

GeneMark

Version 2.5p (09.08.06)

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PROGRAM INFORMATION

Sequence : Arthrobacter phage Mendel complete sequence, 19428 bp, probable terminal proteins, Cluster
Analysis Date : 10/22/17 at 19:00:29
Pages : 11
Sequence Length : 19428 bp
GC Content : 59.83%

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

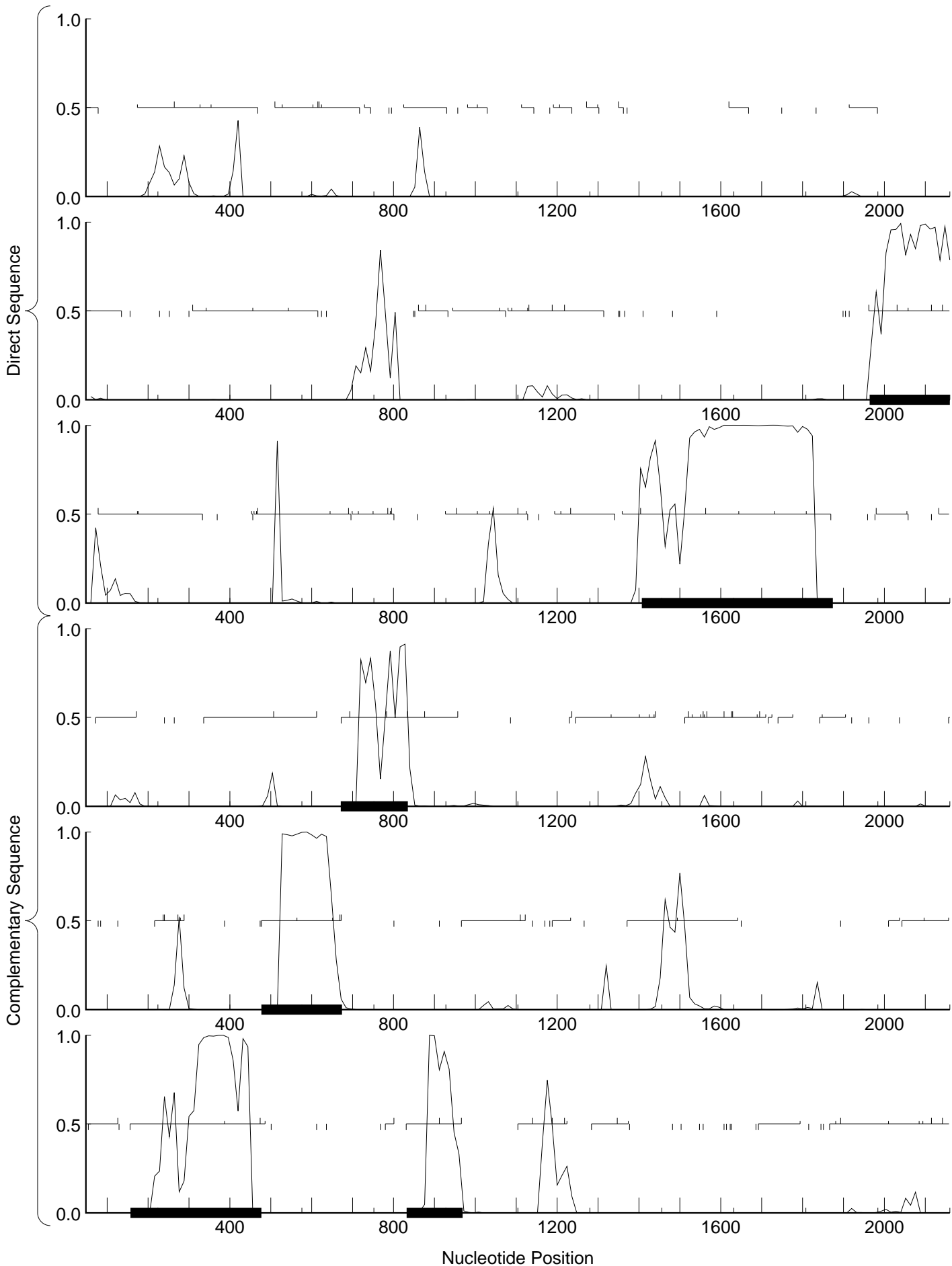
For details on the model building procedure see:
Besemer J. and Borodovsky M.
"Heuristic approach to deriving models for gene finding"
NAR, 1999, Vol. 27, No. 19, pp. 3911-3920

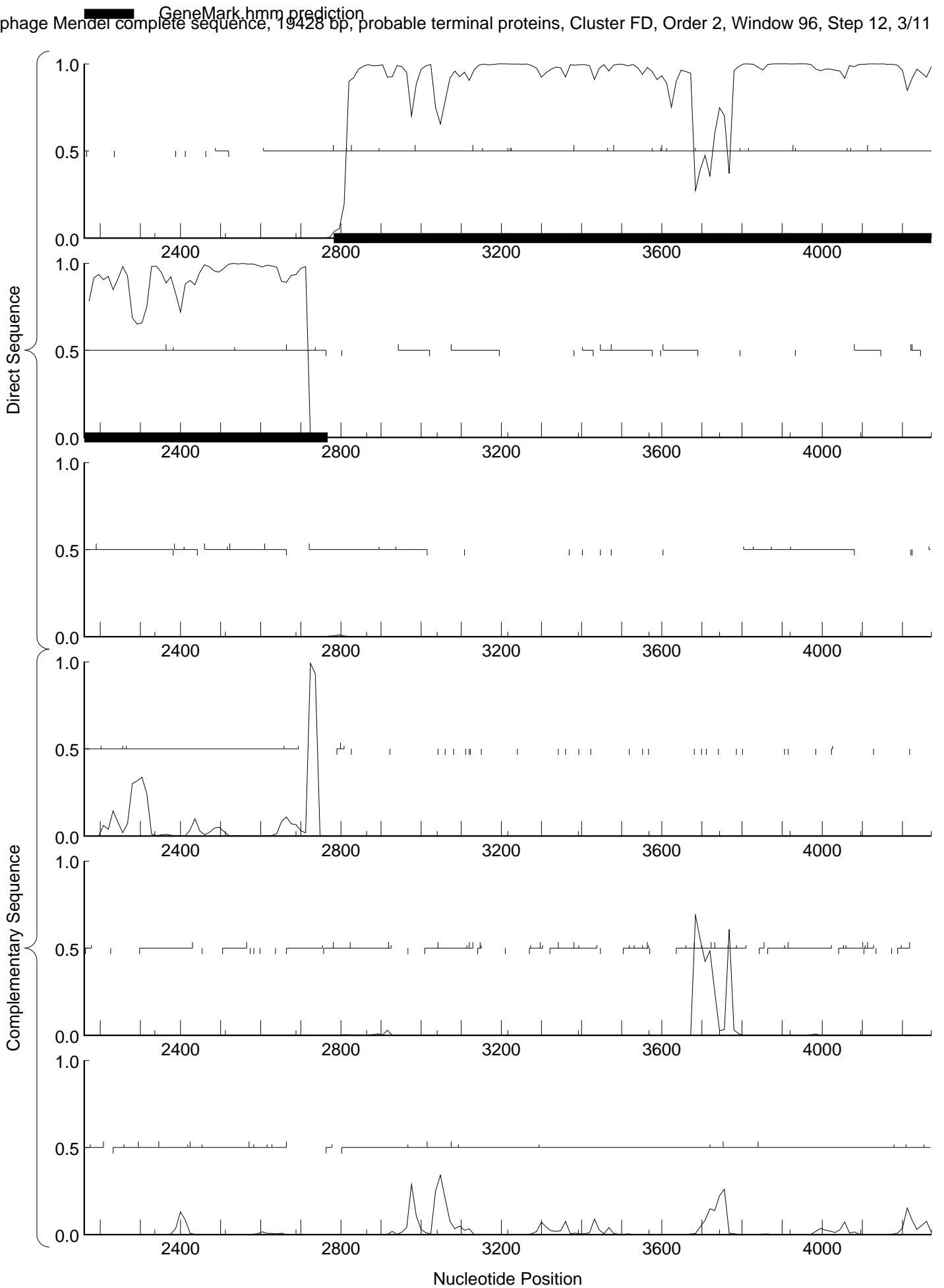
MATRIX INFORMATION

Matrix : Heuristic, GC = 60
Author : Borodovsky Laboratory - Georgia Tech
Order : 2

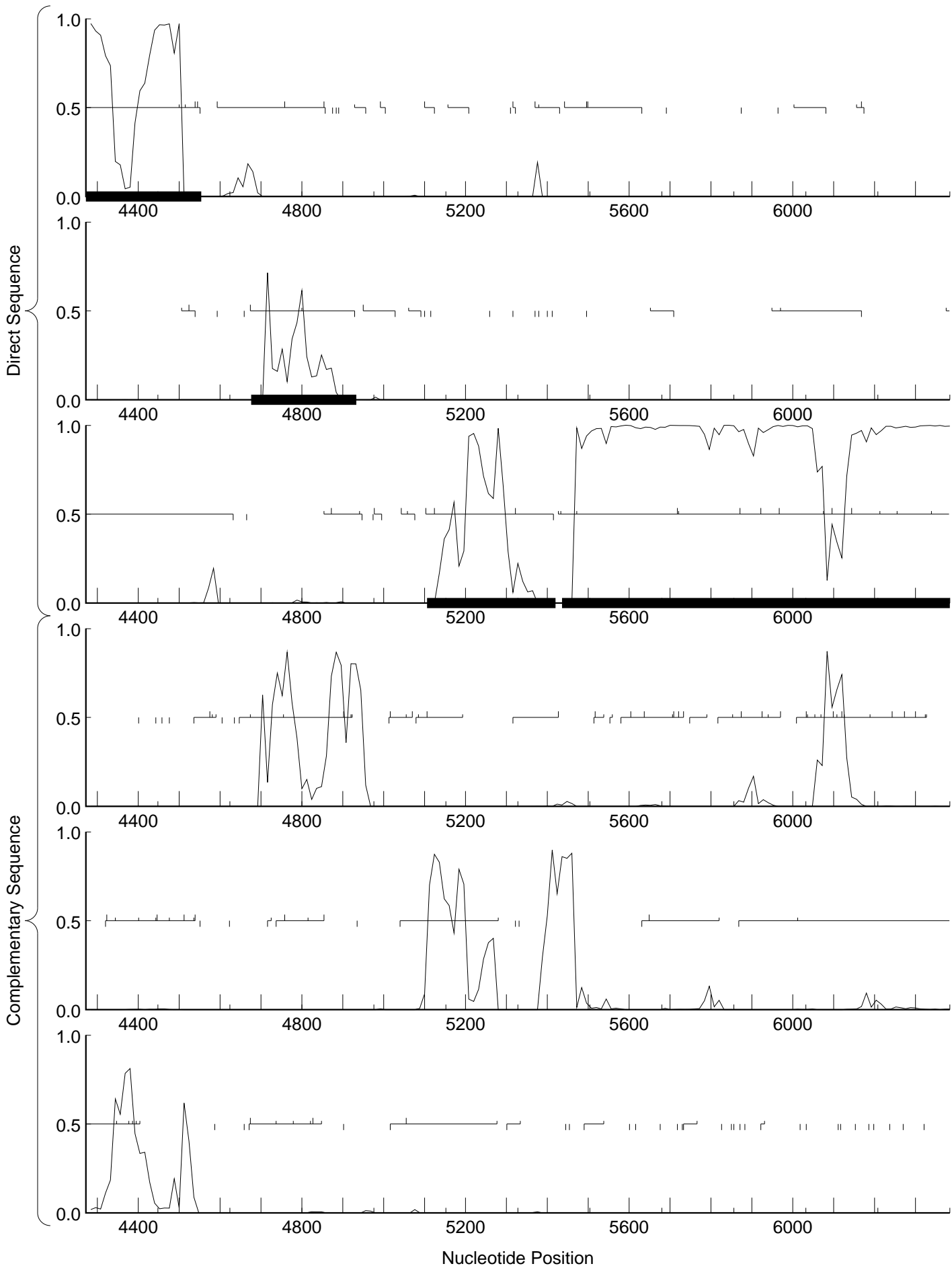
Send questions / comments to:
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Atlanta, GA 30332-0230

GeneMark.hmm prediction

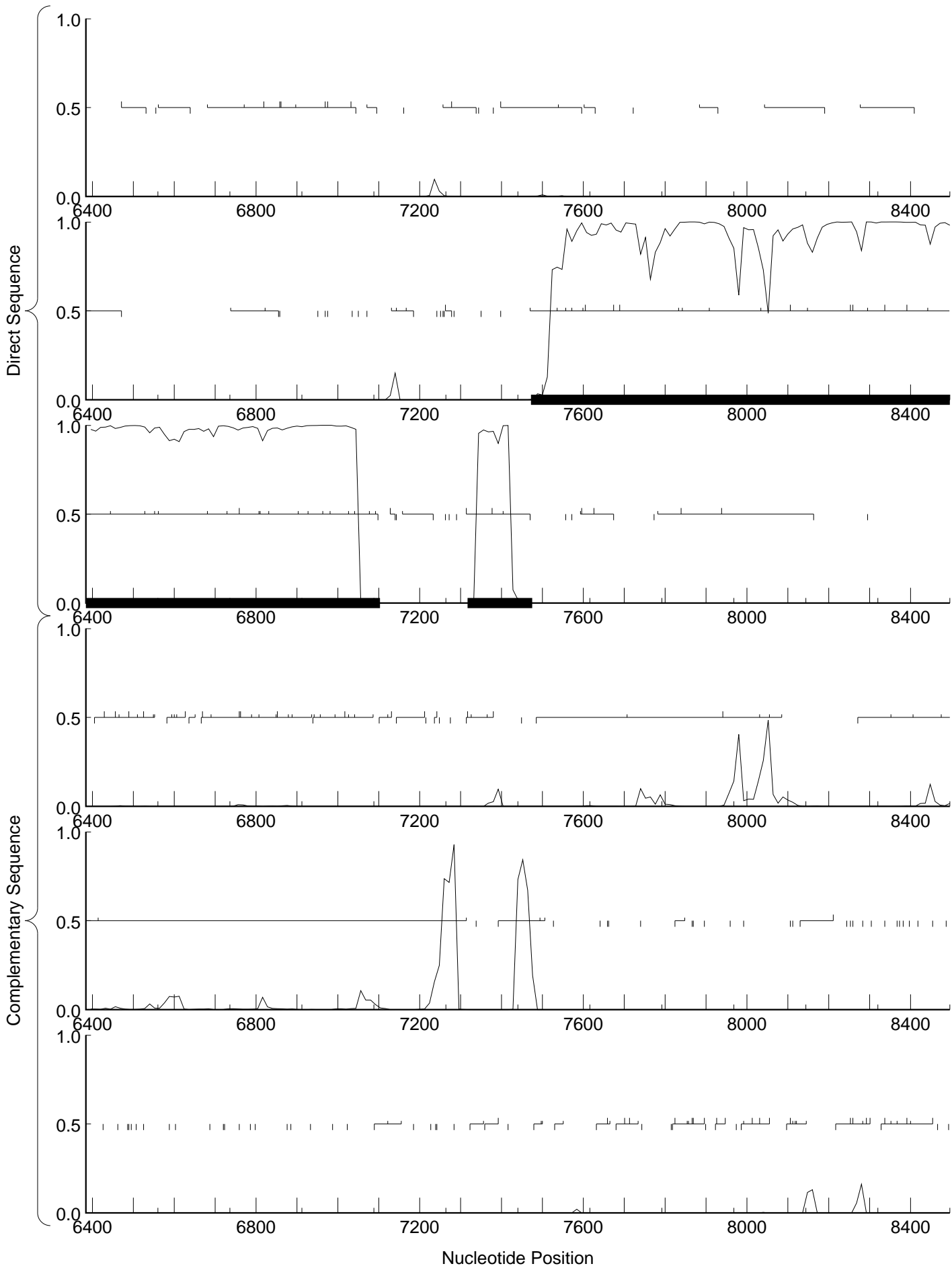




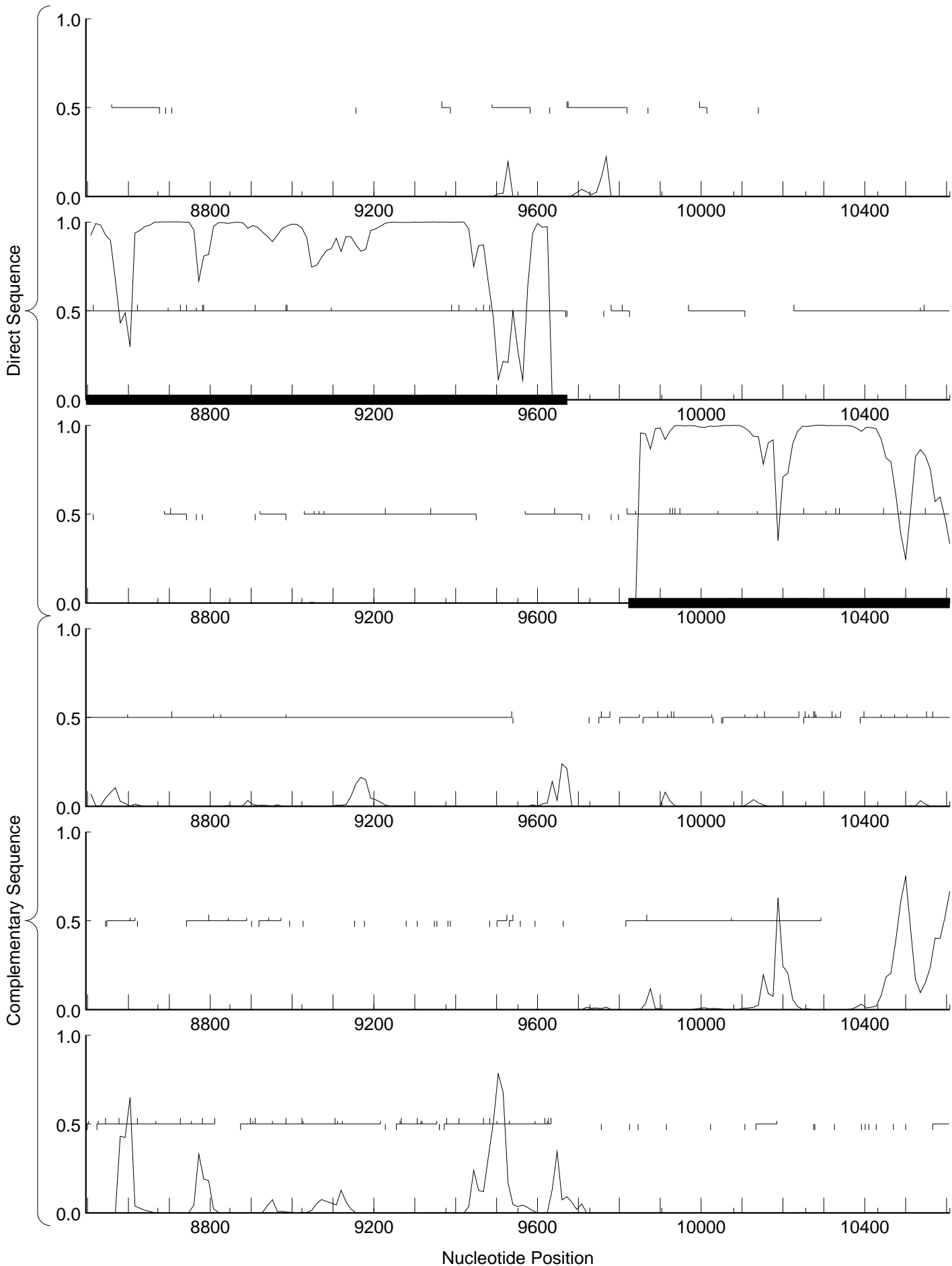
GeneMark.hmm prediction

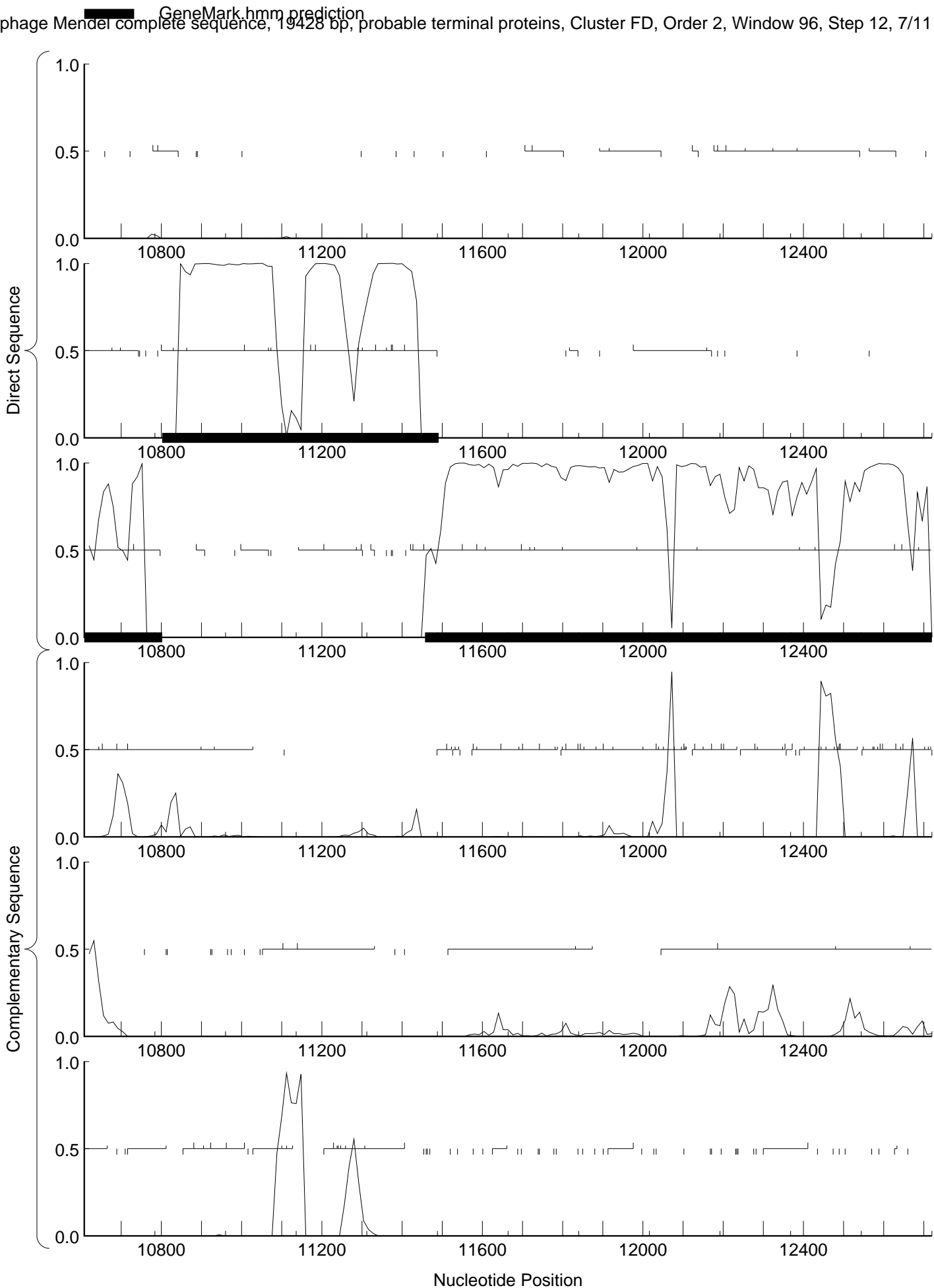


GeneMark.hmm prediction



GeneMark.hmm prediction





GeneMark.hmm prediction

