

GeneMark

Version 2.5p (09.08.06)

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PROGRAM INFORMATION

Sequence : Streptomyces phage Nerdos complete sequence, 49557 bp including 11-base 3' overhang (CGGGCA
Analysis Date : 8/19/17 at 1:45:36
Pages : 25
Sequence Length : 49557 bp
GC Content : 66.22%

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,

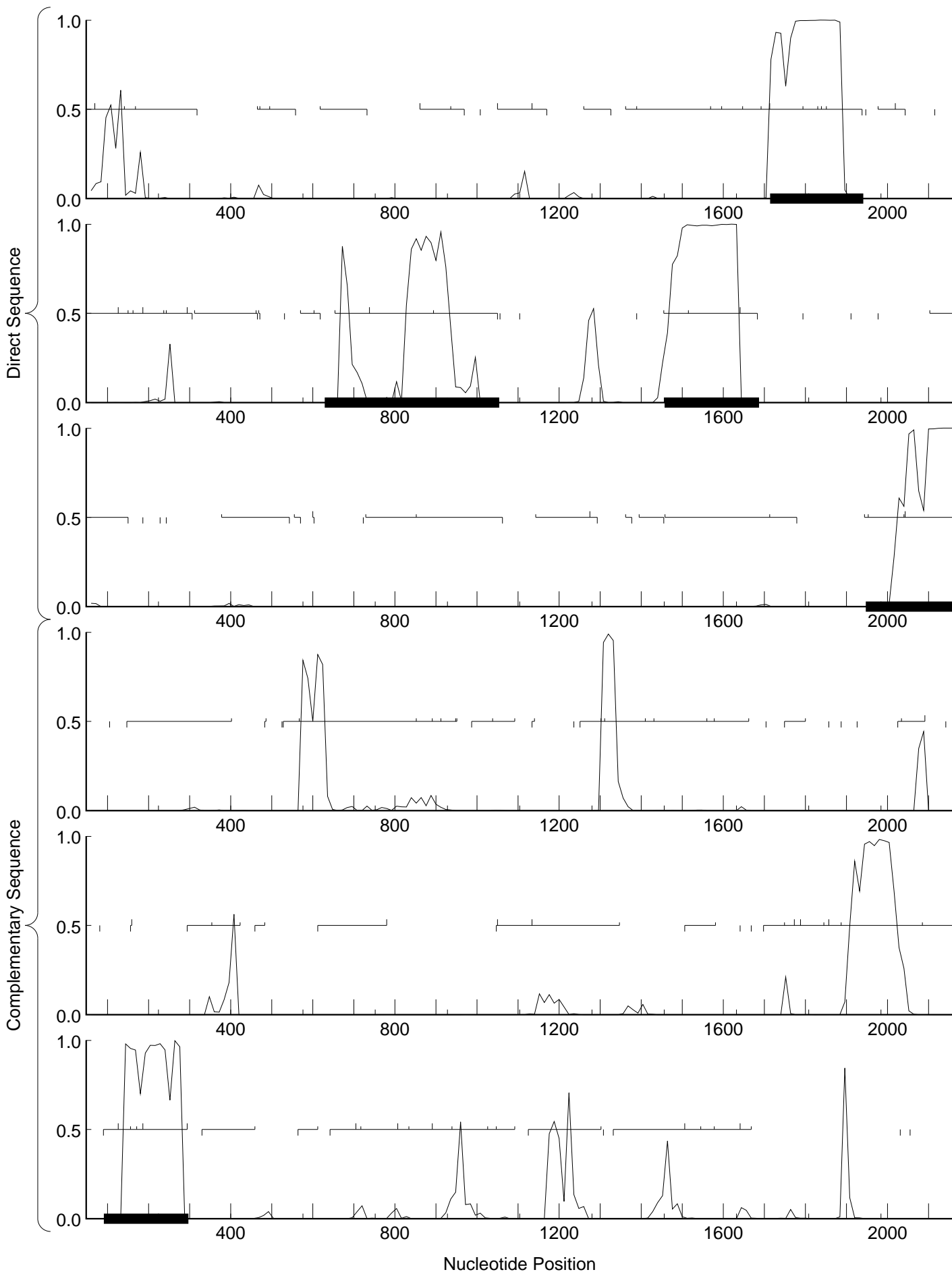
Matrix notes & comments

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

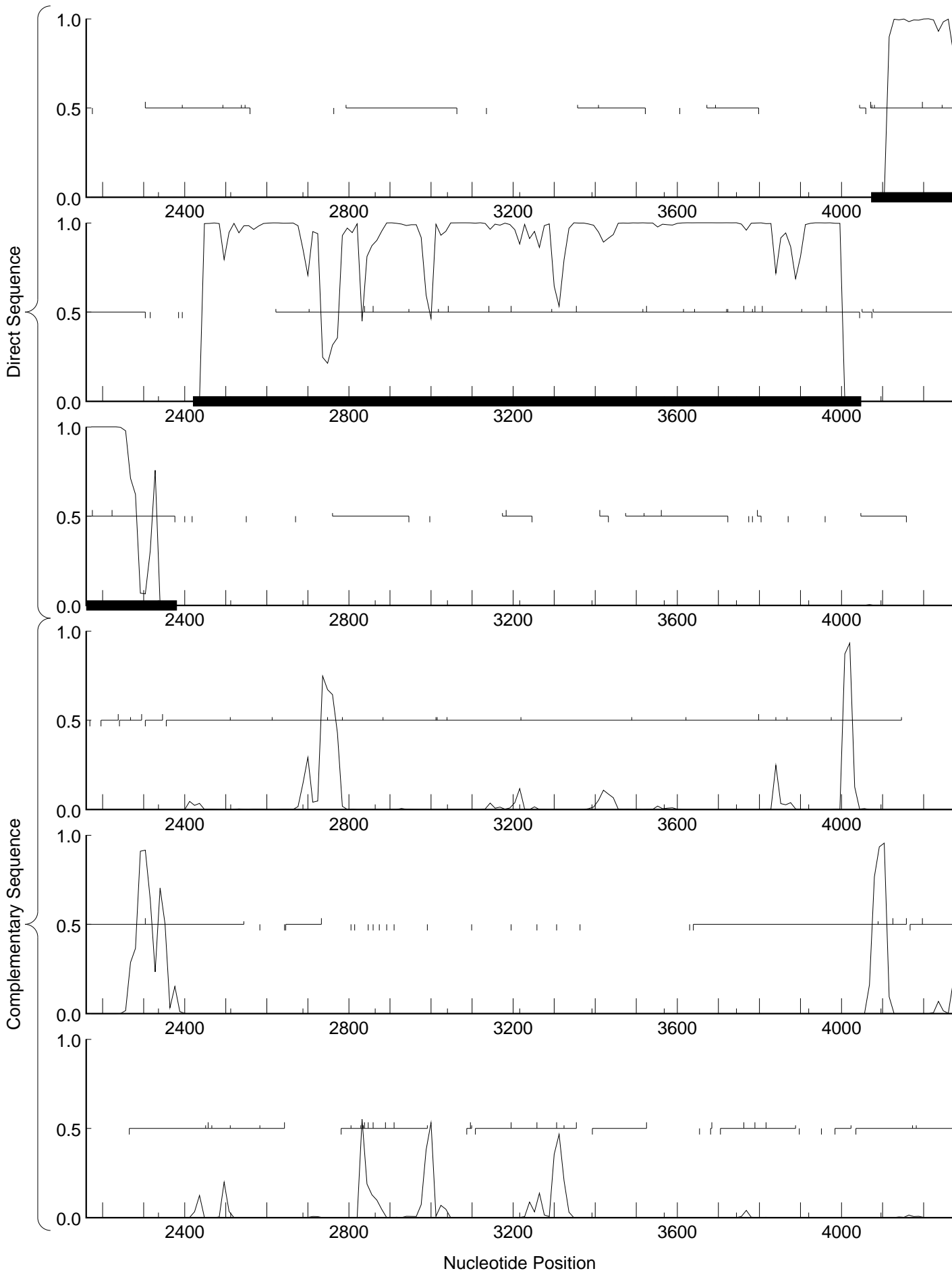
MATRIX INFORMATION

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

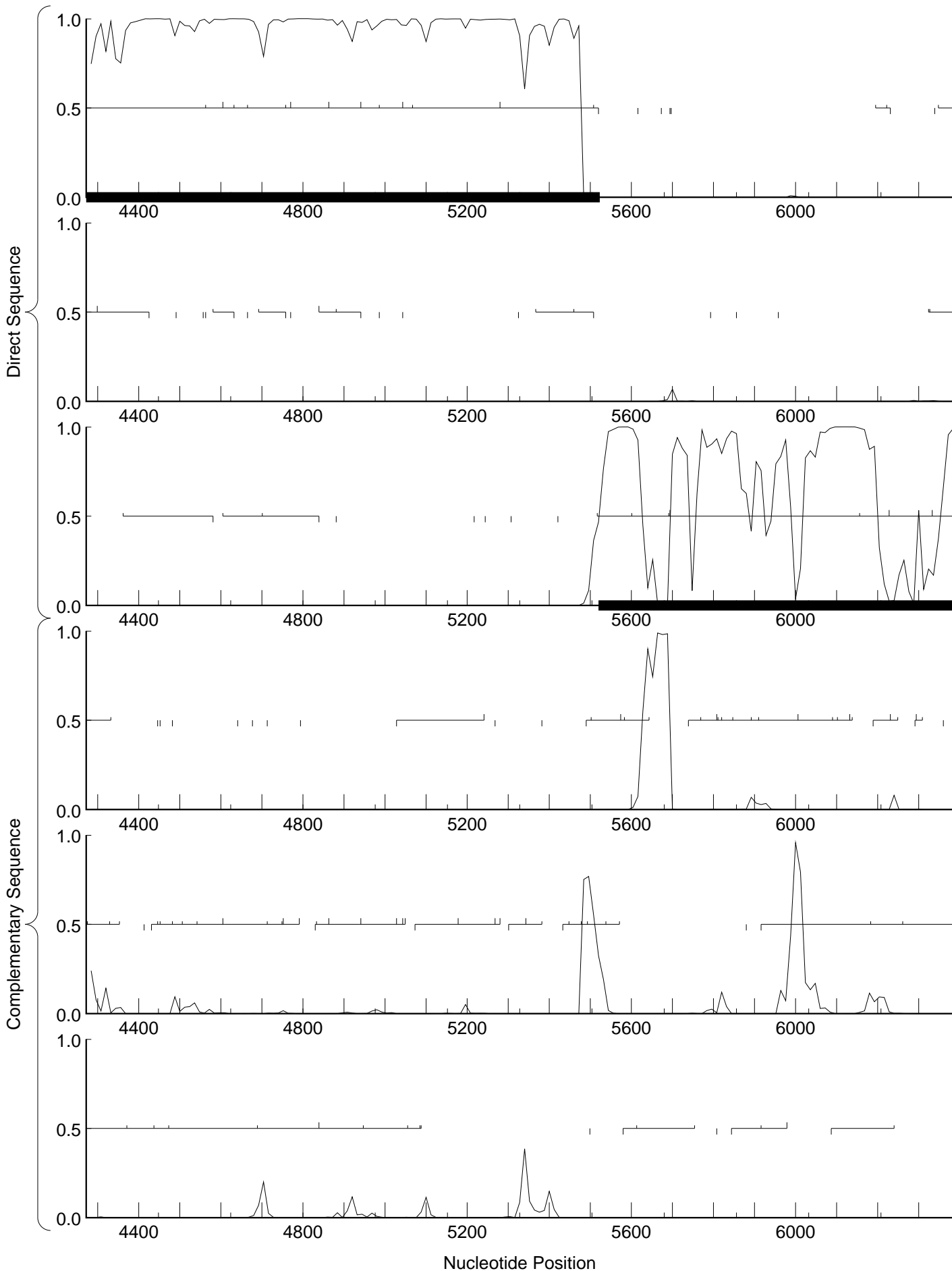
Send questions / comments to:
Dr. M. Borodovsky
Georgia Institute of Technology
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Atlanta, GA 30332-0230



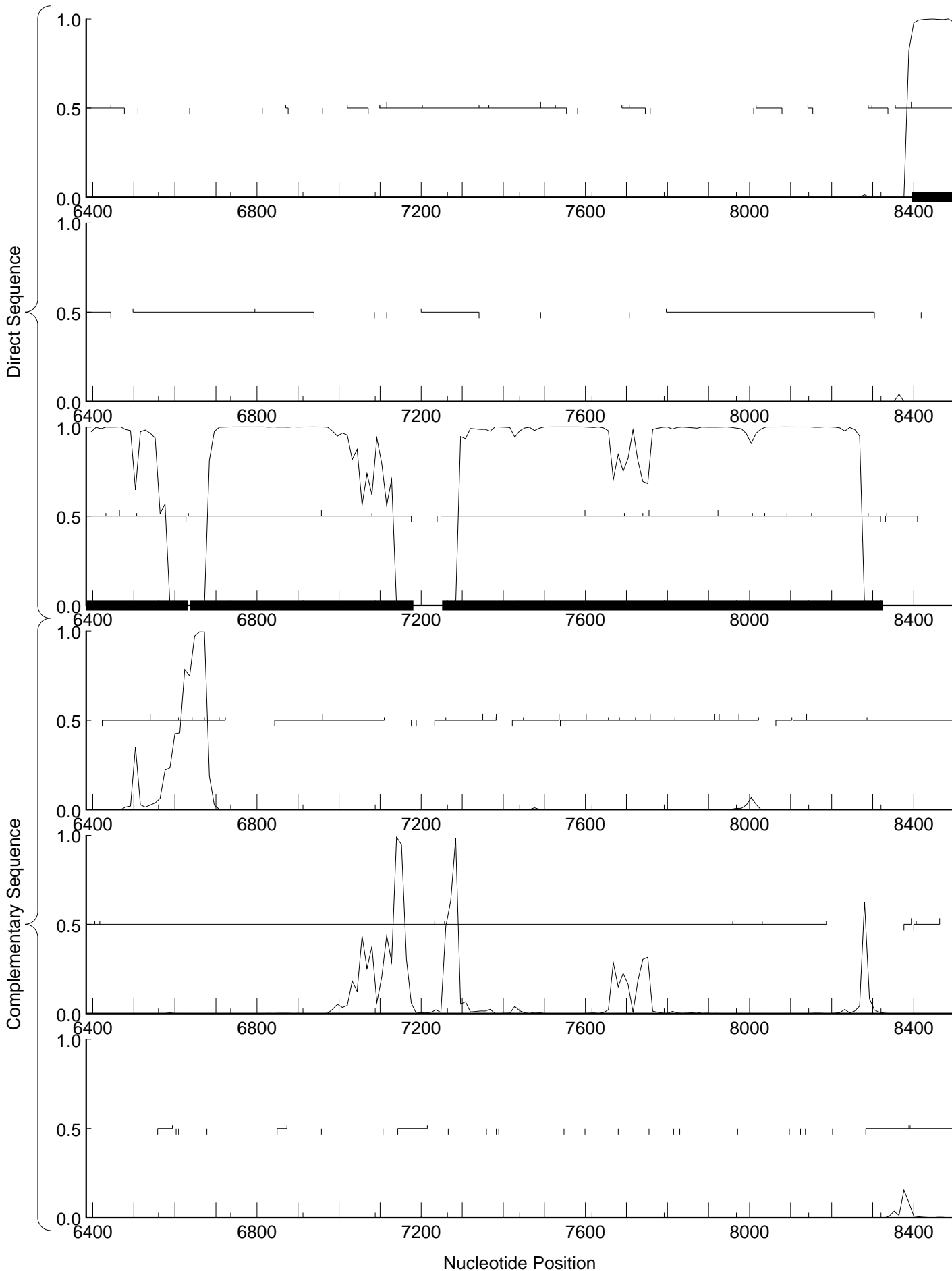
GeneMark, hmm prediction



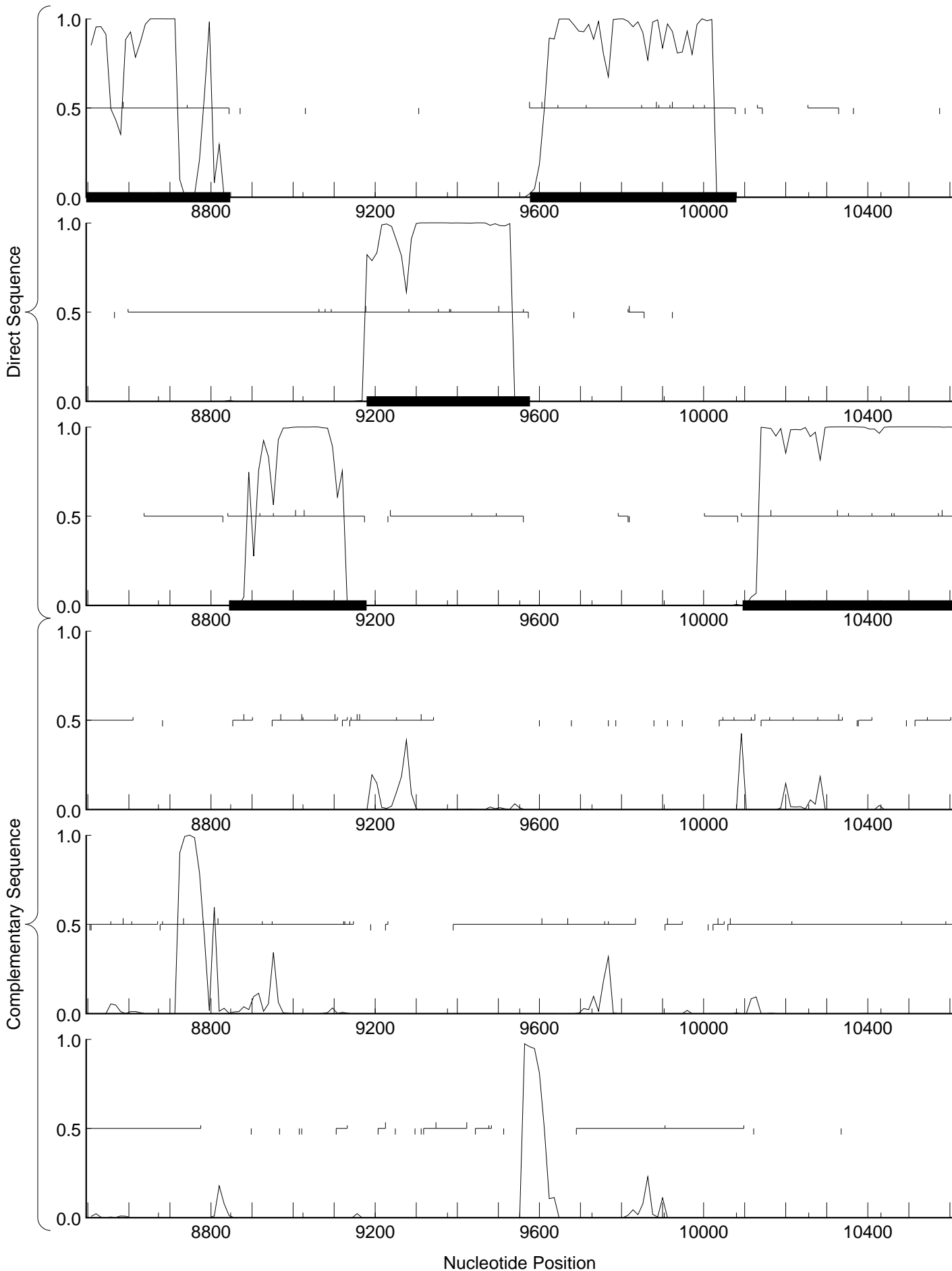
GeneMark, hmm prediction



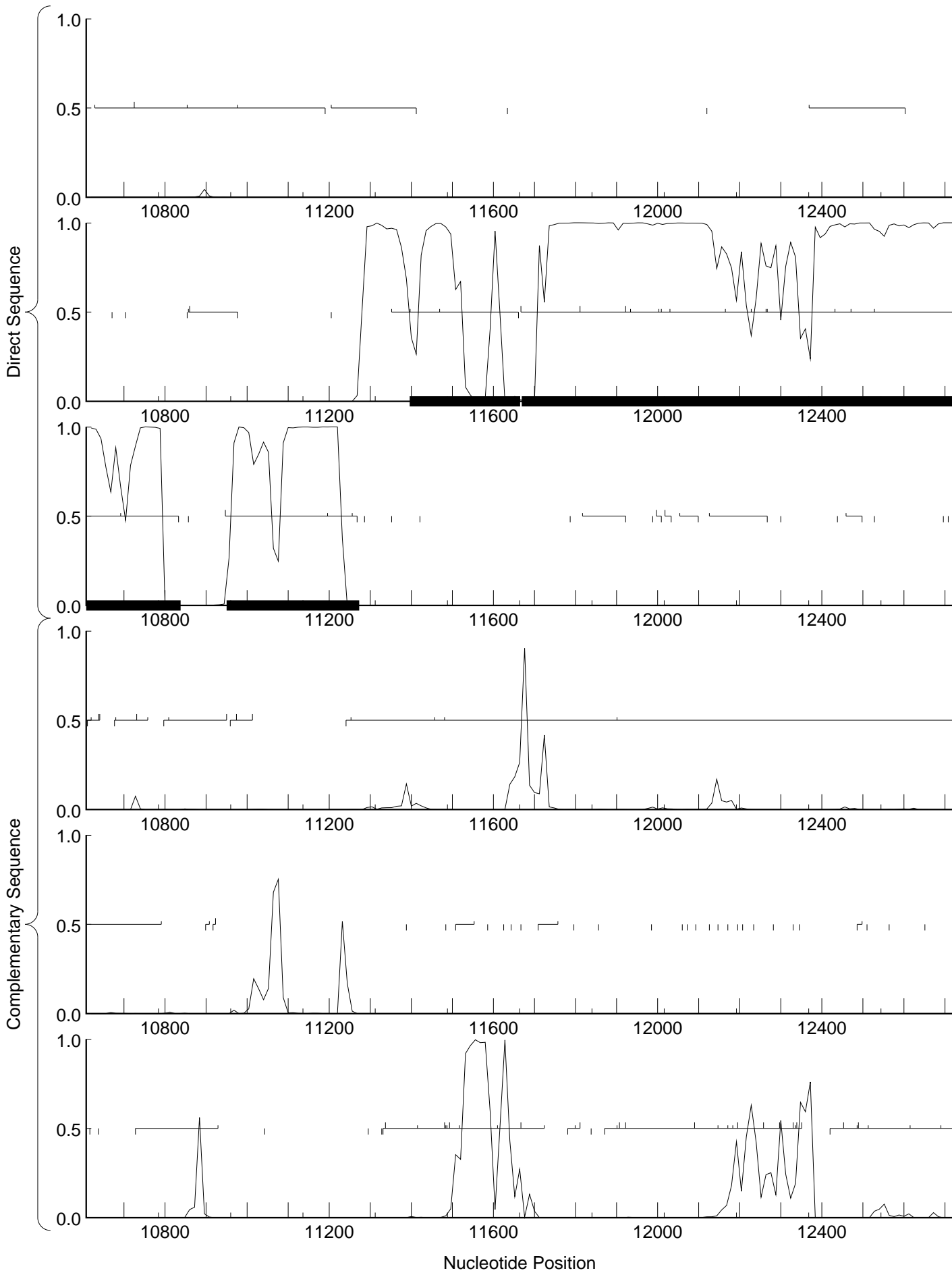
GeneMark, hmm prediction



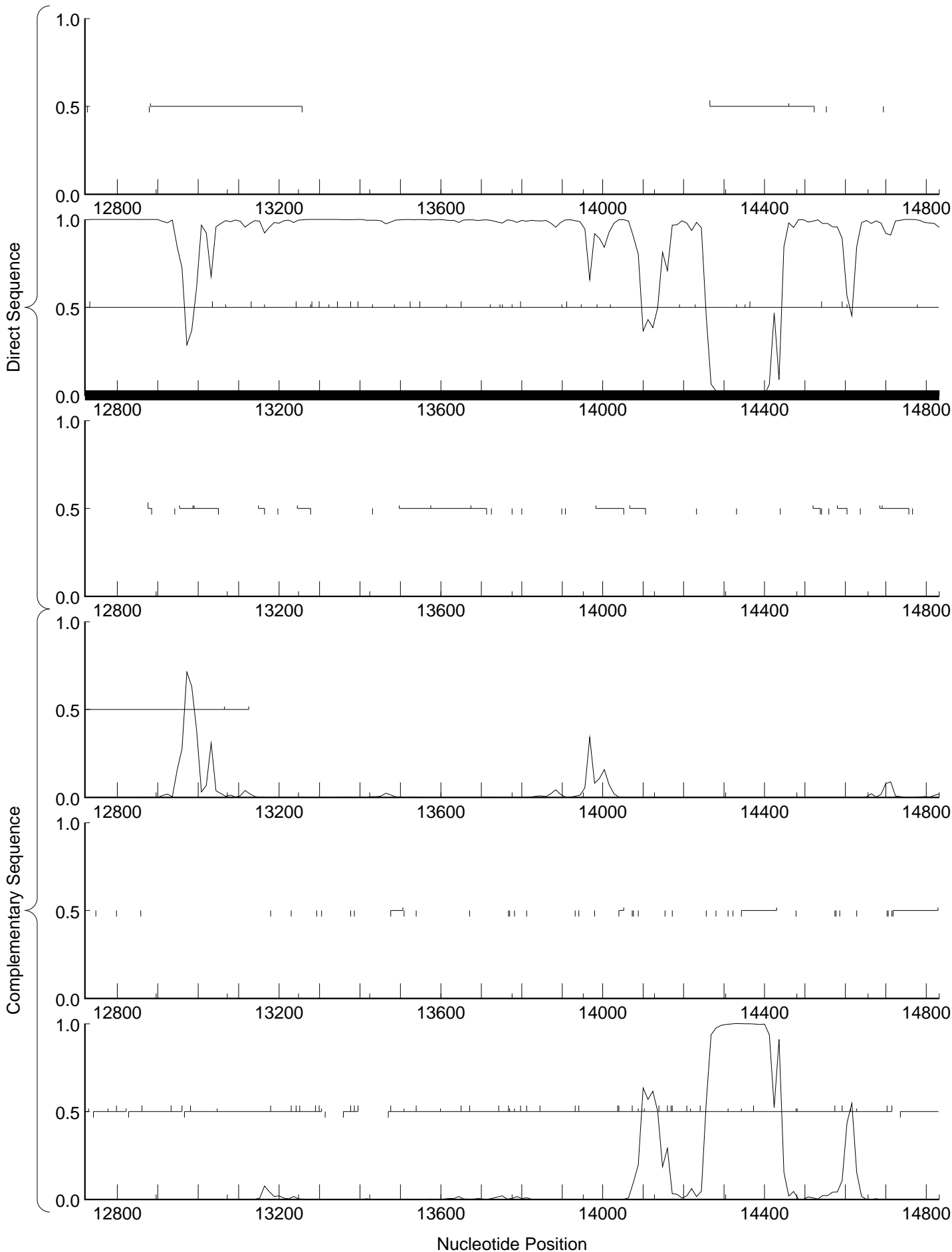
GeneMark, hmm prediction



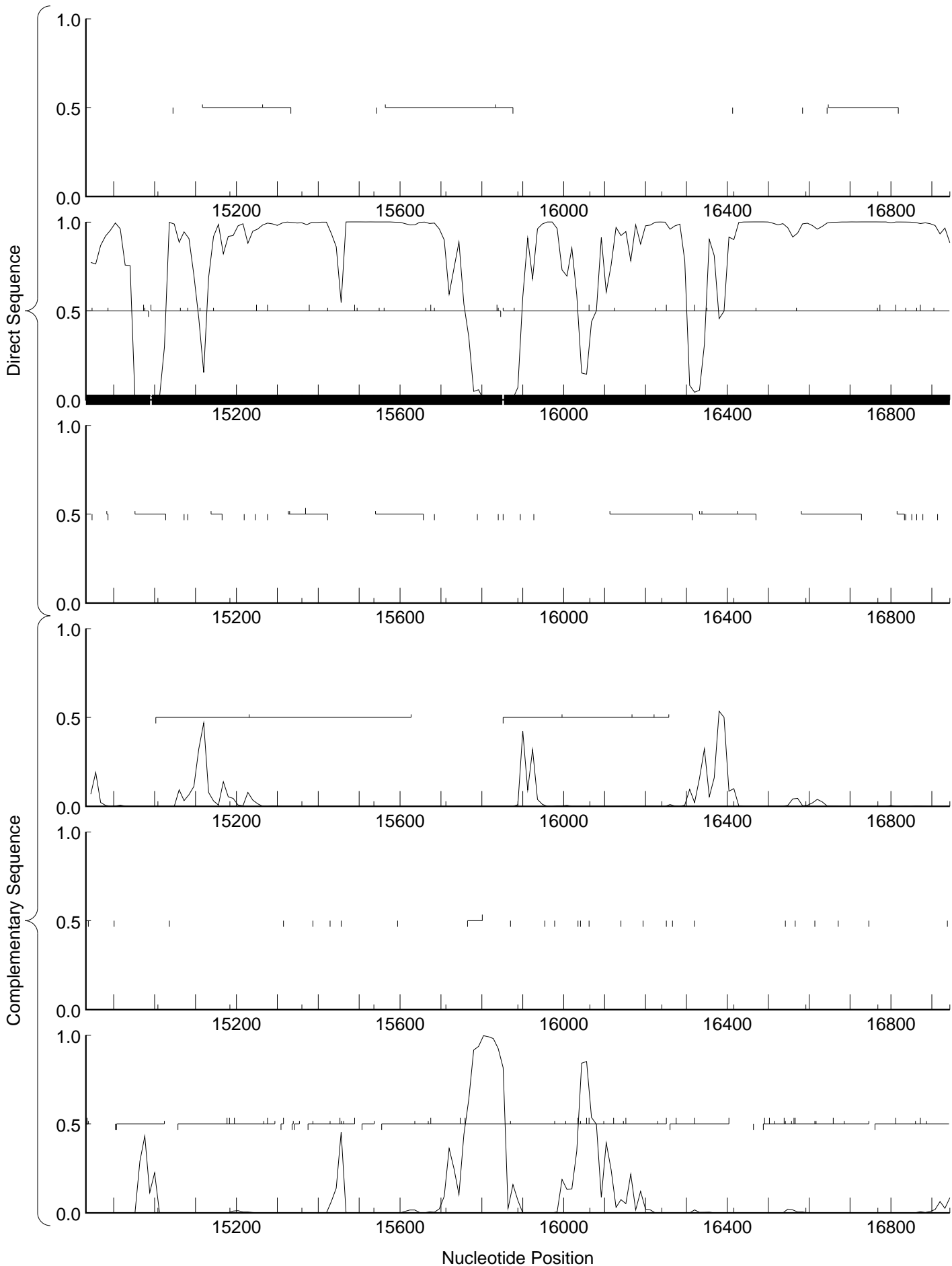
GeneMark, hmm prediction

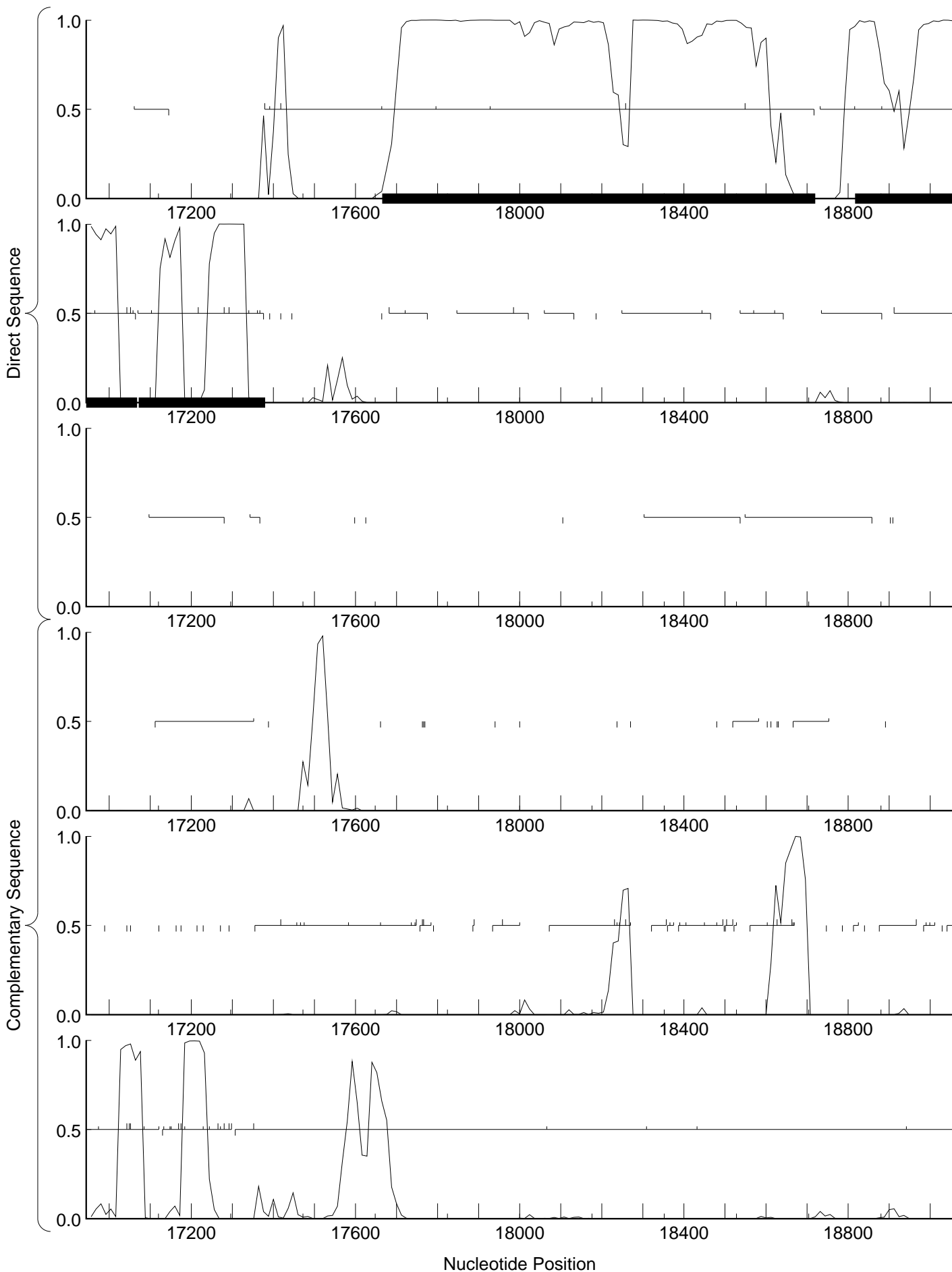


GeneMark, hmm prediction

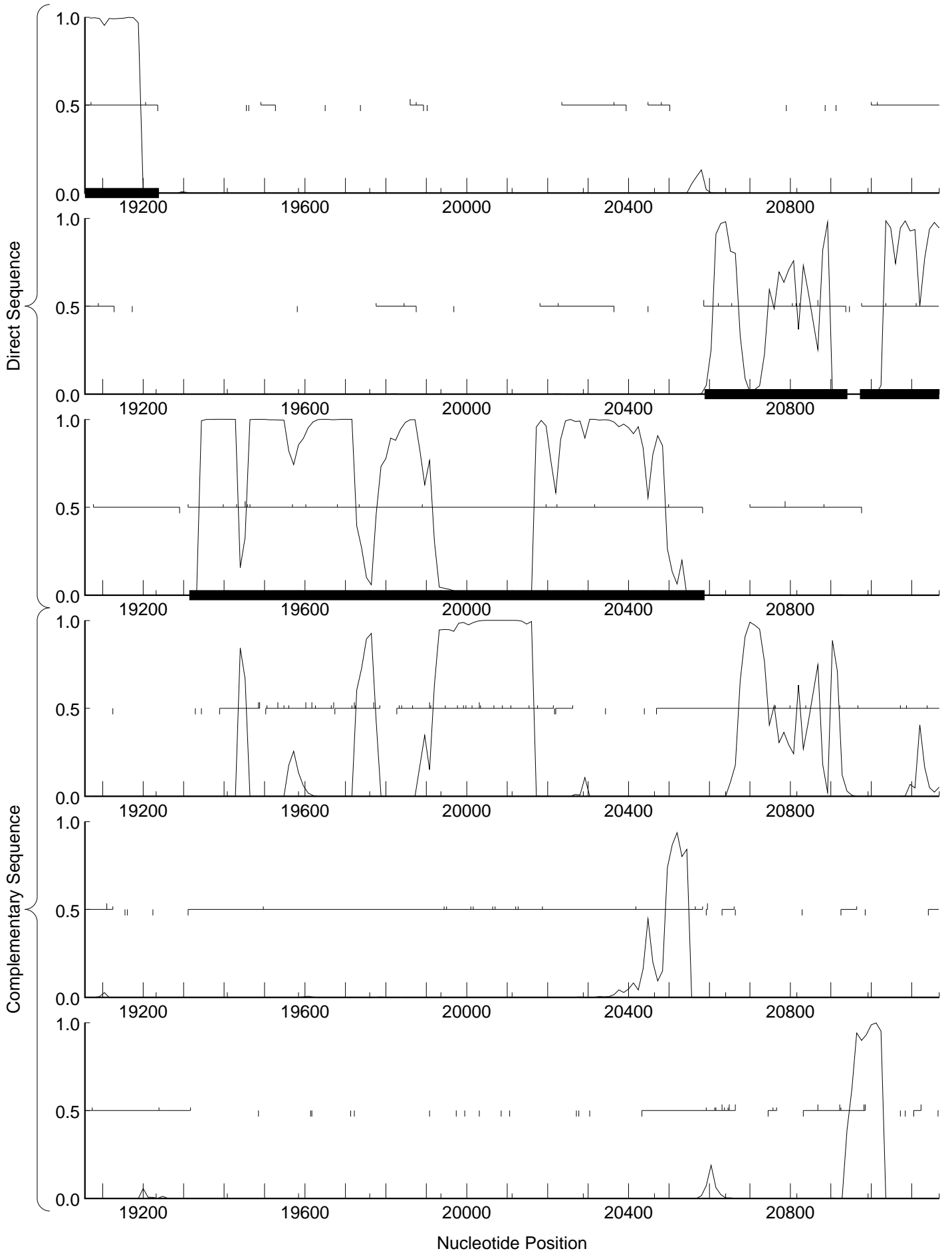


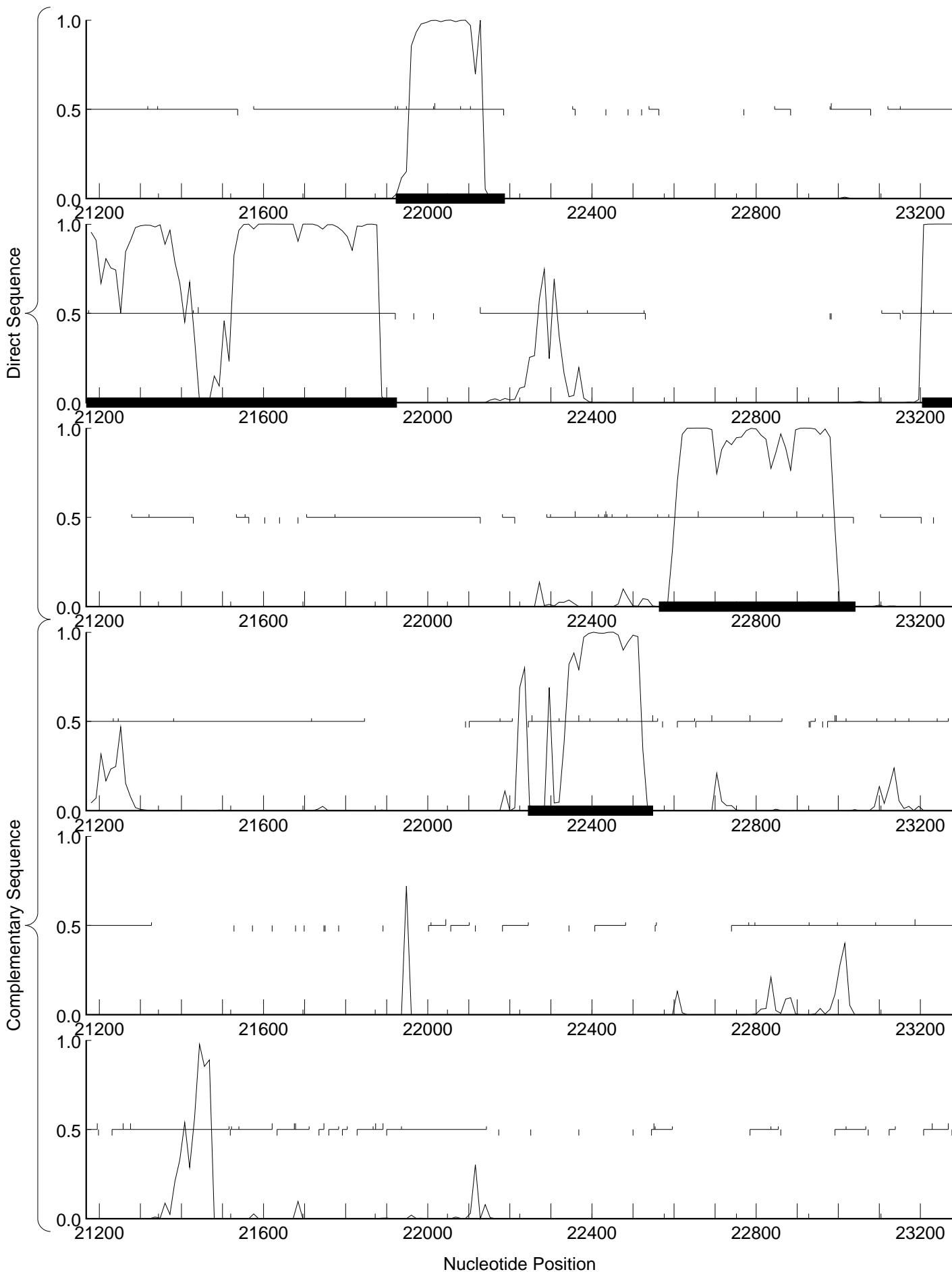
GeneMark, hmm prediction





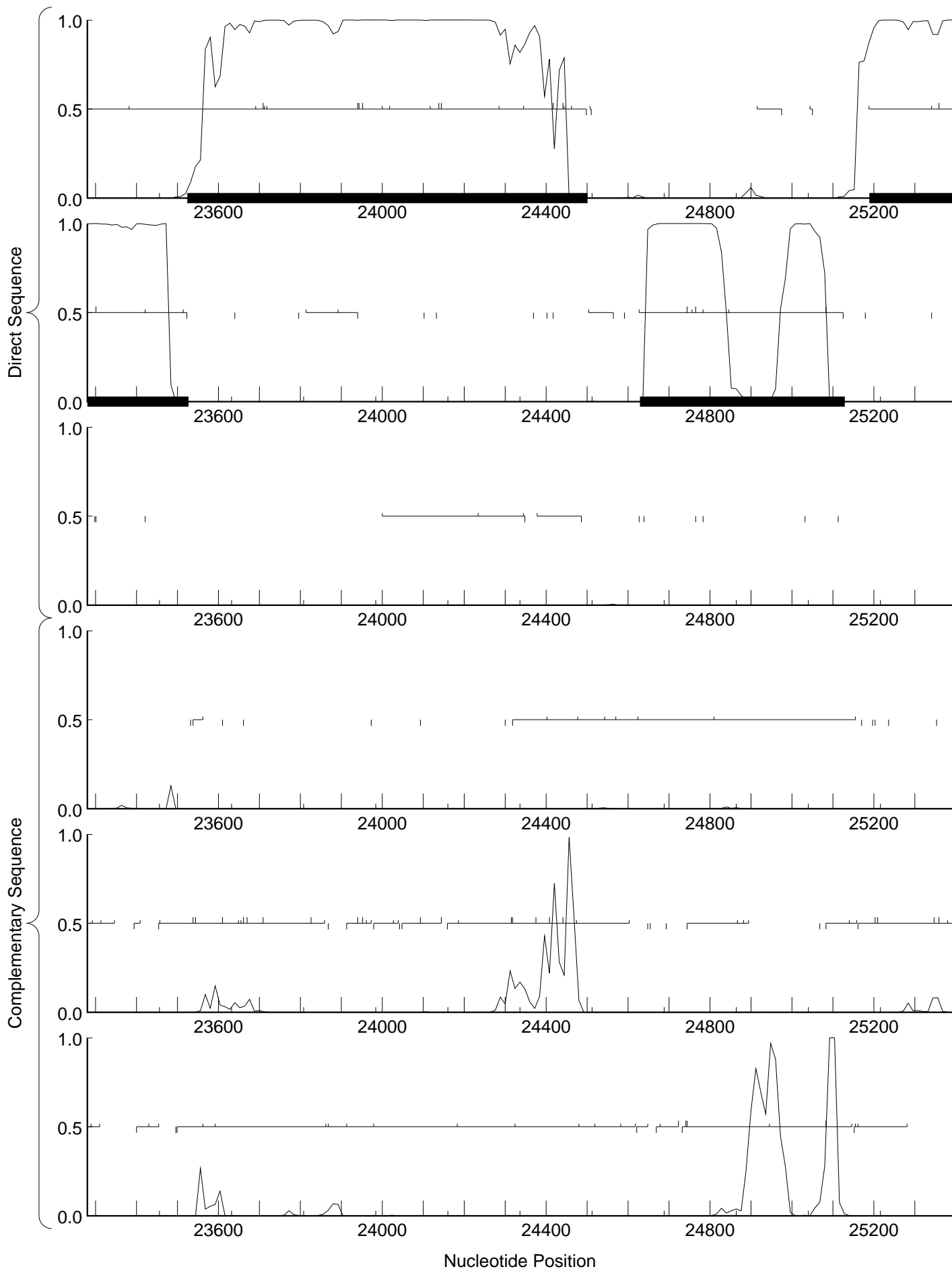
GeneMark, hmm prediction



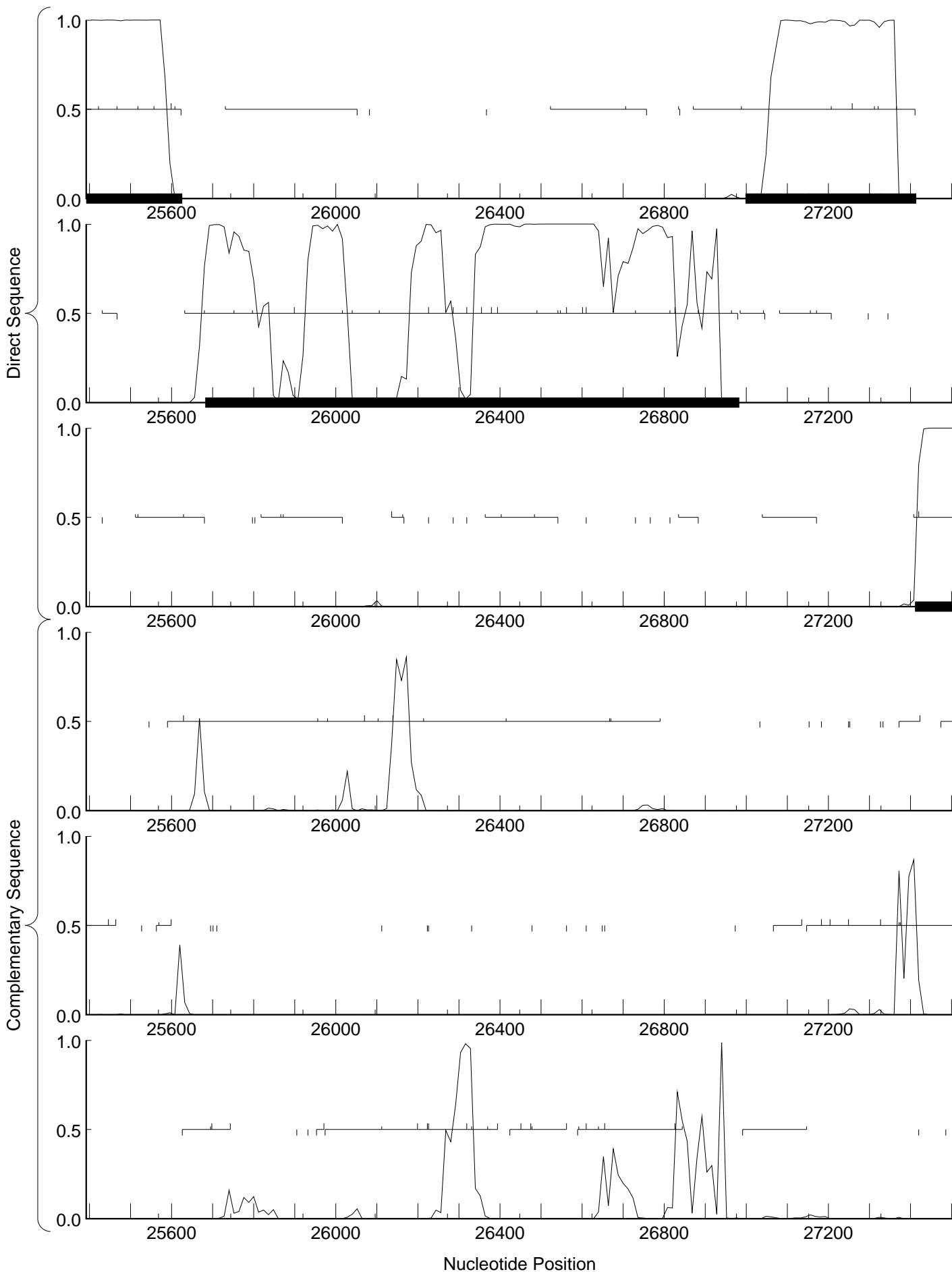


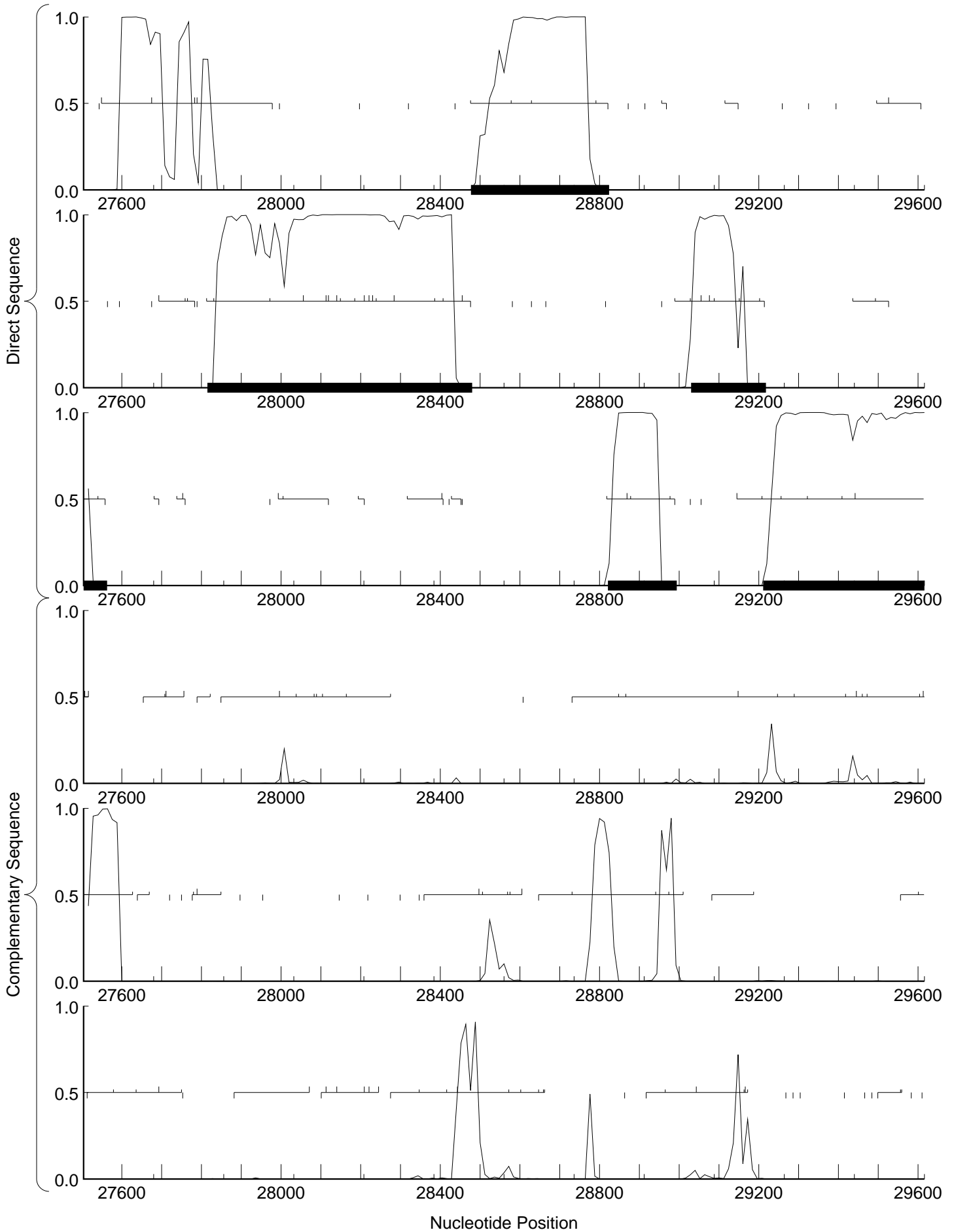
complete sequence, 49557 bp including 11-base 3' overhang (CGGGCAGTGAT), Cluster BD1, Order 2, Window 96, Step 12, 13/25

GeneMark, hmm prediction

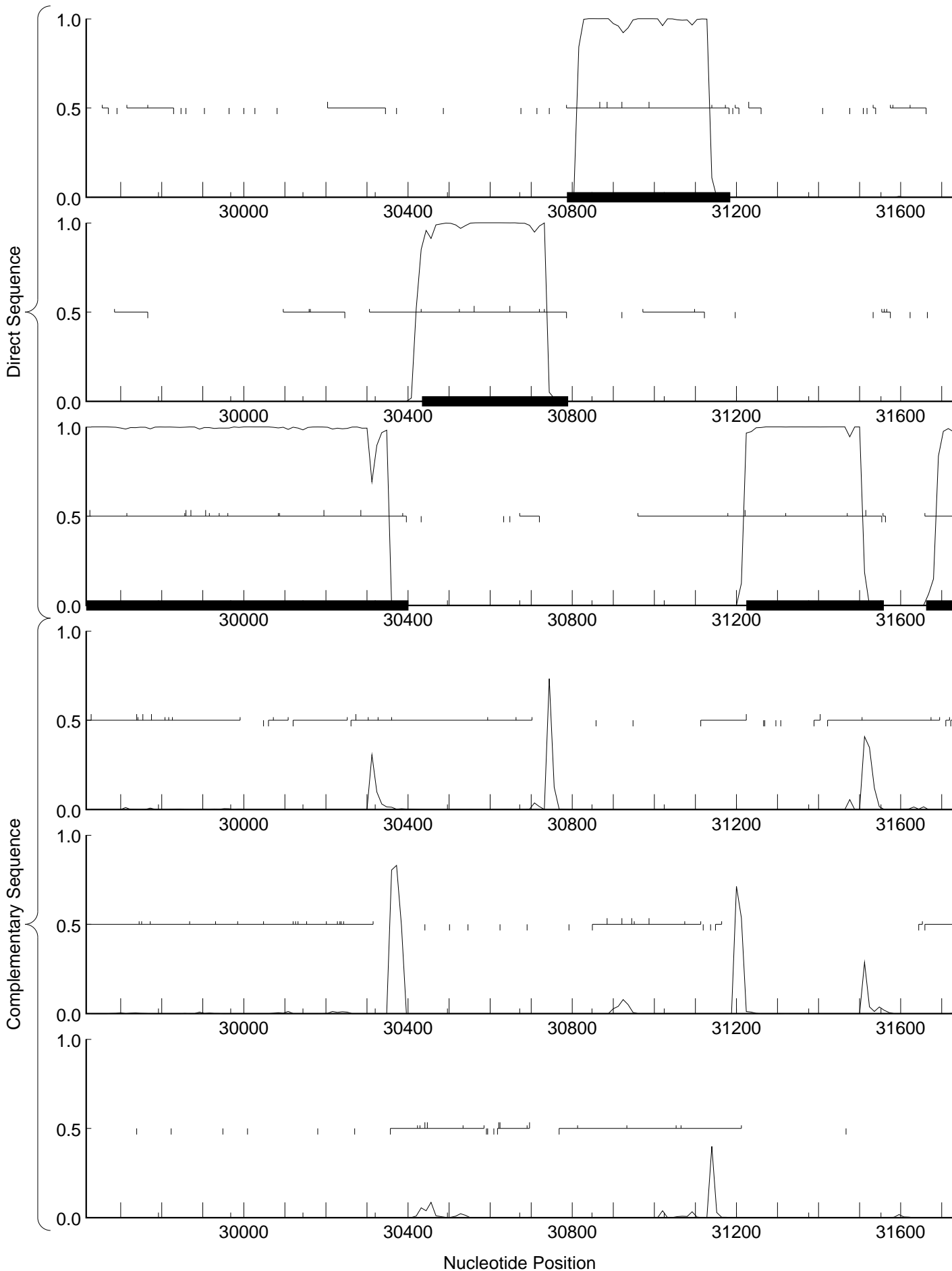


GeneMark, hmm prediction

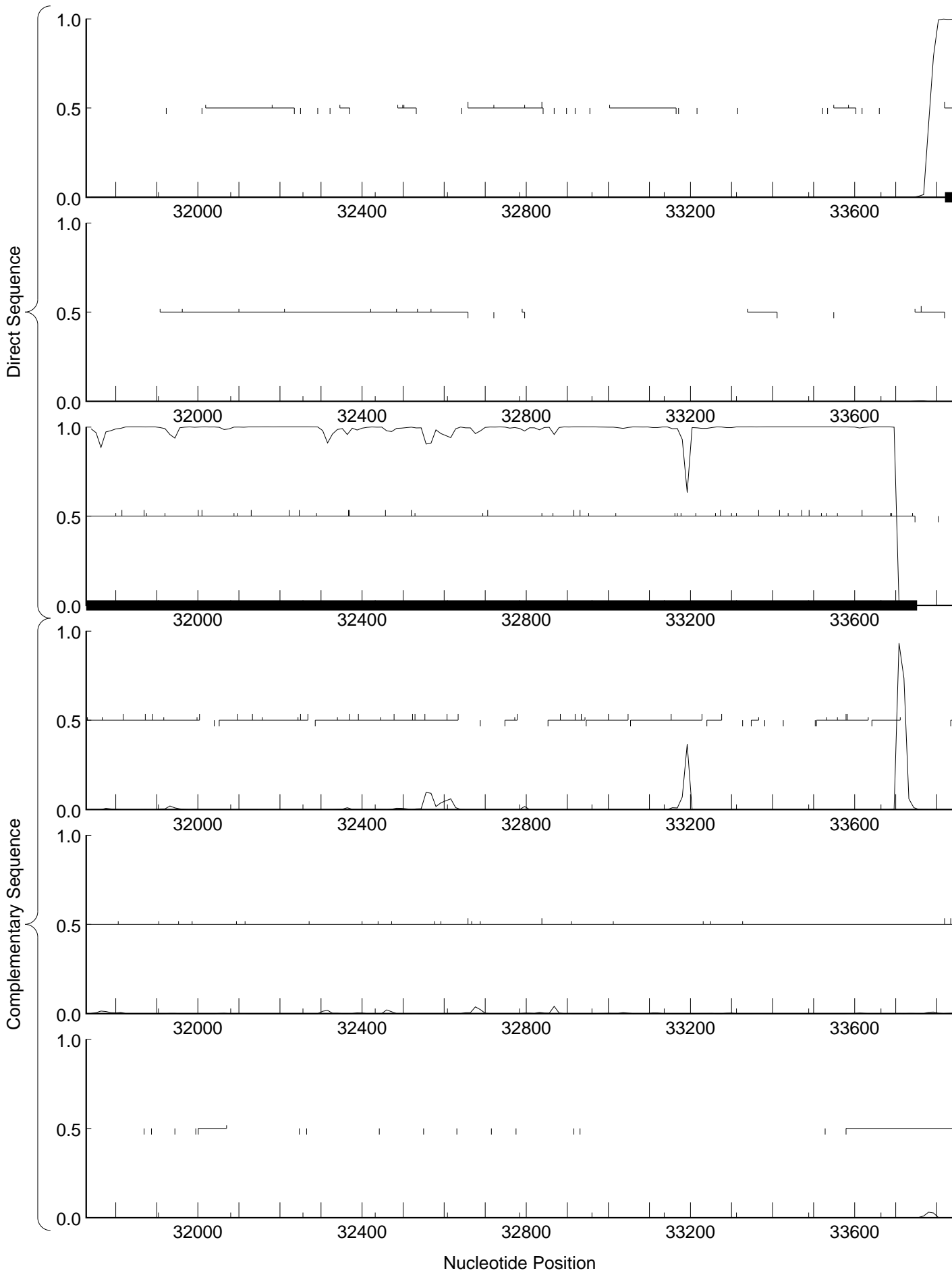




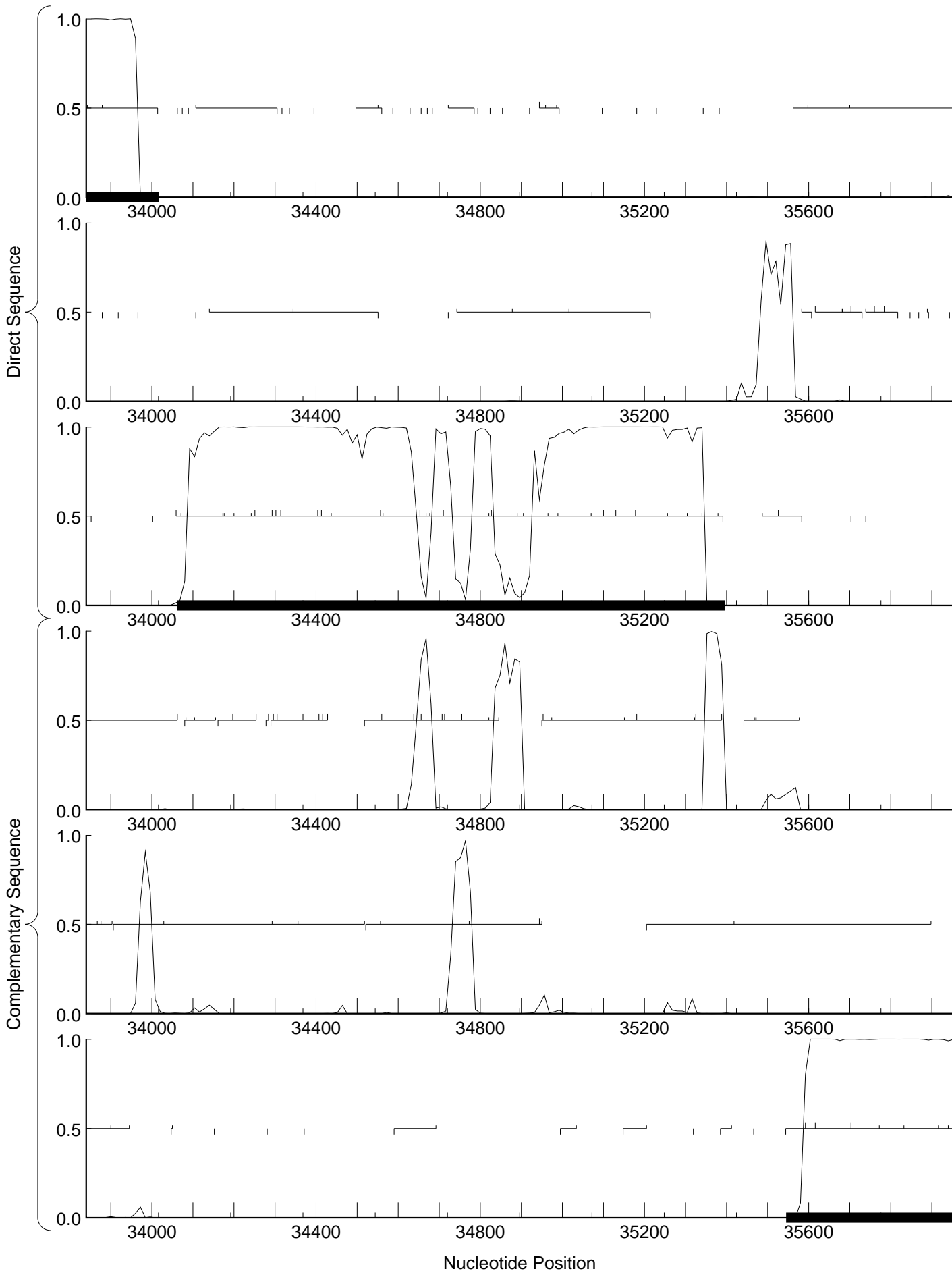
GeneMark, hmm prediction



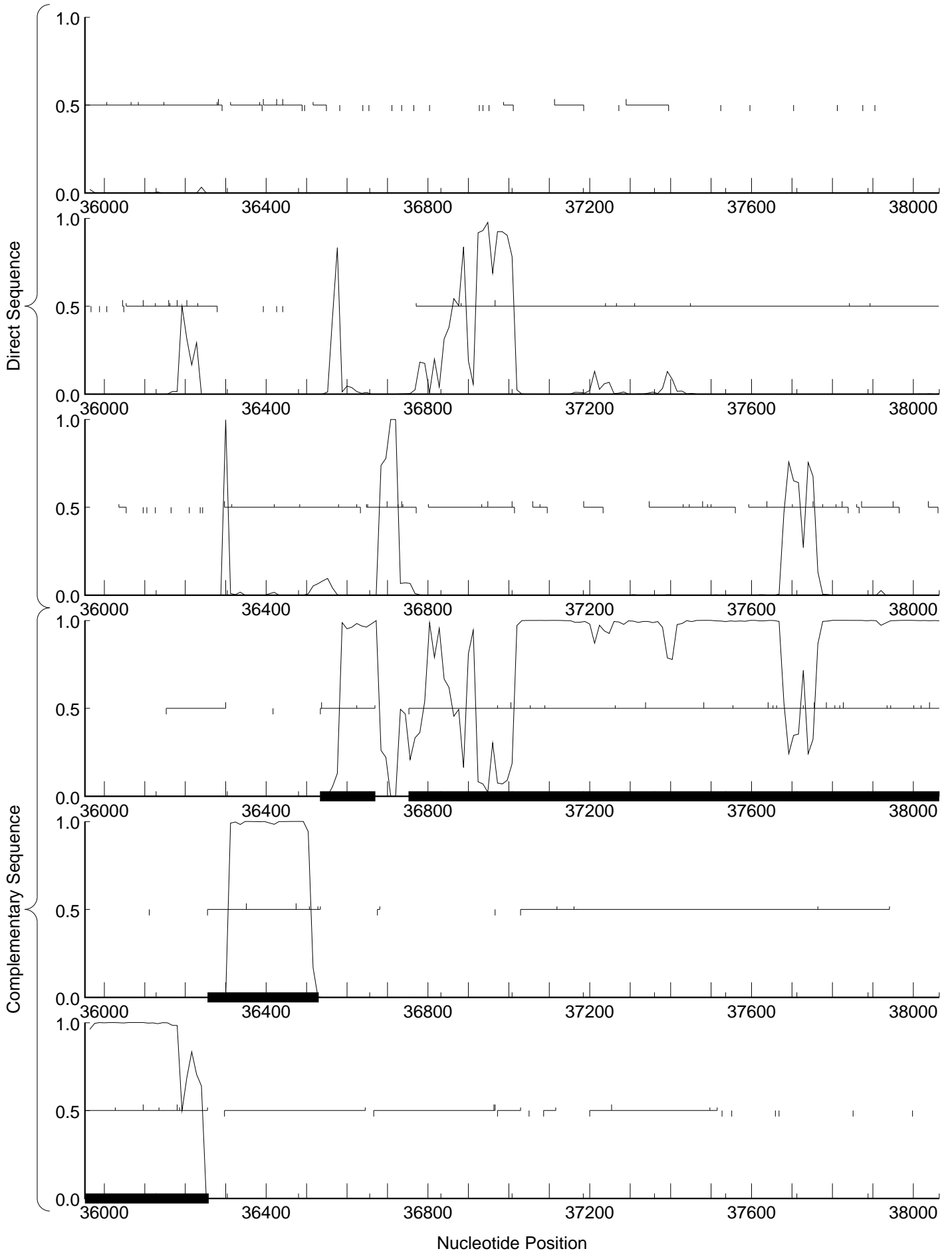
GeneMark, hmm prediction



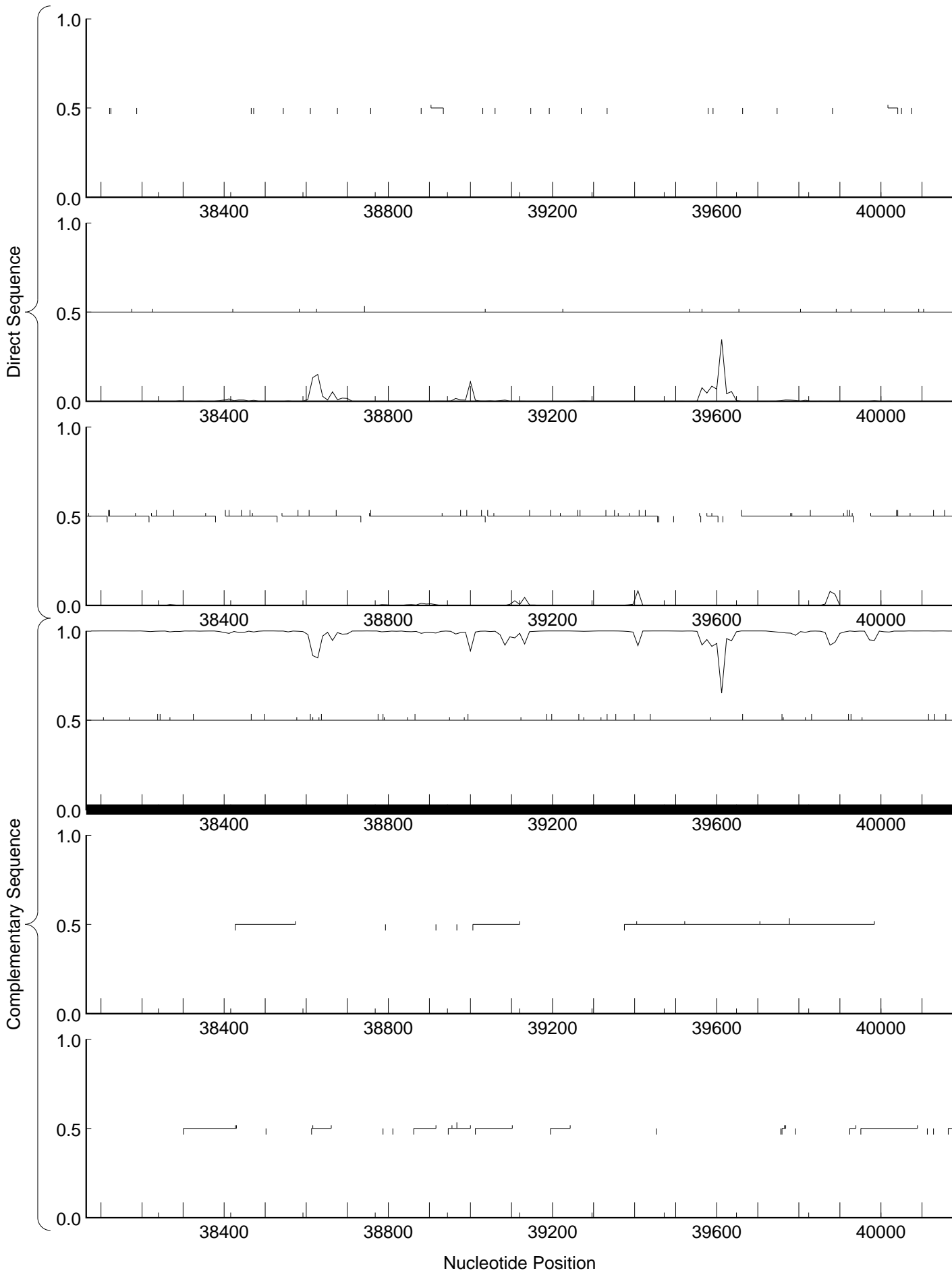
GeneMark, hmm prediction



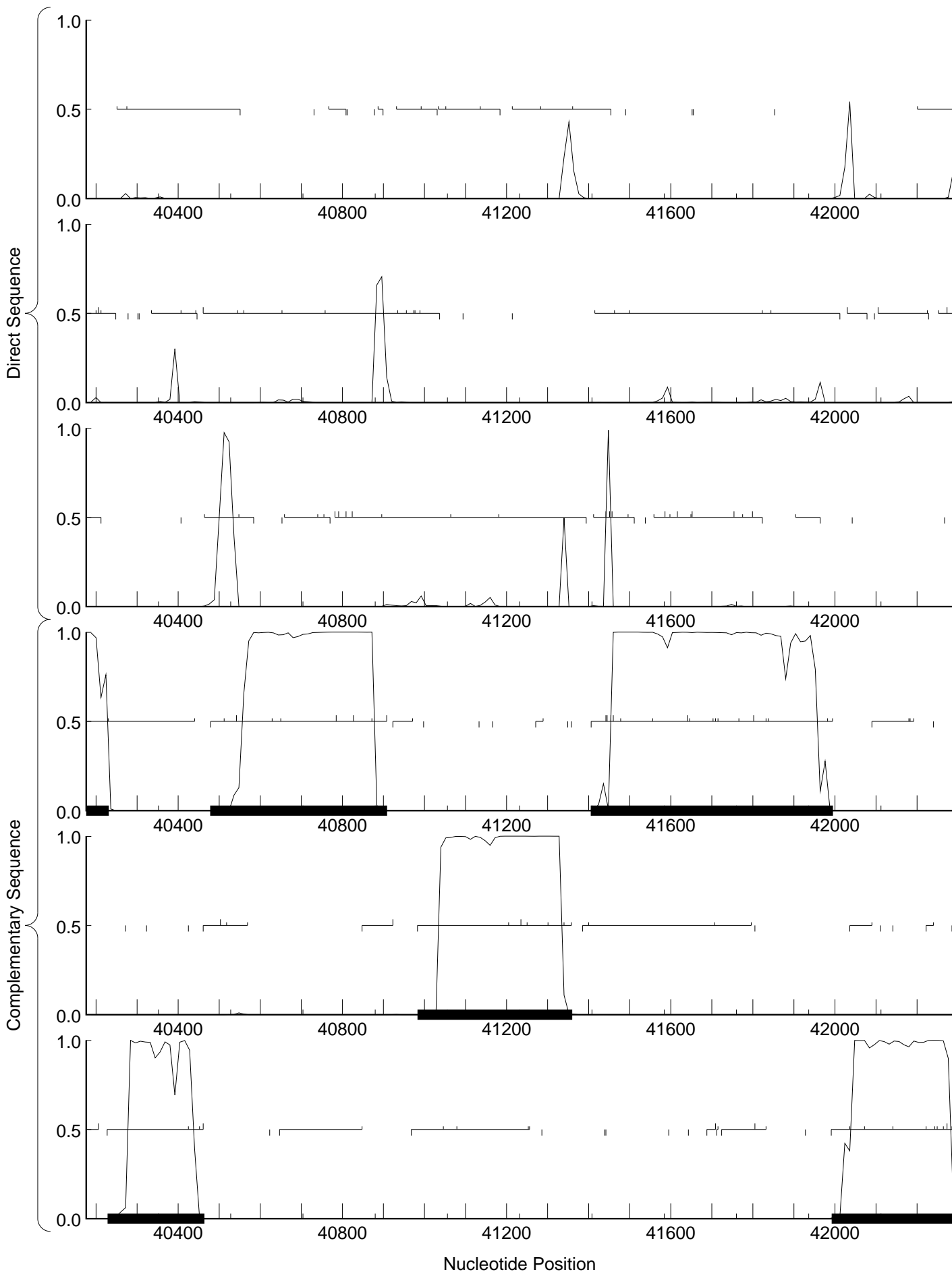
GeneMark, hmm prediction



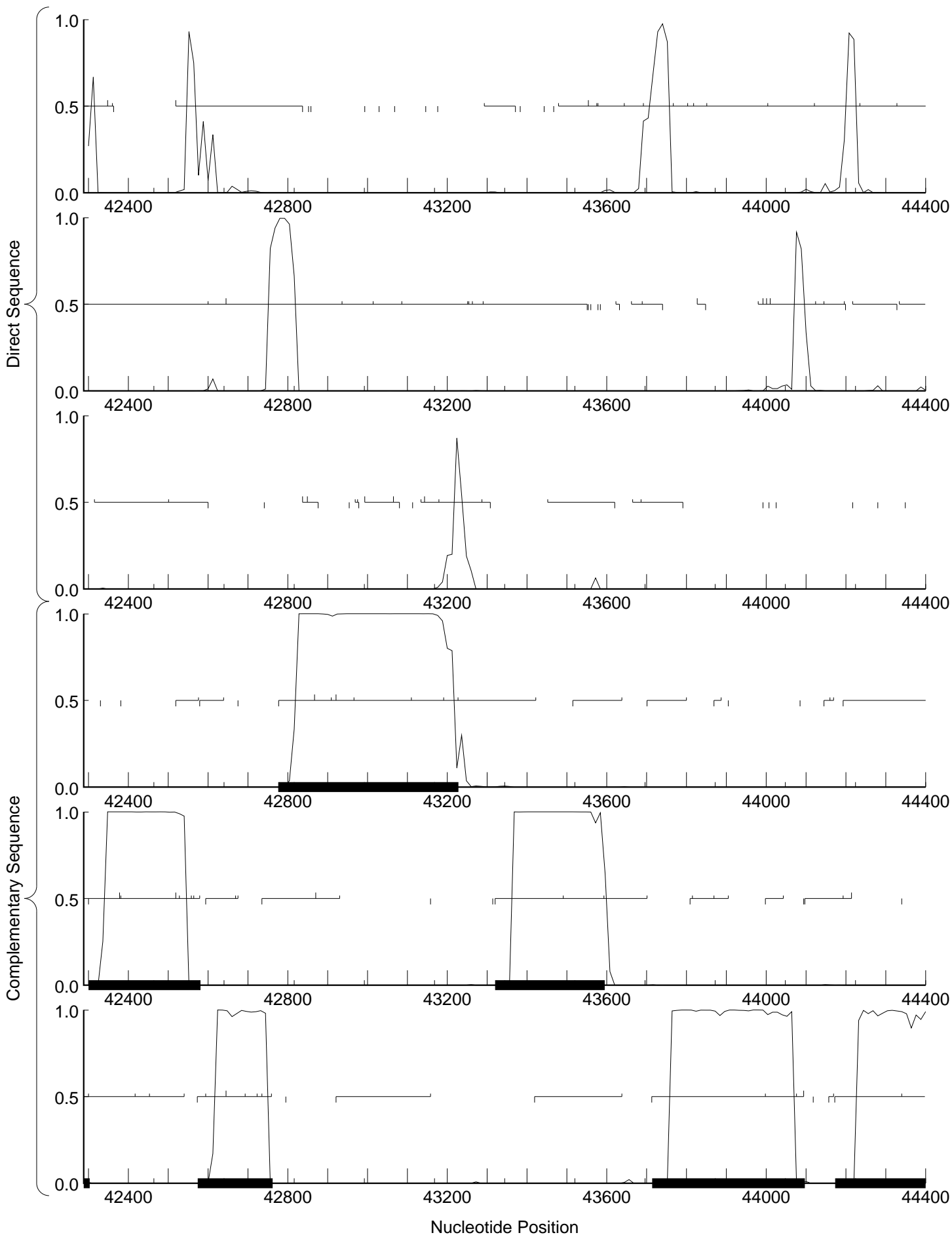
GeneMark, hmm prediction

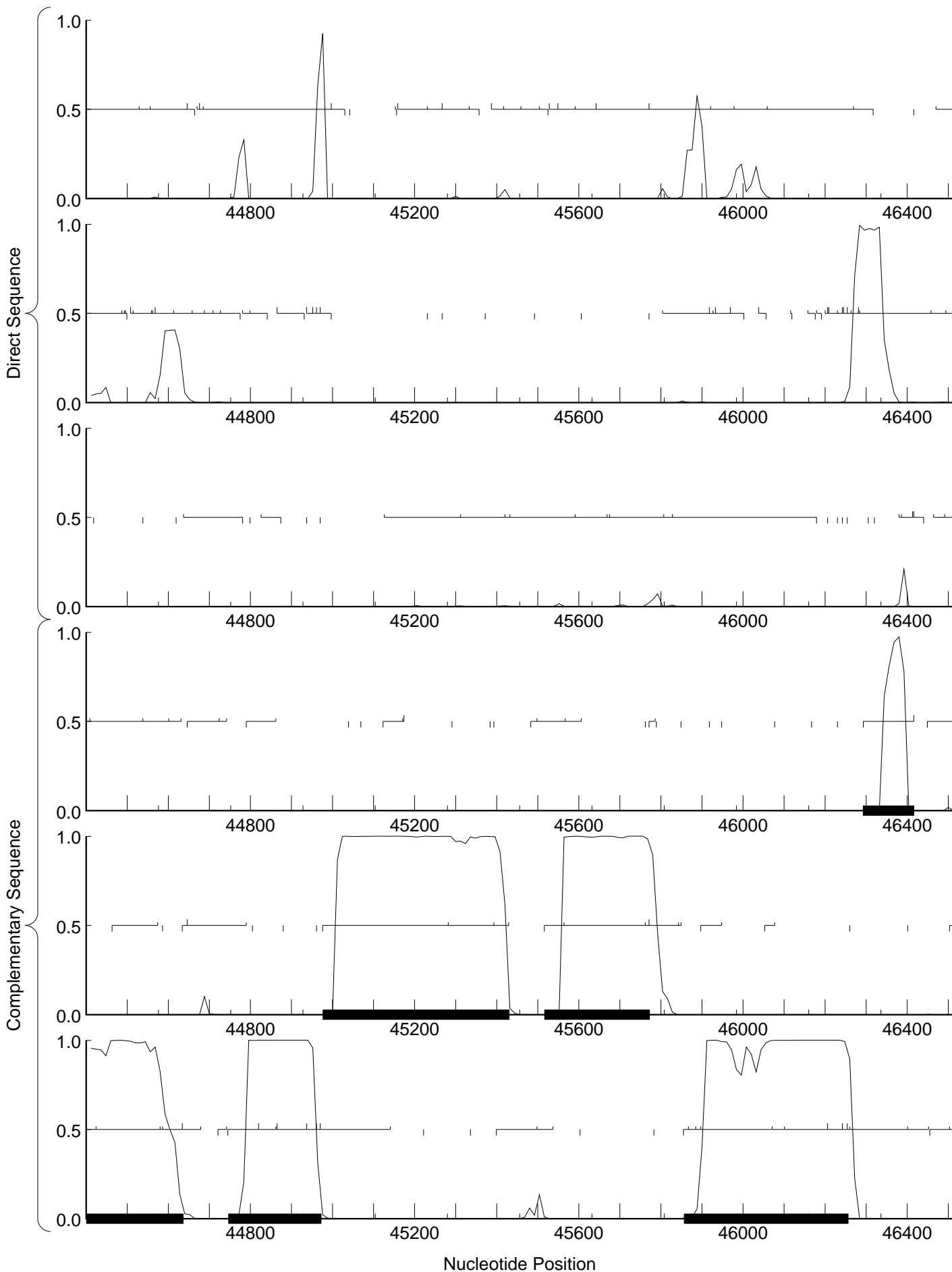


GeneMark, hmm prediction

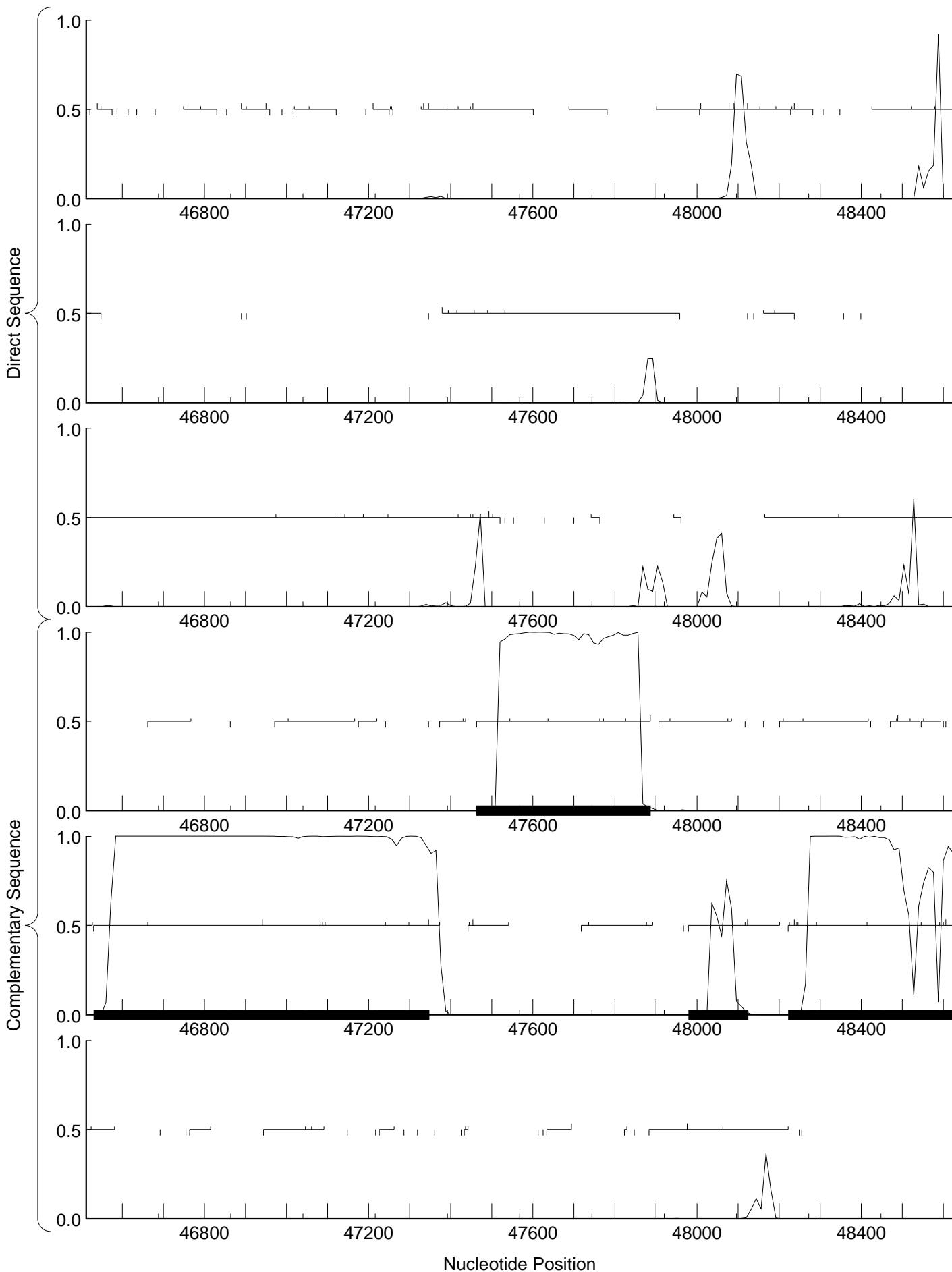


GeneMark, hmm prediction





GeneMark, hmm prediction



GeneMark, hmm prediction

