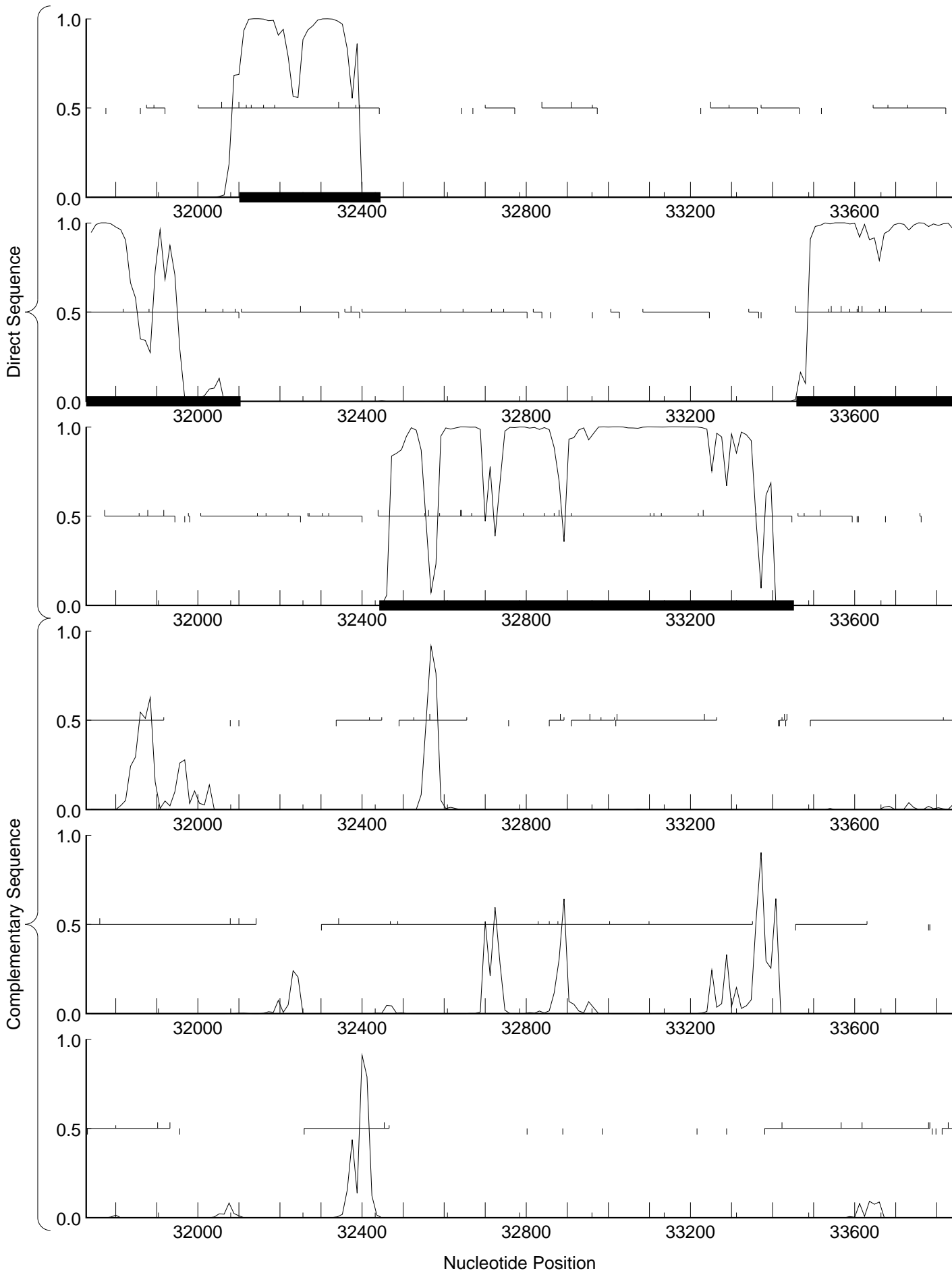


GeneMark.hmm prediction

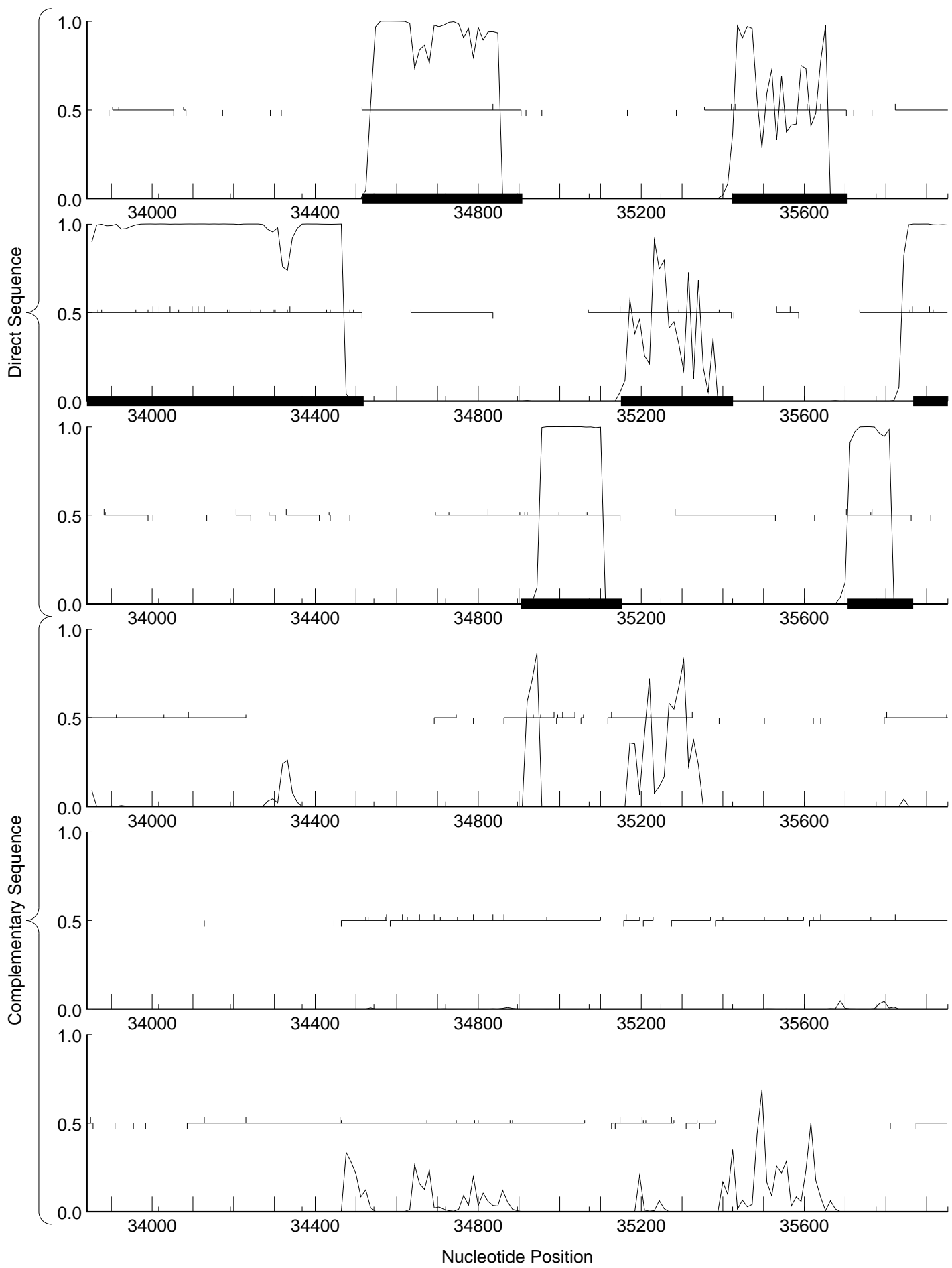




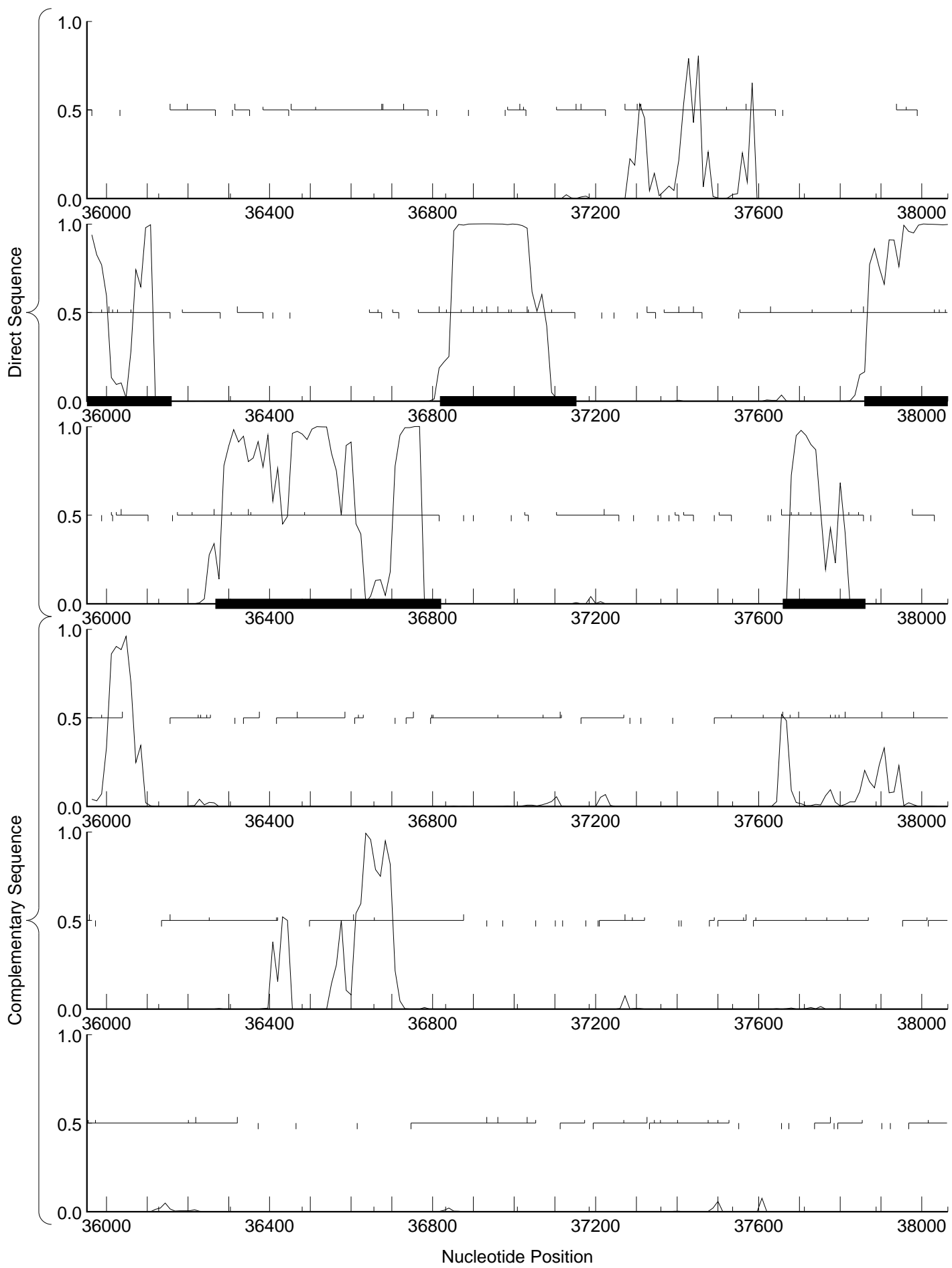




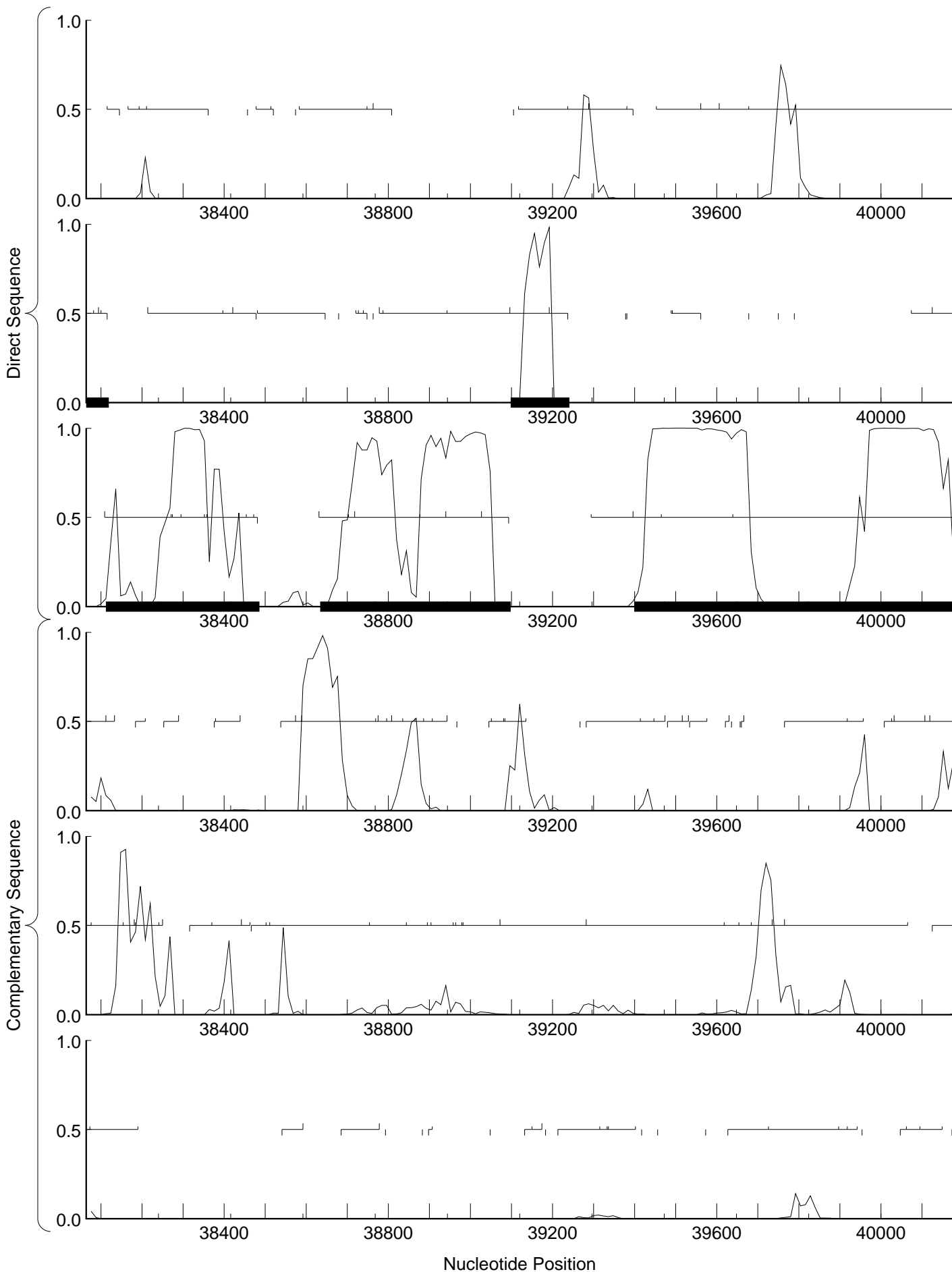
GeneMark.hmm prediction



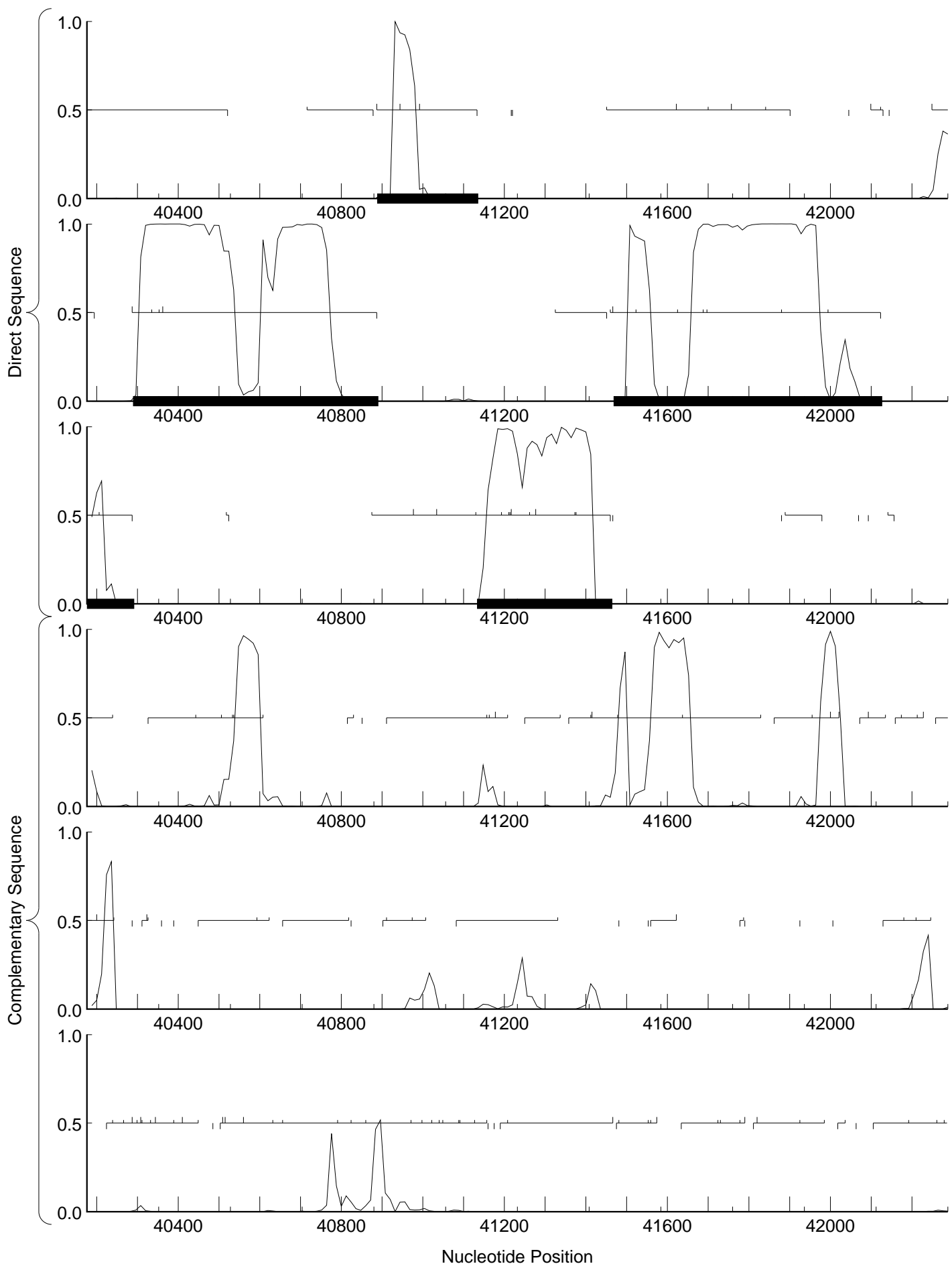
GeneMark.hmm prediction



GeneMark.hmm prediction



GeneMark.hmm prediction



GeneMark.hmm prediction

