

# GeneMark

Version 2.5p (09.08.06)

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## PROGRAM INFORMATION

Sequence : Microbacterium phage Lucky3 complete sequence, 39640 bp, circularly permuted, Cluster EA4  
Analysis Date : 3/17/18 at 16:10:37  
Pages : 20  
Sequence Length : 39640 bp  
GC Content : 64.09%

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,

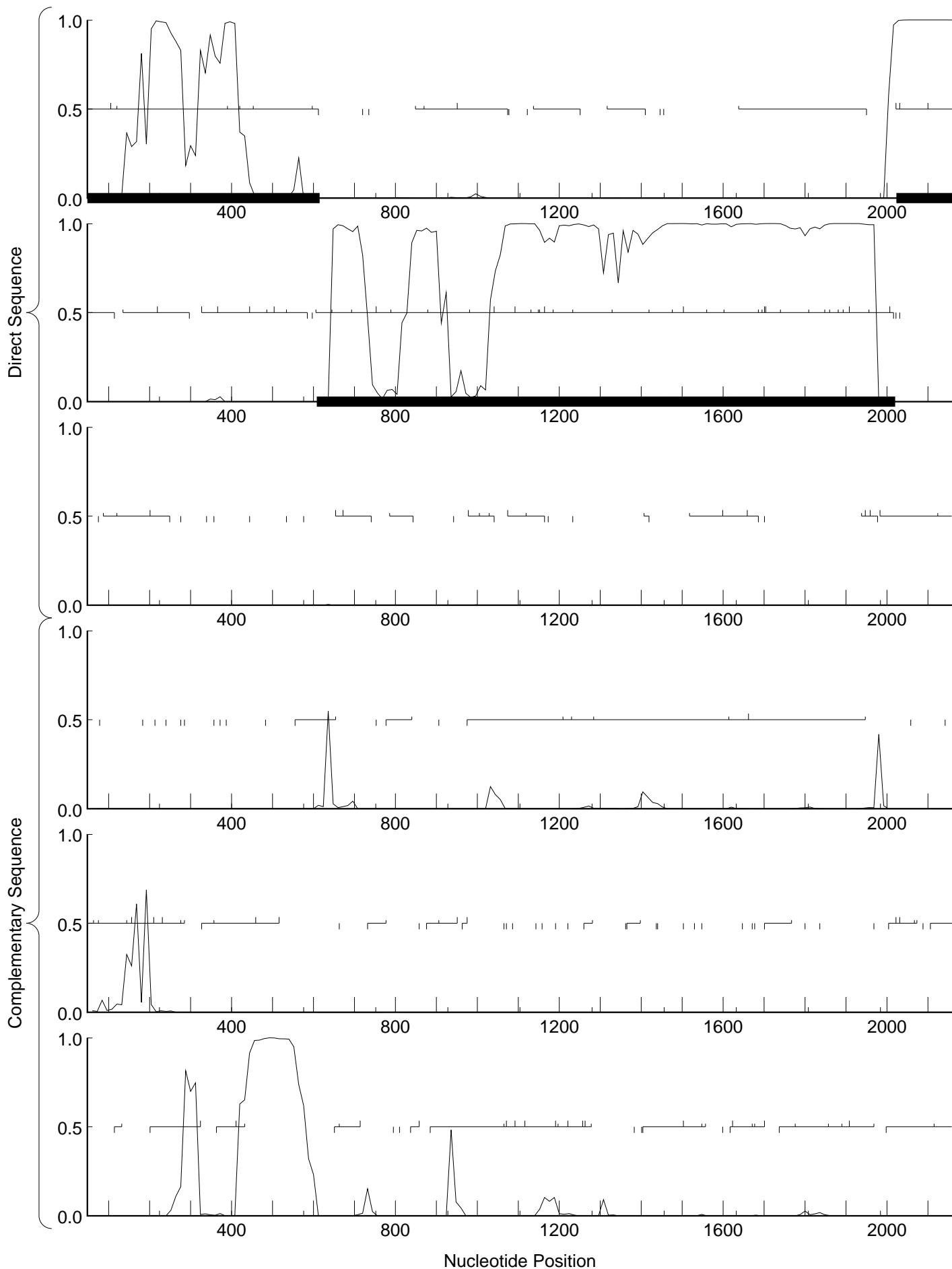
## MATRIX INFORMATION

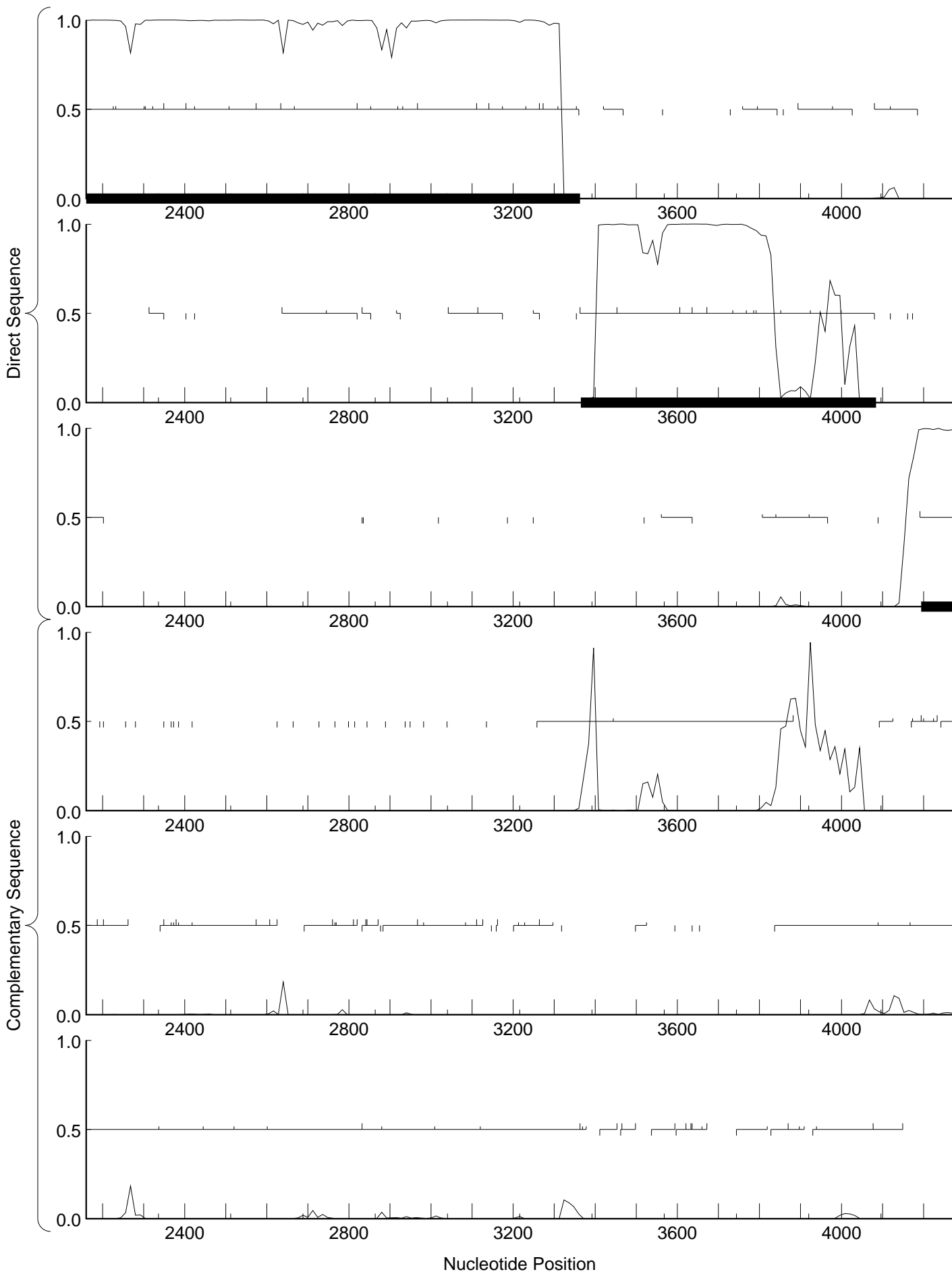
Matrix : Heuristic, GC = 64  
Author : Borodovsky Laboratory - Georgia Tech  
Order : 2

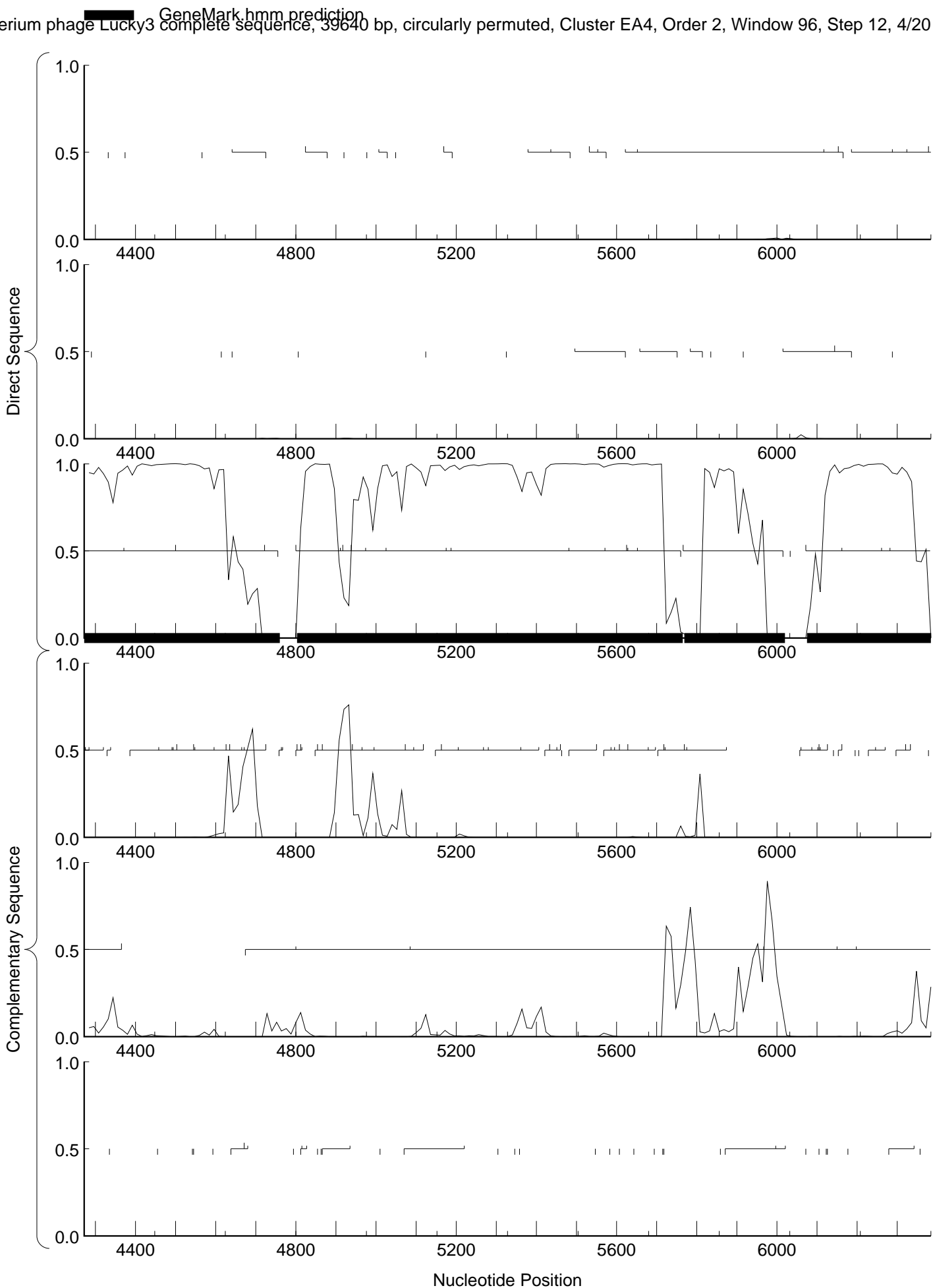
Send questions / comments to:  
Dr. M. Borodovsky  
Georgia Institute of Technology  
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Atlanta, GA 30332-0230

### Matrix notes & comments

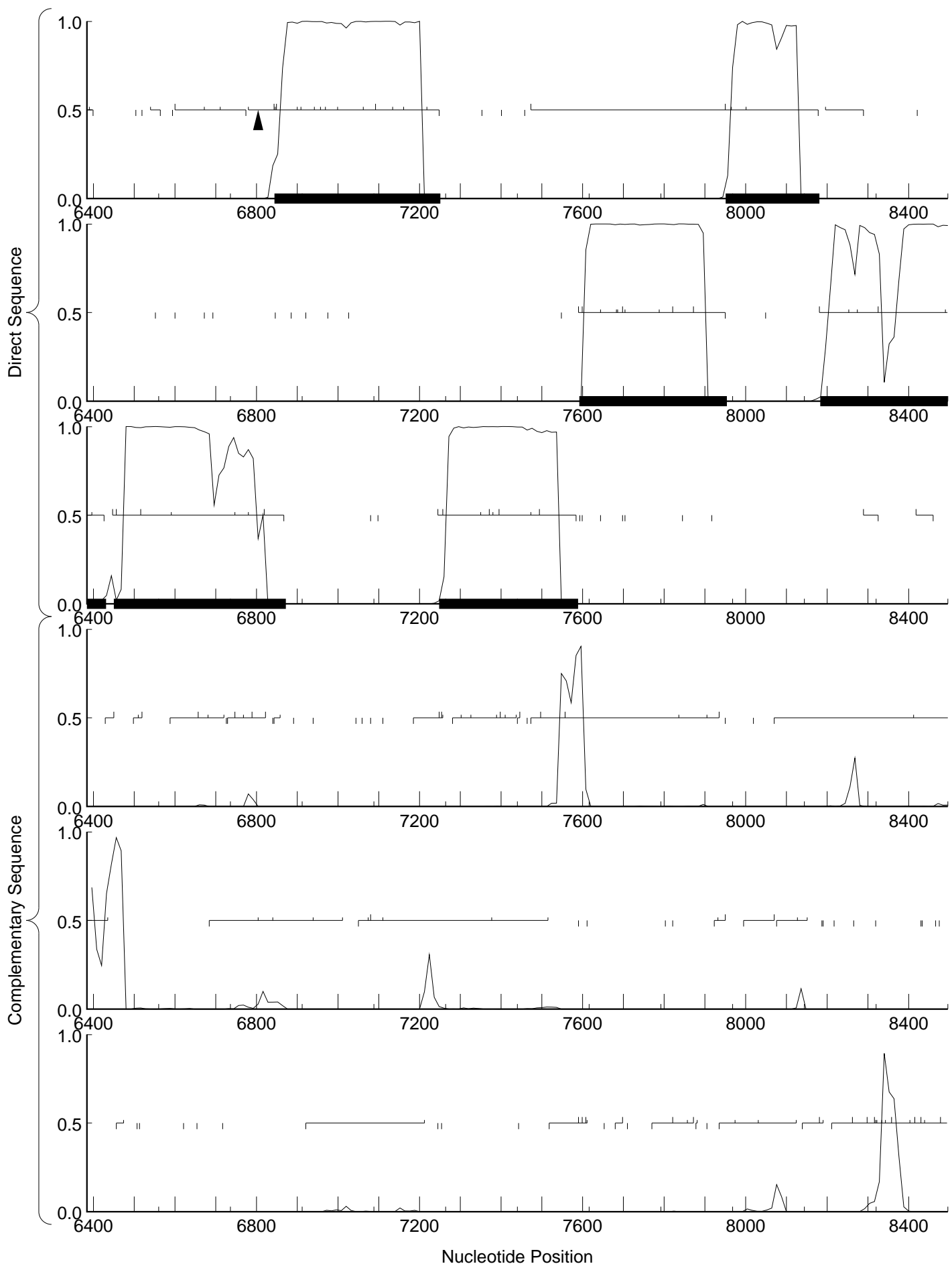
For details on the model building procedure see:  
Besemer J. and Borodovsky M.  
"Heuristic approach to deriving models for gene finding"  
NAR, 1999, Vol. 27, No. 19, pp. 3911-3920



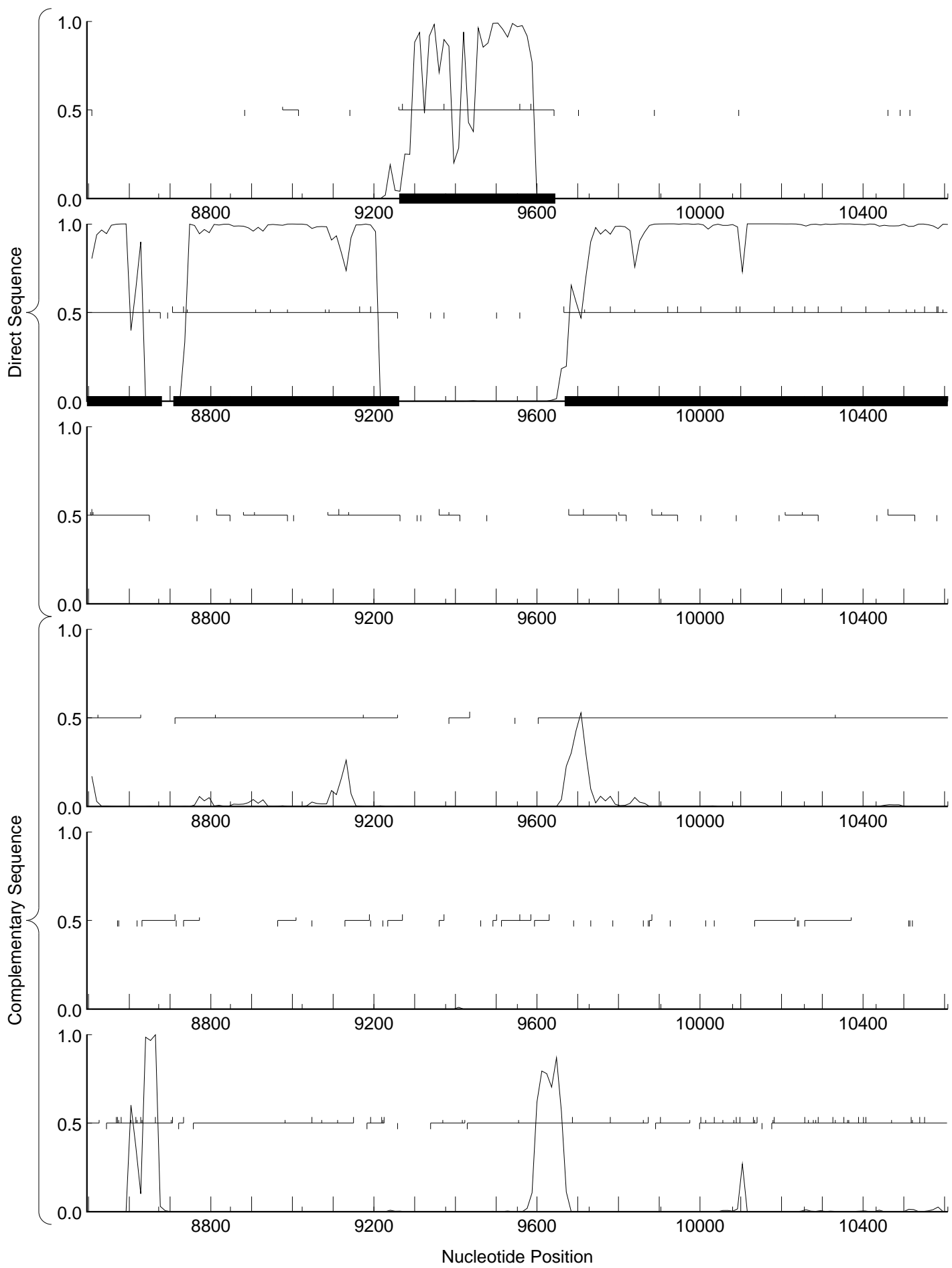




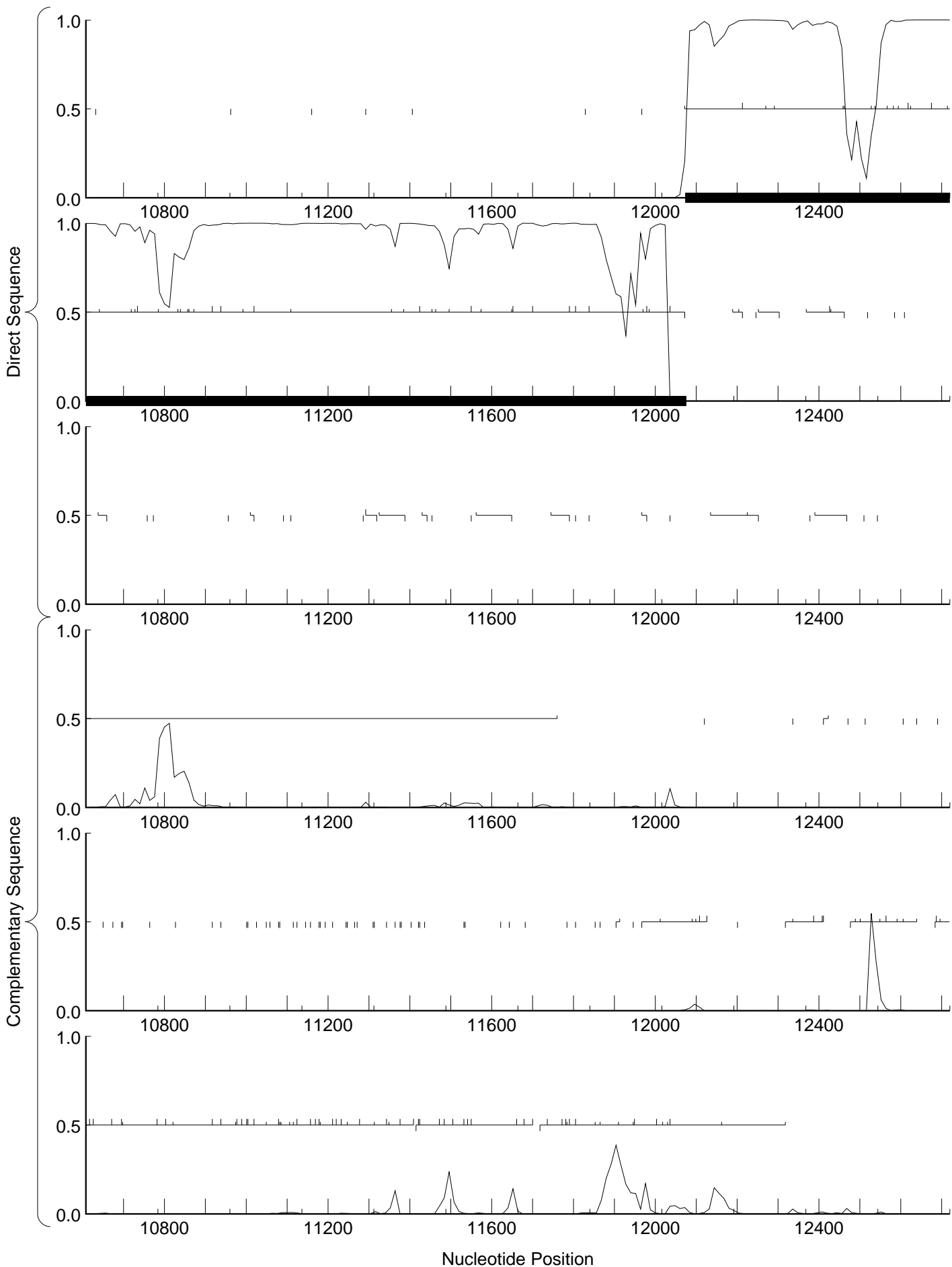
GeneMark.hmm prediction

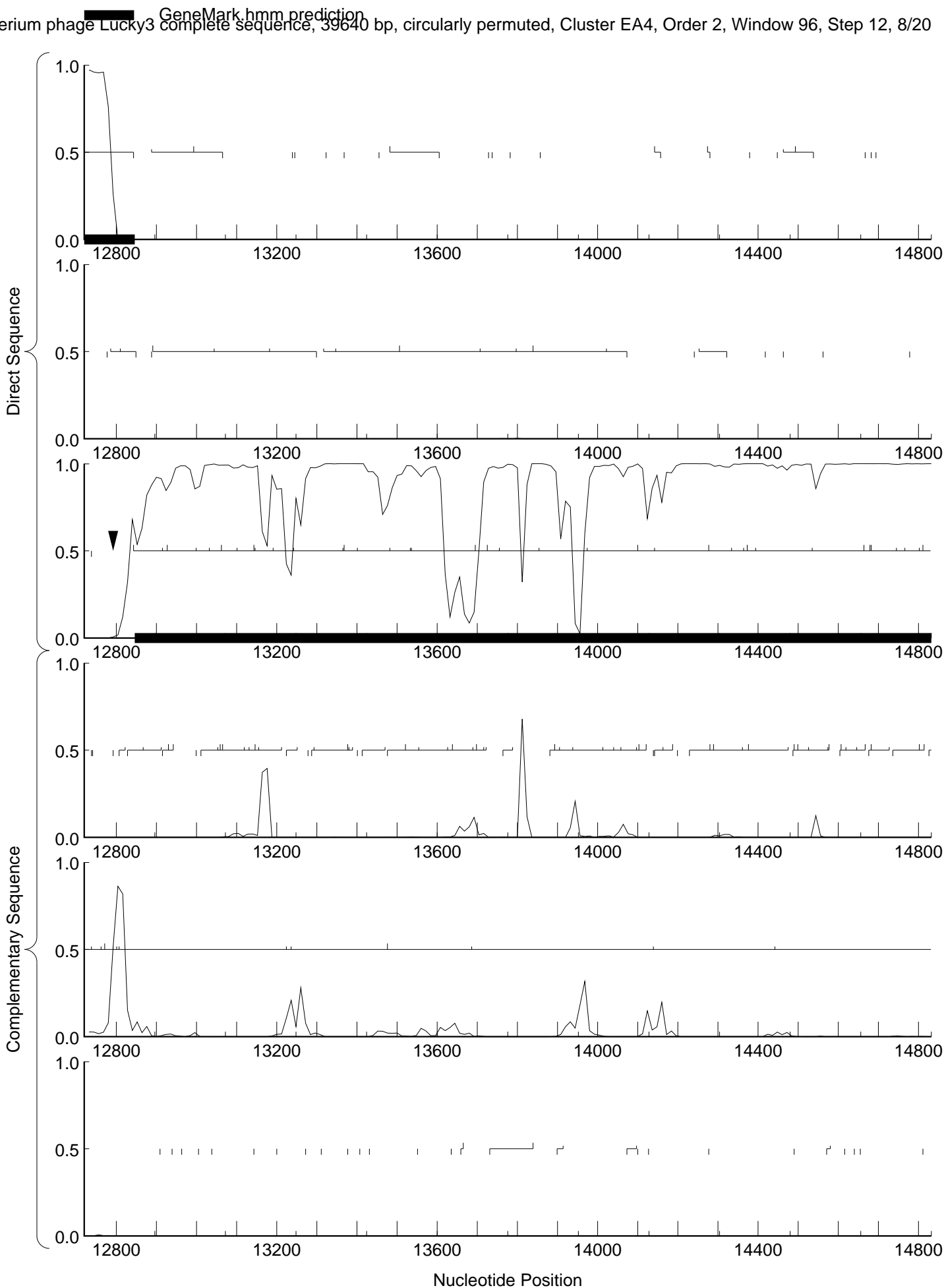


GeneMark.hmm prediction

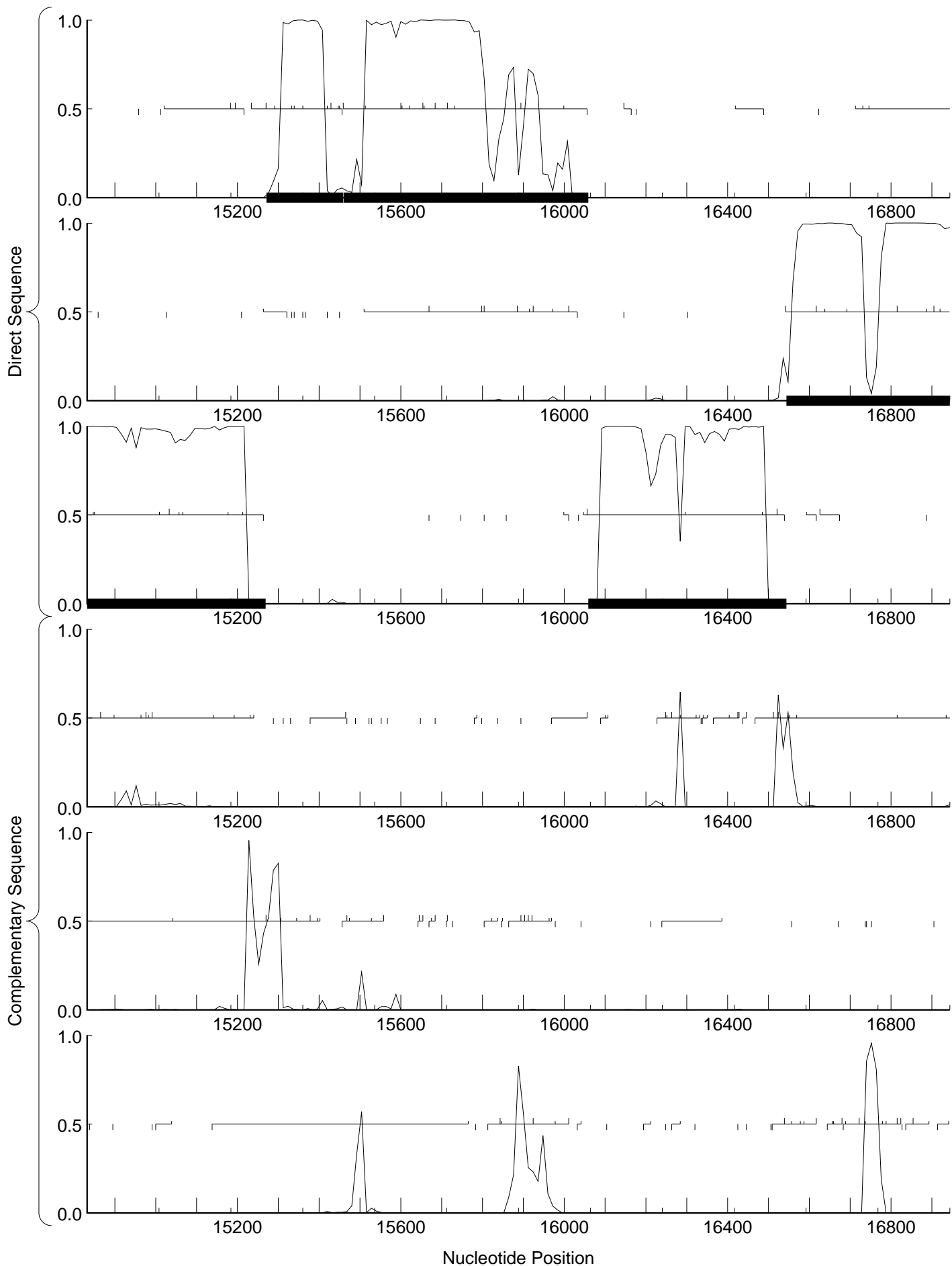


GeneMark.hmm prediction

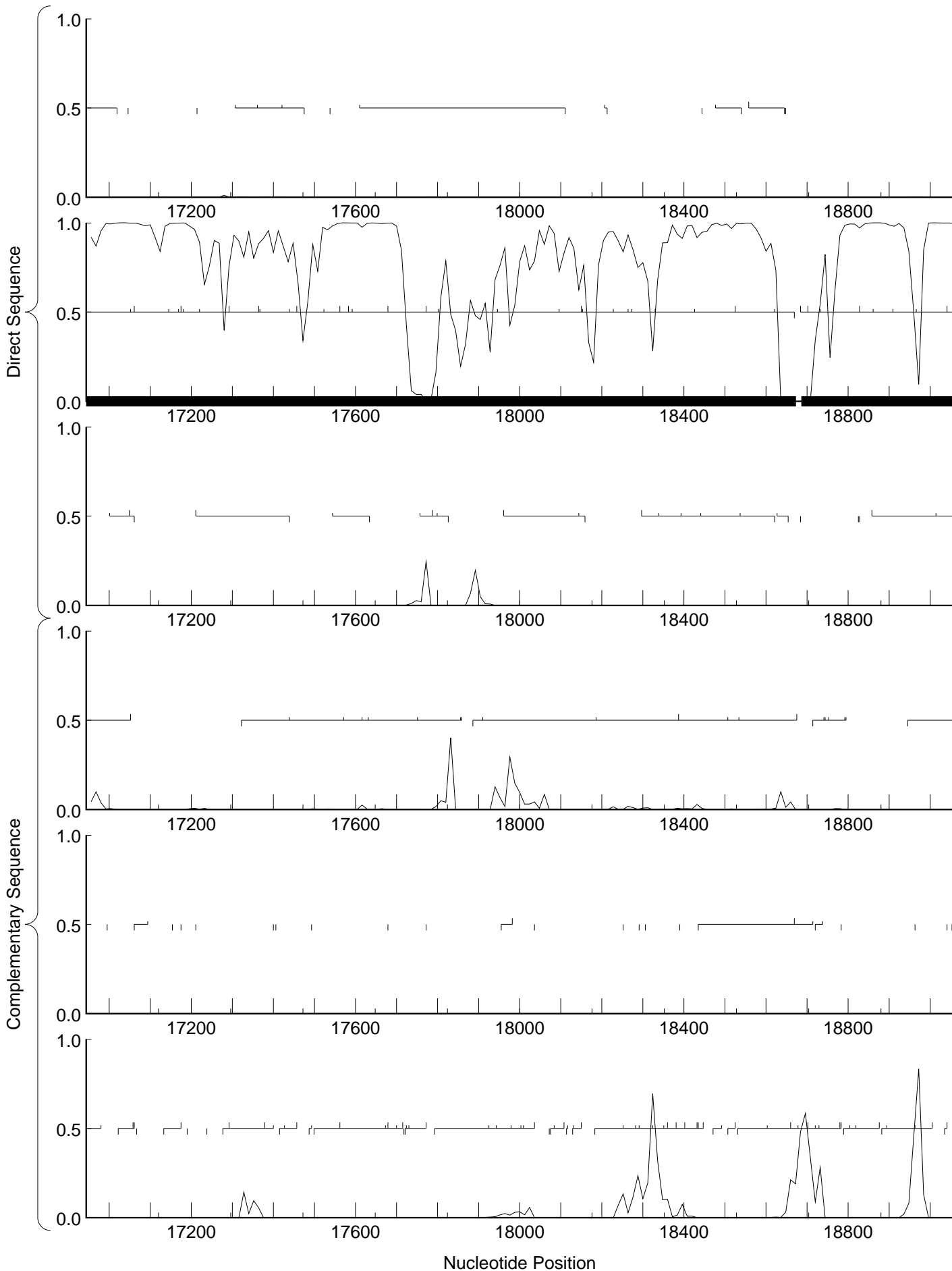


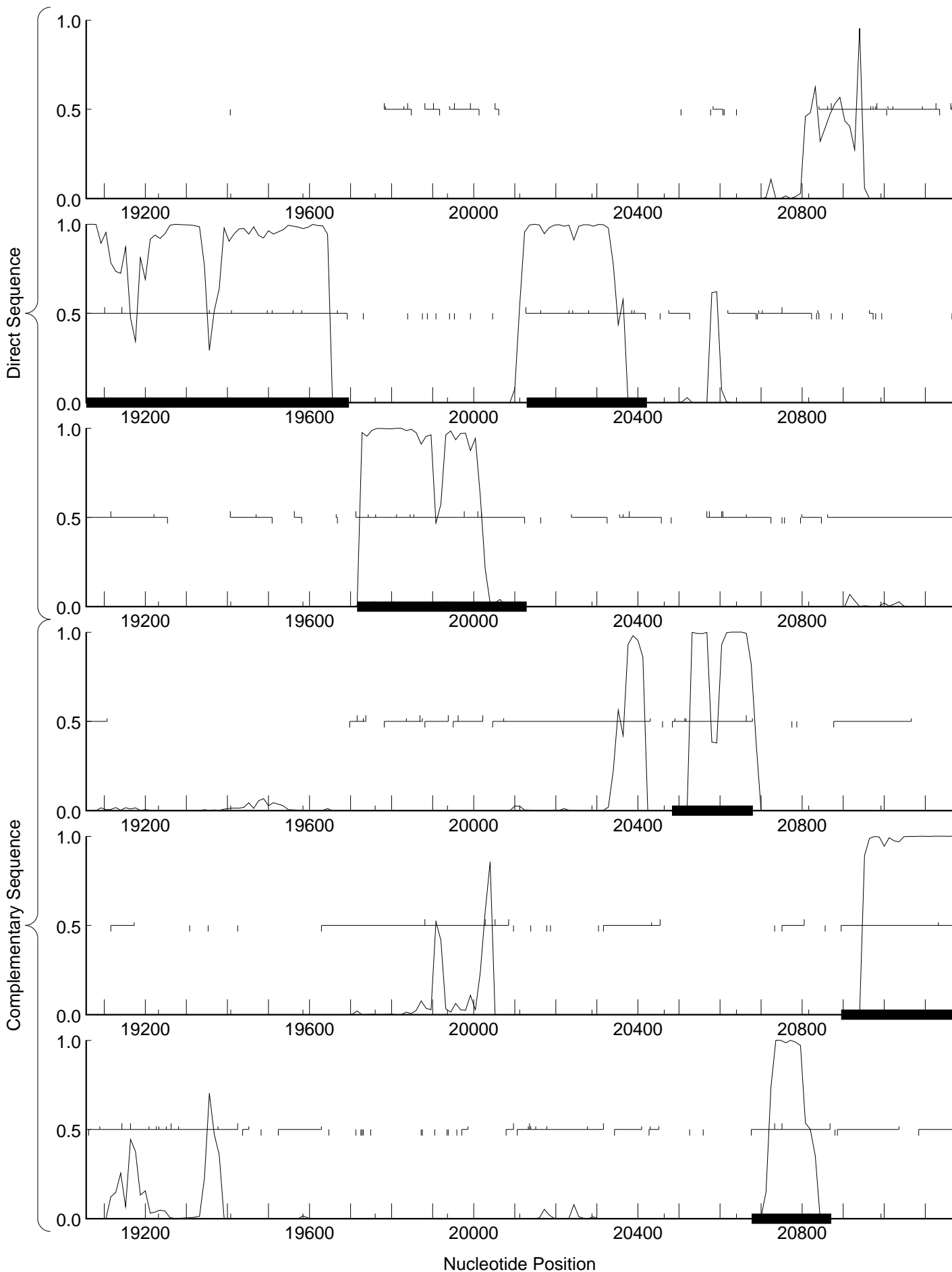


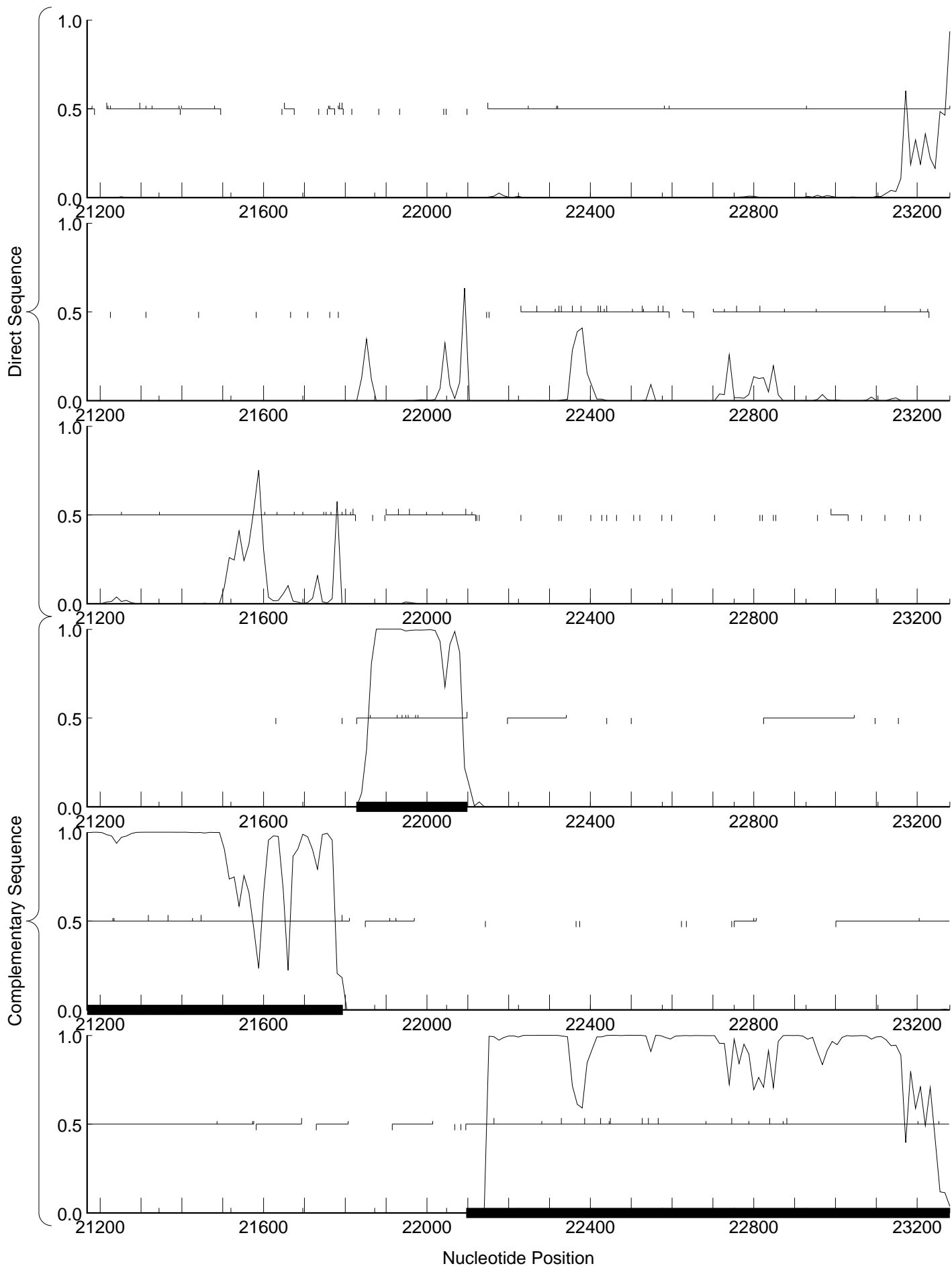


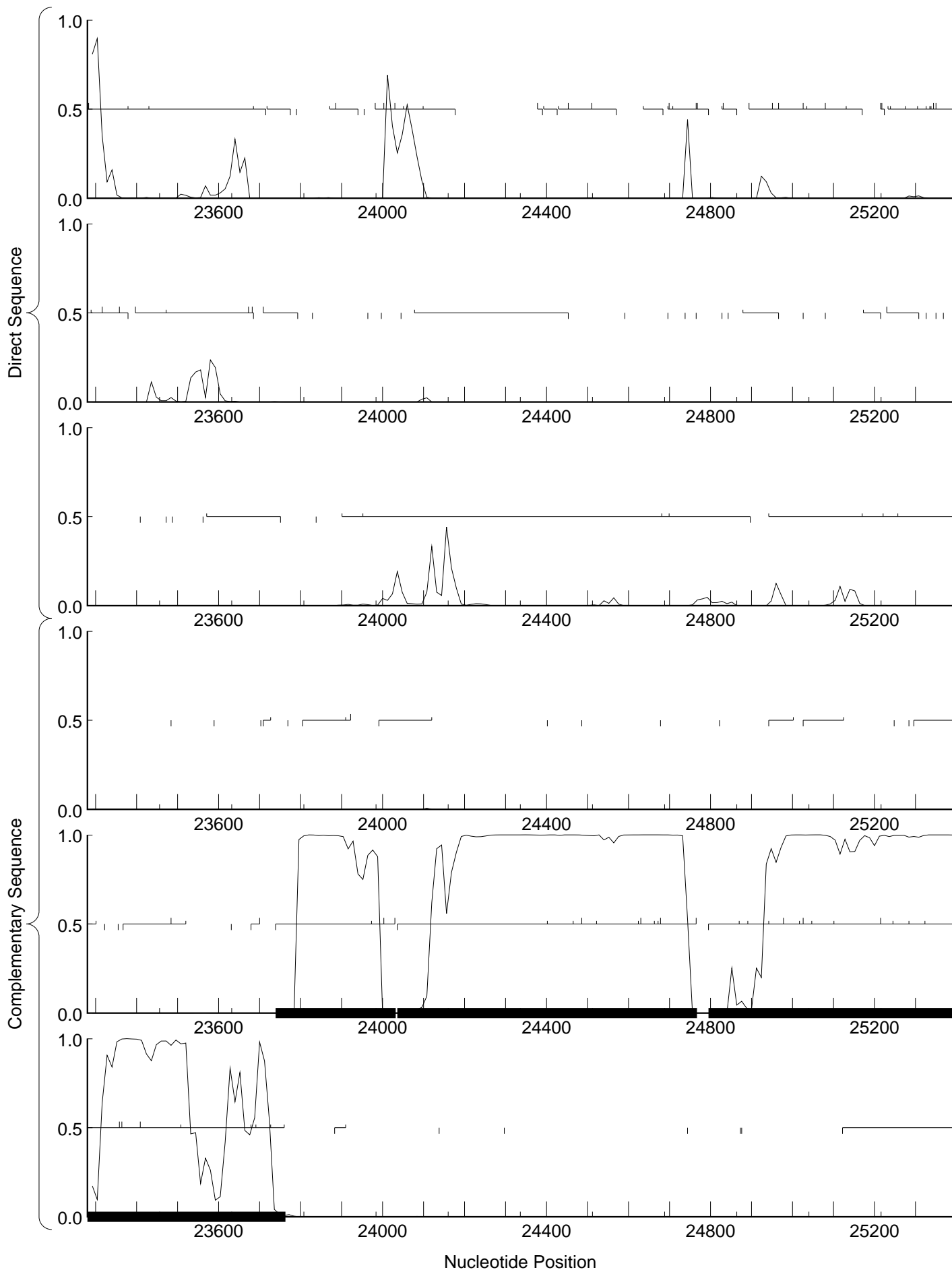


GeneMark.hmm prediction

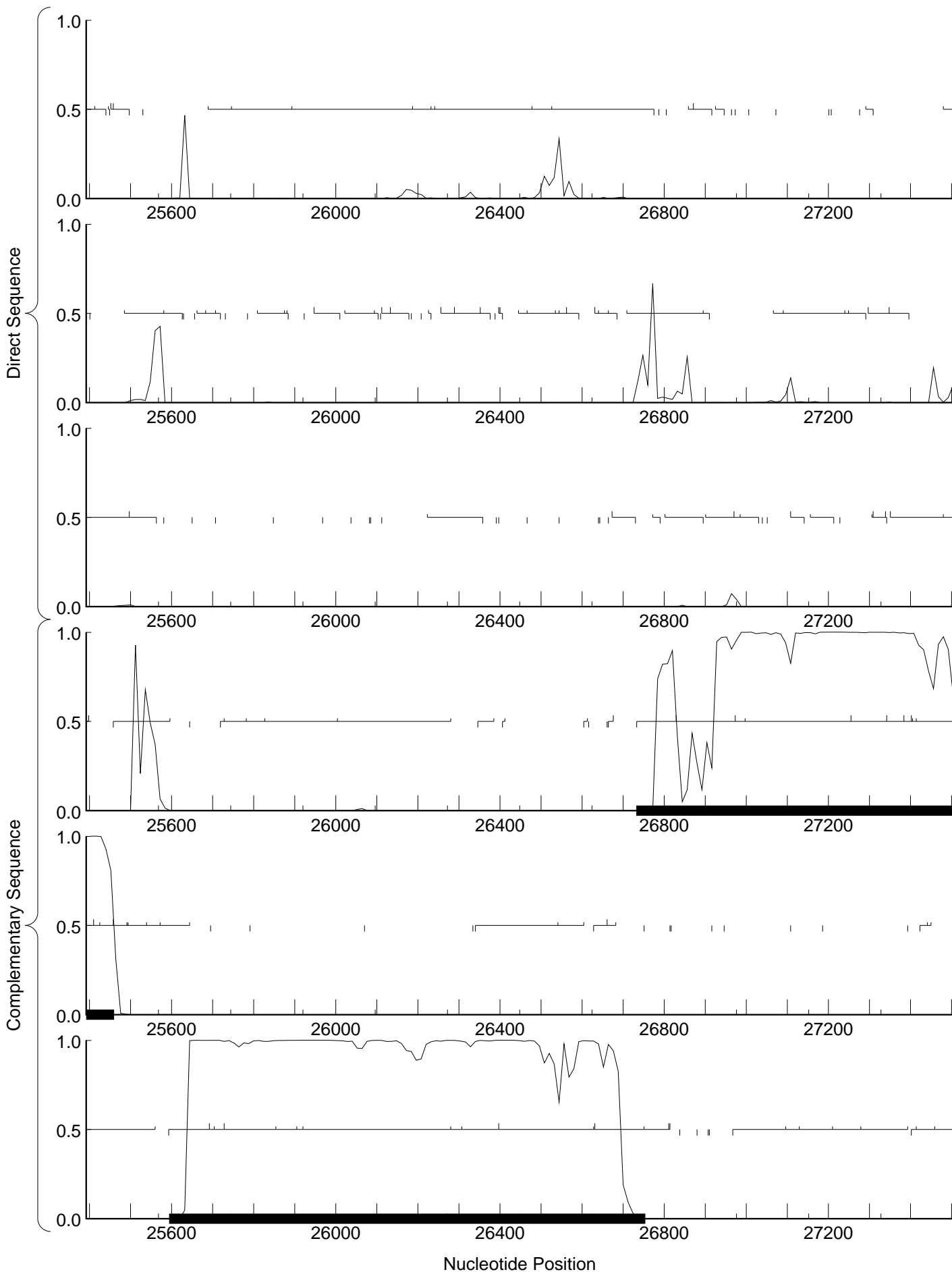




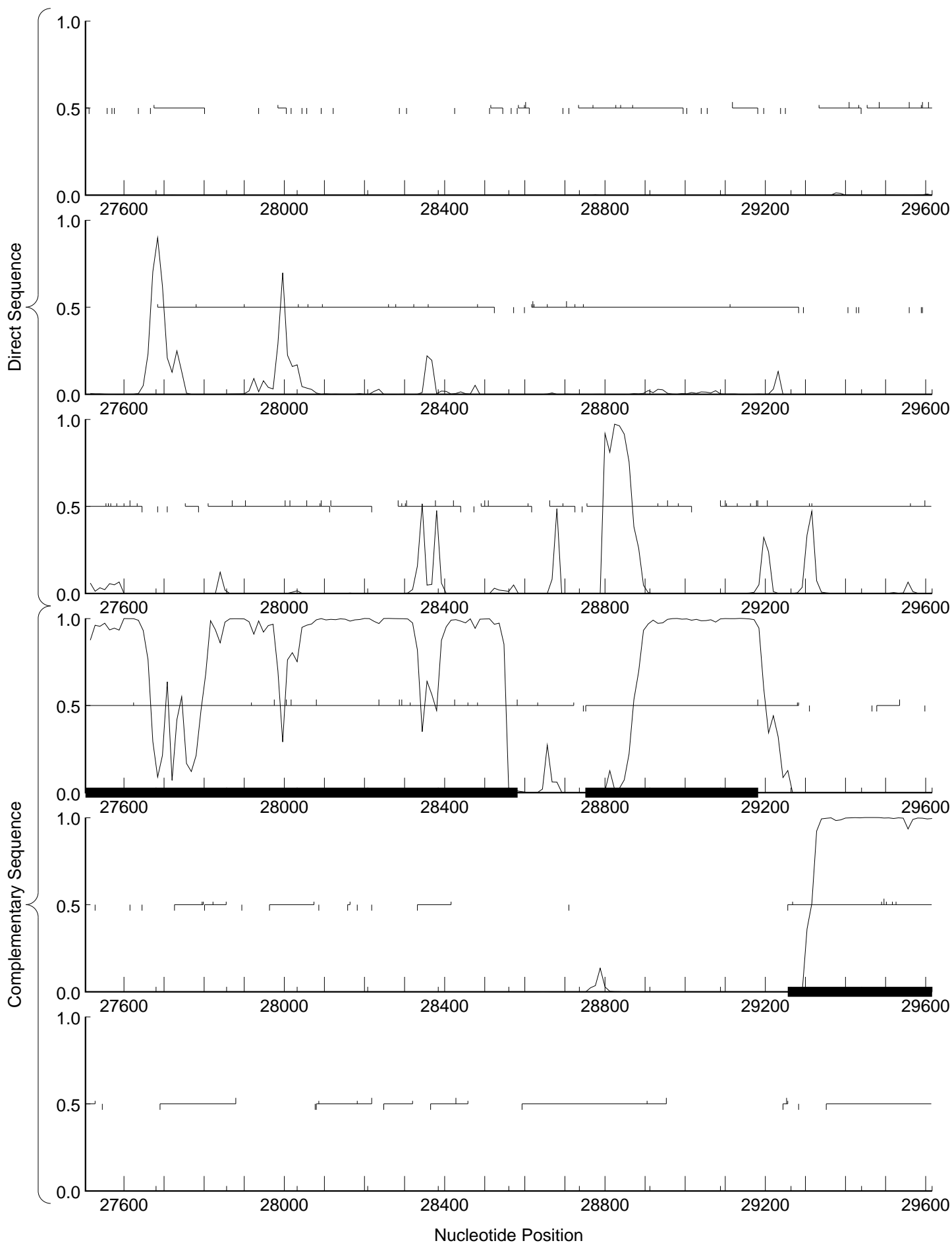




GeneMark.hmm prediction



GeneMark.hmm prediction



GeneMark.hmm prediction

