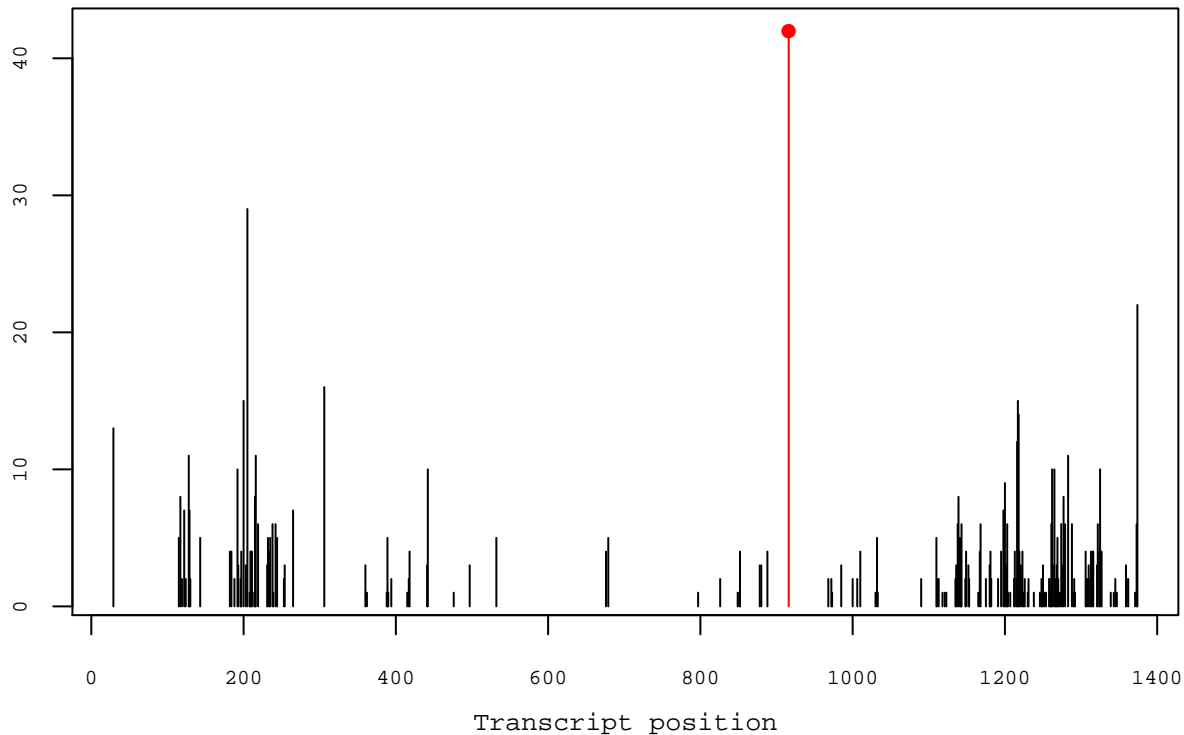


PggD1526_c1_g1_i2

5' CCCAACTCACGTGCCCTGCTTCTCCAATGGTA '3
| | | | | | | | | | | | | | | | | | | | | |
3' TT-GTGCACGGGACGAAGAGGT '5

Fragment Abundance



Cleavage site: 916 Tag abundance: 42 Weighted abundance: 42 Category: 0
sRNA abundance: 13 Alignment score: 2 MFE ratio: 0.95 p-value: 0.005