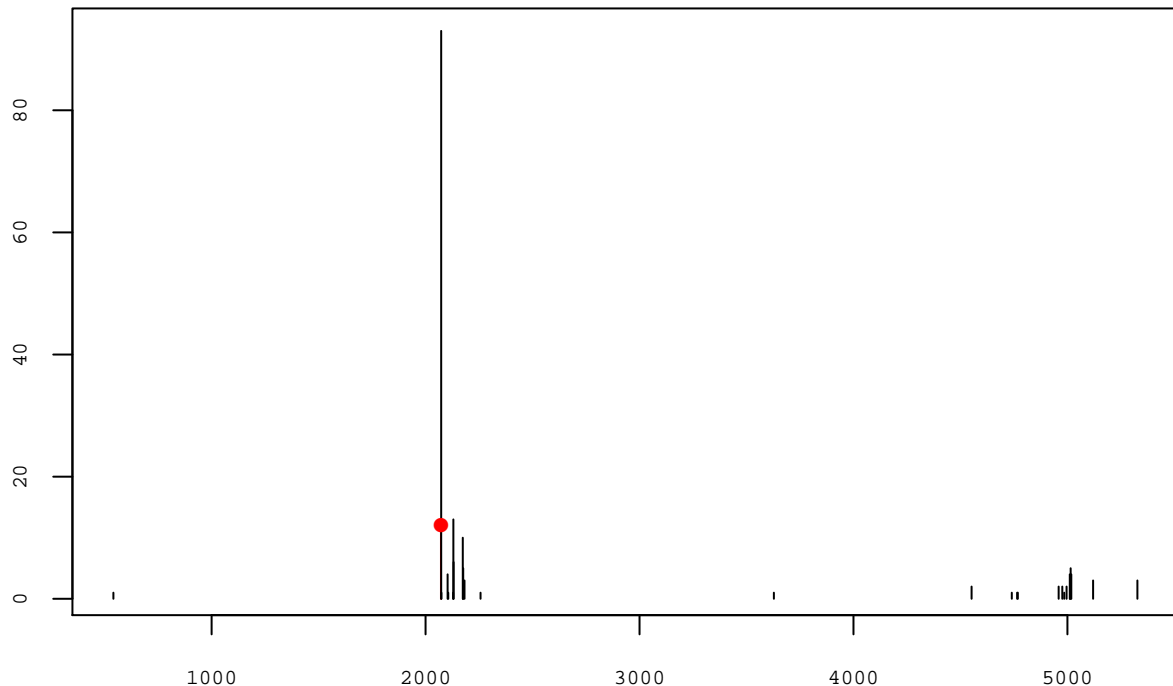


5' ACGAACAAAAAGTCCTACATTGGCTAGGTGTA '3  
| | | | | | | | | | o | | | | o | | | |  
3' CCTGTTTTTCAGGGTGTAGCCGAT '5

Fragment Abundance



Transcript position

Cleavage site: 2072

Tag abundance: 12

Weighted abundance: 0.238

Category: 2

sRNA abundance: 427

Alignment score: 3

MFE ratio: 0.779

p-value: 0.026