

# EDIT-301: An Experimental Autologous Cell Therapy Comprising Cas12a-RNP Modified mPB-CD34+ Cells for the Potential Treatment of SCD

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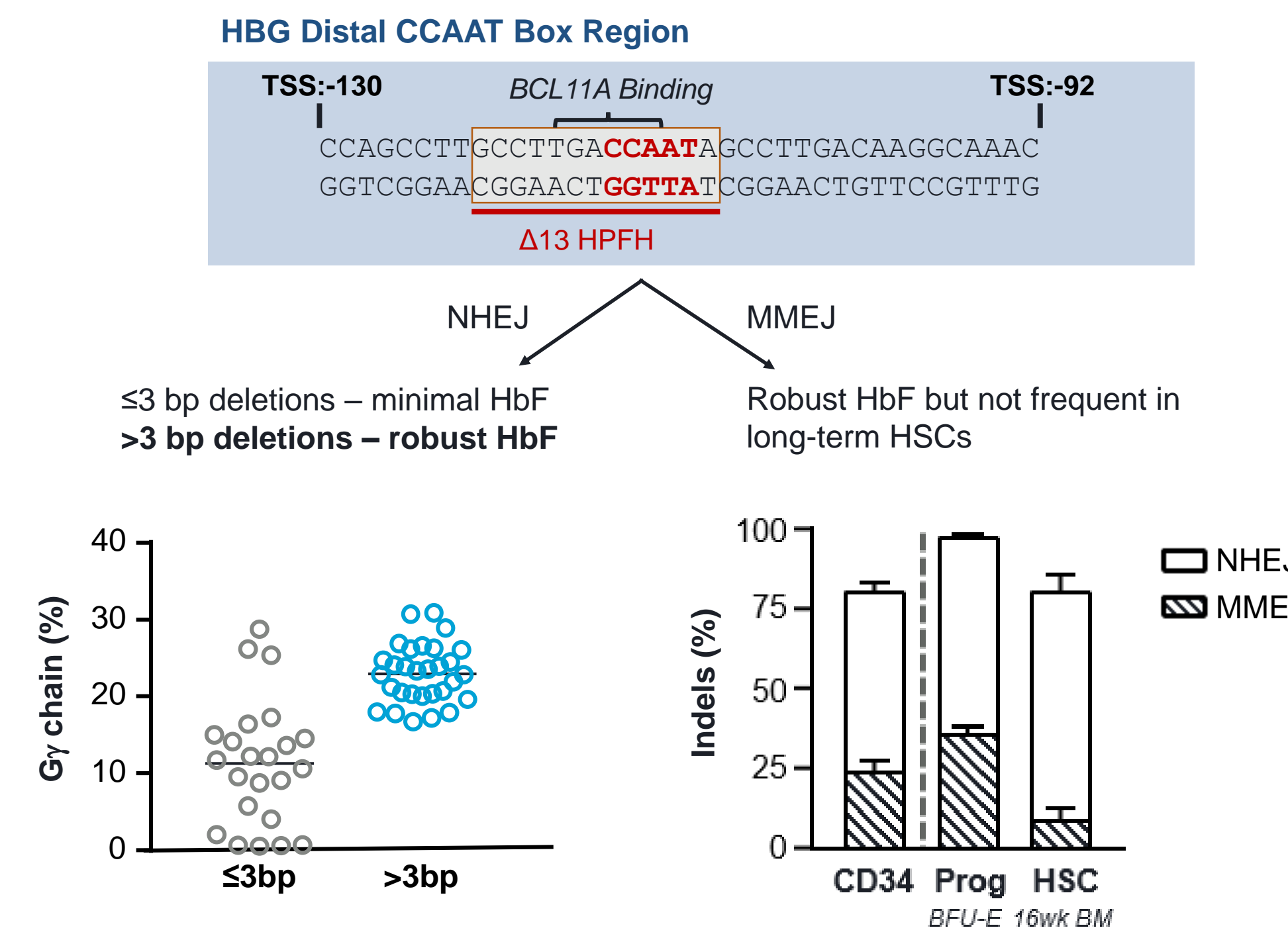
## Introduction

Sickle cell disease (SCD) is caused by a single mutation E6V of the  $\beta$ -globin chain, leading to polymerization of sickle hemoglobin (HbS) and formation of HbS fibers. Fetal hemoglobin (HbF) protects against SCD by inhibiting HbS polymerization.<sup>1</sup> Individuals with compound heterozygosity for HbS and deletional hereditary persistence of fetal hemoglobin (HPFH) express approximately 30% HbF with pancellular distribution and exhibit no features of SCD.<sup>2</sup>

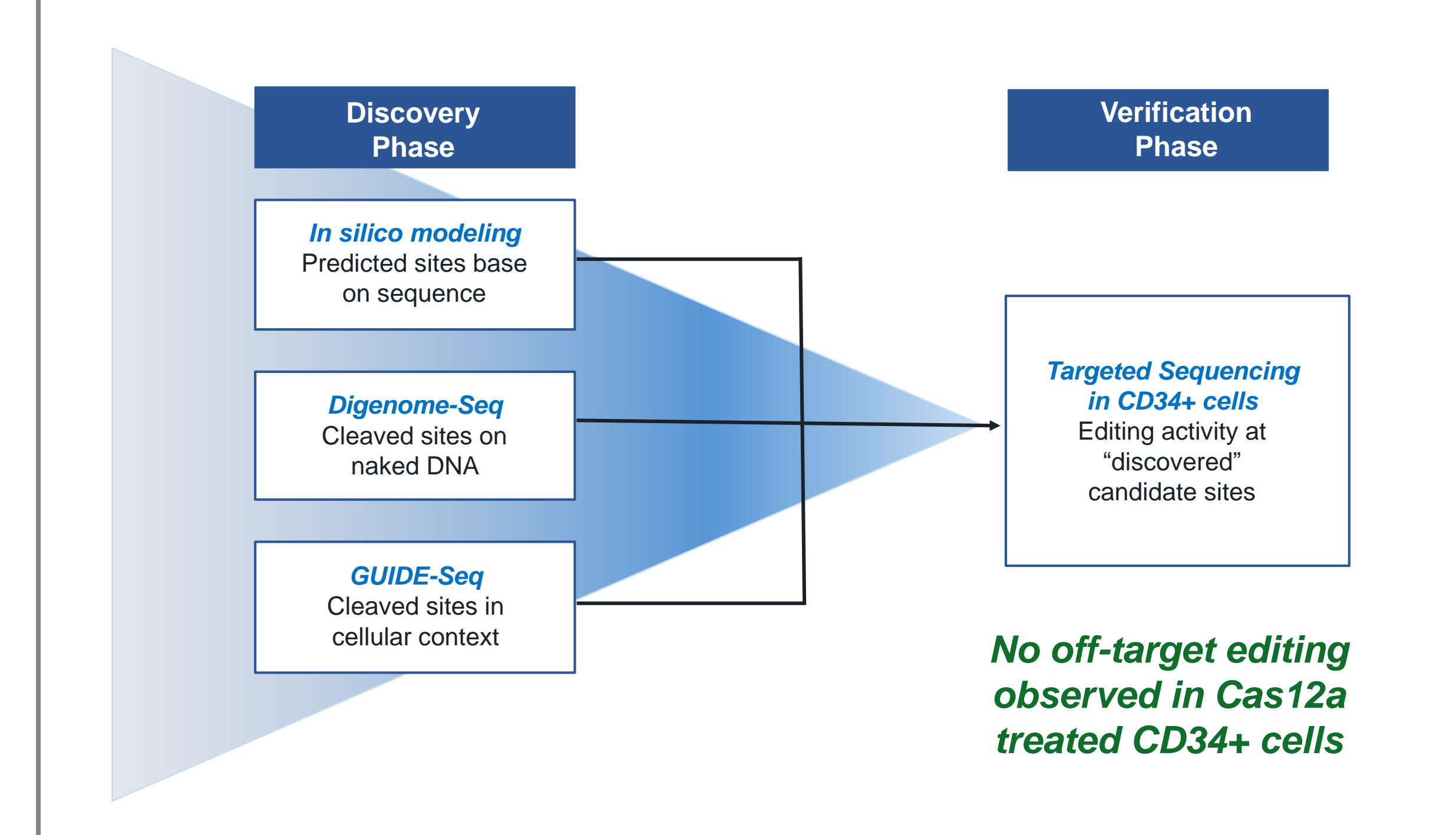
The HBG distal CCAAT box region was identified in our previous screen to be one of the most robust HbF-inducing sites across the beta-globin locus. Several naturally occurring HPFH mutations are also clustered at this region, partially overlapping a BCL11A binding site.<sup>3</sup>

Cas12a, a highly specific gene editing enzyme,<sup>4</sup> was evaluated against spCas9 for its capacity to promote durable and high-HbF inducing indels at the distal CCAAT box. Those studies led us to optimize Cas12a editing for EDIT-301, a potentially best-in-class experimental medicine for SCD.

## Large NHEJ Deletions Are Durable and Induce High Levels of HbF



## EDIT-301 – No Detectable Off-targets



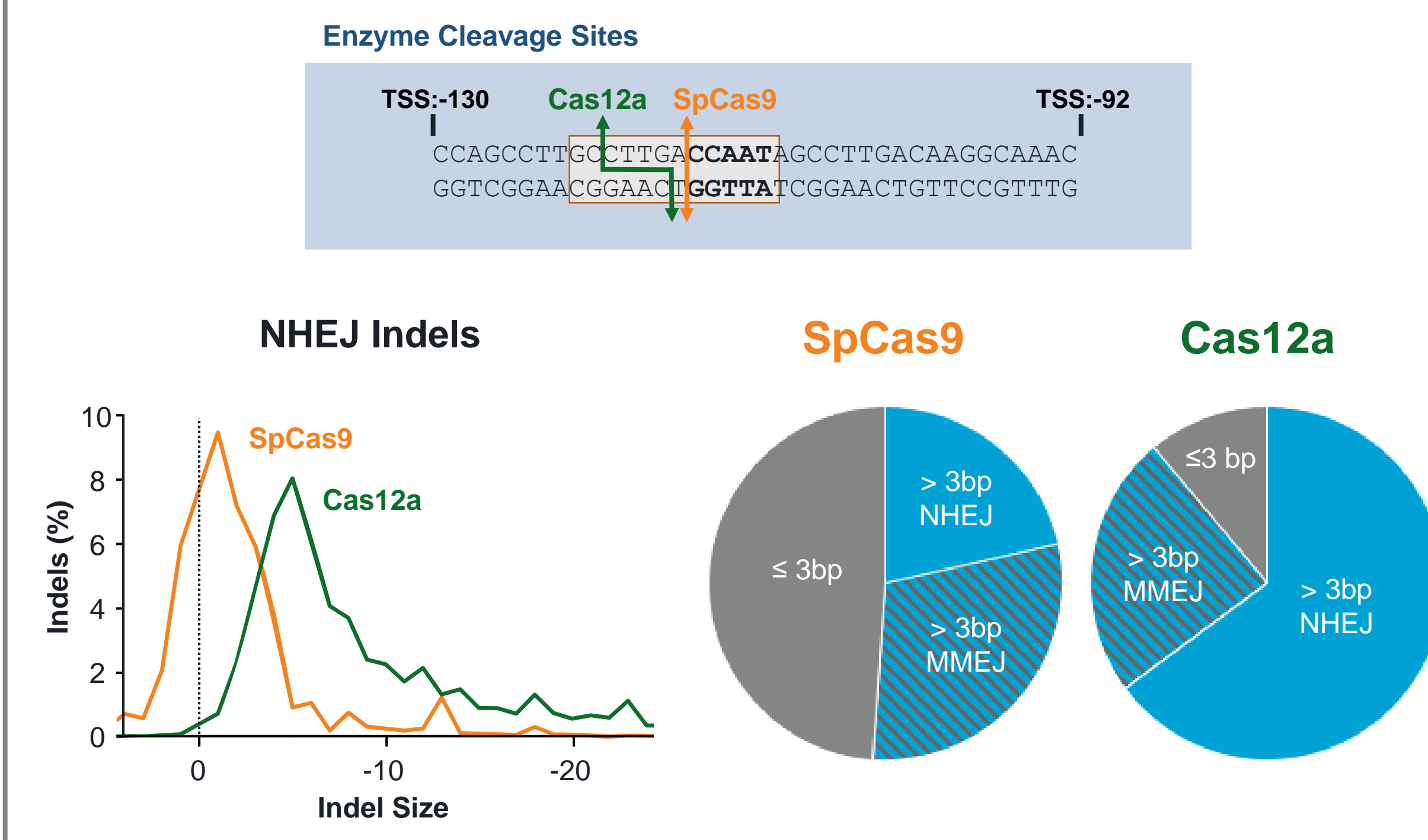
## EDIT-301 – 50% HbF *In Vivo*



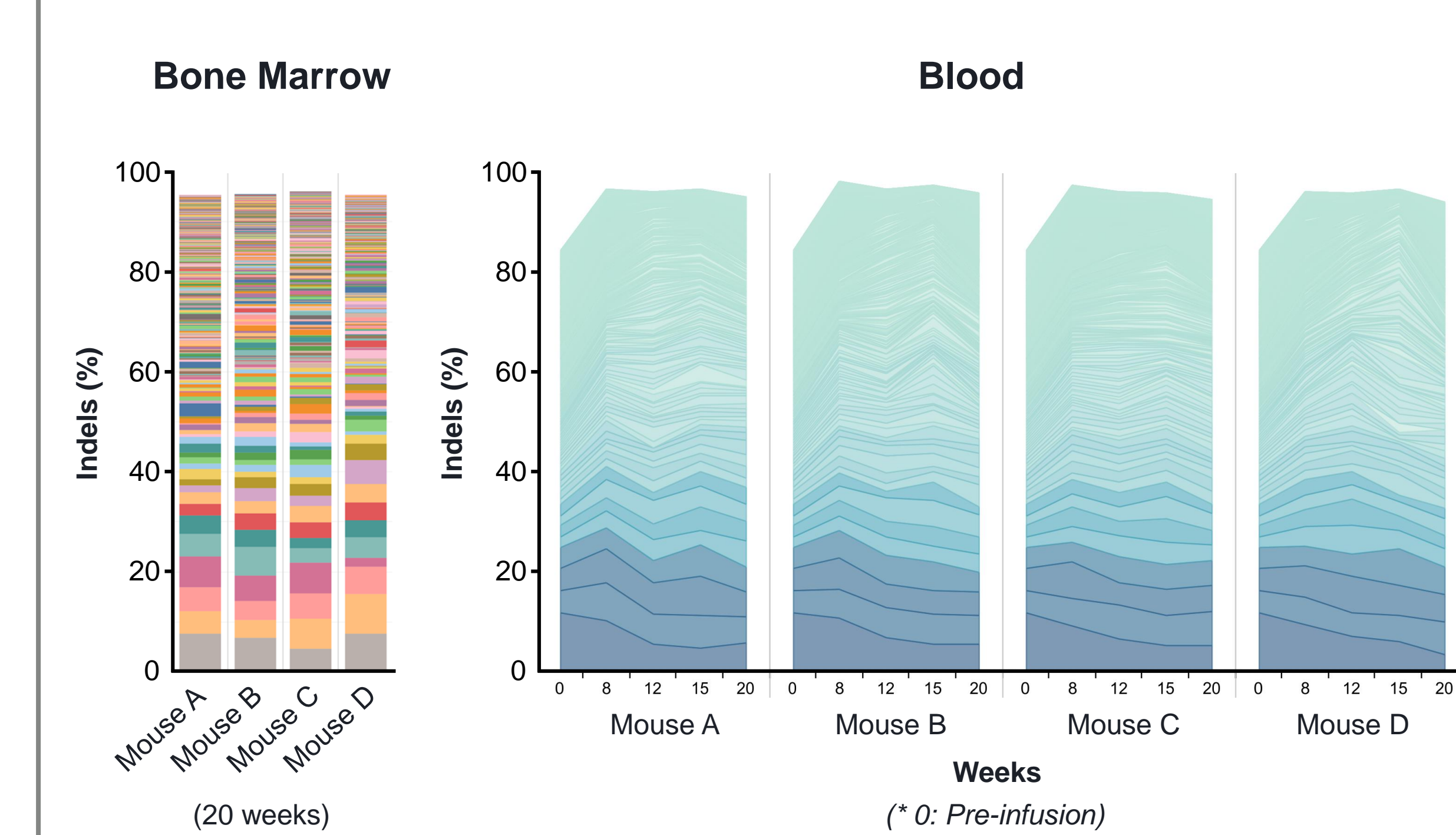
## Methods

- Edited cells were generated by transfection of healthy donor mobilized CD34+ cells with spCas9 or Cas12a ribonucleoproteins (RNPs)
- Targeted Next-Gen Seq (NGS) was conducted for on and off-target editing levels and indel profile analysis. Identification of candidate off-target sites was performed using *in silico* prediction, Digenome and Guide-seq.
- HbF-inducing indels were identified in clonal erythroid cultures, derived from RNP-electroporated CD34+ cells
- *In vivo* studies were performed in NBSGW mice or NSG mice infused with mock or edited CD34+ cells.
- Lineage reconstitution (flow cytometry), editing (NGS), and HbF expression (HPLC and flow cytometry) analyses were conducted 16-20 weeks post engraftment.

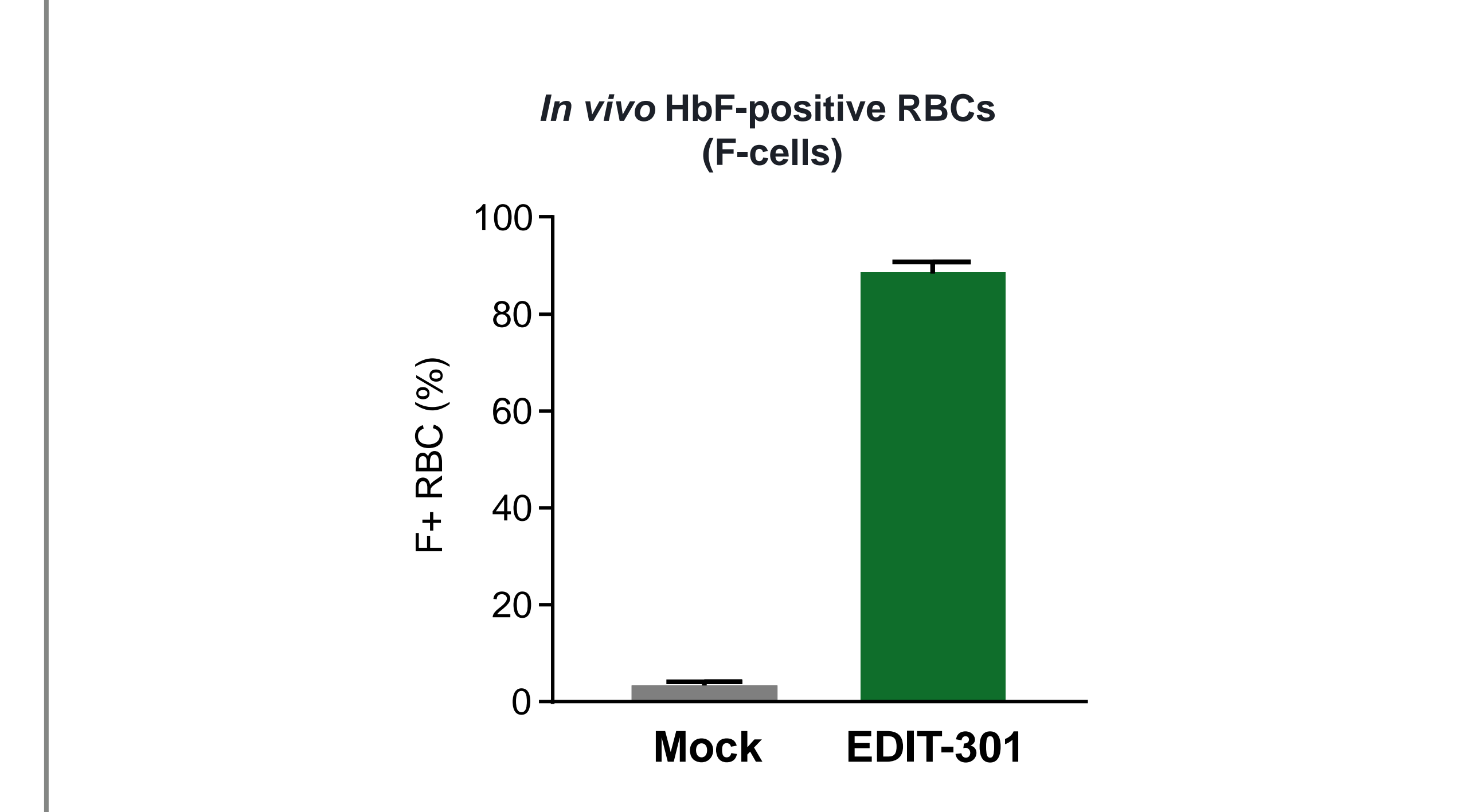
## Cas12a Editing Demonstrates a Better Editing Profile for Persistent and High HbF Expression



## EDIT-301 – High Polyclonality *In Vivo*



## EDIT-301 – Pancellular HbF *In Vivo*



## References

- <sup>1</sup>Akinsheye I, et al. (2011). Blood, 118, 19-27.  
<sup>2</sup>Ngo DA, et al. (2012). Br J Haematol, 156, 259-264.  
<sup>3</sup>Liu N, et al. (2018). Cell, 173, 430-442.  
<sup>4</sup>Strohkendl I et al. (2018). Molecular Cell, 71, 816–824.

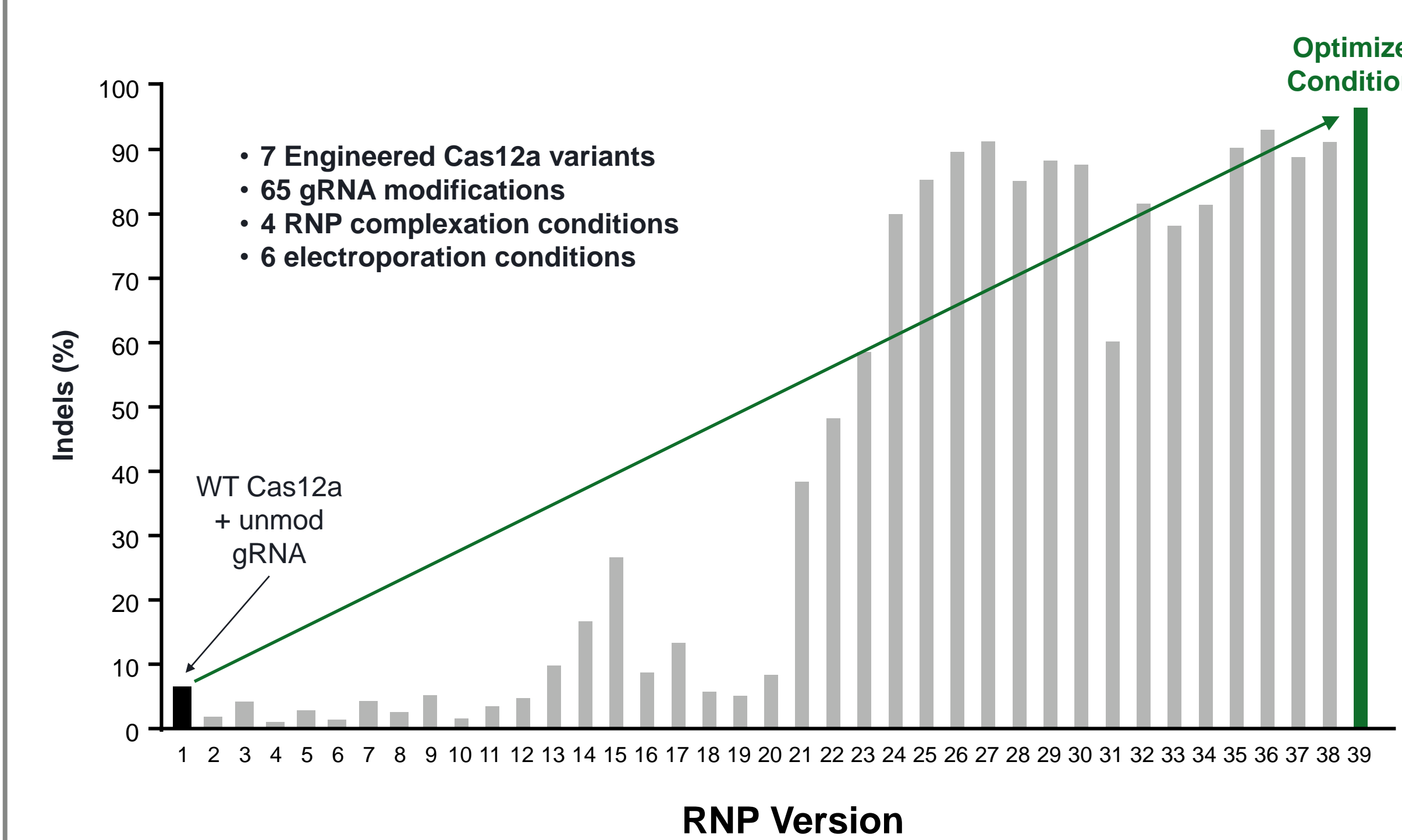
## Acknowledgements

We would like to thank Hayat Abdulkerim, James Bochiochio, Emily Brennan, Georgia Giannoukos, Gregory Gotta, Meltem Isik, Tusneem Janoudi, Mingli Li, Eugenio Marco, Tamara Monesmith, Tanushree Phadke, Jamaica Siwak, Frederick Ta, Diana Tabbaa and Kate Zhang for their scientific contributions.

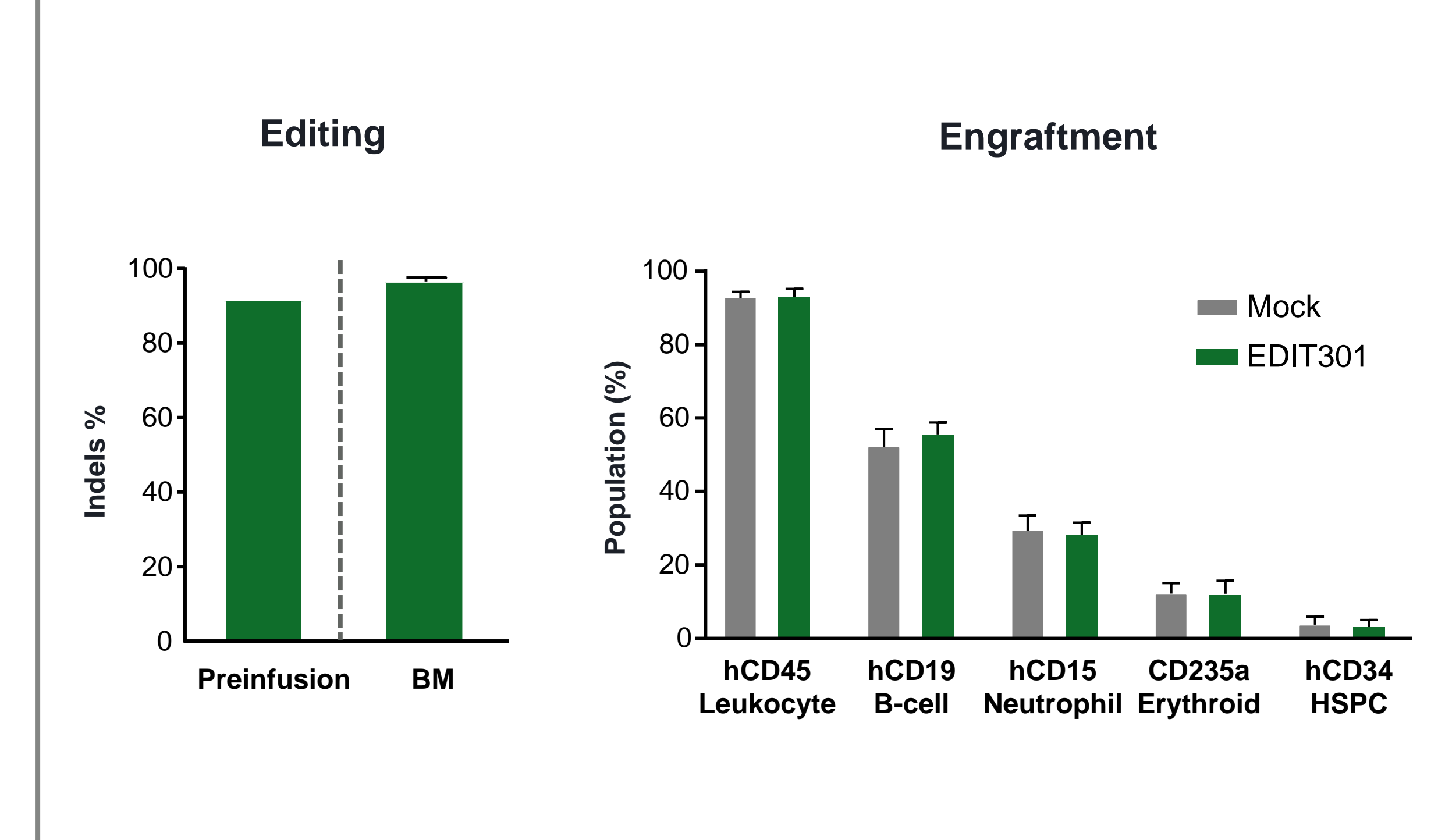
## Disclosures

All authors were Editas employees and shareholders when the research was conducted.

## Optimization Enabled Editing Levels >90%



## EDIT-301 – Efficient Editing without Lineage Skewing *In Vivo*



## Conclusions

- Cas12a produced more long-term HbF-inducing indels than SpCas9 at the HBG distal CCAAT box region.
- Greater than 90% indels were achieved after optimization of electroporation conditions and selection of best performing Cas12a variant and gRNA modifications
- EDIT-301 had no detectable off-target editing and contained highly-edited long-term HSCs (>90% indels) that engrafted mice with high polyclonality and no lineage skewing.
- 50% HbF levels were observed *in vivo* with pancellular distribution.

IND-enabling activities are ongoing for EDIT-301: an experimental autologous cell therapy comprising Cas12a-RNP modified mPB-CD34+ cells for the potential treatment of SCD.