

GeneMark

Version 2.5p (09.08.06)

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PROGRAM INFORMATION

Sequence : Streptomyces phage Bovely complete sequence, 49576 bp including 11-base 3' overhang (CGGGCA
Analysis Date : 8/15/18 at 16:21:49
Pages : 25
Sequence Length : 49576 bp
GC Content : 66.17%

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,

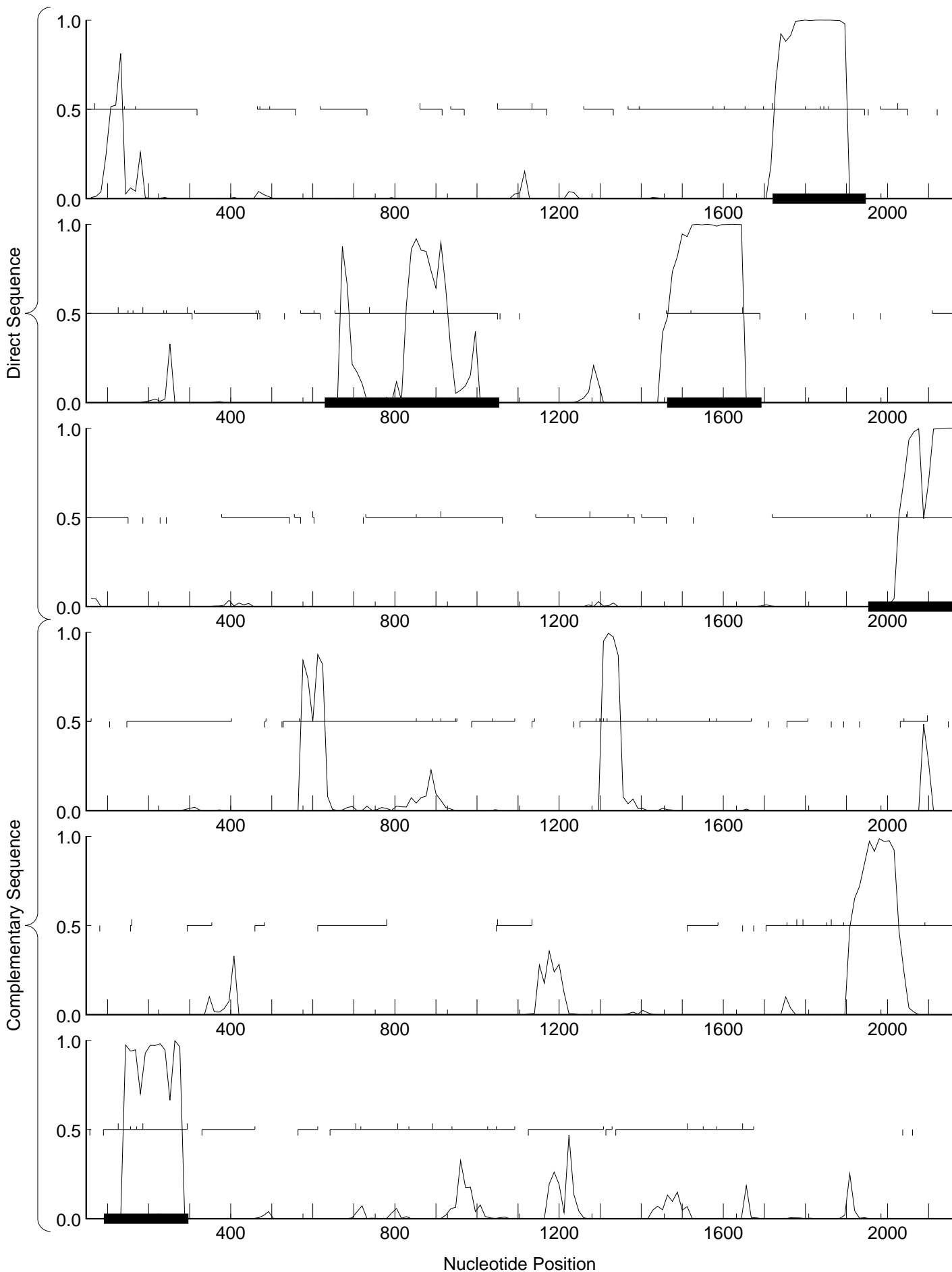
Matrix notes & comments

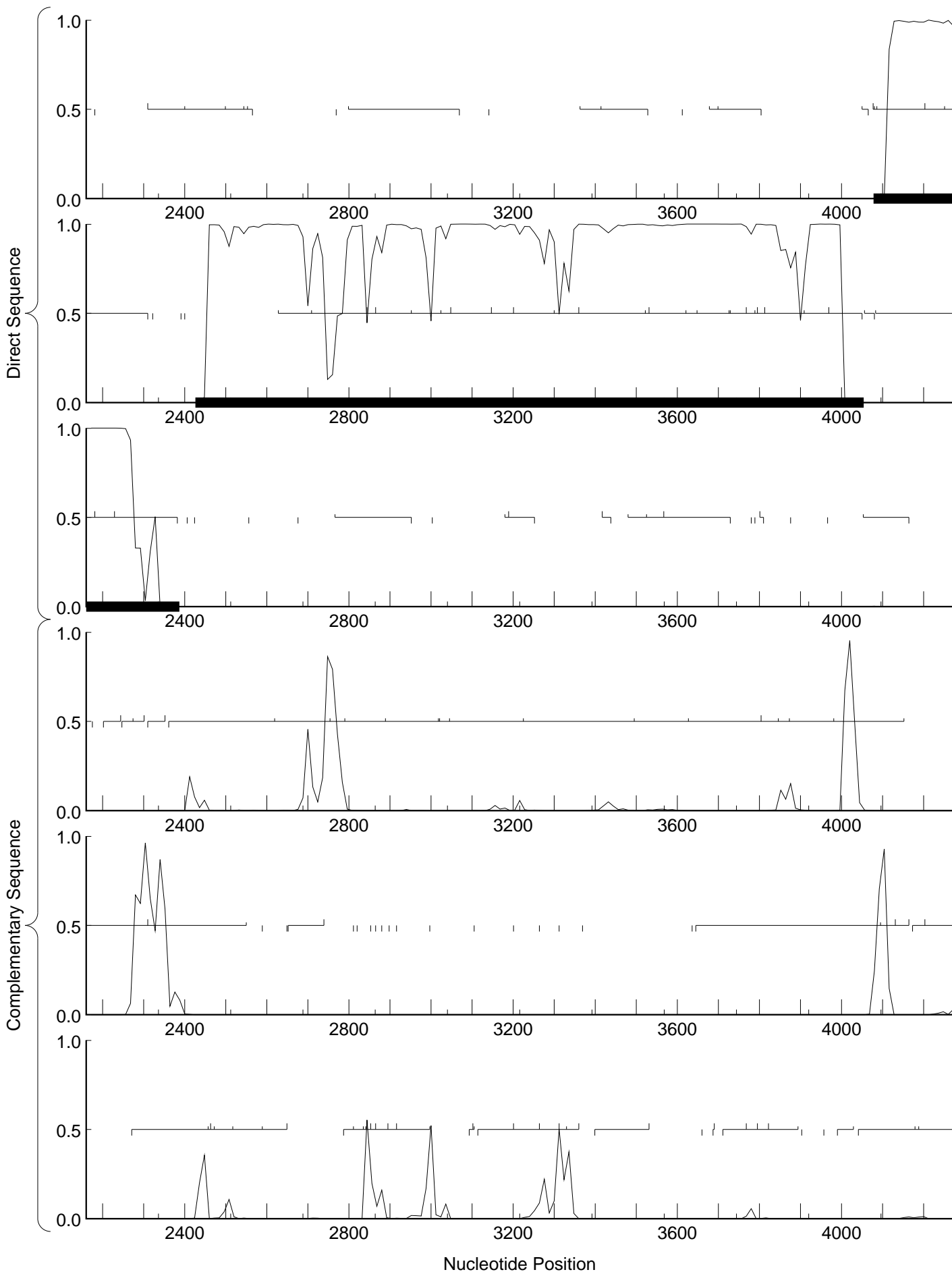
For details on the model building procedure see:
Besemer J. and Borodovsky M.
"Heuristic approach to deriving models for gene finding"
NAR, 1999, Vol. 27, No. 19, pp. 3911-3920

MATRIX INFORMATION

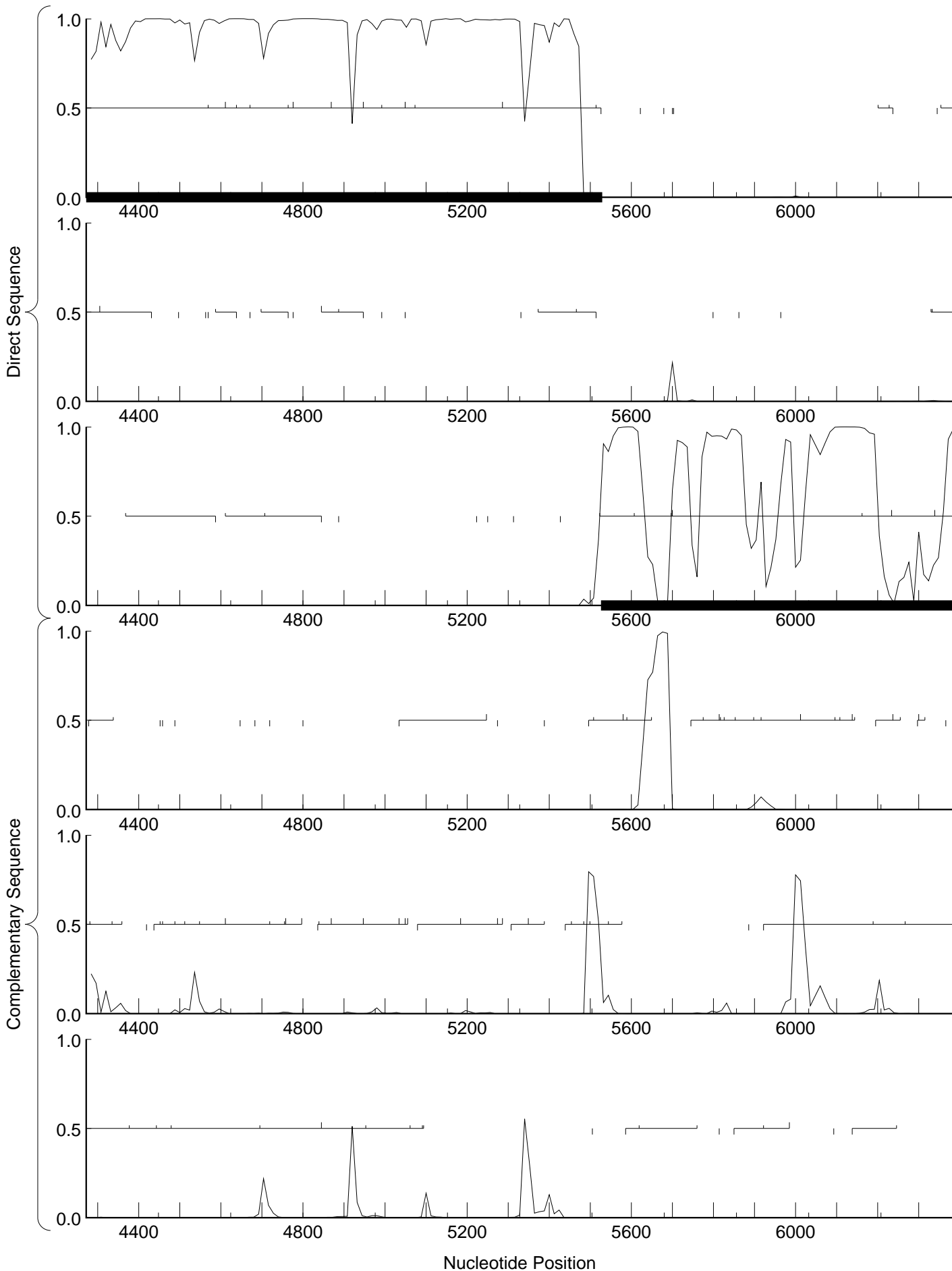
Matrix : Heuristic, GC = 66
Author : Borodovsky Laboratory - Georgia Tech
Order : 2

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

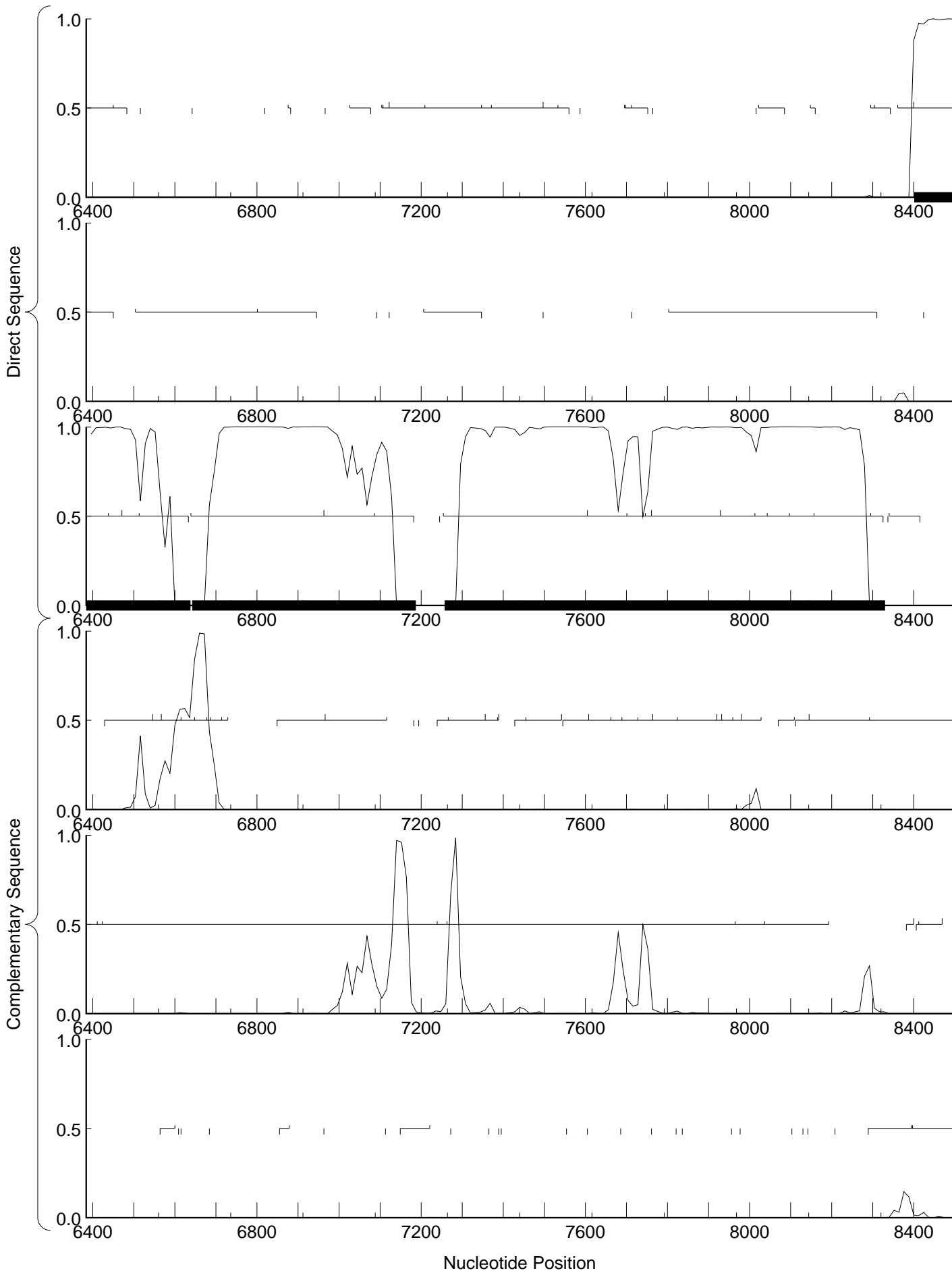




GeneMark, hmm prediction

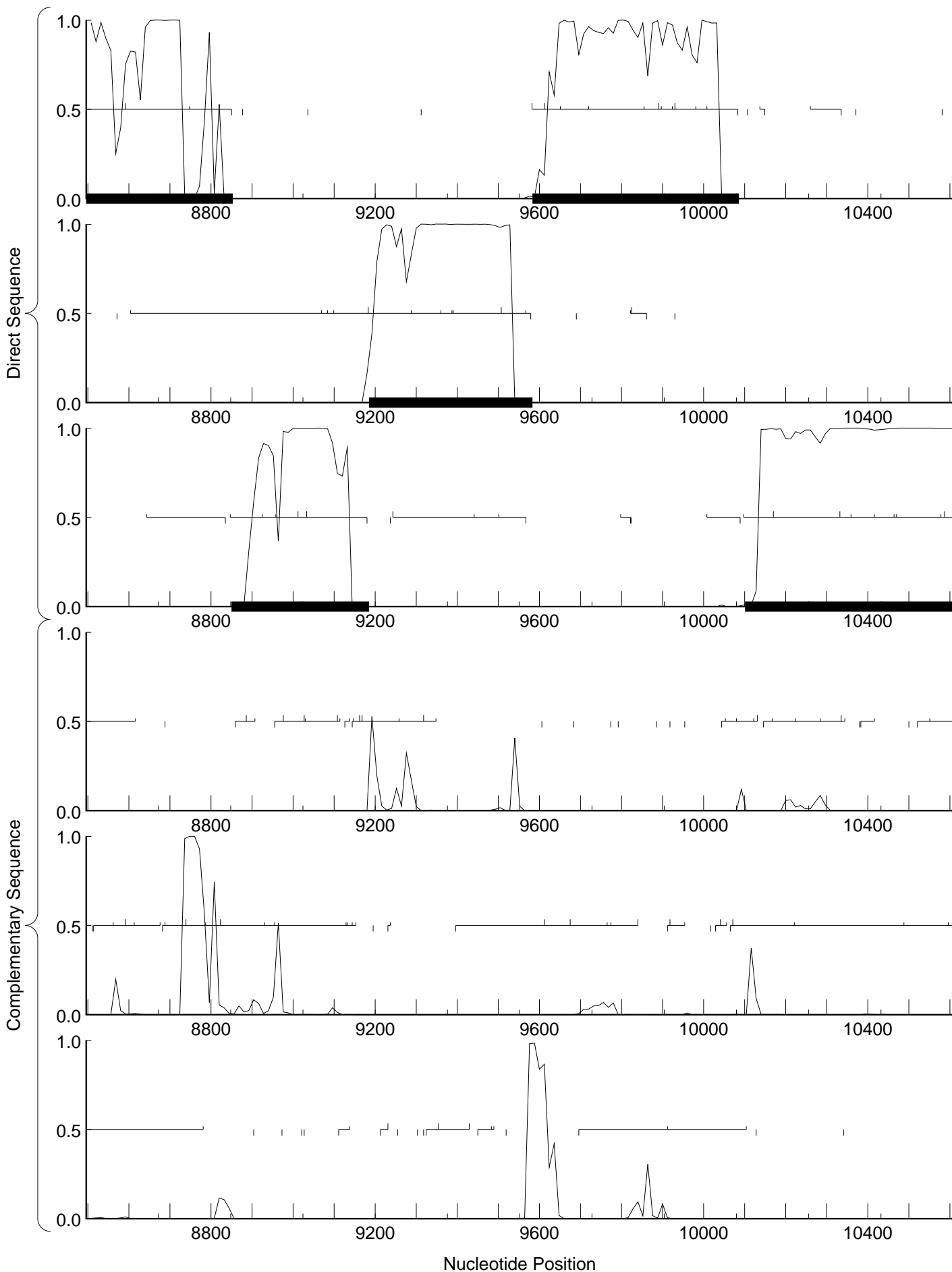


GeneMark, hmm prediction

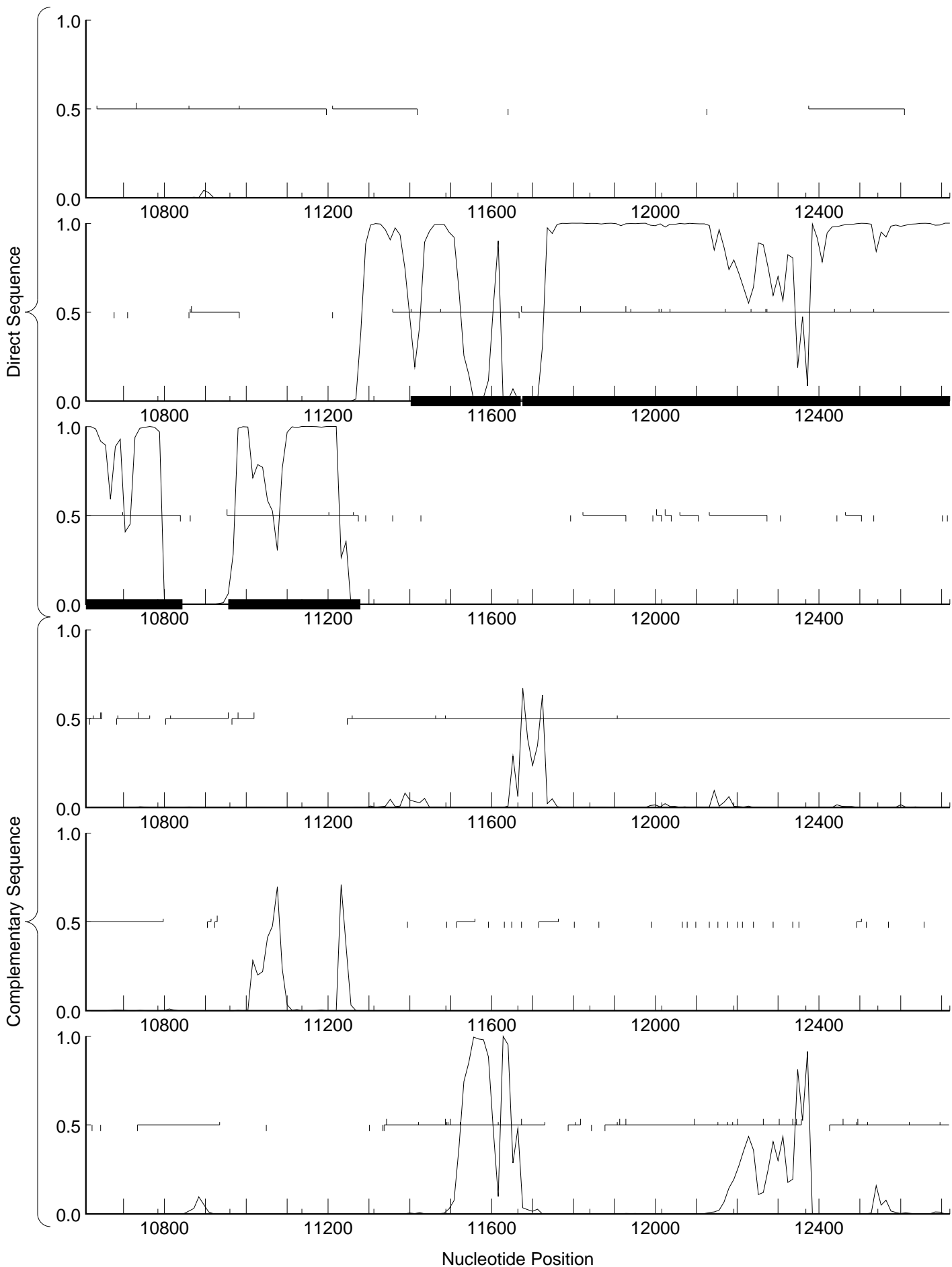


Nucleotide Position

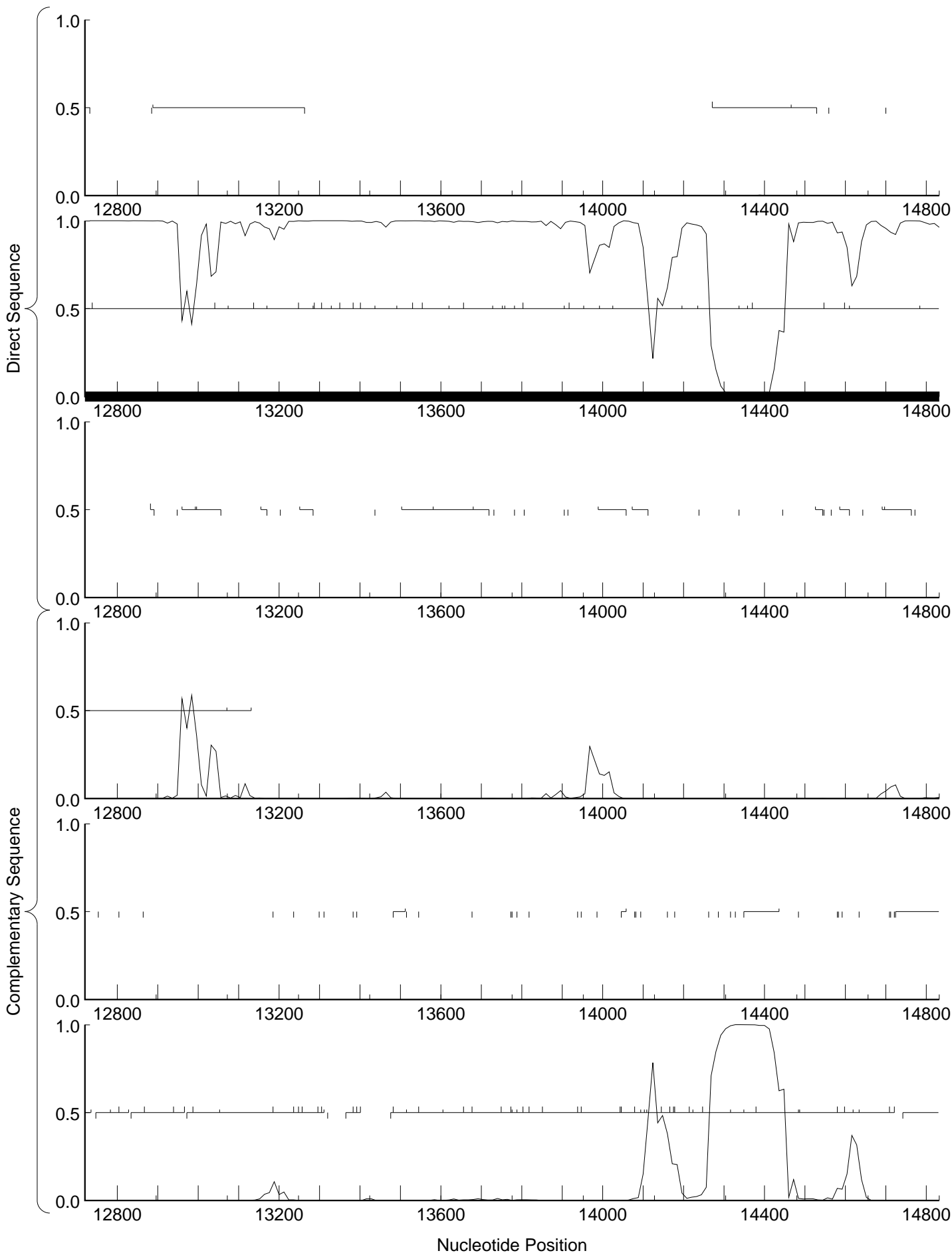
GeneMark, hmm prediction



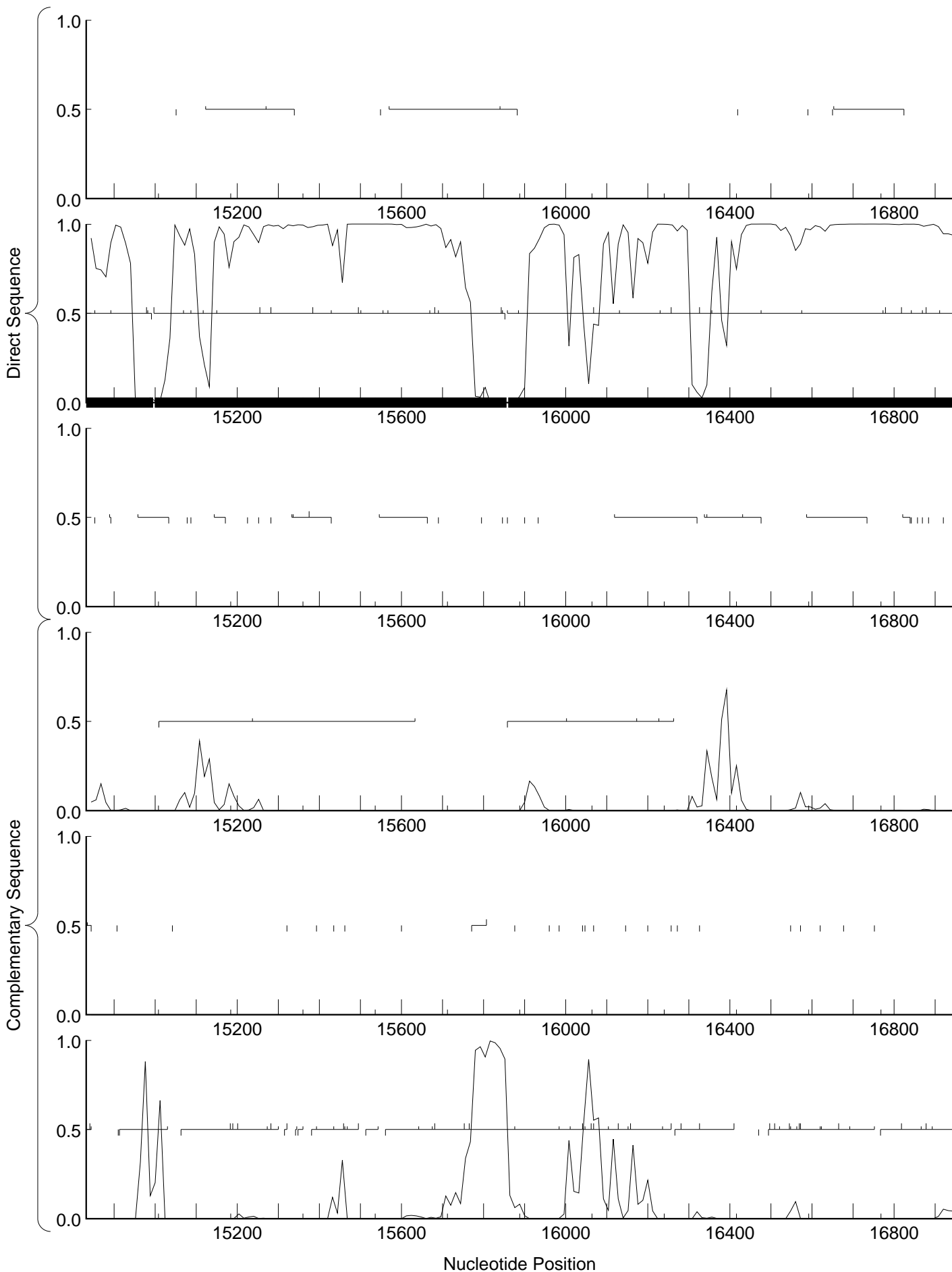
GeneMark, hmm prediction



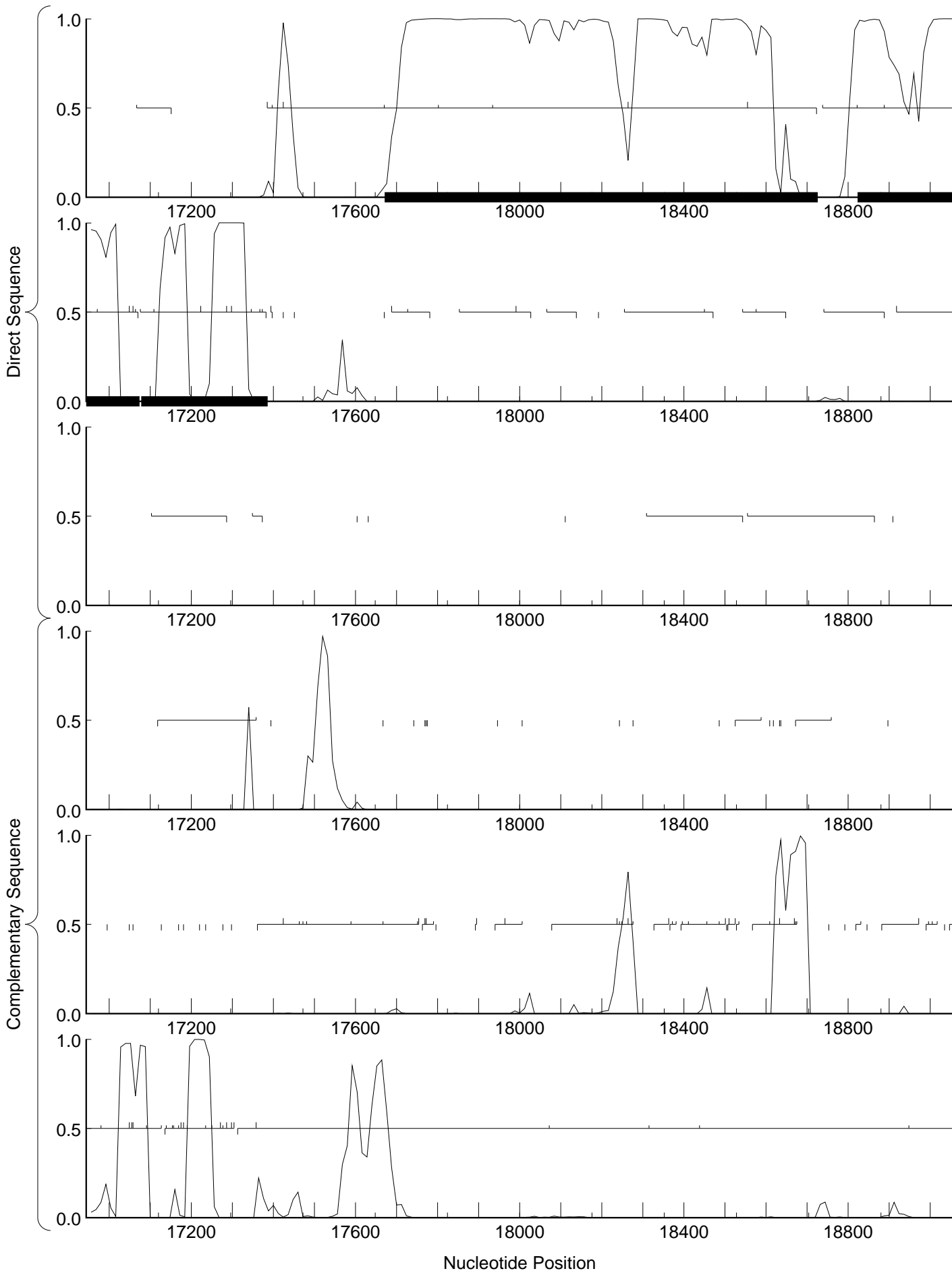
GeneMark, hmm prediction

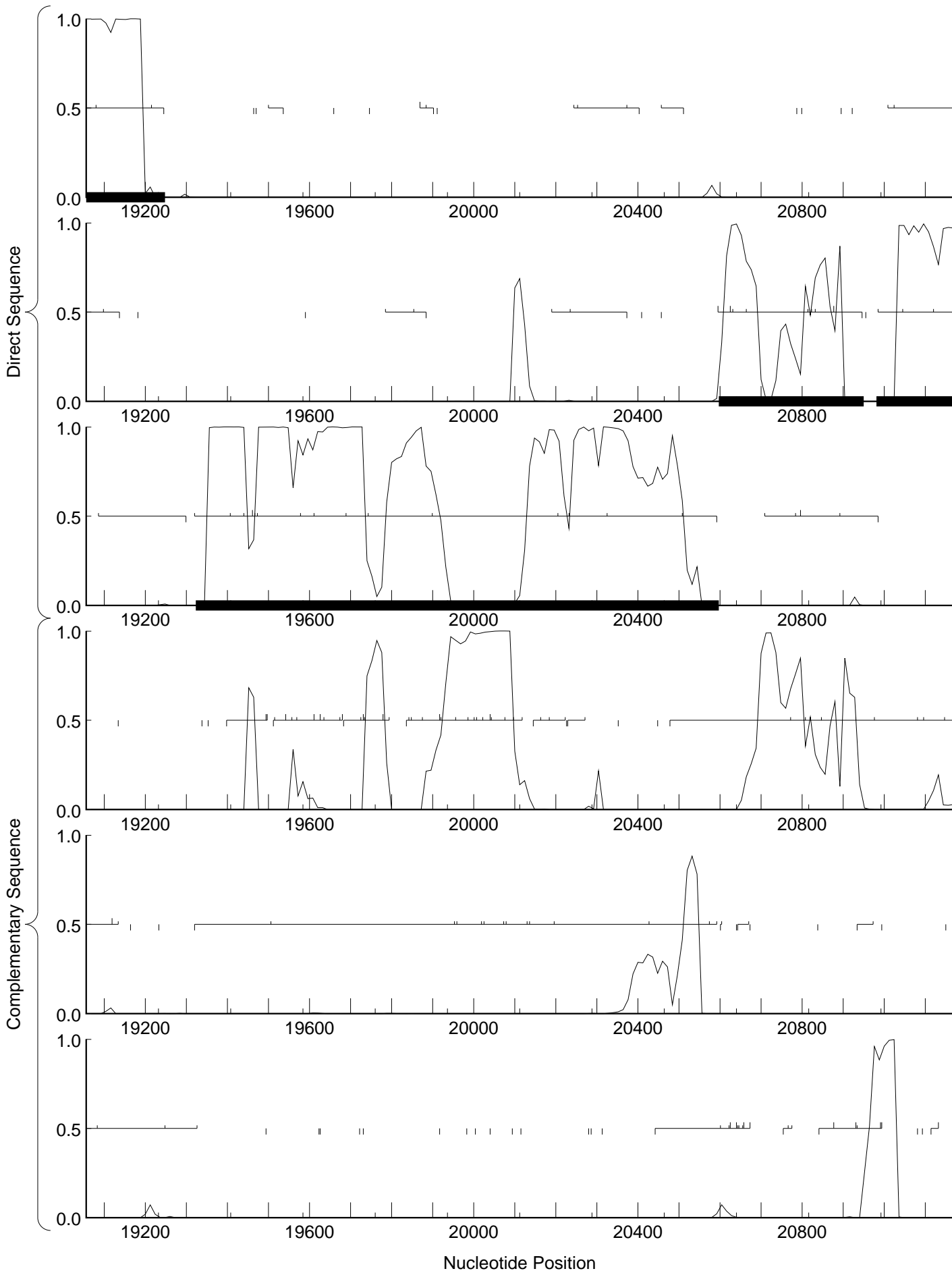


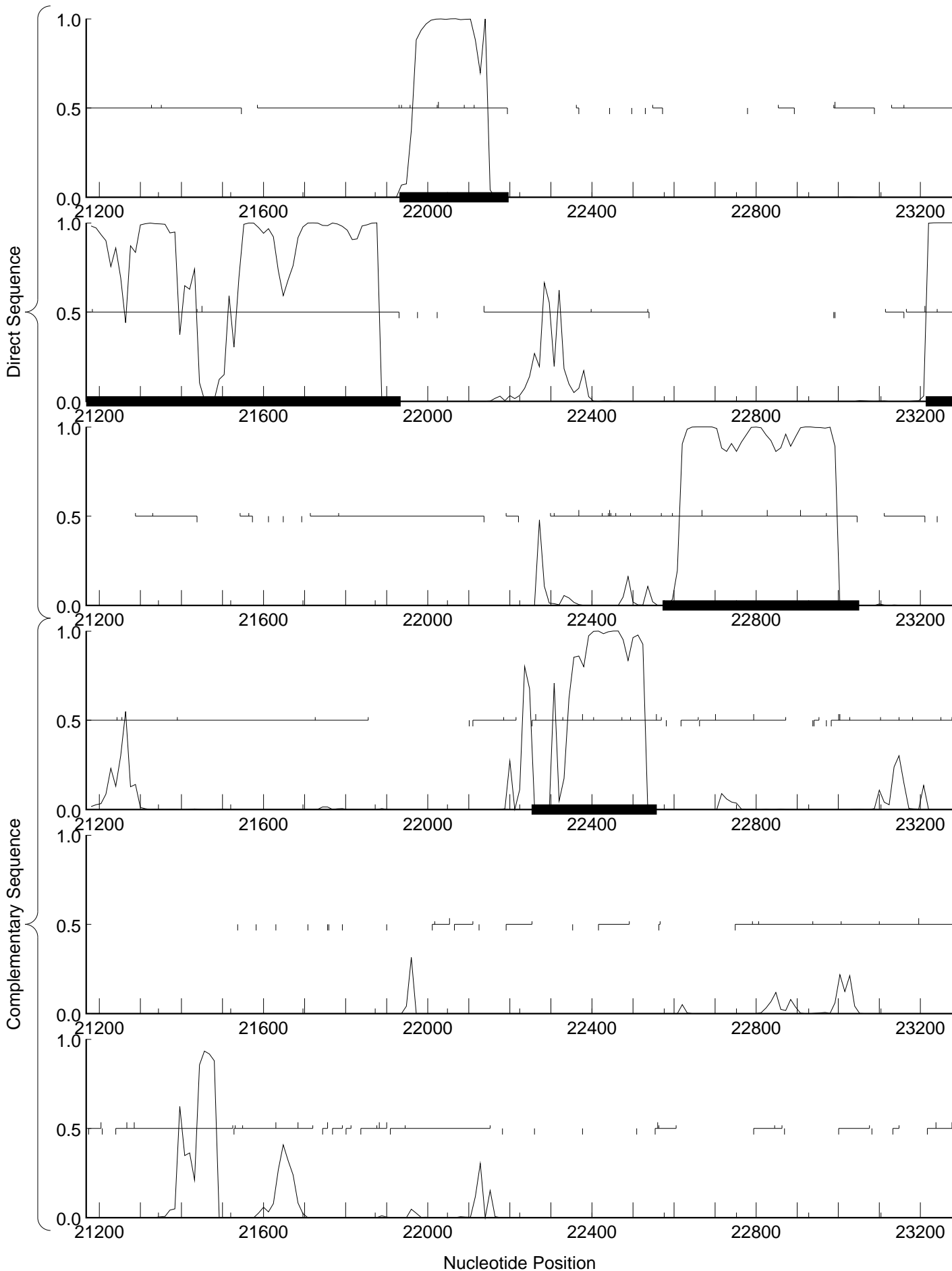
GeneMark, hmm prediction

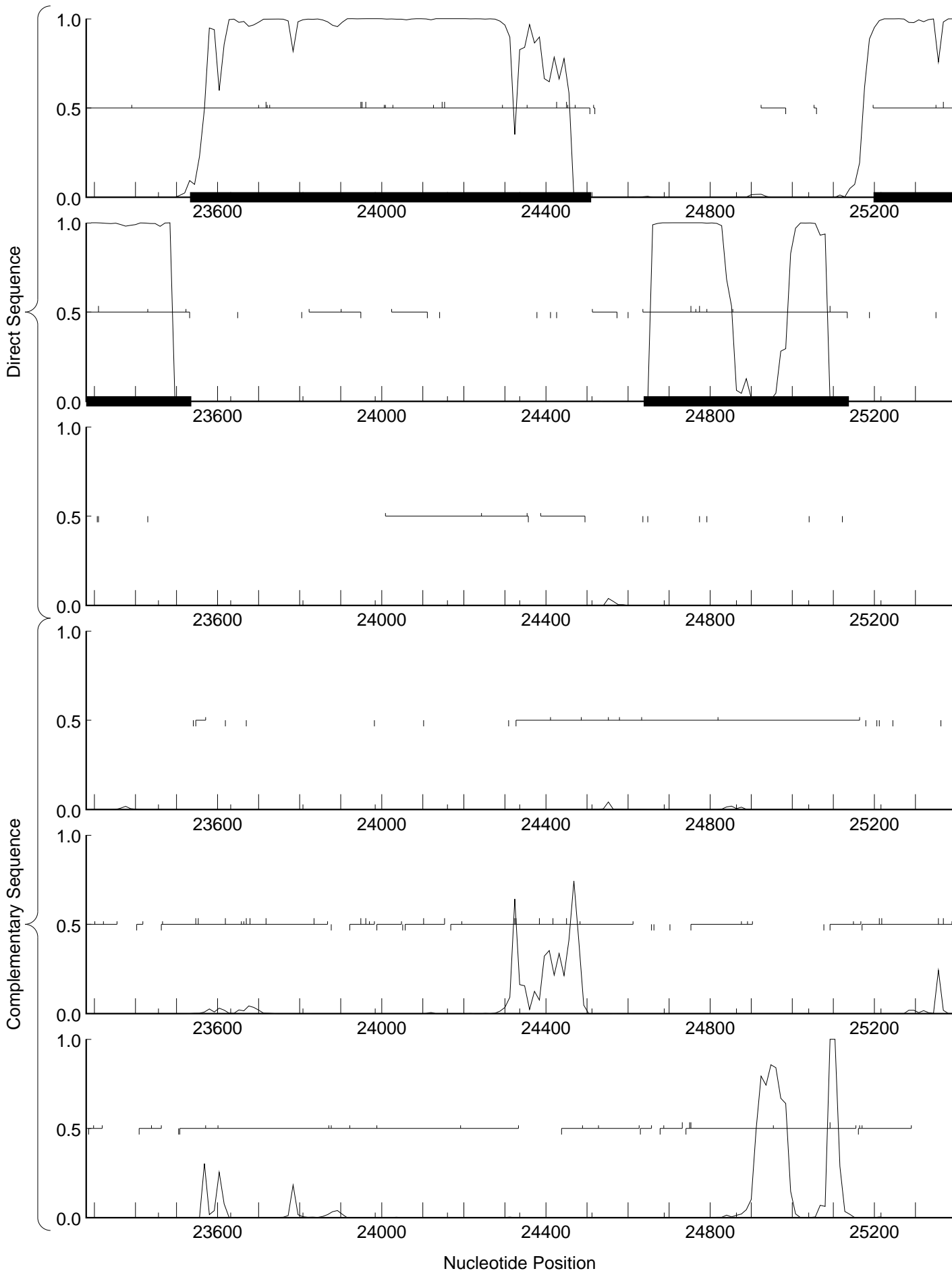


complete sequence, 49576 bp including 11-base 3' overhang (CGGGCAGTGAT), Cluster BD1, Order 2, Window 96, Step 12, 10/25

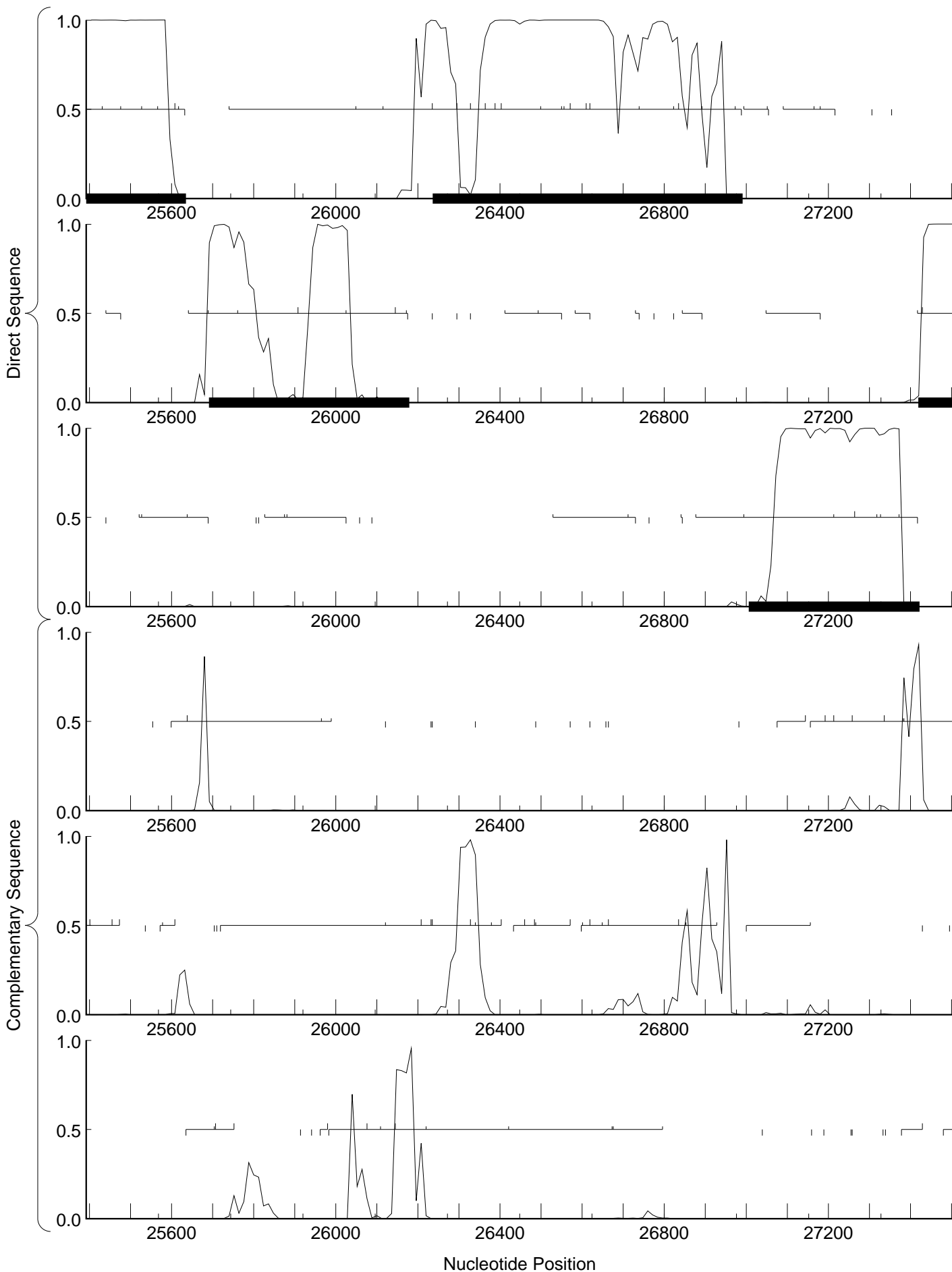




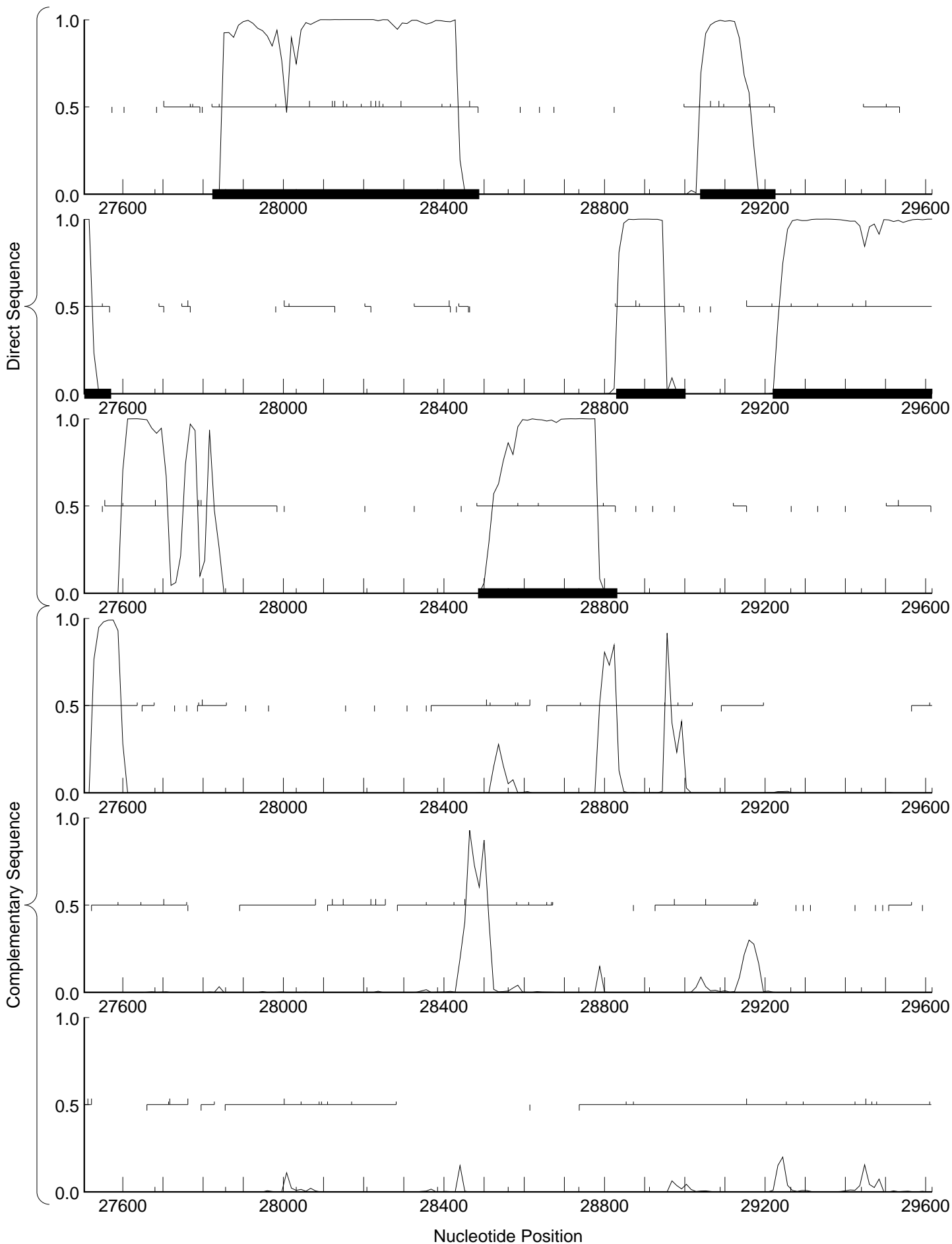




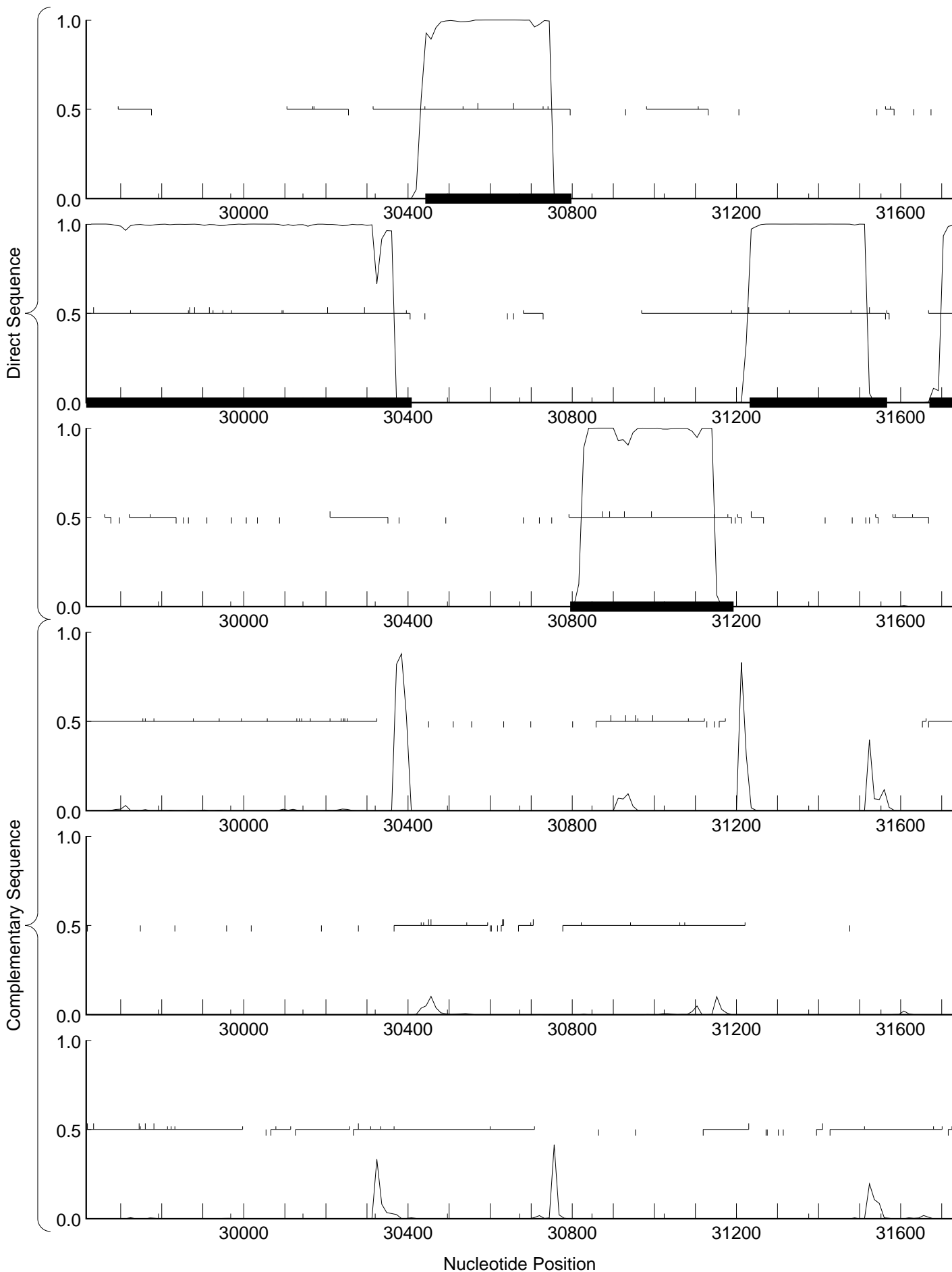
GeneMark, hmm prediction



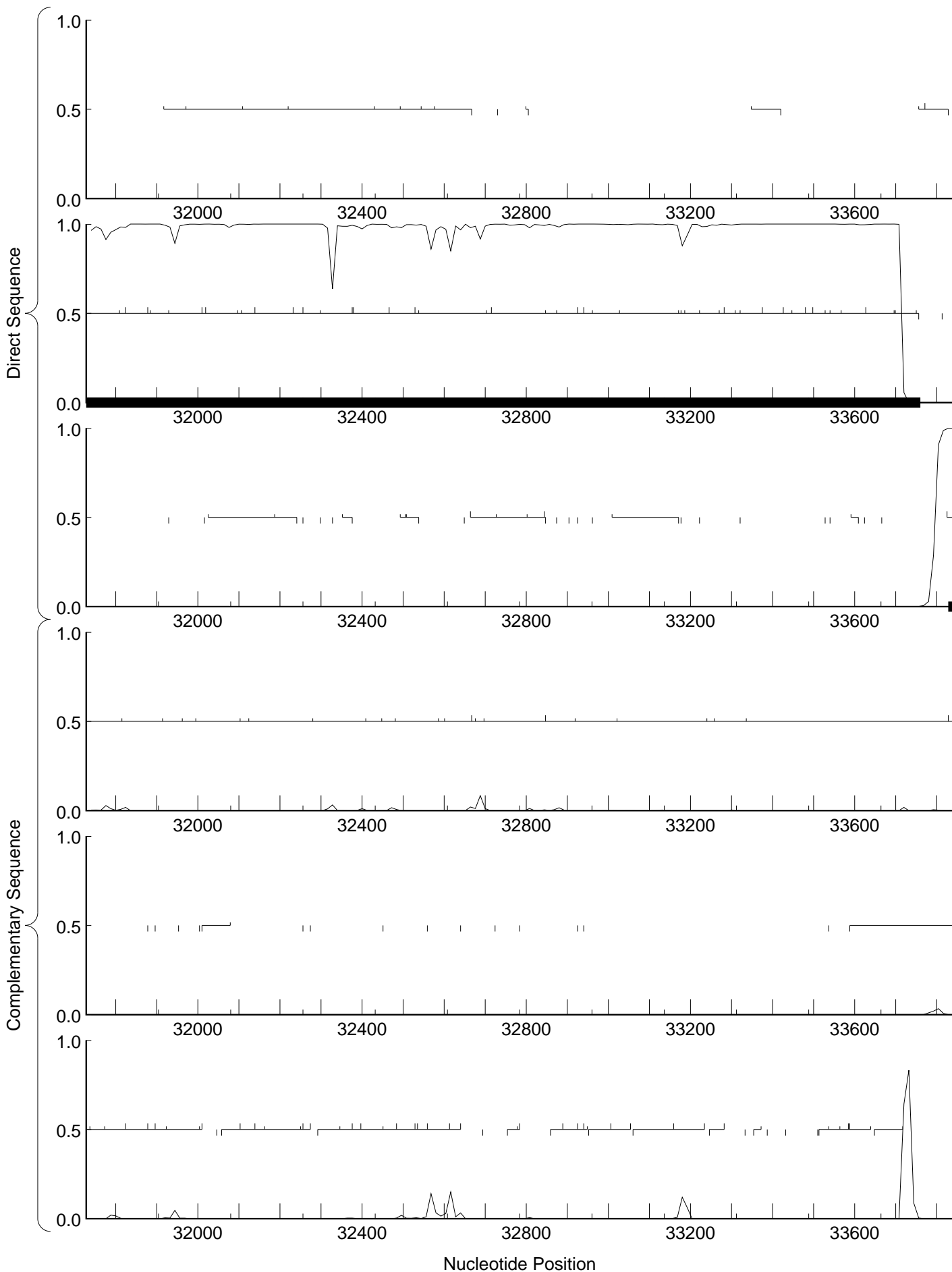
GeneMark, hmm prediction



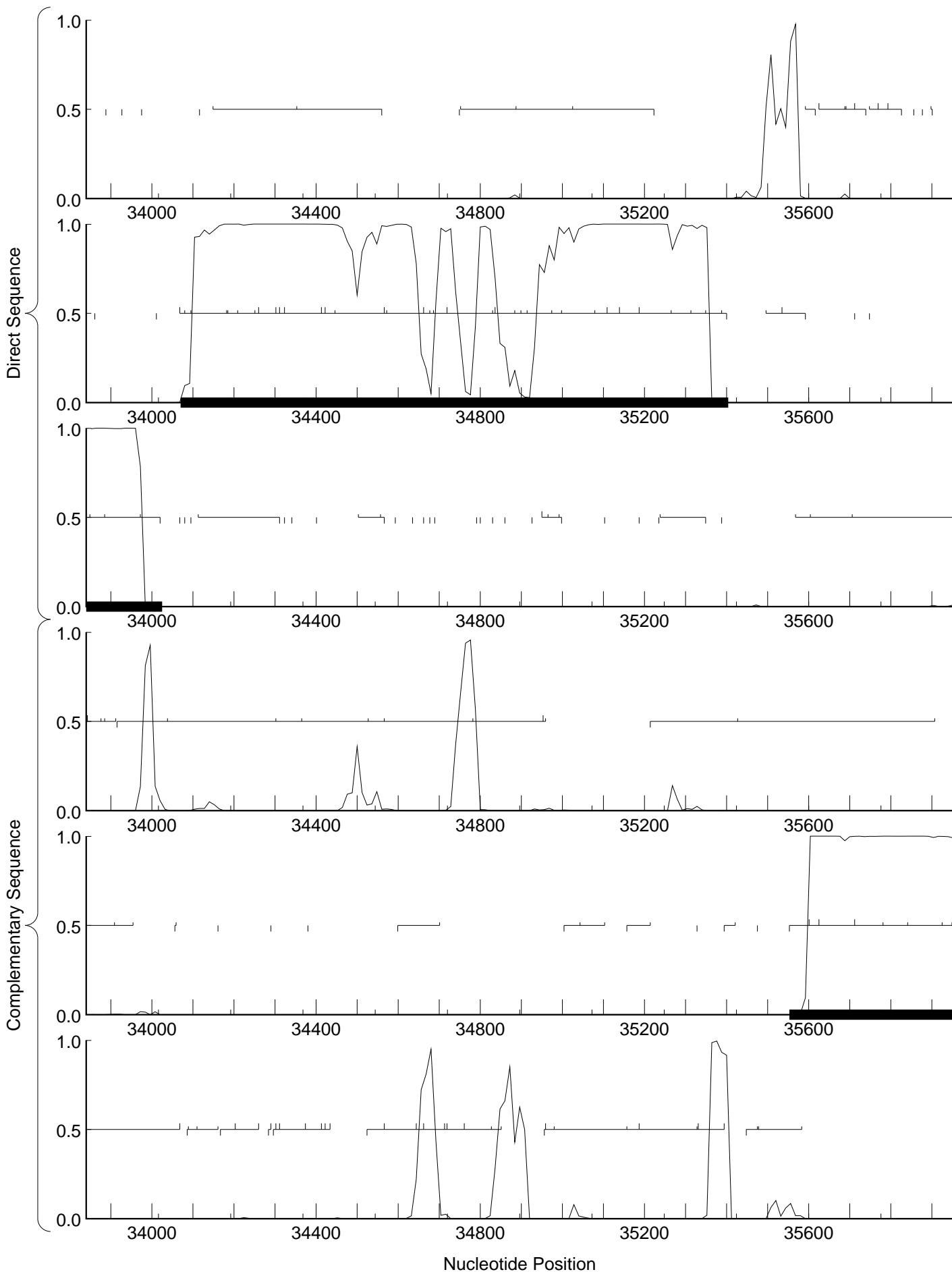
GeneMark, hmm prediction

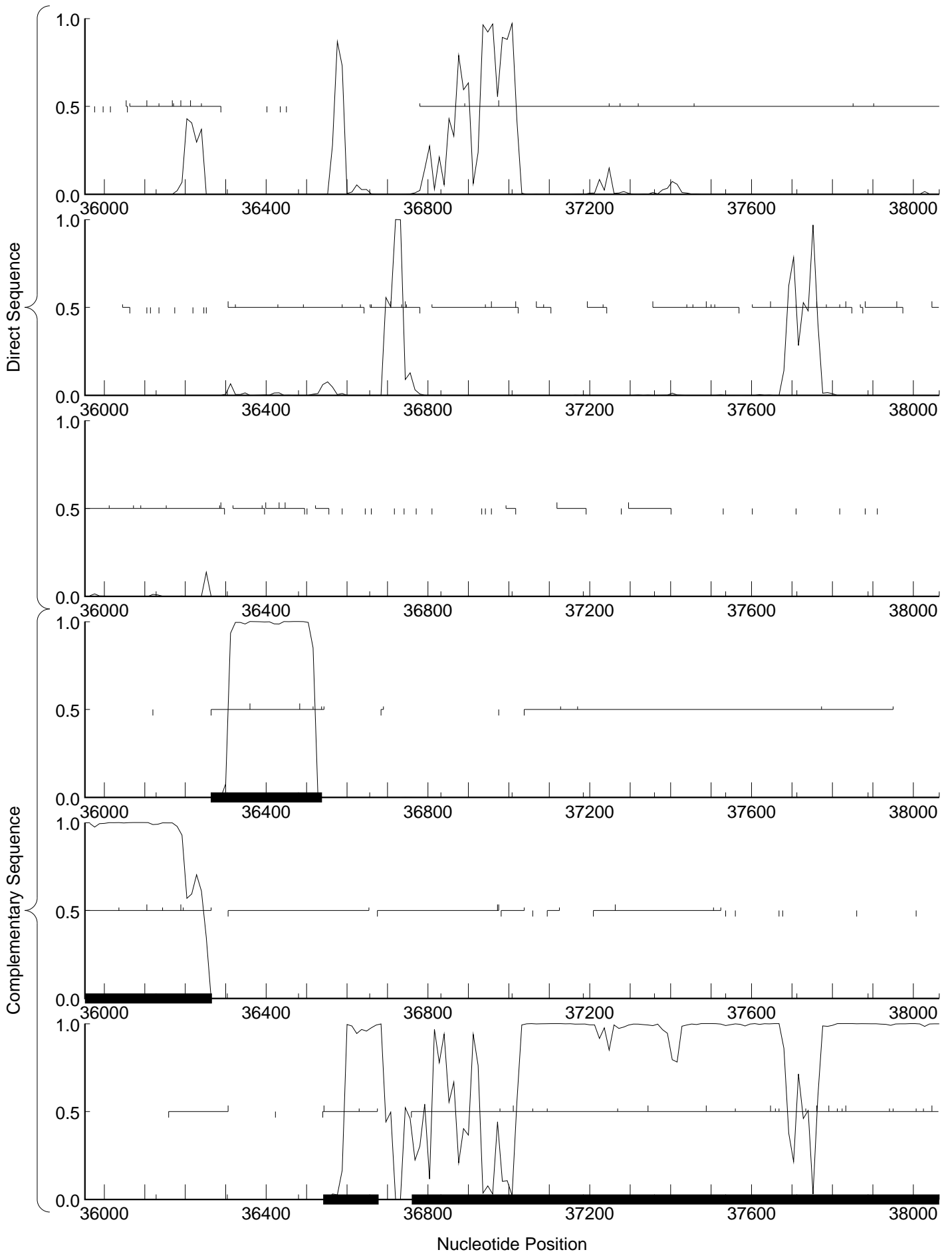


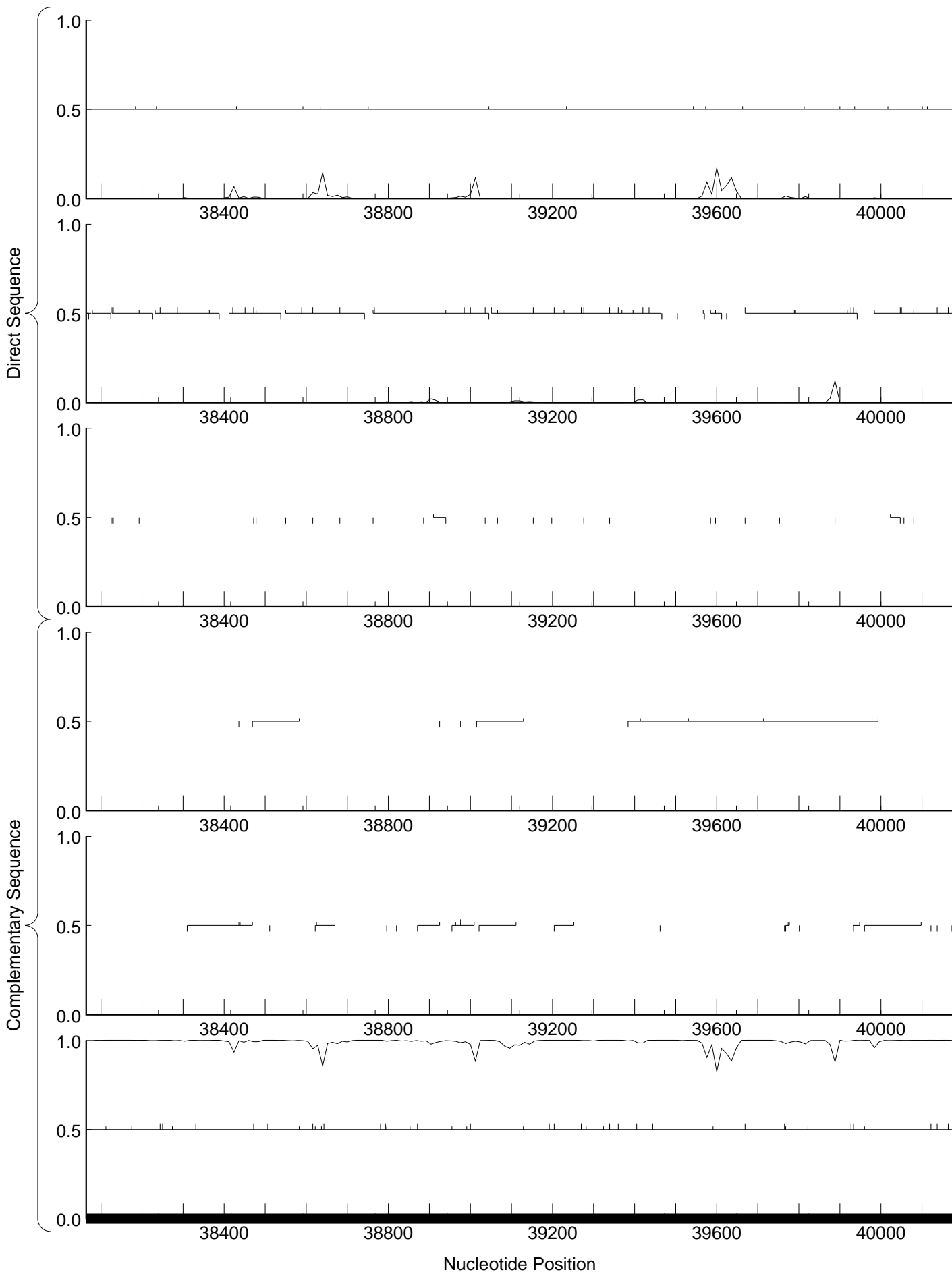
GeneMark, hmm prediction

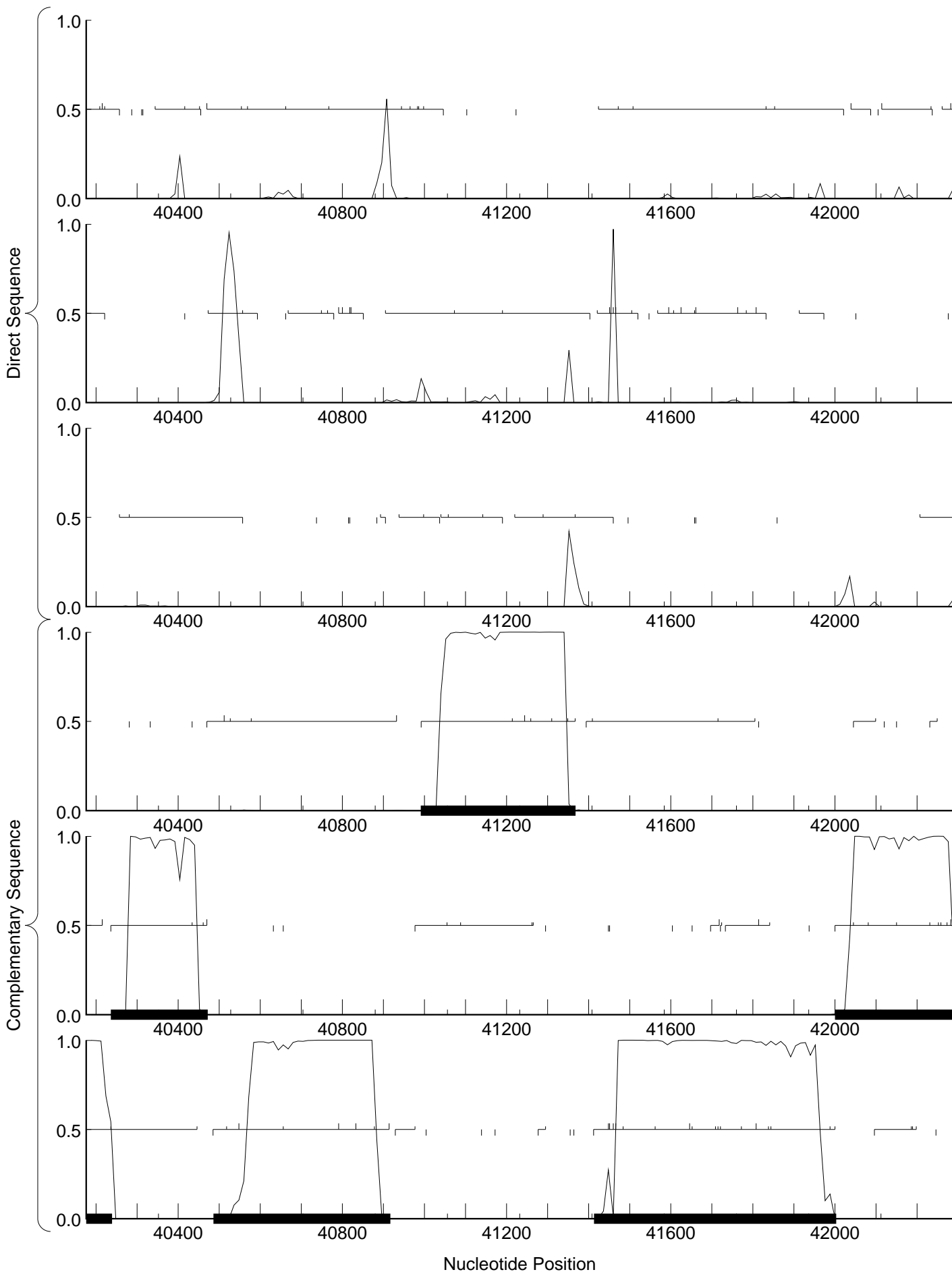


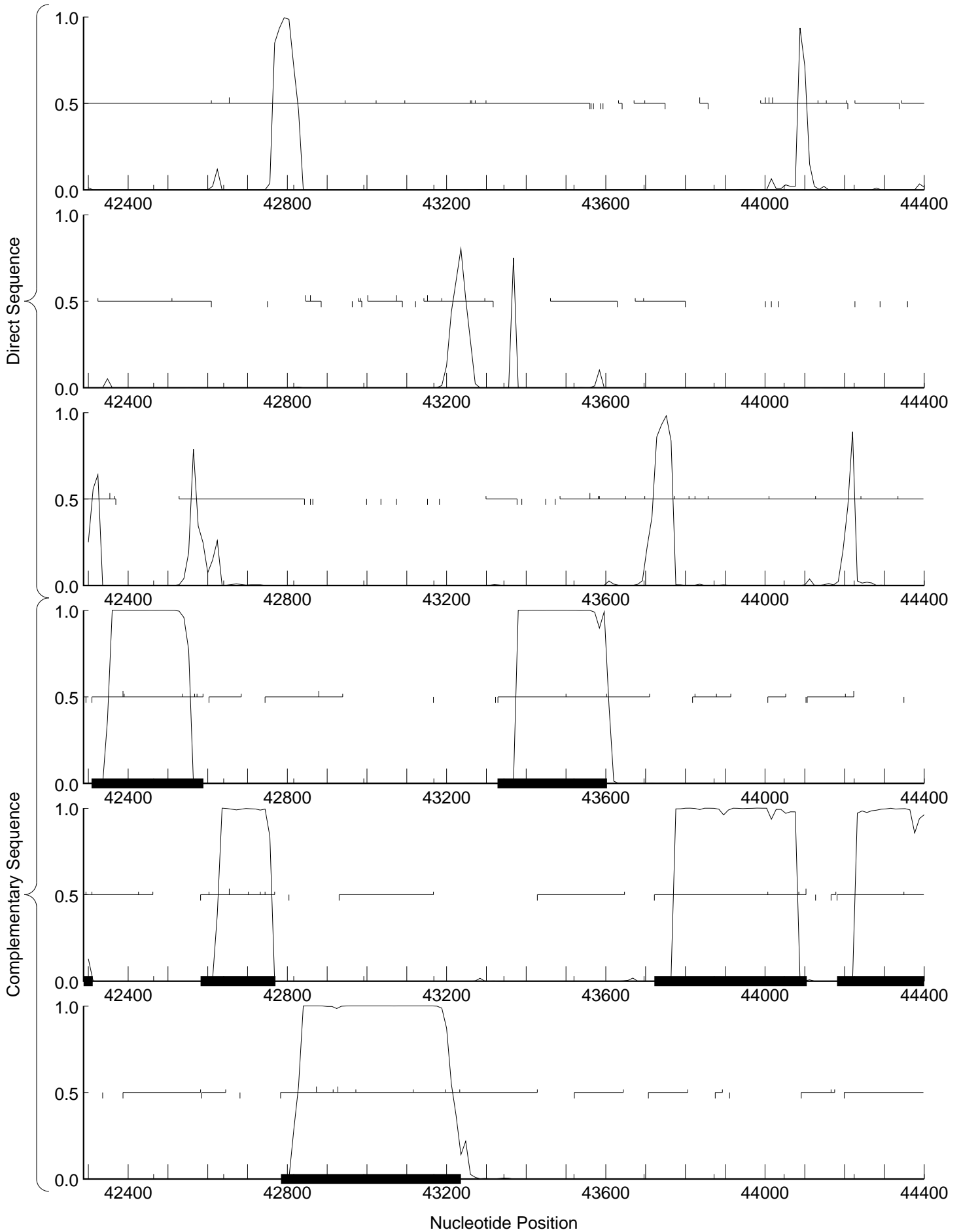
GeneMark, hmm prediction



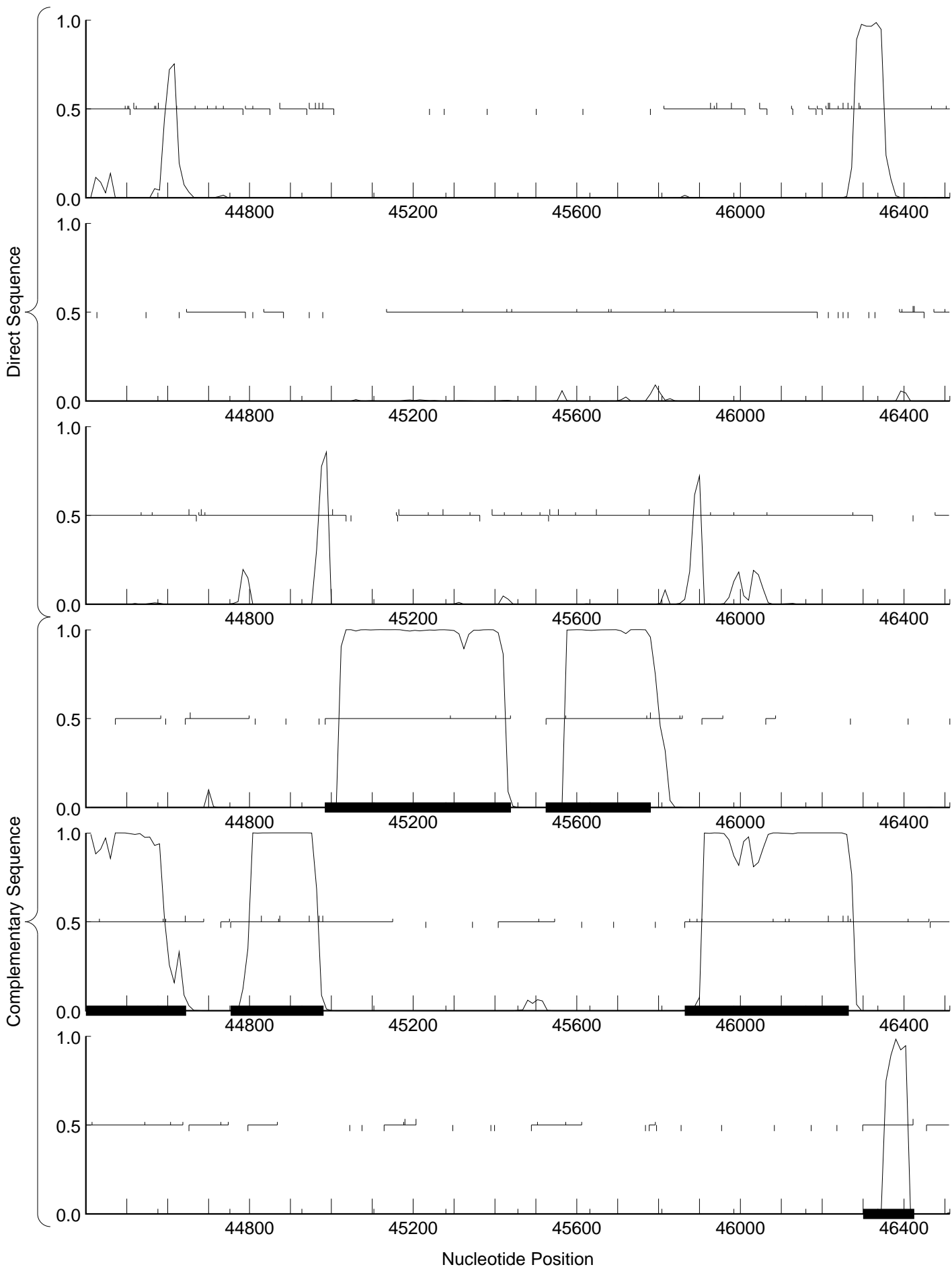




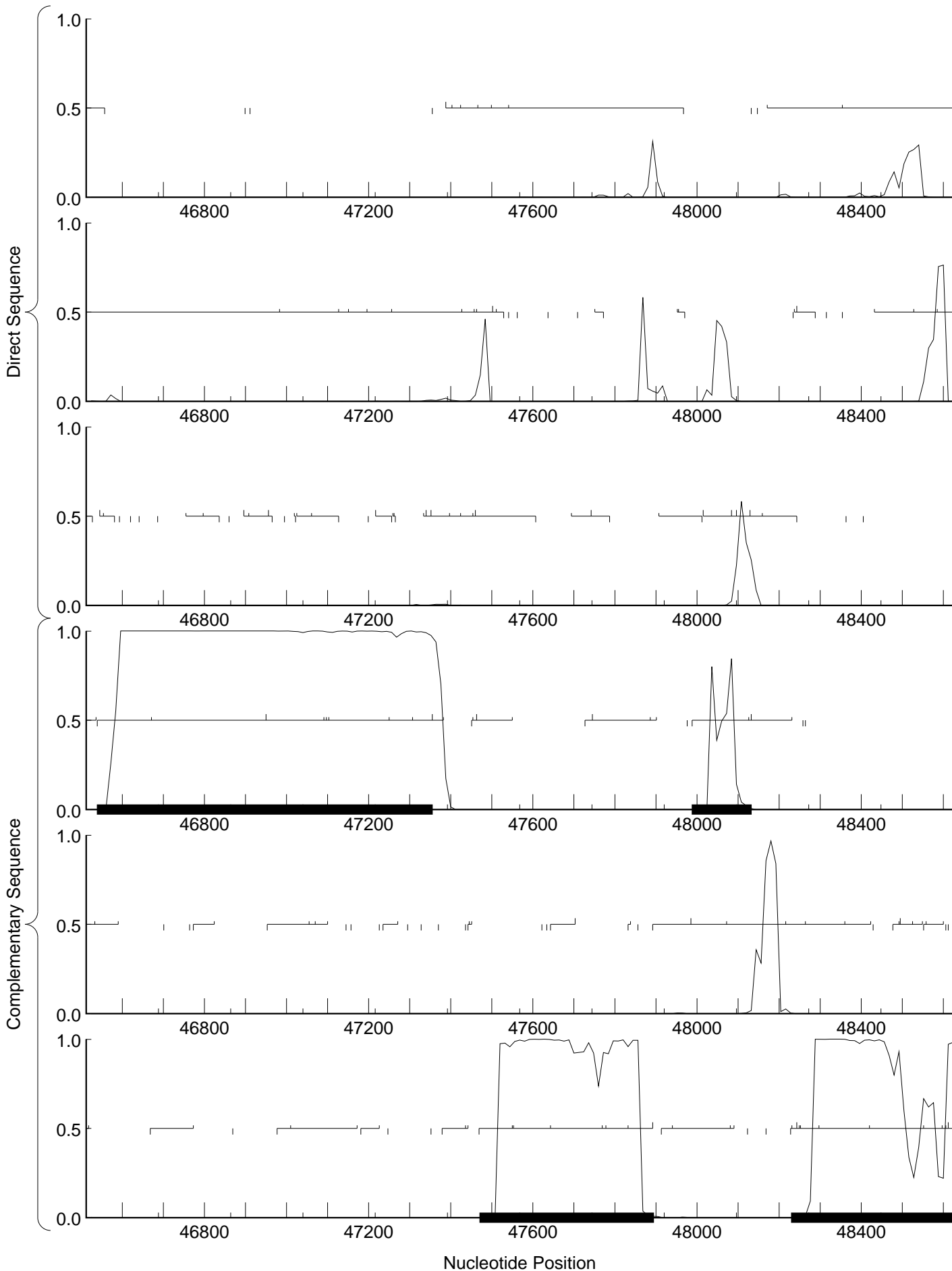




GeneMark, hmm prediction



GeneMark, hmm prediction



GeneMark, hmm prediction

