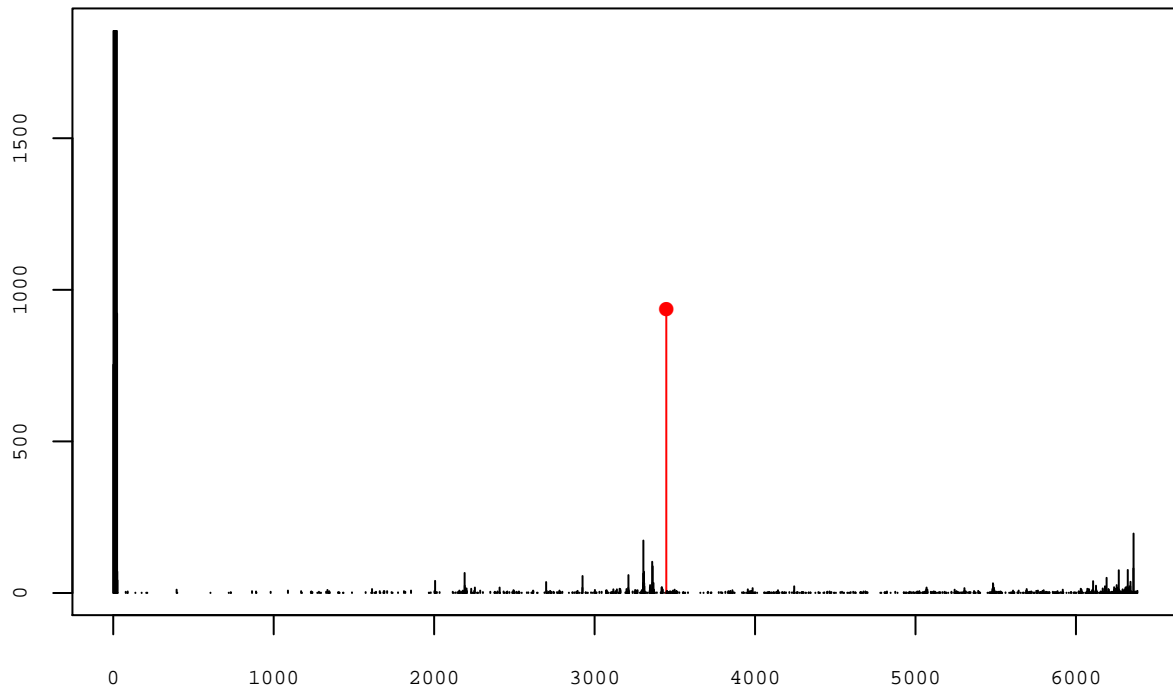


PggD11644\_c3\_g1\_i1

5' ATGAGCTGGATGCAGAGGTCTTATCGATGTCA '3  
|o||||||||| |||||  
3' GGCCTACGTCTCCA-AATAGCT '5

Fragment Abundance



Transcript position

Cleavage site: 3447	Tag abundance: 937	Weighted abundance: 937	Category: 0
sRNA abundance: 3445	Alignment score: 2.5	MFE ratio: 0.872	p-value: 0