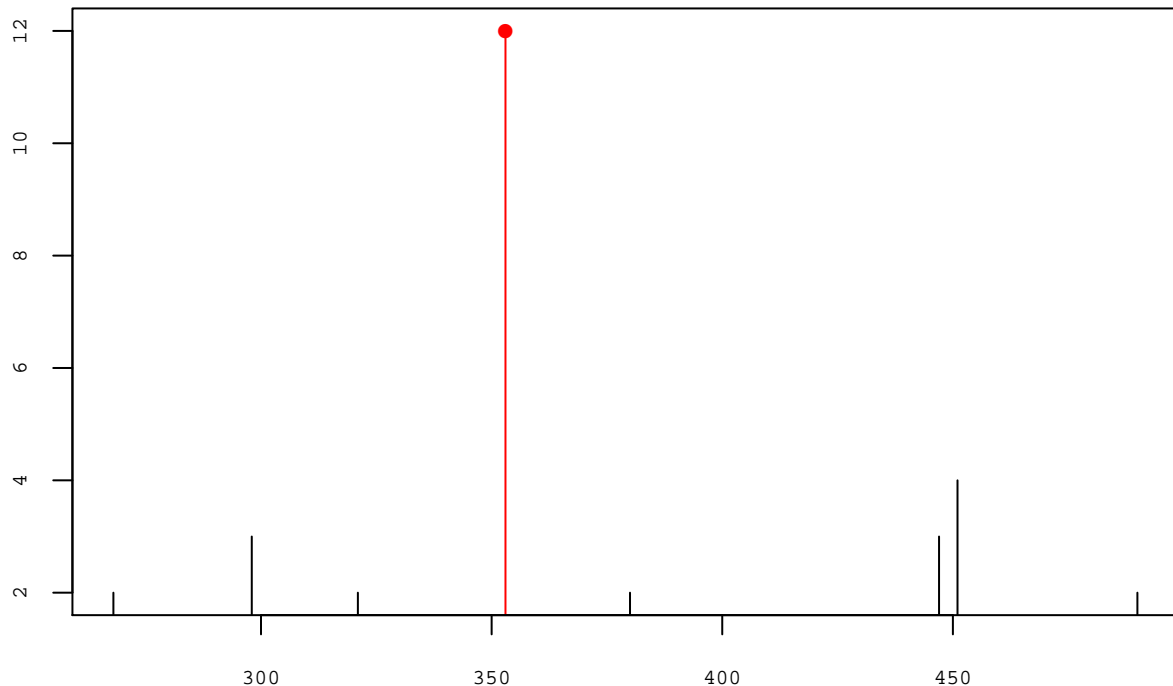


PggD1649_c22_g1_i1

5' AACACGAGCTGTTTCATGAACAAAGAGTTGTTT '3
|||||o|||||
3' GTGCTCGACAAGTGCTTGTATTATC '5

Fragment Abundance



Transcript position

Cleavage site: 353 Tag abundance: 12 Weighted abundance: 2.4 Category: 0
sRNA abundance: 15 Alignment score: 3 MFE ratio: 0.853 p-value: 0.006