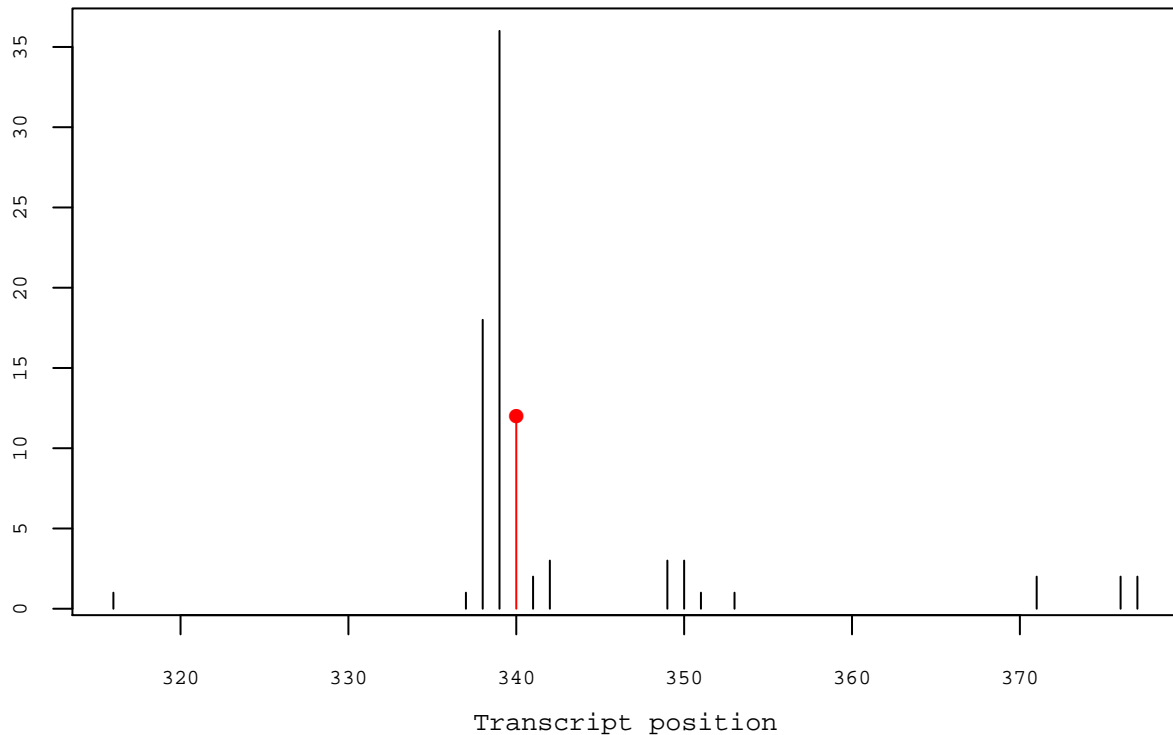


PggD8965_c122_g1_i1

5' CAGCTCGTGTTCCGCTCGTTAAG-AAGCTCGTG '3
||||| ||| ||| |
3' CGAGCACAAGCCGAGCAATTGTT '5

Fragment Abundance



Cleavage site: 340

sRNA abundance: 9

Tag abundance: 12

Alignment score: 4

Weighted abundance: 0.983

MFE ratio: 0.74

Category: 2

p-value: 0.047