

GeneMark

Version 2.5p (09.08.06)

Copyright 1993 - M. Borodovsky, J. McIninch

PROGRAM INFORMATION

Sequence : Gordonia phage Zirinka complete sequence, 52077 bp including 10-base 3' overhang (CGGCTGGGG
Analysis Date : 9/21/17 at 13:43:16
Pages : 26
Sequence Length : 52077 bp
GC Content : 66.67%

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,

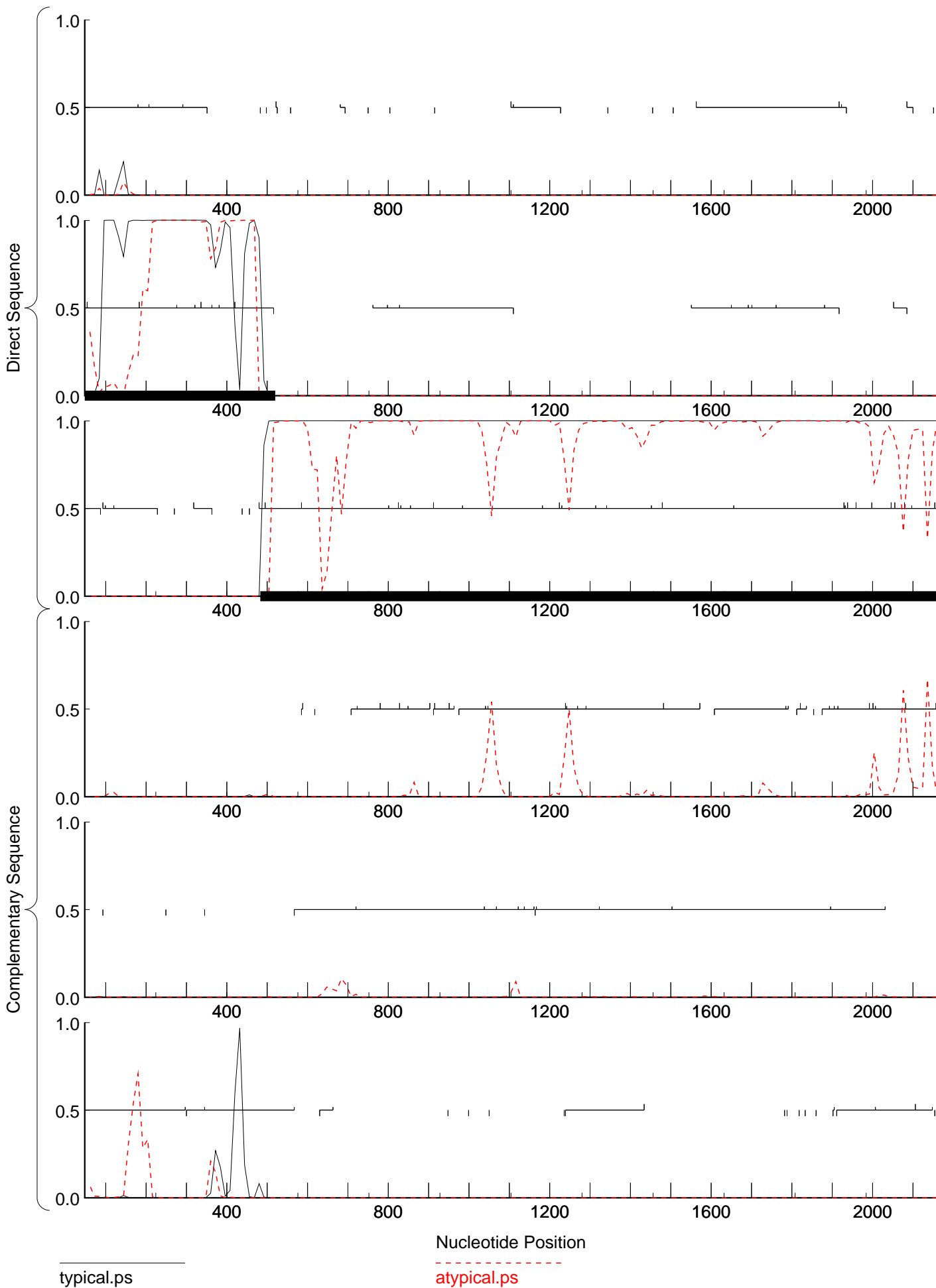
MATRIX INFORMATION

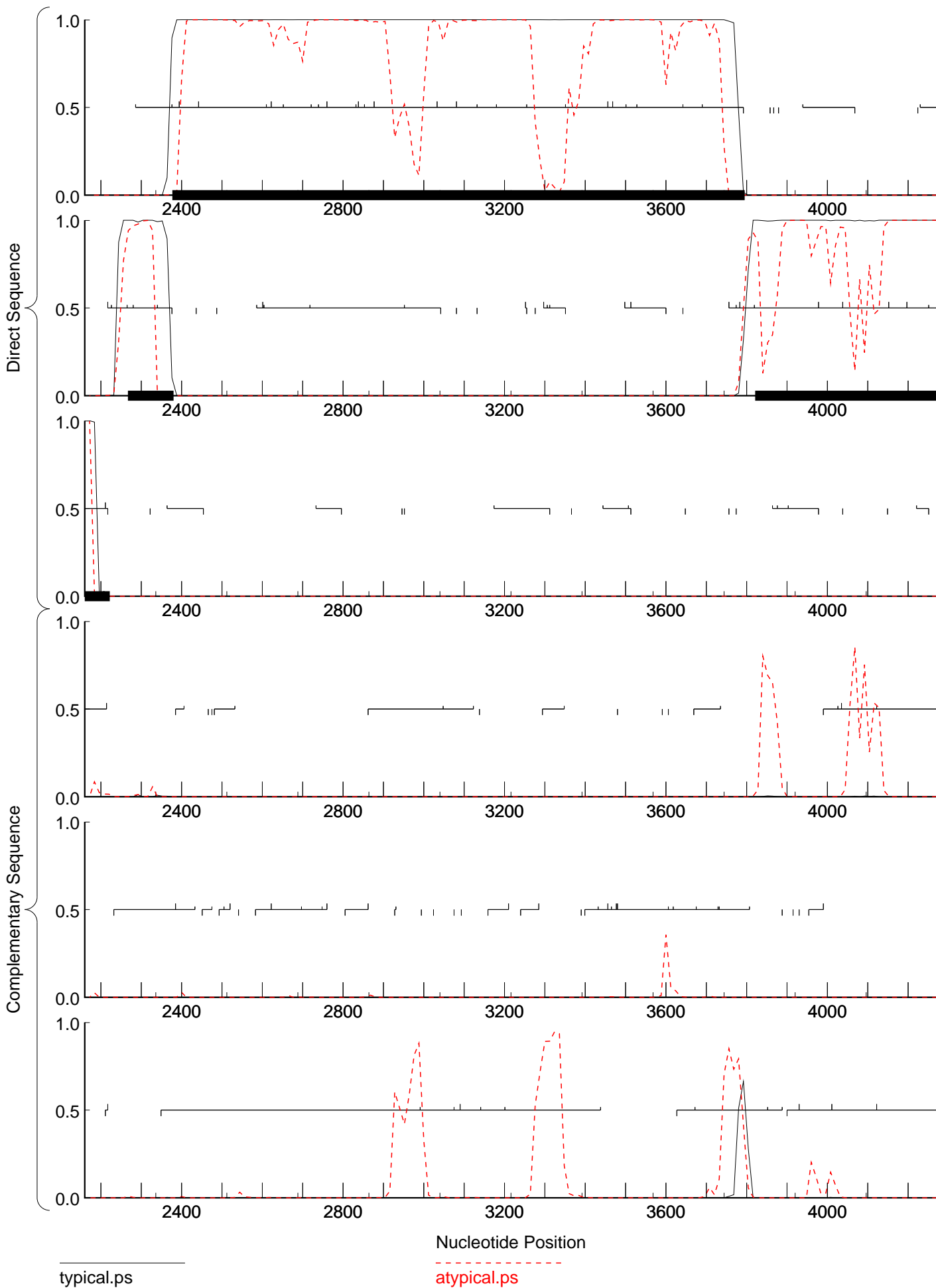
Matrix : -
Author : -
Order : 4

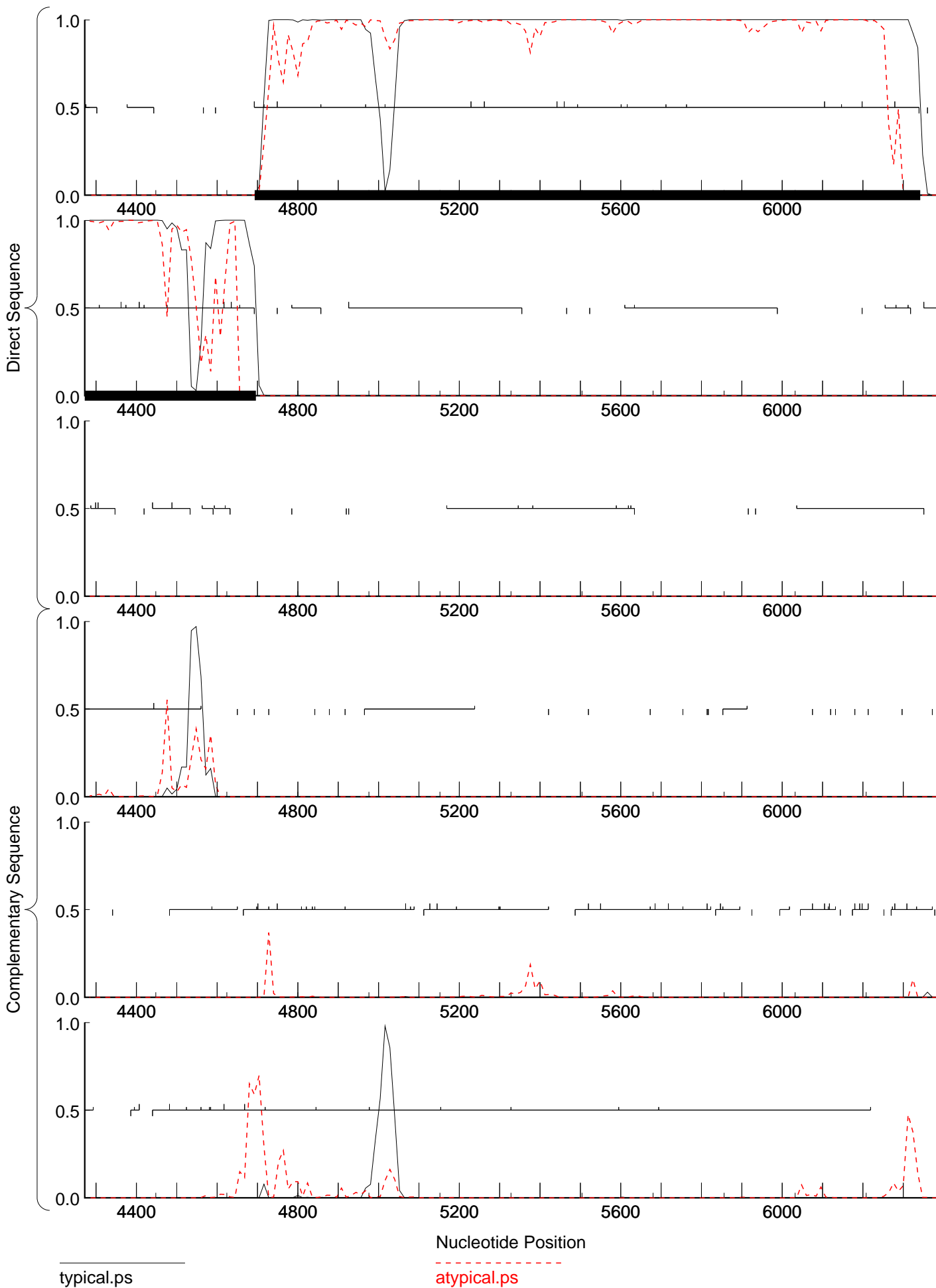
Send questions / comments to:
Dr. M. Borodovsky
Georgia Institute of Technology
School of Biology
Atlanta, GA 30332-0230

Matrix notes & comments

Training set derived by GeneMarkS, 4.30 October 2014
Thu Sep 21 13:43:16 2017

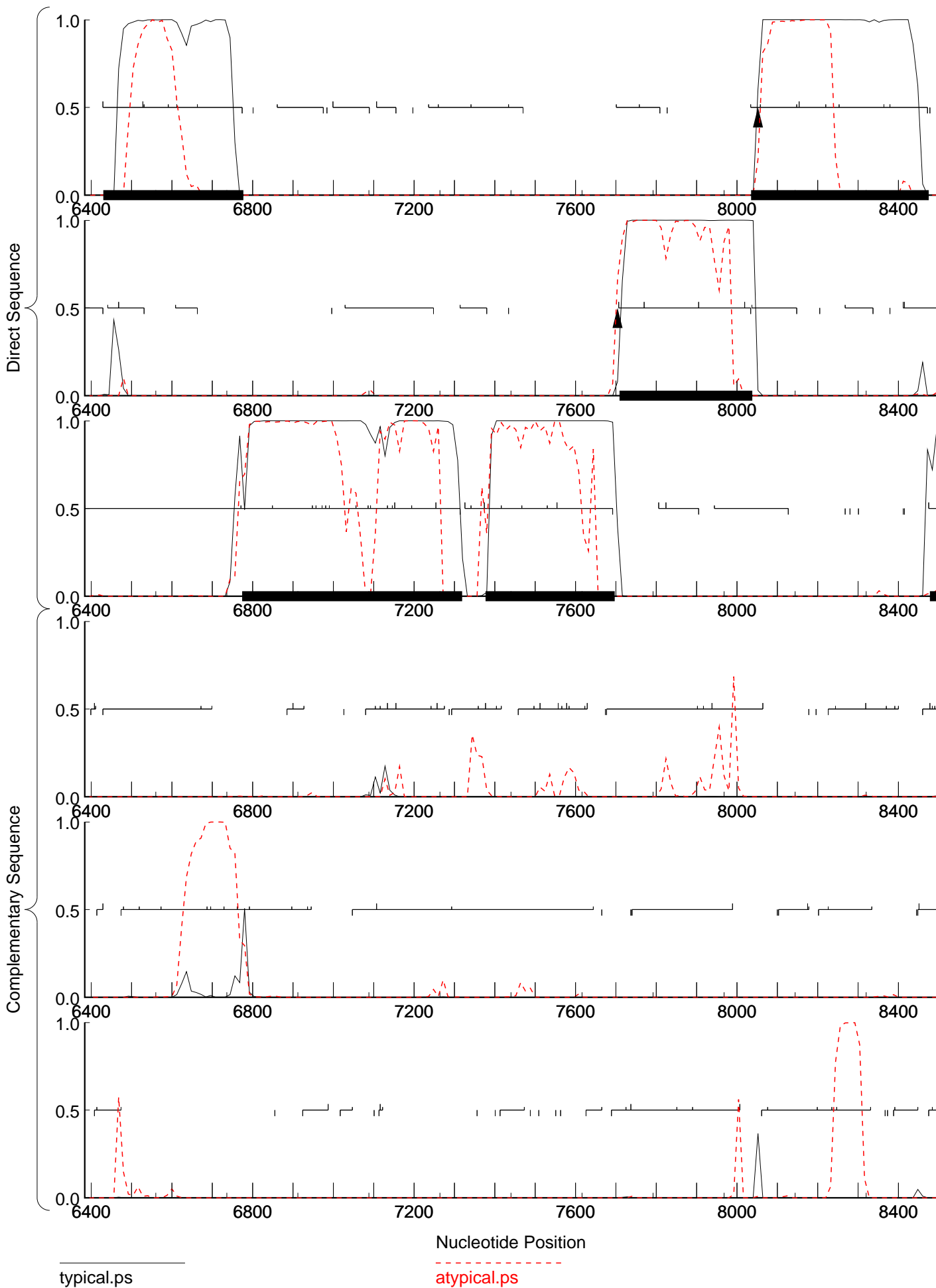




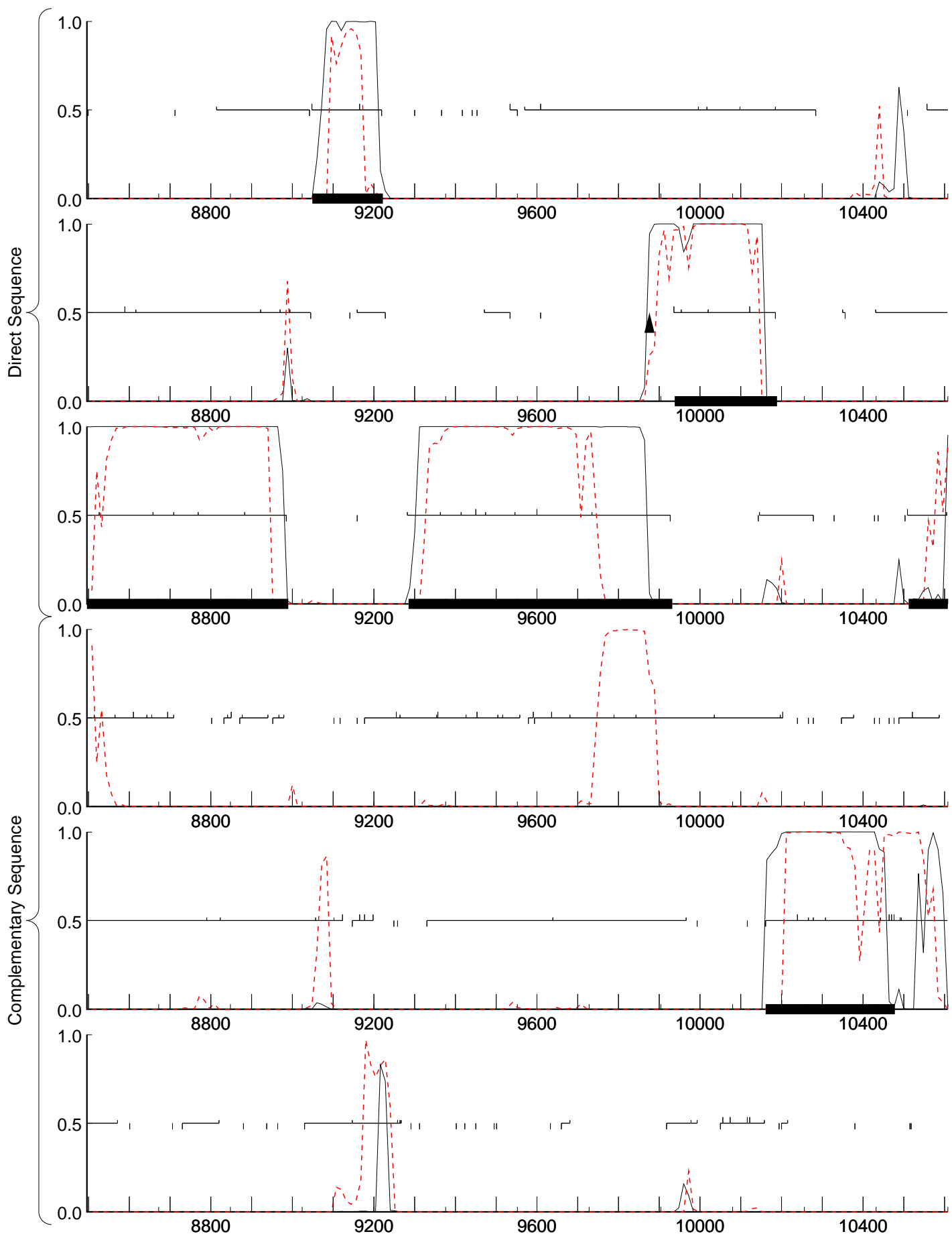


typical.ps

atypical.ps

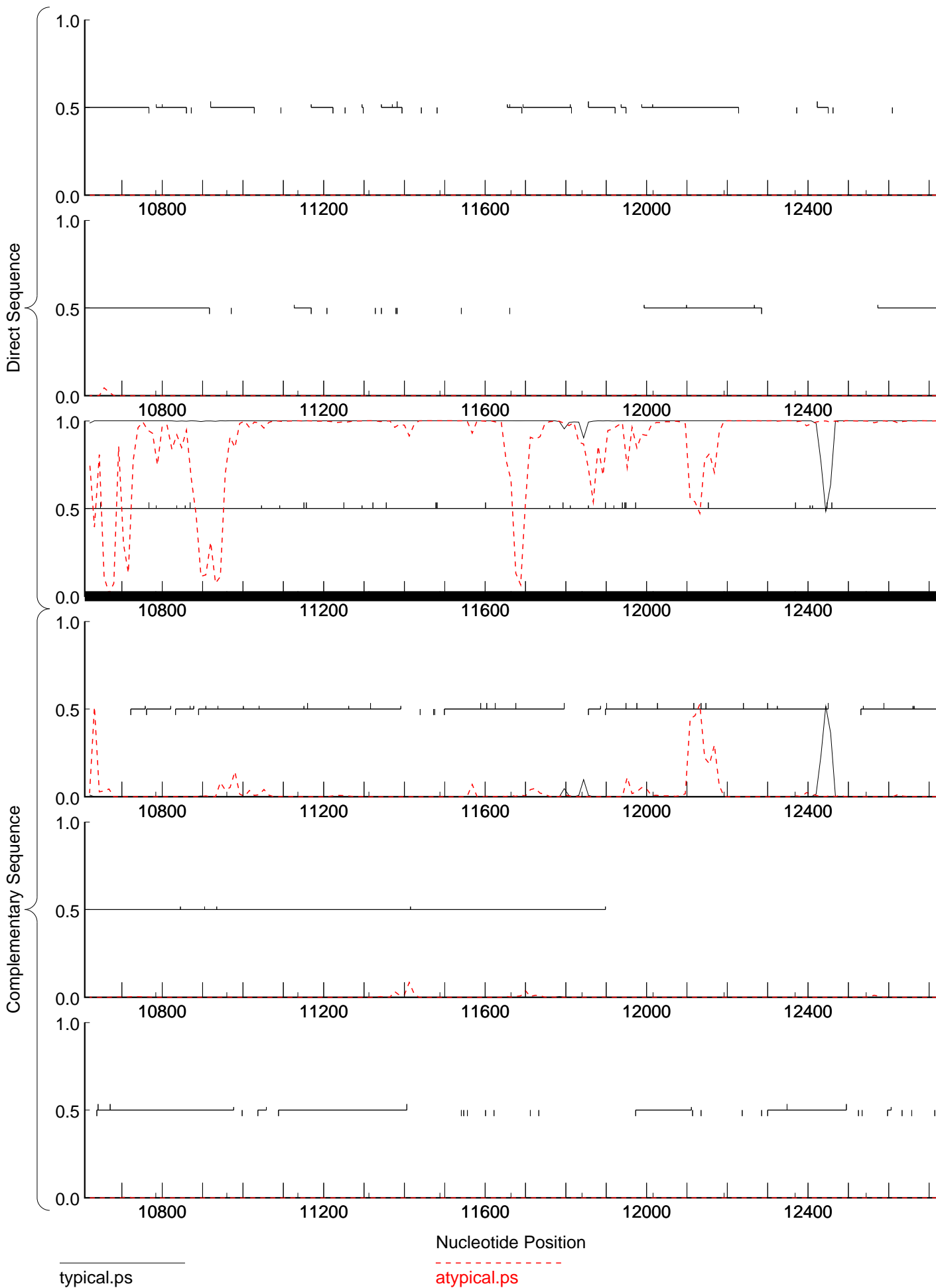


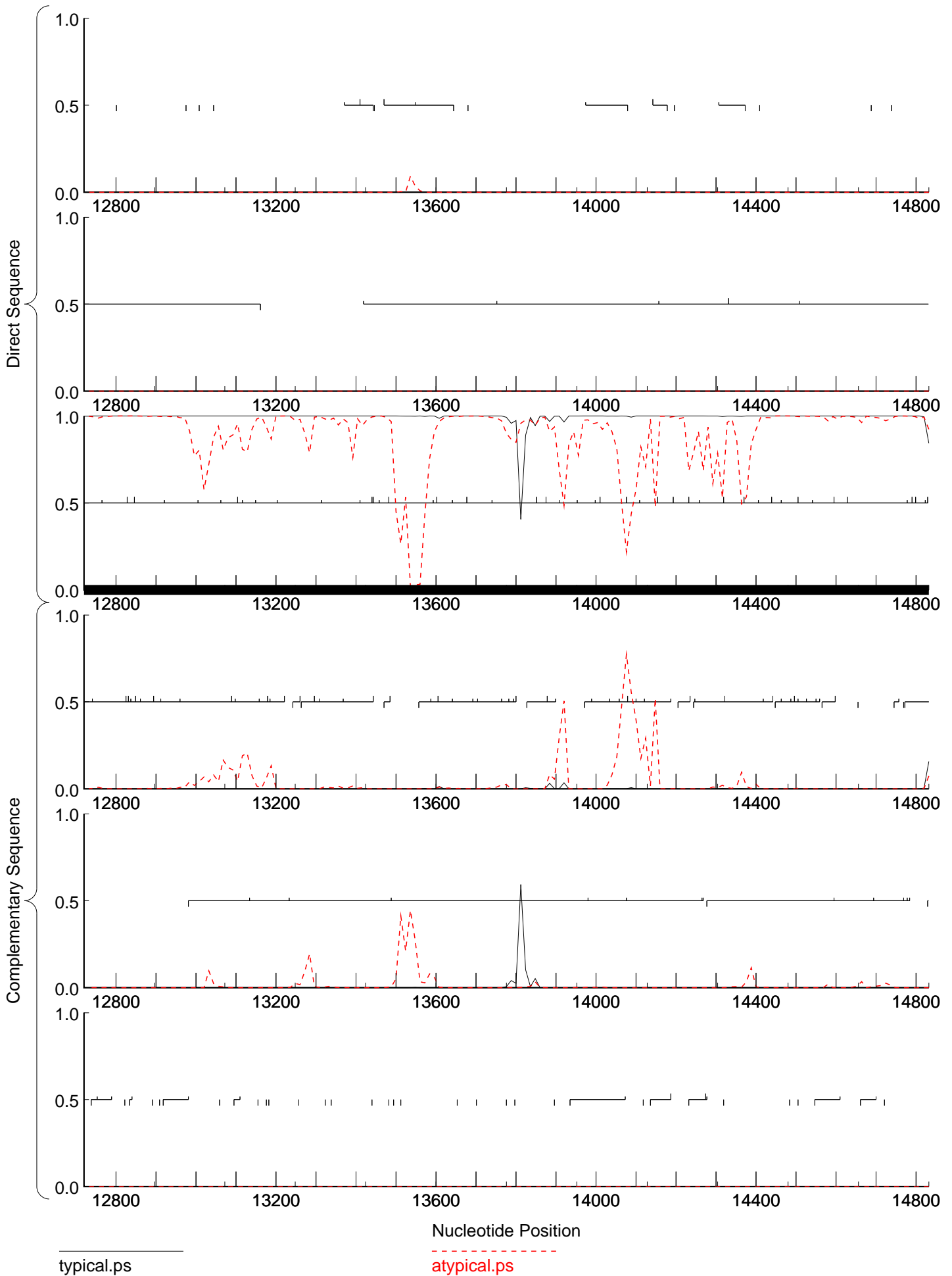
GeneMark.hmm prediction

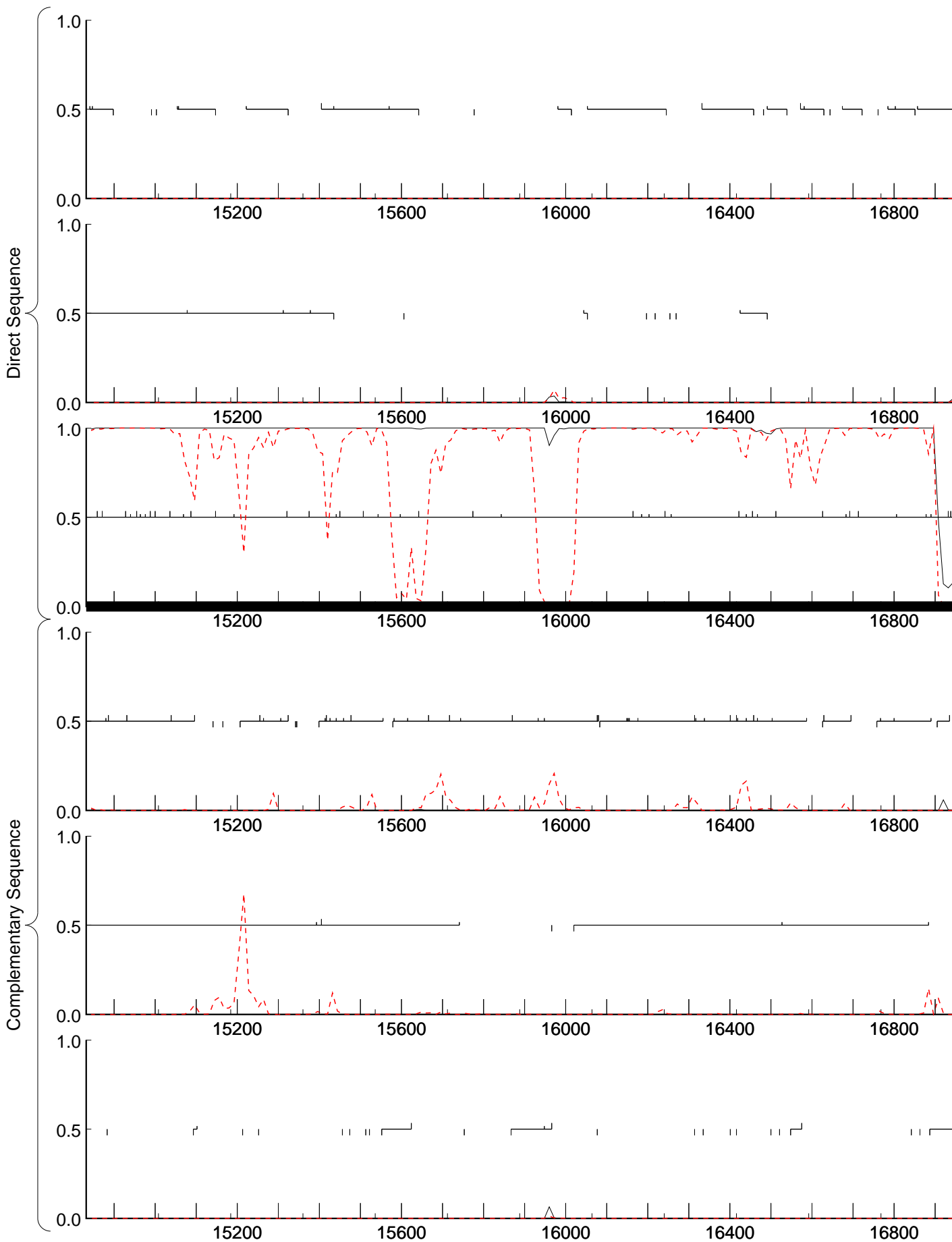


typical.ps

atypical.ps

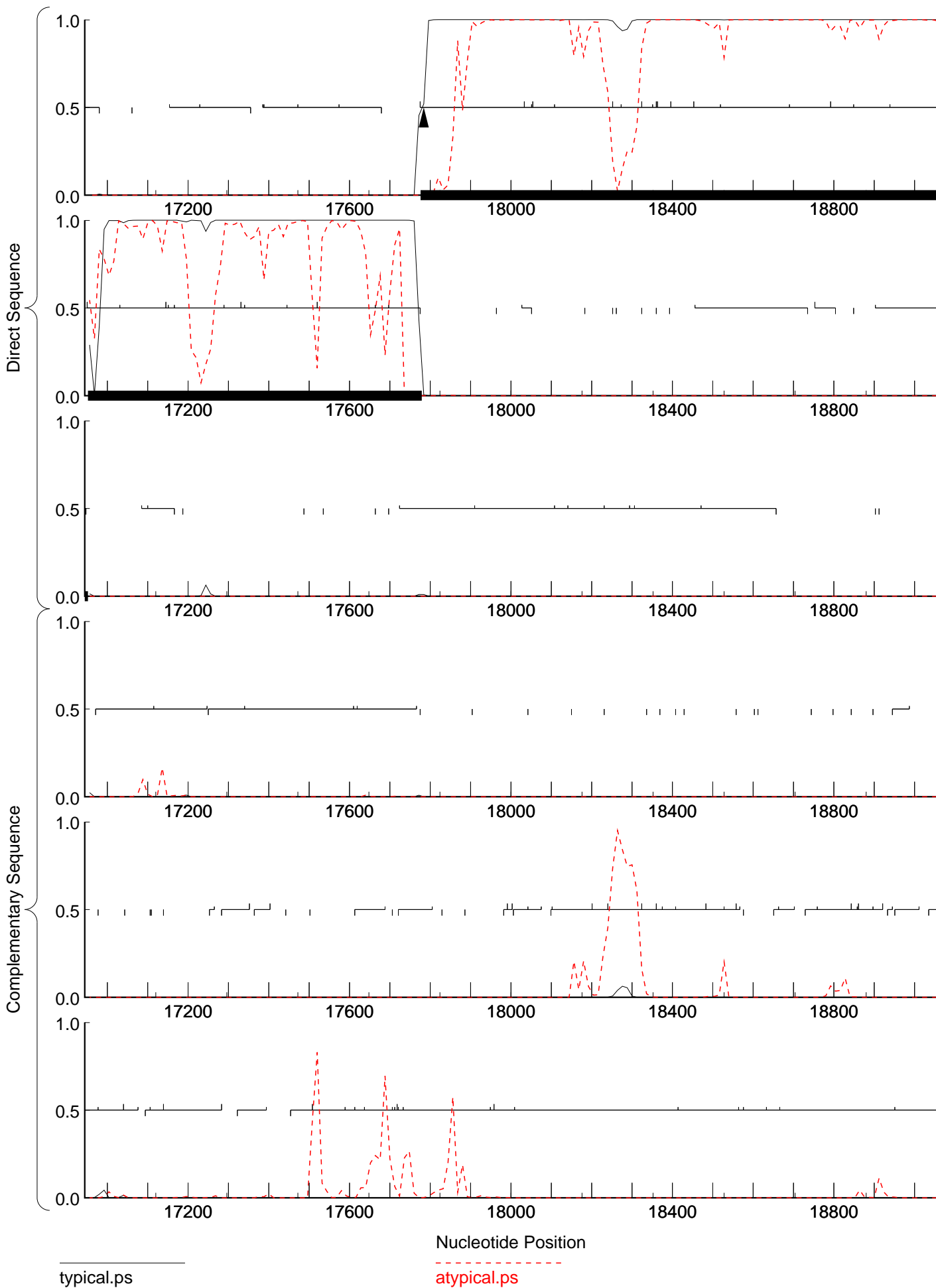


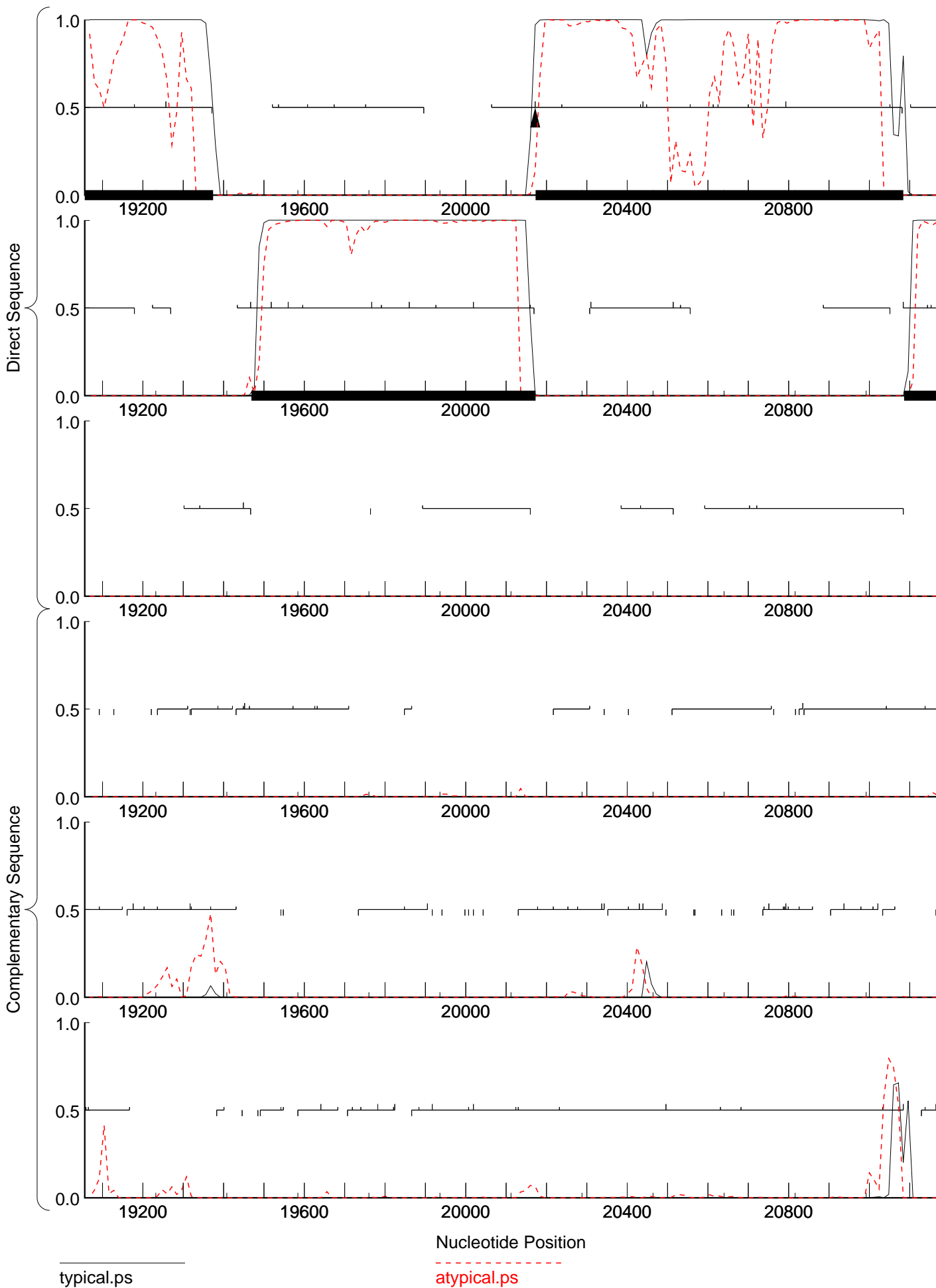


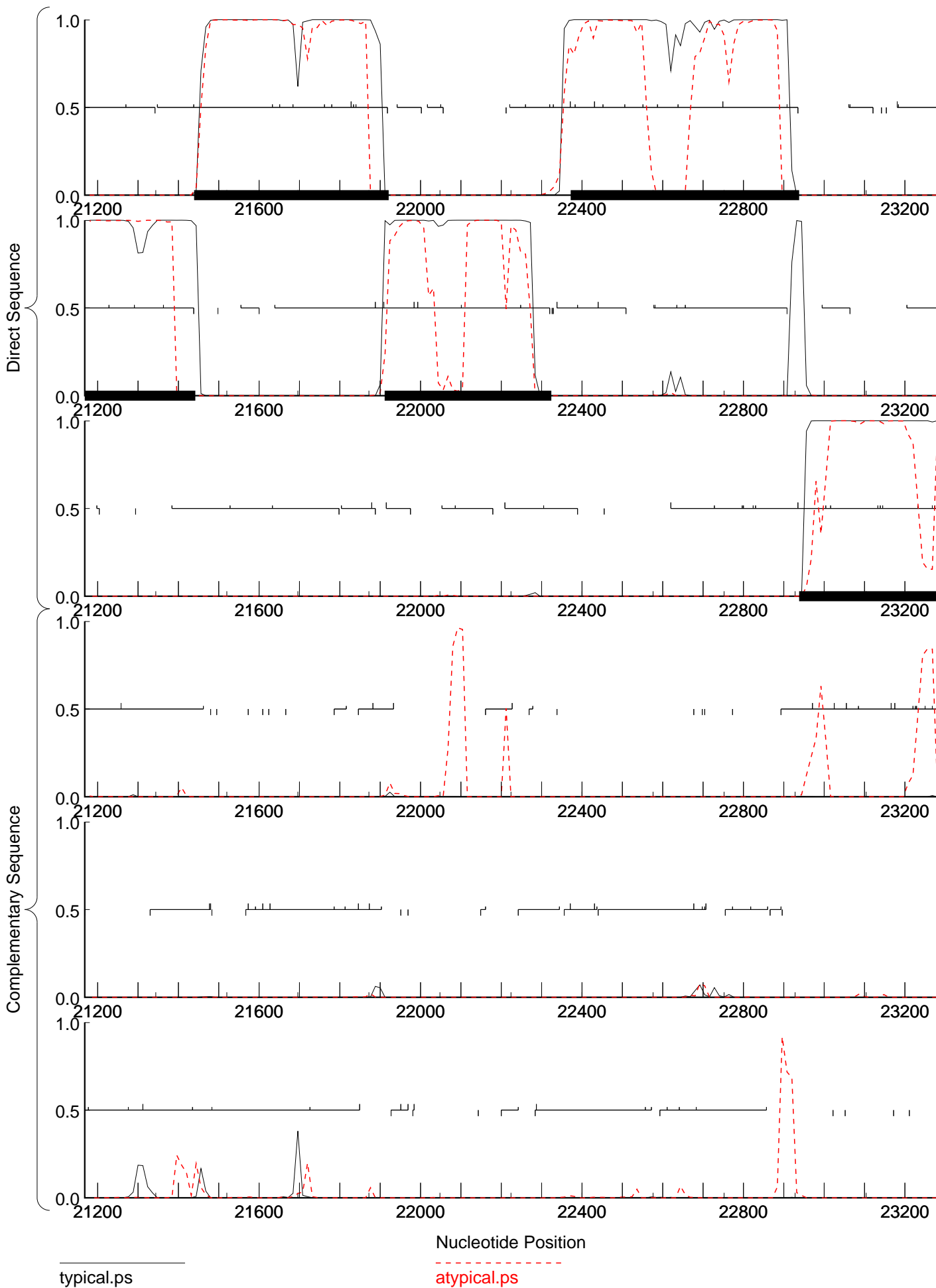


typical.ps

atypical.ps

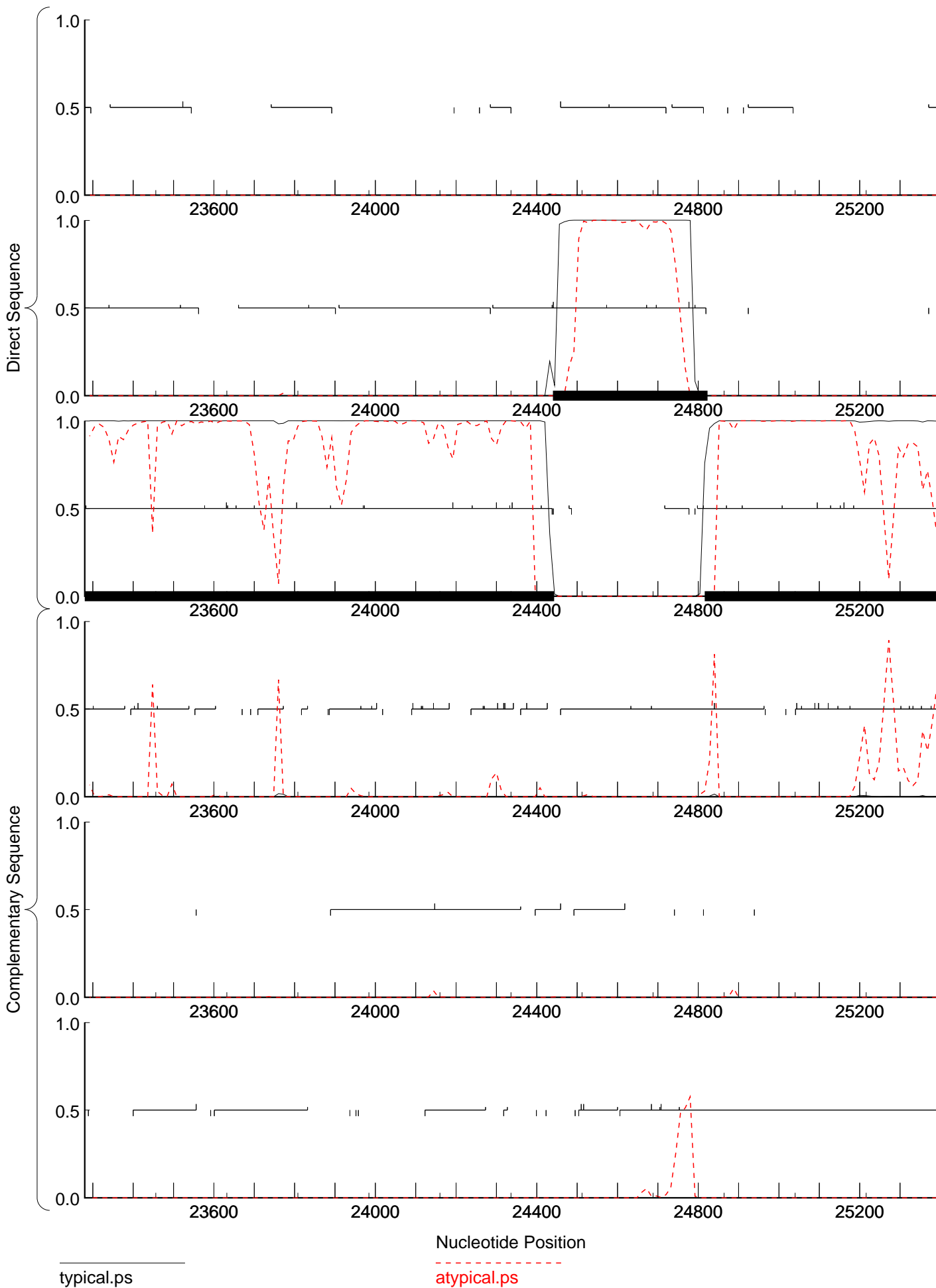






typical.ps

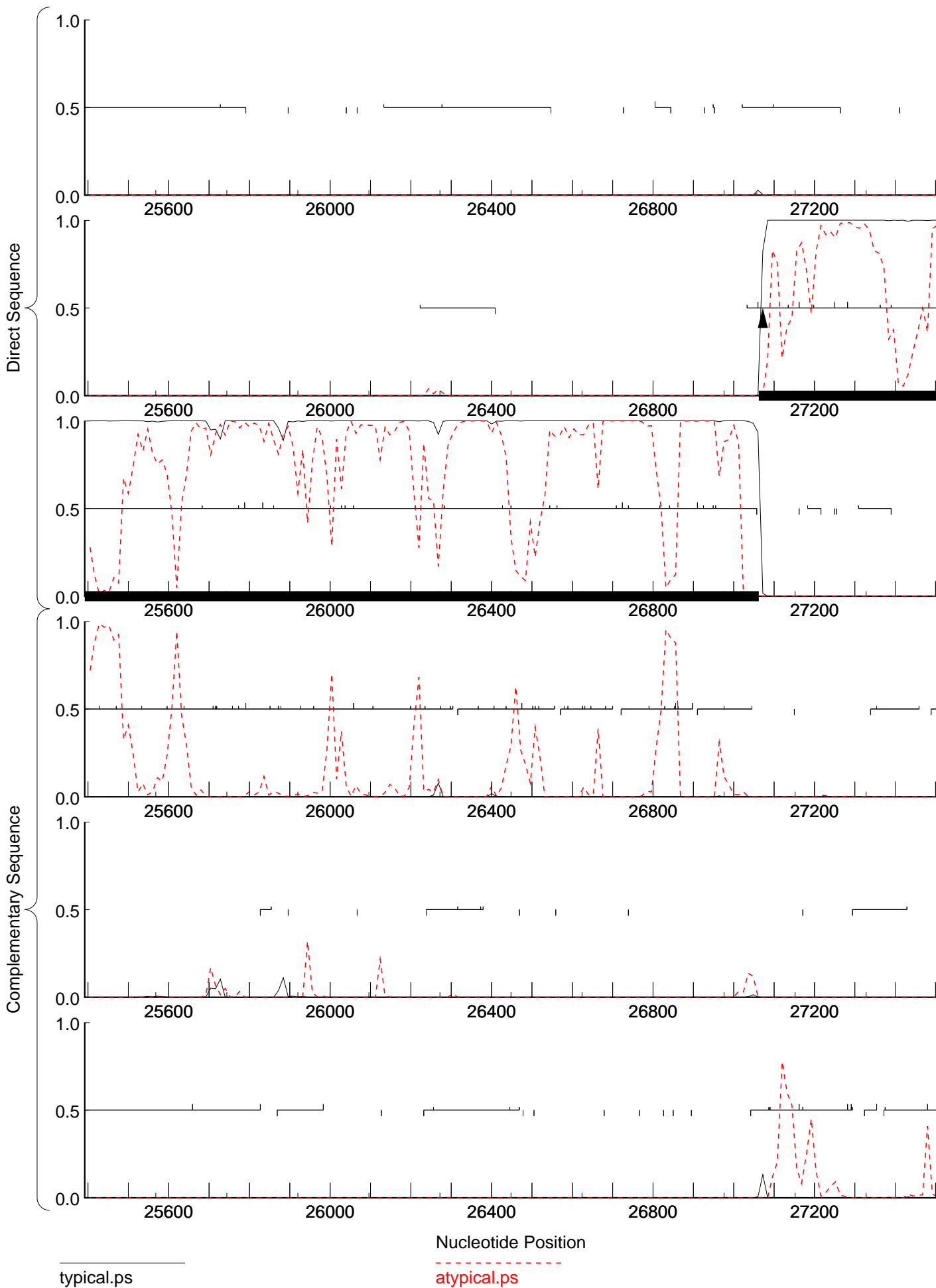
atypical.ps



typical.ps

Nucleotide Position

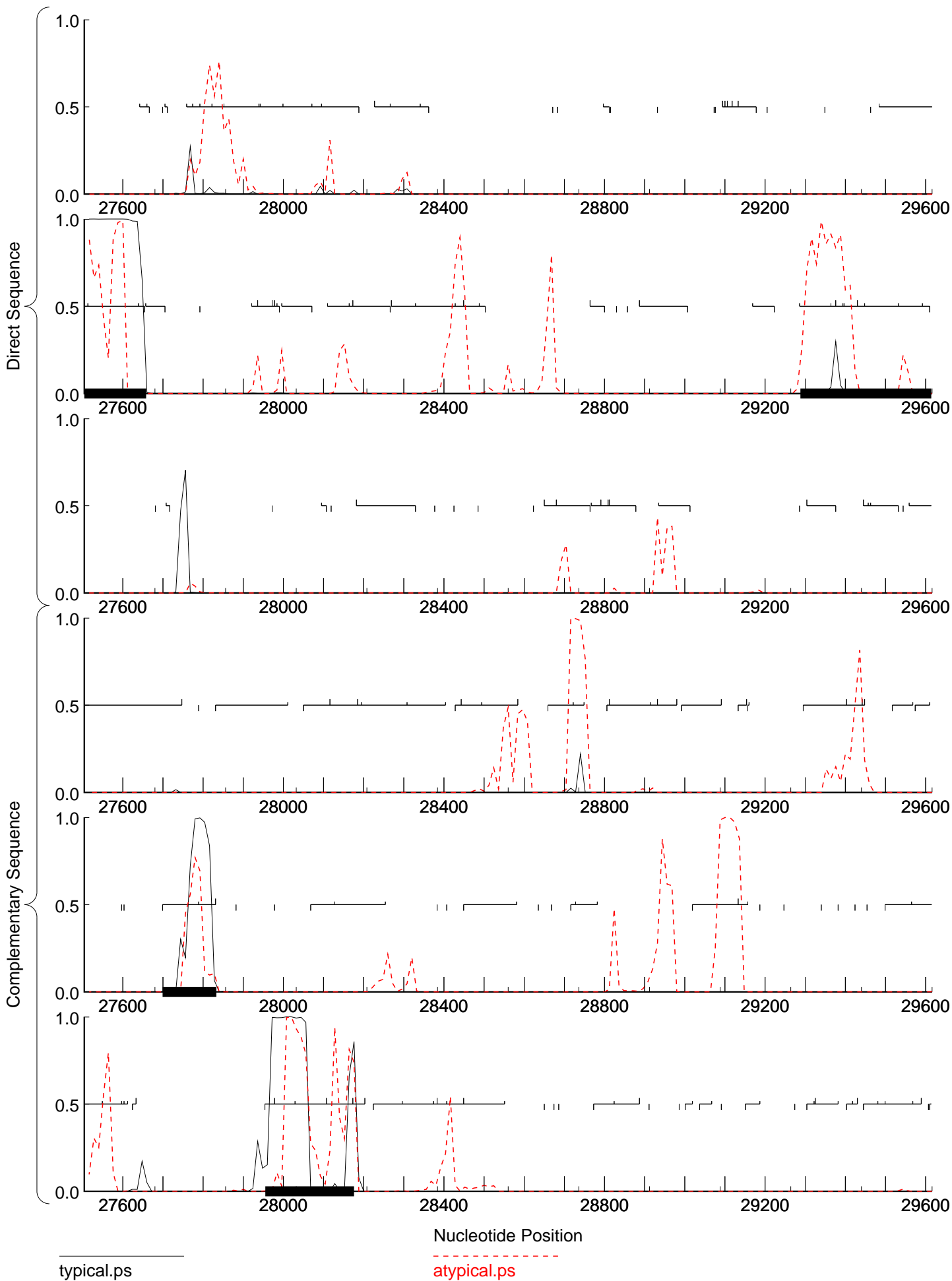
atypical.ps

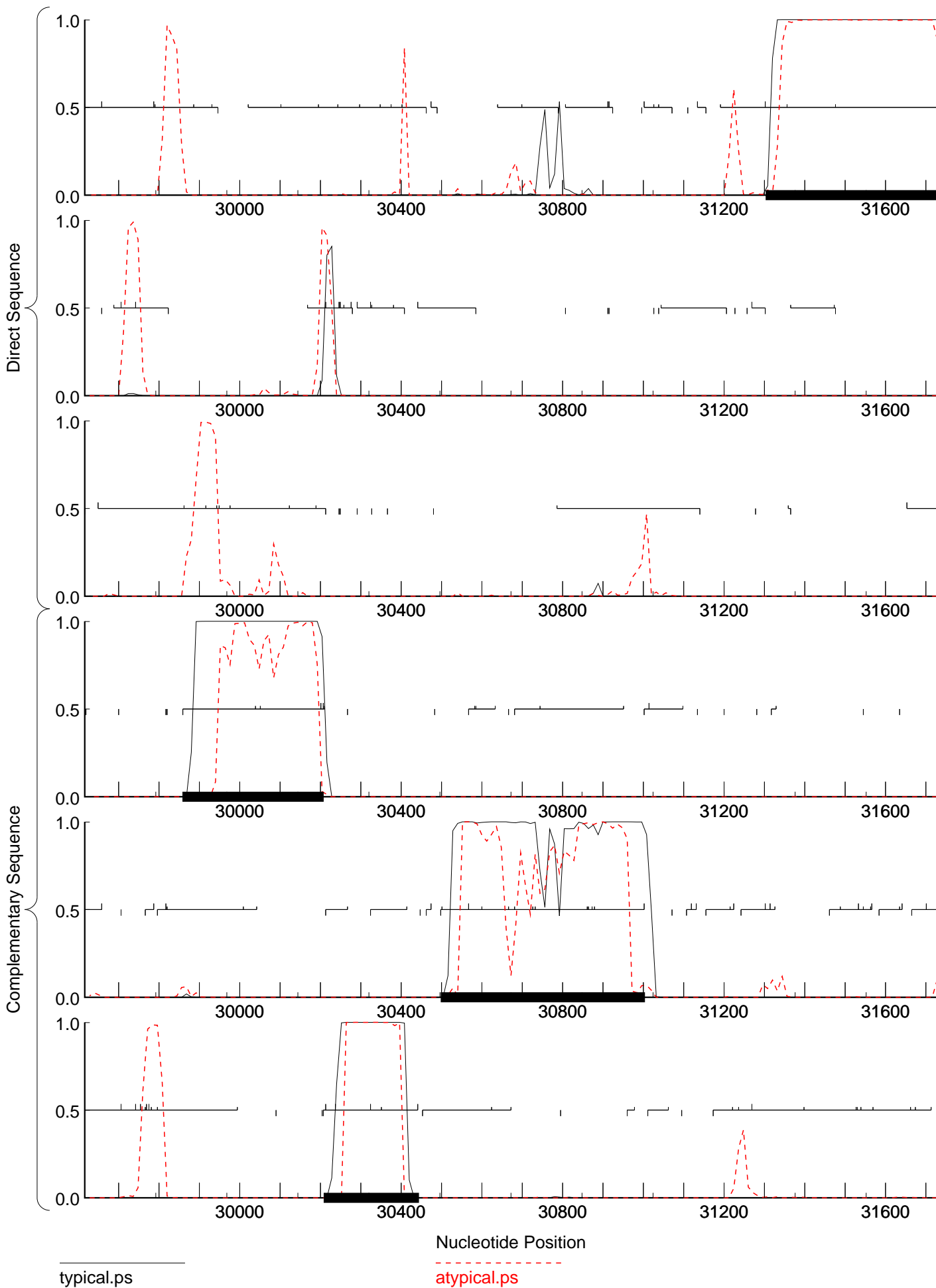


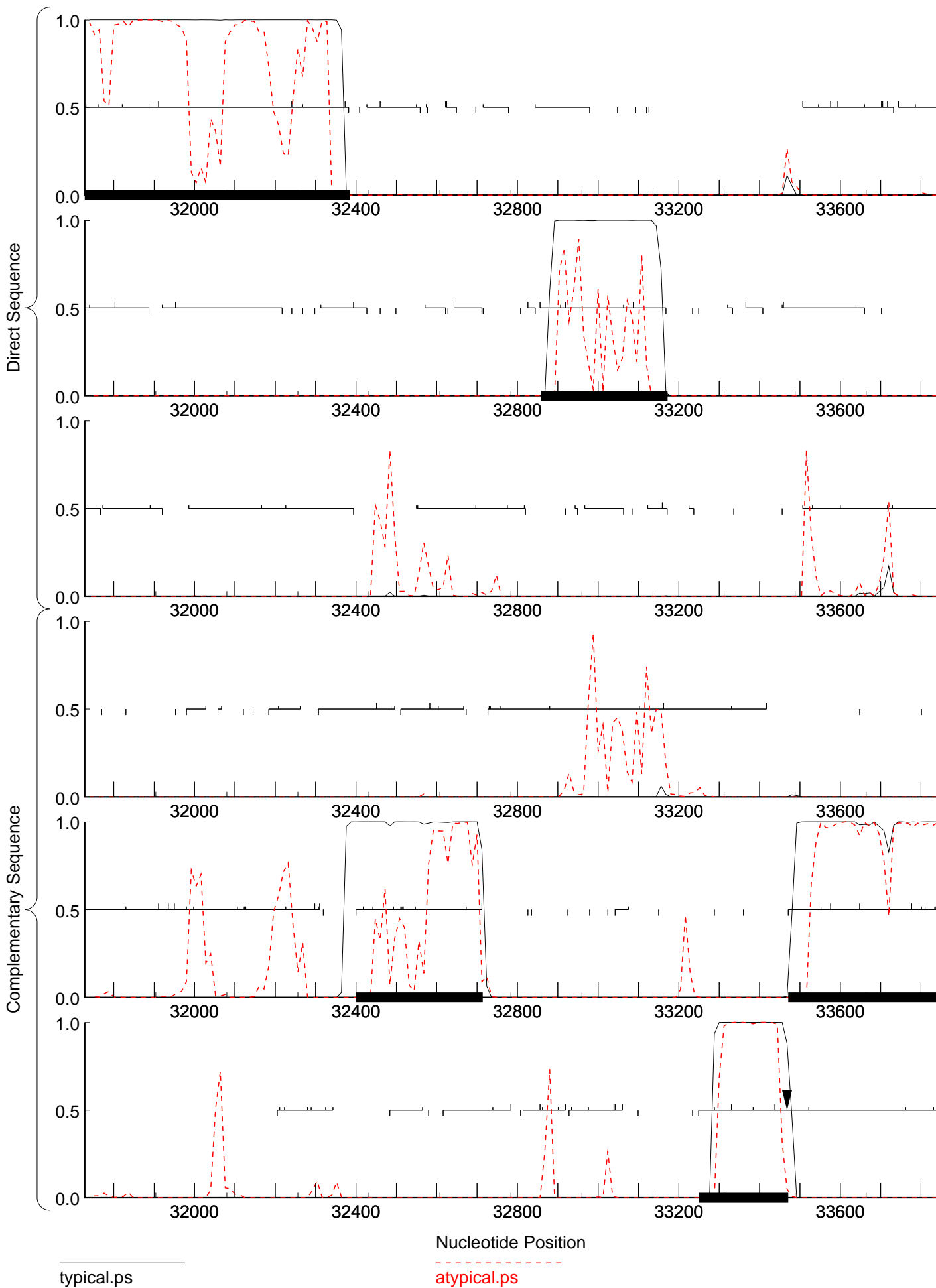
typical.ps

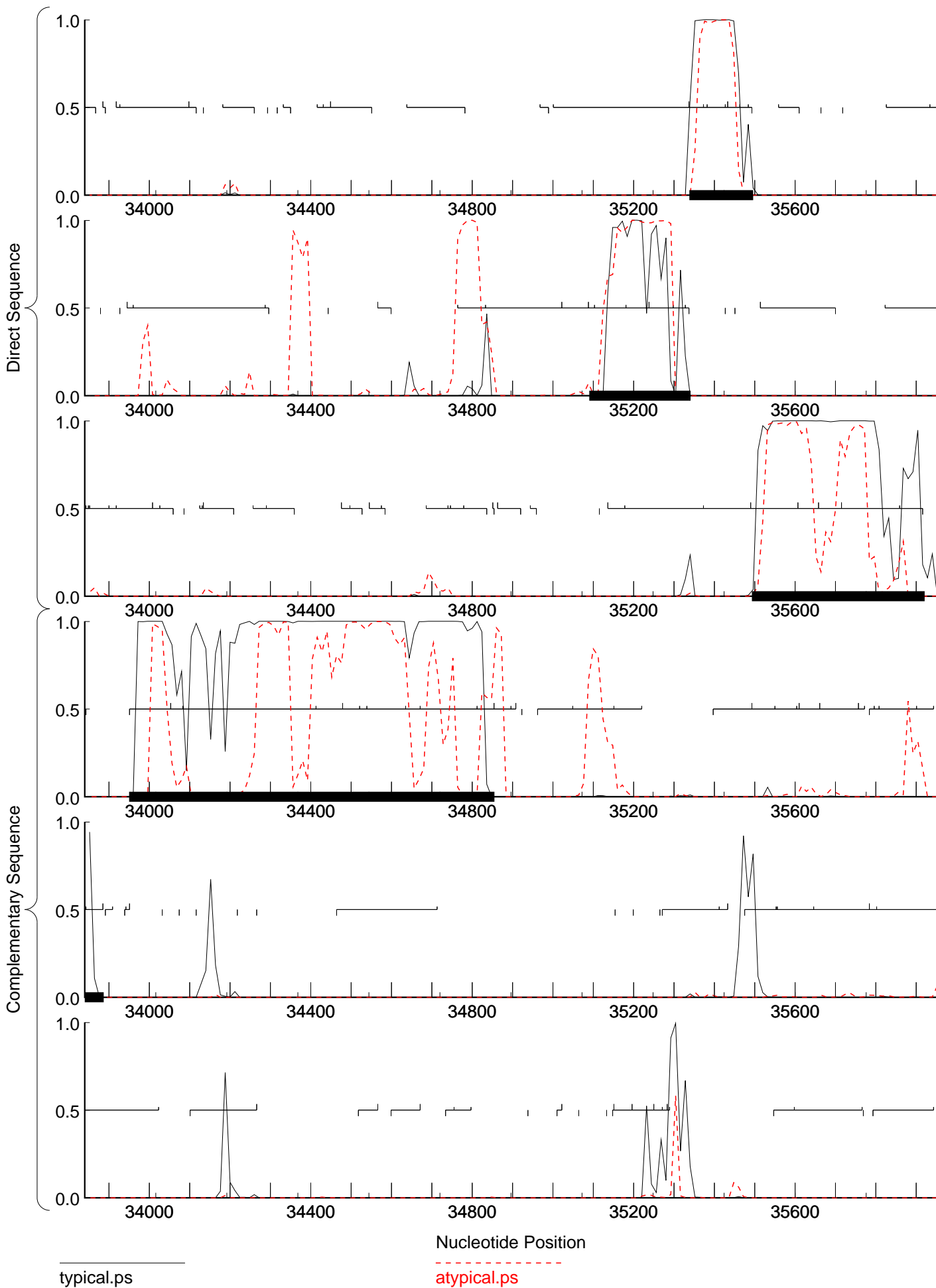
atypical.ps

complete sequence, 52077 bp including 10-base 3' overhang (CGGCTGGGGA), Cluster CZ, Order 4, Window 96, Step 12, 15/26
complete sequence, 52077 bp including 10-base 3' overhang (CGGCTGGGGA), Cluster CZ, Order 2, Window 96, Step 12, 15/26



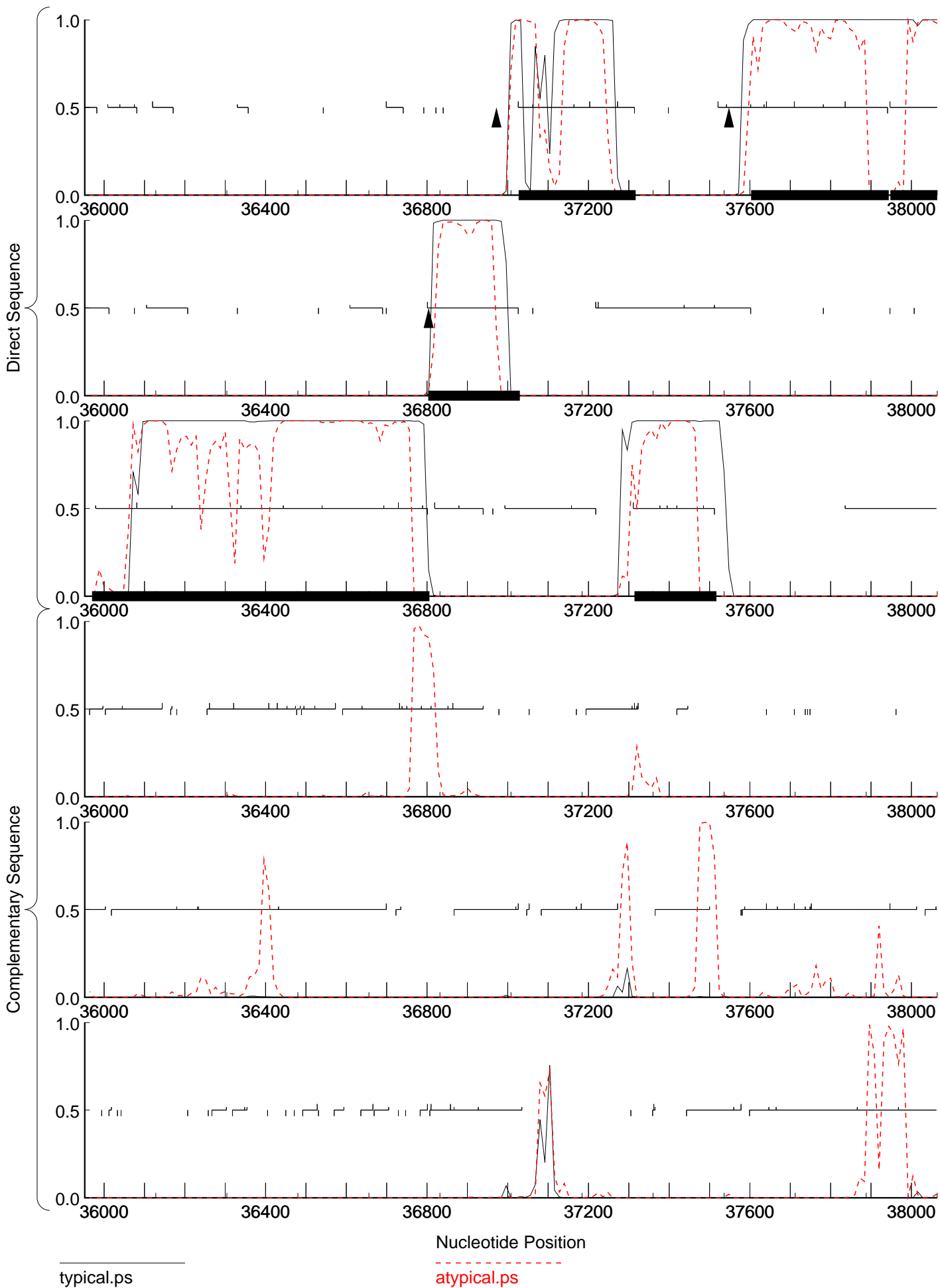


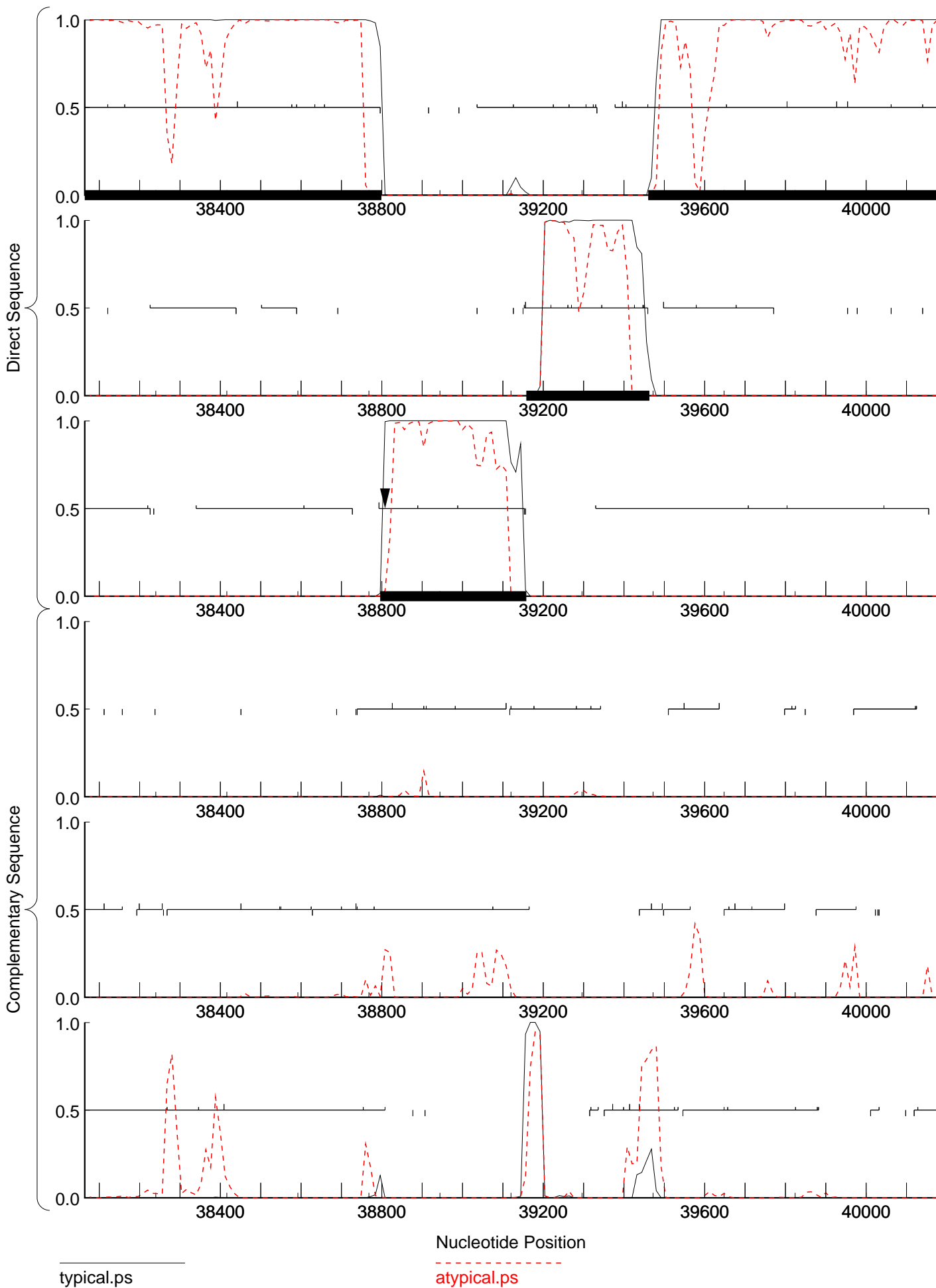


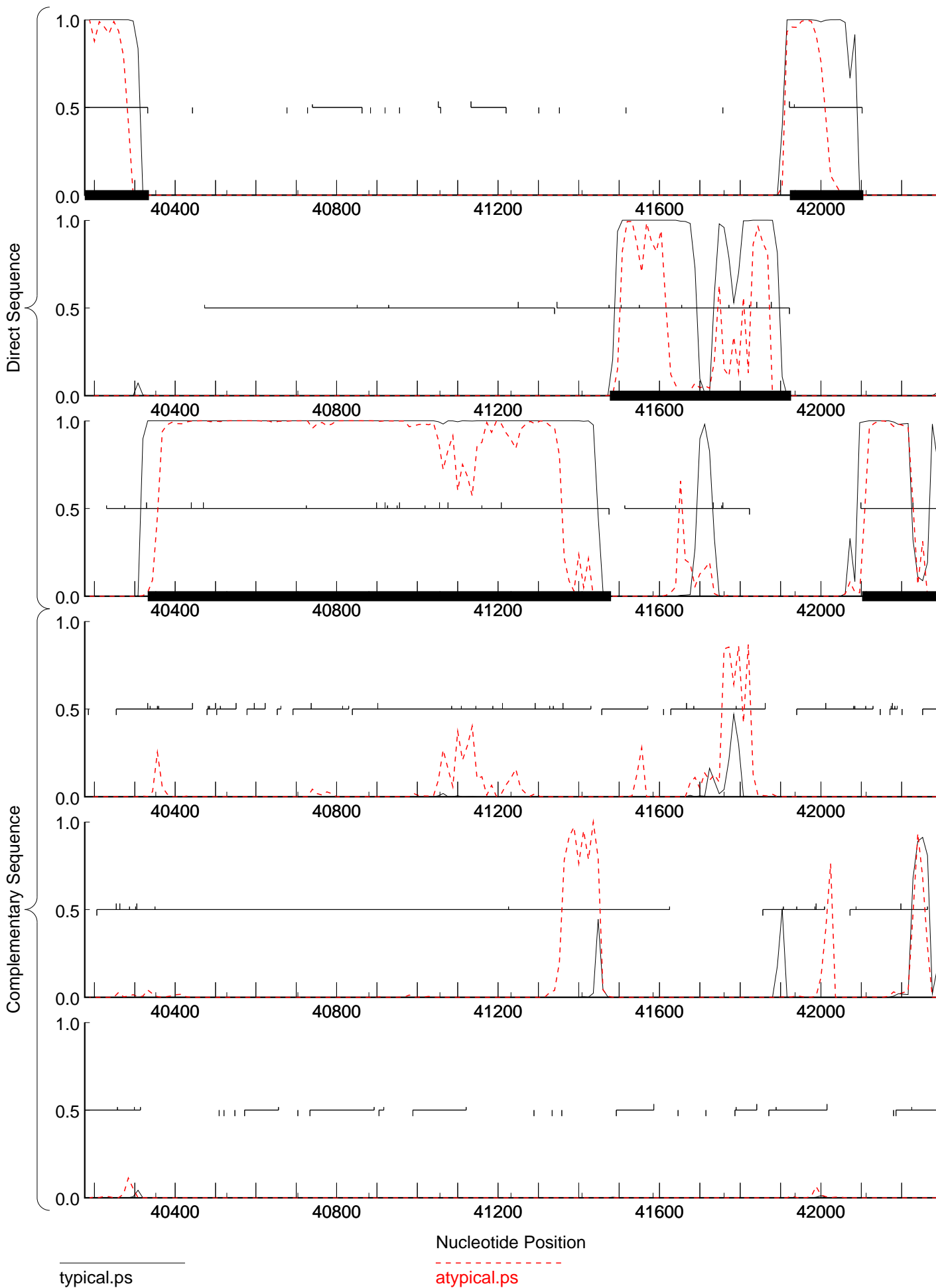


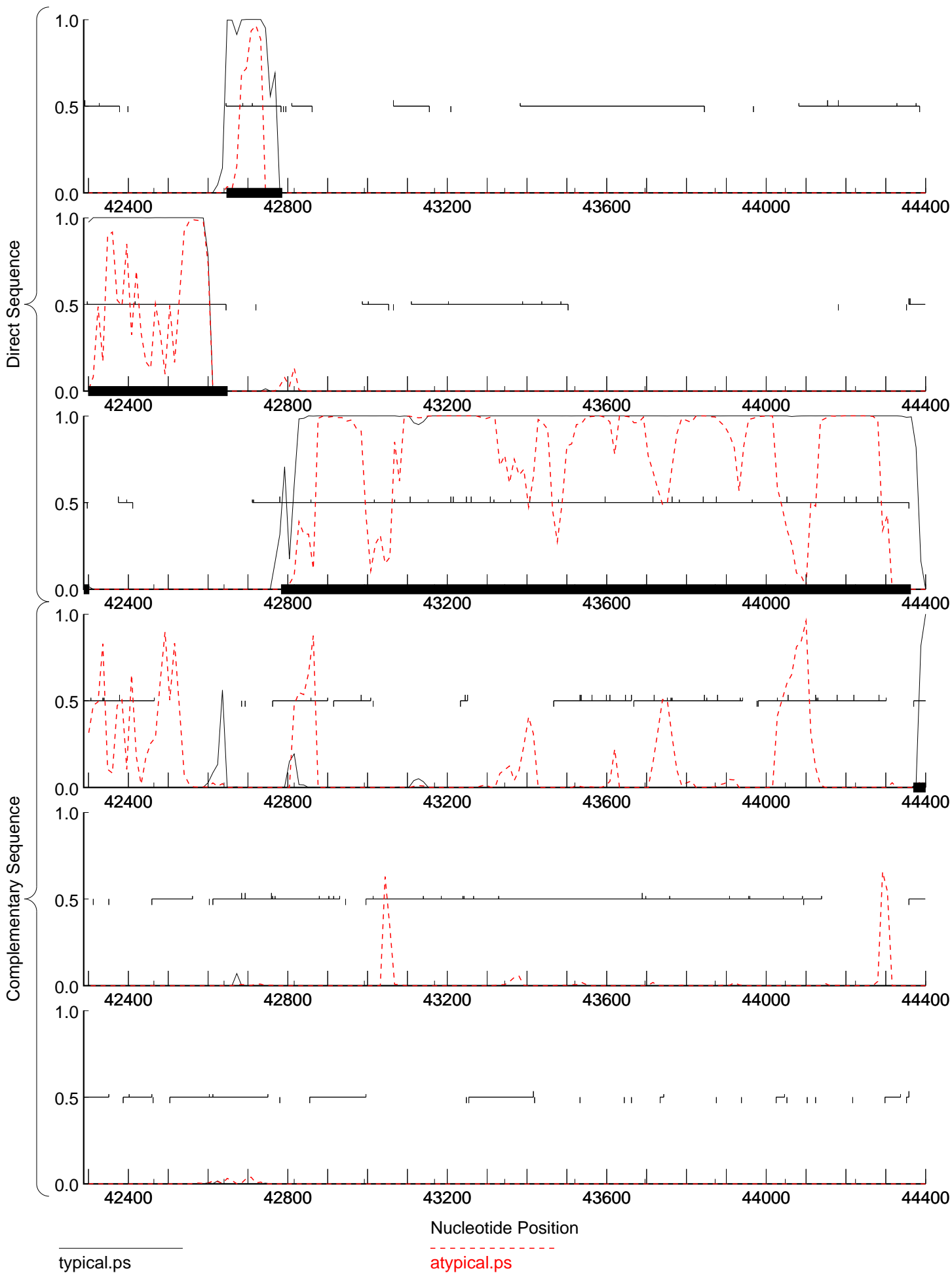
typical.ps

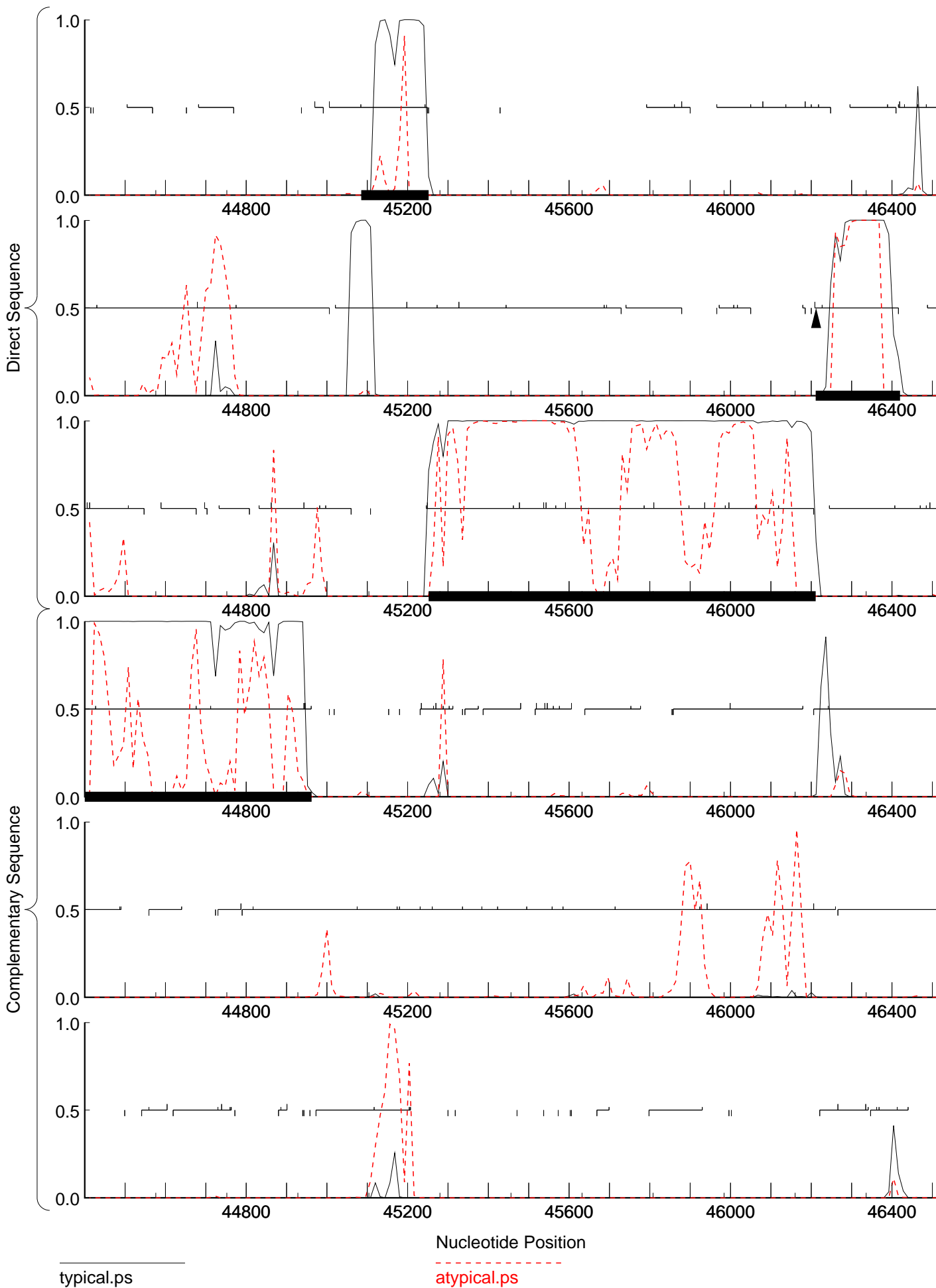
atypical.ps











typical.ps

atypical.ps

