

GeneMark

Version 2.5p (09.08.06)

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PROGRAM INFORMATION

Sequence : Streptomyces phage HaugeAnator complete sequence, 46135 bp including 274 bp terminal repeat
Analysis Date : 8/22/17 at 20:41:41
Pages : 23
Sequence Length : 46135 bp
GC Content : 59.63%

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

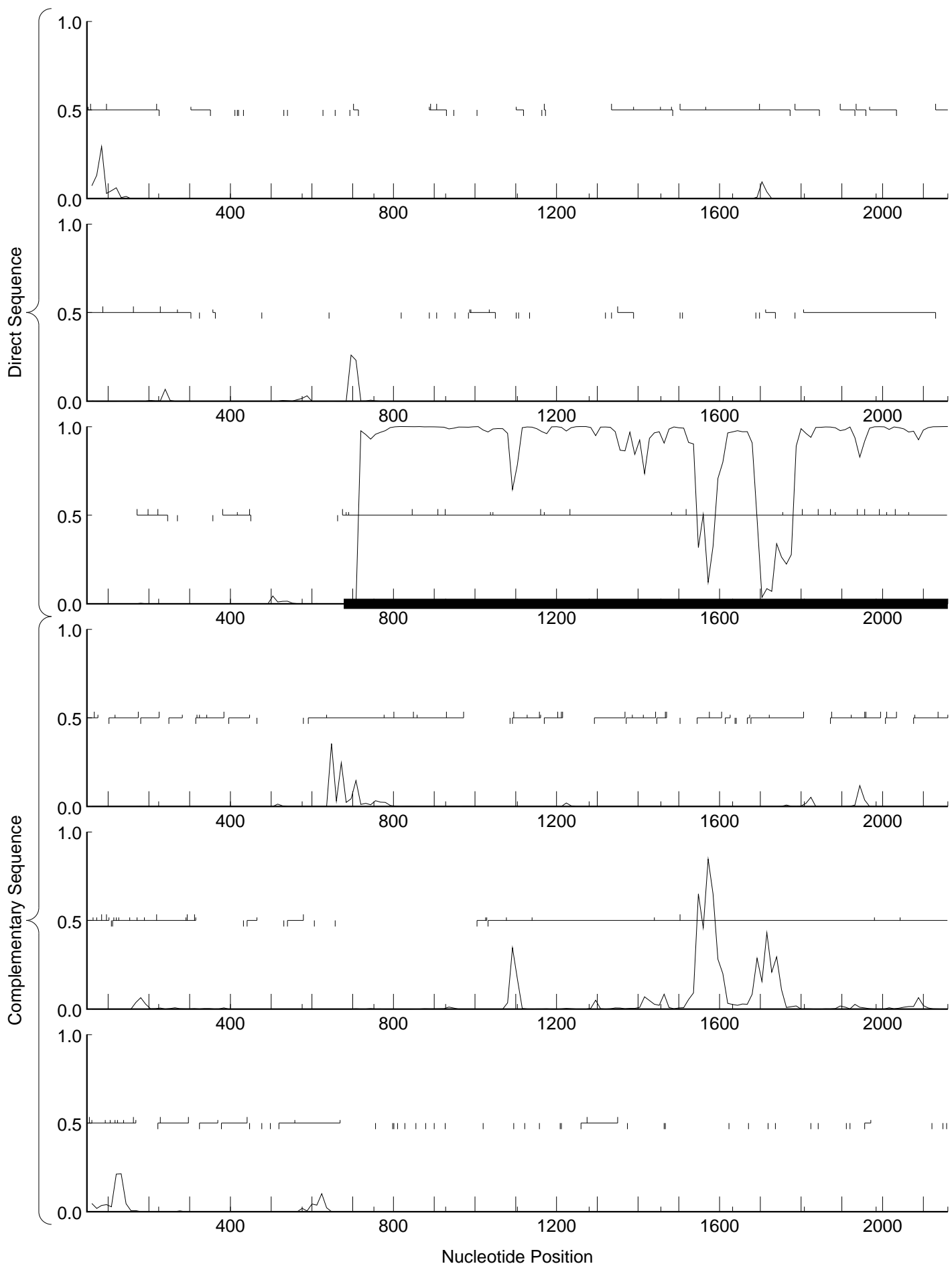
Matrix : Heuristic, GC = 60
Author : Borodovsky Laboratory - Georgia Tech
Order : 2

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

Matrix notes & comments

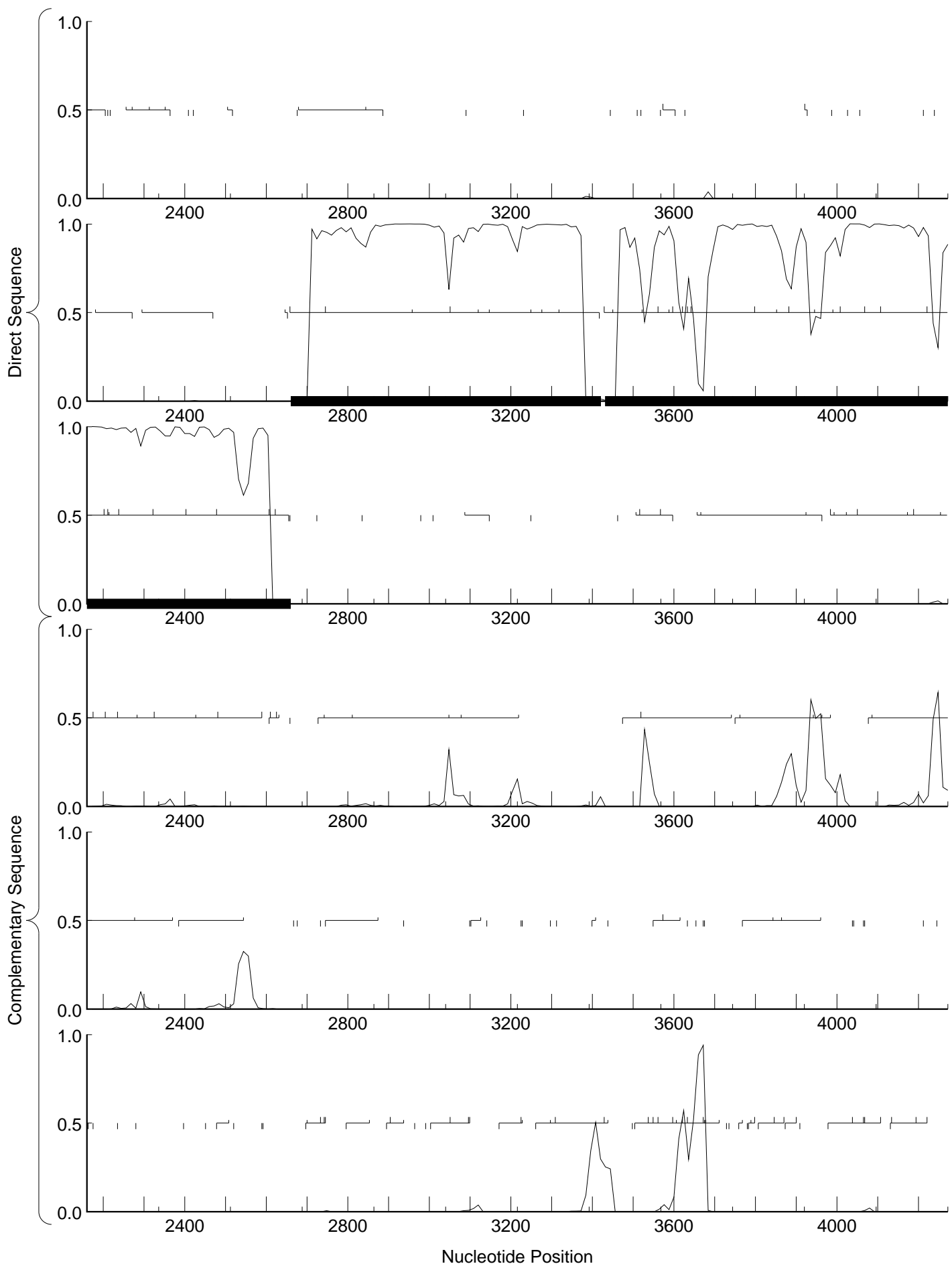
For details on the model building procedure see:
Besemer J. and Borodovsky M.
"Heuristic approach to deriving models for gene finding"
NAR, 1999, Vol. 27, No. 19, pp. 3911-3920

GeneMark, hmm prediction



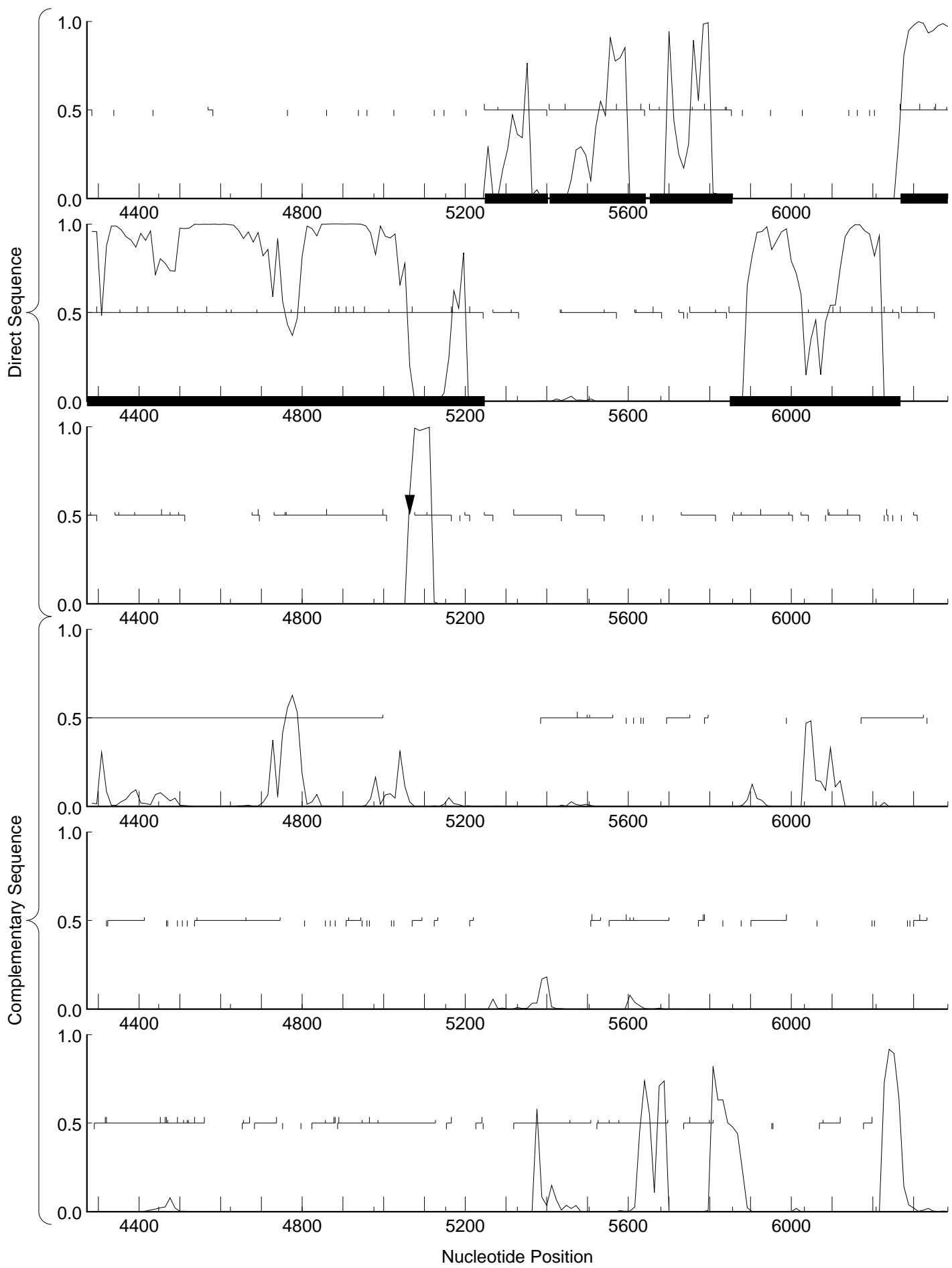
Nucleotide Position

GeneMark, hmm prediction

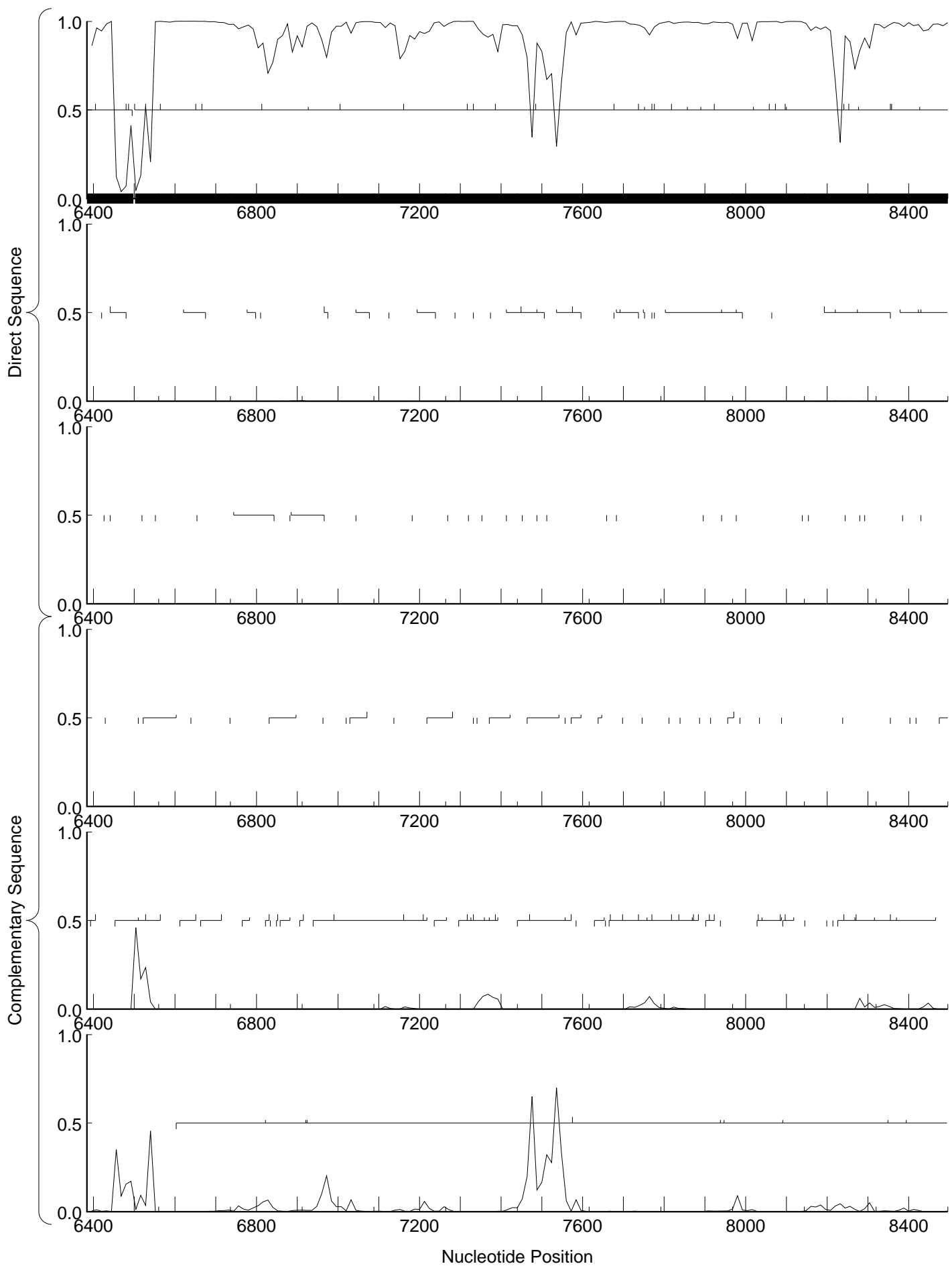


Nucleotide Position

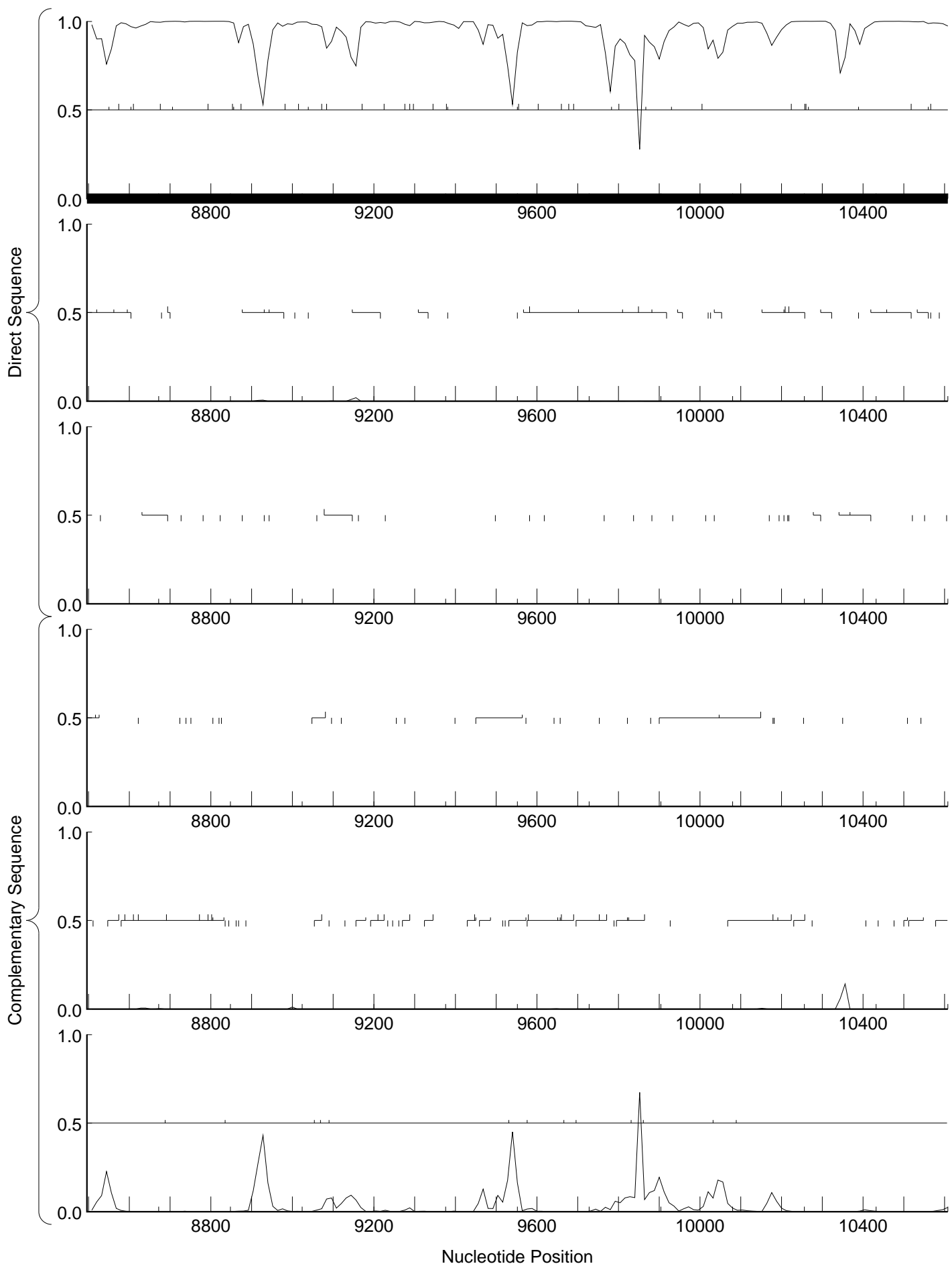
GeneMark, hmm prediction



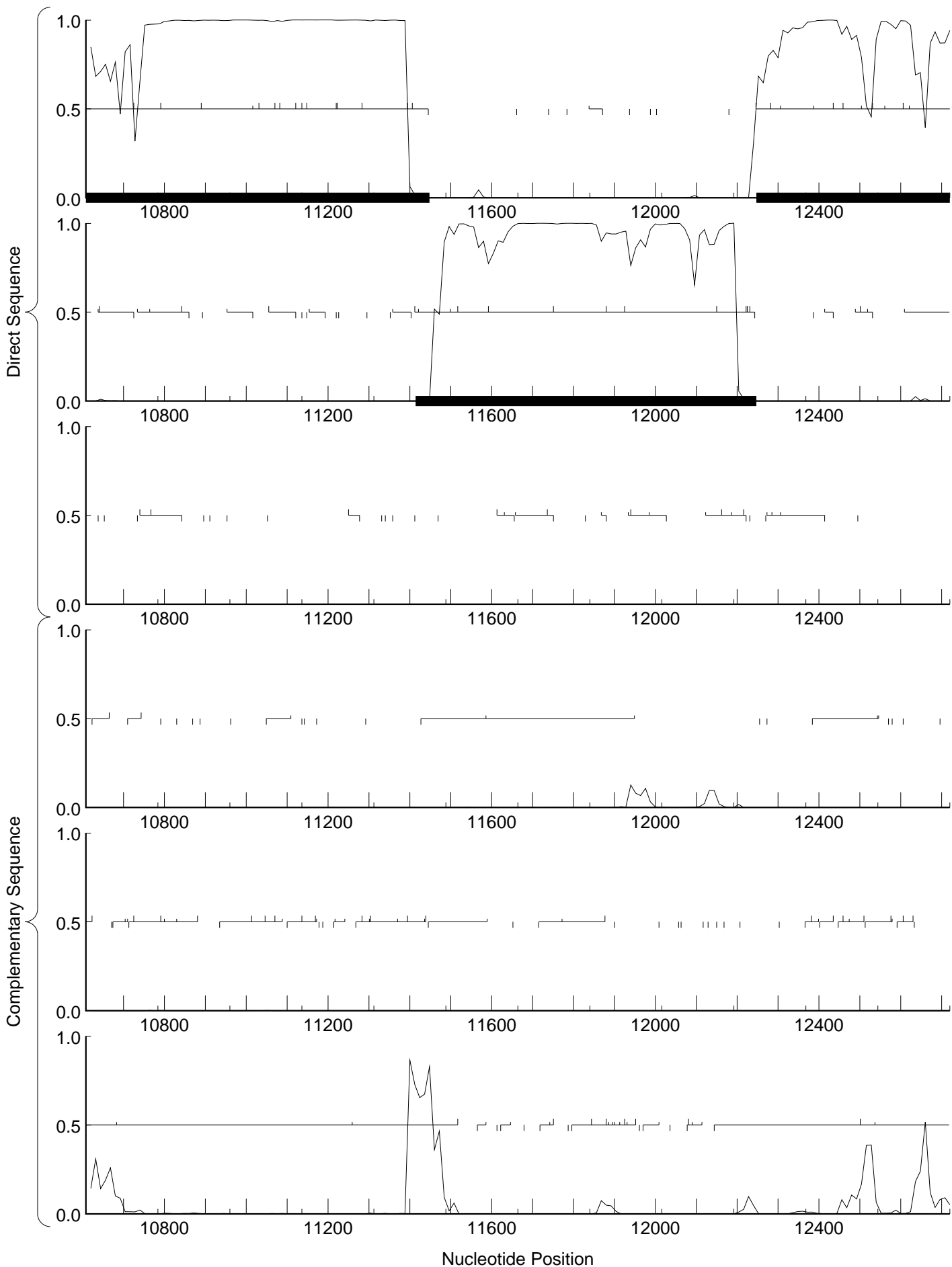
GeneMark, hmm prediction



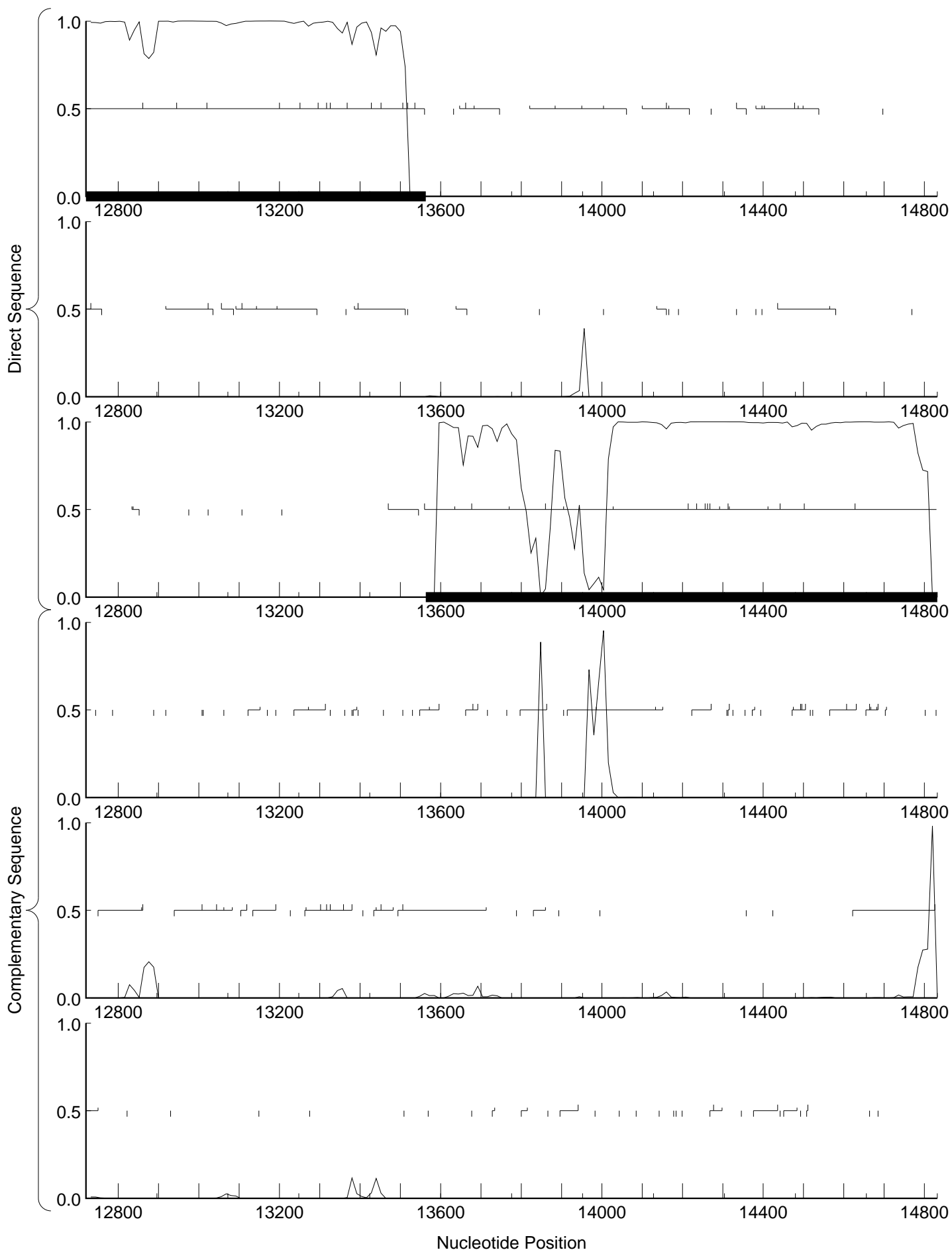
GeneMark, hmm prediction



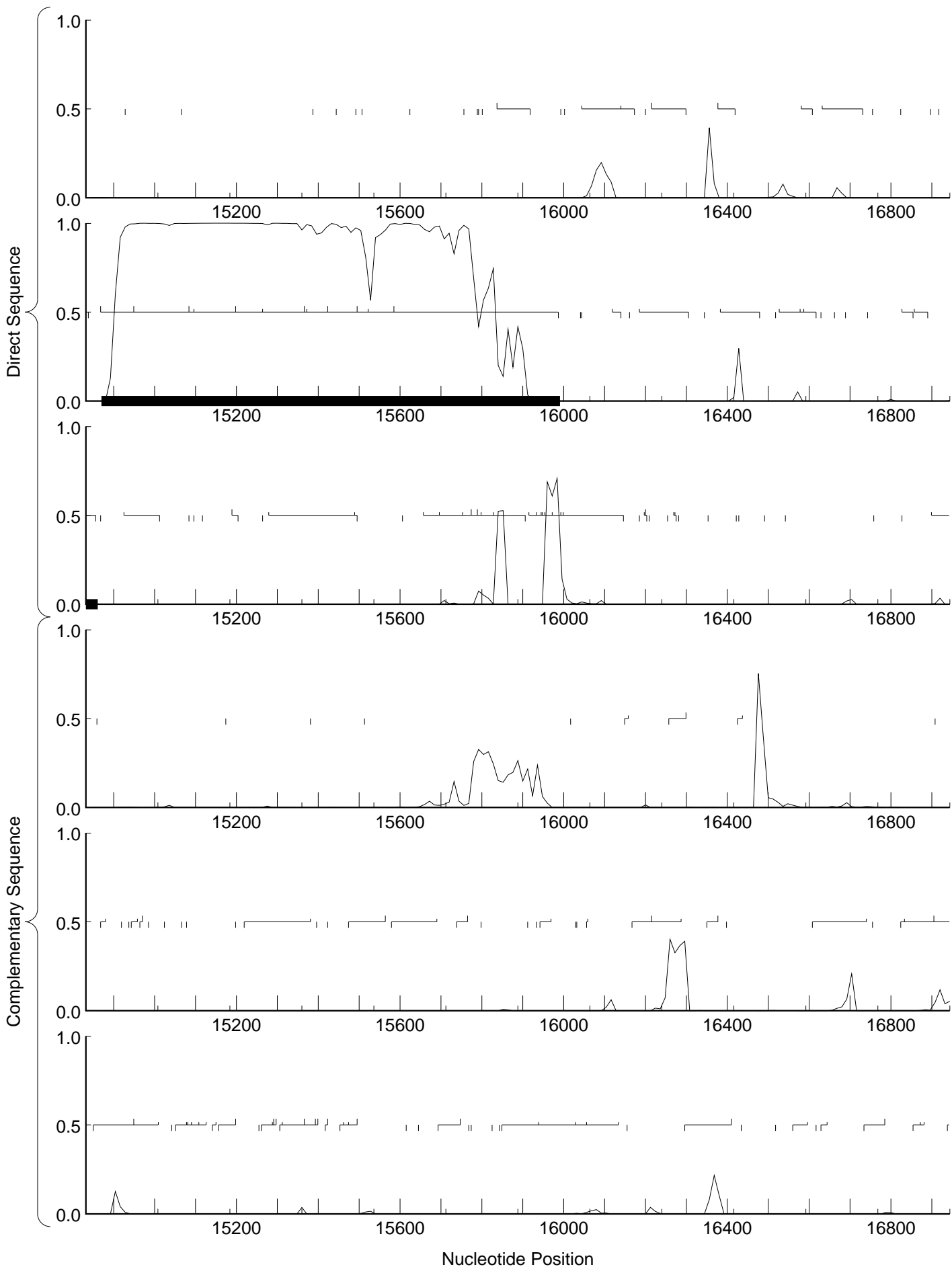
GeneMark, hmm prediction



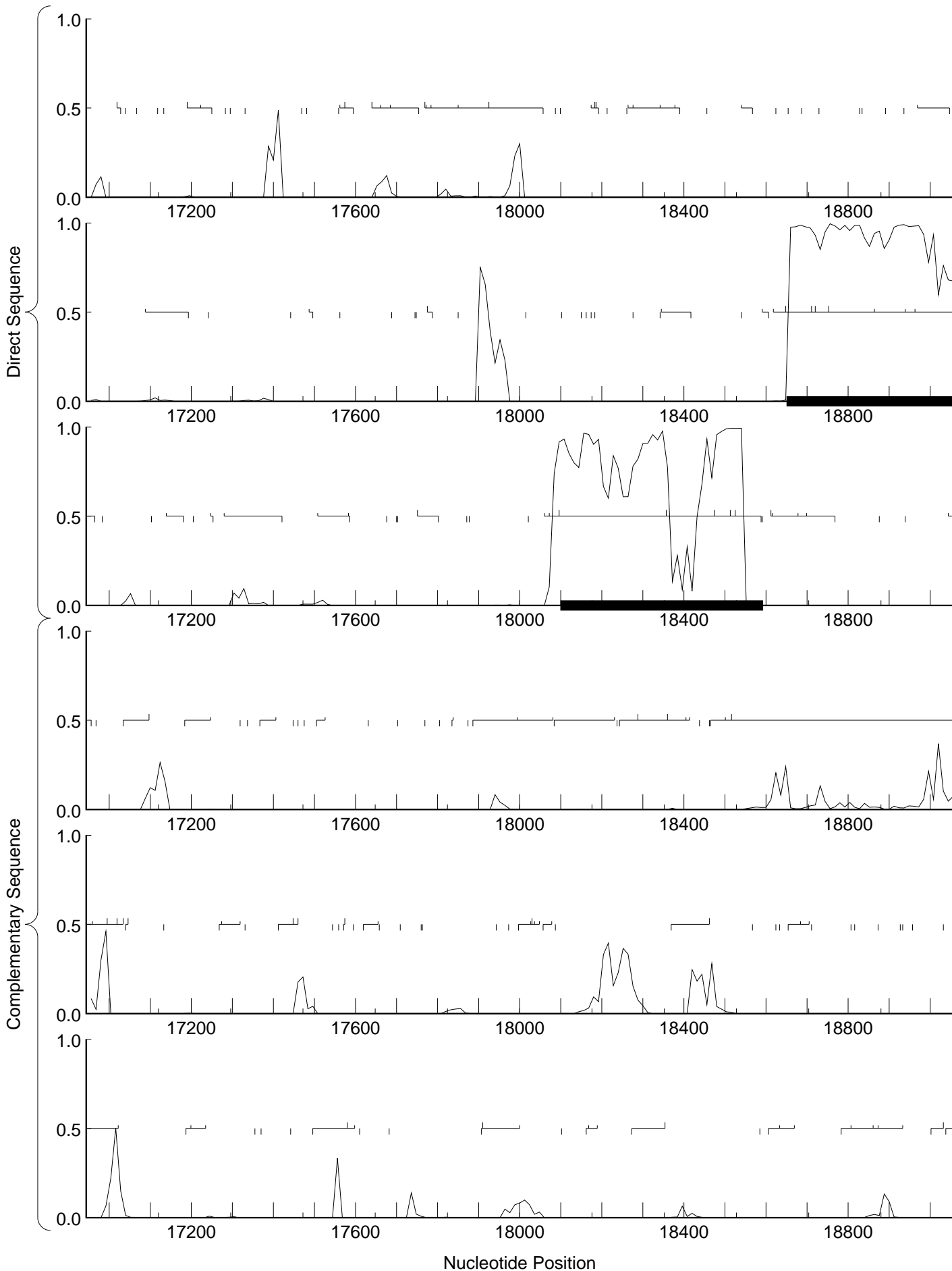
GeneMark, hmm prediction



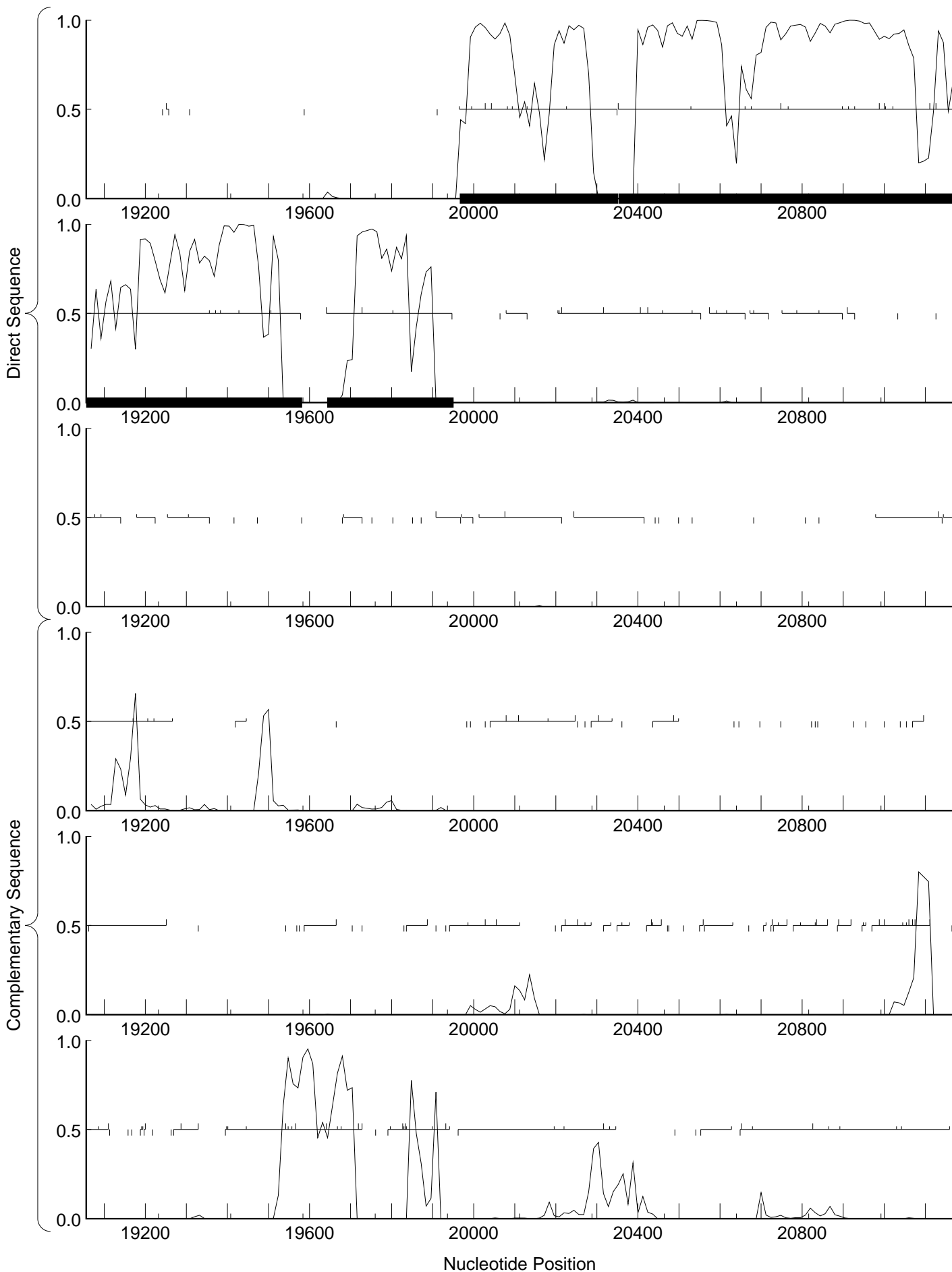
GeneMark, hmm prediction



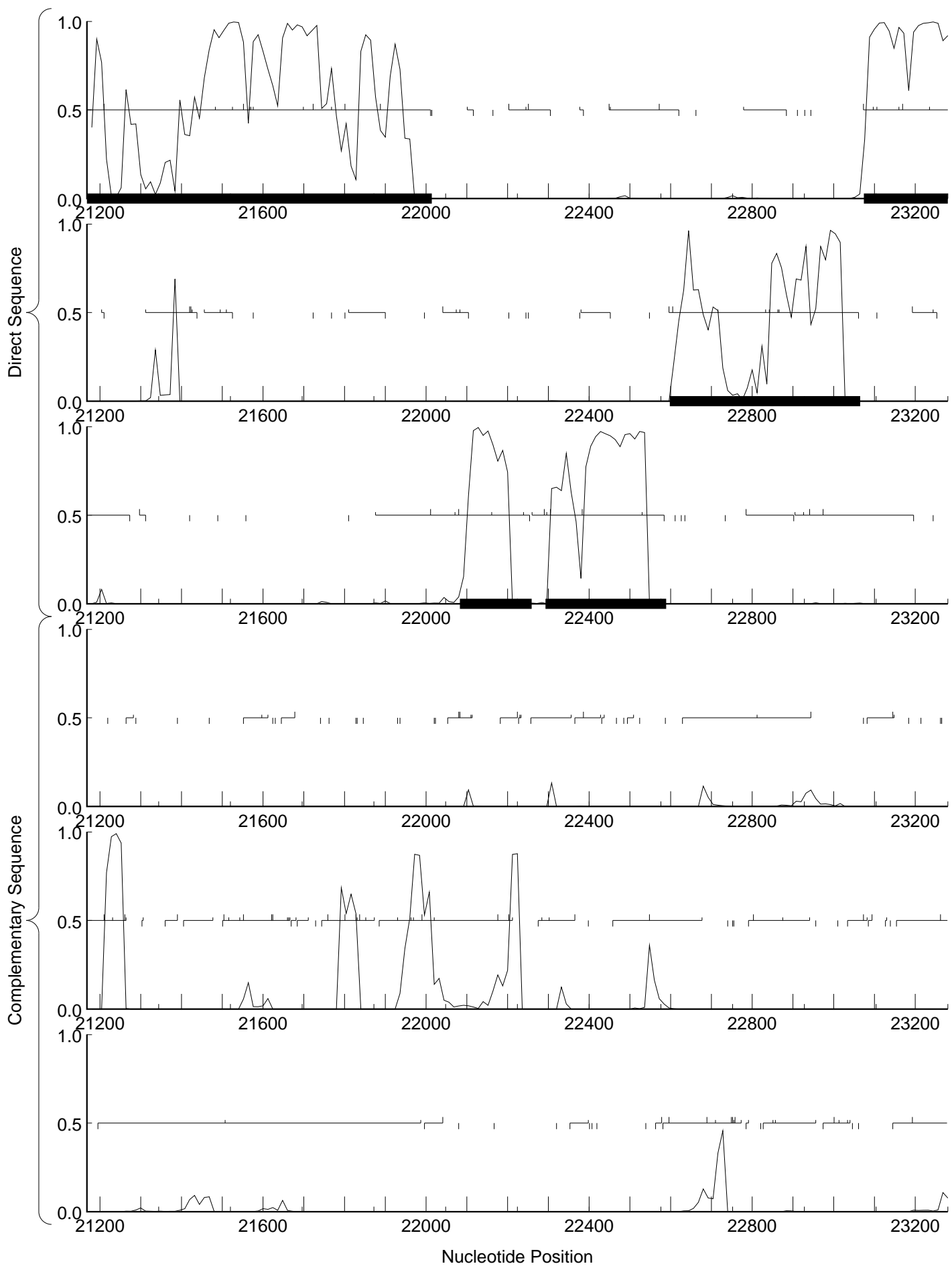
GeneMark.hmm prediction



GeneMark.hmm prediction

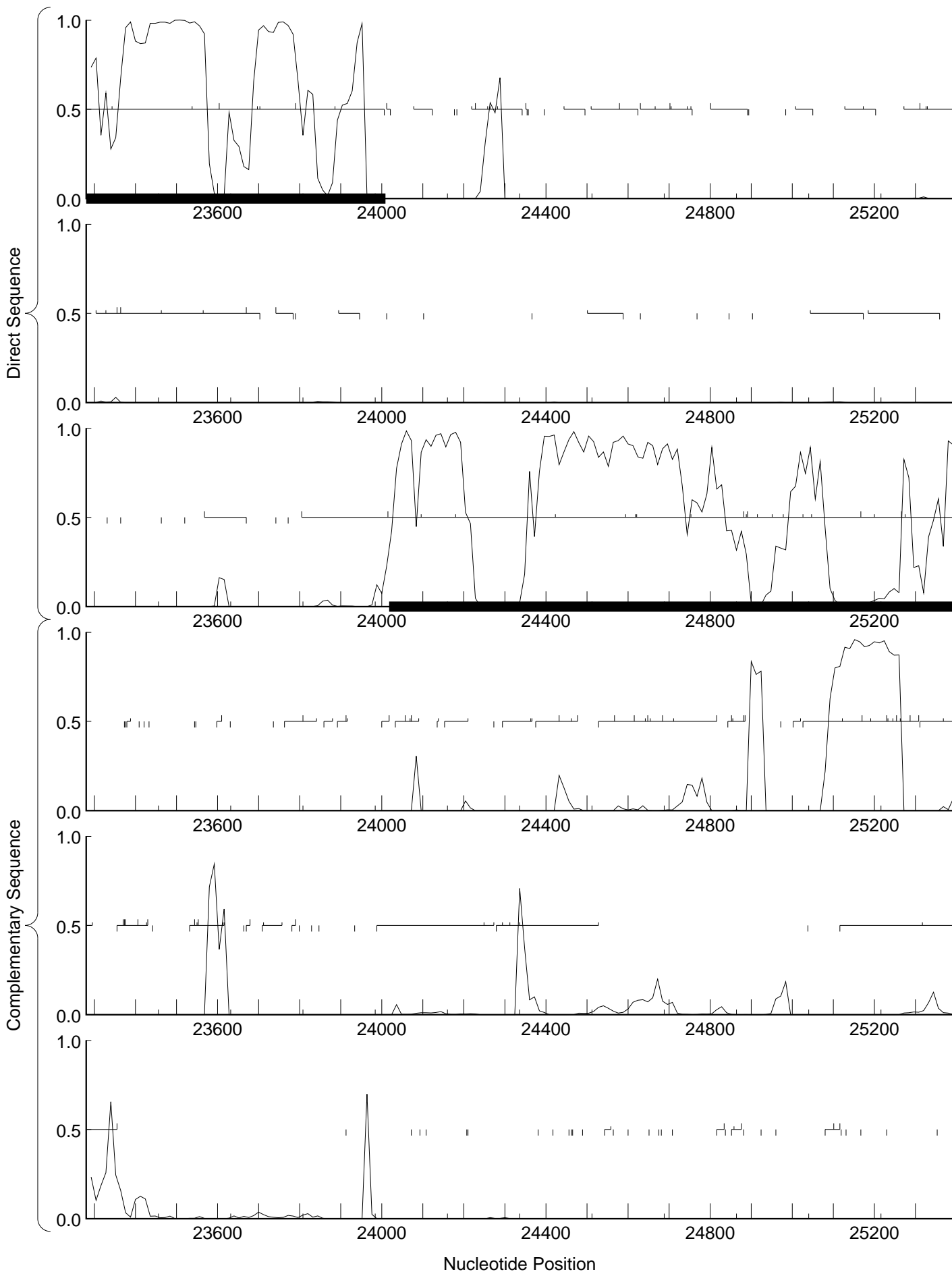


GeneMark.hmm prediction

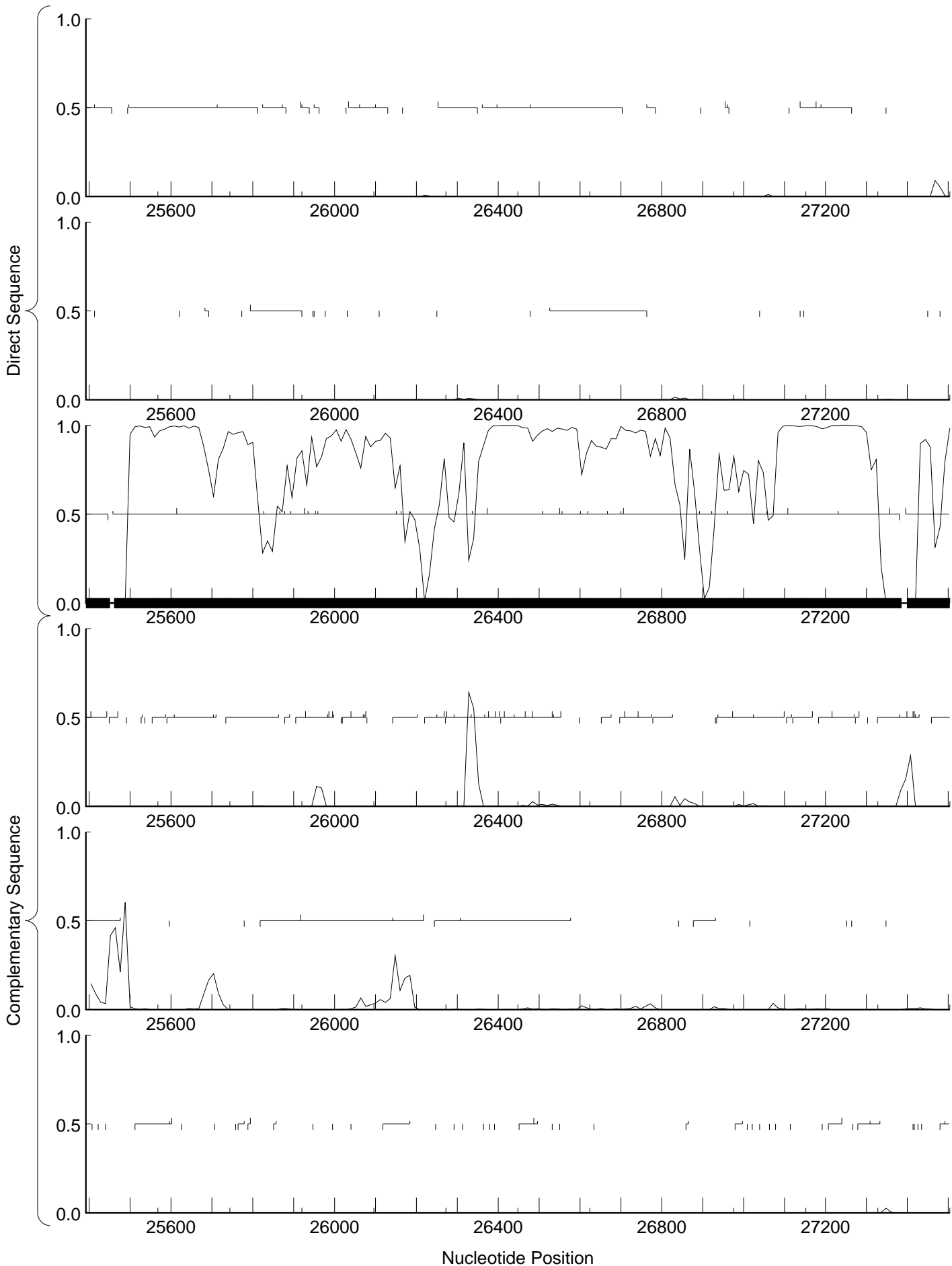


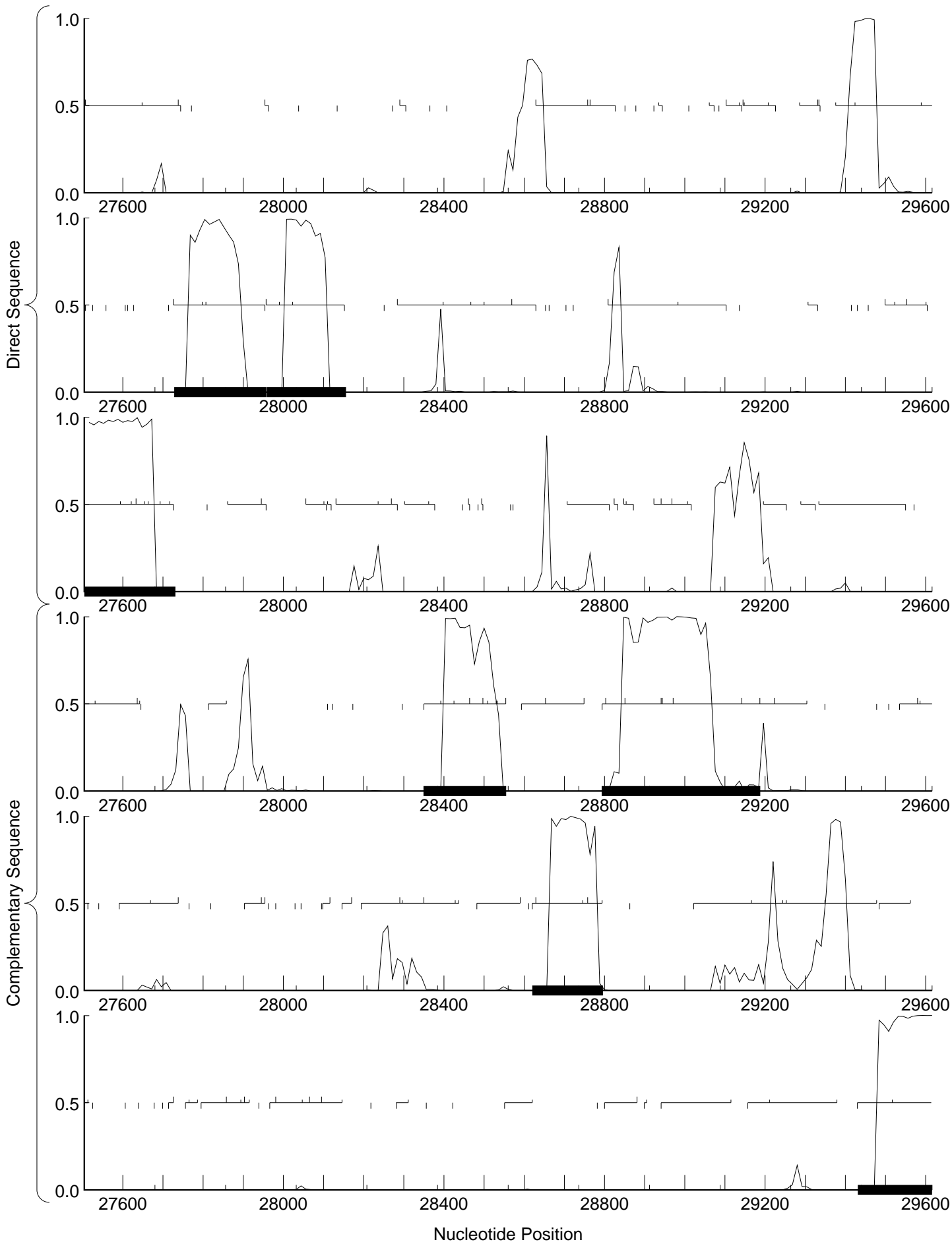


GeneMark_hmm prediction

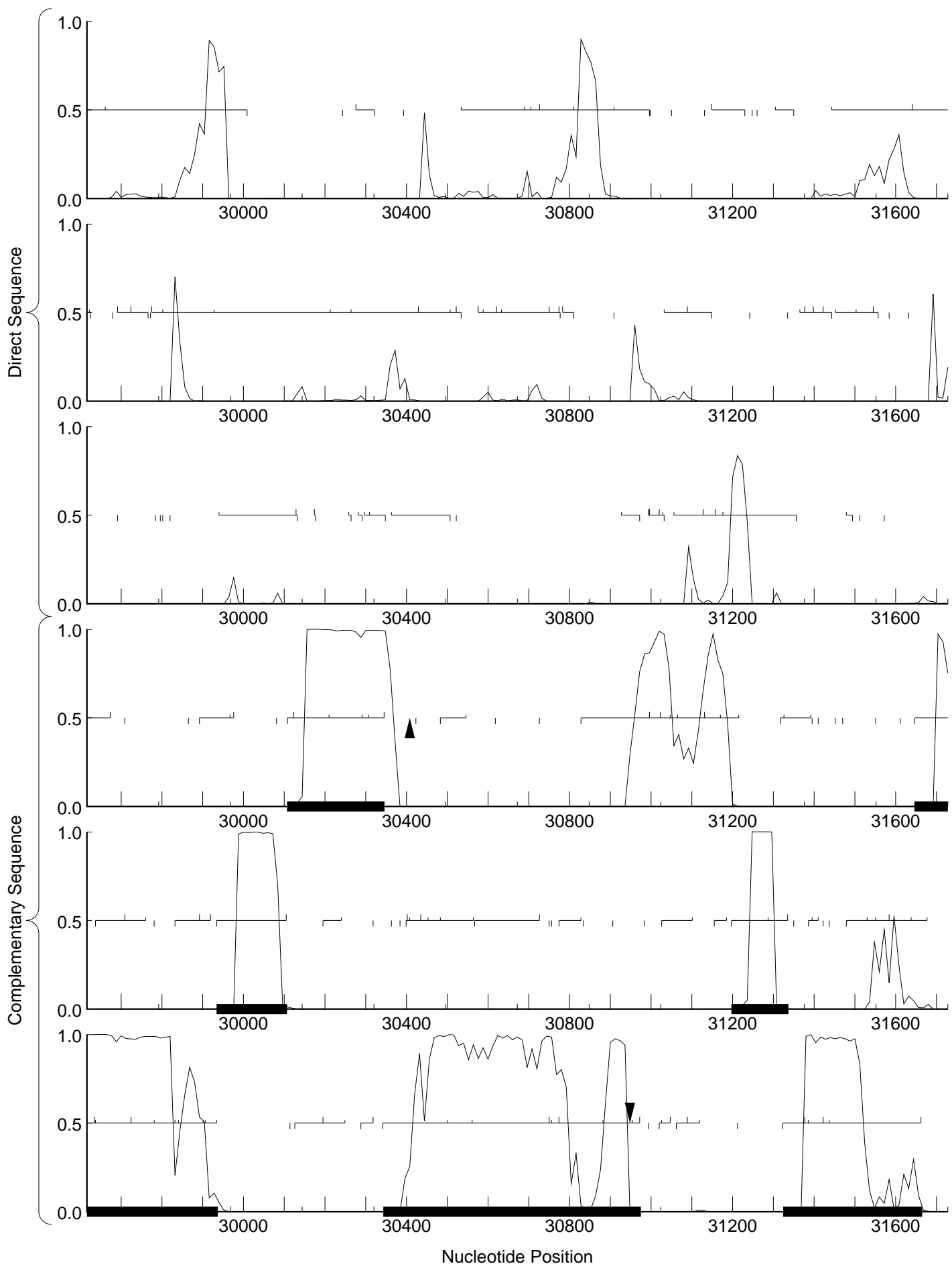


GeneMark.hmm prediction

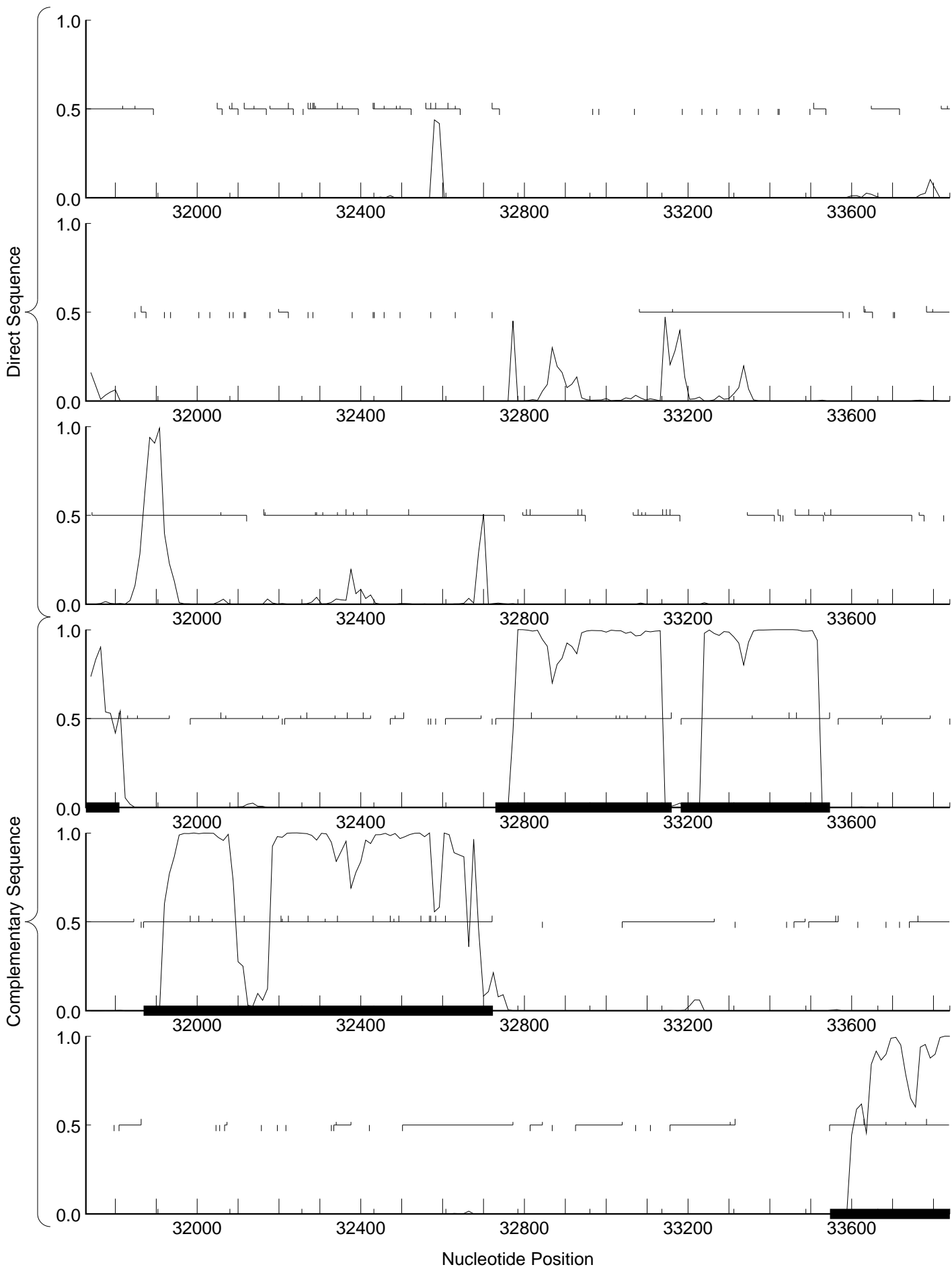




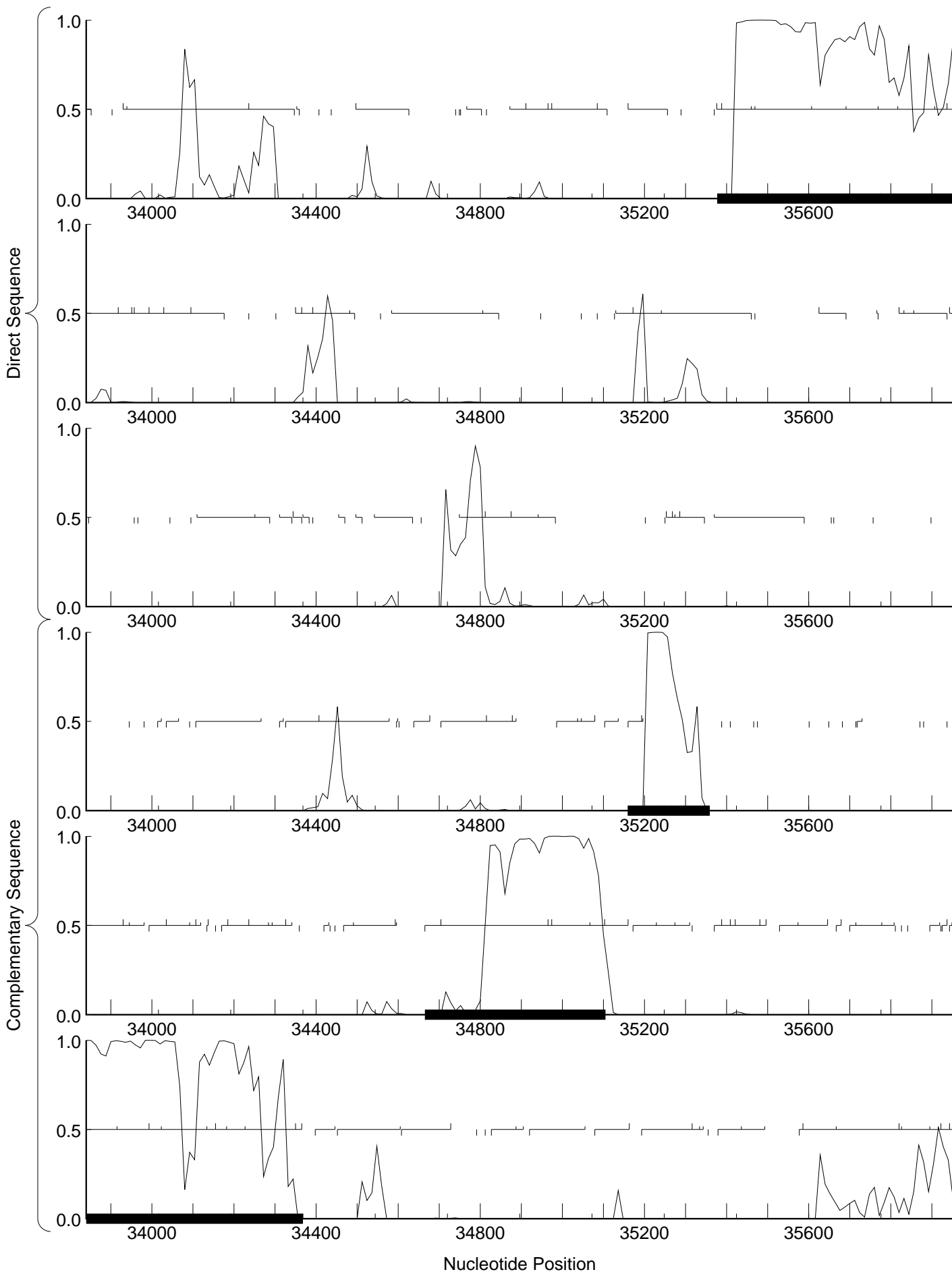
GeneMark_hmm prediction



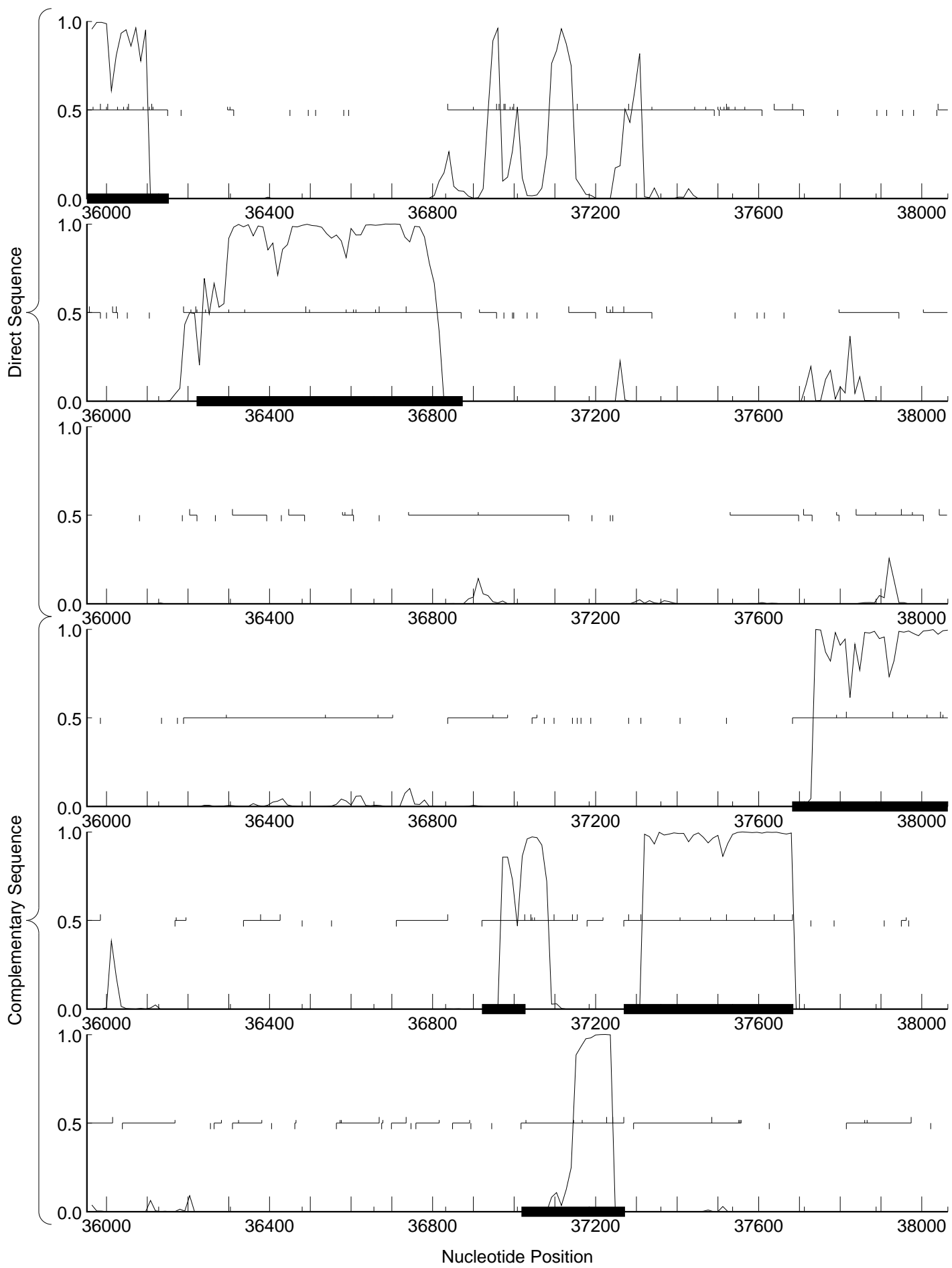
GeneMark.hmm prediction



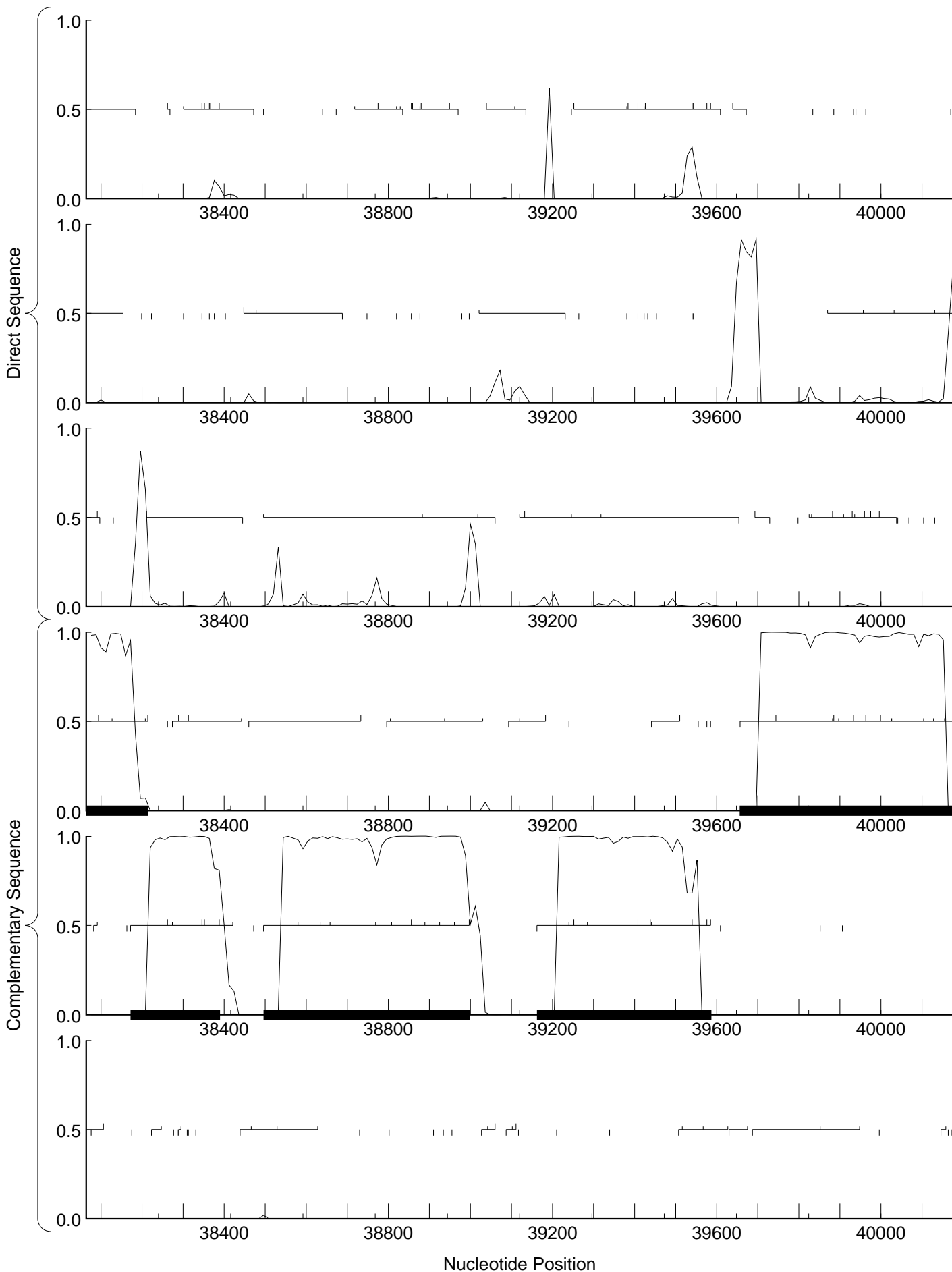
GeneMark.hmm prediction



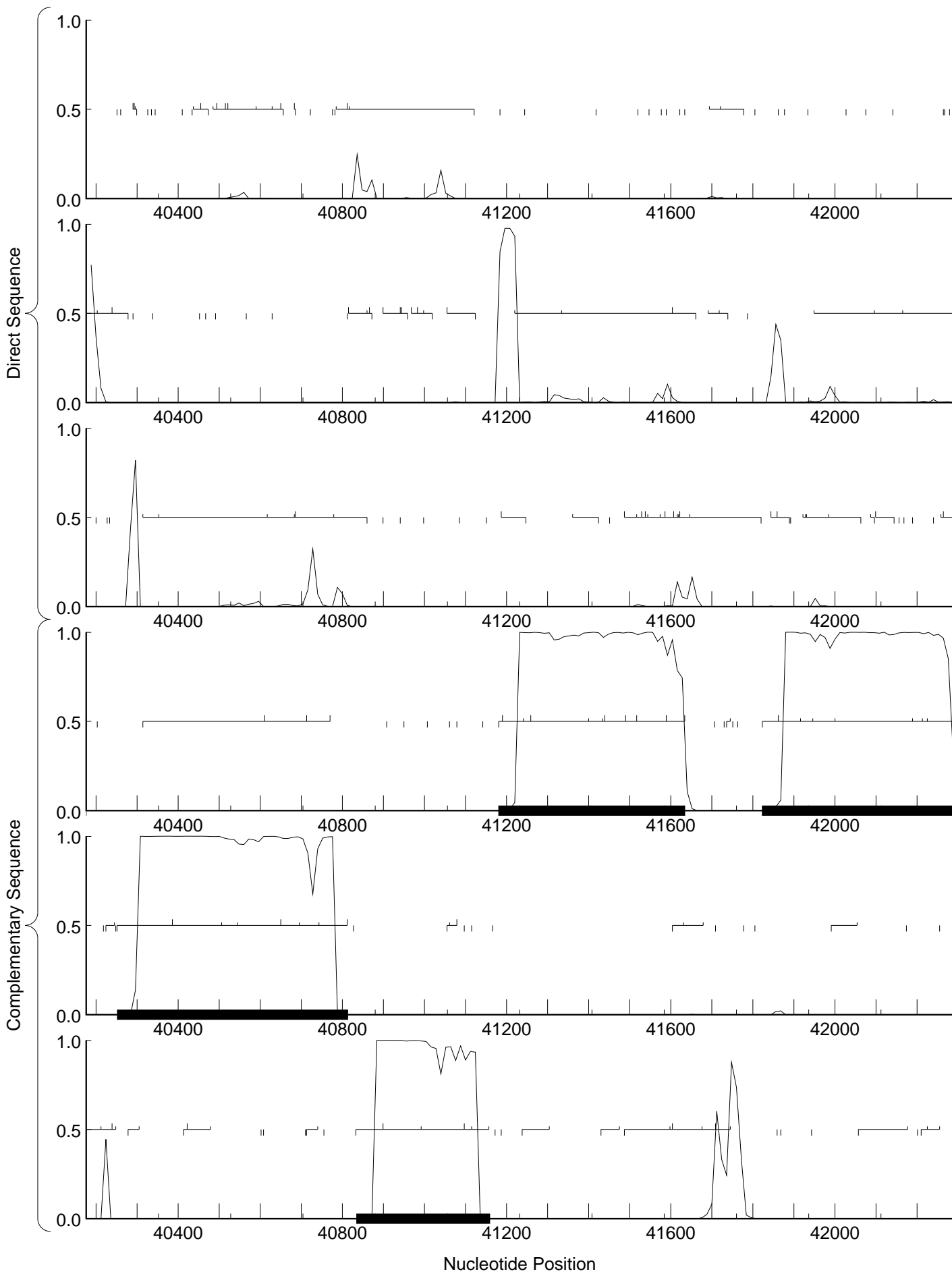
GeneMark.hmm prediction



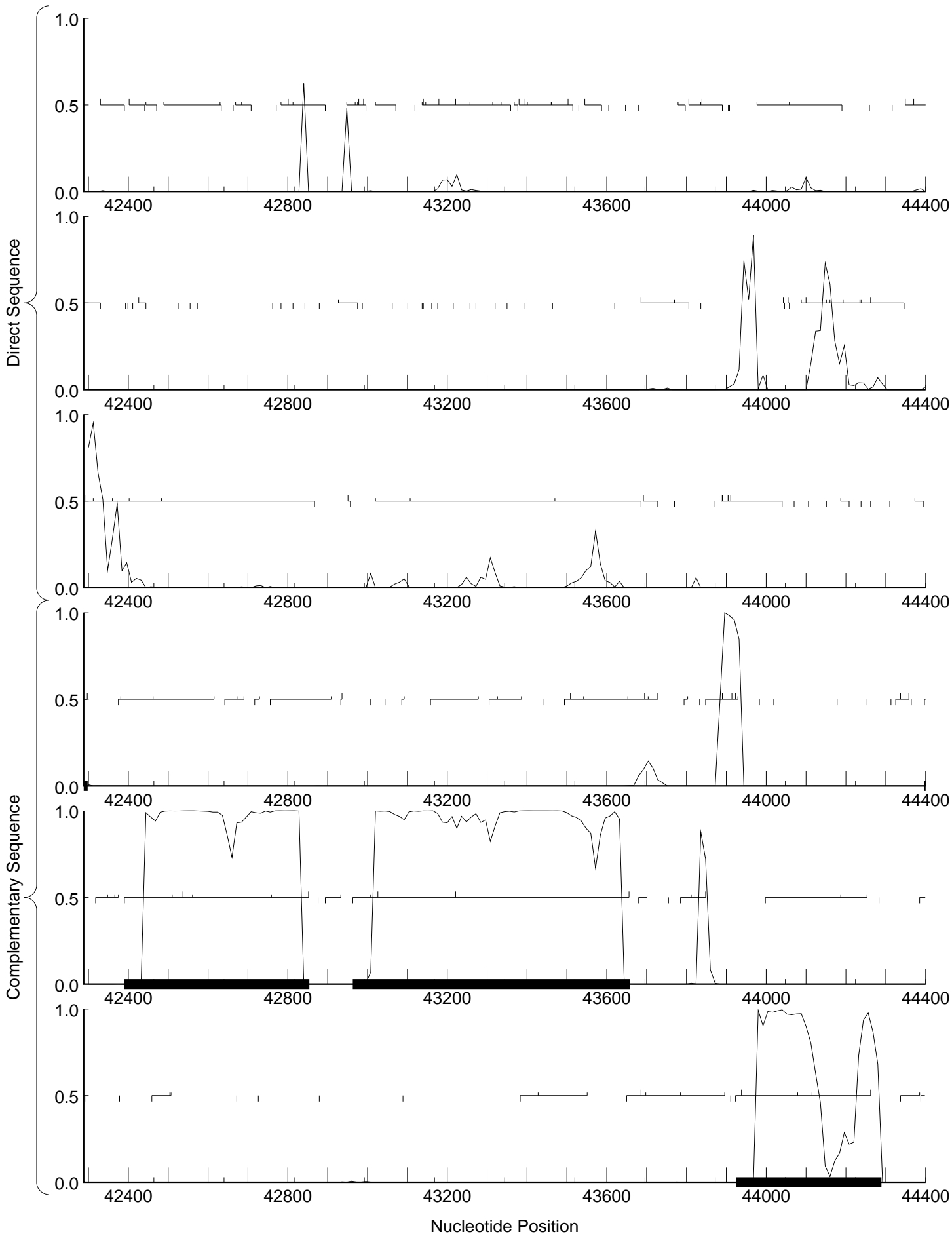
GeneMark.hmm prediction



GeneMark.hmm prediction



GeneMark.hmm prediction





GeneMark_hmm prediction

