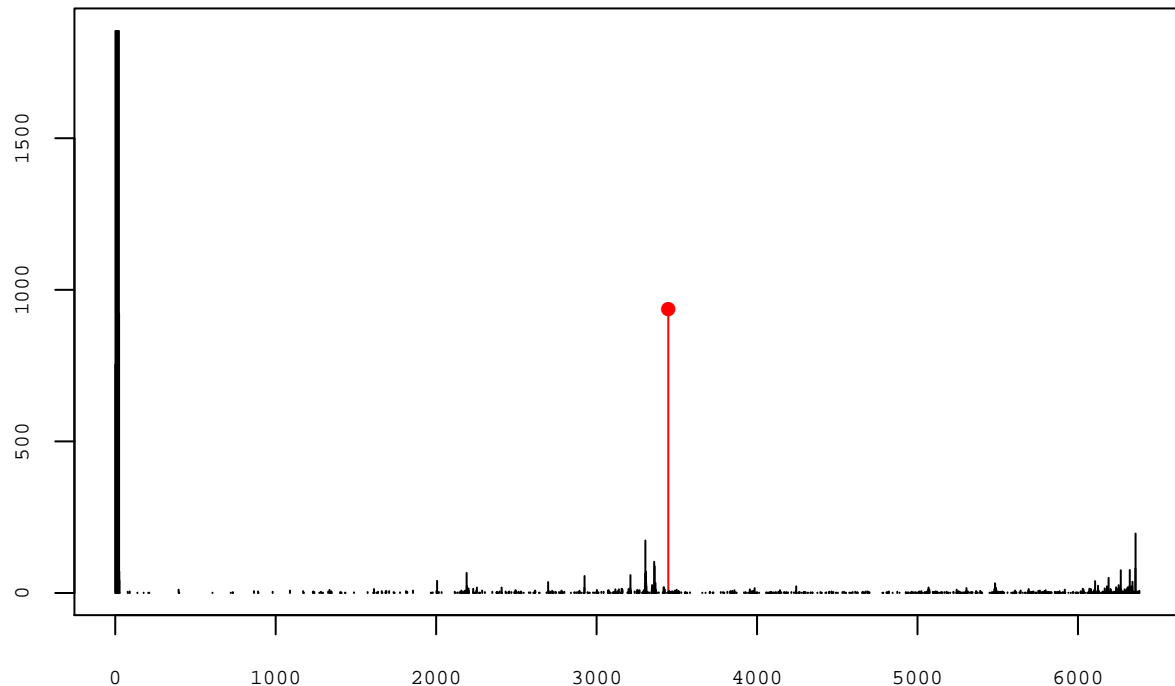


PggD11644_c3_g1_i1

5' ATGAGCTGGATGCAGAGGTCTTATCGATGTCA '3
o|o||||||||| |||||
3' TGGCCTACGTCTCCA-AATAGCT '5

Fragment Abundance



Transcript position

Cleavage site: 3447 Tag abundance: 937 Weighted abundance: 937 Category: 0
sRNA abundance: 1551 Alignment score: 3 MFE ratio: 0.885 p-value: 0