



Controlling Rearrangement Frequencies in the Context of Multigene Genome Editing

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Chief Technology Officer

Genome Engineering: From Mechanisms to
Therapies, February 23, 2019



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VM is an employee and shareholder of Editas Medicine, Inc.

Human Genome Editing Safety Concerns



- Off-target genome editing
 - Sensitivity of off-target screening methods
- Unintended biological consequences of on-target editing
 - Mutagenesis as a result of imprecise DNA repair following on-target editing
- Additional adverse effects due to genomic DNA cleavage at on- and off-target sites
 - Chromosomal translocations, inversions, etc.
- Immunogenicity
- Adverse impact of the delivery system
- In the case of *in vivo* genome editing, off-target cell/tissue editing

Anna Kwilas, Ph.D.

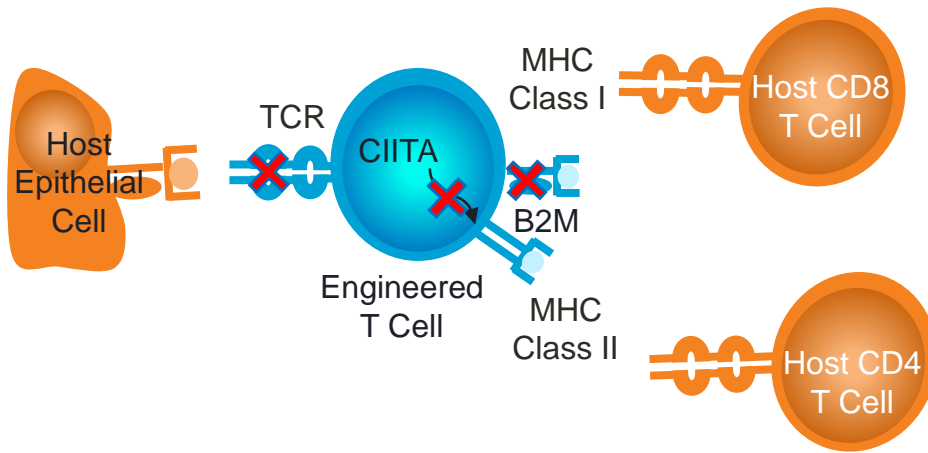
CMC Reviewer, Gene Therapy Branch
Division of Cellular and Gene Therapies
Office of Tissues and Advanced Therapies
Center for Biologics Evaluation and Research
Food and Drug Administration

NIST-FDA Genome Editing Workshop

April 23, 2018

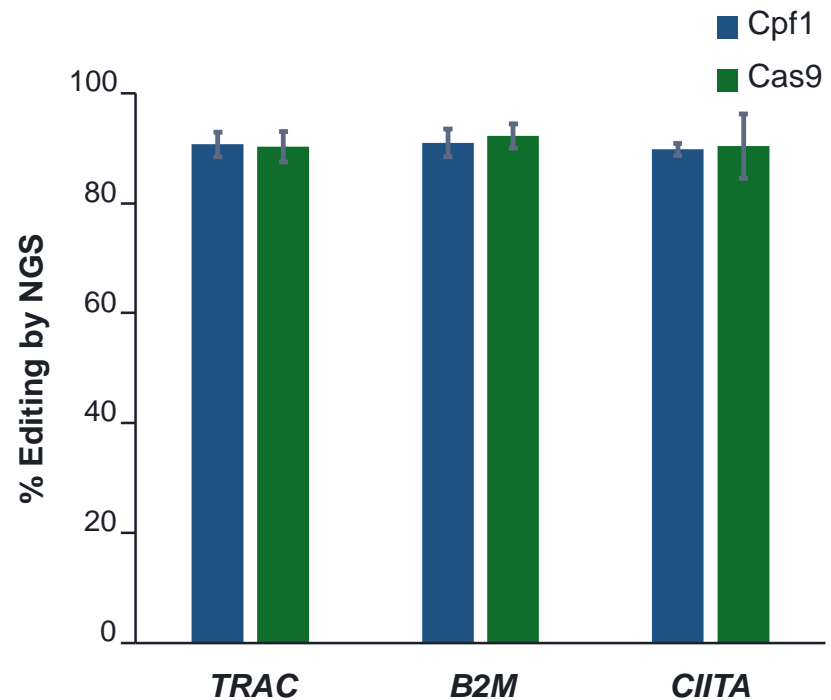


Allogeneic Therapies Will Require Multiple Edits



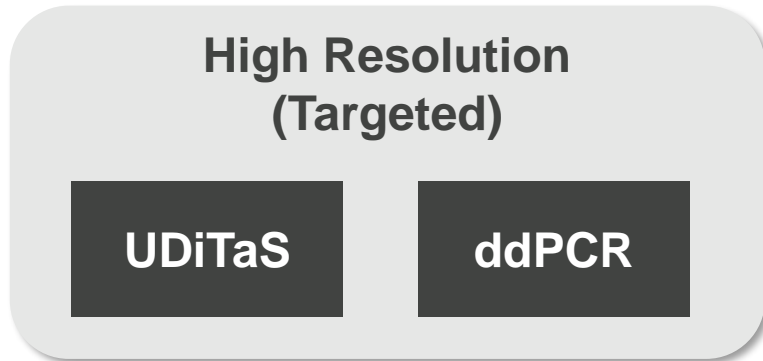
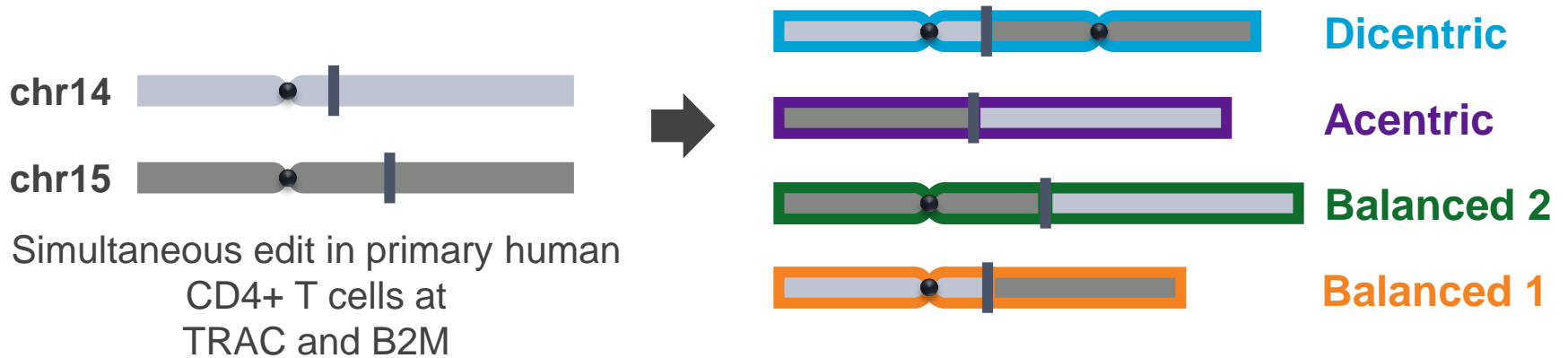
Multiple edits to eliminate the T cell receptor, Class I, and Class II presentation may be required

Highly Active Single Molecules For Cas9 and Cpf1



| Translocation Detection in the Context of Multiplexing

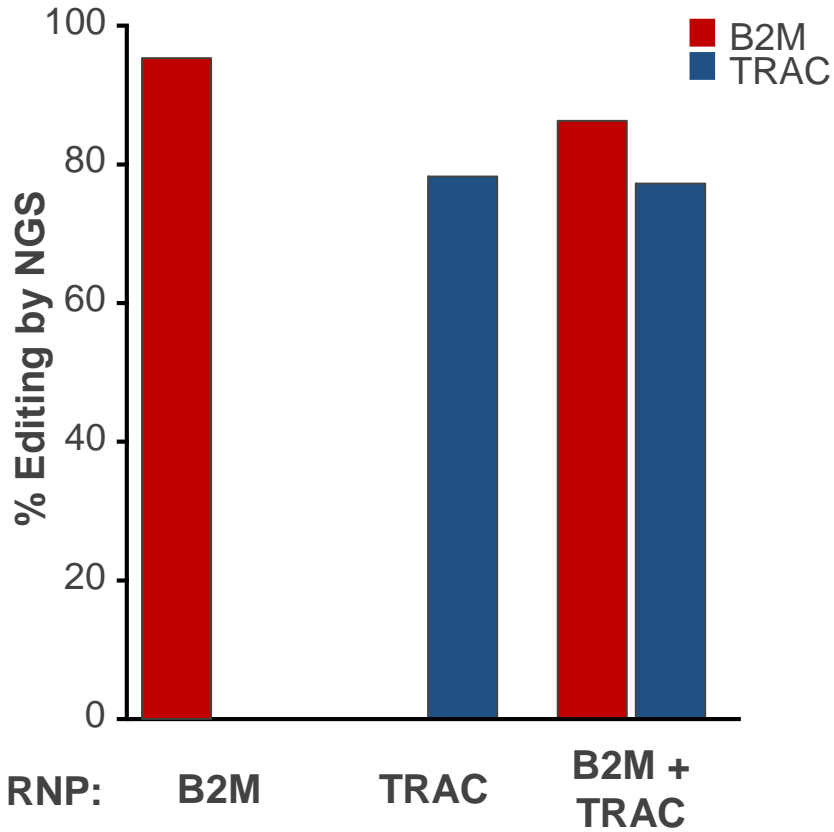
Develop detection methods for accurate quantitation of genome editing induced structural rearrangements.



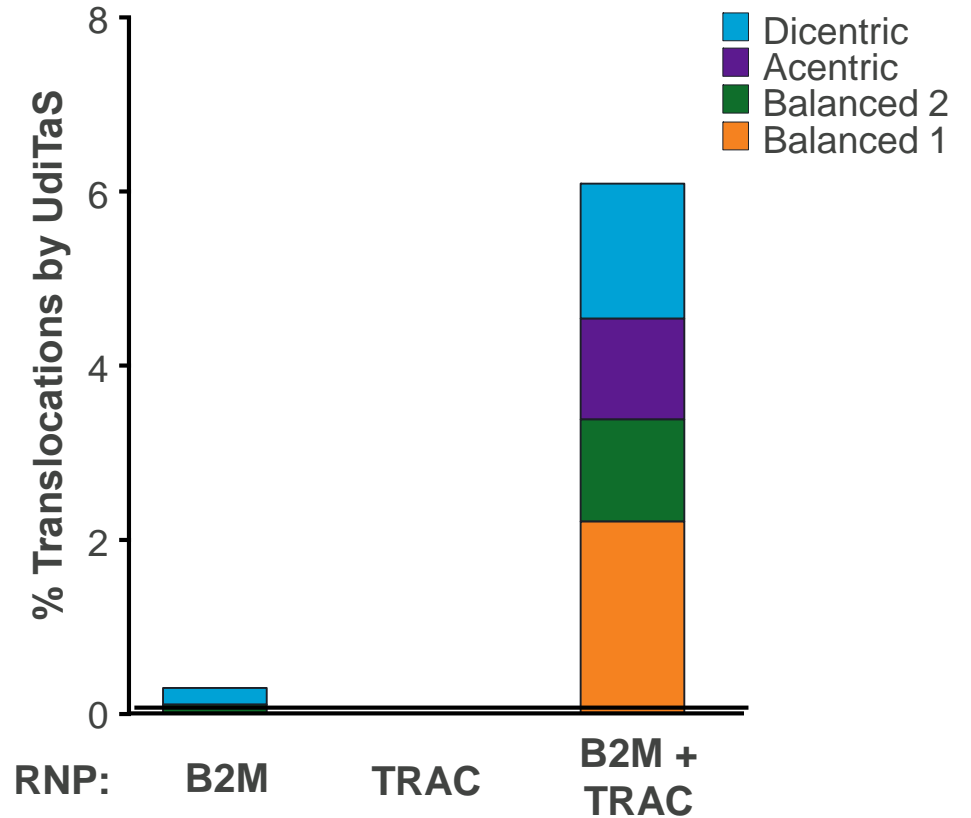


Multiplexing Leads to Translocation Formation

Editing



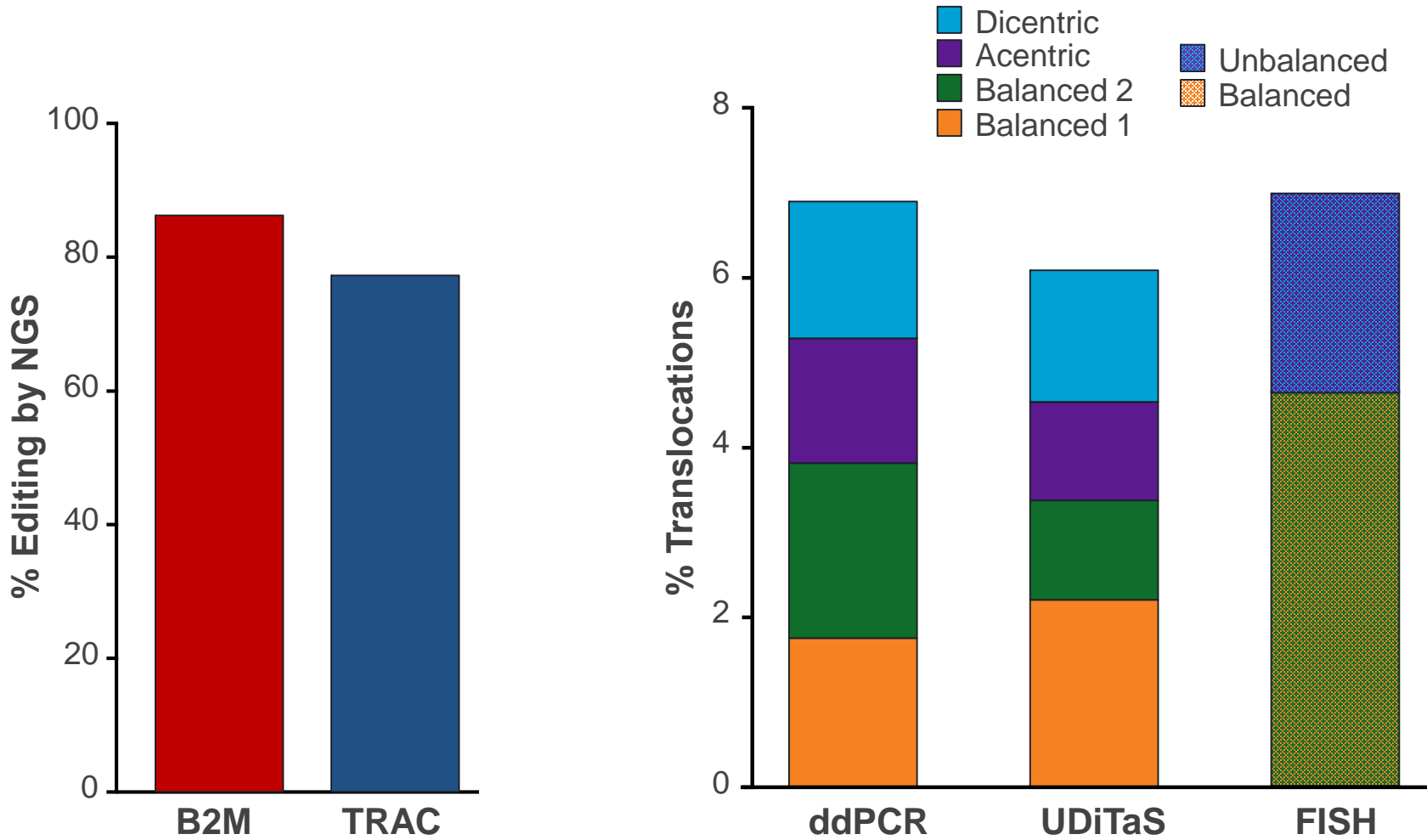
Translocations



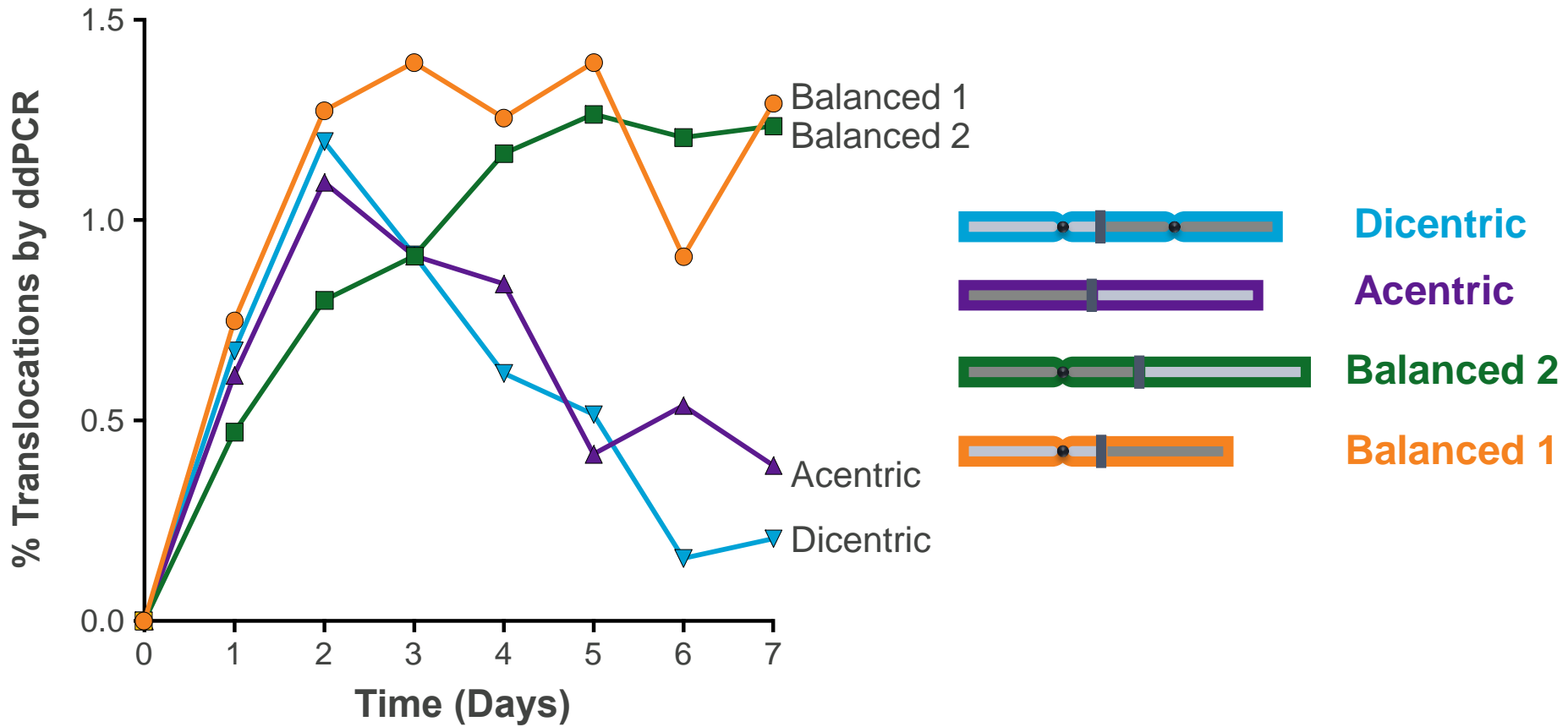
Day 3 Post-nucleofection, Primary human T cells, SpCas9



Targeted and Genome-wide Methods Yield Comparable Translocation Frequencies

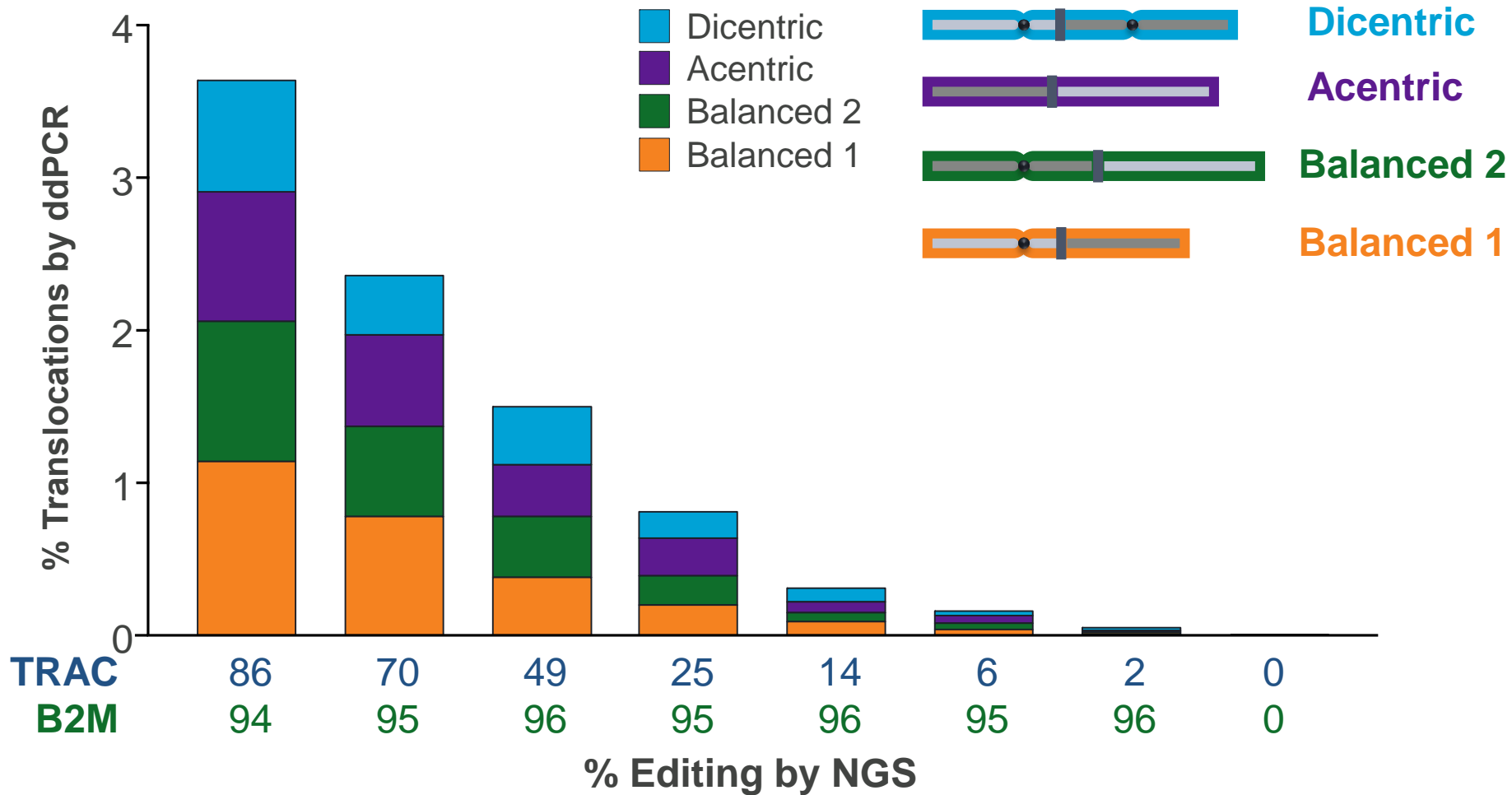


| Balanced Translocations Persist, Unbalanced Do Not



CD4+ Human Primary T Cells, B2M and TRAC, SpCas9

Translocation Rates are Dependent on Editing Rates



- Titrated down TRAC RNP while holding B2M constant

LLOD of ddPCR assay: 0.01%; CD4+ T cells, SpCas9

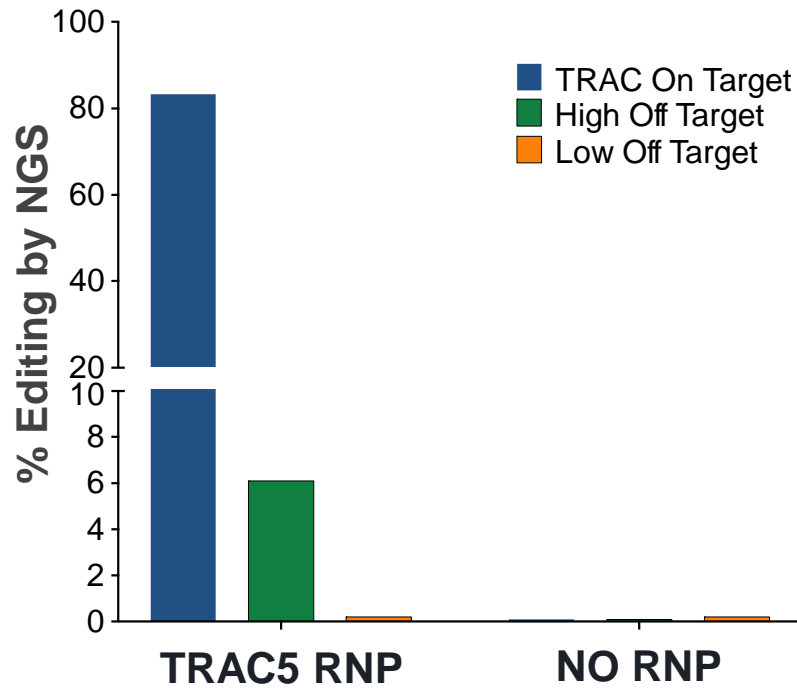


Translocations to Off-Targets for a Dirty Guide

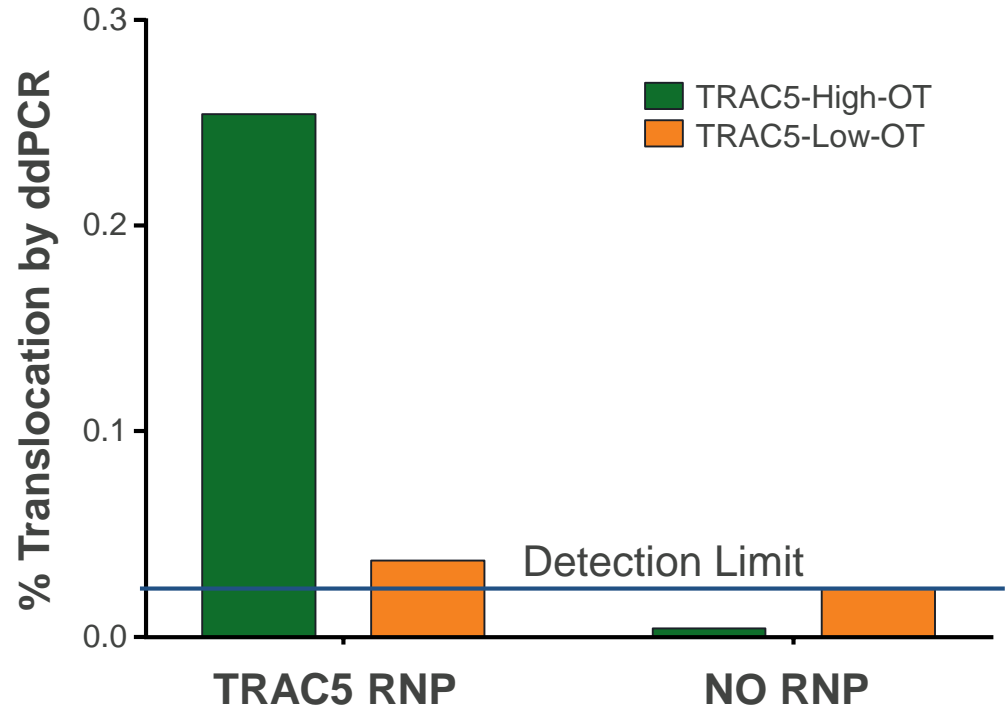
TRAC5 gRNA: Many off targets



Targeted Sequencing

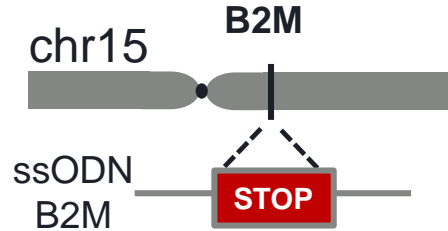


Translocation Detection

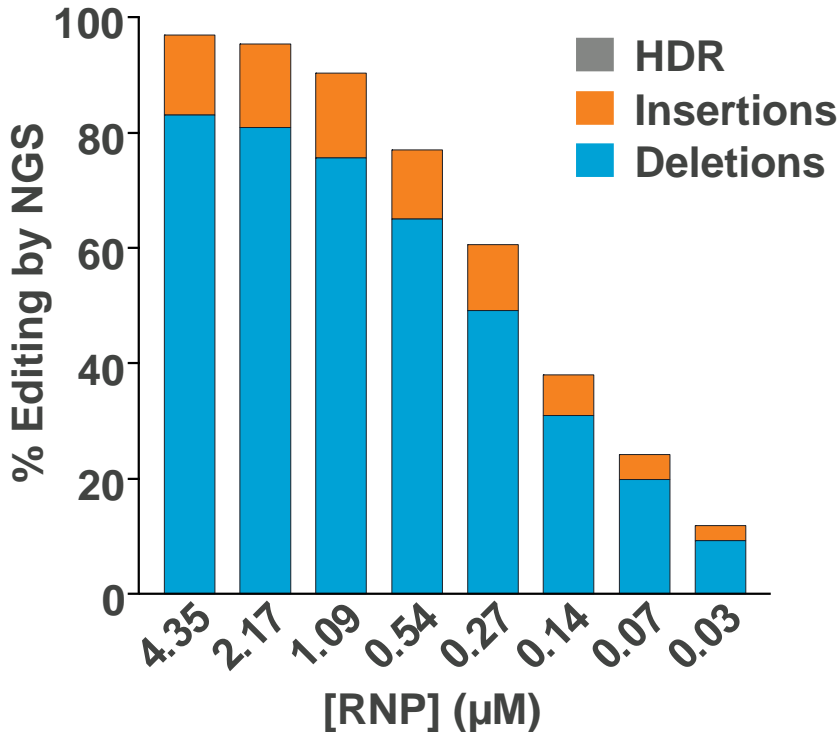


- Highly efficient, multiple edits are achievable but:
 - Translocations happen
 - The rate of translocation is proportional to:
 - # cuts
 - Editing efficiency
- Translocations are not dangerous per se. They become a concern when they drive a phenotype that is unexpected. They *may* reduce your efficacy and/or cellular viability
- Ideally, you want to identify them, track them, understand them, and (if possible) reduce them.
- How would you do that?
 - Modulate repair pathways?
 - Combine enzymes?

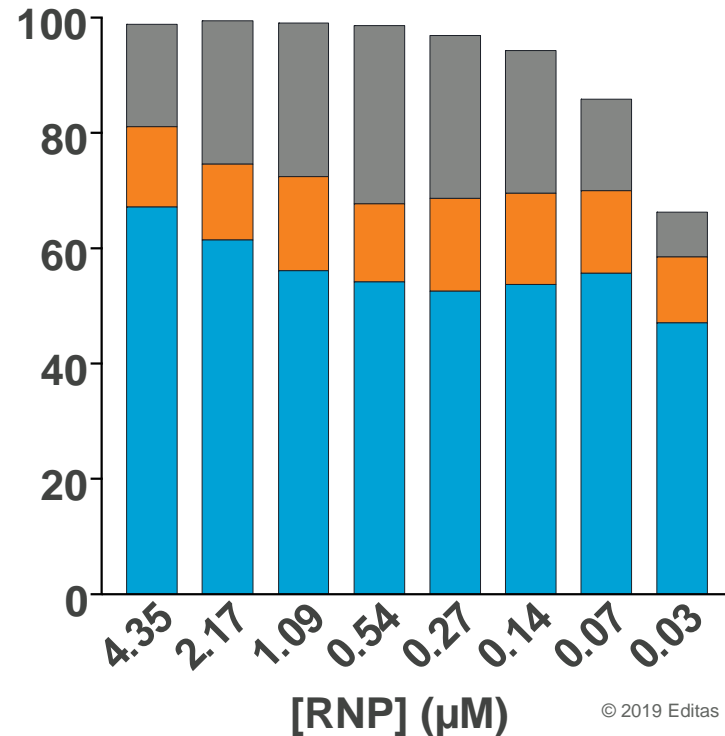
Modulating Repair Pathways: HDR with a DNA Oligo



No Oligo

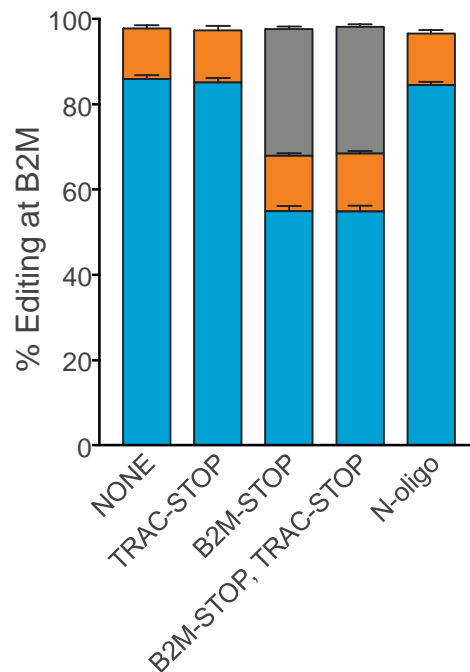
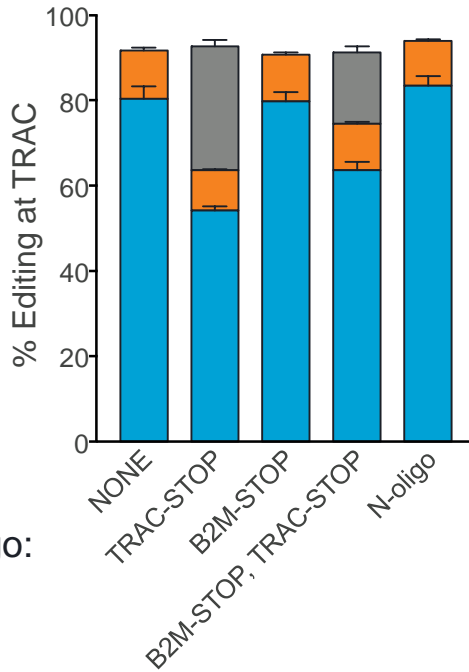
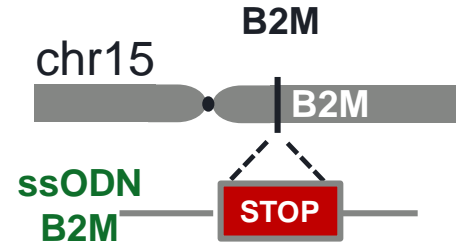
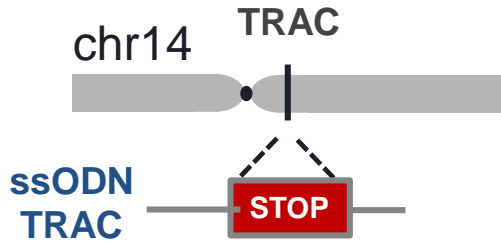


+ Donor Oligo

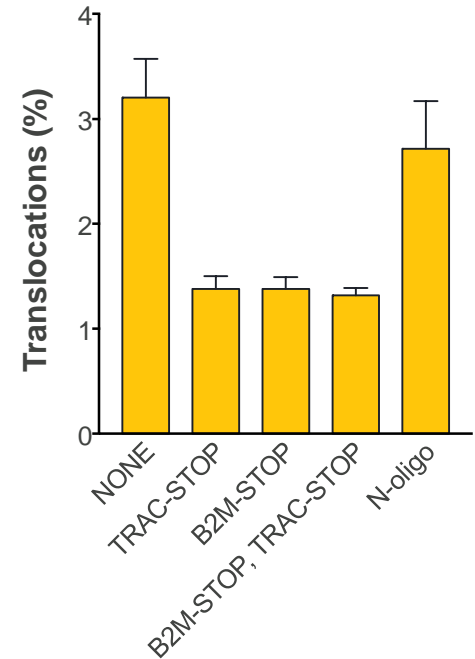




Single Stranded Homologous DNA Oligo Reduces Translocations



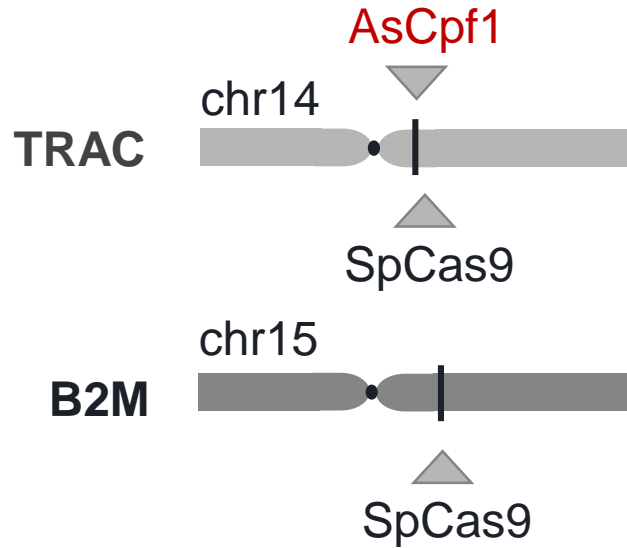
■ Stop
■ Insertions
■ Deletions



- ssODN homologous to either cut site results in repair pathway balance shift from c-NHEJ to HDR with 2-fold decrease in translocations
- ssODN administration enables 2-4 fold reduction of RNP dose

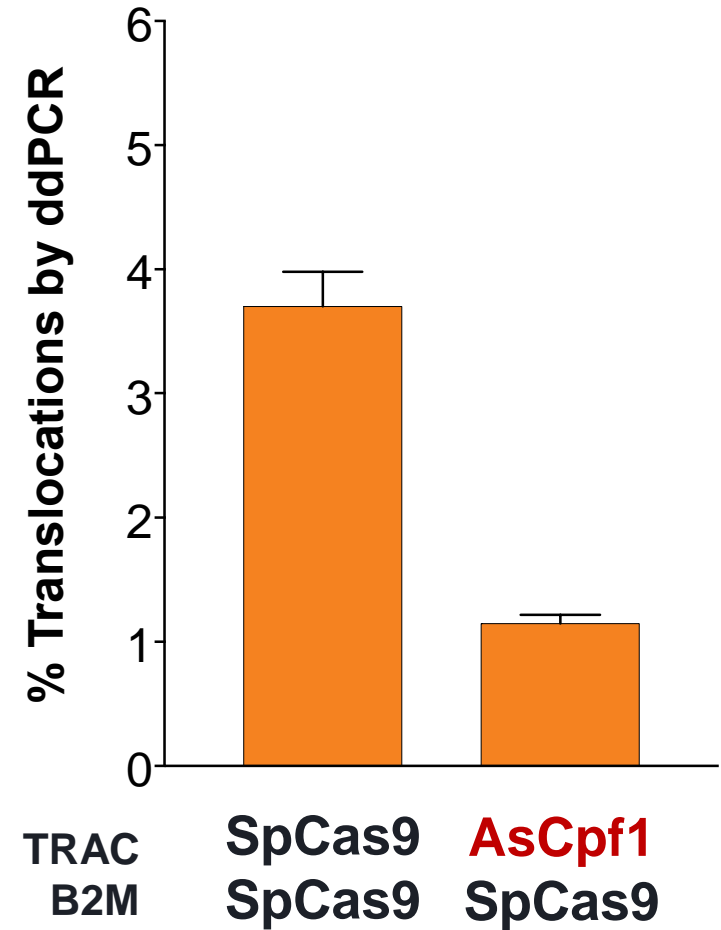


Using Cas9/Cpf1 (Cas12a) for Multiplexing Reduces Translocations



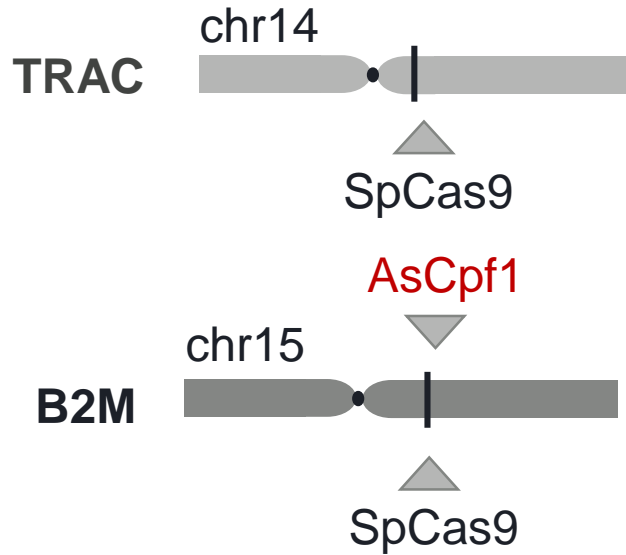
On Target Editing (% by NGS)

Locus	Enzyme		Percent
	B2M	TRAC	
TRAC	Cas9	Cas9	87
	Cas9	Cpf1	94
B2M	Cas9	Cas9	90
	Cas9	Cpf1	94



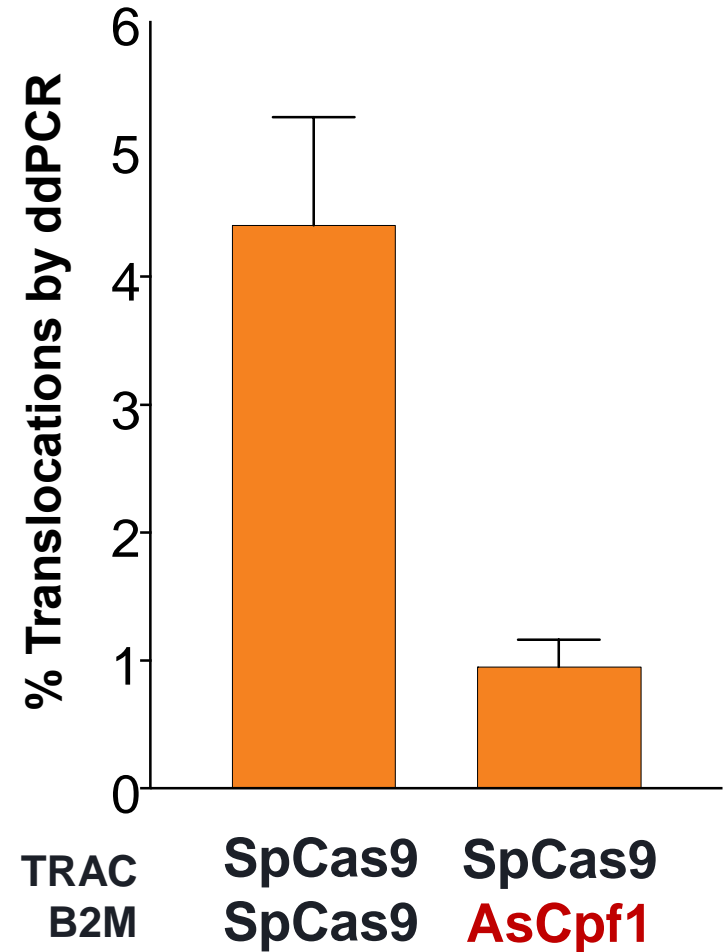


Using Cas9/Cpf1 (Cas12a) for Multiplexing Reduces Translocations



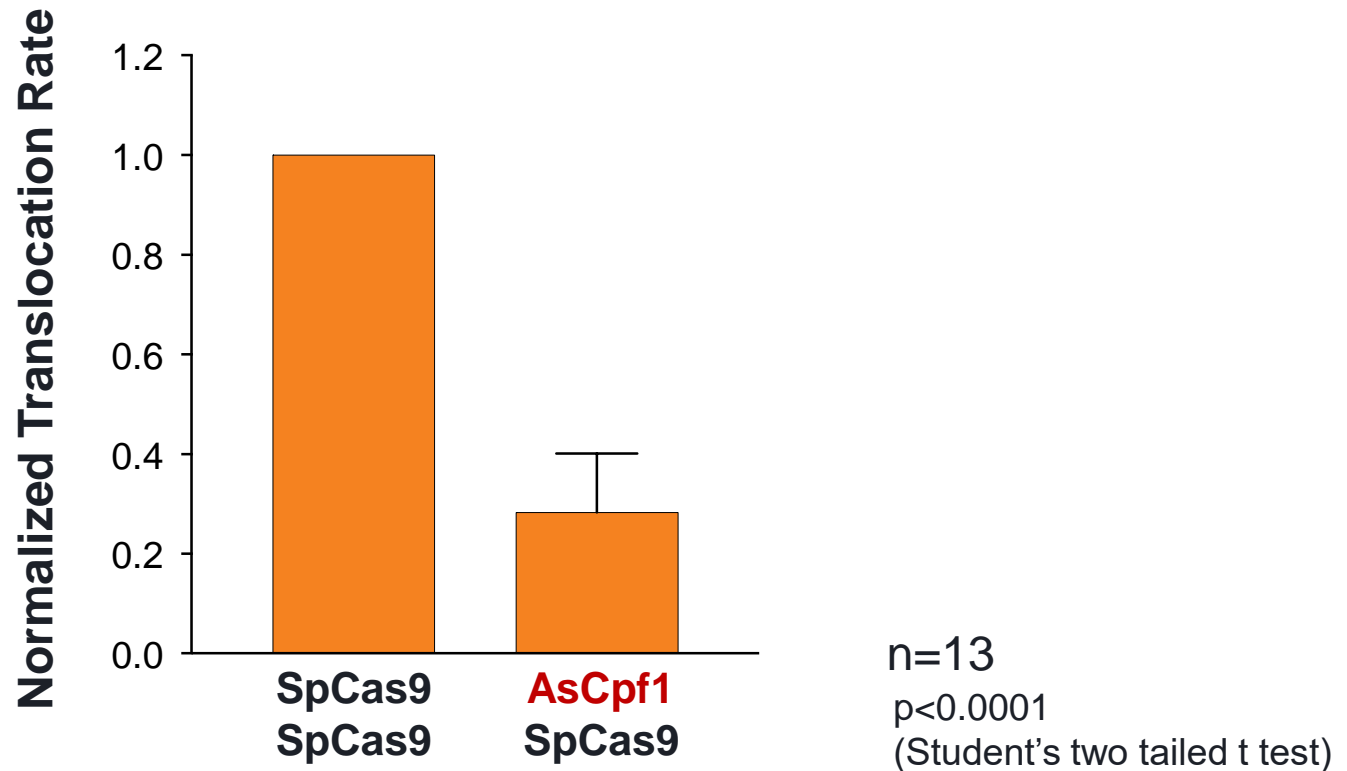
On Target Editing (% by NGS)

Locus	Enzyme		Percent
	B2M	TRAC	
TRAC	Cas9	Cas9	86
	Cpf1	Cas9	89
B2M	Cas9	Cas9	92
	Cpf1	Cas9	88





Using Cas9/Cpf1 (Cas12a) for Multiplexing Reduces Translocations



- Multiplexing with **SpCas9 (WT)/AsCpf1(WT)** significantly reduces translocation rates
- Reduction in translocation rates is independent of assay (UDiTaS/ddPCR), locus, and gRNA

- Highly efficient, multiple edits are achievable but:
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 - # cuts
 - Editing efficiency
- Translocations are not dangerous per se. They become a concern when they drive a phenotype that is unexpected. They *may* reduce your efficacy and/or cellular viability
- Ideally, you want to identify them, track them, understand them, and (if possible) reduce them.
- Translocations *can* be reduced by modulating repair pathways and mixing enzymes appropriately