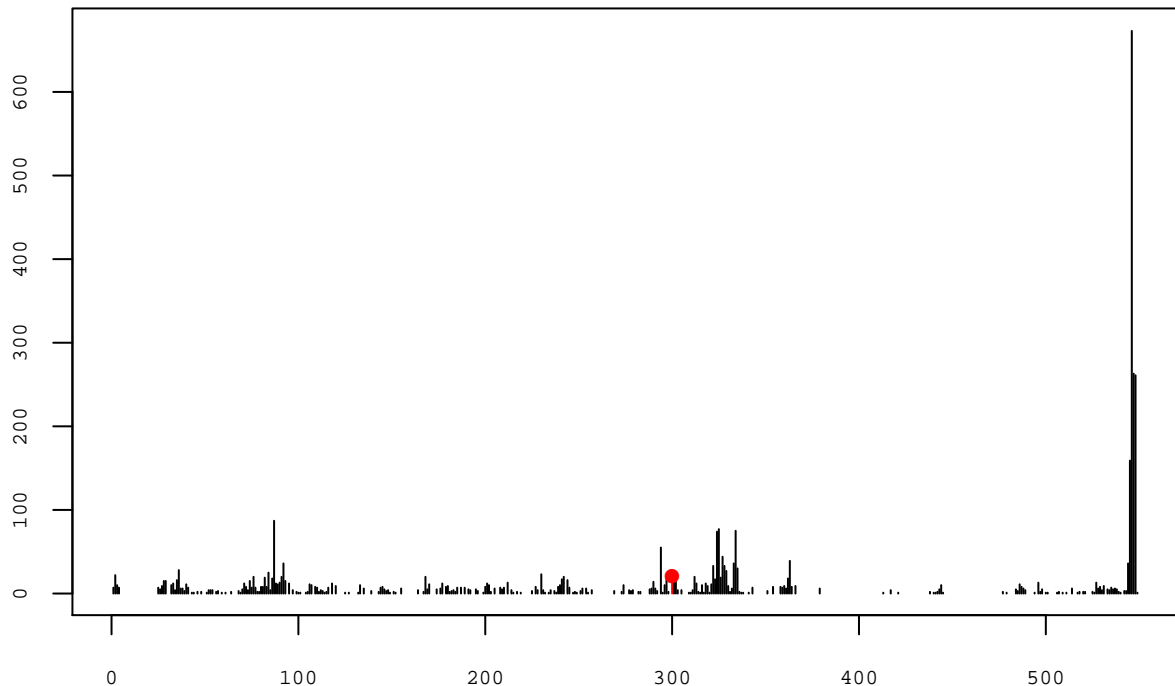


PggD9068_c6_g1_i1

5' GCGGTGTCCGATCCTGACCGTAGATCATGATT '3
||| ||| ||| ||| |o|||
3' CCACAGACTAGGCCTGGCATTAG '5

Fragment Abundance



Transcript position

Cleavage site: 300 Tag abundance: 21 Weighted abundance: 21 Category: 2
sRNA abundance: 108 Alignment score: 4 MFE ratio: 0.767 p-value: 0.042