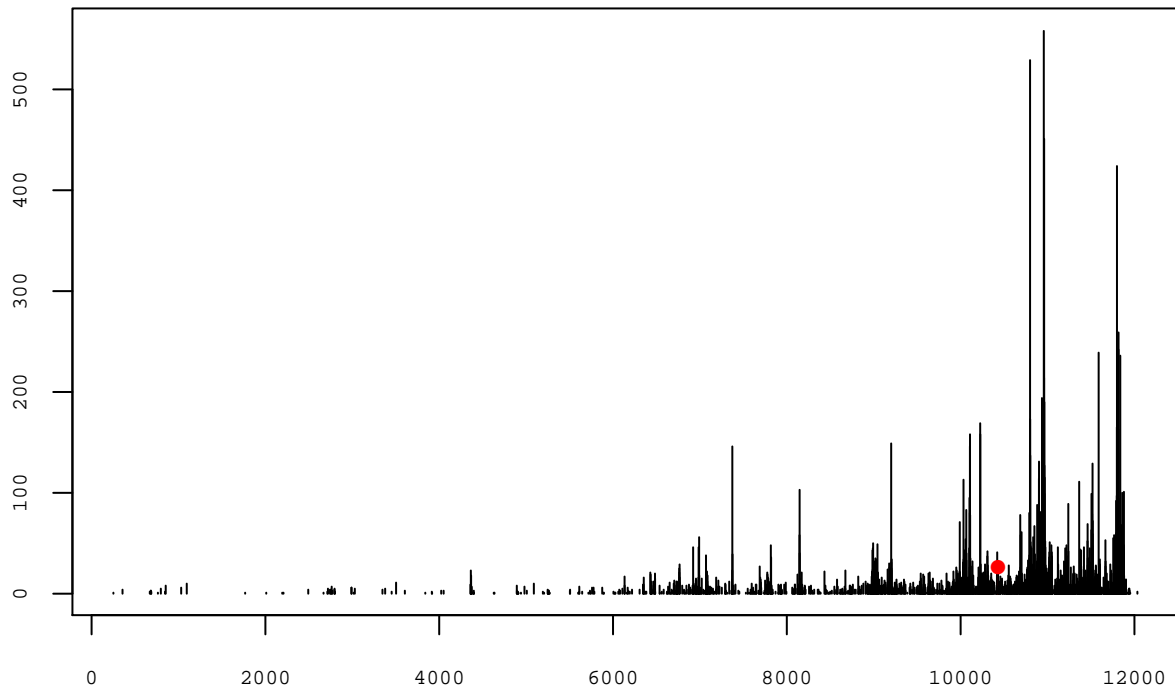


PggD10208_c4_g1_i1

5' CTTGAAGATTCTTATAATCAGCTACGGATGAG '3
||| | ||| o ||| ||| ||| o
3' CTTCTTA-AATGTTAGTCGATGT '5

Fragment Abundance



Transcript position

Cleavage site: 10430 Tag abundance: 26 Weighted abundance: 26 Category: 2
sRNA abundance: 5 Alignment score: 3.5 MFE ratio: 0.762 p-value: 0.033