

GeneMark

Version 2.5p (09.08.06)

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PROGRAM INFORMATION

Sequence : Streptomyces phage ZooBear complete sequence, 46135 bp including 274 bp terminal repeat, Cl
Analysis Date : 8/22/17 at 20:31:21
Pages : 23
Sequence Length : 46135 bp
GC Content : 59.65%

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

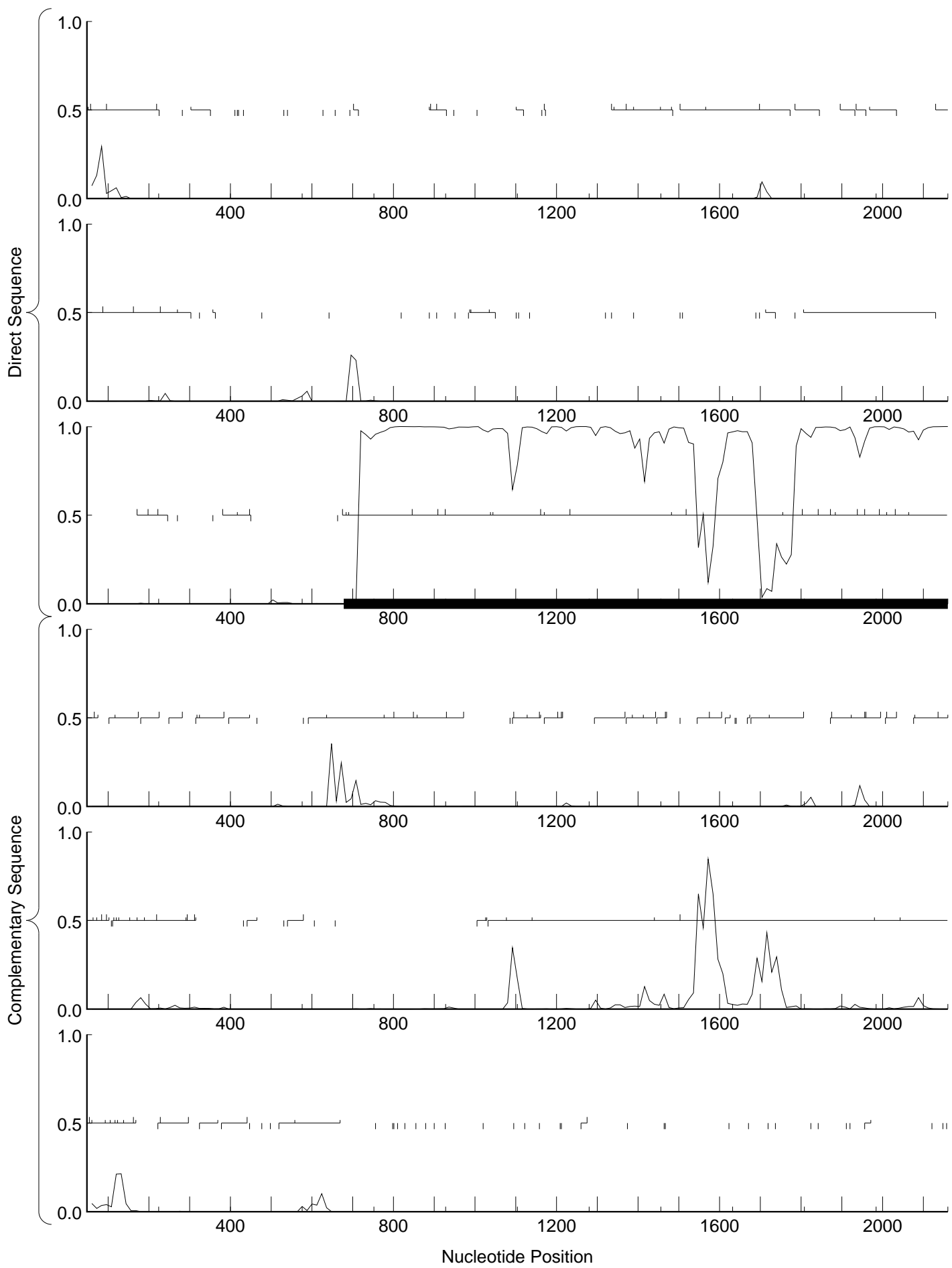
Matrix : Heuristic, GC = 60
Author : Borodovsky Laboratory - Georgia Tech
Order : 2

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

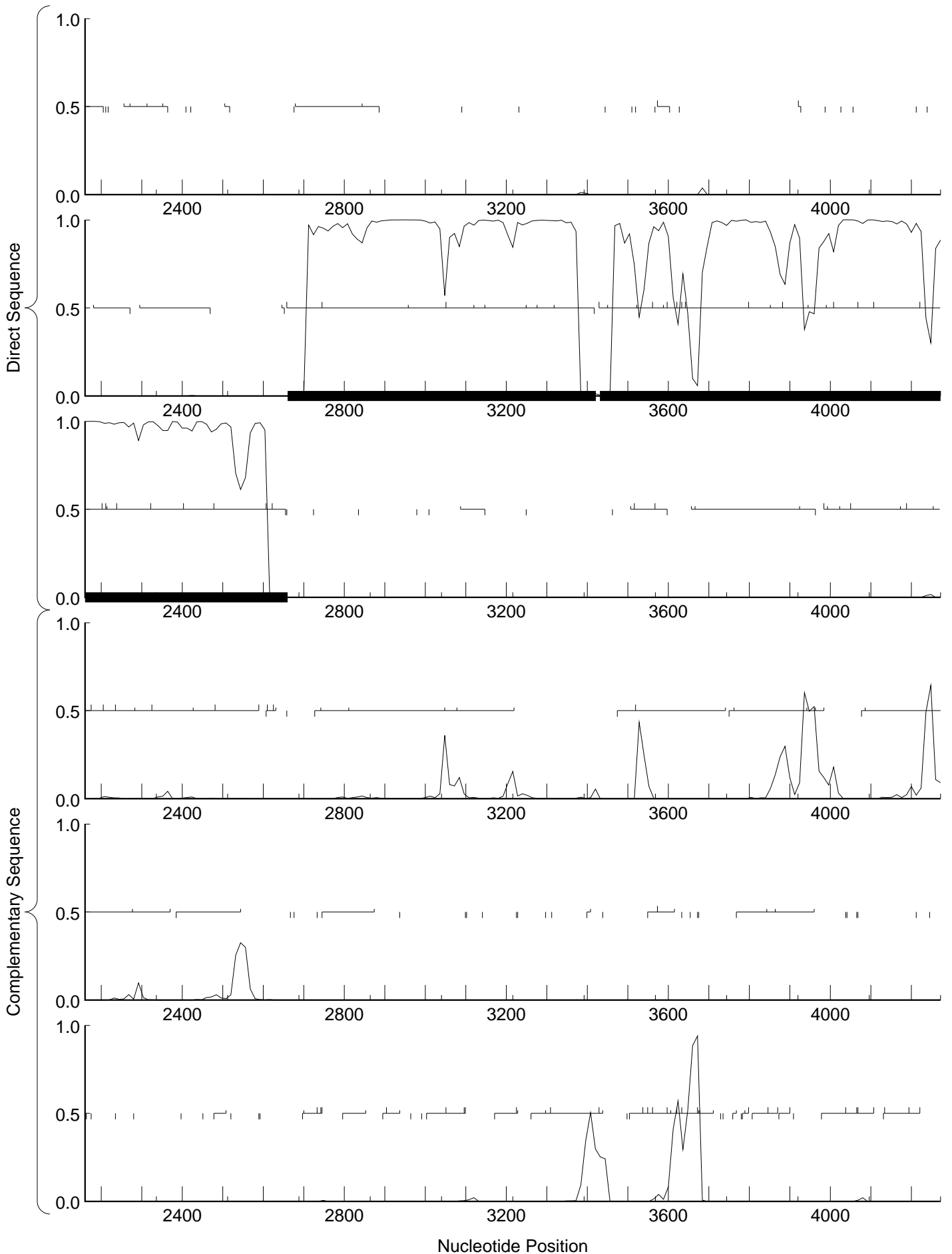
Matrix notes & comments

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

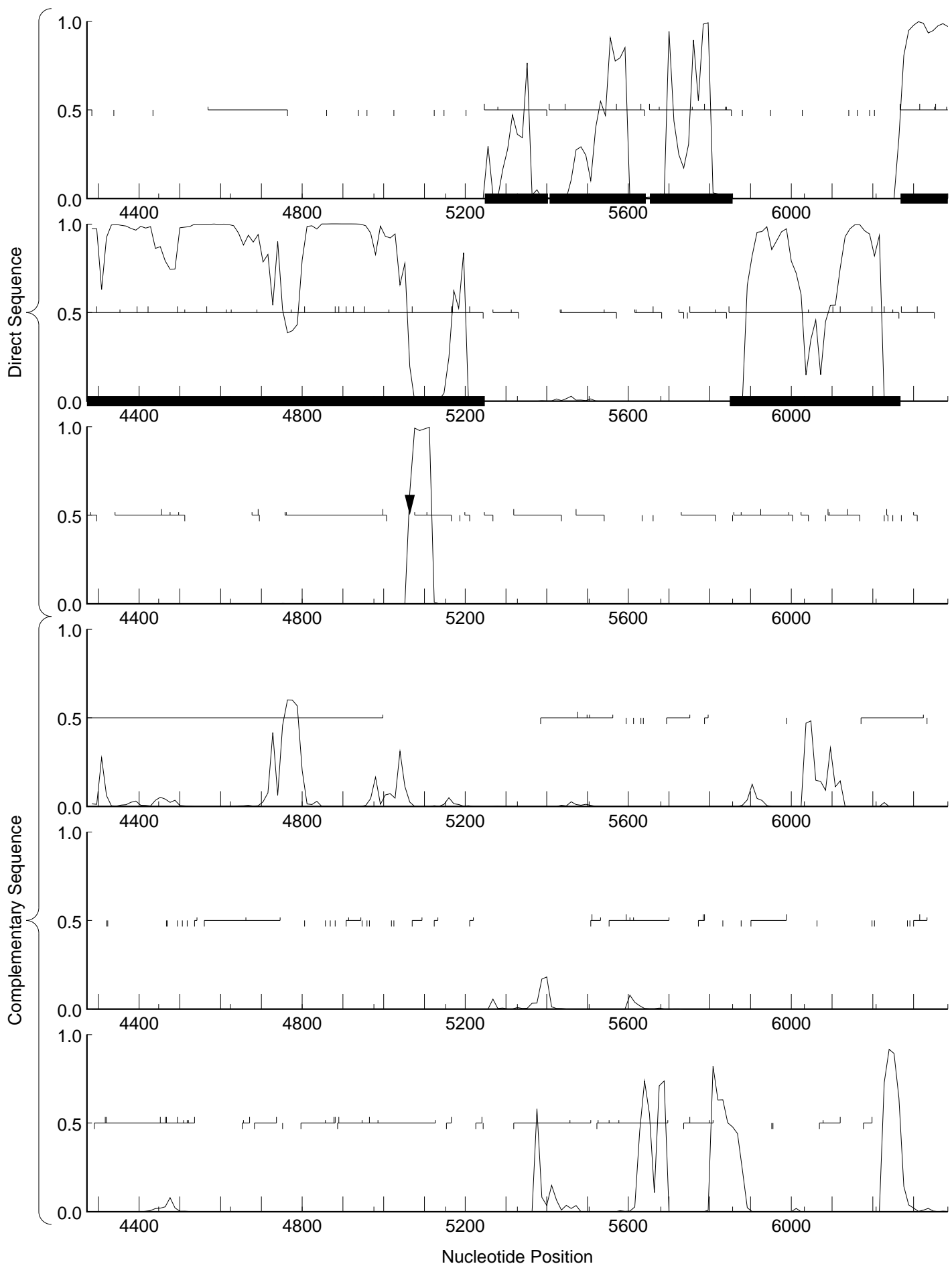
GeneMark, hmm prediction



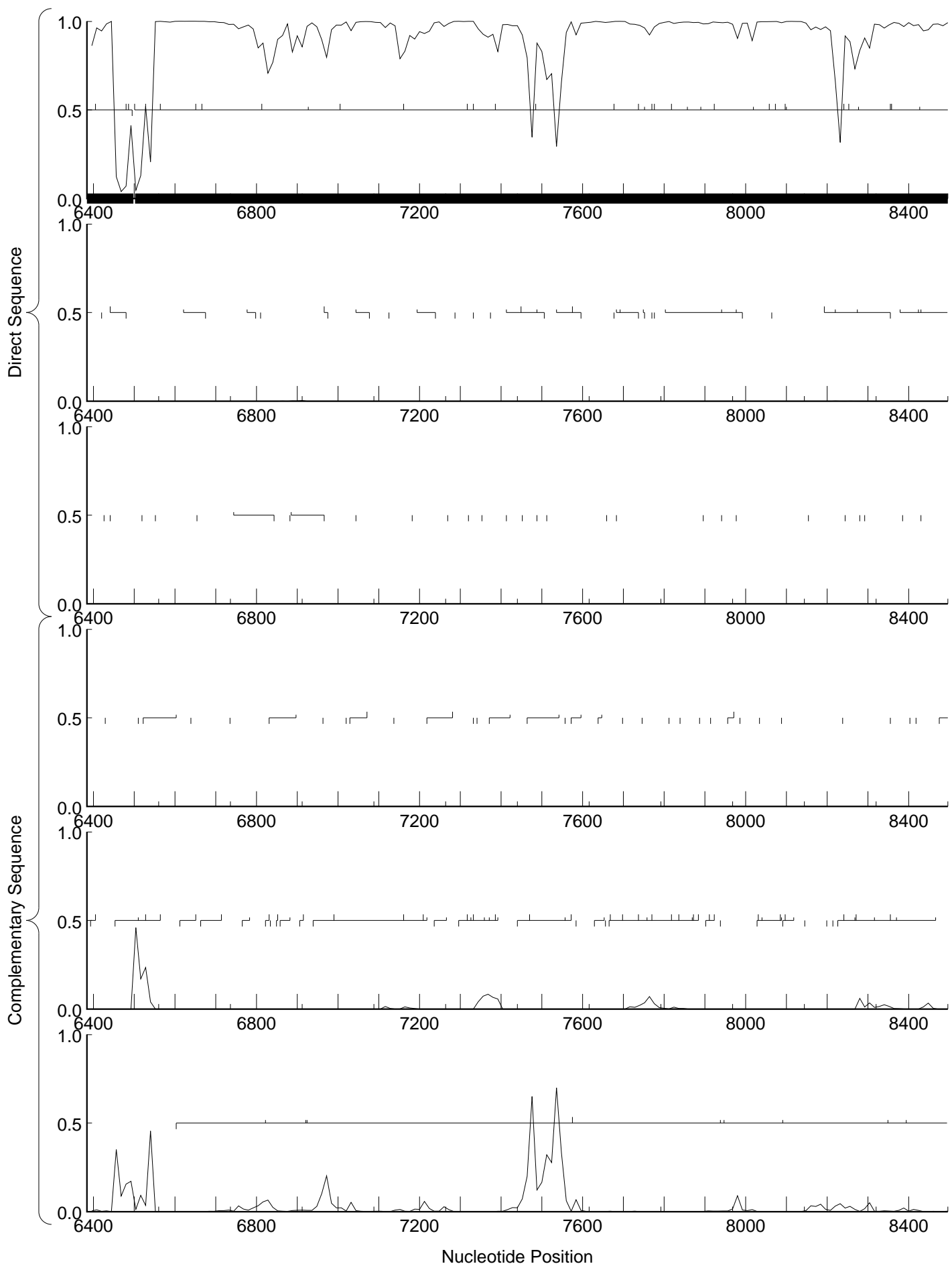
GeneMark, hmm prediction



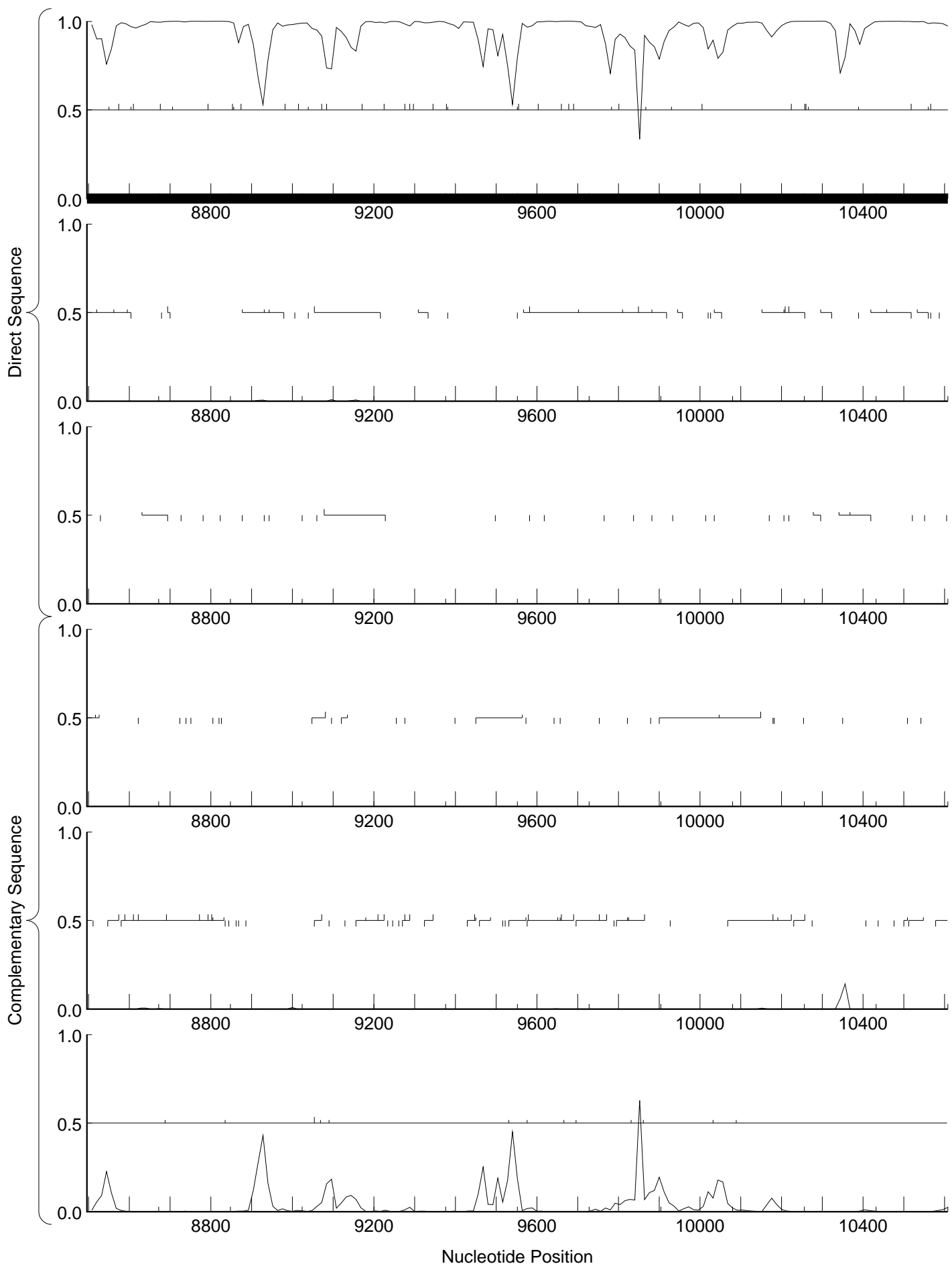
GeneMark, hmm prediction



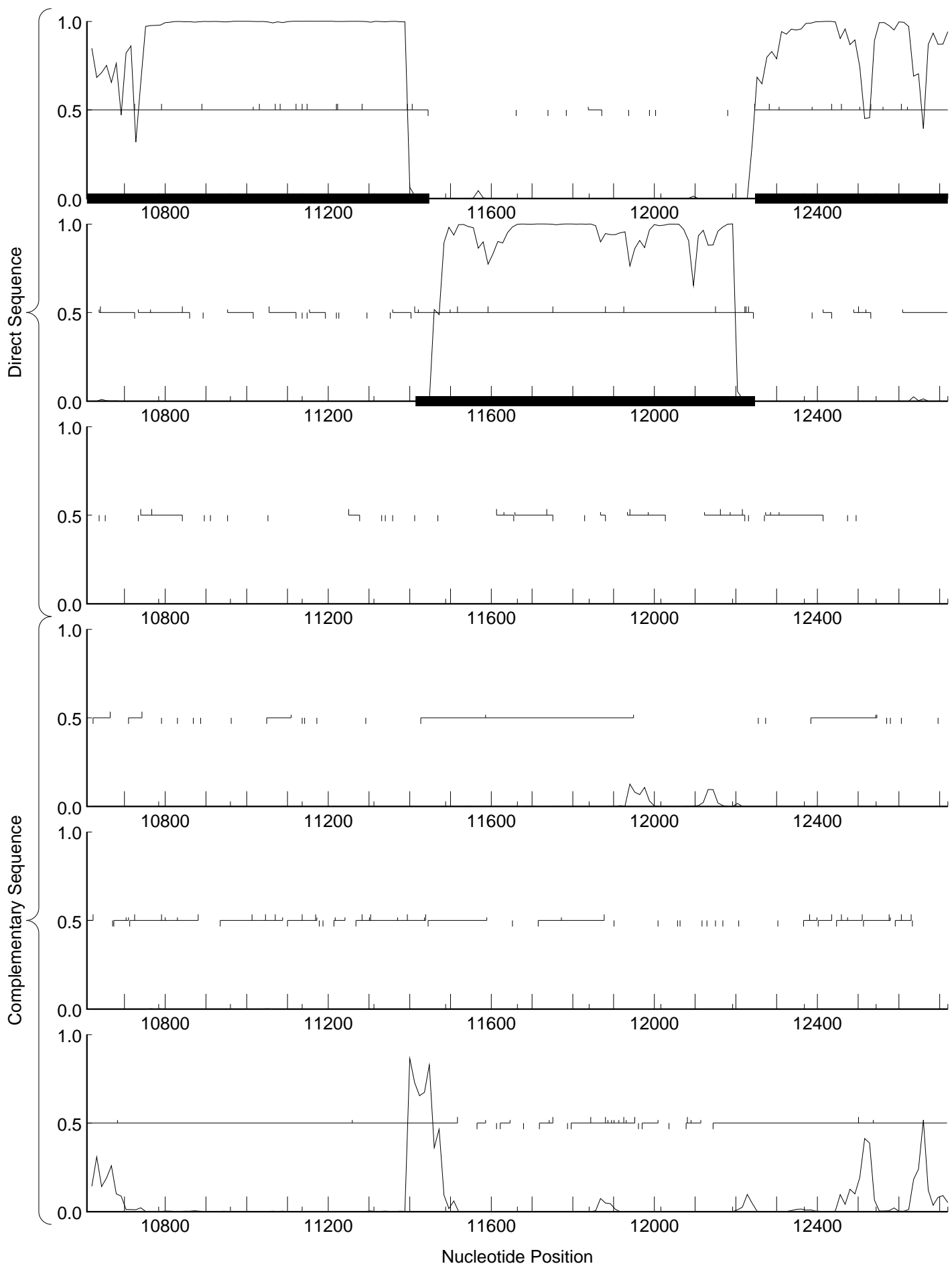
GeneMark_hmm prediction



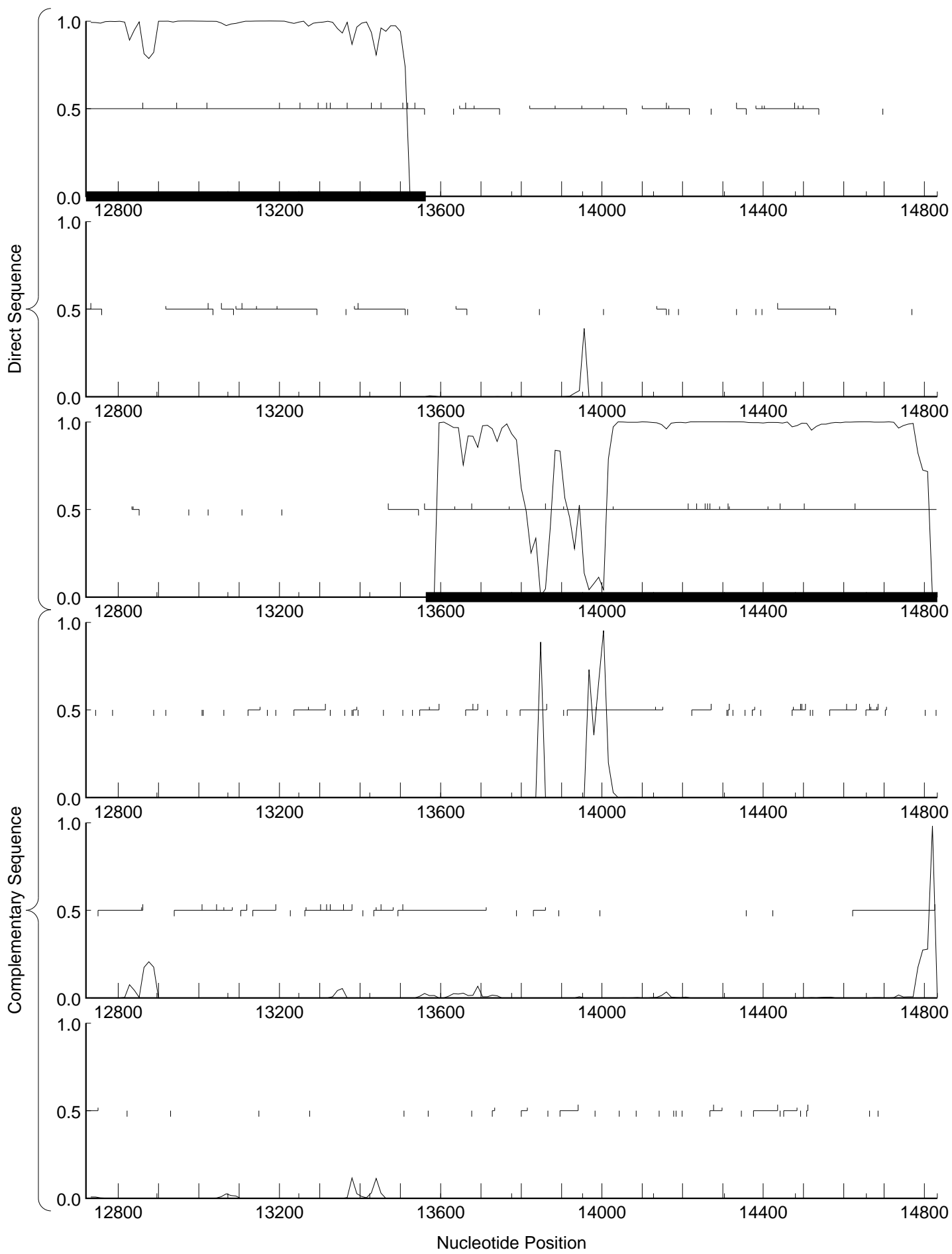
GeneMark, hmm prediction



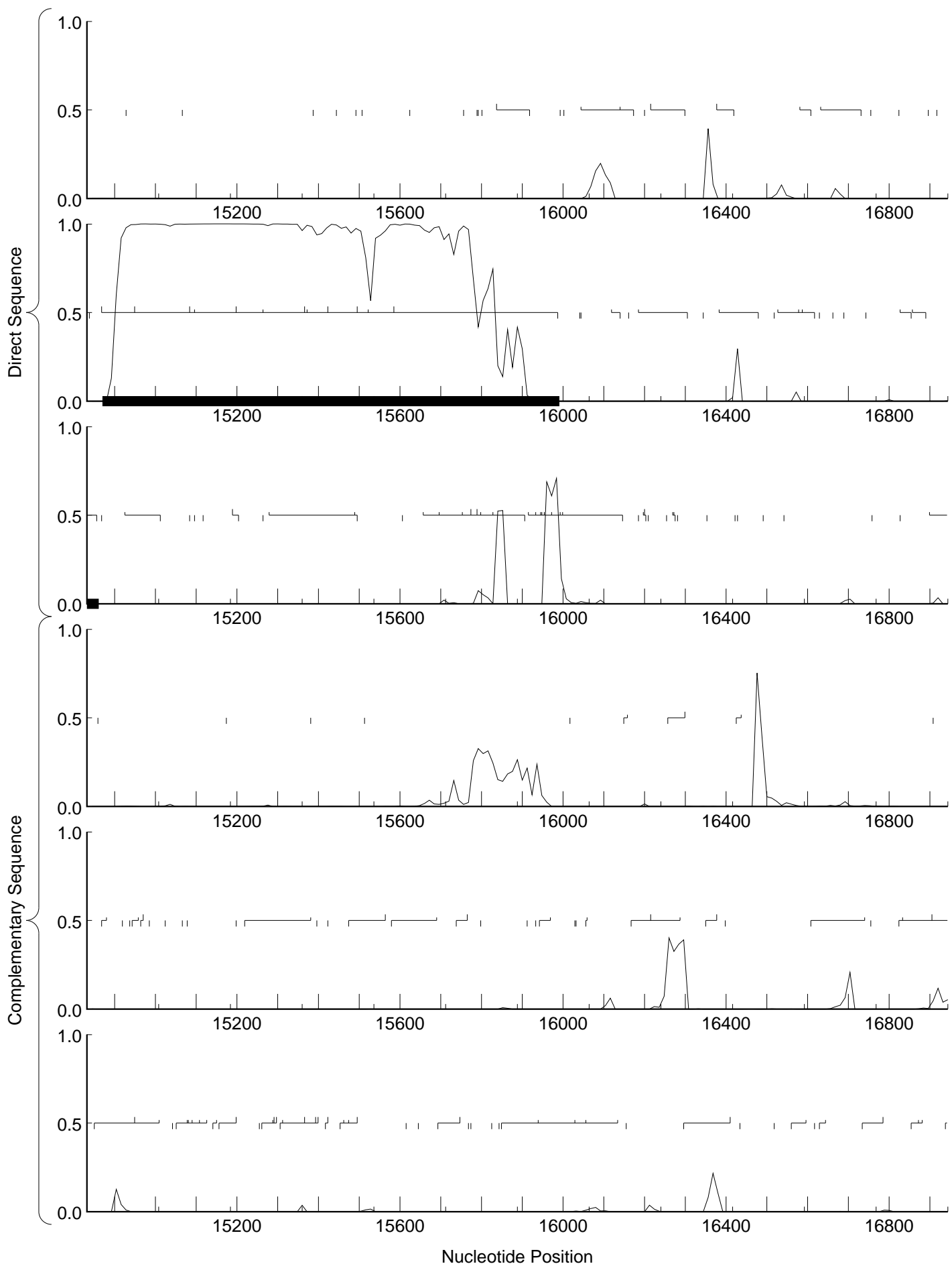
GeneMark, hmm prediction



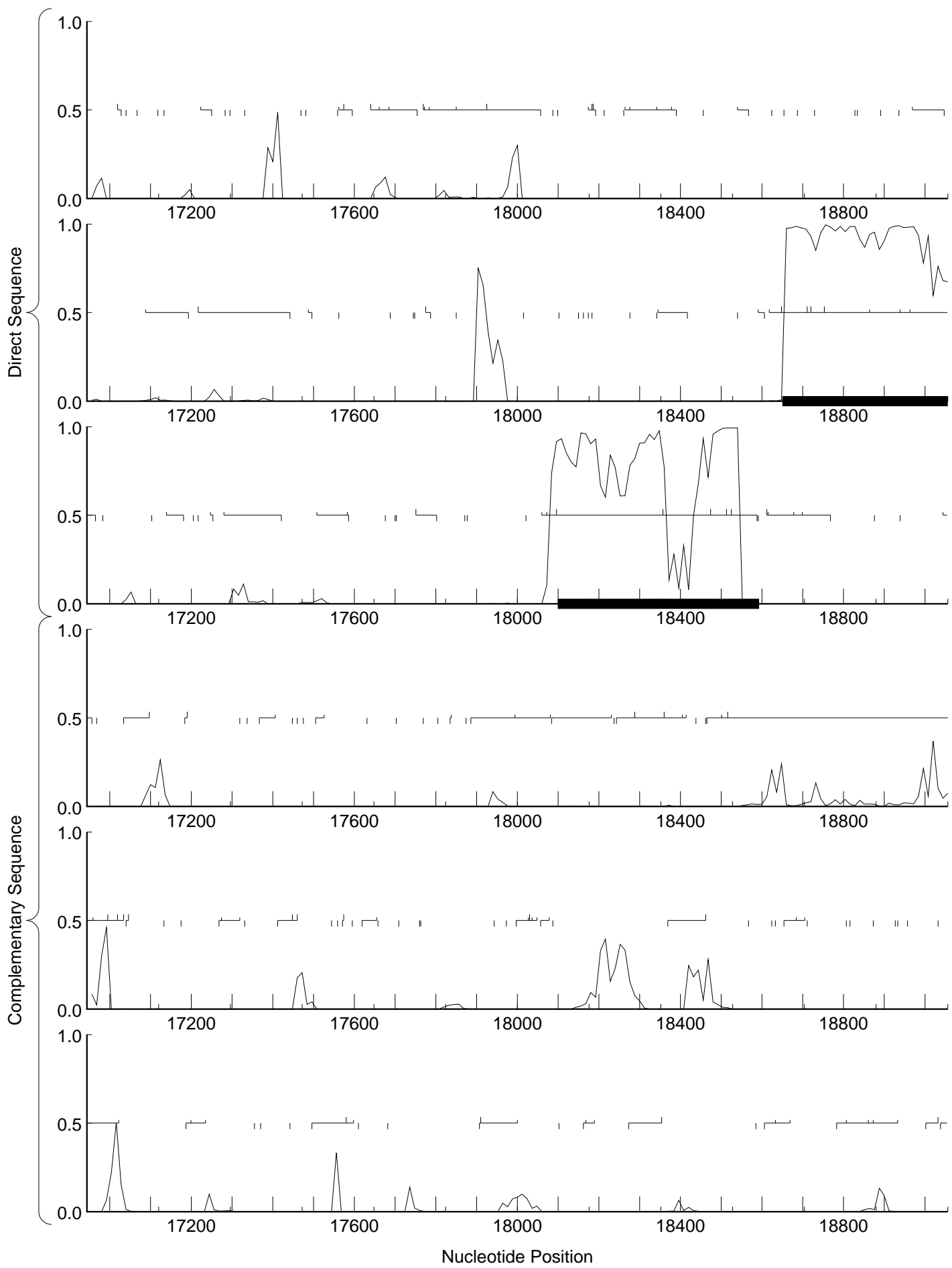
GeneMark, hmm prediction



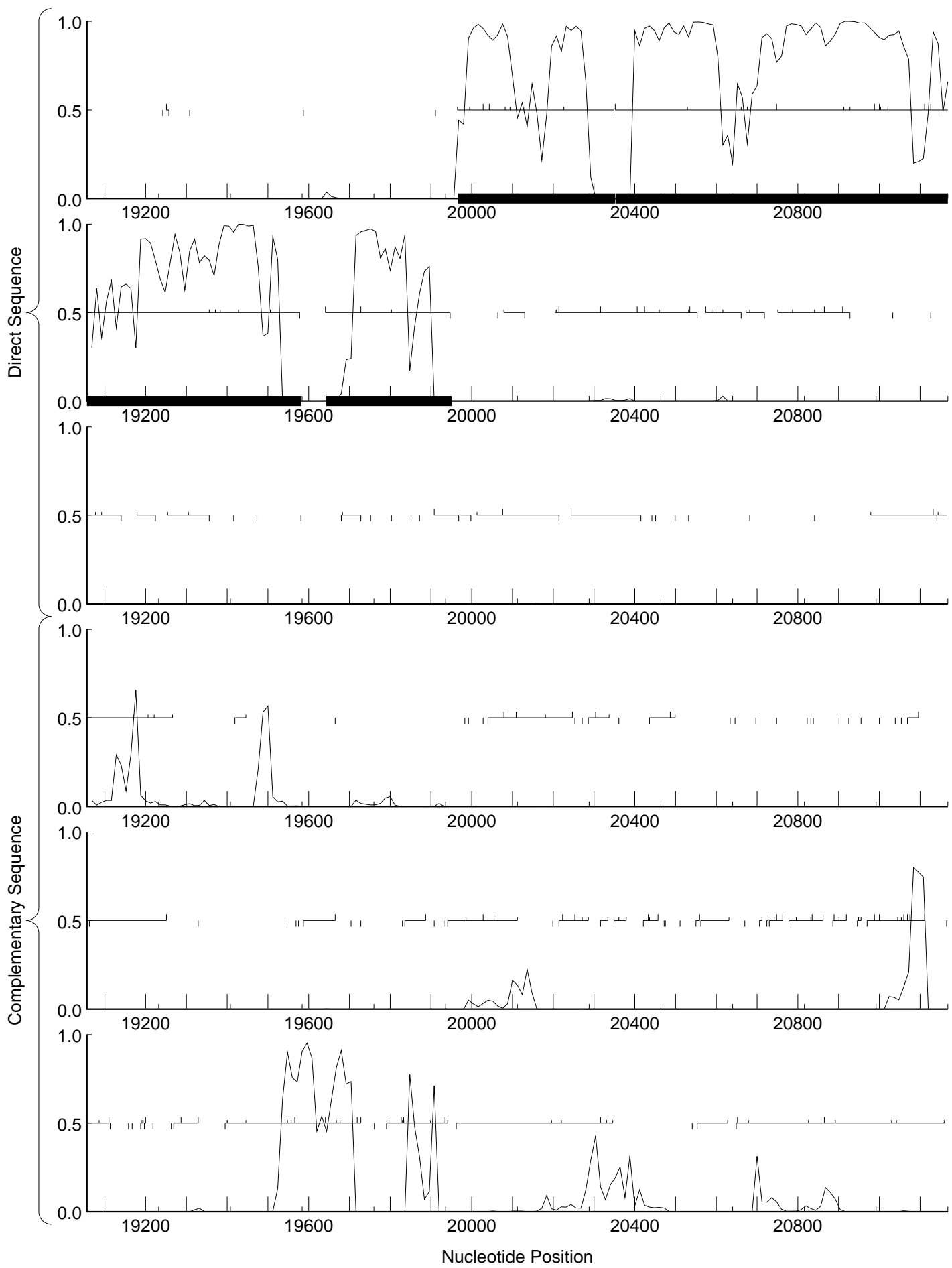
GeneMark, hmm prediction



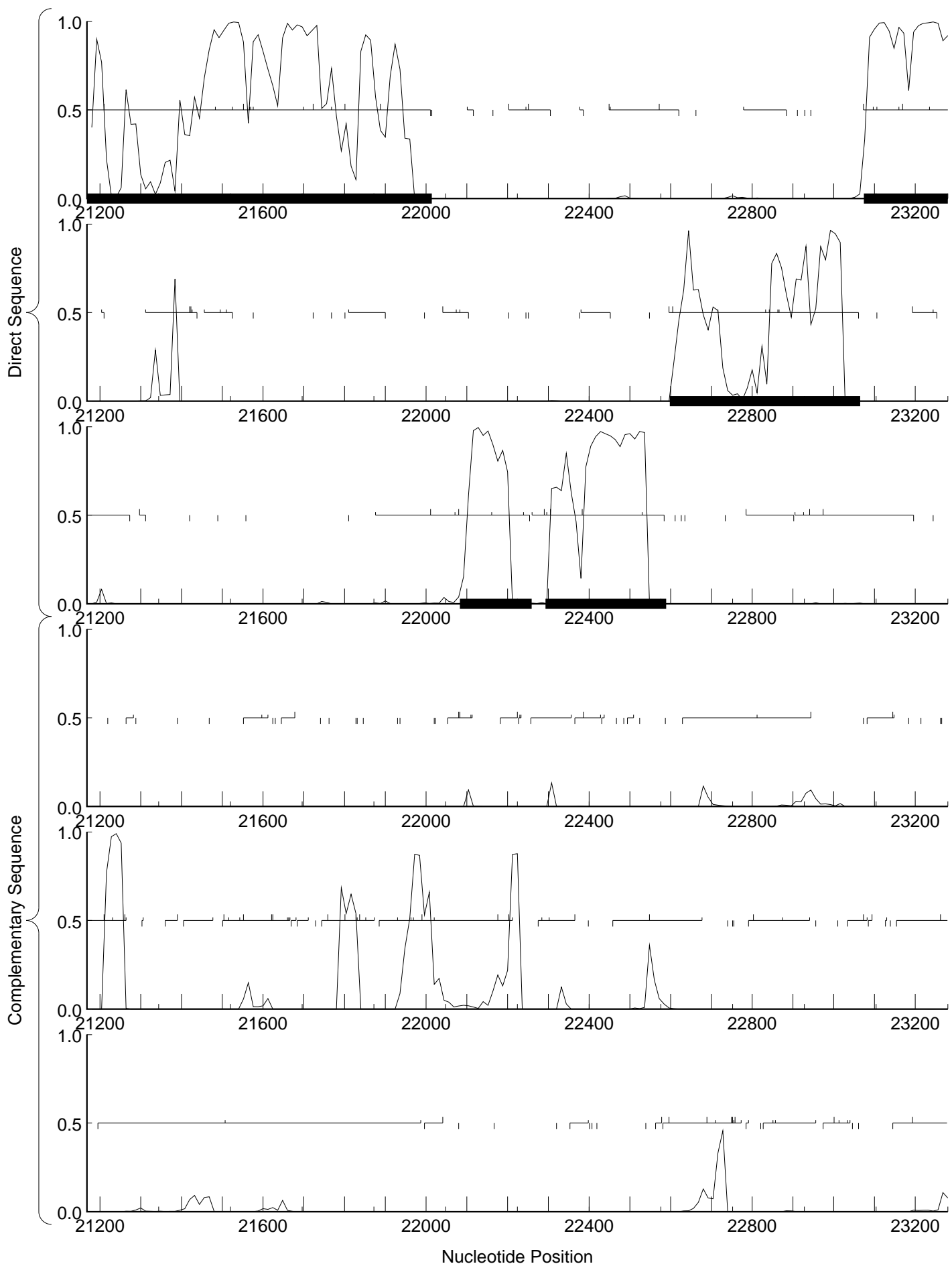
GeneMark.hmm prediction



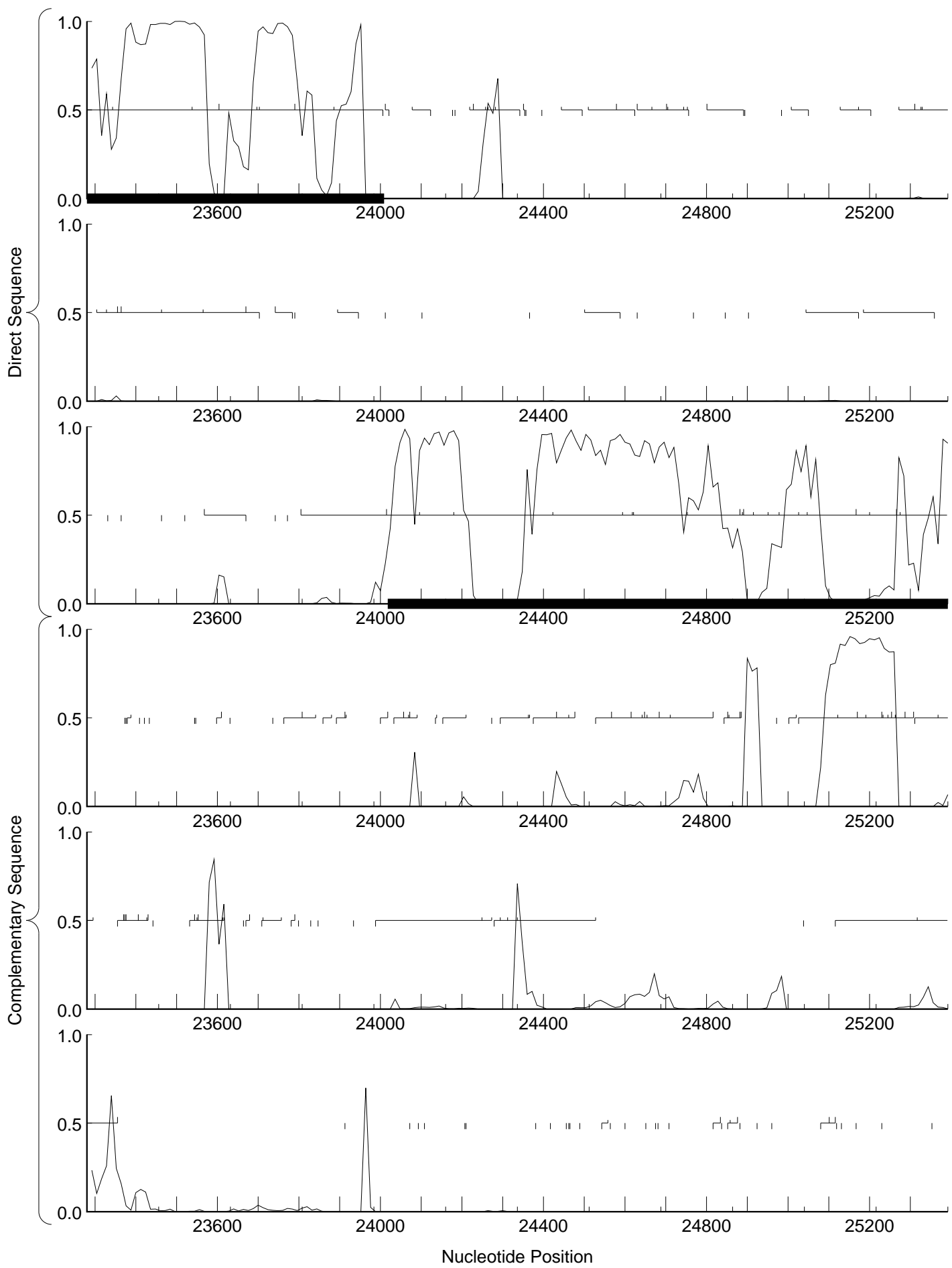
GeneMark_hmm prediction



GeneMark.hmm prediction

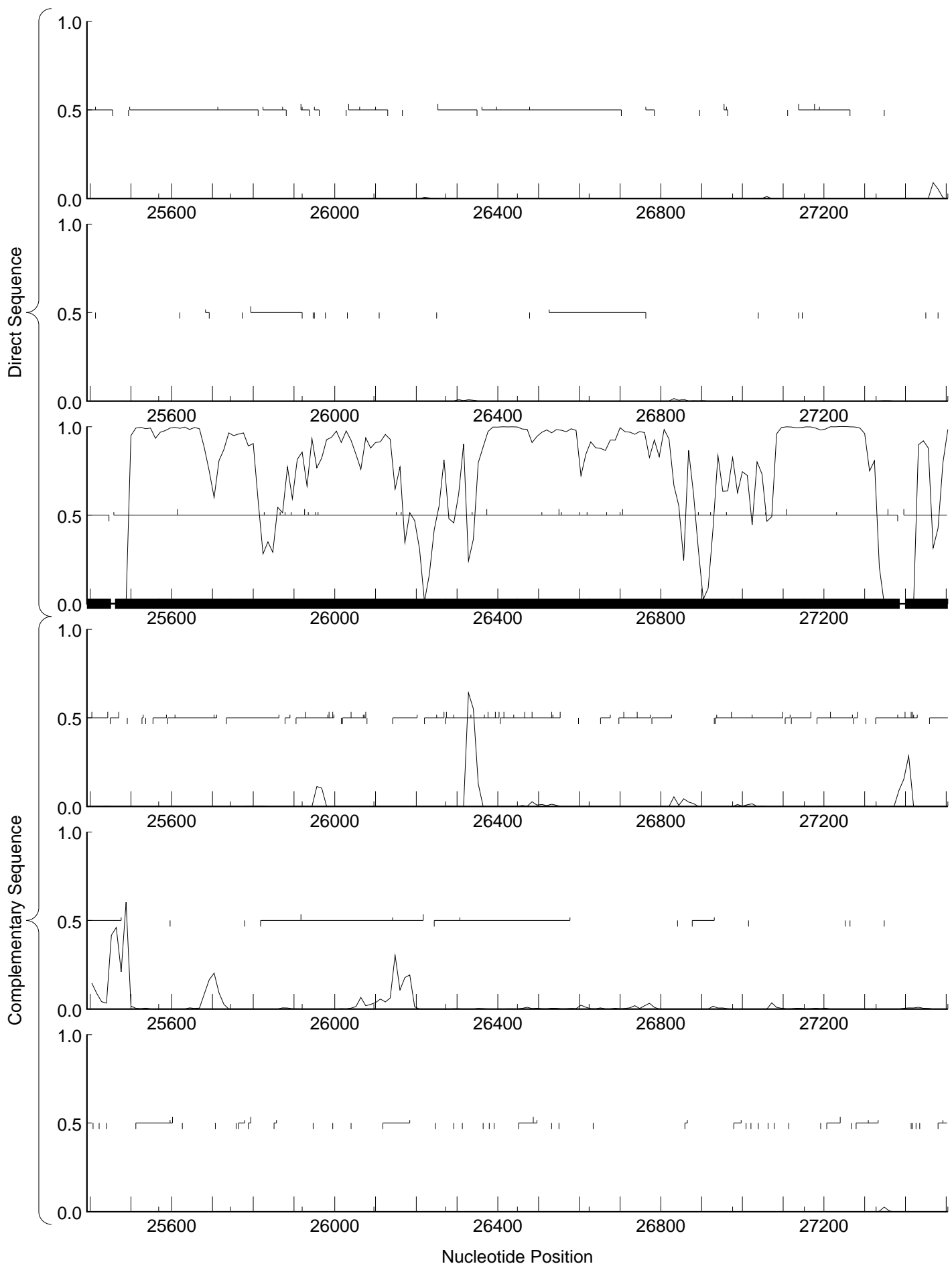


GeneMark.hmm prediction

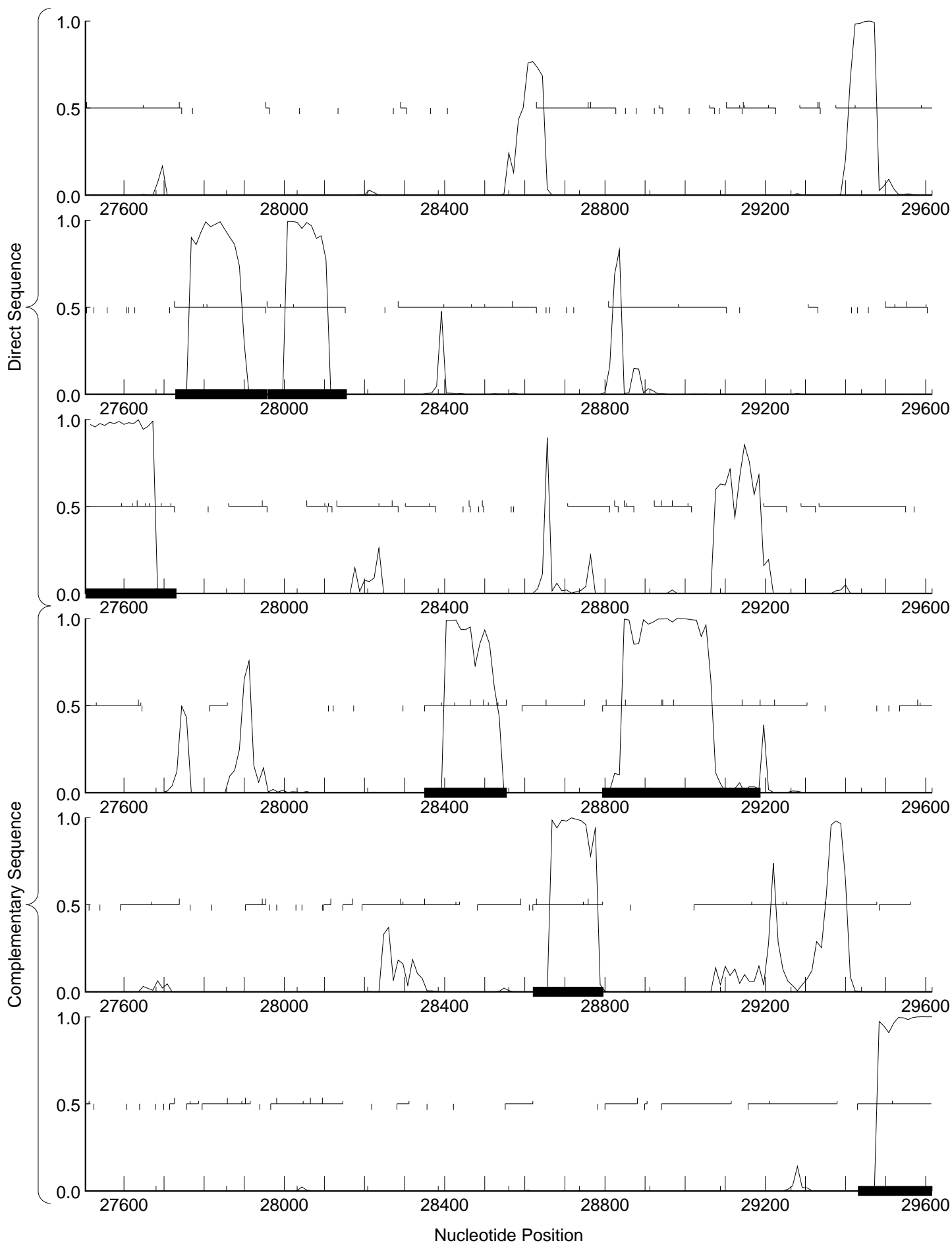


Nucleotide Position

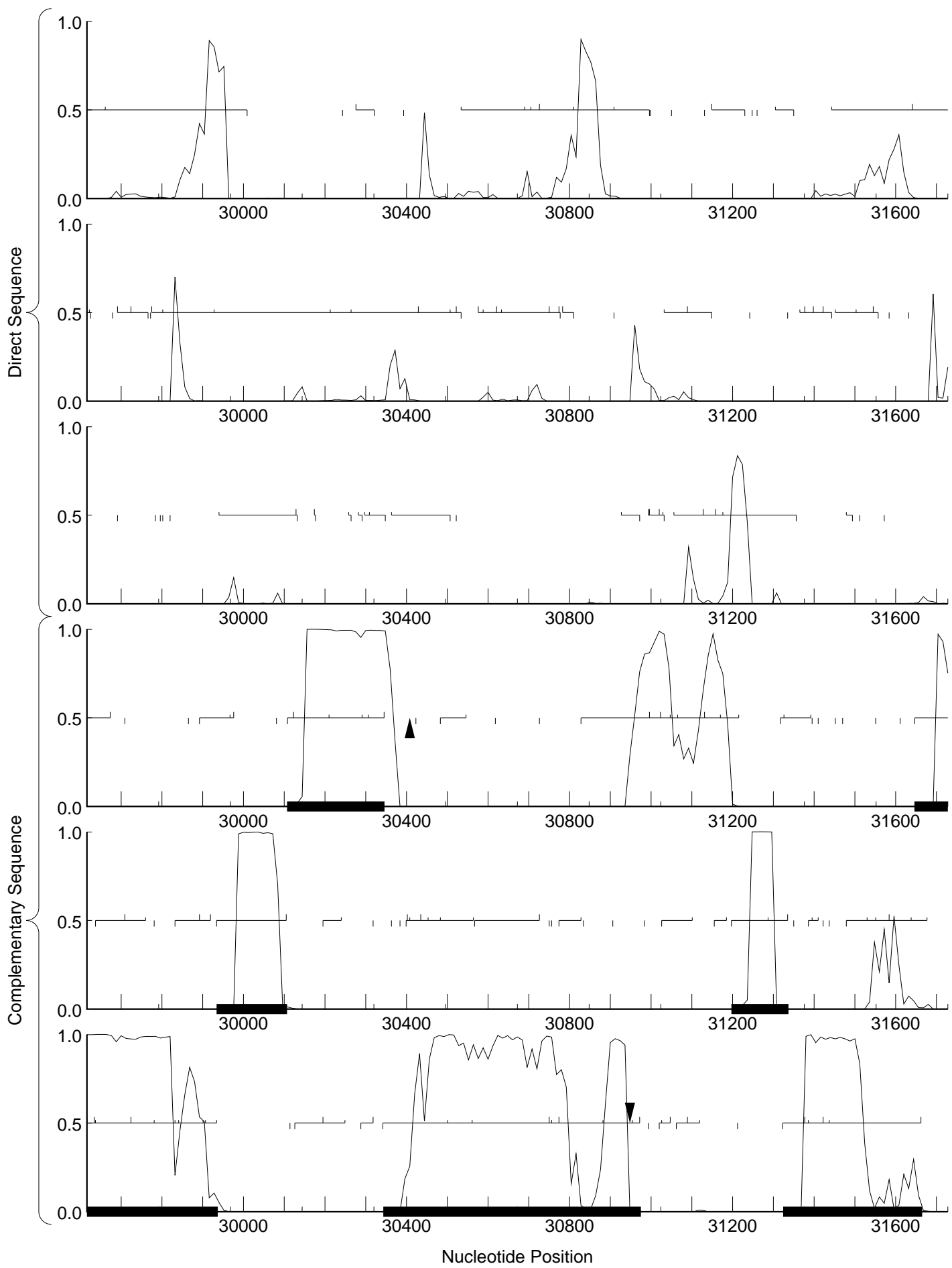
GeneMark.hmm prediction



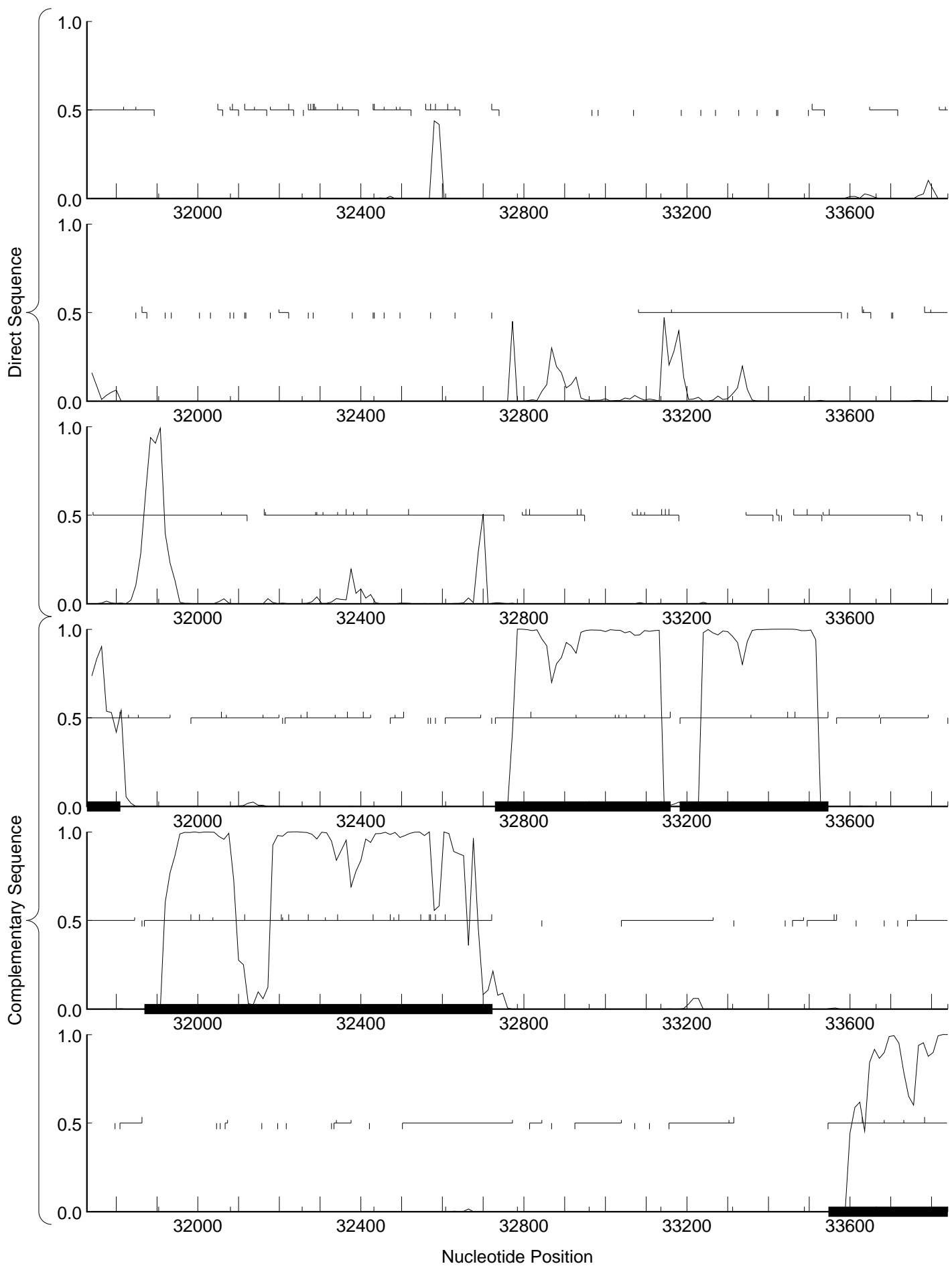
GeneMark.hmm prediction



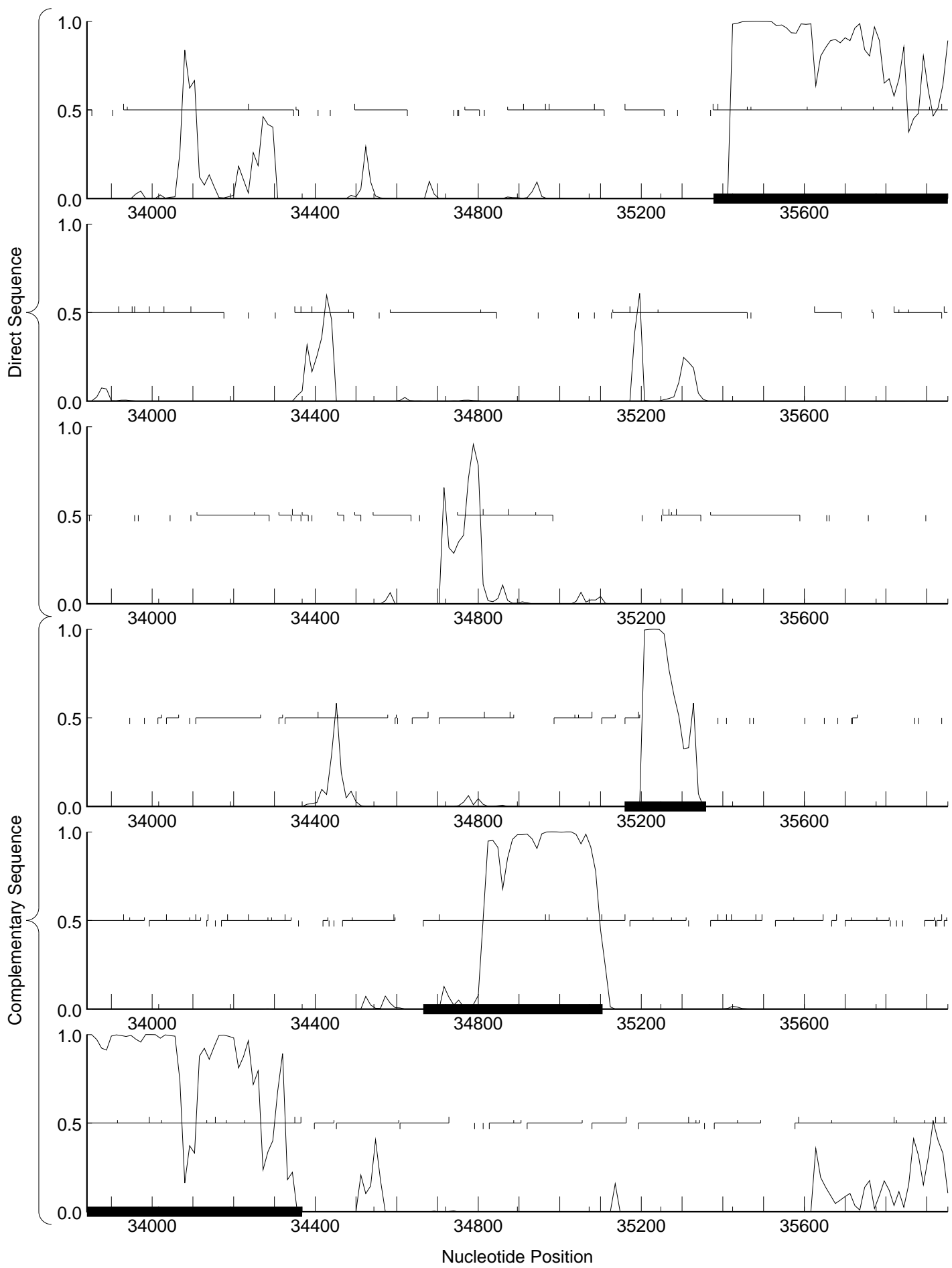
GeneMark_hmm prediction



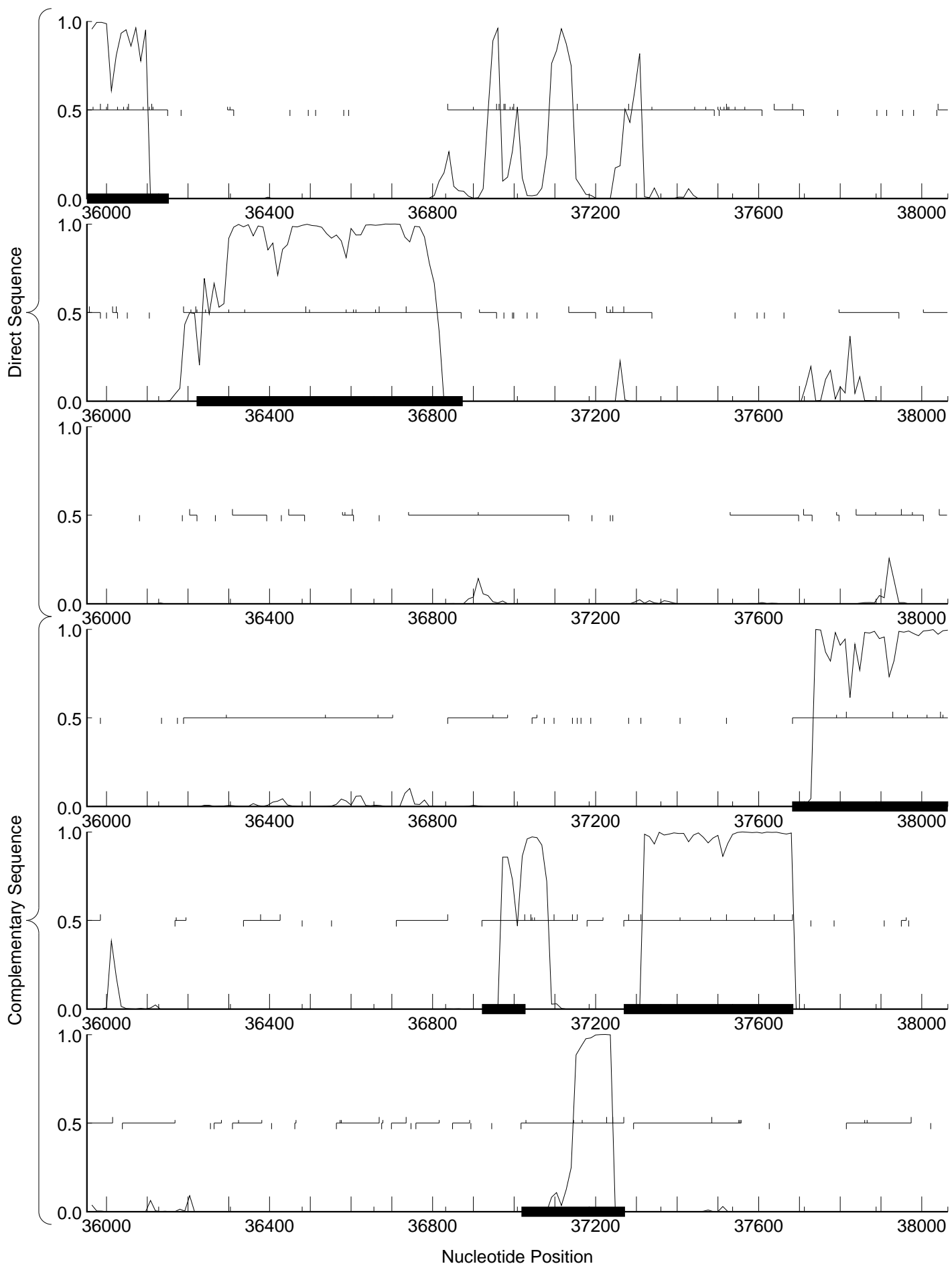
GeneMark_hmm prediction



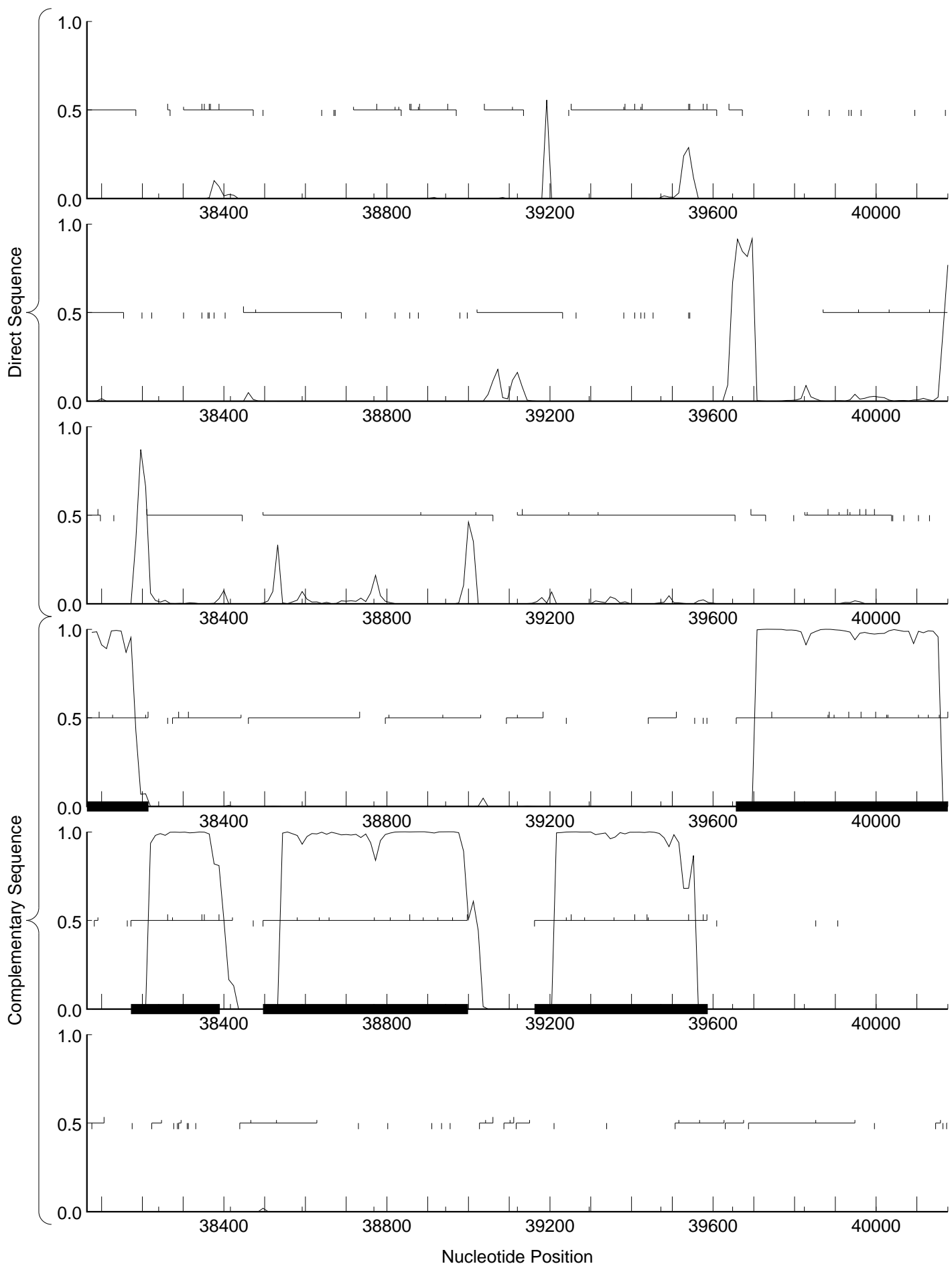
GeneMark.hmm prediction



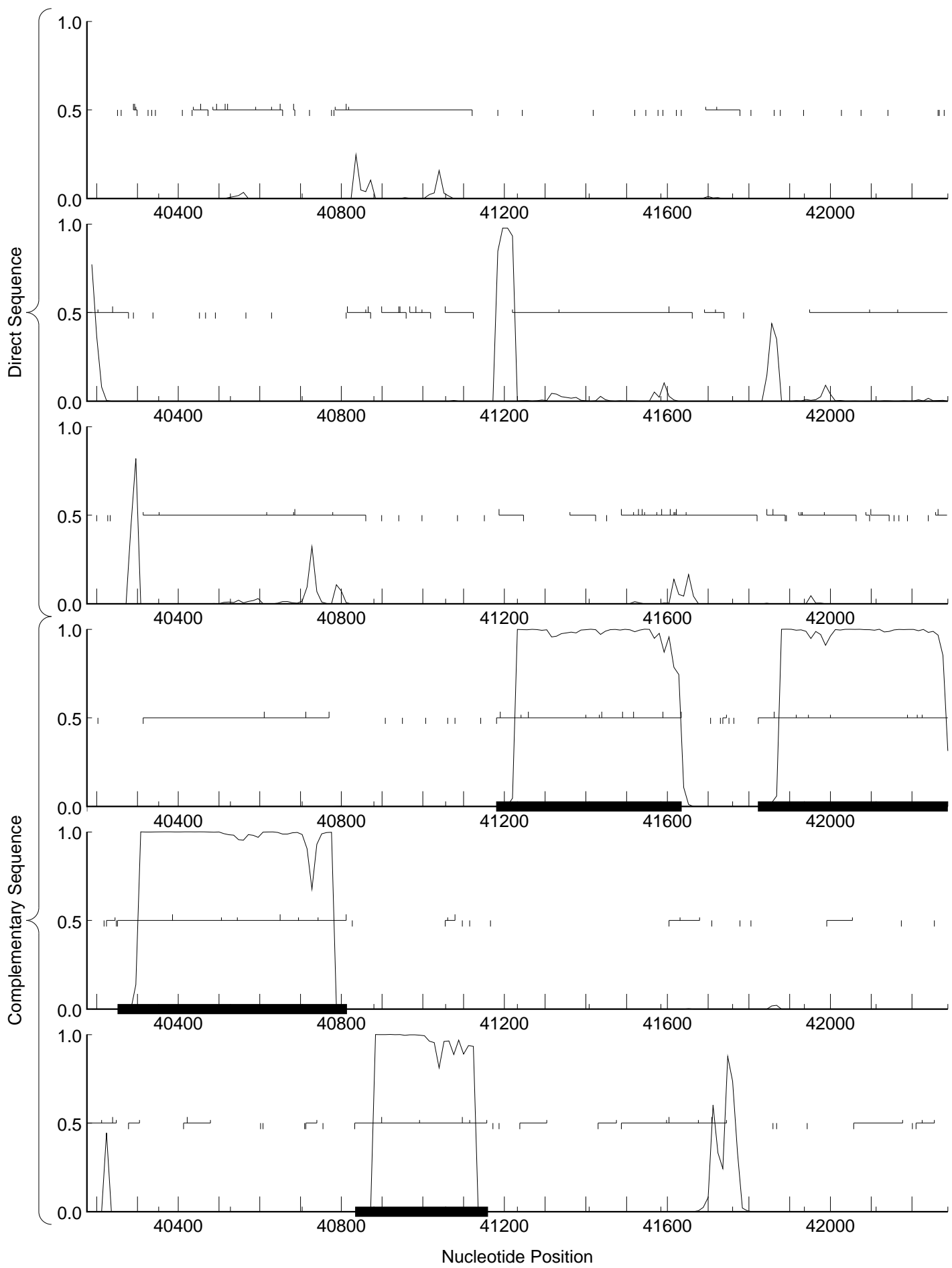
GeneMark.hmm prediction



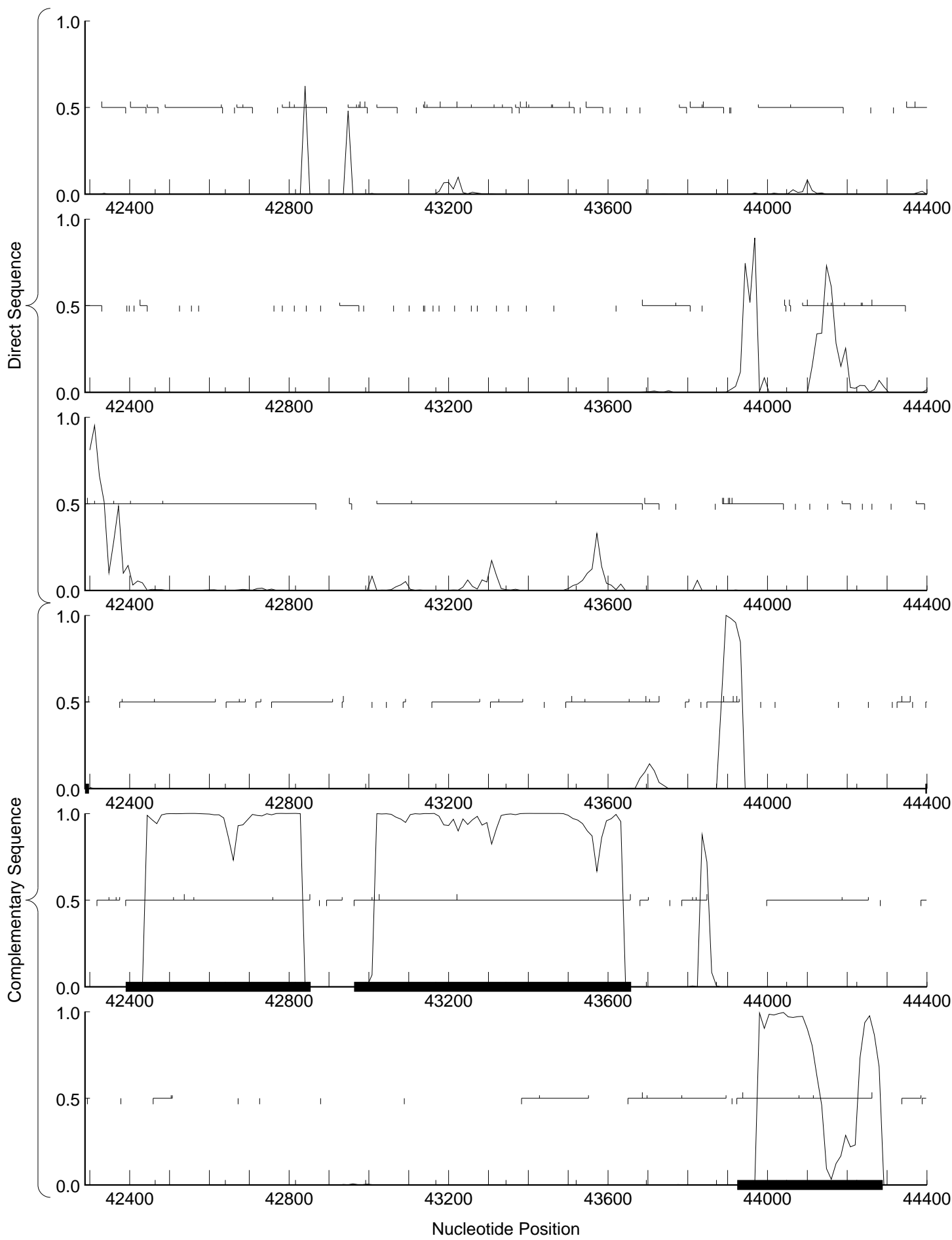
GeneMark.hmm prediction



GeneMark.hmm prediction



GeneMark_hmm prediction



GeneMark_hmm prediction

