

GeneMark

Version 2.5p (09.08.06)

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PROGRAM INFORMATION

Sequence : Mycobacterium phage DMoney complete sequence, 41880 bp including 11-base 3' overhang (CCCCA
Analysis Date : 7/17/18 at 21:22:49
Pages : 21
Sequence Length : 41880 bp
GC Content : 66.56%

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,

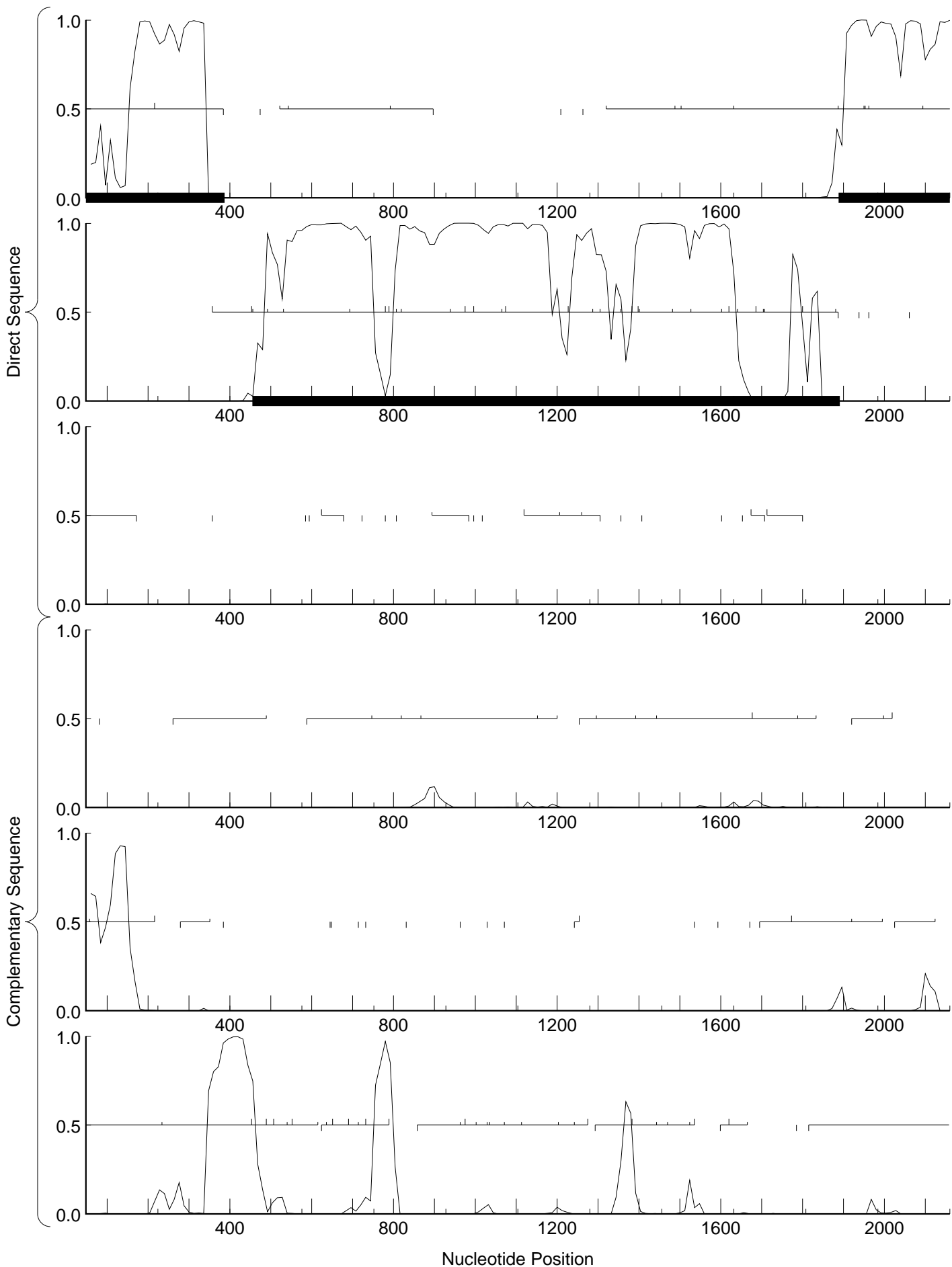
Matrix notes & comments

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

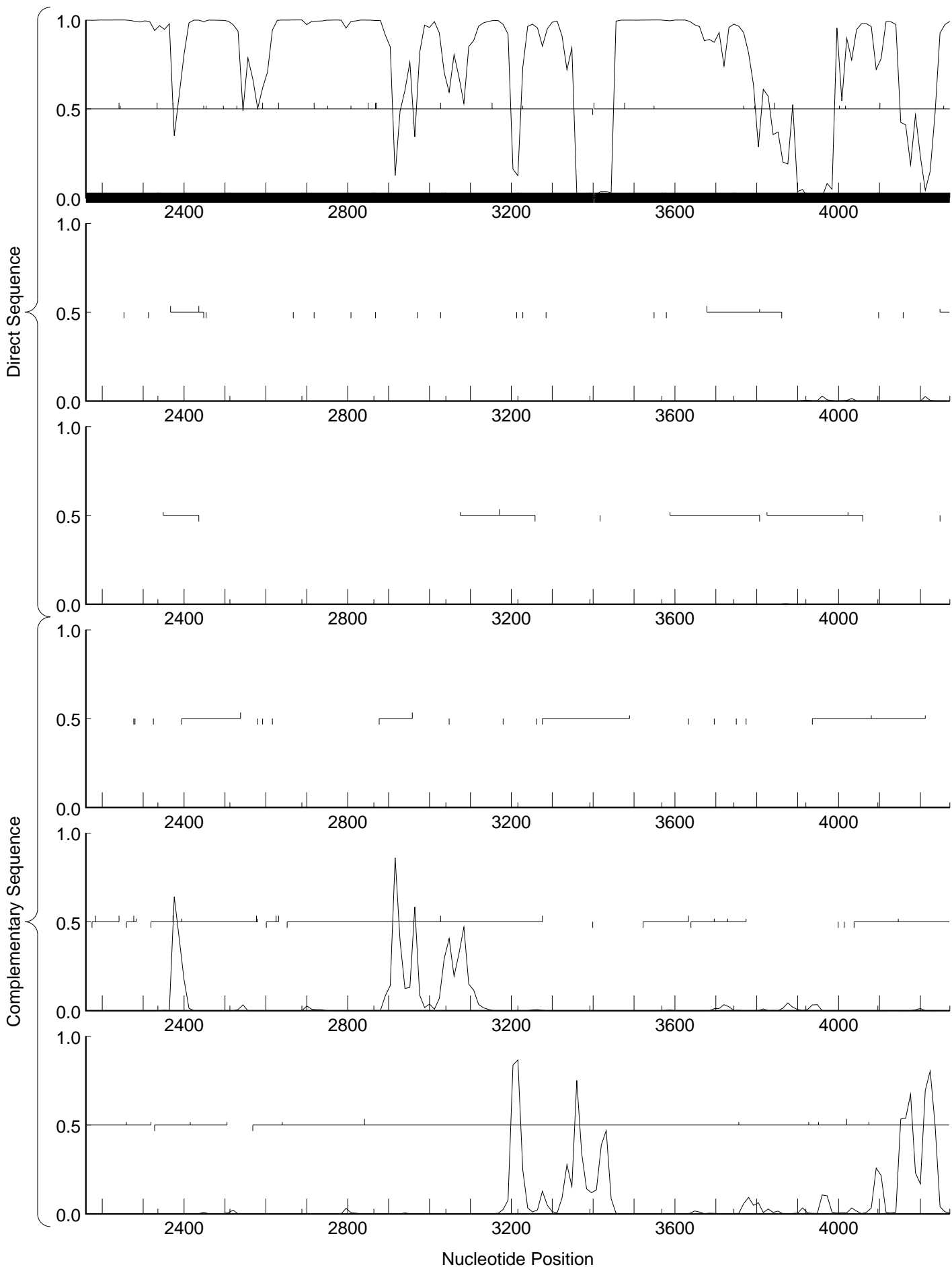
MATRIX INFORMATION

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

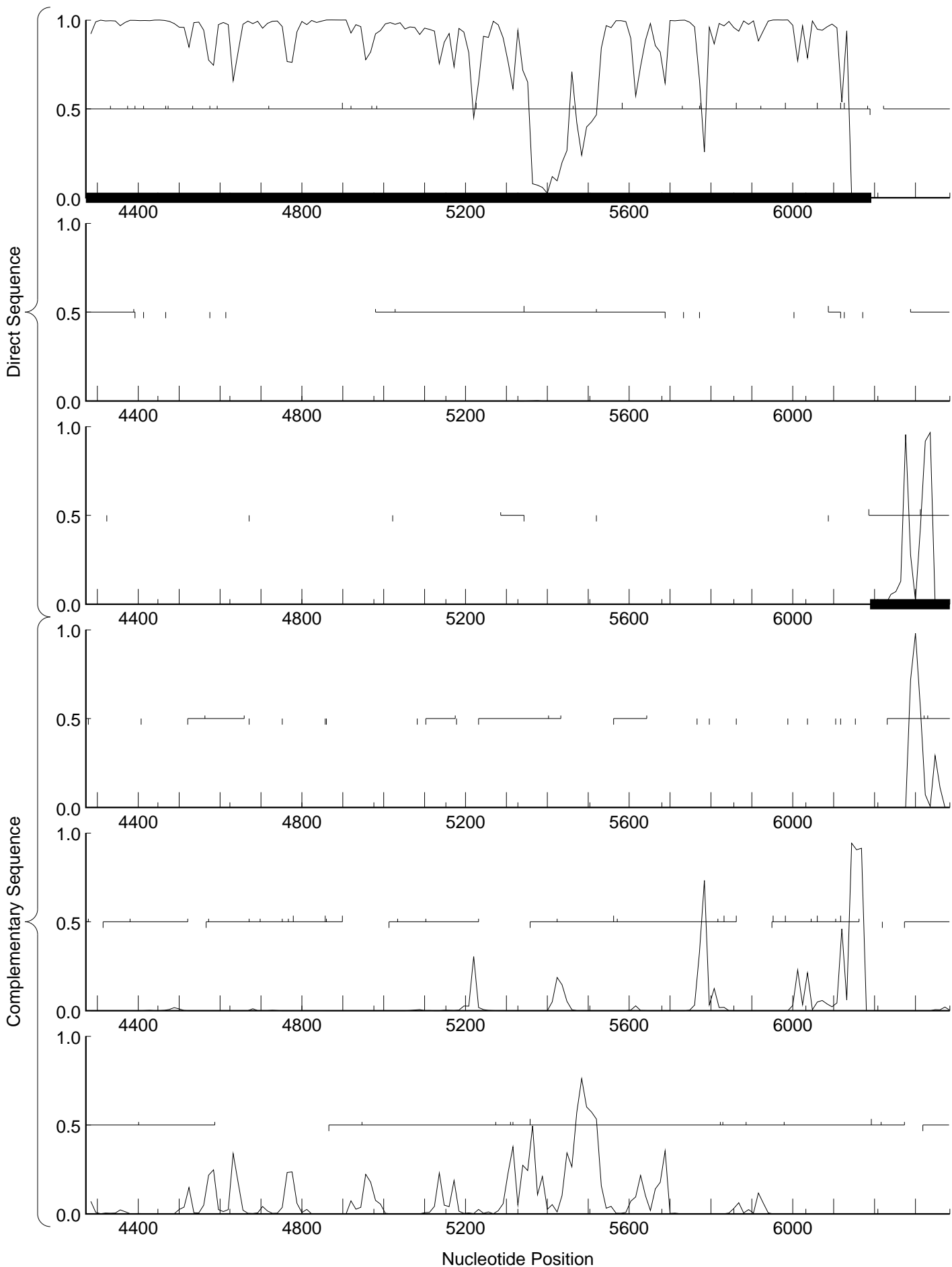
Send questions / comments to:
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School of Biology
Atlanta, GA 30332-0230



complete sequence, 41880 bp including 11-base 3' overhang (CCCCATGGCAT), Cluster G1, Order 2, Window 96, Step 12, 3/21

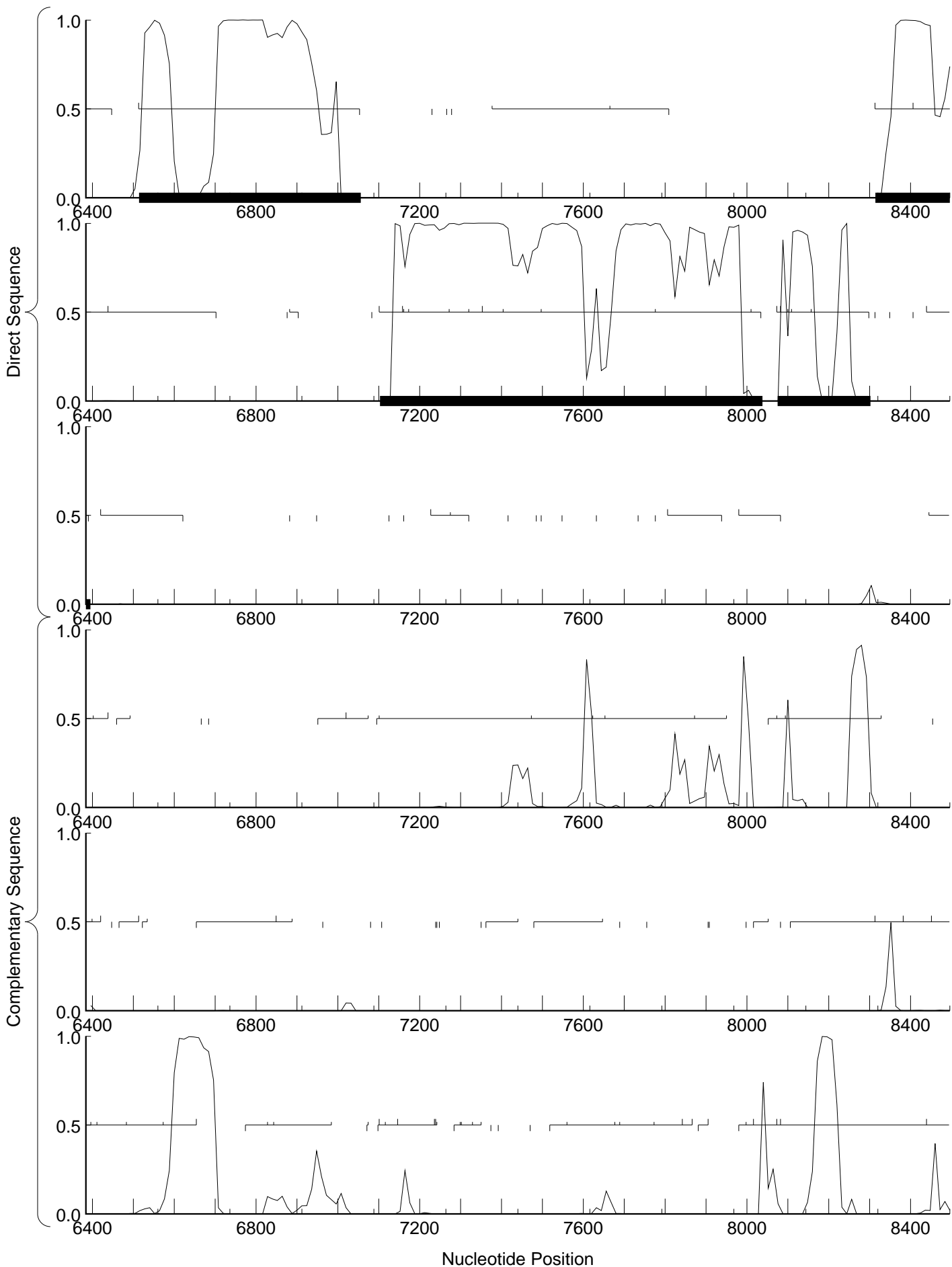


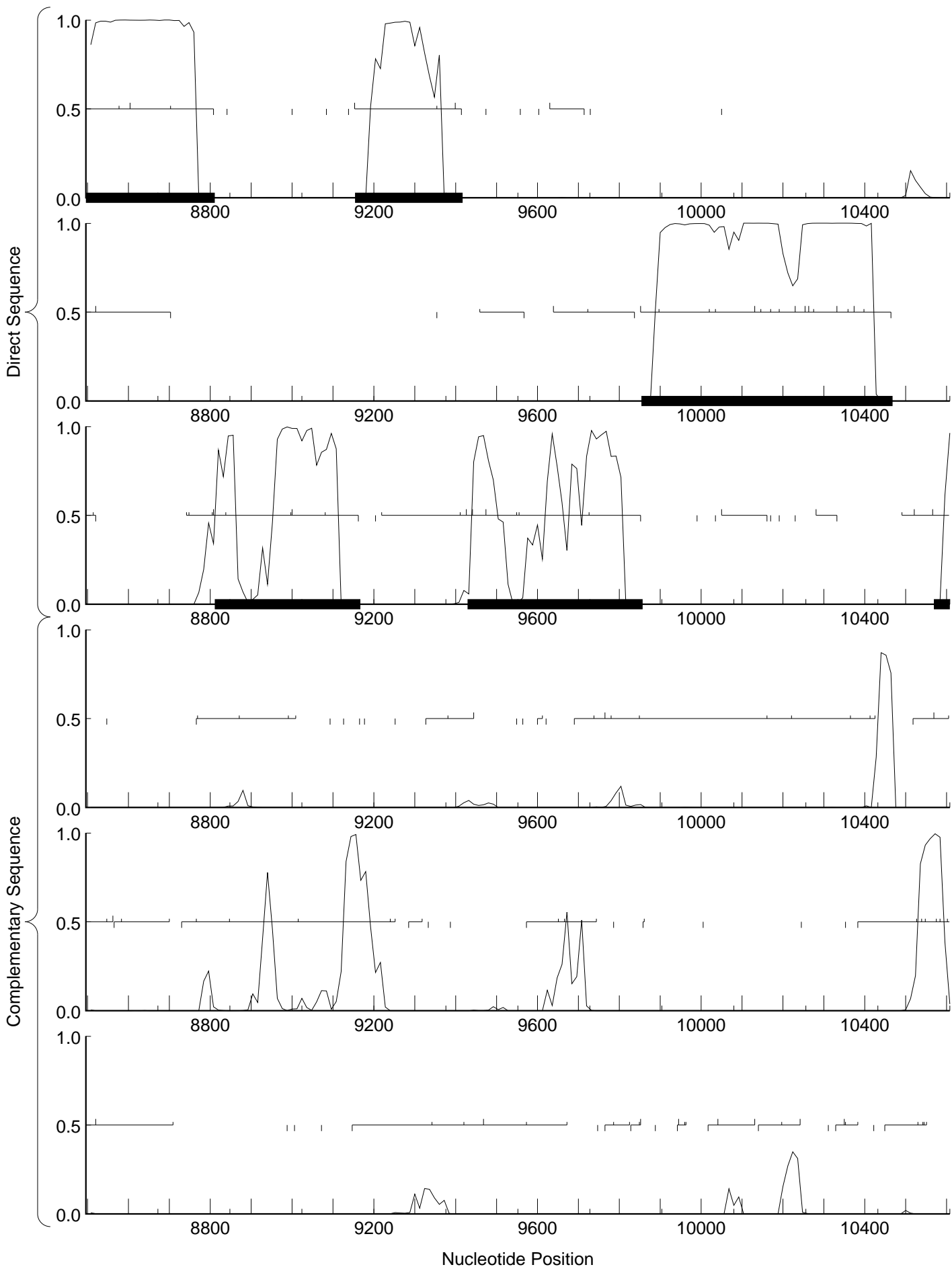
complete sequence, 41880 bp including 11-base 3' overhang (CCCCATGGCAT), Cluster G1, Order 2, Window 96, Step 12, 4/21



complete sequence, 41880 bp including 11-base 3' overhang (CCCCATGGCAT), Cluster G1, Order 2, Window 96, Step 12, 5/21

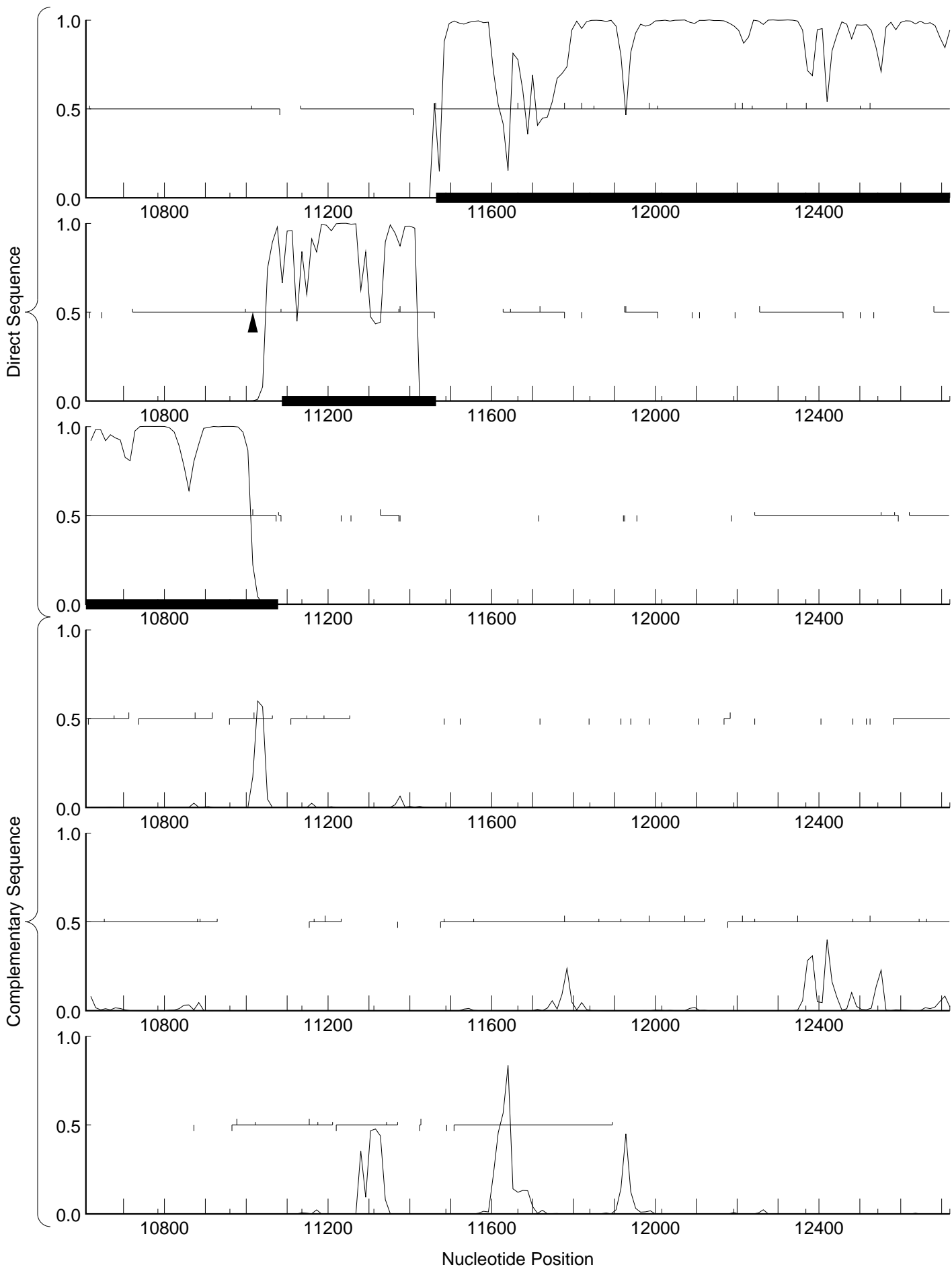
GeneMark.hmm prediction





complete sequence, 41880 bp including 11-base 3' overhang (CCCCATGGCAT), Cluster G1, Order 2, Window 96, Step 12, 7/21

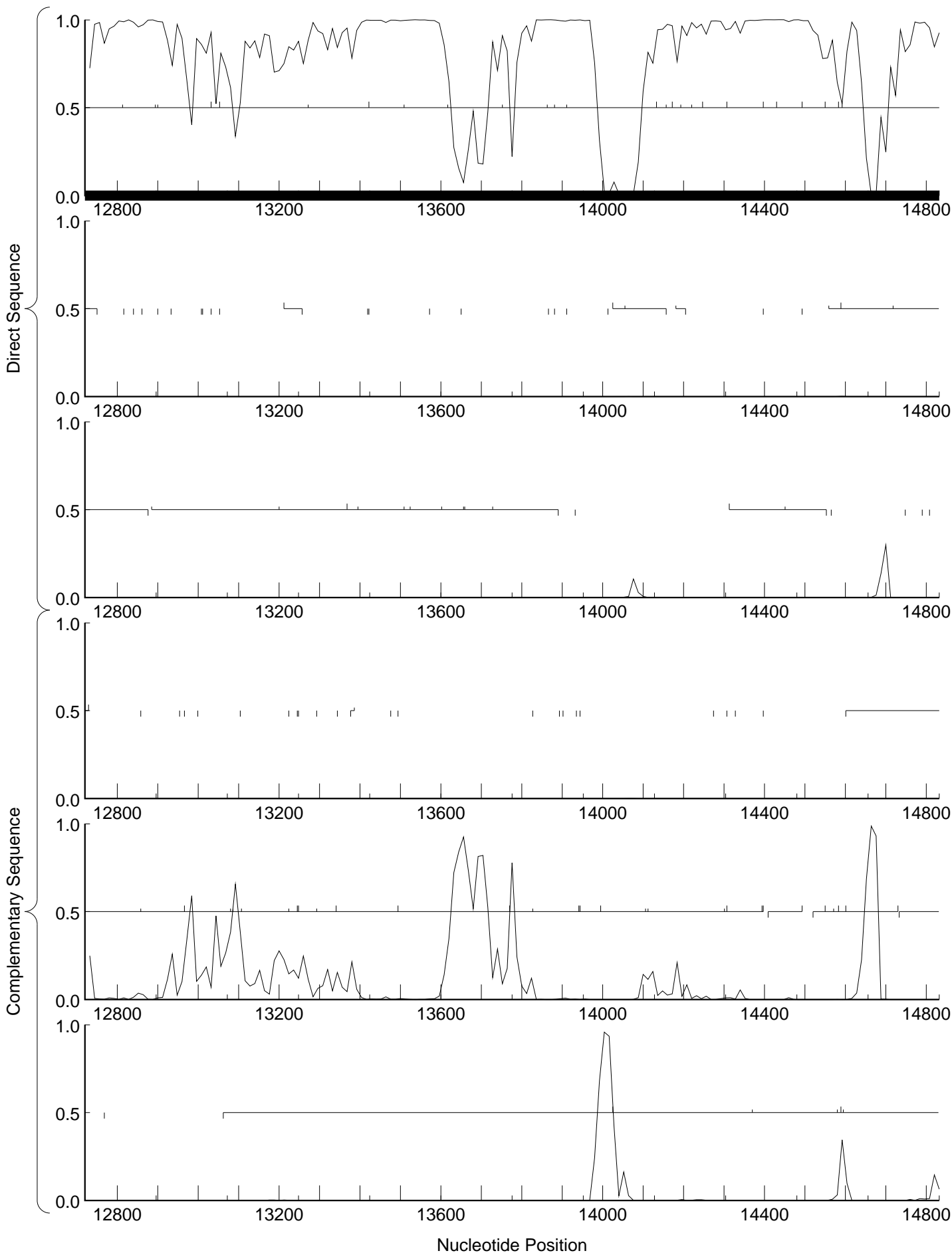
GeneMark.hmm prediction



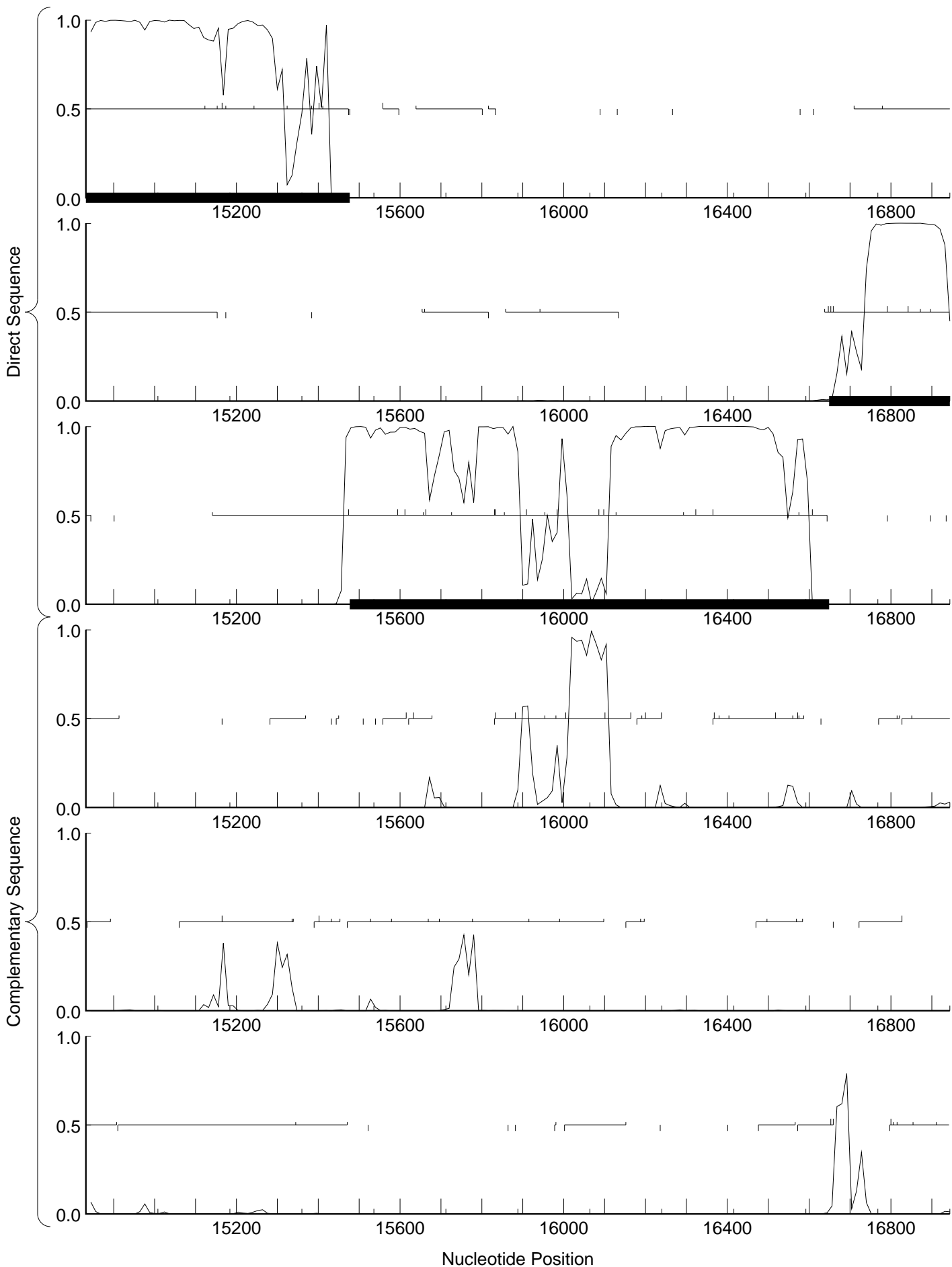
complete sequence, 41880 bp including 11-base 3' overhang (CCCCATGGCAT), Cluster G1, Order 2, Window 96, Step 12, 8/21



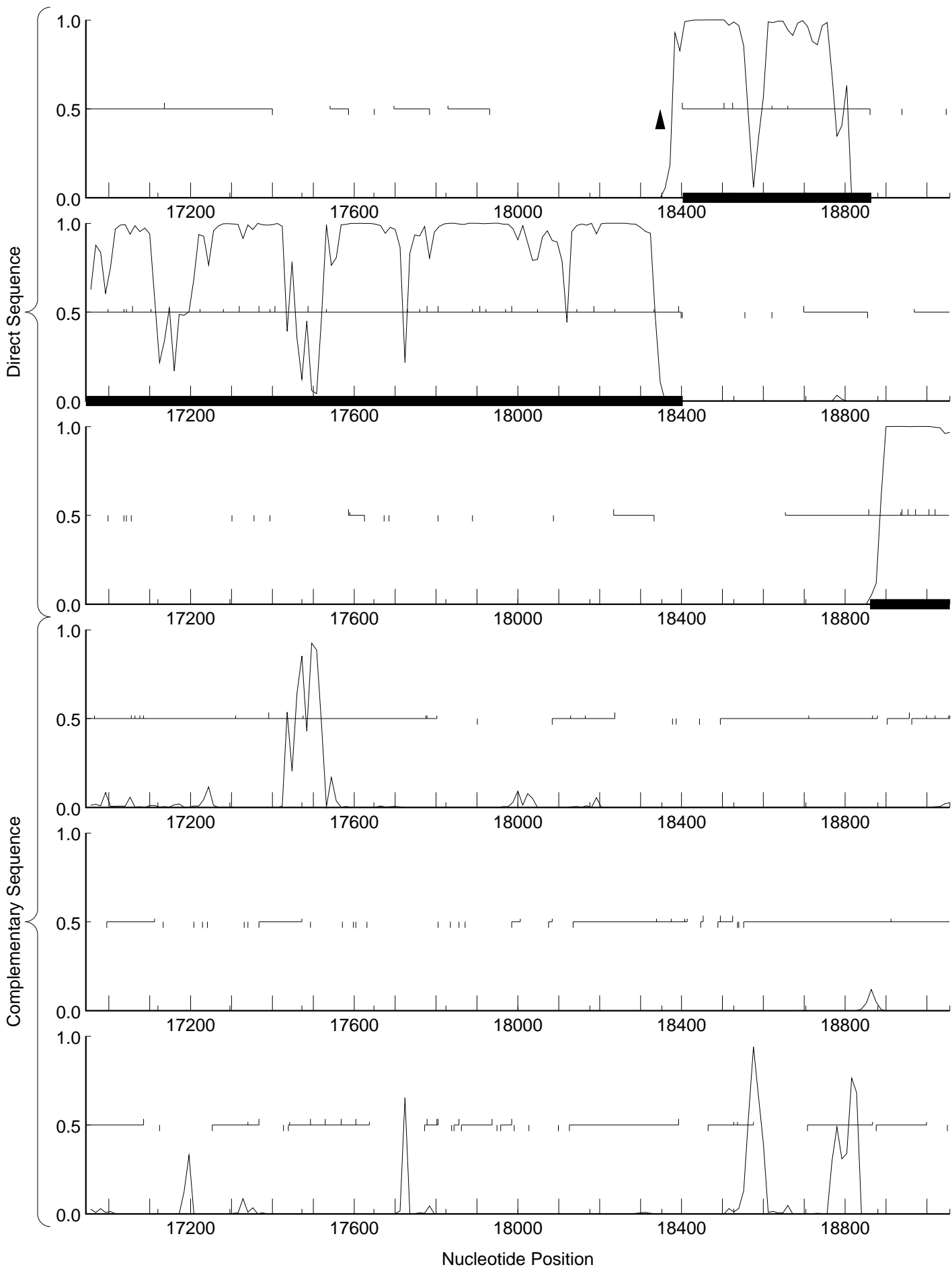
GeneMark.hmm prediction

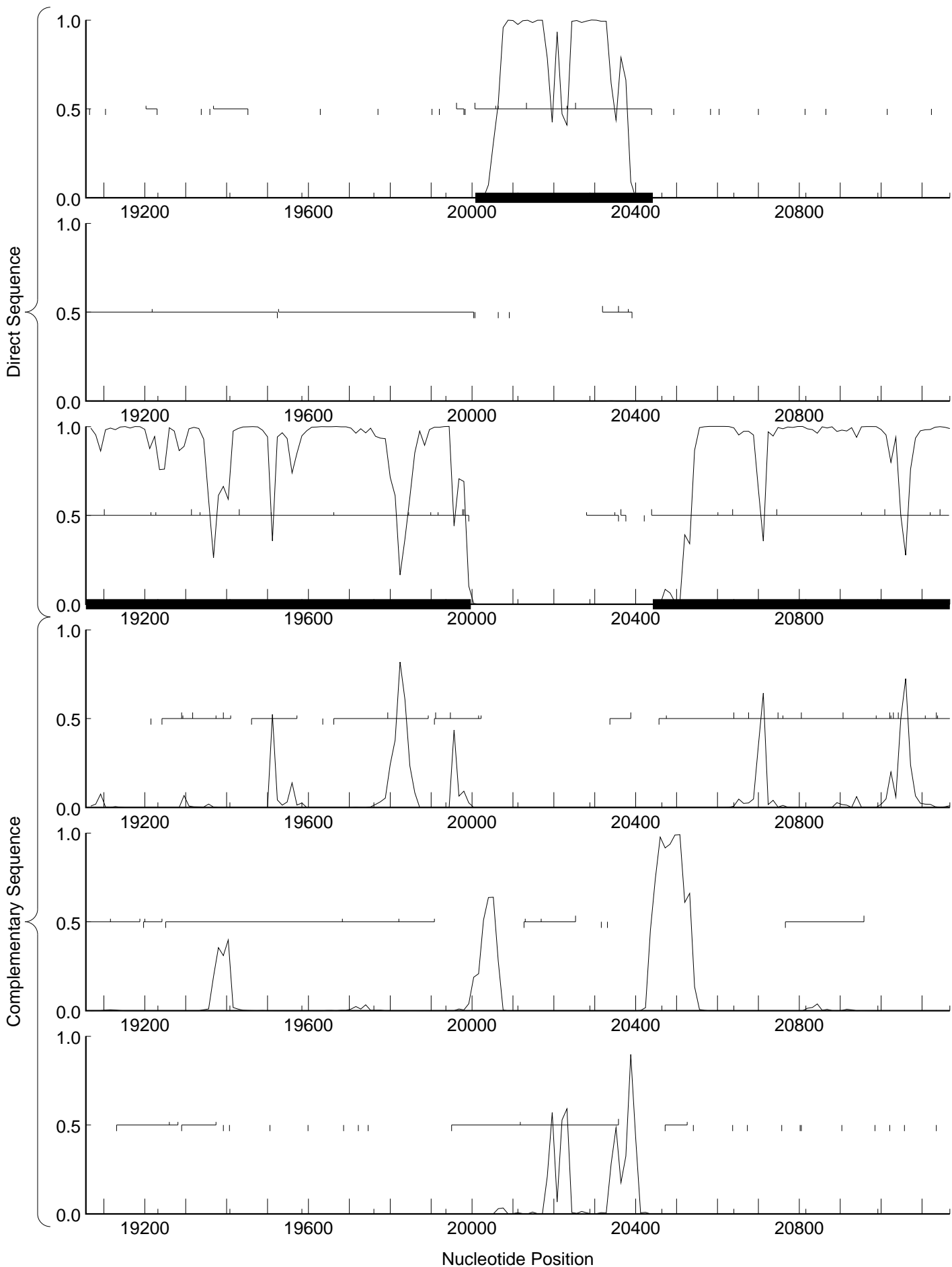


GeneMark.hmm prediction

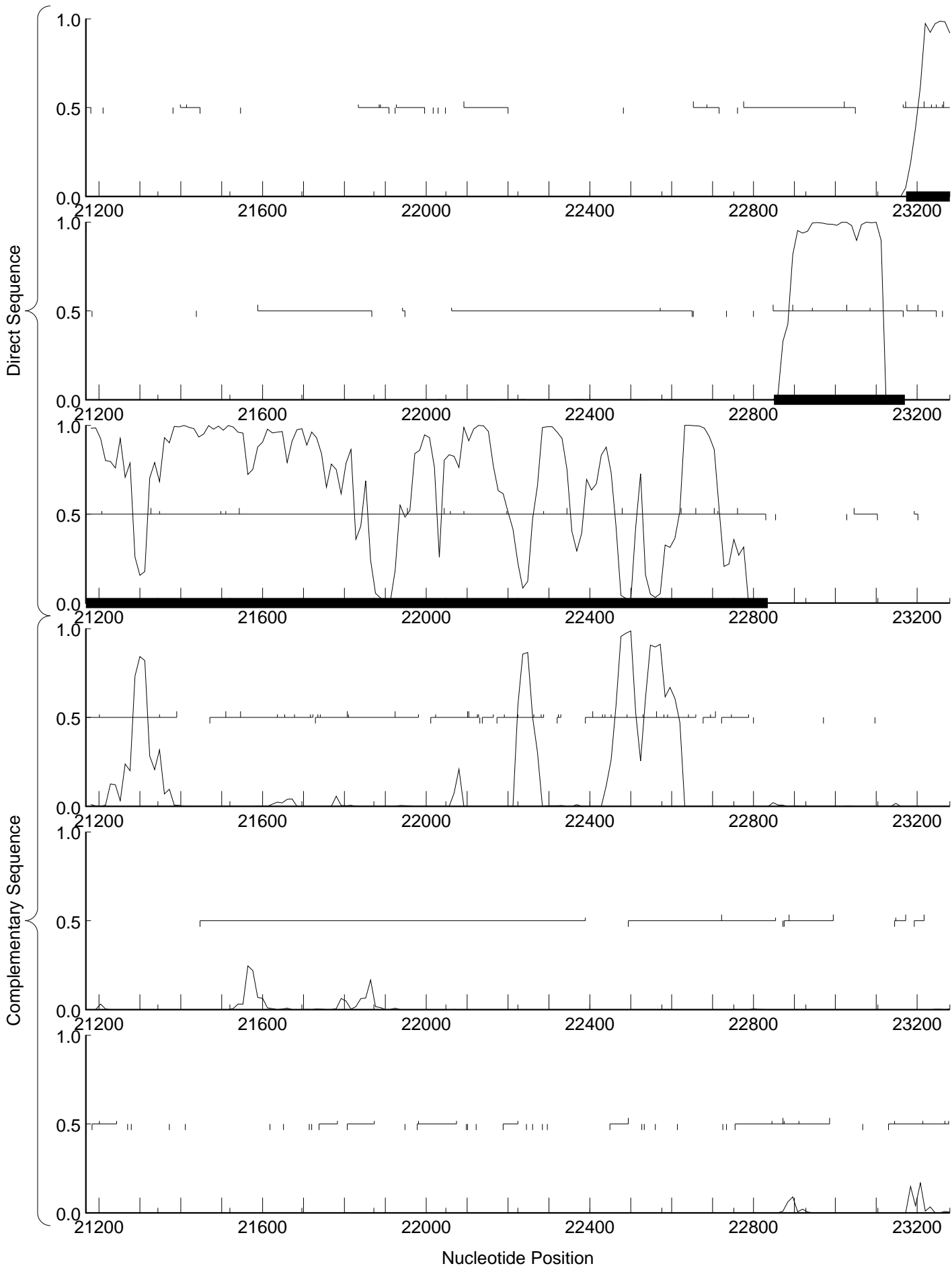


GeneMark.hmm prediction

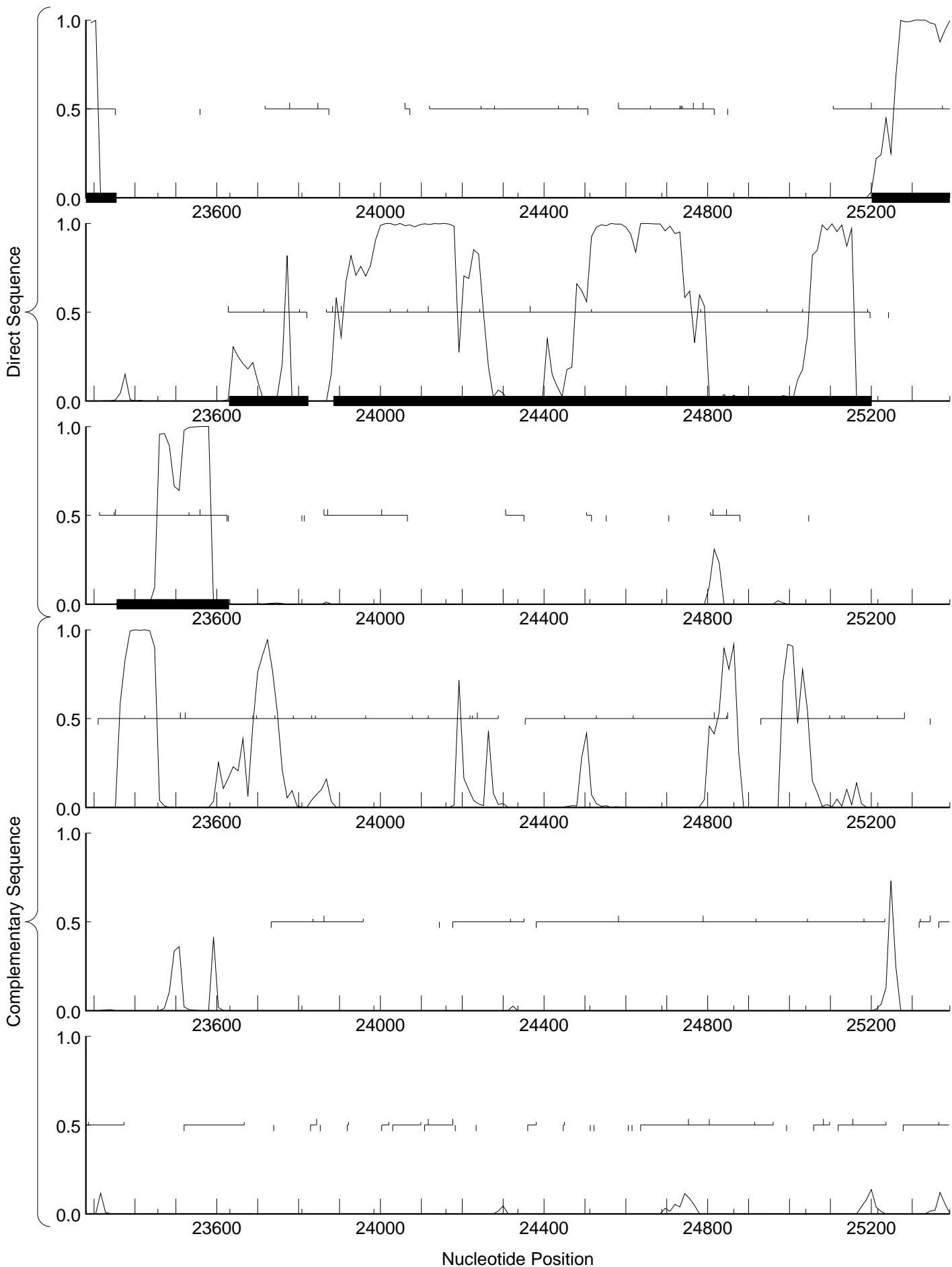




GeneMark.hmm prediction

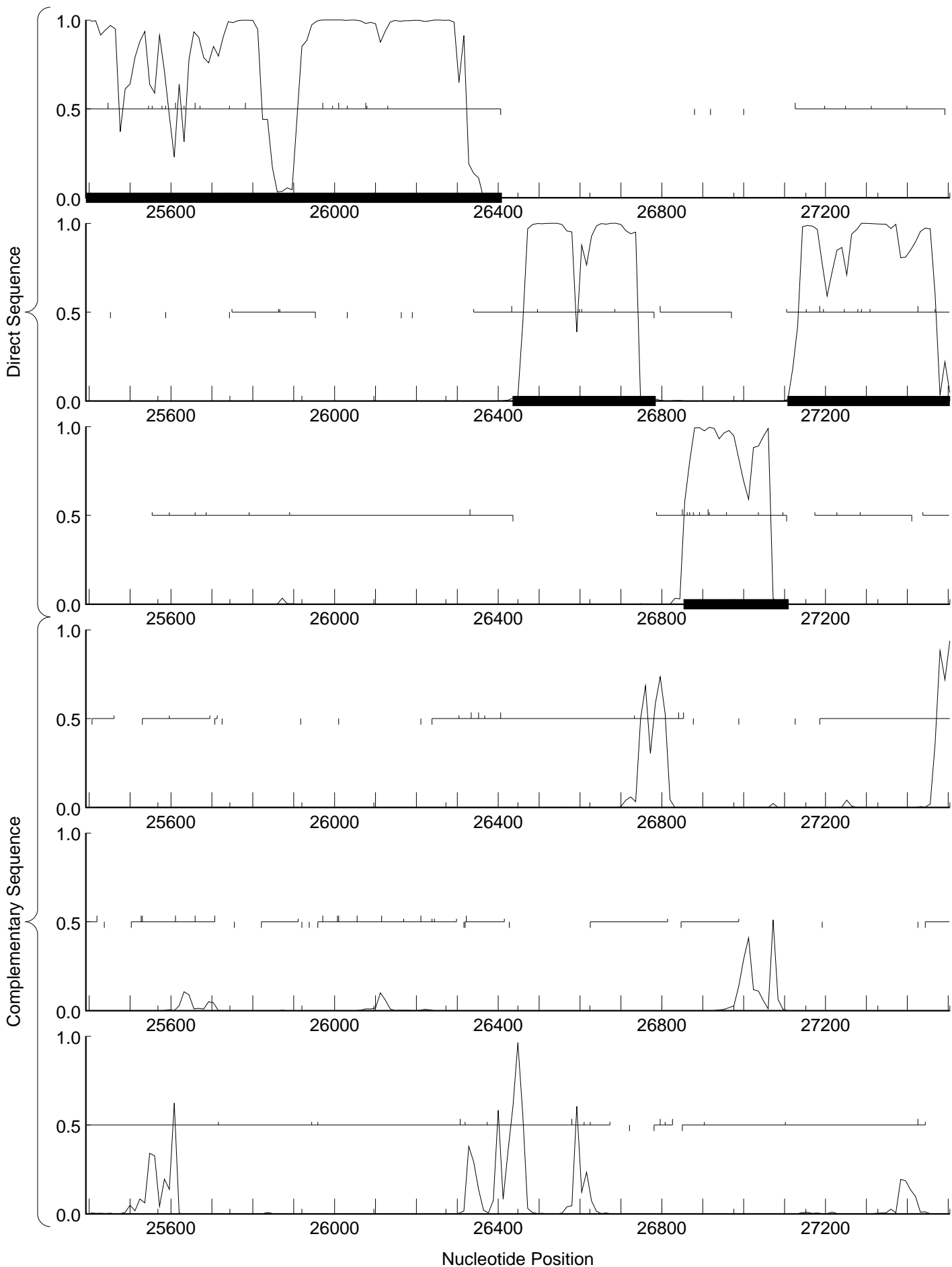


GeneMark.hmm prediction

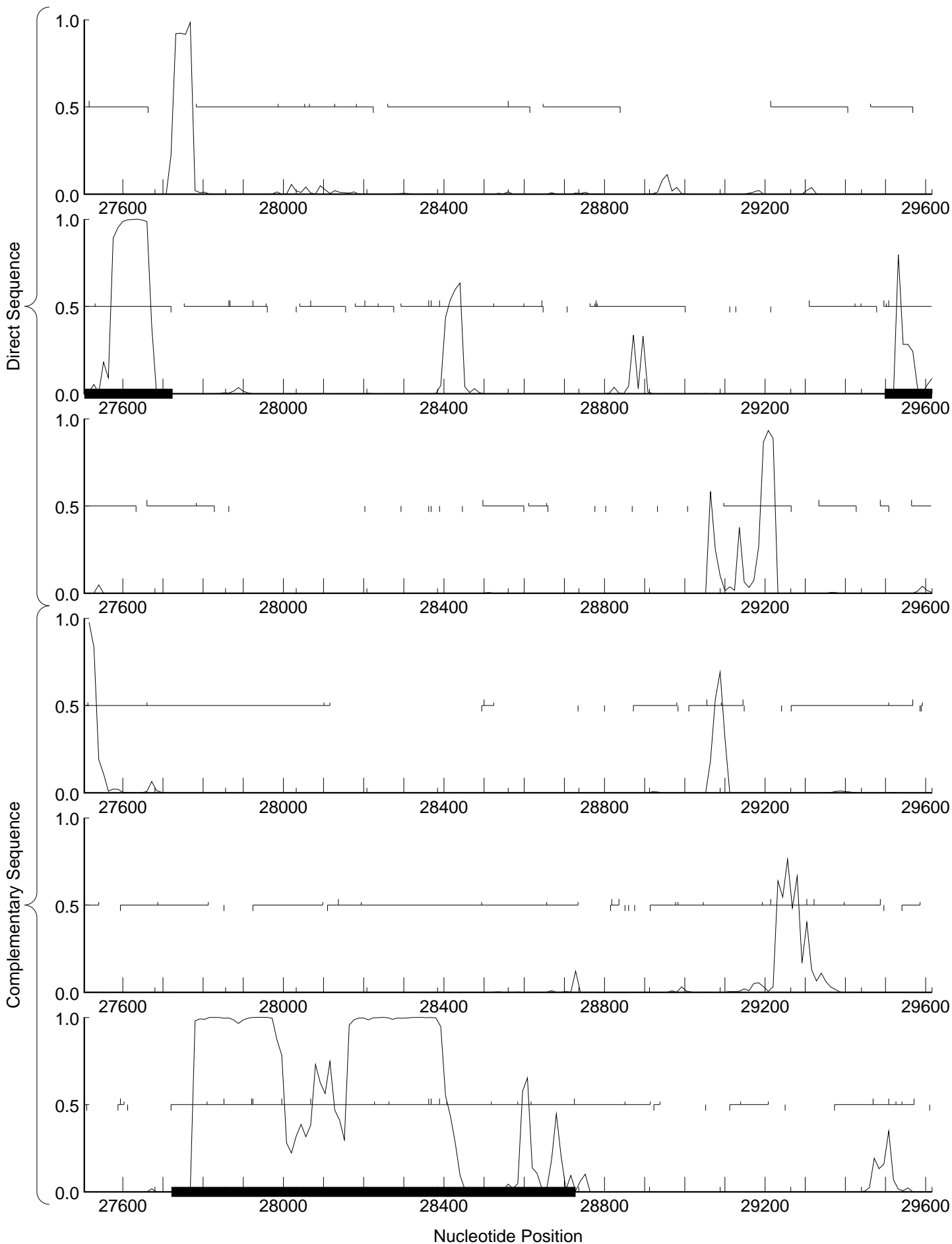


complete sequence, 41880 bp including 11-base 3' overhang (CCCCATGGCAT), Cluster G1, Order 2, Window 96, Step 12, 14/21

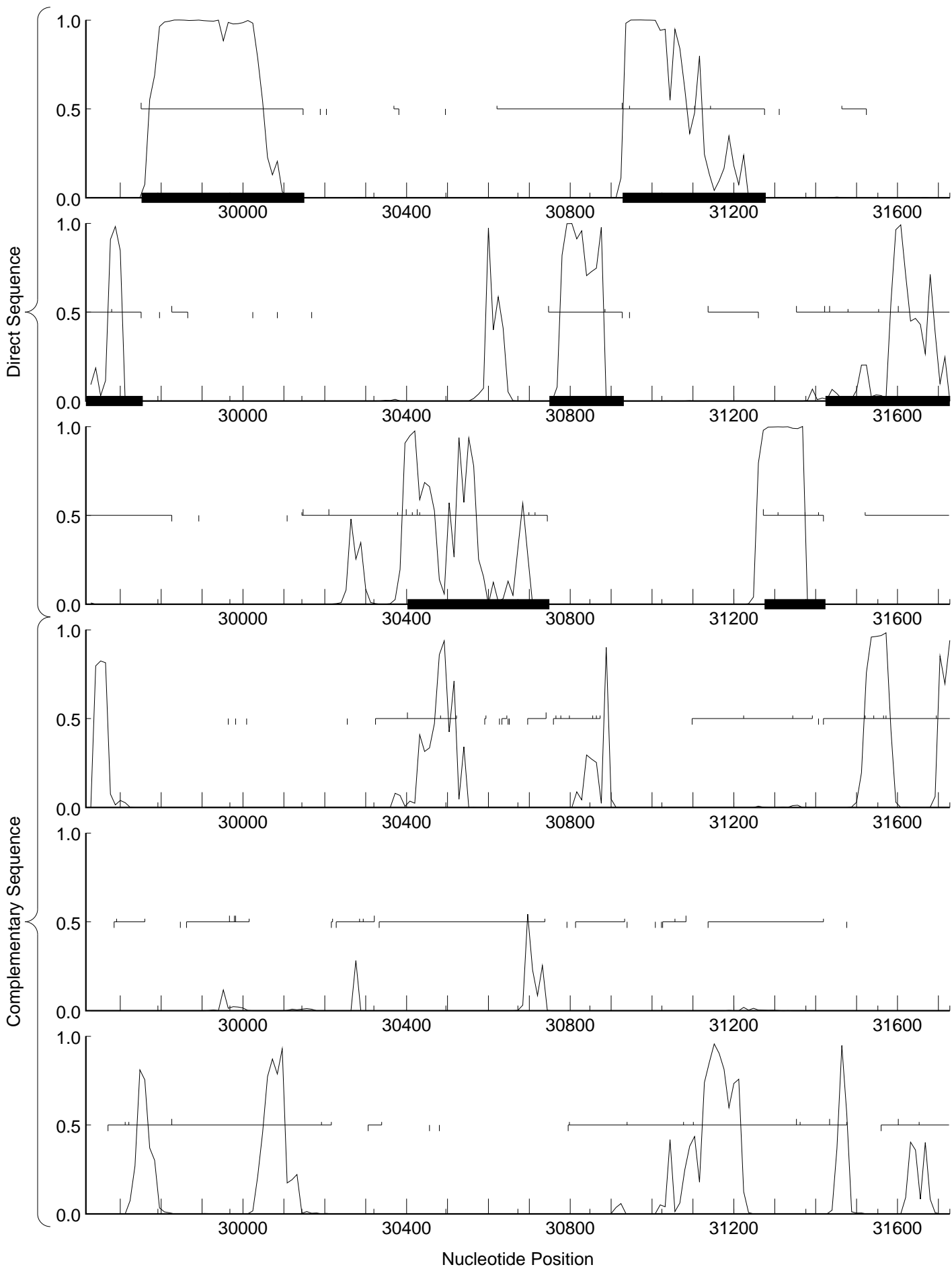
GeneMark.hmm prediction



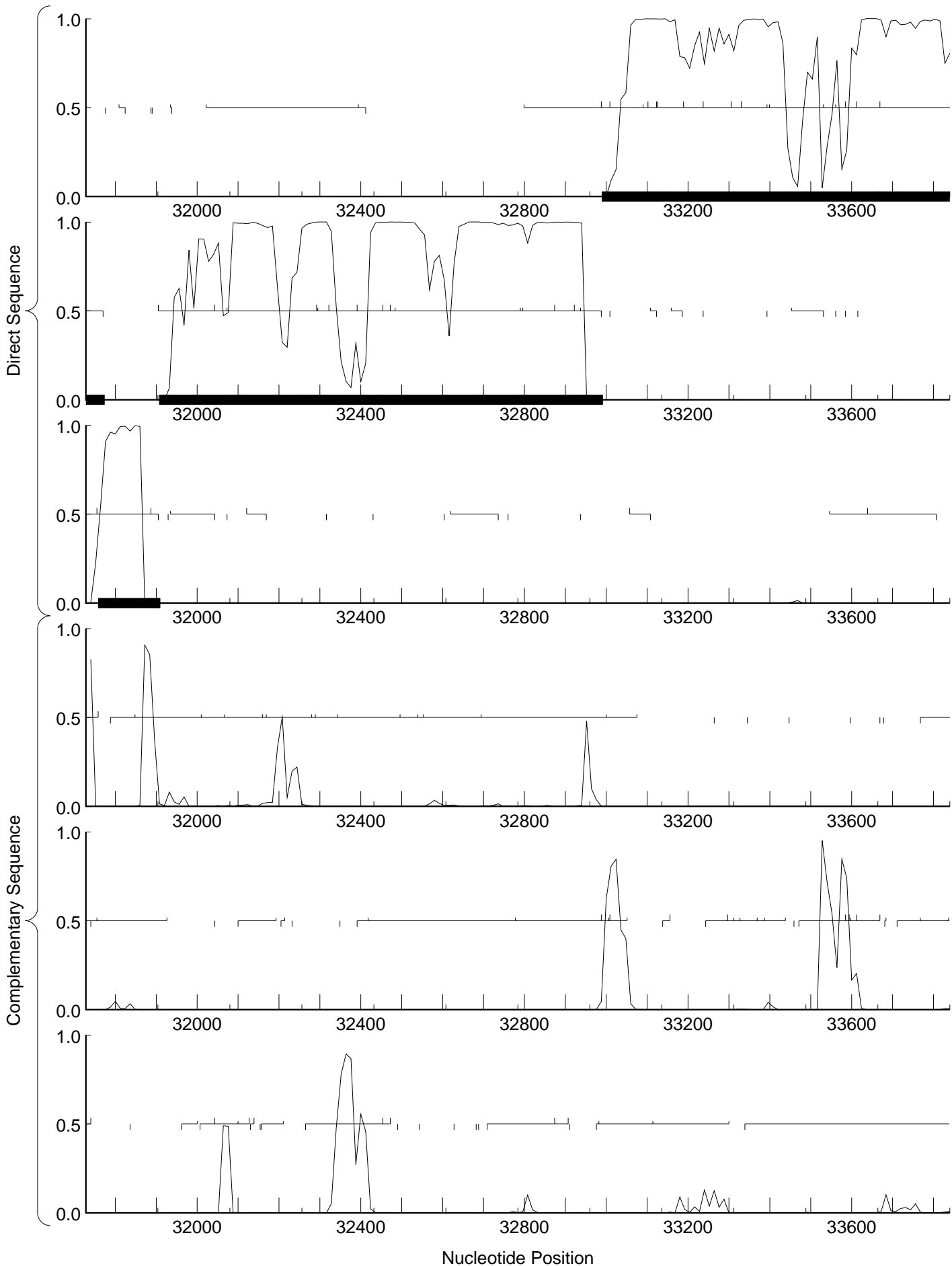
GeneMark.hmm prediction



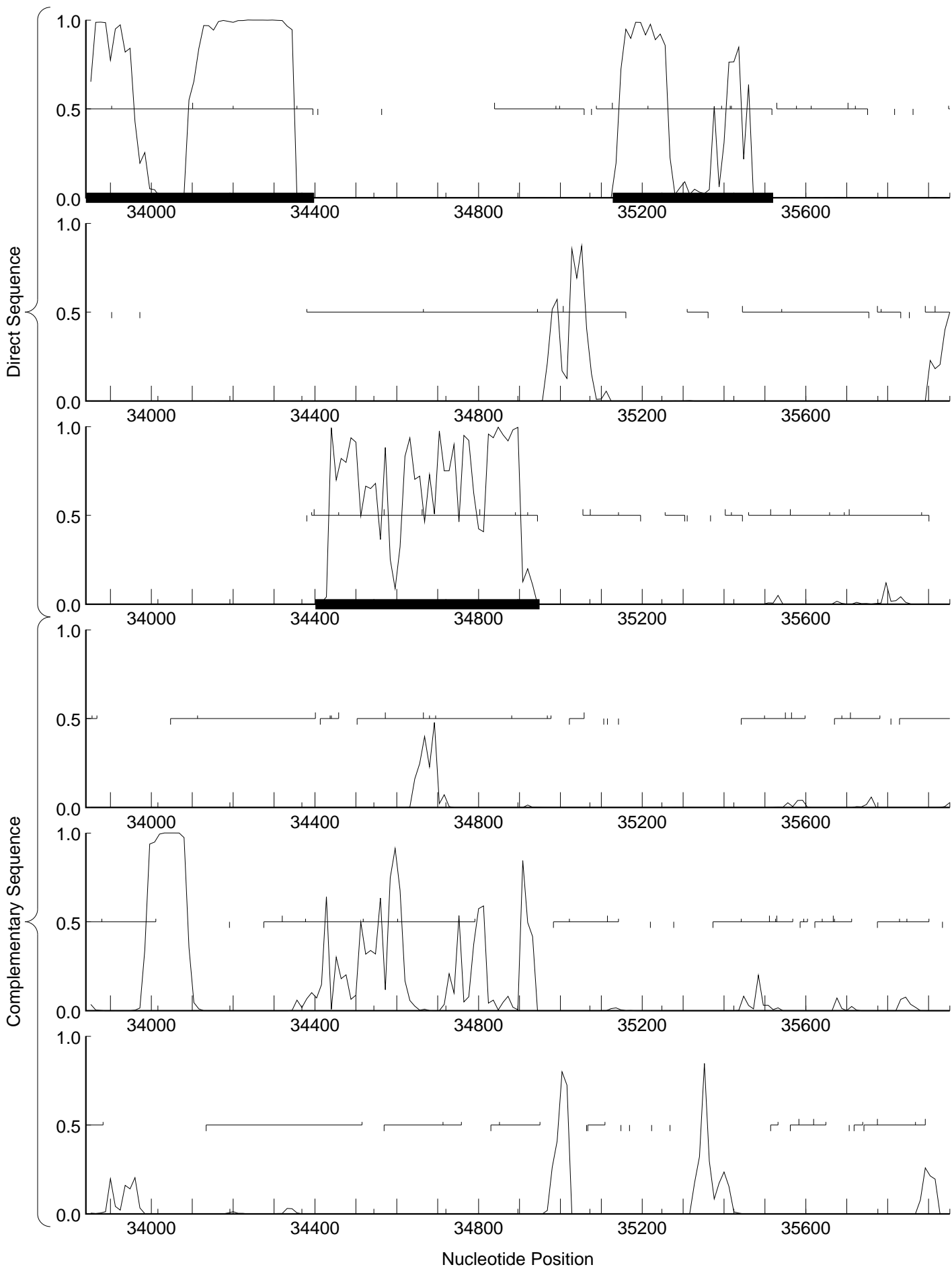
GeneMark.hmm prediction



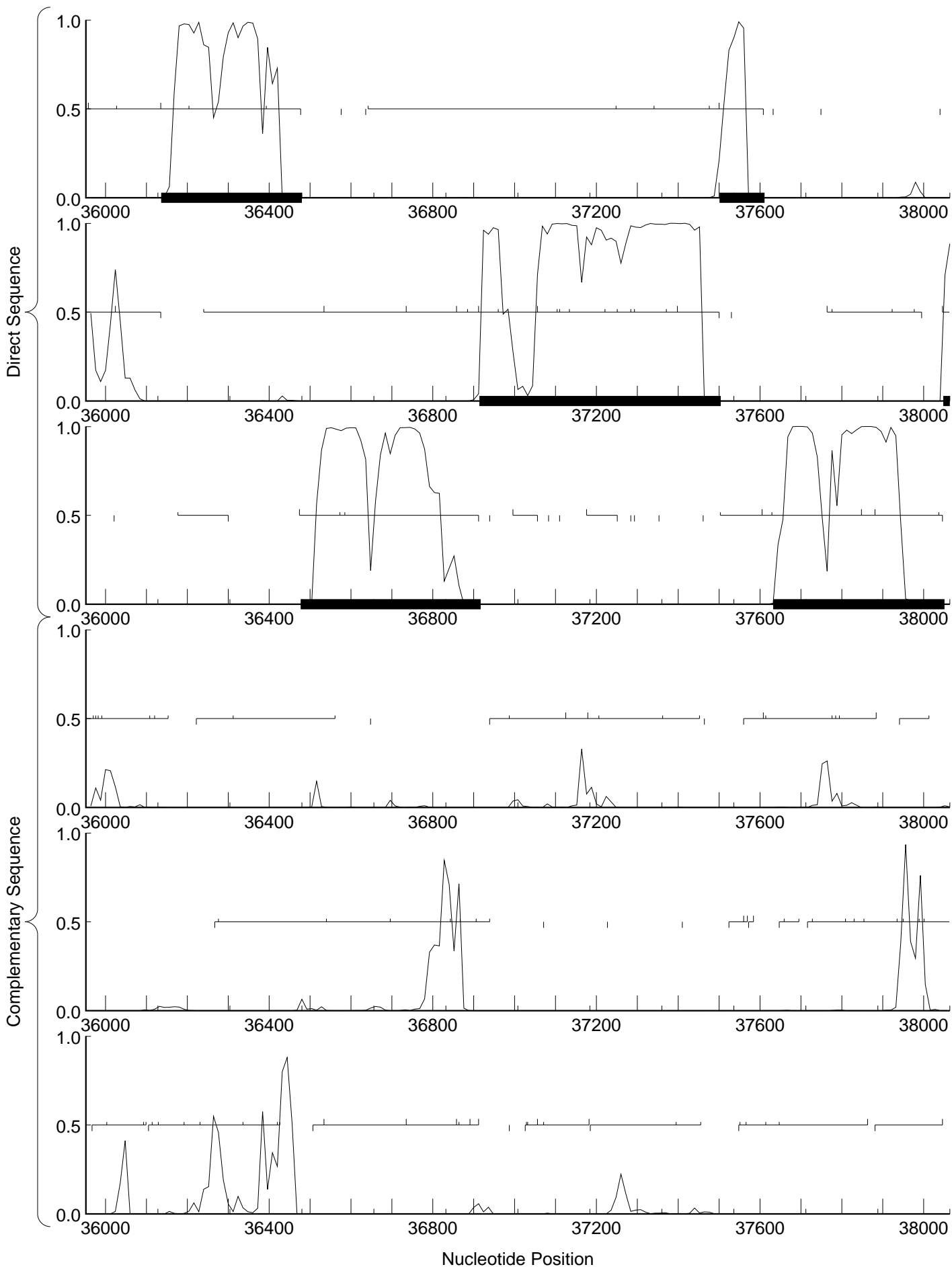
GeneMark.hmm prediction

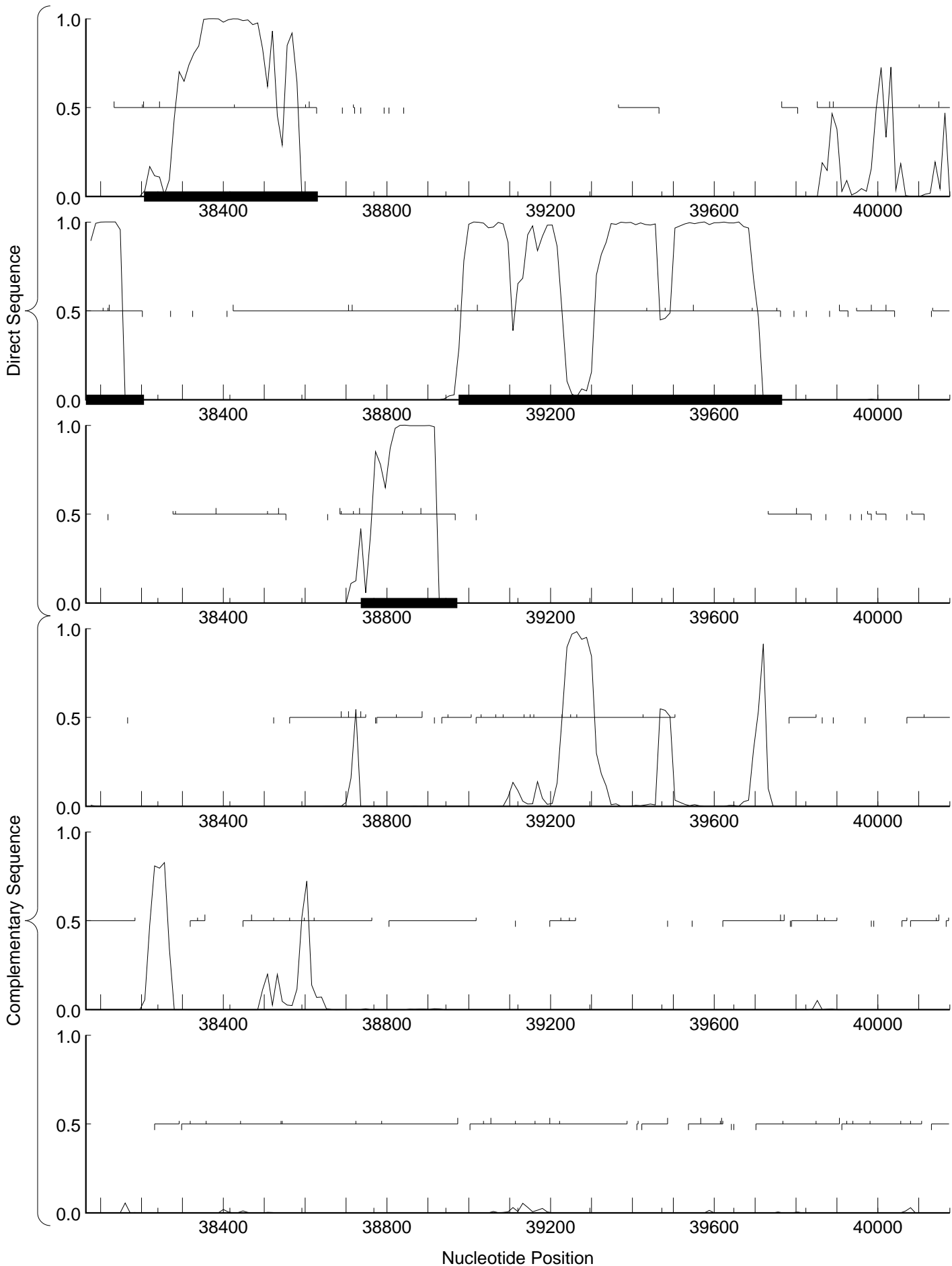


GeneMark.hmm prediction



GeneMark.hmm prediction





GeneMark, hmm prediction

