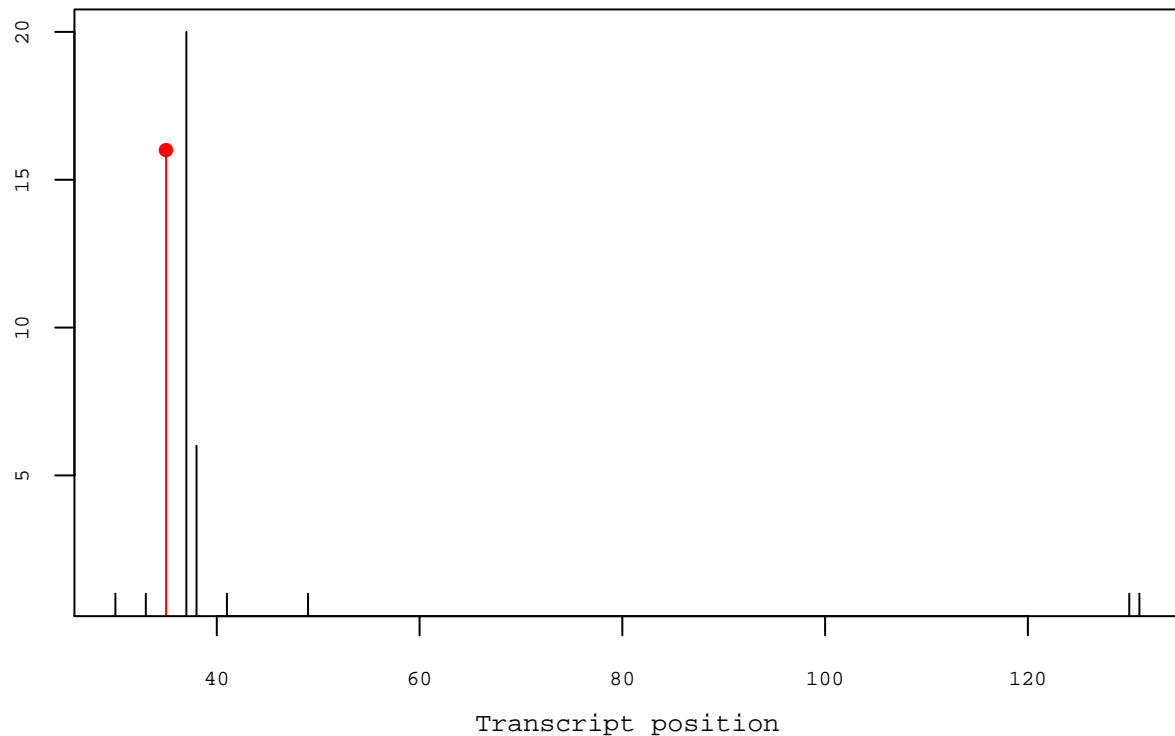


5' CTCATGTAGAACTACGTCAGGAGTCCGGACAG '3
 ||o|||| | ||||| |||||o|||
 3' GTGCATCTCGATGCAGTCCTTAGG '5

Fragment Abundance



Cleavage site: 35 Tag abundance: 16 Weighted abundance: 3.619 Category: 2
 sRNA abundance: 9 Alignment score: 2.5 MFE ratio: 0.816 p-value: 0.042