

GeneMark

Version 2.5p (09.08.06)

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PROGRAM INFORMATION

Sequence : Microbacterium phage Lucky3 complete sequence, 39640 bp, circularly permuted, Cluster EA4
Analysis Date : 11/25/17 at 0:53:42
Pages : 20
Sequence Length : 39640 bp
GC Content : 64.09%

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,

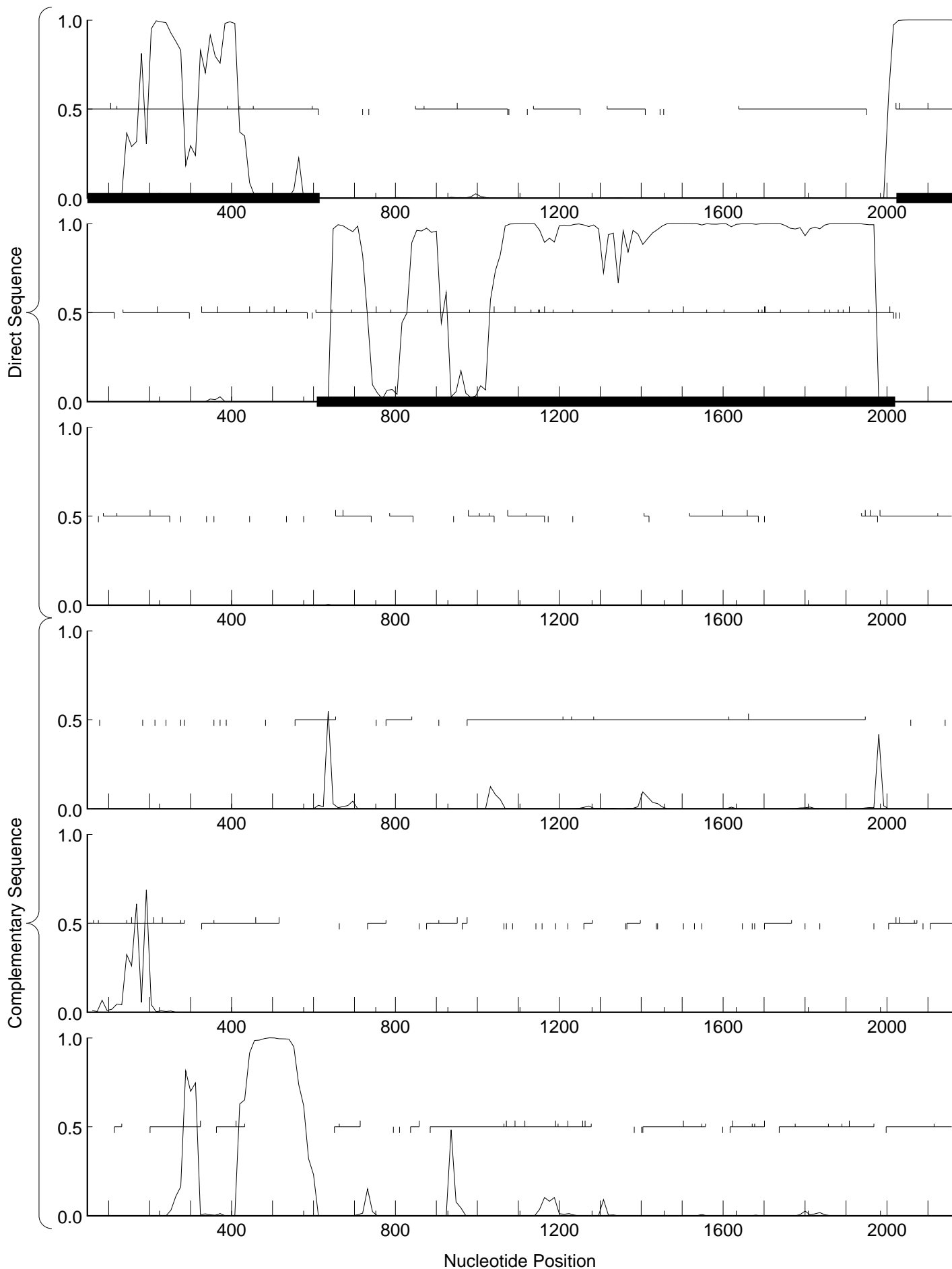
MATRIX INFORMATION

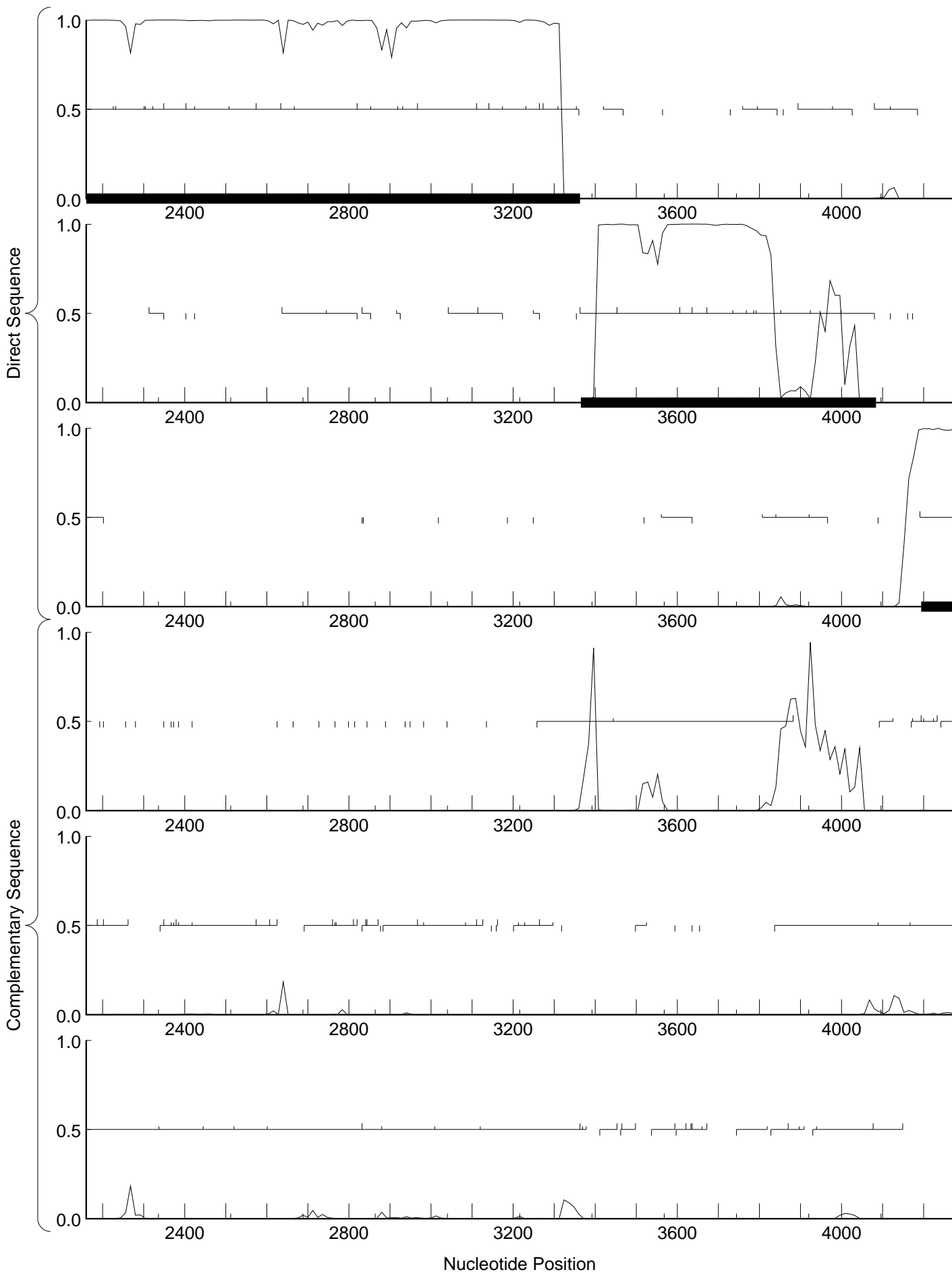
Matrix : Heuristic, GC = 64
Author : Borodovsky Laboratory - Georgia Tech
Order : 2

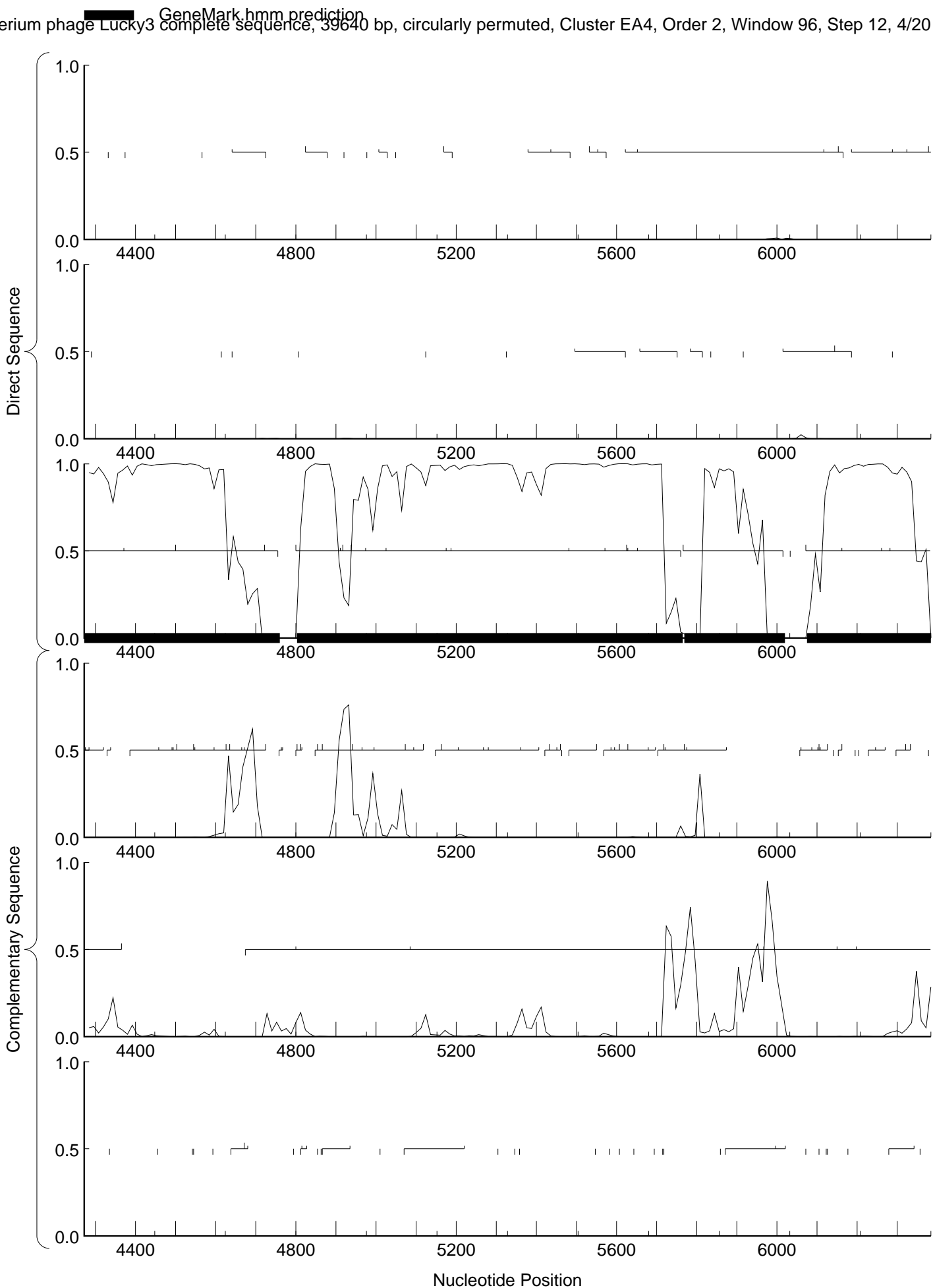
Send questions / comments to:
Dr. M. Borodovsky
Georgia Institute of Technology
School of Biology
Atlanta, GA 30332-0230

Matrix notes & comments

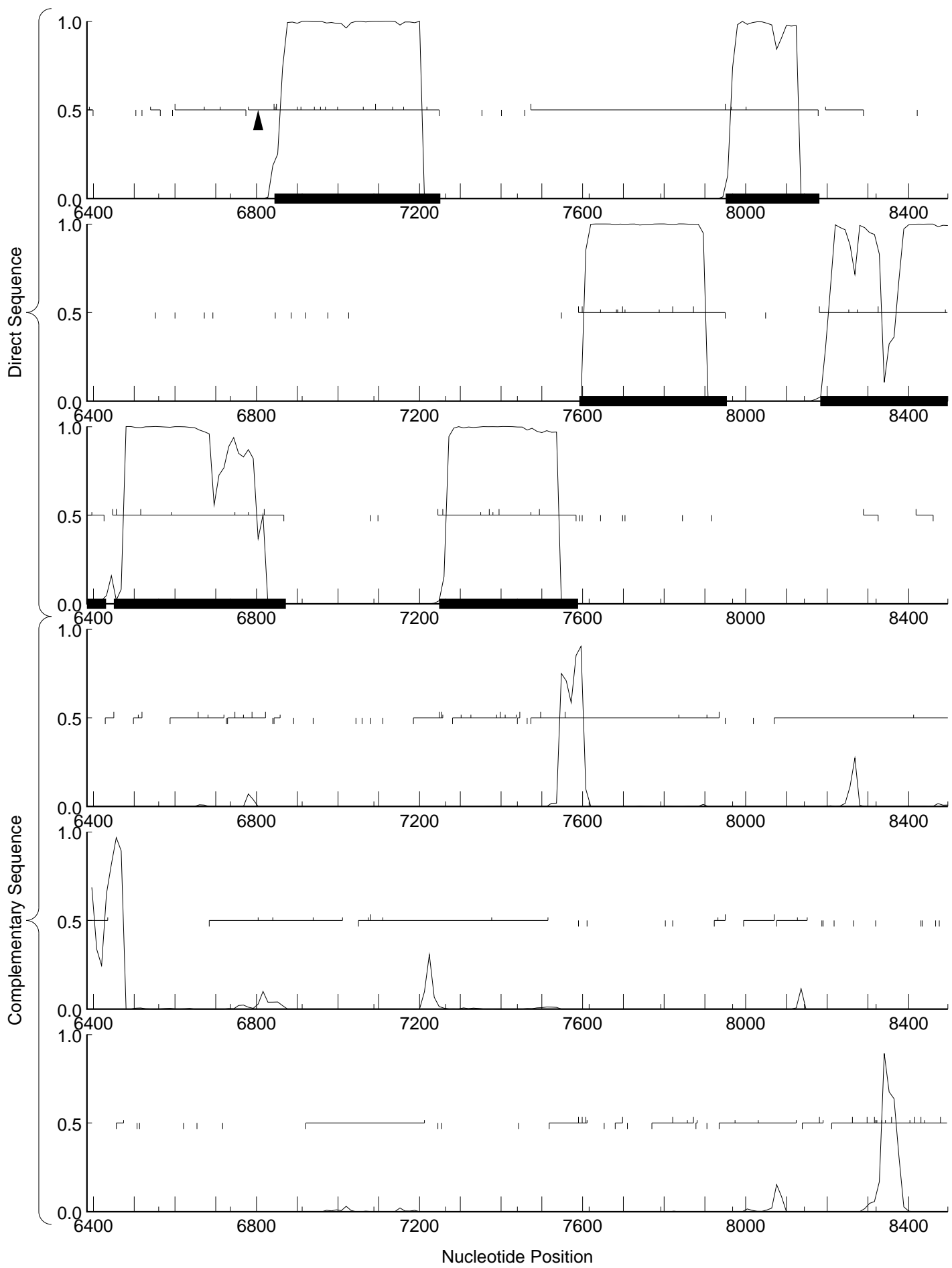
For details on the model building procedure see:
Besemer J. and Borodovsky M.
"Heuristic approach to deriving models for gene finding"
NAR, 1999, Vol. 27, No. 19, pp. 3911-3920



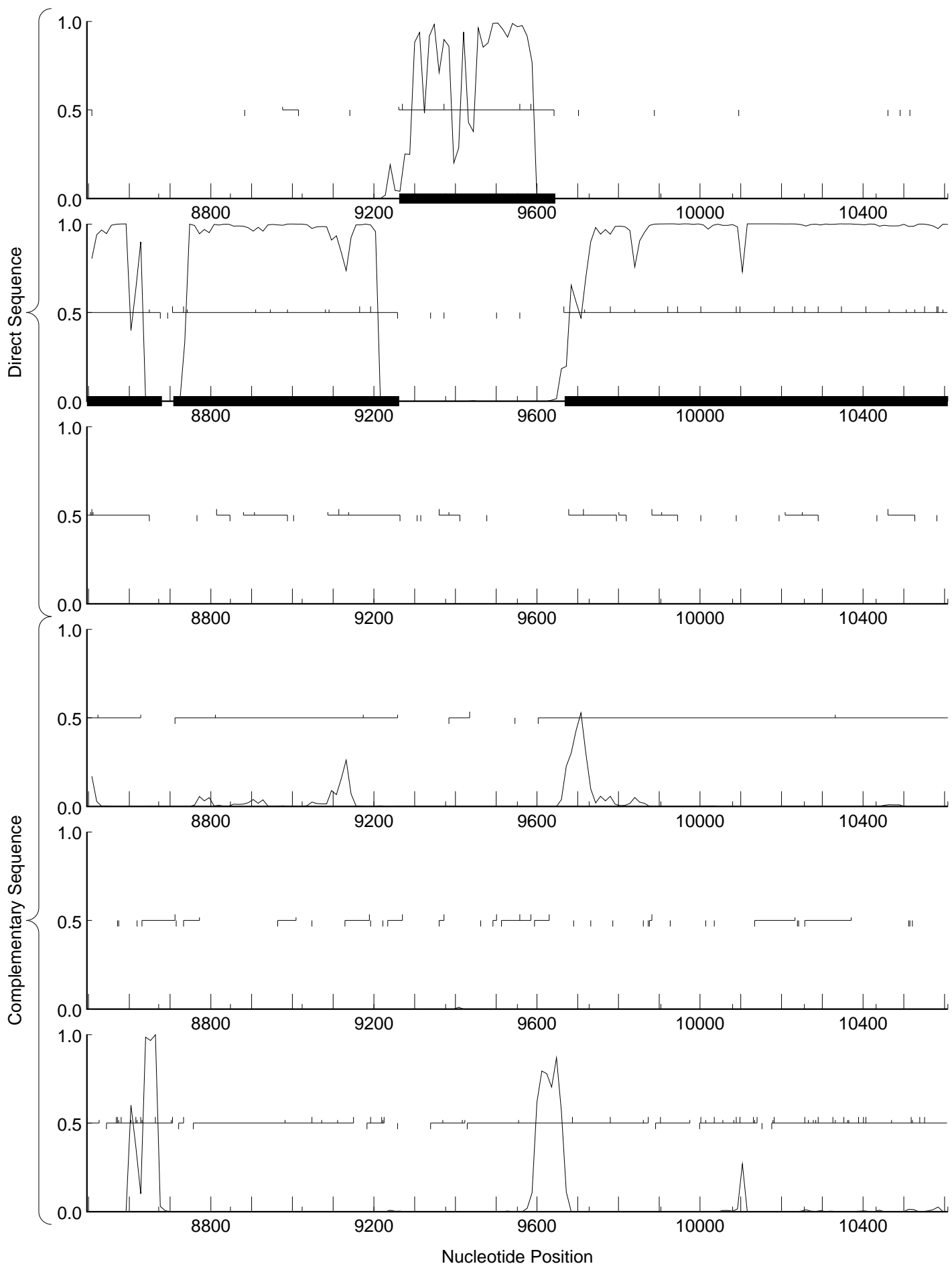




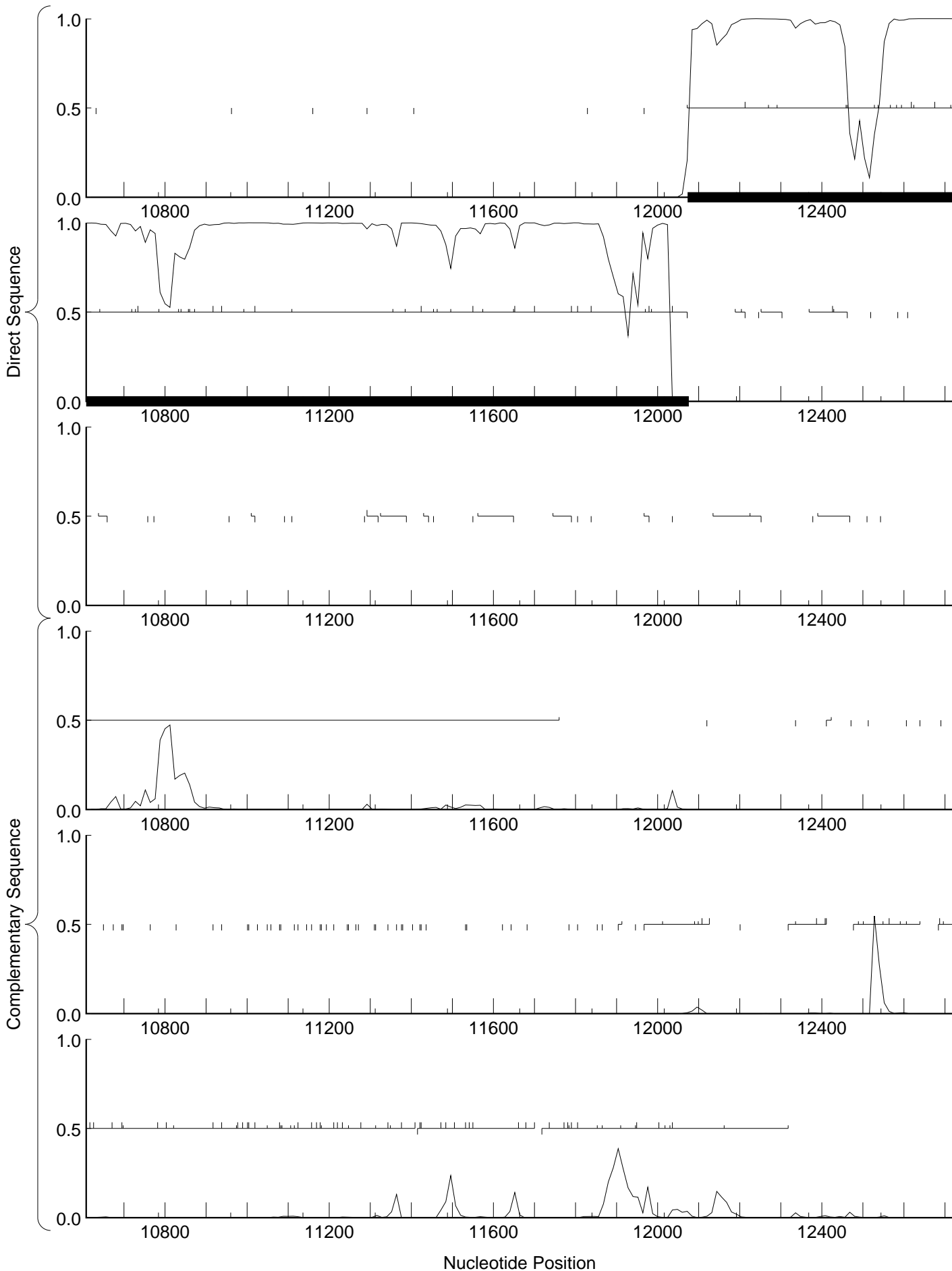
GeneMark.hmm prediction

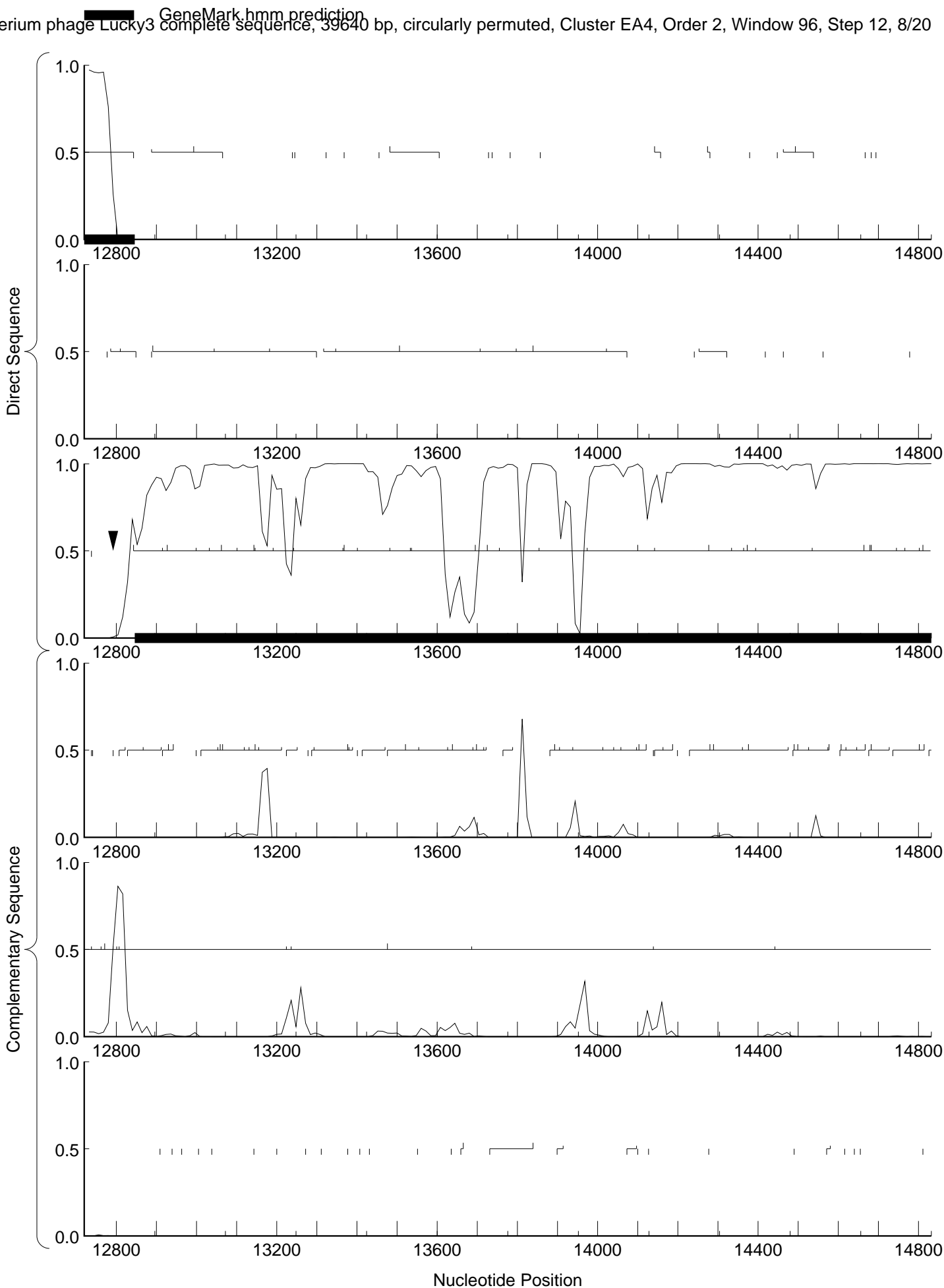


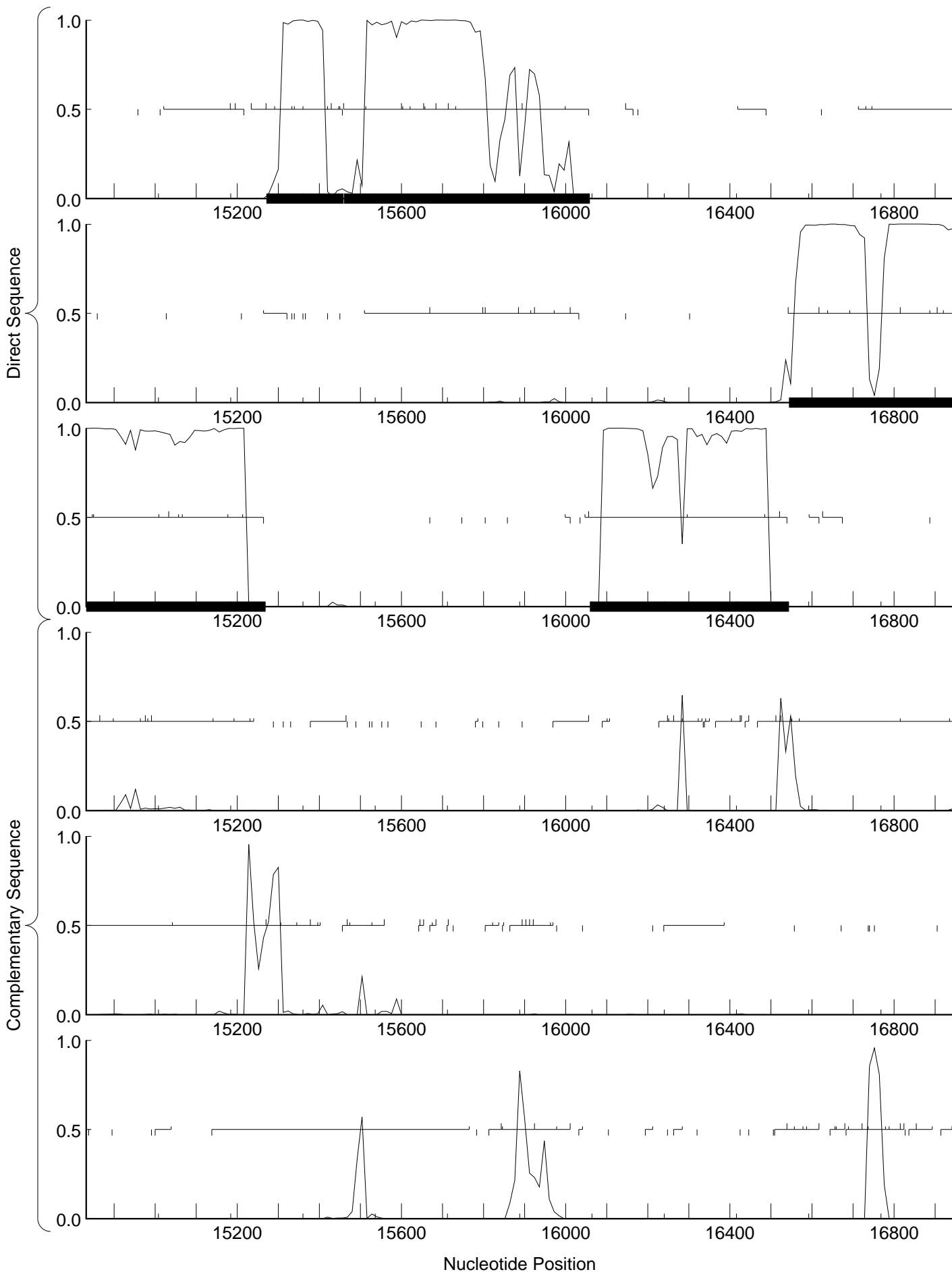
GeneMark.hmm prediction

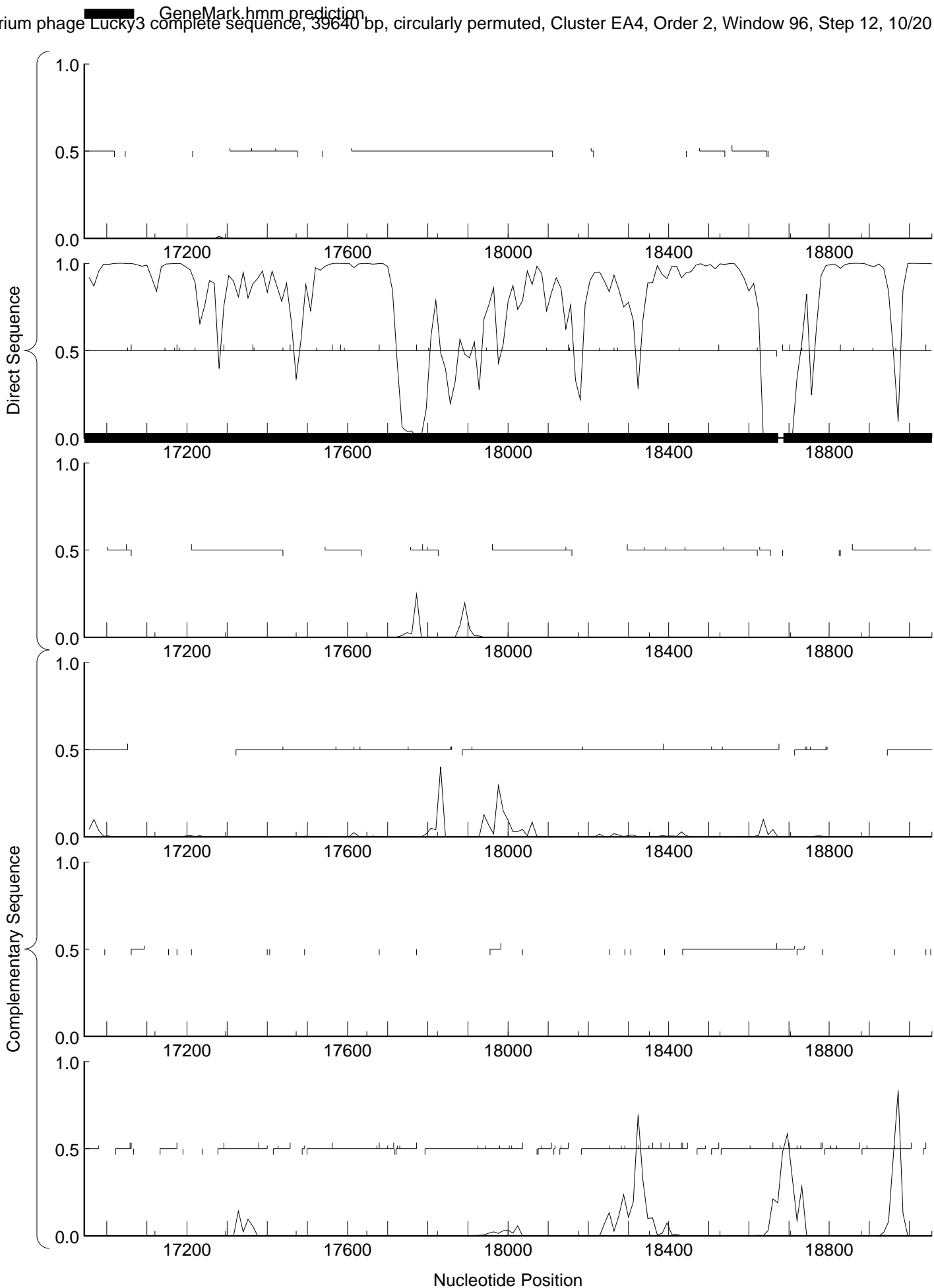


GeneMark.hmm prediction

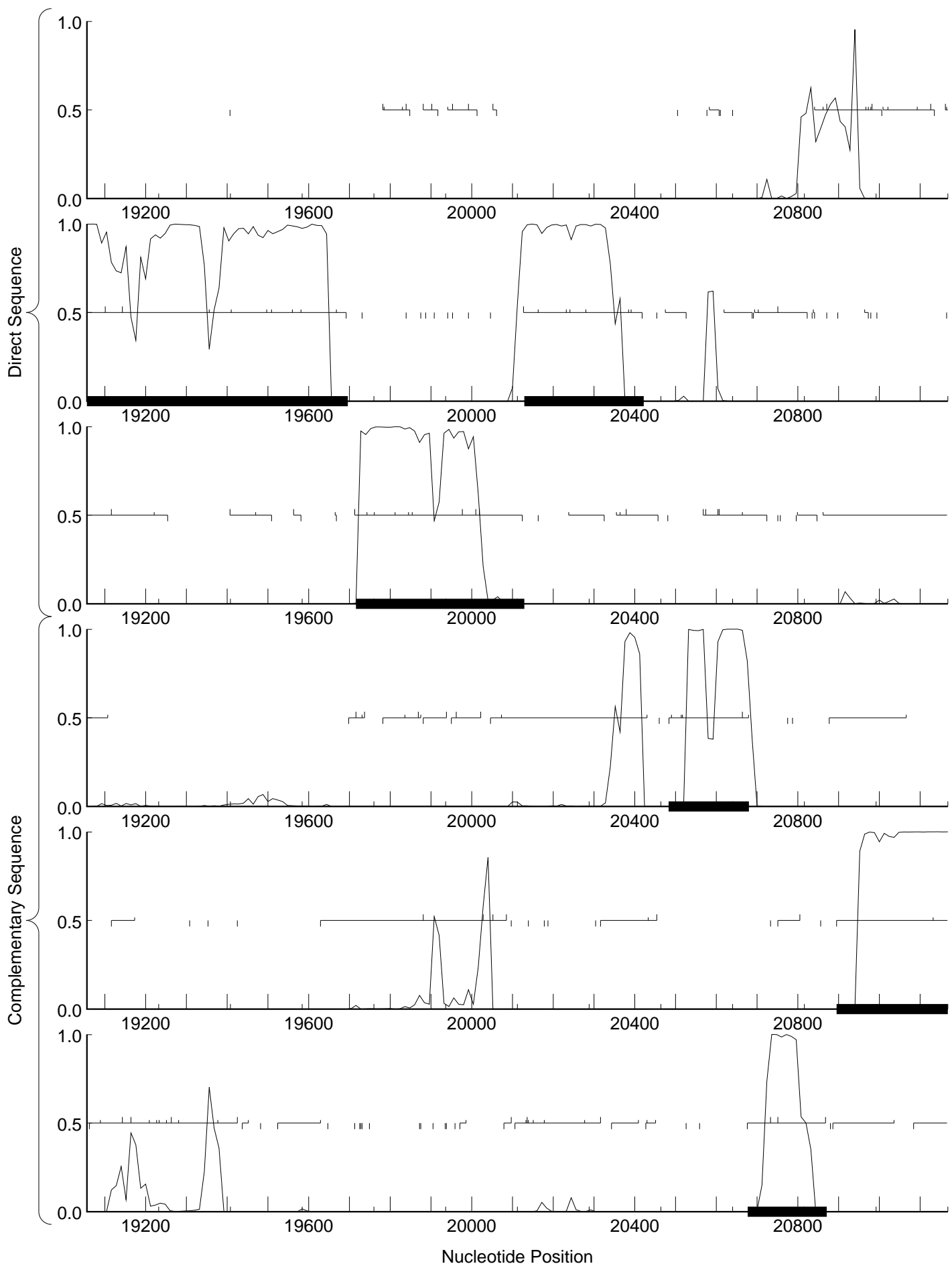


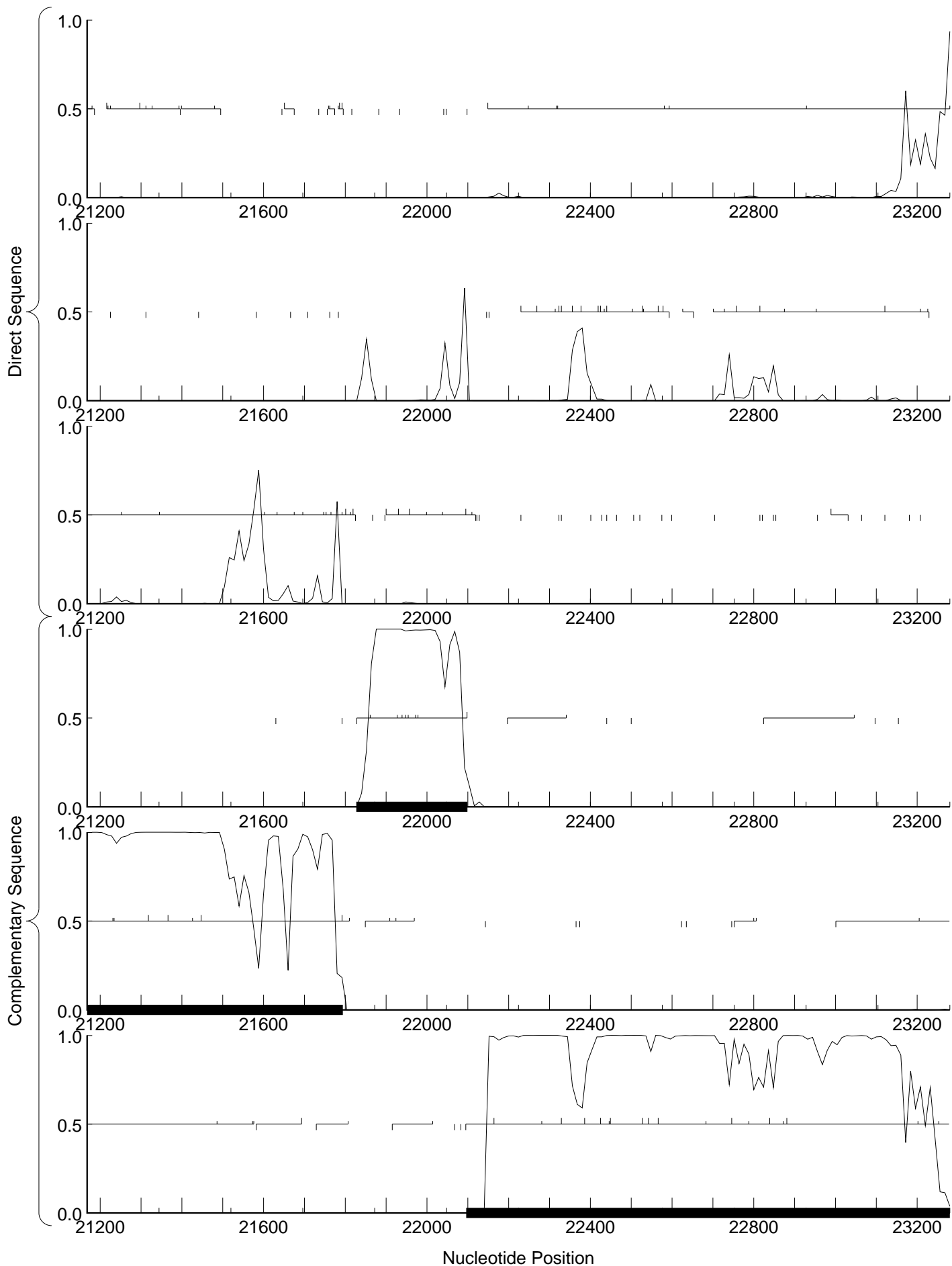


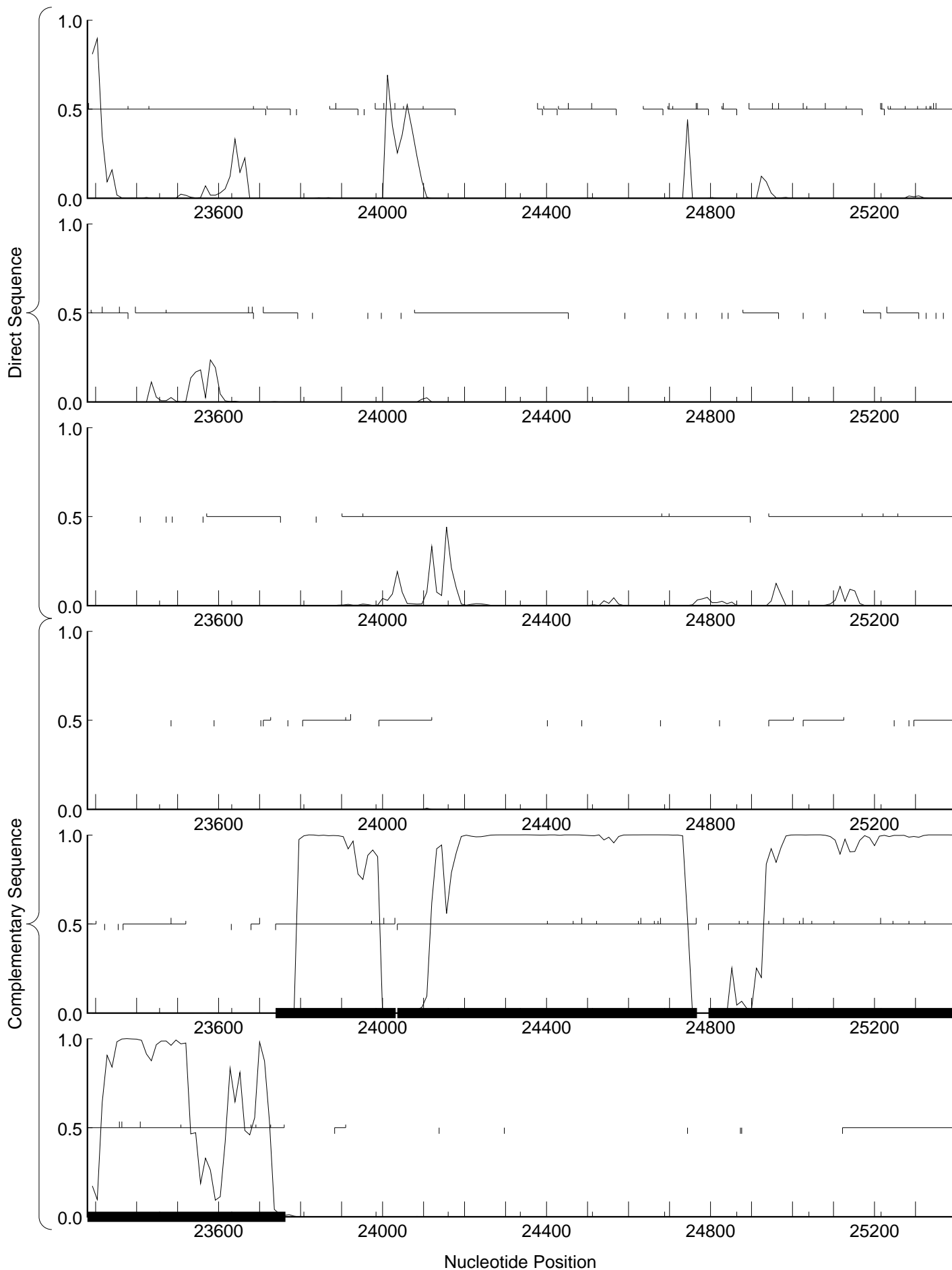




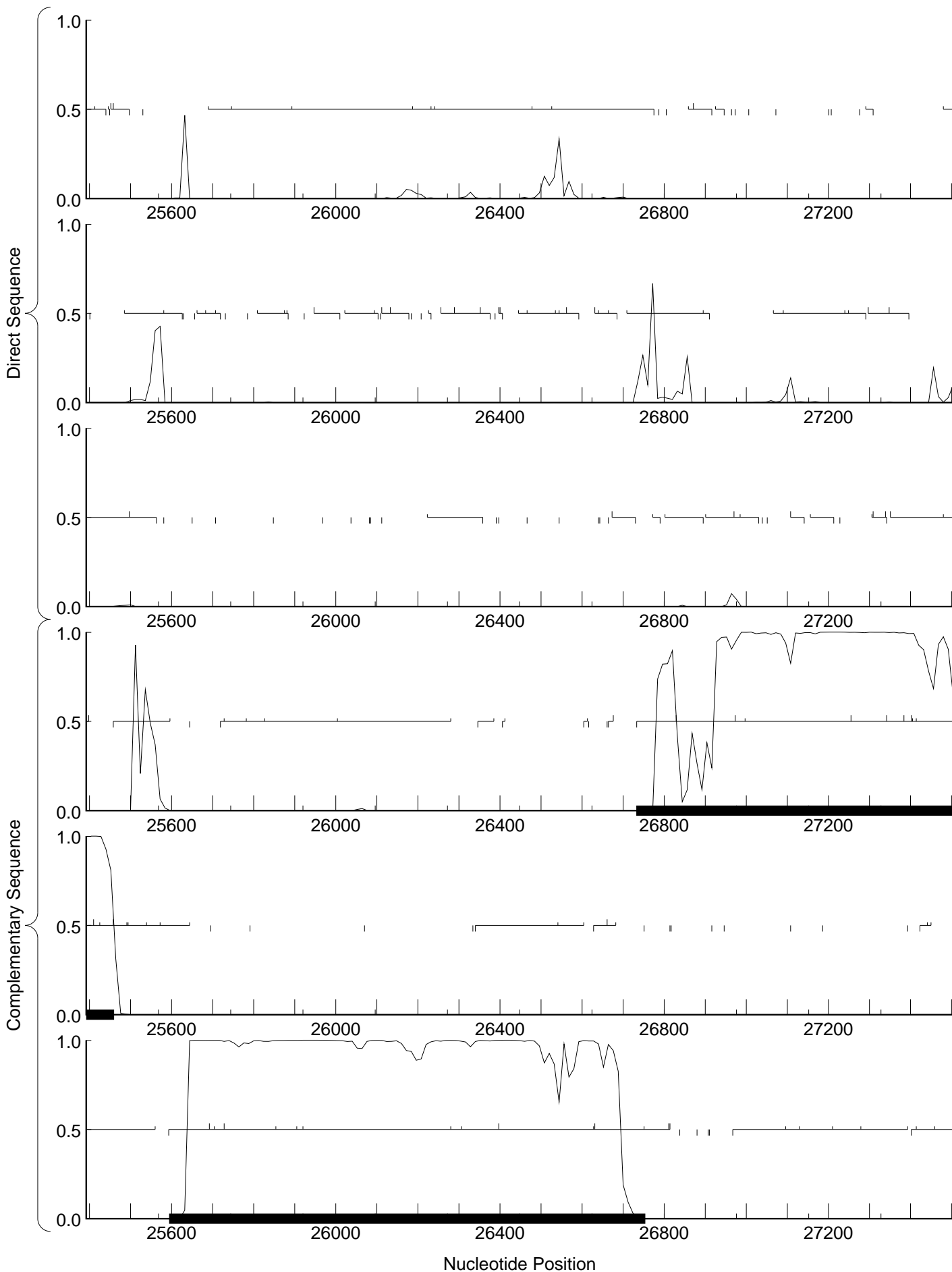
GeneMark.hmm prediction

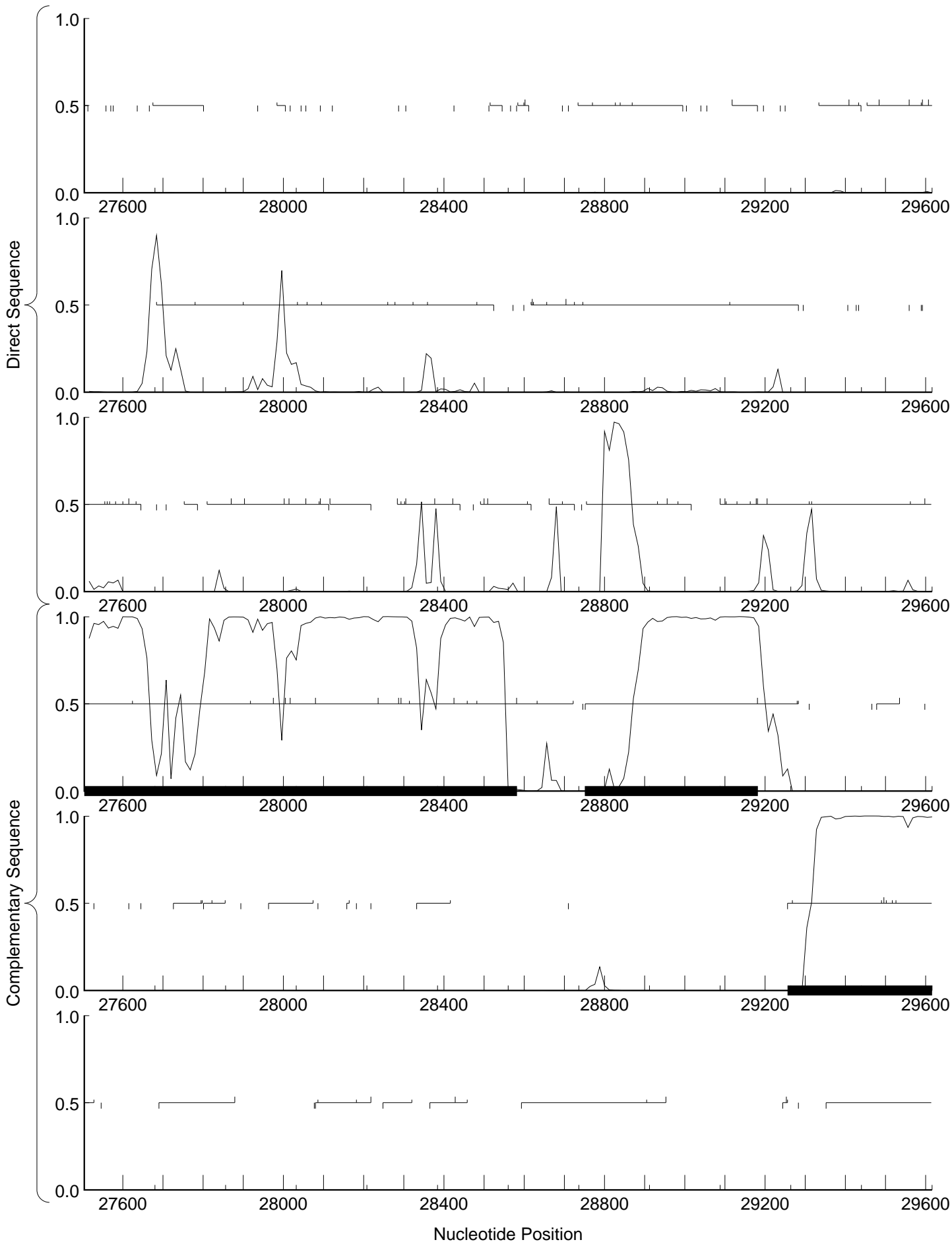






GeneMark.hmm prediction





GeneMark.hmm prediction

