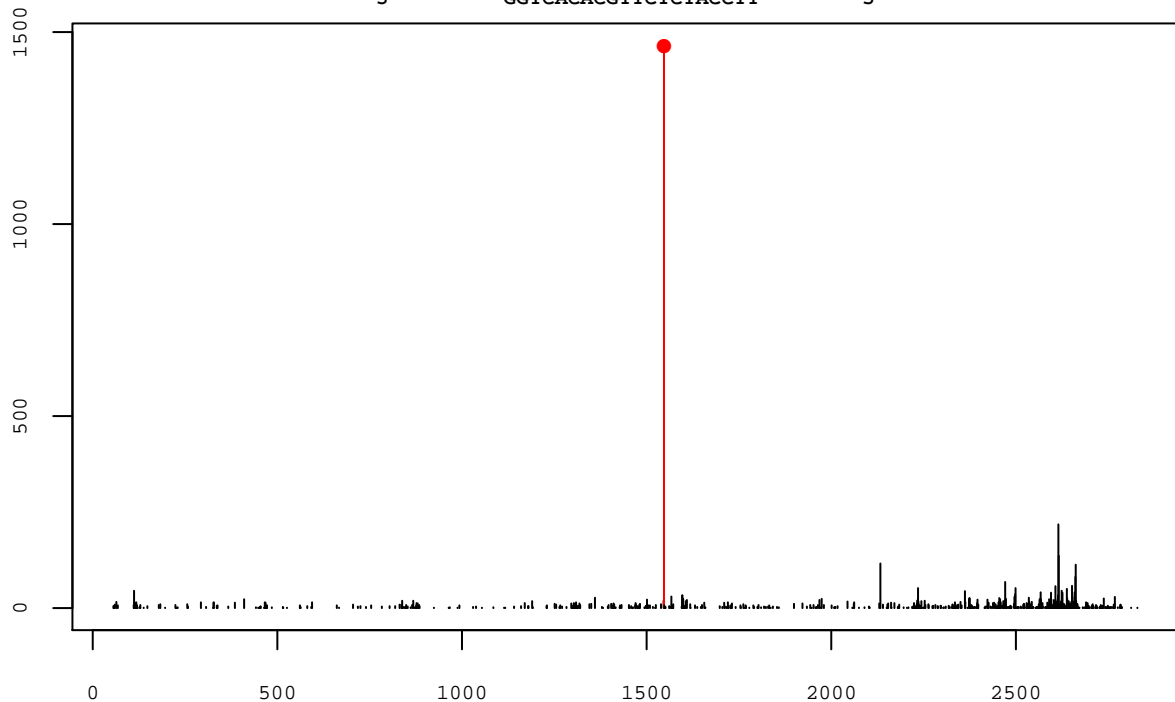


PggD4130\_c0\_g1\_i1

5' GTTCCCTCCAGTA-GCAAGAGATGGACAGATGG '3  
||||| |||||  
3' GGTACACGTTCTCTACCTT '5

Fragment Abundance



Transcript position

Cleavage site: 1547 Tag abundance: 1464 Weighted abundance: 732 Category: 0  
sRNA abundance: 69 Alignment score: 3 MFE ratio: 0.753 p-value: 0.001