

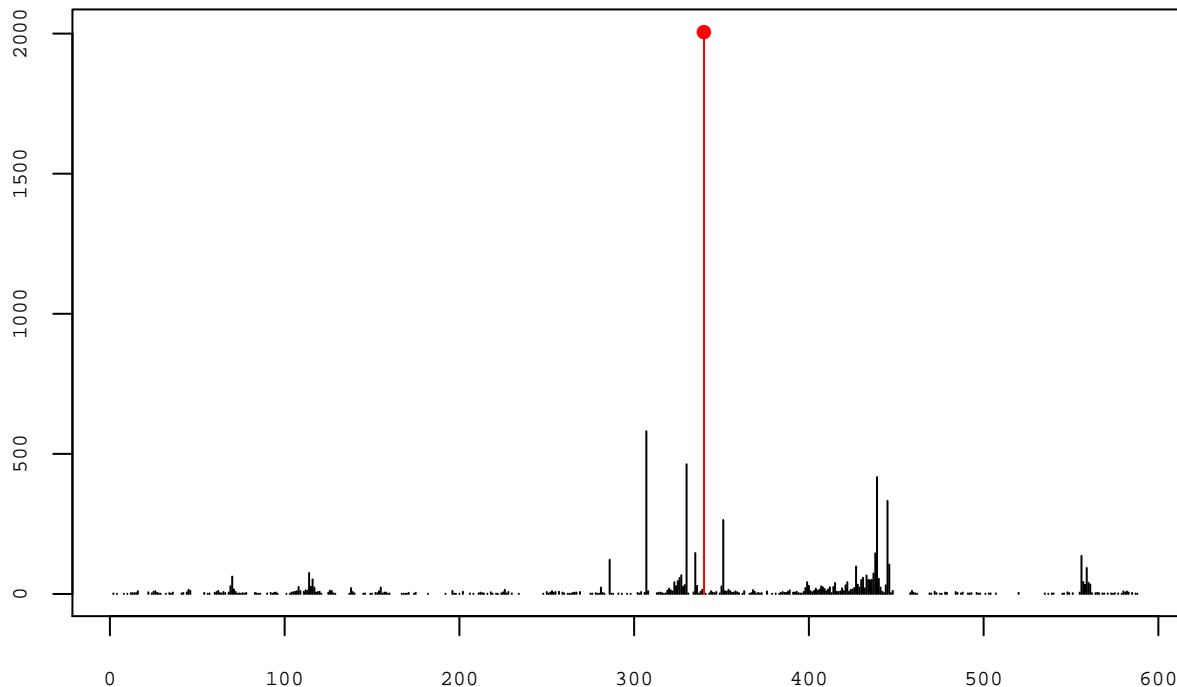
PggD884_c45_g1_i2

5' TCTTTTTT-TGGATTGAAGGGAGCTCTACATCA '3

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3' TCACCTGACTTCCTTCGAGA '5

Fragment Abundance



Transcript position

Cleavage site: 340 Tag abundance: 2006 Weighted abundance: 2006 Category: 0
sRNA abundance: 6 Alignment score: 3.5 MFE ratio: 0.827 p-value: 0.024