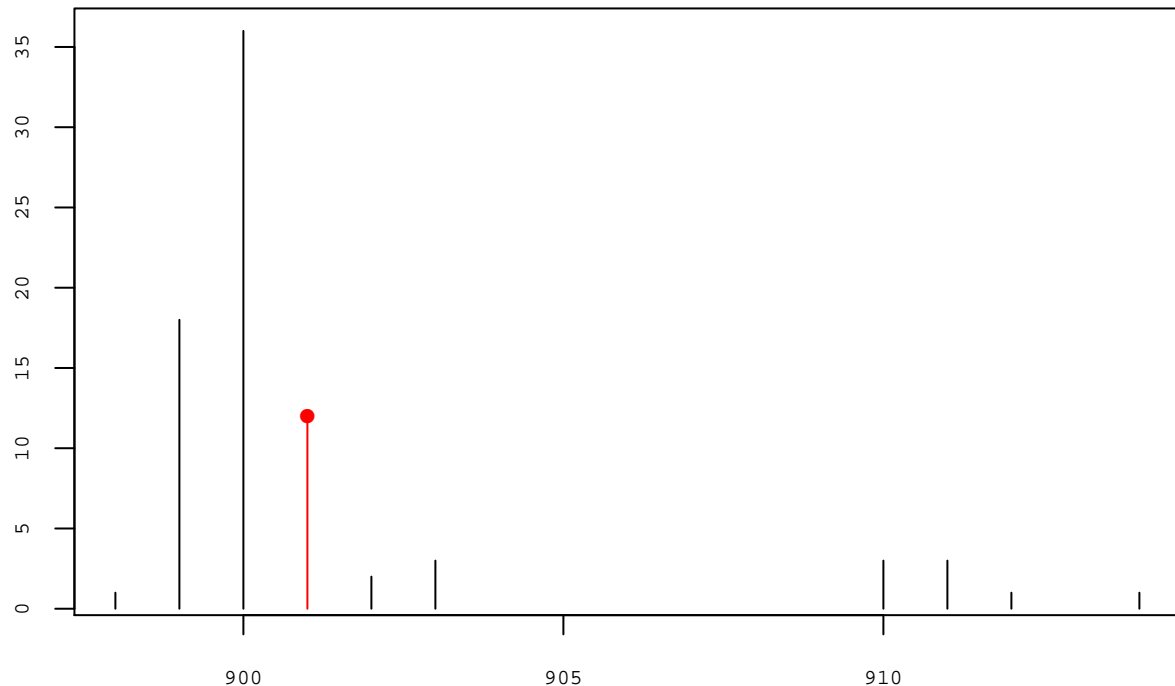


5' CGGCTCGTGTTGGGCTCGTTAAG-AAGCTCGTG '3
 ||||| | |o| ||||| ||
 3' CGAGCACAAGCTGAGCAATTCGTT '5

Fragment Abundance



Transcript position

Cleavage site: 901

sRNA abundance: 22

Tag abundance: 12

Alignment score: 4

Weighted abundance: 0.983

MFE ratio: 0.794

Category: 2

p-value: 0.026