

GeneMark

Version 2.5p (09.08.06)

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PROGRAM INFORMATION

Sequence : Gordonia phage Yeezy complete sequence, 51884 bp including 11-base 3' overhang (TGCCAGGGGGA
Analysis Date : 1/18/18 at 18:47:21
Pages : 26
Sequence Length : 51884 bp
GC Content : 66.69%

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,

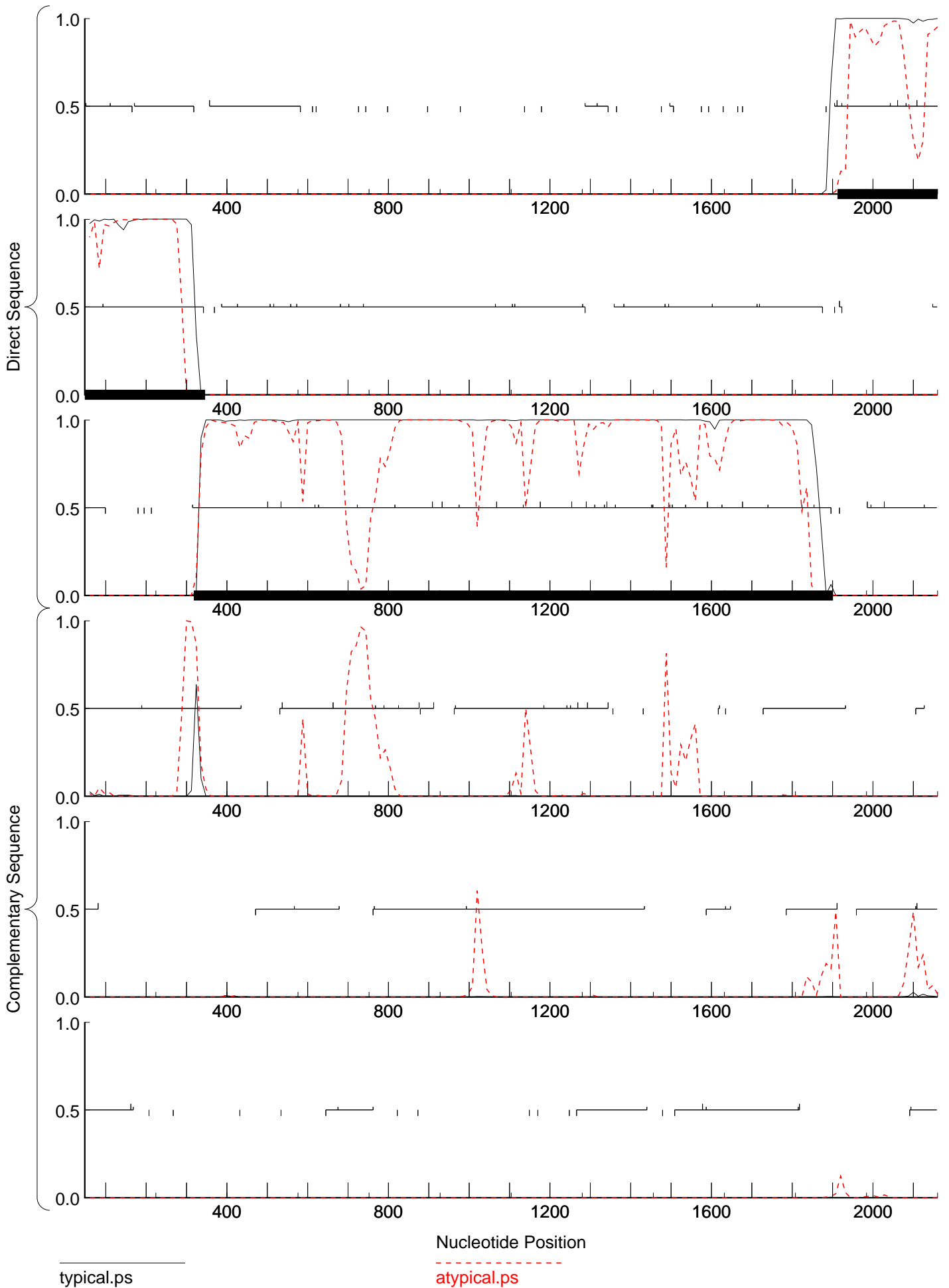
Matrix notes & comments

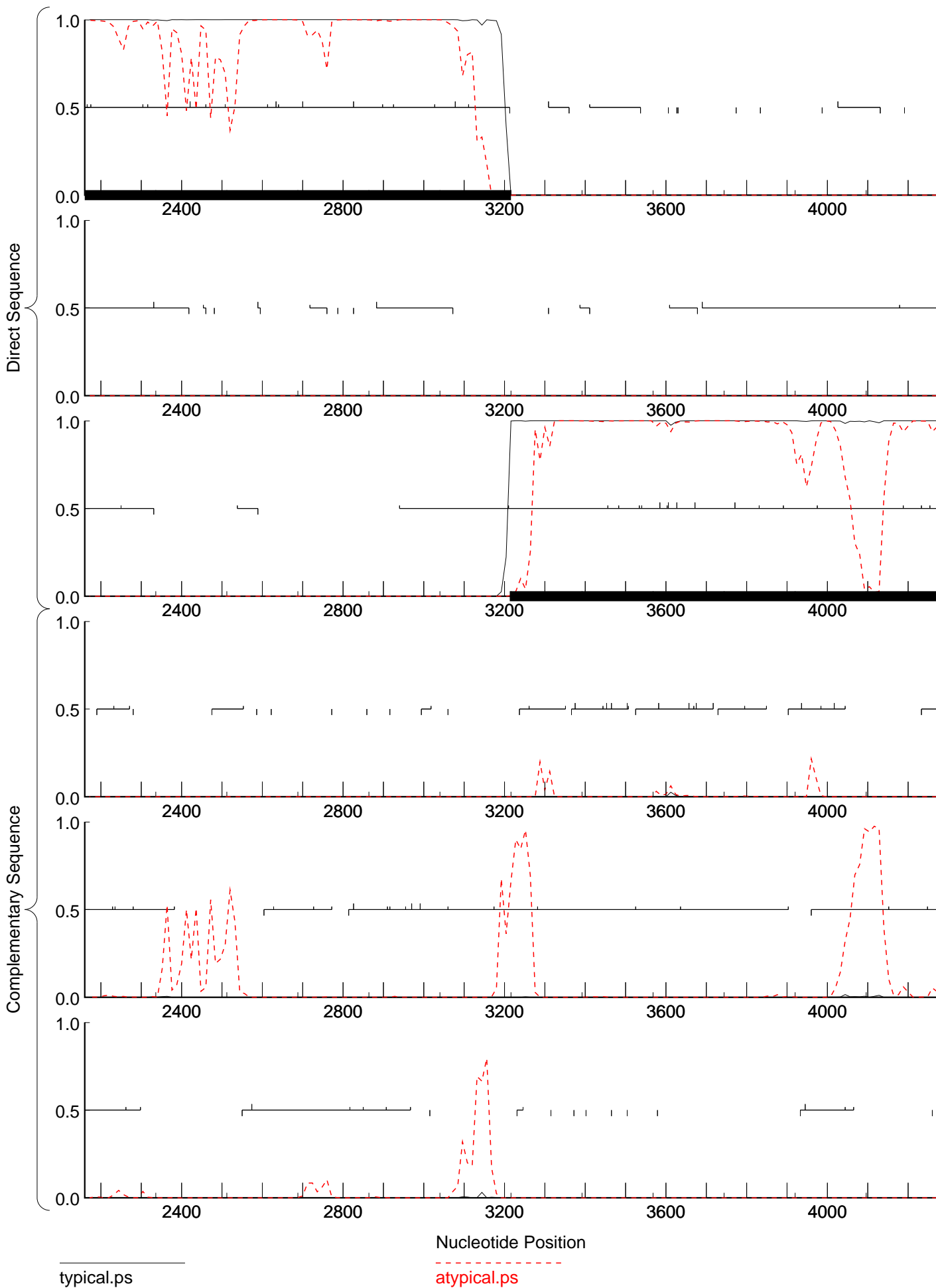
Training set derived by GeneMarkS, 4.30 October 2014
Thu Jan 18 18:47:21 2018

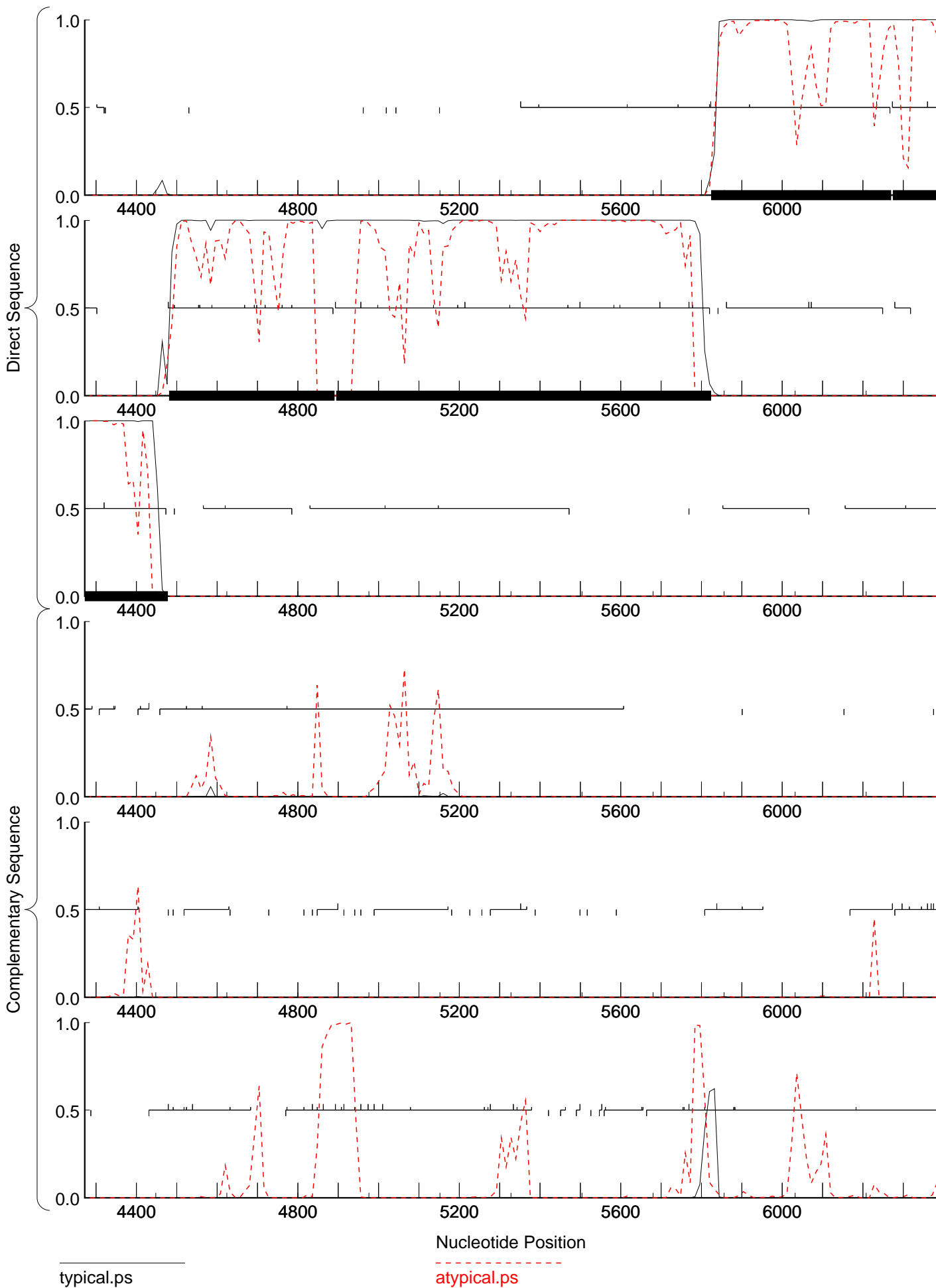
MATRIX INFORMATION

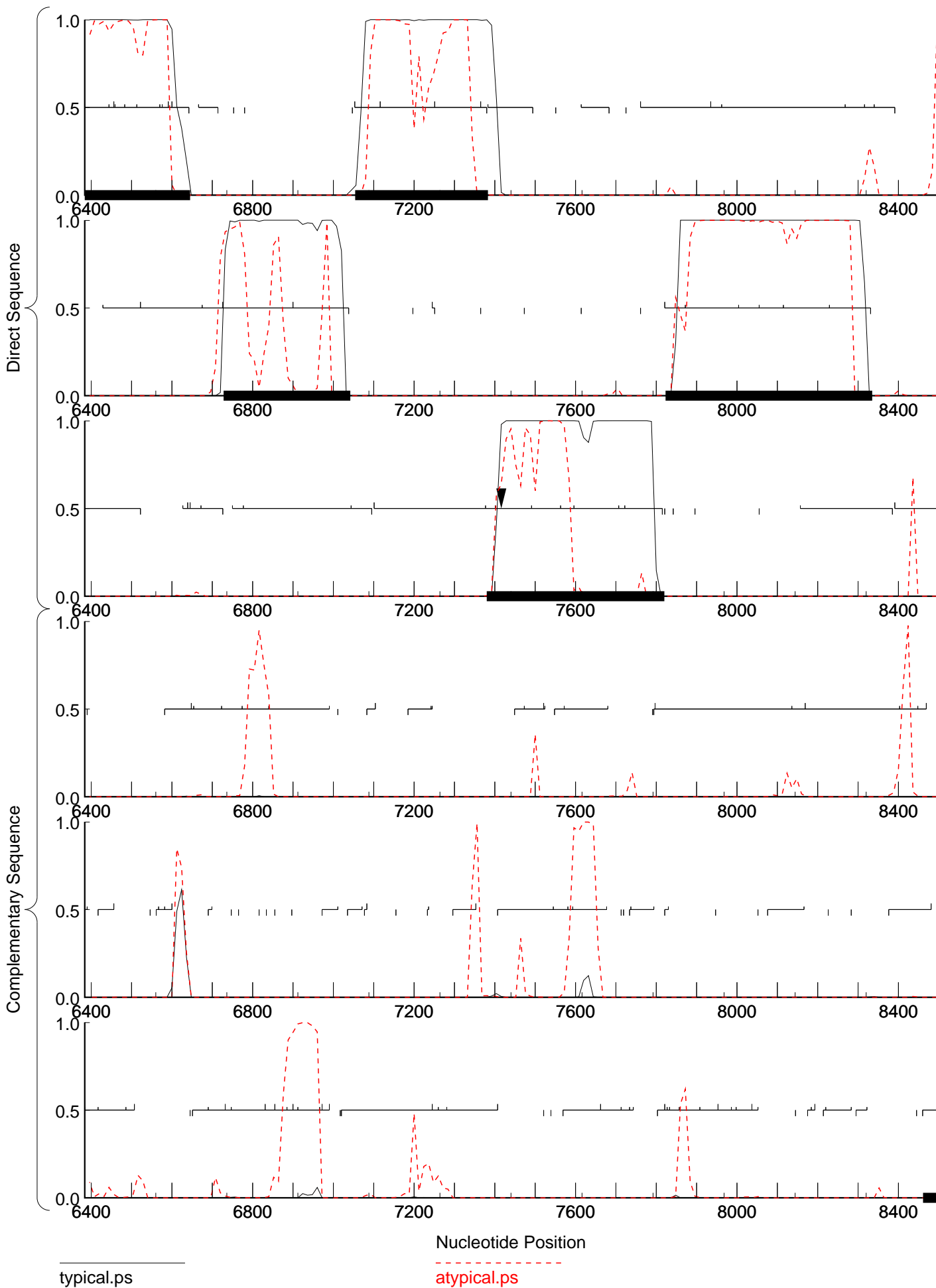
Matrix : -
Author : -
Order : 4

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



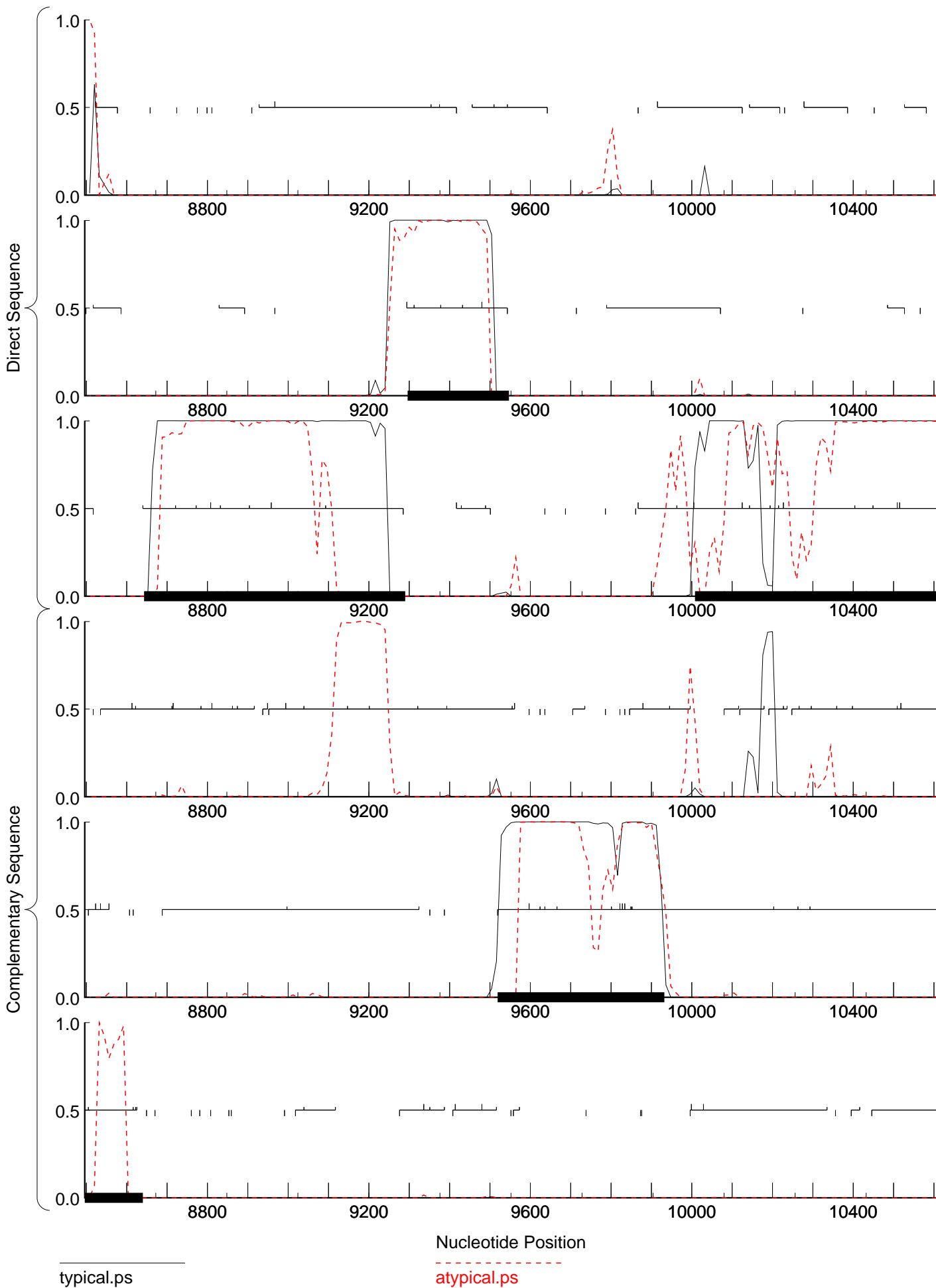


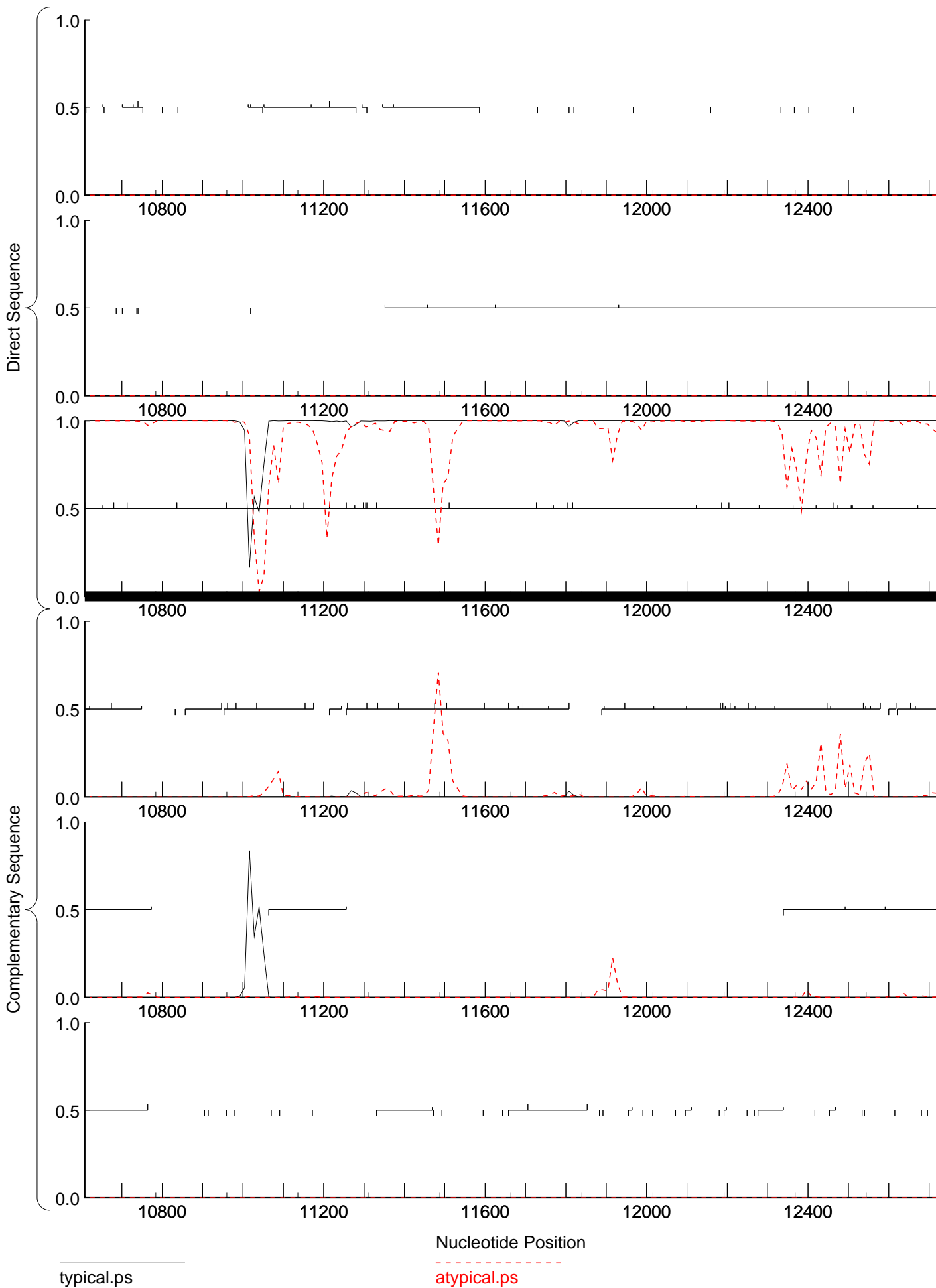


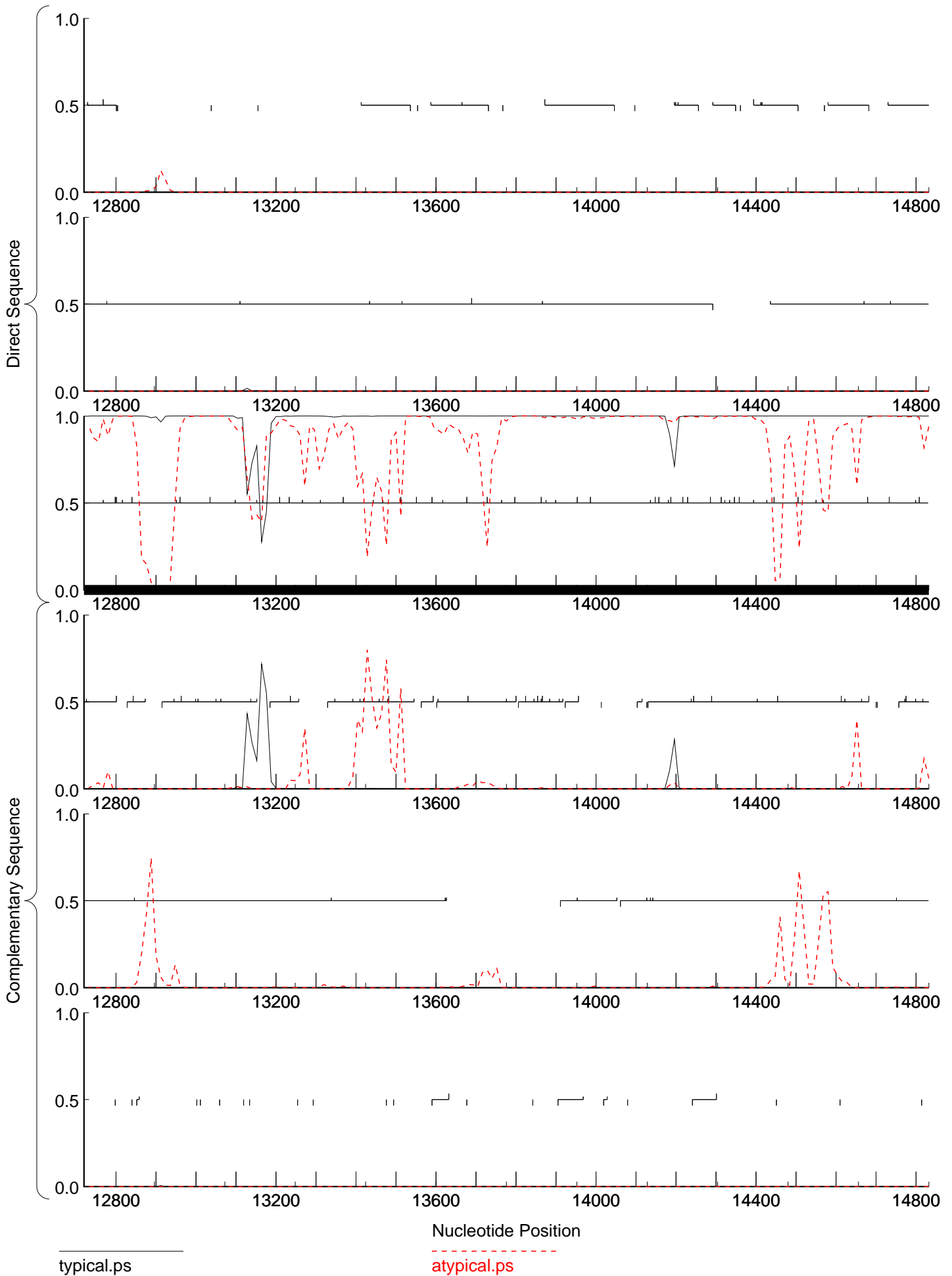


typical.ps

atypical.ps

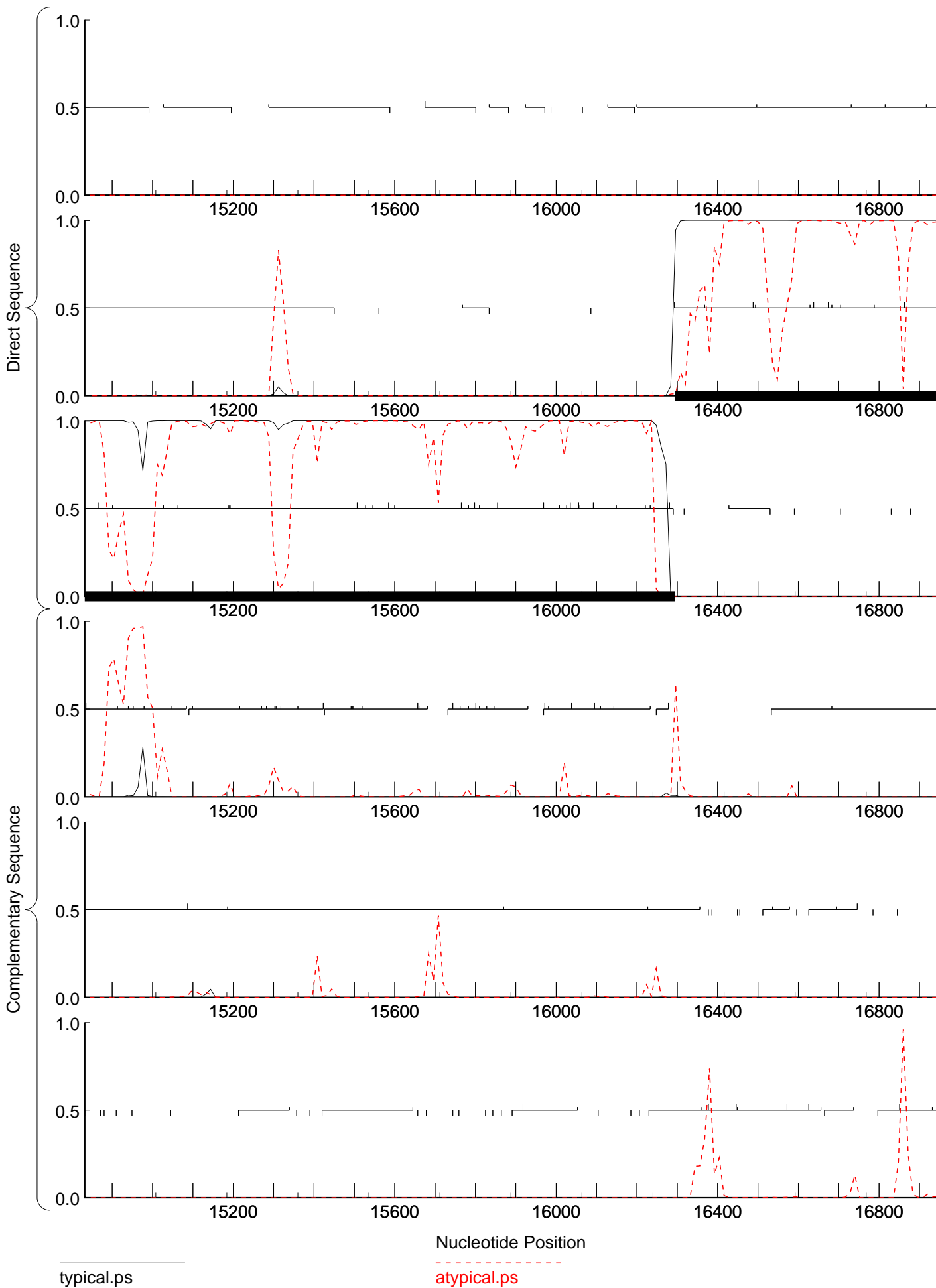




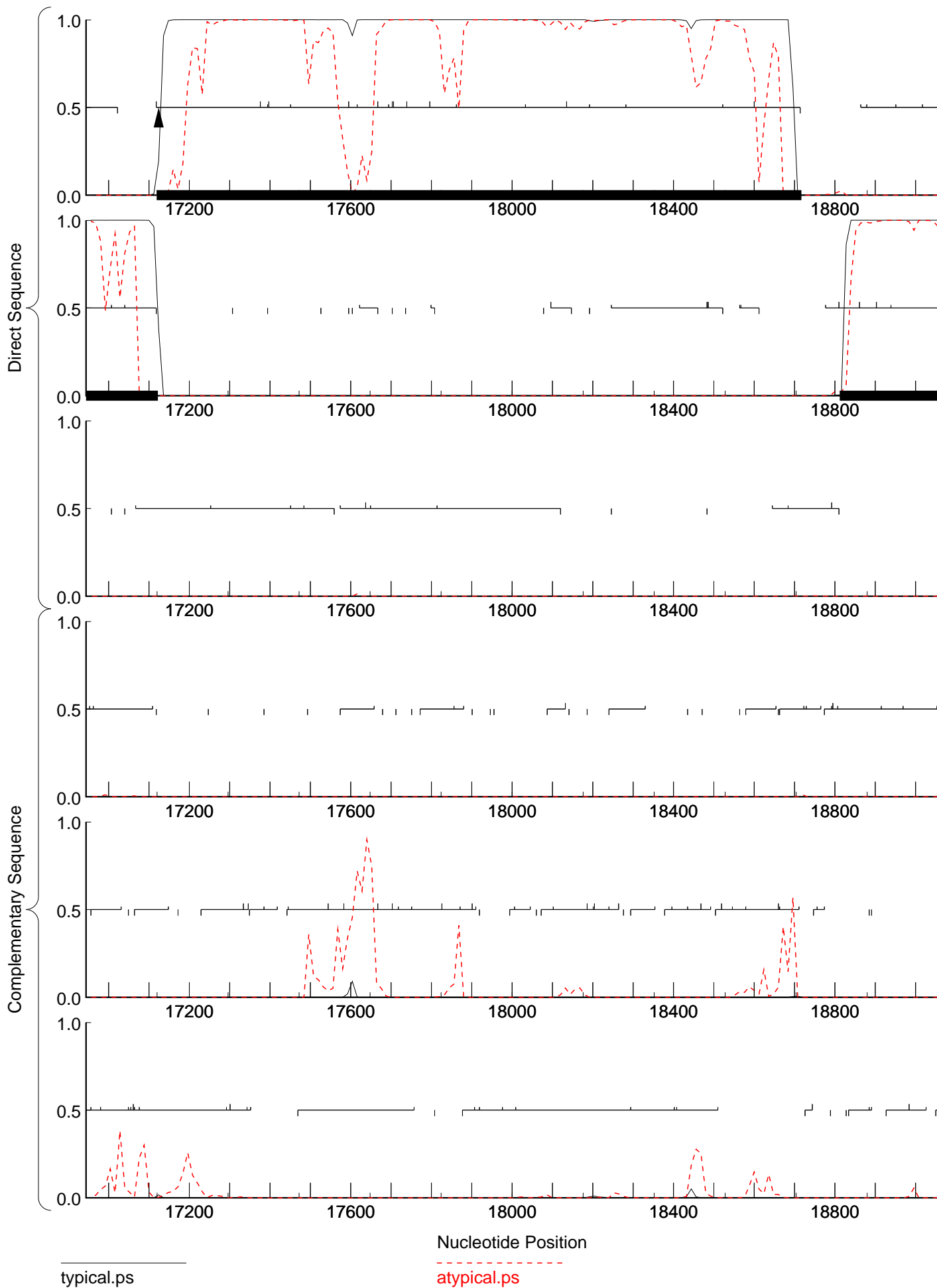


typical.ps

atypical.ps



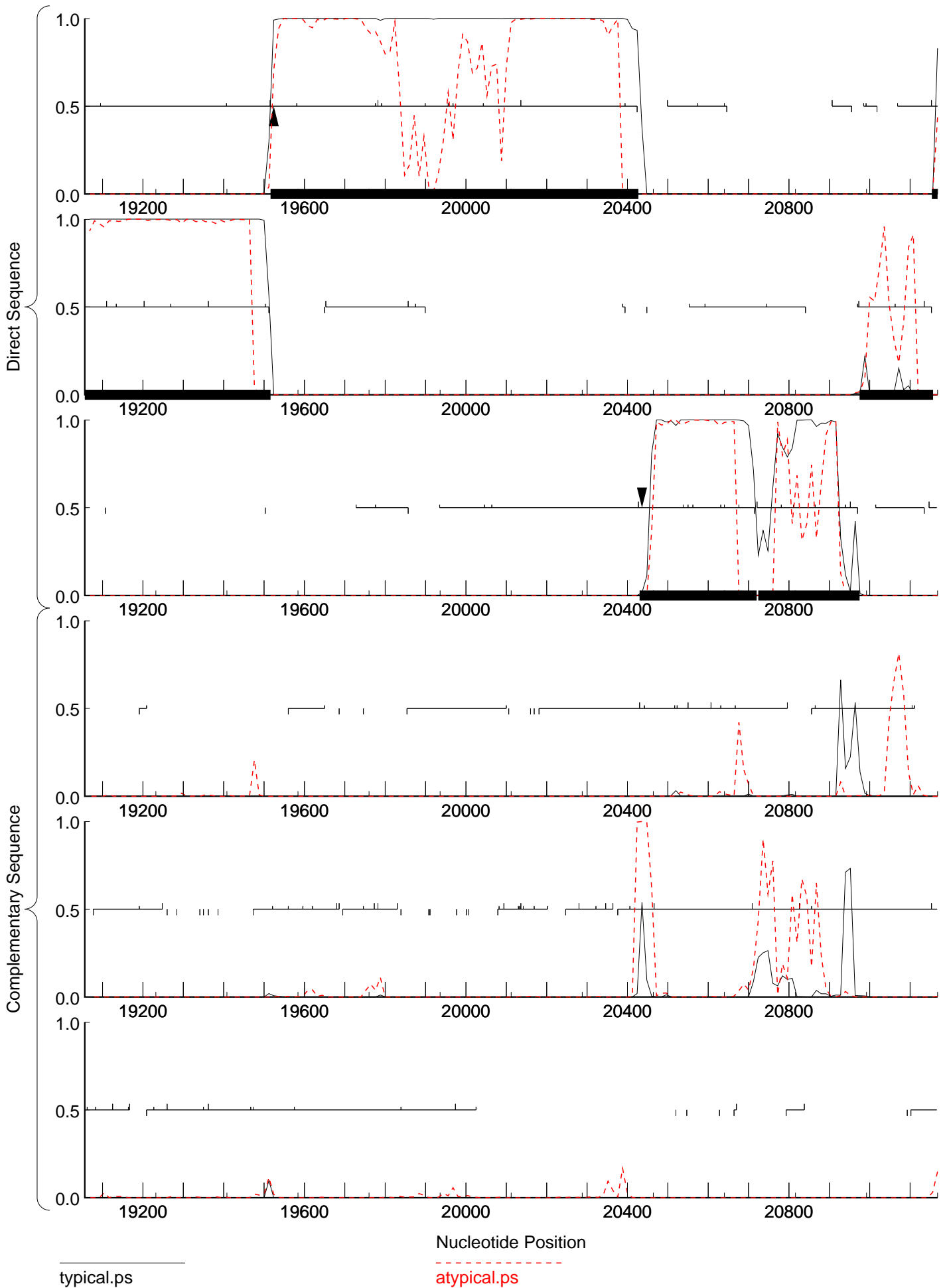
GeneMark.hmm prediction



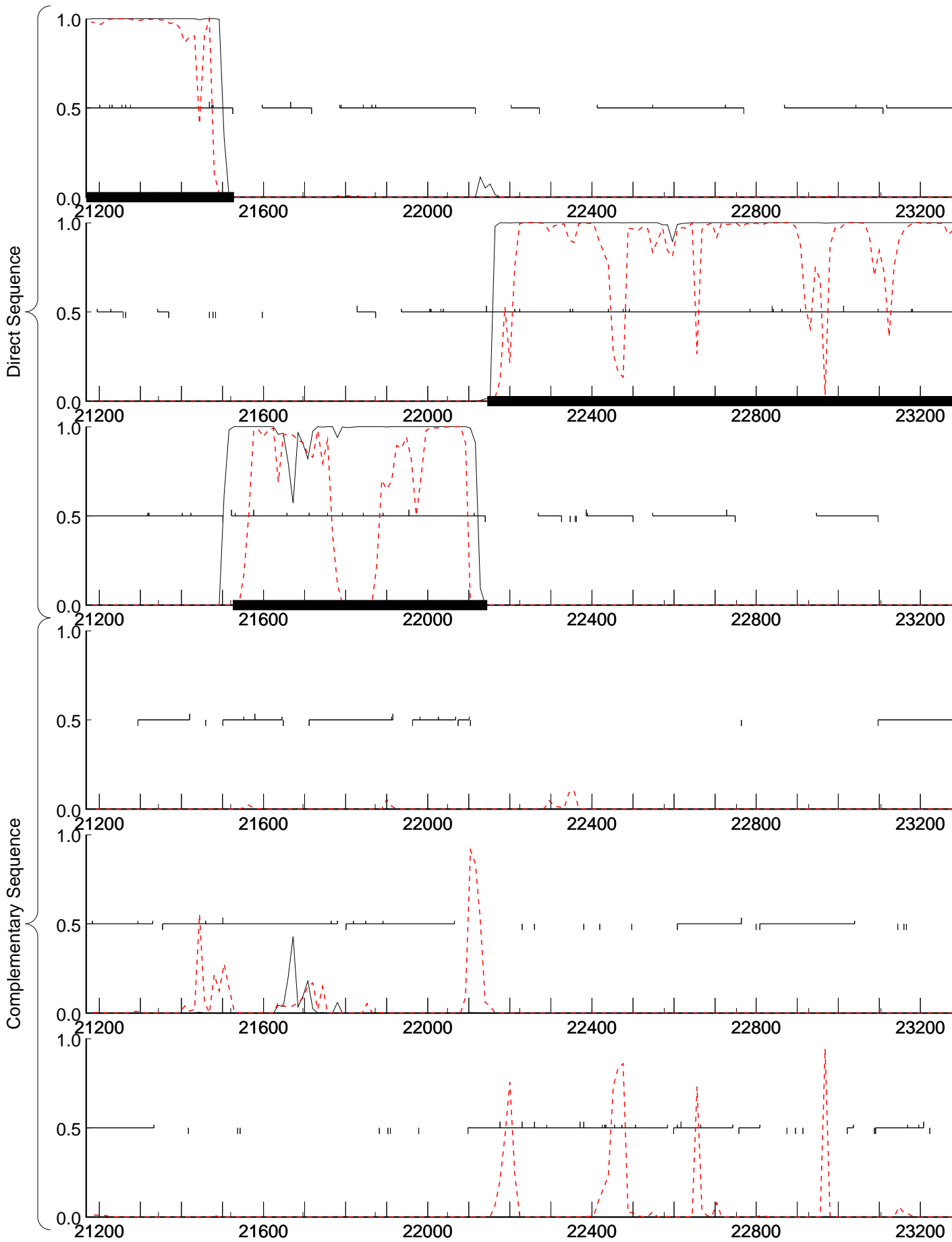
typical.ps

Nucleotide Position

atypical.ps

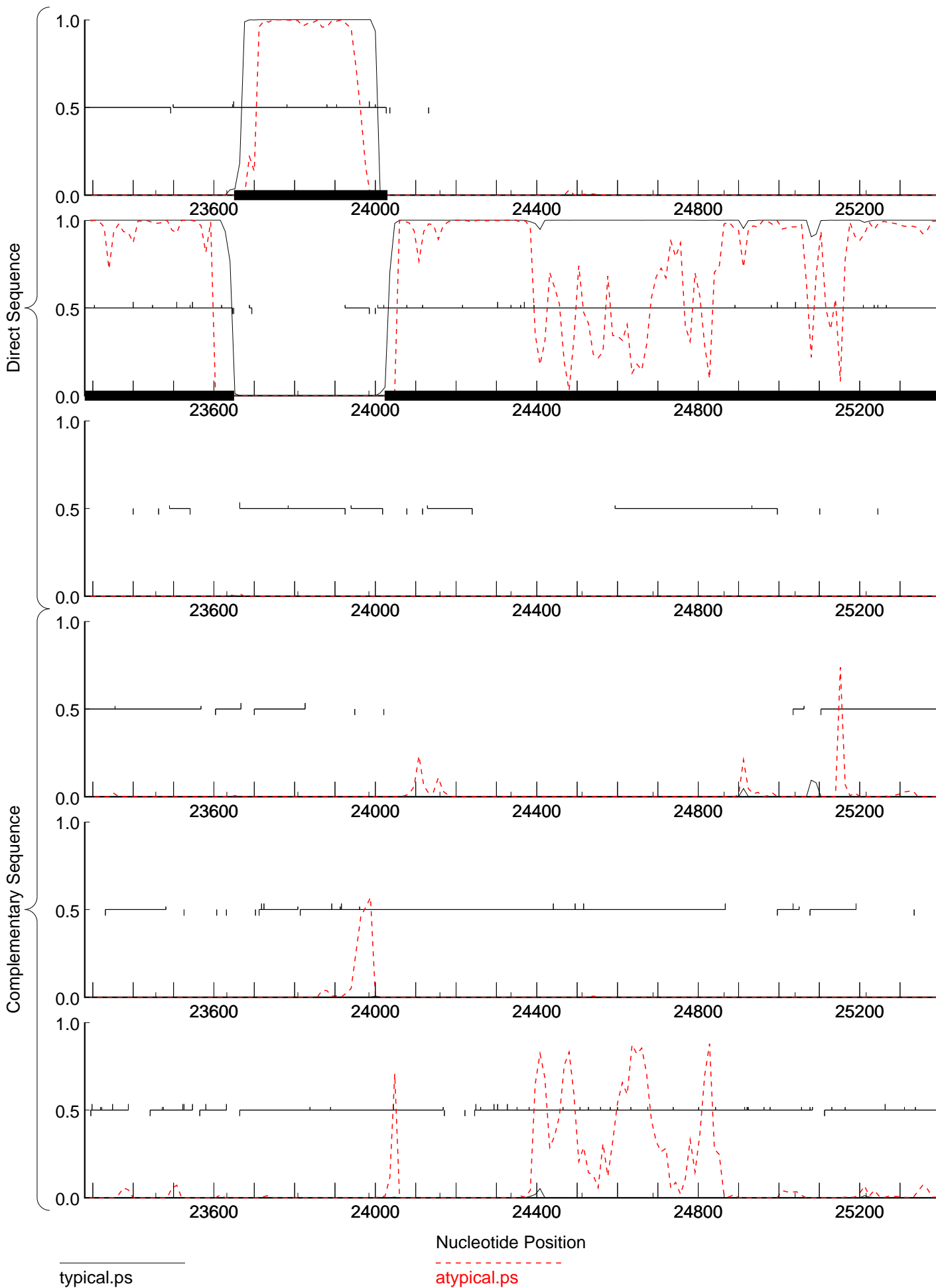


GeneMark.hmm prediction

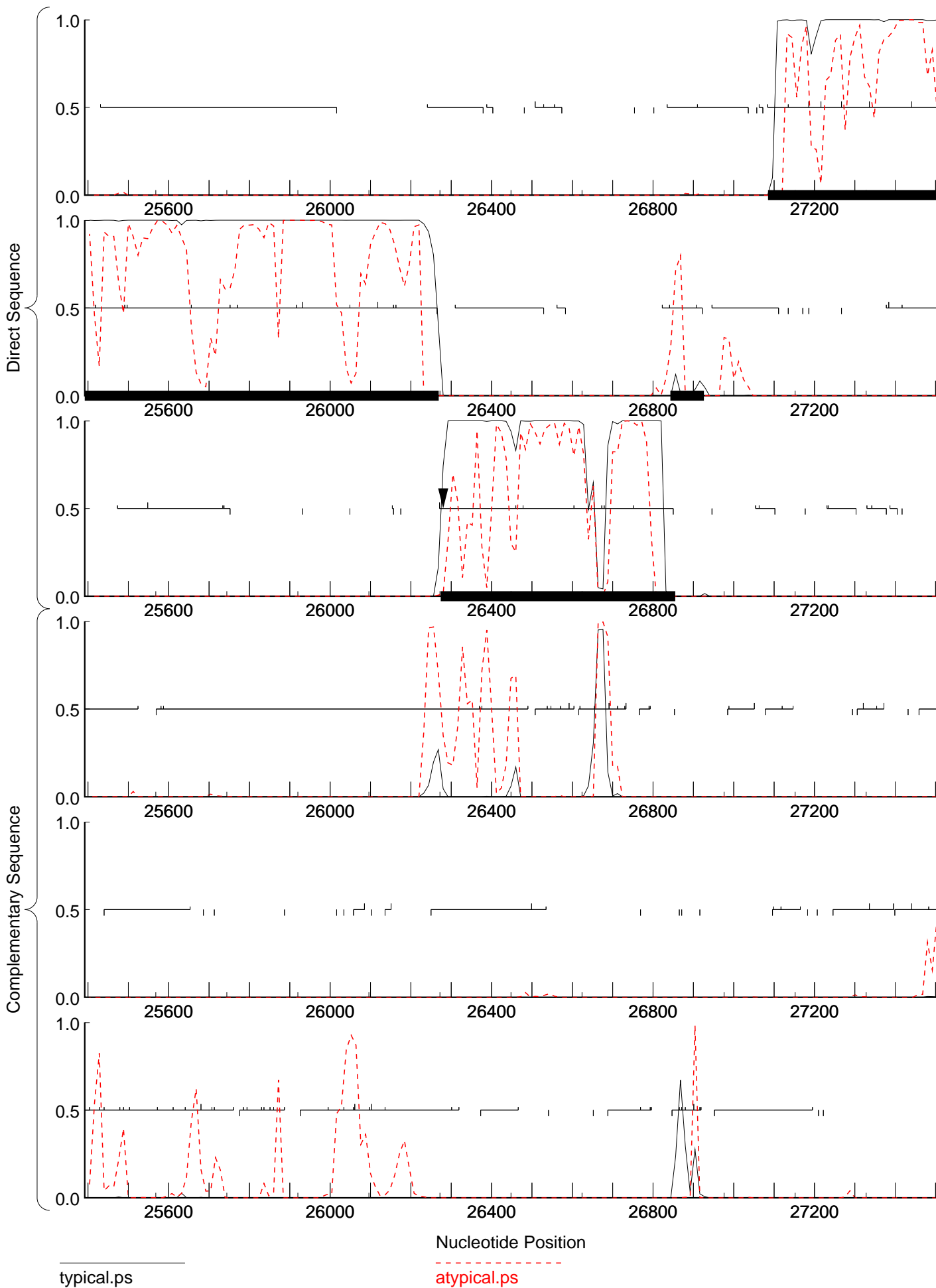


typical.ps

atypical.ps



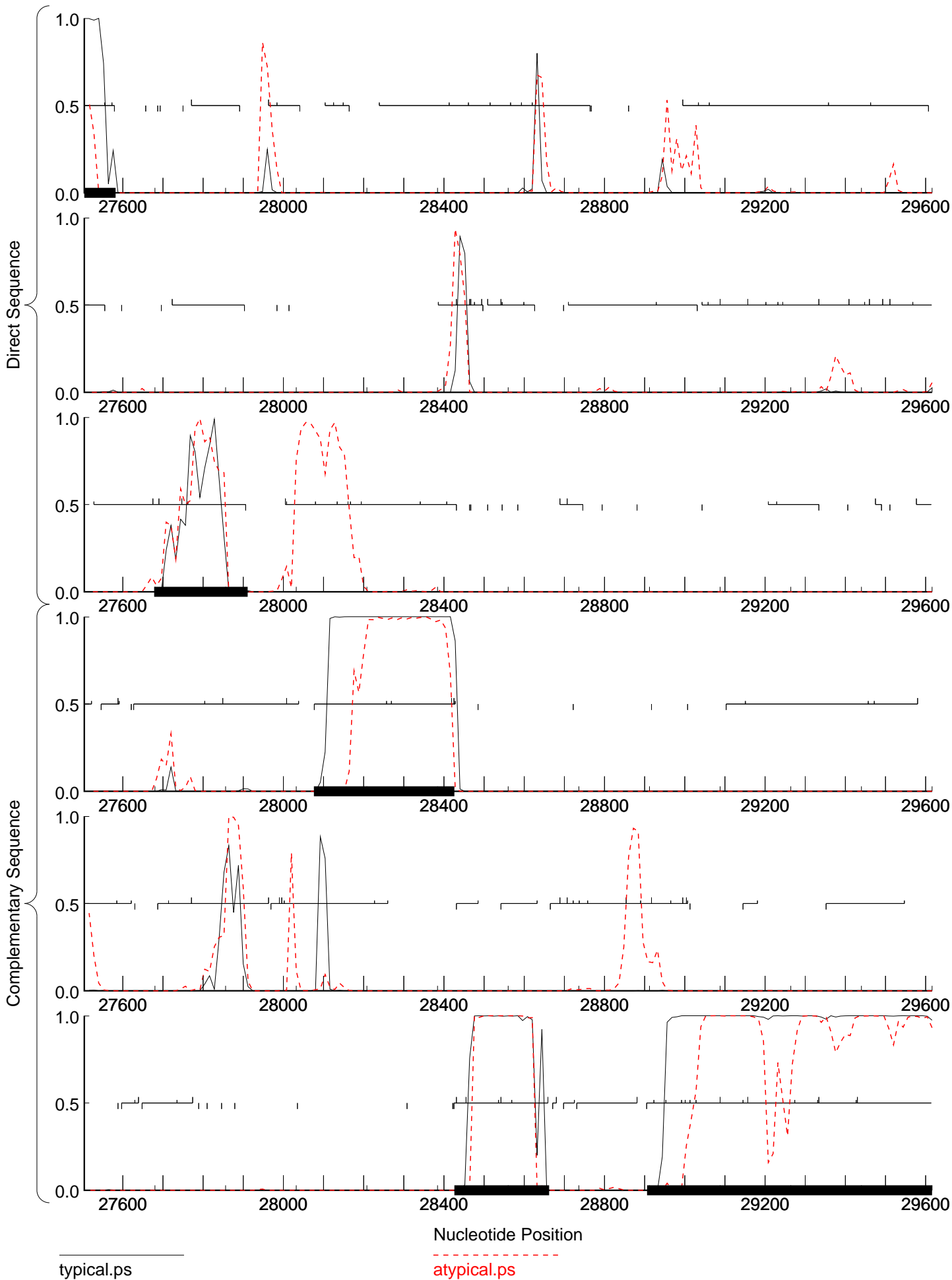
GeneMark.hmm prediction



typical.ps

atypical.ps

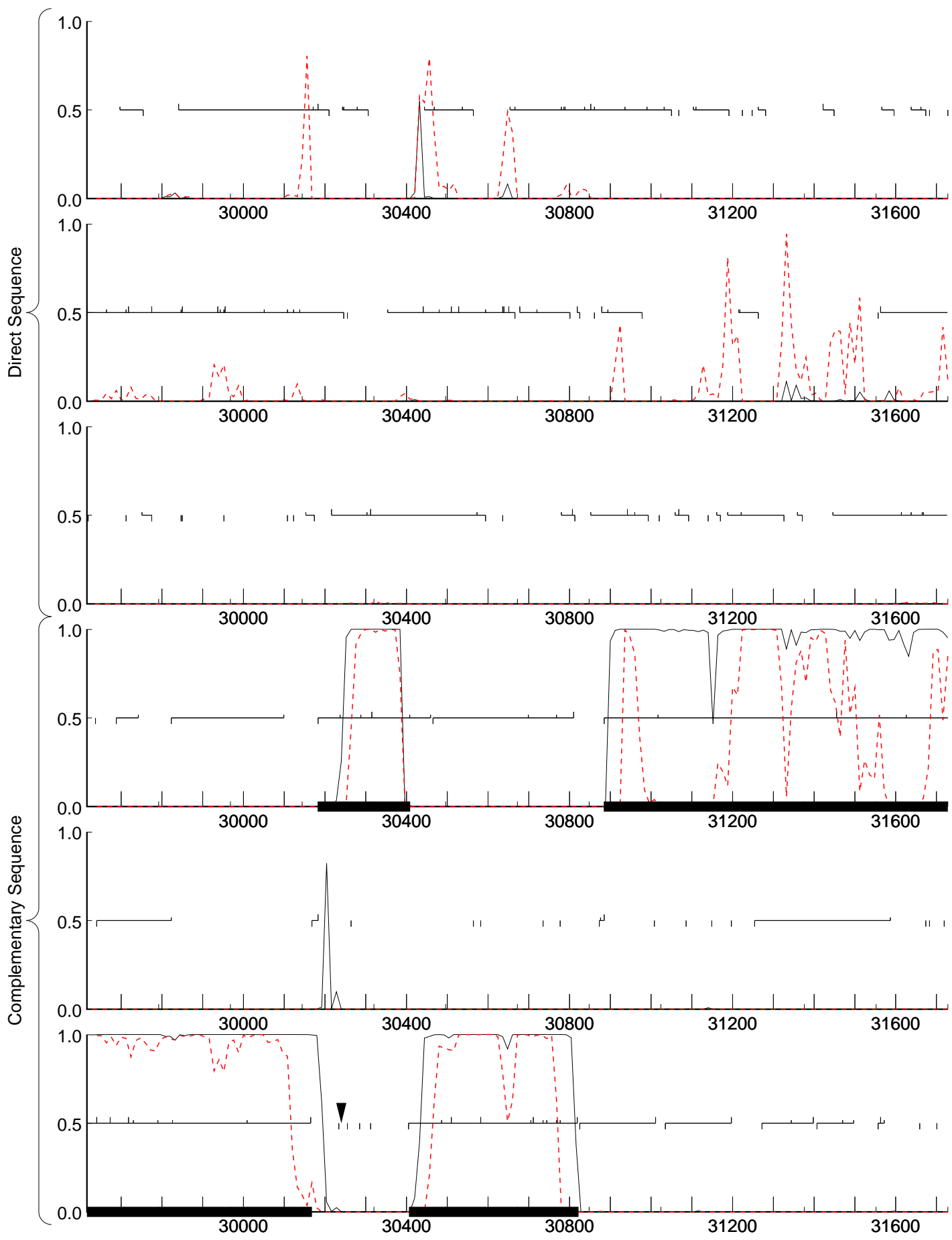
GeneMark.hmm prediction



typical.ps

atypical.ps

GeneMark.hmm prediction

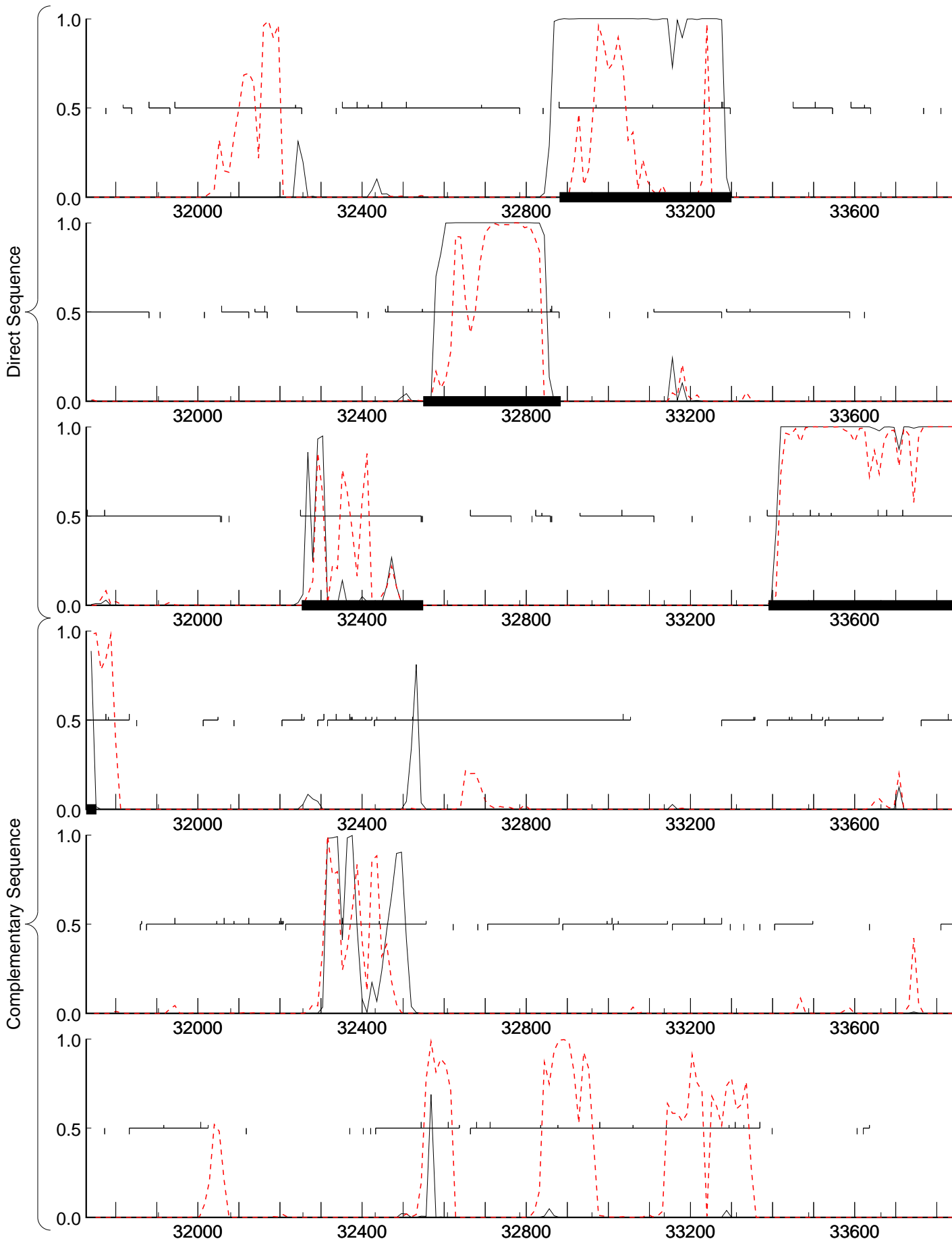


typical.ps

atypical.ps

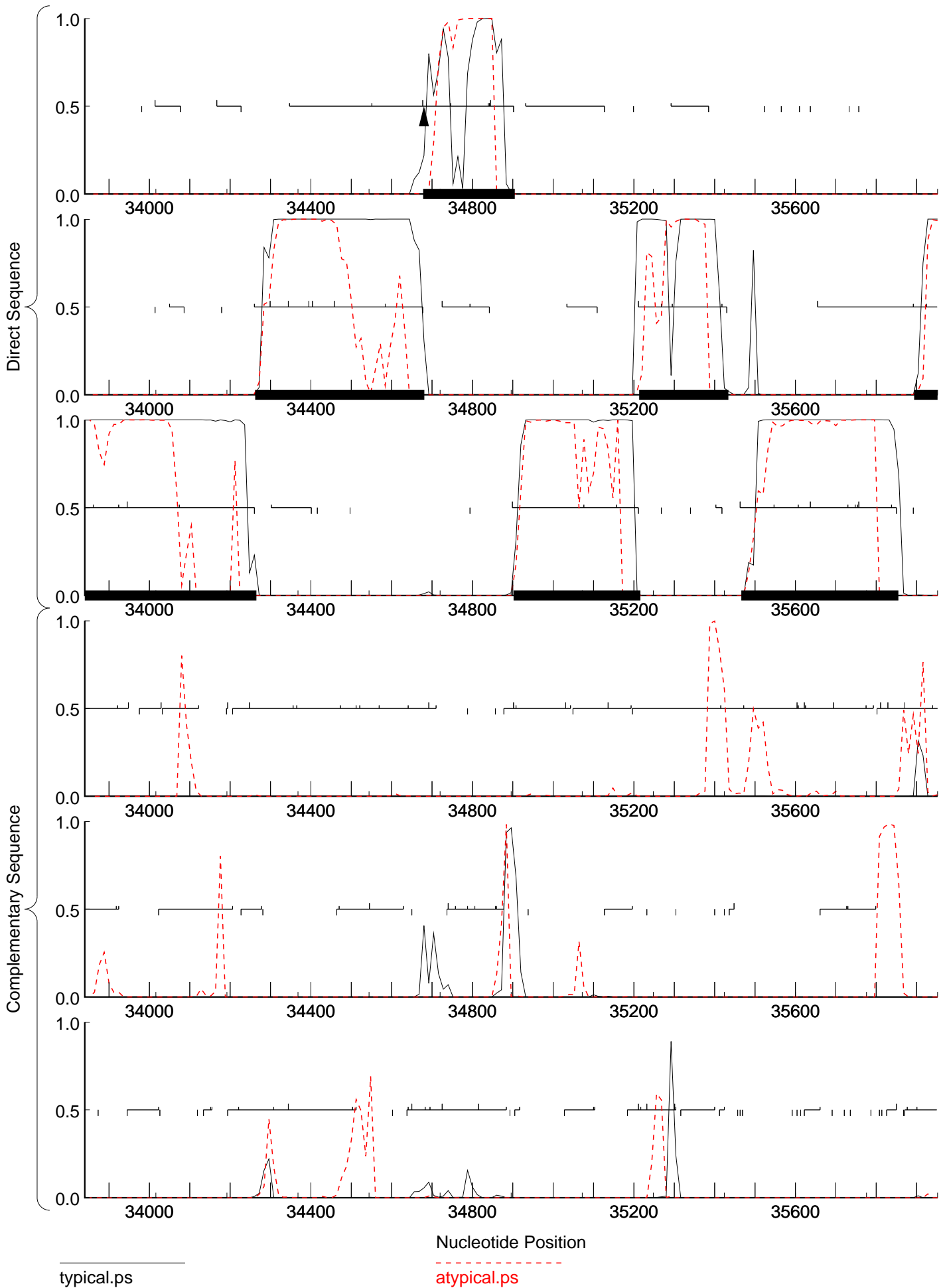
Nucleotide Position

GeneMark.hmm prediction

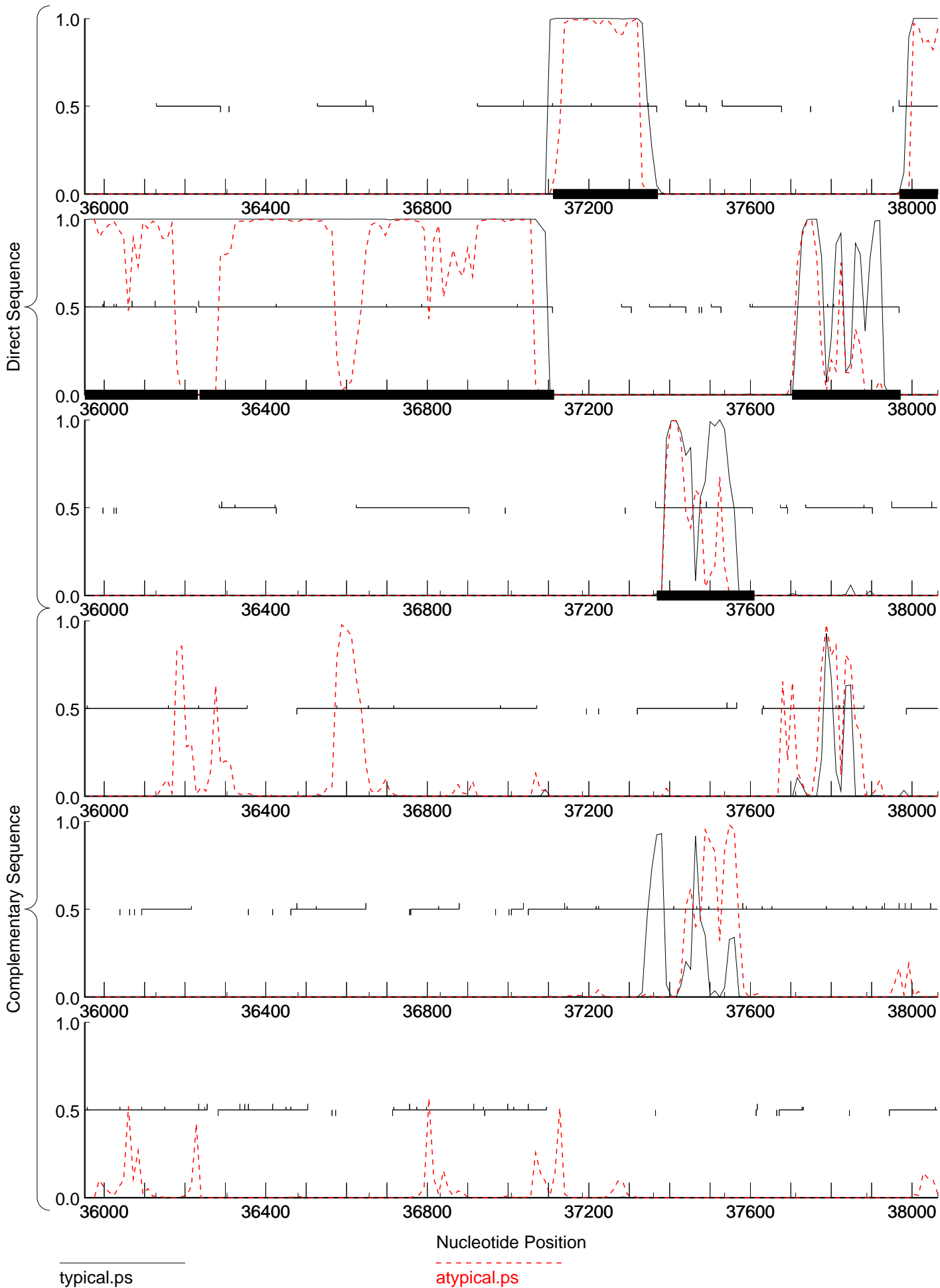


typical.ps

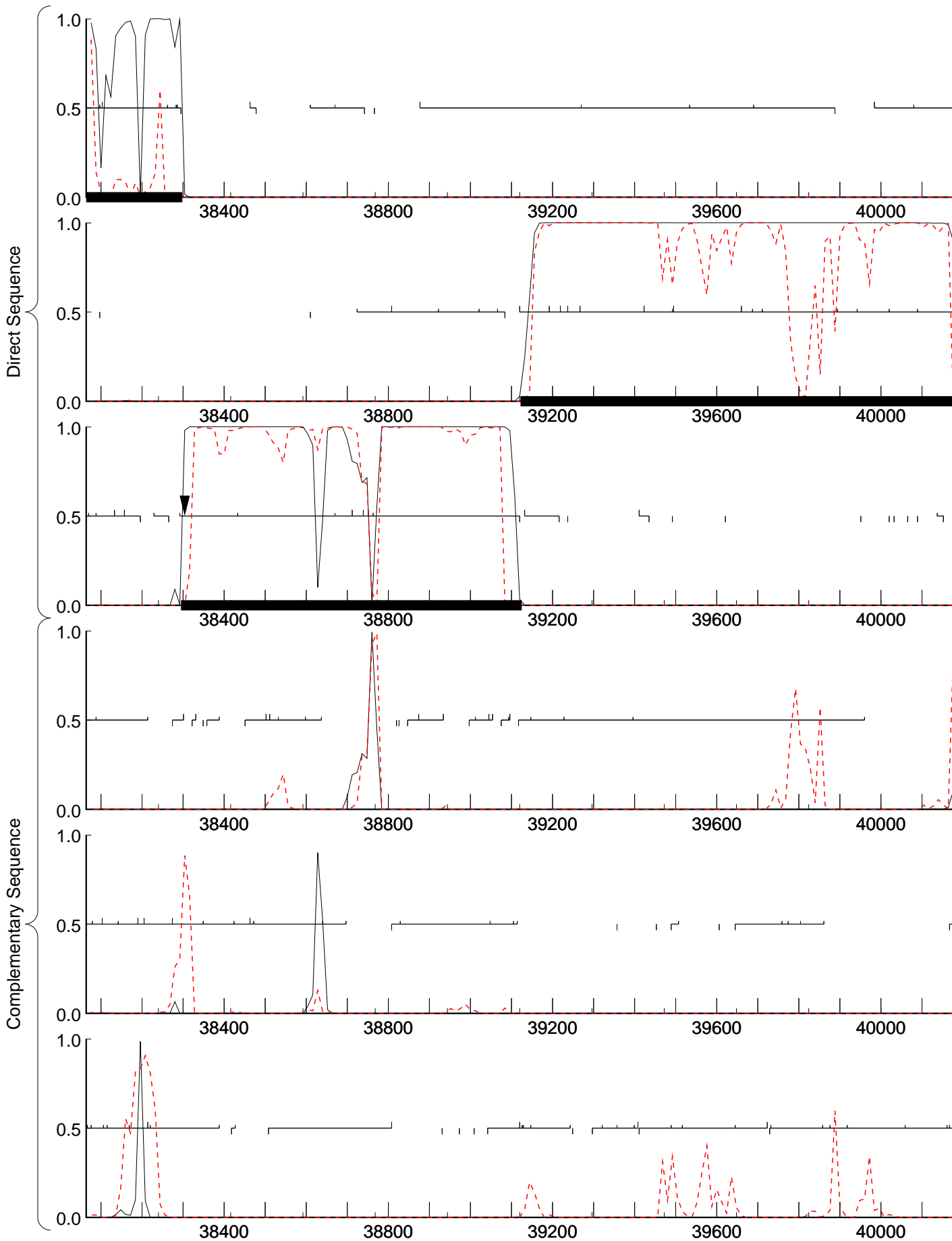
atypical.ps



GeneMark.hmm prediction



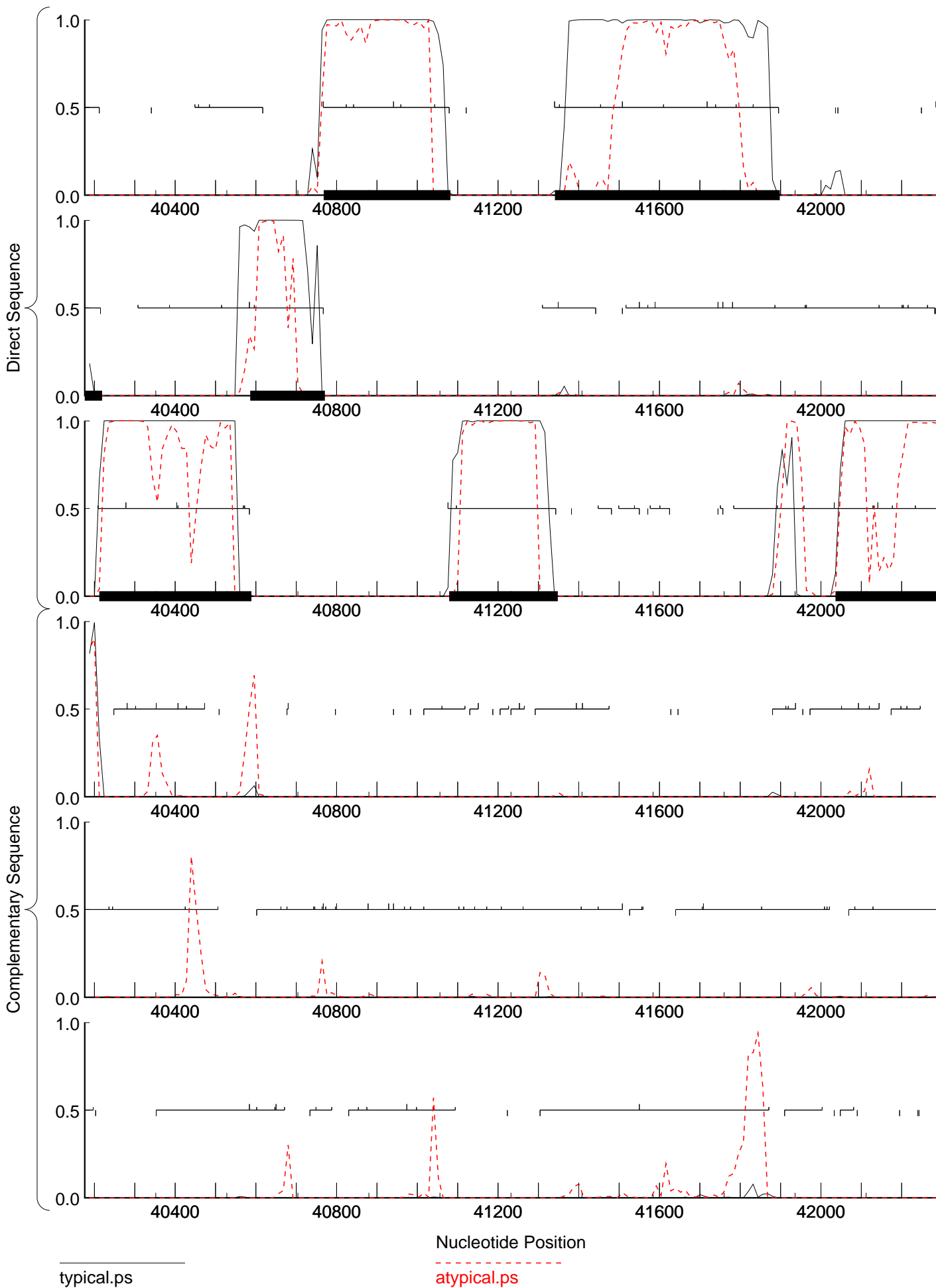
GeneMark.hmm prediction



typical.ps

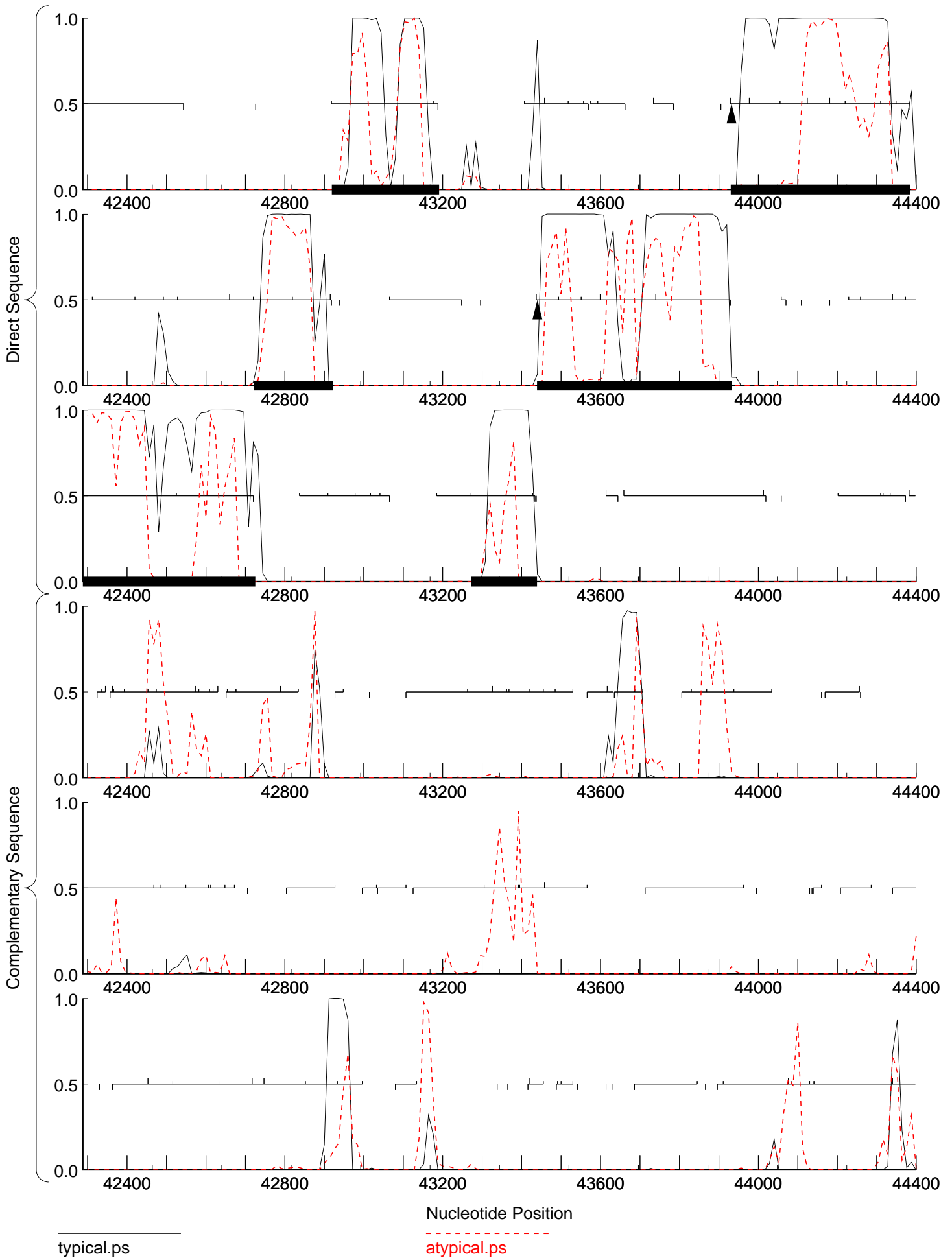
atypical.ps

GeneMark.hmm prediction

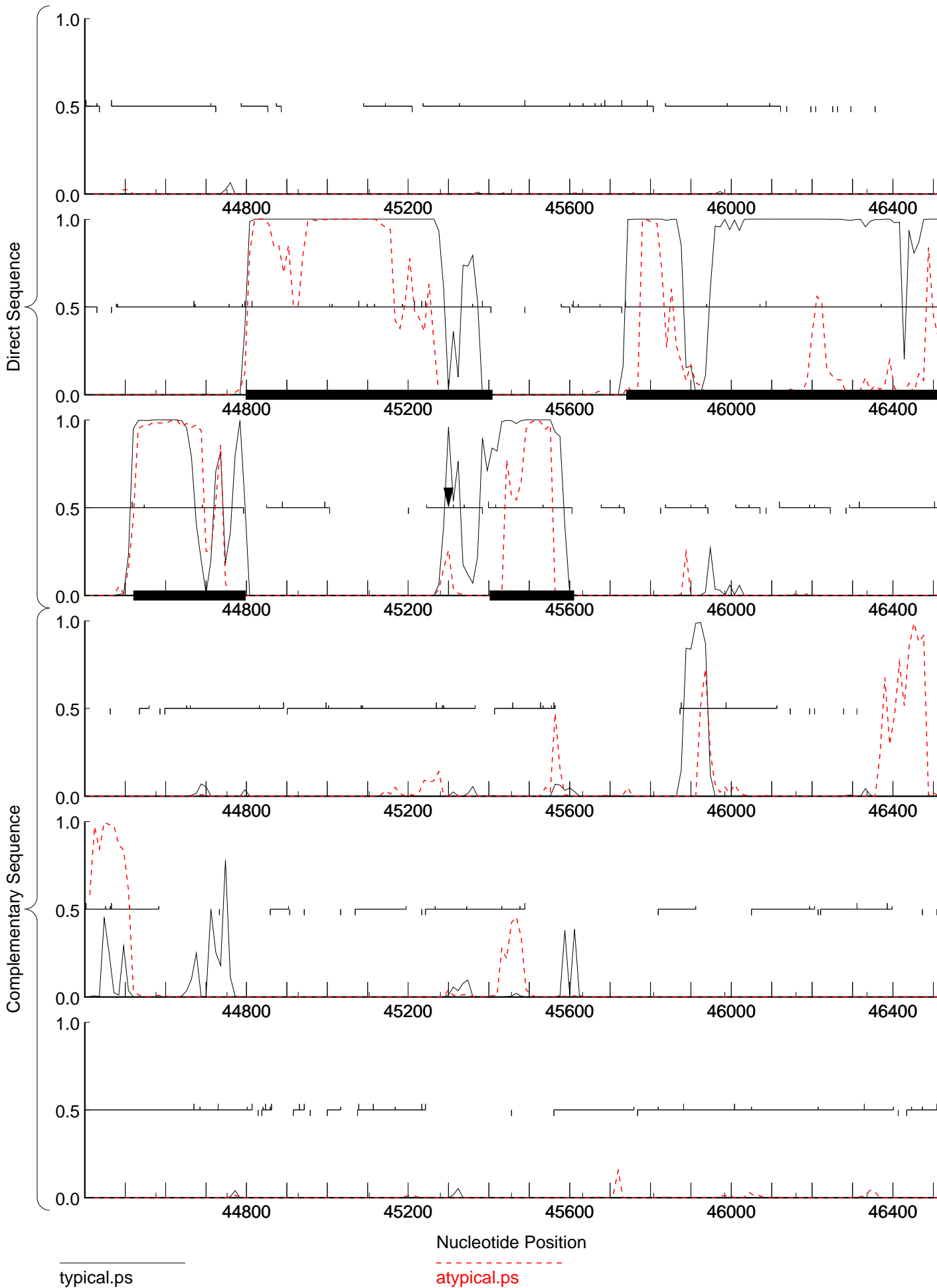


typical.ps

atypical.ps



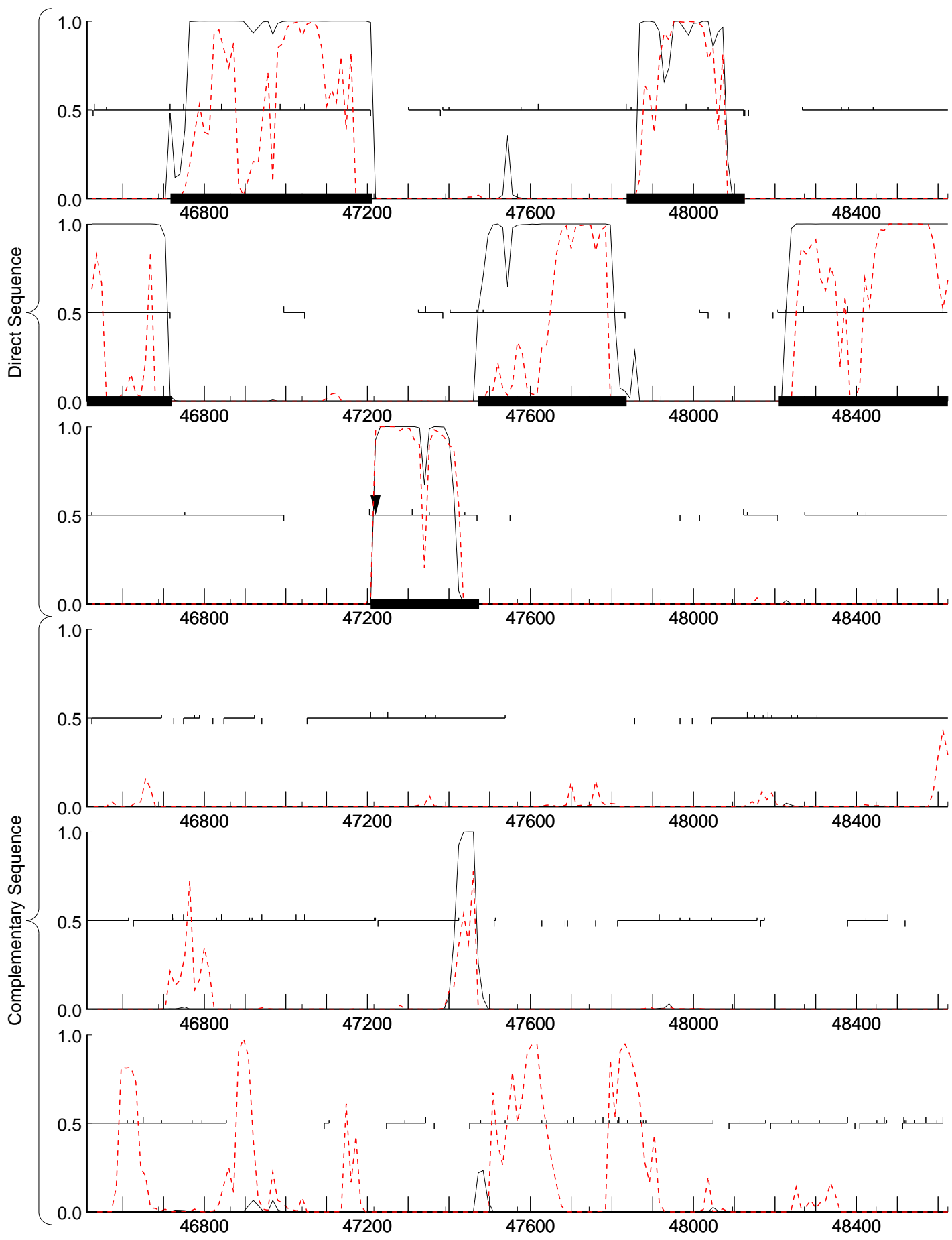
GeneMark.hmm prediction



typical.ps

atypical.ps

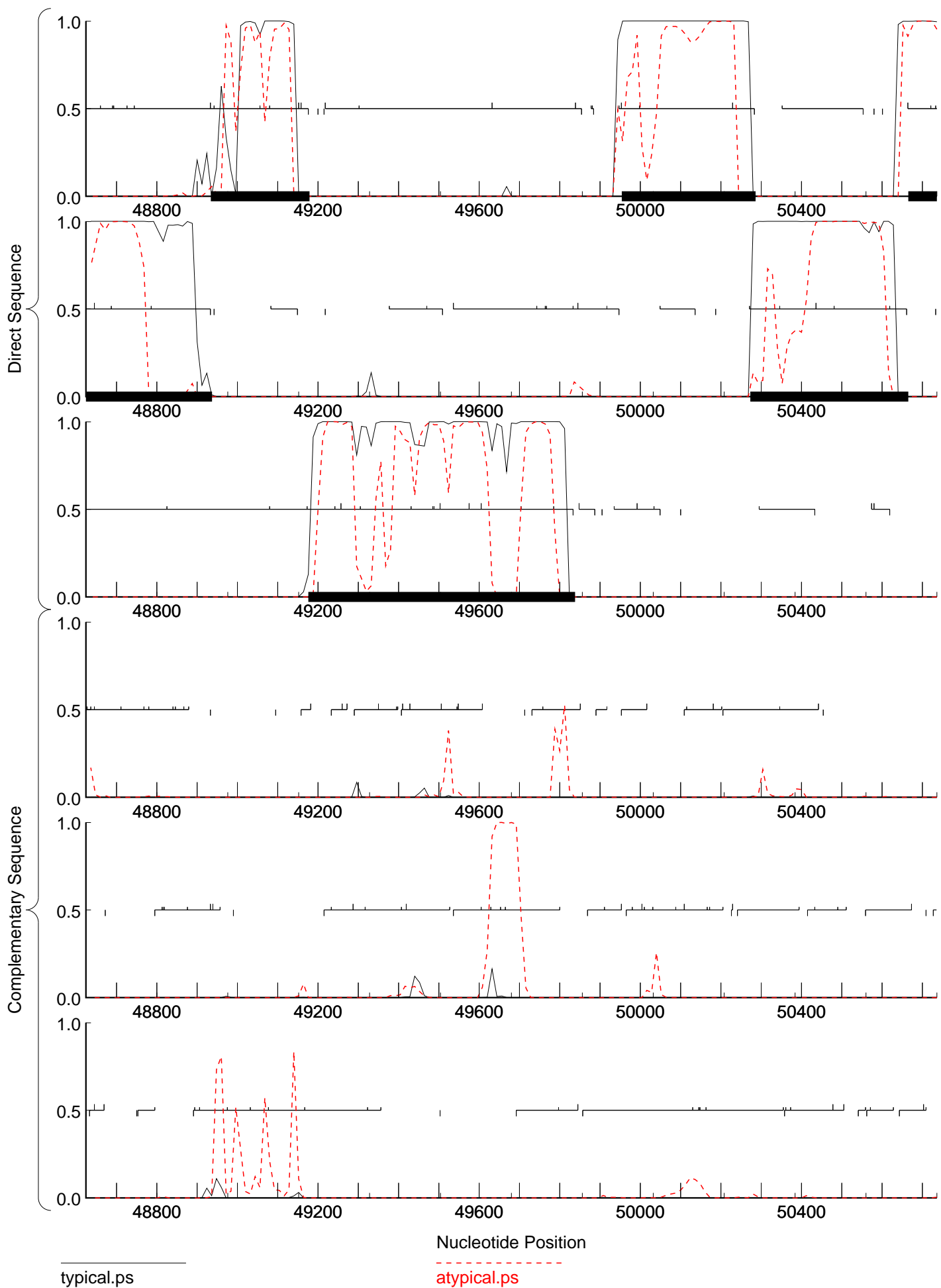
GeneMark.hmm prediction



typical.ps

atypical.ps

GeneMark.hmm prediction



typical.ps

atypical.ps

GeneMark.hmm prediction

