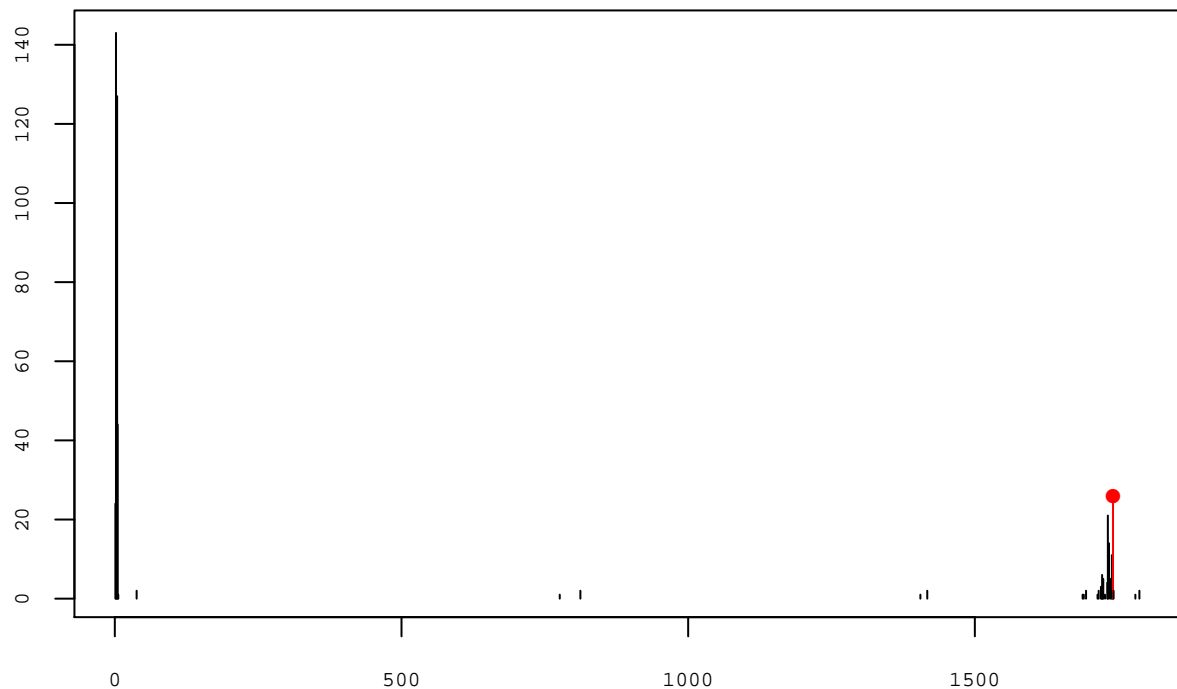


PggD13459_c44_g1_i2

5' GAACACGAGCTGTTACGAACAAA-GAGTCCTT '3
|||||
3' TGTGCTCGACAAGTGCTTGTAT '5

Fragment Abundance



Transcript position

Cleavage site: 1741 Tag abundance: 26 Weighted abundance: 4.143 Category: 0
sRNA abundance: 23 Alignment score: 1.5 MFE ratio: 0.955 p-value: 0.003