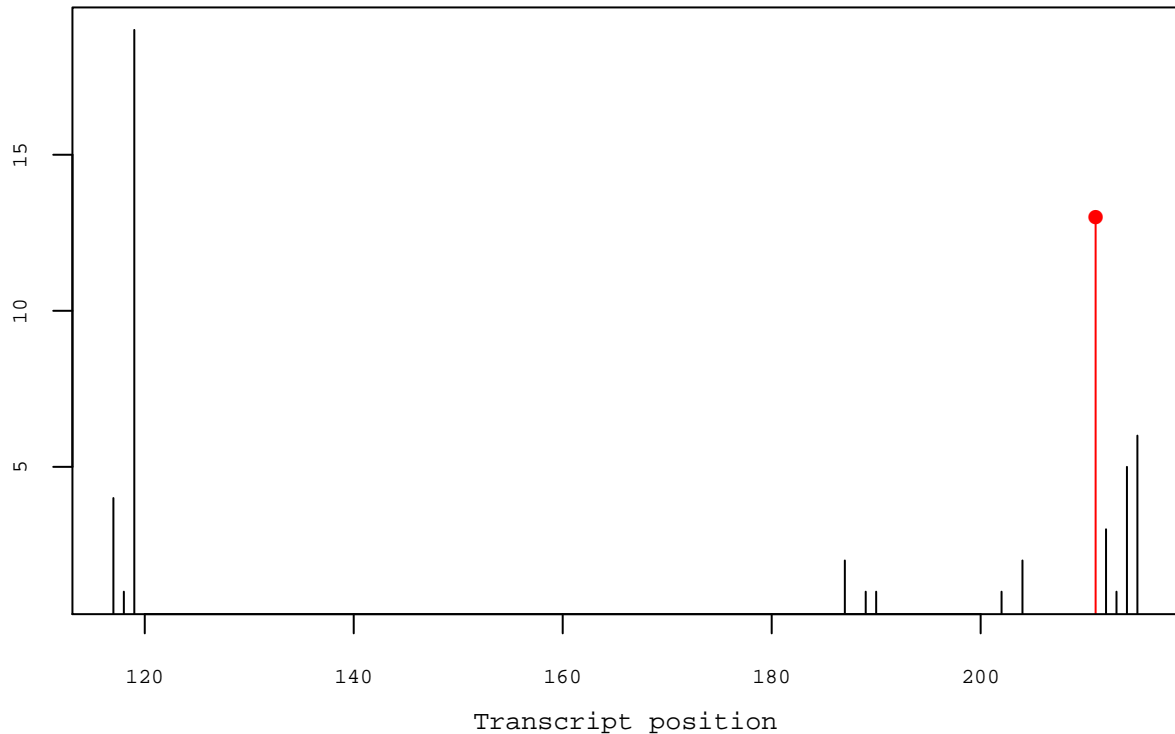


PggD9015_c120_g1_i1

5' CGGACTCTTGACGTAGCTCTACGTGCGGACCA '3
|||o|||||||o|||
3' TGAGGACTGCATCGAGATGTACG '5

Fragment Abundance



Cleavage site: 211 Tag abundance: 13 Weighted abundance: 6.5 Category: 2
sRNA abundance: 8 Alignment score: 1.5 MFE ratio: 0.93 p-value: 0.014