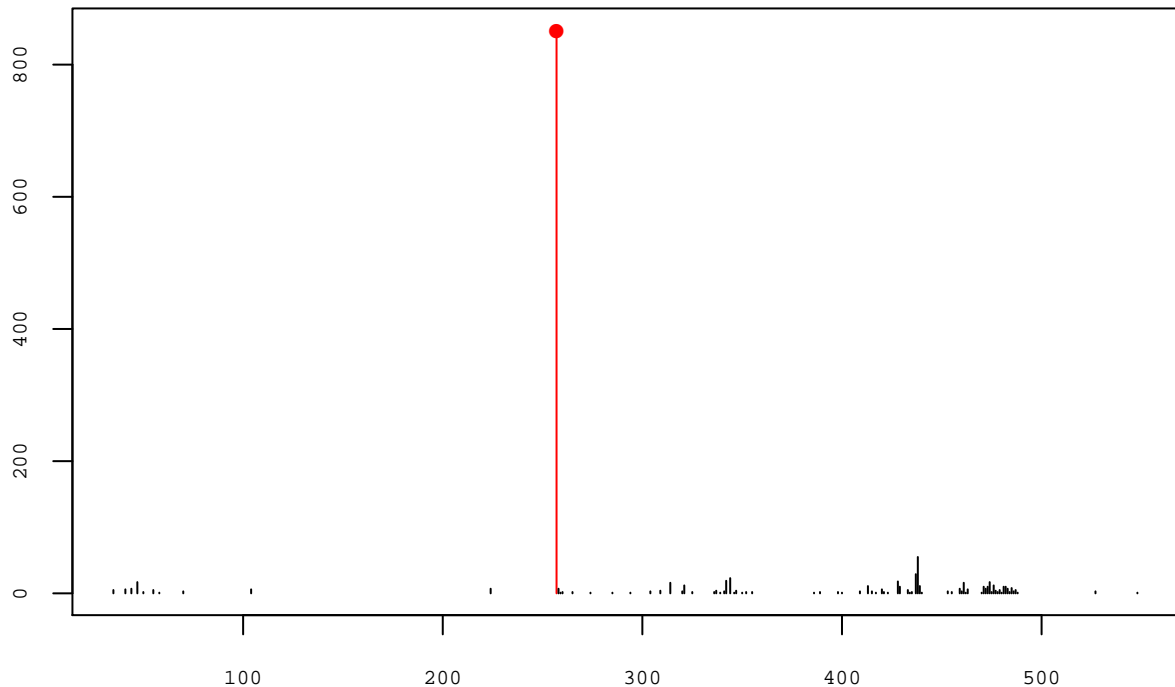


PggD10737\_c261\_g1\_i1

5' GAGAGATCACGTGCCCTGCTTCTCCACATCCG '3  
| | | | | | | | | | | | | | | | | | | | | |  
3' TTGTGCACGGGACGAAGAGGT '5

Fragment Abundance



Transcript position

Cleavage site: 257	Tag abundance: 851	Weighted abundance: 425.5	Category: 0
sRNA abundance: 13	Alignment score: 1	MFE ratio: 0.955	p-value: 0.003