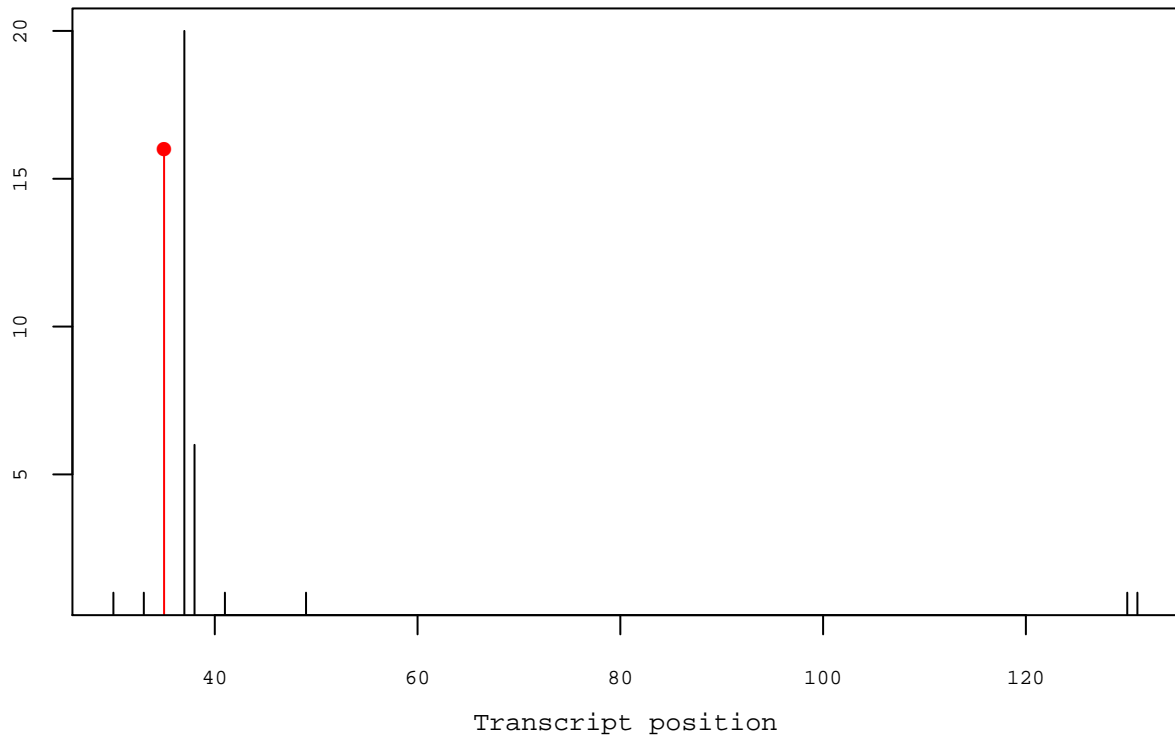


5' CTCATGTAGAACTACGTCAGGAGTCCGGACAG '3
||o||||| ||||| |||||
3' GTGCATCTCGATGCAGGCCTCAGG '5

Fragment Abundance



Cleavage site: 35 Tag abundance: 16 Weighted abundance: 3.619 Category: 2
sRNA abundance: 12 Alignment score: 3.5 MFE ratio: 0.707 p-value: 0.048