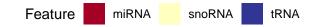
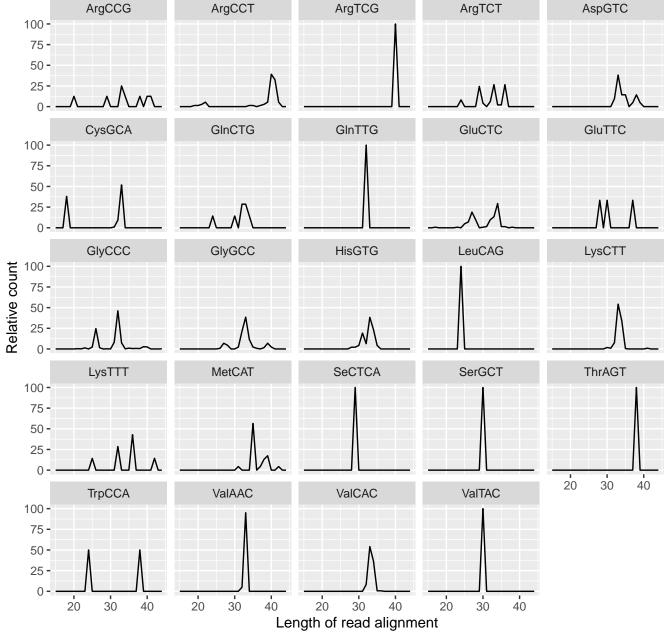


Features identified in CytC vs TotalRNA Raw read counts displayed 3000 -Raw Read Count 1000 -0 -TotalRNA CytC

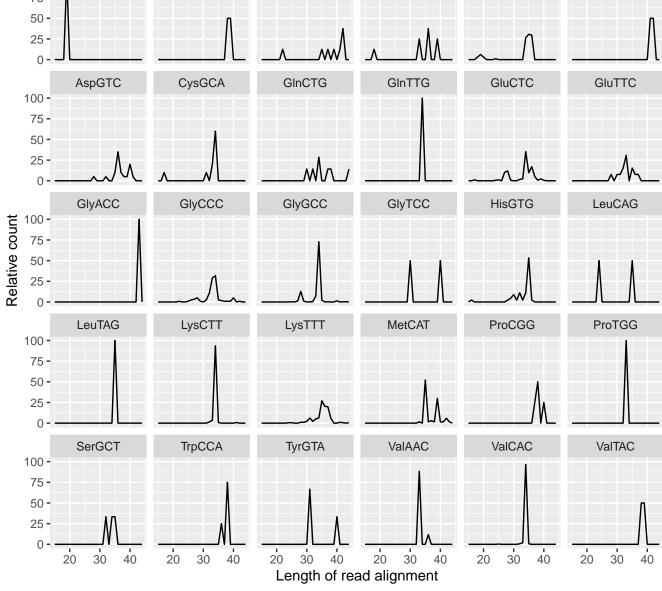


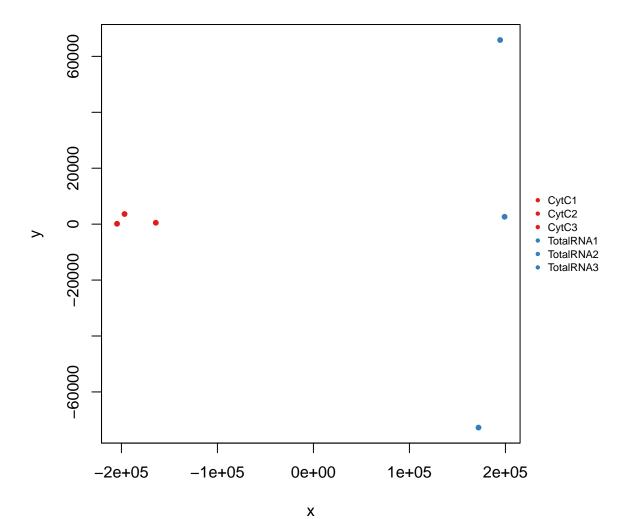
Read Alignment Lengths (CytC)

ArgCCG ArgCCT

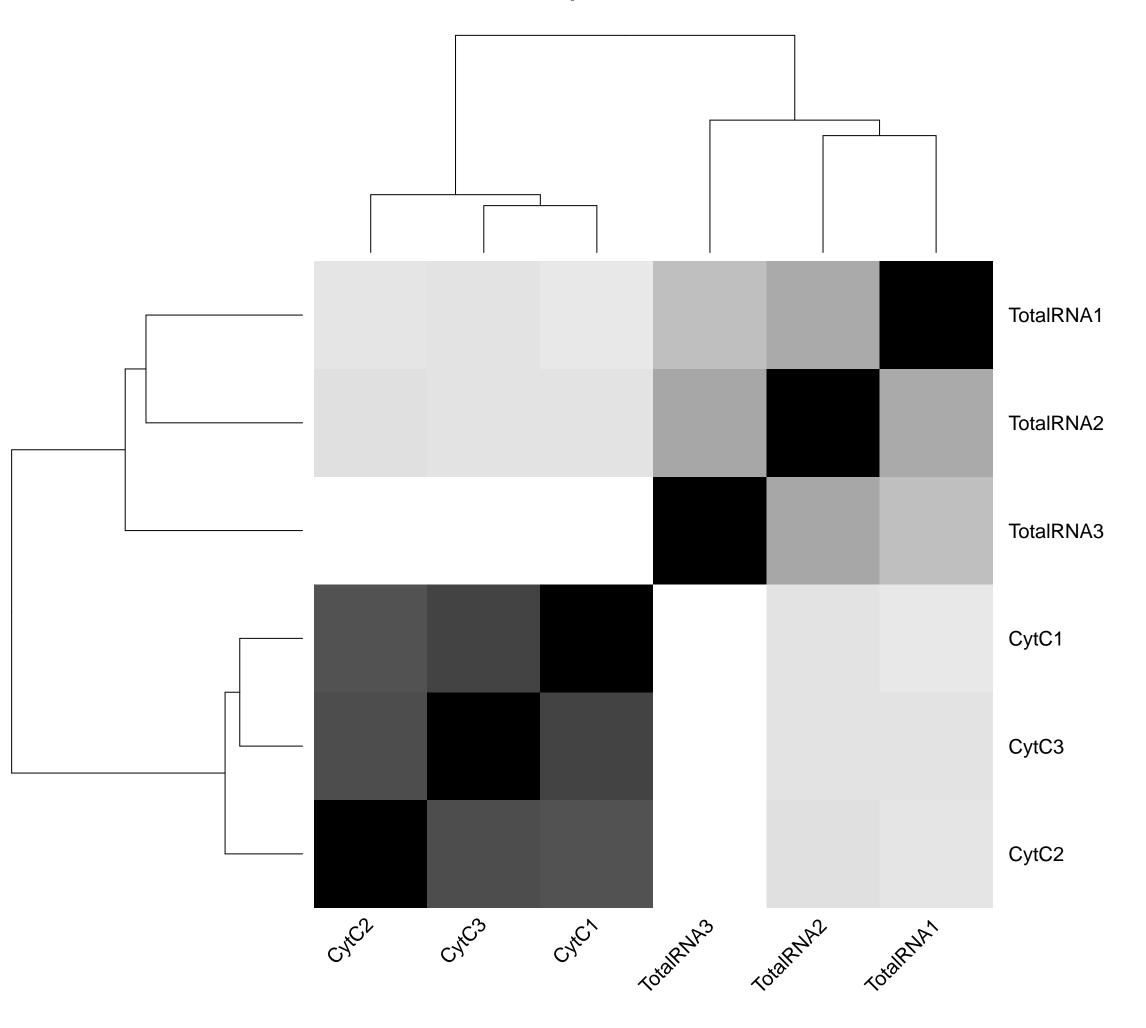


AsnGTT



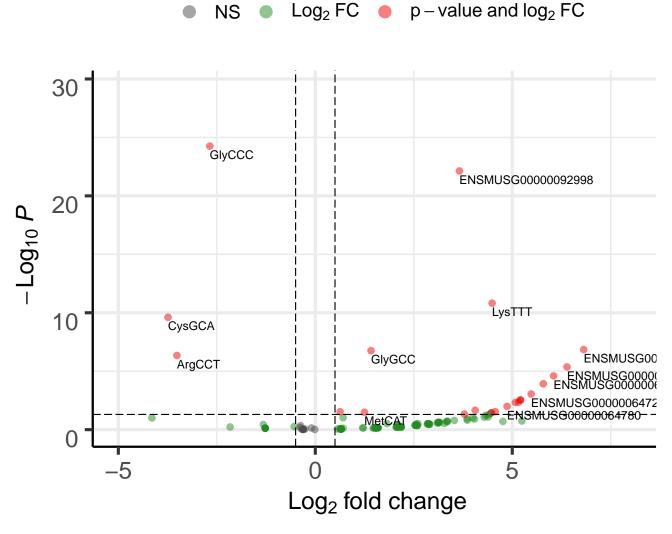


## **Sample Distance Matrix**

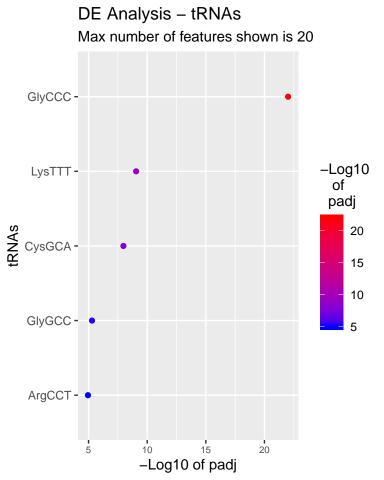


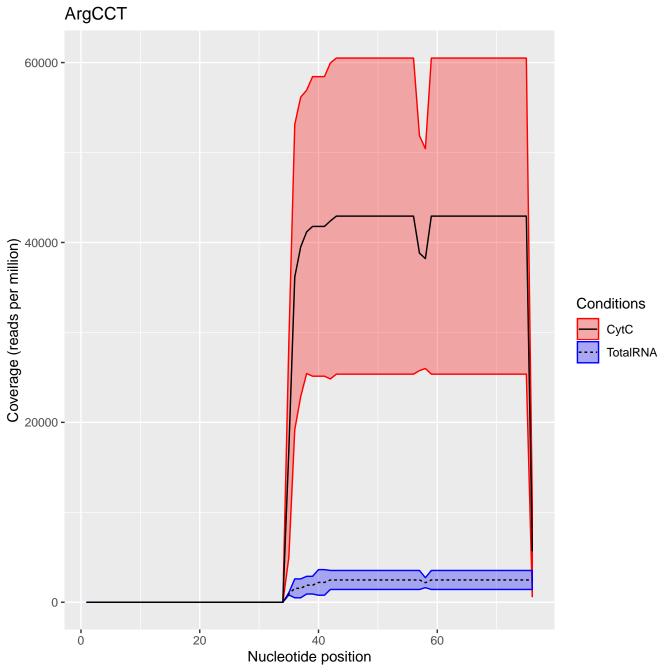
## Volcano plot

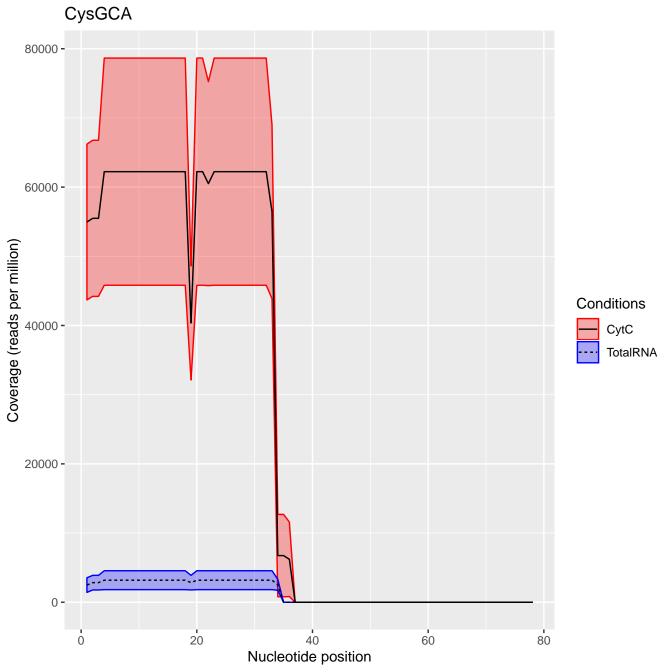
EnhancedVolcano

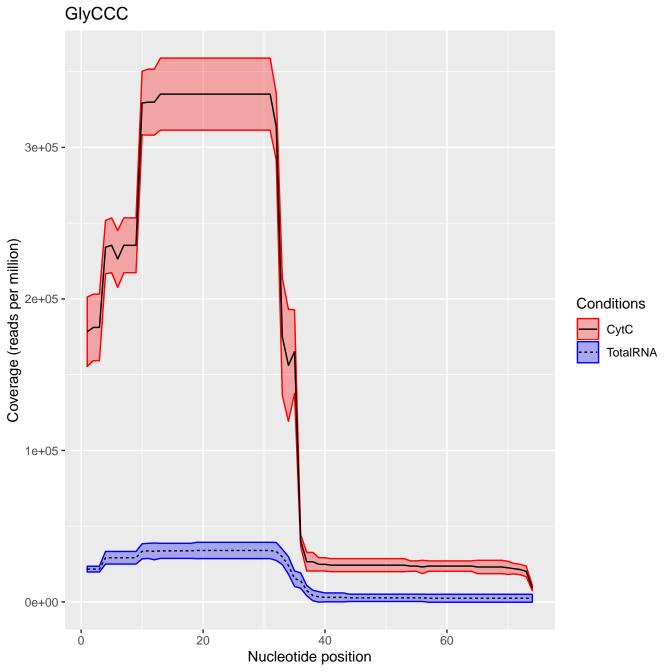


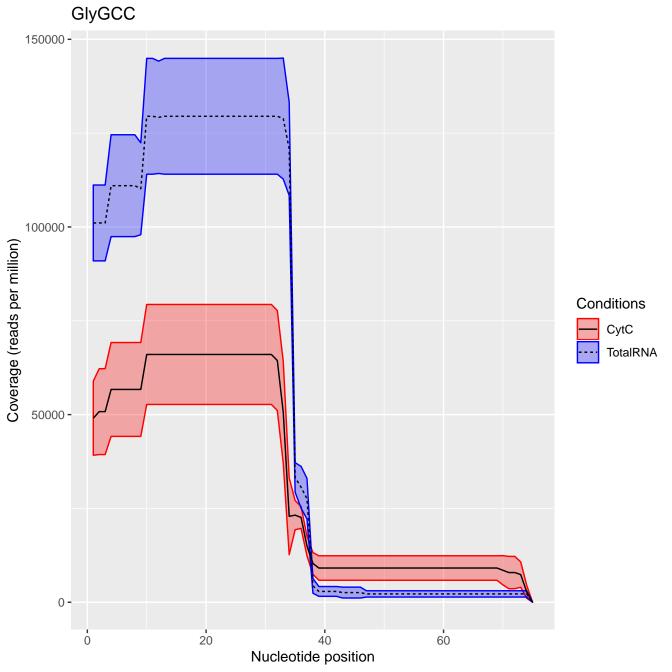
Total = 3370 variables

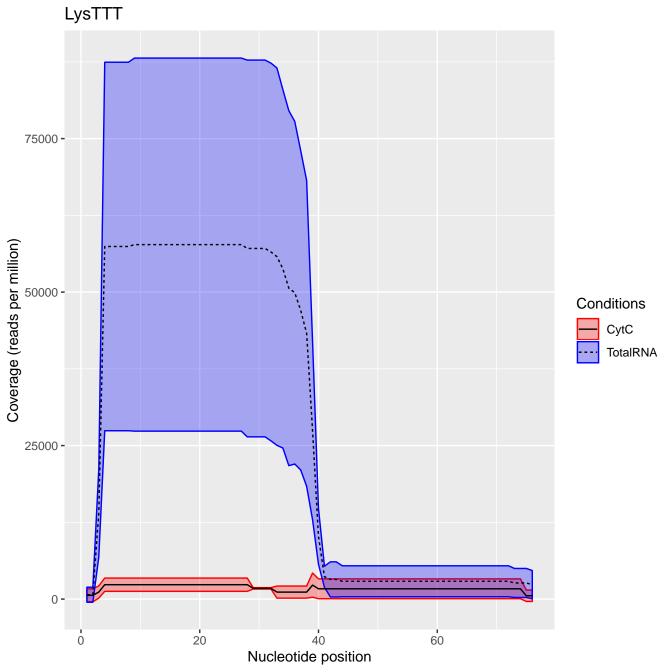




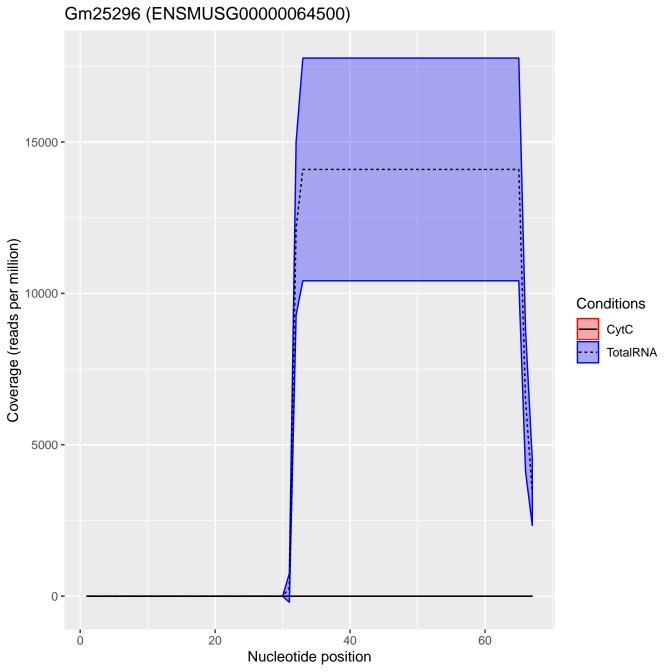


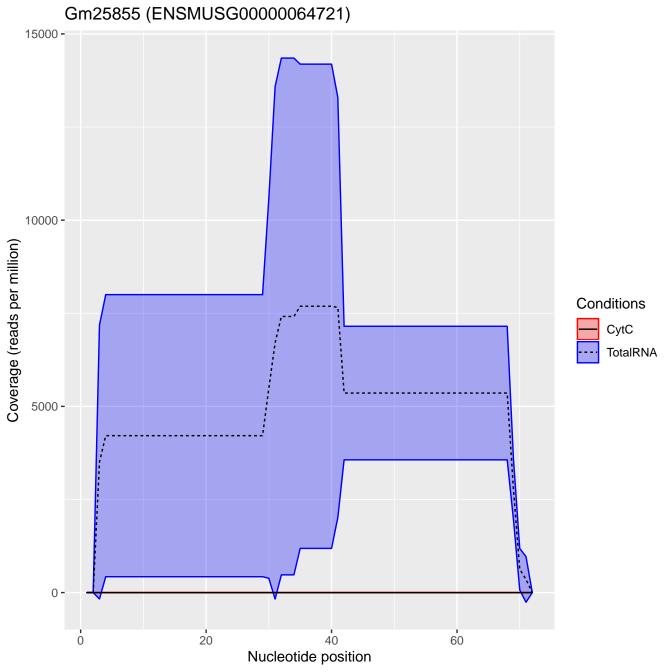


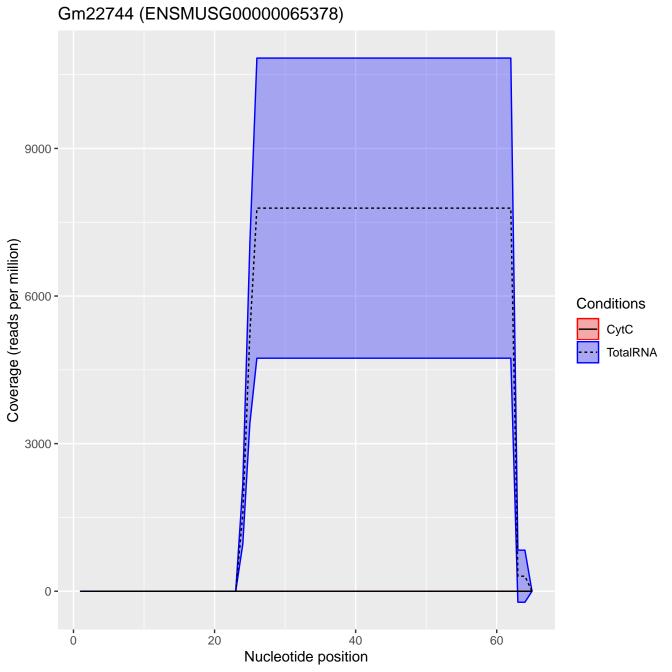


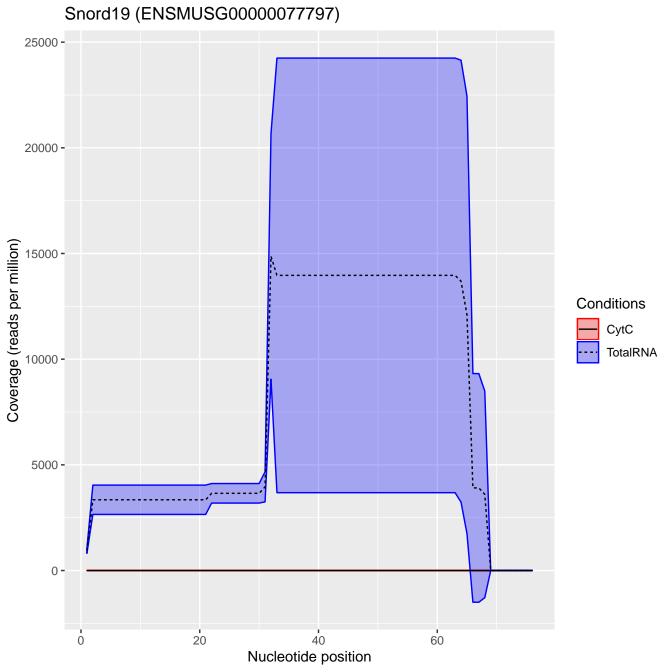


DE Analysis – ncRNAs Max number of features shown is ENSMUSG00000092998 (Mir5099) -ENSMUSG00000084667 (Gm23212) --Log10 ENSMUSG00000077797 (Snord19) padj 20 ENSMUSG00000064500 (Gm25296) ncRNAs 15 ENSMUSG00000093009 (Snord52) -10 5 ENSMUSG00000064721 (Gm25855) - • ENSMUSG00000065378 (Gm22744) - • ENSMUSG00000080463 (Gm22489) - • 20 -Log10 of padi

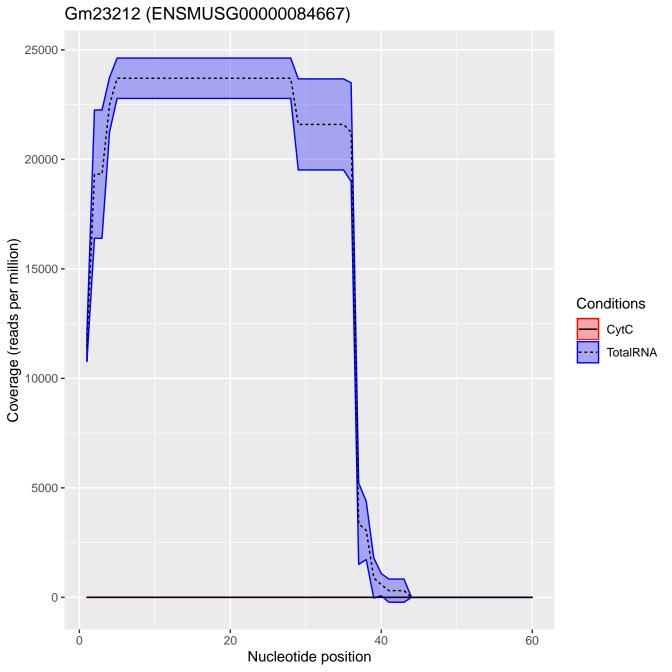


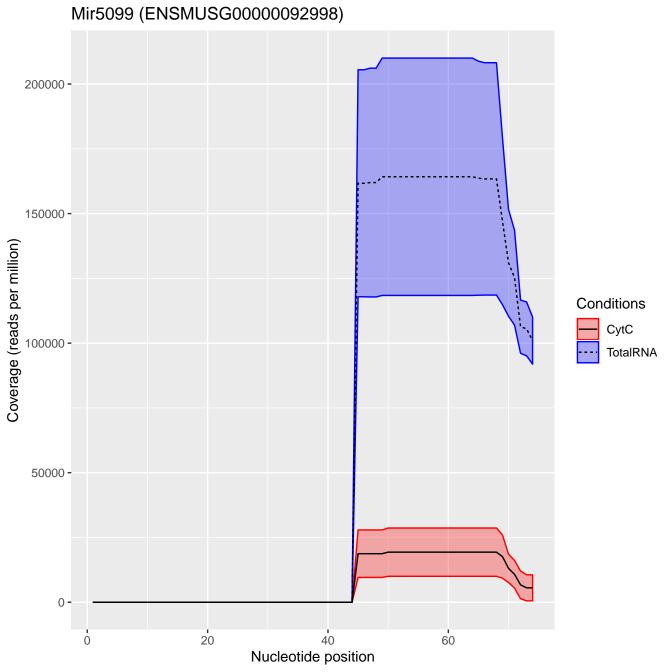


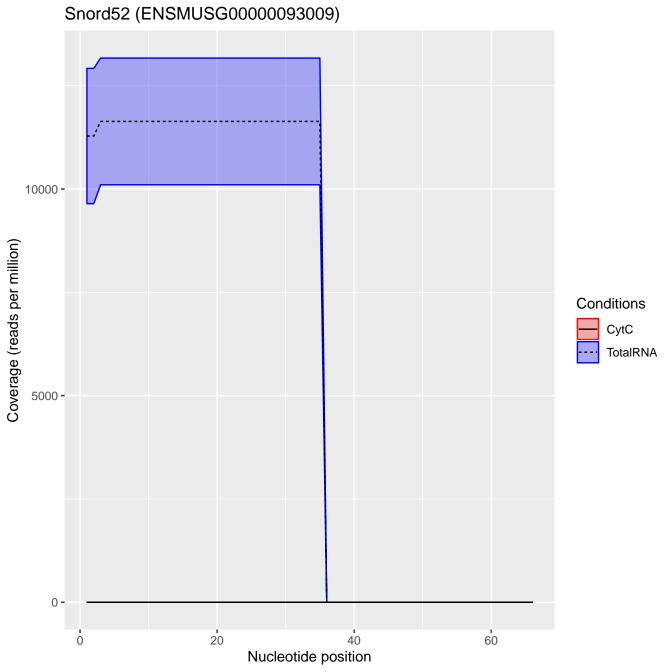




Gm22489 (ENSMUSG00000080463) 12000 -9000 -Coverage (reads per million) Conditions 6000 -CytC TotalRNA 3000 -0 -20 60 40 0 Nucleotide position

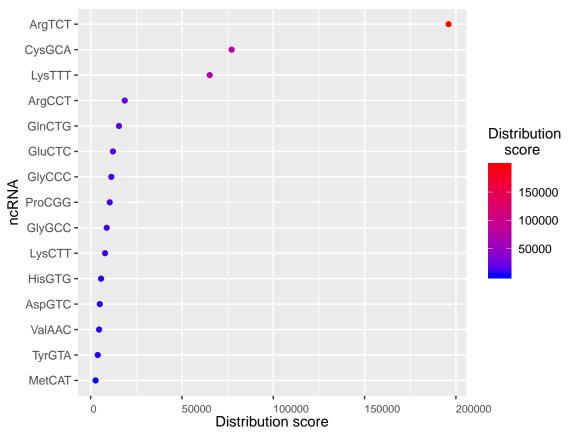


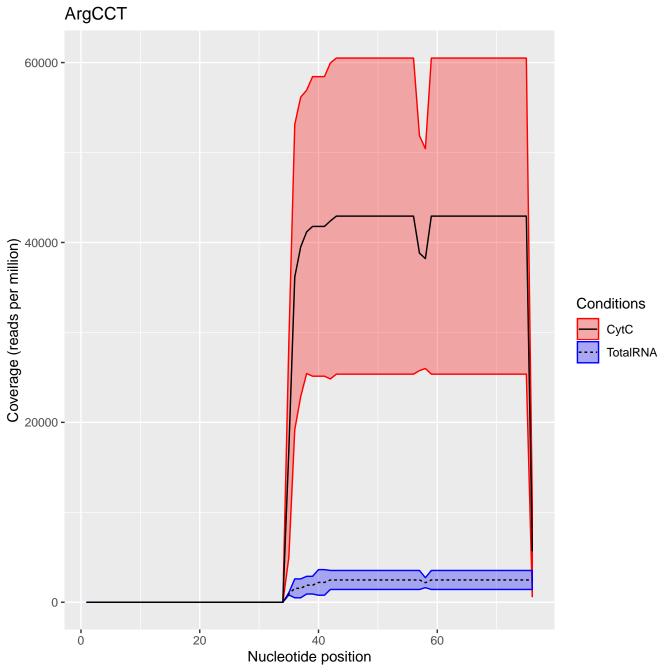


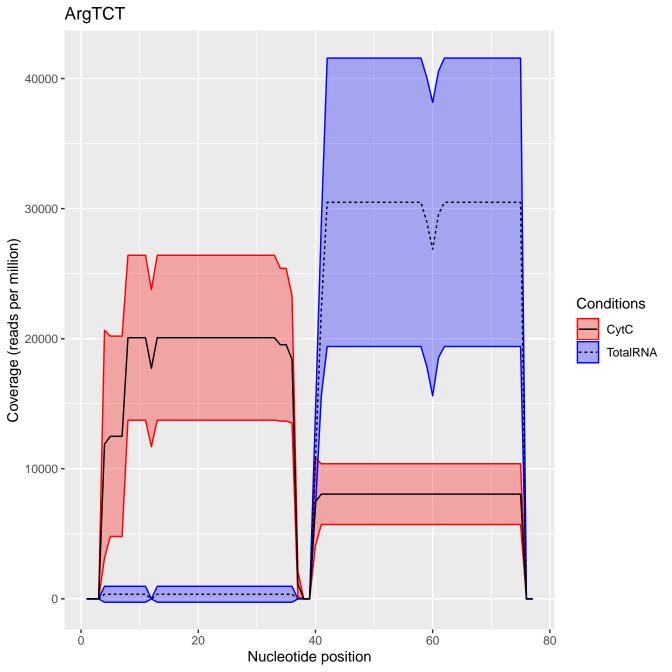


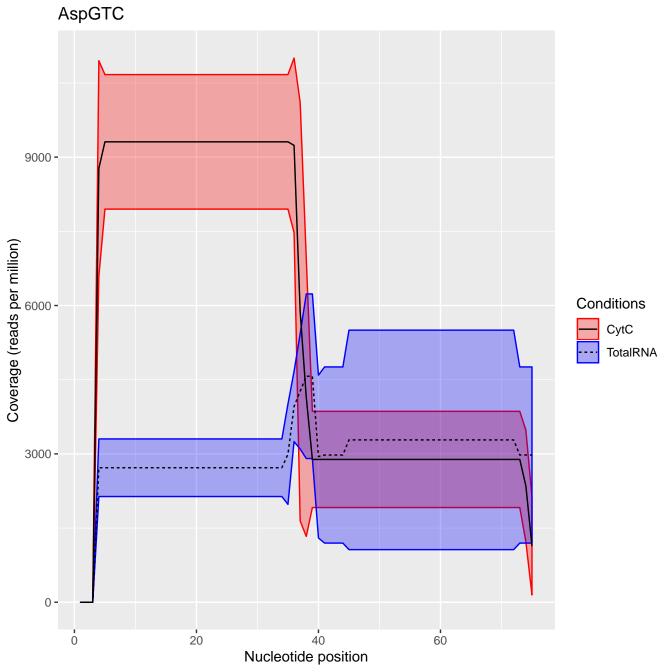
Distribution Score

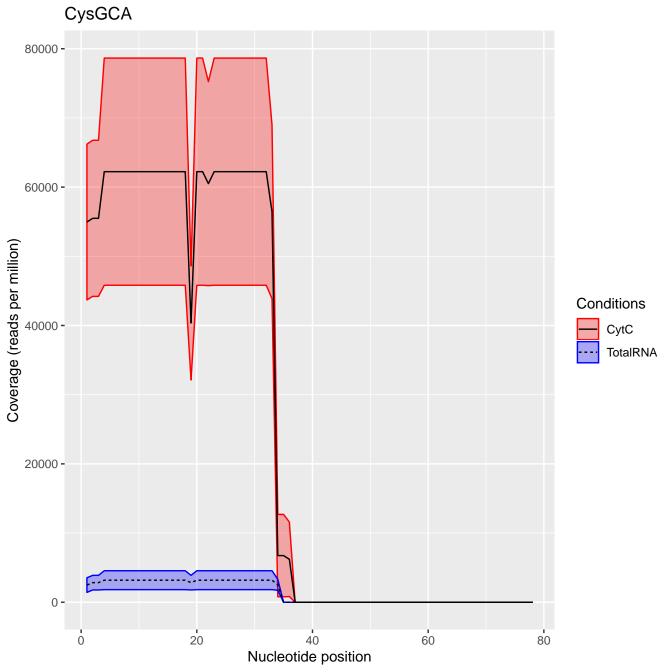
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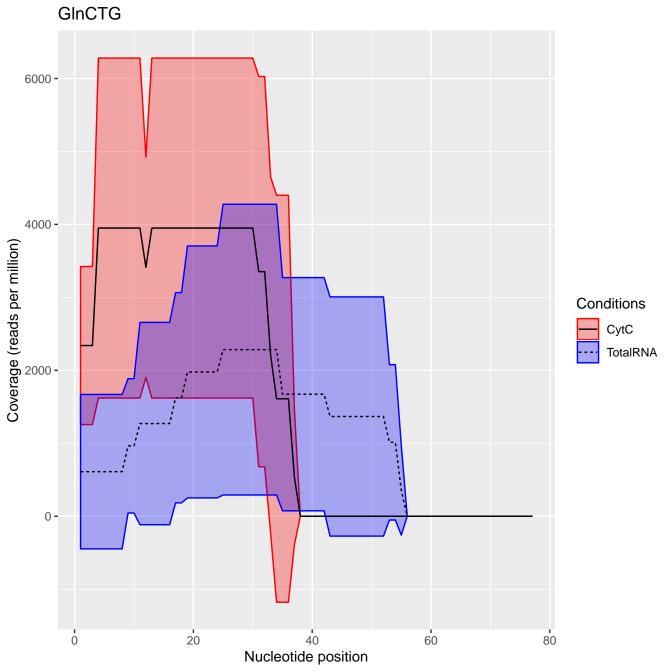


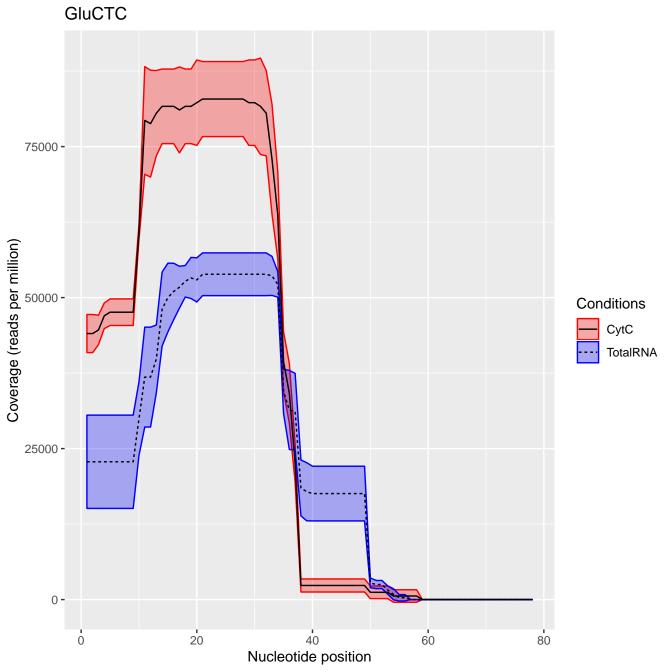


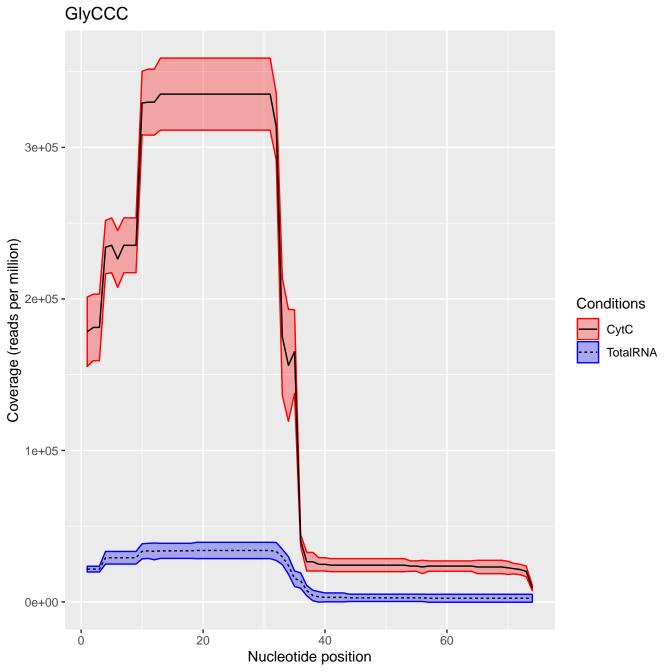


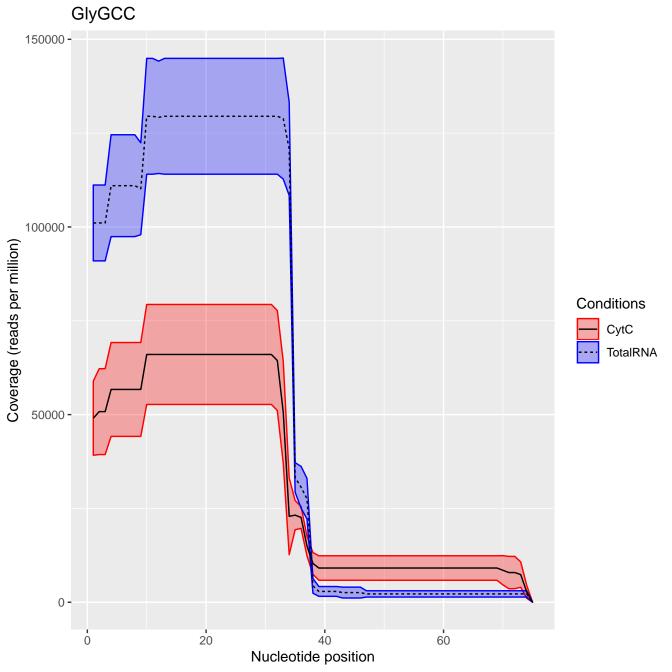


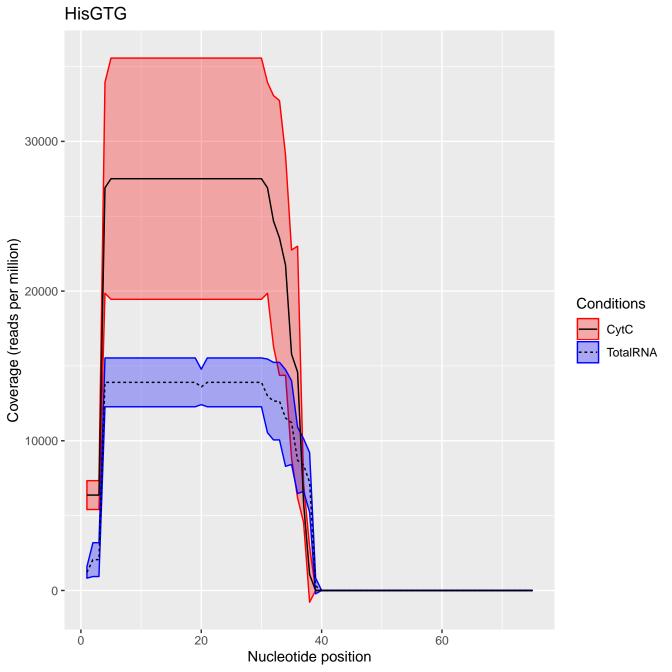


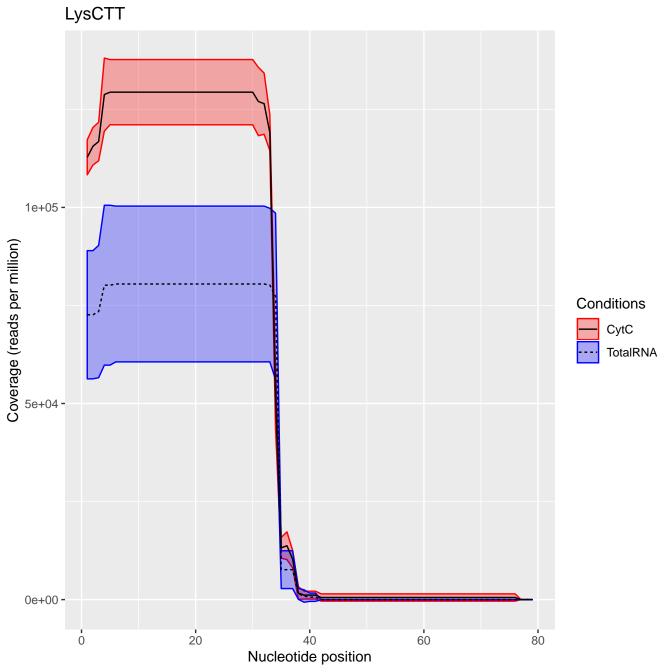


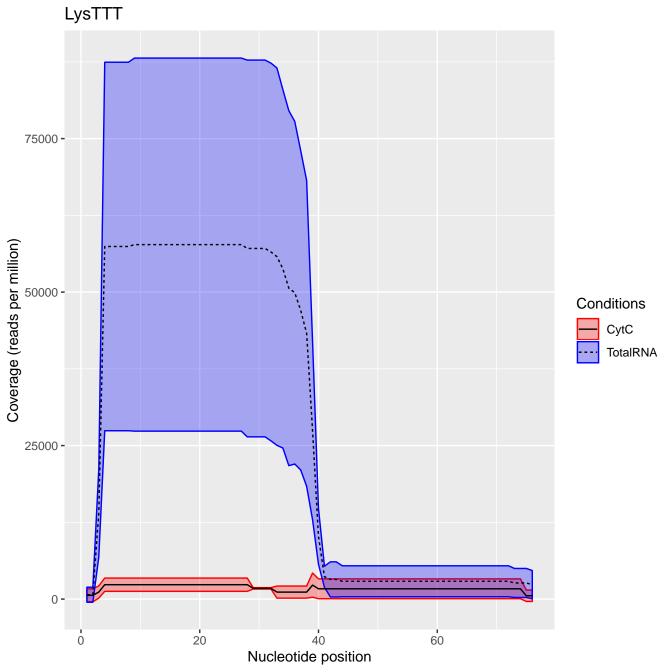


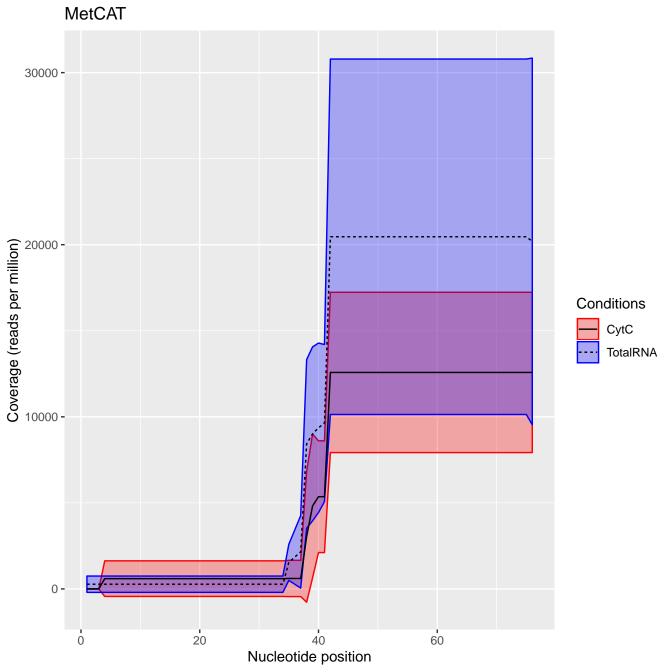


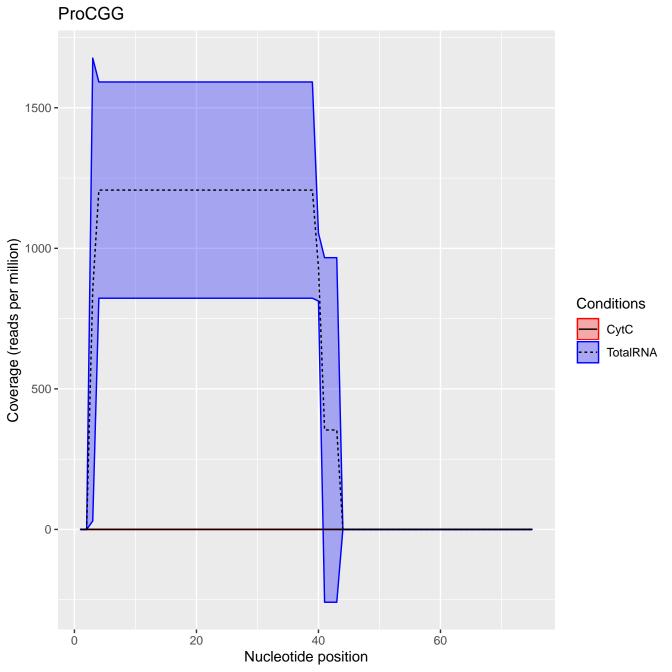


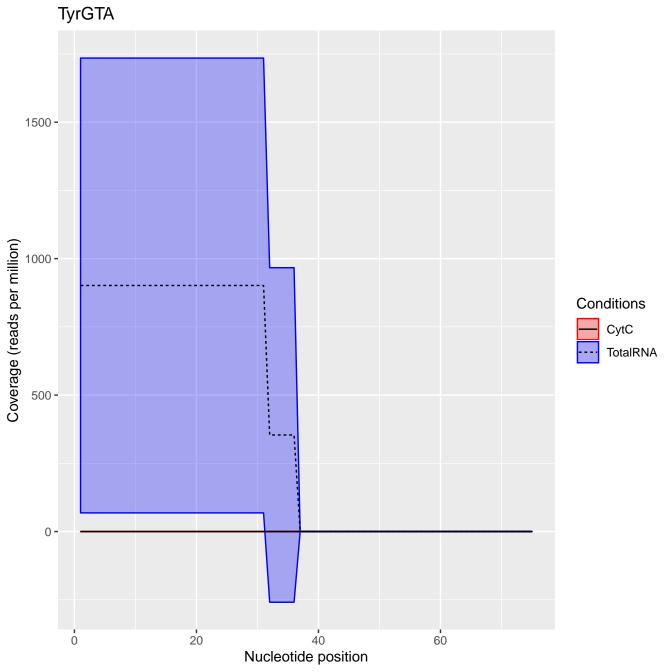


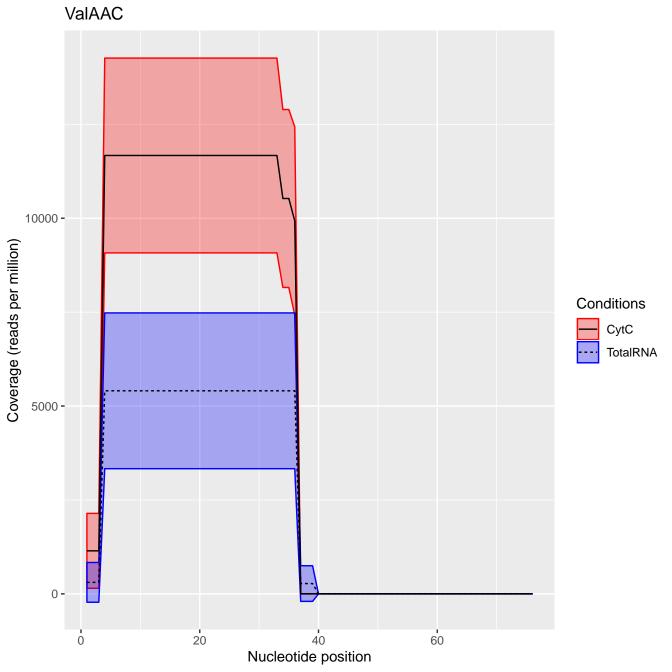






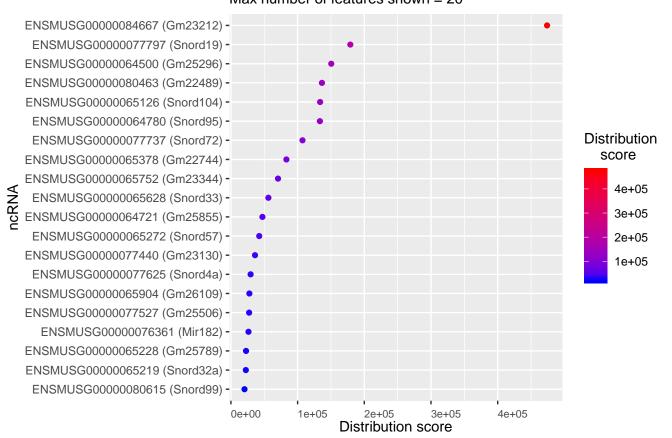


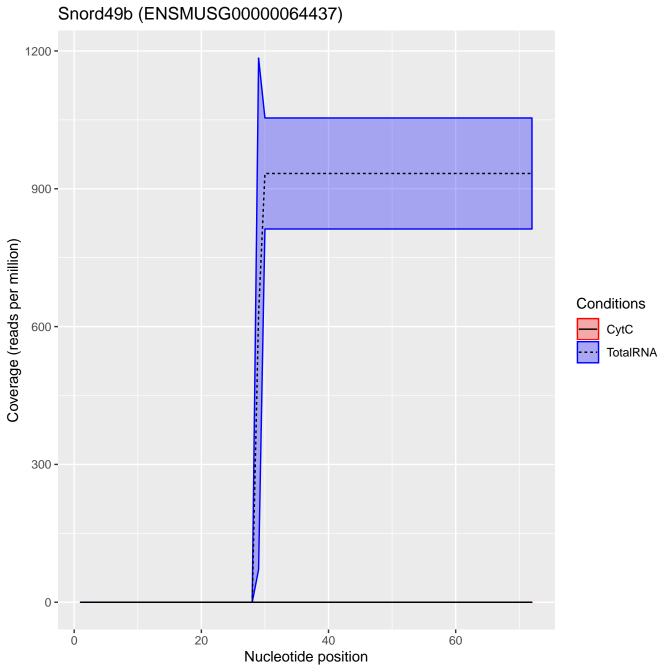


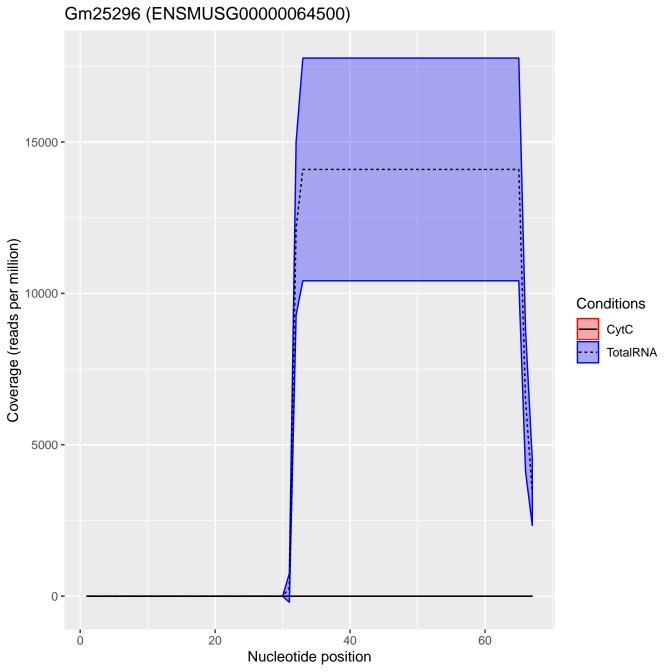


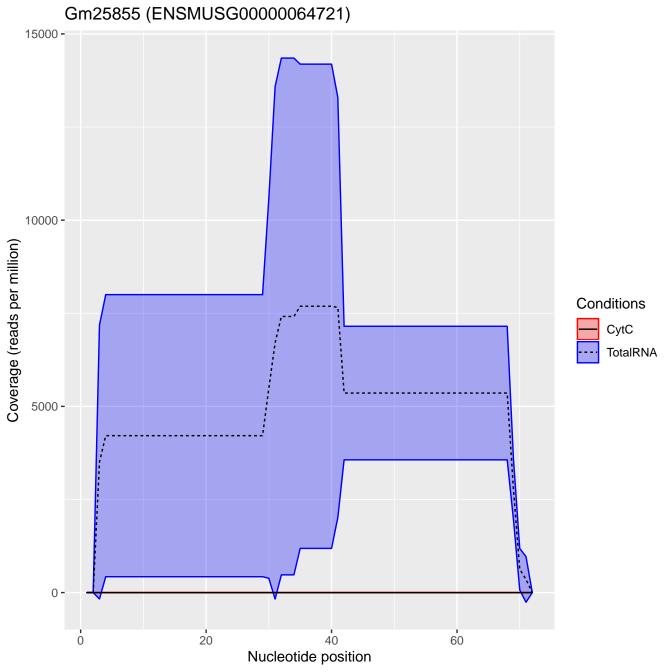
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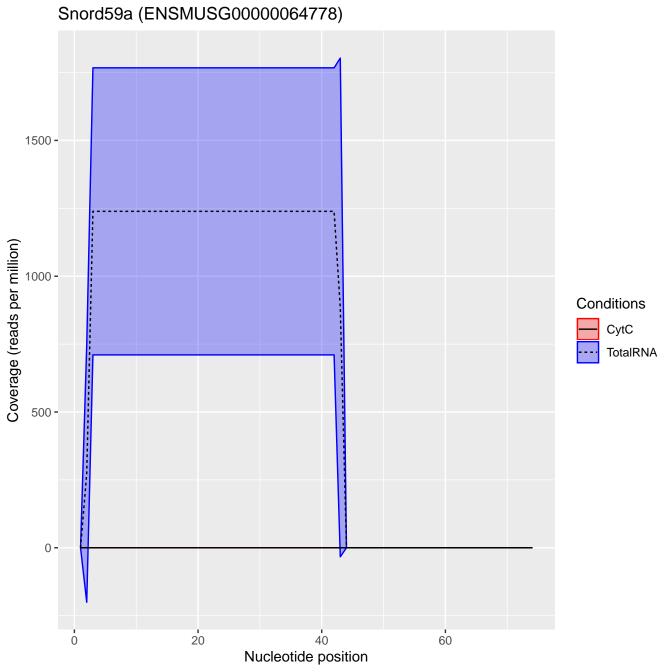
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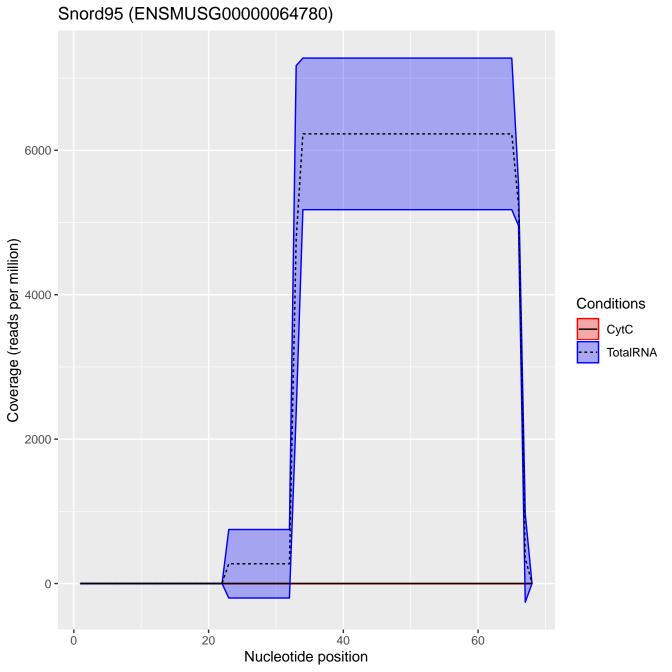


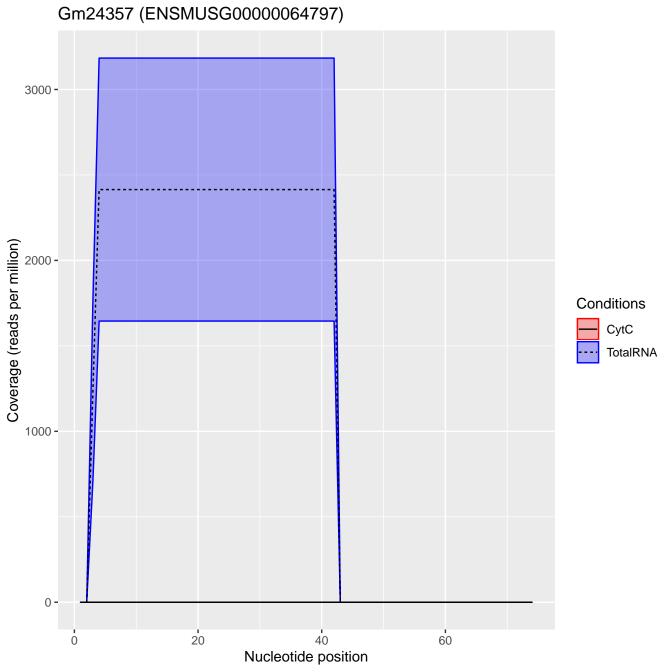


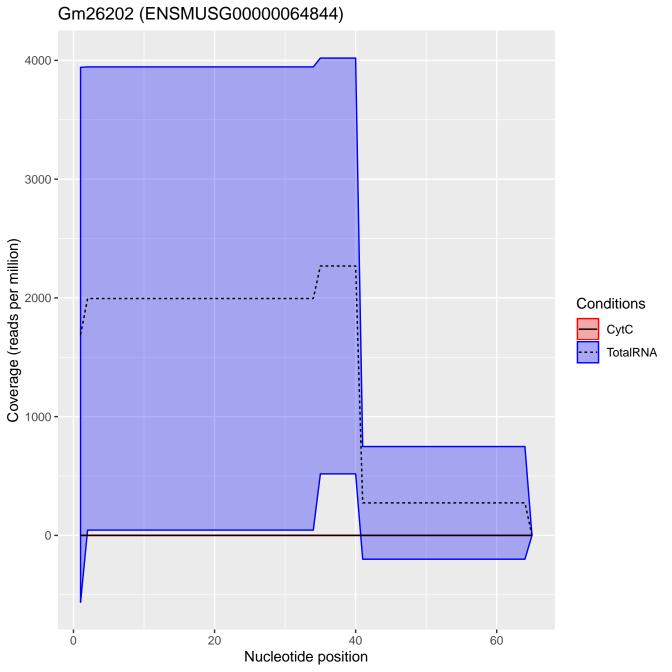


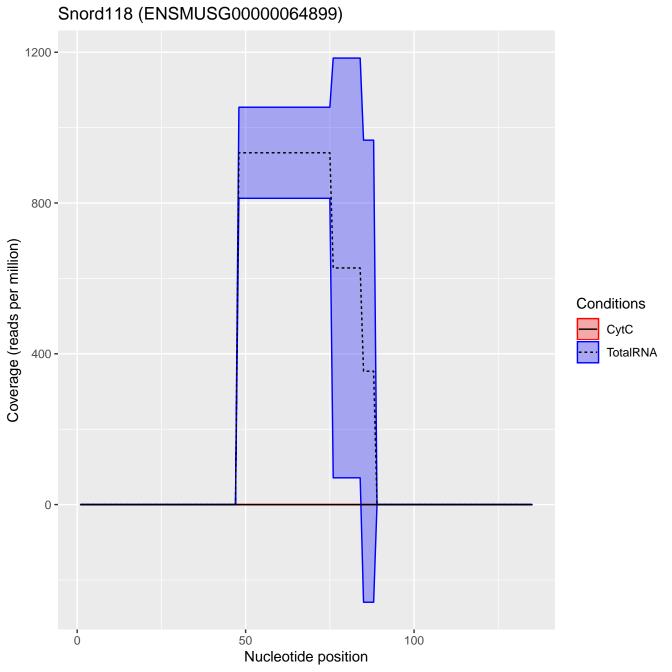


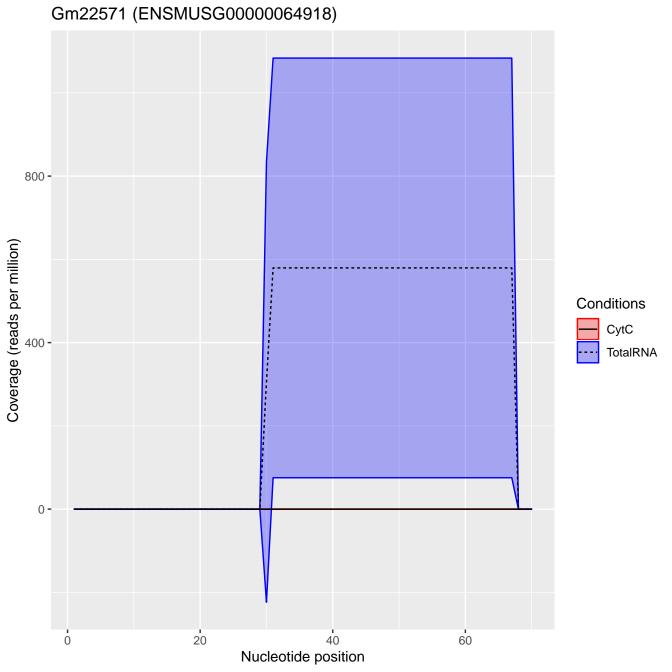


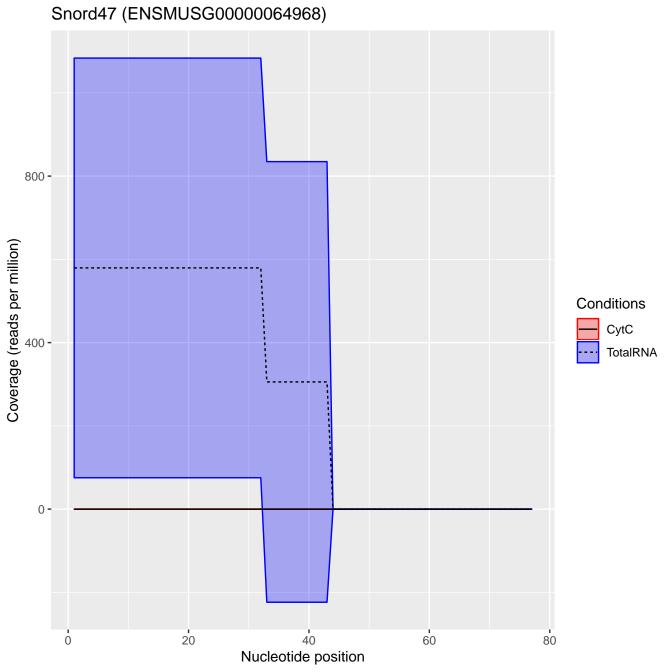


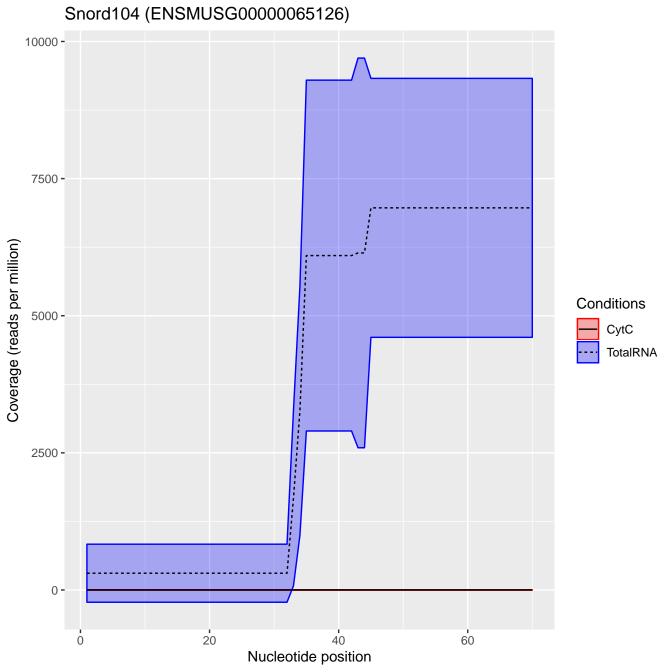


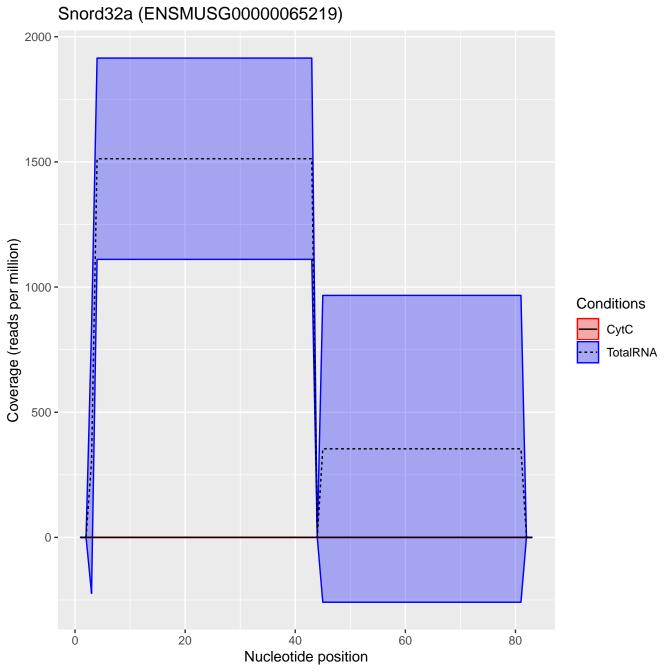


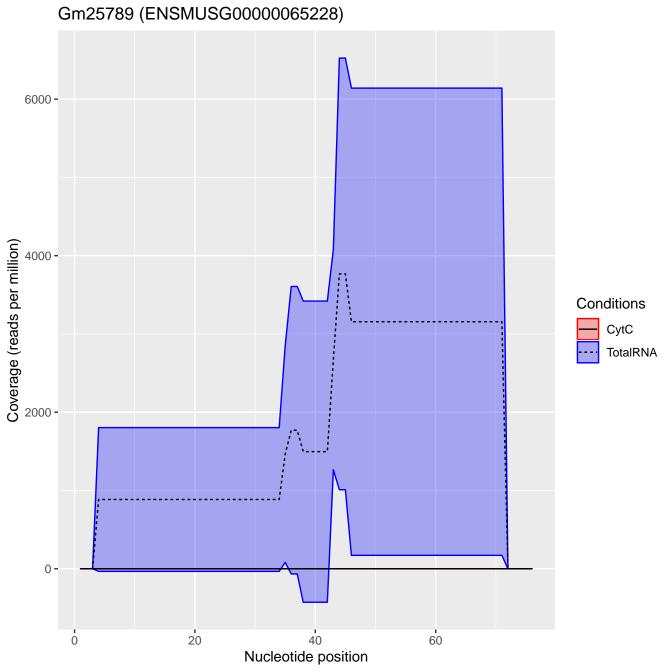


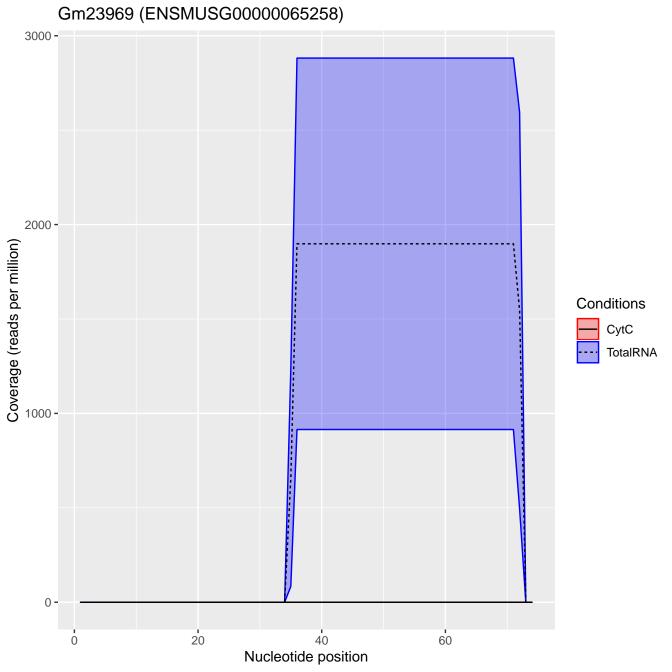


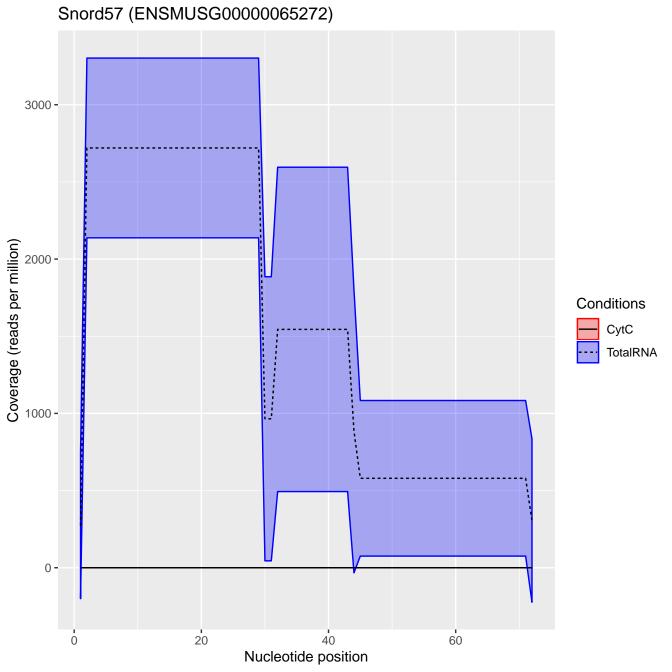


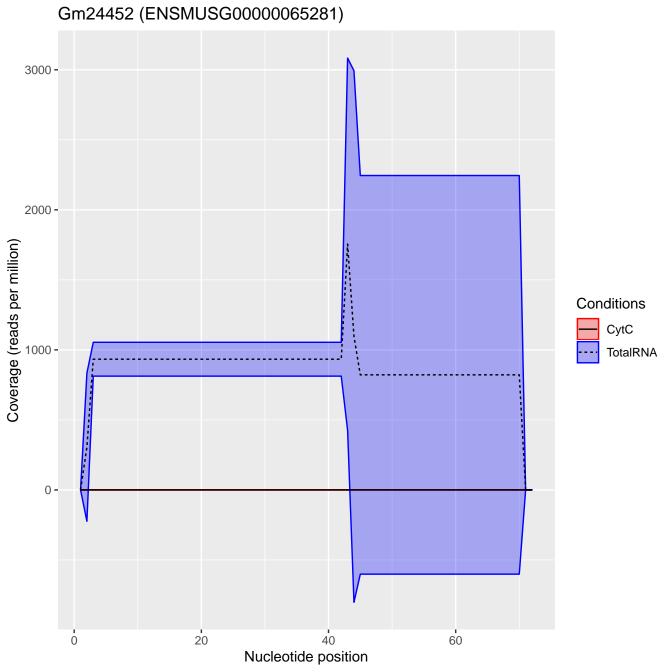


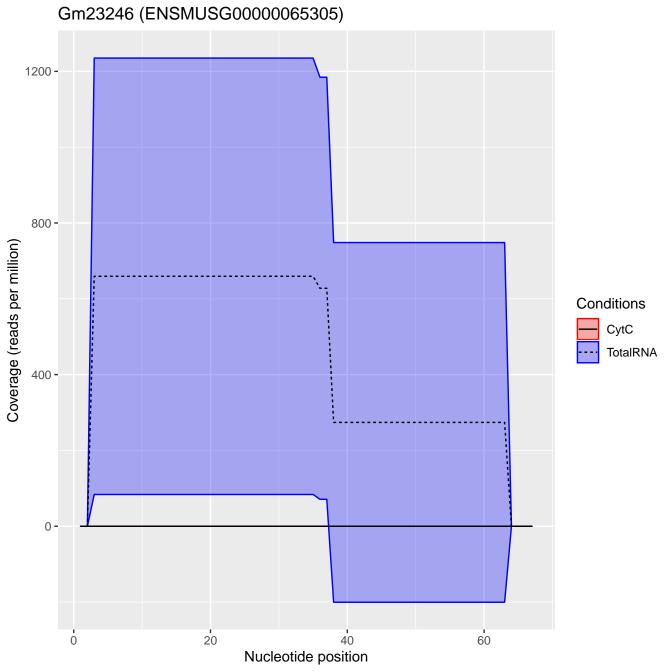


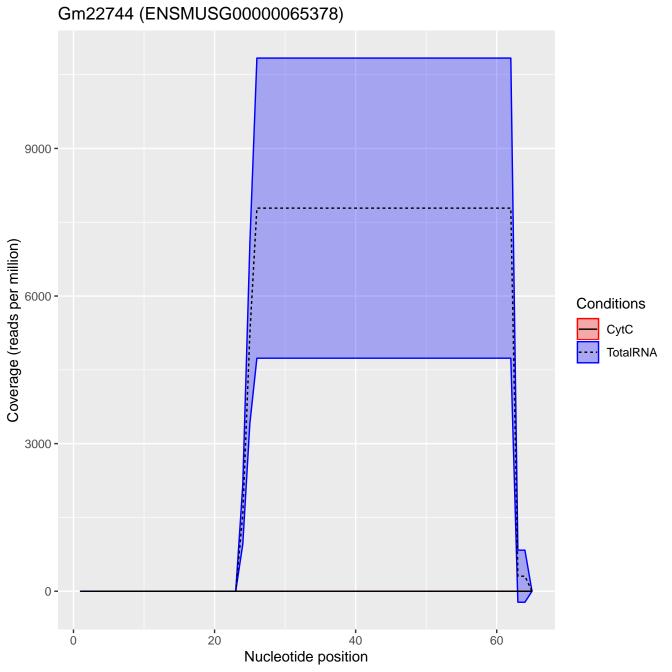


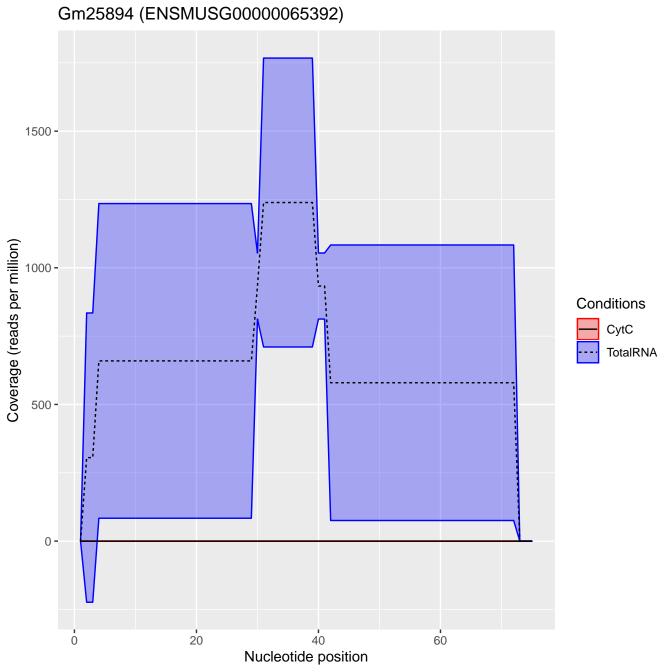




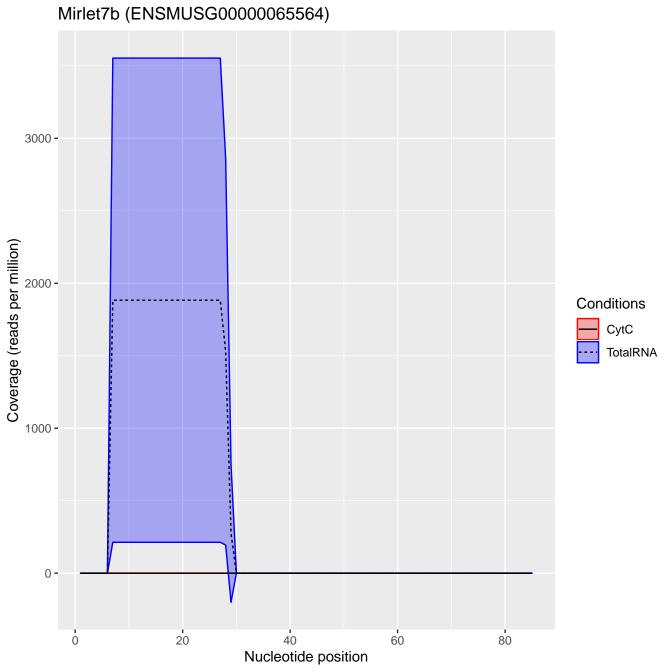




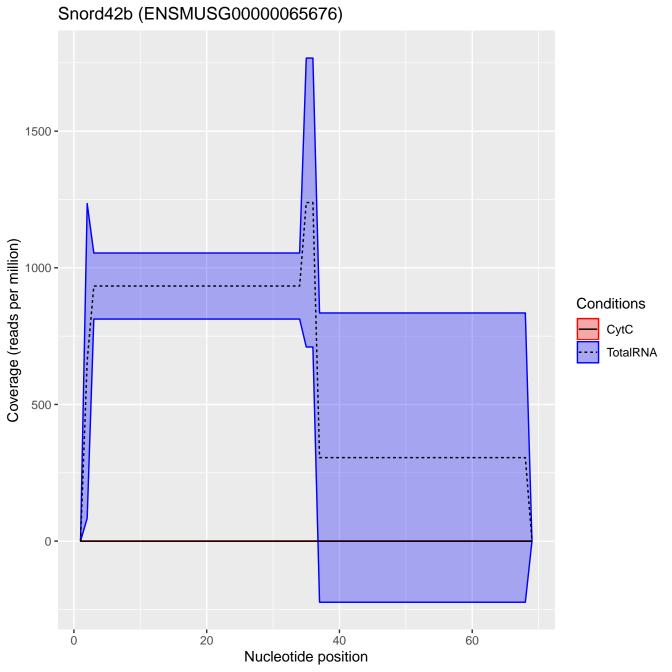


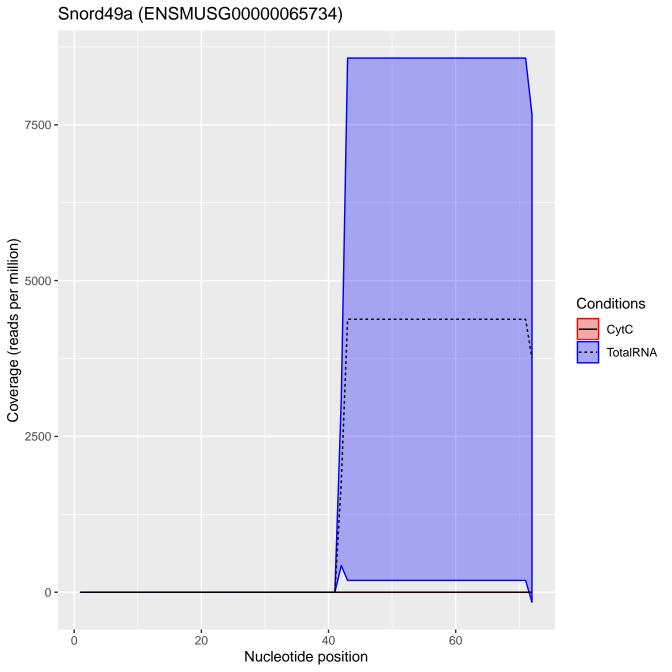


Mir22 (ENSMUSG00000065529) 1500 **-**Coverage (reads per million) Conditions CytC TotalRNA 500 **-**0 -25 75 50 0 Nucleotide position

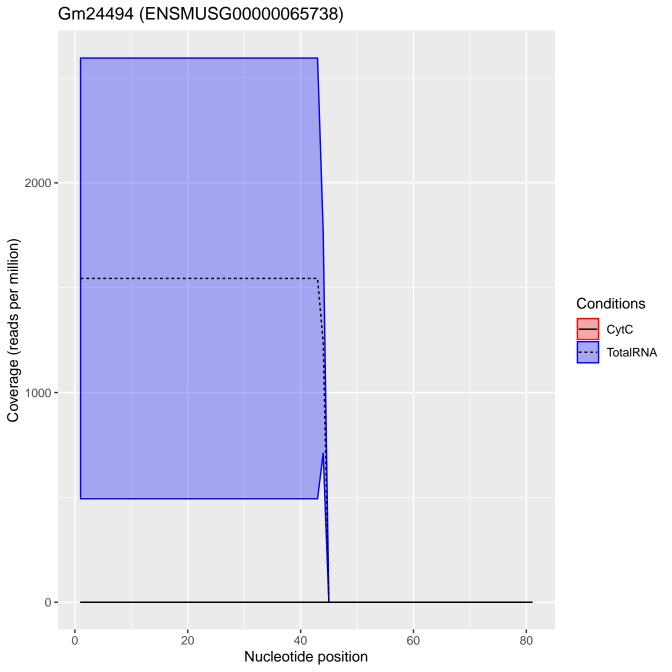


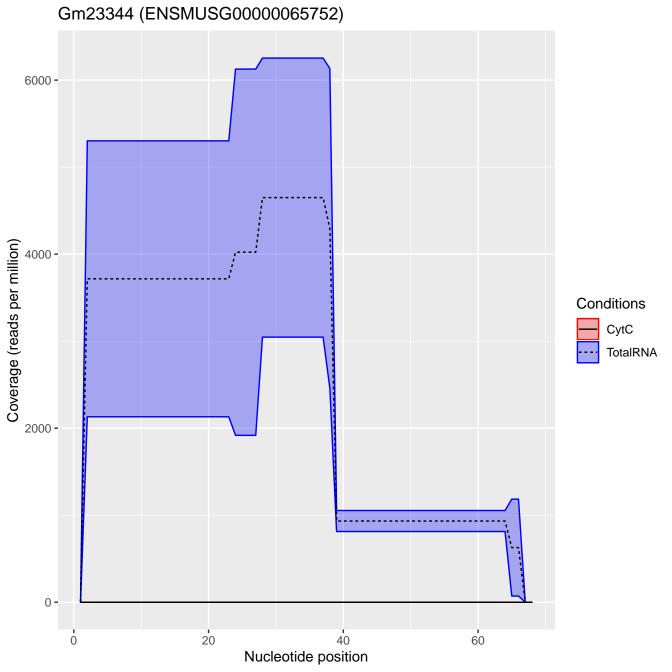
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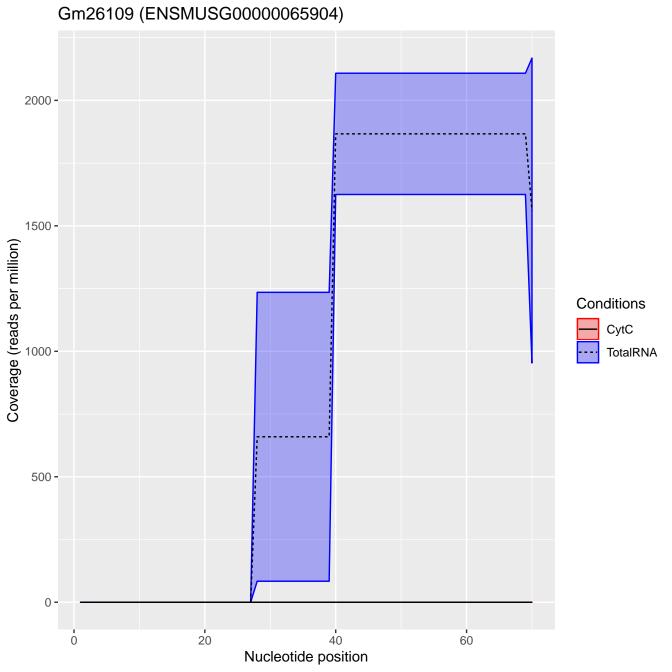


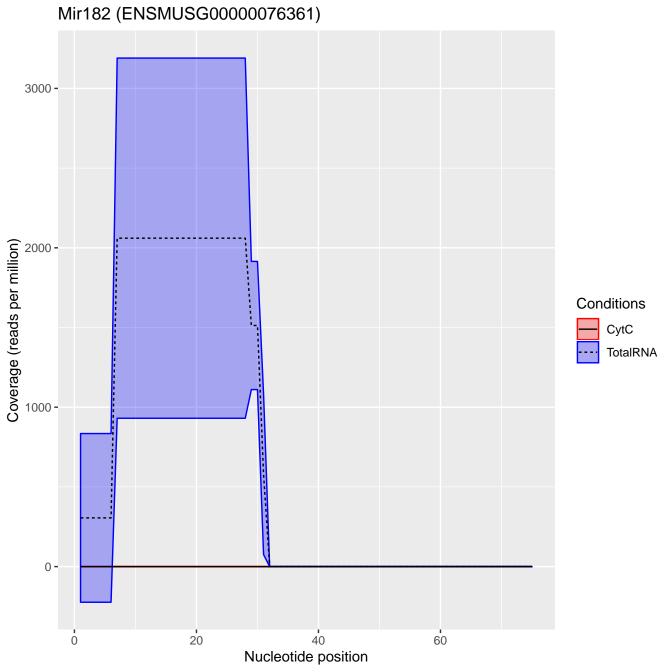


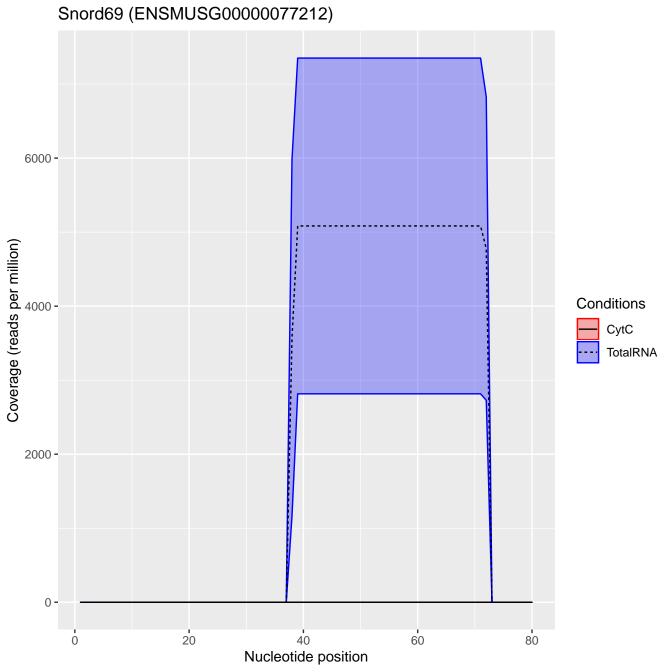
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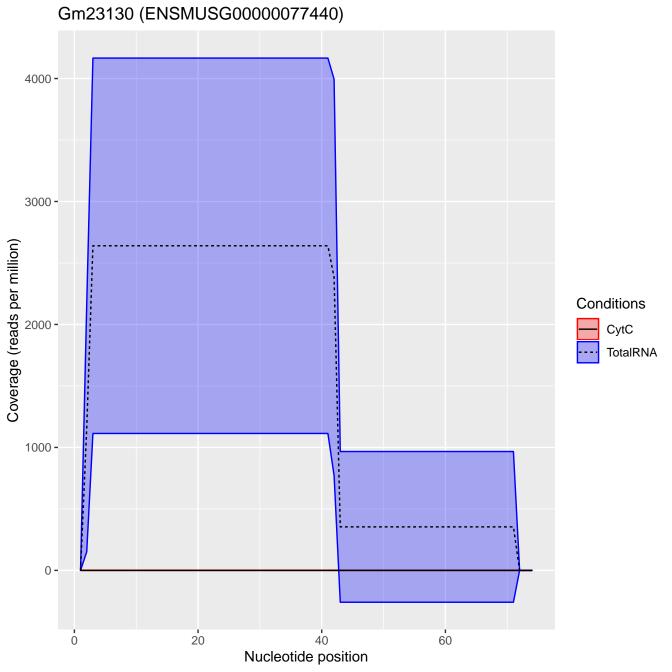




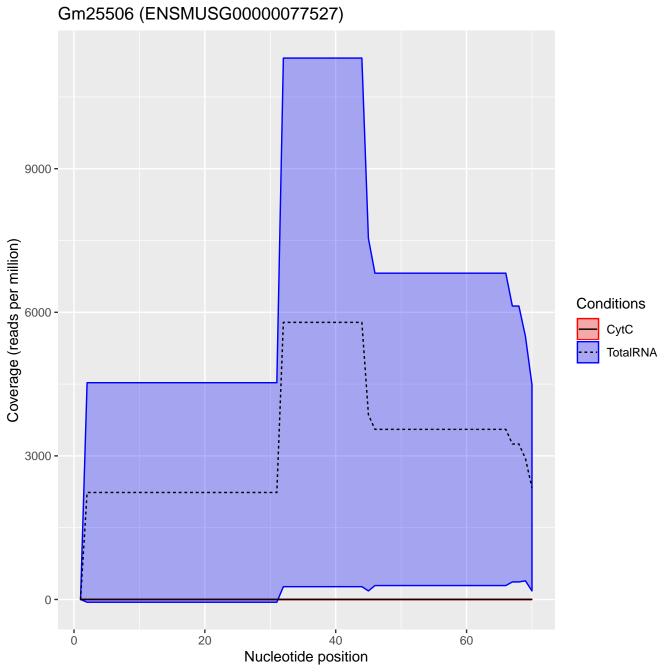


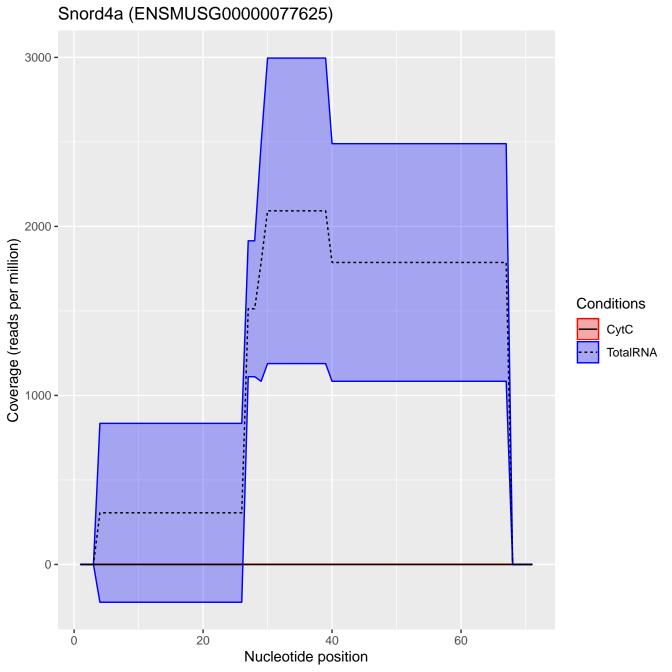


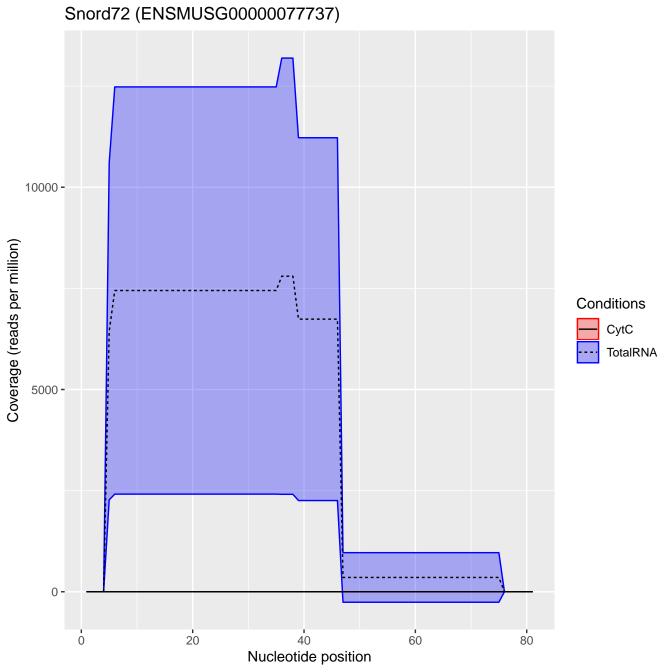


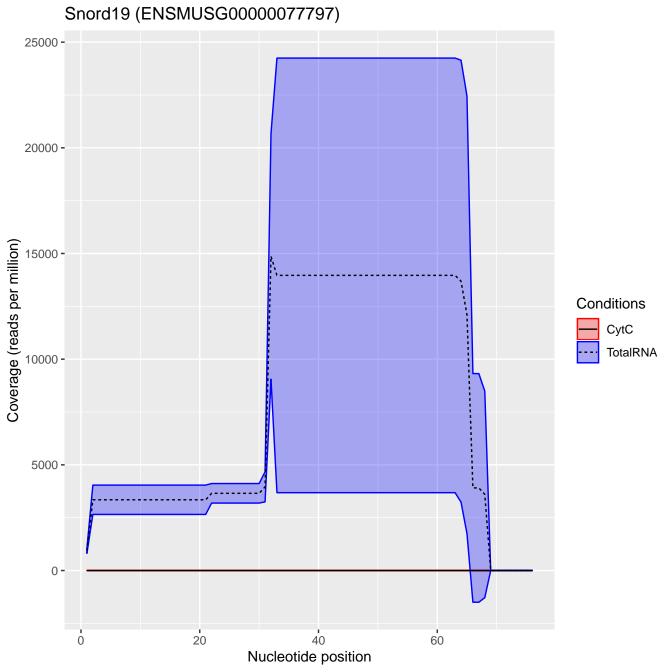


Snord91a (ENSMUSG00000077493) 2000 -1500 -Coverage (reads per million) 1000 -Conditions CytC TotalRNA 500 -0 -0 25 7<sub>5</sub> 50 Nucleotide position

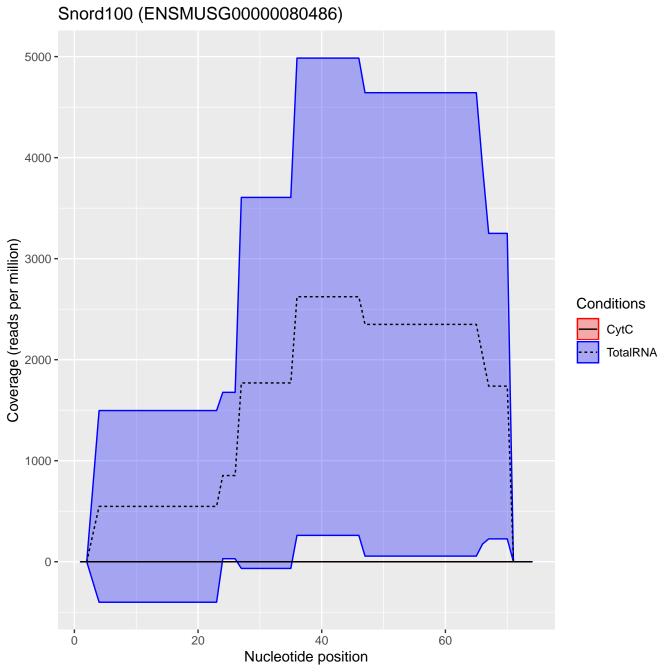


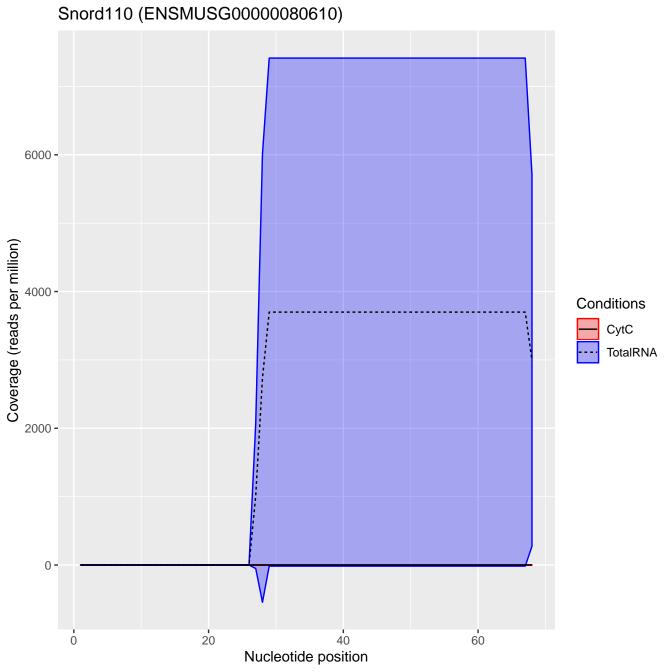


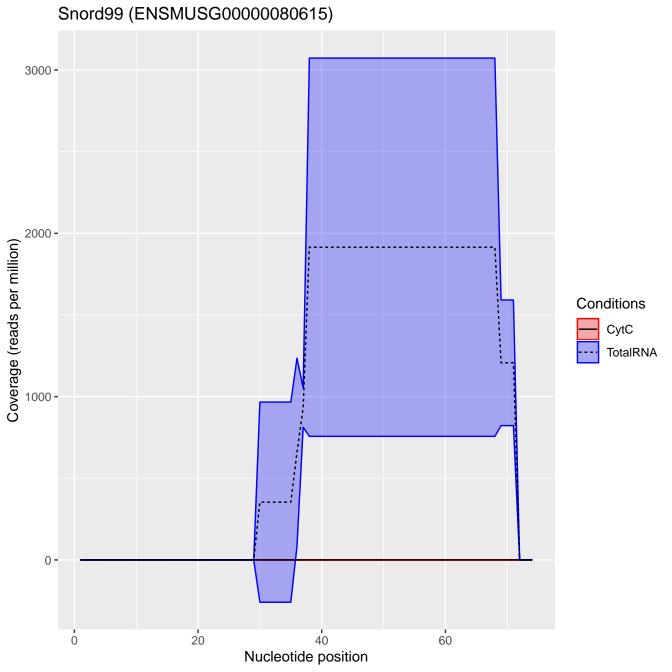


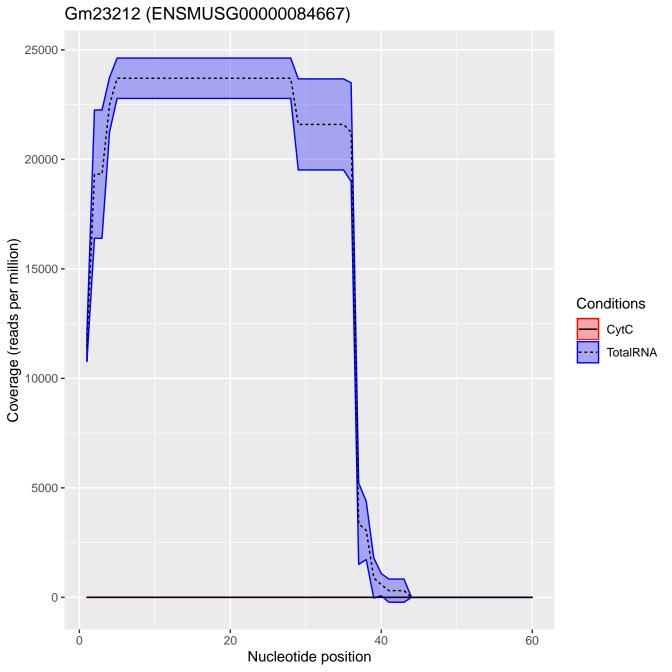


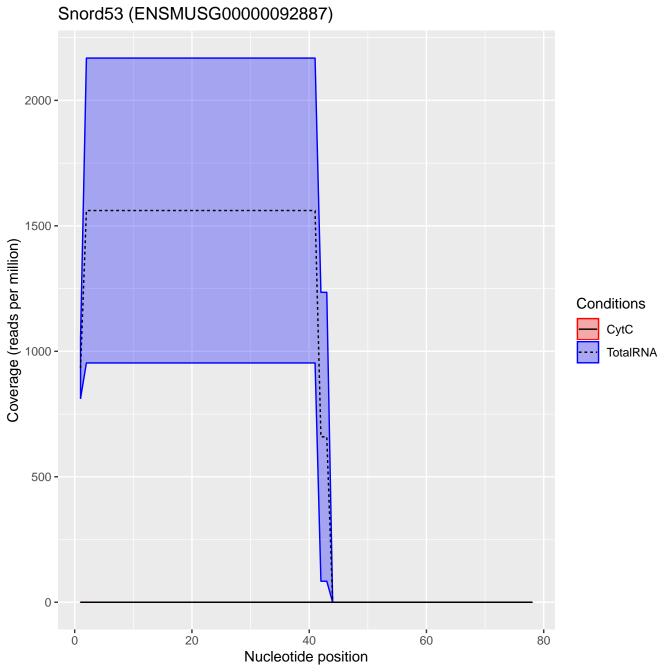
Gm22489 (ENSMUSG00000080463) 12000 -9000 -Coverage (reads per million) Conditions 6000 -CytC TotalRNA 3000 -0 -20 60 40 0 Nucleotide position

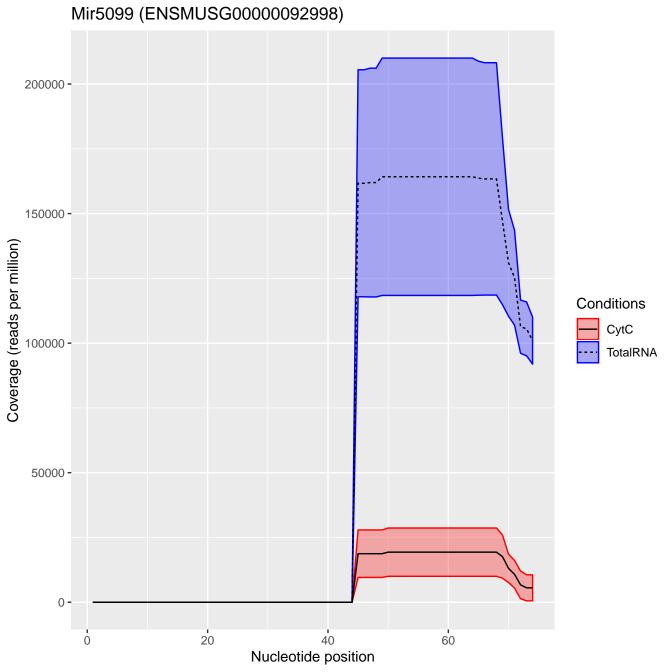


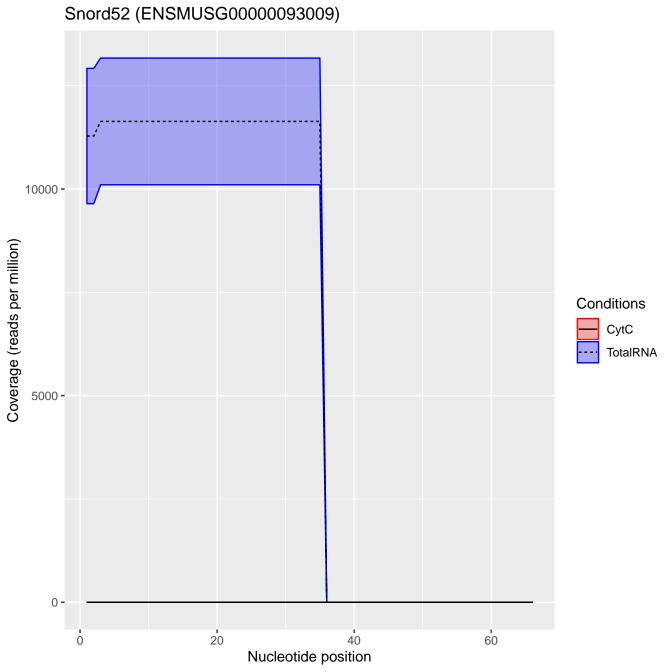




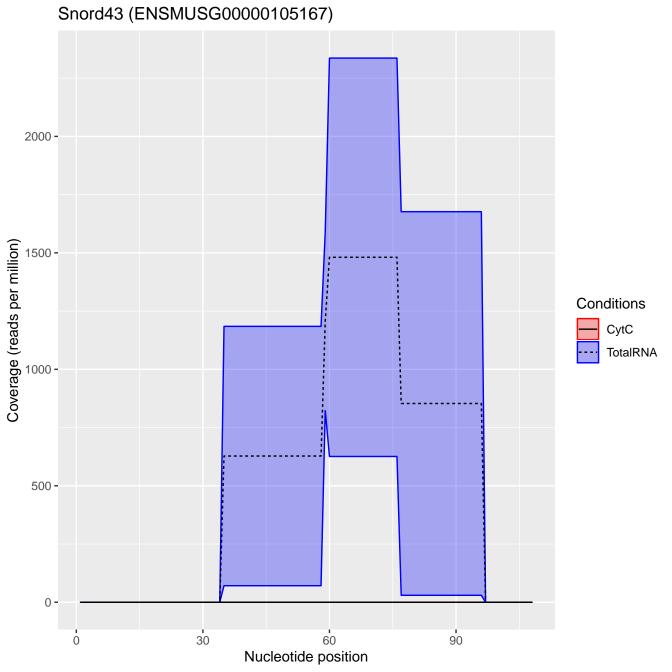








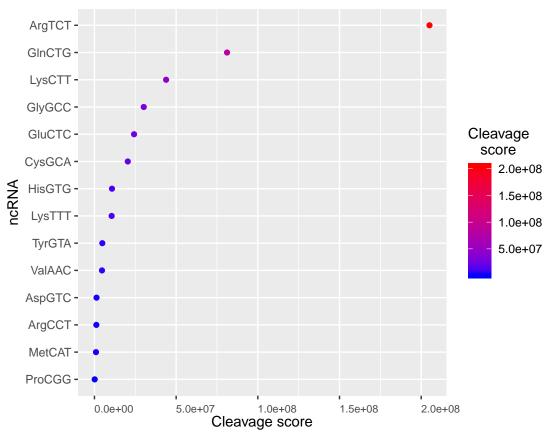
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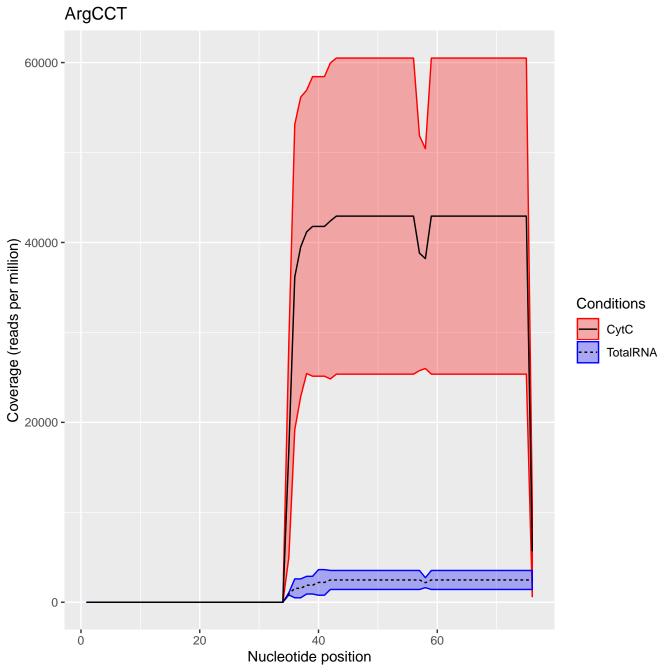


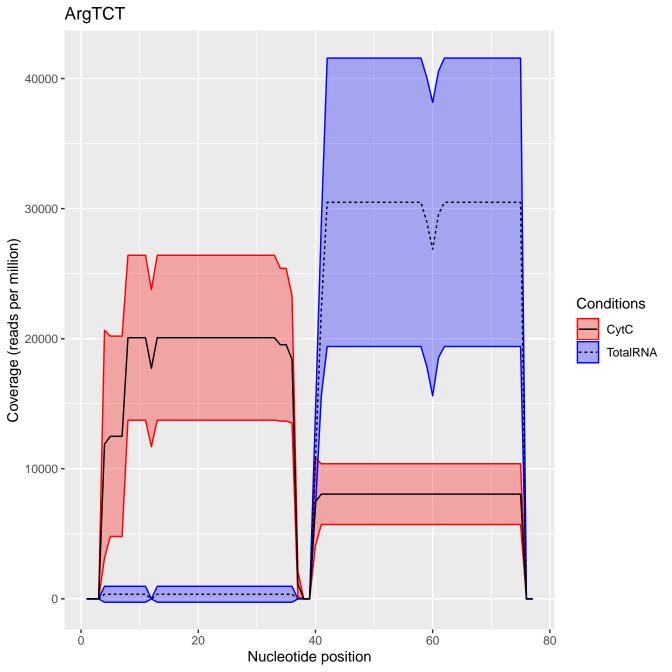
Gm22711 (ENSMUSG00000105884) 1200 -800 -Coverage (reads per million) Conditions CytC TotalRNA 400 **-**0 -Ö 50 100 Nucleotide position

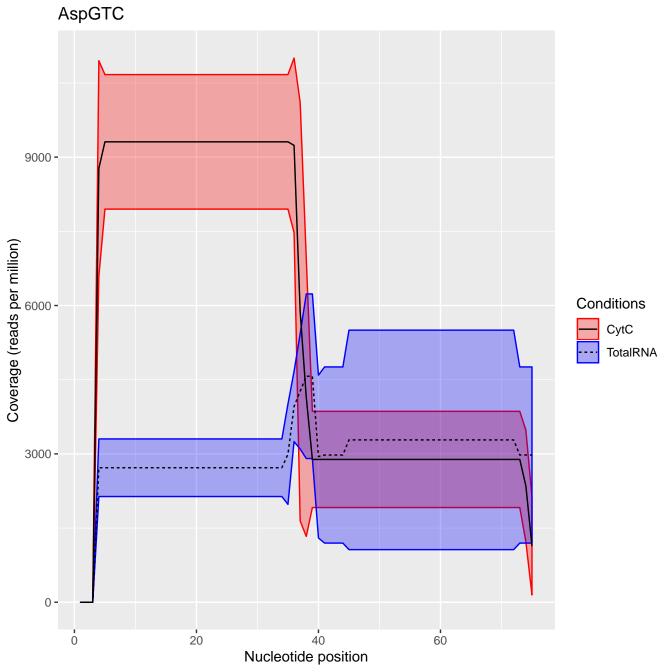
Cleavage score

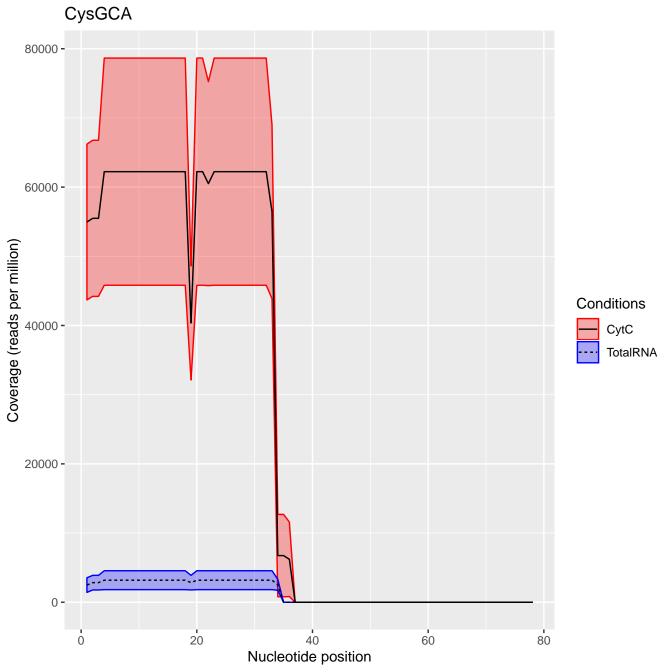
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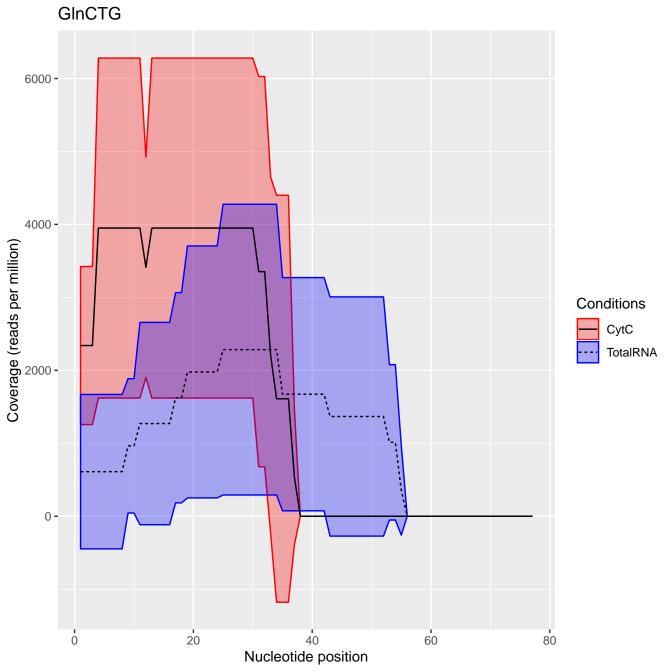


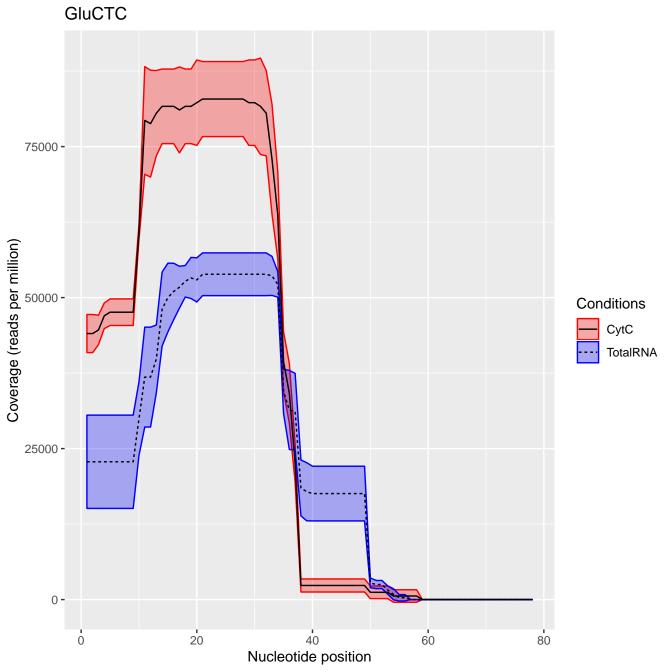


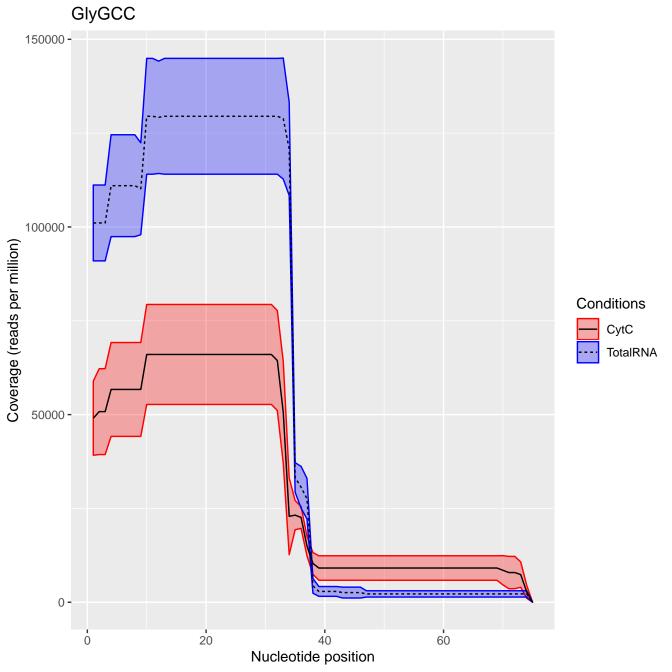


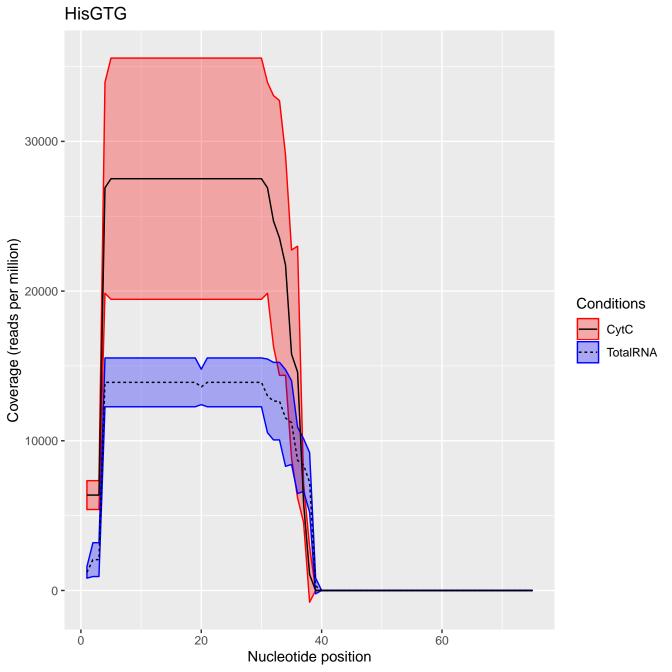


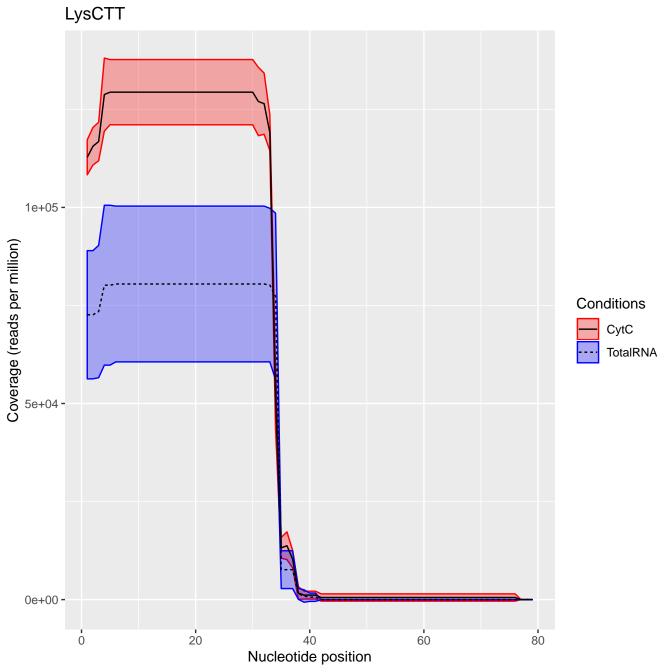


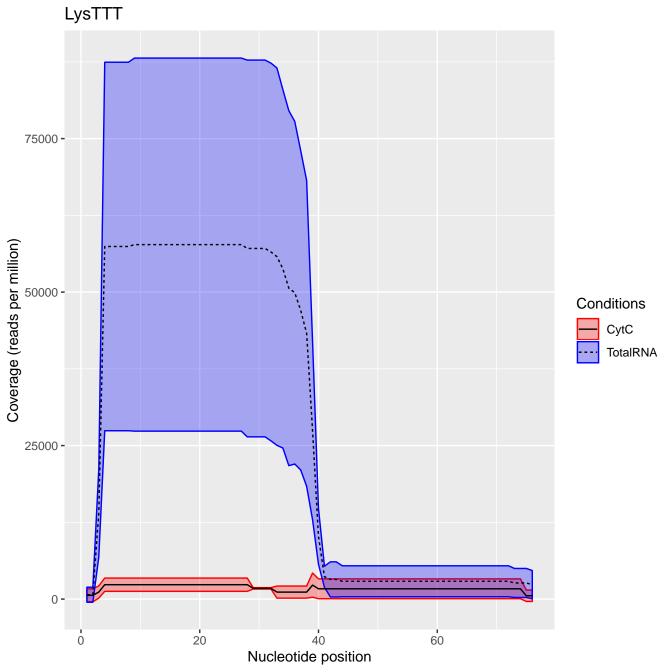


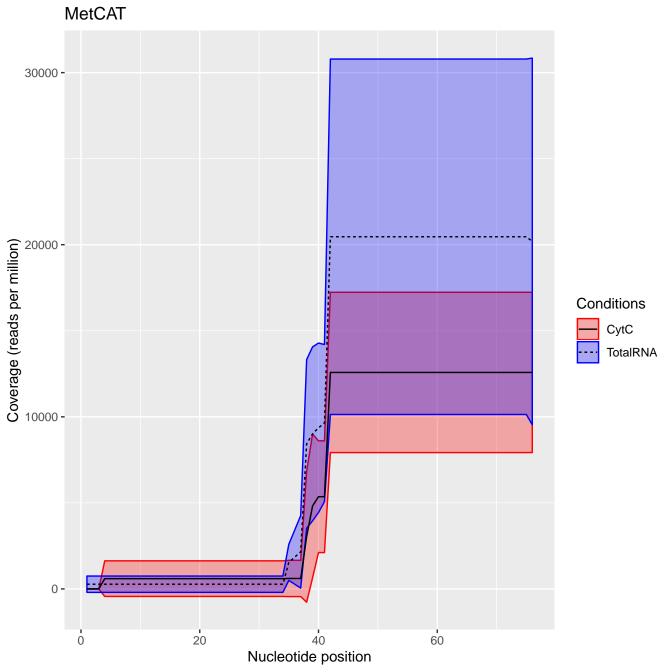


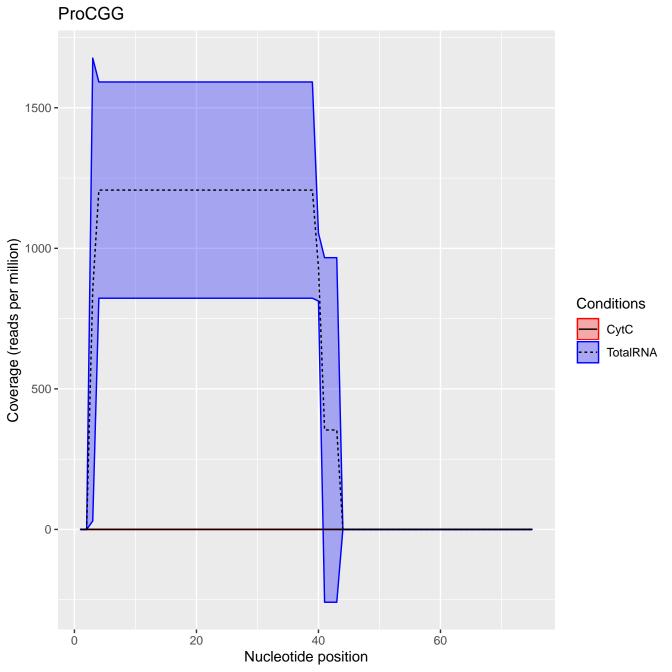


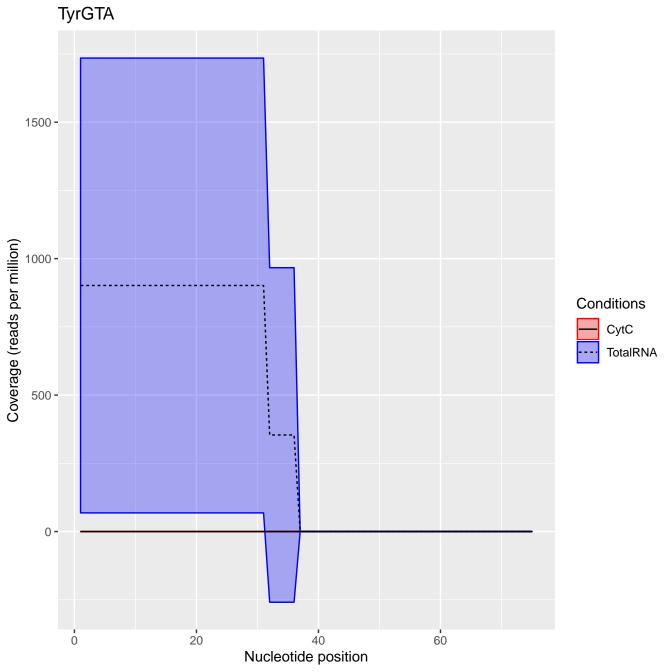


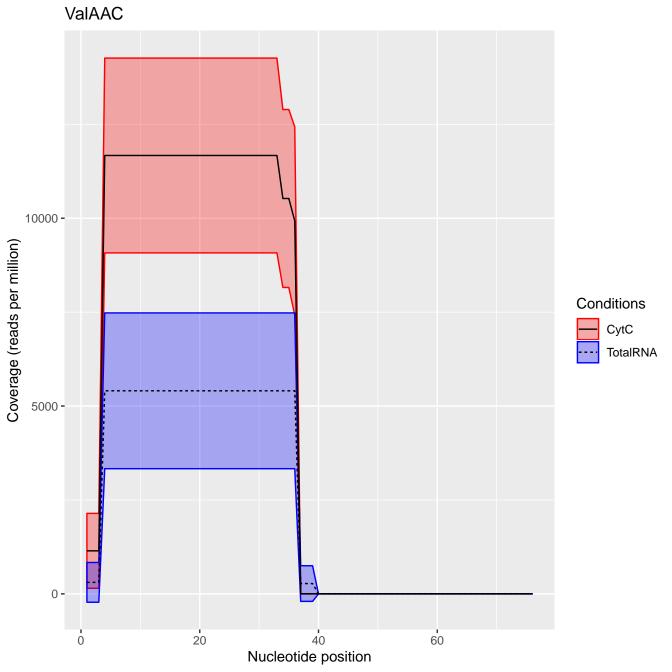






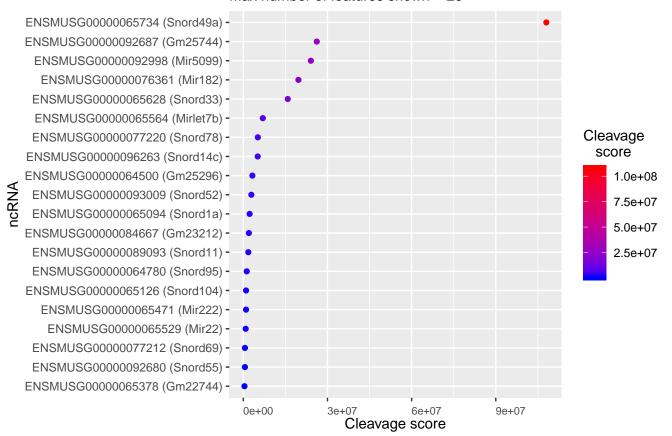


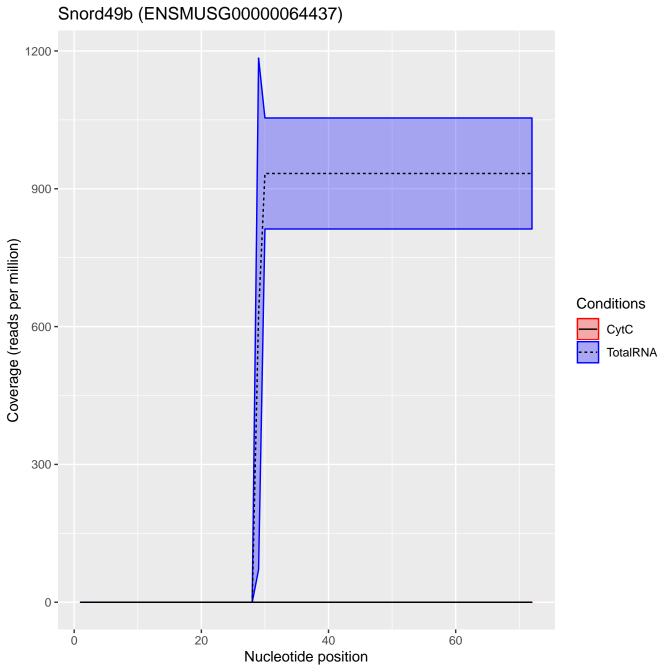


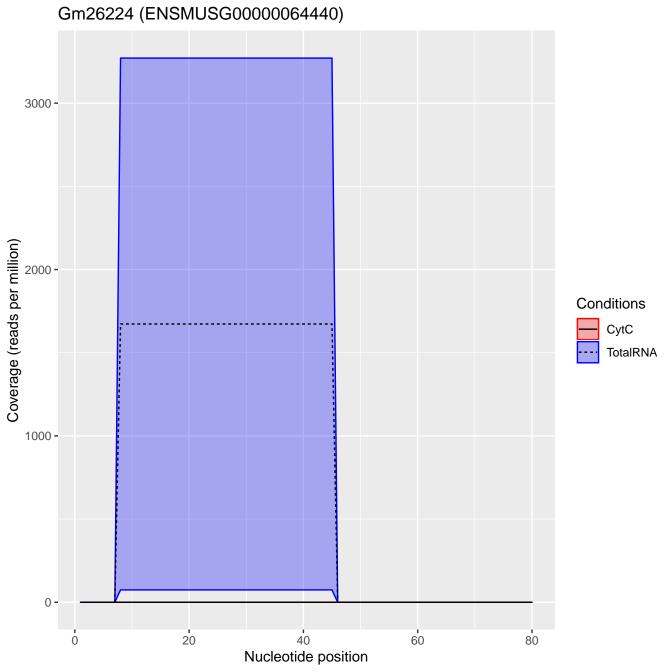


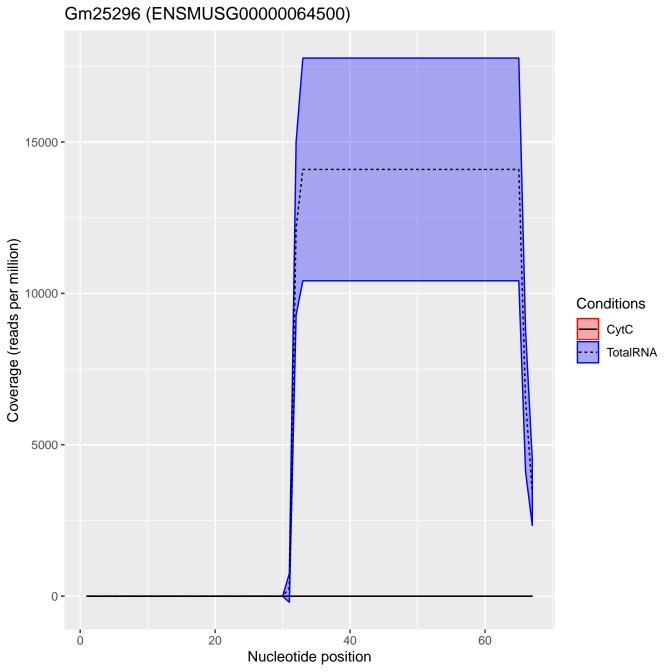
Cleavage score

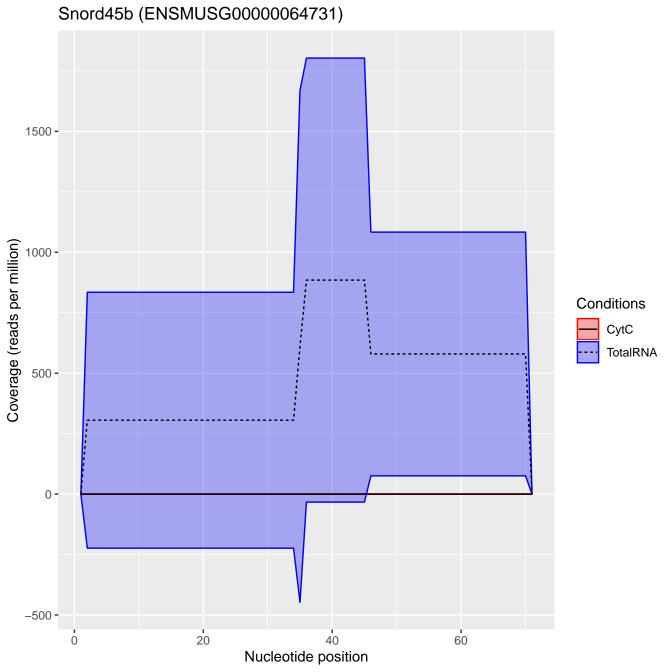
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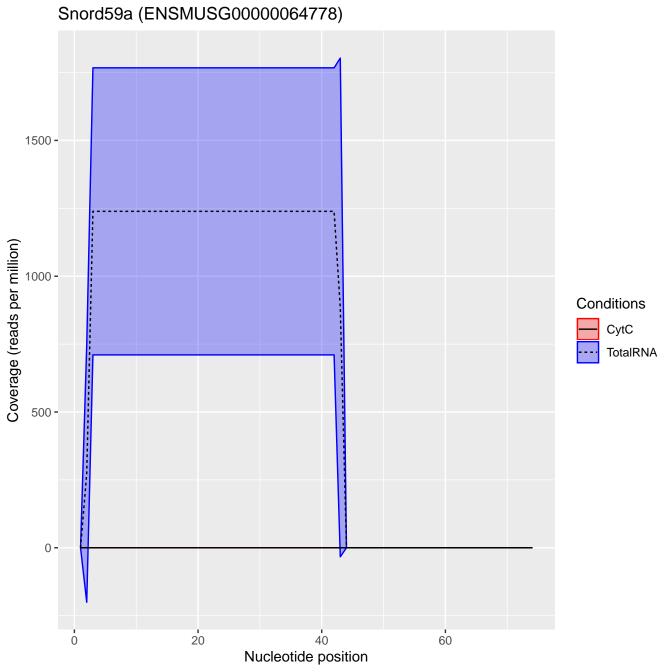


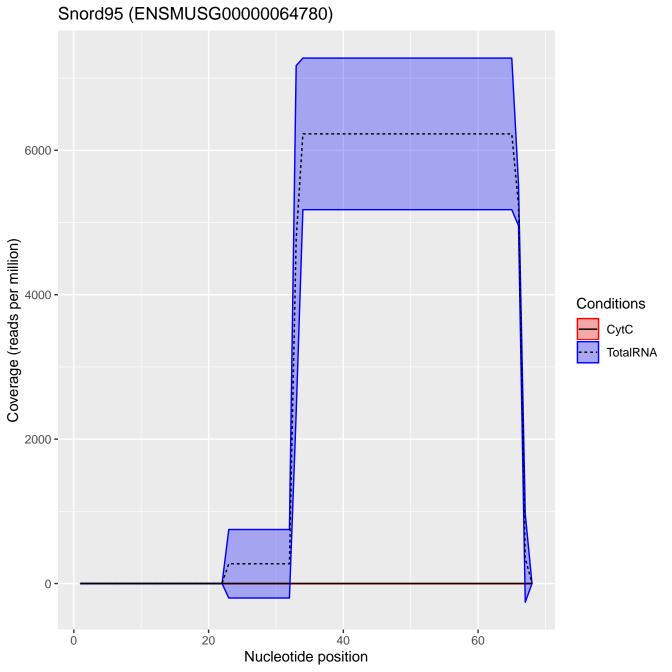


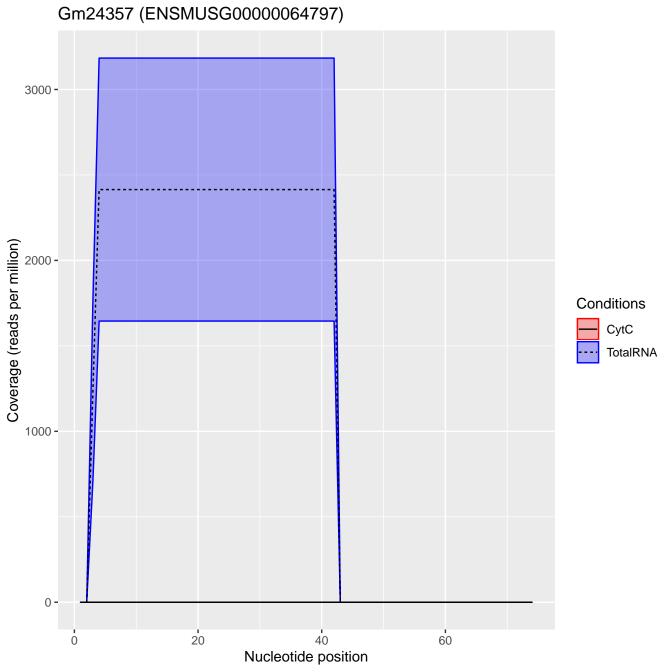


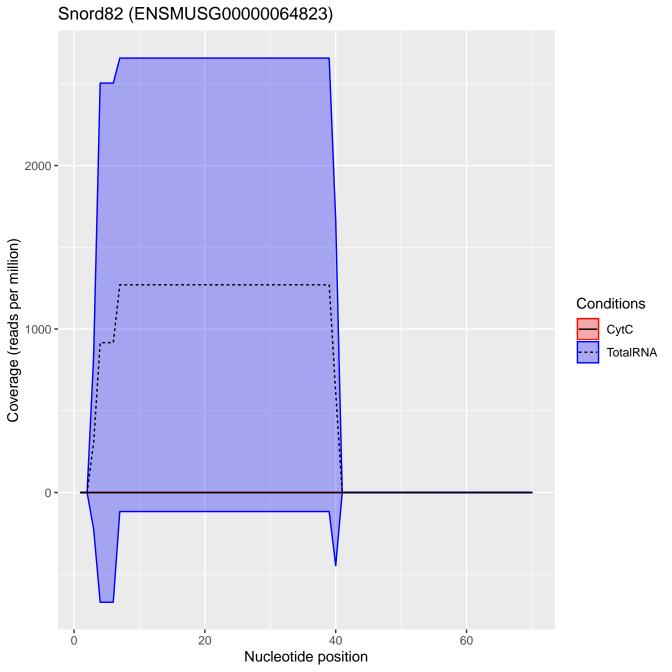


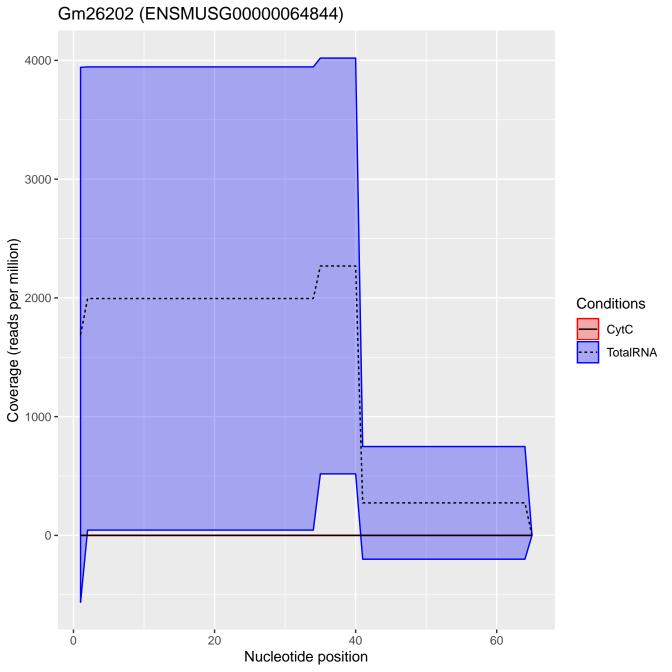


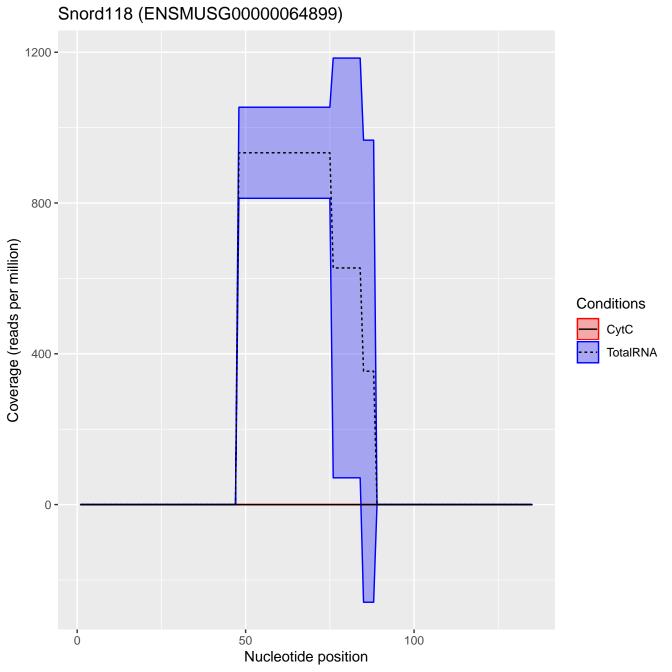


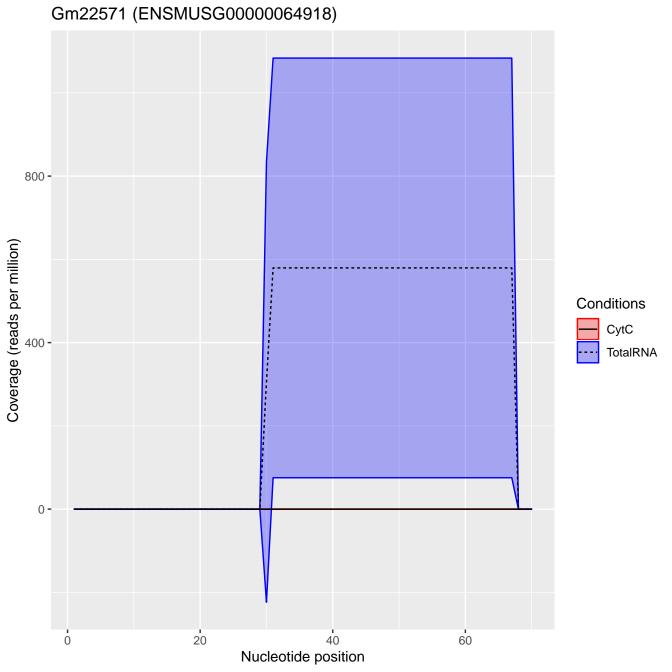


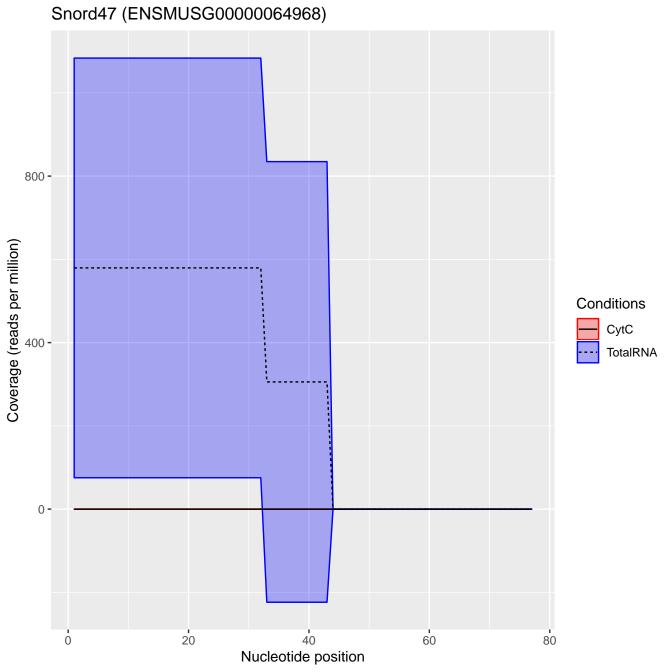


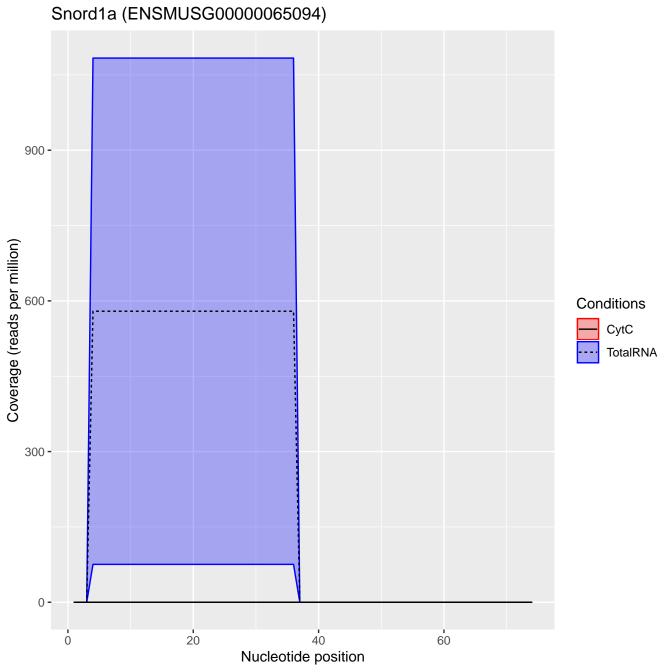


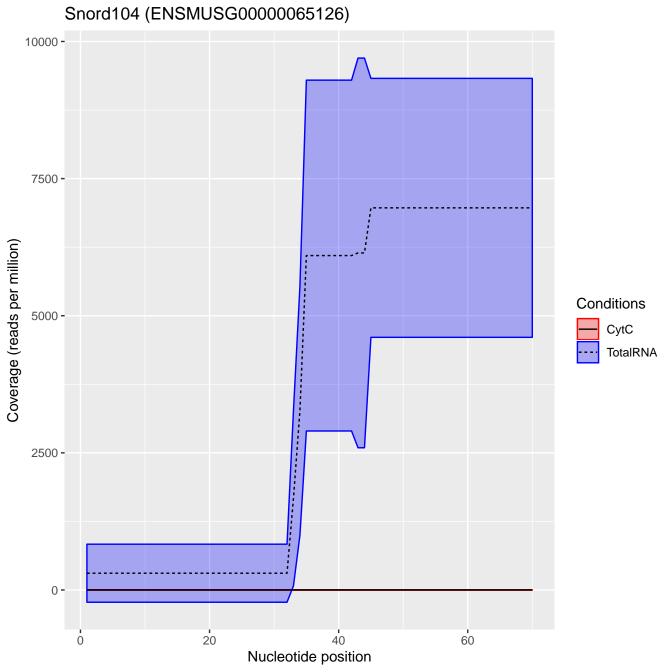


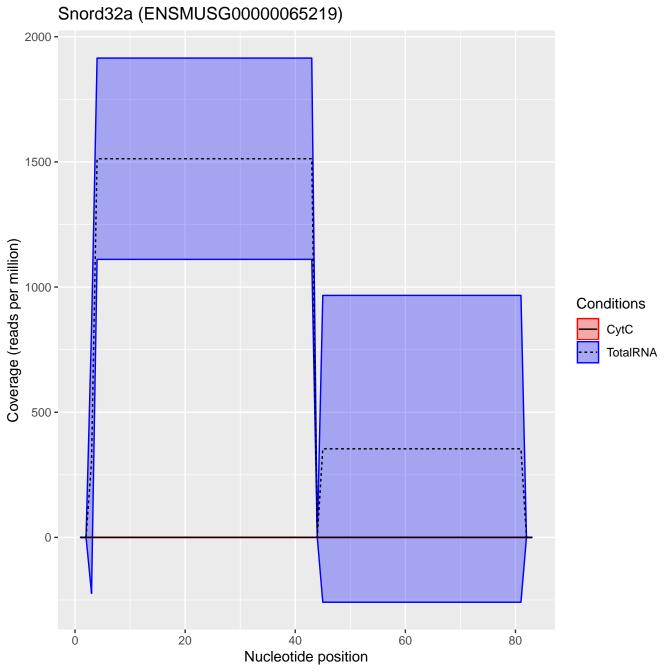


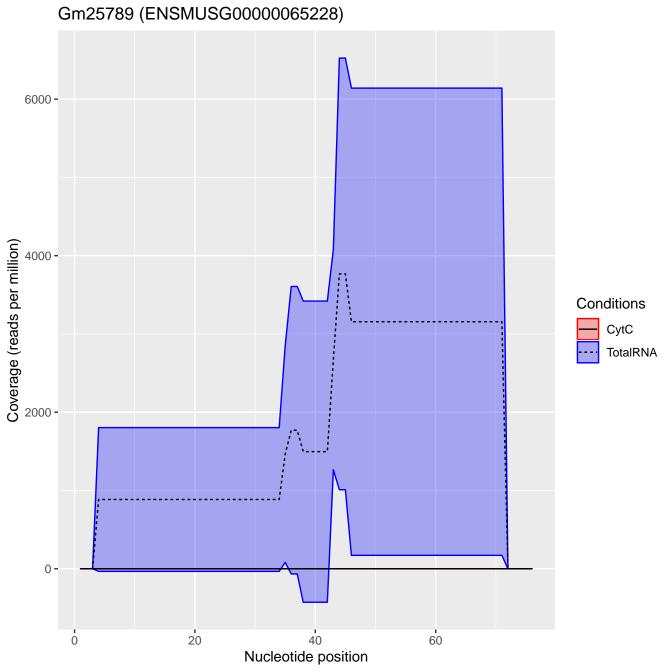


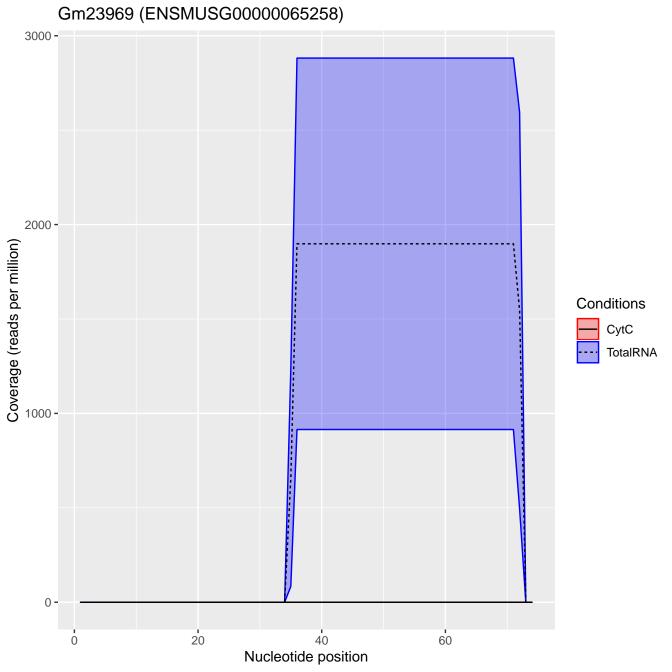


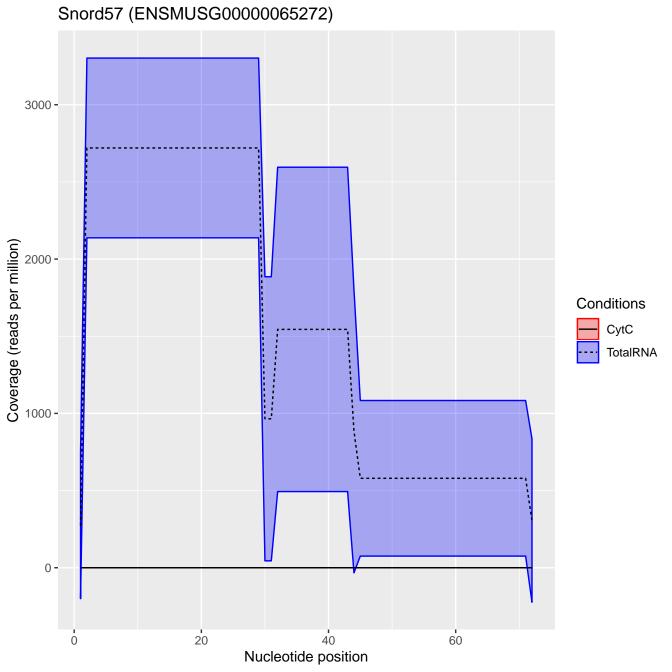


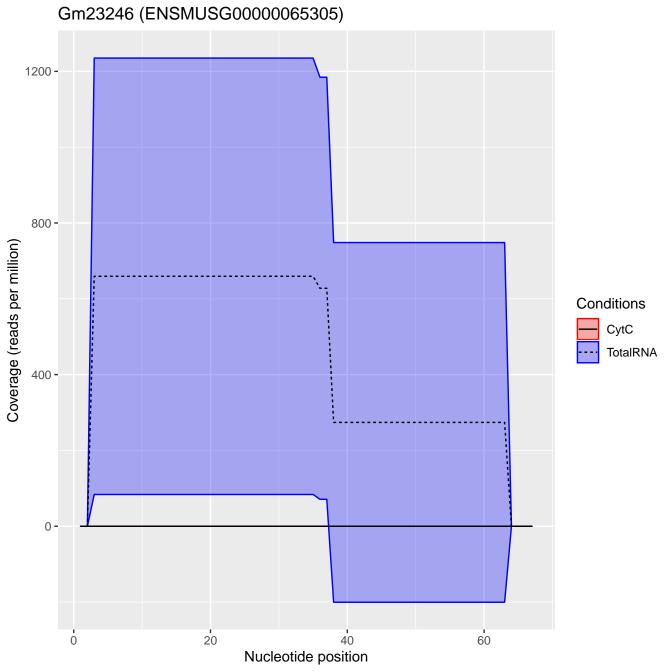


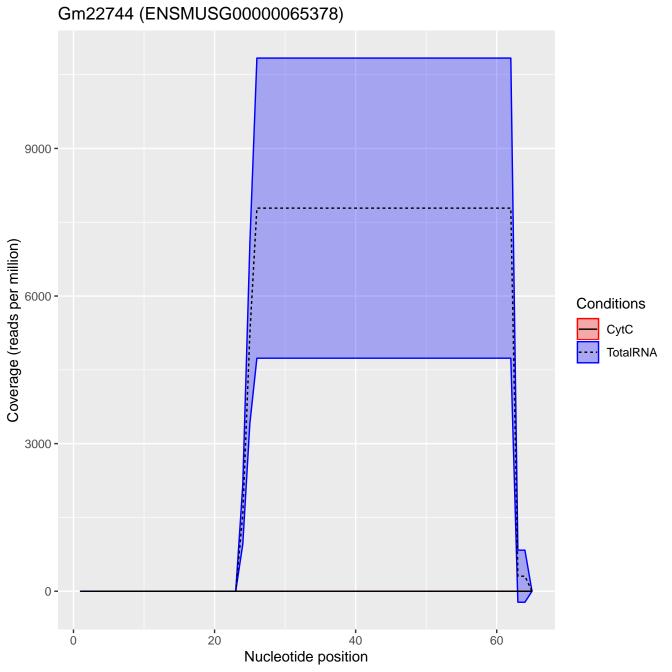


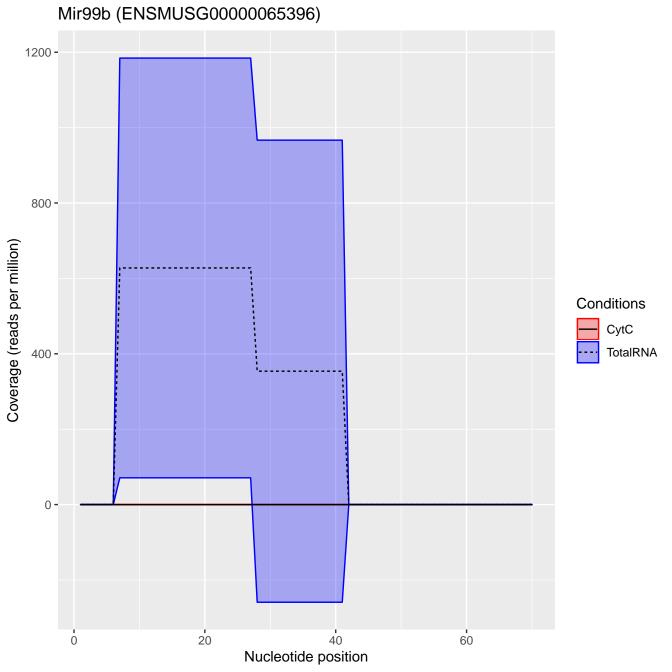


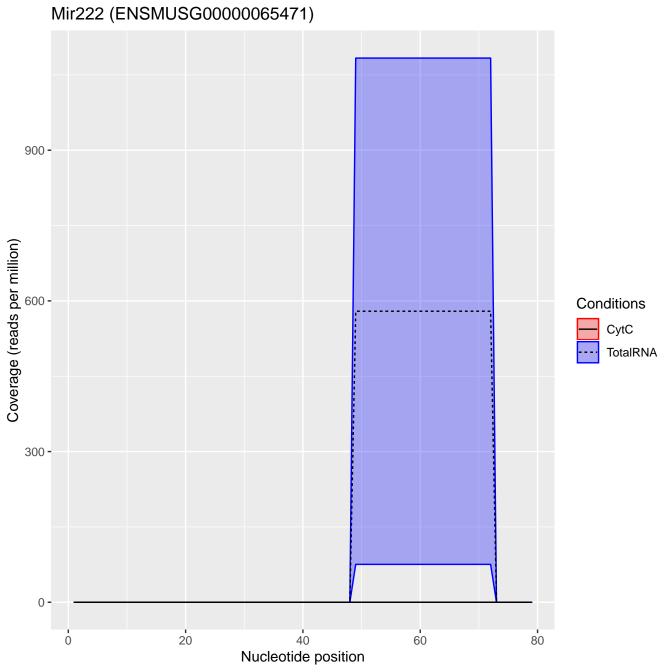




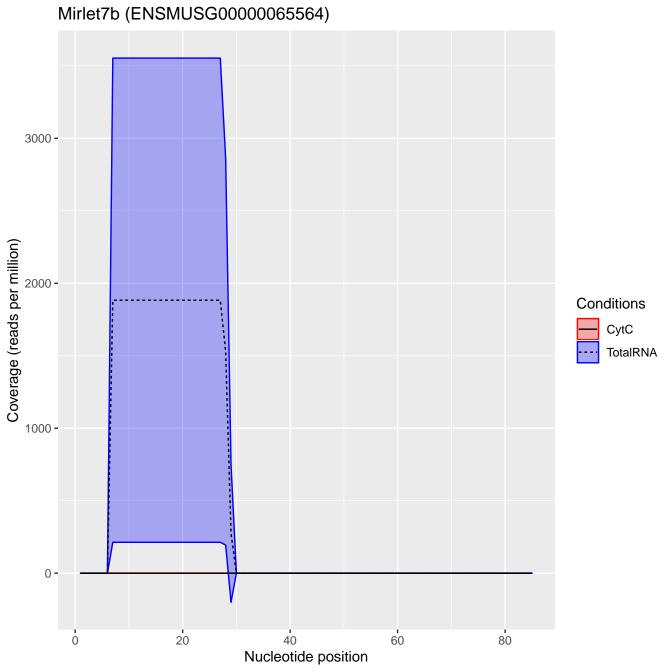




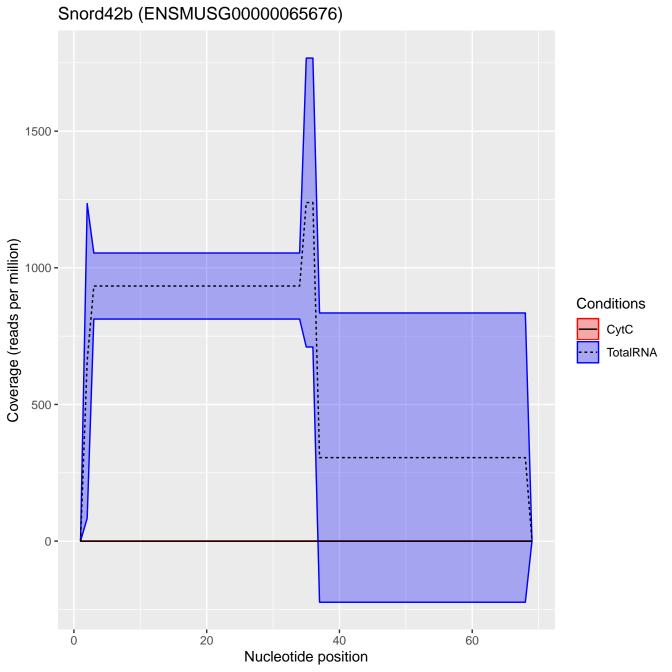


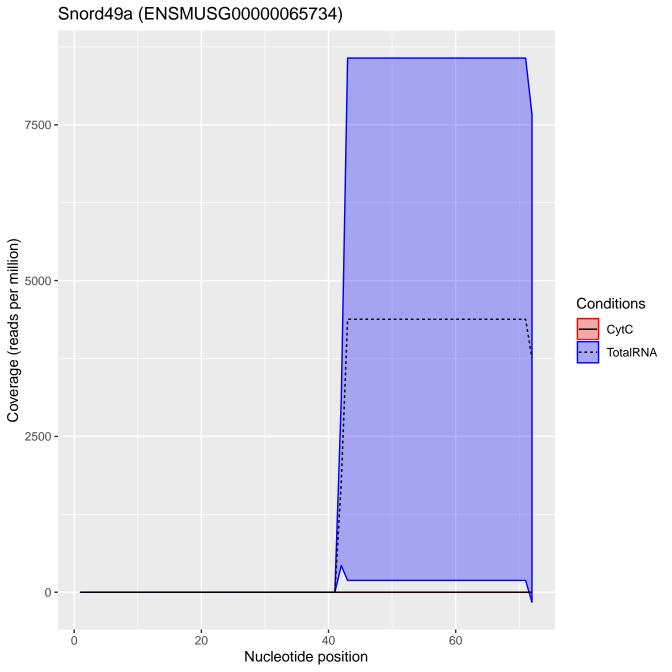


Mir22 (ENSMUSG00000065529) 1500 **-**Coverage (reads per million) Conditions CytC TotalRNA 500 **-**0 -25 75 50 0 Nucleotide position

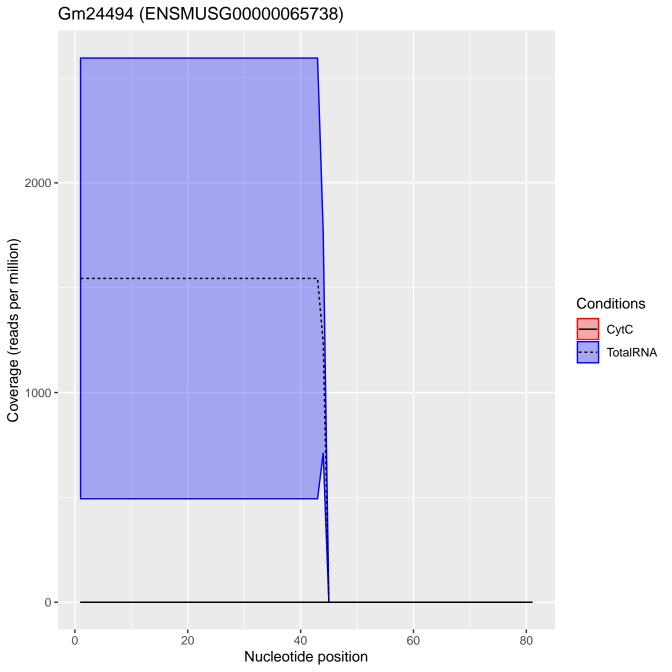


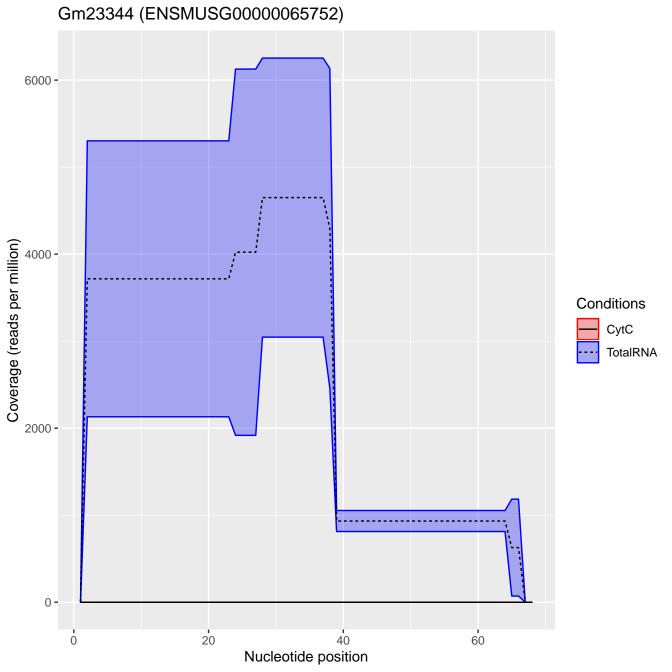
Snord33 (ENSMUSG00000065628) 6000 -Coverage (reads per million) Conditions CytC TotalRNA 0 -40 20 60 80 Nucleotide position

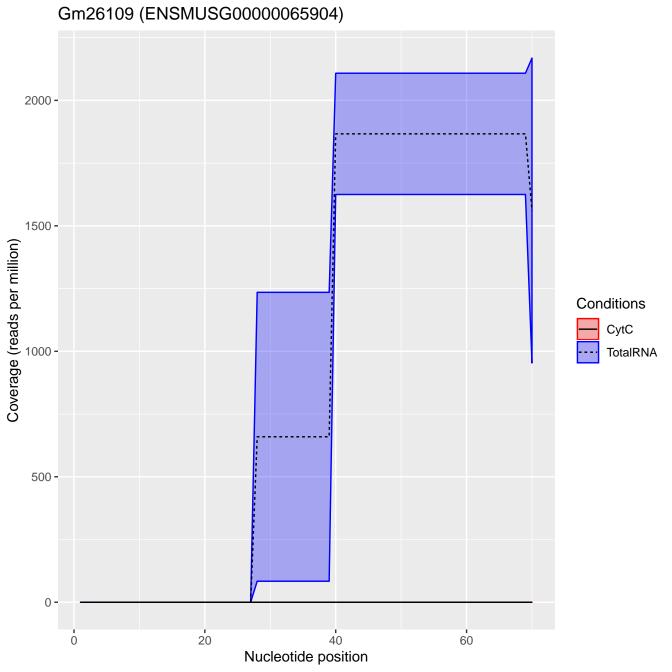


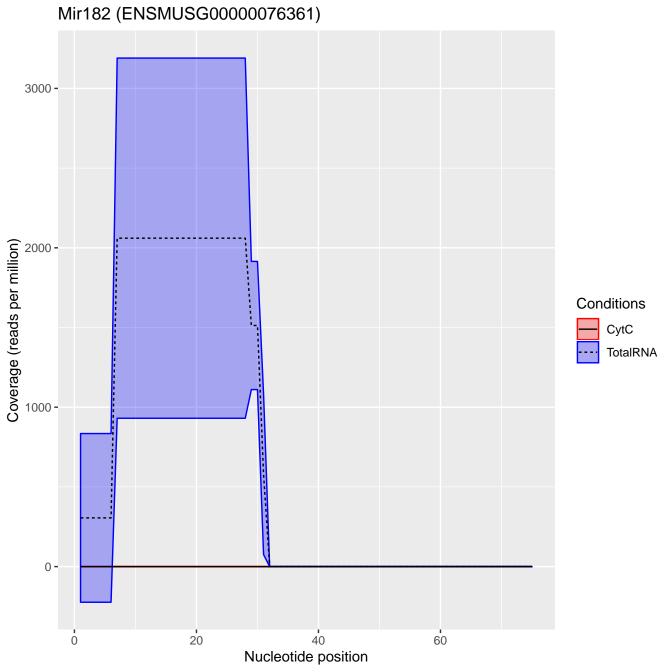


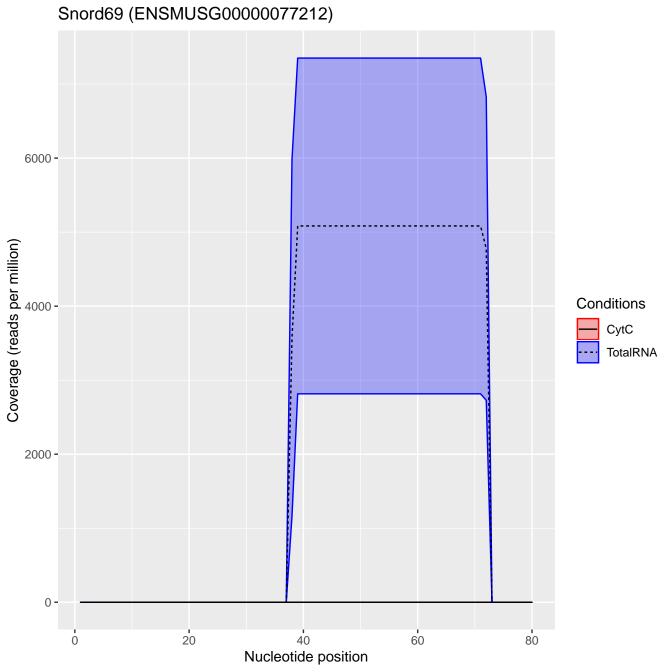
Snord80 (ENSMUSG00000065735) 8000 -6000 -Coverage (reads per million) Conditions CytC TotalRNA 2000 -0 -20 40 60 80 Nucleotide position

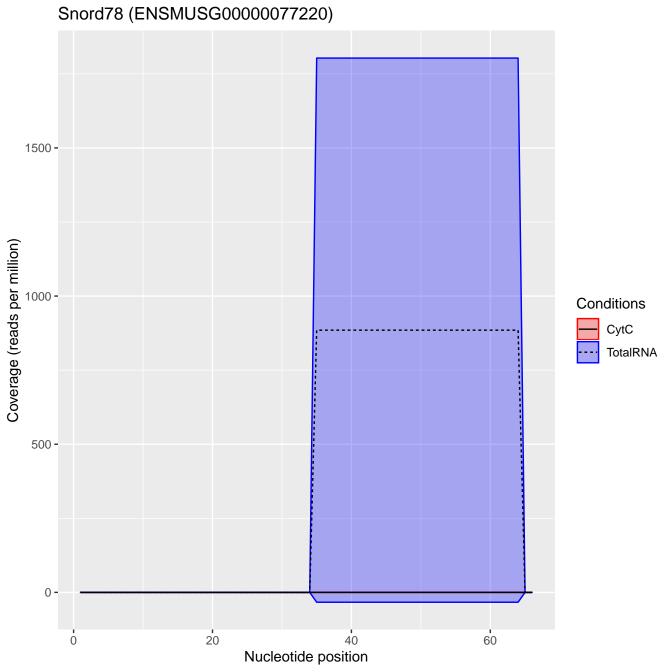


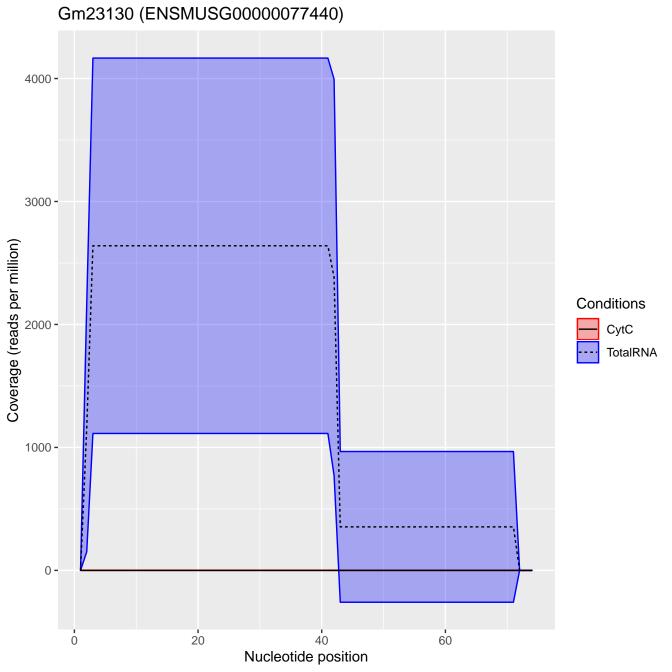




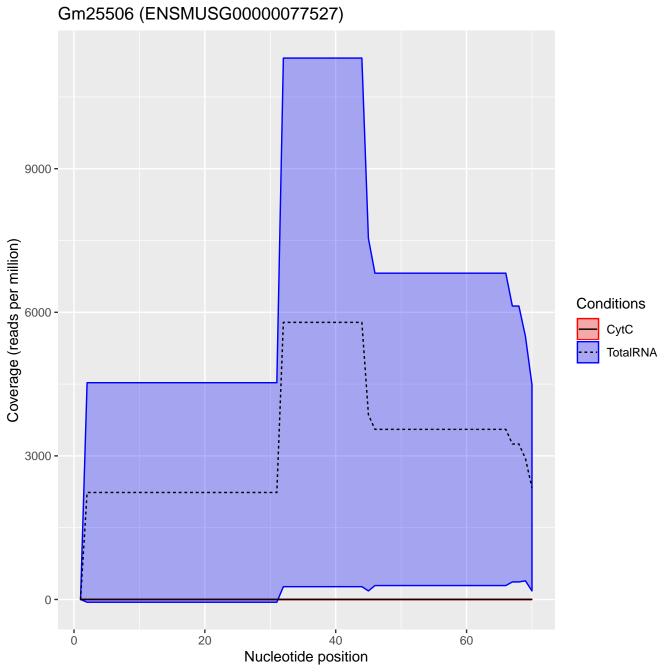




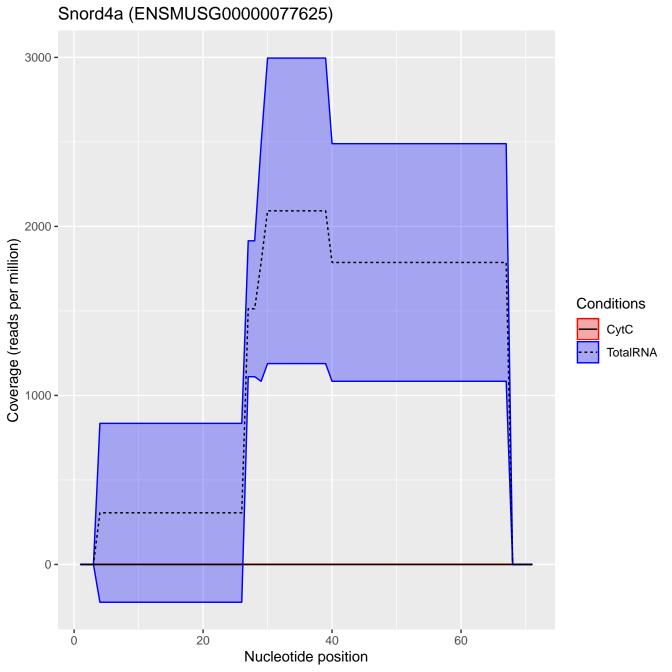


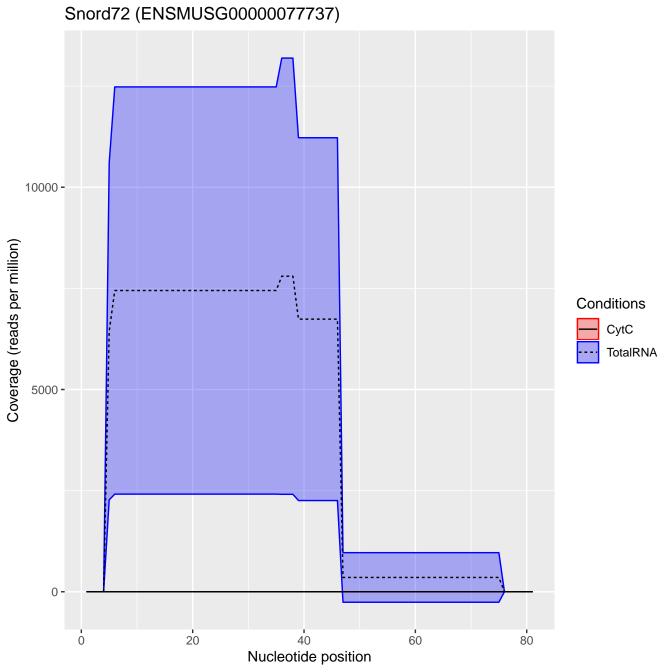


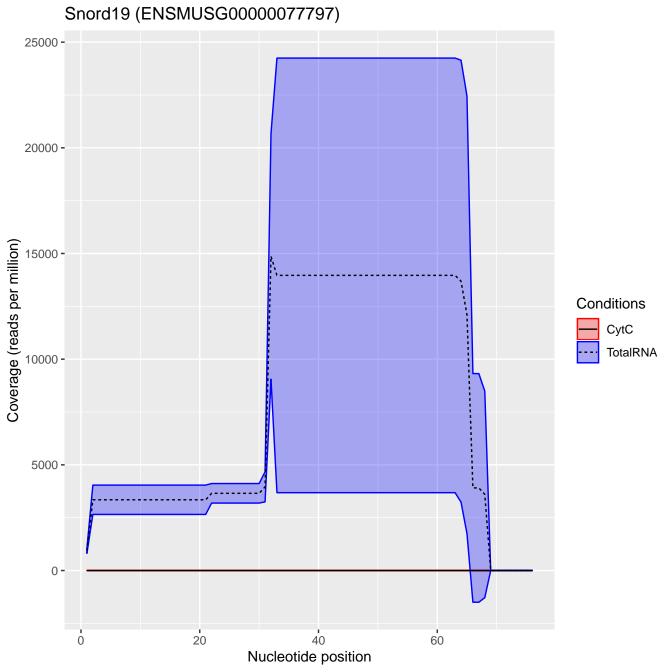
Snord91a (ENSMUSG00000077493) 2000 -1500 -Coverage (reads per million) 1000 -Conditions CytC TotalRNA 500 -0 -0 25 7<sup>5</sup> 50 Nucleotide position



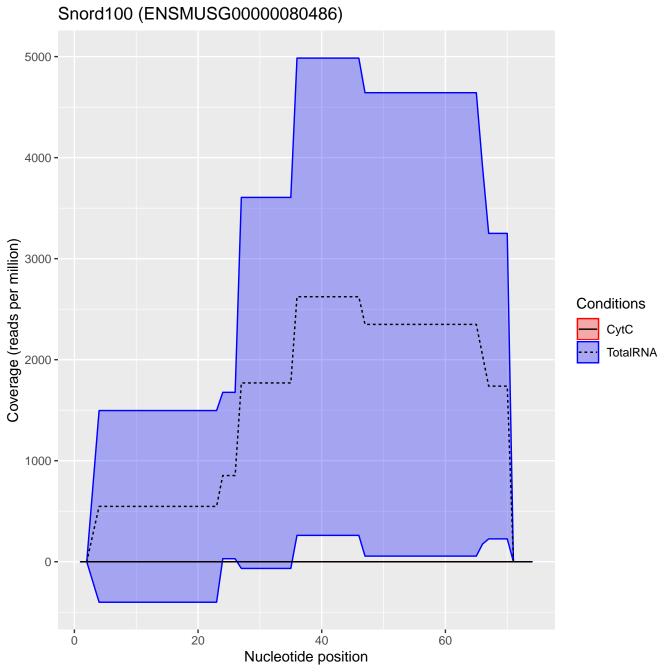
Gm23201 (ENSMUSG00000077565) 900 -Coverage (reads per million) Conditions CytC TotalRNA 300 -0 -25 50 **7**5 0 Nucleotide position

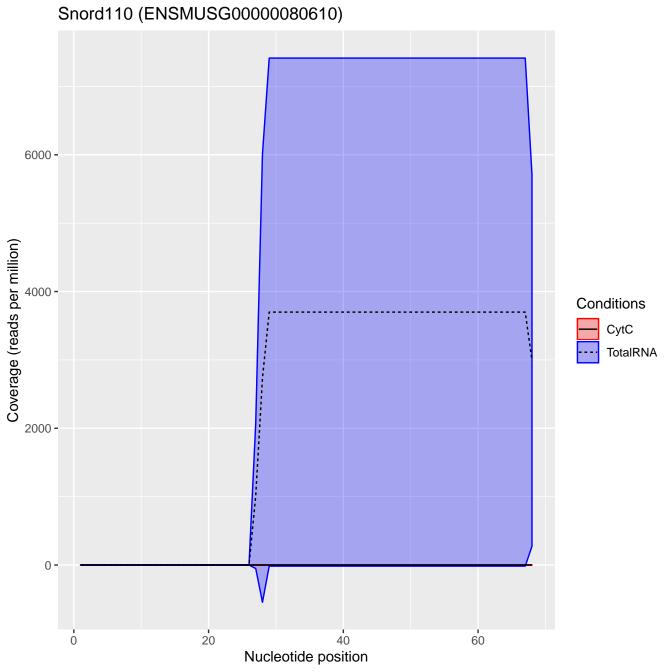


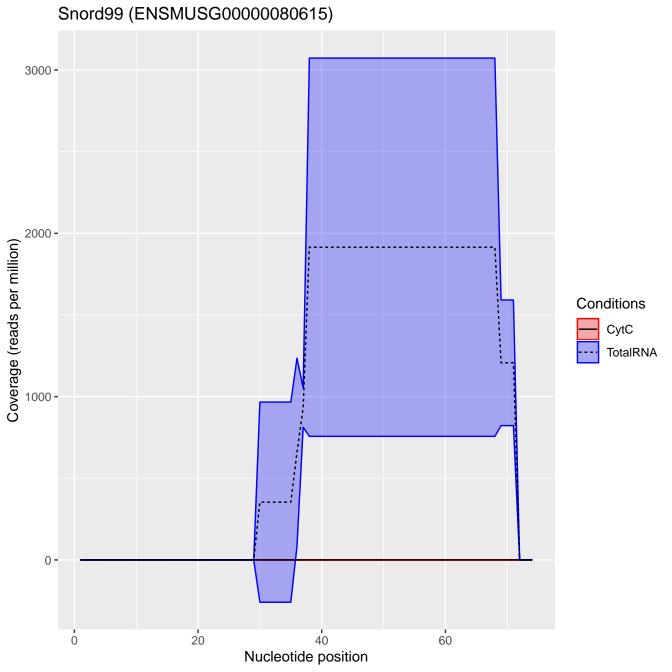


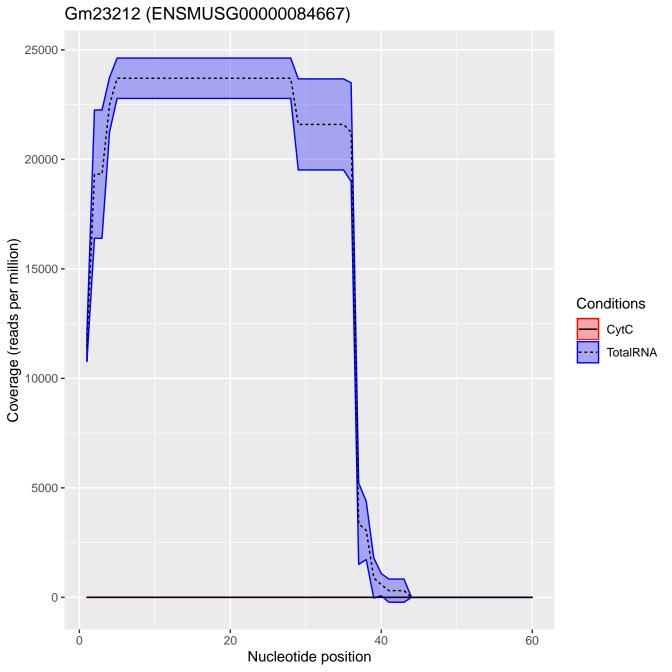


Gm22489 (ENSMUSG00000080463) 12000 -9000 -Coverage (reads per million) Conditions 6000 -CytC TotalRNA 3000 -0 -20 60 40 0 Nucleotide position

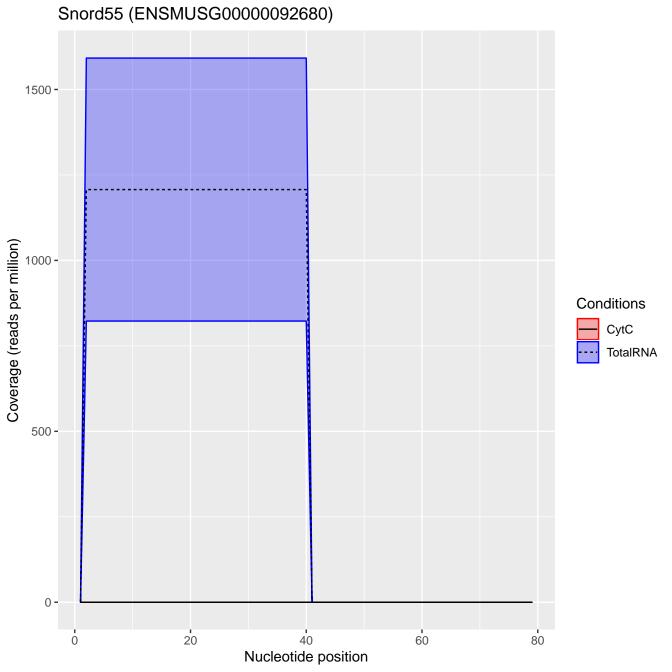


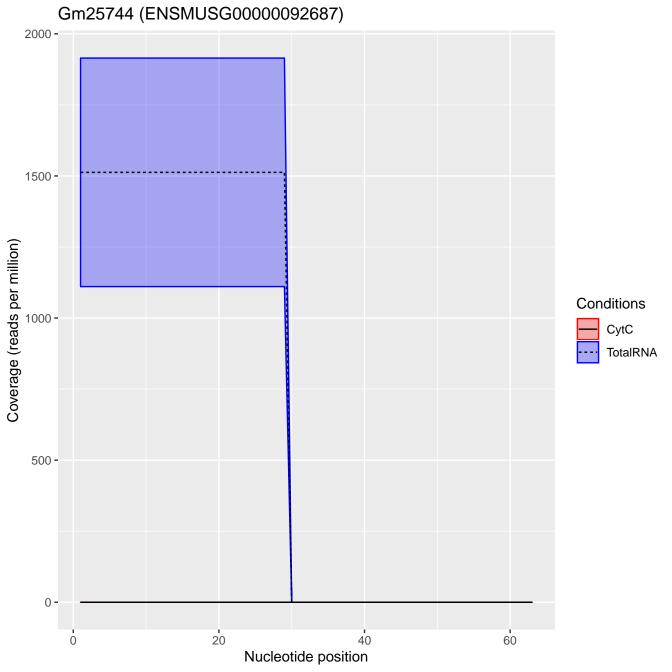


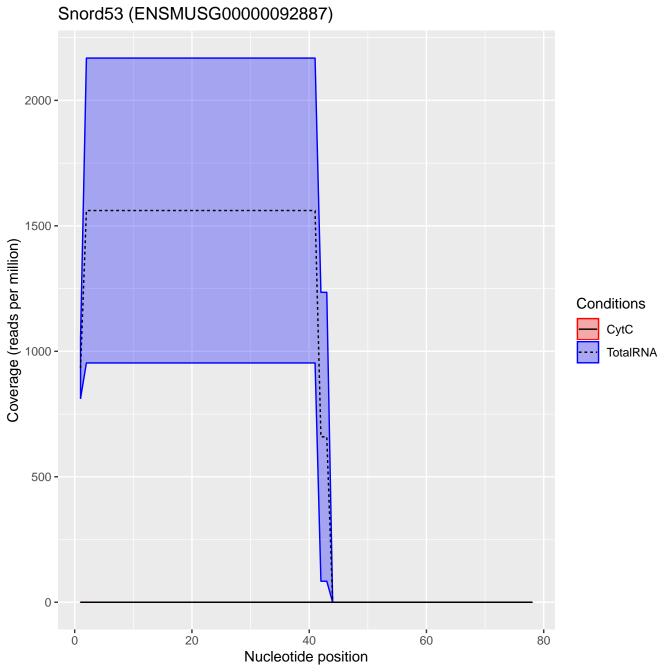


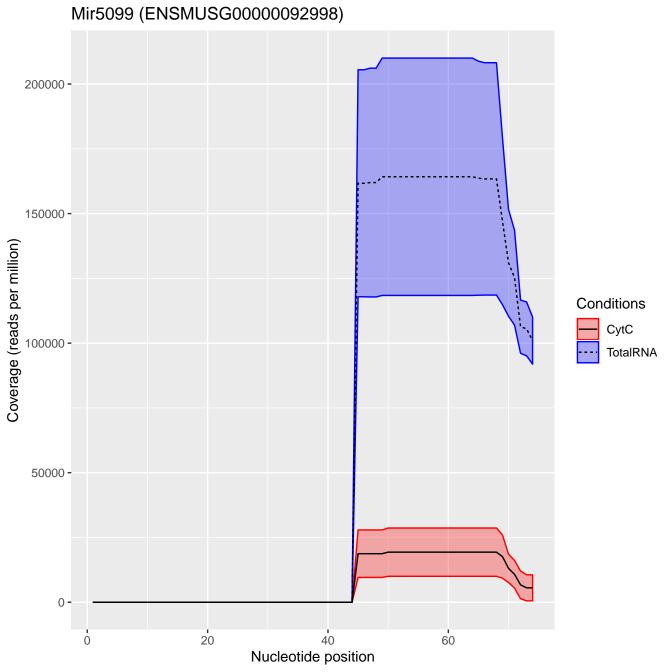


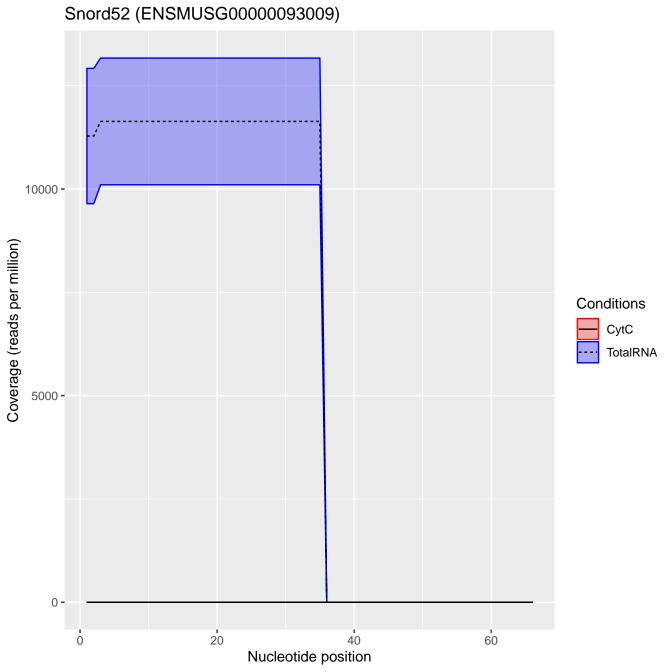
Snord11 (ENSMUSG00000089093) 1200 -900 -Coverage (reads per million) Conditions 600 **-**CytC TotalRNA 300 -0 -20 40 60 80 0 Nucleotide position

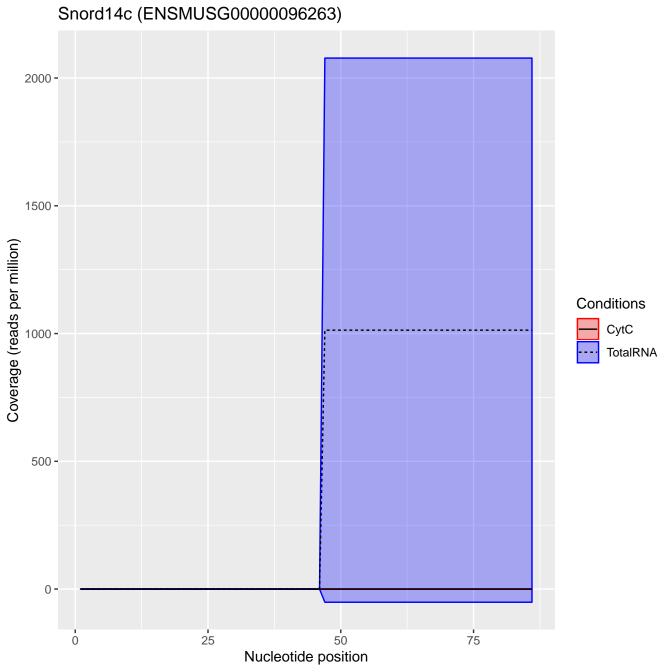




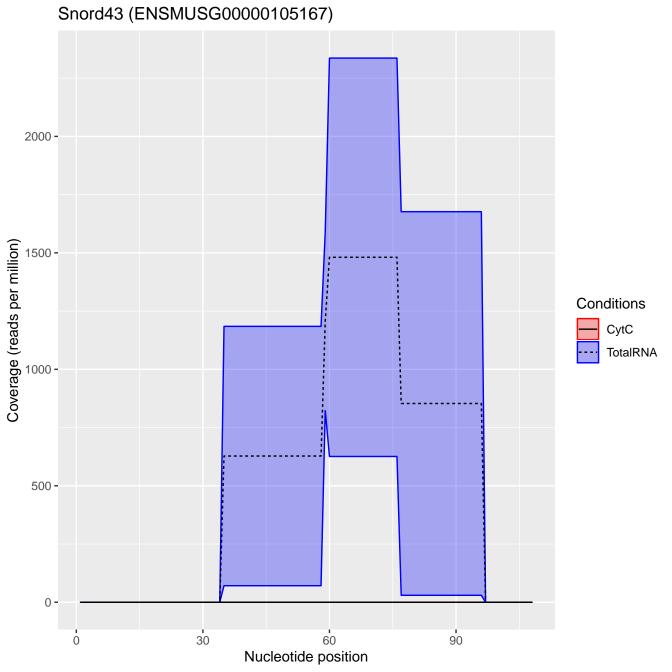








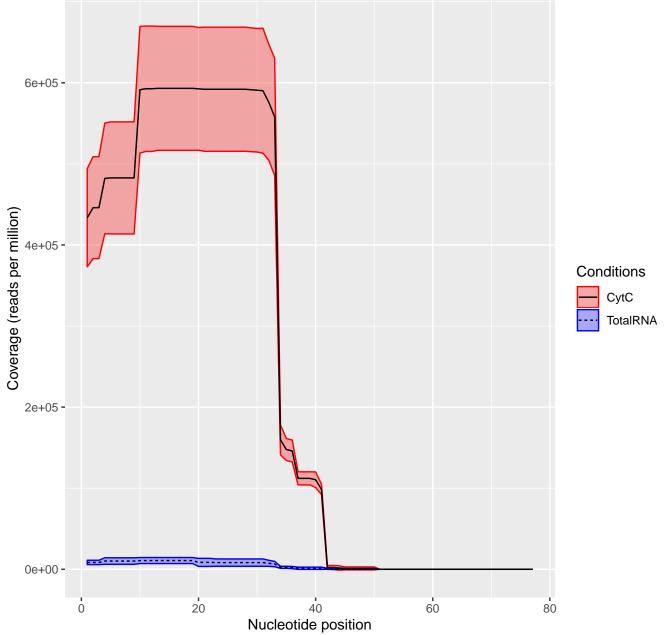
Mir6240 (ENSMUSG00000098343) 10000 -7500 -Coverage (reads per million) Conditions 5000 -CytC TotalRNA 2500 **-**0 -30 60 90 120 Ö Nucleotide position



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)



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