

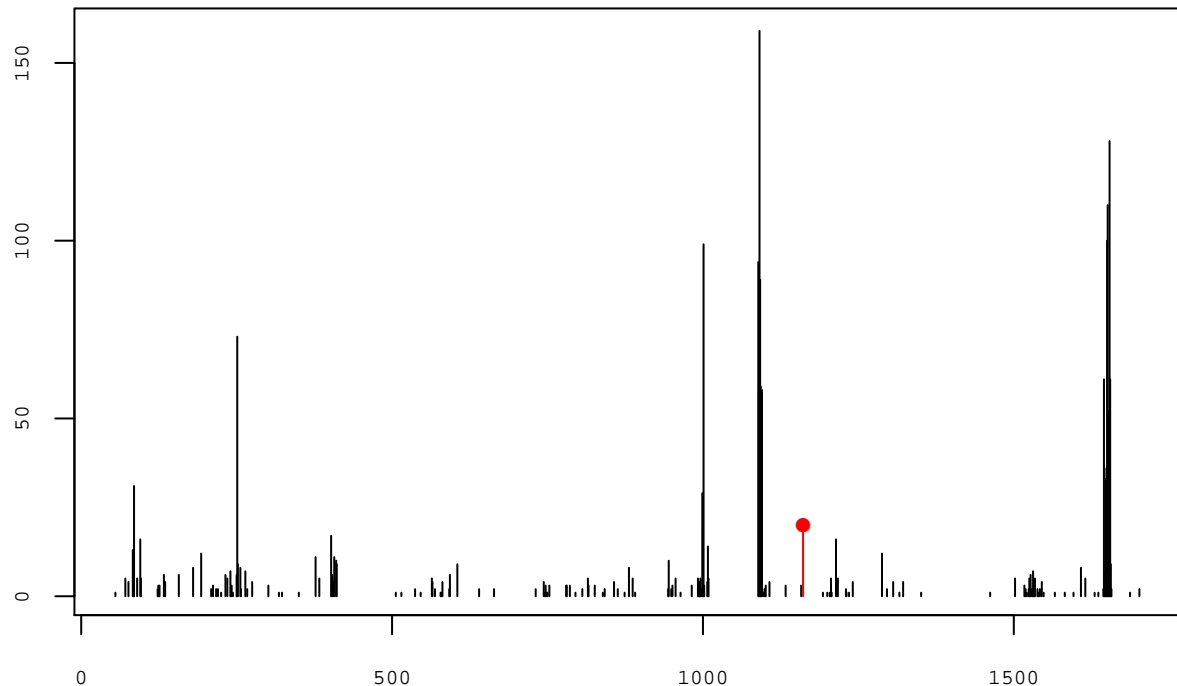
PggD11514_c11_g1_i5

5' TCACCTGATTGACGGTCAGGATCGGACATCAC '3

|||o||o|||||||

3' CTAGATGTCAGTCCTAGCCT '5

Fragment Abundance



Transcript position

Cleavage site: 1161 Tag abundance: 20 Weighted abundance: 20 Category: 2
sRNA abundance: 8 Alignment score: 2.5 MFE ratio: 0.809 p-value: 0.042