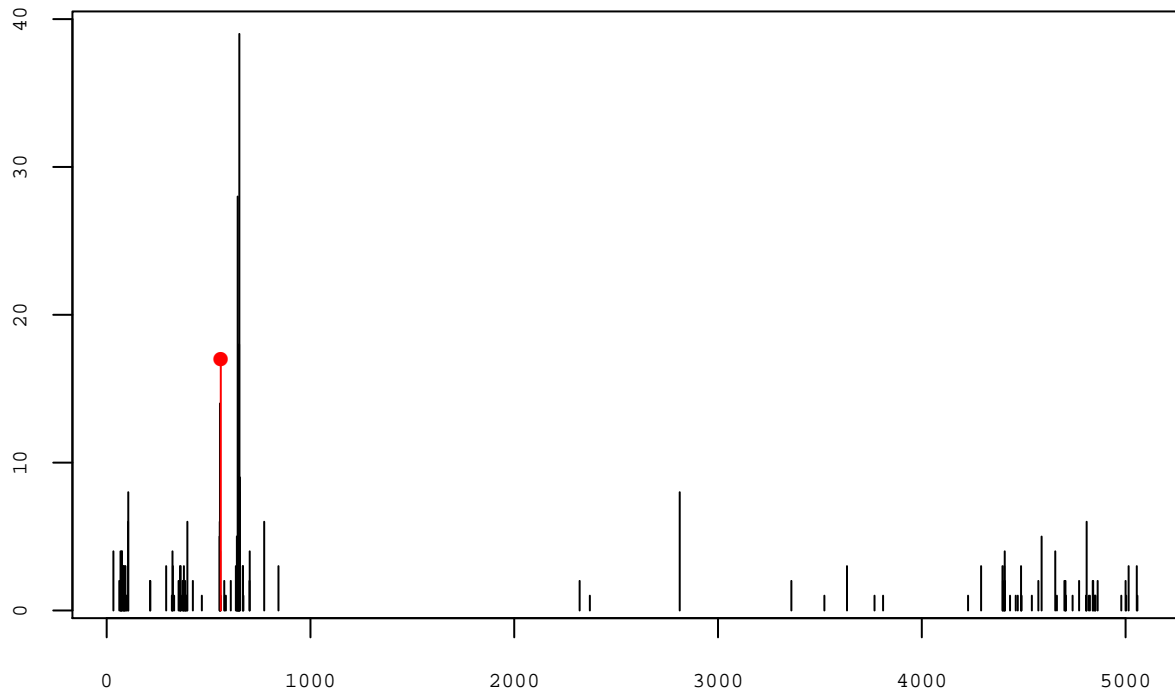


PggD10279_c62_g1_i3

5' AATGCAT-CGGTGTCCGATCCTGACCGTAGATC '3
||| ||||| ||||| ||||| |||||
3' CGTACGCCACAGGCTAAGACTGGC '5

Fragment Abundance



Transcript position

Cleavage site: 560	Tag abundance: 17	Weighted abundance: 5.667	Category: 2
sRNA abundance: 8	Alignment score: 3	MFE ratio: 0.774	p-value: 0.016