

GeneMark

Version 2.5p (09.08.06)

Copyright 1993 - M. Borodovsky, J. McIninch

PROGRAM INFORMATION

Sequence : Streptomyces phage Kradal complete sequence, 186383 bp including ~1053 bp terminal repeat,
Analysis Date : 3/18/18 at 9:41:35
Pages : 90
Sequence Length : 186383 bp
GC Content : 66.72%

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,

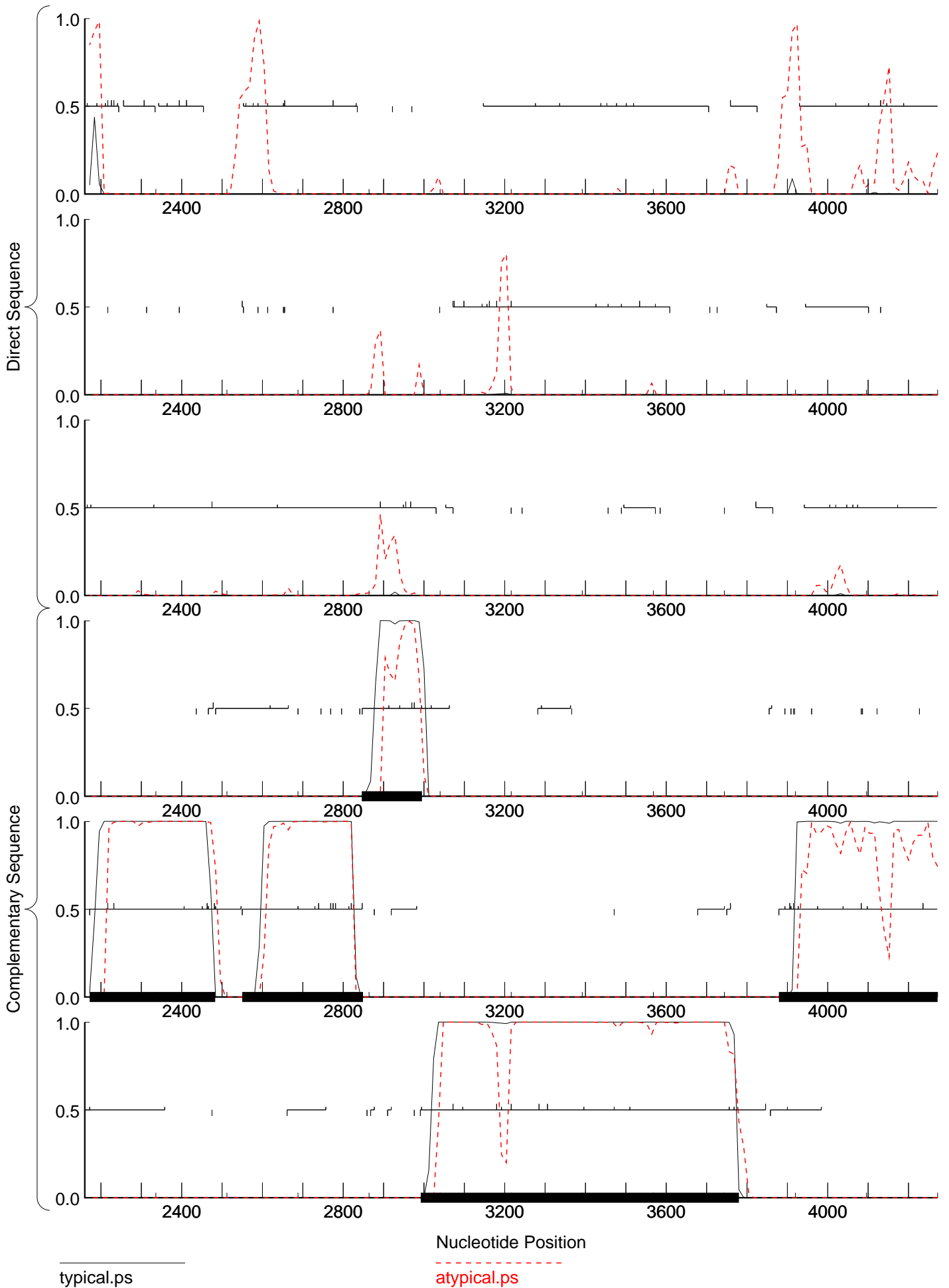
MATRIX INFORMATION

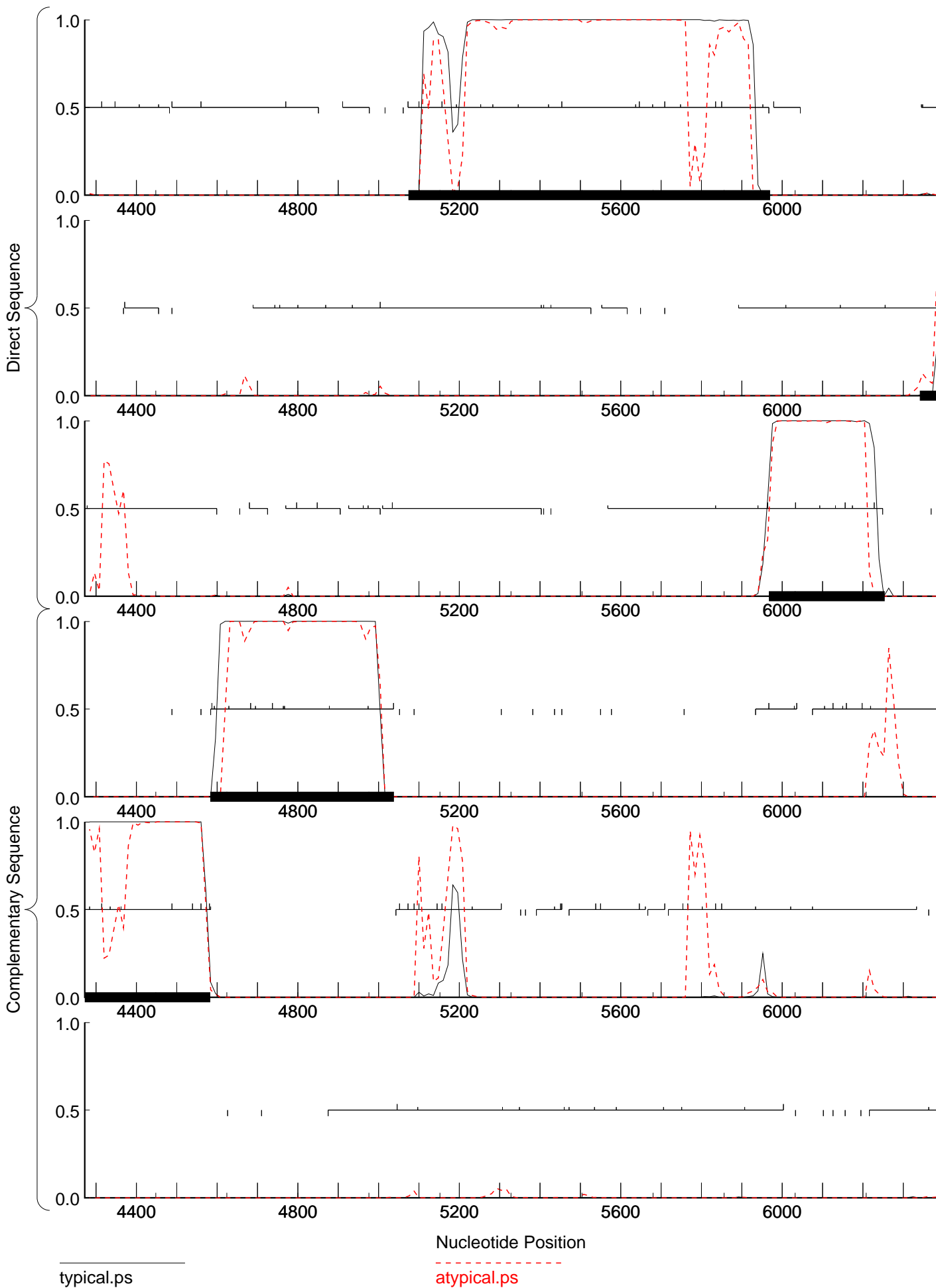
Matrix : -
Author : -
Order : 4

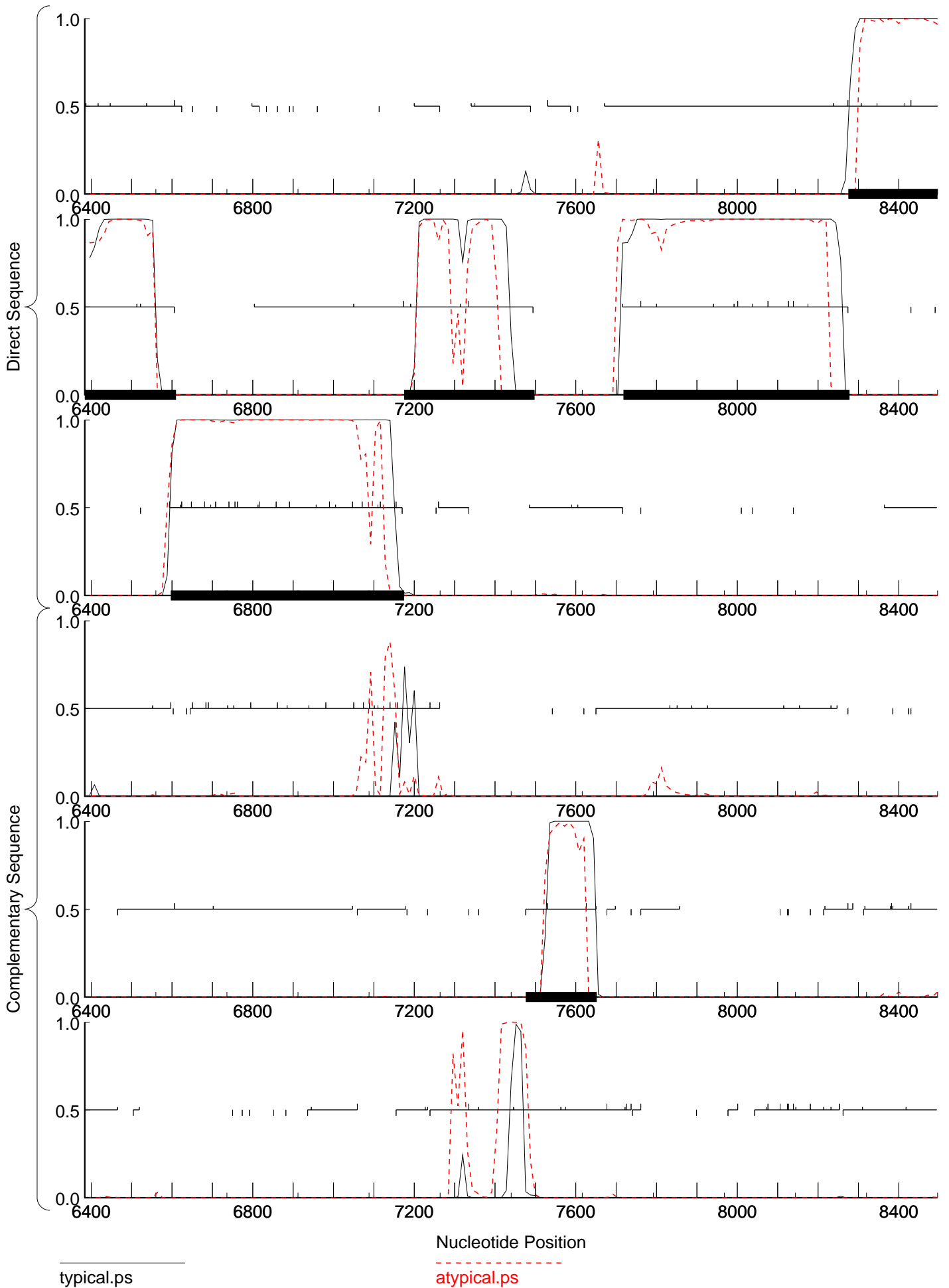
Send questions / comments to:
Dr. M. Borodovsky
Georgia Institute of Technology
School of Biology
Atlanta, GA 30332-0230

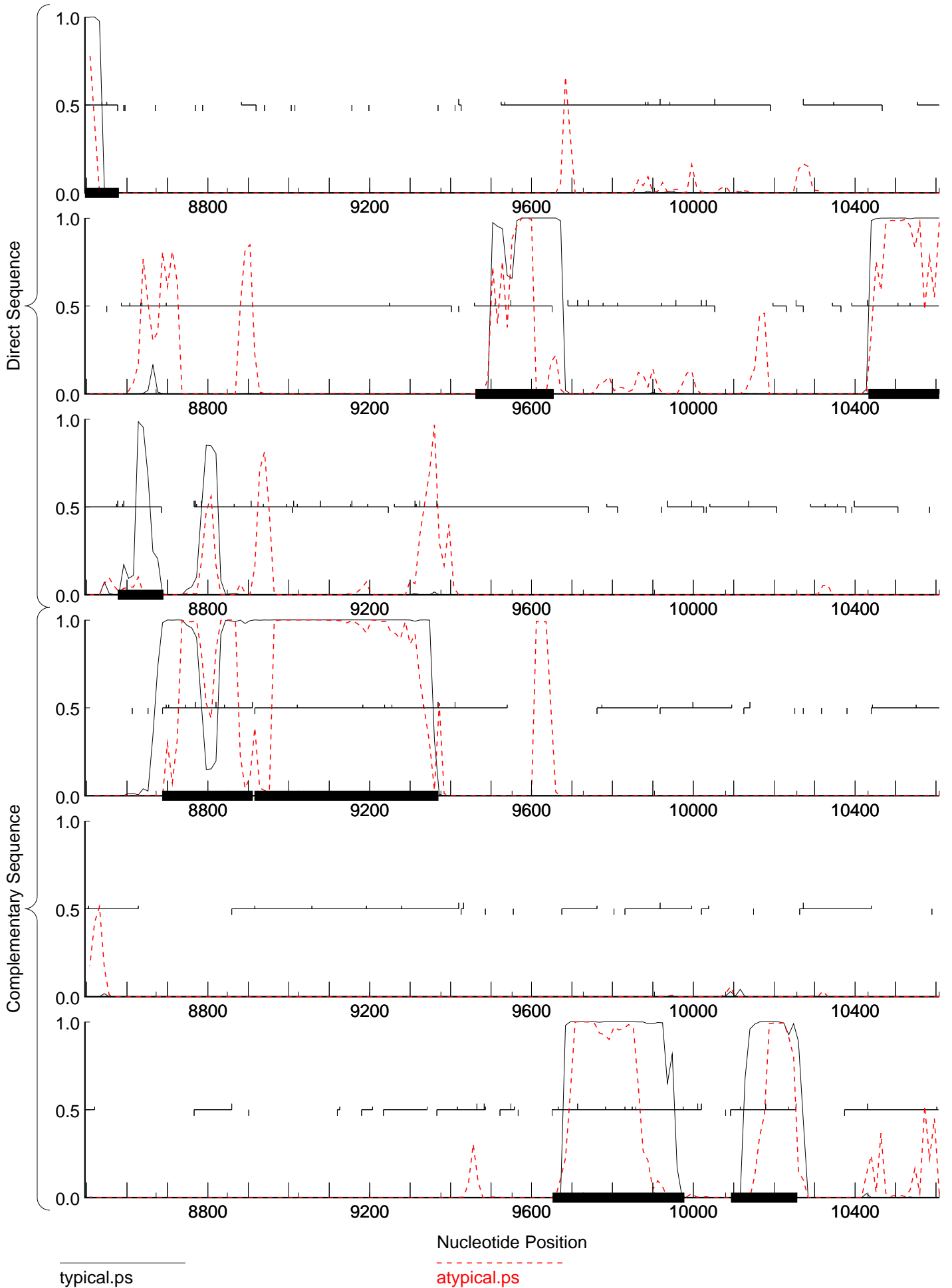
Matrix notes & comments

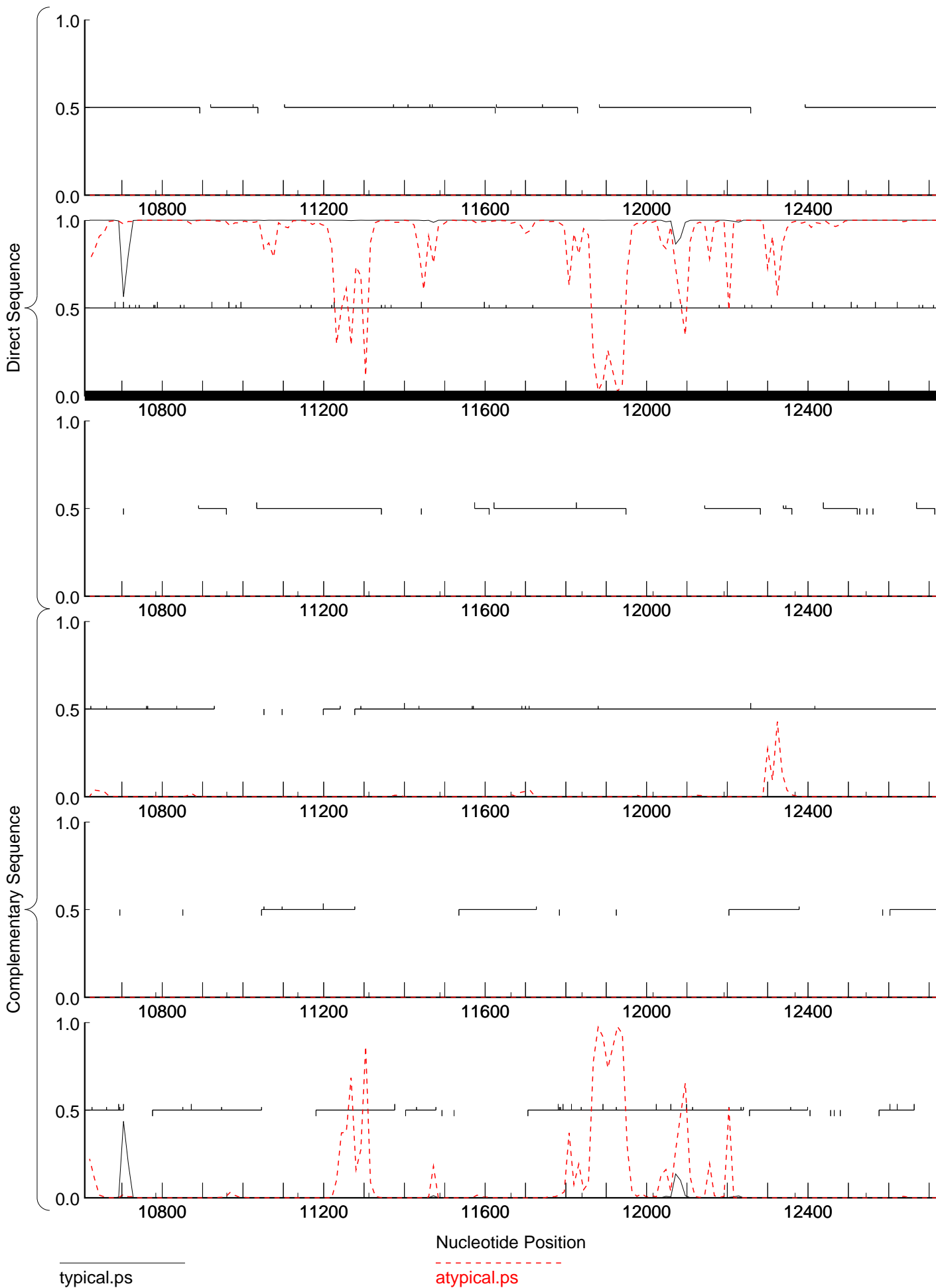
Training set derived by GeneMarkS, 4.30 October 2014
Sun Mar 18 09:41:35 2018

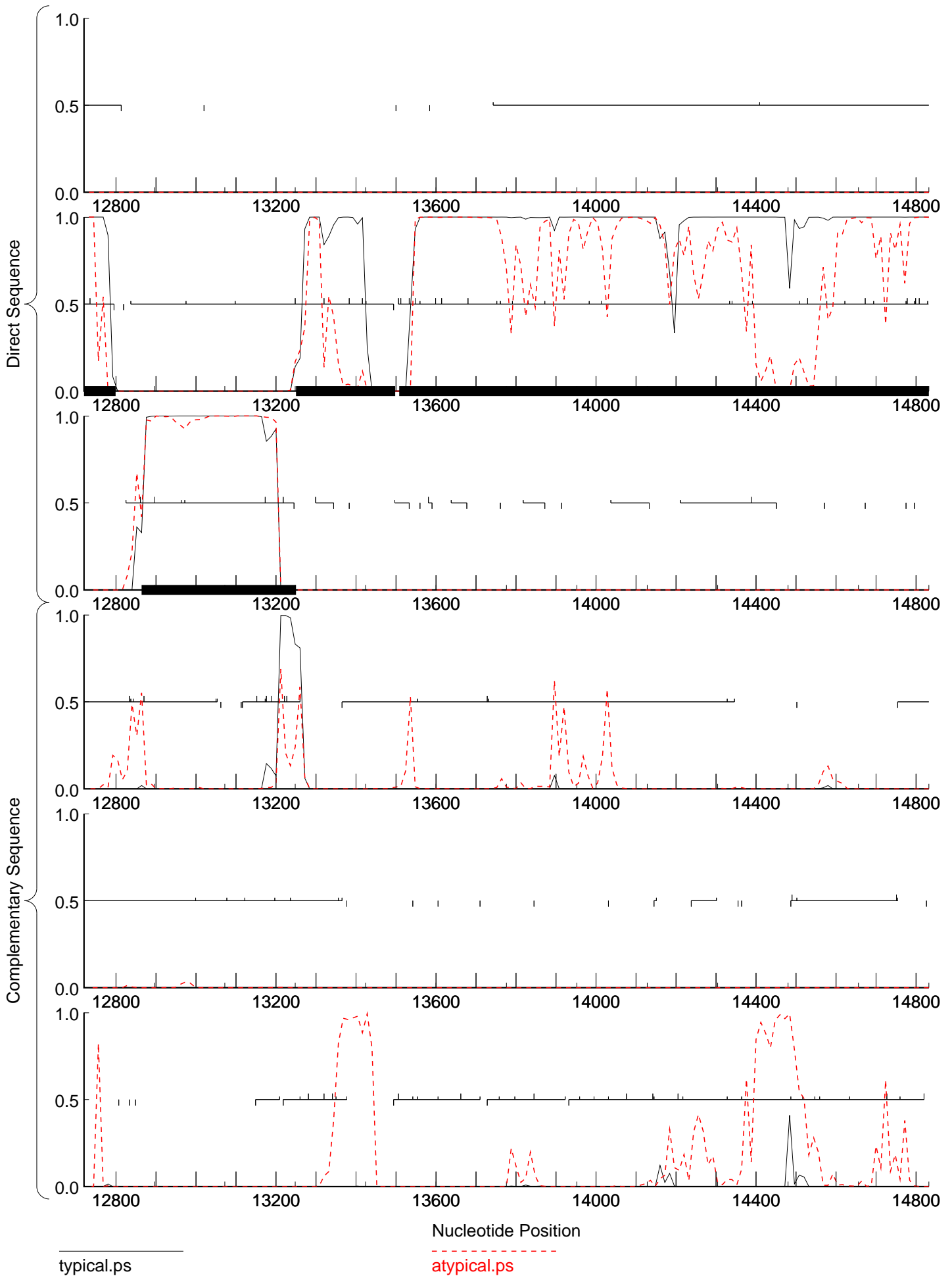


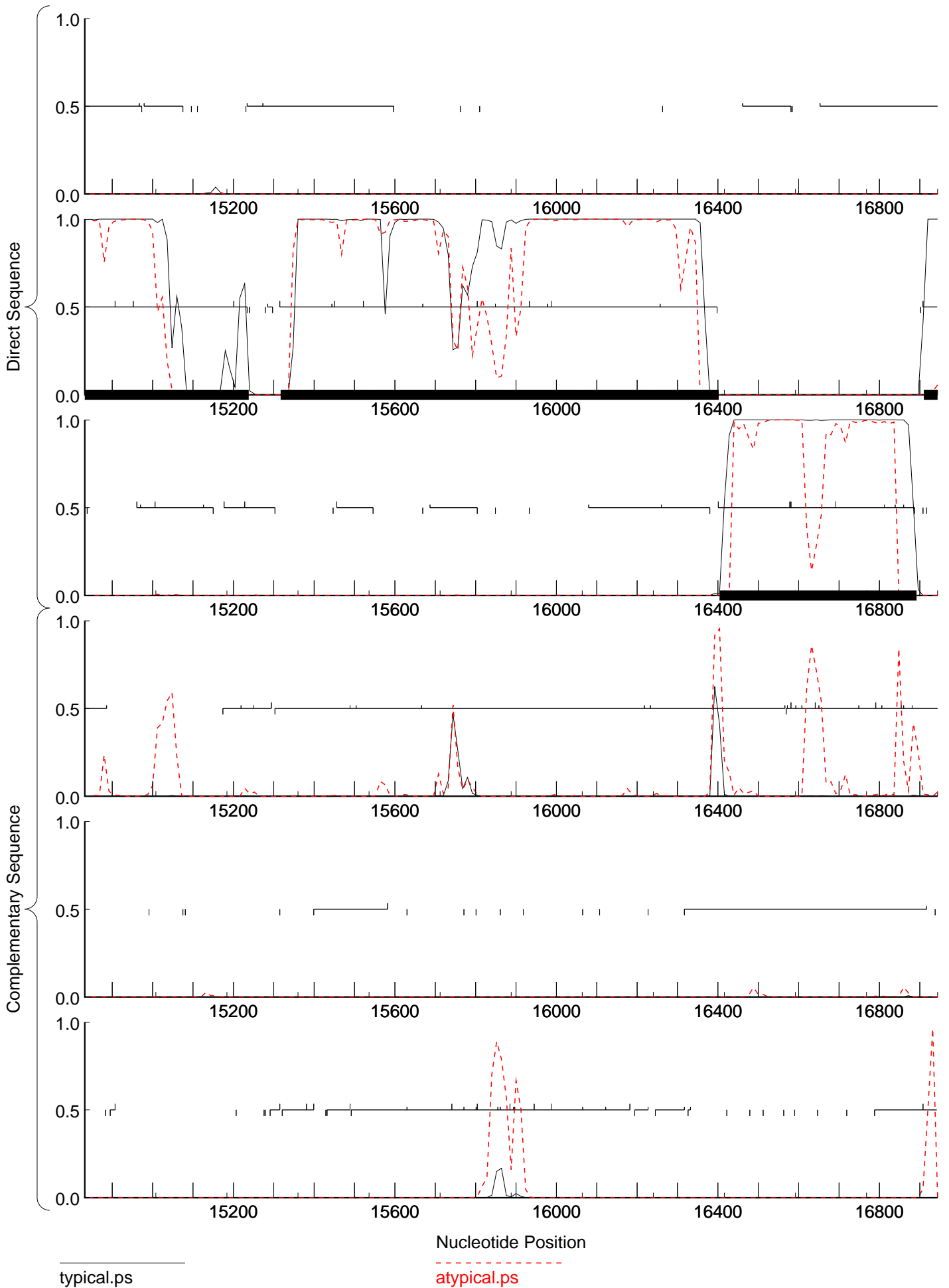


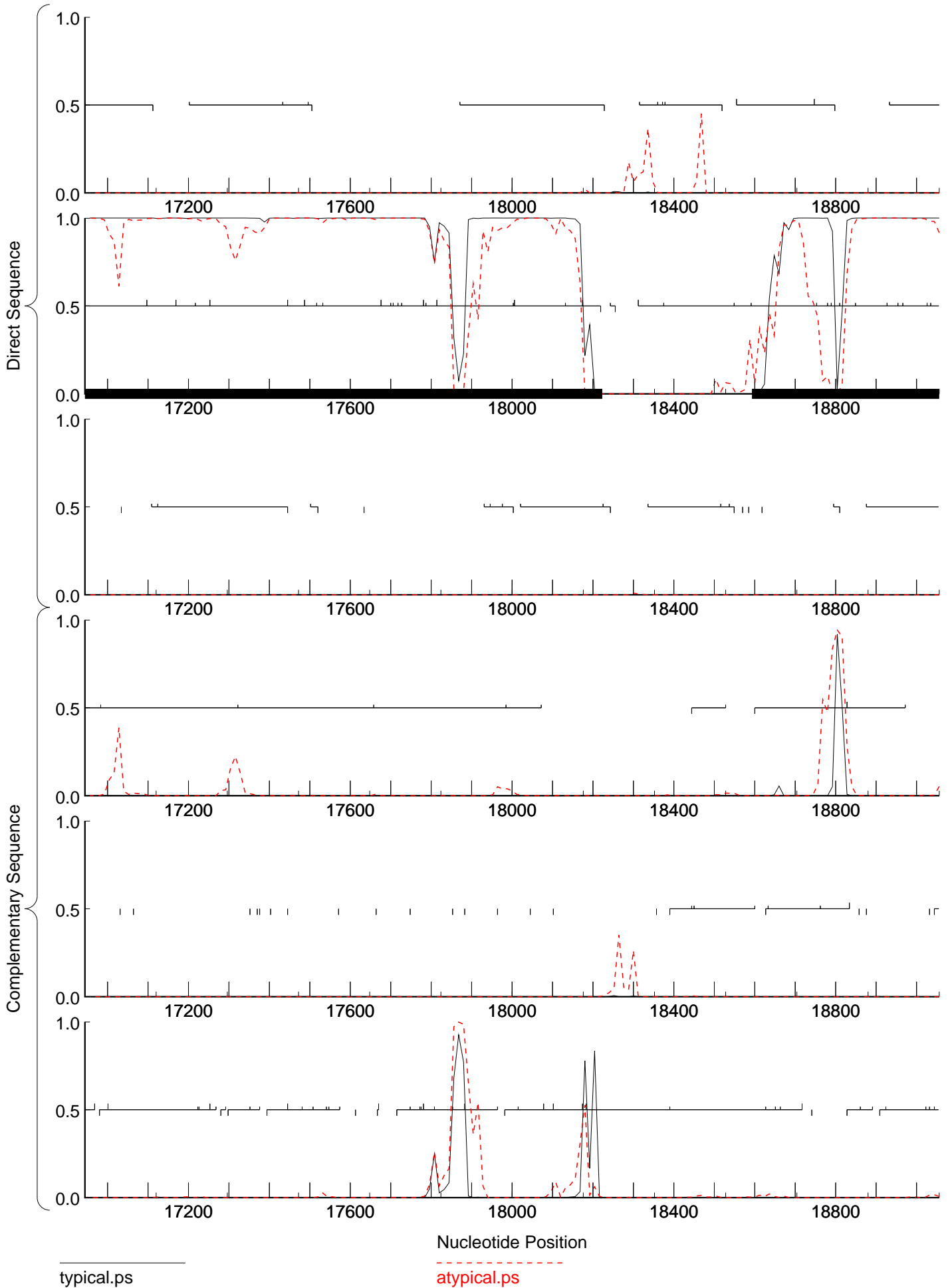


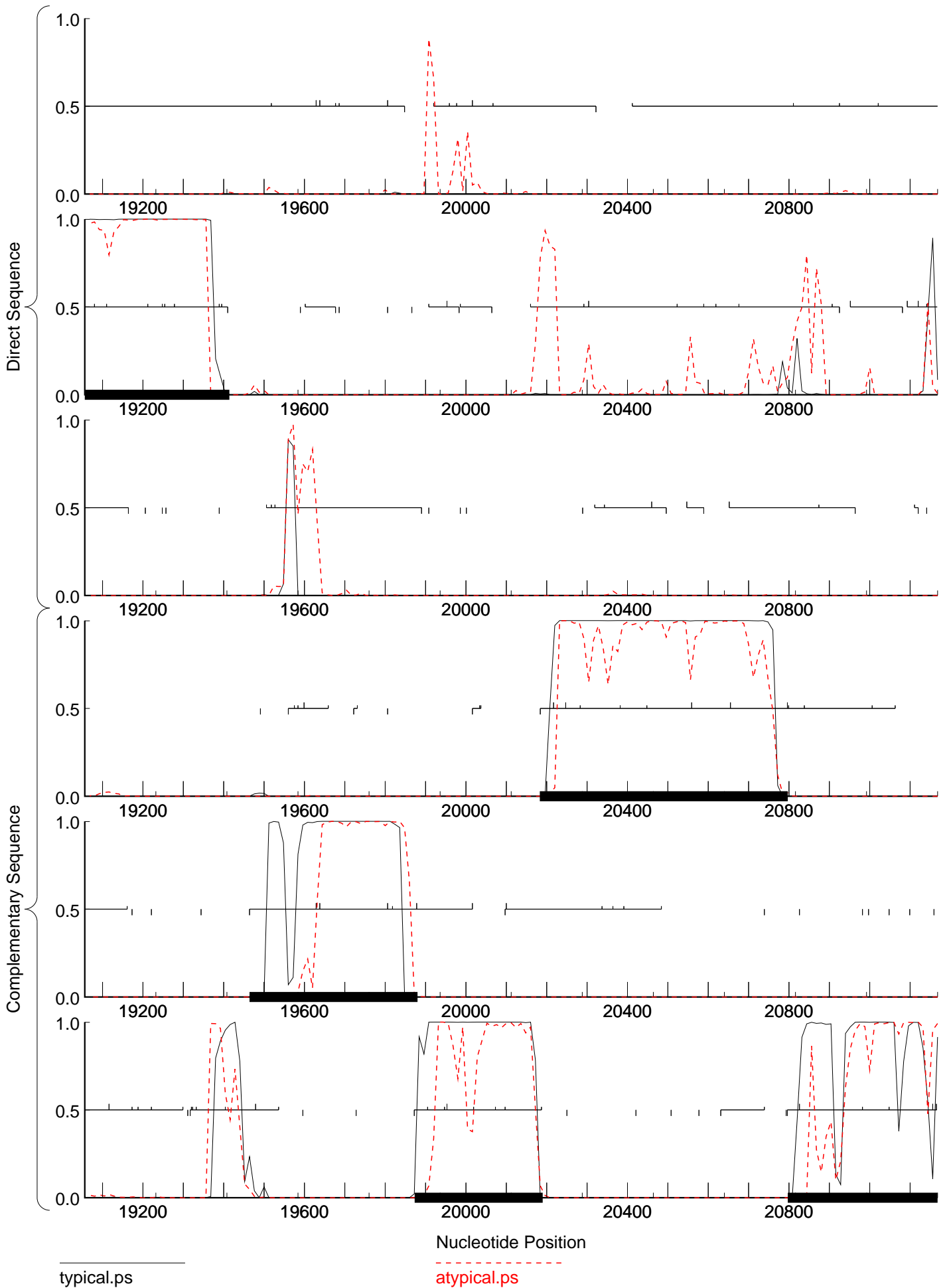


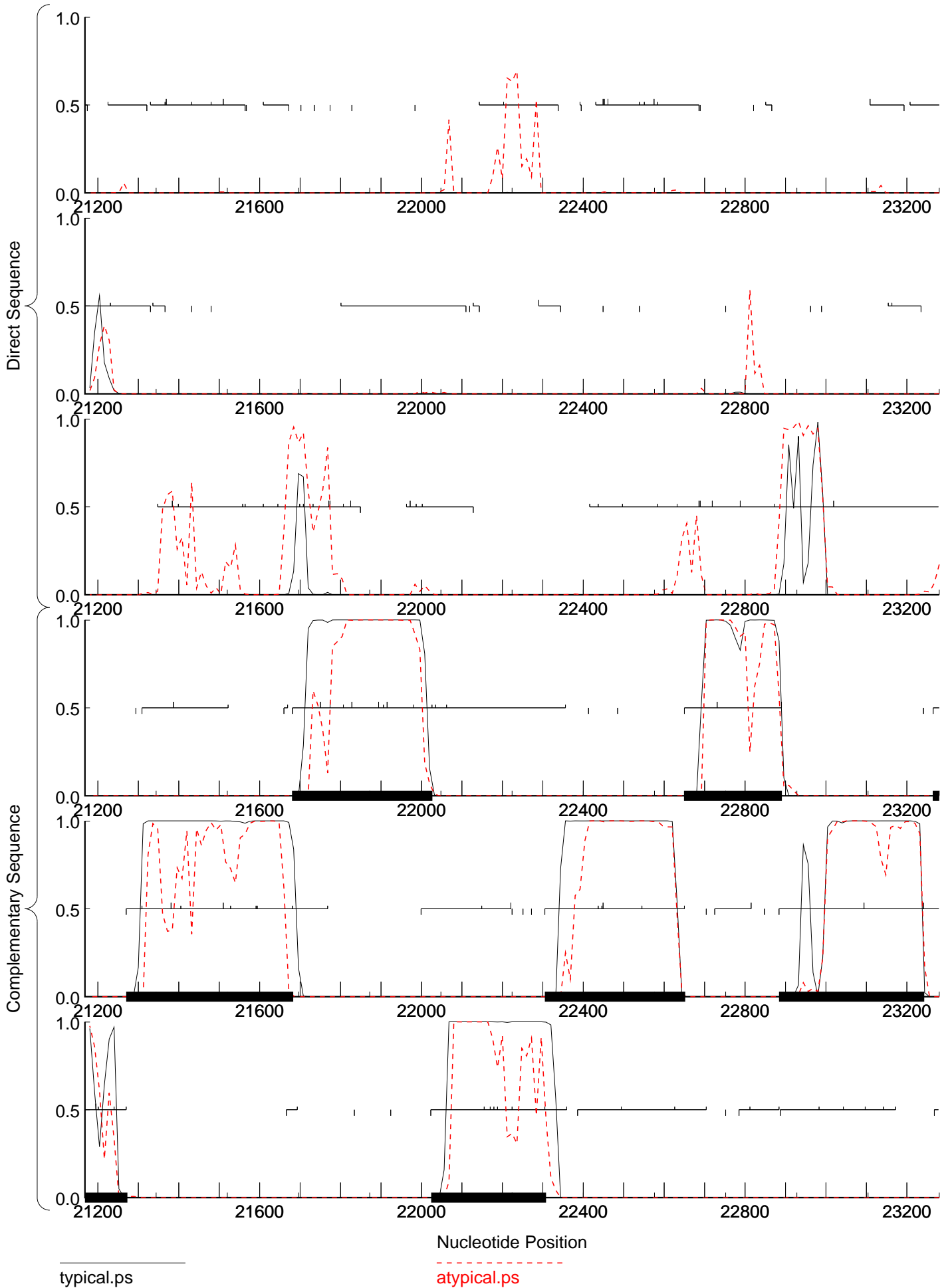


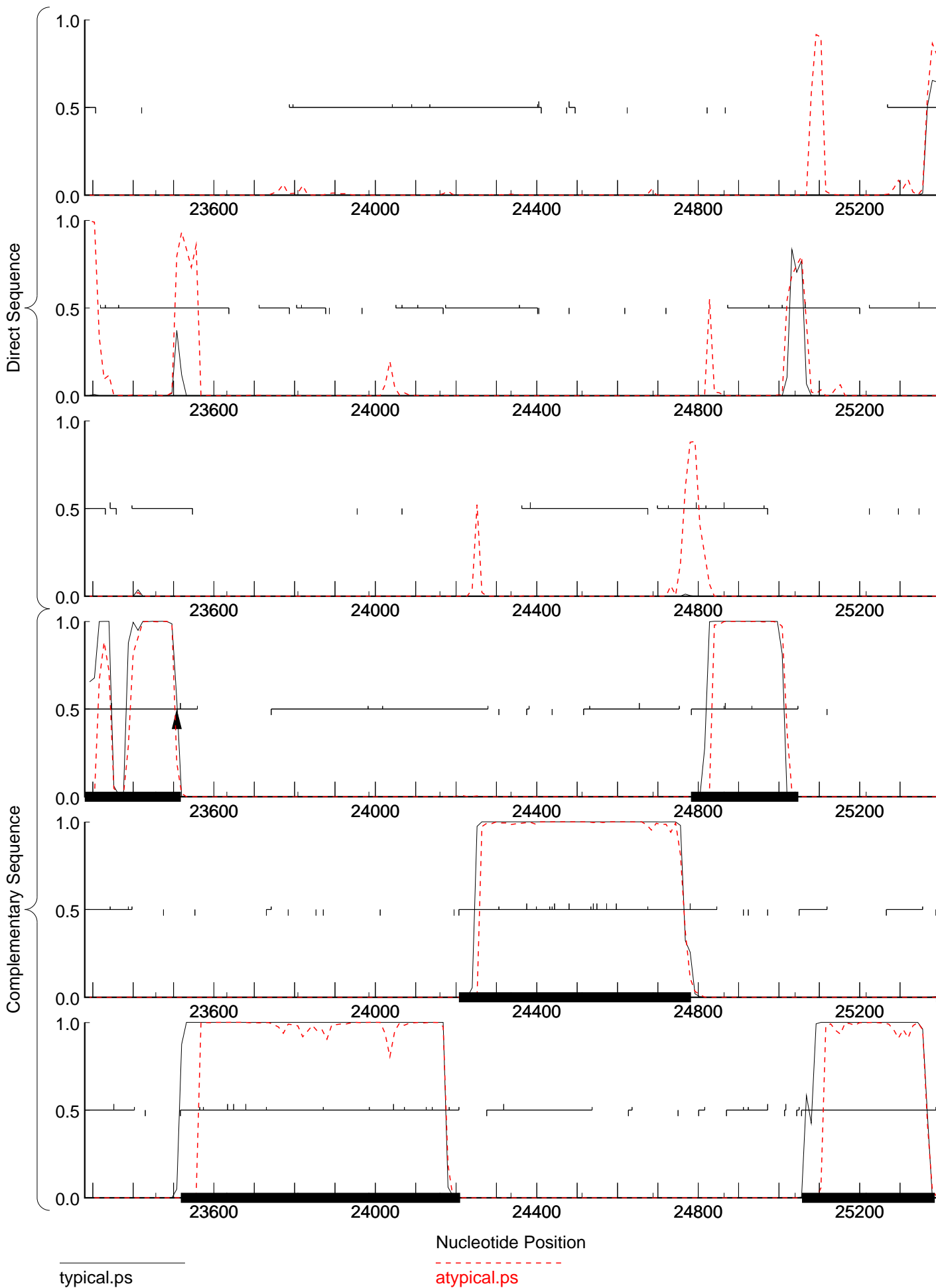


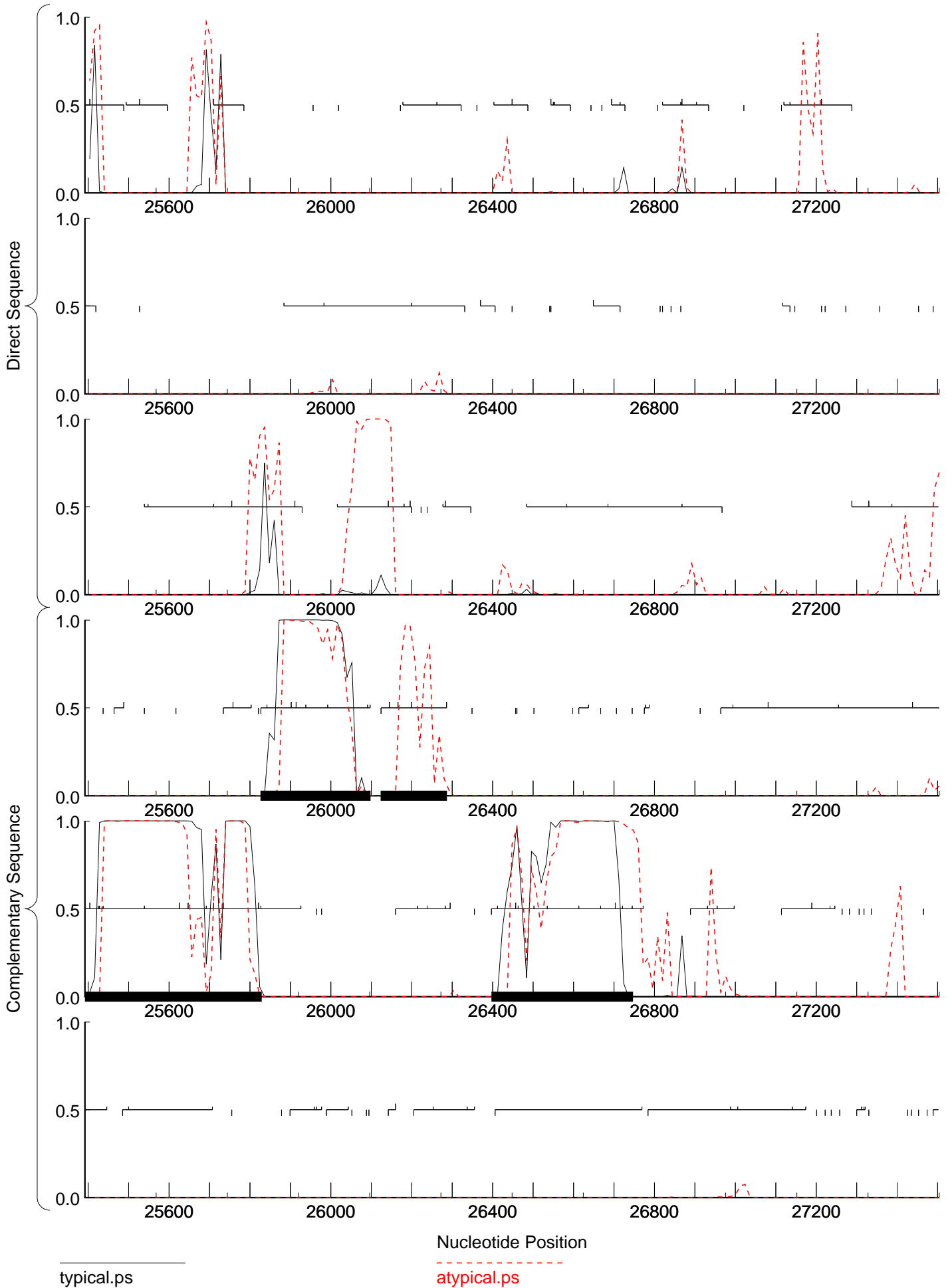






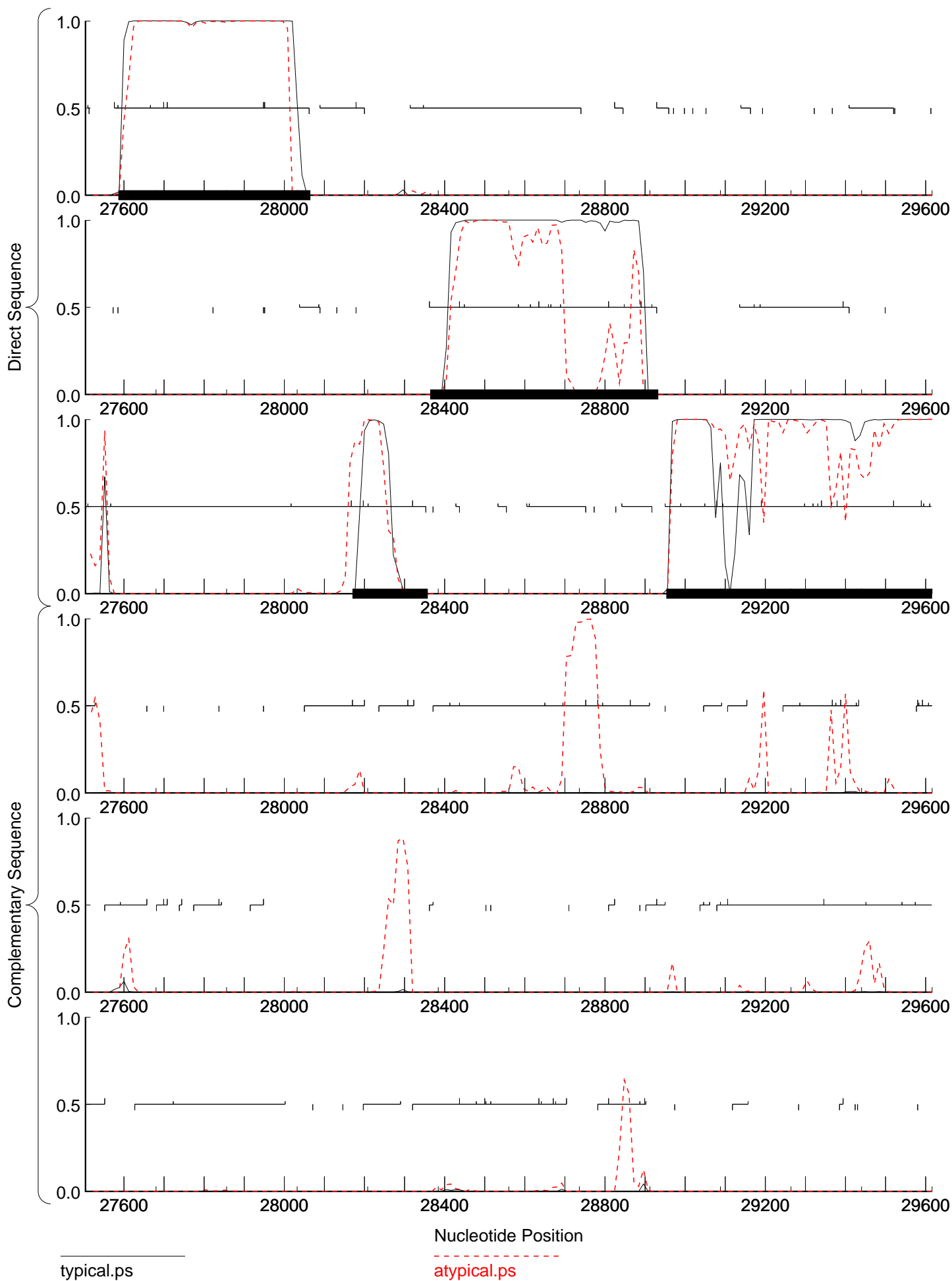


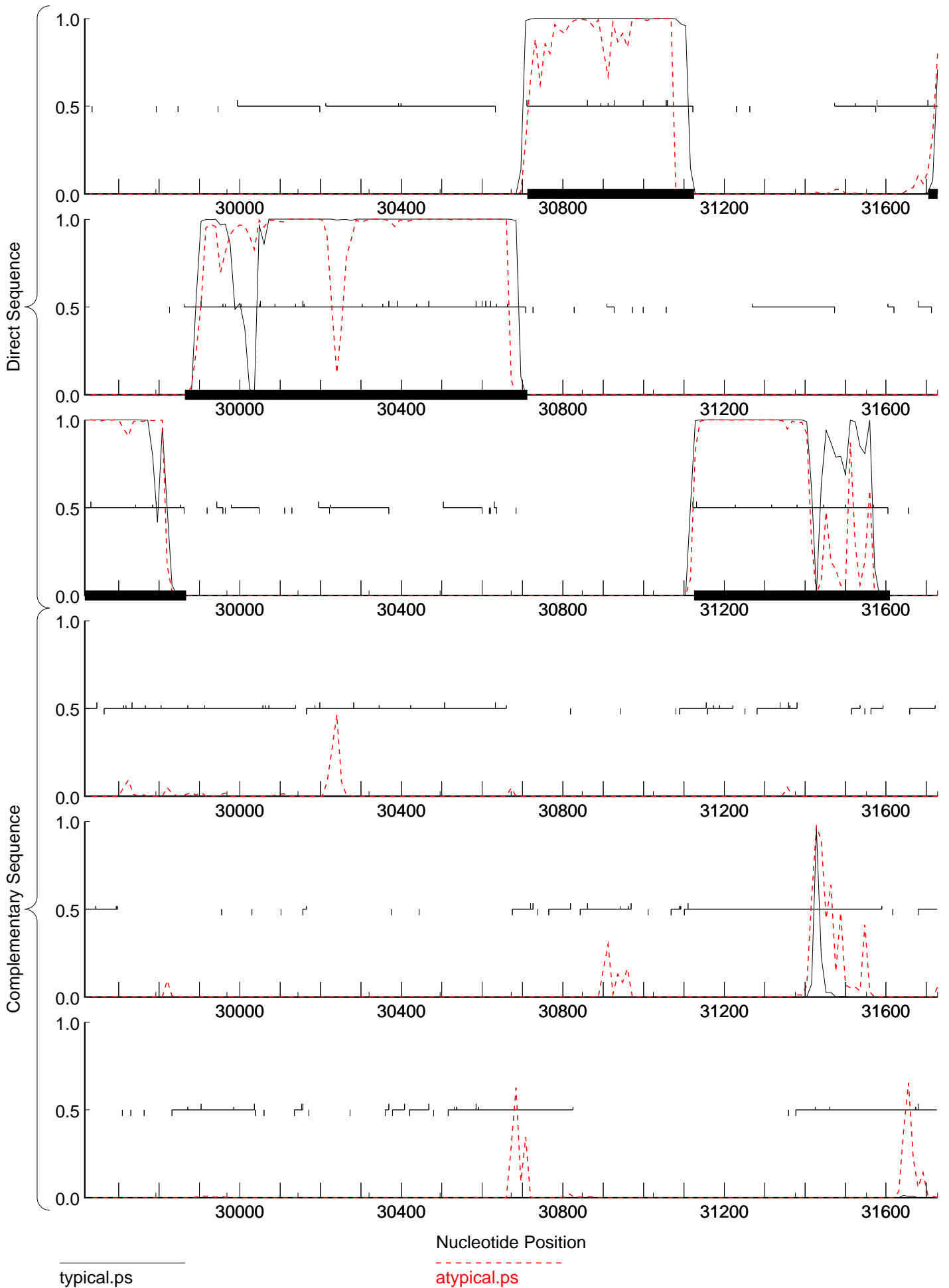


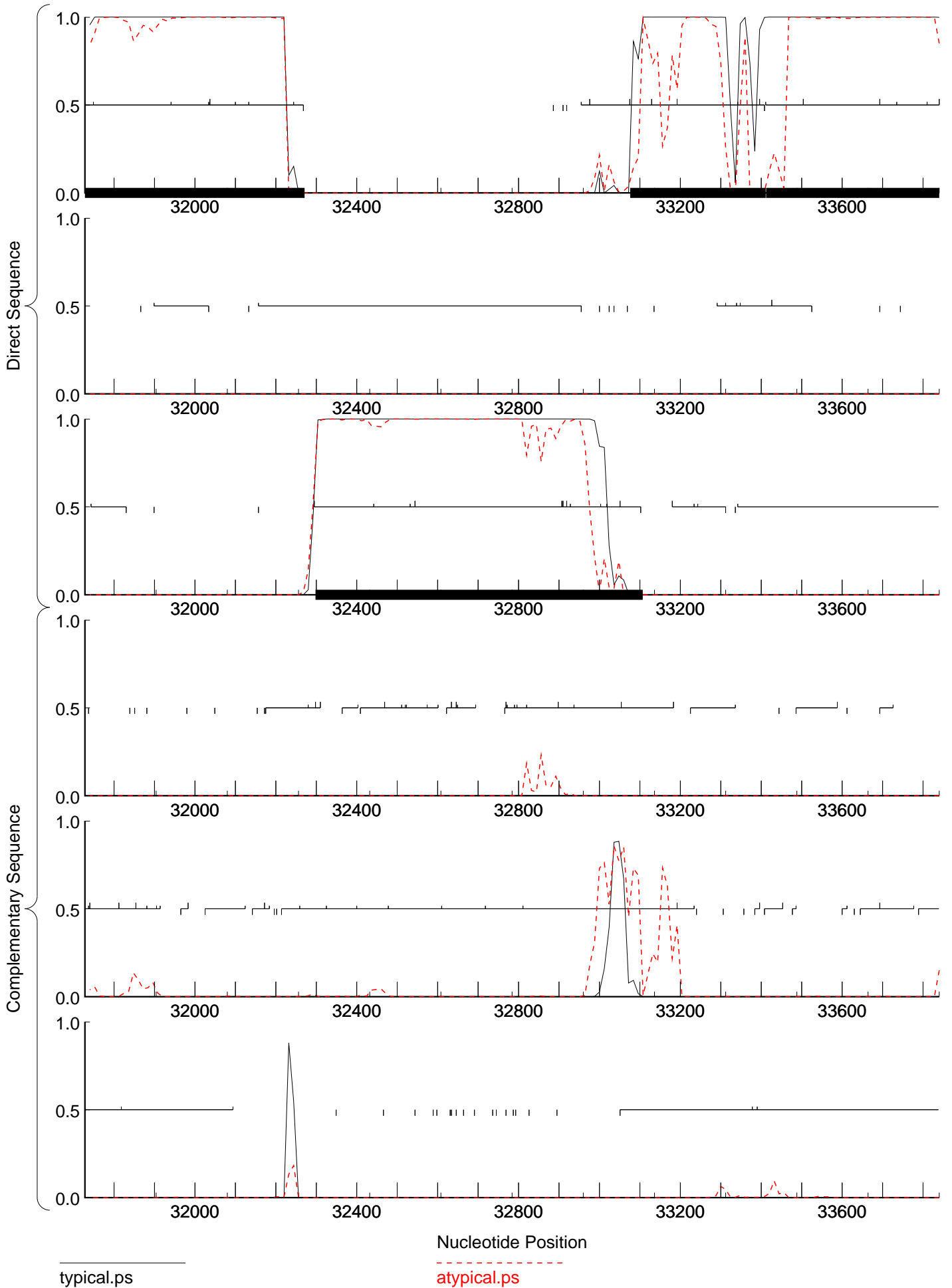


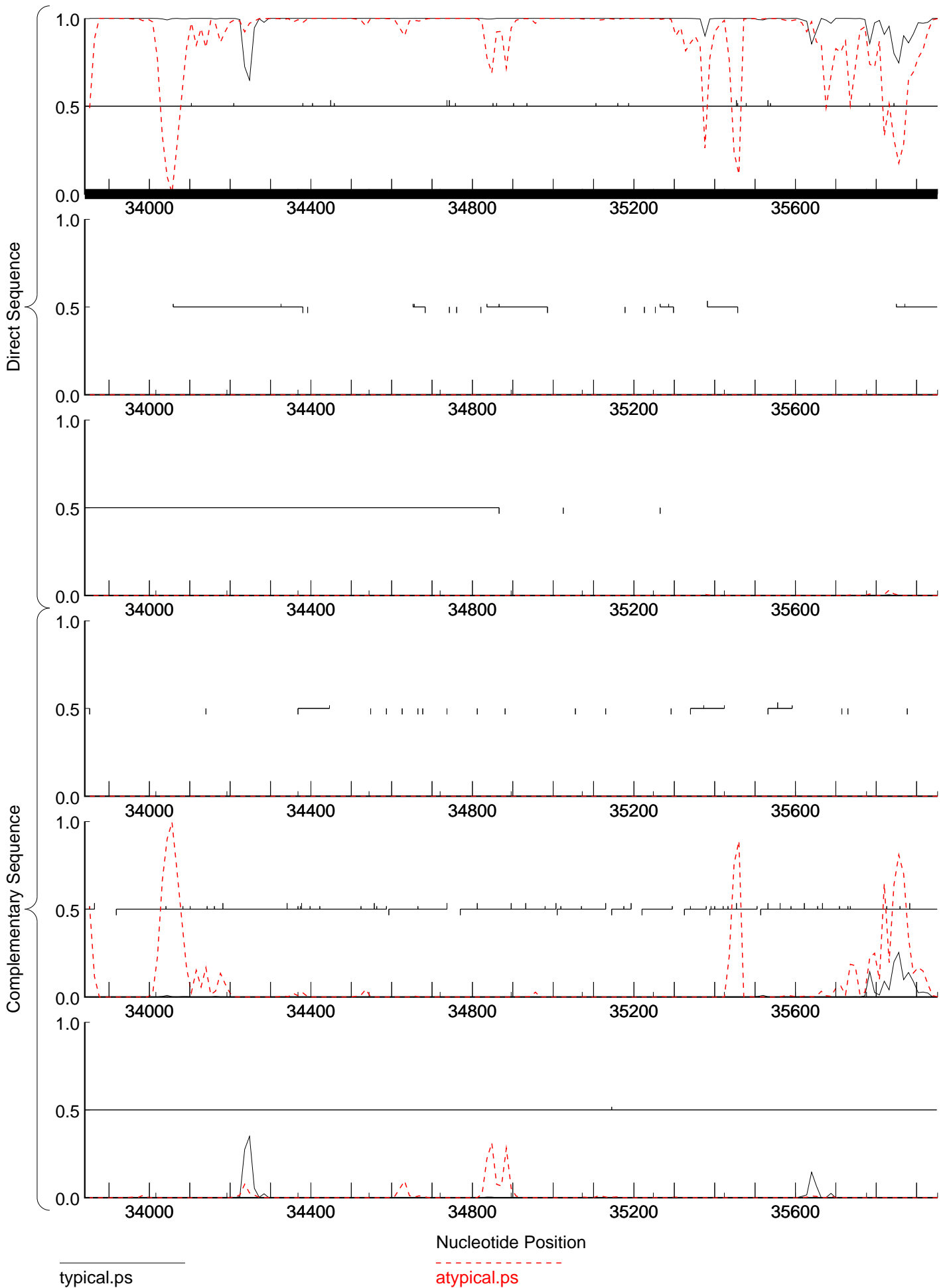
typical.ps

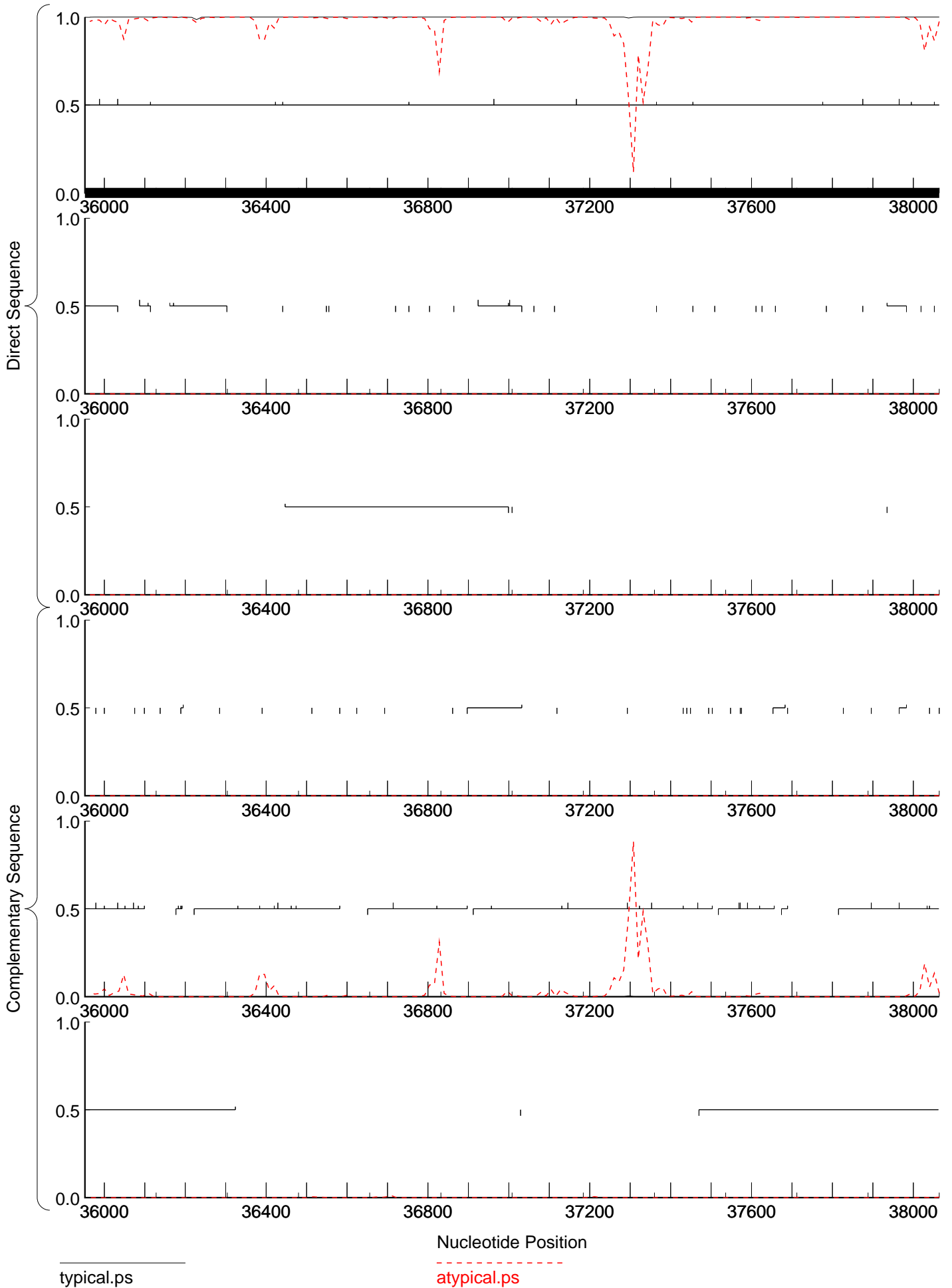
atypical.ps





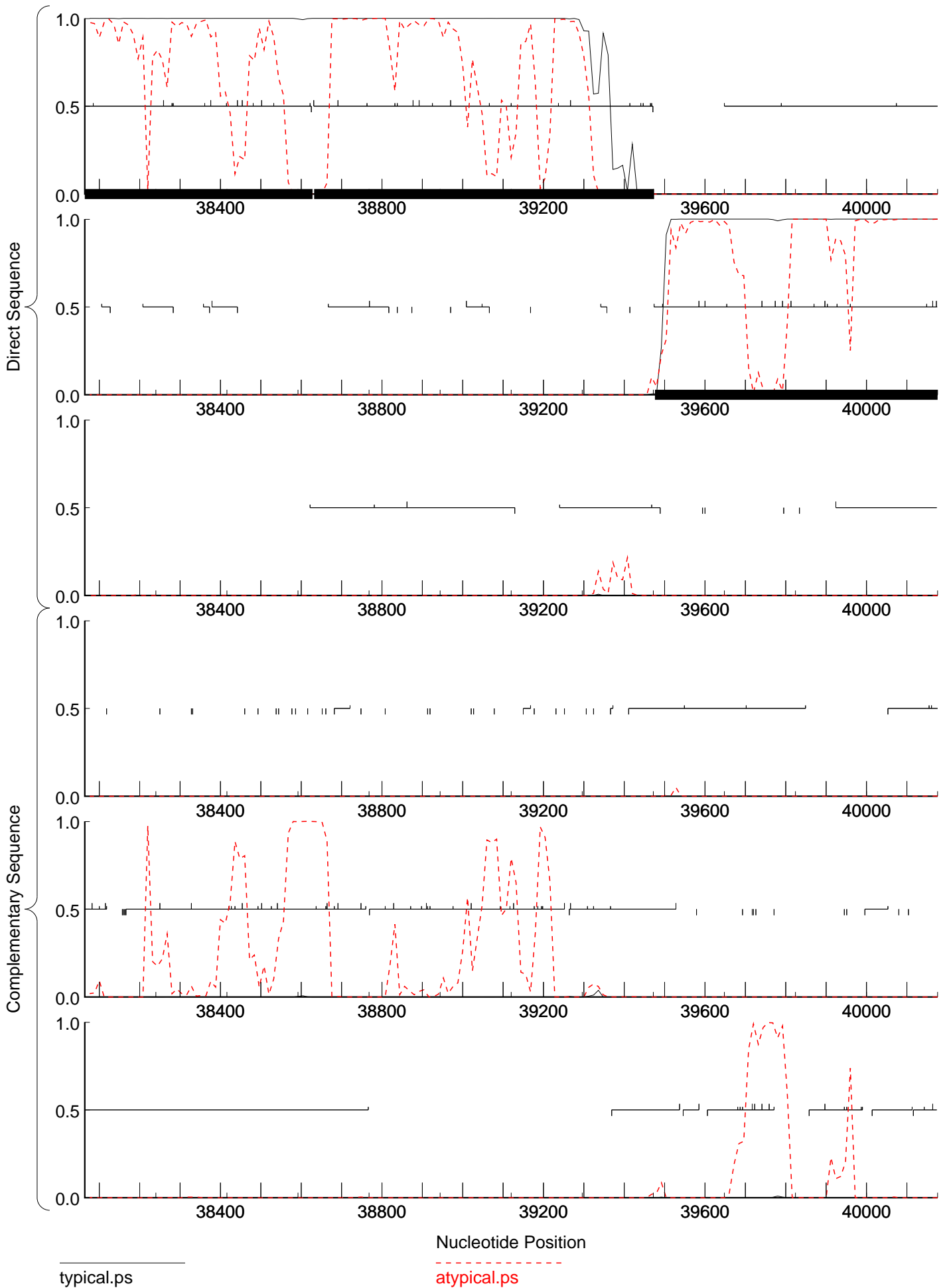


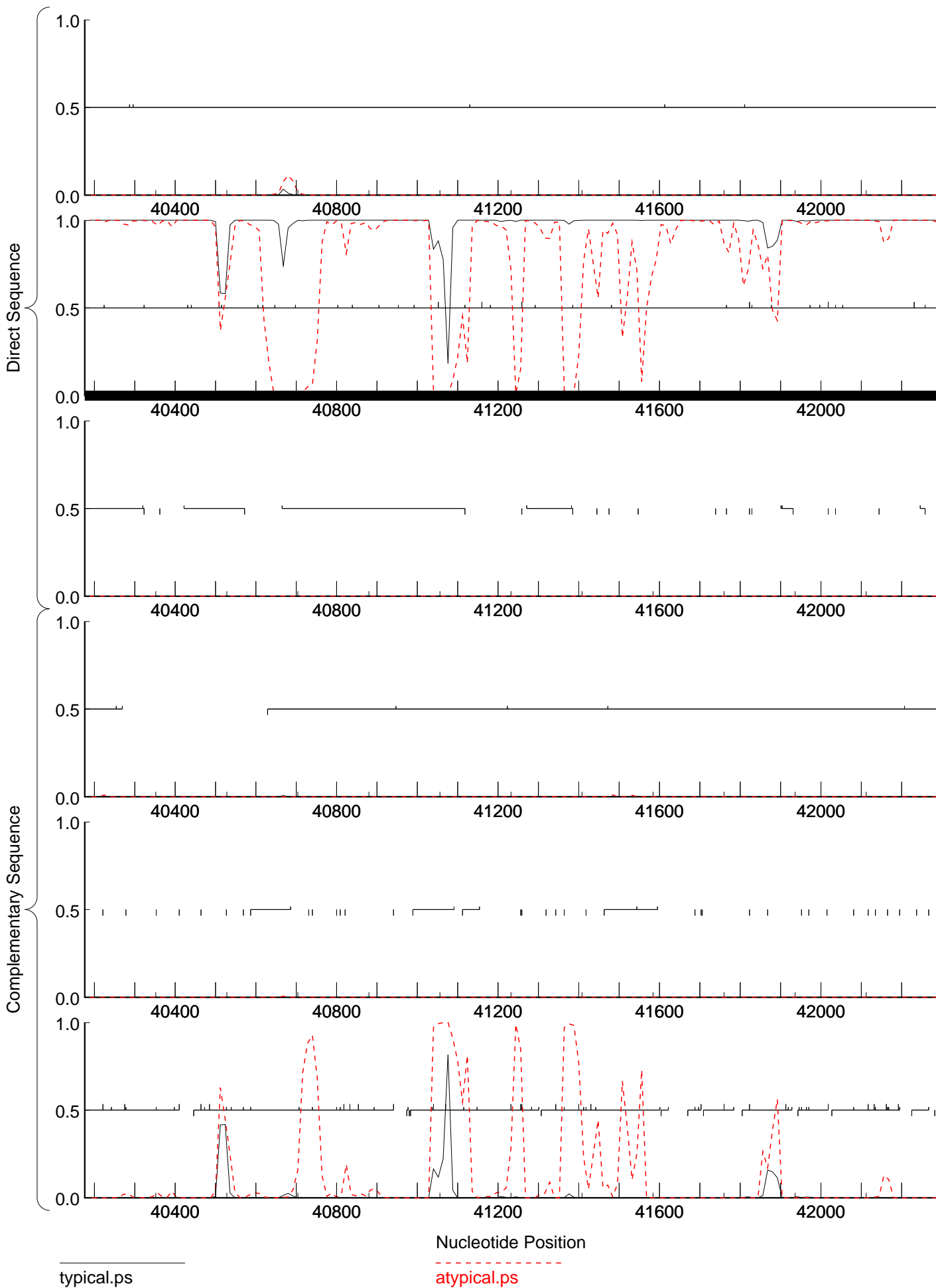




typical.ps

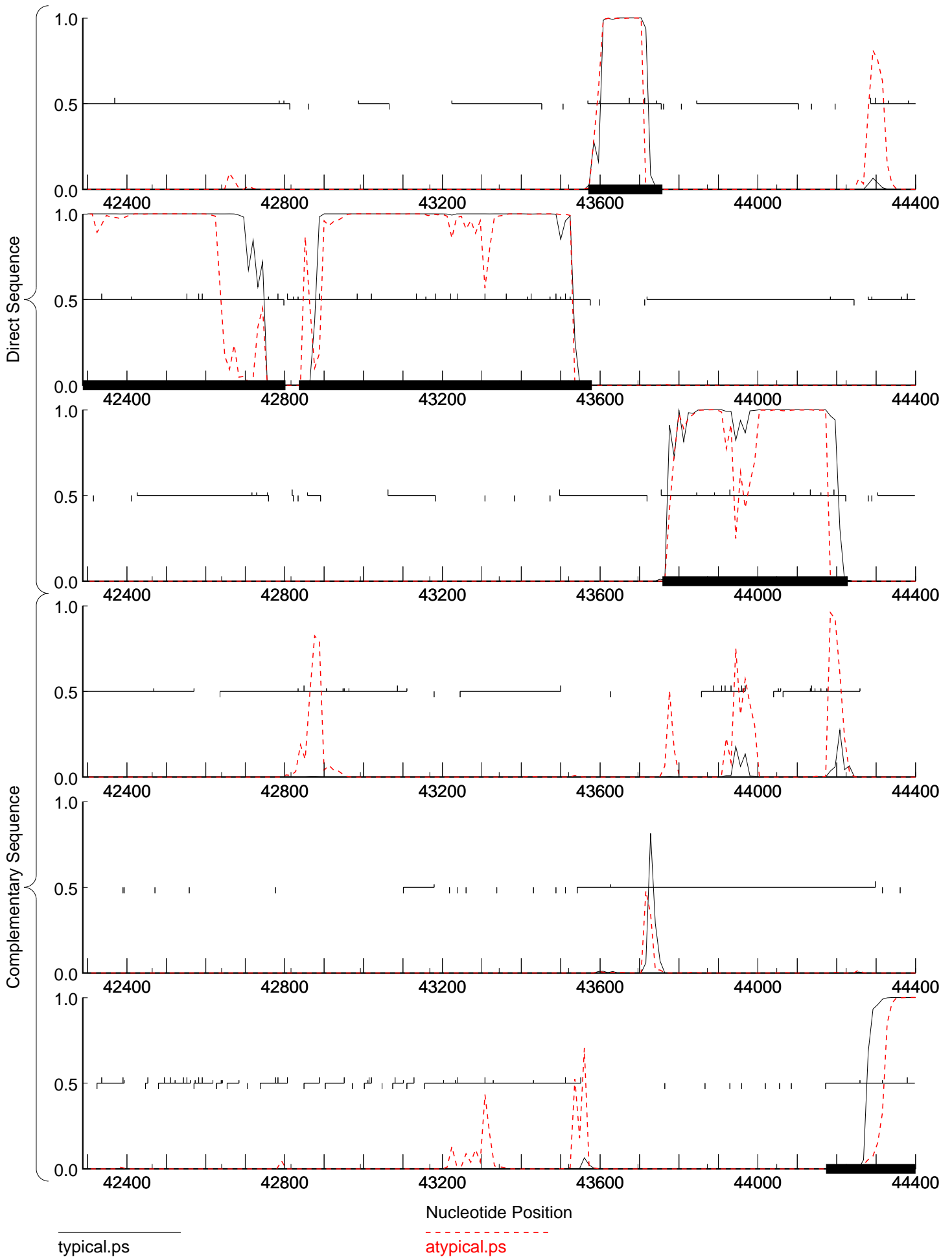
atypical.ps

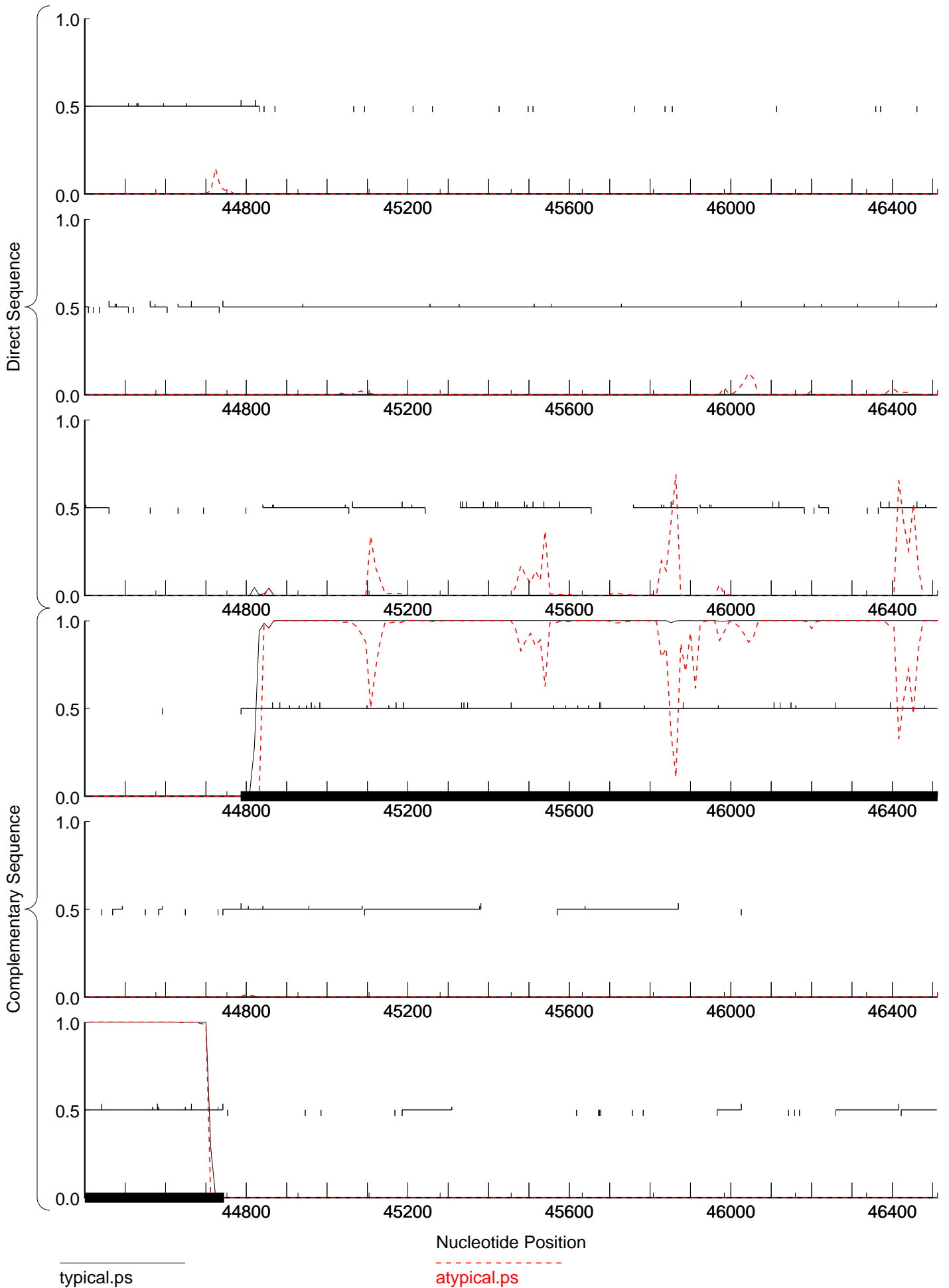


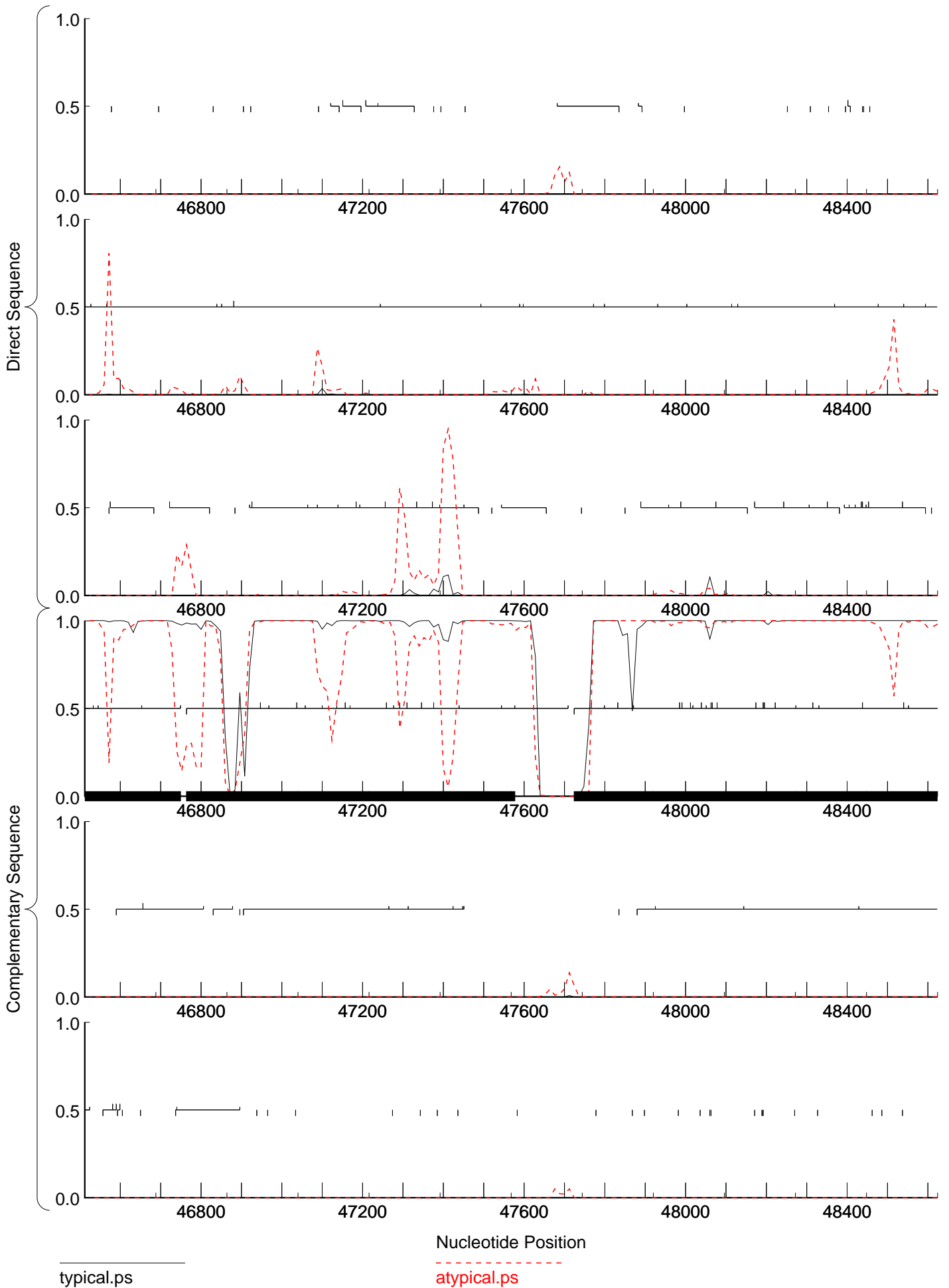


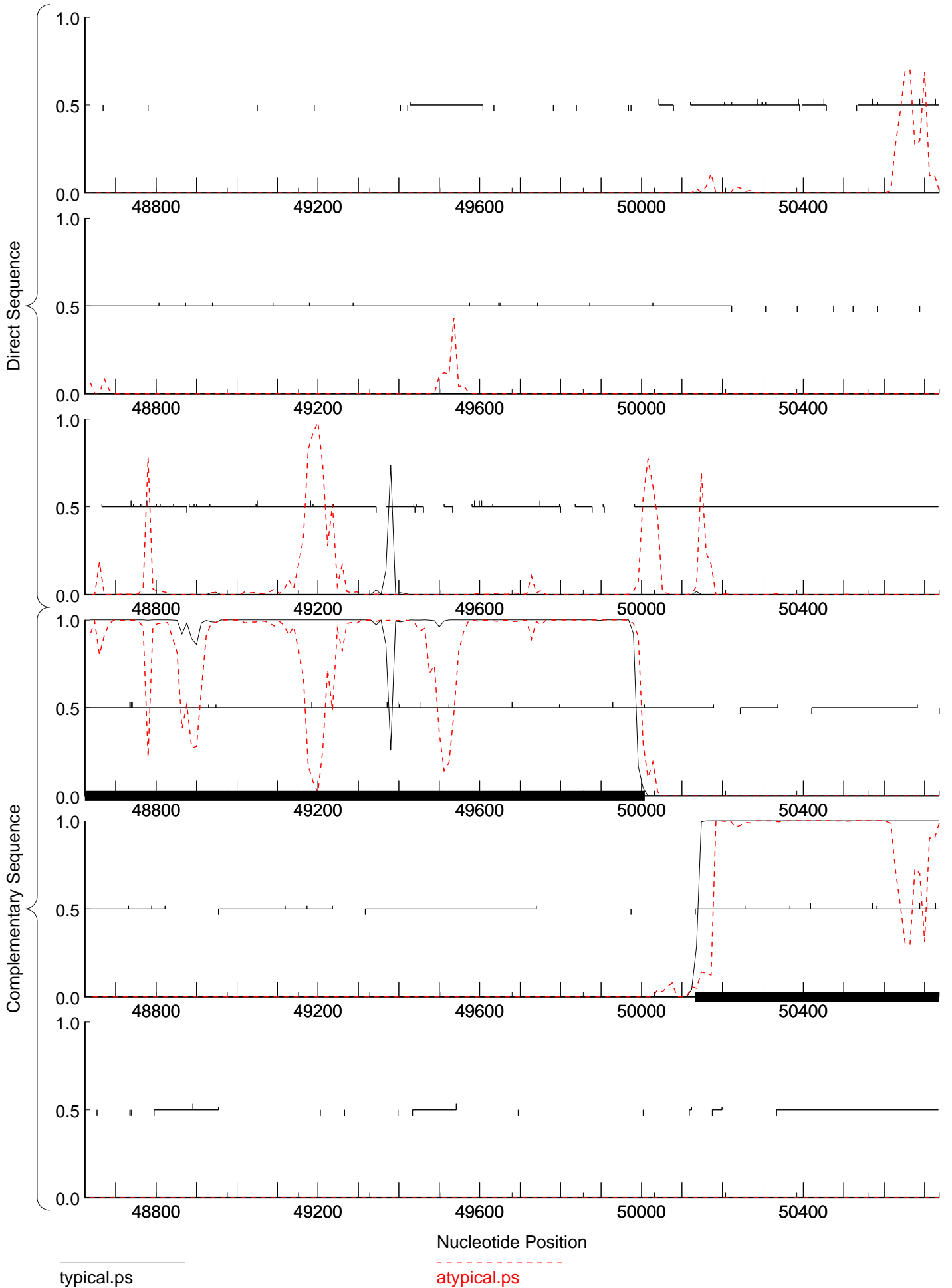
typical.ps

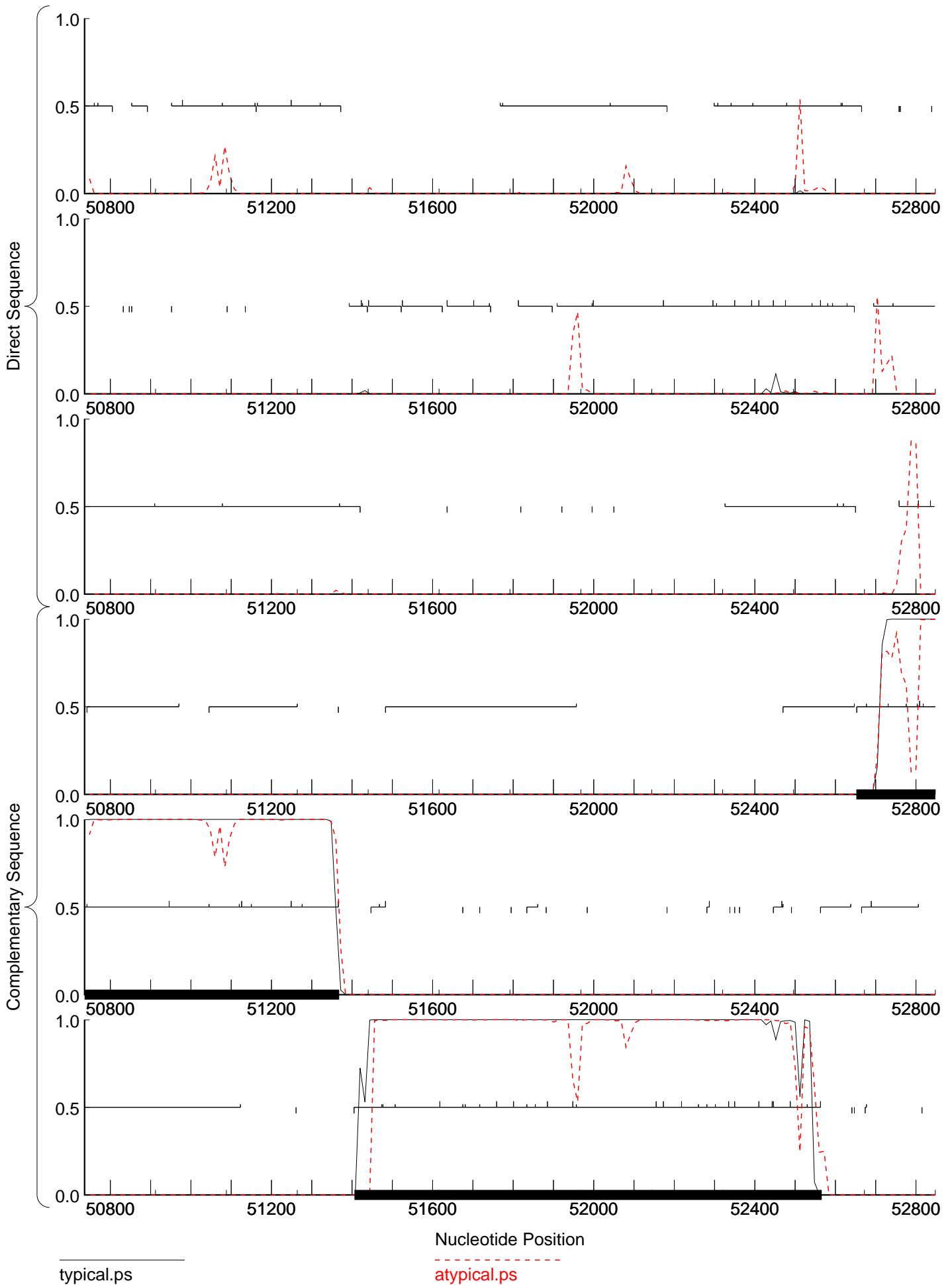
atypical.ps

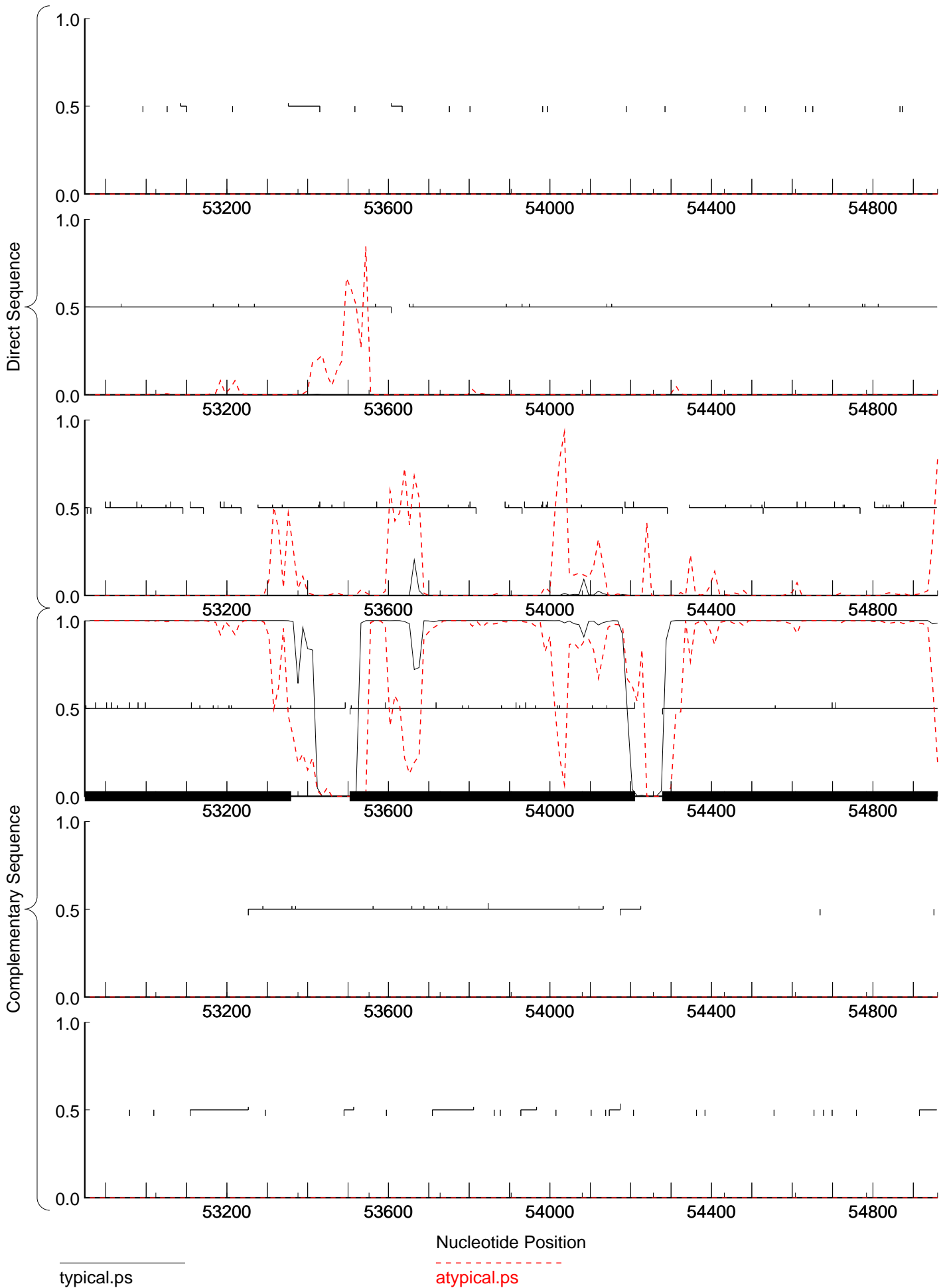


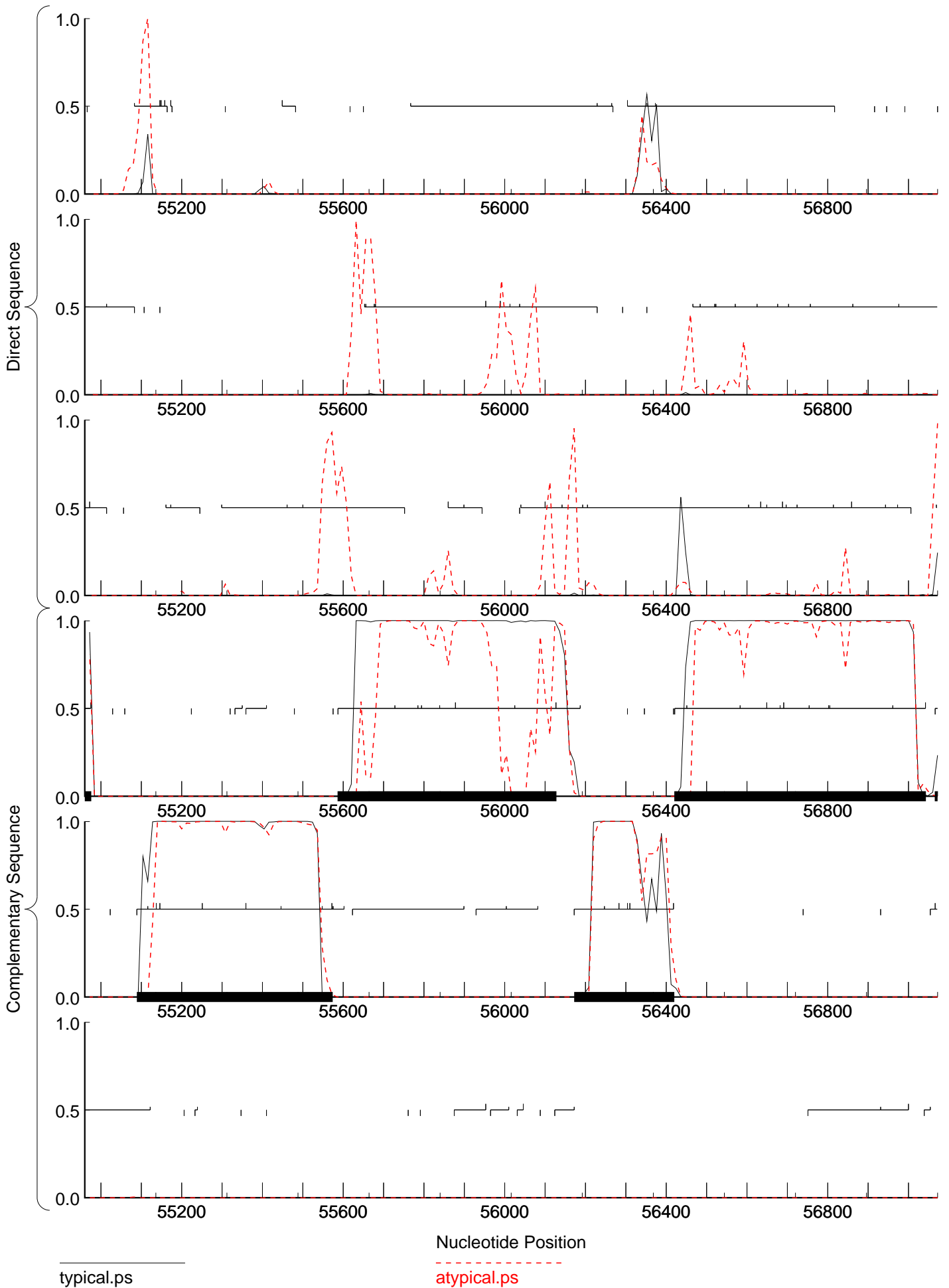


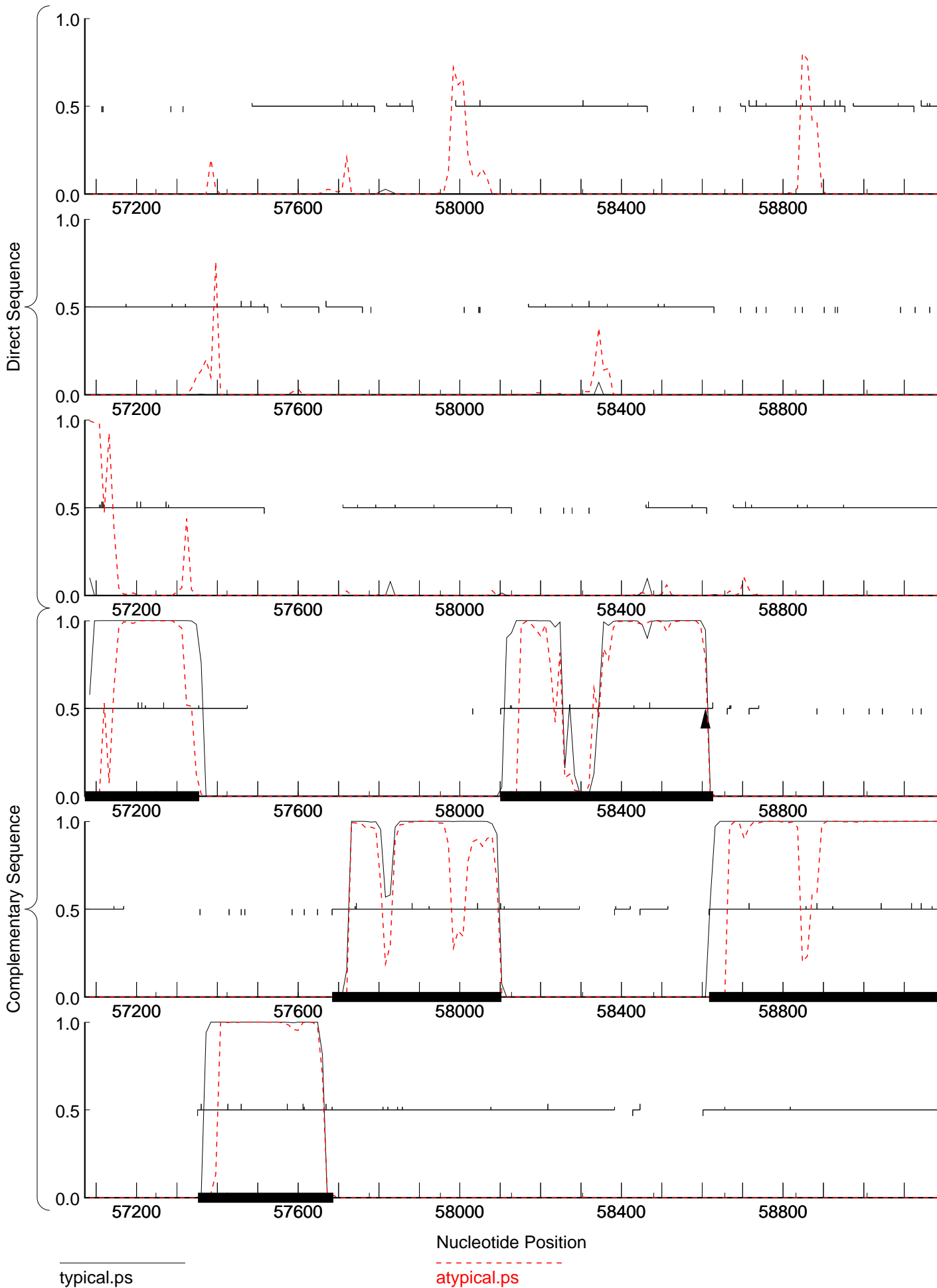


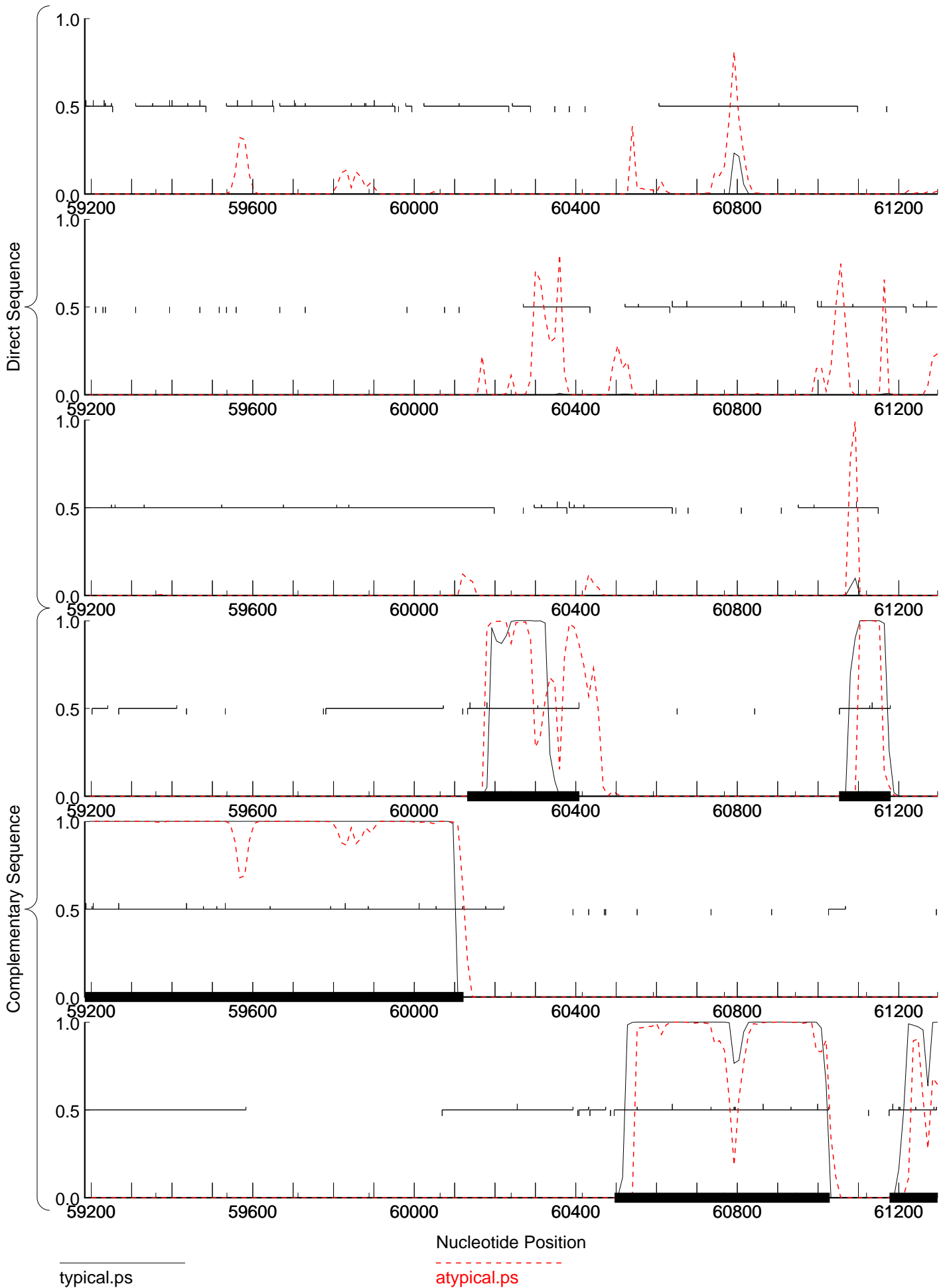


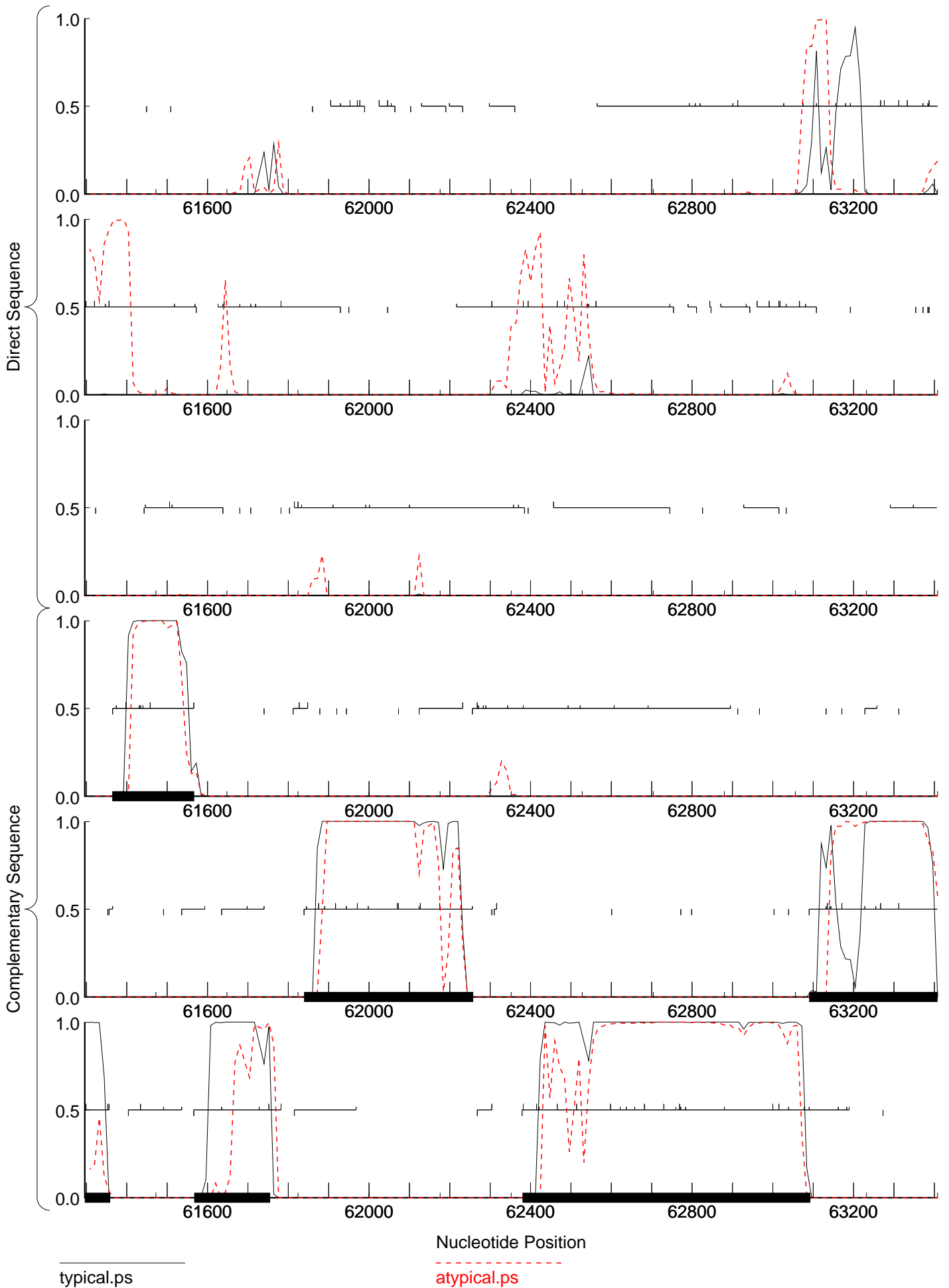


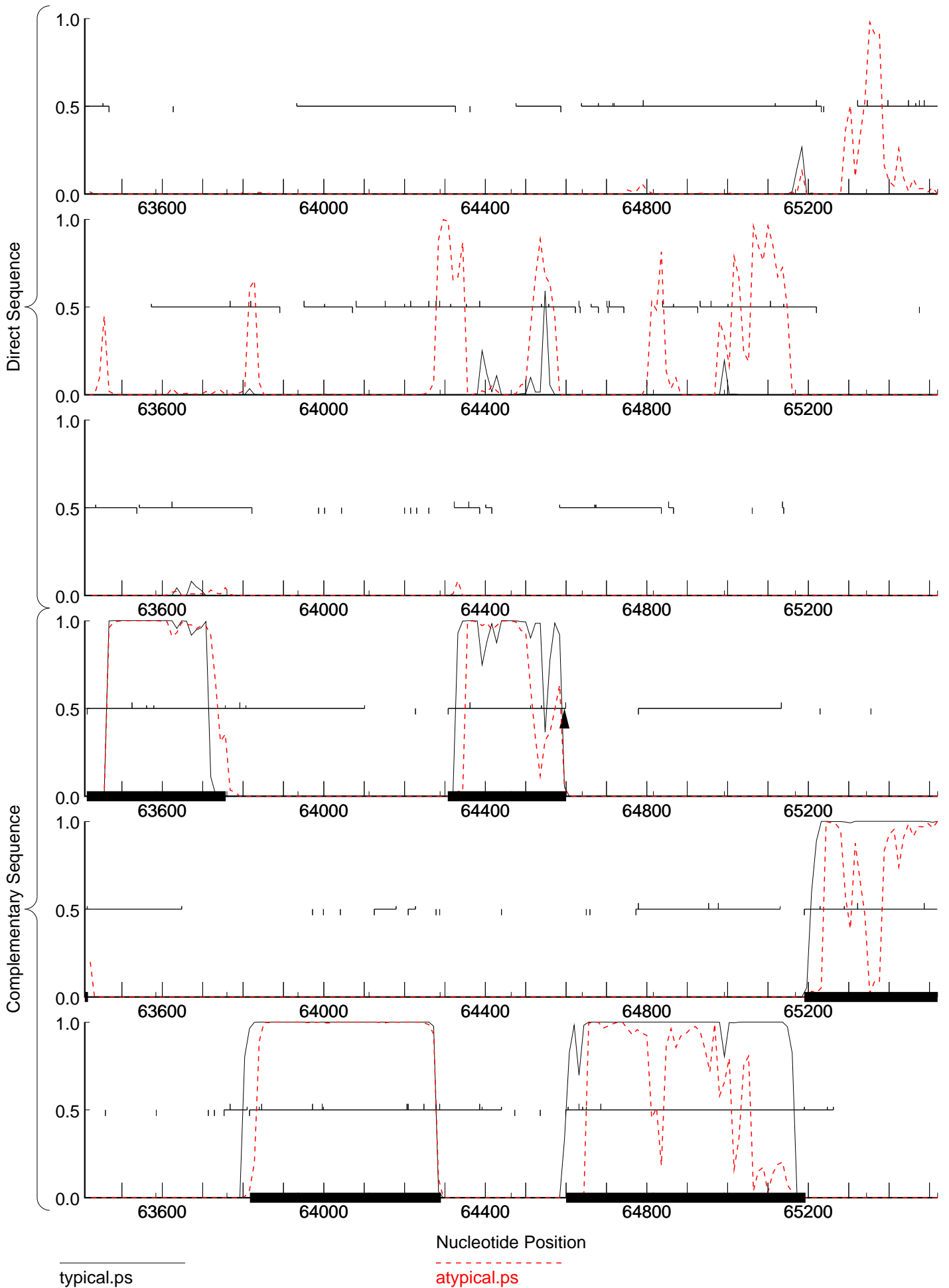


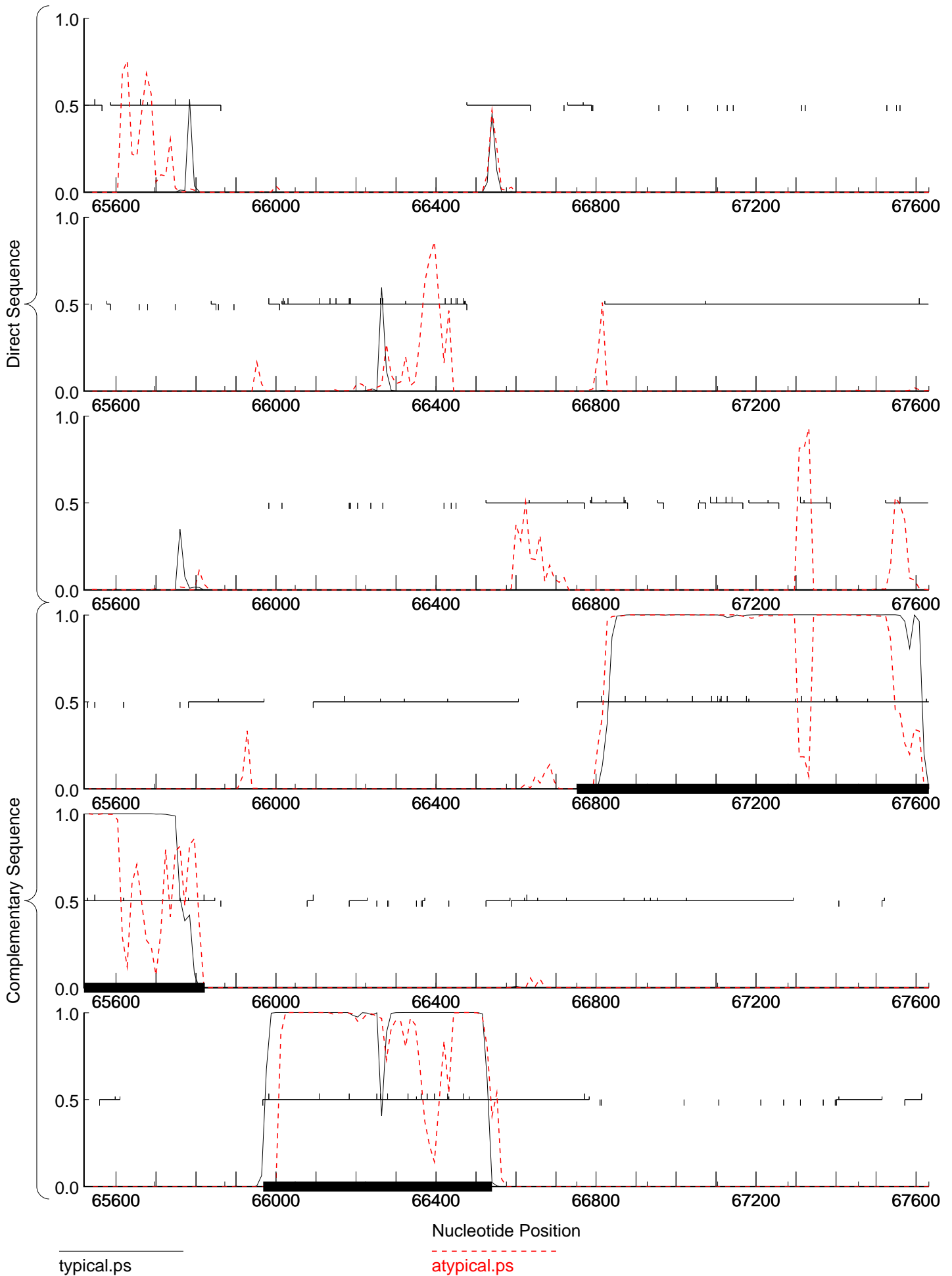






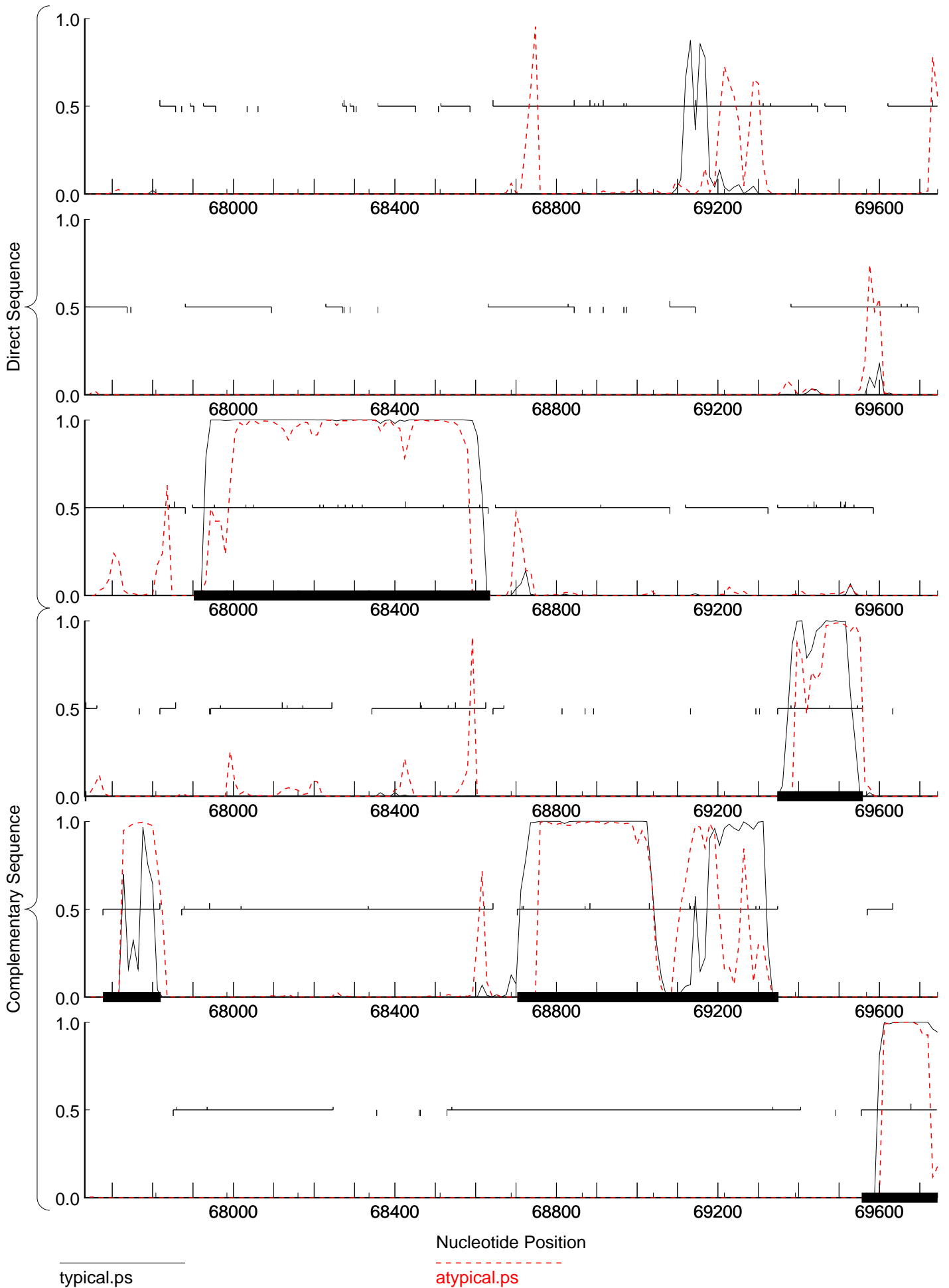


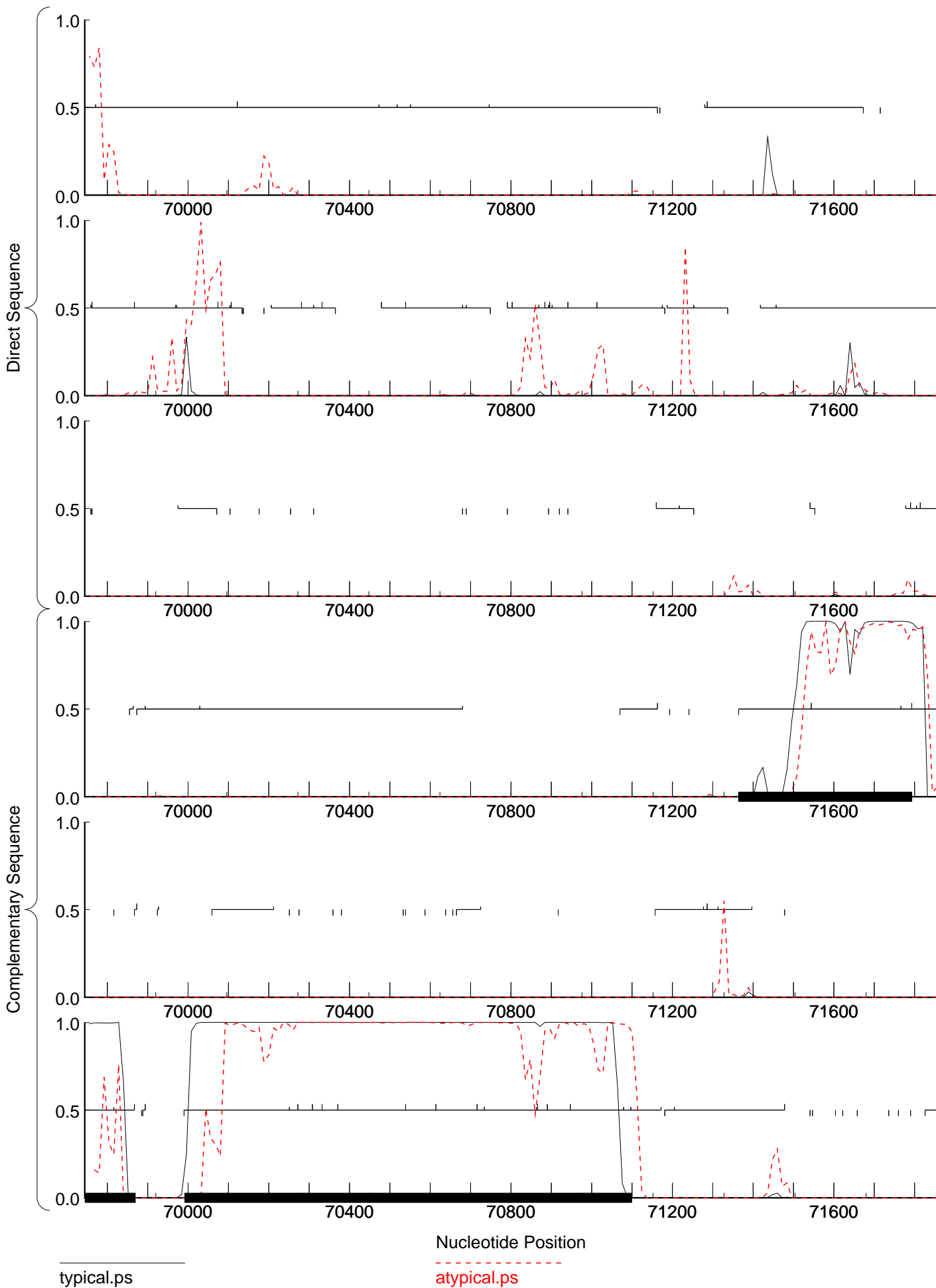




typical.ps

atypical.ps

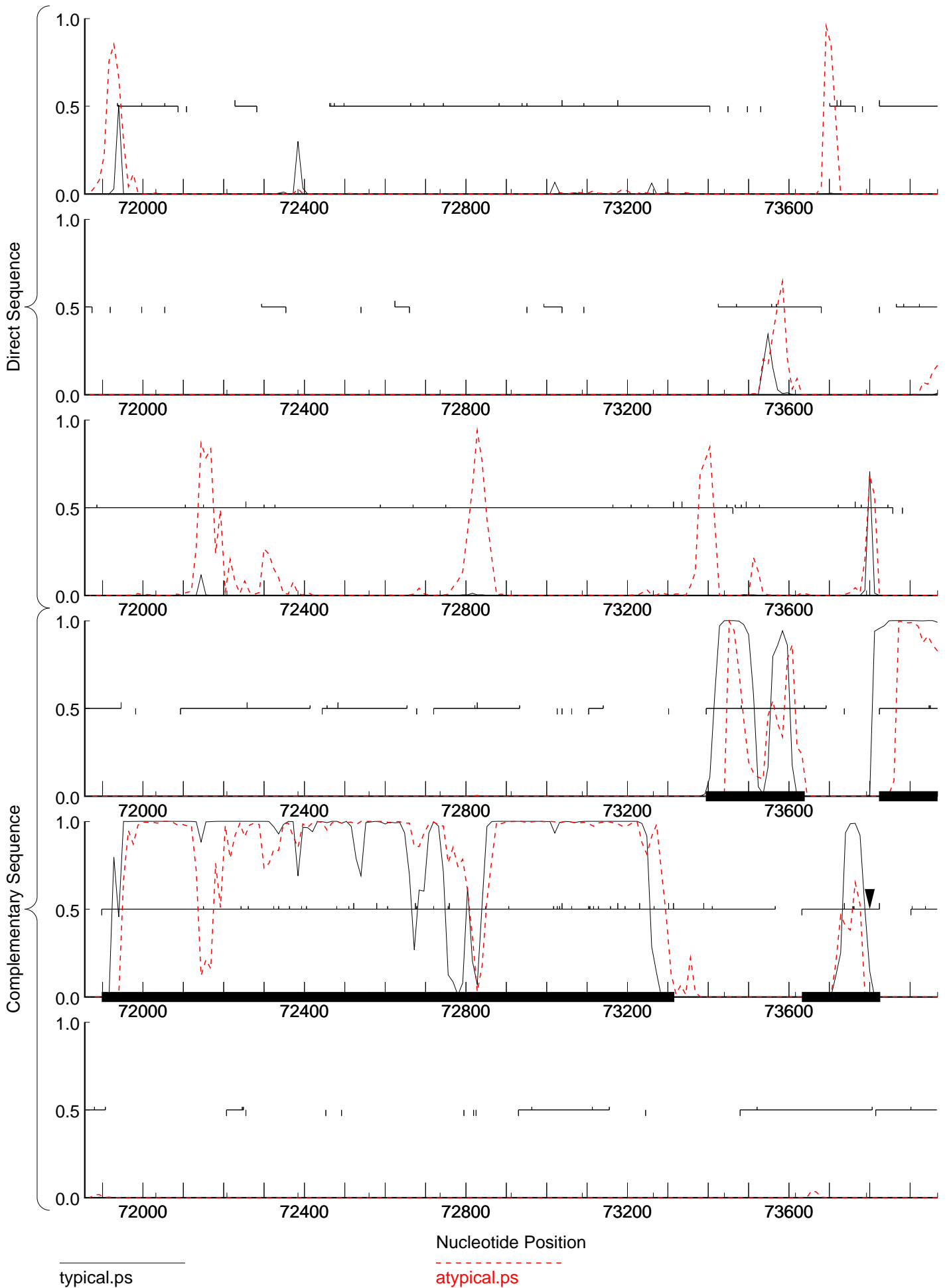


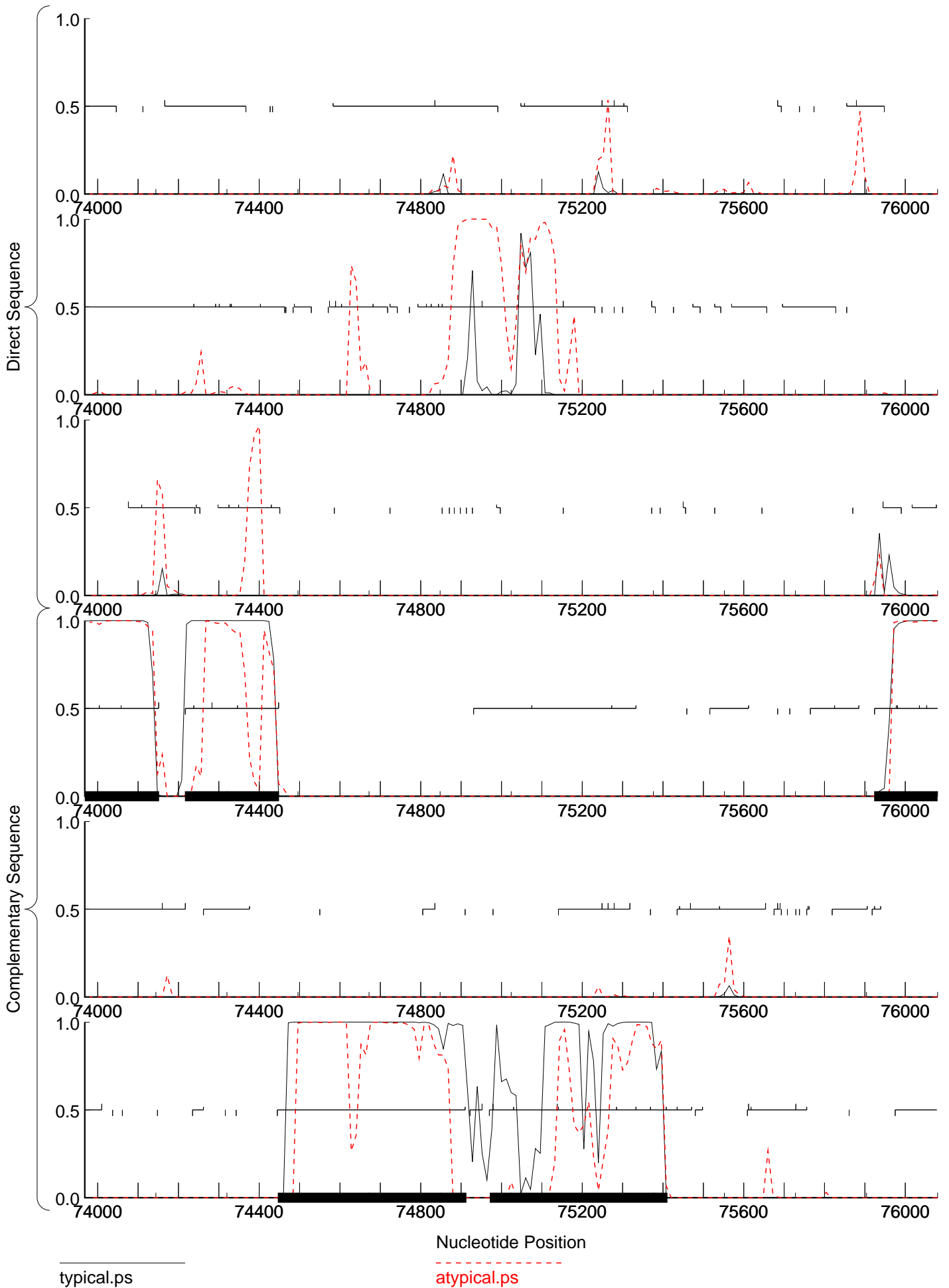


typical.ps

Nucleotide Position

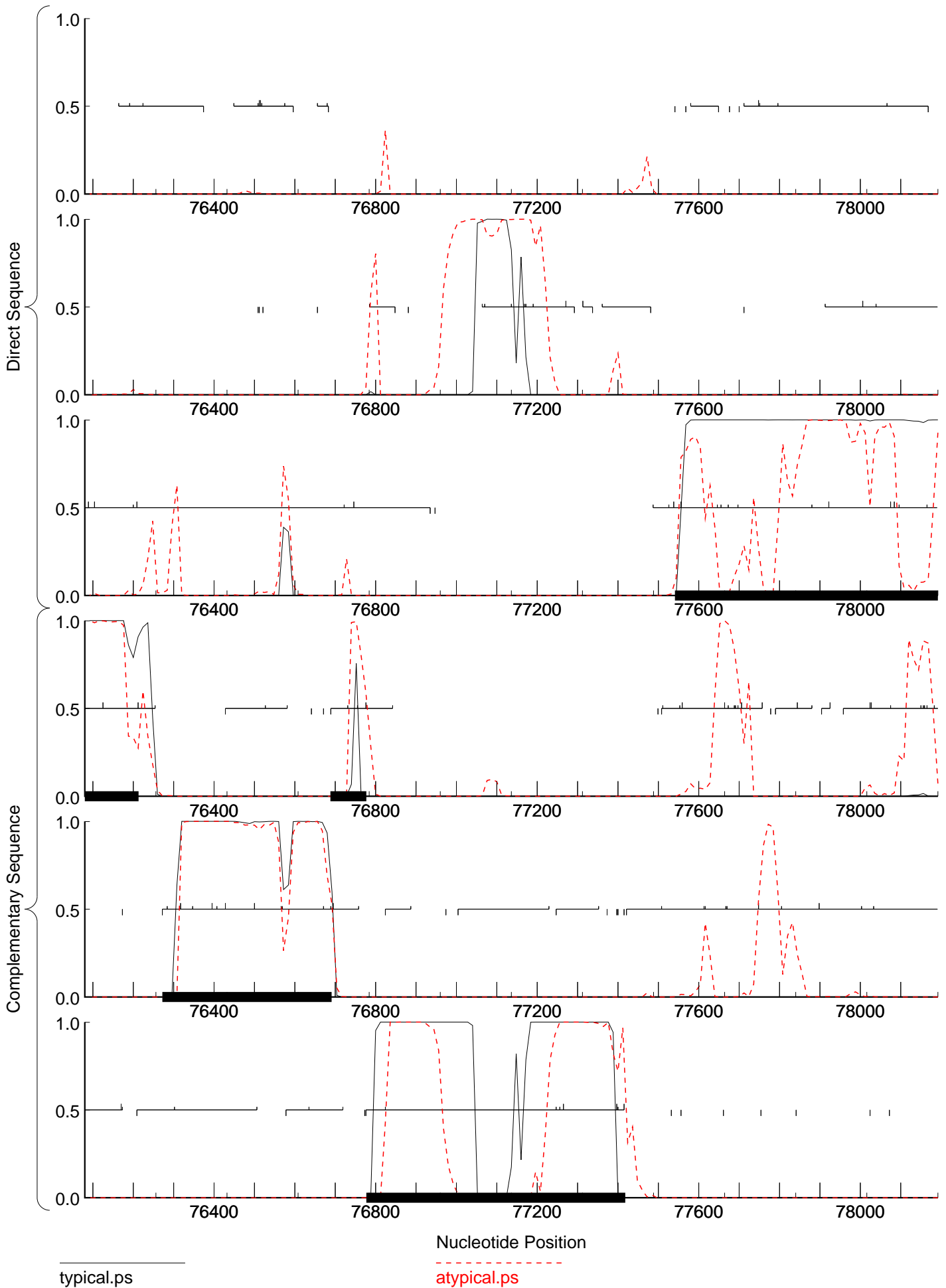
atypical.ps

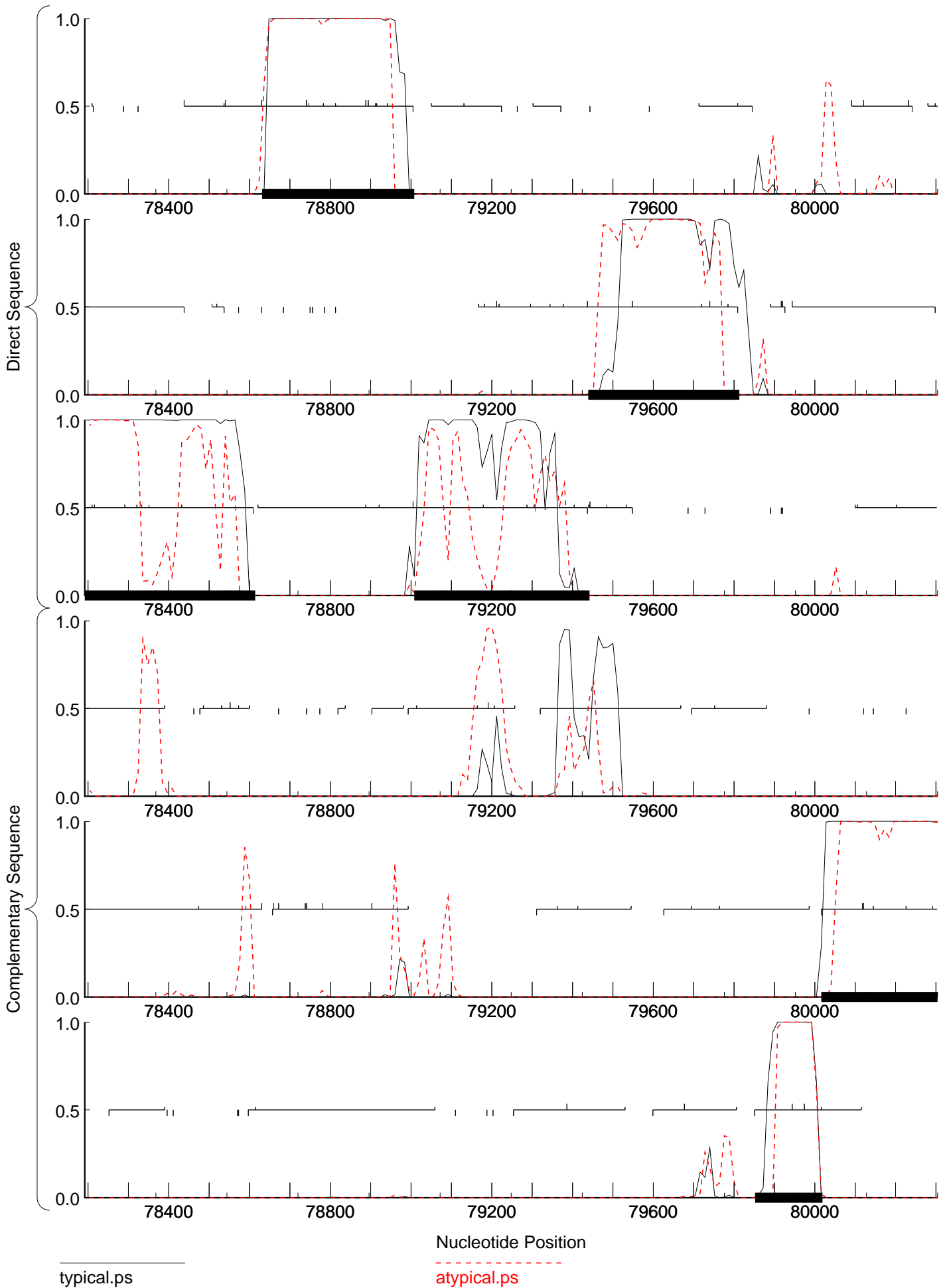


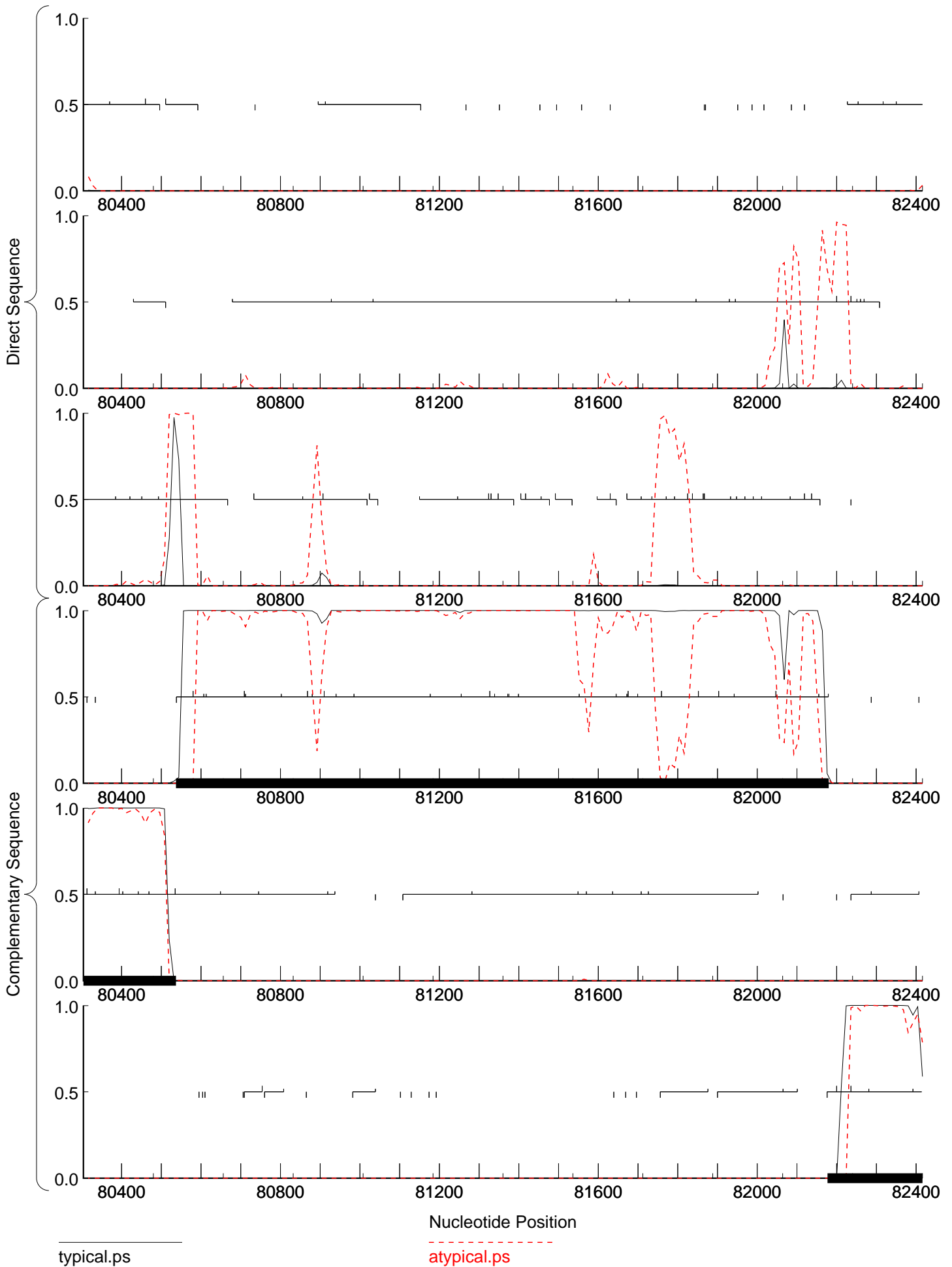


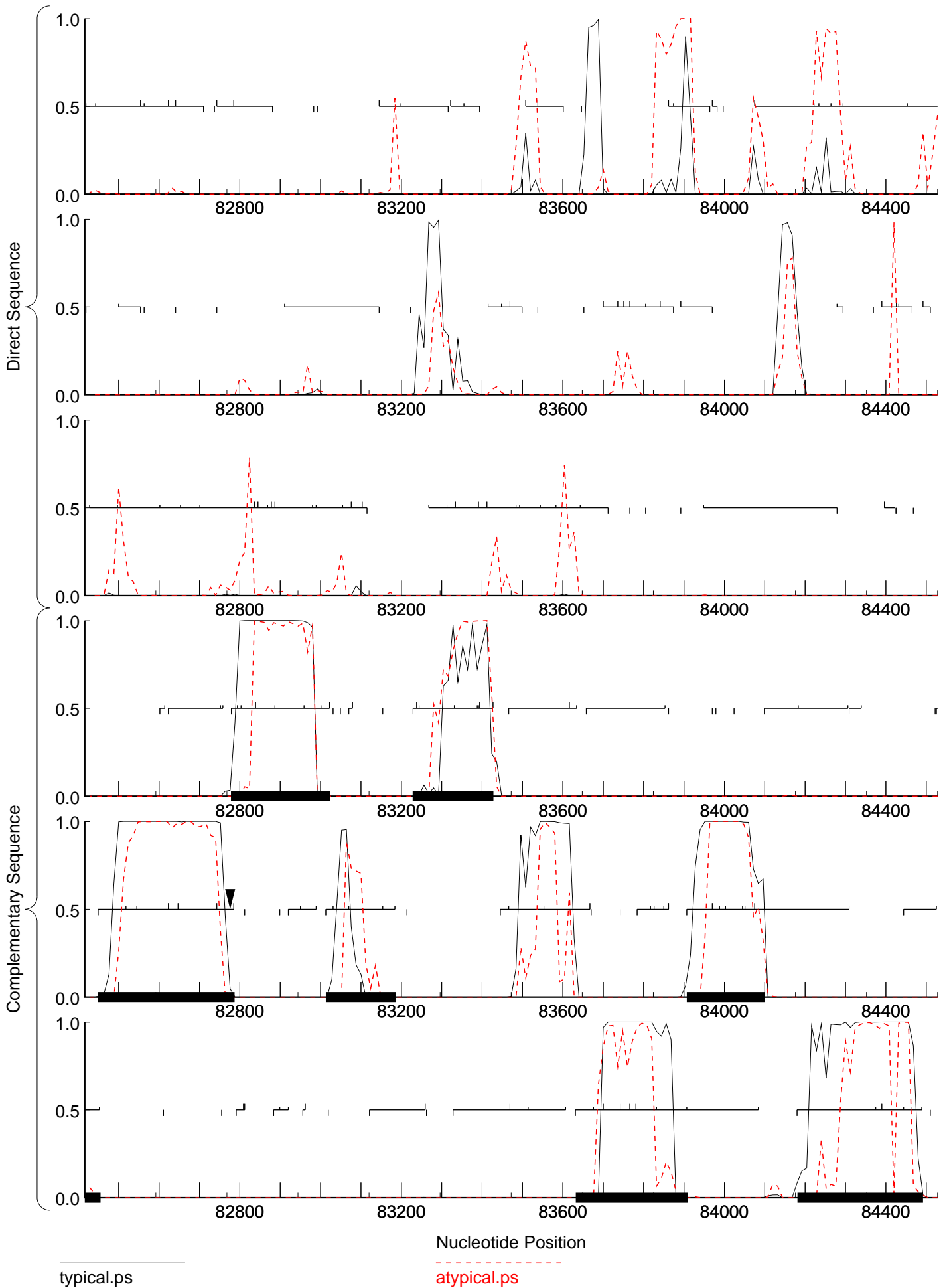
typical.ps

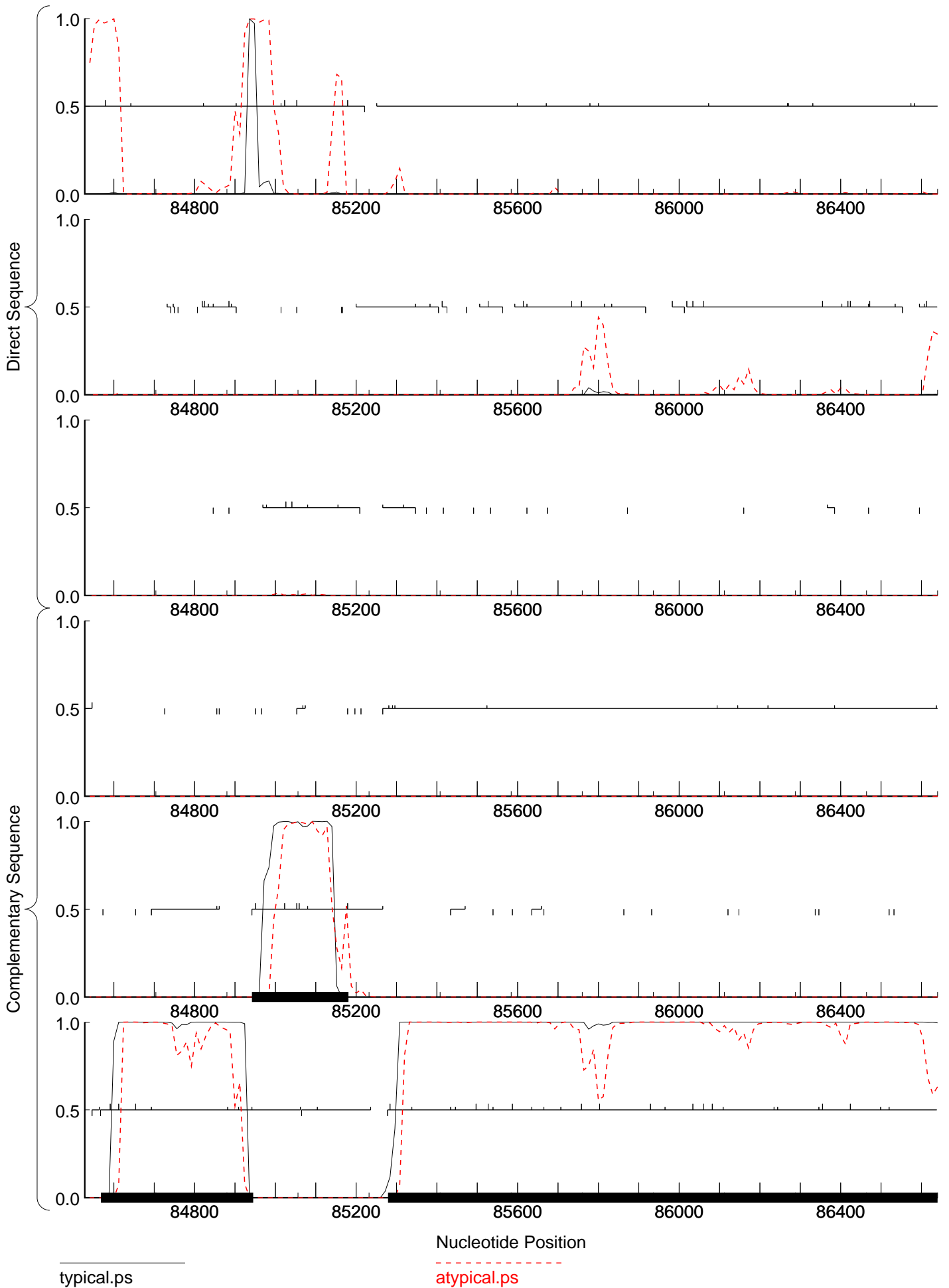
atypical.ps





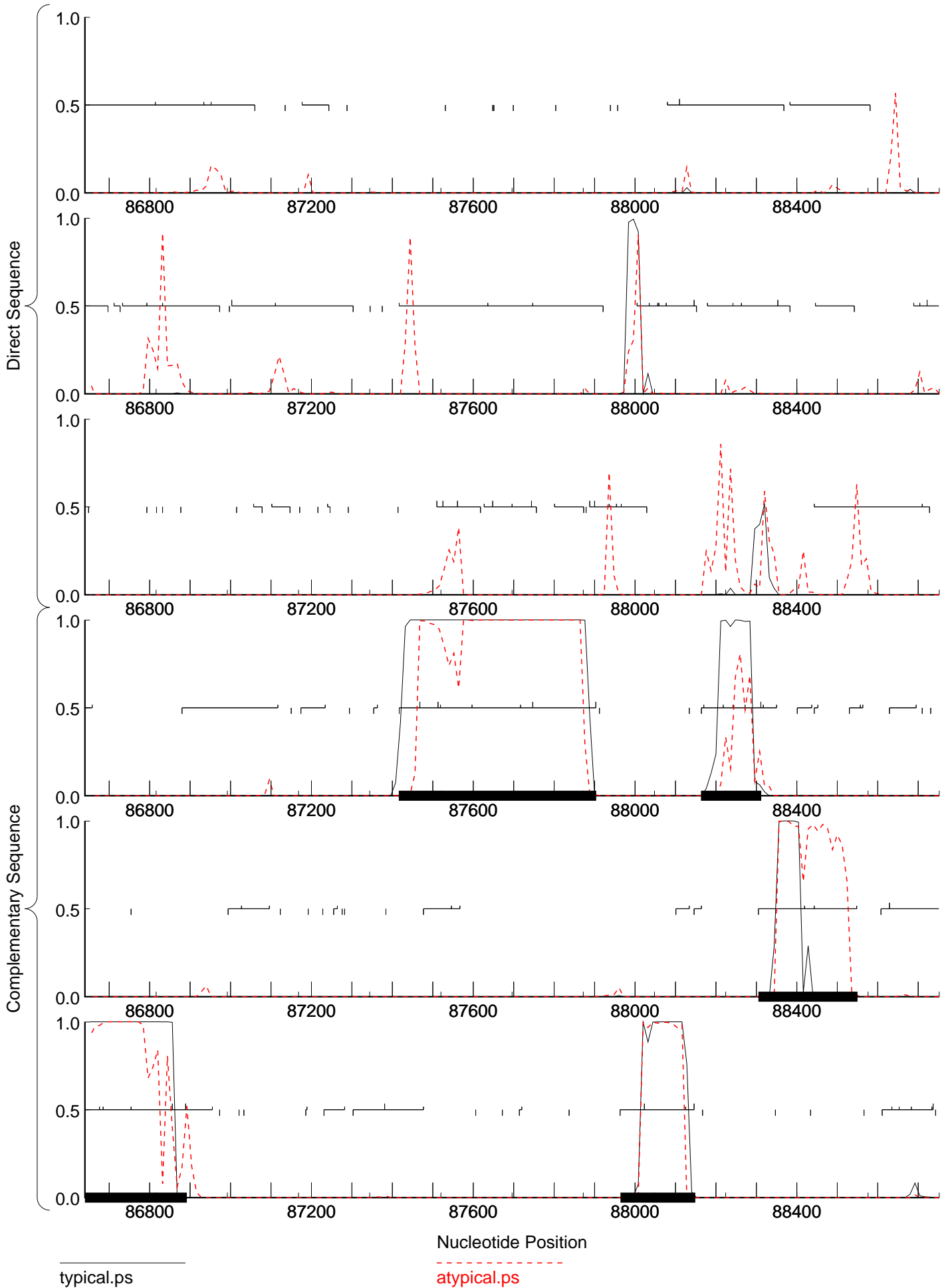






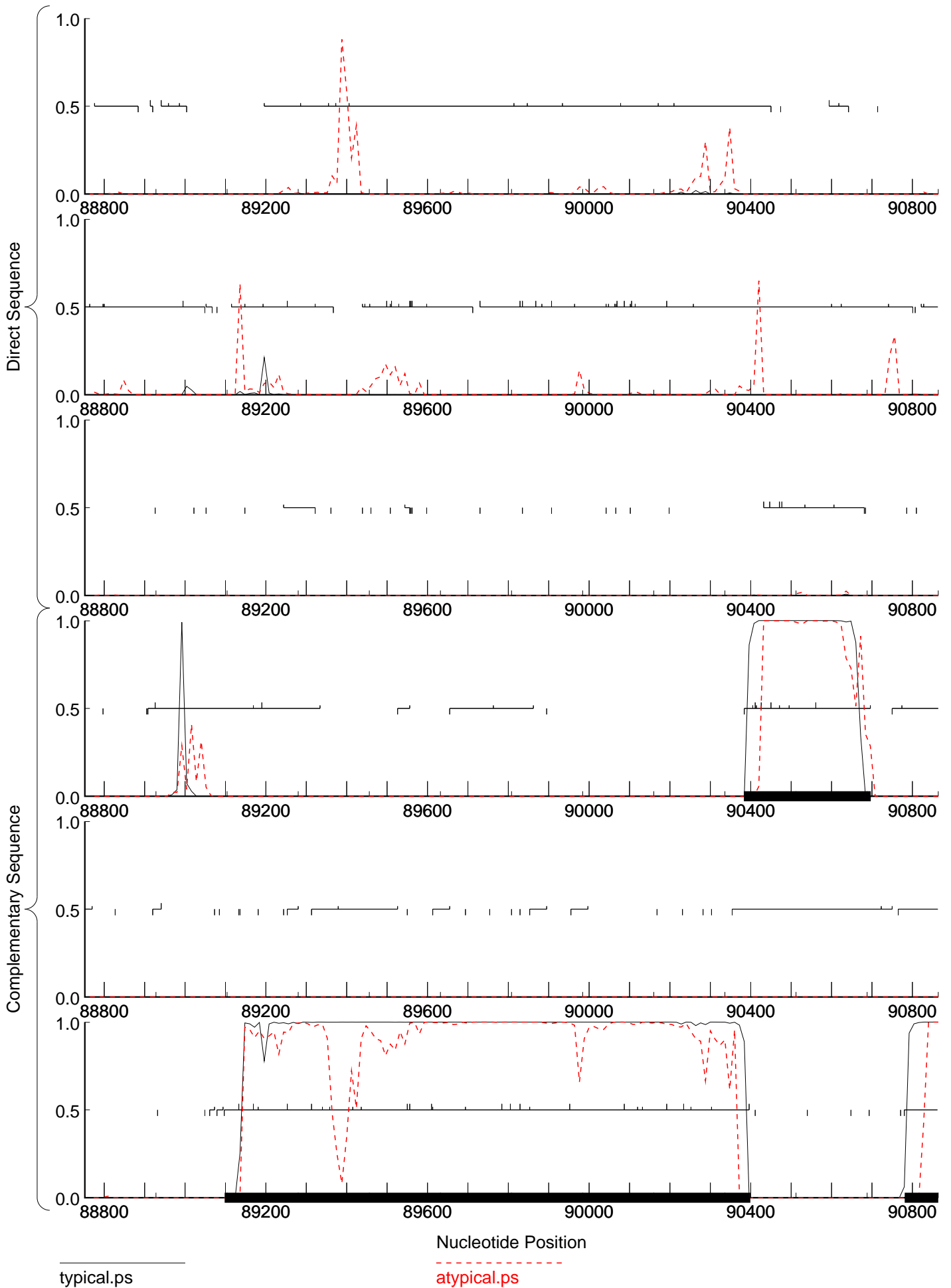
typical.ps

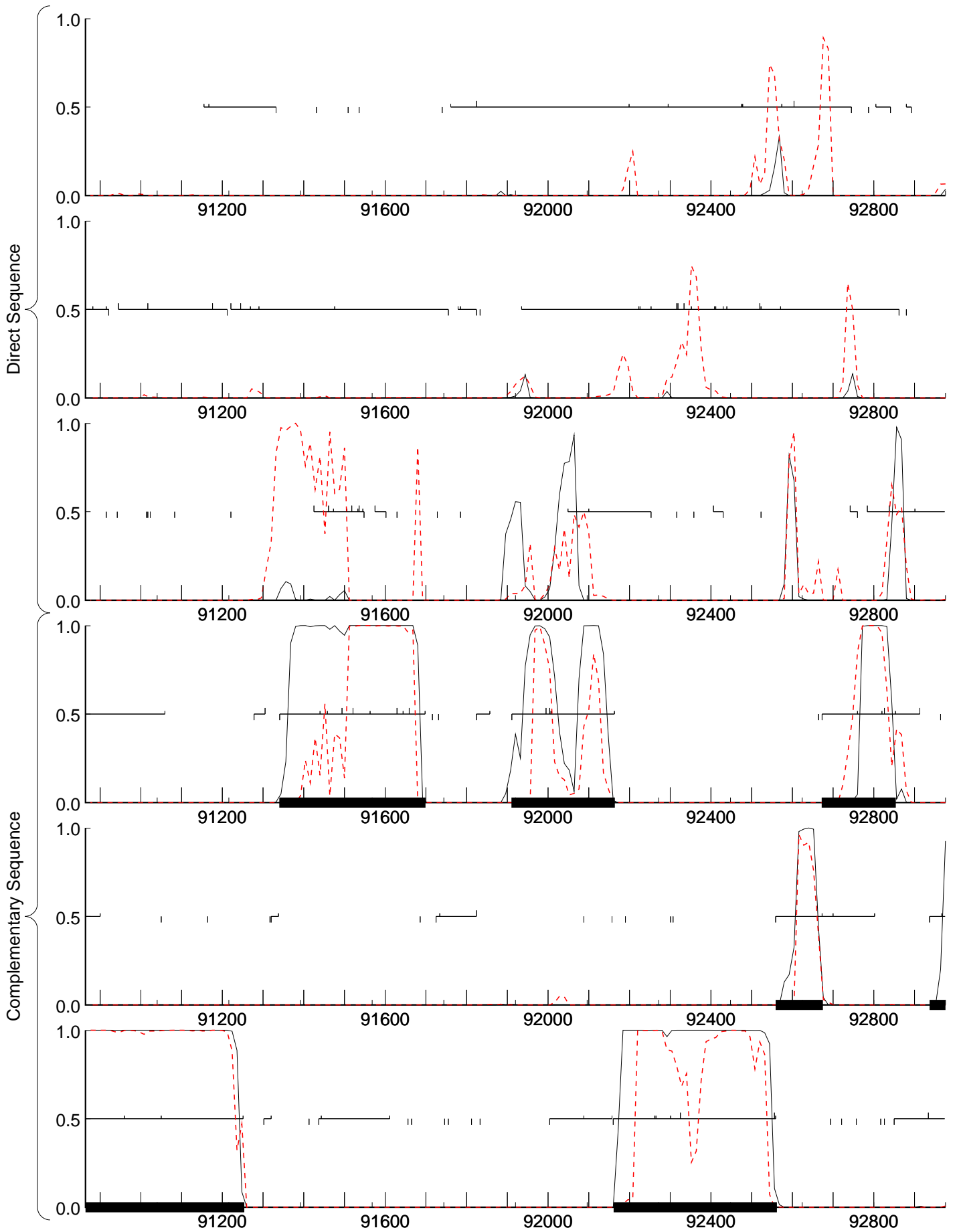
atypical.ps



typical.ps

atypical.ps

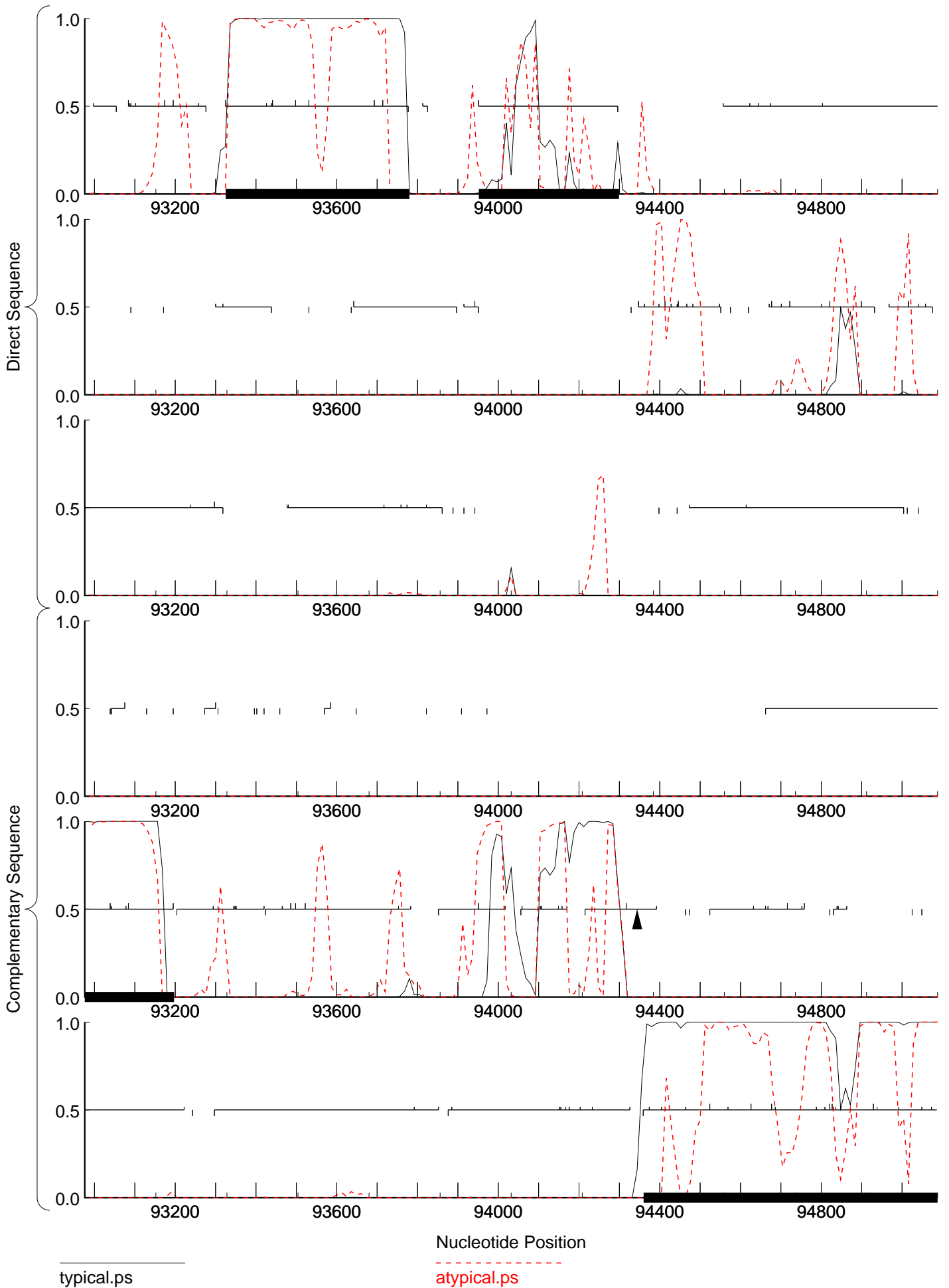


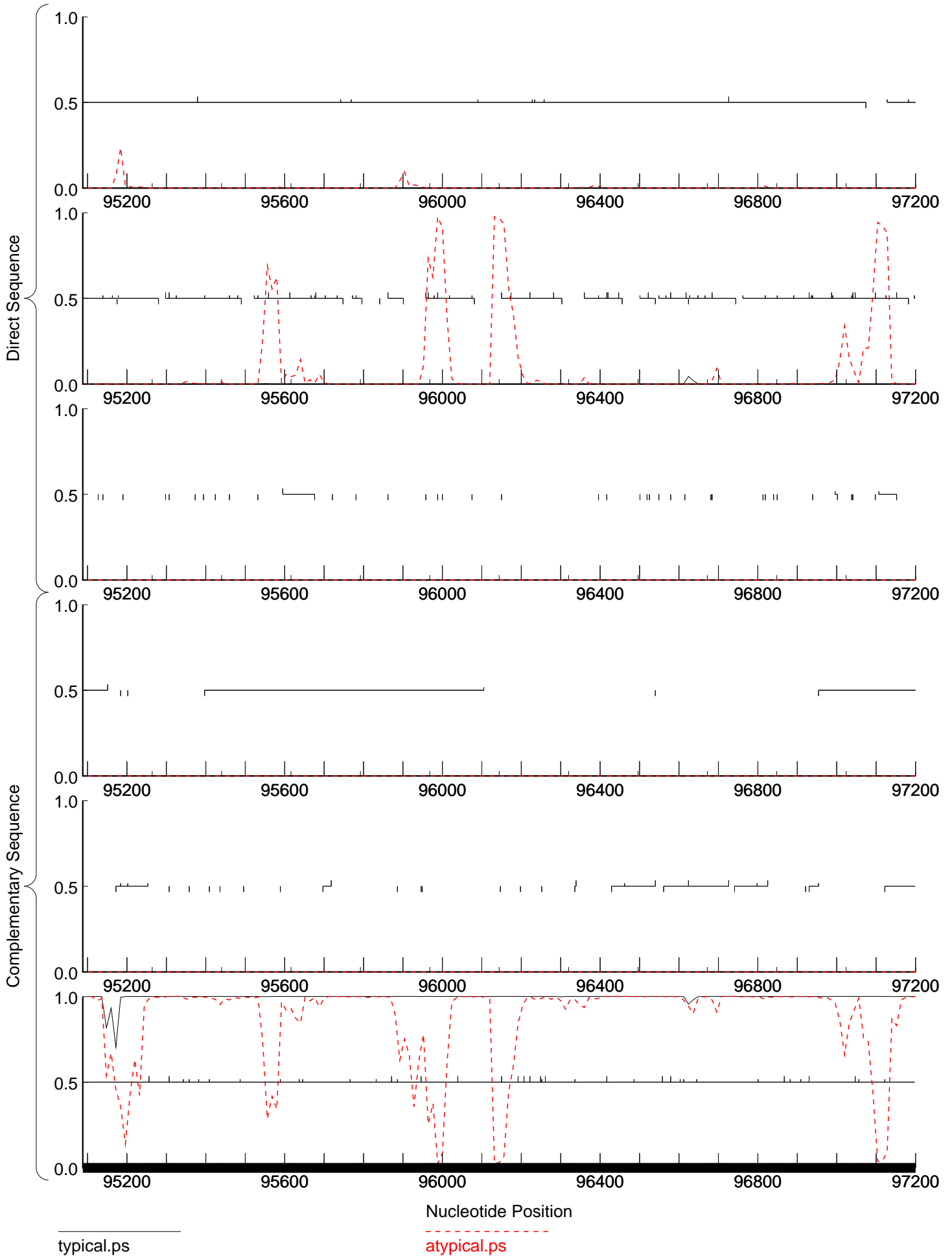


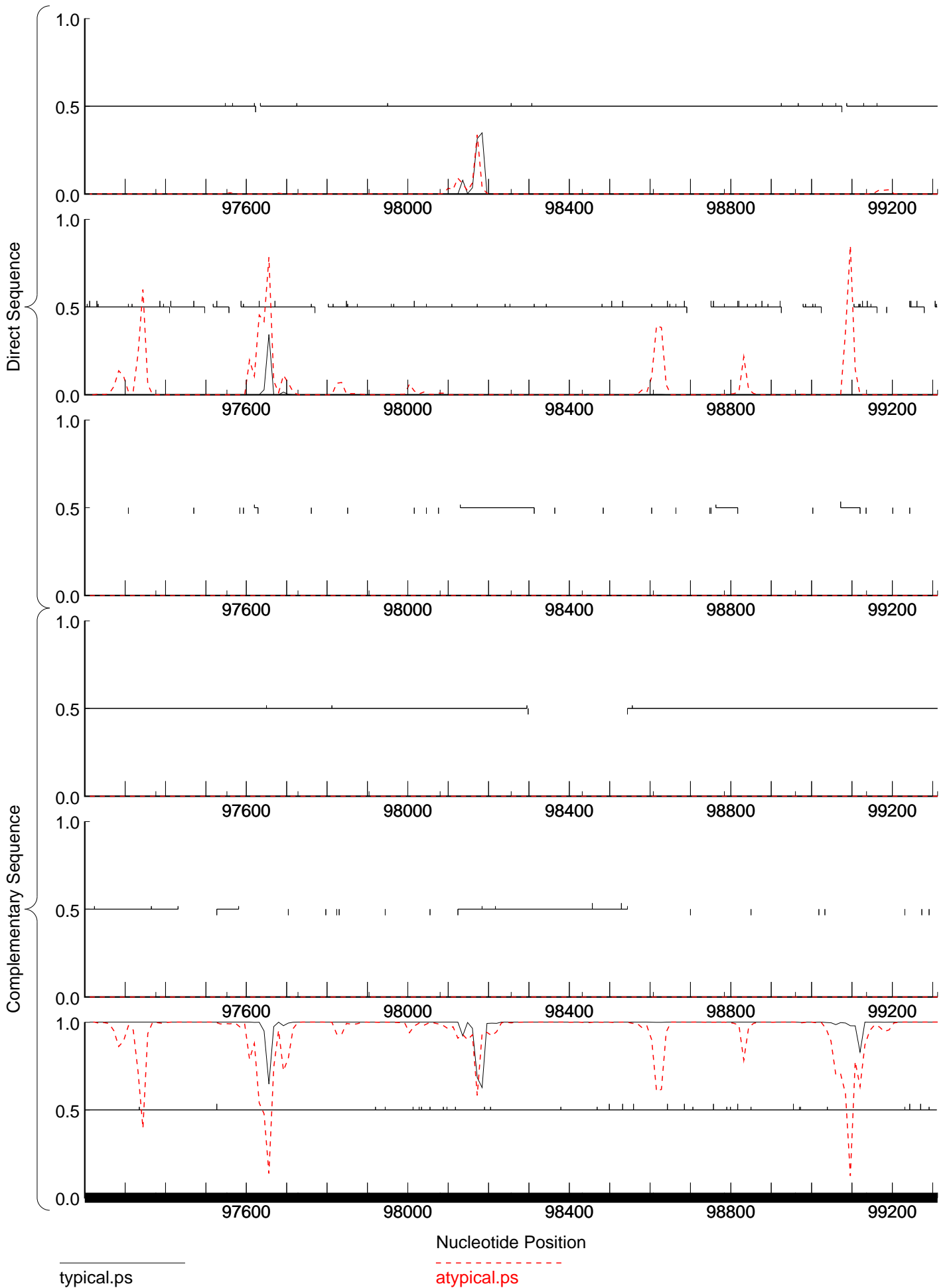
typical.ps

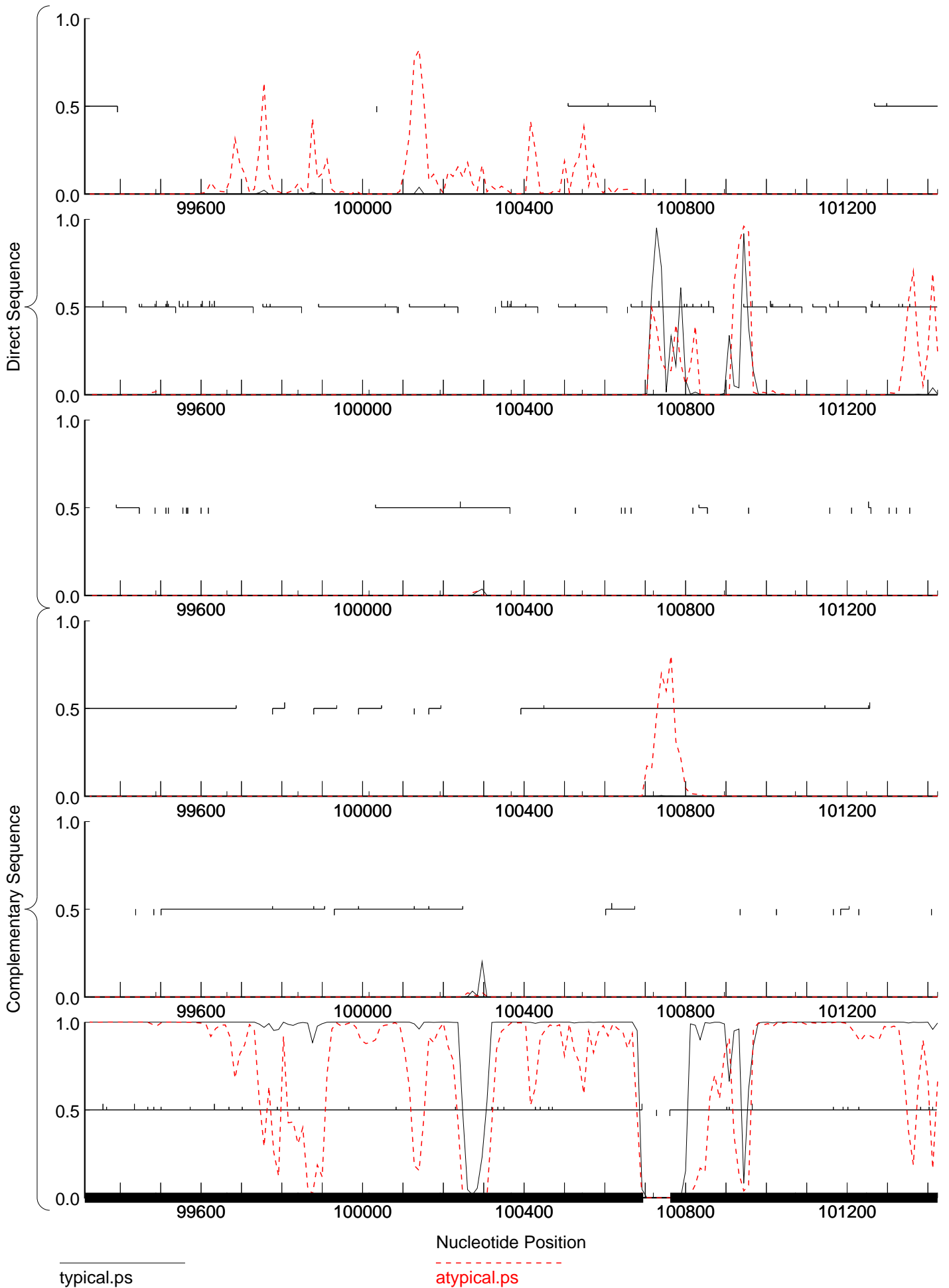
Nucleotide Position

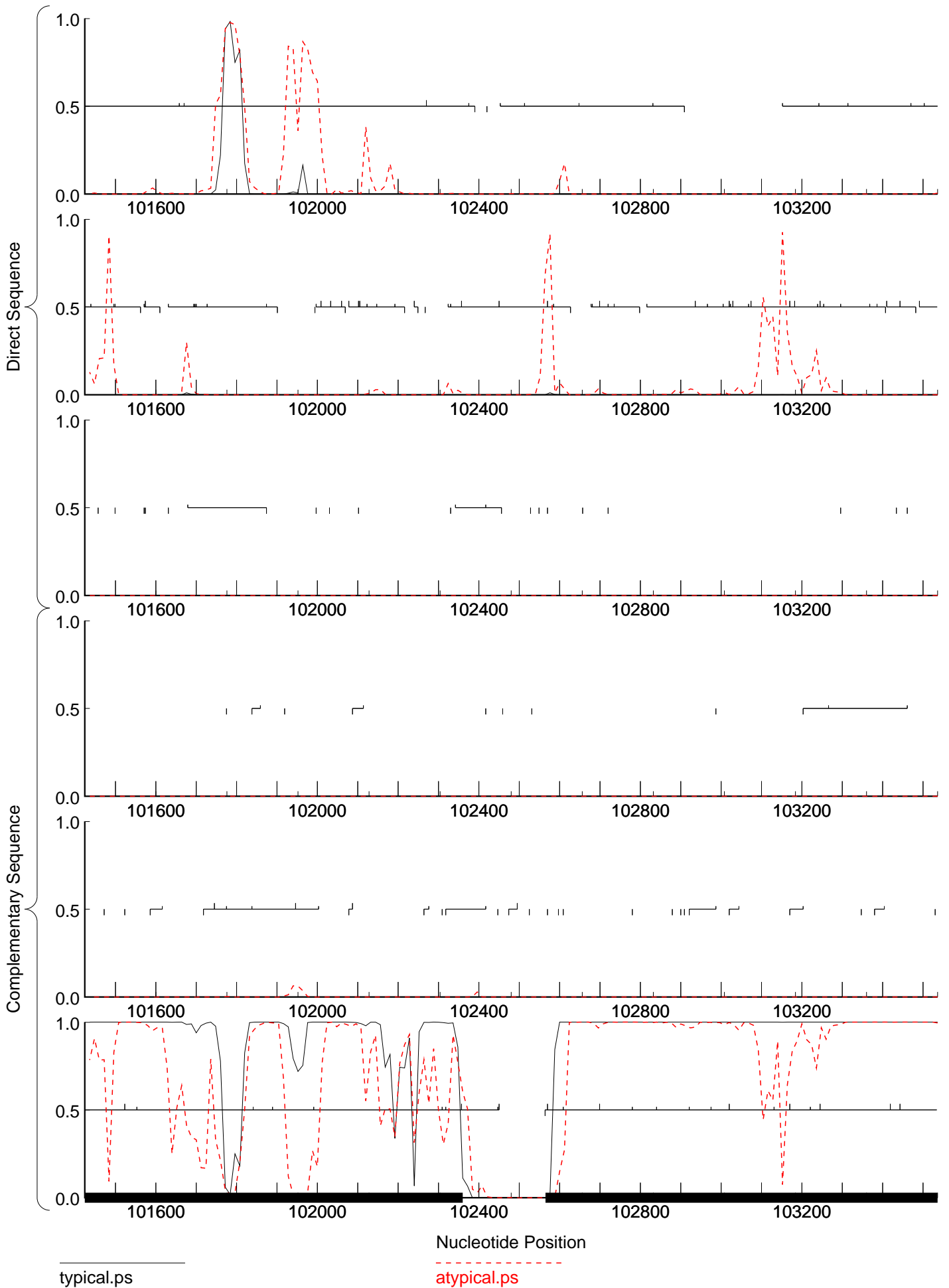
atypical.ps

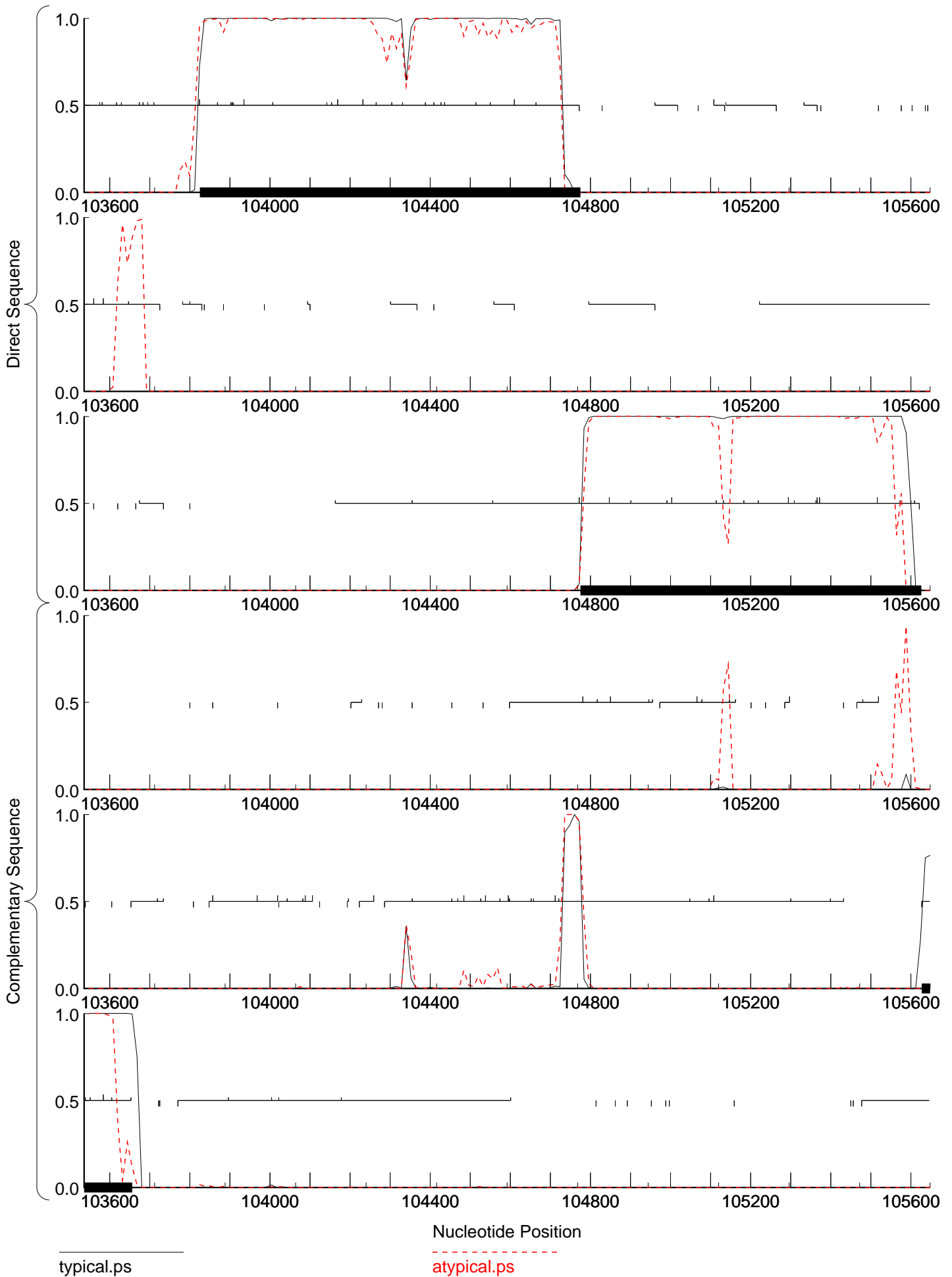


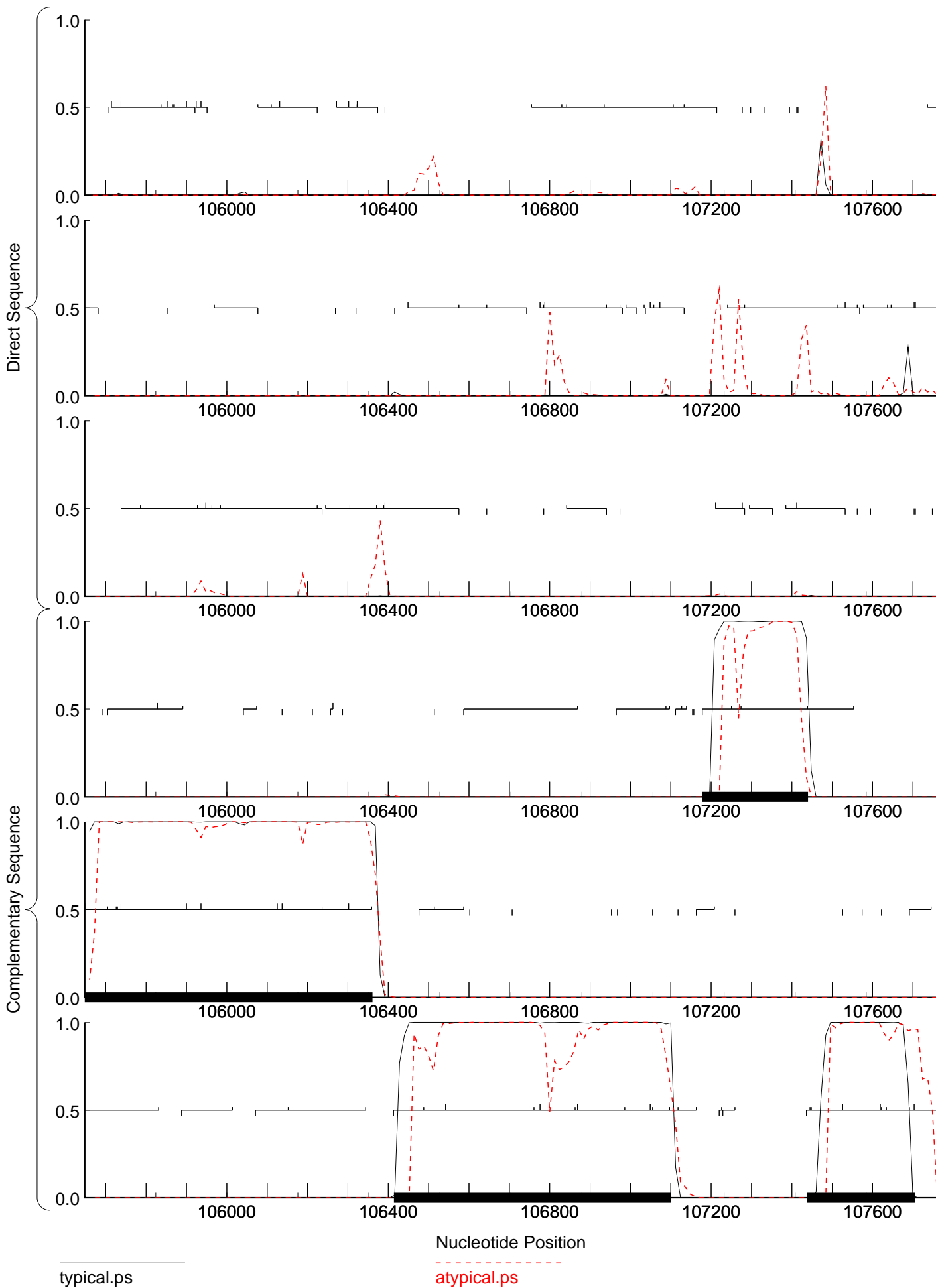






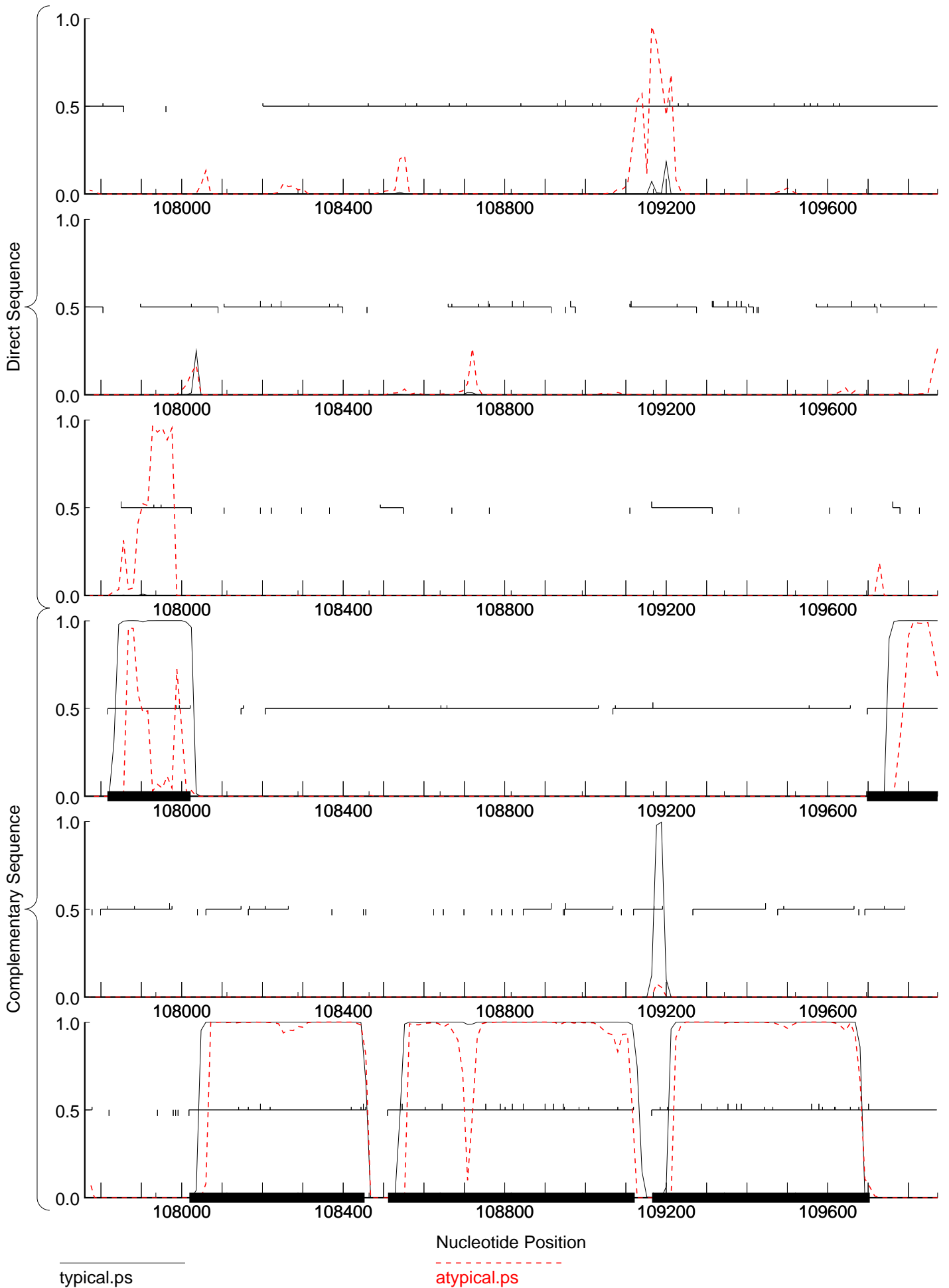


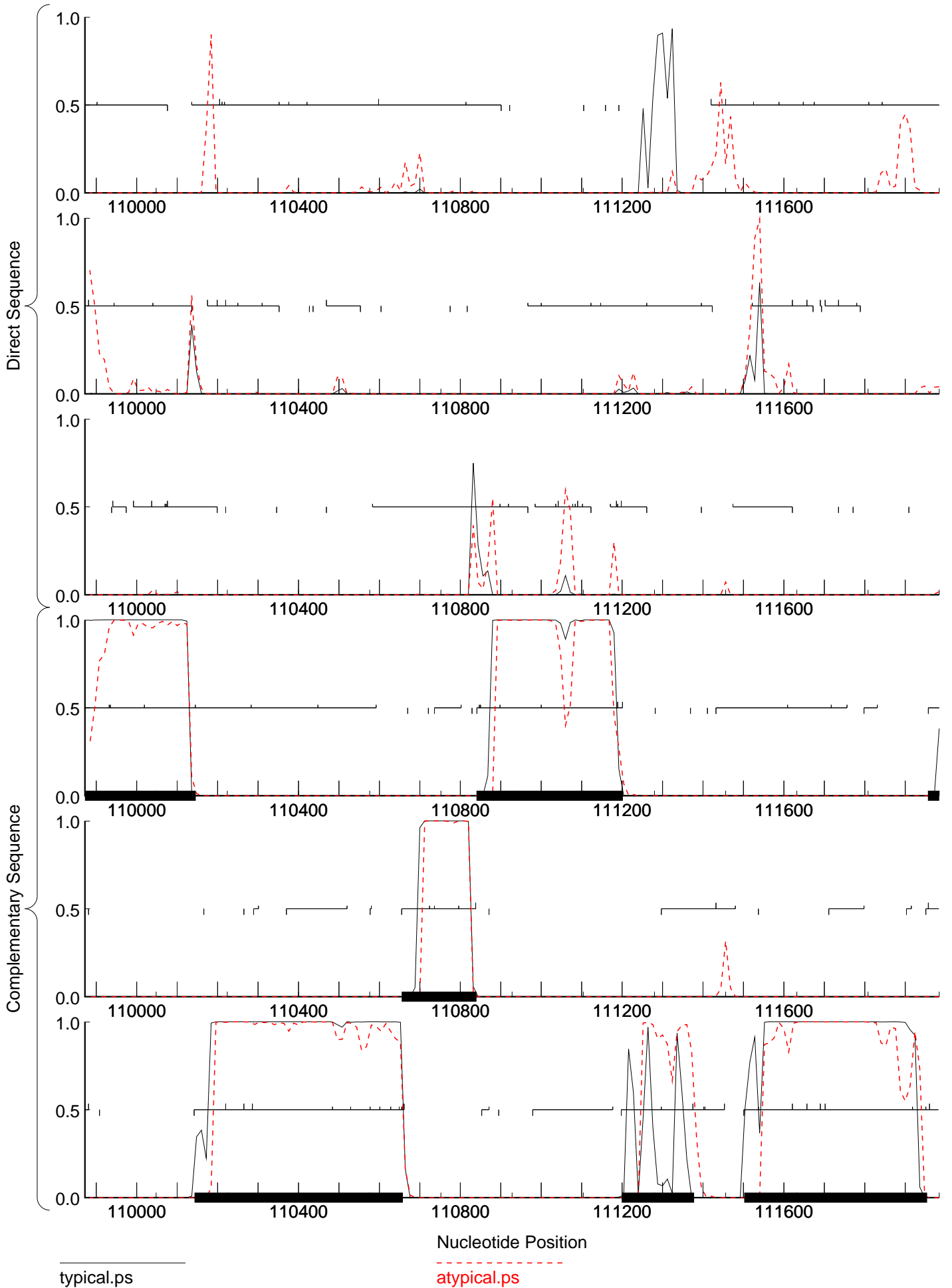


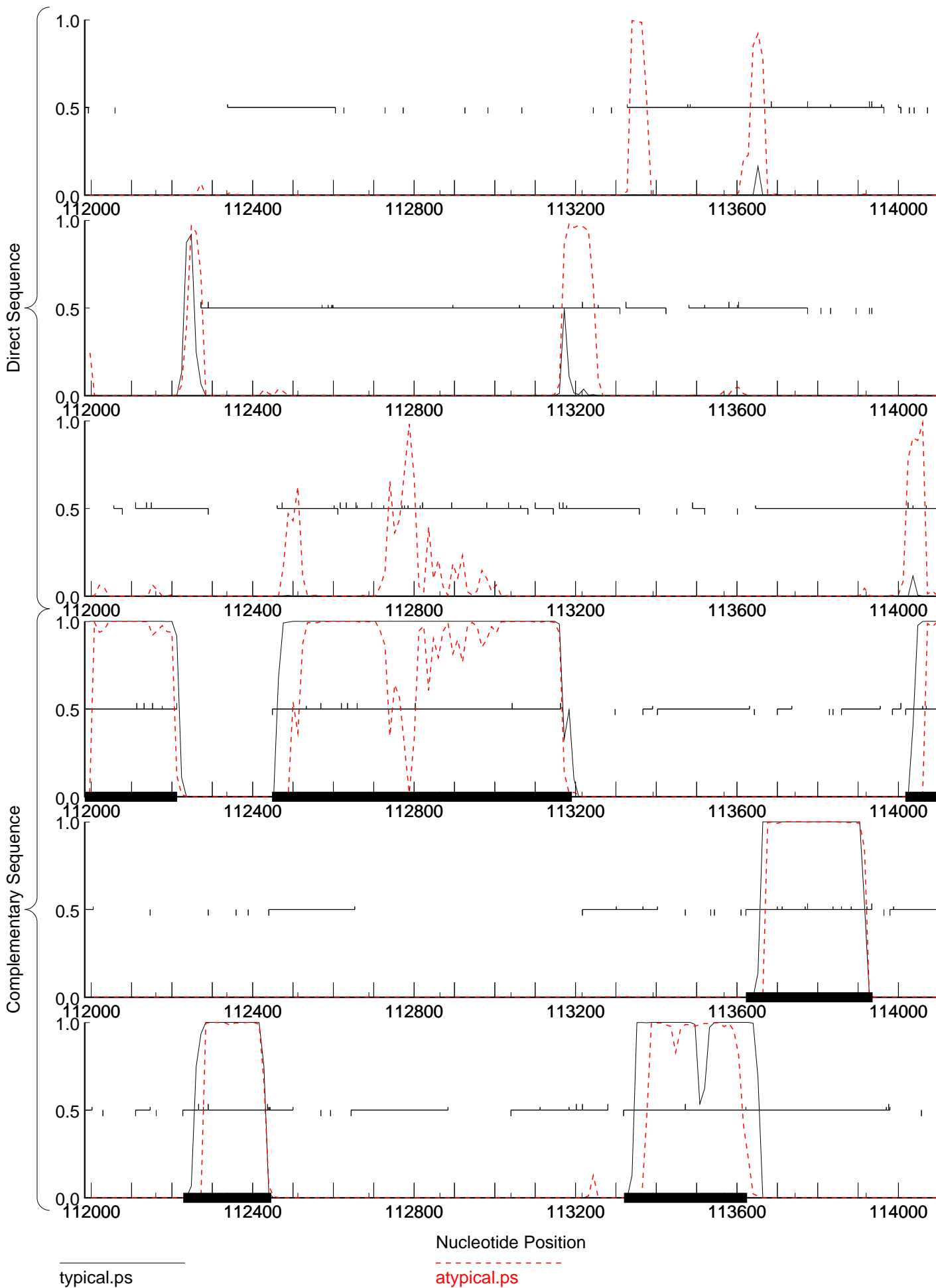


typical.ps

atypical.ps

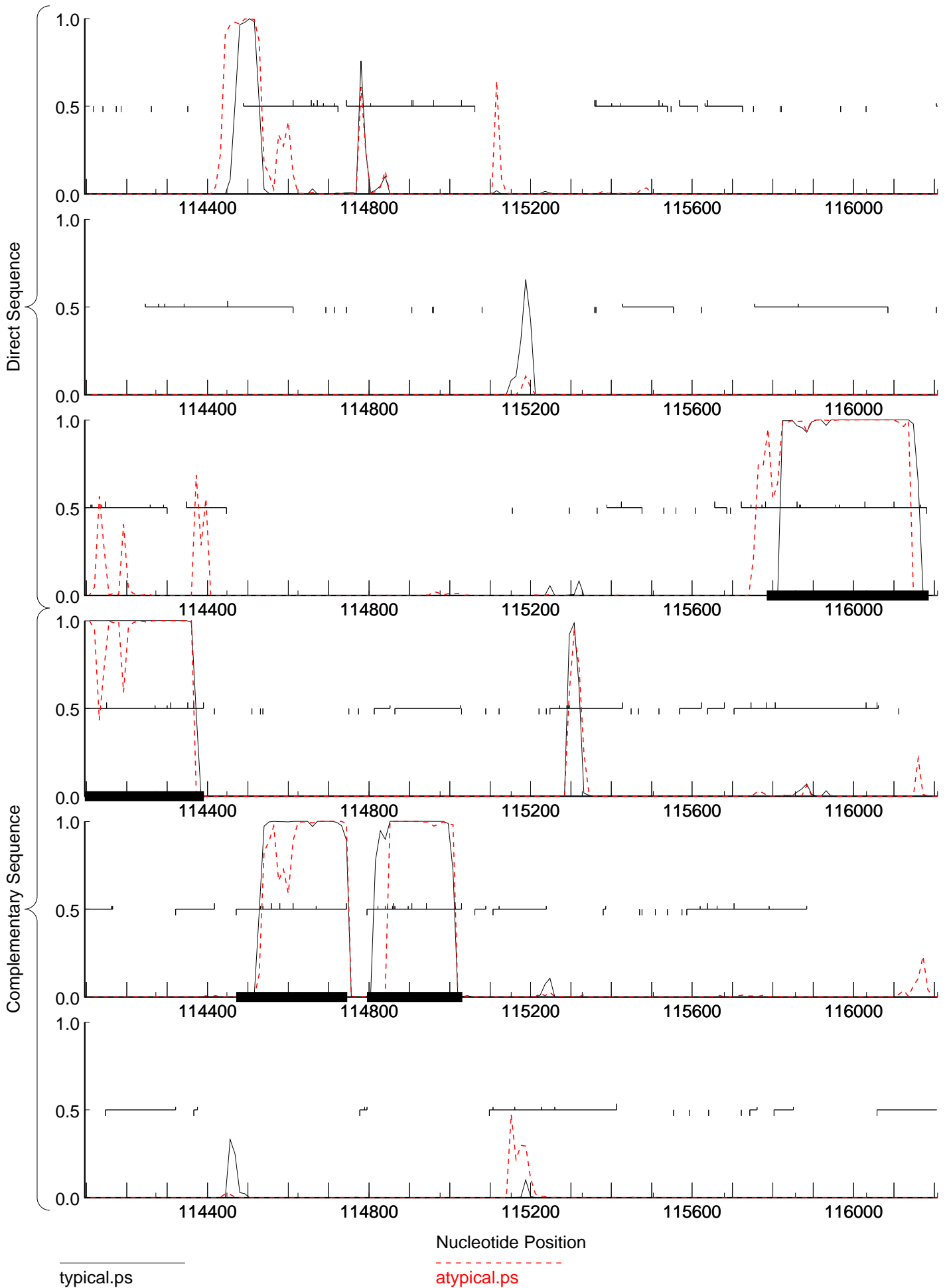


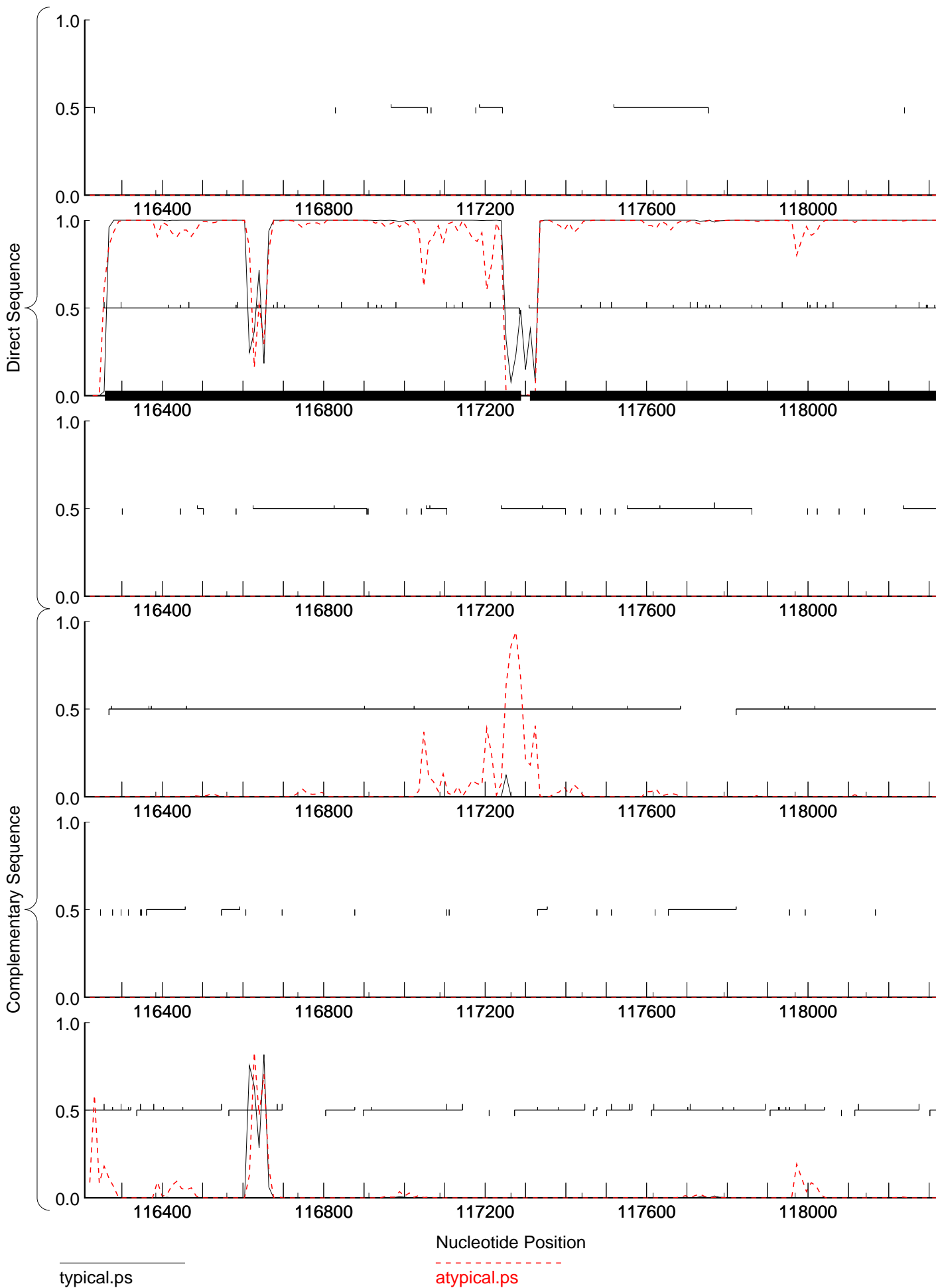


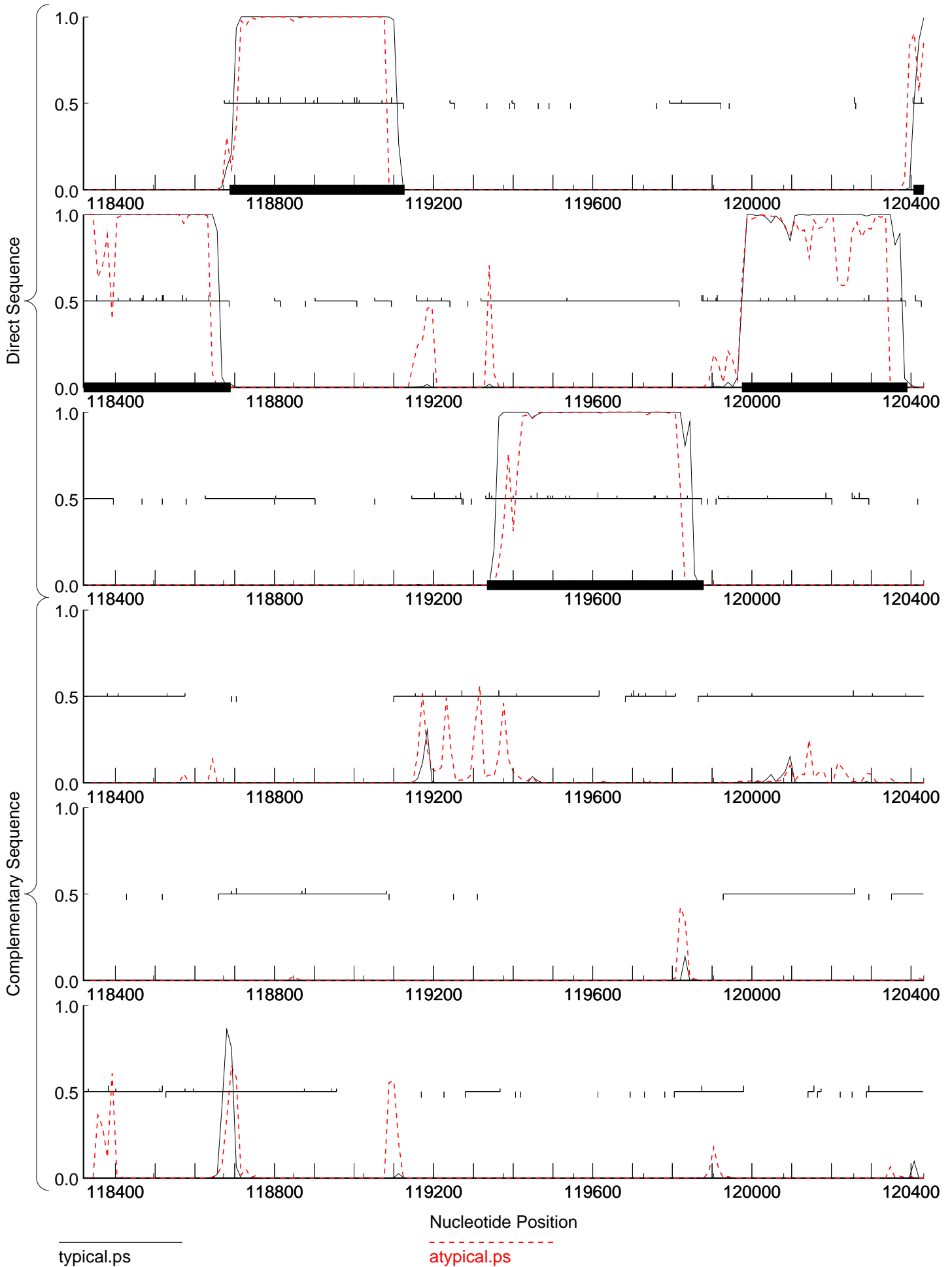


typical.ps

atypical.ps

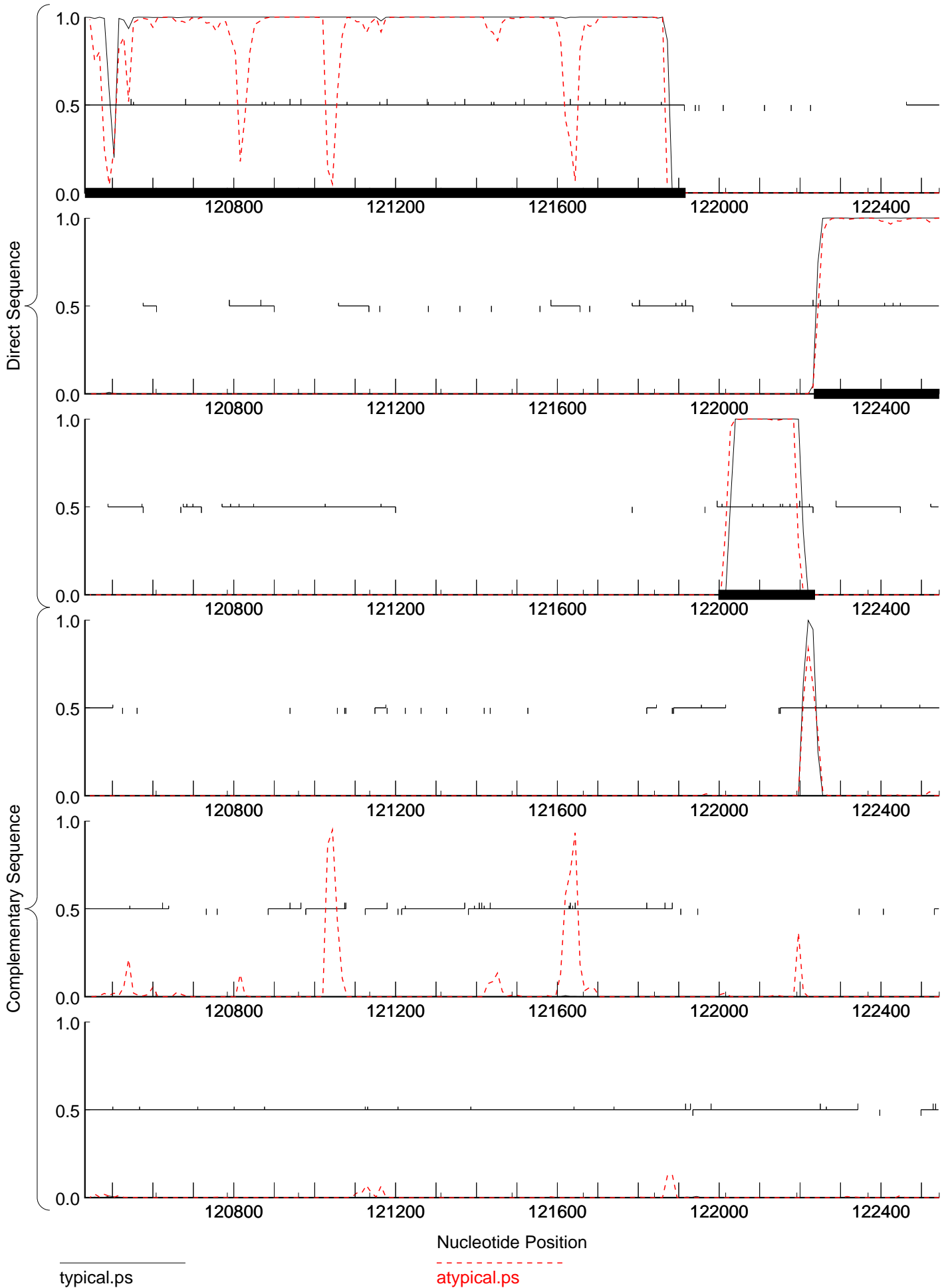


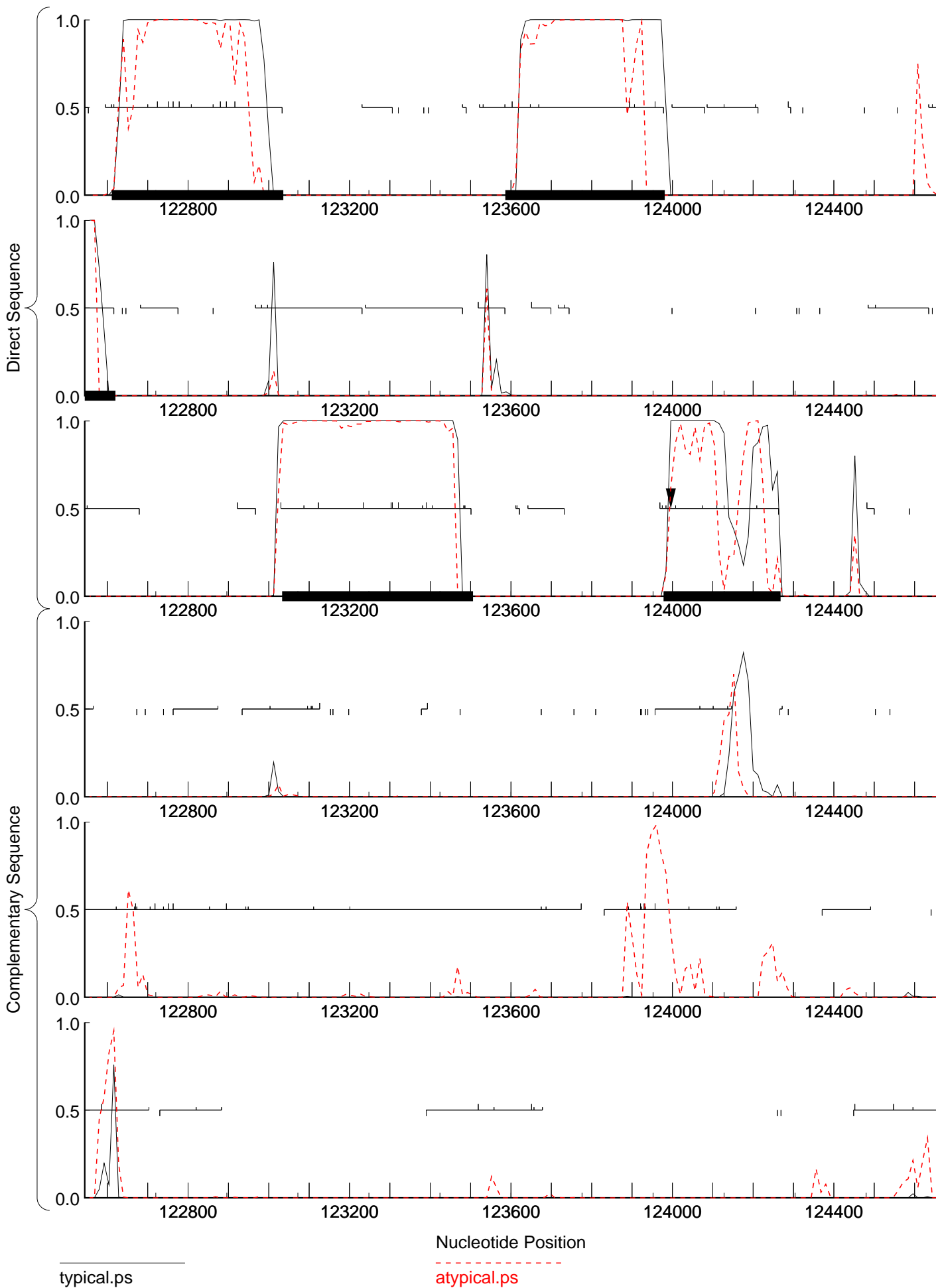




typical.ps

atypical.ps

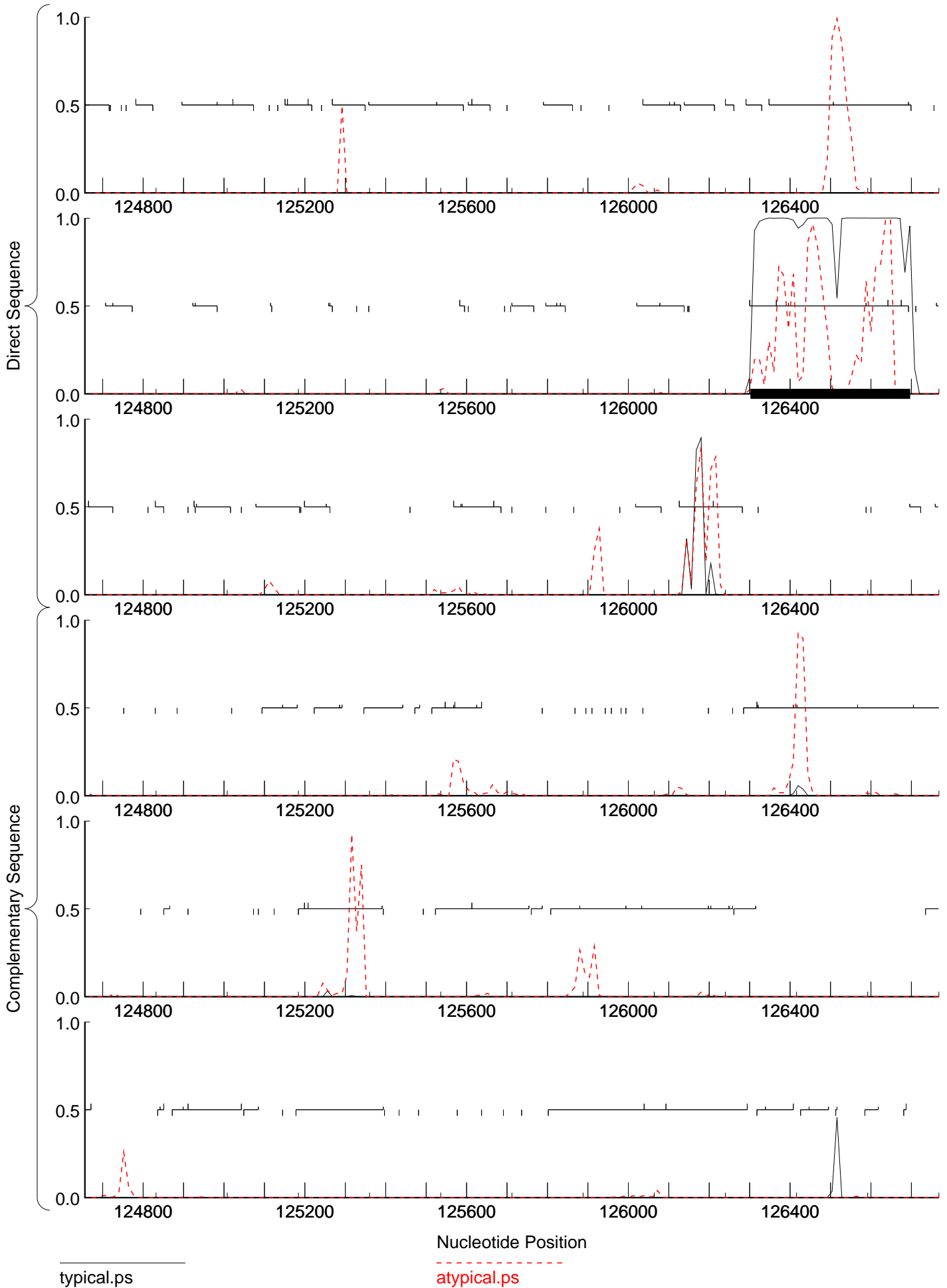




typical.ps

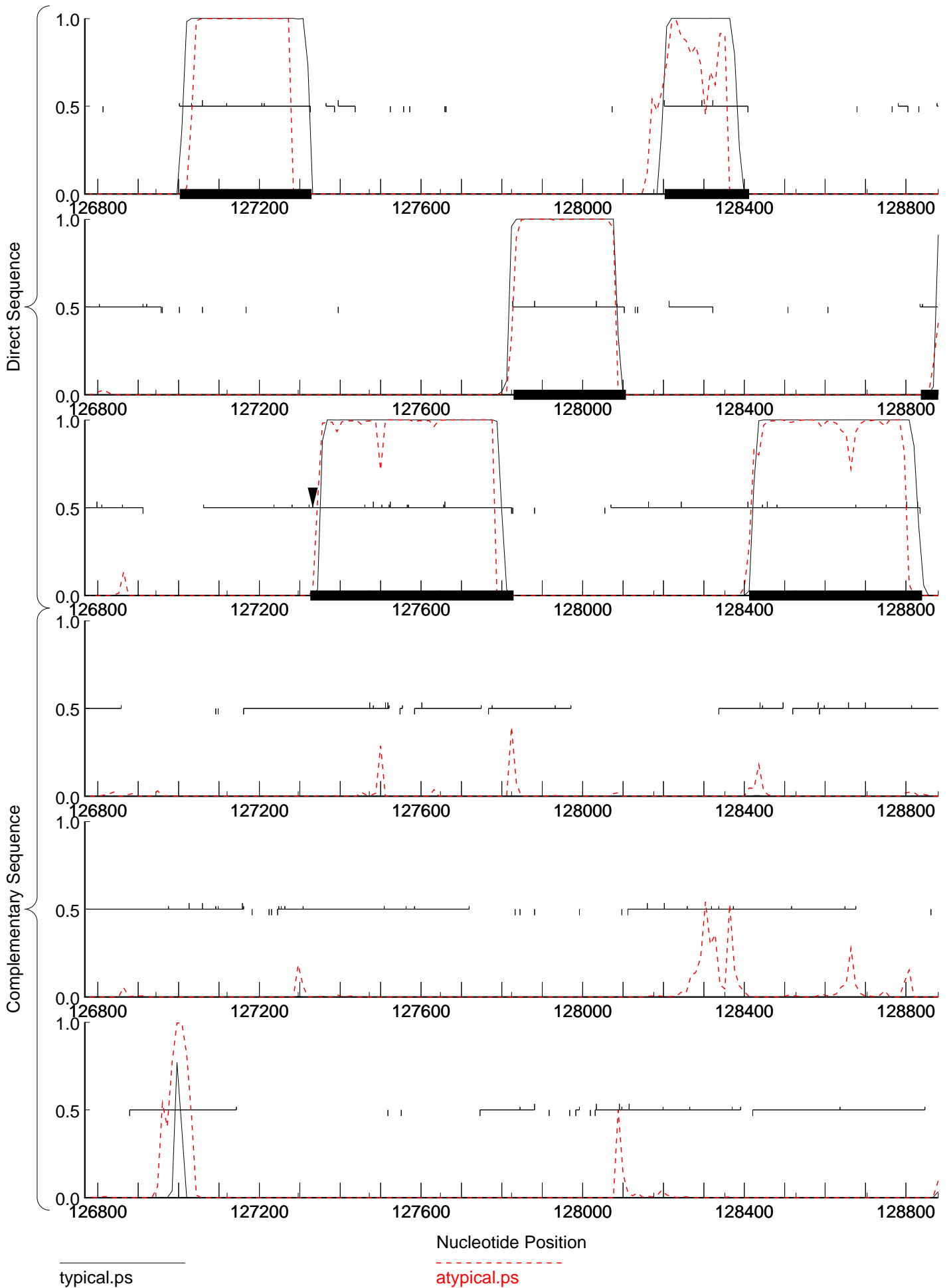
Nucleotide Position

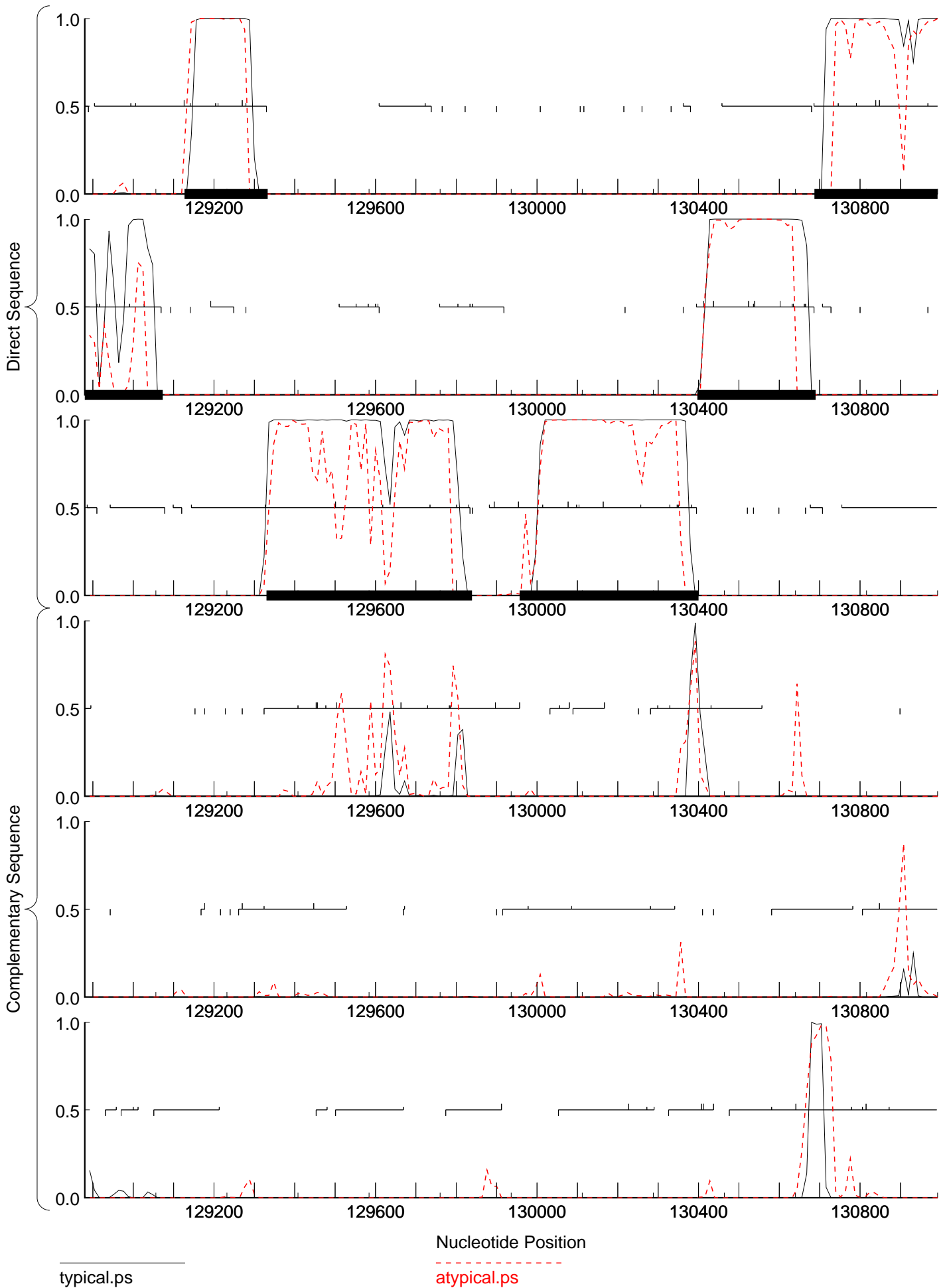
atypical.ps



typical.ps

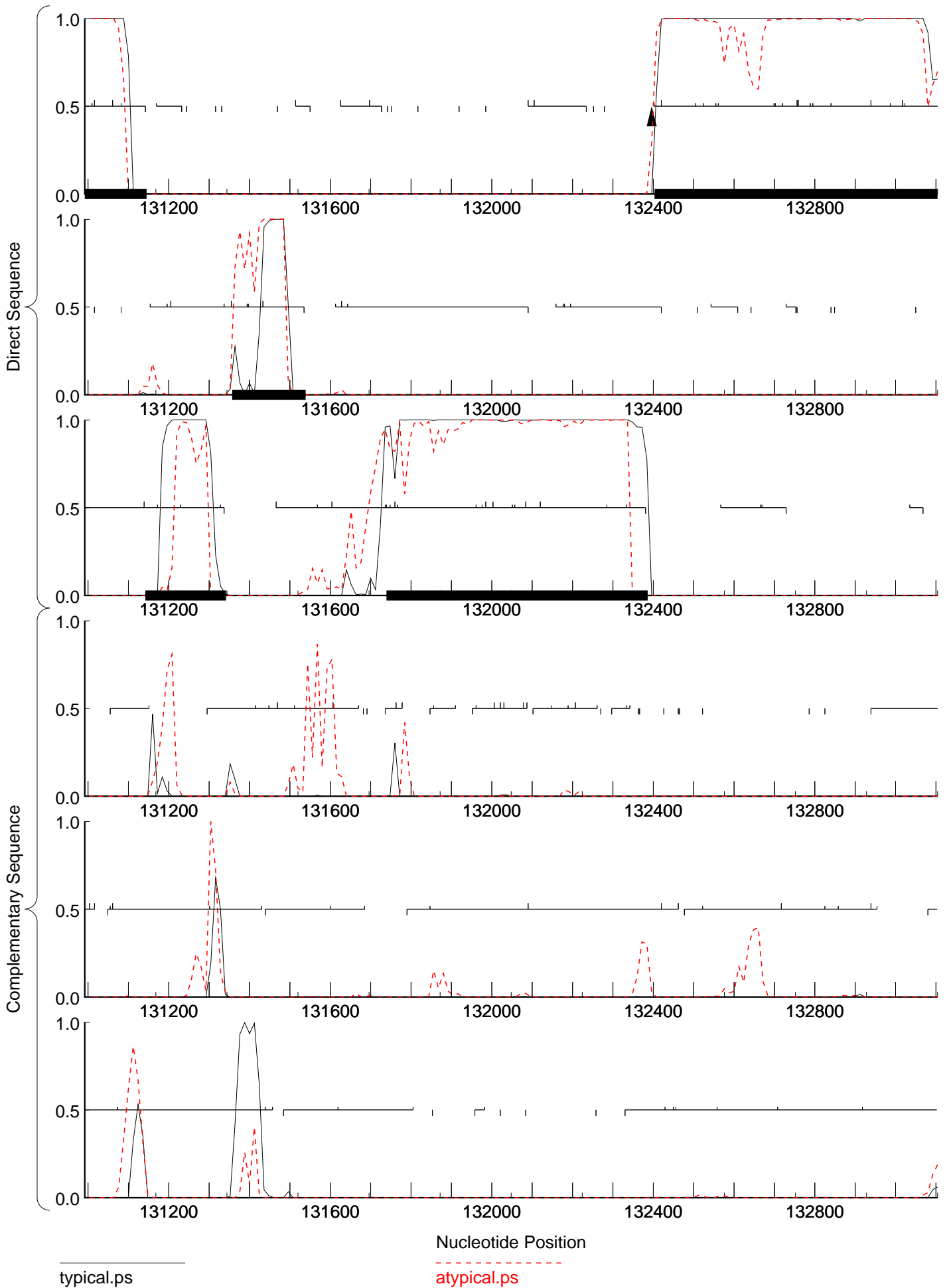
atypical.ps

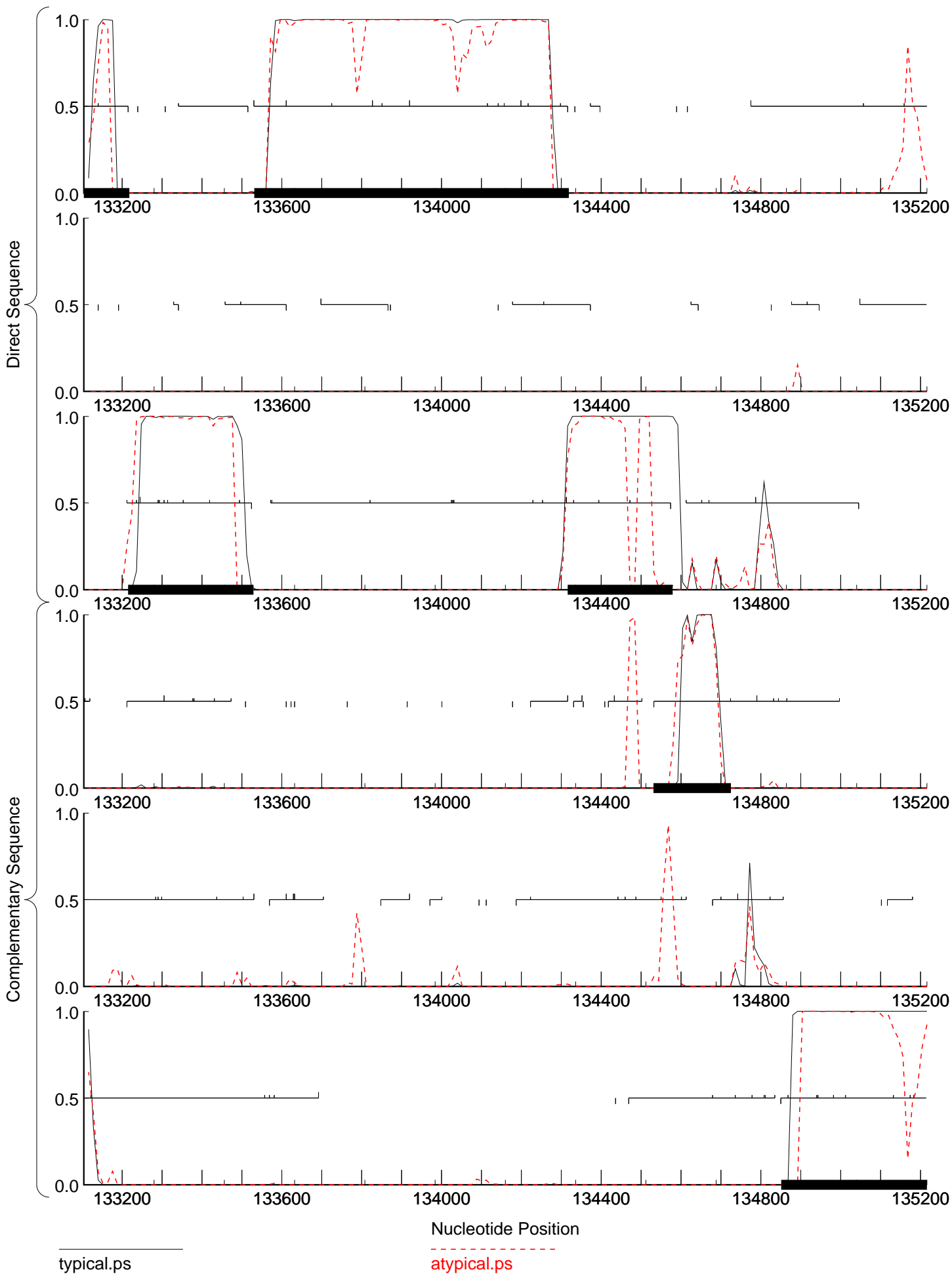


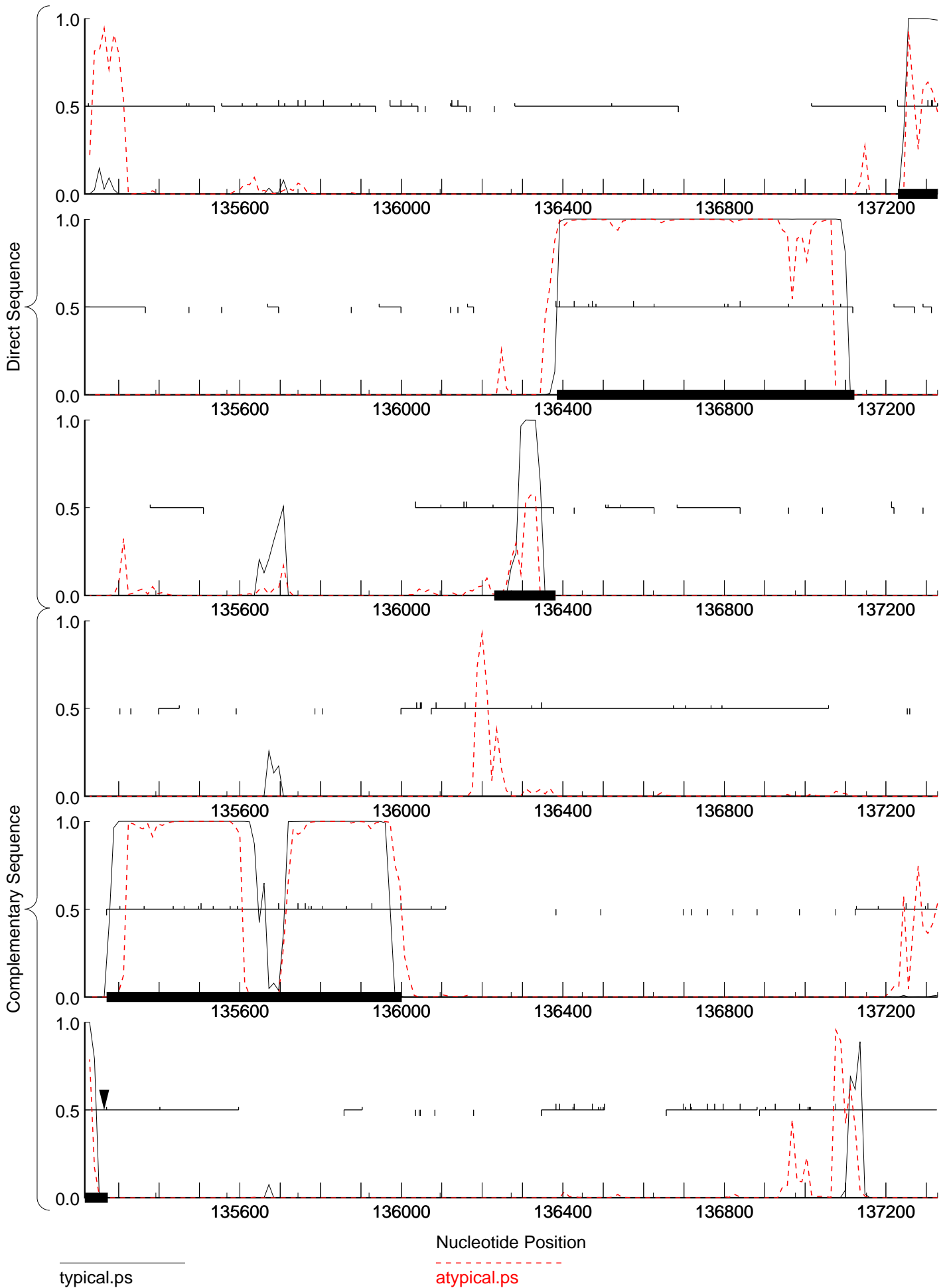


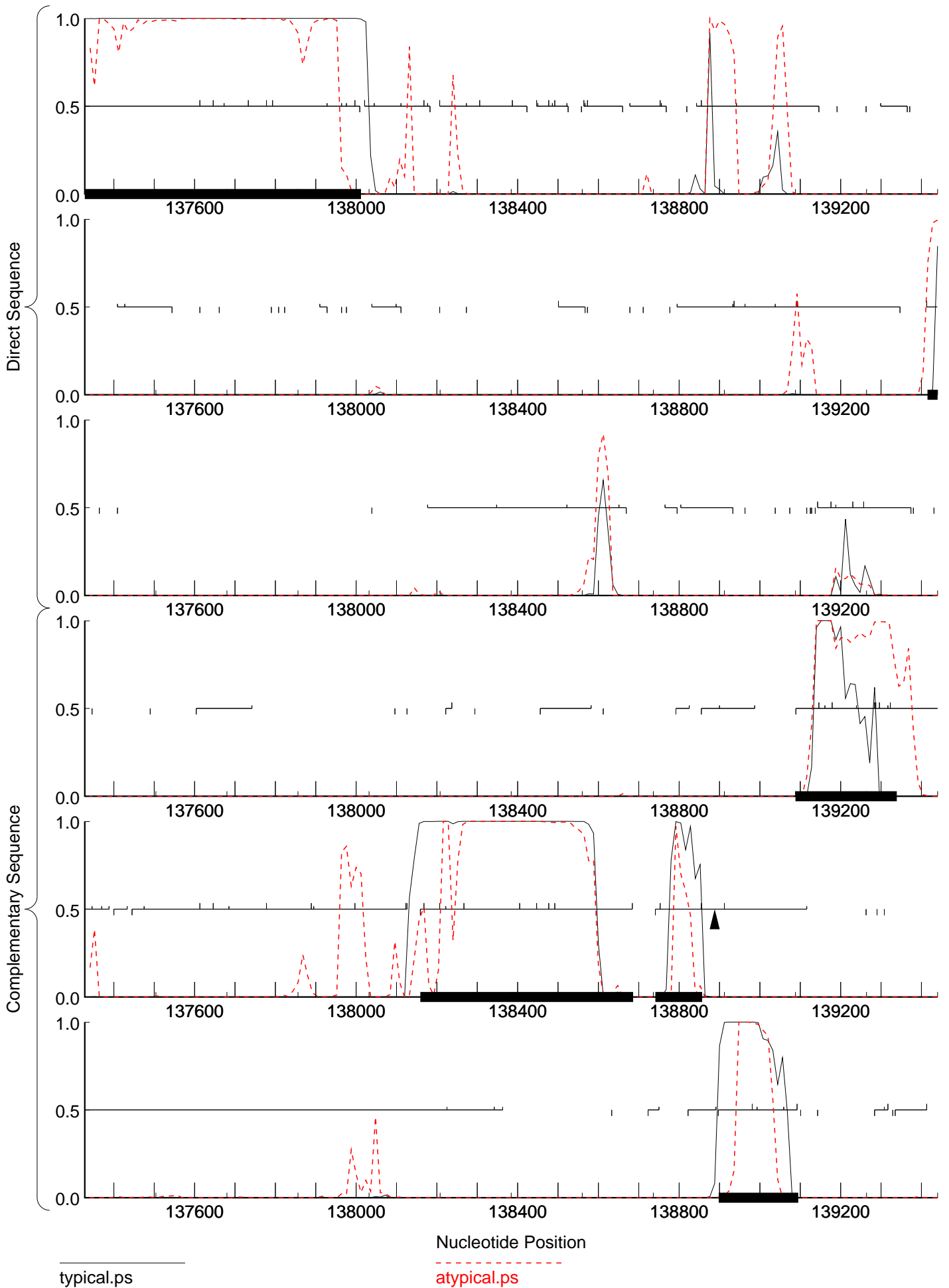
typical.ps

atypical.ps



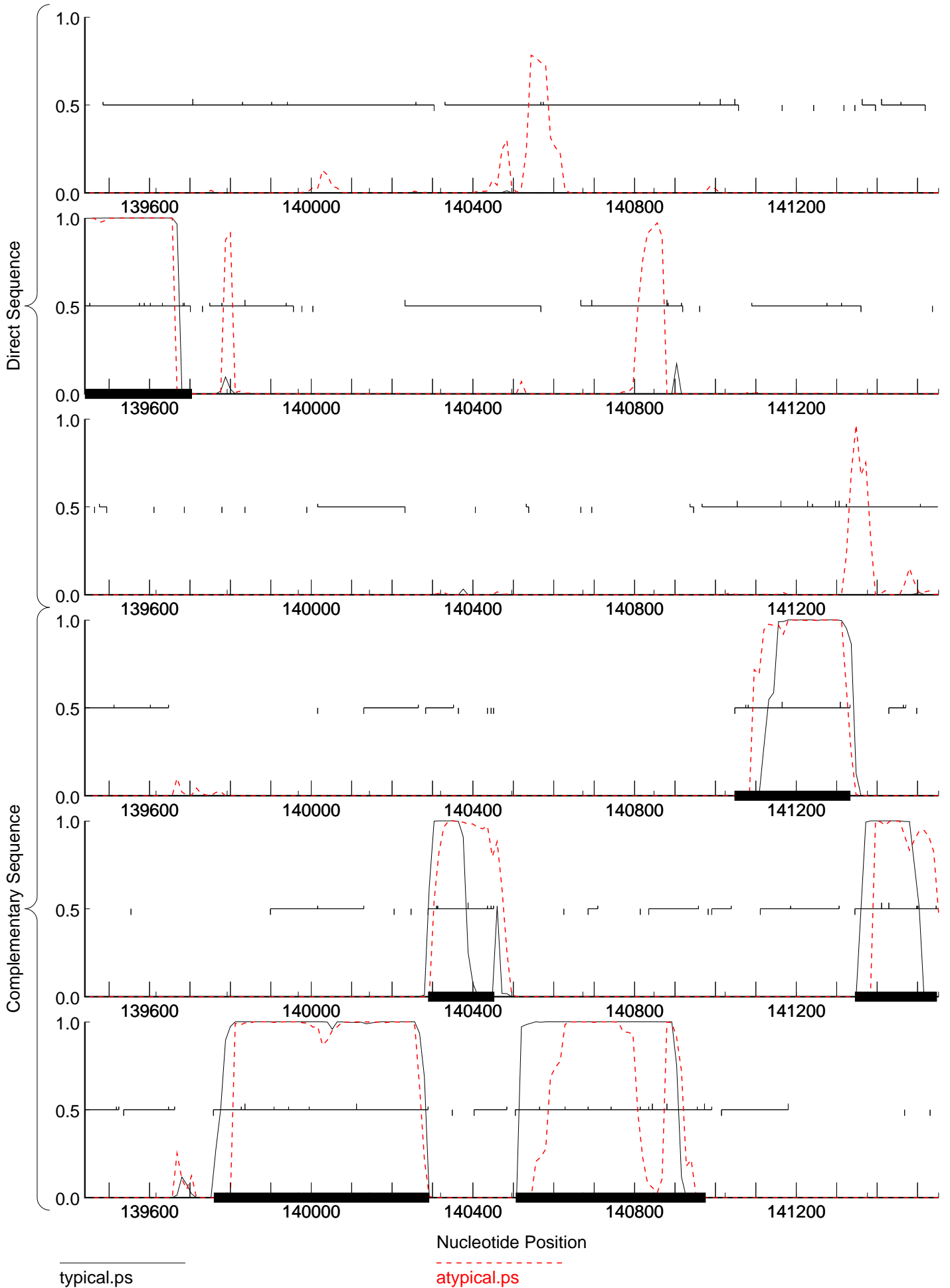


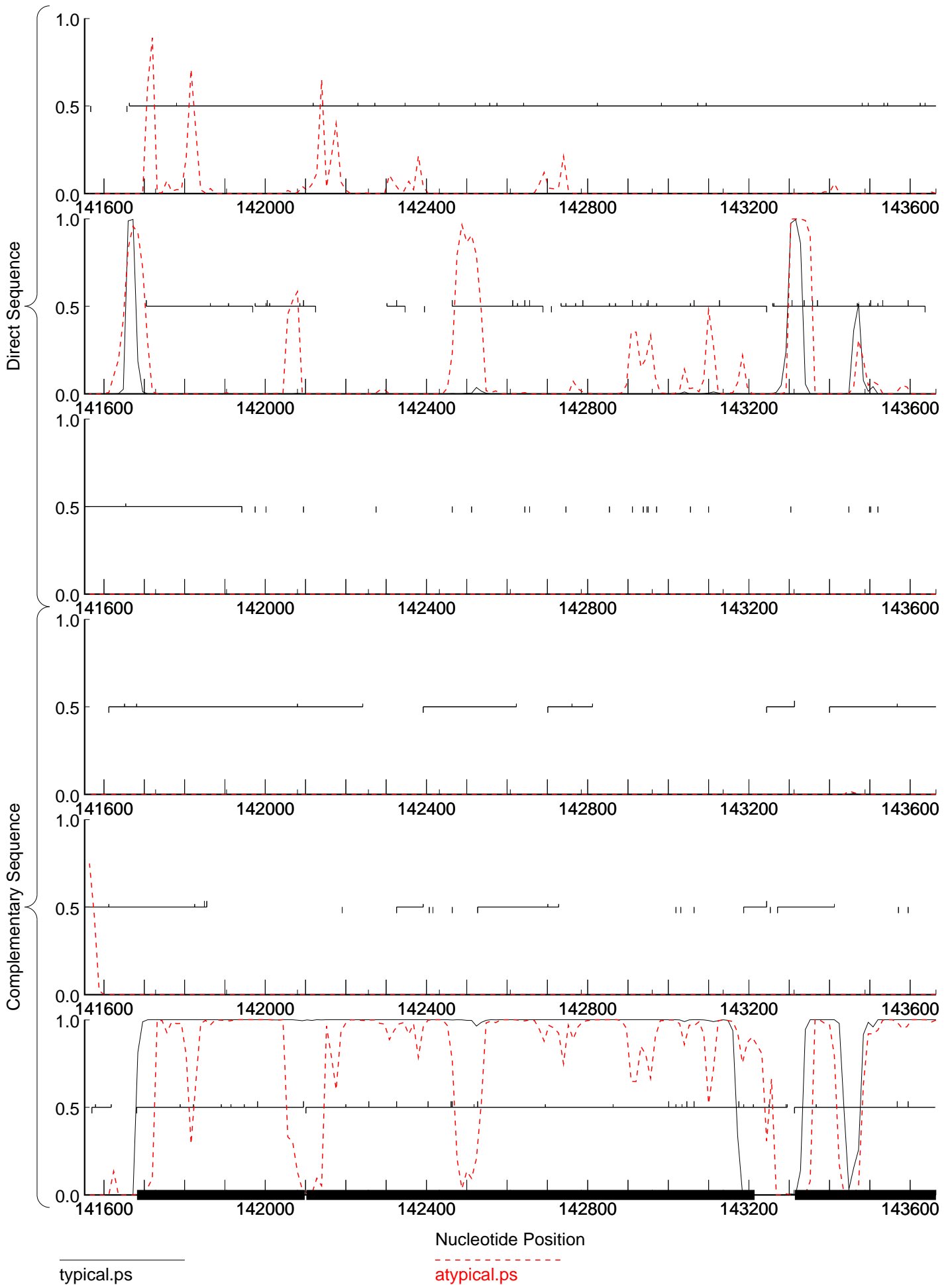


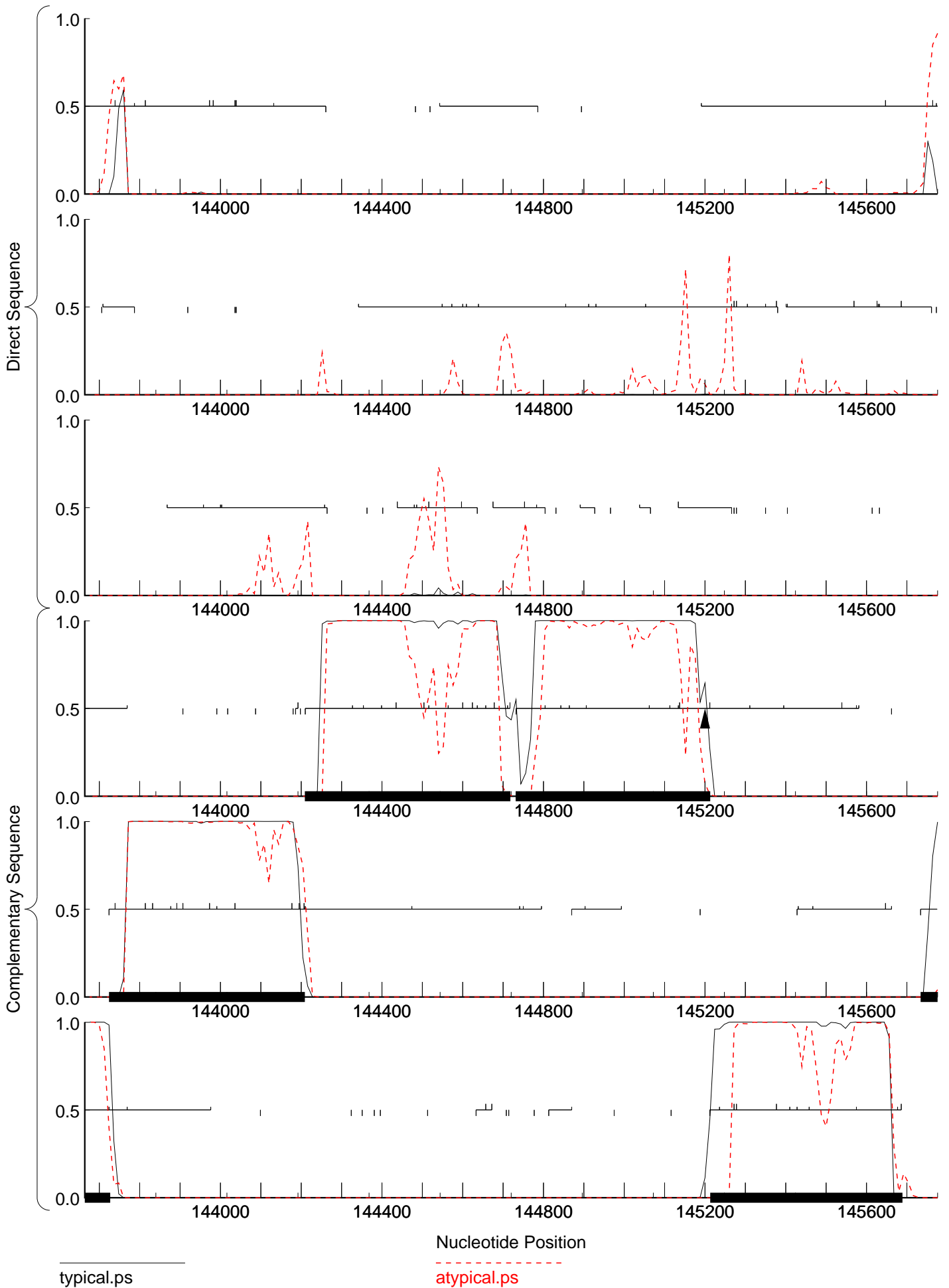


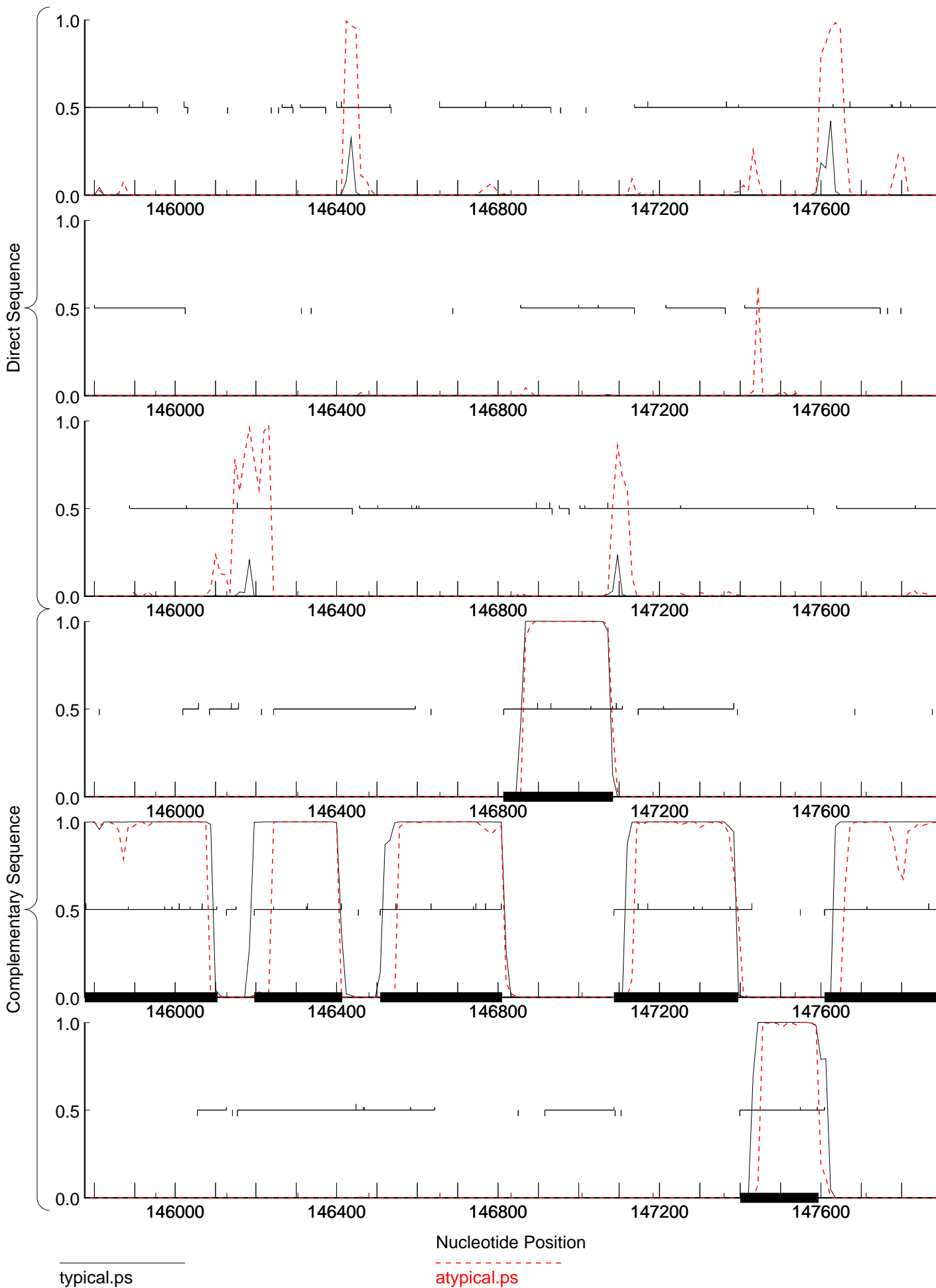
typical.ps

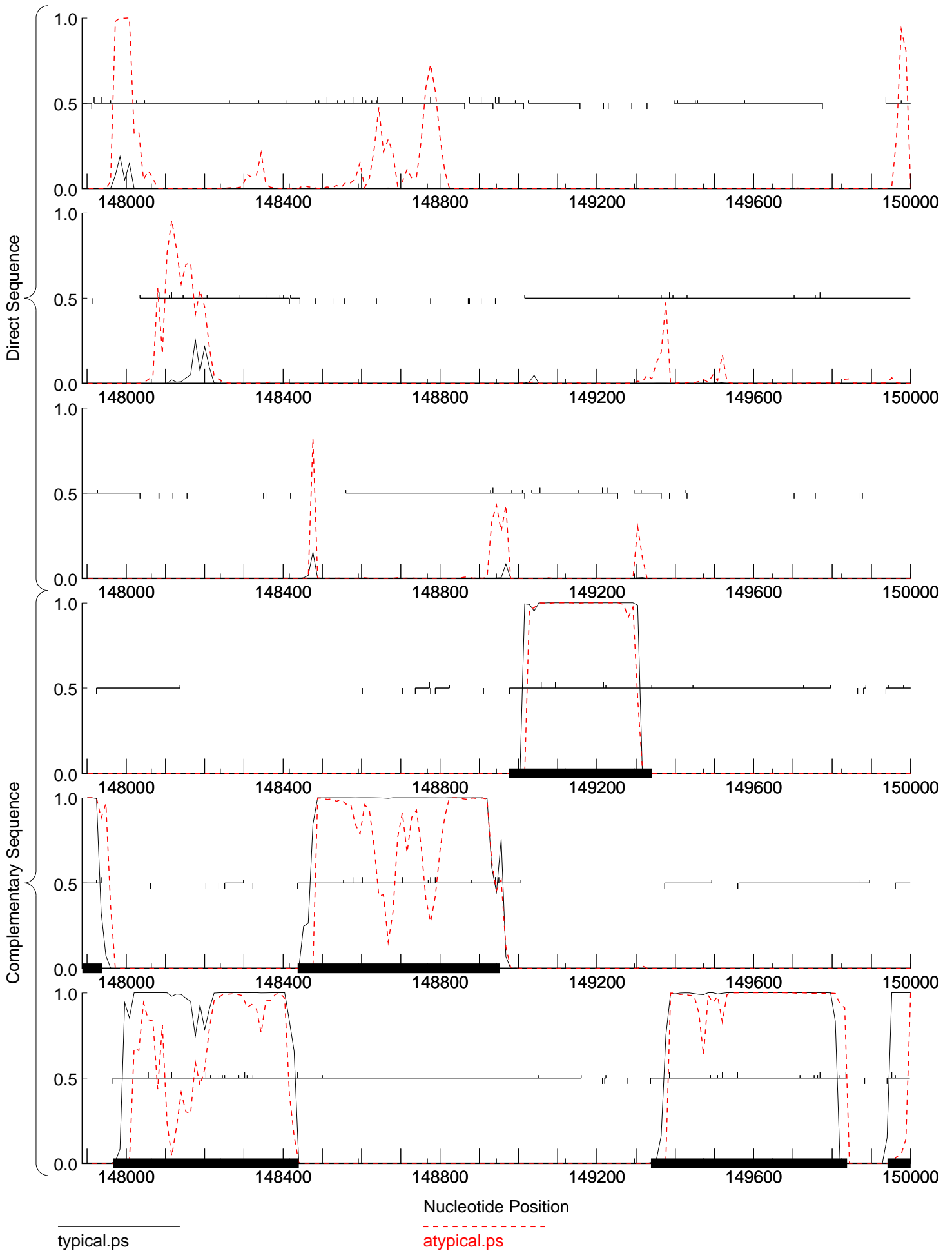
atypical.ps

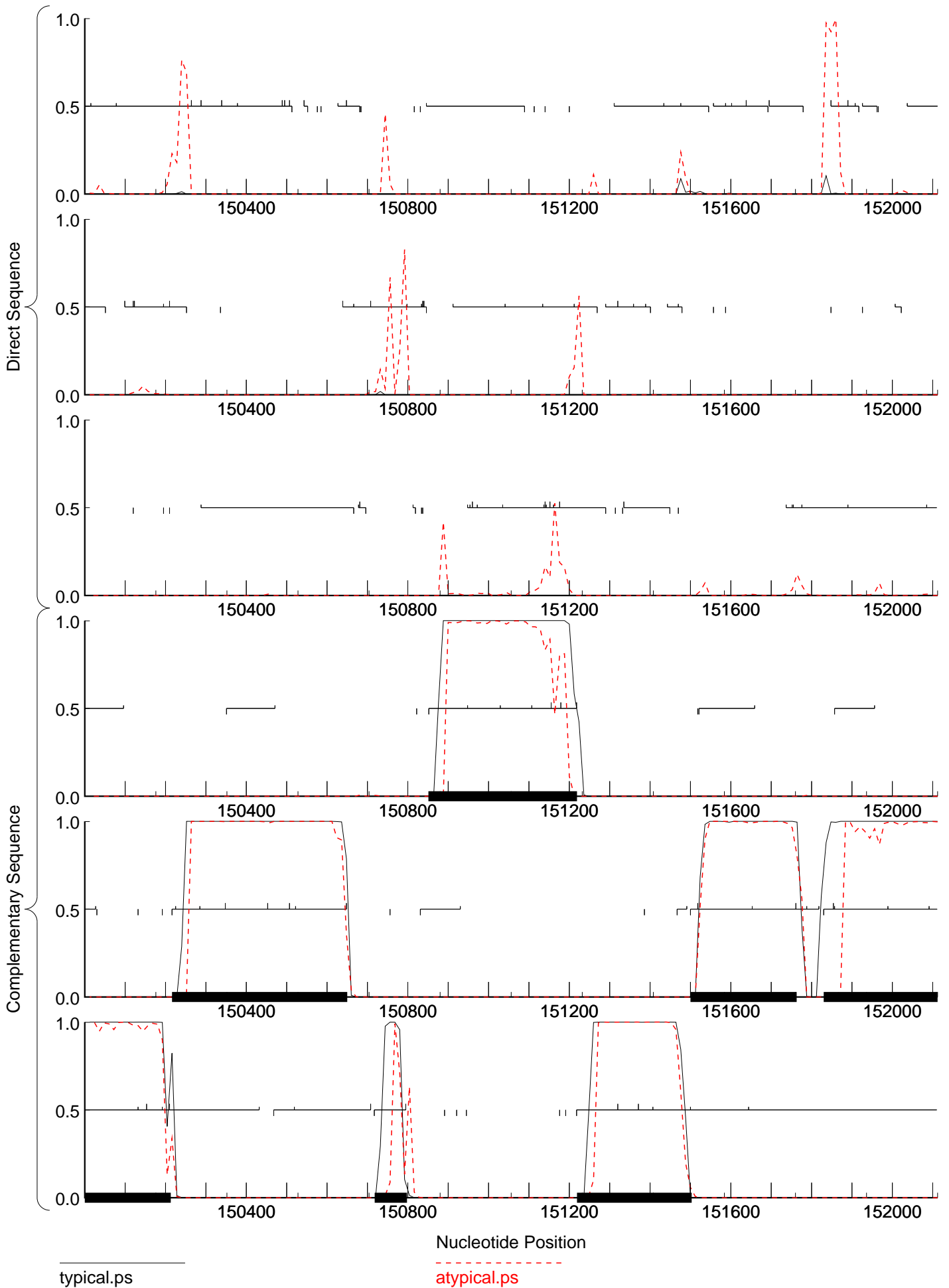


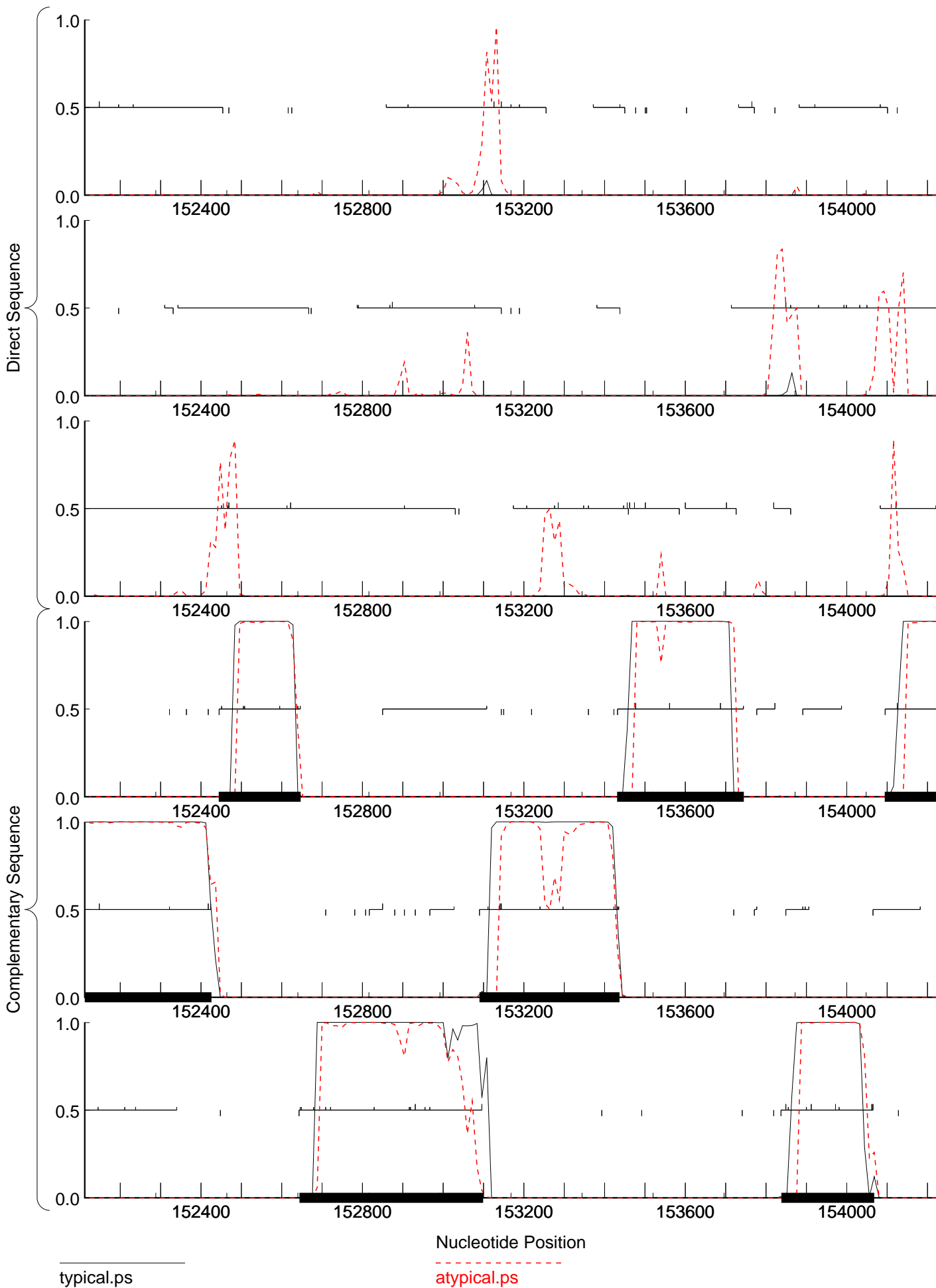






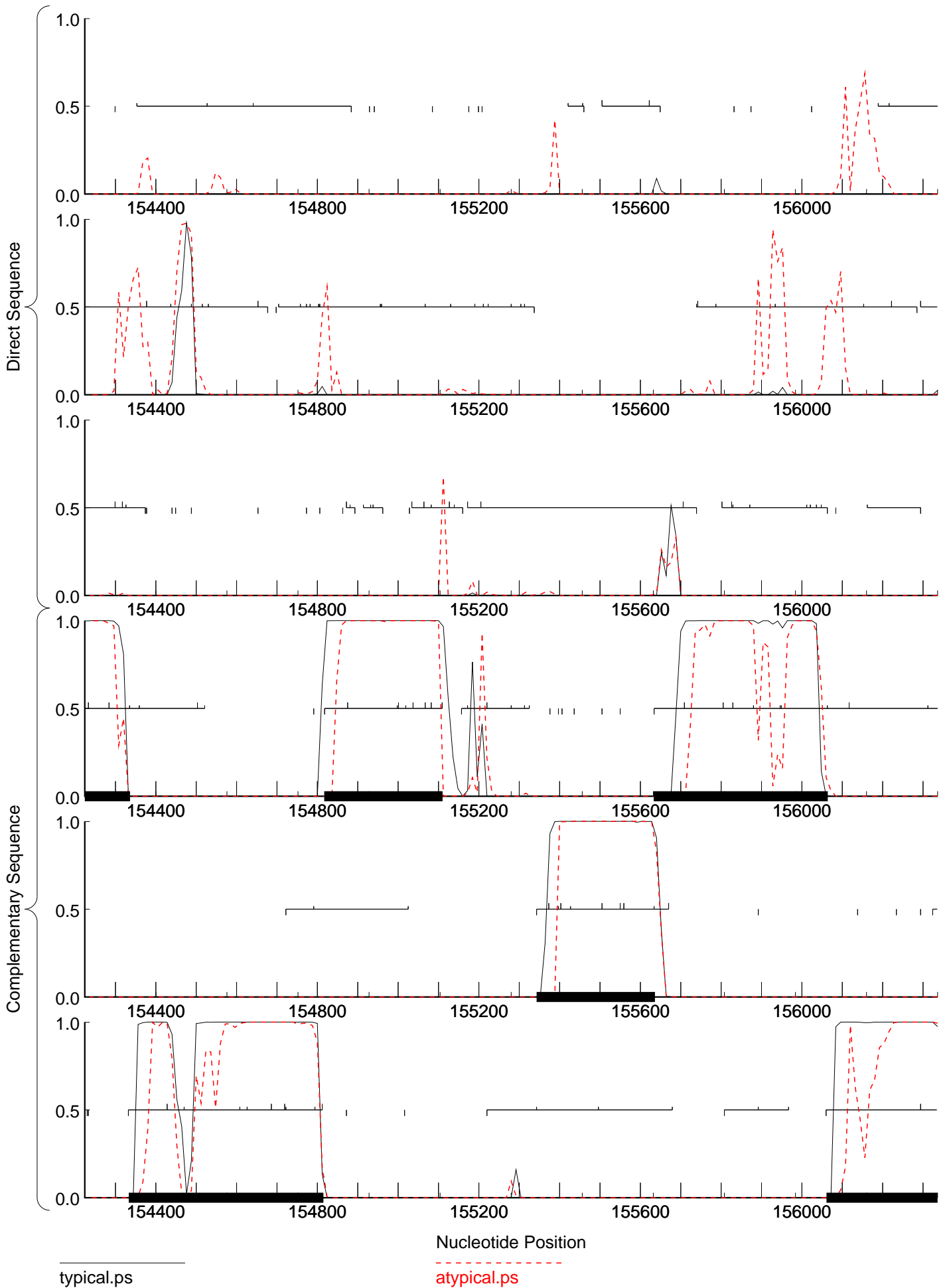


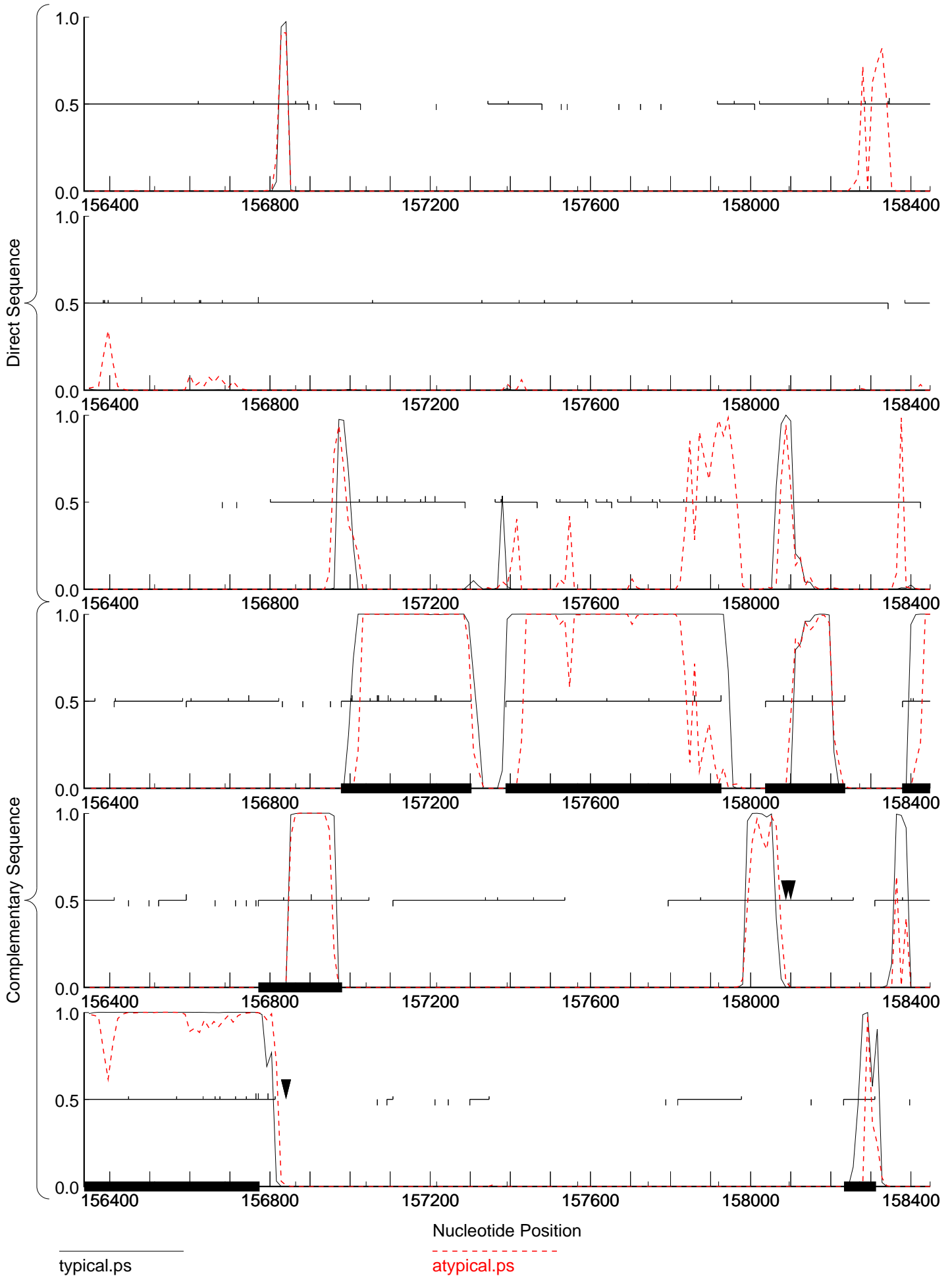


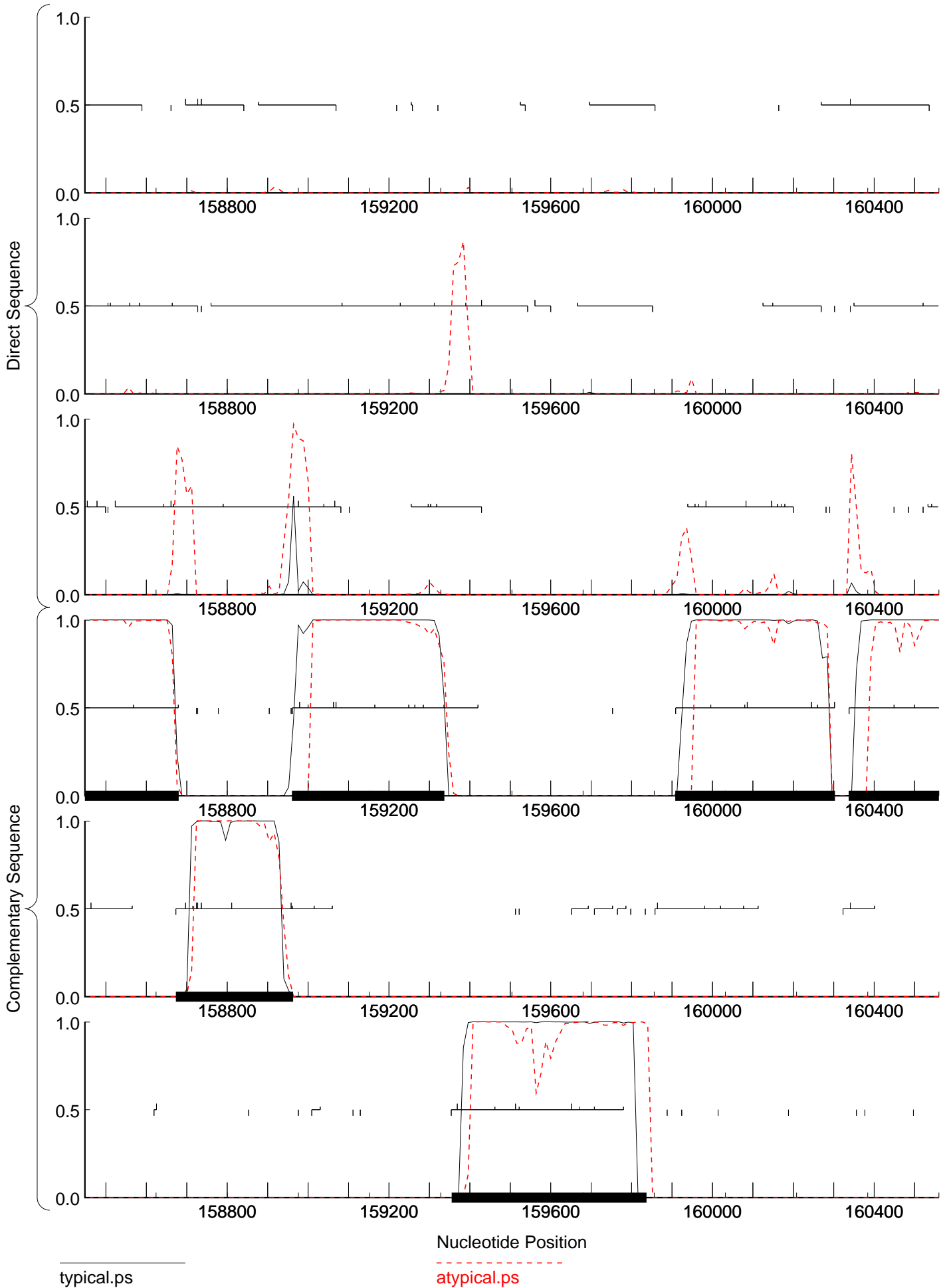


typical.ps

atypical.ps







typical.ps

atypical.ps

