

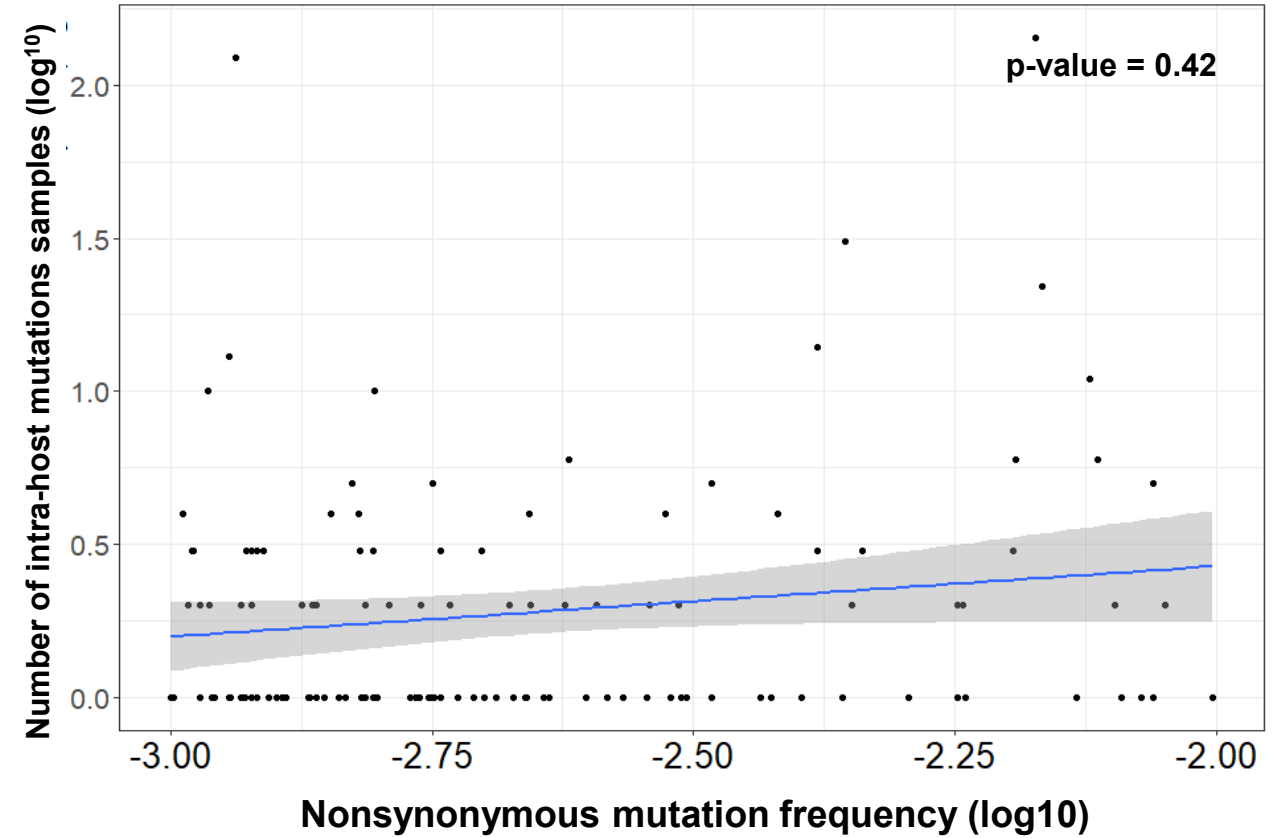
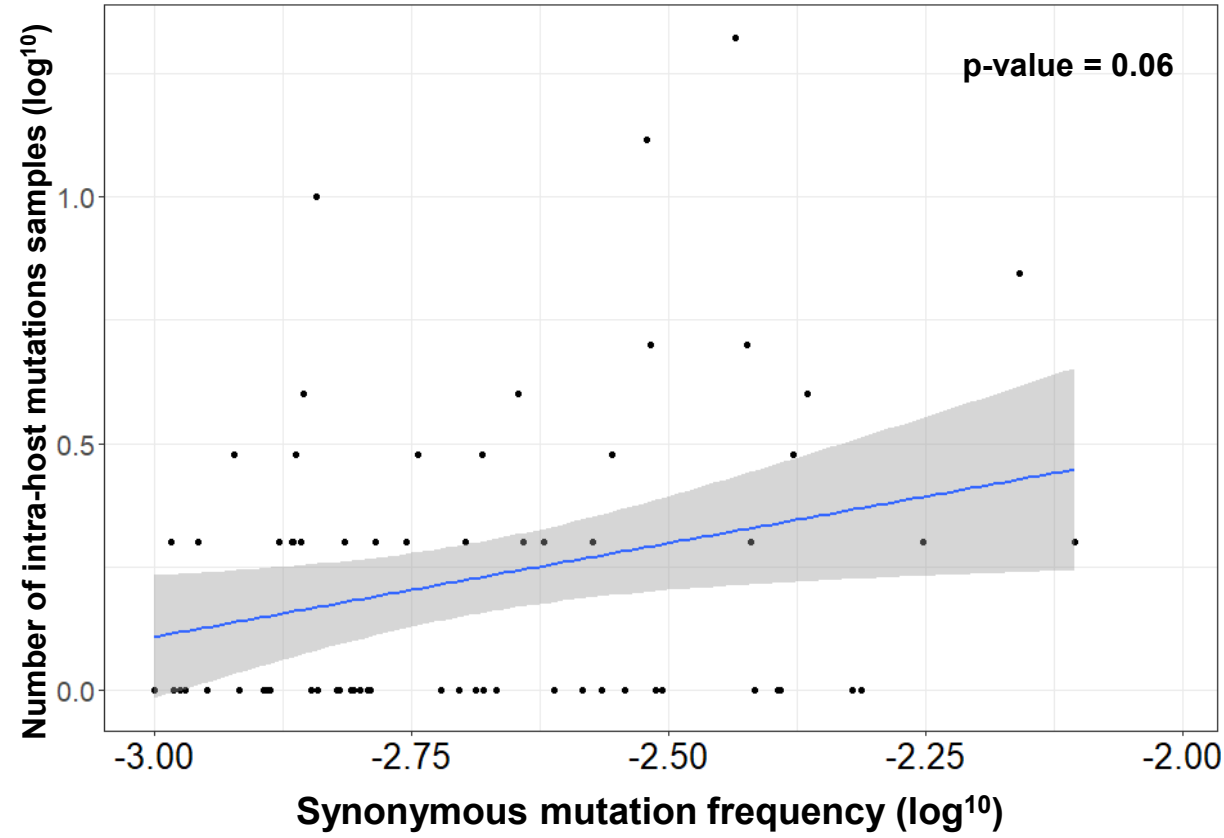


Fig. S1 Correlation of synonymous (left panel, $p=0.06$, Kendall correlation, $\tau=0.17$) and (C) nonsynonymous (right panel, $p=0.42$, $\tau=0.05$) mutation frequency between hosts (X-axis) with number of intra-host variants (Y-axis). The two datasets were collected over identical time interval.

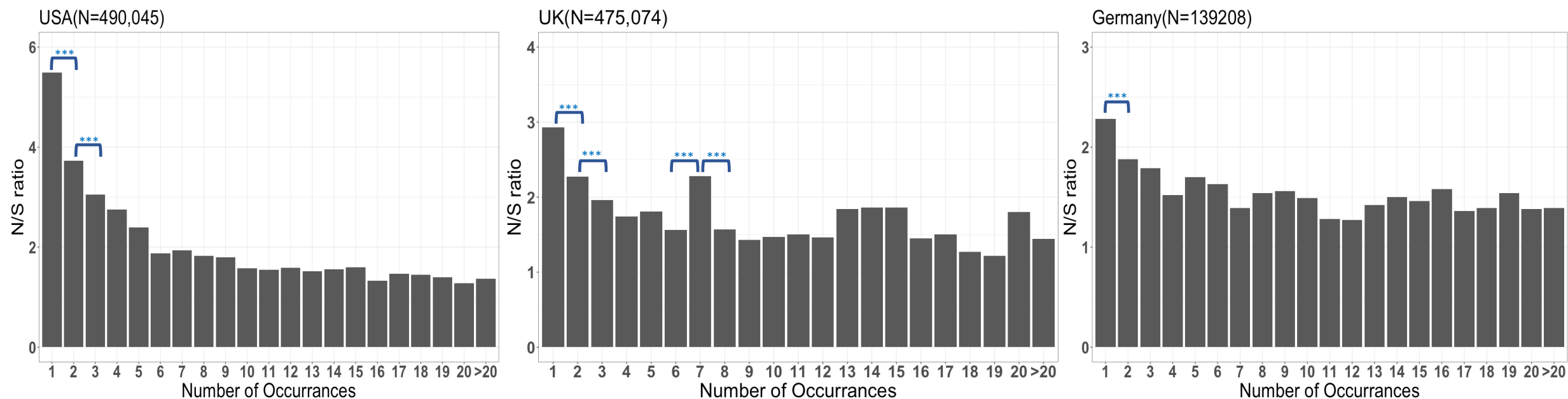


Fig. S2 N/S ratios of mutations that occurred 1 – 20 time in different countries. (***) $p < 10^{-3}$; Chi-square test)

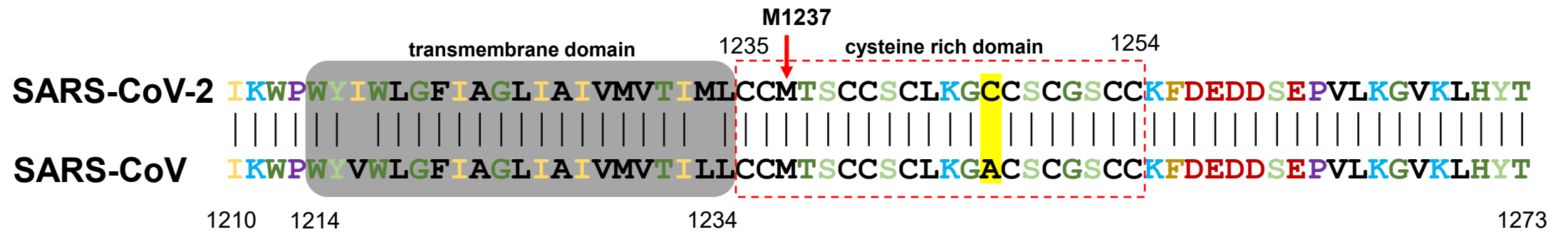


Fig. S3 The amino acid alignment of cytoplasmic tail of the SARS-CoV and SARS-CoV-2 Spike proteins.

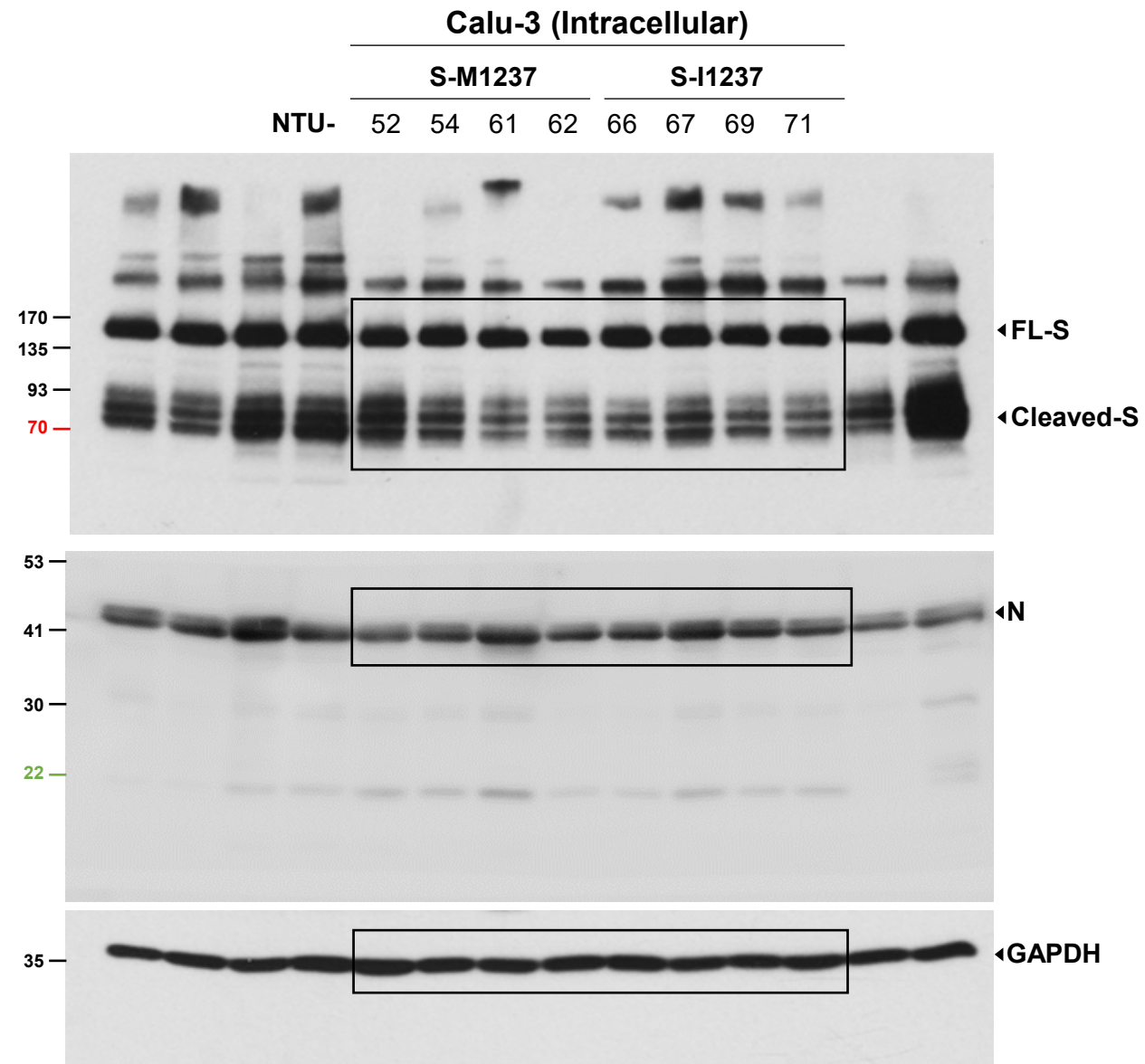


Fig. S4 Full length blot images that were cropped and presented in Figure 3A.

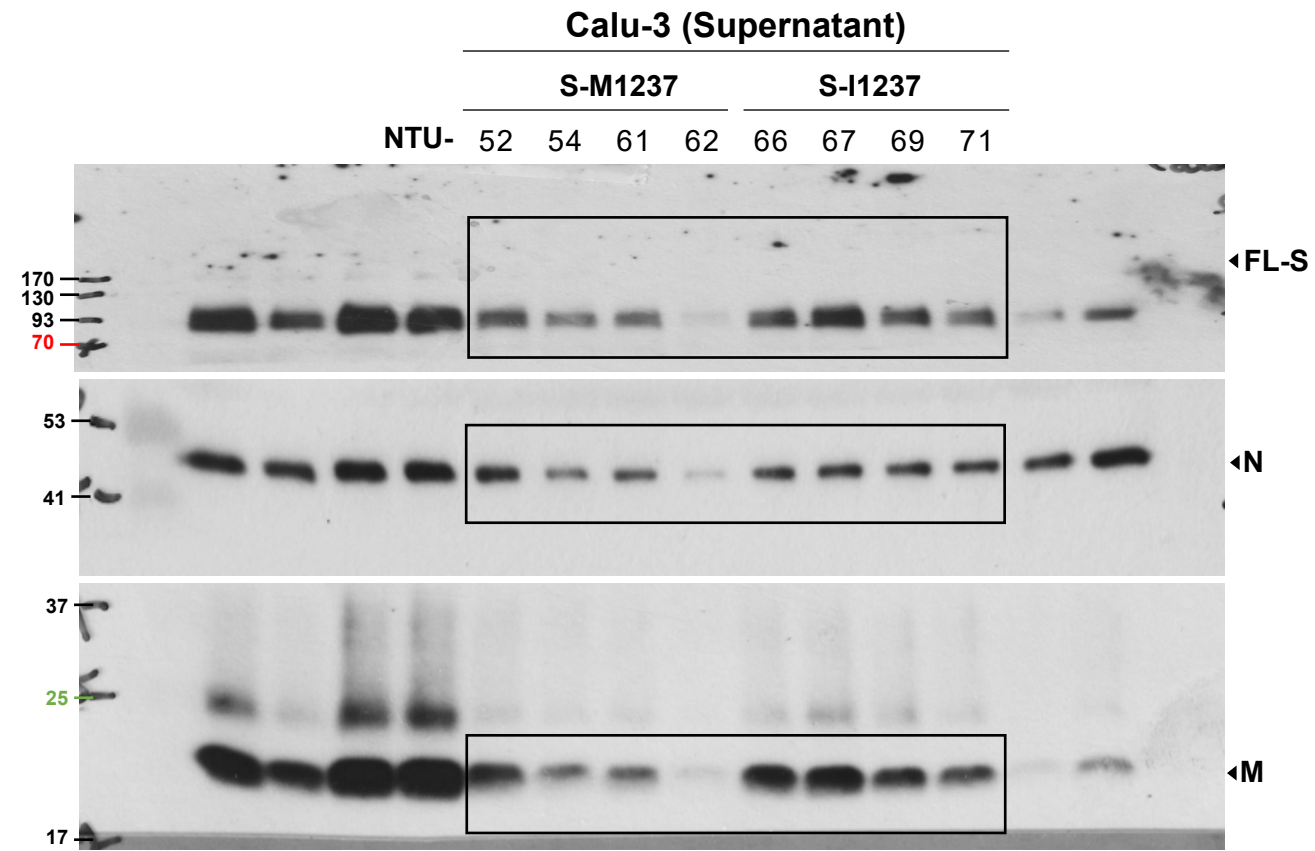


Fig. S5 Full length blot images that were cropped and presented in Figure 3B.

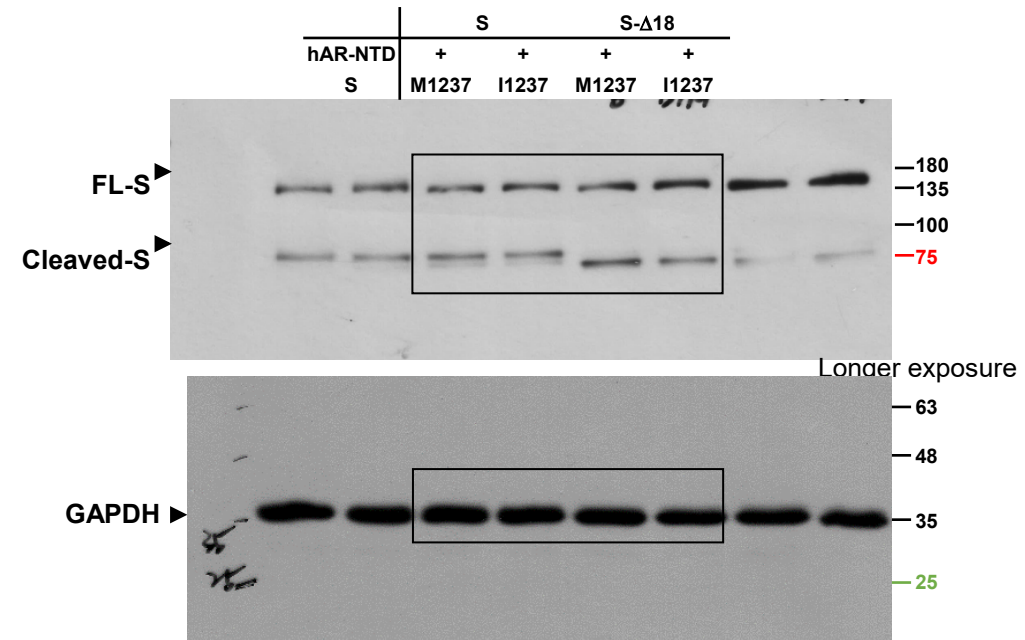


Fig. S6 Full length blot images that were cropped and presented in Figure 4E.