

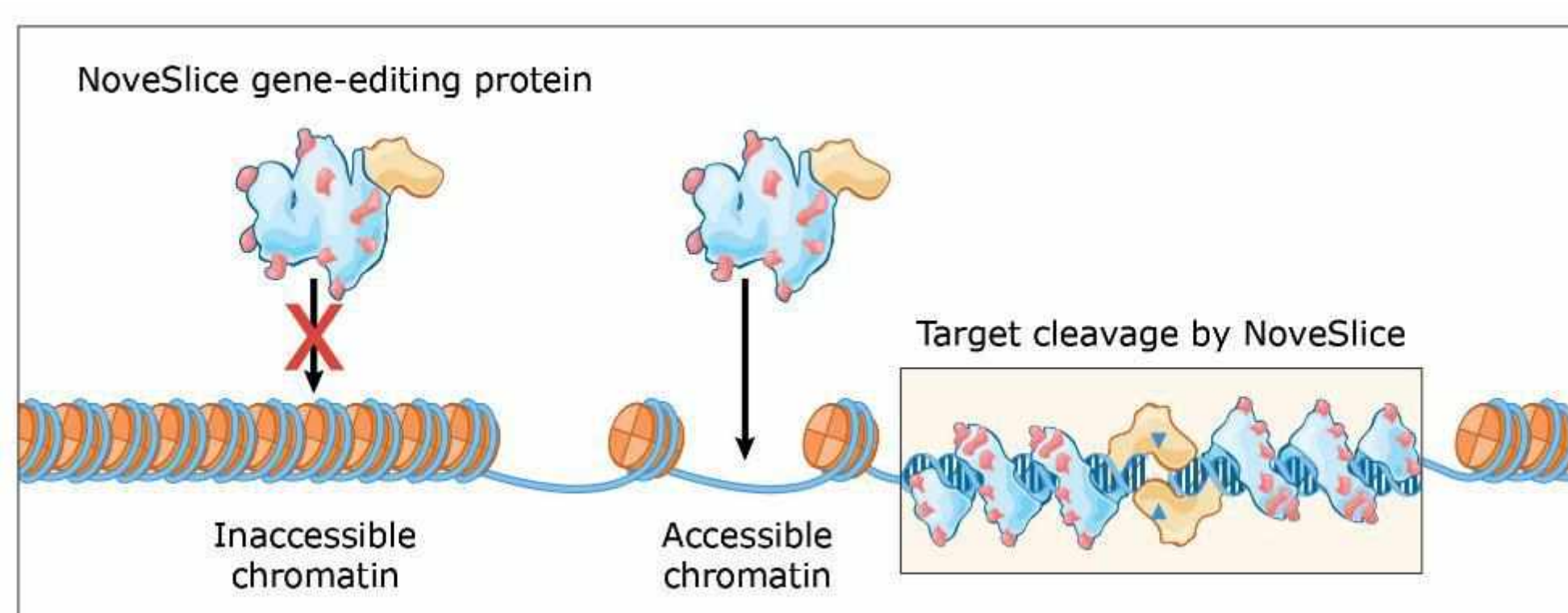
NoveSlice: A Novel Chromatin Context-Sensitive Gene-Editing Endonuclease

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Introduction

Genome-editing endonucleases are currently undergoing early clinical evaluation for the treatment of a wide range of diseases. However, *in vivo* use of gene-editing endonucleases is limited by the risk of potentially harmful off-target effects. It has been previously shown that gene-editing endonucleases are blocked by heterochromatin and show reduced efficiency in nucleosome-associated targets.



Methods

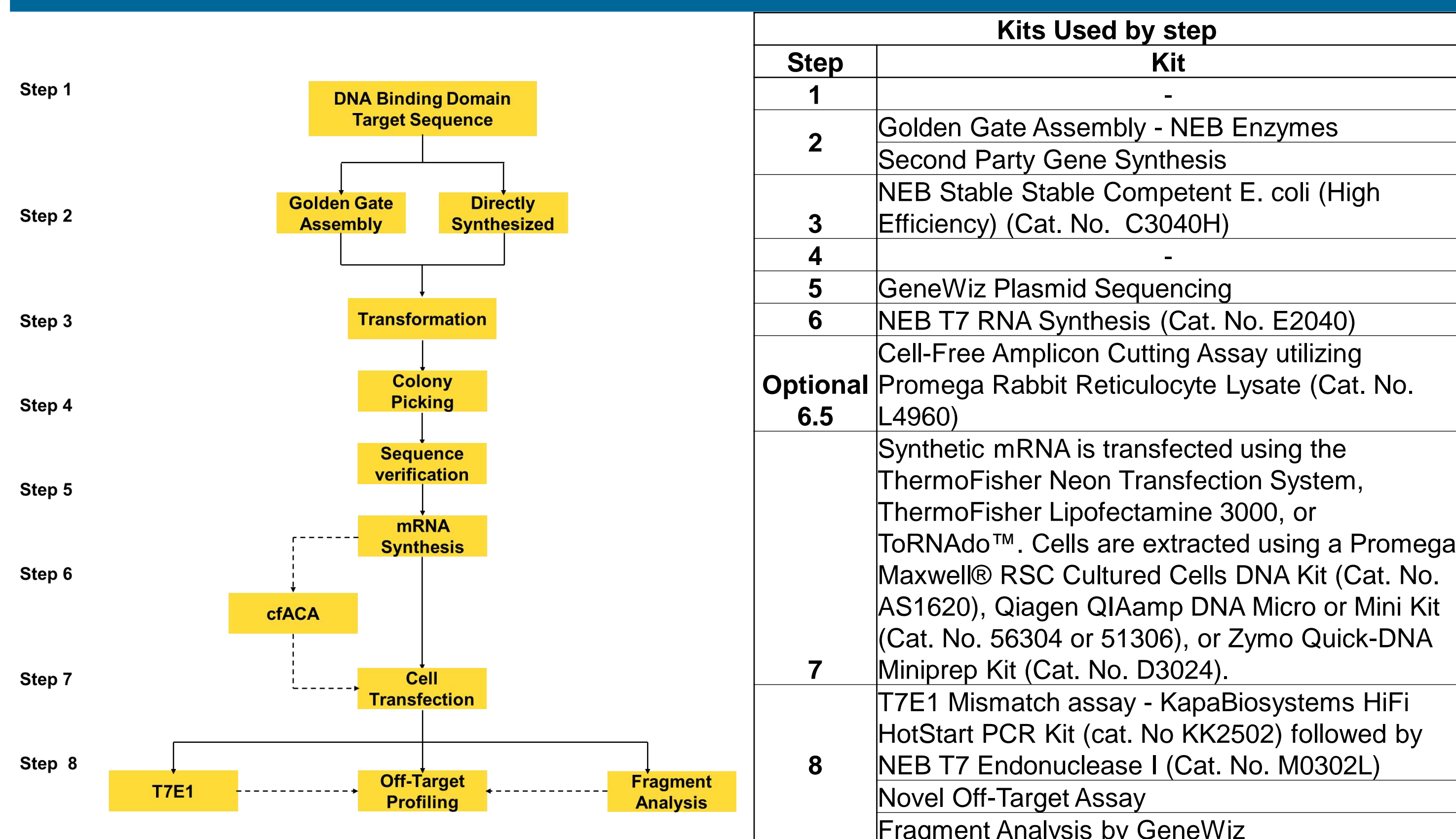


Figure 1 & Table 1: Flow Chart of NoveSlice creation and testing process. The processing and testing procedure for NoveSlice is shown above. The workflow has been streamlined to efficiently process and test gene-editing mRNA. The workflow includes target sequence selection to assess target specificity, off-target effects, insertion rates, and targeting efficiency.

Results

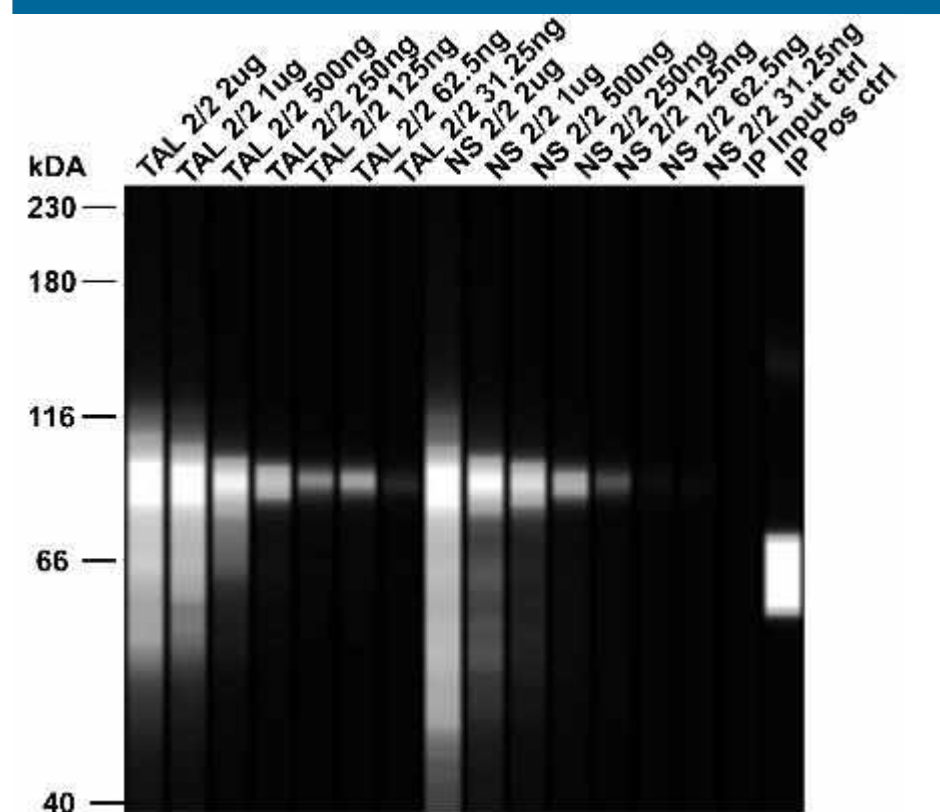
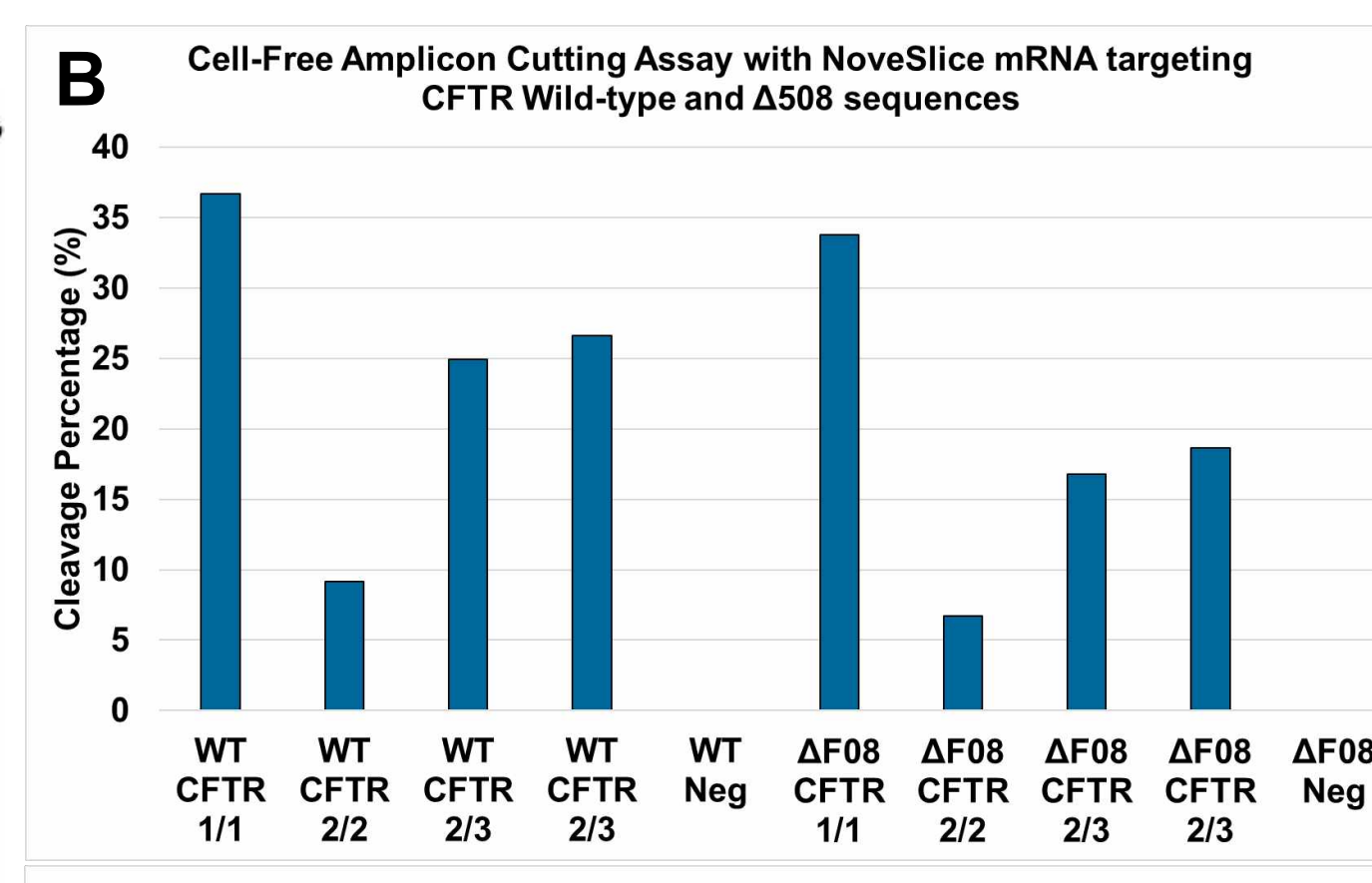
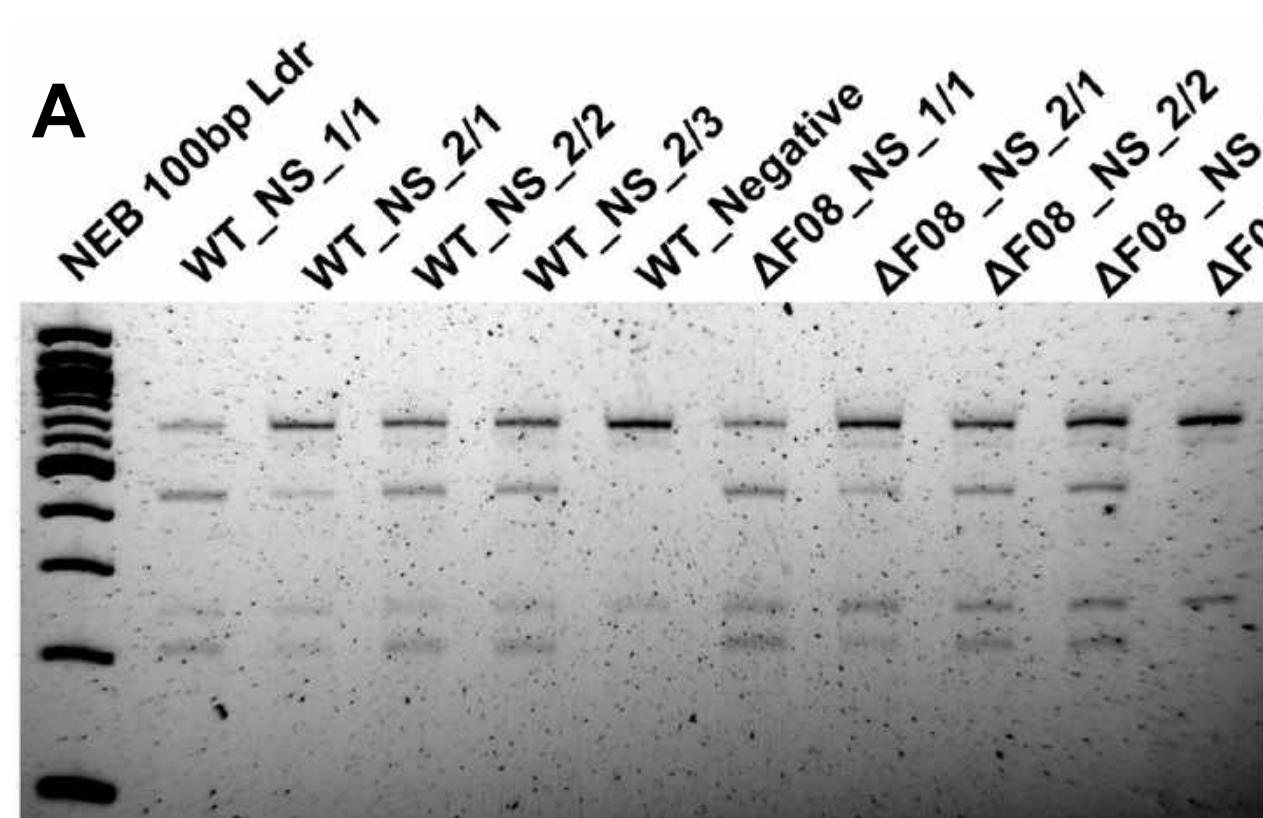


Figure 3: Protein Detection. NoveSlice proteins include a FLAG-tag. Shown here is the result of FLAG-based detection of both NoveSlice and TALENs in a rabbit reticulocyte lysate following immunoprecipitation. After immunoprecipitation, samples were run using FLAG-Tag antibodies on the Biotechne Protein Simple Wes device. Both NoveSlice and TALENs were robustly detected.



| Col7A1E73 Spacing Chart | | | | | |
|-------------------------|----------------|----------------|----------------|----------------|----------------|
| | NS R1 20mer | NS R2 20mer | NS R3 18mer | NS R4 18mer | NS R5 16mer |
| NSL1 20mer | 18 | 16 | 31 | 4 | 6 |
| NSL2 20mer | 20 | 18 | 33 | 6 | 8 |
| NSL3 18mer | 5 | 3 | 18 | -8 | -5 |
| NSL4 19mer | 32 | 30 | 45 | 18 | 20 |
| NSL5 18mer | 0 | 24 | 39 | 12 | 14 |
| NSL6 18mer | 28 | 26 | 41 | 14 | 16 |
| NSL7 18mer | 20 | 18 | 33 | 6 | 8 |

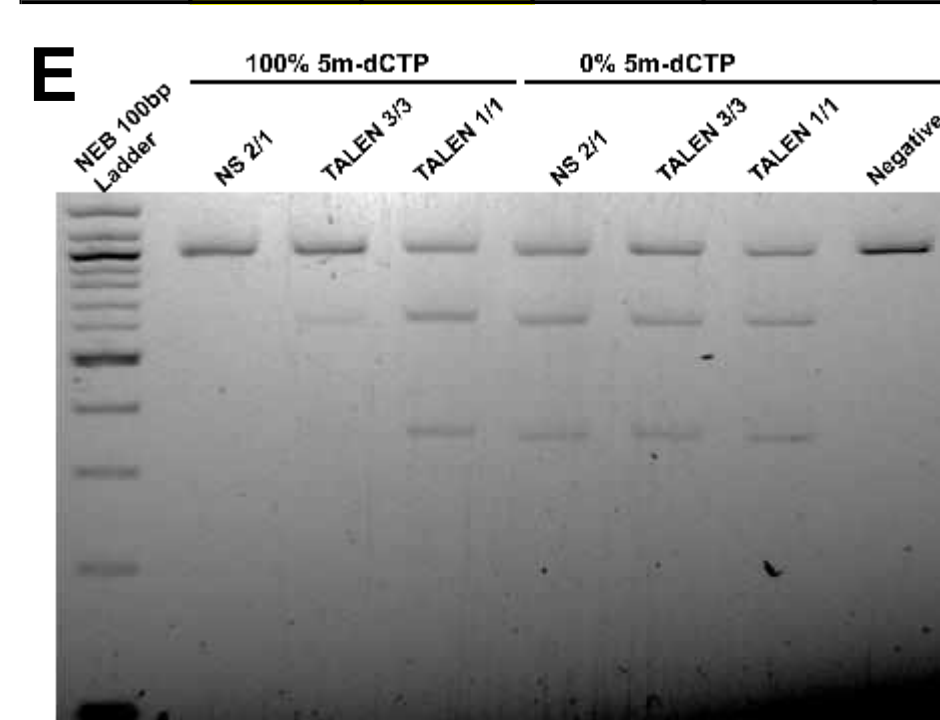
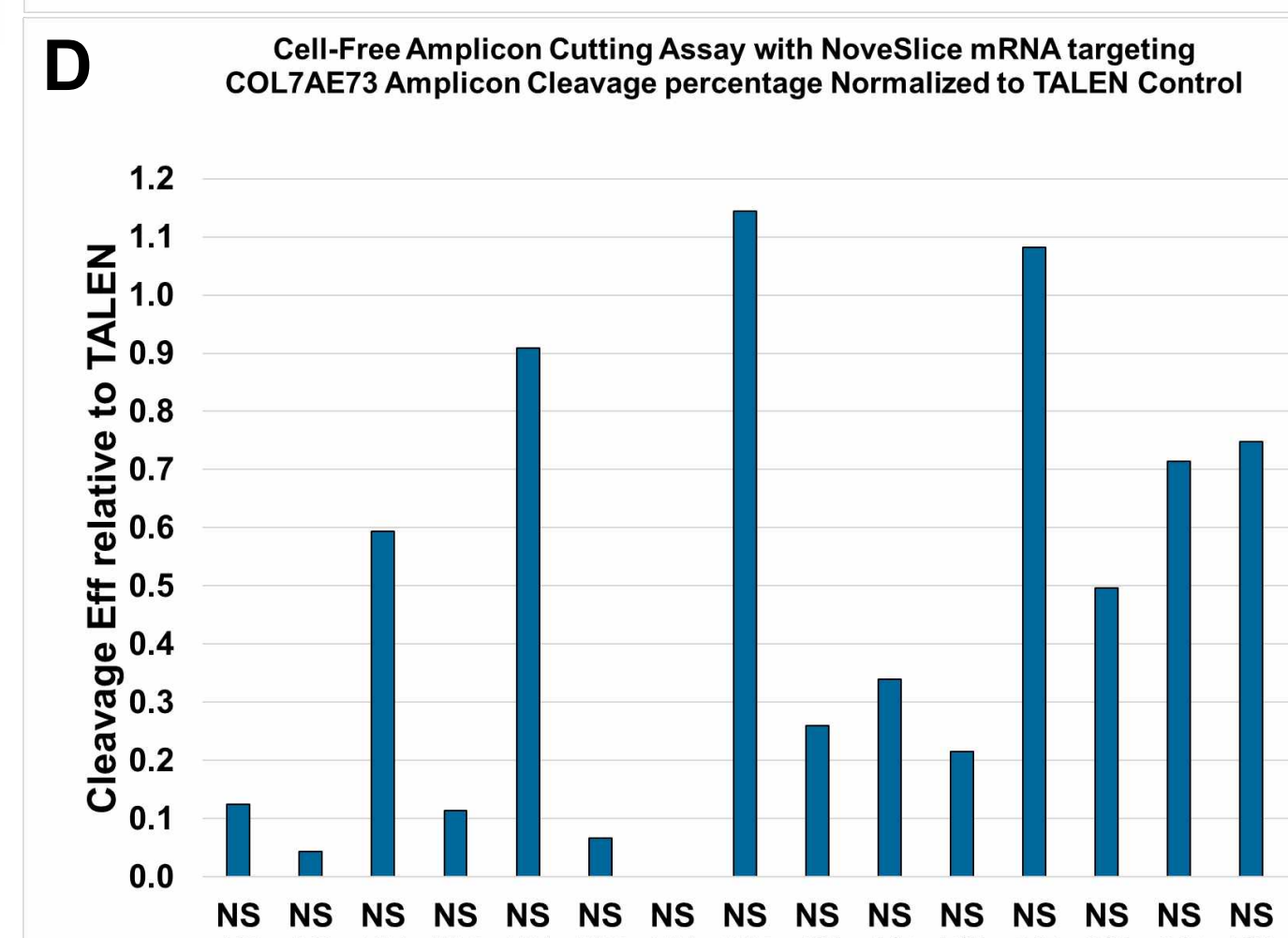


Figure 4: Cell-Free Amplicon-Cutting Assay (cfACA). We developed a rapid method for assessing gene editing proteins using a rabbit reticulocyte lysate system. **A.** gBlocks targeting the WT and ΔF08 mutation in the CFTR gene were synthesized by IDT. **B.** Using ImageJ, cleavage percentage was measured and used to assess different gene-editing pairs. **C.** This table shows spacings of gene-editing protein pairs that were designed to target the splice acceptor for COL7A1 exon 73. **D.** Cleavage efficiency was normalized to the positive control. In this experiment, the effects of converting all NN RVDs to NK were also tested. **E.** dCTP was replaced by 5m-dCTP to create an amplicon that would mimic hypermethylated DNA in the target region. In this case TALEN cut the hypermethylated amplicon, while NoveSlice did not.

| Alias | Sequence |
|-----------|----------|
| NS_Mod_1 | AHDG |
| NS_Mod_2 | GAHD |
| NS_Mod_3 | GTHG |
| NS_Mod_4 | GSGS |
| NS_Mod_5 | NHGG |
| NS_Mod_6 | GSGG |
| NS_Mod_7 | RDHG |
| NS_Mod_8 | IVHG |
| NS_Mod_9 | VHGA |
| NS_Mod_10 | GHGP |
| NS_Mod_11 | RHGD |
| NS_Mod_12 | THGG |
| NS_Mod_13 | GGHD |
| NS_Mod_14 | PHGG |
| NS_Mod_15 | LHGA |
| NS_Mod_16 | GGGG |
| NS_Mod_17 | GRGG |
| NS_Mod_18 | RHGE |
| NS_Mod_19 | AHGA |
| NS_Mod_20 | HRGE |
| NS_Mod_21 | PHDG |
| NS_Mod_22 | GPHD |
| NS_Mod_23 | GKGG |
| NS_Mod_24 | PHGP |
| NS_Mod_25 | IHGM |
| NS_Mod_26 | GPYE |

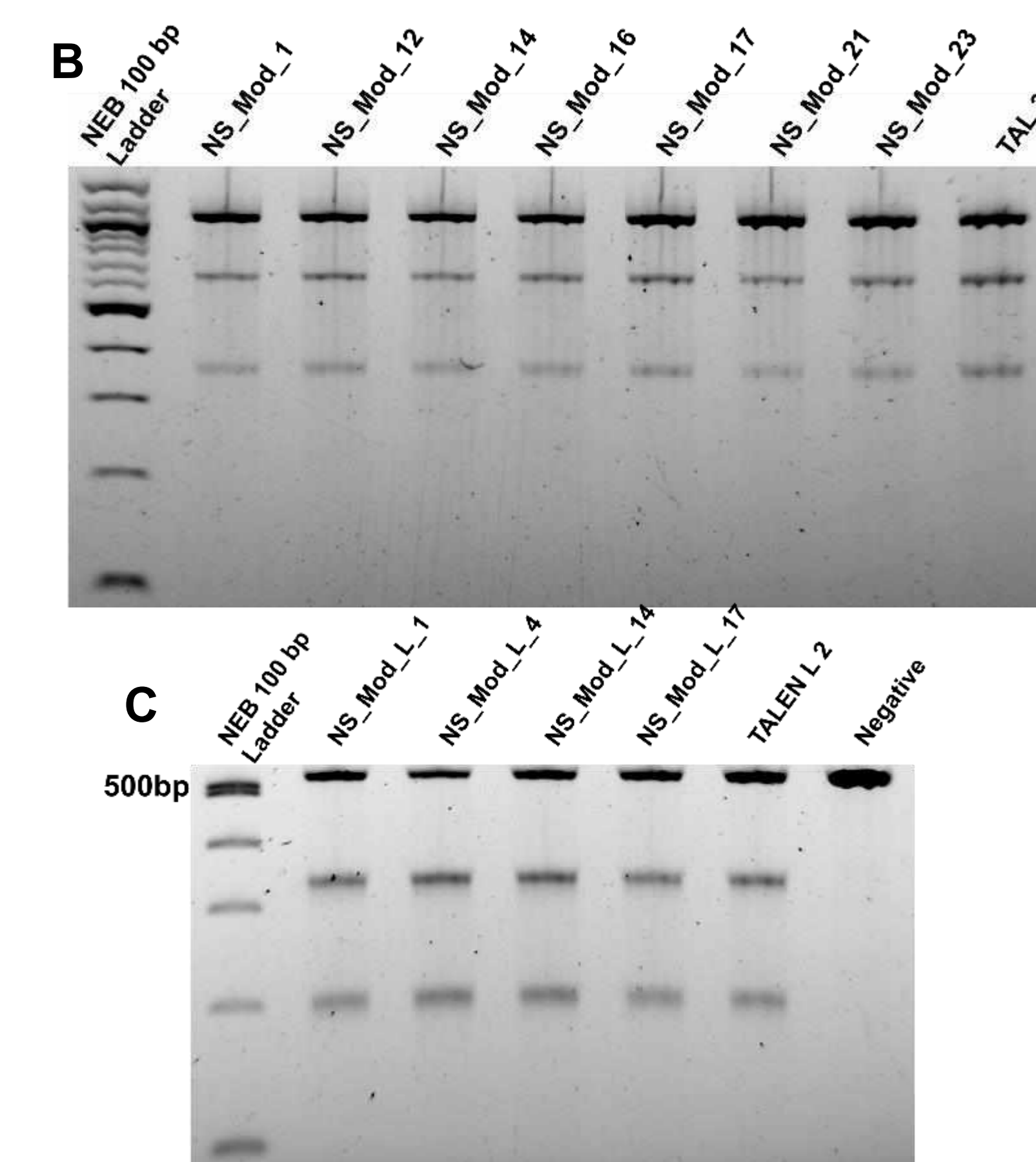


Figure 7: Additional Linkers. **A.** Various linkers were designed and tested. **B.** Cells were transfected with gene editing pairs in which the left gene editing protein contained a modified linker in the second-to-last position. The pairs were designed to target the Human AAVS1 site. Transfections were performed using ToRNA^{do}™ and 500ng of mRNA on Neonatal Human Epidermal Keratinocytes. Cells were extracted 48 hours after transfection and a T7E1 was performed. **C.** iPSCs were transfected gene editing pairs in which the left gene editing protein contained multiple alternative linkers. The pairs were designed to target the human Col7A1 exon 73 splice acceptor site. Transfections where performed using Lipofectamine 3000 and 2ug of mRNA per well of a 6-well plate. Cells were extracted 48 hours after transfection and a T7E1 was performed.

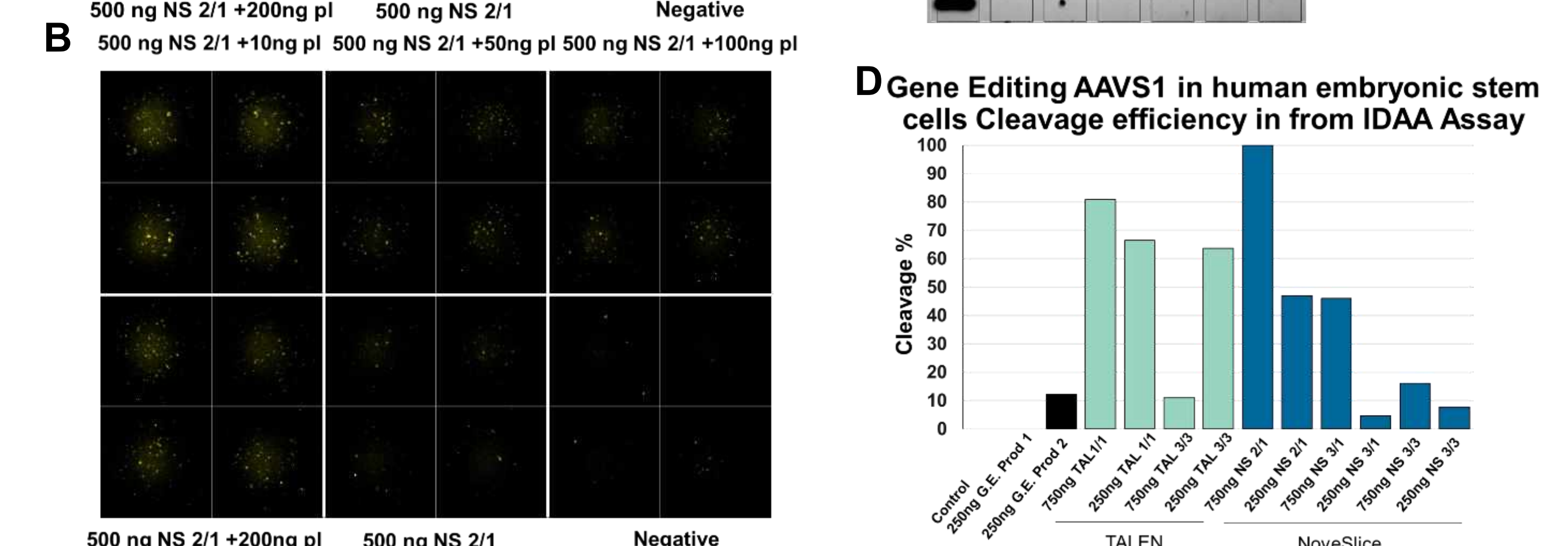
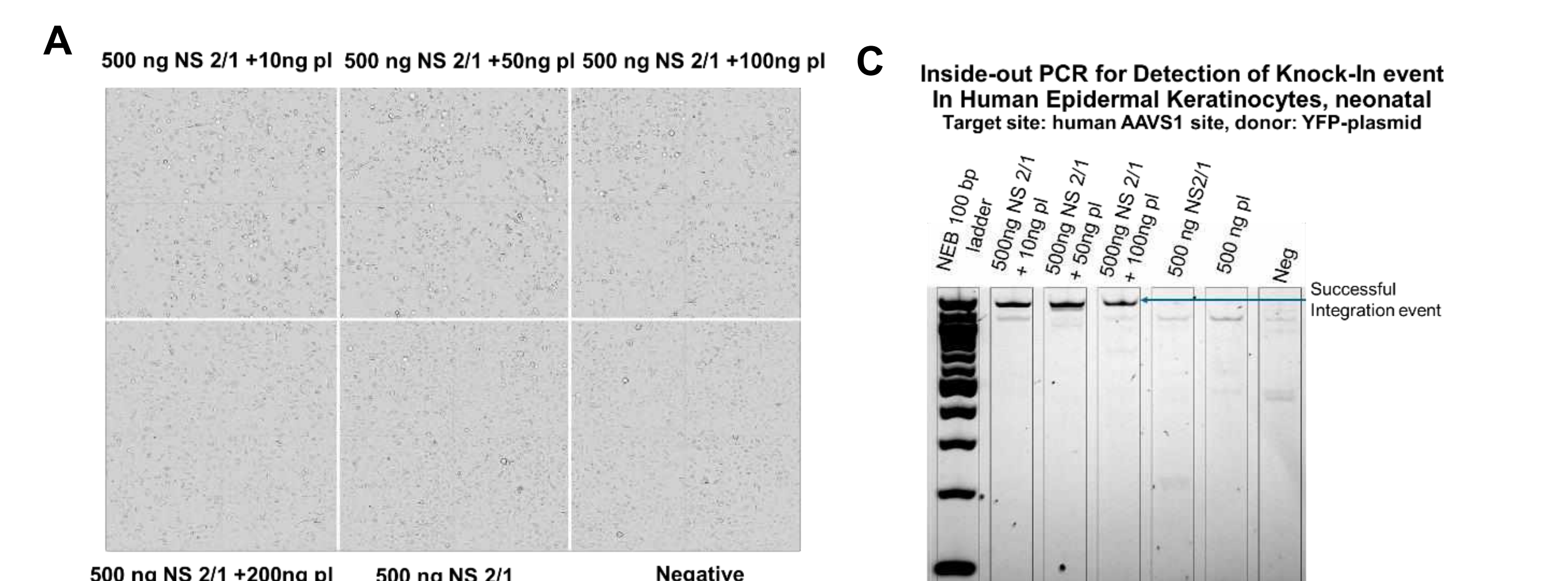
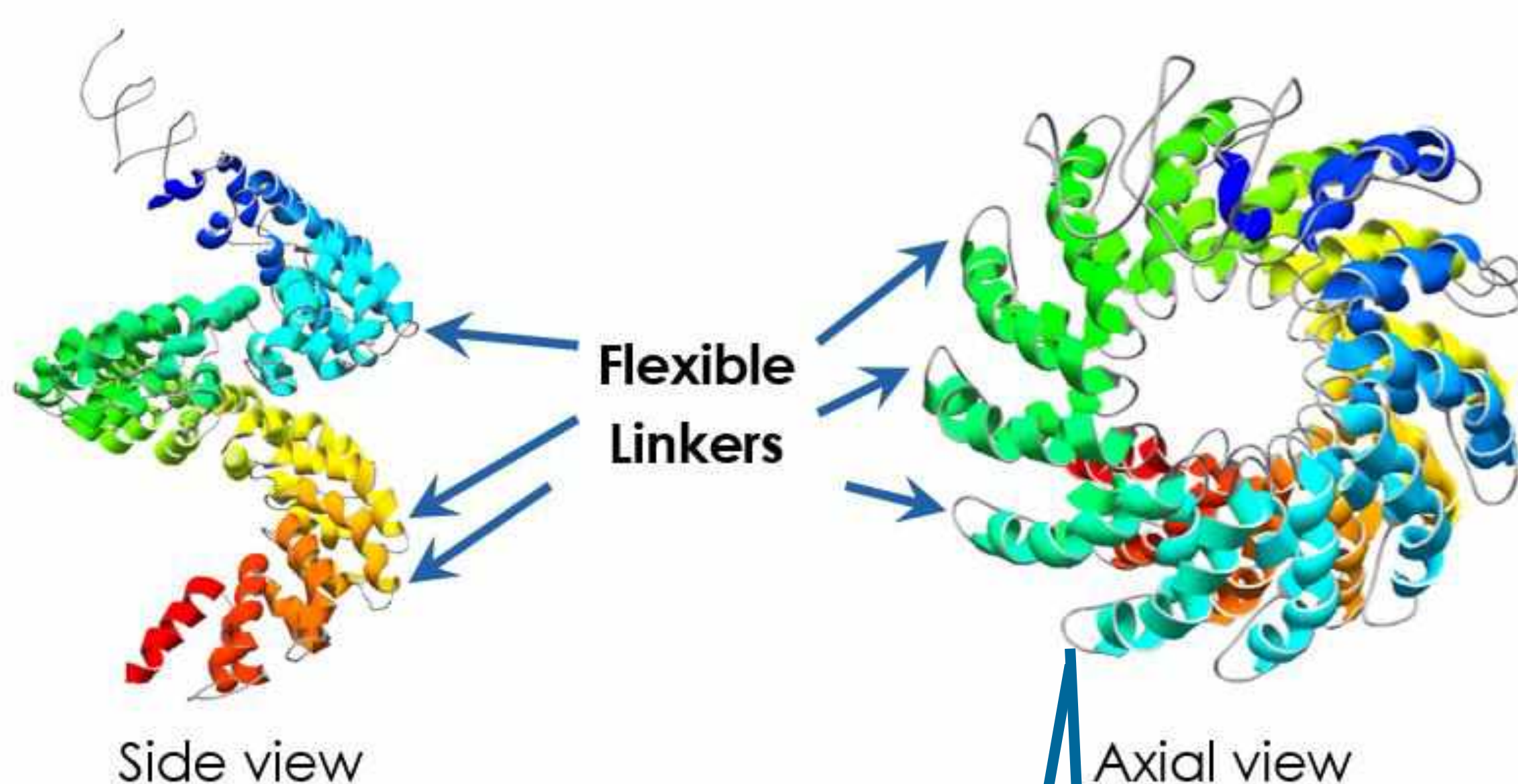


Figure 8: Insertion and Editing Efficiency Quantification. **A-B.** Human neonatal epidermal keratinocytes were transfected and imaged using an Operetta High-Content Imaging System. **C.** DNA was extracted and an inside-out PCR was performed to assess integration. **D.** The IDAA Assay (Yang Z, Steentoft C, Hauge C, et al. Fast and sensitive detection of indels induced by precise gene targeting. Nucleic Acids Res. 2015;43(9):e59. doi:10.1093/nar/gkv126) was used to quantify the editing efficiency of NoveSlice.



Wild-Type Monomer
 LTPEQVVAIAS***RVD***GGKQALETVQRLLPVLCQAHG

Synthetic Flexible Monomer
 LTPEQVVAIAS***RVD***GGKQALETVQRLLPVLCQAGHG

Figure 2: NoveSlice Synthetic Monomers. Flexible linkers are added to the 3' end of monomers. Alternating or non-tandem arrays of synthetic and wild-type monomers were assessed for editing efficiency, toxicity, and chromatin-context sensitivity. The linkers are shown by arrows.

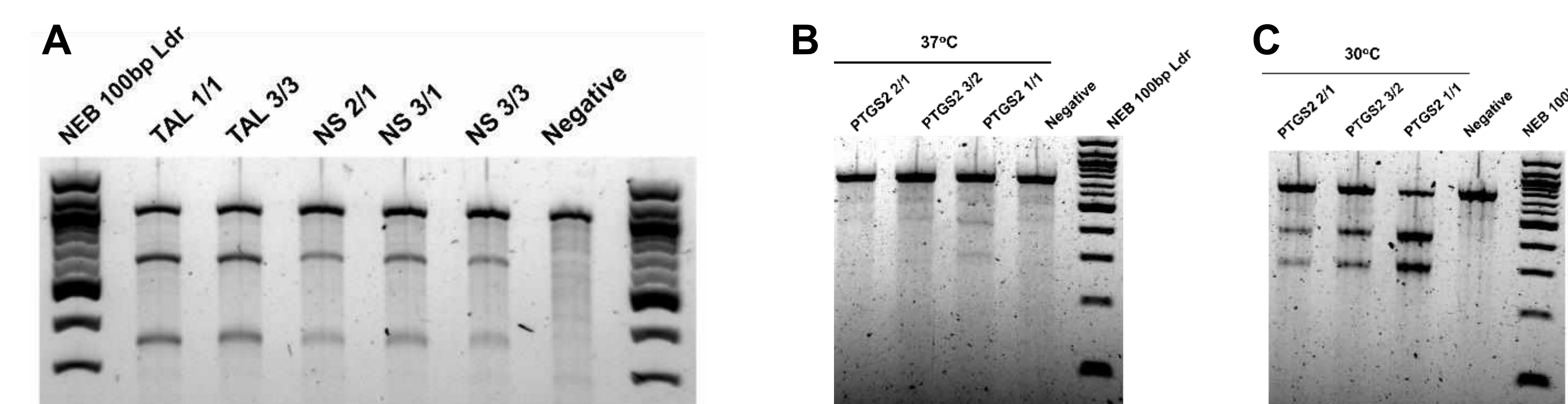


Figure 5: Temperature Sensitivity. **A.** Human neonatal epidermal keratinocytes were transfected using 500ng mRNA targeting the Human AAVS1 site using ToRNA^{do}™ under normal condition (37°C, 19% O₂, and 5% CO₂). Cells were harvested and DNA was extracted 48 hours after transfection. Surveyor PCR and T7E1 was performed. **B-C.** iPSCs were transfected using 500ng mRNA under two different temperature conditions 37°C and 30°C, both at 5% O₂, and 5% CO₂. These experiments demonstrate the temperature sensitivity of NoveSlice, and that transfection at low temperature can restore efficient cutting of targets that are not cut at 37°C.

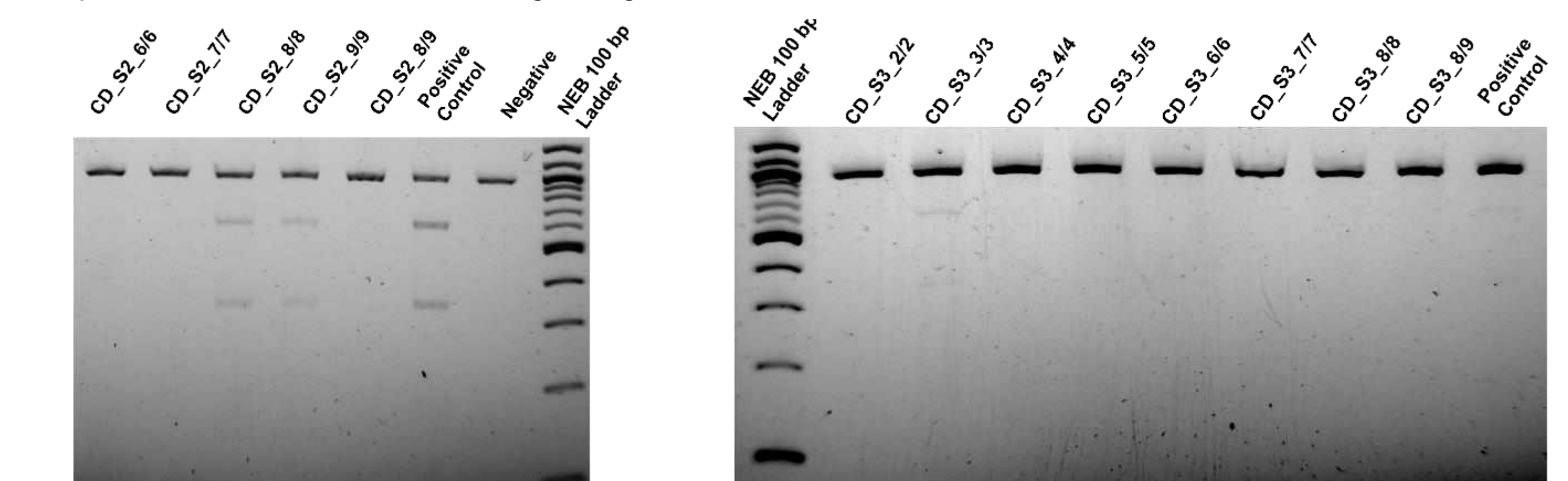


Figure 6: Catalytic Domain. cfACA experiments were performed to assess the relative efficiency of different cleavage domains.

Discussion

While several gene-editing proteins efficiently cut various targets in primary human cells, these data show that the novel NoveSlice gene-editing endonuclease is more sensitive to the chromatin context of the target than an equivalent TALEN pair. The risk of potentially harmful off-target effects has restricted the clinical translation of gene-editing technologies. A gene-editing endonuclease with reduced activity in inaccessible regions of the genome could exhibit reduced off-target effects, and could thus represent a powerful tool for the development of gene-editing therapies. Here we present a novel gene-editing endonuclease that exhibits enhanced sensitivity to the chromatin context of the target. NoveSlice may serve as an important tool for the development of new precision medicines, including *in vivo* gene-editing therapies.

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