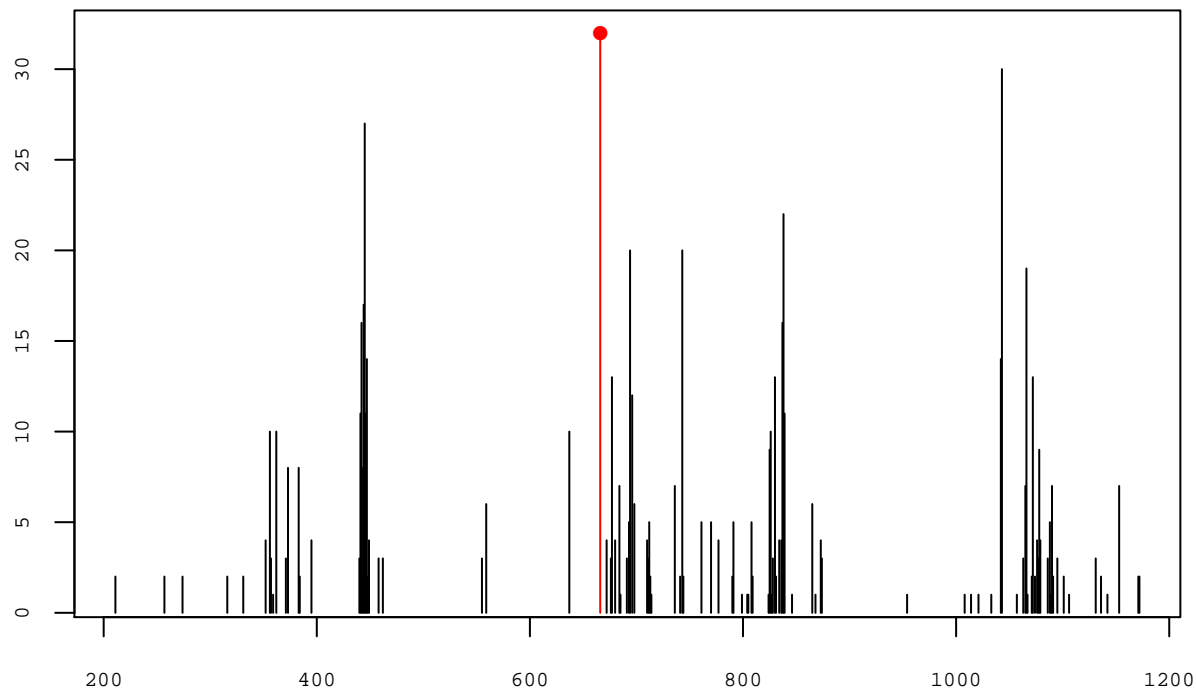


PggD10990_c1_g1_i1

5' GAAATGGAAGCTGCCTTCATTCCAAATGTCAA '3

3' C-TCGAGGGAAGTTAGGTTT '5

Fragment Abundance



Transcript position

Cleavage site: 666

sRNA abundance: 738

Tag abundance: 32

Alignment score: 4

Weighted abundance: 5.333

MFE ratio: 0.711

Category: 0

p-value: 0.036