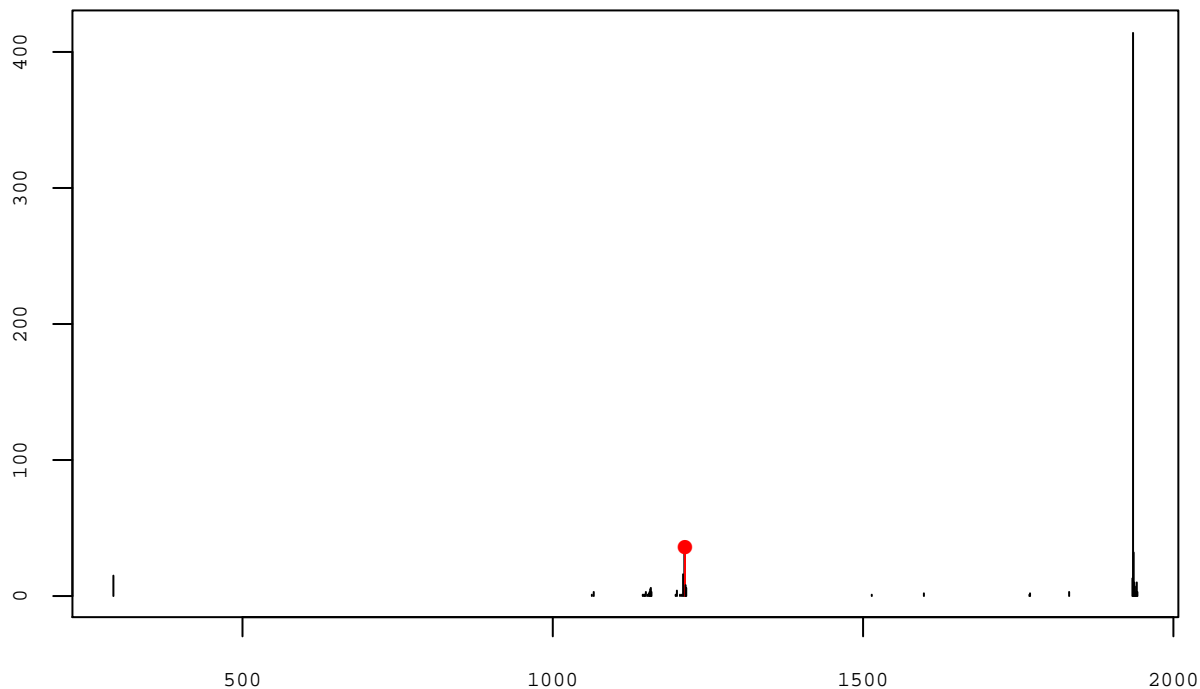


PggD15095\_c245\_g1\_i1

5' ACGTAGAGCTACGTCAGGAGTCCGGACAGAAA '3

||||| ||||| ||||| |||||  
3' ATCTCCATGCAGTCCACAGGCCT '5

Fragment Abundance



Transcript position

Cleavage site: 1213 Tag abundance: 36 Weighted abundance: 18 Category: 2  
sRNA abundance: 6 Alignment score: 3 MFE ratio: 0.745 p-value: 0.001