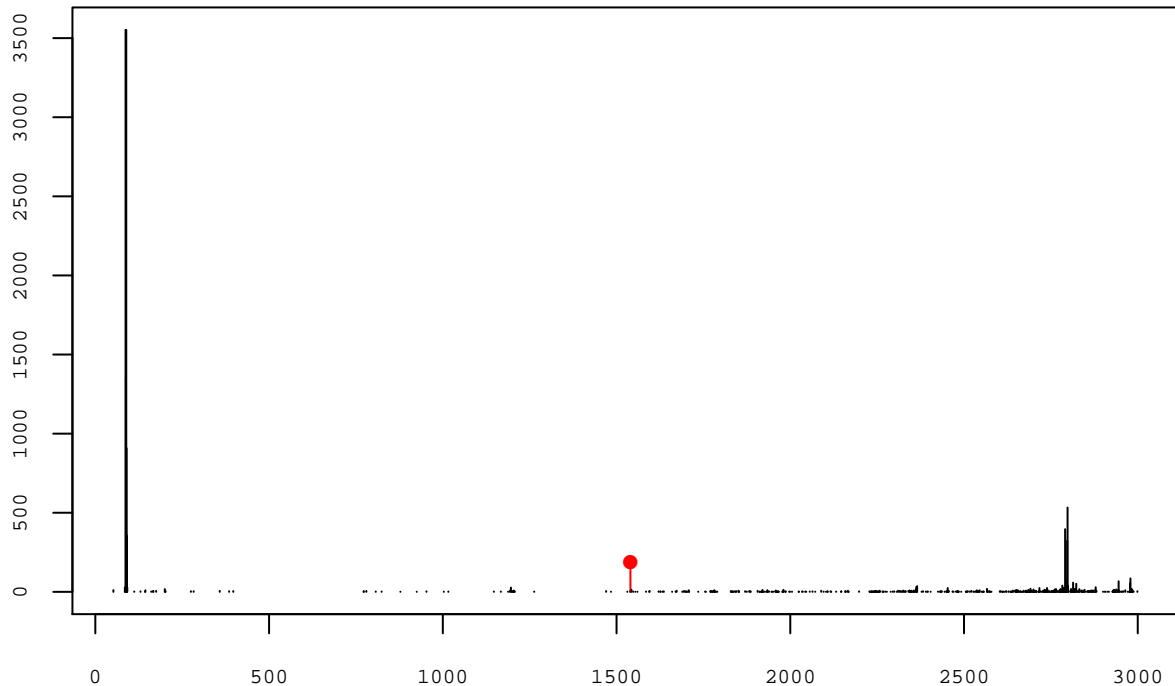


PggD3876\_c10\_g1\_i1

5' GCGCATGG-GATATTGGCGCGGCTCAATCACCA '3

|| |||||o|||||||  
3' CCTCTATAACTGCGCCGAGTT '5

Fragment Abundance



Transcript position

Cleavage site: 1540    Tag abundance: 190    Weighted abundance: 157    Category: 2  
sRNA abundance: 56    Alignment score: 2    MFE ratio: 0.857    p-value: 0.036