



Zinc finger fusions and synthetic DNA donor engineering improve the performance of reprogrammed modular integrases at the TRAC locus

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Sangamo Therapeutics, Inc.

ASGCT, May 11-16, 2026

— Disclosure

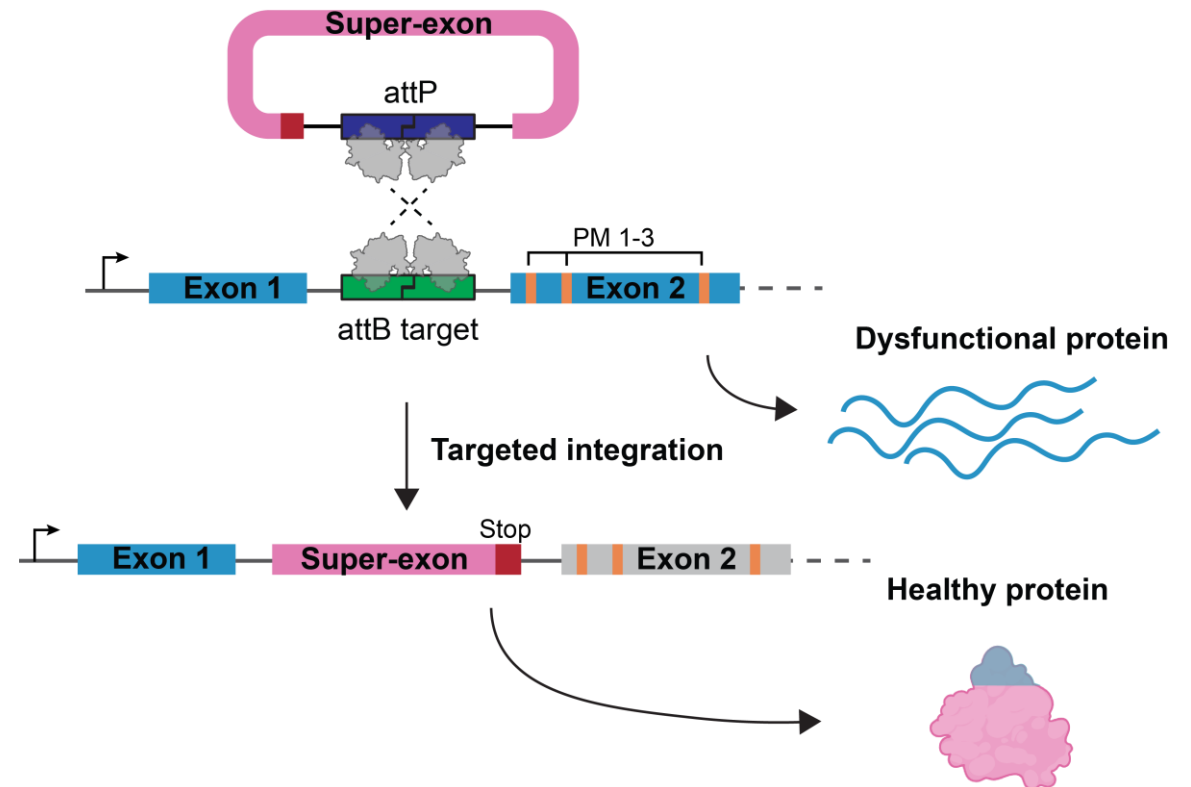
I am a full-time employee of Sangamo Therapeutics

Talk Overview

- **We developed a platform to retarget Large Serine Integrases (LSIs) to therapeutically-relevant sites**
- **We used this platform to retarget Bxb I, an LSI, to the TRAC locus**
- **We achieved ~29% TRAC integration and up to 44% GFP expression in primary human T cells**

Fully programmable gene integration: the ideal genomic medicine approach

- Targeted integration promises a single therapeutic approach to many Patient population Mutations (PM)
- LSI is a strong therapeutic candidate for targeted integration
 - Large payload delivery
 - Irreversible integration: Integrates via attachment sites (**attP** → **attB**)
 - DNA break-free
 - Cell type independence: Does not depend on DNA repair machinery
- Reprogramming existing LSIs to target therapeutically-relevant sites with high precision remains a challenge in the field



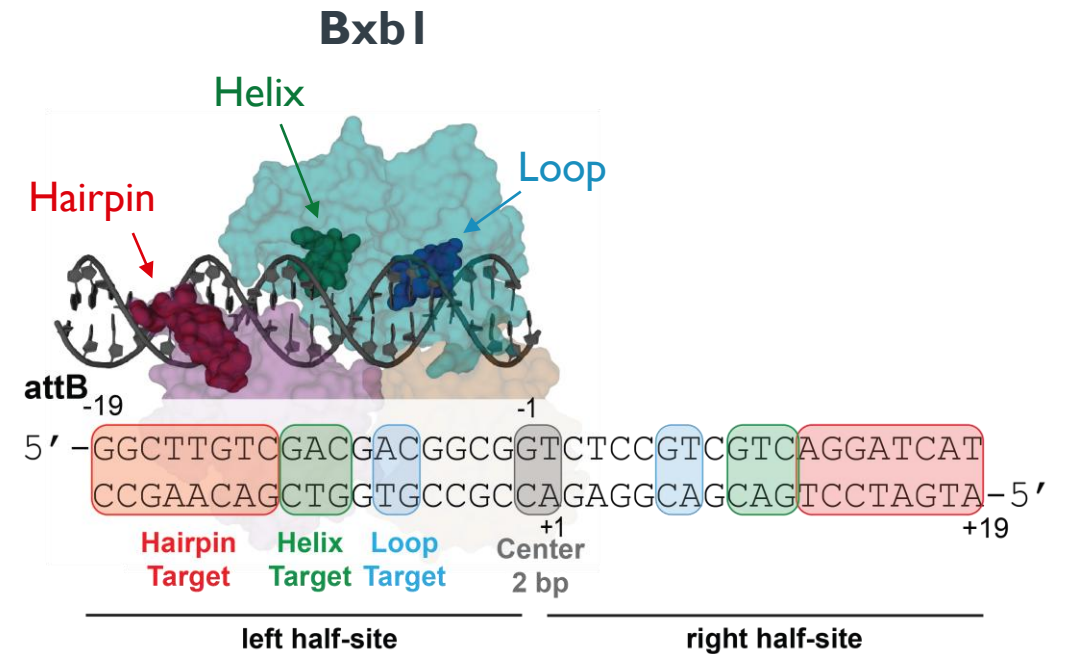
Bxb1 is a Large Serine Integrase with promising therapeutic potential

High activity in human cells, and *in vivo* mouse and NHP studies

High fidelity of cargo integrity after integration via cut and paste mechanism

Low off-target integration levels in human genome

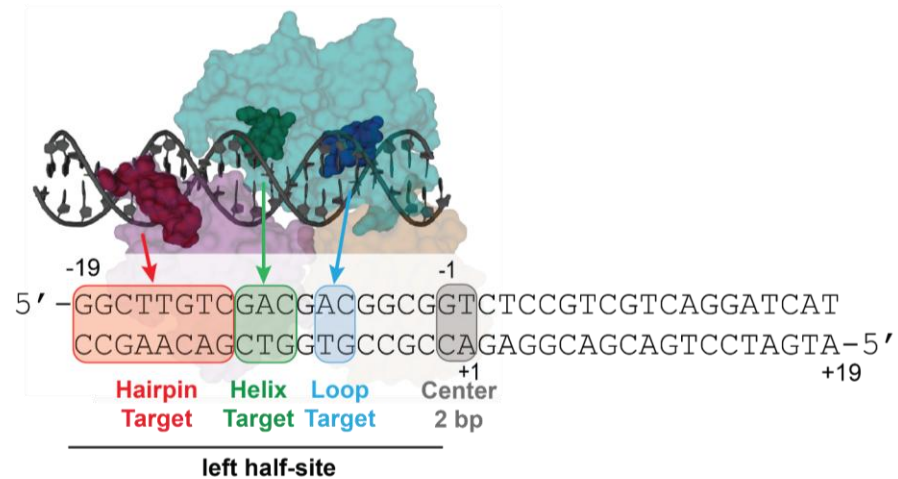
- Structural analysis and scanning mutagenesis studies predicted likely DNA-binding domains and locations of their target sites within attB
- DNA binding by each domain hypothesized to occur in a modular fashion, guiding our approach to retargeting



Our Modular Integrase (MINT™) platform retargeting strategy

1. Bacterial selections to generate each DNA-binding domain

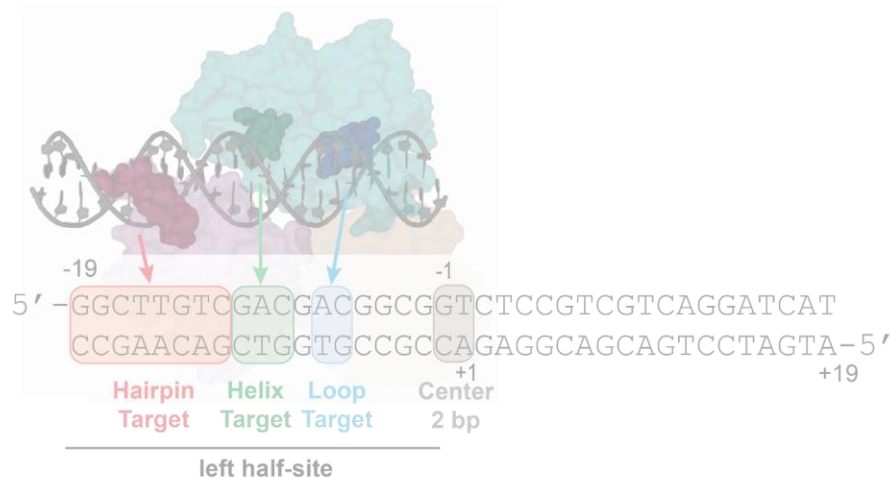
- Built archive of domains for ease of retargeting



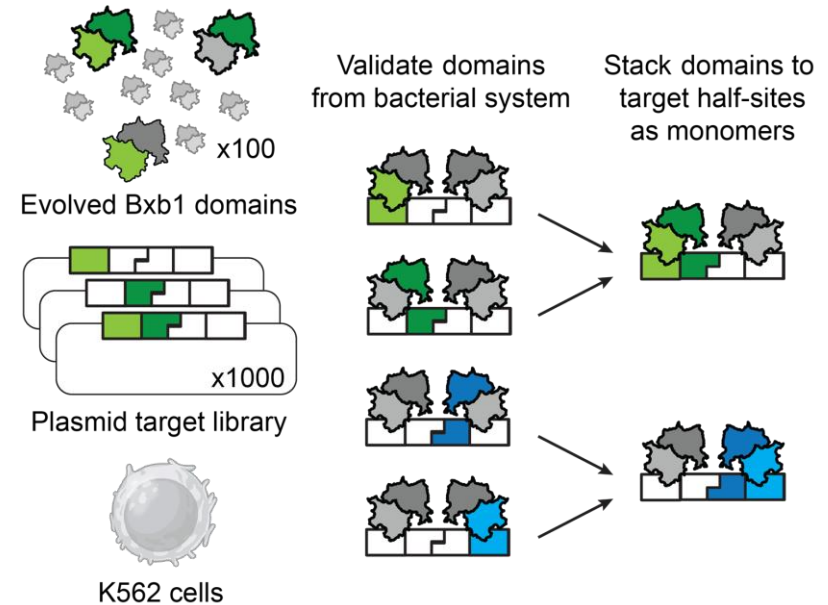
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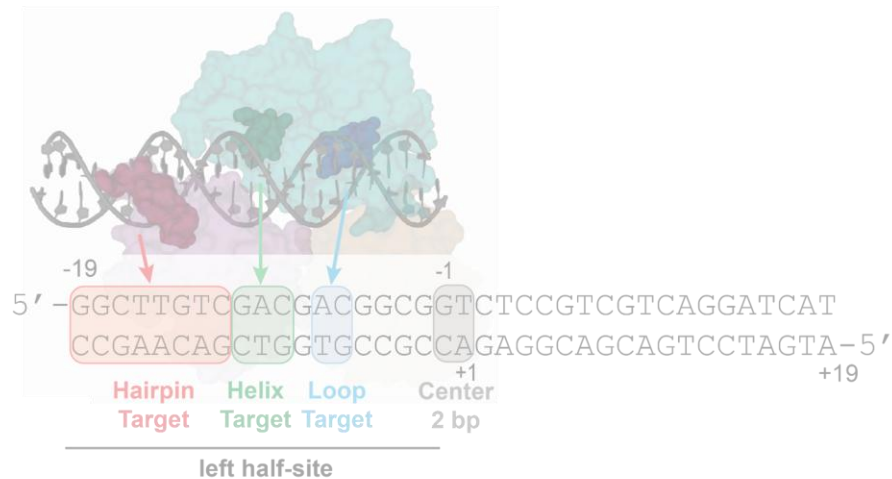
2. Stack domains as monomers to target attB half-sites



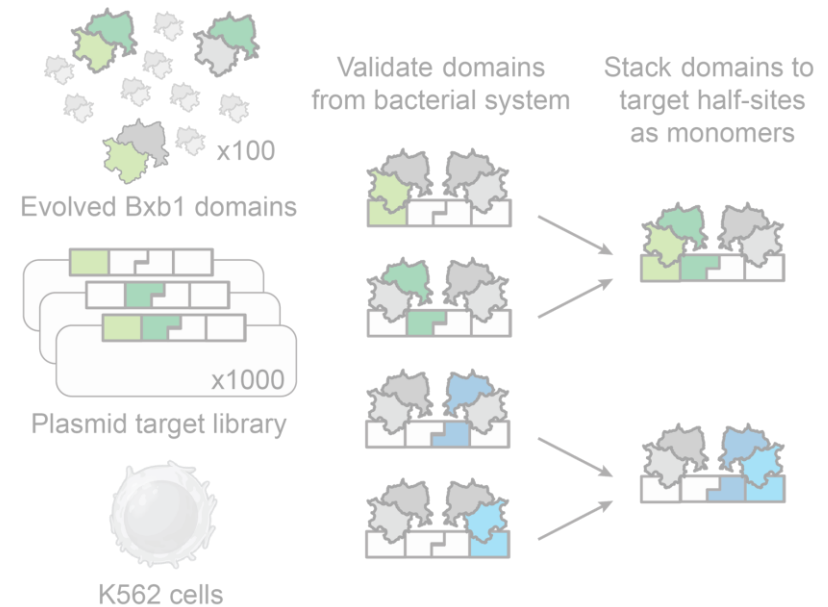
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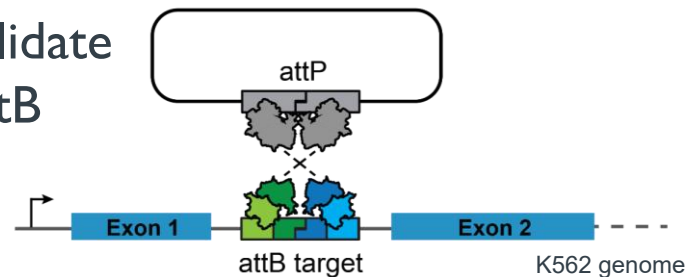
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2. Stack domains as monomers to target attB half-sites

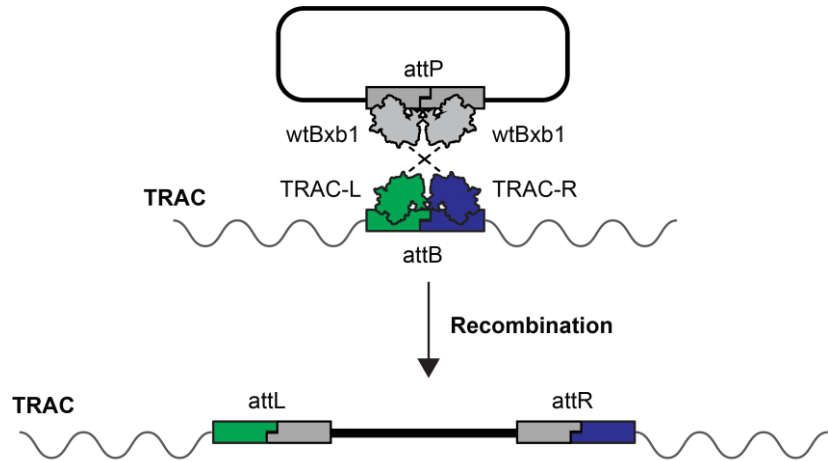


3. Pair monomers and validate activity at full genomic attB target site



We fully retargeted Bxb1 to the human TRAC locus

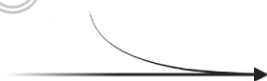
- Domains stacked to make two Bxb1 monomers targeting the left and right TRAC attB half-sites
- Genomic integration assayed in K562 cells



- Plasmid DNA donor
- TRAC-L plasmid DNA
- TRAC-R plasmid DNA
- wtBxb1 plasmid DNA

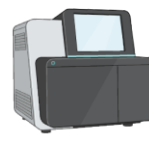


K562 cells



Nucleofection

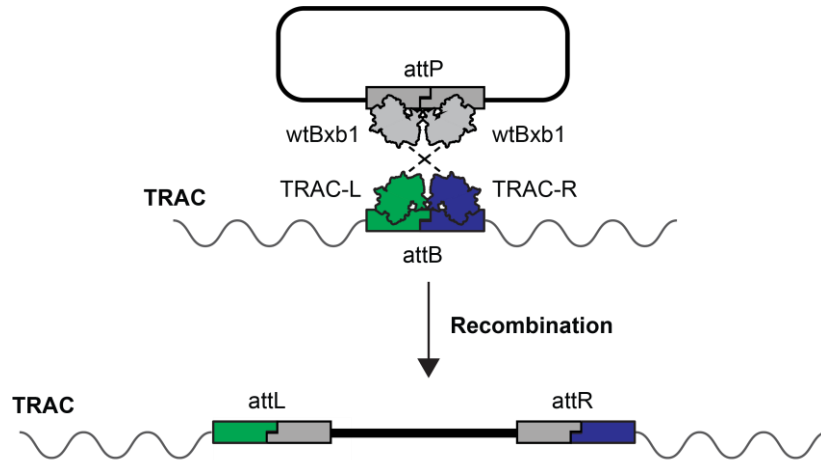
3 days



NGS

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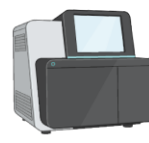


K562 cells

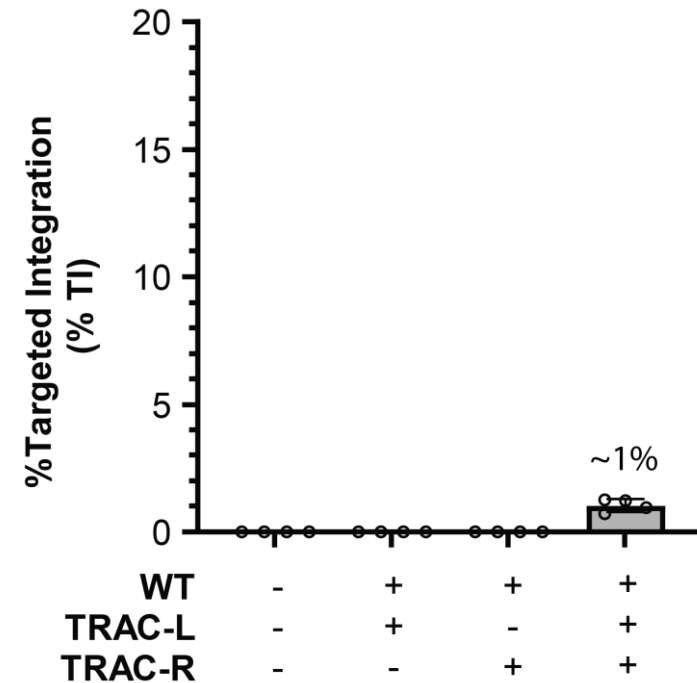


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3 days



NGS

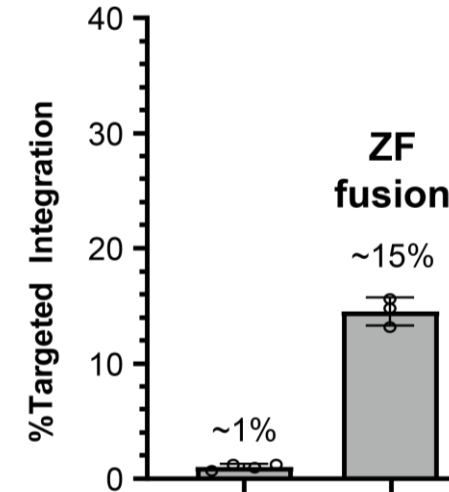
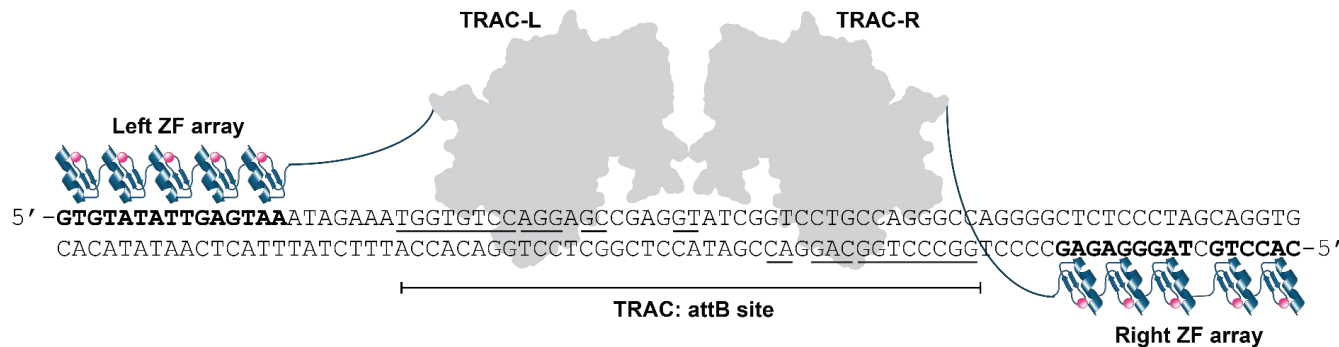


We achieved full re-targeting of Bxb1 to TRAC, achieving 1% TI

Next step: increase activity further

ZF fusions give a 15-fold increase to the on-target activity of MINT reagents

- Zinc Finger (ZF) arrays increase binding affinity by localizing MINT reagents to their intended genomic target site
- Screened a panel of ZF arrays and linkers with TRAC reagents

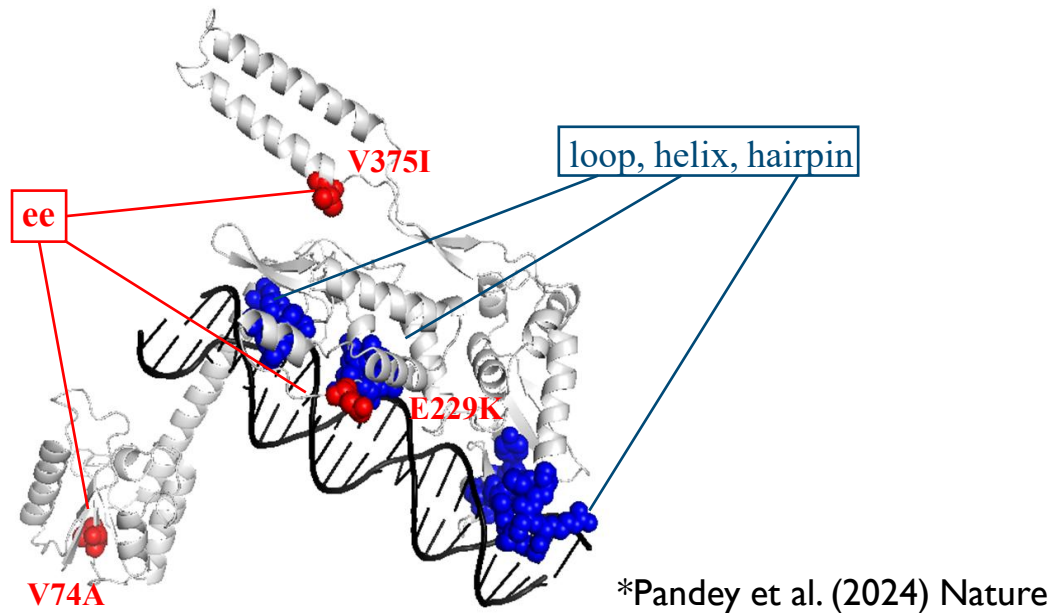


WT	+	+
TRAC-L	+	-
TRAC-R	+	-
TRAC-L-ZF	-	+
TRAC-R-ZF	-	+

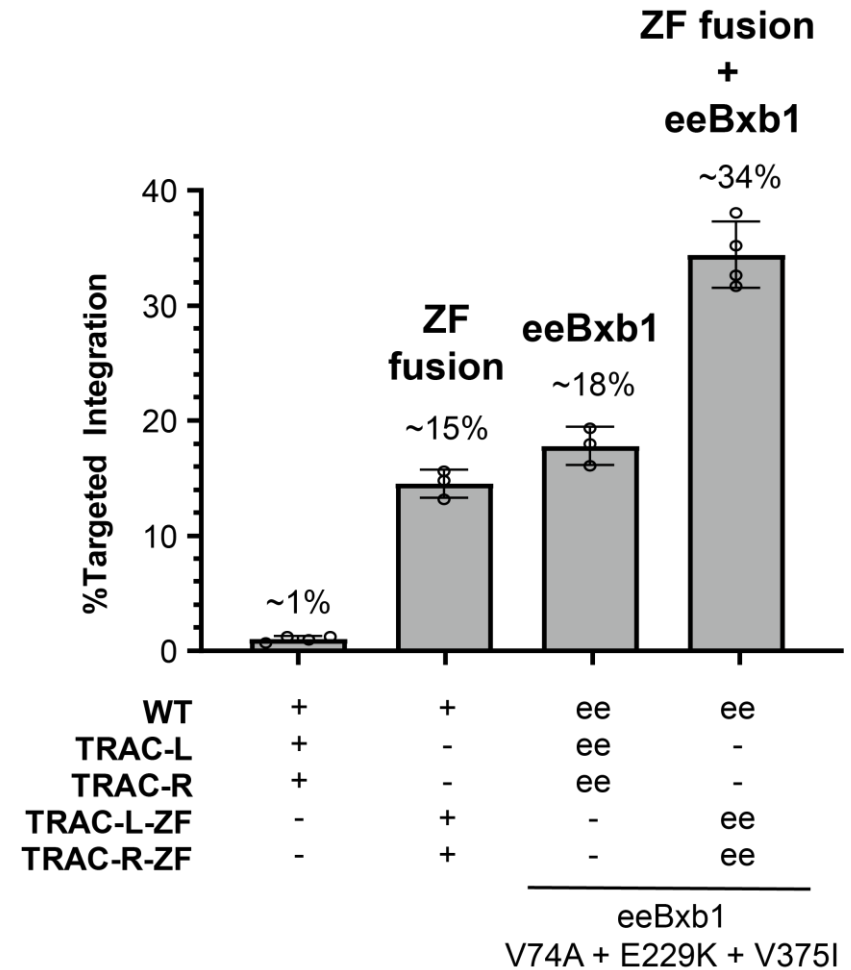
Best set of ZF fusion and linker combinations achieved
15% TI at the TRAC locus in K562 cells

Combining ZF fusions and activity-increasing mutations yield therapeutically-relevant activity with TRAC reagents

- eeBxb1 is an activity-increasing Bxb1 variant developed by David Liu's team at Harvard*

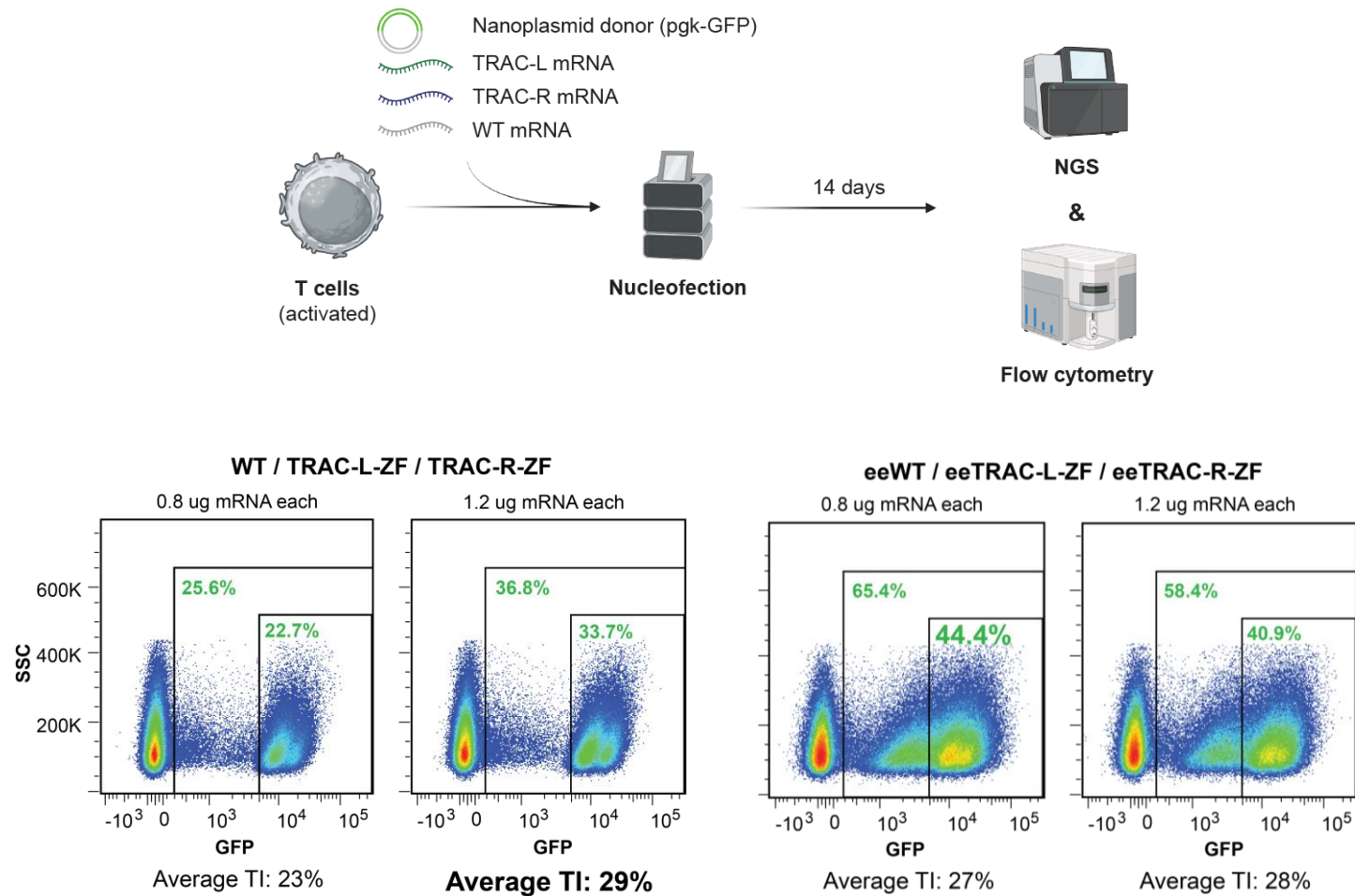


- Combining eeBxb1 with our TRAC reagents drove comparable improvements as ZF fusions



Combining ZF fusions with activity-increasing mutations achieved ~34% TI at the TRAC in K562 cells

We successfully targeted the TRAC locus in primary human T cells

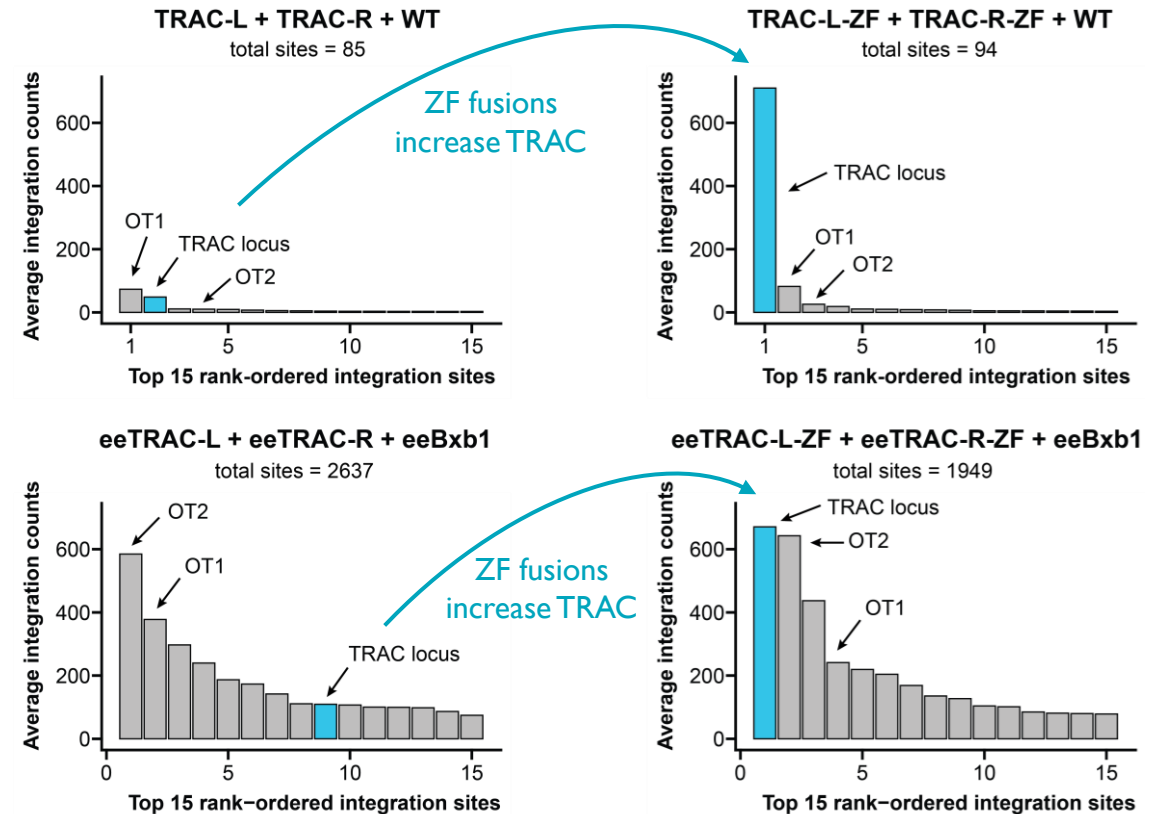


Achieved ~29% TI at the TRAC locus and up to 44% GFP expression in primary human T cells using ZF fusions

ZF fusions improve MINT reagent specificity and on-target activity

Unbiased genome-wide assay nominated off-targets

- Activity-increasing mutations reduced specificity
- ZF-fusions selectively increased the on-target signal
- Validated top two off-target sites in K562 and T cells
 - Relative TI followed similar trends as nomination assay
- No translocations observed across samples
 - Did observe a weak, local genomic inversion only with activity-increasing mutations



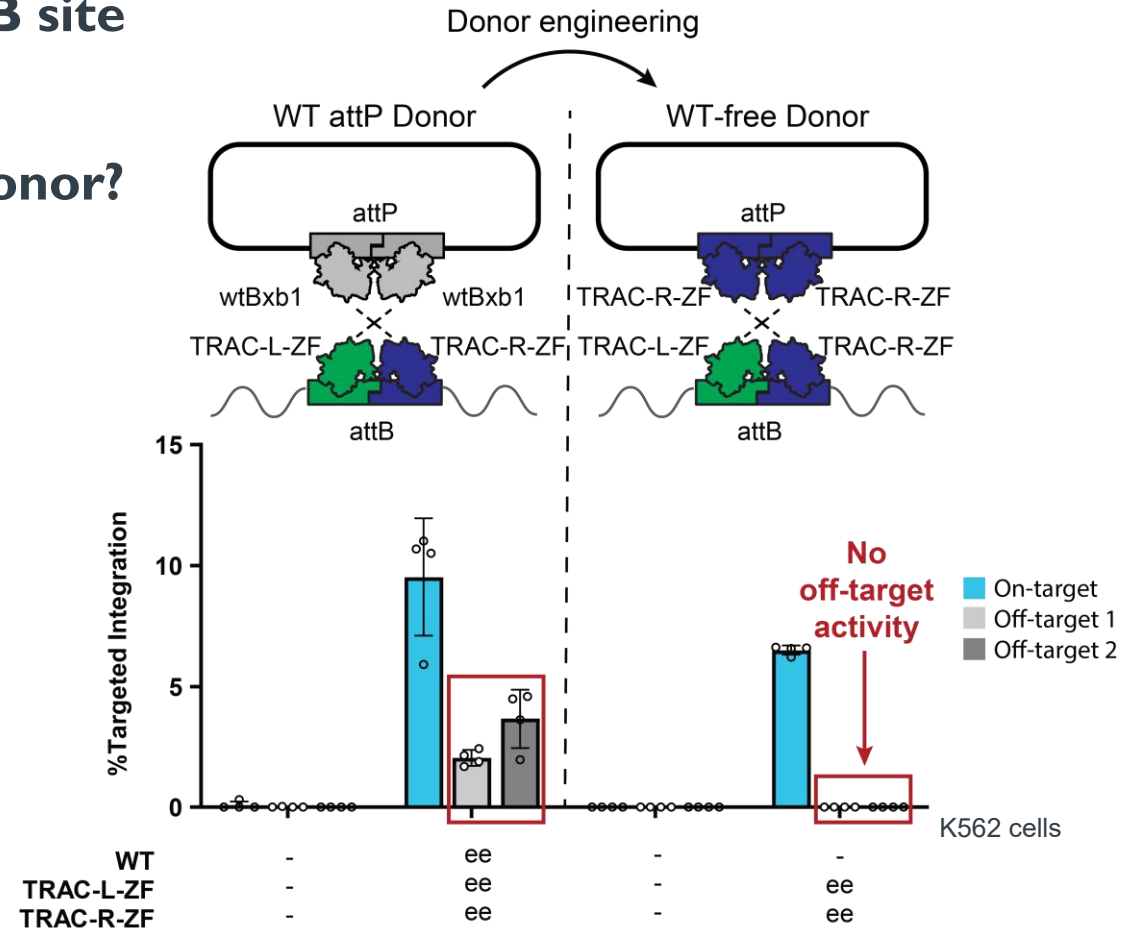
All assays performed in K562 cells

ZF-fused MINT reagents indicate a superior specificity profile

WT-free donor architecture further improves MINT reagent specificity

- We retargeted Bxb1 to the genomic TRAC attB site
- Can we engineer a TRAC-like attP site in the donor?
 - Only requires retargeted MINT reagents for activity
 - Removes need for wild-type Bxb1
 - Reduces off-targets

Donor engineering removed off-targets 1 and 2 for the most active TRAC reagents







Summary

- **MINT platform enables retargeting BxbI to therapeutically-relevant sites**
 - 34% TRAC TI and 29% AAVSI TI in K562 cells
 - Used archive of pre-characterized BxbI DNA-binding domains to target two additional sites
- **Achieved high activity in T cells**
 - 29% integration at TRAC locus
 - 44% GFP-expressing cells
- **ZF fusions improve activity & specificity**
 - WT-free donor engineering further increases specificity

Accepted at **Nature Biotech**

Full preprint of work presented here:

Reprogrammed Serine Integrases Enable Precise Integration of Synthetic DNA

Friedrich Fauser, Sebastian Arangundy-Franklin, Jessica E Davis, Lifeng Liu, Nicola J Schmidt, Luis Rodriguez,  Danny F Xia, Nga Nguyen,  Nicholas A Scarlott, Rakshaa Mureli, Irene Tan, Yuanyue Zhou, Lynn N Truong, Sarah J Hinkley, Bhakti N Kadam, Stephen Lam, Bryan Bourgeois, Emily Tait, Mohammad Qasim, Vishvesha Vaidya, Adeline Chen, Andrew Nguyen, Yuri R. Bendaña, David A. Shivak, Patrick Li, Andreas Reik, David E Paschon,  Gregory D Davis,  Jeffrey C Miller

doi: <https://doi.org/10.1101/2024.05.09.593242>



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May 12
Tuesday

Single-cell characterization of ST-506, a BBB-penetrant epigenetic repressor of Prion protein expression, in the nonhuman primate brain

Victoria Chou, #1469
Poster presentation

ST-503 nonclinical safety studies evaluating zinc finger repressors regulating the expression of the Nav1.7 gene for treatment of small fiber neuropathy

Kathleen Meyer, #1309
Poster Presentation

- Neurology Epigenetic Regulation



Thank You

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