



Genome Editing: Considerations for Therapeutic Applications

Cecilia Fernandez

TIDES, 2017

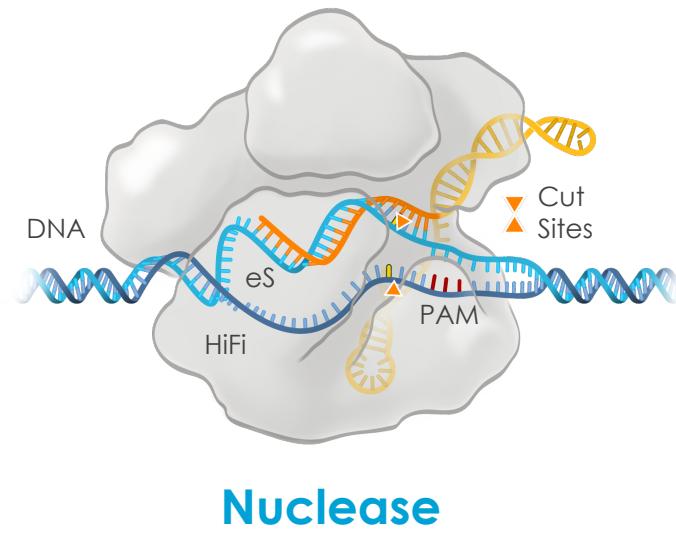


The Potential to Repair Any Broken Gene



Transformative new category of medicines
for genetically-defined and genetically-treatable diseases

Editing machinery can be engineered to target nearly any genomic location



Nuclease

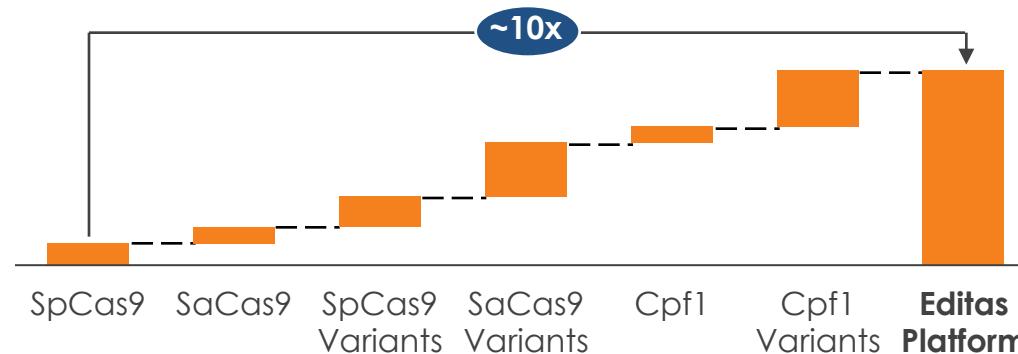
Guide RNA

- Complex of nuclease and guide RNA precisely locates and cuts genomic sites
- Ability to target several sites simultaneously using multiple guide RNAs
- Nuclease can be engineered to reach more sites and to modulate cutting

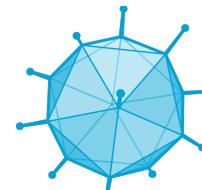
eo | Unparalleled Platform for Gene Editing Medicines



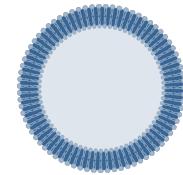
Broad
Range of
Sites



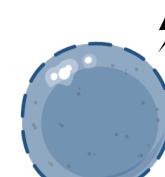
Wide
Delivery
Options



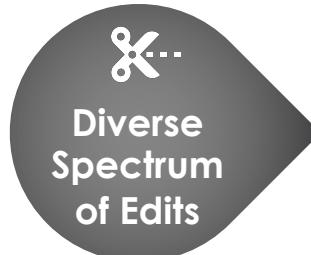
Viral Vector



Lipid Nanoparticle

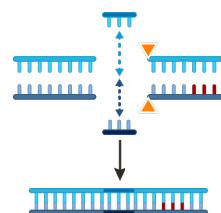


Electroporation

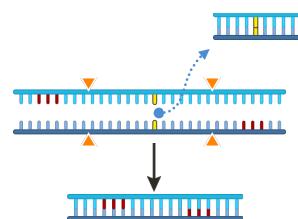


Diverse
Spectrum
of Edits

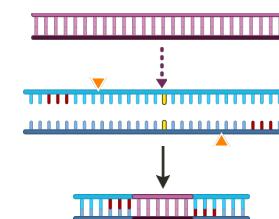
Disrupt



Delete

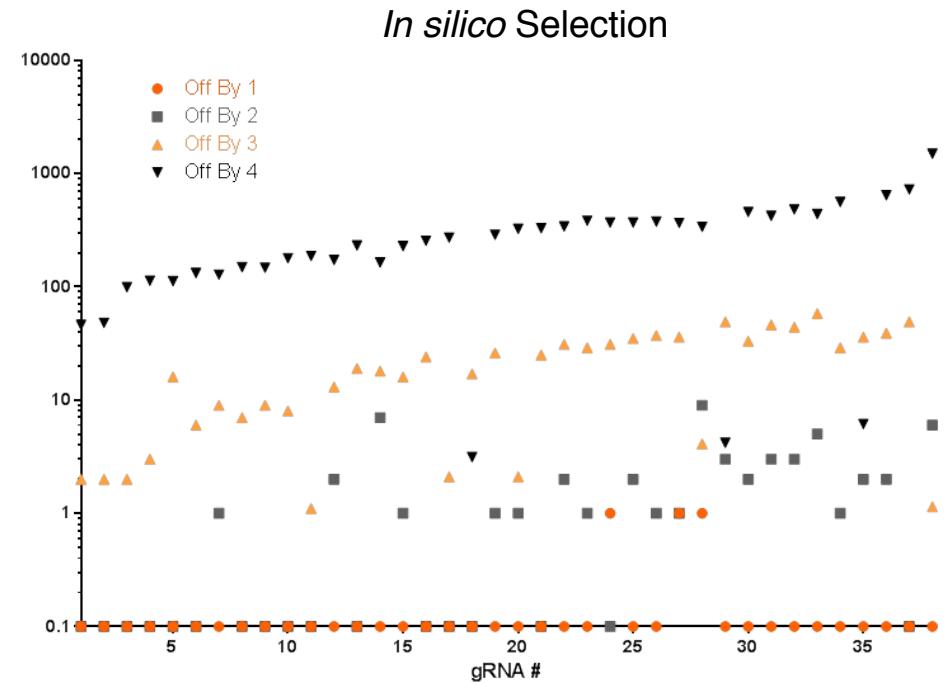


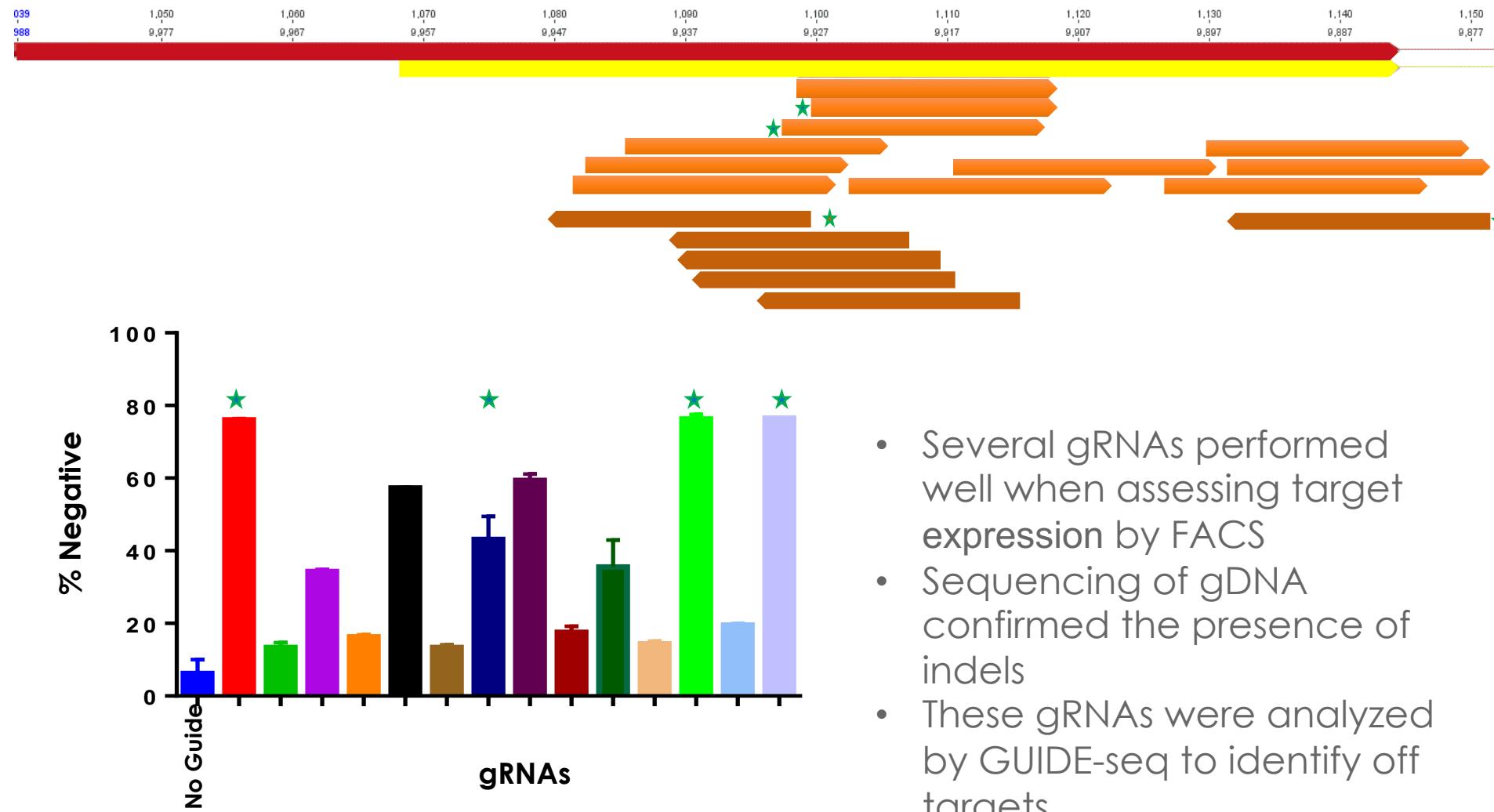
Correct



eo | Lead Finding & Specificity to Select gRNA

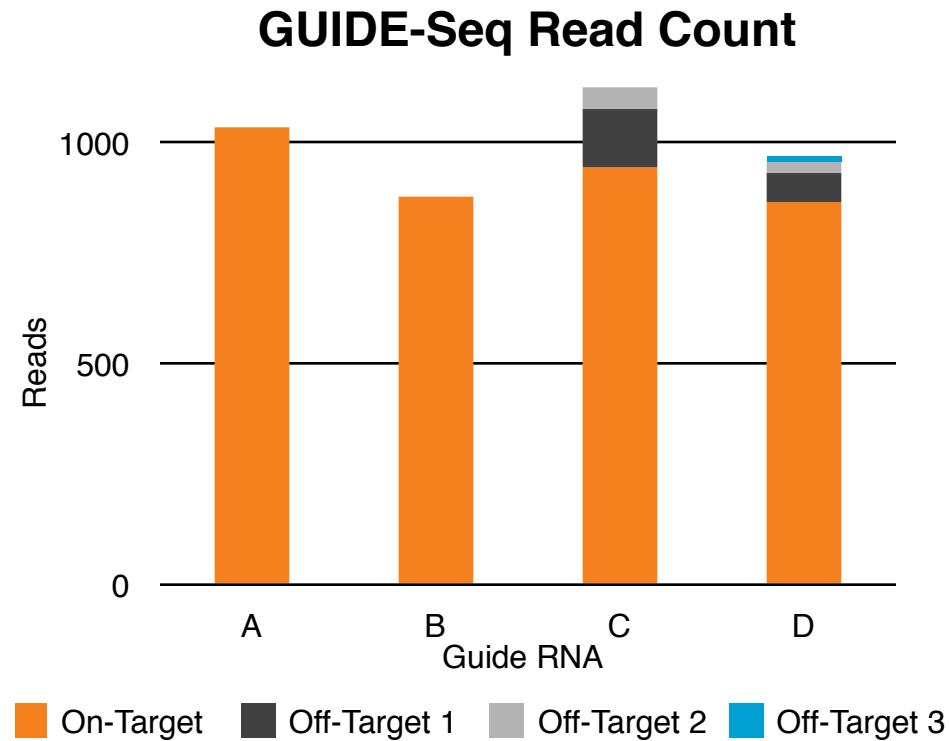
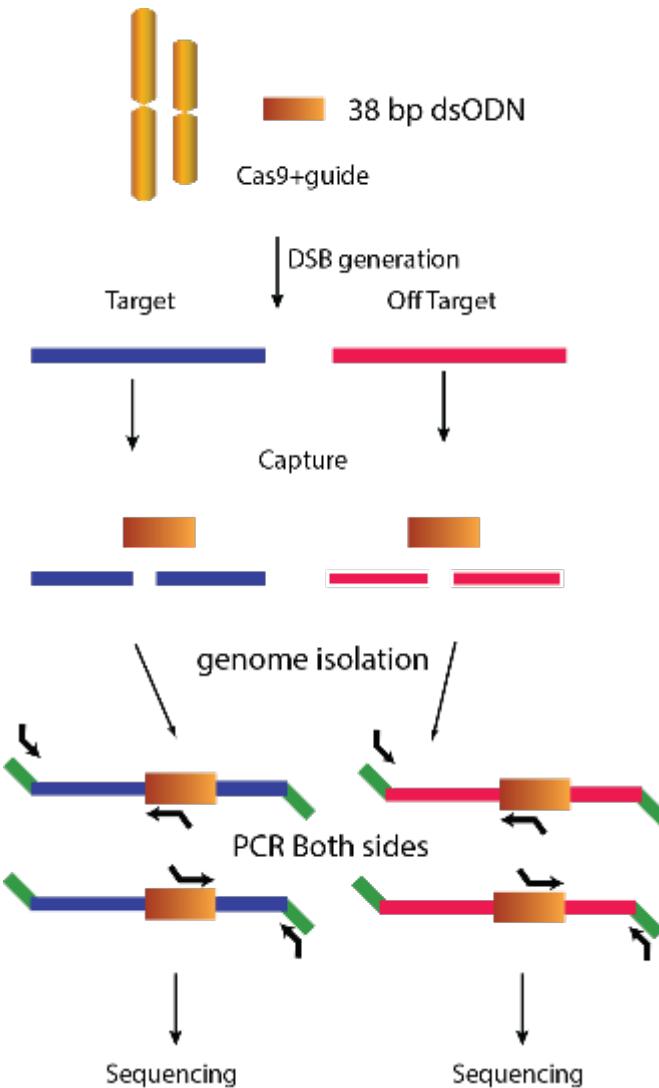
Identify, Measure, Minimize



RNP (*S. pyogenes*) delivery to primary T cells

eo | Control and Specificity to Drive Precision

Guide-seq allows identification of highly selective candidates





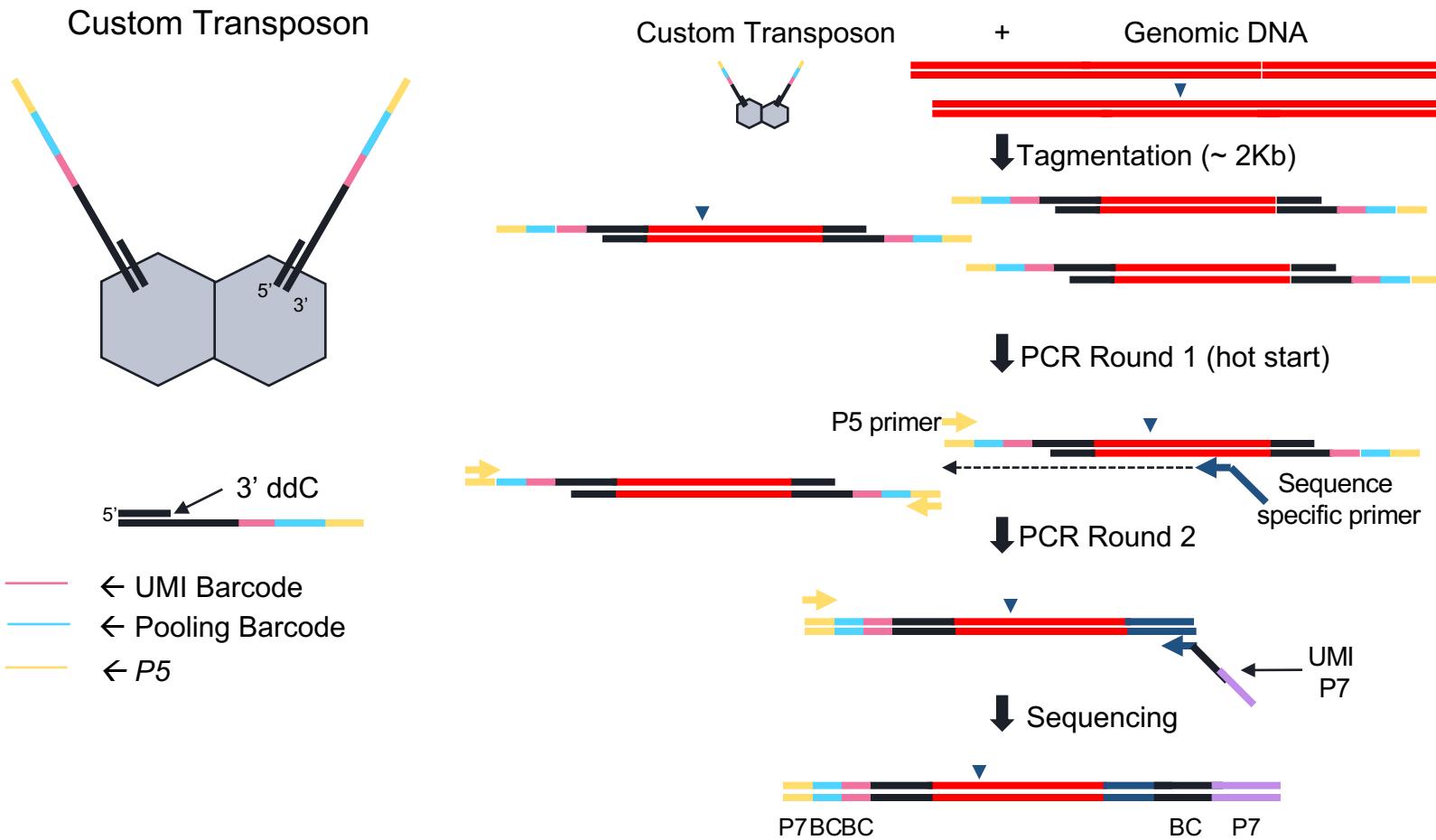
How Do You Best Measure Editing?

A simple question with a complex answer

- Sequence anchored detection approaches are limited to:
 - What is between the primers and
 - Amplicon size
- One cannot detect several events and has to build and “reassemble” answers from disparate technologies (e.g. ddPCR + targeted sequencing):
 - Large insertions
 - Large deletions
 - Inversions
 - Translocations
- Wanted a size insensitive, multiplex compatible, comparatively easy single tube method that can detect all of the above events

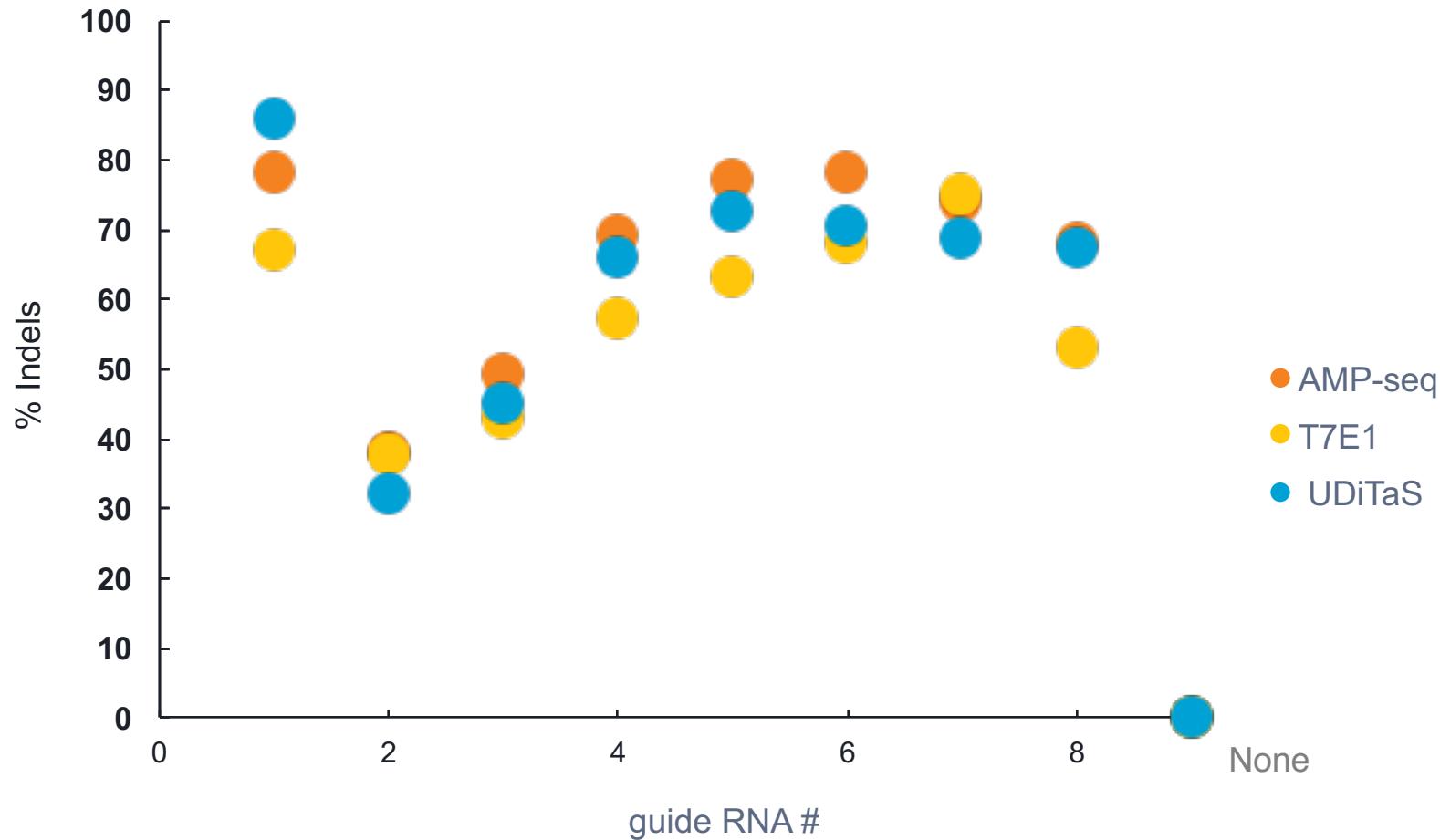
eo | Uni-Directional Targeted Sequencing (UDiTaS™)

Blending tagmentation and AMP-seq



eo | Comparison of Small Indel Measurements

UDiTaS correlates well with targeted sequencing and T7E1 assays

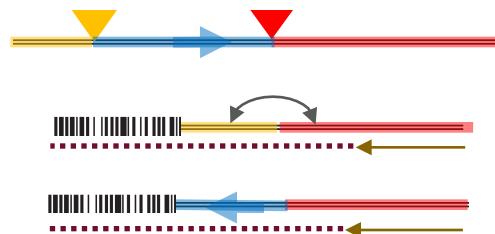


UDiTaS™ (Uni-Directional Targeted Sequencing)

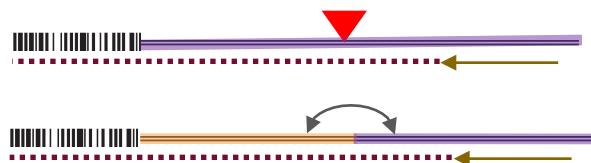
A simple, robust method for capturing complex editing events in a single reaction



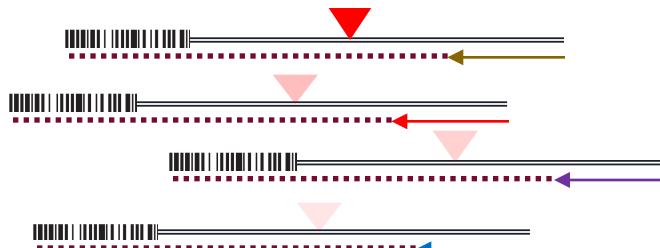
1. Quantitation of editing



2. Quantitation and discovery of large deletions and inversions

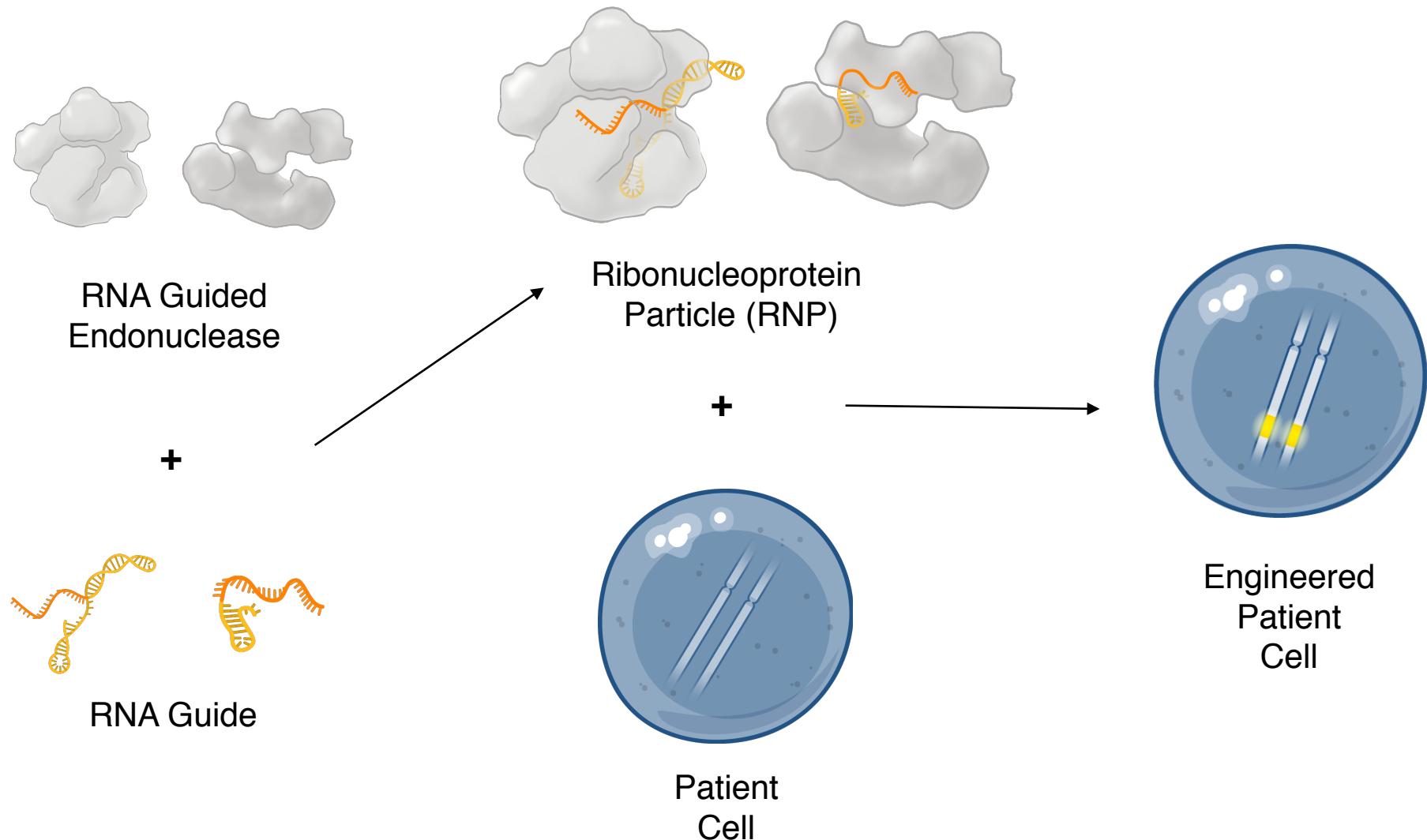


3. Translocation discovery and quantitation



4. Multiplexing

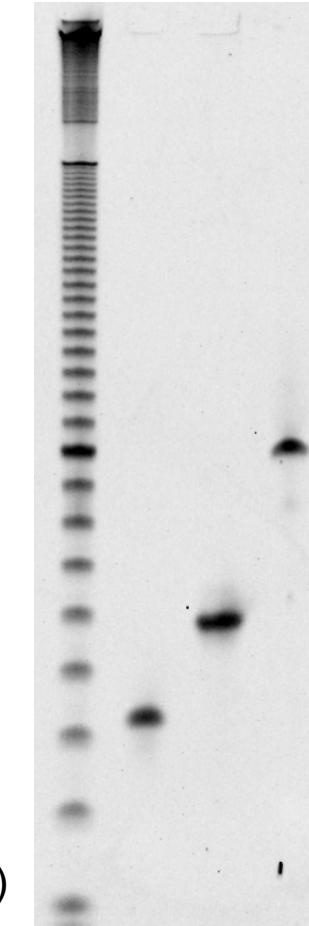
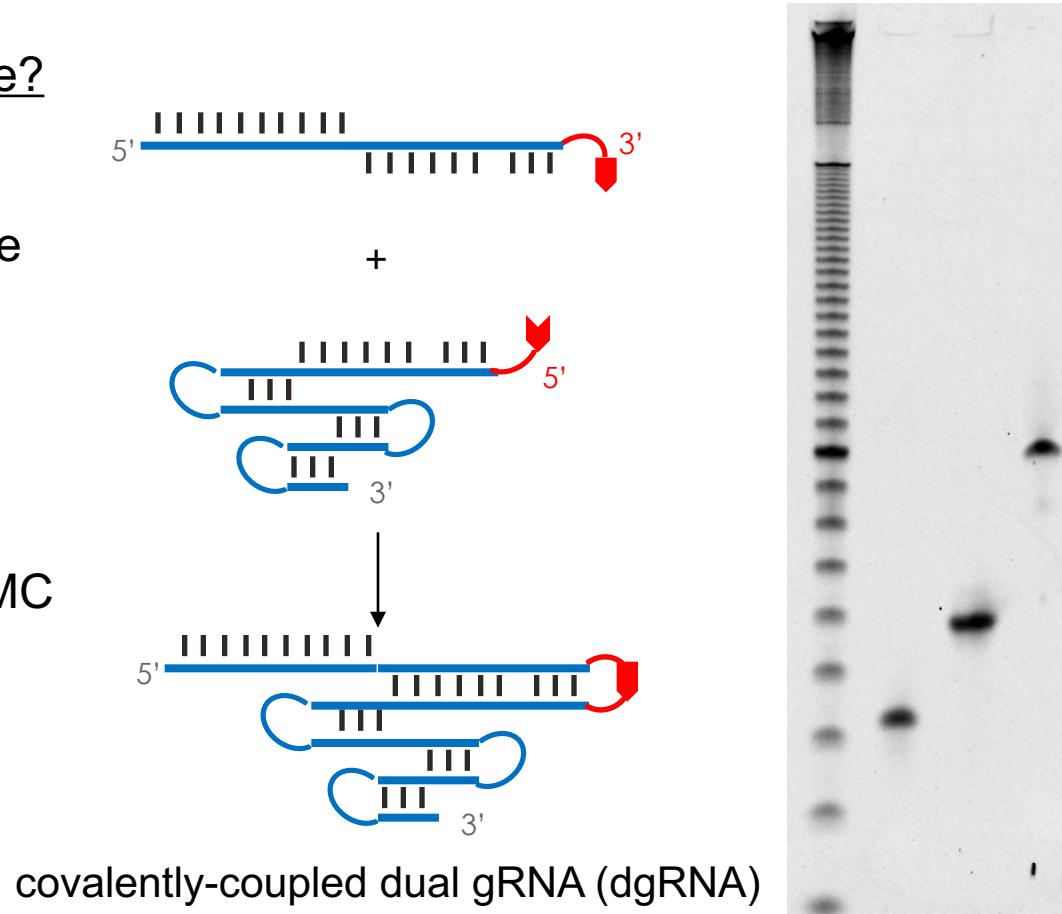
High Quality Ribonucleoprotein Particle Delivery



A completely non-enzymatic process for guide production

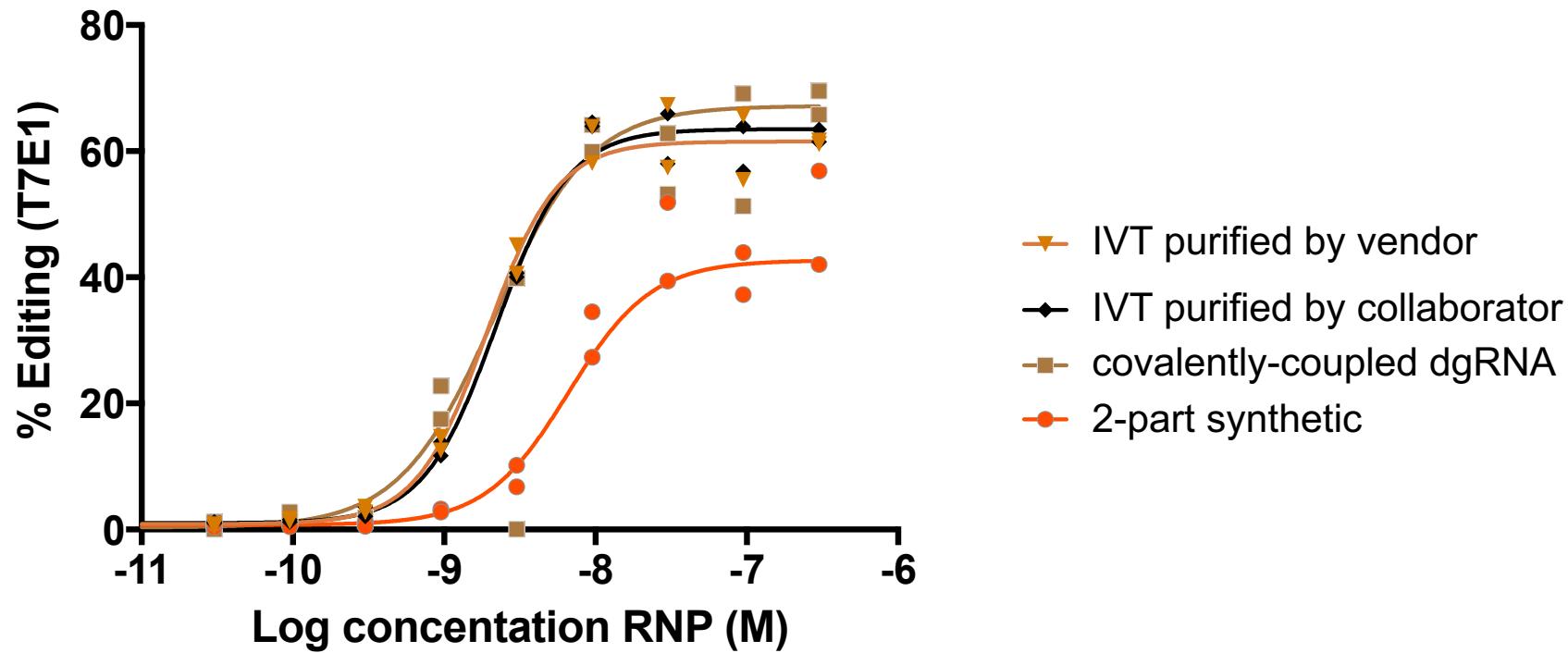
Why make a synthetic guide?

- Targeted chemistries anywhere in the molecule
- Unhindered ends and modifications
- Scale up and purity are more compatible with CMC requirements

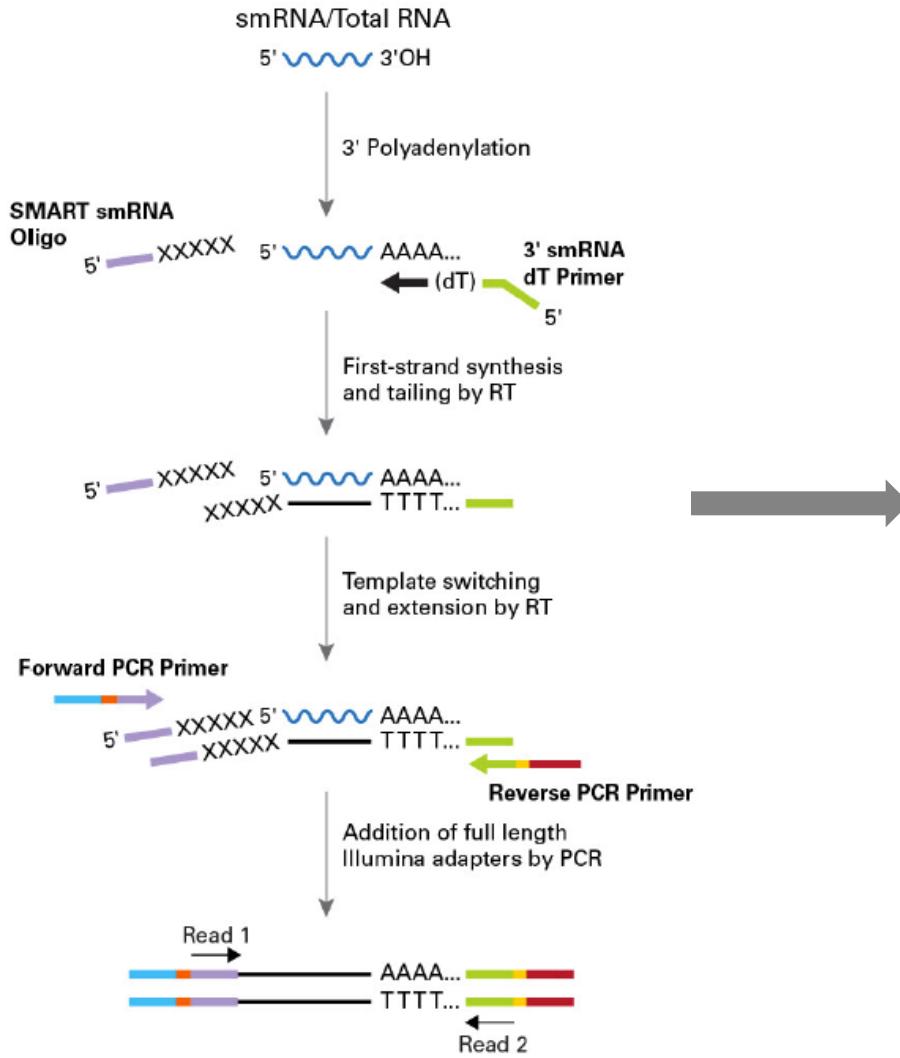


eo | Cellular Editing Activity

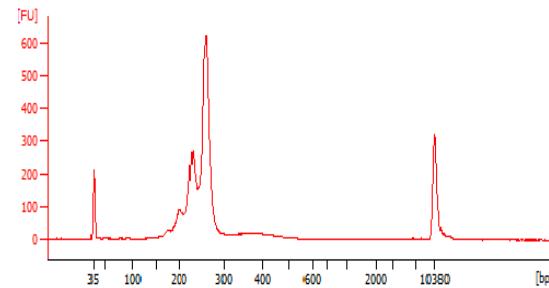
In vitro transcribed and synthetic covalently-coupled dgRNA are equivalent in cells



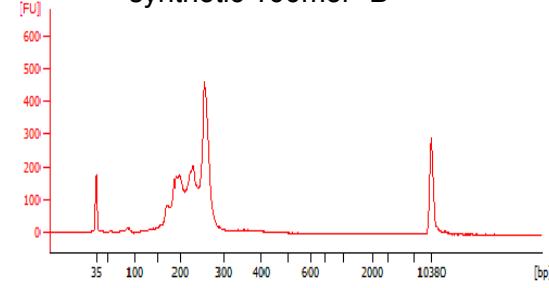
Development of an RNA-Seq based method for gRNA QC



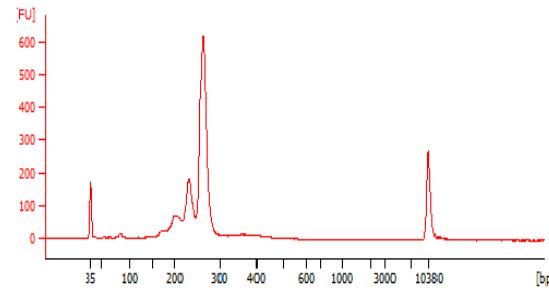
synthetic 100mer "A"



synthetic 100mer "B"



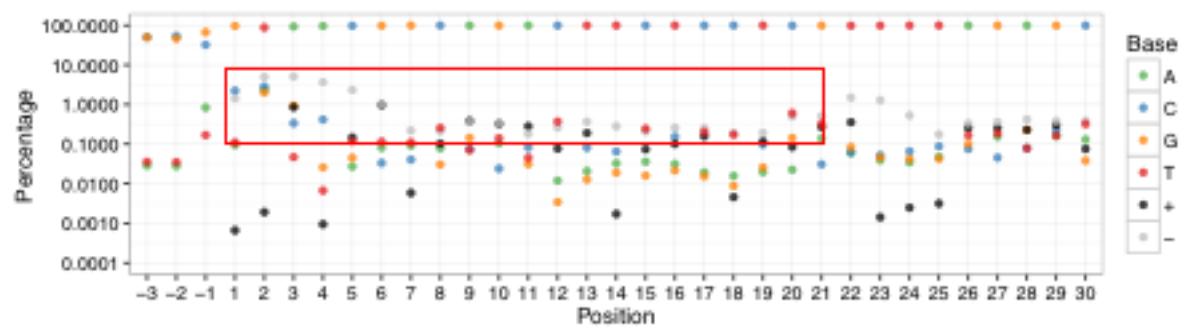
covalently-coupled dgRNA



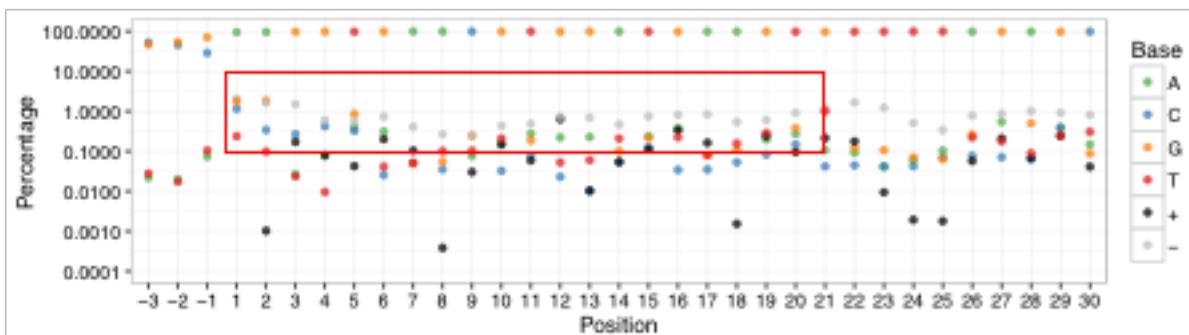
eo | gRNA purity and sequence fidelity

Covalently-coupled dgRNA result in greater sequence fidelity in target region

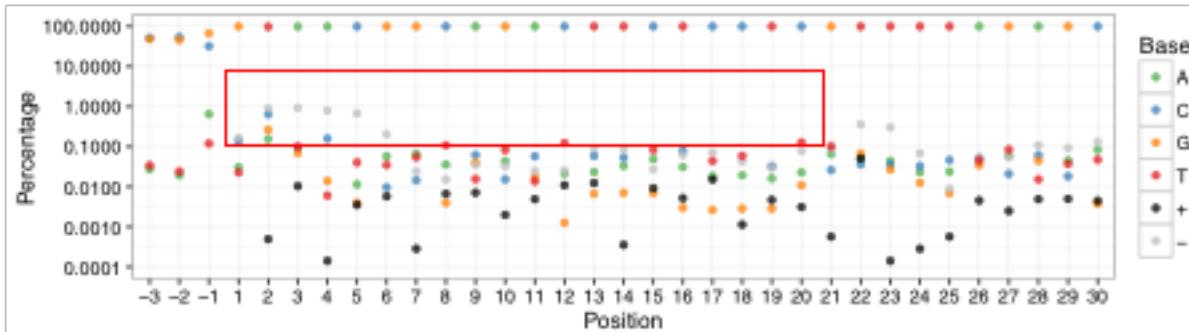
A



B



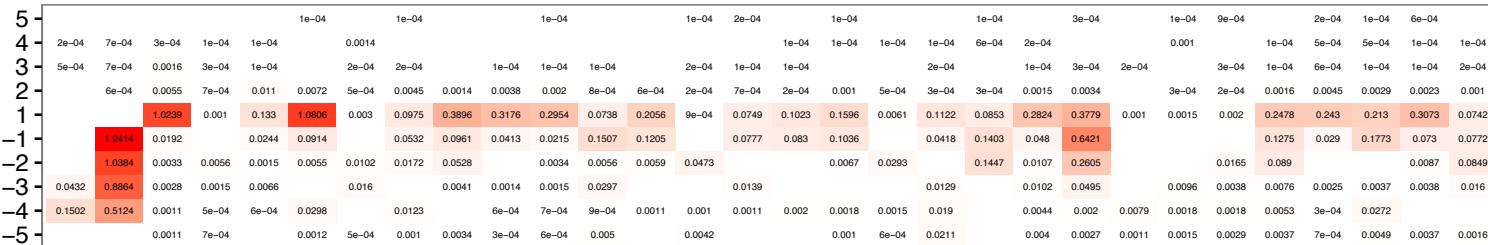
Covalently-Coupled dgRNA



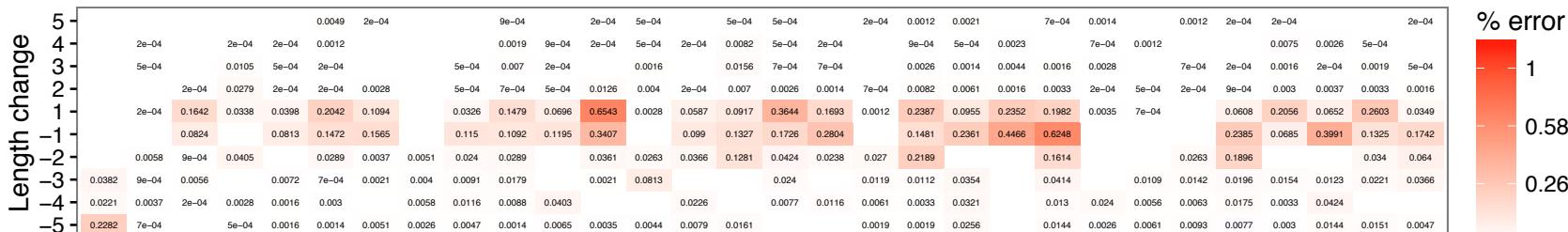
 | gRNA Purity and Sequence Fidelity

Covalently-coupled dgRNA result in fewer truncated molecules

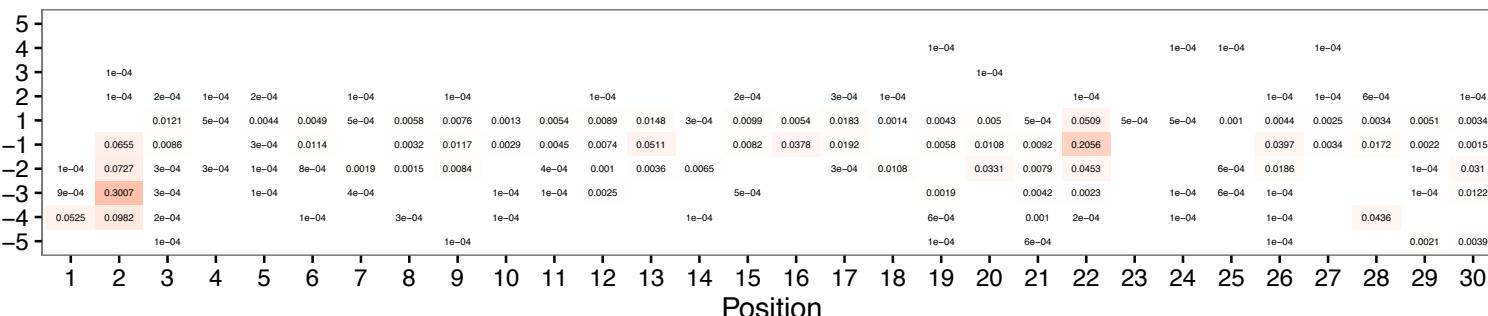
A



B

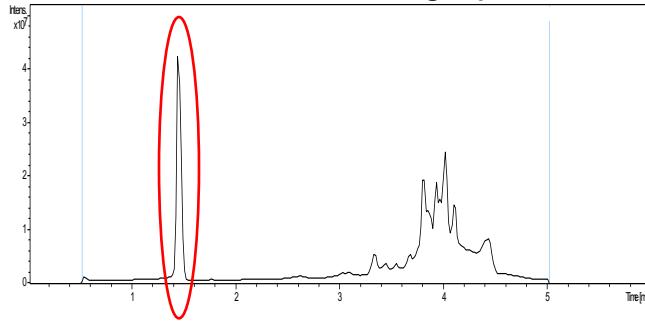


Covalently-Coupled dgRNA

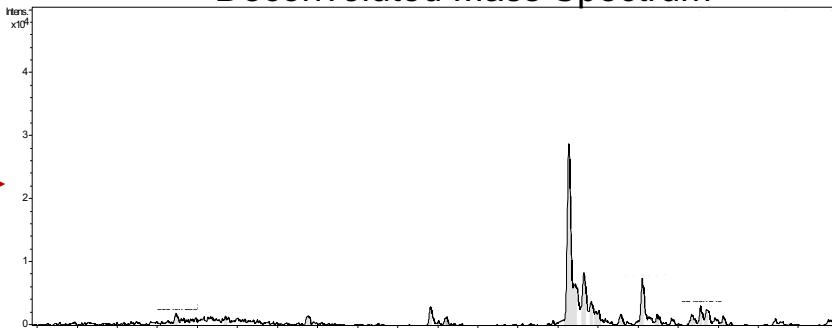


Total Ion Chromatograph

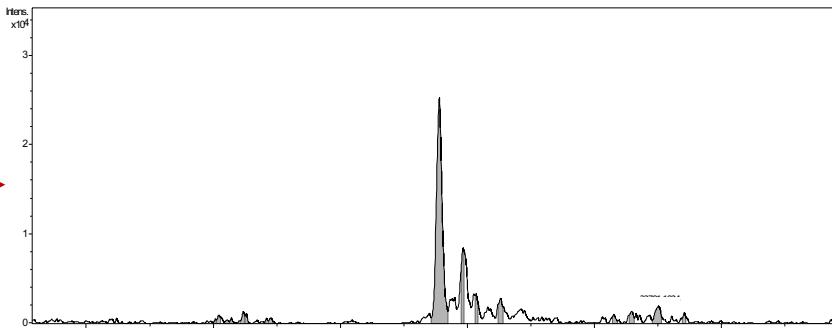
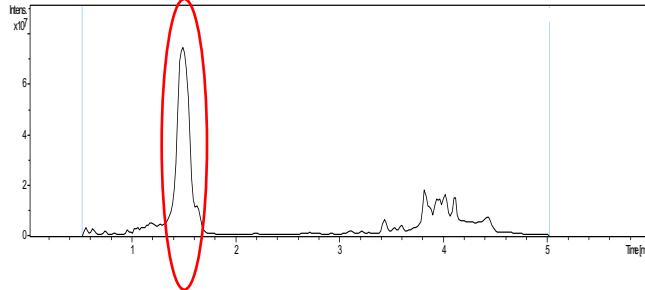
A



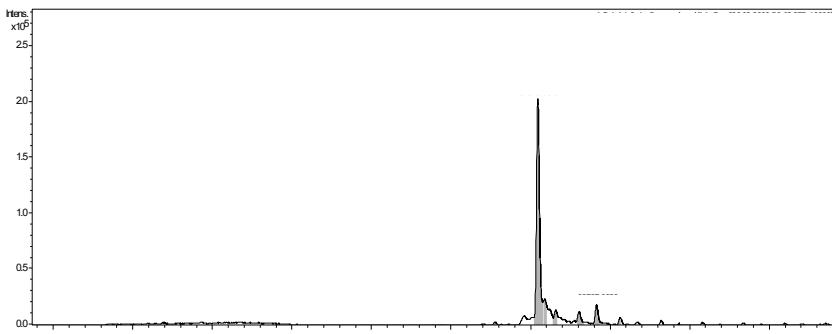
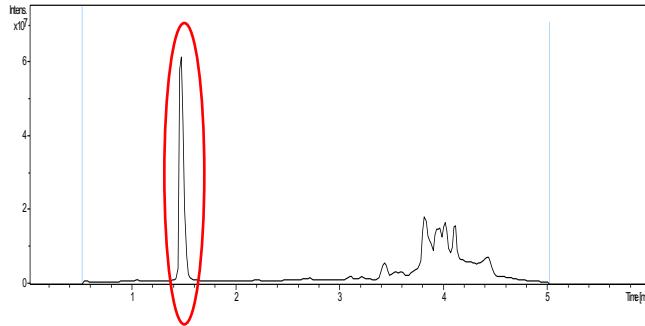
Deconvoluted Mass Spectrum



B



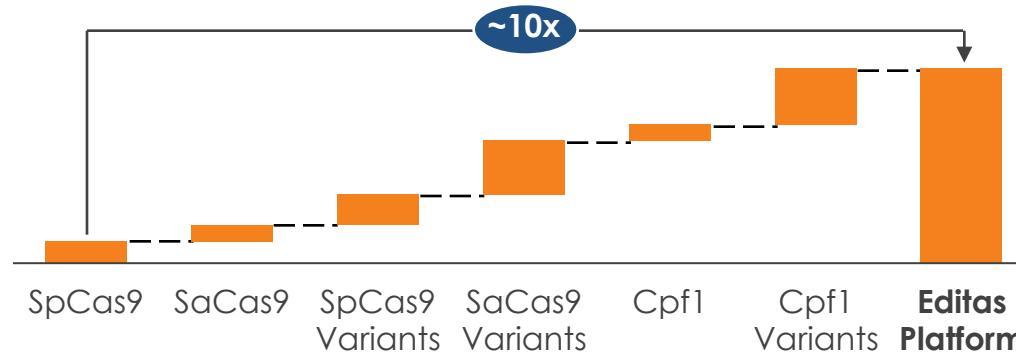
Covalently-coupled dgRNA



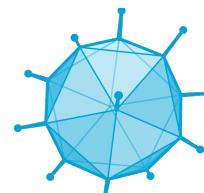
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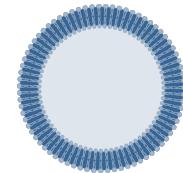
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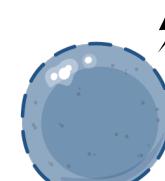
Wide
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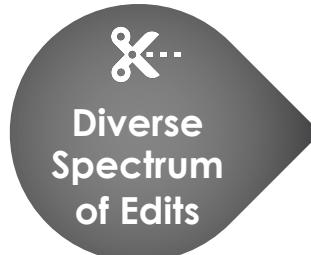
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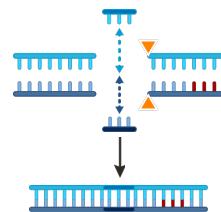


Electroporation

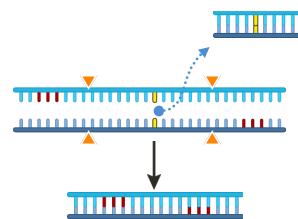


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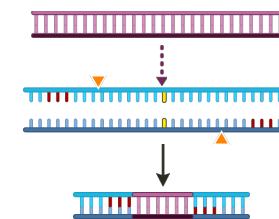
Disrupt



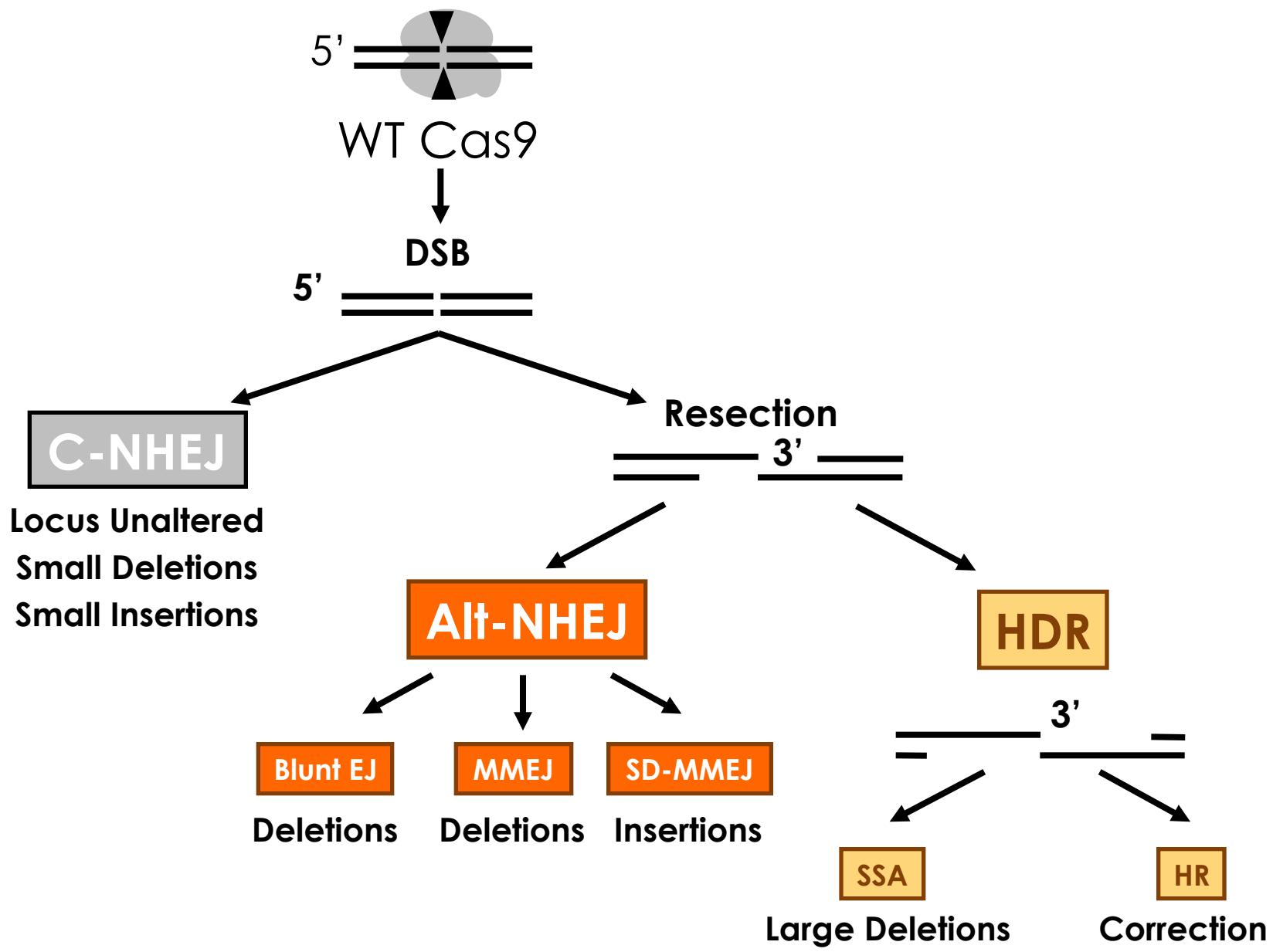
Delete



Correct

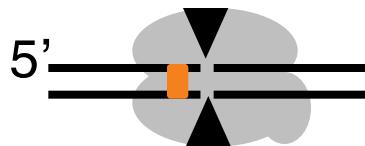


Cas9 Stimulates the Endogenous Repair Pathways



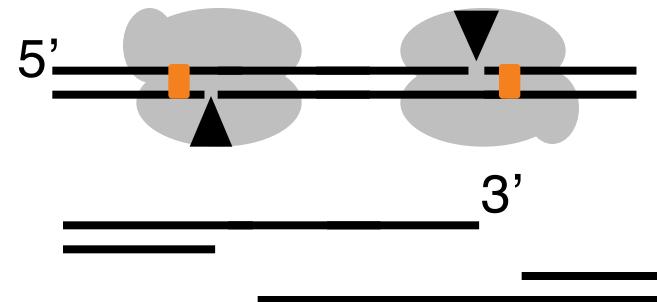
eo | Cas9 is a Flexible Tool

WT Cas9



5'

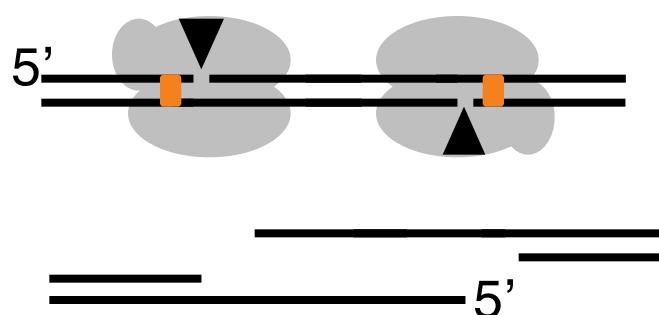
N863A Nickases



5'

3'

D10A Nickases



5'

5'

Blunt

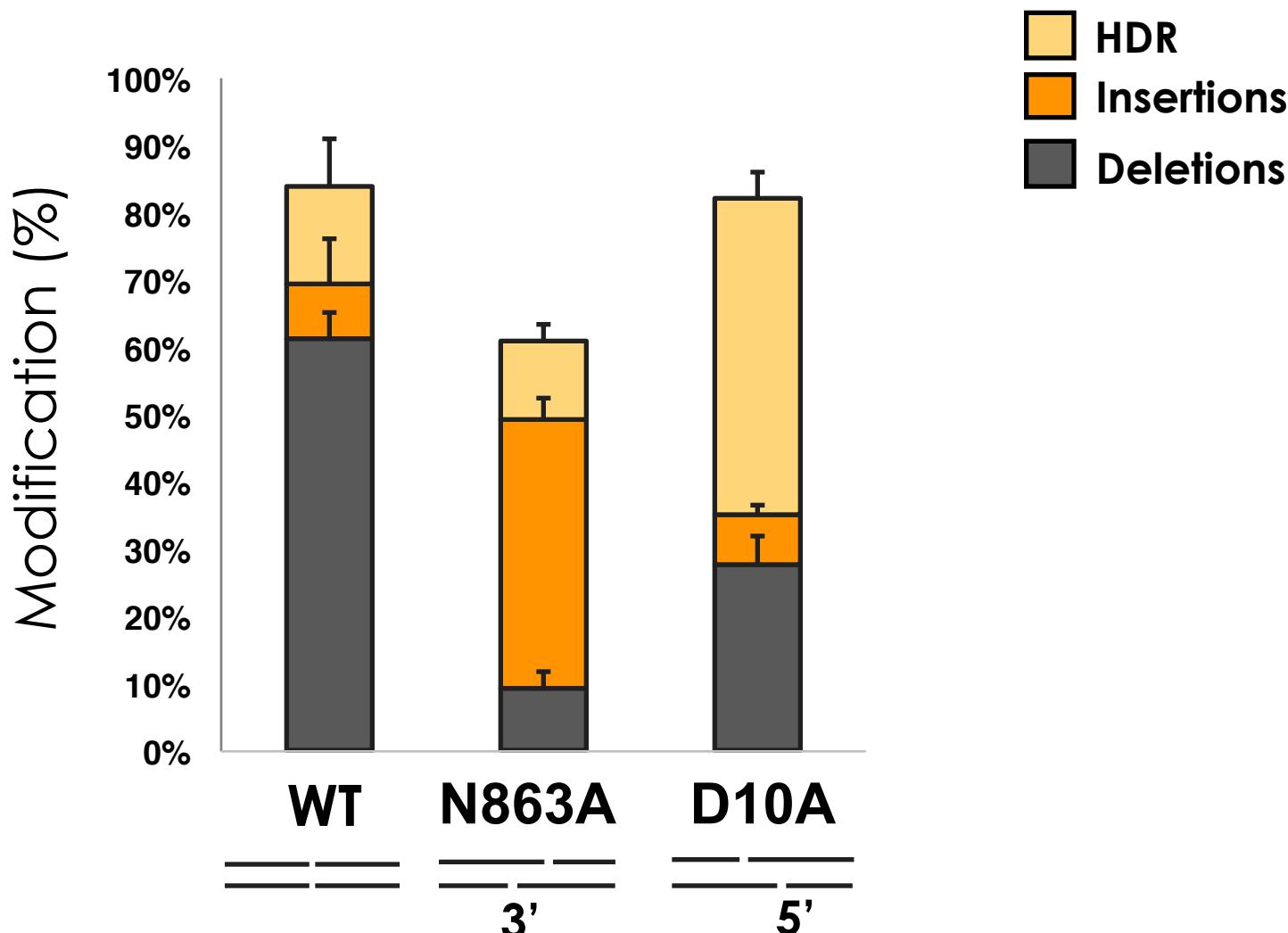
3' Overhang

5' Overhang



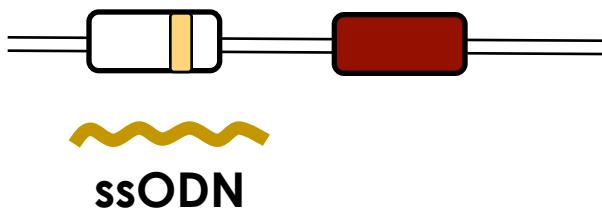
- Could we engage different pathways by using these different variants?
- Could we selectively stimulate HDR?

DSBs Generated by D10A are Predominantly Repaired by HDR

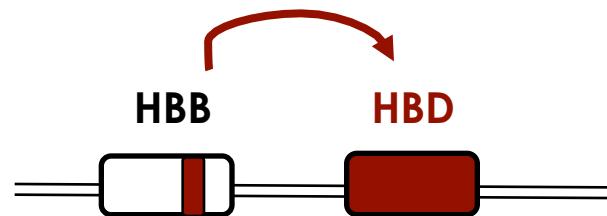


Do Gene Conversion and Gene Correction have the same Genetic Requirement?

Gene Correction

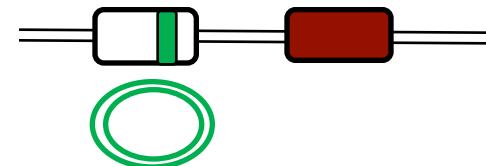
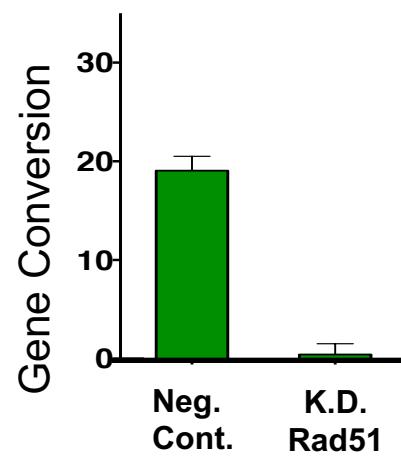
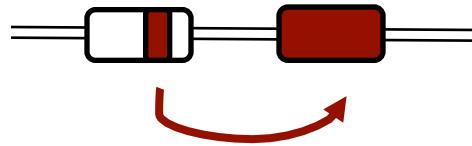
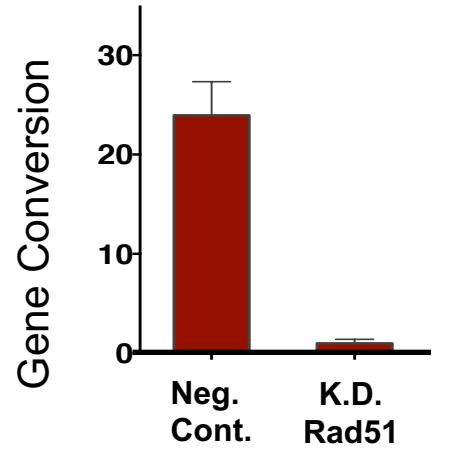
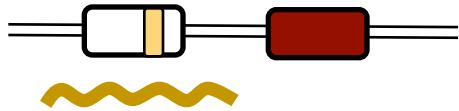
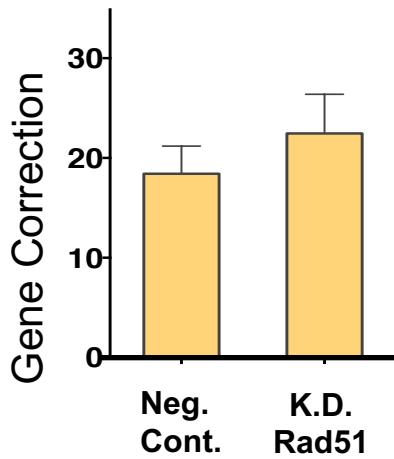


Gene Conversion



Do they both dependent on the HR pathway?

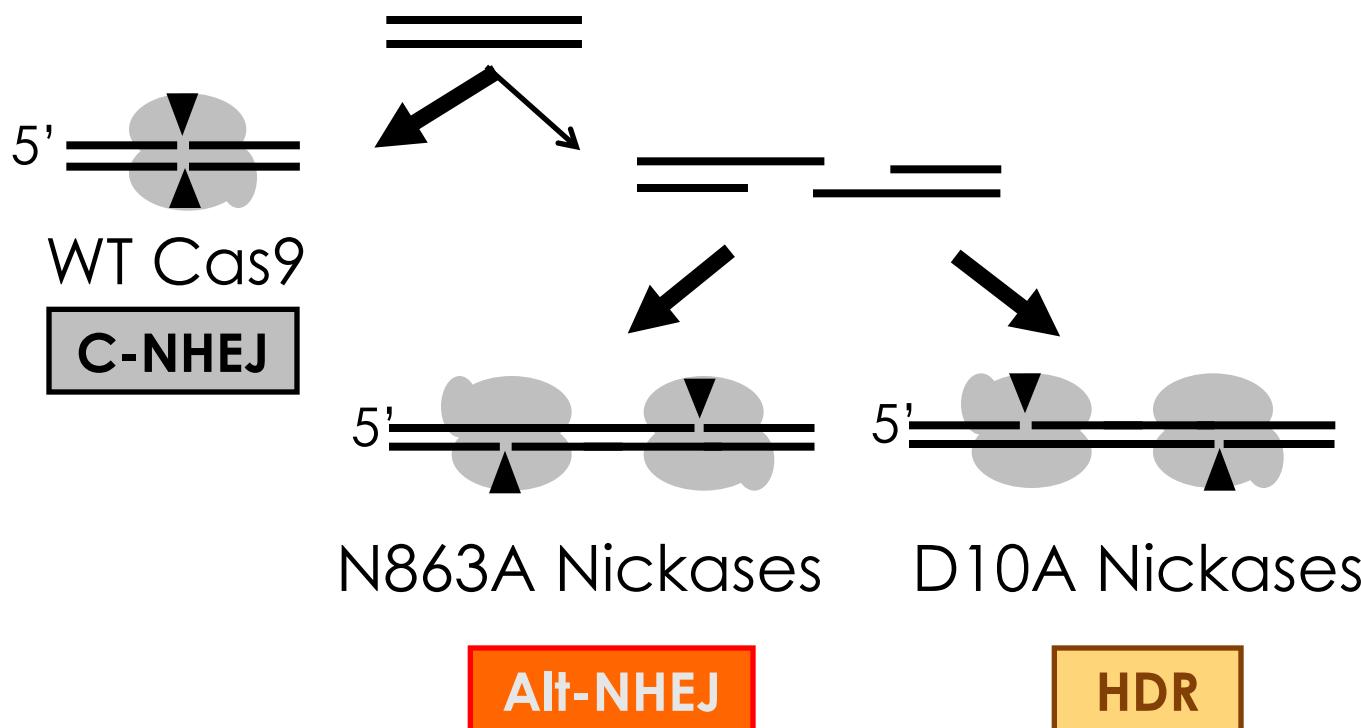
Gene Conversion and Gene Correction have Different Genetic Requirements



HR is required for repair from double stranded donors (endogenous homology tracks or plasmids) but not single stranded donors

Conclusions from the Dual Nick Analysis

- Different ends activate different DNA repair pathways



- Different donors stimulate different pathways

Gene Correction mediated by ssODN is not HR dependent

- We are developing precise and durable therapies by selecting and directing nuclease activity, delivery and the cellular repair response.
- We can effectively measure off-target and other genomic outcomes.
- We can make fully synthetic covalently-coupled dgRNAs of high quality.
- Our understanding of how different lesions are repaired and the connection with the nature of the donor allow us to engineer for the desired outcomes.

Hayat Abdulkerim
Luis Barrera
Anne Bothmer
Frank Buquicchio
Dawn Ciulla
Cecilia Cotta-Ramusino
Georgia Giannoukos
Kiran Gogi

Fred Harbinski
Hari Jayaram
Eugenio Marco
Carrie Margulies
Vic Myer
Tanushree Phadke
Terence Ta
Chris Wilson

i2 Pharmaceuticals team