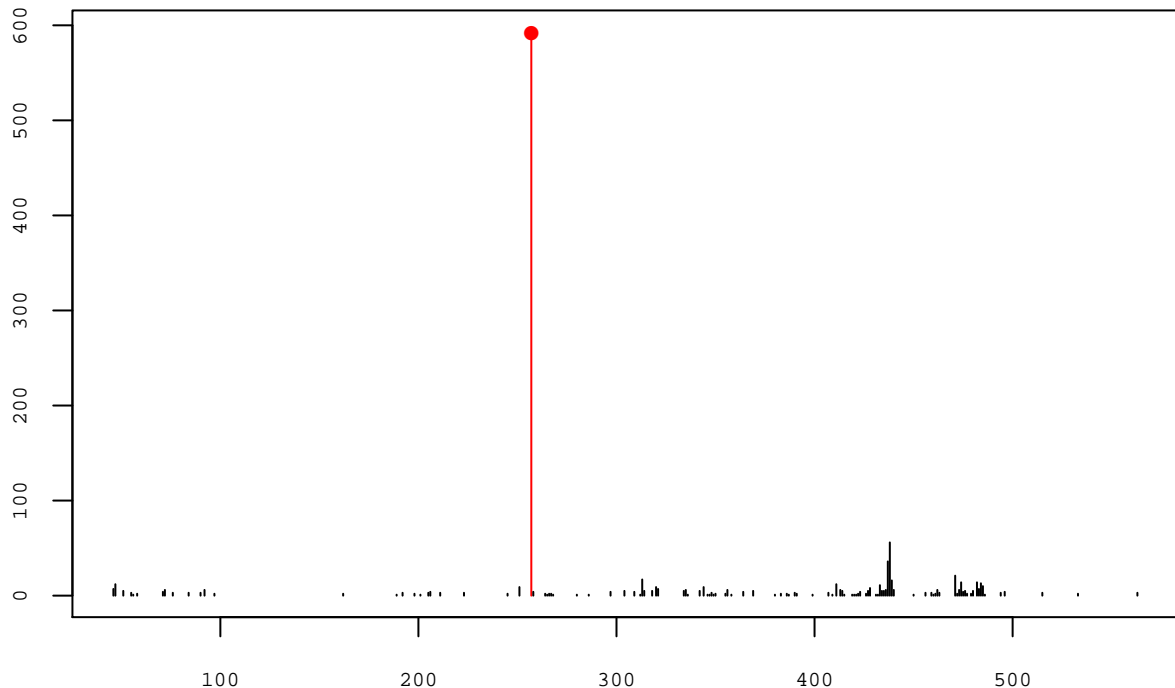


PggD10737\_c261\_g1\_i1

5' GAGAGATCACGTGCCCTGCTTCTCCACATCCG '3  
|||  
3' ACGTGCACGGGACGAAGAGGT '5

Fragment Abundance



Transcript position

Cleavage site: 257 Tag abundance: 592 Weighted abundance: 296 Category: 0  
sRNA abundance: 412 Alignment score: 2 MFE ratio: 0.898 p-value: 0.009