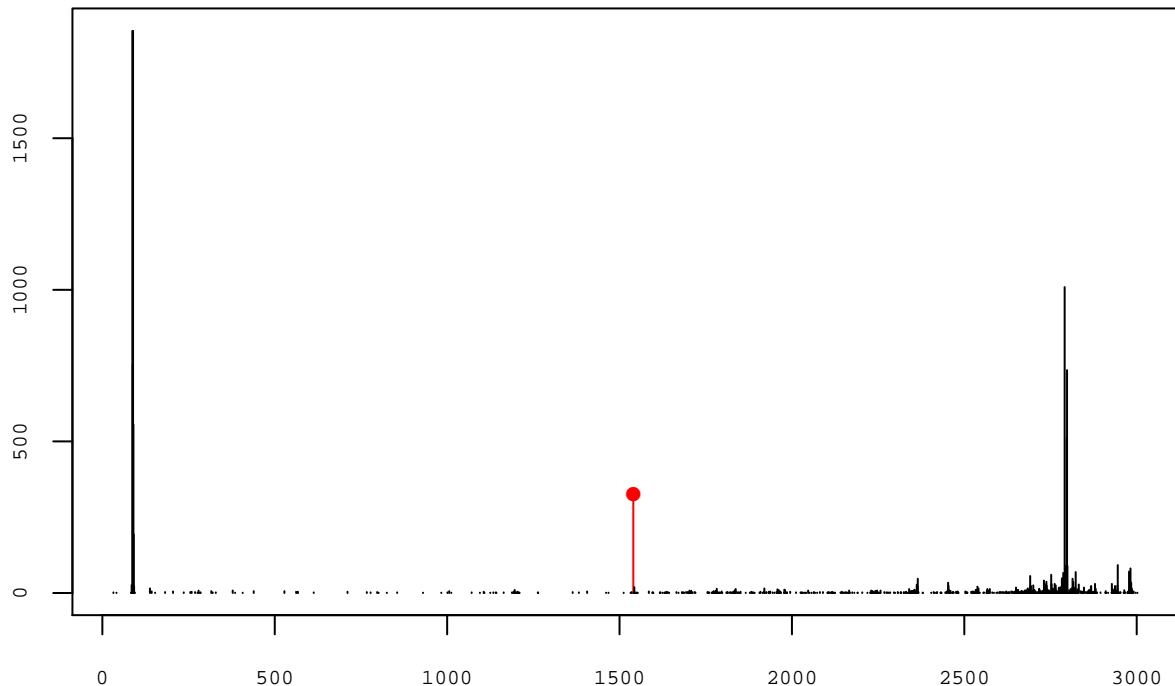


PggD3876\_c10\_g1\_i1

5' GCGCATGG-GATATTGGCGCGGCTCAATCACCA '3  
|| |||||o|||||||  
3' CCTCTATAACTGCGCCGAGTT '5

Fragment Abundance



Transcript position

Cleavage site: 1540	Tag abundance: 326	Weighted abundance: 268.5	Category: 2
sRNA abundance: 102	Alignment score: 2	MFE ratio: 0.857	p-value: 0.043