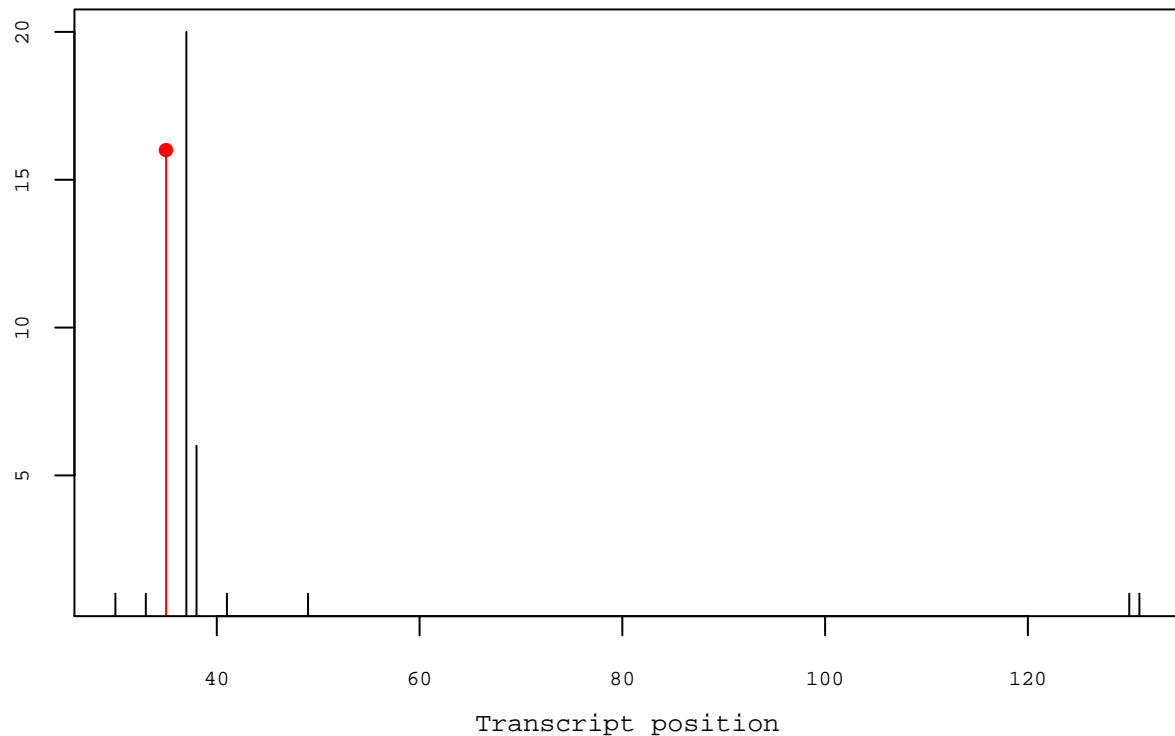


5' CTCATGTAGAACTACGTCAGGAGTCCGGACAG '3  
||o|||| | ||||| ||||| |||  
3' GTGCATCTCGATGCAGTCCTAAGG '5

Fragment Abundance



Cleavage site: 35 Tag abundance: 16 Weighted abundance: 3.619 Category: 2  
sRNA abundance: 6 Alignment score: 3.5 MFE ratio: 0.732 p-value: 0.042