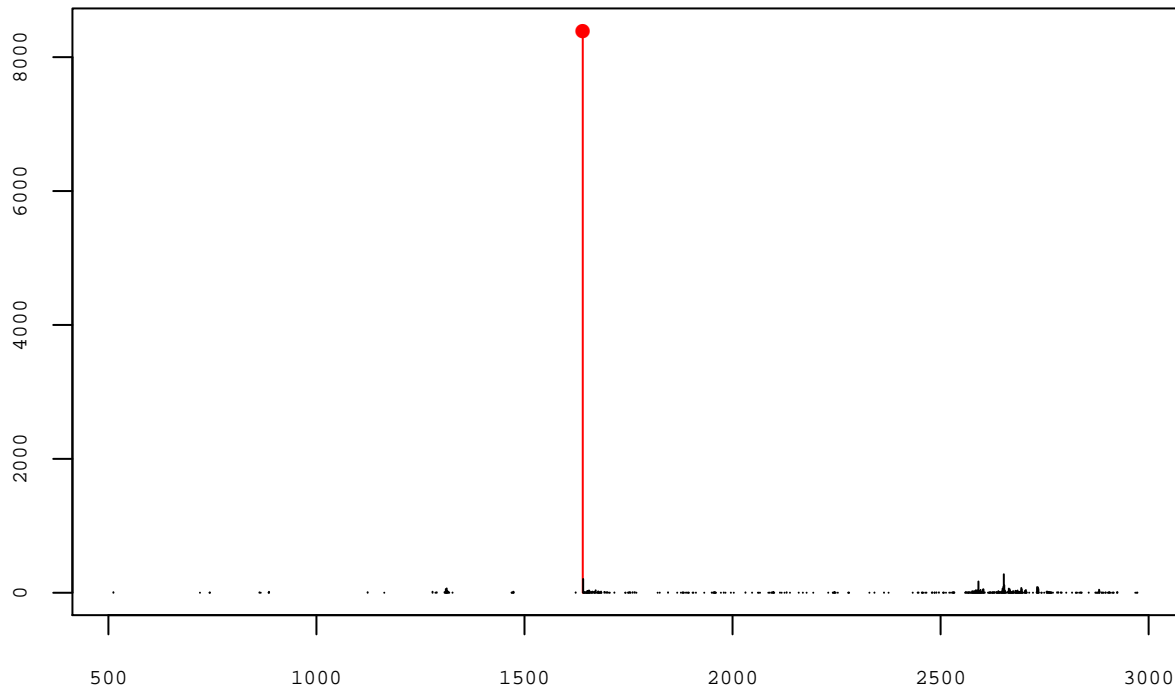


PggD1242_c13_g1_i2

5' GCAGCTAGCATAACAGGGAGCCAGGCAAATTCT 3'
|||||
3' CCGTATGTCCCTCGGTCCGT 5'

Fragment Abundance



Transcript position

Cleavage site: 1640	Tag abundance: 8392	Weighted abundance: 4196	Category: 0
sRNA abundance: 48	Alignment score: 1	MFE ratio: 0.947	p-value: 0.001