

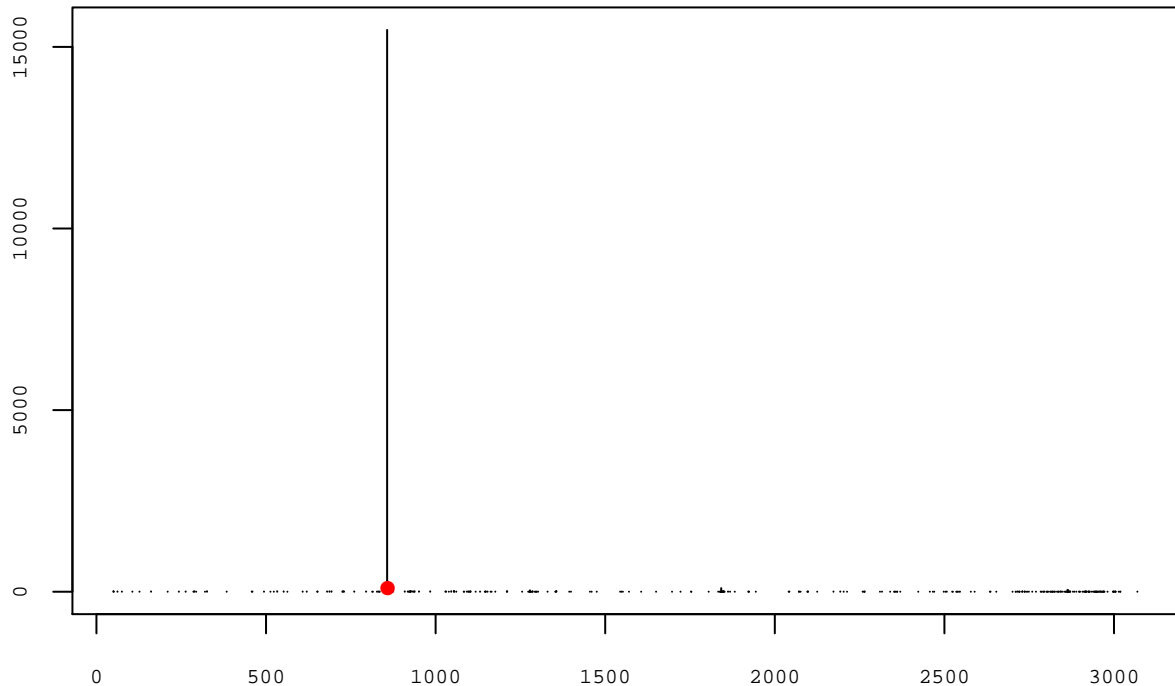
PggD11091_c20_g1_i1

5' TGGTCGGGATGAAGCCTGGTCCG-GATTCTATT '3

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3' CCTTACTTCGGACCAGGCTCT '5

Fragment Abundance



Transcript position

Cleavage site: 859 Tag abundance: 91 Weighted abundance: 45.5 Category: 2
sRNA abundance: 44 Alignment score: 2.5 MFE ratio: 0.869 p-value: 0.002