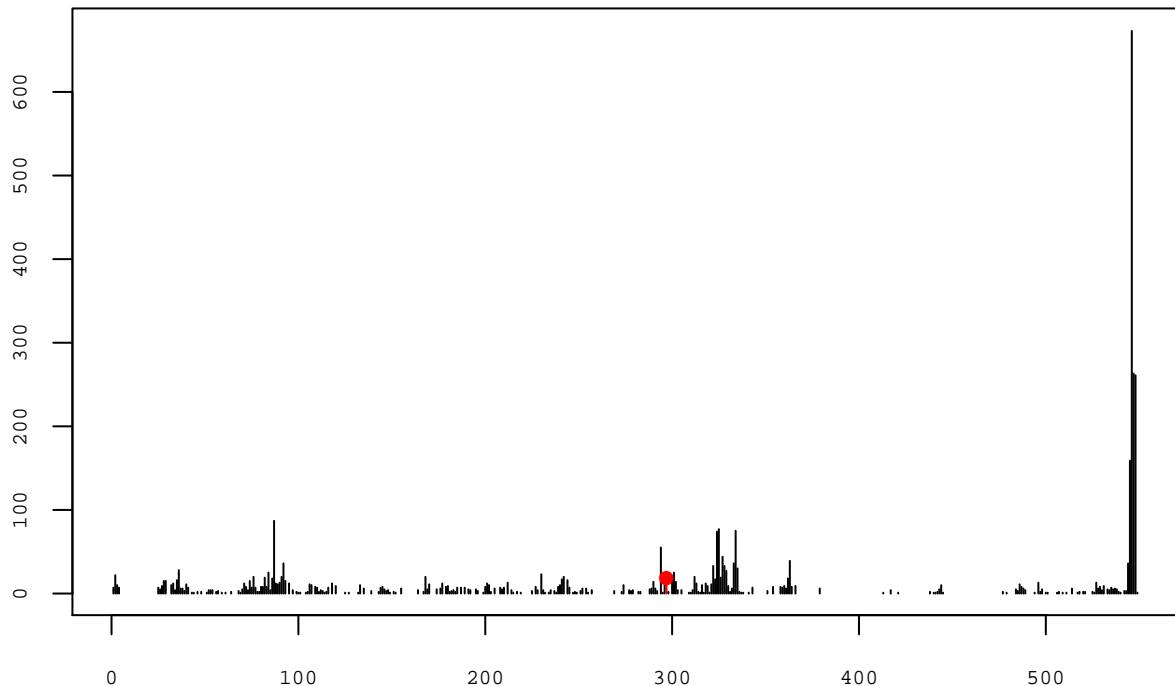


PggD9068_c6_g1_i1

5' CATGCGGTGTCCGATCCTGACCGTAGATCATG '3
 ||||| ||||| ||||| |
3' CCACAGACTAGGCCTGGCATT '5

Fragment Abundance



Transcript position

Cleavage site: 297 Tag abundance: 19 Weighted abundance: 19 Category: 2
sRNA abundance: 7 Alignment score: 3.5 MFE ratio: 0.737 p-value: 0.042