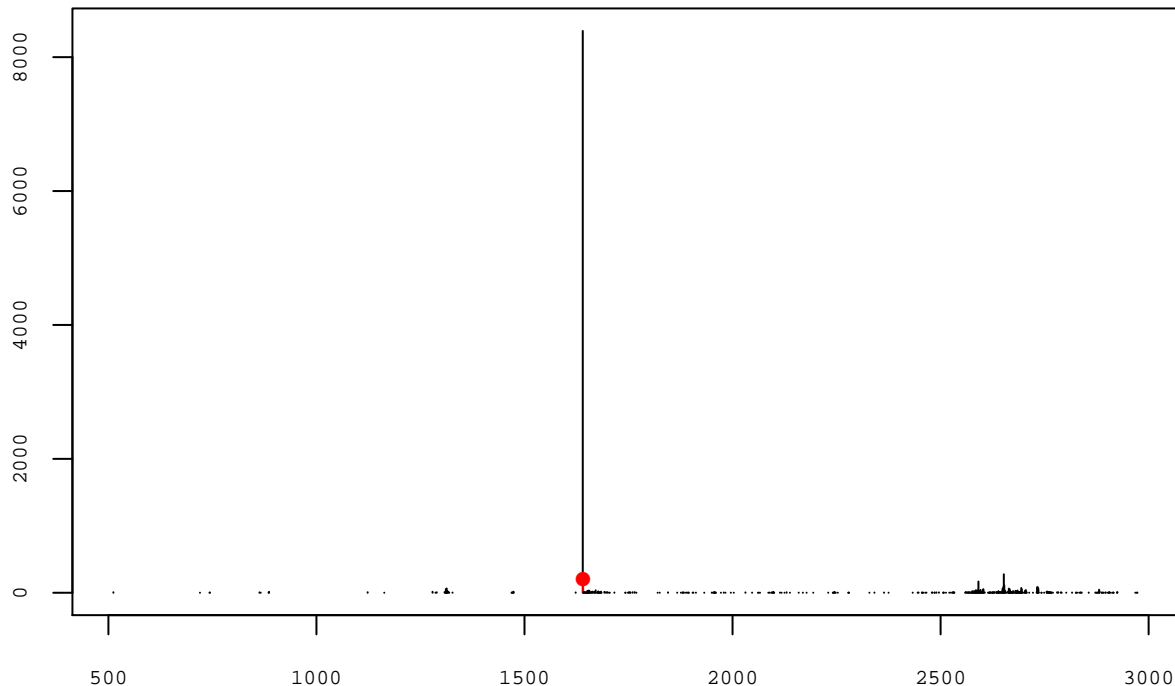


PggD1242_c13_g1_i2

5' CAGCTAGCATACAGGGAGCCAGGCAAATTCTA '3
|||||
3' CCGTATGTCCCTCGGTCCGTA '5

Fragment Abundance



Transcript position

Cleavage site: 1641	Tag abundance: 205	Weighted abundance: 102.5	Category: 2
sRNA abundance: 5	Alignment score: 2	MFE ratio: 0.942	p-value: 0.02