

# GeneMark

Version 2.5p (09.08.06)

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## PROGRAM INFORMATION

Sequence : Mycobacterium phage Rubeelu complete sequence, 41491 bp including 13-base 3' overhang (CCCG)  
Analysis Date : 5/22/18 at 9:40:28  
Pages : 21  
Sequence Length : 41491 bp  
GC Content : 65.82%

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,

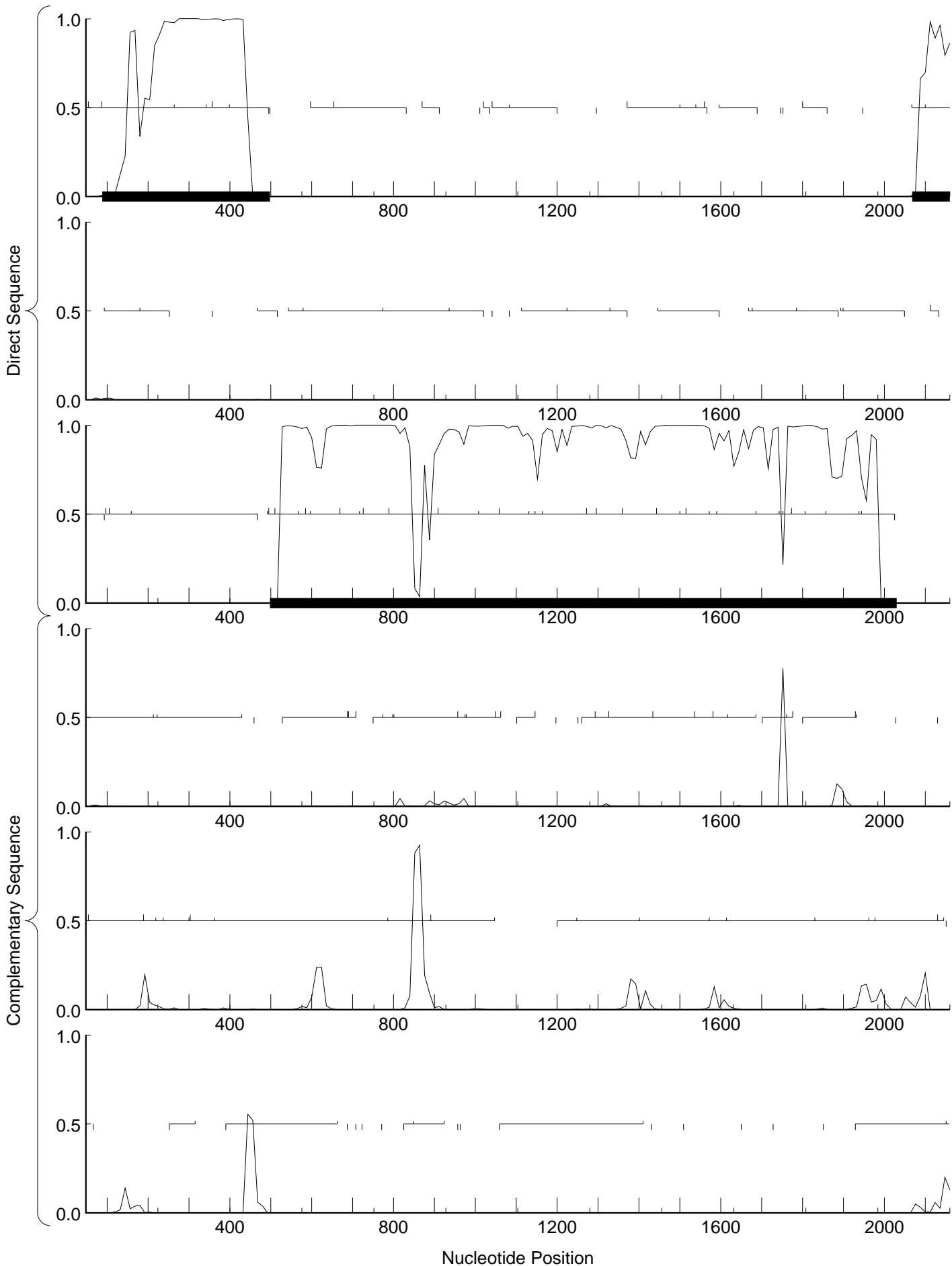
## Matrix notes & comments

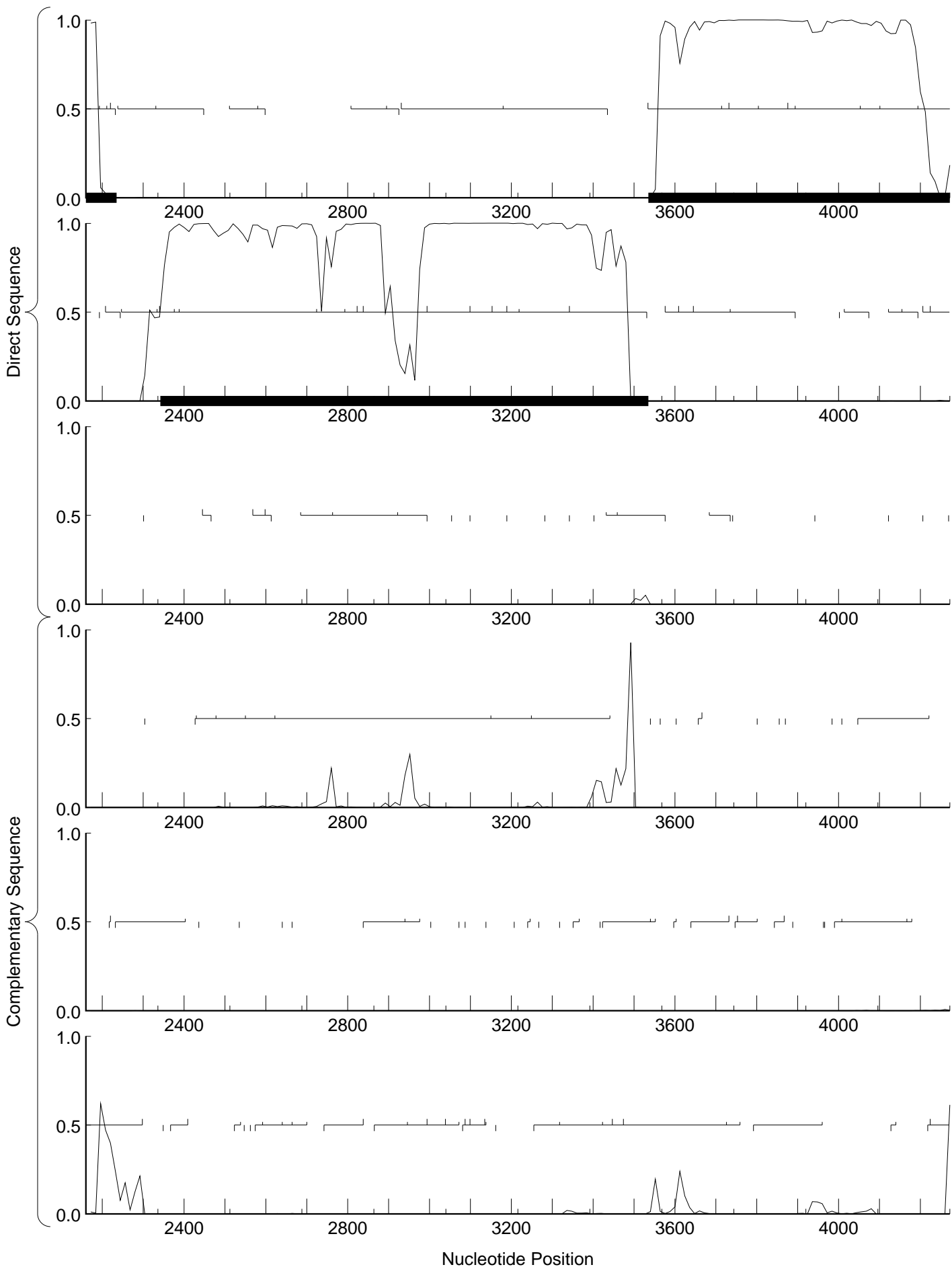
For details on the model building procedure see:  
Besemer J. and Borodovsky M.  
"Heuristic approach to deriving models for gene finding"  
NAR, 1999, Vol. 27, No. 19, pp. 3911-3920

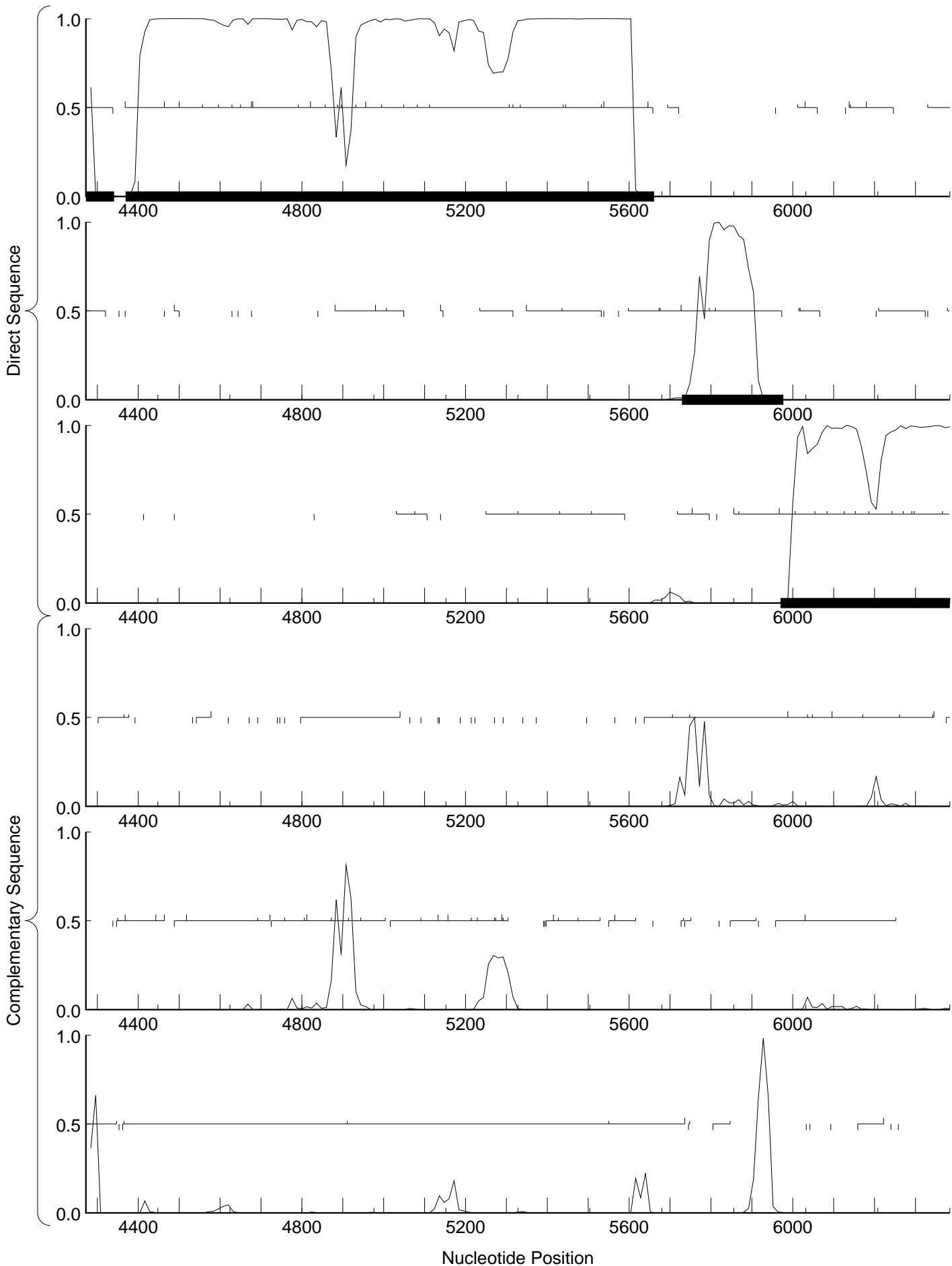
## MATRIX INFORMATION

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

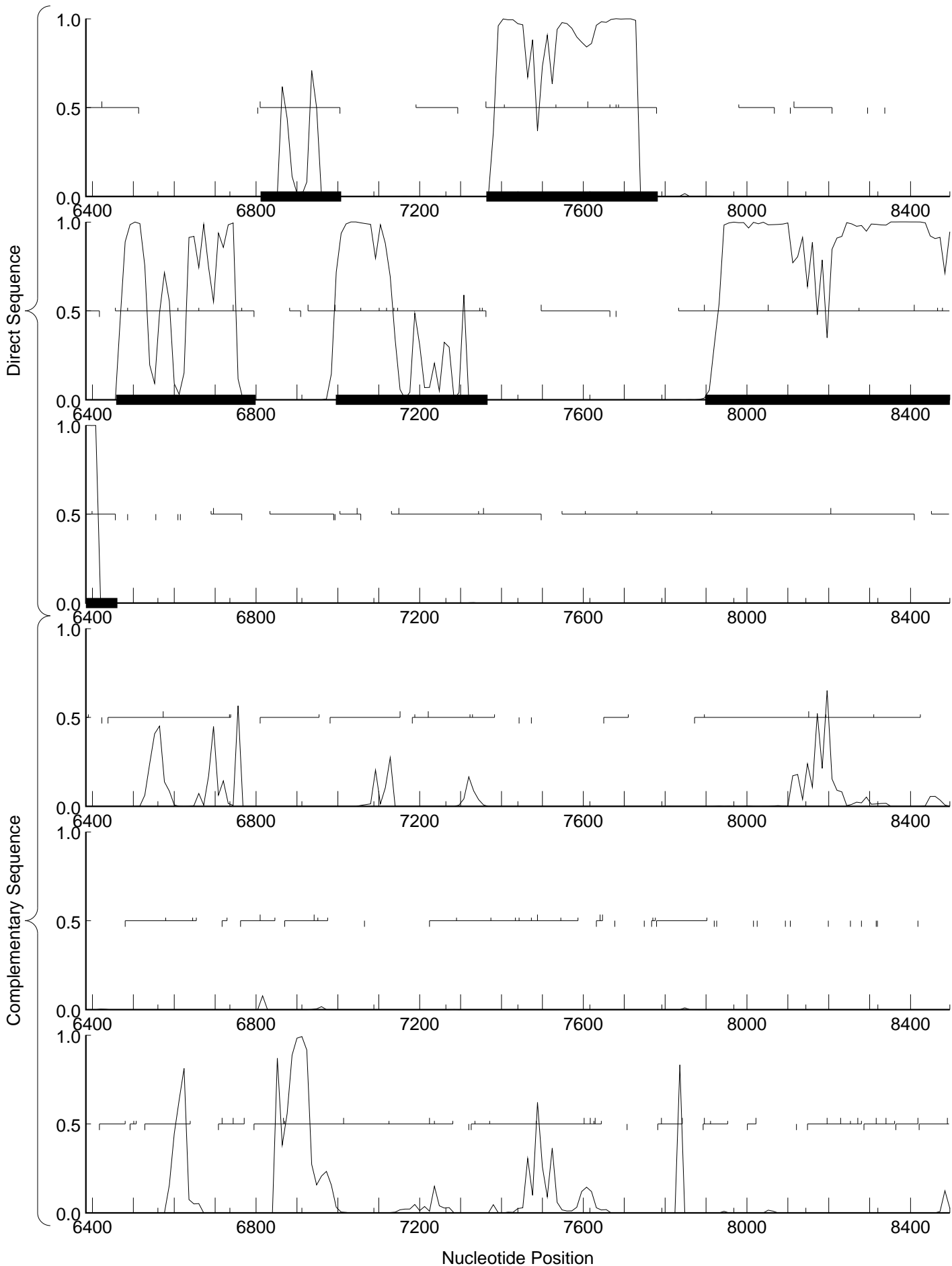
Send questions / comments to:  
Dr. M. Borodovsky  
Georgia Institute of Technology  
School of Biology  
Atlanta, GA 30332-0230

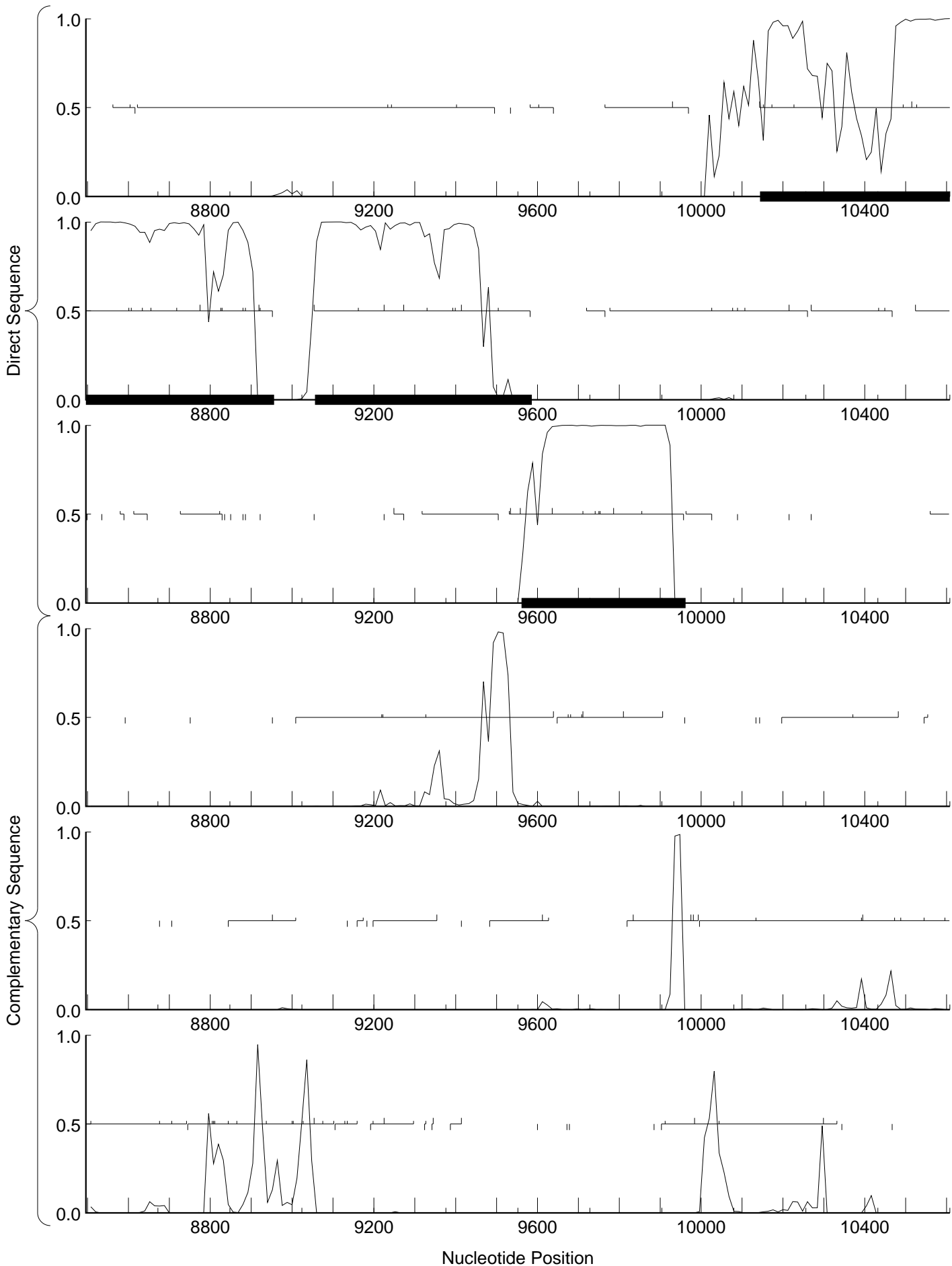






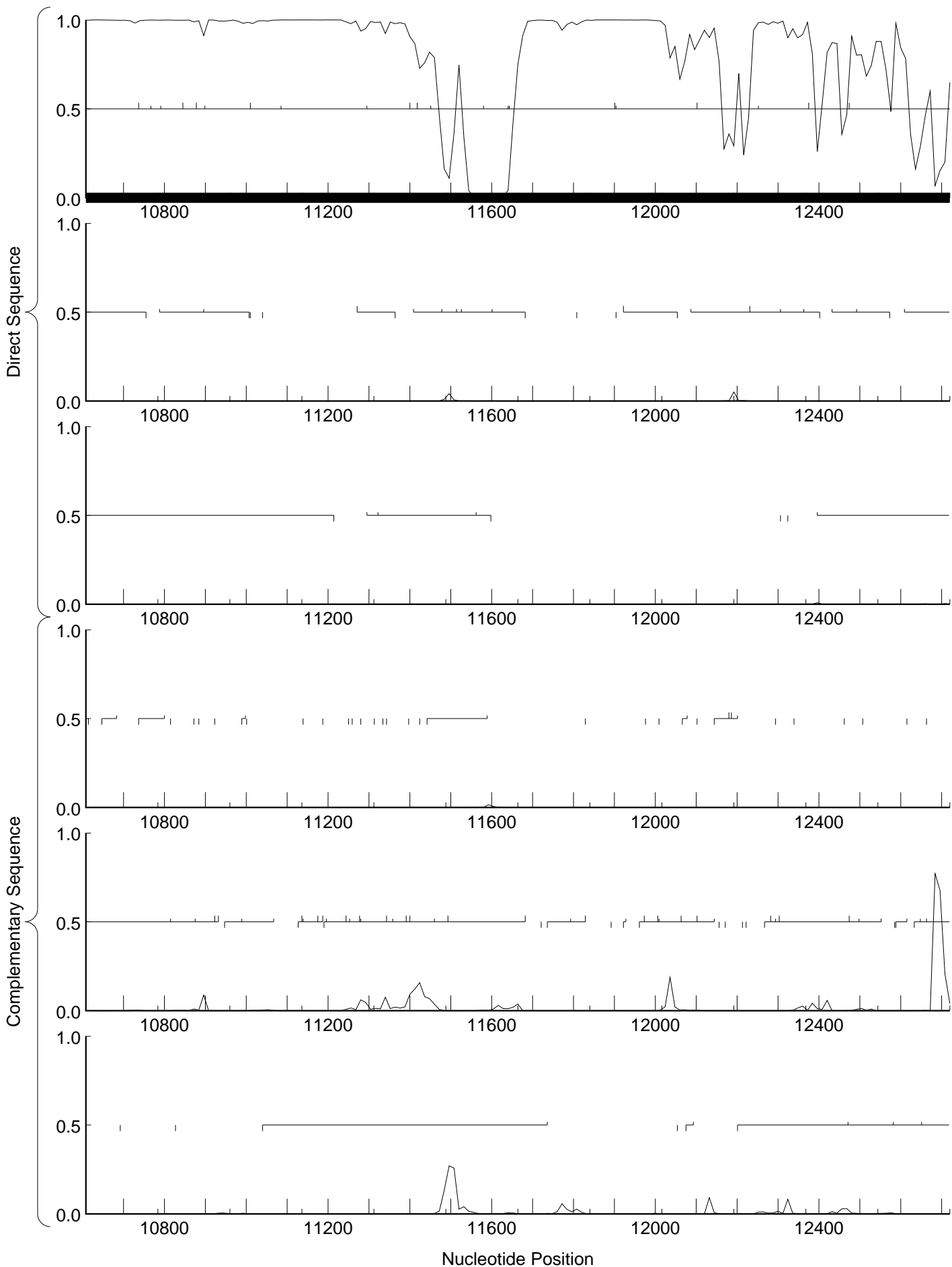
GeneMark\_hmm prediction



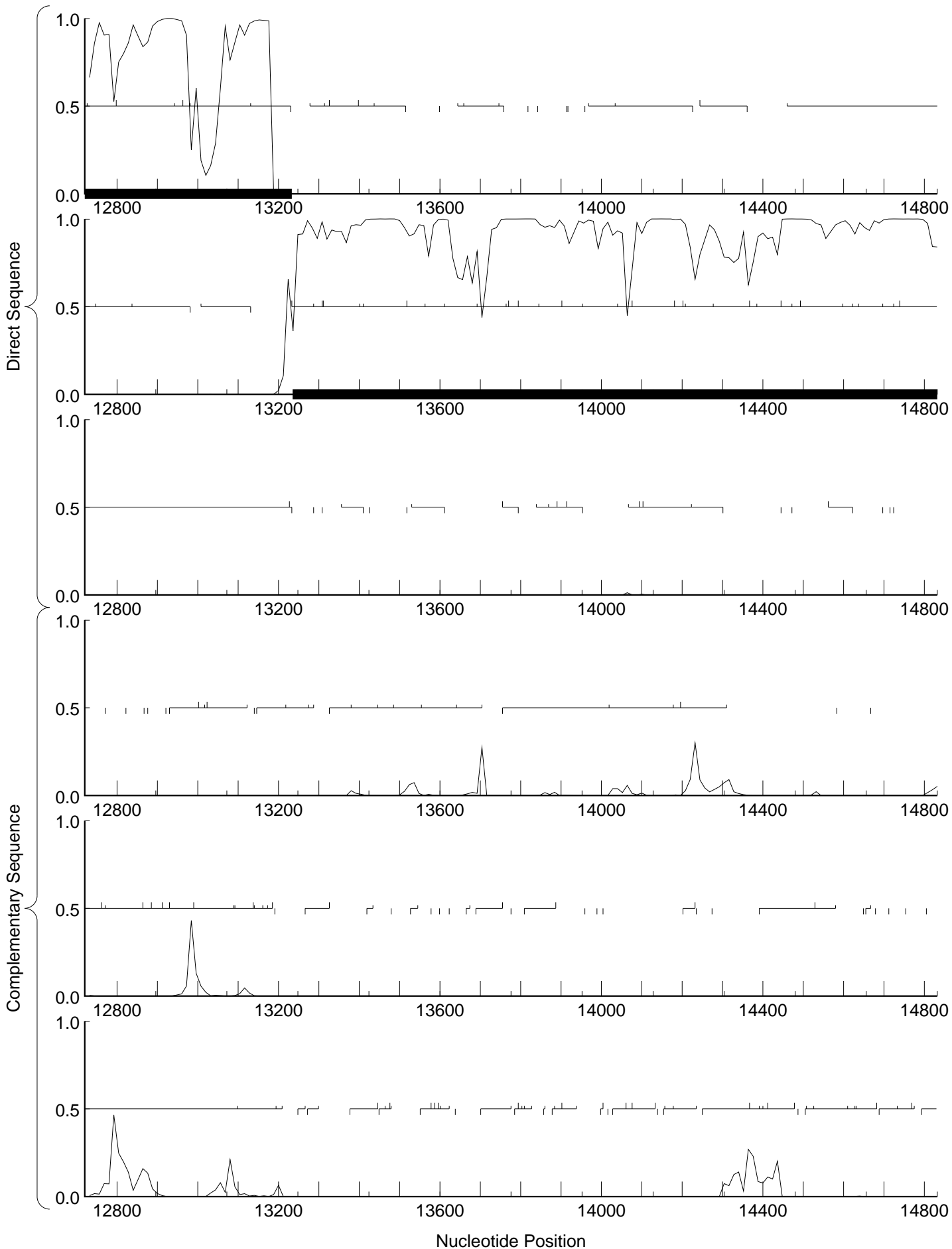


complete sequence, 41491 bp including 13-base 3' overhang (CCCGCCGCCCTCG), Cluster N, Order 2, Window 96, Step 12, 7/21

GeneMark\_hmm prediction



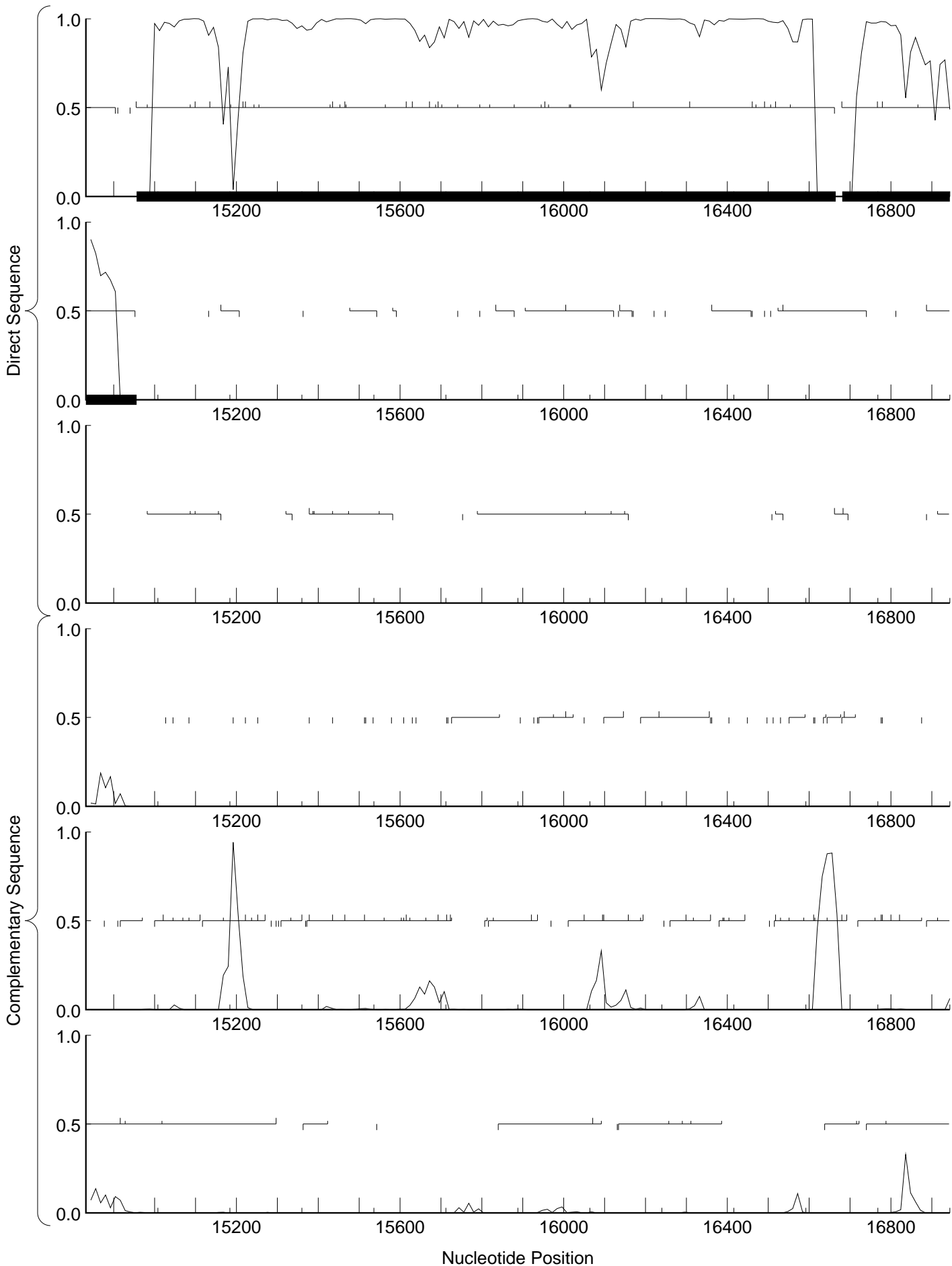
GeneMark\_hmm prediction



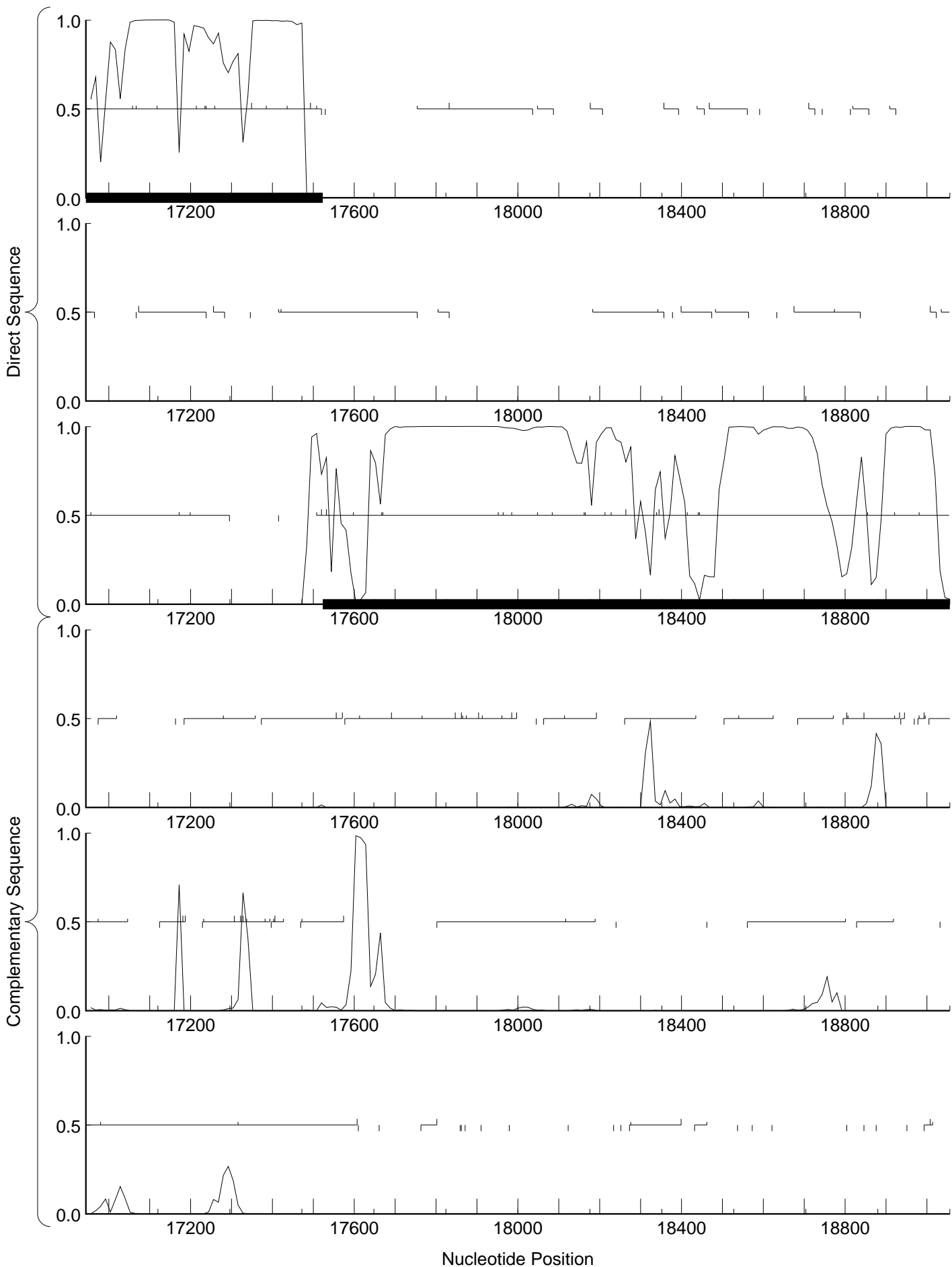


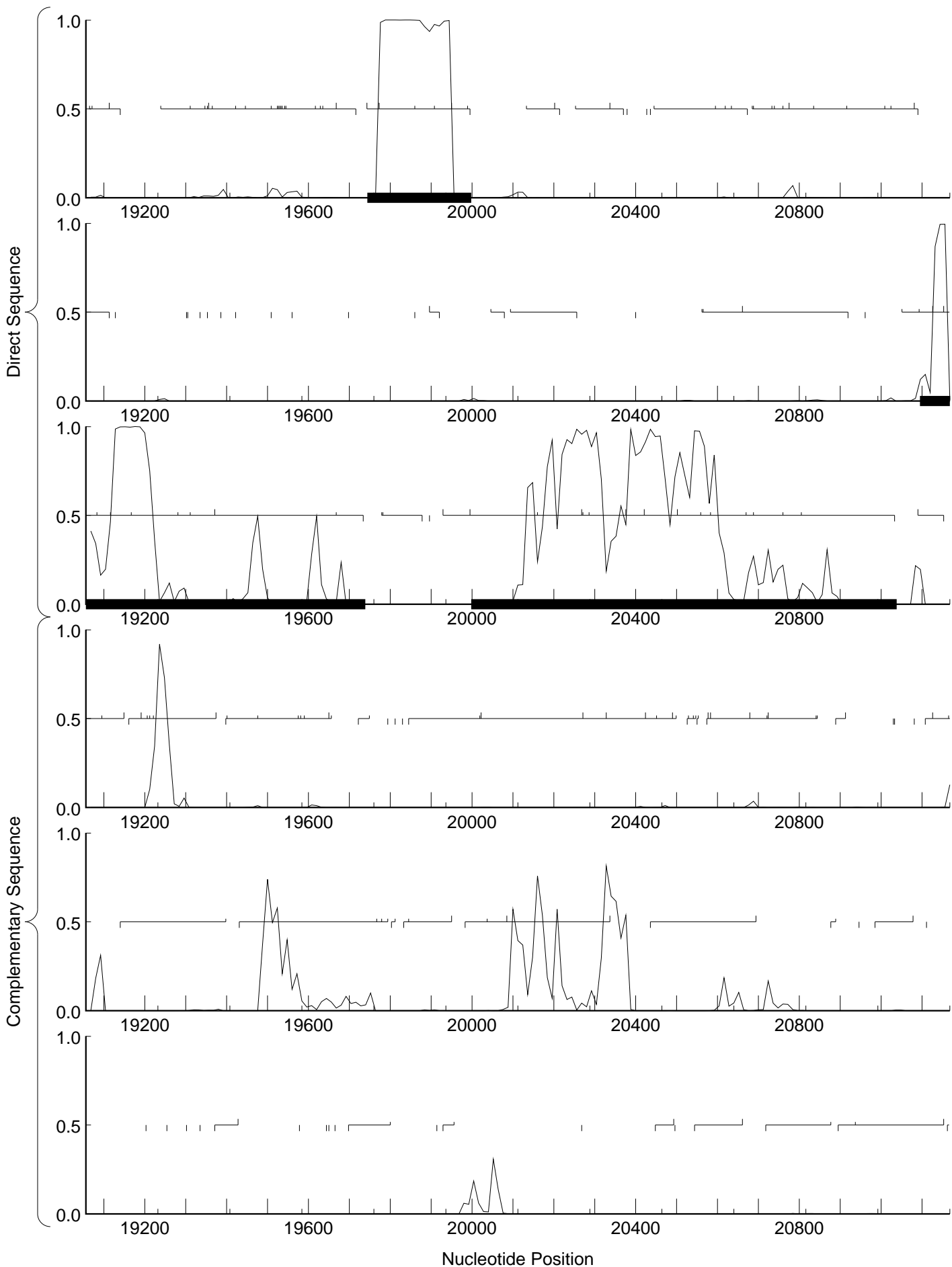
complete sequence, 41491 bp including 13-base 3' overhang (CCCGCCGCCCTCG), Cluster N, Order 2, Window 96, Step 12, 9/21

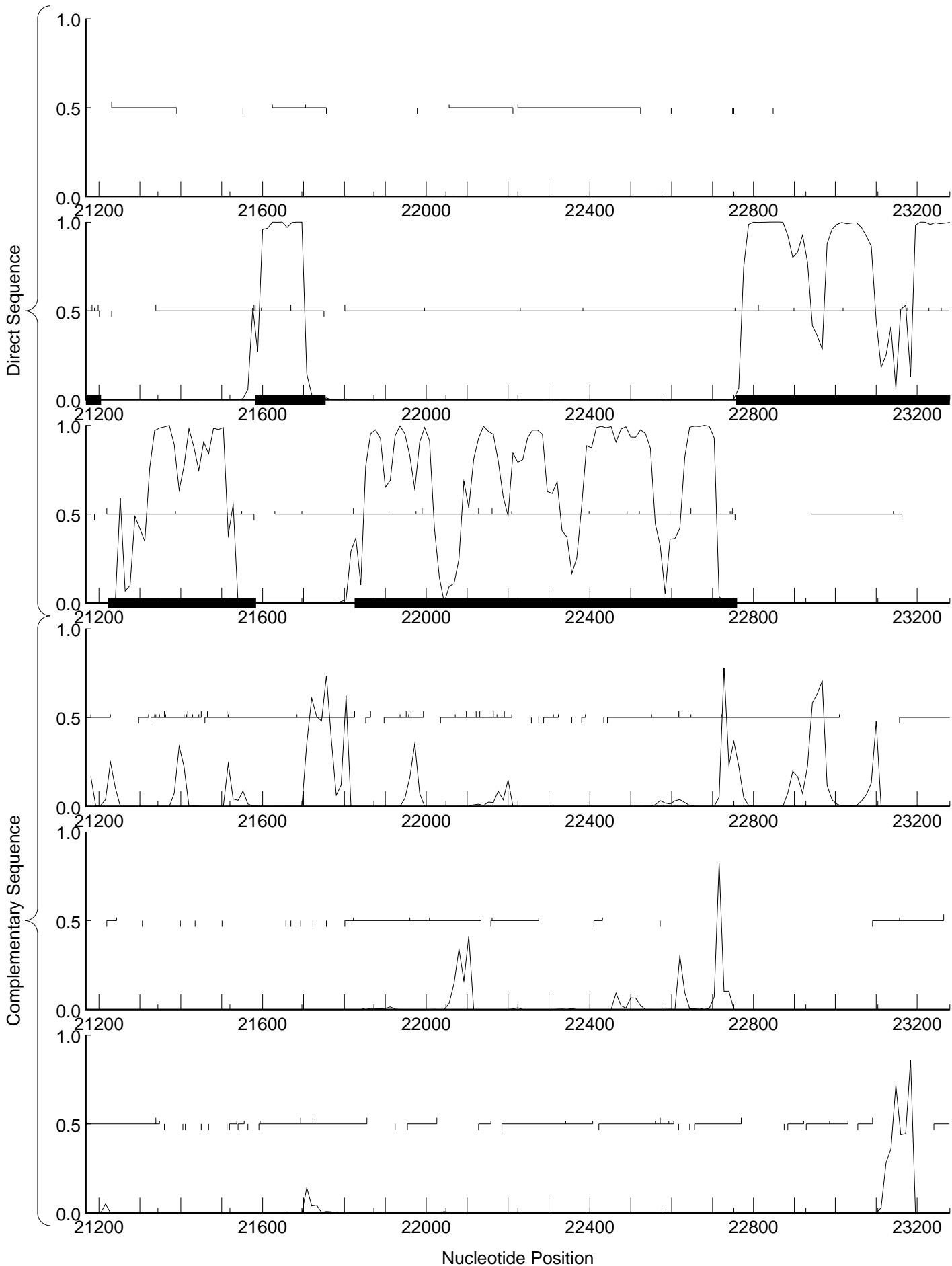
GeneMark\_hmm prediction



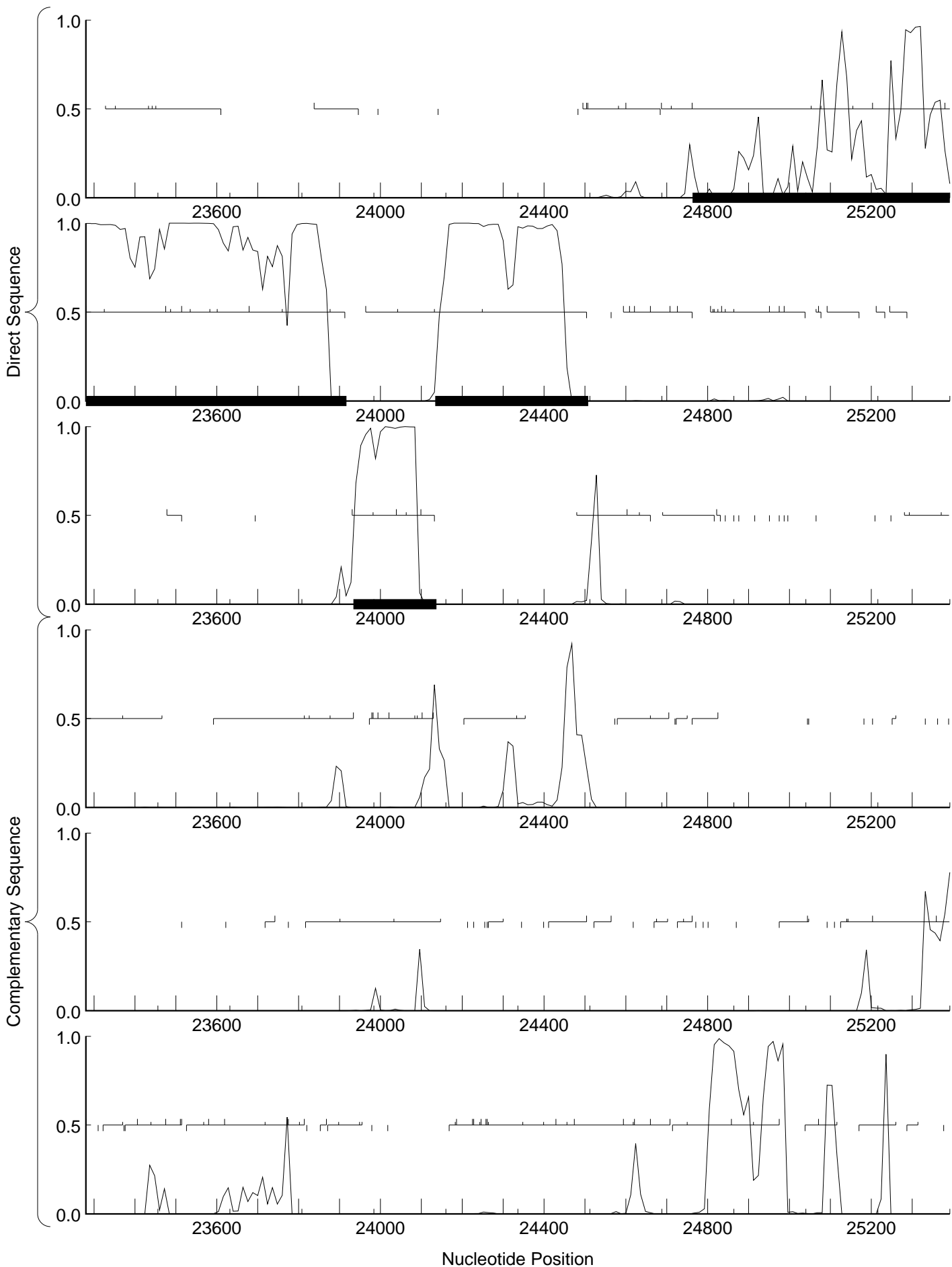
GeneMark.hmm prediction  
complete sequence, 41491 bp including 13-base 3' overhang (CCCGCCGCCCTCG), Cluster N, Order 2, Window 96, Step 12, 10/21



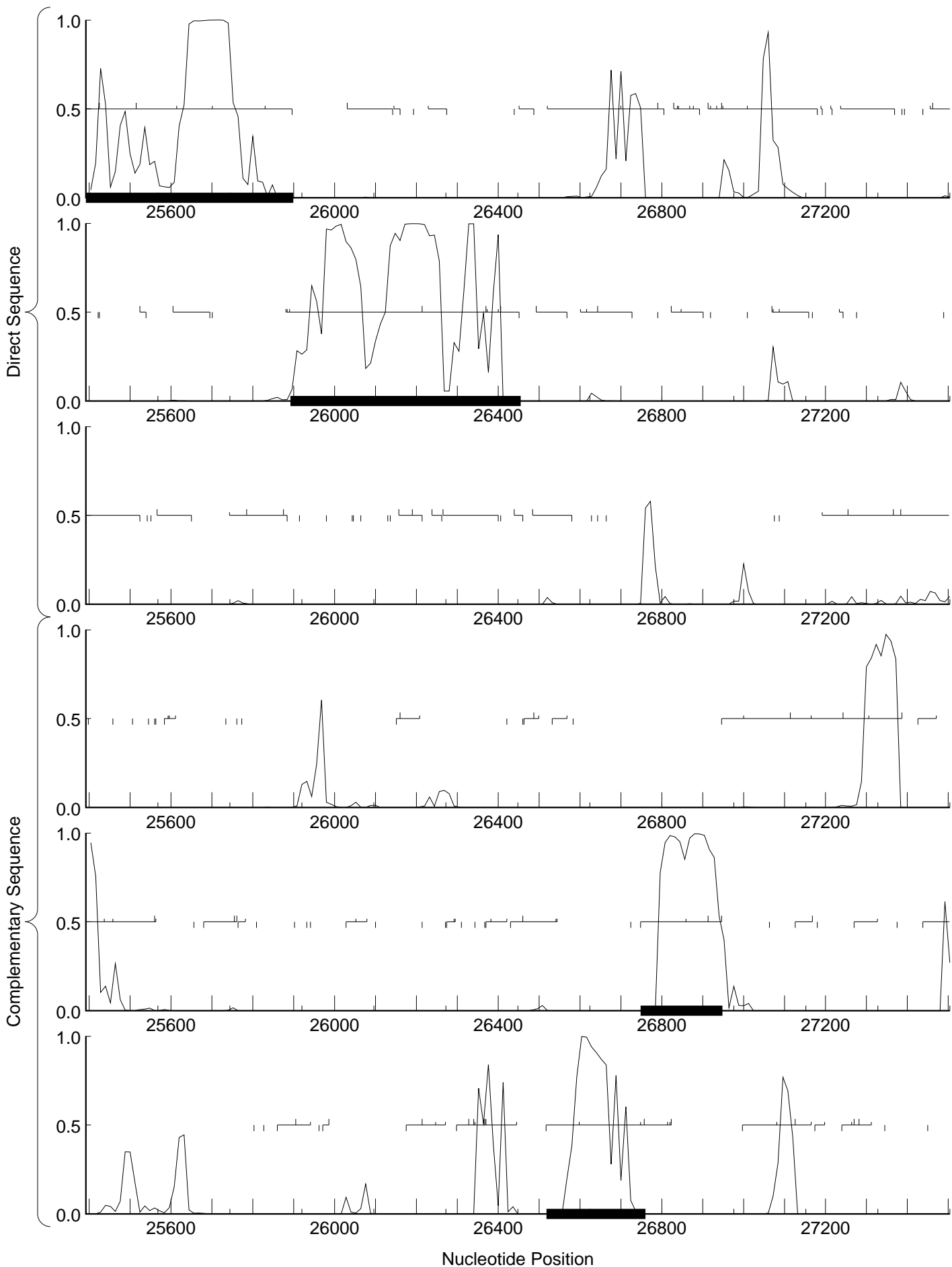




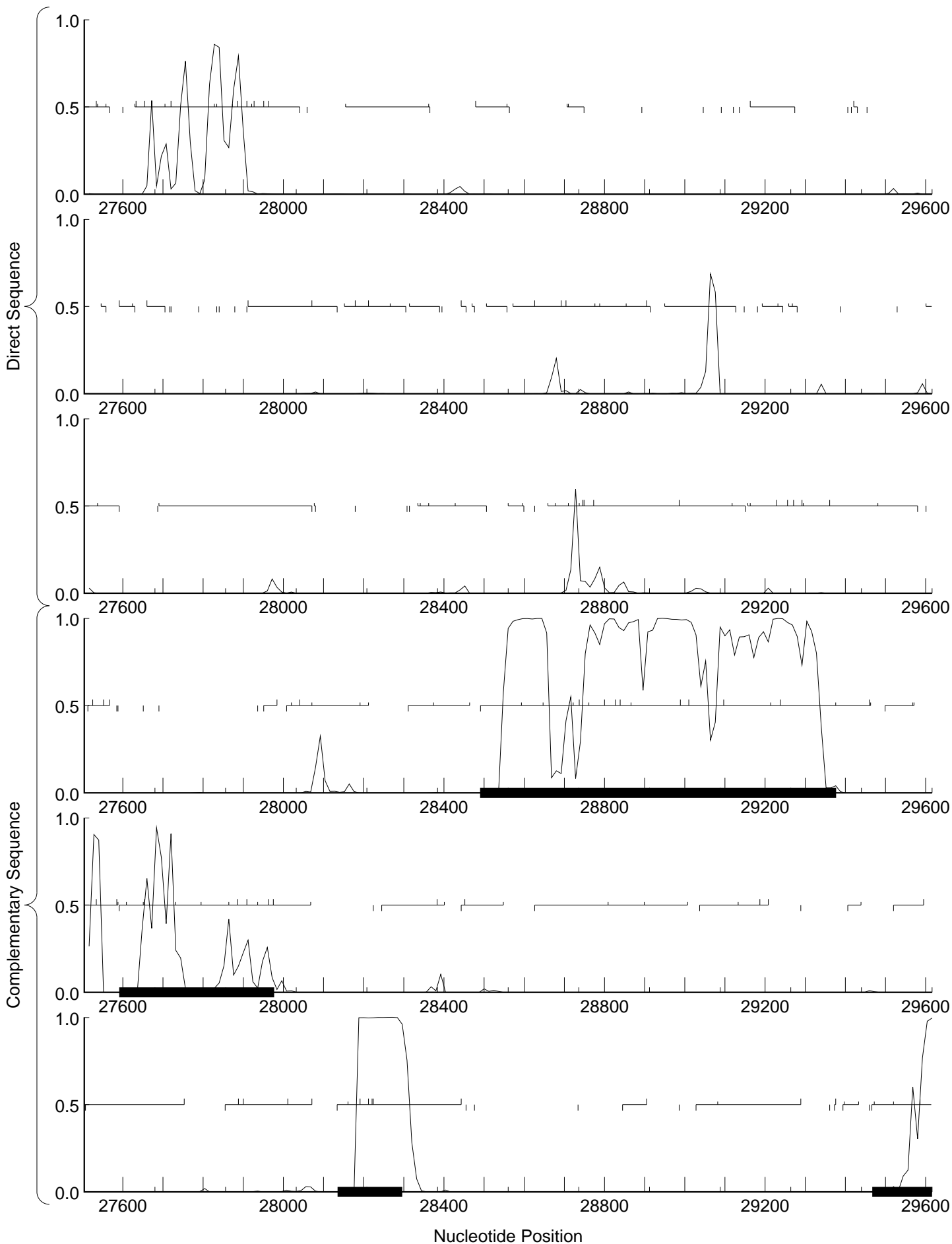
GeneMark.hmm prediction  
complete sequence, 41491 bp including 13-base 3' overhang (CCCGCCGCCCTCG), Cluster N, Order 2, Window 96, Step 12, 13/21



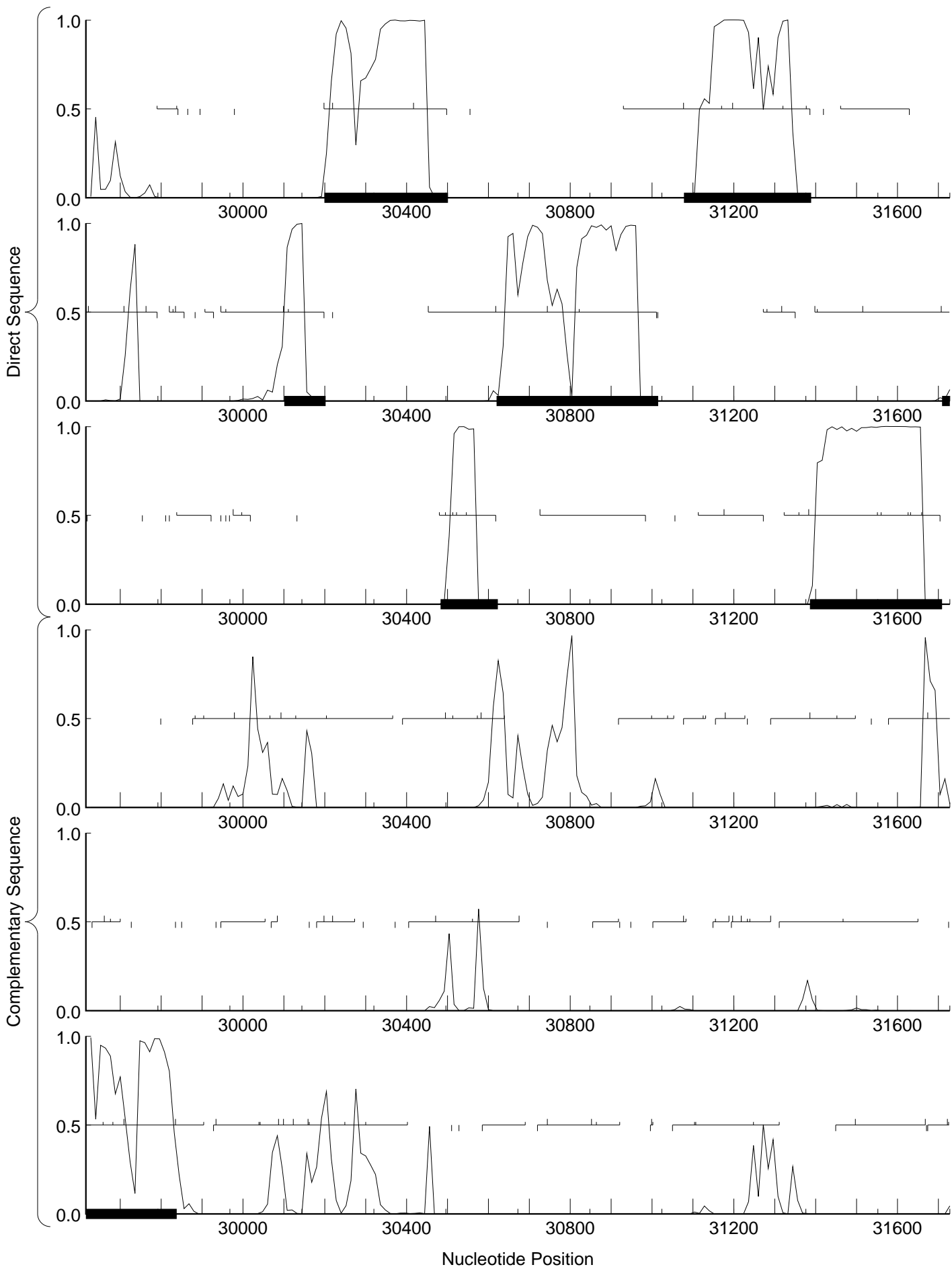
GeneMark.hmm prediction  
complete sequence, 41491 bp including 13-base 3' overhang (CCCGCCGCCCTCG), Cluster N, Order 2, Window 96, Step 12, 14/21



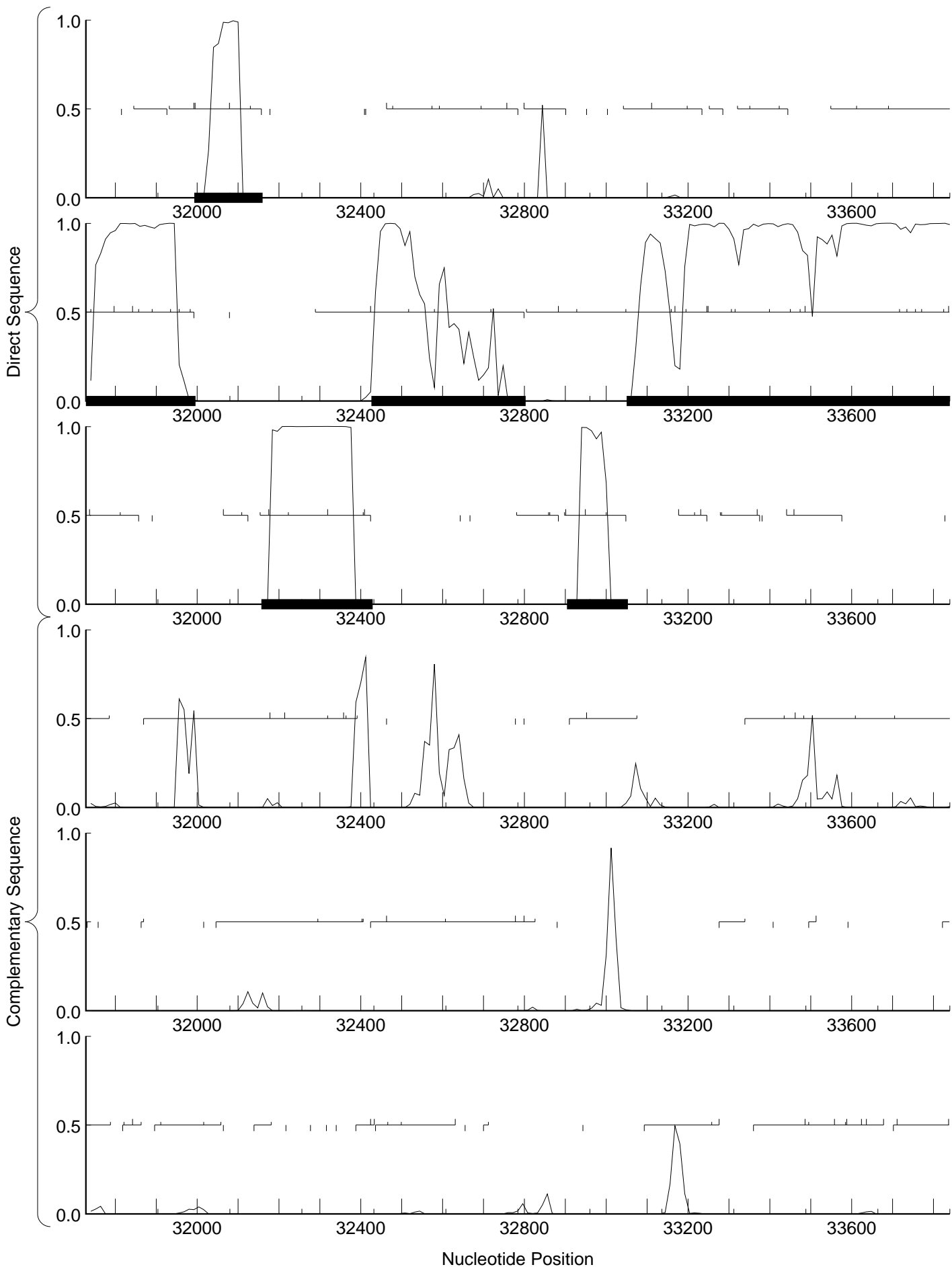
GeneMark.hmm prediction  
complete sequence, 41491 bp including 13-base 3' overhang (CCCGCCGCCCTCG), Cluster N, Order 2, Window 96, Step 12, 15/21



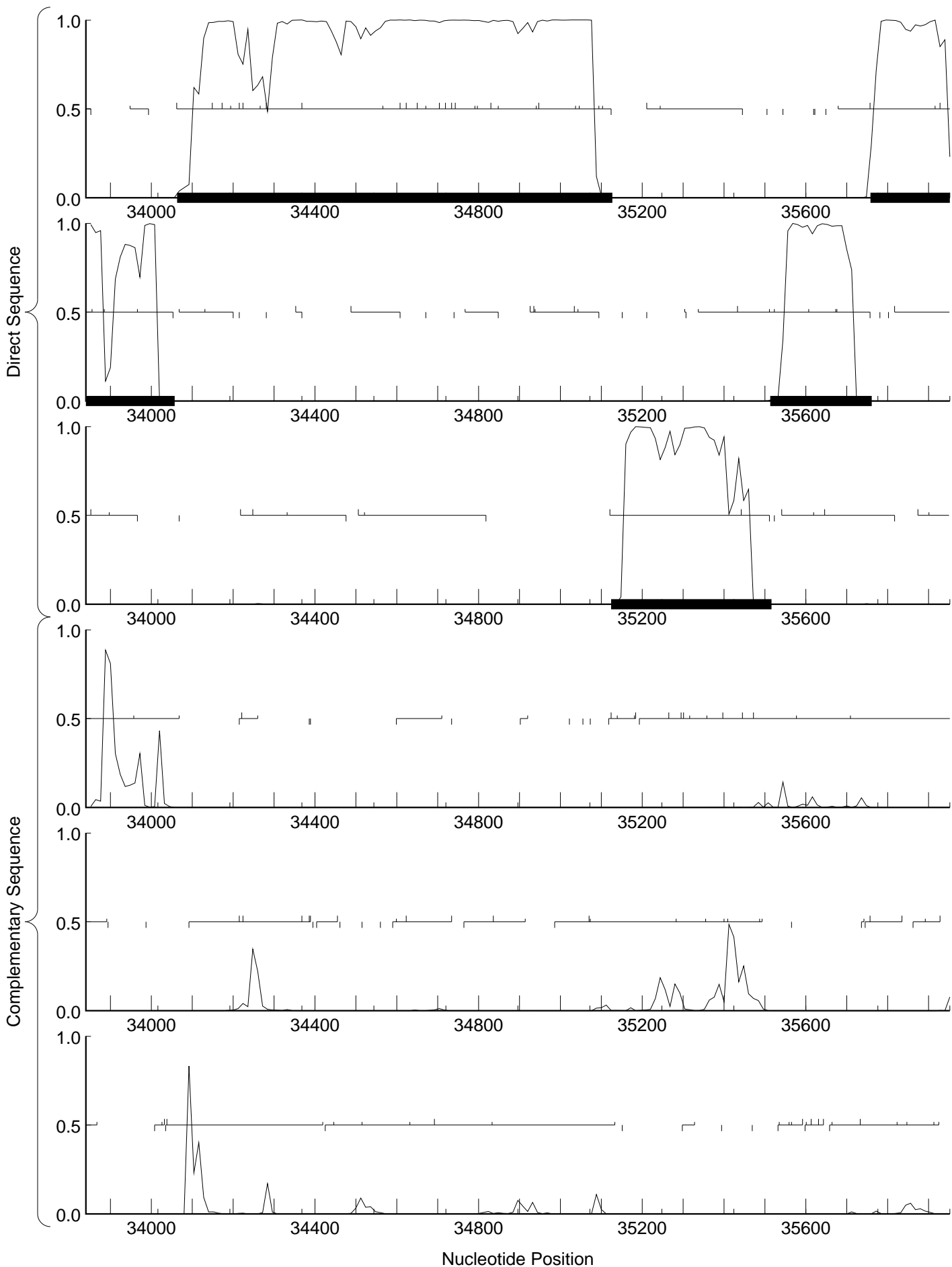
GeneMark.hmm prediction  
complete sequence, 41491 bp including 13-base 3' overhang (CCCGCCGCCCTCG), Cluster N, Order 2, Window 96, Step 12, 16/21

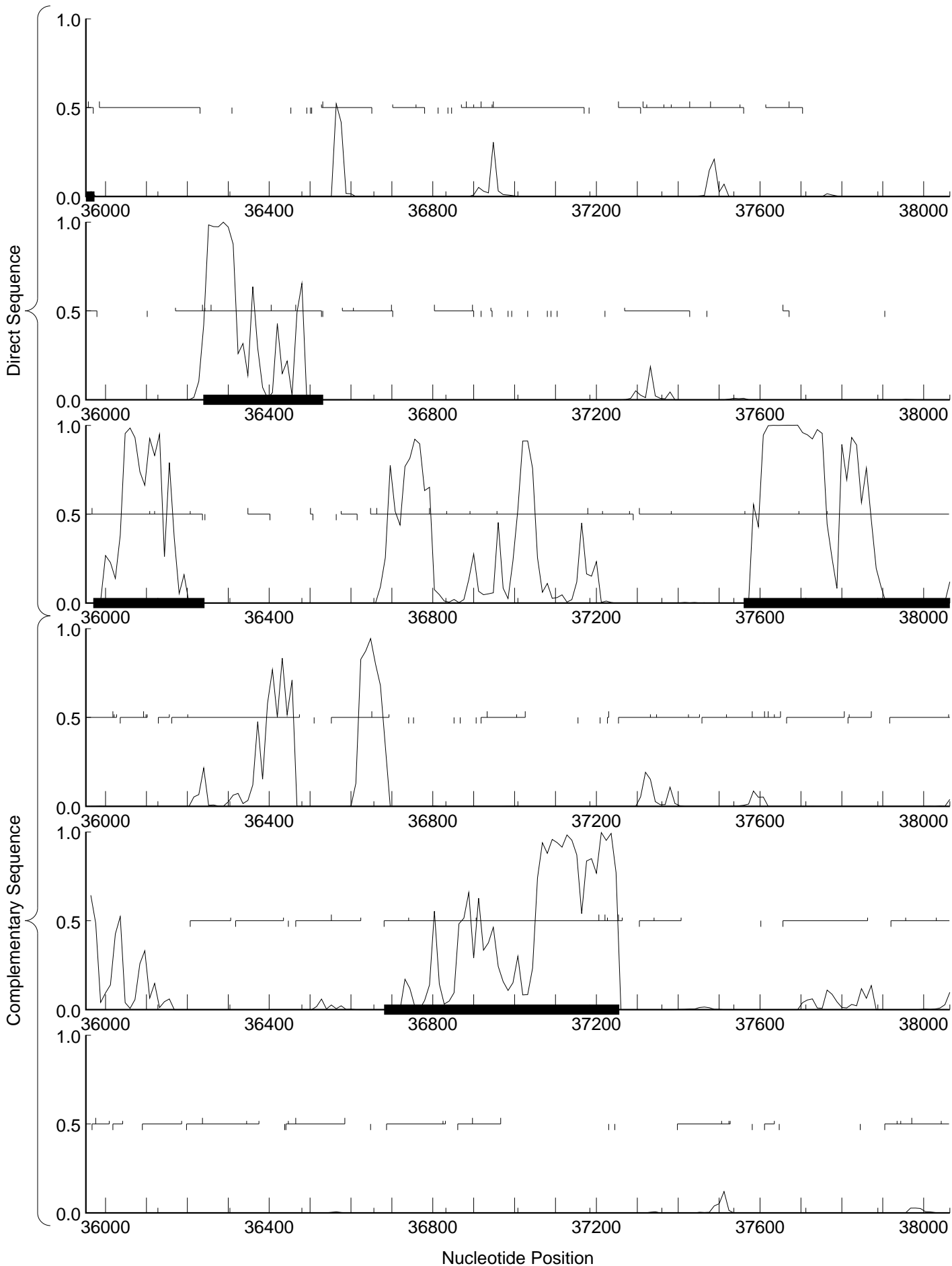


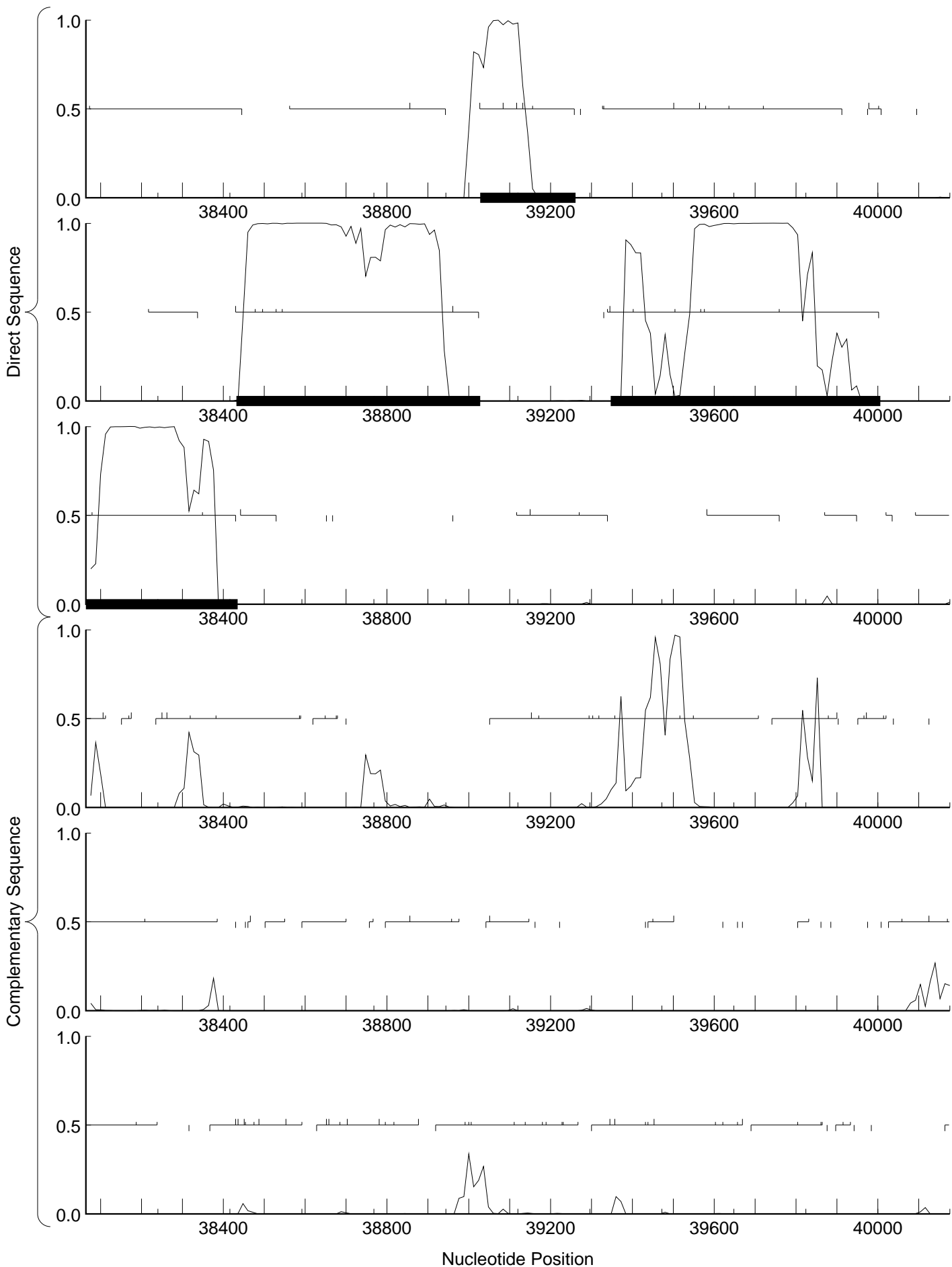




GeneMark.hmm prediction  
complete sequence, 41491 bp including 13-base 3' overhang (CCCGCCGCCCTCG), Cluster N, Order 2, Window 96, Step 12, 18/21







GeneMark.hmm prediction  
complete sequence, 41491 bp including 13-base 3' overhang (CCCGCCGCCCTCG), Cluster N, Order 2, Window 96, Step 12, 21/21

