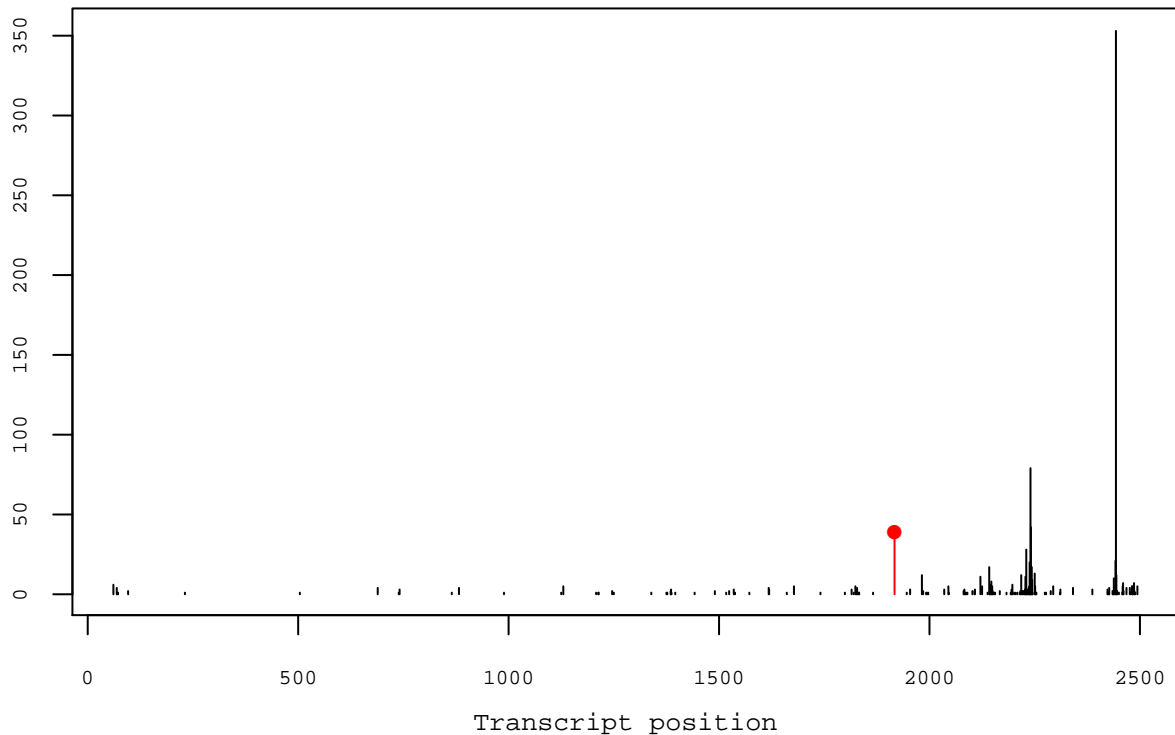


PggD12654_c9_g1_i1

5' CTCTTCTGCAGCATCATCAGGATTCTCAGCCT '3
| | | | | | | | | | | | | | | | | | | |
3' A-ACGTCGTAGTAGTACTAAGA '5

Fragment Abundance



Cleavage site: 1917 Tag abundance: 39 Weighted abundance: 13 Category: 2
sRNA abundance: 20 Alignment score: 3 MFE ratio: 0.863 p-value: 0.042