

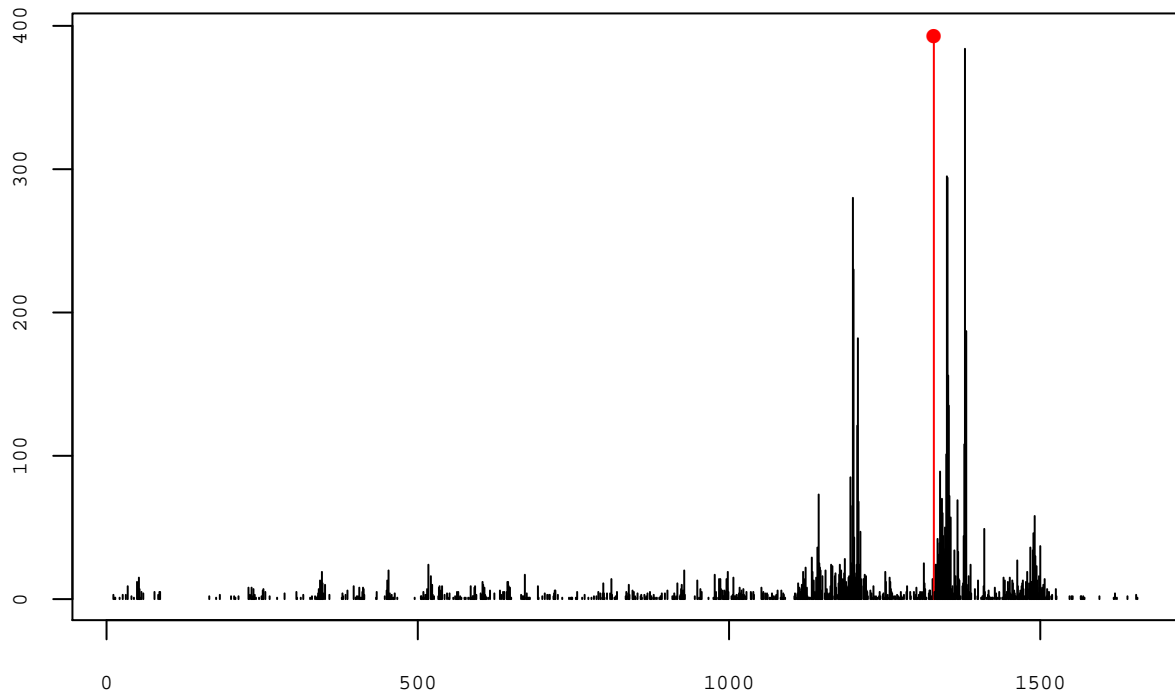
PggD3549_c0_g1_i1

5' TCTCCAAGGCAGC-TCATCGAGGTTCTCTCAAT '3

| | | | | | | | | | | | | | | |

3' TACGTCGTAGTAGTTCTAAGA '5

Fragment Abundance



Transcript position

Cleavage site: 1329

Tag abundance: 393

Weighted abundance: 393

Category: 0

sRNA abundance: 108

Alignment score: 4

MFE ratio: 0.808

p-value: 0.01