

GeneMark

Version 2.5p (09.08.06)

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PROGRAM INFORMATION

Sequence : Mycobacterium phage Tortoise16 complete sequence, 154584 bp, circularly permuted, Cluster C
Analysis Date : 6/22/18 at 1:38:01
Pages : 75
Sequence Length : 154584 bp
GC Content : 64.76%

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,

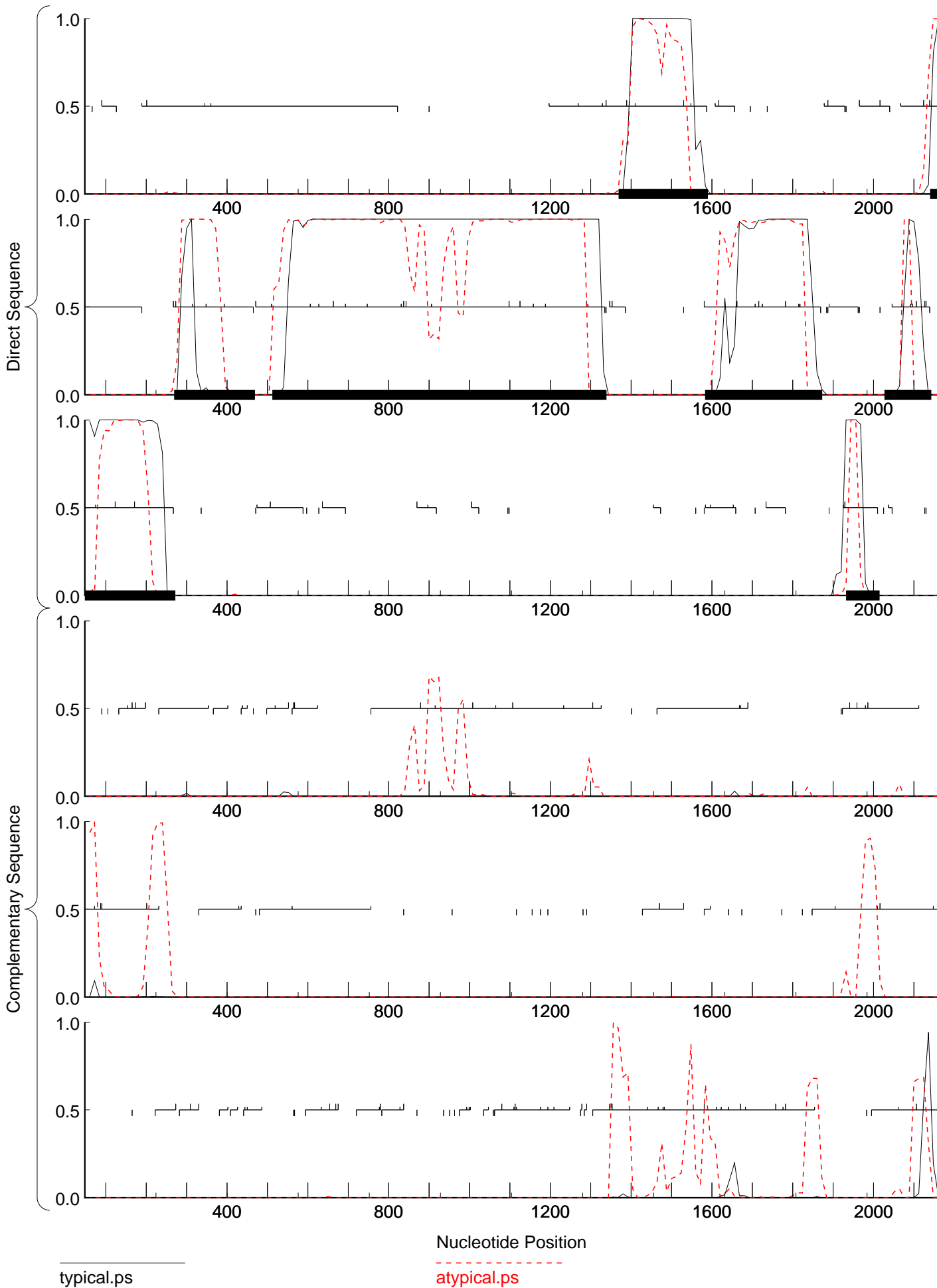
MATRIX INFORMATION

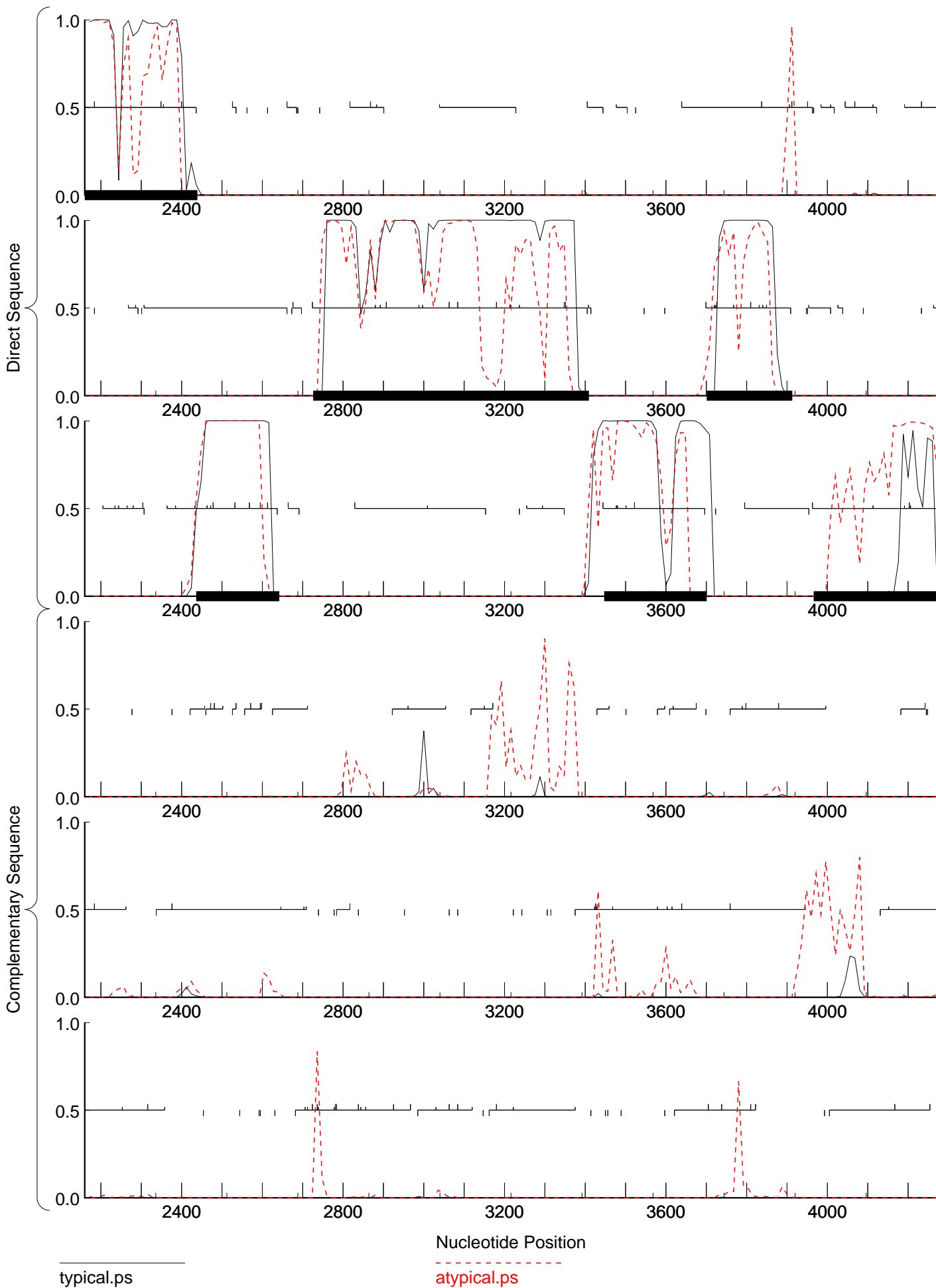
Matrix : -
Author : -
Order : 4

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

Matrix notes & comments

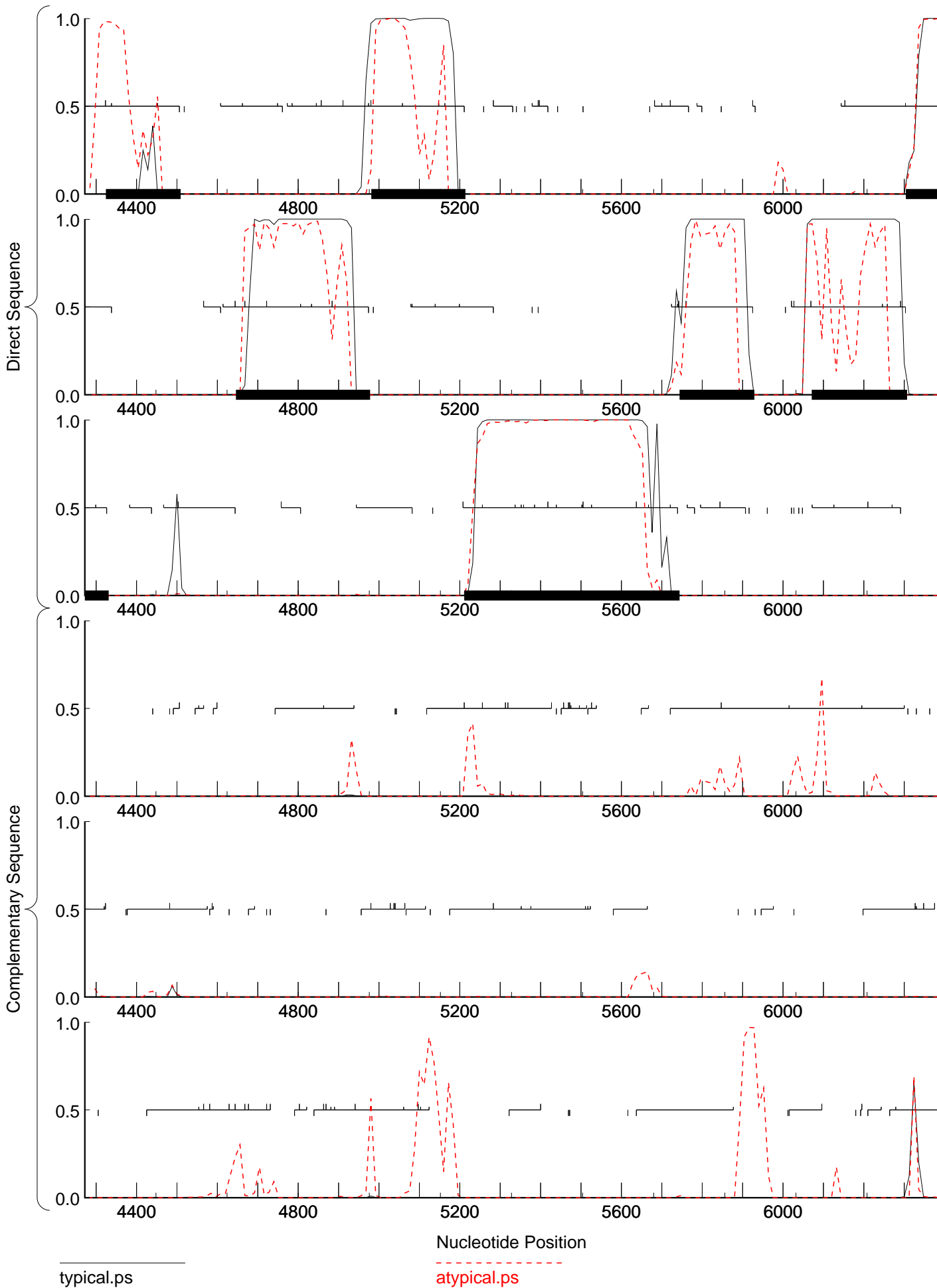
Training set derived by GeneMarkS, 4.30 October 2014
Fri Jun 22 01:38:01 2018





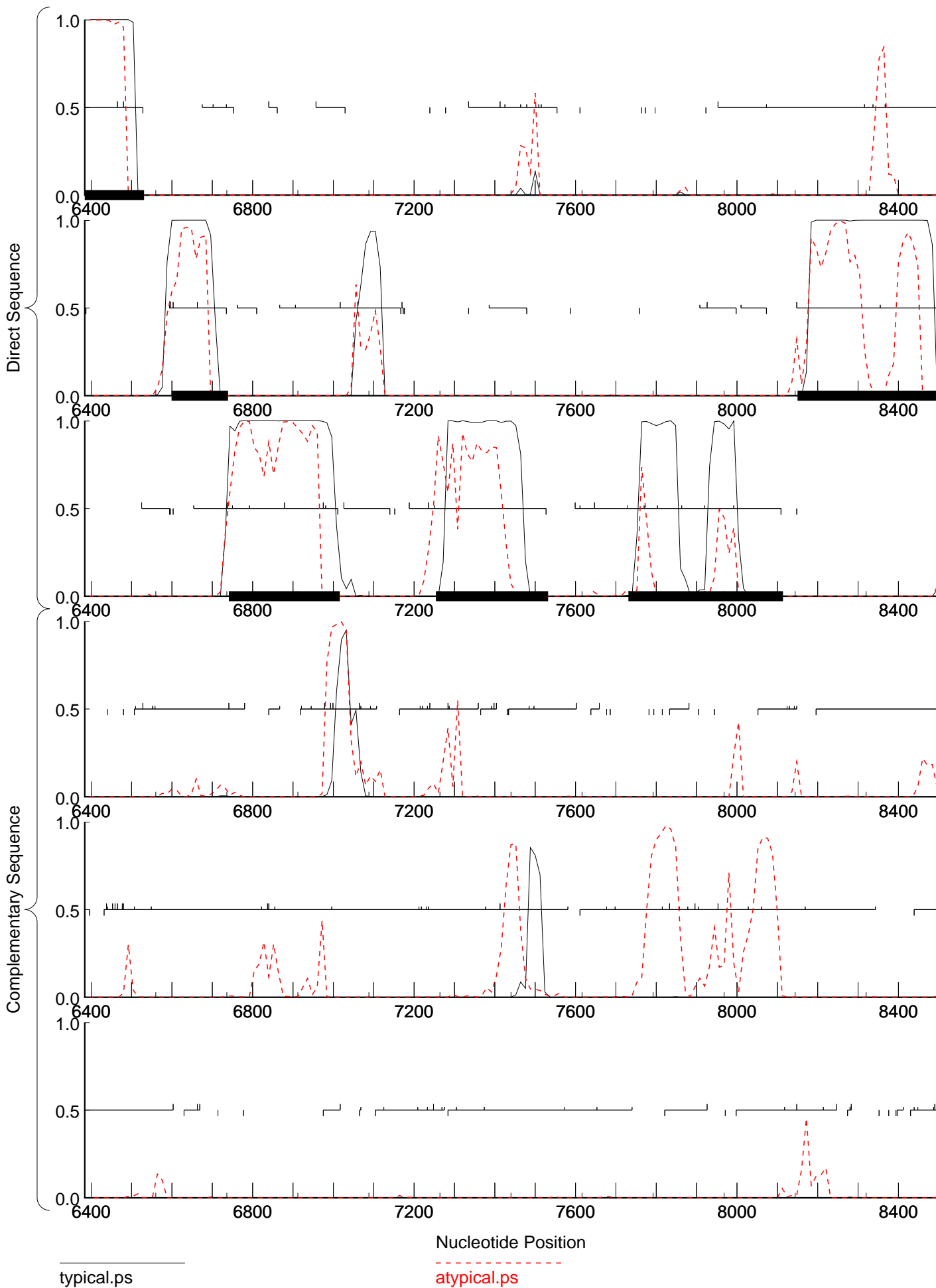
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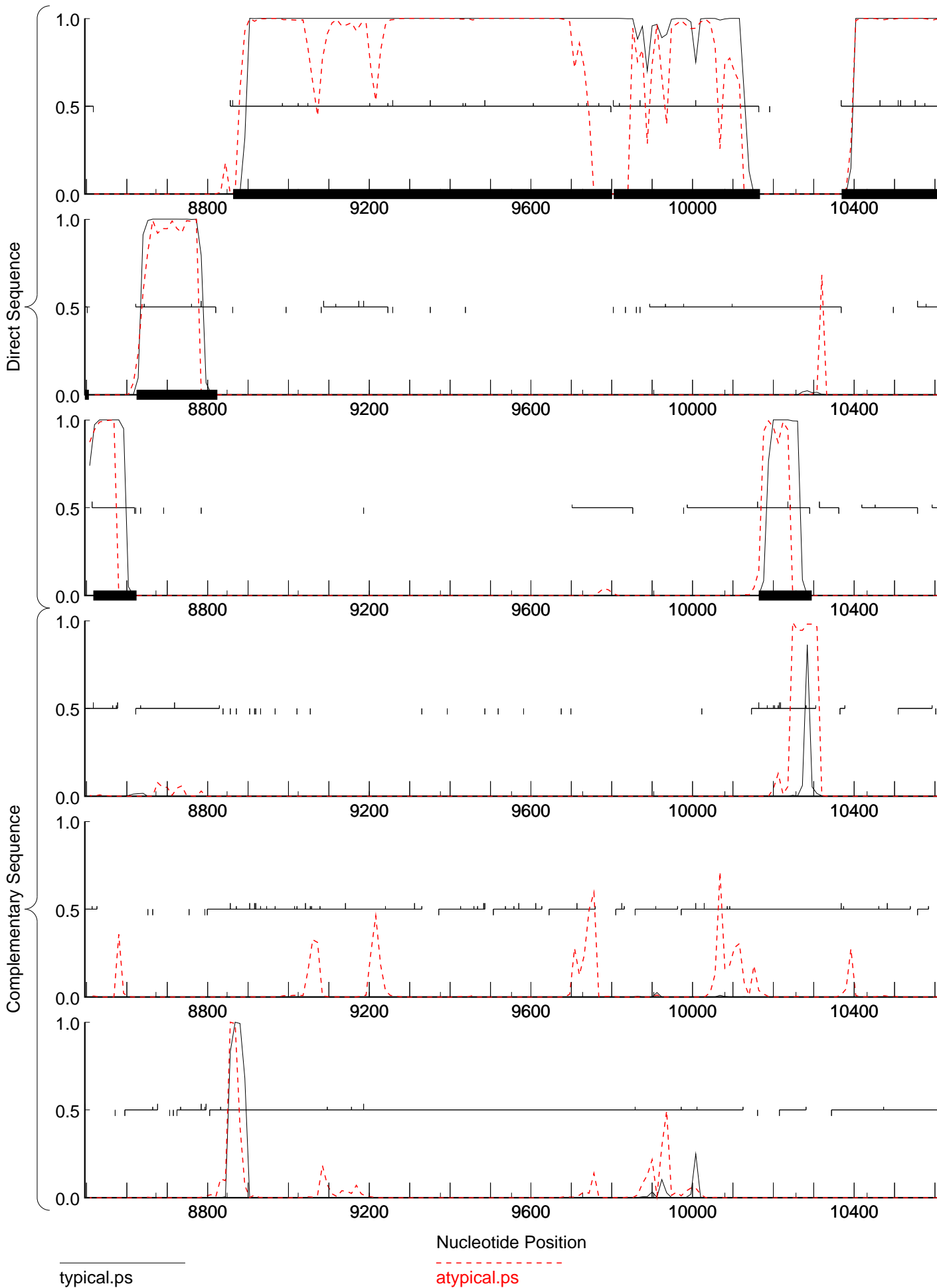
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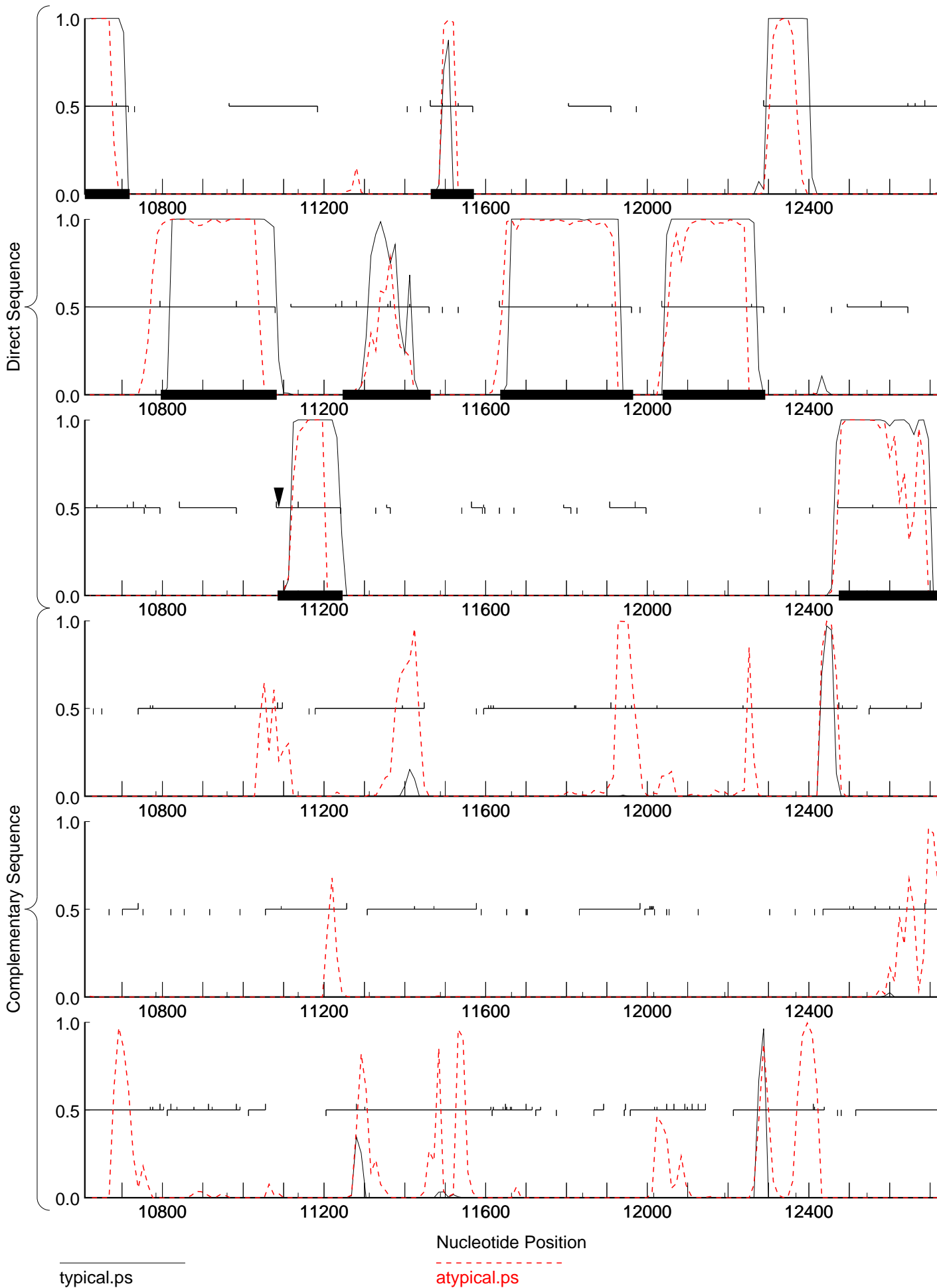


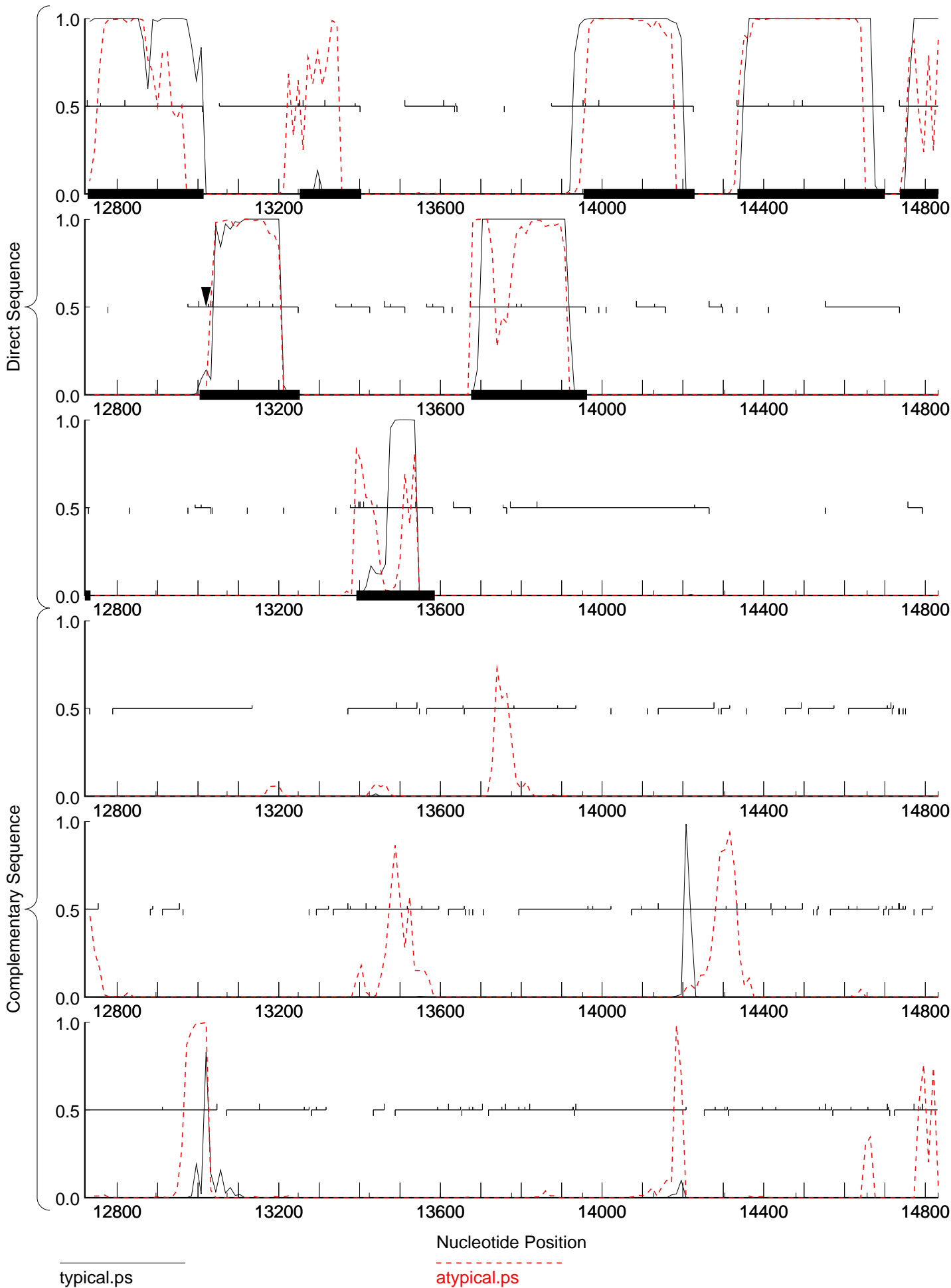
typical.ps

atypical.ps



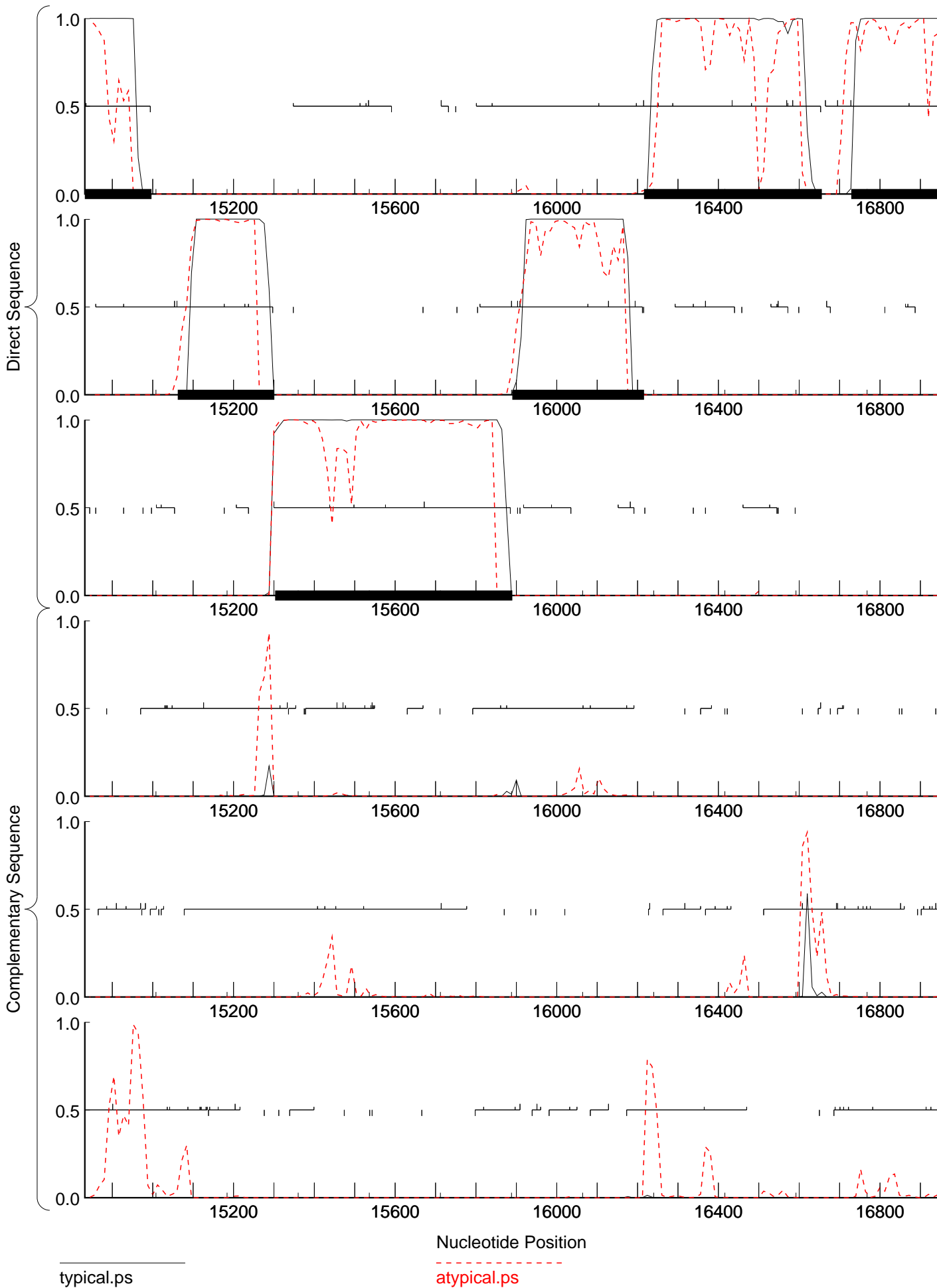




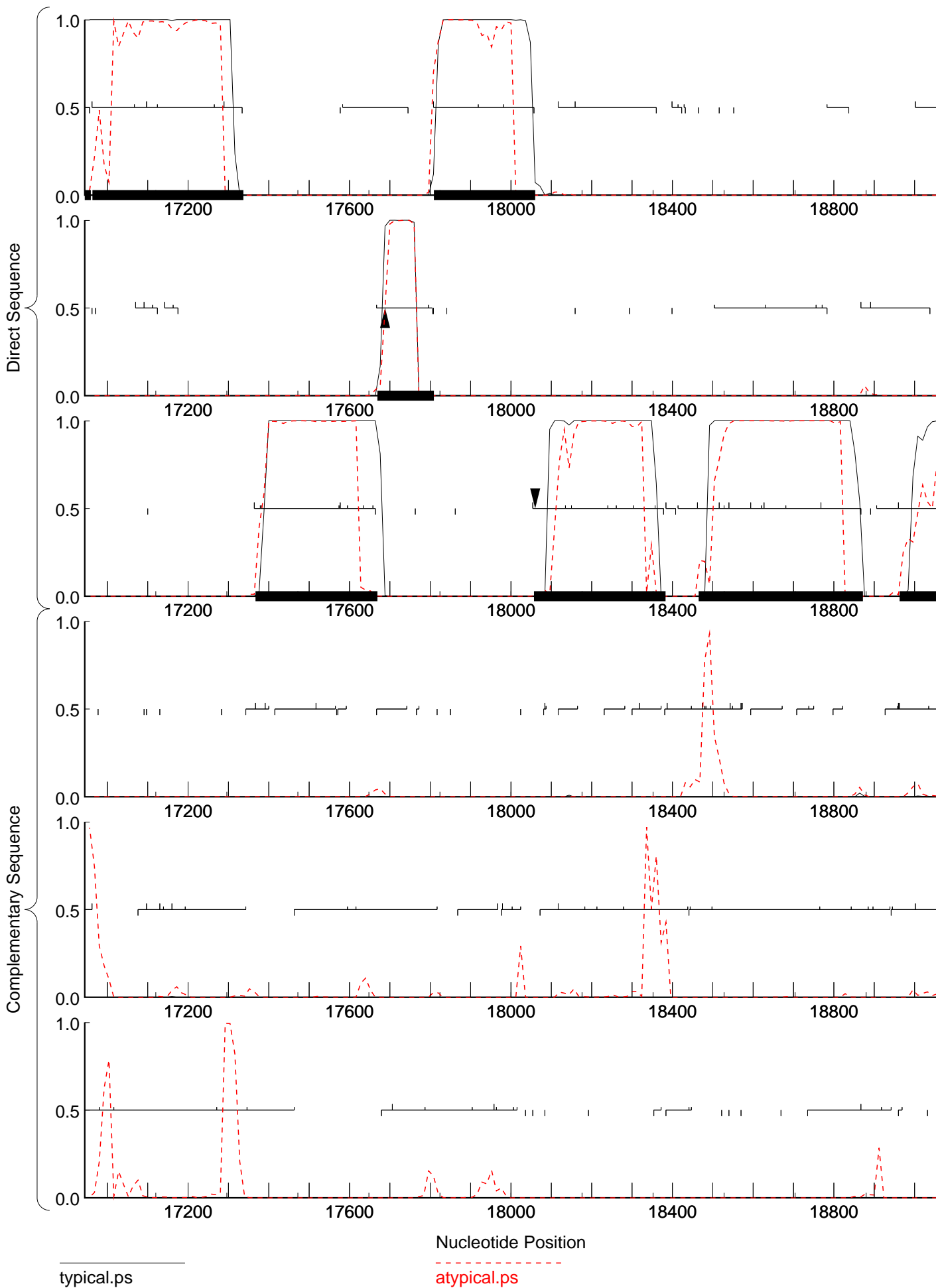


typical.ps

atypical.ps

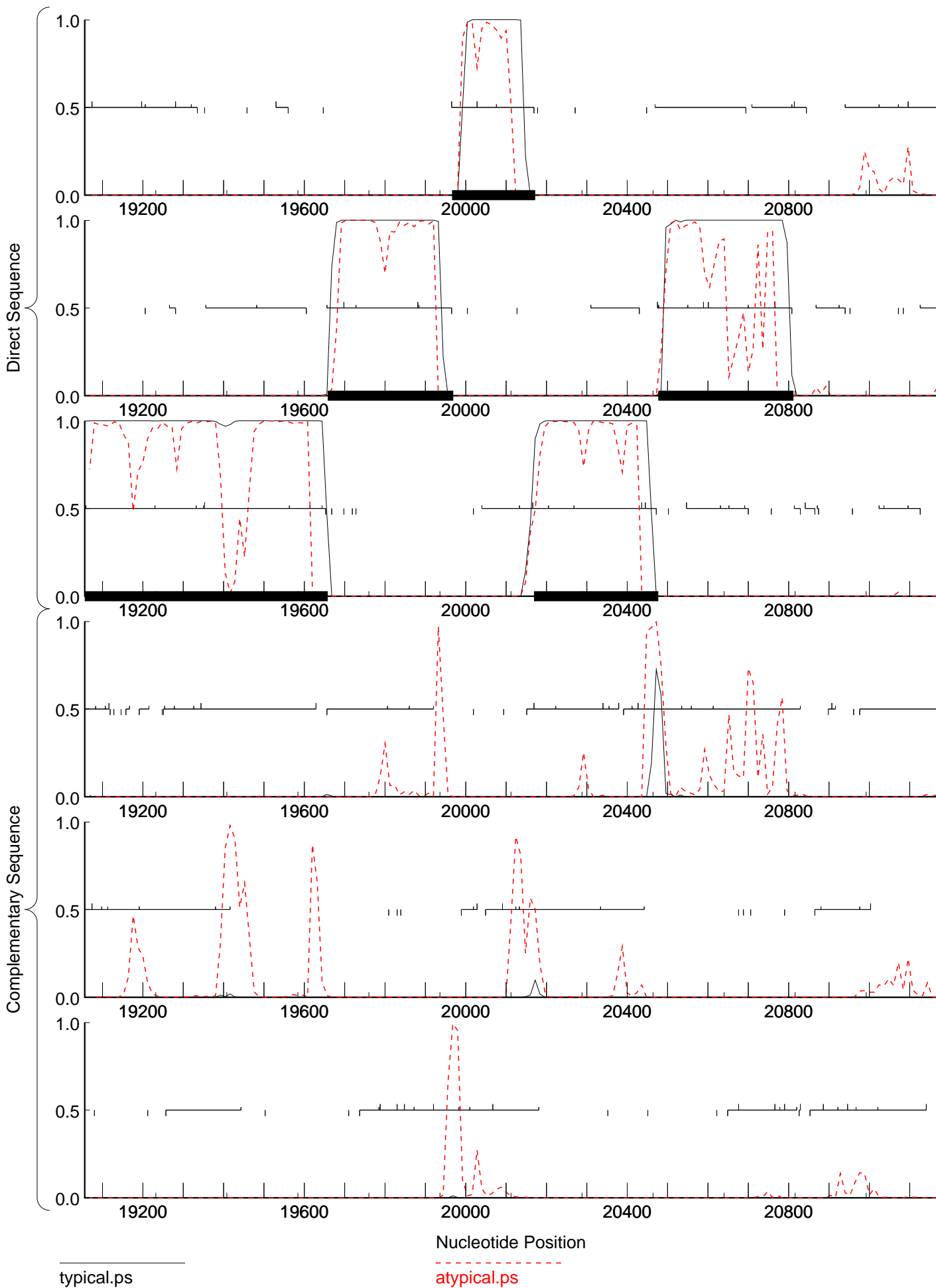


GeneMark.hmm prediction

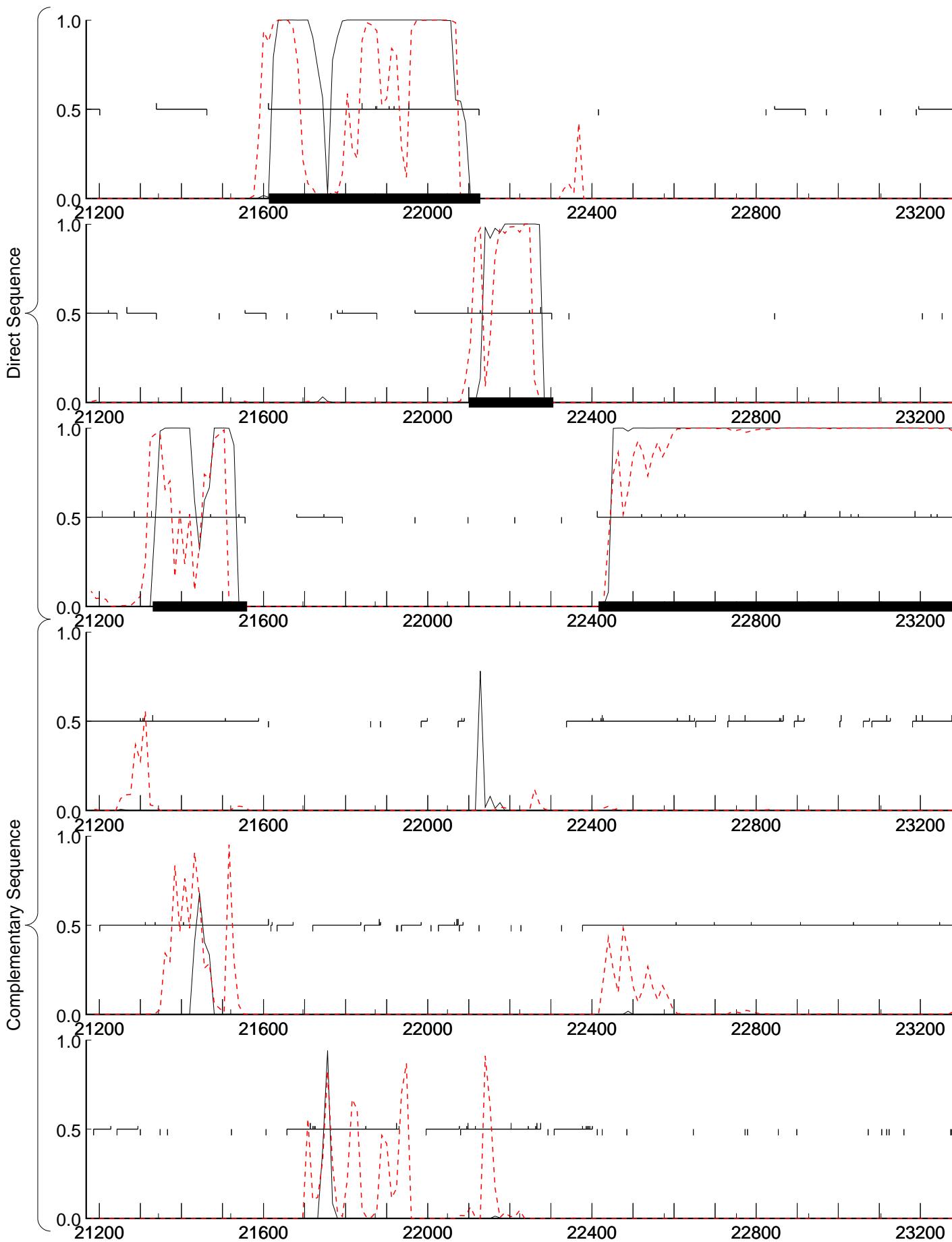


typical.ps

atypical.ps

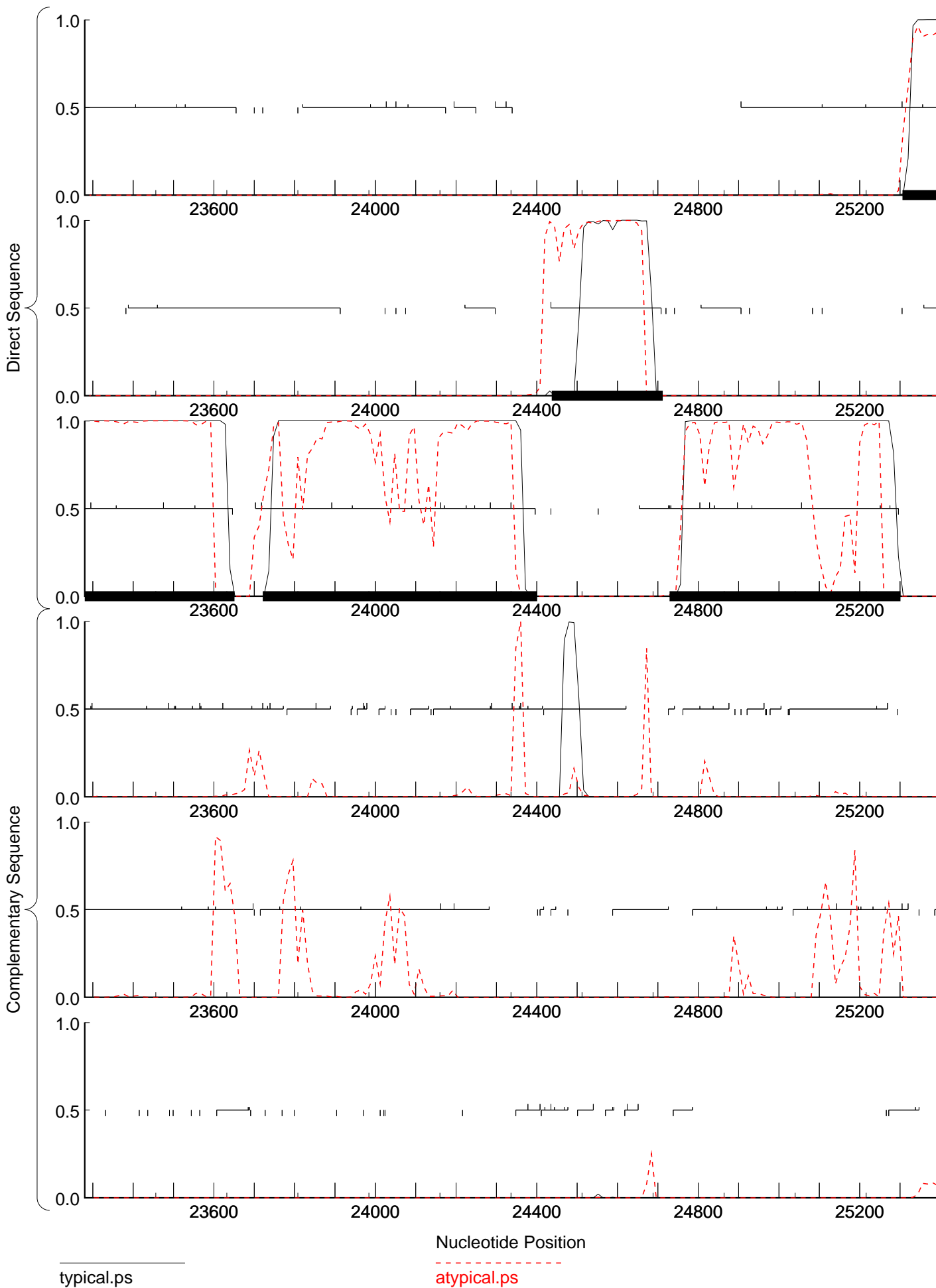


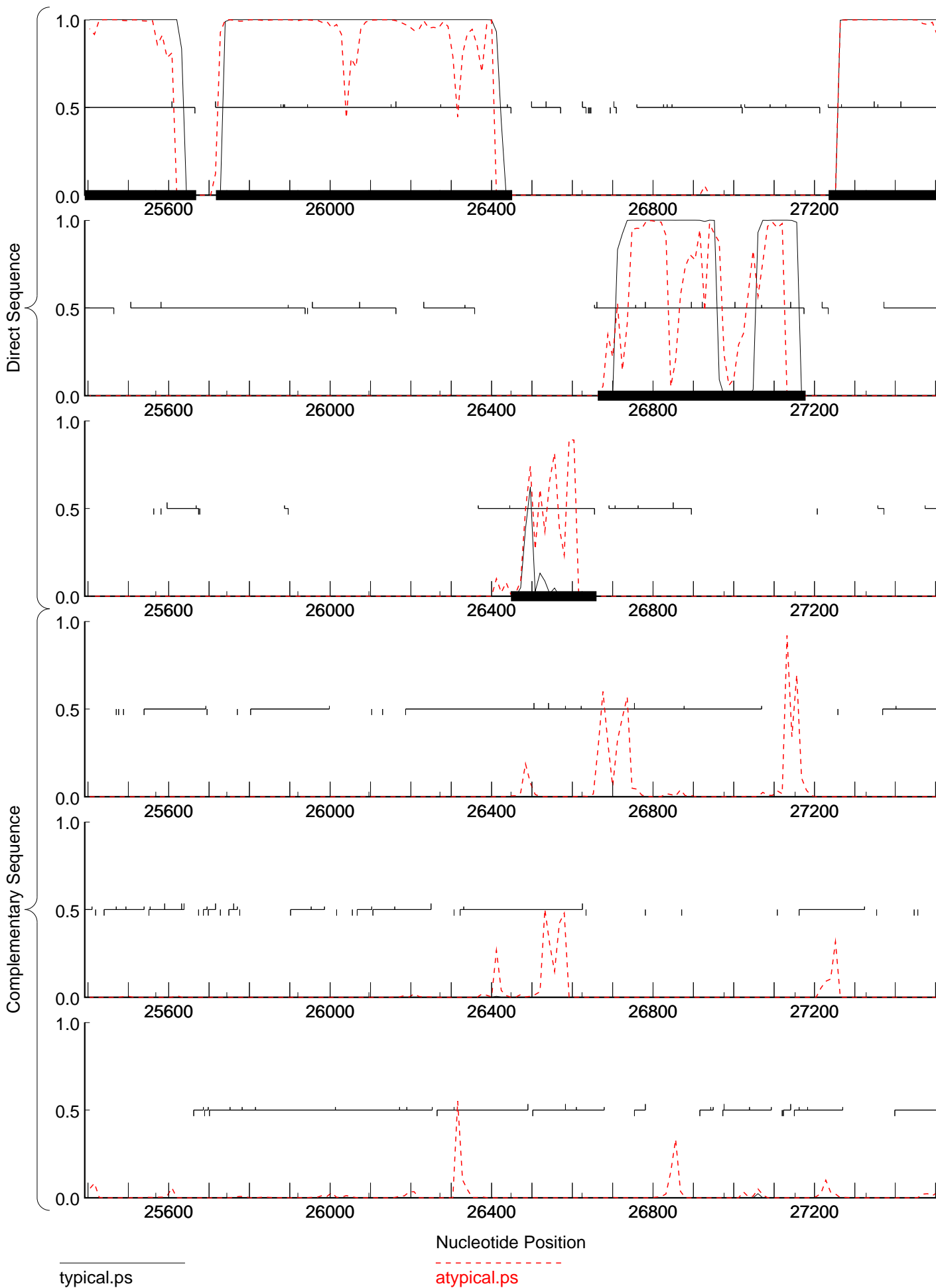
GeneMark.hmm prediction

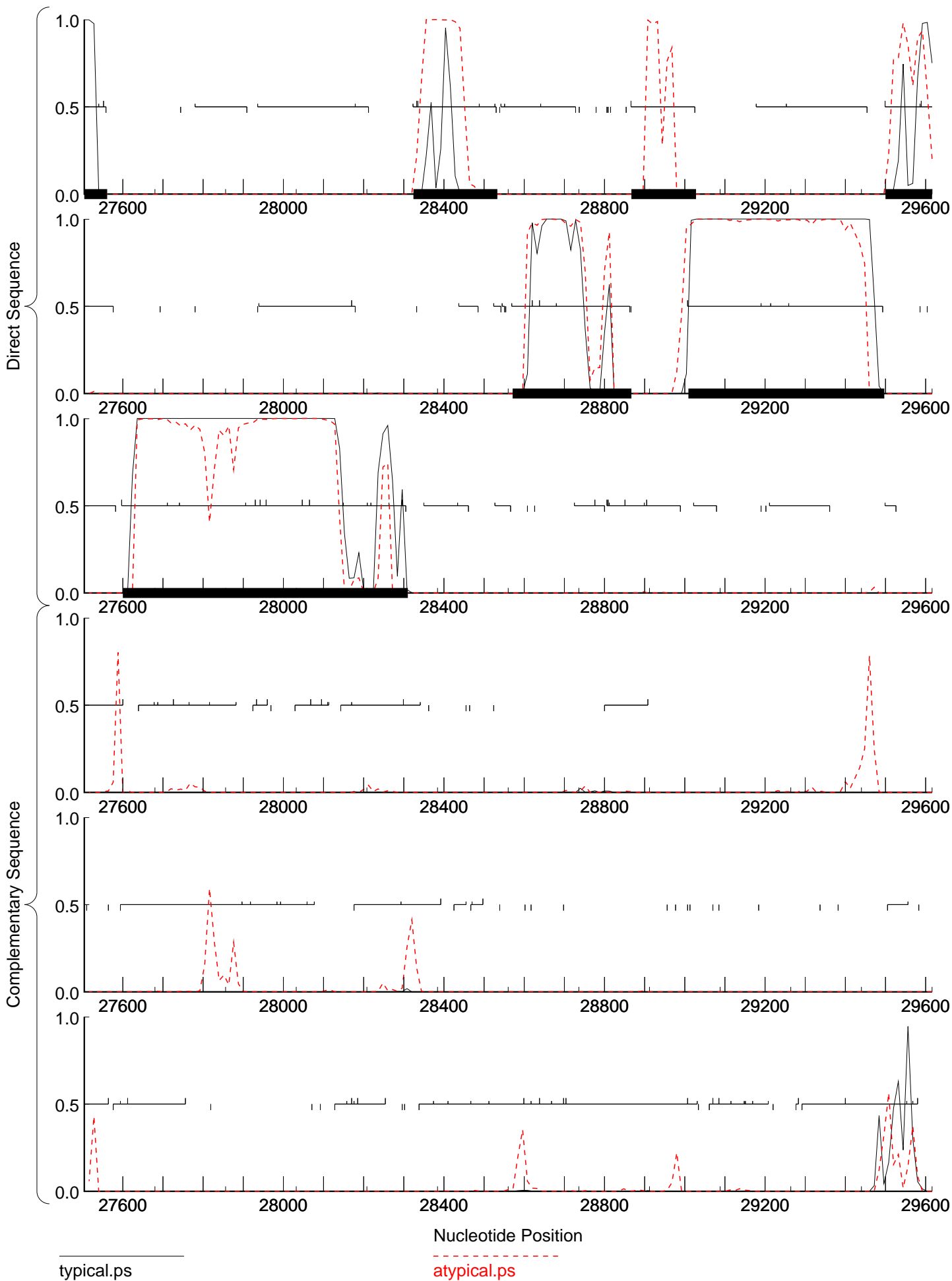


typical.ps

atypical.ps

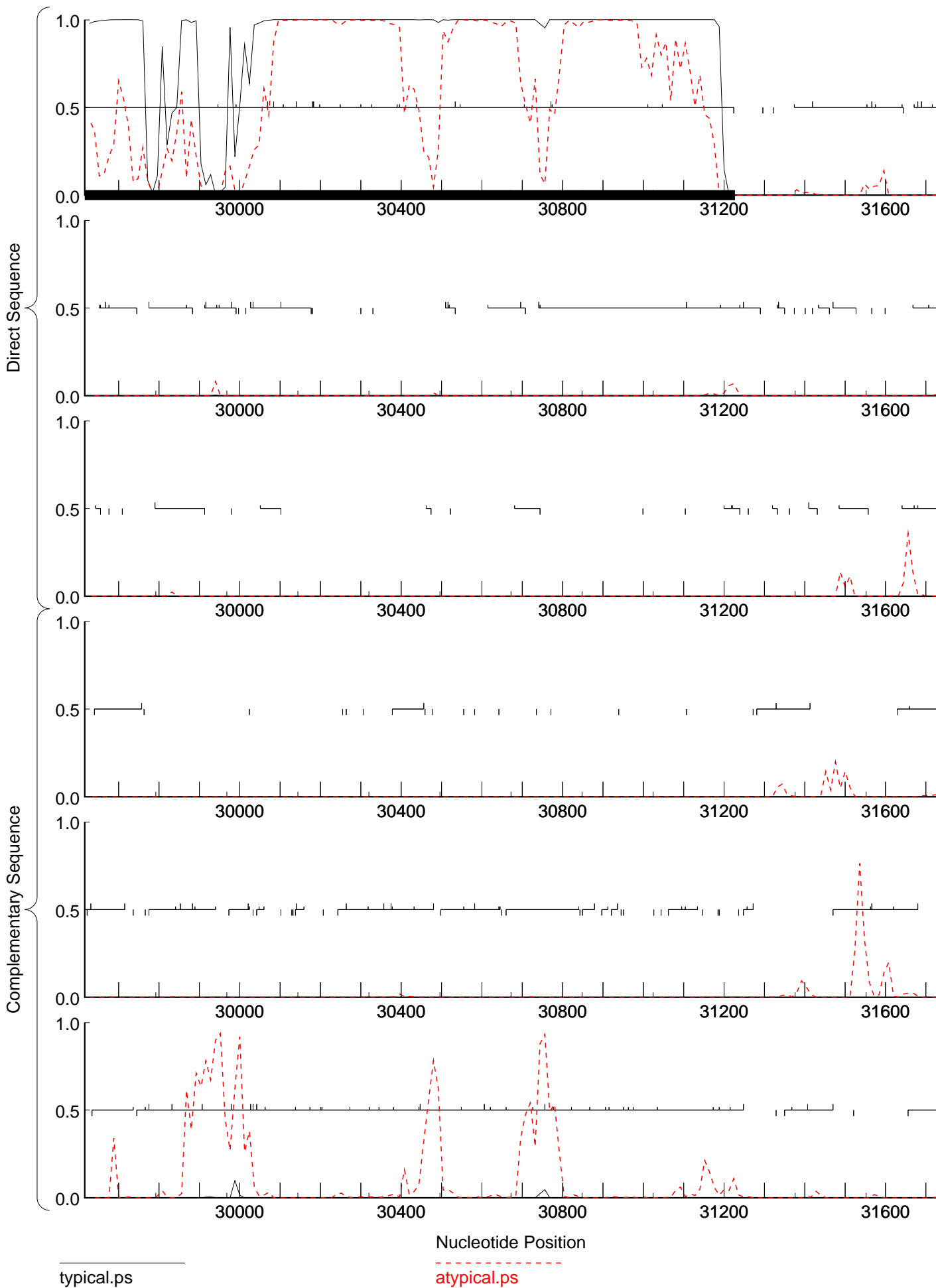


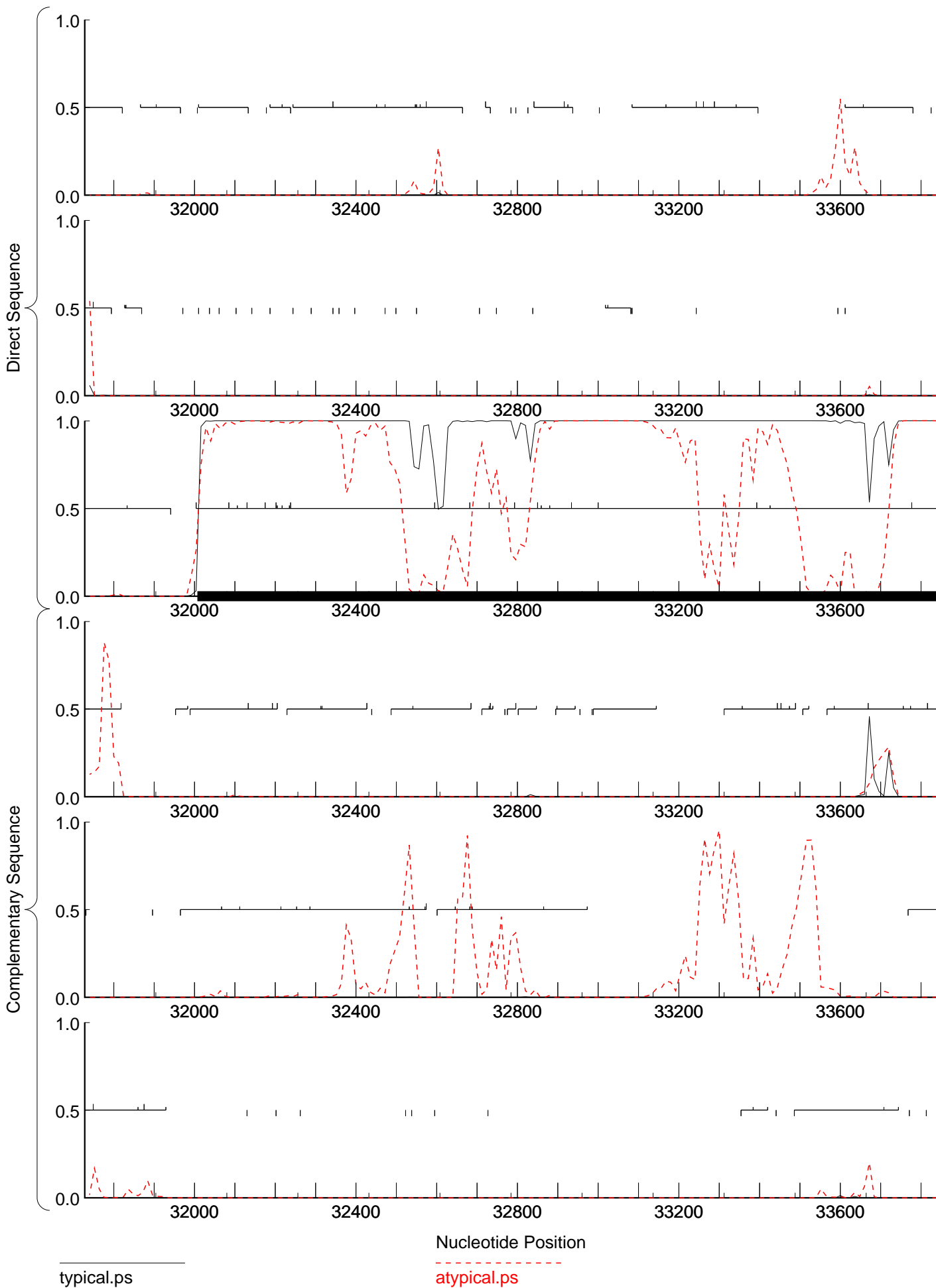


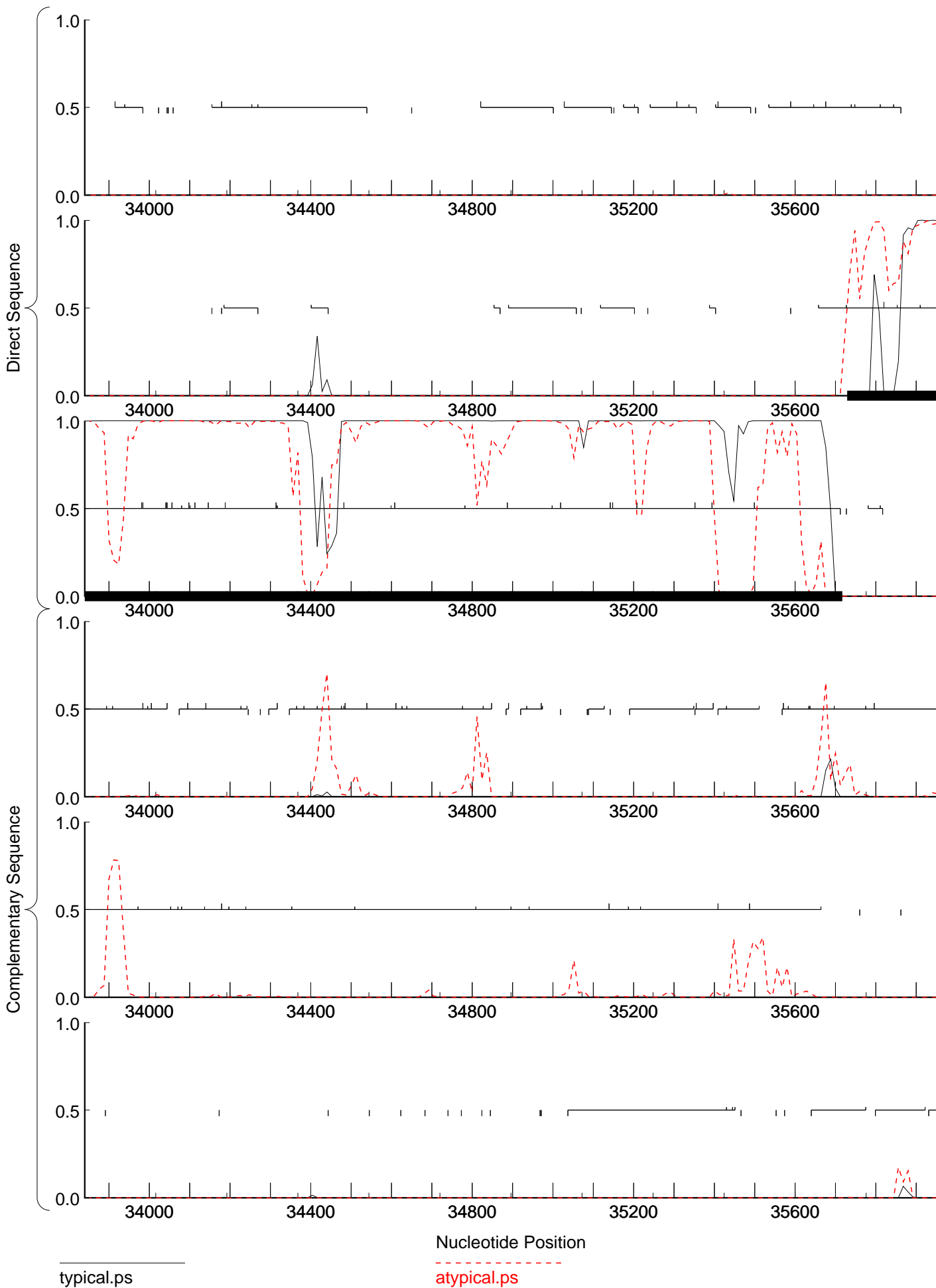


typical.ps

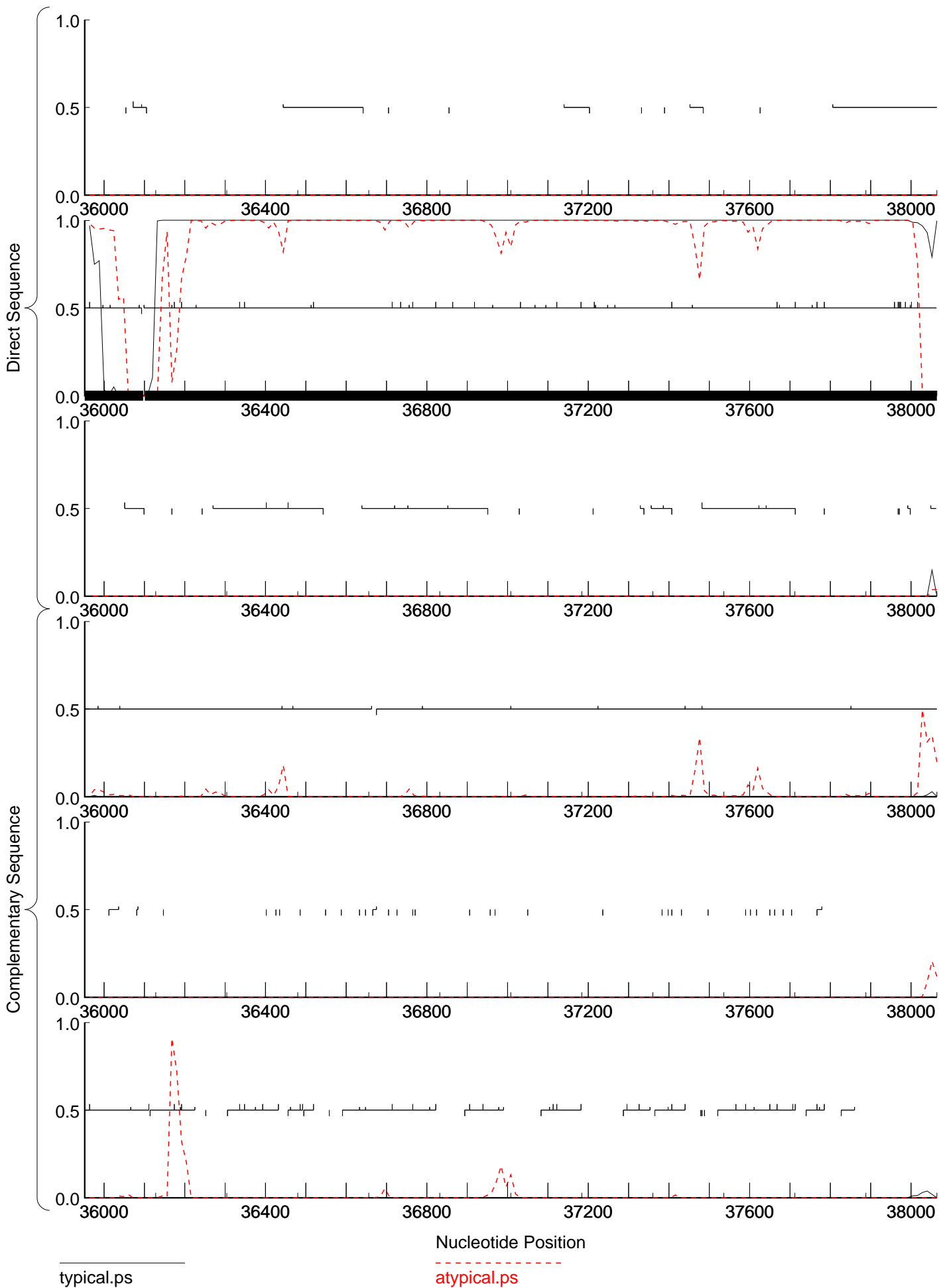
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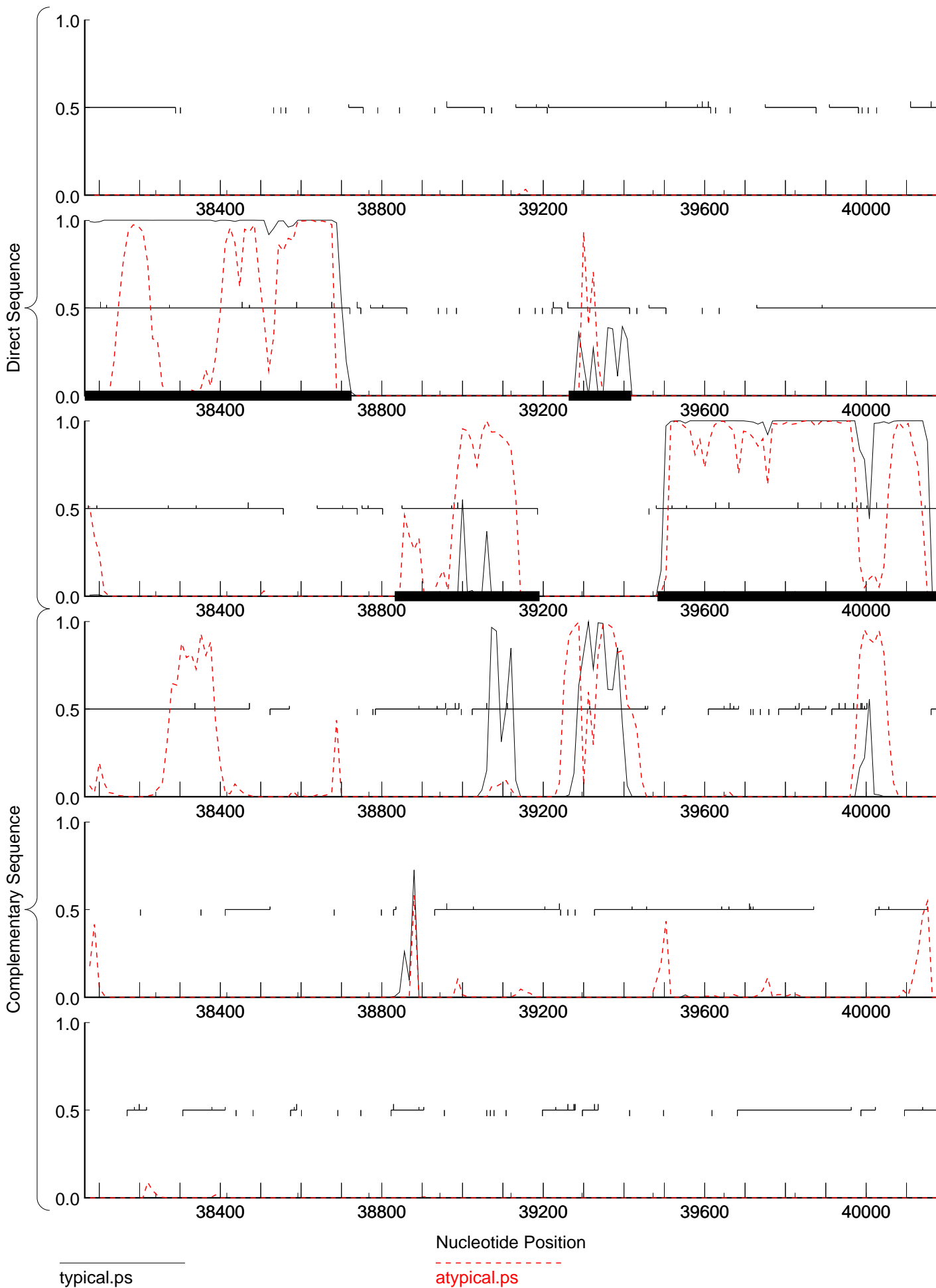




GeneMark.hmm prediction

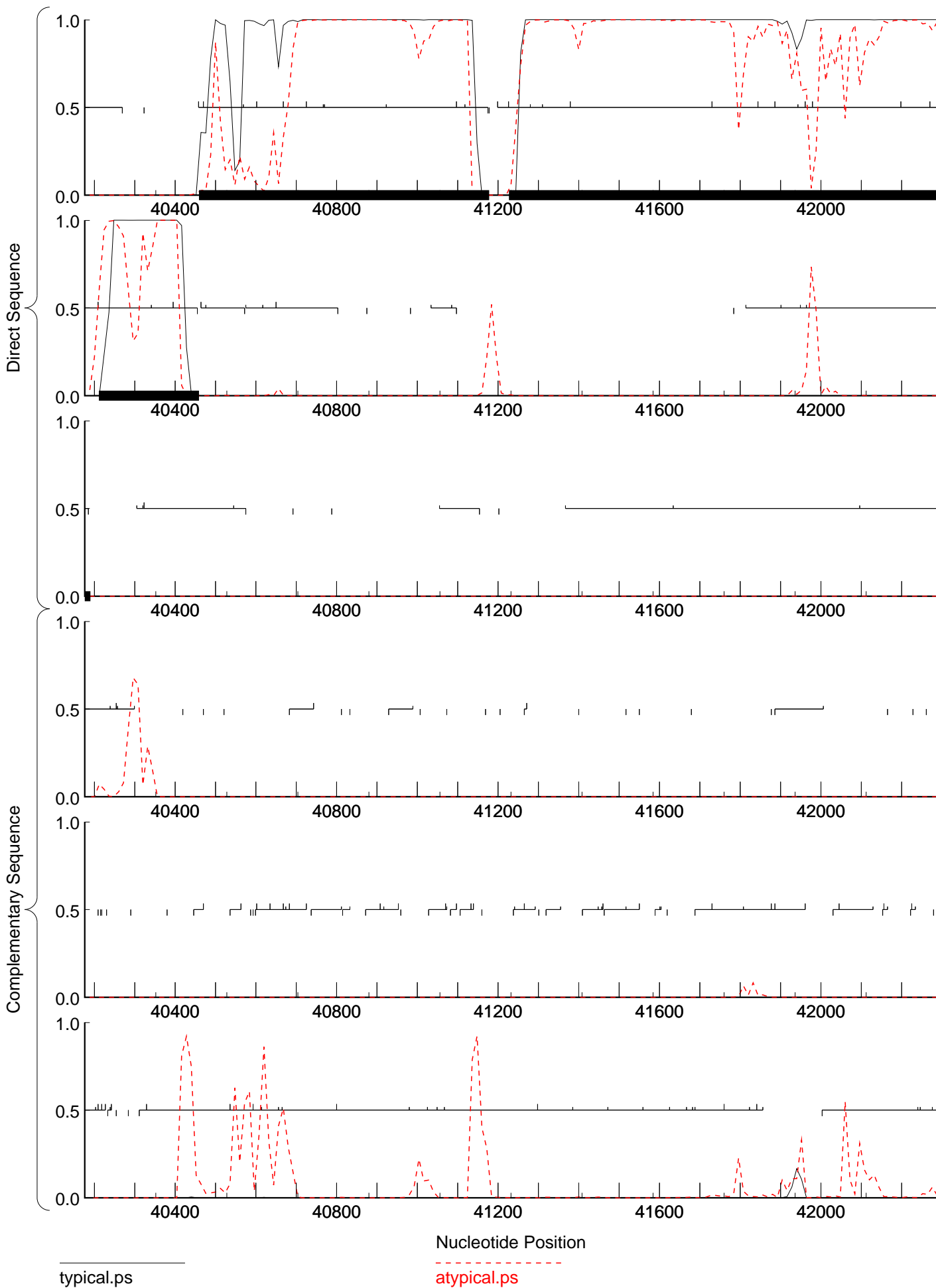


GeneMark.hmm prediction

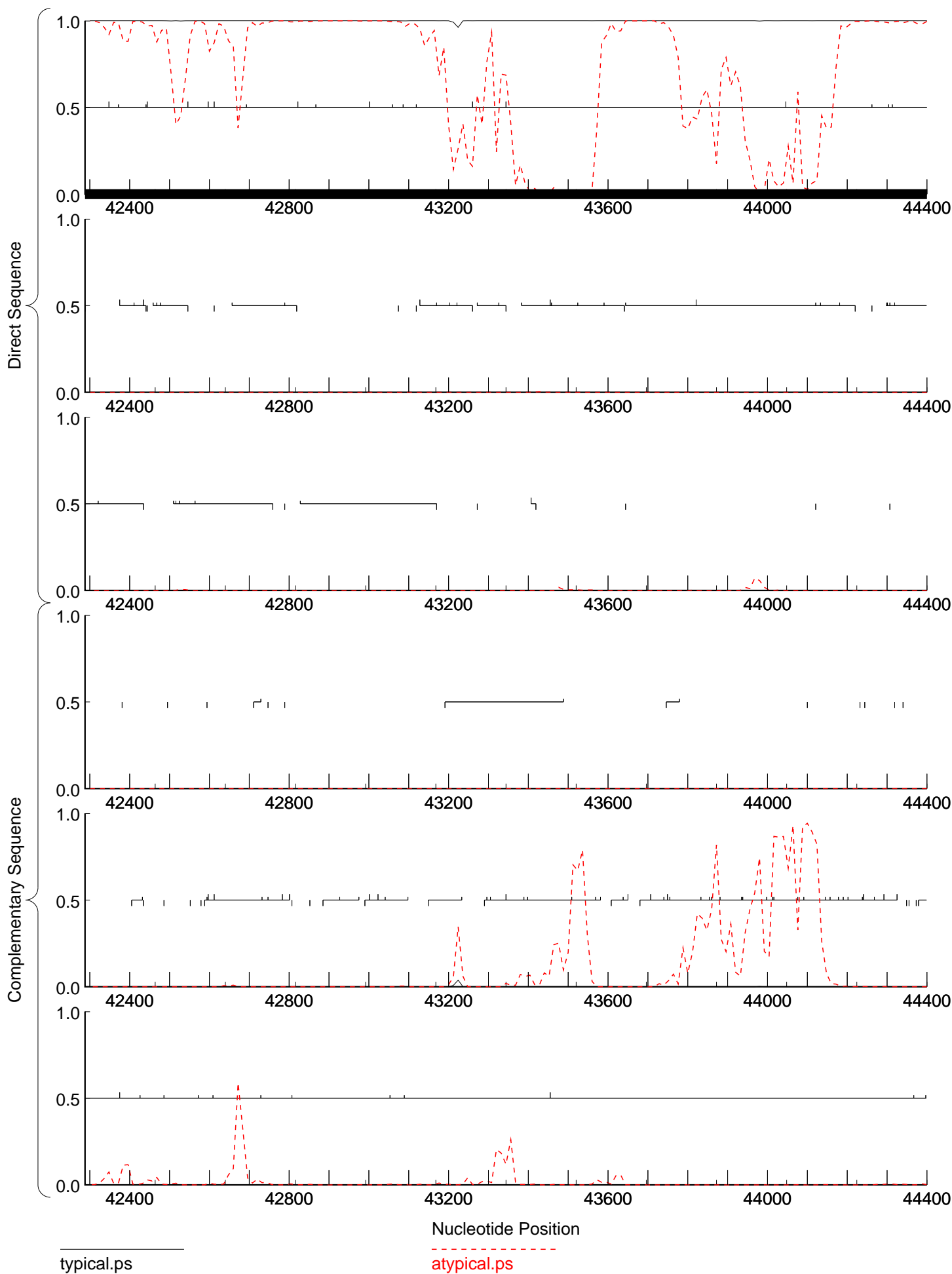


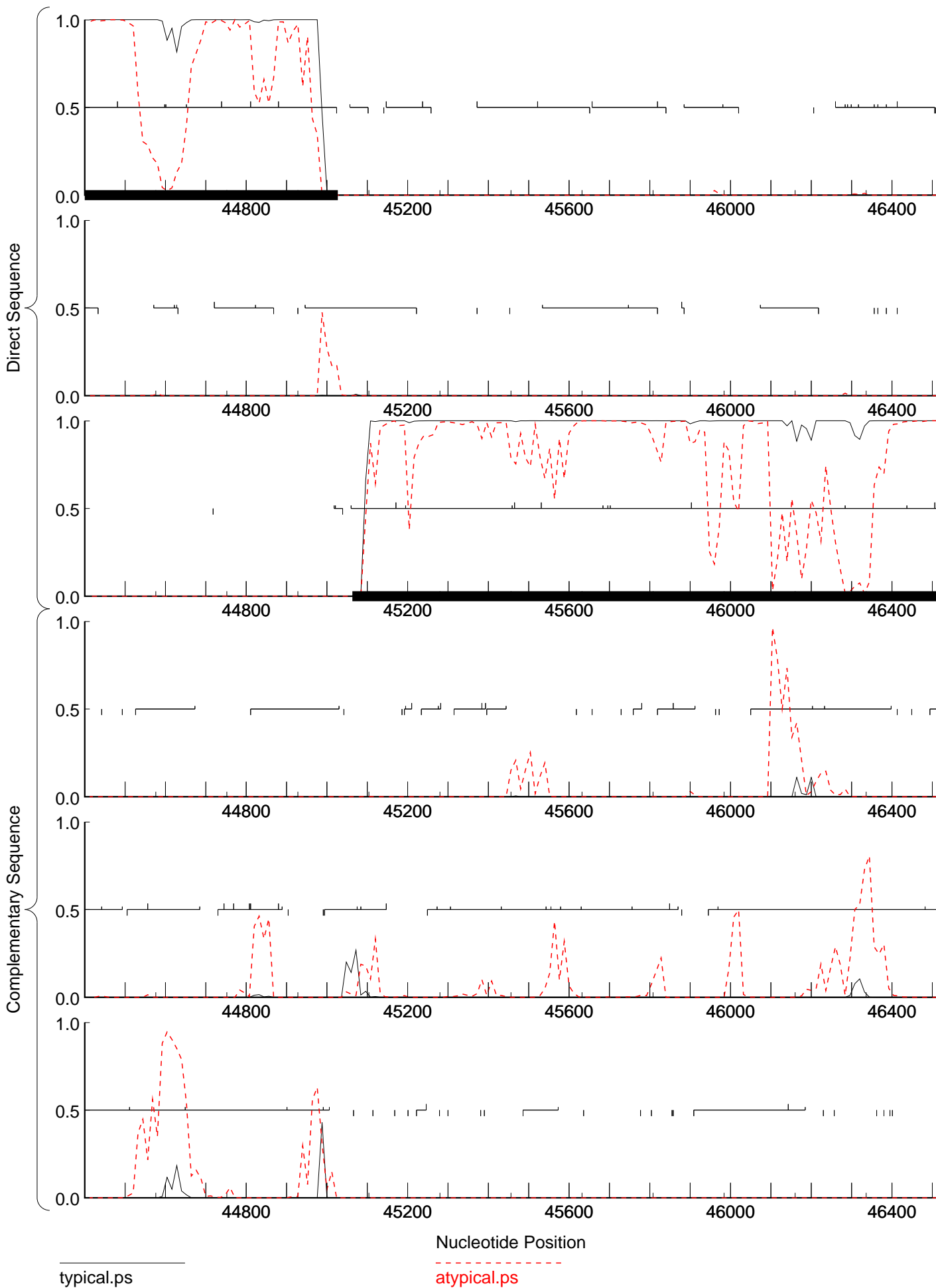
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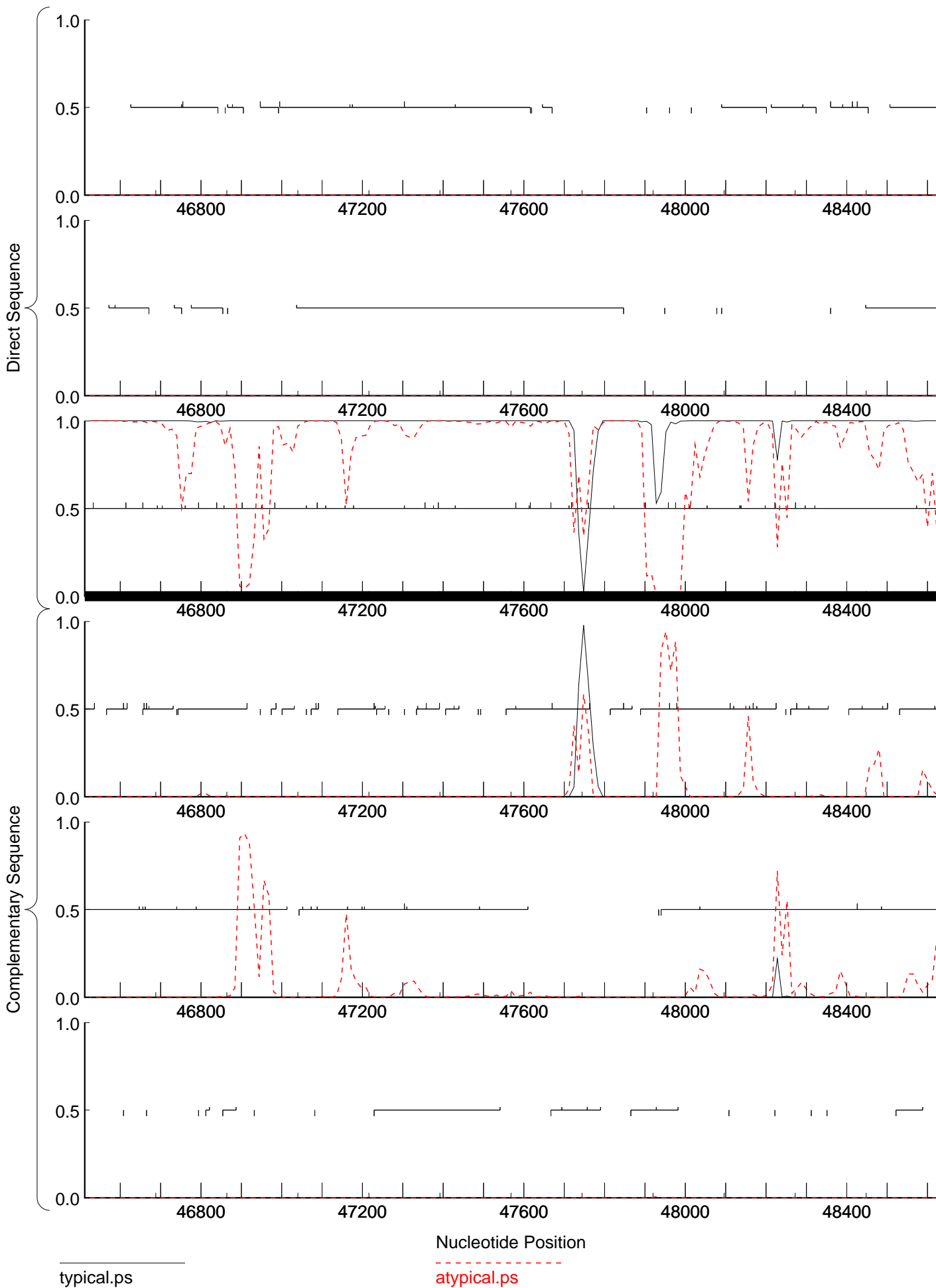
atypical.ps



GeneMark.hmm prediction

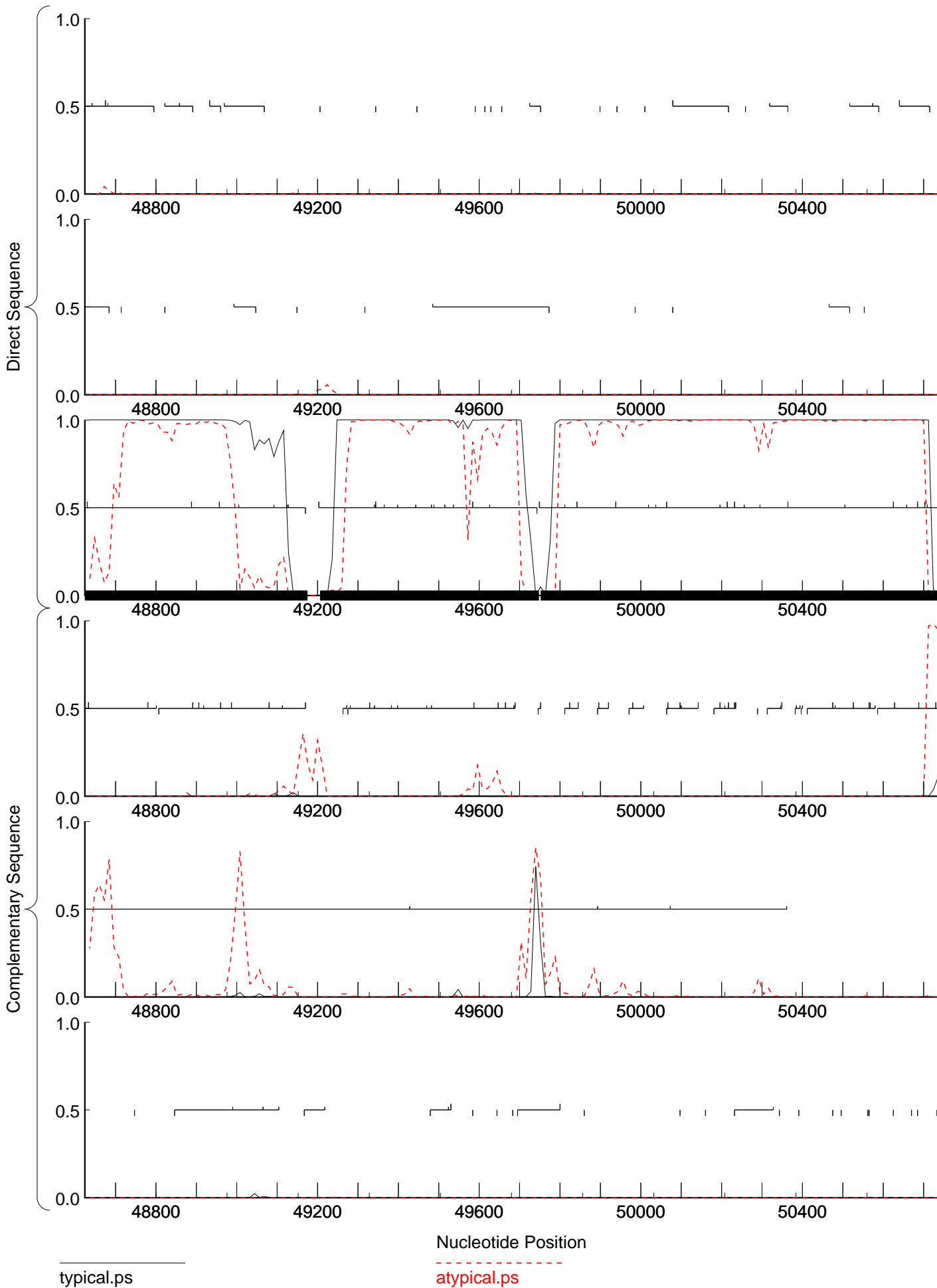




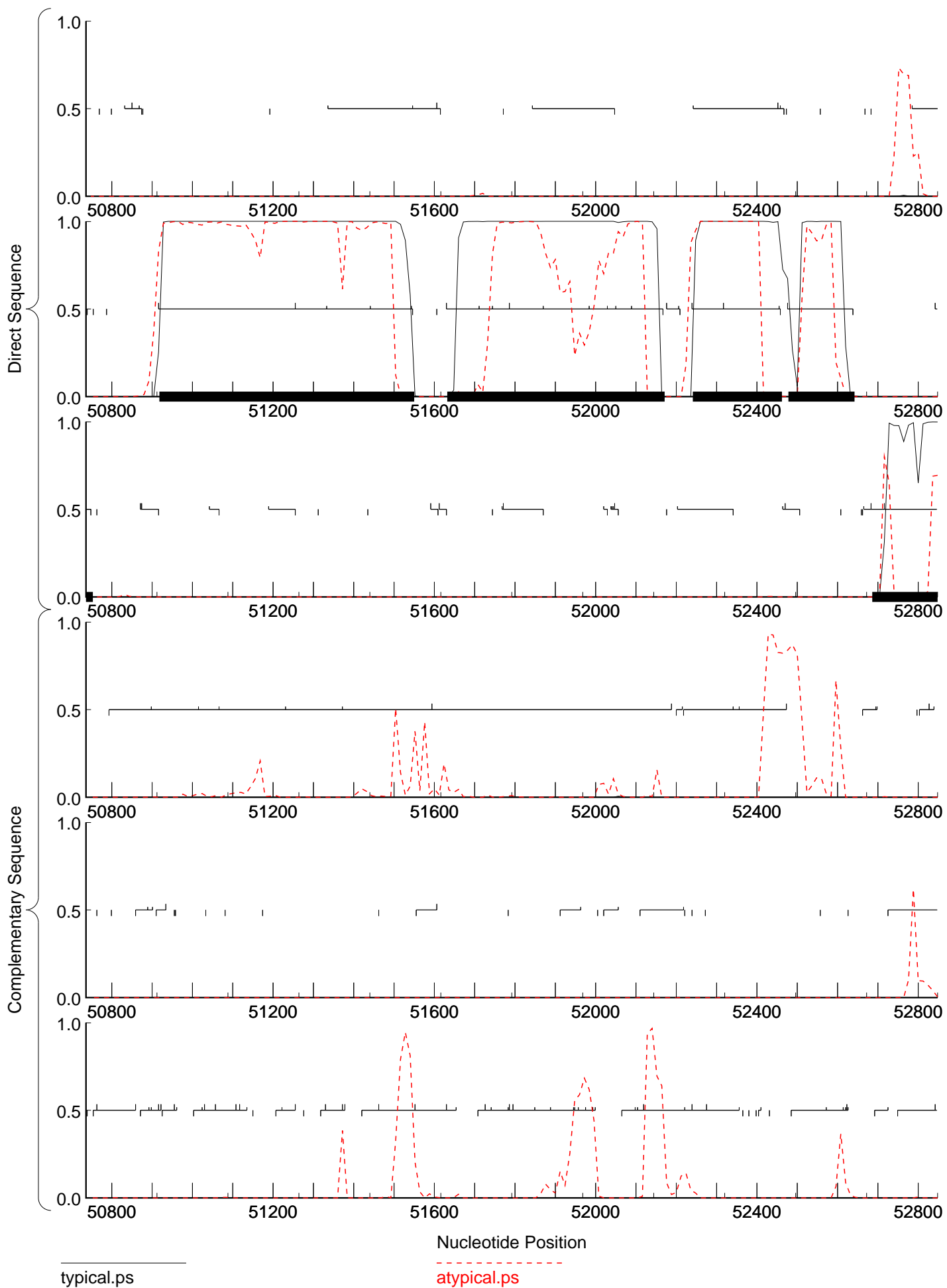


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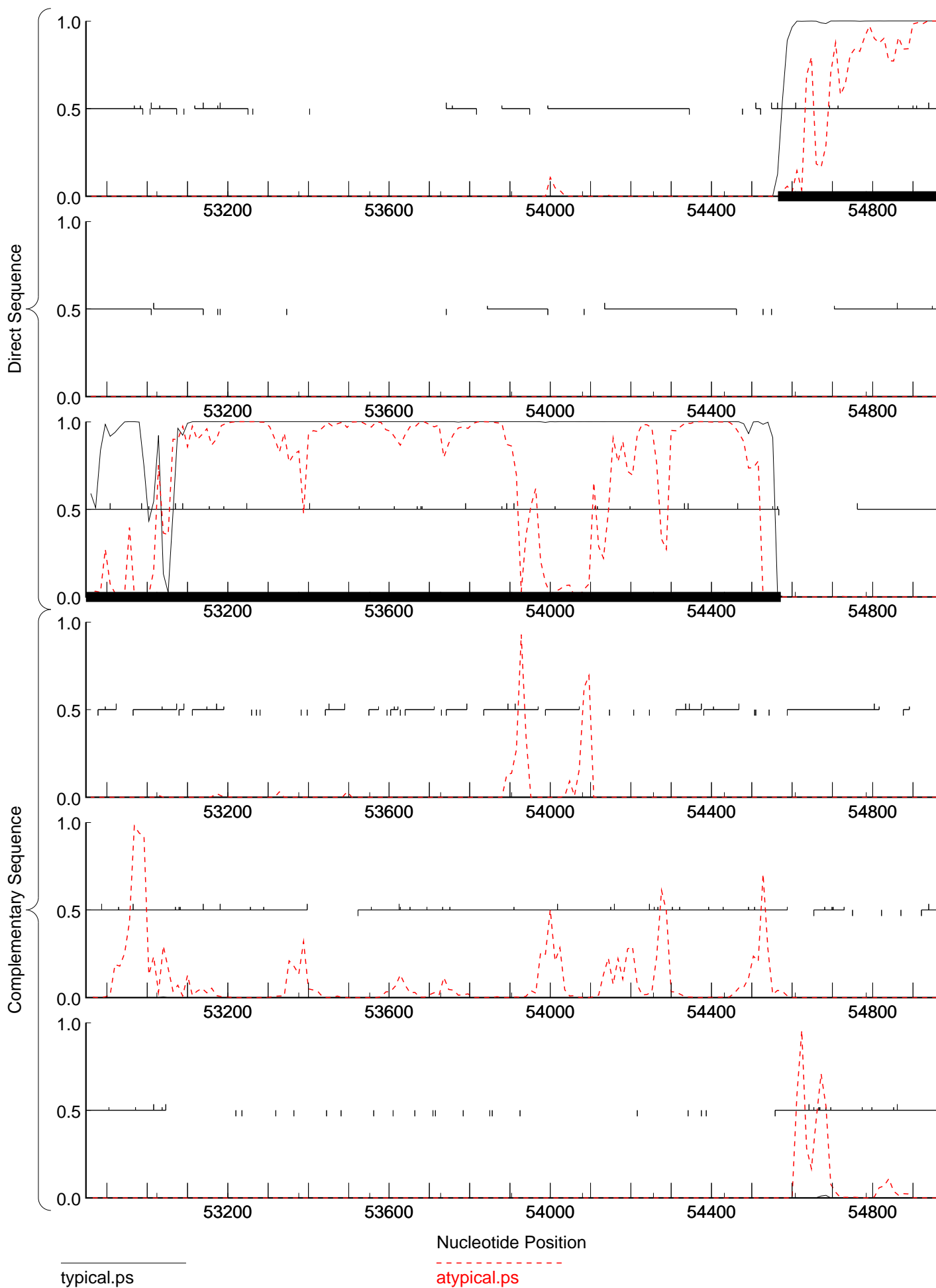
atypical.ps



GeneMark.hmm prediction

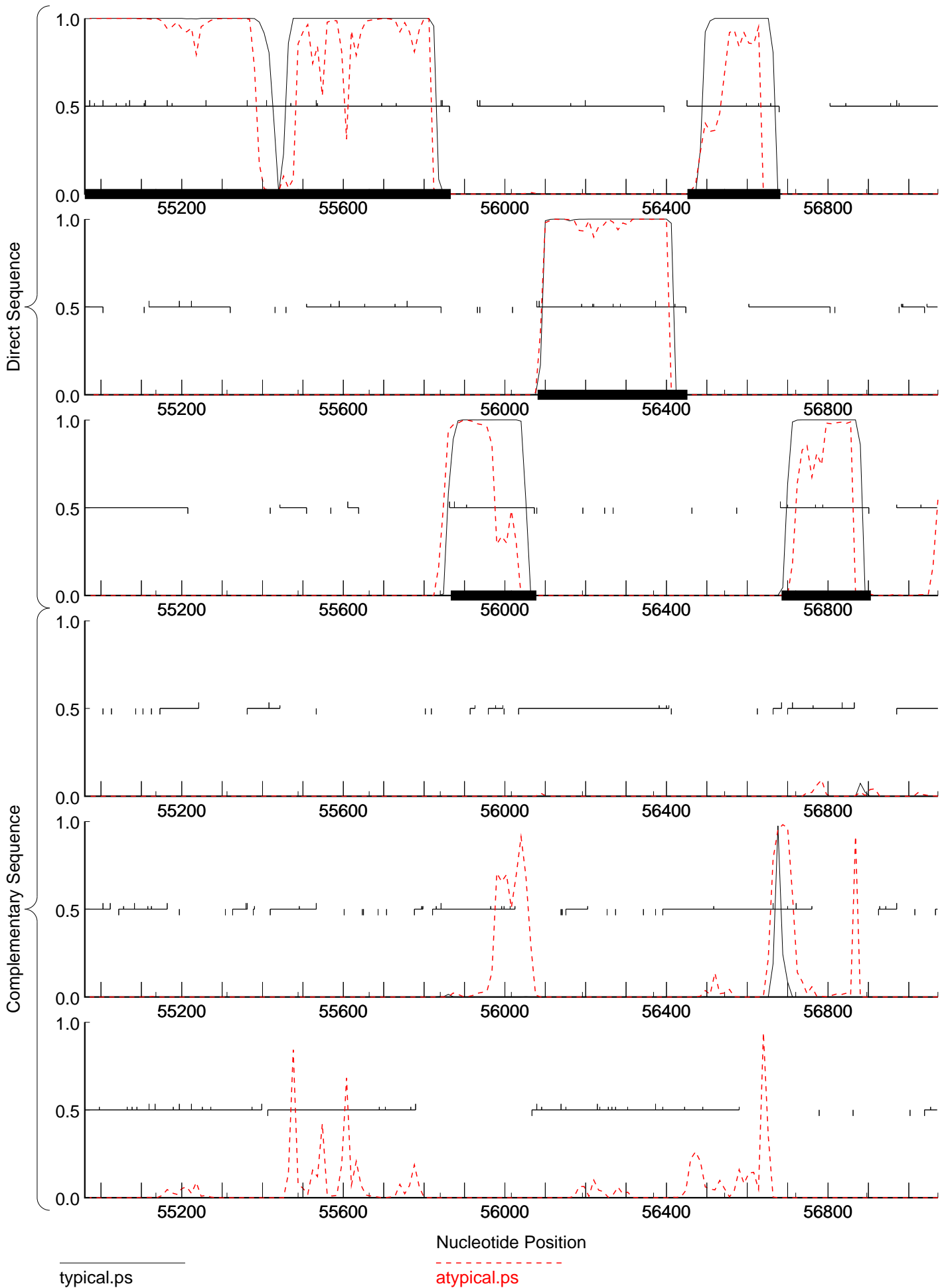


GeneMark.hmm prediction

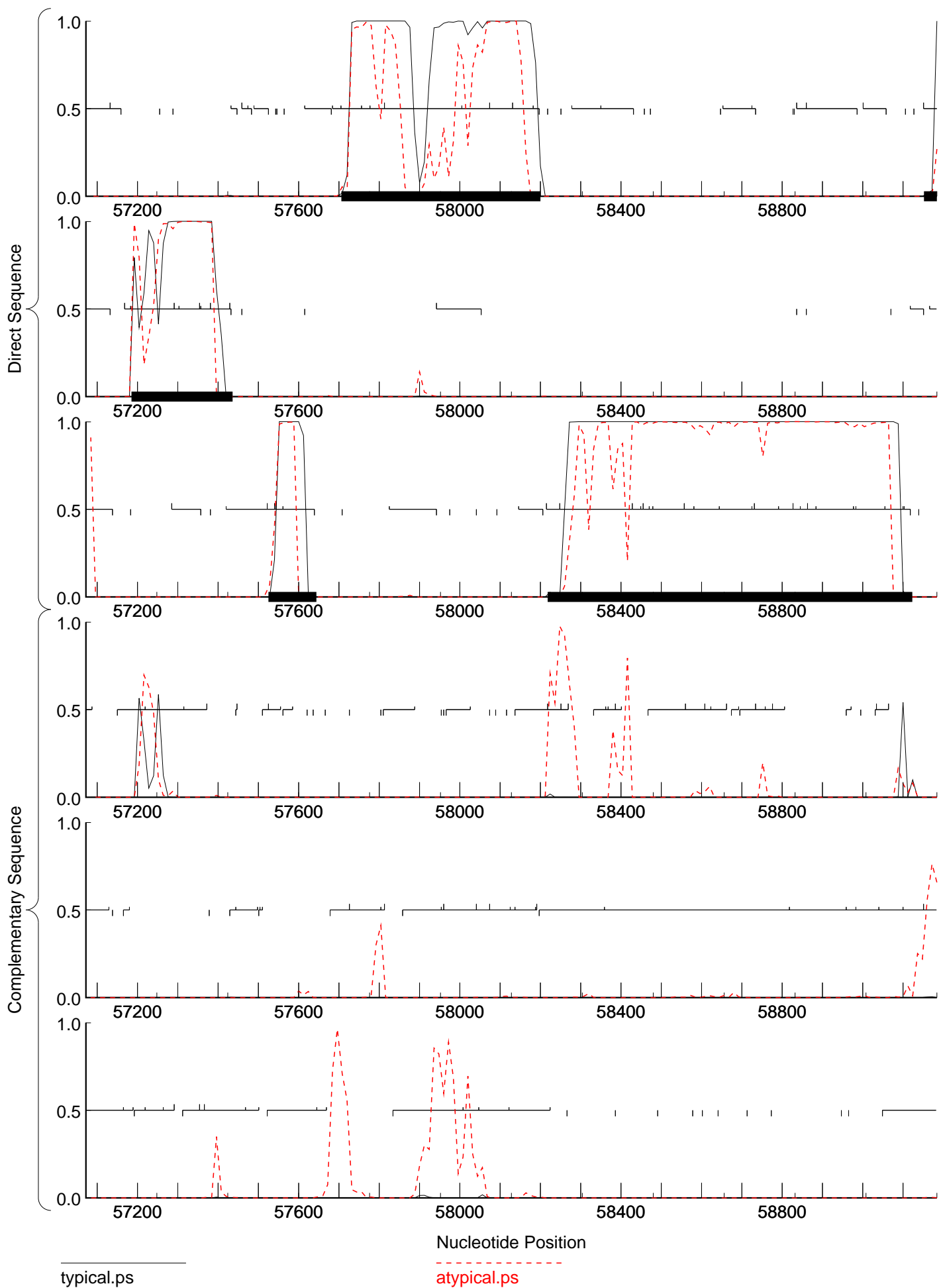


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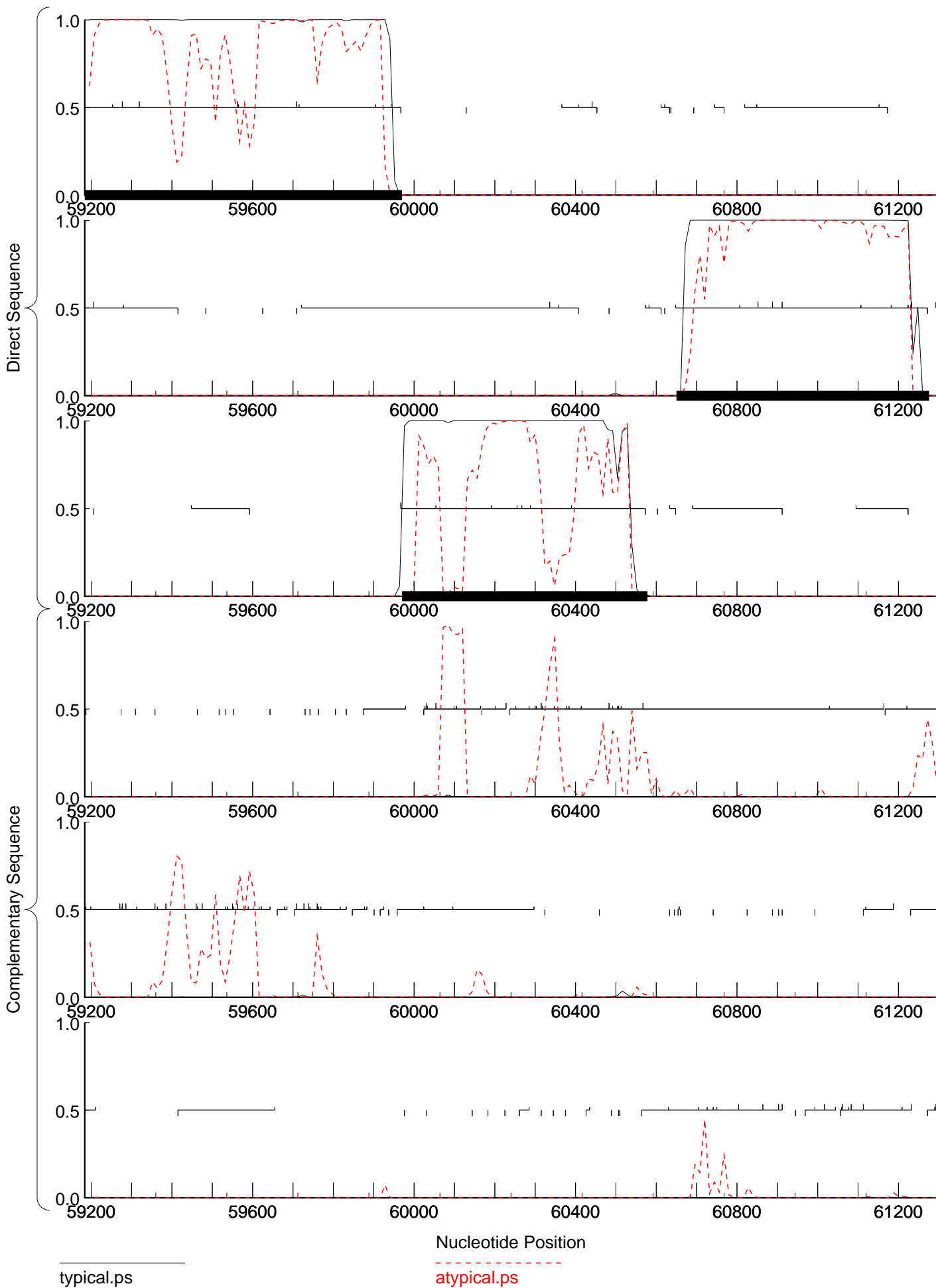
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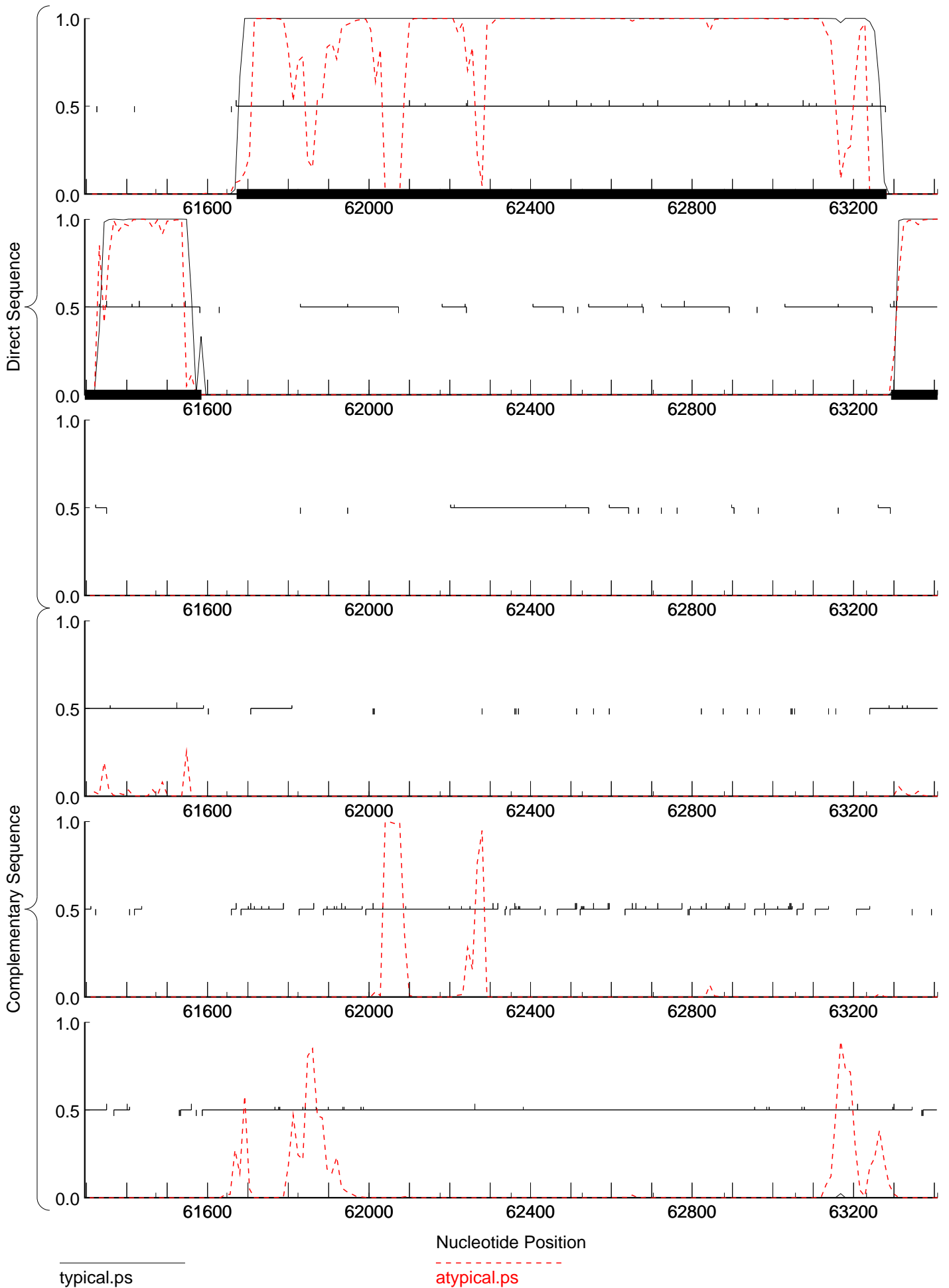


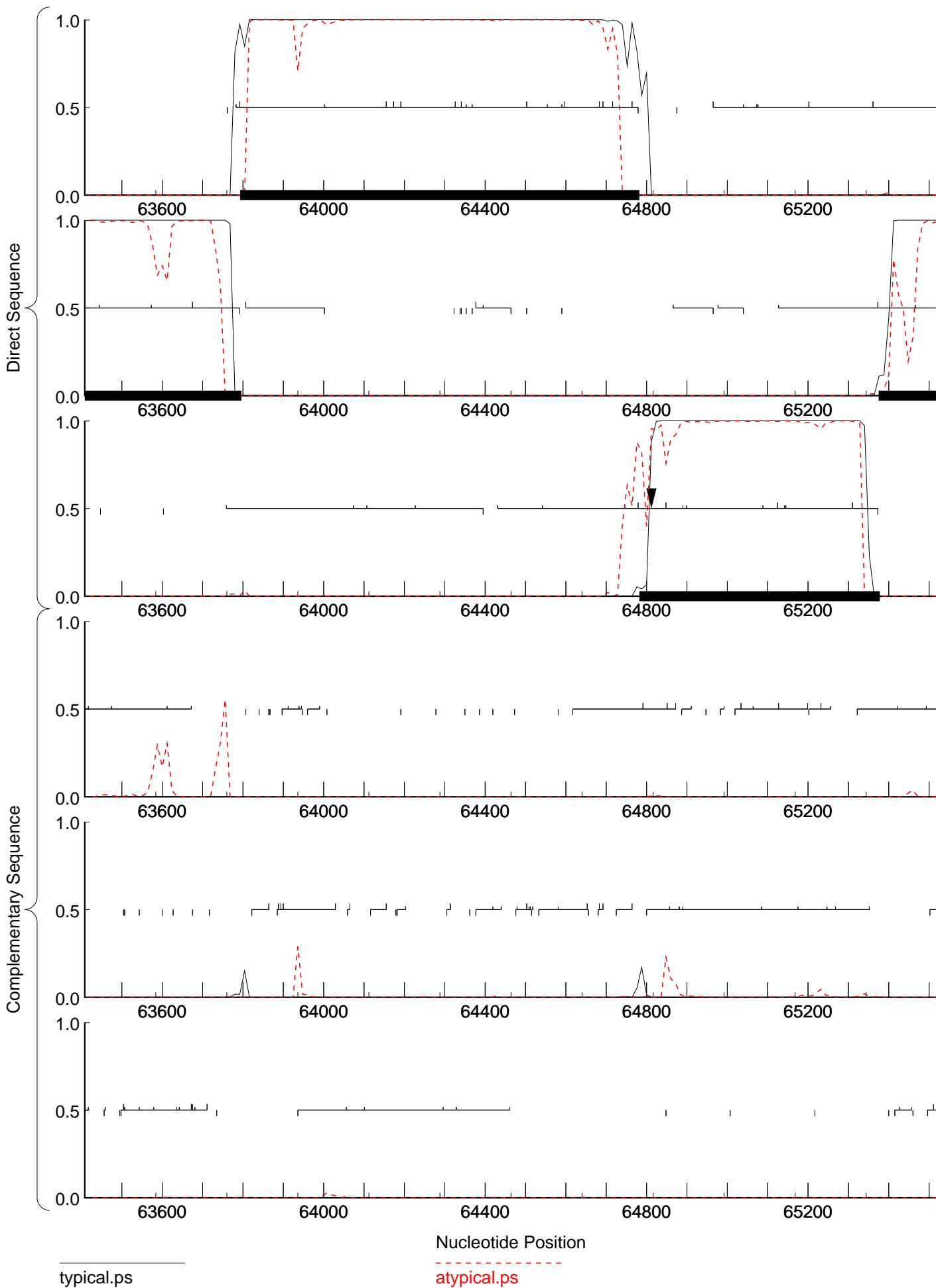
GeneMark.hmm prediction



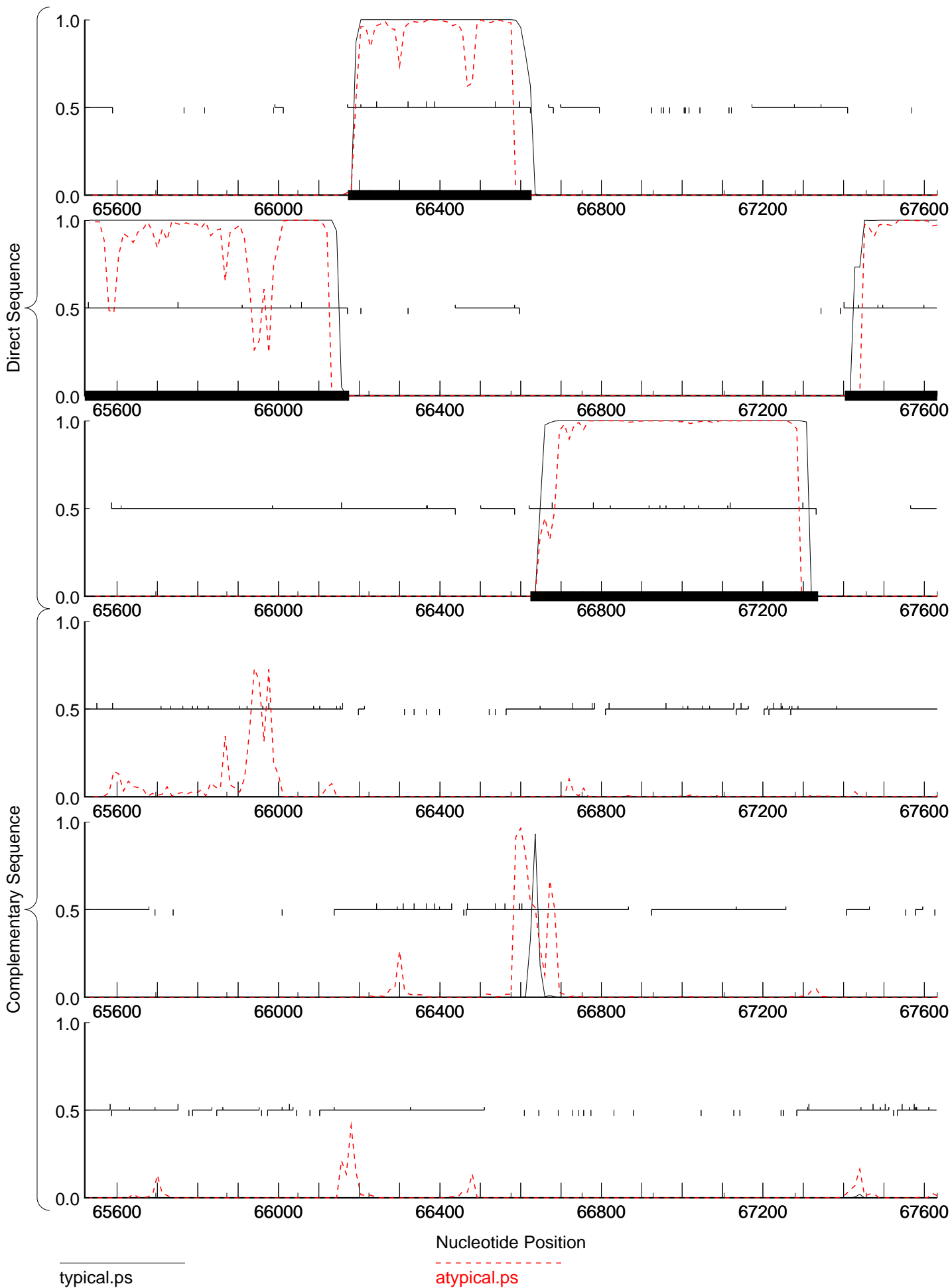
GeneMark.hmm prediction



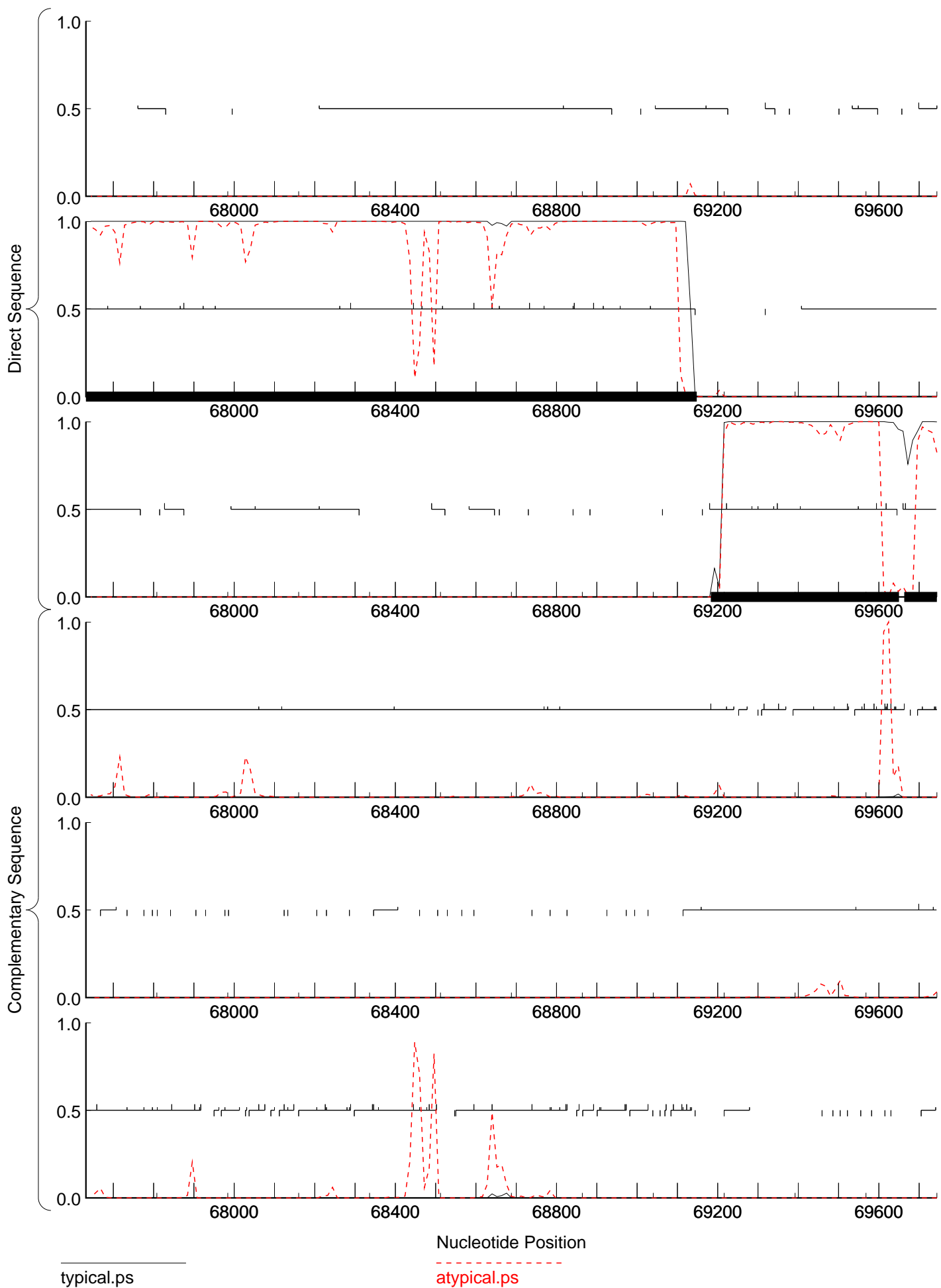




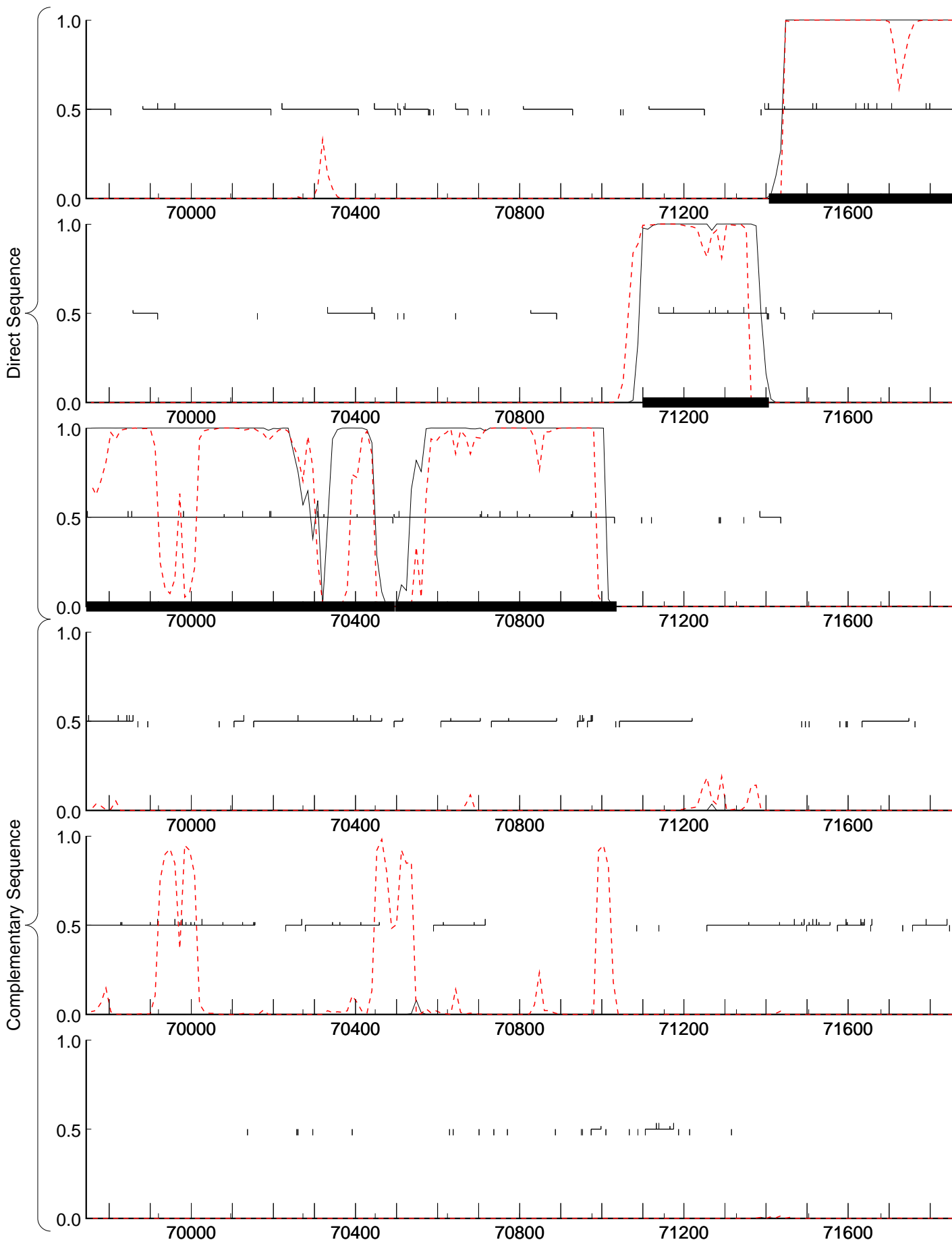
GeneMark.hmm prediction



GeneMark.hmm prediction



GeneMark.hmm prediction

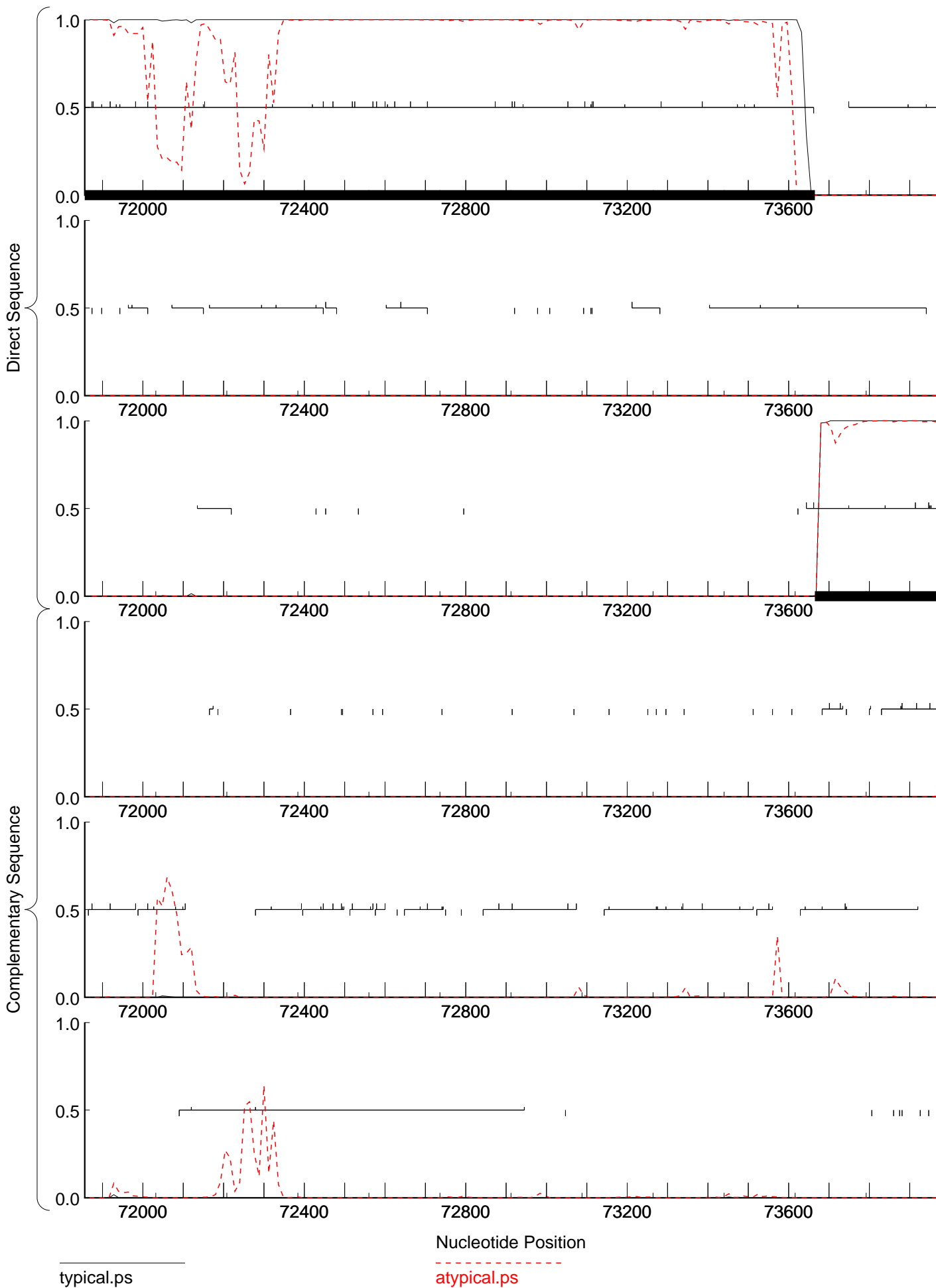


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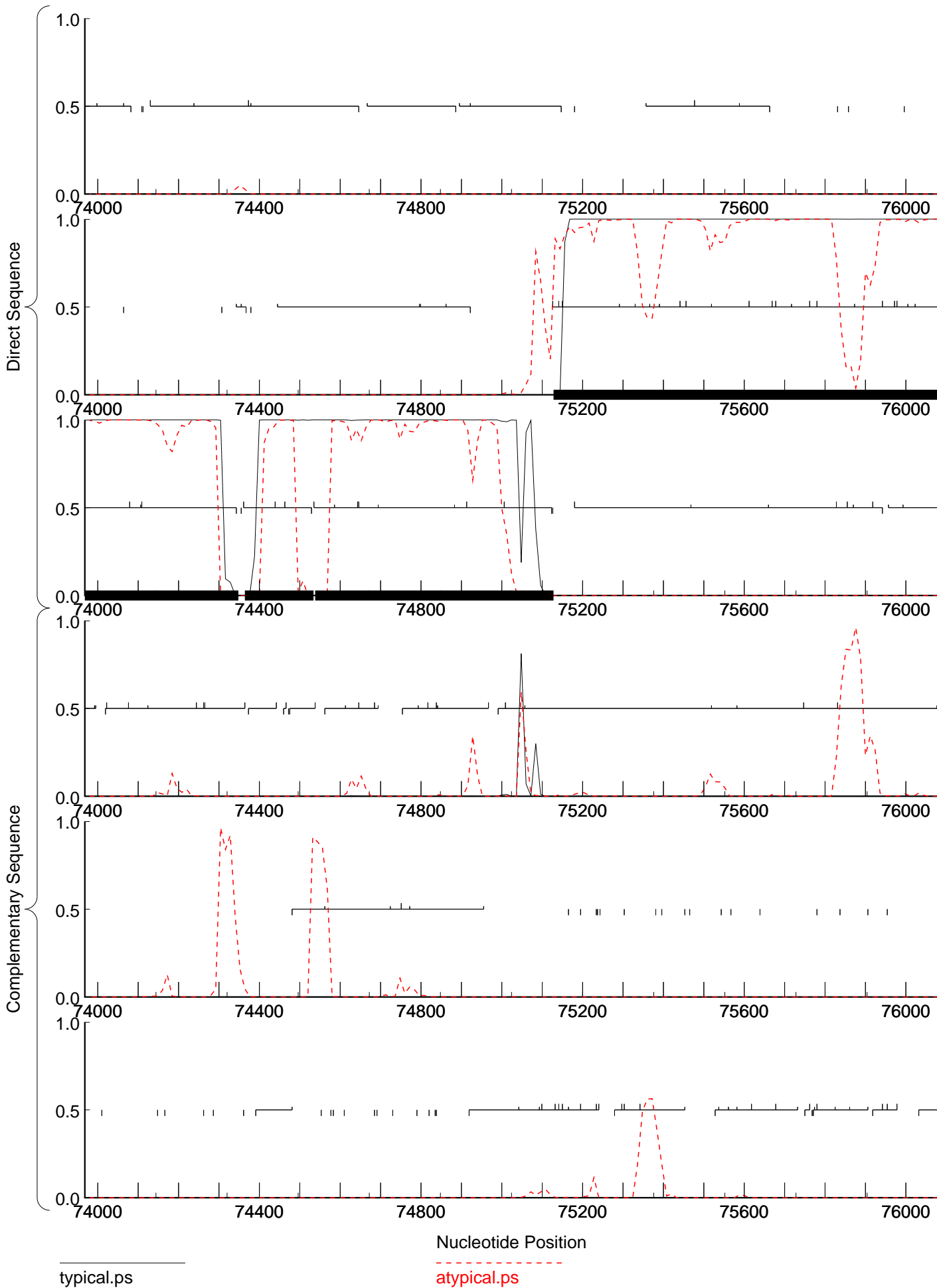
Nucleotide Position

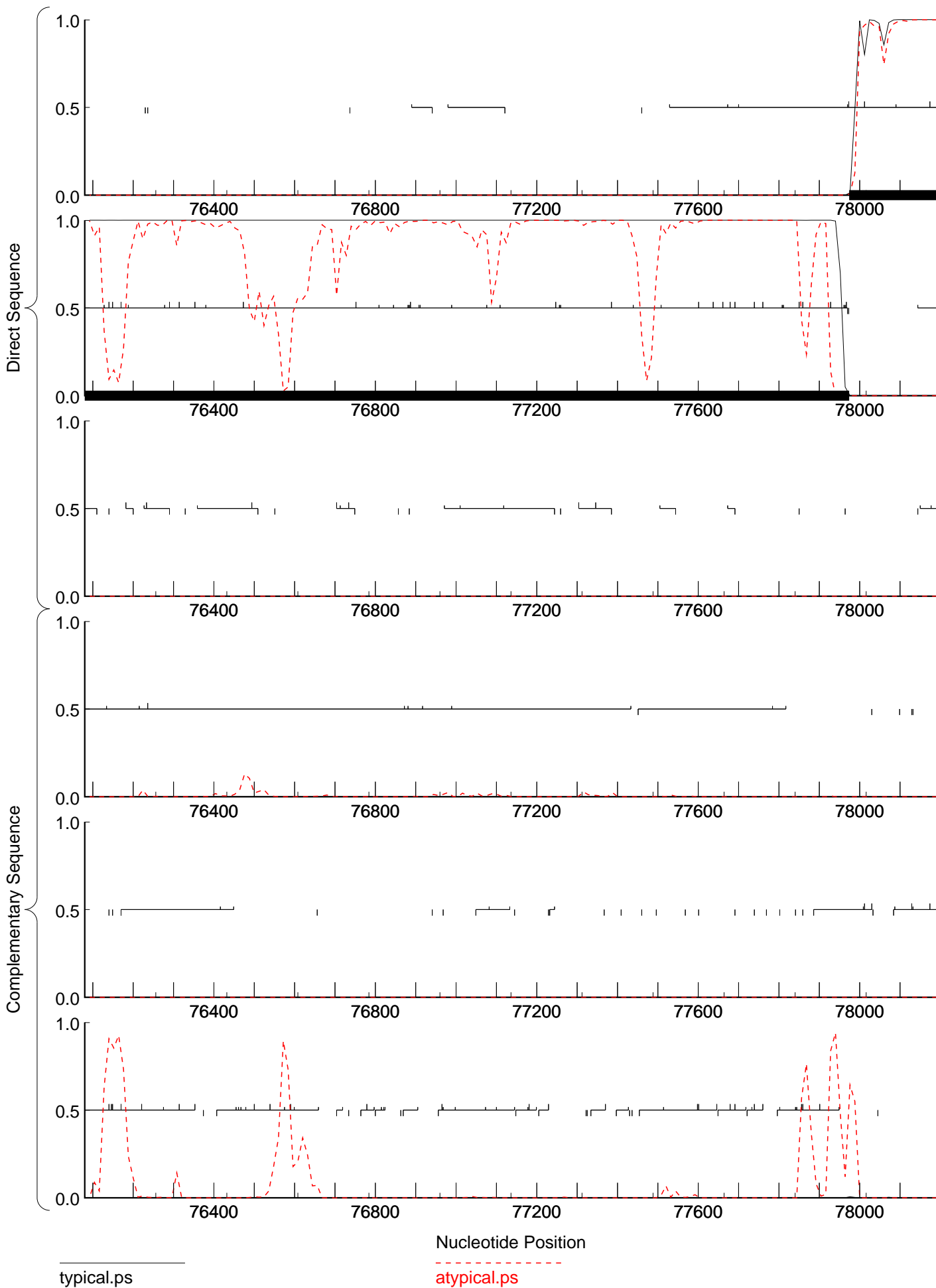
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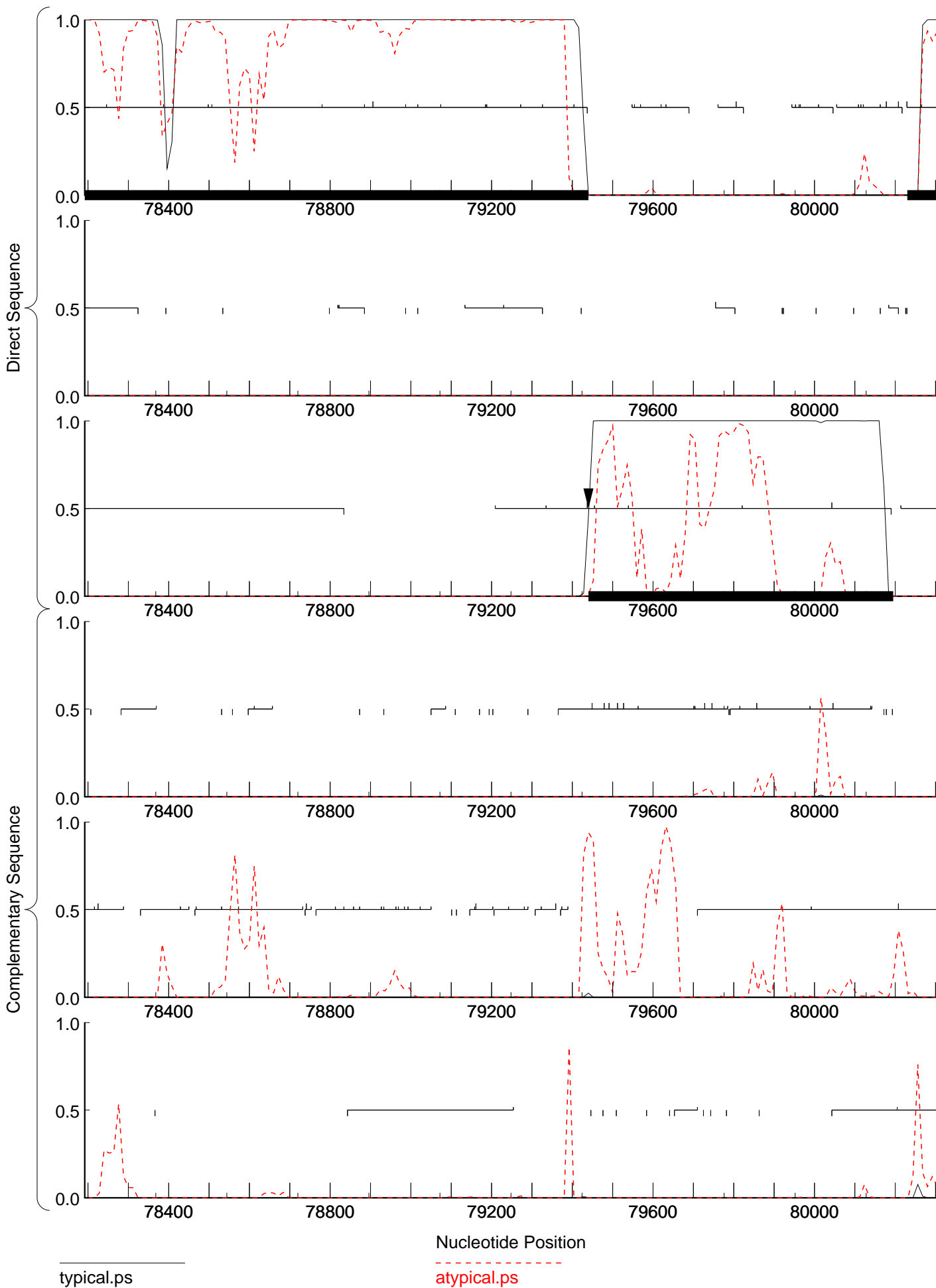
GeneMark.hmm prediction



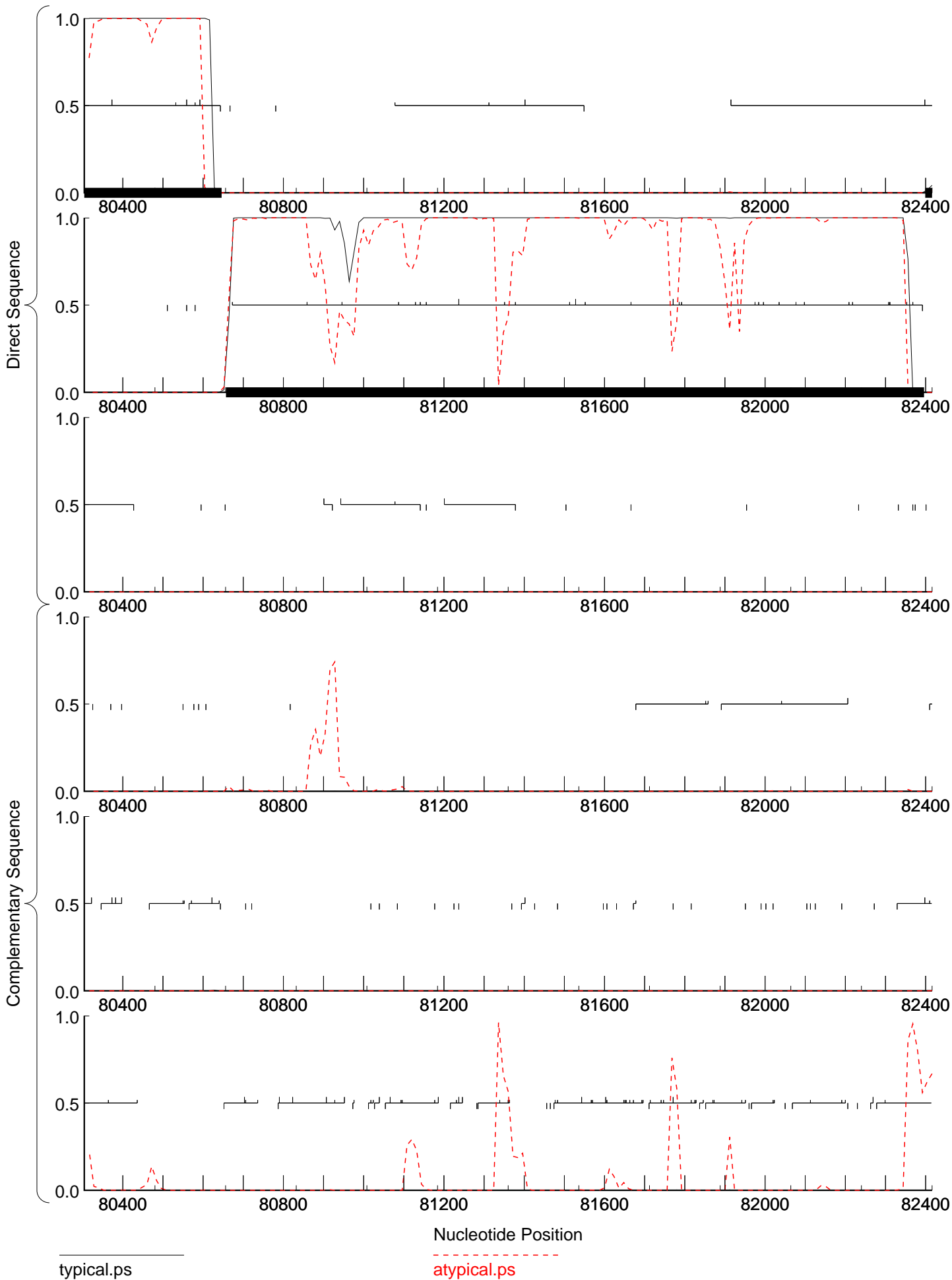
GeneMark.hmm prediction

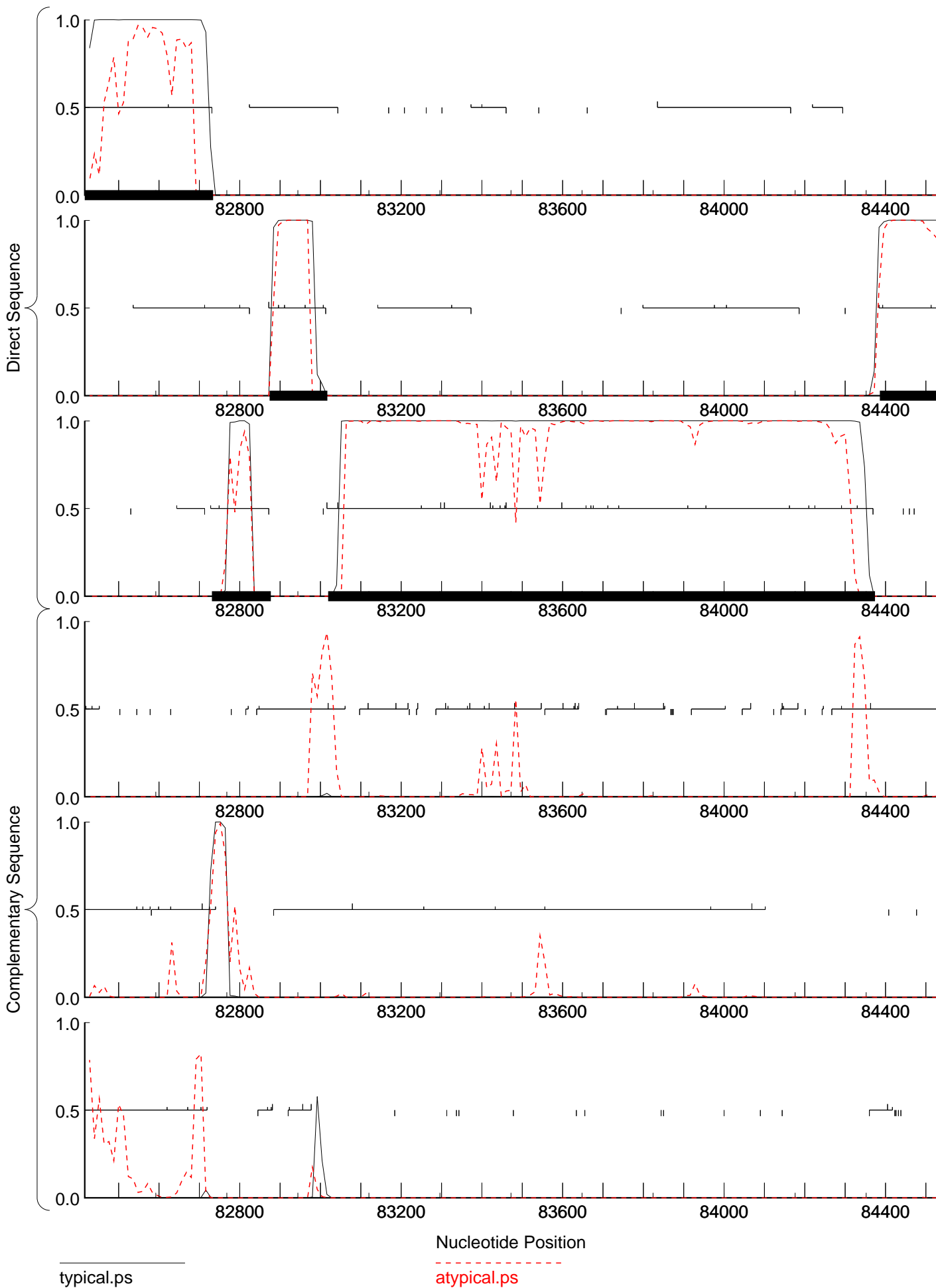


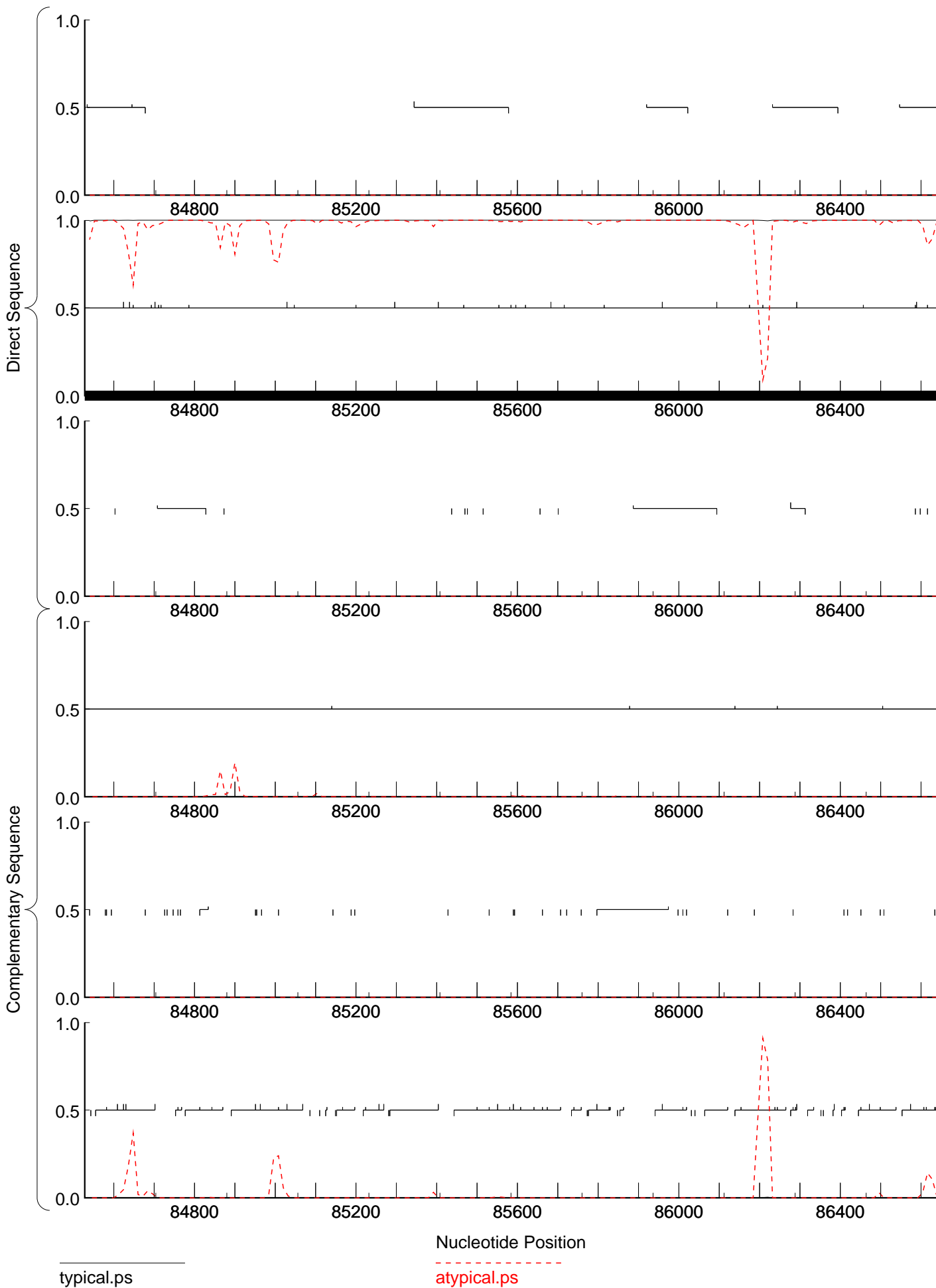




GeneMark.hmm prediction



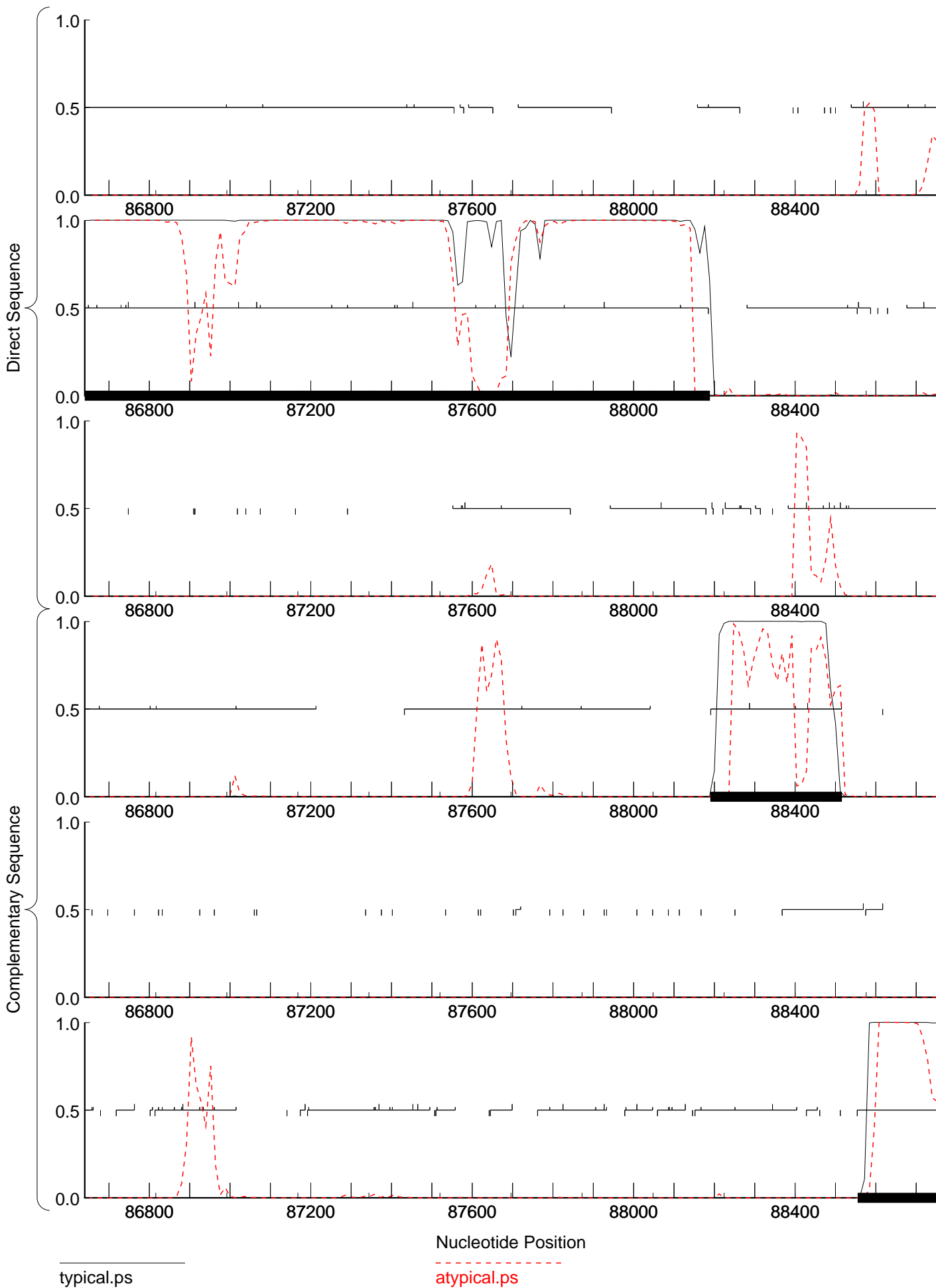




typical.ps

atypical.ps

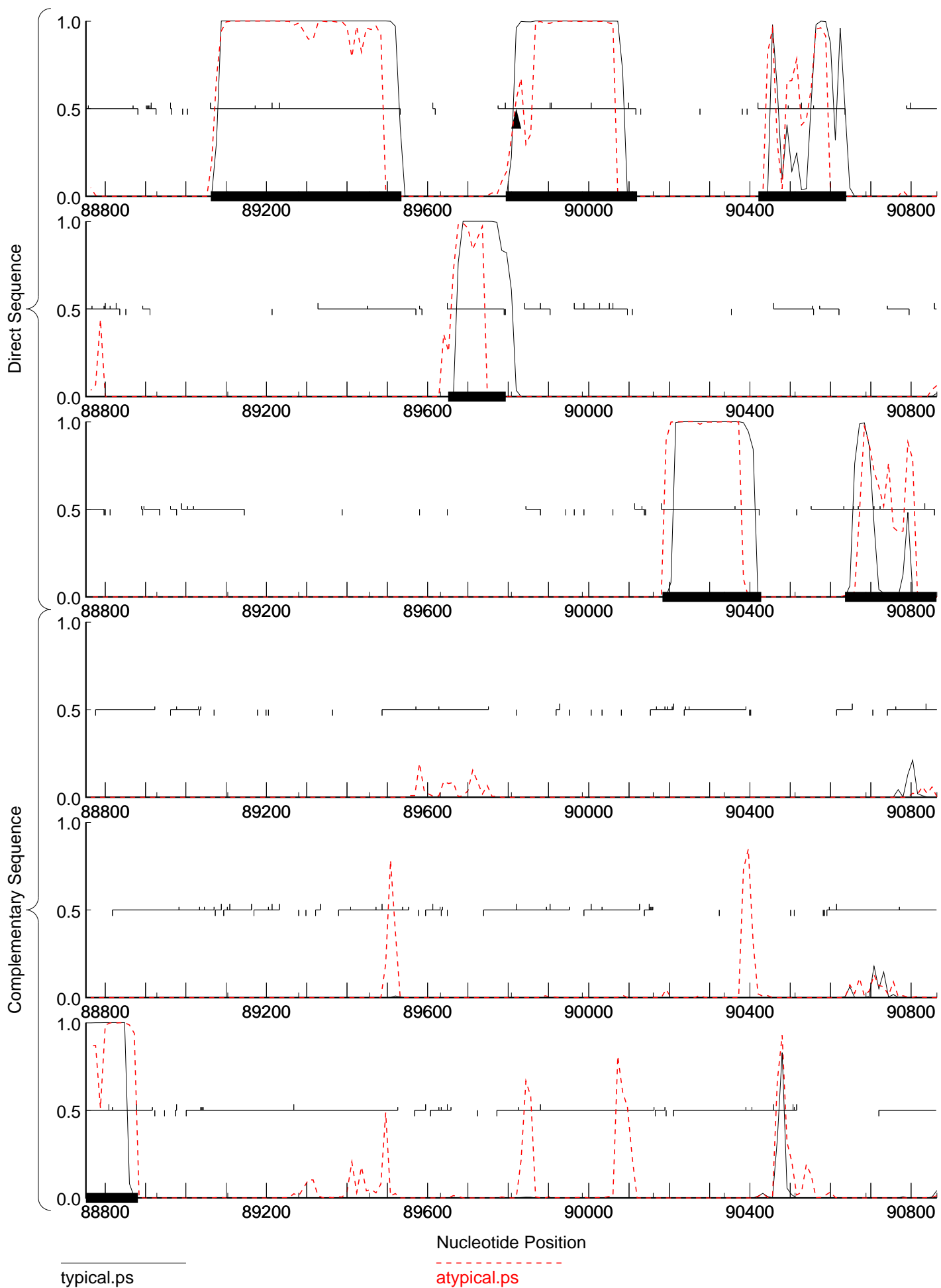
GeneMark.hmm prediction



typical.ps

atypical.ps

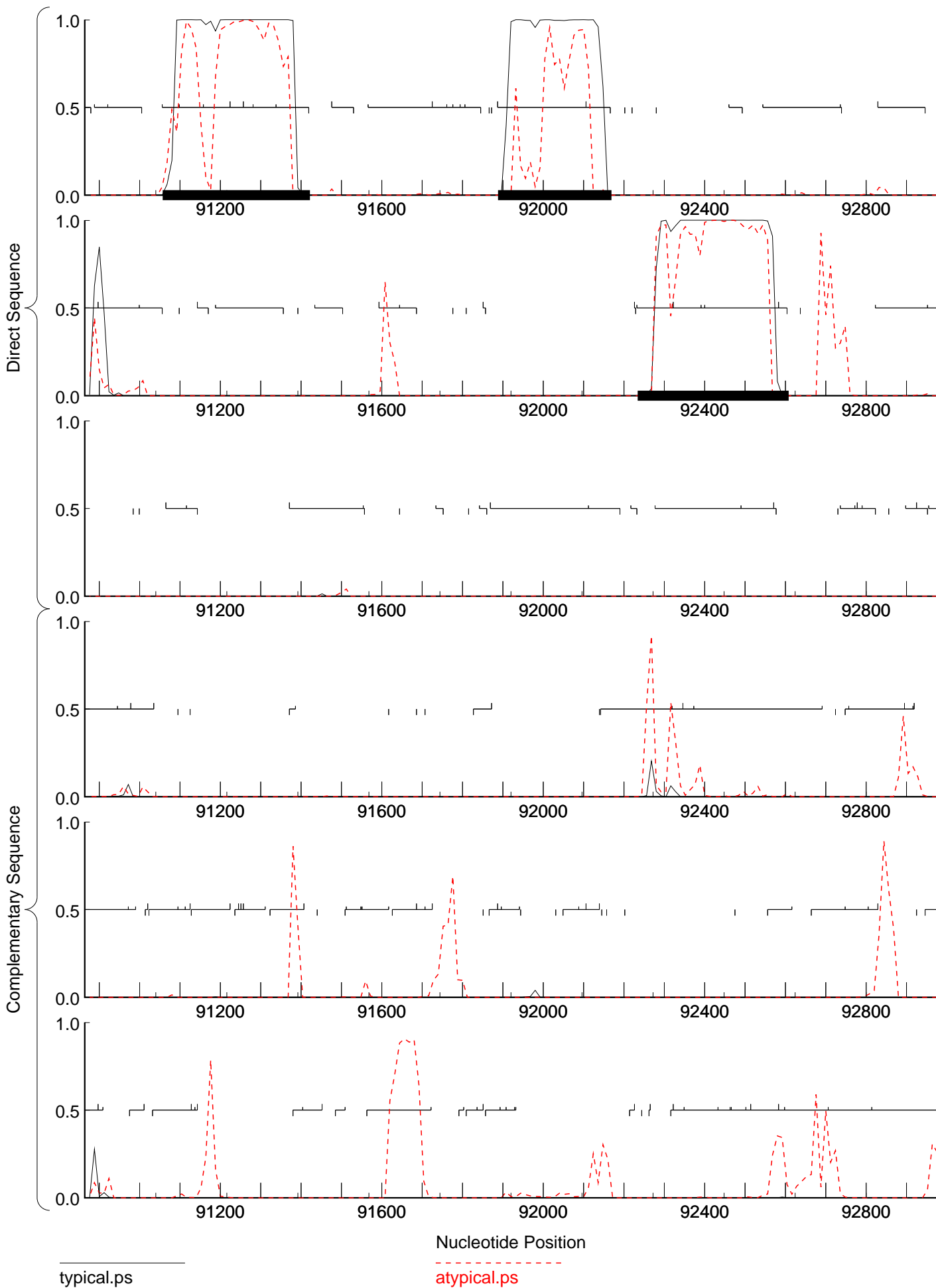
GeneMark.hmm prediction



typical.ps

atypical.ps

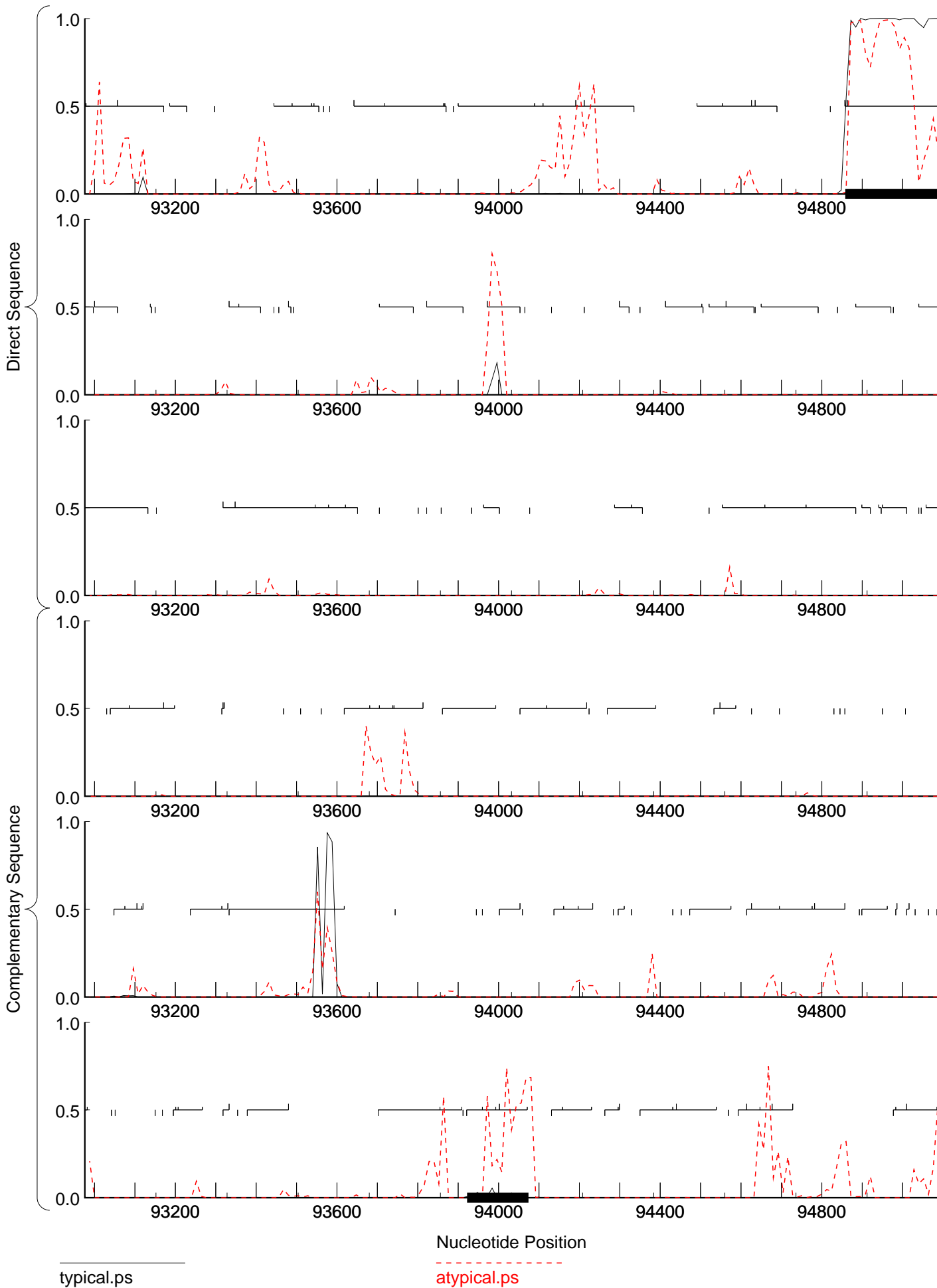
GeneMark.hmm prediction



typical.ps

atypical.ps

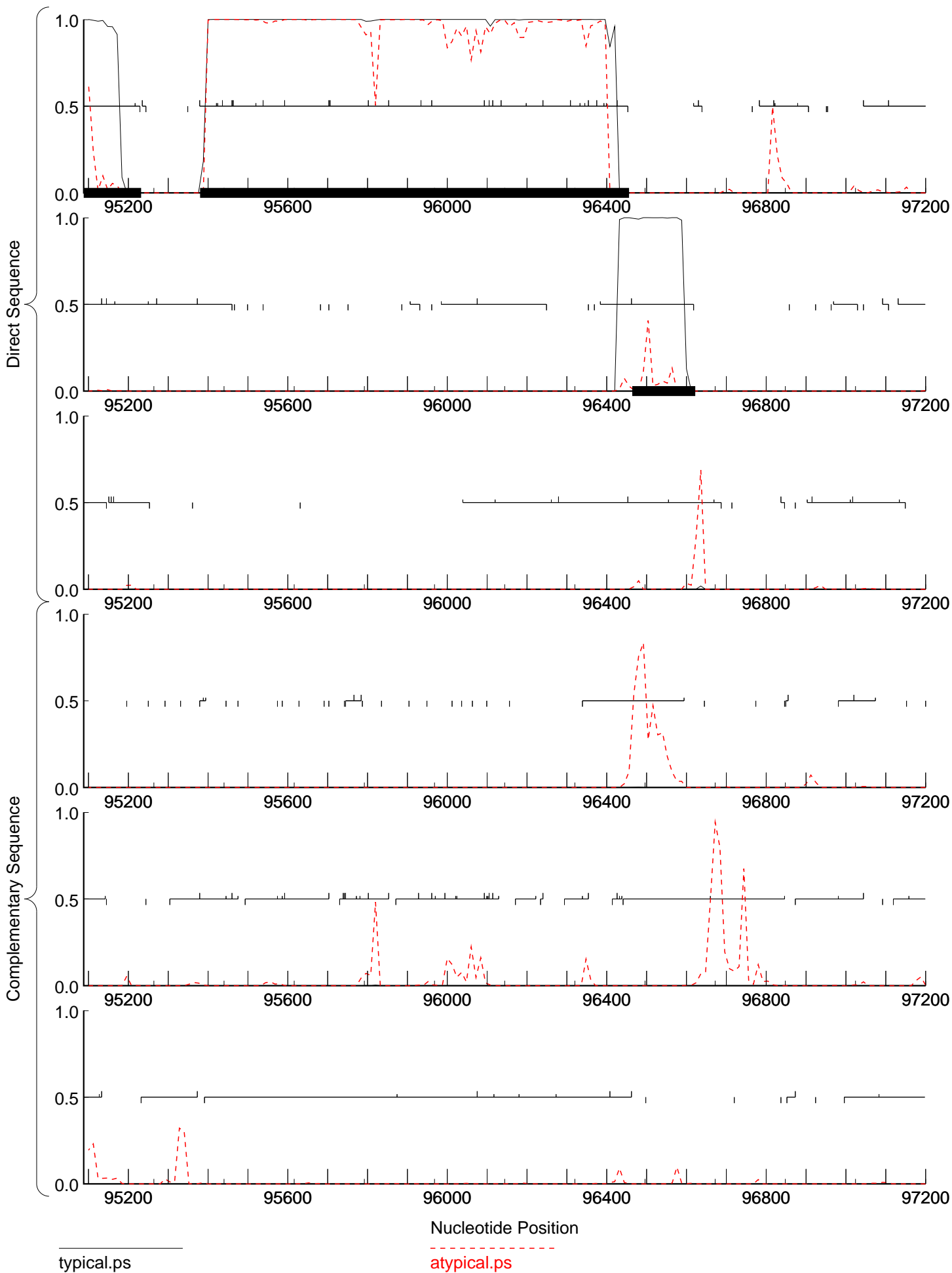
GeneMark.hmm prediction

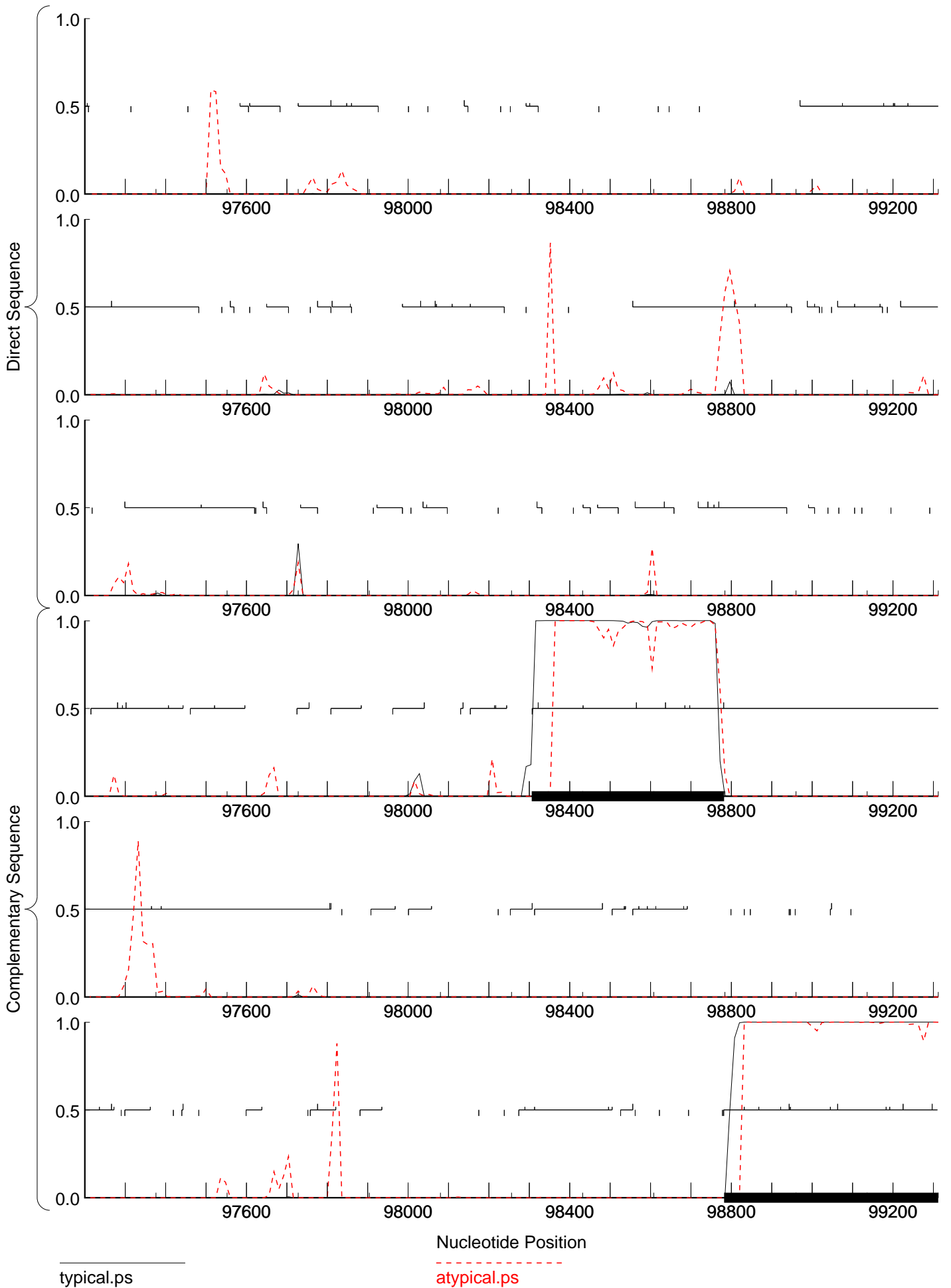


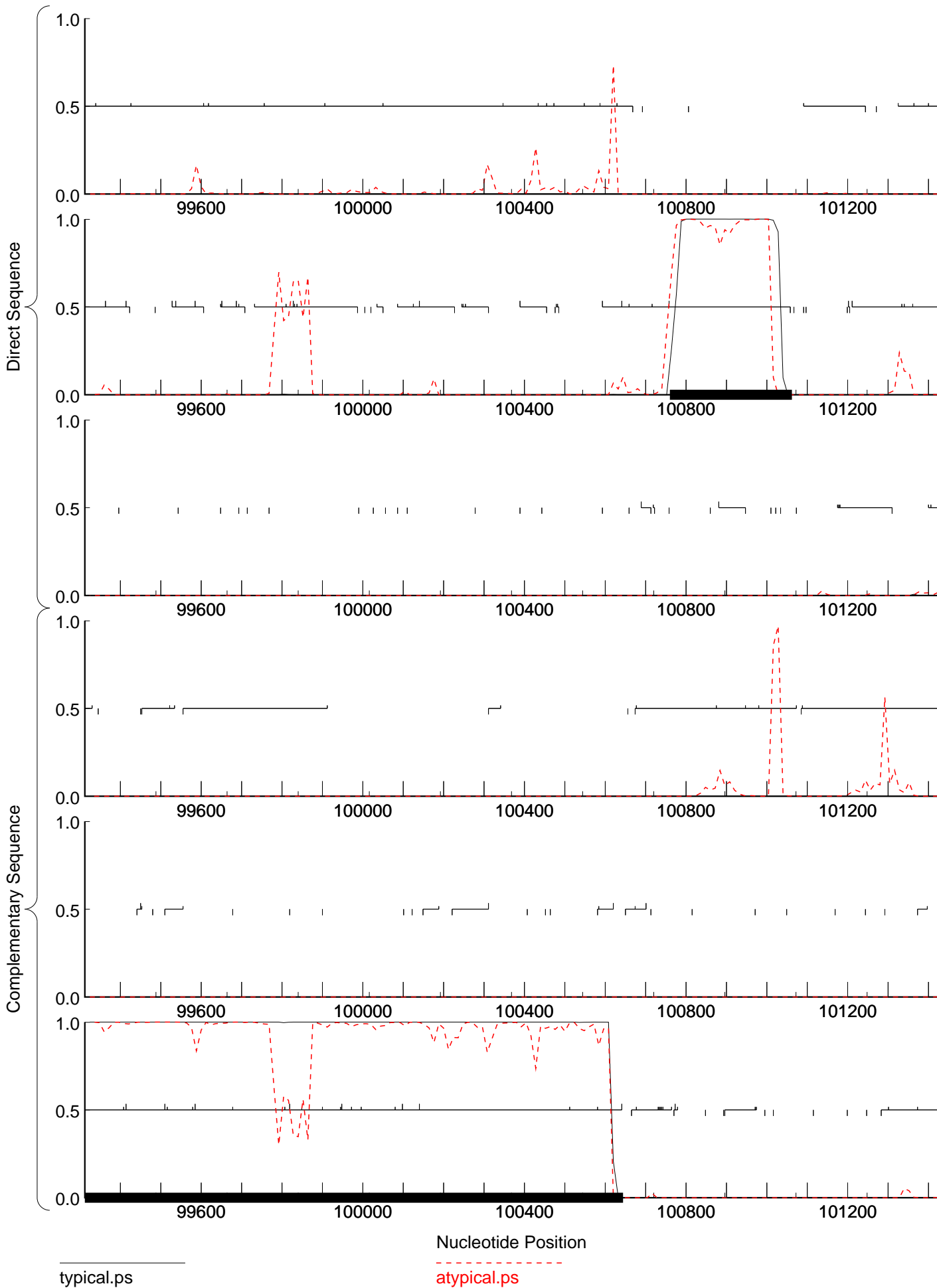
typical.ps

atypical.ps

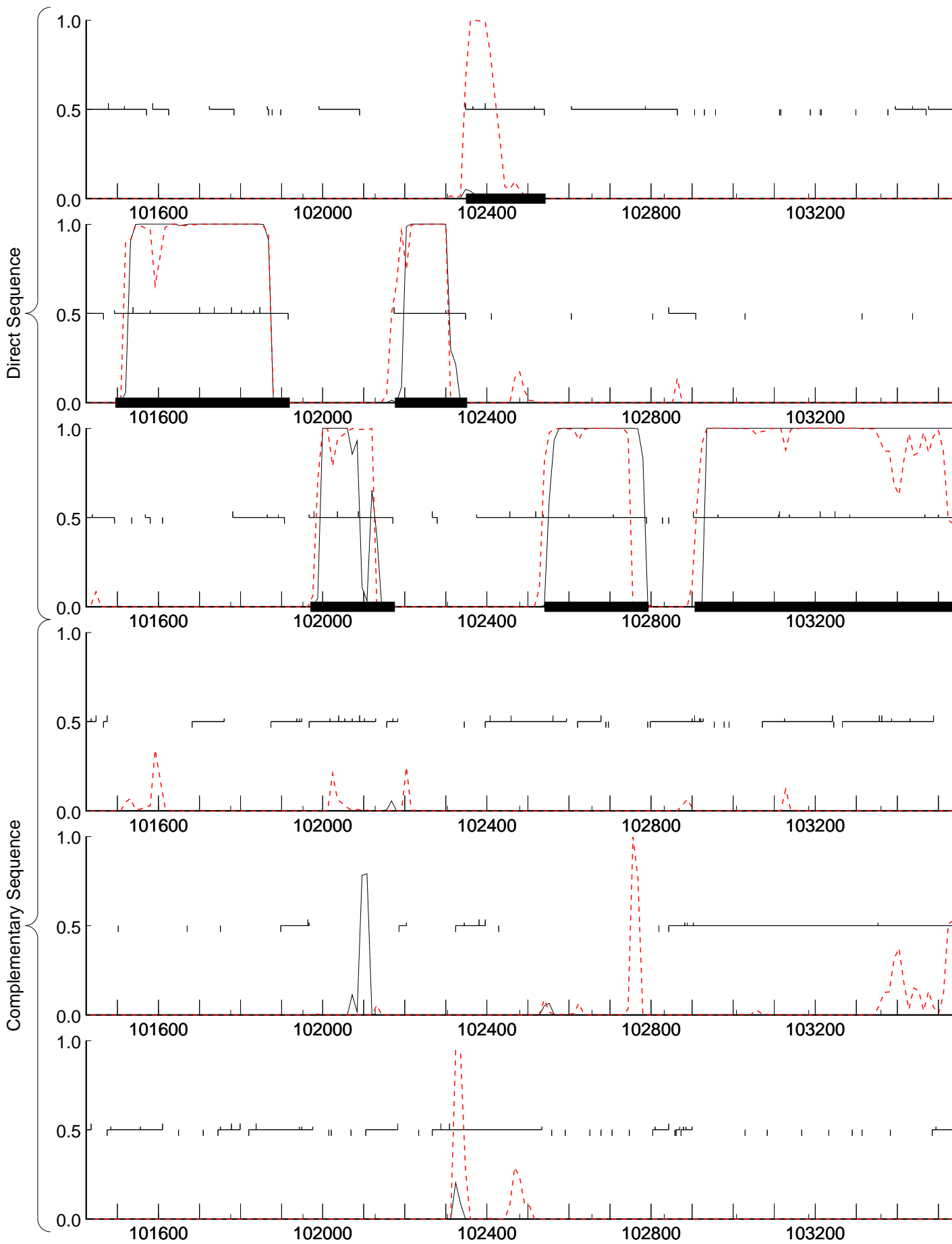
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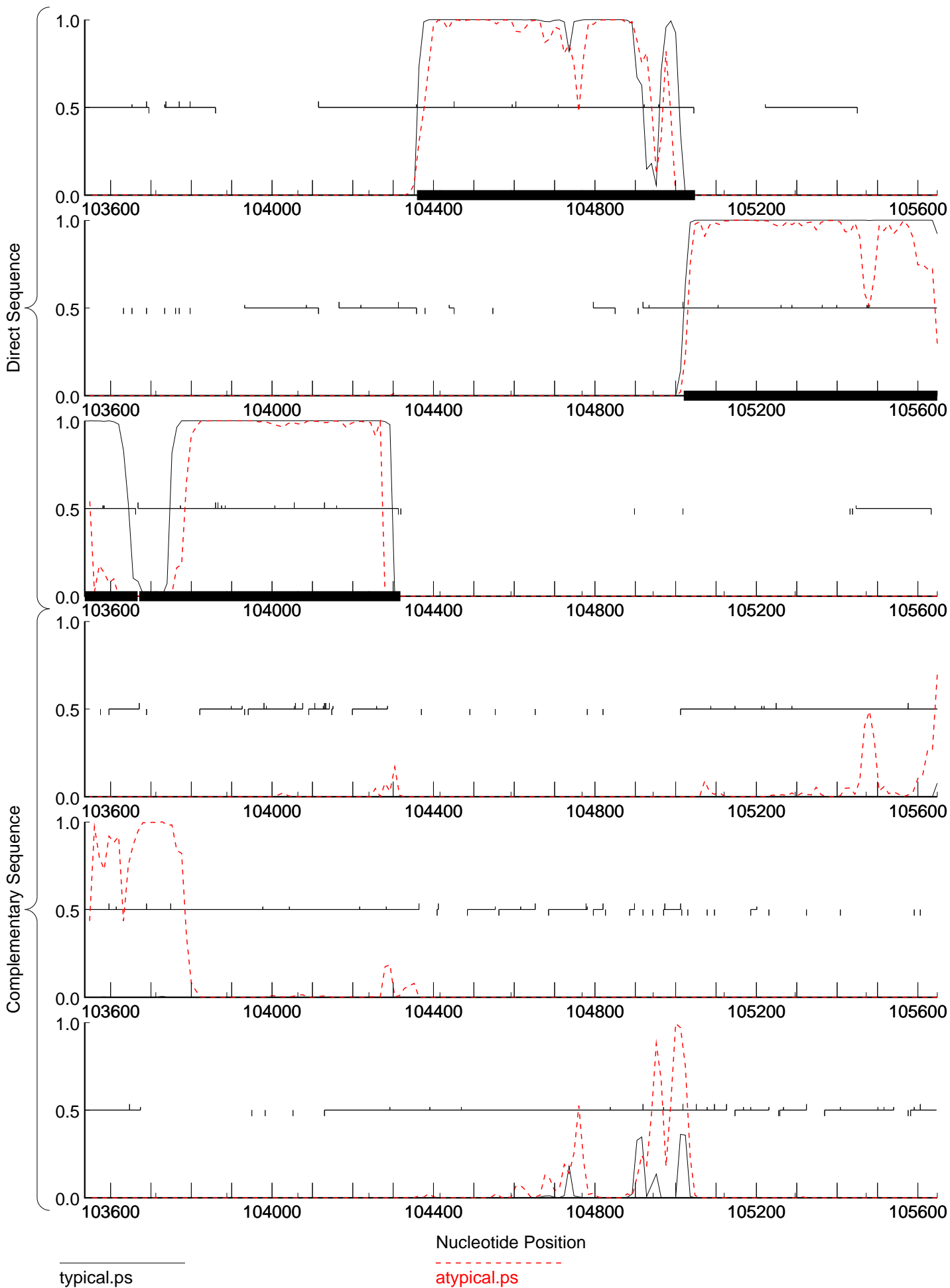
GeneMark.hmm prediction



typical.ps

atypical.ps

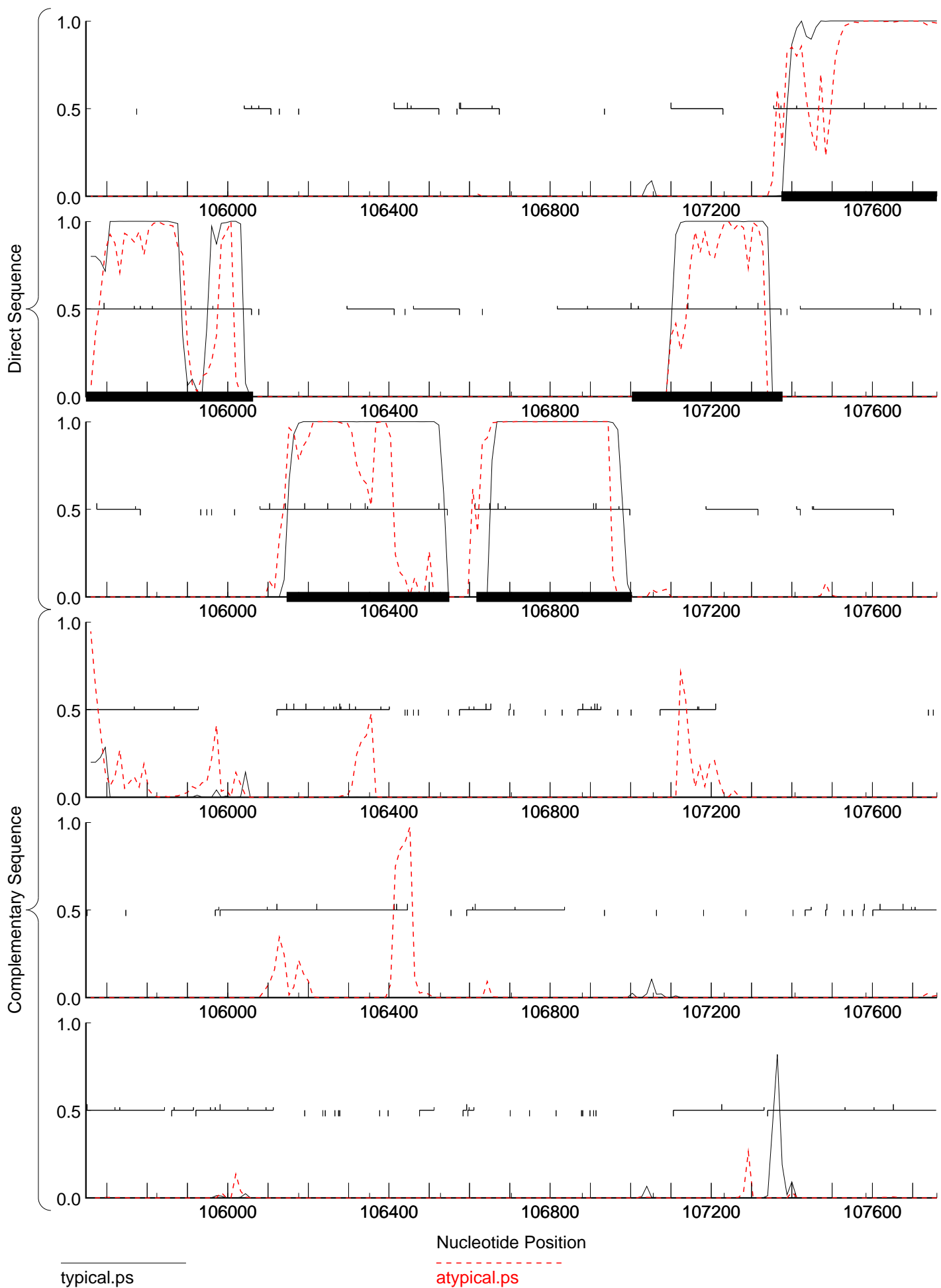
GeneMark.hmm prediction



typical.ps

atypical.ps

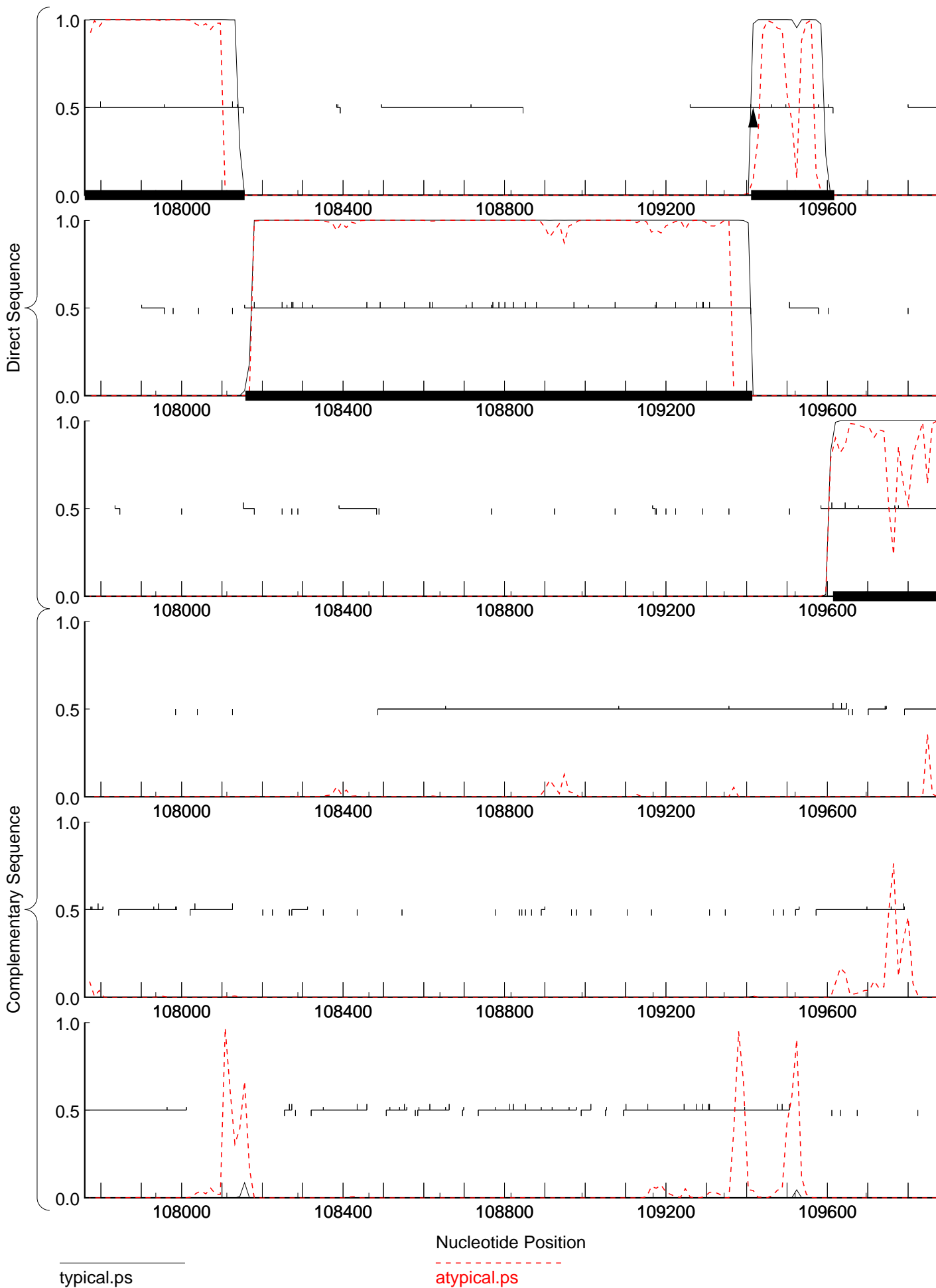
GeneMark.hmm prediction



typical.ps

atypical.ps

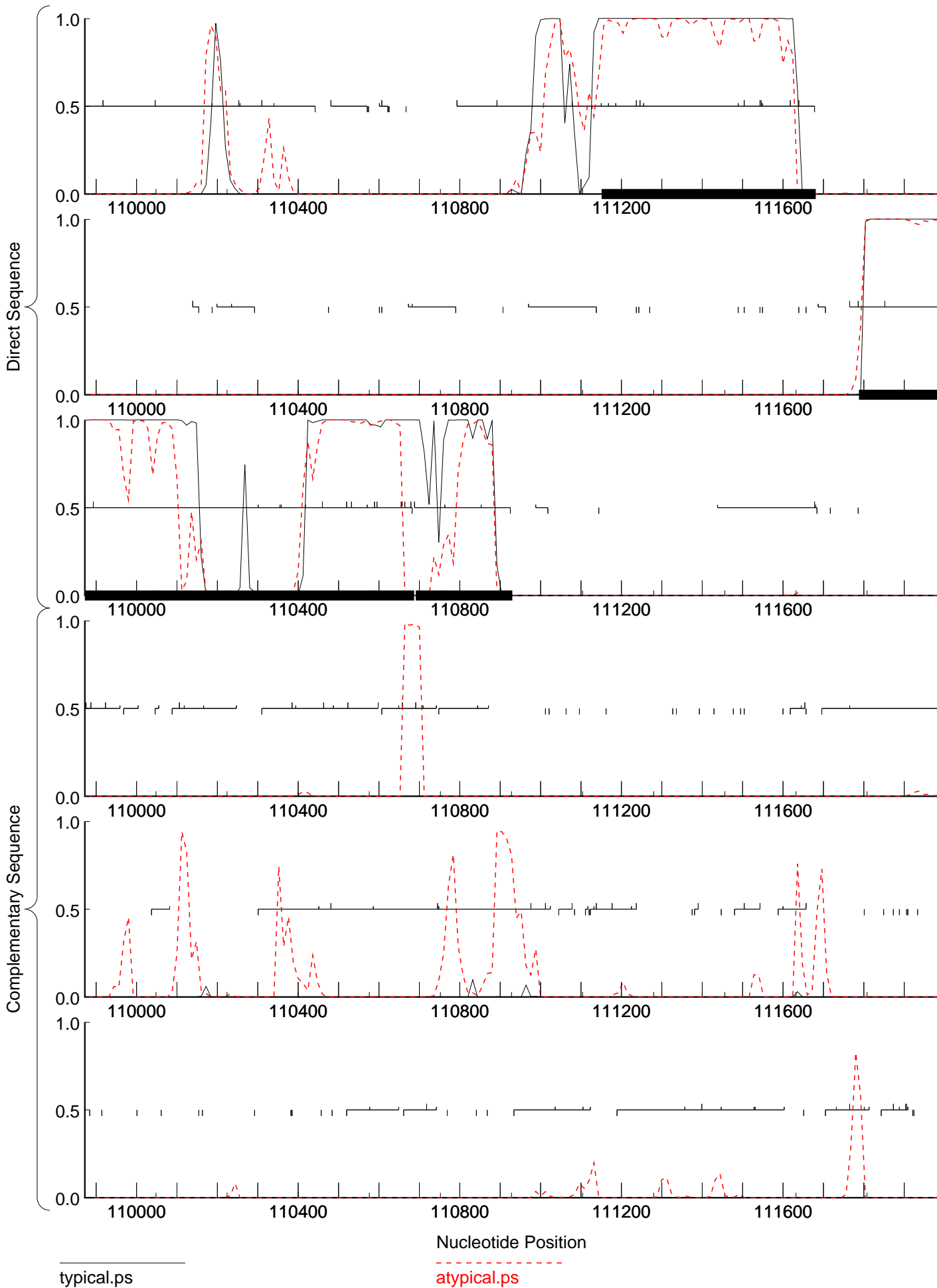
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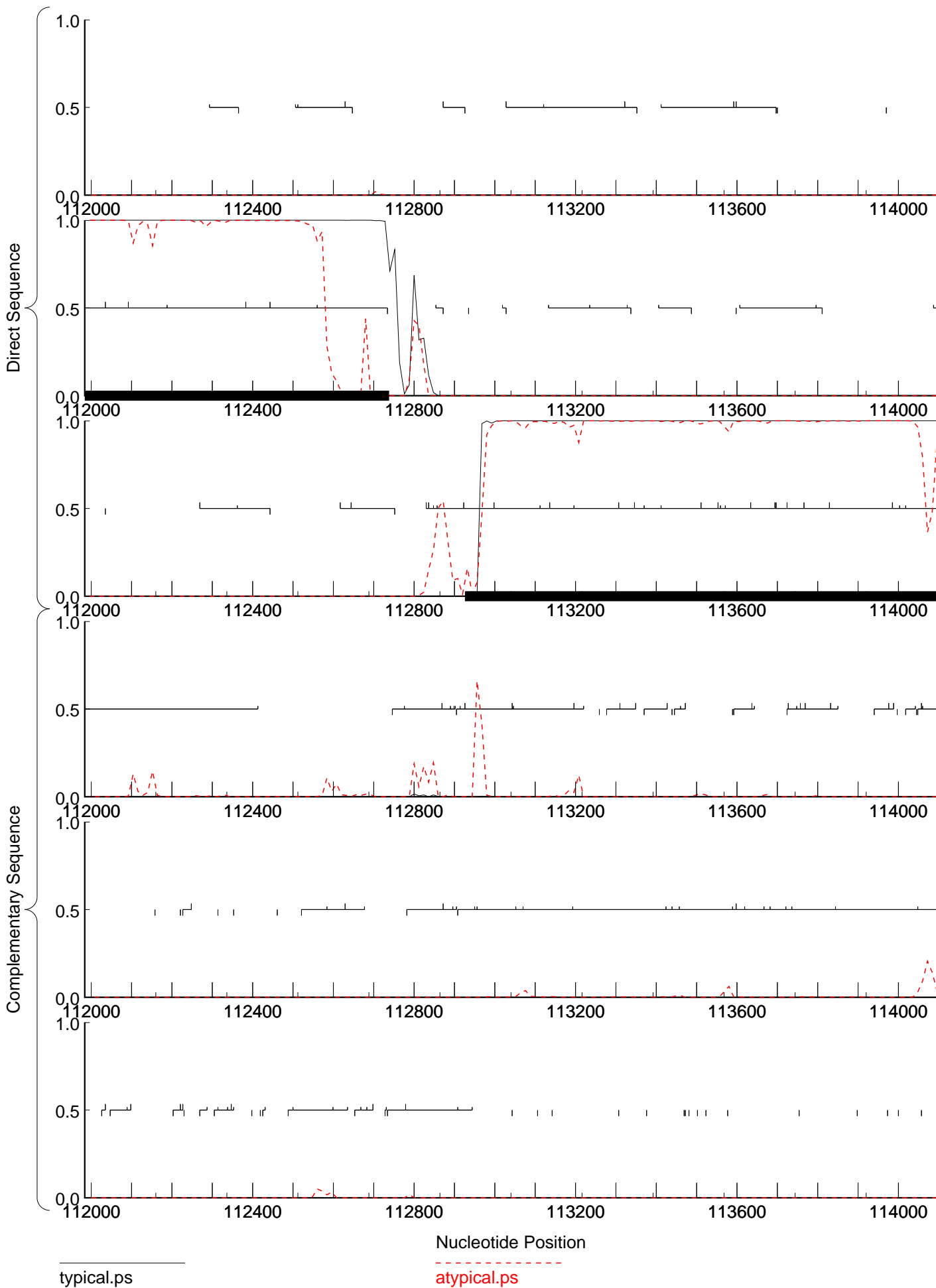


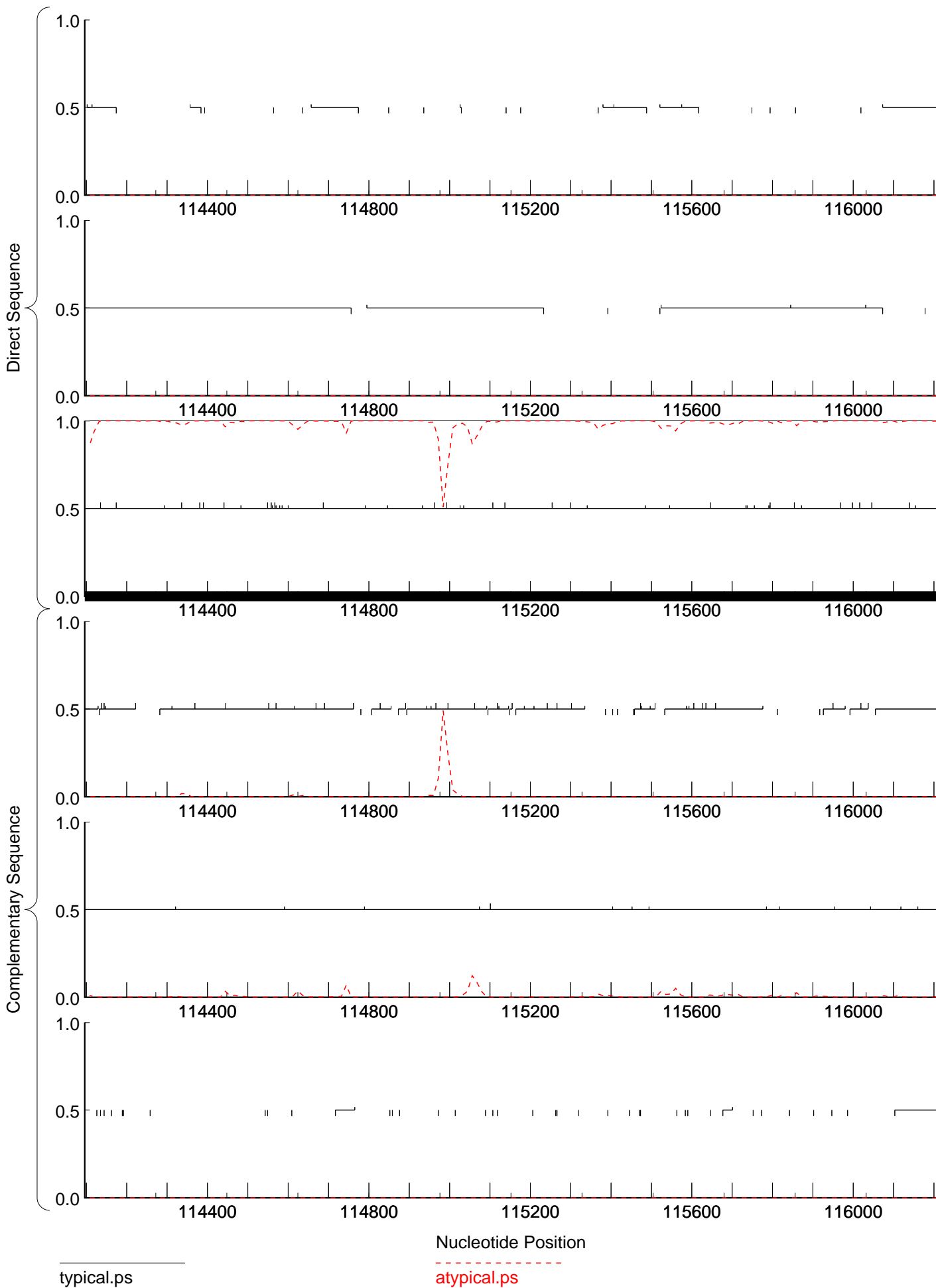
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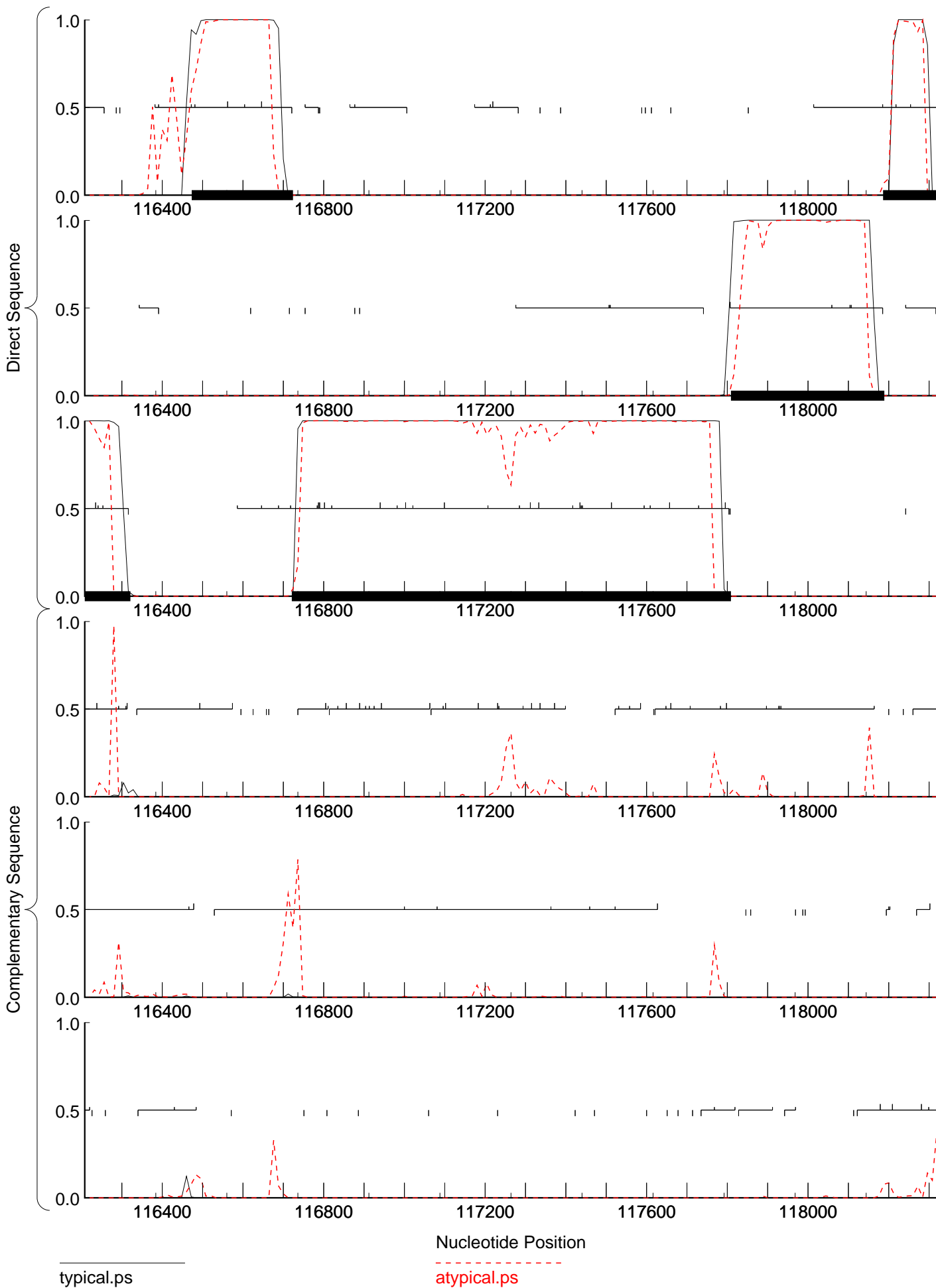
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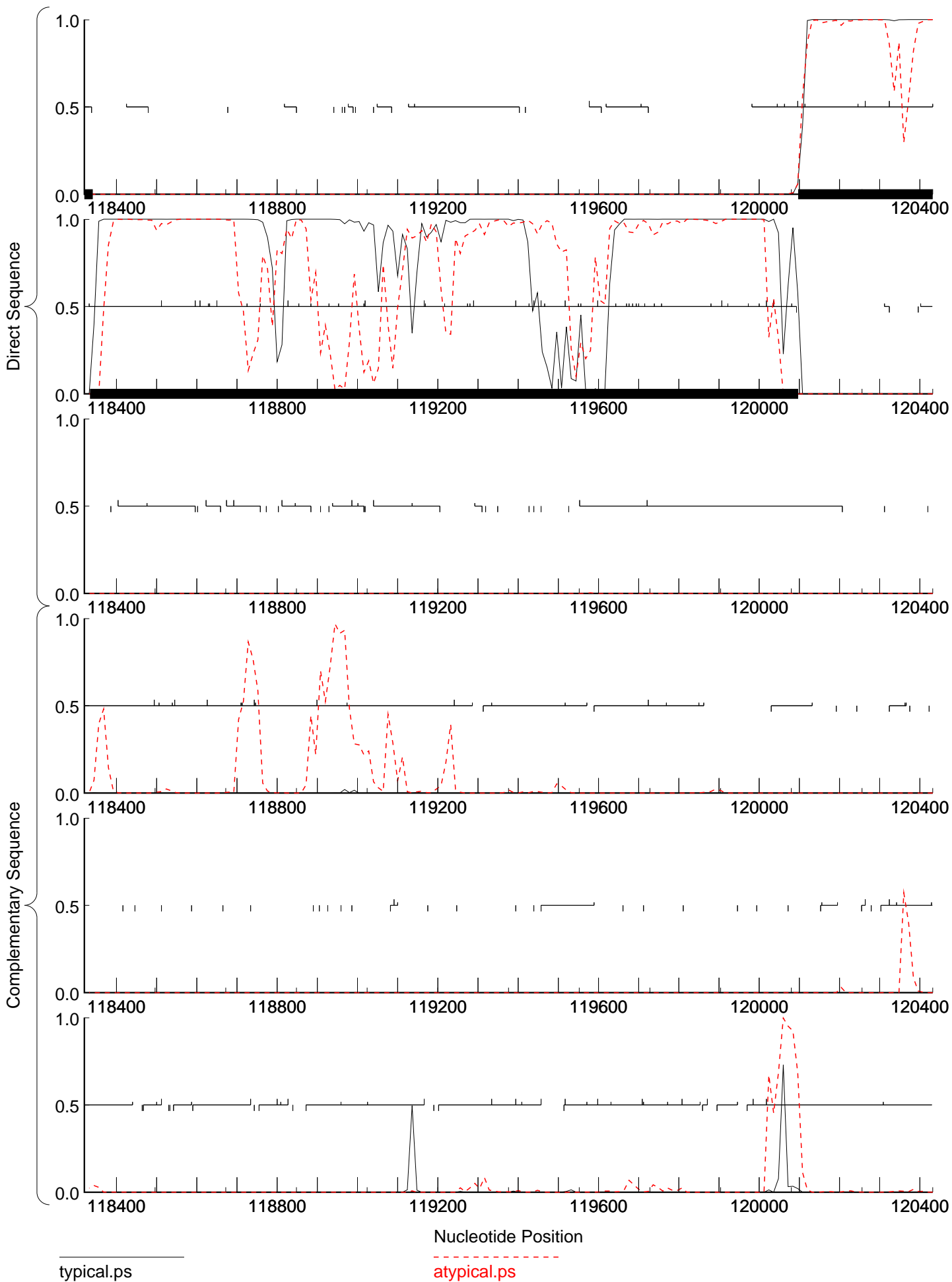
GeneMark.hmm prediction



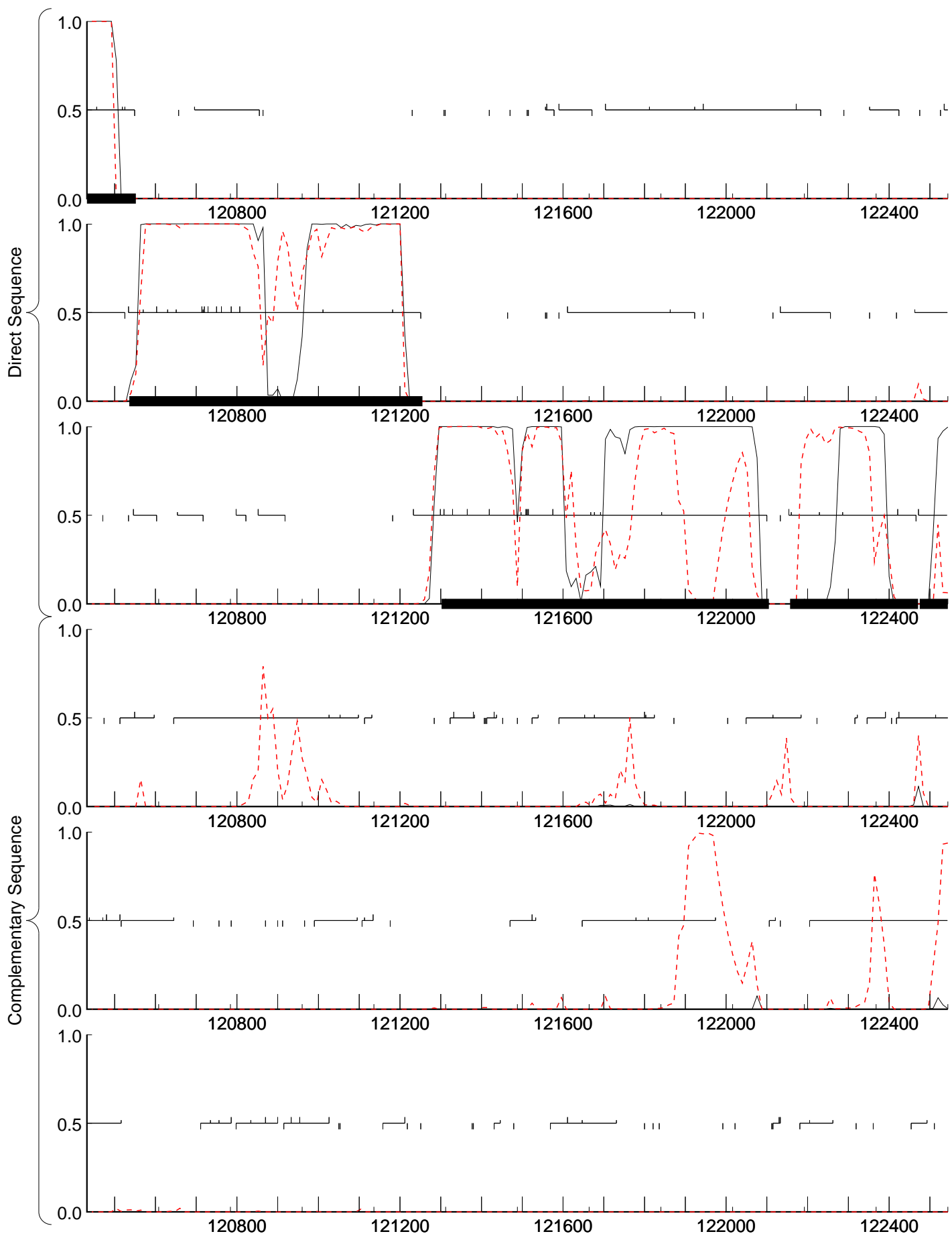








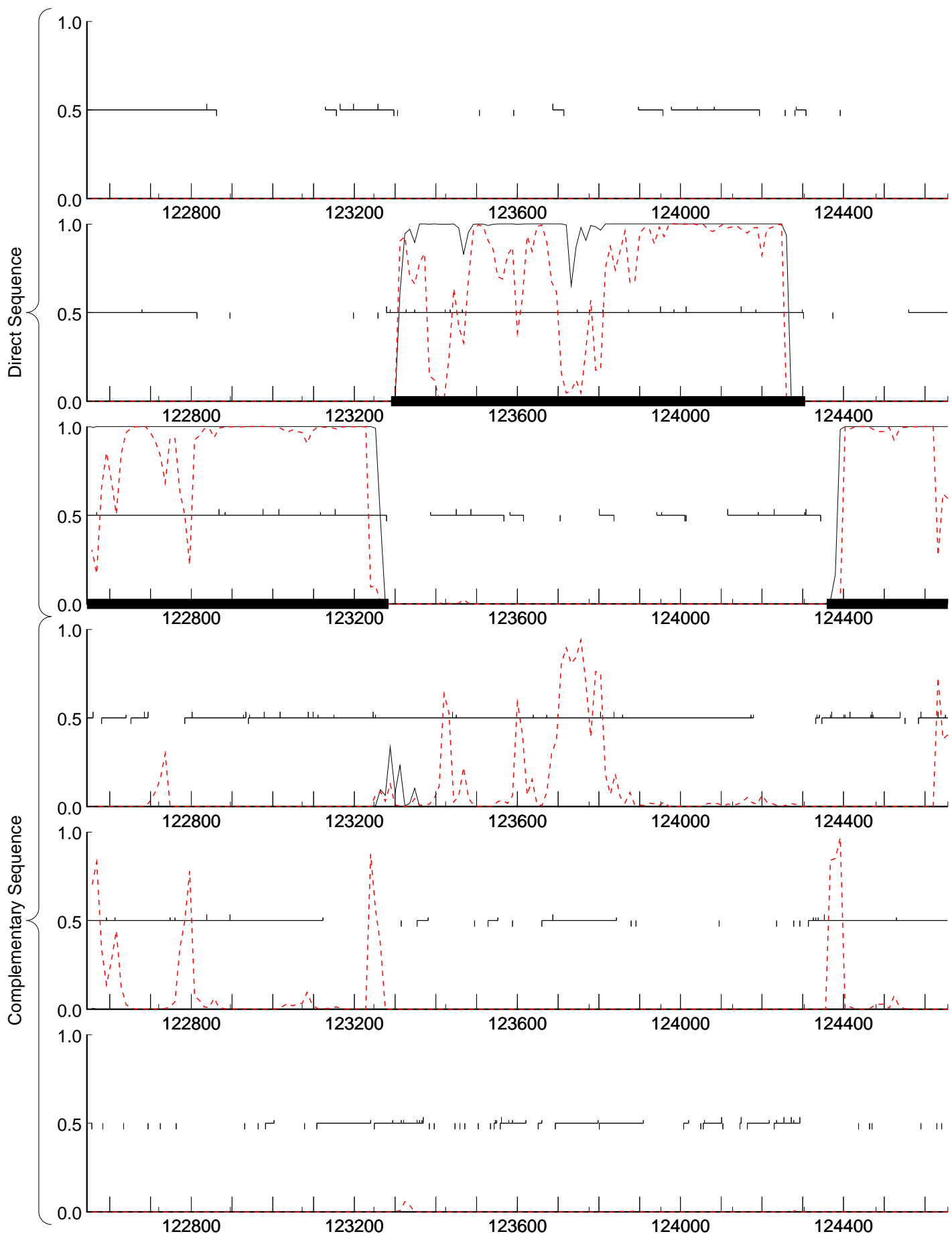
GeneMark.hmm prediction



typical.ps

atypical.ps

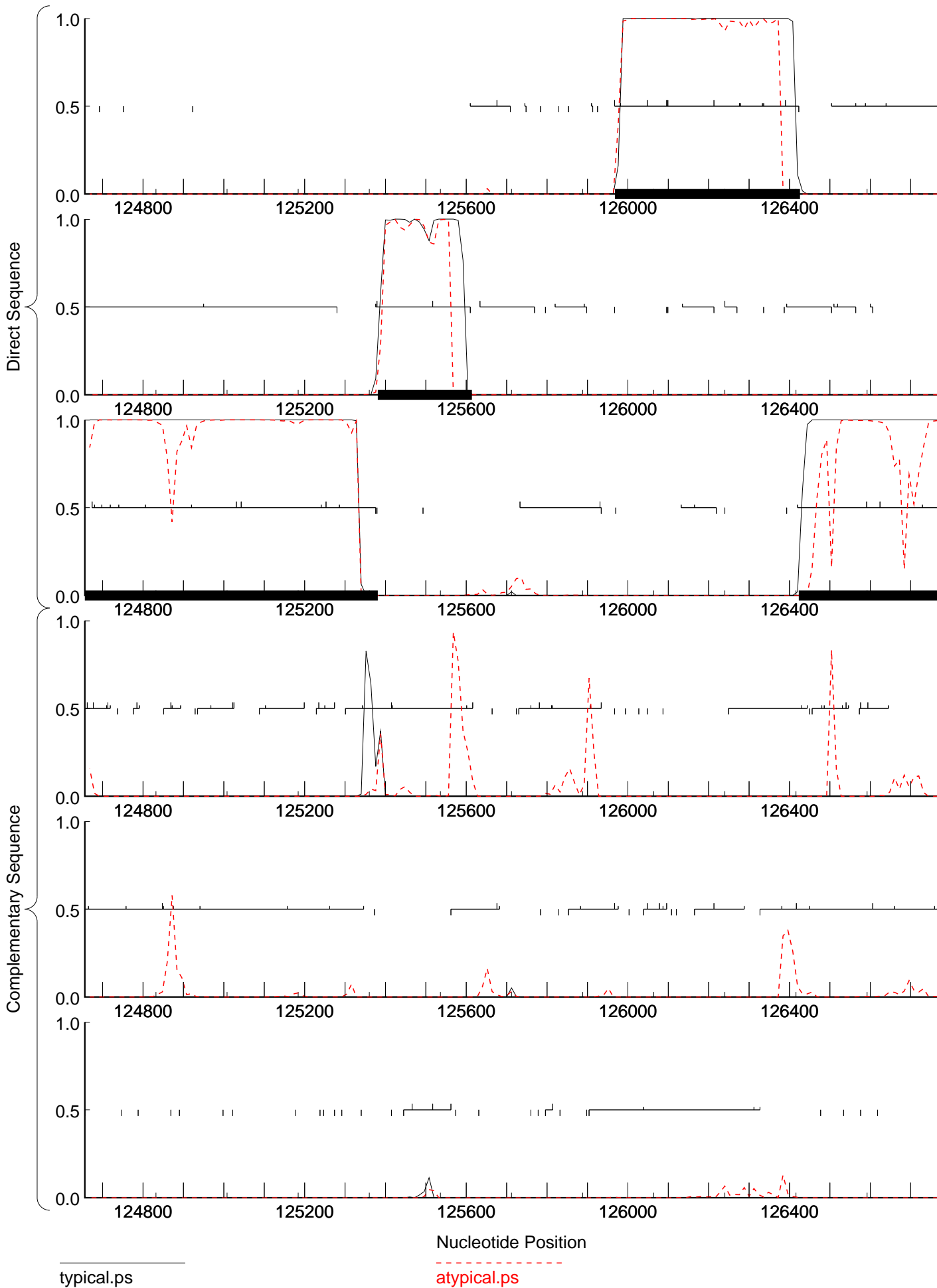
GeneMark.hmm prediction



typical.ps

atypical.ps

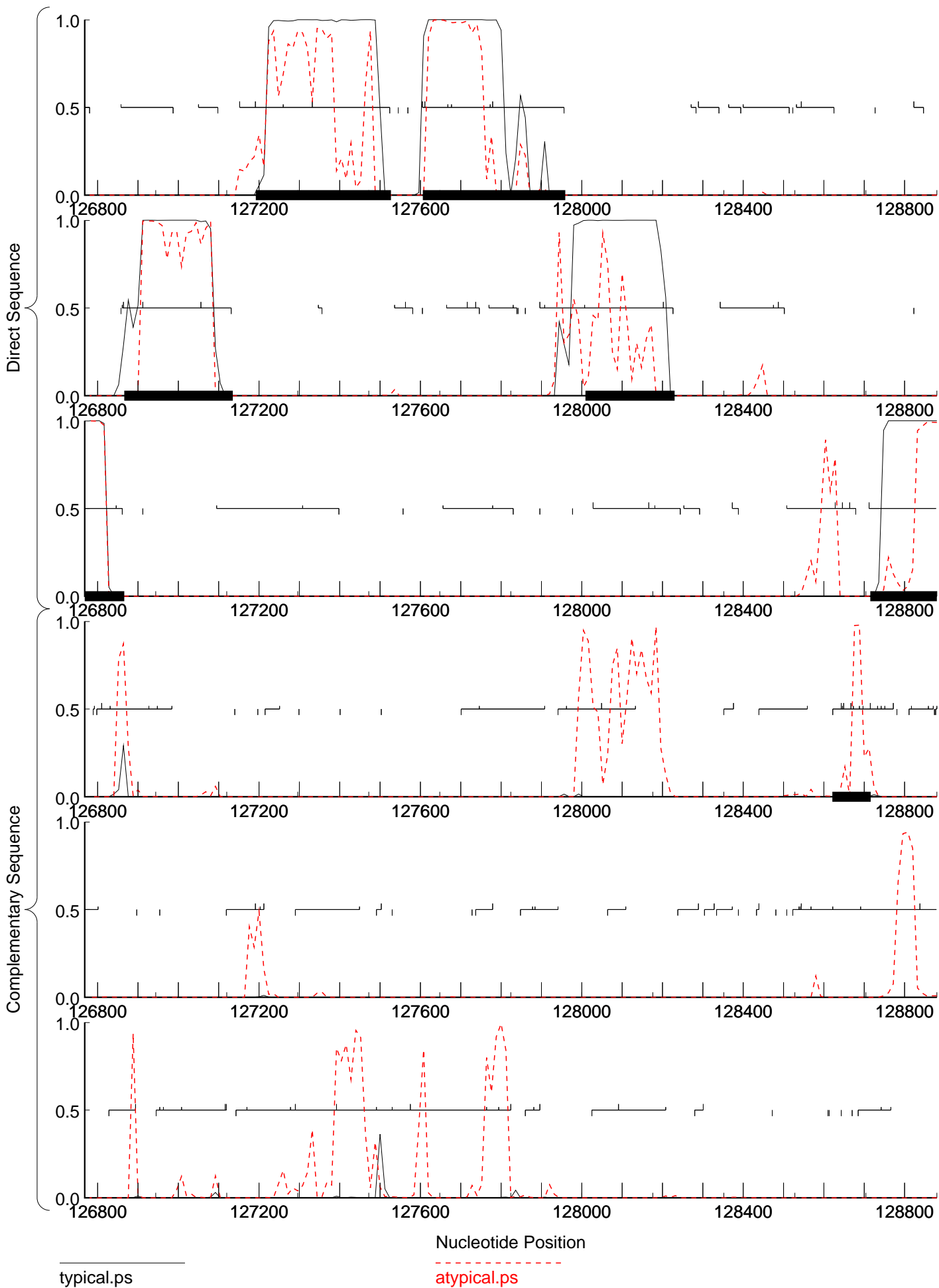
GeneMark.hmm prediction



typical.ps

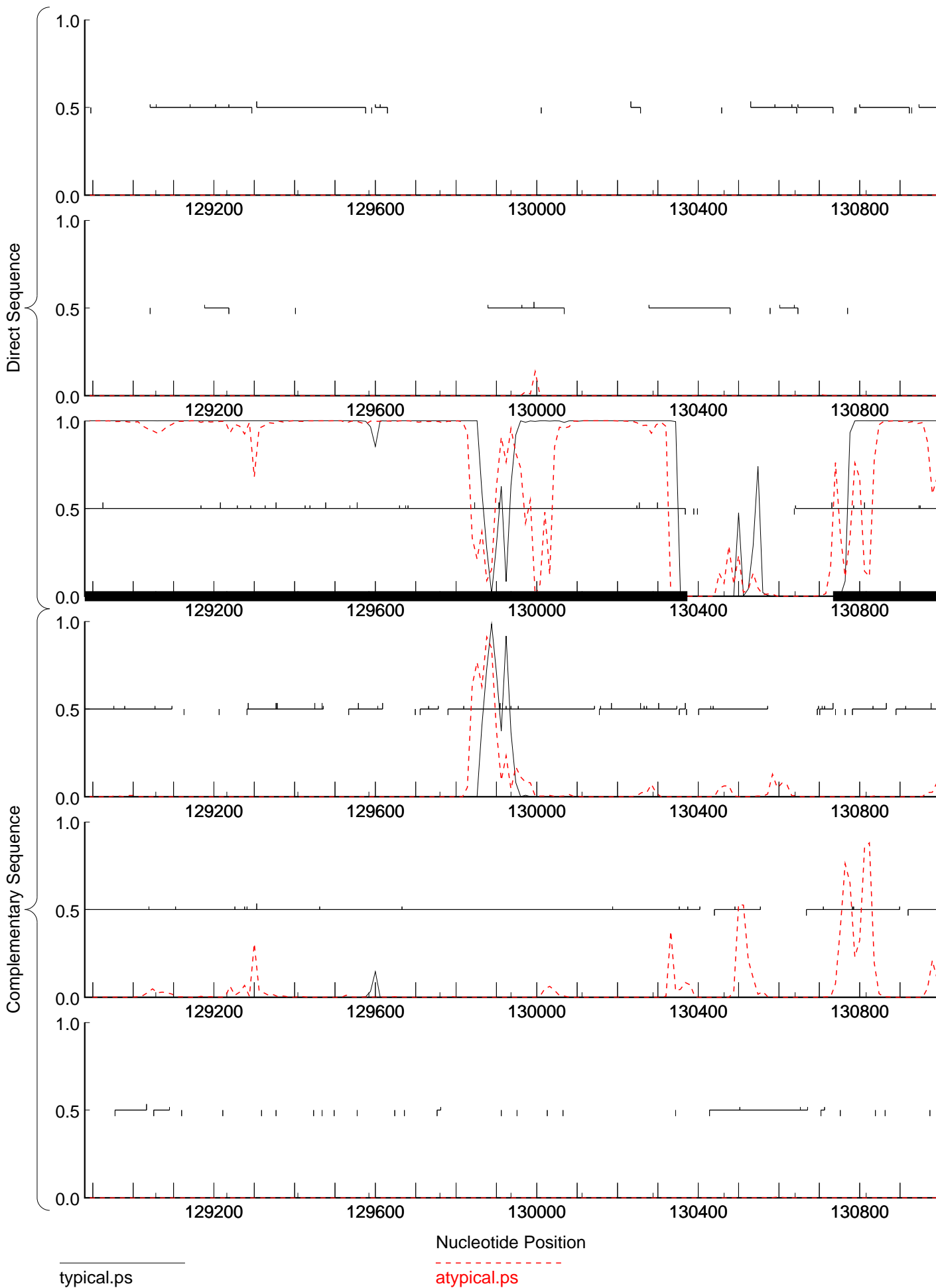
atypical.ps

GeneMark.hmm prediction



typical.ps

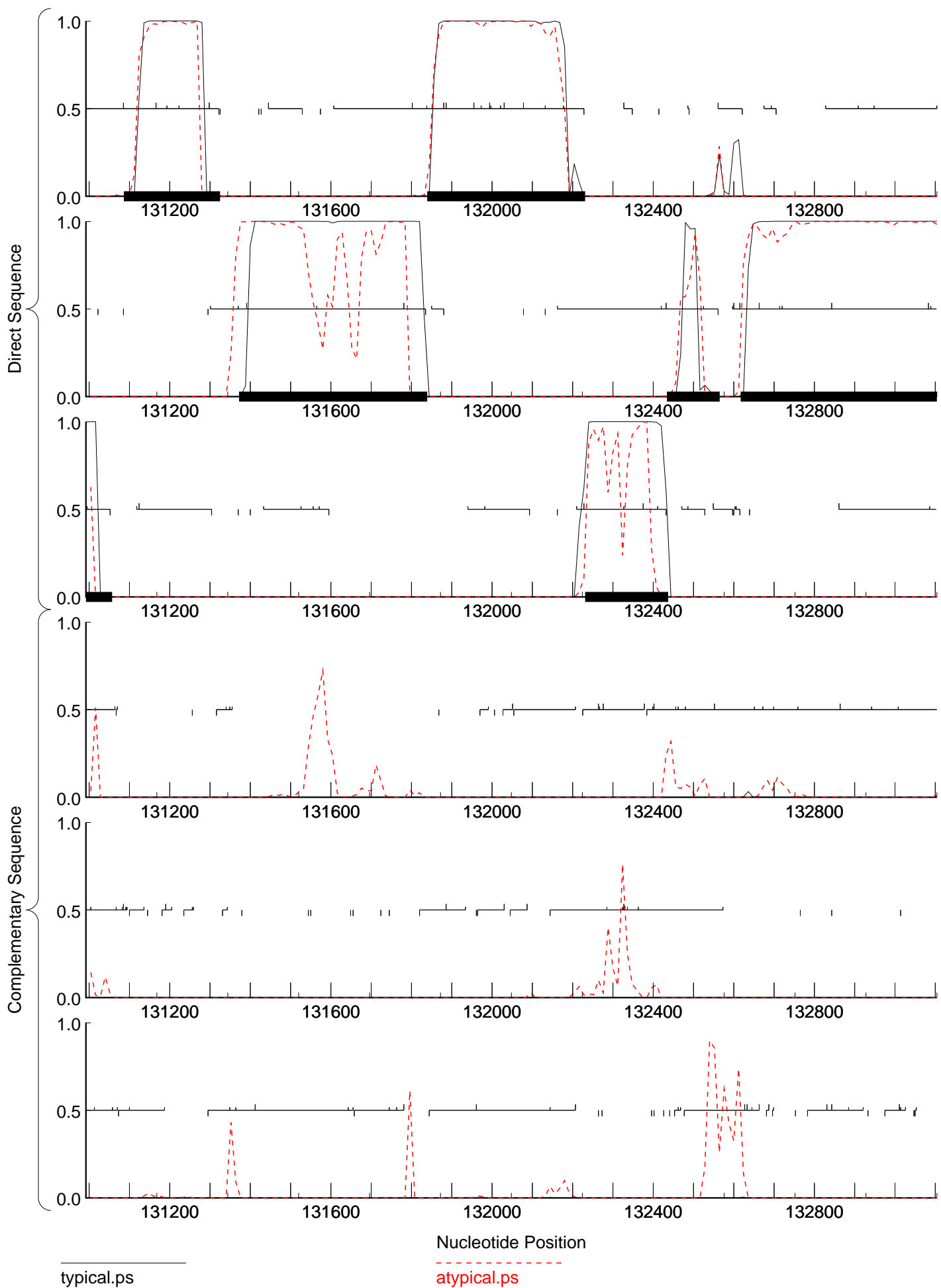
atypical.ps



typical.ps

atypical.ps

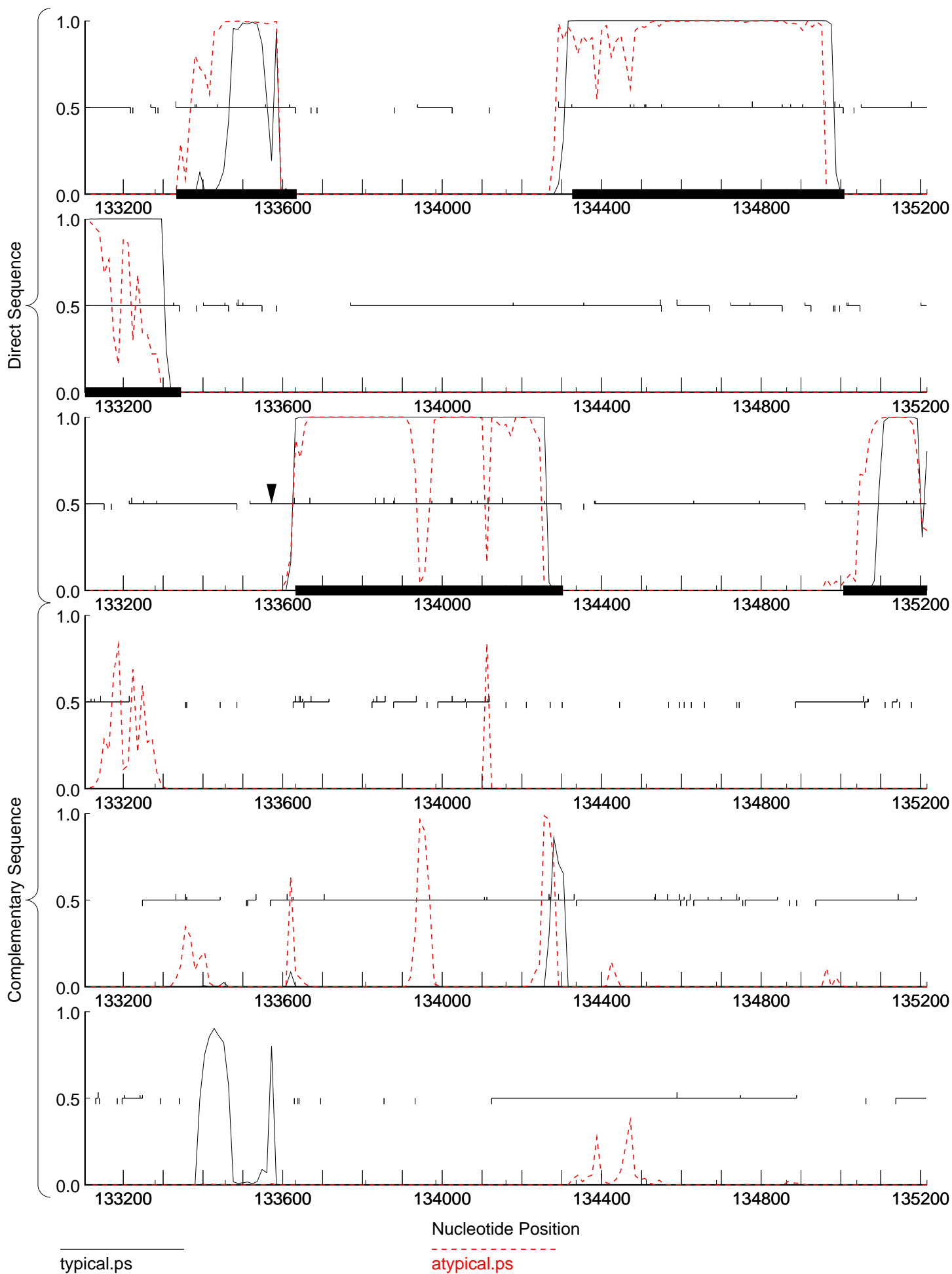
GeneMark.hmm prediction



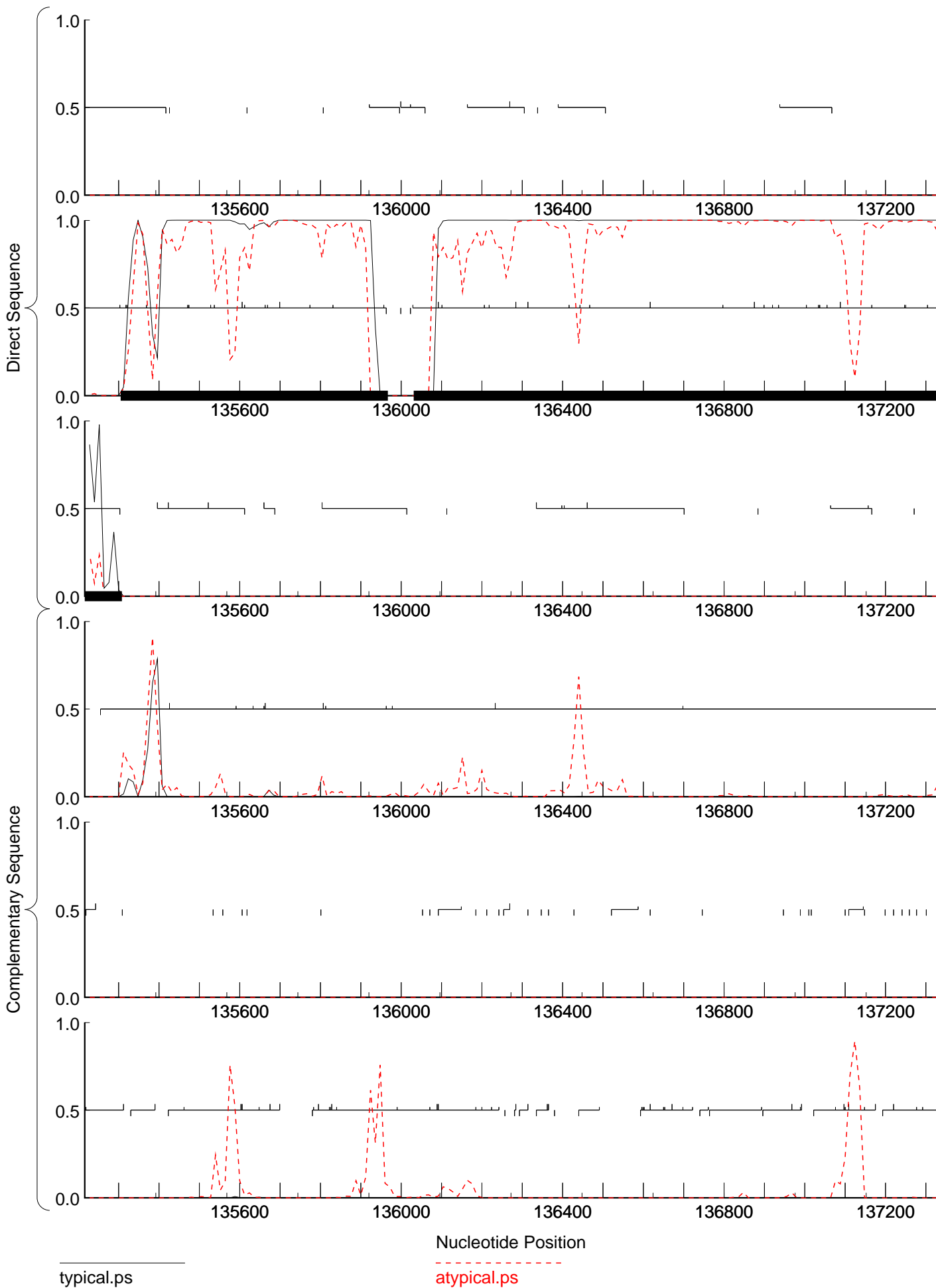
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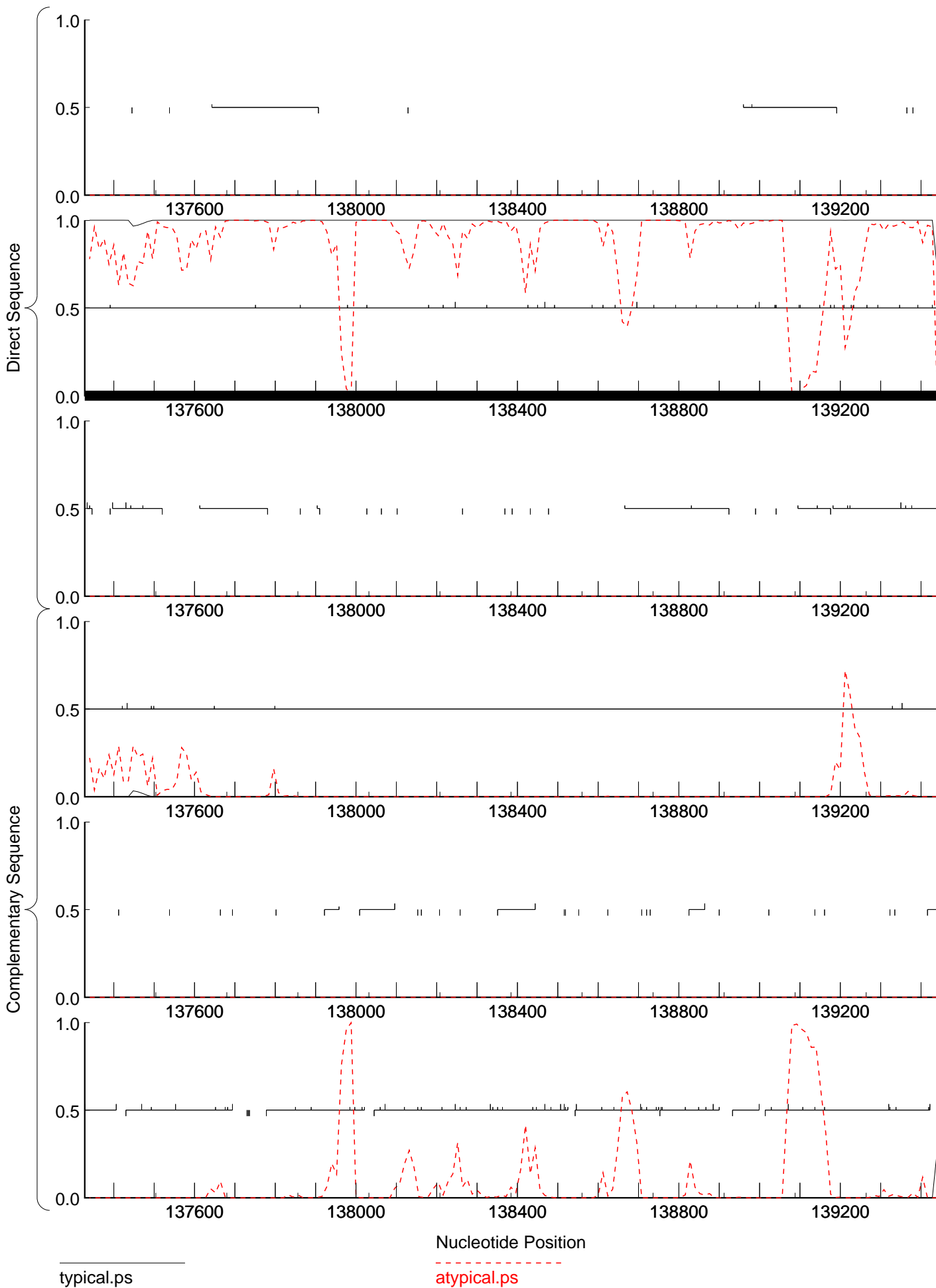
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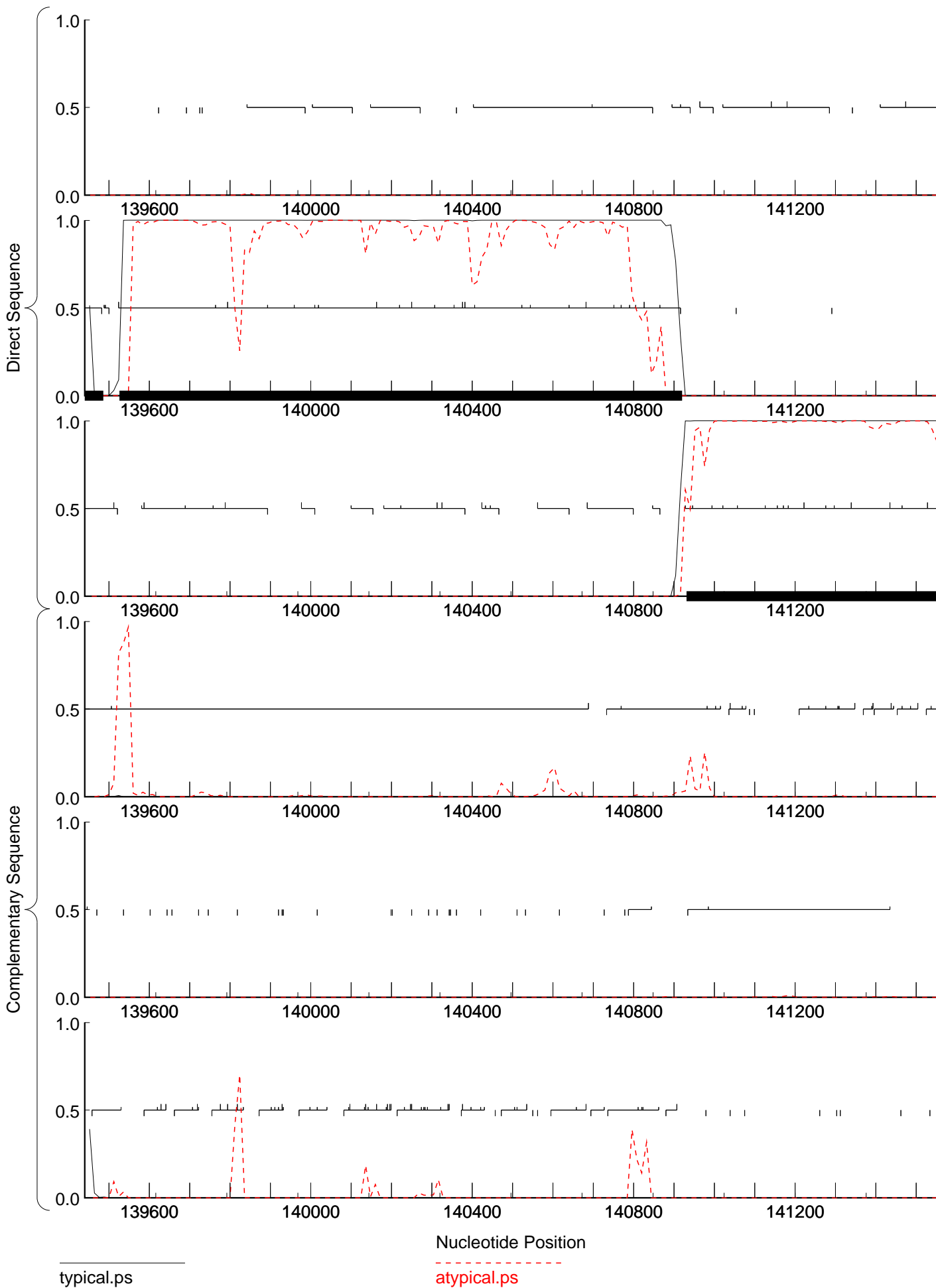
GeneMark.hmm prediction



GeneMark.hmm prediction



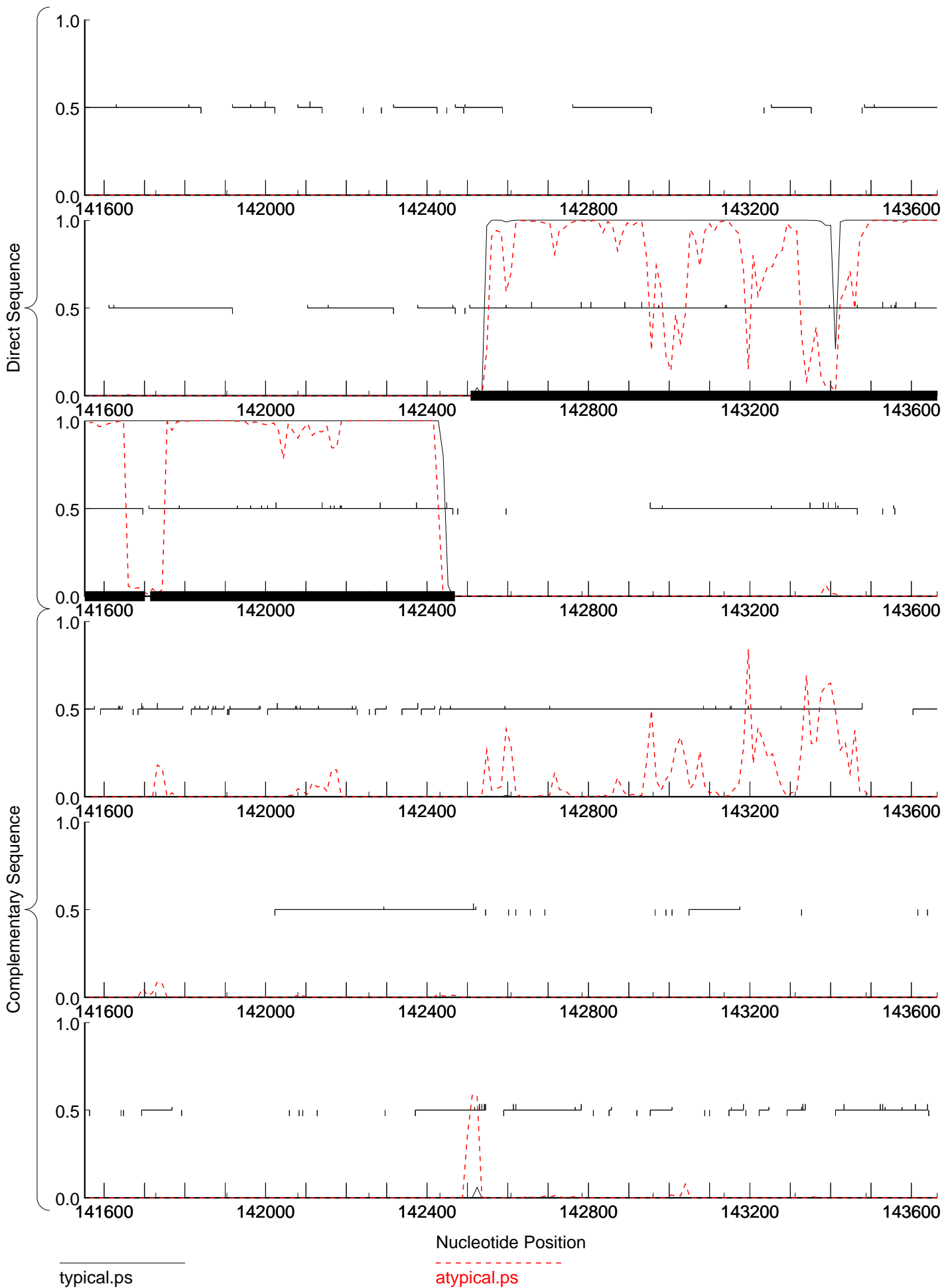




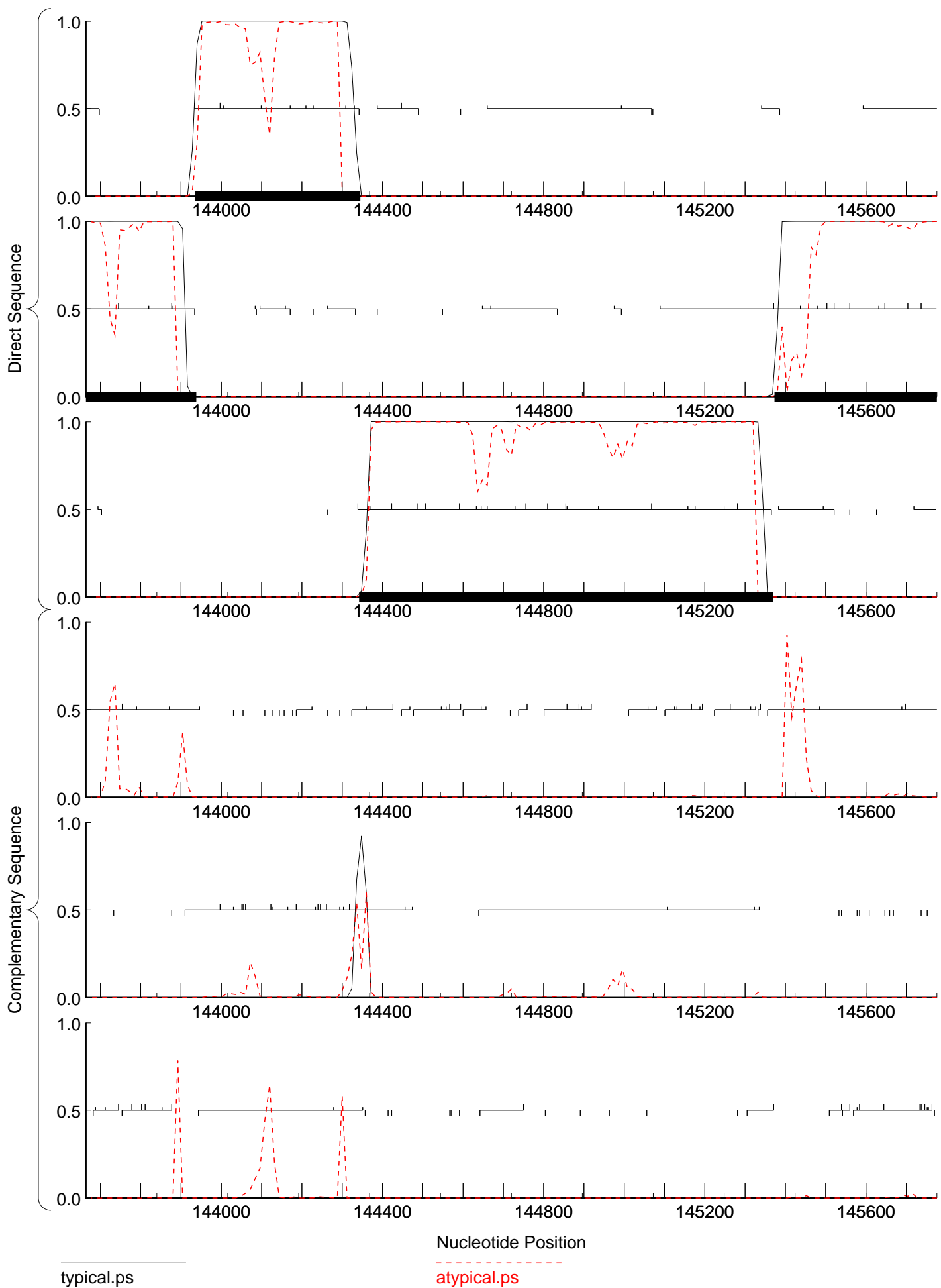
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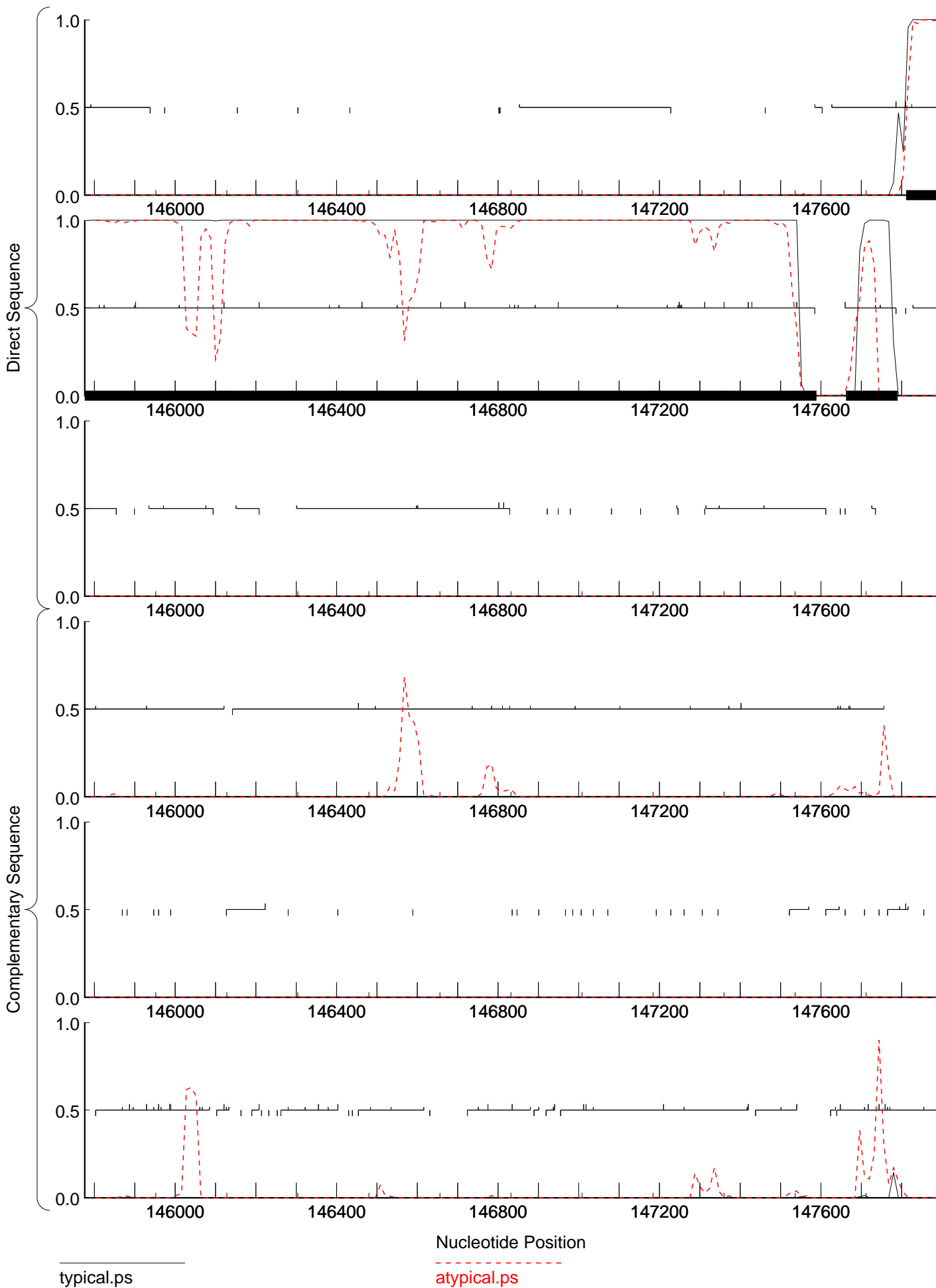
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GeneMark.hmm prediction

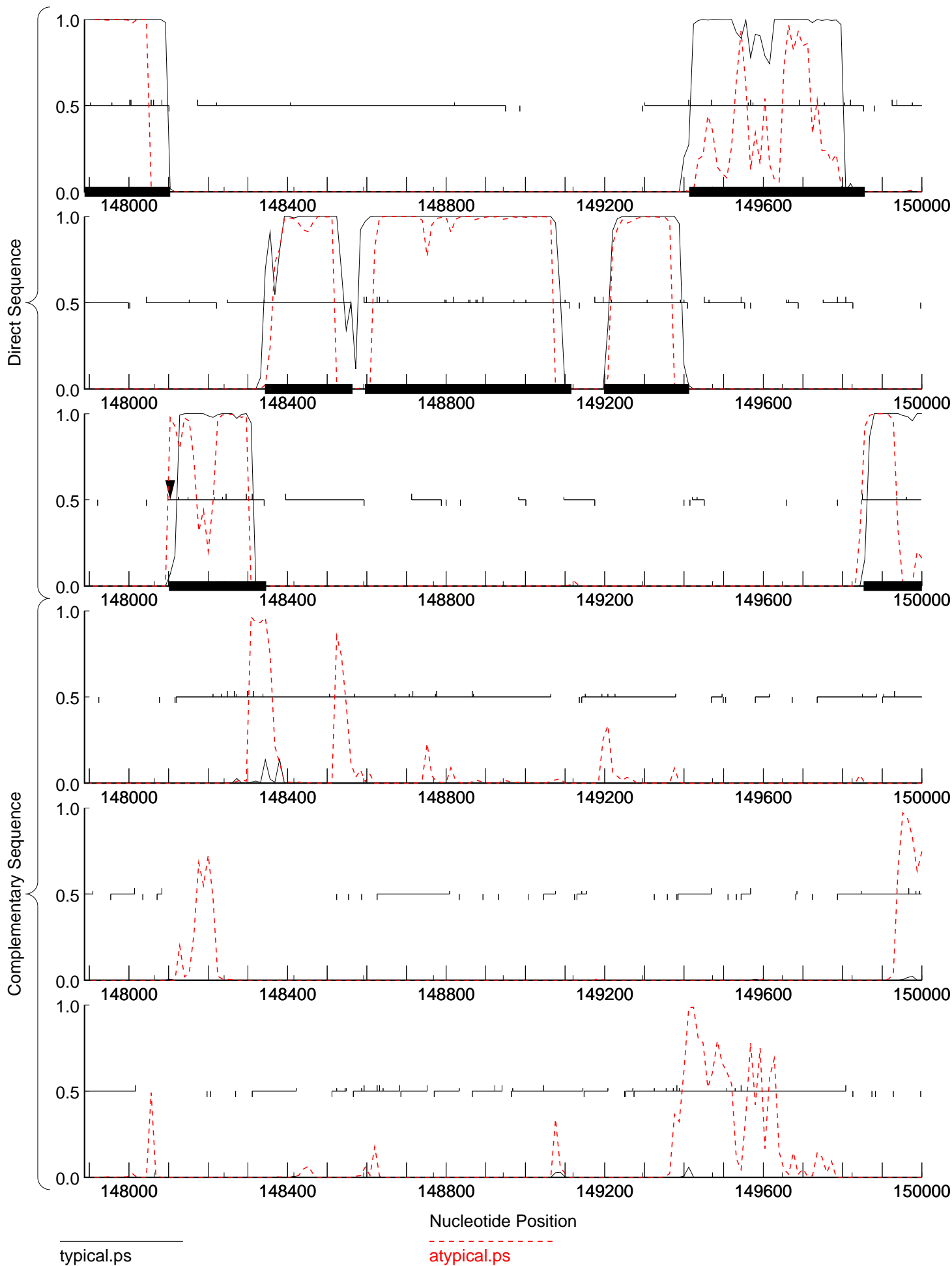


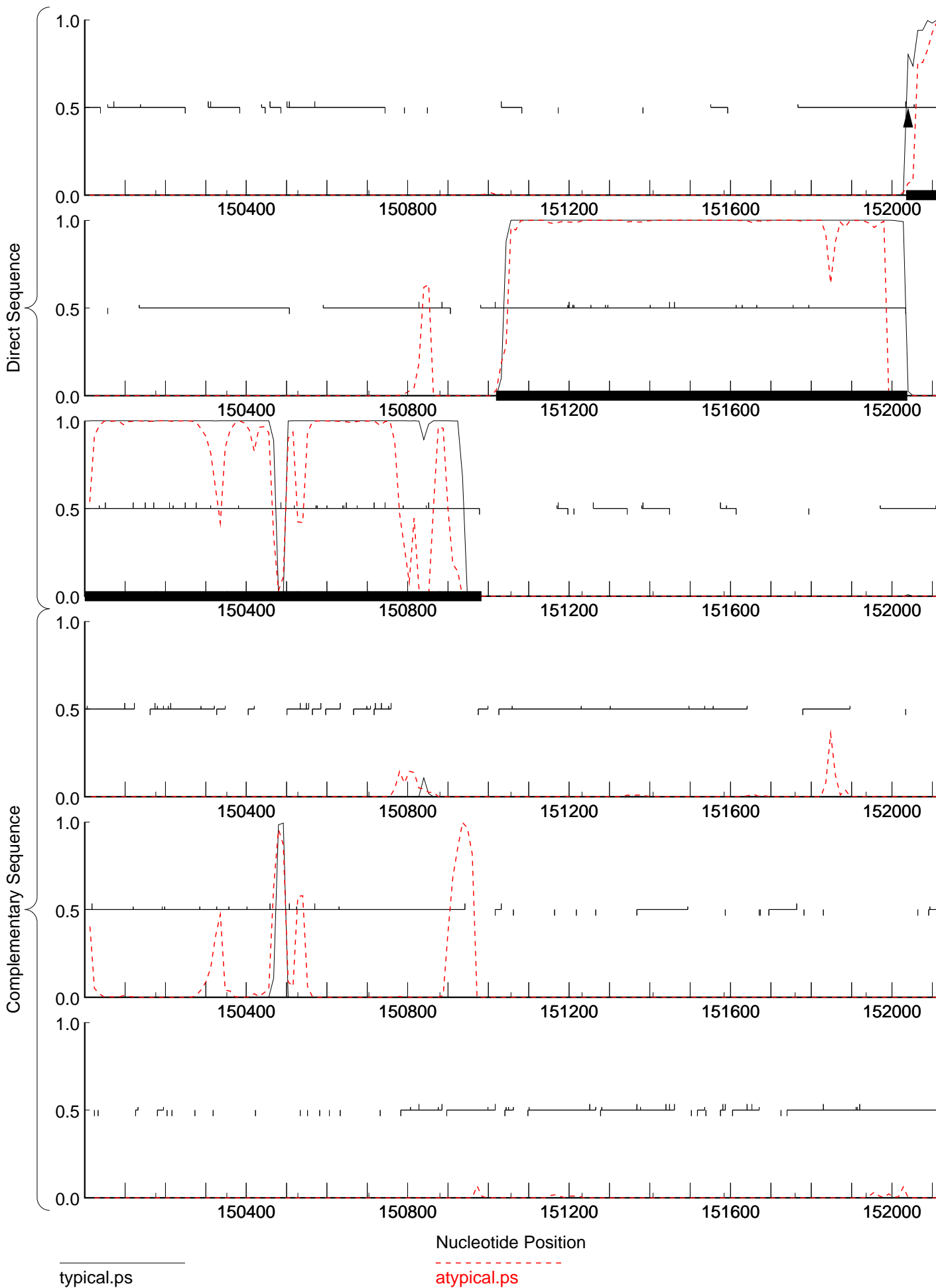
GeneMark.hmm prediction



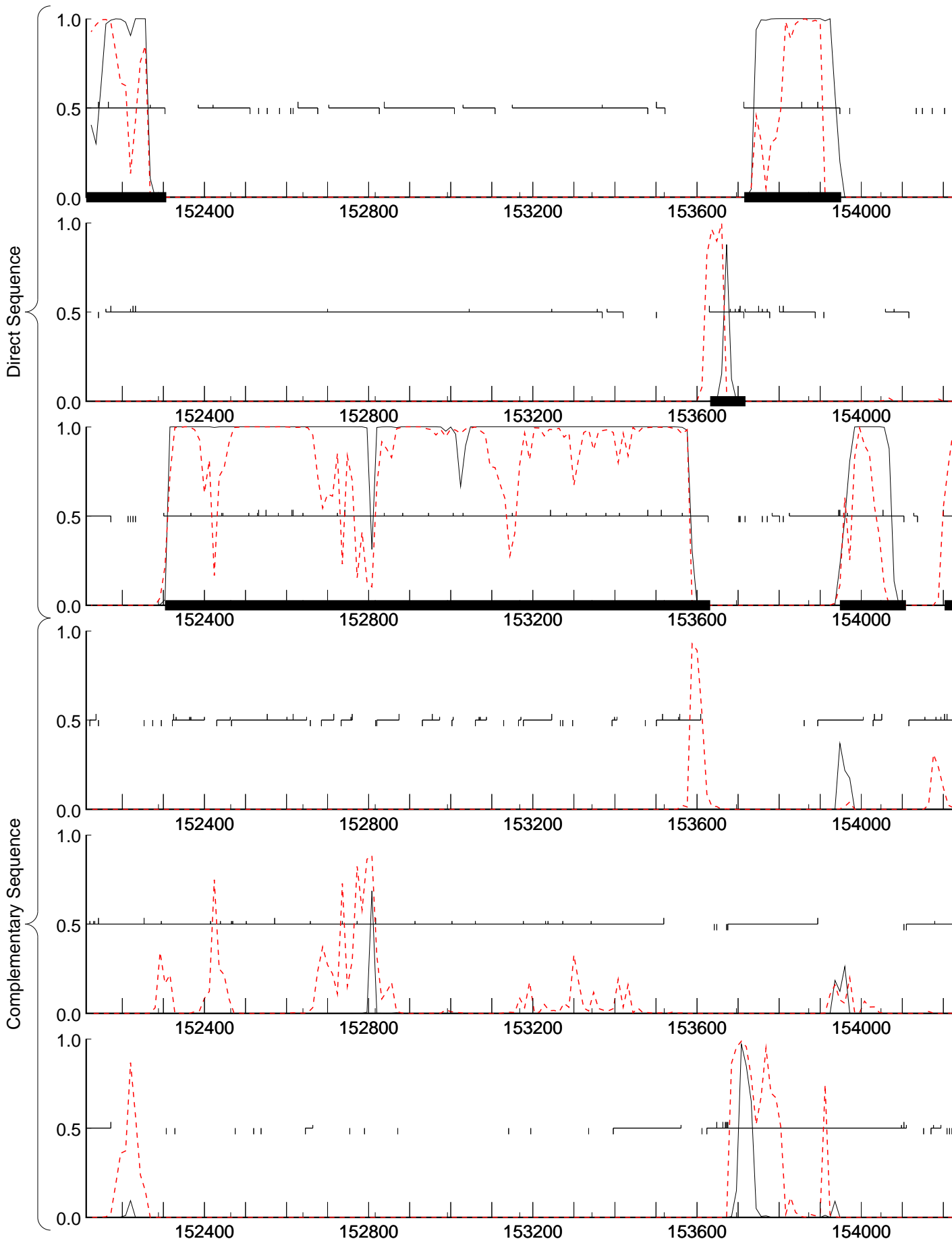


GeneMark.hmm prediction





GeneMark.hmm prediction



typical.ps

Nucleotide Position

atypical.ps

GeneMark.hmm prediction

