

GeneMark

Version 2.5p (09.08.06)

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PROGRAM INFORMATION

Sequence : Arthrobacter phage QuinnAvery complete sequence, 43177 bp including 12-base 3' overhang (TC
Analysis Date : 12/13/24 at 20:18:58
Pages : 22
Sequence Length : 43177 bp
GC Content : 64.93%

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,

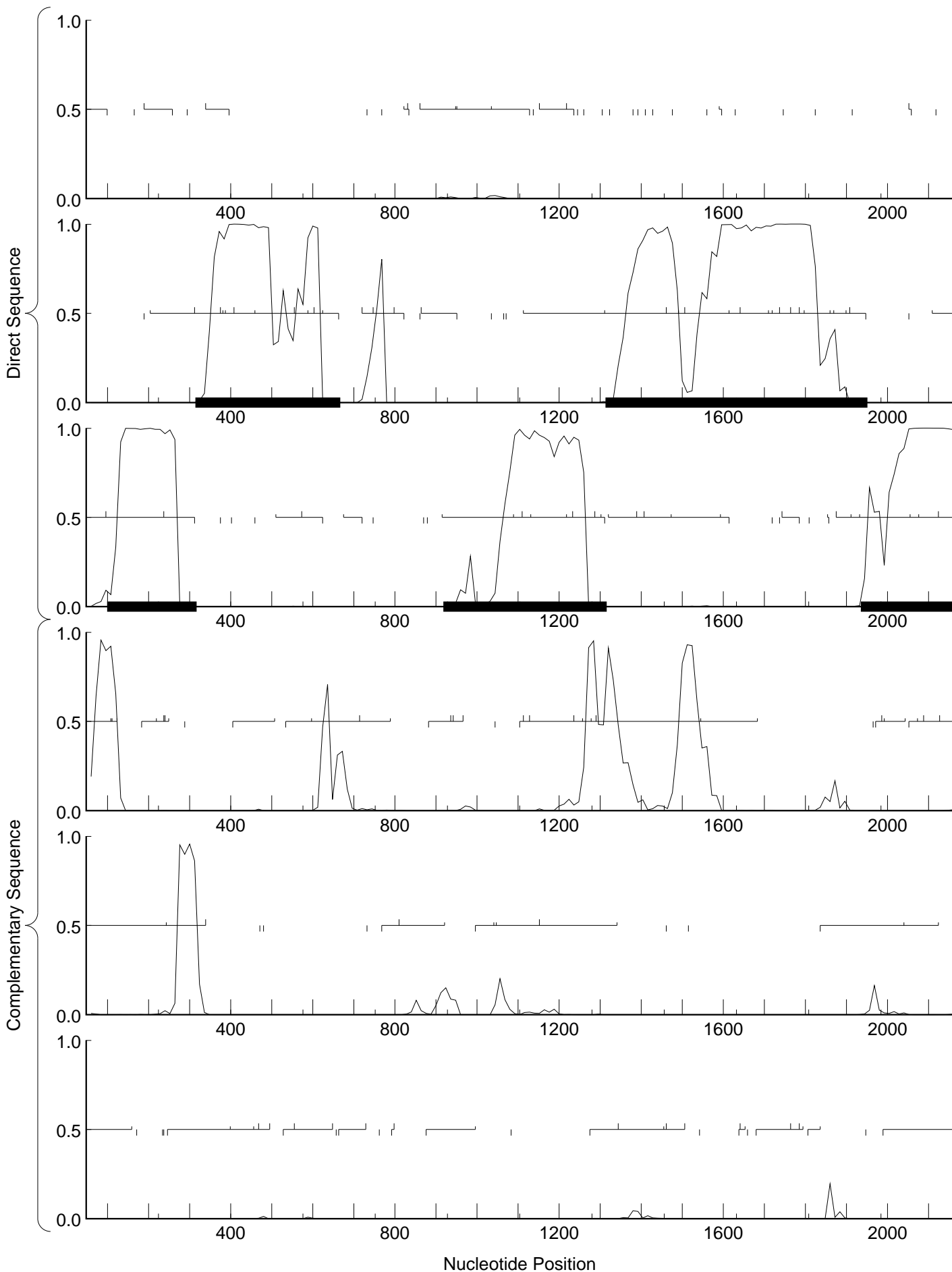
MATRIX INFORMATION

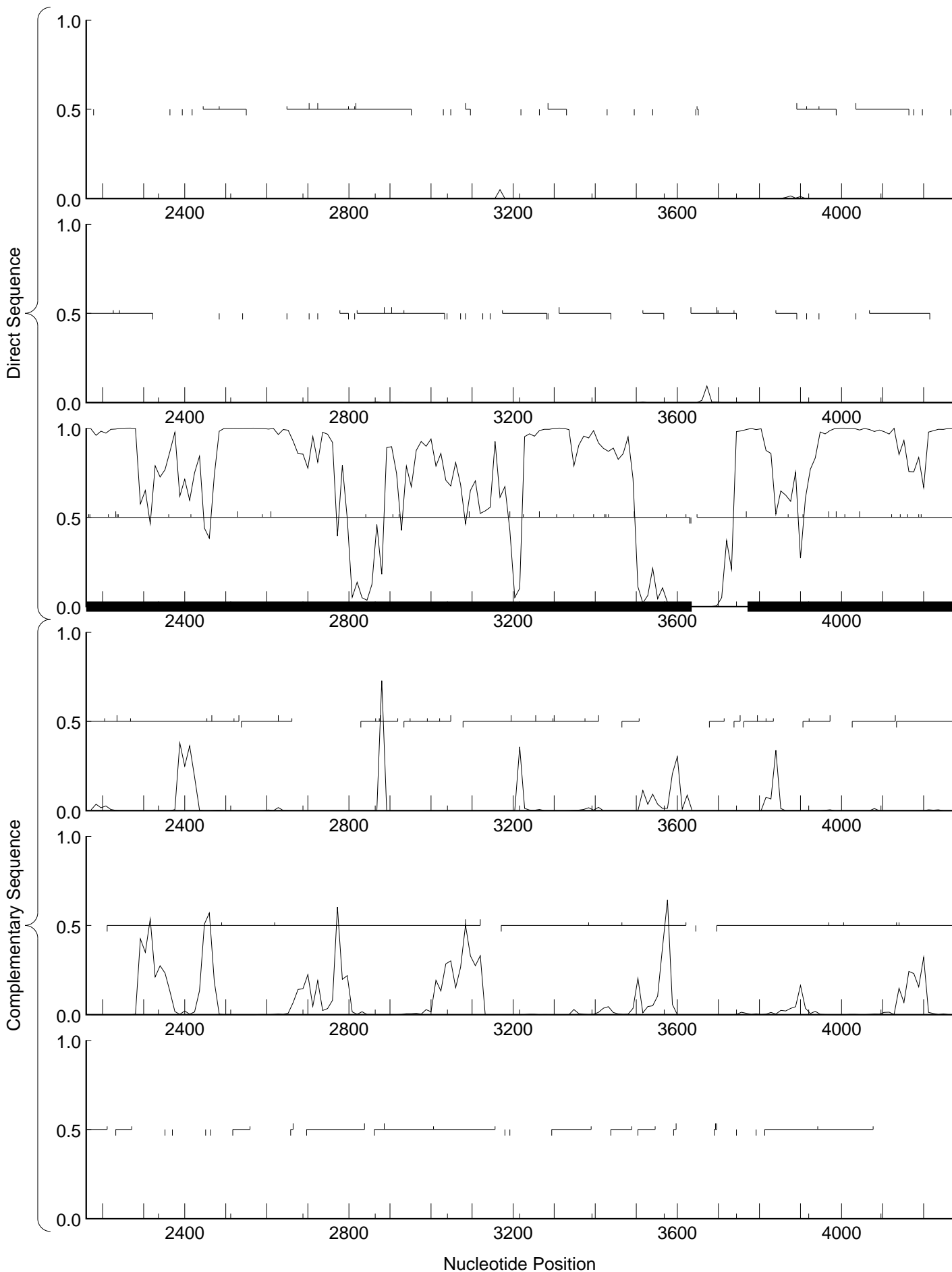
Matrix : Heuristic, GC = 65
Author : Borodovsky Laboratory - Georgia Tech
Order : 2

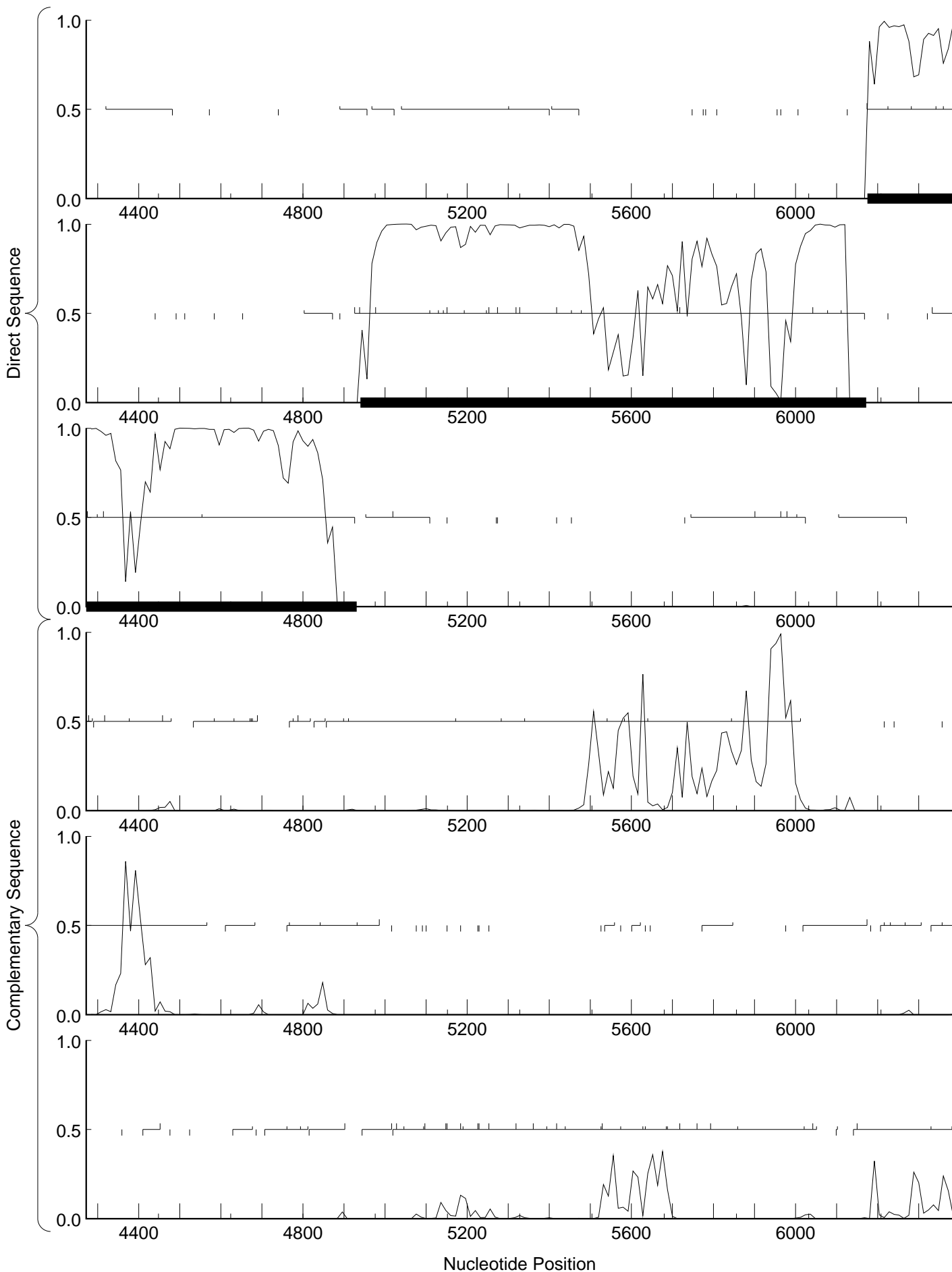
Send questions / comments to:
Dr. M. Borodovsky
Georgia Institute of Technology
School of Biology
Atlanta, GA 30332-0230

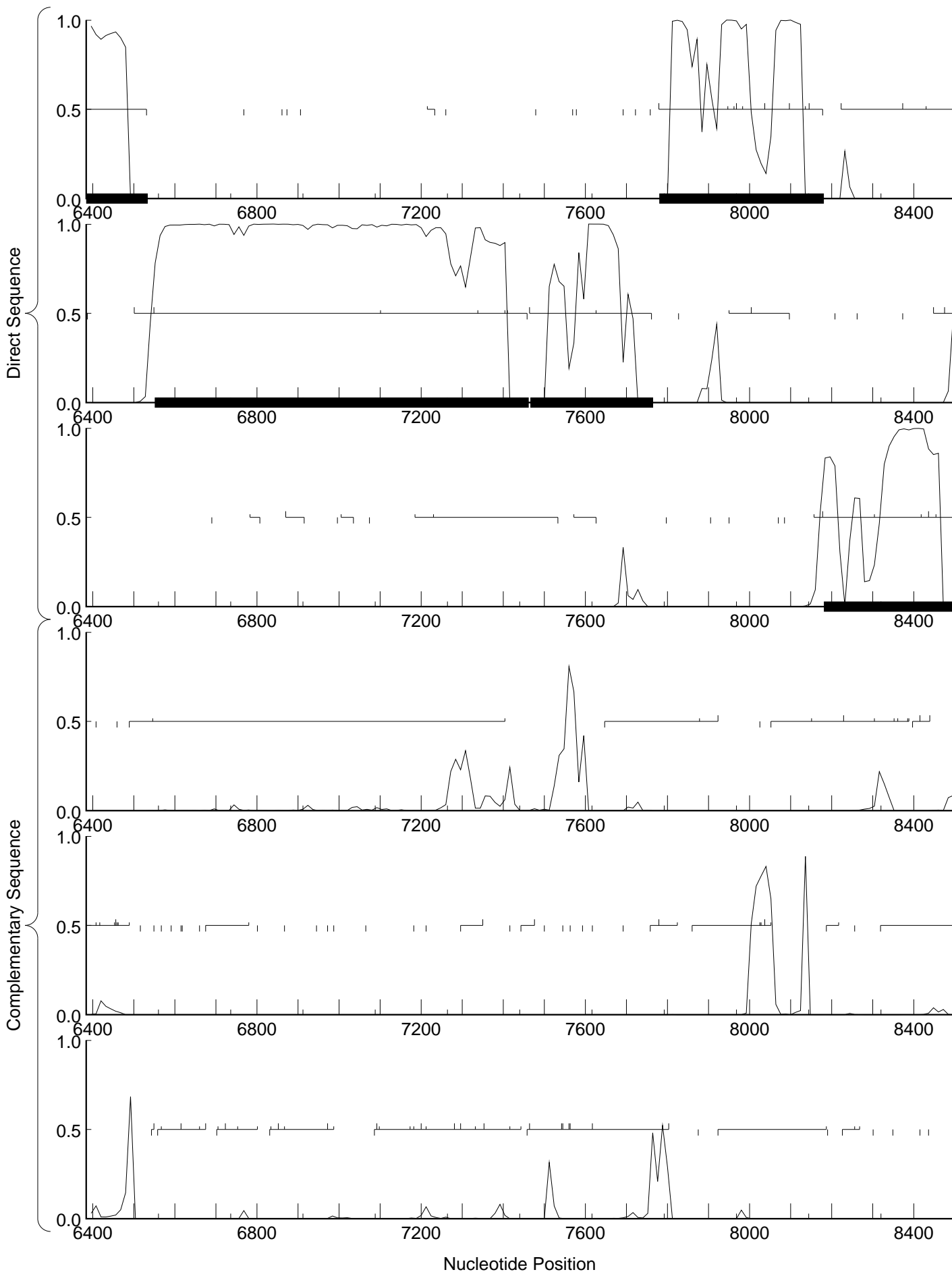
Matrix notes & comments

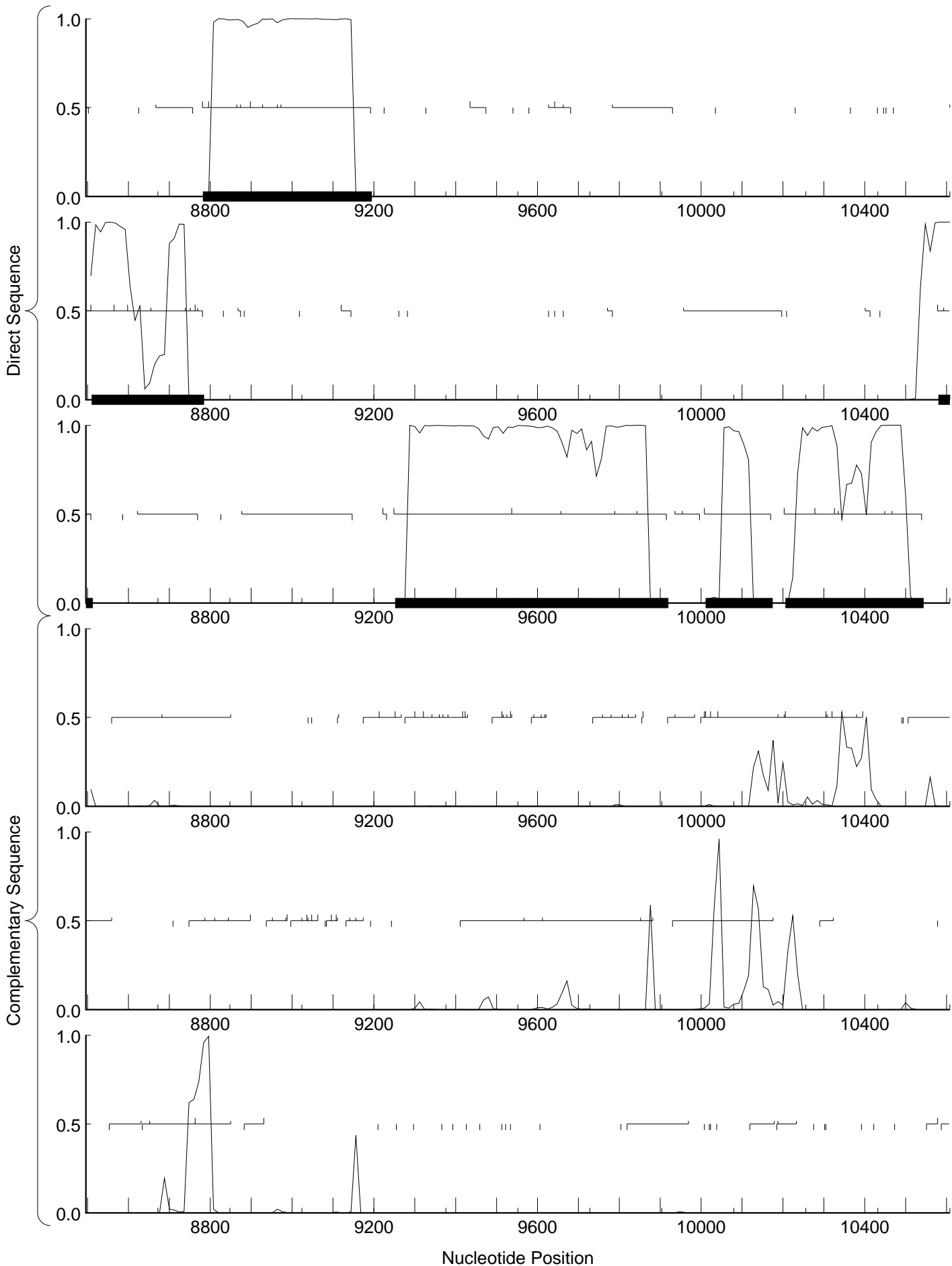
For details on the model building procedure see:
Besemer J. and Borodovsky M.
"Heuristic approach to deriving models for gene finding"
NAR, 1999, Vol. 27, No. 19, pp. 3911-3920

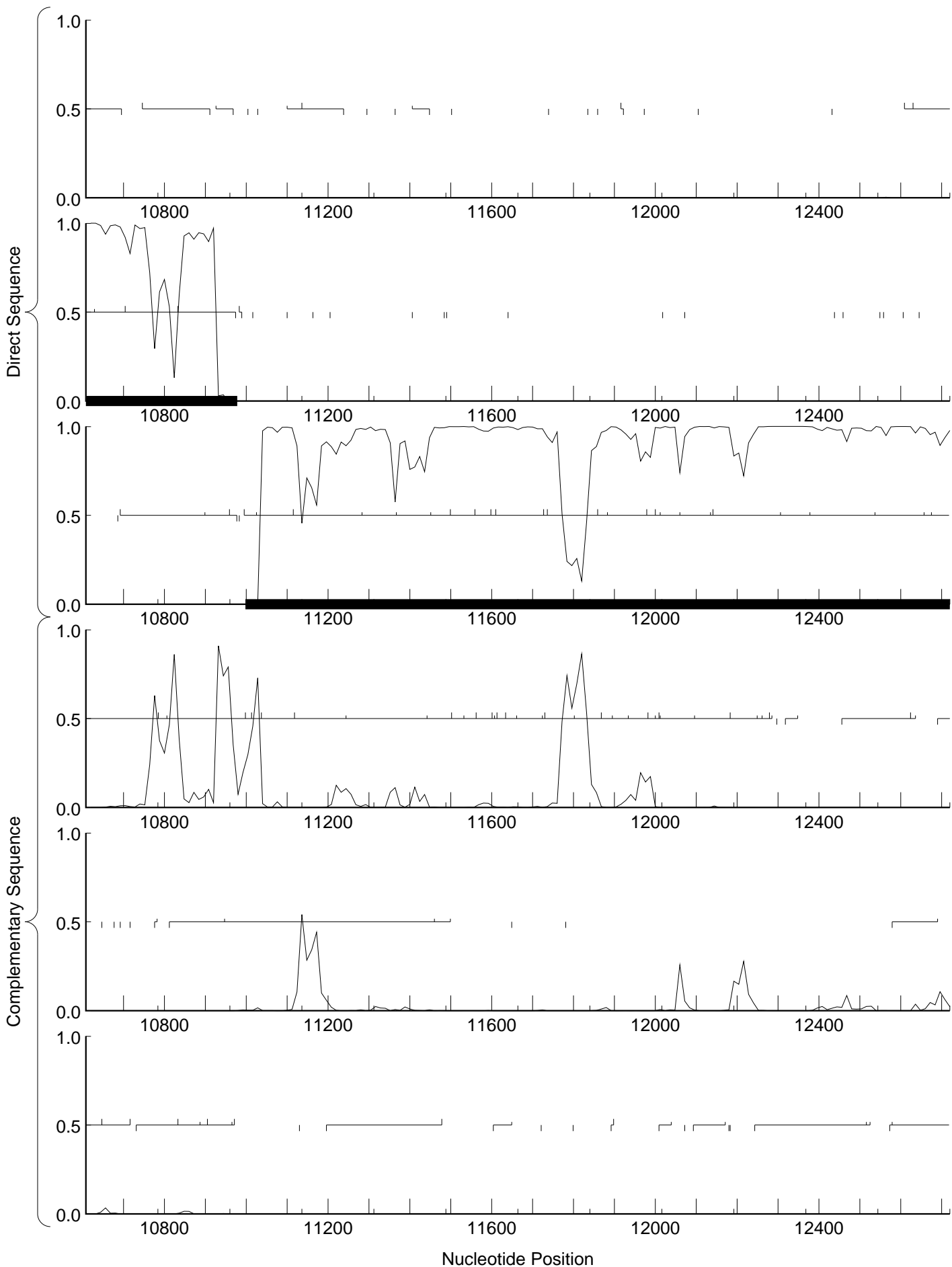


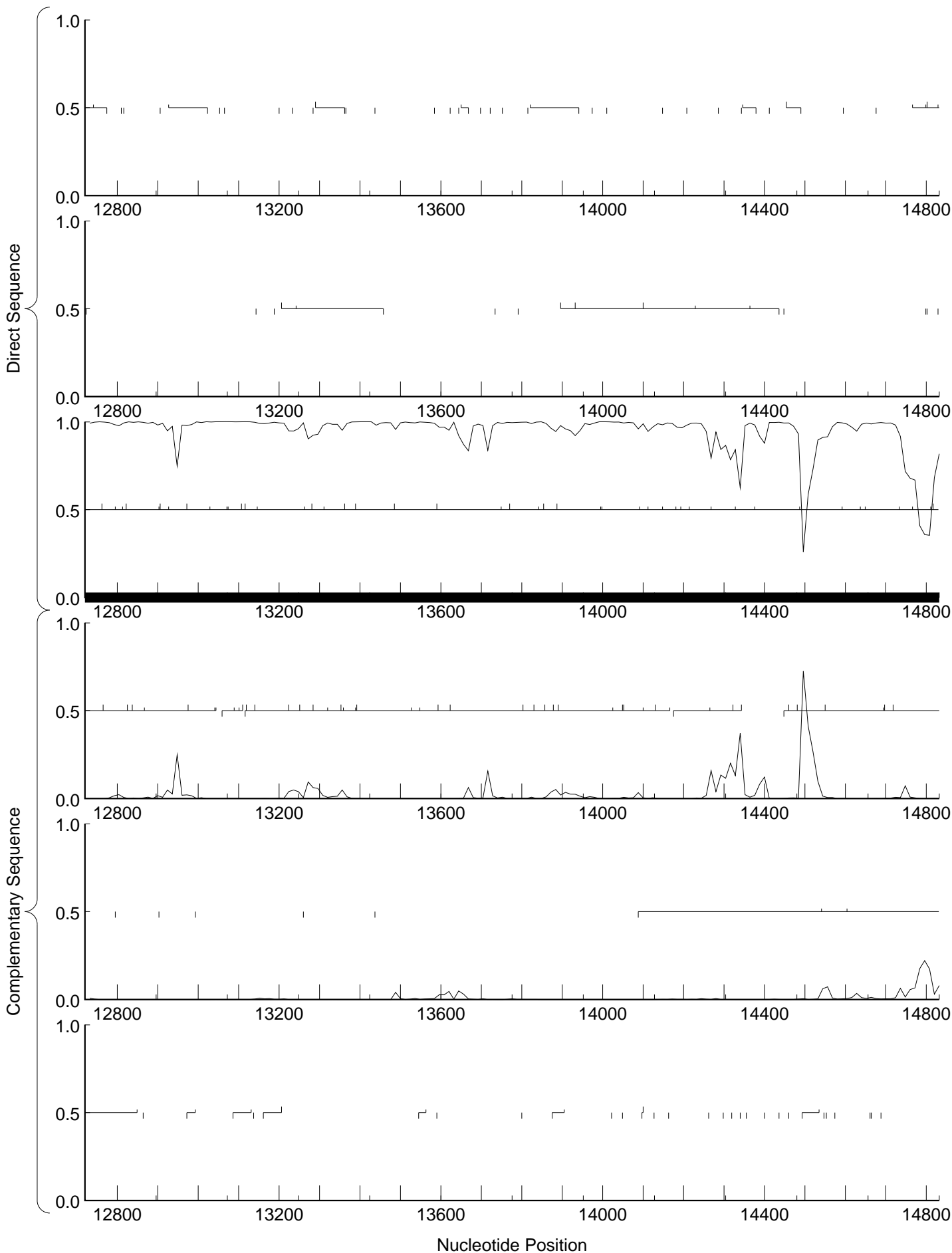


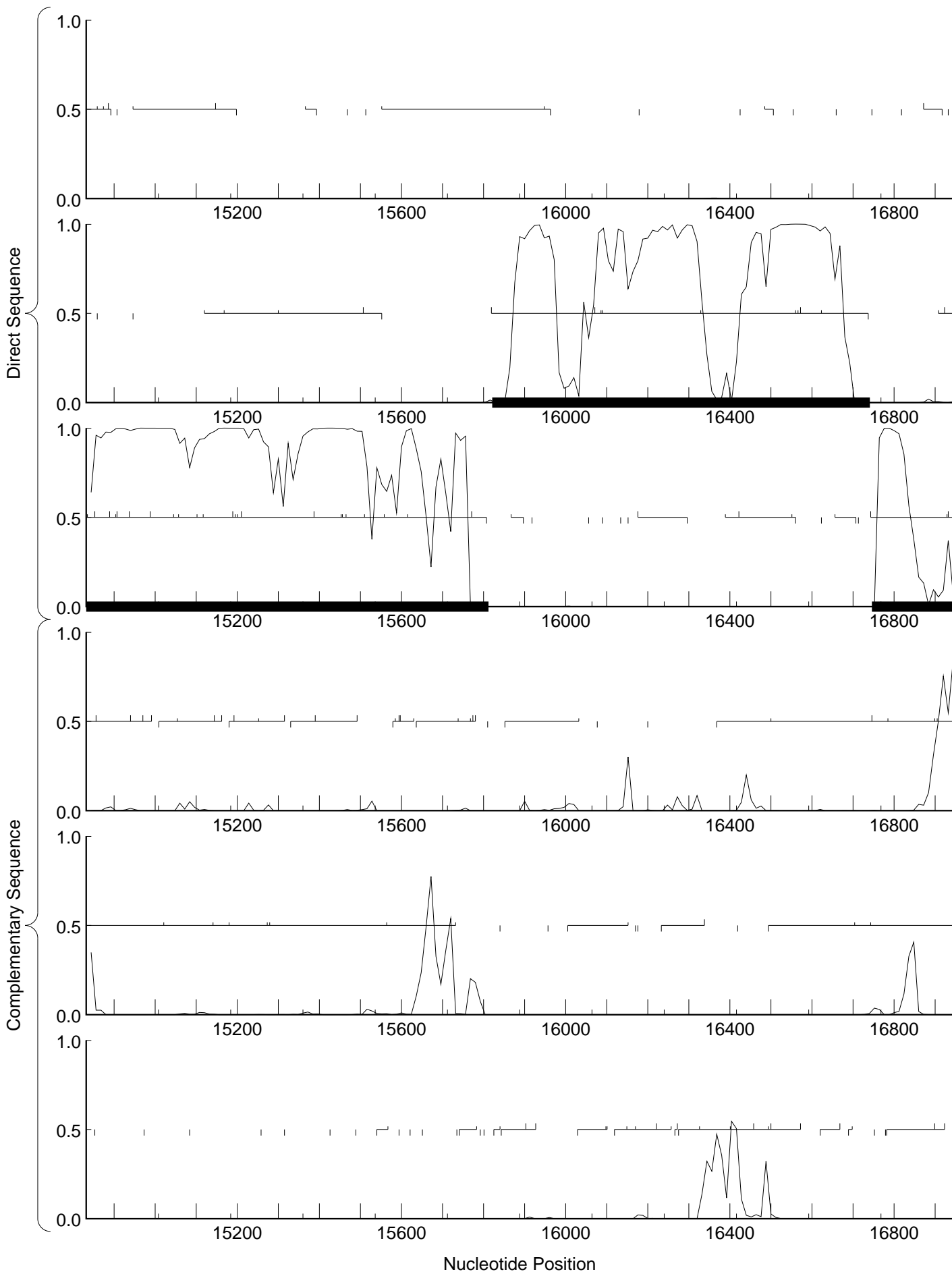




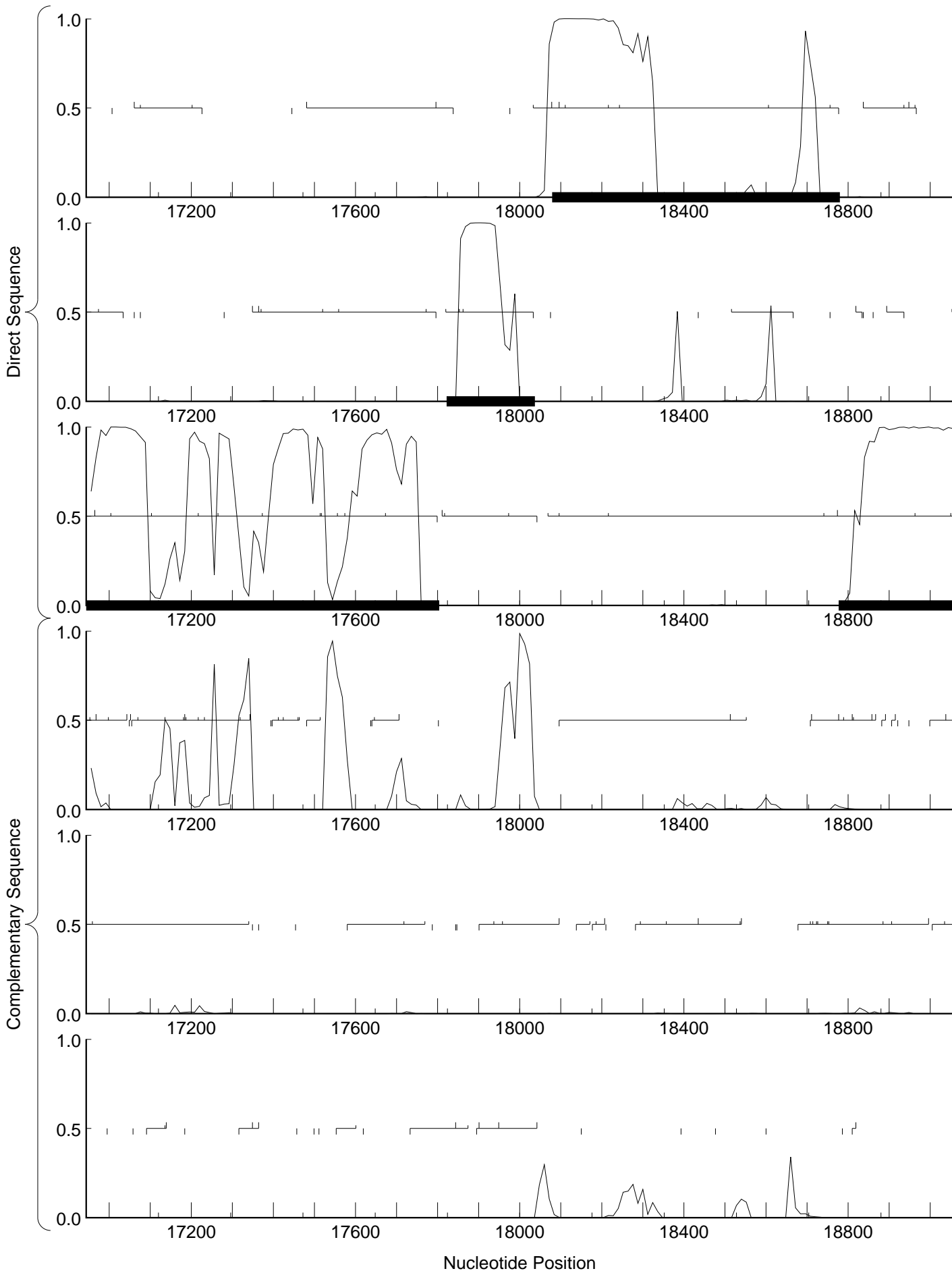


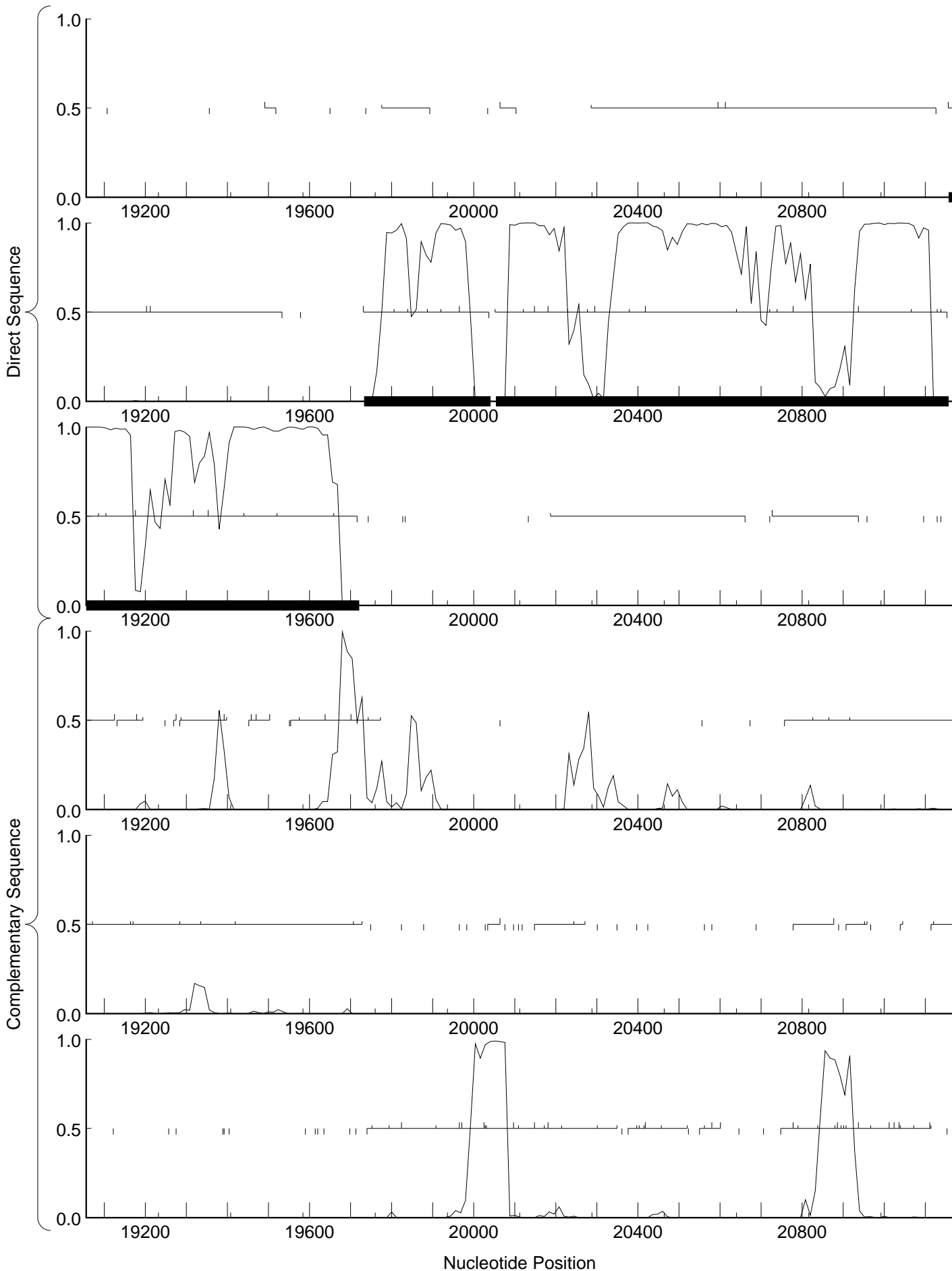




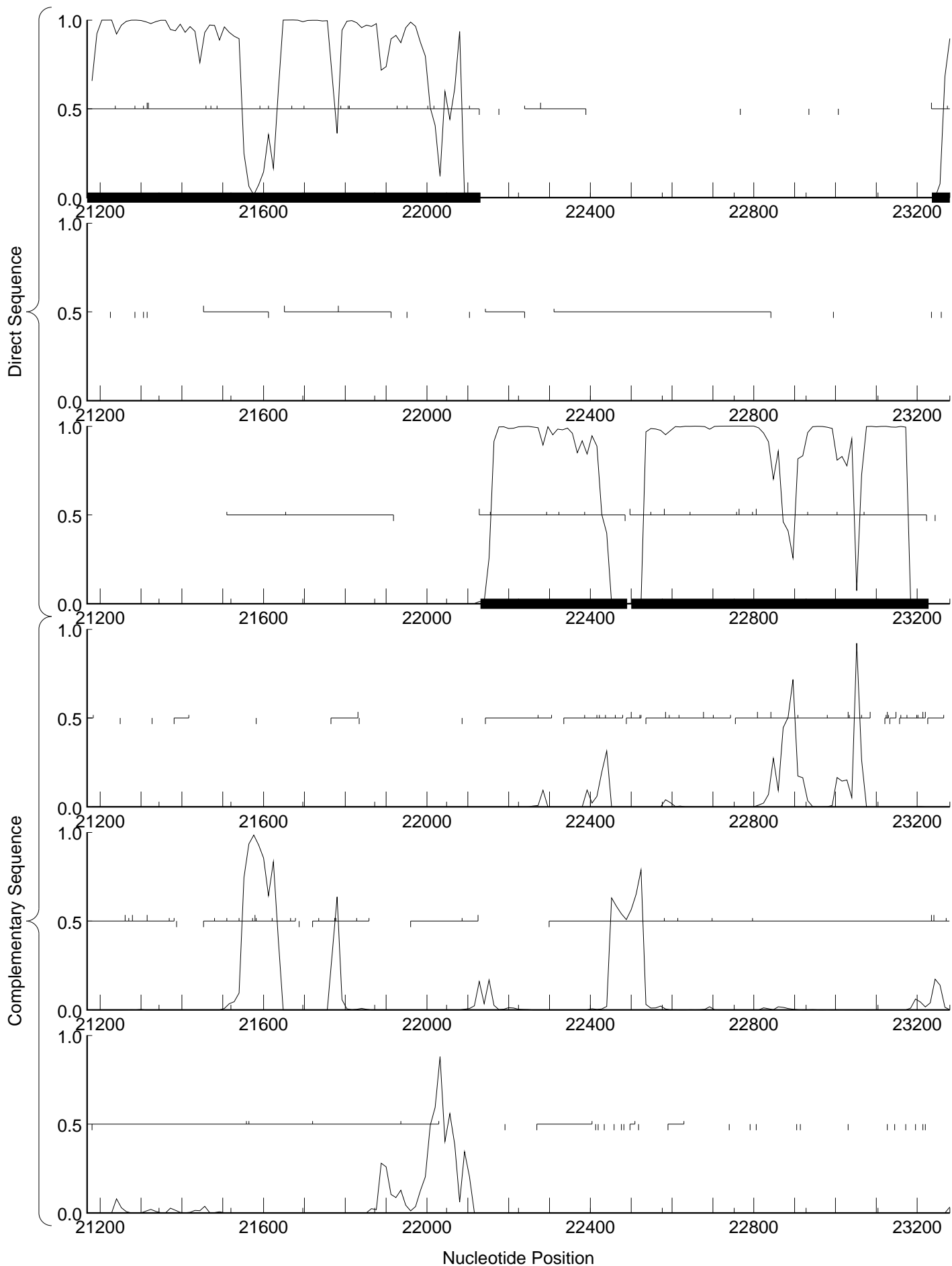


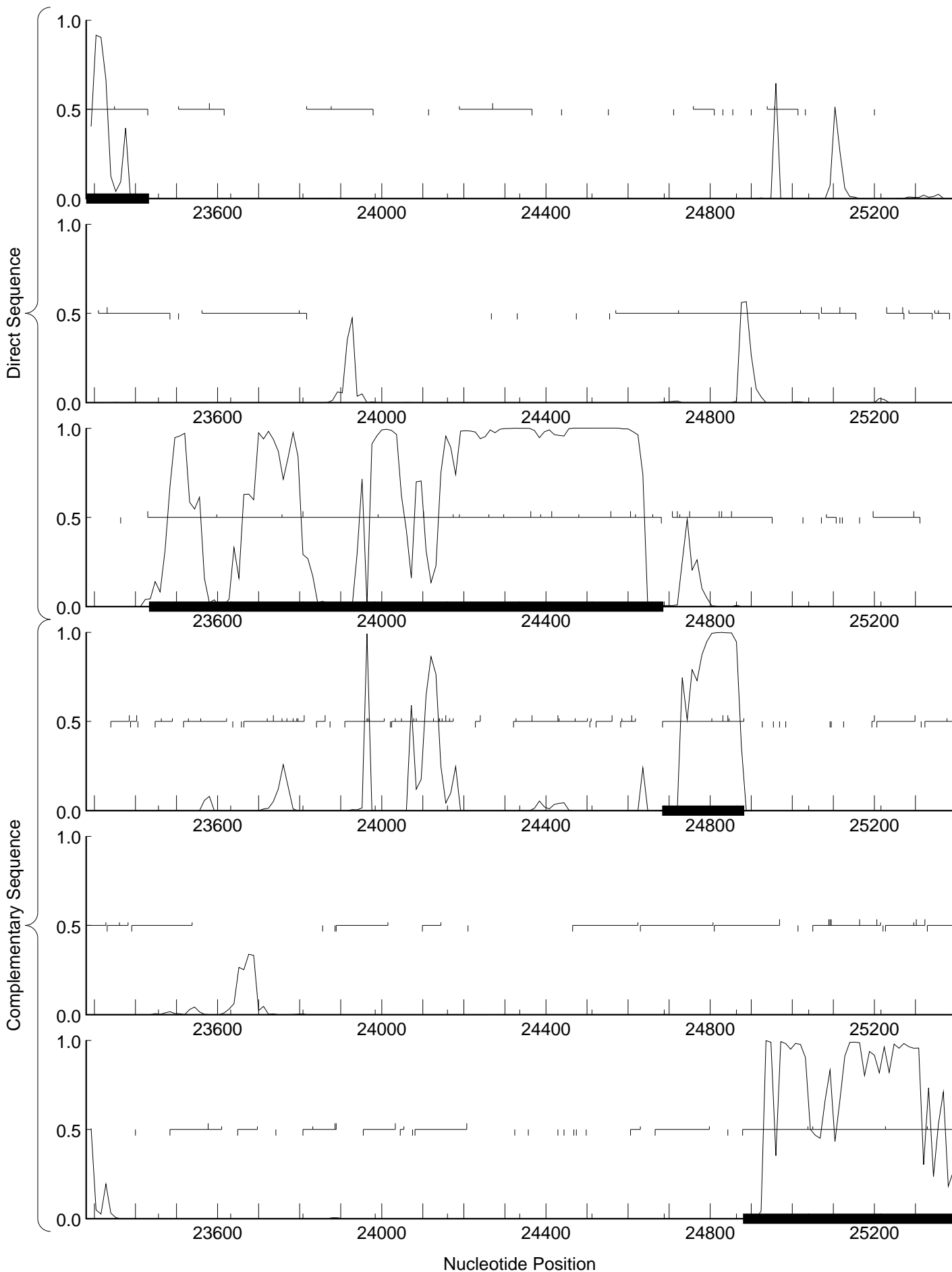
GeneMark_hmm_prediction

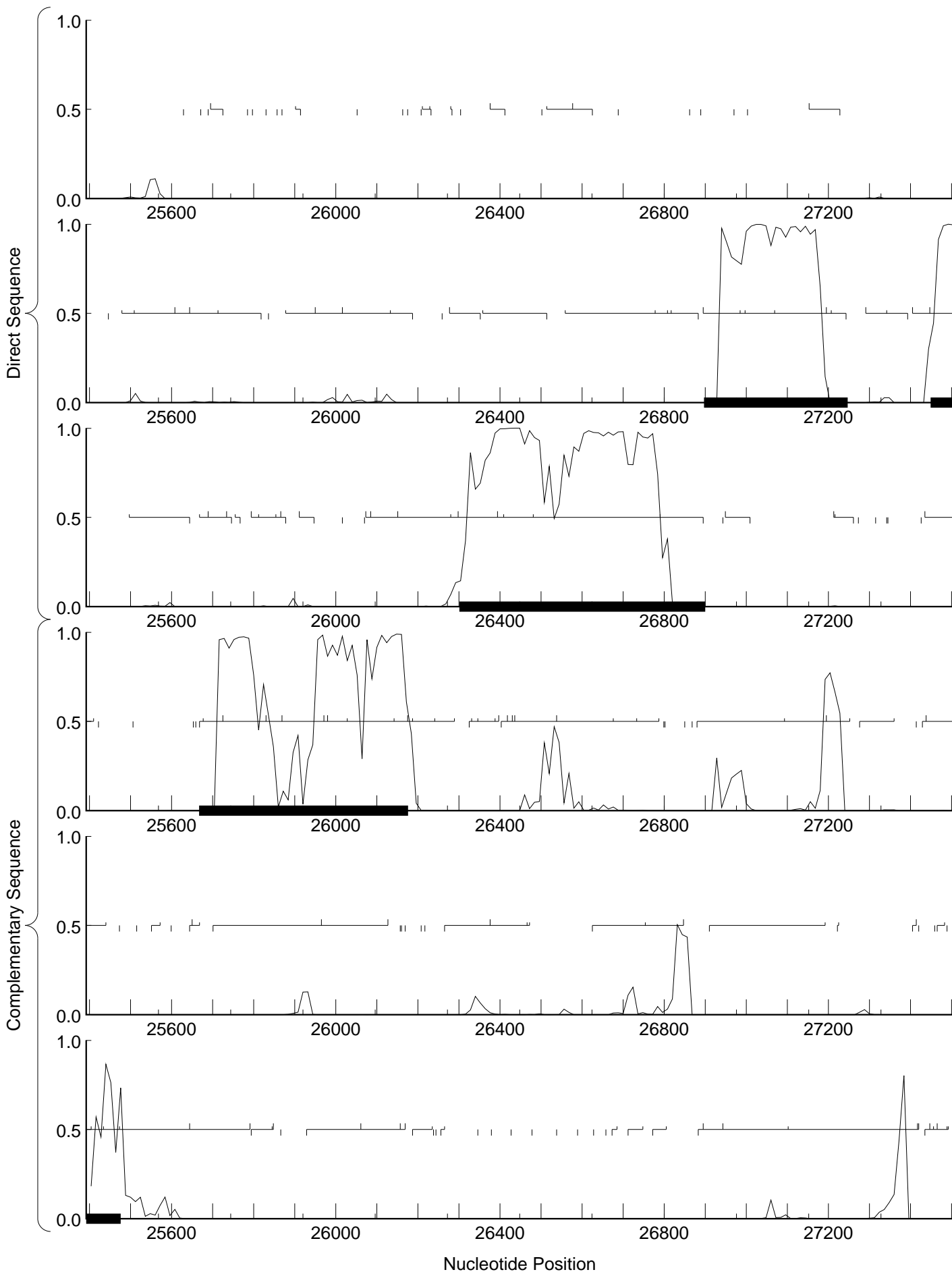


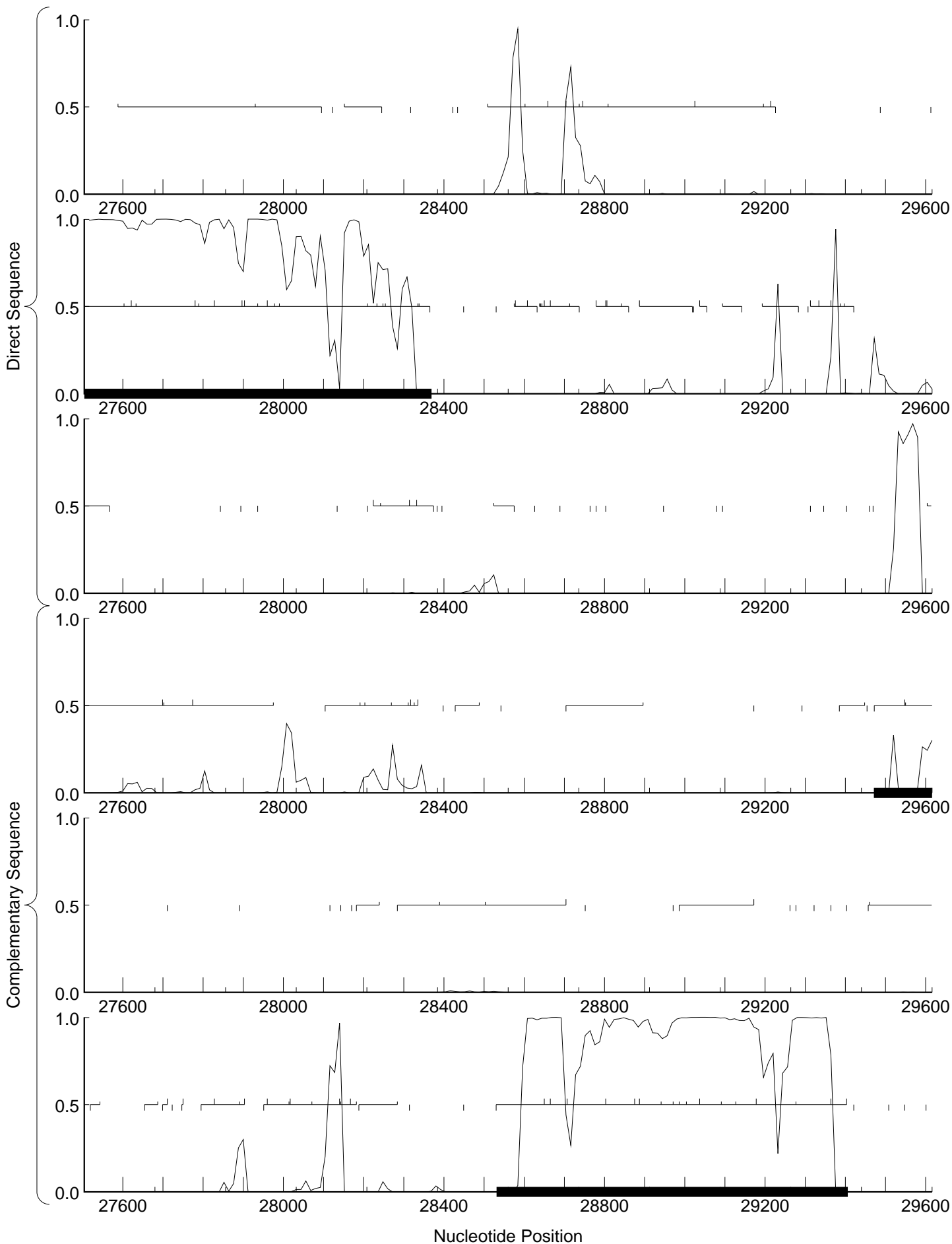


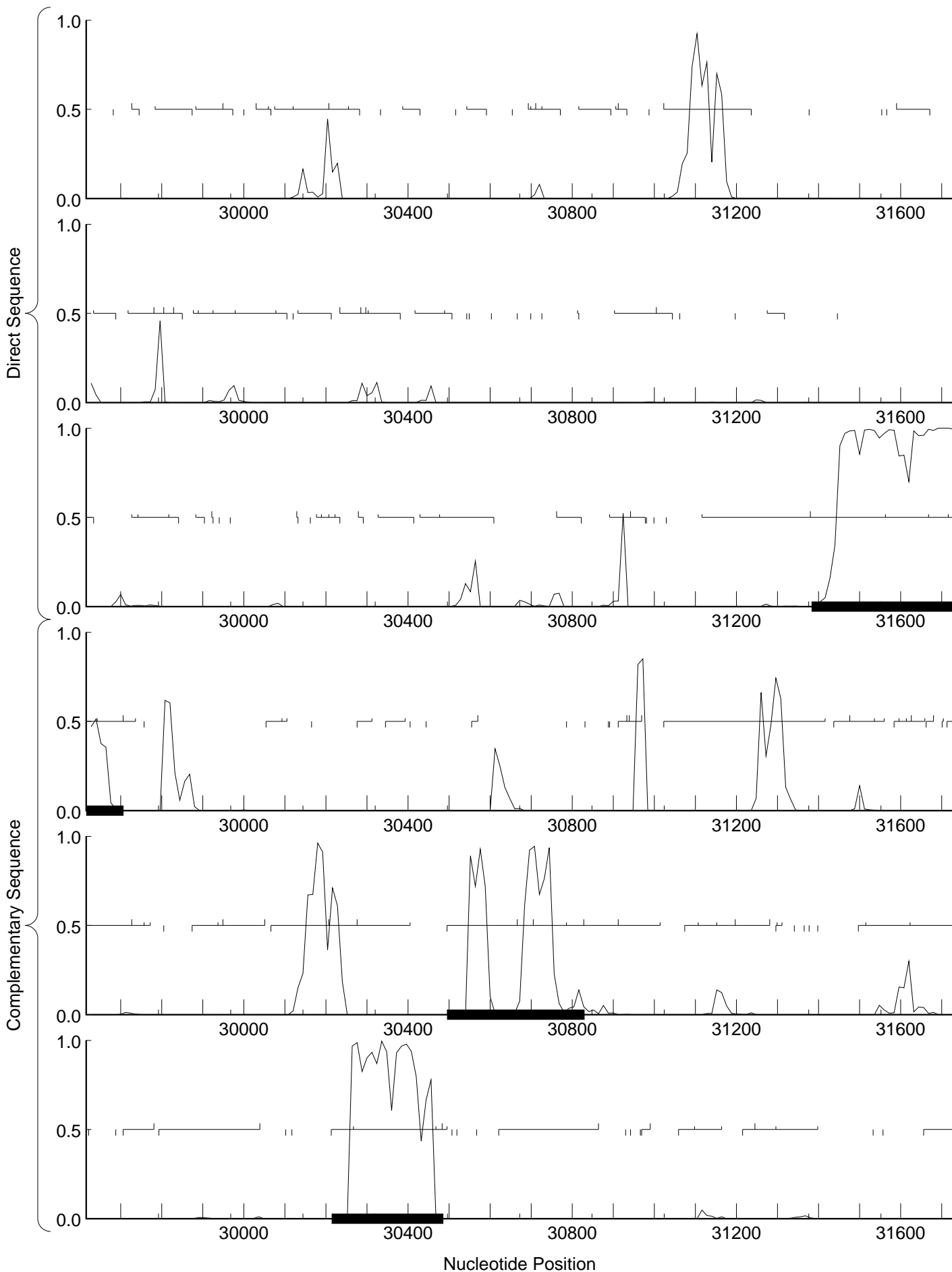
GeneMark.hmm prediction





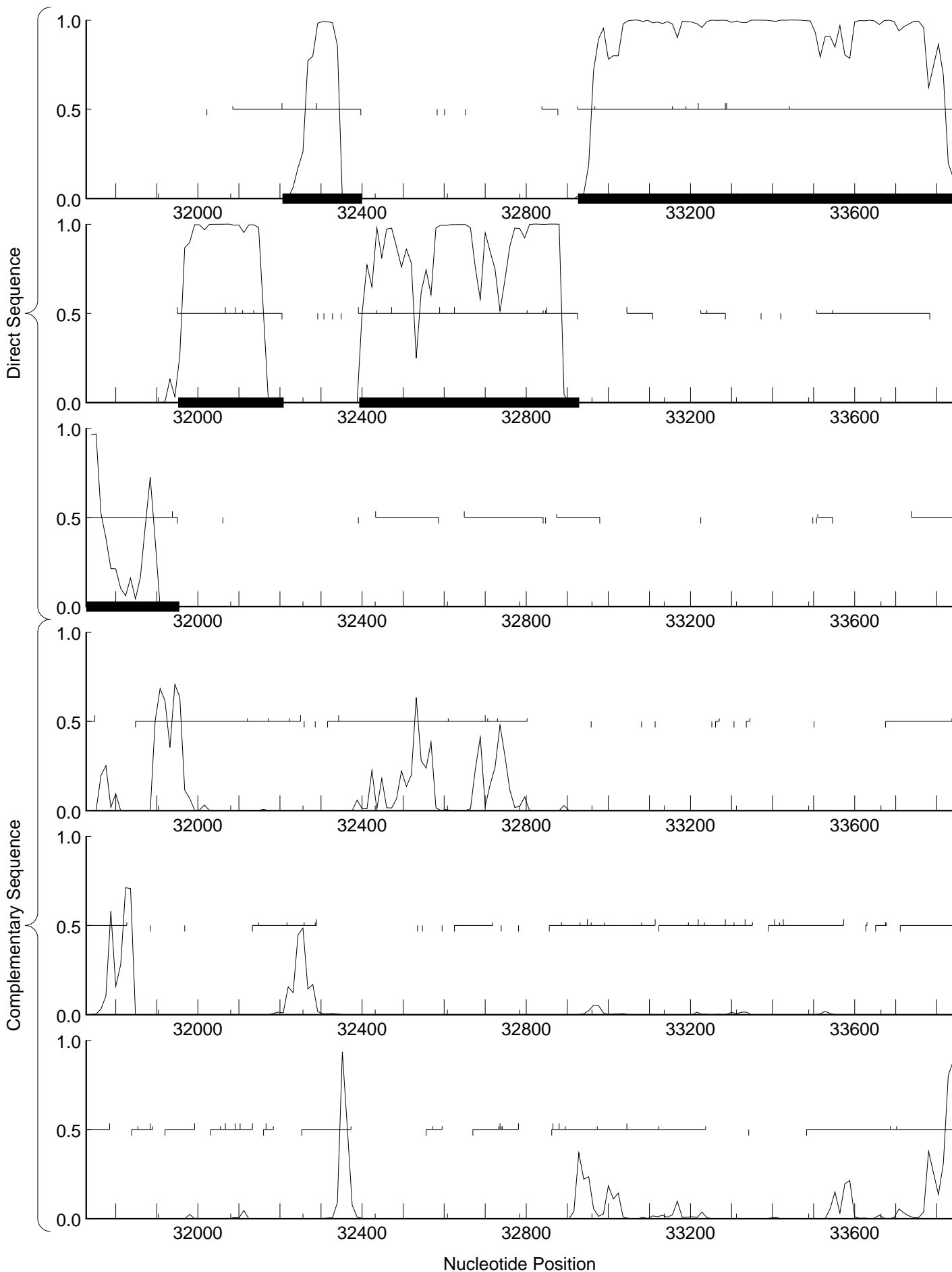




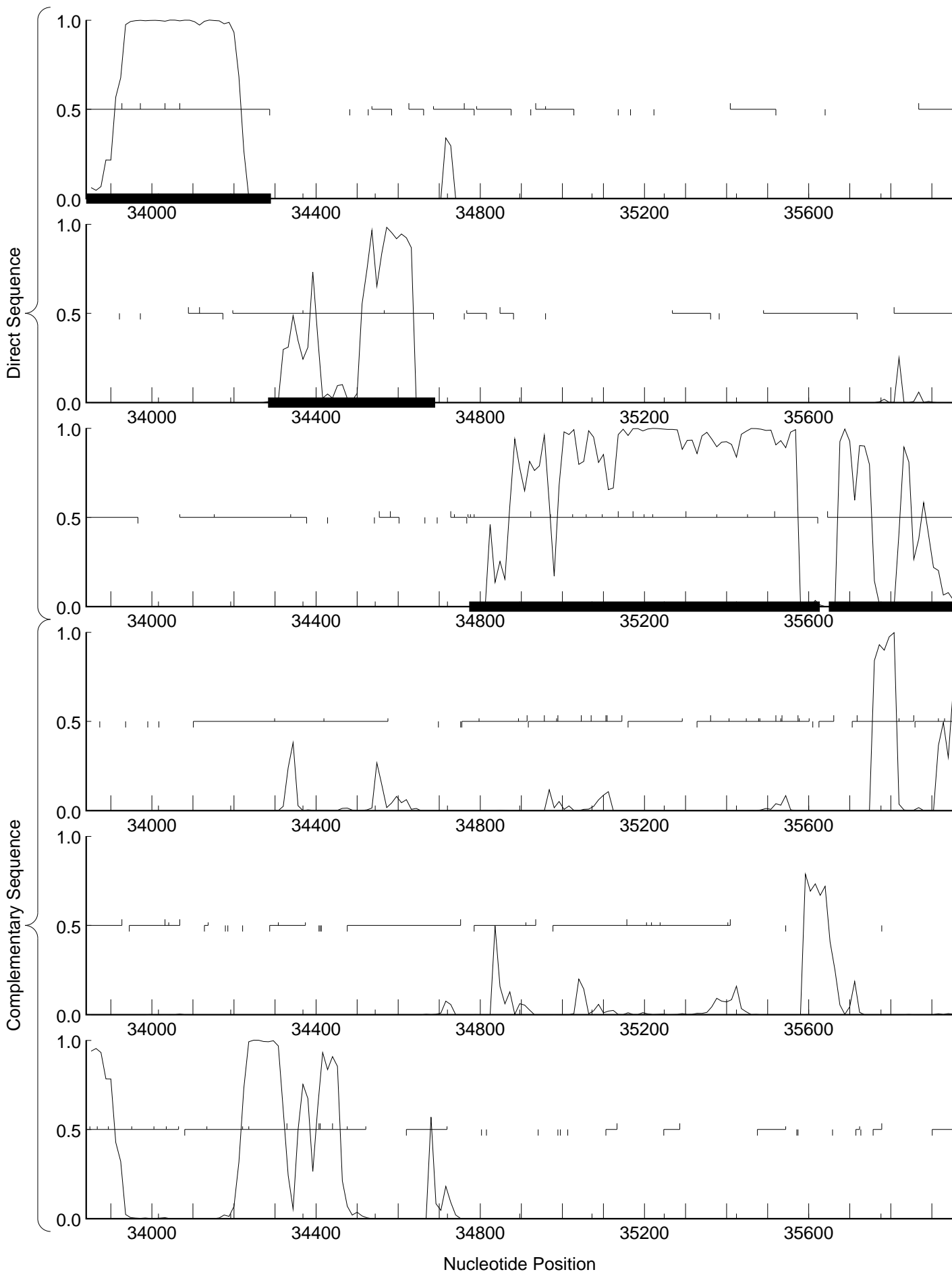


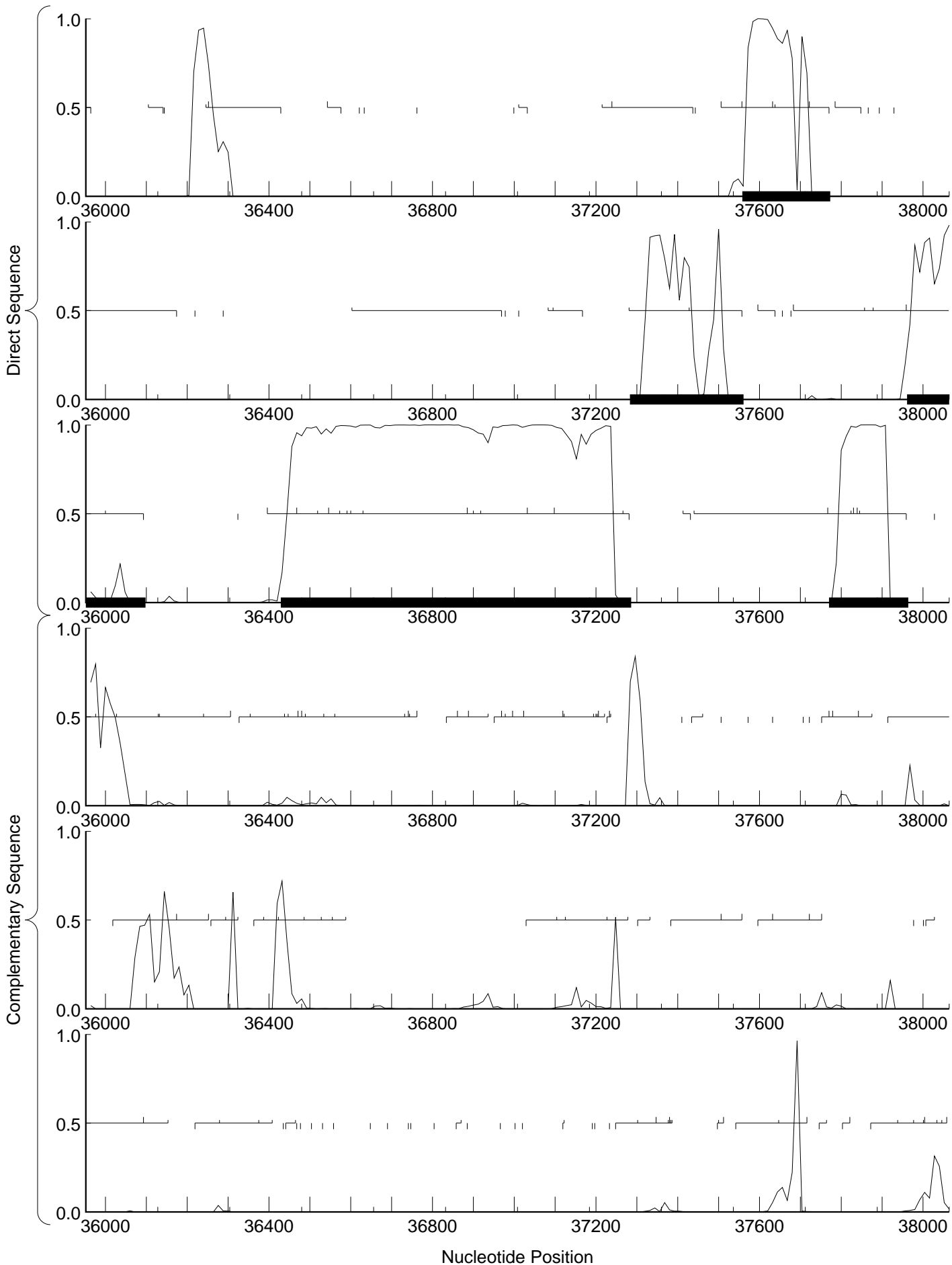
complete sequence, 43177 bp including 12-base 3' overhang (TCCGCCGCGTGA), Cluster FF, Order 2, Window 96, Step 12, 17/22

GeneMark_hmm prediction

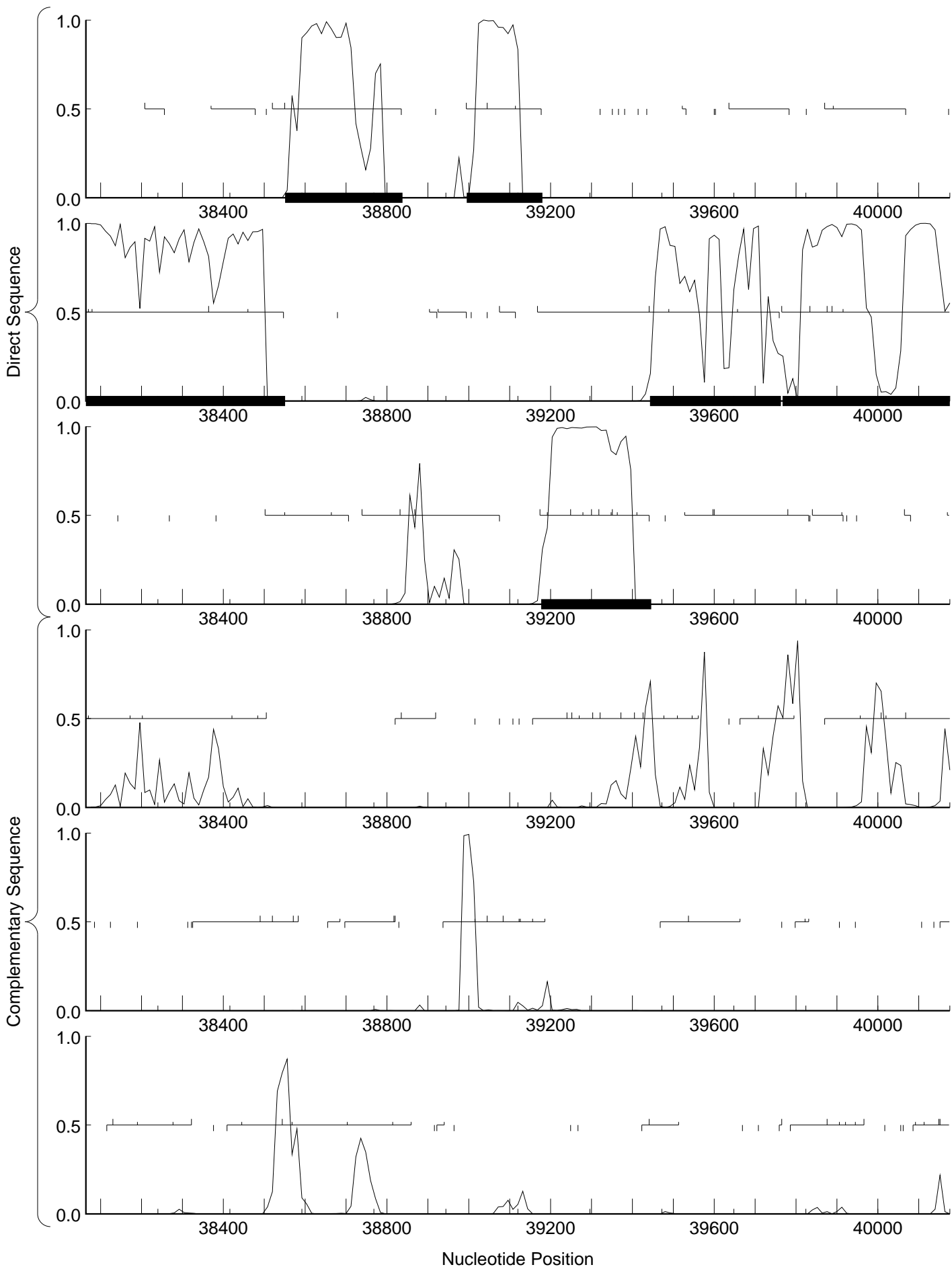


GeneMark_hmm_prediction

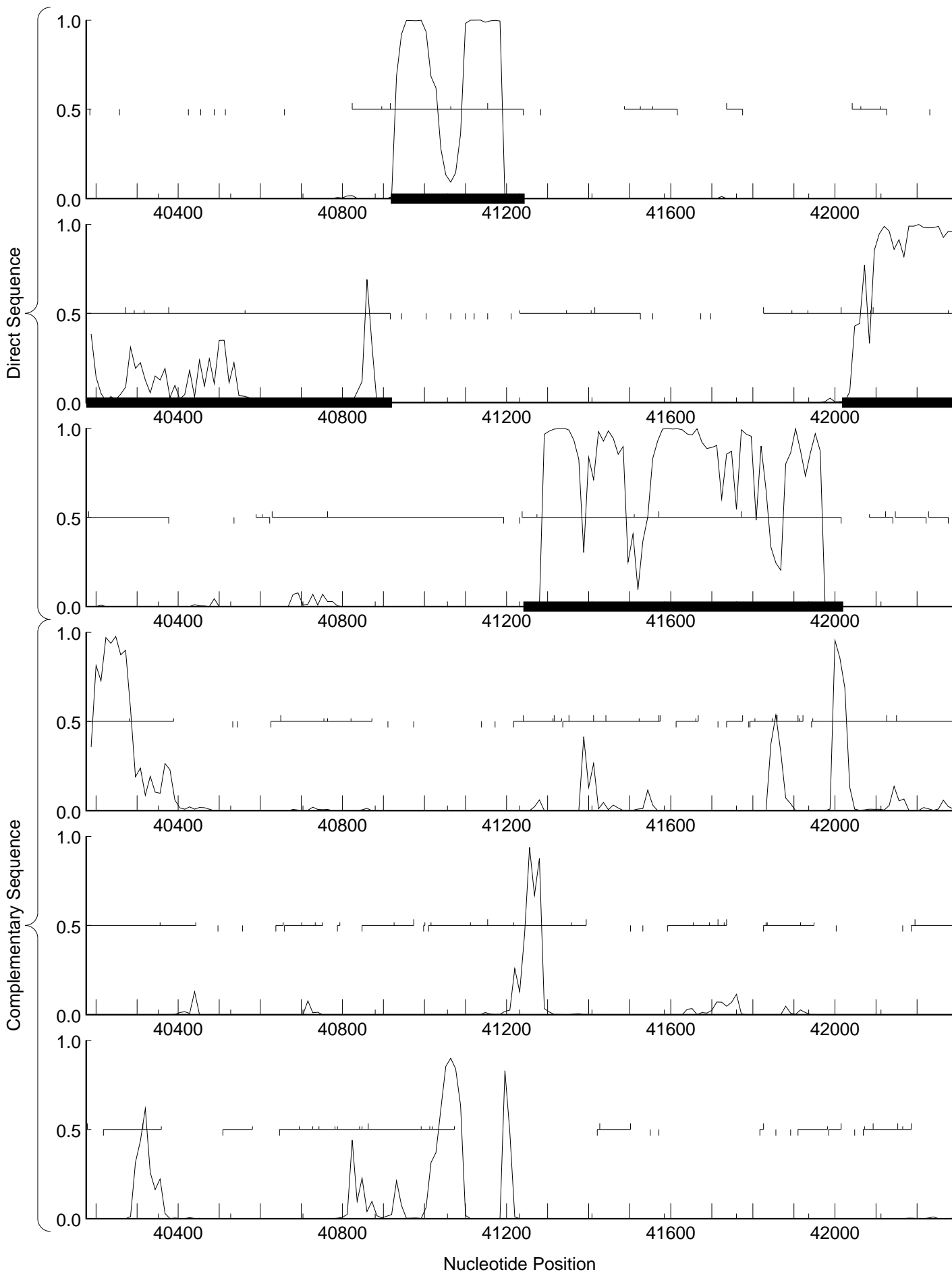




GeneMark.hmm prediction



GeneMark_hmm prediction



GeneMark.hmm prediction

