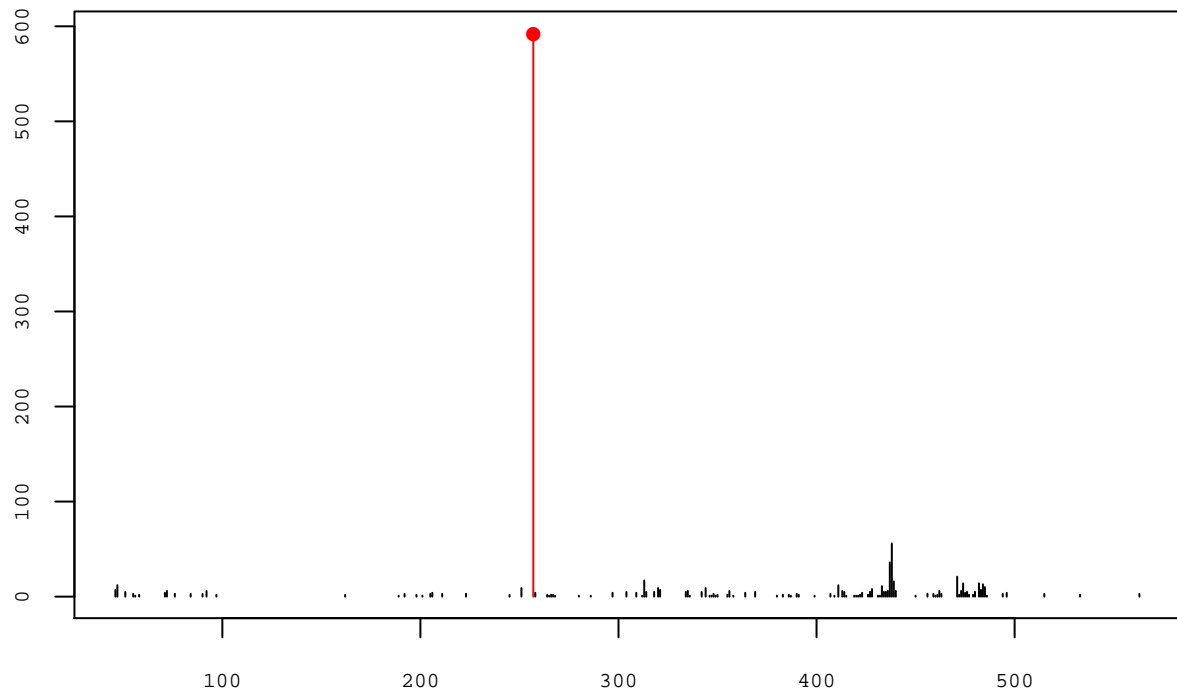


PggD10737_c261_g1_i1

5' GAGAGATCACGTGCCCTGCTTCTCCACATCCG 3'

|||||
3' CGTGCACGGGACGAAGAGGT 5'

Fragment Abundance



Transcript position

Cleavage site: 257 Tag abundance: 592 Weighted abundance: 296 Category: 0
sRNA abundance: 74 Alignment score: 1 MFE ratio: 0.932 p-value: 0.009