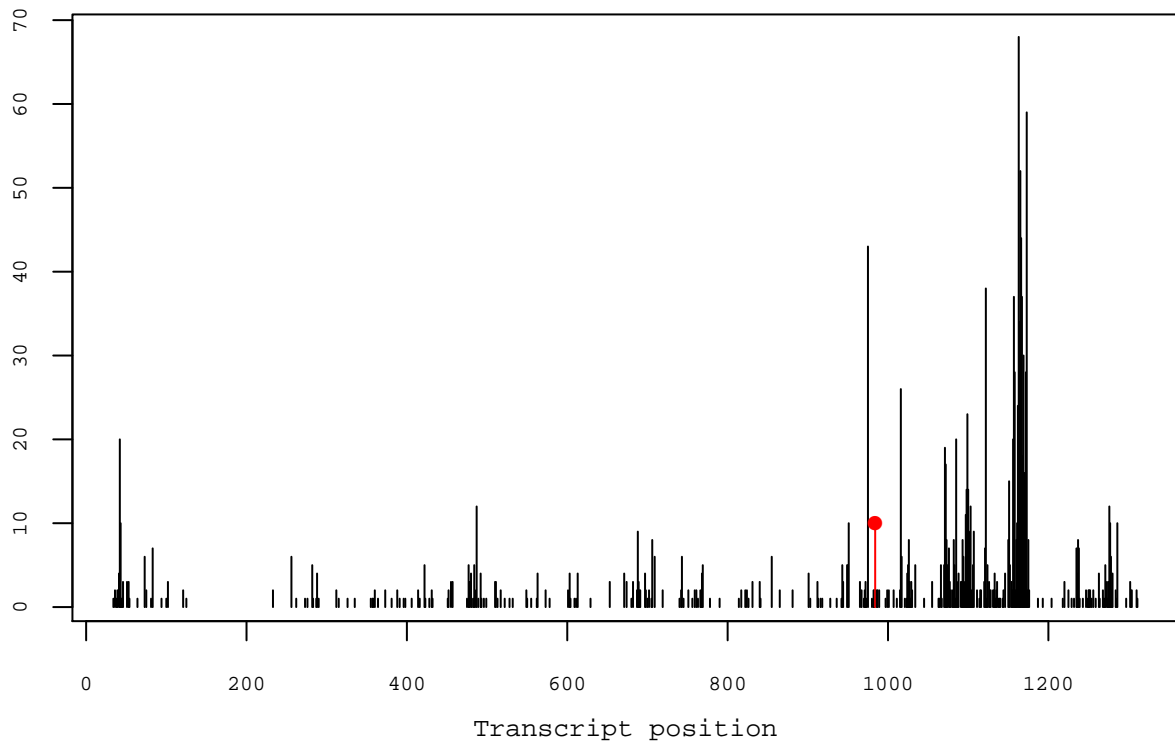


PggD3714\_c28\_g1\_i2

5' TGACTTCAAATAATGCCGAAATAACTCTGCAA '3  
|||o|||||o|||||||  
3' TGAGGTTTATTGCGGCTTTATTGA '5

Fragment Abundance



Cleavage site: 984 Tag abundance: 10 Weighted abundance: 10 Category: 2  
sRNA abundance: 8 Alignment score: 1.5 MFE ratio: 0.875 p-value: 0.036