NIST Genome Editing Consortium Overview October 6, 2021 AEIC Fall meeting



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The value of Standards



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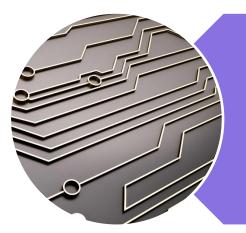
Standards are Enabling and Empowering! NIST



Validity of data



Confidence in and comparability of data



More rapid, integrated technology development



✓ Validity of data ✓ Confidence in and comparability of data ✓ More rapid, integrated technology development

Common Understanding (terms, data interpretation)

STANDARDS

Common Practices



Common Requirements

Common

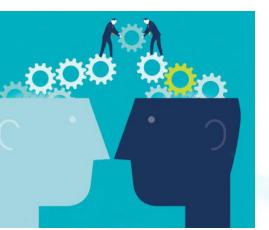
Operational &

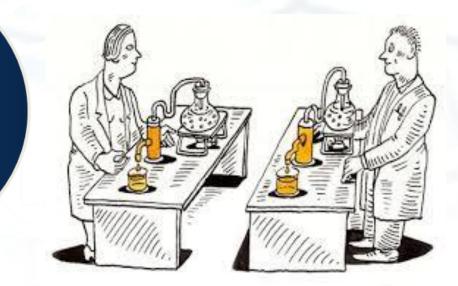
Management

Systems

Traceable Materials











MATERIAL MEASUREMENT LABORATORY

Reproducibility ≠ High Confidence

Just because a value can be reproduced does not mean you can be confident in the measurement

Sources of pre-analytical/analytical variability must be accounted for in order to appropriately tease out and attribute <u>true biologic signal</u>







How confident are you that the answer is correct?

What is the consequence if it is wrong?

...What can be done to understand if the answer is correct?



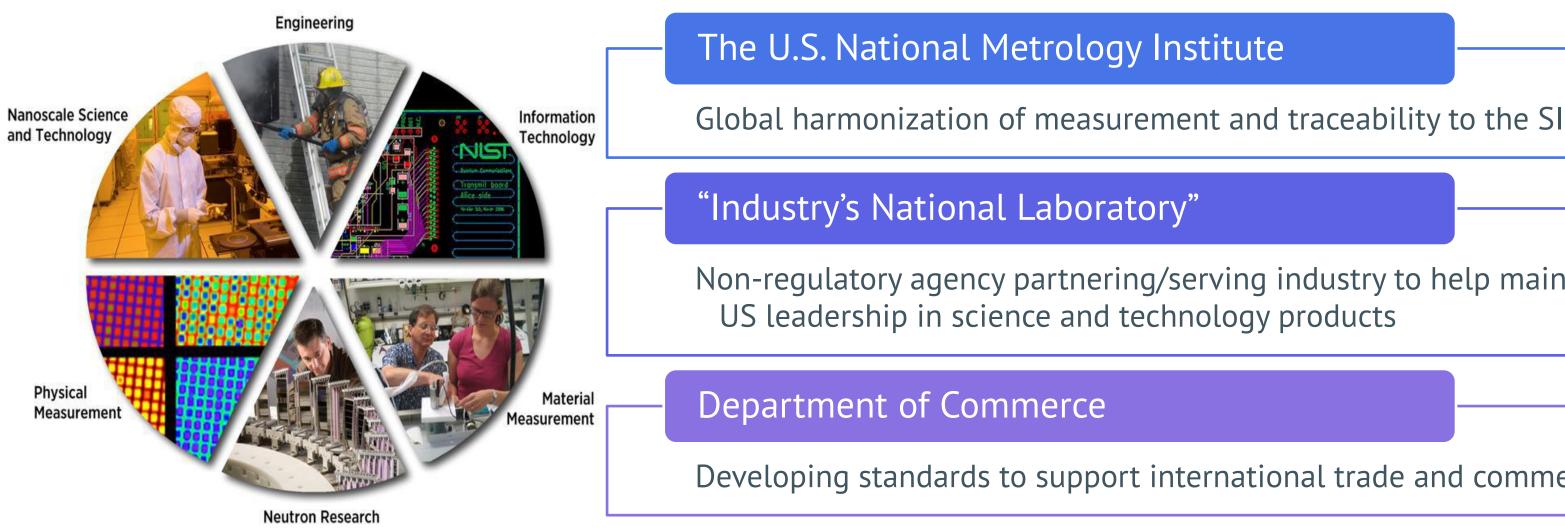
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it is wrong? rstand if the ?

NIST – National Institute of Standards & Technology NIST

MISSION

To promote U.S. innovation and industrial competitiveness by advancing **measurement** science, standards, and technology in ways that enhance economic security and improve our quality of life

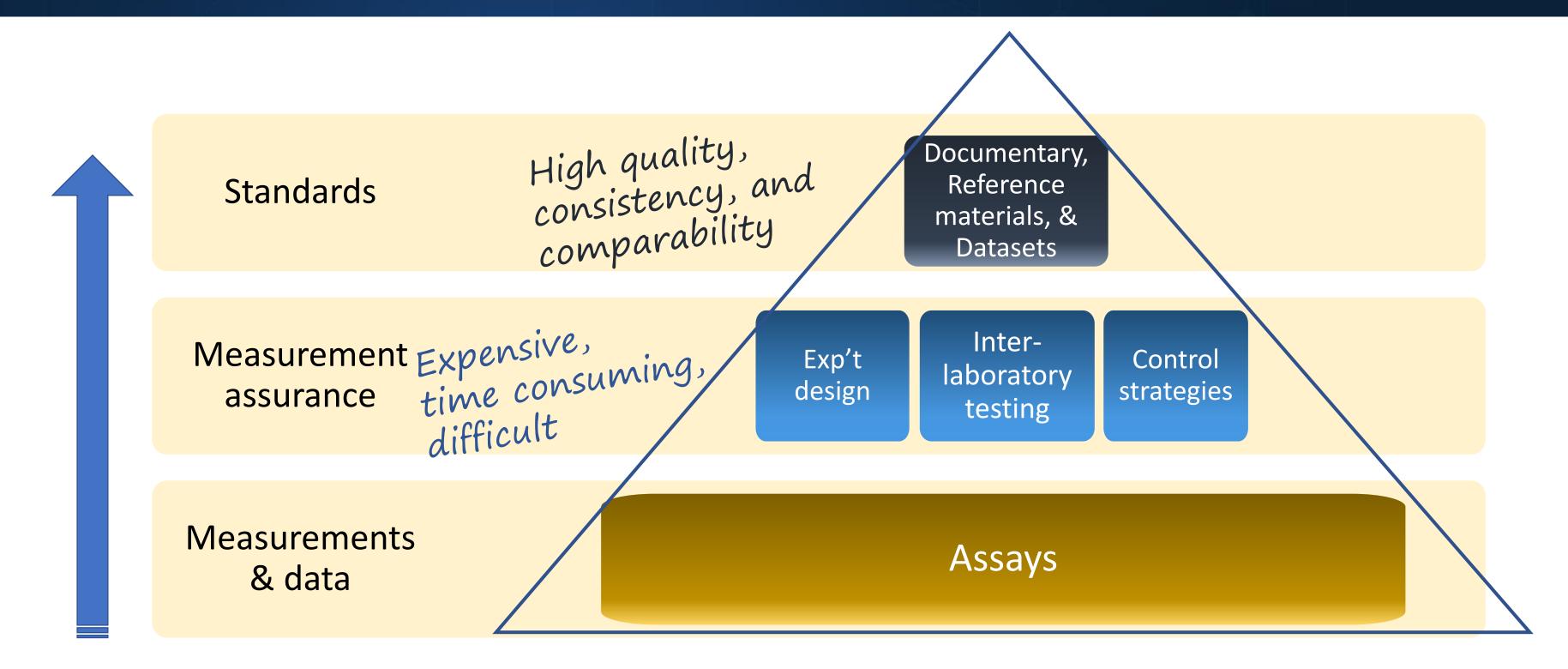




- Non-regulatory agency partnering/serving industry to help maintain

Developing standards to support international trade and commerce

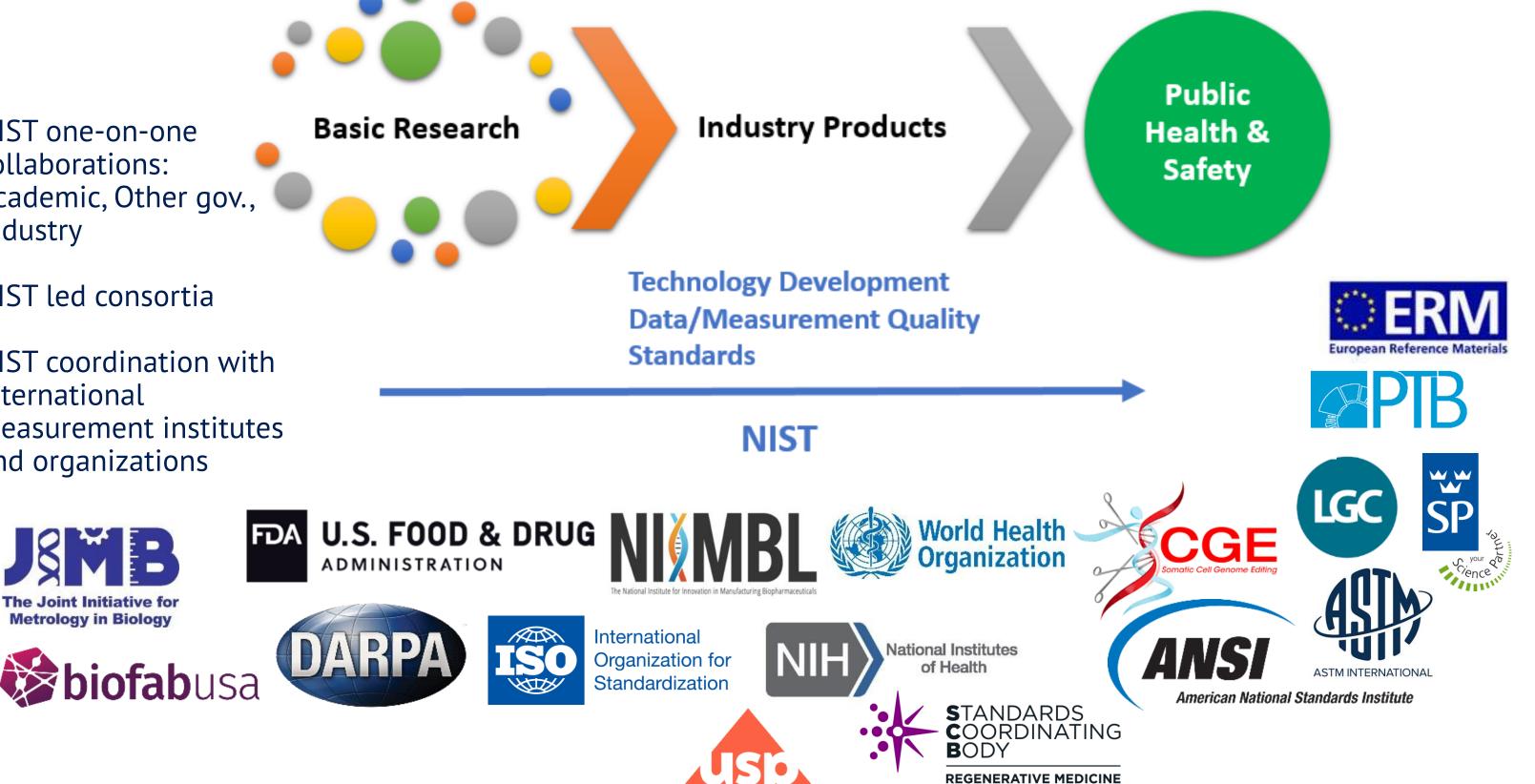
Advanced Biometrology: Measurement Assurance NIST



Demonstration of measurement assurance strategies: <u>https://www.nist.gov/mml/bbd/measurement-assurance-strategies</u>

How does NIST work with communities to meet needs? NIST

- NIST one-on-one collaborations: Academic, Other gov., Industry
- NIST led consortia
- NIST coordination with international measurement institutes and organizations



NIST-FDA Collaborations on Standards

Leveraging unique expertise

NIST engages in discussions and collaborates with industry and others on precompetitive technologies

NIST expertise in measurement sciences address specific analytical challenges

FDA scientific and regulatory expertise ensure that standards:

- do not conflict with FDA regulation and policy

- address significant regulatory challenges that recur across the field





Cytotherapy Volume 20, Issue 6, June 2018, Pages 779-784



Reports

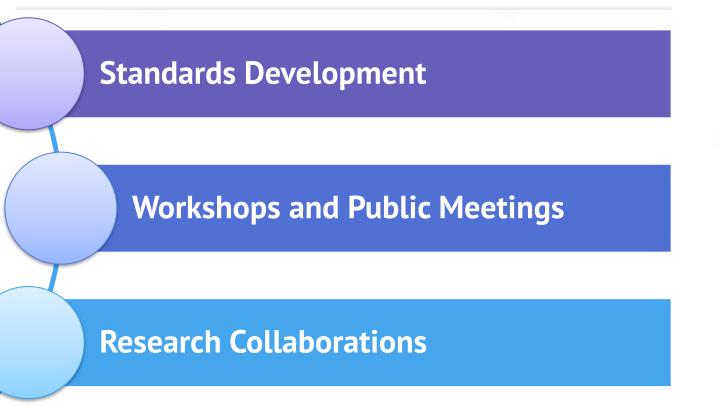
FDA and NIST collaboration on standards development activities supporting innovation and translation of regenerative medicine products

Judith A. Arcidiacono ¹ $\stackrel{\circ}{\sim}$ $\stackrel{\boxtimes}{\sim}$, Steven R. Bauer ¹, David S. Kaplan ², Clare M. Allocca ³, Sumona Sarkar ⁴, Sheng Lin-Gibson ⁴

Show more

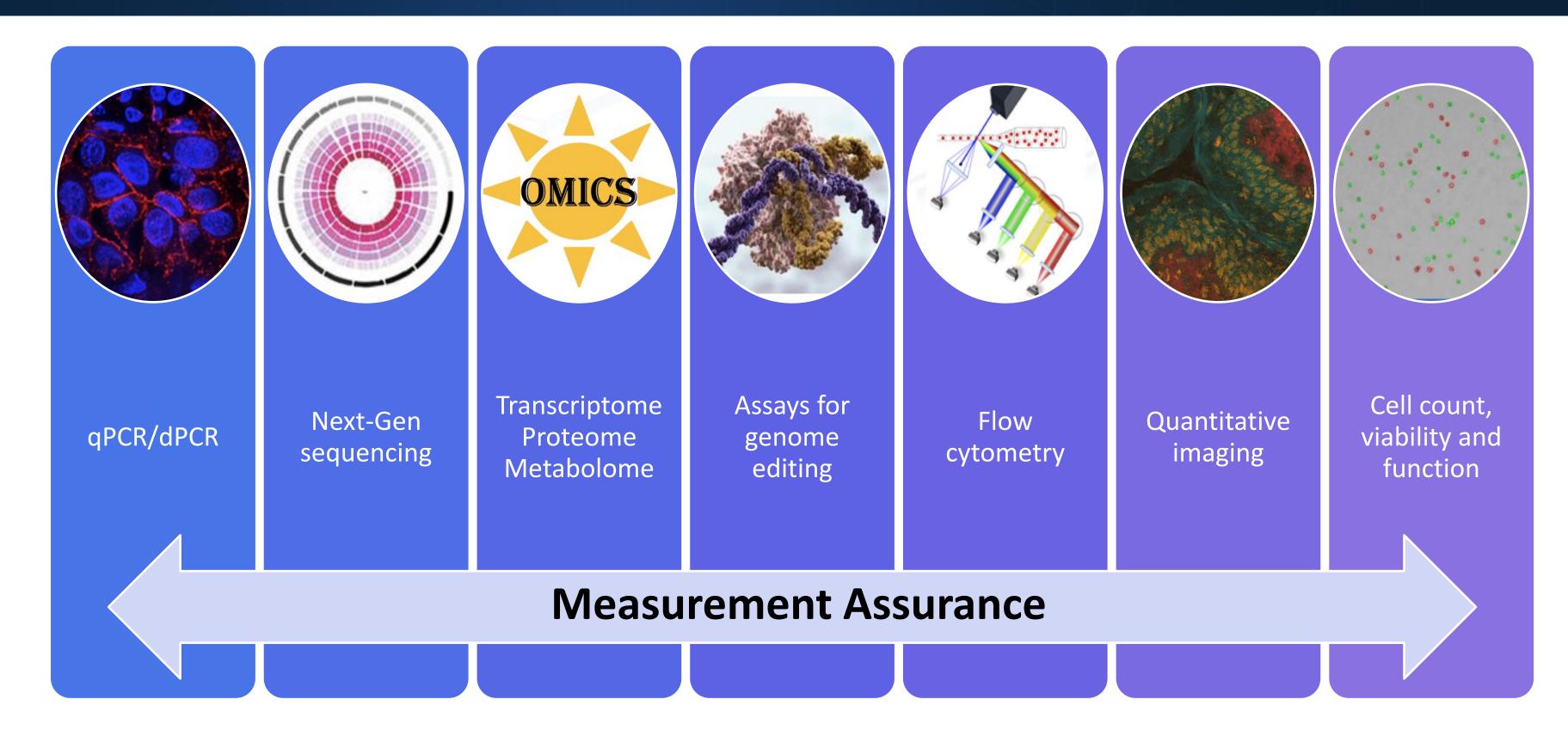
https://doi.org/10.1016/j.jcyt.2018.03.039

Get rights and content



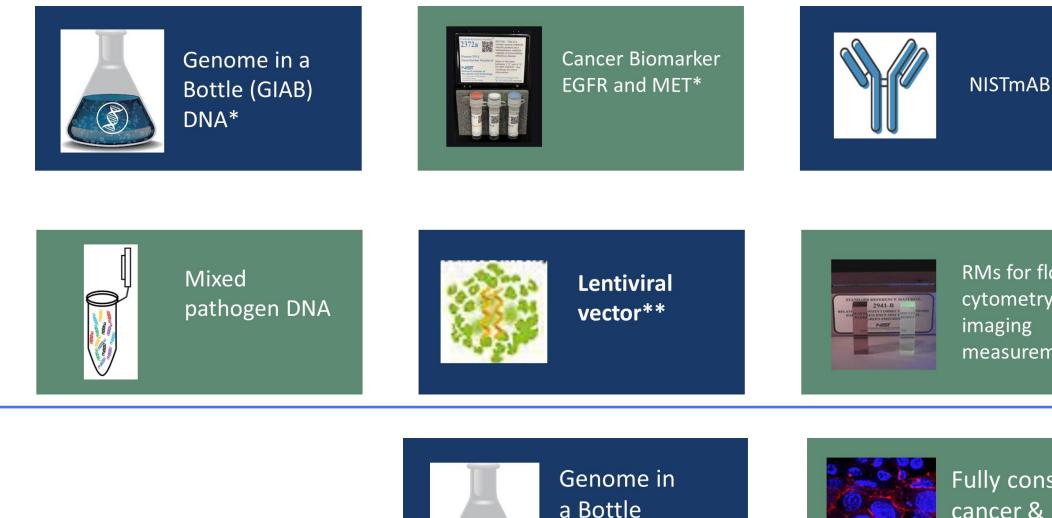
MATERIAL MEASUREMENT LABORATORY

Select Measurement platforms





Advanced biological reference materials NIST



Advanced "living" reference materials



Genetically tagged strain of yeast

(GIAB)

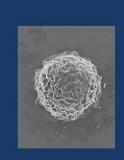
cells*



* Currently available ** High value material donation via MTA from an industry leader

RMs for flow cytometry and imaging measurements

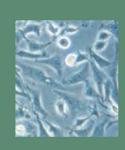
Fully consented cancer & normal cells



Jurkat cells with different VCNs**



Microbial whole cell RMs



NIST_CHO

NIST Consortia

New





E

GENOME EDITING CONSORTIUM

Provides authoritative characterization of benchmark human genomes

POC: Justin Zook

Addresses the measurements and standards needed to increase confidence and lower the risk

POC: Samantha Maragh

FLOW CYTOMETRY STANDARDS CONSORTIUM

Addresses the measurements and standards needed for flow cytometry applications

POC: Lili Wang

NIST

New



RAPID MICROBIAL TESTING METHODS CONSORTIUM

Addresses the measurements and standards needed to increase confidence and lower the risk

POC: Nancy Lin

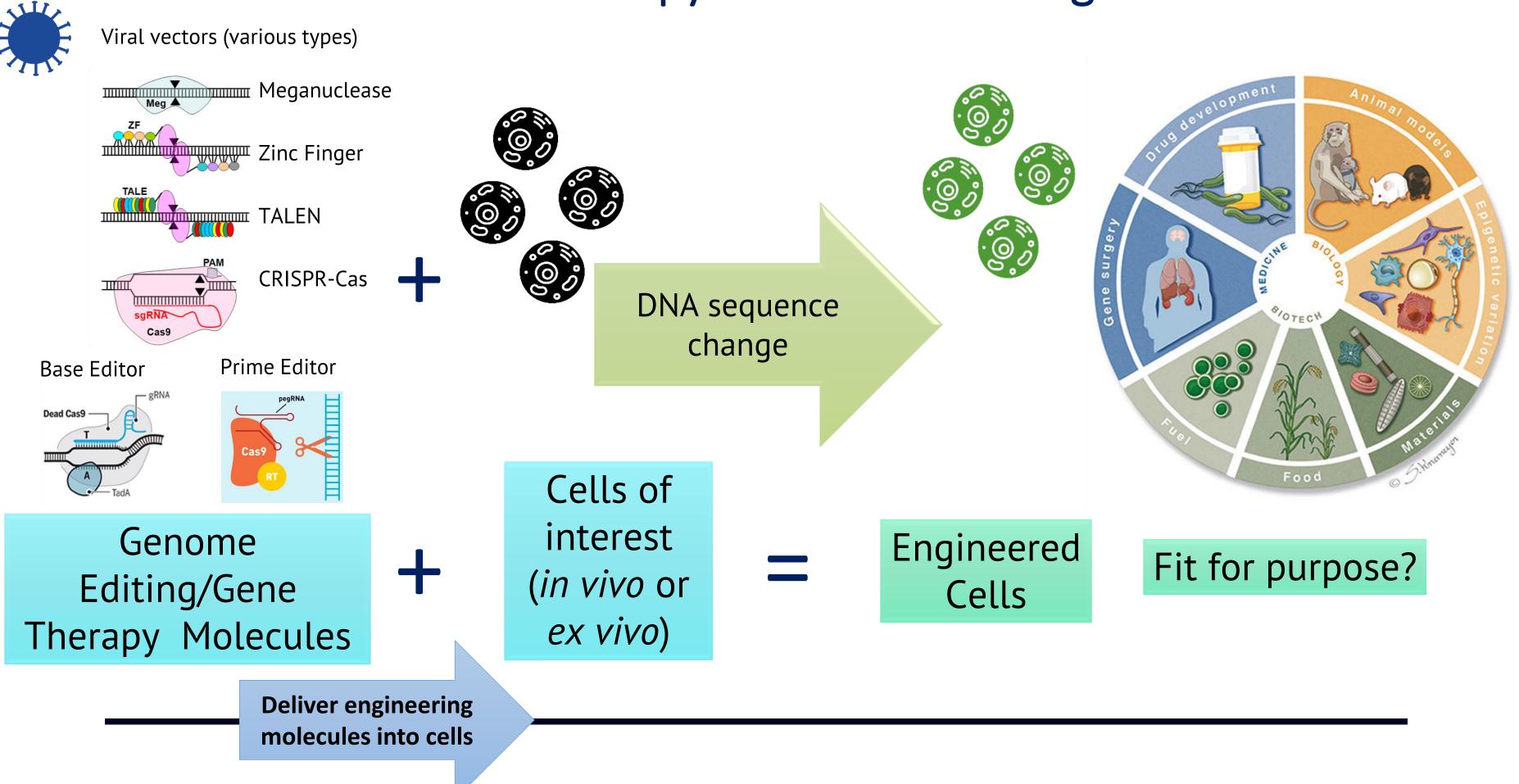
Genome Editing overview



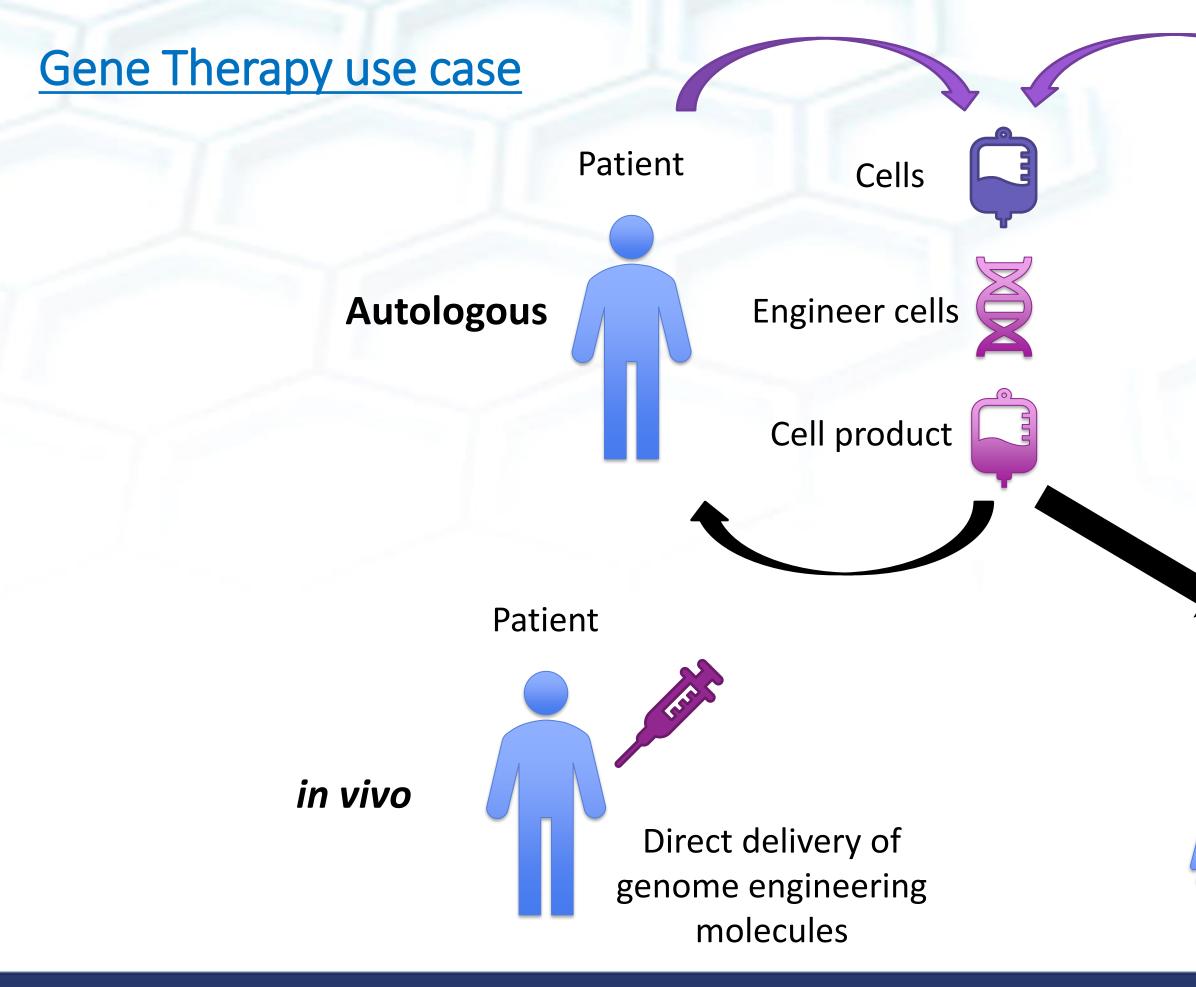
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Gene Therapy & Genome Editing





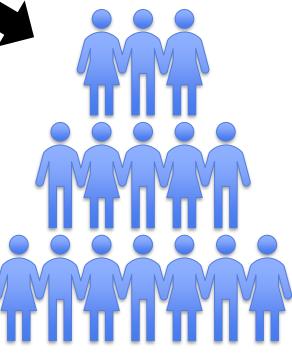






Allogenetic

Patients



MATERIAL MEASUREMENT LABORATORY

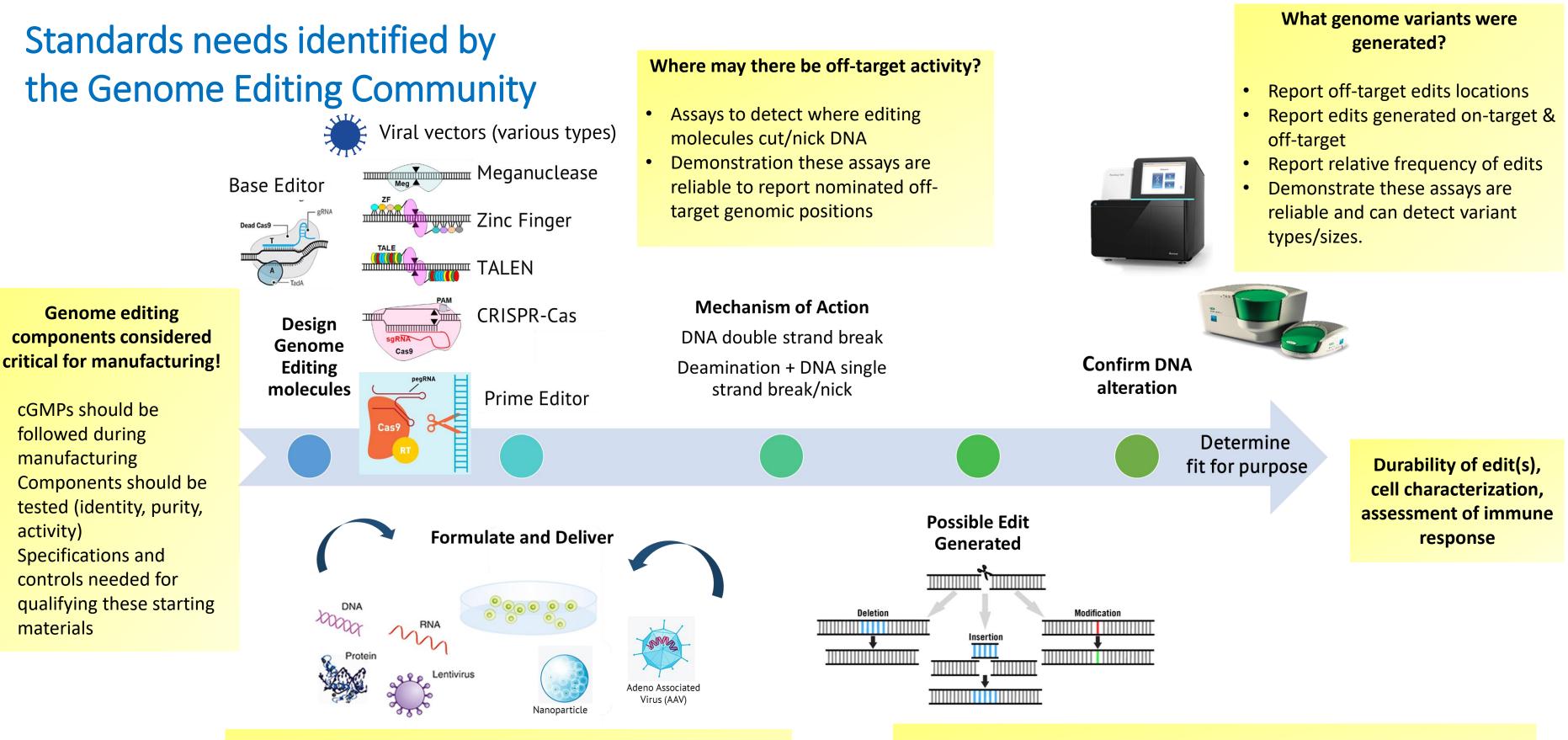
Standards needs identified by the Genome Editing Community

followed during

manufacturing

activity)

materials



How do we evaluate and compare delivery systems?

Delivery systems are varied and expanding, may be part of an *ex vivo* cell engineering process or your final product, but there are no norms on how to evaluate them and compare

- •

What are resources or practices to get most use our of data, understand if data is comparable, and understand bioinformatics performance?

Metadata norms and infrastructure to capture and share metadata Standard datasets and interlab comparisons

Confidence in existing assays

New assays for unmet measurement needs

Control materials

or contraction of the second s NIST **Genome Editing** Program

(consortium + other NIST projects)

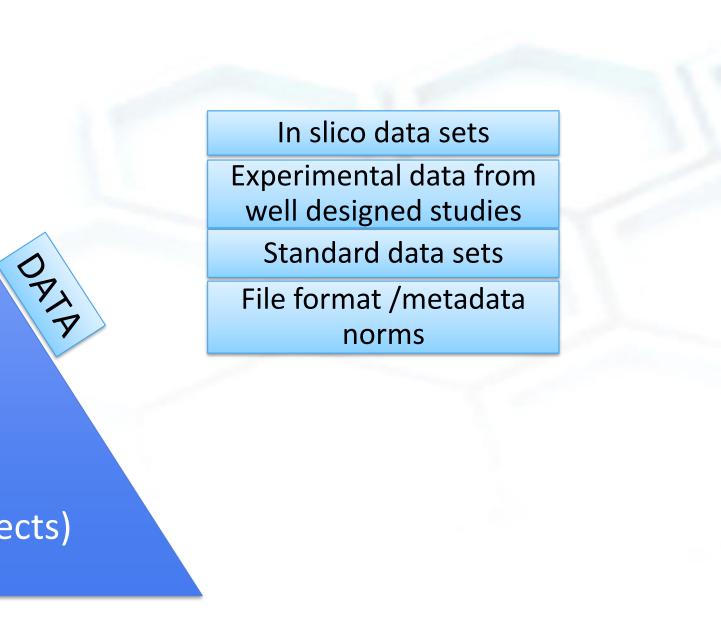
Recommended practices?

DOCUMENTARY

Standard lexicon

Metadata minimum information standards Guidelines for comparing informatics pipelines





MATERIAL MEASUREMENT LABORATORY

Select NIST Genome Editing Program Projects NIST

of Health

St. Jude Children's

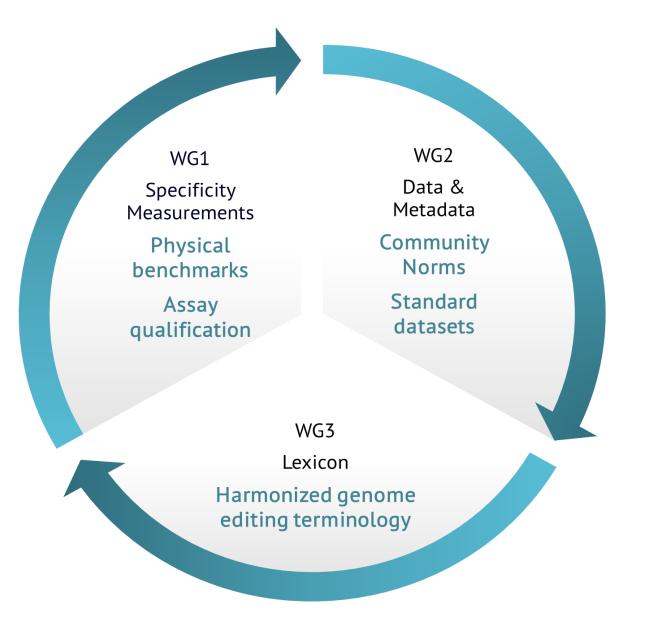
Research Hospital

ALSAC . Danny Thomas, Founde

CHANGE-seq

NIST Genome Editing Consortium (launched October 2018)

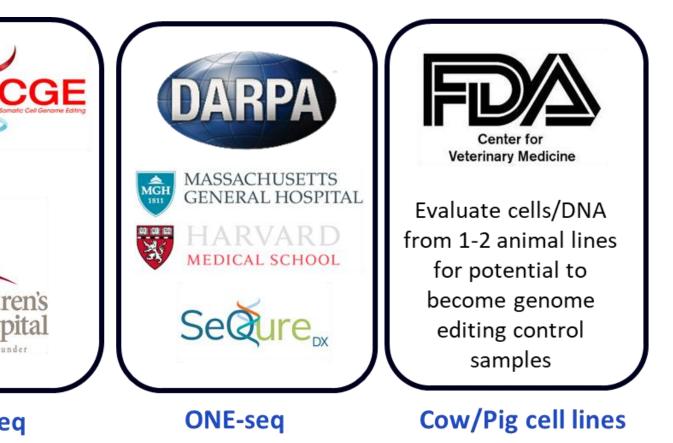
Collaboration with genome editing stakeholders to define <u>measurement challenges for utilizing existing measurement</u> <u>capabilities</u> and develop shared solutions

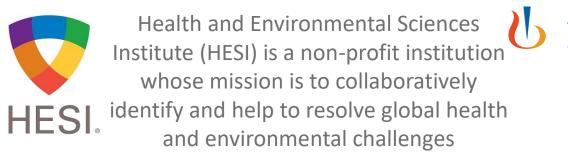


Ongoing/extended through Dec, 1 2025

NIST characterization of developing measurement capabilities (e.g. "off-target assays")

Collaboration with the assay developers and government to <u>add measurement assurance</u> (including bioinformatics) and SOPs for recently developed assays of broad interest for the genome editing field for evaluating precision of genome editing tools used to engineer cells







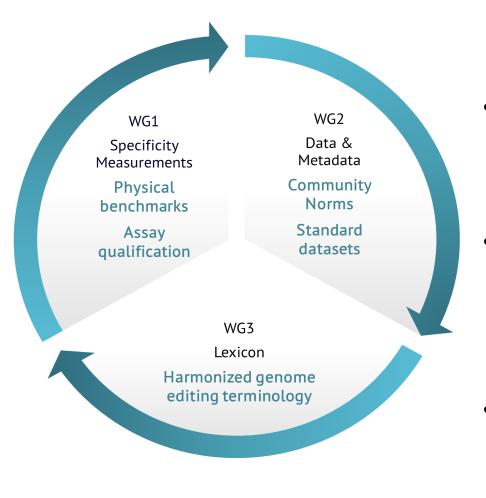
INDUCE-seq

NIST Genome Editing Consortium (launched October 2018)

MISSION

Convene experts across academia, industry, non-profit & government to addresses the measurements and standards needed to increase confidence of utilizing genome editing technologies in research and commercial products

ORGANIZATION



MEMBER BENEFITS

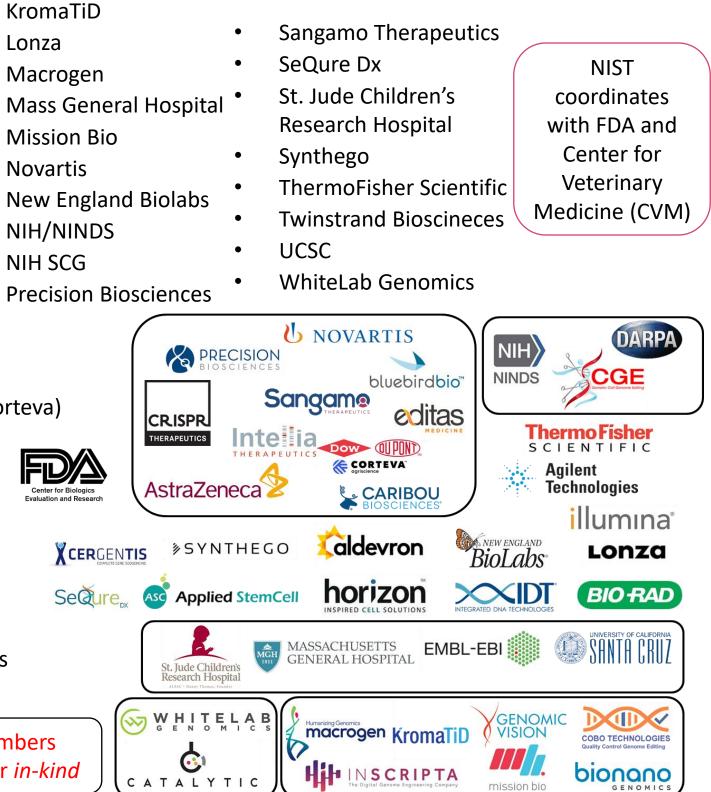
- Access to a neutral forum for addressing precompetitive needs
- Participation in the development of experimental benchmarks, guidelines and terminology
- Access to tools developed by the consortium ahead of public release

- Agilent
- Aldevron
- Applied StemCell
- AstraZeneca
- Bionano Genomics
- Bio-Rad
- Bluebird bio
- Caribou Biosciences
- Catalytic Data Science
- Cergentis
- .
- COBO Technologies
- CRISPR Therapeutics
- DARPA
- DowDuPont Agroscience (Corteva)
- Editas Medicine
- EMBL-EBI
- FDA CBER
- Genomic Vision
- Horizon Discovery
- Illumina
- Inscripta
- Integrated DNA Technologies
- Intellia Therapeutics

Cost sharing model. All members contribute \$20,000 annually or *in-kind*

NIST

MEMBERS

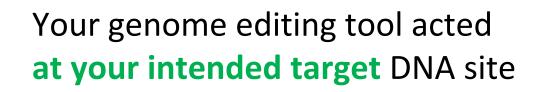


Genome Editing Challenges of note

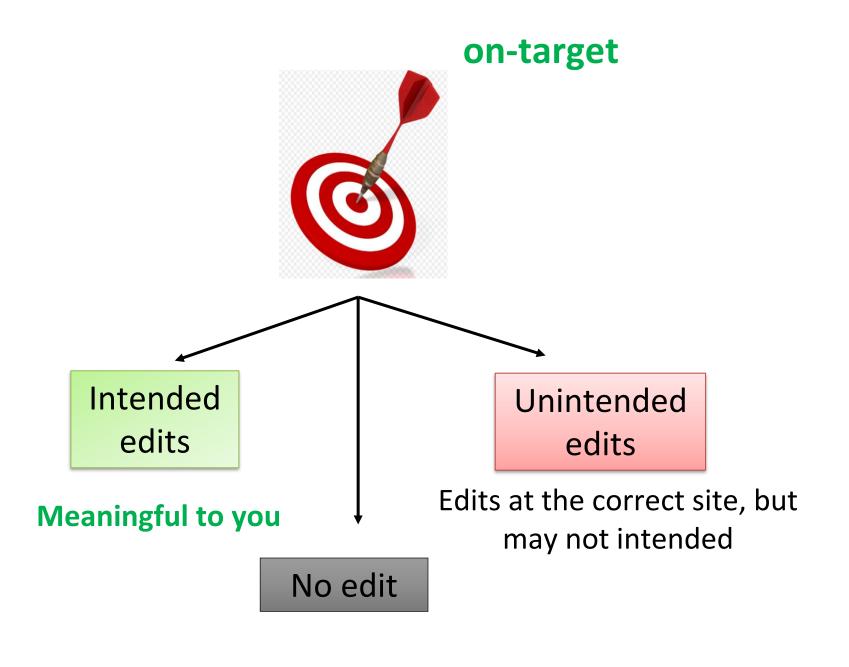


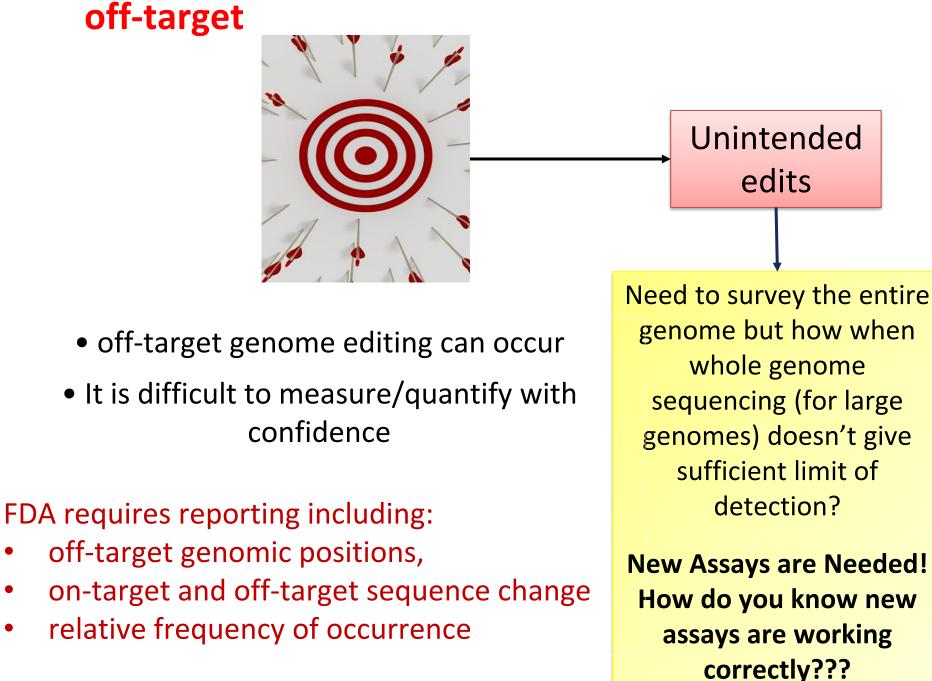
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Outcomes of Genome Editing



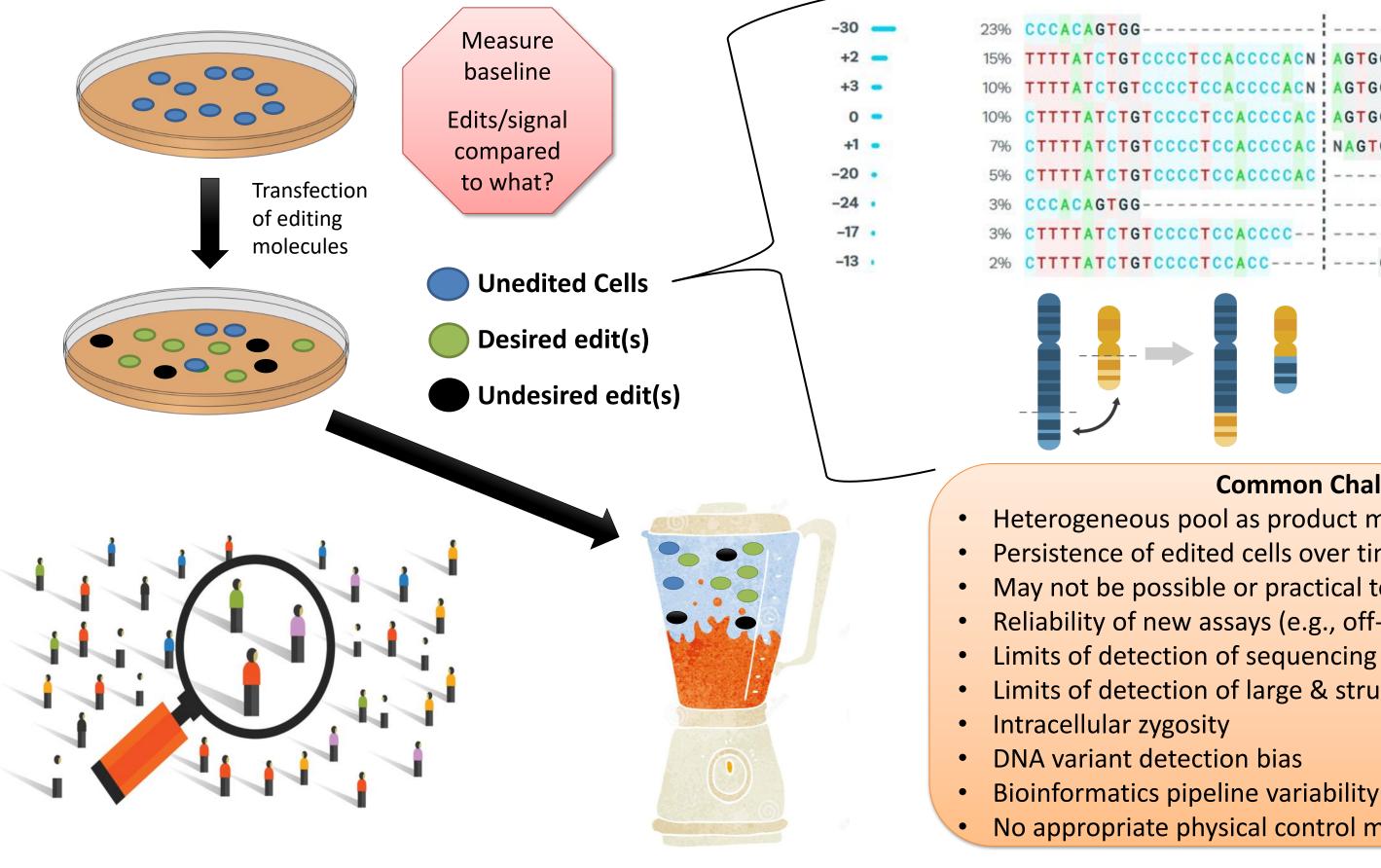






Your genome editing tool acted at a DNA site different from your target

Genome Editing Outcomes are Complex!





G G	AGCCCCATCCTTAGGCCTCCTC
GTCCCCTCCACCCCACN	AGTGGGGCCACTAGGGACAGN GATTGGTGACAGAAA
GTCCCCTCCACCCCACN	AGTGGGGCCACTAGGGACAGNN GATTGGTGACAGAA
TGTCCCCTCCACCCCAC	AGTGGGGCCACTAGGGACAGGATTGGTGACAGAAAAG
TGTCCCCTCCACCCCAC	NAGTGGGGCCACTAGGGACAGGATTGGTGACAGAAAA
TGTCCCCTCCACCCCAC	GATTGGTGACAGAAAA
G G	CAGAAAAGCCCCATCCTTAGGCCTCCTC
TGTCCCCTCCACCCC	GACAGGATTGGTGACAGAAAAG
TGTCCCCTCCACC	GGGCCACTAGGGACAGGTGACAGAAAA

This type of heterogeneity within a cell pools is possible at on-target and each off-target site

Common Challenges:

Heterogeneous pool as product most often Persistence of edited cells over time (fitness) May not be possible or practical to do single cell analysis Reliability of new assays (e.g., off-target nomination assays) Limits of detection of large & structural variants No appropriate physical control materials

How confident are you that the answer is correct?

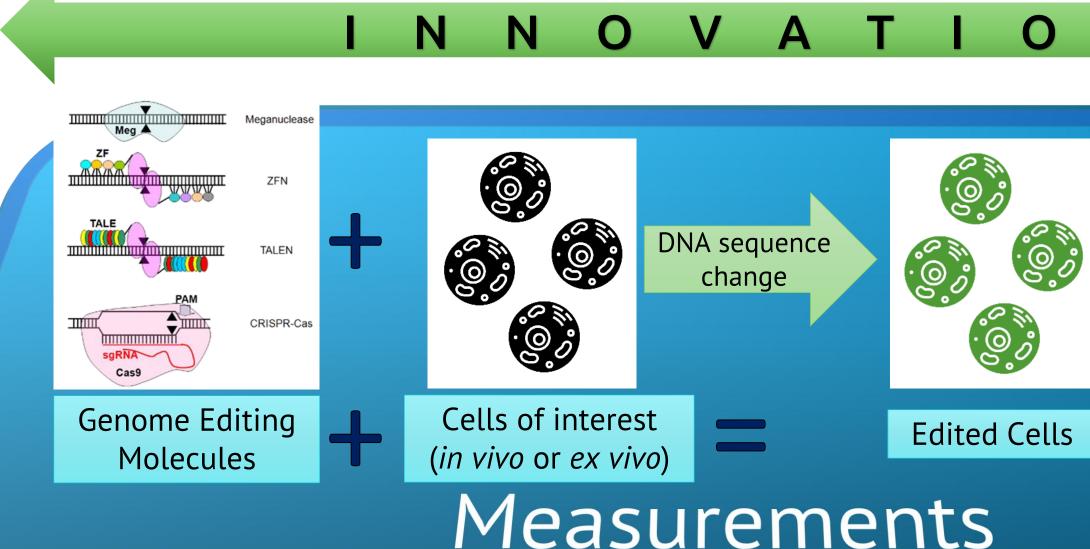
What is the consequence if it is wrong?

...What can be done to understand if the answer is correct?

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Genome Editing Process



Data

Metadata

Ν



Fit for purpose?

Specificity working group

Assay Qualification 1.

2. Physical control materials



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Condensed Genome Editing Process NST

Source sample Editing Target Editing molecule Editing molecule sequence Editing molecule formulation Delivery

Look editing molecule activity

Targeted

(e.g., T7 Endonuclease, TIDE, IDAA, ICE...)

Genome Wide off-target assays:

(e.g., BLESS/BLISS, GUIDE-seq, Digenome-seq, CHANGE-seq, SITE-seq, Discover-seq, END-seq, INDUCE-seq...)

Which assay(s) is/are critical to qualify? Is the assay generalizable? Will there be something new? What could be generalizable control material?

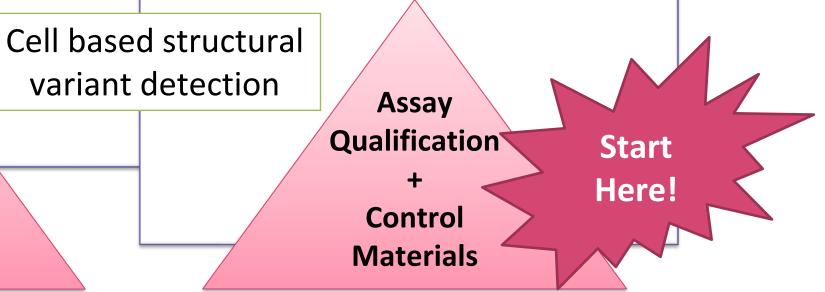
New Assays Assay Qualification Control Materials

Confirm sequence change

Targeted (sequencing, dPCR, hybridization)

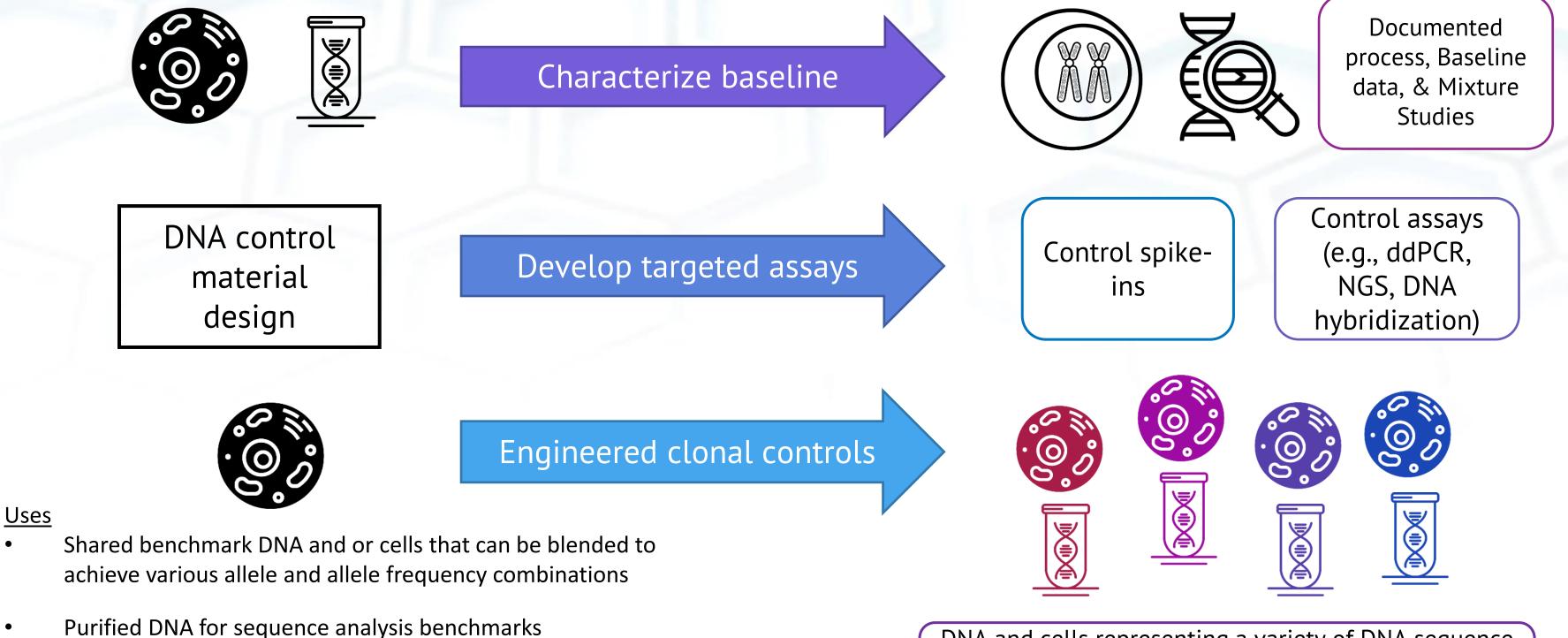
Whole exome sequencing

Whole genome sequencing



SPECIFICITY MEASUREMENTS: DNA CONTROLS AND INTERLAB STUDIES

Is your process, instrument, regents, operator (ect.) working? Controls that mimic genome edited cells/DNA and interlab studies



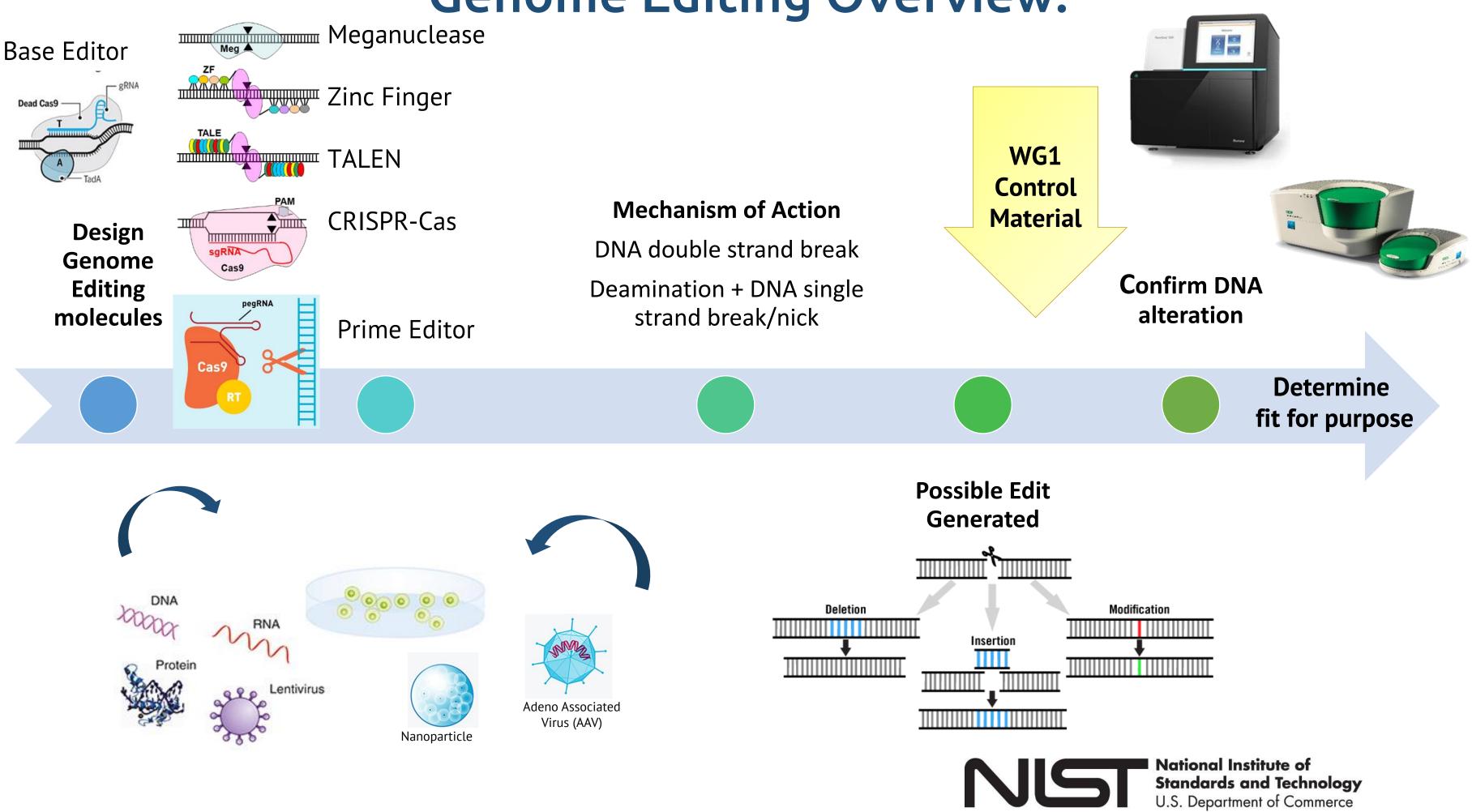
- Cells for sequence analysis benchmarks
- Purified DNA for manipulation (e.g. in vitro cleavage)
- Cells for manipulation



DNA and cells representing a variety of DNA sequence benchmarks "looks like a genome editing output" Deeply characterized at benchmark locations

MATERIAL MEASUREMENT LABORATORY

Genome Editing Overview:





Data & metadata working group

- Identify community norms for data formats and tools for benchmarking data analysis 1. including in silico and experimental data sets.
- Determine the type of **metadata** that would be needed to be shared, housed, and 2. interrogated from genome editing experiments



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Data & Metadata

✓ Transfer of Knowledge ✓ Reproducibility

What are the data we are generating?

When do we need to collect the metadata?

How do we store data and metadata?

Where do we store data and metadata

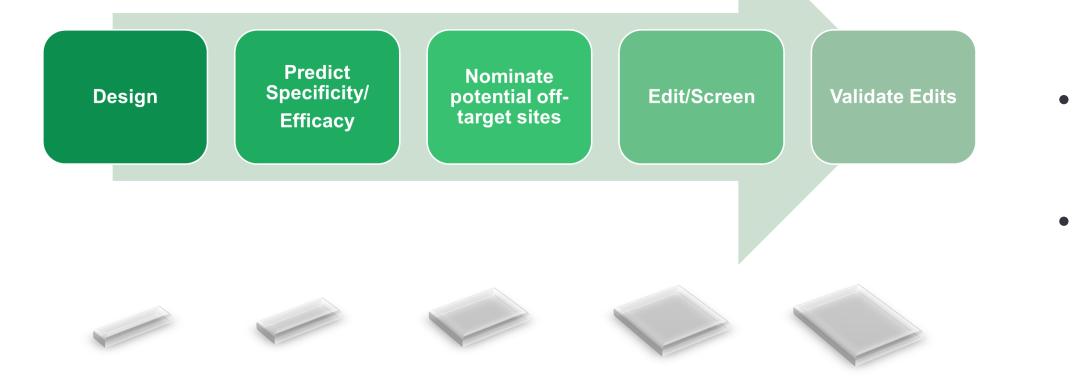
metadata from consortium studies & benchmark datasets as shared resources for the community



Data & Metadata use cases

Transfer/Document experimental process and results

- Within an organization (private)
- Between collaborators (limited access)
- Public databases (wide access)
- Regulatory agencies (e.g., FDA)







- Streamline integration of products with a well-established genome editing process
- Learning from and leveraging information within datasets (both public and private data)
- Benchmark datasets to compare bioinformatics pipelines and tools
- Exposure to potential customers/collaborators

Data & Metadata

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What are the data we are generating?

When do we need to collect the metadata?

How do we store data and metadata?

Where do we store data and metadata

metadata from consortium studies & benchmark datasets as shared resources for the community

Metadata file format (GEM)

JSON format

- 1 Human readable
- 2. Database ready
- 3. Can be validated (JSON Schema)
- Already used by NIST 4.
- 5. Easy to extend

Metadata entry curation: (how can this be normalized and low burden for a user)

		Metadata entry	Metadata ID	Metadata Type	Metadata example
					Genome engineering using the CRISPR-
Title		Study / publication title	study_title	string	Cas9 system
Targ	et	Species	target_species	string	Homo sapiens
Targ	et	Strain	target_strain	string	C57BL/6
Targ	et	Substrain	target_substrain	string	C57BL/6N
Targ	et	Biosample (Cell line/primary cell type)	target_biosample	Ontology	Ontology based e.g. EFO_0001185
Targ	et	Biosample modifications	target_biosample_modifications	string	Plasmid GFP introduction
Targ	et	Genome assembly	target_genome_assembly	string Controlled	hg19
Targ	et	Target (gene vs. other genomic region)	target_region	vocabulary	{gene body,enhancer,intergenic}

Metadata access

Design and feasibility of a database with easy user interface

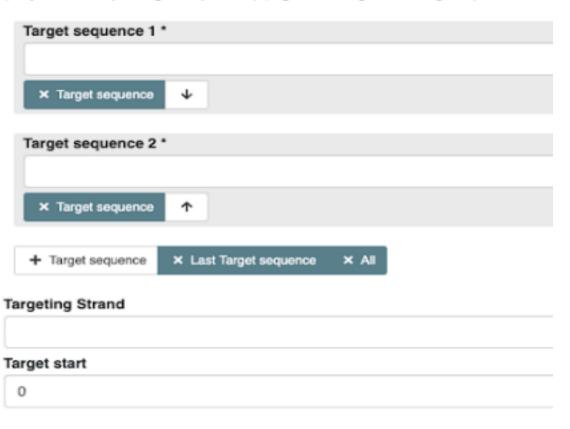
Datasets as control data and linked to metadata





Target sequences

(may have multiple target sequences) (region of the genome targeted).



Lexicon working group



Identify terms and related definitions to form a common genome editing community lexicon

- (e.g., FDA, USDA)



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enable clear communication of scientific results

facilitate effective communication with regulators

have the potential for international acceptance

Lexicon contributing drafting organizations and expert commenters

Industry and commerce – large industry

- Novartis
- <u>AstraZeneca</u>
- <u>Thermo Fisher</u> <u>Scientific</u>
- New England Biolabs
- Illumina
- Lonza
- Johnson & Johnson

Industry and commerce – SMEs

- <u>Bluebird bio</u>
- <u>Caribou Biosciences</u>
- <u>Cortevea Agroscience</u>
- **CRISPR** Therapeutics
- Editas Medicine
- Horizon Discovery
- <u>Integrated DNA</u> <u>Technologies</u>
- Intellia Therapeutics
- Precision Biosciences
- <u>Sangamo</u> <u>Therapeutics</u>
- <u>Synthego</u>
- Casebia Bio

Government	Ac
• FDA	• <u>H</u>
• USDA	• <u>H</u> • <u>S</u>
• NIH	<u>r</u> (
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NIST

ademic and research bodies

- Harvard University St Jude Children's Sesearch hospital The Broad Institute
- MIT Stanford University <u>Jniversity of</u> California Berkeley The Jackson Labs
- The University of
- Copenhagen
- The CRISPR Journal
- NC State University
- The University of
- Massachusetts
- Medical School
- JCSF
- UCSC

Non-governmental organizations

- <u>EMBL-EBI</u>
- The World Health Organization
- Alliance for Regenerative Medicine
- USP

Genome Editing Concepts

Gene editing Genome editing Genome engineering Specificity Target Off-target

Genome Editing Tools

General

Site-directed nuclease Site-directed DNA modification enzyme Repair template

CRISPR-Specific

Guide RNA (gRNA) CRISPR RNA (crRNA) tracrRNA (trans-activating CRISPR RNA) sgRNA (single-guide RNA) PAM (protospacer adjacent motif) RNP (ribonucleoprotein) Cas nuclease target site Target strand

Genome Editing Tools

Meganuclease - Specific

Meganuclease Meganuclease single chain Meganuclease linker Meganuclease target site

TALEN - Specific

TALEN TALEN linker Repeat variable diresidue (RVDs) TALEN target site

megaTAL - Specific

megaTAL megaTAL linker megaTAL target site

ZFN - Specific

Zinc Finger Nuclease (ZFN) ZFN linker Zinc Finger Protein (ZFP) Zinc Finger Recognition helix ZFN target site

Terms v1

Genome Editing Outcomes

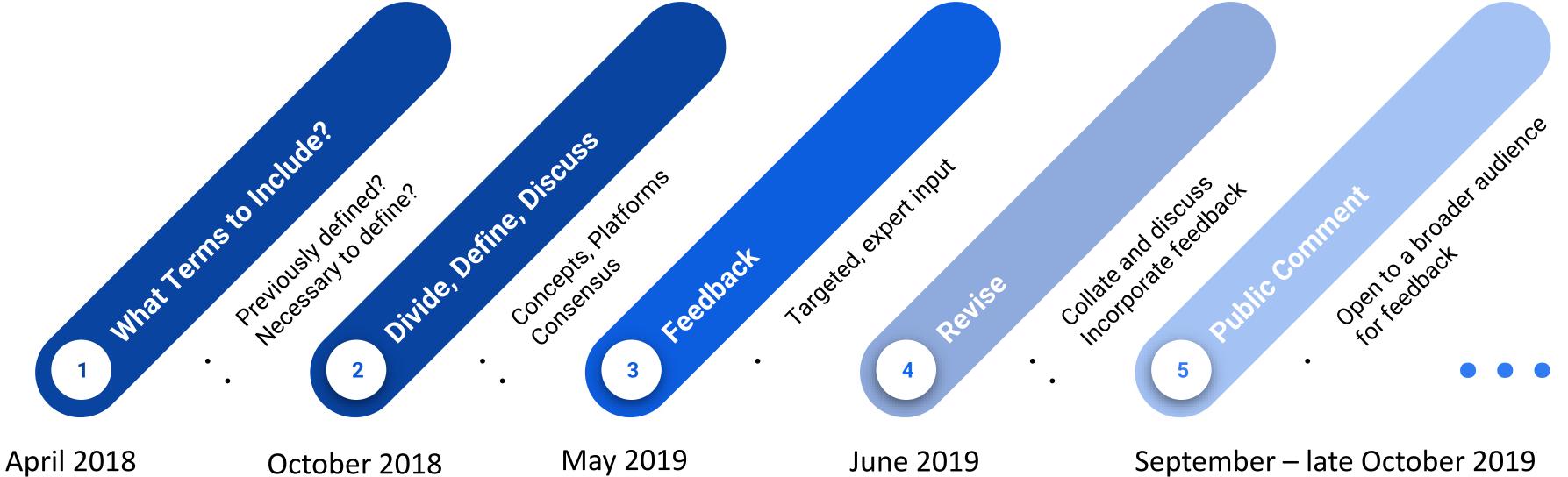
Edit Unintended edit Intended edit HDR (homology-directed repair) NHEJ (non-homologous end-joining) Microhomology-Mediated End Joining Repair (MMEJ) InDel mutation

ISO Standard *Genome Editing Part 1: Vocabulary* is in the last stage of approval

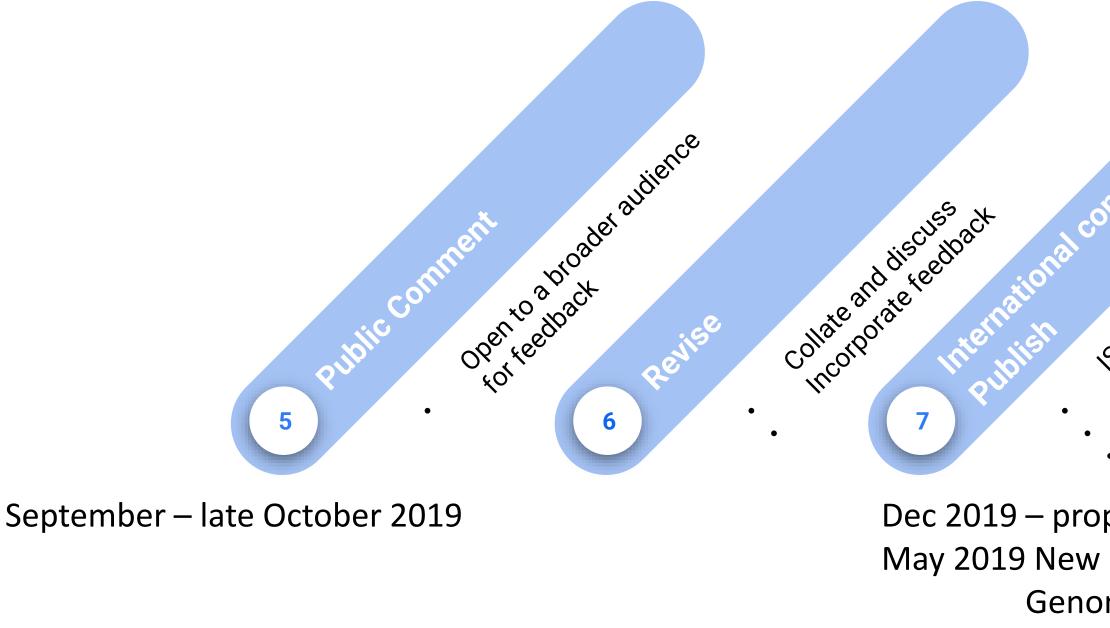


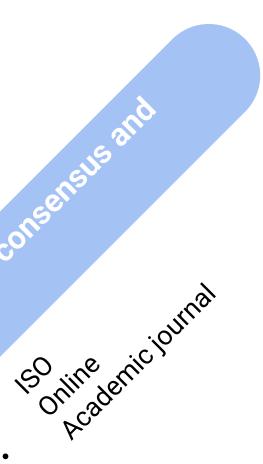
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Process prior to ISO submission



Process prior to ISO submission continued





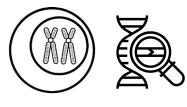
Dec 2019 – proposed as new project at ISO meeting May 2019 New Project ISO standard: Genome Editing Terminology initiated.... Estimated ISO standard publication Q4 2021/Q1 2022

NIST Genome Editing Consortium Progress

WG1: Specificity Measurements

Develop cell and DNA based control materials and test via interlab analysis (Genome in a Bottle and Human iPSCs)

<u>@</u>



Documented process, baseline data, mixture studies, interlab studies, benchmark data

WG2: Data & Metadata

- Community norms for data formats and tools for benchmarking data analysis (in *silico* and experimental data sets)
- Identify metadata that would be needed to be shared, housed, and interrogated from genome editing experiments and develop tools to accelerate metadata sharing

WG3: Lexicon

Identify terms and related definitions to form a common genome editing community lexicon

WG1 – Progress:

- completed

WG2 – Progress:

WG3 – Progress:

expert review and public comment

\$ DNA and cells representing a variety of DNA sequence benchmarks "looks like a genome editing output" Deeply

characterized at benchmark locations

✓ Transfer of Knowledge Reproducibility

What are the data we are generating? When do we need to collect the metadata? How do we store data and metadata? Where do we store data and metadata

metadata from consortium studies and benchmark datasets as shared resources for the community





A set of Phase 1 DNA and cell based control materials have been generated and an interlab study has been launched

Samples have been qualified by NIST and sent to members for interlab comparison of DNA sequences detected and limit of detction

Additional clonal engineered cell controls are in progress with some lines

Phase 1 metadata entries and template completed Testing use cases and user interfaces, and interoperability of a metadata standard format and database(s) to house records.

A first version lexicon has been generated that has gone through targeted https://www.nist.gov/programs-projects/nist-genome-editing-lexicon

An updated internationally harmonized version is in the last stages of approval to be released as an ISO Standard for *Genome Editing Vocabulary*

Keeping pace with technology



Gene Therapy, Genome Editing Technologies and related capabilities (e.g. delivery systems) are rapidly growing and an intentional effort must be made to keep up with advances in knowledge and technology



It is important that standards are not limited to only the potential of current technology, but 'future proofed' to help with comparability and qualification of new technology advancements and comparability between current and future technologies that may be beneficial to take advantage even during the development lifetime of a product.



The NIST Genome Consortium is currently active through Dec 2025, to address standards needs identified by members and expert community. Additional members are welcome.



Additional engagement and expert community collaborative activities are critical for identifying standards needs and working towards consensus solutions and developing needed data and products



For commercial products, regulation will be different across countries, and it is important to appreciate key policies and positions from regulatory bodies particularly regarding safety



Thank You NIST Colleagues!





Natasha Kolmakova

Alex Tona



Tara Eskandari



Sierra Miller

Simona

Patange



Justin Zook



Nate Olson



Zach Trautt



Arlin Stoltzfus



Hua-Jun He



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https://www.nist.gov/programs-projects/nist-genome-editing-consortium

Funding Collaborators

NIST Genome Editing Consortium Members



Jamie Almeida









- Shengdar Tsai •
- Cicera Lazzarotto
- Yichao Li \bullet