

GeneMark

Version 2.5p (09.08.06)

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PROGRAM INFORMATION

Sequence : Mycobacterium phage Crespo complete sequence, 41902 bp including 11-base 3' overhang (CCCCA
Analysis Date : 3/17/18 at 2:21:34
Pages : 21
Sequence Length : 41902 bp
GC Content : 66.56%

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,

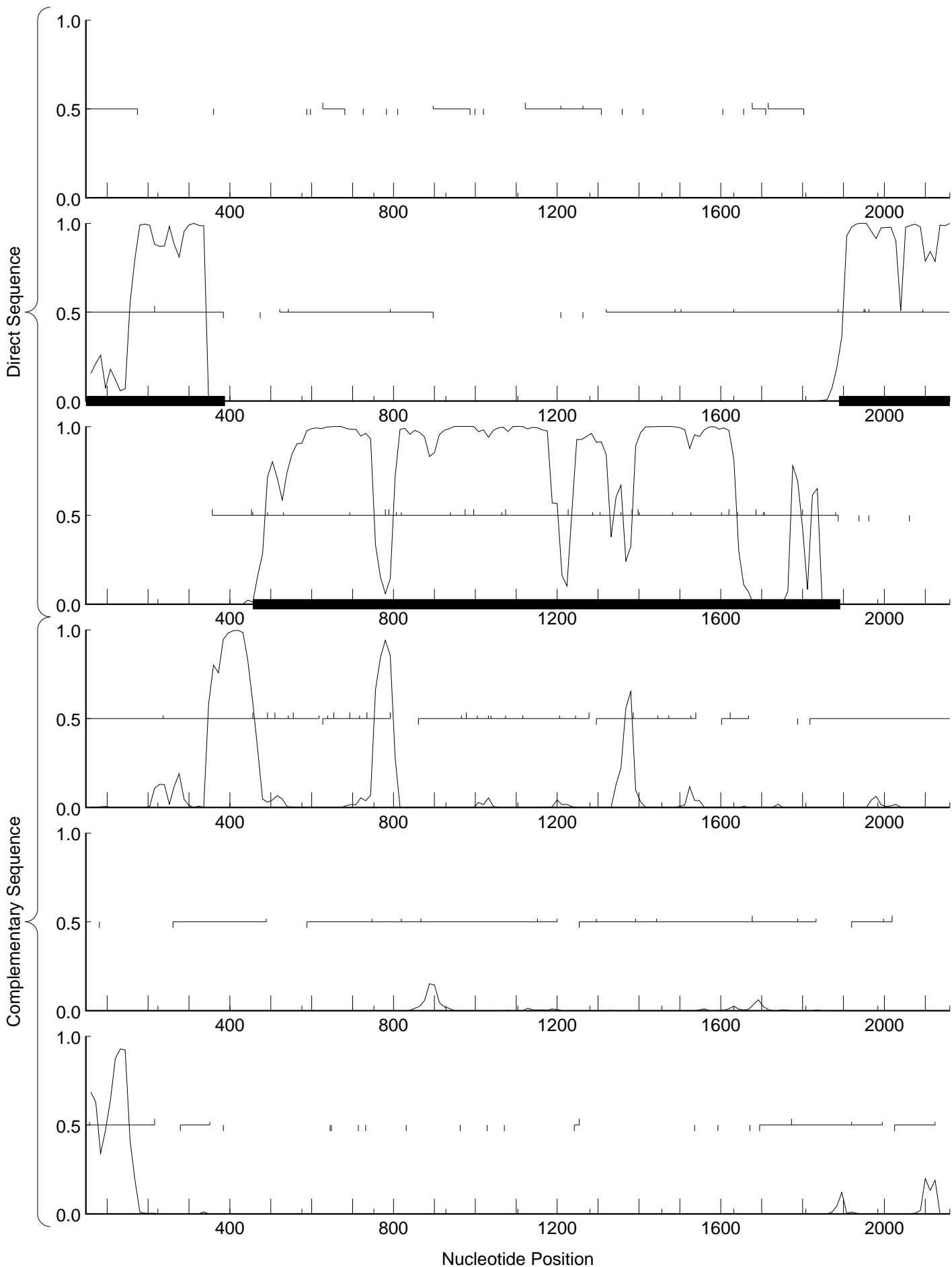
Matrix notes & comments

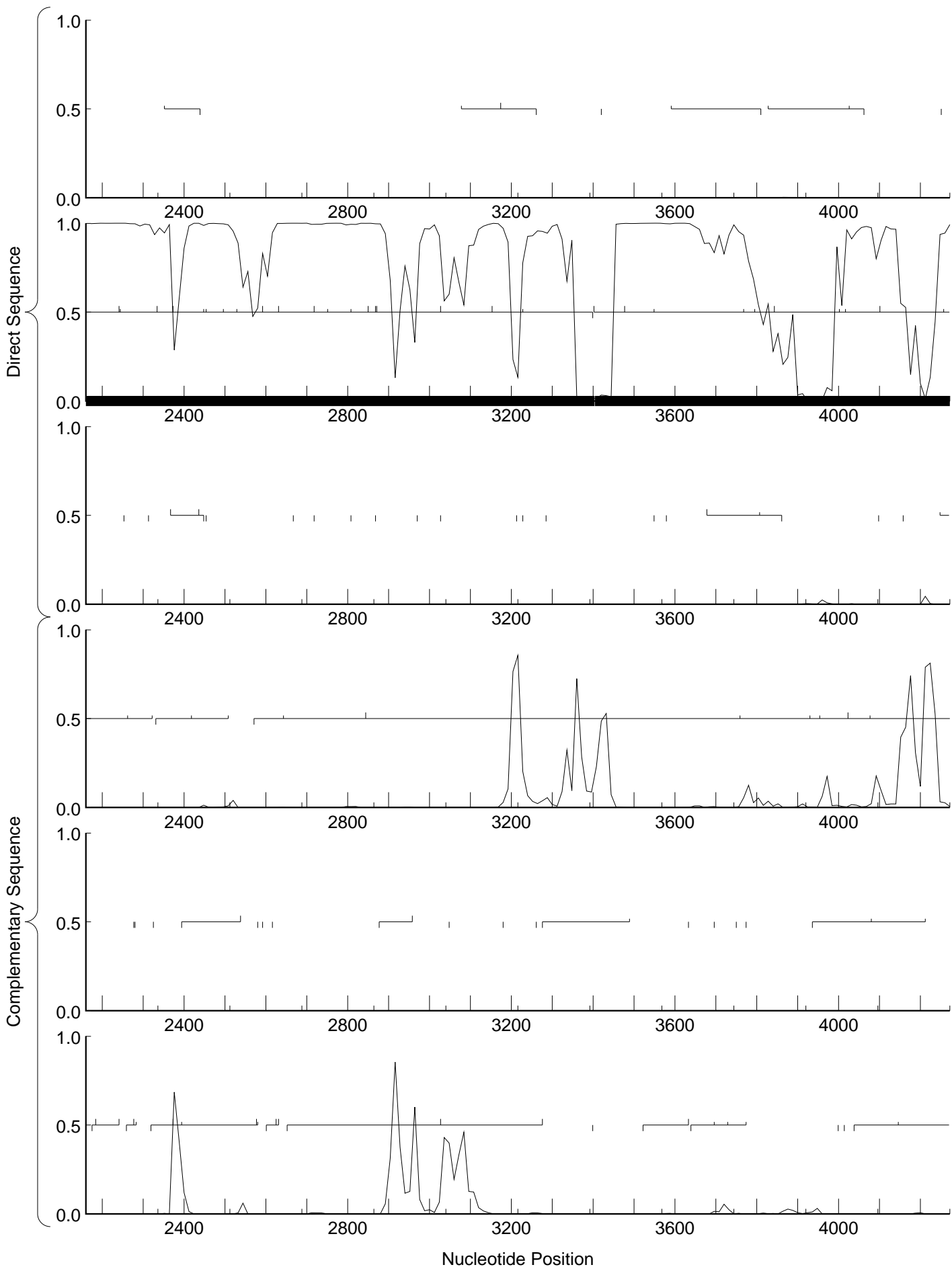
For details on the model building procedure see:
Besemer J. and Borodovsky M.
"Heuristic approach to deriving models for gene finding"
NAR, 1999, Vol. 27, No. 19, pp. 3911-3920

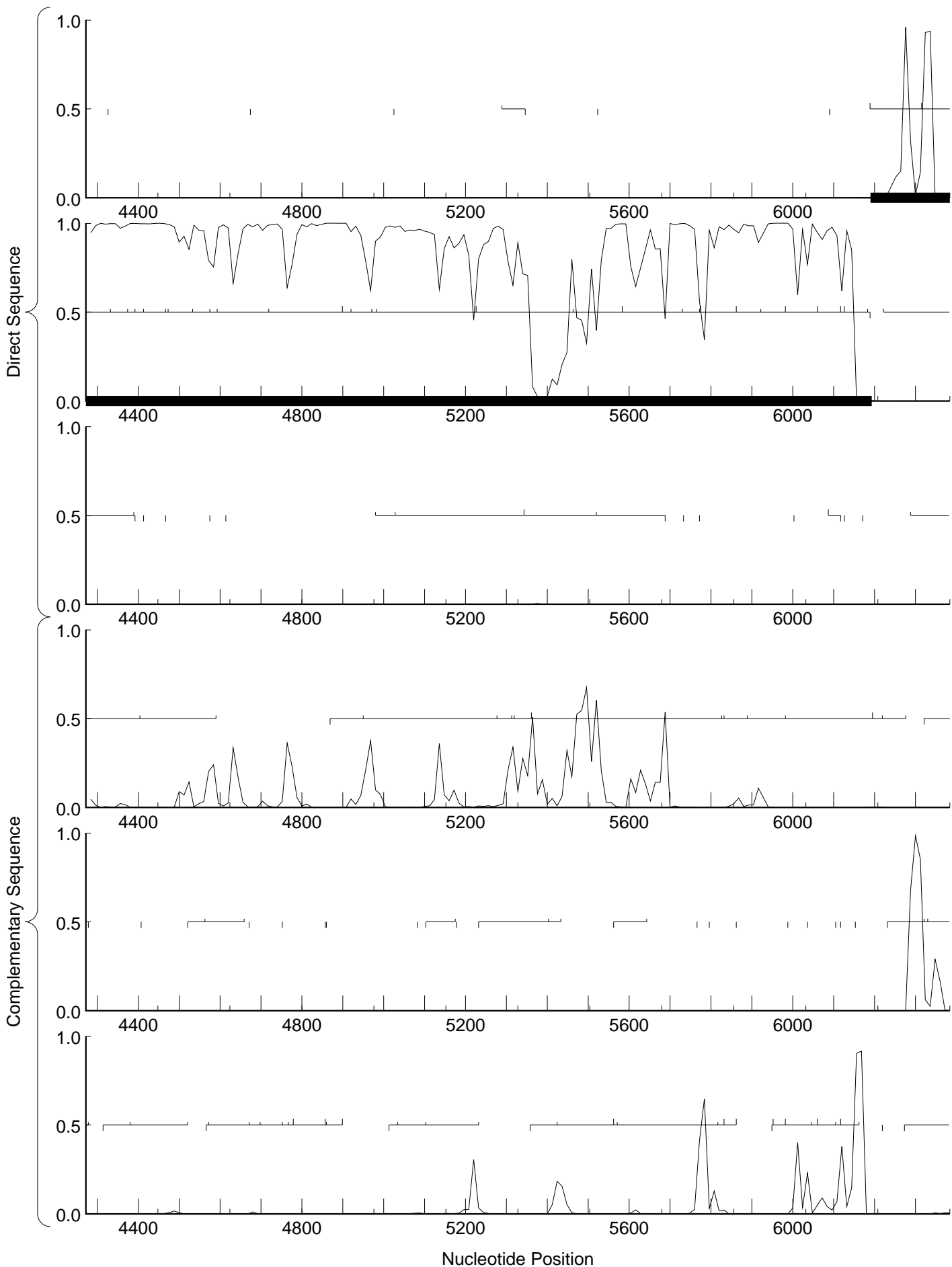
MATRIX INFORMATION

Matrix : Heuristic, GC = 67
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

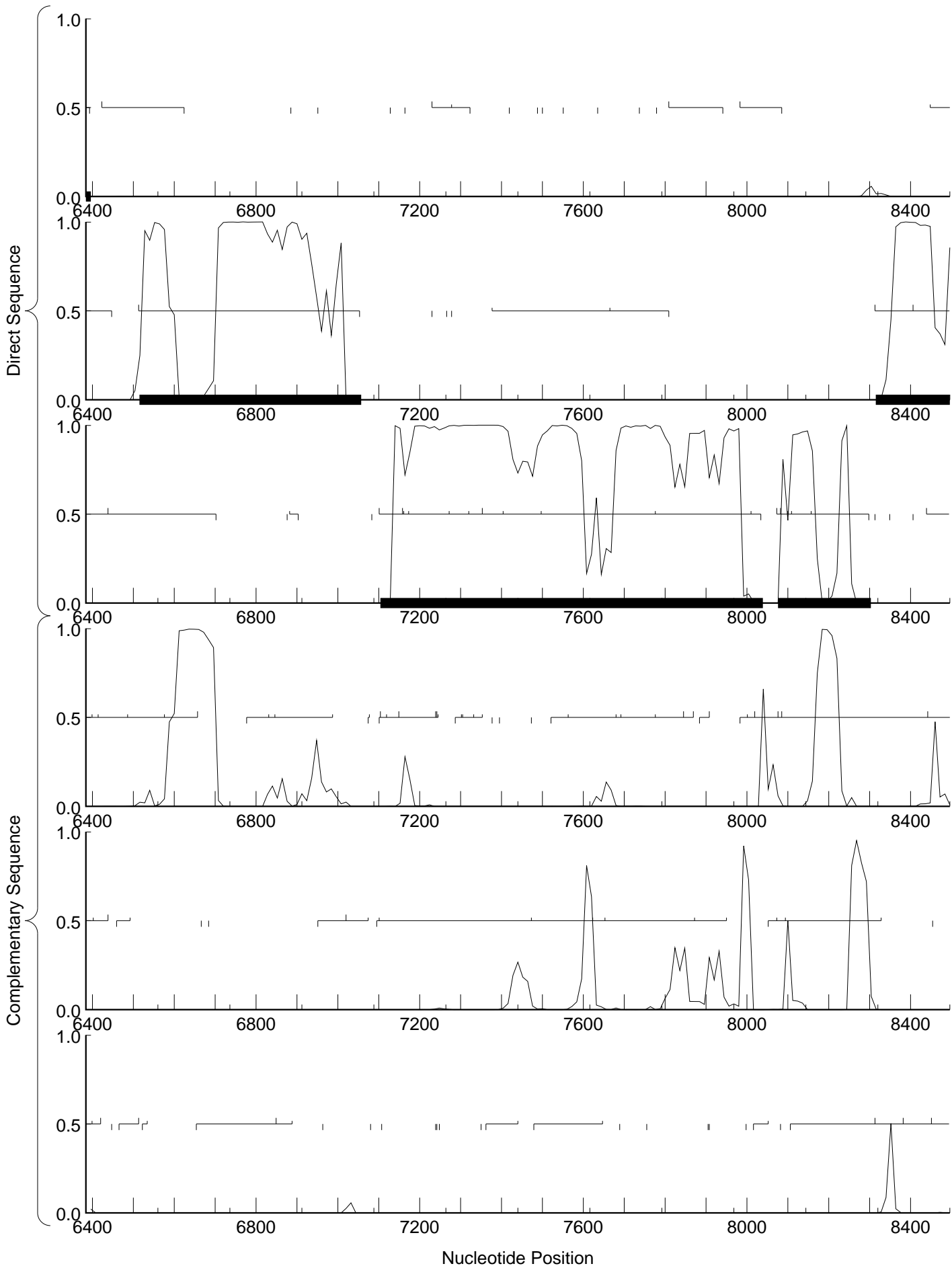


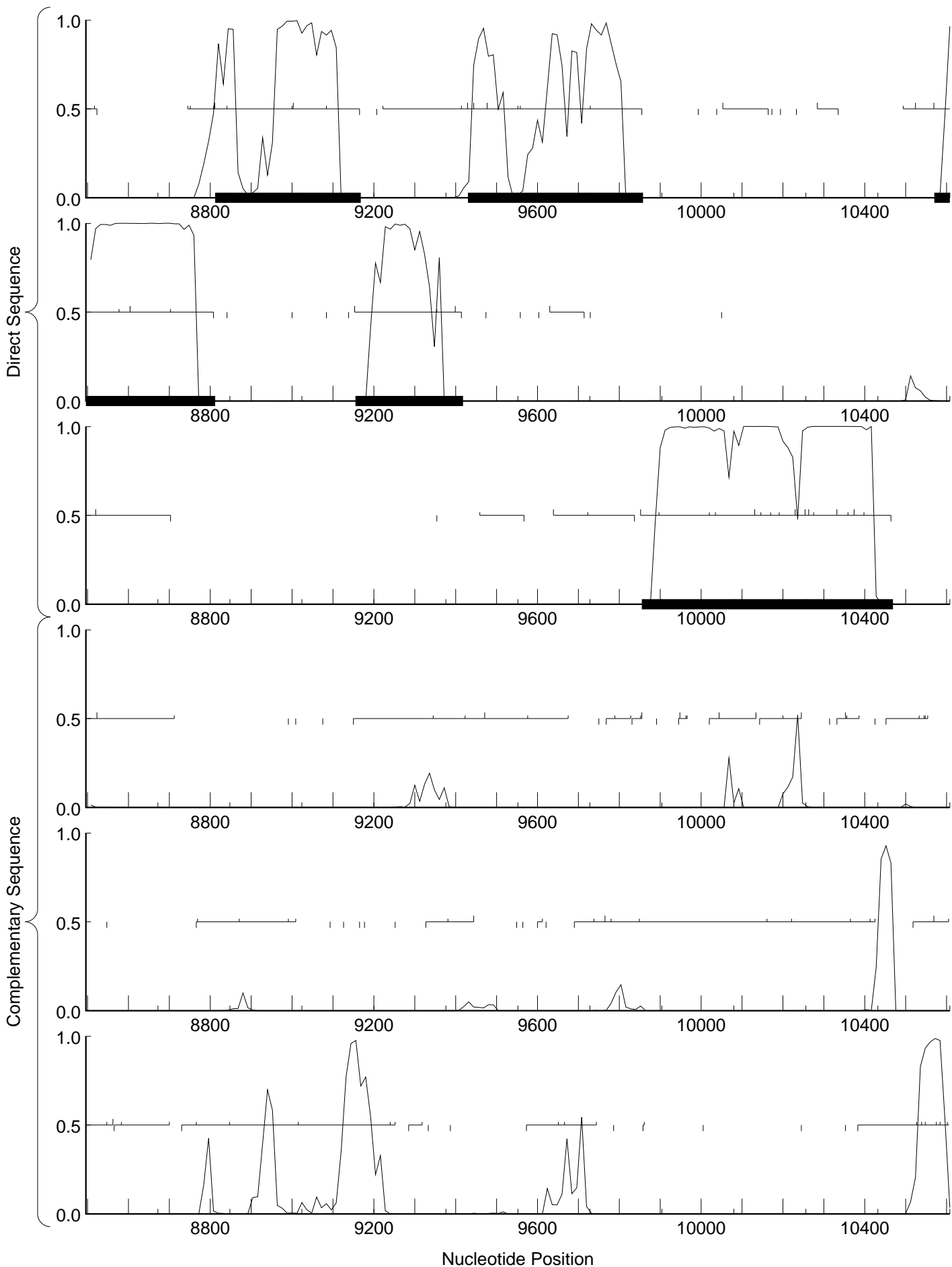




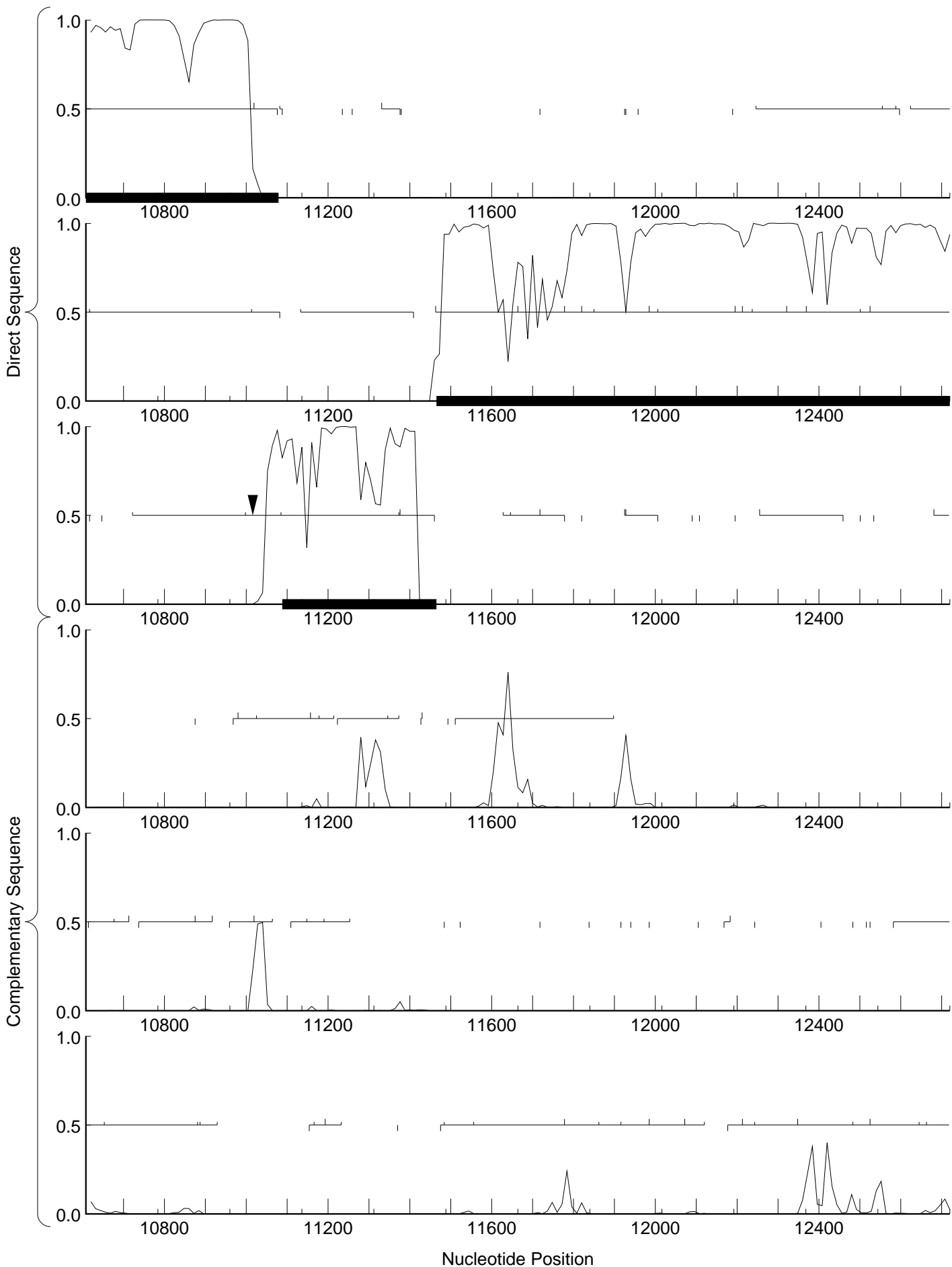
██████████

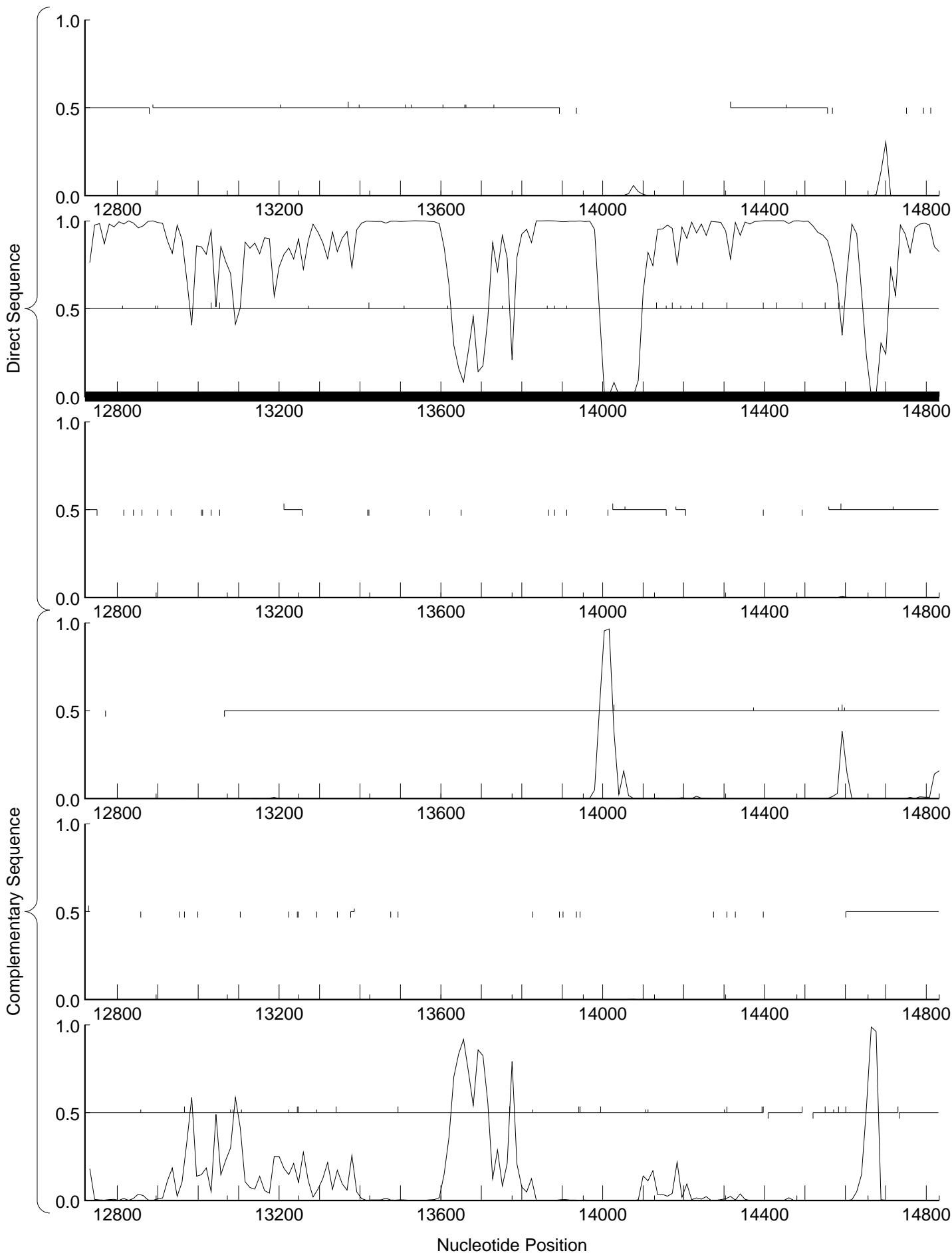
GeneMark.hmm prediction





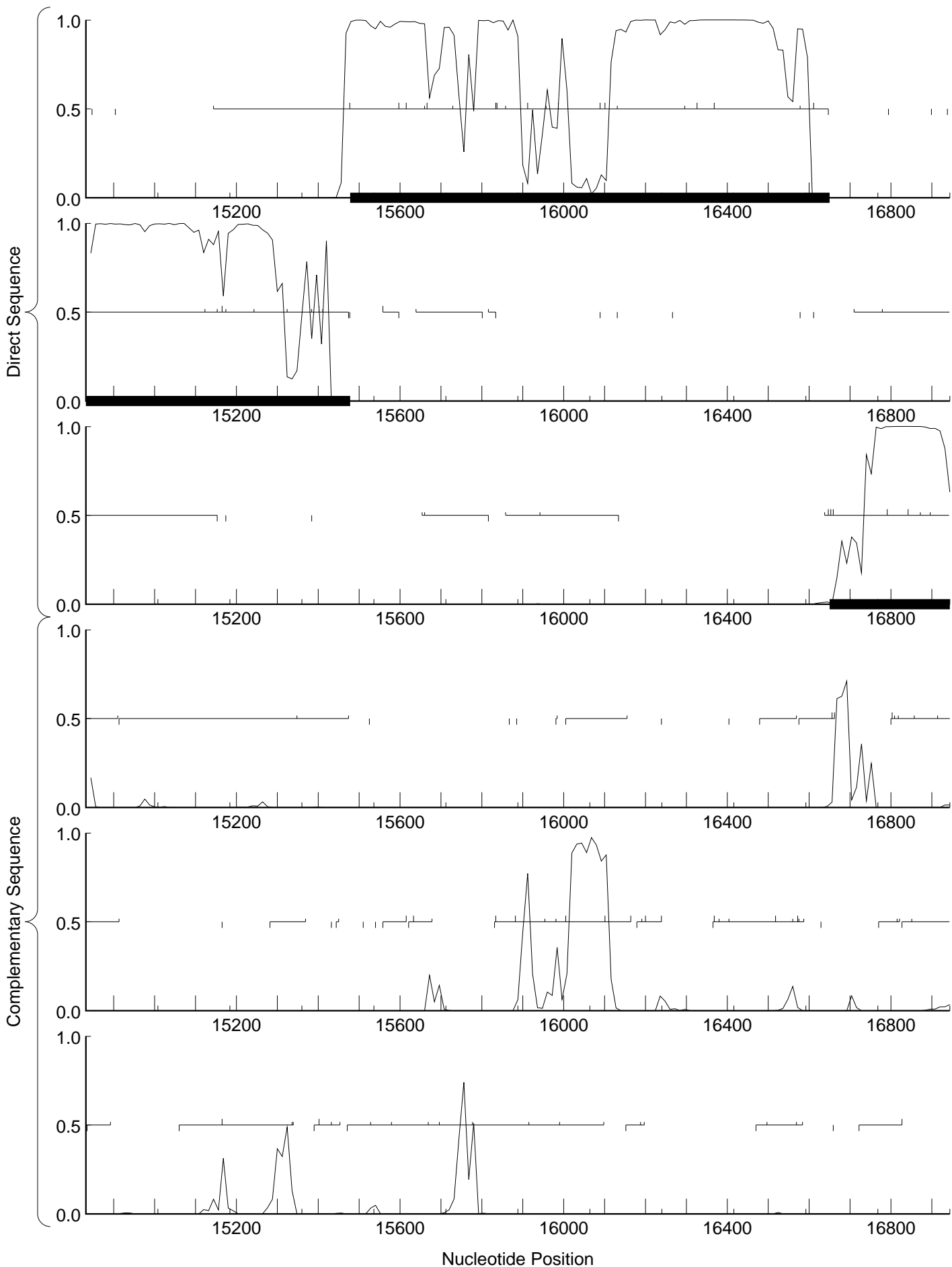
GeneMark.hmm prediction



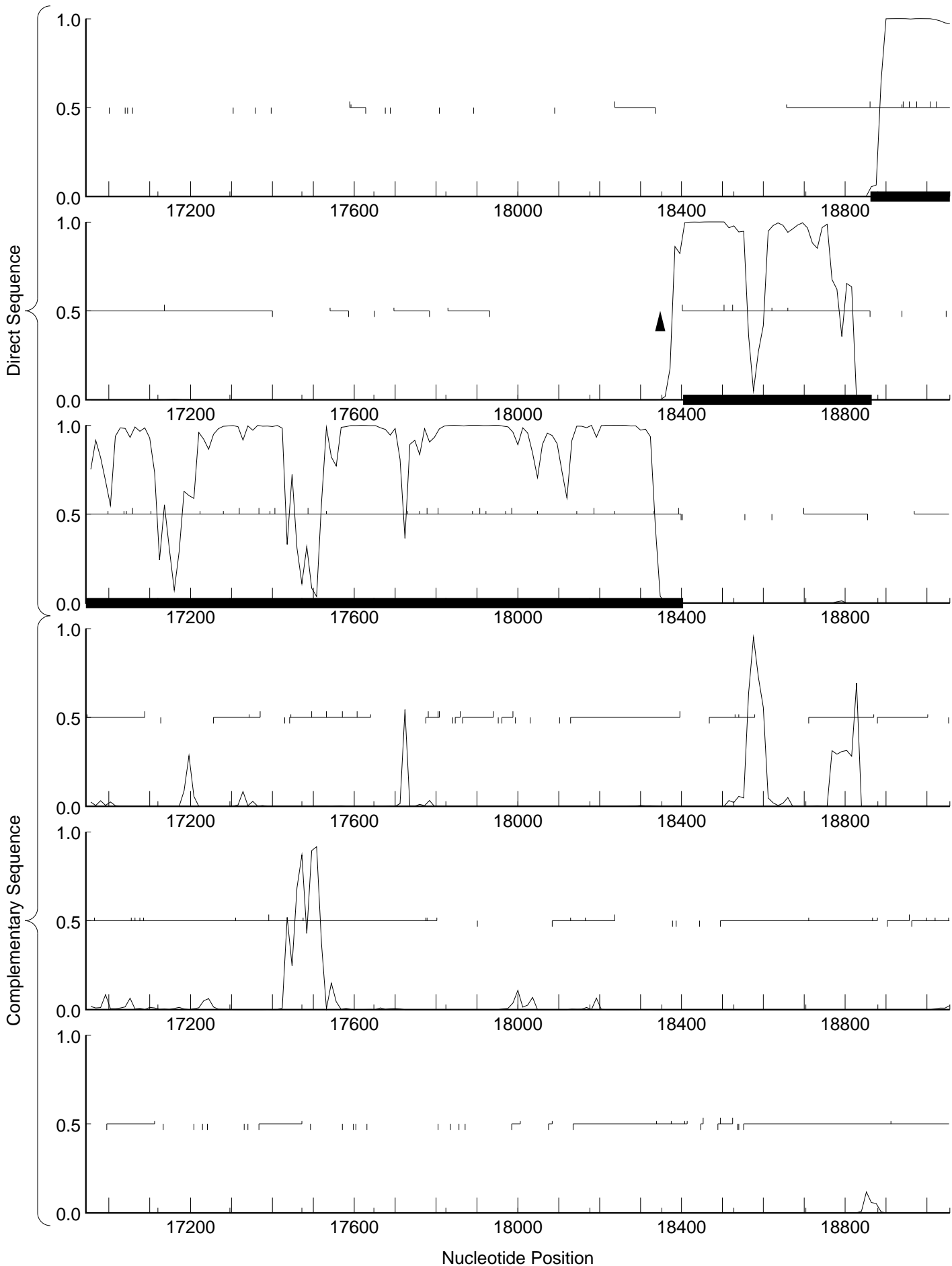


██████████

GeneMark.hmm prediction

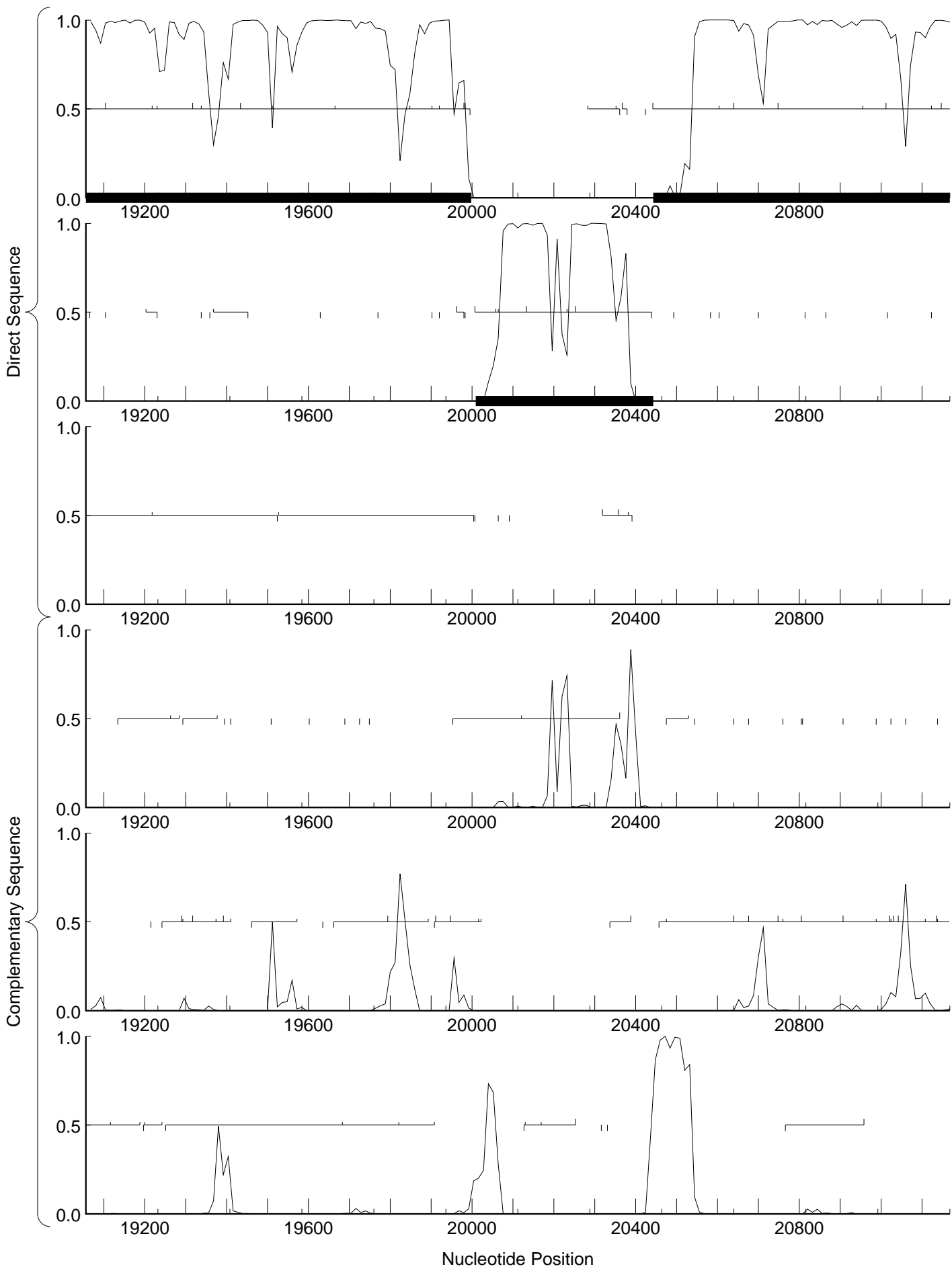


GeneMark.hmm prediction



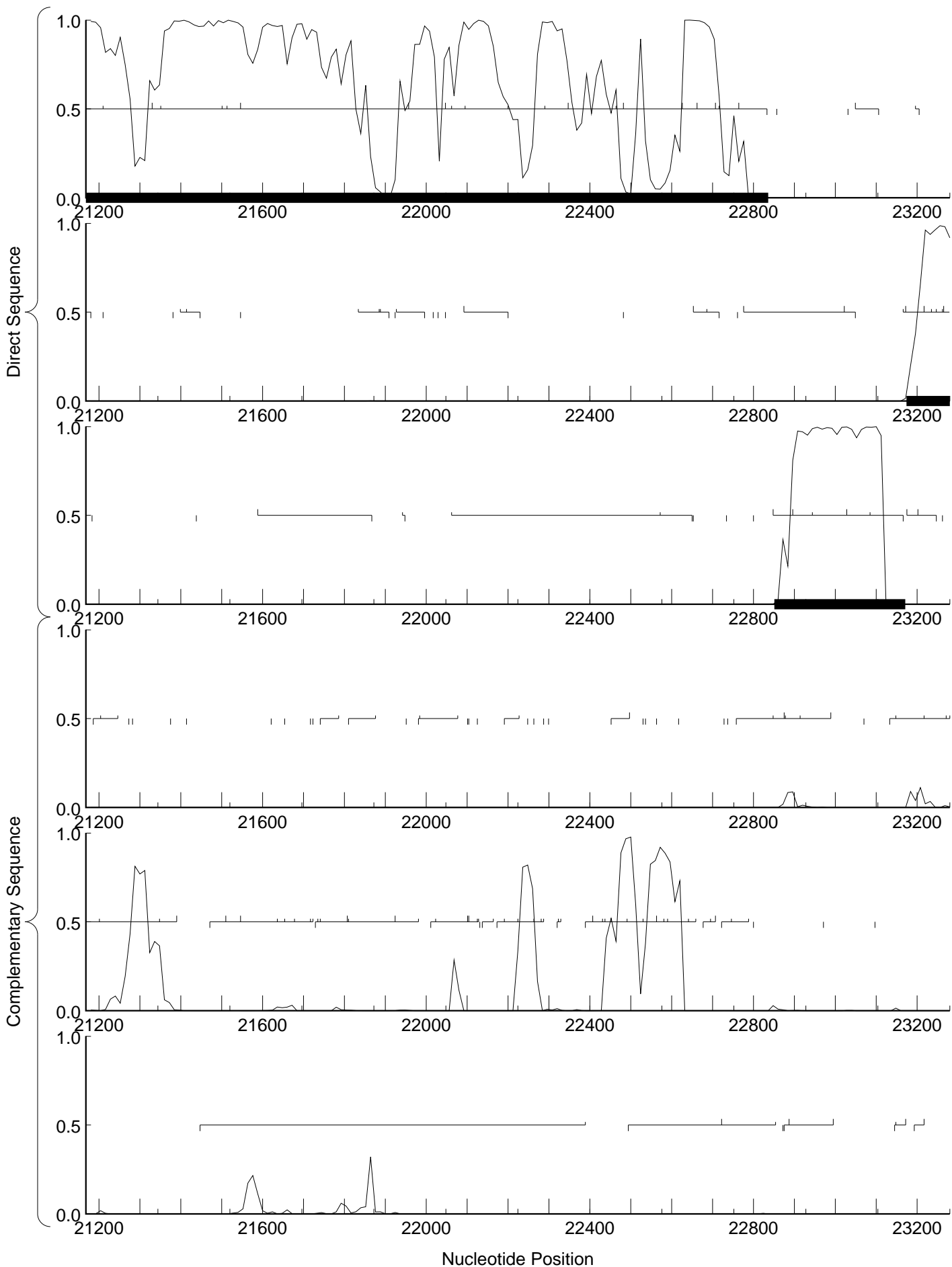
██████████

GeneMark.hmm prediction

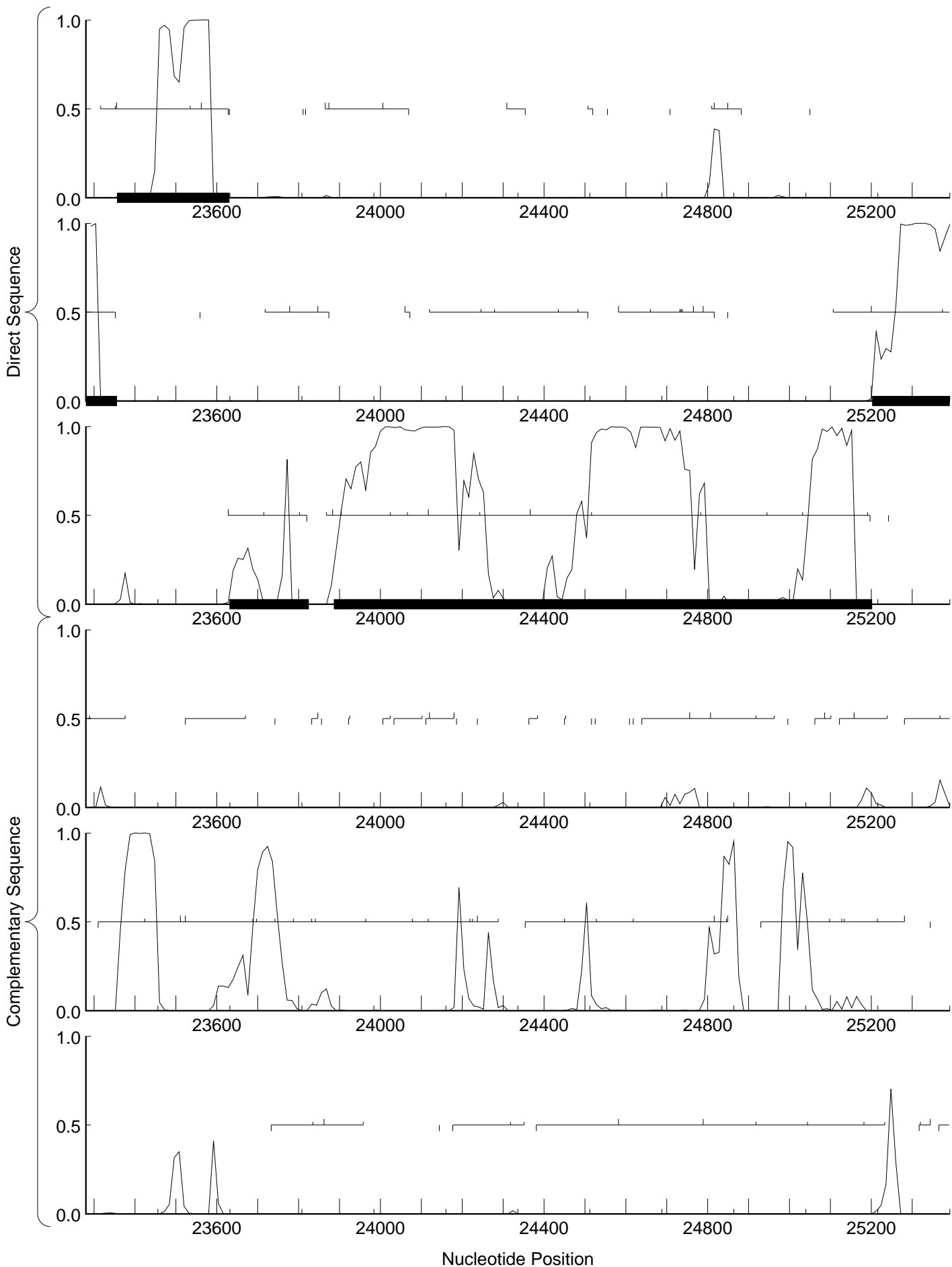


complete sequence, 41902 bp including 11-base 3' overhang (CCCCATGGCAT), Cluster G1, Order 2, Window 96, Step 12, 12/21

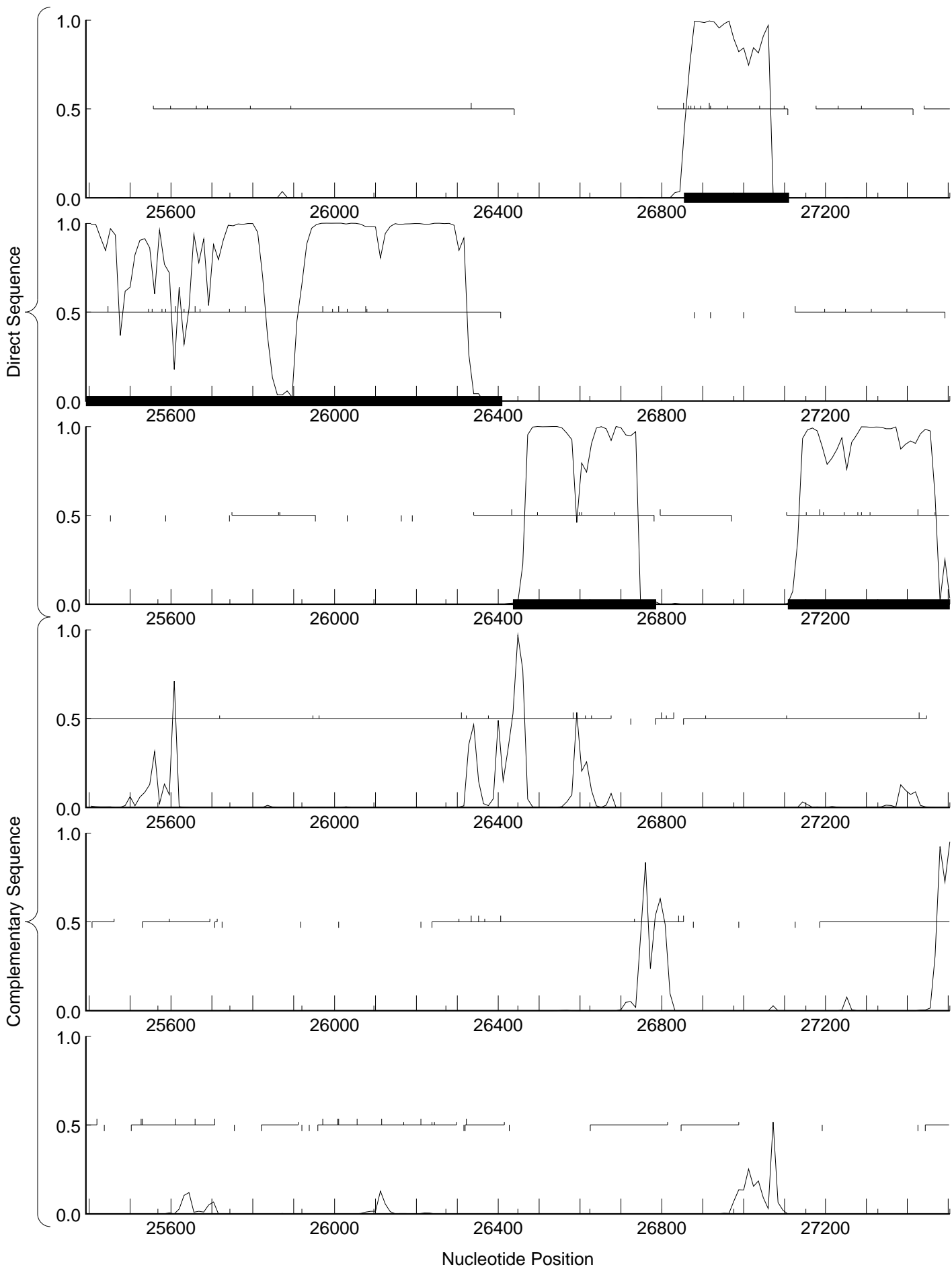
GeneMark.hmm prediction



GeneMark.hmm prediction

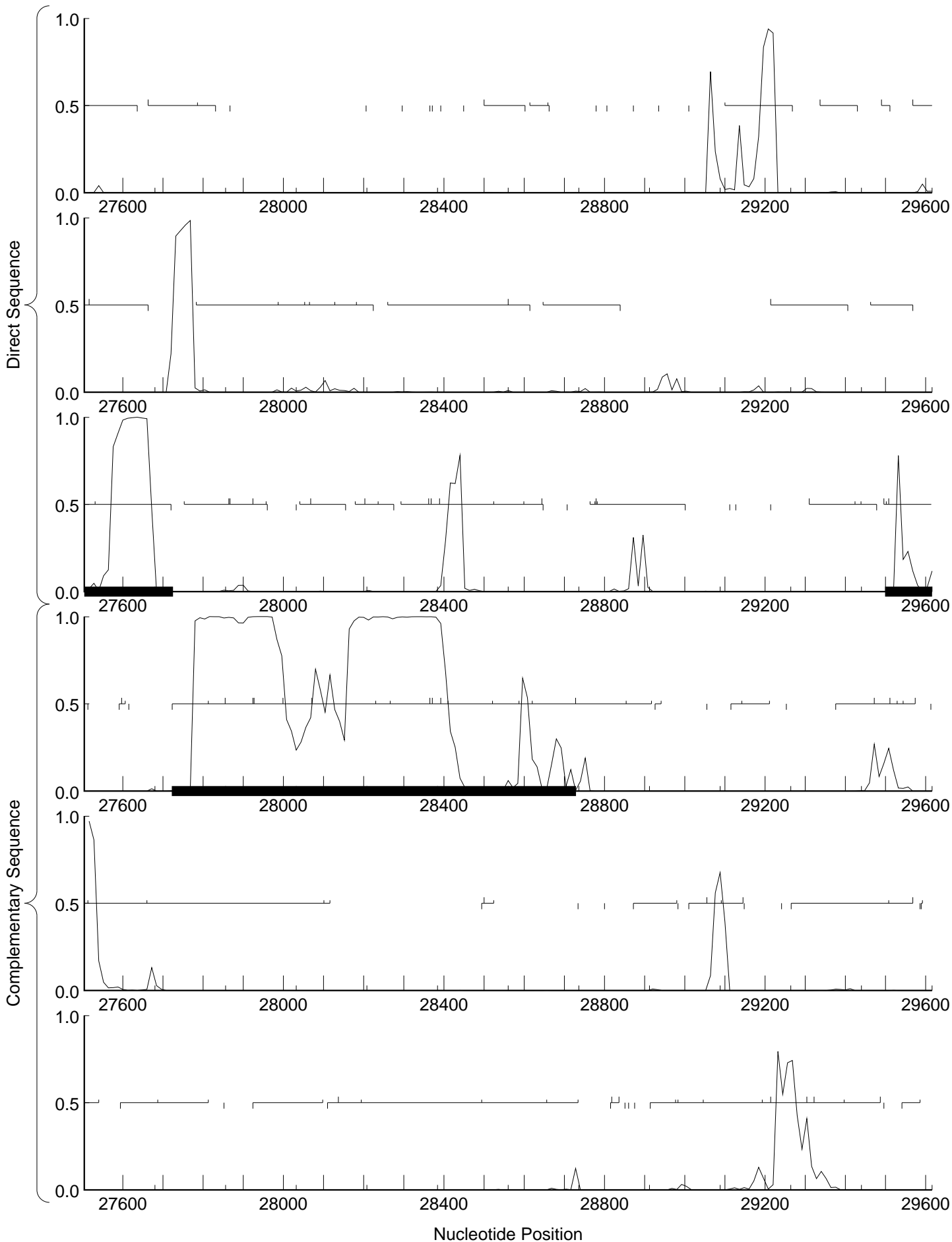


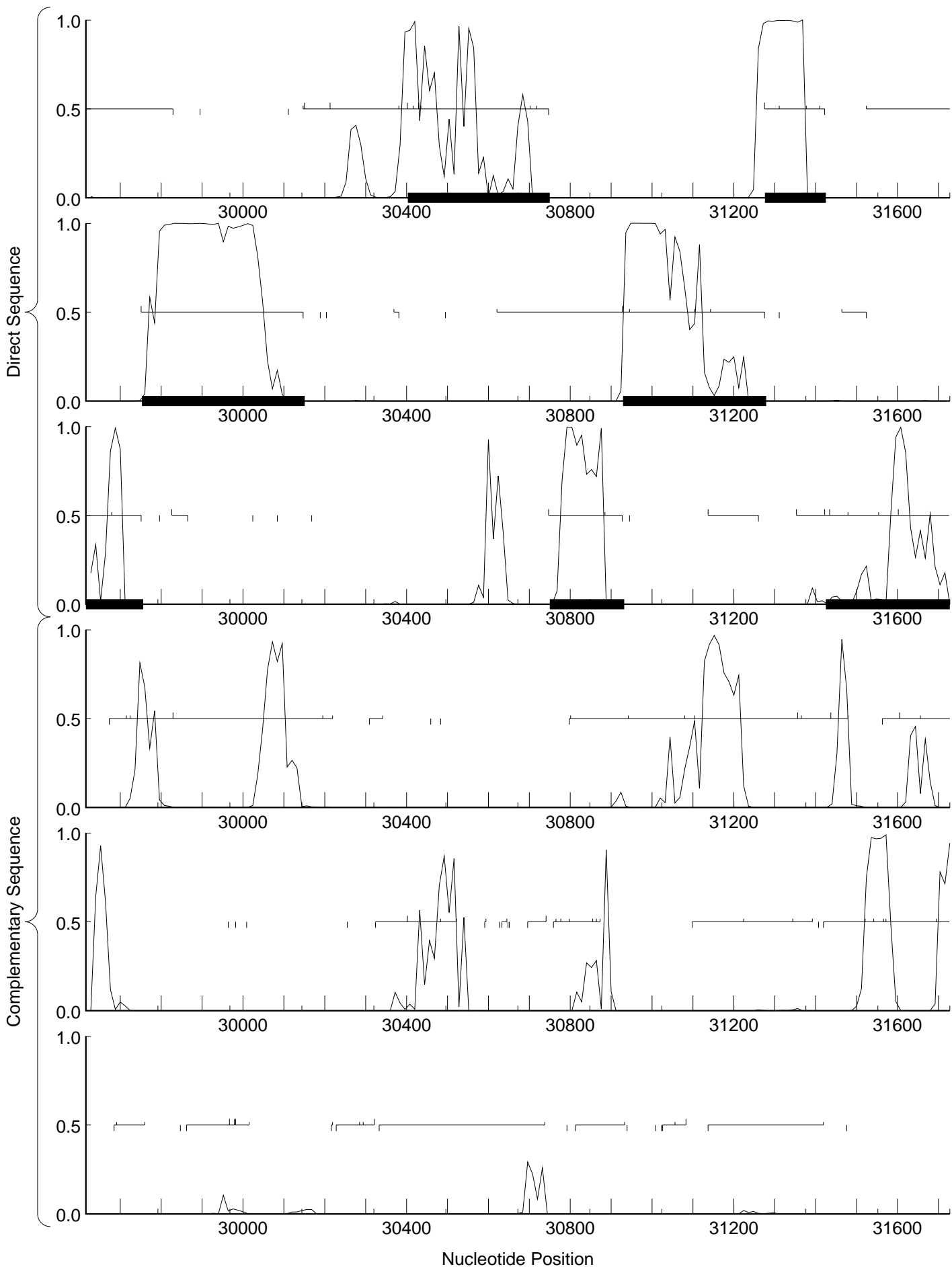
GeneMark.hmm prediction



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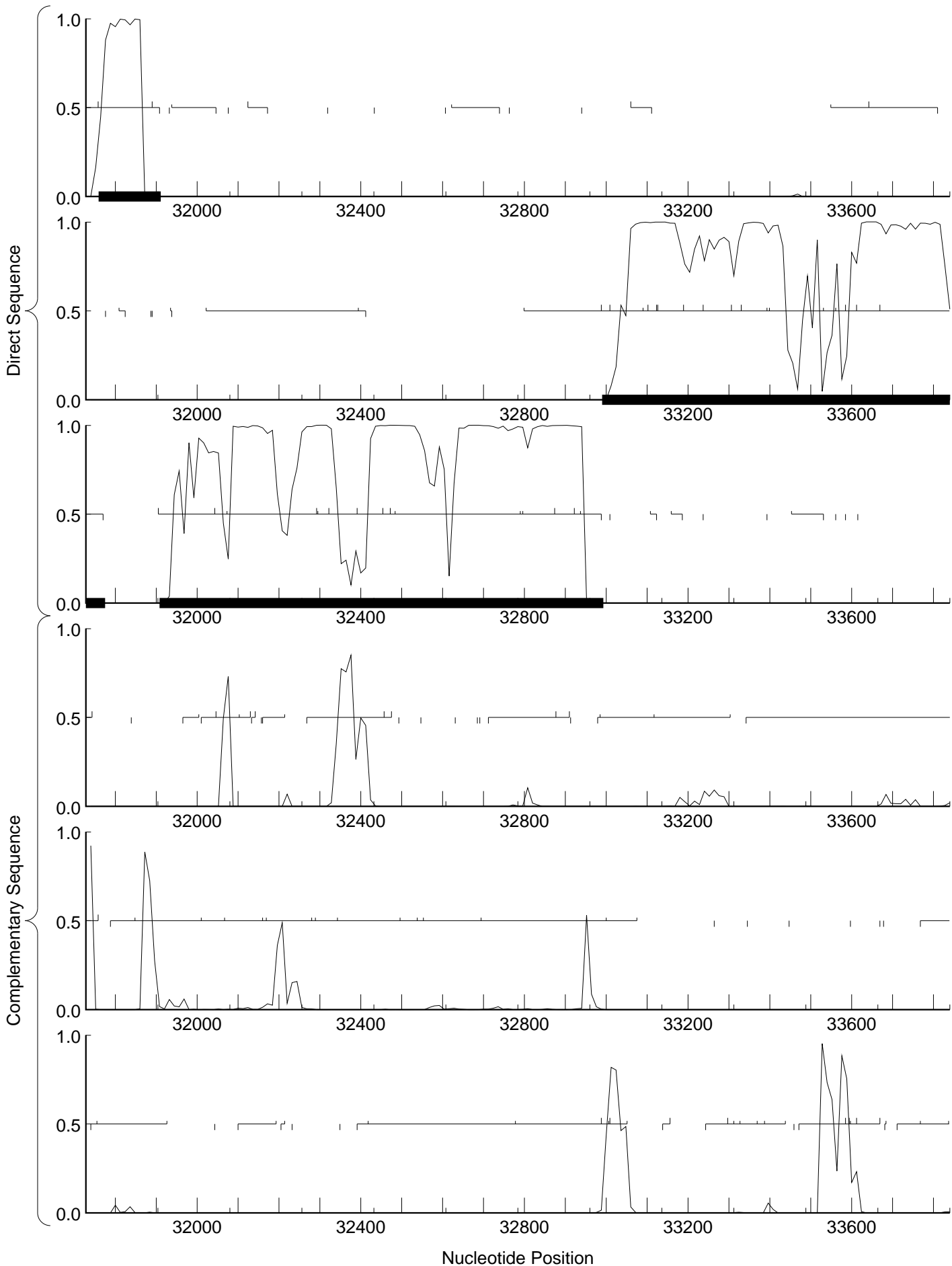
GeneMark.hmm prediction





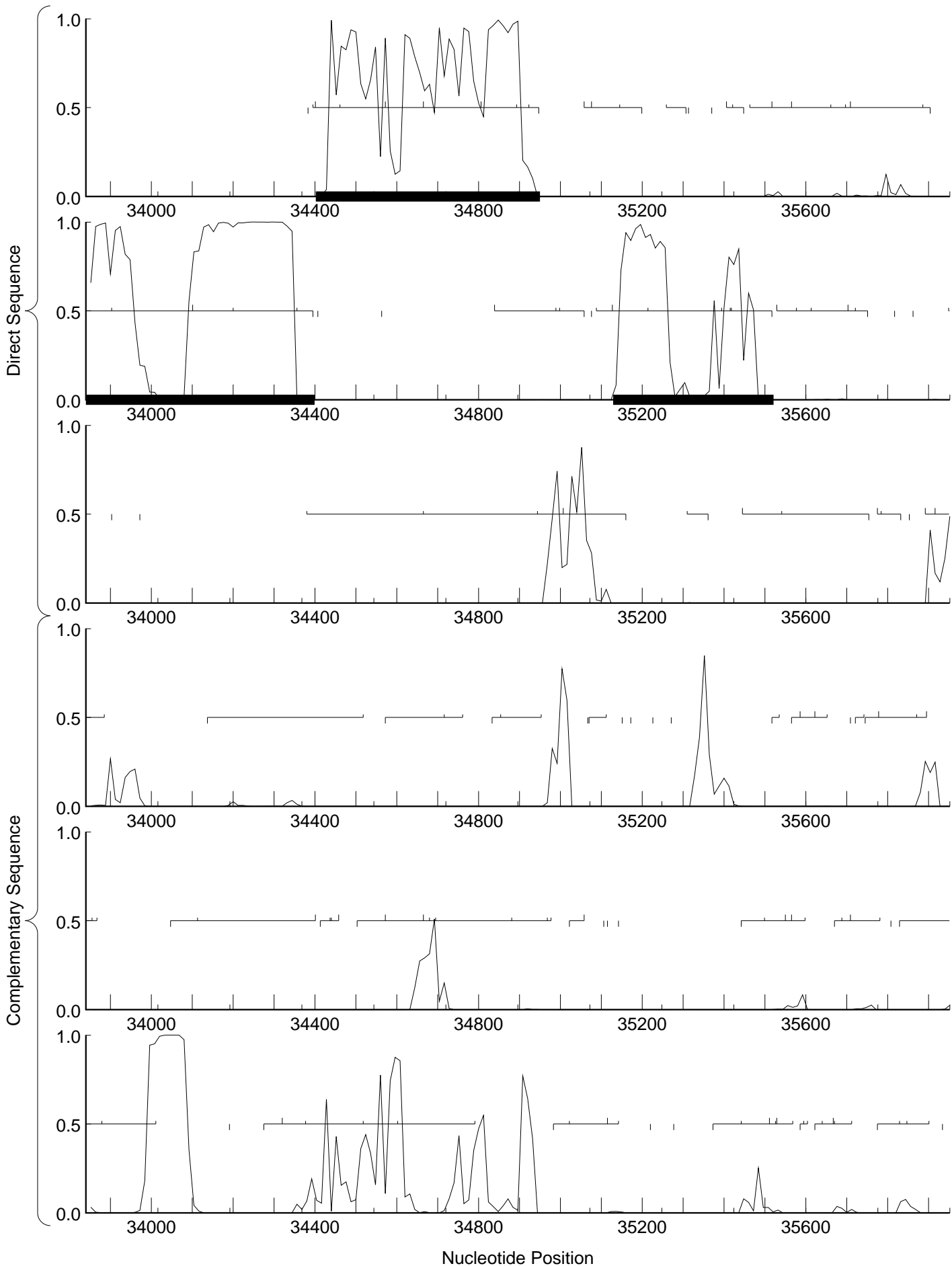
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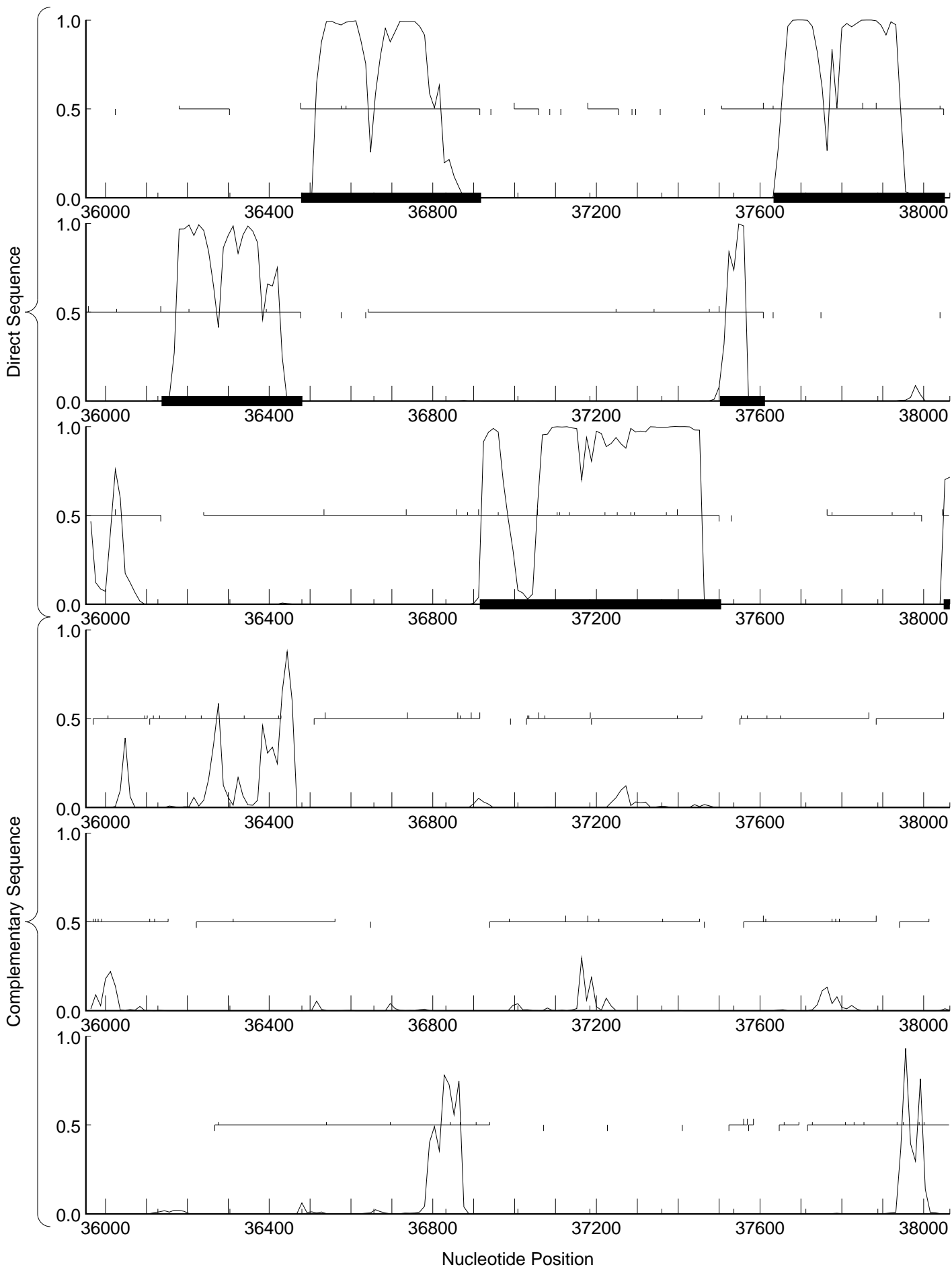
GeneMark.hmm prediction

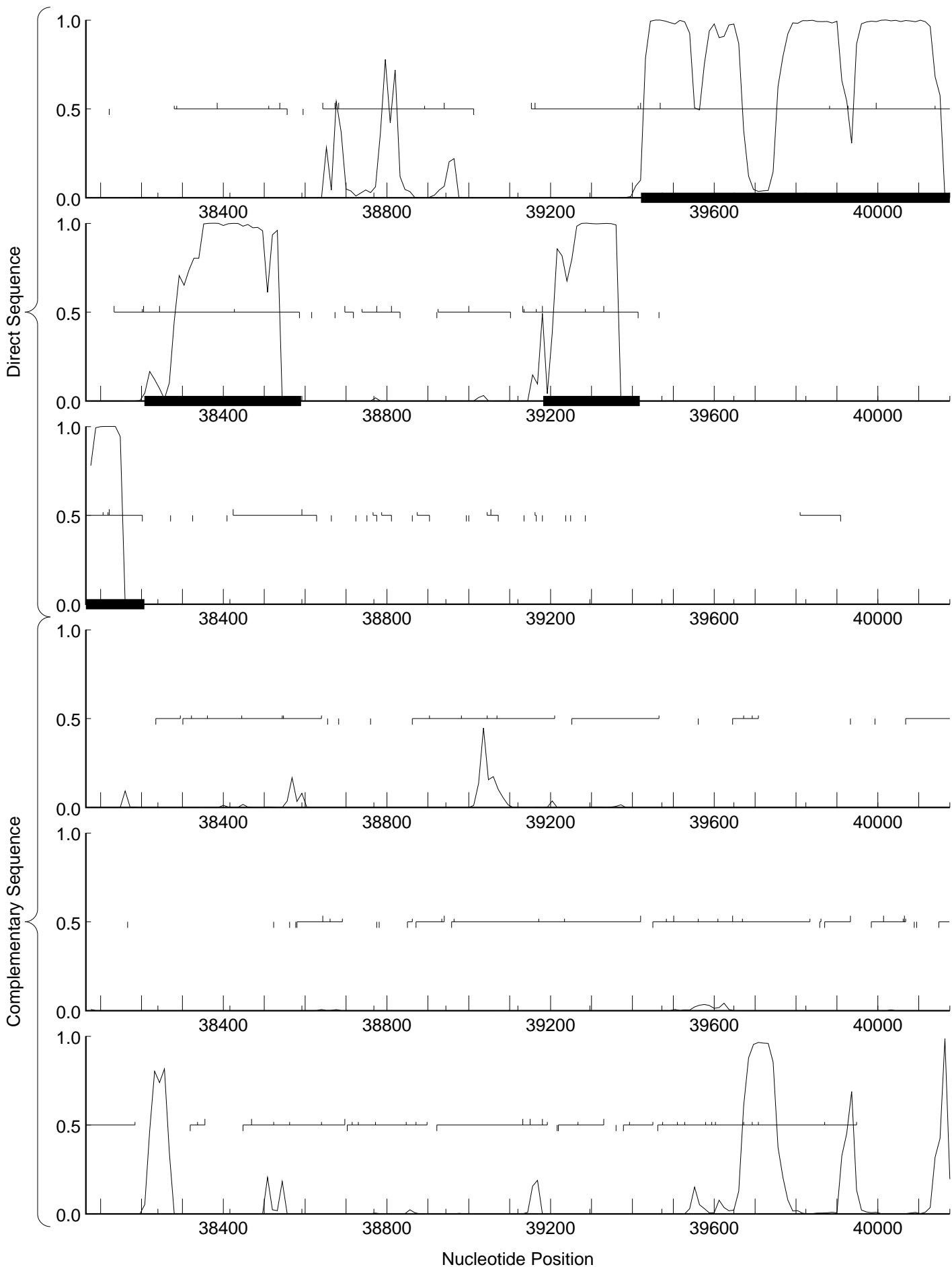


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GeneMark.hmm prediction







GeneMark.hmm prediction

