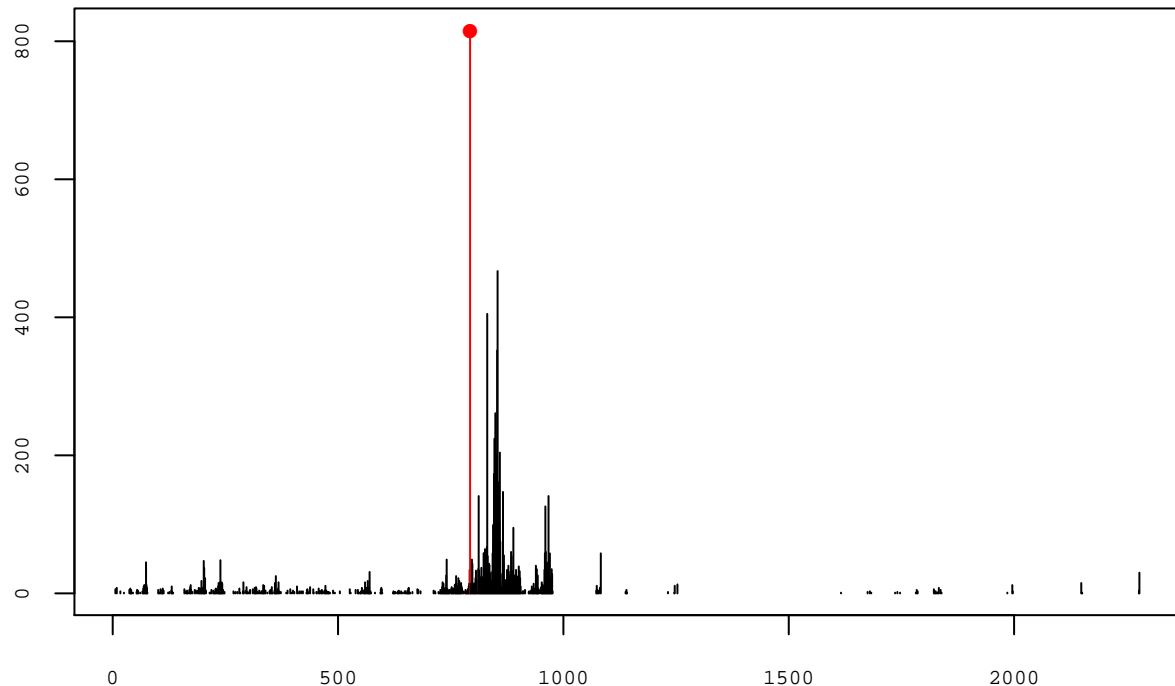


PggD6617_c1_g2_i1

5' TCAAGCATGCTTGCTCTCTTCTGTCCTAGAT '3

|||||oo|||||||
3' ACGAGTGAGAGAAGACAGT '5

Fragment Abundance



Transcript position

Cleavage site: 793 Tag abundance: 815 Weighted abundance: 815 Category: 0
sRNA abundance: 6 Alignment score: 1 MFE ratio: 0.907 p-value: 0.008