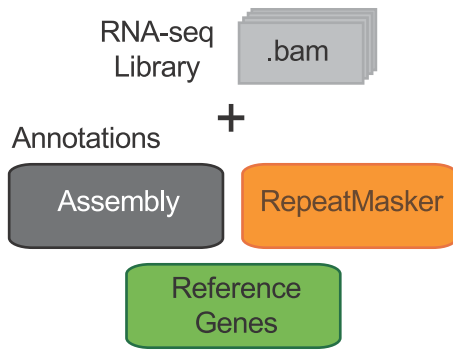
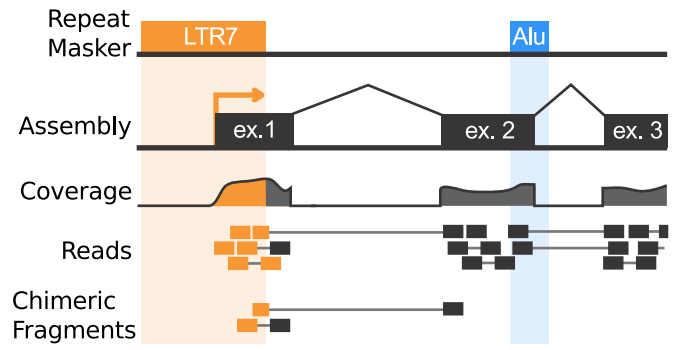


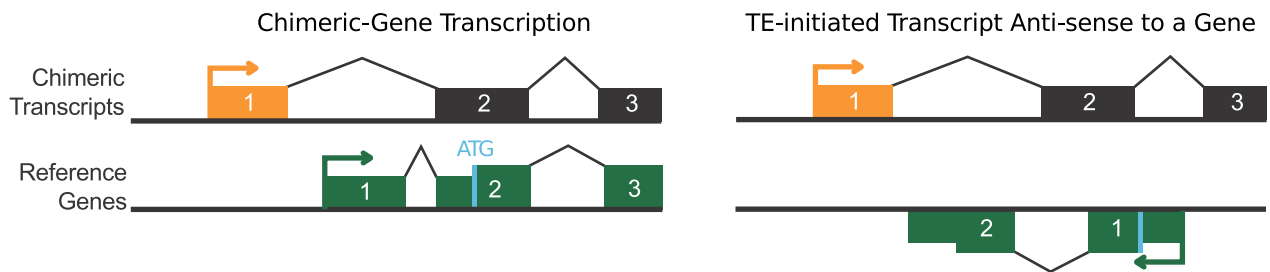
### A) i. Input



### ii. Detect & Classify TE-Derived Transcripts

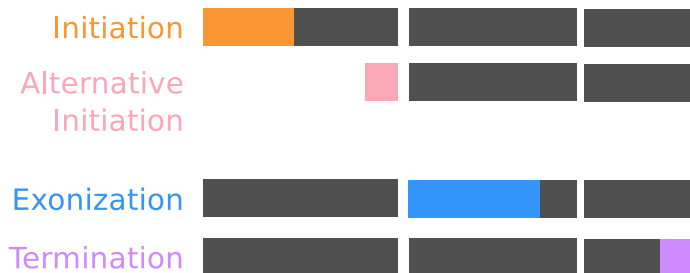
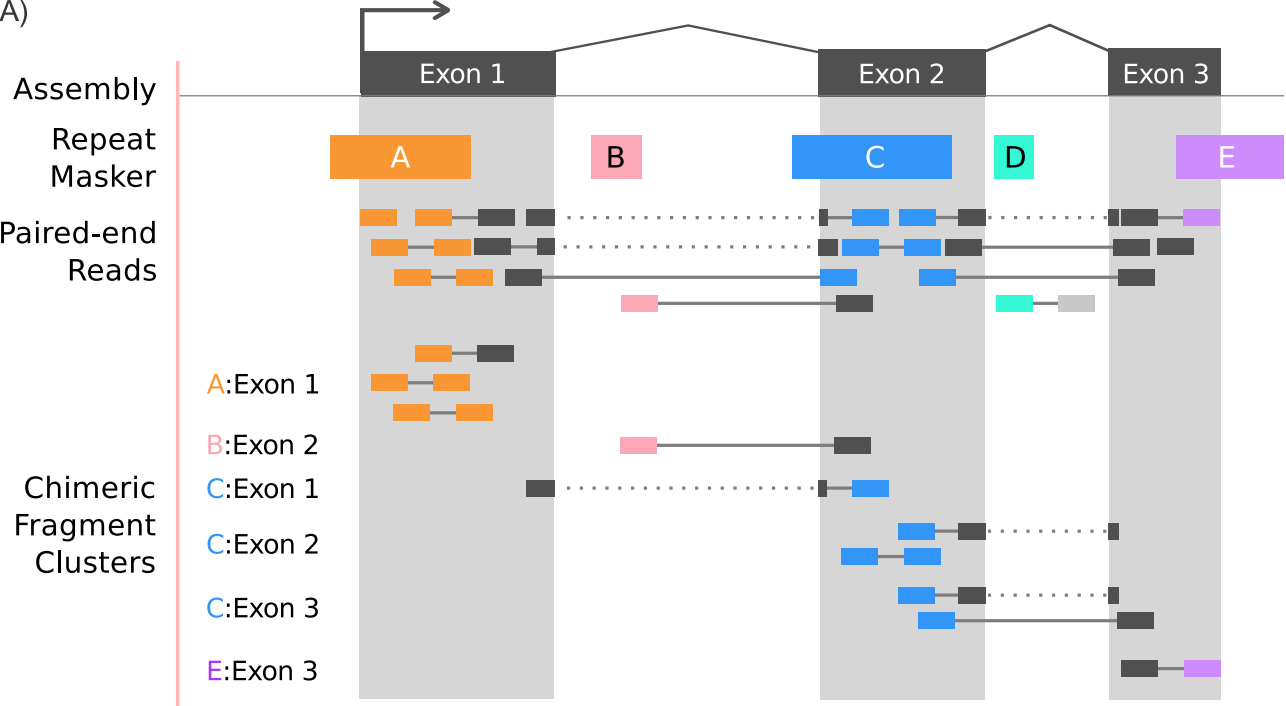


### iii. Intersect TE-Derived Transcripts to Reference Genes

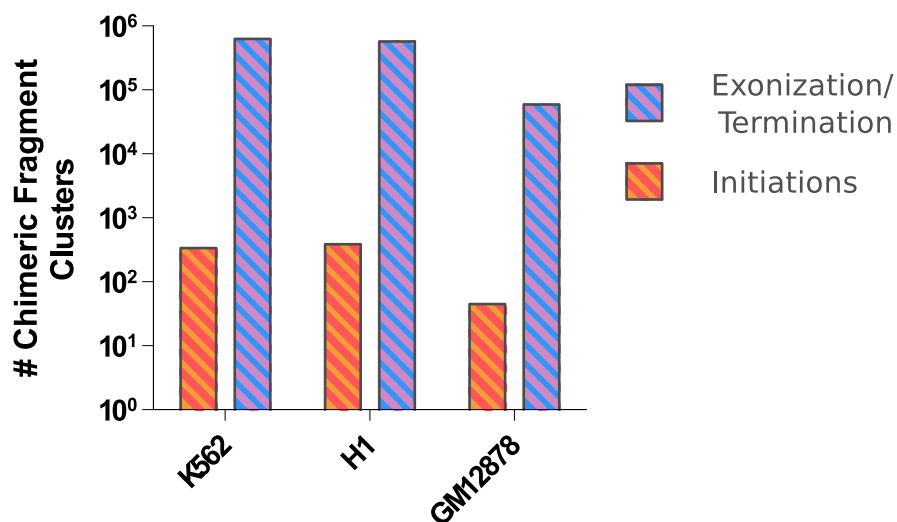


### B)

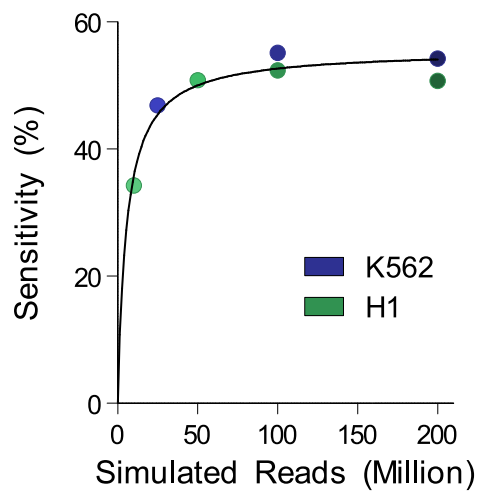




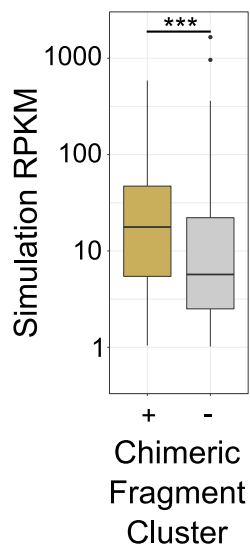
B)



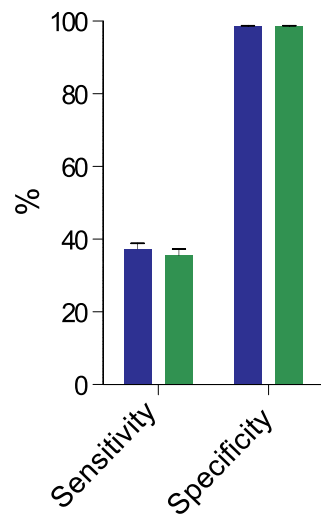
A



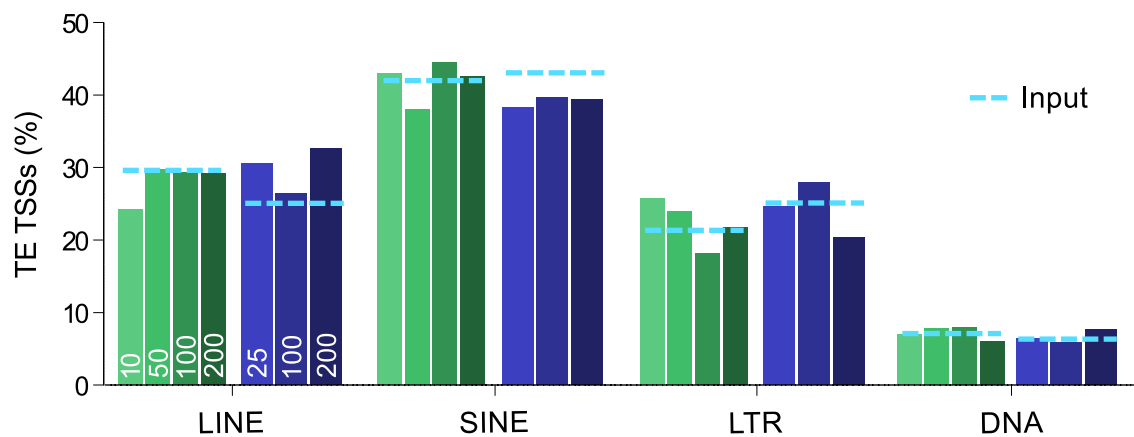
B

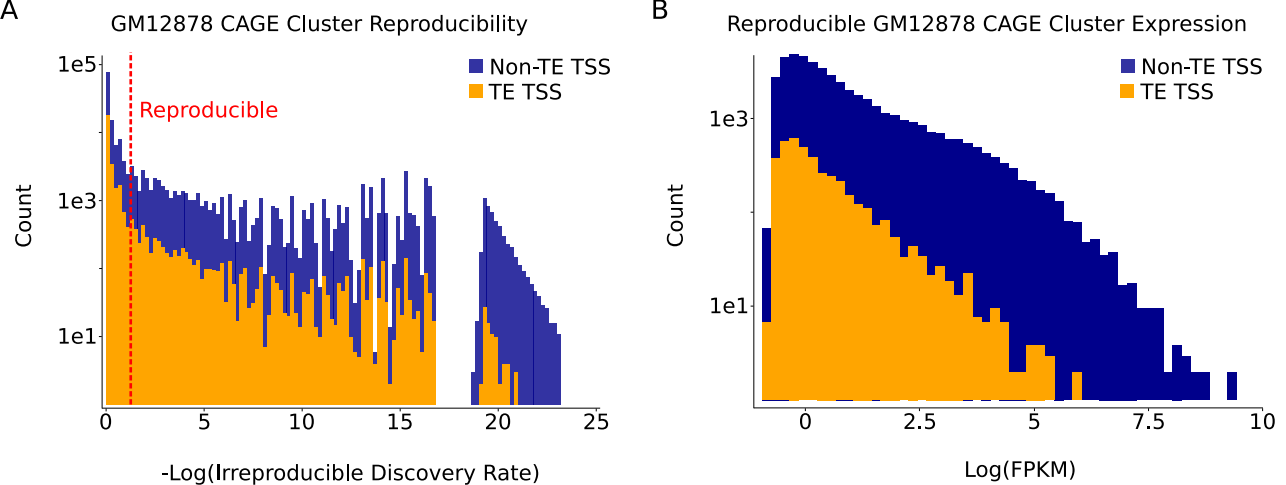


C



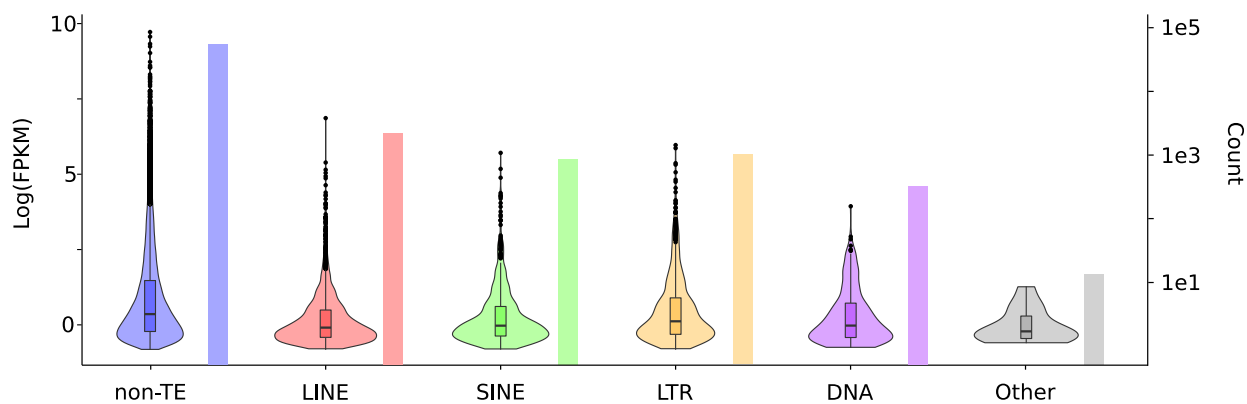
D

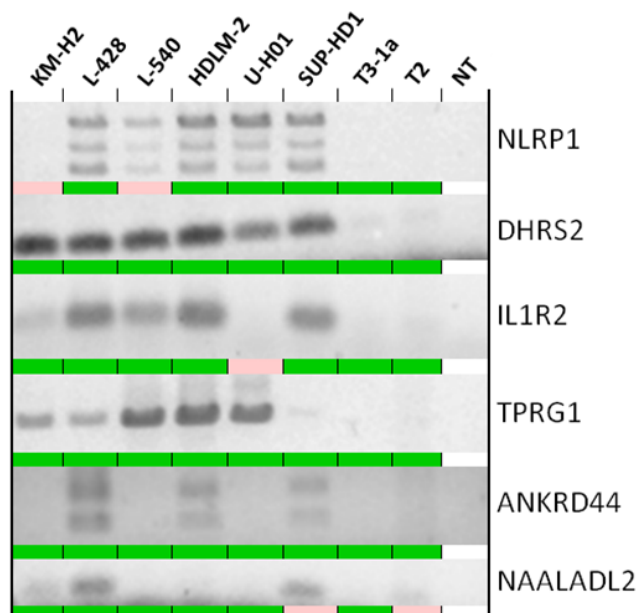




**C**

Reproducible CAGE Cluster Expression and Count by TE Class

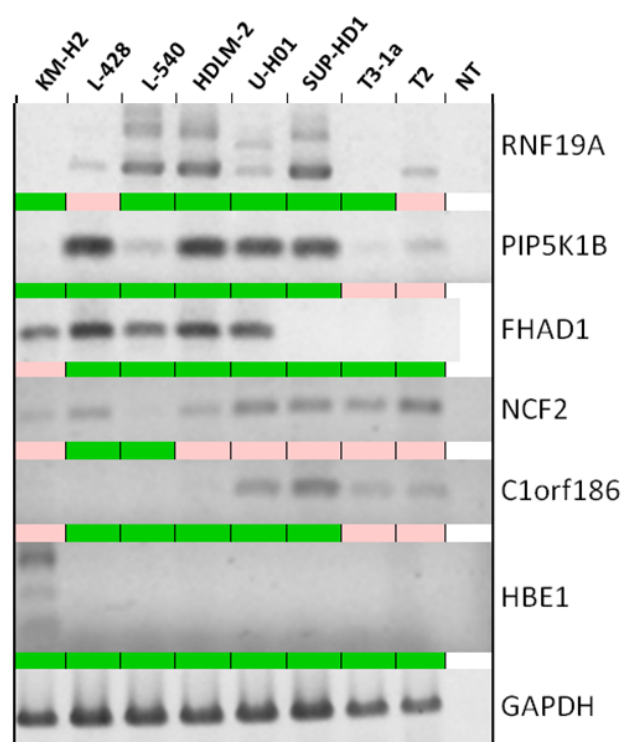




Specificity = 89.2 %

Sensitivity = 55.41 %

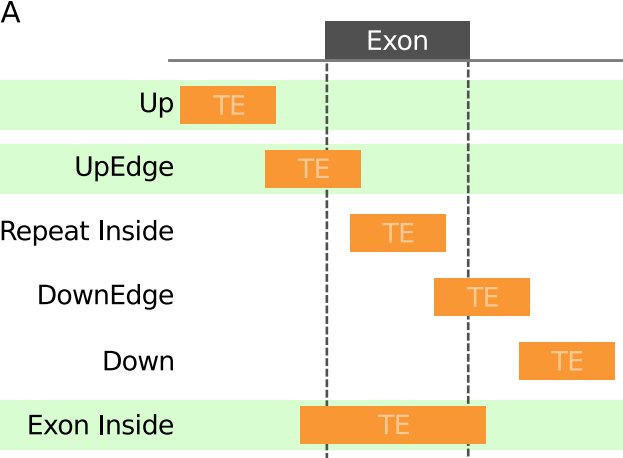
False Discovery Rate = 0.089



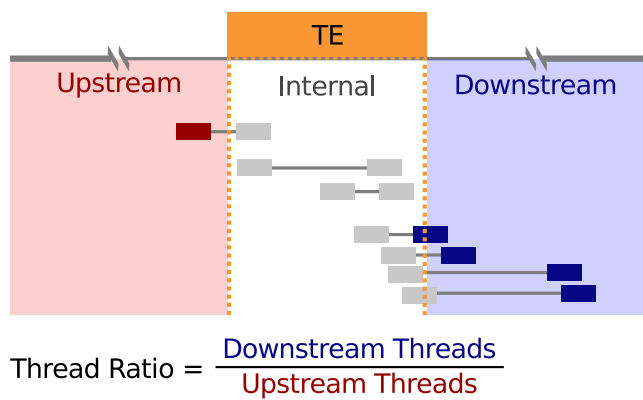
■ LIONS = RT-PCR

■ LIONS ≠ RT-PCR

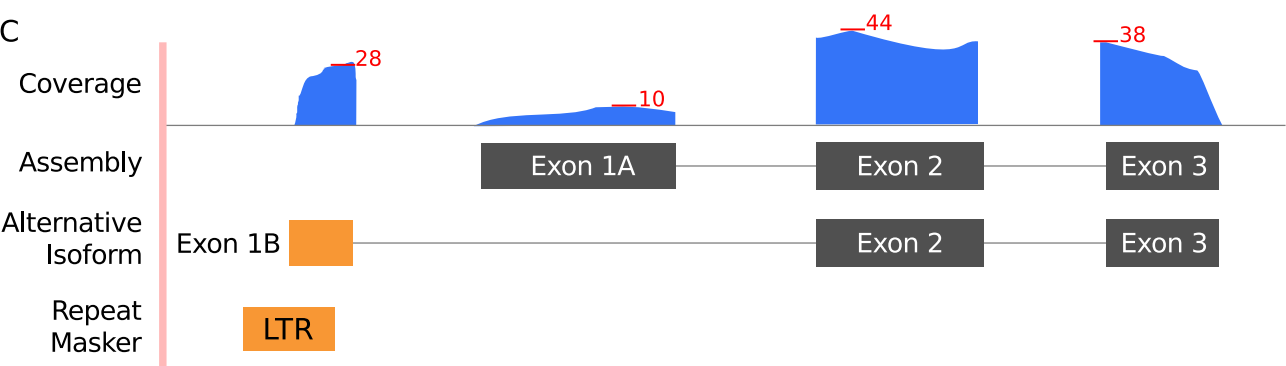
A



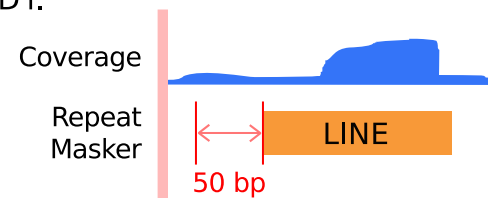
B



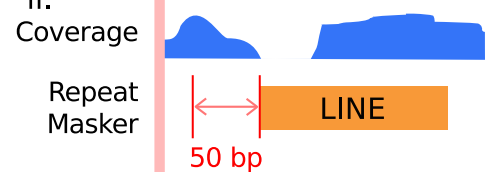
C



D i.



ii.



E

