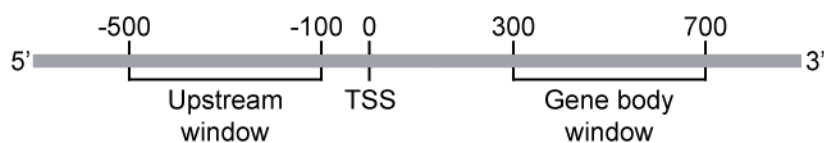
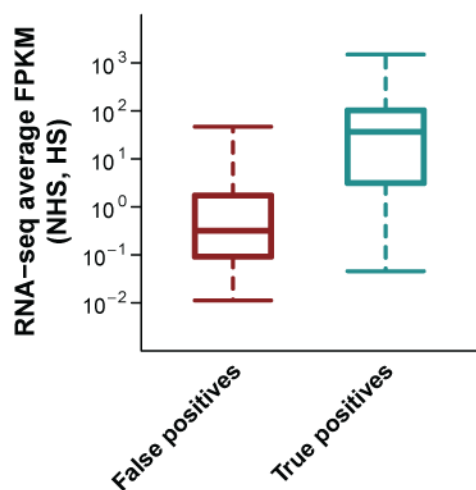


A

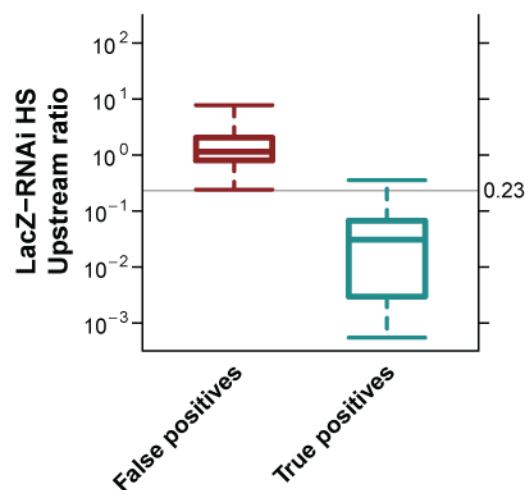


$$\text{Upstream ratio} = \frac{\text{Upstream reads/mappable bases}}{\text{Gene body reads/mappable bases}}$$

B



C



D

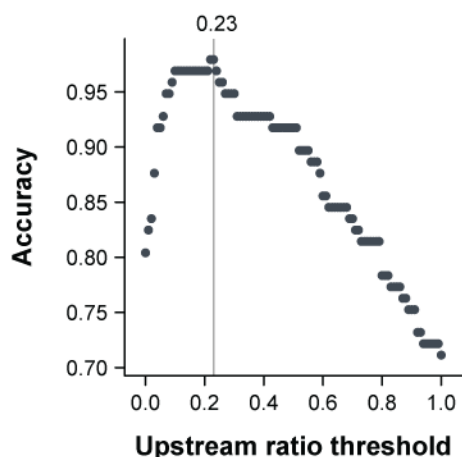


Figure S9: Validation of the upstream transcription filter implemented in our study. (A) Diagram of the *upstream ratio* metric that was used to filter out false positive genes generated by run-through transcription. (B) Box-plot of the average RNA-seq FPKM (NHS and HS) for the true (n=22) and false (n=78) positive subsets classified by visual inspection of 100 randomly selected activated genes. (C) Box-plot of the upstream ratio for the LacZ-RNAi HS condition for true and false positive genes. The 0.23 cutoff that was used to separate true from false positives is shown in the plot. (D) Accuracy metric ((true positives + true negatives)/total) of upstream ratio filter as a function of tested cutoffs. The cutoff with highest accuracy (0.23) is shown in the plot.