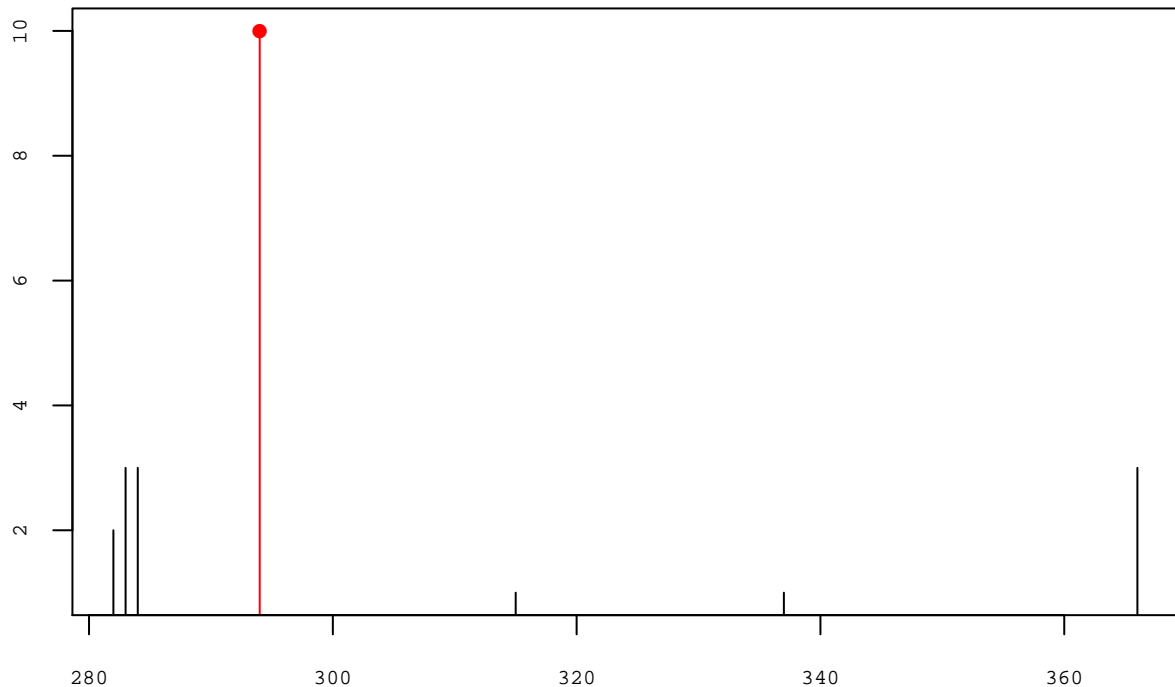


PggD11615\_c455\_g1\_i1

5' GCGGTGTCCGATCCGGACCGTAAATCACTTCT '3  
||||| |||||  
3' CCACAGACTAGGCCTGGCATTAG '5

Fragment Abundance



Transcript position

Cleavage site: 294 Tag abundance: 10 Weighted abundance: 10 Category: 0  
sRNA abundance: 12 Alignment score: 1 MFE ratio: 0.898 p-value: 0.007