

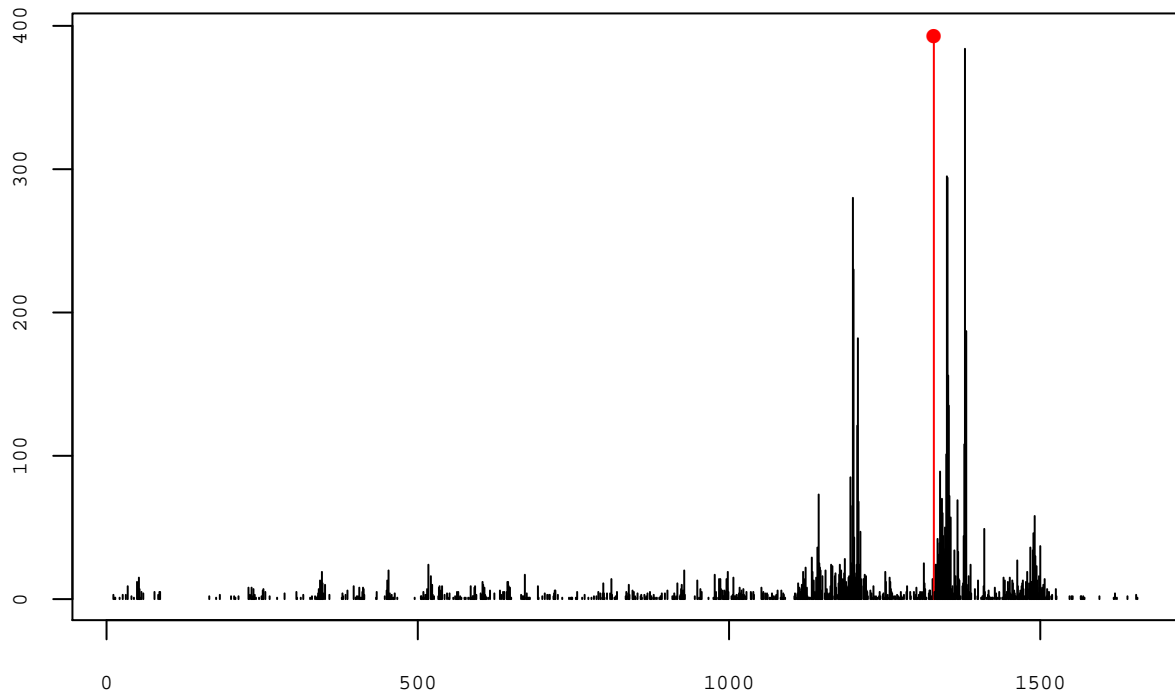
PggD3549_c0_g1_i1

5' TCTCCAAGGCAGC-TCATCGAGGTTCTCTCAAT '3

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3' TCCGTCGTAGTAGTTCTAAGA '5

Fragment Abundance



Transcript position

Cleavage site: 1329 Tag abundance: 393 Weighted abundance: 393 Category: 0
sRNA abundance: 139 Alignment score: 3 MFE ratio: 0.855 p-value: 0.008