

GeneMark

Version 2.5p (09.08.06)

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PROGRAM INFORMATION

Sequence : Microbacterium phage VitulaEligans complete sequence, 17534 bp, including 9-base 3' overhang
Analysis Date : 3/20/18 at 3:50:30
Pages : 10
Sequence Length : 17534 bp
GC Content : 68.77%

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,

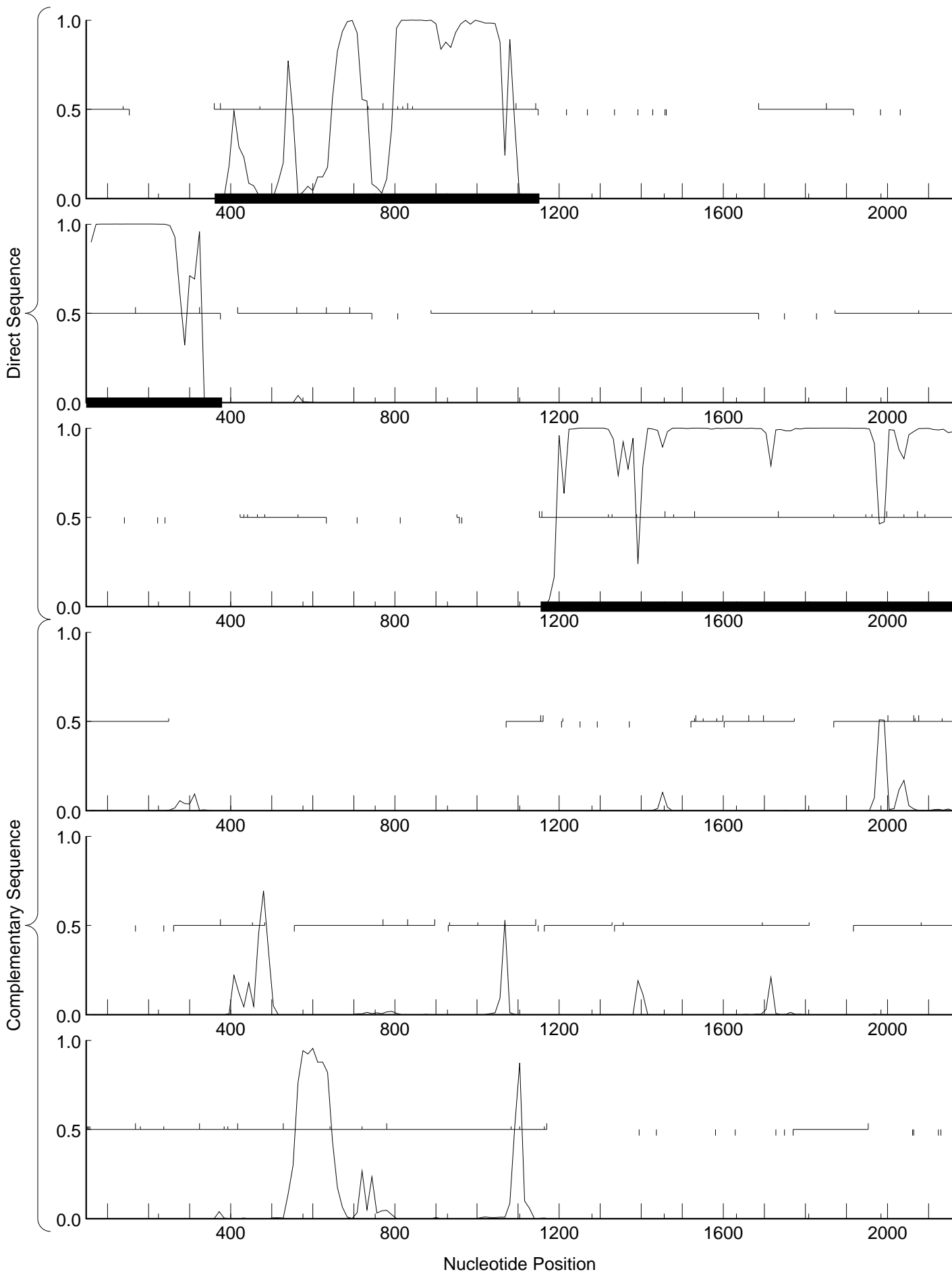
MATRIX INFORMATION

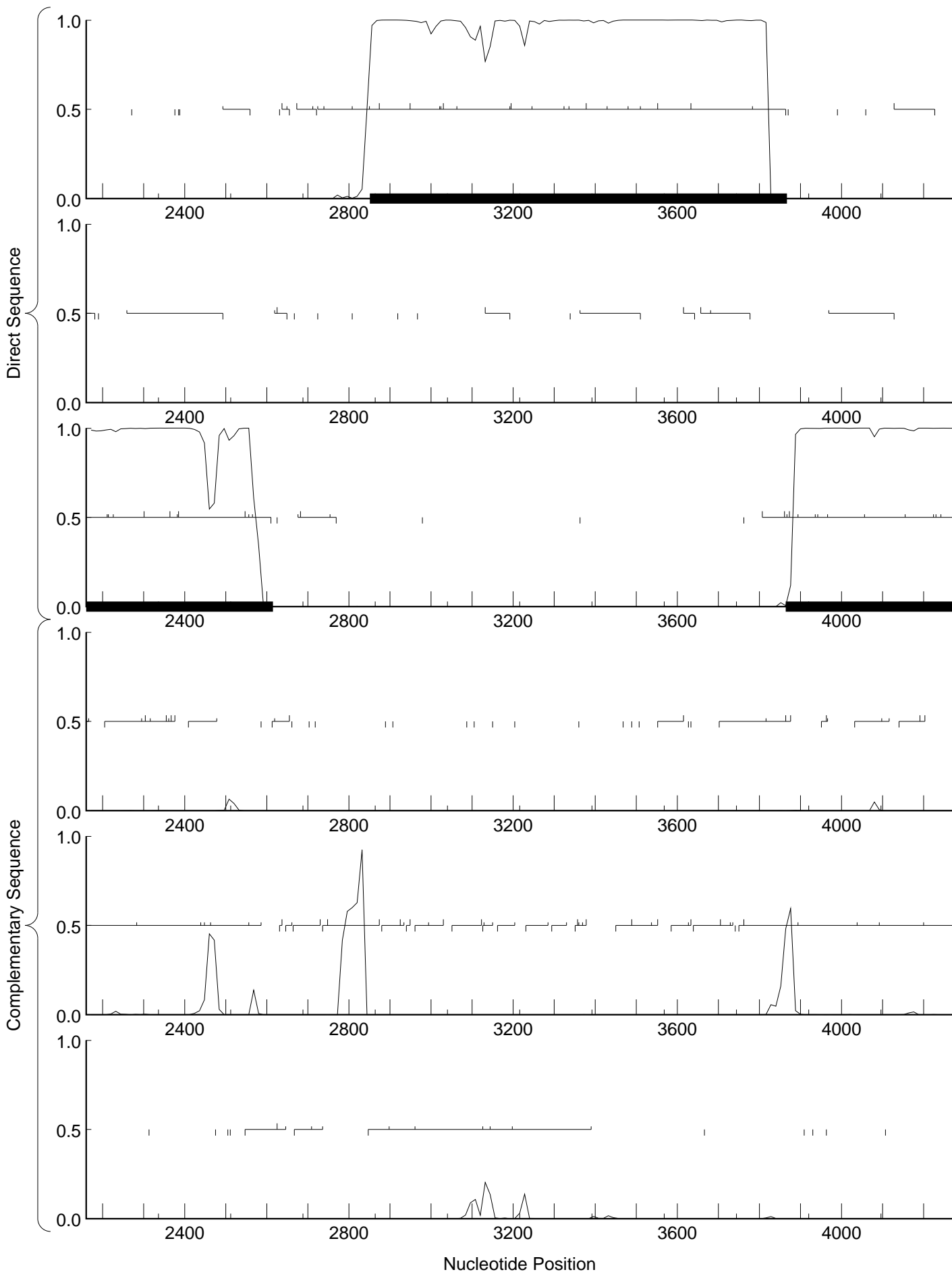
Matrix : Heuristic, GC = 69
Author : Borodovsky Laboratory - Georgia Tech
Order : 2

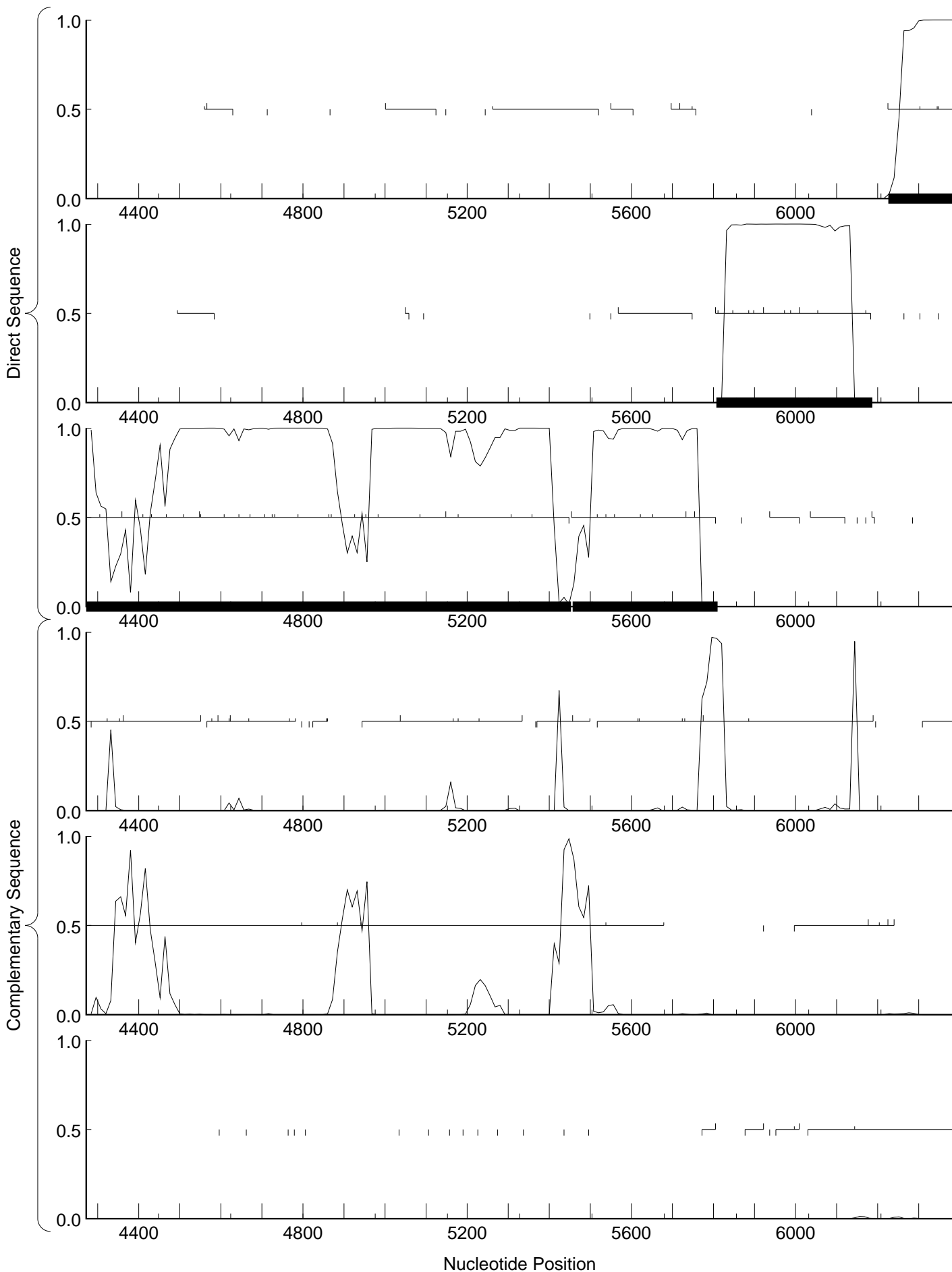
Send questions / comments to:
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Atlanta, GA 30332-0230

Matrix notes & comments

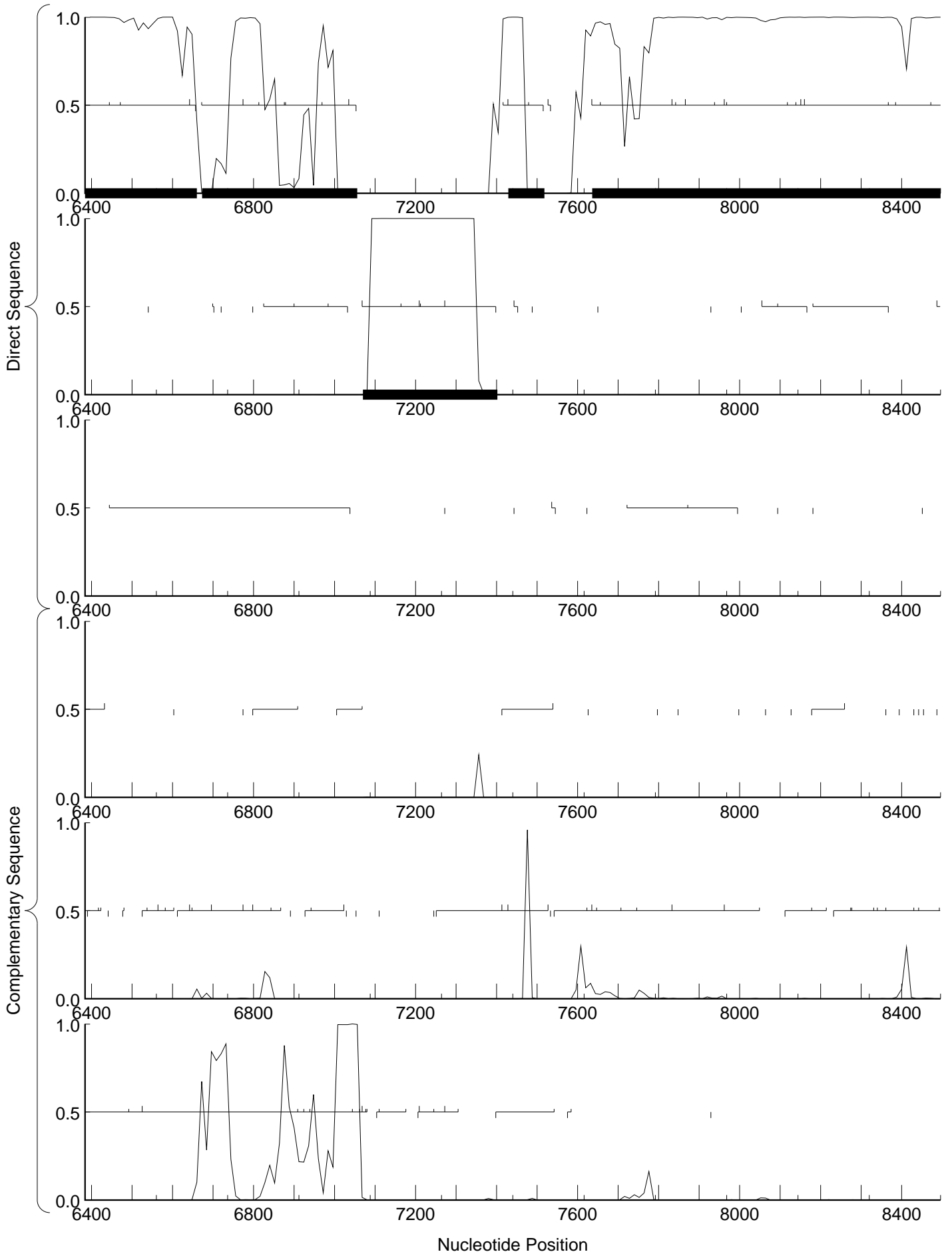
For details on the model building procedure see:
Besemer J. and Borodovsky M.
"Heuristic approach to deriving models for gene finding"
NAR, 1999, Vol. 27, No. 19, pp. 3911-3920

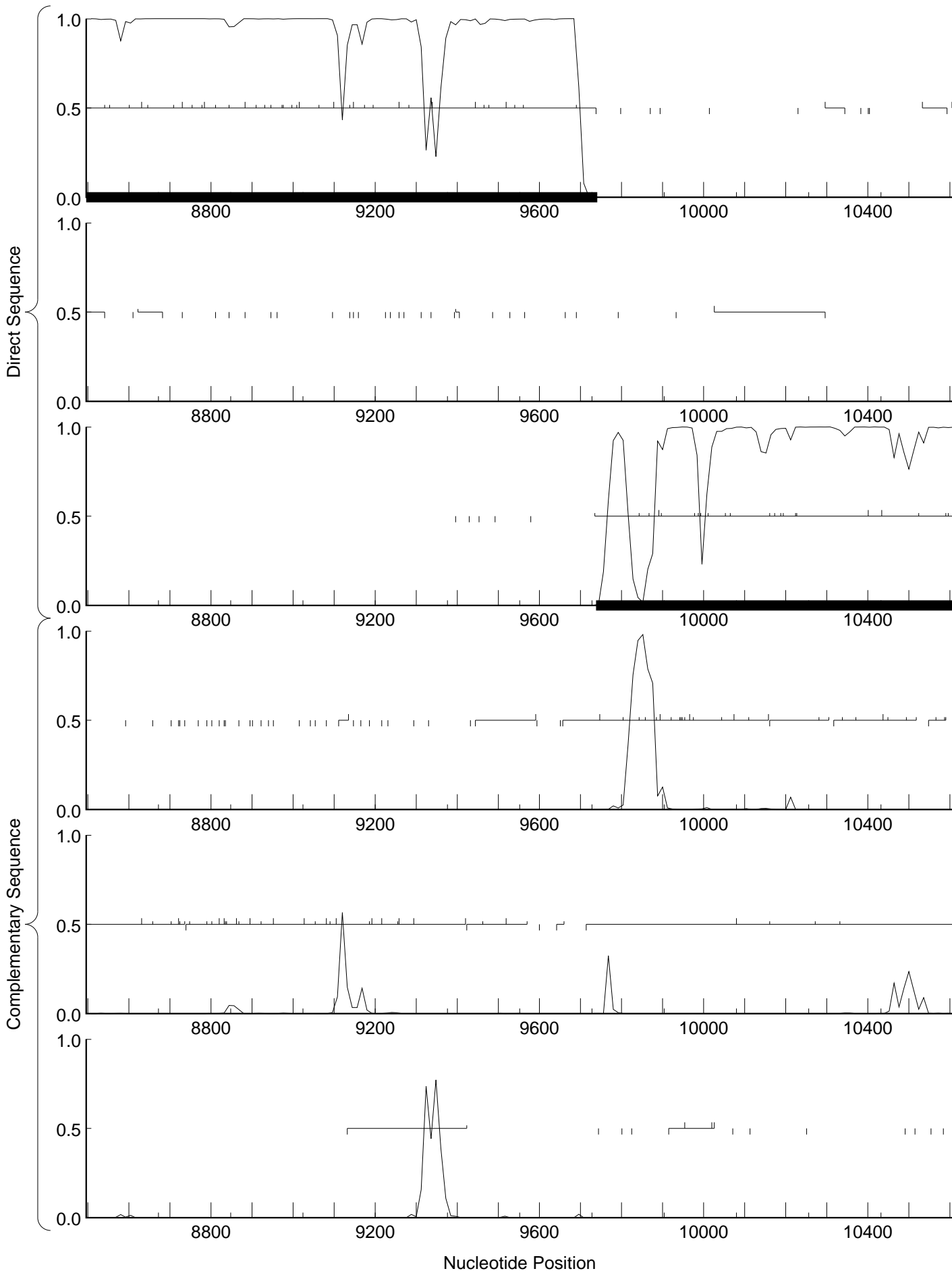




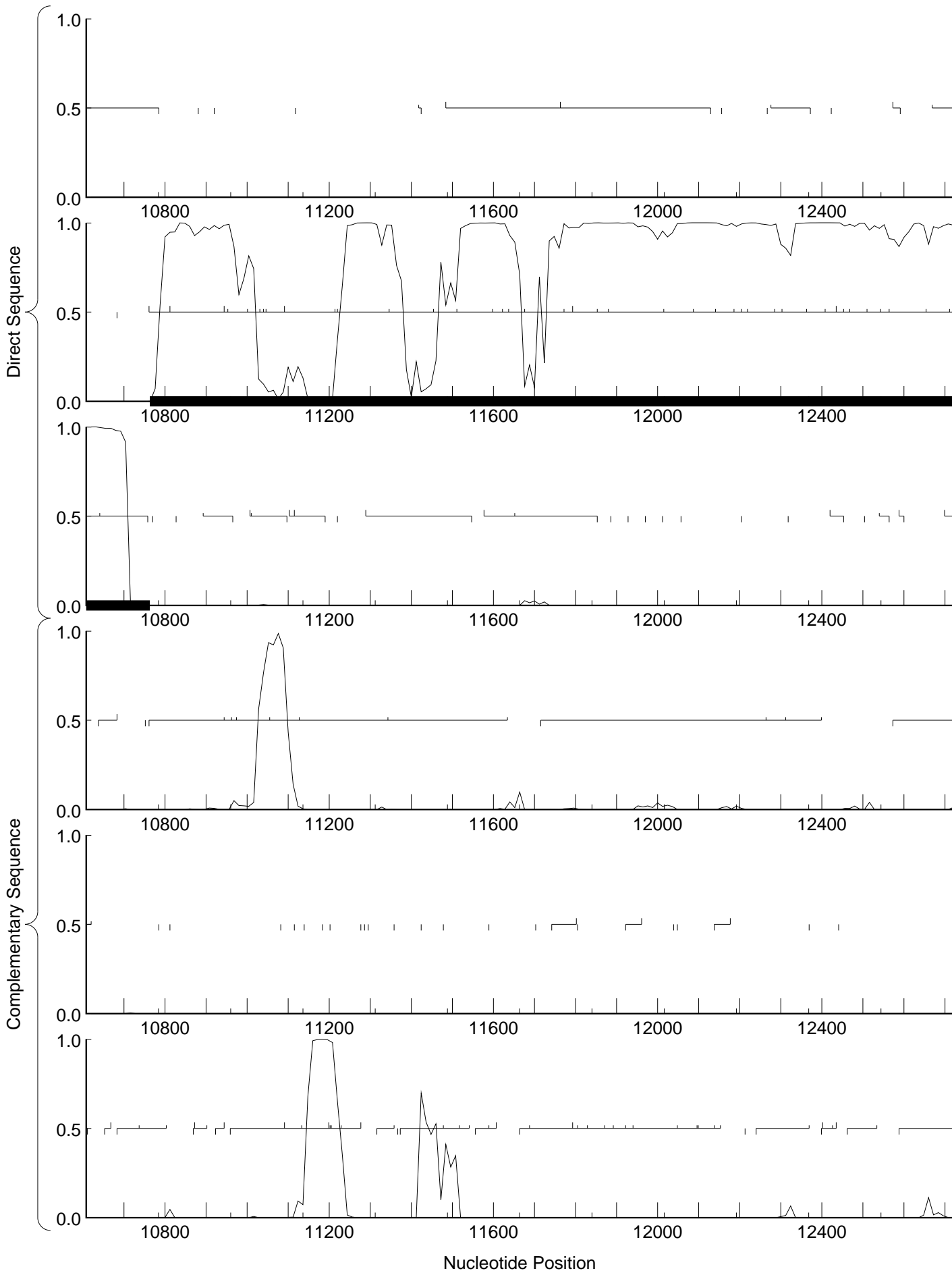


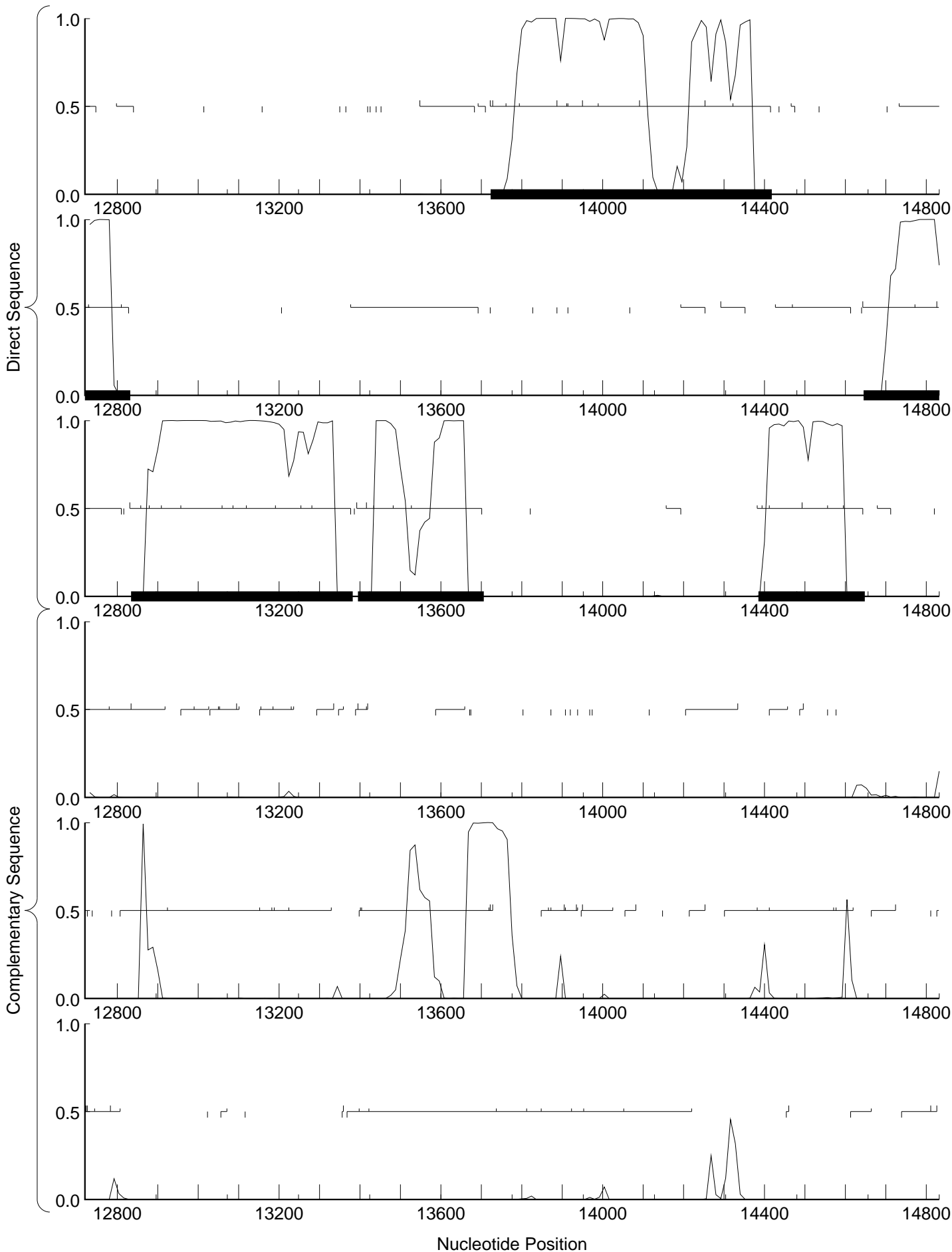
GeneMark.hmm prediction
ans complete sequence, 17534 bp, including 9-base 3' overhang (CCCGCCCCA), Cluster EE, Order 2, Window 96, Step 12, 5/10

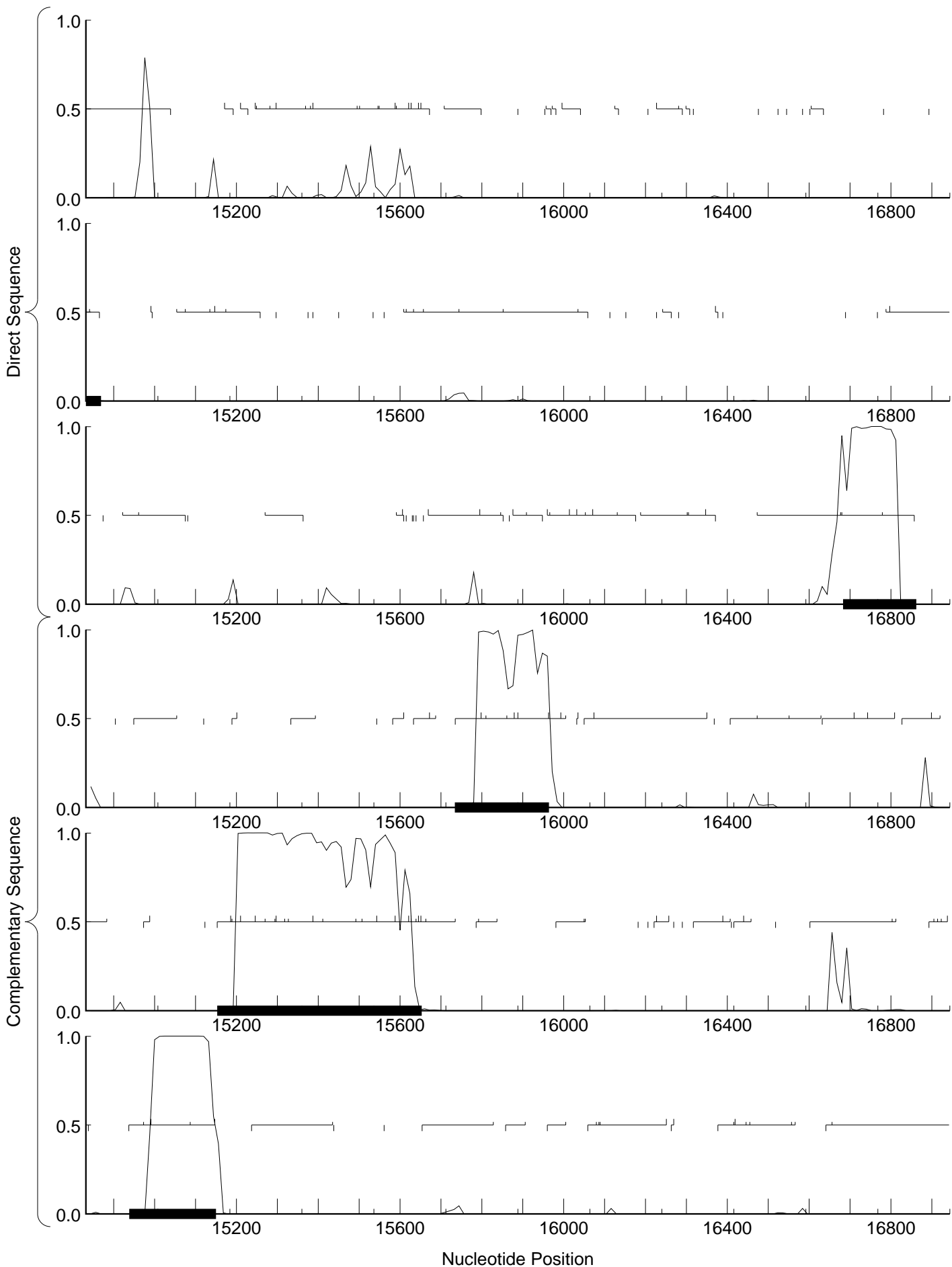




GeneMark.hmm prediction







GeneMark.hmm prediction
Complete sequence, 17534 bp, including 9-base 3' overhang (CCGCCCCA), Cluster EE, Order 2, Window 96, Step 12, 10/10

