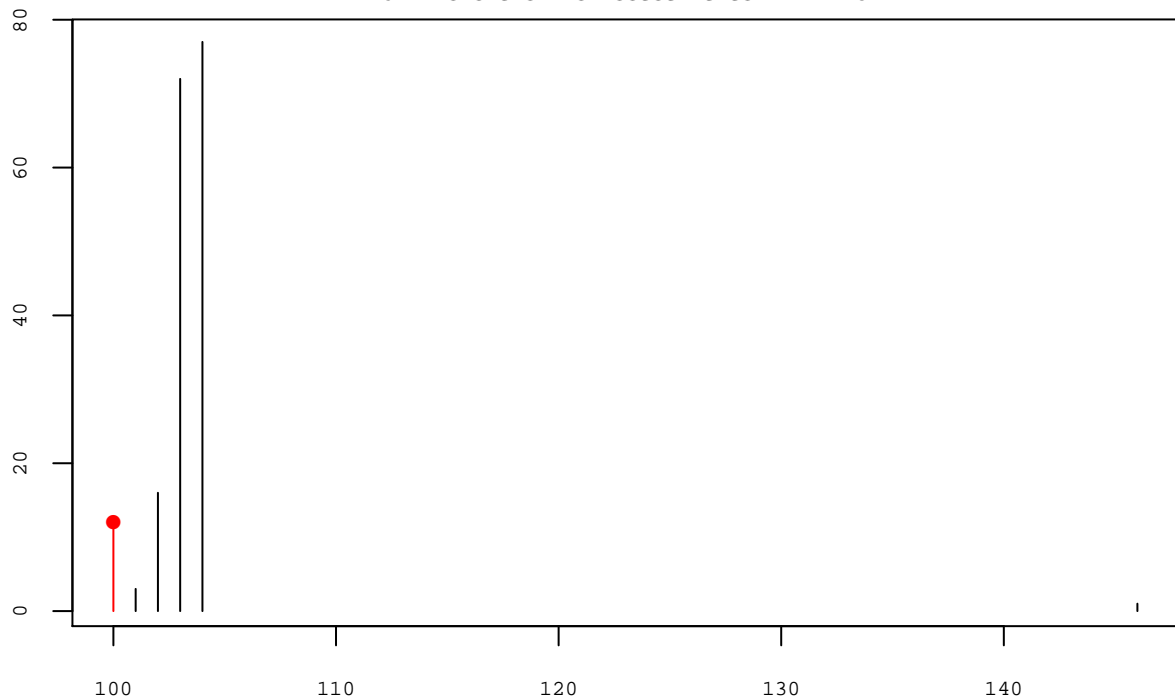


5' GCTGCTGTCATACAGTCGCGATGTGCGGCTGT '3

oo|||||||oo|||||||

3' GTGACAGTATGTTGGCGCTACACG '5

Fragment Abundance



Transcript position

Cleavage site: 100

Tag abundance: 12

Weighted abundance: 3.917

Category: 3

sRNA abundance: 45

Alignment score: 3

MFE ratio: 0.845

p-value: 0.024