

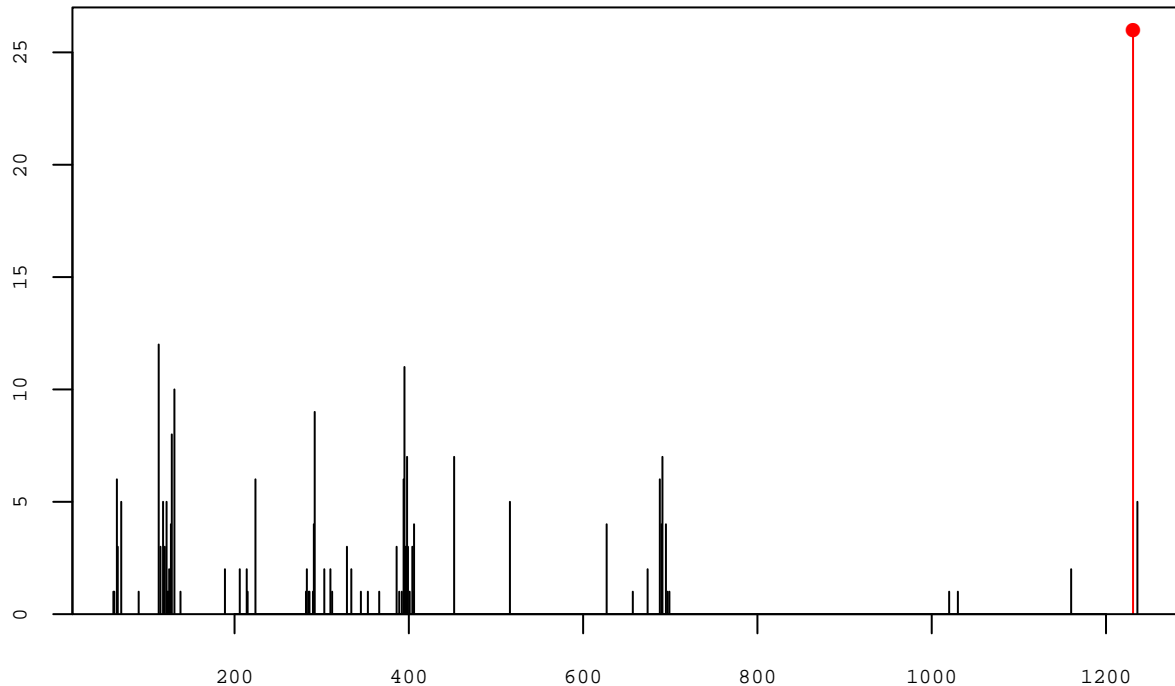
PggD10737_c31_g1_i1

5' CATGTAACCTCTTTGCAGGTTACAGACGTACG '3

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3' TTGTACAAACGTCCAATGTCT '5

Fragment Abundance



Transcript position

Cleavage site: 1231

Tag abundance: 26

Weighted abundance: 1.083

Category: 0

sRNA abundance: 10

Alignment score: 2

MFE ratio: 0.704

p-value: 0.006