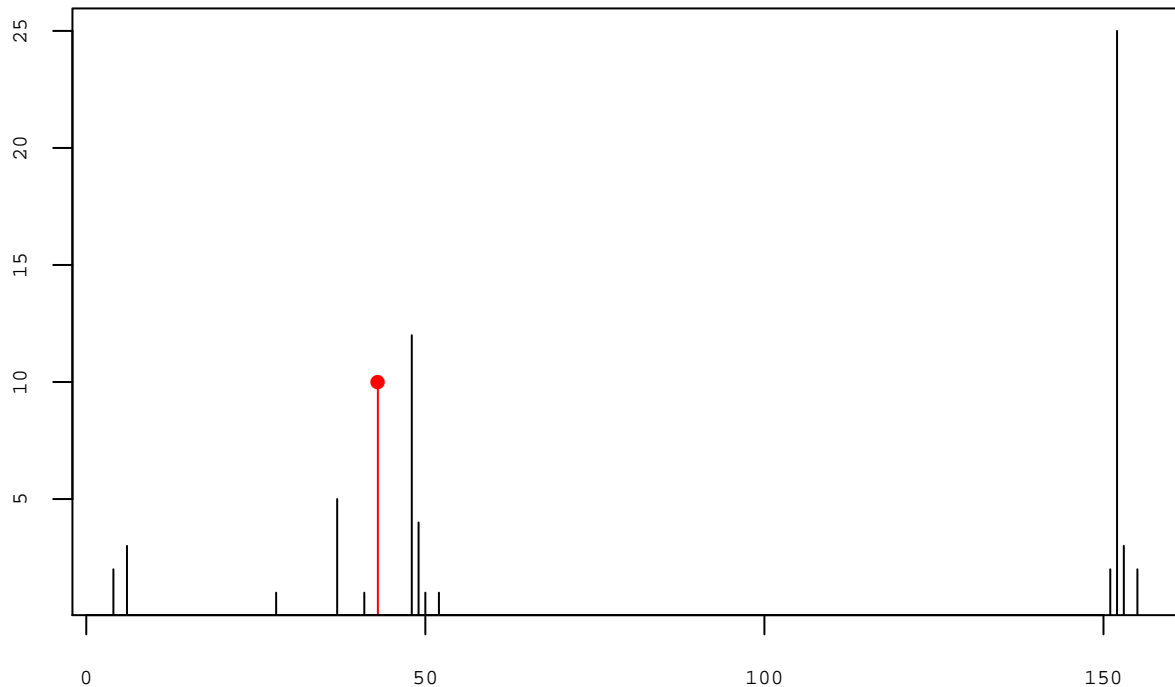


5' TAACTTGGTACGCACGTAGAGTTACGTCAGGA '3
||||| | ||||| | |
3' TGAACCAGACGTGCATCTCGATGC '5

Fragment Abundance



Transcript position

Cleavage site: 43 Tag abundance: 10 Weighted abundance: 10 Category: 2
sRNA abundance: 7 Alignment score: 3 MFE ratio: 0.776 p-value: 0.006