

GeneMark

Version 2.5p (09.08.06)

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PROGRAM INFORMATION

Sequence : Arthrobacter phage Azathoth complete sequence, 15556 bp including 11-base 3' overhang (CCCG)
Analysis Date : 11/19/17 at 19:06:43
Pages : 9
Sequence Length : 15556 bp
GC Content : 60.11%

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

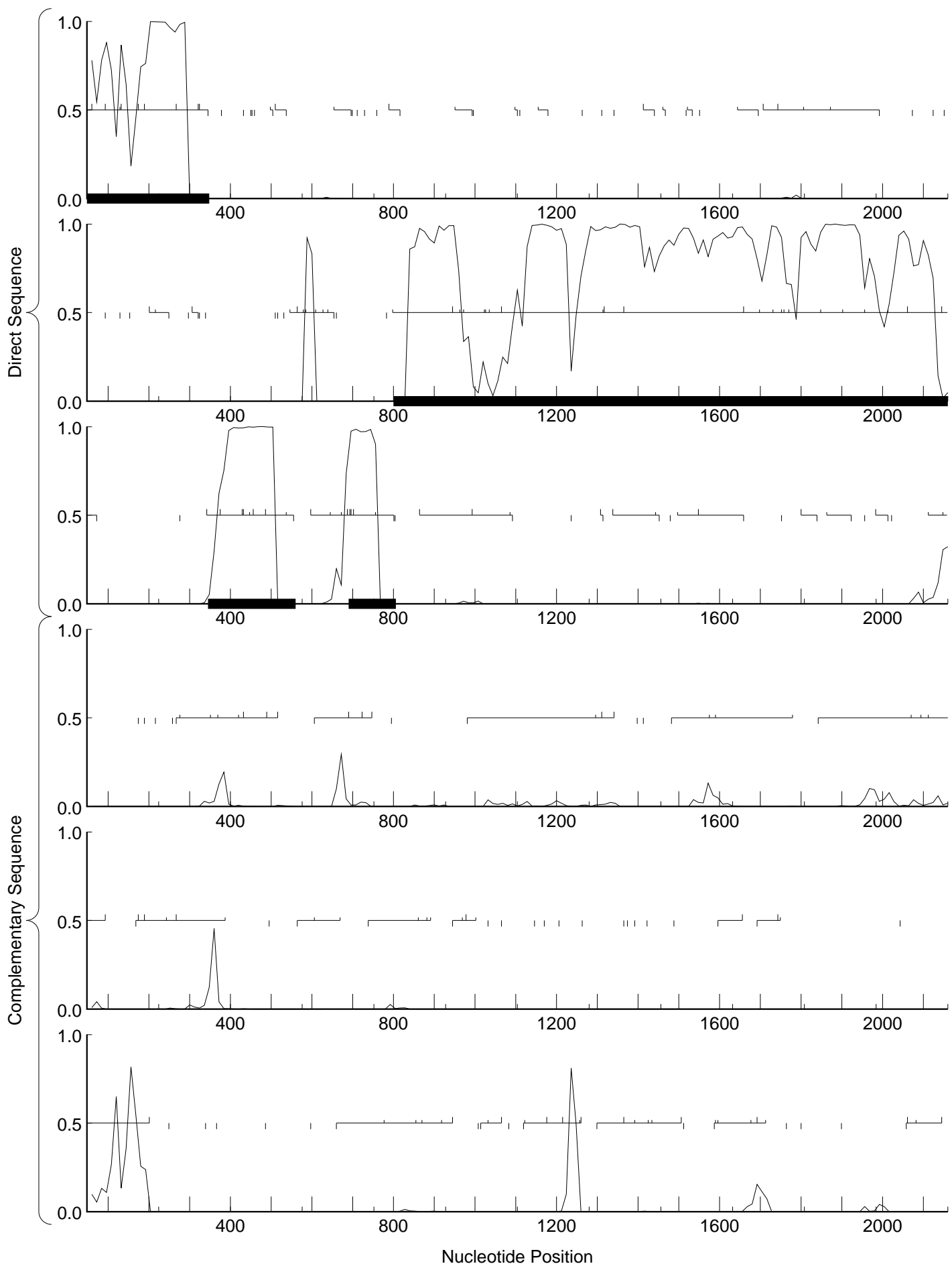
For details on the model building procedure see:
Besemer J. and Borodovsky M.
"Heuristic approach to deriving models for gene finding"
NAR, 1999, Vol. 27, No. 19, pp. 3911-3920

MATRIX INFORMATION

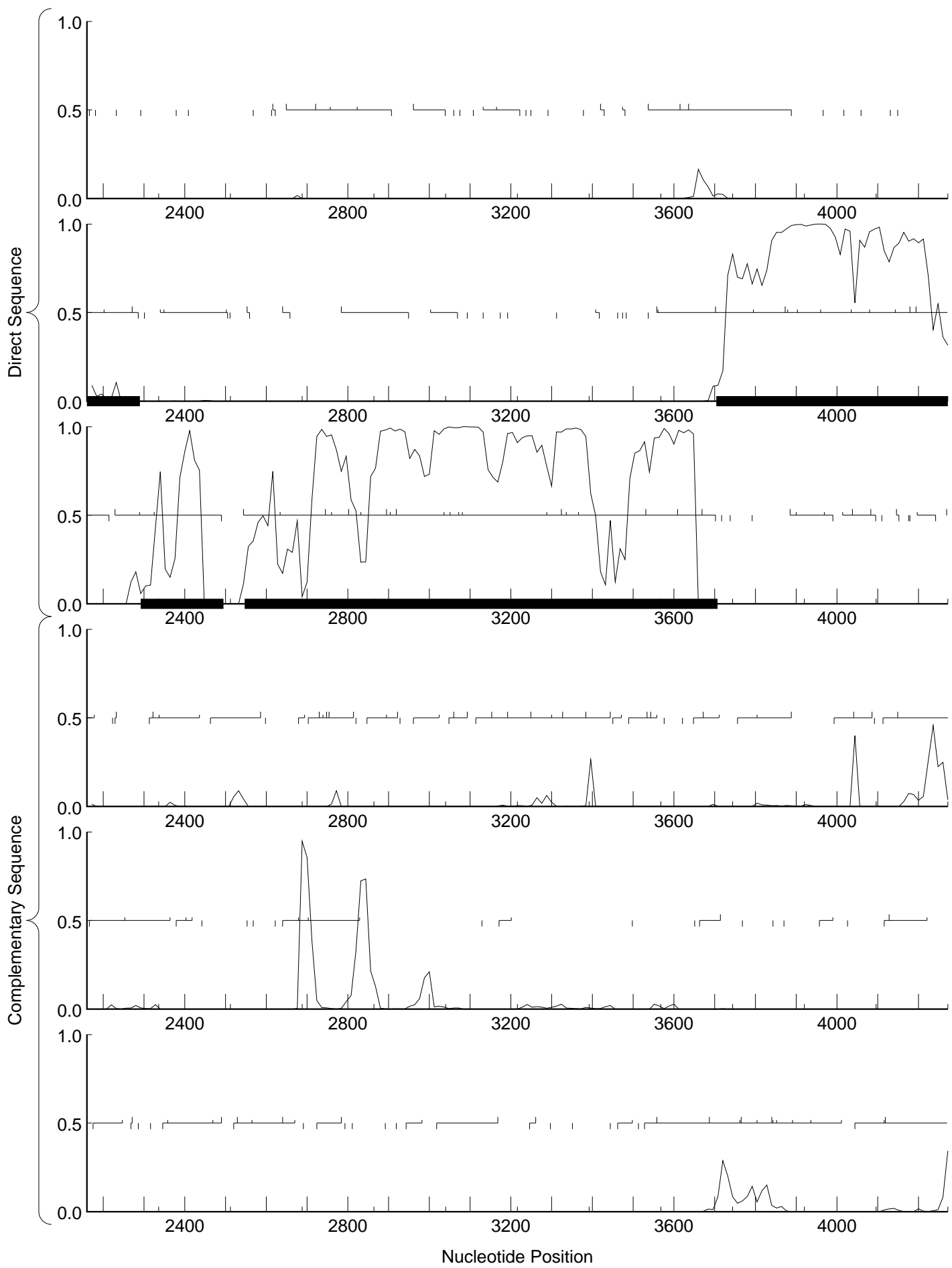
Matrix : Heuristic, GC = 60
Author : Borodovsky Laboratory - Georgia Tech
Order : 2

Send questions / comments to:
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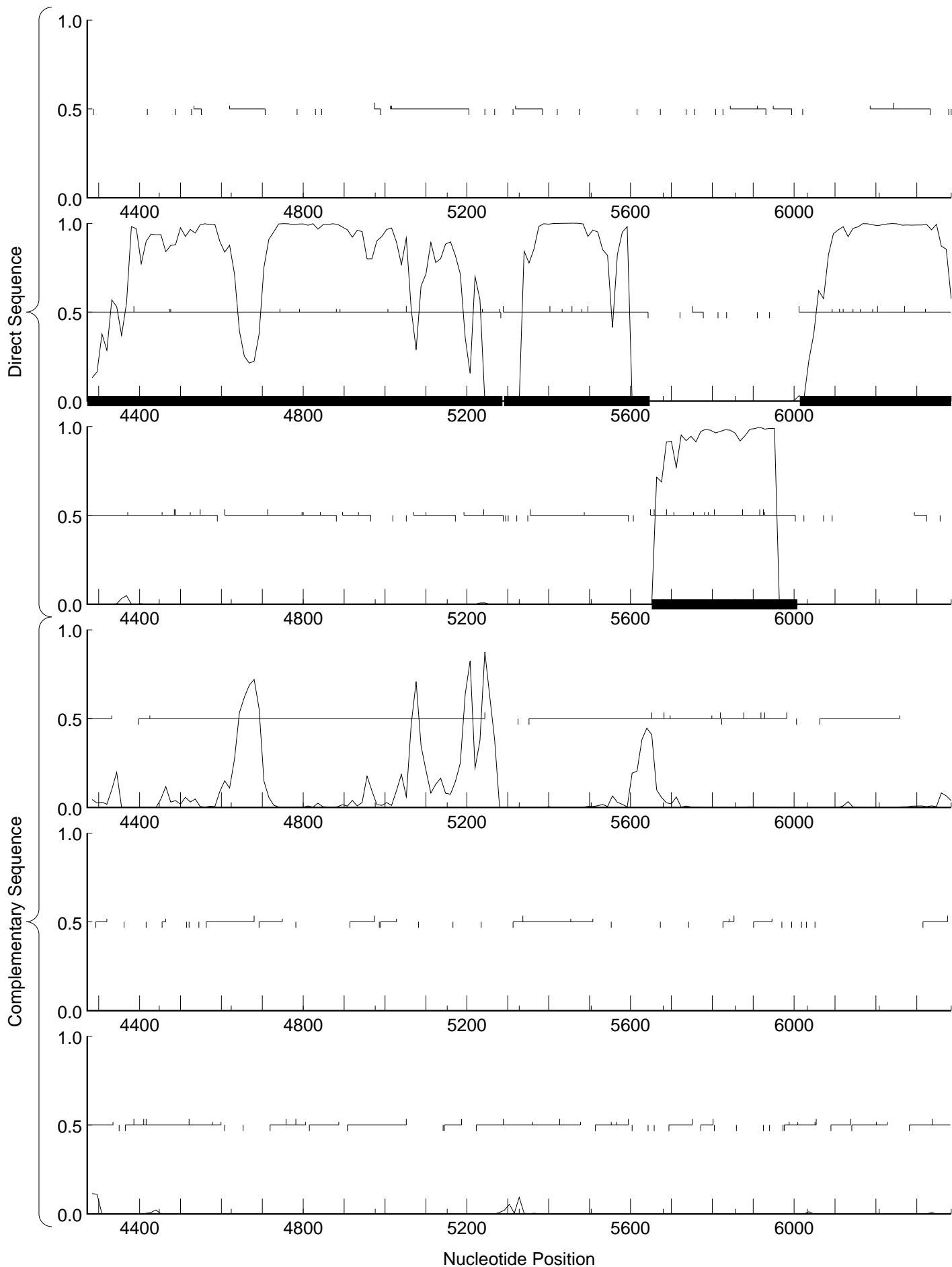
GeneMark.hmm prediction



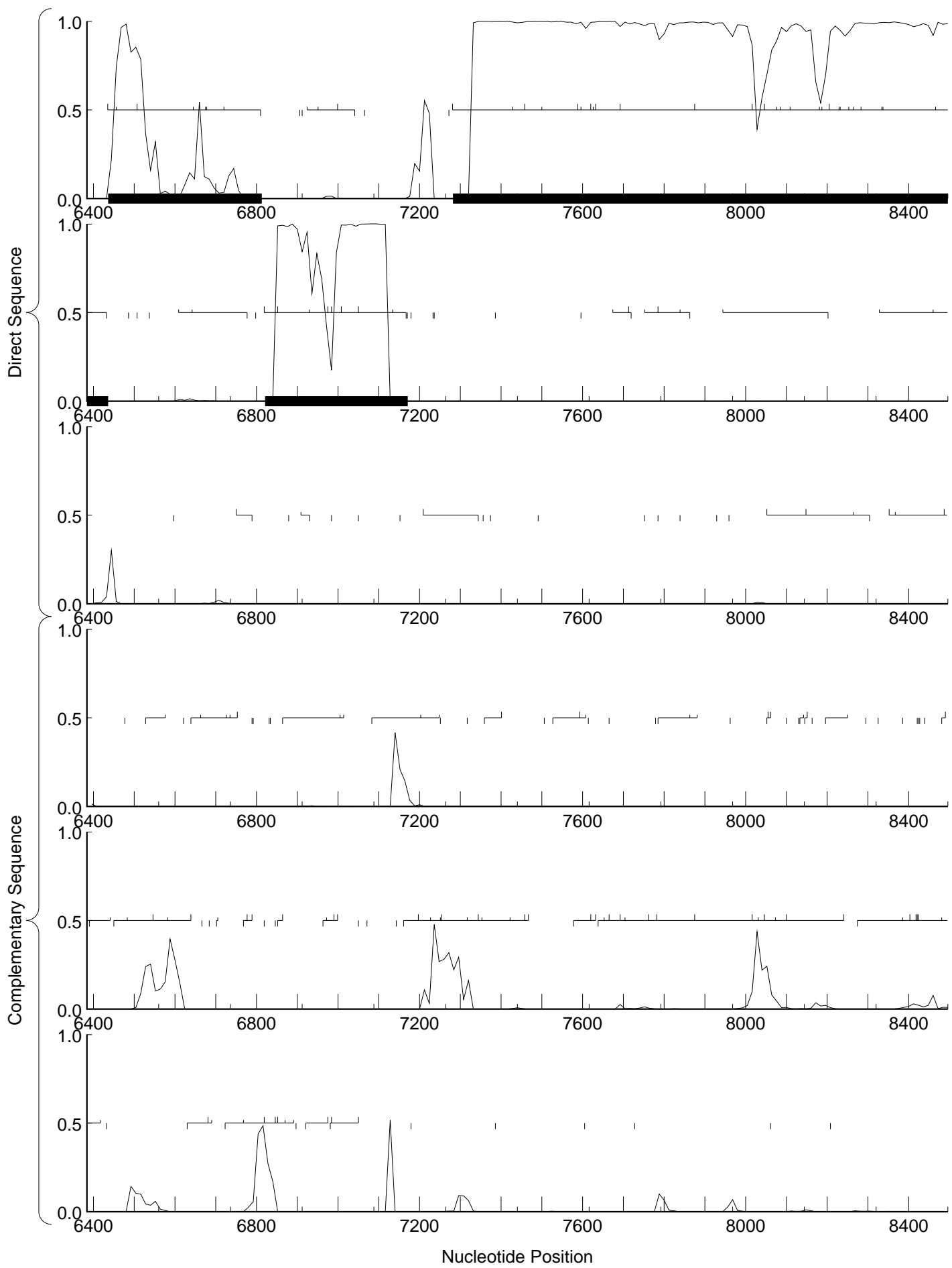
GeneMark.hmm prediction



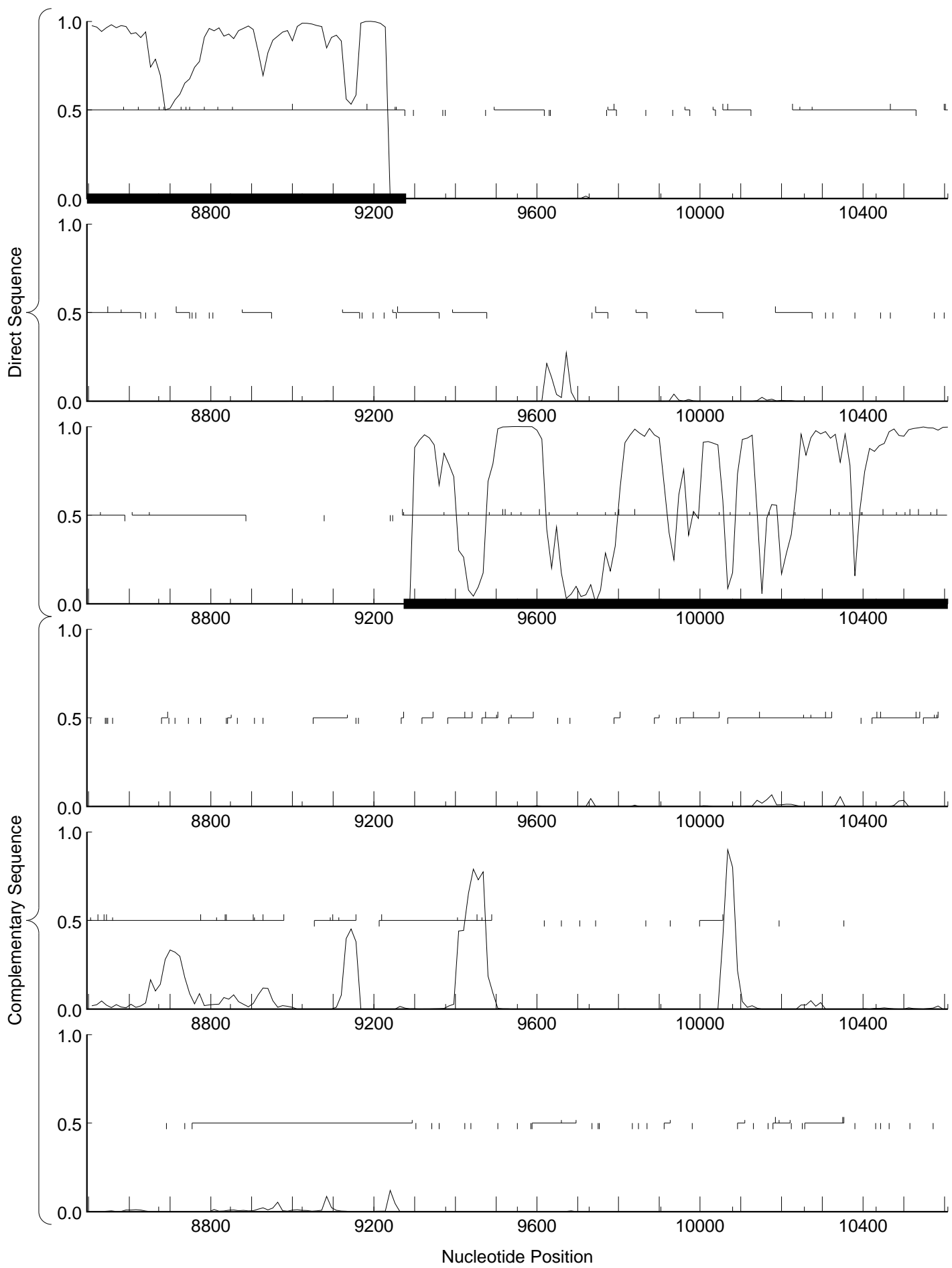
GeneMark.hmm prediction



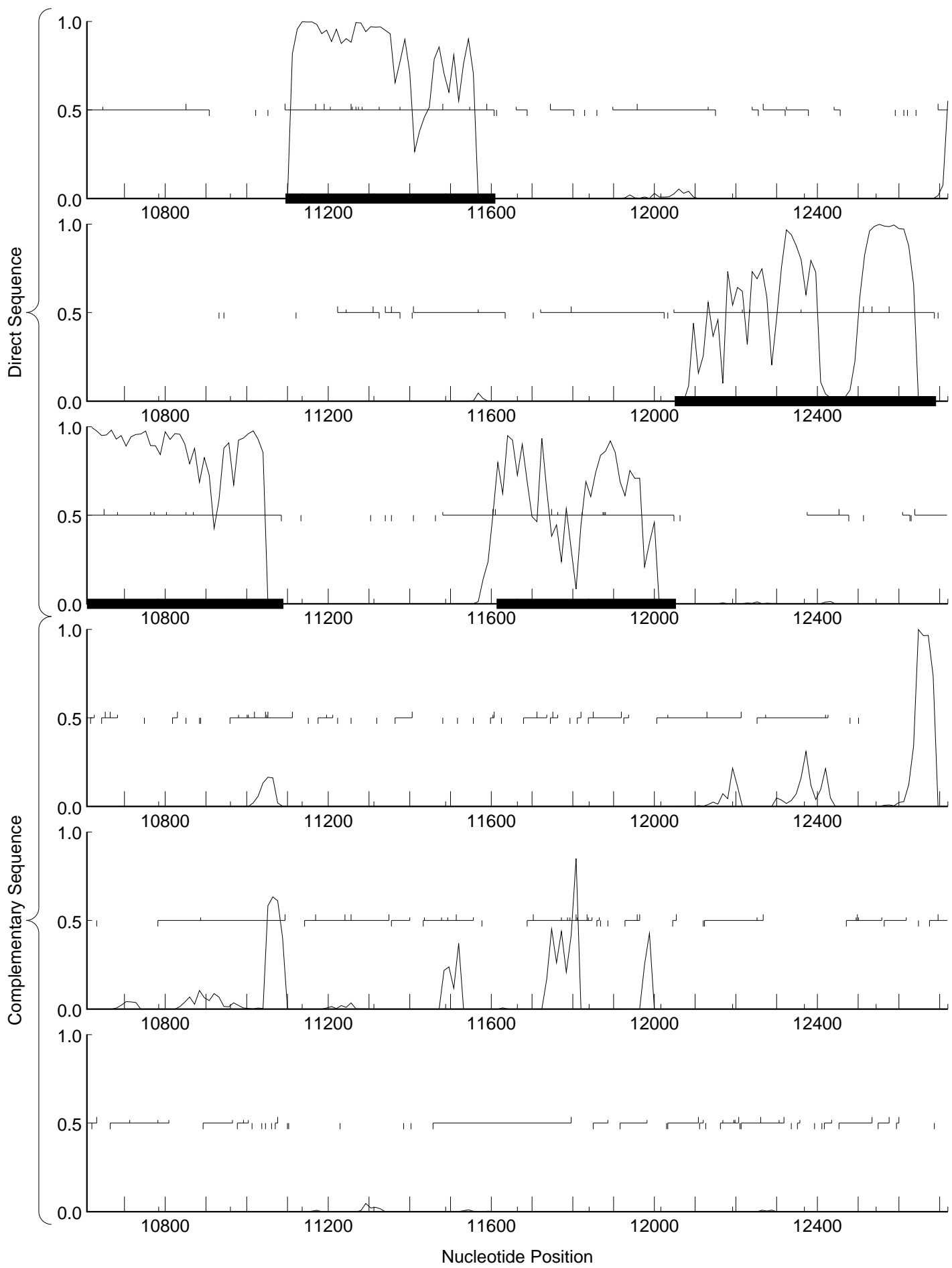
GeneMark.hmm prediction



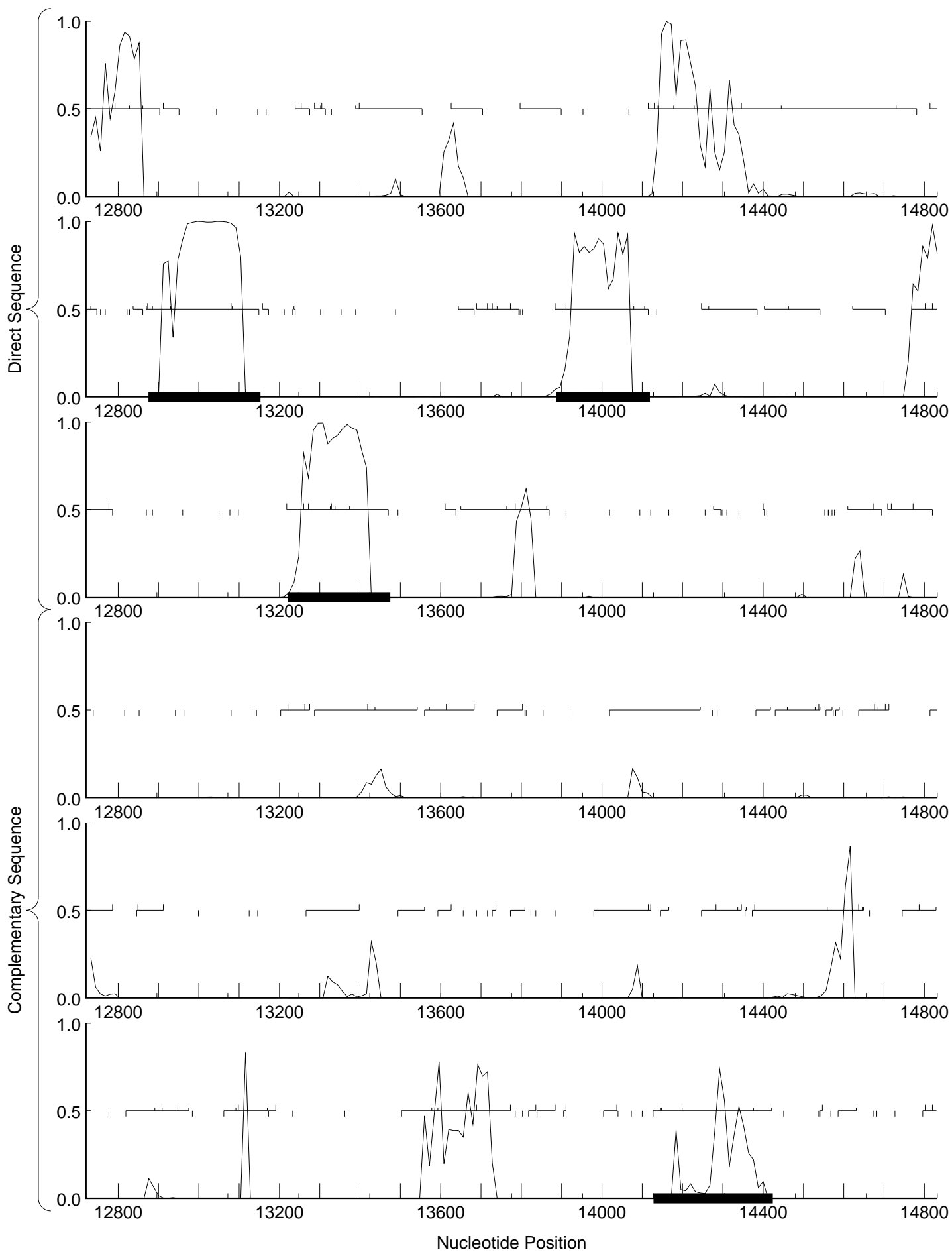
GeneMark.hmm prediction



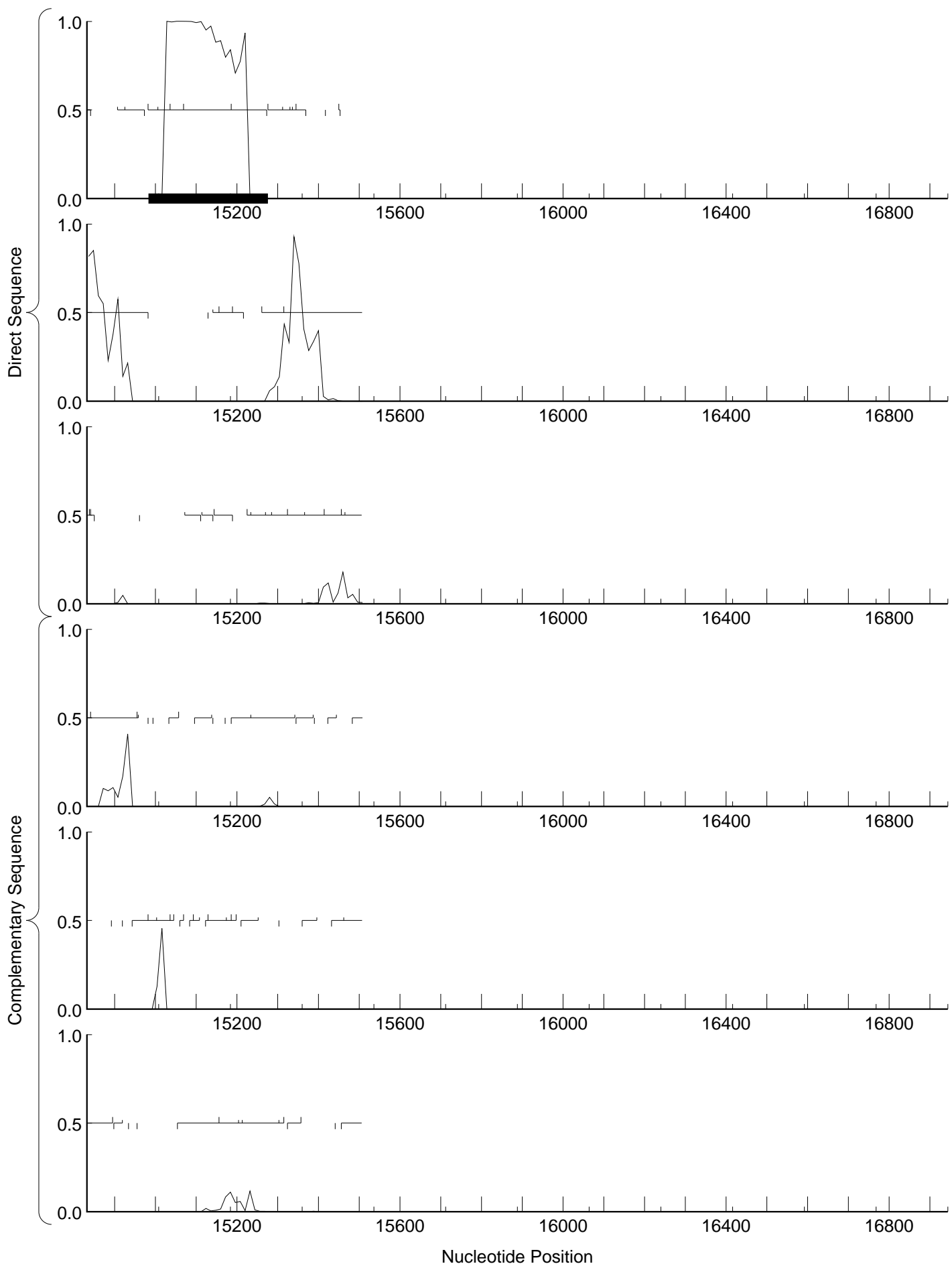
GeneMark.hmm prediction



GeneMark.hmm prediction



GeneMark.hmm prediction



Nucleotide Position