

GeneMark

Version 2.5p (09.08.06)

Copyright 1993 - M. Borodovsky, J. McIninch

PROGRAM INFORMATION

Sequence : Mycobacterium phage Purgamenstris complete sequence, 42595 bp including 13-base 3' overhang
Analysis Date : 7/17/18 at 21:22:30
Pages : 22
Sequence Length : 42595 bp
GC Content : 66.14%

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,

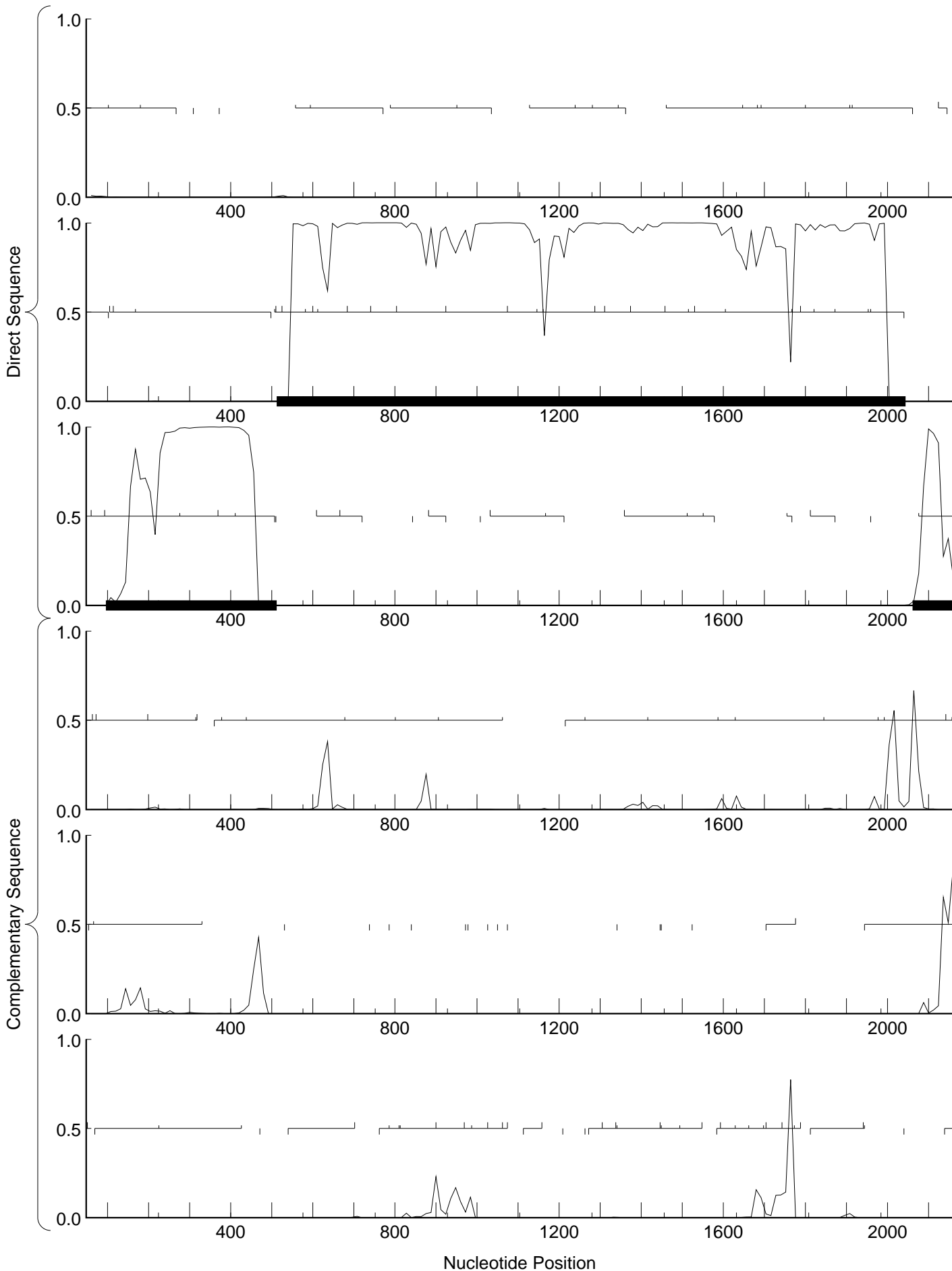
MATRIX INFORMATION

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

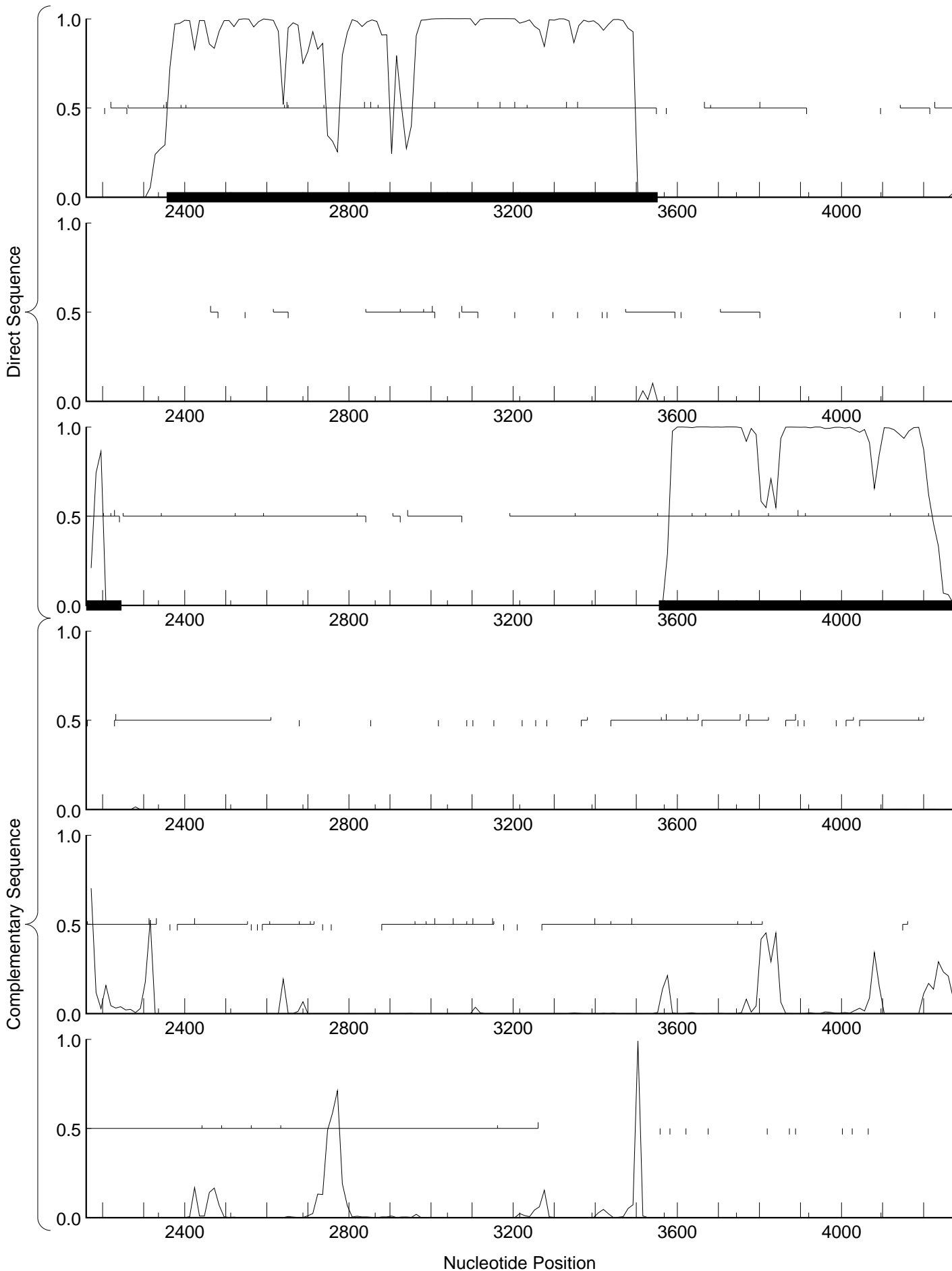
Send questions / comments to:
Dr. M. Borodovsky
Georgia Institute of Technology
School of Biology
Atlanta, GA 30332-0230

Matrix notes & comments

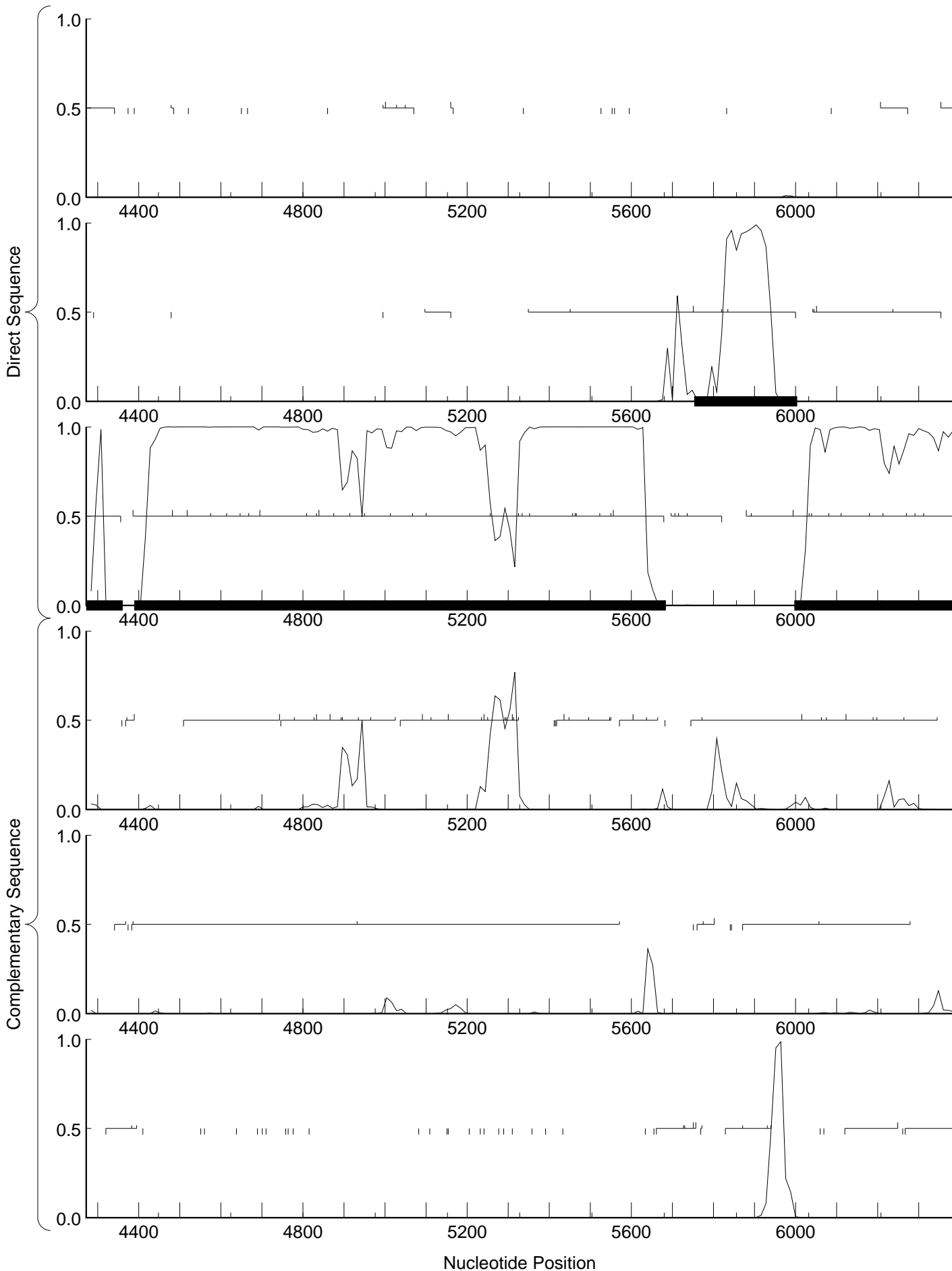
For details on the model building procedure see:
Besemer J. and Borodovsky M.
"Heuristic approach to deriving models for gene finding"
NAR, 1999, Vol. 27, No. 19, pp. 3911-3920



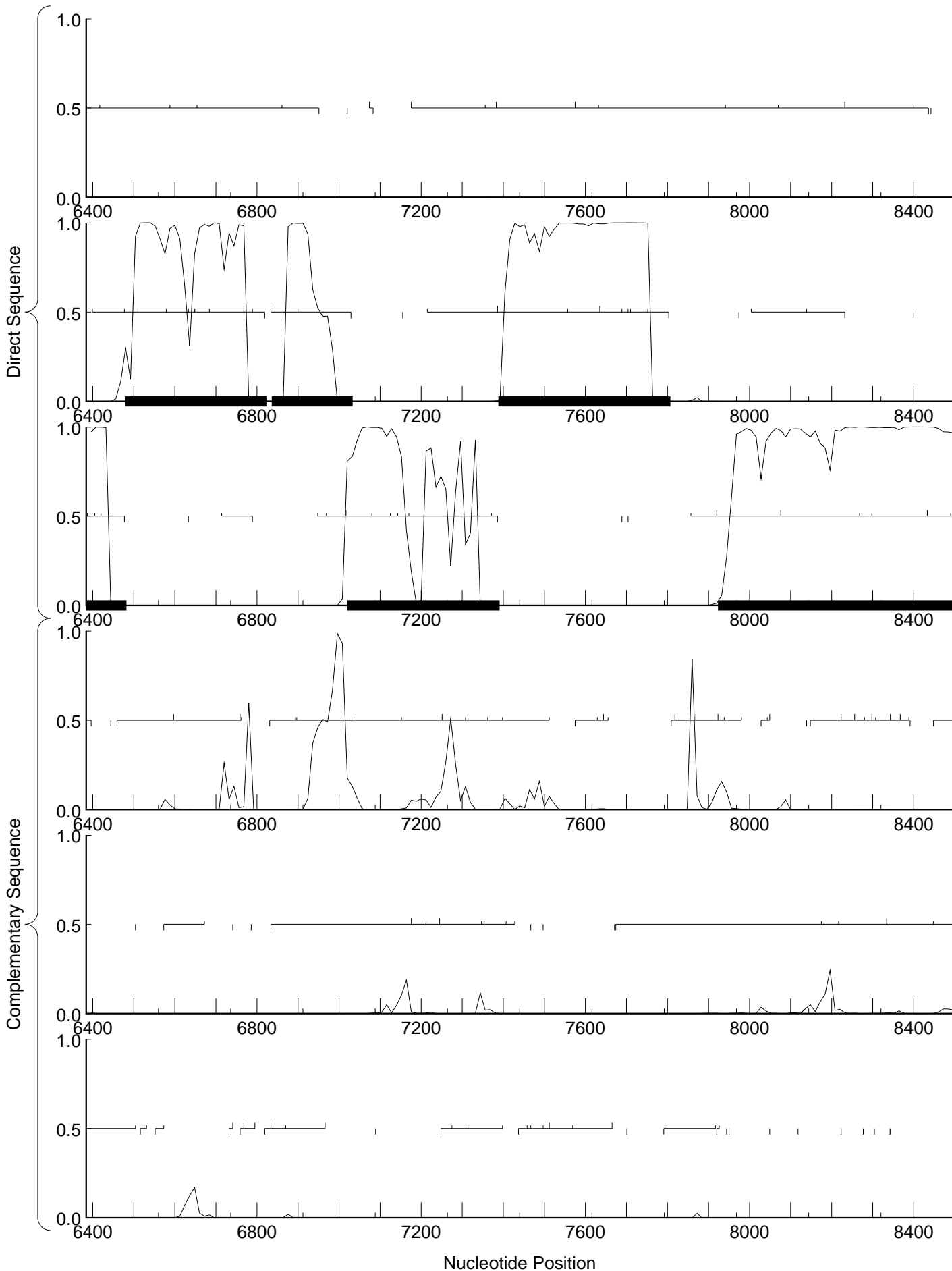
GeneMark.hmm prediction



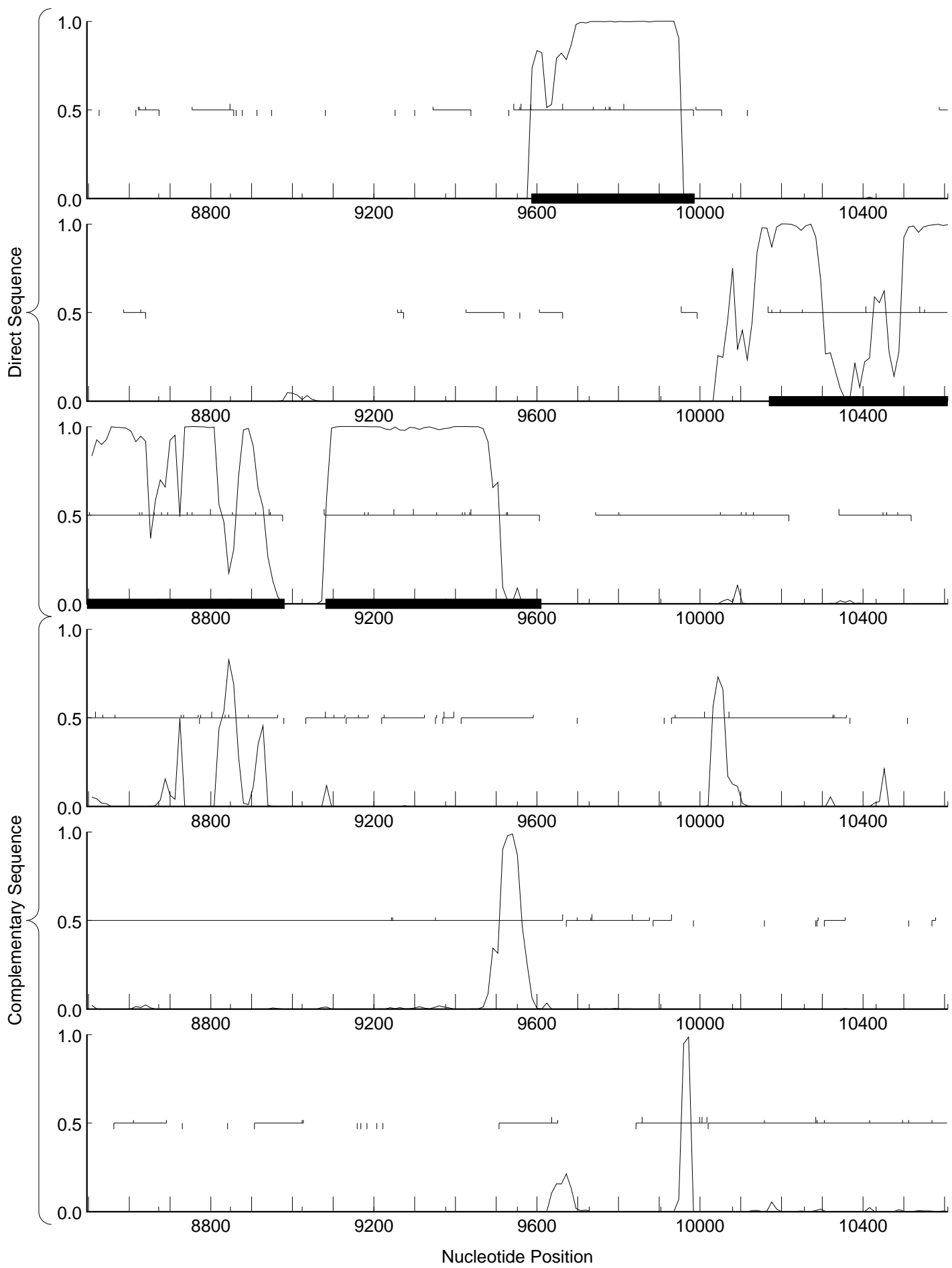
GeneMark.hmm prediction

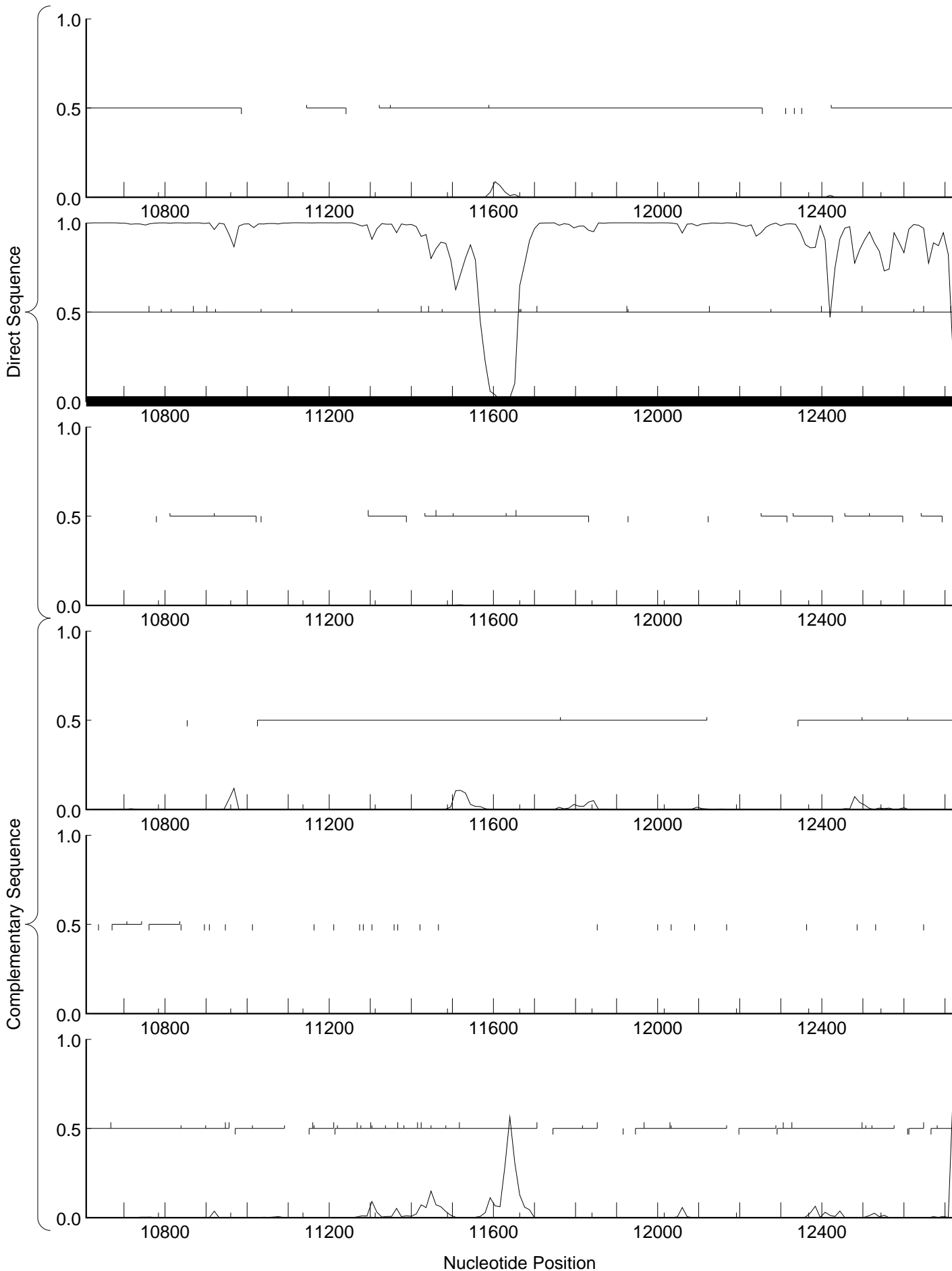


GeneMark_hmm prediction

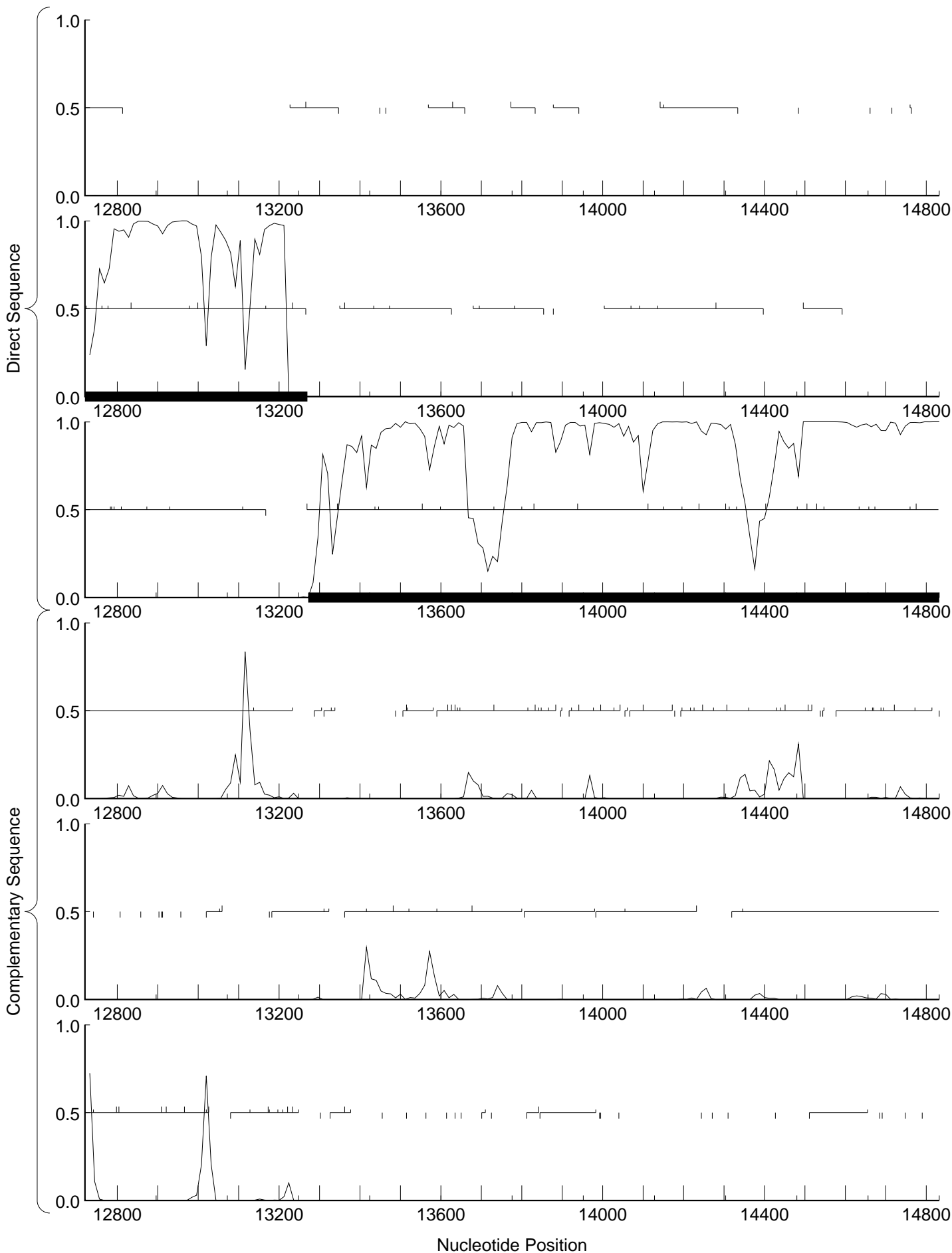


GeneMark.hmm prediction

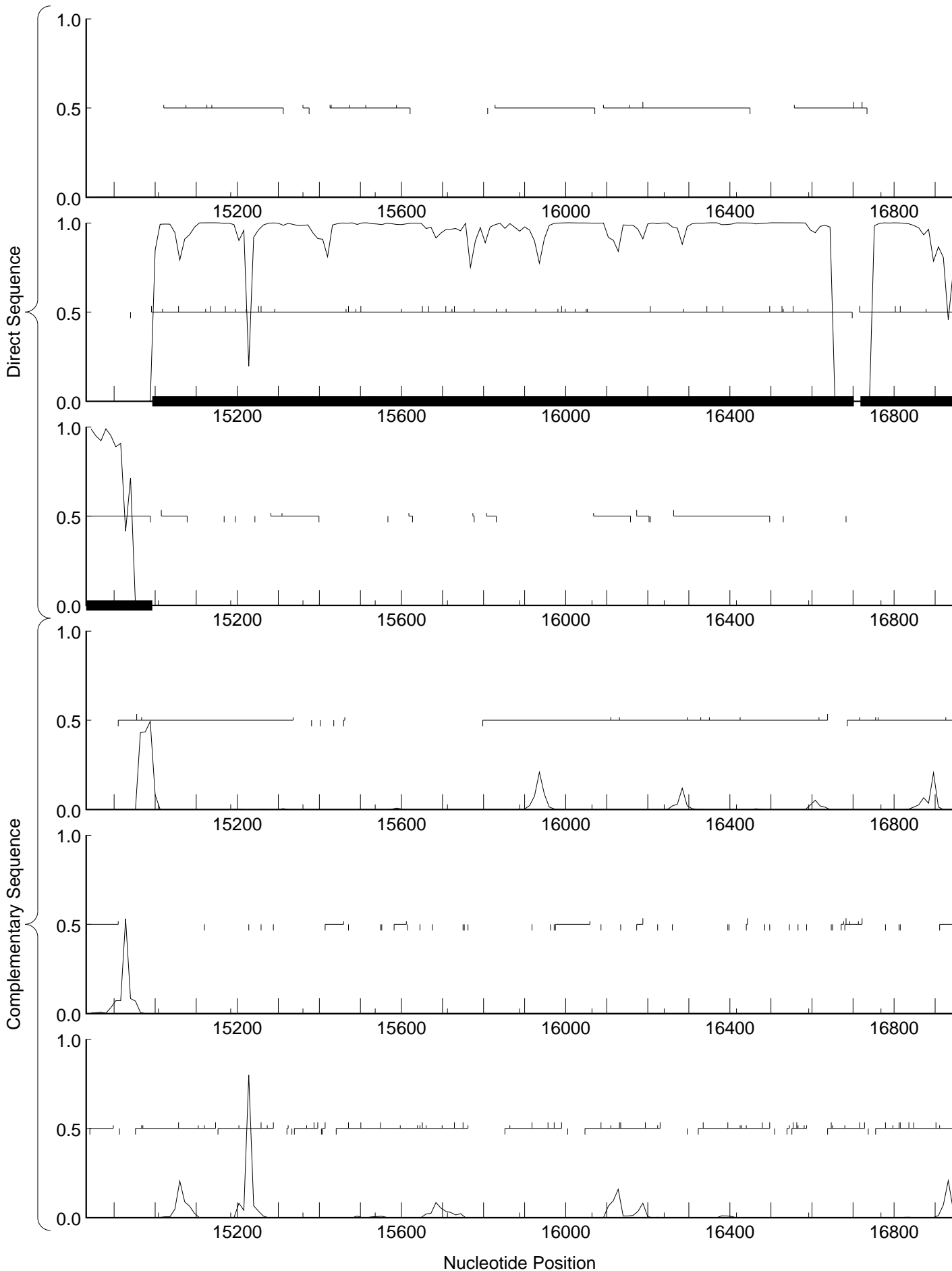


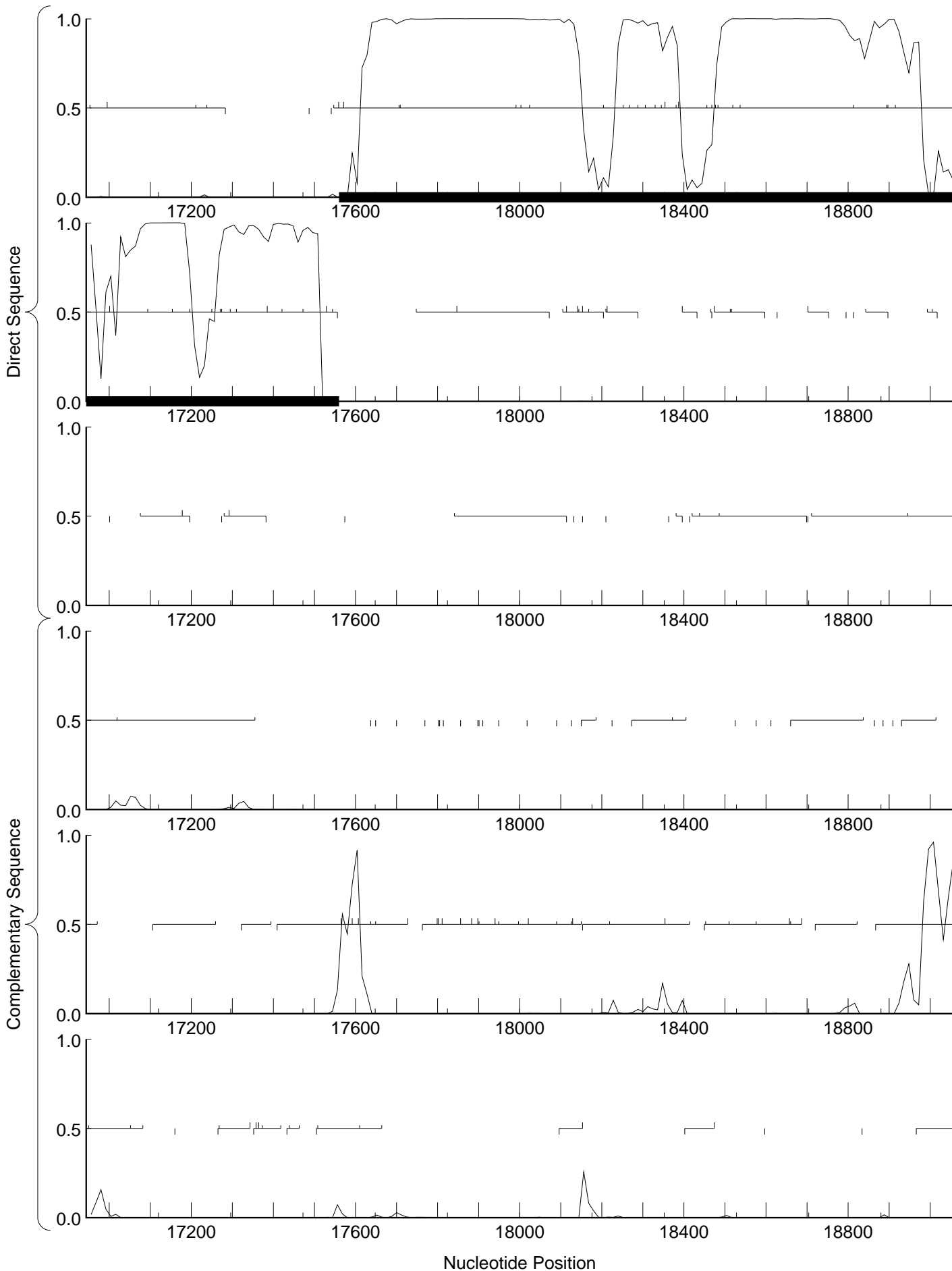


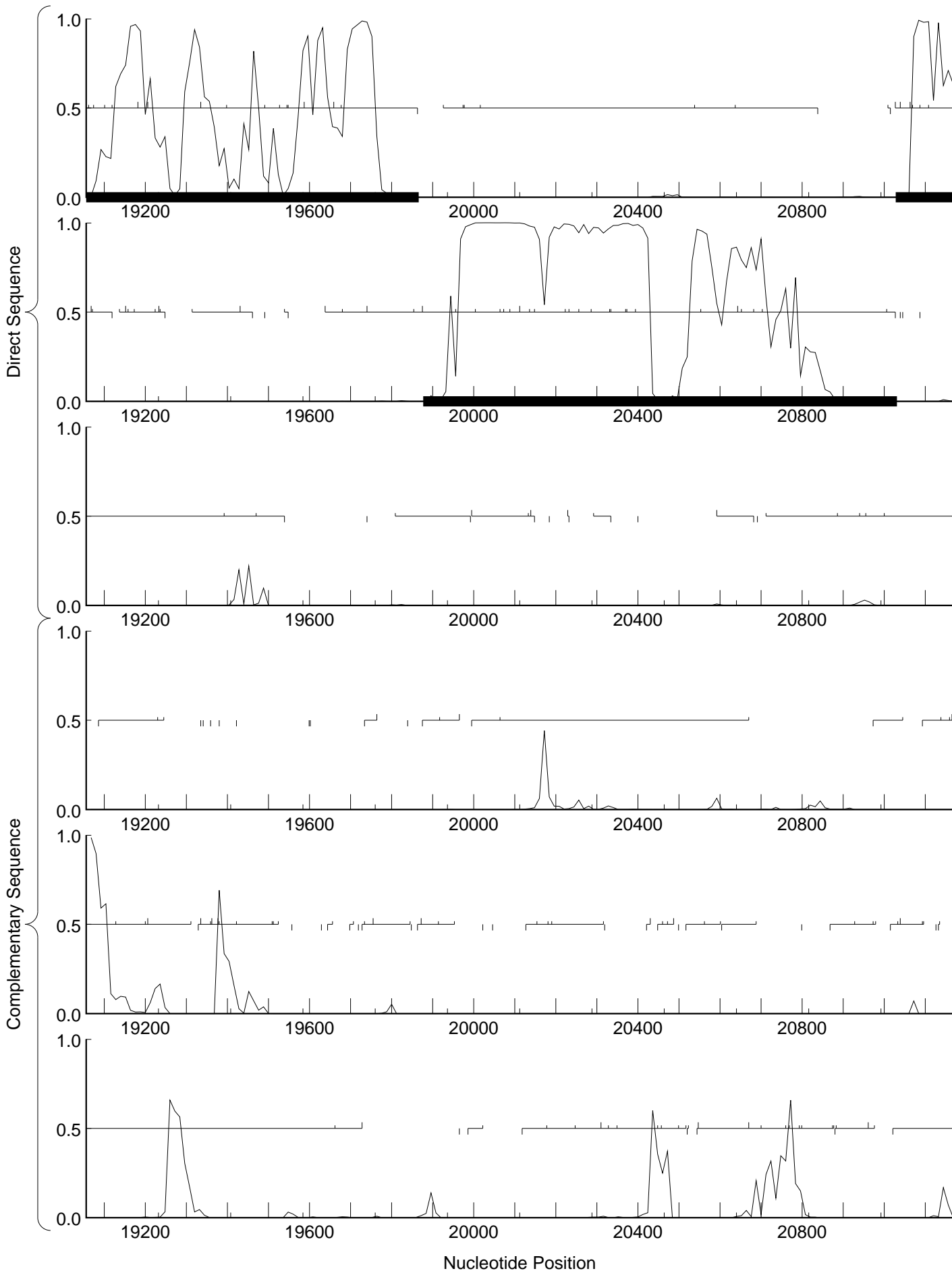
GeneMark.hmm prediction

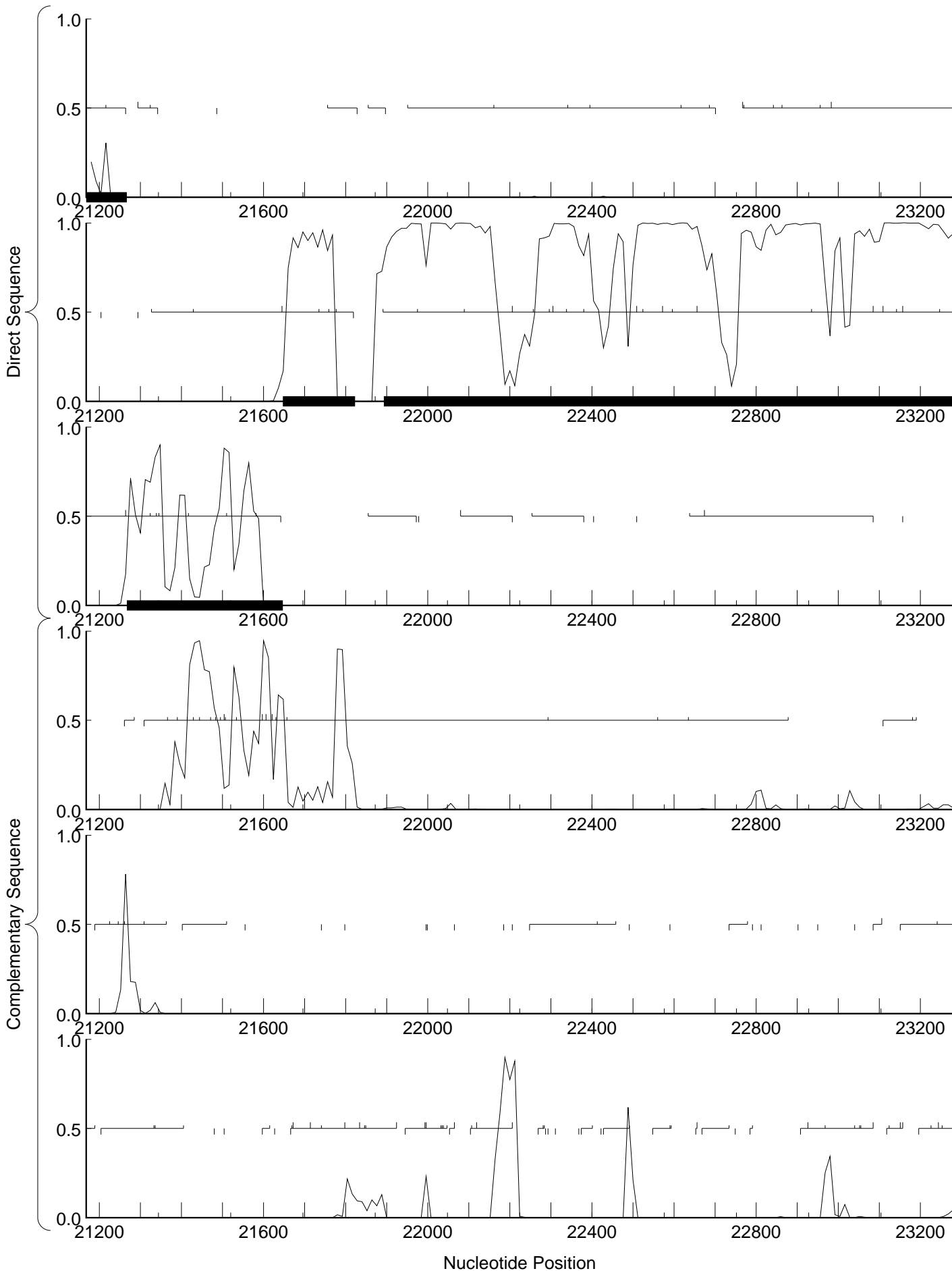


GeneMark_hmm prediction

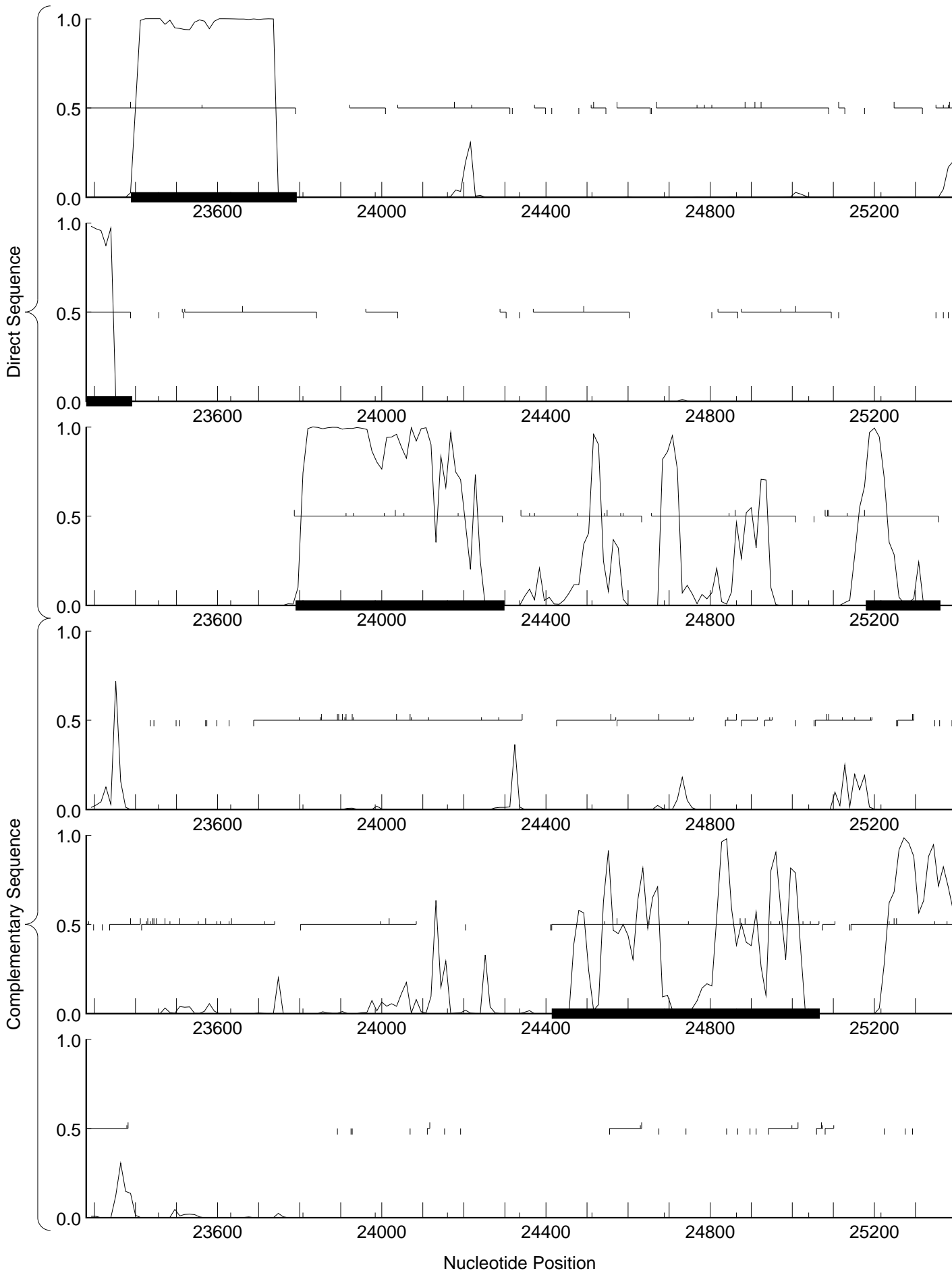




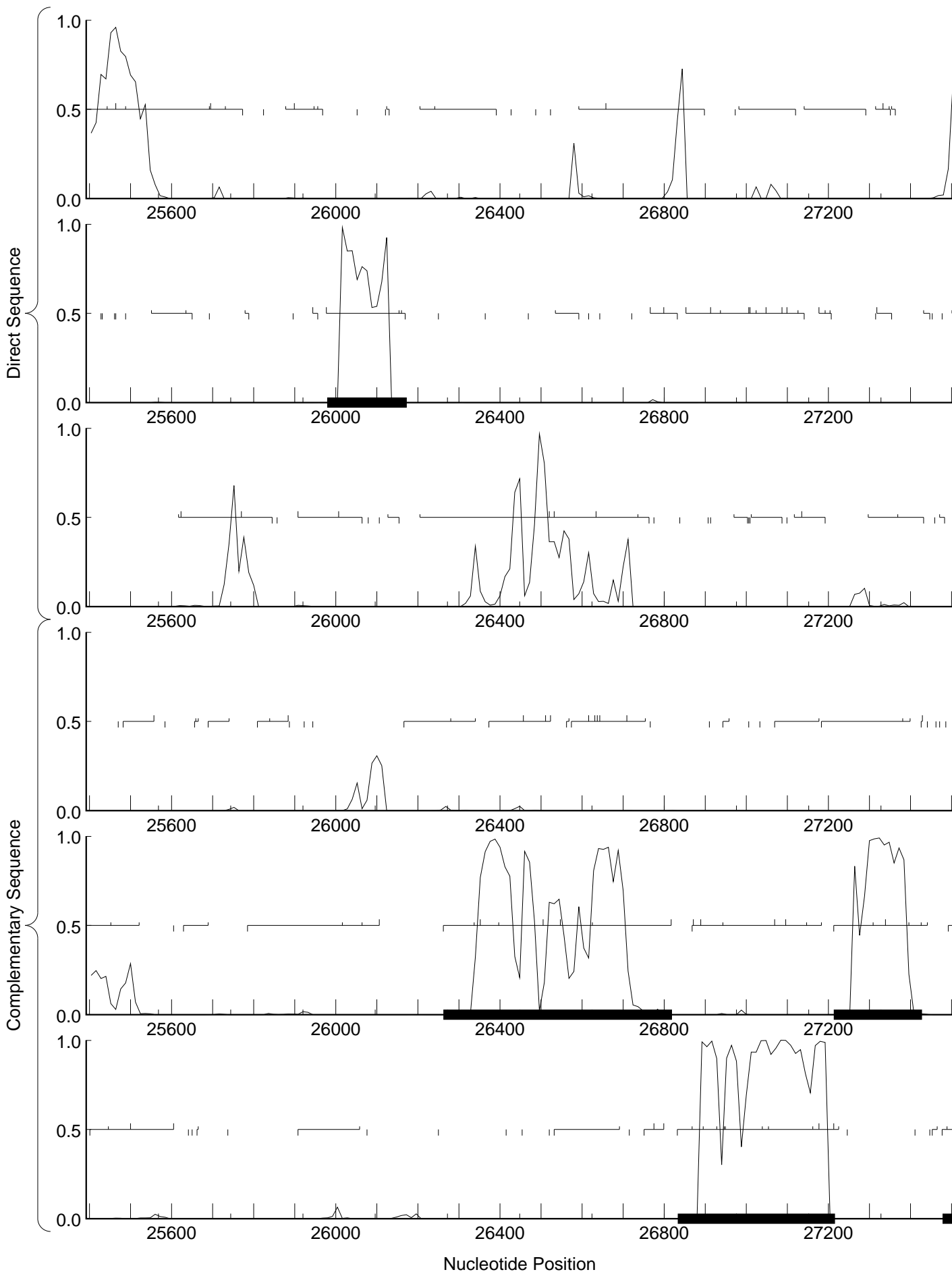


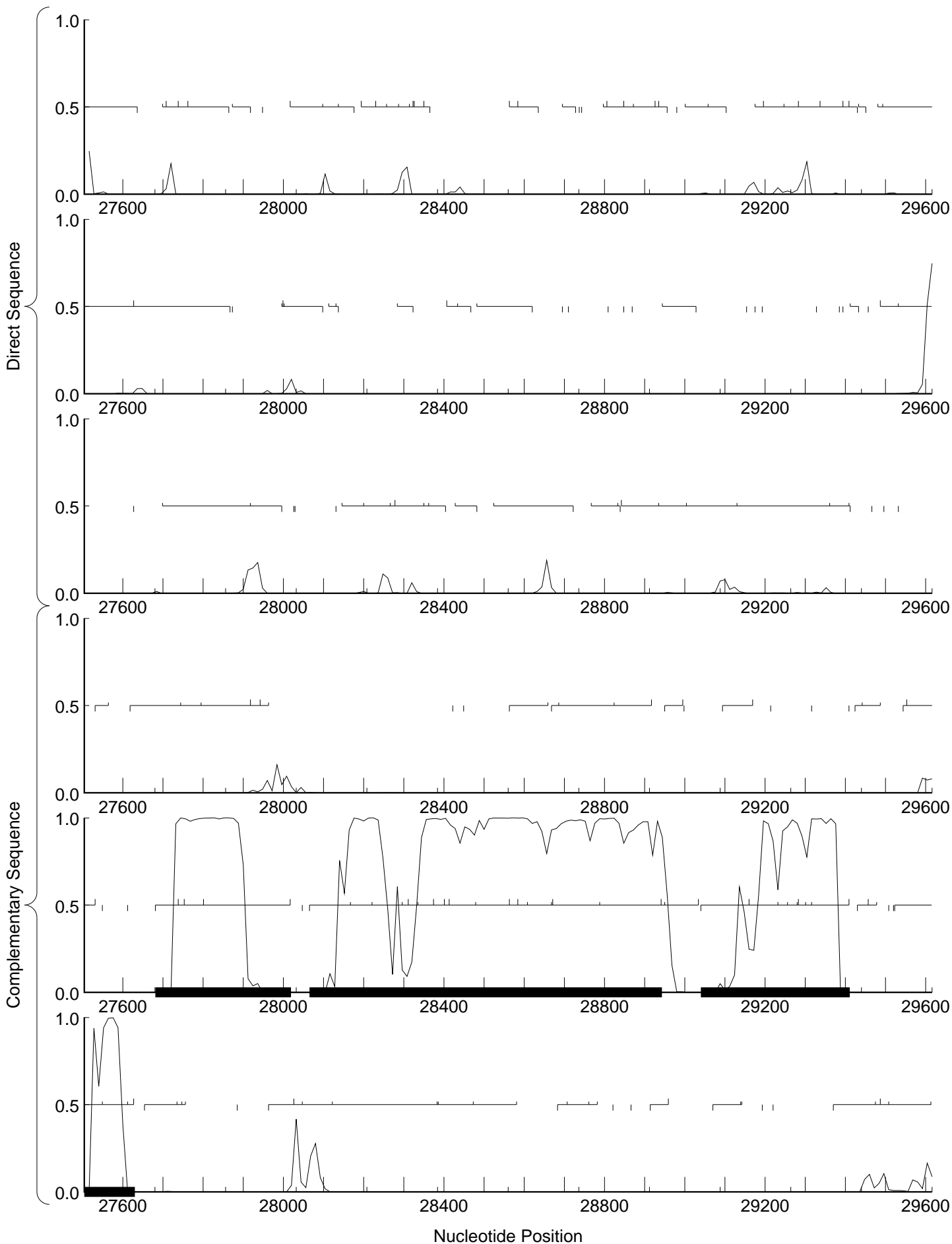


GeneMark.hmm prediction
complete sequence, 42595 bp including 13-base 3' overhang (CCCGCCGCCTTGG), Cluster N, Order 2, Window 96, Step 12, 13/22

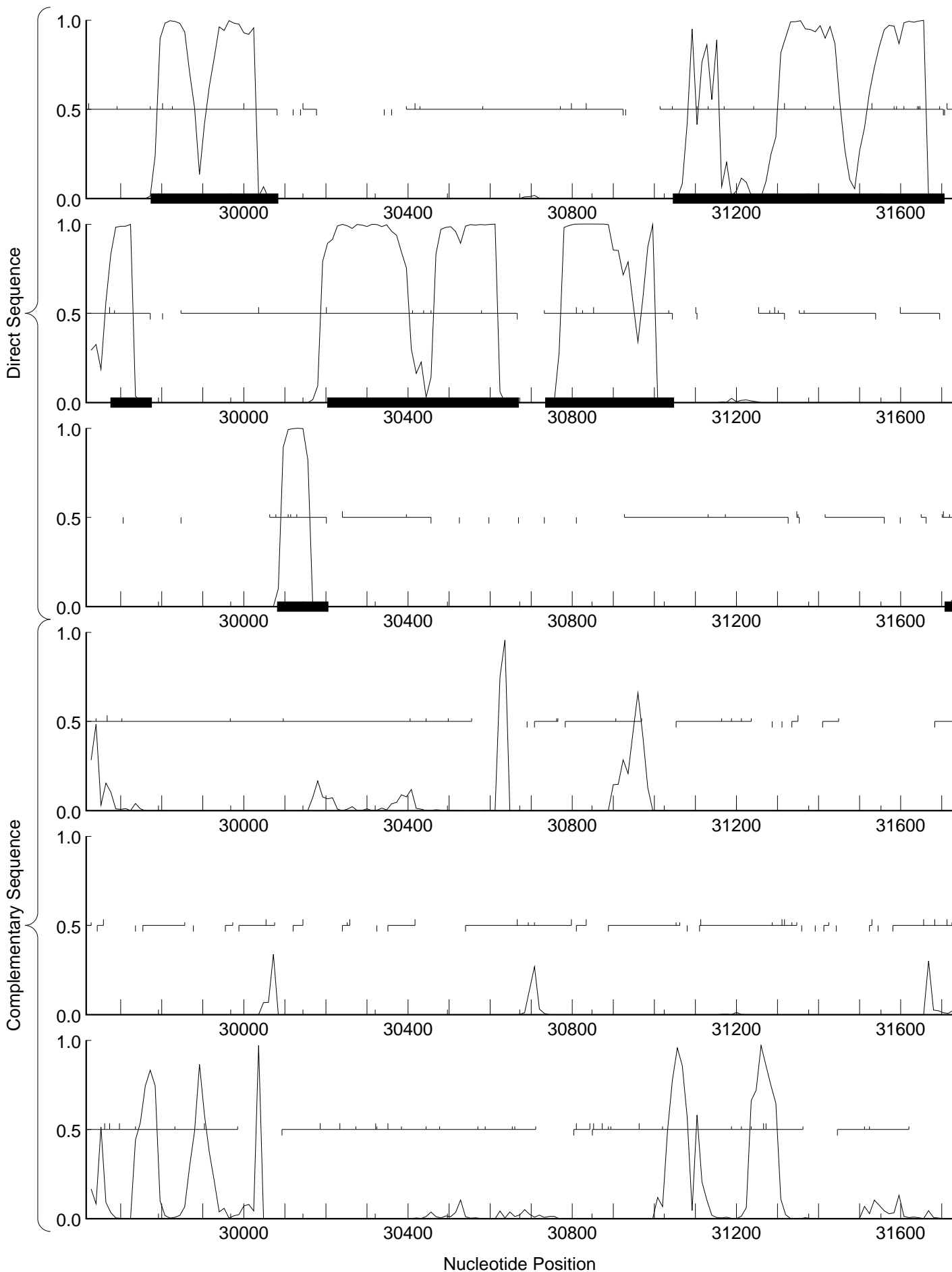


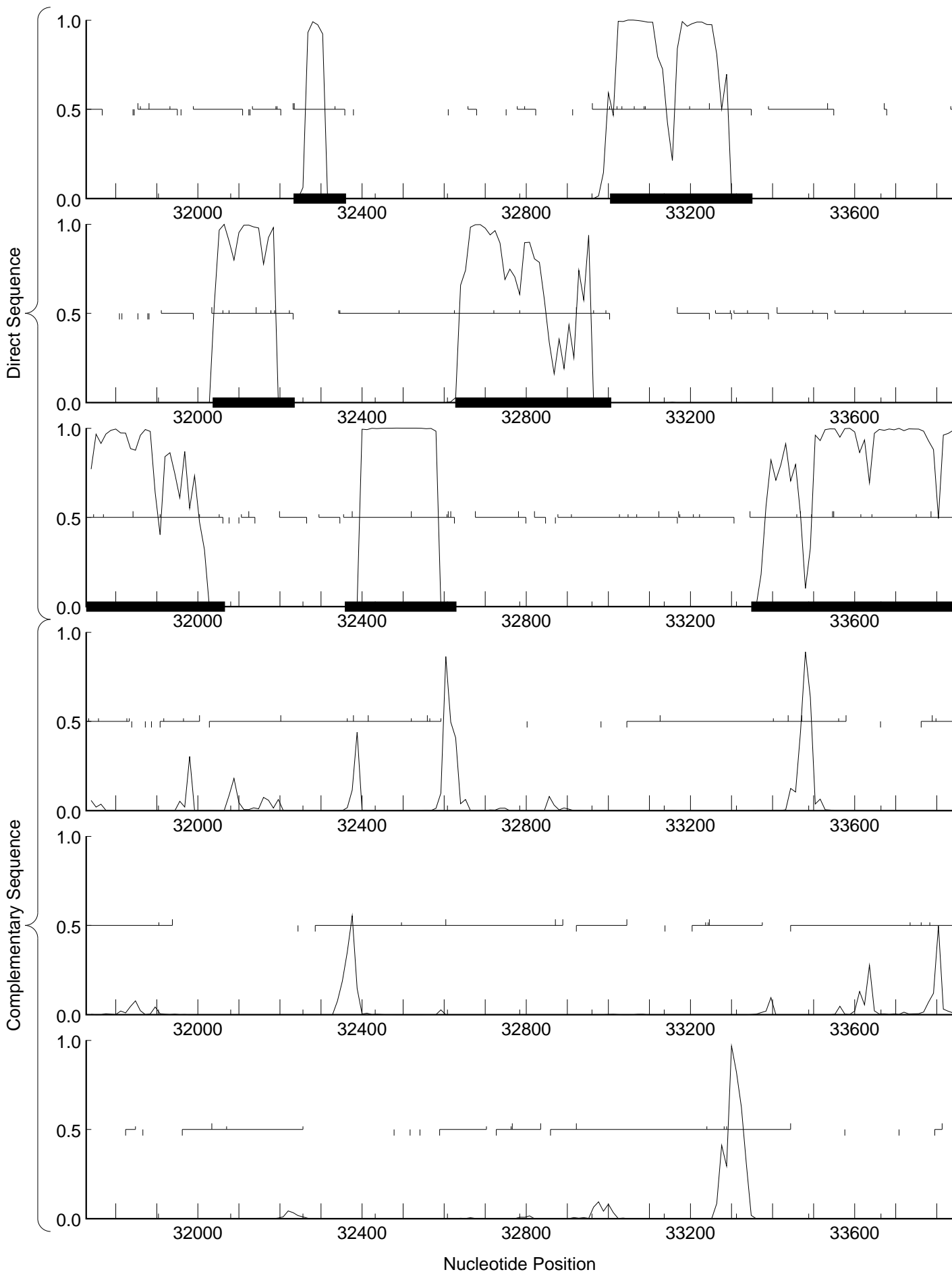
GeneMark.hmm prediction
complete sequence, 42595 bp including 13-base 3' overhang (CCCGCCGCCTTGG), Cluster N, Order 2, Window 96, Step 12, 14/22

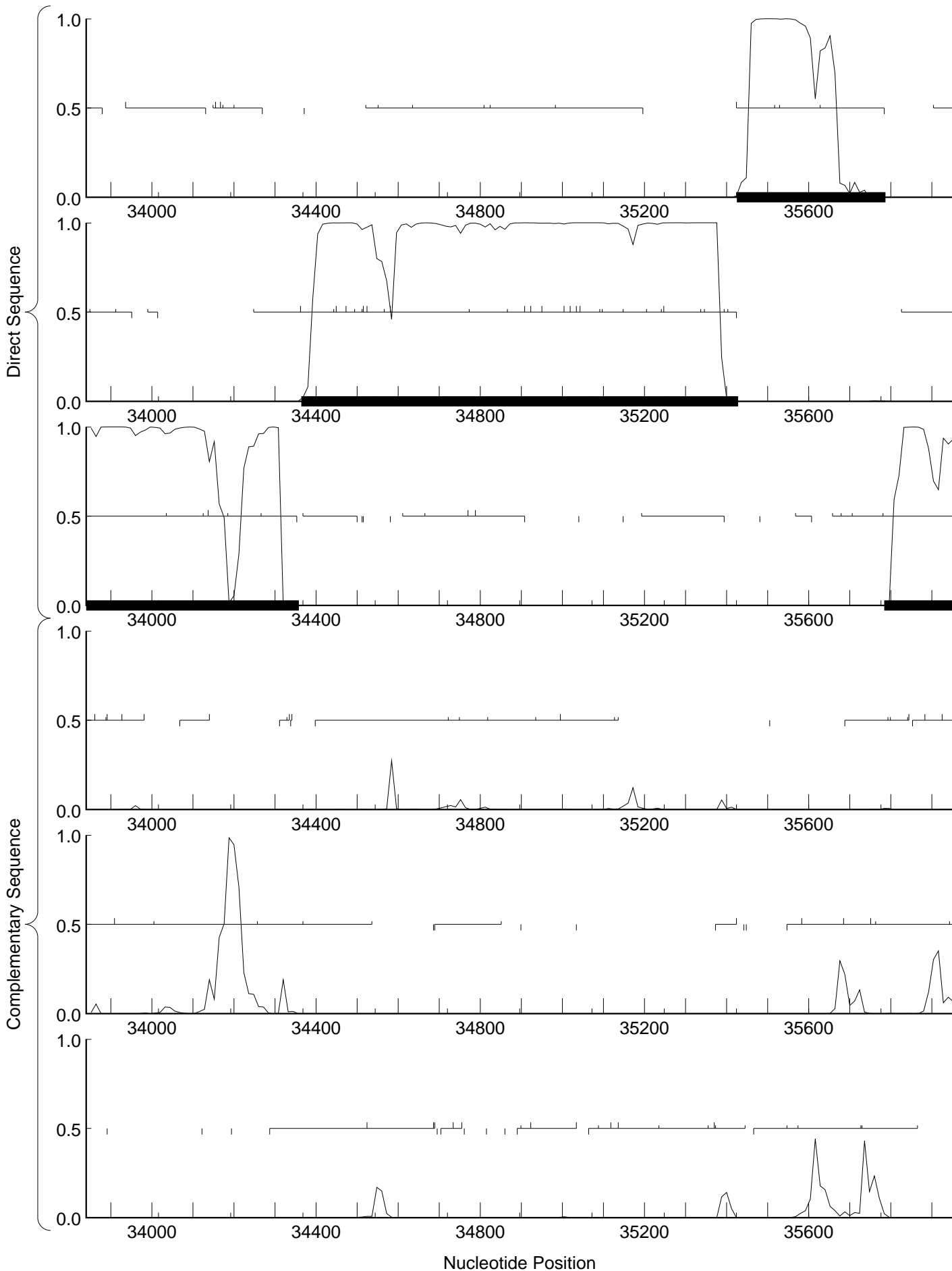




GeneMark.hmm prediction
complete sequence, 42595 bp including 13-base 3' overhang (CCCGCCGCCTTGG), Cluster N, Order 2, Window 96, Step 12, 16/22







GeneMark.hmm prediction
complete sequence, 42595 bp including 13-base 3' overhang (CCCGCCGCCTTGG), Cluster N, Order 2, Window 96, Step 12, 19/22

