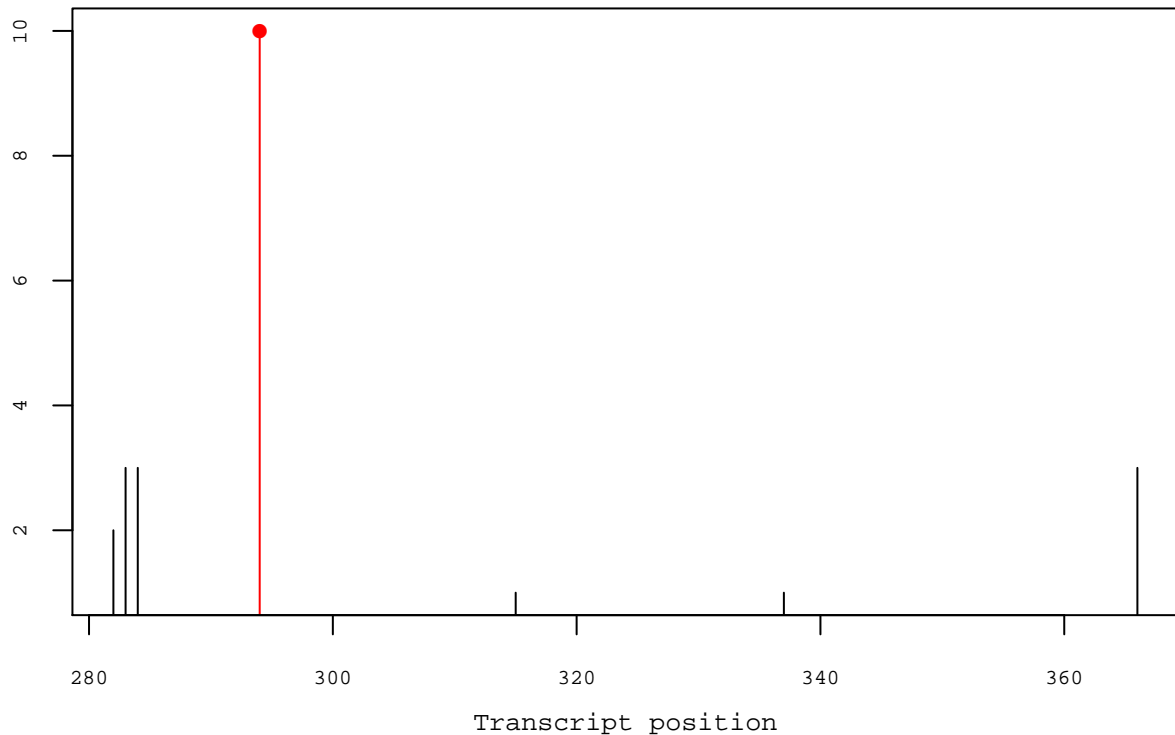


PggD11615_c455_g1_i1

5' GCGGTGTCCGATCCGGACCGTAAATCACTTCT '3
|||||o|||||
3' CCACAGGCTAGGTCTGGCATTAG '5

Fragment Abundance



Cleavage site: 294 Tag abundance: 10 Weighted abundance: 10 Category: 0
sRNA abundance: 56 Alignment score: 1 MFE ratio: 0.985 p-value: 0.007