



Advancing CRISPR Technologies for Therapeutic Application

Vic Myer

Keystone Genome Editing Meeting

January, 2017

Drug Development Fundamentals

- Reliably manufacture high quality drug substance
- Key understandings:
 - Pharmacokinetics: “what the body does to the drug”
 - Pharmacodynamics: “what the drug does to the body”

Current Recommendations to Assess Safety of Gene Editing Products



Celia Witten,
OTAT→CBER→FDA
Cell and Gene Meeting
on the Mesa
La Jolla, California,
October 6, 2016

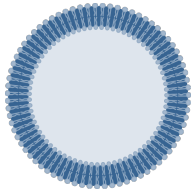
- **Kinetics of nuclease cleavage and persistence of cleavage activity**
- **Percentage of cleavage at the on- and off-target sites**
- **Identification and characterization of off-target events in cells/tissues, including chromosomal translocations**
- **Evaluation of the profile of insertions and deletions and types of mutations generated**

Strategy to Widely Enable Efficient Delivery

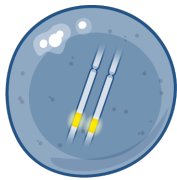
Success across a spectrum of delivery modalities in preclinical studies

MODALITY

Nanoparticle



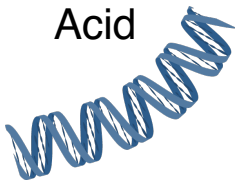
Engineered Cell



Viral Vector



Nucleic Acid



DELIVERY

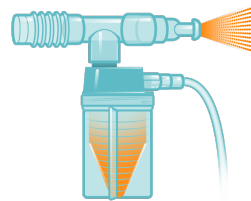


IV Infusion



Direct Injection

Inhalation



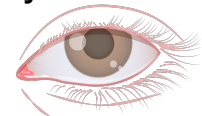
TARGET TISSUE

Bone Marrow & Blood

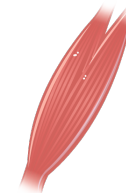


Liver

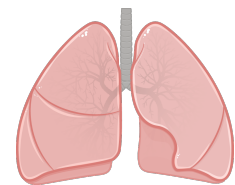
Eye



Muscle



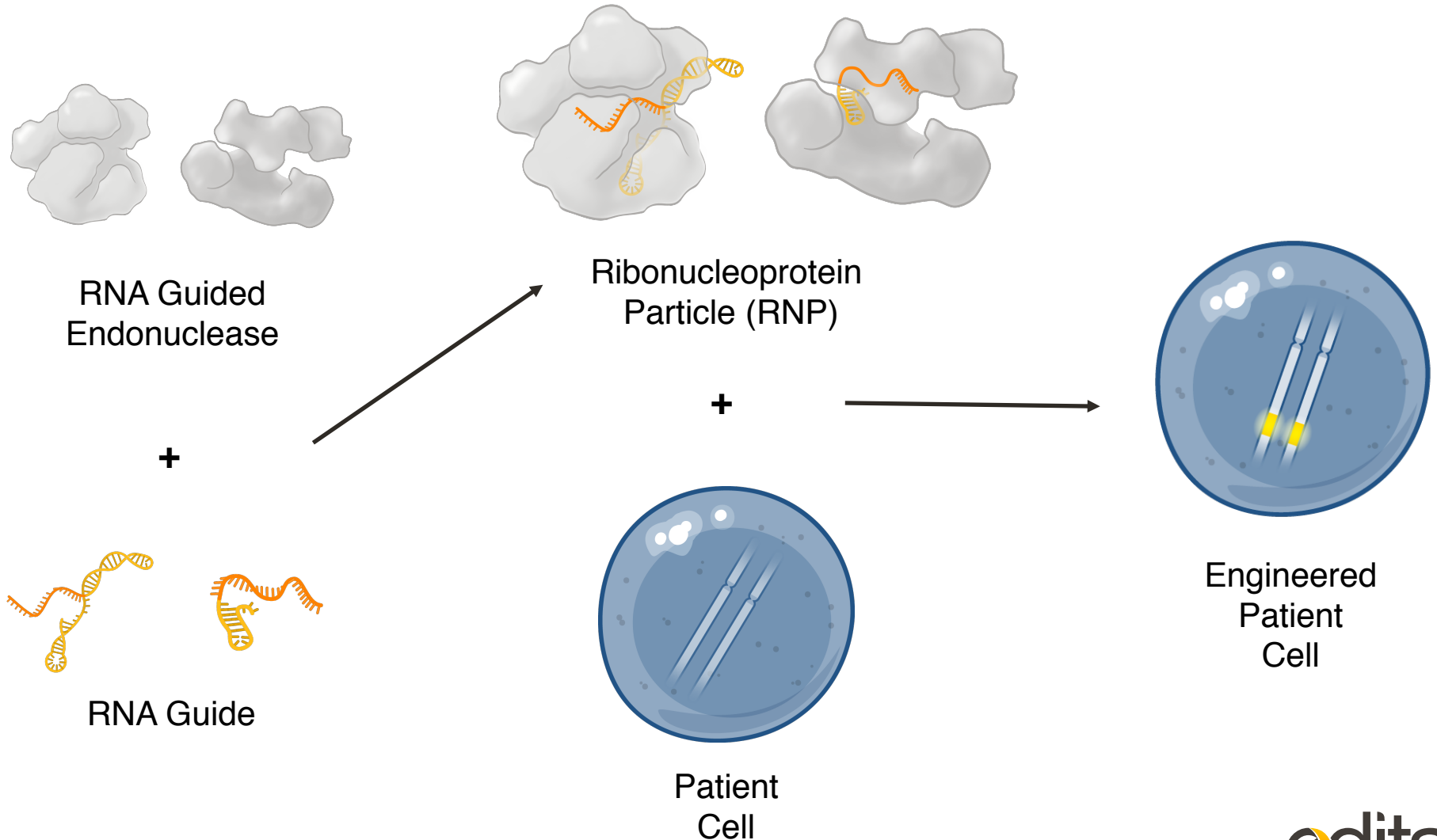
Lungs



- Tailor delivery approach for each product candidate to match specific disease
- Leverage existing technologies while investing in new approaches

High Quality Autologous Drug Development

Engineered autologous therapy requires multiple components

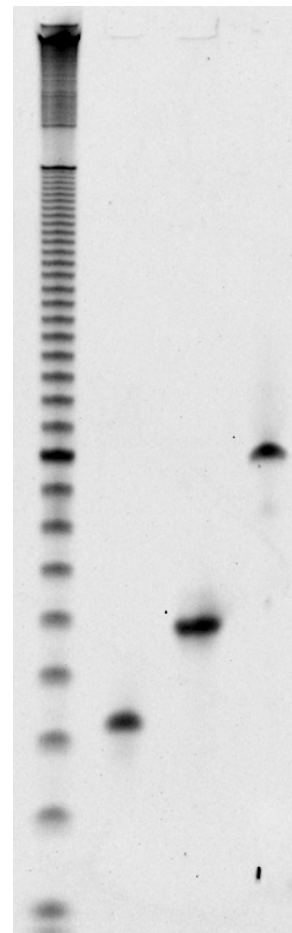
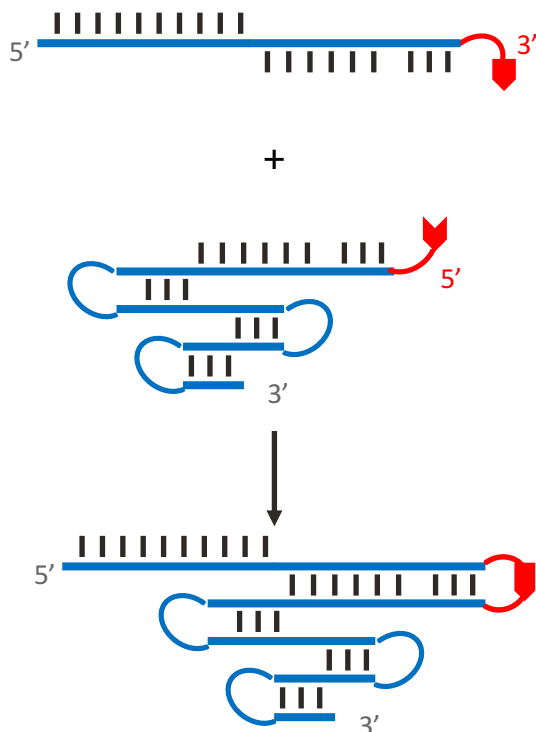


Generating Synthetic Single gRNA

A completely non-enzymatic process for guide production

Why make a synthetic guide?

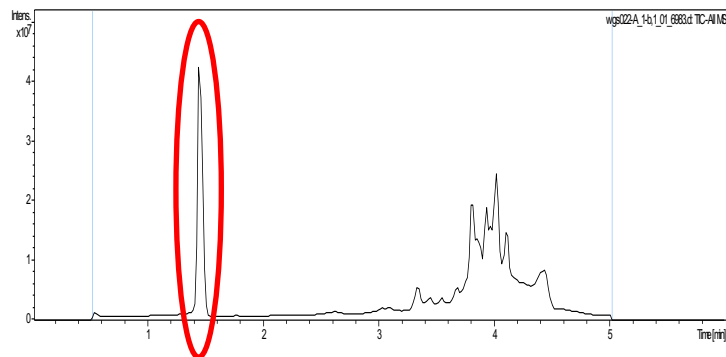
- Targeted chemistries anywhere in the molecule
- Unhindered ends and modifications
- Scale up and purity are more compatible with CMC requirements



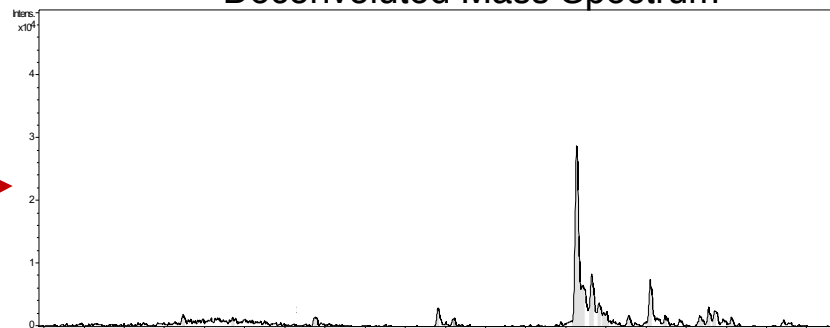
Analytics Demonstrates High Quality Material

Total Ion Chromatograph

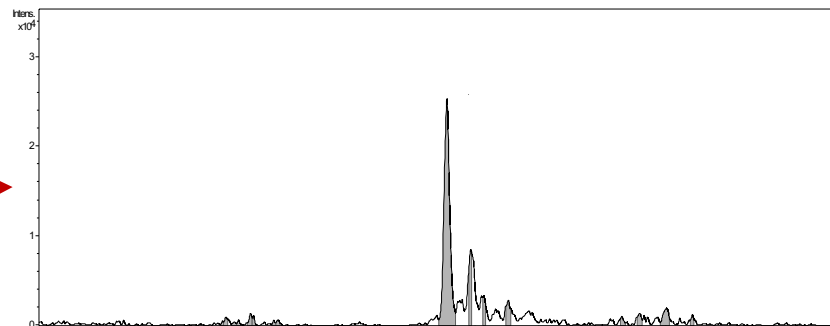
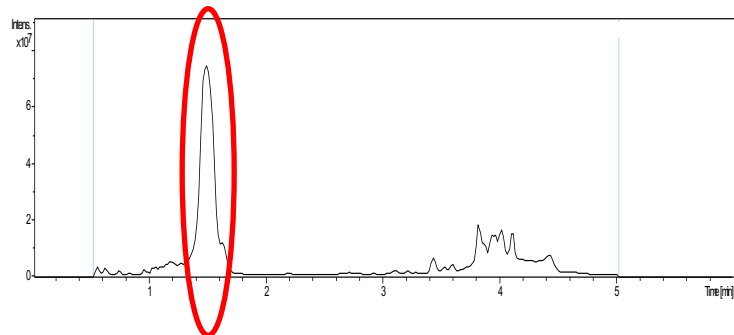
A



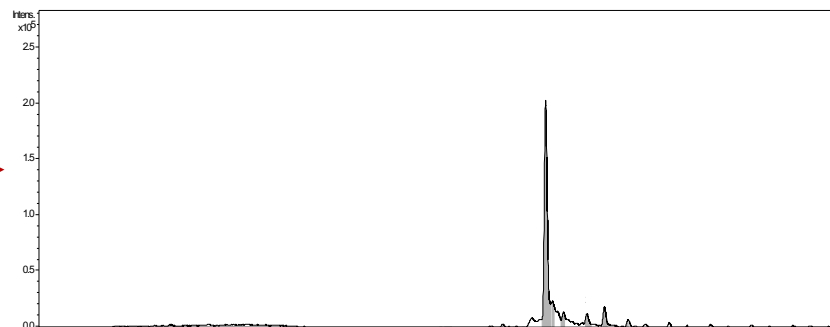
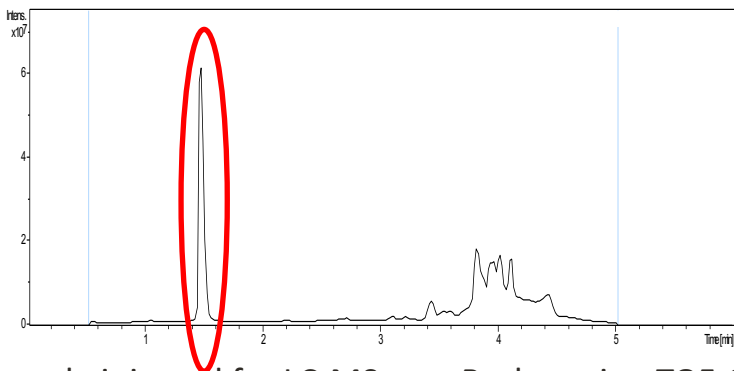
Deconvoluted Mass Spectrum



B



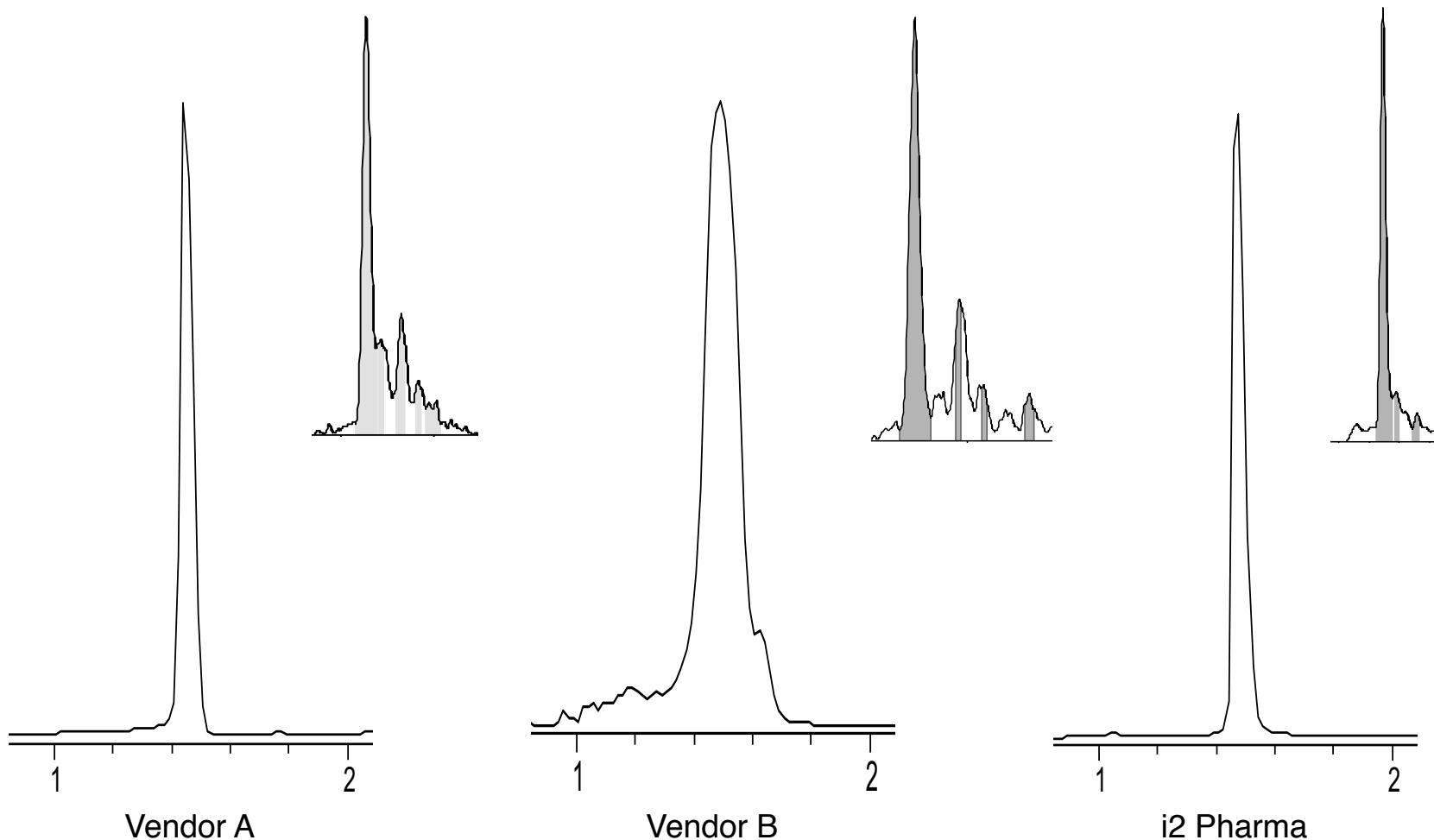
i2 Pharma



100 pmole injected for LC-MS on a Bruker microTOF-QII mass spec equipped with a Waters ACQUITY UPLC system (C18 column)

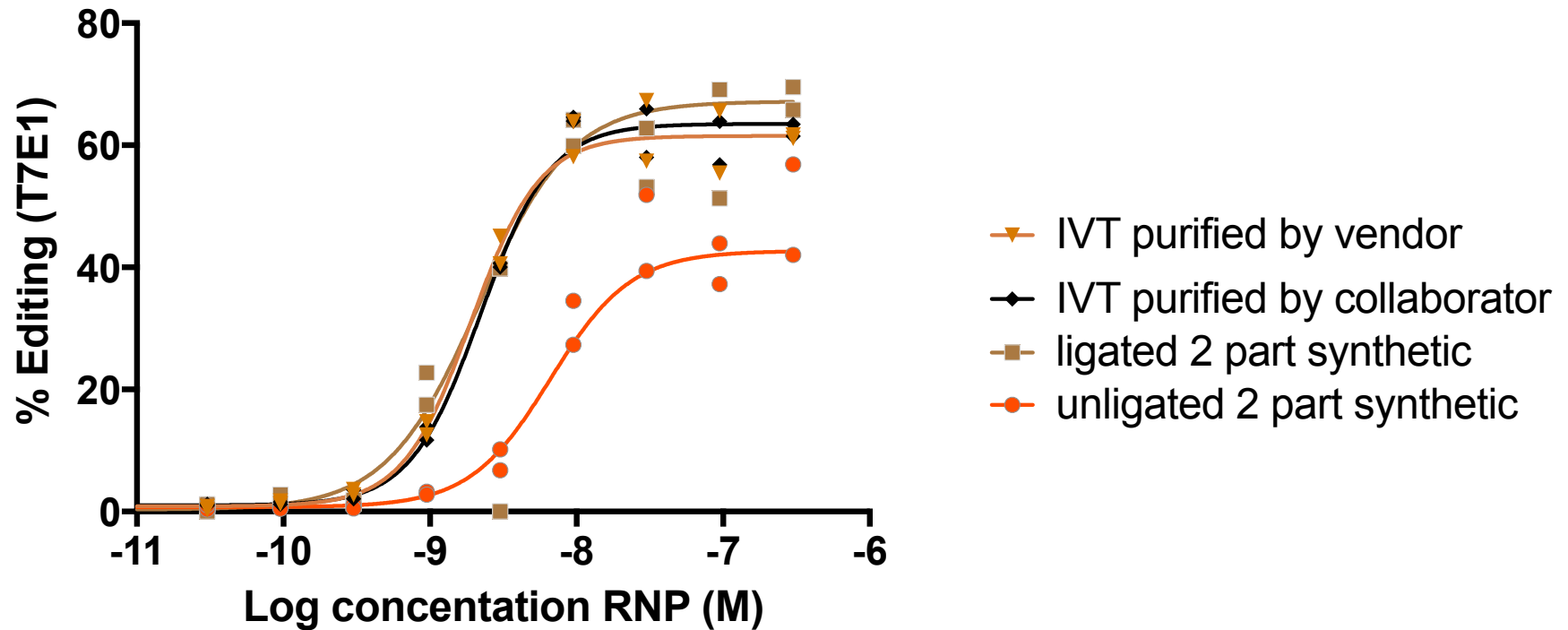
Comparative Mass Spec Data

Our strategy yields high quality research grade molecules



Cellular Editing Activity

In vitro transcribed & synthetic gRNAs are equivalent in cells



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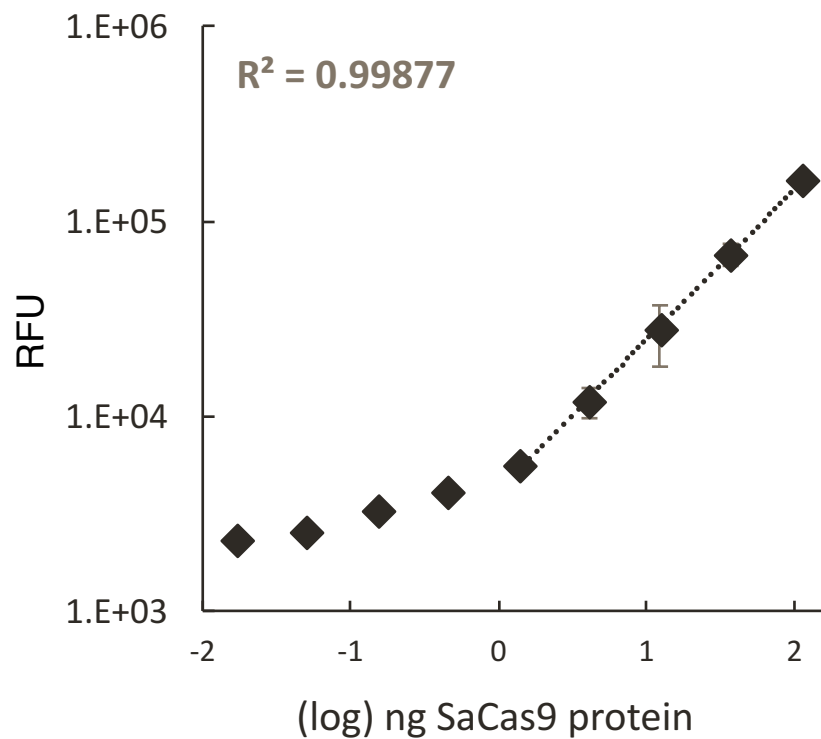
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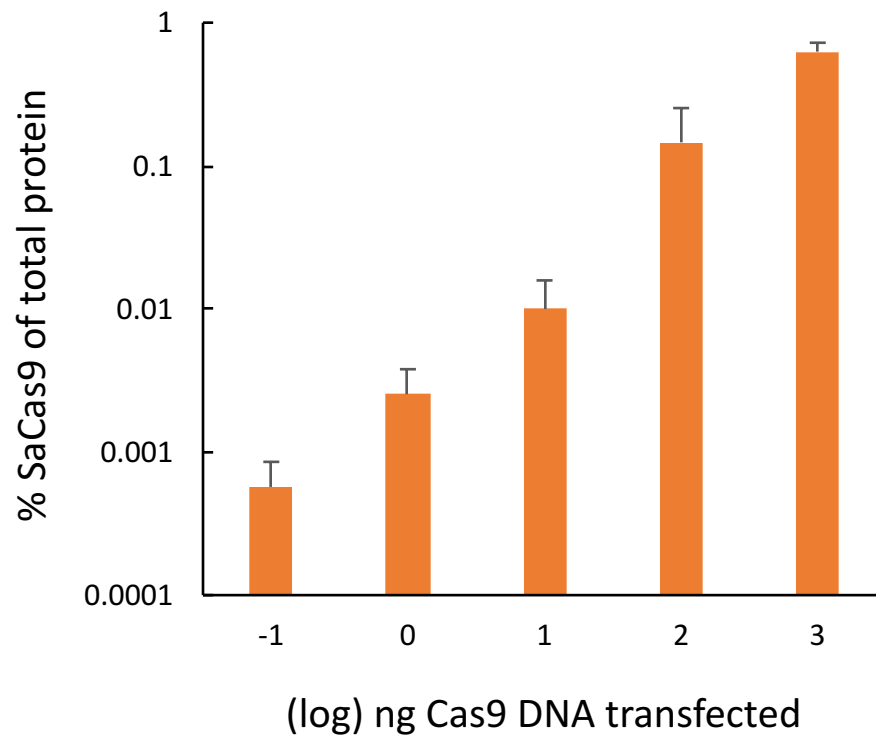
Sensitive Detection of SaCas9 Protein

AlphaLISA protein assay with 2-3 logs linear sensitivity

AlphaLISA standard curve for SaCas9



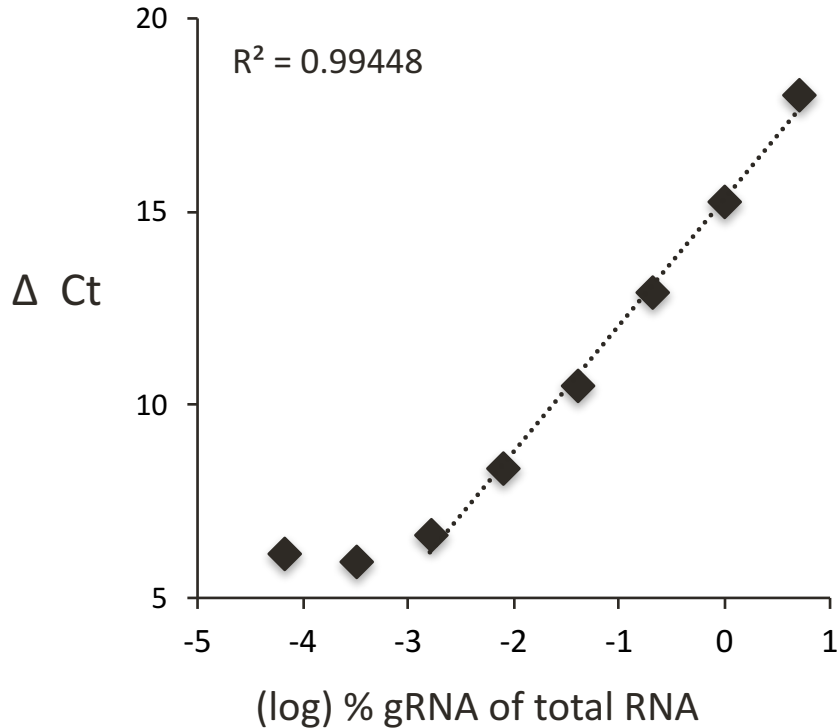
Dose response in transfected cells



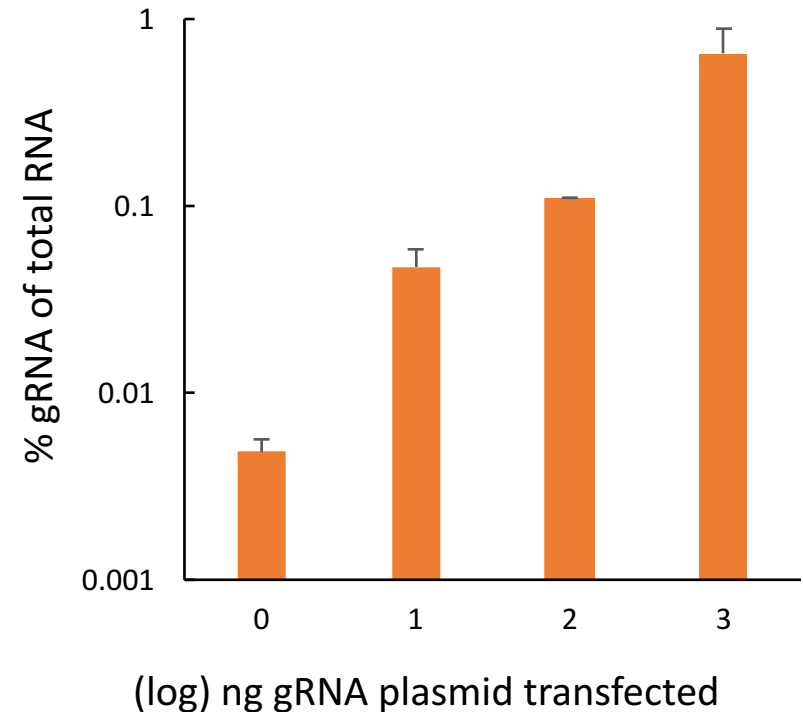
Sensitive Detection of *S.aureus* gRNAs

Generic gRNA detection assay with 4 logs linear sensitivity

RT-qPCR for SaCas9 gRNA TRACR
standard curve



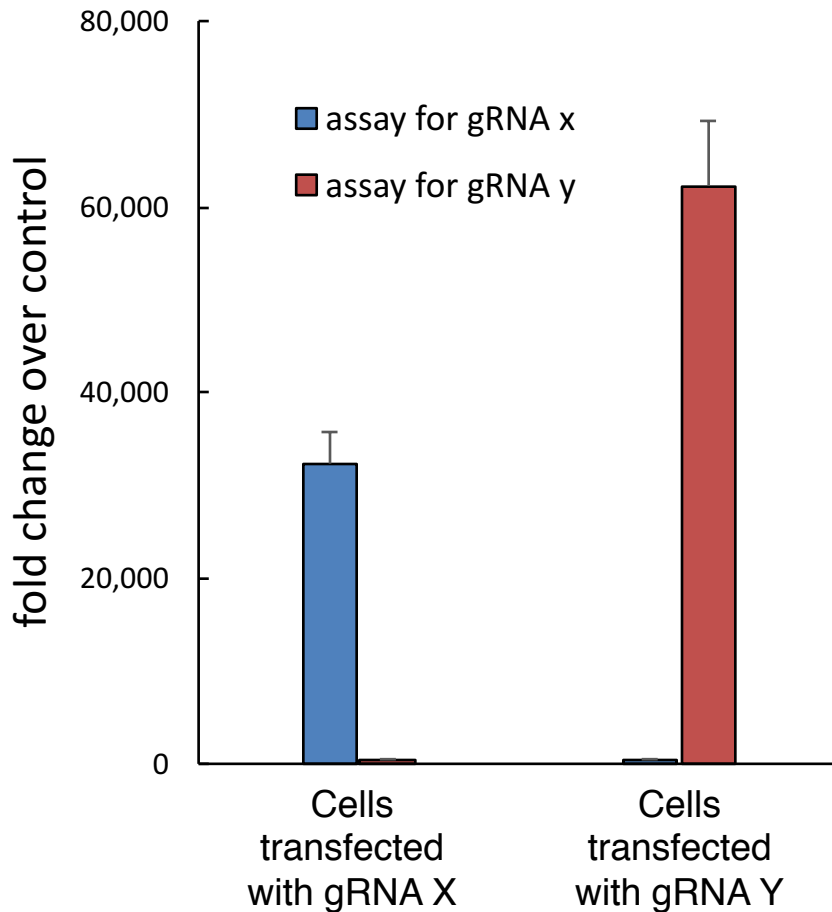
Dose response in transfected cells



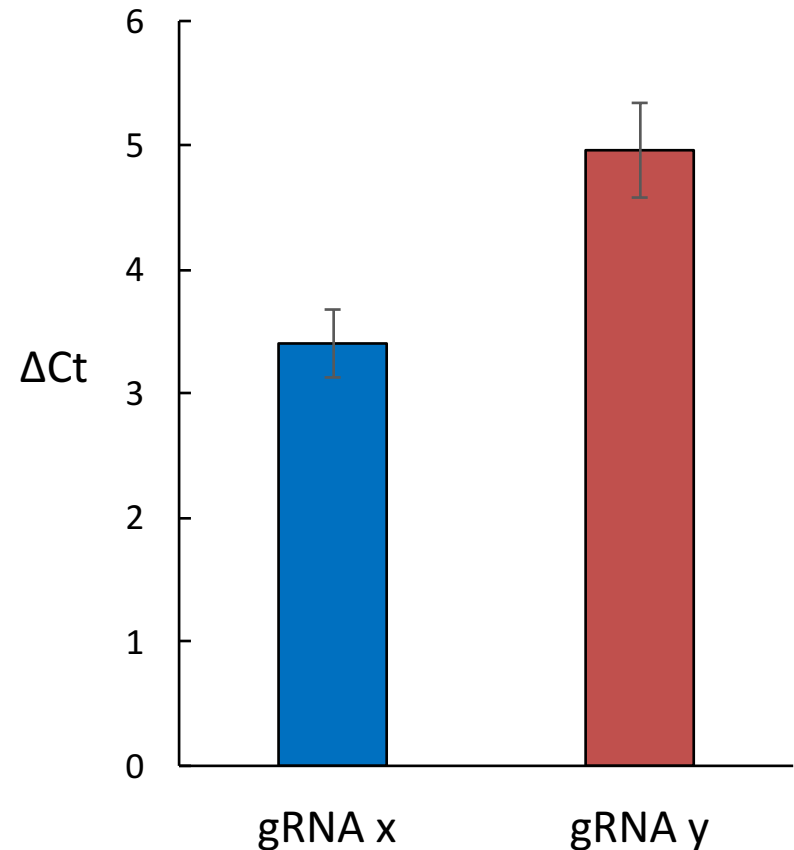
Sensitive and Specific Detection of gRNAs

Multi gRNA edits require specific assays

Taqman assays are specific for each gRNA



Expression differences *in vivo* with dual gRNA AAV



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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

Single Primer Approaches Achieve Many Goals

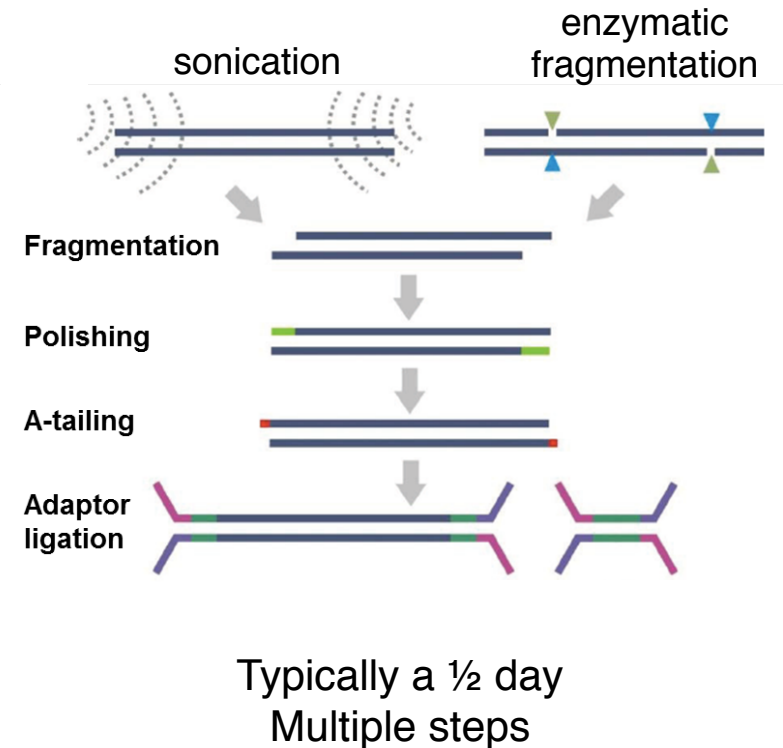
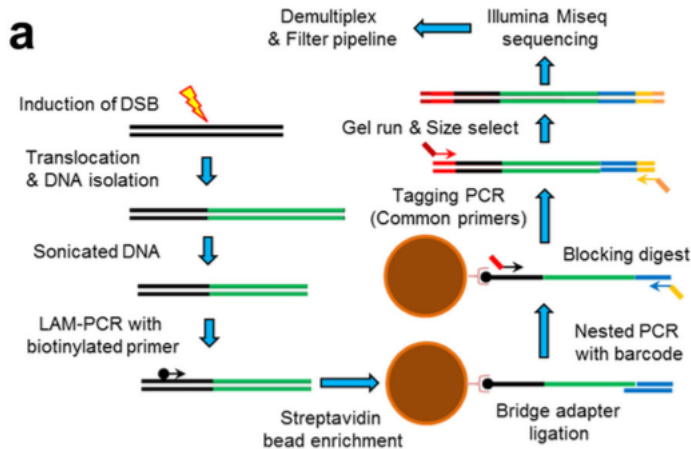
While effective, these approaches (HTGTS, AMP-Seq) can be cumbersome

Genome-wide detection of DNA double-stranded breaks induced by engineered nucleases

Richard L. Frock^{1,2,3,4}, Jiazhi Hu^{1,2,3,4}, Robin M. Meyers^{1,2,3}, Yu-Jui Ho^{1,2,3}, Erina Kii^{1,2,3}, and Frederick W. Alt^{1,2,3,5}

Anchored multiplex PCR for targeted next-generation sequencing

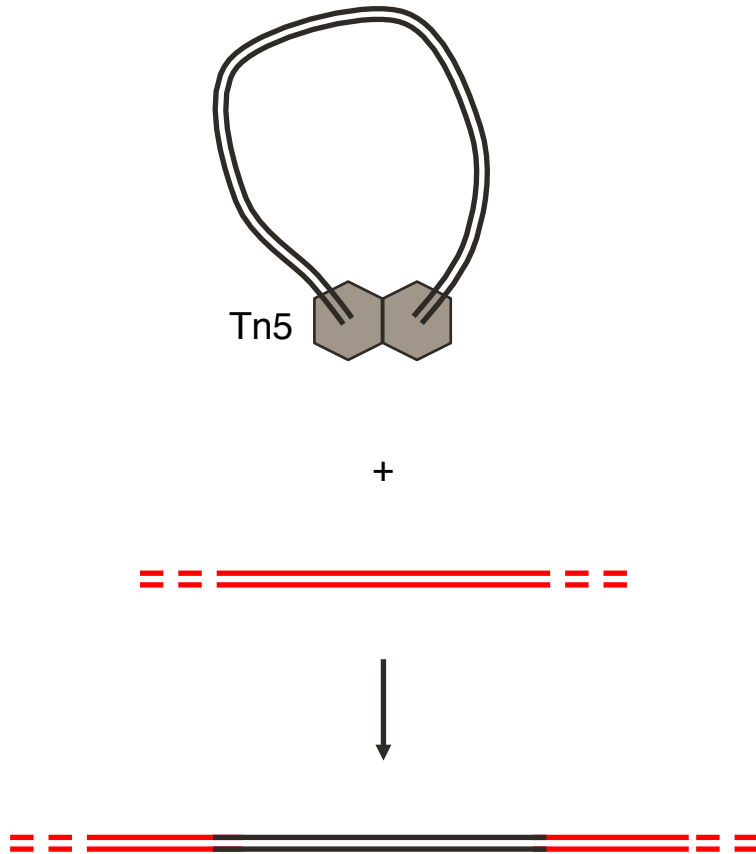
Zongli Zheng^{1,2}, Matthew Liebers¹, Boryana Zhelyazkova¹, Yi Cao¹, Divya Panditi¹, Kerry D Lynch¹, Juxiang Chen^{1,3}, Hayley E Robinson¹, Hyo Sup Shim^{1,4}, Juliann Chmielecki⁵, William Pao⁵, Jeffrey A Engelman⁶, A John Iafrate^{1,6} & Long Phi Le^{1,6}



Adey, A., et al.(2010). Rapid, low-input, low-bias construction of shotgun fragment libraries by high-density in vitro transposition. *Genome Biology*, 11(12), R119. <http://doi.org/10.1186/gb-2010-11-12-r119>

Transposase Engineering for Sequencing

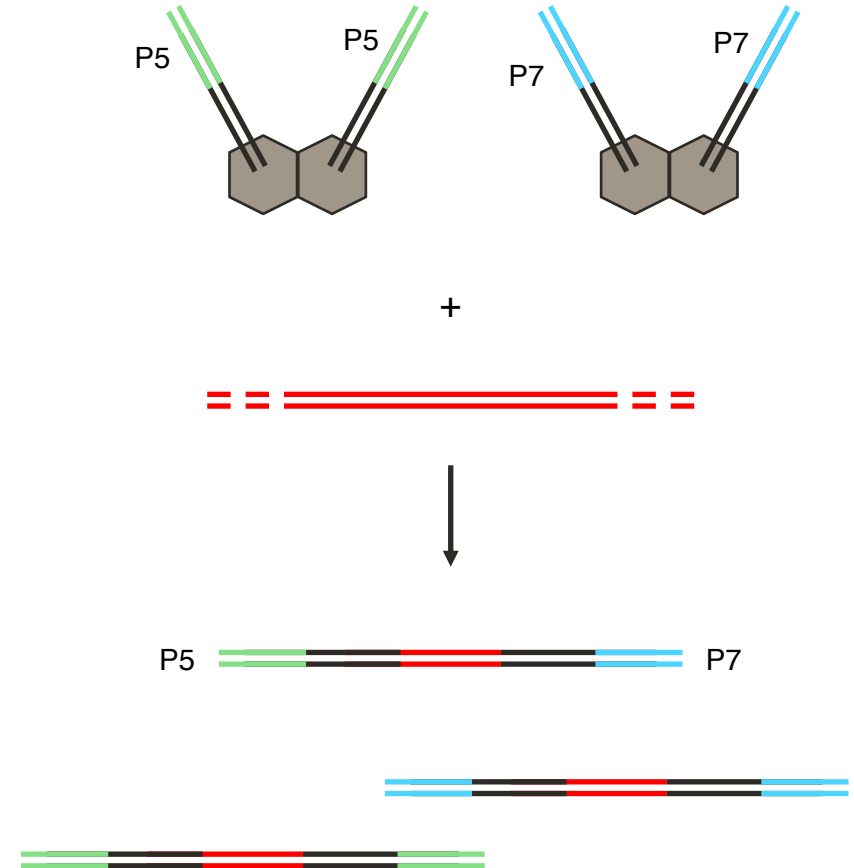
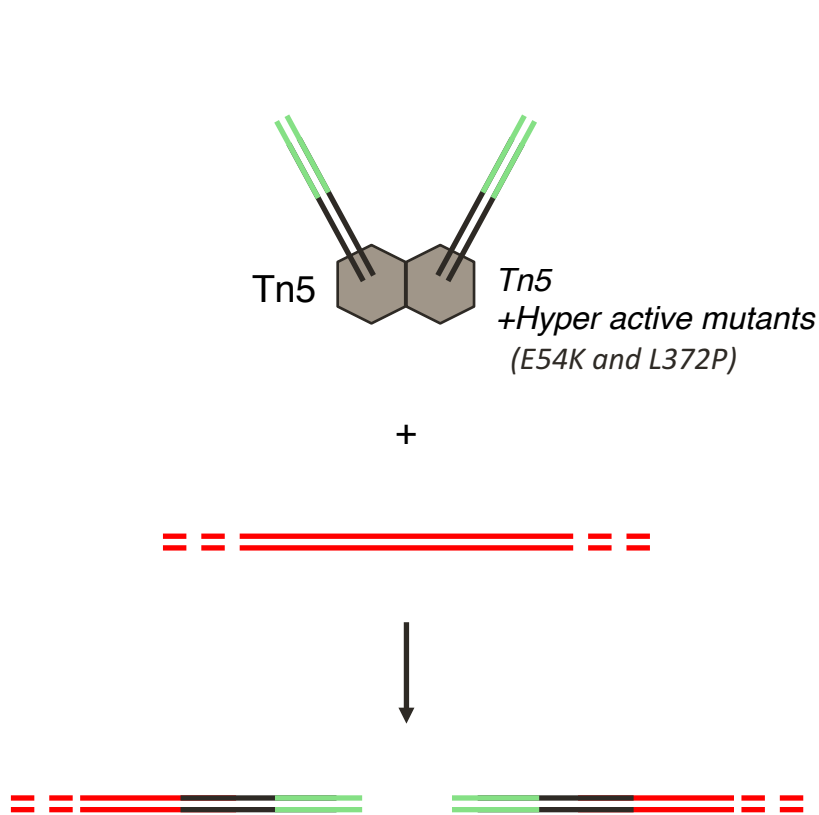
Highly efficient and scalable



Adey, A., et al.(2010). Rapid, low-input, low-bias construction of shotgun fragment libraries by high-density in vitro transposition. *Genome Biology*, 11(12), R119.
<http://doi.org/10.1186/gb-2010-11-12-r119>

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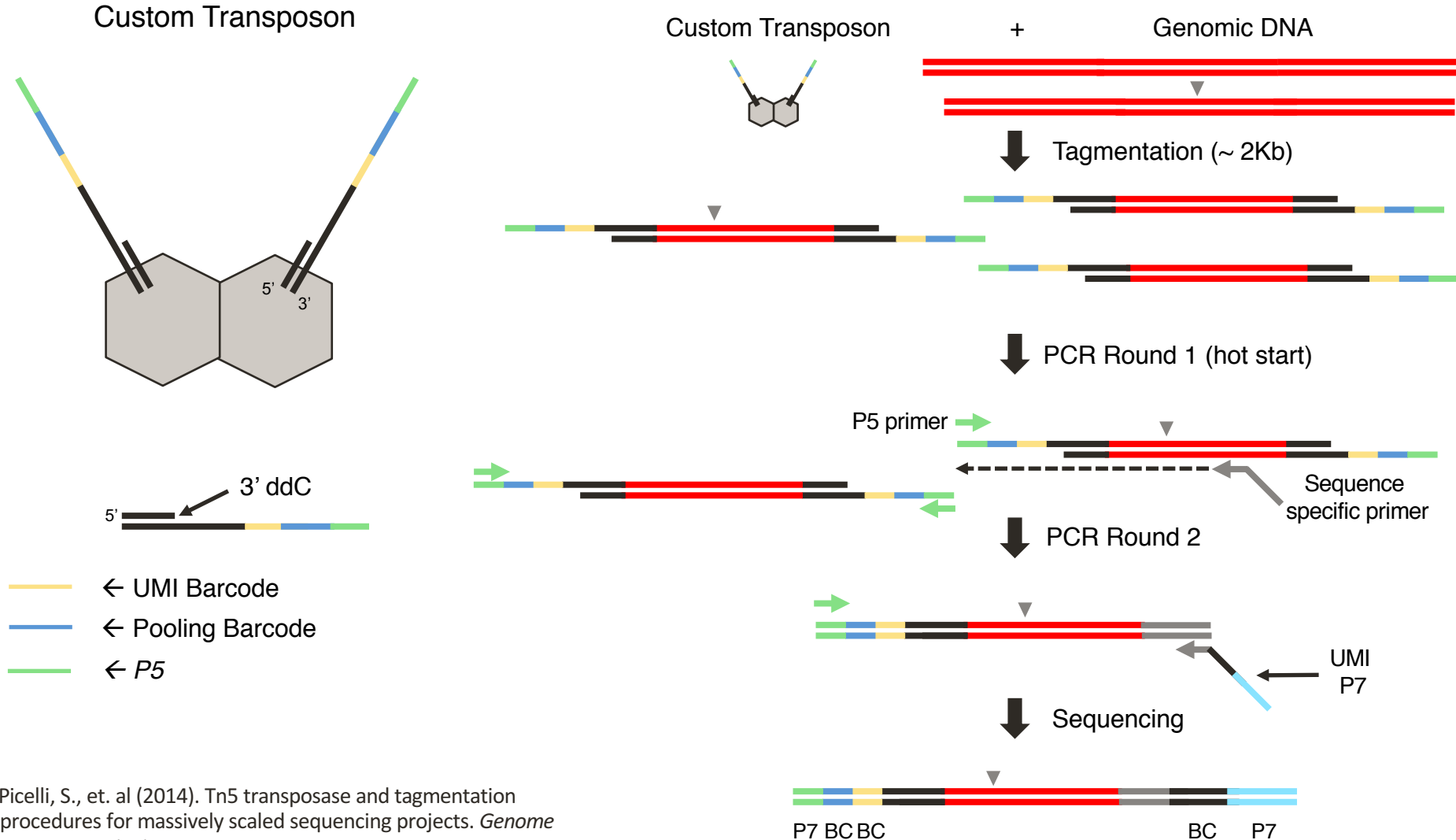


10 min single reaction

Adey, A., et al.(2010). Rapid, low-input, low-bias construction of shotgun fragment libraries by high-density in vitro transposition. *Genome Biology*, 11(12), R119. <http://doi.org/10.1186/gb-2010-11-12-r119>

Uni-Directional Targeted Sequencing (UDiTaS)

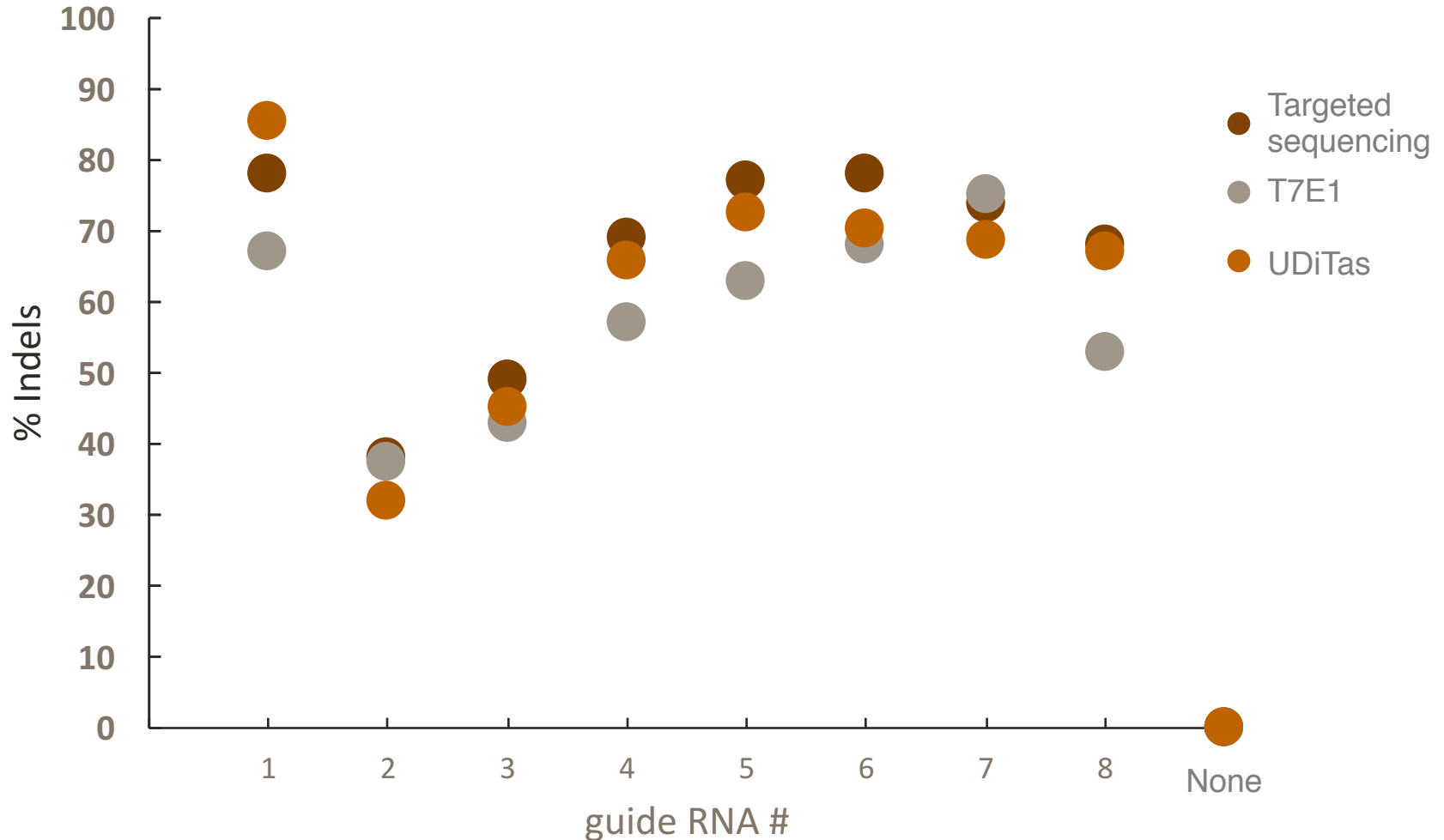
Blending tagmentation and AMP-seq



Picelli, S., et. al (2014). Tn5 transposase and tagmentation procedures for massively scaled sequencing projects. *Genome Research*, 24(12), 2033–2040.

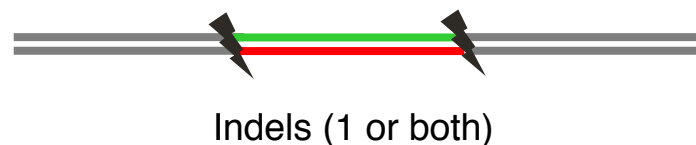
Comparison of Small Indel Measurements

UDiTaS correlates well with targeted sequencing and T7E1 assays



Intra-Chromosomal Rearrangement Detection

Dual guide edits have multiple possible outcomes



Digital Droplet PCR: measures the ratio of 2 qPCR assays on single molecules of genomic DNA

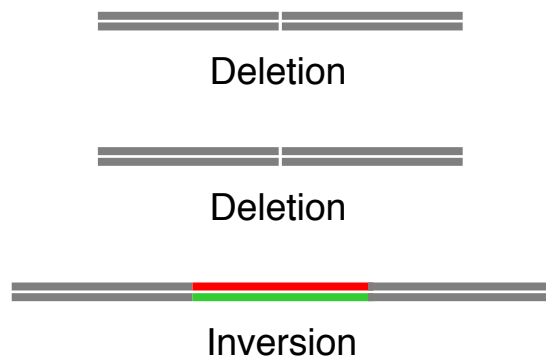


Uditas: counts the sequences post junction

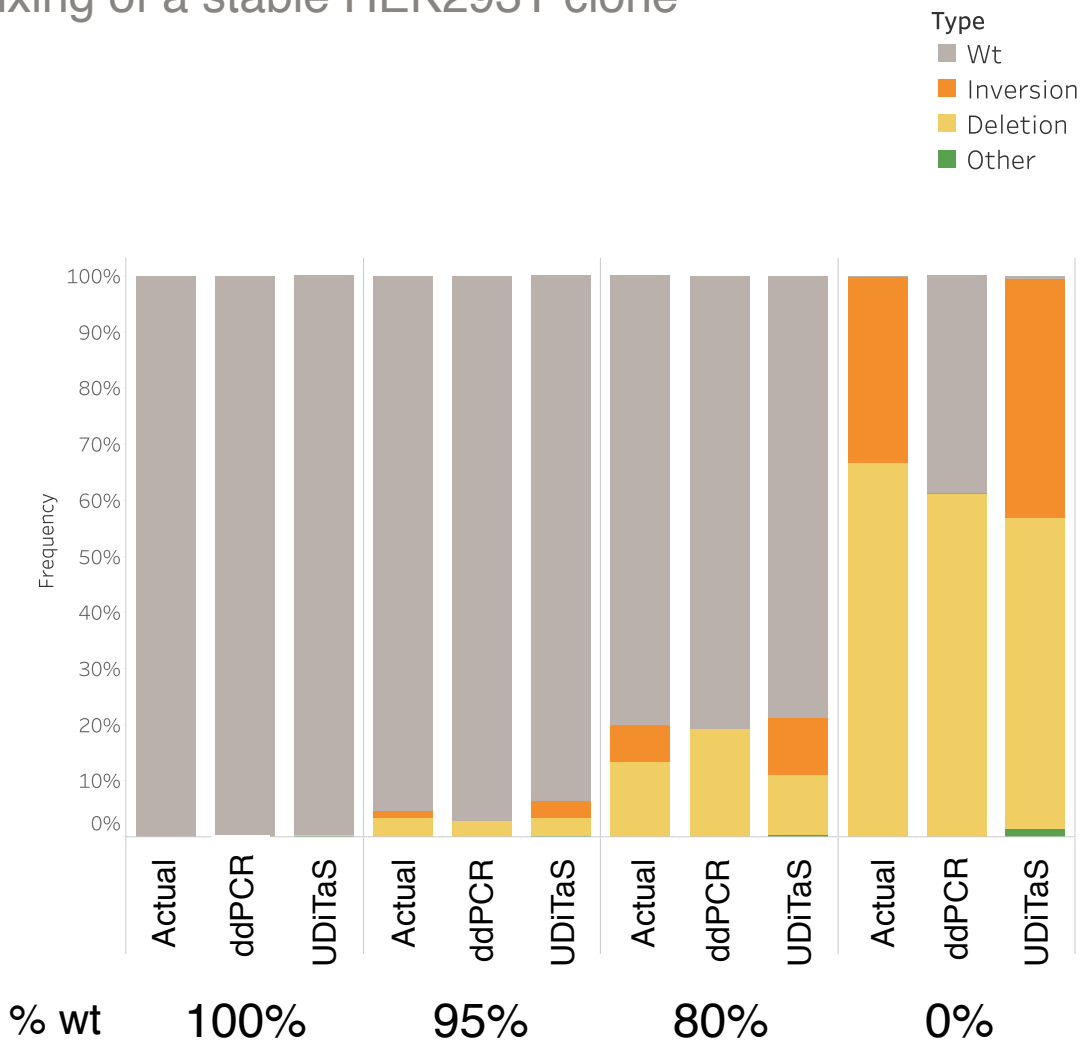
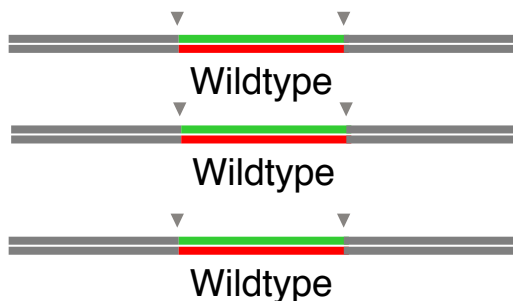
Intra-Chromosomal Rearrangement Detection

Validation using genomic DNA mixing of a stable HEK293T clone

Stable HEK293T Clone

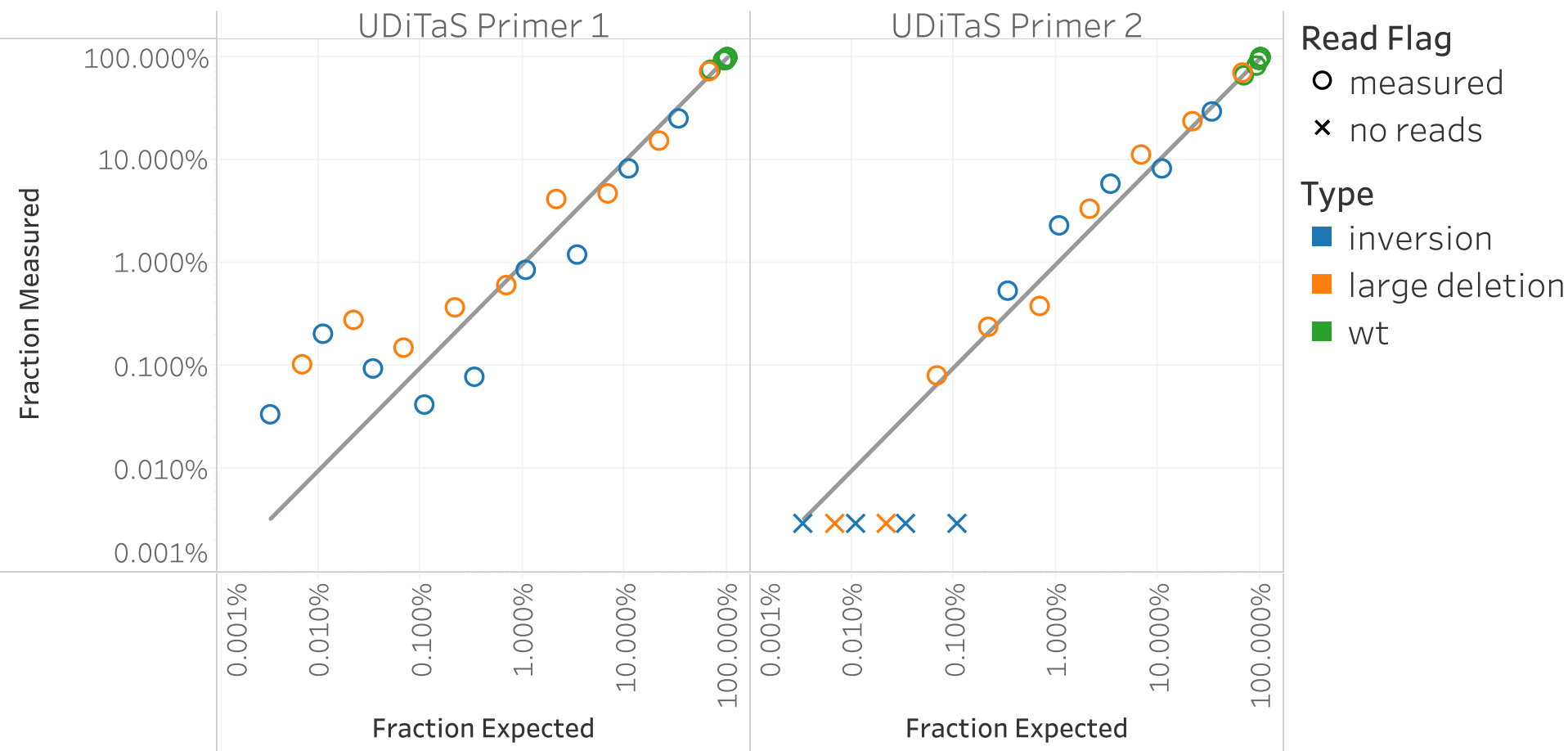


Parent HEK293



Intra-Chromosomal Rearrangement Detection

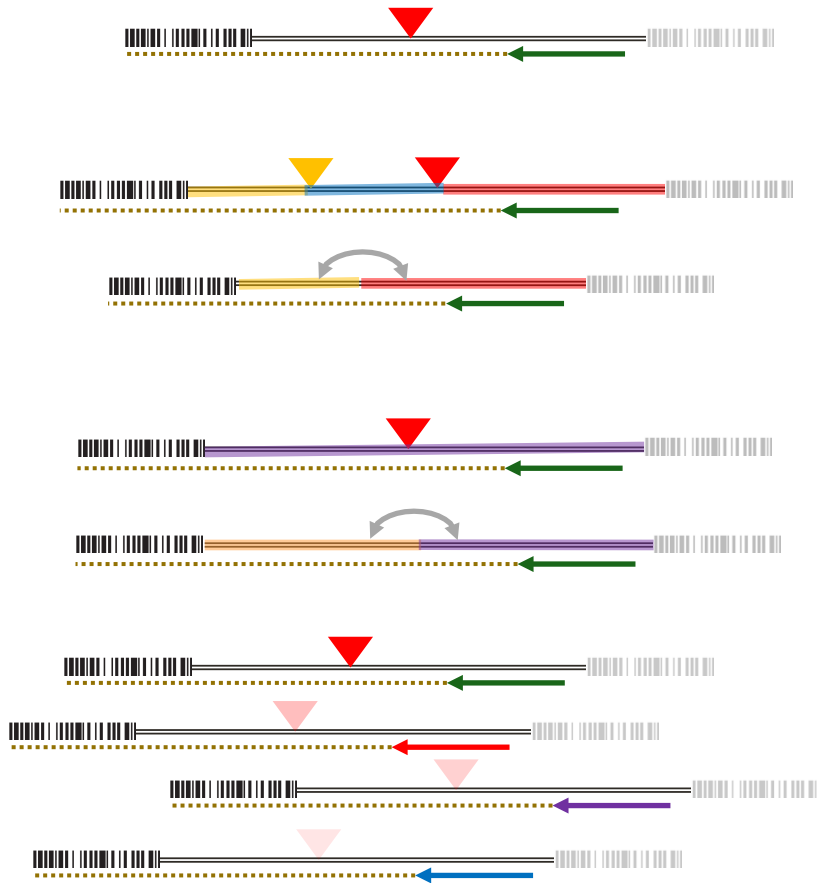
Follow up experiment defines LLOD (limited by input material and sequencing depth)



3,500 input genomes

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
3. Translocation discovery and quantitation
4. Multiplexing assays
5. Robust and shorter process

Summary

- We can make fully synthetic single gRNAs of high quality
- Pharmacokinetics: high sensitivity and specificity assays measure drug levels
- Pharmacodynamics: UDiTaS is a simple, robust method for capturing complex editing events in a single reaction

Reshica Baral
Luis Barrera
Dawn Ciulla
Cecilia Fernandez
Ari Friedland
Georgia Giannoukos
Sebastian Gloskowski
Kiran Gogi
Jenn Gori
Fred Harbinski

Jack Heath
Joy Horng
Hari Jayaram
Morgan Maeder
Eugenio Marco
Rina Mepani
Andrew Sadowski
Will Selleck
Terence Ta
Chris Wilson

Bruce Eaton &
The i2 Pharma team