

GeneMark

Version 2.5p (09.08.06)

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PROGRAM INFORMATION

Sequence : Rhodococcus phage Shuman complete sequence, 46544 bp including 10-base 3' overhang (CGGCCGT
Analysis Date : 4/20/18 at 1:00:33
Pages : 24
Sequence Length : 46544 bp
GC Content : 58.65%

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,

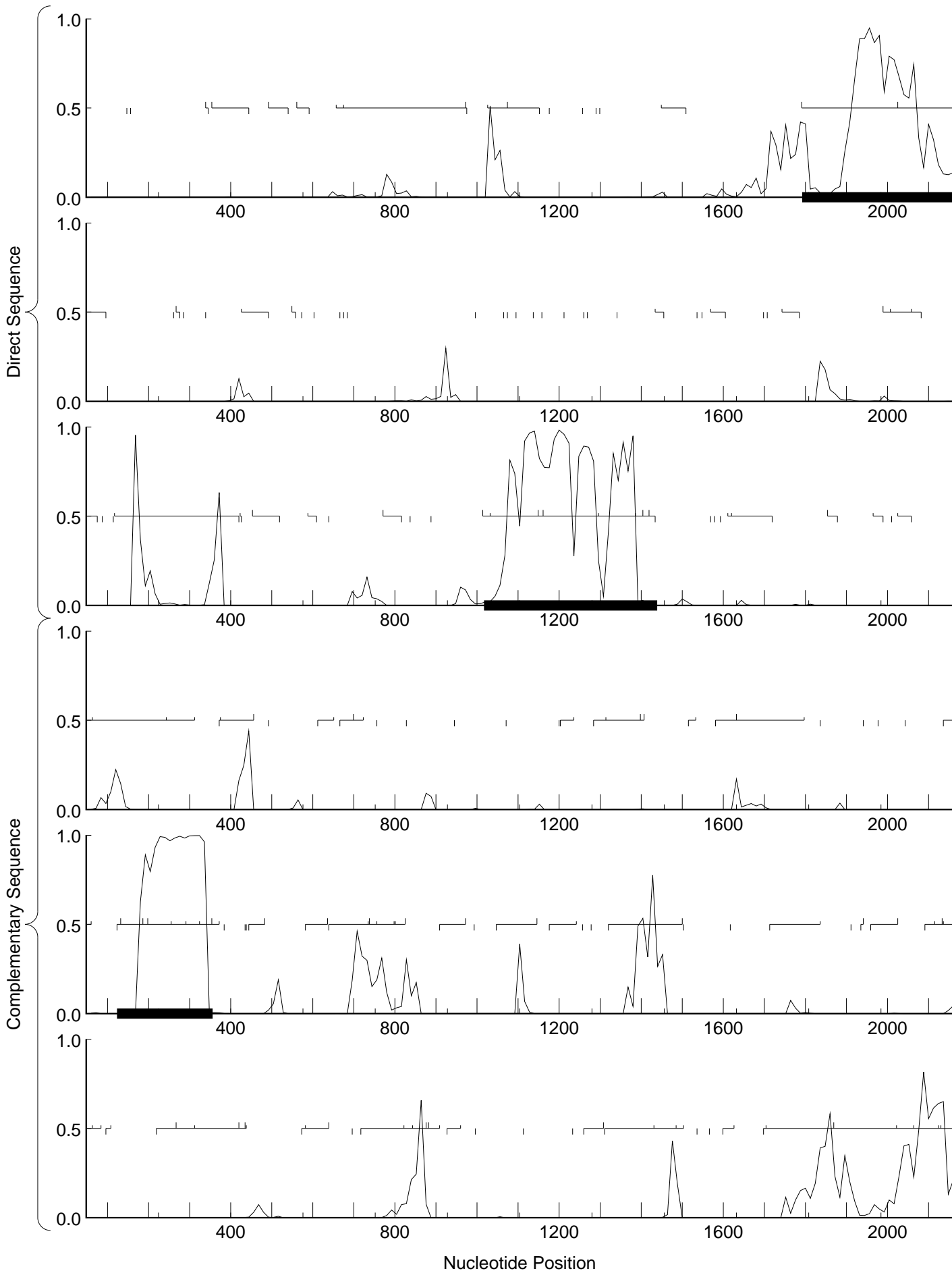
Matrix notes & comments

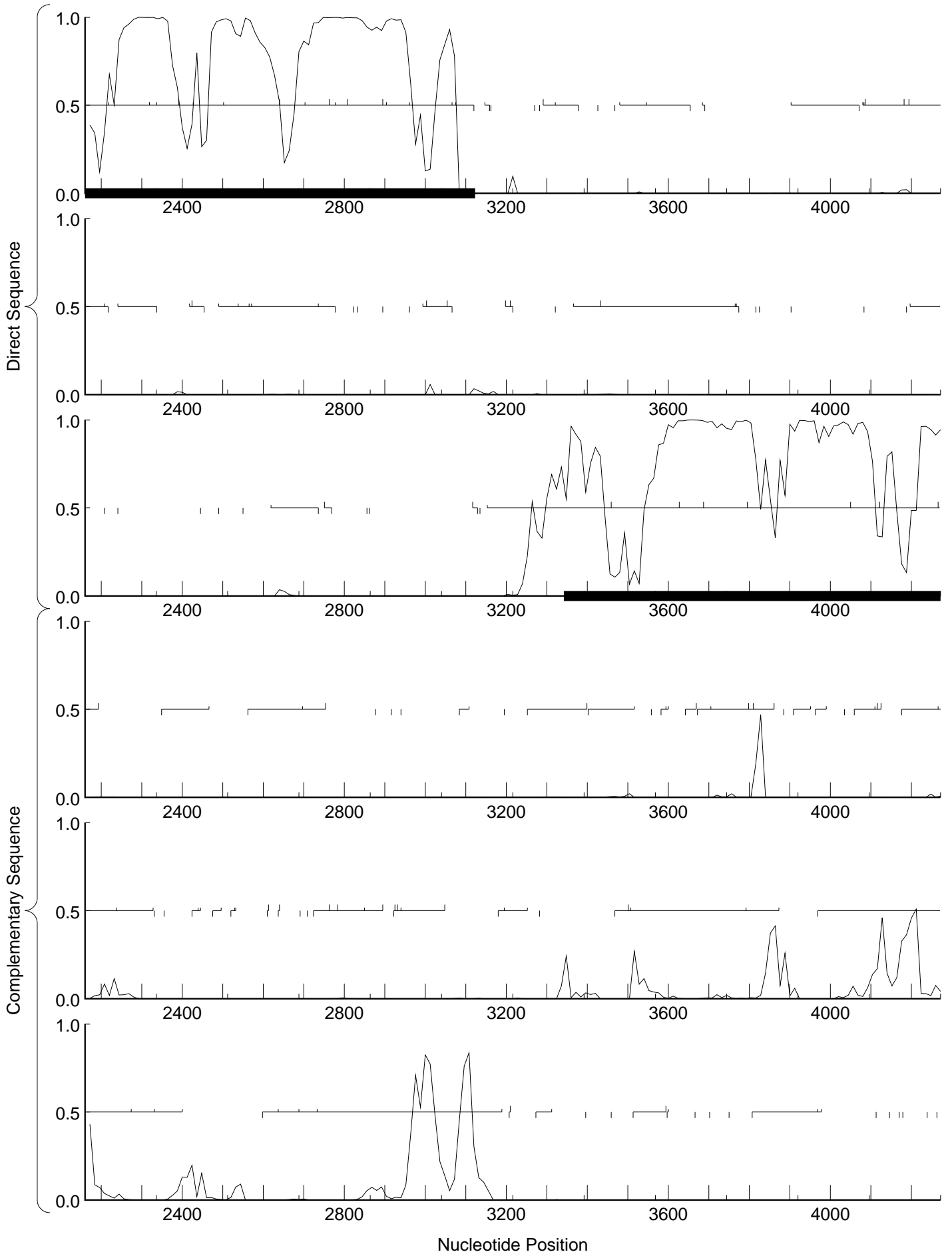
For details on the model building procedure see:
Besemer J. and Borodovsky M.
"Heuristic approach to deriving models for gene finding"
NAR, 1999, Vol. 27, No. 19, pp. 3911-3920

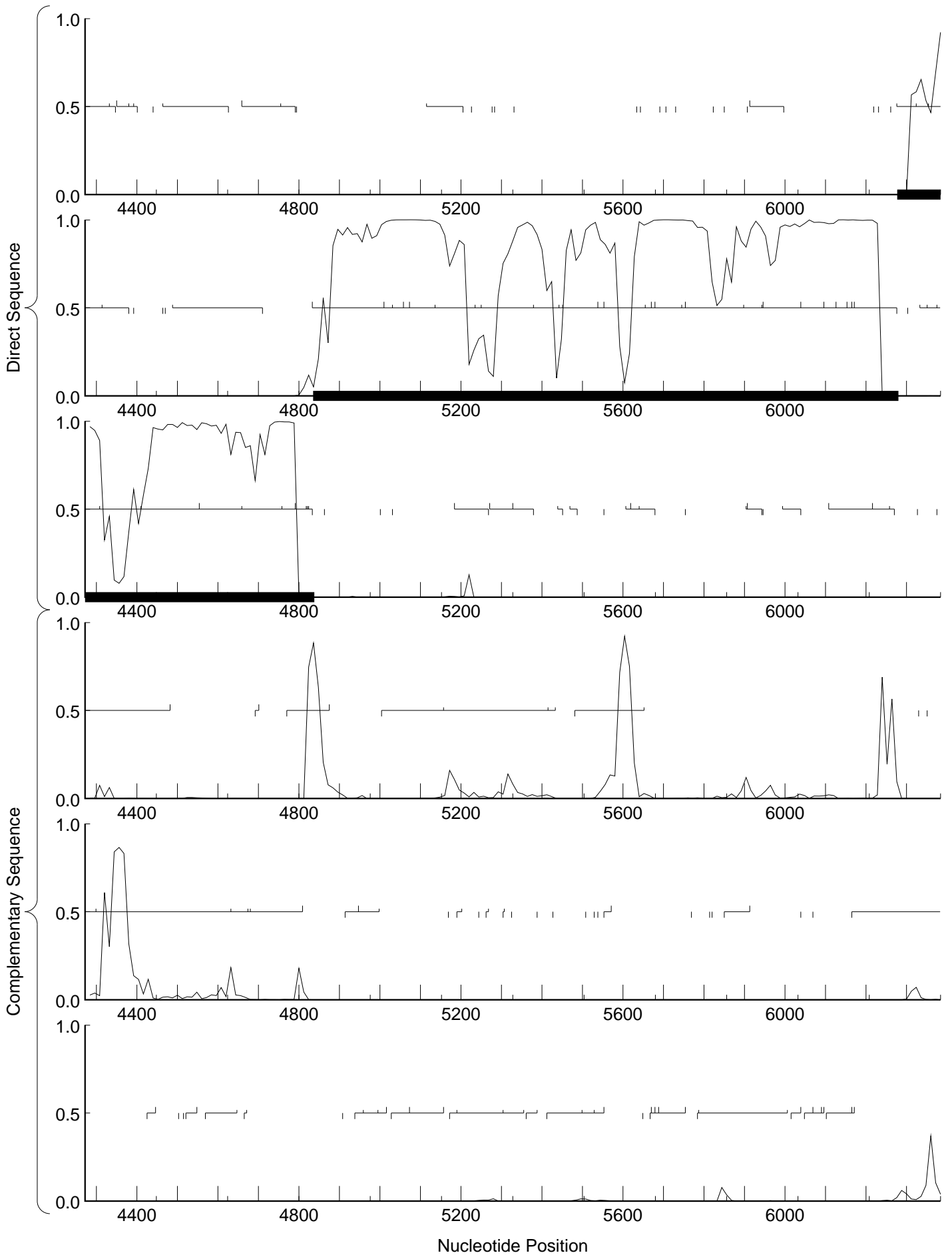
MATRIX INFORMATION

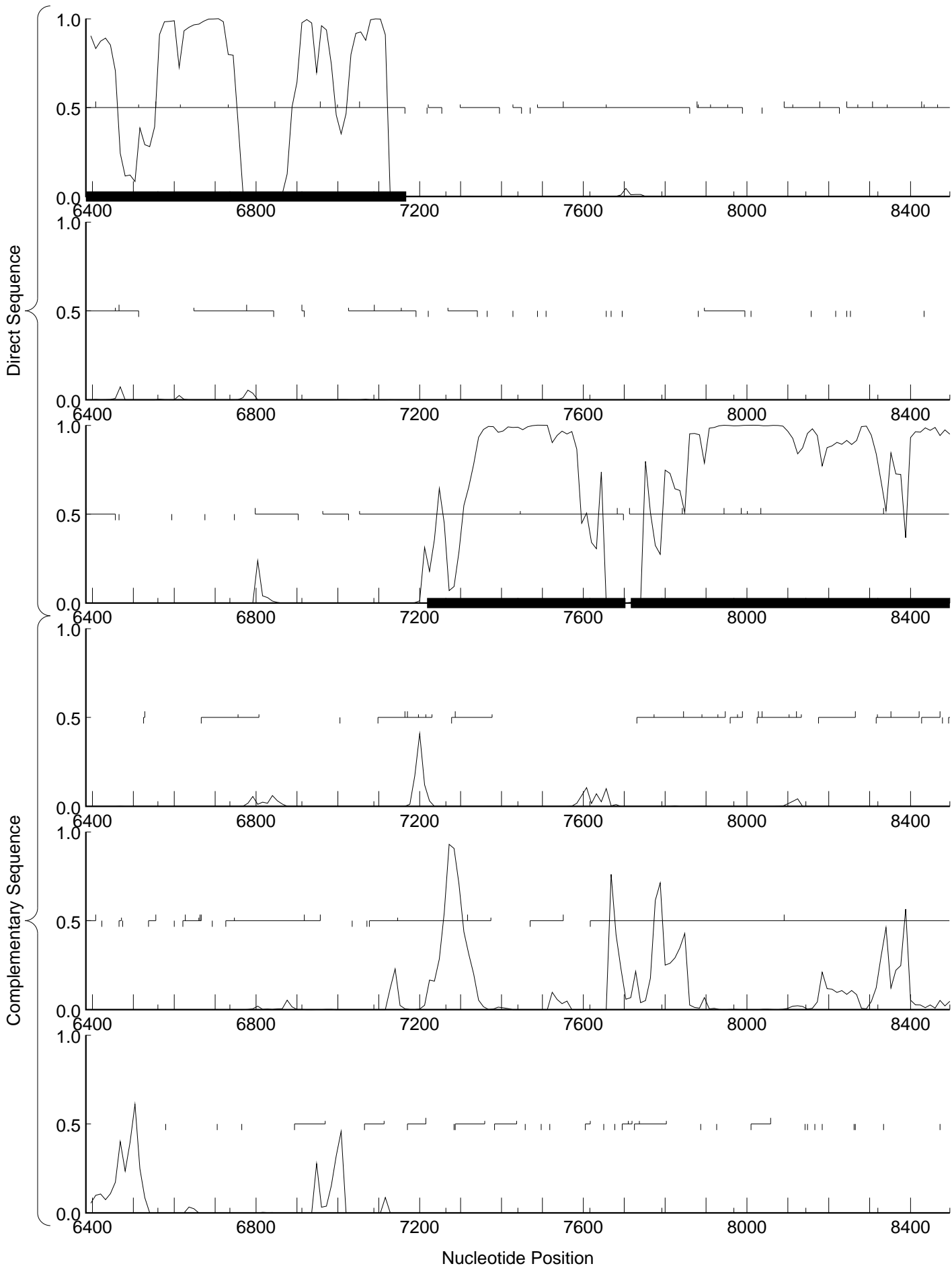
Matrix : Heuristic, GC = 59
Author : Borodovsky Laboratory - Georgia Tech
Order : 2

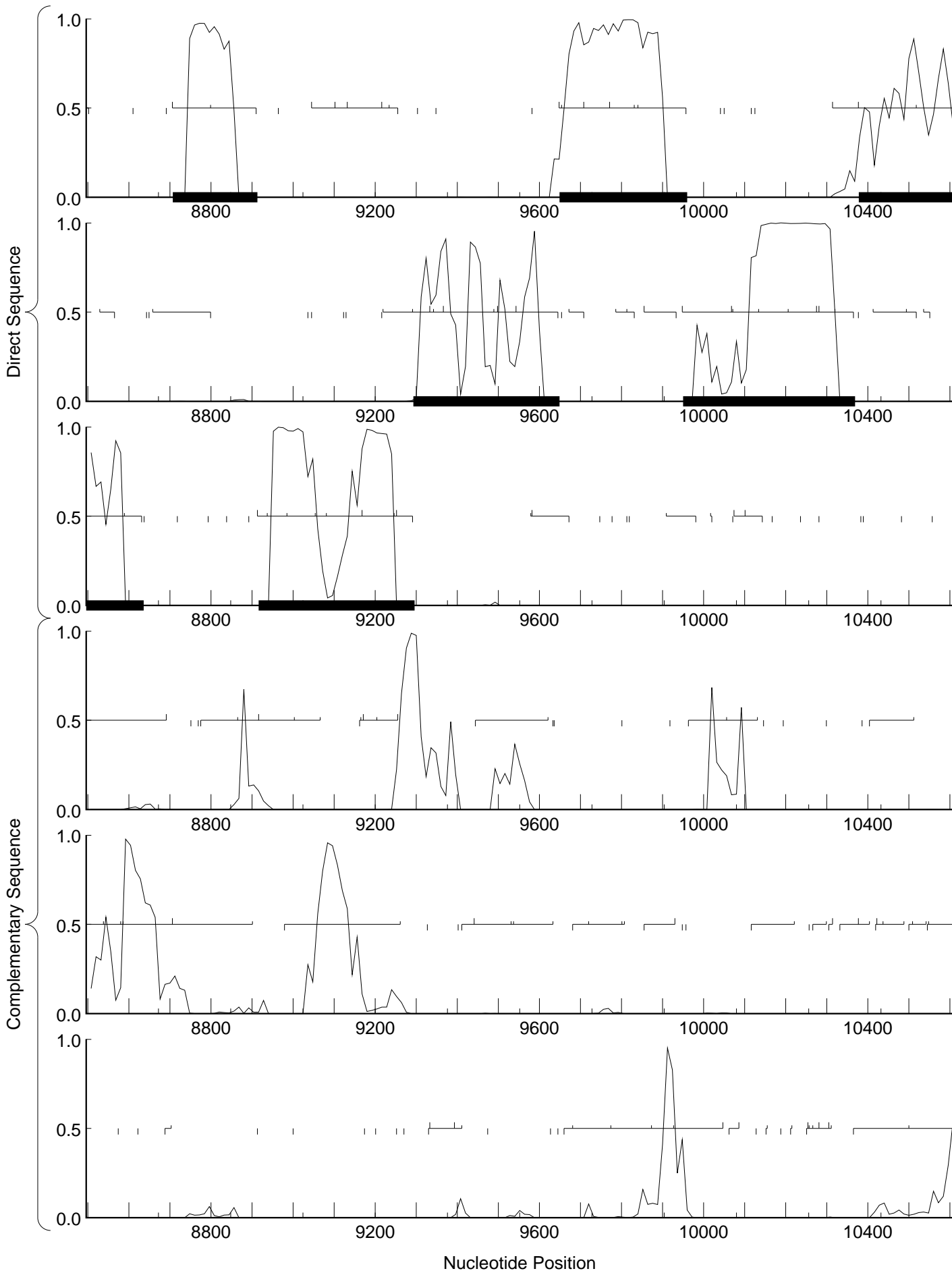
Send questions / comments to:
Dr. M. Borodovsky
Georgia Institute of Technology
School of Biology
Atlanta, GA 30332-0230

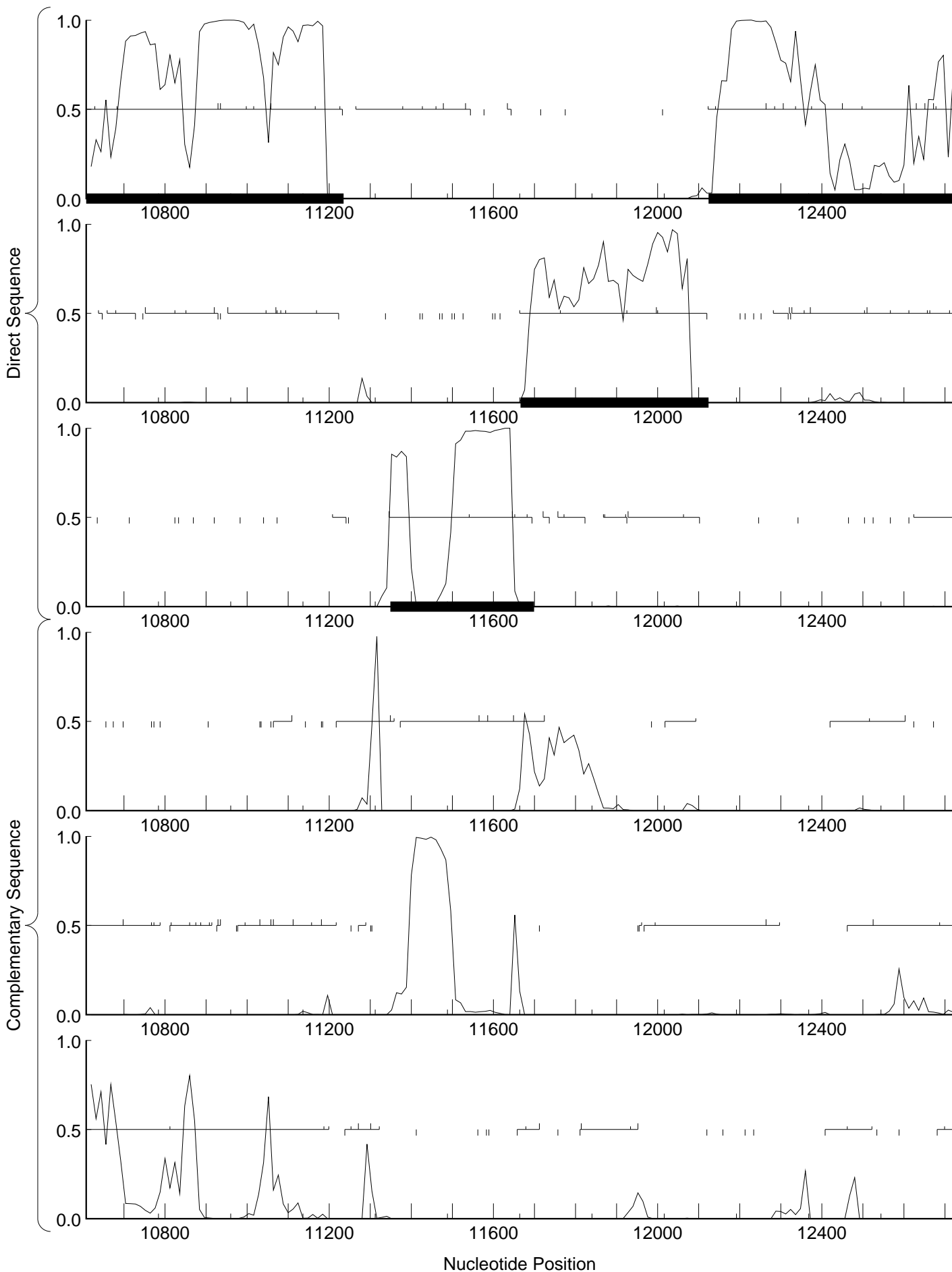


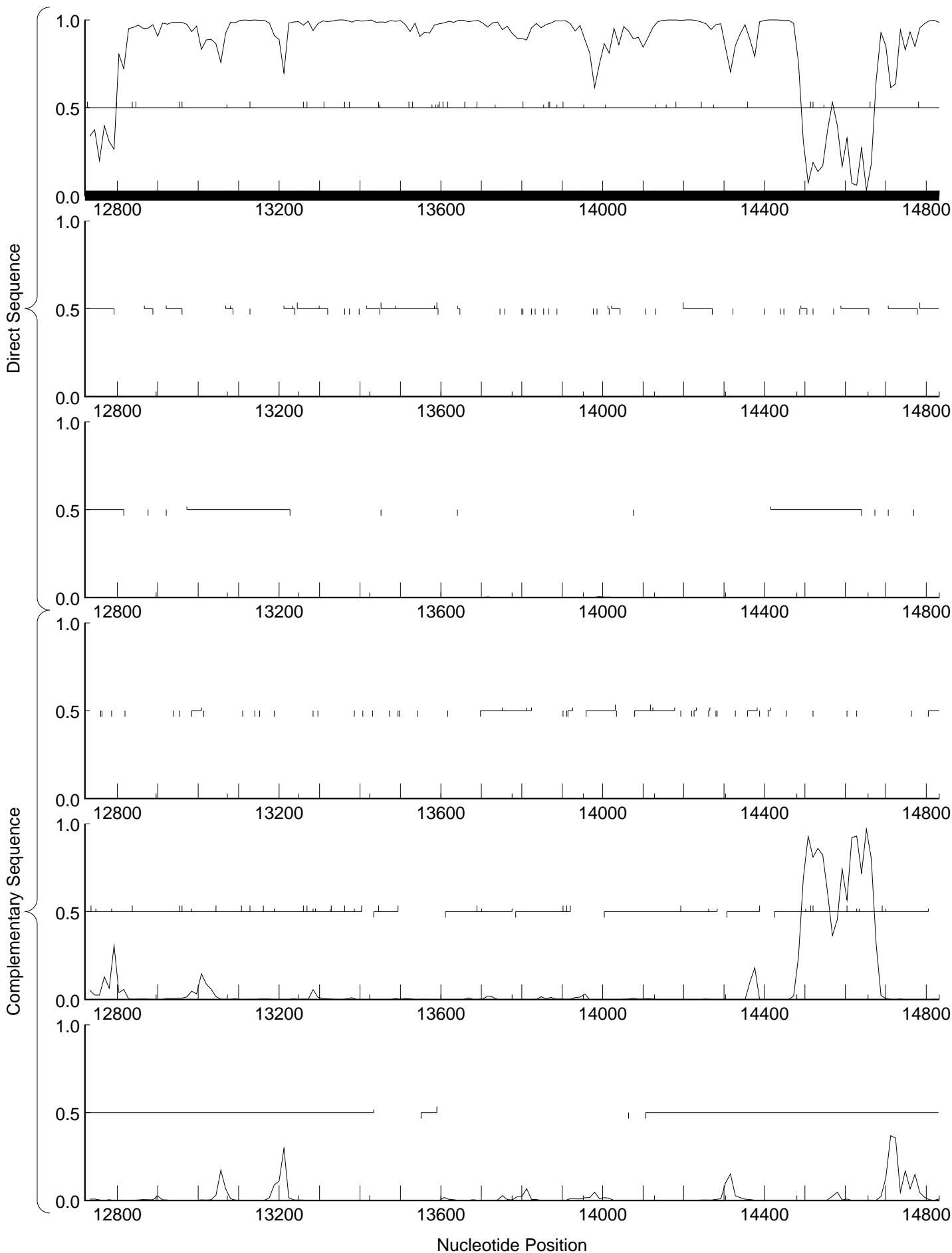


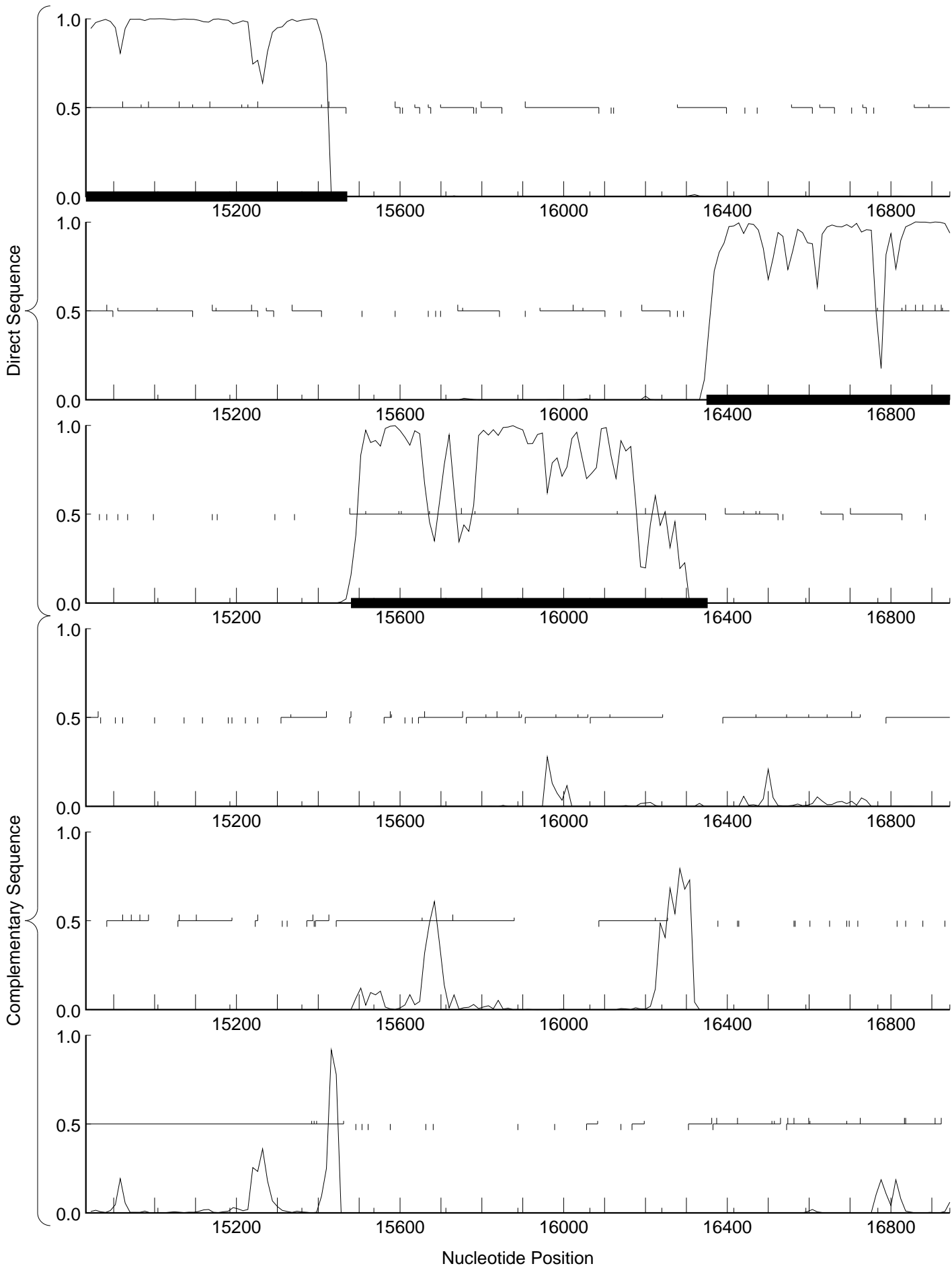




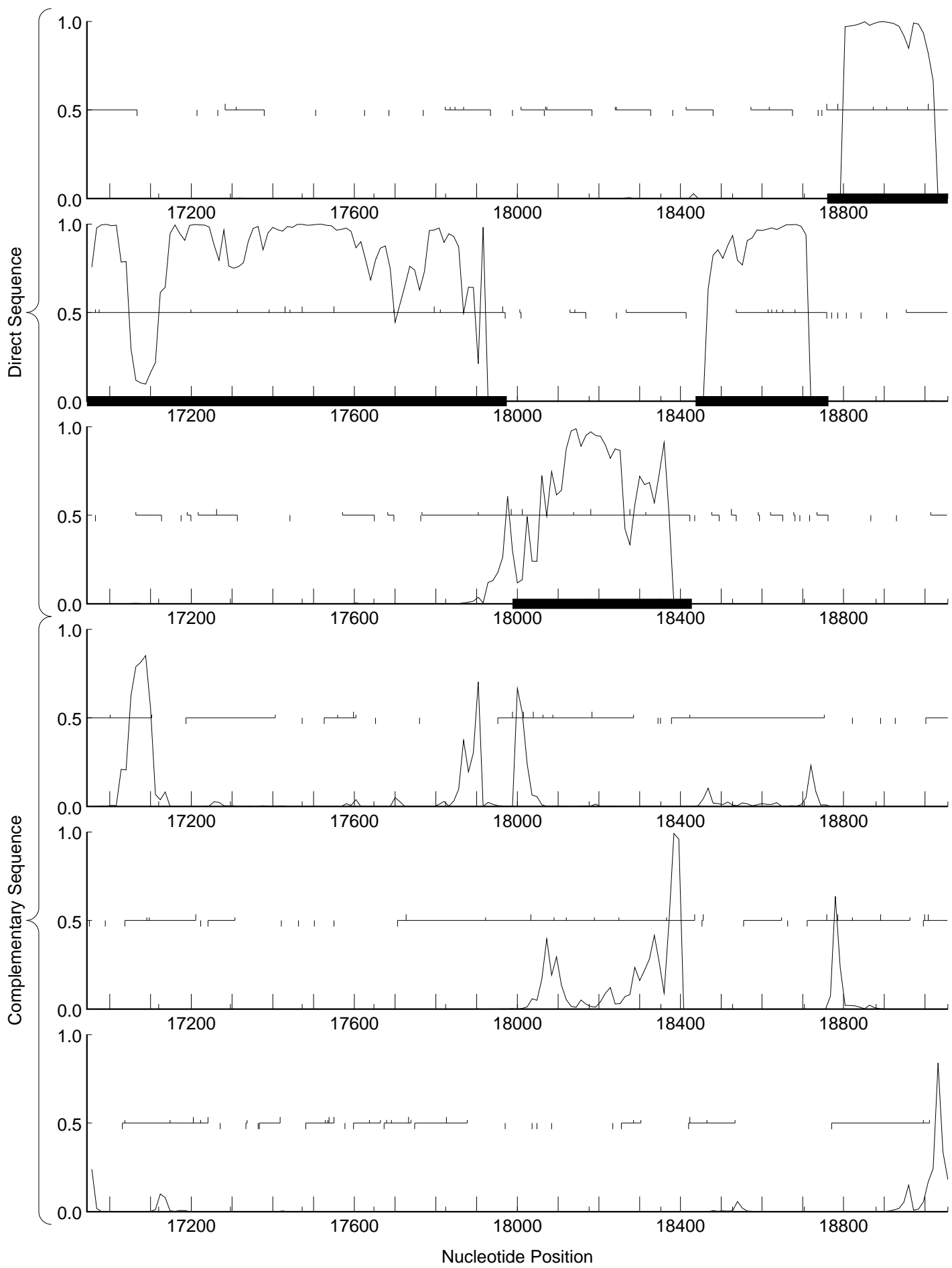




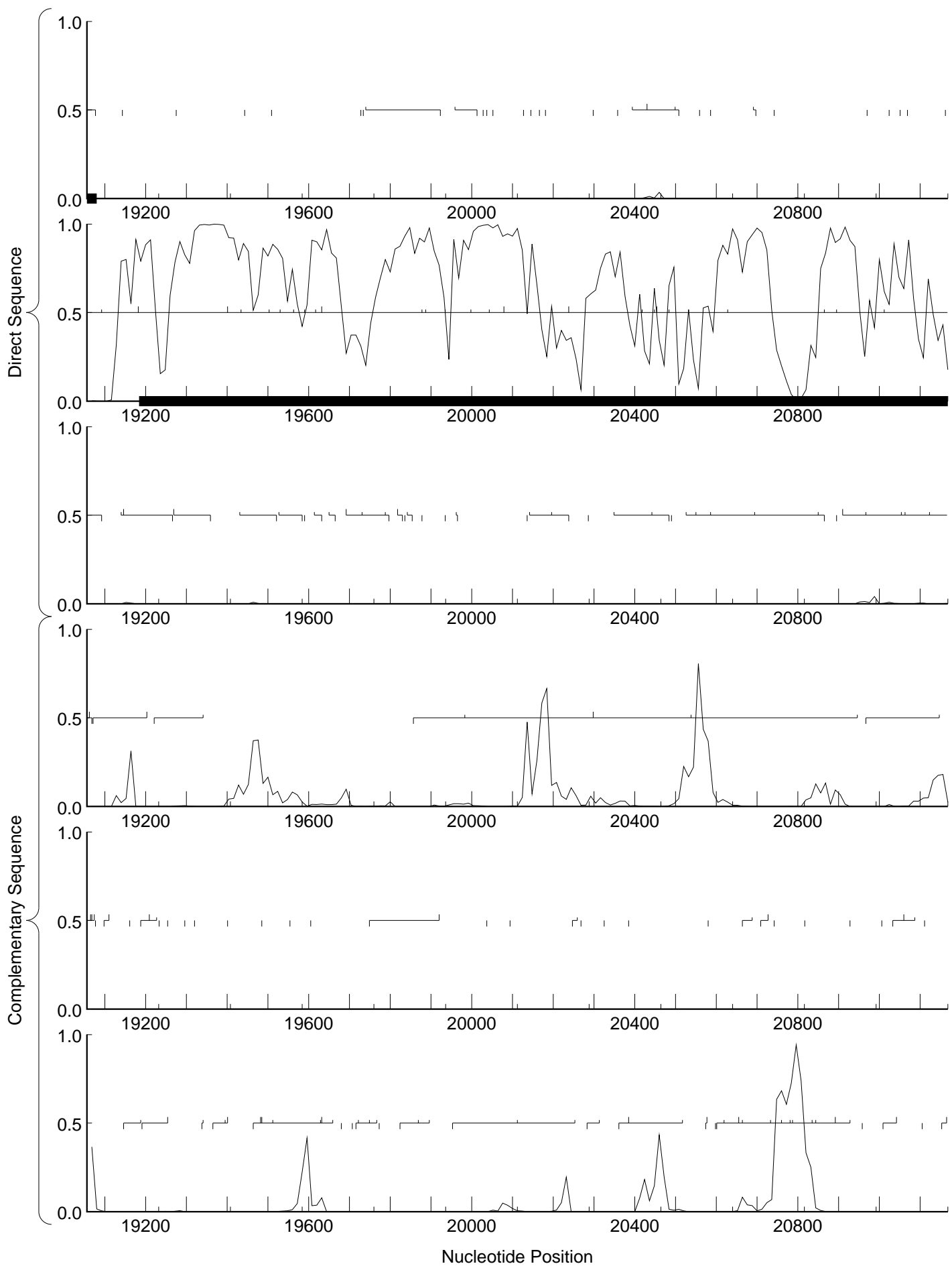




GeneMark.hmm prediction

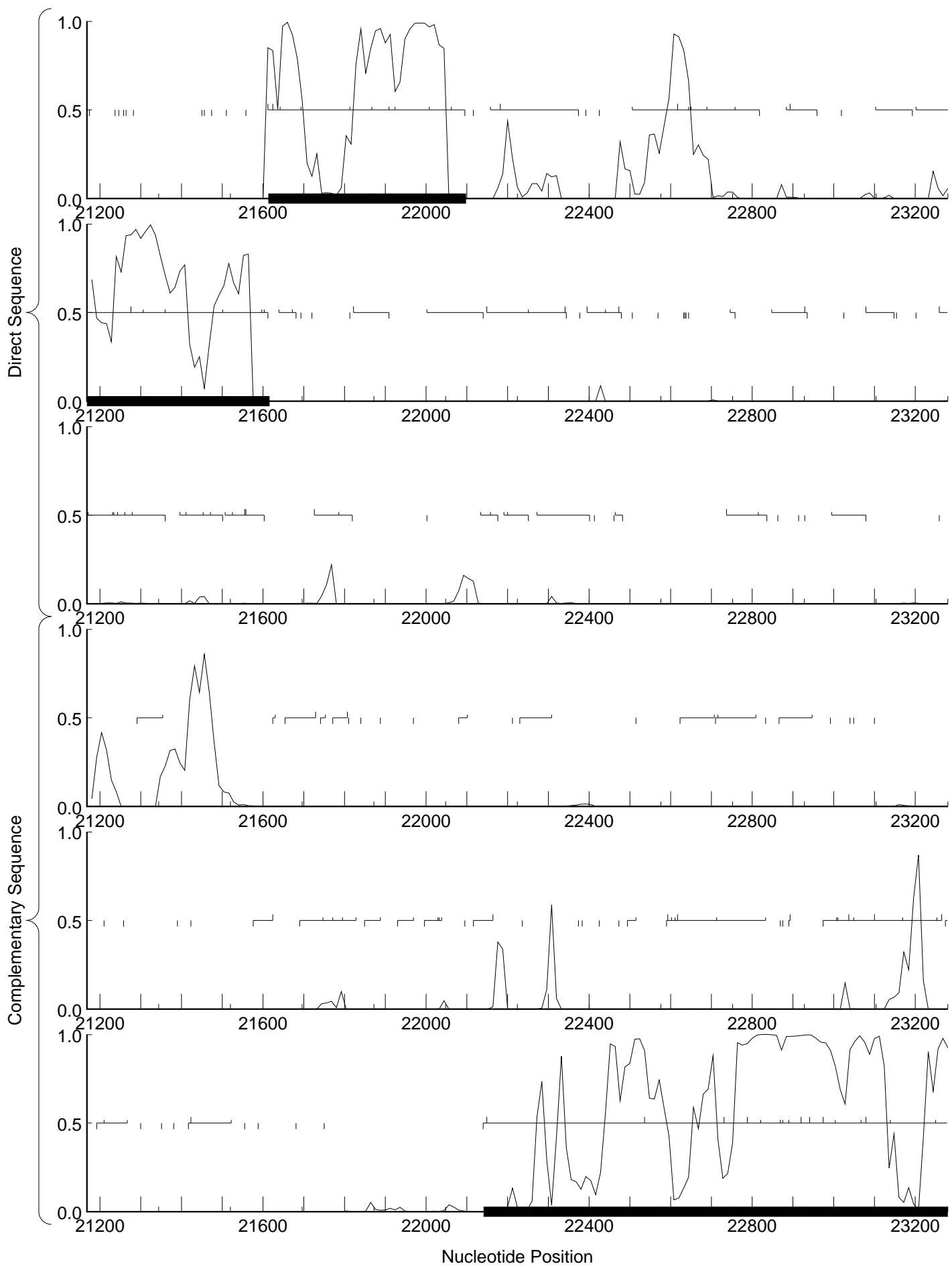


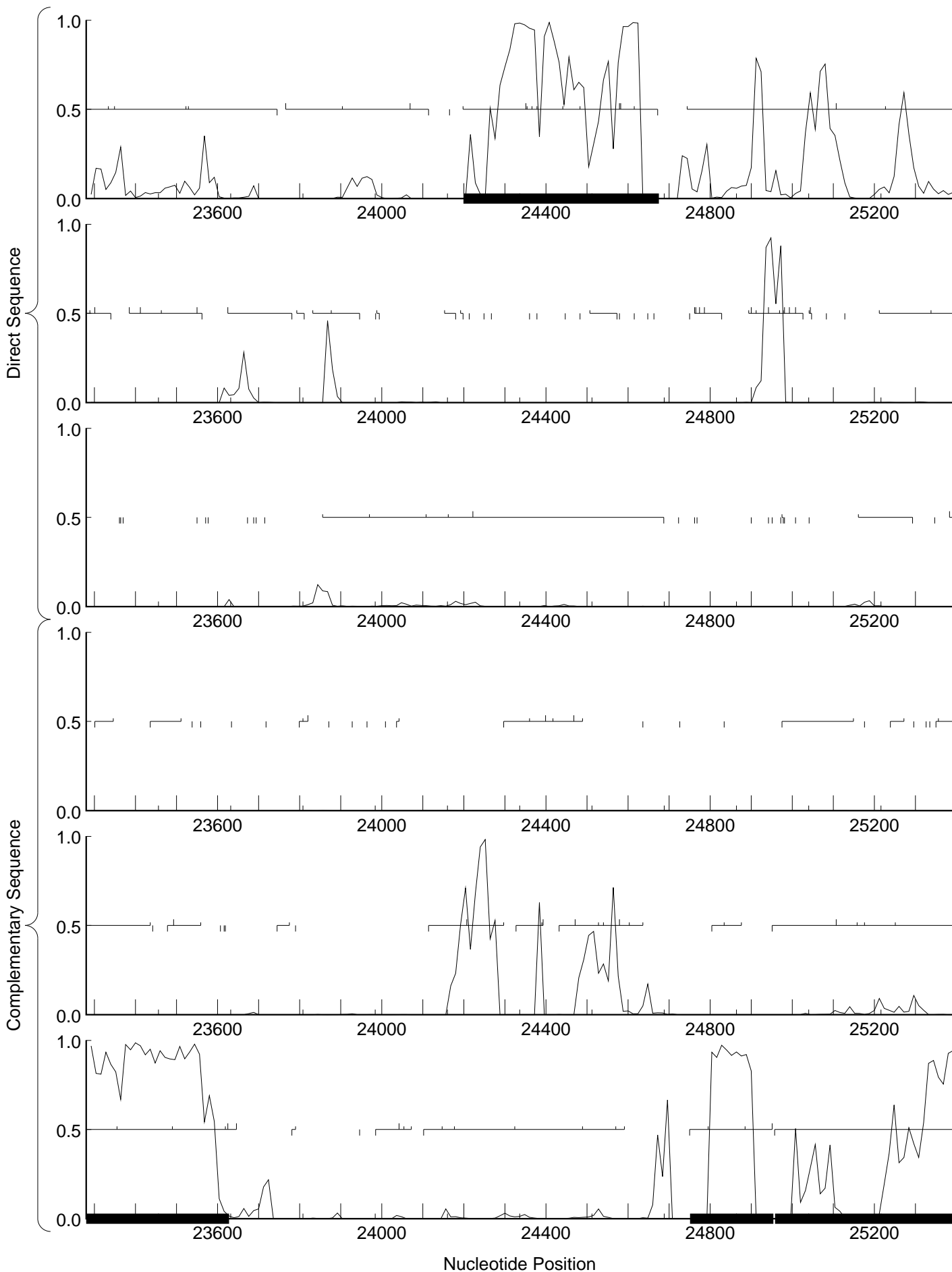
GeneMark.hmm prediction



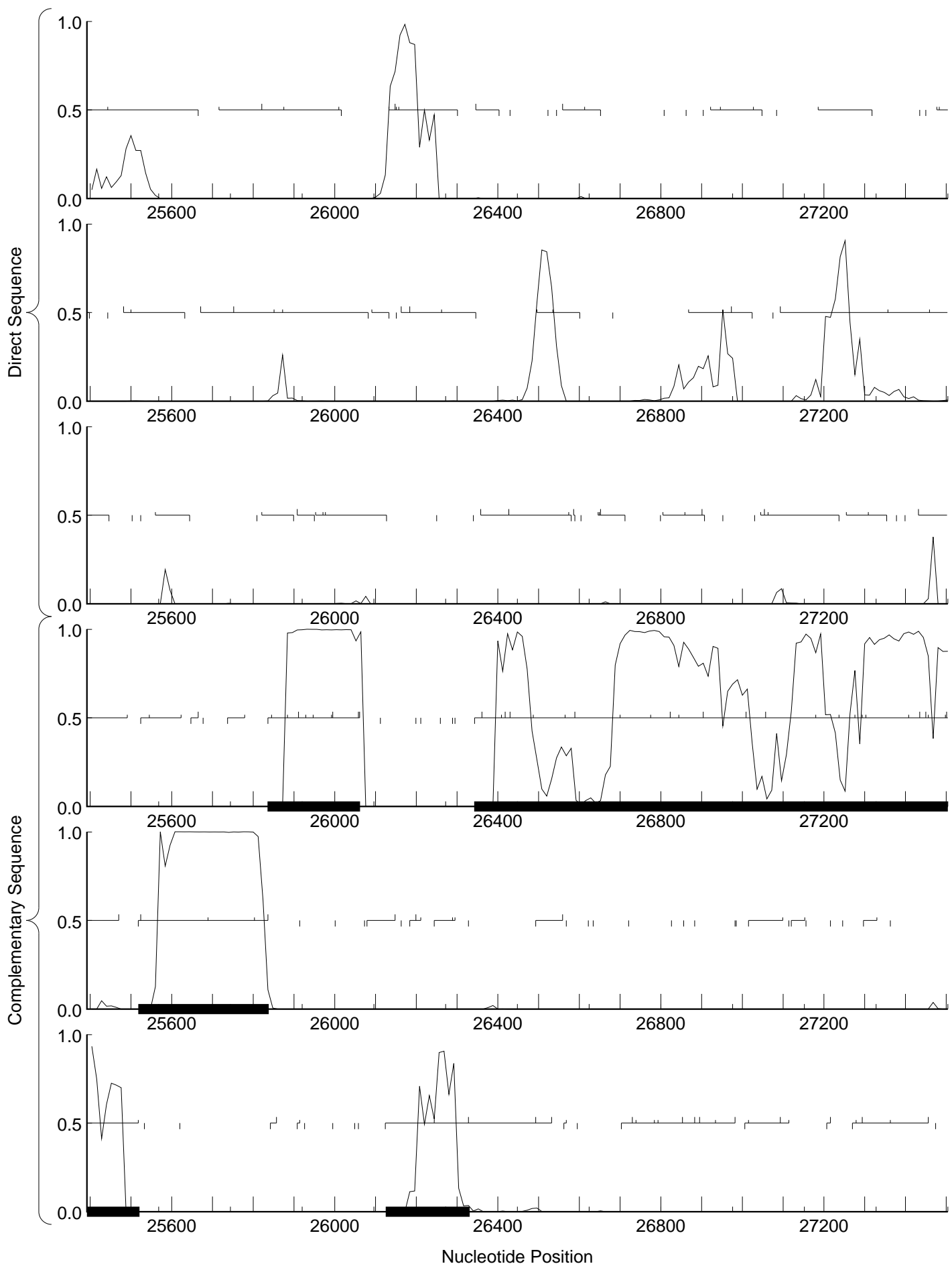
Nucleotide Position

GeneMark.hmm prediction



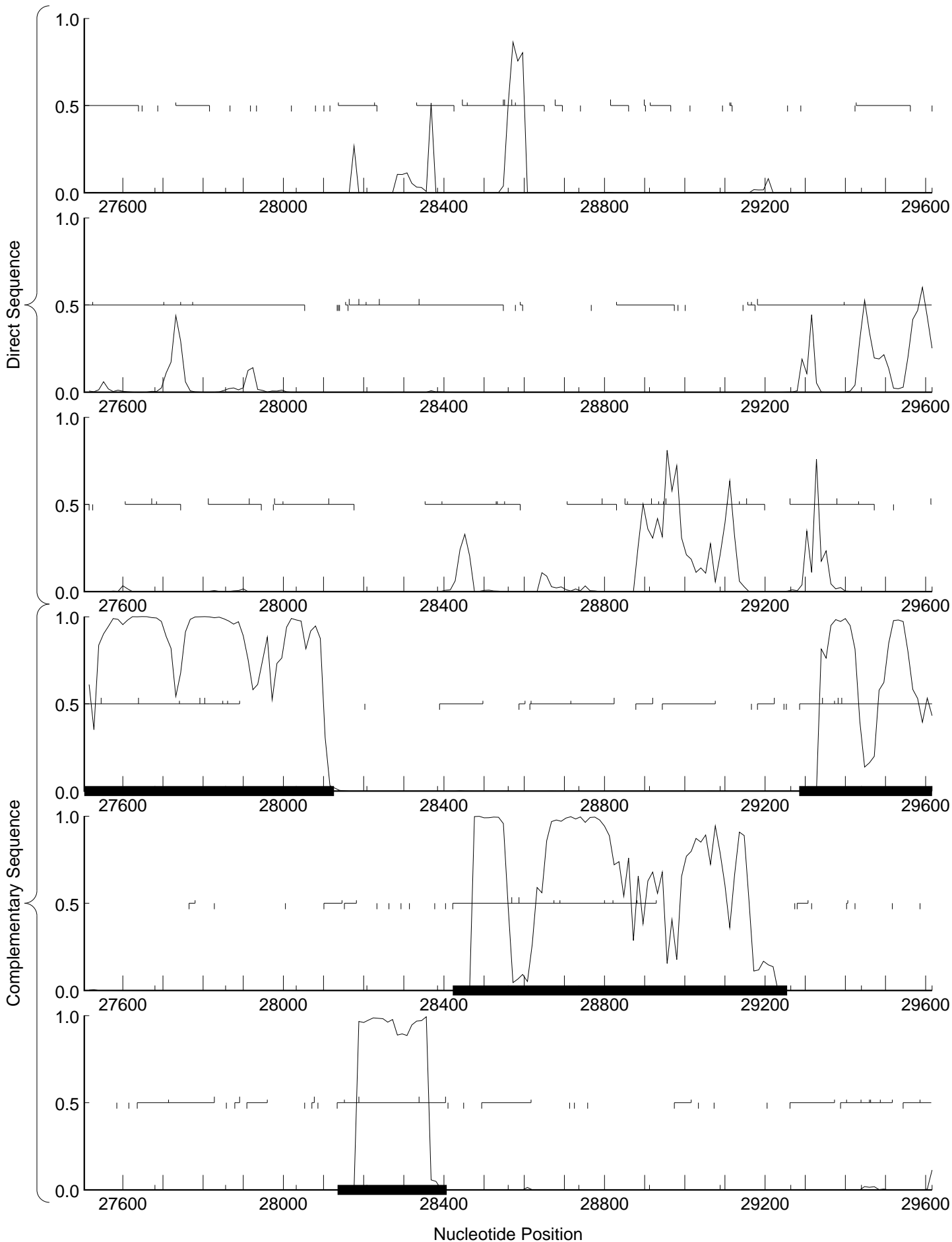


GeneMark.hmm prediction

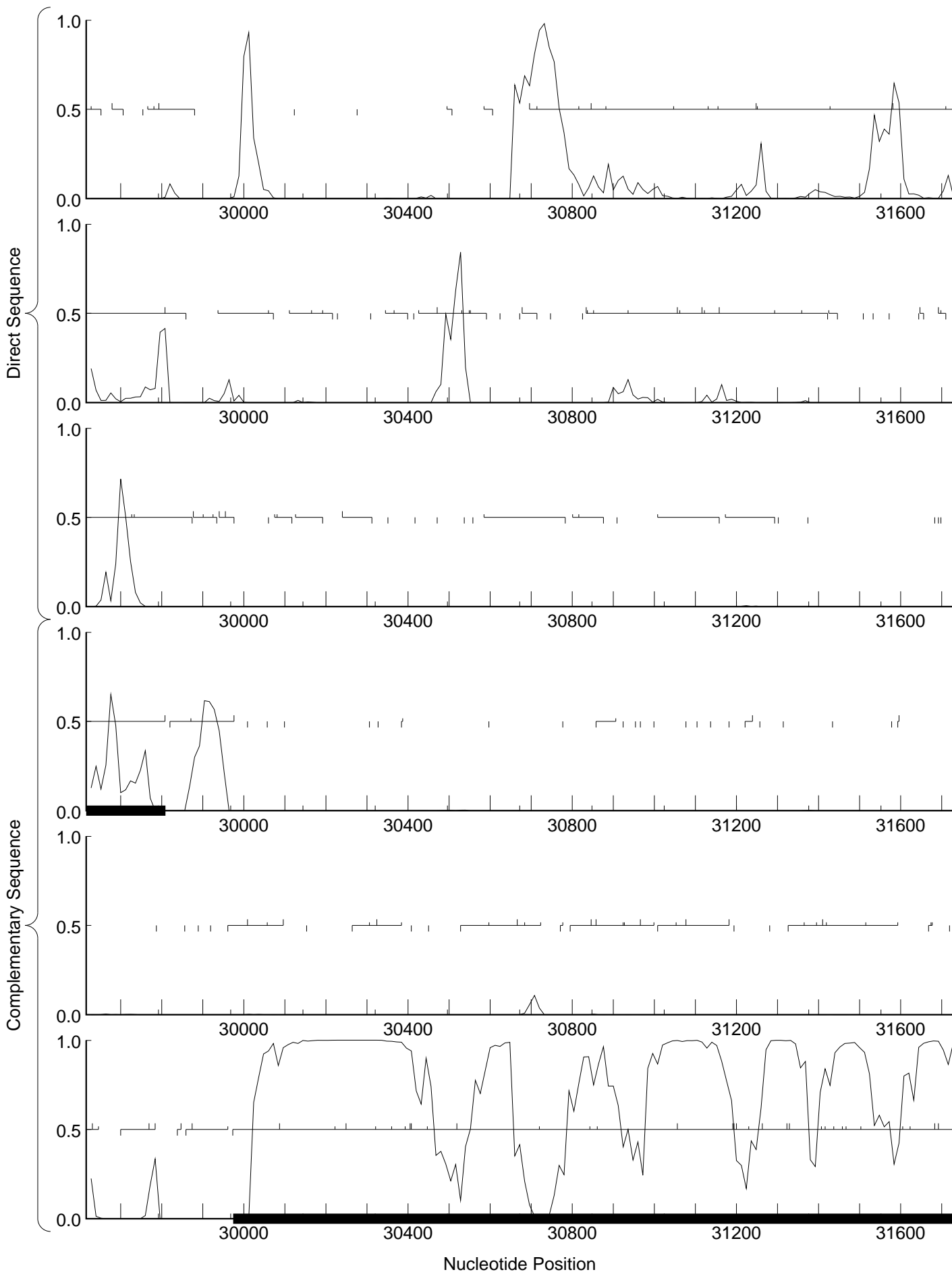


██████████

GeneMark.hmm prediction

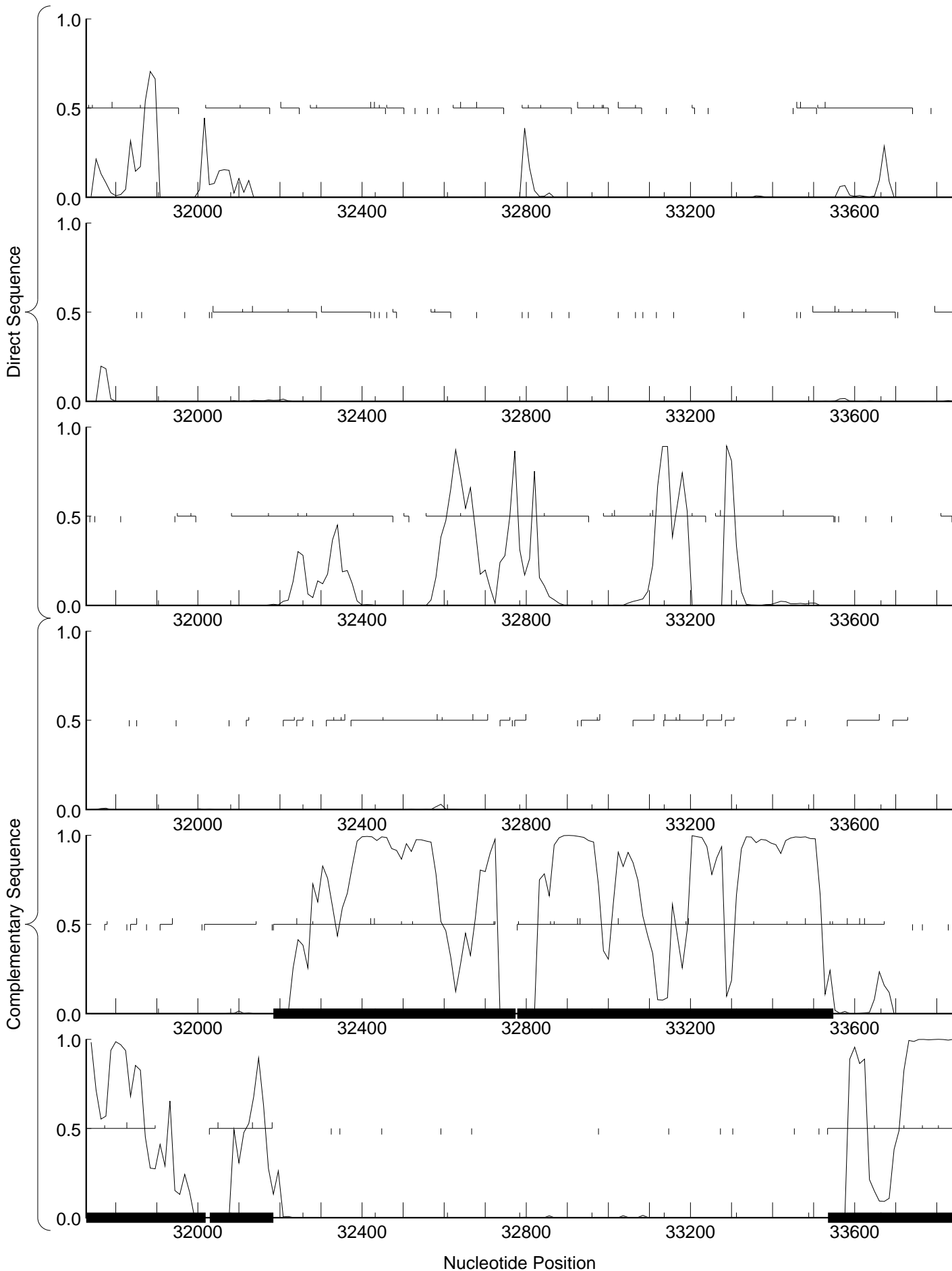


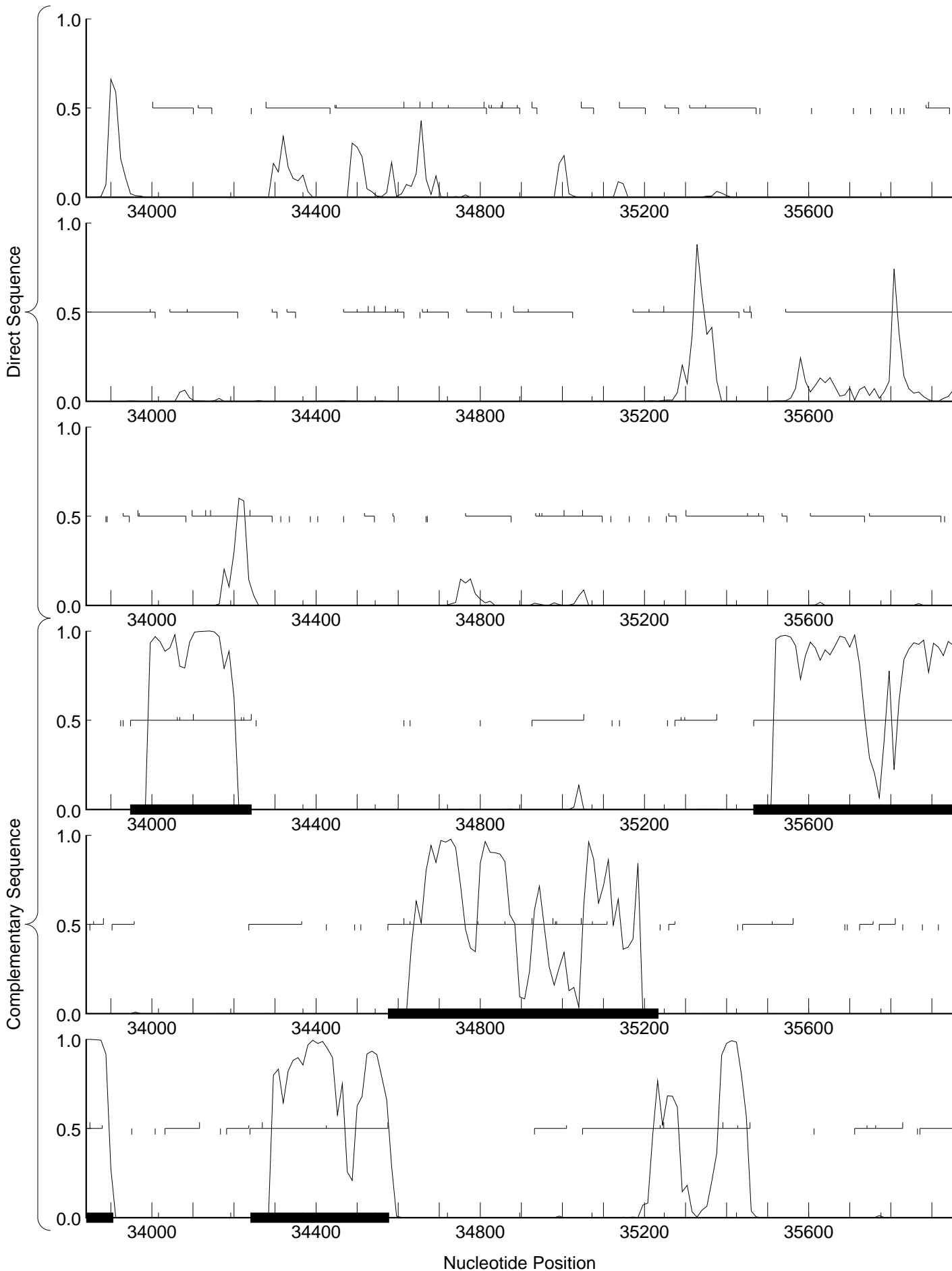
complete sequence, 46544 bp including 10-base 3' overhang (CGGCCGTGAT), Cluster CA, Order 2, Window 96, Step 12, 16/24

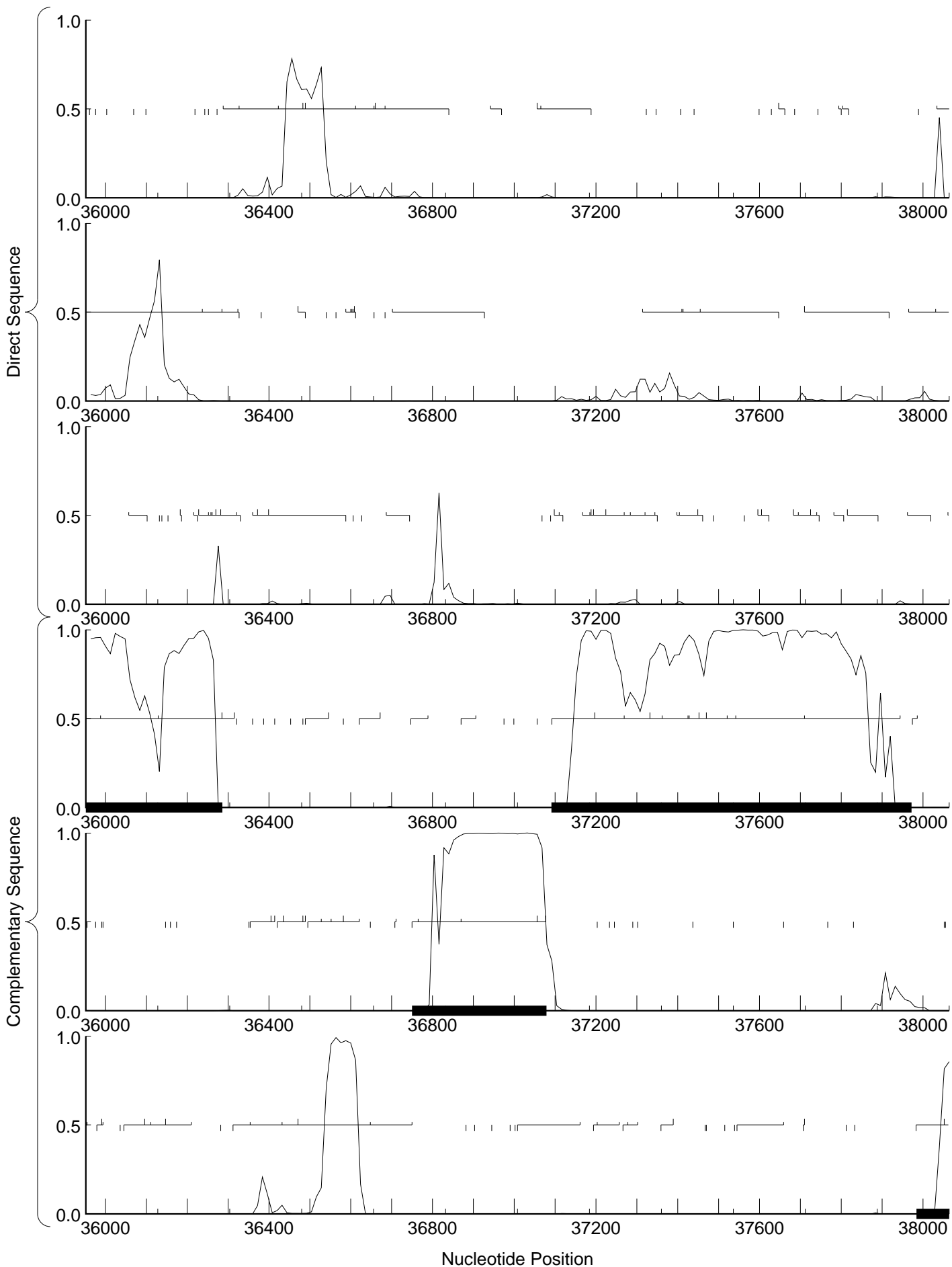


██████████

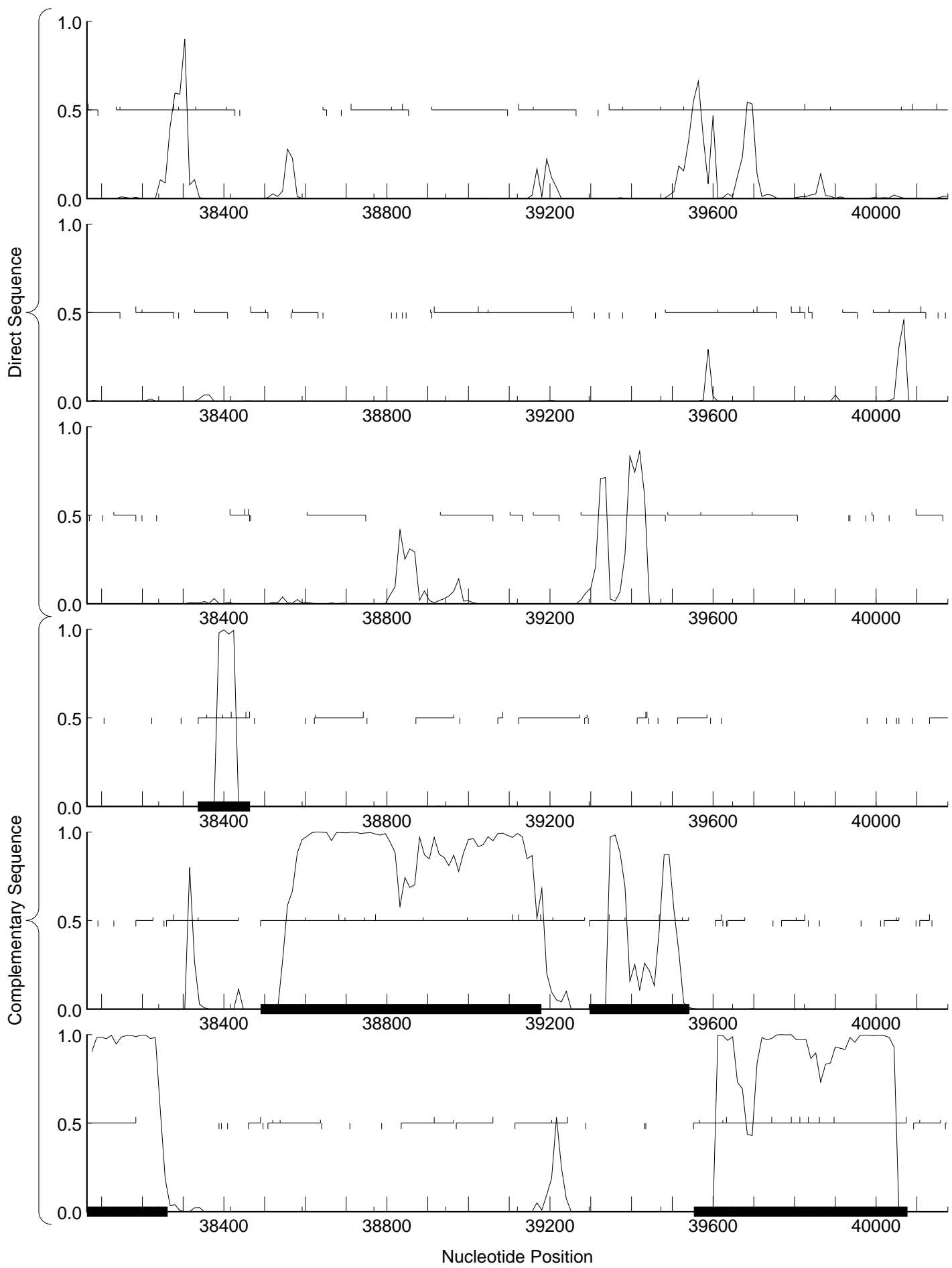
GeneMark.hmm prediction

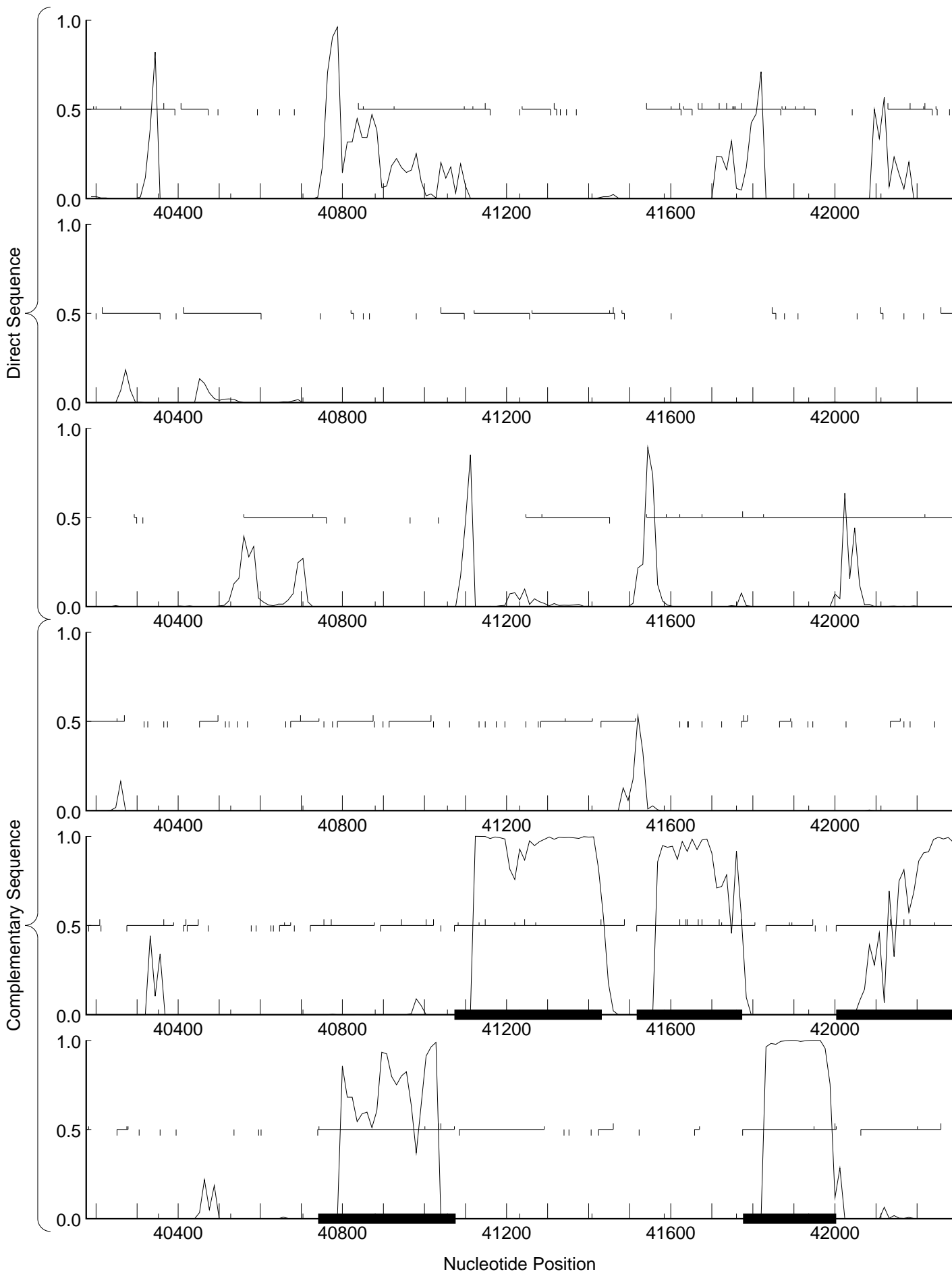






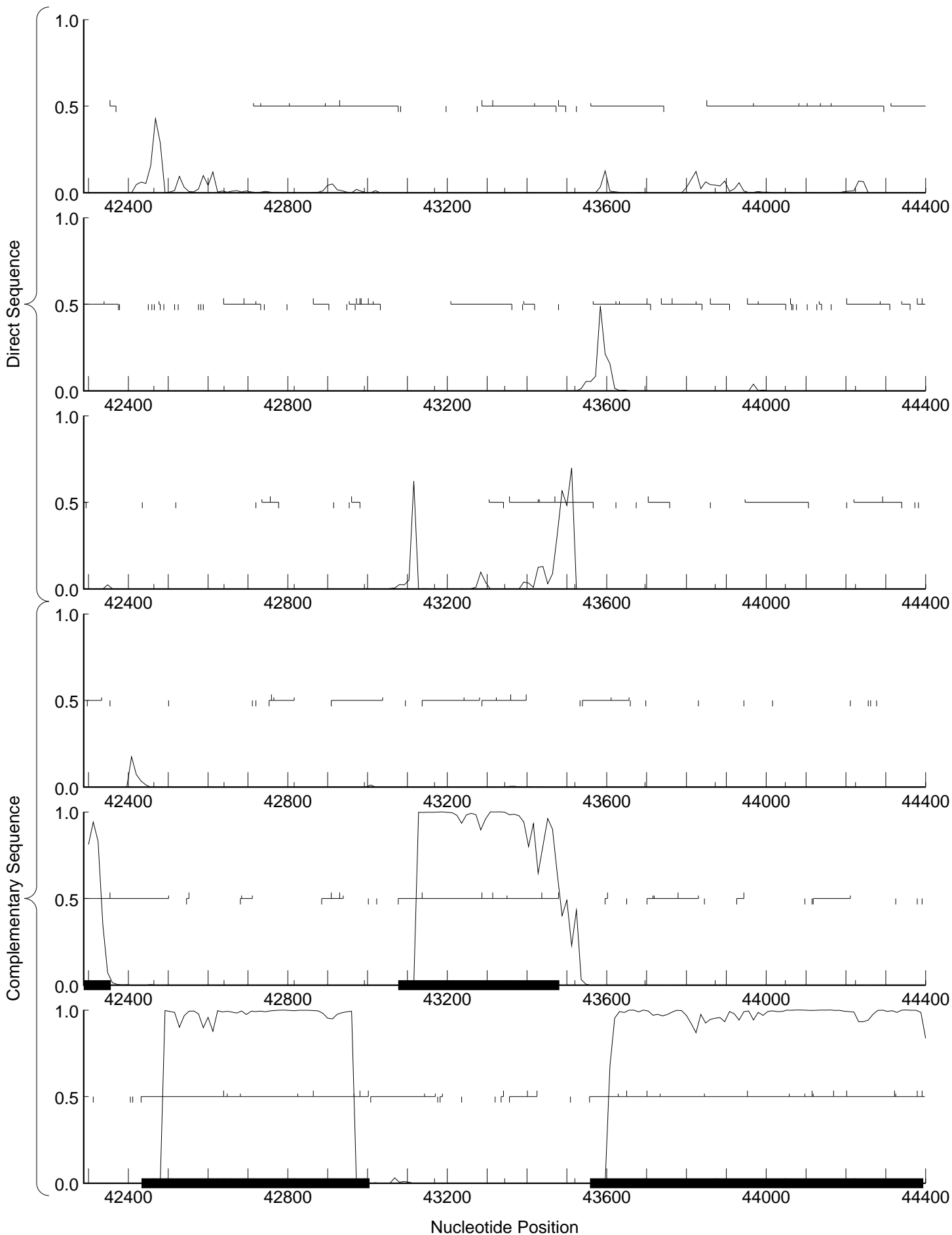
GeneMark.hmm prediction





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GeneMark.hmm prediction



GeneMark.hmm prediction

