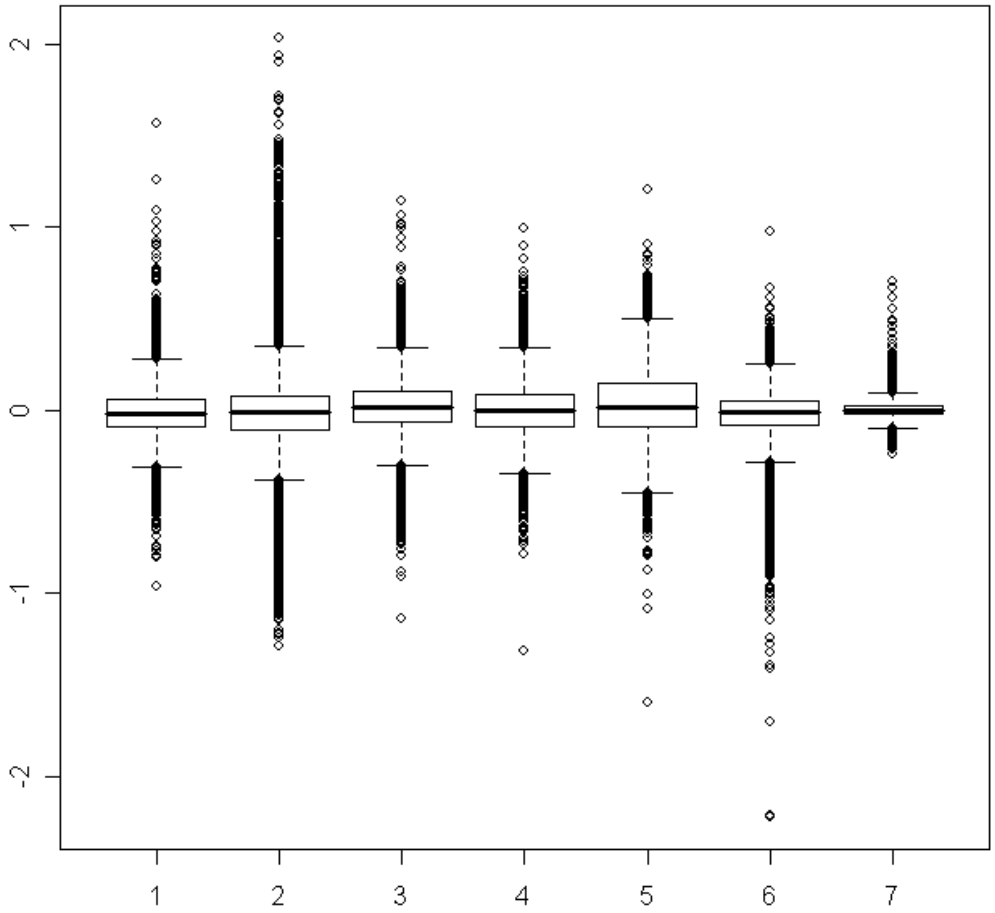
Supplementary Figures and Tables
Supplementary Figure 1: Goodness of fit of the exponential decay model

A.



RNA degradation was modeled with an exponential decay model, which corresponds to fitting a linear model on the vsn transformed data. The per-gene residuals of the linear model for proliferating cells on the 7 different time points (0, 10, 20, 30, 60, 150, 480 minutes) are displayed as a boxplot (50% of all residuals in the box, 75% of all residuals between the horizontal stripes). The plot shows that the linear model fits the data well since the median of the residuals is close to zero for each time point. The residuals for the 480 minutes time point are smallest, demonstrating that this datapoint has the largest influence on the fit. This is expected since this time point is furthest away from the other time points (lever effect) and also wanted because RNAs with average to long half-life will only be significantly changed at this particular time point. Plot for differentiated cells is highly similar.
Principal component analysis on the residuals of the fit of the linear model for genes with slopes significantly different from zero ($p<0.0001$) was performed to analyze in more detail the goodness of fit for individual genes and time points. The biplots (genes in grey; time points in red) shown below for proliferating (Figure 1B) and differentiated cells (Figure 1C) demonstrate no major trends, although in both cases the 150 minutes time

points appear to have a larger number of negative residuals than would be expected with a perfect fit. However, the effect is not large and will not have a major influence on the data.

For modeling decay at the level of probe sets, we used the exact same model as for the gene level data. Results of the fits for individual probe sets were essentially similar to the fits for genes.

Figure 1B.

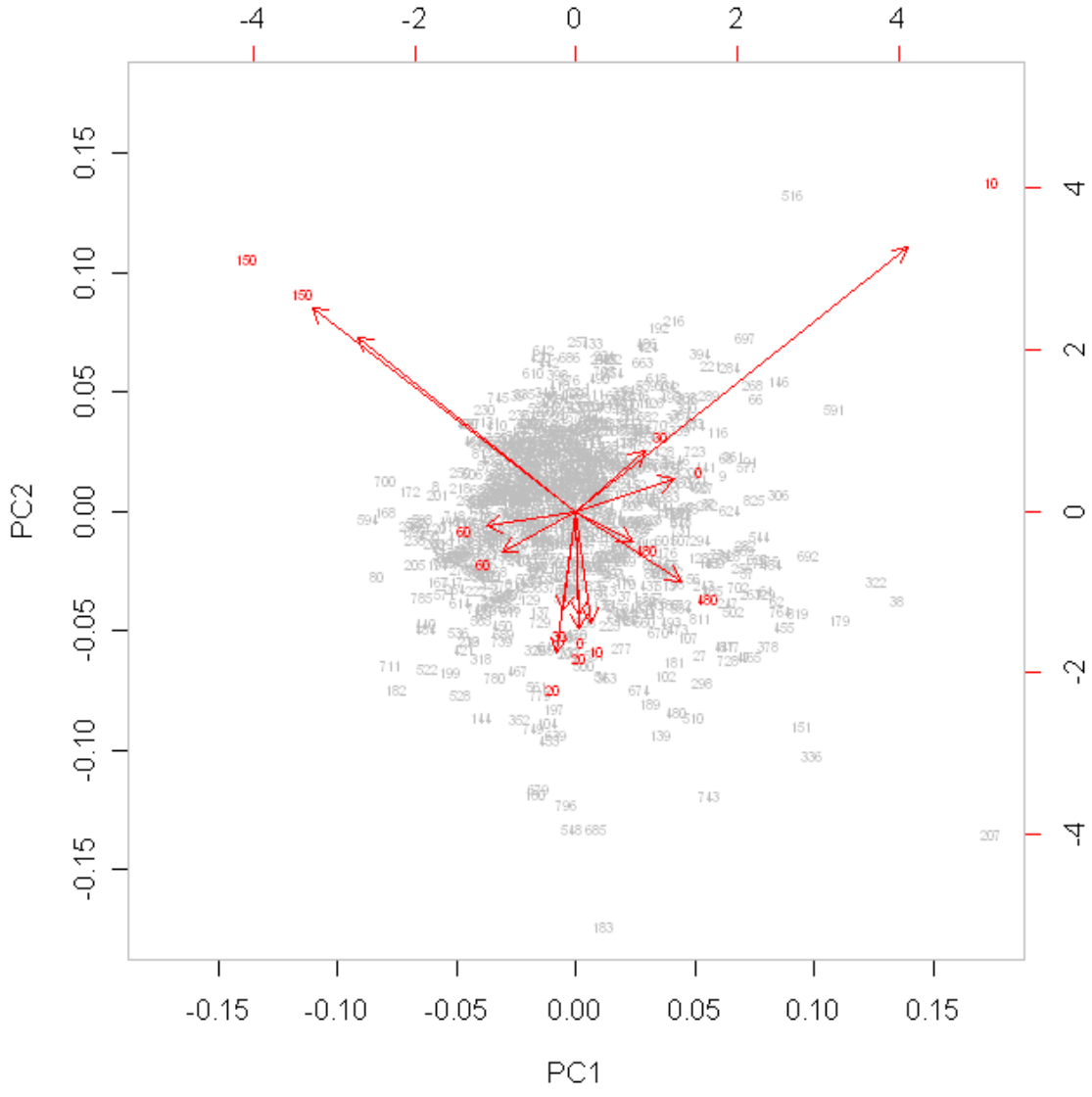
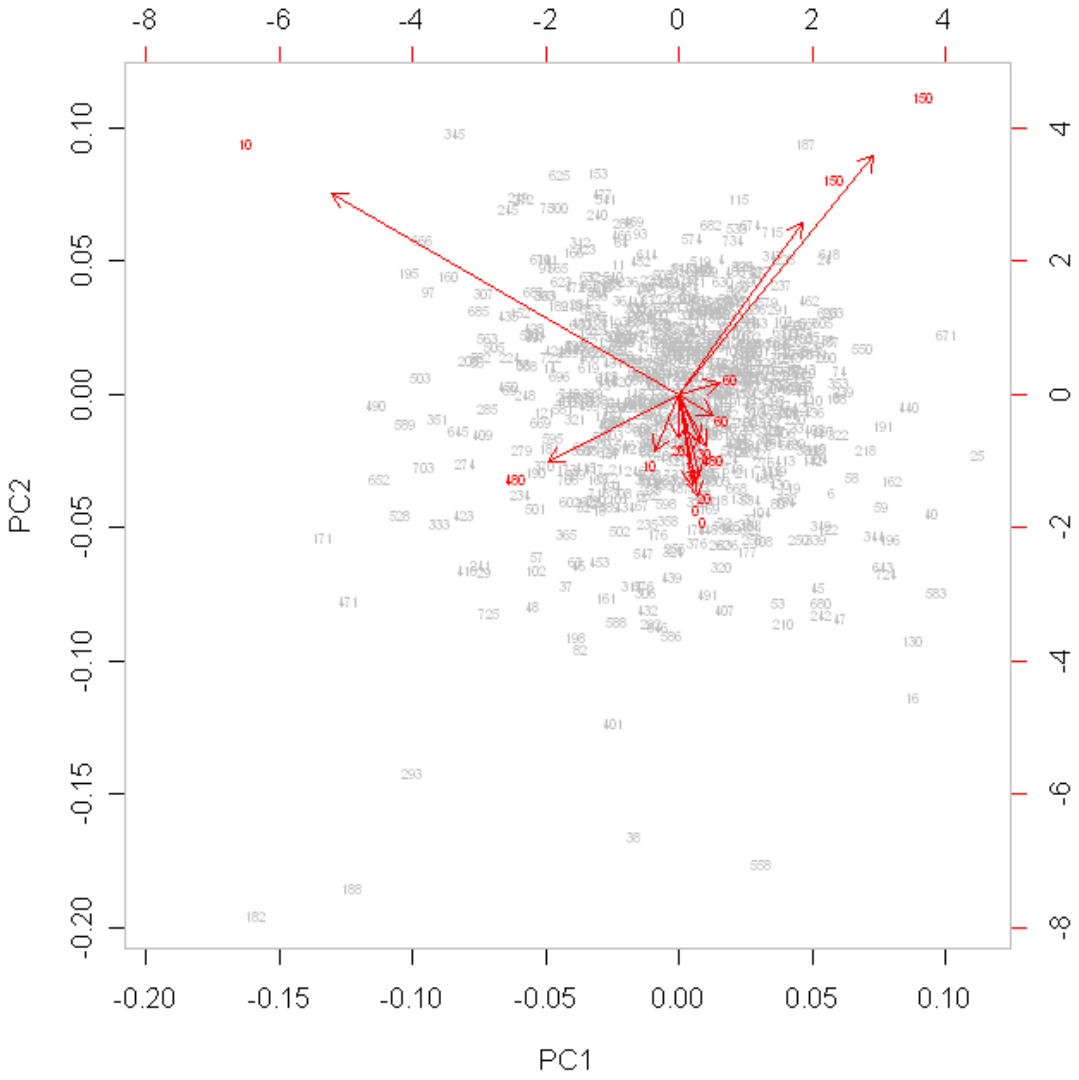
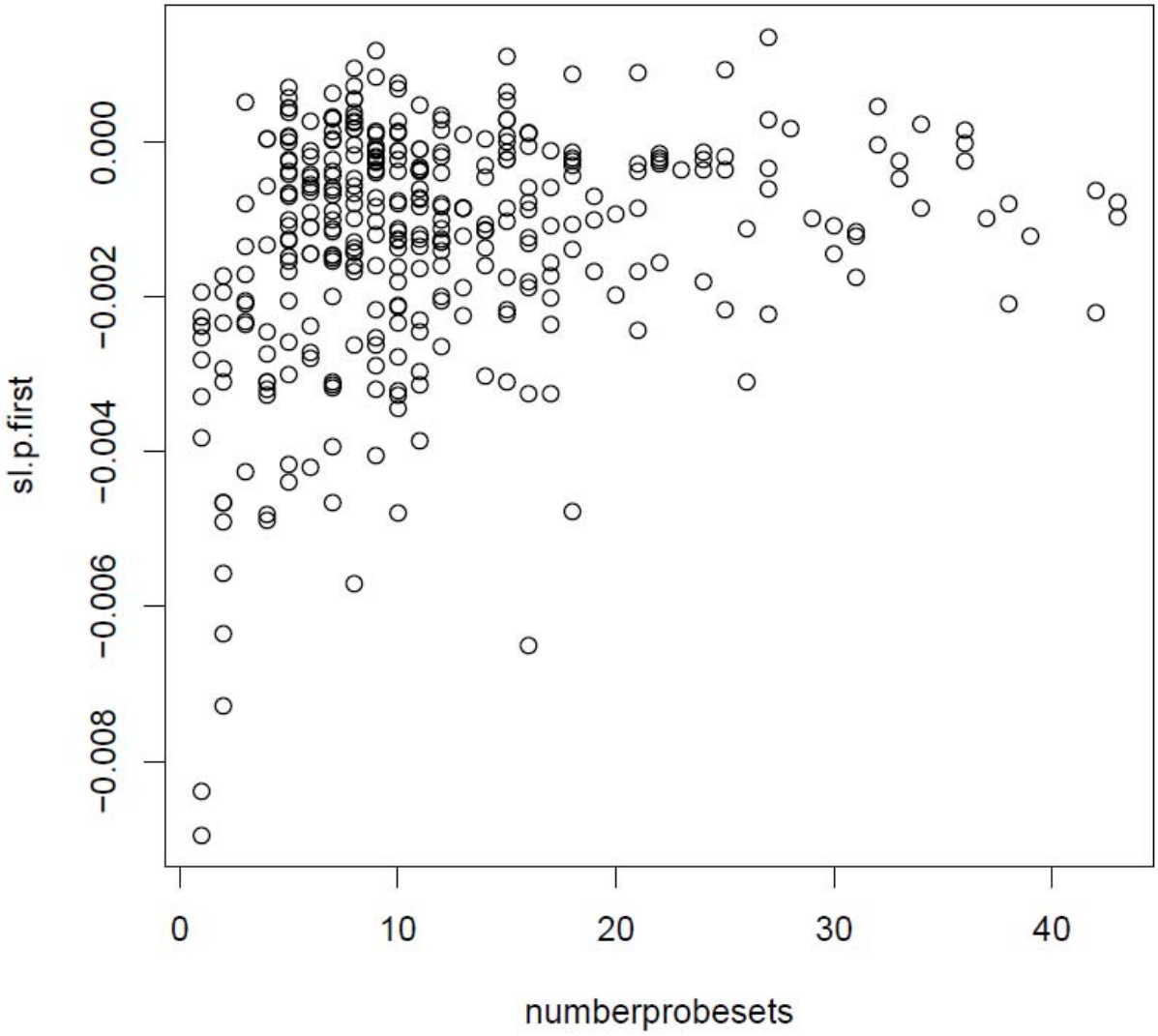


Figure 1C

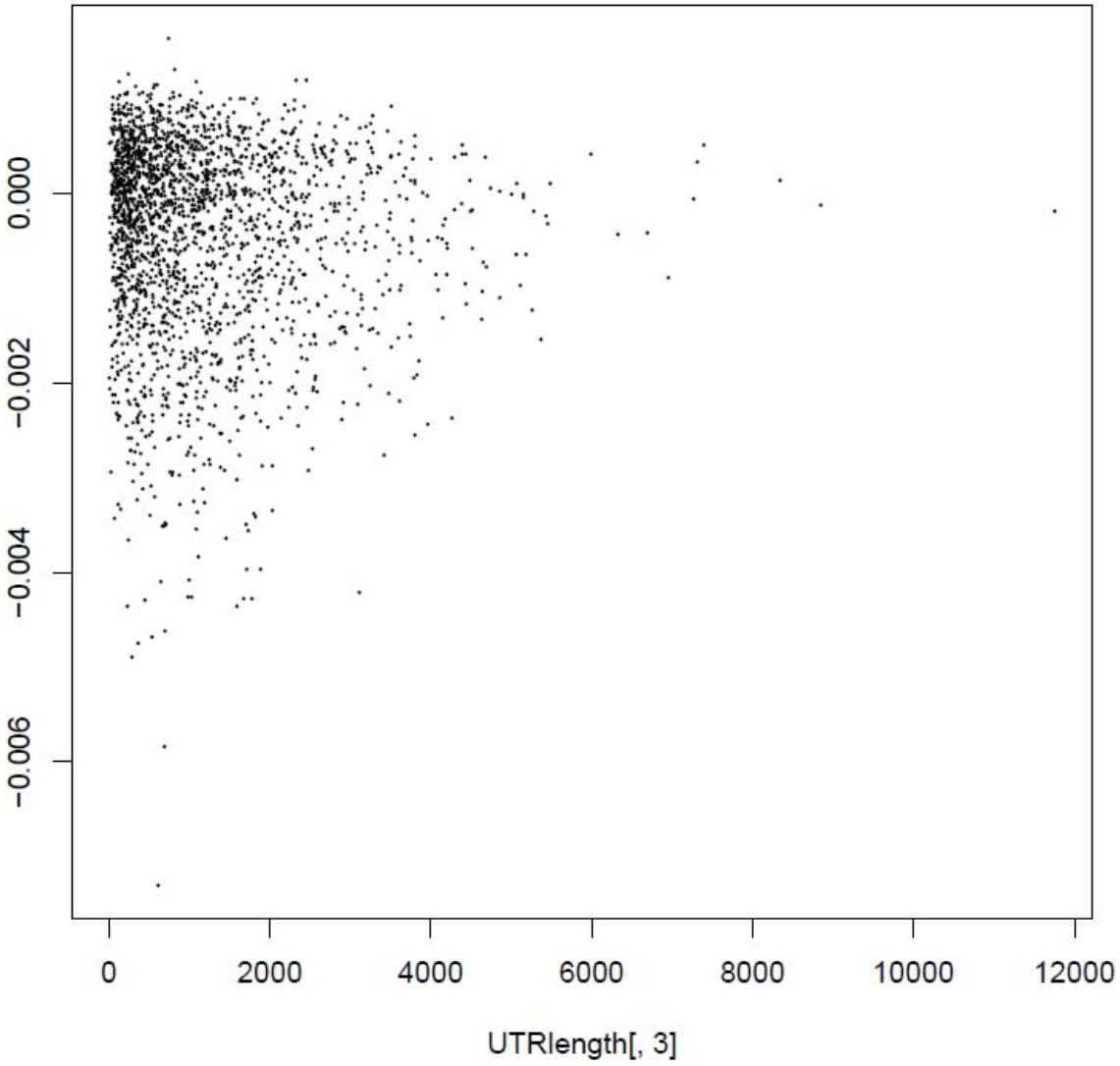

-8
-6
-4
-2
0
2
4
0.10
0.05
0.00
-0.05
-0.10
-0.15
-0.20
PC2
PC1
-0.20
-0.15
-0.10
-0.05
0.00
0.05
0.10
4
2
0
-2
-4
-6
-8

Supplementary Figure 2: Correlation between degradation rate and gene length



The slope (degradation rate constant) of the first exon of a particular gene is plotted as a function of the number of probe sets for the gene. The plot only reflects fast decaying genes (average slope < -.002) in proliferating cells. The plot for differentiated cells is highly similar. Genes with one exon tend to have short half lives, while there is not a strong correlation between the degradation rate constant and the gene length (represented by number of probe sets per gene).

Supplementary Figure 3: Correlation between degradation rate and length of 3'-UTR



The average slope for all probesets in a transcript (y-axis) is plotted against the length of the 3'-UTR of the transcript, as annotated in the Ensembl database (x-axis). There is no strong correlation between degradation rate and UTR length, but genes with longer 3'-UTRs tend to be more stable than genes with shorter 3'-UTRs.