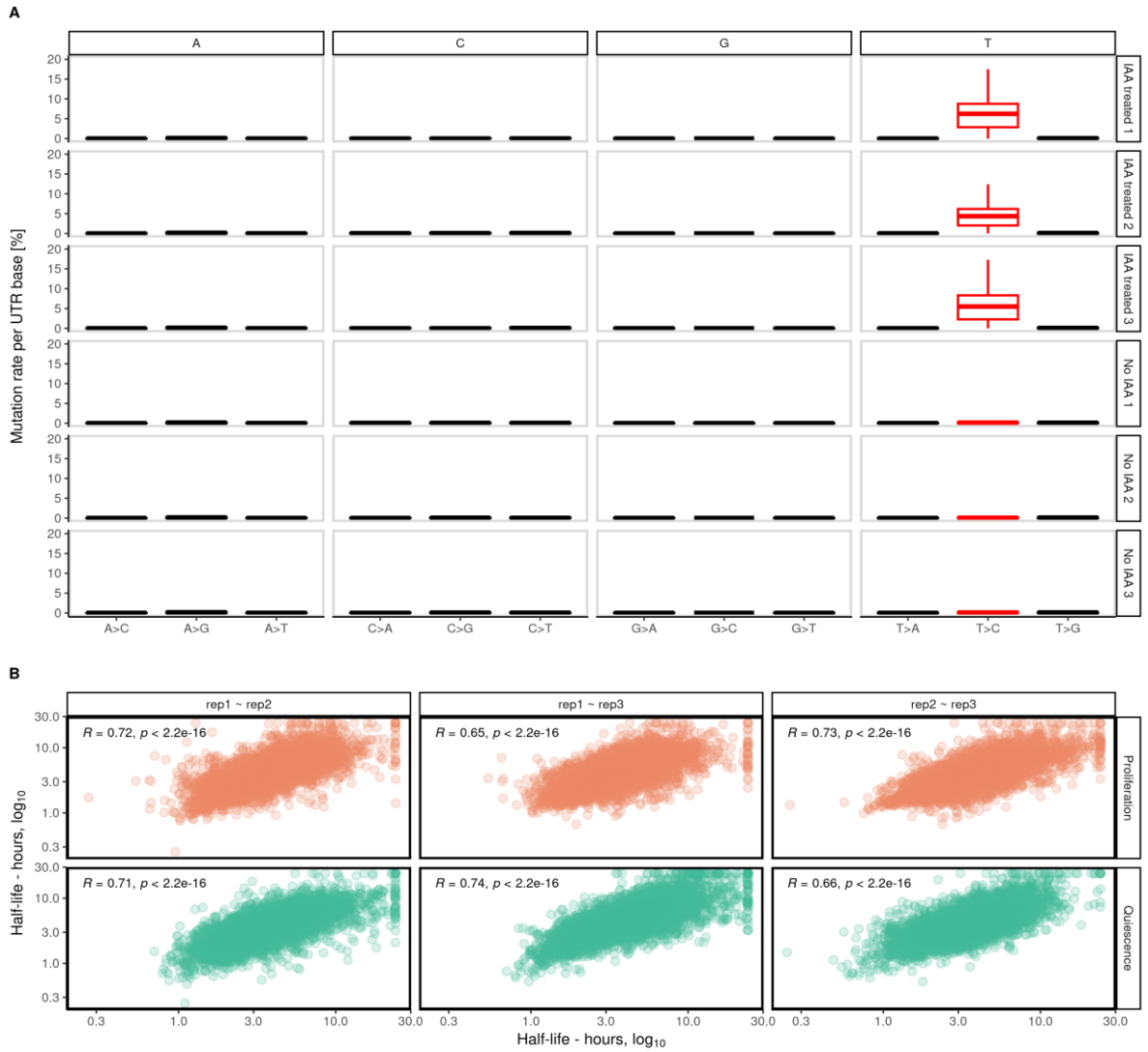
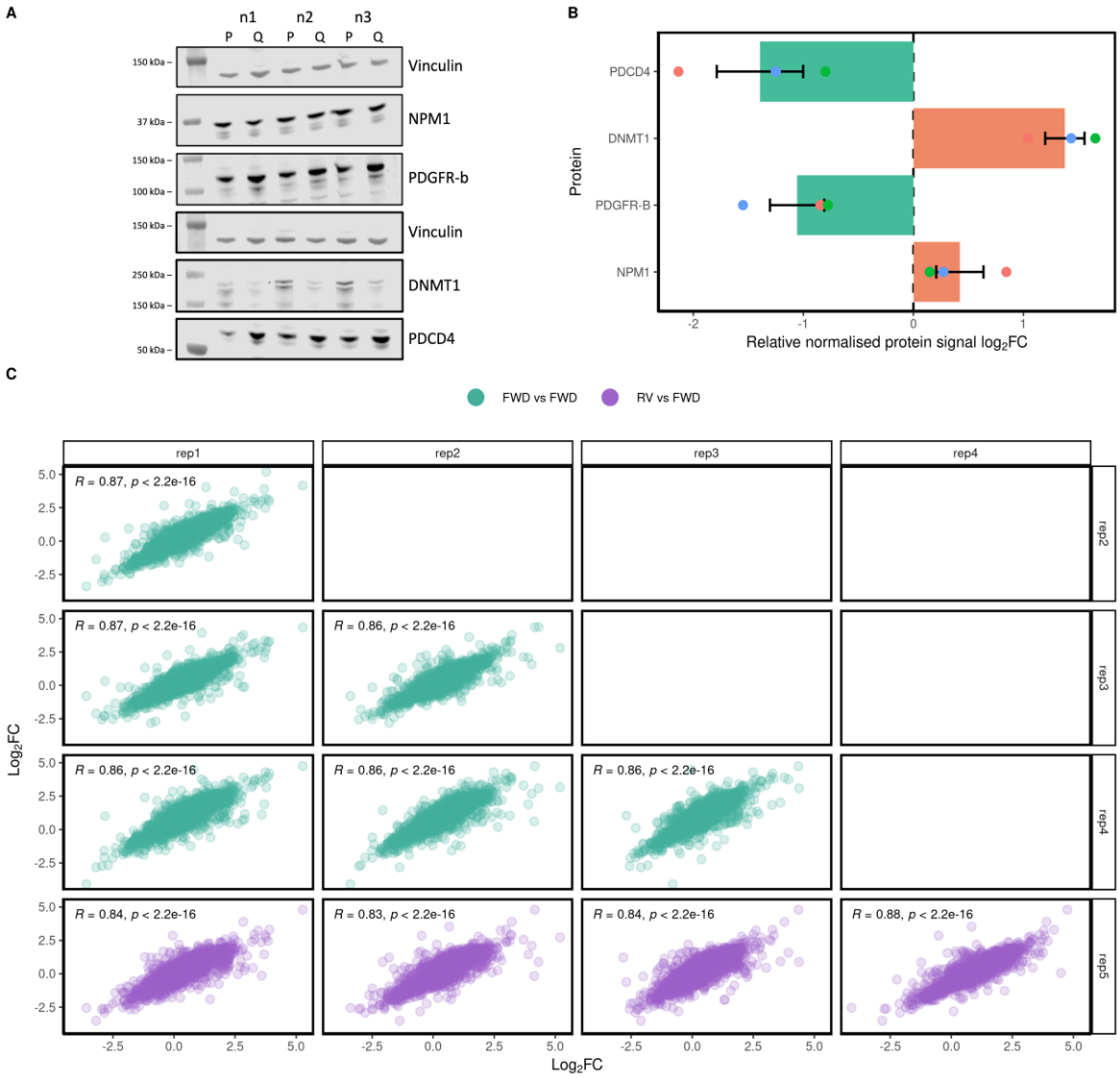
Supplemental figures



Supplemental Figure 1: SLAM-seq QC shows expected mutational signature and good correlation between replicates

A. T>C mutational signature is enriched in the 3' UTR of fed BJ5Ta cells treated with s4U at 0-hour timepoint with IAA treatment. This signature is not present without IAA treatment. Boxplot of percentage of reads mapping to the 3' UTR with mutations indicated from 3' UTR sequencing. Three biological replicate experiments were performed.

B. Good correlation of predicted mRNA half-lives between replicates in proliferative (orange) and quiescent (green) BJ5Ta cells. For each independent replicate, the half-life of a given gene was calculated independently. Spearman's rank correlation (R) is indicated along with p. adjusted value.

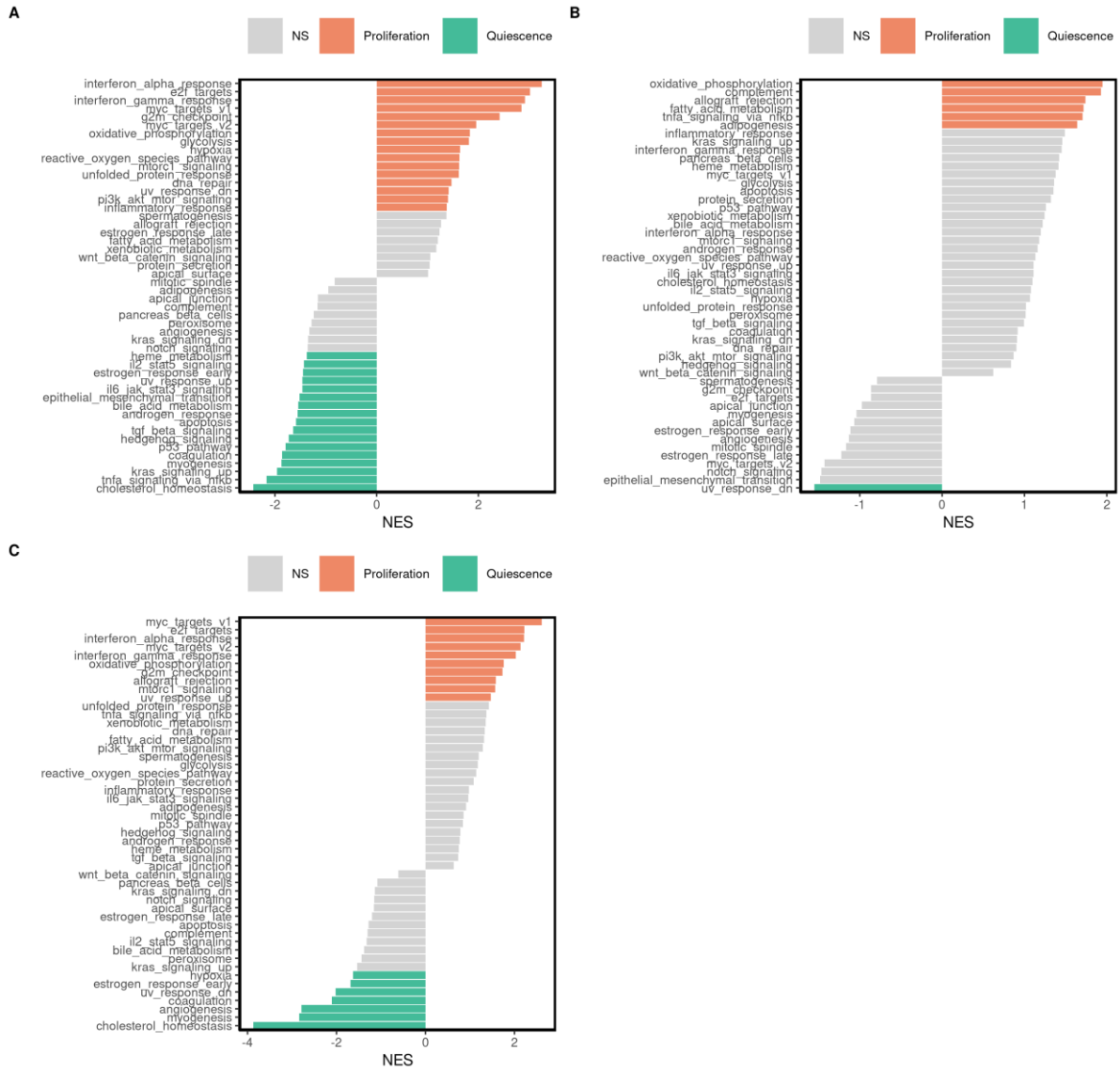


Supplemental Figure 2: pulsed SILAC QC shows expected changes in protein level and good correlation between replicates

A. Western blot of four proteins identified by pSILAC as being differentially produced in quiescence or proliferation conditions with three independent replicates indicated as "n*" and proliferation (P) and quiescence (Q). NPM1 and DNMT1 are associated with proliferation, PDGFR-b and PDCD4 are associated with quiescence. Vinculin expression is shown as a loading control.

B. Quantification of Western blots. Bar indicates mean log2FC relative signal intensity of each protein relative to Vinculin with standard error of the three replicates in proliferative (orange) and quiescent (green) BJ5Ta cells. Replicates displayed as points and coloured according to experiment number.

C. Replicate correlation of pulse SILAC experiments was good, even when labelling was switched. Ratio of proliferation:quiescent labelled protein was calculated for each protein. Spearman correlation and p. adjusted value indicated. Forward and reverse SILAC experiments were compared. Forward comparison to forward is highlighted in green, and in purple are forward experiments challenged to reverse experiments.

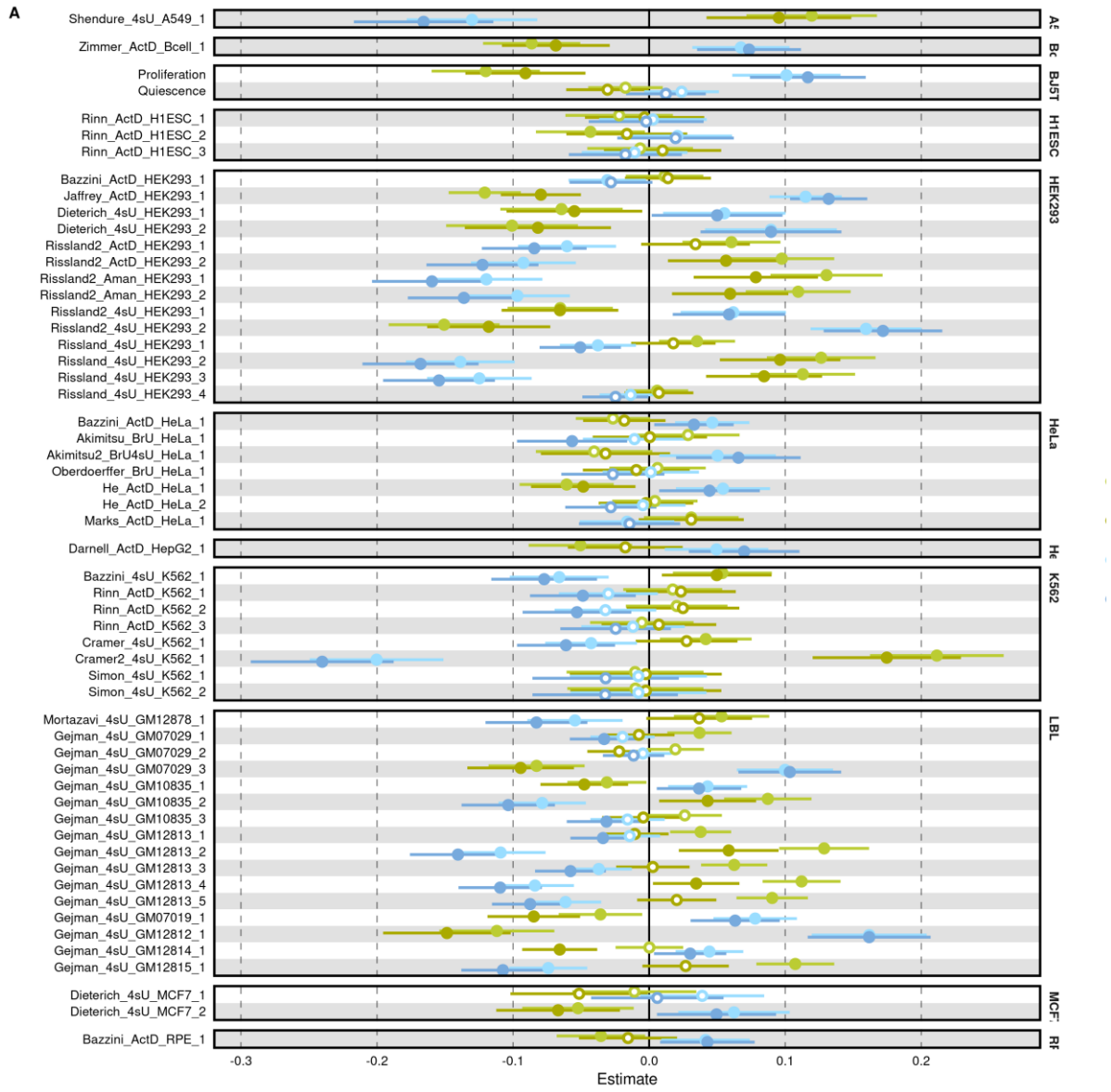


Supplemental Figure 3: Proliferation pathways are changing at the RNA and protein level, but not at the mRNA half-life level.

A. Enrichment of pathway specific stability between proliferation and quiescence-related transcripts. GSEA was performed using Hallmark gene-sets (Liberzon et al. 2015). Normalised enrichment score on the x-axis, highlighted if significant (p. adj < 0.05) in proliferative conditions in orange and if towards quiescence in green. *t*-statistic was used as ranking metric for RNAseq.

B. As A, with $-\log^{10}$(p. adjusted value)/sign $\log_2$(FC) utilised for half-life ranking.

C. As B, but with pSILAC data, using $-\log^{10}$(p. adjusted value)/sign $\log_2$(FC) for ranking.



Supplemental Figure 4: Codon Stability Coefficients from other studies

A broad sampling of half-life data was used from the literature to understand how both cell line and method of half-life capture affect the codon stability coefficient calculation (Agarwal and Kelley 2022). As per Figure 3C. Row names: GroupID, method, cell line, and sample N.