

# GeneMark

Version 2.5p (09.08.06)

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## PROGRAM INFORMATION

Sequence : Gordonia phage Clark complete sequence, 47716 bp including 11-base 3' overhang (TGCCAAGGGGA  
Analysis Date : 11/23/17 at 8:00:08  
Pages : 24  
Sequence Length : 47716 bp  
GC Content : 66.53%

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 = 67  
Author : Borodovsky Laboratory - Georgia Tech  
Order : 2

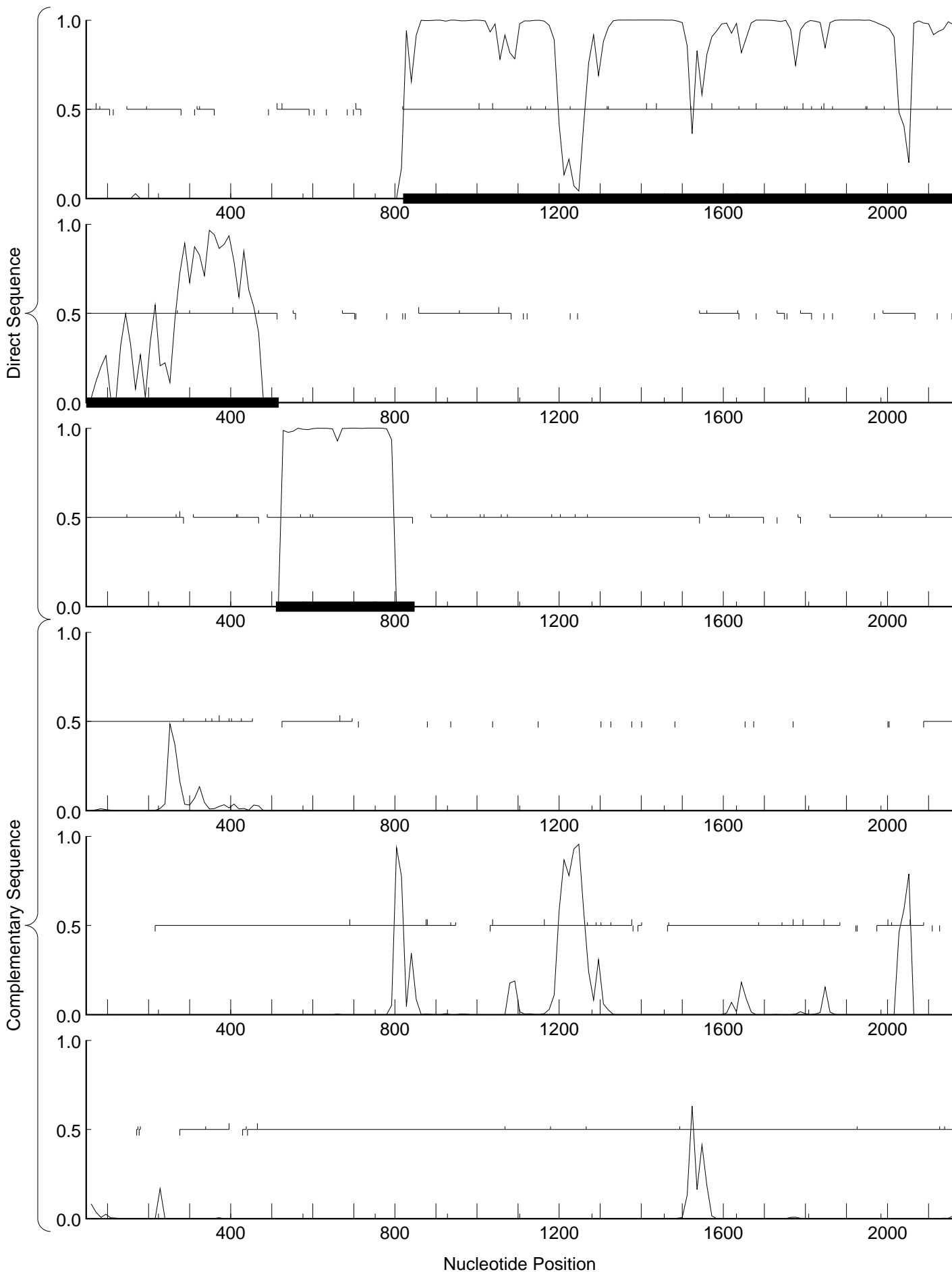
Send questions / comments to:  
Dr. M. Borodovsky  
Georgia Institute of Technology  
School of Biology  
Atlanta, GA 30332-0230

### Matrix notes & comments

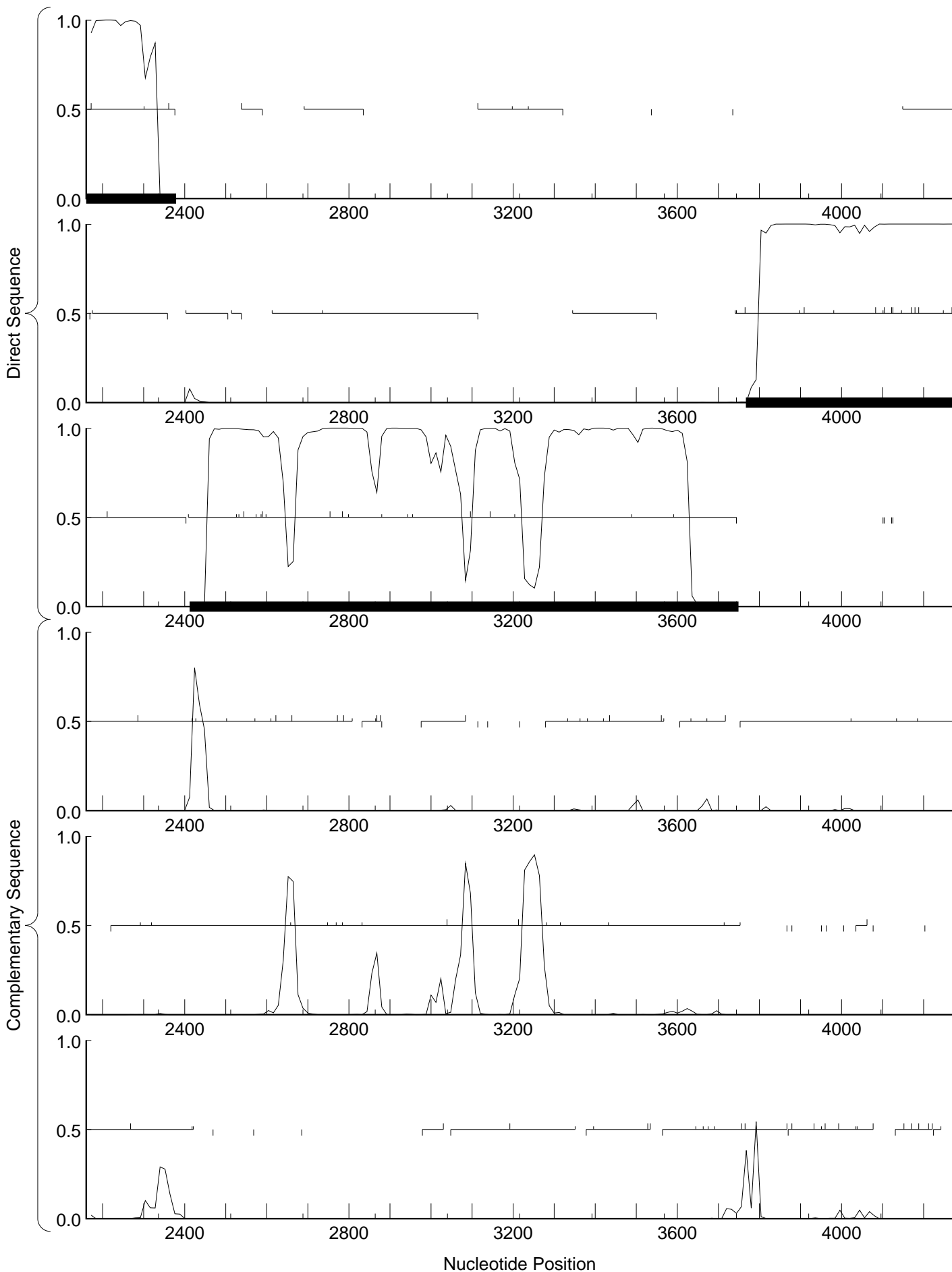
For details on the model building procedure see:  
Besemer J. and Borodovsky M.  
"Heuristic approach to deriving models for gene finding"  
NAR, 1999, Vol. 27, No. 19, pp. 3911-3920

complete sequence, 47716 bp including 11-base 3' overhang (TGCCAAGGGGA), Cluster CZ, Order 2, Window 96, Step 12, 2/24

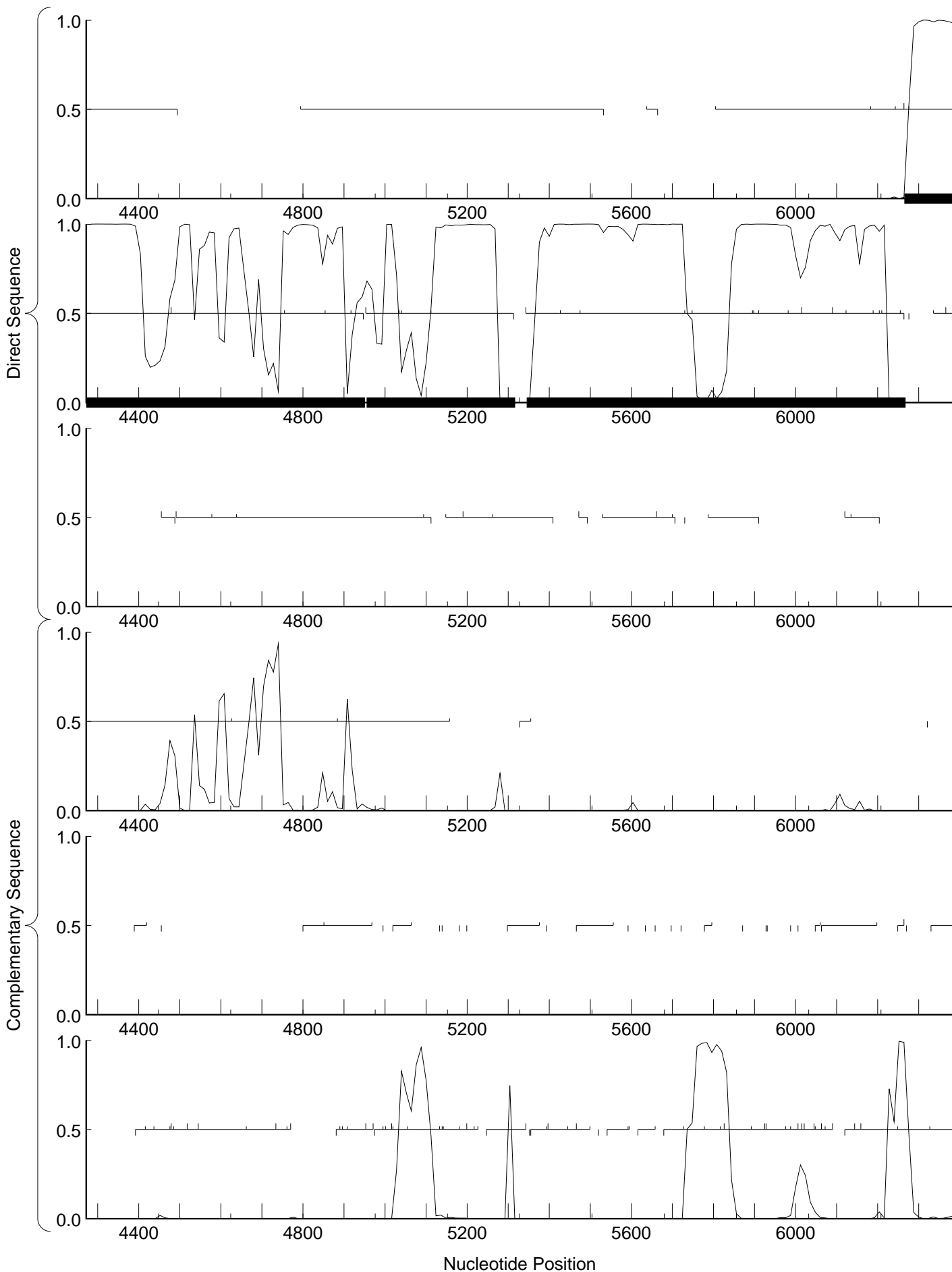
GeneMark.hmm prediction



complete sequence, 47716 bp including 11-base 3' overhang (TGCCAAGGGGA), Cluster CZ, Order 2, Window 96, Step 12, 3/24

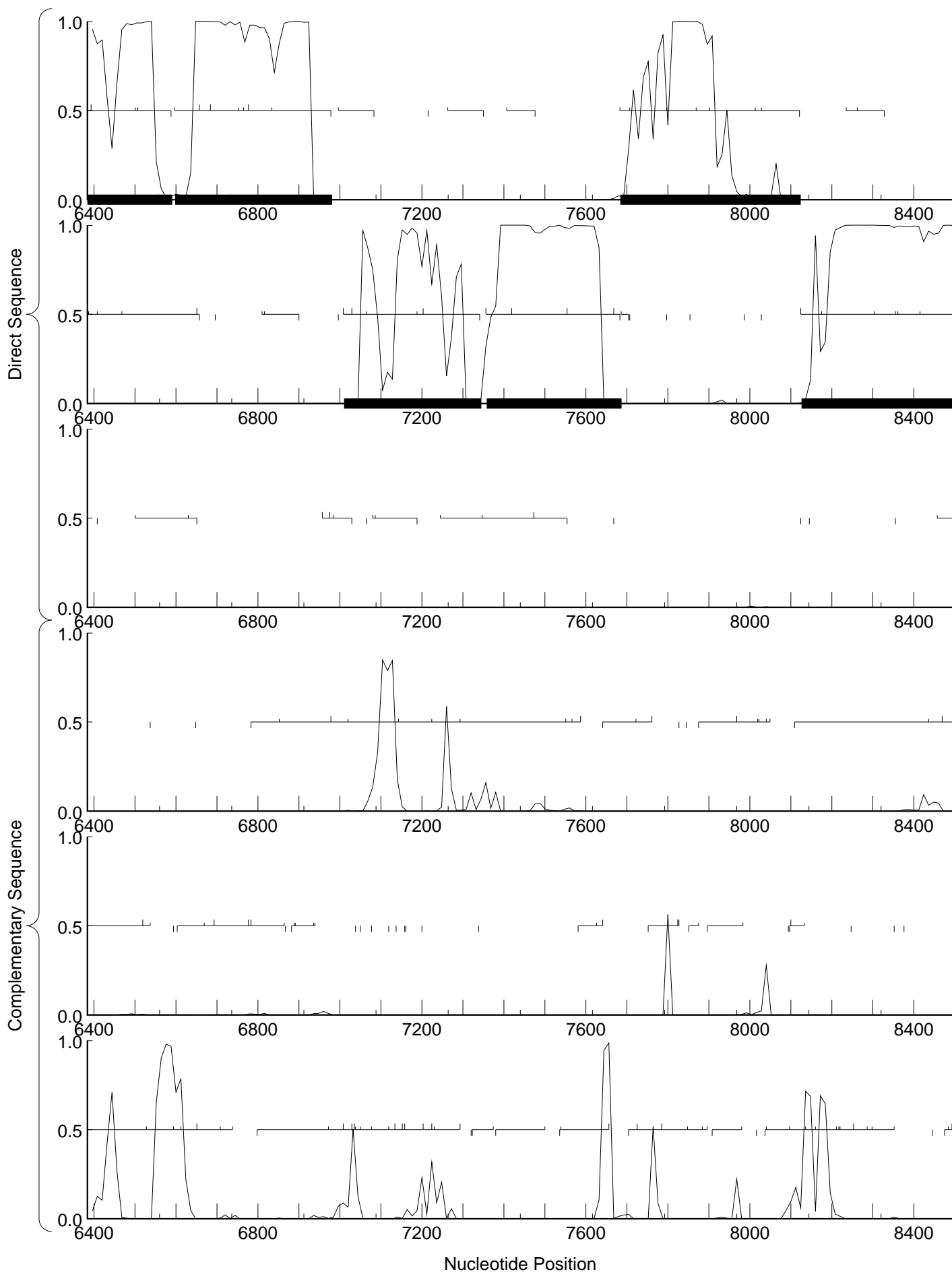


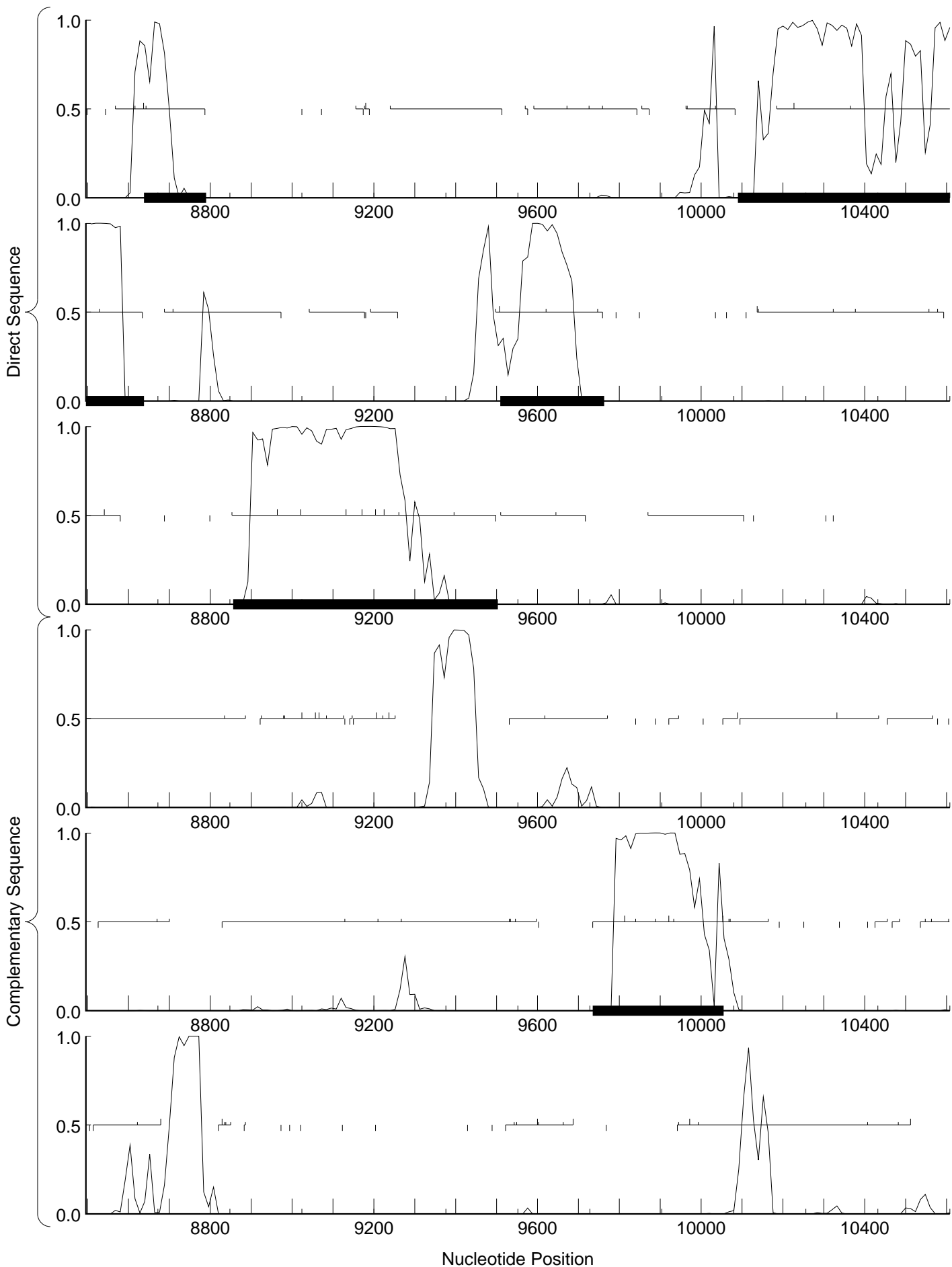
GeneMark.hmm prediction



complete sequence, 47716 bp including 11-base 3' overhang (TGCCAAGGGGA), Cluster CZ, Order 2, Window 96, Step 12, 5/24

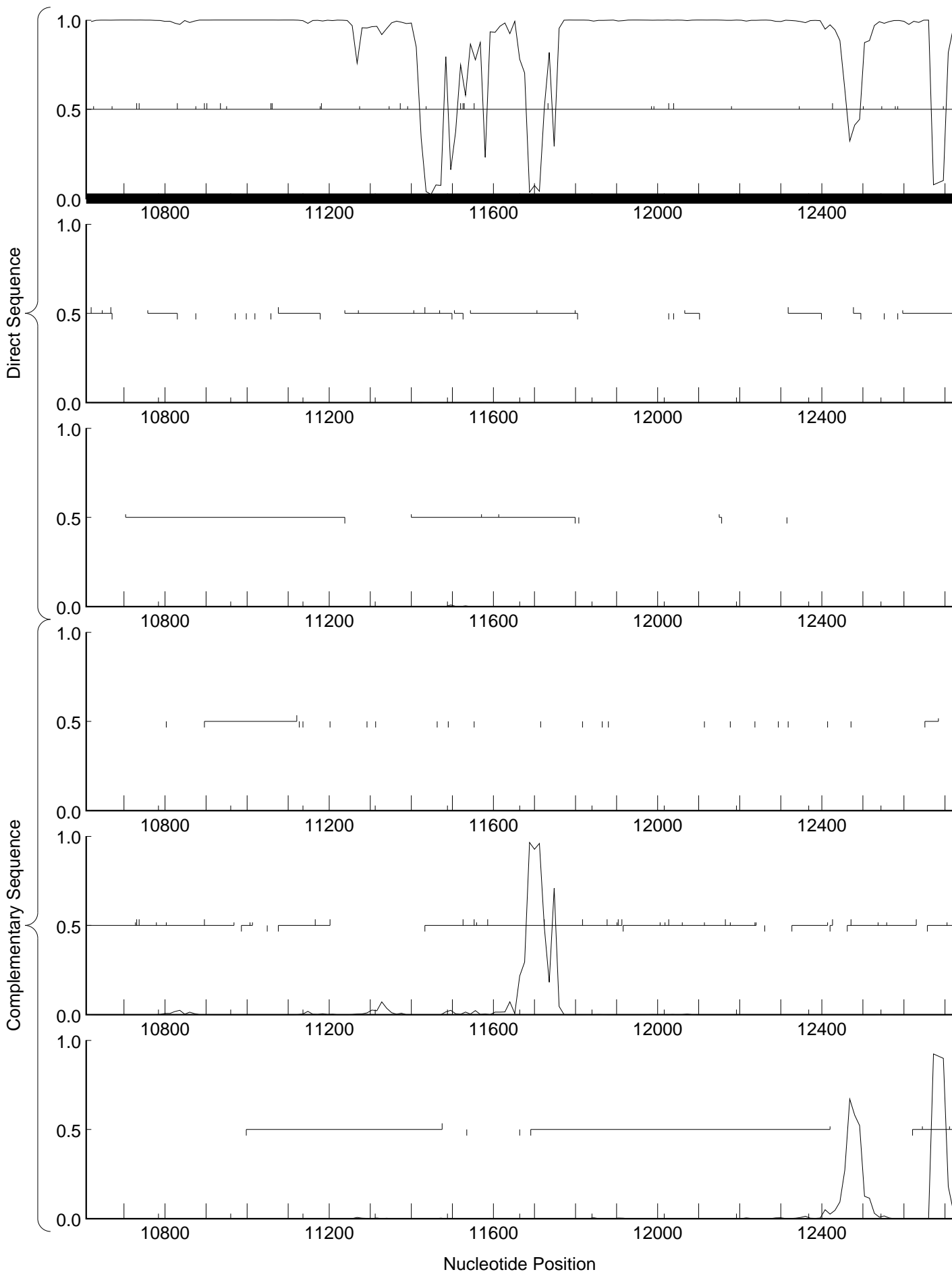
GeneMark.hmm prediction





complete sequence, 47716 bp including 11-base 3' overhang (TGCCAAGGGGA), Cluster CZ, Order 2, Window 96, Step 12, 7/24

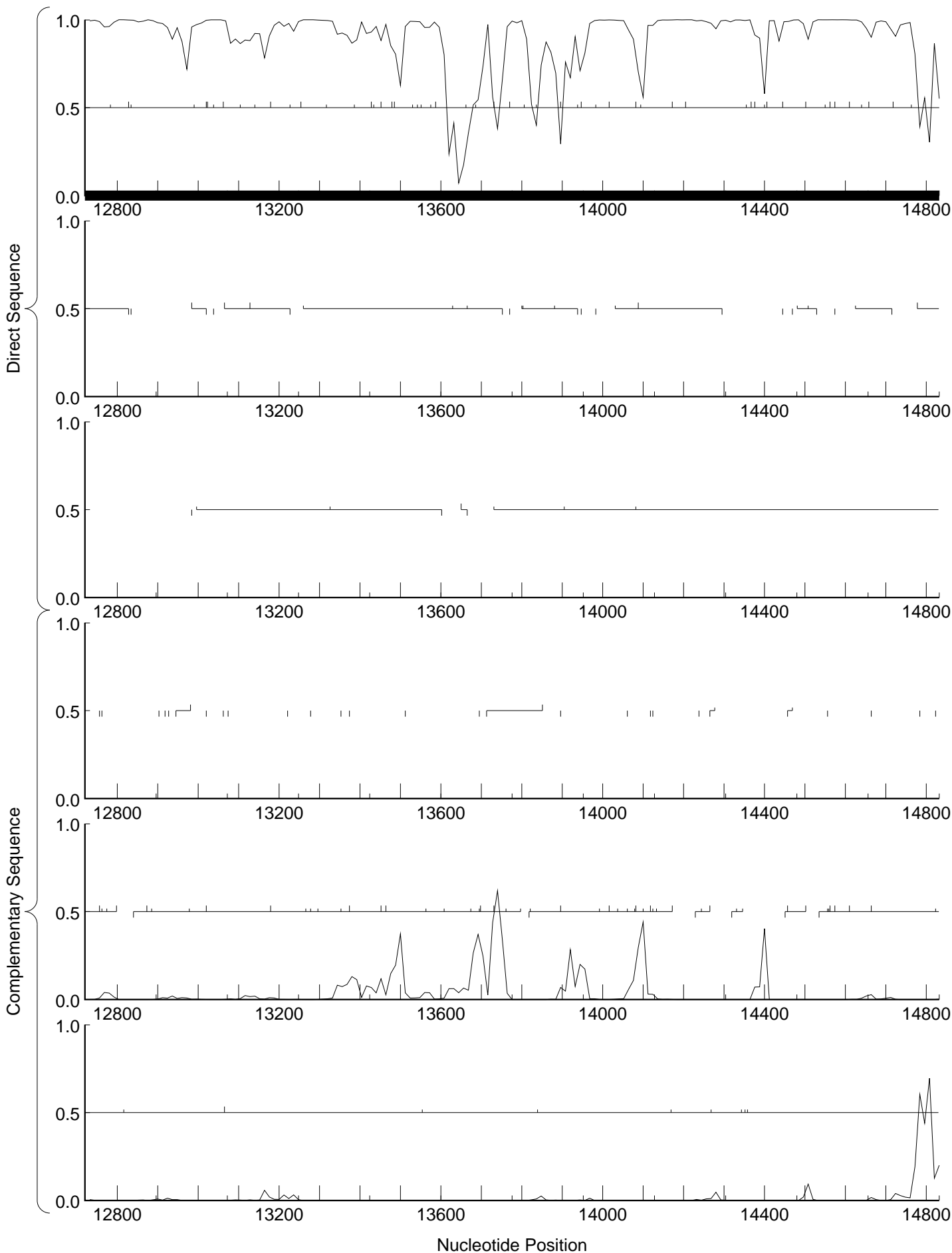
GeneMark.hmm prediction



complete sequence, 47716 bp including 11-base 3' overhang (TGCCAAGGGGA), Cluster CZ, Order 2, Window 96, Step 12, 8/24

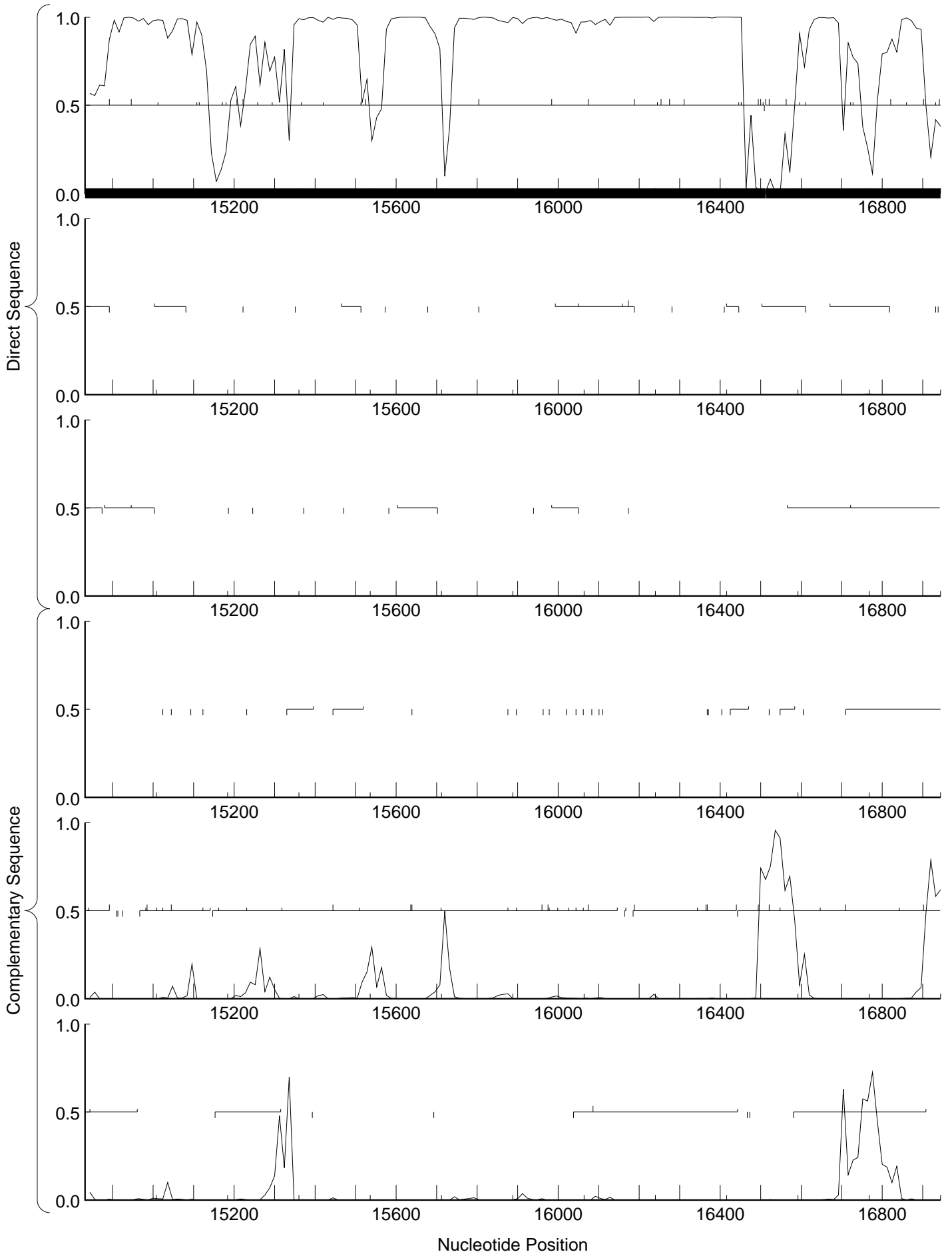
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GeneMark.hmm prediction

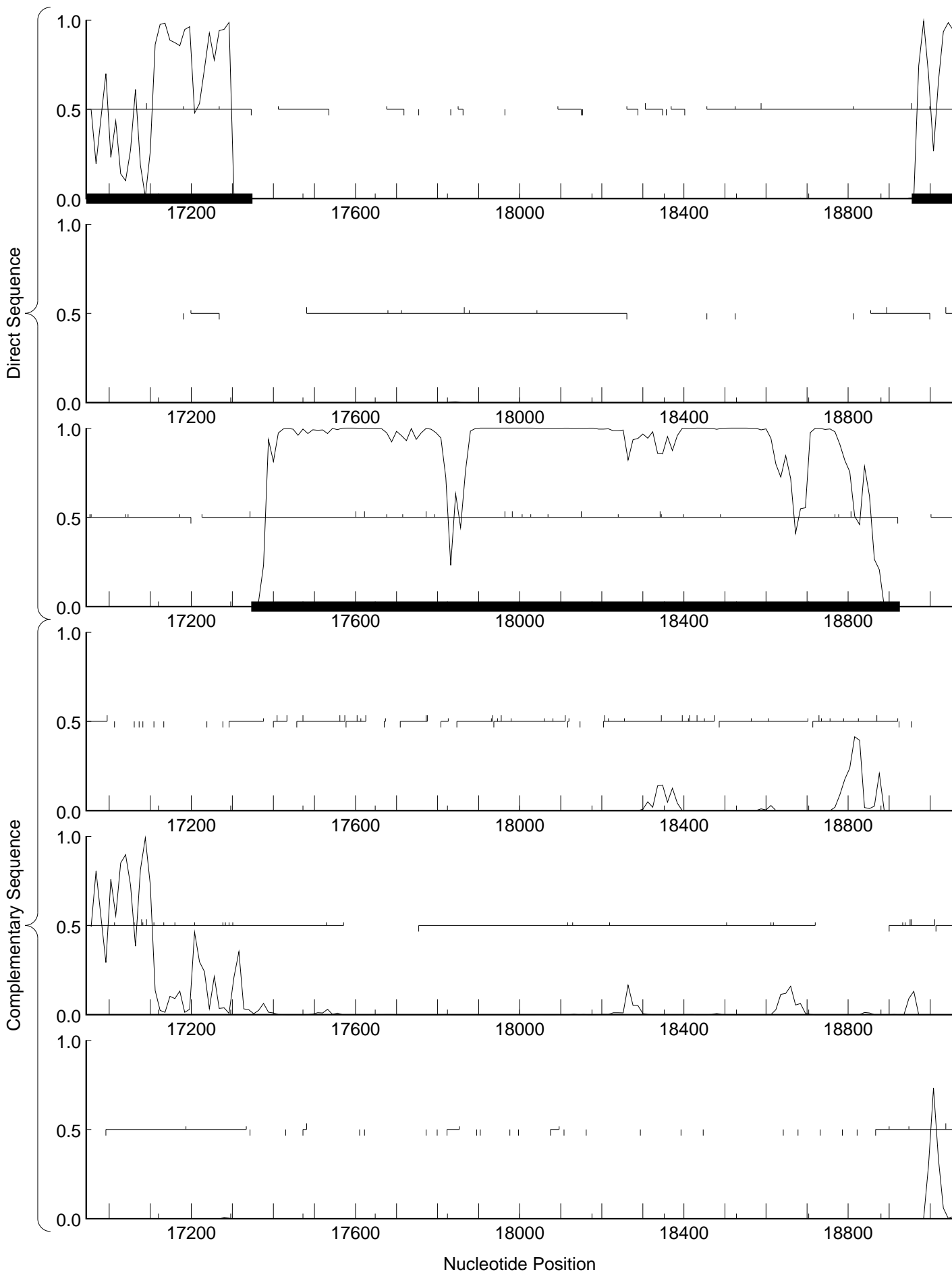




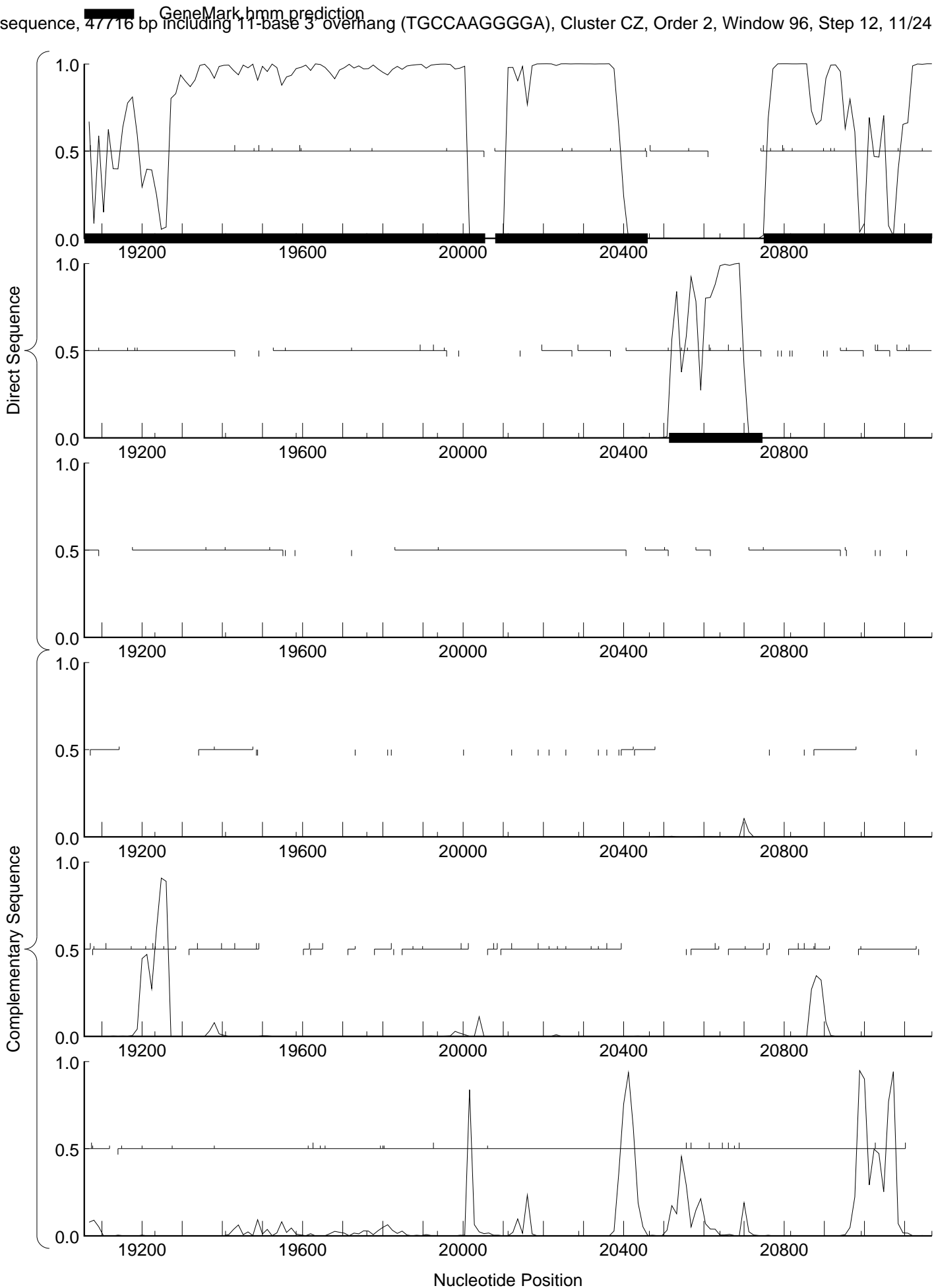
complete sequence, 47716 bp including 11-base 3' overhang (TGCCAAGGGGA), Cluster CZ, Order 2, Window 96, Step 12, 9/24

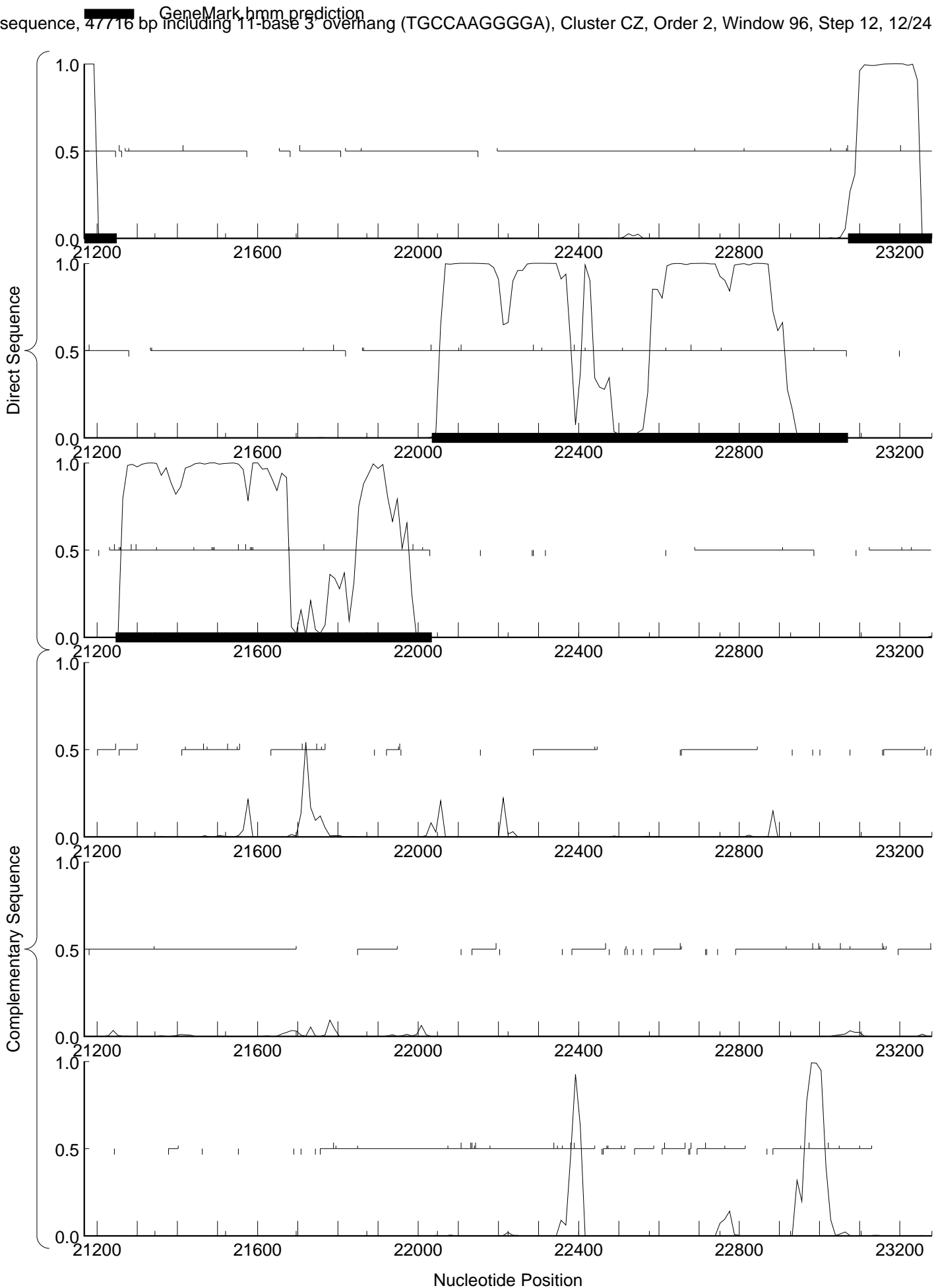


GeneMark, hmm prediction



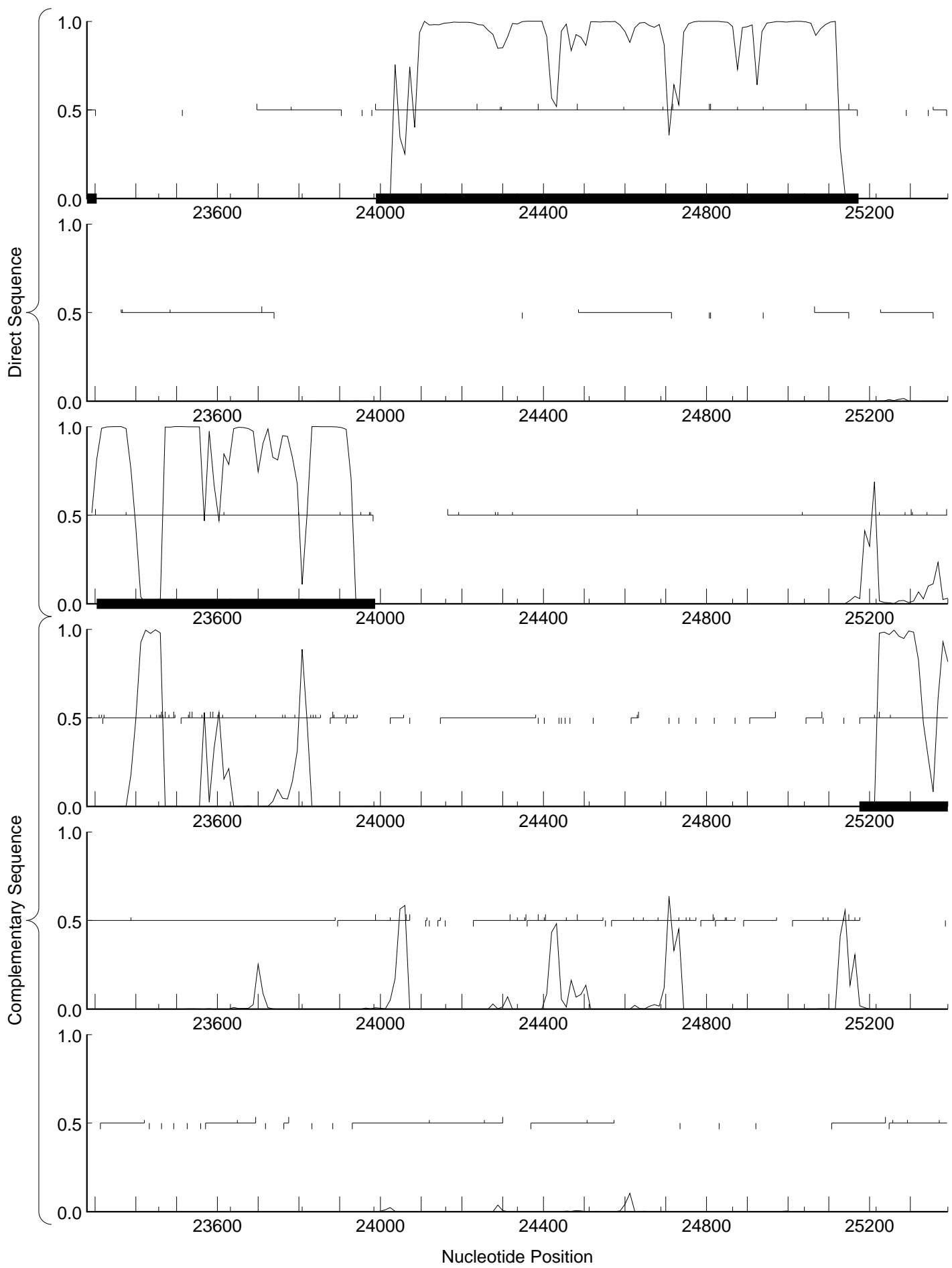
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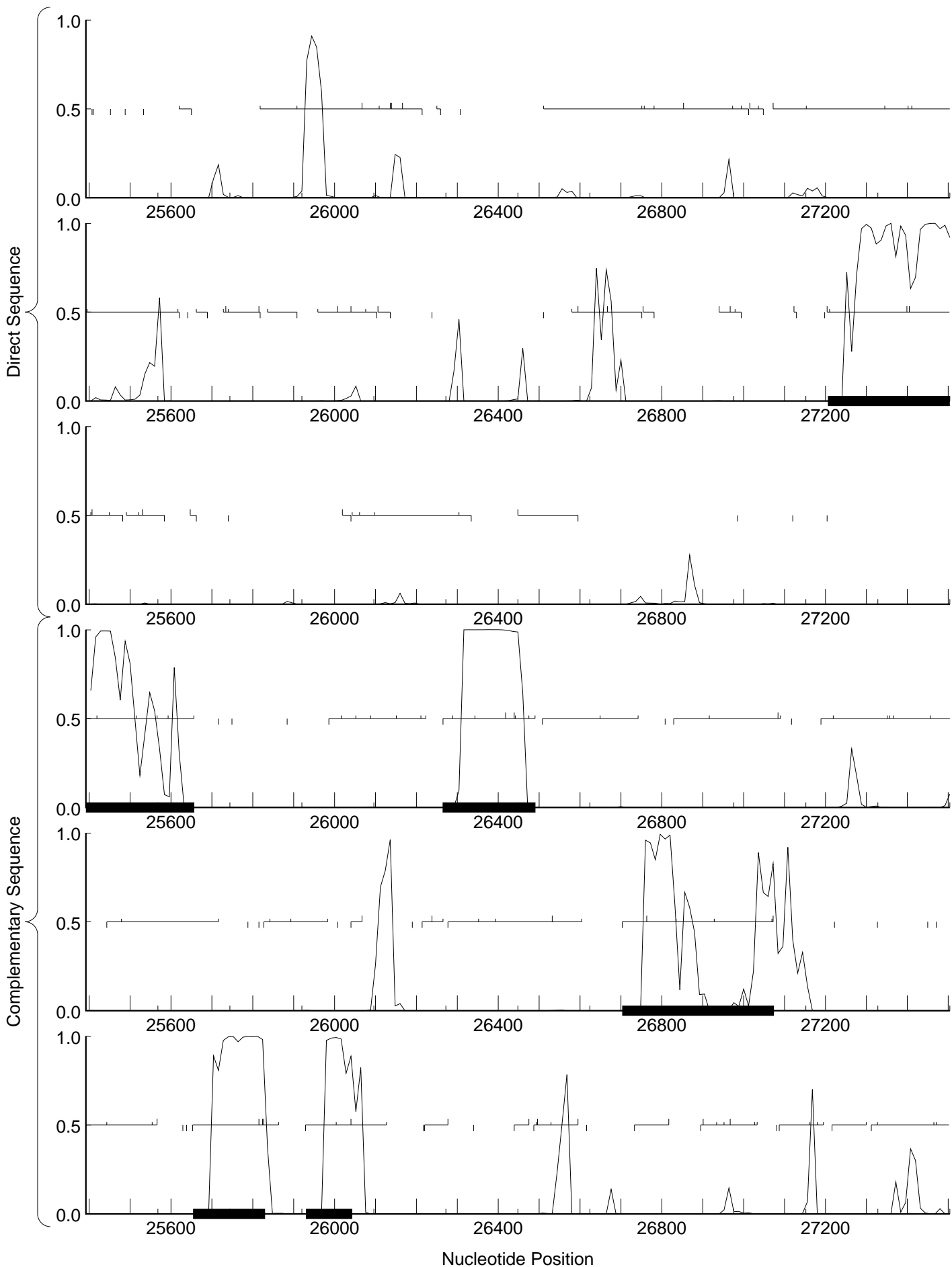


complete sequence, 47716 bp including 11-base 3' overhang (TGCCAAGGGGA), Cluster CZ, Order 2, Window 96, Step 12, 13/24

GeneMark, hmm prediction

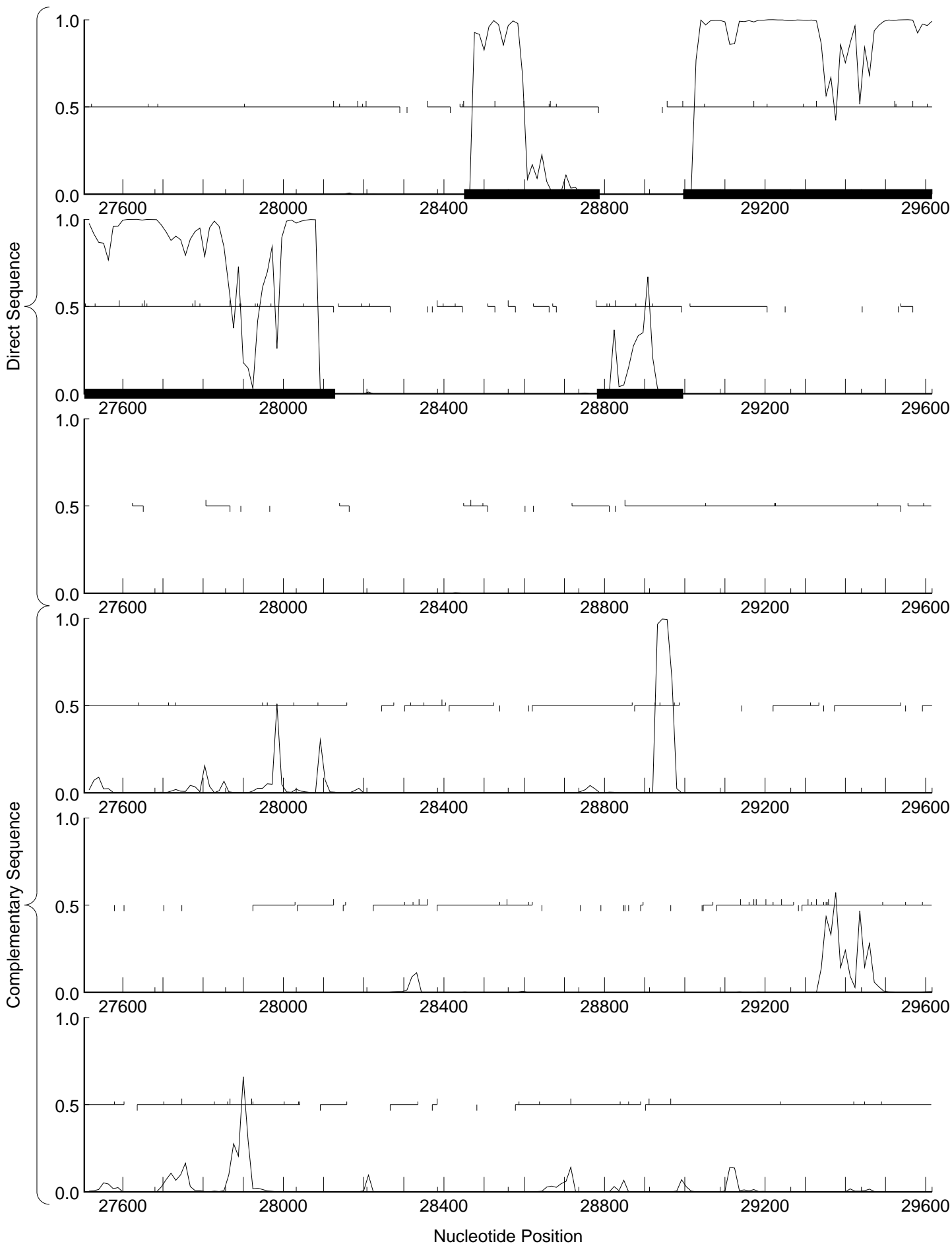


GeneMark, hmm prediction



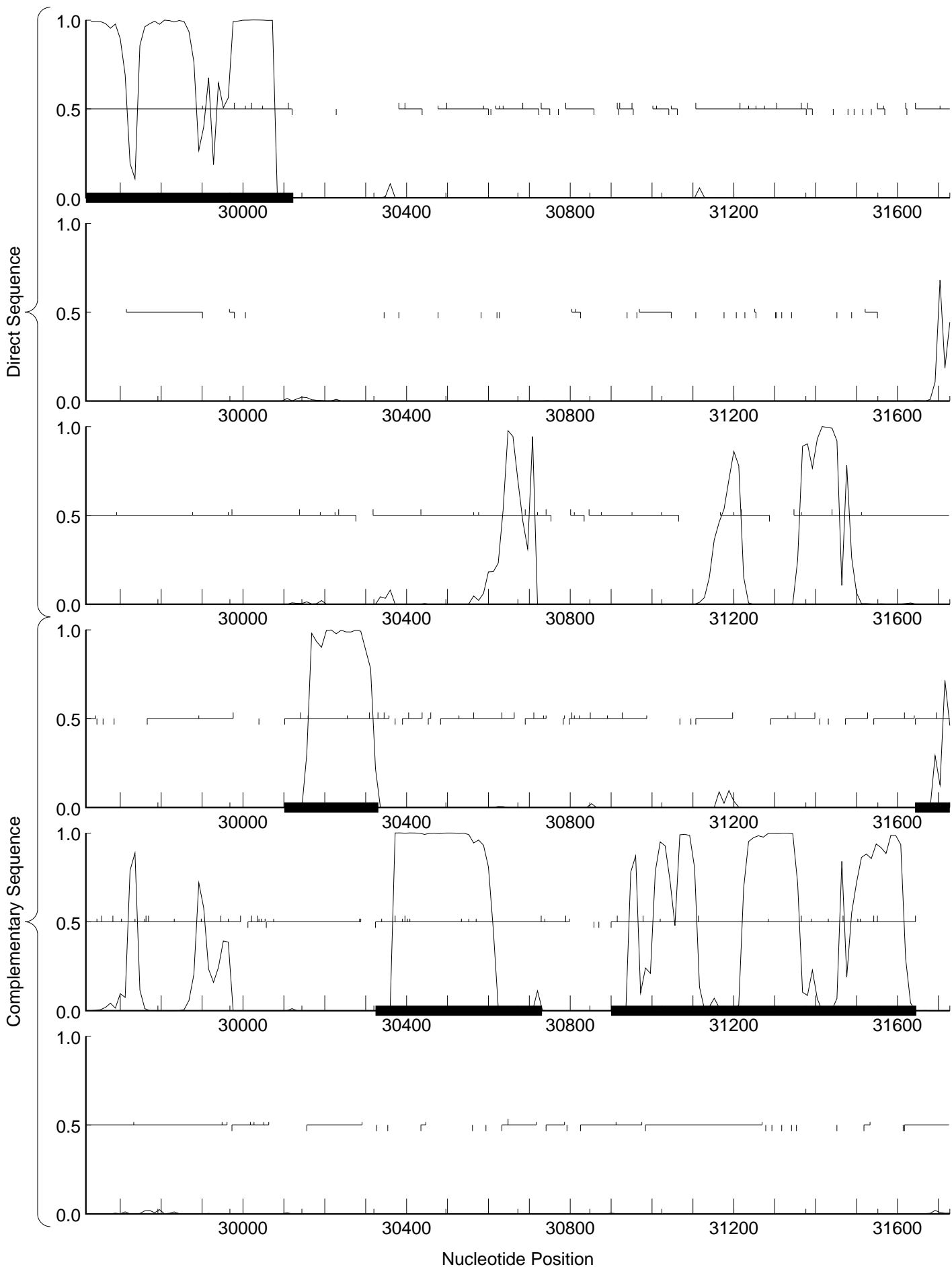
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GeneMark, hmm prediction

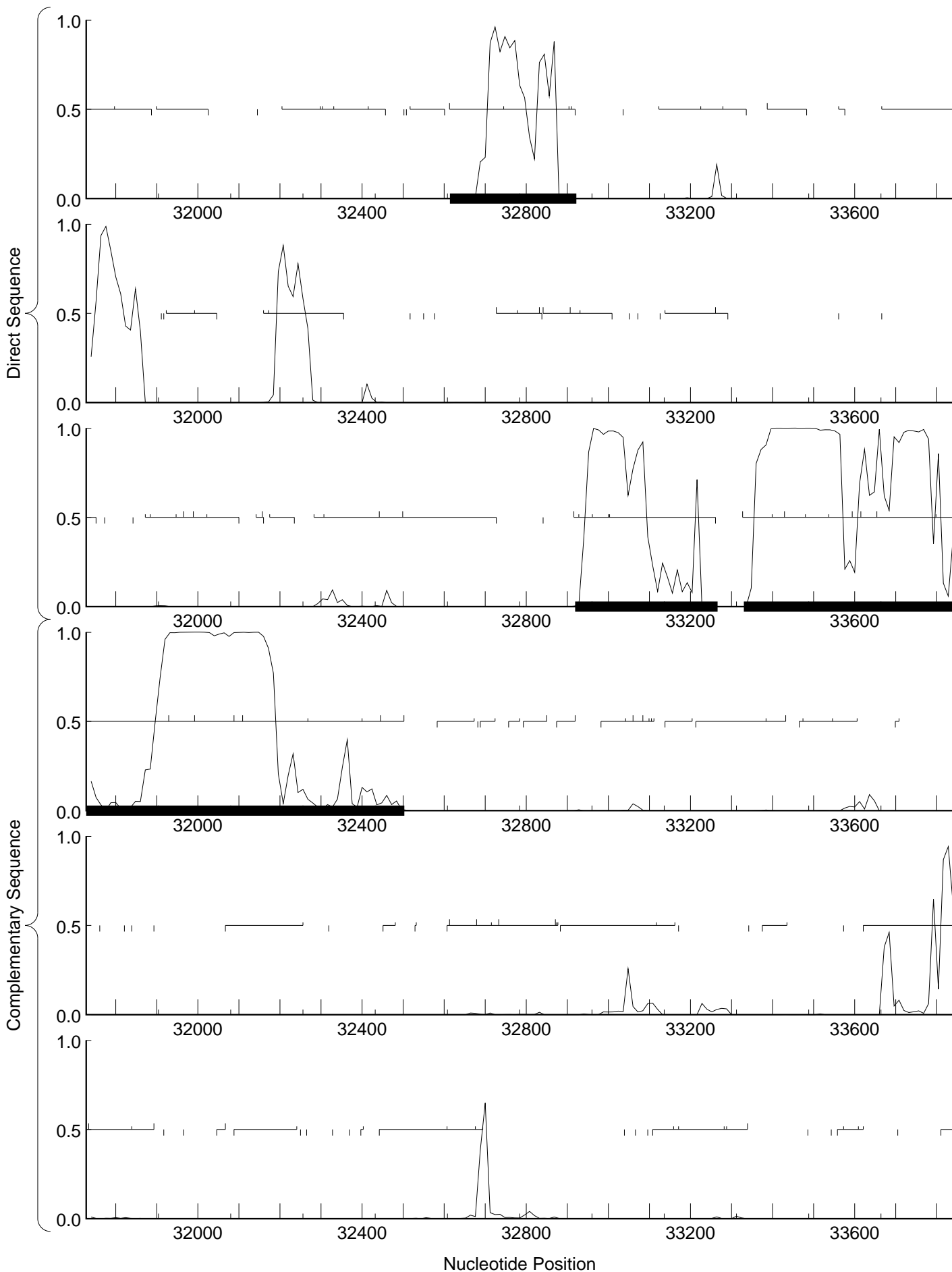


complete sequence, 47716 bp including 11-base 3' overhang (TGCCAAGGGGA), Cluster CZ, Order 2, Window 96, Step 12, 16/24

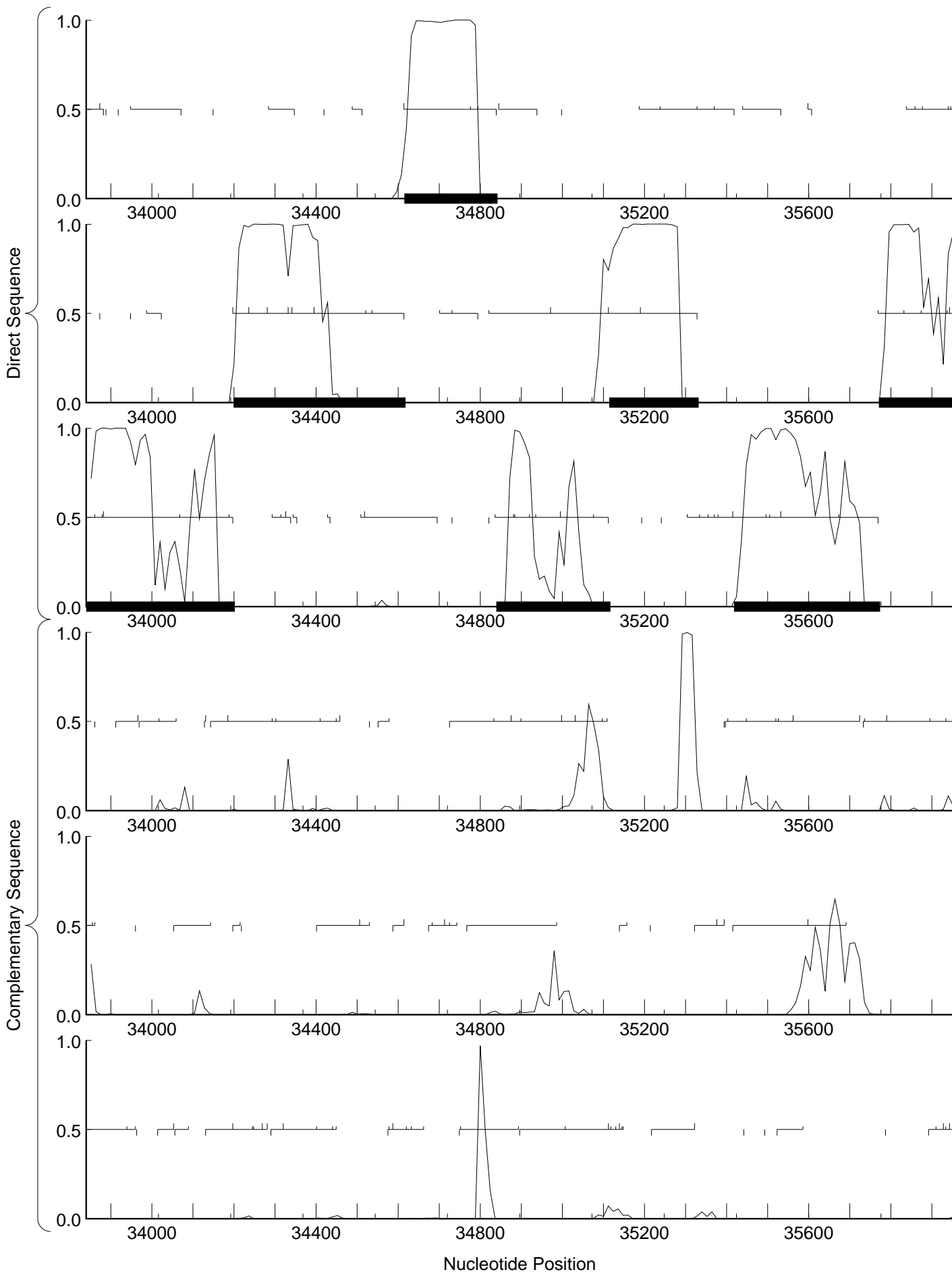
GeneMark, hmm prediction





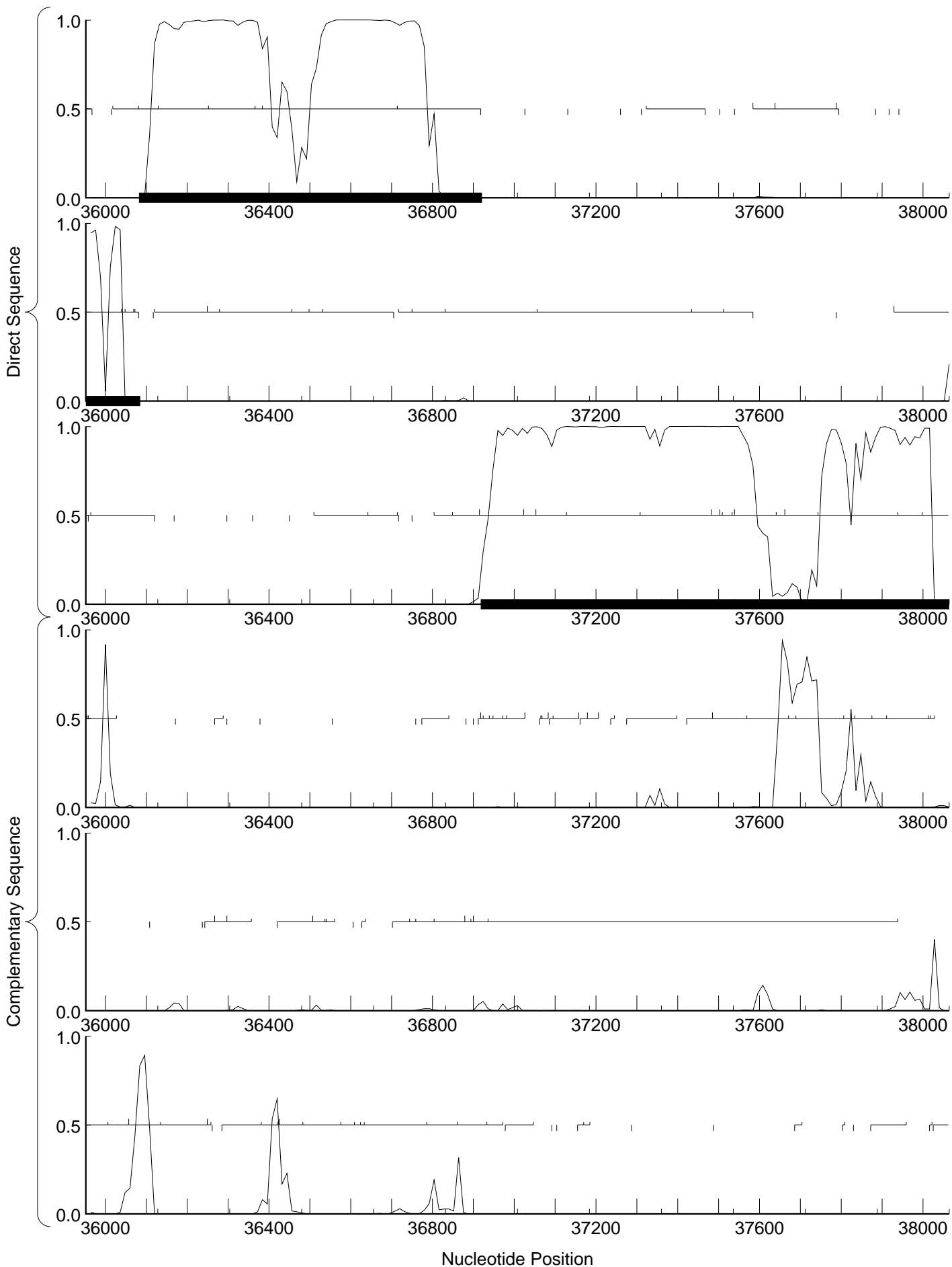


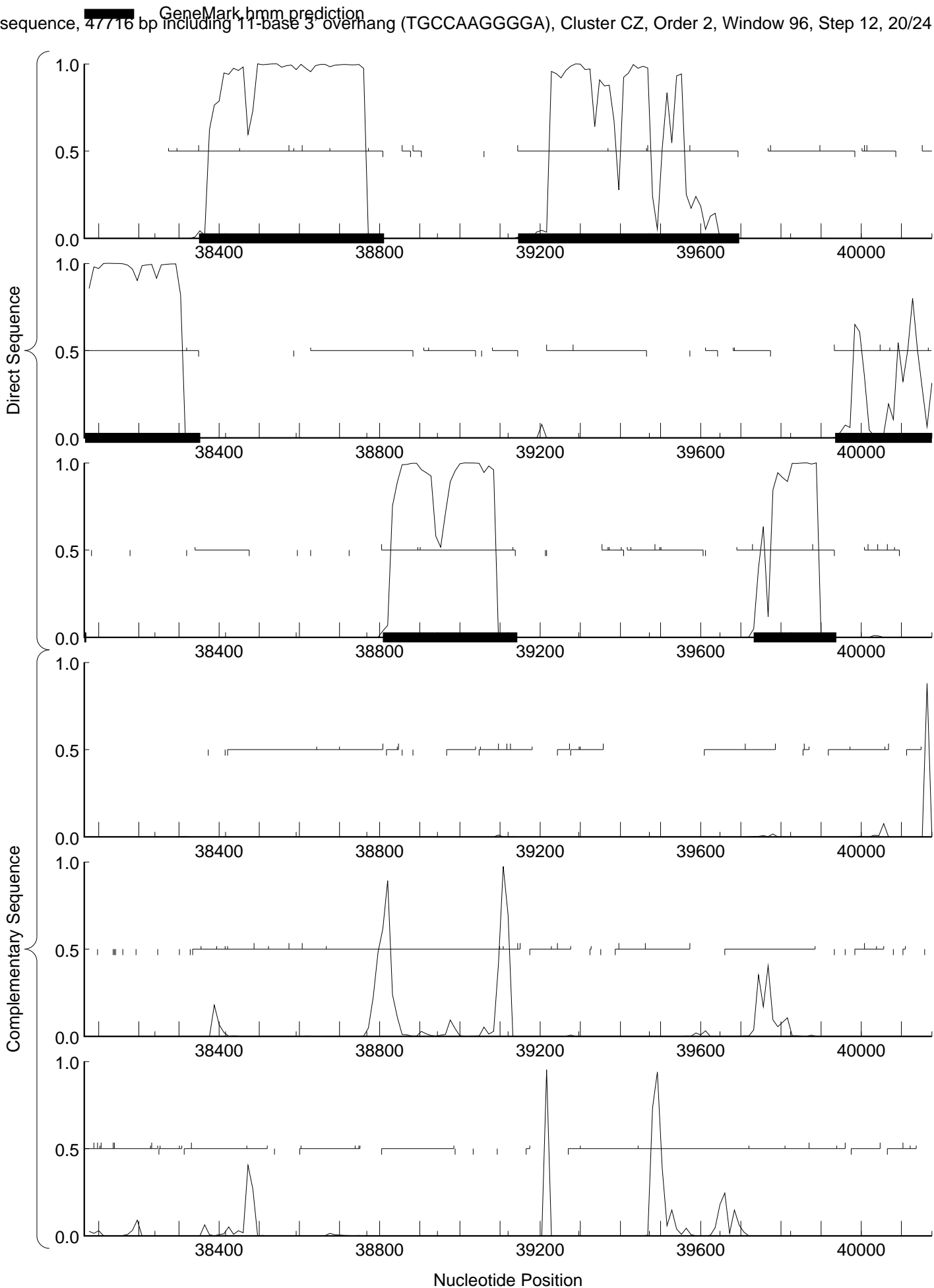
GeneMark, hmm prediction



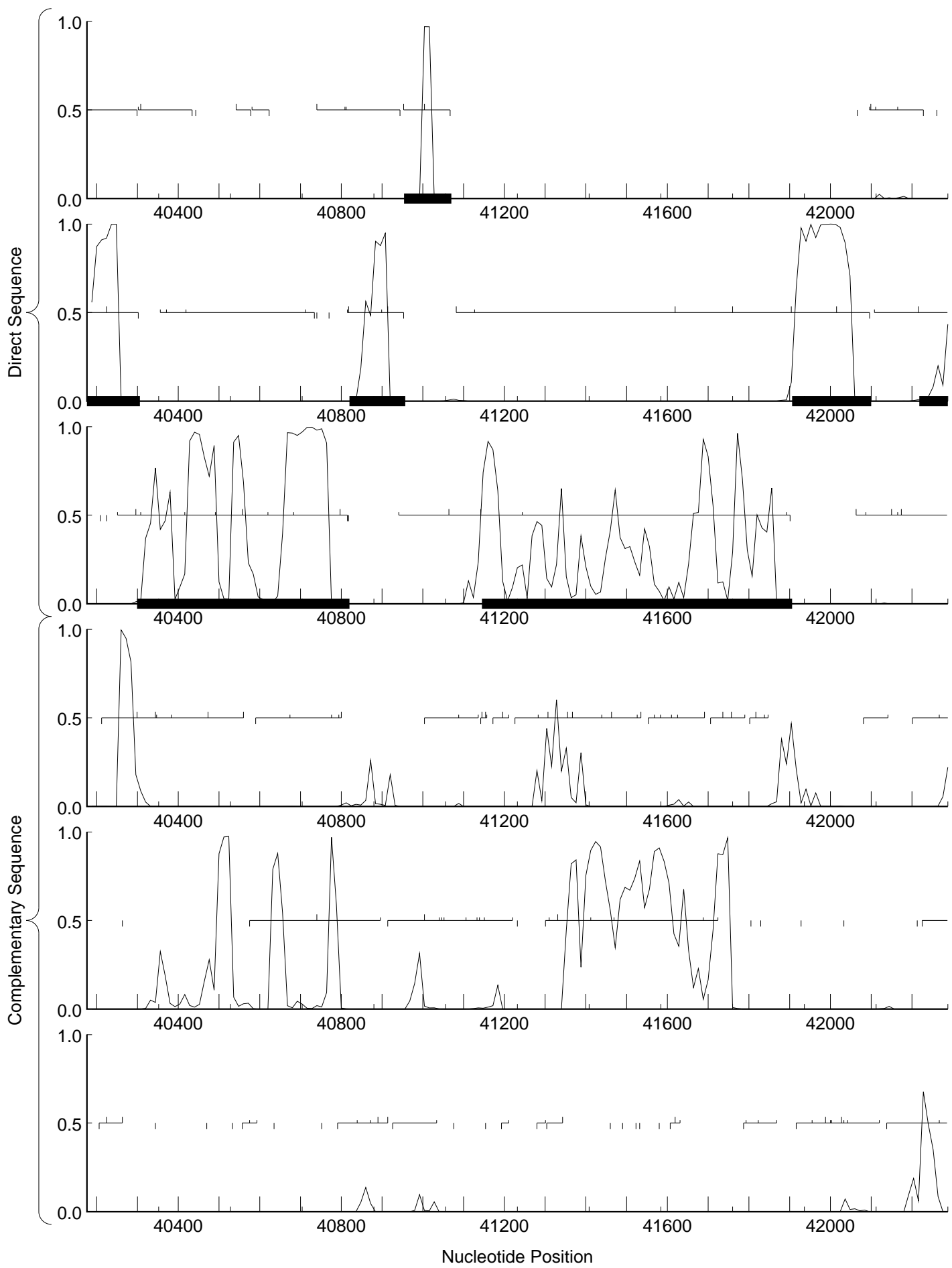
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GeneMark, hmm prediction



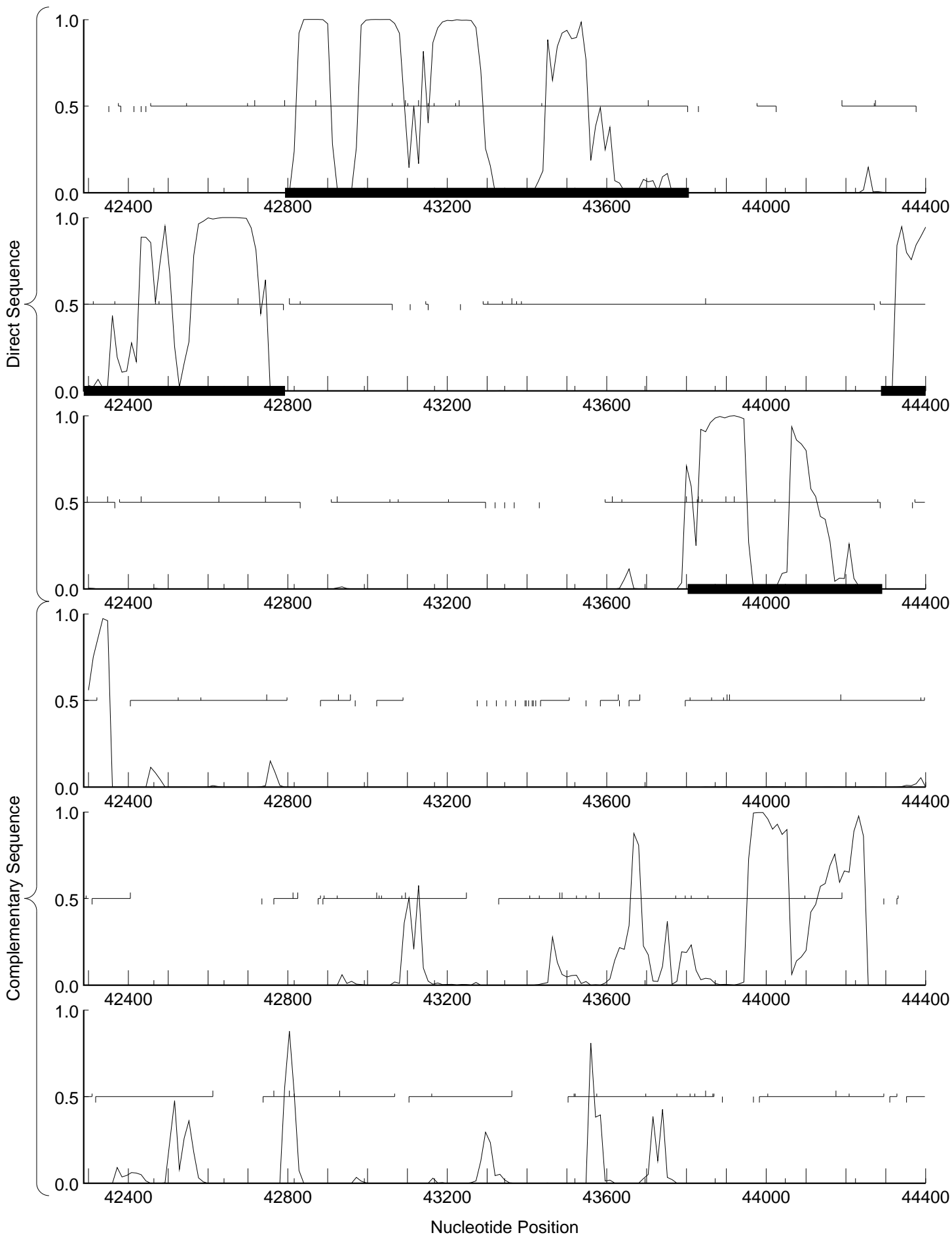


GeneMark, hmm prediction



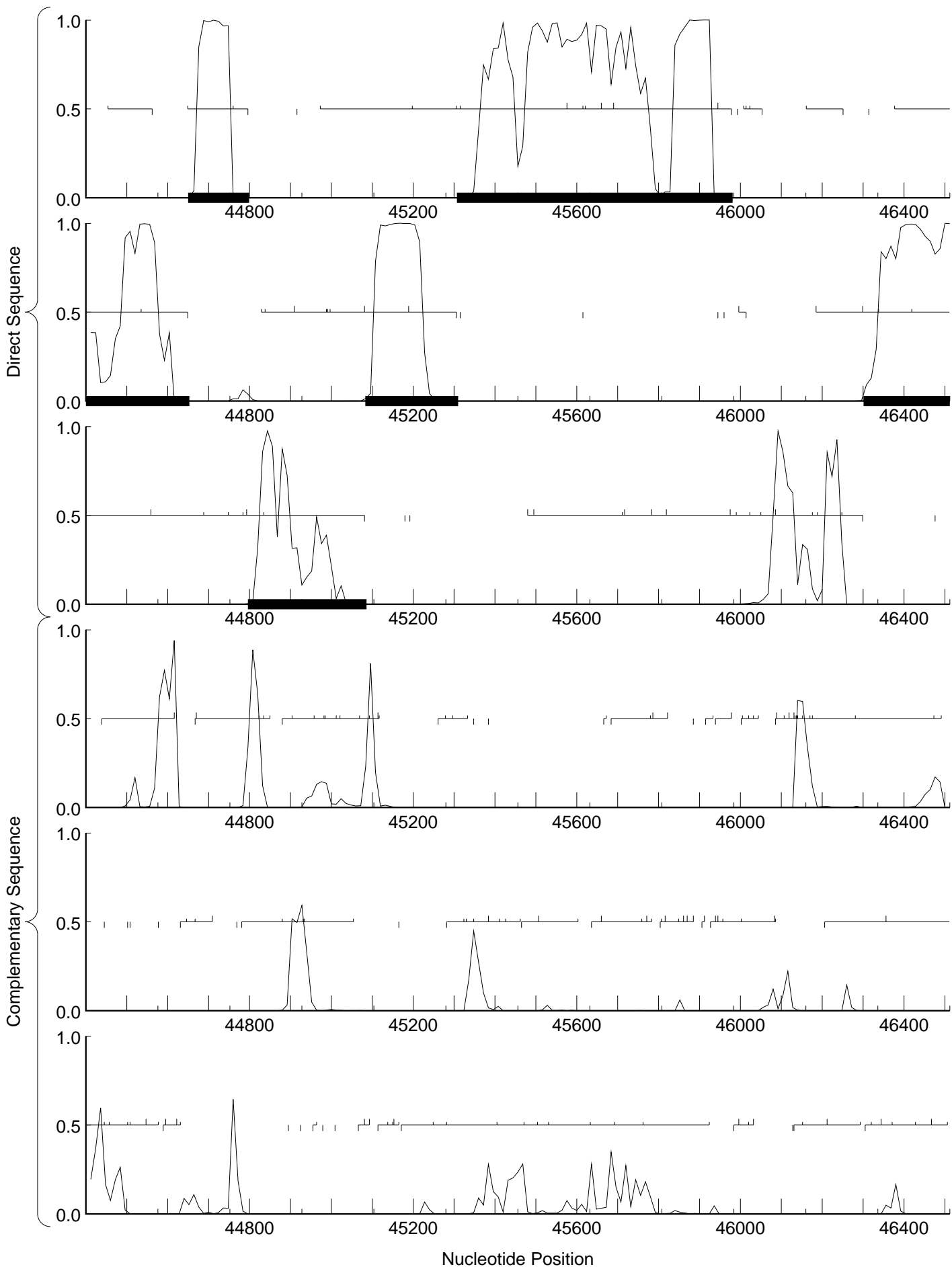
complete sequence, 47716 bp including 11-base 3' overhang (TGCCAAGGGGA), Cluster CZ, Order 2, Window 96, Step 12, 22/24

GeneMark, hmm prediction



complete sequence, 47716 bp including 11-base 3' overhang (TGCCAAGGGGA), Cluster CZ, Order 2, Window 96, Step 12, 23/24

GeneMark, hmm prediction



complete sequence, 47716 bp including 11-base 3' overhang (TGCCAAGGGGA), Cluster CZ, Order 2, Window 96, Step 12, 24/24

