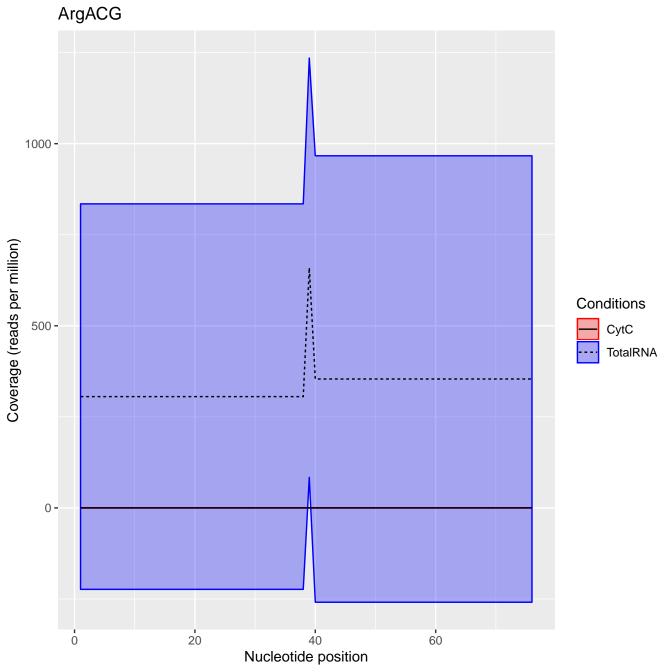
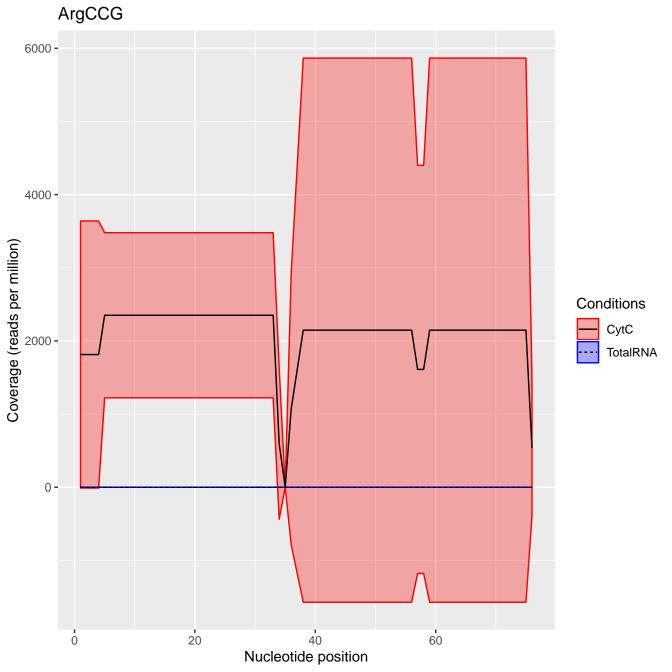
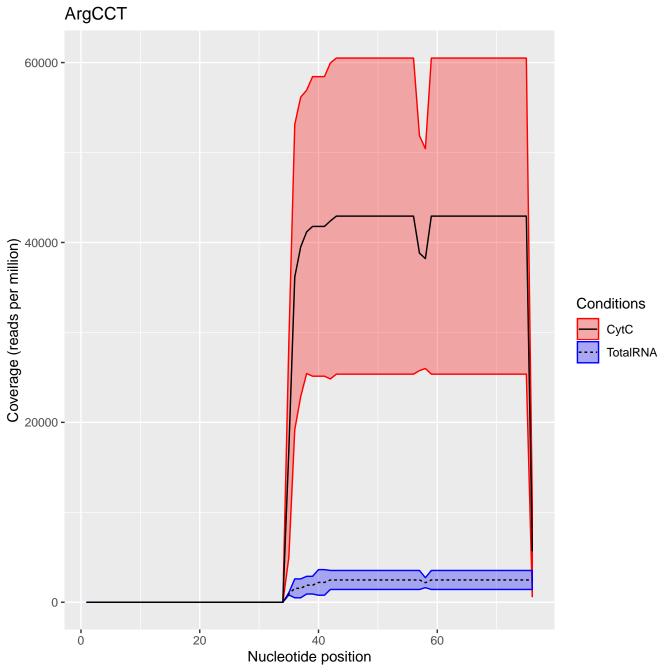
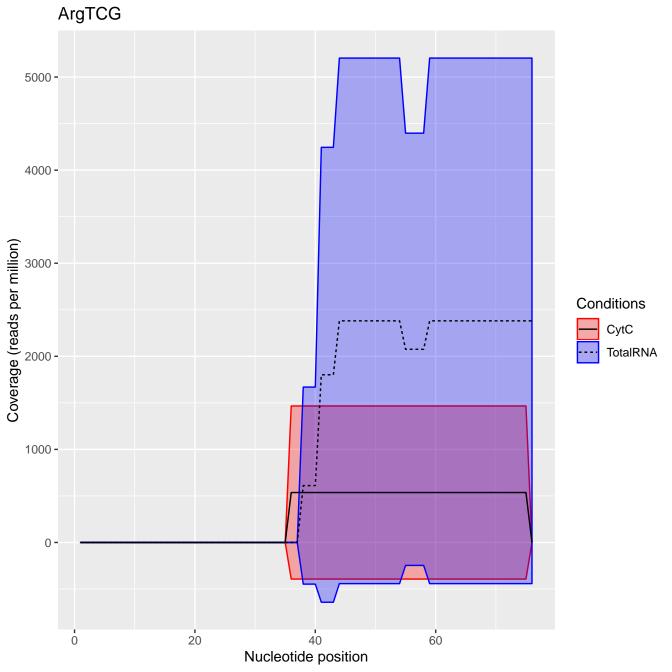


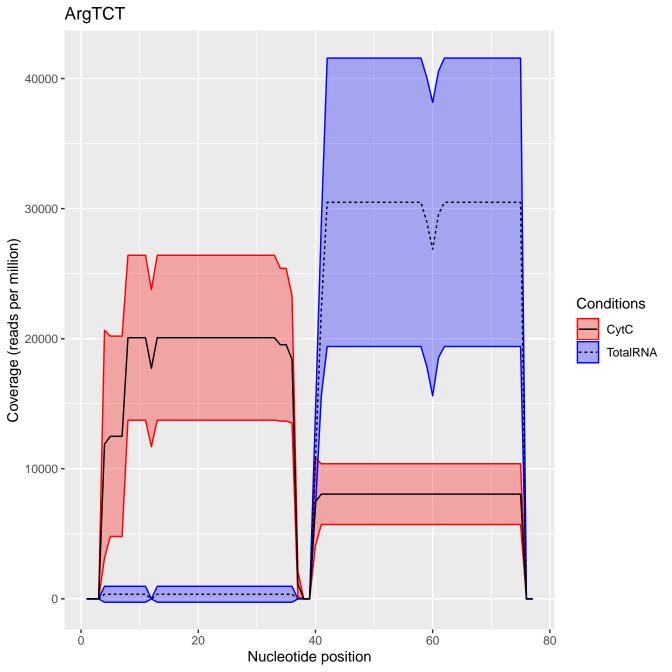
Arg (plot of multi-mapping reads where isoacceptor could not be identified) 3000 -Coverage (reads per million) Conditions CytC TotalRNA 0 -25 50 75 0 Nucleotide position

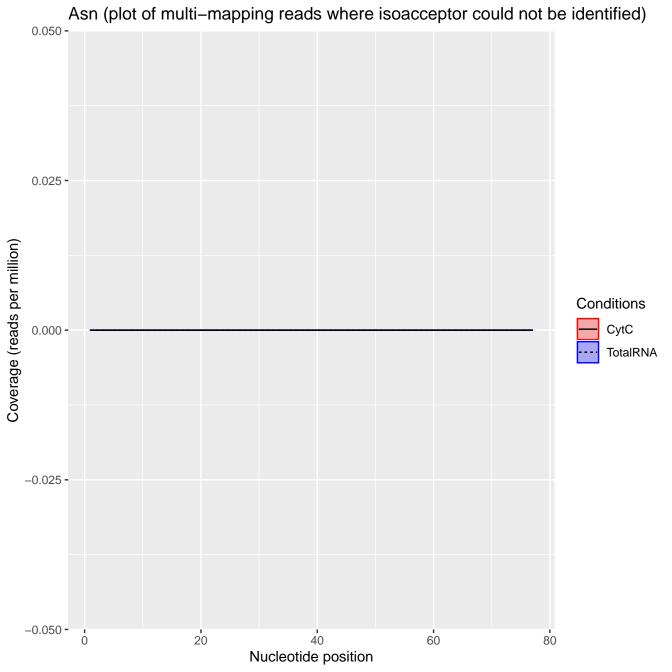


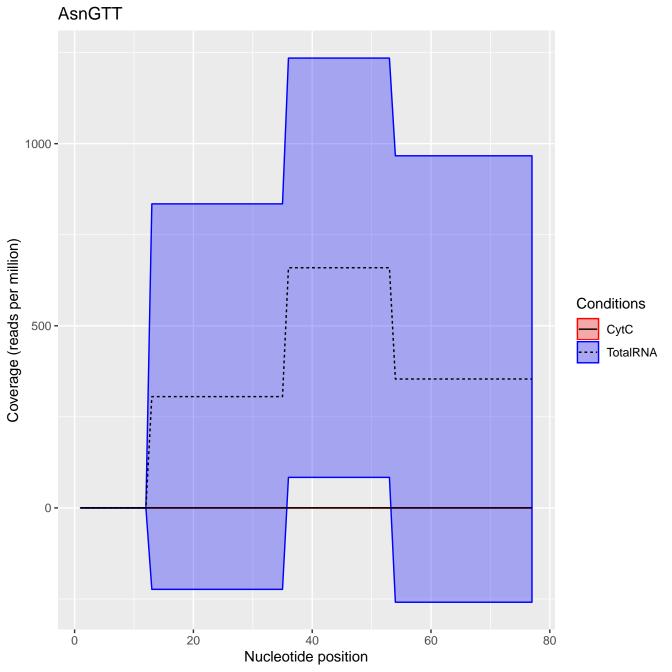


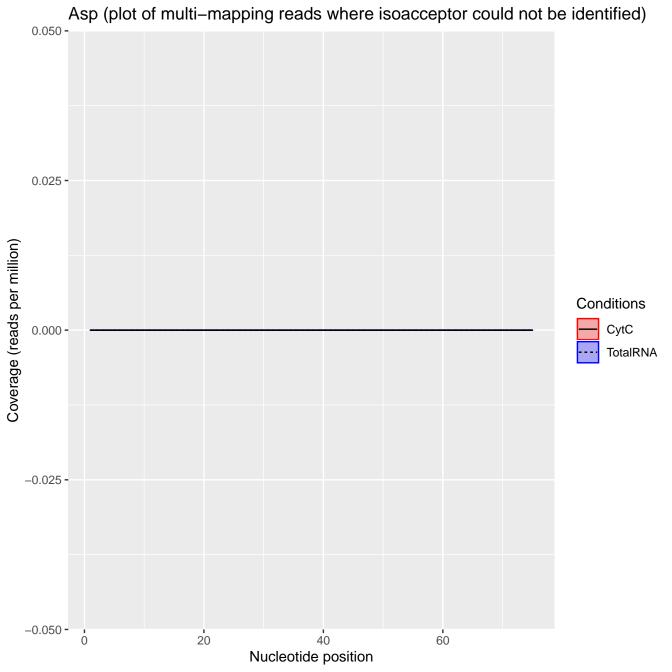


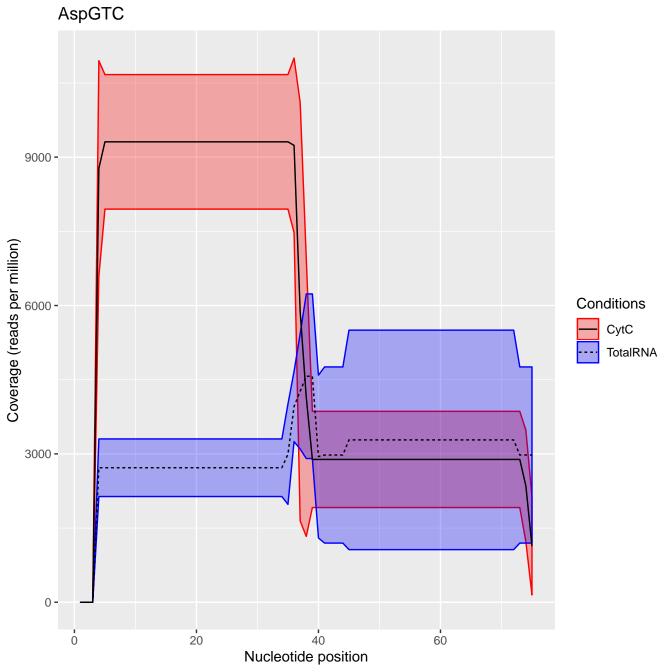


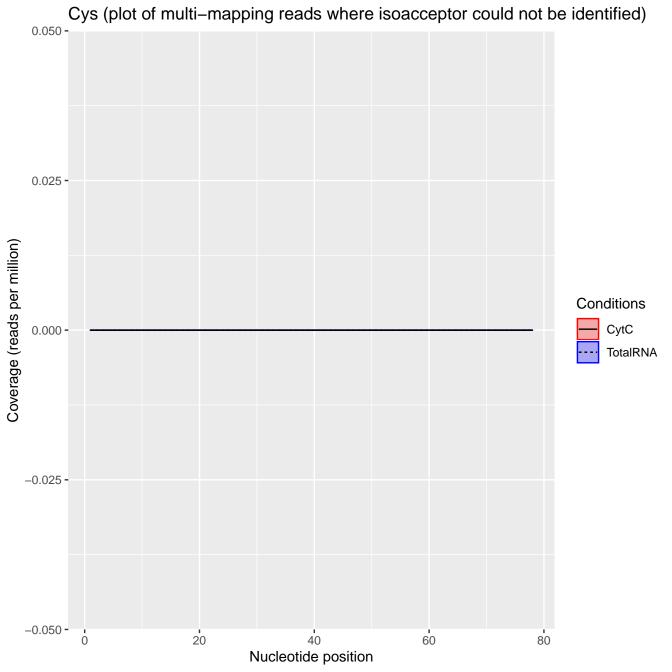


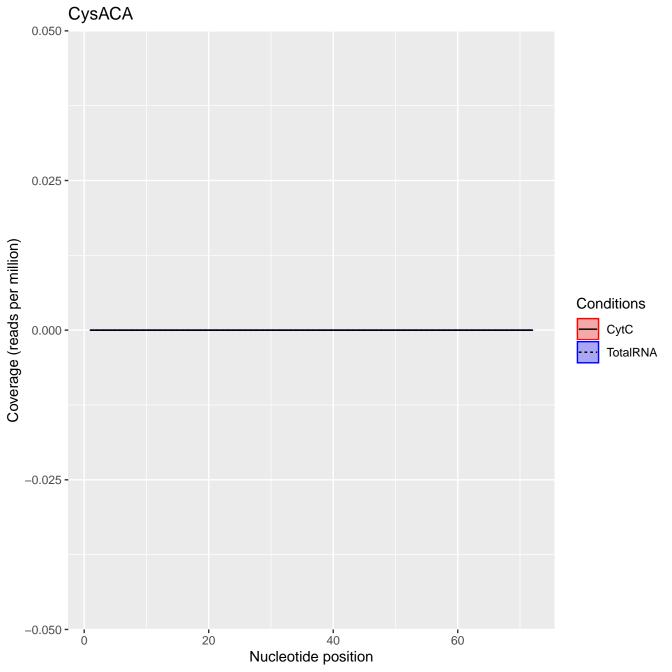


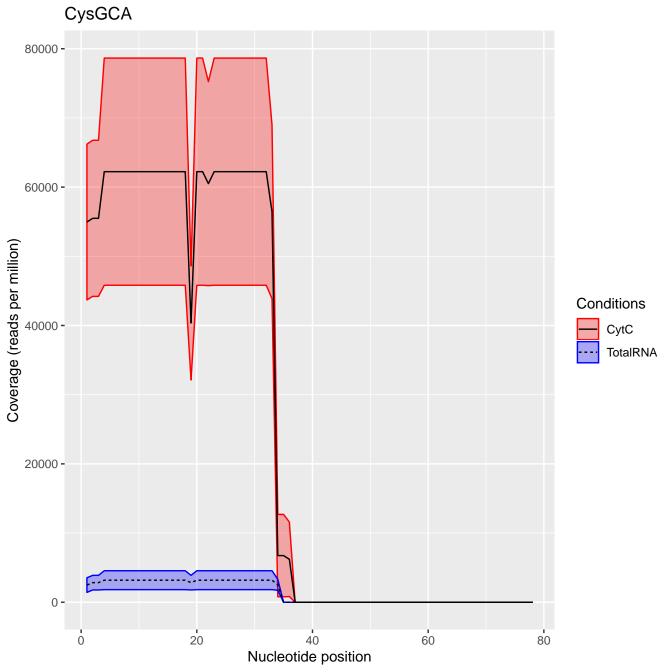


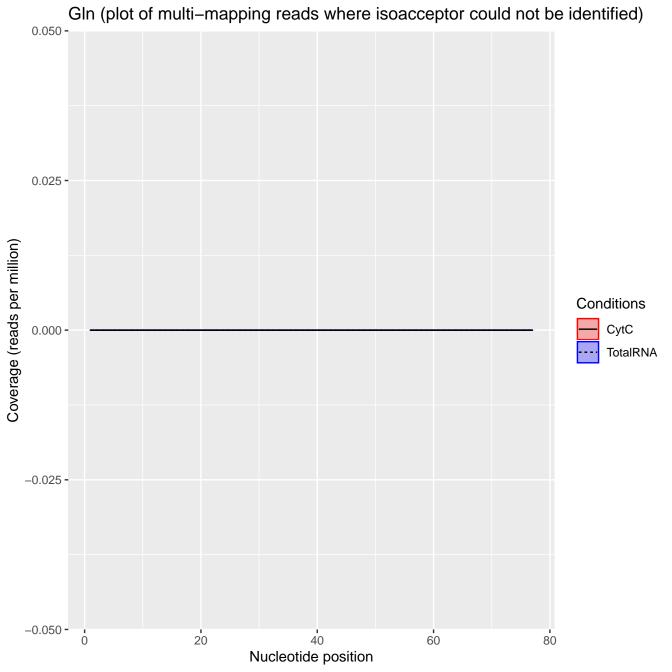


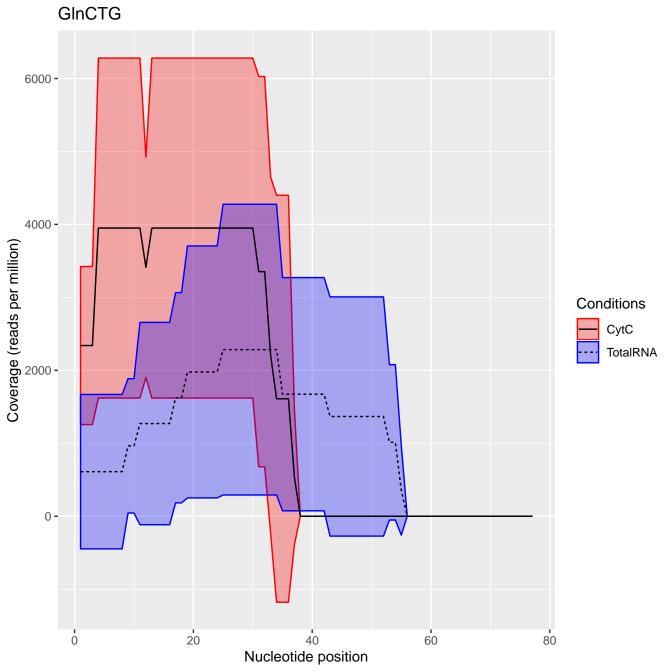


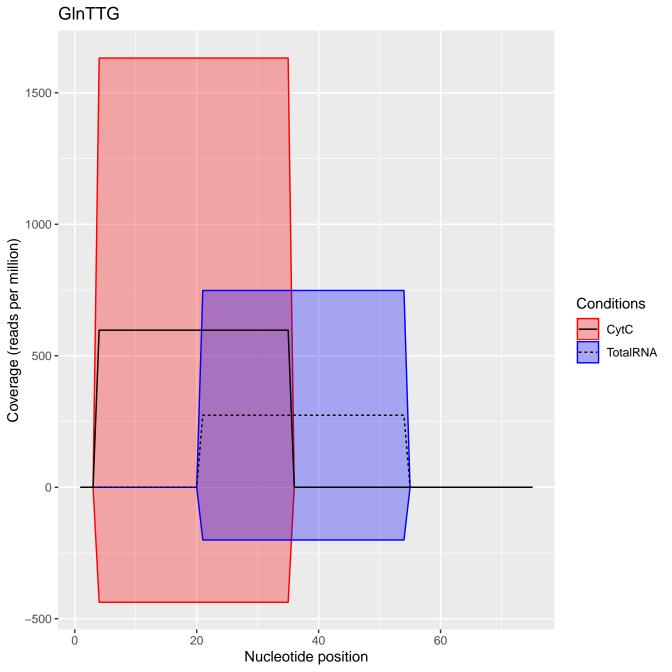




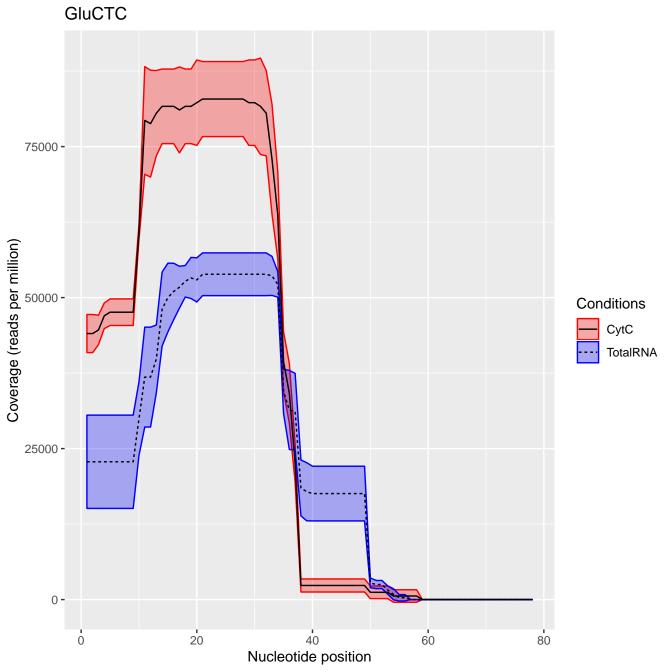


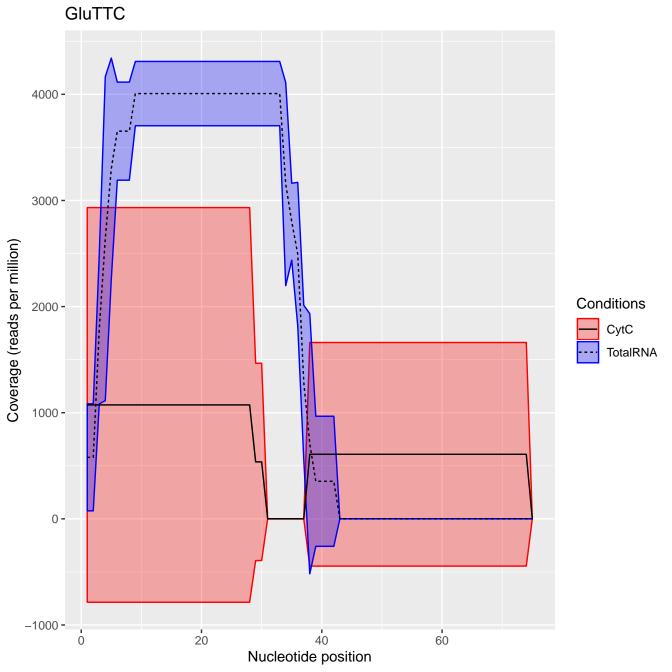




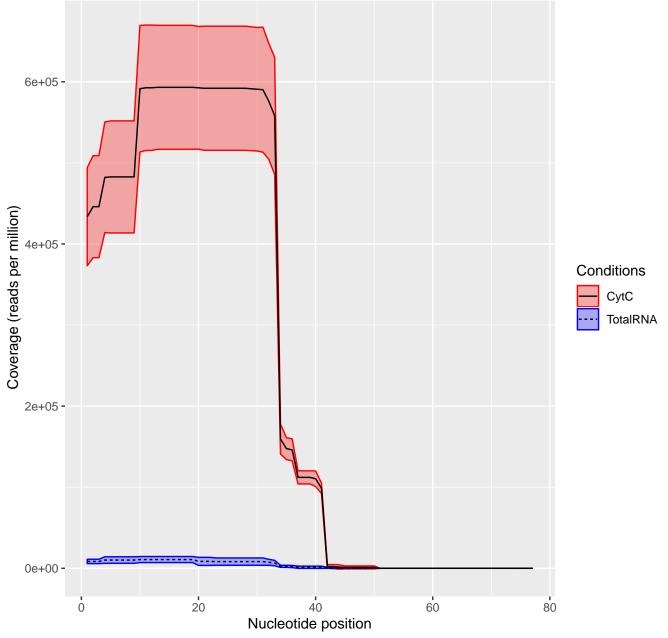


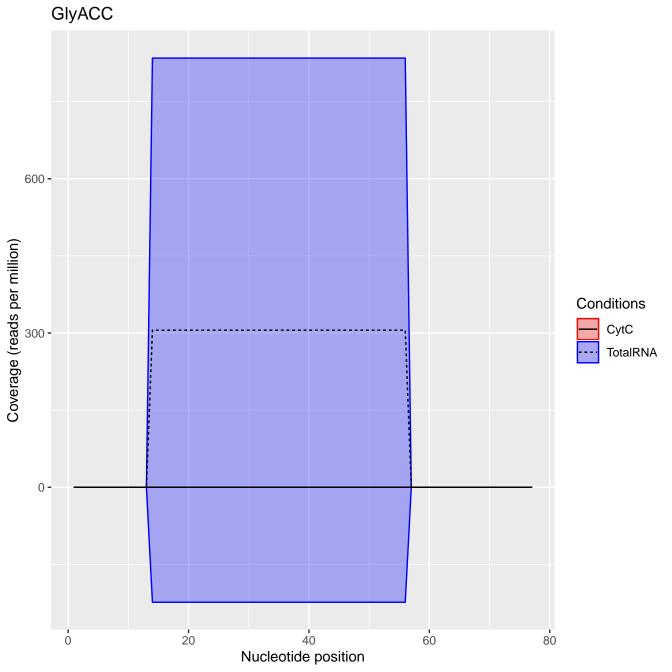
Glu (plot of multi-mapping reads where isoacceptor could not be identified) 6000 -Coverage (reads per million) Conditions CytC TotalRNA 2000 -0 -40 60 20 80 Nucleotide position

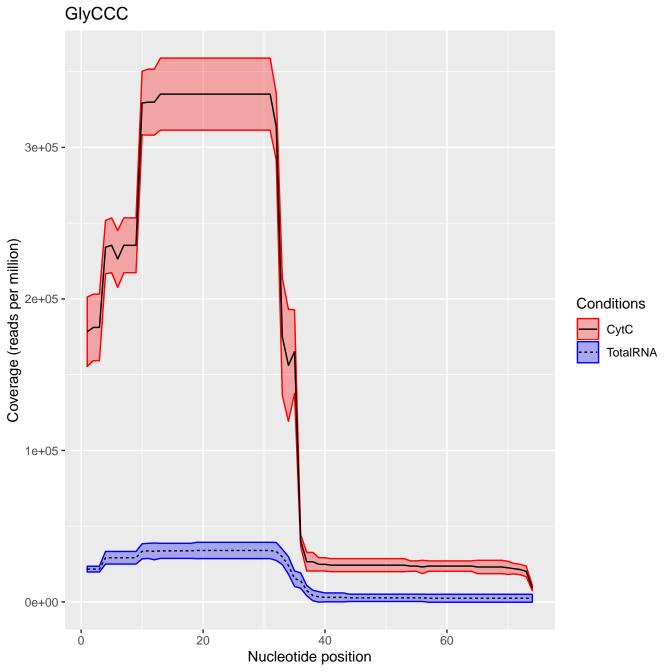


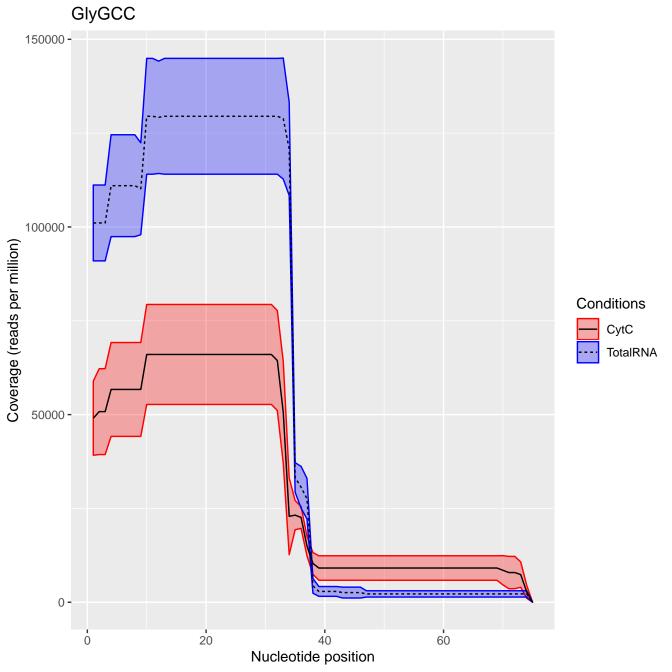


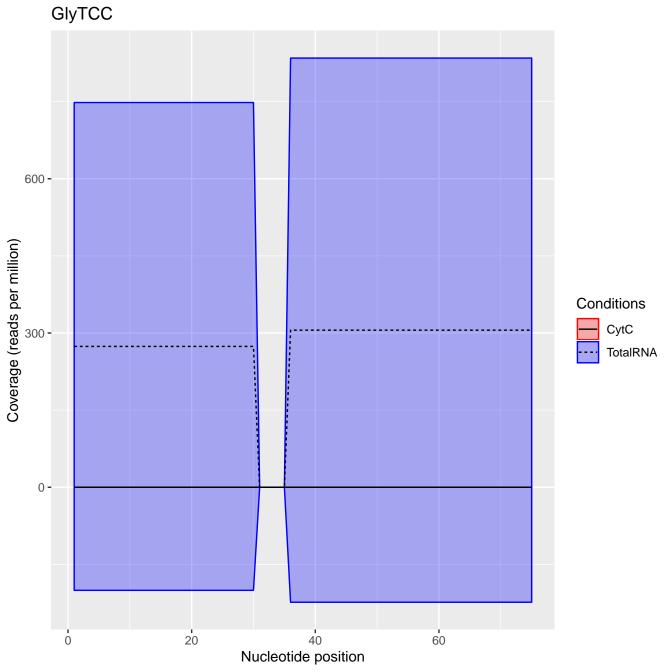
Gly (plot of multi-mapping reads where isoacceptor could not be identified)

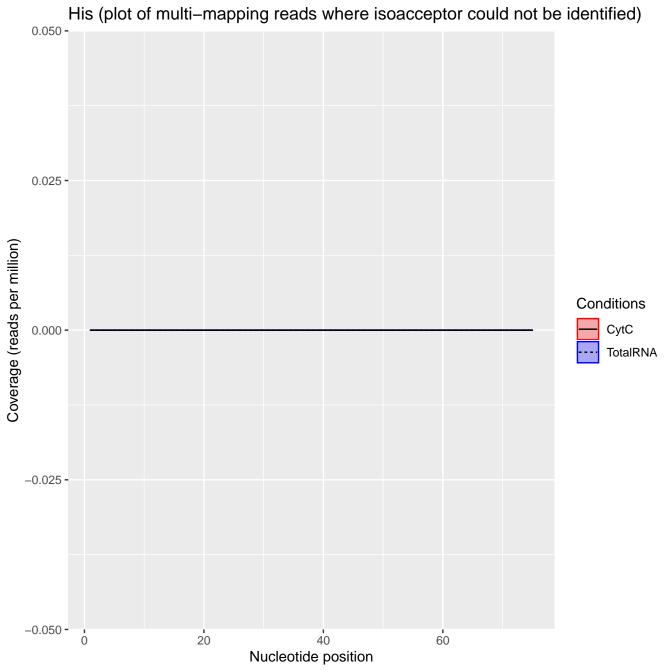


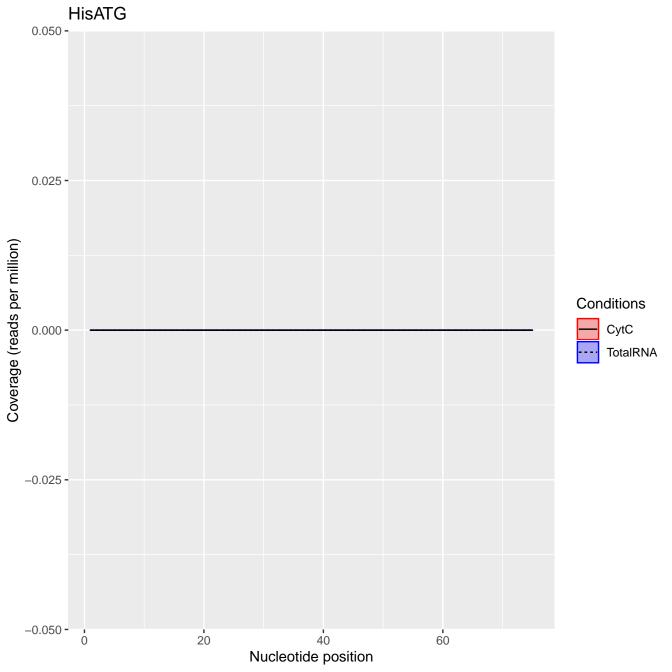


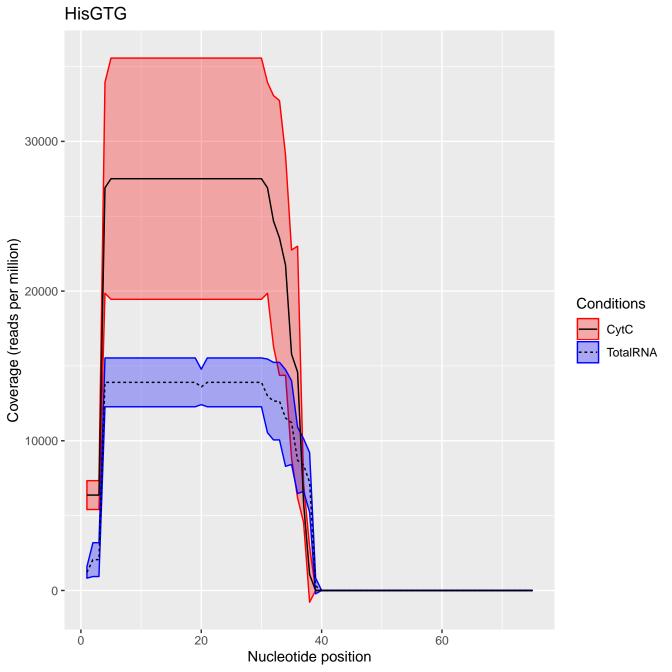


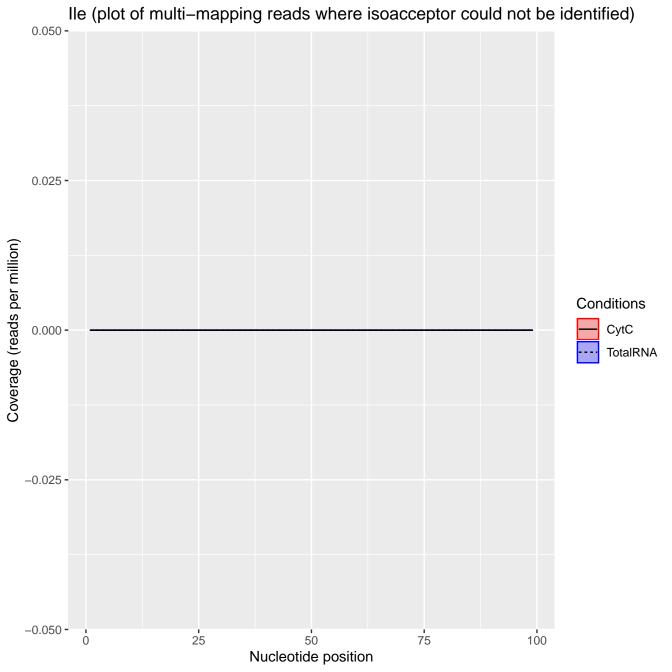


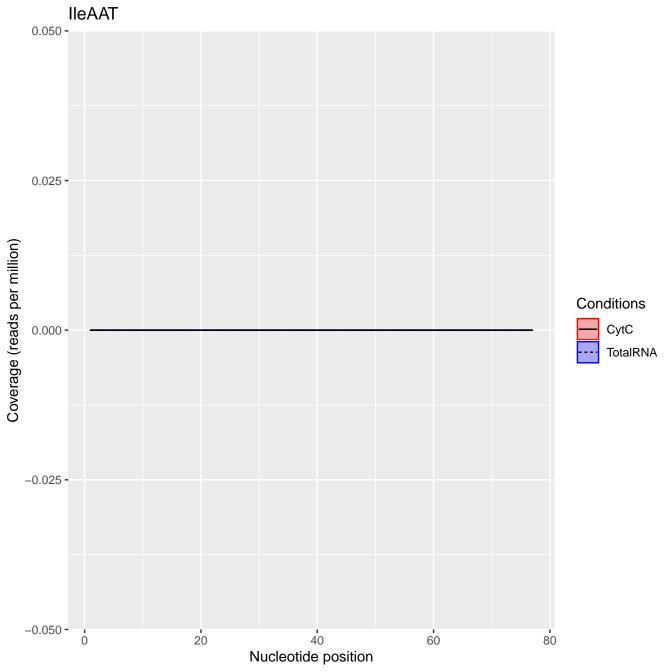


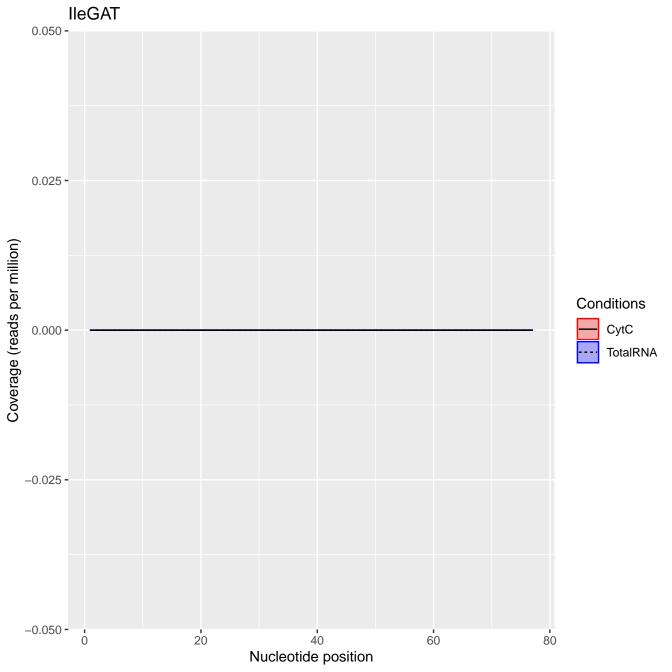


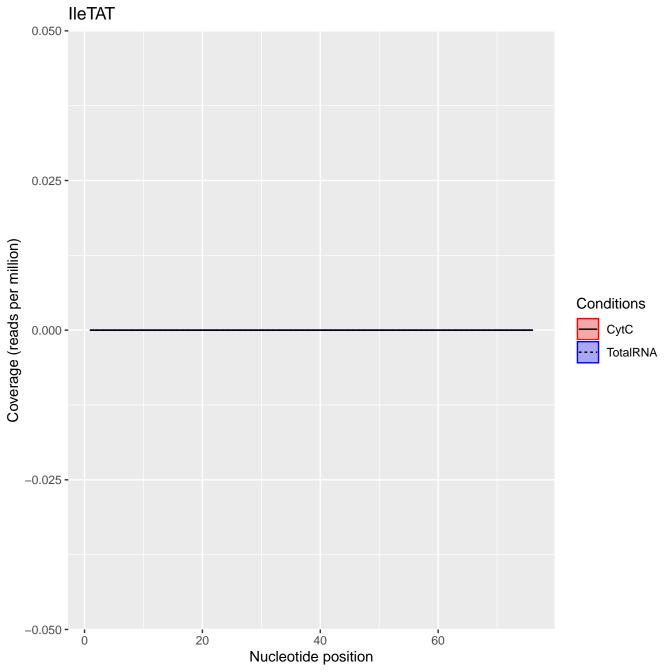




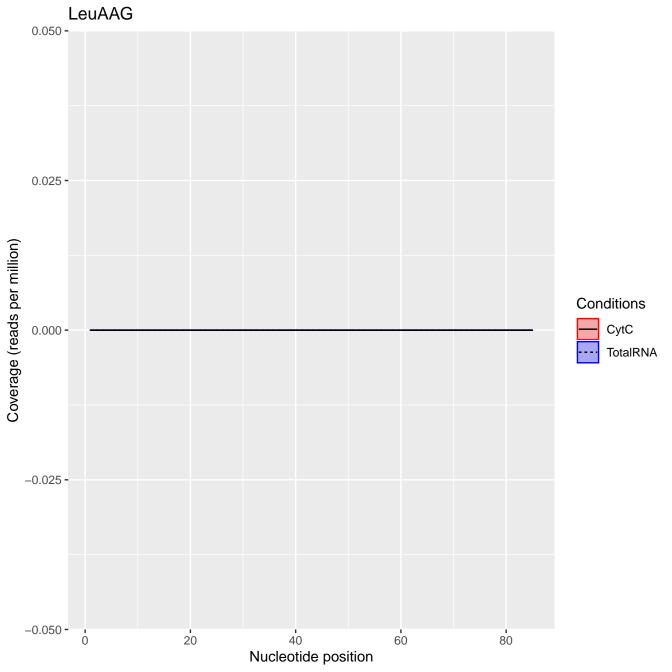


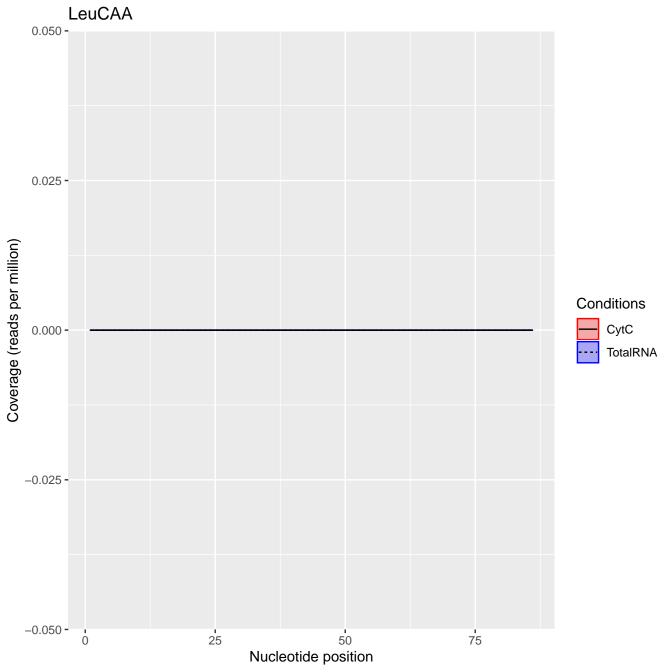


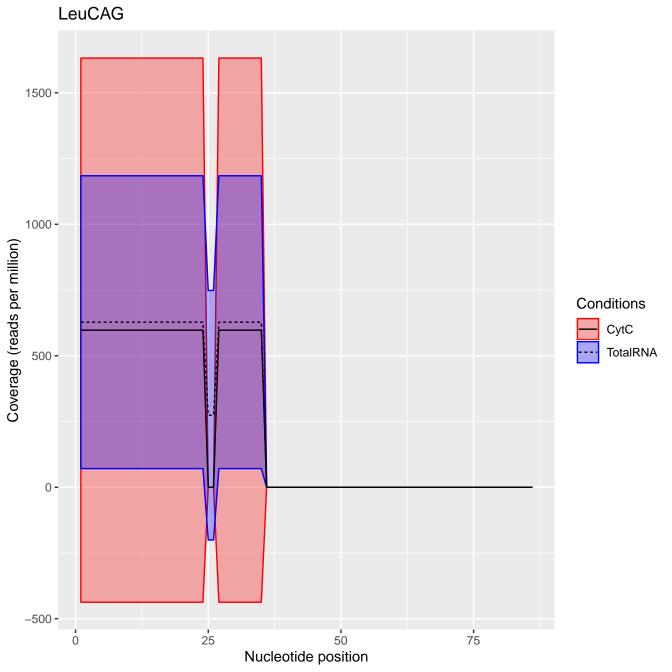


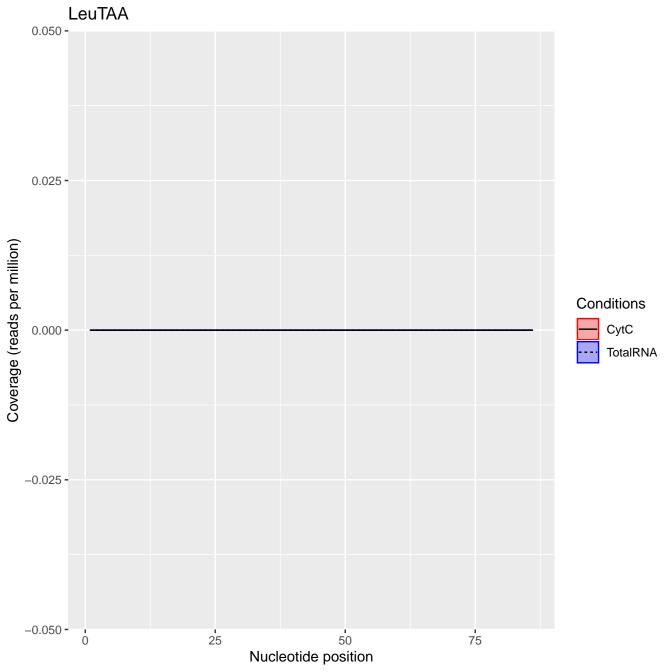


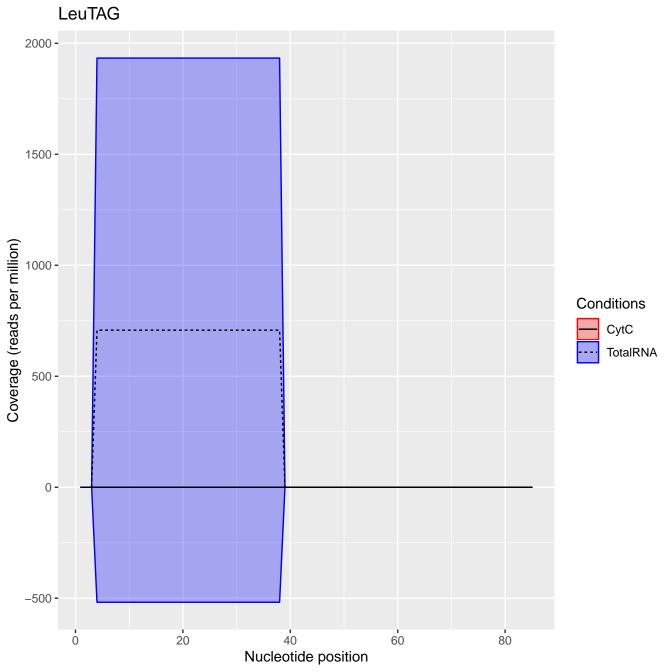
Leu (plot of multi-mapping reads where isoacceptor could not be identified) 1000 -750 **-**Coverage (reads per million) 500 -Conditions CytC TotalRNA 250 **-**0 --250 **-**0 30 60 90 Nucleotide position



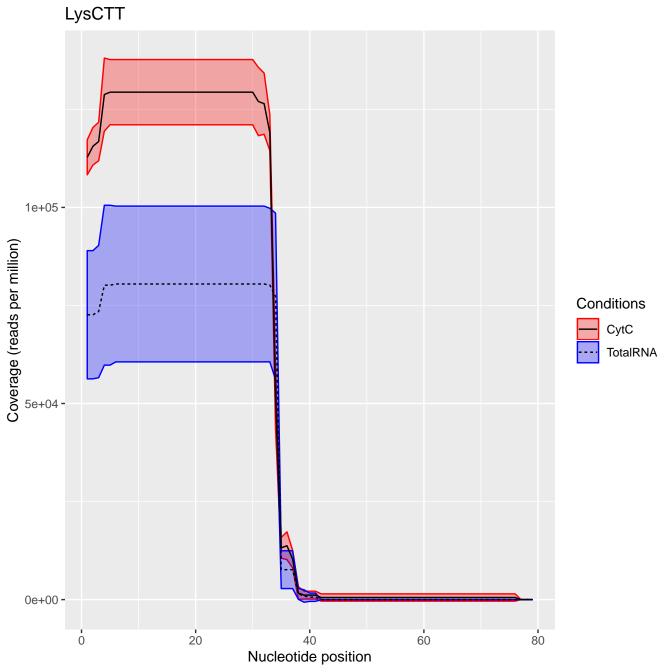


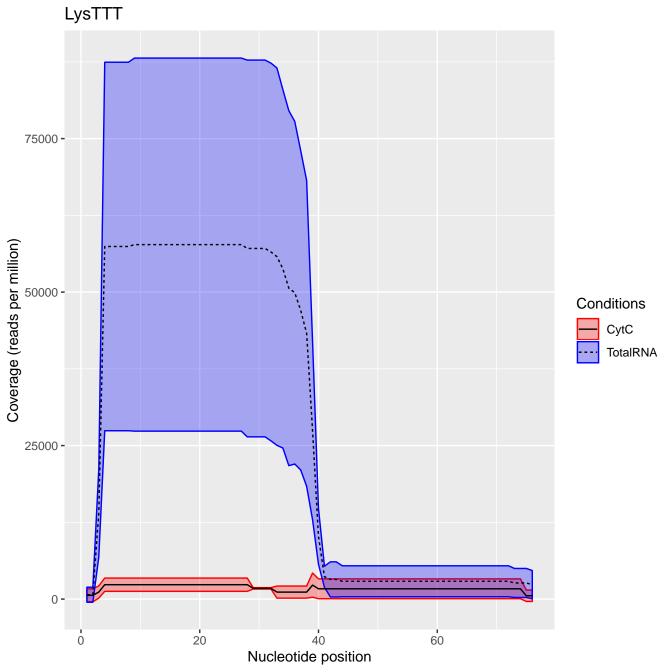


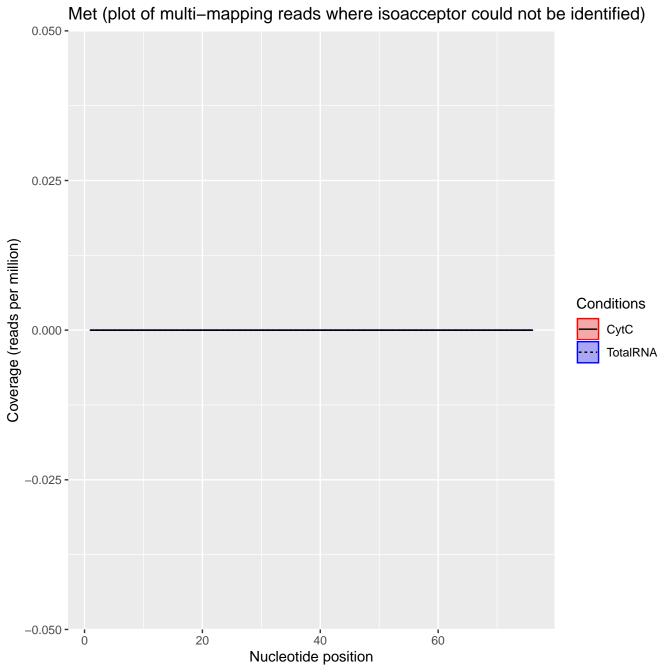


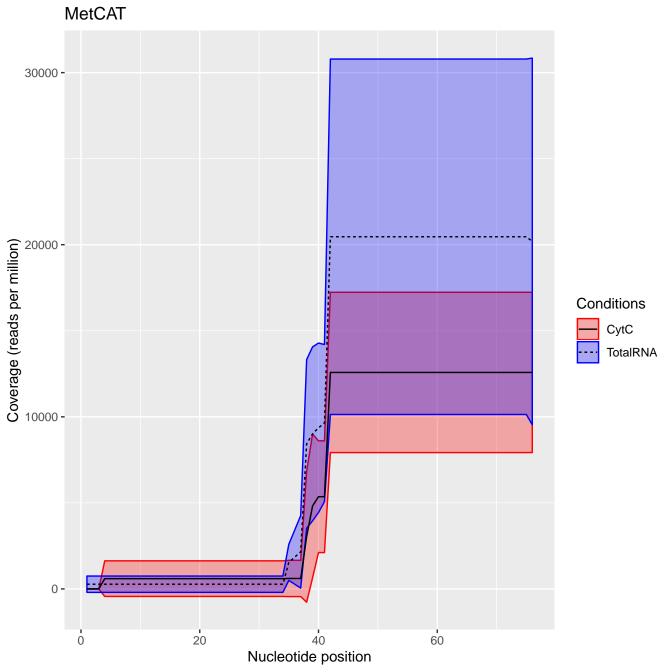


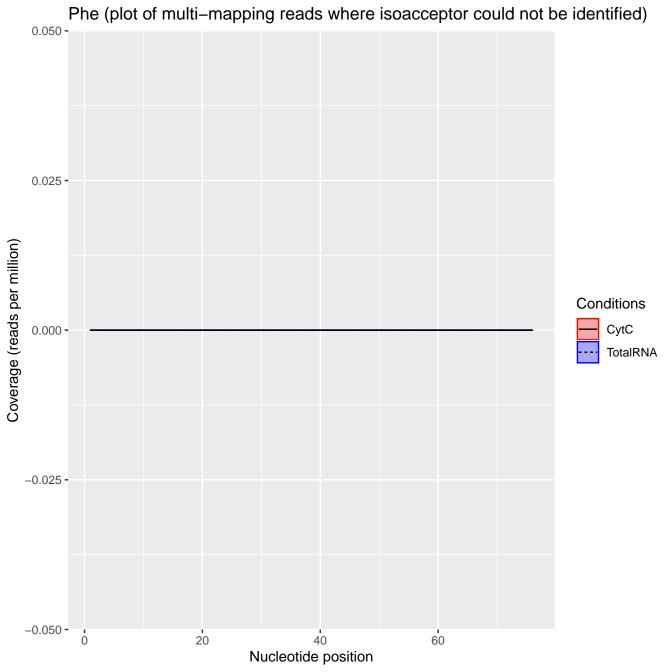
Lys (plot of multi-mapping reads where isoacceptor could not be identified) 750 **-**500 **-**Coverage (reads per million) Conditions CytC TotalRNA 0 -20 40 60 80 Ö Nucleotide position

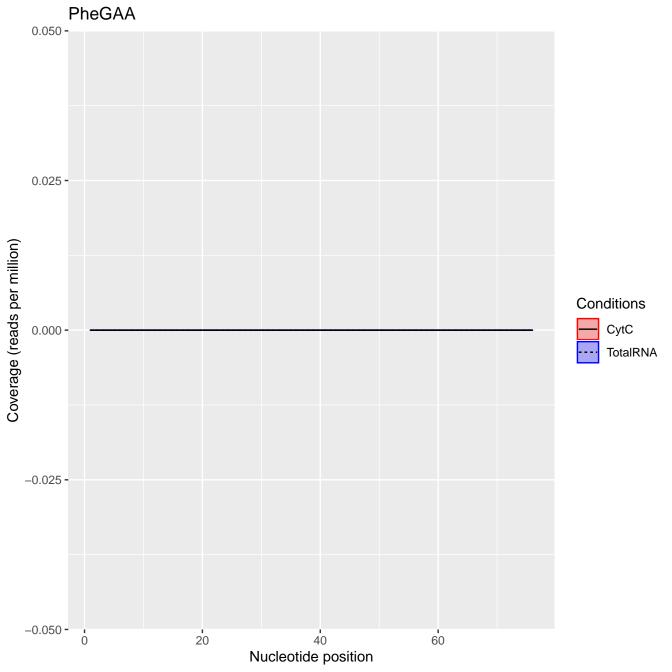




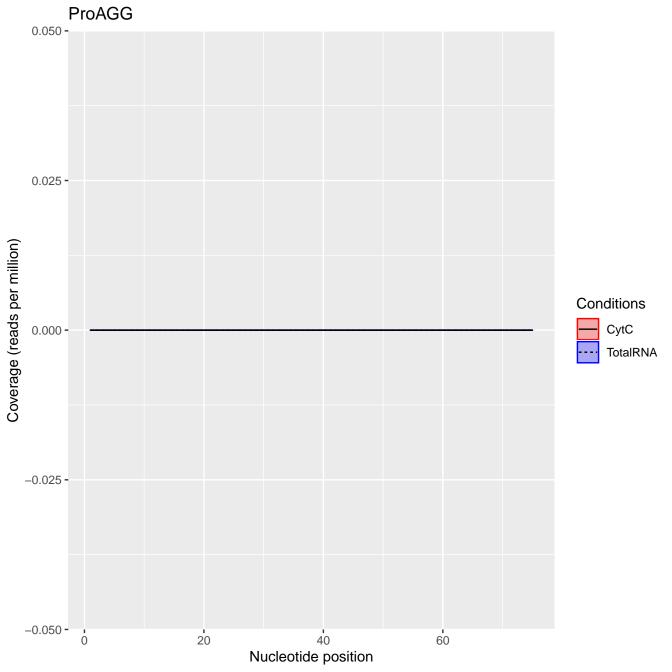


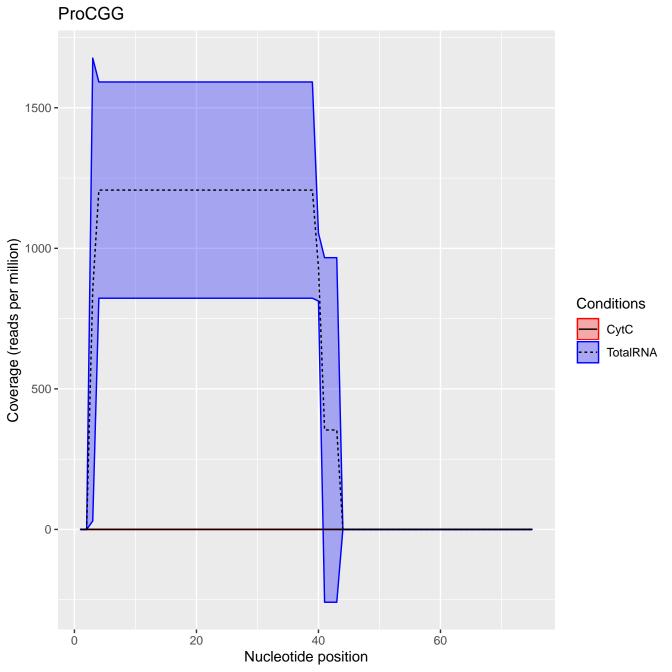


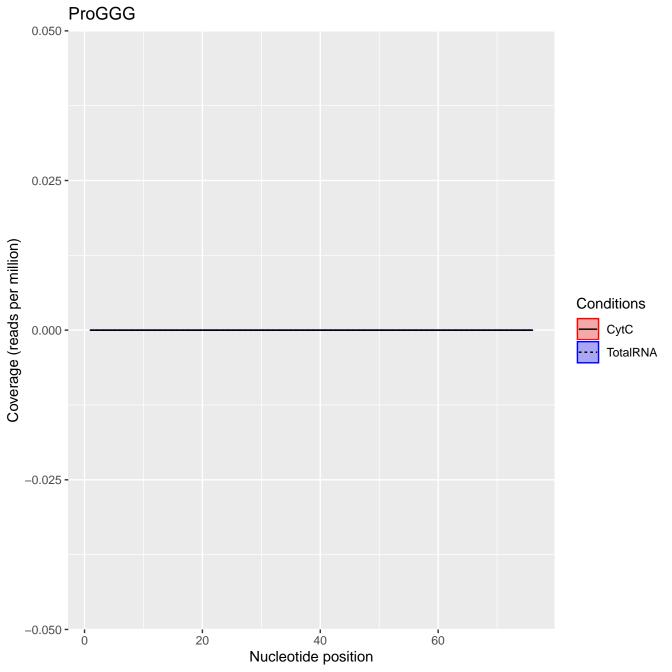


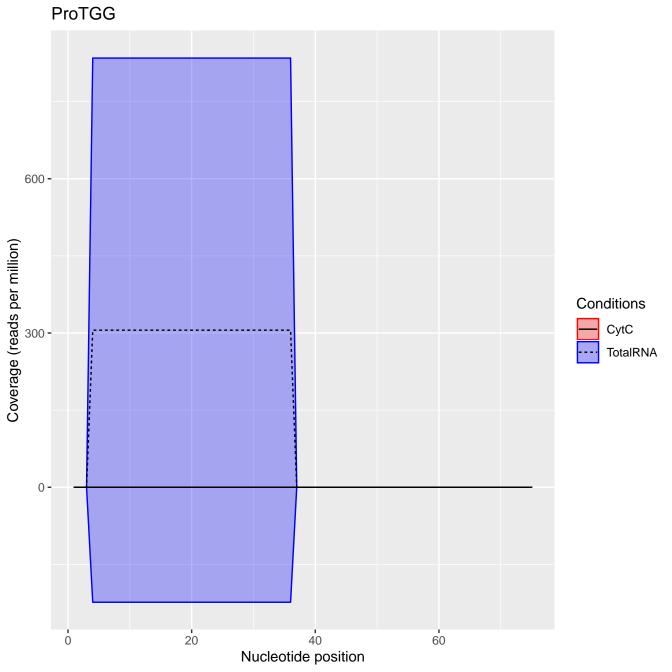


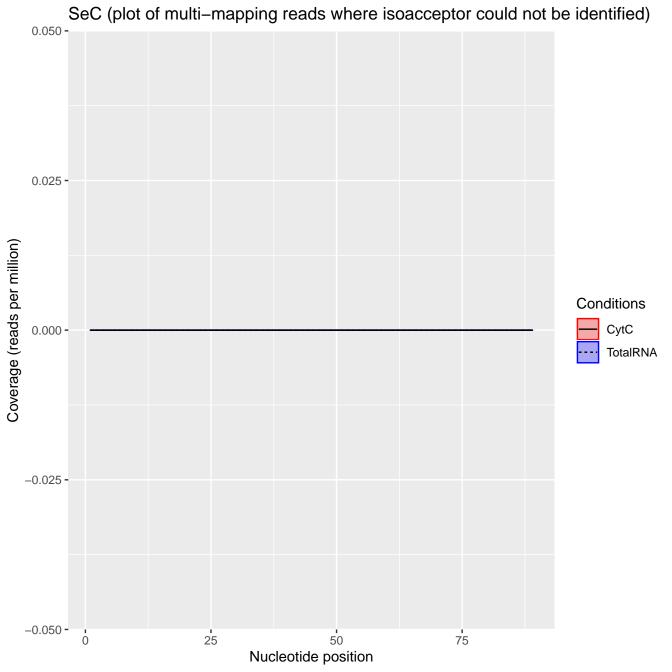
Pro (plot of multi-mapping reads where isoacceptor could not be identified) 6000 -Coverage (reads per million) Conditions CytC TotalRNA 0 -60 20 40 Nucleotide position

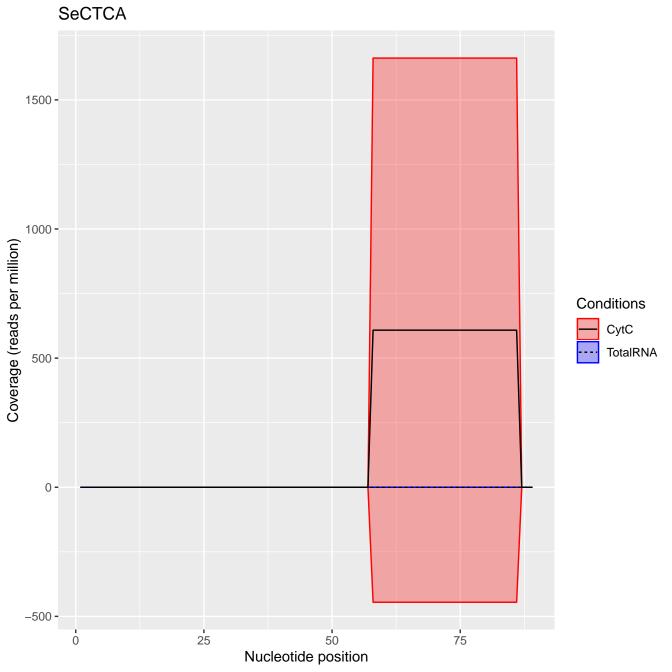


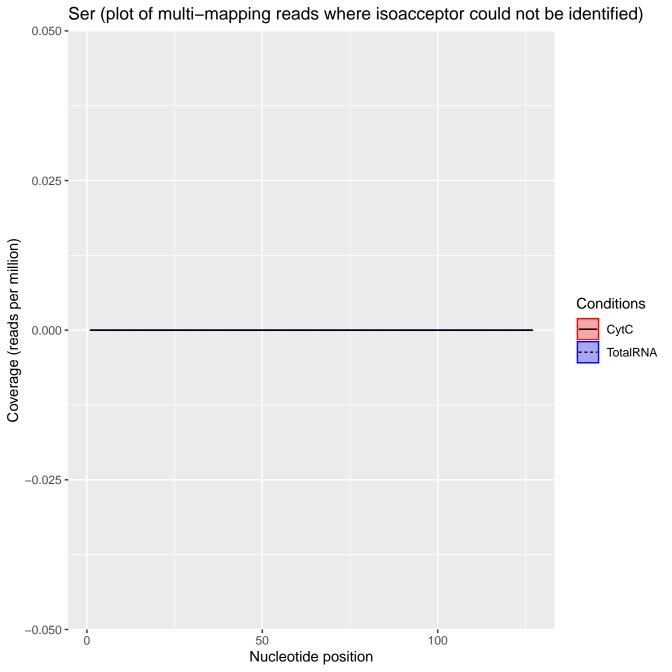


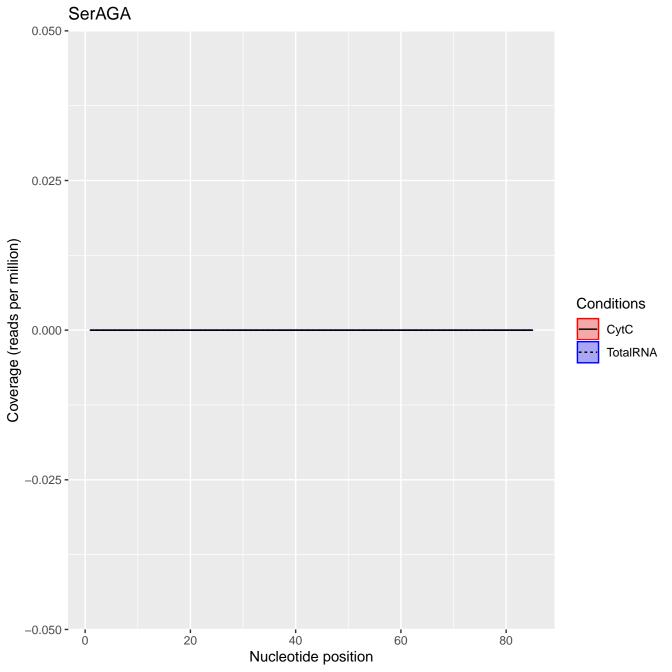


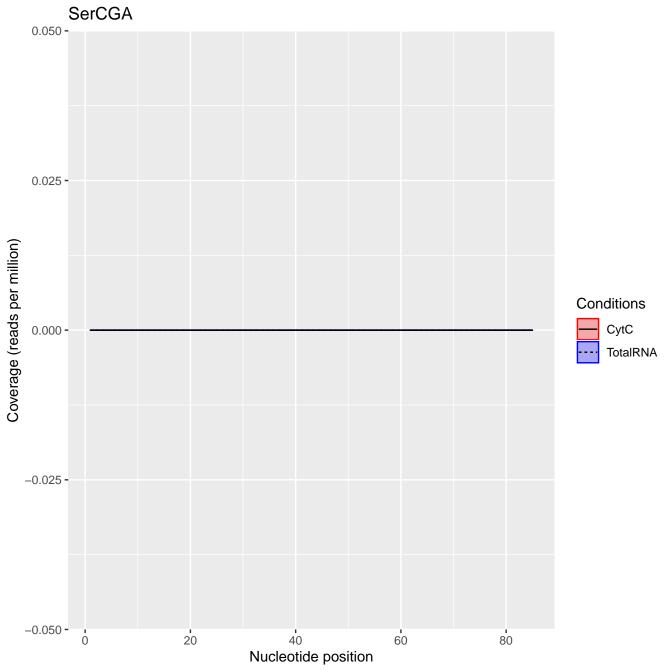


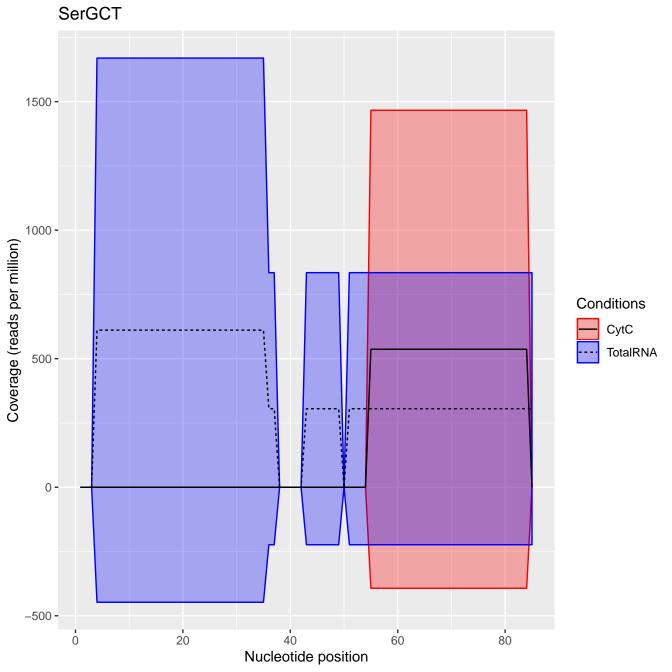


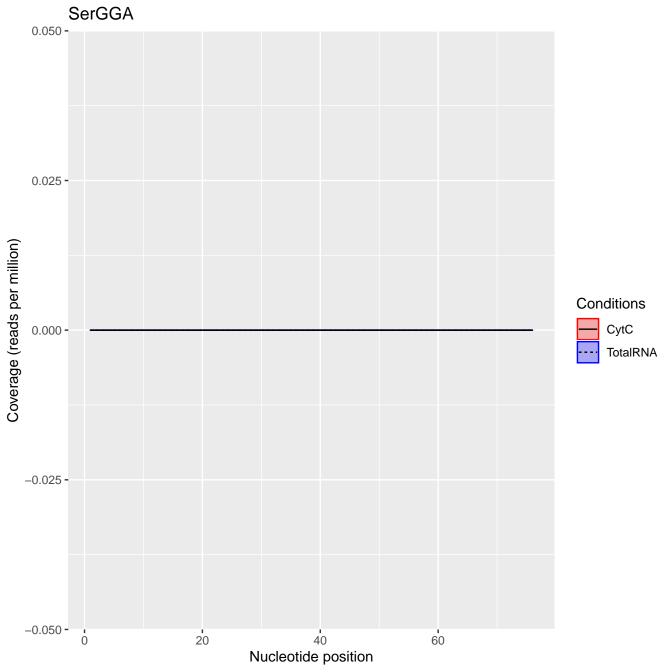


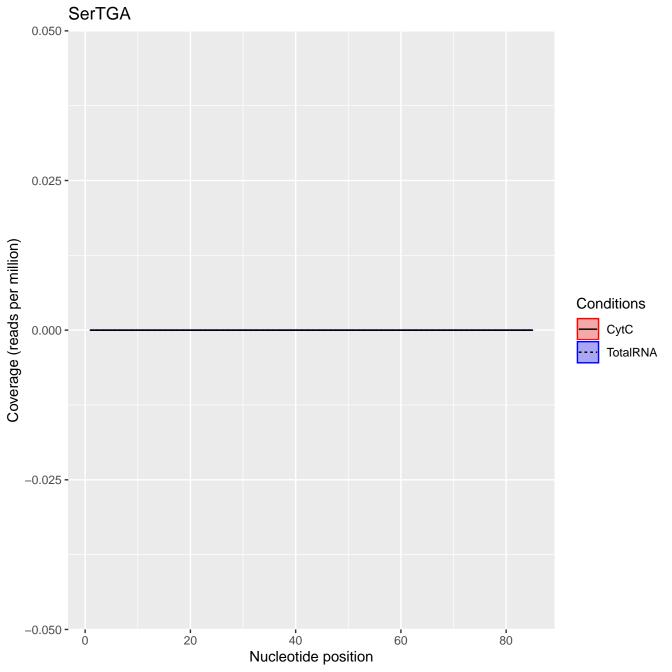


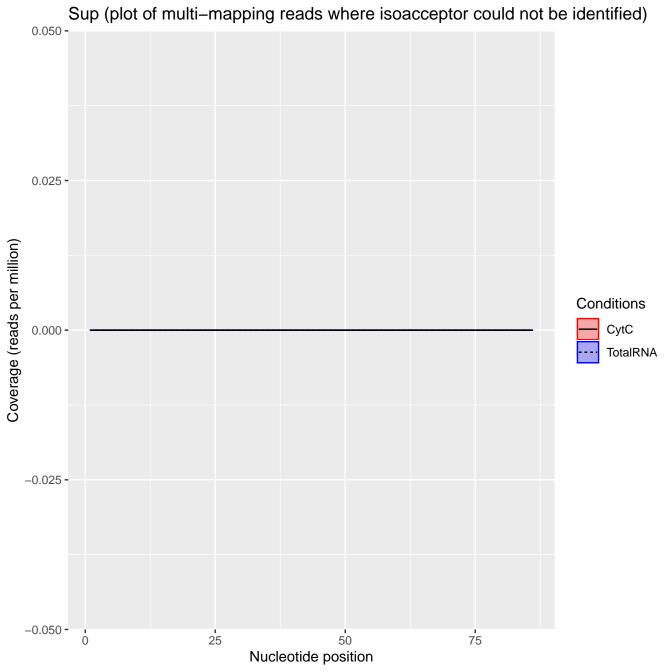


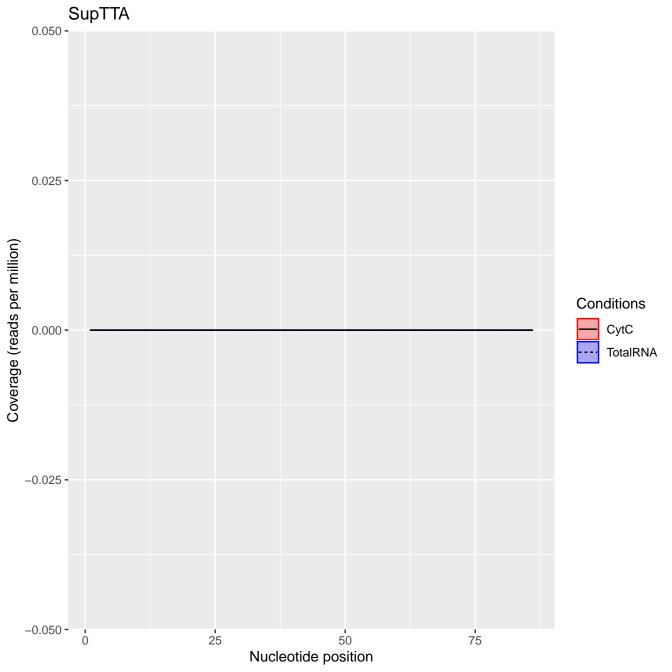


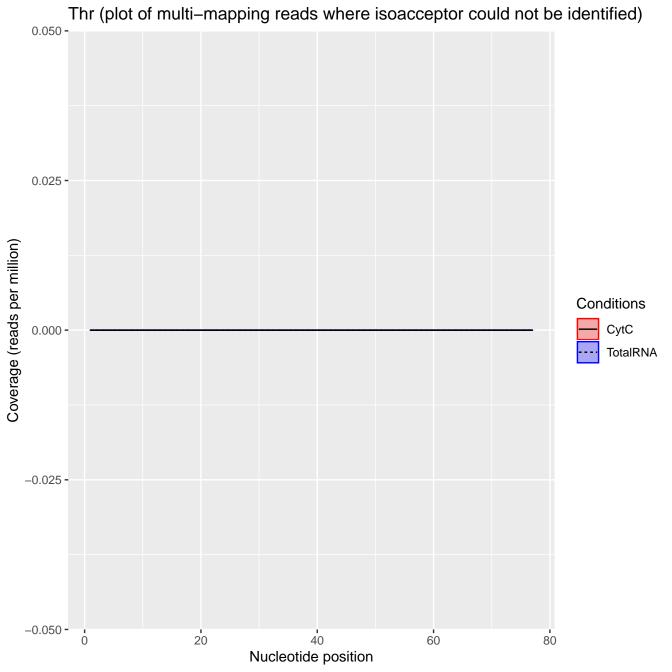


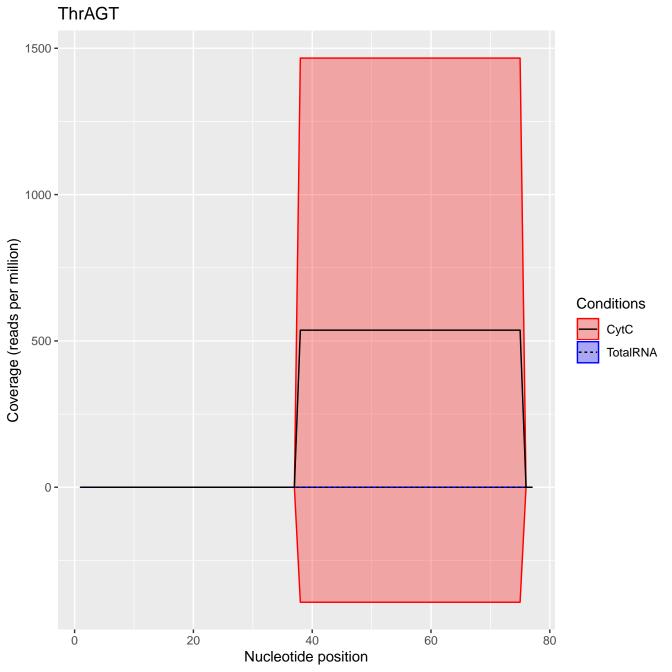


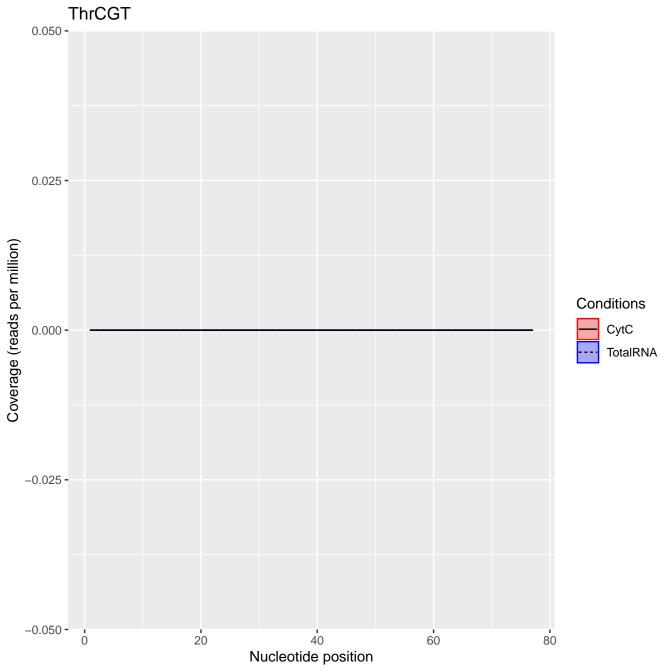


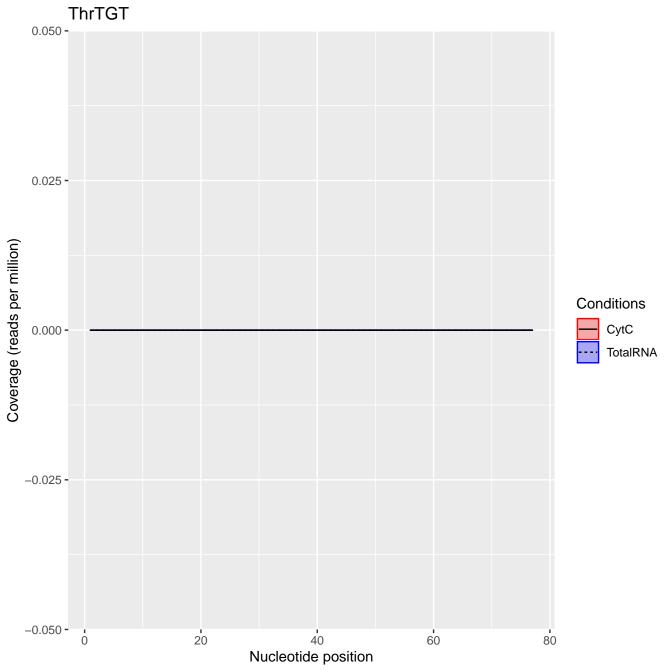


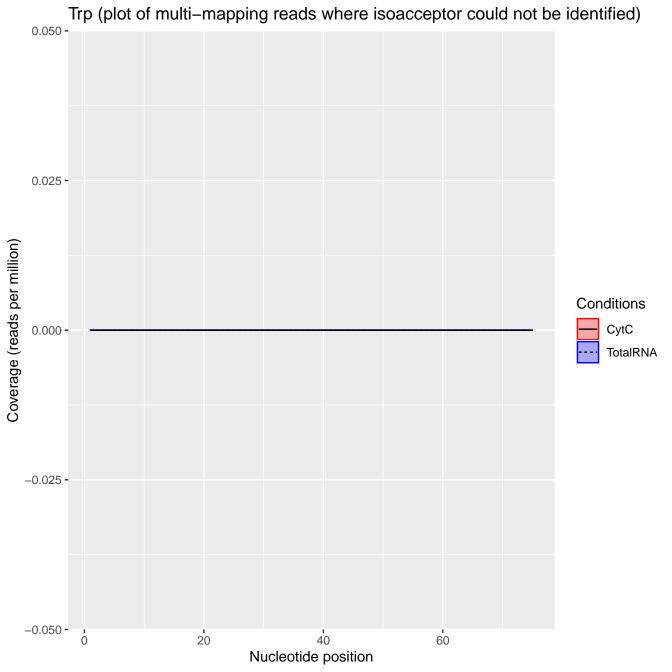


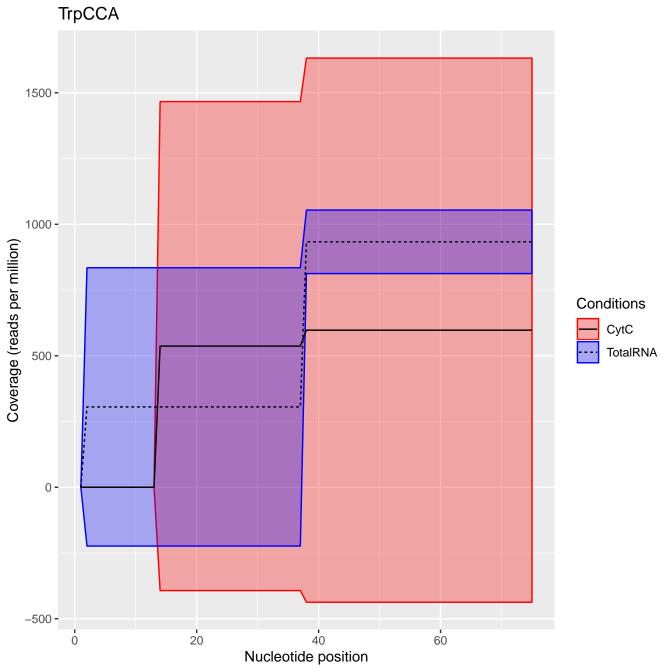


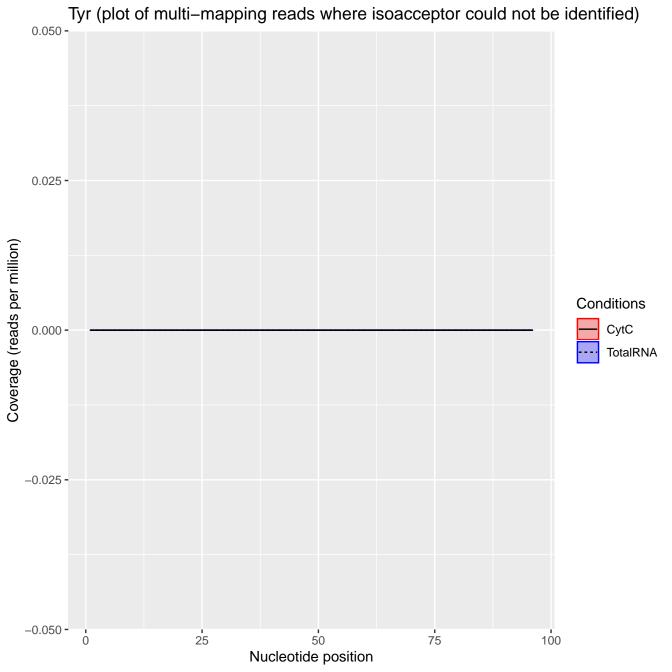


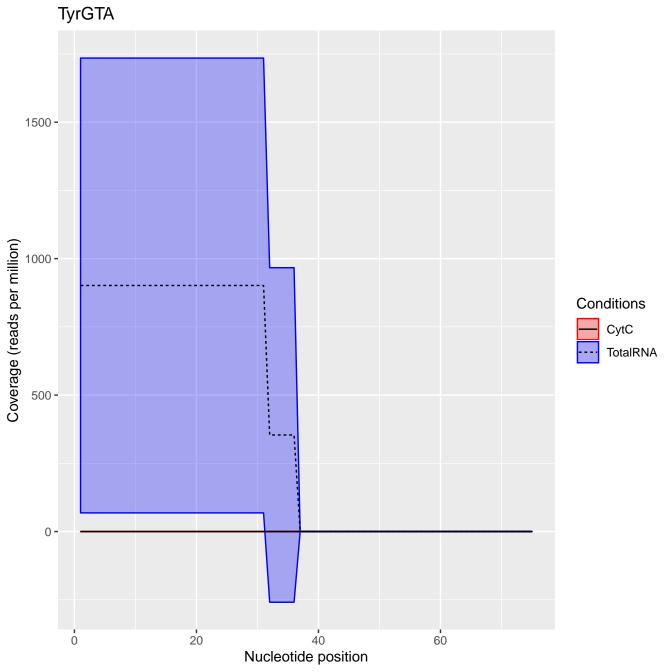


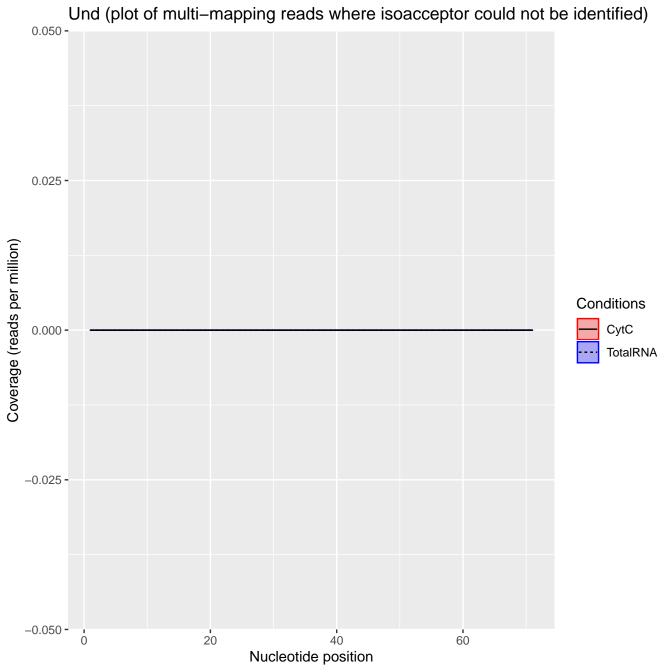












Val (plot of multi-mapping reads where isoacceptor could not be identified) 1200000 -900000 -Coverage (reads per million) Conditions 600000 -CytC TotalRNA 300000 -0 -20 40 60 0 80 Nucleotide position

