

GeneMark

Version 2.5p (09.08.06)

Copyright 1993 - M. Borodovsky, J. McIninch

PROGRAM INFORMATION

Sequence : Microbacterium phage Armstrong complete sequence, 39928 bp including 10-base 3' overhang (A
Analysis Date : 5/26/18 at 2:16:24
Pages : 20
Sequence Length : 39928 bp
GC Content : 67.14%

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,

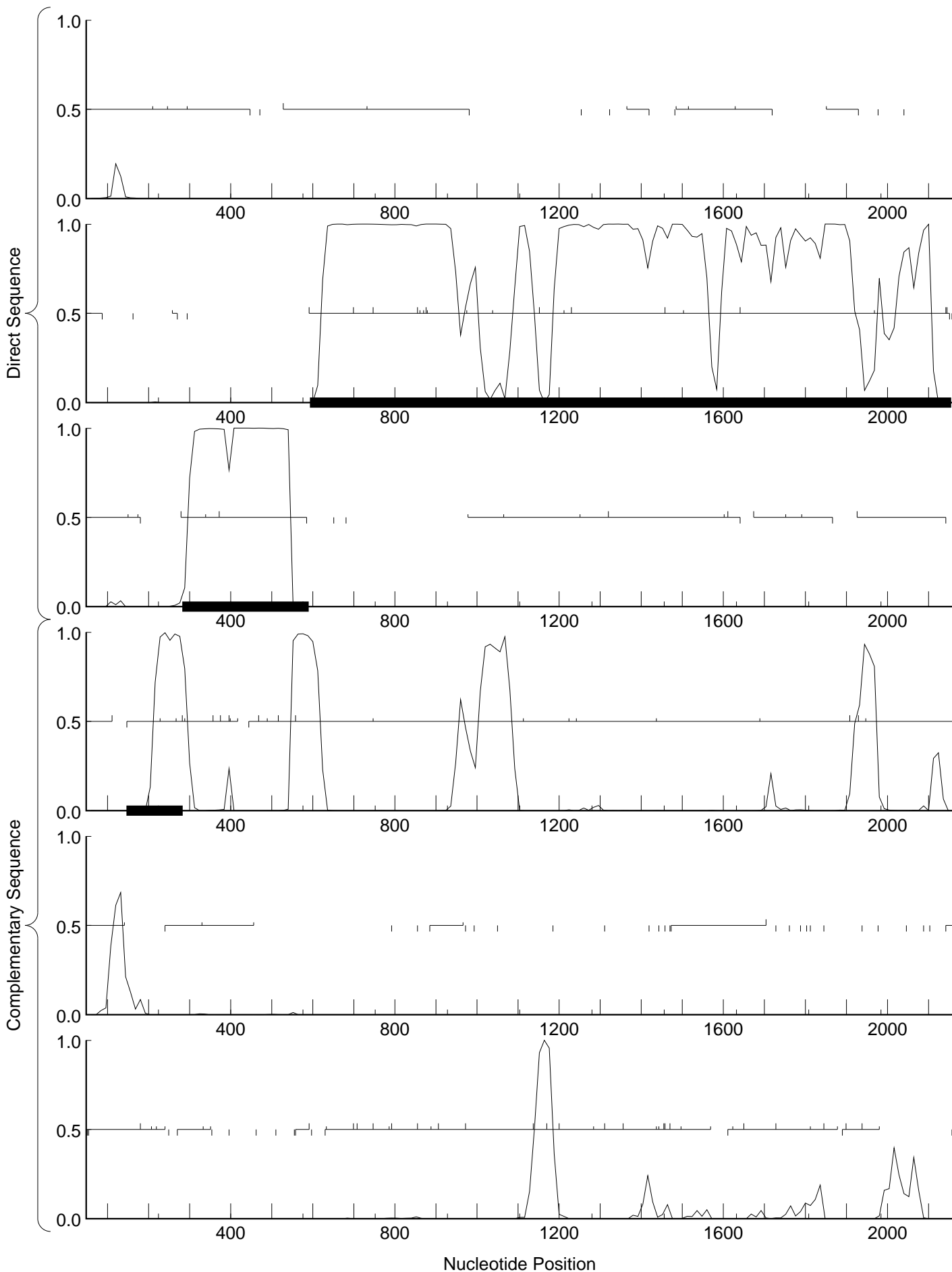
Matrix notes & comments

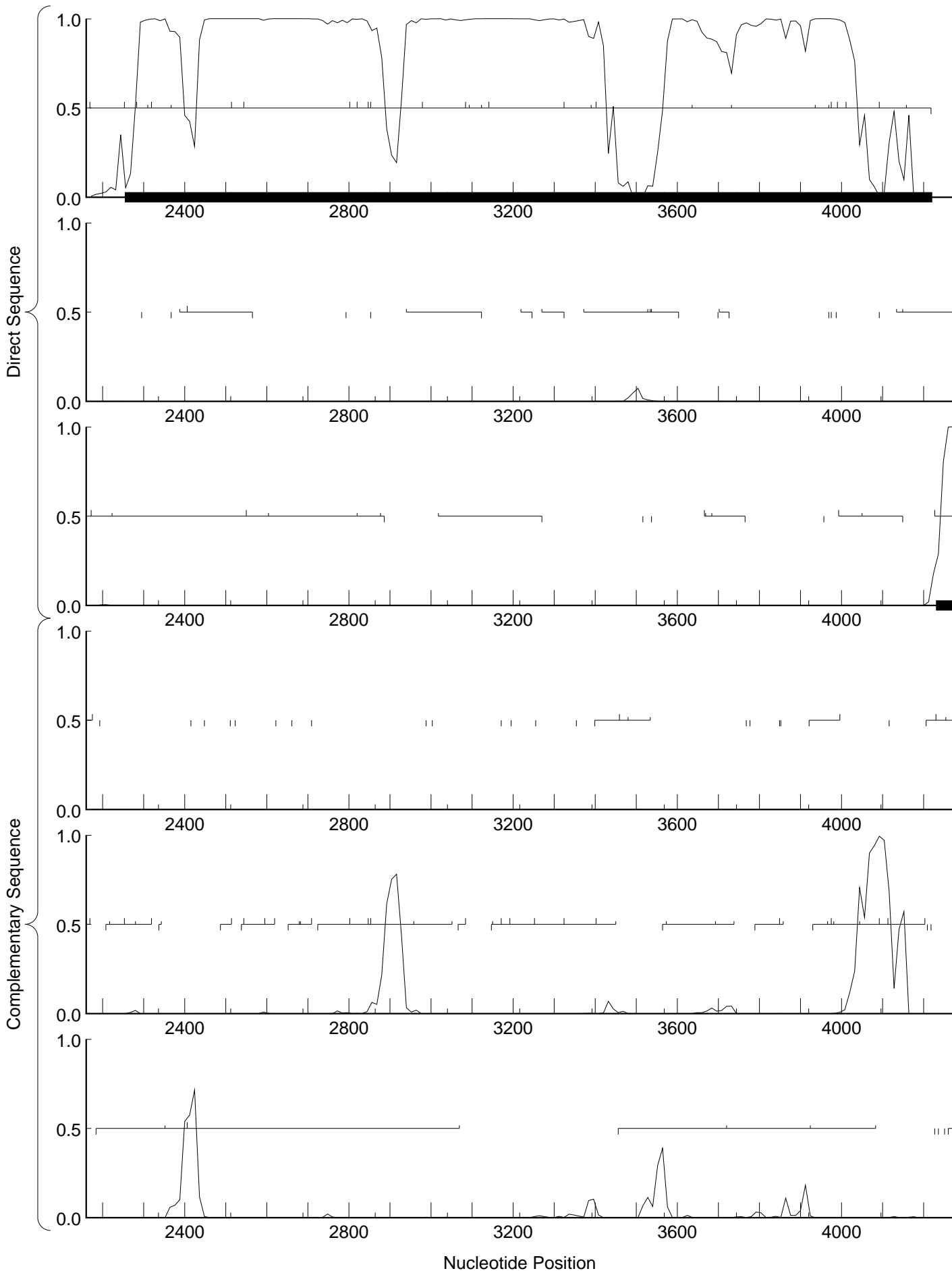
For details on the model building procedure see:
Besemer J. and Borodovsky M.
"Heuristic approach to deriving models for gene finding"
NAR, 1999, Vol. 27, No. 19, pp. 3911-3920

MATRIX INFORMATION

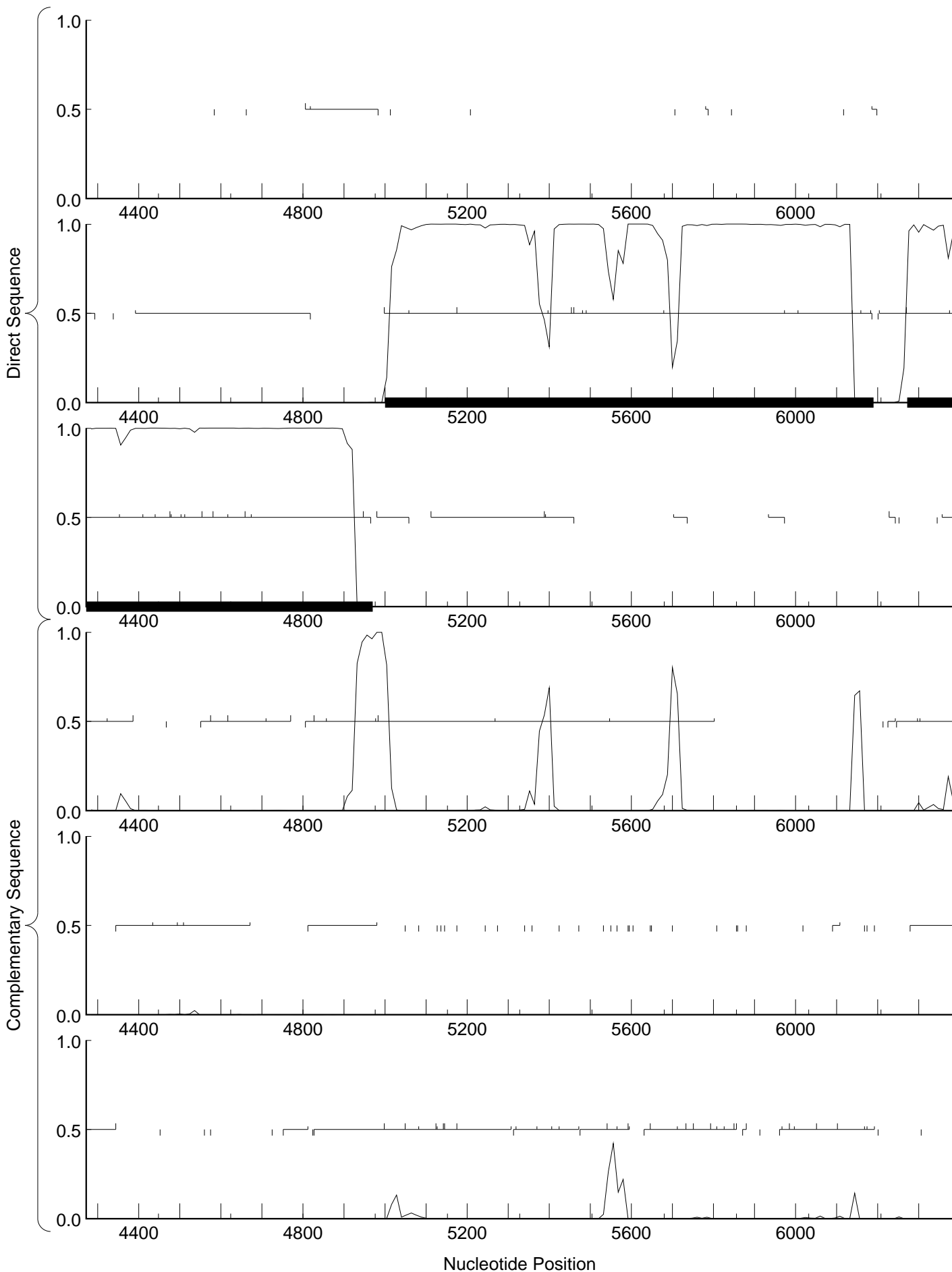
Matrix : Heuristic, GC = 67
Author : Borodovsky Laboratory - Georgia Tech
Order : 2

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

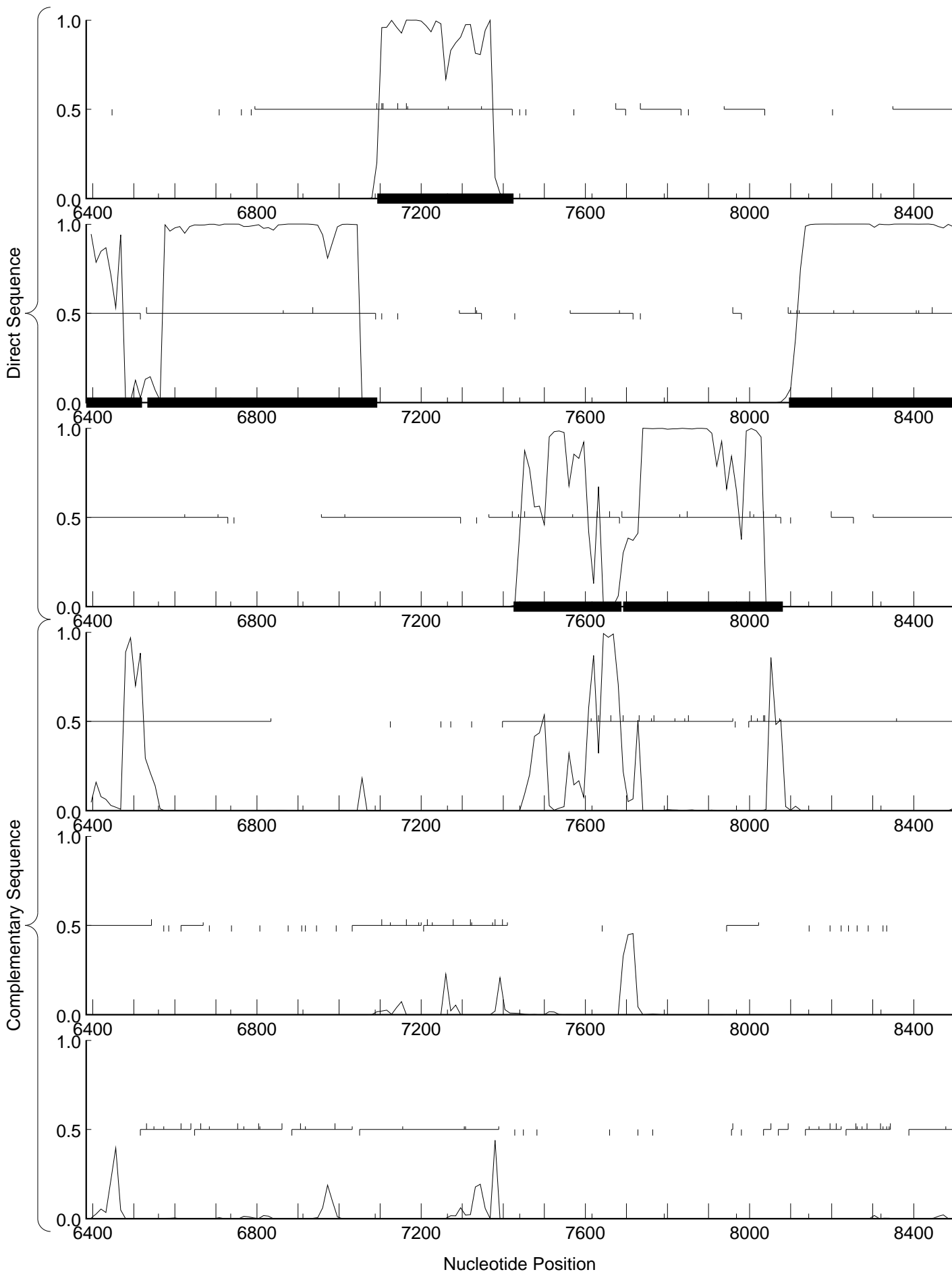




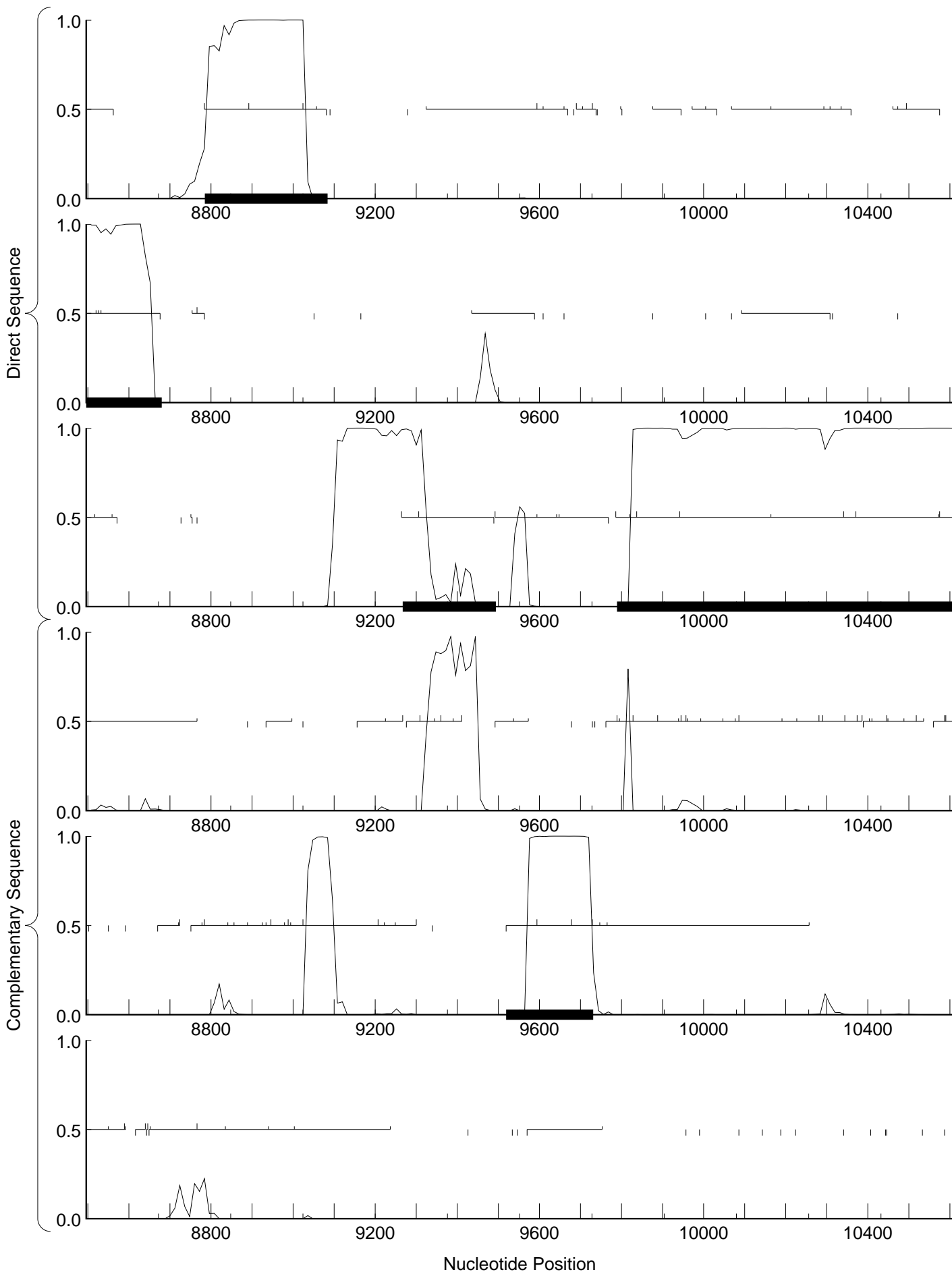
GeneMark.hmm prediction



GeneMark.hmm prediction

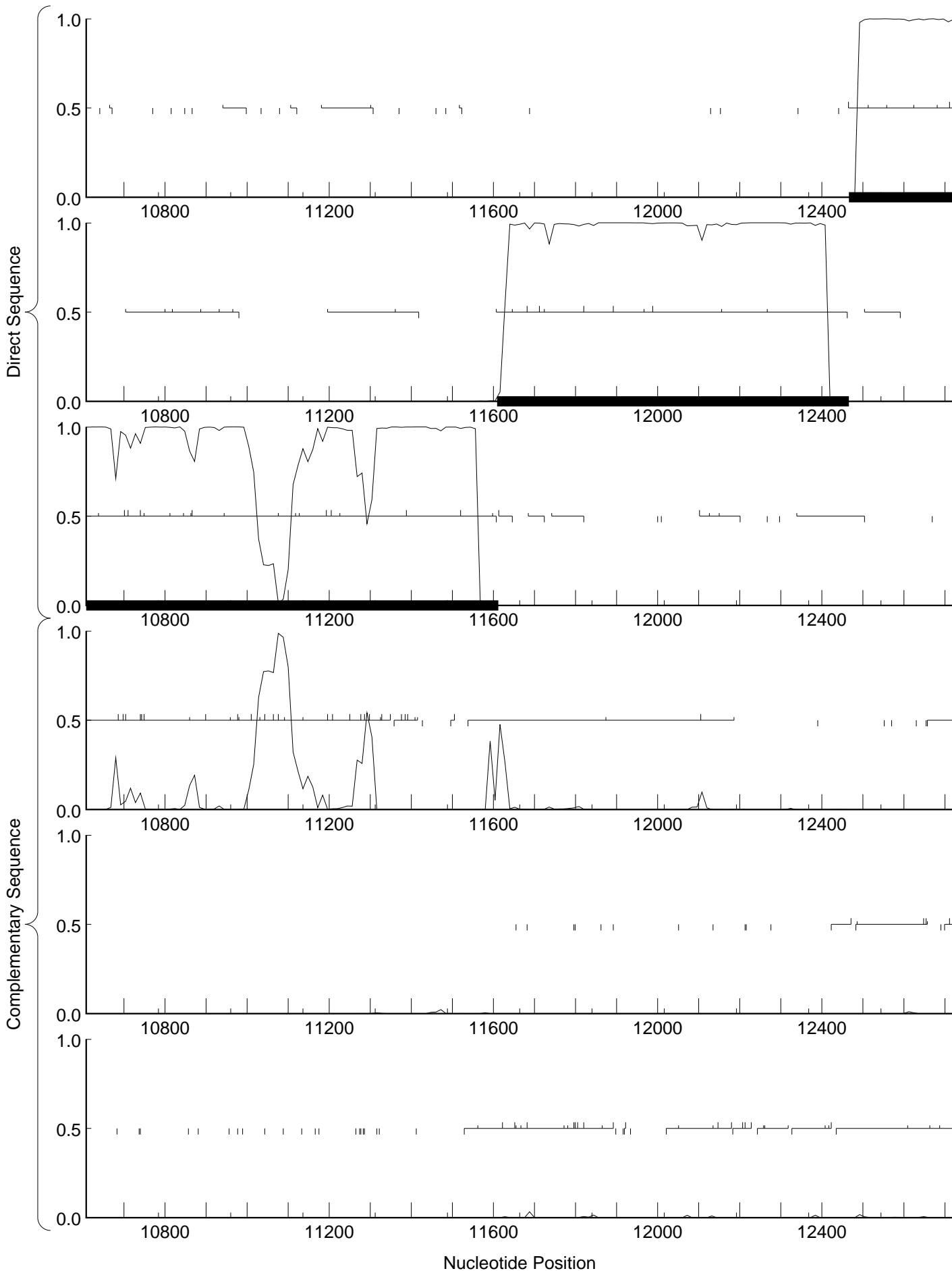


GeneMark.hmm prediction



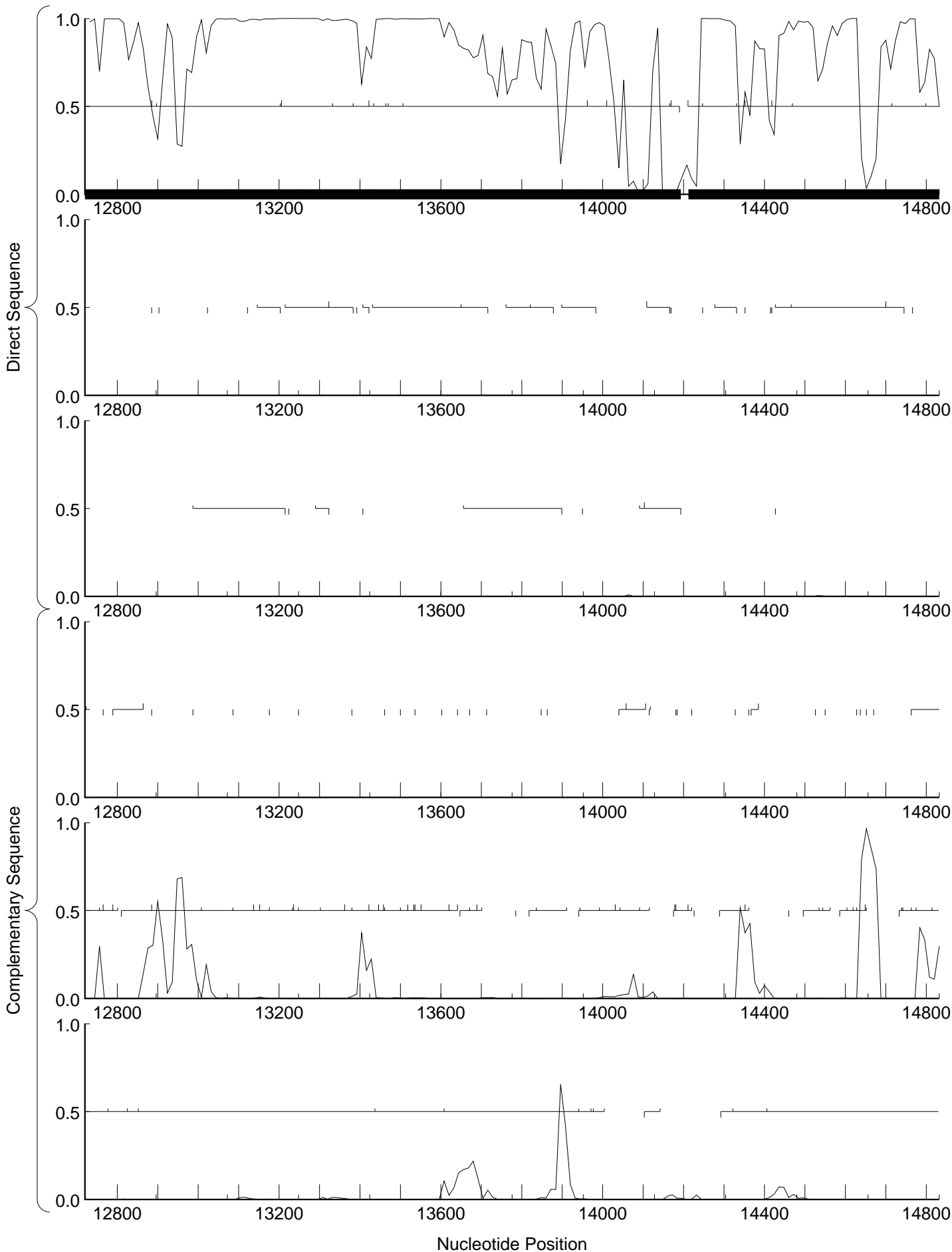
██████████

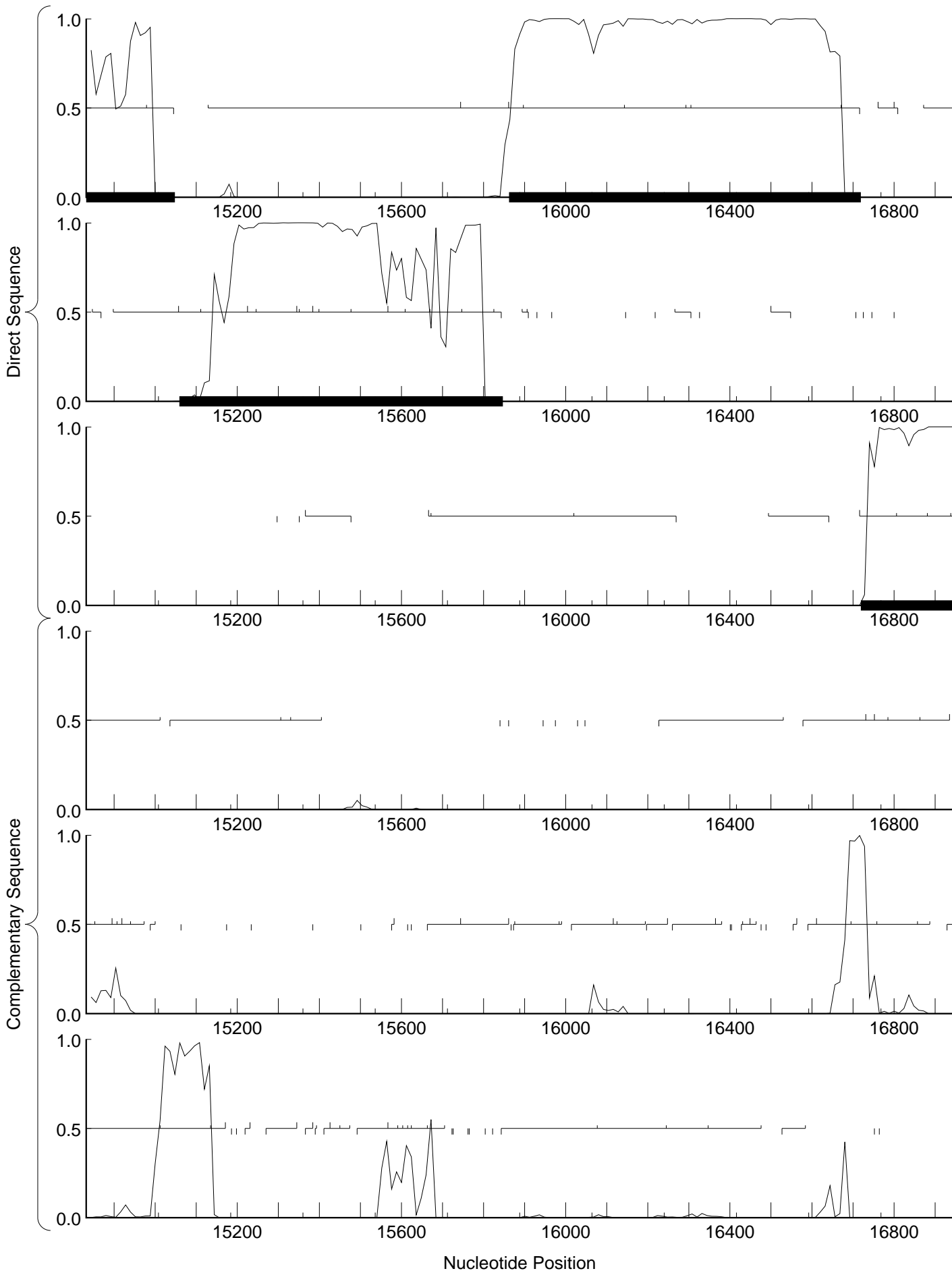
GeneMark.hmm prediction



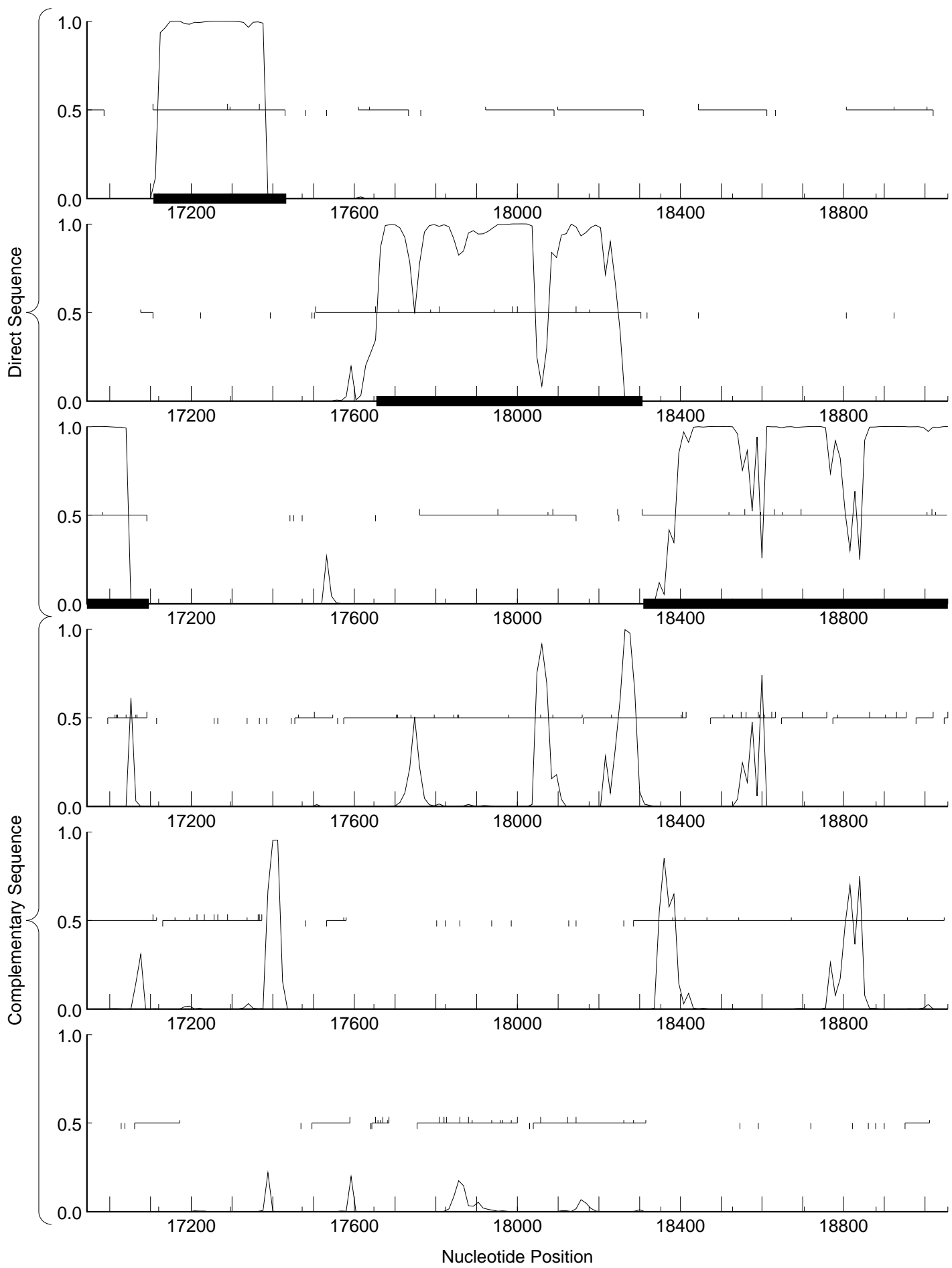


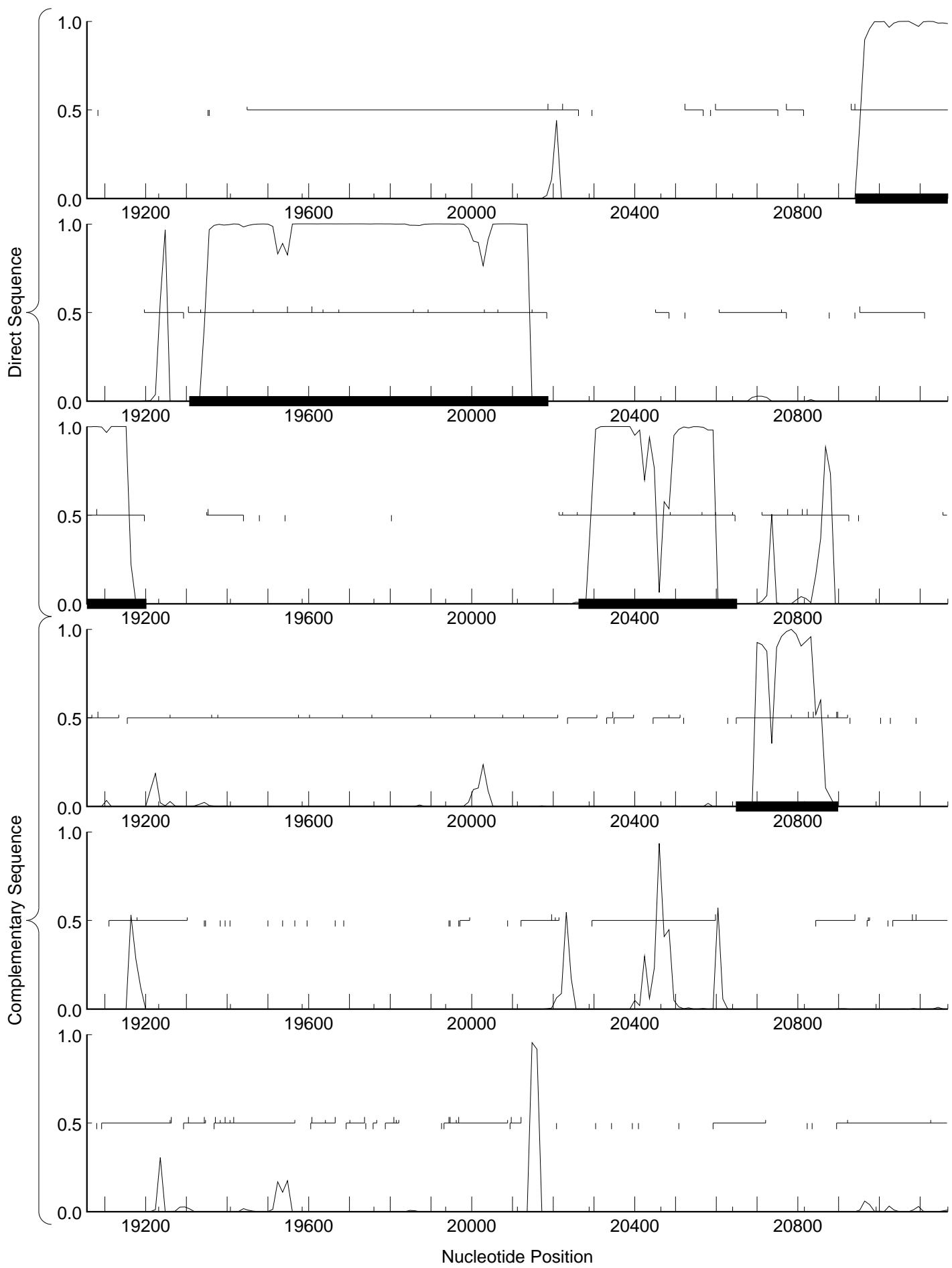
GeneMark.hmm prediction



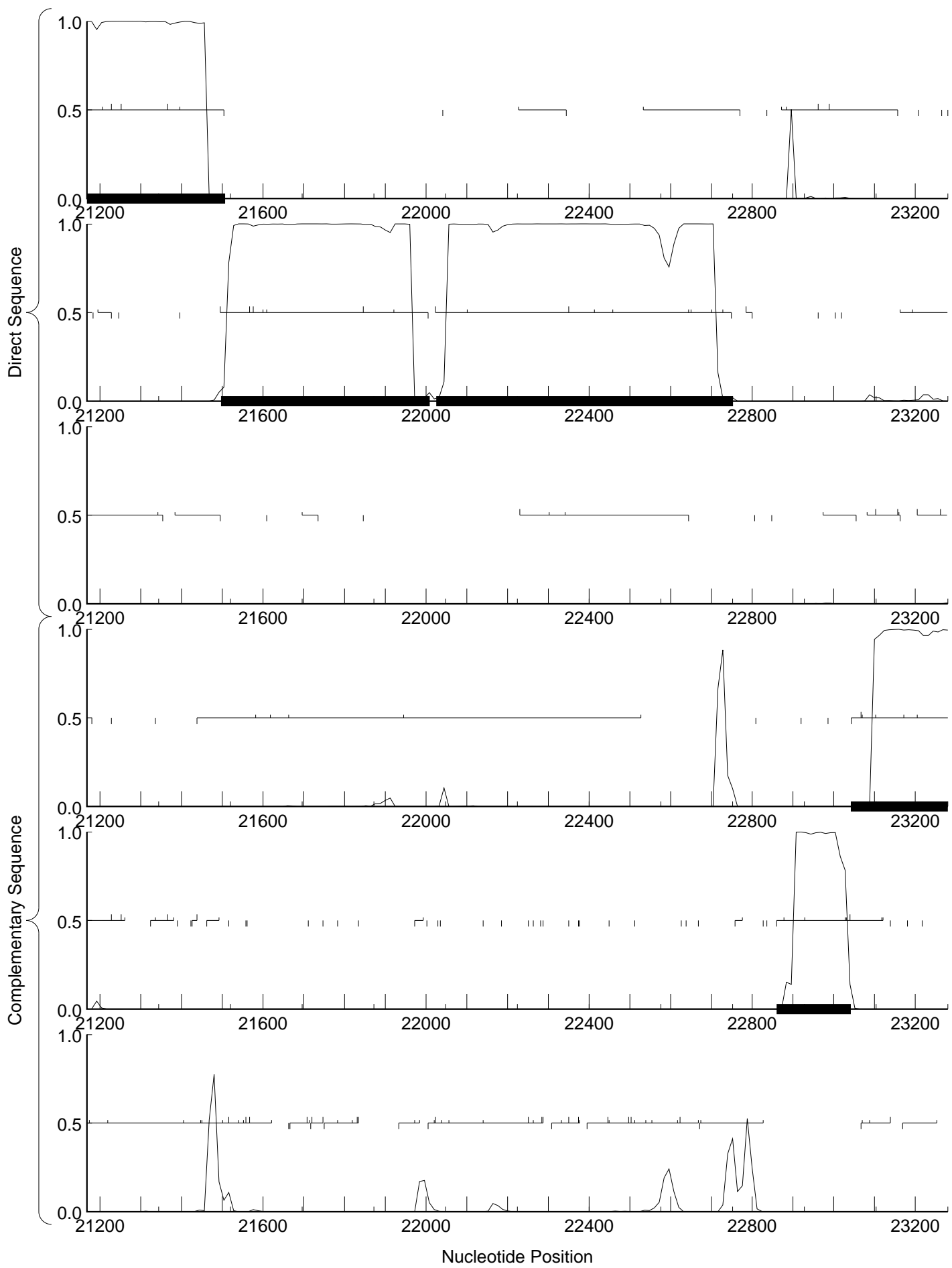


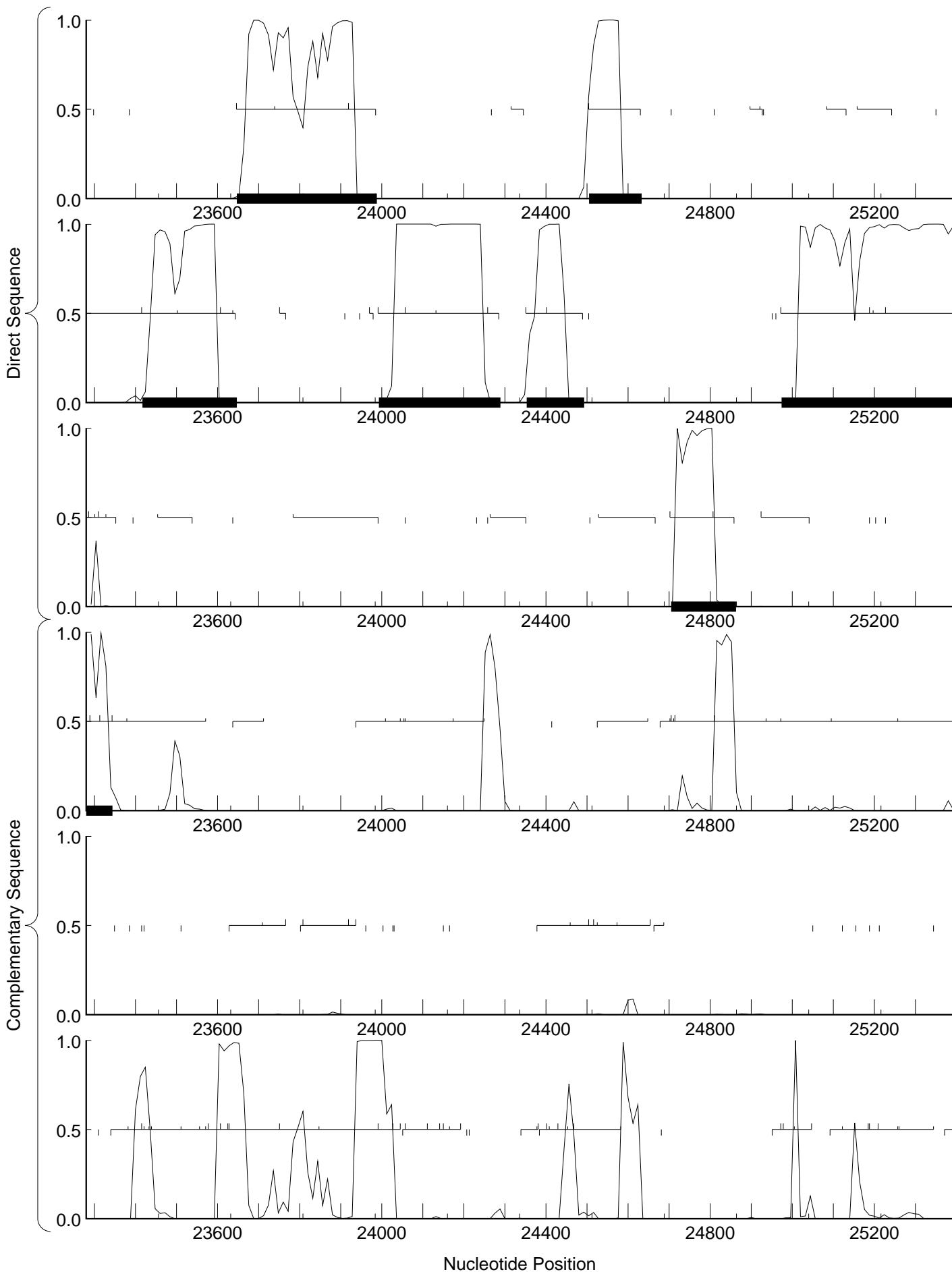
GeneMark.hmm prediction

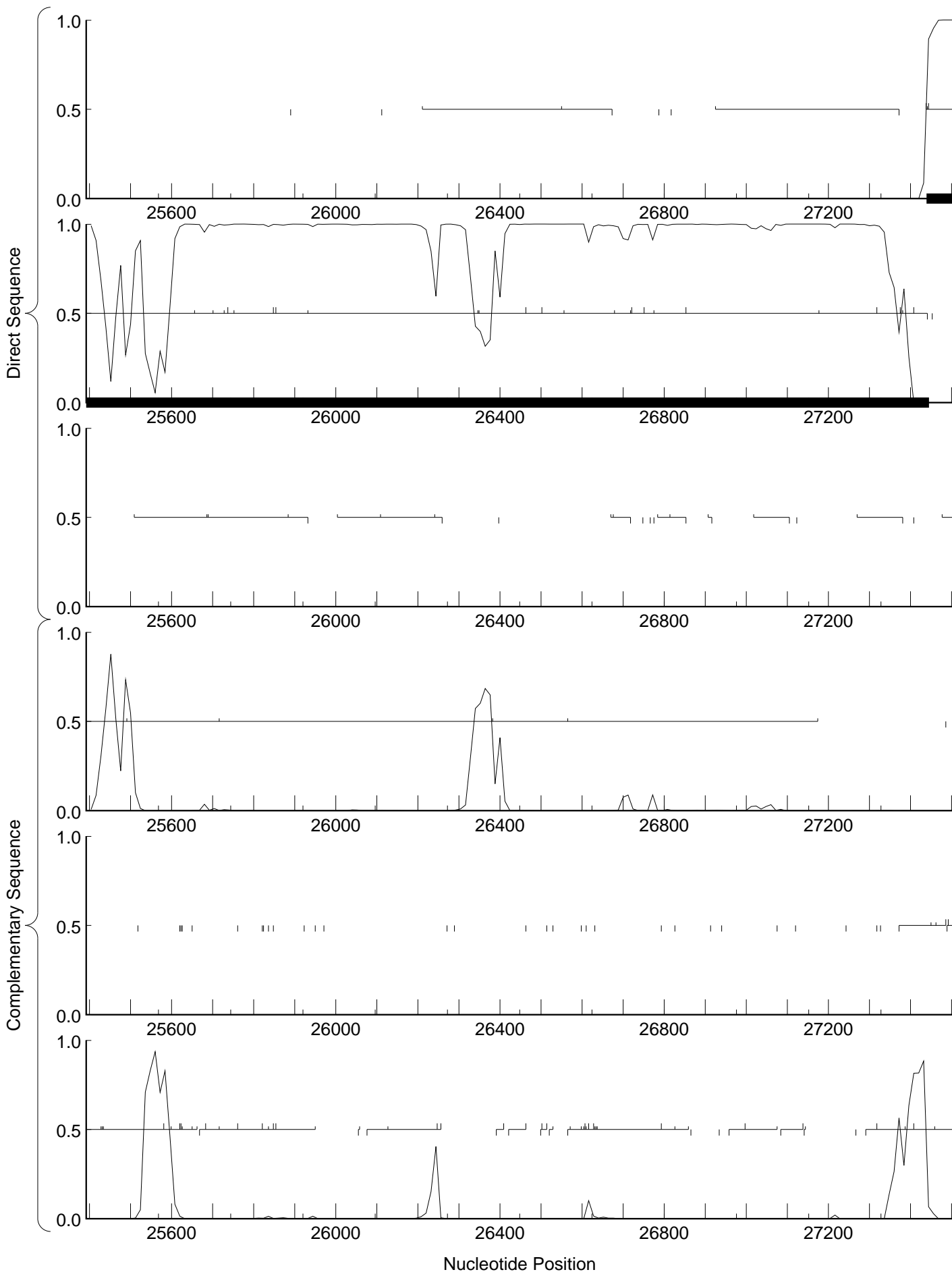




GeneMark.hmm prediction

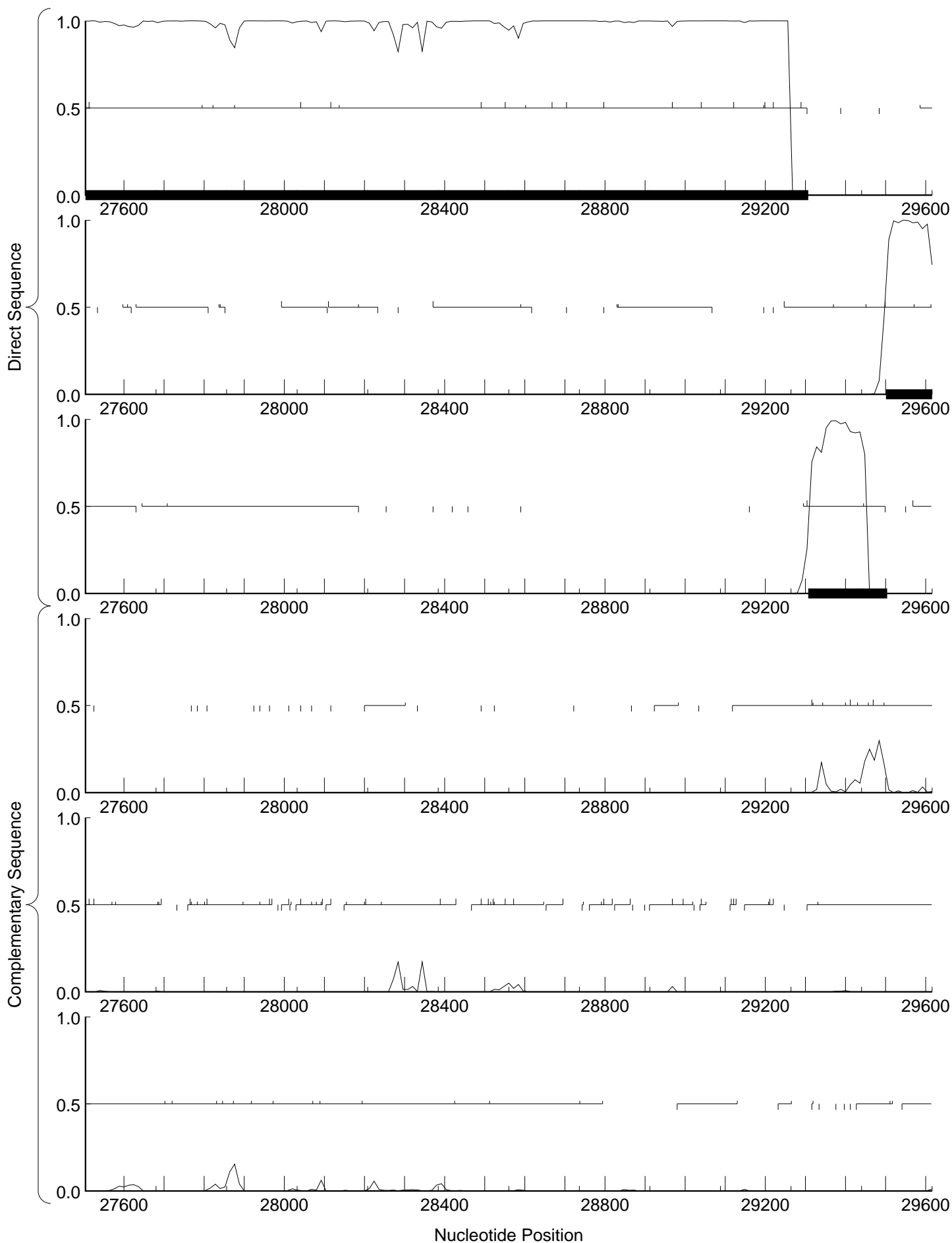


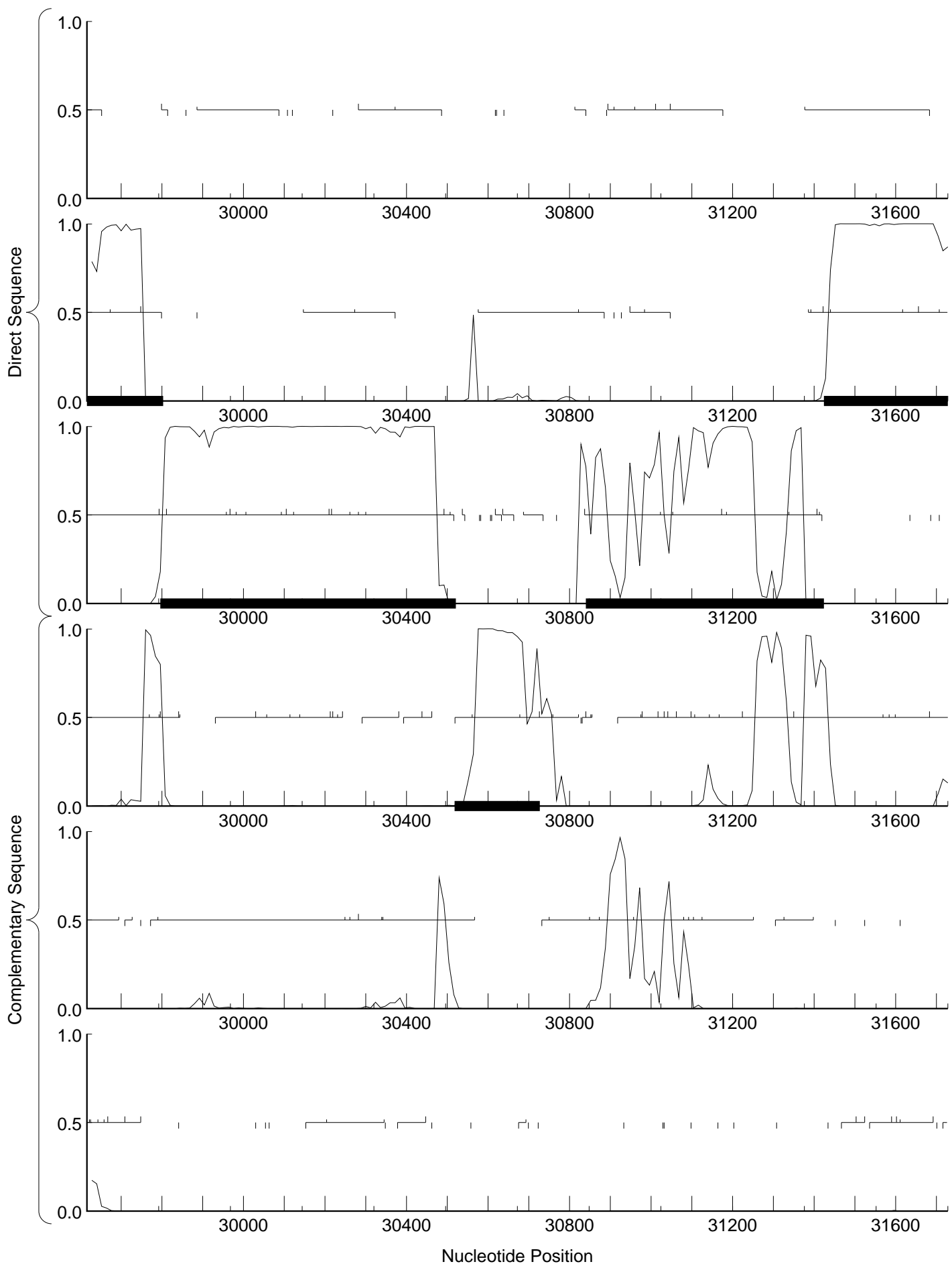




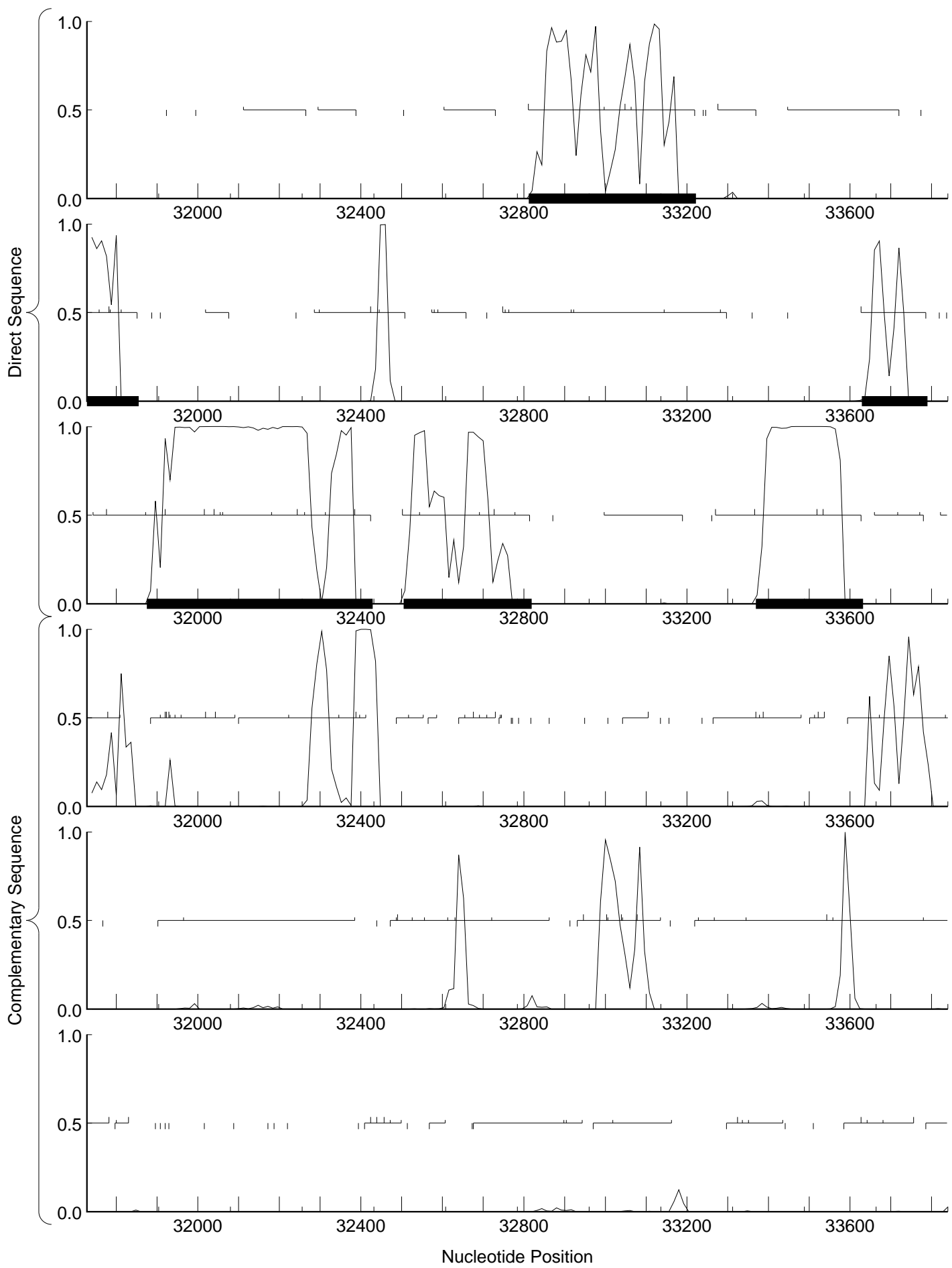
complete sequence, 39928 bp including 10-base 3' overhang (ACTCCCGGCA), Cluster EB, Order 2, Window 96, Step 12, 15/20

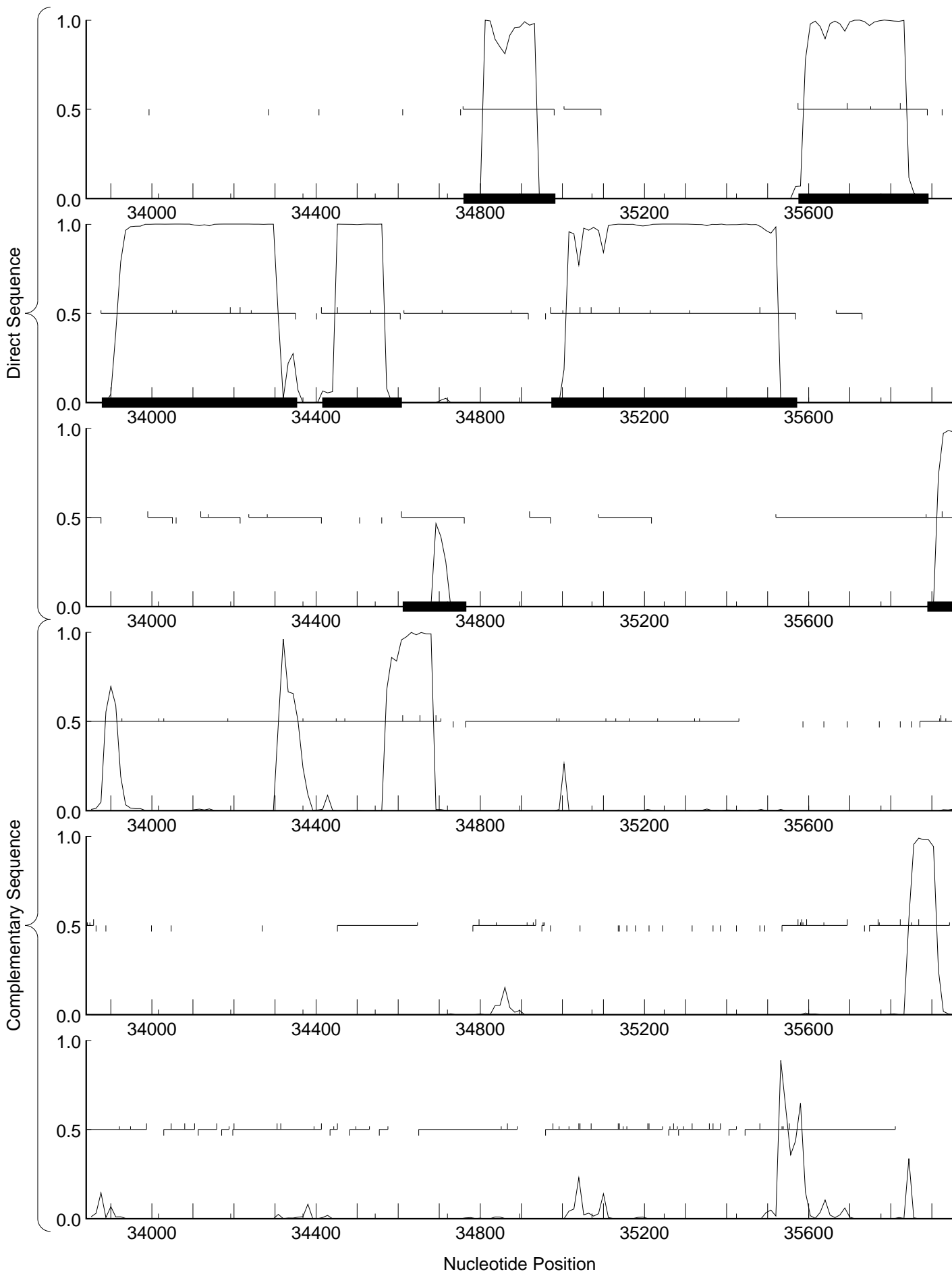
GeneMark.hmm prediction



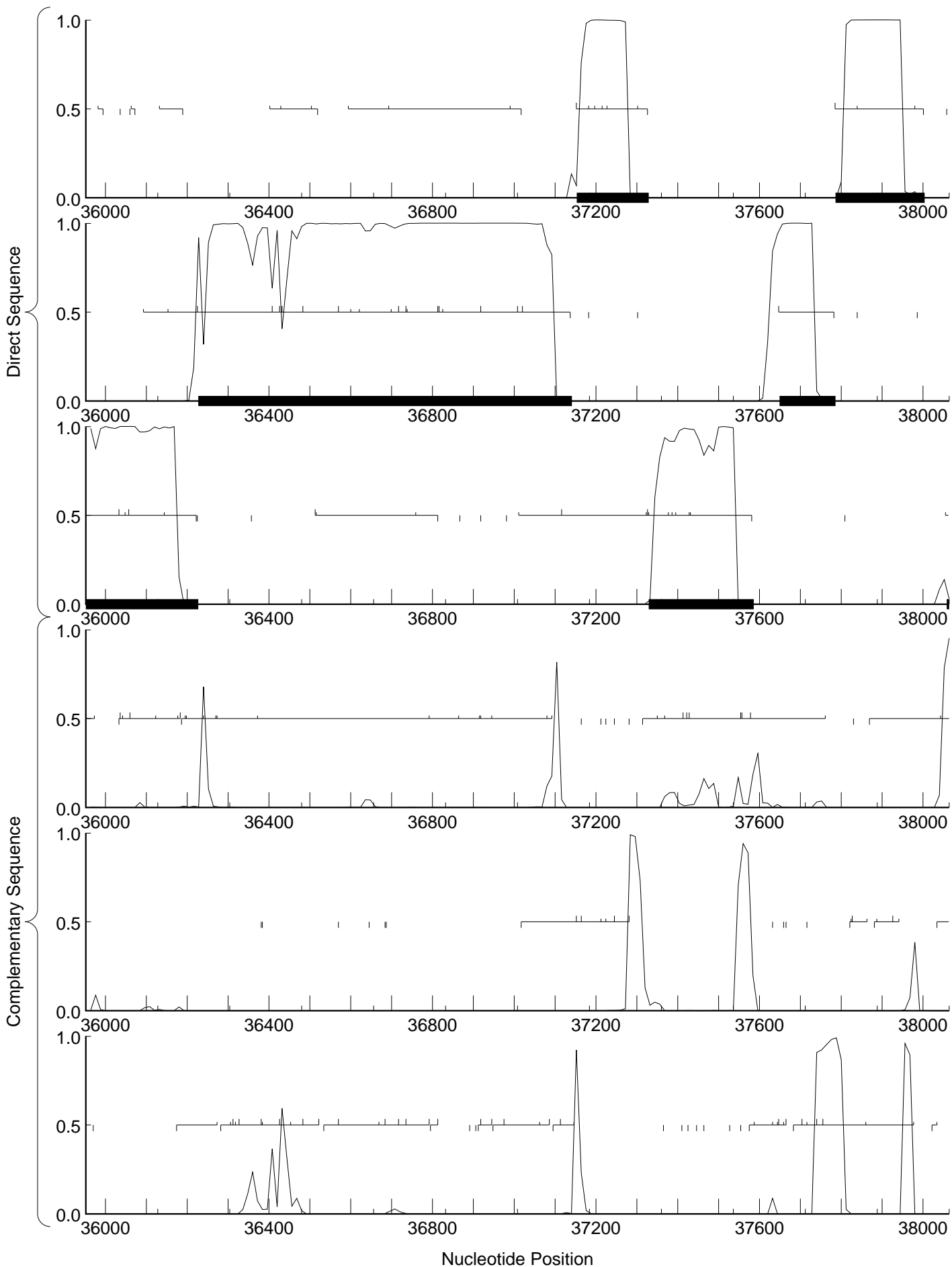


GeneMark.hmm prediction





complete sequence, 39928 bp including 10-base 3' overhang (ACTCCCGGCA), Cluster EB, Order 2, Window 96, Step 12, 19/20



GeneMark.hmm prediction

