

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 : 1/18/18 at 22:30:38
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

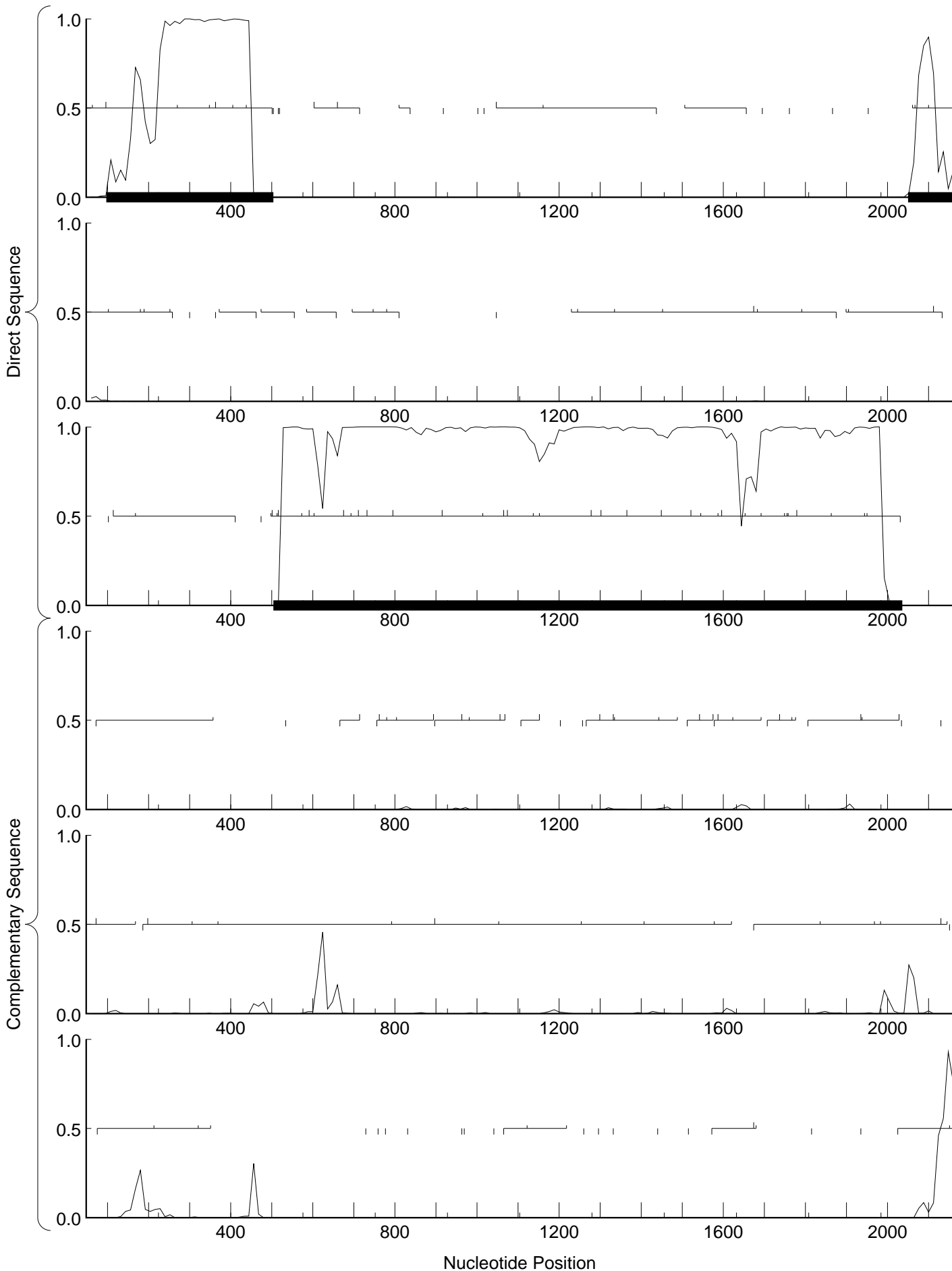
Send questions / comments to:
Dr. M. Borodovsky
Georgia Institute of Technology
School of Biology
Atlanta, GA 30332-0230

Matrix notes & comments

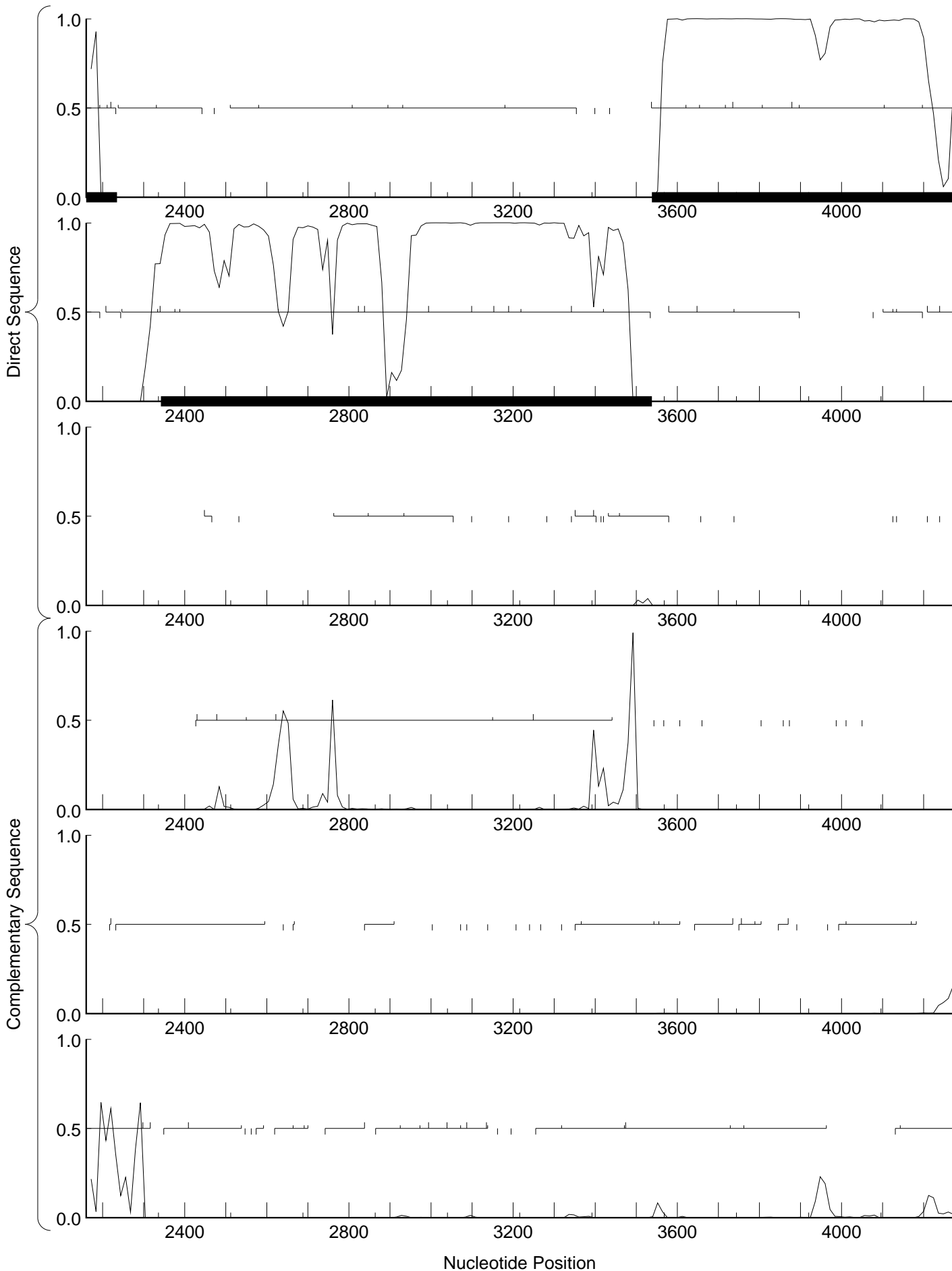
For details on the model building procedure see:
Besemer J. and Borodovsky M.
"Heuristic approach to deriving models for gene finding"
NAR, 1999, Vol. 27, No. 19, pp. 3911-3920

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

GeneMark_hmm prediction

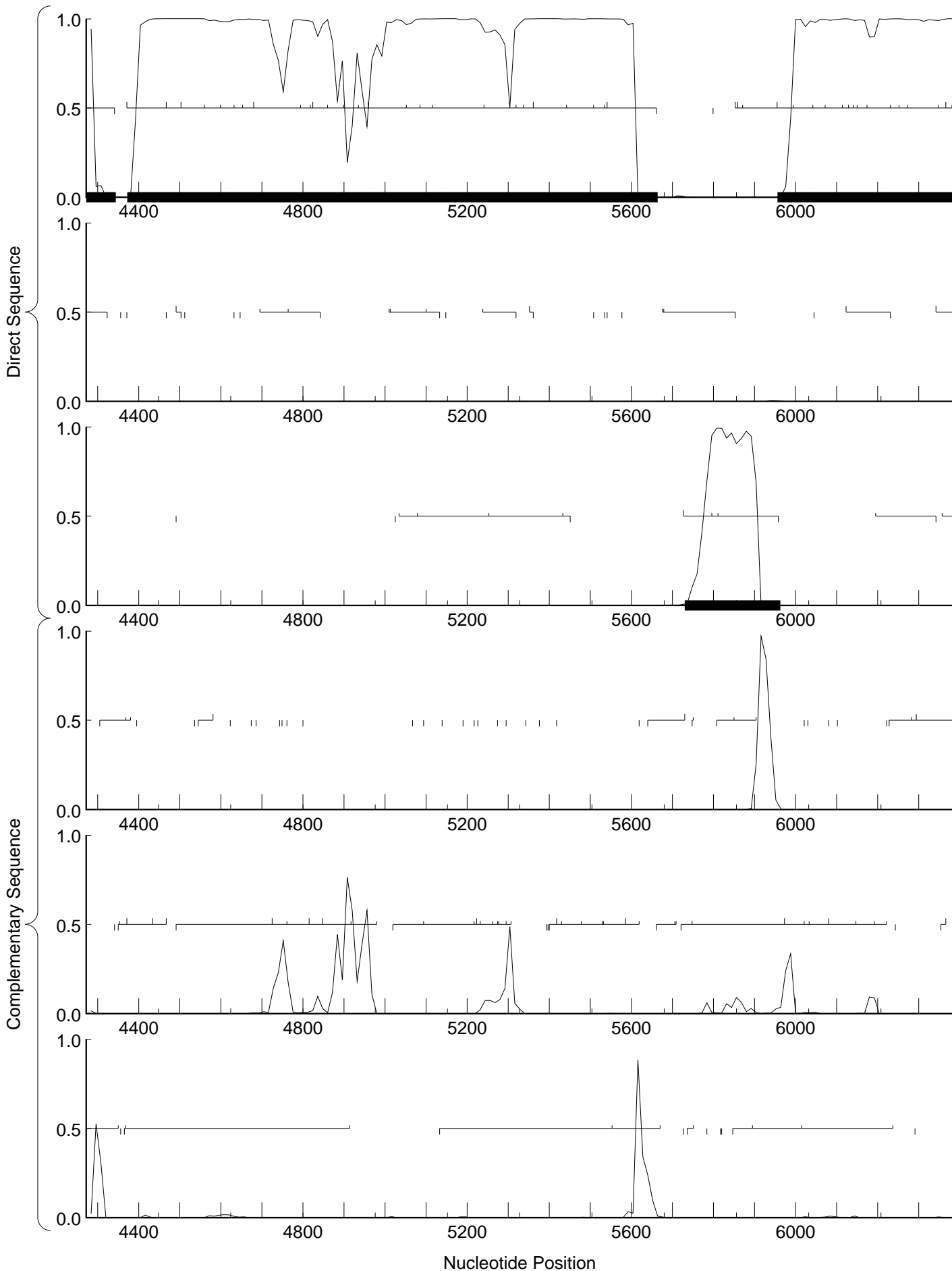


complete sequence 43575 bp including 13-base 3' overhang (CCGCCGCAATGG), Cluster N, Order 2, Window 96, Step 12, 3/22

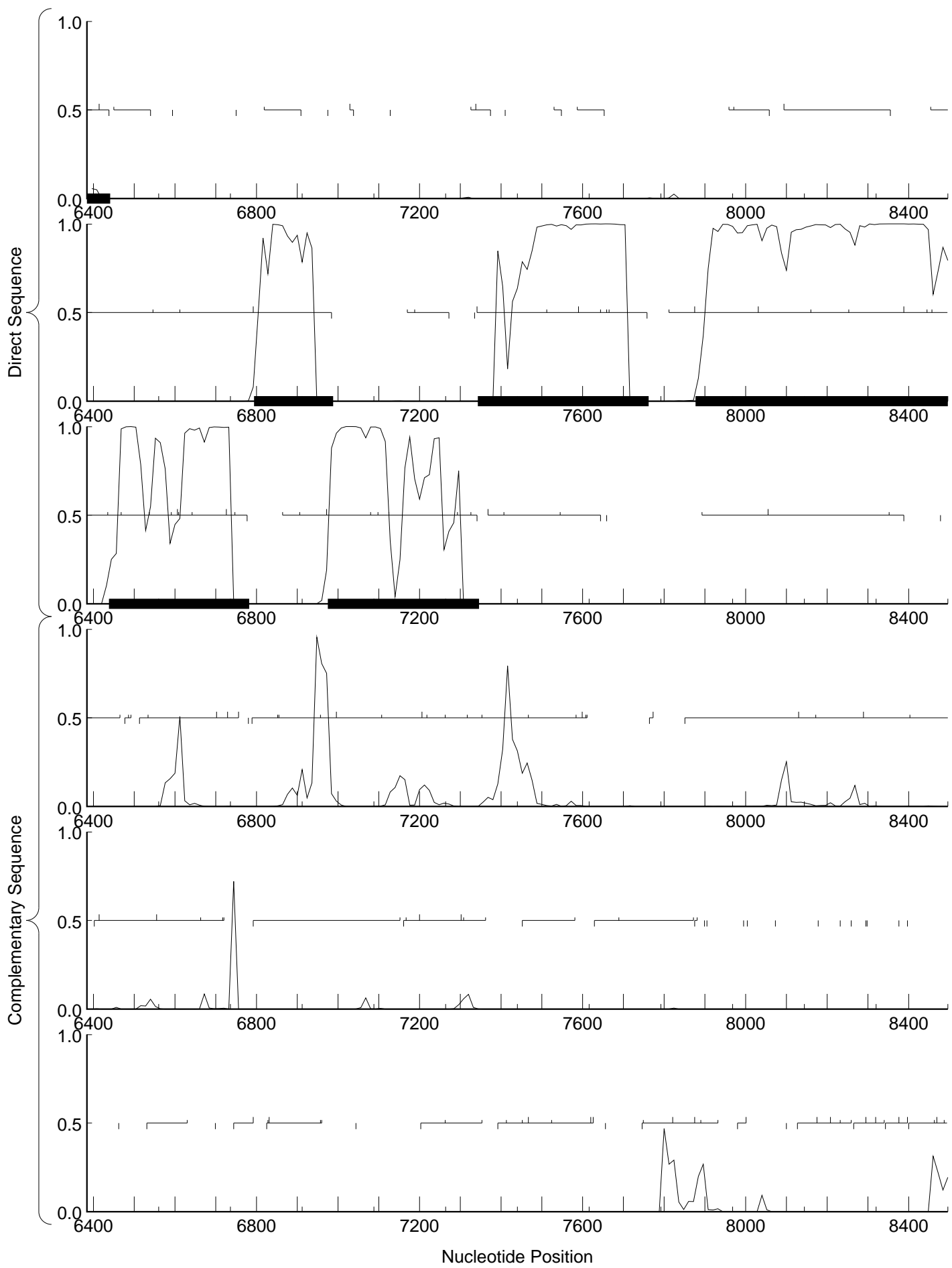


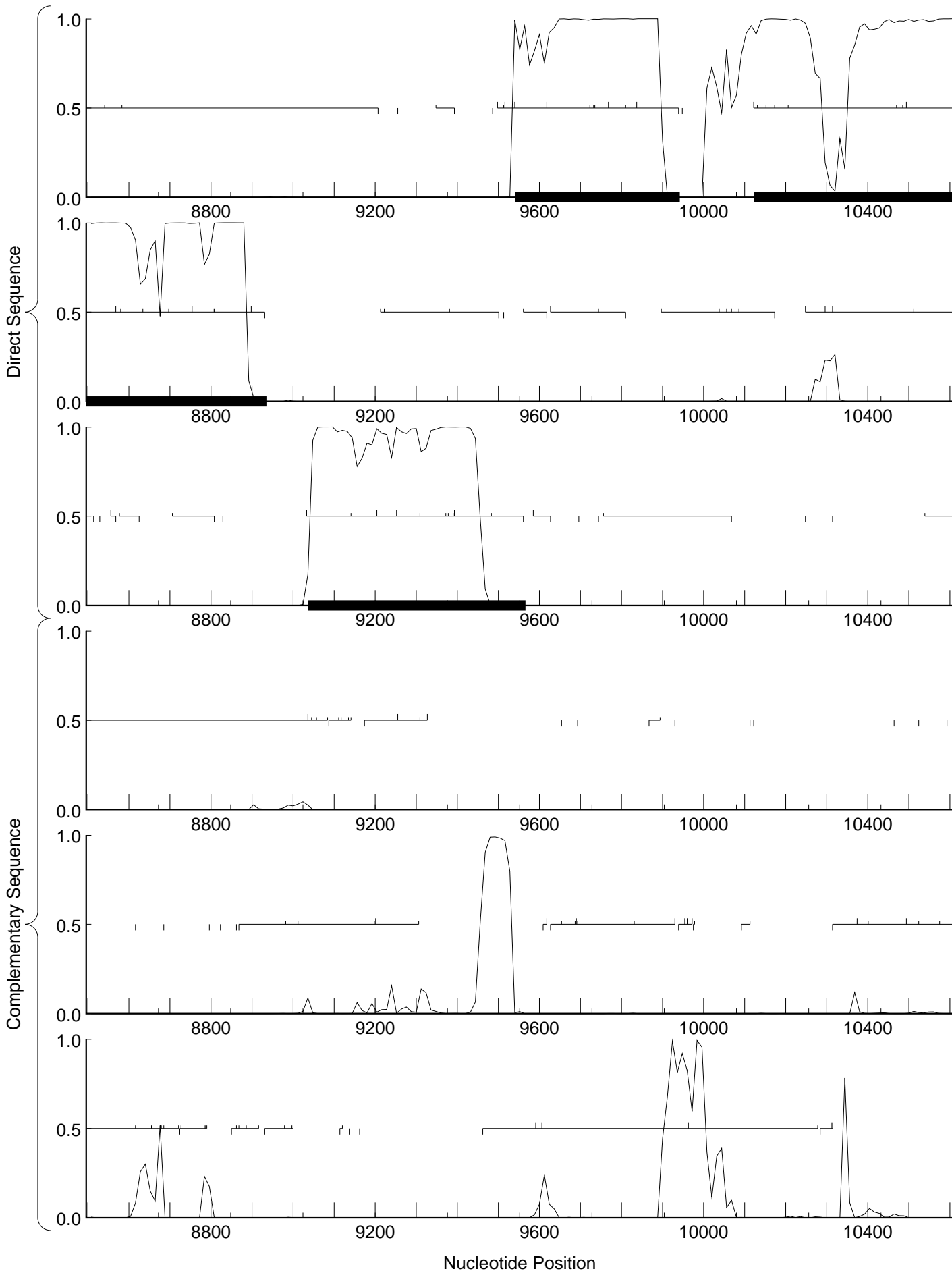
complete sequence 43575 bp including 13-base 3' overhang (CCGCGCAATGG), Cluster N, Order 2, Window 96, Step 12, 4/22

GeneMark.hmm prediction



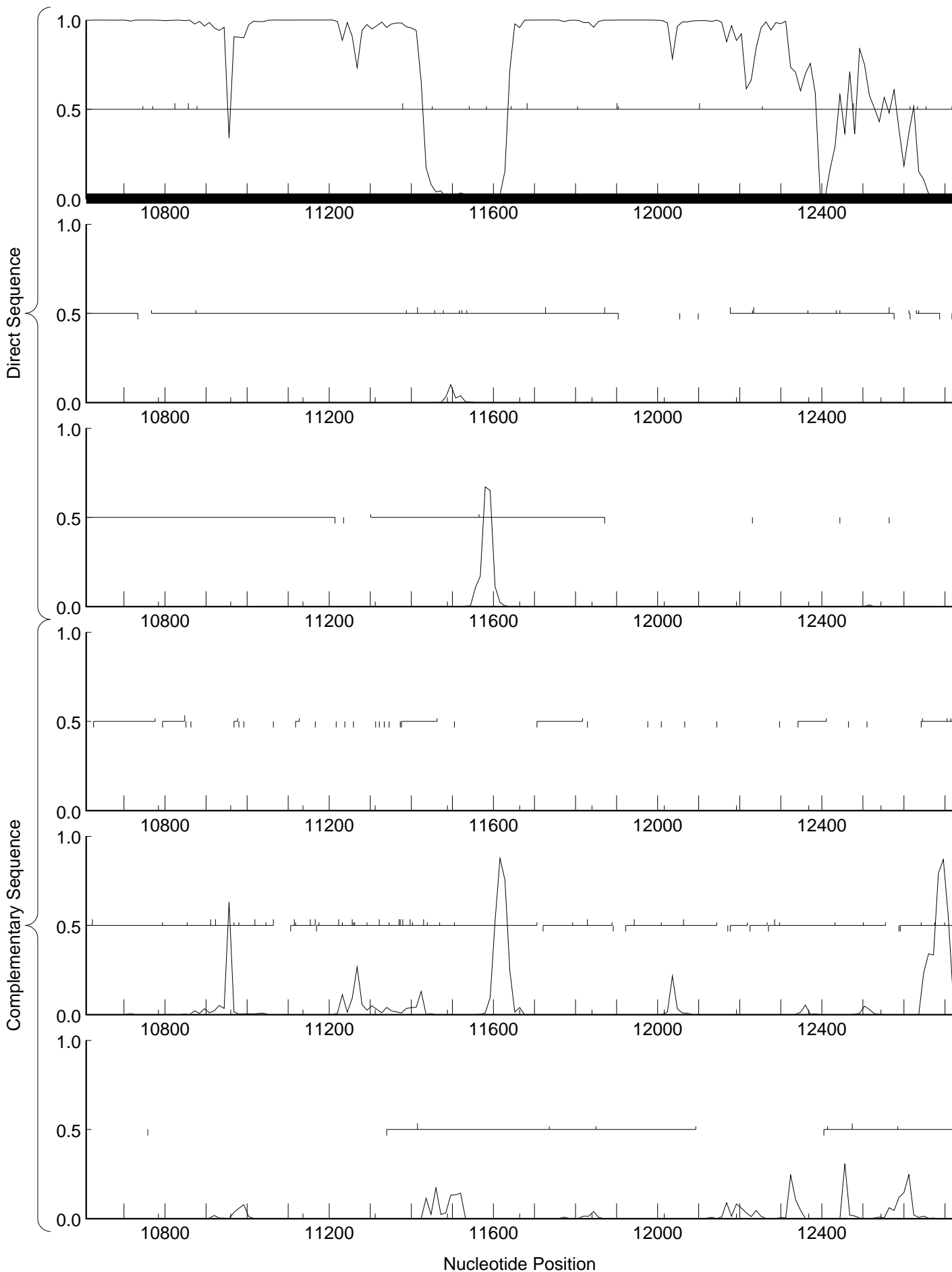
GeneMark.hmm prediction



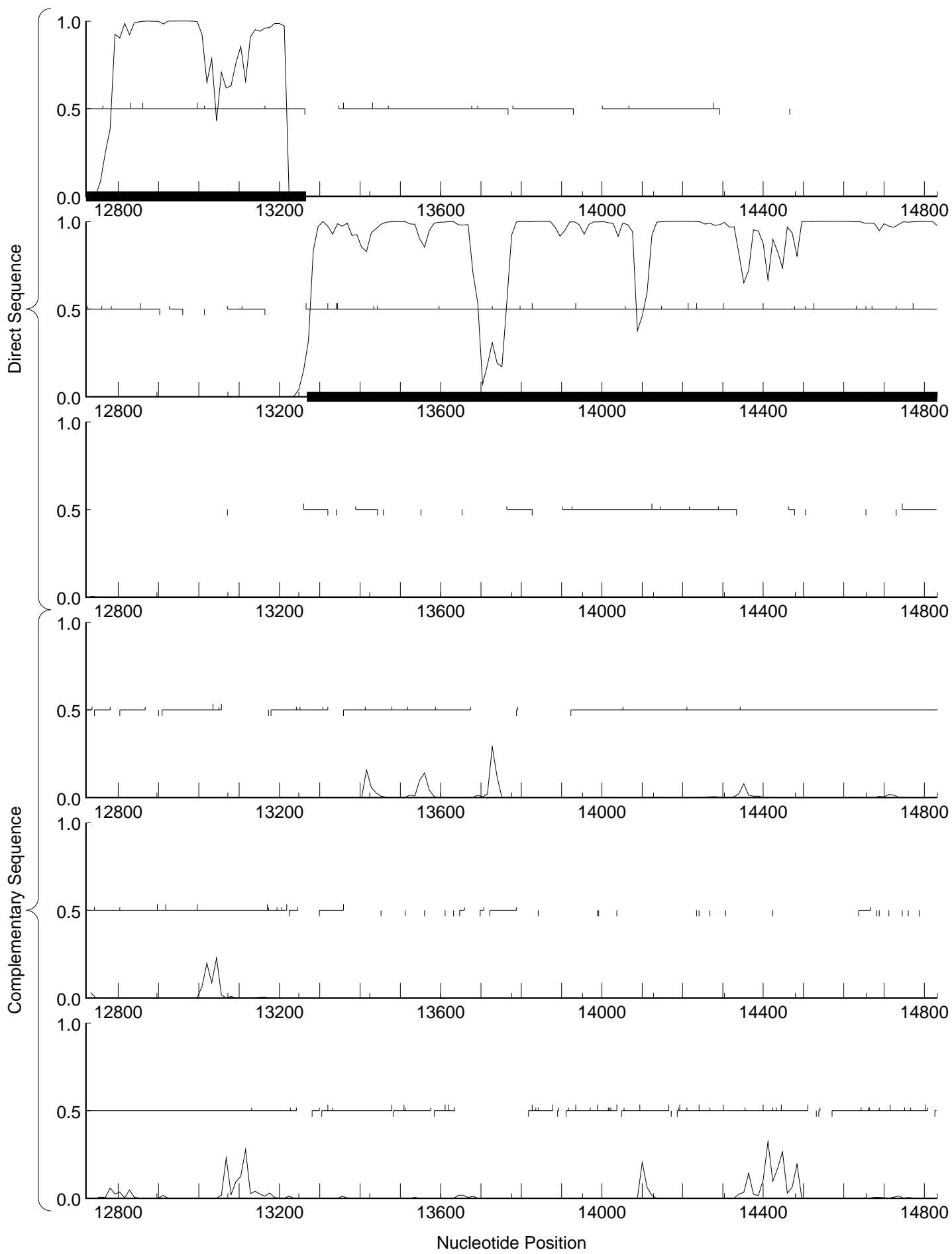


complete sequence 43575 bp including 13-base 3' overhang (CCGCCGCAATGG), Cluster N, Order 2, Window 96, Step 12, 7/22

GeneMark.hmm prediction

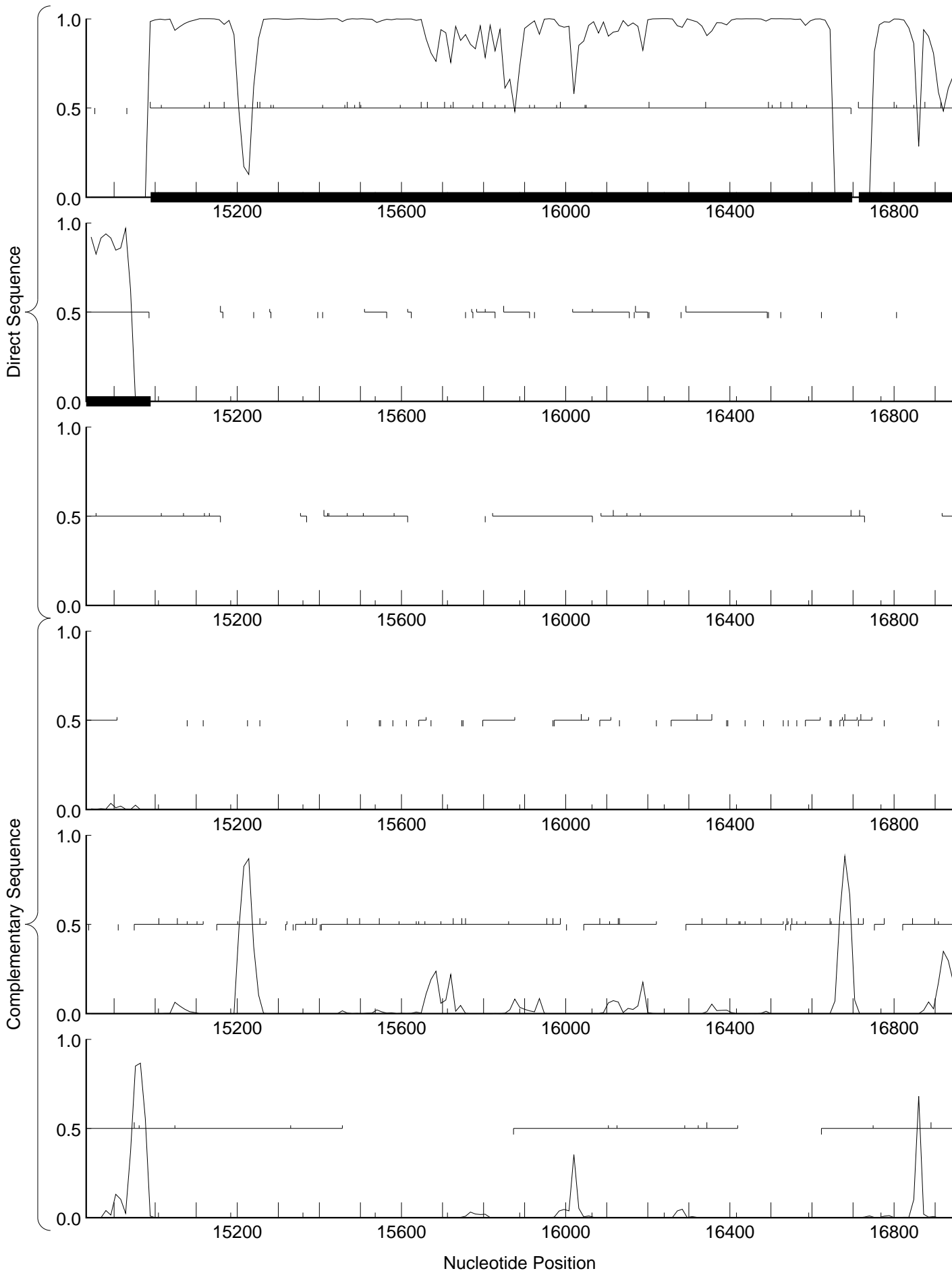


GeneMark.hmm prediction

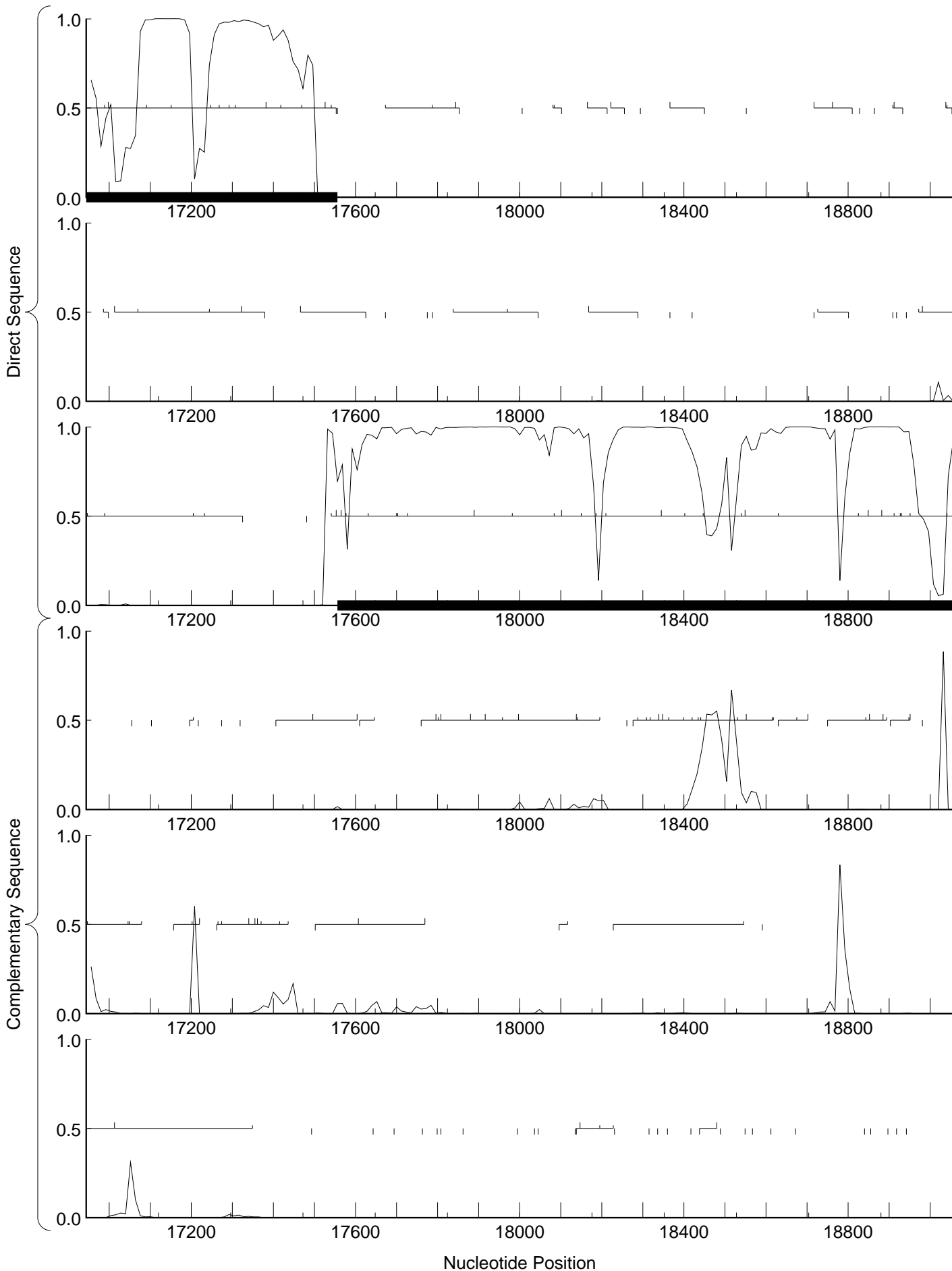


complete sequence 43575 bp including 13-base 3' overhang (CCGCGCAATGG), Cluster N, Order 2, Window 96, Step 12, 9/22

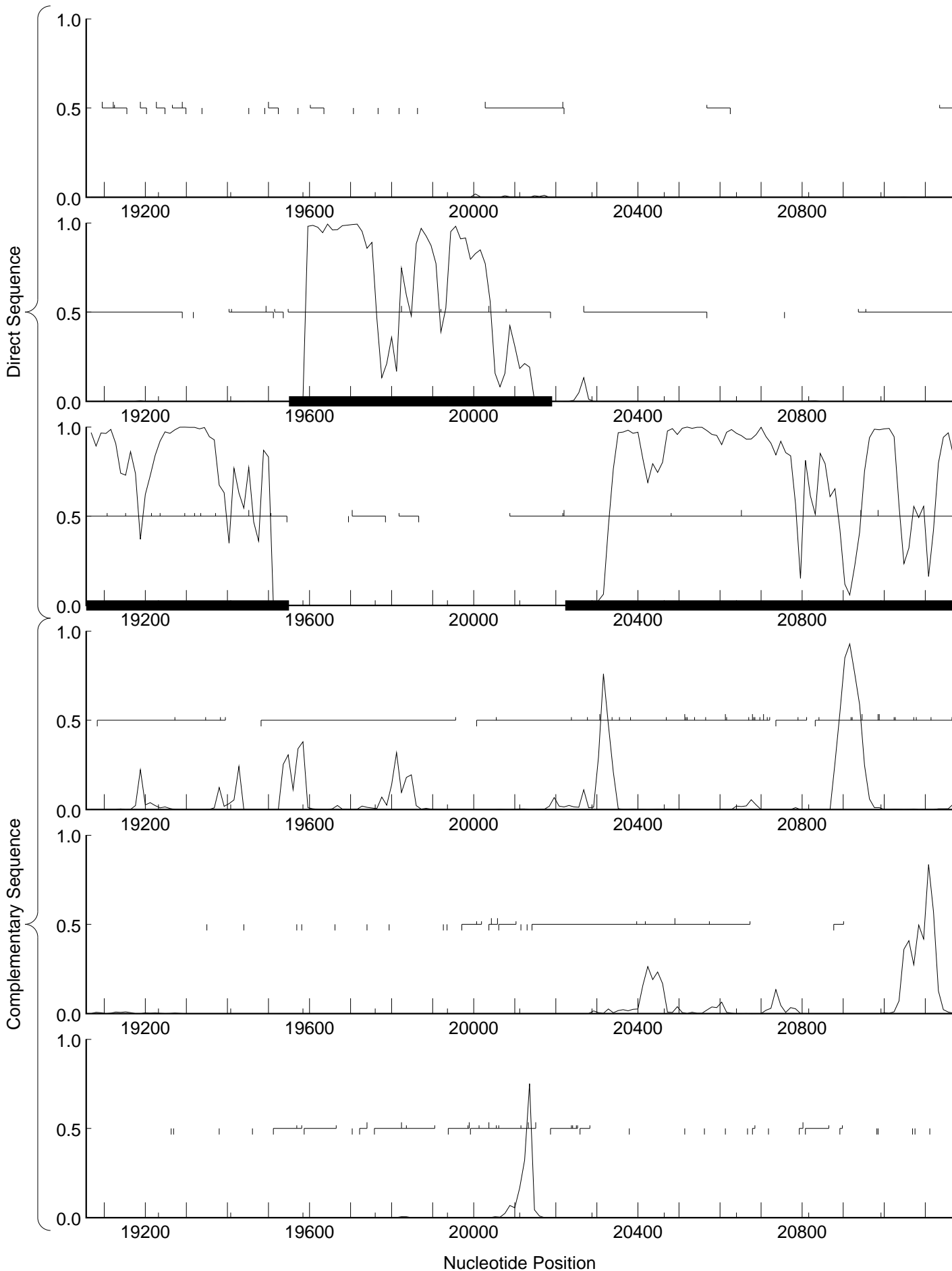
GeneMark.hmm prediction

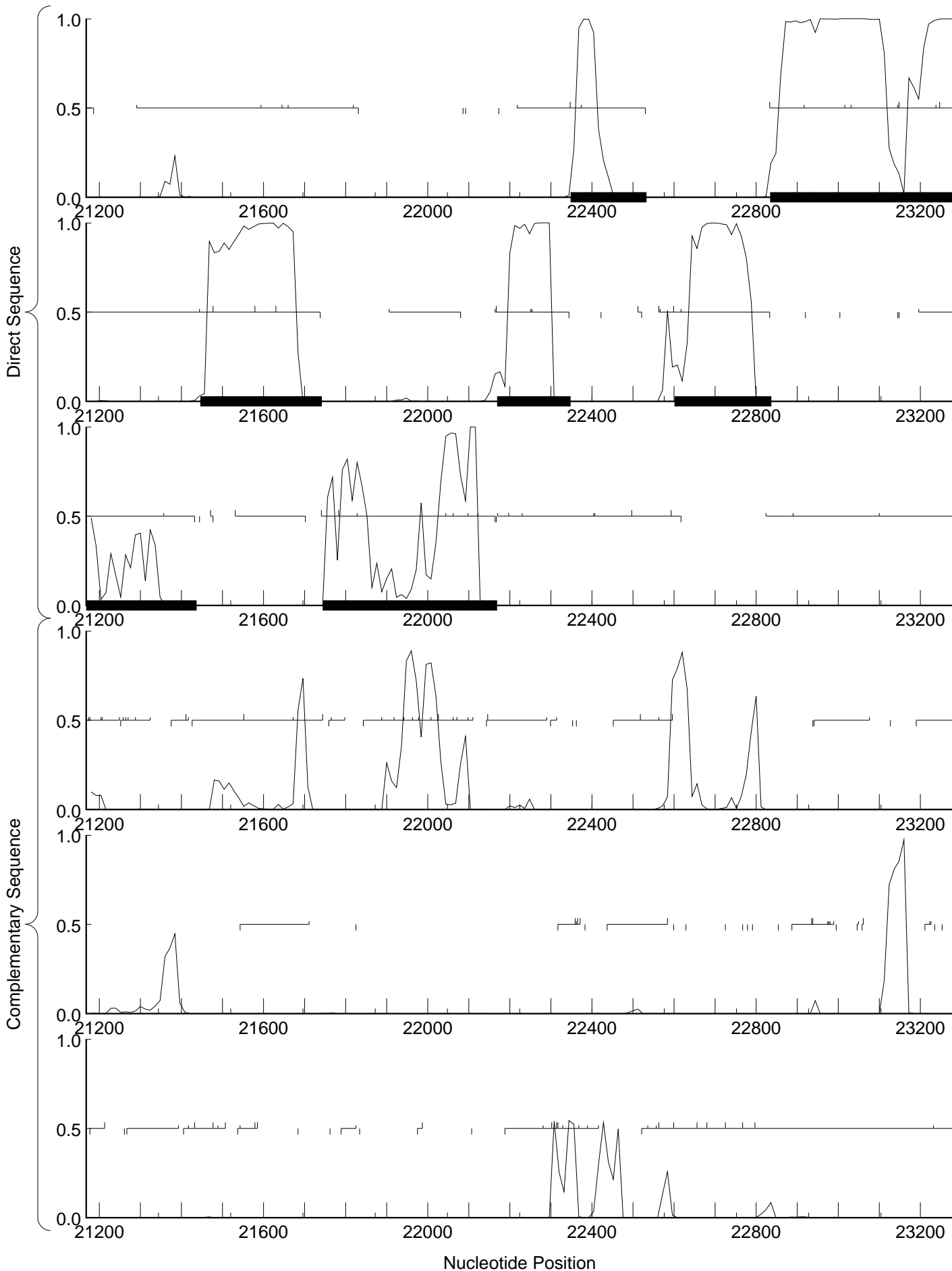


GeneMark.hmm prediction



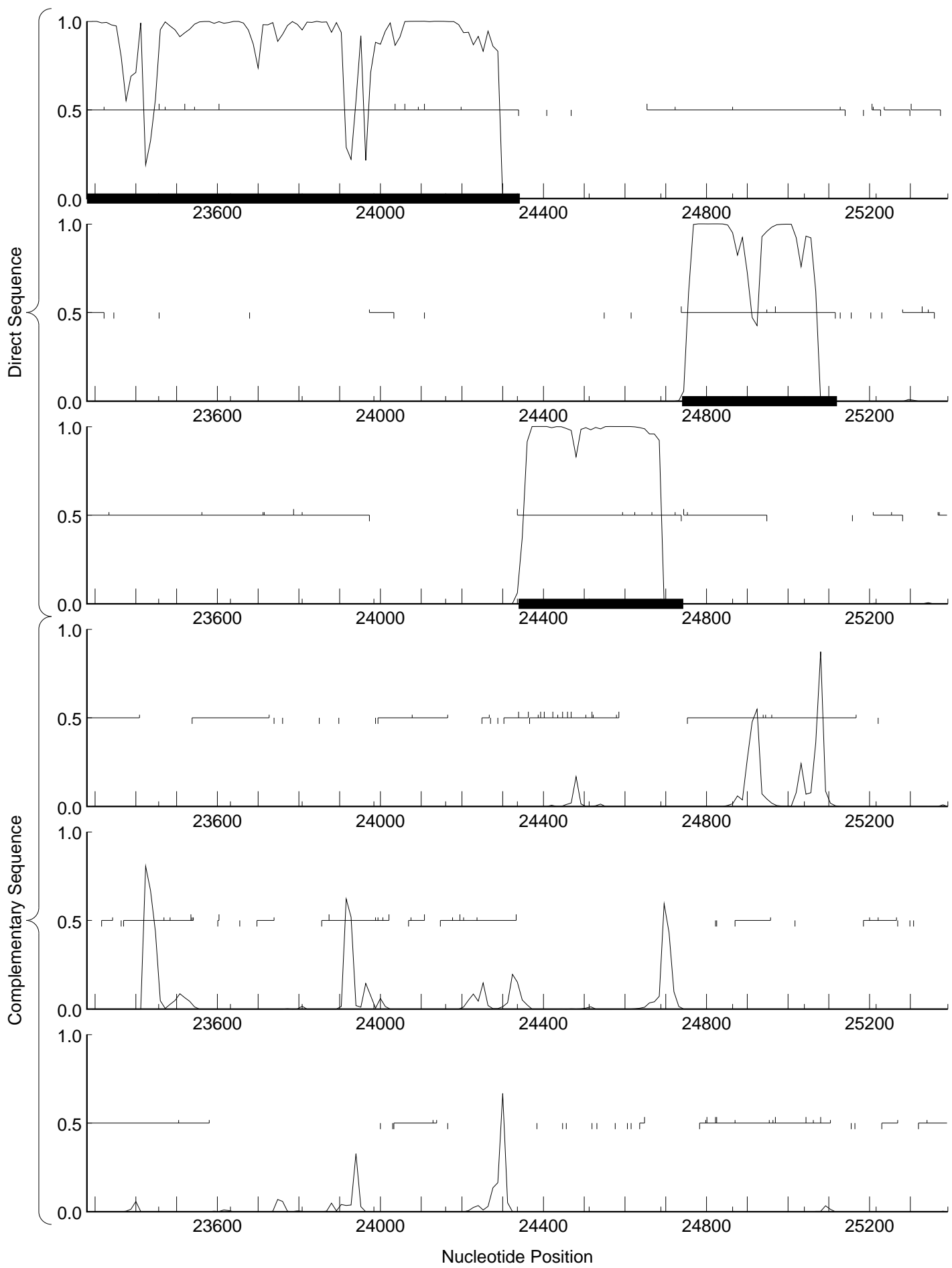
GeneMark.hmm prediction

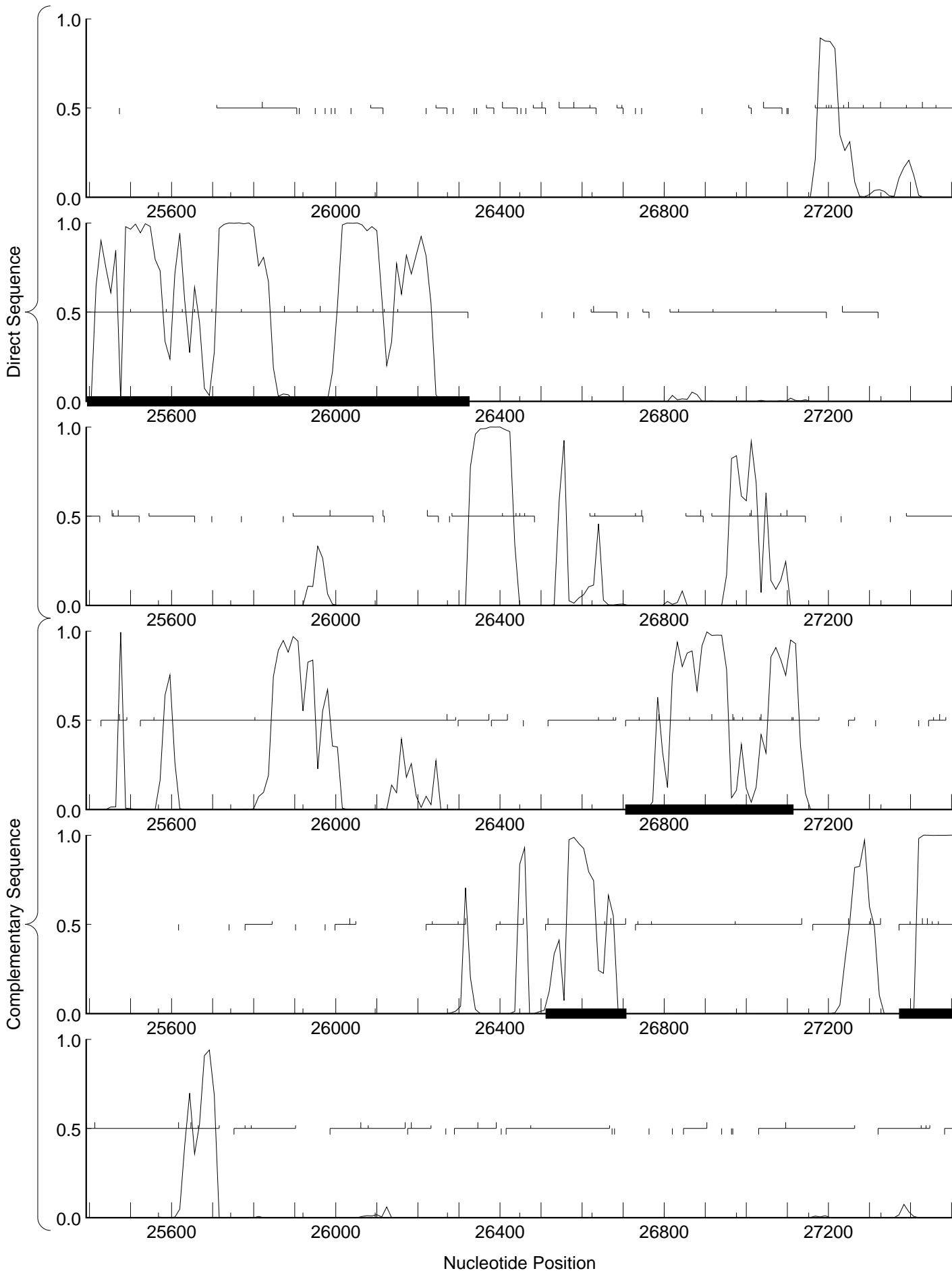




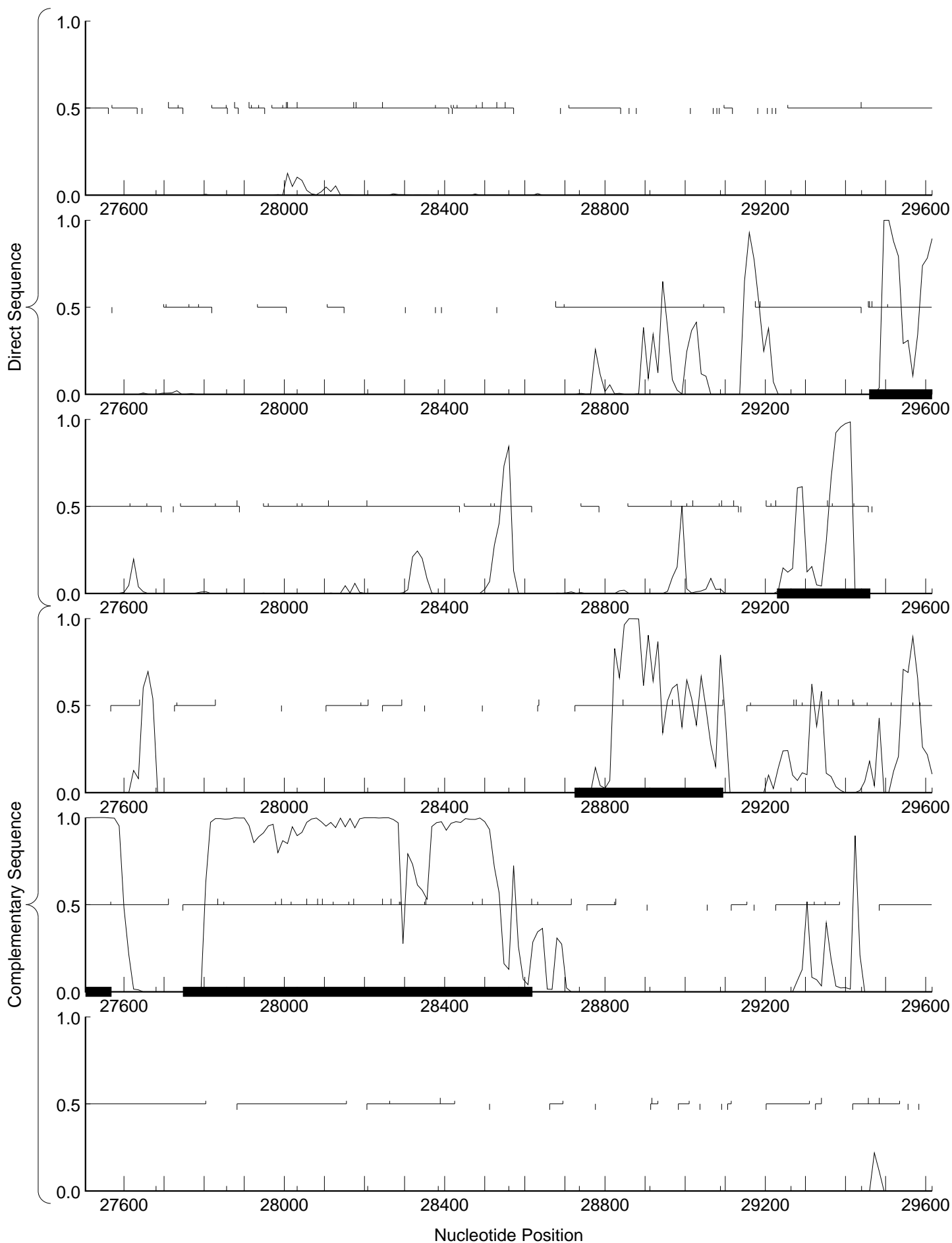
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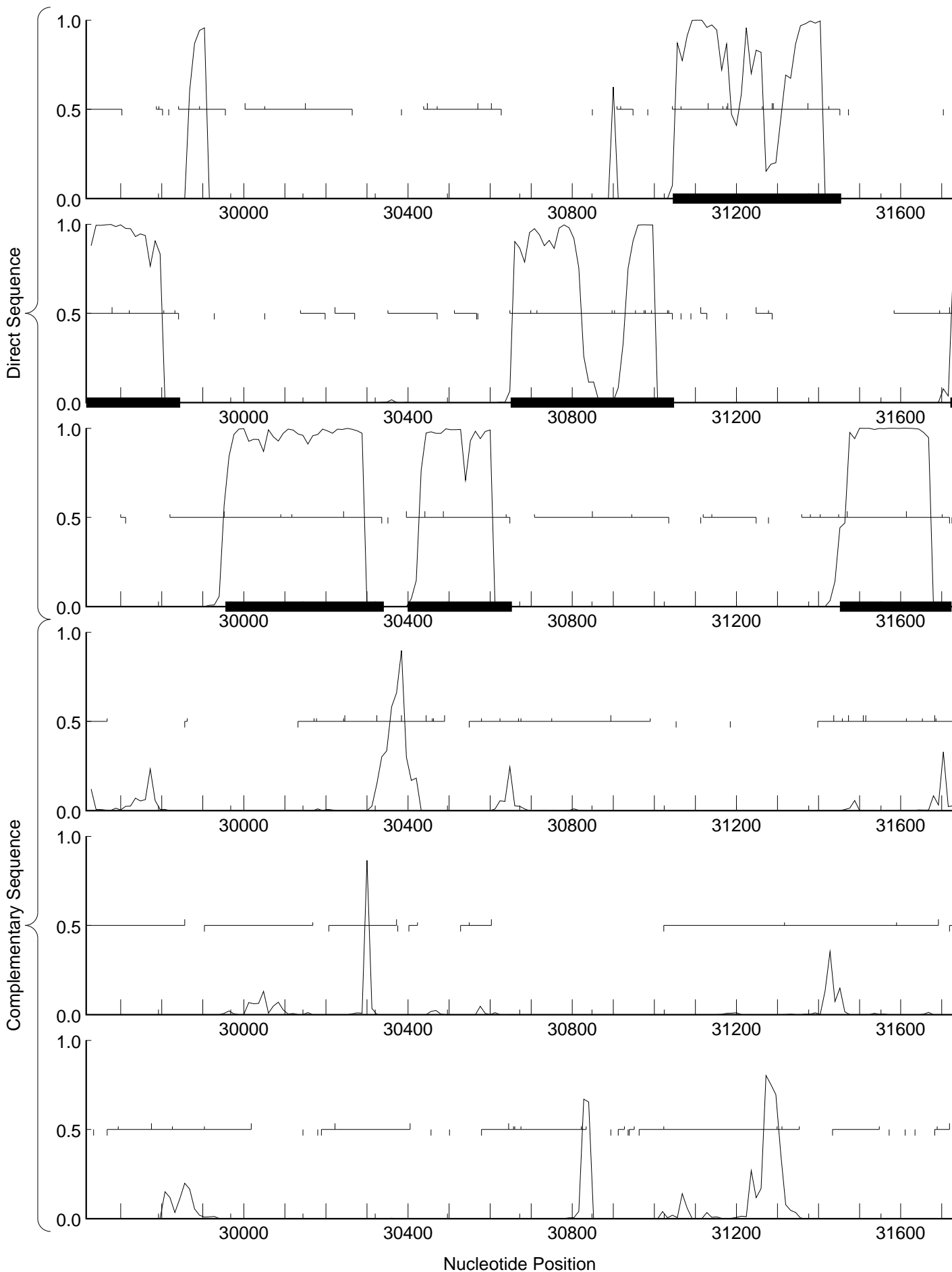
GeneMark.hmm prediction



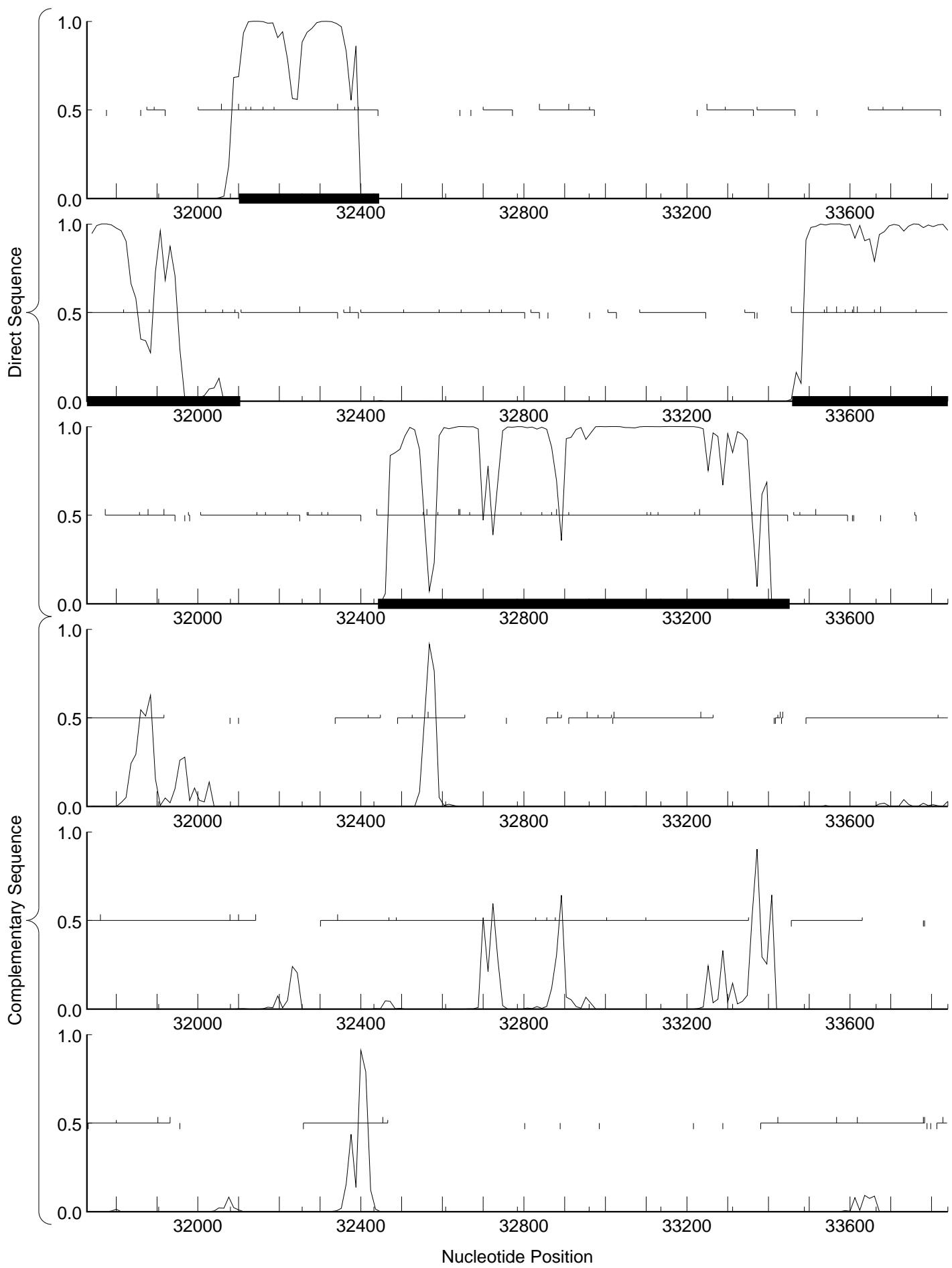


GeneMark.hmm prediction

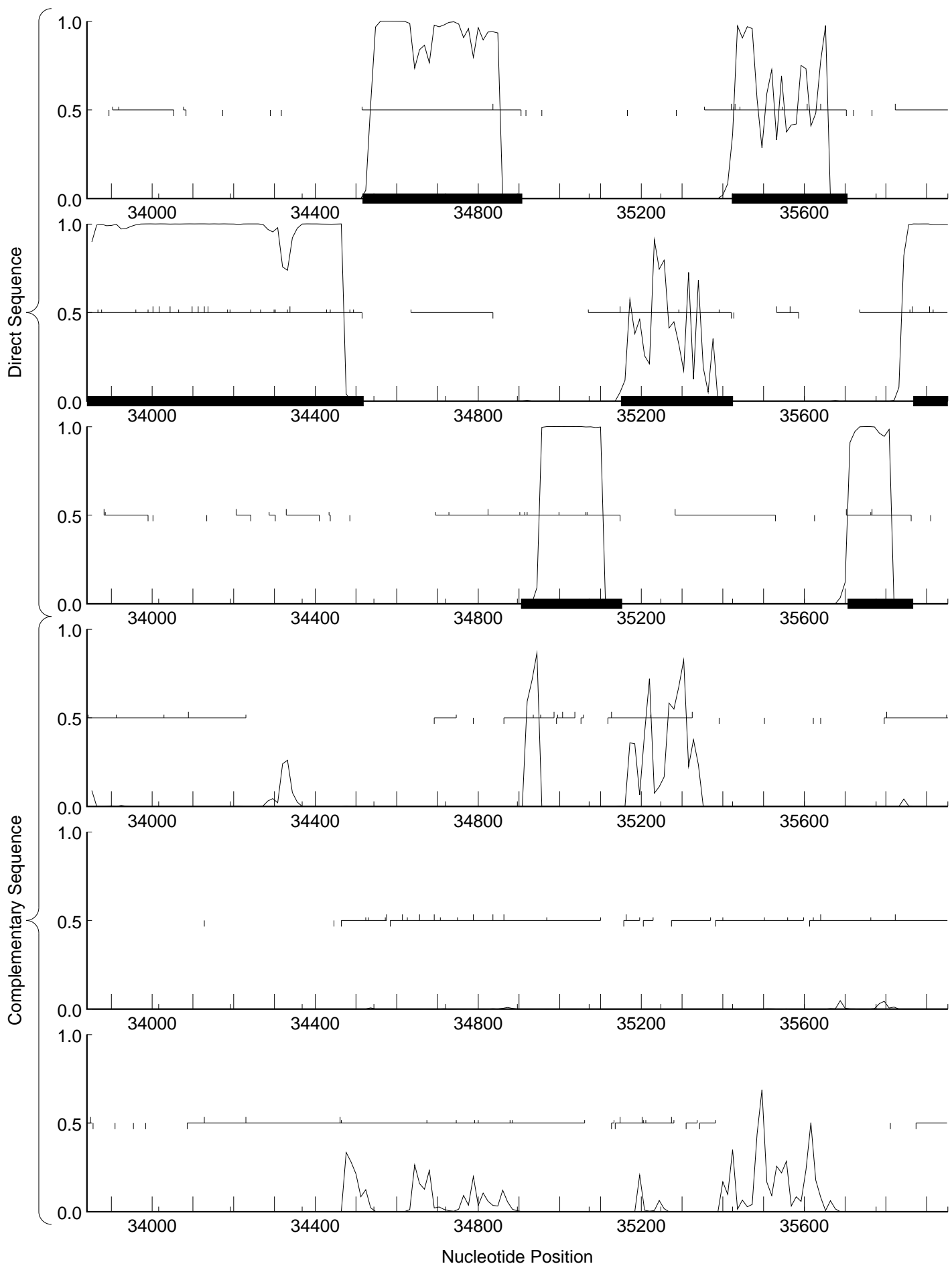




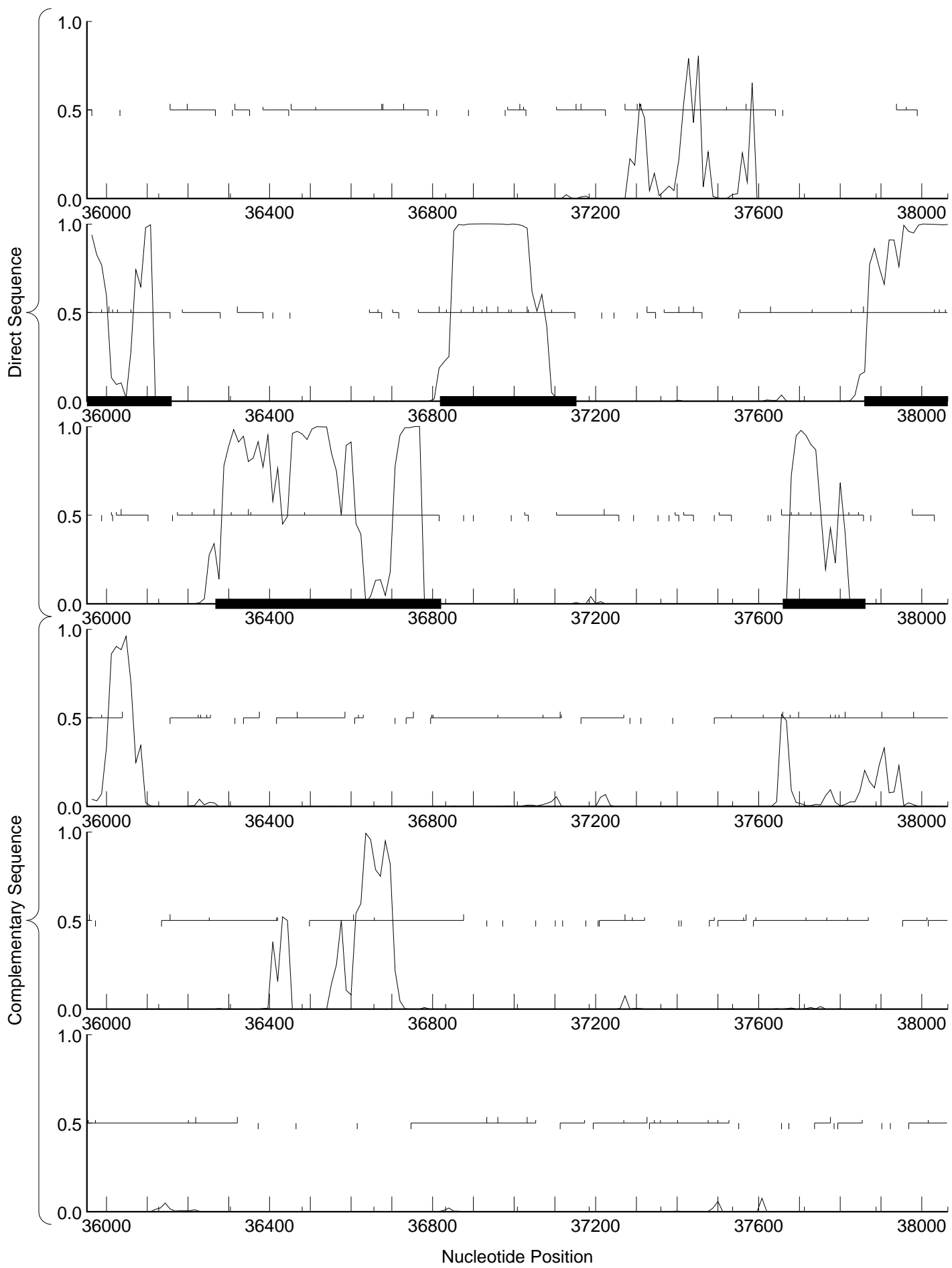
GeneMark.hmm prediction



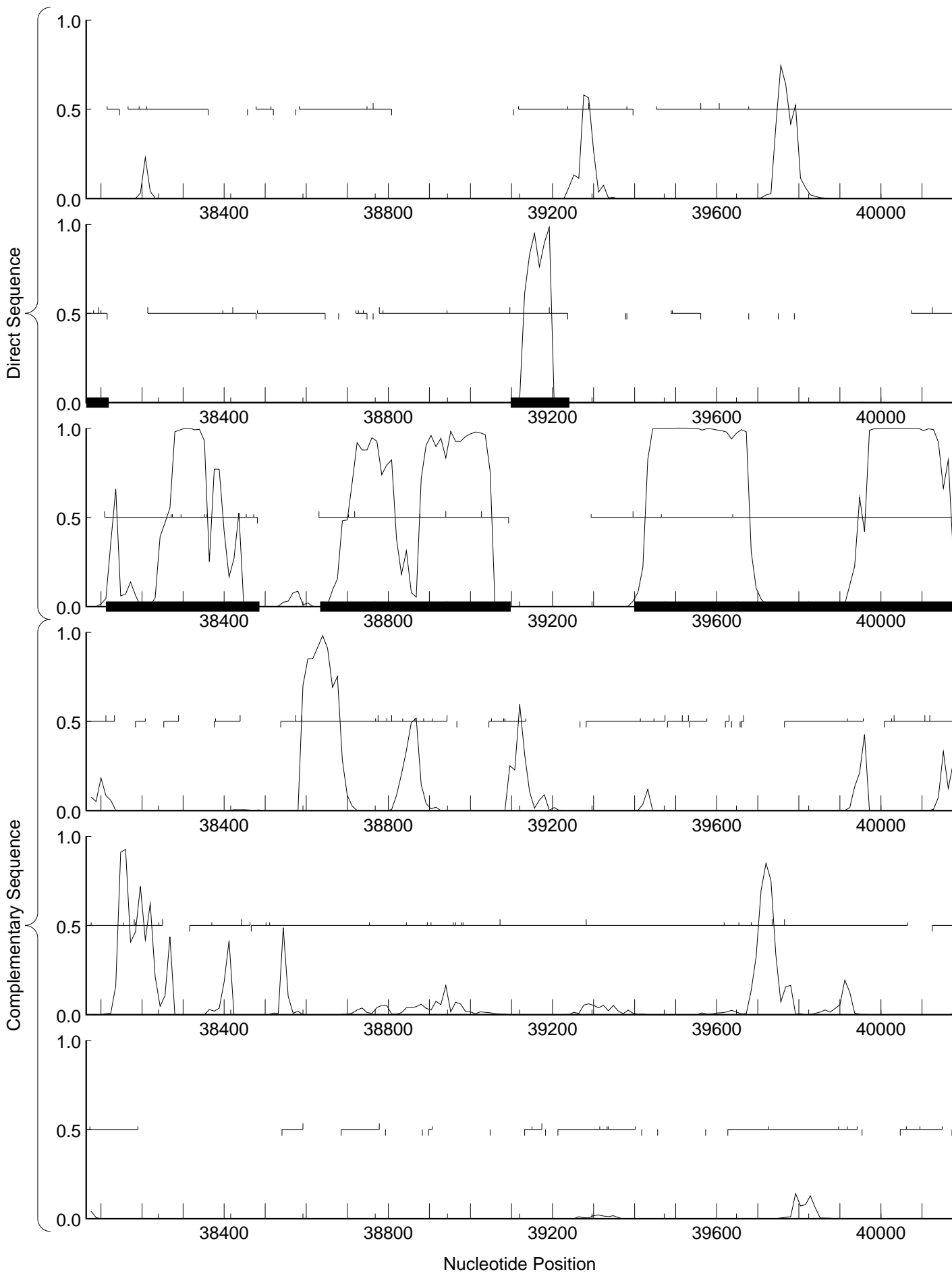
GeneMark.hmm prediction



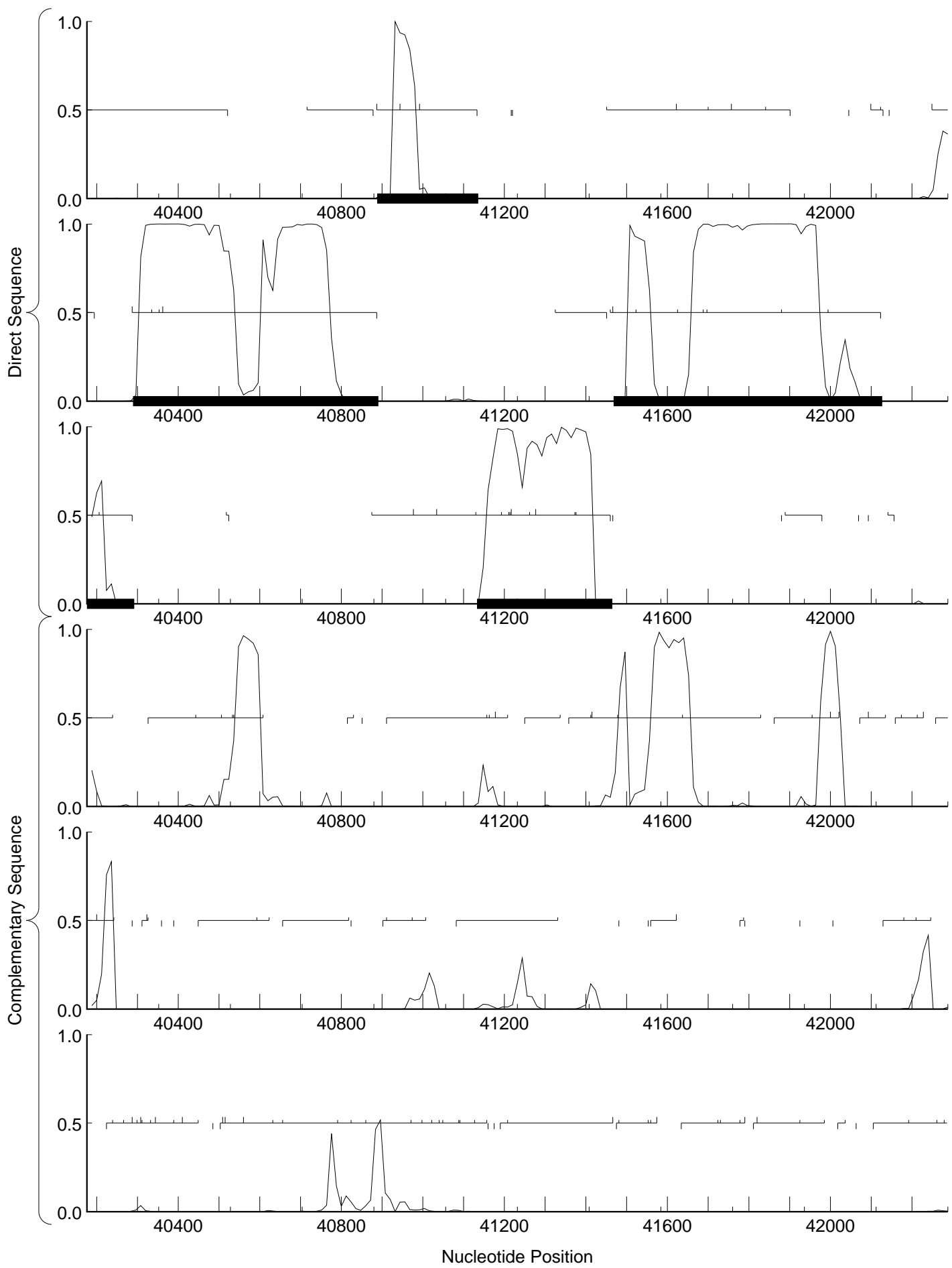
GeneMark.hmm prediction



GeneMark.hmm prediction



GeneMark.hmm prediction



GeneMark.hmm prediction

