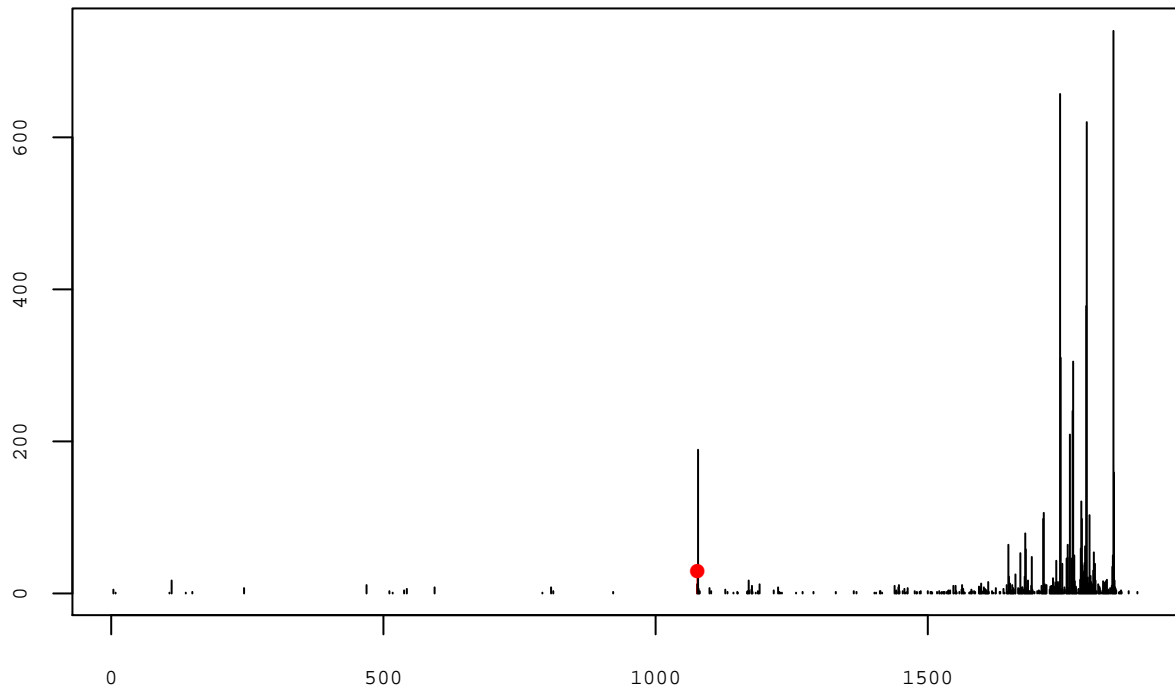


PggD8298_c47_g1_i1

5' TGAAGCTGGAGCTCCCTTCACTCCAATGTCCA '3
|| o ||||| ||||| |||||
3' CG-TCTCGAGGGAAGTTAGGTT '5

Fragment Abundance



Transcript position

Cleavage site: 1077 Tag abundance: 29 Weighted abundance: 14.5 Category: 2
sRNA abundance: 2575 Alignment score: 3.5 MFE ratio: 0.821 p-value: 0.04