

GeneMark

Version 2.5p (09.08.06)

Copyright 1993 - M. Borodovsky, J. McIninch

PROGRAM INFORMATION

Sequence : Mycobacterium phage Roots515 complete sequence, 156288 bp, circularly permuted, Cluster C1
Analysis Date : 8/24/17 at 0:51:36
Pages : 75
Sequence Length : 156288 bp
GC Content : 64.70%

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,

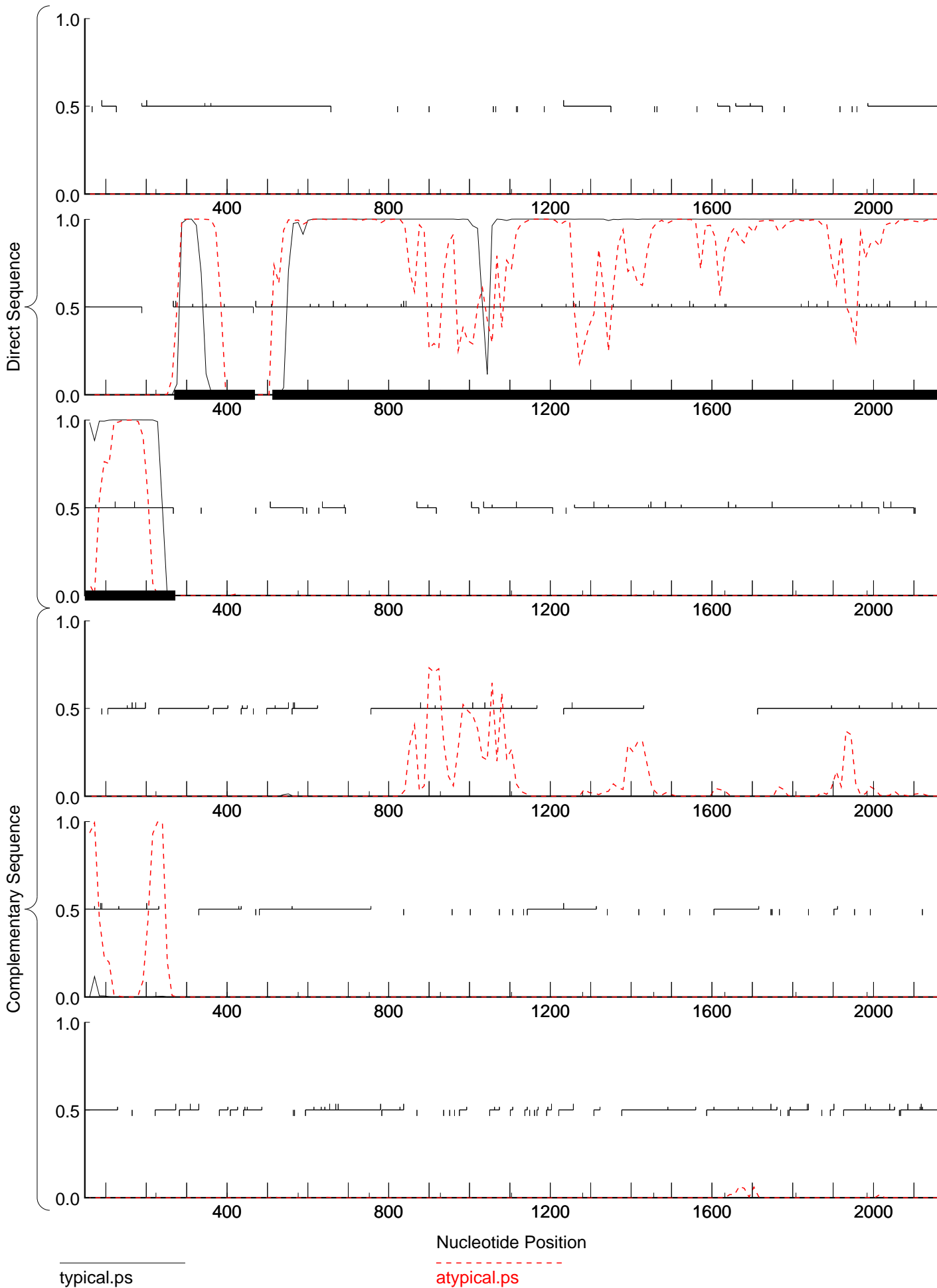
Matrix notes & comments

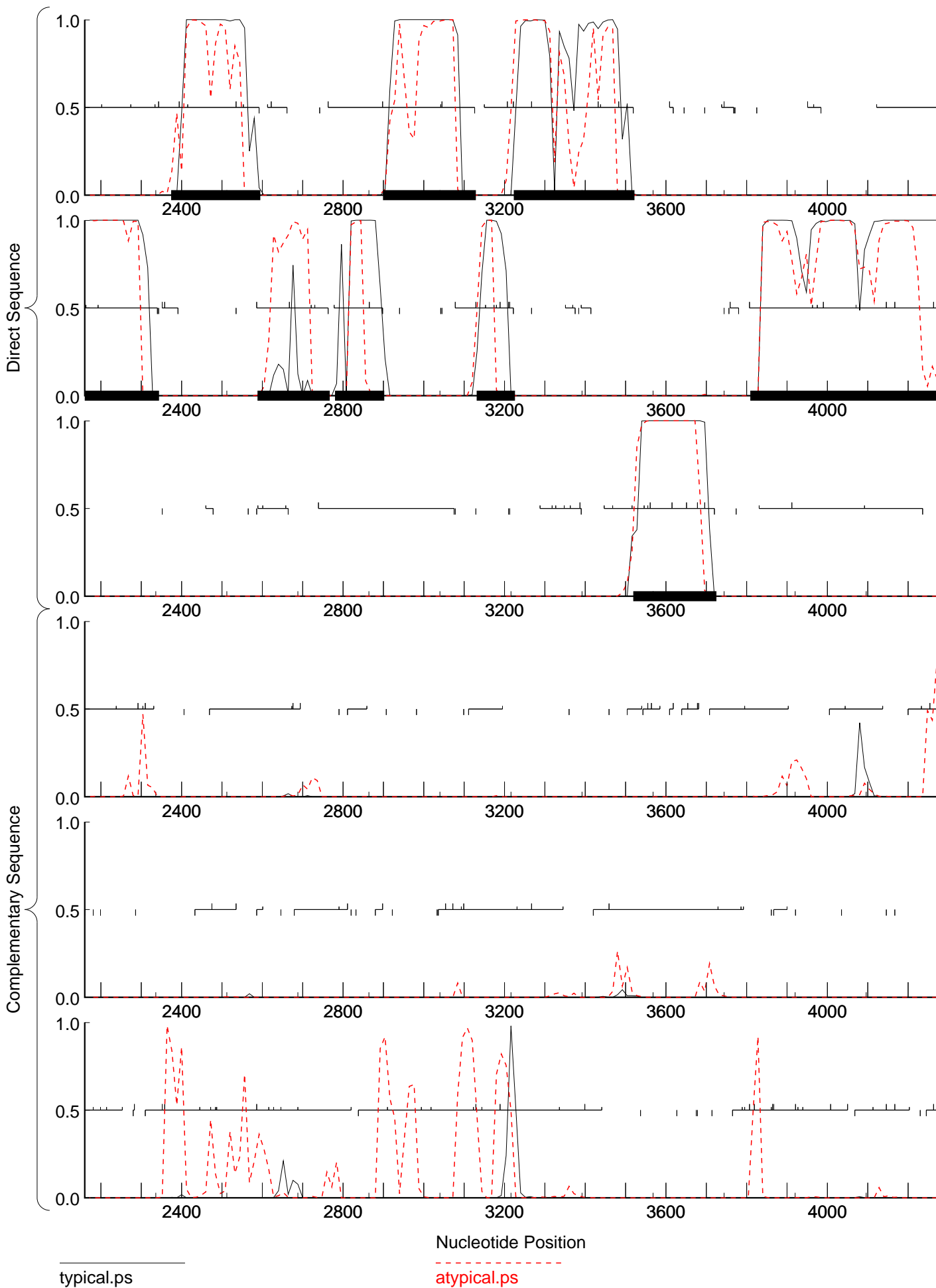
Training set derived by GeneMarkS, 4.30 October 2014
Thu Aug 24 00:51:36 2017

MATRIX INFORMATION

Matrix : -
Author : -
Order : 4

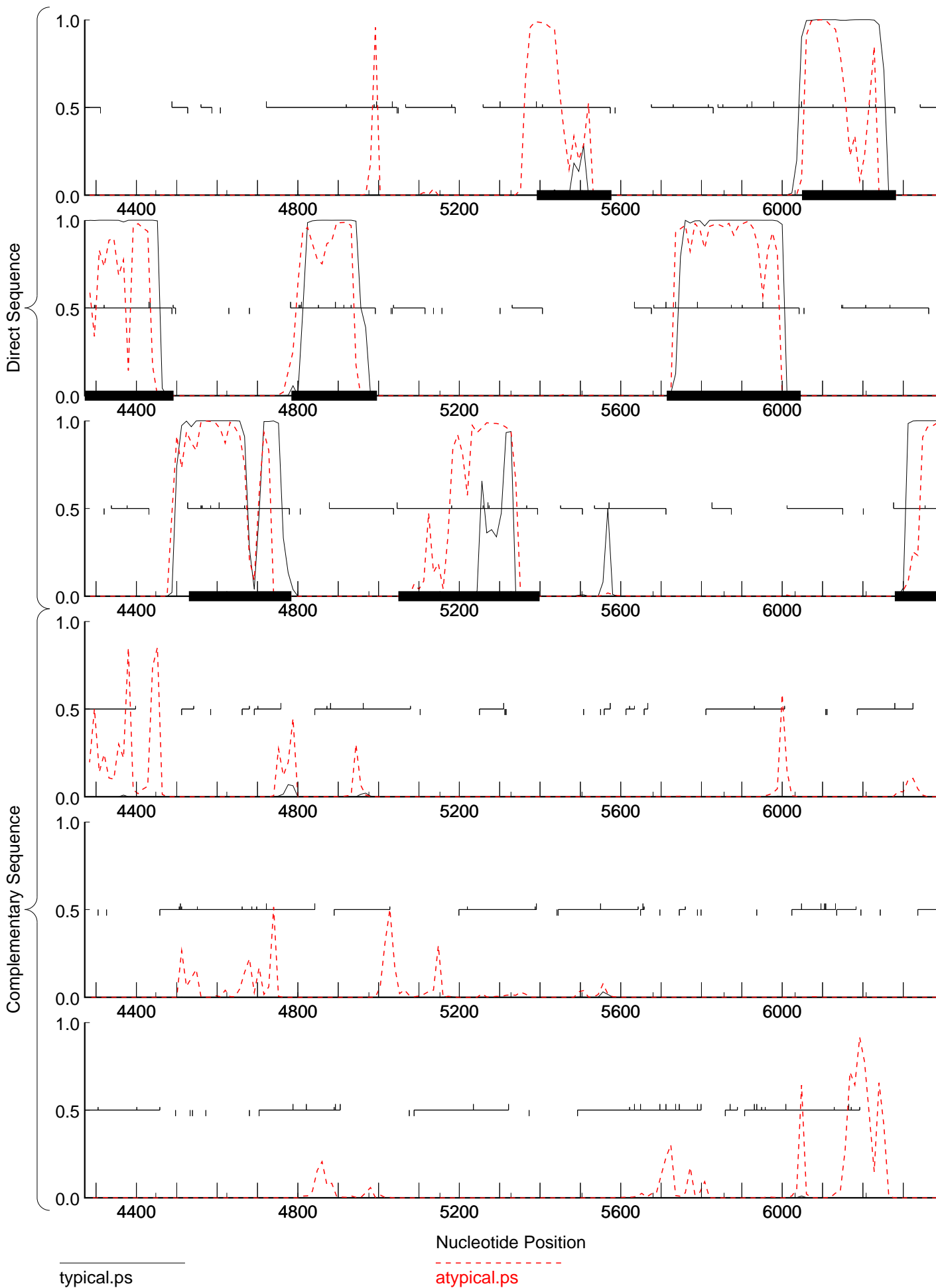
Send questions / comments to:
Dr. M. Borodovsky
Georgia Institute of Technology
School of Biology
Atlanta, GA 30332-0230

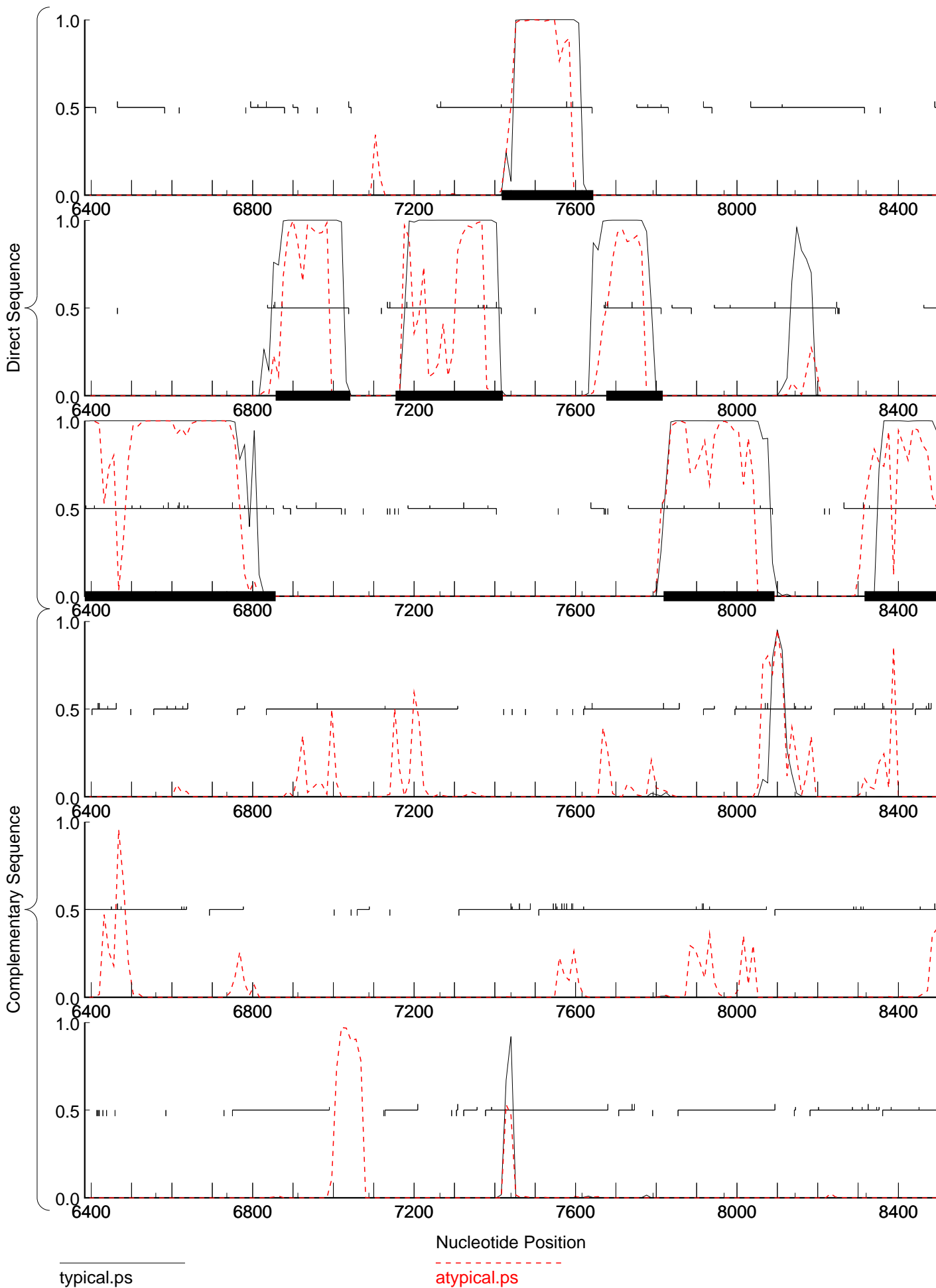


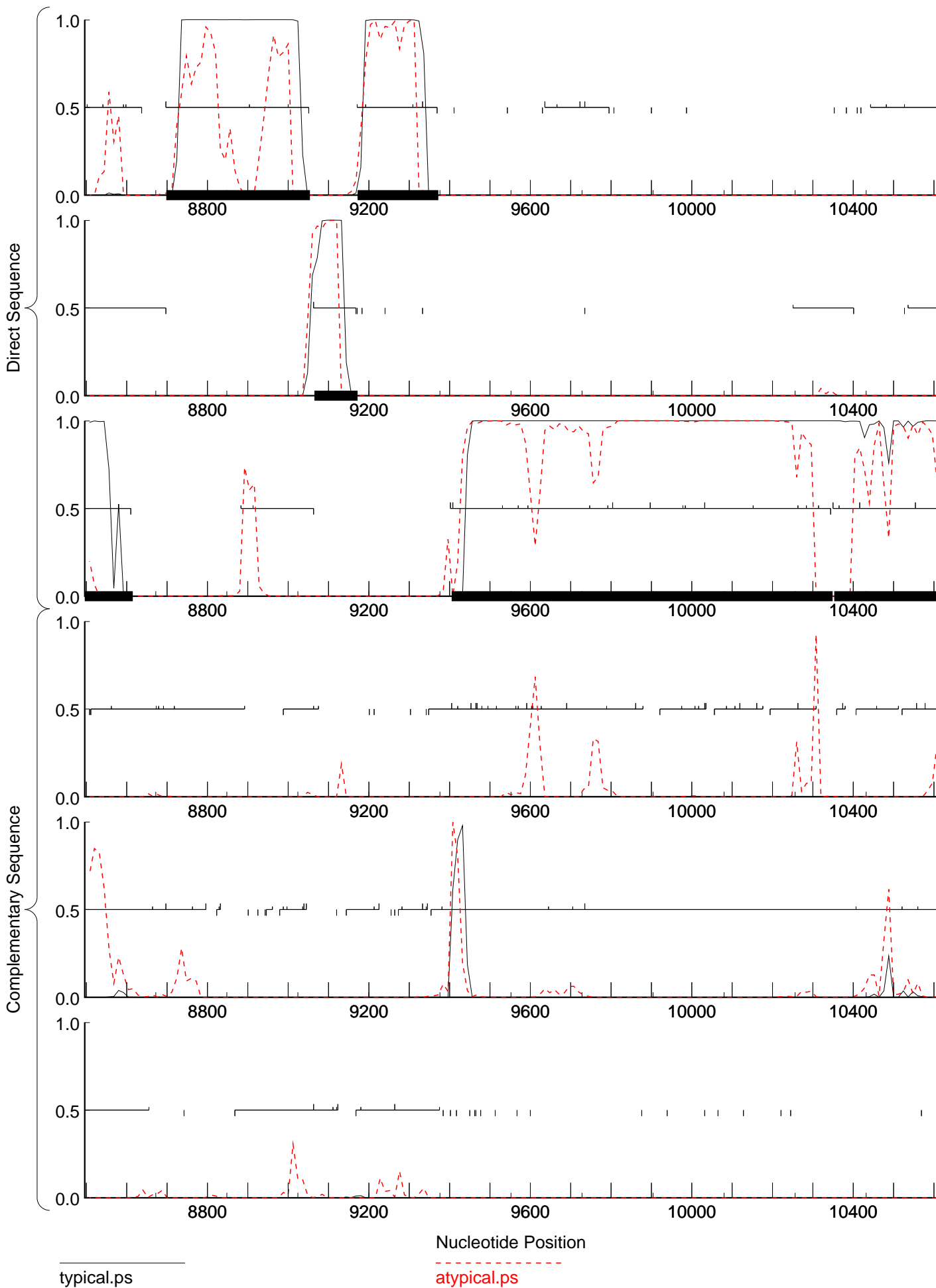


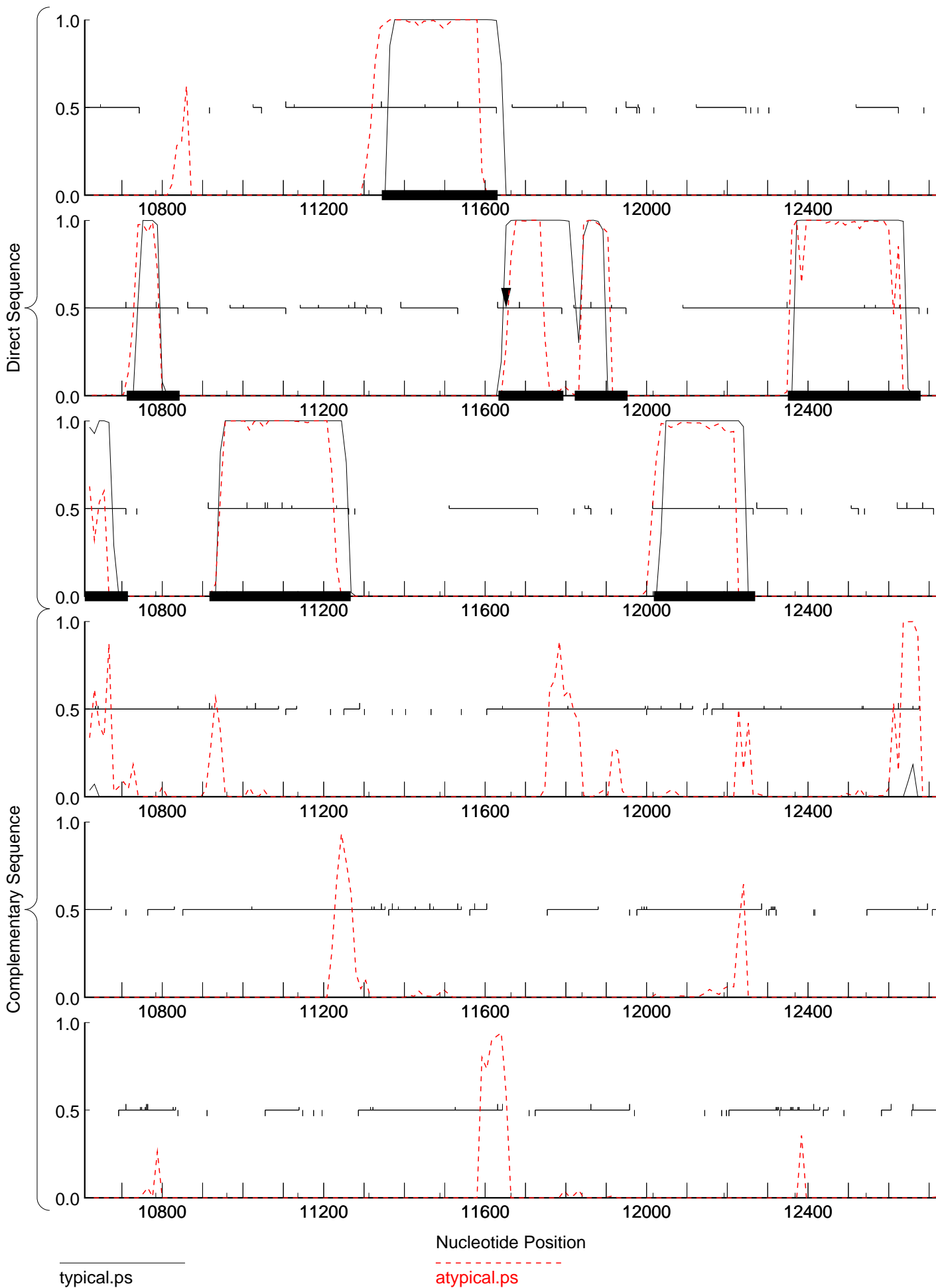
typical.ps

atypical.ps



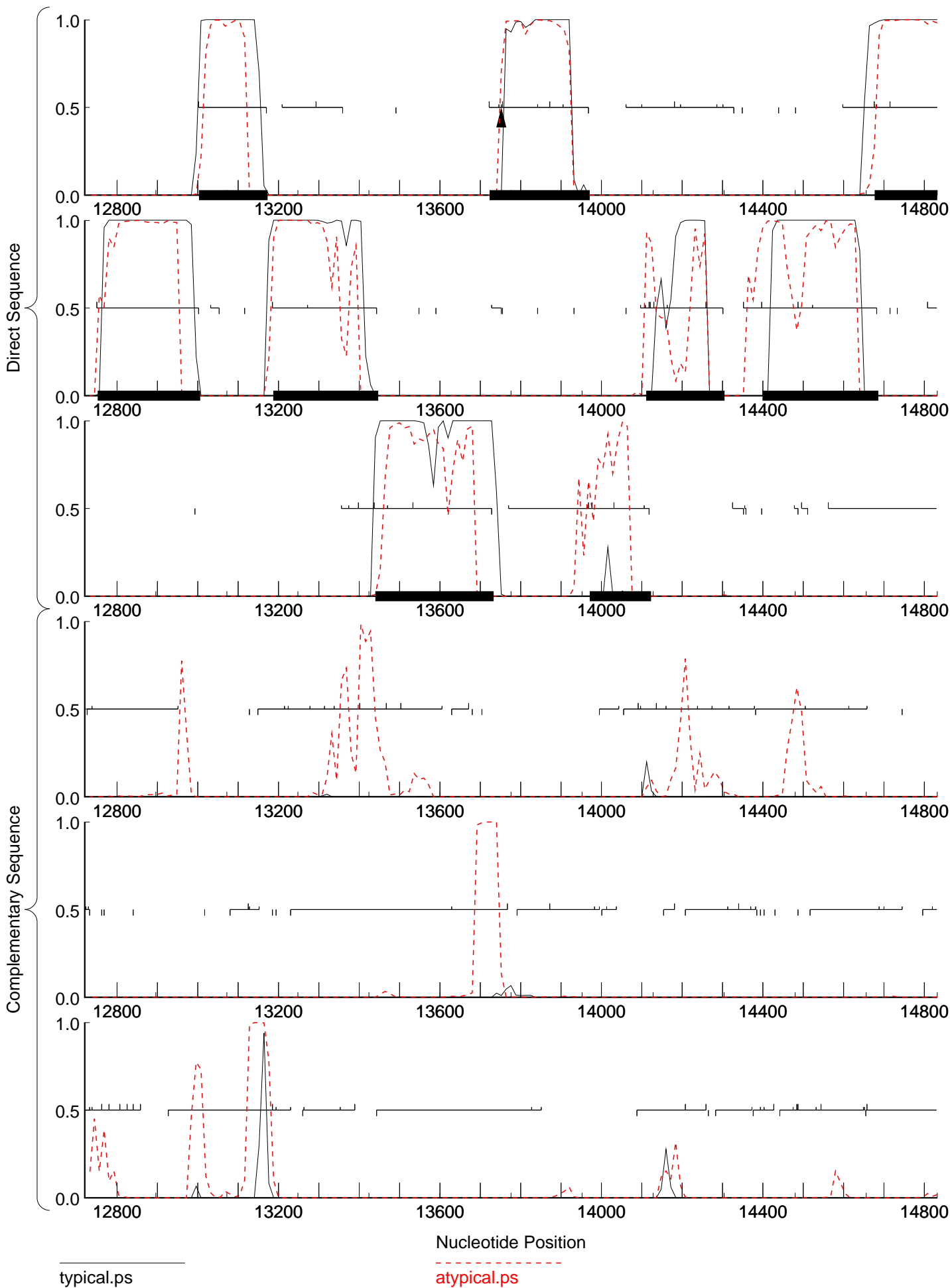


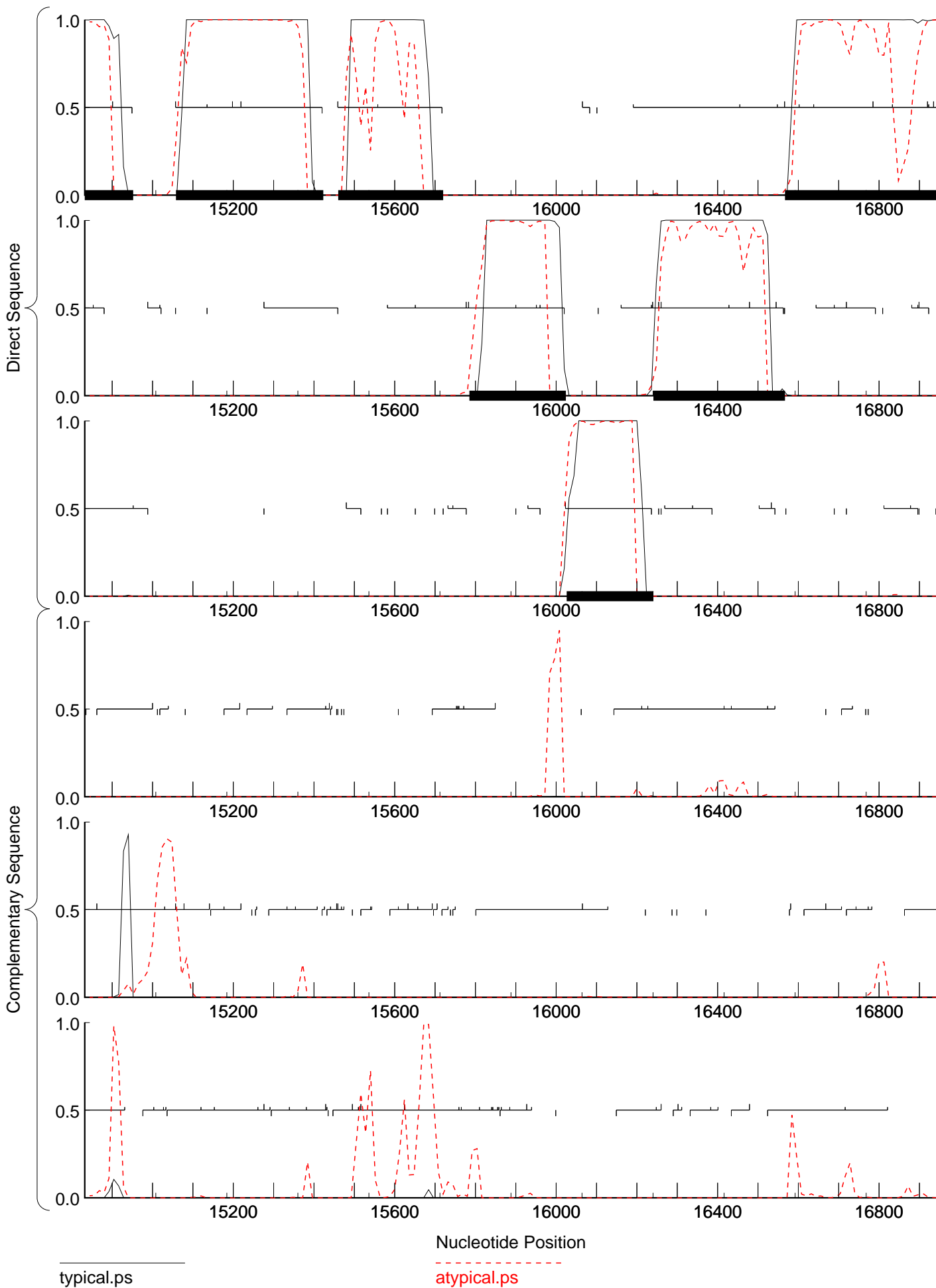




typical.ps

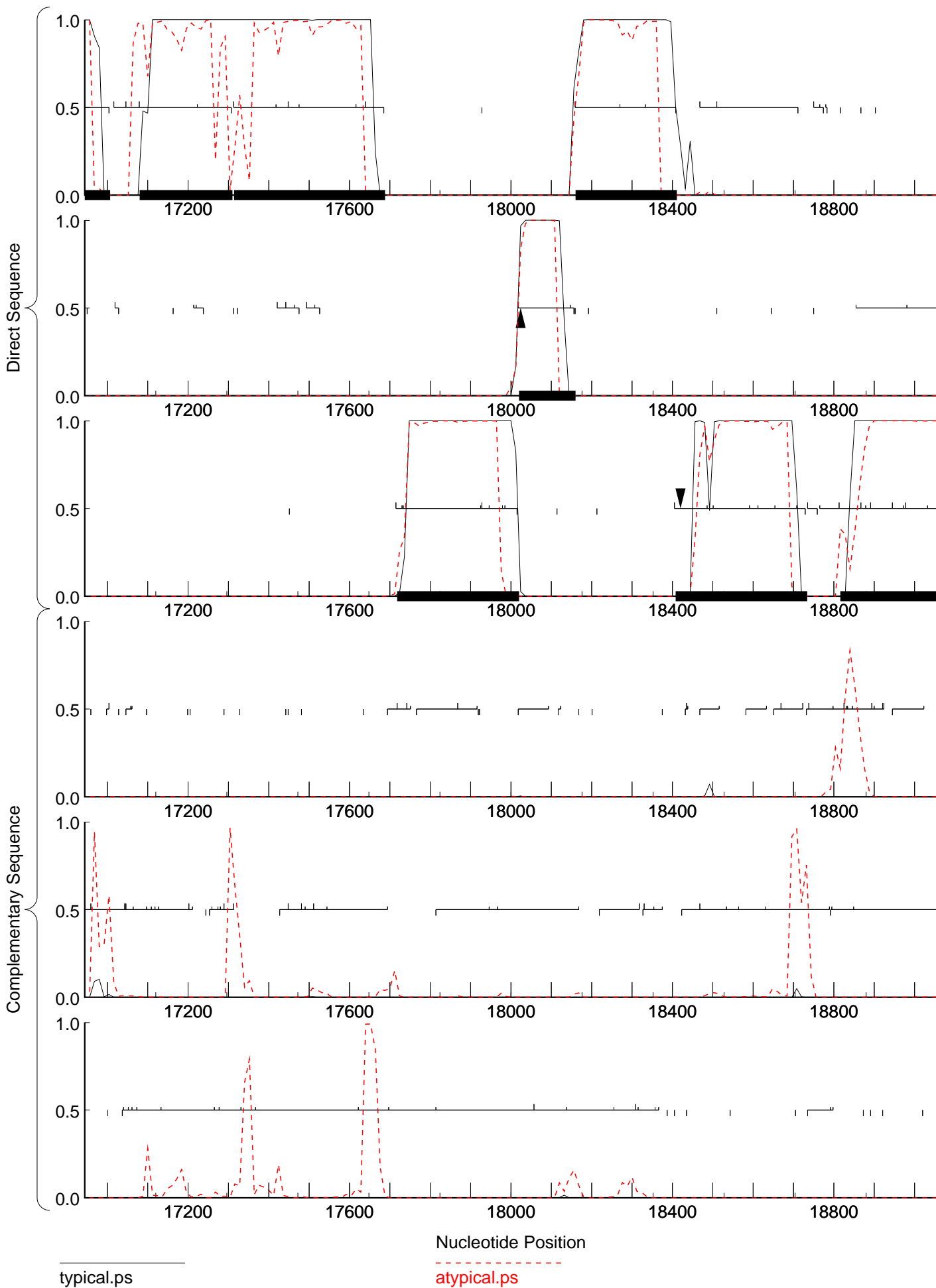
atypical.ps

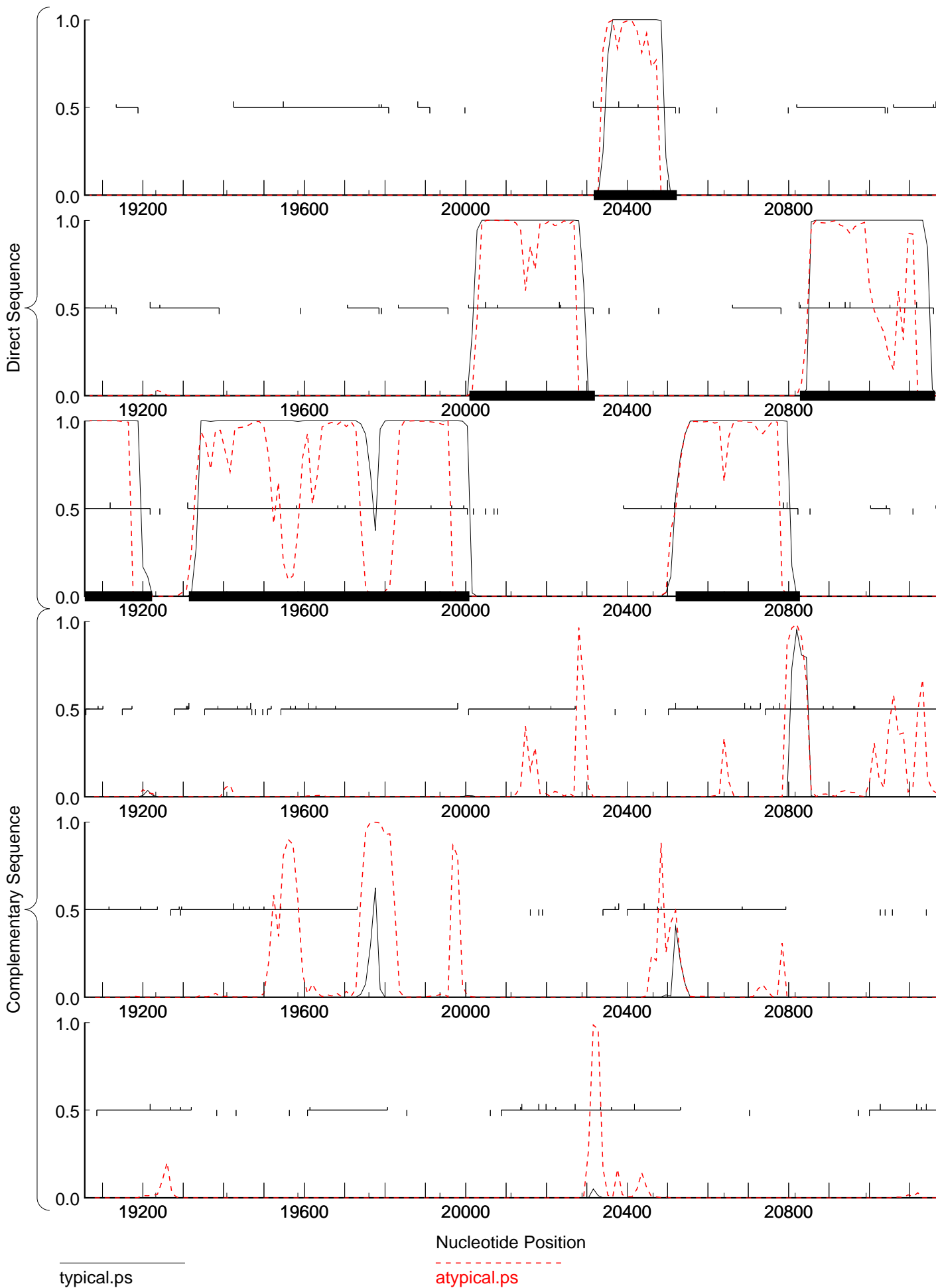




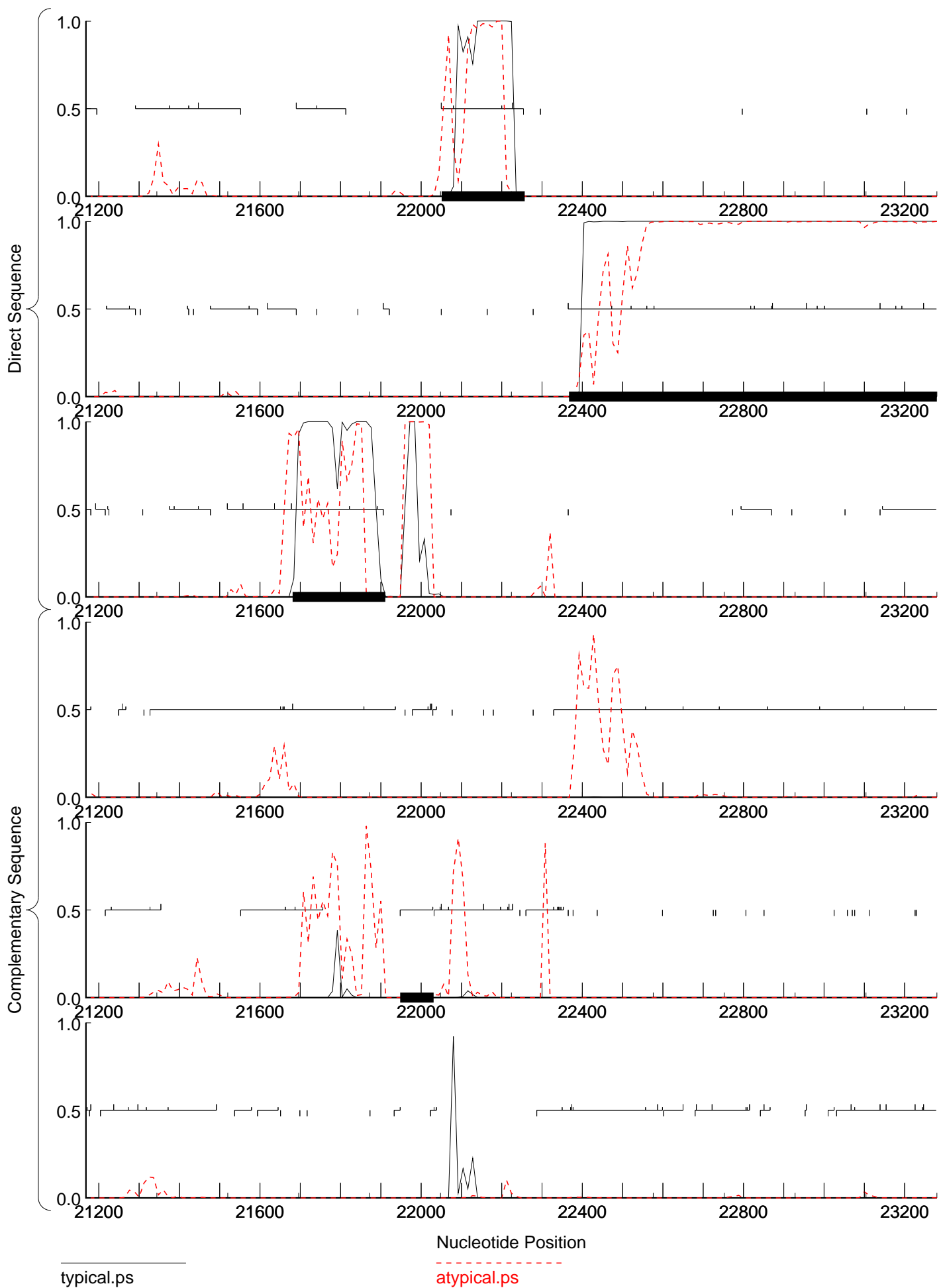
typical.ps

atypical.ps



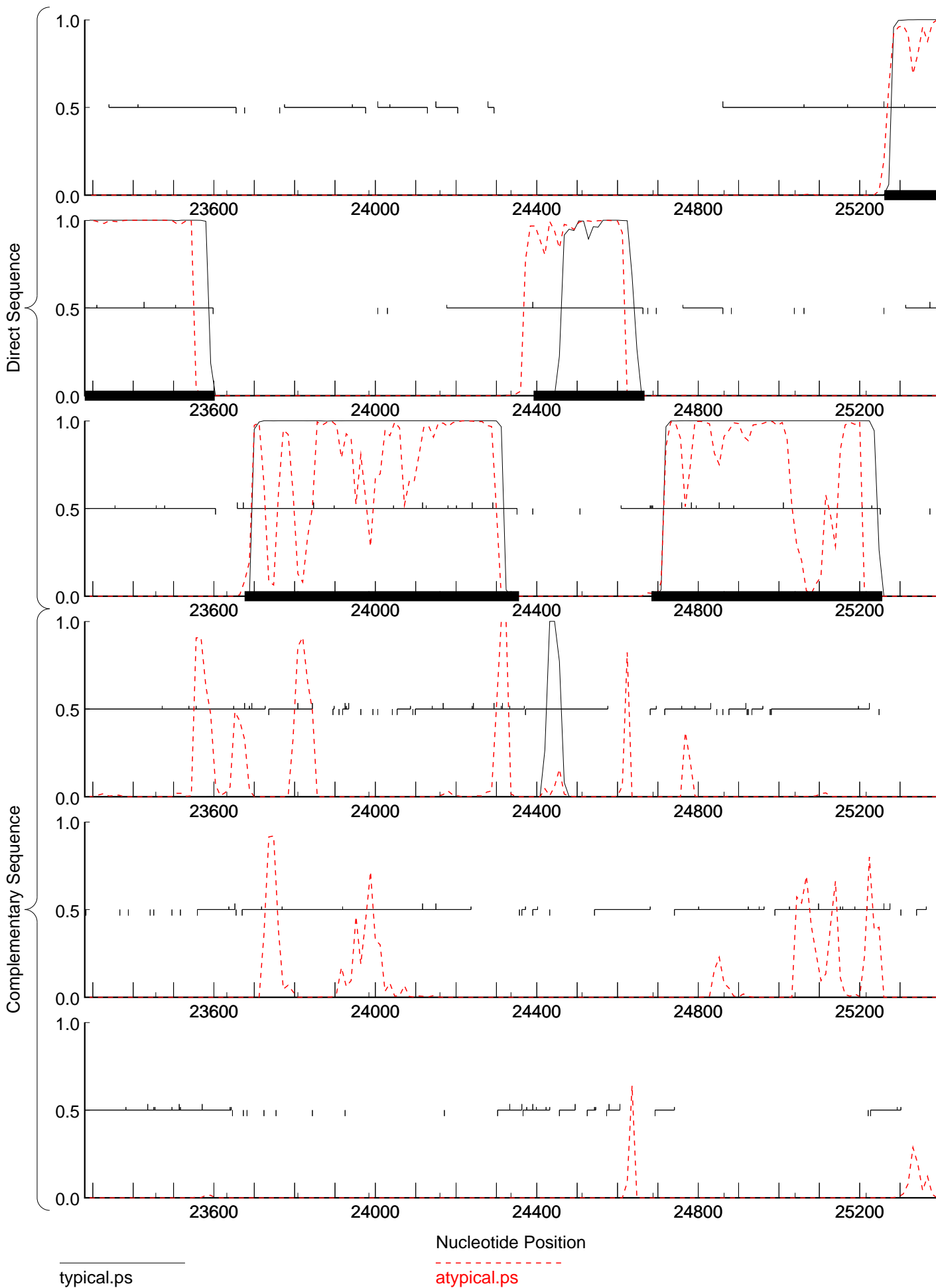


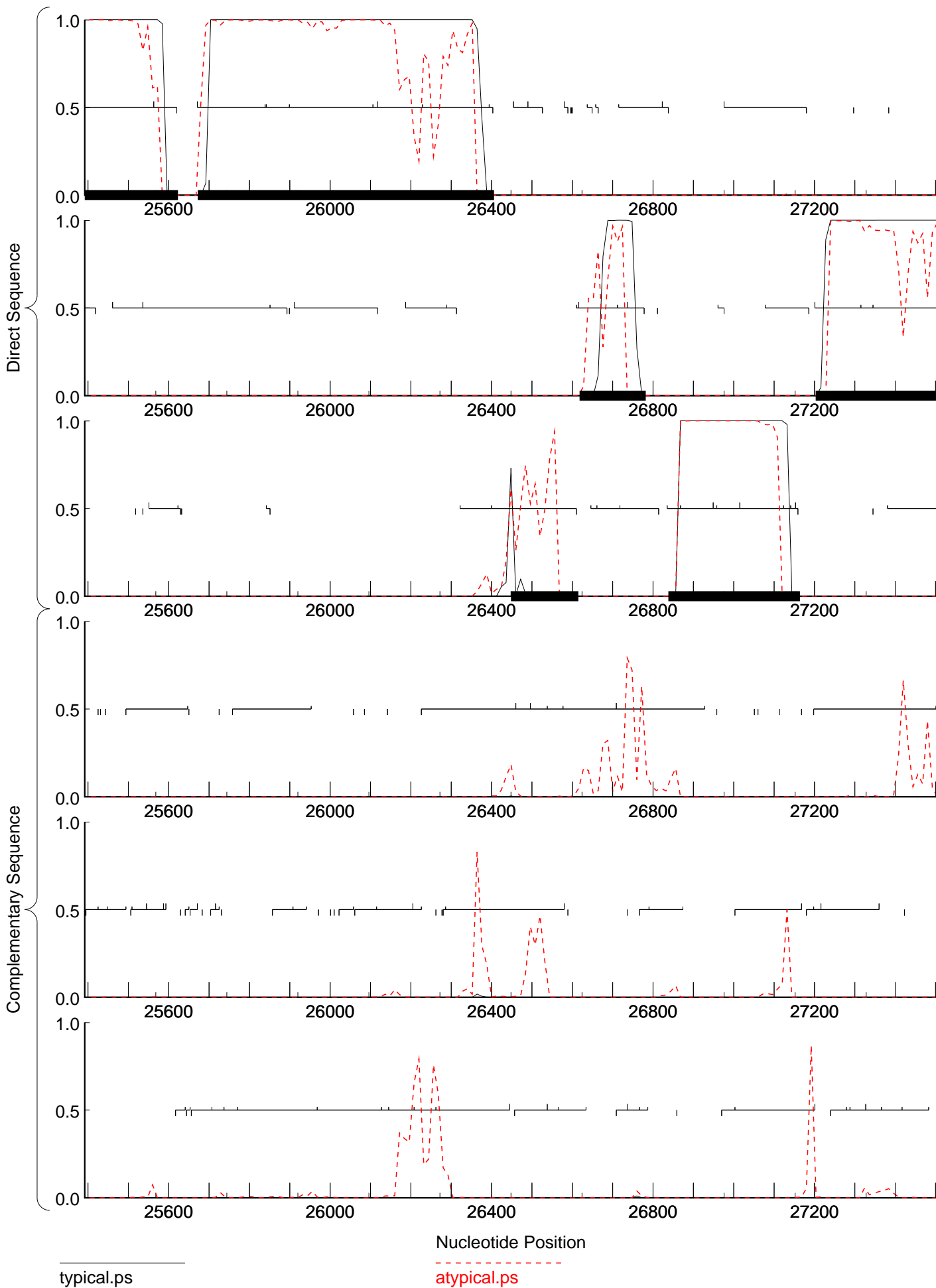
GeneMark.hmm prediction



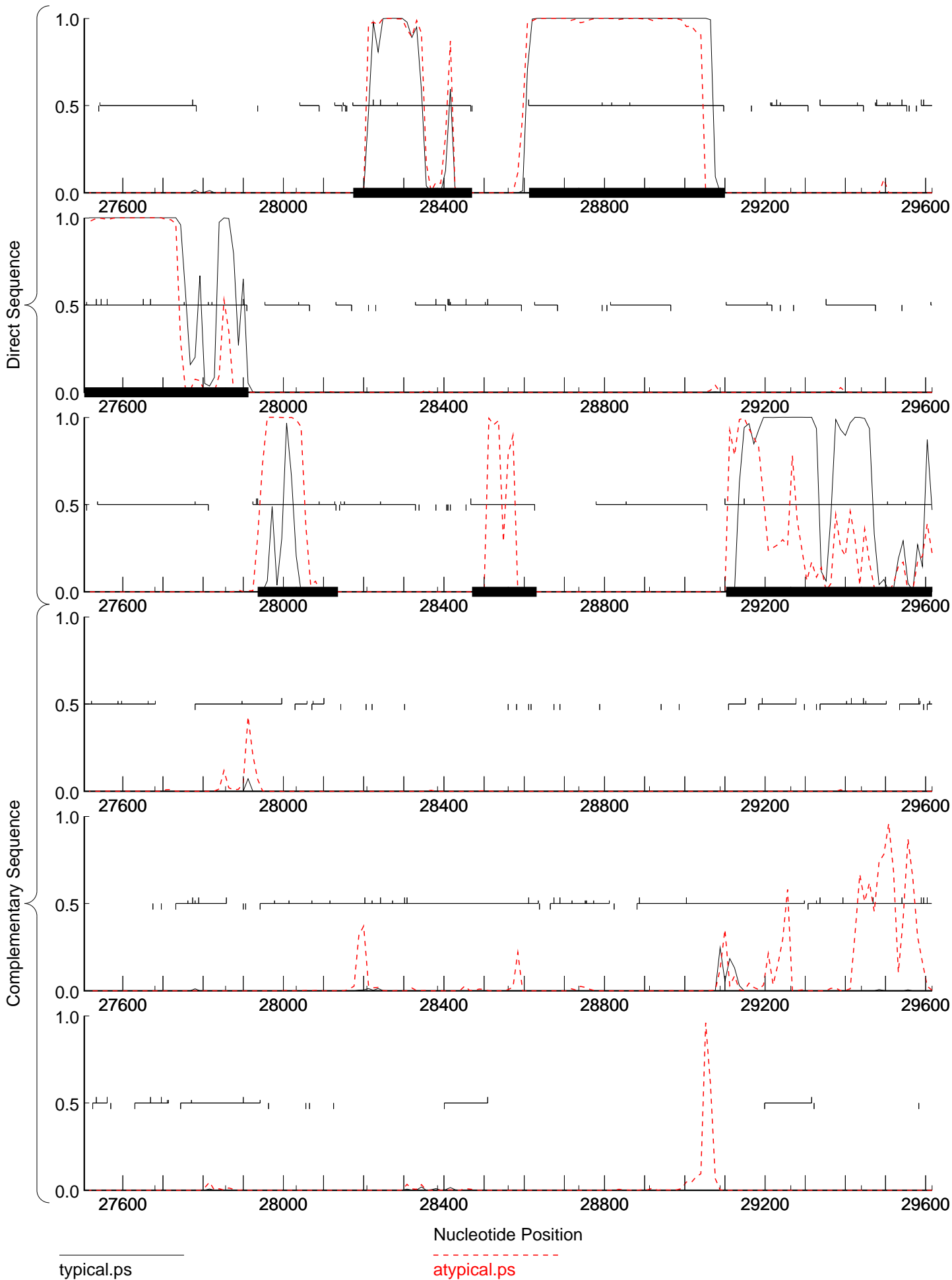
typical.ps

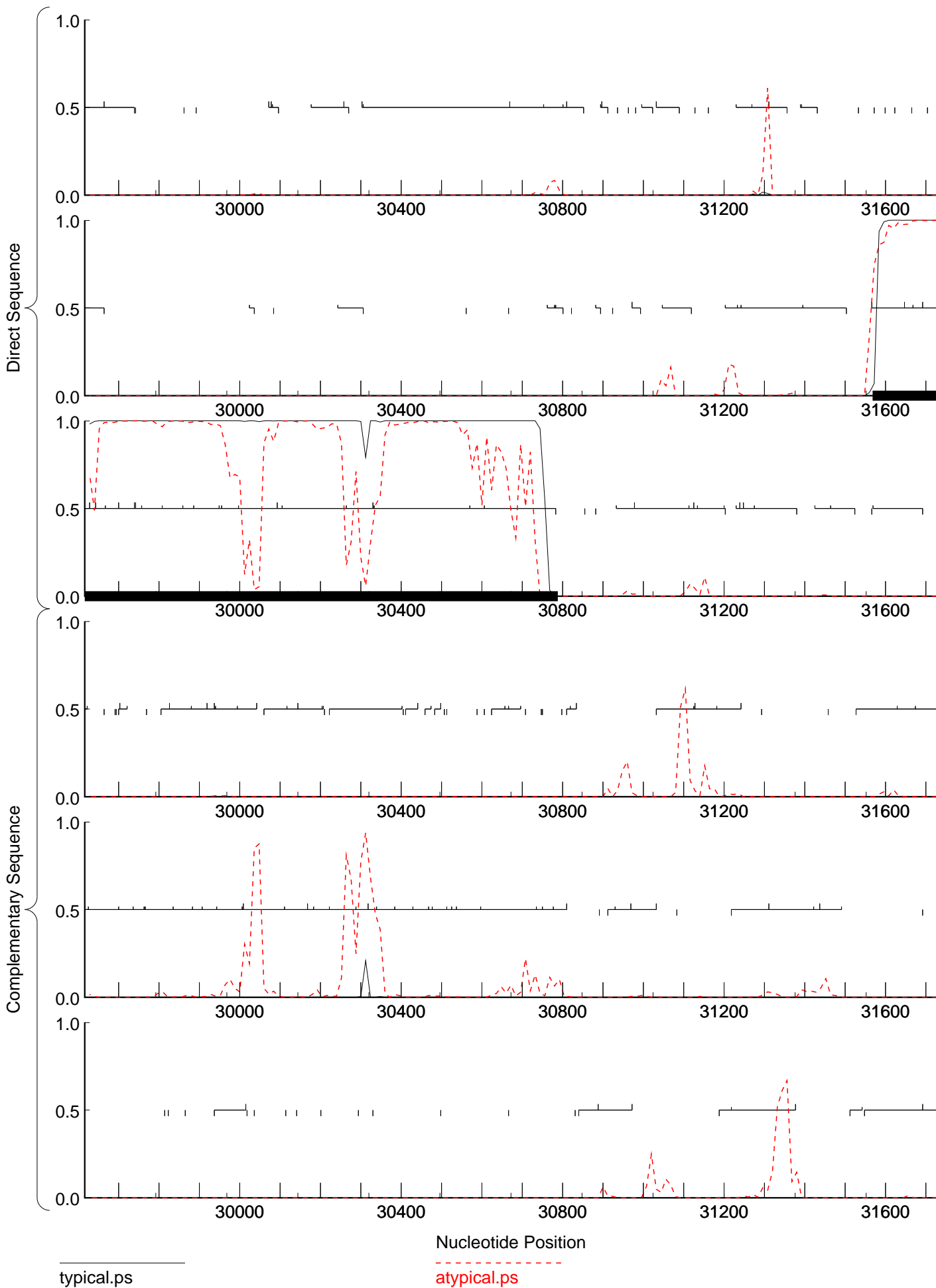
atypical.ps

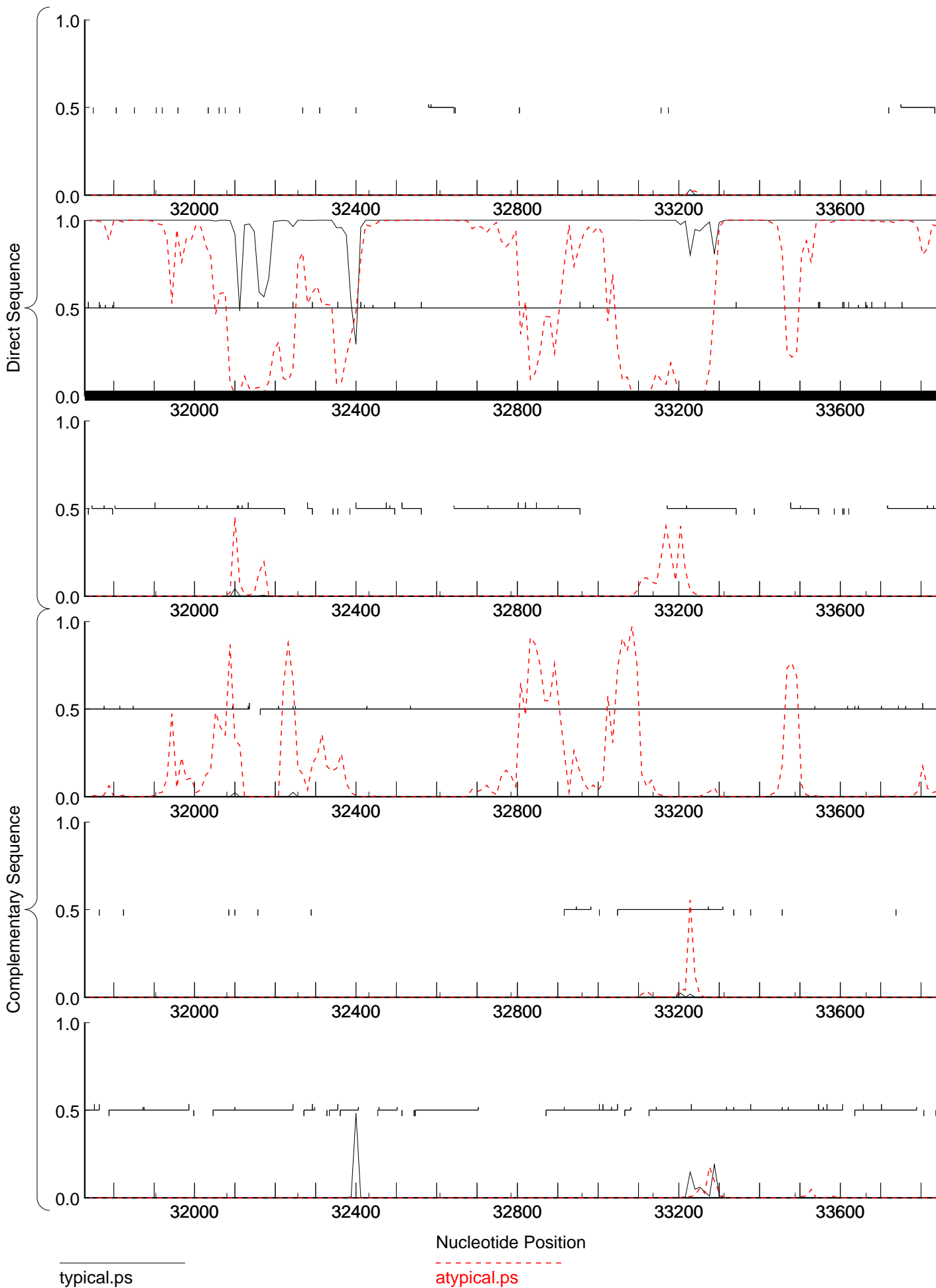


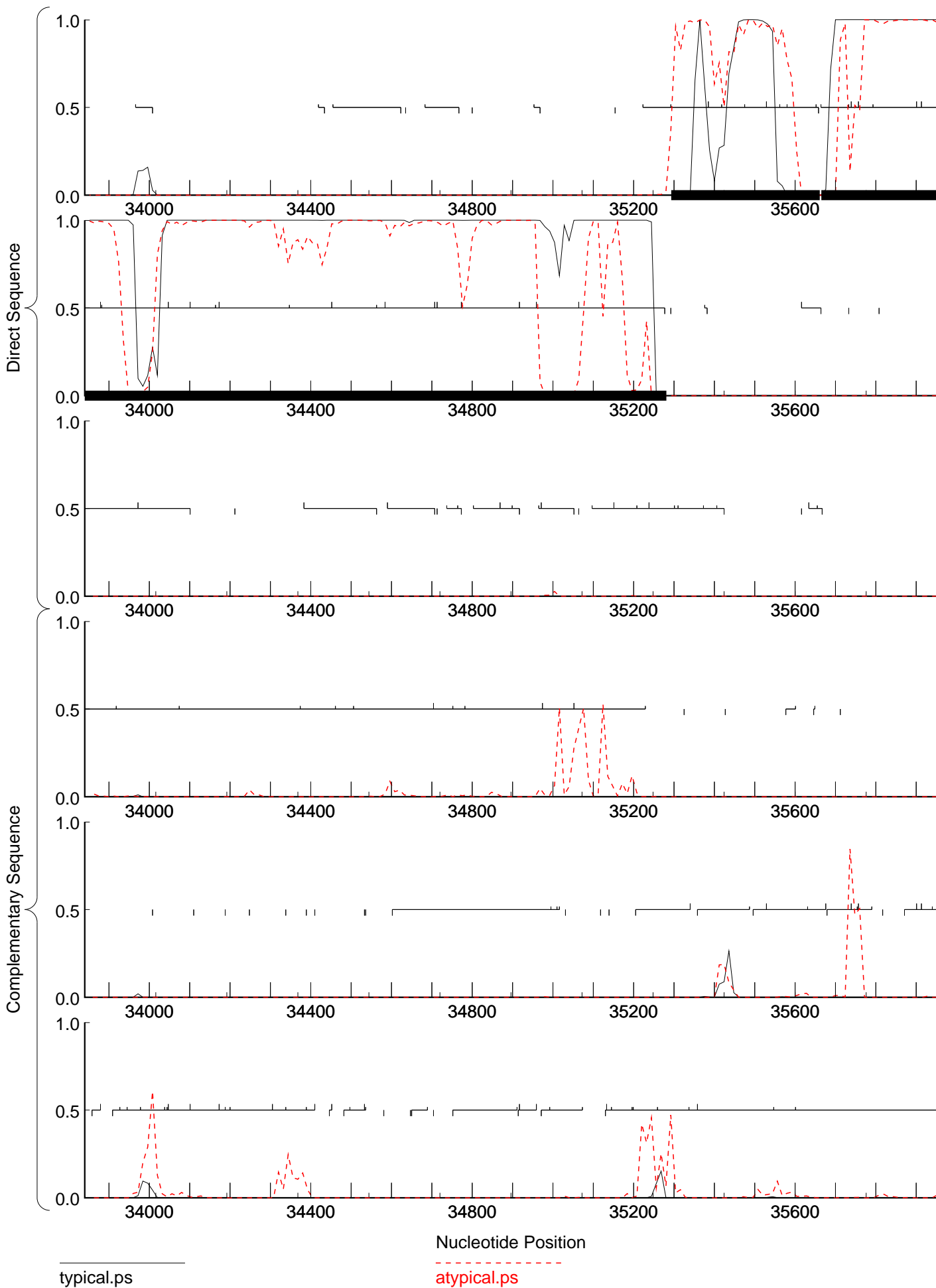


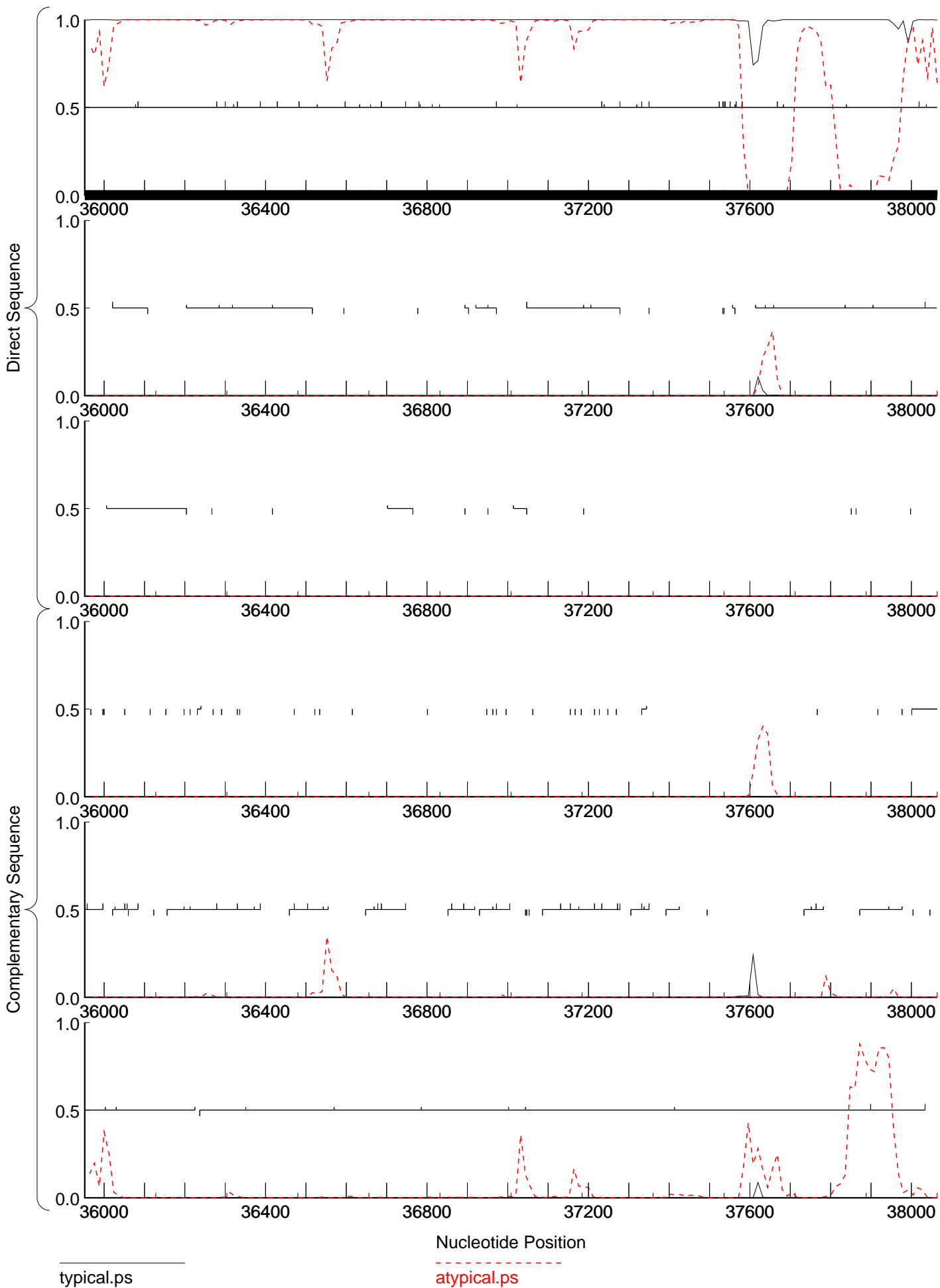
GeneMark.hmm prediction







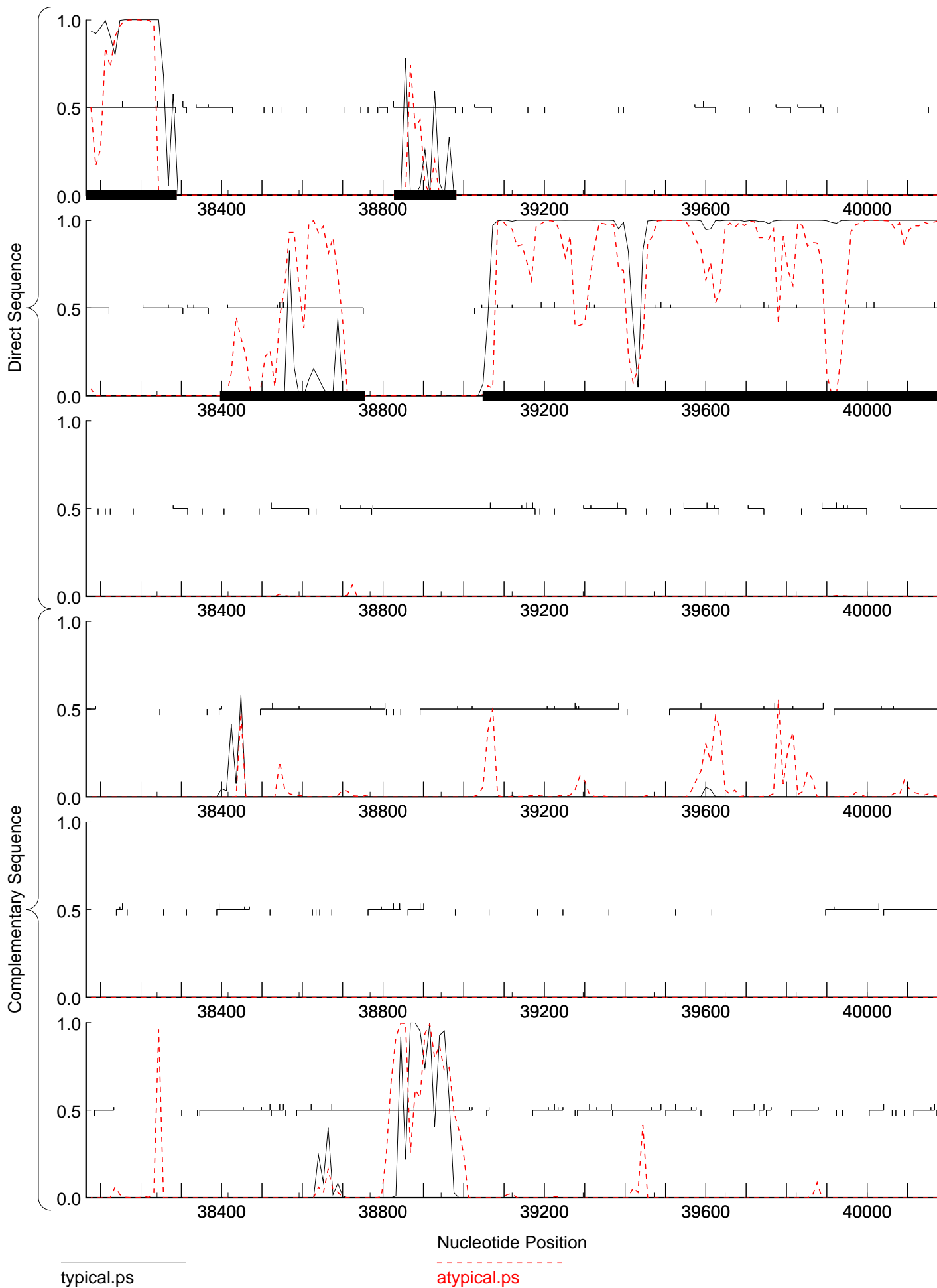




typical.ps

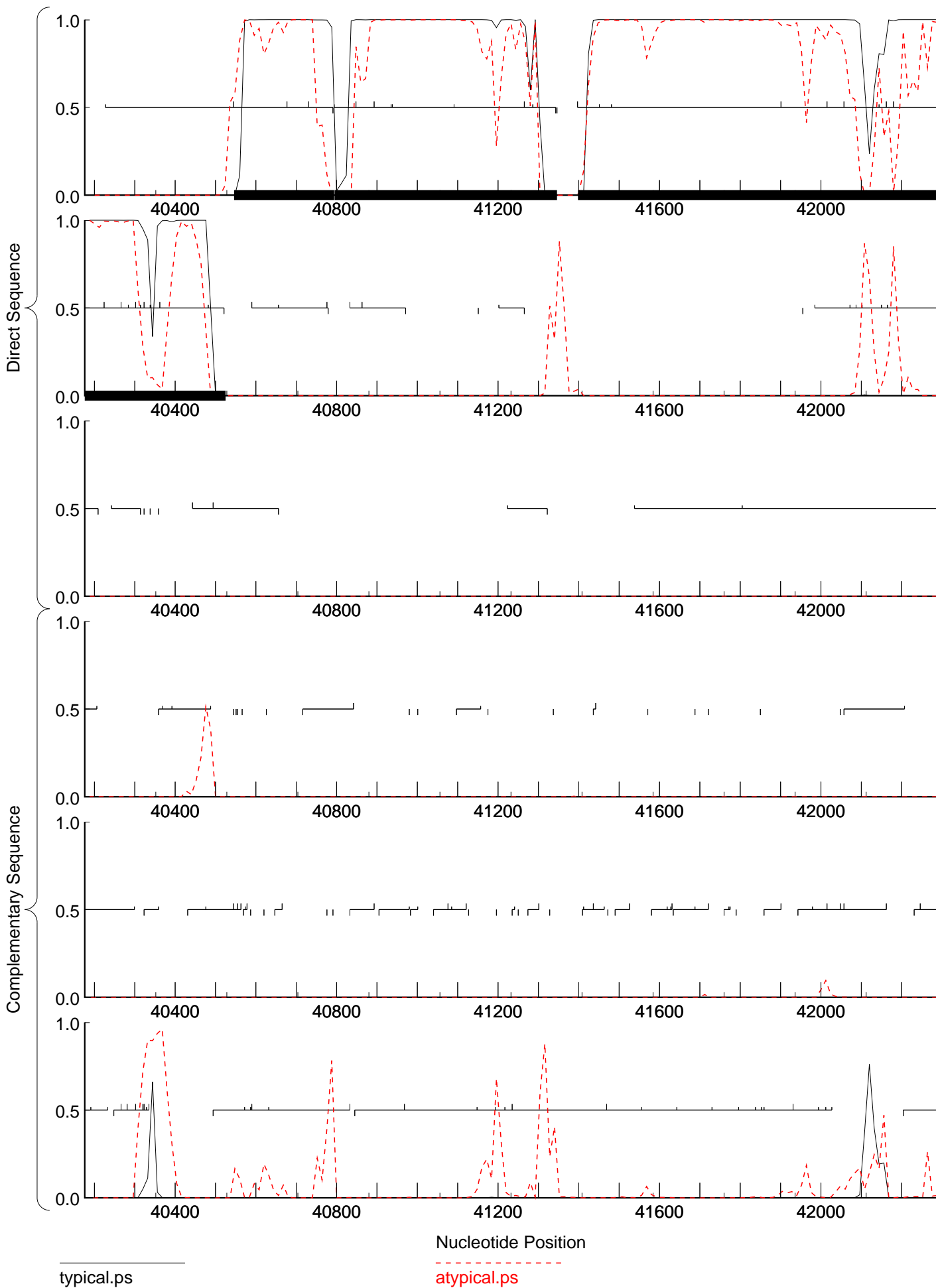
atypical.ps

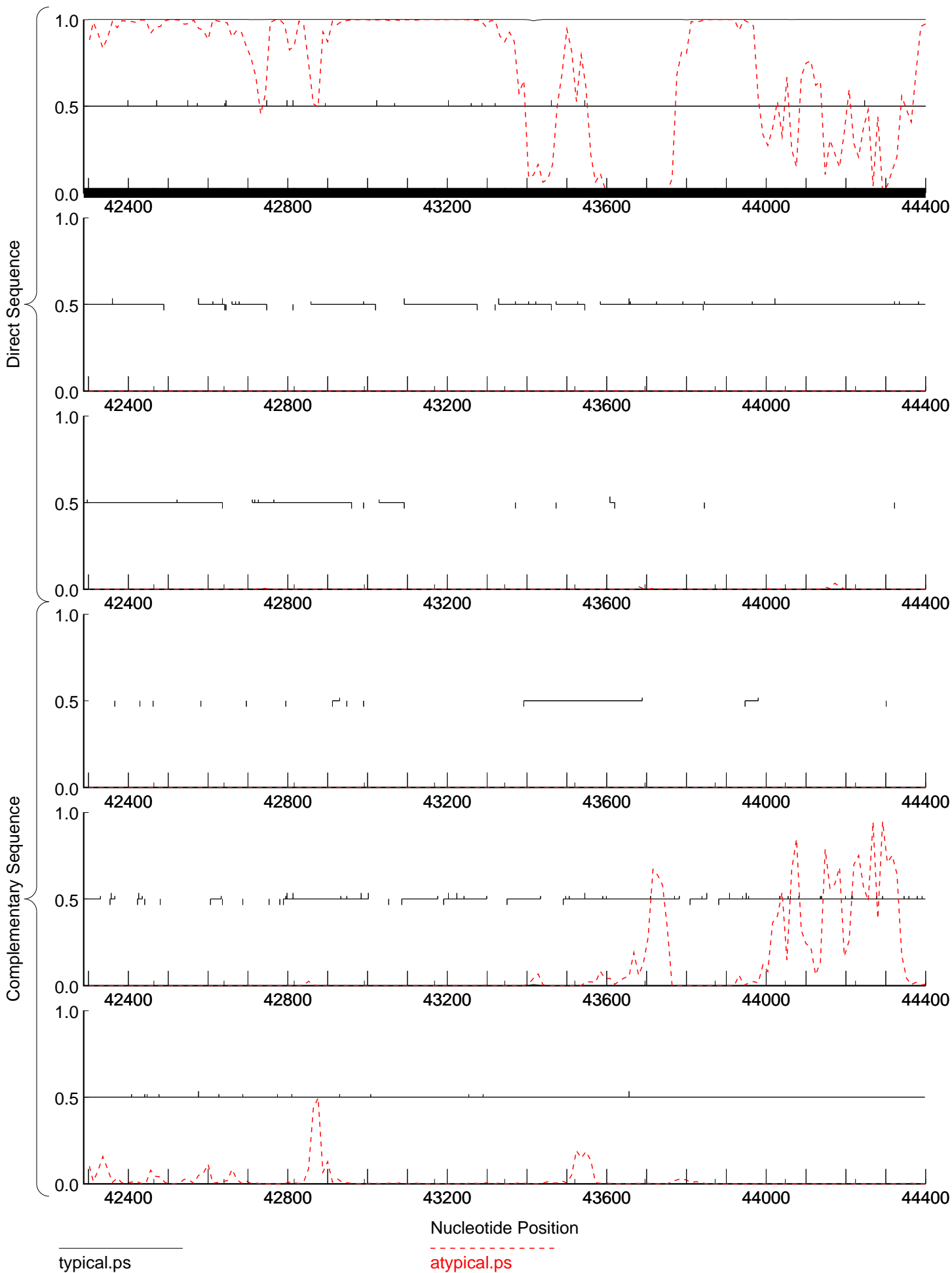
GeneMark.hmm prediction

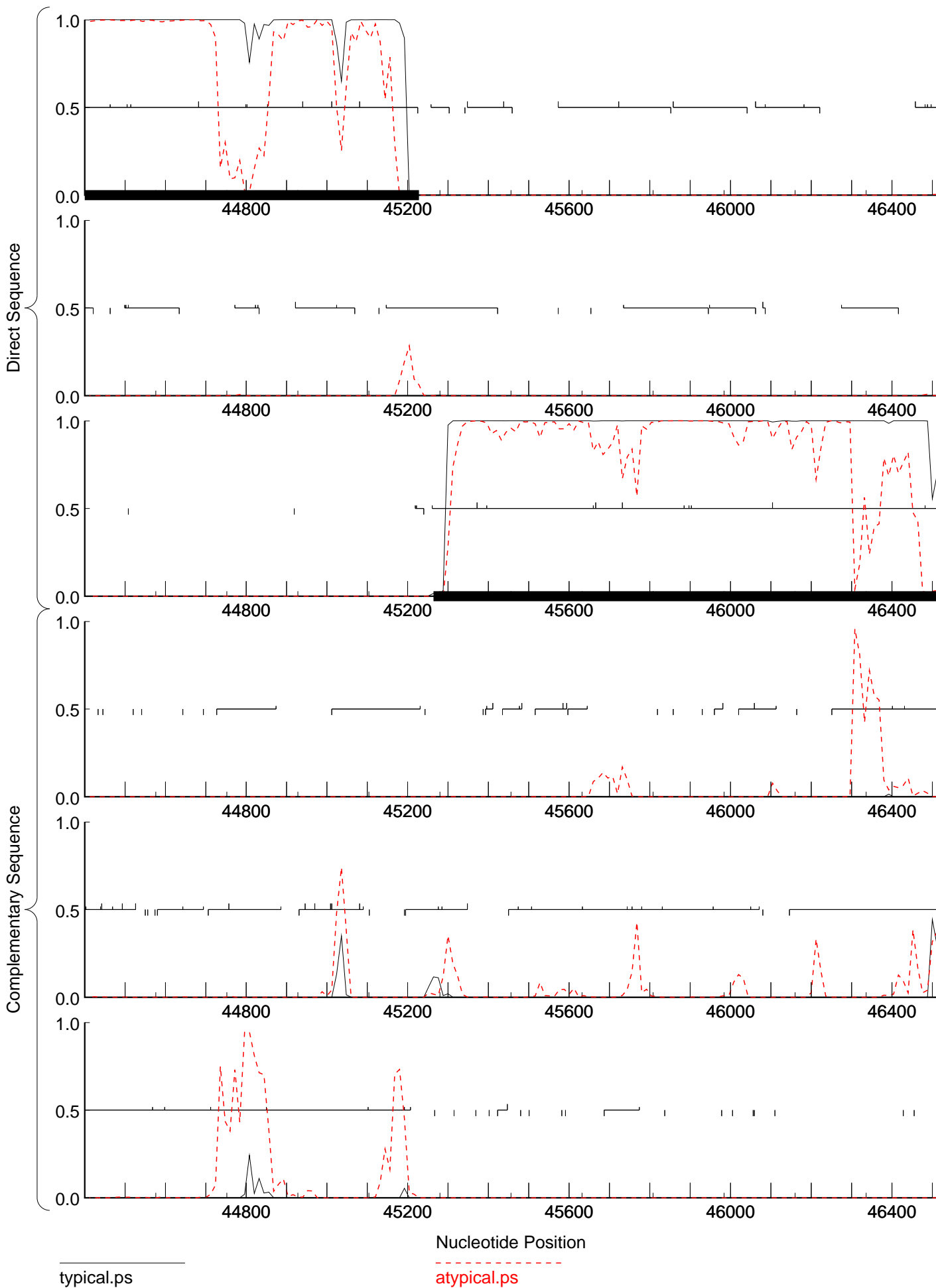


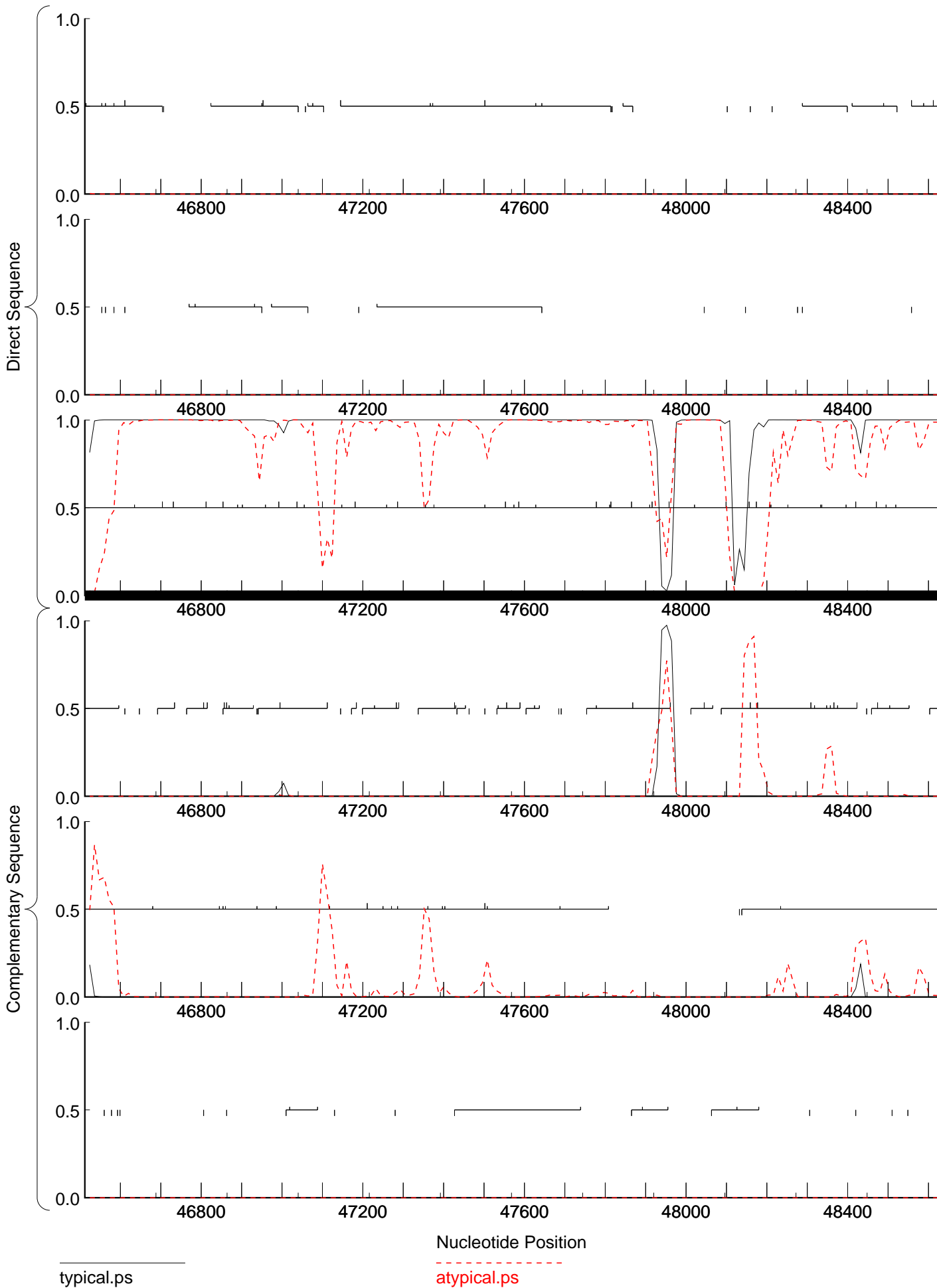
typical.ps

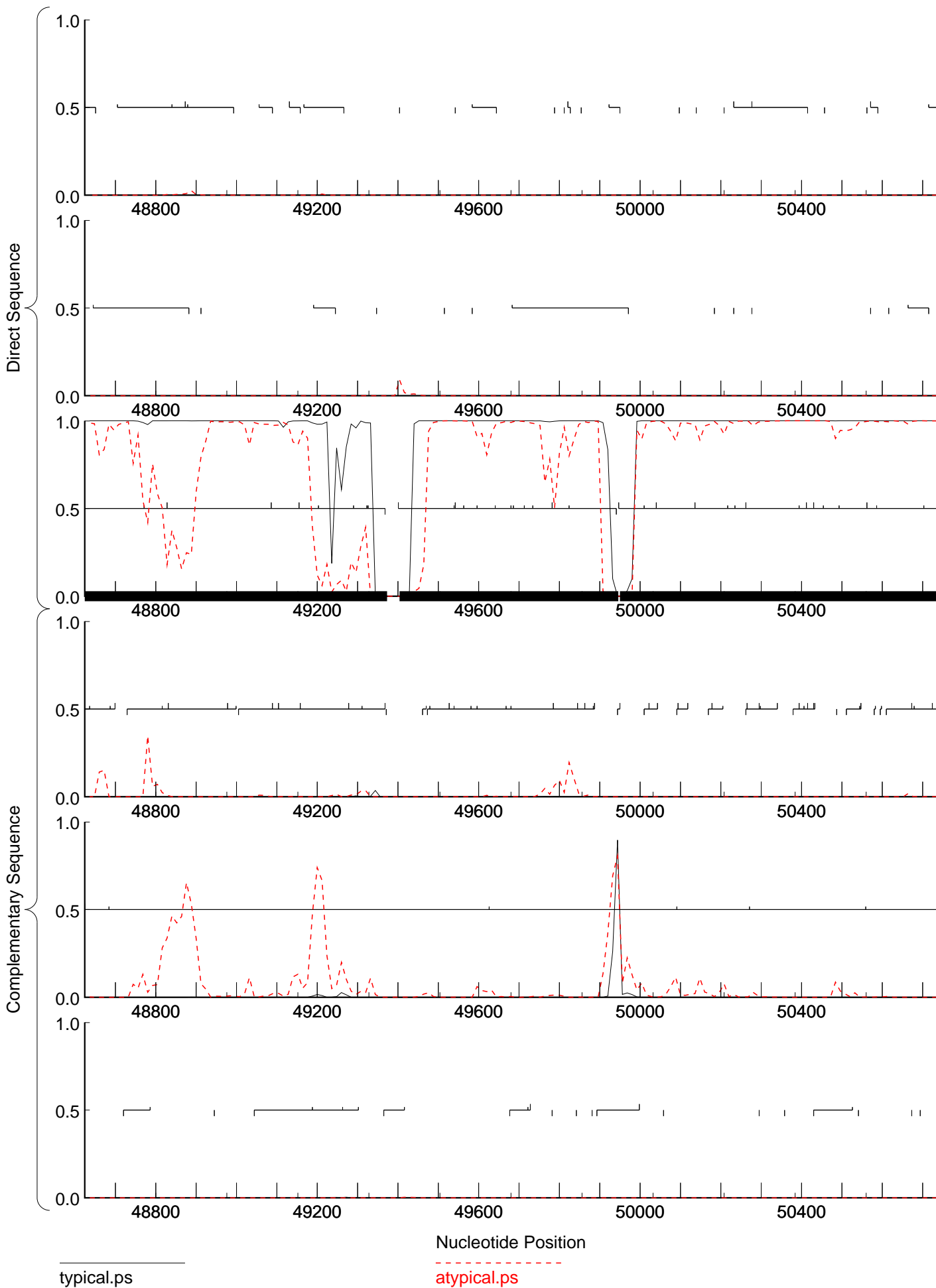
atypical.ps

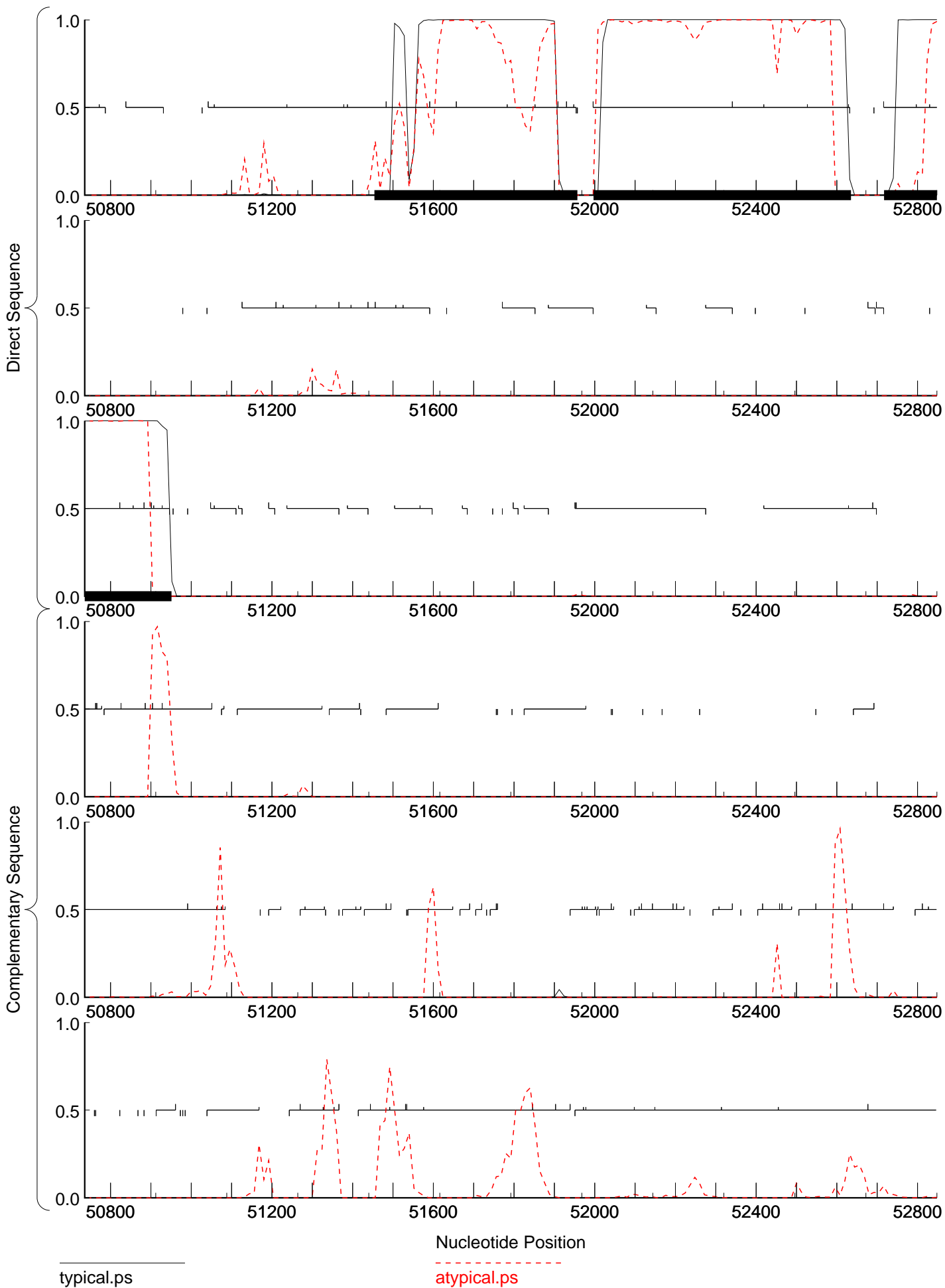


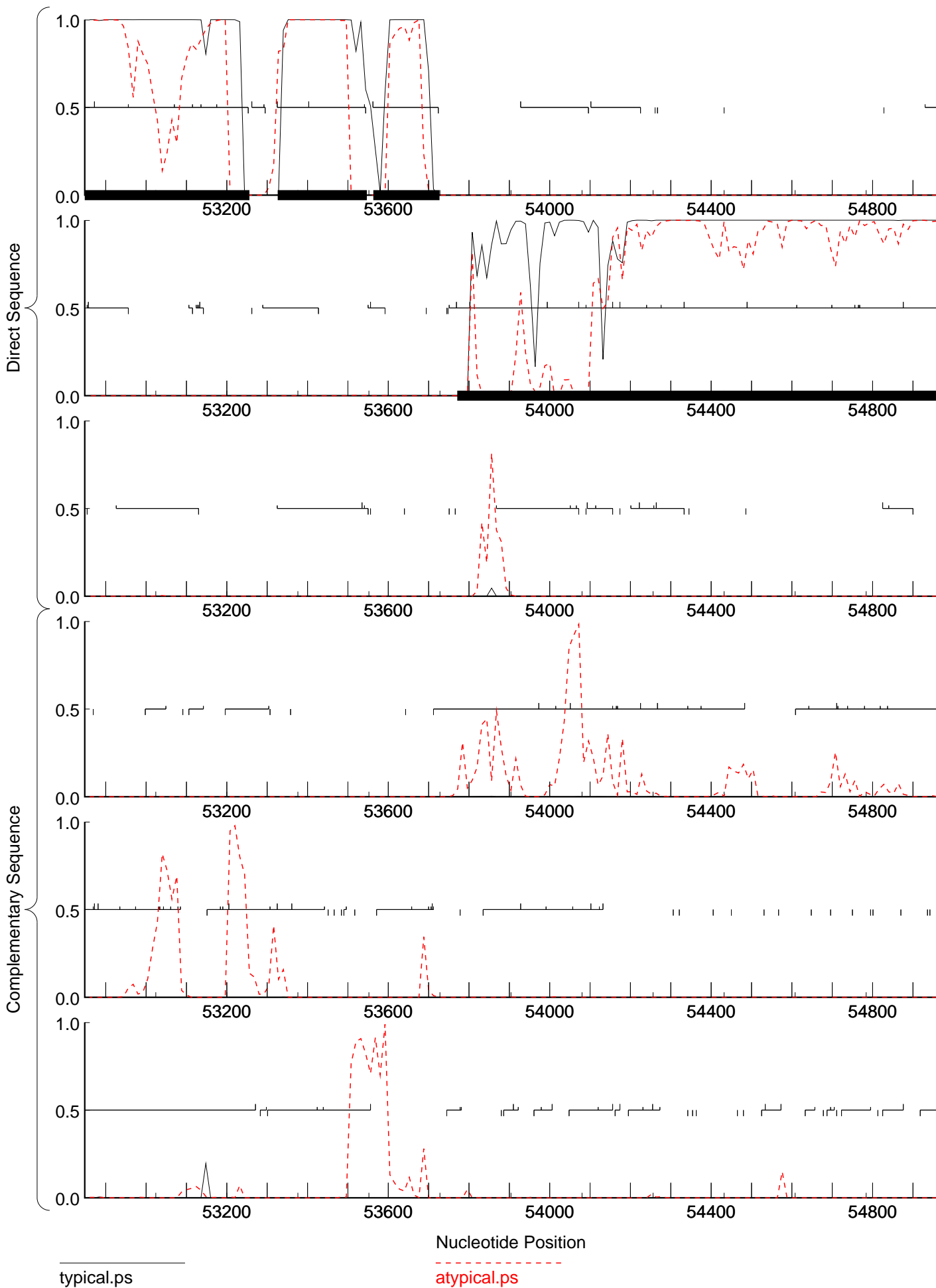


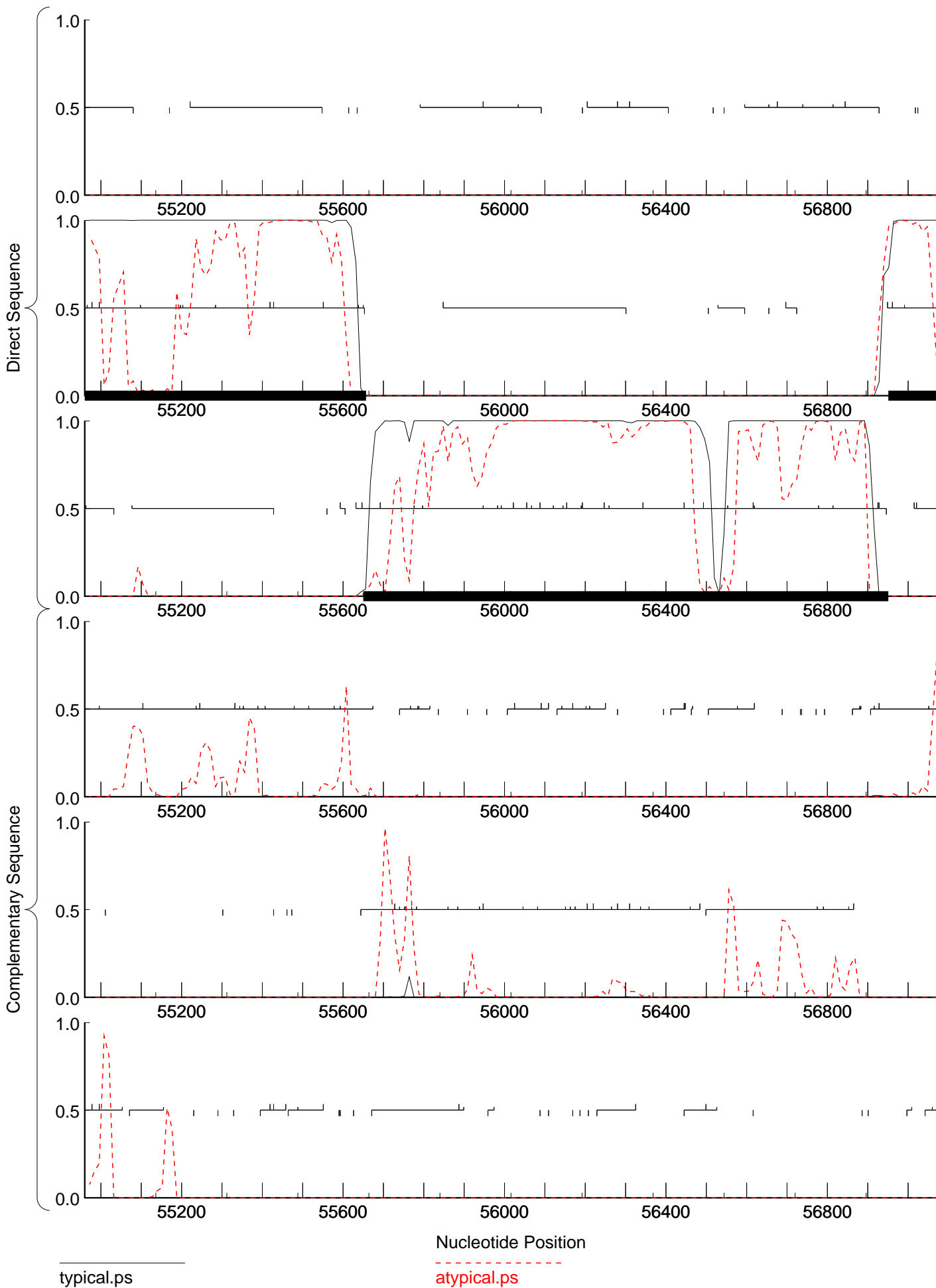






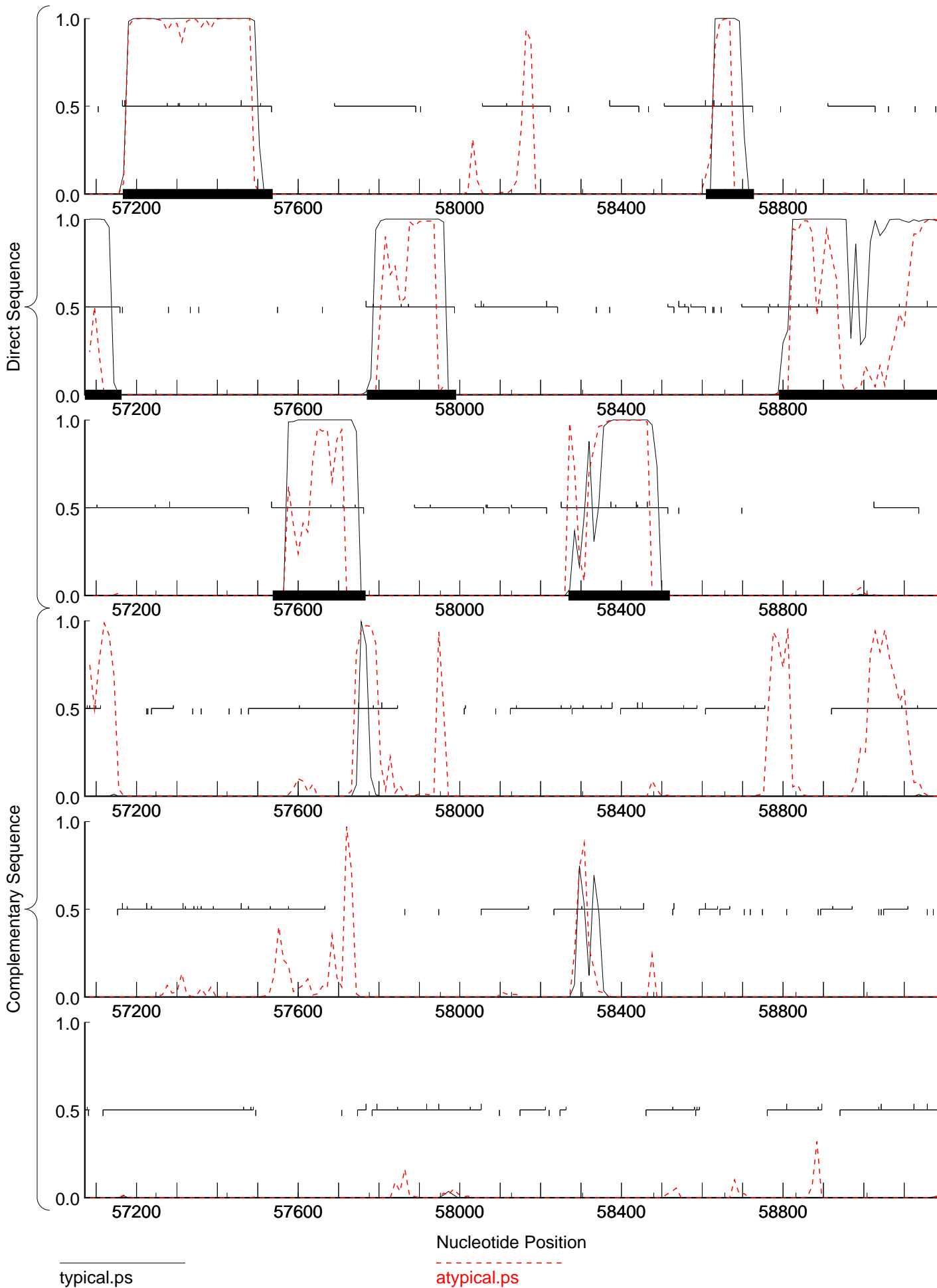


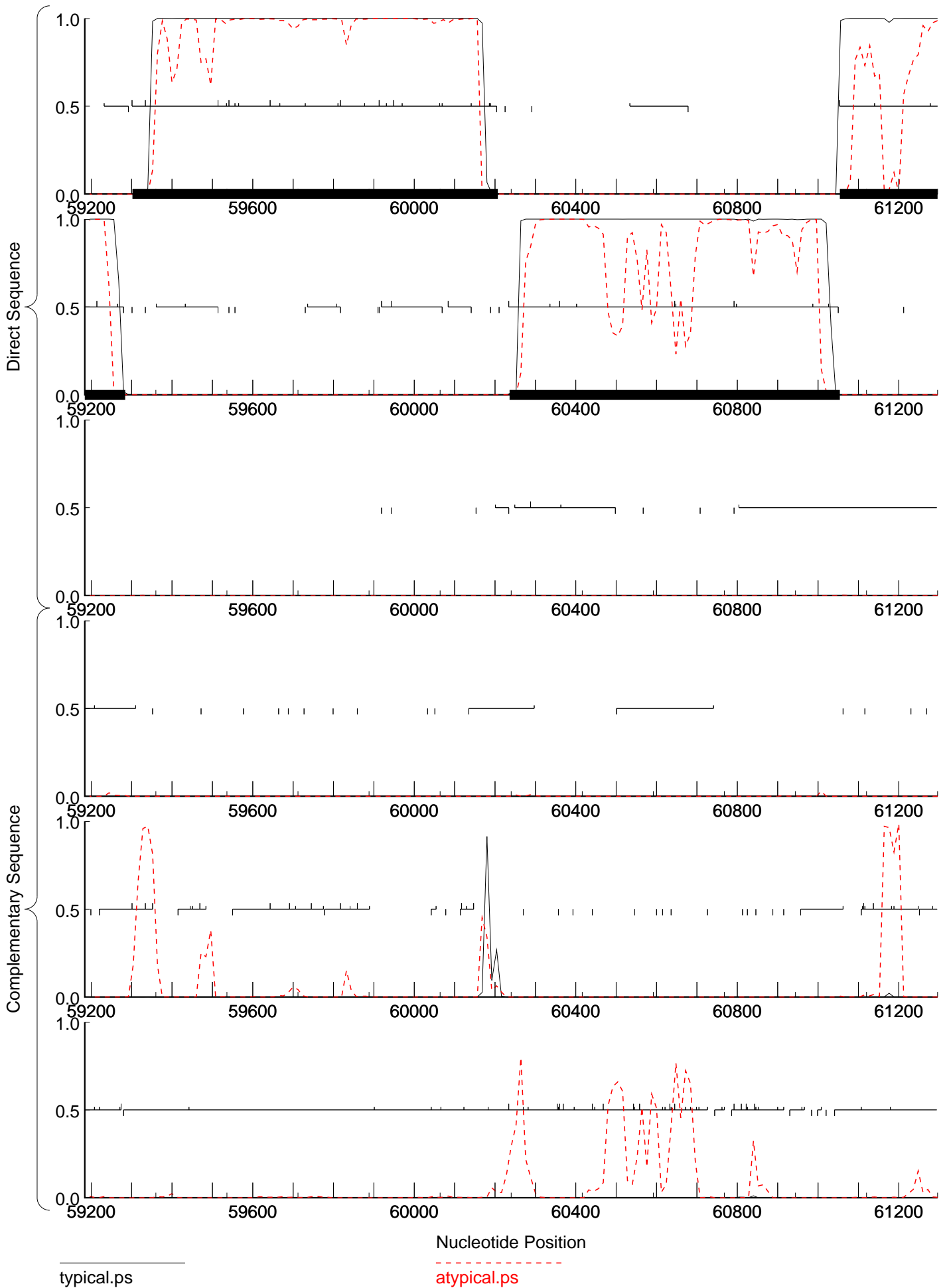


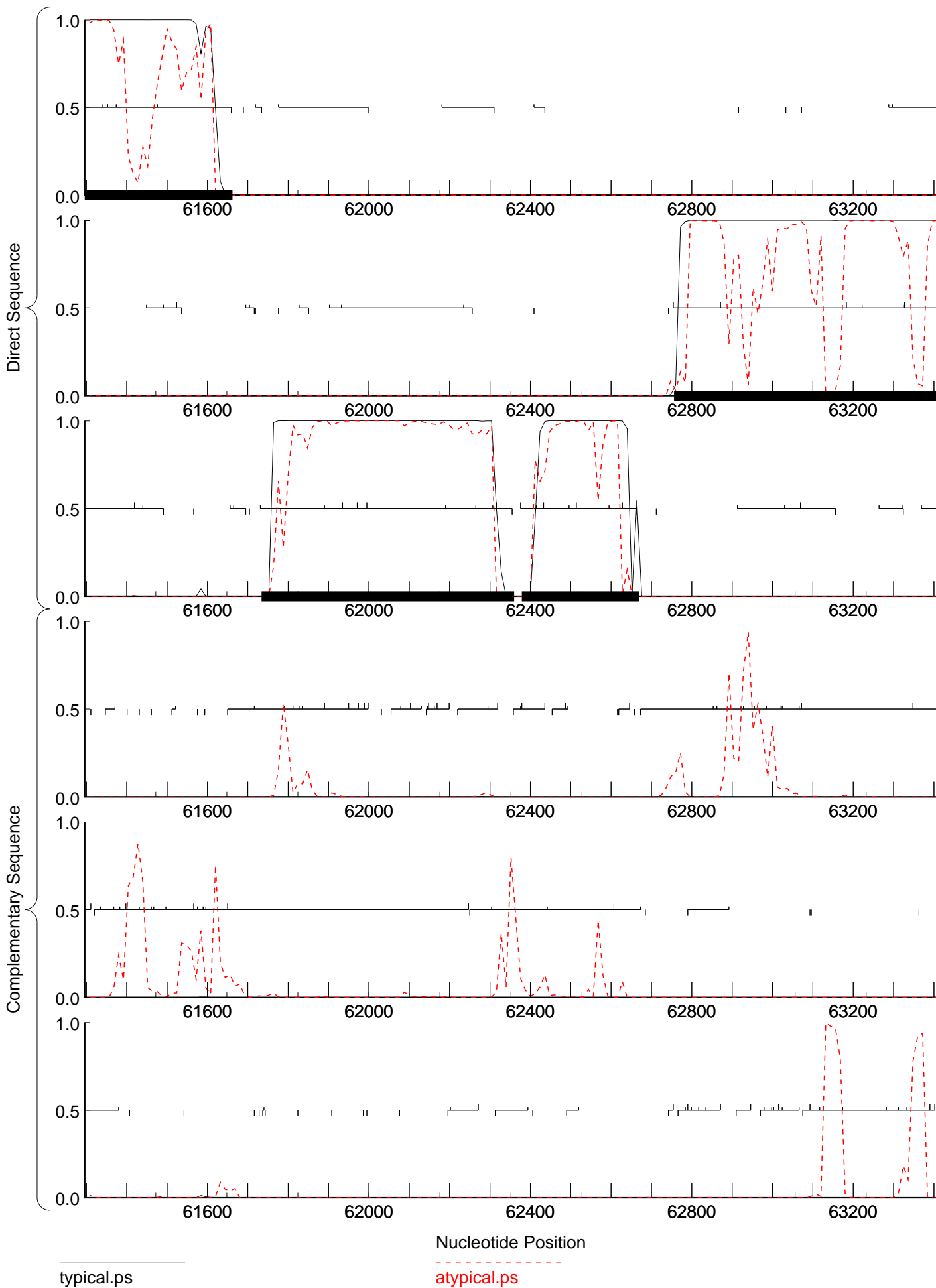


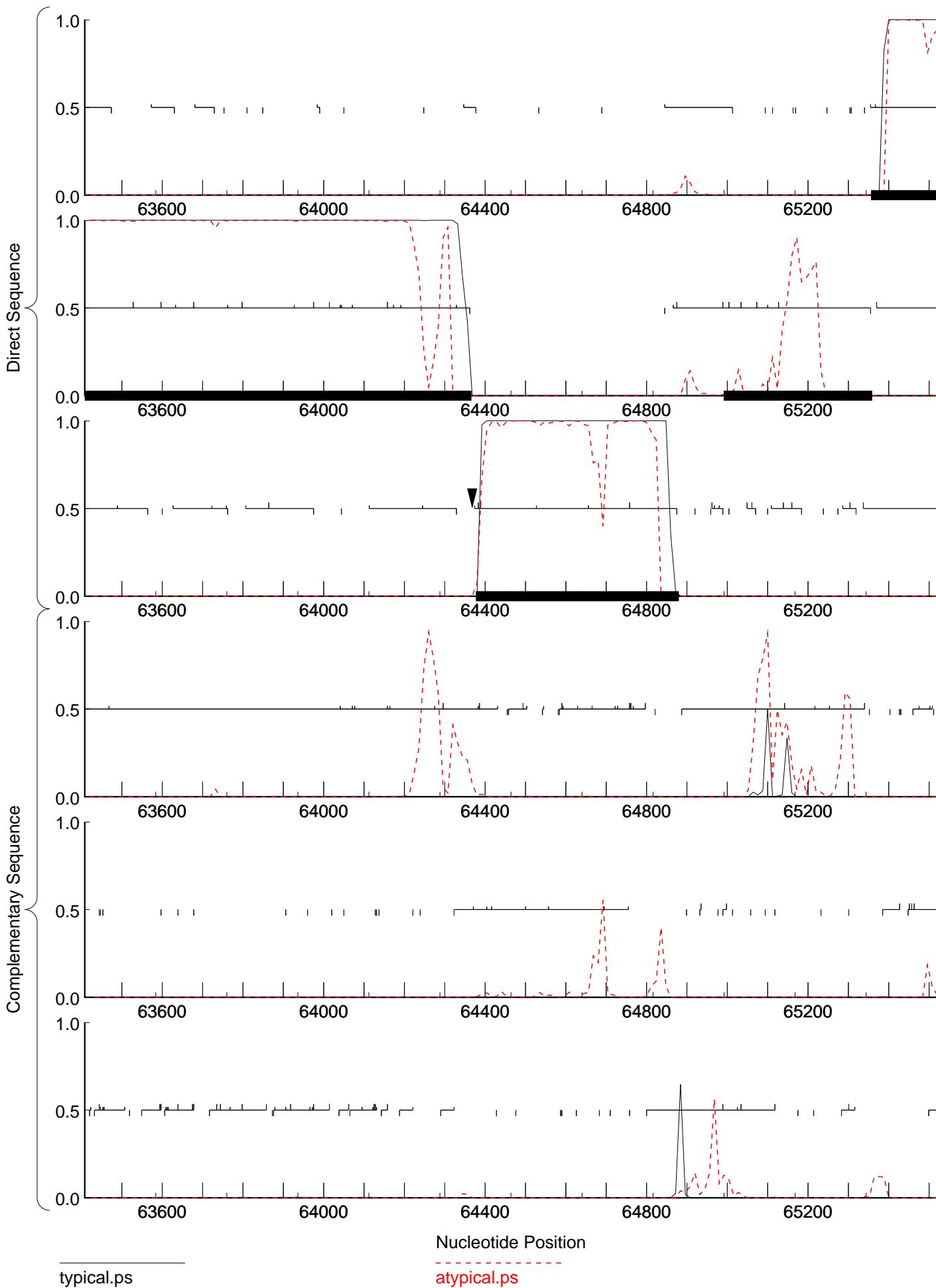
typical.ps

atypical.ps





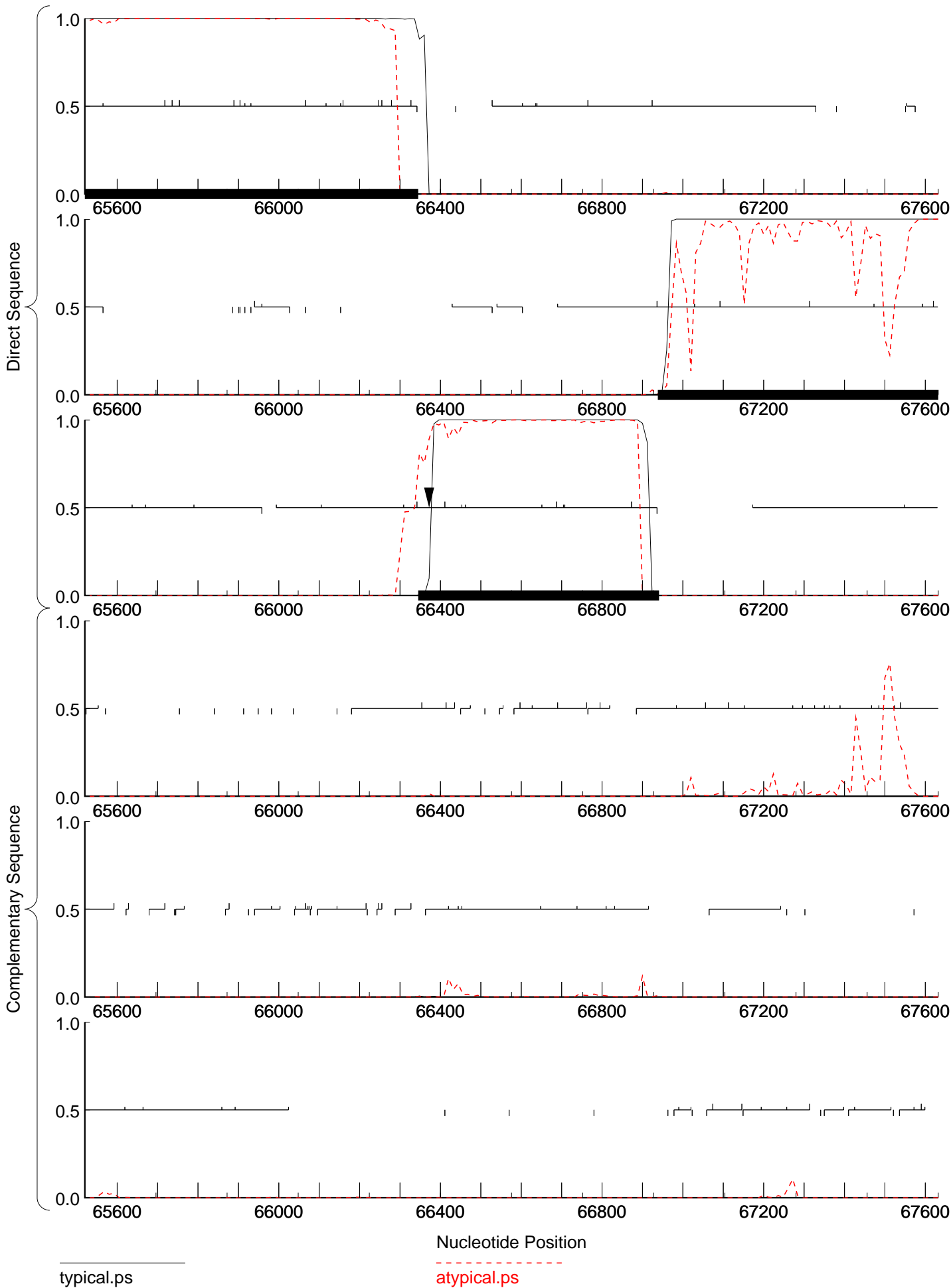




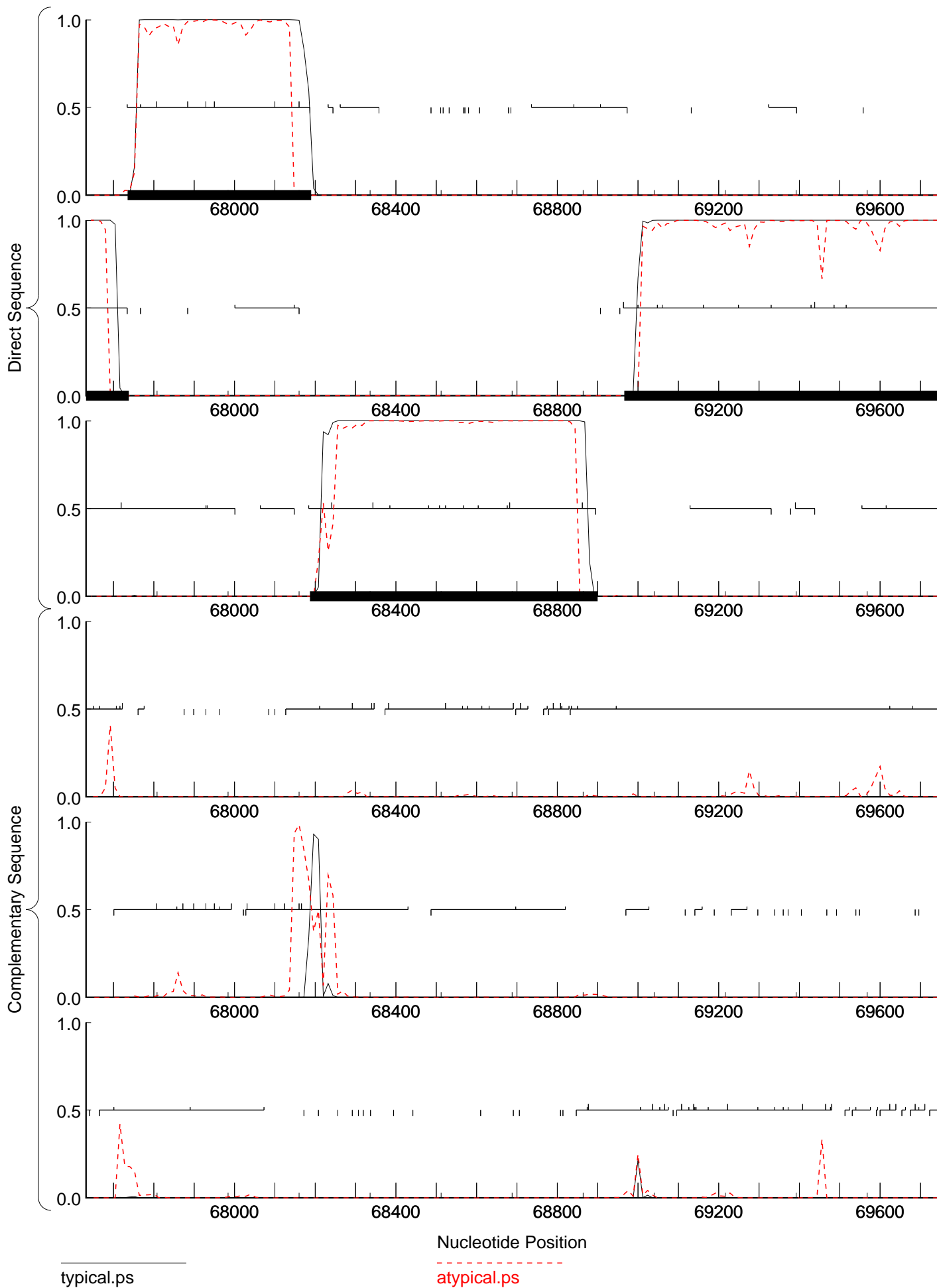
typical.ps

atypical.ps

GeneMark.hmm prediction

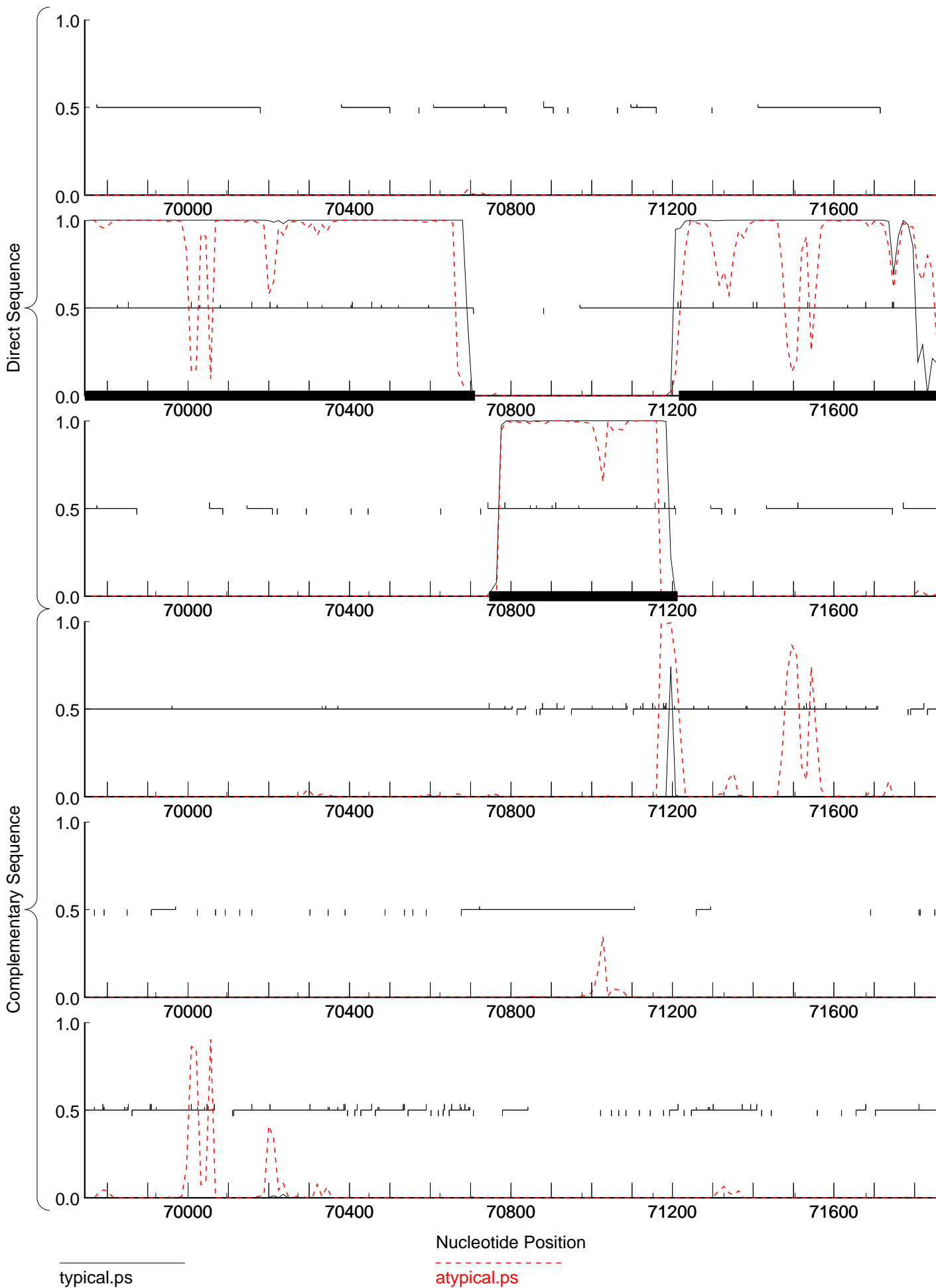


GeneMark.hmm prediction



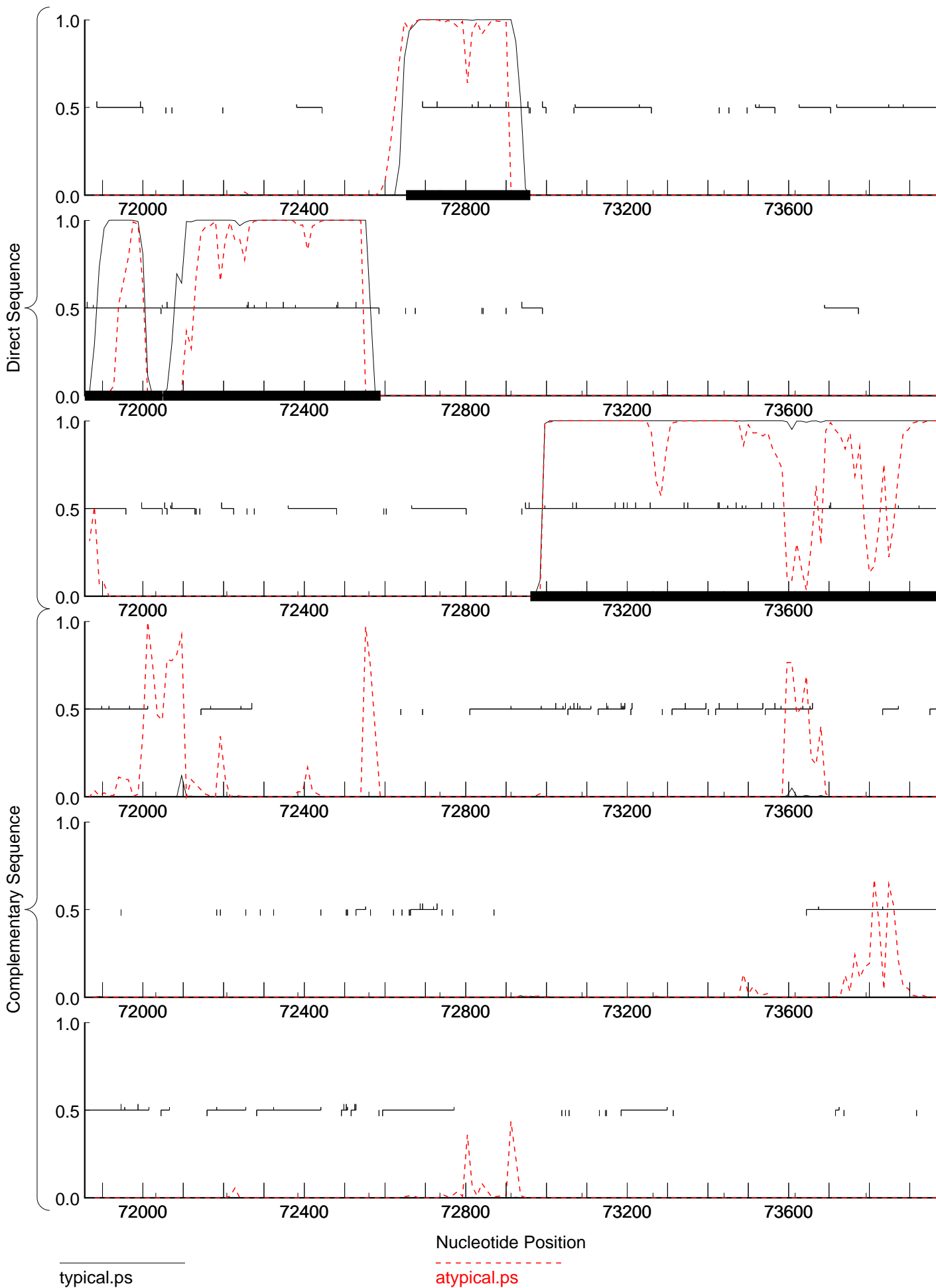
typical.ps

atypical.ps



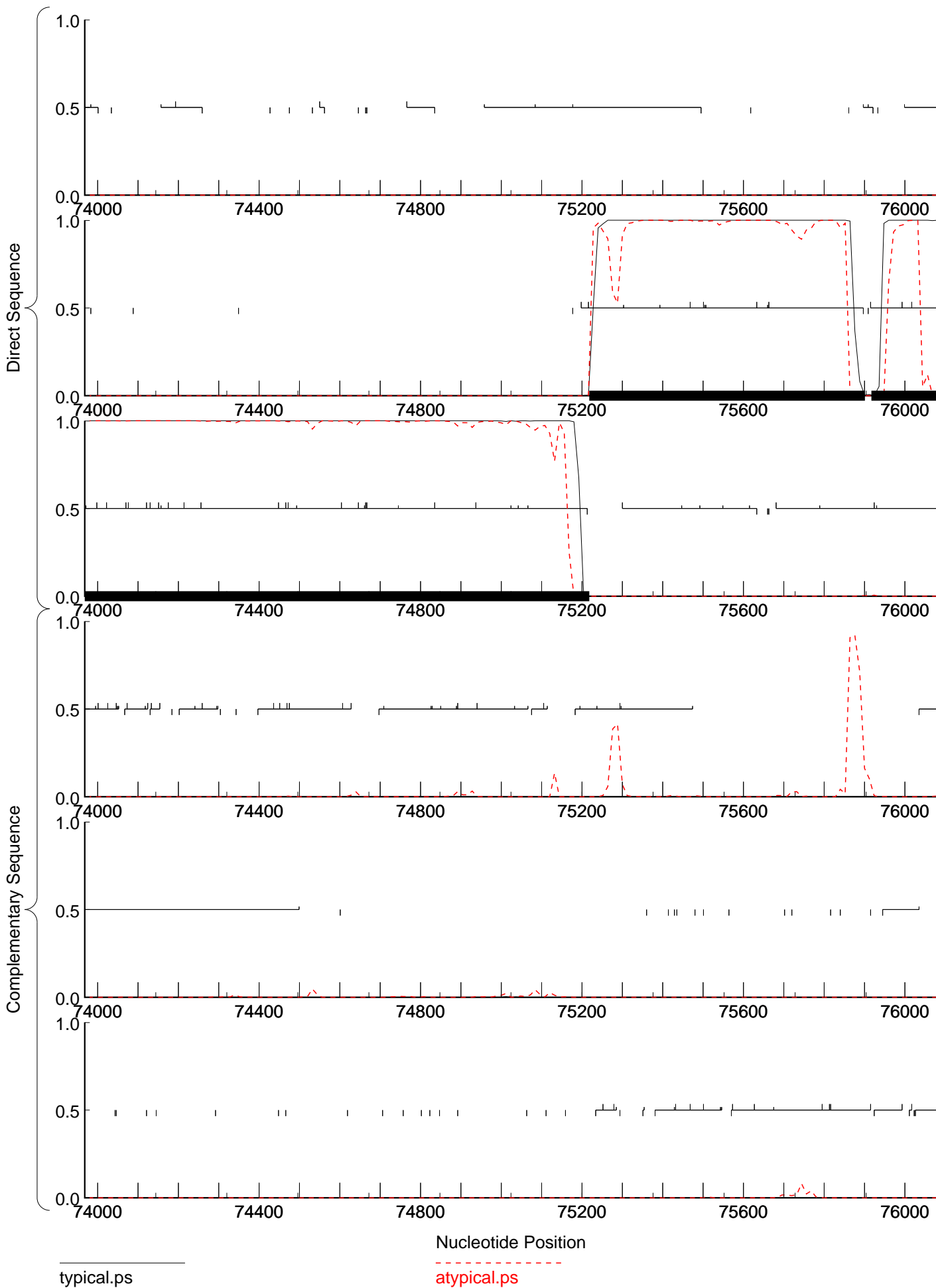
typical.ps

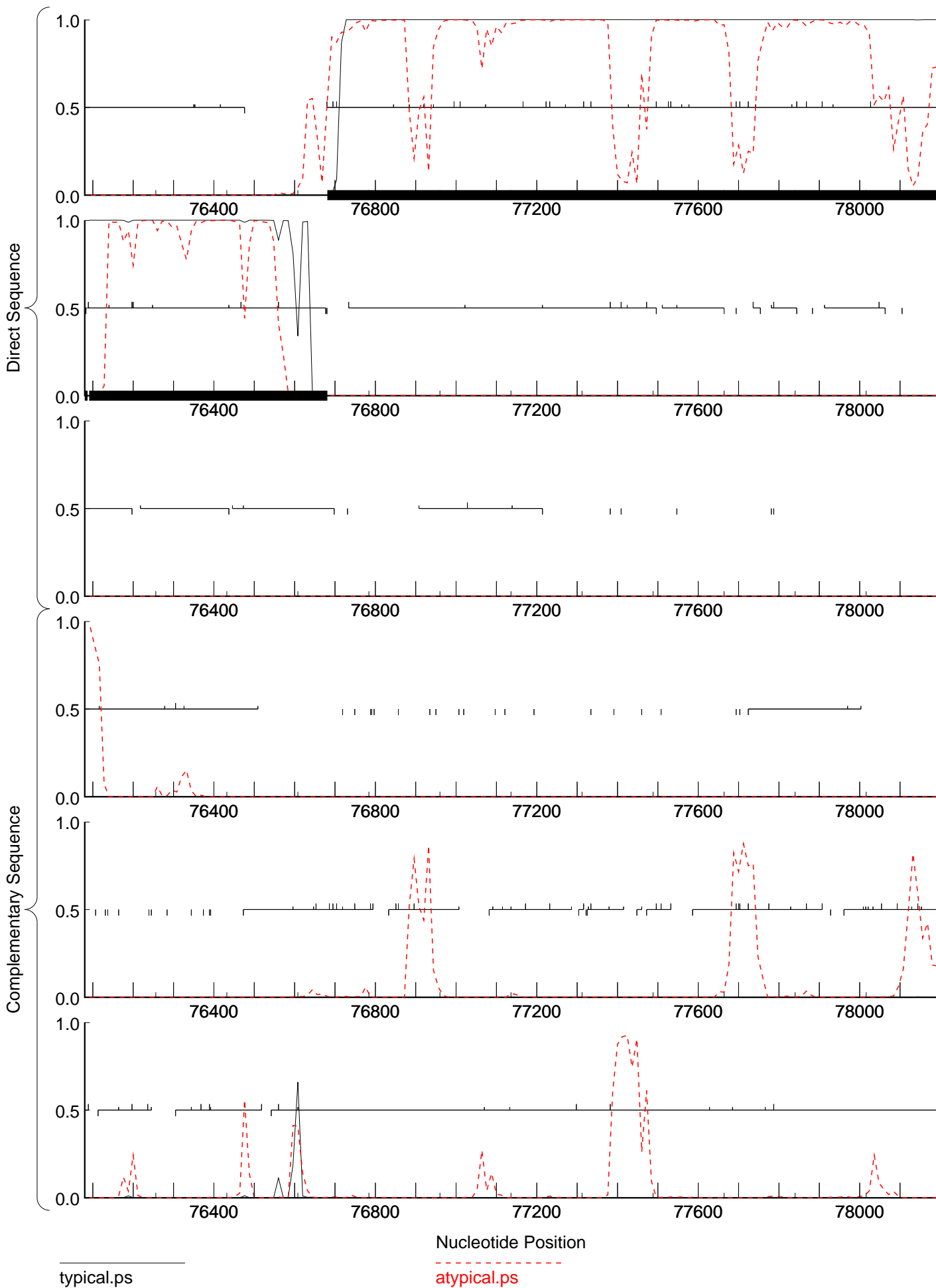
atypical.ps

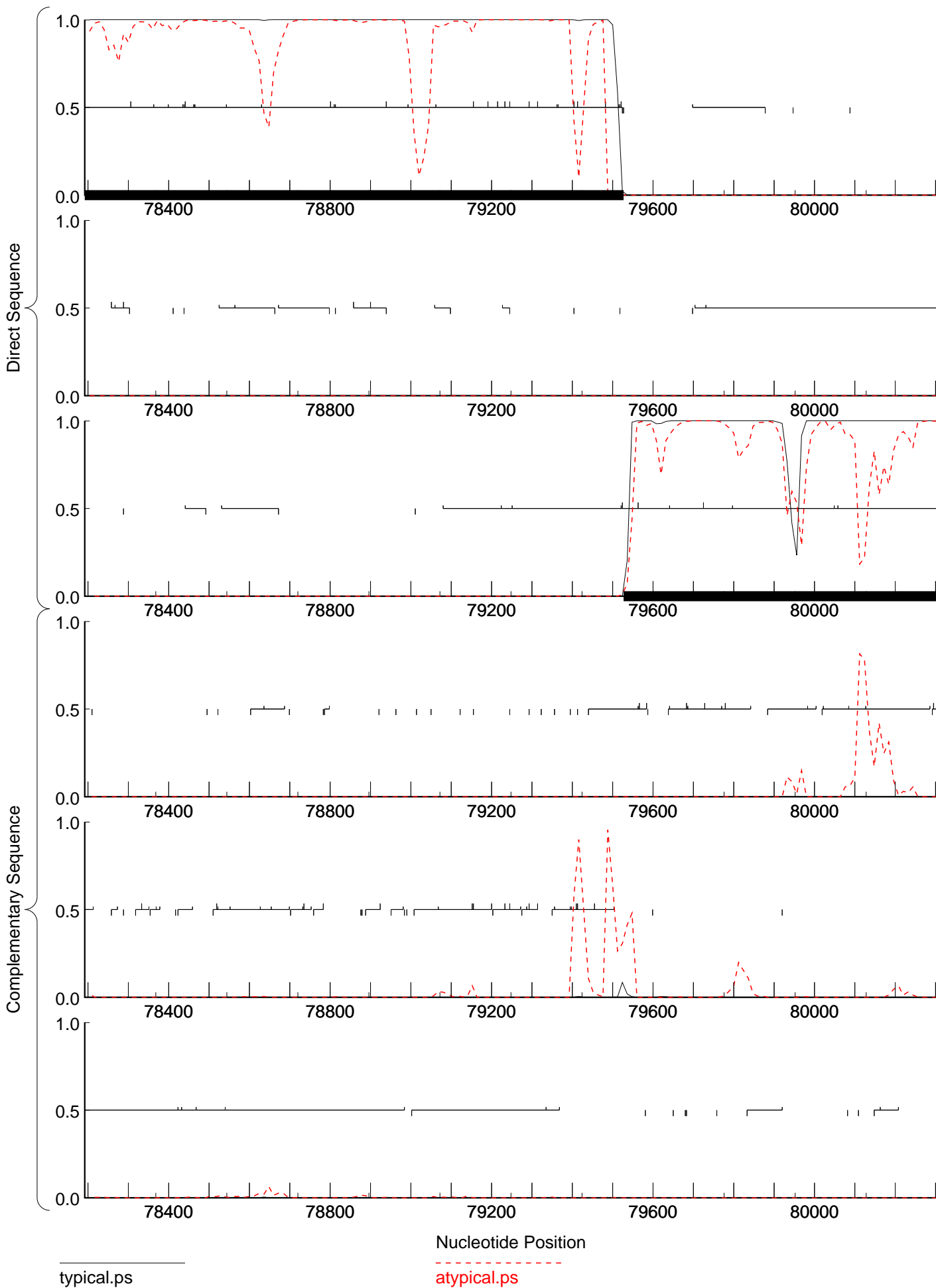


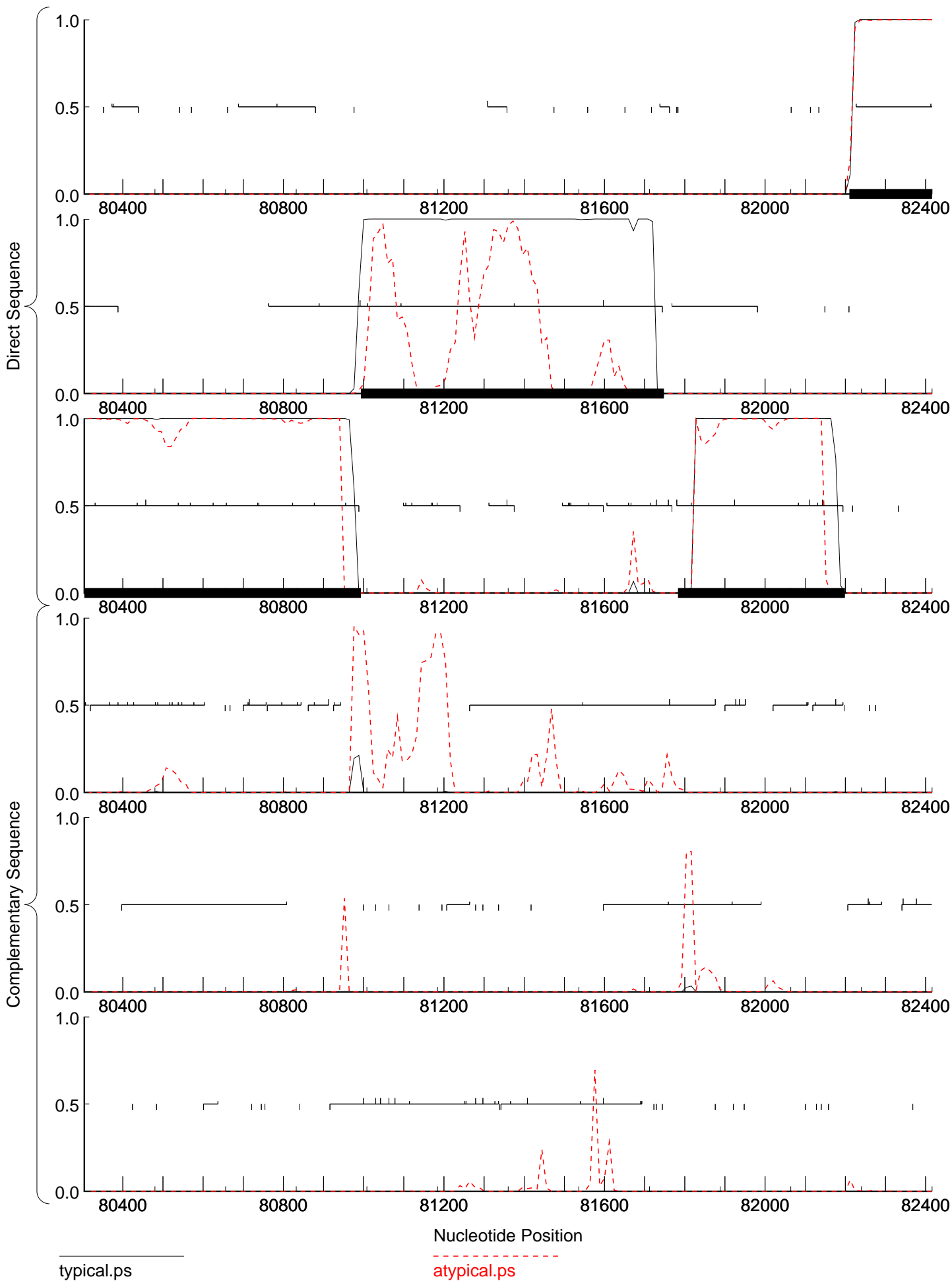
typical.ps

atypical.ps



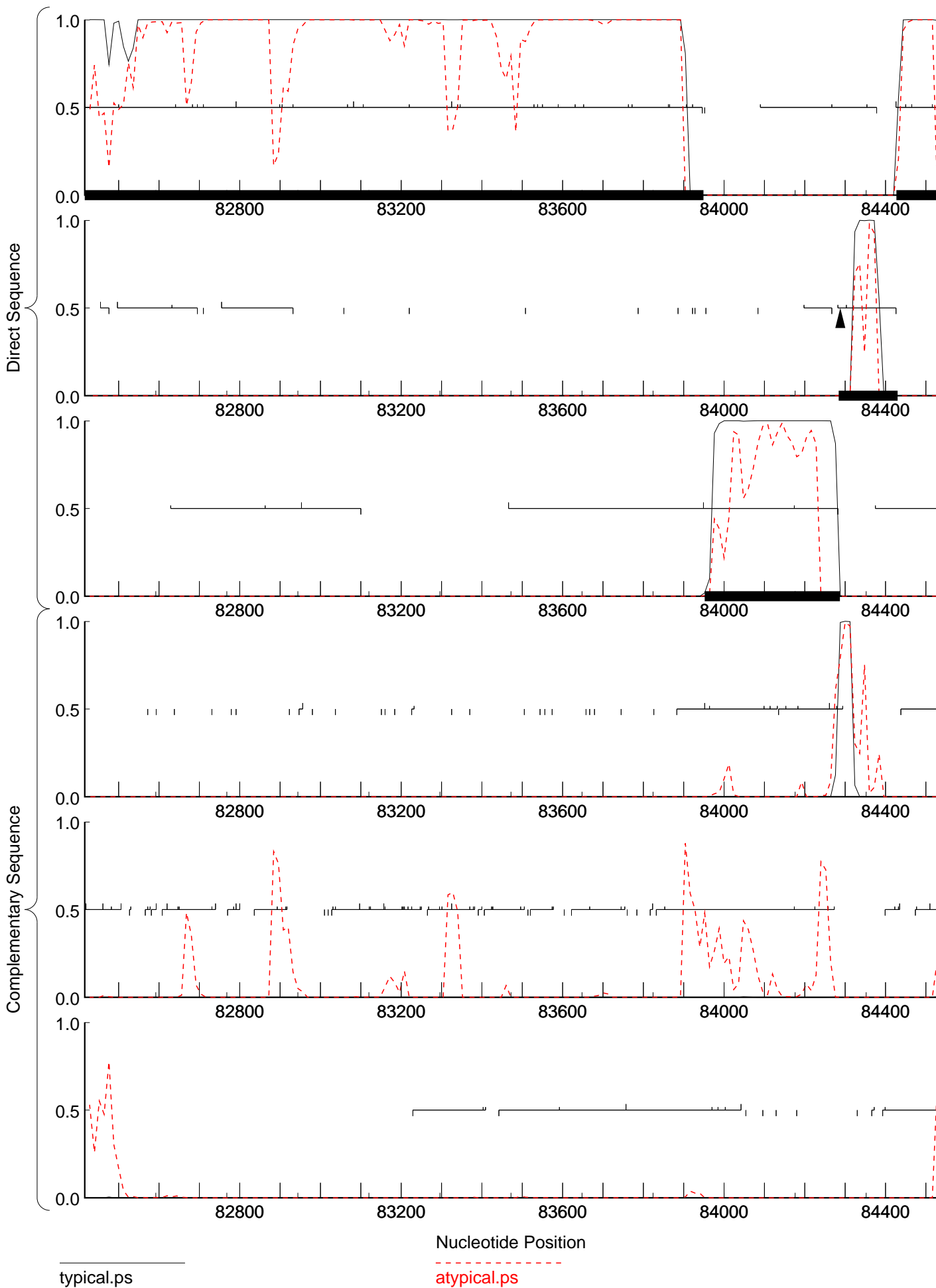






typical.ps

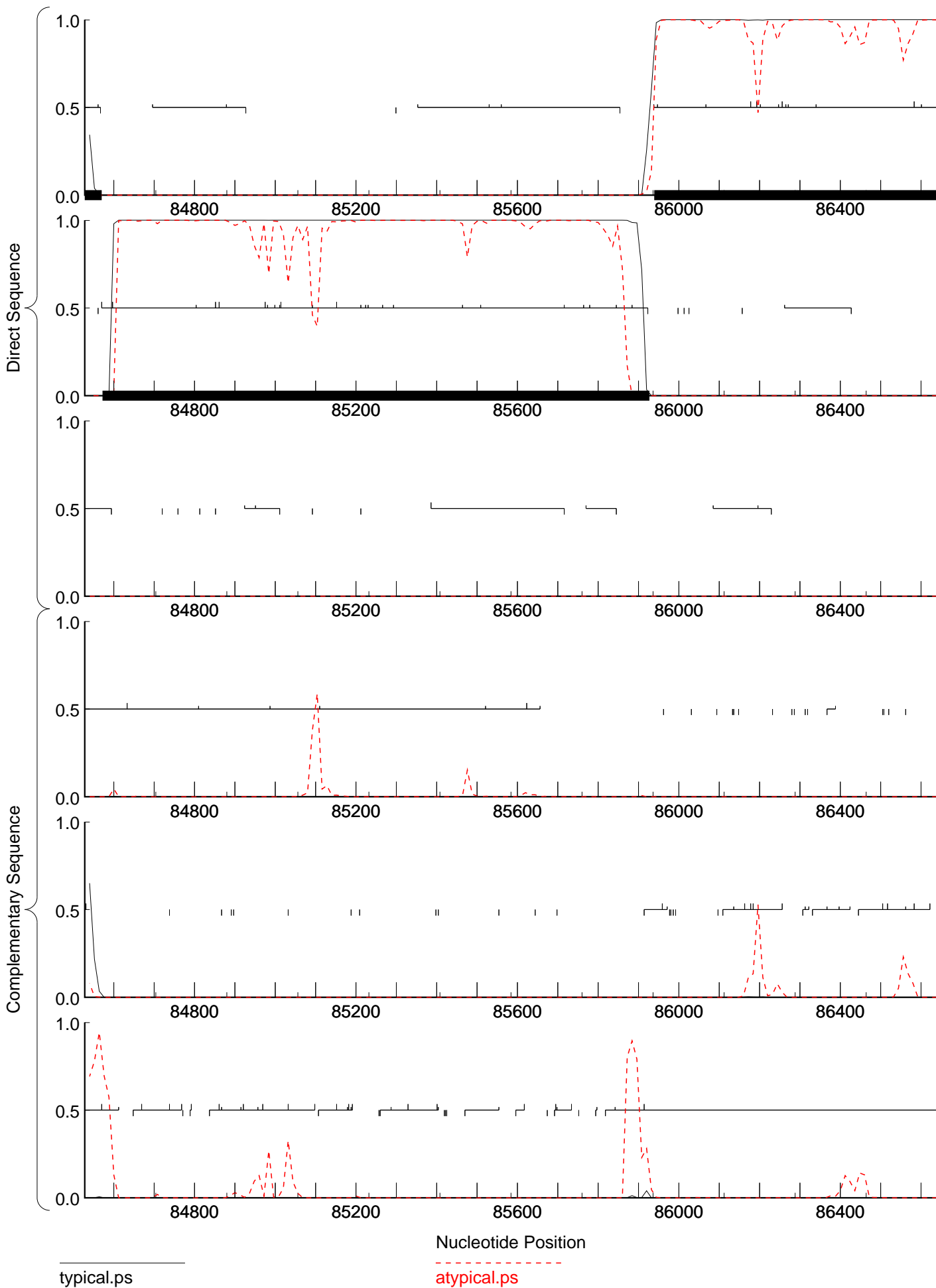
atypical.ps

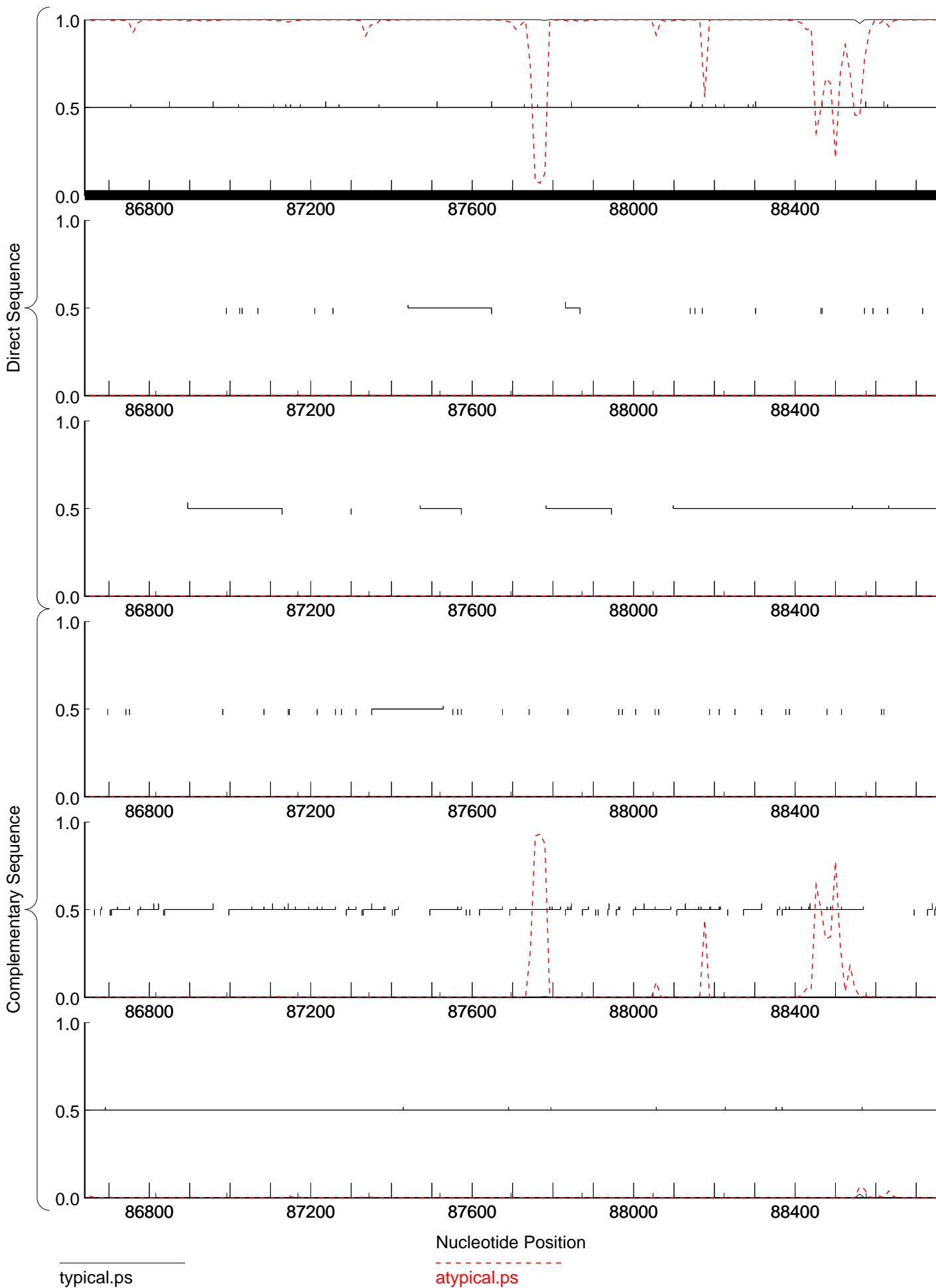


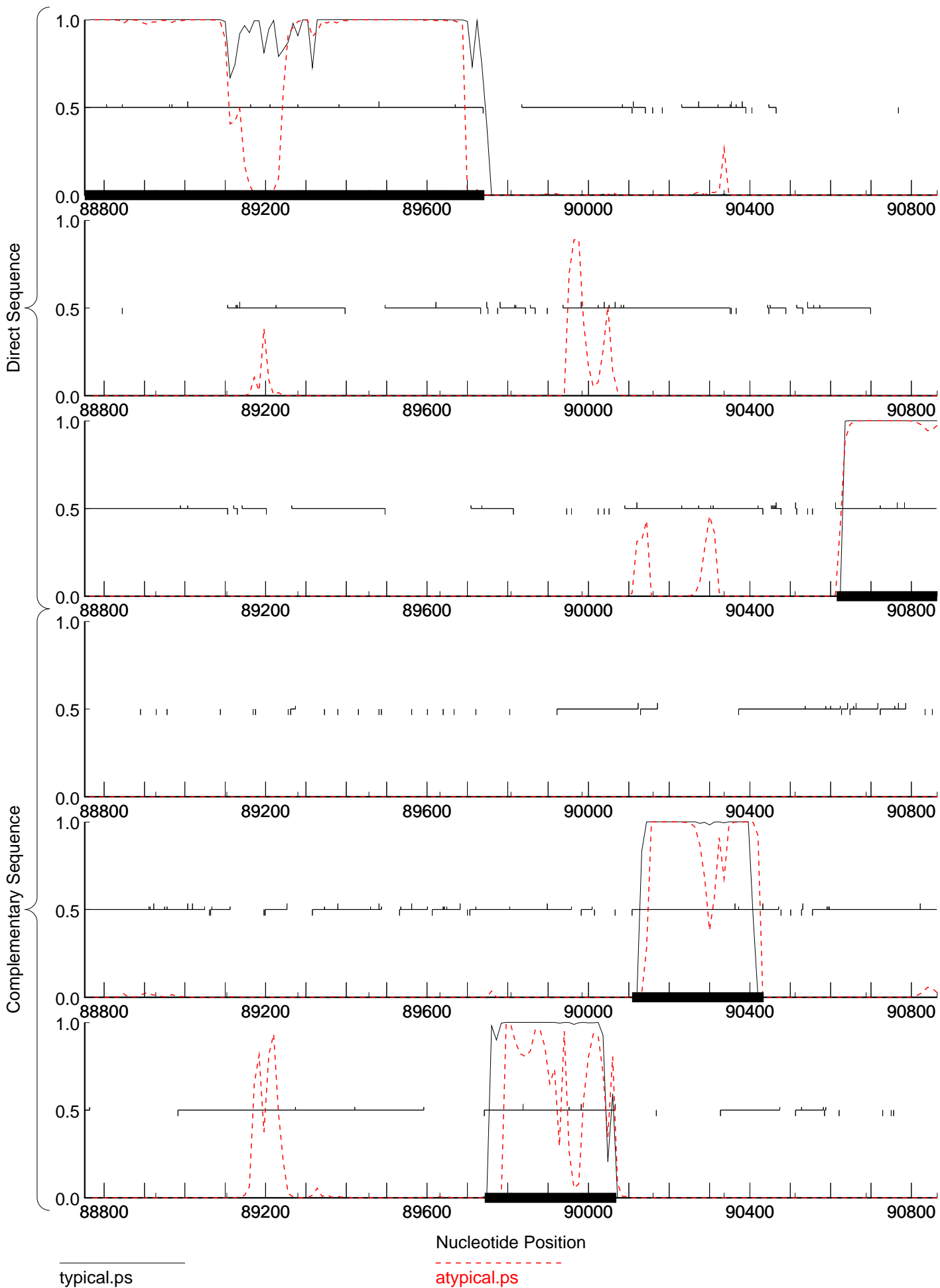
typical.ps

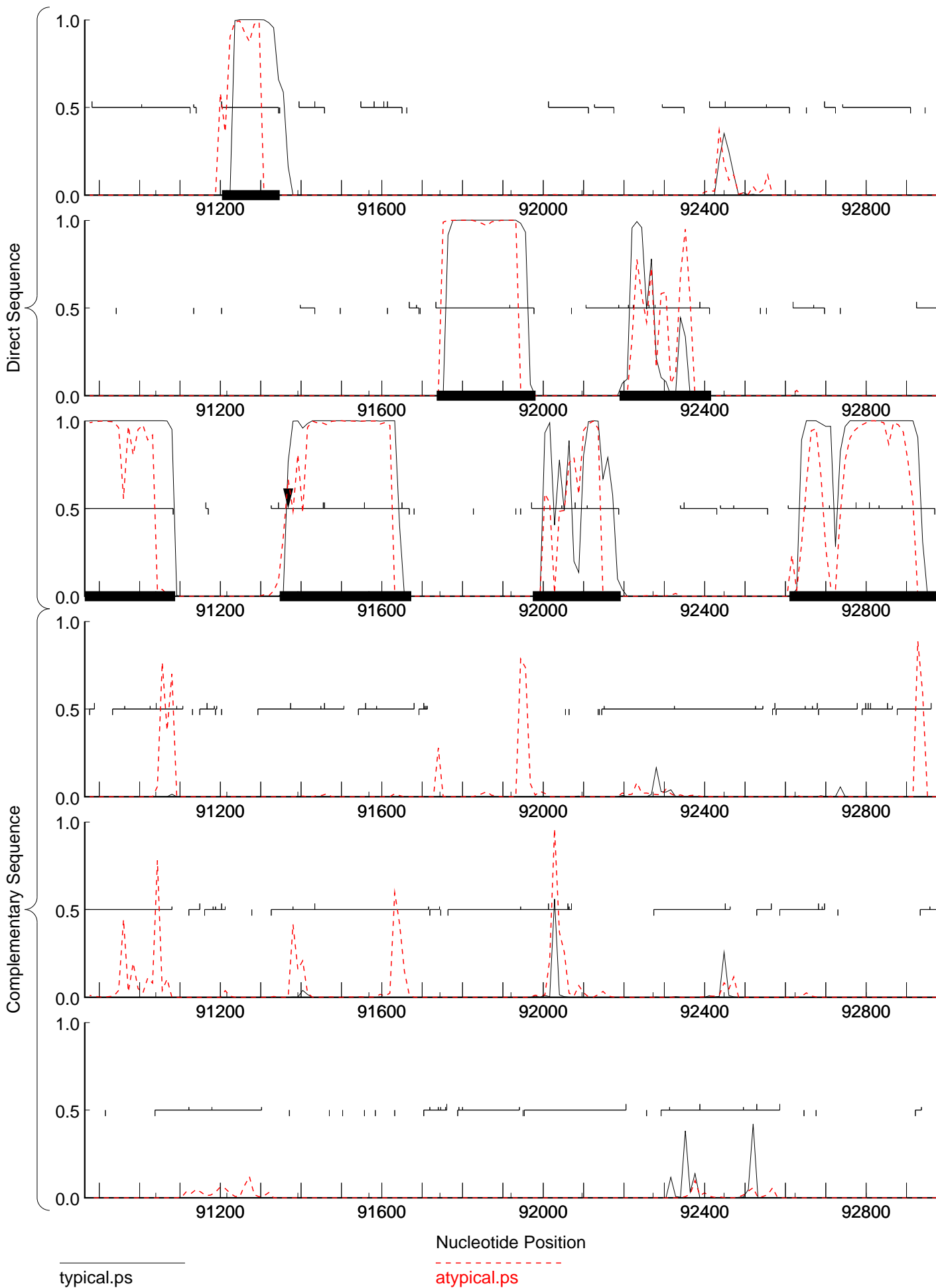
atypical.ps

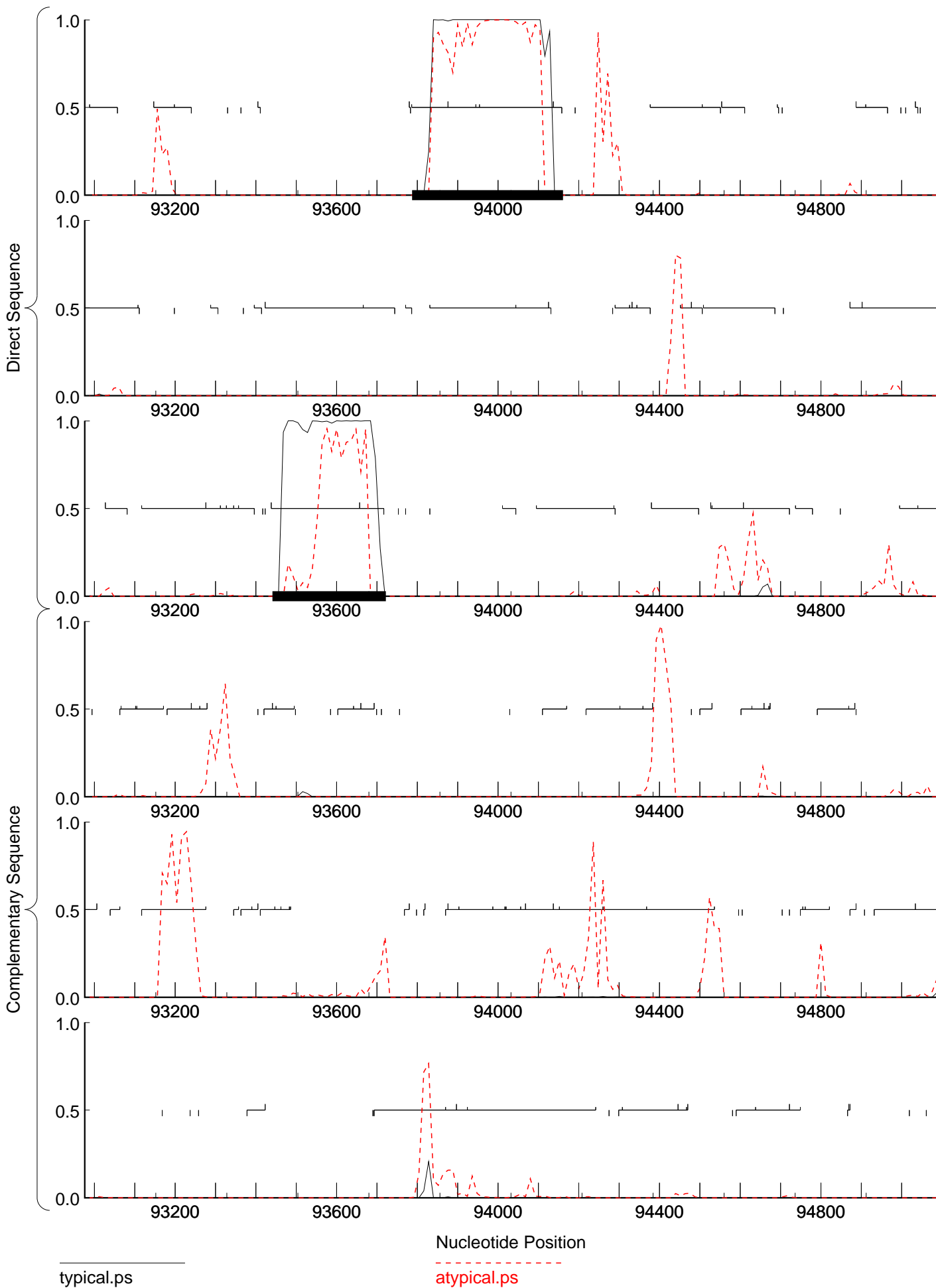
GeneMark.hmm prediction



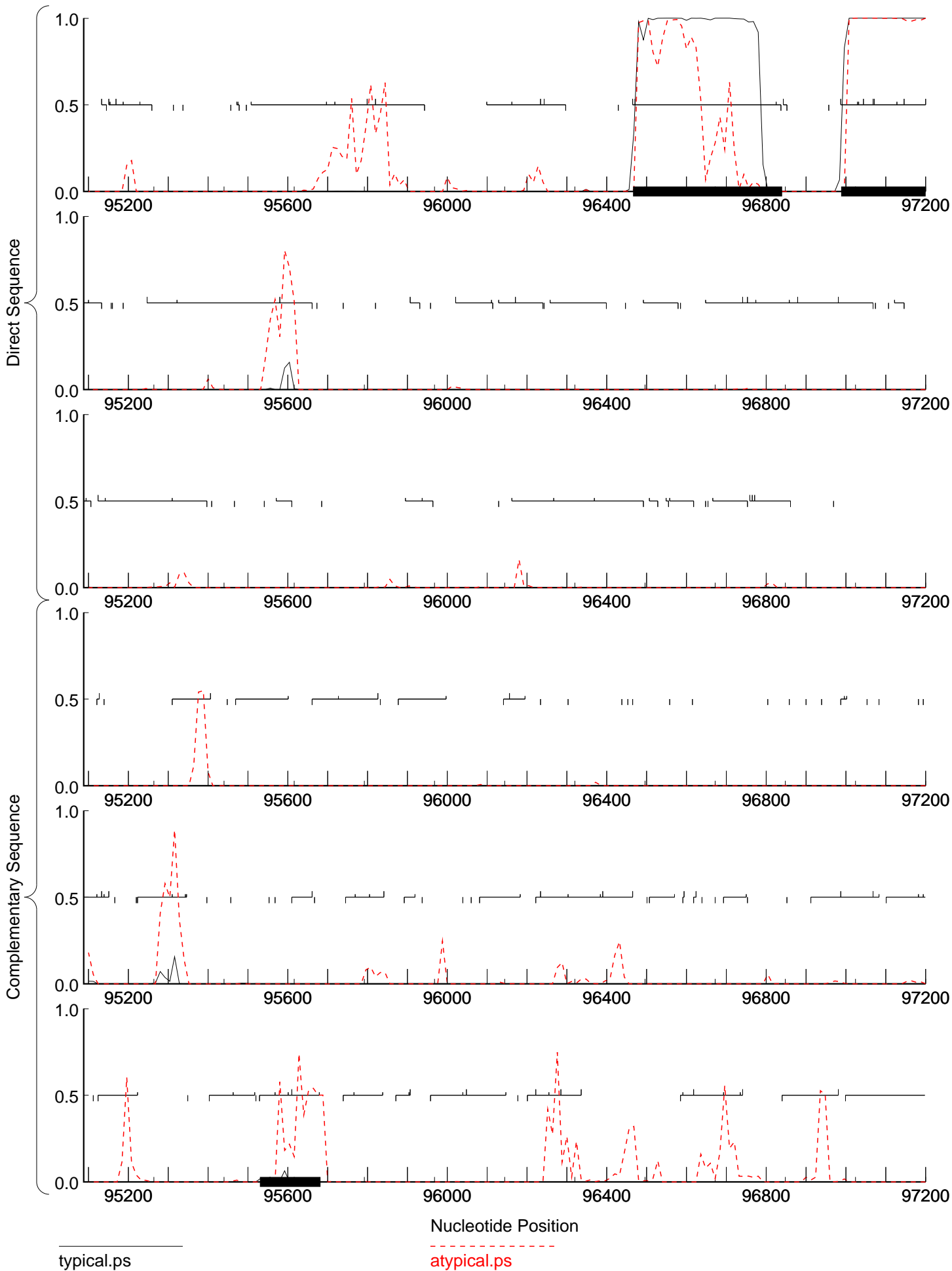








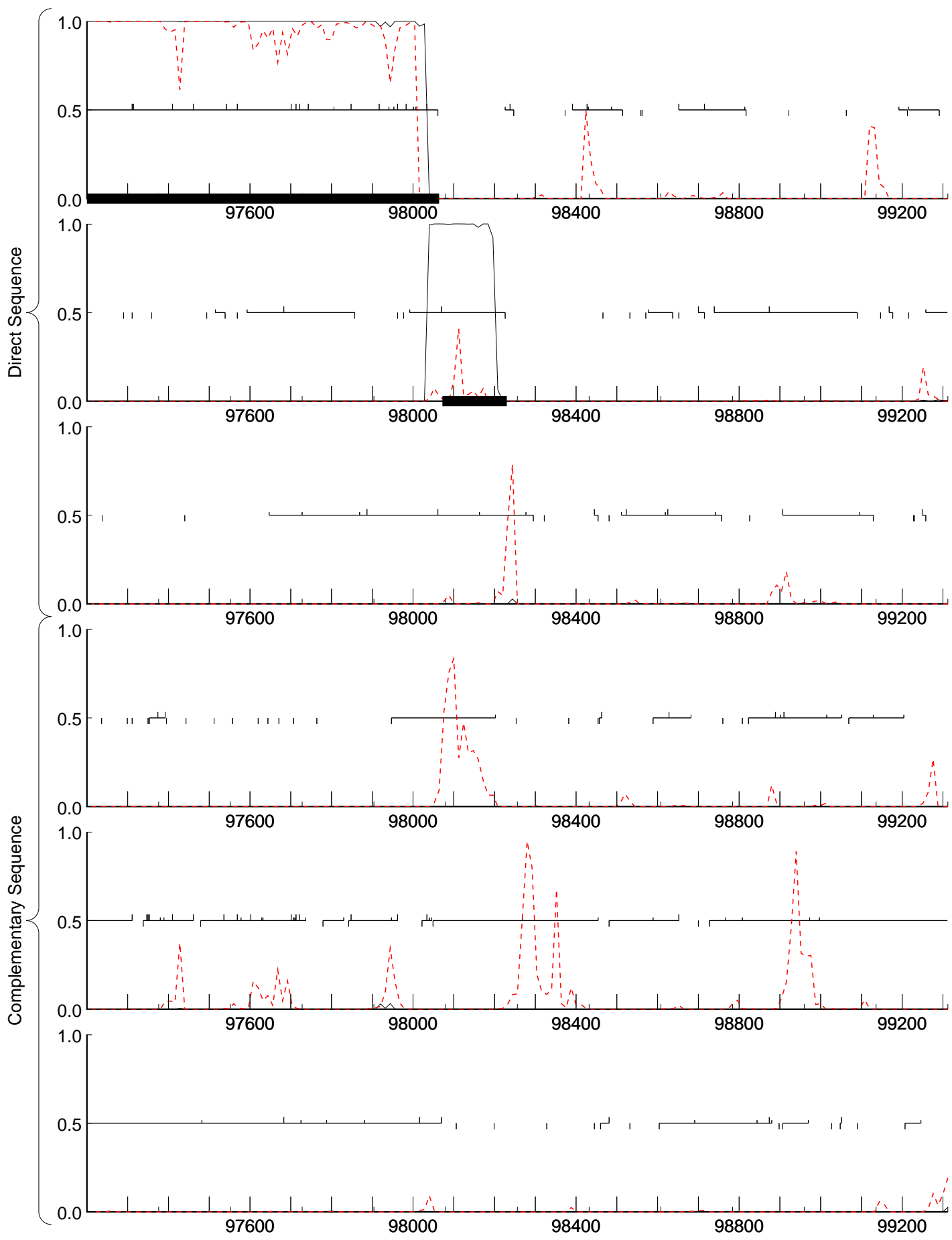
GeneMark.hmm prediction



typical.ps

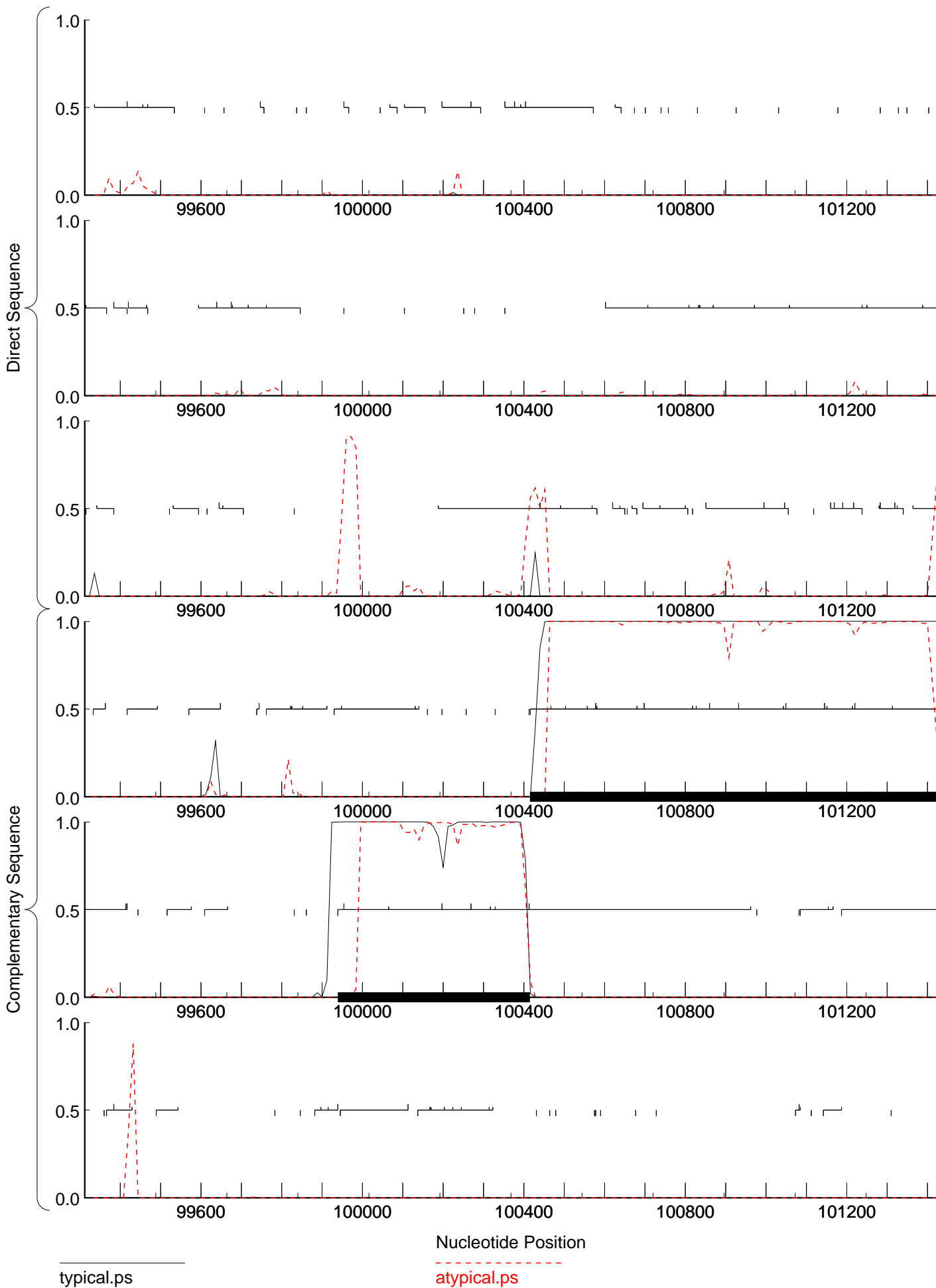
atypical.ps

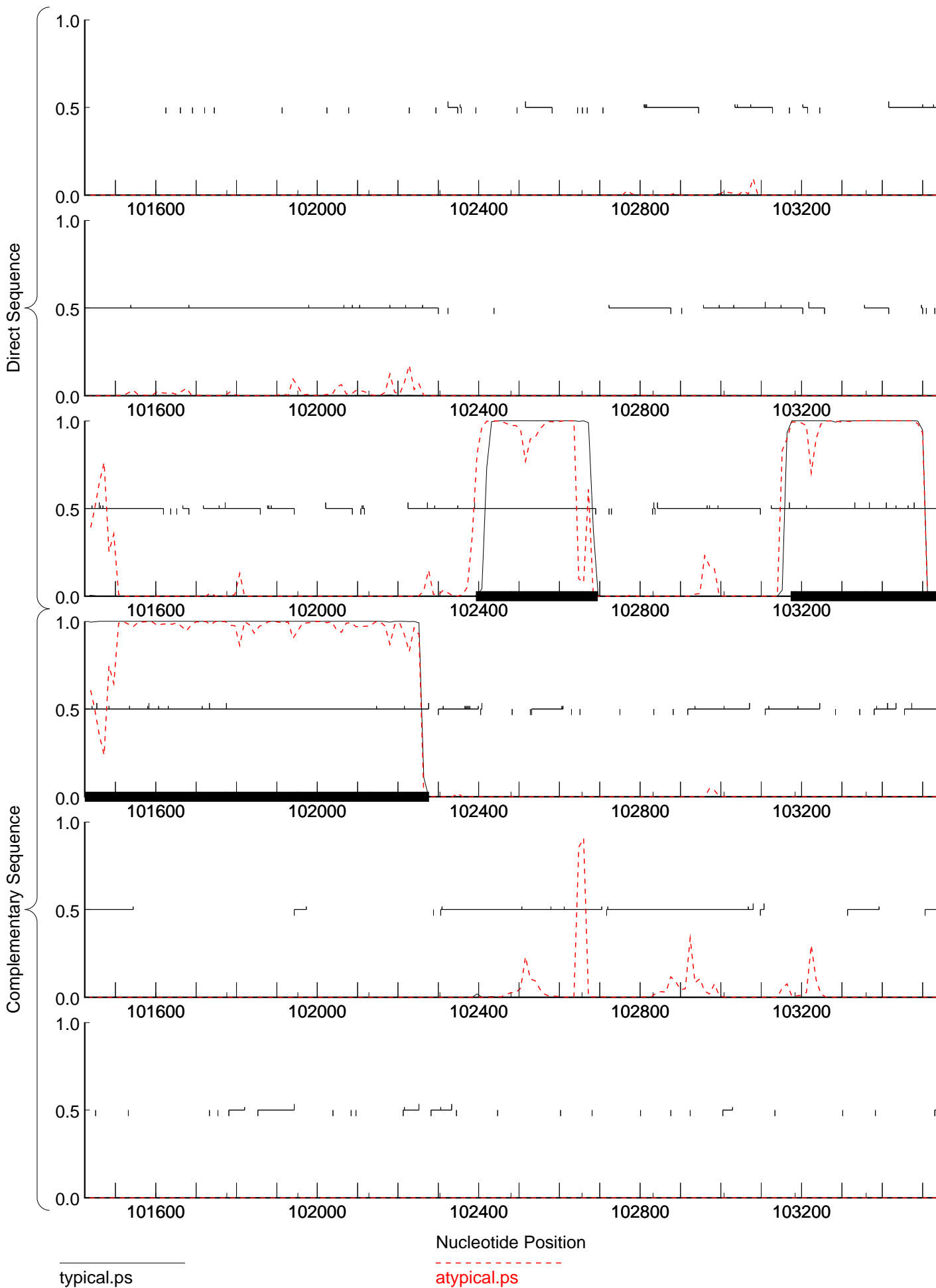
GeneMark.hmm prediction



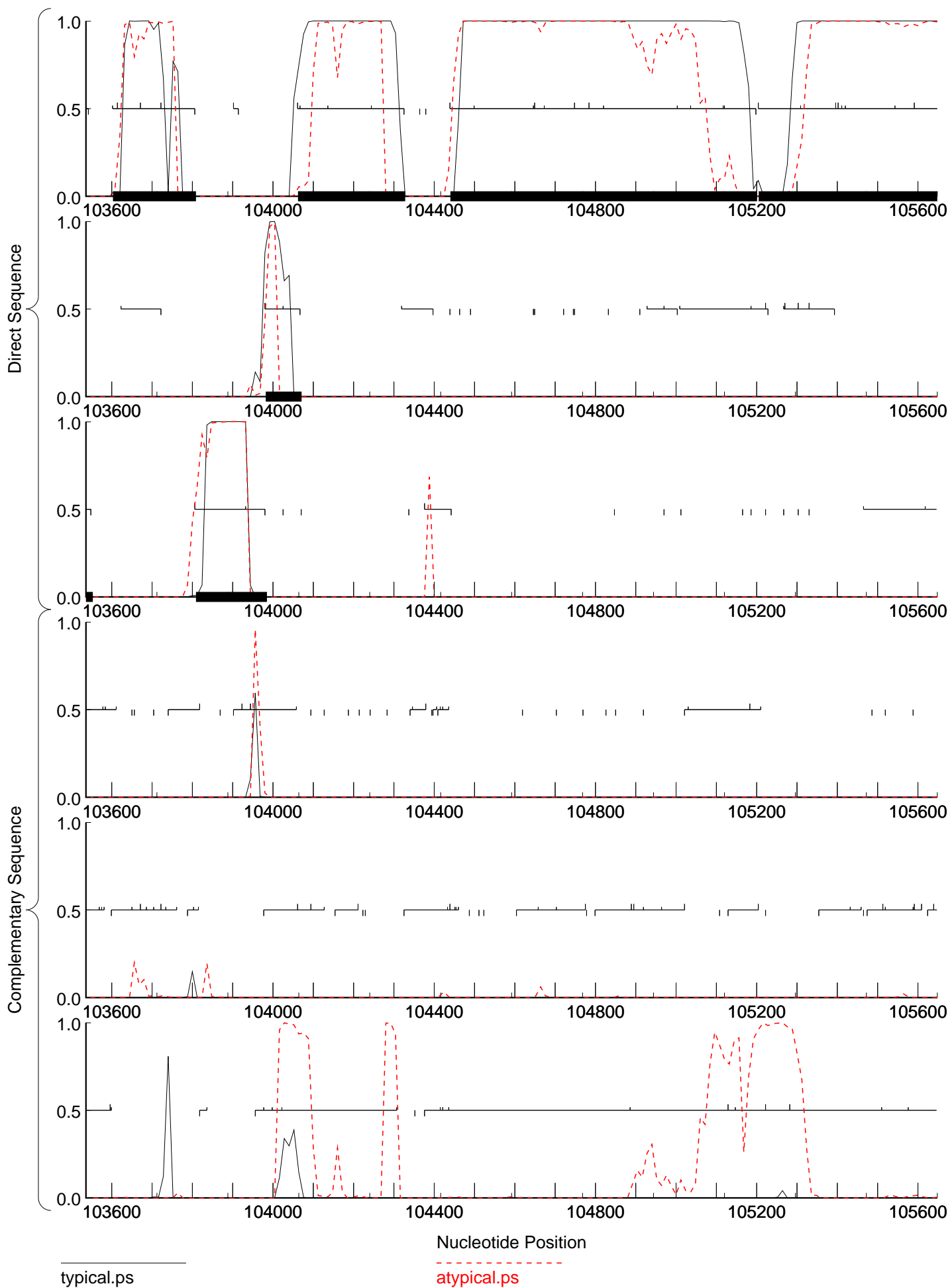
typical.ps

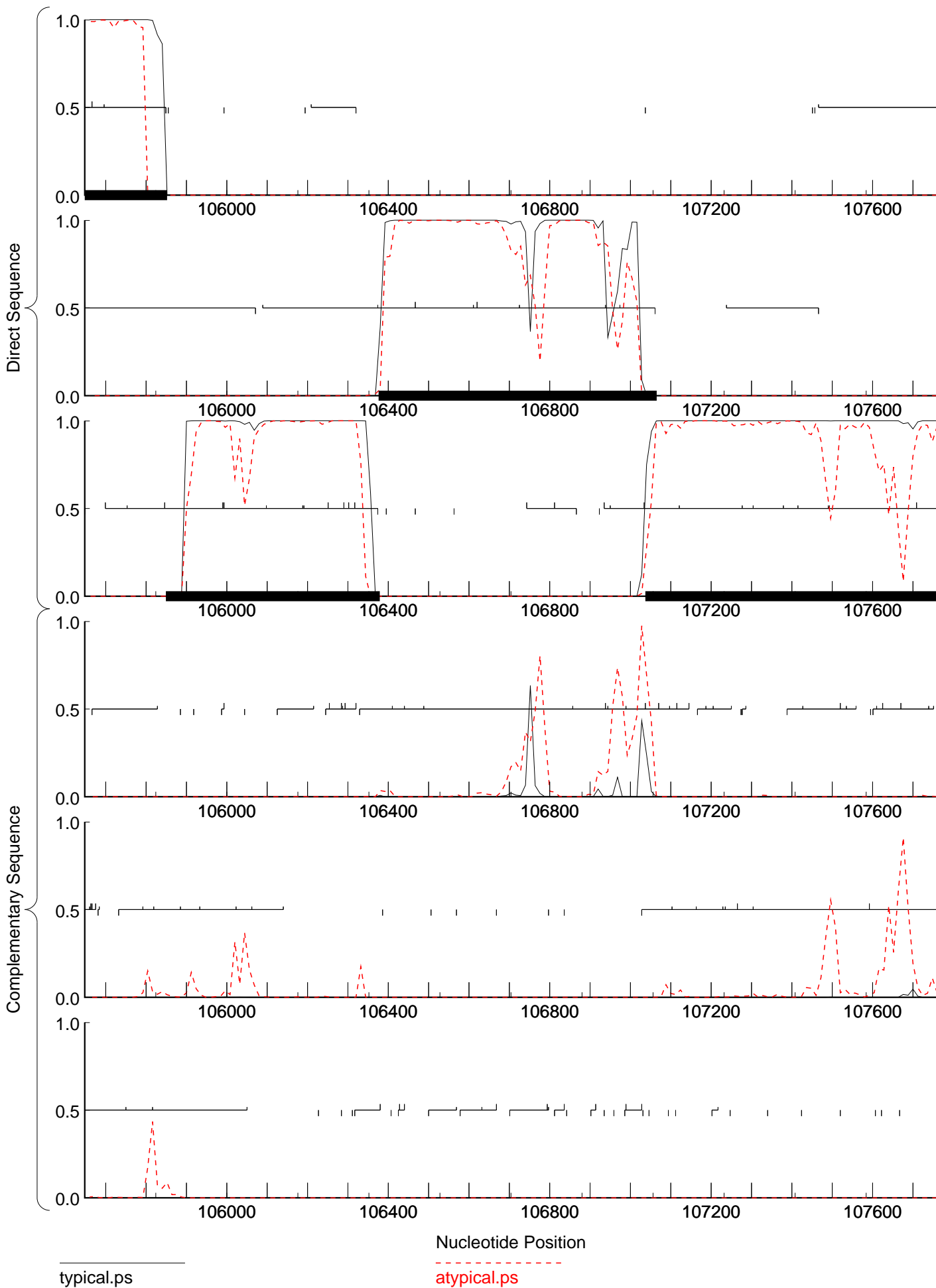
atypical.ps

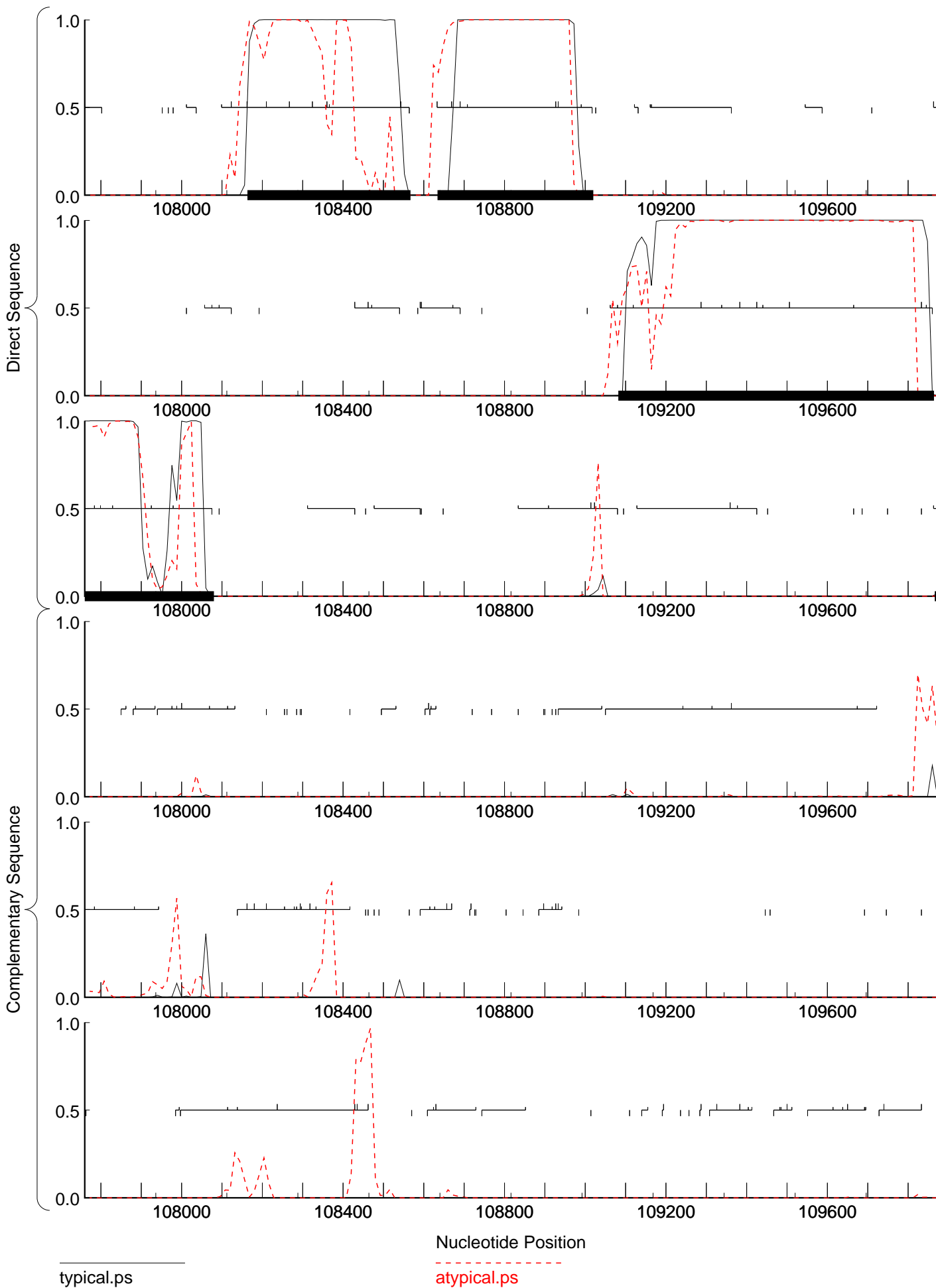


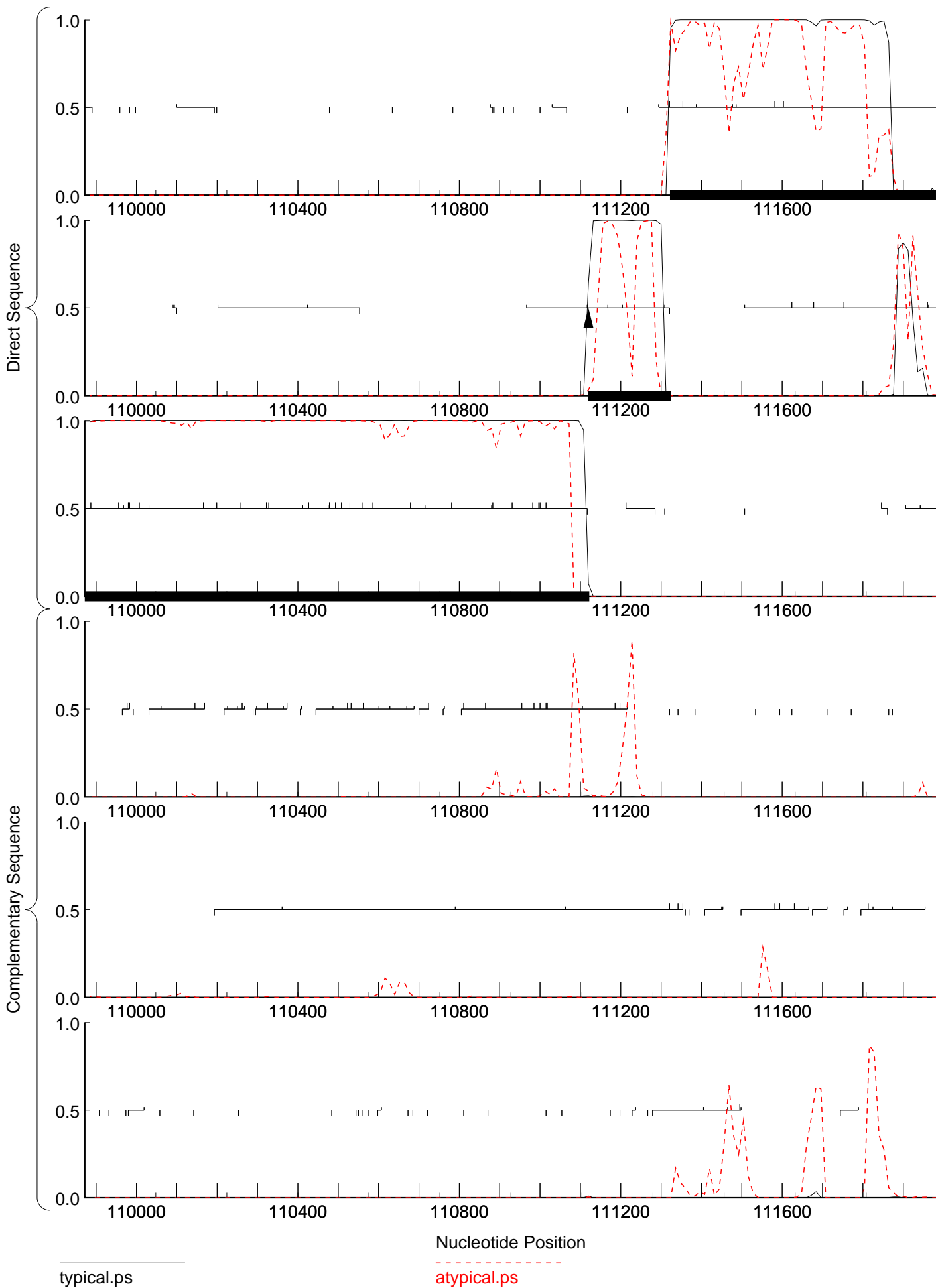


GeneMark.hmm prediction

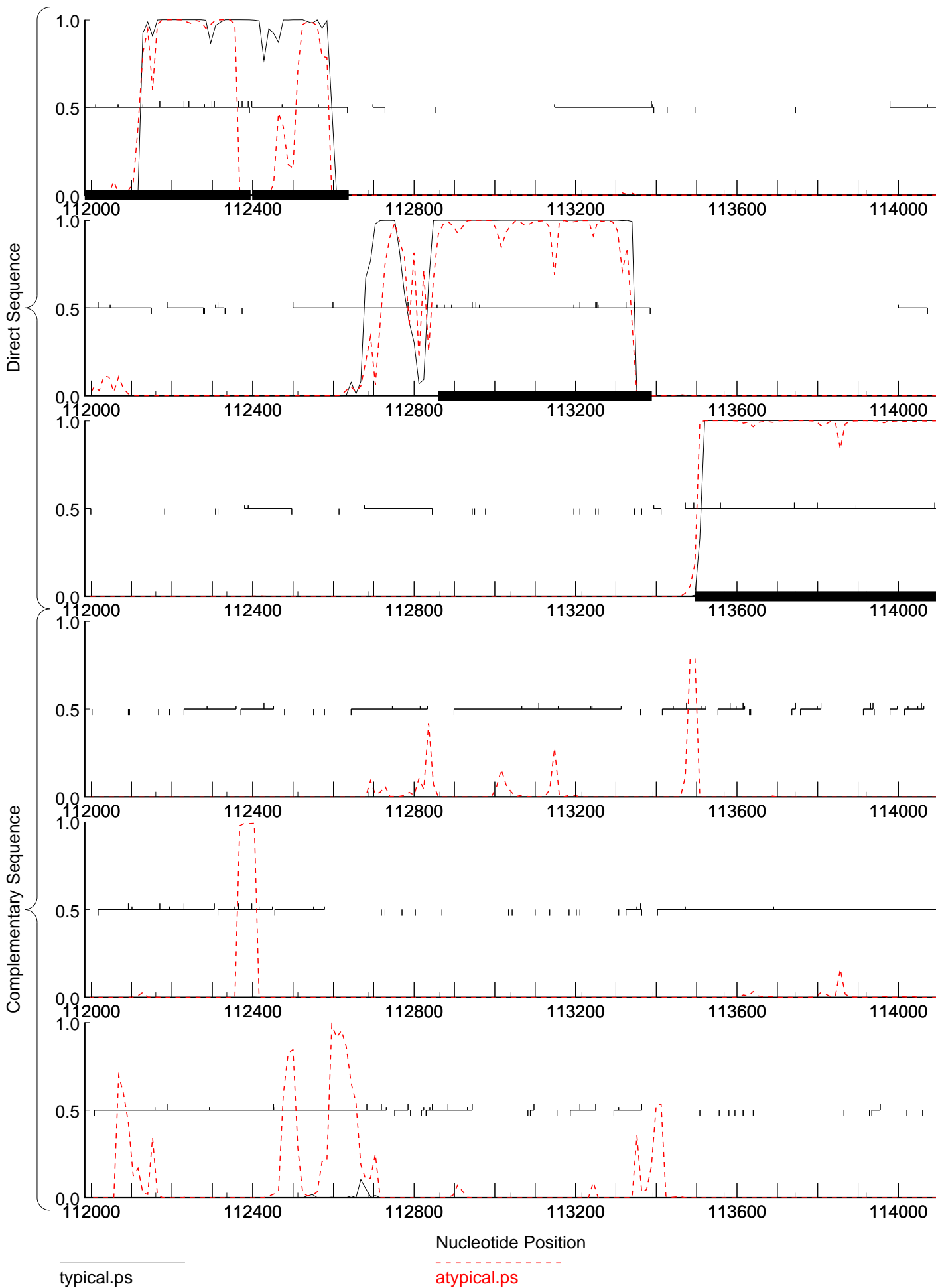


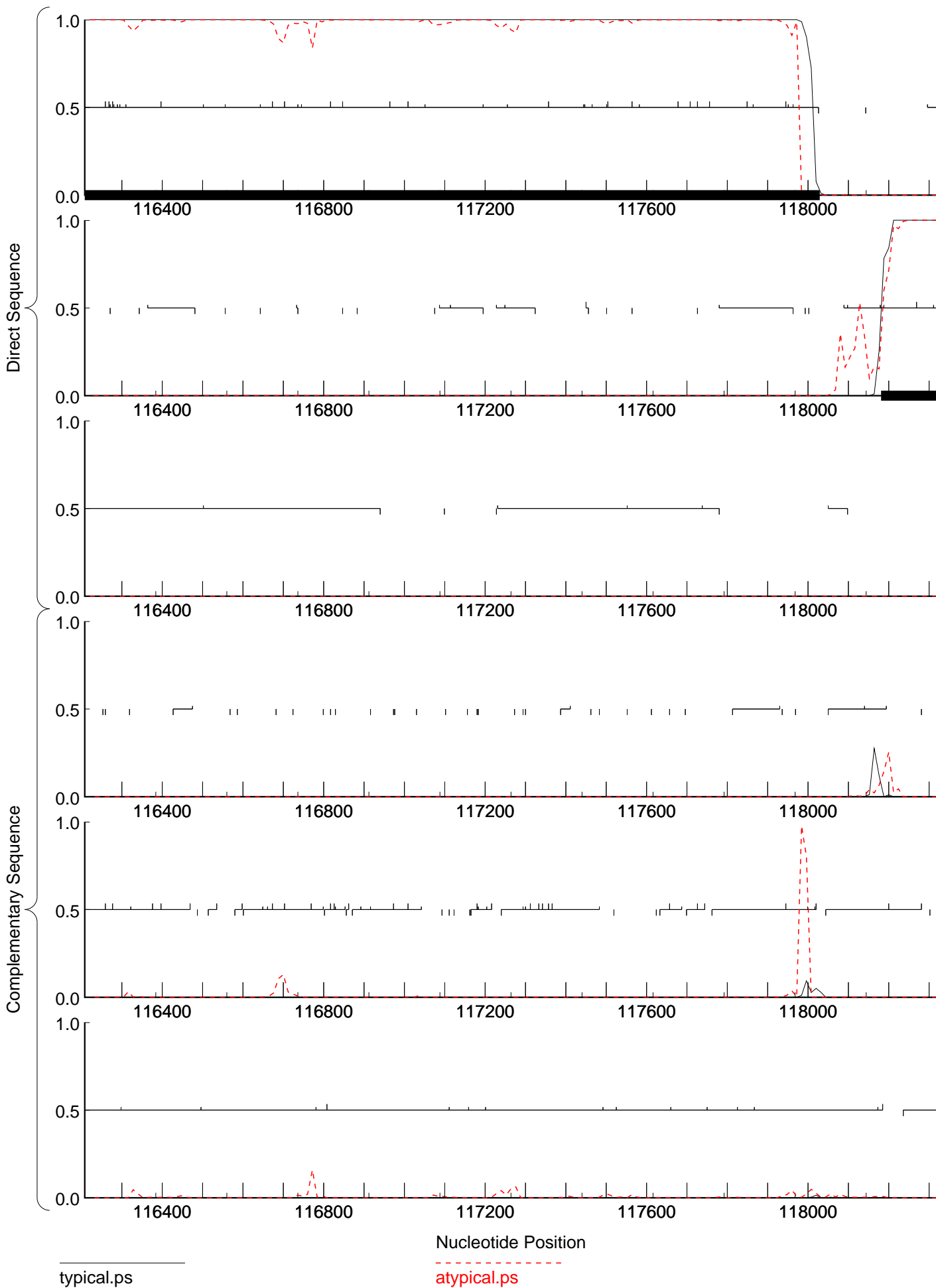


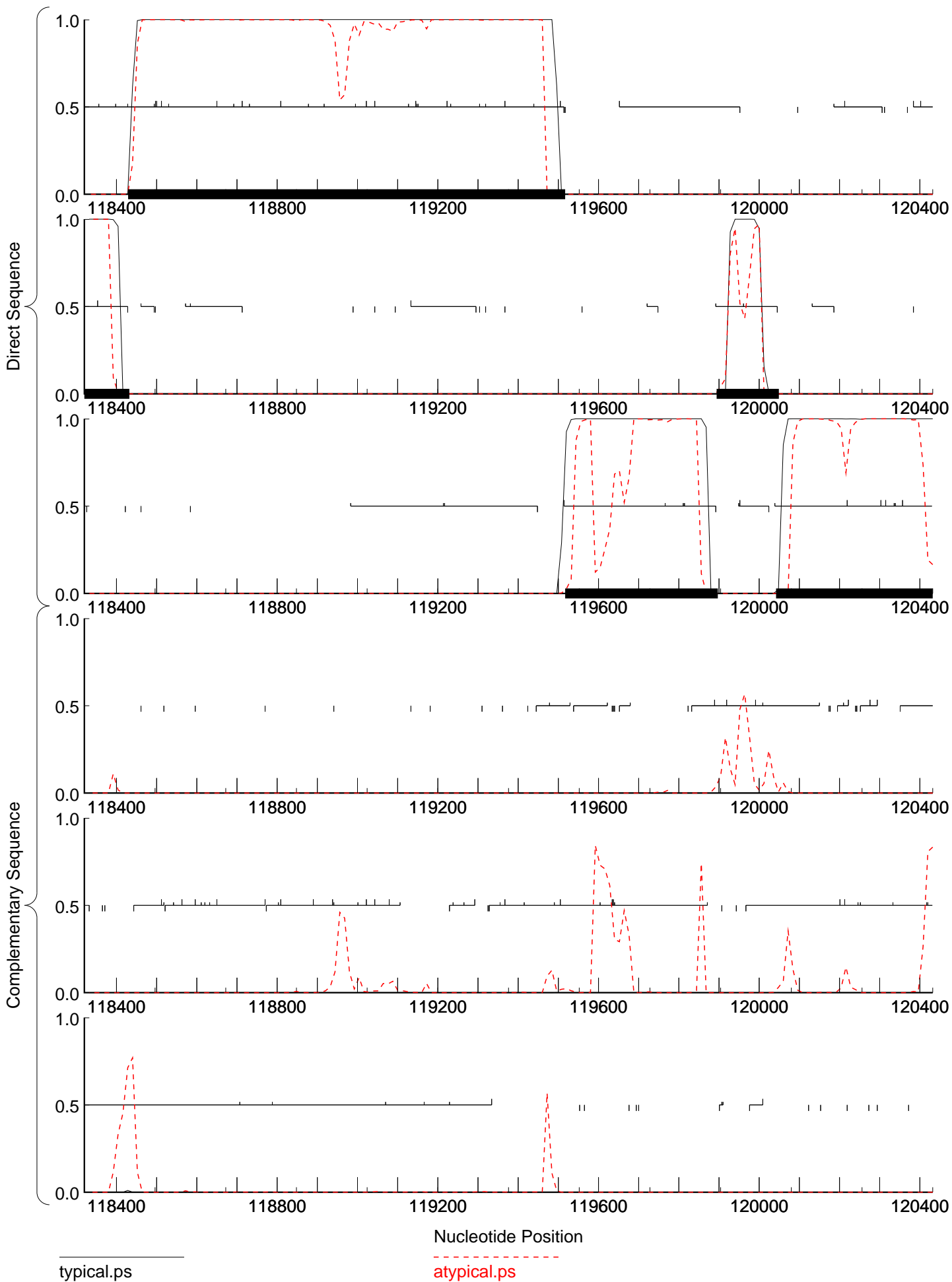


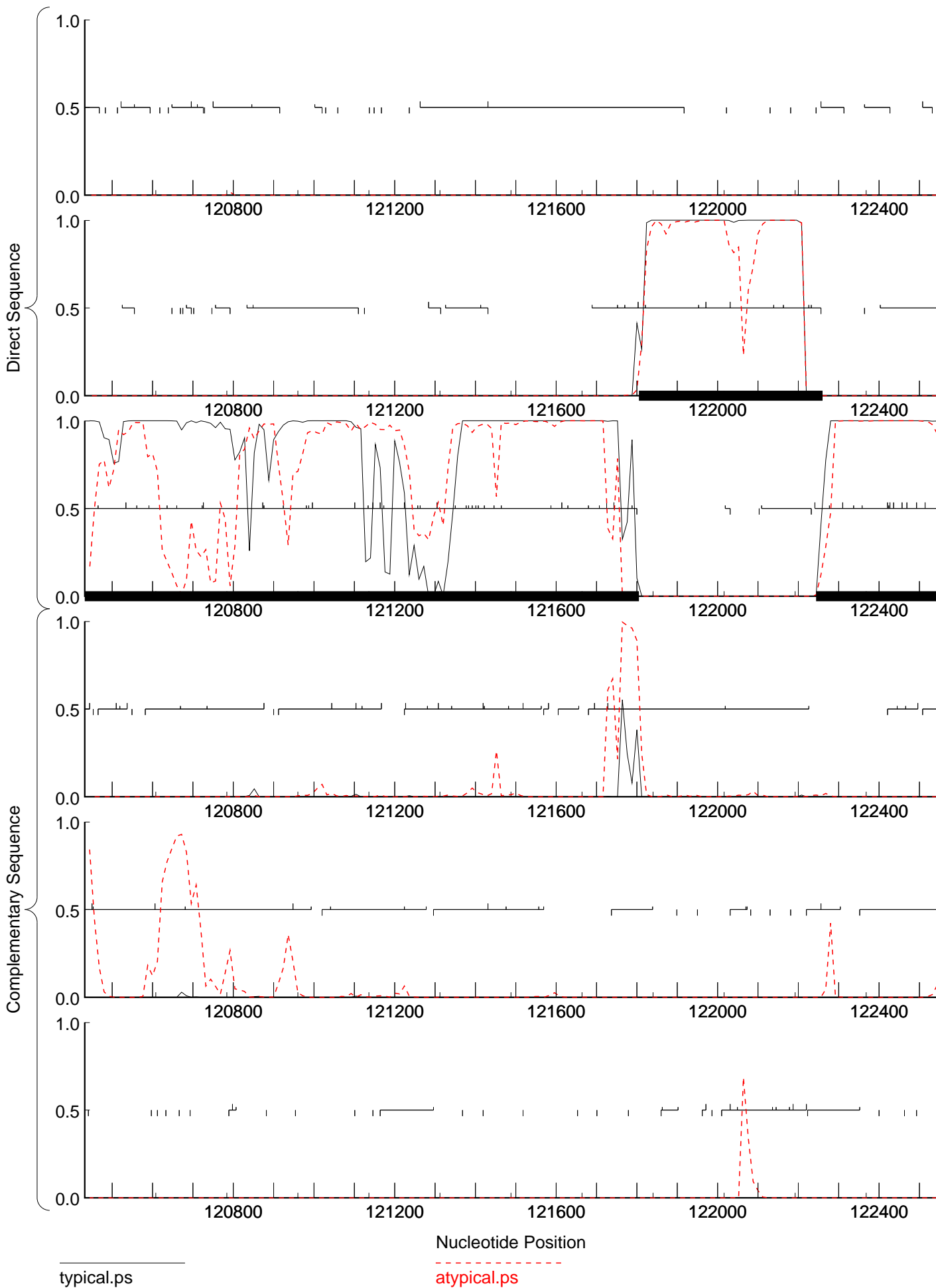


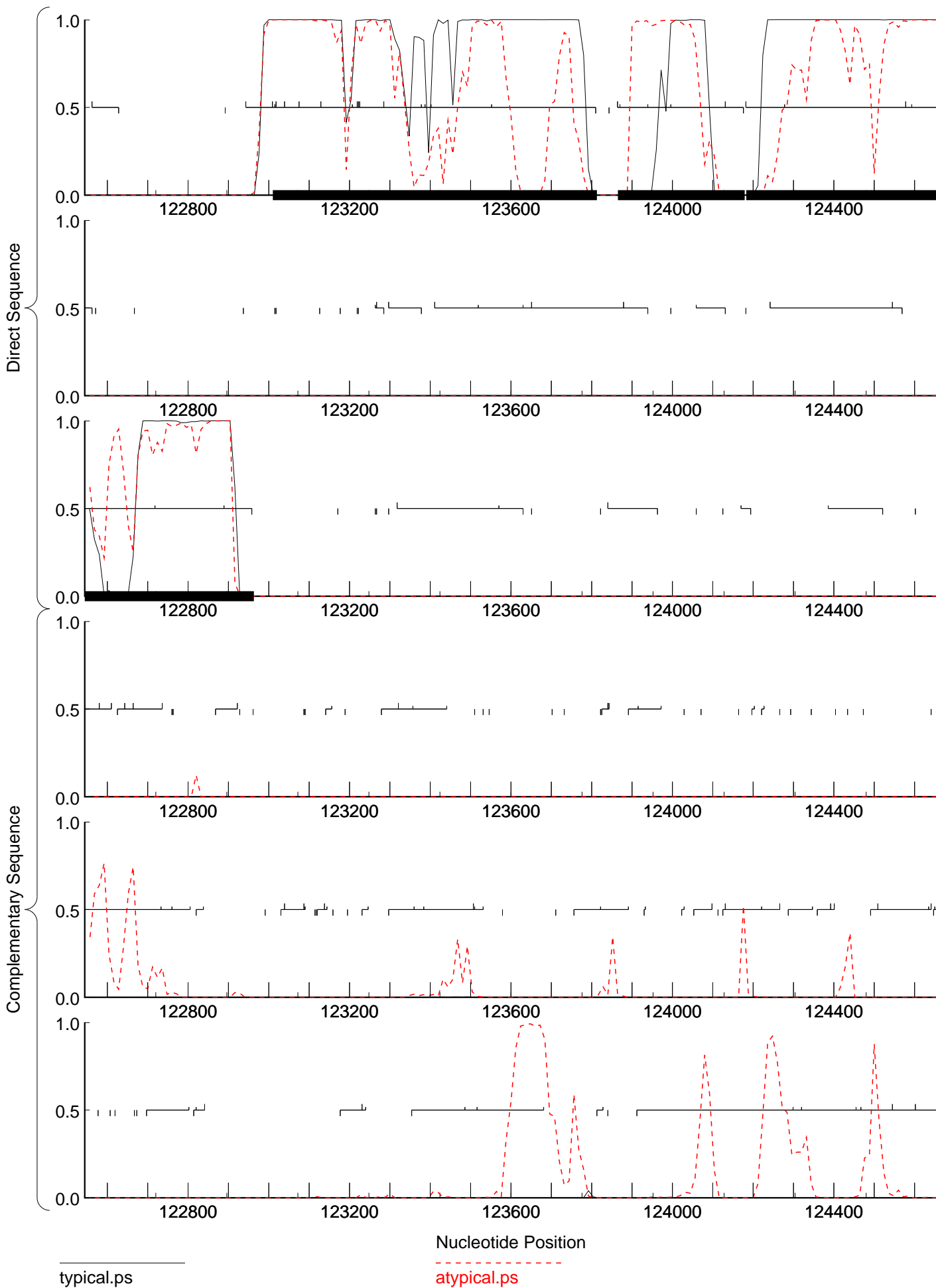
GeneMark.hmm prediction

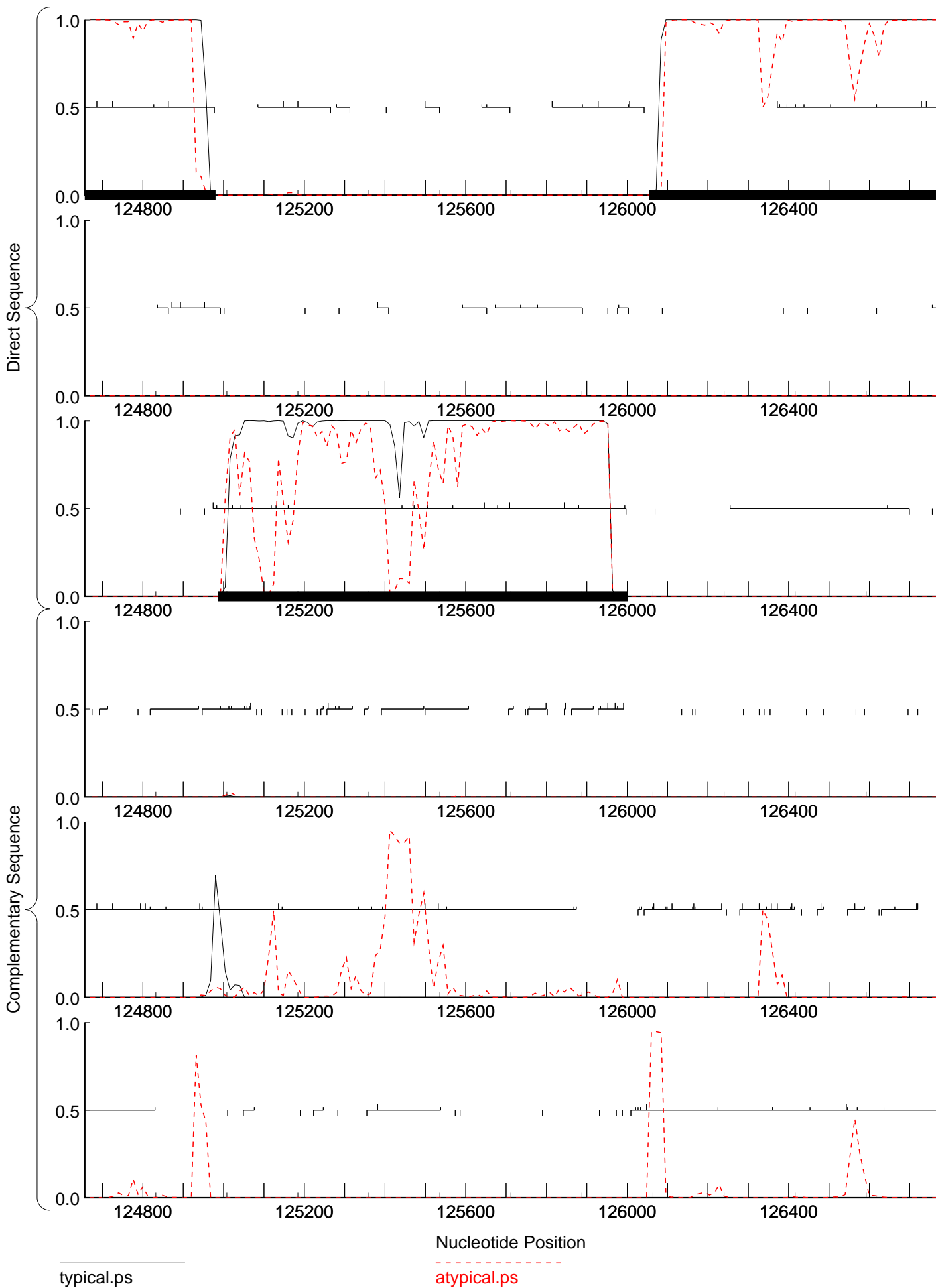


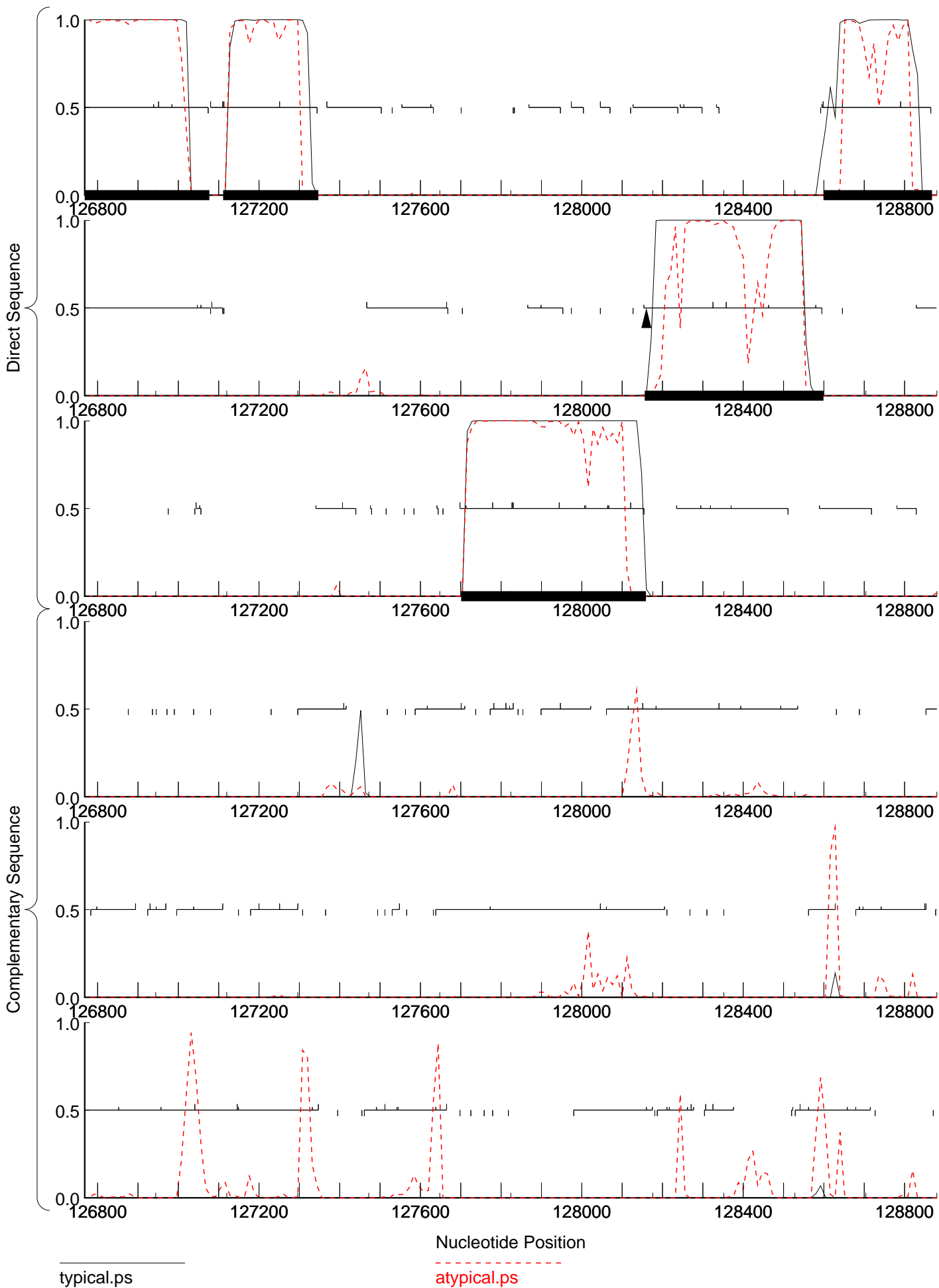


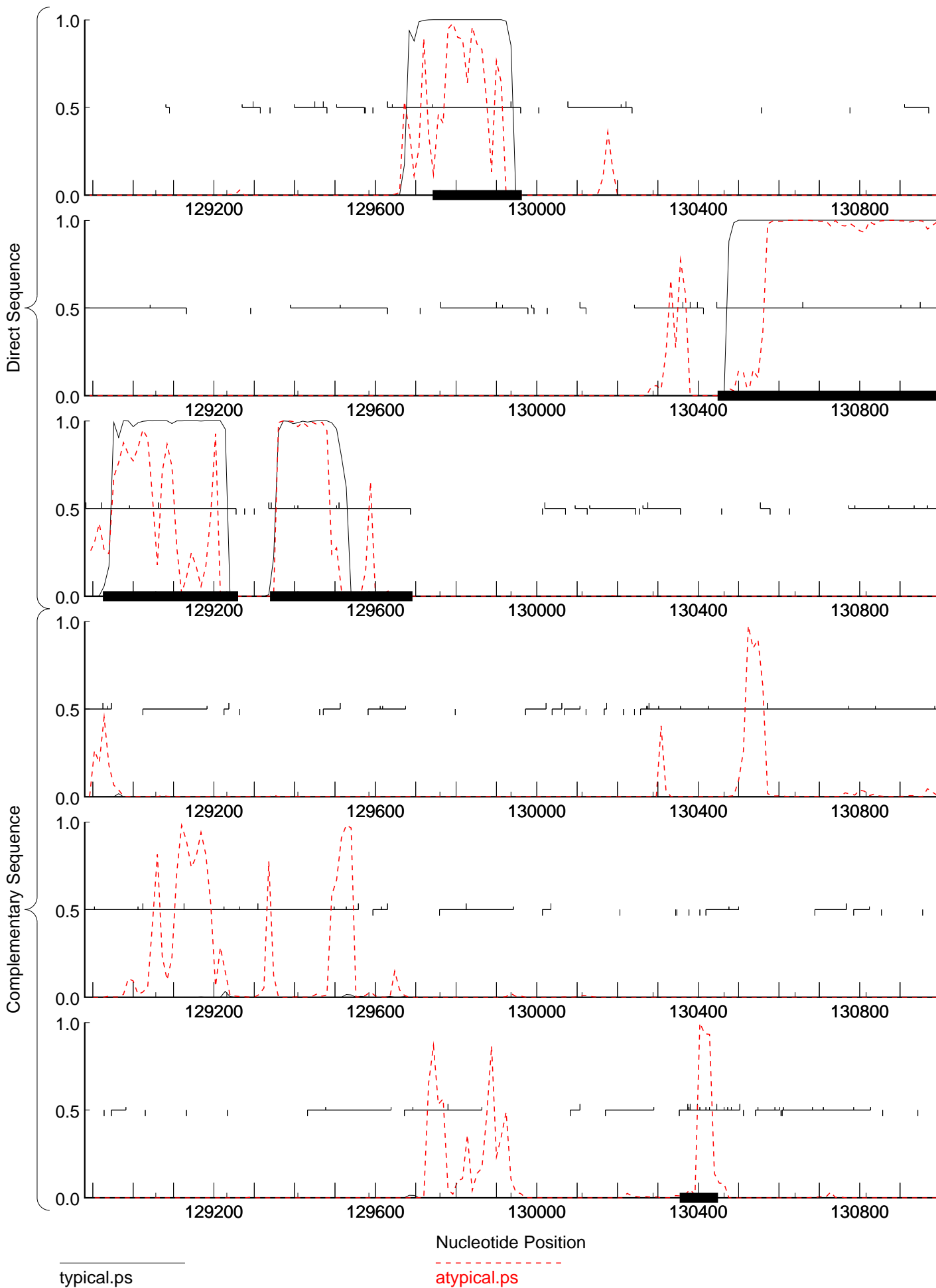






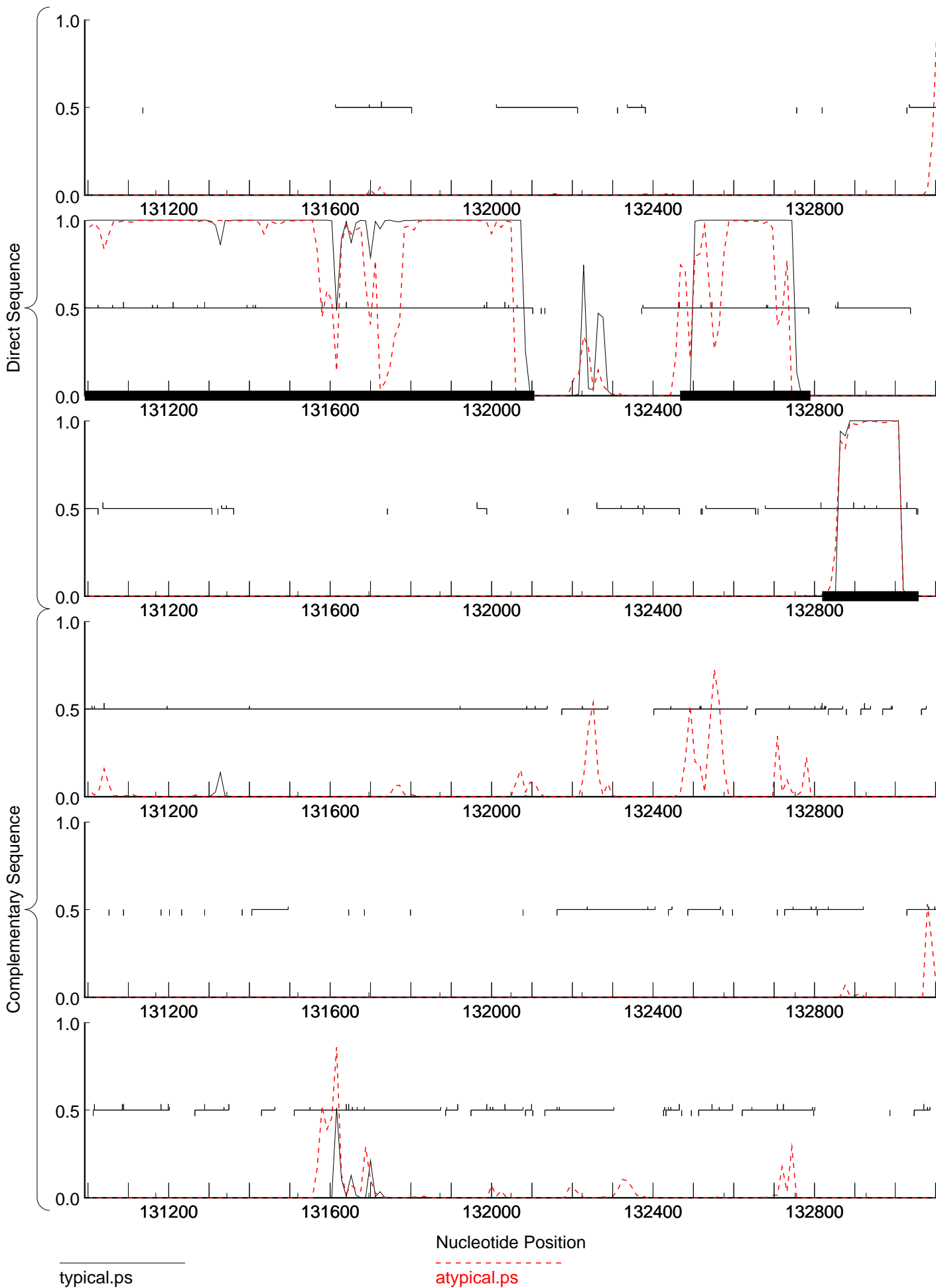


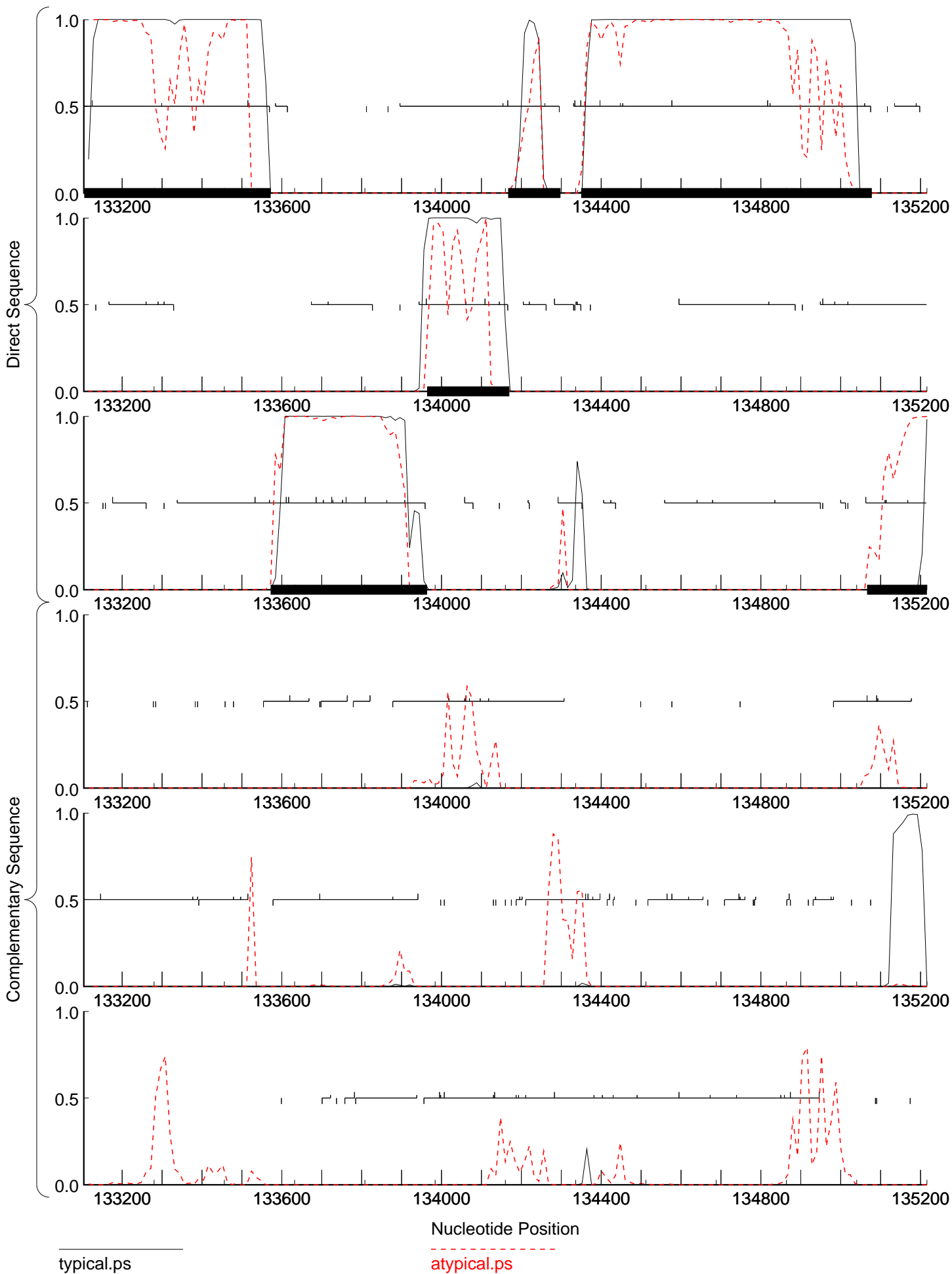


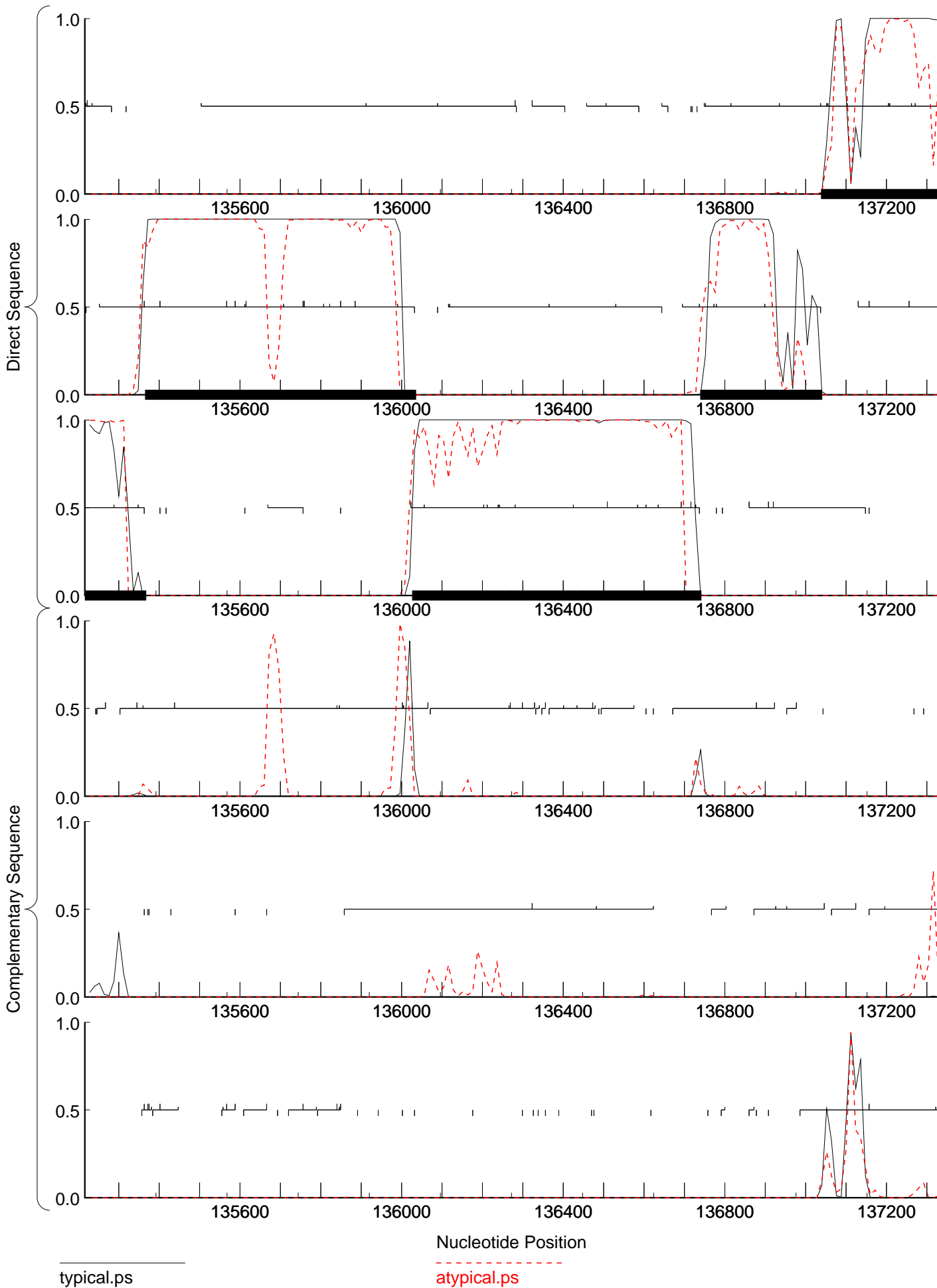


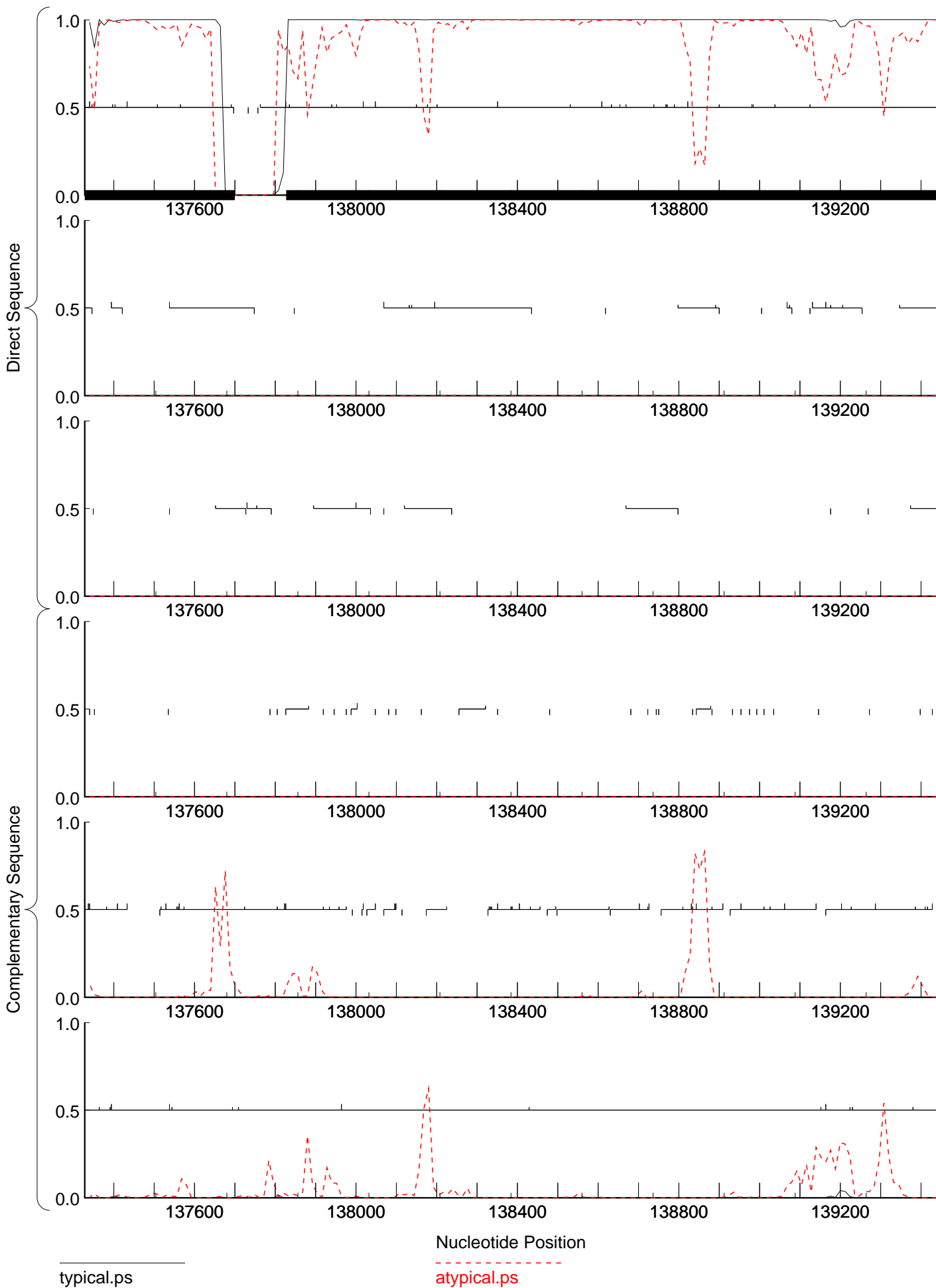
typical.ps

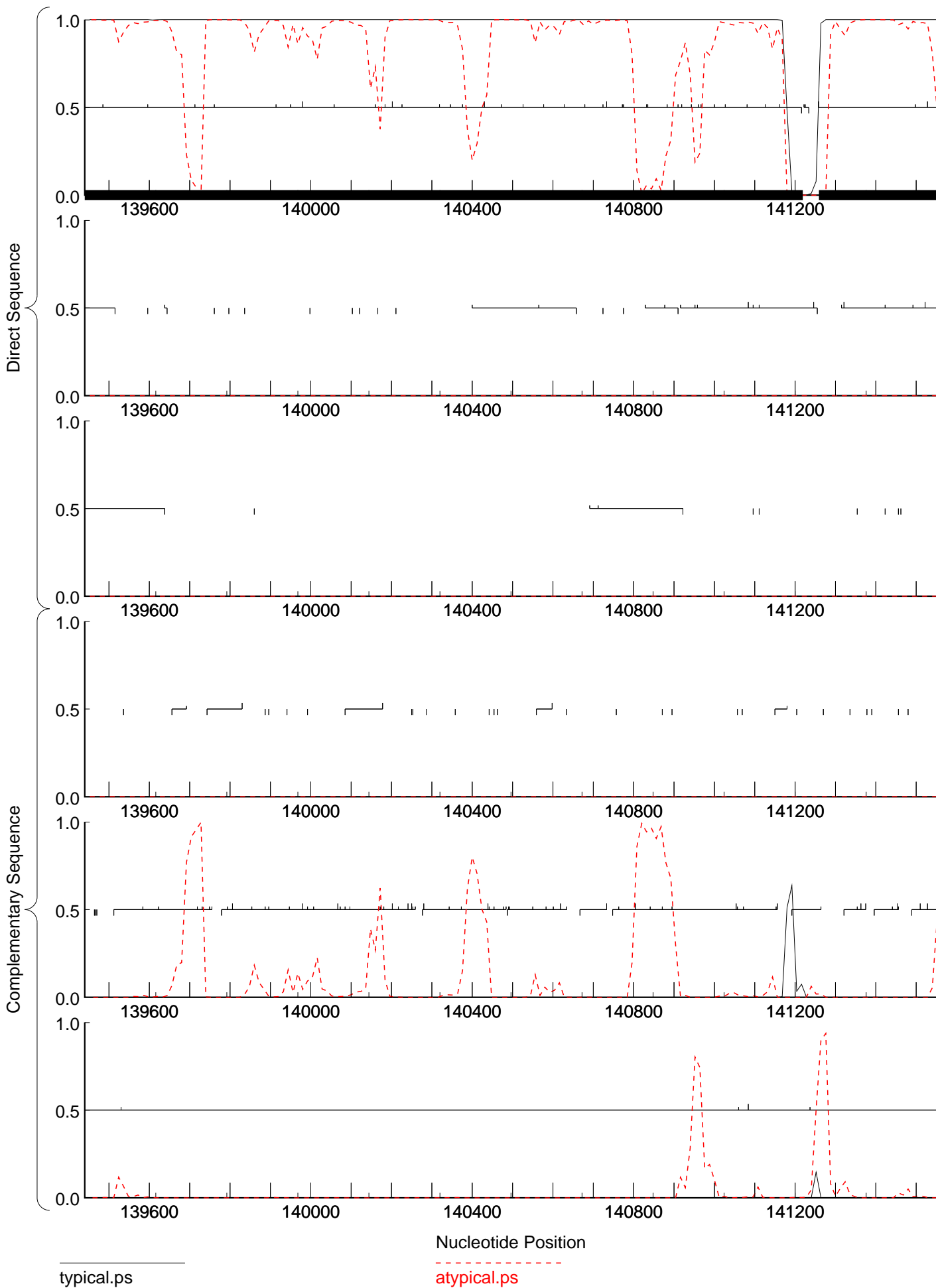
atypical.ps

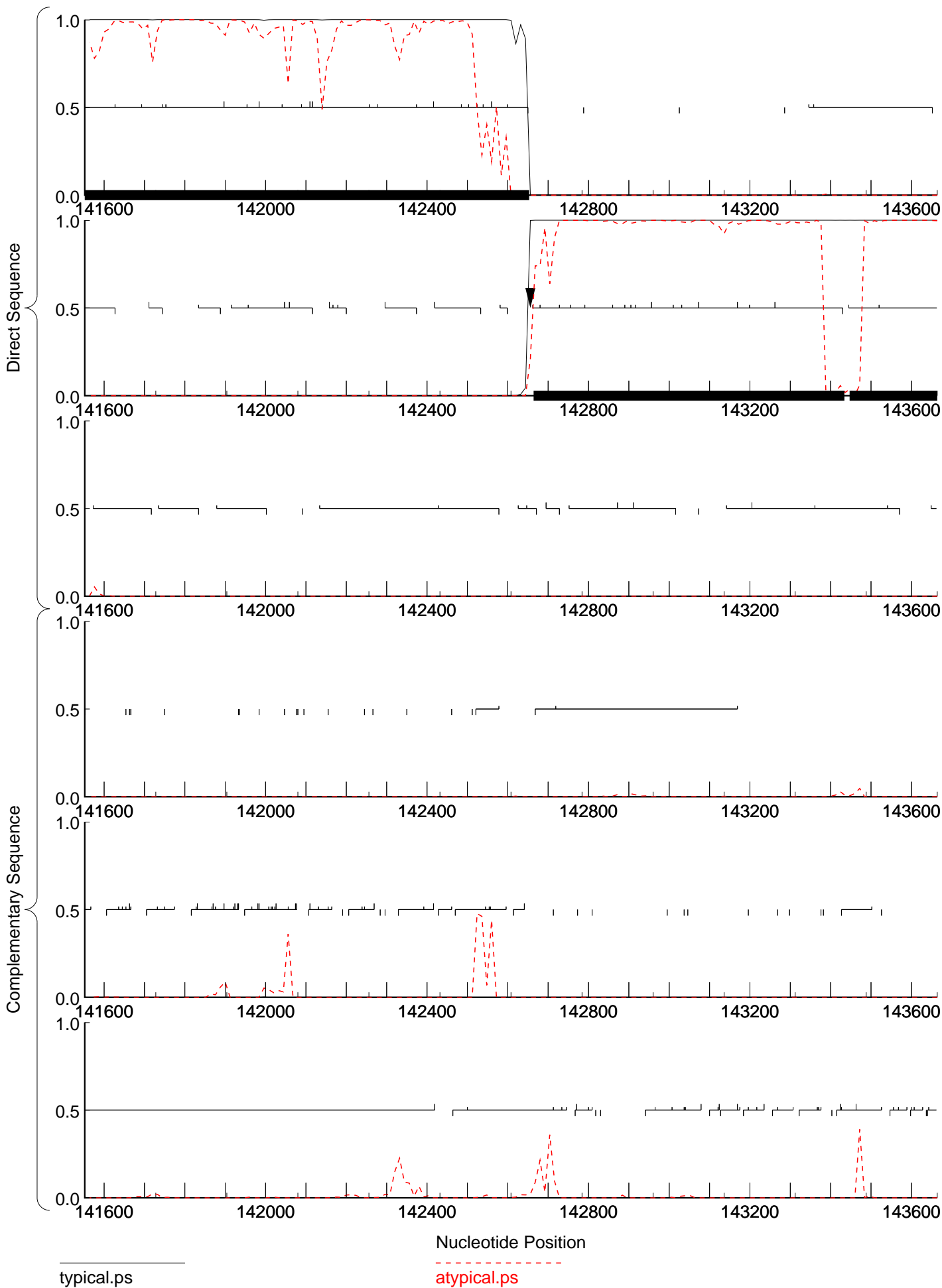


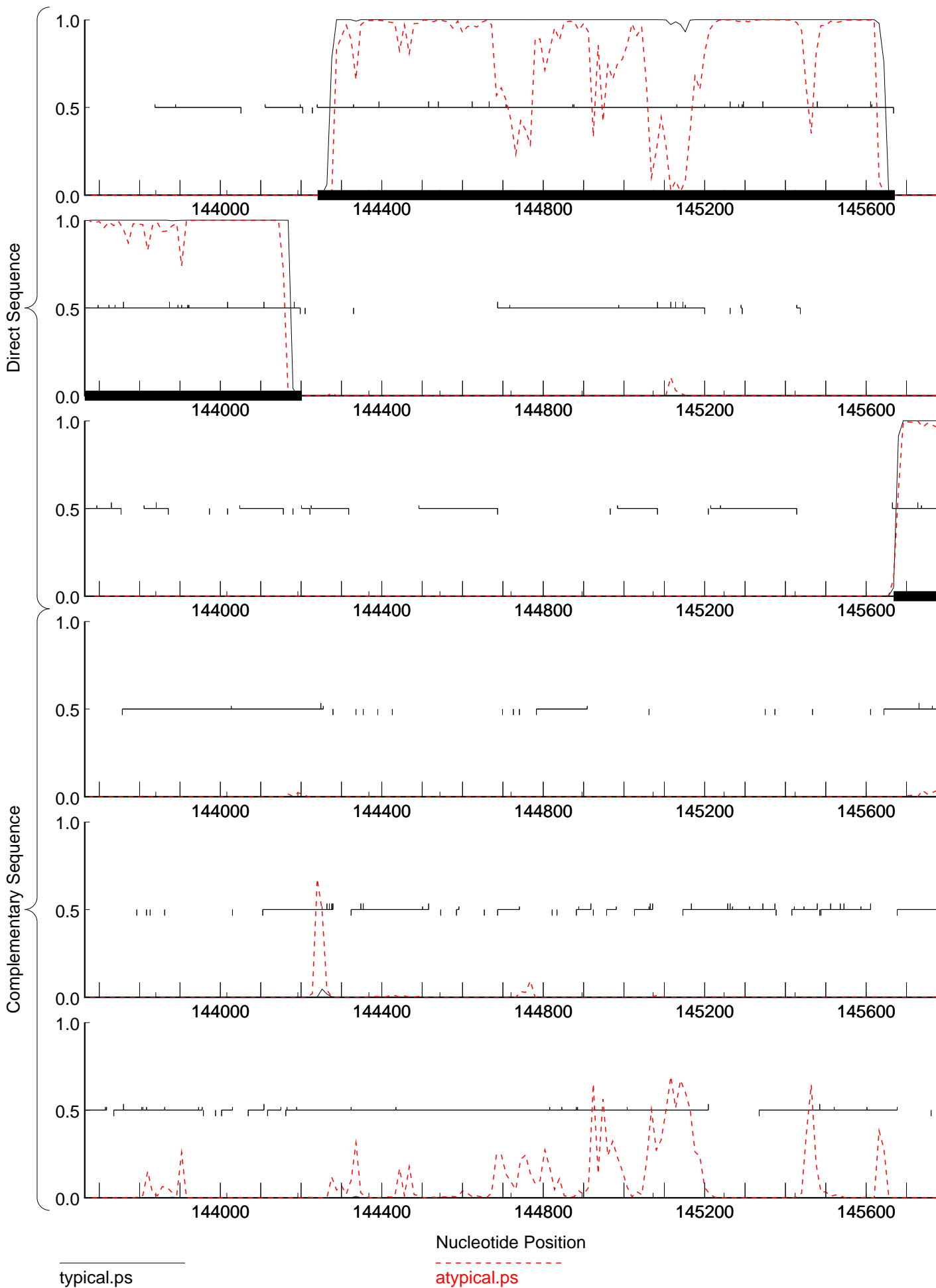


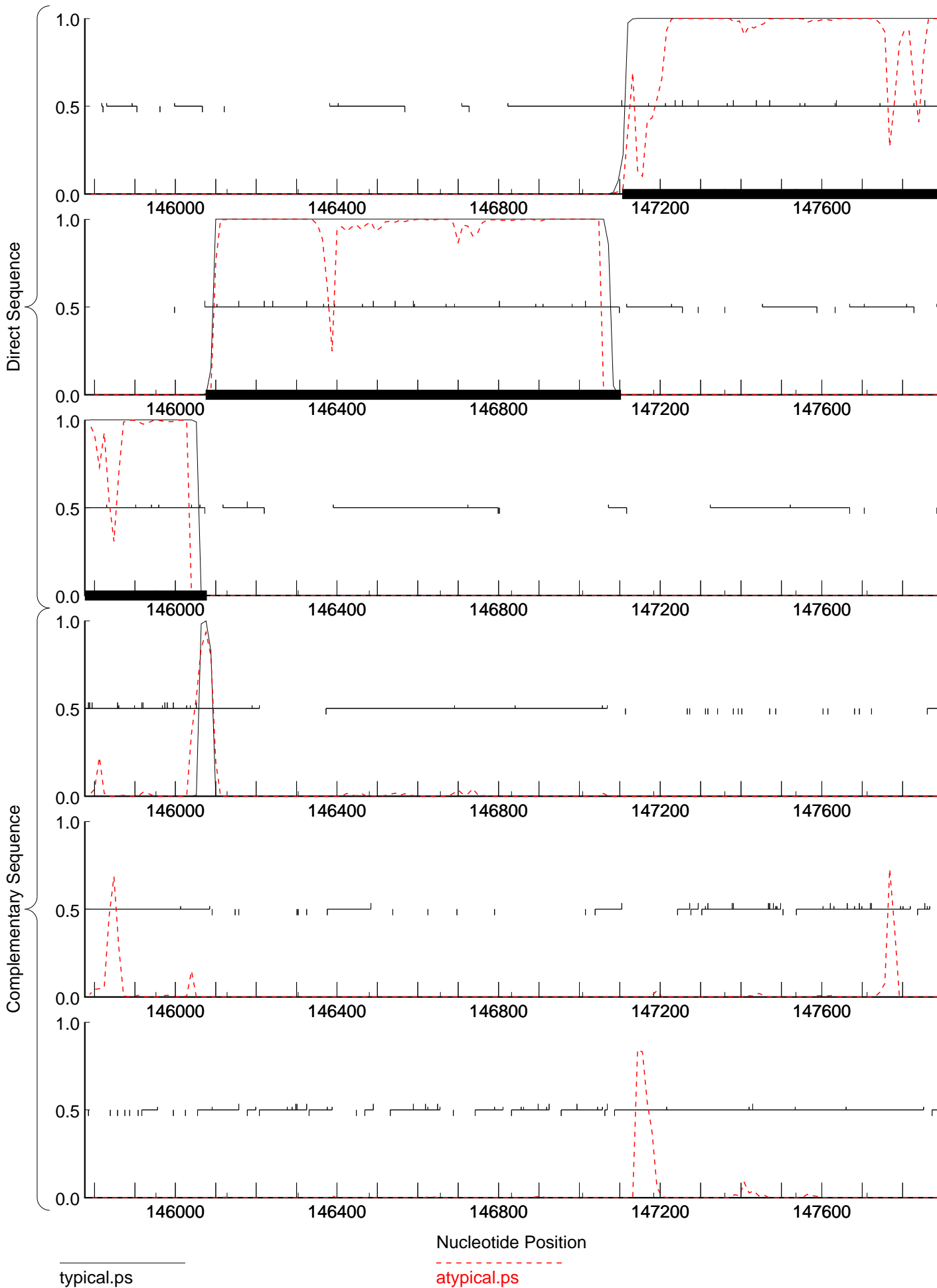






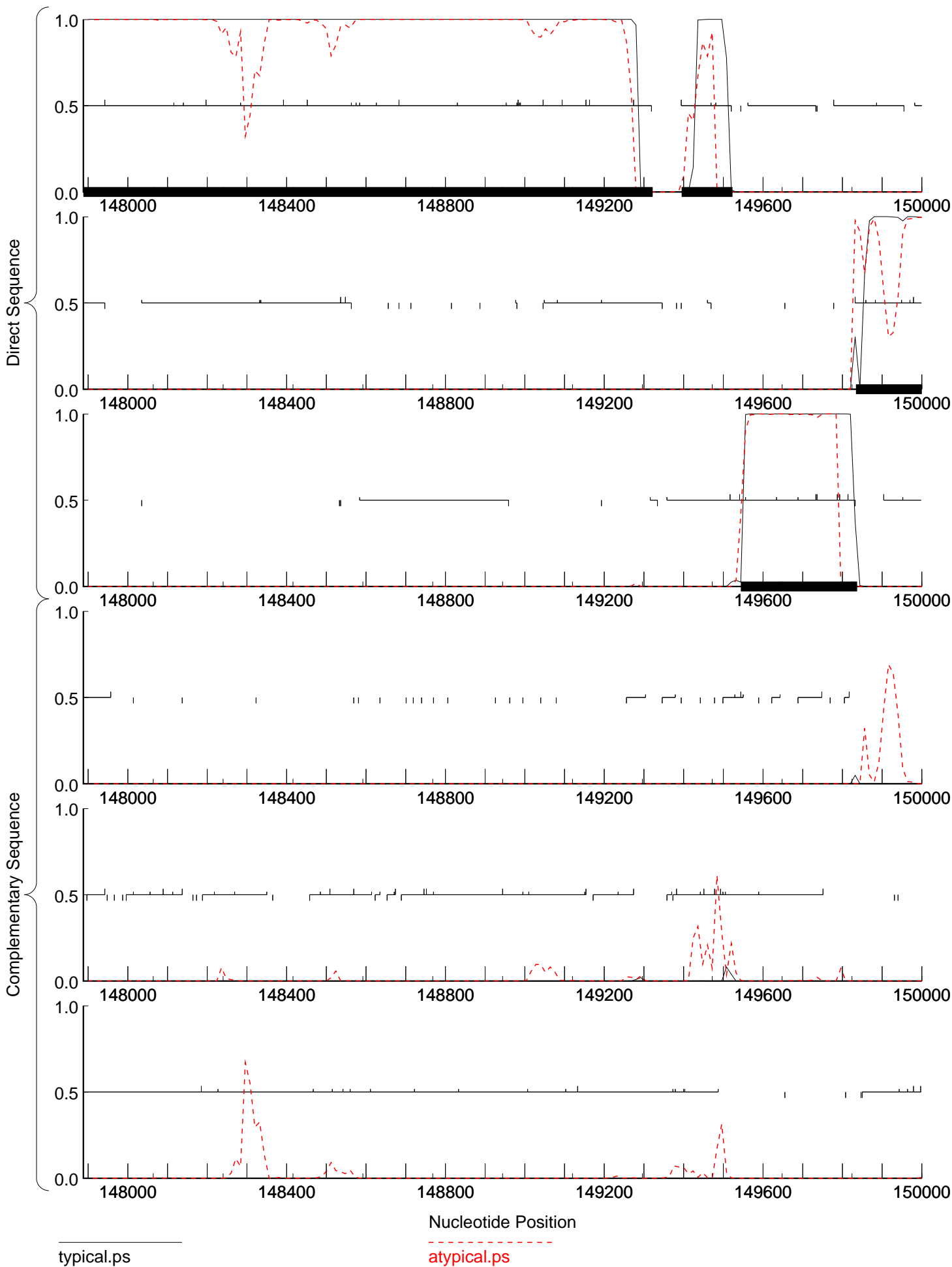


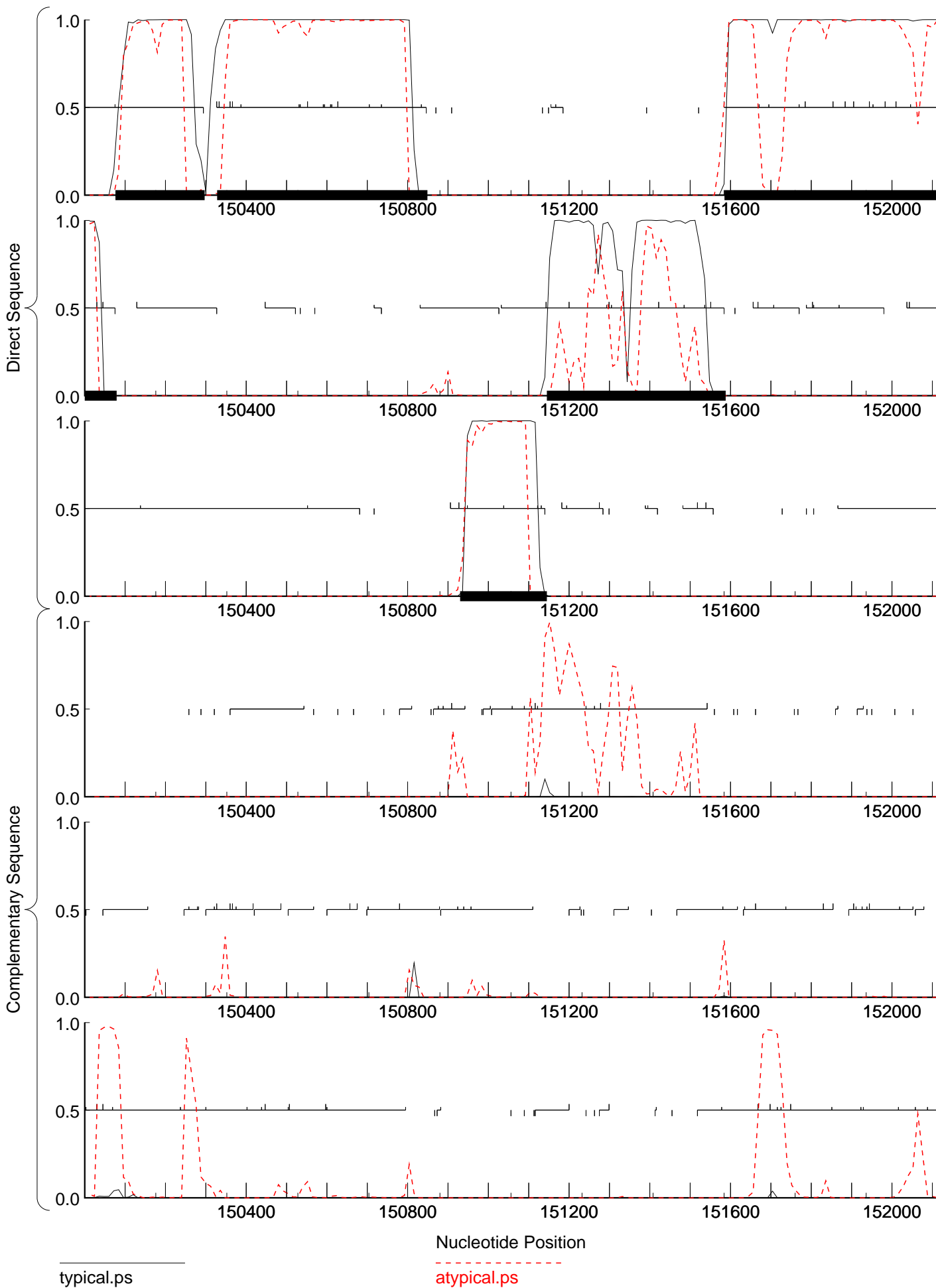




typical.ps

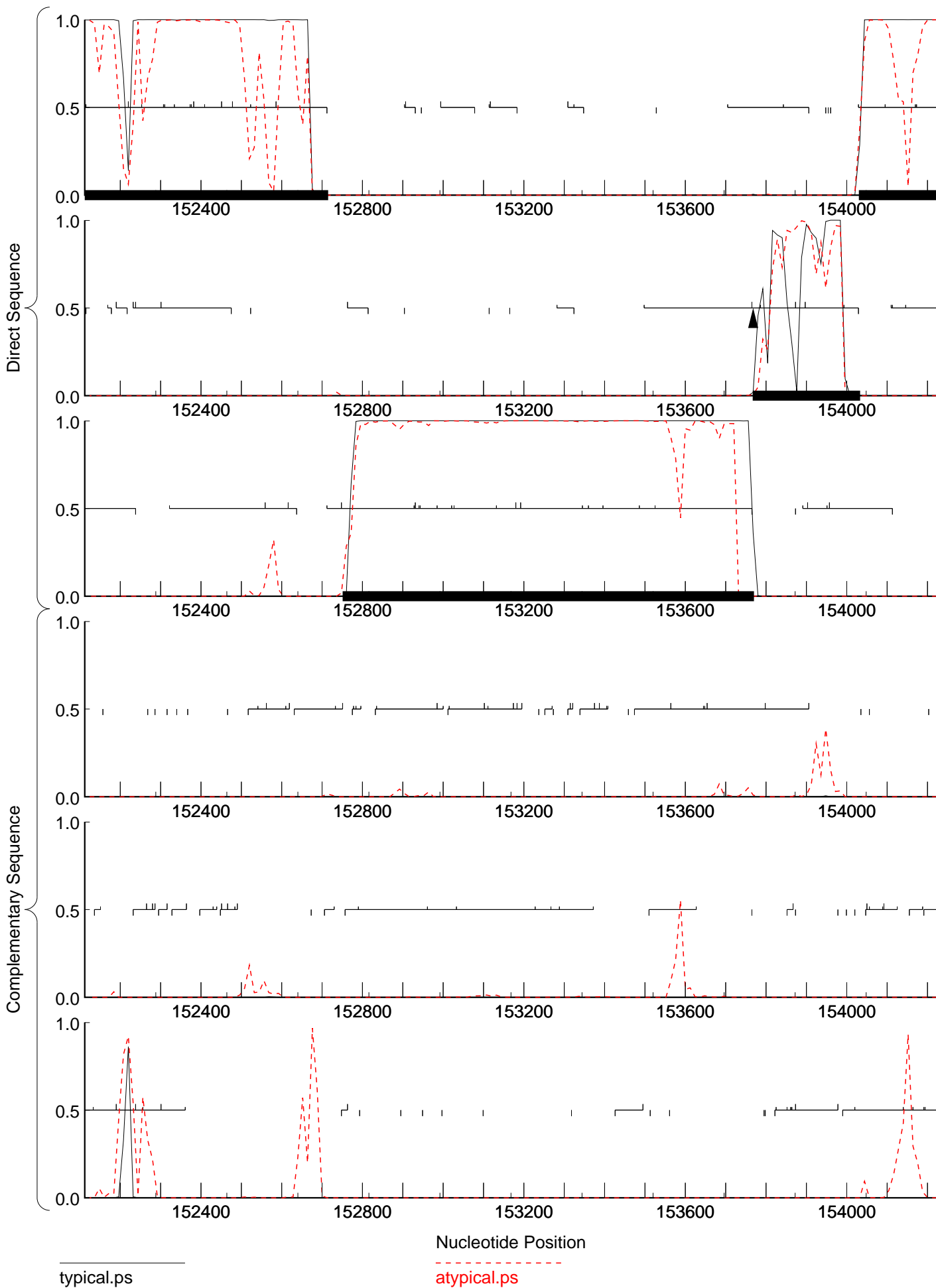
atypical.ps

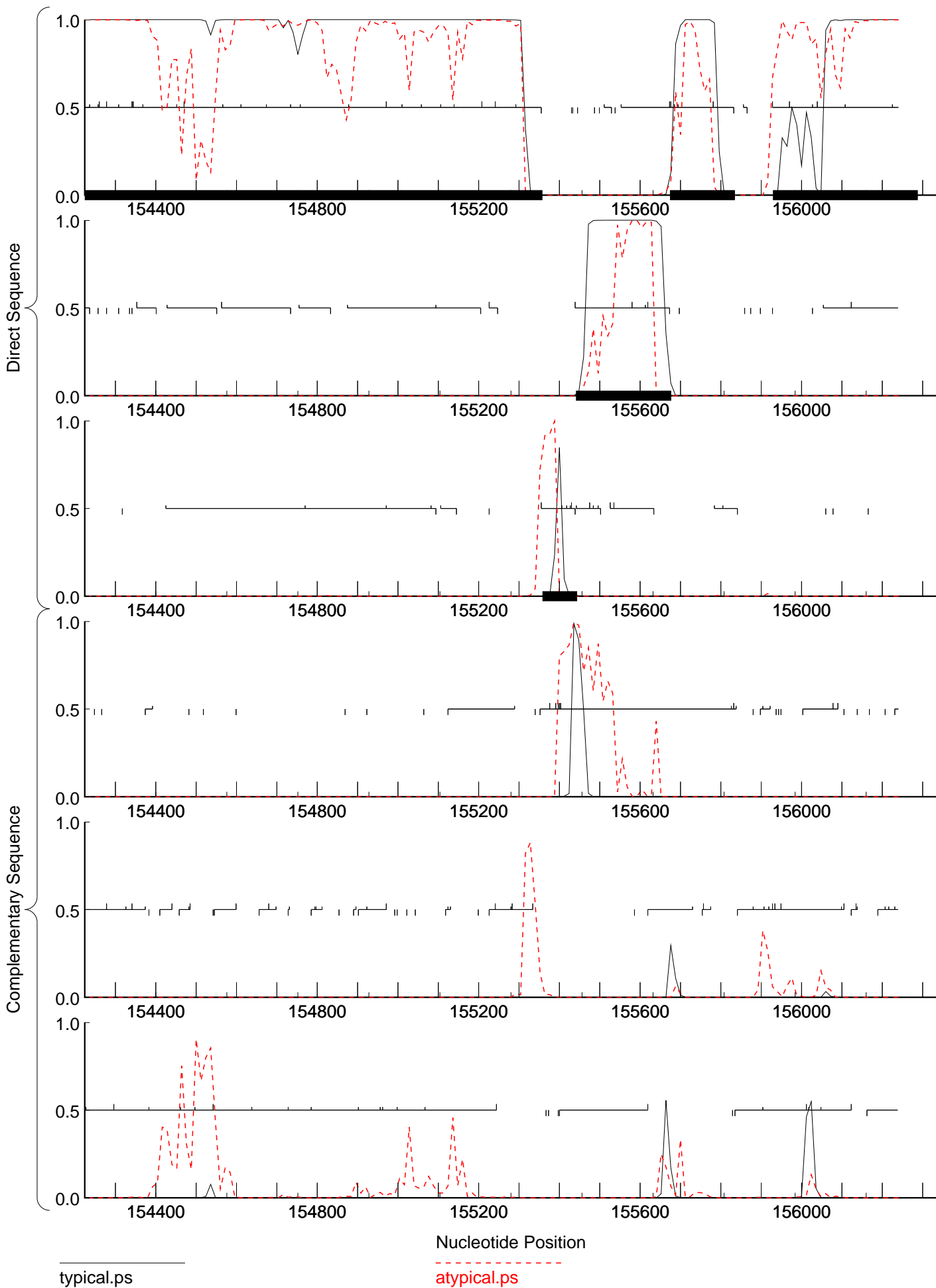




typical.ps

atypical.ps





typical.ps

atypical.ps