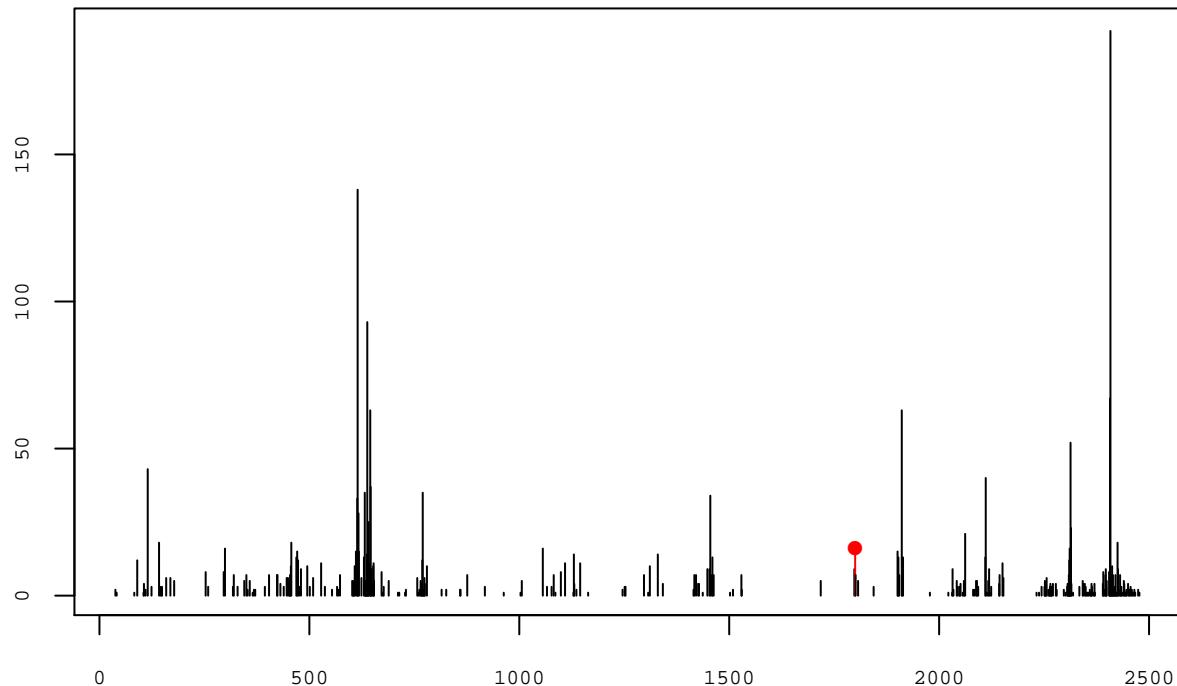


PggD12101_c37_g1_i9

5' AGTGGTCATTTTGTCTTAGAGTTTATAGAAG '3
 ||||| |||oo|||||
3' CCAGTAAAATCAGGGTCTCAAAT '5

Fragment Abundance



Transcript position

Cleavage site: 1800 Tag abundance: 16 Weighted abundance: 16 Category: 2
sRNA abundance: 5 Alignment score: 3 MFE ratio: 0.743 p-value: 0.021