



# Investor Day

May 21, 2026

# Emily Leproust

CEO and Co-founder

*Welcome*



# Legal Disclaimer

This presentation contains forward-looking statements. All statements other than statements of historical facts contained herein are forward-looking statements the current beliefs and expectations of management made pursuant to the safe harbor provisions of the Private Securities Litigation Reform Act of 1995, including, but not limited to, projections labeled “FY 2026 Guidance”, statements regarding future growth and expansion, estimated turnaround times, drivers of future revenue and gross margin growth, market size and growth, estimated annual 2026 revenues, ability and timing to achieve profitability, ability and timing to achieve adjusted EBITDA breakeven and ability to maintain or increase gross margins and Twist’s other expectations regarding its future operations plans and financial performance, introduction of new products, and newly announced partnerships. Forward-looking statements involve known and unknown risks, uncertainties, and other important factors that may cause Twist’s actual results, performance, or achievements to be materially different from any future results, performance, or achievements expressed or implied by the forward-looking statements. Such risks and uncertainties include, among others, the ability to attract new customers and retain and grow sales from existing customers; the ability of Twist to achieve sufficient revenue to achieve or maintain positive cash flow from operations or profitability in any given period; risks and uncertainties of rapidly changing technologies and extensive competition in synthetic biology that could make the products Twist is developing obsolete or noncompetitive; the ability to integrate and leverage artificial intelligence and machine learning technologies to improve operational efficiency, product development, and customer solutions; the ability to expand DNA synthesis manufacturing capacity; dependence on one supplier for a critical component; dependence on key personnel; additional regulations that could increase Twist’s costs and delay commercialization efforts; changes in U.S. trade policies and other trade actions that could result in increased costs and supply chain disruptions; the ability to maintain and enforce intellectual property protection; uncertainty as to economic and market conditions and the impact of adverse economic conditions; and the ability to obtain financing when necessary. For a description of the risks and uncertainties that could cause actual results to differ from those expressed in these forward-looking statements, as well as risks relating to Twist’s business in general, see Twist’s risk factors set forth in Twist’s Annual Report on Form 10-K filed with the SEC on November 17, 2025. Any forward-looking statements contained in this presentation speak only as of the date hereof, and Twist specifically disclaims any obligation to update any forward-looking statement, whether as a result of new information, future events or otherwise.

The presentation also contains supplemental financial information determined by methods other than in accordance with U.S. generally accepted accounting principles (“GAAP”). These non-GAAP measure are not in accordance with, or an alternative for, measures prepared in accordance with generally accepted accounting principles (GAAP) and may be different from non-GAAP measures used by other companies. In addition, these non-GAAP measures are not based on any comprehensive set of accounting rules or principles. A reconciliation of these non-GAAP financial measures may be found starting on page 233 of this presentation.

A reconciliation of adjusted EBITDA for the fourth quarter of fiscal 2026 to a corresponding GAAP financial guidance measure is not available on a forward-looking basis because the Company does not provide guidance on GAAP net loss and is not able to present the various reconciling cash and non-cash items between GAAP net loss and adjusted EBITDA without unreasonable effort. In particular, stock-based compensation expense is impacted by the Company’s future hiring and retention needs, as well as the future fair market value of its common stock, all of which are difficult to predict and are subject to change. The actual amount of these expenses during fiscal 2026 will have a significant impact on Twist’s future GAAP financial results.

# Science Without Limits. Solutions without Compromise.

Twist Bioscience Investor Day 2026

# Agenda

- **Welcome**
  - Tour
  - DSPS Strategy Session
  - Fireside Chat with Dr. Frances Arnold
  - Customer Presentations
- 

## Lunch

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- NGS Strategy Session
- Customer Presentations
- Financial Overview
- Culture
- Q&A

# Twist Bioscience is Writing the Future

## Delivering Products Across the Biological Continuum

### Proprietary

silicon-based DNA  
synthesis platform

**\$442 - \$447M**  
guided FY26 revenue  
(May 4, 2026)

**~\$377M**

revenue  
(FY 2025)

**~1,000**  
employees

### Enabling

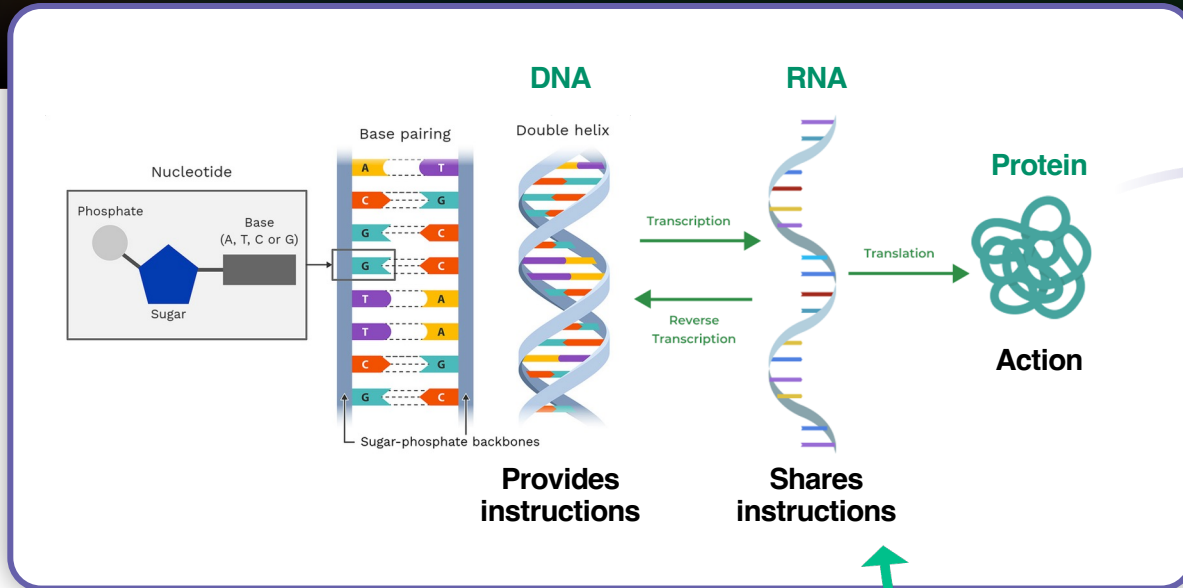
therapeutics, diagnostics, research, industry,  
and applied markets

**Multi-billion \$**  
growing markets

## Established global footprint, capacity for growth



# Biology Is Increasingly Understood Through Reading and Writing DNA: Twist at the Forefront



**Twist DNA Synthesis and Protein Solutions**

## Twist NGS Applications

**Biology**

Biology is the outcome we read, understand and engineers

|  |   |  |   |
|--|---|--|---|
| <br><b>Research</b><br>Advance knowledge and uncover biology | <br><b>Diagnostics</b><br>Detect, monitor and guide decisions | <br><b>Therapeutics</b><br>Discover and develop transformative therapies | <br><b>Applied/Industrial</b><br>Engineer biology for health, sustainability and beyond |
|--|---|--|---|

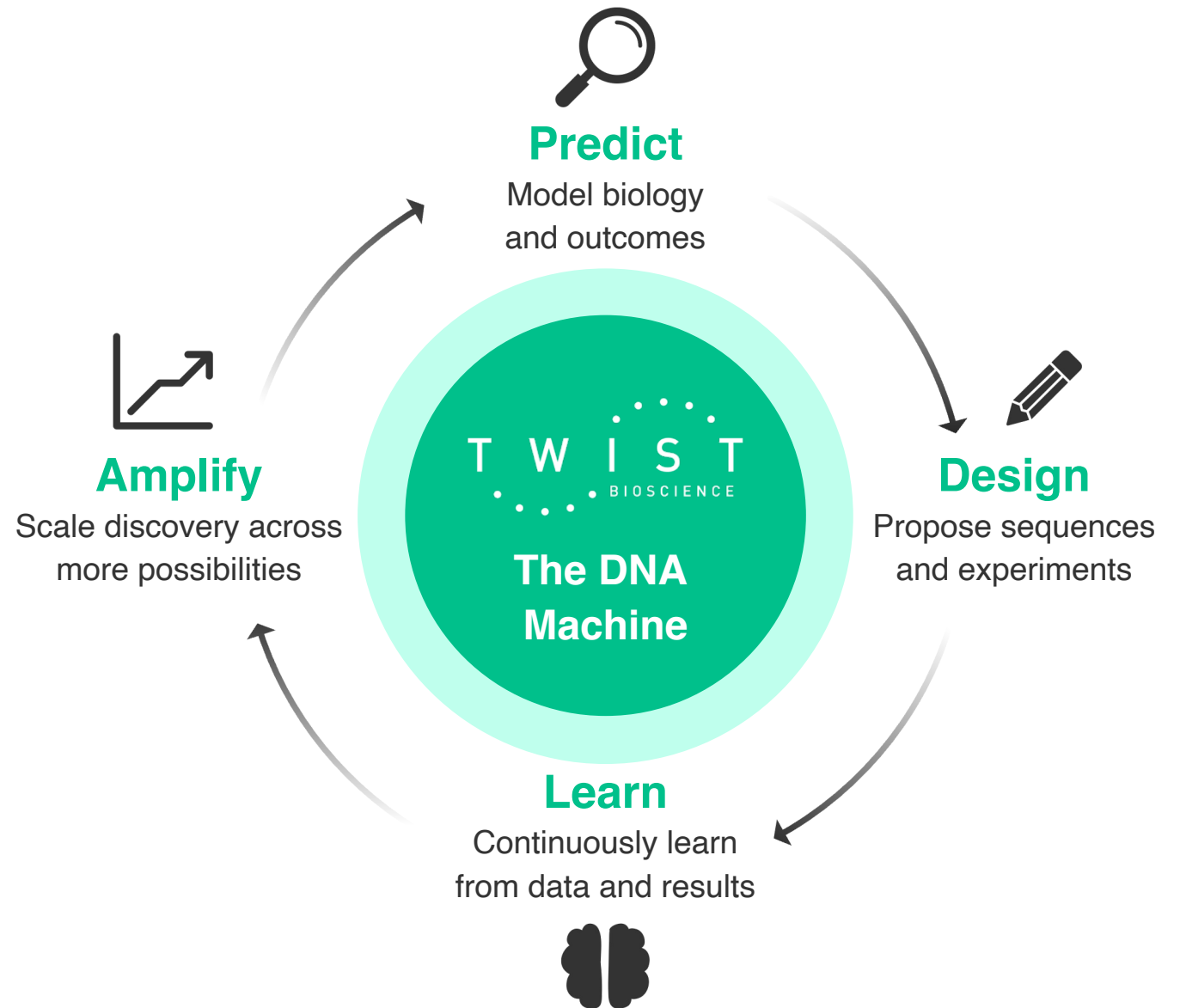
# Uniquely Positioned at the Intersection of Biology and AI

Reading and writing DNA is increasingly important to drive biological insights and clinical action

## AI makes discovery more DNA-driven

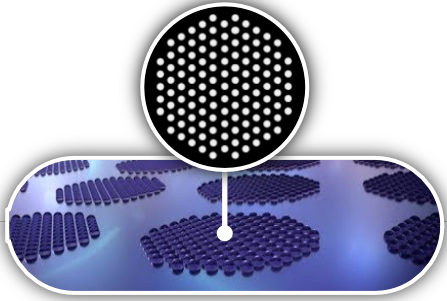
DNA-driven discovery accelerated by AI: shifting paradigm from trial-and-error to systematic, scalable sequence design

**Twist is the DNA Machine:** leadership in DNA synthesis creates a critical data flywheel that is informing the future of biology



# Power of the Platform

Our differentiation is  
**the silicon chip**



**Expanding Revenue-  
Generating Workflows on  
the Same Infrastructure**

## You'll see today:

- Best-in-class, proprietary platform built for scale
- Scalable, purpose-built manufacturing infrastructure + software
- Continued innovation to drive tech optimization and new product launches
- Ability to serve large and rapidly growing markets

# Differentiated Versatile Advantage

## Miniaturized proven chemistry

- Cost advantage (less reagent, waste)
- Higher throughput
- Customization at scale

## Uniquely enables critical applications

- AI Discovery
- MRD Express
- Enzyme Engineering
- Nucleic Acid Therapeutics

# Purpose-Built Platform to Power Large Growth Opportunities

## **Proprietary**

DNA synthesis  
technology platform

## **Robust and Flexible**

product portfolio

## **Premium white-glove**

service capabilities

## **Experienced team**

## **Manufacturing**

prosess paired with  
automation excellence

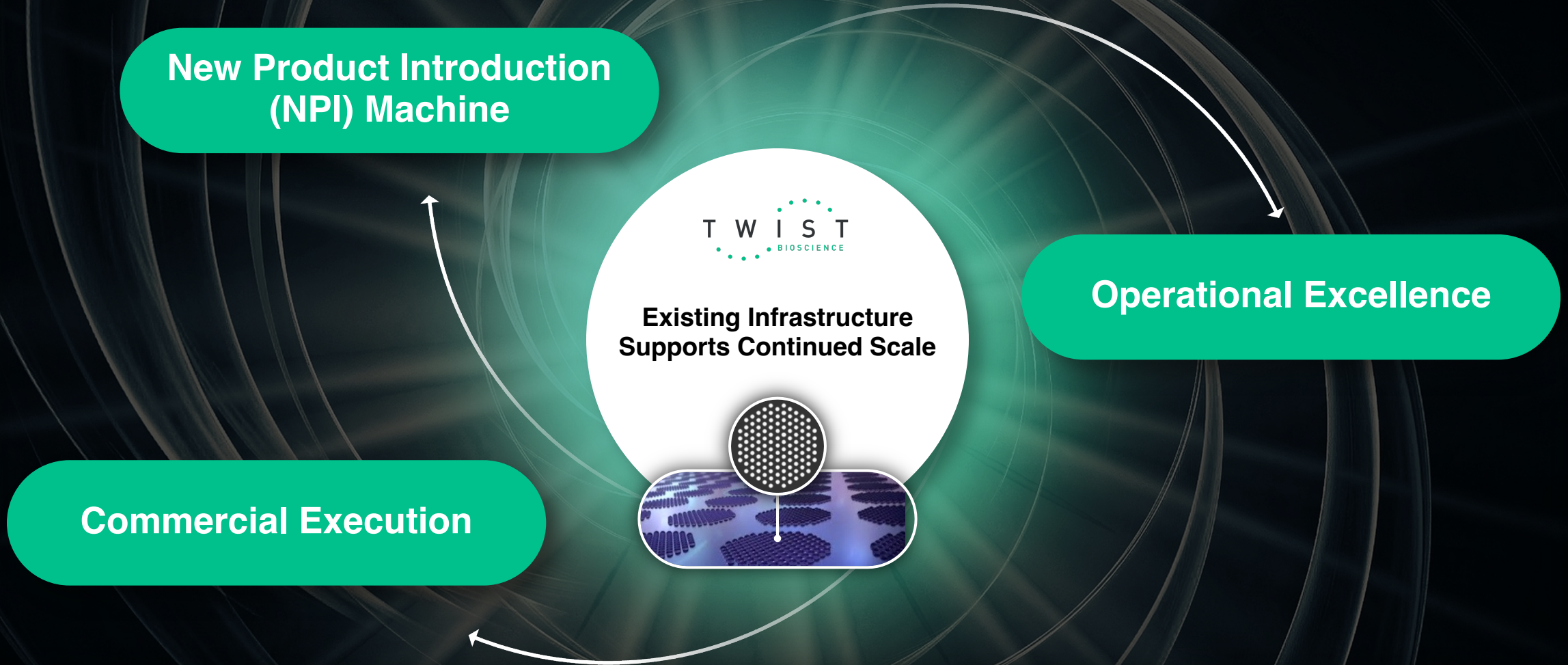
## **Diversified**

customer base in  
multiple markets

## **Meet Customers** where they are

## **Unique growth opportunities**

# How Twist Operates Sets Us Apart from Others



# Twist Bioscience: NPI Machine

## Expand

Expand available opportunity by adding new products to open multi-billion dollar markets (e.g. FlexPrep™)

## Build

Build portfolio of innovative products to load more on the chip, increasing throughput, lowering cost (e.g. MRD Express)



## Invest

Invest and scale infrastructure ahead of demand inflections (e.g. proteins, AI)

## Deploy

Rapidly deploy capabilities into emerging opportunities (e.g. Ab characterization)

# Operational Excellence Underpins Success

1

Quality &  
Reliability

2

Customization

3

Scale

4

Structural  
cost advantage

## KEY ENABLERS



Innovative software



Proprietary silicon-based platform

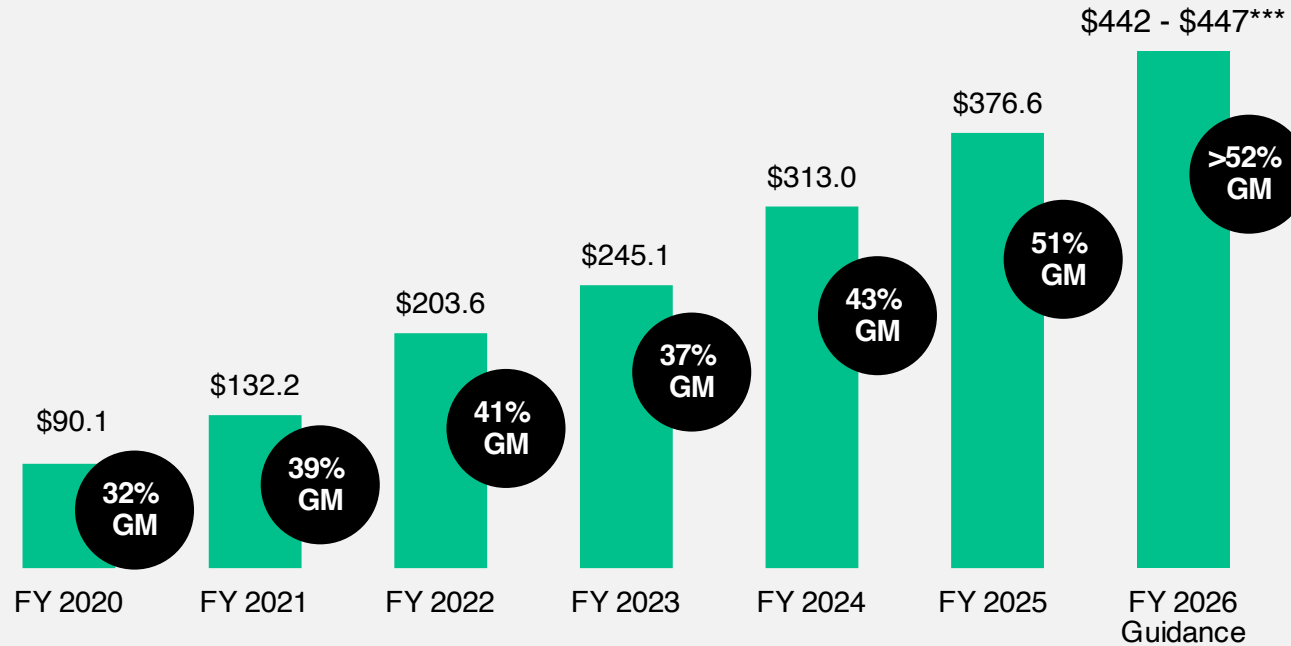


Automation, state-of-the-art manufacturing system

# Proven Commercial Execution, Financial Discipline

## Annual Revenue

\$ Millions



**33% CAGR**  
over last 6 years

**20% points**  
margin improvement

**Diversified**  
revenue base

|                          |           |            |            |            |           |           |
|--------------------------|-----------|------------|------------|------------|-----------|-----------|
| <b>Adjusted OpEx*</b>    | \$126M    | \$164M     | \$248M     | \$260M     | \$253M    | \$262M    |
| <b>Adjusted EBITDA**</b> | (\$93.8M) | (\$106.5M) | (\$152.8M) | (\$147.3M) | (\$93.6M) | (\$46.9M) |

\* Adjusted OpEx is defined as SG&A and R&D expenses excluding depreciation and amortization and stock-based compensation expense. See adjusted OpEx reconciliation on page 234

\*\*Adjusted EBITDA is defined as net income (loss) adjusted to exclude interest income, income tax expense, depreciation and amortization, other income/expense, net, stock-based compensation expense and other items detailed in the reconciliation table below that we believe are not indicative of our ongoing results. See page 233 for Adjusted EBITDA Reconciliation

\*\*\*Guidance as of May 4, 2026

# One Platform, Many Customized Solutions

Meeting customers where they are, powering growth across expanding platforms

## How we win



**Operational excellence**



**NPI machine**



**Commercial execution**

T W I S T  
BIOSCIENCE

Differentiated  
Silicon Platform  
Speed and Scale



**AI-enabled antibody discovery workflows**

AI-ready wet-lab at scale



**Molecular residual disease**

Personalized diagnostic research at scale



**Enzyme-engineered NGS**

Better performance, integrated workflow



**Nucleic acid therapeutics**

Future growth frontier

**Twist culture**

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# Manufacturing Facility Tour

Manufacturing front end

Manufacturing back end (genes, IgG proteins, data characterization)

A few Twisters

Labs

Manufacturing Execution System Software

**\*No photos, no videos, no recording, no Meta glasses**

# James Diggans

VP, Biosecurity and Policy

*Manufacturing Execution System Demonstration*



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# DNA Synthesis and Protein Solutions

Advancing scientific discovery across traditional and AI-enabled workflows with scalable DNA synthesis and protein solutions

# Siyuan Chen

Chief Technology Officer

*Silicon Technology, Operational Excellence*



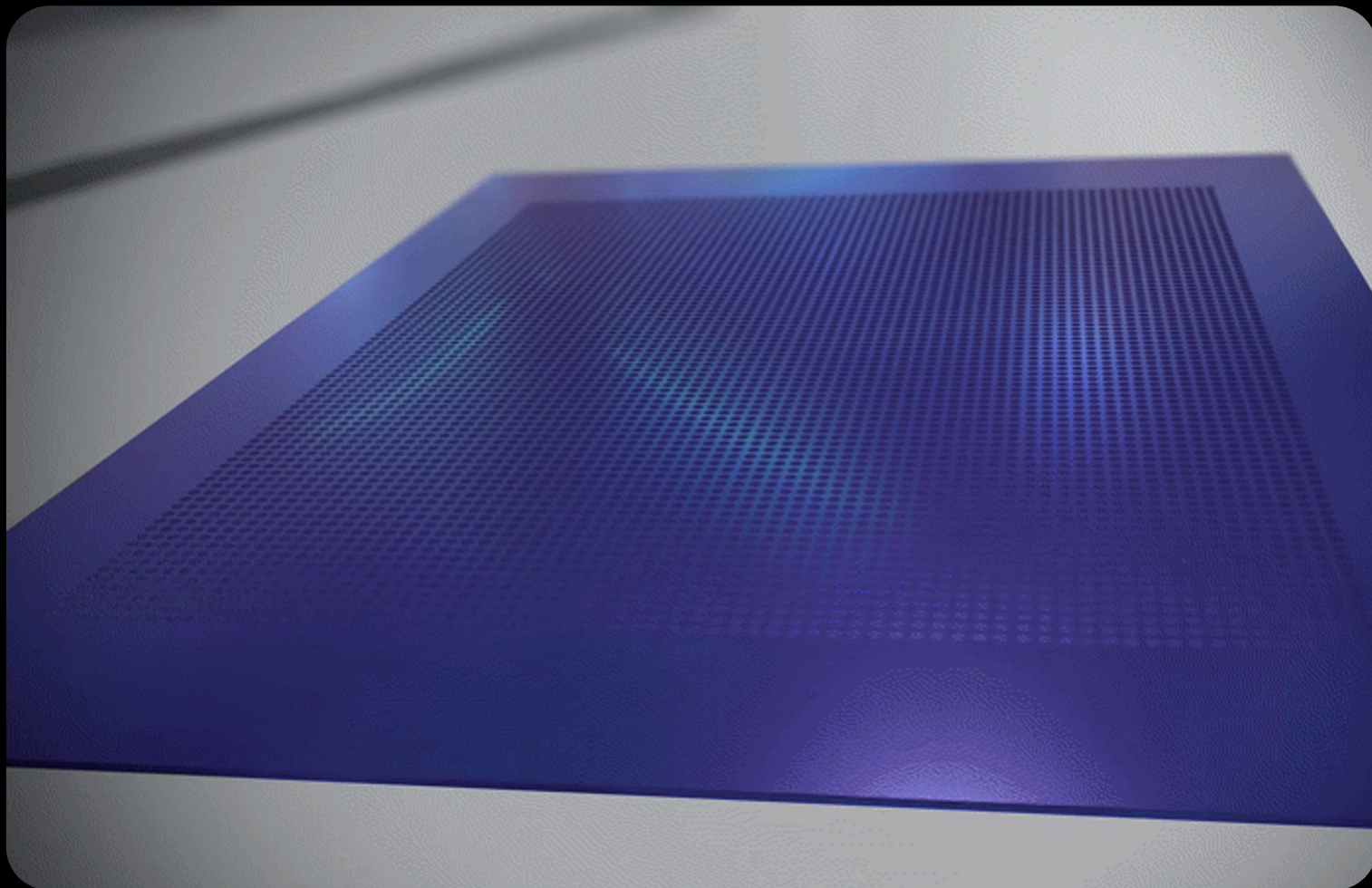
# It All Starts with Our Silicon Technology – And Automation

## DNA SYNTHESIS

Oligos, Variant libraries, MGF, Gene pools,  
Fragments, Clonal genes, IgG, siRNA/ASO  
oligos, mRNA (coming soon)

## PROTEIN SOLUTIONS

*In vitro* antibody discovery, *in vivo* antibody  
discovery, protein production, antibody  
characterization



**>32 million**  
oligonucleotides  
per day capacity

Direct synthesis  
up to **500 bases**

Industry leading  
**accuracy**

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**Enzyme-engineered NGS**

Better performance, integrated workflow

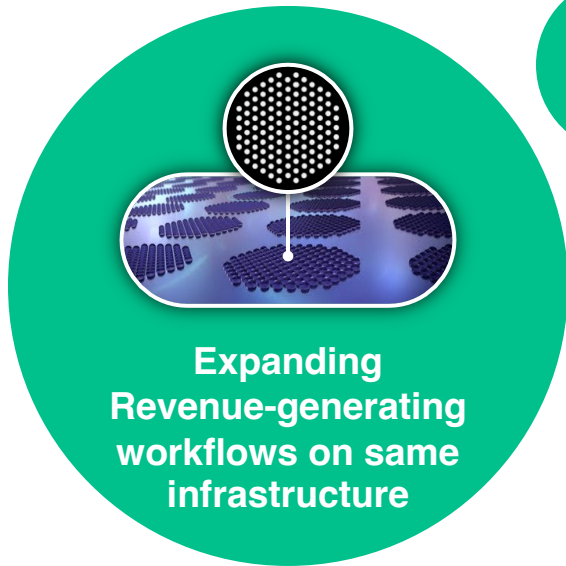


**Nucleic acid therapeutics**

Next growth frontier

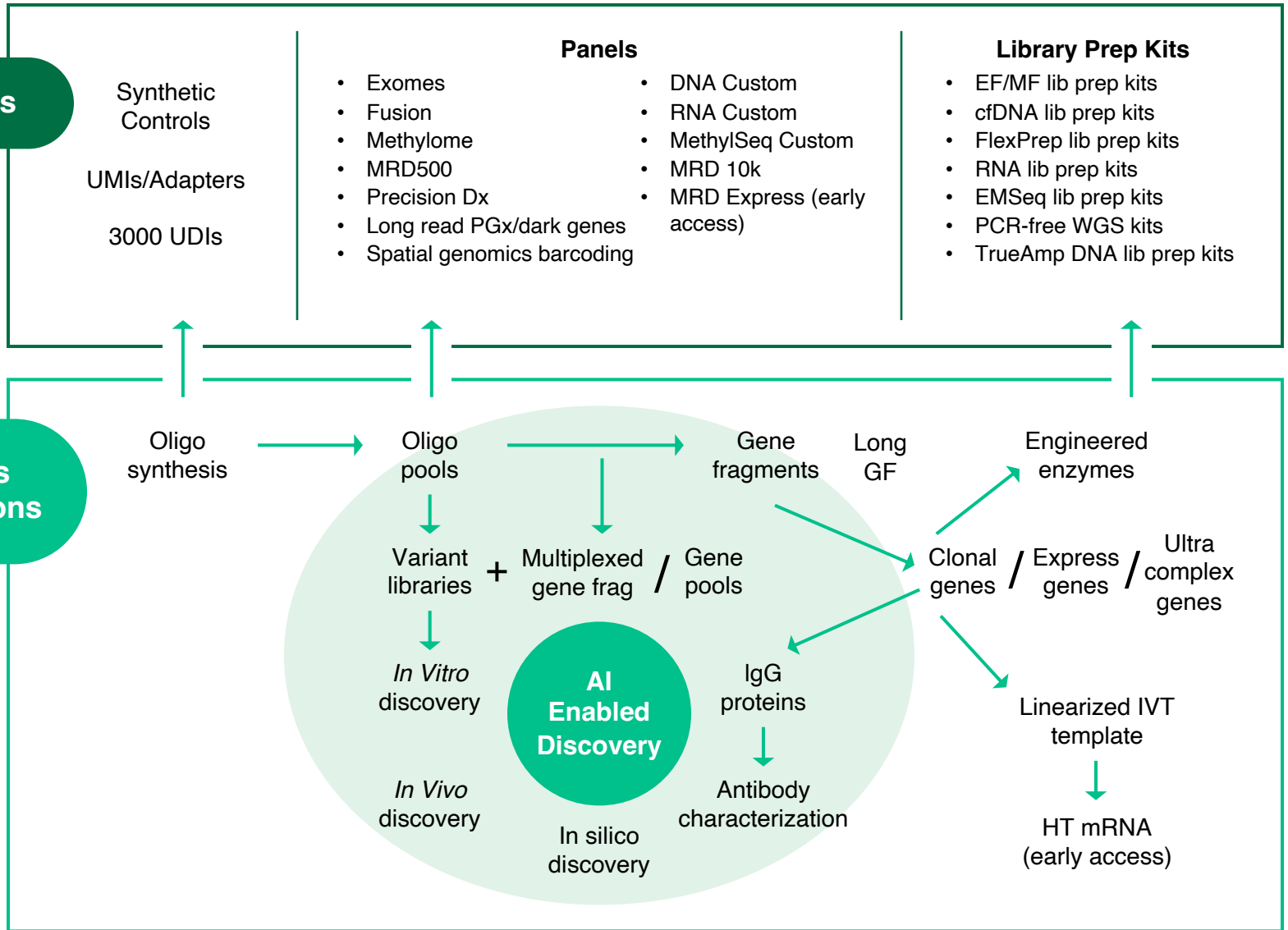
**Twist culture**

# Synergistic Solutions that Work Together



## NGS applications

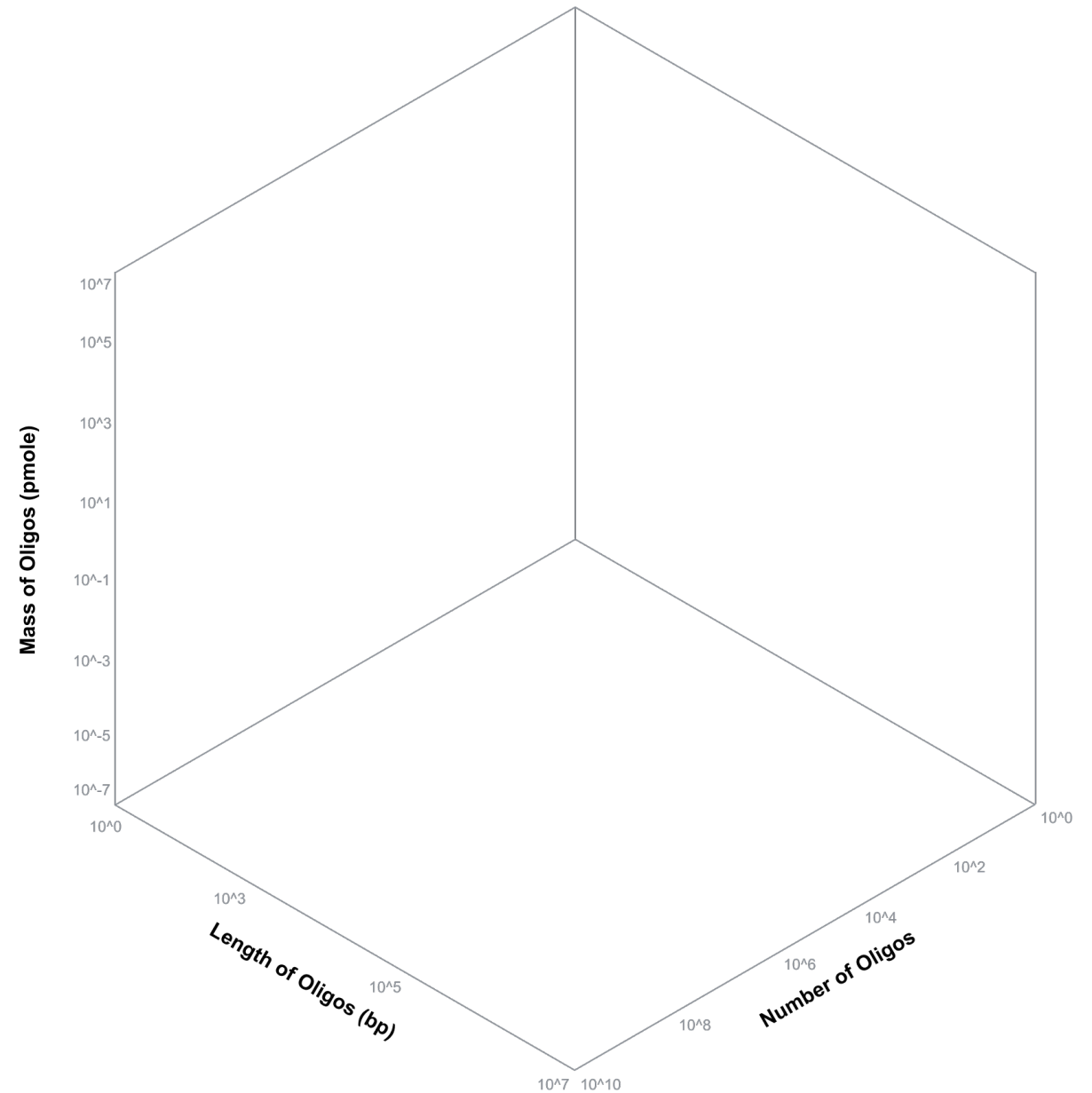
## DNA synthesis & protein solutions



# Applications mapped by oligo number, mass, and length

## Group

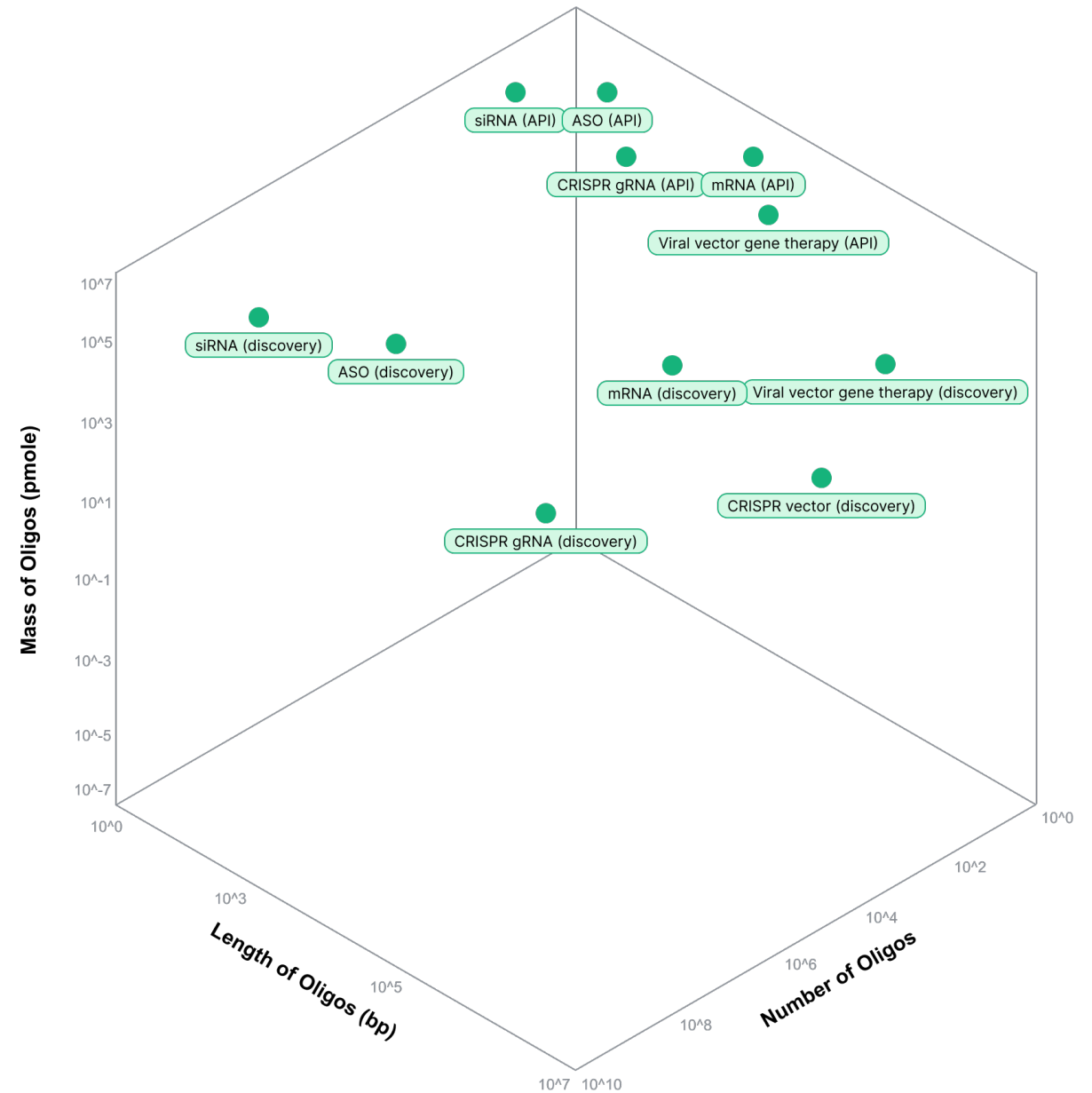
- Therapeutics
- Diagnostics
- Genomics
- Protein engineering



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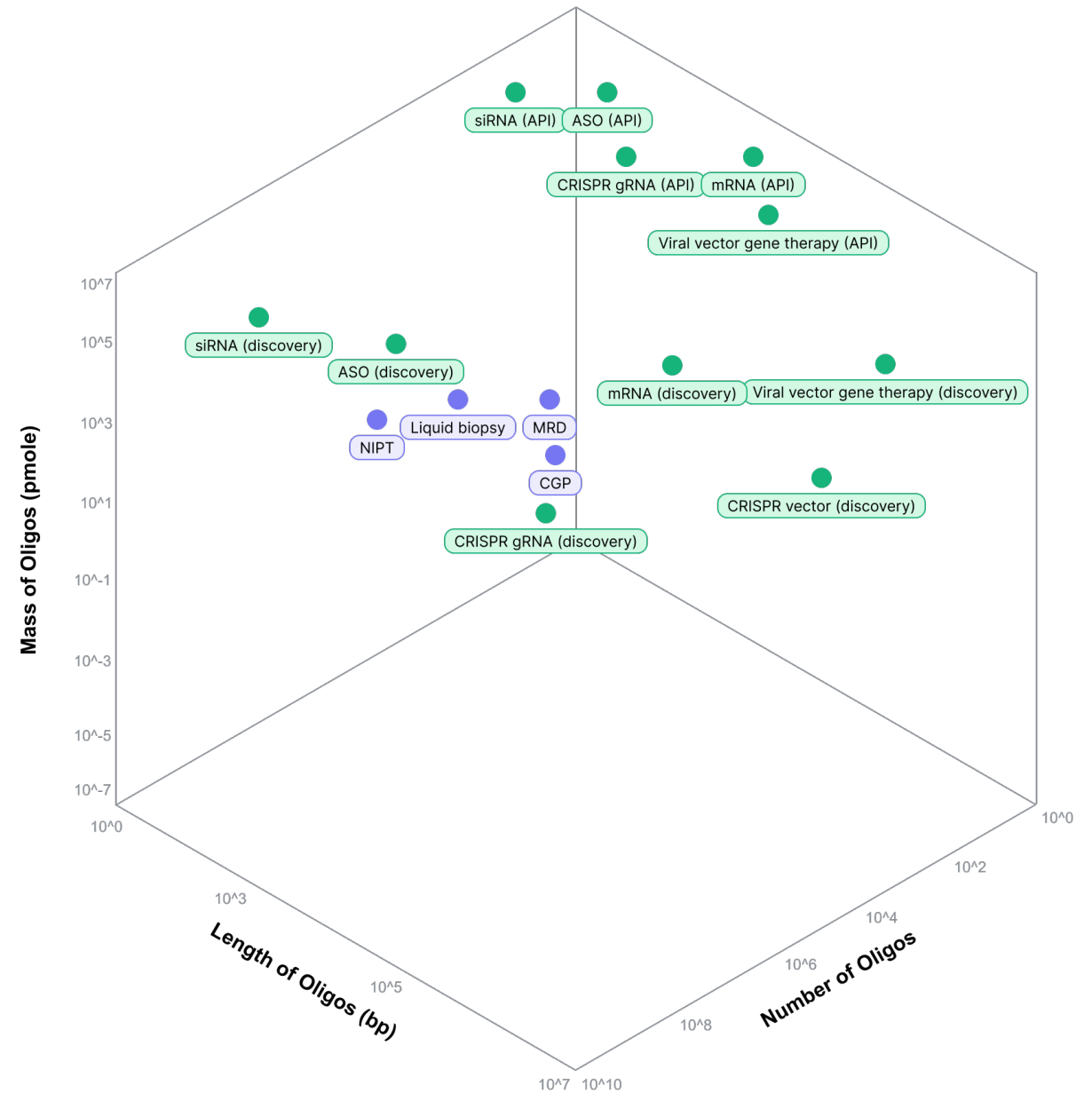
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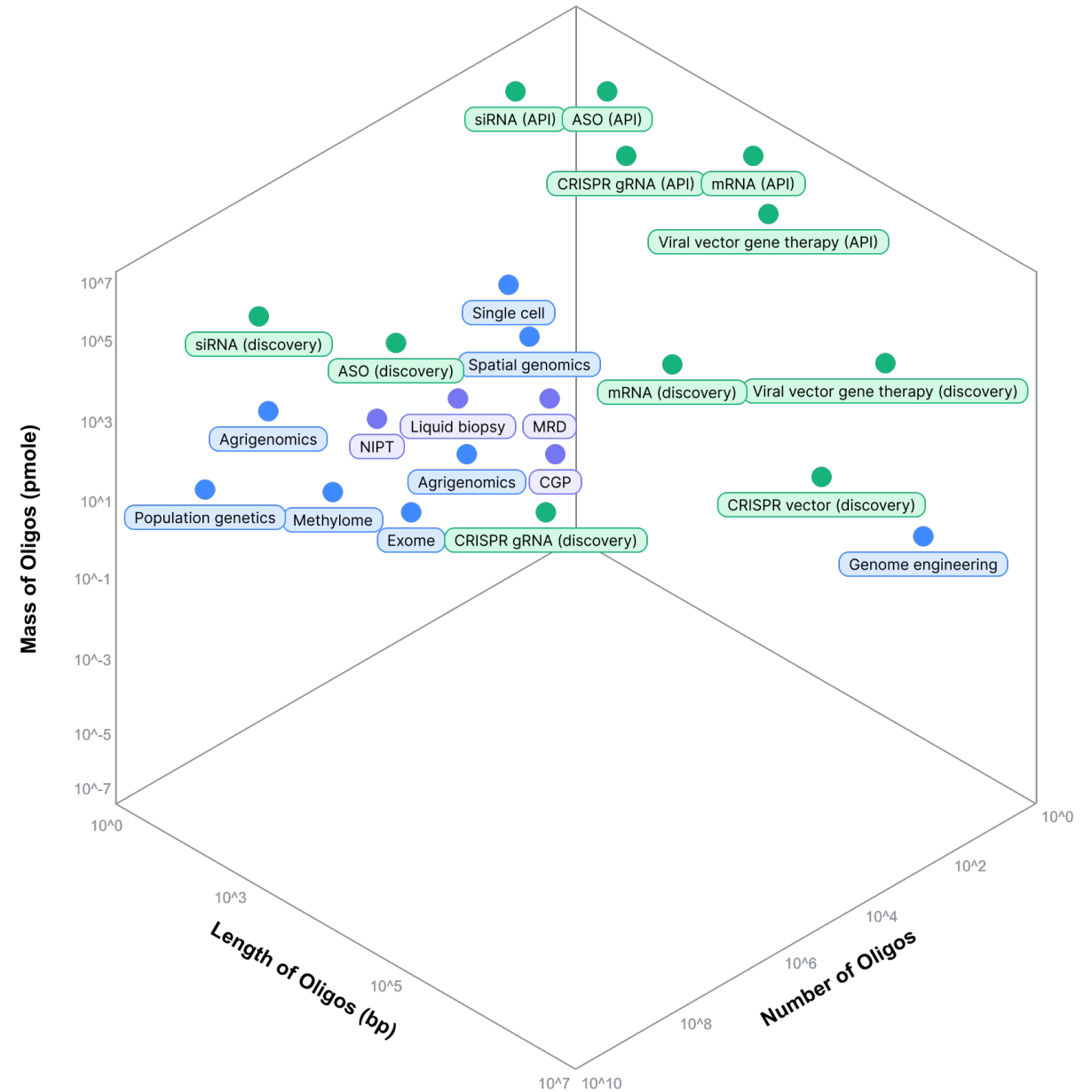
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# Applications mapped by oligo number, mass, and length

## Group

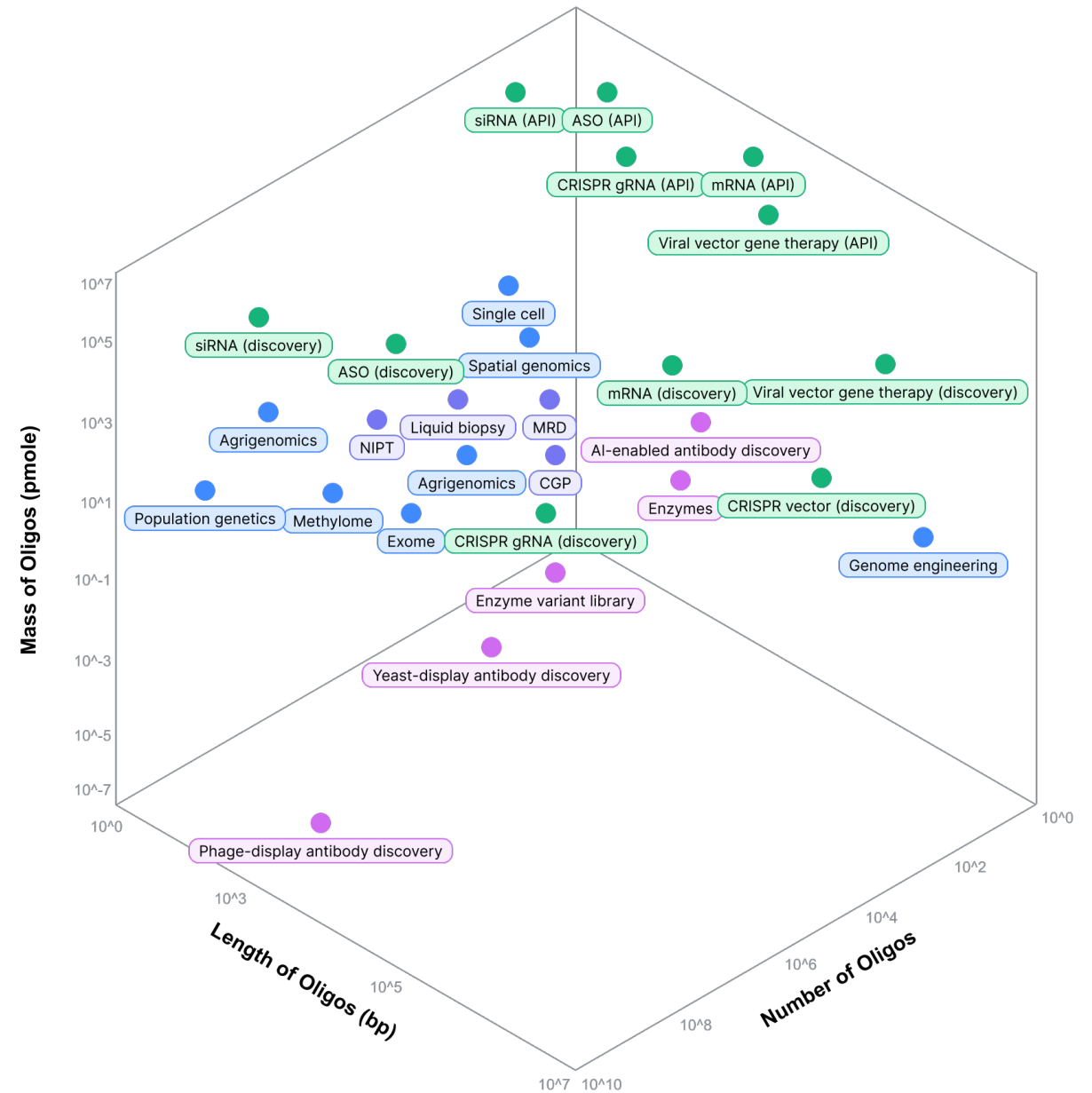
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# Applications mapped by oligo number, mass, and length

## Group

- Therapeutics
- Diagnostics
- Genomics
- Protein engineering



# Oligo Application Reference Table

| Application                      | Group               | # Sequences    | Mass (pmol) | Length (bp) |
|----------------------------------|---------------------|----------------|-------------|-------------|
| siRNA (discovery)                | Therapeutics        | 10,000         | 1           | 21          |
| ASO (discovery)                  | Therapeutics        | 10,000         | 1           | 25          |
| siRNA (API)                      | Therapeutics        | 10             | 100,000     | 21          |
| ASO (API)                        | Therapeutics        | 10             | 150,000     | 25          |
| CRISPR gRNA (discovery)          | Therapeutics        | 100,000        | 0.1         | 200         |
| CRISPR vector (discovery)        | Therapeutics        | 100            | 0.1         | 12,000      |
| CRISPR gRNA (API)                | Therapeutics        | 10             | 100,000     | 200         |
| Viral vector GT (discovery)      | Therapeutics        | 1,000          | 100         | 10,000      |
| Viral vector GT (API)            | Therapeutics        | 10             | 100,000     | 10,000      |
| mRNA (discovery)                 | Therapeutics        | 1,000          | 100         | 5,000       |
| mRNA (API)                       | Therapeutics        | 10             | 1,000,000   | 5,000       |
| MRD                              | Diagnostics         | 2,000          | 0.1         | 120         |
| Liquid biopsy                    | Diagnostics         | 15,000         | 0.1         | 120         |
| CGP                              | Diagnostics         | 25,000         | 0.1         | 120         |
| NIPT                             | Diagnostics         | 100,000        | 1           | 50          |
| Spatial Genomics                 | Genomics            | 50,000         | 10          | 150         |
| Agrigenomics (200k)              | Genomics            | 200,000        | 10          | 80          |
| Exome                            | Genomics            | 400,000        | 0.1         | 120         |
| Methylome                        | Genomics            | 1,500,000      | 0.1         | 120         |
| Single cell                      | Genomics            | 10,000         | 10          | 60          |
| Agrigenomics (20k)               | Genomics            | 20,000         | 1           | 70          |
| Population Genetics              | Genomics            | 1,000,000      | 0.1         | 120         |
| Genome engineering               | Genomics            | 10             | 0.1         | 1,000,000   |
| AI-enabled antibody discovery    | Protein Engineering | 1,000          | 1           | 1,500       |
| Phage-display antibody discovery | Protein Engineering | 10,000,000,000 | 0.000001    | 1,500       |
| Yeast-display antibody discovery | Protein Engineering | 1,000,000      | 0.0001      | 1,500       |
| Enzymes                          | Protein Engineering | 1,000          | 0.1         | 3,000       |
| Enzyme variant library           | Protein Engineering | 100,000        | 0.01        | 3,000       |

## Group

● Therapeutics

● Diagnostics

● Genomics

● Protein engineering

# One Platform, Many Customized Solutions

Meeting customers where they are, powering growth across expanding platforms

## How we win



**Operational excellence**



**NPI machine**



**Commercial execution**

T W I S T  
BIOSCIENCE

Differentiated  
Silicon Platform  
Speed and Scale



**AI-enabled antibody discovery workflows**

AI-ready wet-lab at scale



**Molecular residual disease**

Personalized diagnostic research at scale



**Enzyme-engineered NGS**

Better performance, integrated workflow



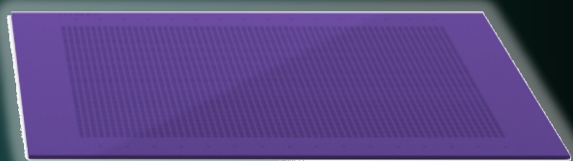
**Nucleic acid therapeutics**

Next growth frontier

**Twist culture**

# Continuing to Iterate and Improve Proprietary Platform

- Continuing low error rate with improved consistency
- Continue to reduce reagent cost and chemical waste
- Faster synthesis increases writer capacity, enhances products, and expands throughput
- Enables new product introductions

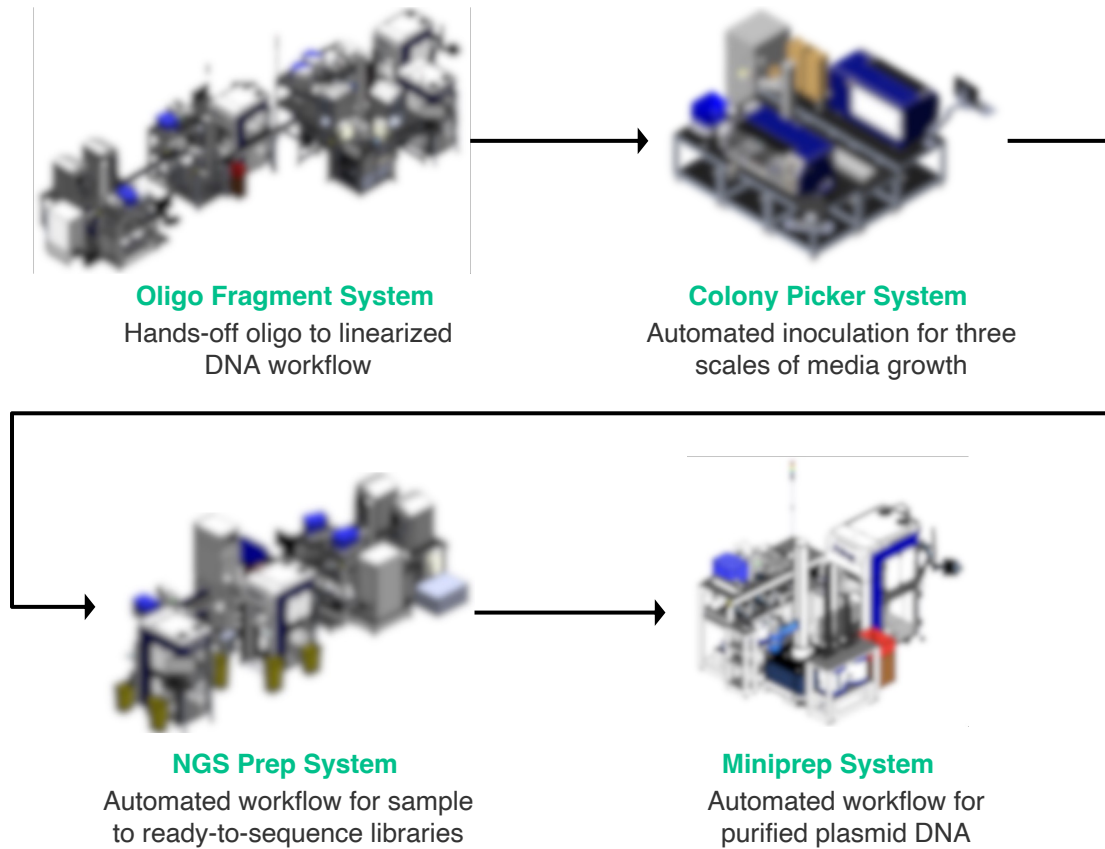


All data is for ~1,000,000 oligos at femtomole scale



# Automated from Start to Finish

## Automate key bottleneck steps



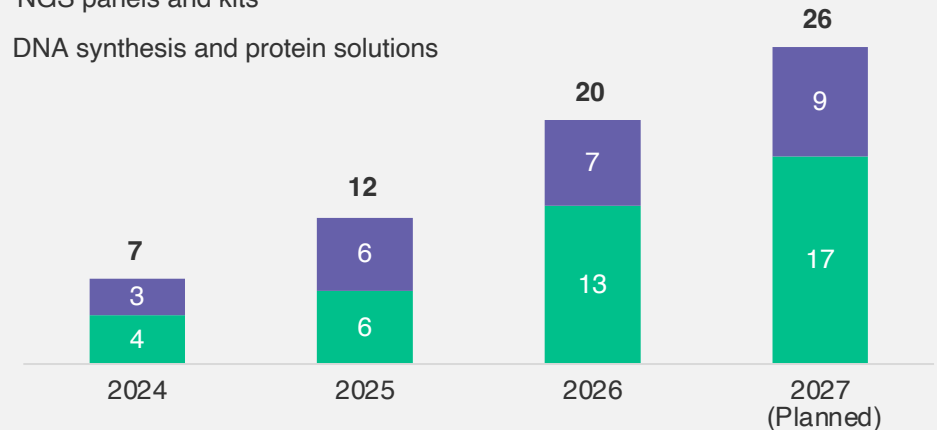
Building scalable process so that **multiple processes can run on the same tools** (e.g. complexity process with minimum addition of equipment)

## Enable scaling with more integrated systems

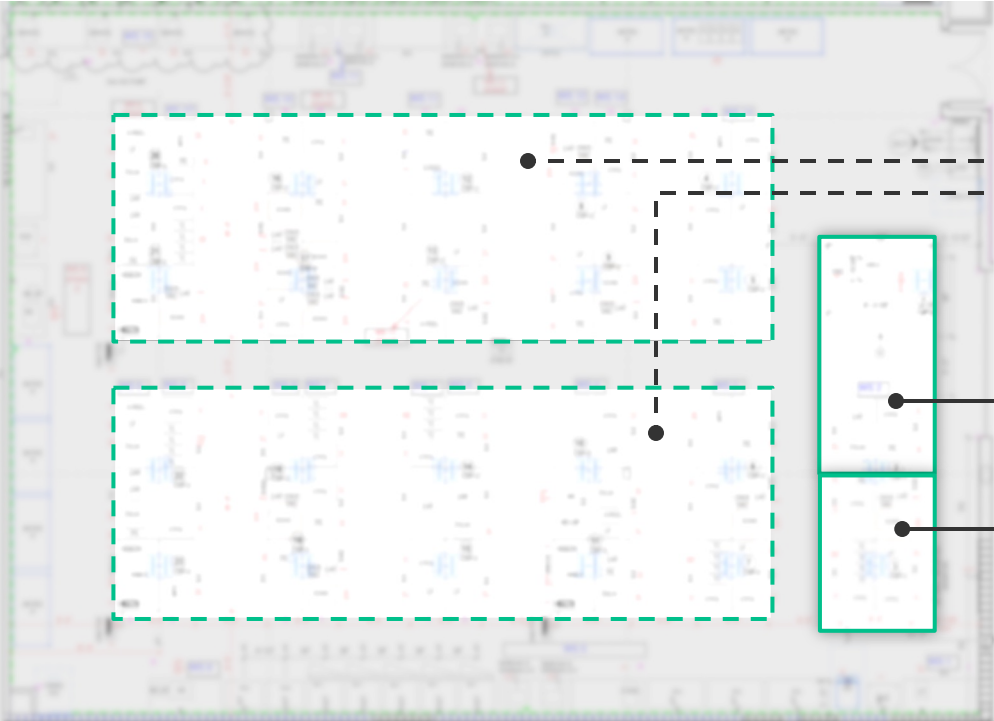
Number of integrated systems

● NGS panels and kits

● DNA synthesis and protein solutions



# Automating the Automation: Doubling Throughput in 20% of Physical Footprint



**Then**  
 Gene fragment workstation  
 (step 1 and step 2)  
 ~950 sq.ft. + ~950 sq.ft.

**Now**  
 2 integrated systems  
 System 1 ~150 sq.ft. + System 2 ~160 sq.ft.

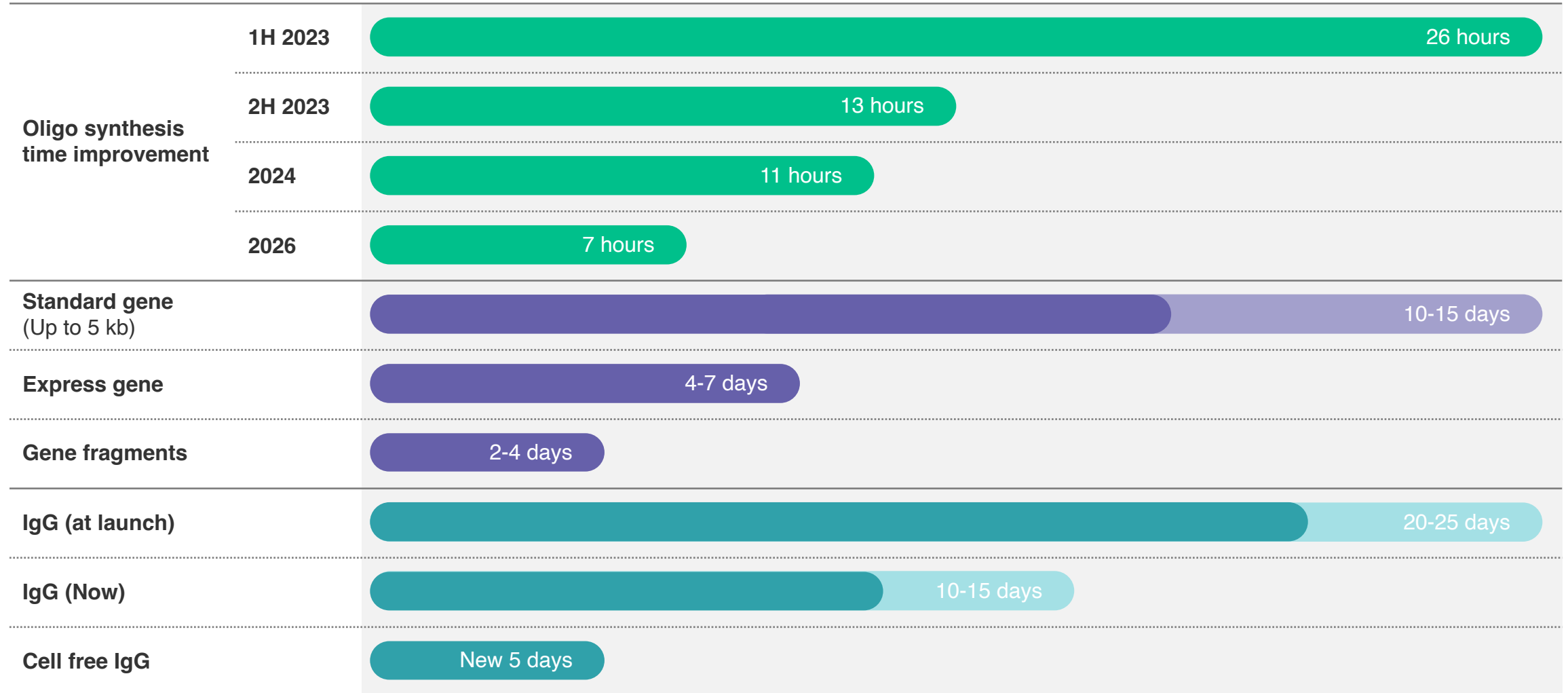
|                       | Automated                   | Integrated |
|-----------------------|-----------------------------|------------|
| # of operators        | 3-4                         | 1-2        |
| Hands-on time (hours) | 9-10                        | 1-2        |
| Batch size            | 12 plates                   | 16 plates  |
| Tracking steps        | 50% reduction in integrated |            |

Now, we are manufacturing  
**2x gene fragments in  
 1/5 the space**

We “automated the automation”

- ↑ Increased capacity
- ↑ Increased productivity
- ↓ Reduced headcount required

# In Pursuit of Speed: Decreased TAT over Time



# Operational Excellence Delivers Consistent Value to Margins and Cash Position

## FY24:

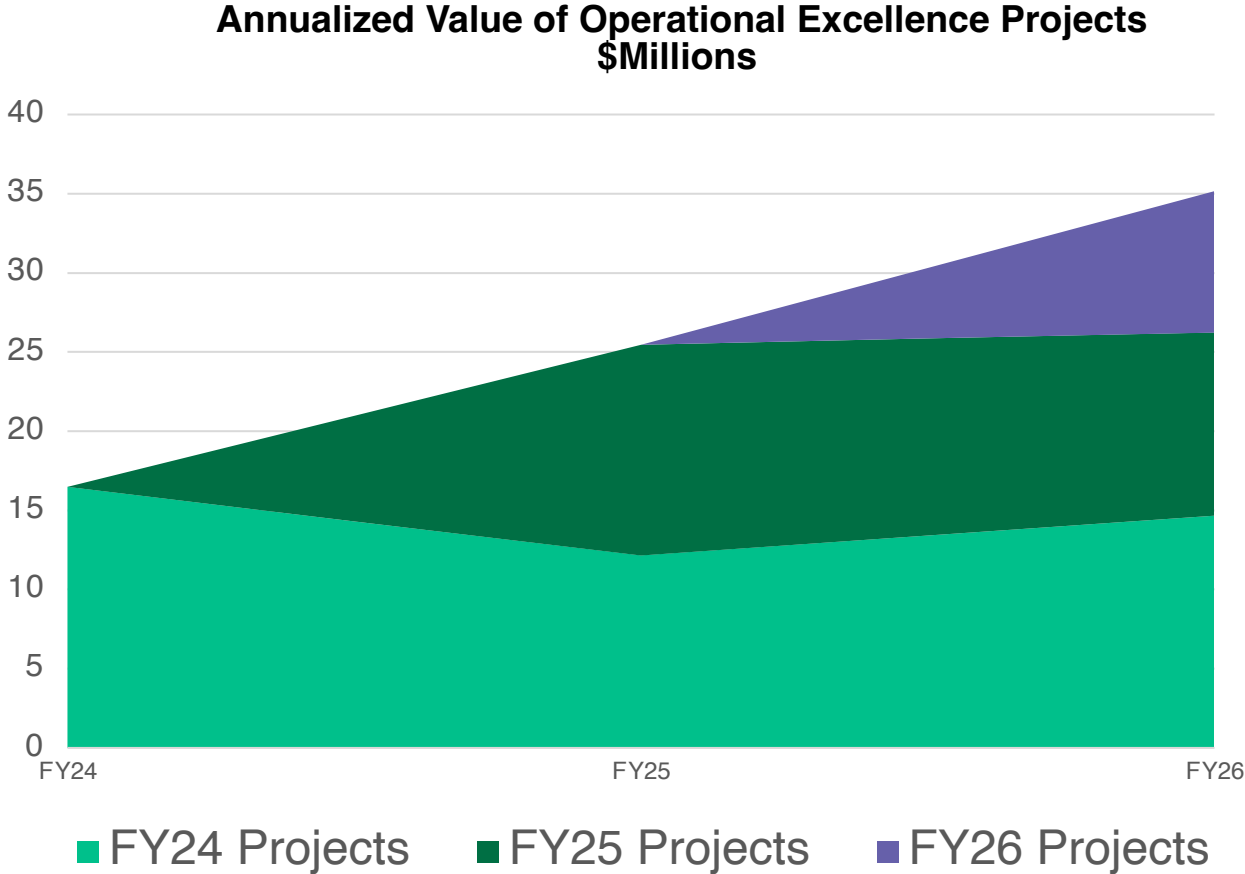
18 projects worth **\$17M**

## FY25:

28 projects worth **\$13M**, and additional **\$12M carry-forward** from FY24

## 1H'FY26:

18 projects worth **\$9M** (annualized) with **\$26M carry-forward** from FY24 and FY25



# Operational Excellence: Panel Synthesis Advancement

Customers launching bespoke MRD assays need additional capacity for their product line



## Results

Enabled full use of **walkaway system**

Upgraded hardware and software and leveraging our exceptional engineering and software teams

With a fixed headcount, we increased capacity by **10X** and reduced turnaround time **significantly**

Consumables savings of ~\$2M+ first year savings

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# Dr. Frances H. Arnold

Nobel Laureate and Linus Pauling Professor  
of Chemical Engineering, Bioengineering and Biochemistry;  
Director, Donna and Benjamin M. Rosen Bioengineering  
Center at the California Institute of Technology

*Fireside Chat with Dr. Emily Leproust*



# Colby Souders

Chief Scientific Officer

*AI-Enabled Drug Discovery*



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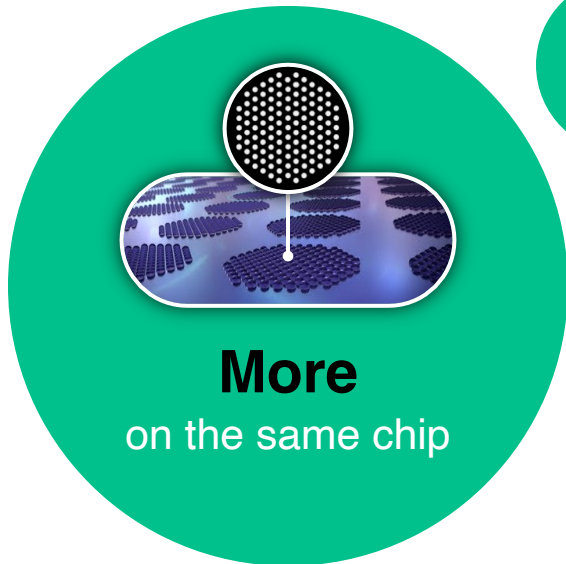
**Nucleic acid therapeutics**

Next growth frontier

**Twist culture**

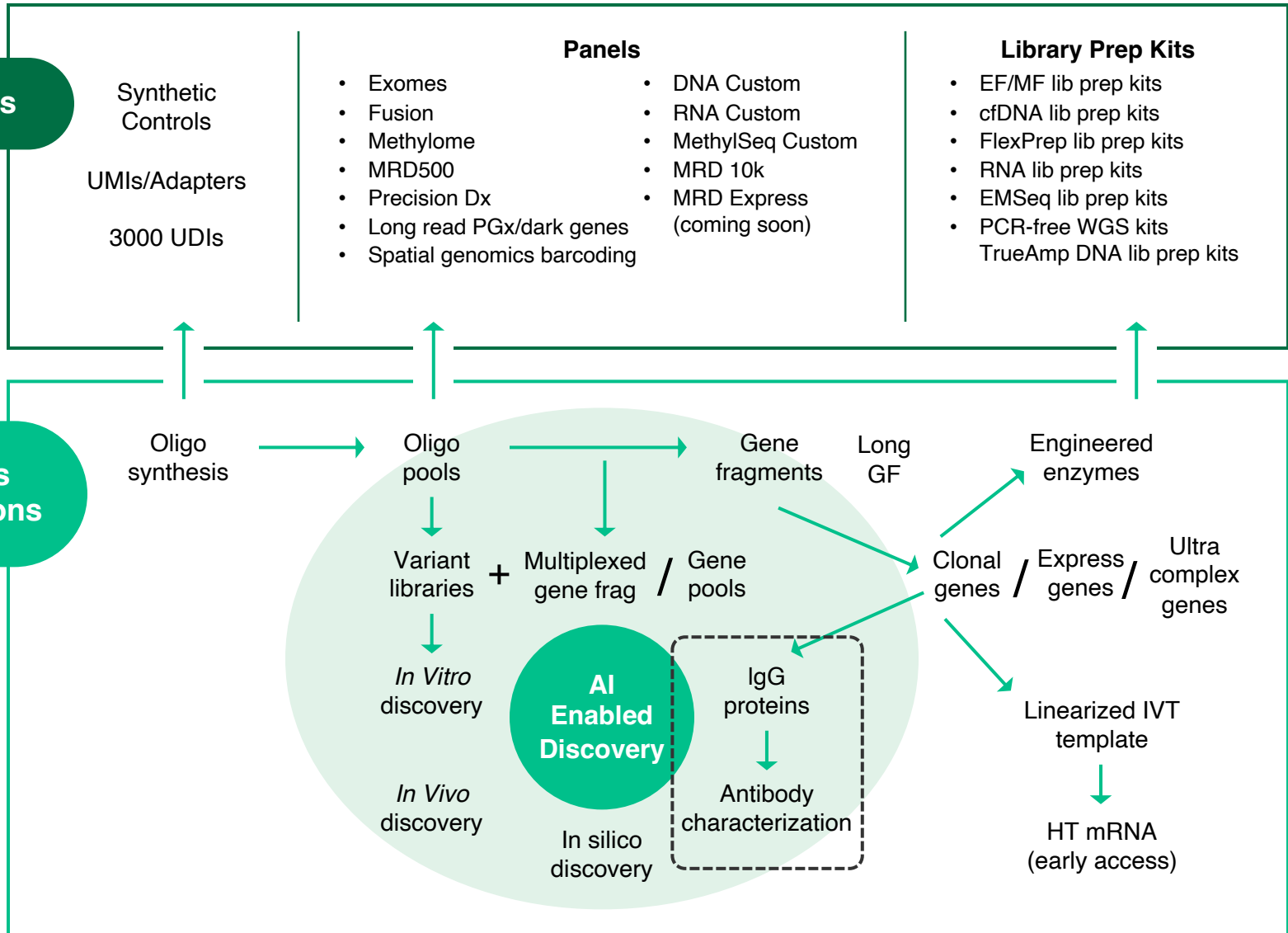
# Synergistic Solutions that Work Together

2026



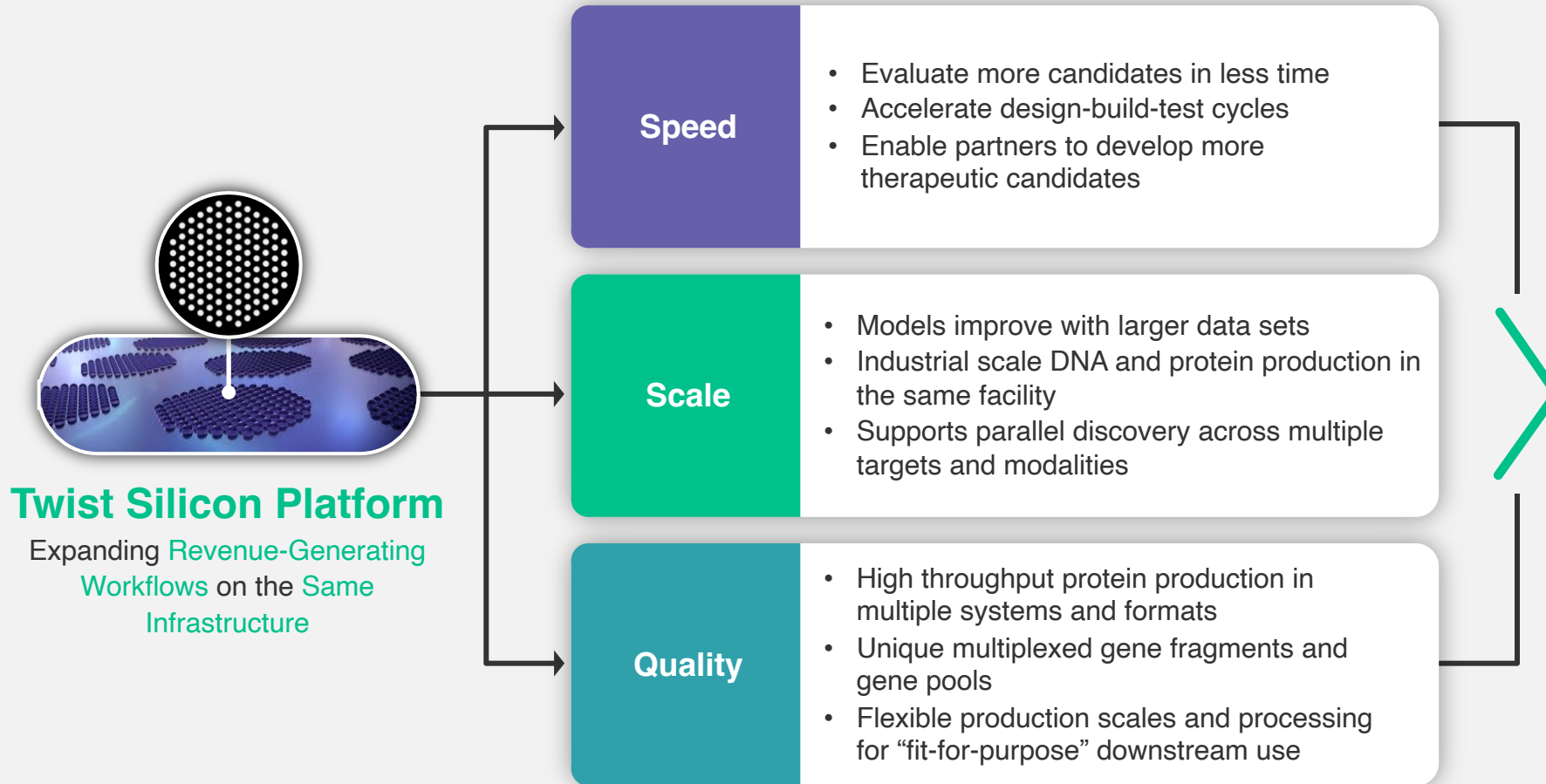
## NGS applications

## DNA synthesis & protein solutions



\*Introduced in 2025

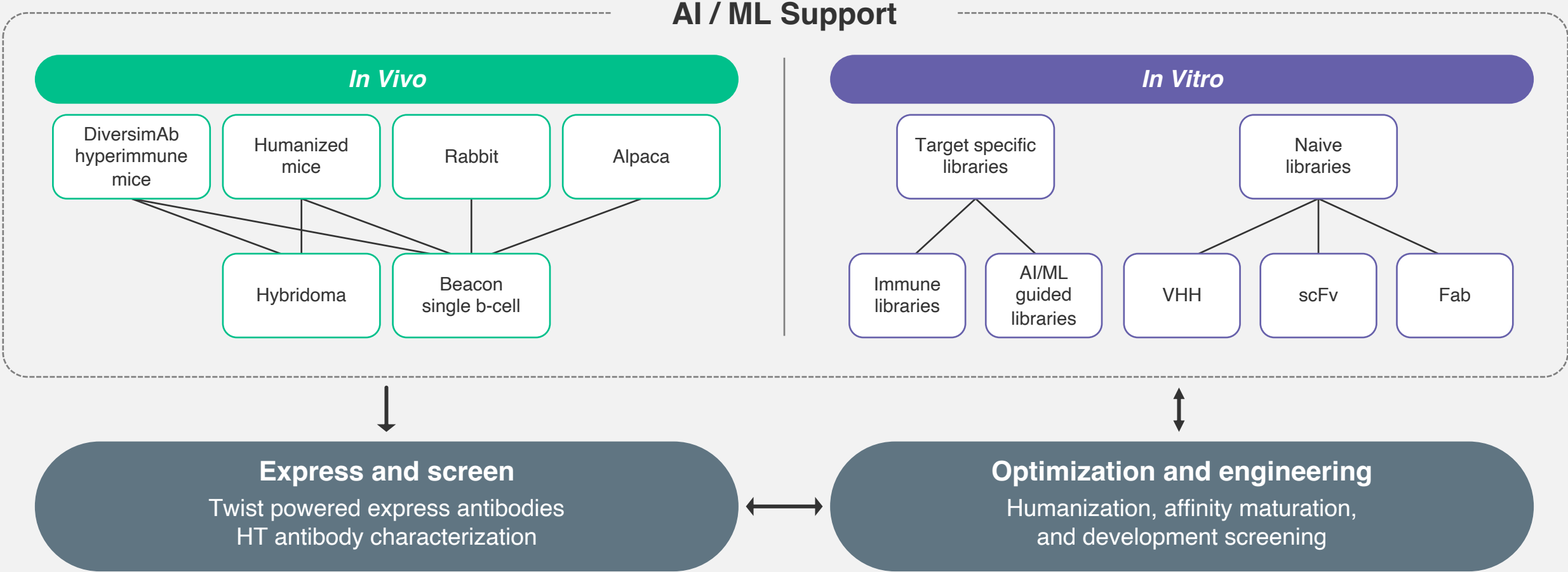
# AI-Enabled Antibody Discovery: DNA Determines Speed, Scale, Quality of Data



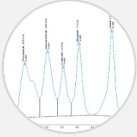
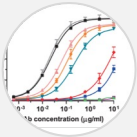
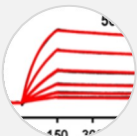
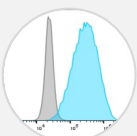

**AI-ready sequence**  
→ **protein** → binding/  
characterization  
data sets

**AI protein and antibody discovery starts with DNA.** Twist’s silicon-based synthesis platform turns the key input bottleneck into a strategic advantage

# We Partner with Researchers to Provide Comprehensive Support for Therapeutic Discovery



# Diverse, Scalable Assay Capabilities for Antibody and Protein Characterization

|   |   |  |
|---|---|--|
| <p><b>Automated throughput protein production</b></p>           |    | <p><b>Protein purification</b></p> <ul style="list-style-type: none"> <li>• High throughput automated small-scale purification</li> <li>• Medium to large scale purification of immunogens, reagents &amp; up to 100 mg+ of mAbs</li> </ul>  |
| <p><b>Binding evaluation</b></p>                                |    | <p><b>ELISA</b></p> <ul style="list-style-type: none"> <li>• Antibody screening with crude/unpurified samples</li> <li>• Screening of purified mAbs and various protein formats</li> <li>• Indirect and capture formats available</li> </ul>   |
| <p><b>Antibody functional assessment</b></p>                    |    | <p><b>SPR and BLI</b></p> <ul style="list-style-type: none"> <li>• Reagent validation (binding affinity &amp; target specificity)</li> <li>• Binding kinetics &amp; multiple blocking formats available</li> <li>• Epitope binning</li> </ul>  |
| <p><b>Antibody functional assessment</b></p>                    |   | <p><b>Flow cytometry and cell-based assays</b></p> <ul style="list-style-type: none"> <li>• Binding validation on engineered and primary cell lines</li> <li>• Screening of purified mAbs for on-cell apparent <math>K_D</math></li> <li>• Functional assays (internalization, cell signaling, agonist/antagonist activity)</li> </ul> |
| <p><b>Quality, stability, and developability assessment</b></p> |  | <p><b>Developability assessment</b></p> <ul style="list-style-type: none"> <li>• SEC, CIC, HIC, AC-SINS, BVP-ELISA (or OVA) off-target</li> <li>• DLS and nDSF: <math>T_m</math>, <math>T_{onset}</math>, <math>T_{agg}</math>, <math>rH</math>, <math>T_{size}</math></li> </ul>  |

## Broad and deep capabilities



Big Tuna



MicroLab STAR



AKTA pure



HPLC



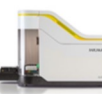
LabChip



Carterra LSA



Octet RH96



iQue



Sony MA900



NanoTemper Panta



Lunatic



Uncle

# AI Discovery Expands Twist from a DNA Supplier to a Broader Protein and Data Partner



## Differentiator: Deep antibody discovery expertise

- Proprietary antibody discovery CRO business
- We know what AI customers need from data quality and workflow design

**Differentiates Twist from other high-throughput manufacturers and traditional CROs**



## Protein generation

- High-throughput production at customer scale
- Expression of full-length IgG proteins



## Data generation

- Expertise in characterization workflows
- Scalable plate-based 96 / 384 well formats
- Existing CROs lack ability to operate at this AI-required scale

## Foundation: DNA making

Industry-leading TAT

Highest throughput

Strong capability

Exceptional quality

## Required foundation: best-in-class DNA writing

DNA synthesis, high fidelity, and large-scale manufacturing capacity



## Scaling customization

High-throughput automation

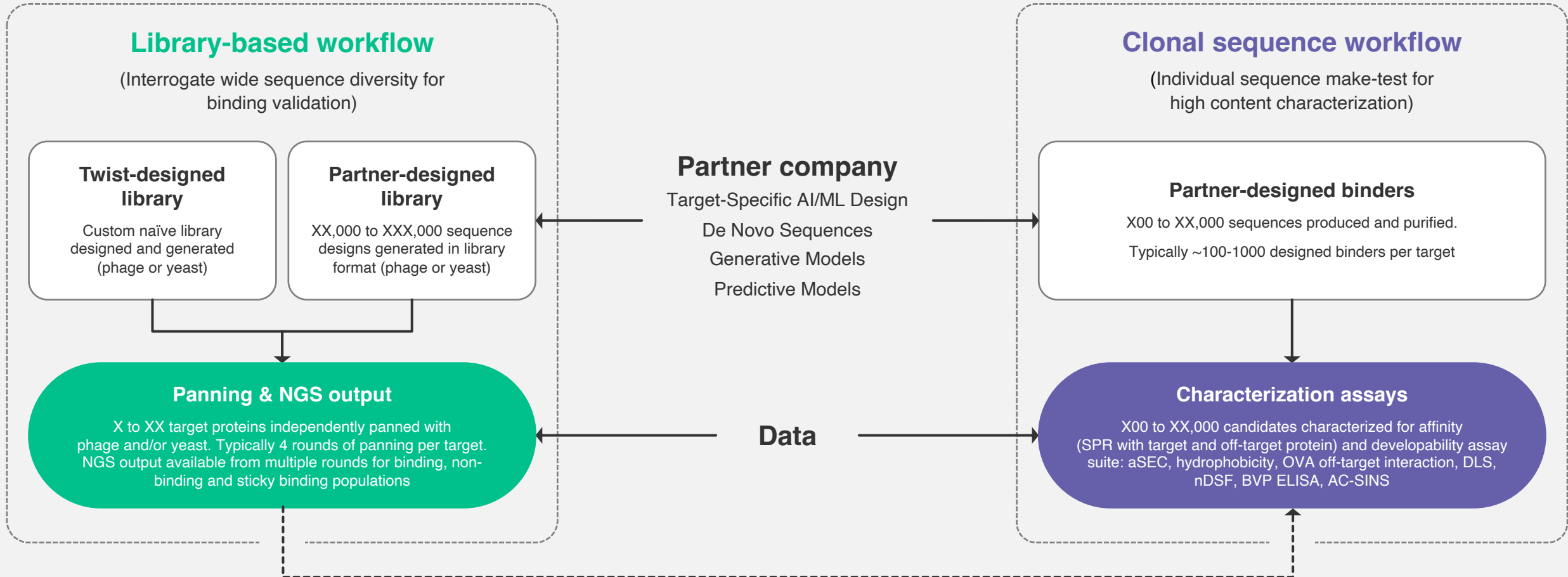
Manufacturing Execution System

Logistics infrastructure

Twist combines an unmatched DNA foundation, scaled protein and data generation, and deep discovery expertise to **serve AI antibody discovery workflows**

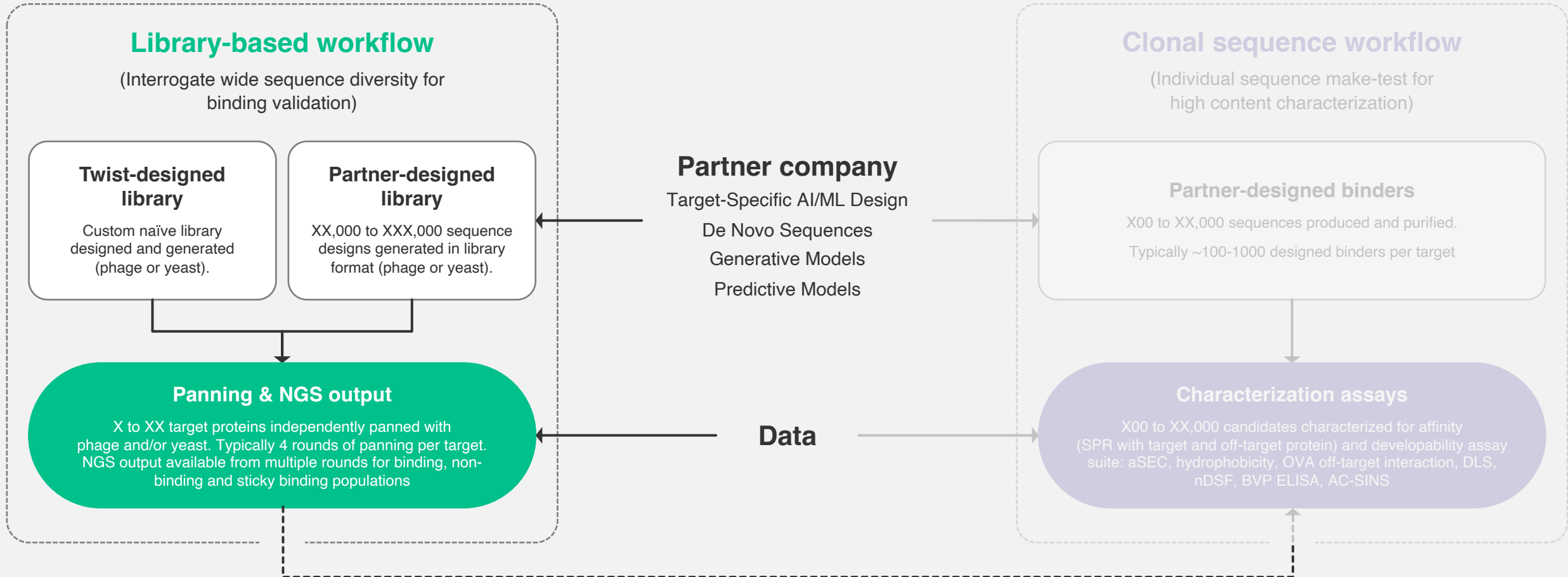
# Powering Antibody Engineering and Biologics Discovery

Multiple starting and ending points available in Twist Protein Solutions workflow



# Powering Antibody Engineering and Biologics Discovery

Multiple starting and ending points available in Twist Protein Solutions workflow



# Baker Lab *de novo* Design of Single Domain Antibodies

Custom library production for AI/ML model training, validation and refinement of 36,000 exact sequence designs



Atomically accurate *de novo* design of single-domain antibodies

Nathaniel R. Bennett, Joseph L. Watson, Robert J. Ragotte, Andrew J. Borst, Déjanaé L. See, Connor Weidle, Riti Biswas, Ellen L. Shrock, Phillip J.Y. Leung, Buwei Huang, Inna Goreschnik, Russell Ault, Kenneth D. Carr, Benedikt Singer, Cameron Criswell, Dionne Vafeados, Mariana Garcia Sanchez, Ho Min Kim, Susana Vázquez Torres, Sidney Chan, David Baker

- AI-generated VHH designs: RFDiffusion + ProteinMPNN created 9,000 unique VHHs per target
- Fully designed CDRs: All 3 loops tailored to 4 distinct epitopes
- Twist-built libraries: 4 multiplexed gene fragment pools of 9,000 VHHs each
- Target specificity validated: Cryo-EM & SPR confirmed correct binding and folding

“Make me a VHH against my target”



AI

LKVATGALNNYV...  
LKVWTGALNTYV...  
LKVWTGCLNTYV...  
DNA synthesis



Wet Lab

Final drug

RFDiffusion  
“Design binders”

ProteinMPNN  
“CDR Sequence Design”

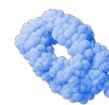
RosettaFold  
“Structure-based Filtering”



4 x 9,000 variant pools synthesized for screening

Validated target specific VHH

Multiplexed Gene Fragments



CDR1

CDR2

CDR3

Multiplexed Gene Fragments span full VHHs for AI-driven design

# De Novo Single Domain Antibodies for Amazon's MSK Discovery Project

AI-designed nanobody candidates validated against a previously untargeted cancer antigen

## Library data generation in weeks

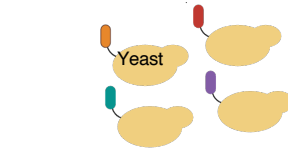
- **>300,000** sequences identified across **12** populations from **~24M** NGS reads
- **~500** individual clones sorted for binding and non-binding populations



**MSK Case Study**  
REPORT AND RESULTS



Displayed VHH



1e5 Designed Sequences  
1.4e8 Transformed Yeast

Decrease in Antigen

Increase in Washes

Round 1

+ and -  
Selection

Round 2

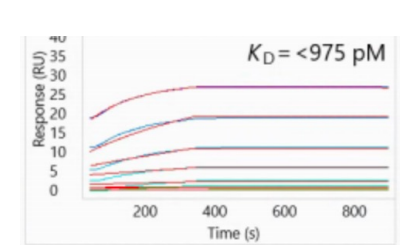
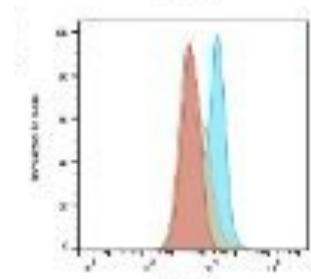
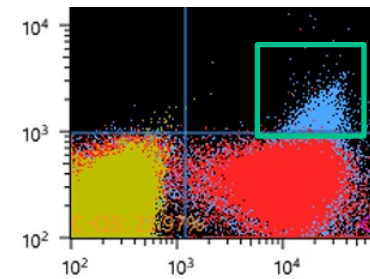
+ and -  
Selection

Round 3

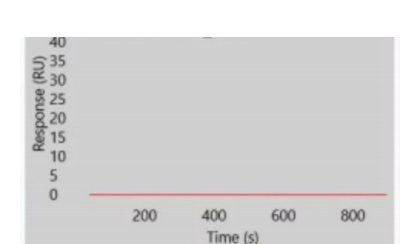
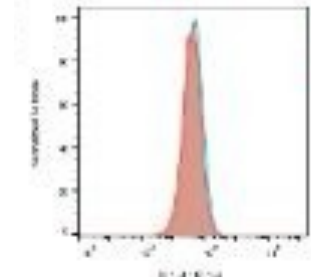
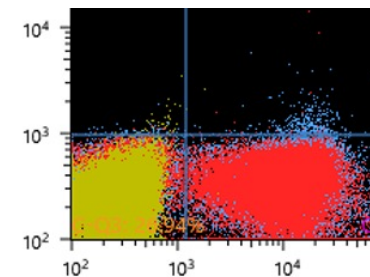
High [Target]  
Sort and NGS

Low [Target]  
Sort and NGS

Target

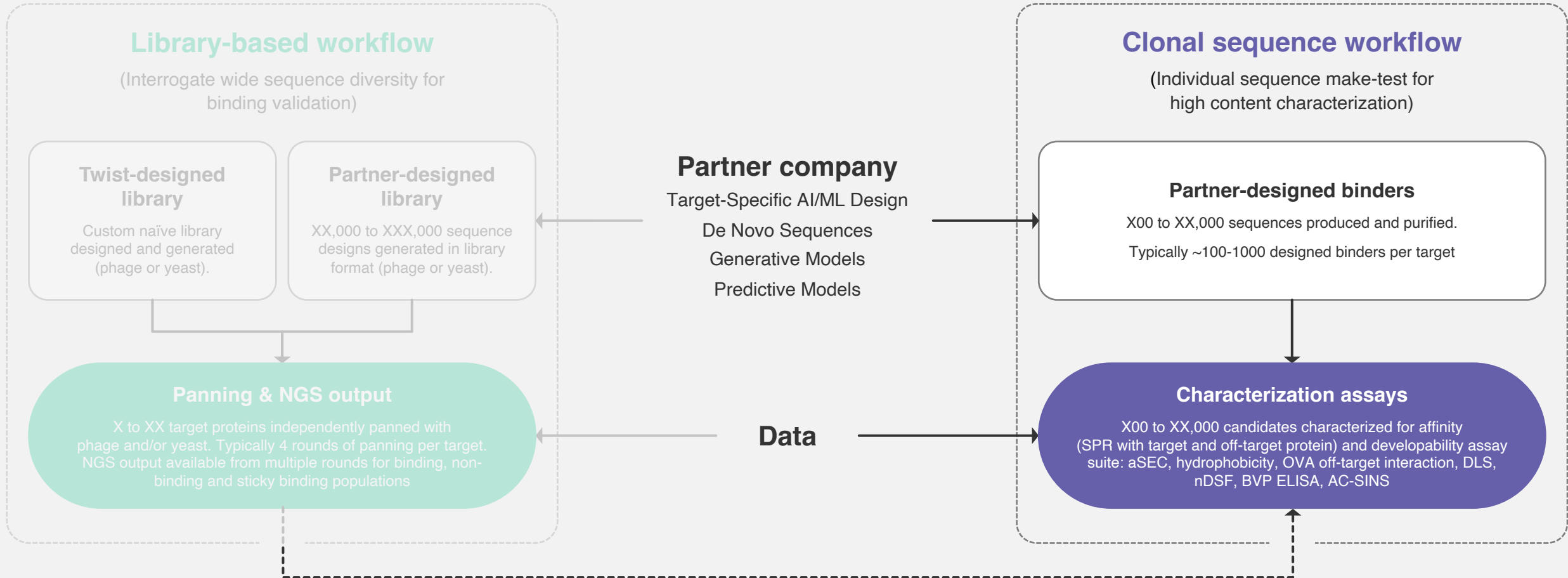


Off-target



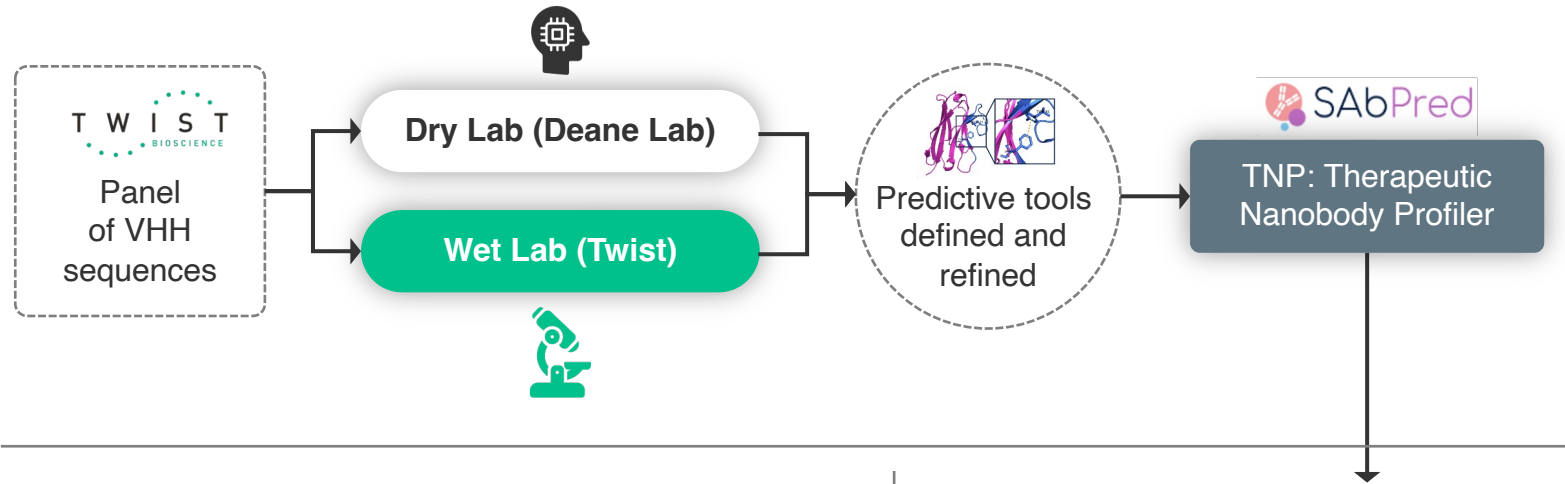
# Powering Antibody Engineering and Biologics Discovery

Multiple starting and ending points available in Twist Protein Solutions workflow

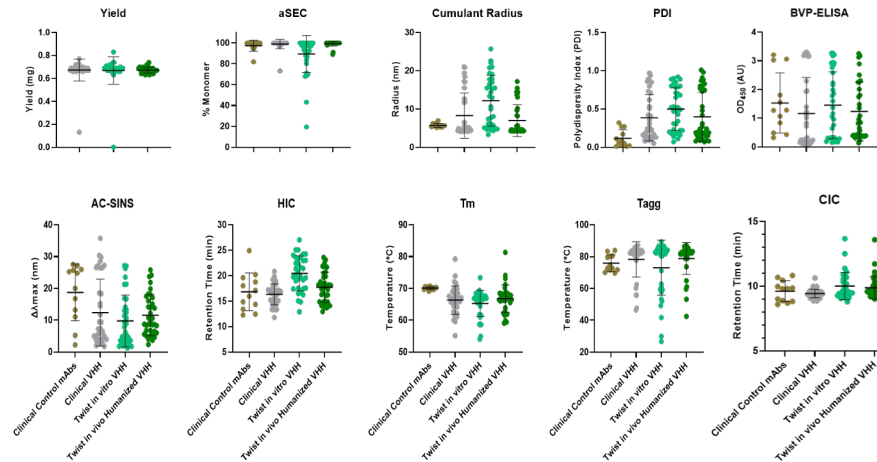


# Production and Characterization of VHHs for Therapeutic Nanobody Profiler

High throughput expression and characterization for AI/ML model training, validation and refinement



## High Throughput Production and Developability Assessment Assay Suite



## Final Open-Source Model Developed

[nature](#) > [communications biology](#) > [articles](#) > [article](#)

Article | [Open access](#) | Published: 31 January 2026

### Characterising nanobody developability to improve therapeutic design using the Therapeutic Nanobody Profiler

[Gemma L. Gordon](#), [João Gervasio](#), [Colby Souder](#) & [Charlotte M. Deane](#) ✉

[Communications Biology](#), Article number: (2026) | [Cite this article](#)

# Production and Characterization of IgG and VHH for Amazon Bio Discovery Benchmark Dataset

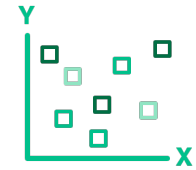
This experimental dataset provides the benchmarking foundation for evaluating AI models on antibody binding and developability prediction

Twist's experimental capabilities act as essential infrastructure for evaluating and improving AI models



**5,000**

sequences produced across 50 independent targets



**70,000**

data points generated across 7 assays

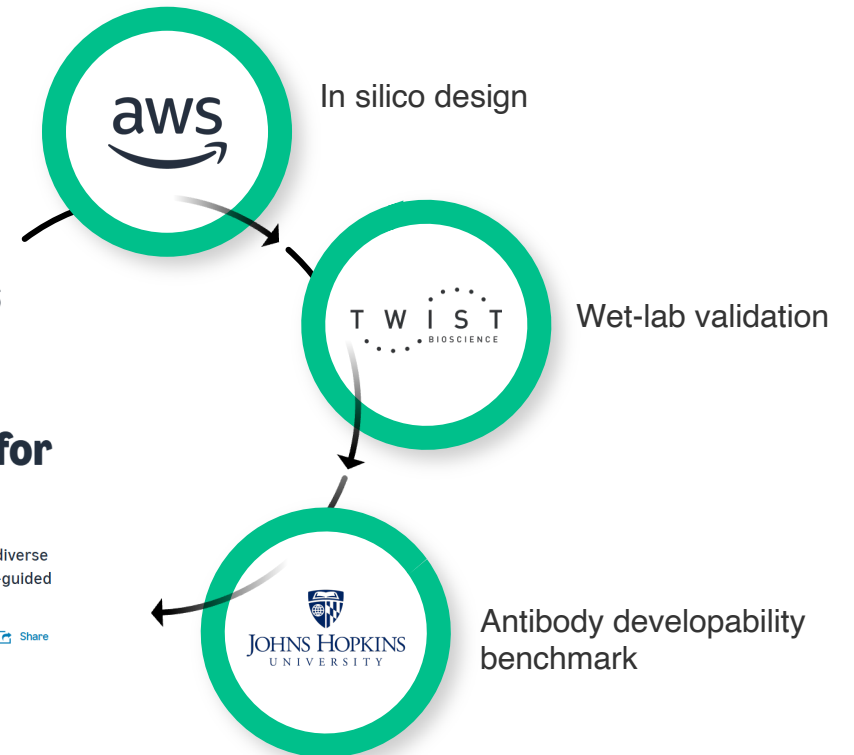
Machine learning

## AWS and Gray Lab at Johns Hopkins Whiting School of Engineering announce groundbreaking database for AI/ML antibody design

The Antibody Developability Benchmark is powered by one of the most diverse antibody datasets, enabling transparent performance evaluation for AI-guided antibody design.

By Staff writer  
April 14, 2026 | 10 min read

Share

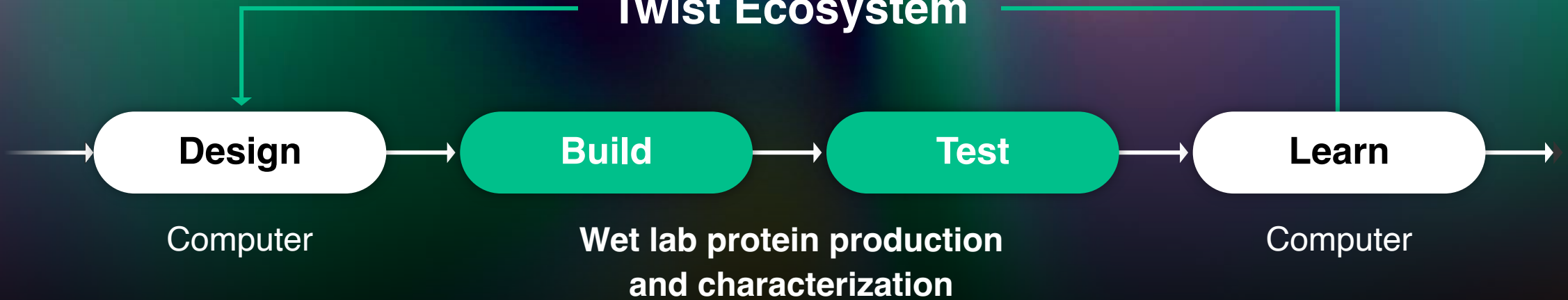




# The Customer Journey

What, How and How Much: **Real Stories**

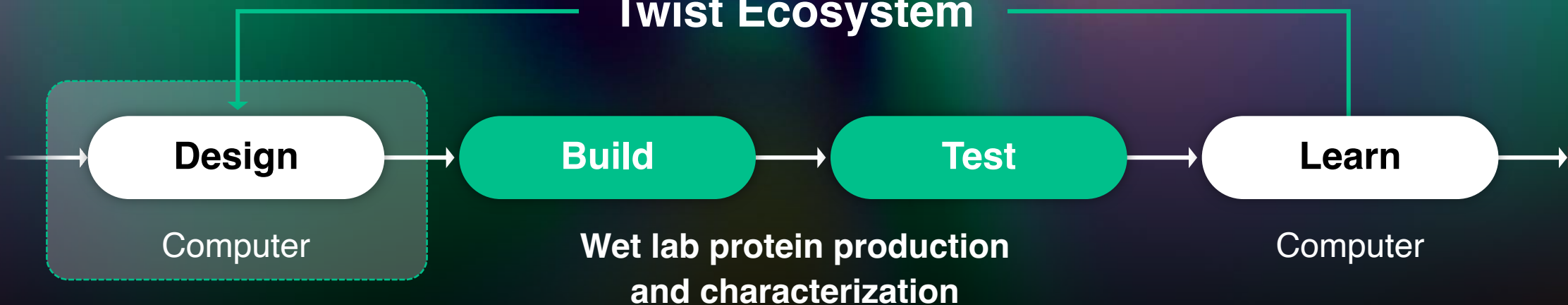
## Twist Ecosystem



## Model Building Stage

- Initial pilot study:
  - 10s-100s of sequences
- Production and characterization at Twist with 'known' sequences from Partner
- Completed within 20 days for \$10k-\$100k

## Twist Ecosystem

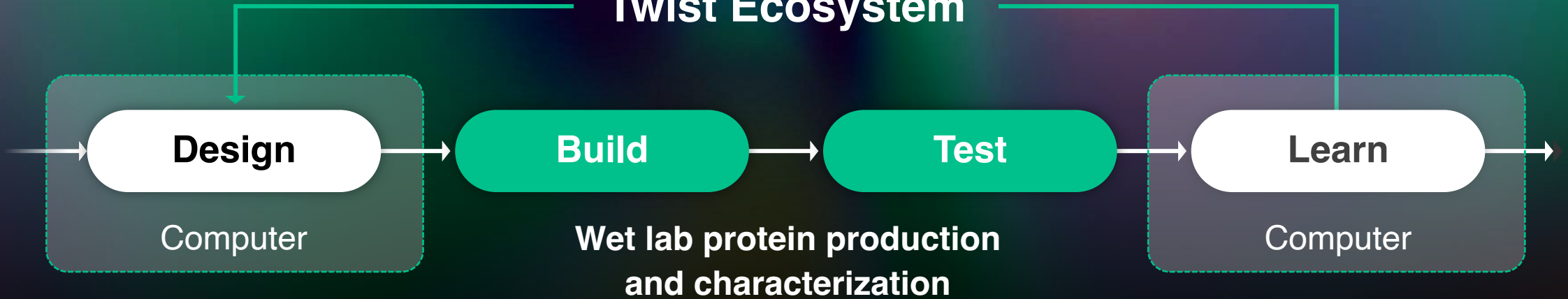


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- First round of training:
  - 1,000s of new sequence designs from Partner
- Produced and characterized at Twist
- Completed in 20-30 days for <\$1M

# Twist Ecosystem



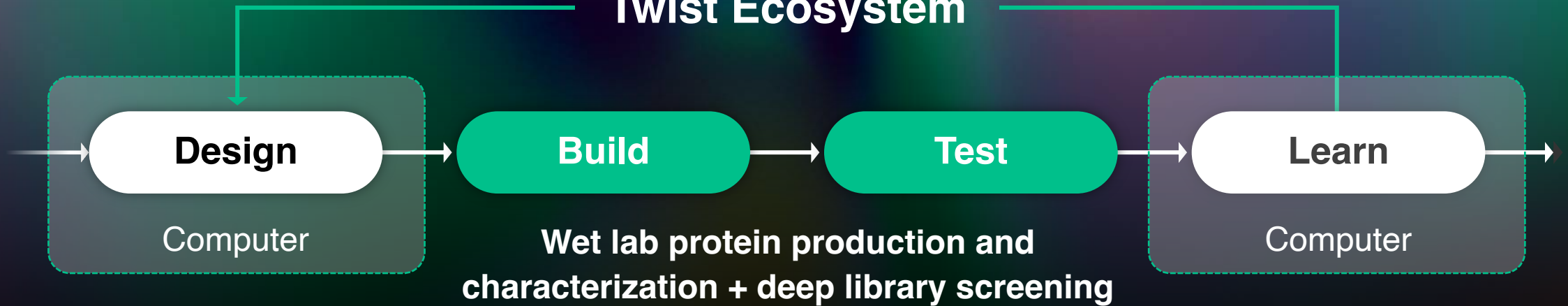
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- Produced and characterized at Twist
- Completed in 20-30 days for <\$1M

- Two to five additional rounds:
  - Fine-tune training
- 1,000s of new sequence designs from Partner based on learning from previous rounds
- Long term relationship established and final models enabled by Twist Build and Test cycle

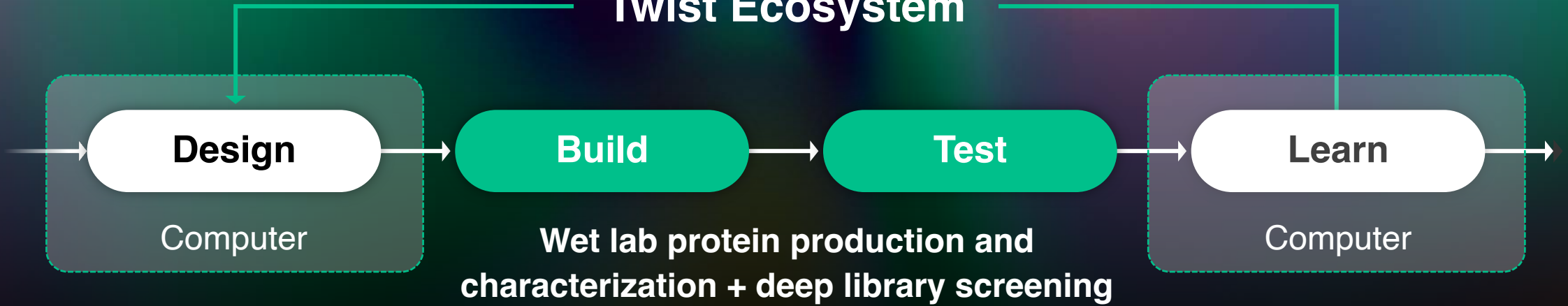
# Twist Ecosystem



## Foundational Model Required

- 10,000s to 100,000s of sequence designs for each of 5 to 50 independent targets
- Twist builds large sequence library
- Twist screens libraries to generate binding data and NGS sequence datasets
- Completed in weeks for \$100,000s to \$1Ms

# Twist Ecosystem

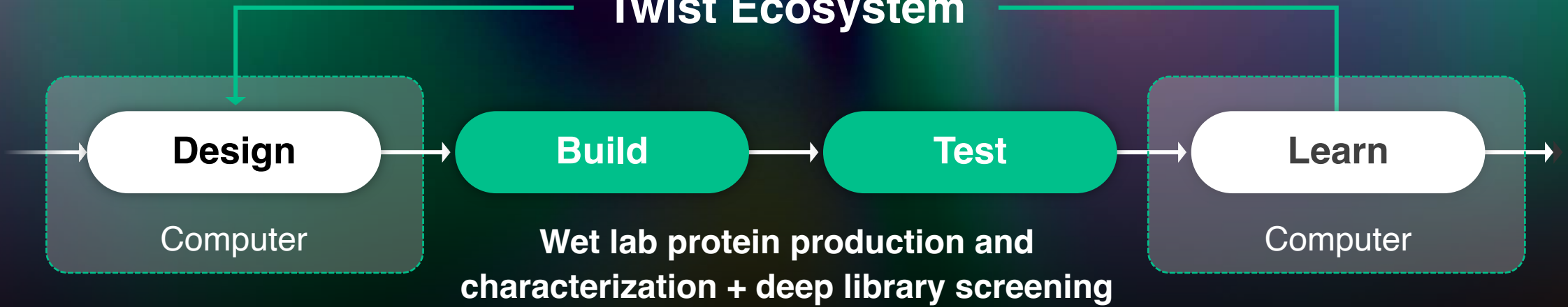


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# Twist Ecosystem



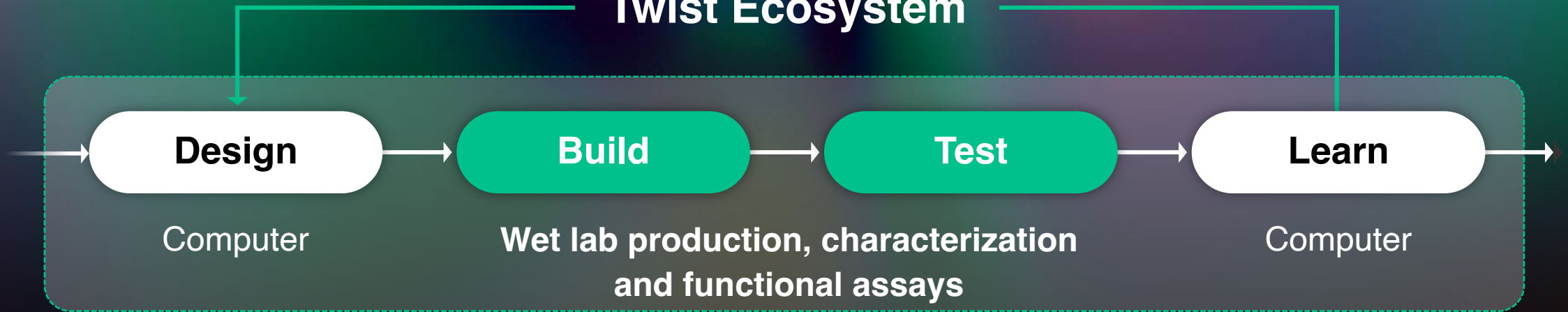
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- Validation data:
  - 1,000s of new sequence designs from Partner
- Produced and characterized at Twist
- Completed in 20-30 days for <\$1M

- Two to five additional rounds
  - Fine-tune training for multi-property criteria
- 1,000s of new sequence designs from Partner based on learning from previous rounds
- Deploy model for therapeutic discovery

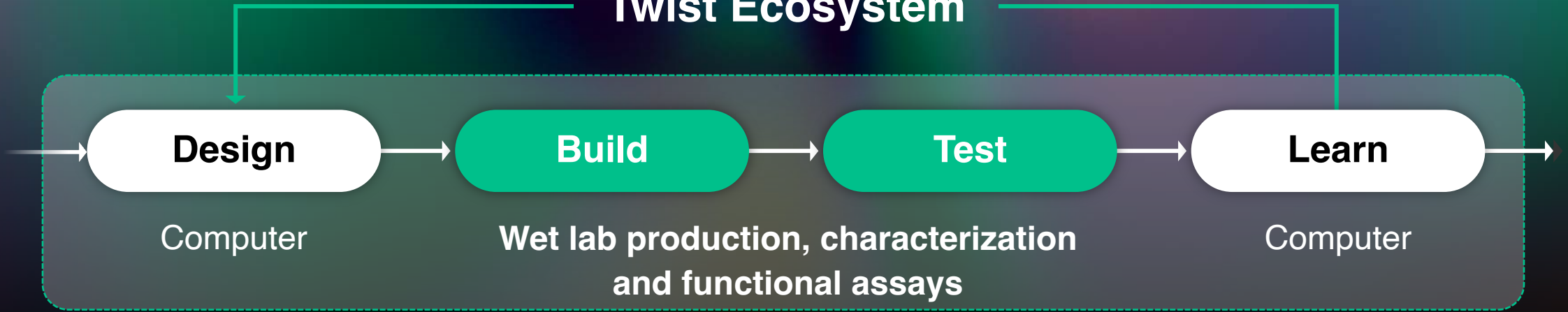
## Twist Ecosystem



## AI-Based Therapeutic Discovery

- Established, fine-tuned foundational models generate 100s to 1000s of candidates
- Twist produces and performs initial basic characterization
- Leads proceed to advanced characterization assays
- Completed in <30 days for <\$1M

# Twist Ecosystem

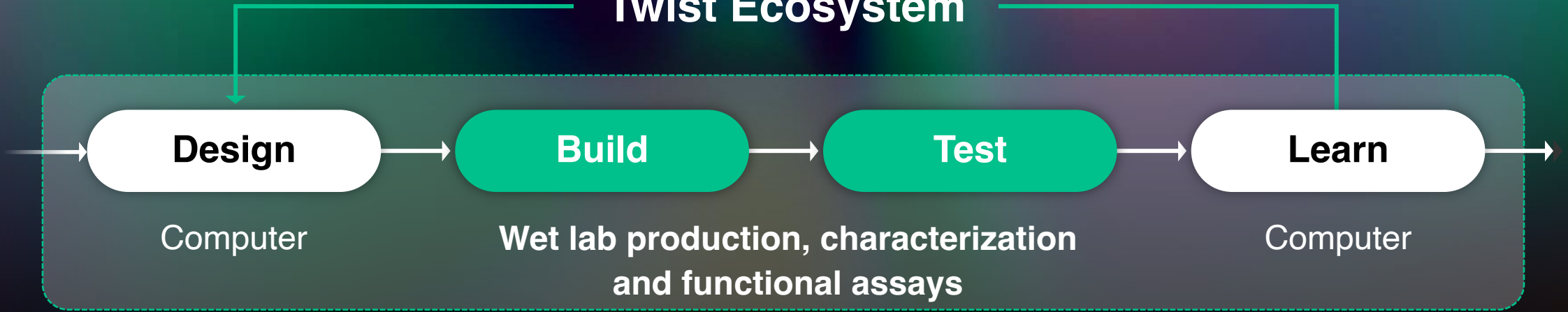


## AI-Based Therapeutic Discovery

- Established, fine-tuned foundational models generate 100s to 1000s of candidates
- Twist produces and performs initial basic characterization
- Leads proceed to advanced characterization assays
- Completed in <30 days for <\$1M

- Top candidates fed into Optimization Models
- 100s to 1000s of optimized designs produced and characterized at Twist
- Leads proceed to advanced characterization assays
- Completed in <30 days for <\$1M

# Twist Ecosystem



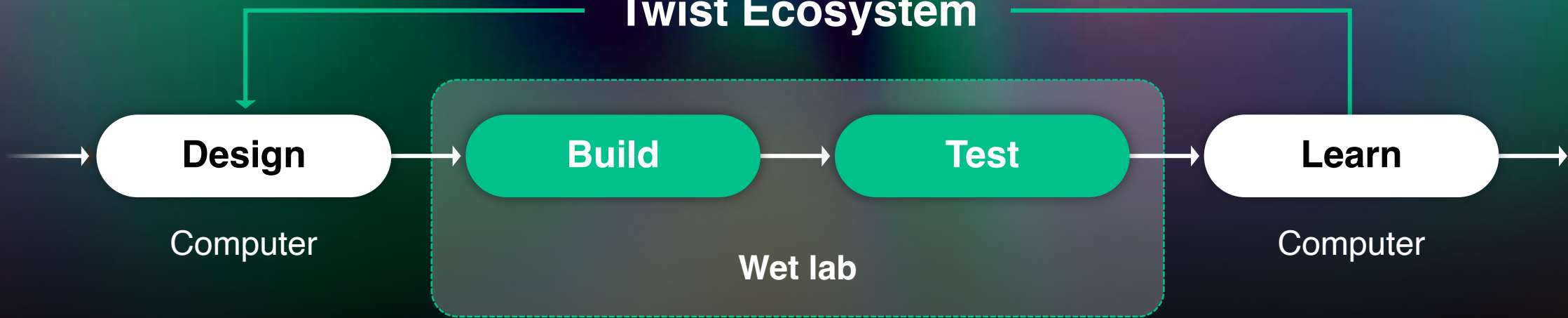
## AI-Based Therapeutic Discovery

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- Completed in <30 days for <\$1M

- Top candidates fed into Optimization Models
- 100s to 1000s of optimized designs produced and characterized at Twist
- Leads proceed to advanced characterization assays
- Completed in <30 days for <\$1M

- Partner nominates lead(s) for further preclinical testing in efficacy and tox models at CDMO
- Candidate enters Partner's therapeutic pipeline

# Twist Ecosystem

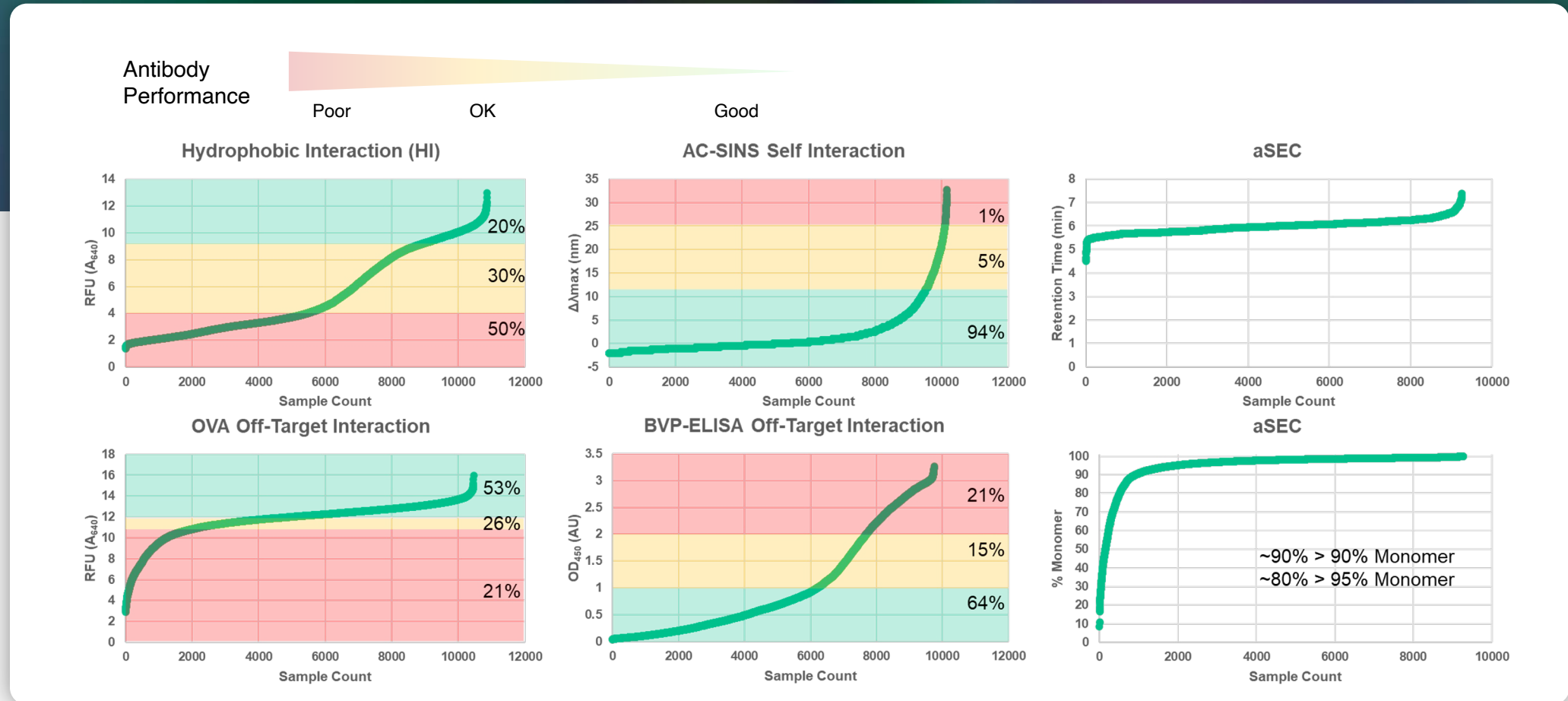


|                                     |                                    |
|-------------------------------------|------------------------------------|
| <b>200k+</b><br>Proteins Expressed  | <b>130k+</b><br>Antibodies Assayed |
| <b>7M+</b><br>Data Points Generated | <b>Dozens</b><br>Customers Served  |

As of March 5, 2026

# Large Scale, High Content Data Generation: 20 days

10,000s of datapoints for metadata capture in high-content developability assays for model building

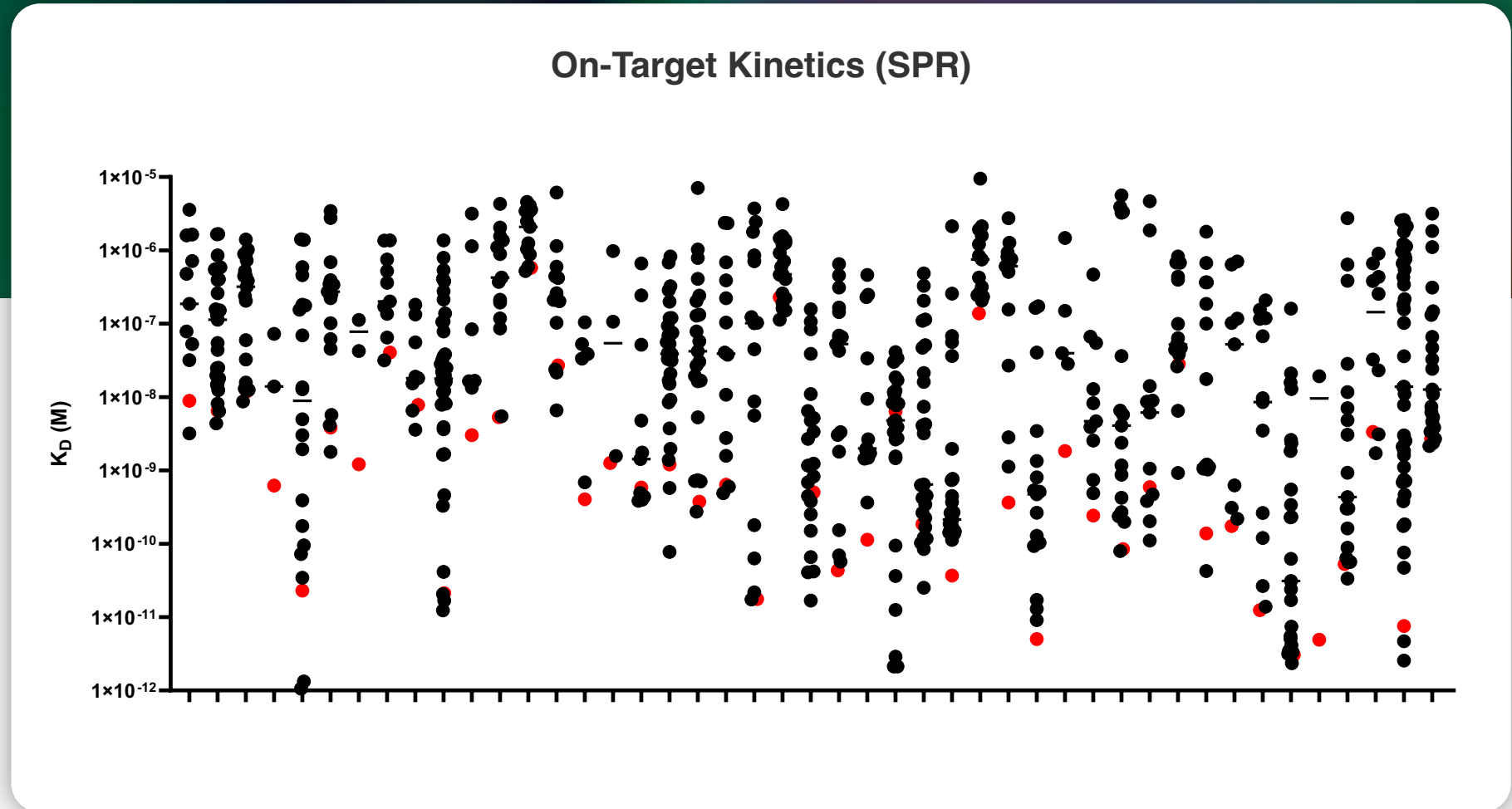


# Large Scale, High Content Data Generation: Optimization

10,000s of datapoints for metadata capture in binding kinetics assays for model validation and candidate optimization

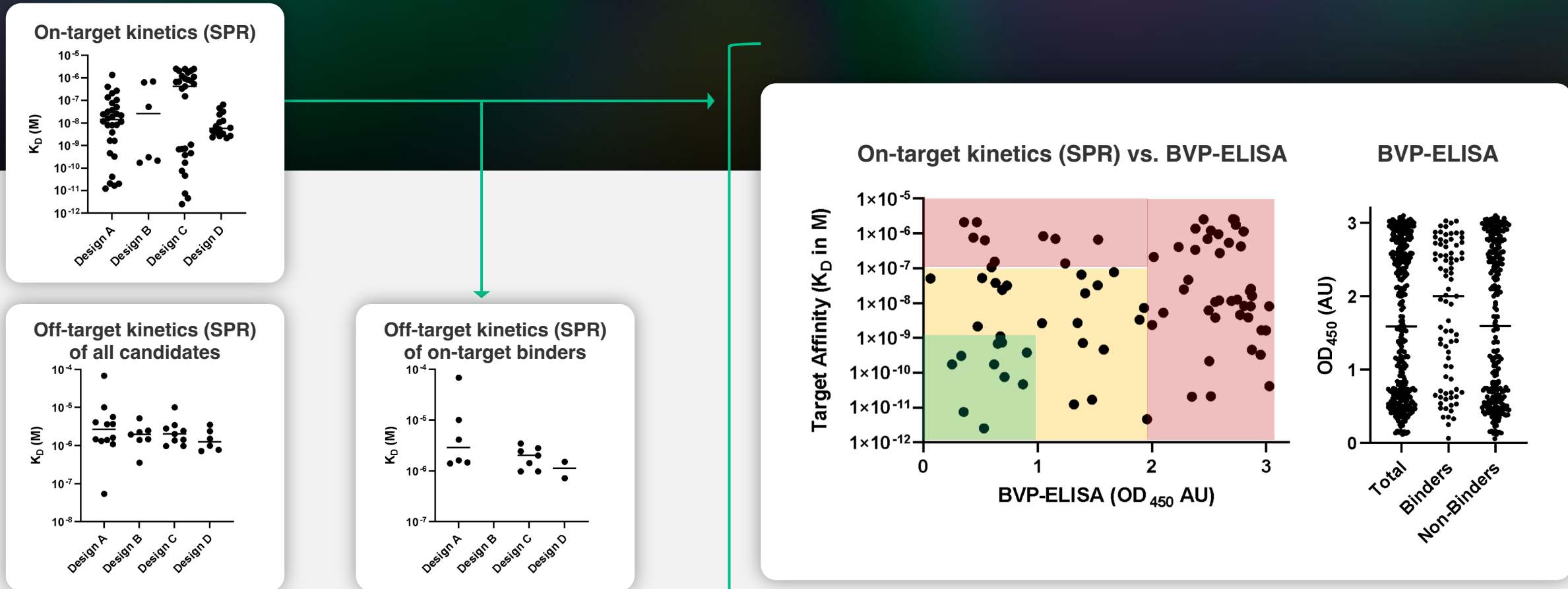
Binding kinetics: ~5000 sequence designs based on 50 different independent targets assessed in multipoint SPR on Catterra LSA-XT

Binders in  $\mu\text{M}$  to pM range; compared vs. benchmark sequence (red).



# Large Scale, High Content Data Generation: Lead Candidate Selection

Multi-parameter optimization to select lead therapeutic candidates

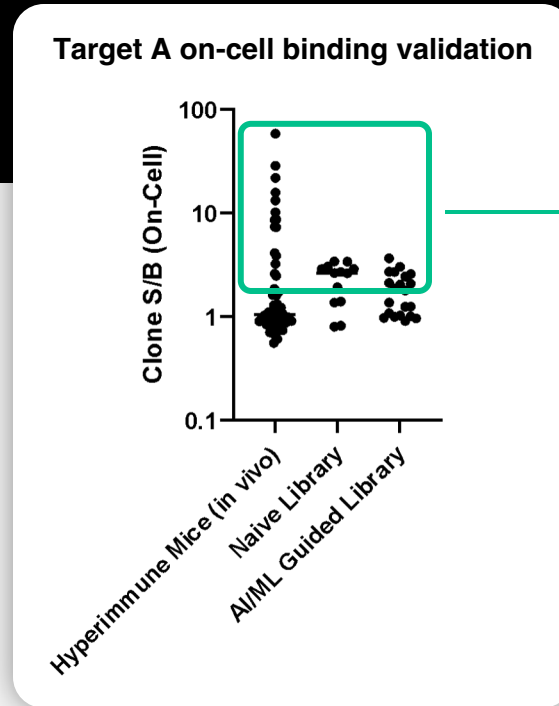
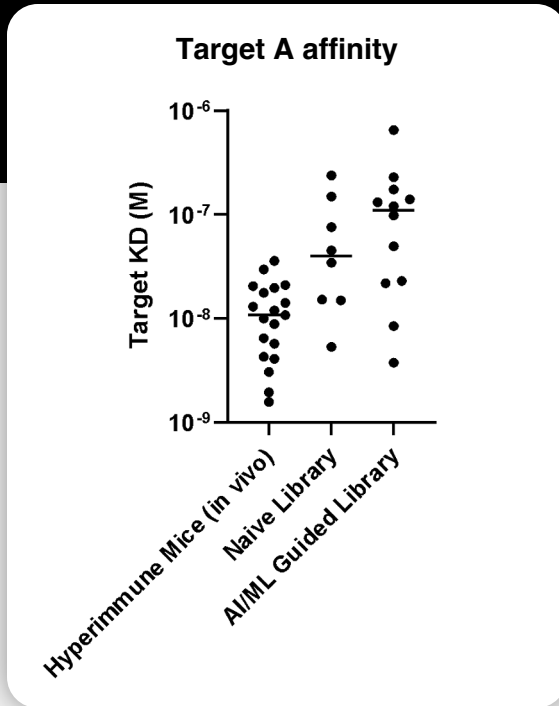


# Generative Protein Design Guided Library for Therapeutic Candidate Selection of Challenging Targets

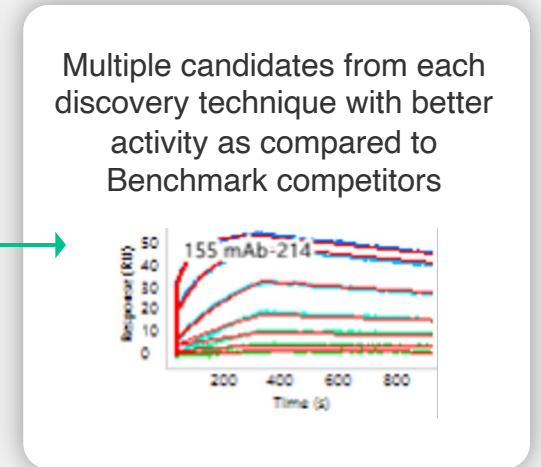
End-to-End: AI library design, build and panning for difficult cell surface target

## Results:

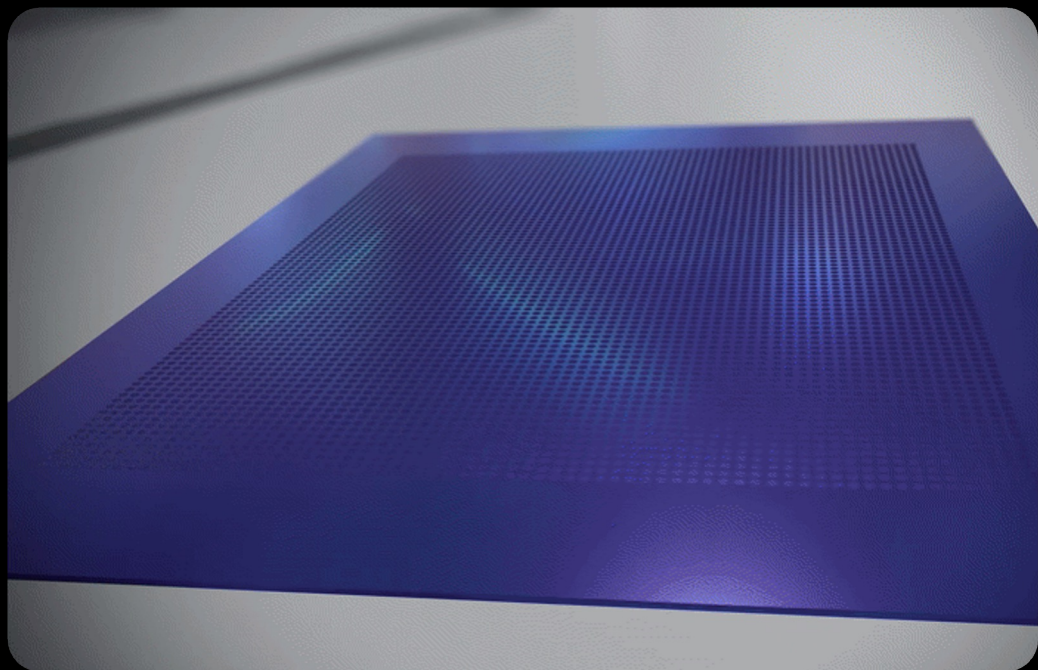
- Single- and double-digit nM binders obtained from three discovery methods (*in vivo*, naïve *in vitro* library and AI/ML guided *in vitro* library)
- On-cell binding validated, and top candidates progressed to functional validation in downstream signaling assay
- Unique candidates from each method progressed as project leads



| Source                     | Functional IC50 (nM) |
|----------------------------|----------------------|
| Hyperimmune Mice (in vivo) | 1.1                  |
|                            | 1.6                  |
|                            | 0.7                  |
| Naïve Library              | 15.0                 |
|                            | 0.8                  |
| AI/ML Guided Library       | 3.3                  |
|                            | 0.03                 |
| Benchmark A                | 28.7                 |
| Benchmark B                | 41.8                 |
|                            | 3.9                  |

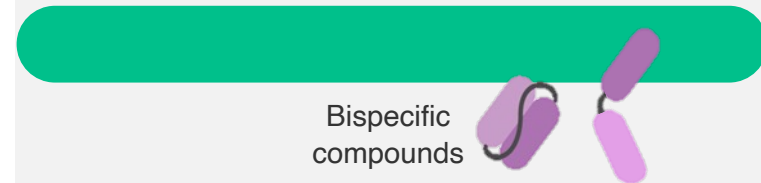


# The Future is Written on the Twist Platform



## Gene Pools

(Early Access)  
Paired Heavy+Light Chain Libraries (scFV); Precisely Paired Bispecific VHHs  
1800 bp



## Multiplexed Gene Fragments

VH, VL, VHH and Miniproteins  
500 bp



## Twist Oligos

Paired or Unpaired CDRs  
300 nts



350 nts



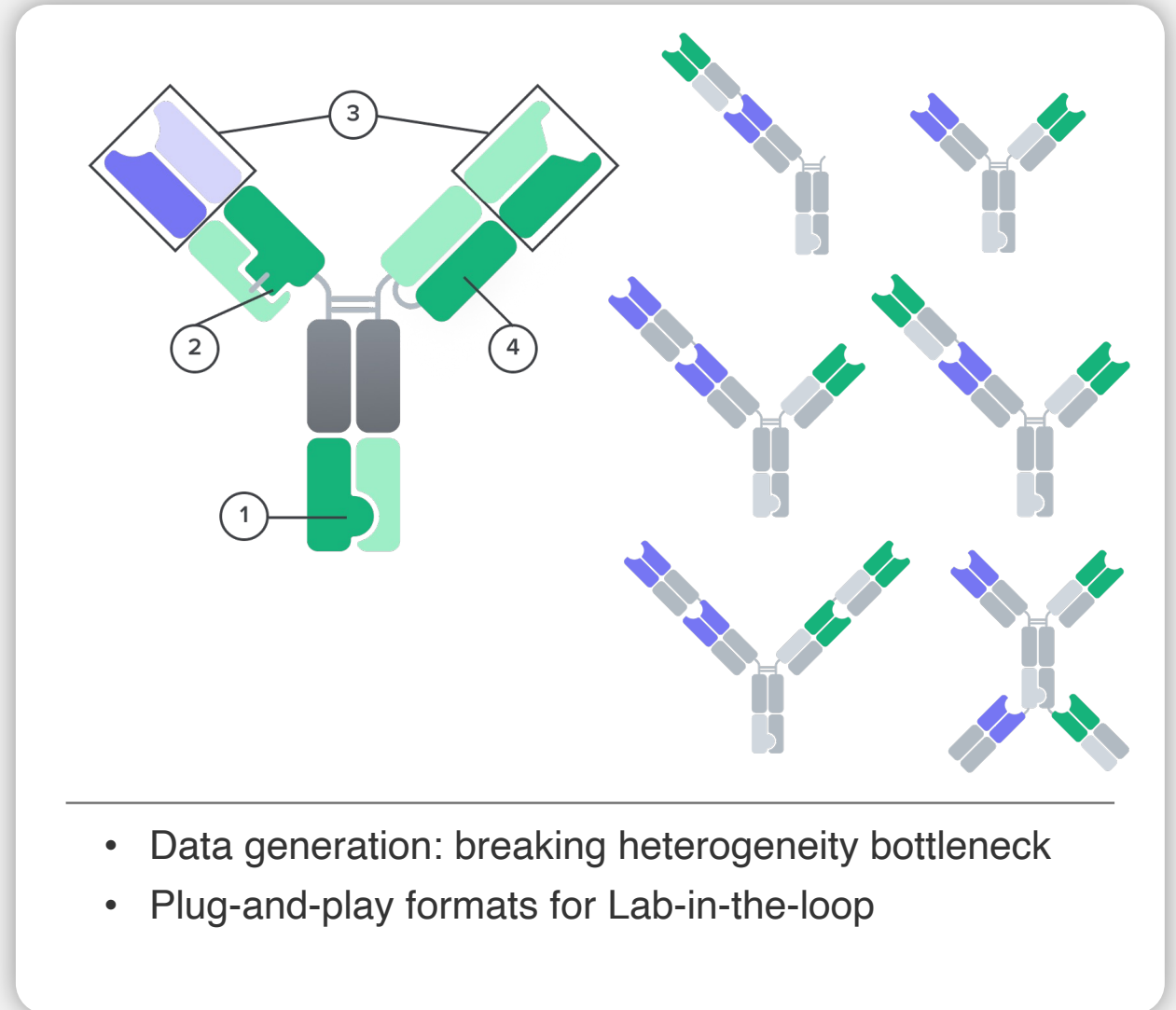
170 nts



# A Unique Bispecific Platform to Standardize “Hardware” into AI “Software”

## CMC driven innovation

- ① **Fc Region: Clinically Validated Knobs-into-Holes**
  - Drives heavy chain heterodimerization
- ② **Fab Arm: Proprietary CH3 Domains to Drive Heterodimerization**
  - Substitutes for CH1/CL in one Fab Arm
  - Solves light chain mispairing issue
  - Novel CH3 mutations, without knobs-into-holes or charge pairs
  - pl asymmetry streamlines polishing steps
- ③ **Heavy & Light Chains: Proprietary Symmetrical Inversions**
  - Enhances expression yield and stability
  - Facilitates one-step purification
  - Compatible with a wide variety of variable domain sources
- ④ **Sole CH1 Domain: Allows a Level of Purification Beyond Protein A/IEX**
  - Facilitates one-step purification with anti-CH1 resins
  - Simplifies in-format discovery
  - Removes homodimers and other impurities in one pass



# One Platform, Many Customized Solutions

Meeting customers where they are, powering growth across expanding platforms

## How we win



**Operational excellence**



**NPI machine**



**Commercial execution**

T W I S T  
BIOSCIENCE

Differentiated  
Silicon Platform  
Speed and Scale



**AI-enabled antibody discovery workflows**

AI-ready wet-lab at scale



**Molecular residual disease**

Personalized diagnostic research at scale



**Enzyme-engineered NGS**

Better performance, integrated workflow



**Nucleic acid therapeutics**

Next growth frontier

**Twist culture**

# DNA Synthesis Platform Drives Scale, Speed for AI-Enabled Discovery

**200,000+**

Proteins expressed

**130,000+**

Antibodies assayed

**7 million**

Data points for AI training

**15 days**

To Deliver AI-ready data

**6,000+**

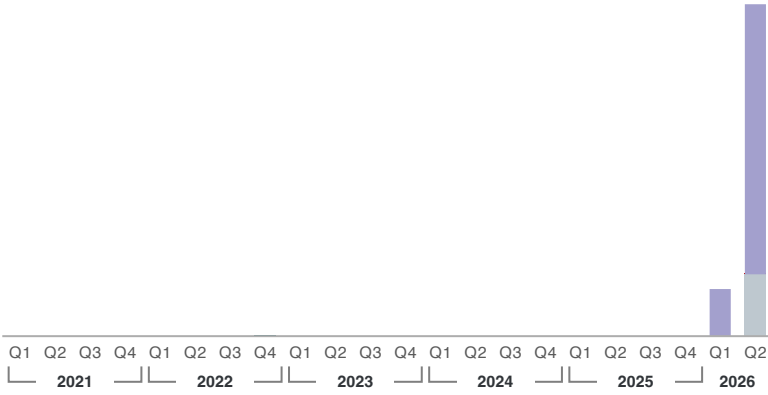
IgGs per week

**445+**

Partner organizations

As of March 5, 2026

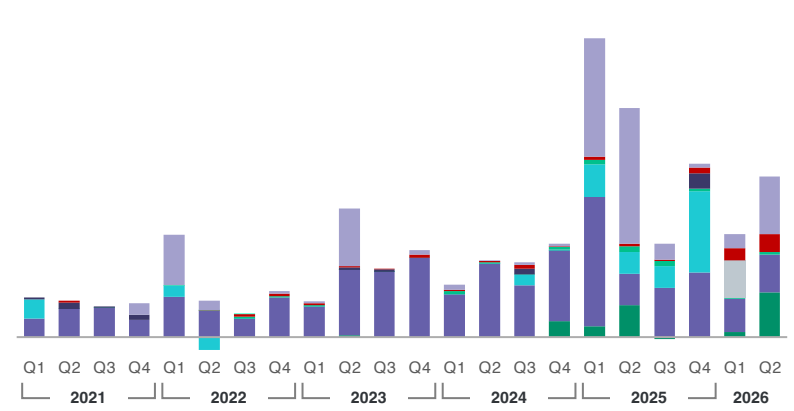
### Frontier AI Lab



**AI Enabled  
Discovery**

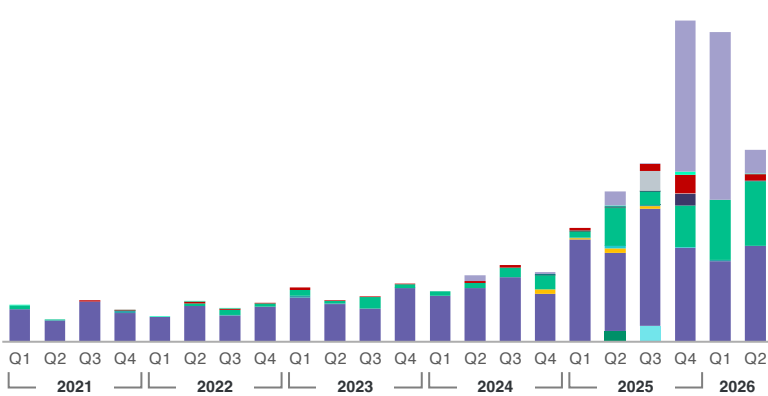
**Different Approach**  
for Every Customer  
All Adding IgG/Characterization

### Large Pharma

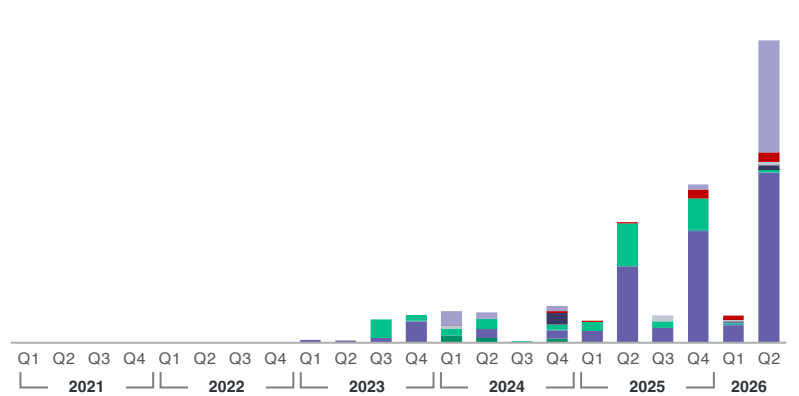


- Biopharma Services
- Gene Fragments
- Other
- Custom Vector Onboarding
- Multiplexed Gene Fragments
- Custom Panel
- Libraries
- Custom Production
- Library Prep
- Clonal Genes
- Kits and Reagents
- IgG+ Characterization
- Fixed Panel
- Oligo Pools

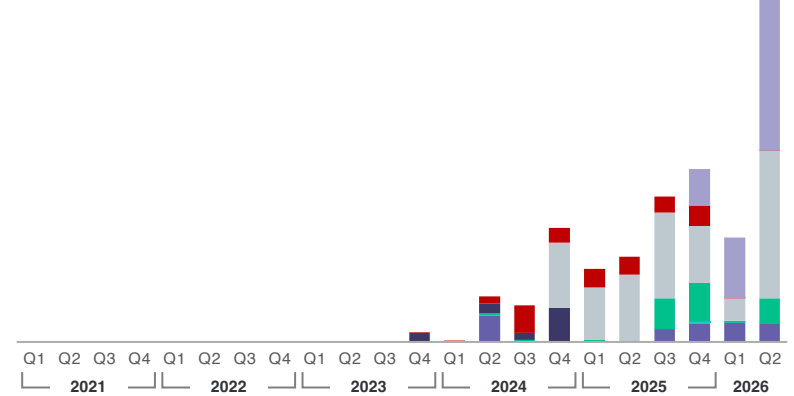
### Large Pharma



### AI-Native Biotech



### Dry Lab Biotech



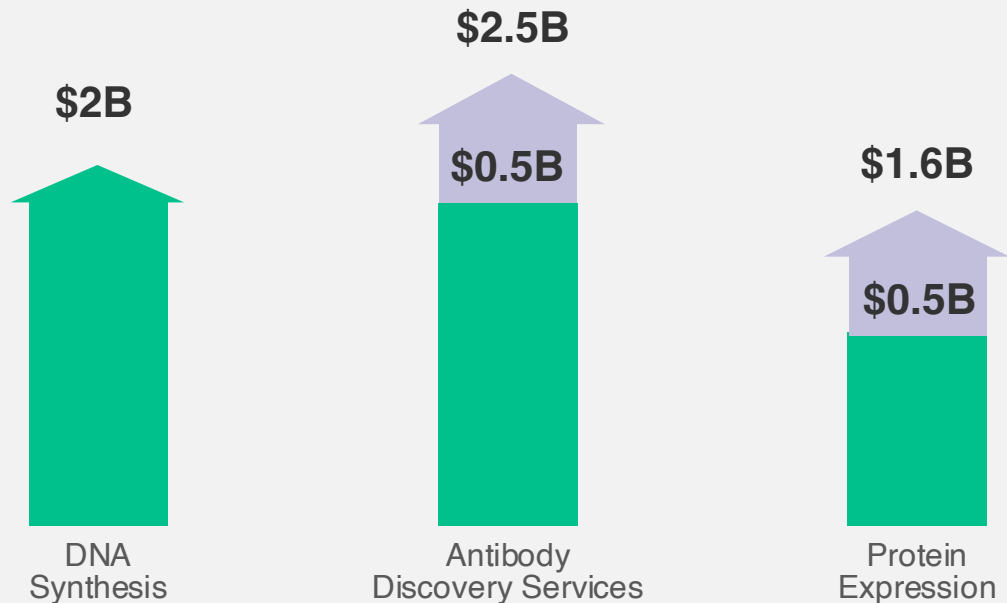
\* Revenue charts not presented on uniform scale

# Future Market Opportunity for AI-Enabled Discovery Adds \$1B in 2030

**\$7B+ SAM\***

- AI-enabled Drug Discovery
- DNA Synthesis and Protein Solutions

**\$18B+ TAM**



## AI-Enabled Drug Discovery

Estimate includes efforts to **build** foundational models and **use** of those models for antibody discovery.

Assumptions include:

- **No dominant model** for either binding prediction or other characterization – iteration continues
- **Scope** of preclinical development work using models continues to expand
- **For Twist**, On track for triple digit order growth in FY26 vs FY25

\*BCC reports, DeciBio, Grand View, Antibodies – recombinant protein market stat; Twist internal estimates

# Beyond Protein, AI Driving Additional DNA-Intensive Applications Platform Enables Broad Set of Applications Including

Build an AI generated  
**CRISPR** nuclease

Train a model to identify optimal  
3'UTRs for **mRNA** expression

Develop lab-in-the-loop **protein**  
design and optimization workflow

CSH Cold Spring Harbor Laboratory  
bioRxiv THE PREPRINT SERVER FOR BIOLOGY

**Design of highly functional genome editors by modeling the universe of CRISPR-Cas sequences**

Jeffrey A. Ruffolo, Stephen Nayfach, Joseph Gallagher, Aadyot Bhatnagar, Joel Beazer, Riffat Hussain, Jordan Russ, Jennifer Yip, Emily Hill, Martin Pacesa, Alexander J. Meeseck, Peter Cameron, Ali Madani  
doi: <https://doi.org/10.1101/2024.04.22.590591>

The diagram illustrates the design workflow for CRISPR-Cas proteins. It starts with 'Training' using 'Universal PUM (pre-trained decoder)' and 'CRISPR-Cas PUM (fine-tuned decoder)'. This leads to 'Diverse proteins' (DGM123PA, WNT1E2LL, WNT19AAE) and 'Diverse CRISPR-Cas proteins' (Cas1, Cas2, Cas3, Cas4, Cas5, Cas6, Cas7, Cas8, Cas9, Cas10, Cas11, Cas12, Cas13, Cas14, Cas15, Cas16, Cas17, Cas18, Cas19, Cas20, Cas21, Cas22, Cas23, Cas24, Cas25, Cas26, Cas27, Cas28, Cas29, Cas30, Cas31, Cas32, Cas33, Cas34, Cas35, Cas36, Cas37, Cas38, Cas39, Cas40, Cas41, Cas42, Cas43, Cas44, Cas45, Cas46, Cas47, Cas48, Cas49, Cas50, Cas51, Cas52, Cas53, Cas54, Cas55, Cas56, Cas57, Cas58, Cas59, Cas60, Cas61, Cas62, Cas63, Cas64, Cas65, Cas66, Cas67, Cas68, Cas69, Cas70, Cas71, Cas72, Cas73, Cas74, Cas75, Cas76, Cas77, Cas78, Cas79, Cas80, Cas81, Cas82, Cas83, Cas84, Cas85, Cas86, Cas87, Cas88, Cas89, Cas90, Cas91, Cas92, Cas93, Cas94, Cas95, Cas96, Cas97, Cas98, Cas99, Cas100). This leads to 'Diverse Cas10 proteins' (Cas10A, Cas10B, Cas10C, Cas10D, Cas10E, Cas10F, Cas10G, Cas10H, Cas10I, Cas10J, Cas10K, Cas10L, Cas10M, Cas10N, Cas10O, Cas10P, Cas10Q, Cas10R, Cas10S, Cas10T, Cas10U, Cas10V, Cas10W, Cas10X, Cas10Y, Cas10Z) and 'gRNA Model (pre-trained decoder)'. This leads to 'Diverse Cas10 proteins' (Cas10A, Cas10B, Cas10C, Cas10D, Cas10E, Cas10F, Cas10G, Cas10H, Cas10I, Cas10J, Cas10K, Cas10L, Cas10M, Cas10N, Cas10O, Cas10P, Cas10Q, Cas10R, Cas10S, Cas10T, Cas10U, Cas10V, Cas10W, Cas10X, Cas10Y, Cas10Z) and 'Complete Type I effectors' (Cas1, Cas2, Cas3, Cas4, Cas5, Cas6, Cas7, Cas8, Cas9, Cas10, Cas11, Cas12, Cas13, Cas14, Cas15, Cas16, Cas17, Cas18, Cas19, Cas20, Cas21, Cas22, Cas23, Cas24, Cas25, Cas26, Cas27, Cas28, Cas29, Cas30, Cas31, Cas32, Cas33, Cas34, Cas35, Cas36, Cas37, Cas38, Cas39, Cas40, Cas41, Cas42, Cas43, Cas44, Cas45, Cas46, Cas47, Cas48, Cas49, Cas50, Cas51, Cas52, Cas53, Cas54, Cas55, Cas56, Cas57, Cas58, Cas59, Cas60, Cas61, Cas62, Cas63, Cas64, Cas65, Cas66, Cas67, Cas68, Cas69, Cas70, Cas71, Cas72, Cas73, Cas74, Cas75, Cas76, Cas77, Cas78, Cas79, Cas80, Cas81, Cas82, Cas83, Cas84, Cas85, Cas86, Cas87, Cas88, Cas89, Cas90, Cas91, Cas92, Cas93, Cas94, Cas95, Cas96, Cas97, Cas98, Cas99, Cas100).

**Nuclease**  
SpCas9  
OpenCRISPR-1

**Deaminase**  
ABE8.20  
PF-DEAM-1  
PF-DEAM-2

N-terminal fusion

CSH Cold Spring Harbor Laboratory  
bioRxiv THE PREPRINT SERVER FOR BIOLOGY

**ML-driven design of 3'UTRs for mRNA stability**

Alyssa K. Morrow, Ashley Thornal, Elise Duboscq Flynn, Emily Hoeltzl, Meimei Shan, Gökrem Garipis, Rory Kirchner, Aniketh Janardhan Reddy, Sophia Tabchouri, Ankit Gupta, Jean-Baptiste Michel, Uri Laserson

The diagram shows the ML-driven design of 3'UTRs for mRNA stability. It includes a table comparing different methods and a flowchart of the design process.

| Method                        | Standard 3'UTR (wild-type) | Standard 3'UTR (mutated) | Standard 3'UTR (synthetic) |
|-------------------------------|----------------------------|--------------------------|----------------------------|
| Genetic algorithm             | ✓                          | ✓                        | ✓                          |
| Simulated annealing           | ✓                          | ✓                        | ✓                          |
| SeqSnp                        | ✓                          | ✓                        | ✓                          |
| QASQAS                        | ✓                          | ✓                        | ✓                          |
| Mutagenesis (ML selected)     | ✓                          | ✓                        | ✓                          |
| Motif shuffling (ML selected) | ✓                          | ✓                        | ✓                          |

**A**

**B**

Design  
Train x3  
Measure

**C**

normalized half-life (hr)

Iteration 0 ML Iteration 1 ML Iteration 2 ML Iteration 3

genomic synthetic (non-ML) ml

10.2 10.6 11.0 11.0

\*\* \*\*\*\* n.s. \*\*\*\*

CSH Cold Spring Harbor Laboratory  
bioRxiv THE PREPRINT SERVER FOR BIOLOGY

**Lab-in-the-loop therapeutic antibody design with deep learning**

Nathan C. Frey, Isidro Hötzel, Samuel D. Stanton, Ryan Kelly, Robert G. Alberstein, Emily Mskowski, Karolis Martinus, Daniel Berenberg, Jack Bevers III, Tyler Bryson, Pamela Chan, Alicja Czuby, Tamica D'Souza, Henri Dwyer, Anna Dziejewska, James W. Fairman, Allen Goodman, Jennifer Hofmann, Henry Isaacson, Aya Ismail, Samantha James, Taylor Joren, Simon Kelow, James R. Kiefer, Matthieu Kirchmeyer, Joseph Kleinhenz, James T. Koerber, Julien Lafrance-Vanasse, Andrew Leaver-Fay, Jae Hyeon Lee, Edith Lee, Donald Lee, Wei-Ching Liang, Joshua Yao-Yu Lin, Sidney Lisanza, Andreas Loukas, Jan Ludwiczak, Sai Pooja Mahajan, Omar Mahmood, Homa Mohammadi-Peyhani, Sarazrupi Nerki, Ji Won Park, Jaewoo Park, Stephen Ra, Sarah Robinson, Saeed Saremi, Franziska Seeger, Imee Sinha, Anna M. Sokol, Natasa Tagasovska, Hao To, Edward Wagstaff, Amy Wang, Andrew M. Watkins, Blair Wilson, Shuang Wu, Karina Zadorozhny, John Marioni, Aviv Regen, Yan Wu, Kyunghyun Cho, Richard Bonneau, Vladimir Gilgorijević

The diagram illustrates the lab-in-the-loop therapeutic antibody design with deep learning workflow. It shows the iterative process of design, training, and measurement, leading to the optimization of antibody sequences.

# Agenda

- Welcome
  - Tour
  - DSPS Strategy Session
  - Fireside Chat with Dr. Frances Arnold
  - **Customer Presentations**
- 

## Lunch

---

- NGS Strategy Session
- Customer Presentations
- Financial Overview
- Culture
- Q&A

# Chai Discovery



# Thank you

ELSIE BIOTECHNOLOGIES / GSK

**Enhancing Oligonucleotide Screening Efficiency  
with DNA Encoded Library Technology**

**Dillon Flood**

Co-Founder and Scientific Director

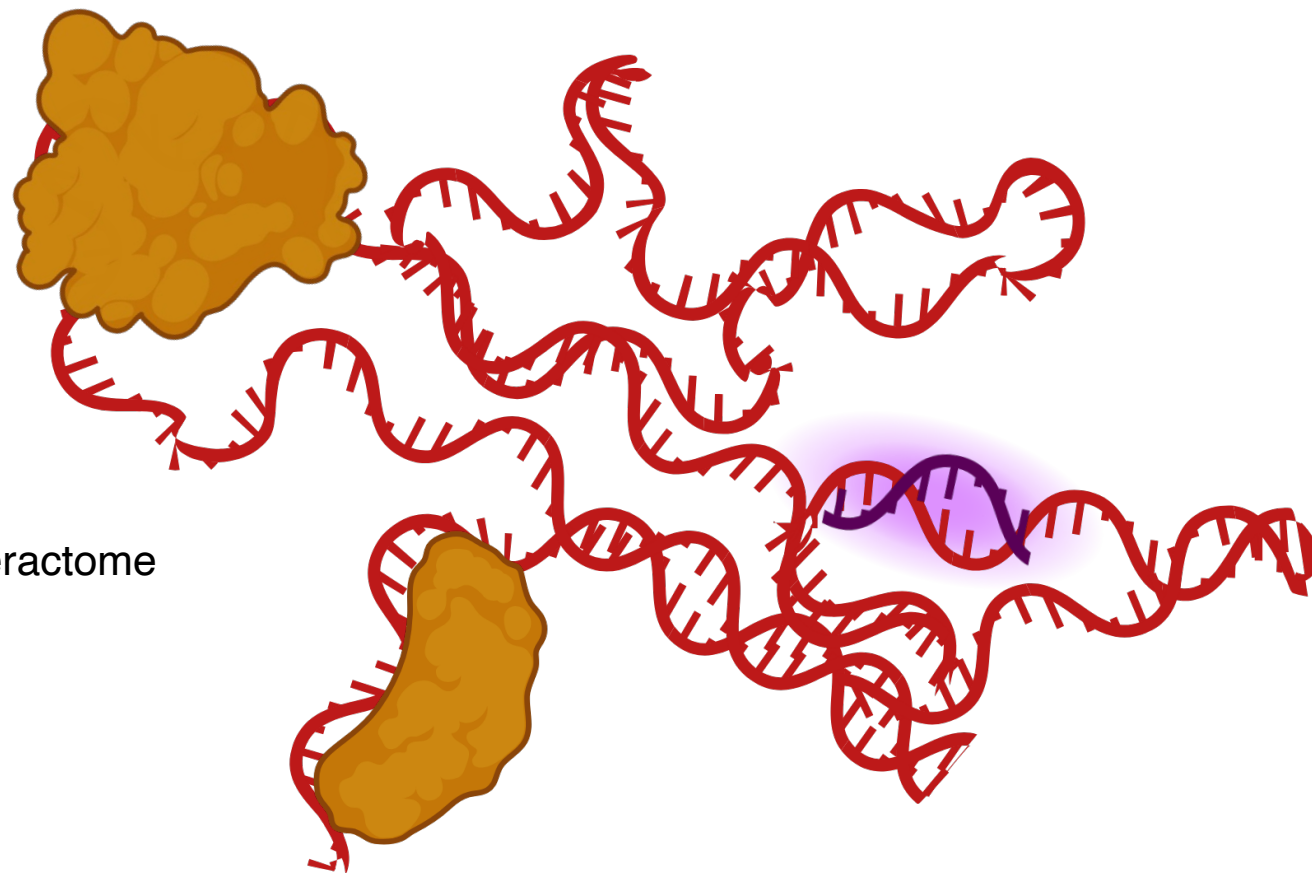
# Difficulties with oligo sequence definition

## Tx sequence prediction challenges

- RNA structure is dynamic
- Long range structure prediction limited
- Undefined protein interactome

## ROSALIND answers:

- Empirically assay vast sequence space
- Recapitulate native target structure and protein interactome
- Discover improved leads



# Pooled screening eliminates the oligo design question

Traditional screening = individually testing oligos

## Sequence



Sequence = (n)  
1,000's

## Modifications



Modifications (m) &  
patterns (g & l)  
10's & 10,000's

## Linkage ID & stereochem



Linkage ID &  
stereochem (2l-1)  
10's & 10,000's

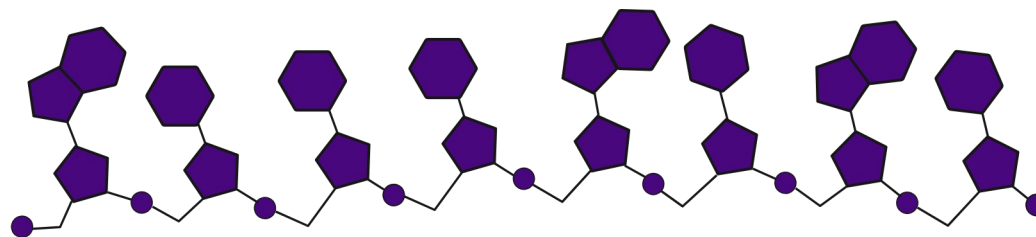
Total chemical diversity:

$$\sum_{l=l_{min}}^{l_{max}} (n - l + 1) 2^{l-1} m^{l-g} = 10^{12} \text{ possible combinations}$$

# ROSALIND: DNA-encoded discovery engine

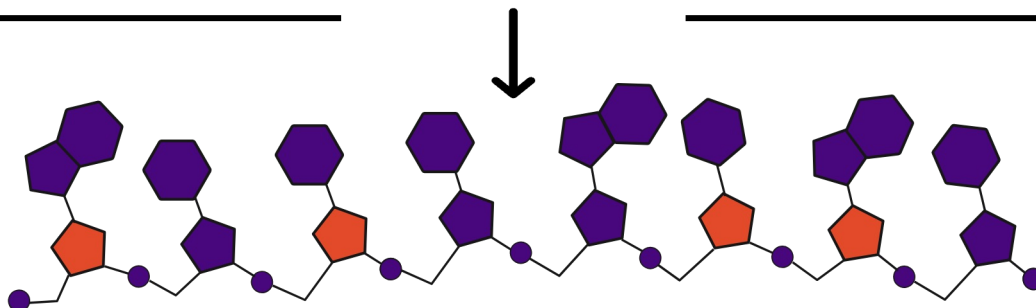
Screening oligos in a pooled format

**Sequence**  
Gen 1 Leads



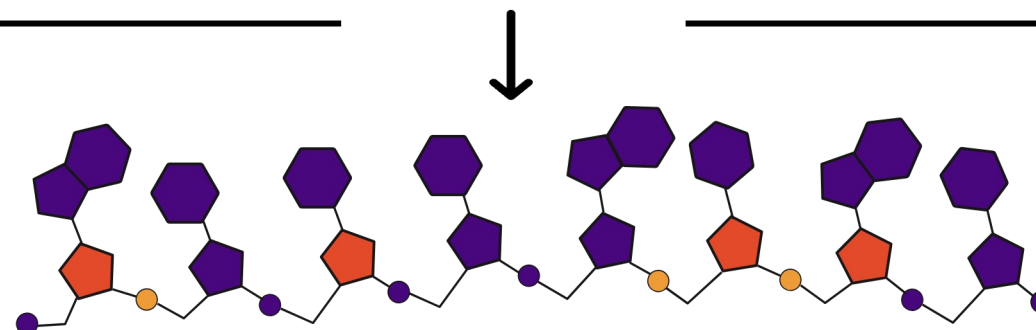
**10K-100K**  
Oligos screened to define activity & selectivity

**Modification pattern**  
Gen 2 Leads



**10K-50K**  
Oligos screened to define toxicity & PK/PD

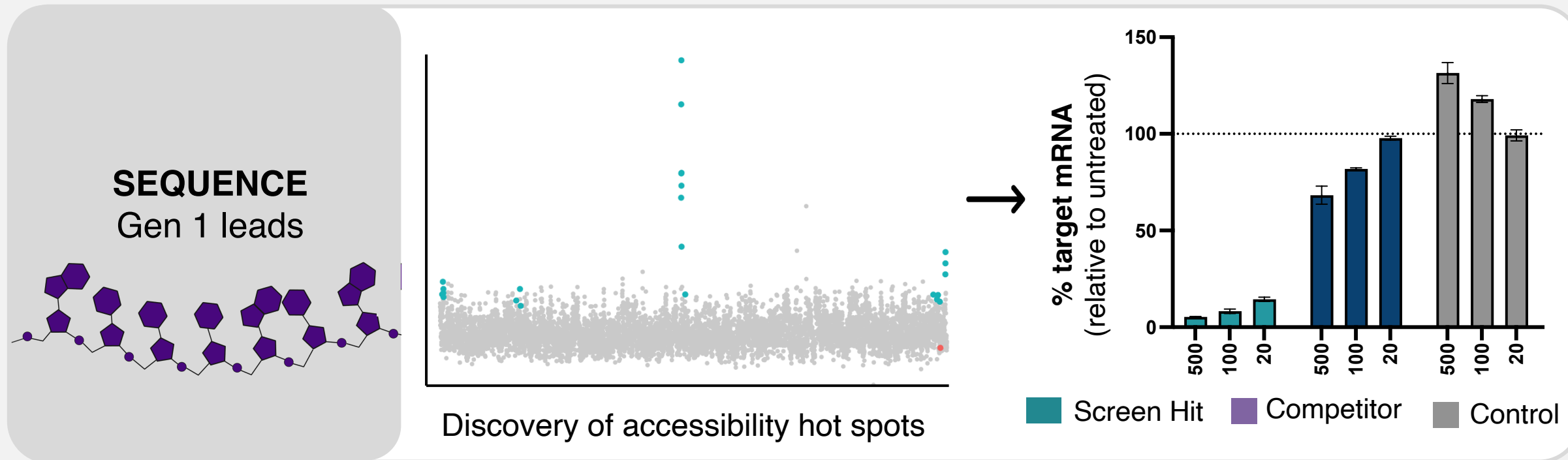
**Linkage and stereochem**  
Gen 3 Leads



**100-1000's**  
Oligos screened allow fine-tuning of drug properties

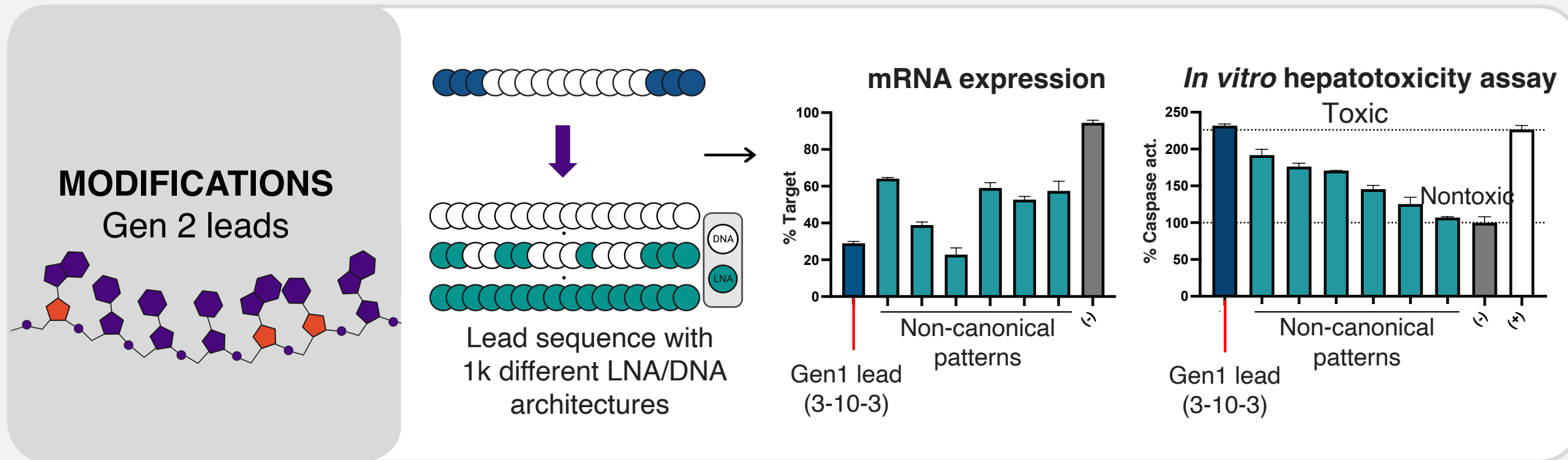
# Accessibility drives activity

Sequence optimized Gen1 ASOs demonstrate superior activity to clinical phase molecules



# Patterns impact properties

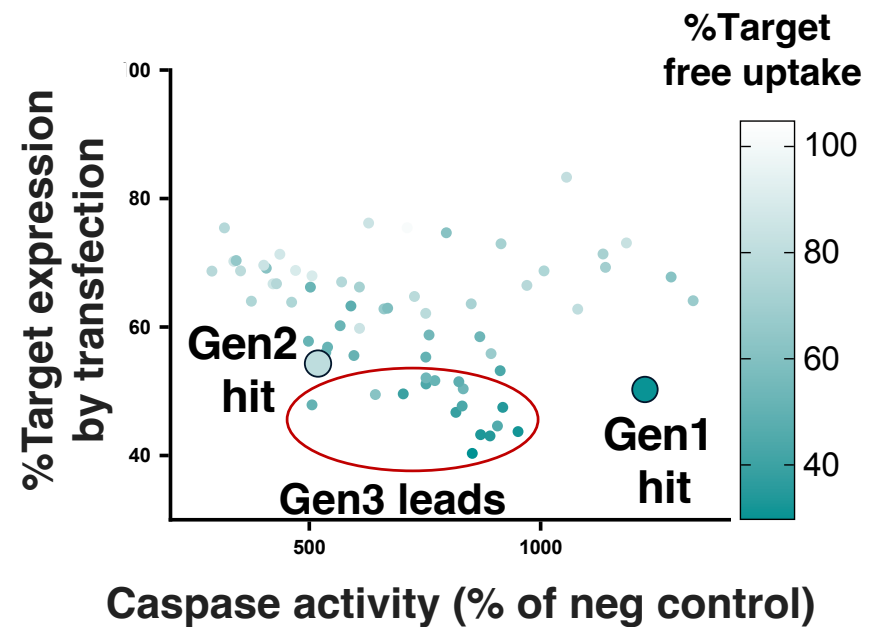
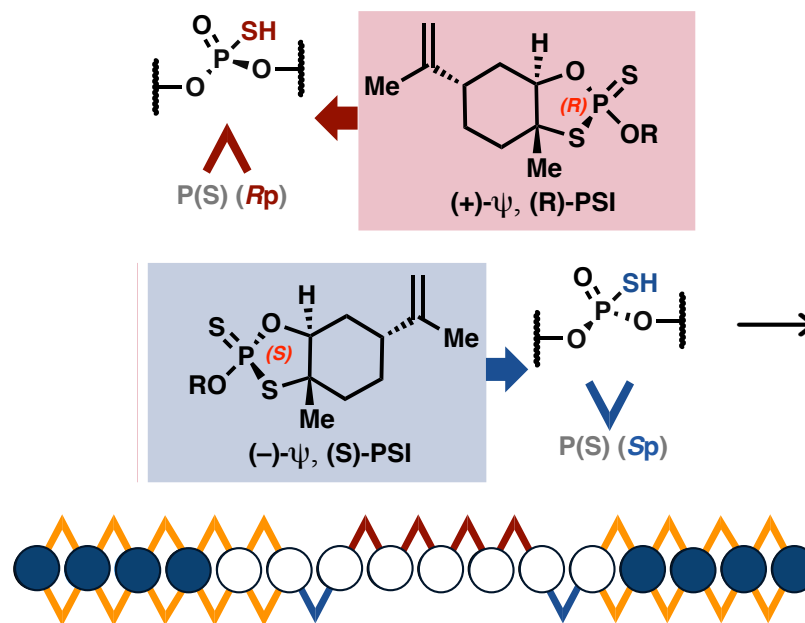
Gen 2 ASOs with non-canonical chemical architectures display decreased toxicity



# Chemistry imparts control

Gen 3 ASOs with controlled stereochemistry

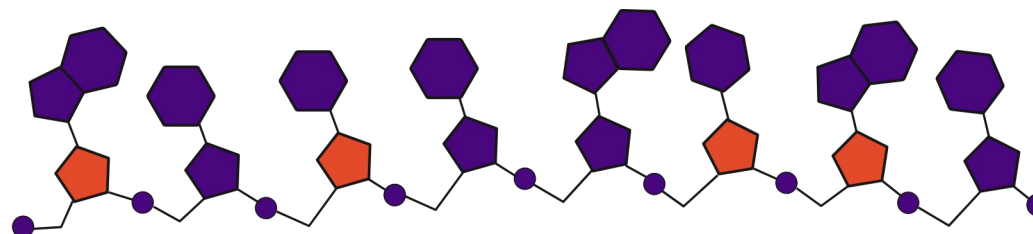
**LINKAGE & STEREOCHEM**  
Gen 3 leads



# Chemistry development was needed to enable innovation

Screening oligos in a pooled format require chemistry optimization

**Modification pattern**  
Gen 2 Leads

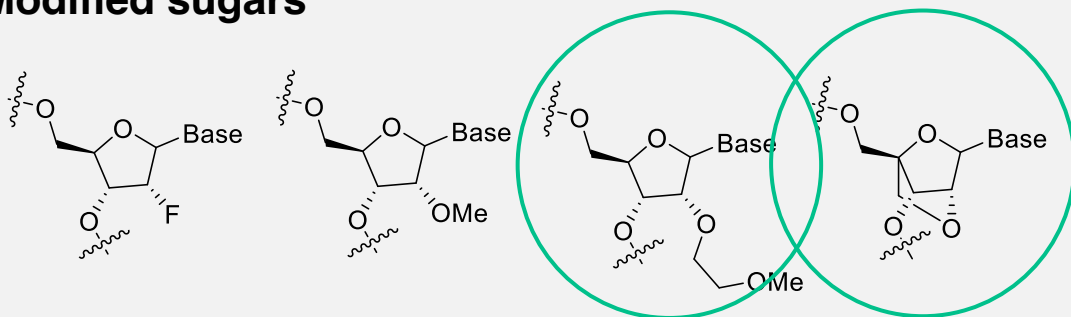


10K-50K

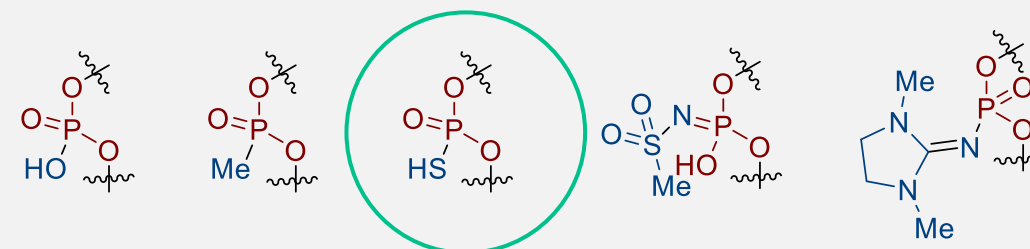
Oligos screened to define toxicity & PK/PD



**Modified sugars**

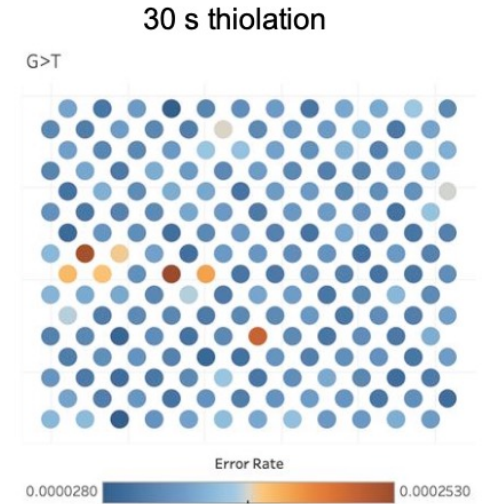
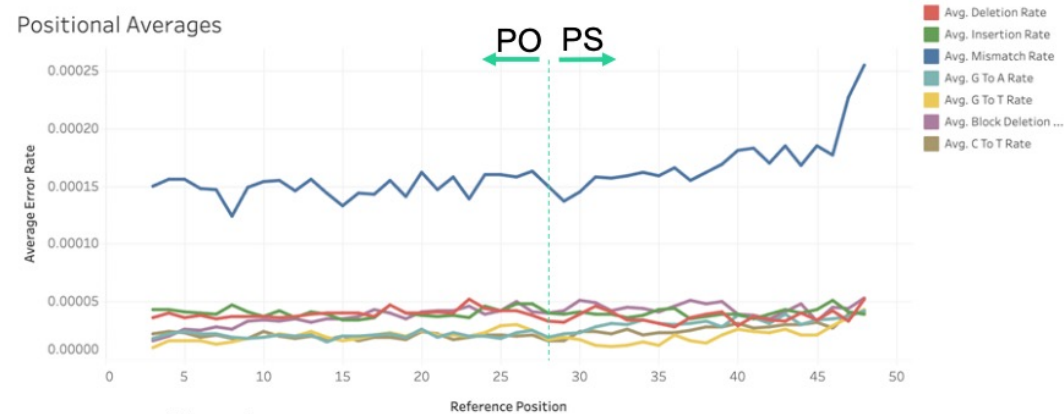


**Modified phosphodiester mimics**

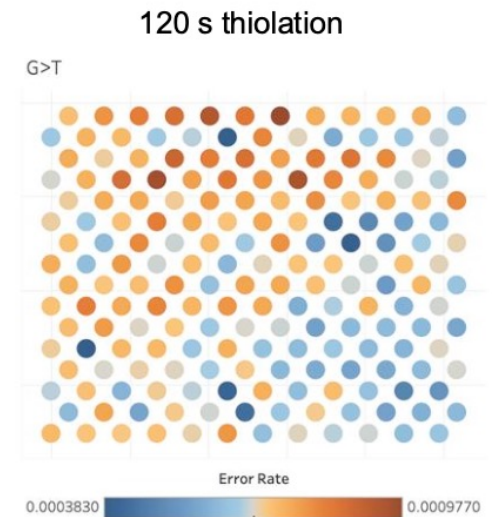
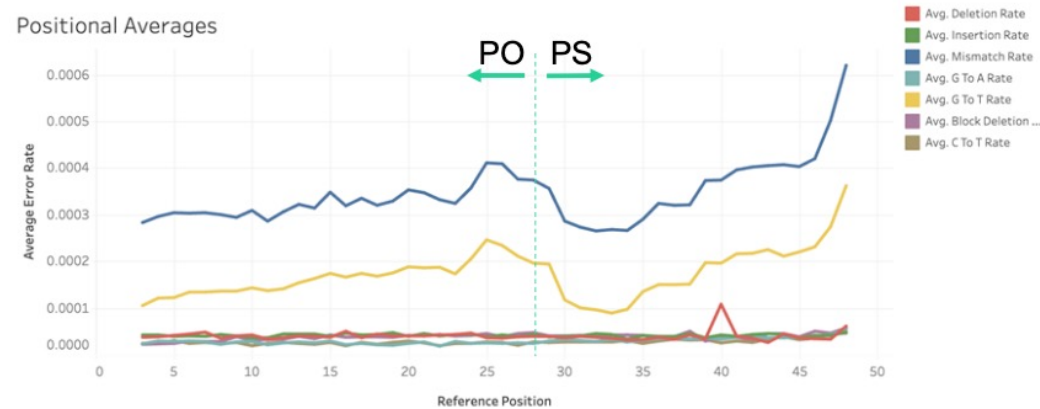


# Chemistry collaboration enabled high throughput screening

**30 second thiolation:**  
Error rate 1 in 3200



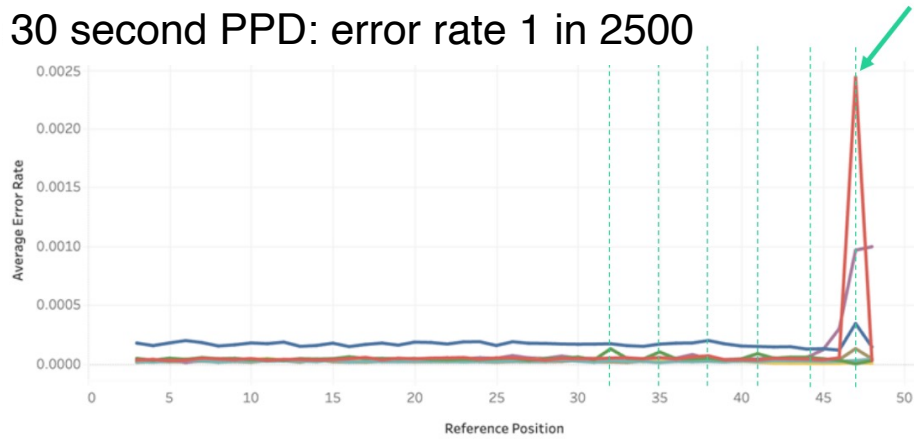
**120 second thiolation:**  
Error rate 1 in 2500



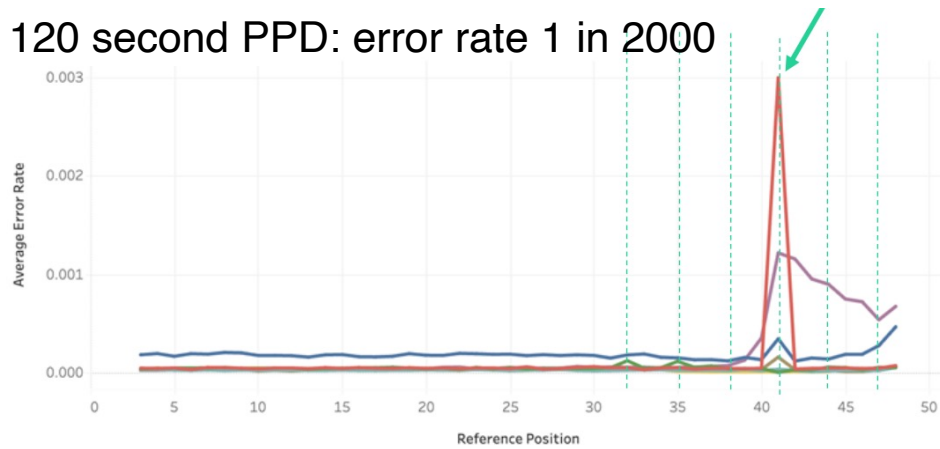
# Chemistry collaboration enabled high throughput screening

## MOE incorporation

30 second PPD: error rate 1 in 2500

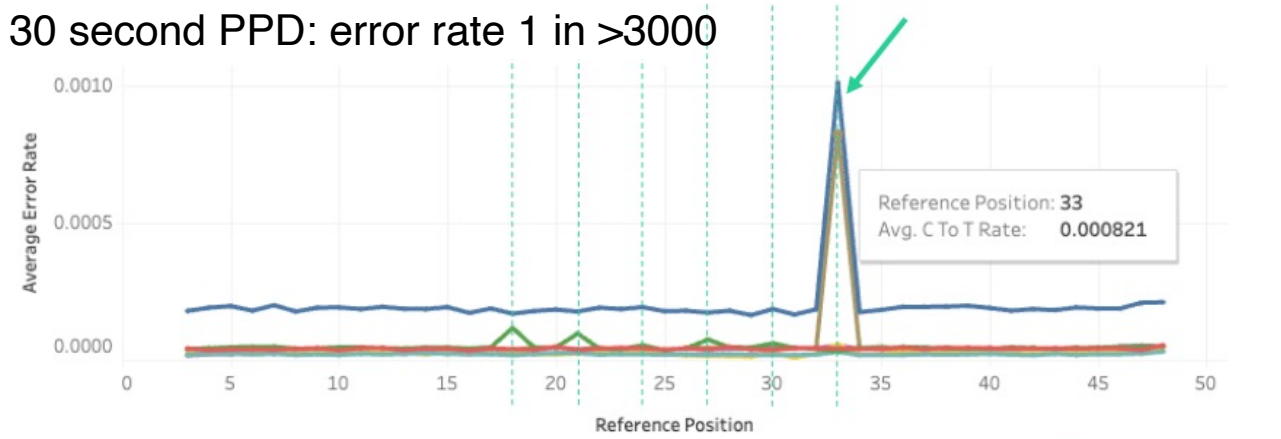


120 second PPD: error rate 1 in 2000

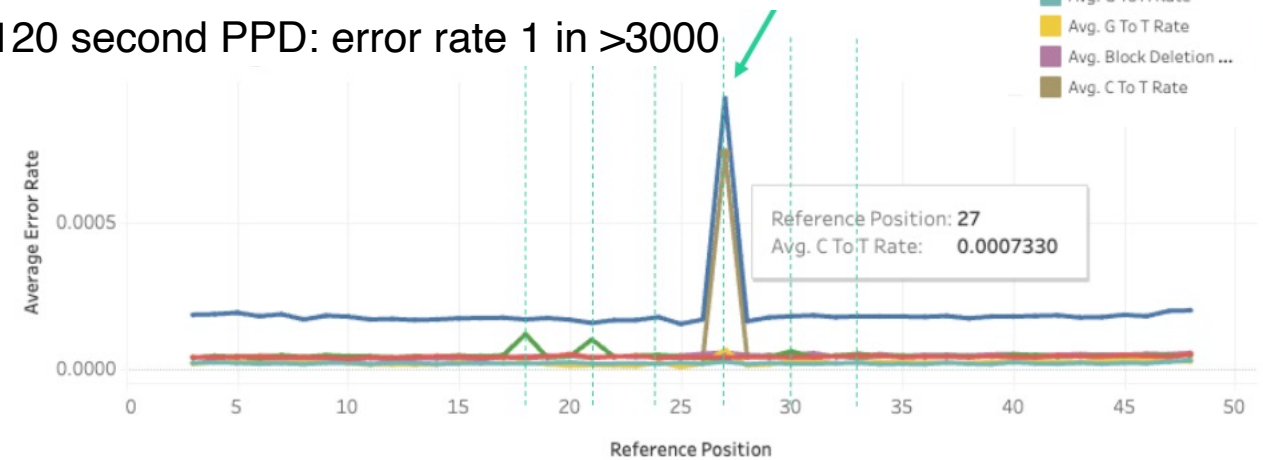


## LNA incorporation

30 second PPD: error rate 1 in >3000



120 second PPD: error rate 1 in >3000

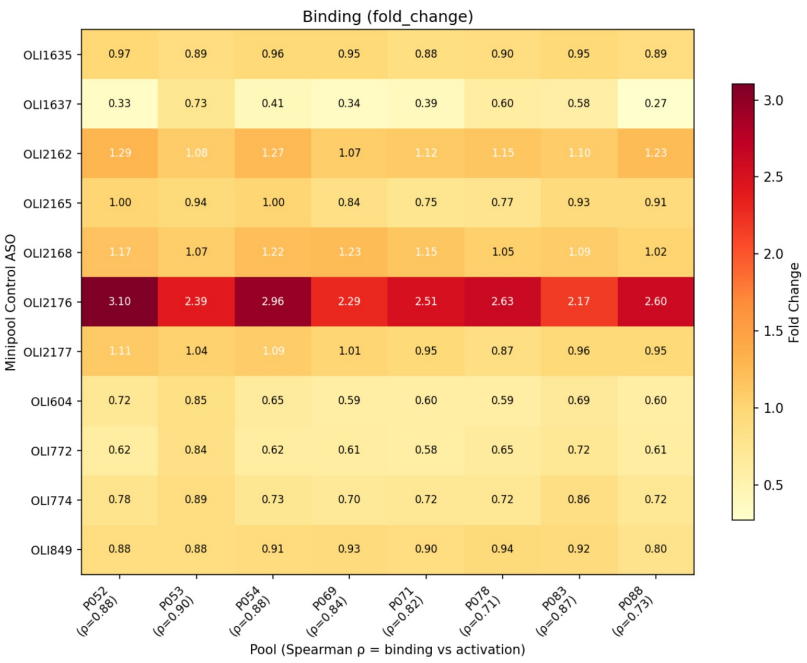


- Avg. Deletion Rate
- Avg. Insertion Rate
- Avg. Mismatch Rate
- Avg. G To A Rate
- Avg. G To T Rate
- Avg. Block Deletion ...
- Avg. C To T Rate

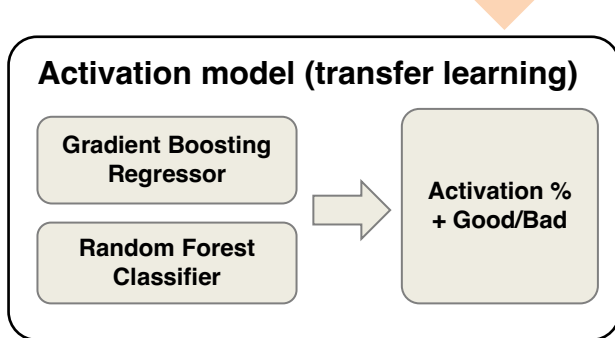
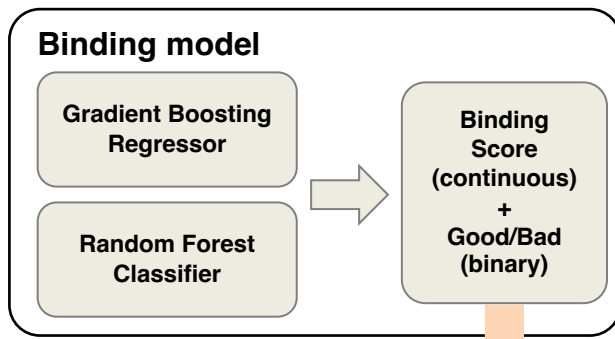
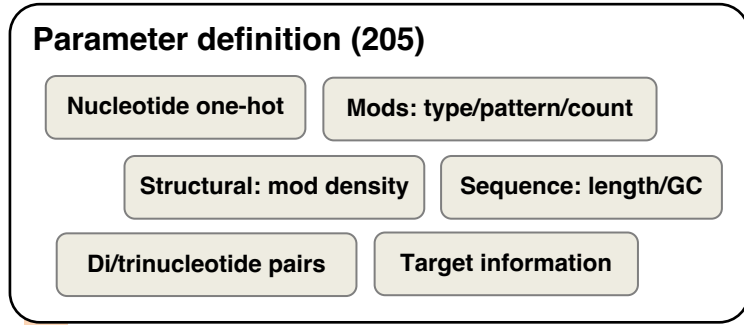
# Selections at scale enable modeling and data asset creation

## Gen 2 ROSALIND and in vitro datasets

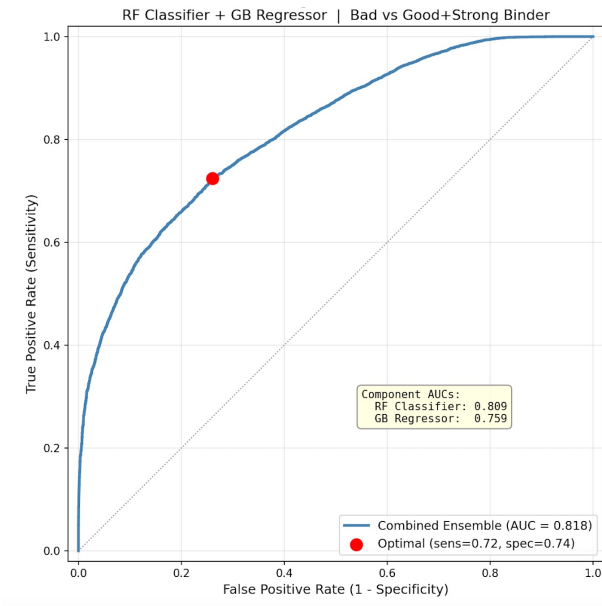
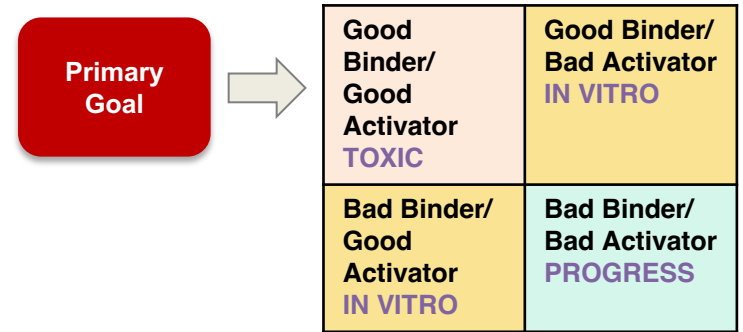
- 100,000+ unique datapoints per assay
- Spike-in controls allow QC validation
- Data pre-processing for unified input



## Model development and evaluation



## Validation and deployment



# Acknowledgements



Amanda McCrae  
Henry Qiu  
Deepakshi Kasat  
Kyle Knouse  
Daniel Nations

Alberto Carreno  
Tereza Shea  
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Kyle Masukawa  
Akiyo Ogawa

Richard Redman  
James Ducker  
Dianne Agarwal  
LJ Lim



Christine Donahue  
Chloe Jones  
Jack Brown  
Rajeev Chorghade  
Chris Dimitri  
Daisy Flemming

Patrick Neal  
Kristina Gans  
Robert Hale  
Angelina Heyler  
Boyko Kakaradov  
Amy Lancaster



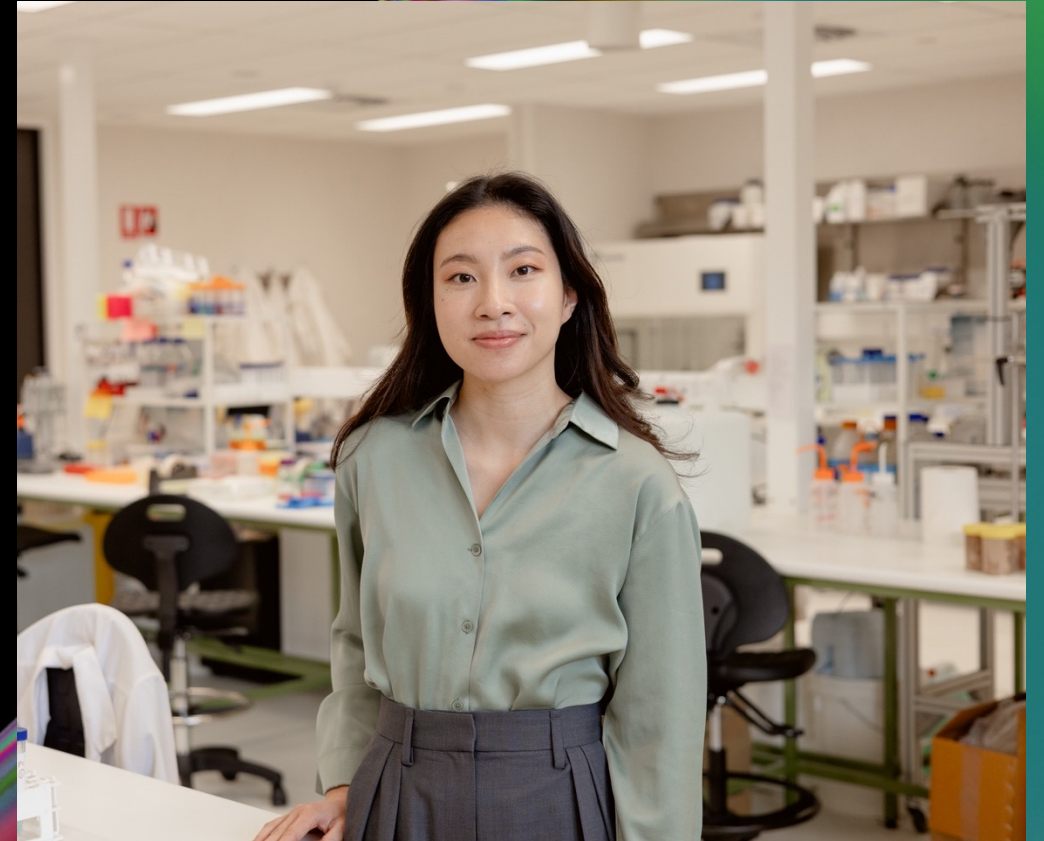
# Thank you

SAMSARA ECO

# Dr Vanessa Vongsouthi

Research Founder

Head of Bioengineering and Discovery Research



# Creating circularity for the world's most valuable materials



10%  
of plastics are  
recycled

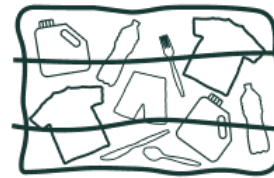
0.3%  
TEXTILE-TO-TEXTILE  
RECYCLING

# Our technology platform

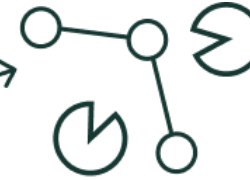
Twist Clonal Genes  
96-well plate format



ENGINEERED  
ENZYMES



PLASTIC  
WASTE



ENZYMATIC  
DEPOLYMERISATION



MONOMERS  
PURIFICATION



VIRGIN-LIKE  
PLASTICS



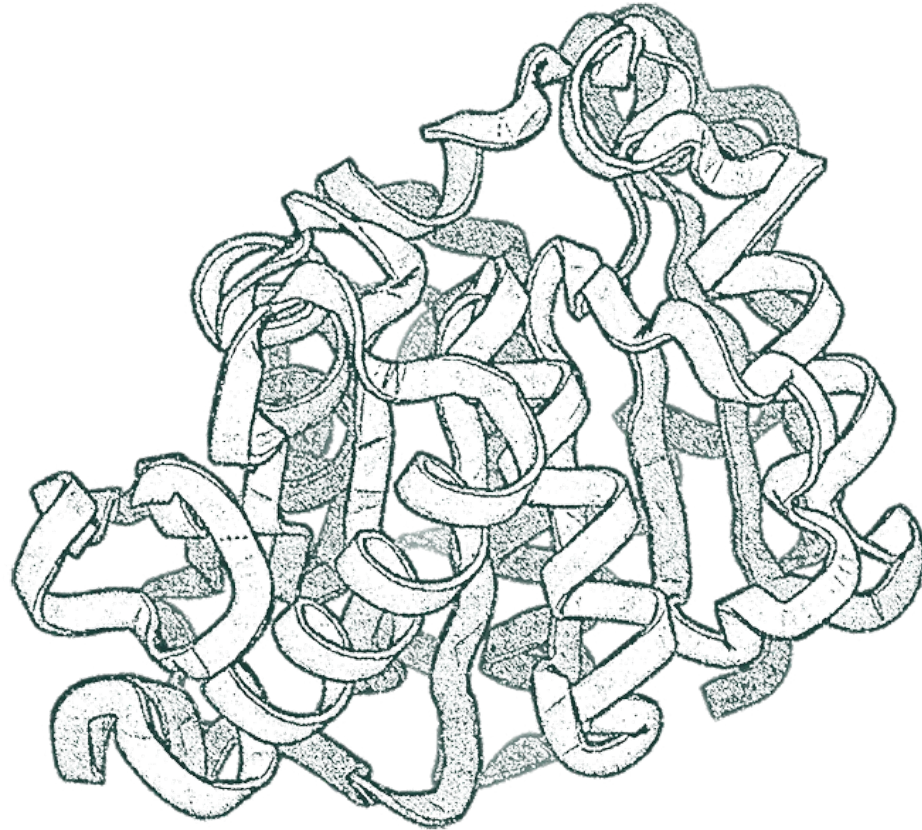
GREEN  
CHEMICALS



NEW  
PRODUCTS

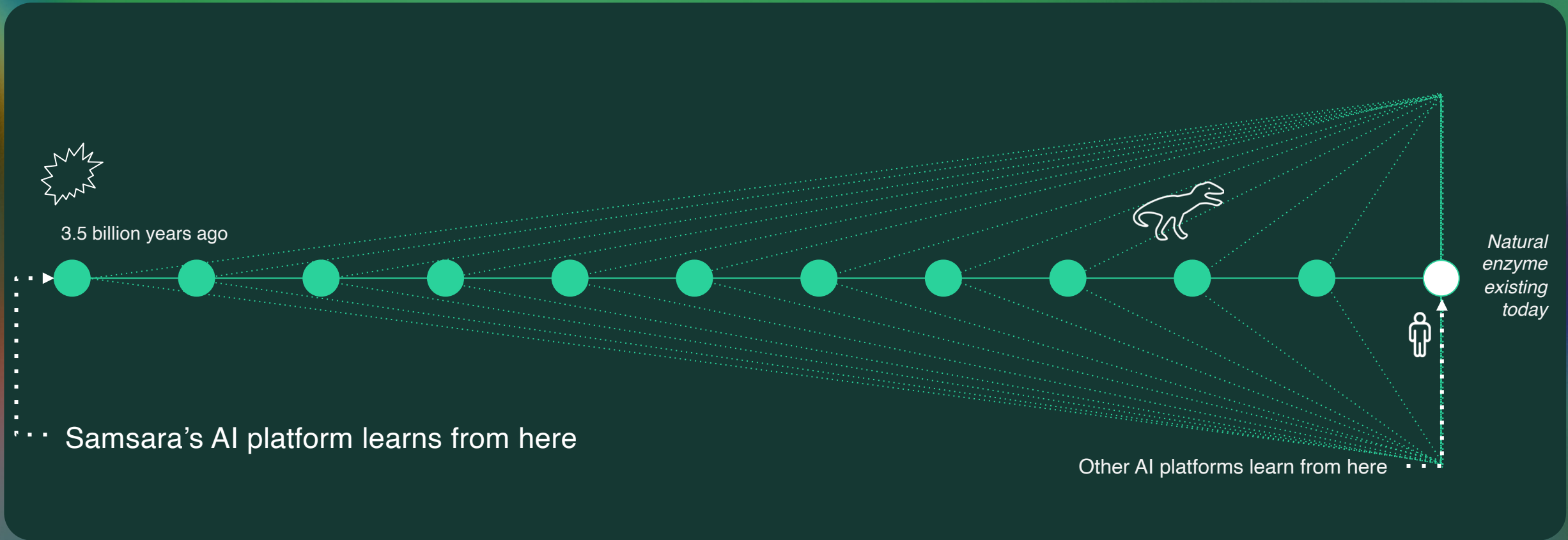
Turning end-of-life products into  
**virgin-identical, circular materials.**

New-to-nature  
enzymes uniquely  
designed to break  
down plastics at  
speed, scale and  
with precision.





# Our enzyme design platform learns across evolutionary history – from ancestral enzymes to natural enzymes existing today



# Our enzymatic advantage

|                                   | MECHANICAL RECYCLING | CHEMICAL RECYCLING   | SAMSARA TECHNOLOGY |
|-----------------------------------|----------------------|----------------------|--------------------|
| CLOSED-LOOP CIRCULARITY           | ✗                    | ✓                    | ✓                  |
| HANDLES MIXED PLASTICS/COMPOSITES | ✗                    | ✗                    | ✓                  |
| LOW CARBON FOOTPRINT              | ✓                    | ✗                    | ✓                  |
| VIRGIN IDENTICAL                  | ✗                    | Not yet demonstrated | ✓                  |
| END PRODUCT                       | Chips                | Monomers             | Monomers           |

# World-first partnerships and global scale



World 1<sup>st</sup> Nylon  
6,6 Garment




Lululemon 10-year agreement  
to supply 20% fibre portfolio




First plant open  
in Australia



Clear rPET Bottle



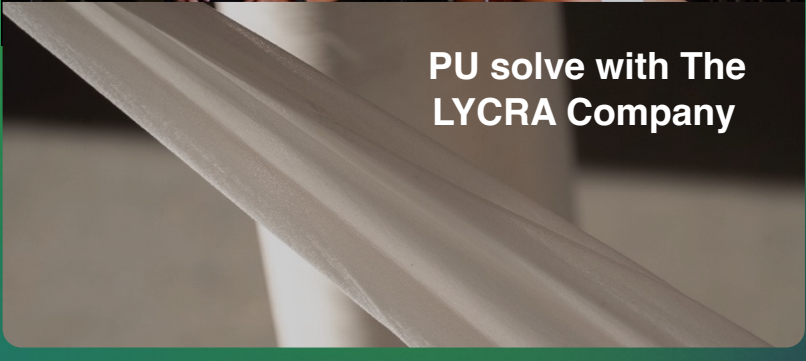
LSKD 10-year agreement



USD \$107M  
backing



lululemon x Samsara  
Eco retail collection

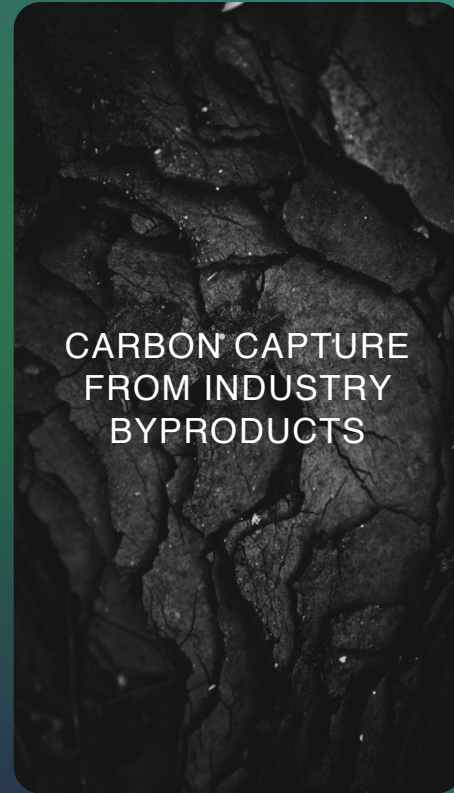
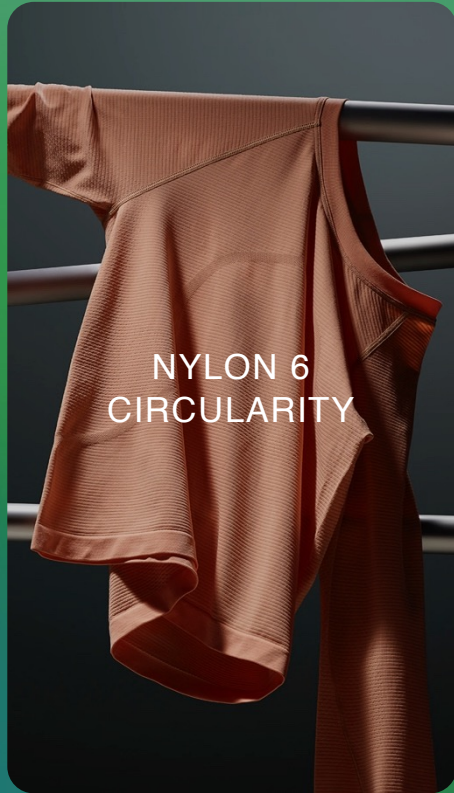


PU solve with The  
LYCRA Company



Commercial plant  
opening 2028

# Circularity for other valuable resources



AI-enabled platform supporting the development of new-to-nature proteins and enzymes to create value from waste





# Thank you

Reach out with questions to:  
[vanessa.vongsouthi@samsaraeco.com](mailto:vanessa.vongsouthi@samsaraeco.com)

Follow us on LinkedIn: /samsaraeco

# Agenda

- Welcome
  - Tour
  - DSPS Strategy Session
  - Fireside Chat with Dr. Frances Arnold
  - Customer Presentations
- 

## Lunch

---

- **NGS Strategy Session**
- Customer Presentations
- Financial Overview
- Culture
- Q&A

# NGS Solutions

Enabling efficient and effective customized, scalable research solutions for cancer, inherited and rare disease diagnostics

# Jimmy Jin

SVP, Product and Marketing

*Next Generation Sequencing Tools*



# One Platform, Many Customized Solutions

Meeting customers where they are, powering growth across expanding platforms

## How we win



**Operational excellence**



**NPI machine**



**Commercial execution**

T W I S T  
BIOSCIENCE

**Differentiated Silicon Platform  
Speed and Scale**

Twist products are for research use only. The products presented here are not intended for the diagnosis, prevention, or treatment of a disease or condition. Twist Bioscience assumes no liability regarding use of the product for applications in which it is not intended. The results are specific to the institution to which they were obtained. The results presented are customer-specific and should not be interpreted as indicative of performance across all institutions.



**AI-enabled antibody discovery workflow**

AI-ready wet-lab at scale



**Molecular residual disease**

Personalized diagnostic research at scale



**Enzyme-engineered NGS**

Better performance, integrated workflow



**Nucleic acid therapeutics**

Next growth frontier

**Twist culture**

# NGS Applications



## Products

Quality

Uniformity and lower sequencing cost

Comprehensive workflows

Rapid customization

Fast throughput

Sequencer agnostic

## Services

NGS **20,000 samples per day**  
(Gene production)

Deep NGS **expertise and at cost** consumables

Strong **pharma partnerships** who outsource NGS

Why We Win

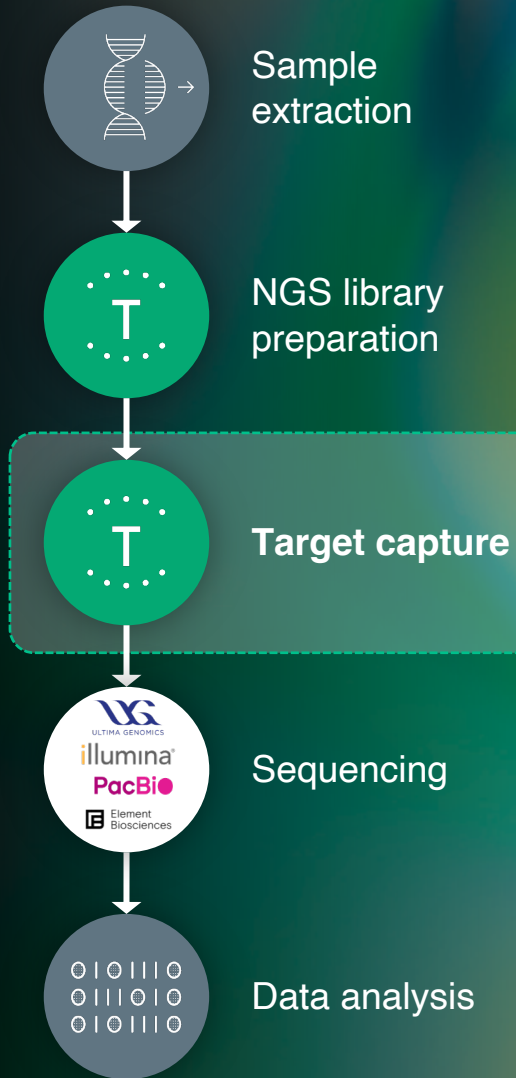
## Products

- Fixed panels
- Custom panels
- Alliance panels
- Library prep kits
- Reagents
- Controls and standards

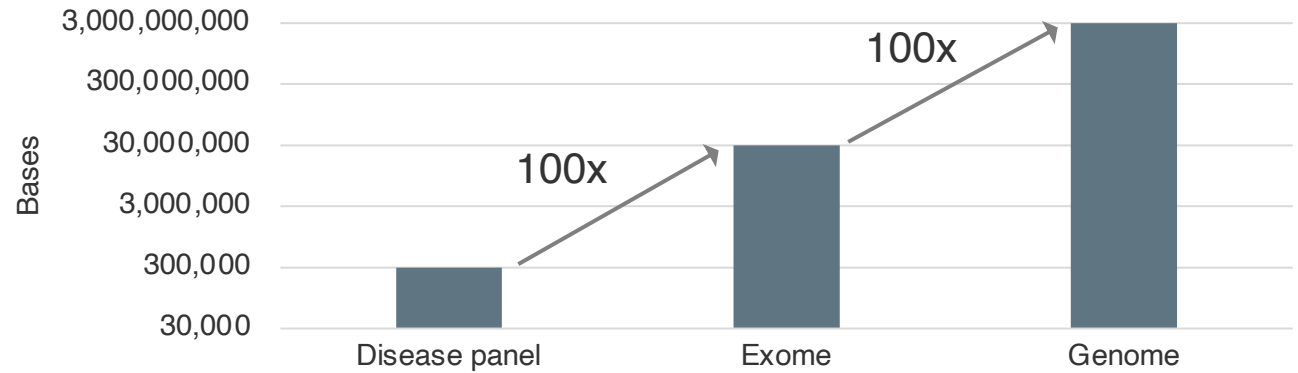
## Services

- Pre and post-sale application support
- Bioinformatics
- Automation
- Service Lab
- Pilot Lab

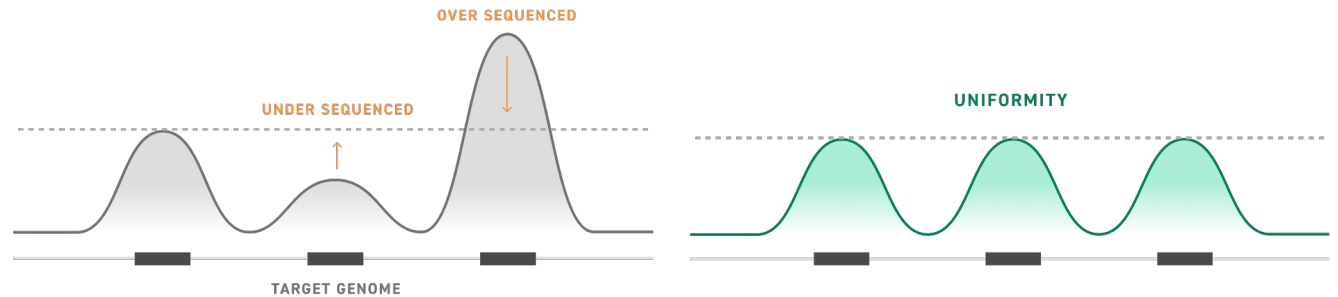
# If Not WGS, It Will Be Twist



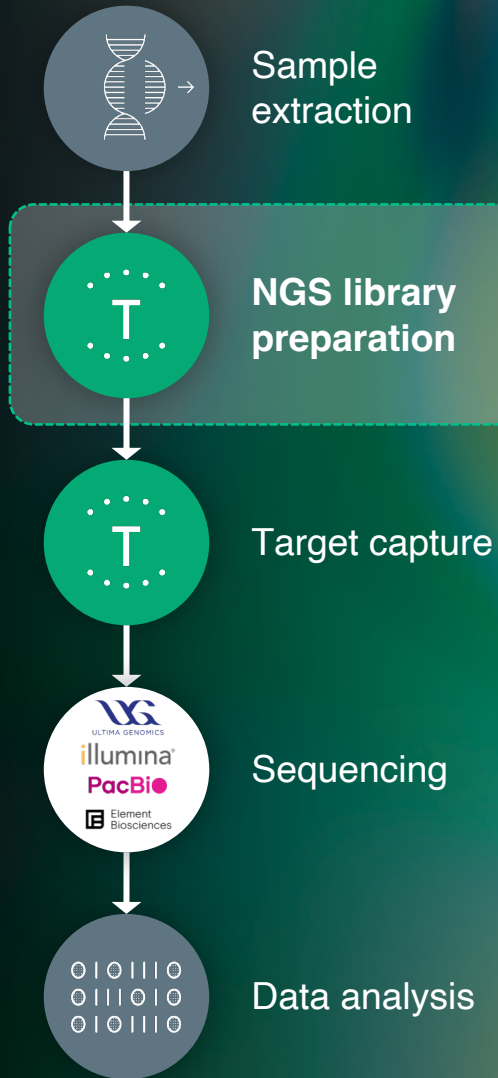
Cost of sequencing went from \$6 per Gb in 2021 to \$1-2 in 2026



Twist probes = High uniformity → Lower sequencing costs  
Low failure rates



# If WGS, It Should Still Be Twist



## What's in a library preparation kit?

Buffers

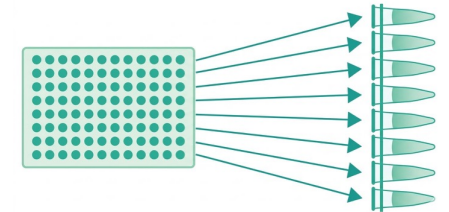
DNA

Enzymes

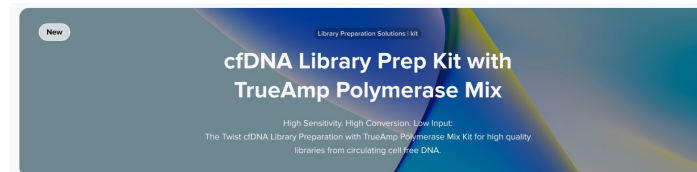
Highest throughput PCR-Free WGS kit on the market –  
1536 full-length UDI adapters

Highest throughput  
Library preparation  
kit in general

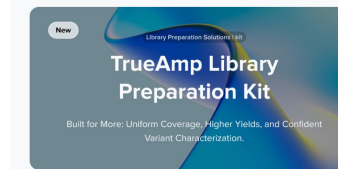
- 3000 HT Unique Dual indexing
- FlexPrep 1152 samples in a 96-well plate



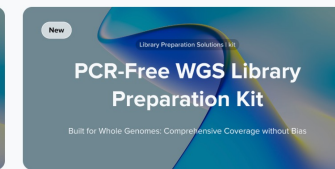
High  
performance



Conversion  
efficiency



Low input &  
FFPE



# Quality Starts at the Chip

Large scale, quality oligo synthesis is the cornerstone of our portfolio

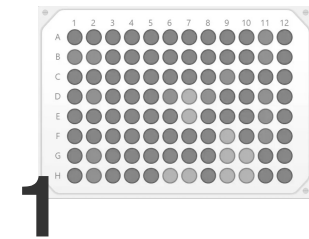


121

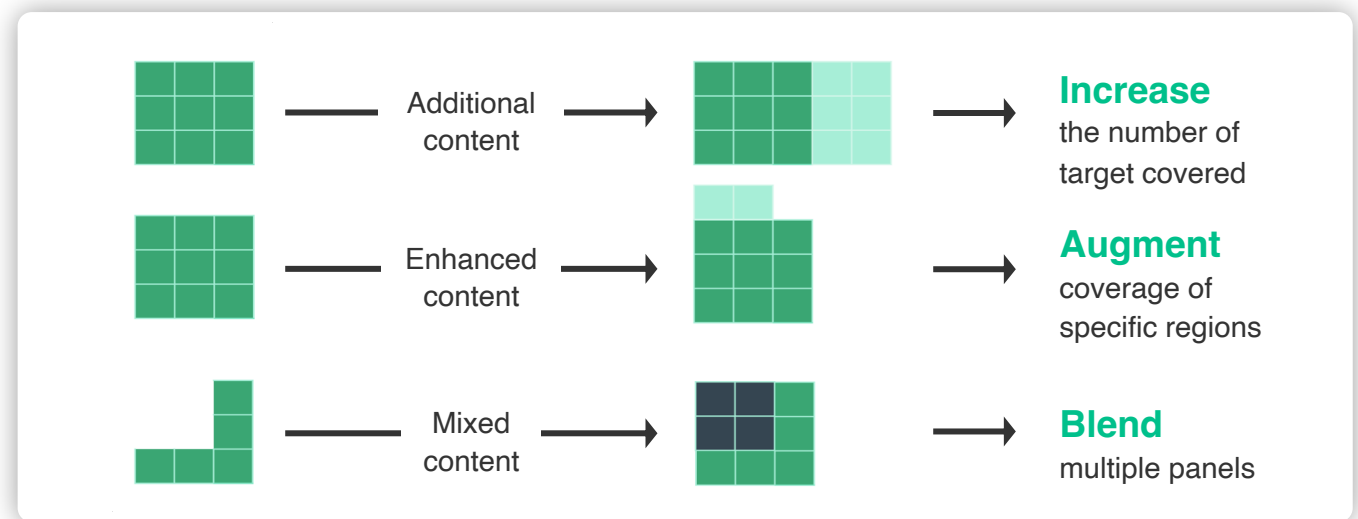


Our silicon platform enables the precision synthesis of millions of probes.

# Scale. Quality. Flexibility. Economy.



- Machines and batches
- Pipetting



# Twist NGS Powers Liquid Biopsy Dx and Research



## Early cancer detection

Leading supplier w/ Twist Methylo and Methylation detection system

## Therapy selection

Leading supplier w/ Twist custom Comprehensive Genomic Profiling (CGP) panels

## MRD

Key supplier w/ Twist exome, 5-day MRD500 & MRD10k panels



We are not in the horse race  
We don't bet on a horse  
**We win**

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# Patient Journey



Linda S.

**Age:** 63  
**Gender:** Female  
**Occupation:** Retired teacher  
**Location:** Suburban Midwest, USA  
**Diagnosis:** Stage II colon cancer  
**Treatment /test context:**  
**Month 1:** Surgery complete.  
 Treatment decision for adjuvant chemotherapy.

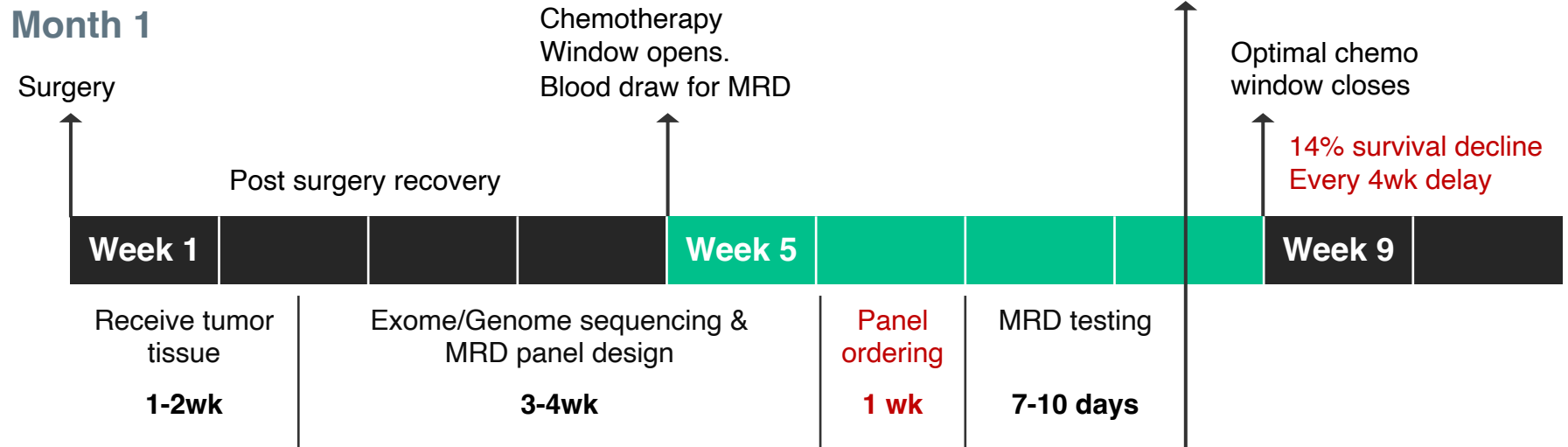
**Month 7:**  
 Return for surveillance test

*For illustrative purposes only*

# Racing Against Time and Pushing Against Limits

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## Month 1



## Month 7

| Site                | Approximate incidence | MRD sensitivity needed (ppm) | False negative risks |
|---------------------|-----------------------|------------------------------|----------------------|
| Liver               | 30–50% of recurrences | 100                          | Low                  |
| Lung                | 10–25%                | 10-100                       | Medium               |
| Peritoneum          | 10–20%                | <10                          | High                 |
| Distant lymph nodes | 5–10%                 | 10                           | High                 |
| Local recurrence    | 5–10%                 | <10                          | High                 |
| Bone                | <5%                   | <10                          | High                 |
| Brain/CNS           | <2%                   | <1?                          | Very high            |

# NPI Machine: MRD Express

Speed and sensitivity will never be in conflict



## Ultra-sensitive

Detects true ctDNA across thousands of tumor-specific targets

**10,000**

Tumor-specific targets



## Lightning fast panels

Direct synthesis in < 24 hours

**1 Day**

Panel order to shipment turnaround



## Built for scale

Express panels, cfDNA kits, UMI adapters, reference standards, and API/LIMS integration — automation-ready for high-volume labs and biopharma.

**0 compromise**

On quality and workflow

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- Type of targets
- # of targets
- Signal to noise quality of targets

## MRD Methods Scan

---

- Fragmentomics
- WGS / AI
- Fixed panels / Methylation
- MultiOmics

- Personalized dPCR / Structural variants
- Personalized PCR Amplicon panels / Phased variants
- Personalized Target enrichment panels
- Selected enrichment of tumor variants

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# The Inevitable March Towards Tumor Informed Twist Panels



The more targets

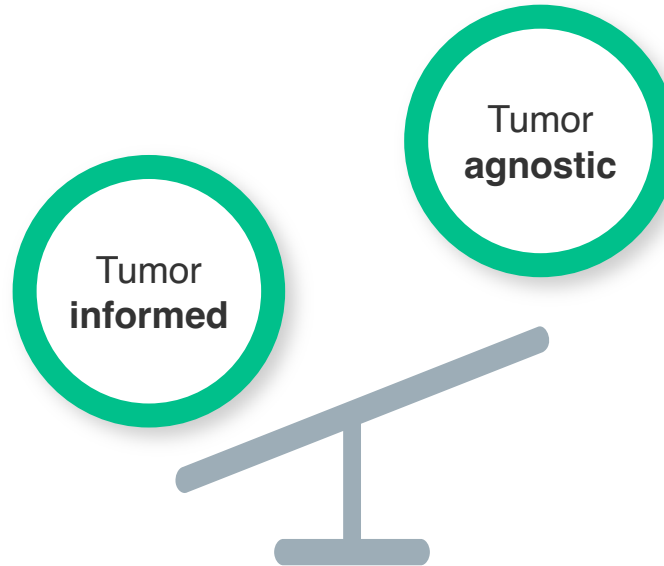


The more you know about them

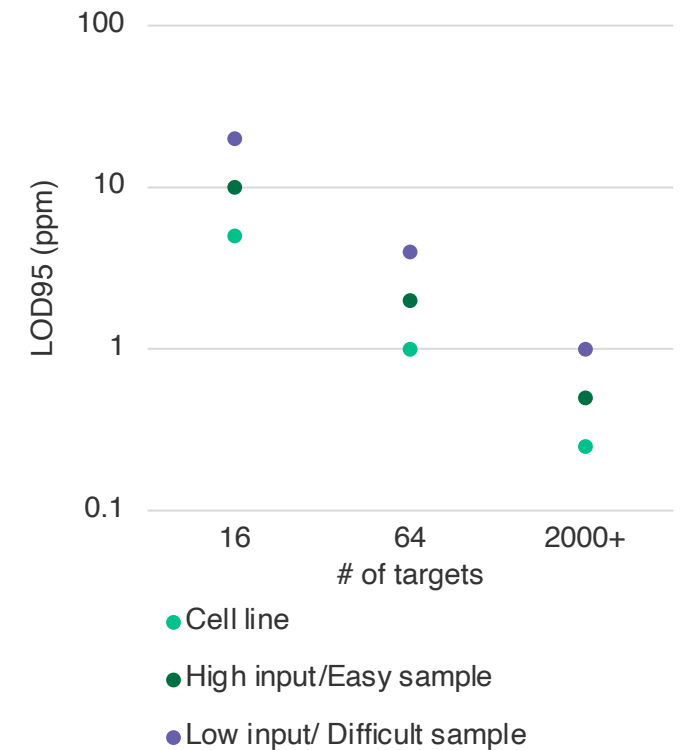


The **easier** they are to spot

The more you **know**  
about the targets



## The more targets



*For illustrative purposes only*

# MRD Express: In Focus

- Blazing **fast** synthesis in <24hours
- Industry best synthesis **quality**
- **ISO13485**
- Modified base capability for even **greater** performance
- **Future proof capacity**



## Twist MRD probe capacity planning

2,300,000 MRD assays / year

1,150,000 MRD panels / year (2 assays / tumor)

2,300,000,000 probes / year (~2000 probes / panel)

4,600,000,000 oligos / year (2x oligos / probe)

4,600 Chips / year (1M oligos / chip)

16 Chips / day (300 days / year)

4 dedicated MRD writers (4 chips / writer / day)

## Alternative Primers approach

230,000,000 targets / year (~200 targets / panel)

460,000,000 oligos / year (2x oligos / target)

1,500,000 oligos / day (300 days / year)

150,000 oligos / day (Primer vendor capacity)

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# Patrick Finn

President and COO

*Enzyme Engineering and Nucleic Acid Therapeutics*



# One Platform, Many Customized Solutions

Meeting customers where they are, powering growth across expanding platforms

## How we win



**Operational excellence**



**NPI machine**



**Commercial execution**

T W I S T  
BIOSCIENCE

Differentiated  
Silicon Platform  
Speed and Scale



**AI-enabled antibody discovery workflows**

AI-ready wet-lab at scale



**Molecular residual disease**

Personalized diagnostic research at scale



**Enzyme-engineered NGS**

Better performance, integrated workflow



**Nucleic acid therapeutics**

Next growth frontier

**Twist culture**

# Best-in-Class Enzyme Portfolio



Enhanced performance

Reduce dependency on external partners,  
more agility than competitors

Opens up OEM and NPI opportunities

# The Twist Advantage for Enzyme Engineering

## **AI-guided design compresses the search space**

Moves enzyme engineering from blind trial-and-error to targeted empirical validation

## **Unlock incremental functionality with differentiated performance and larger design pool**

Traditional methods are technologically constrained and can only support limited enzyme designs

## **DNA synthesis expertise and scale enable more shots on goal**

Twist can rapidly build large variant libraries to test more hypotheses

Rapid DNA enables testing of more hypotheses and faster design-build-test-learn iterations

## **Product-relevant screening closes the loop**

We measure what matters: yield, conversion, bias, speed, low-input performance, robustness, and automation compatibility

## **Application proximity drives commercial relevance**

Enzymes are engineered directly for NGS kit requirements, not isolated biochemical activity

## **Vertical integration converts innovation into revenue**

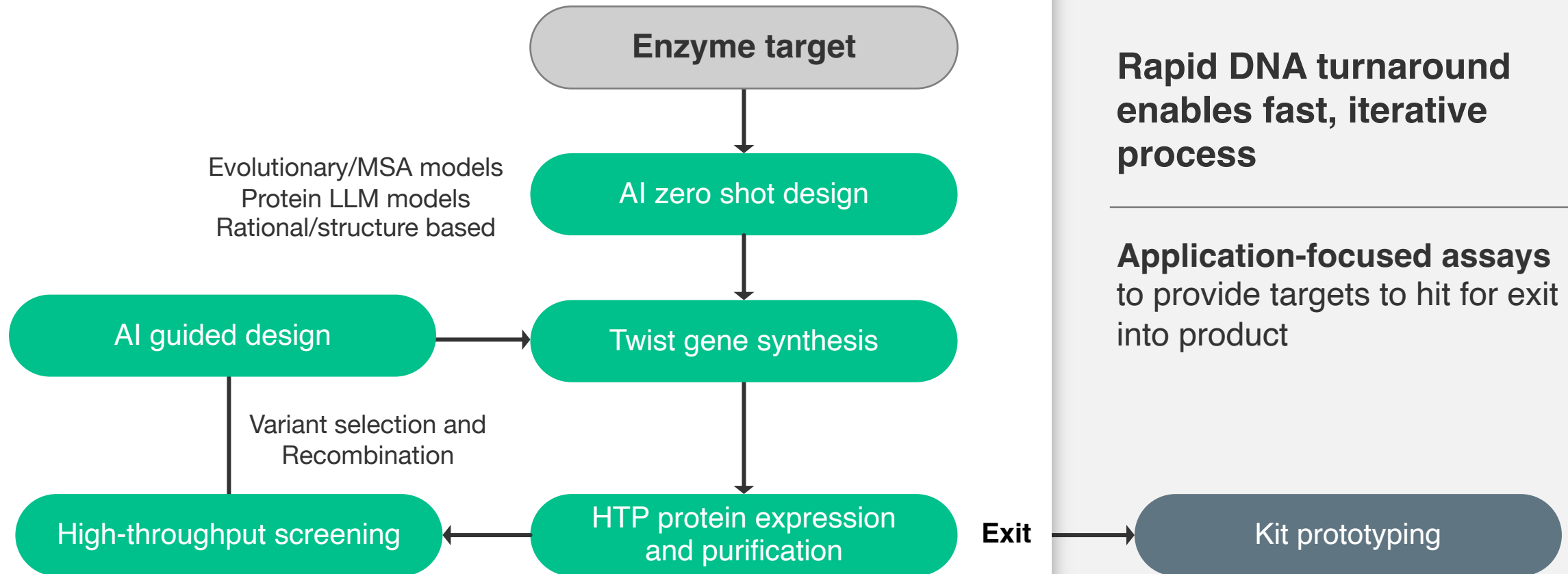
Better enzymes become differentiated products with improved performance, supply control, and margin potential

## **Each cycle creates proprietary learning**

Sequence-function data improves future design and compounds the platform advantage

# Our Experimental Workflow to Optimize Results

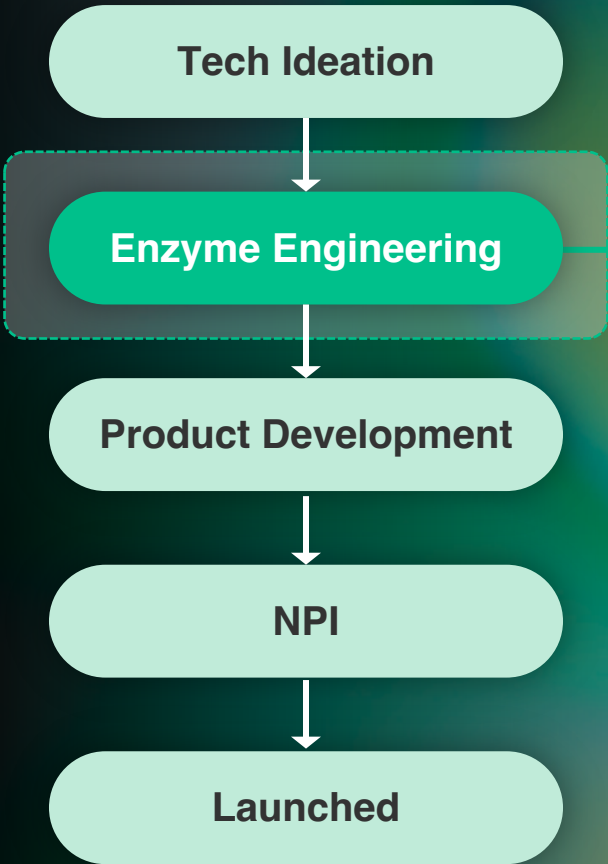
10 Days/Cycle



**Rapid DNA turnaround enables fast, iterative process**

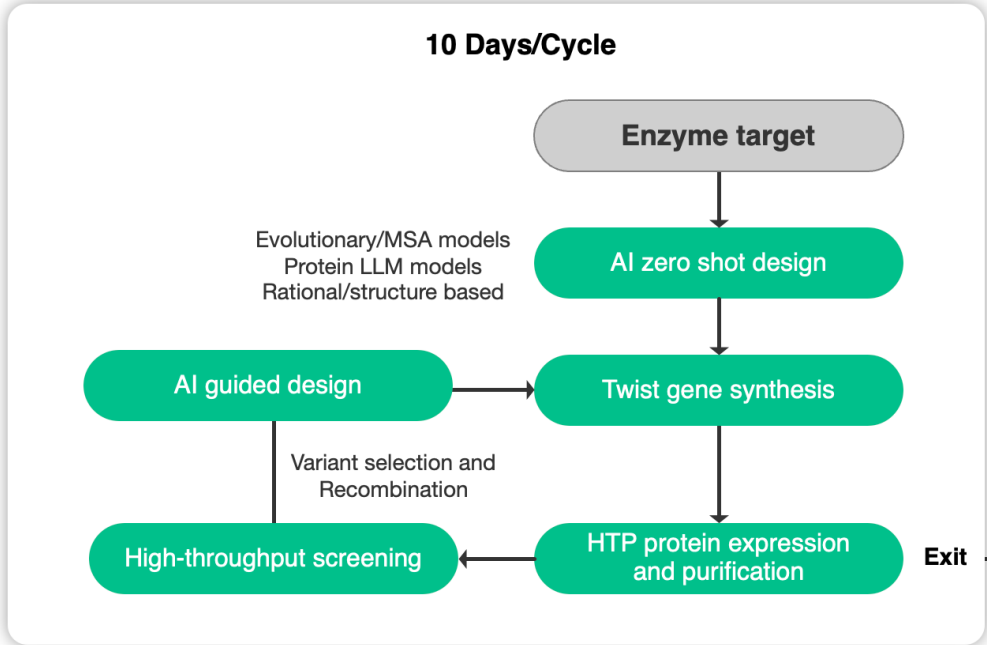
**Application-focused assays to provide targets to hit for exit into product**

# NGS and Enzyme Engineering



## Expand catalog of enzymes

- Drive healthy pipeline of engineered enzymes
- Capitalize on robust infrastructure established for enzyme discovery, engineering, buffer DoE and manufacturing



**Rapid DNA turnaround enables fast, iterative process**

**Application-focused assays** to provide targets to hit for exit into product

# Case Study: Ligase into NGS Kits

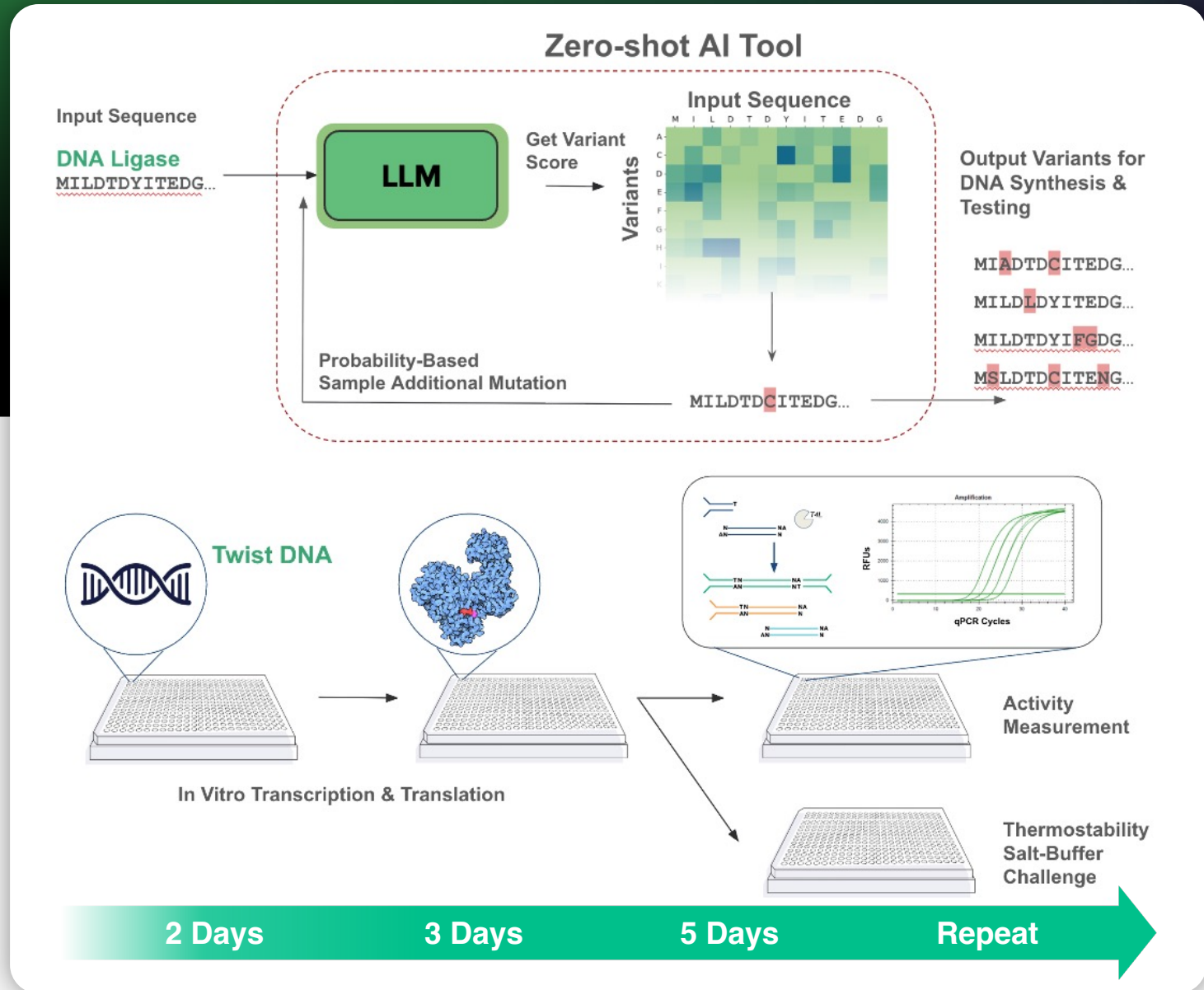
**Challenge:** Low input cfDNA for tests, impacted conversion efficiencies, buffer sensitivity of ligase

**Goal:** Engineer a Robust, best-in-class efficiency DNA ligase that works with Low input DNA

**Strategy:** Utilize LLM-based design tools to introduce beneficial stability and activity mutations. Leveraged **Twist Gene Fragments** to produce screening scale enzymes. 13 rounds of High-throughput assays to screen for desirable properties.

Used **Twist Clonal DNA** for large scale purification and validation. No molecule left behind.

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# Case Study: Ligase into NGS Kits Engineering Outcome

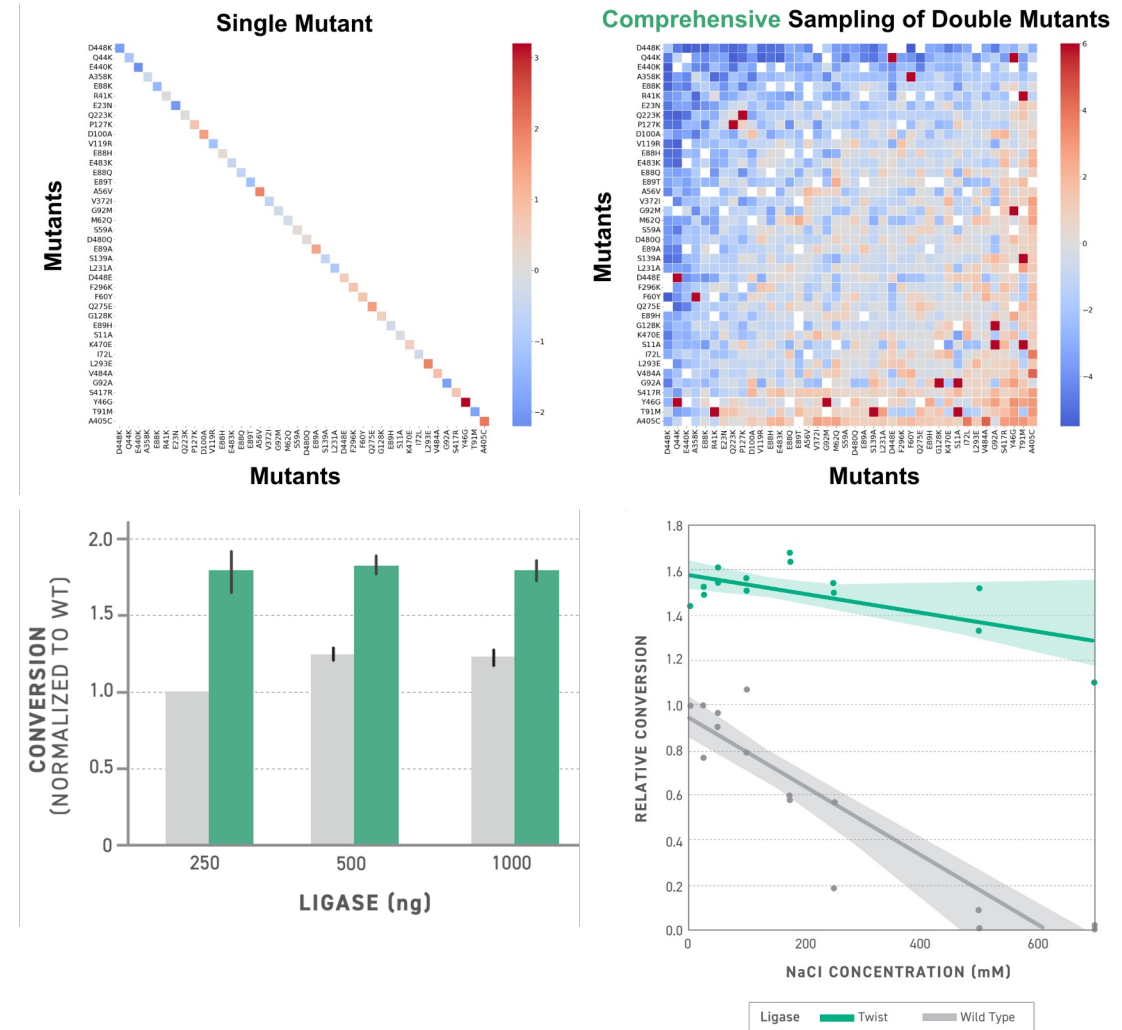
## Advantages:

- Rapid DNA turnaround time for weekly iterations
- Low price point
- Best-in-class conversion of low input DNA

Twist leverages this DNA ligase in NGS Library Prep product portfolio

Twist uses **10x less ligase** internally for high conversion

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# Case Study: Polymerase

**Challenge:** GC amplification bias in complex libraries

**Goal:** Engineer a **high-fidelity DNA polymerase** solution with a **high-performance buffer** for best-in-class uniformity

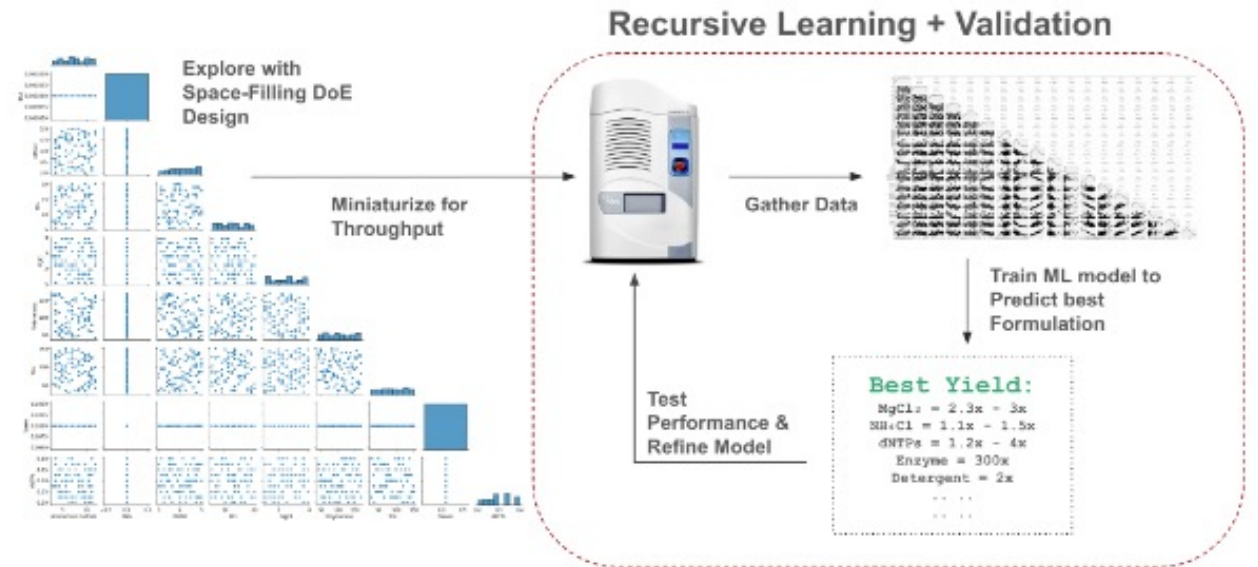
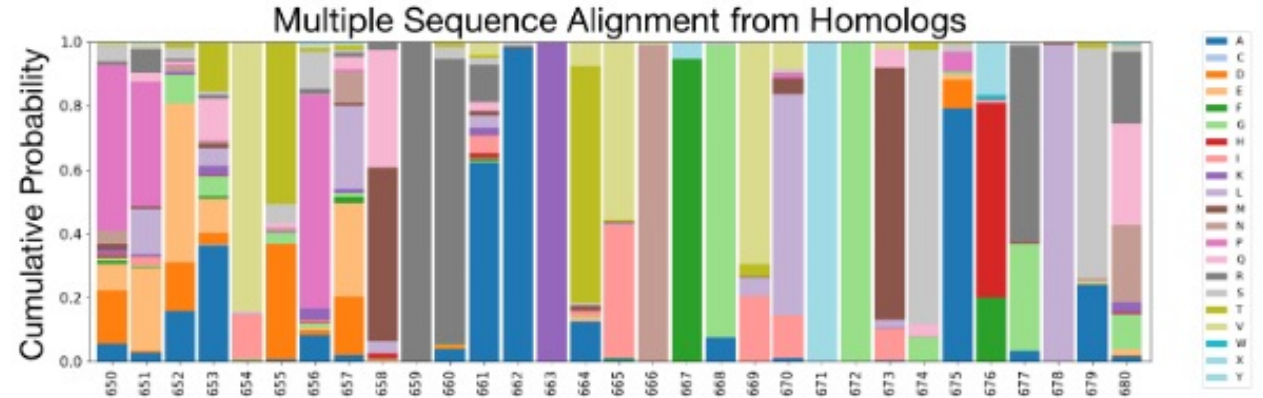
## Enzyme Strategy

Utilize **LLM** and **Multiple Sequence Alignment (MSA)** Tools and **Structure Modeling** to sample mutations in functional hot-spots

## Buffer Strategy

Utilize **space-filling Design of Experiments (DoE)** approaches to broadly sample and **supervised learning** to predict best buffer compositions

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# Case Study: Polymerase Results

Engineered Polymerase to provide robust and uniform coverage across various GC regions  
Uniform coverage enables tracking of sequence-challenging variants

## Twist Polymerase solution encompasses

1. High-Fidelity Polymerase
2. Robust and High-Performance Buffer

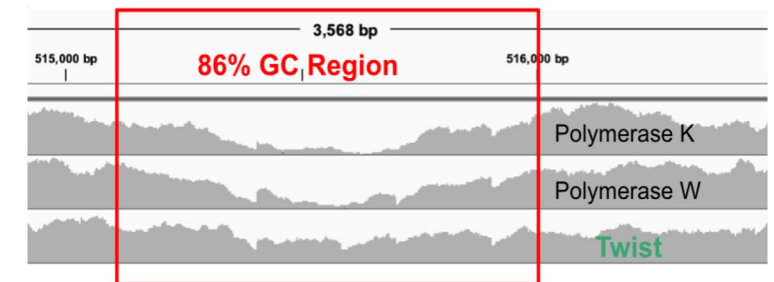
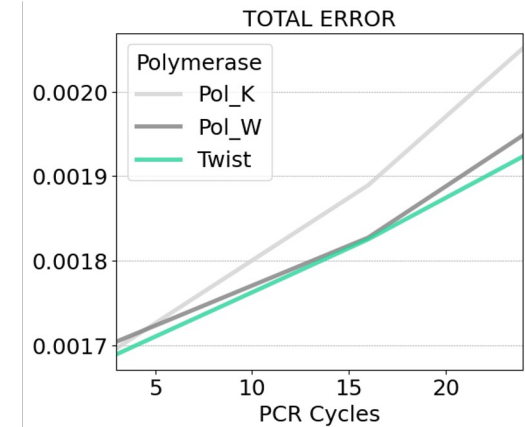
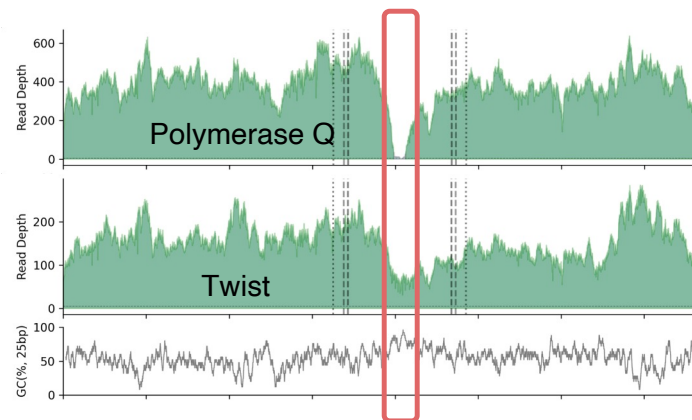
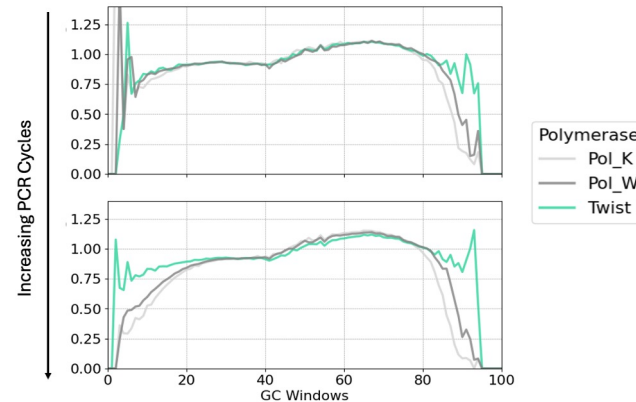
## Results

Leveraged Twist Express Clonal Genes and Twist Cloned Single Variant Libraries (SVL) for E.coli expression, purification and arrayed screening to identify winning mutations for improved activity and fidelity

## Outcome

### Best-in-class uniformity

Twist leverages this DNA polymerase in sequencing confirmation of every gene that is delivered in DNA Synthesis Portfolio



# New Twist DNA Library Prep: Leveraging Enzyme Engineering for Superior NGS Performance

## Introducing Twist TrueAmp and PCR-Free WGS: A New Standard in Enzymatic Fragmentation Library Prep



### TrueAmp Library Prep

Library prep samples  
that are degraded or  
have low input



### PCR-Free WGS Library Prep

Library prep for whole  
genome sequencing

## Proprietary innovation via enzyme engineering

Integrating our engineered fragmentation module, T4 DNA ligase, and TrueAmp Polymerase, these kits deliver **low-bias, high-uniformity** libraries with **strong yields**, even from **FFPE or ultra-low inputs** down to 0.1 ng.

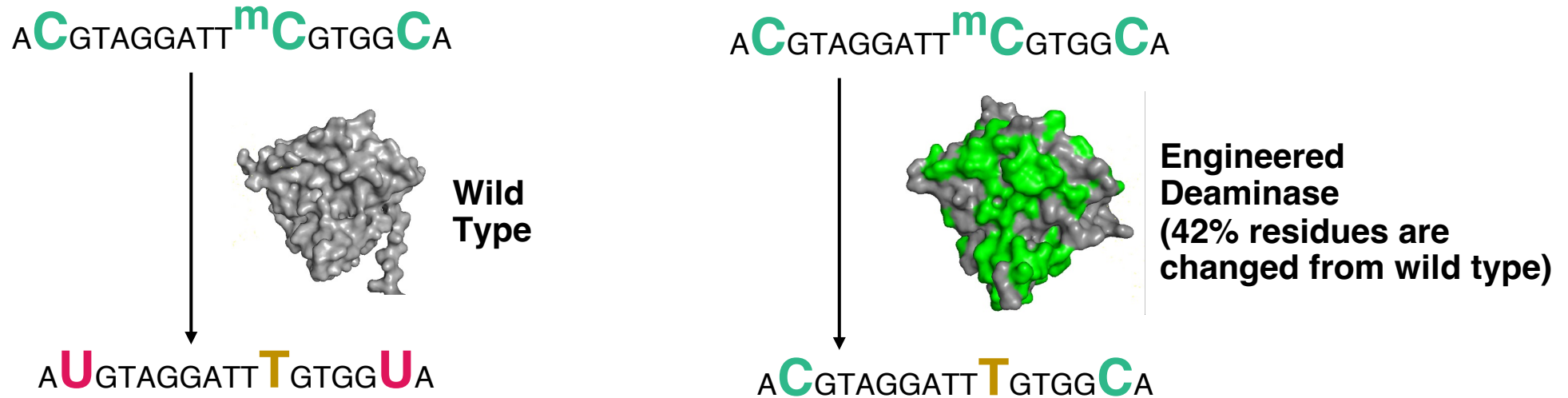
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## High-performance solutions for any scale

The **TrueAmp** and **PCR-Free WGS** kits provide comprehensive, high-performance solutions for diverse sequencing needs. While the TrueAmp kit offers tunable enzymatic fragmentation with minimal bias, the PCR-Free workflow utilizes high ligation efficiency to eliminate amplification bias entirely.

# Methylation: New Enzyme Differentiation

Twist-engineered C-deaminase distinguishes mC and C



## Engineered for:

- High targeted specificity towards mC > T conversion, maintaining genome complexity
- High thermal stability
- High activity to enable <30min reaction time

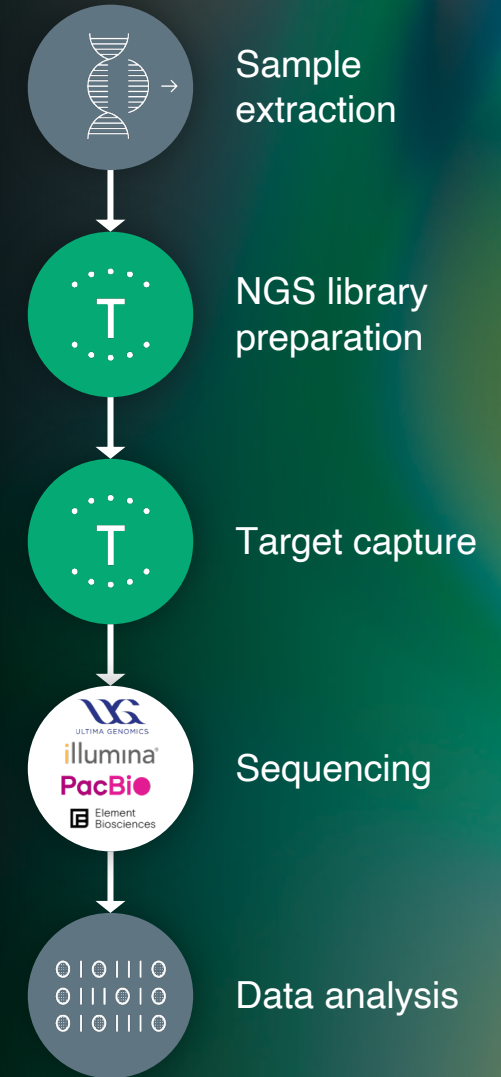
# NPI Machine: Regulated Products for Clinical Customers

## Unlocking new market opportunities

- In Vitro Diagnostic Medical Device Regulation (IVDR) poses major shift in the European regulatory landscape for NGS diagnostics
- EMEA growing area of Twist business
- Proactively pursuing rigorous compliance efforts across all key areas to introduce Twist Precision Dx kit
- Pairs well with product portfolio for clinical customers

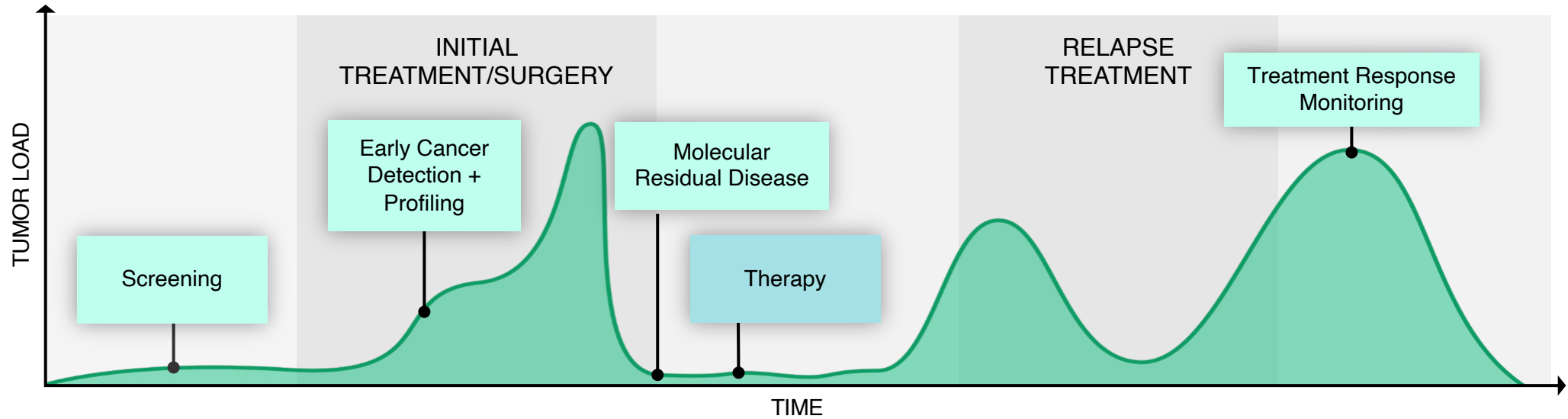
## Our CE-marked Twist Precision Dx Products are available in 3 configurations

| Products                                | Content   |
|---|---|
| Twist Precision Exome Dx Kit            | <b>Comprehensive exome workflow</b> with library prep, target enrichment, and exome panel |
| Twist Precision Prep and Enrichment Kit | <b>Panel agnostic</b> library prep and enrichment   |
| Twist Precision Exome Dx Panel          | <b>Exome panel</b> that can be integrated with other workflows                            |



For in vitro diagnostic use. Not available in all regions and countries.

# Twist Powers the Continuum of Care in Cancer Research



| DIAGNOSTIC                                |   |   |   |   |   | THERAPEUTIC        |              |
|---|---|---|---|---|---|--------------------|--------------|
| SCREENING                                 |   | EARLY DETECTION + PROFILING                   |   | MINIMAL RESIDUAL DISEASE                    |   | NEOANTIGEN THERAPY |              |
| WGS + WES<br>High throughput applications | RNA-Seq<br>Low input, FFPE, Whole transcriptome | WGS + WES<br>High throughput applications     | Methylation<br>Epigenetic biomarker detection | Express MRD<br>1 BD TAT personalized panels | WGS + WES<br>High throughput applications       | mRNA               | Clonal Genes |
| Library Prep + Enrichment                 | Custom Panels (HLA)<br>Multi-allelic coverage   | Liquid Biopsy<br>Deep sequencing applications | CGP Panels<br>Oncology detection              | Custom Panels<br>Targeted tumor naïve tests | cfDNA LP<br>Ultra sensitive library preparation | Antibody Discovery | HT IgG       |

# One Platform, Many Customized Solutions

Meeting customers where they are, powering growth across expanding platforms

## How we win



**Operational excellence**



**NPI machine**



**Commercial execution**

T W I S T  
BIOSCIENCE

Differentiated  
Silicon Platform  
Speed and Scale



**AI-enabled antibody discovery workflows**

AI-ready wet-lab at scale



**Molecular residual disease**

Personalized diagnostic research at scale



**Enzyme-engineered NGS**

Better performance, integrated workflow



**Nucleic acid therapeutics**

Next growth frontier

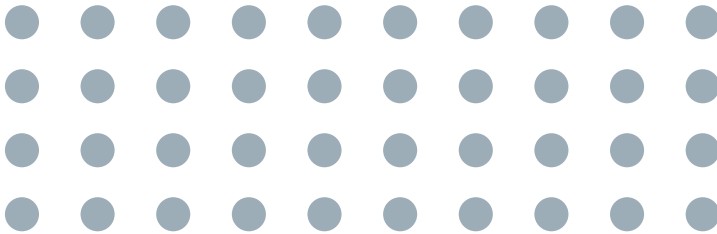
**Twist culture**

# Powering a New Era of Therapeutics with Future Product Introductions

2020

Building UP

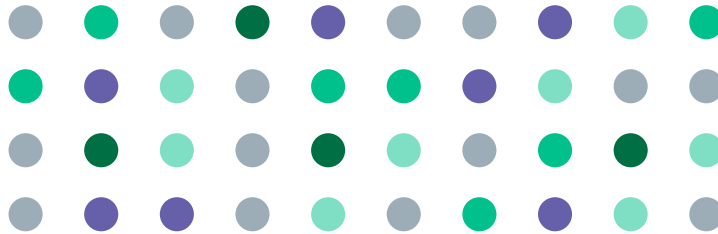
One therapy  
for millions of people



2026

Building OUT

Personalized therapies  
for millions of people



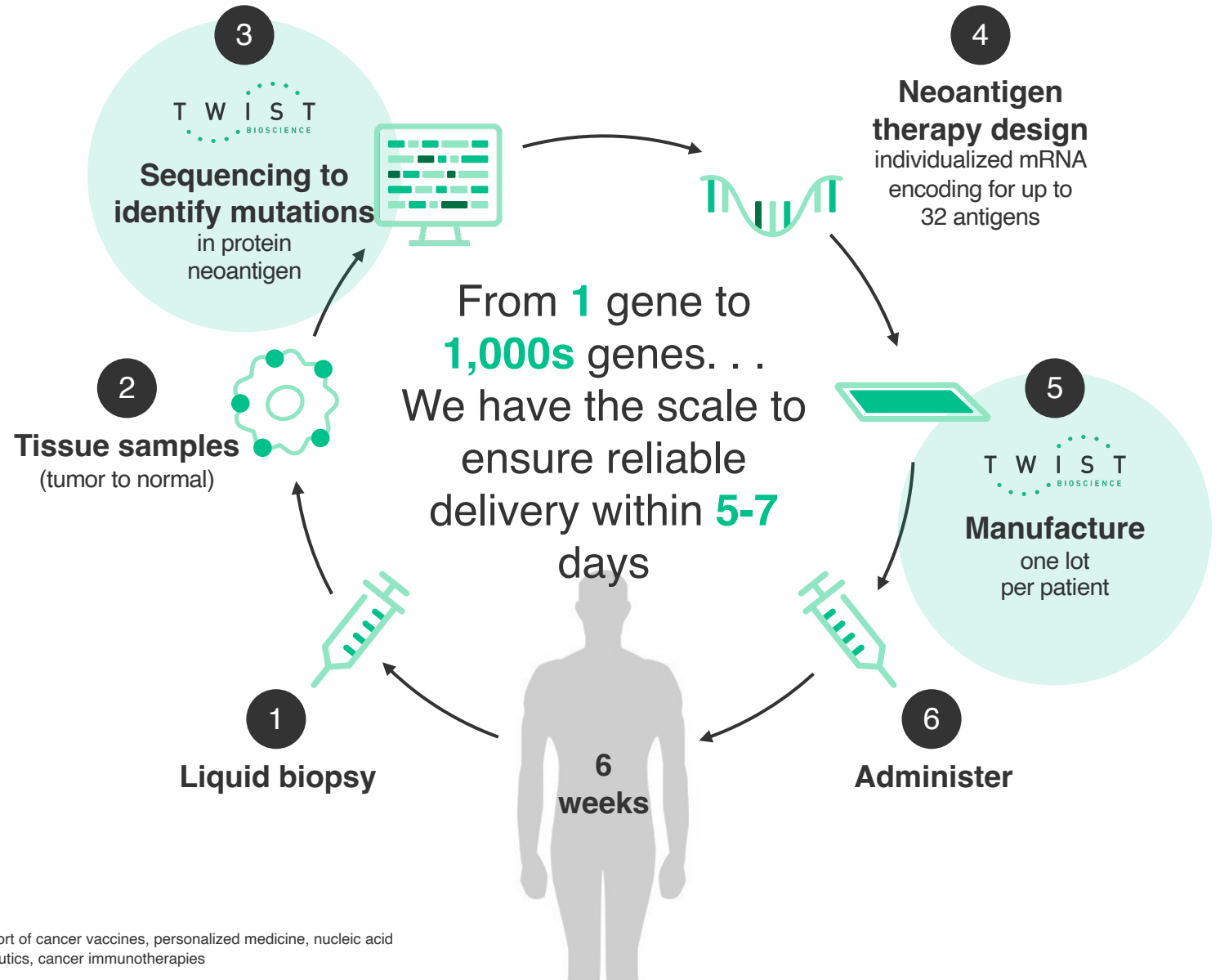
The Need

Capacity, scale, and pricing for needle-to-needle success

# Supporting Tools for Personalized Therapy Workflows at Scale\*













## Example Customer Workflow



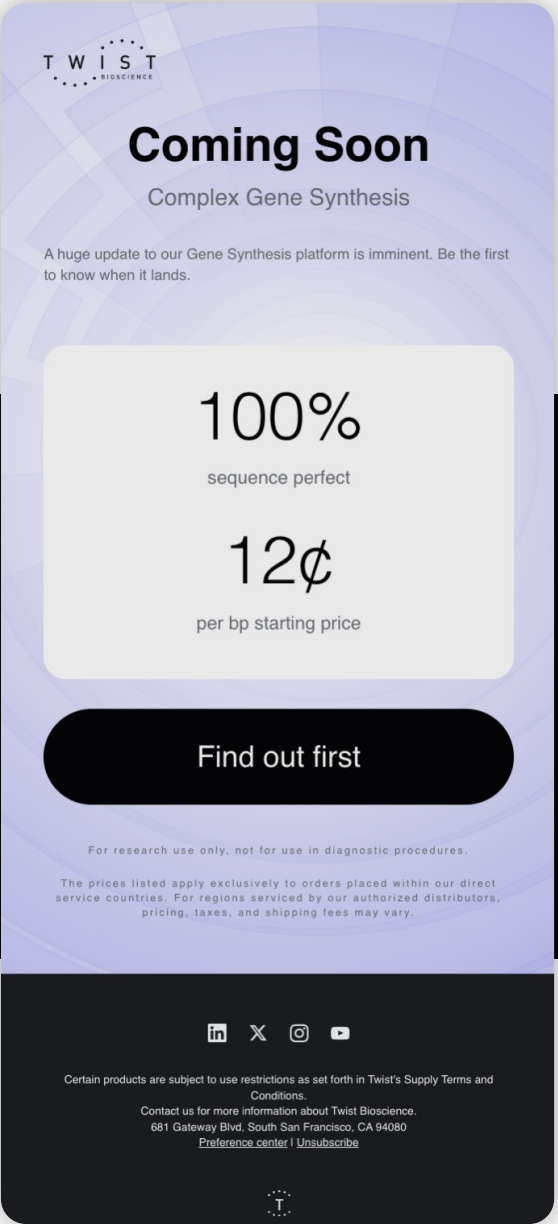
\* In support of cancer vaccines, personalized medicine, nucleic acid therapeutics, cancer immunotherapies

# Robust Product Portfolio Supports Complexity of Nucleic Acid Therapeutics

Ability to address **99.9%** of DNA sequences

|   |   |  |  |   |
|---|---|--|--|---|
| <br><b>Affordable price</b><br> | <br><b>High quality</b><br> | <br><b>Scale</b><br> | <br><b>Speed</b><br> | <br><b>Complexity</b><br> |
|---|---|--|--|---|

Robust product portfolio



**Coming Soon**  
Complex Gene Synthesis

A huge update to our Gene Synthesis platform is imminent. Be the first to know when it lands.

**100%**  
sequence perfect

**12¢**  
per bp starting price

**Find out first**

For research use only, not for use in diagnostic procedures.  
The prices listed apply exclusively to orders placed within our direct service countries. For regions serviced by our authorized distributors, pricing, taxes, and shipping fees may vary.

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# Twist is Writing the Future of Nucleic Acid Therapeutics

We deliver what nucleic acid therapeutics require today

## Perfect quality nucleic acid synthesis

Lowest error rates, highest quality in the industry

## Scale to build out individual sequences to serve the patient community

Deliver millions of genes per year with capacity to scale to support future global demand

## High-quality and fast DNA synthesis, at scale

Delivering clonally perfect DNA in 4-7 days, no compromise to turnaround time, quality or purity

## Minimal carbon footprint

Massively reduced carbon footprint vs. traditional methods

## Unmatched unit economics

< \$1,000 per patient

**Our DNA synthesis platform future-proofs supply chain for generations**

# One Platform, Many Customized Solutions

Meeting customers where they are, powering growth across expanding platforms

## How we win



**Operational excellence**



**NPI machine**



**Commercial execution**

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**Molecular residual disease**

Personalized diagnostic research at scale



**Enzyme-engineered NGS**

Better performance, integrated workflow



**Nucleic acid therapeutics**

Next growth frontier

**Twist culture**

# Twist's Commercial Philosophy



- We are in the business of **delighting our customers**
- Every Twister is **passionate** about our customers'
- Go into a market with the ambition of a world where **we are #1 and there's no #2**
- There is only one way to go for our sales results: **13 consecutive quarters** of sequential (QoQ) growth
- We readily **OEM out our best products to competition**, as we must and we will outsell anyone
- As a salesperson, **you are what your numbers say you are**
- As a commercial leader, if you don't fix the problem, **you are the problem**
- We **reward performance** and regularly identify and remove people who are **better off working for competition**

# Driving Broad Access to DNA through Flexible Commercial Model

1

## Relationship-led sales channels

### Direct sales

General account managers serving broad commercial accounts

### Key account management

Dedicated coverage for large and strategic customers

### Academic / government sales

Specialized support for research institutions and public sector buyers

2

## Scaled growth channels

### Inside sales

Customer acquisition and long-tail account growth

### Digital channel

Scientists and end user order directly from Twist

eCommerce

B2B punchout

API ordering

Self-service ordering for institutions and high-volume accounts

3

## Partner channels

### OEM channel

Twist supplies third parties that sell Twist products under their own brand

Expands reach through embedded partner distribution



Scientists



Labs



Institutions



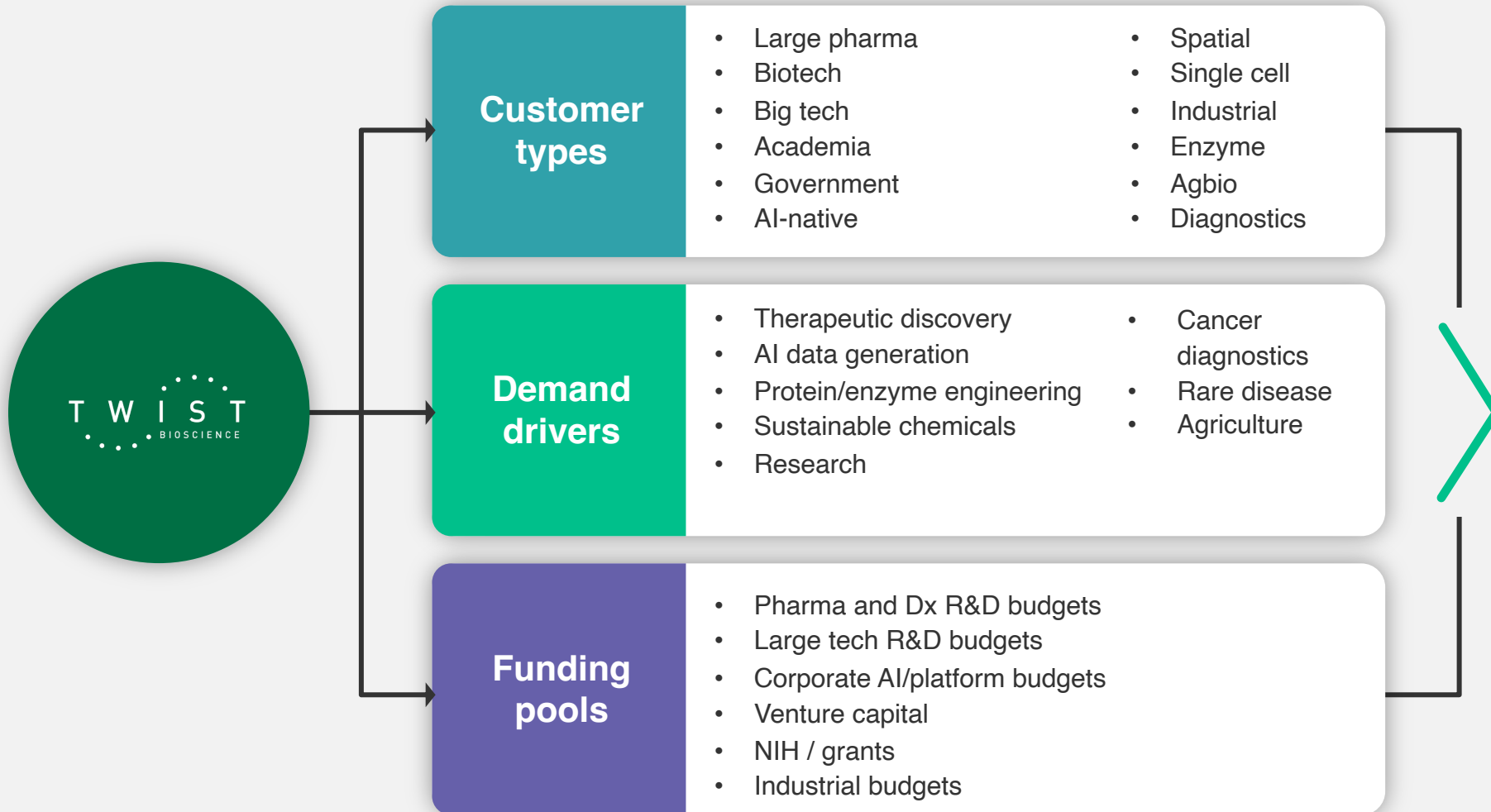
Enterprise accounts



OEM partners

A multi-channel commercial model allows Twist to **serve everyone from individual scientists to strategic enterprise and OEM partners**

# Diversified Customer and End-Market Exposure Supports Durable Demand



## Resilient Demand Profile

✓ End market pressures offset by other growth drivers

✓ Funding cycles do not determine DSPS demand

✓ Increasing application diversity expands market opportunity

Twist's diversified customer types, demand drivers, and budget pools **reduce dependence on any single customer**

# Agenda

- Welcome
  - Tour
  - DSPS Strategy Session
  - Fireside Chat with Dr. Frances Arnold
  - Customer Presentations
- 

## Lunch

---

- NGS Strategy Session
- **Customer Presentations**
- Financial Overview
- Culture
- Reception

REGENERON GENETICS CENTER

**Sequence more samples, not more bases**

# John Overton, PhD

Chief Sequencing Officer, Regeneron Genetics Center

Vice President, Regeneron Pharmaceuticals

Why targeted sequencing is still the smarter bet for drug discovery research — even as whole genome sequencing costs continue to fall.

# The RGC sequences the genome to discover the genetic causes of disease

- The RGC has built one of the world's largest human genetics research databases, ~3.5M participants, by combining high-throughput whole exome sequencing and genotyping to create imputed genomes
- With WGS costs rapidly falling, why not just sequence the whole genome?
- For our purposes, discovering the genetic causes of disease for therapeutic intervention, we believe that a well-imputed genome performs just as well as WGS
- We have empirically assessed the utility of whole genome sequencing versus an imputed genome for studies of complex traits and the results are clear

## **APPROACH 1 — Genotyping + Imputation (IMP)**

**Mostly assesses known variation in non-coding regions of the genome; imputation fills in the gaps**

- Panels commonly target 500K–1.5M known variant sites across the genome
- Imputation against reference genomes creates an imputed genome covering common variation; lowest cost per sample

## **APPROACH 2 — Whole exome sequencing (+ Imputation, WES+IMP) ★ RGC standard**

**Targets coding regions for rare and common variation, combined with genotyping to create an imputed genome**

- ~20,000 coding variants per person (ancestry-dependent)
- Genotyping adds 500K–1.5M non-coding sites; imputation fills in gaps to create an imputed genome

## **APPROACH 3 — Whole Genome Sequencing (WGS)**

**Captures the full genome — ~3.6M variants per person — but at significant cost and time**

- Most WGS variants are rare, non-coding, and not amenable to many tools available for large-scale association analyses (e.g., gene-burden tests)
- 3–10× more expensive per sample, creates a large data footprint, and exome+genotyping sequencing is 20X faster than whole genome sequencing

# The UK Biobank, a cohort of 500K volunteers, has been genotyped, exome sequenced (at the RGC), and whole genome sequenced – enabling direct comparison of sequencing approaches

Article <https://doi.org/10.1038/s41588-024-01930-4>



## Panel a – variants captured (N~150,000 participants) WGS detects ~5× more variants than WES+IMP

- WES: 17M, IMP: 111M, WES+IMP: 126M, and WGS: 599M variants
- Coding variant counts are essentially identical between WES+IMP and WGS platforms
- The extra 473M in the WGS cohort not seen in the WES+IMP data are all non-coding

## Panels b+c+d – WGS variants are non-coding and ultra-rare ~97% of coding variants are shared; WGS non-coding variants are almost all ultra-rare

- Only ~3% of coding variants are unique to one platform
- Mean coding variants per person (panel c) are nearly identical: 20,000 (WGS) vs. 20,039 (WES+IMP)
- 80% of non-coding variants are WGS-only; most seen in only 1 person, virtually all in ≤3 people (panel d)

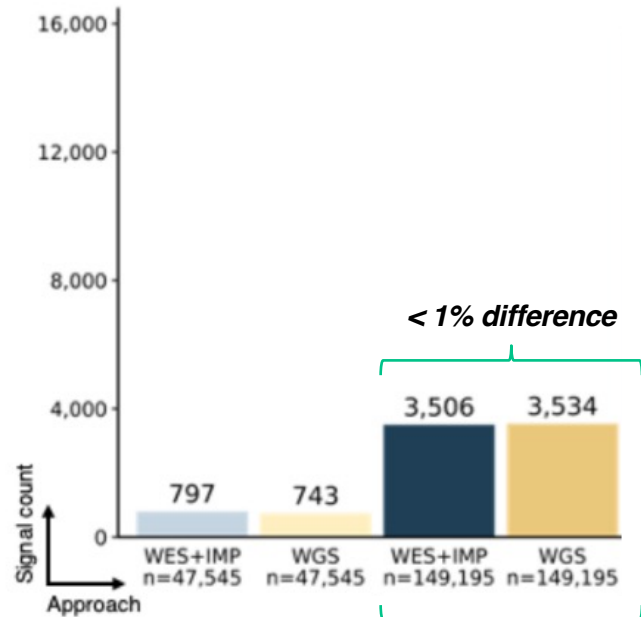
## The implication

### The extra bases in WGS add cost, not insight

- Coding variants – the primary source of actionable drug targets – are captured equally well by WES+IMP and WGS
- Ultra-rare non-coding variants seen in 1–3 people, if real, will not reach statistical significance in association studies (ultra-rare variants in coding regions can be combined for analyses)
- The question is not how many variants are found – it's whether they can be used

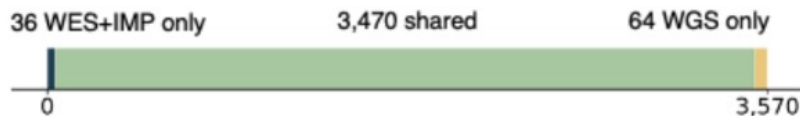
# Across 100 phenotypic traits – 80 quantitative + 20 binary phenotypic traits at fixed sample sizes, WGS and WES+IMP show nearly identical genetic association results

Single variant association yield



Same sample size,  
different approach

Contributions to single variant signals (n=149,195)



## Total association signals

Signal counts differ by less than 1% at ~150,000 samples

- WES+IMP: 3,506 signals vs. WGS: 3,534 signals — a <1% difference
- 3,470 of 3,570 loci shared between platforms — 97% overlap — and almost all point to the exact same variant in the genome

## Platform-unique signals

Platform-unique signals are weak associations and artifacts that often do not replicate

- Only 36 WES+IMP-only and 64 WGS-only unique signals out of 3,570 total
- Weak p-values near threshold — often fail to replicate in later analyses

## Gene-based tests

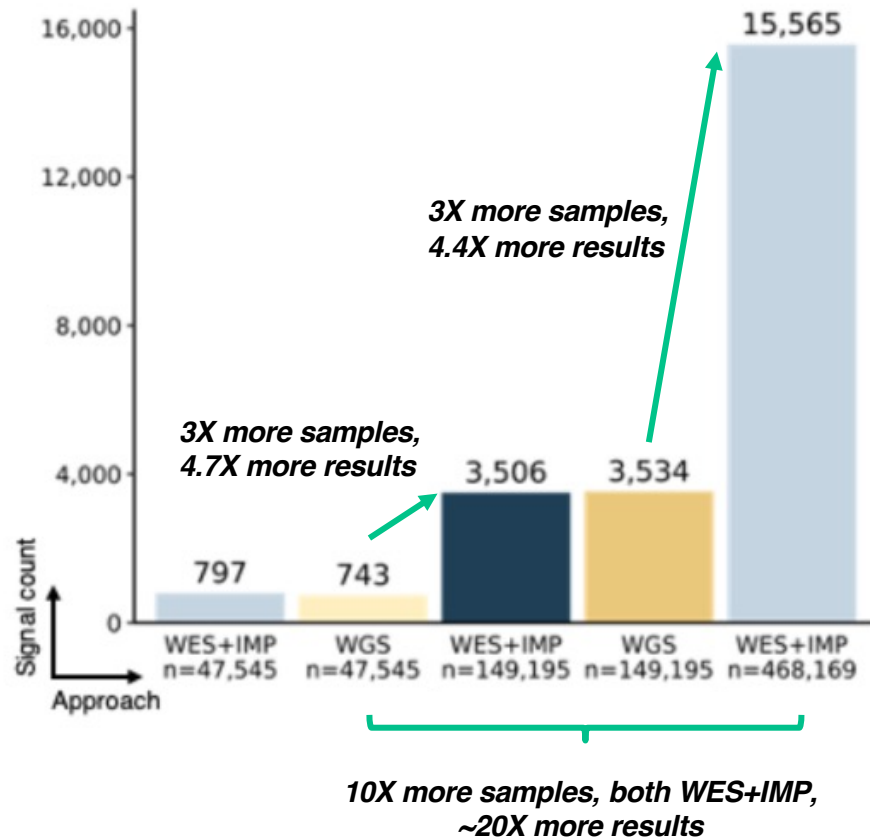
Gene-based results are concordant — the same conclusion holds

- Gene-burden analyses show identical discovery yield between WES+IMP and WGS at matched sample sizes
- Results hold across both quantitative and binary traits

# On a fixed budget, having more samples is more important than more variants per sample: a three-fold increase in sample numbers results in ~5-fold more associations

Cost-matched comparison: WES+IMP cohort 3× larger than WGS at current cost differential; also modelled at 10× cost efficiency

Single variant association yield



## At 3× cost efficiency

### 3× more samples yields 4-5× more single-variant signals

- WGS: 743 signals at n=48K → WES+IMP: 3,506 signals at n=149K
- WGS: 3,534 signals at n=149K → WES+IMP: 15,565 signals at n=468K
- More samples — not more bases per sample — drives discovery

## At 10× cost efficiency

### At 10× cost efficiency, exomes buy far more samples — and the discovery advantage compounds

- WGS: 743 signals at n=48K → WGS+IMP: 15,565 signals at n=468K
- At 3× cost: 4× more results — at 10× cost: >20× more results
- The cost advantage of targeted sequencing will continue to grow as sequencing costs continue to fall

# Genotyping arrays failed to take advantage of the advancements in sequencing technology – the RGC and Twist built a solution that does

## The problem

### Standard arrays couldn't scale with our ambitions — or serve diverse cohorts

- As we scaled to millions of samples, we needed to move genotyping beyond arrays
- We wanted to create an assay that could replace array genotyping, be processed as quickly and easily as exomes, and cover all genetic ancestries equally well

**We needed something that didn't exist...**

## The SNP diversity panel

### Co-developed with Twist in 2019–2020: Ancestry-agnostic, scalable, comprehensive

**GSA: ~600K variants → SNP Diversity Panel: ~1.5M variants**  
~2.5× more variants, via ~600K probes

- Ancestry-agnostic by design — performs equally well across genetically diverse cohorts
- Combined with exome capture in a single workflow; used on >2.5M RGC samples
- Imputation results comparable to the largest available arrays — closing the quality gap for non-European cohorts

# The data is clear: sequence more samples, not more bases

## 01 WGS and WES+IMP deliver nearly identical genetic associations at matched sample sizes

WGS captures 5× more variants — but they are overwhelmingly non-coding, ultra-rare, and largely unusable; the extra bases add cost, not insight.

## 02 On a fixed budget, WES+IMP buys 3–10× more samples — yielding 4–20× more discoveries

Sample count — not base count — is the true driver of genetic discovery; as sequencing costs continue to fall, this advantage only grows.

## 03 The RGC's SNP Diversity Panel extends this advantage

Co-developed with Twist, the SNP Diversity Panel brings ancestry-agnostic, sequencing-scale genotyping to cohorts of any size.



# Thank you

HUDSONALPHA INSTITUTE  
FOR BIOTECHNOLOGY

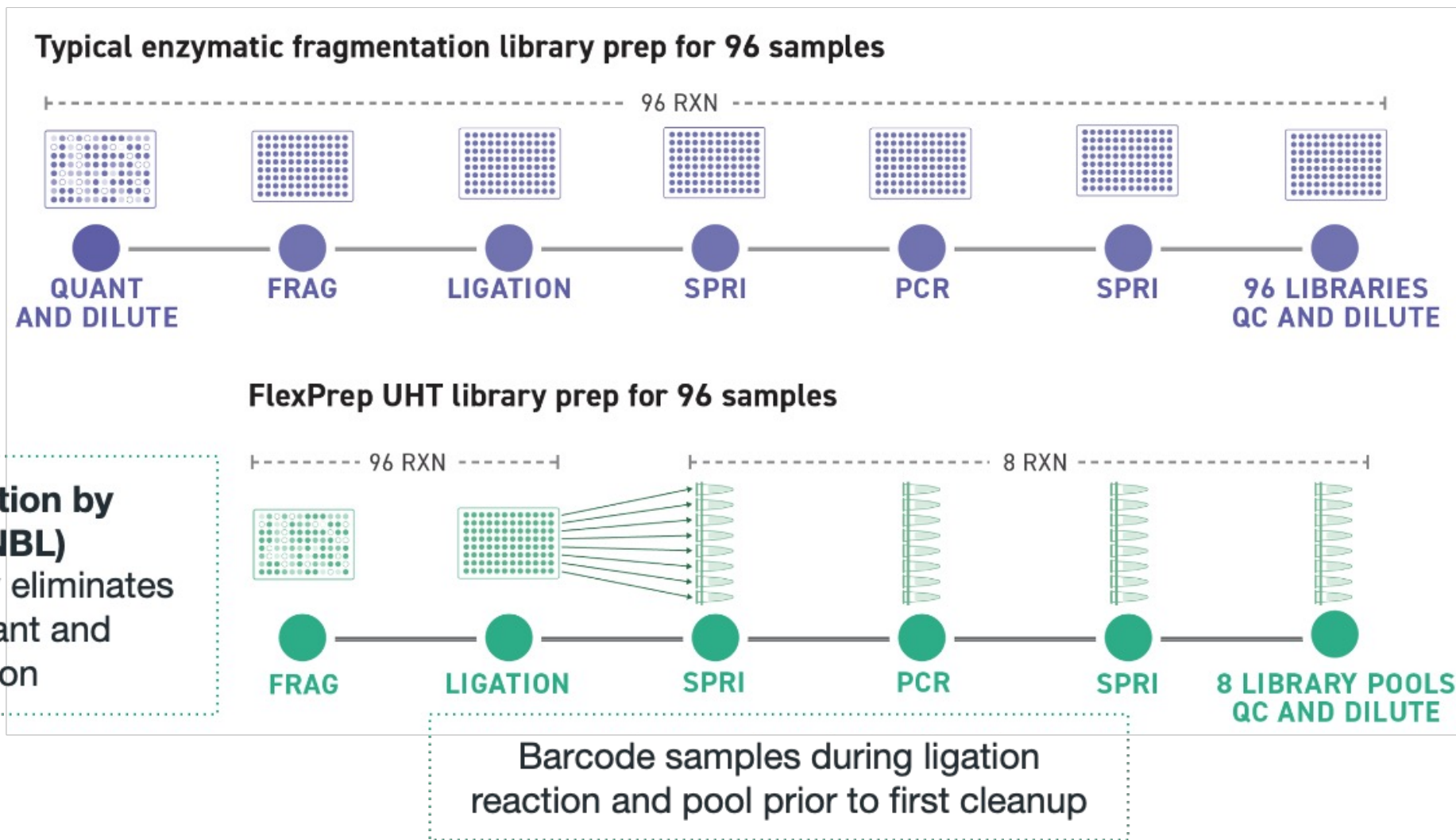
# Josh Clevenger

Faculty Investigator



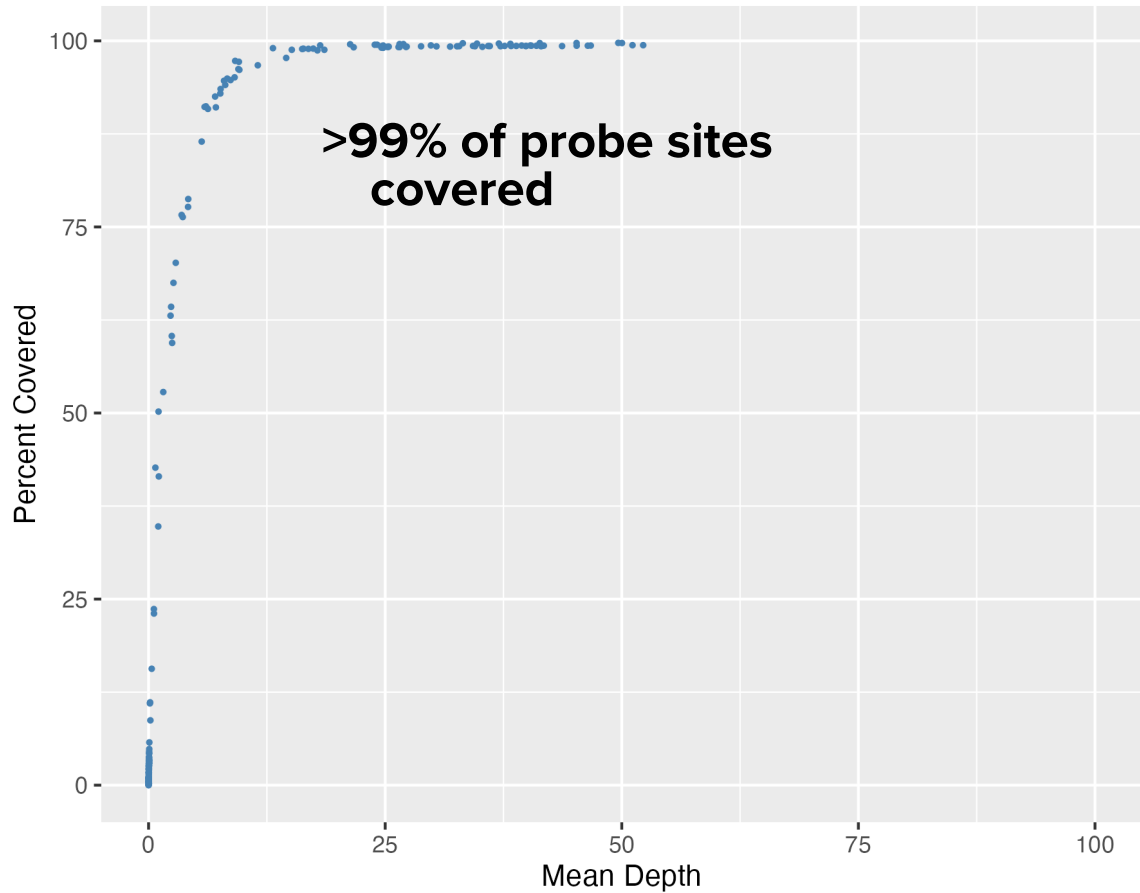
My lab has been built on  
Twist library prep

# FlexPrep UHT workflow emphasizes auto-normalization

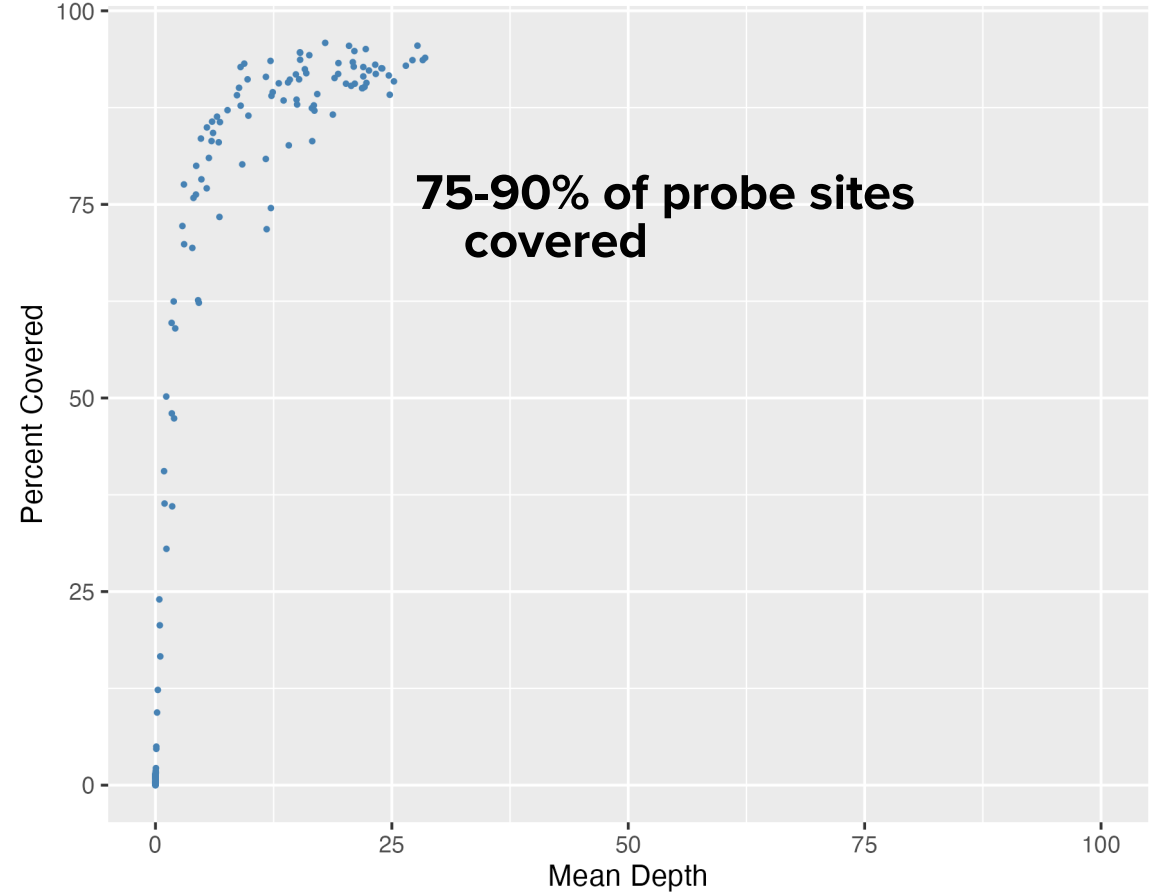


# Library complexity makes enrichment sequencing highly accurate

FlexPrep Mean depth vs Percent Covered



**FlexPrep**



**Competitor Prep**

# The young scientists who make an impact with FlexPrep



## **Zack Myers**

Develops algorithms to discover genes from scaled sequencing data

## **Hallie Wright**

Uses genomics to improve finger millet for east Africa

## **Ashmita Upadhyay**

Develops AI models to use scaled sequencing to improve crop varieties

# The young scientists who make an impact with FlexPrep



**Catherine Davis**  
Supports breeding programs  
all over the world



**Justin Vaughn**  
Translates pangenomes  
into genotypes for gene  
discovery



**Ambreal White**  
Can prepare more than 100  
species of plants and animal  
DNA for library prep

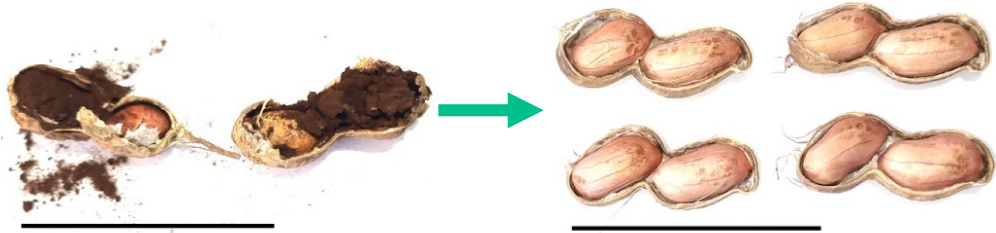


**Ethan Thompson**  
Discovers insights that  
transform agricultural  
industries

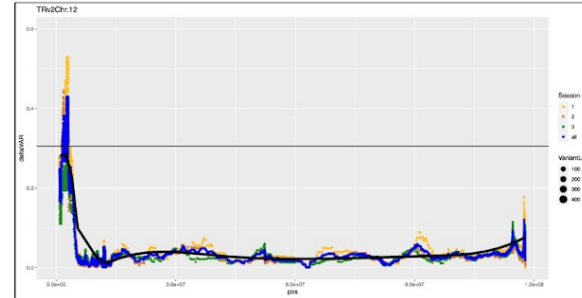
# Genomics protects our food supply

# Scaled genomics helps protect our food supply

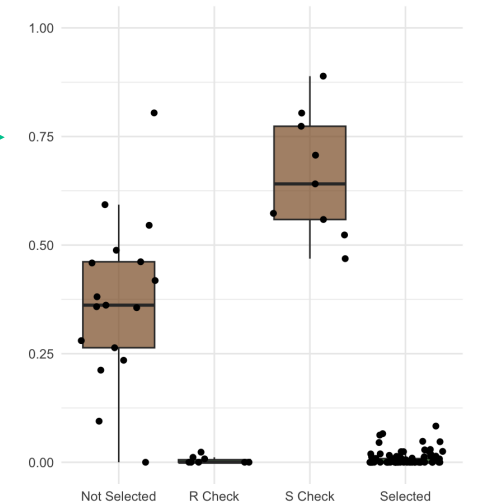
Smut is a major threat to global peanut supply chain



Mapping resistance



Pangenomics and gene discovery





Accelerated cultivar development



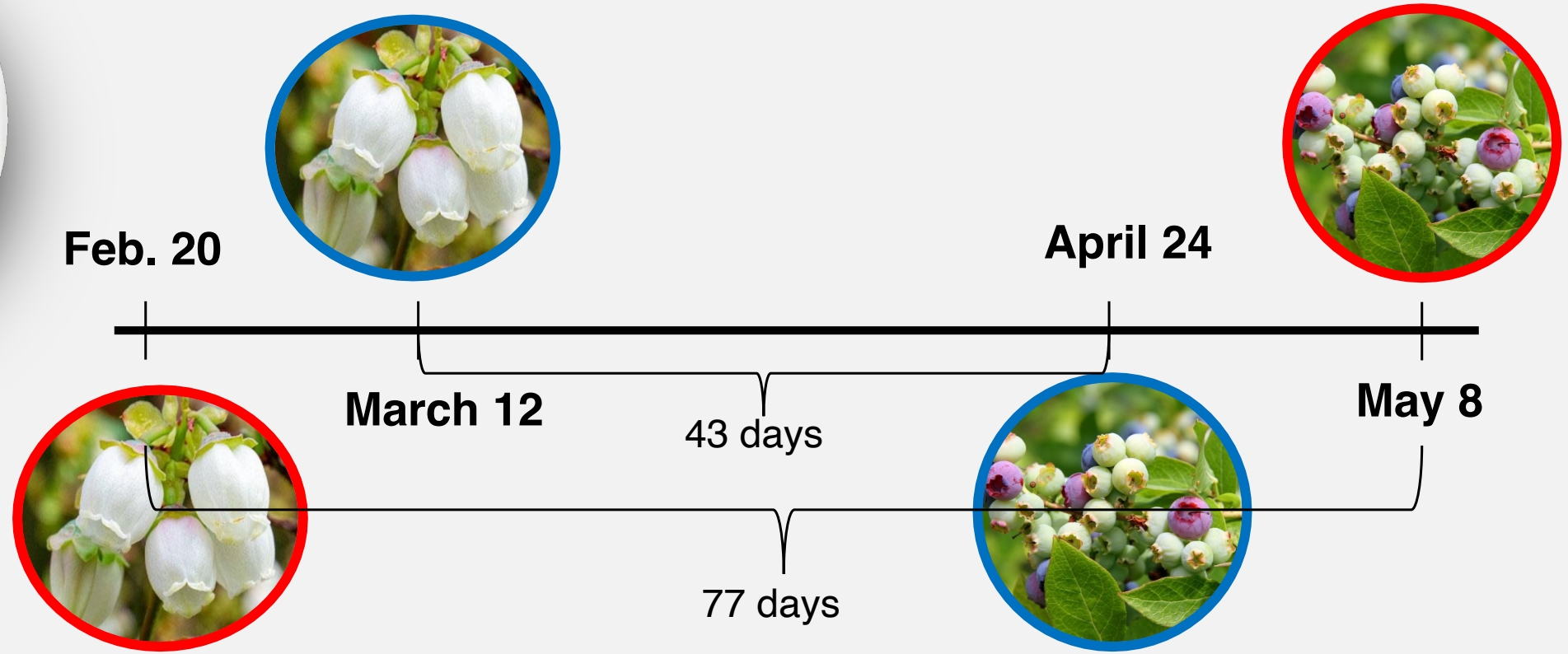
Resistant peanuts have been developed and released in North and South America **in just 3 years**

# Scaled sequencing helps protect blueberry production

 = favorable allele combo  
 = unfavorable allele combo



**Kendall Lee**  
Transforming  
blueberry breeding  
with scaled  
sequencing



# Scaled sequencing helps protect the future of sorghum germplasm and improvement



**Kelly Goode**

Executing sequencing of hundreds of thousands of samples



We have teamed with Doreen Ware, PhD to create a digital backup of the entire 45,000 sorghum collection

# Scaled genomics trains the next generation of scientists and impact makers



**Yanbing wang**  
Improving peanuts in  
collaboration with  
high schools

**WIREGRASS PEANUT PROJECT**

WIREGRASS  
**Peanut Project**

Centrifuge to  
cell debris  
dissolved  
comp

Visitor

Parker

**HUDSONALPHA**  
INSTITUTE FOR BIOTECHNOLOGY  
WIREGRASS

The banner features three photographs: a woman in a blue shirt and safety glasses working with a student in a lab coat; a man in a dark blue polo shirt with a 'Visitor' name tag talking to a student in a lab coat; and a student in a white lab coat with a 'Parker' name tag using a pipette. The background is black with a blue hexagonal pattern at the bottom left.



# Thank you

OncoDNA

# Koenraad Eycken

CPO - Sales & Business Development



# Christophe Van Huffel

Co-Founder & CSO - OncoRNA



# The challenge is real



“As oncologists, our mission is to deliver the right treatment to the right patient at the right time”

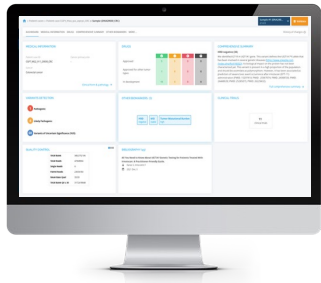
**Dr. Cheng Boon,**  
UK registered oncologist, private and NHS

# OncoDNA – Making tumor profiles actionable



Improve all patients' health through precision care.

# OncoDNA – Making tumor profiles actionable



CANCER TYPE: Thyroid cancer | PATIENT ID: OncoDEEP Kit Demo 4 | VALIDATED ON: Nov, 25 2024 | Page 1 / 17

**OncoDNA**  
THE CANCER THERAPEUTIC COMPASS

### Analysis Report

**Patient**  
Cancer Type: Thyroid cancer

**KEY GENOMIC ALTERATIONS\***  
None

**GENOMIC SIGNATURES**  
 TMB: Low (1.67 Mut/Mb) | MSI: Stable (8.81%) | HRD: Negative (29.0)

**ADDITIONAL BIOMARKERS**  
 CCDC6:RET Fusion: YES

**RELEVANT GENES WITH NO ACTIONABLE ALTERATIONS\*\***  
 BRAF

\* Only variants classified as pathogenic and likely pathogenic are reported here. The full list of identified variants is available in the report.  
 \*\* Cancer type specific

**THERAPIES ASSOCIATED WITH CLINICAL BENEFIT**

| Drug Name                                   | Class                               | Status                           | Indicated for        |
|---|-------------------------------------|----------------------------------|----------------------|
| Associated Biomarker: CCDC6:RET Fusion: YES |                                     |                                  |                      |
| Pralsetinib                                 | RET inhibitors                      | FDA / NCCN / ESMO / EMA approved | patient's tumor type |
| Selpercatinib                               | RET inhibitors                      | FDA / NCCN / ESMO / EMA approved | patient's tumor type |
| alectinib                                   | Receptor tyrosine kinase inhibitors | Approved for other               | other tumor types    |

**CLINICAL TRIALS**

| Name  | Phase   | Countries   | NCT ID      |
|---|---------|---|-------------|
| A Study of Selpercatinib (LOXO-292) in Participants With Advanced Solid Tumors, RET Fusion-Positive Solid Tumors, and Medullary Thyroid Cancer (LIBRETTO-001) | Phase 2 | FR GB HK IL SG AU CA CH DE DK ES US IT JP KR TW                               | NCT03157128 |
| CRAFT: The NCT-PMO-1602 Phase II Trial  | Phase 2 | DE  | NCT04551521 |
| Tumor Agnostic Precision Immuno-Oncology and Somatic Targeting Rational for You (TAPISTRY) Platform Study   | Phase 2 | FR GB HK IL NL SG AU BE BR CA CH CN DE DK ES US IT JP KR NZ PL PR PT RU TW ZA | NCT04589845 |

**CLINICAL FORM**

|                        |   |
|------------------------|---|
| Metastasis             | - |
| Previous medication    | - |
| Comorbidities          | - |
| Concomitant medication | - |
| Macro-dissection ?     | - |

(Continues on next page)

**OncoKDM™** | ONCOKDM VERSION: 24.0.22

CANCER TYPE: Thyroid cancer | PATIENT ID: OncoDEEP Kit Demo 4 | VALIDATED ON: Nov, 25 2024 | Page 3 / 17

| Gene   | Cat. | Exon | Var. Freq. / Copy Nb | cDNA | AA | Drugs related to gene | Drugs related to patient |
|--------|------|------|----------------------|------|----|-----------------------|--------------------------|
| CDKN2A | LOH  | -    | 1.00                 | -    | -  |                       |                          |

**BIOLOGICAL IMPACT: LIKELY PATHOGENIC**  
 This variant is associated with the loss of one copy of CDKN2A, while the remaining copy could be non-functional. The CDKN2A gene encodes the tumor suppressors p16INK4 and p14ARF (PMID:24449825). Therefore, this variant produces truncated proteins leading to a loss of function of the proteins.

**THERAPEUTICAL IMPACT: TIER III**  
 There are currently no drugs that directly target loss of CDKN2A. Because p16INK4a is known to inhibit Cdk4, tumors with CDKN2A alterations may be sensitive to Cdk4/6 inhibitors (PMID:7606716; PMID:9529249). Clinical trials of Cdk4/6 inhibitors, including PD-0332991, BAY1000394, and LEE011 are currently underway in multiple tumor types (PMID:21610706). p14ARF has been reported to function as a tumor suppressor through stabilization and activation of p53 through Mdm2 inhibition (PMID:16869746; PMID:20549699). However, the relevance of those drugs is unknown because the impact of this CDKN2A alteration on p14ARF function has not been characterized. Moreover the loss of function of the other copy for the gene should be confirmed by NGS result.

**INCIDENTAL FINDING**  
 This variant has not been associated with any inherited disease.

| Gene  | Cat. | Exon | Var. Freq. / Copy Nb | cDNA | AA | Drugs related to gene | Drugs related to patient |
|-------|------|------|----------------------|------|----|-----------------------|--------------------------|
| FANCG | LOH  | -    | 1.00                 | -    | -  |                       |                          |

**BIOLOGICAL IMPACT: LIKELY PATHOGENIC**  
 This variant is associated with the loss of one copy of FANCG, while the remaining copy could be non-functional. Hence, it could lead to a probable loss of function of the protein.

**THERAPEUTICAL IMPACT: TIER III**  
 No therapeutic impact has been associated with this variant. However, the loss of function of the other allele should be confirmed by the NGS results.

**INCIDENTAL FINDING**  
 This variant is associated with Fanconi anemia (http://www.uniprot.org/uniprot/O15287).

| Gene  | Cat. | Exon | Var. Freq. / Copy Nb | cDNA | AA | Drugs related to gene | Drugs related to patient |
|-------|------|------|----------------------|------|----|-----------------------|--------------------------|
| KEAP1 | LOH  | -    | 1.00                 | -    | -  |                       |                          |

**BIOLOGICAL IMPACT: LIKELY PATHOGENIC**  
 This variant is associated with the loss of one copy of KEAP1, while the remaining copy could be non-functional. An abnormality in the Nrf2-Keap1 system may facilitate the growth of cancer cells because oxidative and electrophilic stresses cause many diseases, including cancer. The activation of Nrf2 through reduced Keap1 activity, either through a nonsense variant leading to a loss-of-function, provides growth advantages to lung cancer cells under homeostatic conditions. Indeed, there is a high incidence/frequent occurrence of loss of Keap1 function in patient with lung cancer and this loss of function enhanced the nuclear accumulation of Nrf2 and elevated the expression of antioxidant and antioxidant stress enzymes and drug efflux pumps, suggesting cancer cells with weakened. Keap1 acquire multiple advantages for proliferation (PMID:18316592).

**THERAPEUTICAL IMPACT: TIER III**  
 The loss of function of the other allele should be confirmed by the NGS results.

Activation of the Nrf2 pathway is critical for resistance to chemotherapeutic agents (PMID:25014534; PMID:25337579). At this moment there is no Nrf2 inhibitors FDA approved or available through clinical trials. By screening natural products, data identified an antineoplastic compound brusatol as an Nrf2 inhibitor that enhances the chemotherapeutic efficacy of cisplatin (PMID:21205897). No therapeutic impact has been associated with this variant.

**OncoKDM™** | ONCOKDM VERSION: 24.0.22

CANCER TYPE: Thyroid cancer | PATIENT ID: OncoDEEP Kit Demo 4 | VALIDATED ON: Nov, 25 2024 | Page 6 / 17

### DETECTED VARIANTS LIST

| Gene   | Cat.     | Var. Freq. / Copy Nb | cDNA                      | AA              | Biological Impact | Therapeutical Impact | Incidental Findings | Depth |
|--------|----------|----------------------|---------------------------|-----------------|-------------------|----------------------|---------------------|-------|
| CDKN2B | CNV LOSS | 0.00                 | -                         | -               | Pathogenic        | Tier III             | NO                  | -     |
| CDKN2A | LOH      | 1.00                 | -                         | -               | Likely Pathogenic | Tier III             | NO                  | -     |
| FANCG  | LOH      | 1.00                 | -                         | -               | Likely Pathogenic | Tier III             | YES                 | -     |
| KEAP1  | LOH      | 1.00                 | -                         | -               | Likely Pathogenic | Tier III             | NO                  | -     |
| P TEN  | LOH      | 1.00                 | -                         | -               | Likely Pathogenic | Tier III             | NO                  | -     |
| RAD54L | LOH      | 1.00                 | -                         | -               | Likely Pathogenic | Tier III             | NO                  | -     |
| RET    | SNV      | 32.63%               | NM_020975.6:c.2428G>A     | p.(G810S)       | Likely Pathogenic | Tier III             | NO                  | 377   |
| STK11  | LOH      | 1.00                 | -                         | -               | Likely Pathogenic | Tier III             | YES                 | -     |
| ZFXH3  | INS      | 19.19%               | NM_006885.4:c.3255_325dup | p.(C1086Sfs*26) | Likely Pathogenic | Tier III             | NO                  | 615   |
| ZRSR2  | DEL      | 24.44%               | NM_005089.4:c.50del       | p.(K175fs*6)    | Likely Pathogenic | Tier III             | NO                  | 487   |
| BRAF   | WT       | 0.00                 | -                         | -               | Wild type         | Tier IA              | NO                  | -     |
| AURKA  | SNV      | 99.68%               | NM_198437.3:c.169A>G      | p.(I57V)        | VUS               | Tier III             | NO                  | 940   |
| CASP8  | SNV      | 59.10%               | NM_001080125:c.1069A>G    | p.(I357V)       | VUS               | Tier III             | NO                  | 802   |
| CYP2D6 | SNV      | 20.26%               | NM_000106.6:c.1457G>C     | p.(S486T)       | VUS               | Tier III             | NO                  | 311   |
| CYP2D6 | SNV      | 79.86%               | NM_000106.6:c.1453G>C     | p.(V485L)       | VUS               | Tier III             | NO                  | 293   |
| IDH2   | SNV      | 20.62%               | NM_002168.4:c.47G>A       | p.(G16D)        | VUS               | Tier III             | NO                  | 97    |
| MET    | DEL      | 9.58%                | NM_000245.4:c.3029-721del | -               | VUS               | Tier III             | NO                  | 689   |
| MET    | SNV      | 36.11%               | NM_000245.4:c.3259+845G>T | -               | VUS               | Tier III             | NO                  | 767   |
| MET    | INS      | 6.38%                | NM_000245.4:c.3259+969dup | -               | VUS               | Tier III             | NO                  | 564   |
| MET    | SNV      | 35.27%               | NM_000245.4:c.3260-111G<T | -               | VUS               | Tier III             | NO                  | 1049  |

(Continues on next page)

**OncoKDM™** | ONCOKDM VERSION: 24.0.22

# OncoDNA at a glance



**100**

collaborators  
in **6** countries

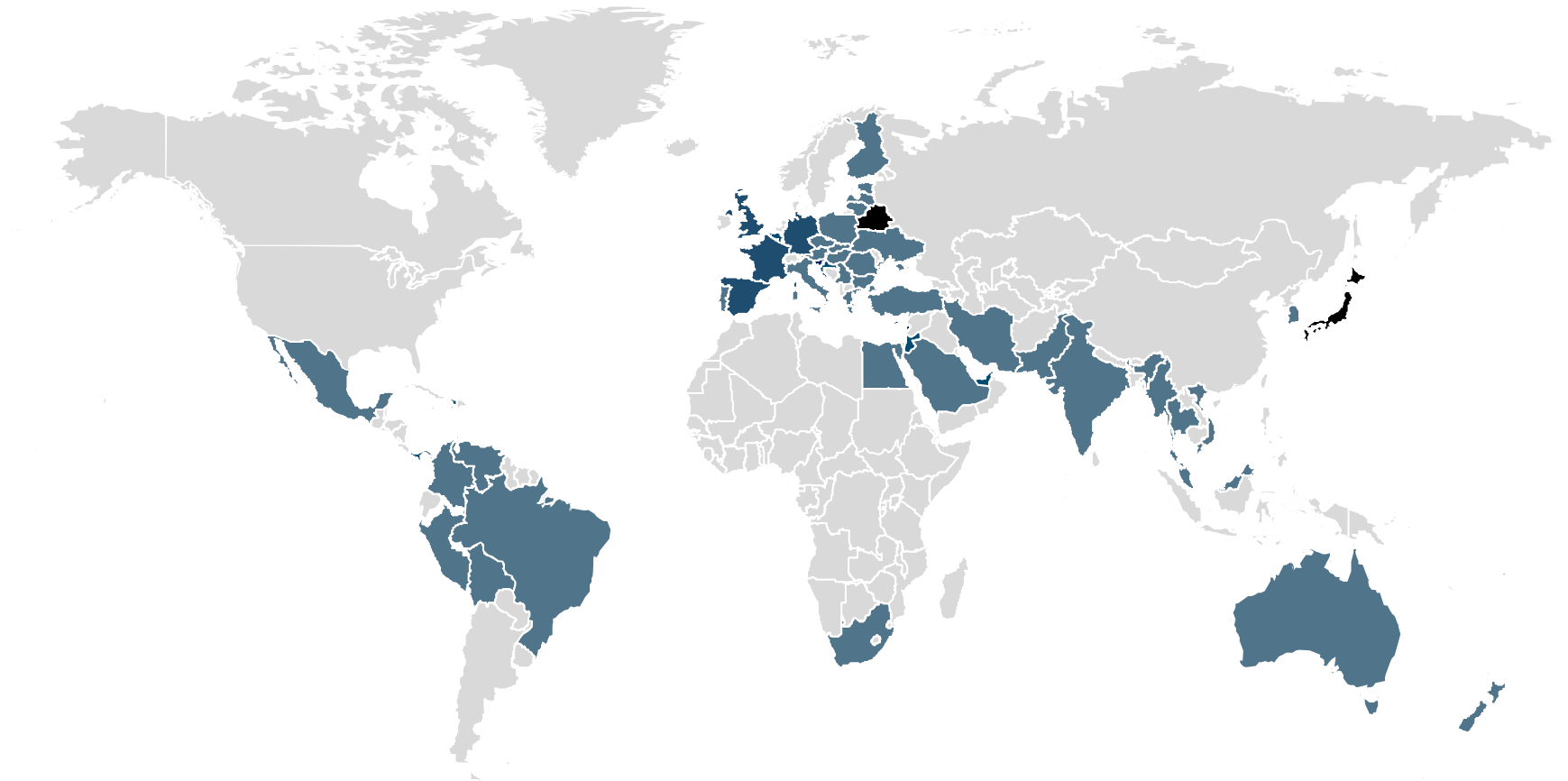
**45**

distributors  
active on all continents

## Global presence

-  Local presence
-  Distribution Network

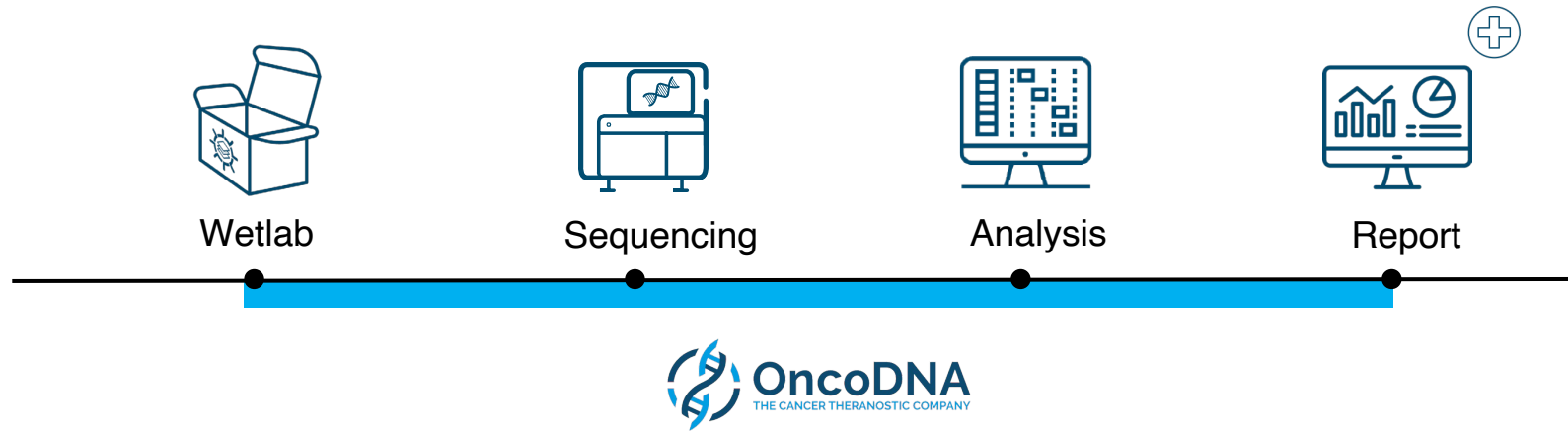
Founded in **2012**, over **100,000 tests** performed



# Twist as a catalyst for growth

**Before  
Twist**

## Centralized workflow



# Twist makes the difference

## Quality & reliability

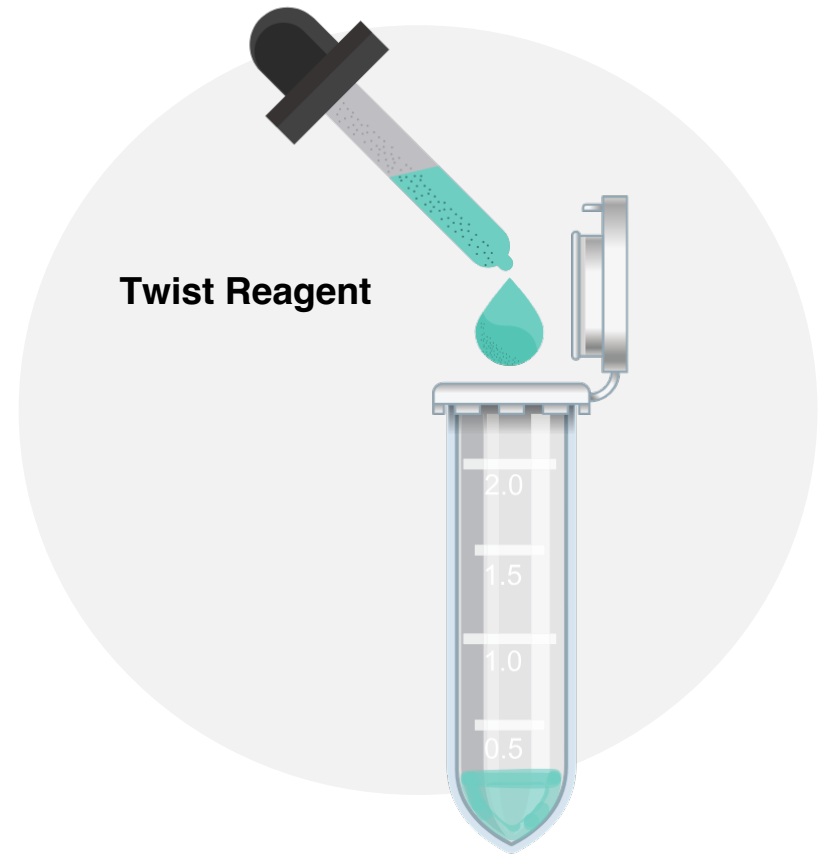
- ✓ High-quality sequencing data
- ✓ Reliable and interpretable results

= **Report with recommendations based on reliable data**

## Throughput & cost efficiency

- ✓ More samples per run
- ✓ Lower cost per sample

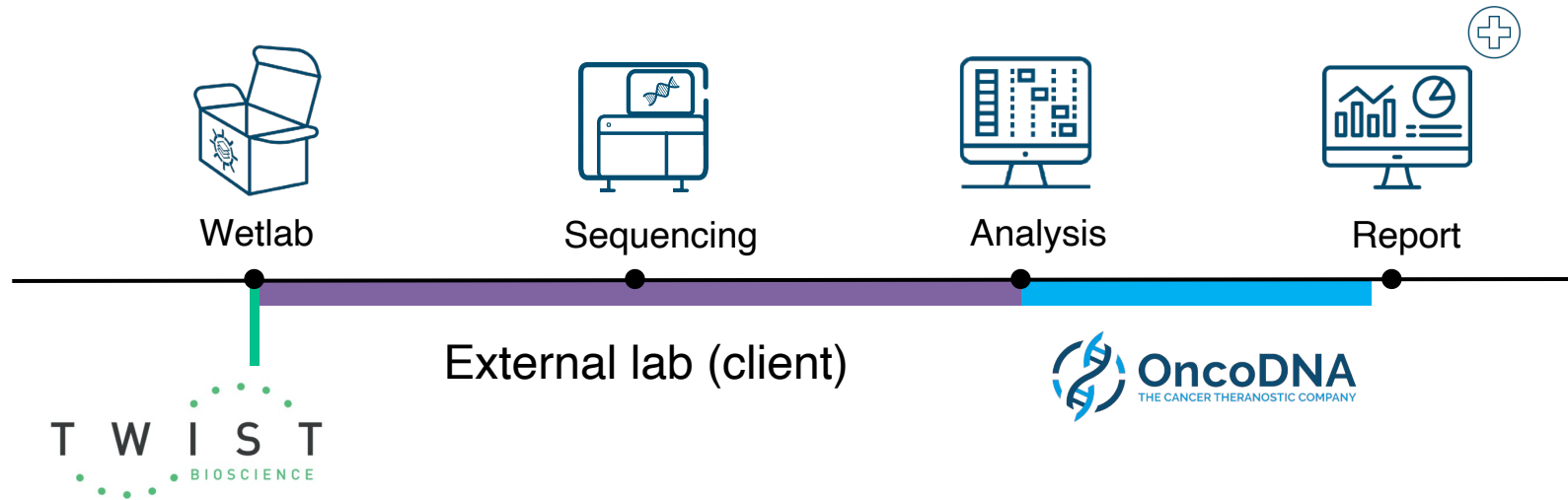
= **More patients analyzed**



Move to Twist capture based technology allows us to do better DNA fingerprinting and better characterization of patient DNA

# Twist as a catalyst for growth

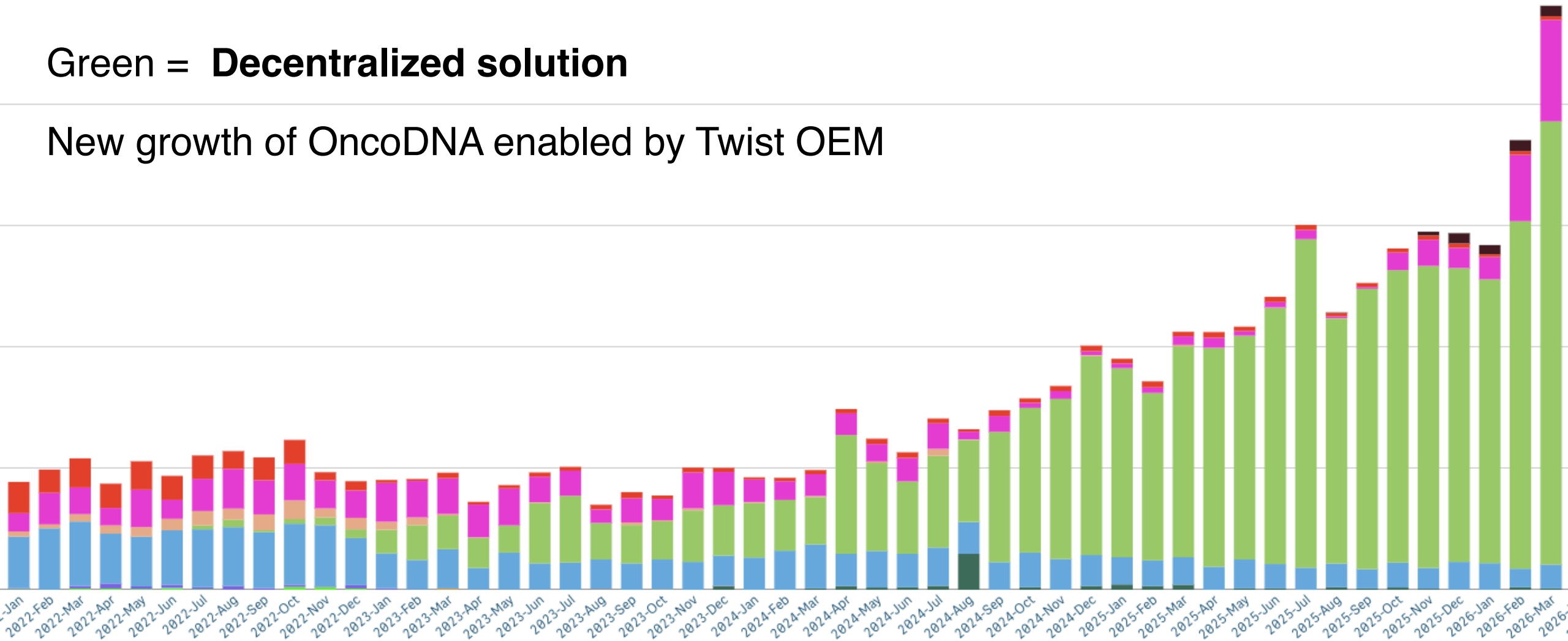
## Decentralized workflow



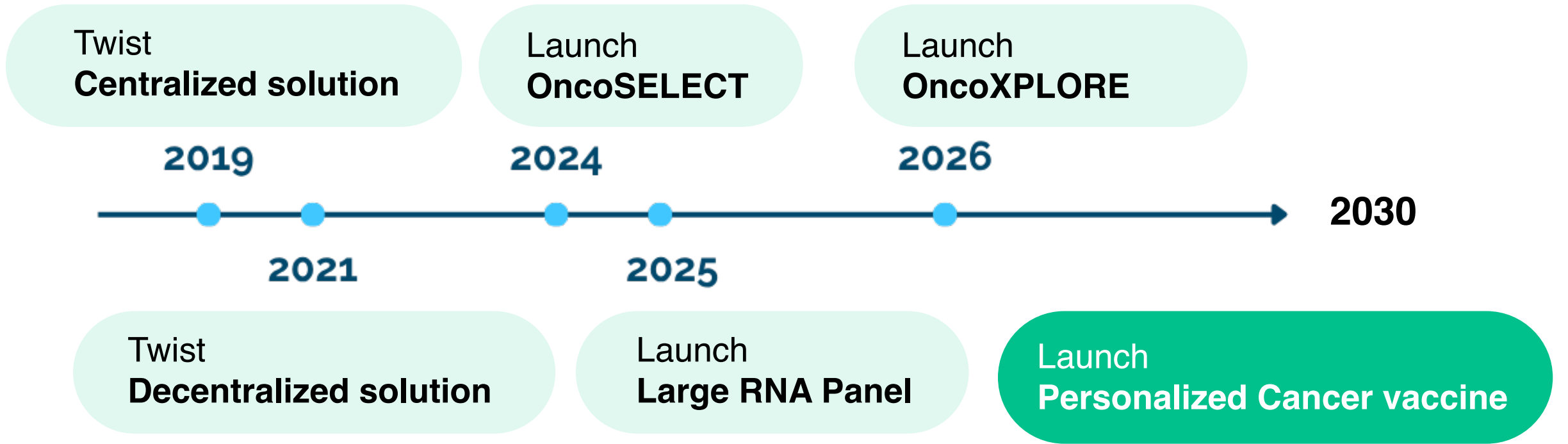
# Switch in business: Decentralized model

Green = **Decentralized solution**

New growth of OncoDNA enabled by Twist OEM



# Successful collaboration with Twist



# OncoSELECT<sup>®</sup> Gene Panel

OncoSELECT is suited for solid cancer patients' testing, and covers many alterations associated with targeted/ hormonal therapies

**Total : 74 Genes:** SNVs / Indels / CNVs/ TERT promotor / Intron aberrations (*translocations, unusual splicing*) / HRR

Optimised process to achieve **greater sensitivity and specificity**

**LOD: 0.25 % AF**

SNV sensitivity: 99 %

INDEL sensitivity: 95.6 %

SNV and INDEL specificity: > 99.9 %

## Whole CDSs

|        |        |        |
|--------|--------|--------|
| ARID1A | CHEK2  | NBN    |
| ATM    | FANCA  | NF1    |
| ATR    | FANCL  | PALB2  |
| BARD1  | FGFR1  | PTEN   |
| BRCA1  | FGFR2  | RAD51C |
| BRCA2  | FGFR3  | RAD51D |
| BRIP1  | H3C2   | RAD54L |
| CDK12  | KEAP1  | STK11  |
| CDKN2A | MLH1   |        |
| CHEK1  | MRE11A |        |

## Hotspots

|        |        |              |
|--------|--------|--------------|
| AKT1   | GNAQ   | NTRK1        |
| ALK    | GNAS   | NTRK2        |
| AR     | H3F3A  | NTRK3        |
| ARAF   | H3F3B  | PDGFRA       |
| BRAF   | HRAS   | PIK3CA       |
| CTNNB1 | IDH1   | POLE         |
| DICER1 | IDH2   | RAD51B       |
| EGFR   | KIT    | RET          |
| ERBB2  | KRAS   | ROS1         |
| ERBB4  | MAP2K1 | TERT (pTERT) |
| ESR1   | MET    | TP53         |
| FOXL2  | MYOD1  |              |
| GNA11  | NRAS   |              |

## Fusions

|       |       |         |
|-------|-------|---------|
| ALK   | FGFR2 | NTRK2   |
| BRAF  | FGFR3 | NTRK3*  |
| CD74  | KIF5B | RET     |
| EGFR  | KIT   | ROS1    |
| EML4  | MET   | SDC4    |
| ETV6  | NPM1  | SLC34A2 |
| EZR   | NRG1  |         |
| FGFR1 | NTRK1 |         |

## Unusual splicing genes

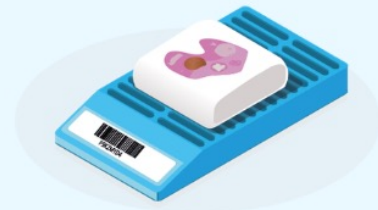
**BRCA1**  
**BRCA2**  
**MET**

\*NTRK3 fusion is detected via its common rearrangement partner ETV6

# OncoFOLLOW workflow



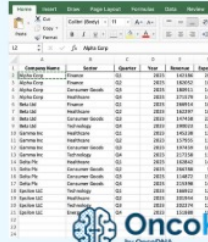
## 1 Solid biopsy & variant selection



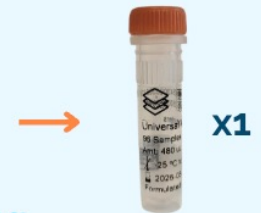
 **OncoDEEP**<sup>®</sup>  
by OncoDNA

 **OncoDEEP WES**<sup>®</sup>  
by OncoDNA

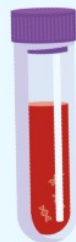
## 2 Custom reagent design based on variant selection



| Chromosome | Gene  | Variant   | Assays          |
|------------|-------|-----------|-----------------|
| 1          | BRCA1 | 184743748 | BRCA1_184743748 |
| 1          | BRCA1 | 184743749 | BRCA1_184743749 |
| 1          | BRCA1 | 184743750 | BRCA1_184743750 |
| 1          | BRCA1 | 184743751 | BRCA1_184743751 |
| 1          | BRCA1 | 184743752 | BRCA1_184743752 |
| 1          | BRCA1 | 184743753 | BRCA1_184743753 |
| 1          | BRCA1 | 184743754 | BRCA1_184743754 |
| 1          | BRCA1 | 184743755 | BRCA1_184743755 |
| 1          | BRCA1 | 184743756 | BRCA1_184743756 |
| 1          | BRCA1 | 184743757 | BRCA1_184743757 |
| 1          | BRCA1 | 184743758 | BRCA1_184743758 |
| 1          | BRCA1 | 184743759 | BRCA1_184743759 |
| 1          | BRCA1 | 184743760 | BRCA1_184743760 |
| 1          | BRCA1 | 184743761 | BRCA1_184743761 |
| 1          | BRCA1 | 184743762 | BRCA1_184743762 |
| 1          | BRCA1 | 184743763 | BRCA1_184743763 |
| 1          | BRCA1 | 184743764 | BRCA1_184743764 |
| 1          | BRCA1 | 184743765 | BRCA1_184743765 |
| 1          | BRCA1 | 184743766 | BRCA1_184743766 |
| 1          | BRCA1 | 184743767 | BRCA1_184743767 |
| 1          | BRCA1 | 184743768 | BRCA1_184743768 |
| 1          | BRCA1 | 184743769 | BRCA1_184743769 |
| 1          | BRCA1 | 184743770 | BRCA1_184743770 |
| 1          | BRCA1 | 184743771 | BRCA1_184743771 |
| 1          | BRCA1 | 184743772 | BRCA1_184743772 |
| 1          | BRCA1 | 184743773 | BRCA1_184743773 |
| 1          | BRCA1 | 184743774 | BRCA1_184743774 |
| 1          | BRCA1 | 184743775 | BRCA1_184743775 |
| 1          | BRCA1 | 184743776 | BRCA1_184743776 |
| 1          | BRCA1 | 184743777 | BRCA1_184743777 |
| 1          | BRCA1 | 184743778 | BRCA1_184743778 |
| 1          | BRCA1 | 184743779 | BRCA1_184743779 |
| 1          | BRCA1 | 184743780 | BRCA1_184743780 |
| 1          | BRCA1 | 184743781 | BRCA1_184743781 |
| 1          | BRCA1 | 184743782 | BRCA1_184743782 |
| 1          | BRCA1 | 184743783 | BRCA1_184743783 |
| 1          | BRCA1 | 184743784 | BRCA1_184743784 |
| 1          | BRCA1 | 184743785 | BRCA1_184743785 |
| 1          | BRCA1 | 184743786 | BRCA1_184743786 |
| 1          | BRCA1 | 184743787 | BRCA1_184743787 |
| 1          | BRCA1 | 184743788 | BRCA1_184743788 |
| 1          | BRCA1 | 184743789 | BRCA1_184743789 |
| 1          | BRCA1 | 184743790 | BRCA1_184743790 |
| 1          | BRCA1 | 184743791 | BRCA1_184743791 |
| 1          | BRCA1 | 184743792 | BRCA1_184743792 |
| 1          | BRCA1 | 184743793 | BRCA1_184743793 |
| 1          | BRCA1 | 184743794 | BRCA1_184743794 |
| 1          | BRCA1 | 184743795 | BRCA1_184743795 |
| 1          | BRCA1 | 184743796 | BRCA1_184743796 |
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| 1          | BRCA1 | 184743799 | BRCA1_184743799 |
| 1          | BRCA1 | 184743800 | BRCA1_184743800 |



## 3 Liquid biopsy & patient variant monitoring



X12

 **OncoFOLLOW**<sup>™</sup>  
by OncoDNA **KIT**

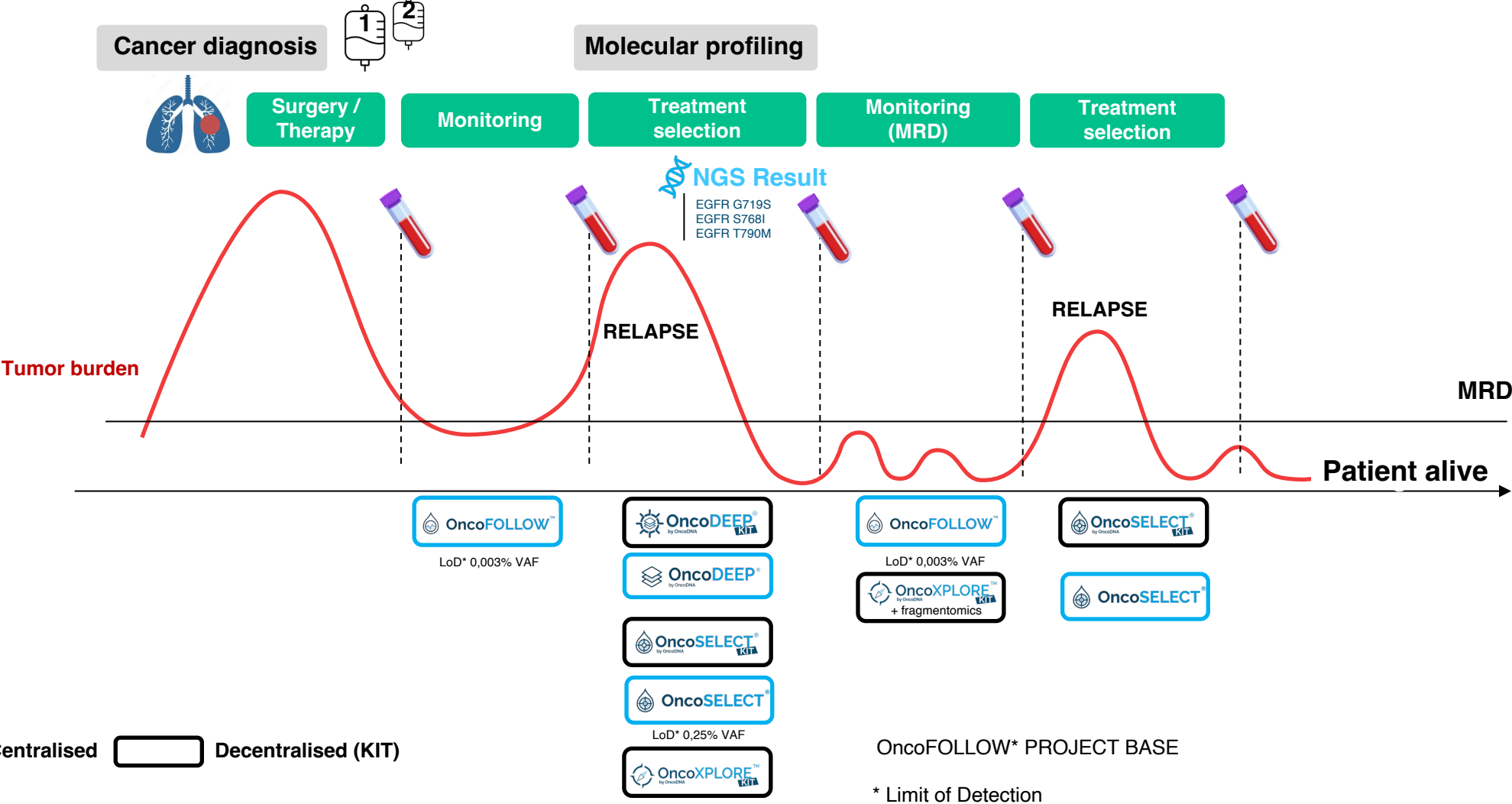


## 4 Results interpretation



 **OncoKDM**<sup>®</sup>  
by OncoDNA

# Solutions that empower oncologist to select the right treatment at the right time regardless to the lab expertise – based on Twist technology



# OncoRNA – A solution for patients for whom there is no treatment available

## A personalized anticancer vaccine in 3 weeks



**OncoRNA**  
PERSONALIZED CANCER VACCINE

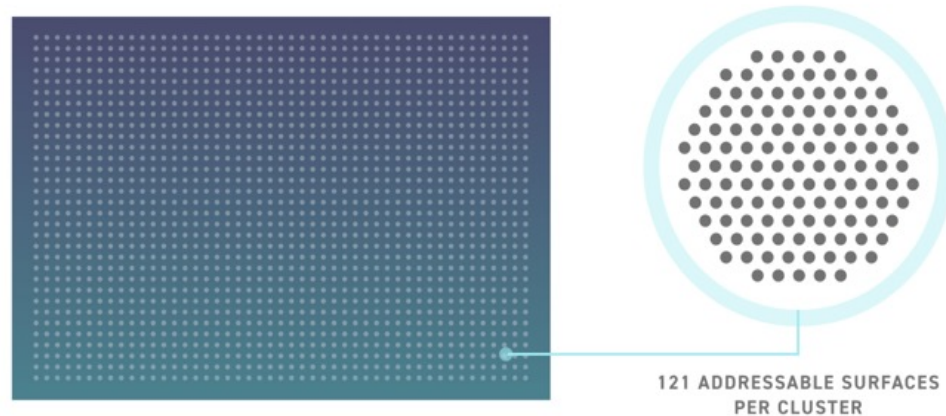
In collaboration with:



**Siyuan Chen**  
Chief Technology Officer at  
Twist Bioscience

# Twist: the only technology that unlocks this

Long-oligo pool synthesis — unavailable anywhere else



Twist Bioscience chip — 121 individually addressable synthesis clusters per pool

**Each cluster synthesizes a unique oligo sequence up to 300 nt. No competitor matches this.**

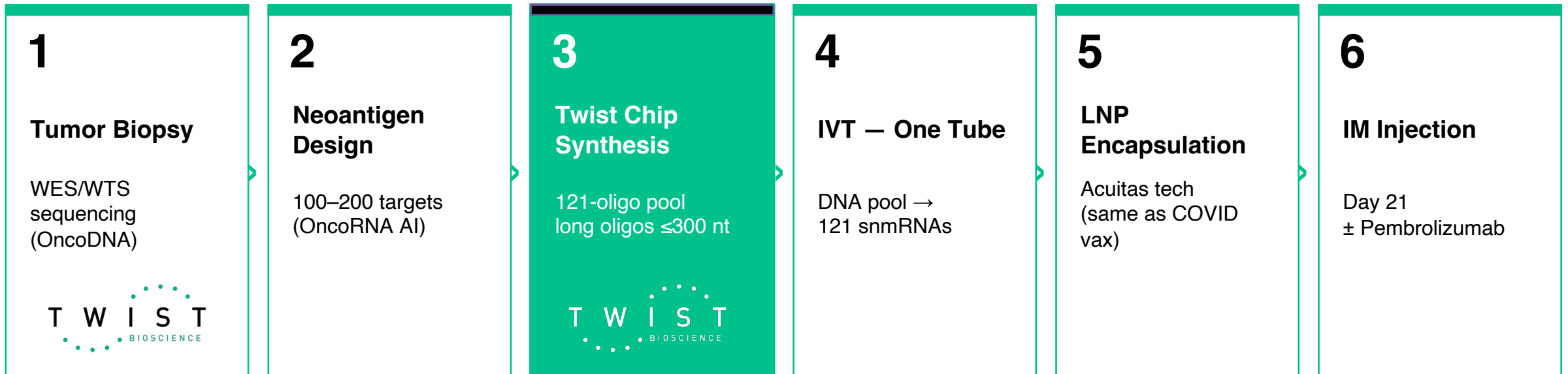
- |           |  |
|-----------|--|
| <b>01</b> | <b>Long oligos — up to 300 nt</b><br>Standard providers cap at 120 nt, requiring 6+ oligos per 500 bp with multiple error-prone assembly events. TWIST encodes a full neoantigen in just TWO long oligos — one clean assembly. Cleaner. Faster. Cheaper.               |
| <b>02</b> | <b>121-pool format = personalized vaccine</b><br>High tumor mutation burden (TMB) yields 100–400 actionable neoantigens. TWIST's 121-cluster chip maps perfectly to this clinical need: one synthesis run = one patient's complete personalized mRNA vaccine template. |
| <b>03</b> | <b>No practical limit on pool diversity</b><br>The scale of TWIST chip synthesis means virtually unlimited unique sequences per pool. Competitors using standard oligo synthesis cannot replicate this format at any price point.                                      |

**Twist is not just a supplier. Twist is the reason this technology exists.**

OncoRNA was specifically designed around the Twist chip format — 121 oligos, long sequences, pool synthesis at therapeutic grade.

# OncoRNA: what Twist chip technology makes possible

The 6-step pipeline — Step 3 is the Twist advantage



Step 3 is the key — without Twist long-oligo pool synthesis, steps 4–6 cannot exist at this scale or cost.

# The strategic partnership at the heart of the next cancer vaccine breakthrough

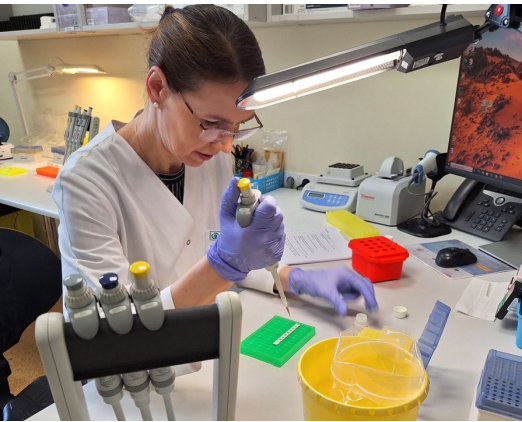


## Proof that Twist chip synthesis enables what nothing else can.

- ✓ **>100 neoantigens**  
vs. 20–30 for all plasmid-based competitors
- ✓ **3-week TAT**  
vs. 3+ months — the only clinically viable timeline
- ✓ **90% CD8+ response**  
pre-clinical proof with TWIST-synthesized pool
- ✓ **€31M EU grant**  
non-dilutive · scientific & commercial validation

## The DNA synthesis infrastructure behind the next generation of personalized medicine

**NASDAQ: TWST**  
Market cap ~\$3 Billion



# Thank you for being part of the mission





# Thank you

# Agenda

- Welcome
  - Tour
  - DSPS Strategy Session
  - Fireside Chat with Dr. Frances Arnold
  - Customer Presentations
- 

## Lunch

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- NGS Strategy Session
- Customer Presentations
- Enzymes at Twist
- **Financial Overview**
- Culture
- Q&A

# Adam Laponis

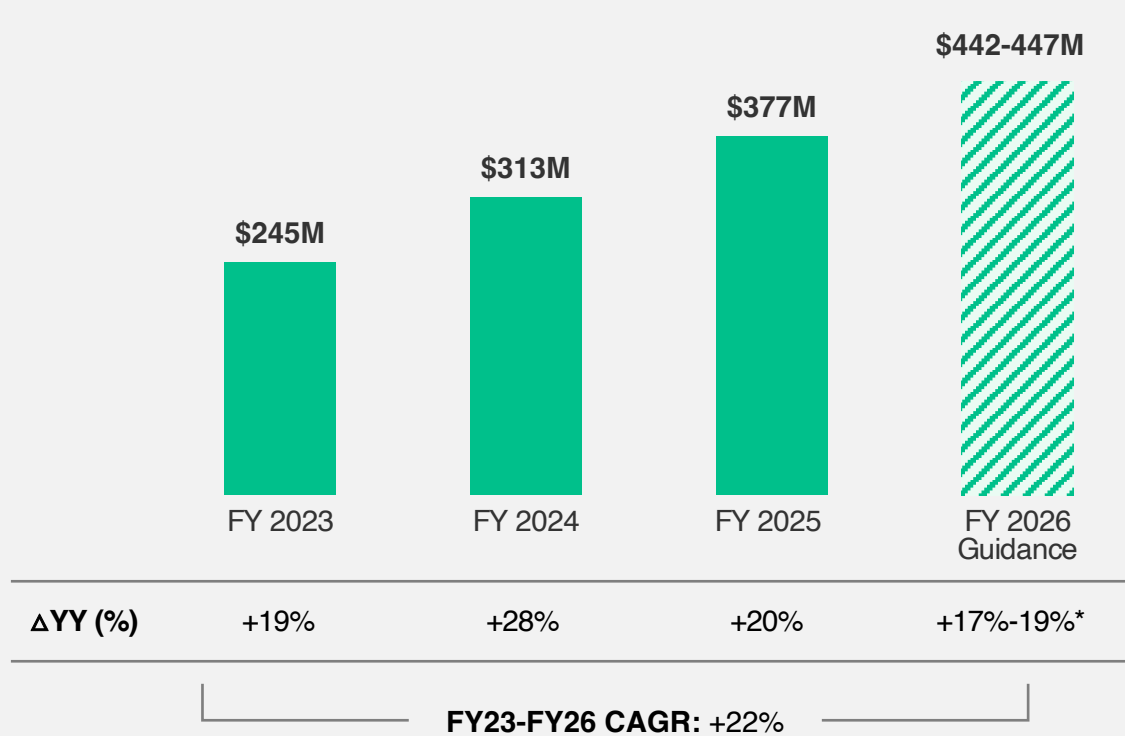
Chief Financial Officer

*Financial and Operational Overview*

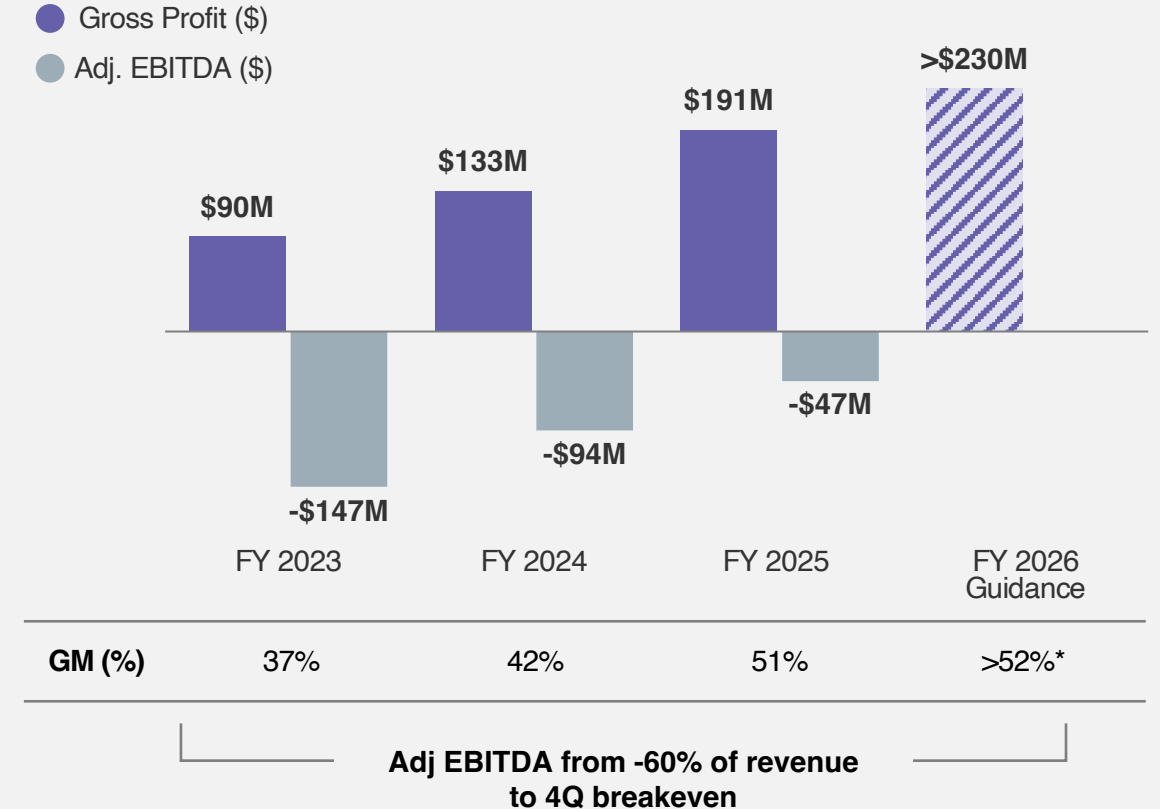


# Twist FY23 through Today: 'Platform Build-Out'

## Revenue



## Gross margin & adjusted EBITDA\*\*



**FY23-FY26 Twist Revenue CAGR of +22% vs. global peers broadly ~flat**

\* As of financial guidance provided on May 4, 2026.

\*\*See page 233 or Adjusted EBITDA Reconciliation.

# FY27 to FY31: Profitable Growth Inflection Point

Strong growth trajectory  
to more than double  
revenue from  
**organic growth**

**Adjusted EBITDA breakeven**  
Q4 FY26 and beyond

**Self-funded, targeted**  
**re-investment** to power NPI machine

Line of sight to **long term GM%** above **60%**  
as business grows and matures

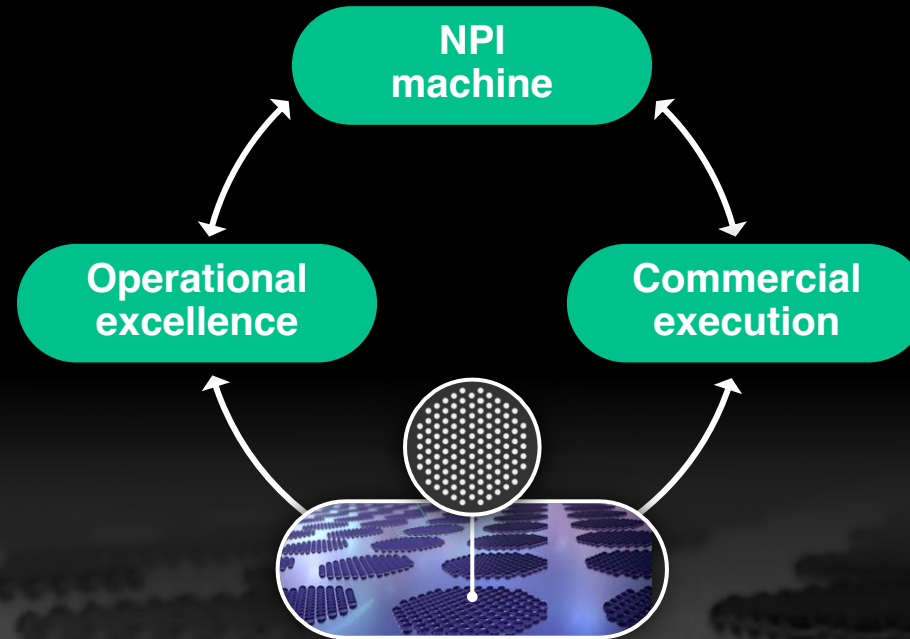
Significant operating leverage and clear  
path to **>\$1B per year of revenue capacity**  
with sustaining levels of CapEx investment

## DSPS drivers

- Continuing broader workflow integration, enabled by **expanding product menu, customization and scale**
- **Increasing custom technical/complex capabilities** and services (e.g., AI-enabled discovery, siRNA, bispecifics, mRNA, GMP for nucleic acid therapeutics, special apps)
- Leveraging **automation** to enable rapid scale of new products alongside emerging market demand (e.g., antibody characterization lab)
- Design-Build-Test-Learn **flywheel** enables customers of all sizes while expanding Twist's wallet share over time

# Multi-Year Growth Outlook and SAM Expansion

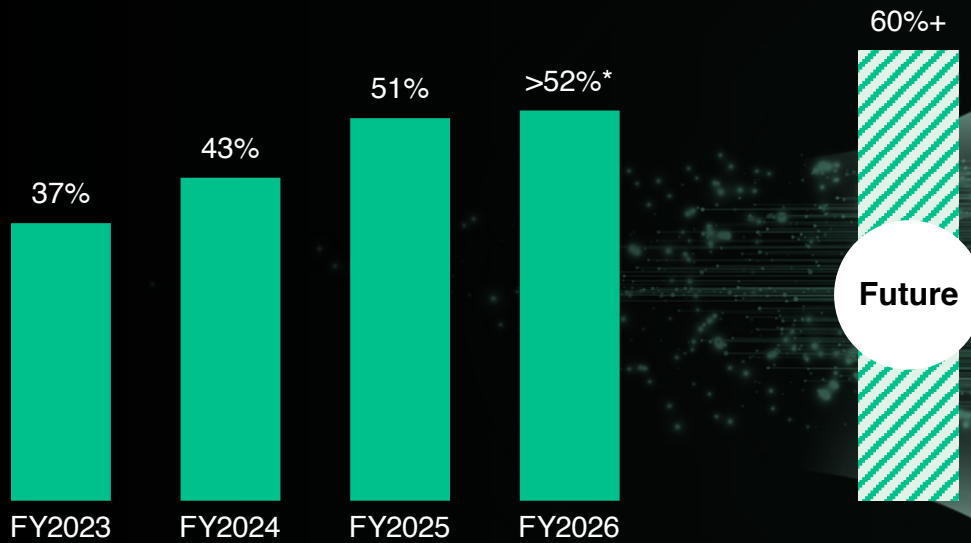
We continue loading **more on the same chip**



## NGS application drivers

- Key supplier for large and growing markets such as liquid biopsy for oncology Dx and rare disease drives **robust validation pipeline**
- Early innings of commercial Dx contributions, with **sticky, recurring revenue streams**
- MRD applications scaling to material revenue; **uniquely positioned esp. for tumor-informed MRD**
- Broad sequencing cost reductions **unlocking new markets, geographies, applications** – positioned to benefit from NGS market expansion

# Revenue Growth, Automation and Continuous Process Improvements Enable GM expansion



From FY23 to H1 FY26  
Gross Margin Expanded  
**+15% percentage points**

Path to long  
term GM  
above **60%**

Relatively **flat fixed costs** (people + D&A + facility) while revenue grew **+22% CAGR** last 3 years

Since FY23 revenue grew **8x** faster than manufacturing headcount, driven by automation

Process re-engineering (e.g. writer cycle time) & automation (e.g. 2x capacity in 20% of the space for Gene Lab 1) drive additional GM expansion

Target all products to have **+75%** incremental revenue drop to the GM line based on automation and continuous process improvements

\* As of financial guidance provided on May 4, 2026.

# Infrastructure to Support >\$1B of Annual Revenue Capacity by 2030

## Current footprint

### Wilsonville

### ~210,000 sq. feet total space

- Primary capacity for DNA synthesis and protein solutions
- 4 writers today
- Includes 65,000 additional sq. feet available

### SSF

### ~90,000 sq. feet total space

- Primary capacity for NGS applications
- 4 writers today
- 3<sup>rd</sup> floor expansion in process without incremental cost
- Option to expand to 4<sup>th</sup> floor

## Facility Runway

- Automation efforts to support NPI introductions and protein characterization business
- 8 writers today at ~50% capacity
- 4 writers on order now
- Current footprint supports up to 22 writers across both sites with ability to expand
- Roughly 3X today's writer capacity available within current facilities

# CapEx Discipline and Capital Allocation Strategy

## Self-funded organic investment

- Self-funded investment to power innovation, NPI machine, automation and commercial execution
- Collaborations with leading customers to establish key positions in emerging markets (e.g., AI Drug Discovery, MRD, AgBio)
- CapEx generally in line with depreciation to support \$1B of revenue capacity by 2030

## Opportunistic M&A

- Inorganic focus on 'bolt-on' technology **accretive** to our platform
- Committed to investment agreements that **support our long-term FCF trajectory and margin profile**

**Central Criteria:**  
Bring more volume onto our platform  
where we can continue to improve the unit economics

# Medium and Long-term Financial Summary

## Revenue growth

- FY27-31: More than double revenue from organic growth
- Driven by NPIs, market share expansion, category growth, customer expansion and commercial ramp
- Opportunity for upside from both organic and inorganic investment
- Expect long-term growth to be balanced across DSPS and NGS Applications

## Adj. EBITDA & FCF positivity

- On track for Adj. EBITDA breakeven in Q4 FY26
- Adjusted EBITDA positive in FY27 and beyond with significant operating leverage opportunities
- Confidence in path to FCF positive with capital on hand

## Gross margin trajectory

- Revenue growth and fixed cost leverage enable long term GM >60%
- Automation and continuous process improvements enable capacity expansion within existing facilities
- Continue to expect all products to have +75% incremental revenue drop to the GM line based on automation and continuous process improvements

## Capital allocation & CapEx

- Self-funded investment to power NPI machine, automation and commercial execution
- \$1B annual revenue capacity in existing locations with continued CapEx investment in line with depreciation
- Bolt-on M&A strategy in emerging areas can accelerate growth

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- 

## Lunch

---

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- Customer Presentations
- Financial Overview
- **Culture**
- Q&A

# Paula Green

SVP, HR and Facilities

*The Culture Advantage*





**We make synthetic  
DNA to improve health  
and sustainability**

## Mission

We work in service of customers who are changing the world for the better. In fields such as medicine, agriculture, and industrial chemicals by using our synthetic DNA tools, our customers are developing ways to better lives and improve the sustainability of the planet

# Our History: Writing DNA from Concept to Creation

*How it started*



*How it's going*



# Who We Are: Driven to Win



## **We operate like a sports team, not a family**

- Best player for each position
- Expect team play
- Competition is outside the company
- Employ commercial execution, with kindness
- Demand performance

# Who We Are: We Work by Our Four Guiding Principles

## Grit



### Passionate drive, fierce determination

- Always strive for excellence and persevere
- Adapt resiliently and learn from each attempt
- Drive strategic and sustainable outcomes
- Take ego-less ownership and focus on resolution

## Impact



### Bold ideas, daily incremental contributions

- Skillfully deliver on ambitious goals and stay humble
- Collaborate and share knowledge to create value
- Diligently improve quality, velocity and cost
- Voice your ideas, commit the time, find new ways

## Service



### Always ask, what can I do for you?

- Listen, hear and dialogue empathetically
- Relentlessly focus on internal and external customer needs
- Communicate to deliver outstanding service
- Build mutually beneficial, long-lasting relationships

## Trust



### Vigilant stewardship, transparent interactions

- Provide products designed and intended for public benefit
- Protect the well-being of people and our planet
- Demonstrate integrity and ethical behavior
- Interact in an accountable, respectful and transparent manner

**Who We Are:**

**Culture as a  
Competitive  
Advantage**

## **Culture Drives Outsized Success**

Experts across multiple disciplines:

- Relentless innovation
- Operational excellence paired with startup velocity
- Customer obsession and scientific partnership
- Precision, quality, reliability as expectation
- Automation and scalability mindset
- Boldness and willingness to disrupt legacy approaches
- Cross functional integration and adaptability
- Motivated to change the world and make money

## **One Twist Team**

# Who We Are: People Philosophy

**Goal:** Twist is the best place our employees have ever worked

## Our people are what make Twist great:

- People-first, servant leadership
- People-first compensation, benefits and policies
- Recruit and retain A players
- Everything is done the Twist way



How we compete

# Commercial execution

## *with Kindness*

We pursue every win with relentless intensity and total respect. Commercial execution is not about ego. It's about protecting our customers and creating lasting advantage.

### **Partner**

Listen to customer needs, bring those back to the organization.

### **Enable**

From deep science to implementation, go above and beyond to support customers.

### **One Twist team**

Win gracefully. Compete with conviction. Competition is on the outside.



How we operate

# Customer-Centricity

## Listen first

Understand workflows, pain points, and goals before proposing anything

## Serve proactively

Anticipate needs. Don't wait to be asked. Surprise and delight at every touchpoint



**THE  
CUSTOMER**

## Deliver reliably

Consistency, quality, and speed — every order, every time, at every scale

## Grow together

Our customers' breakthroughs are our purpose. We're invested in their long game

How we operate

# Enterprise Discipline

## Enterprise discipline

### Commitment culture

We say what we are going to do and we do what we say  
Accountability and alignment are at the heart of our operations

### Quality is non-negotiable

Every unit shipped reflects the Twist standard. No exceptions at any scale

### Automation and software to scale

New products reuse existing infrastructure. Automate the automation to improve efficiency

### As product scales, take costs out

OpEx reduction is a growth lever implemented once product begins commercial ramp

## Startup velocity

### Launch with alpha customers

Good and launched beats perfect and delayed. Customers tell us what they really need when the products are in their hands

### Decisions at the edge

Bold decisions made by leadership drive new opportunities

### Fail fast, fix fast

A failed experiment is data. An ignored experiment is waste. We learn and move

### Remain nimble to embrace emerging opportunities

A product today may not have been imagined 2 years ago. We remain flexible to embrace new opportunities quickly

# Agenda

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- 

## Lunch

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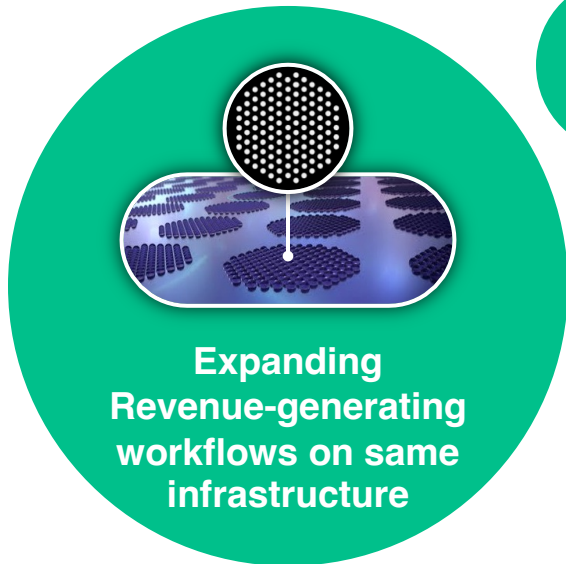
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- Financial Overview
- Culture
- **Q&A**

# Q&A

# Synergistic Solutions that Work Together

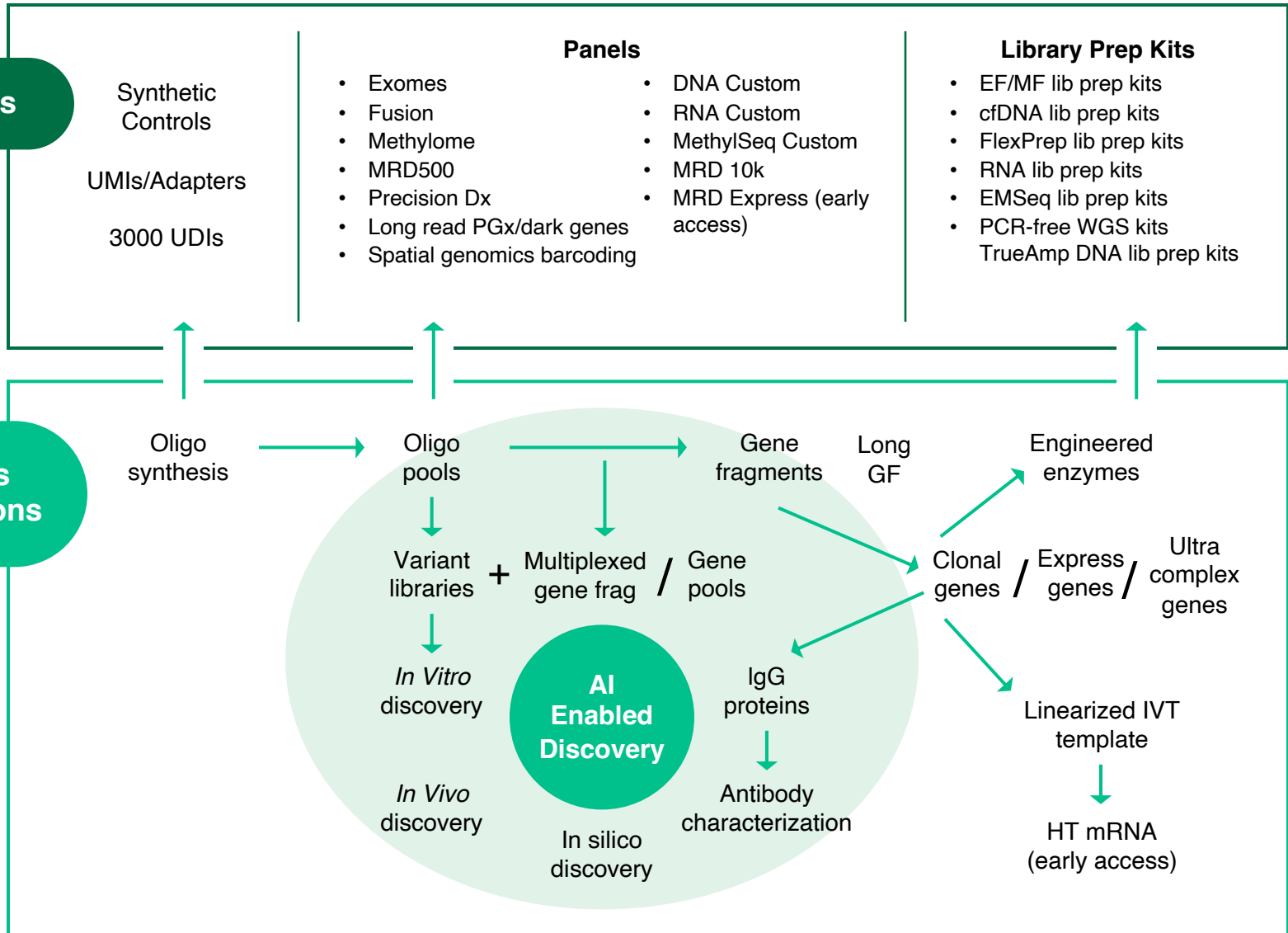
2021

& prior



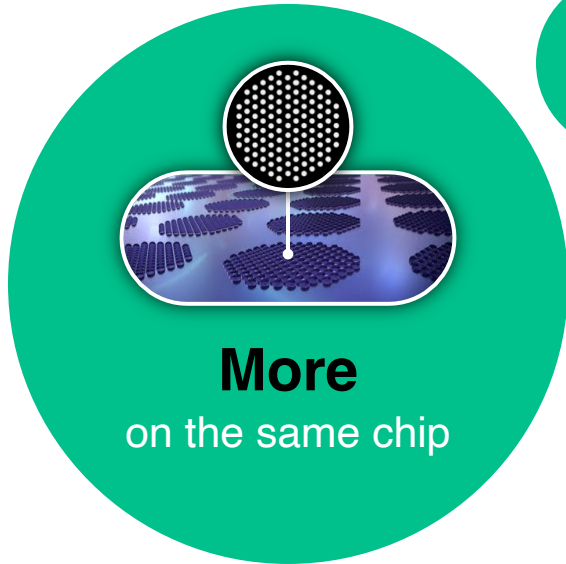
## NGS applications

## DNA synthesis & protein solutions



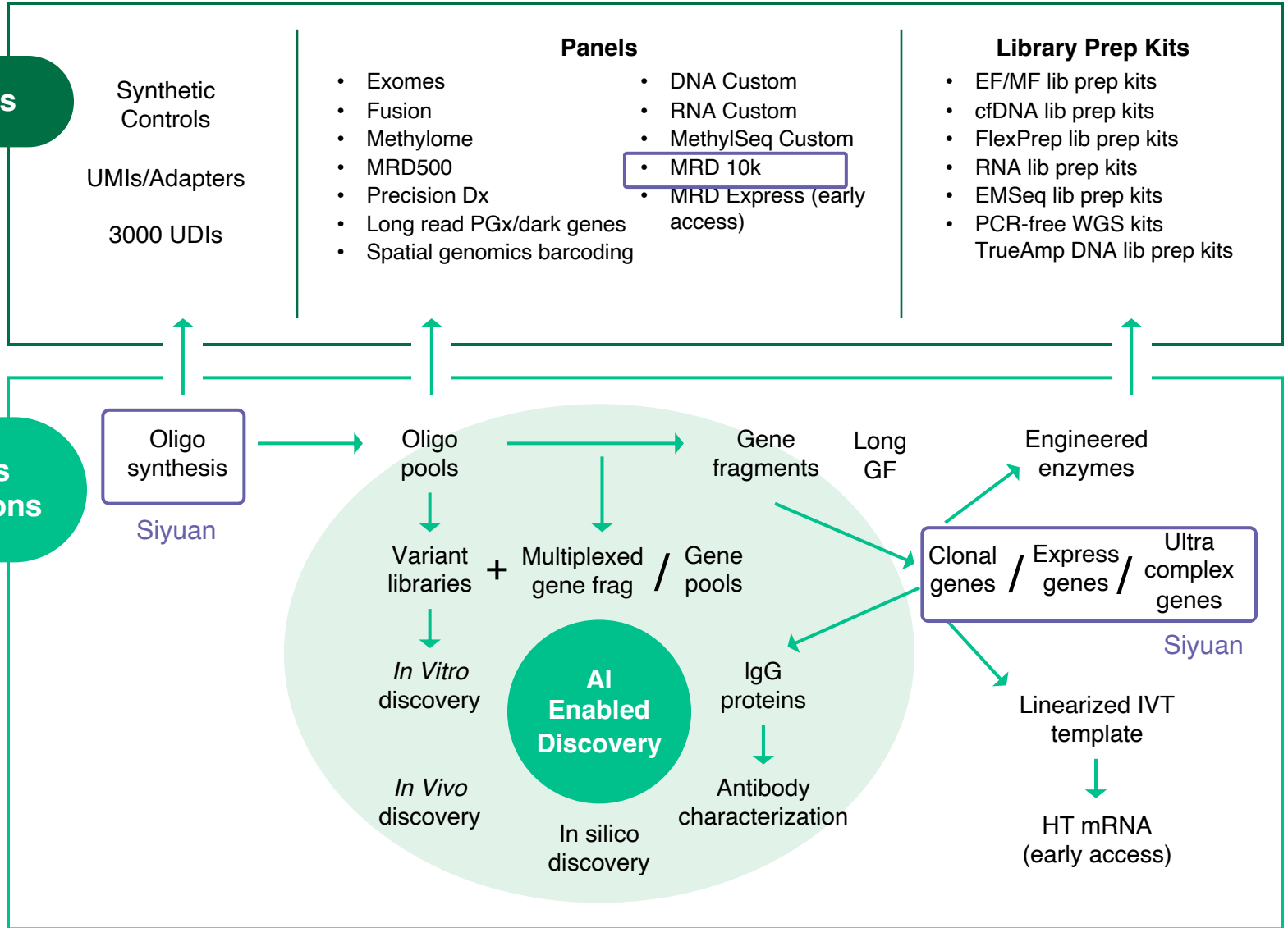
# Synergistic Solutions that Work Together

2026



**NGS applications**

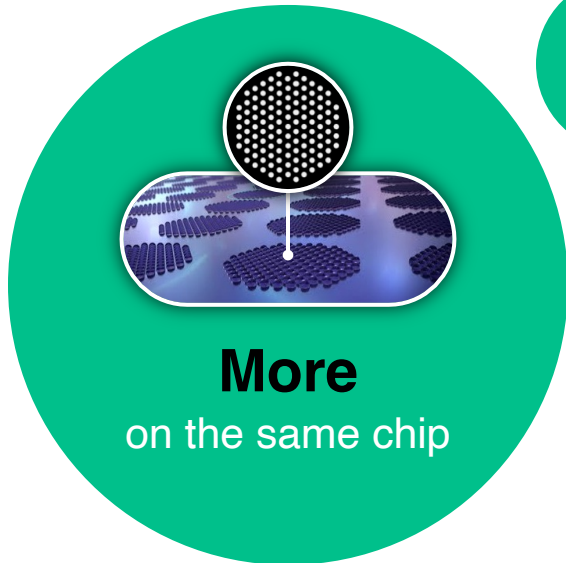
**DNA synthesis & protein solutions**



\*Introduced in 2025

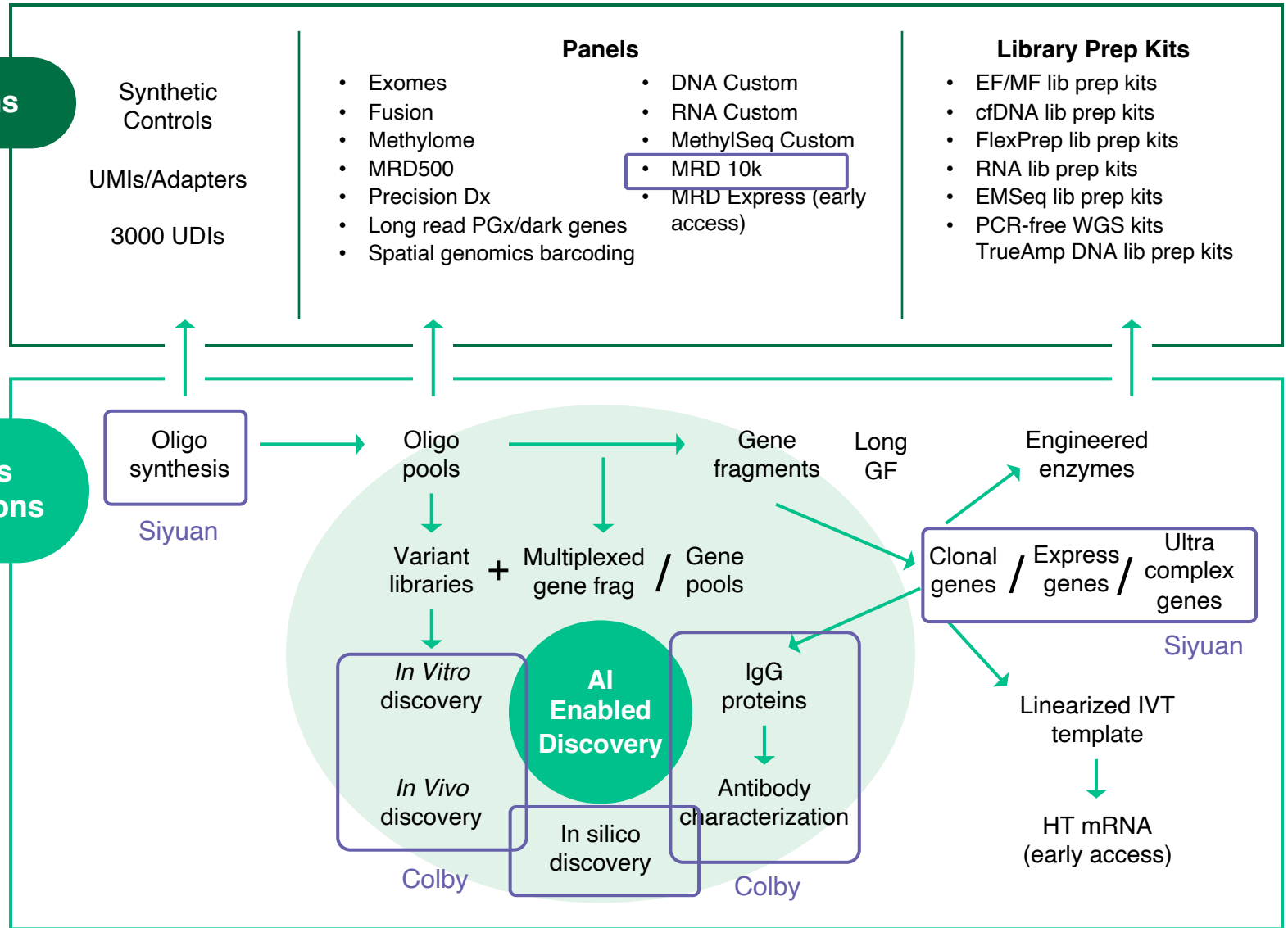
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2026



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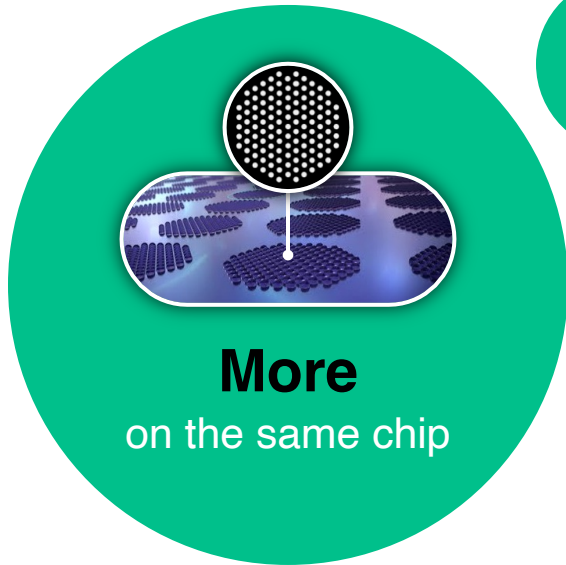
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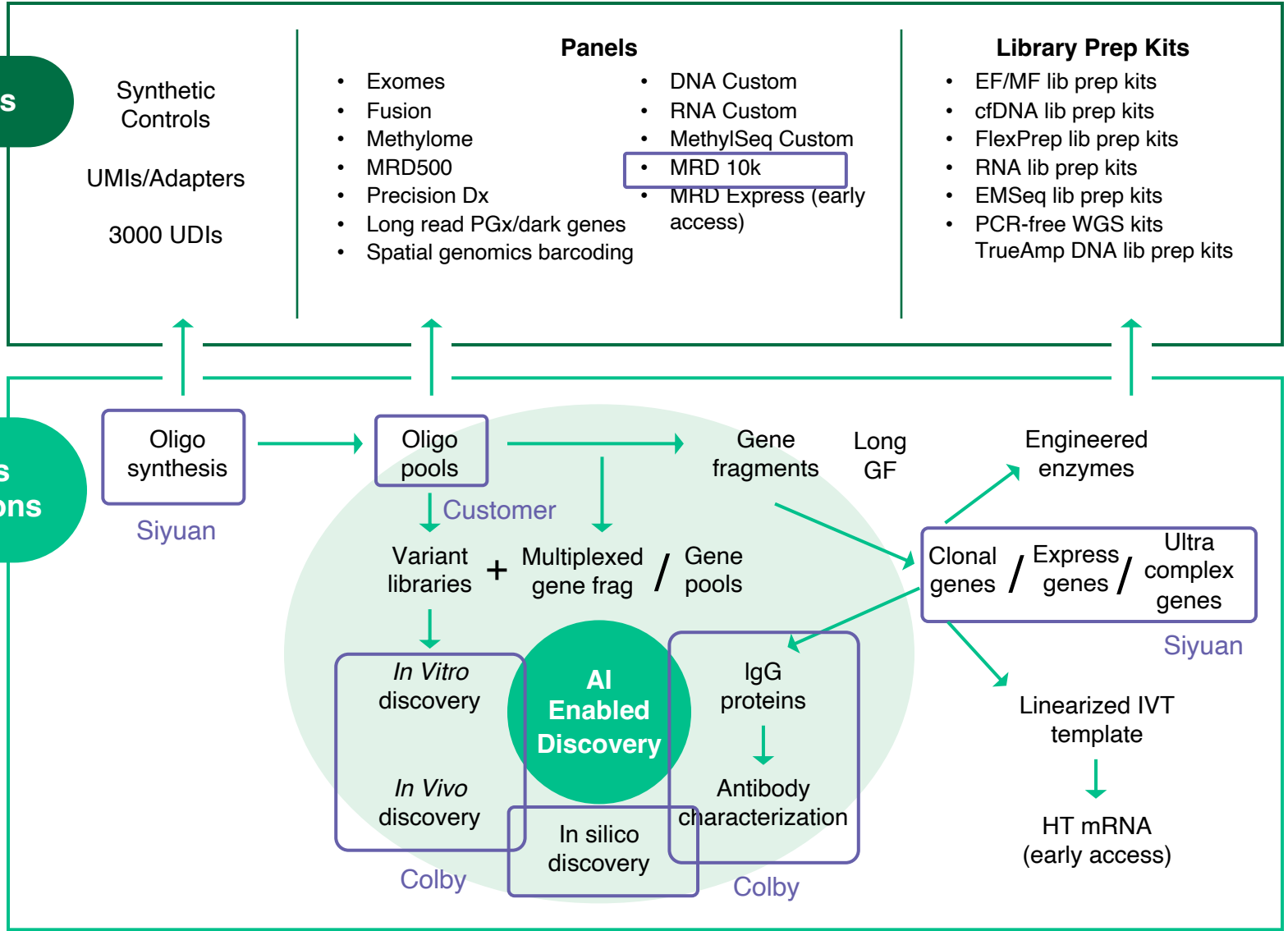
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2026



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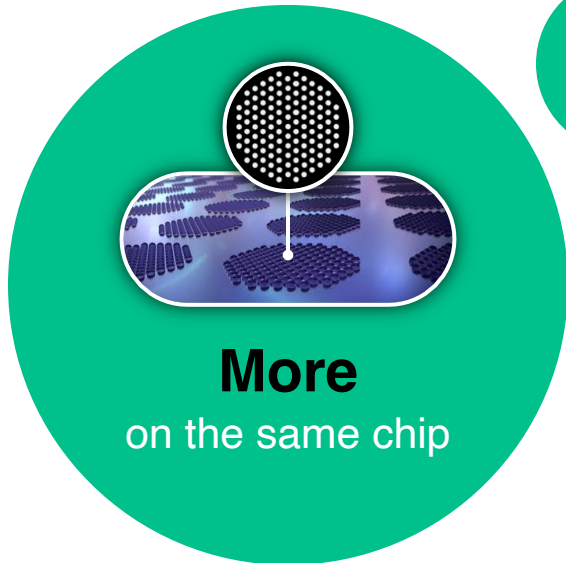
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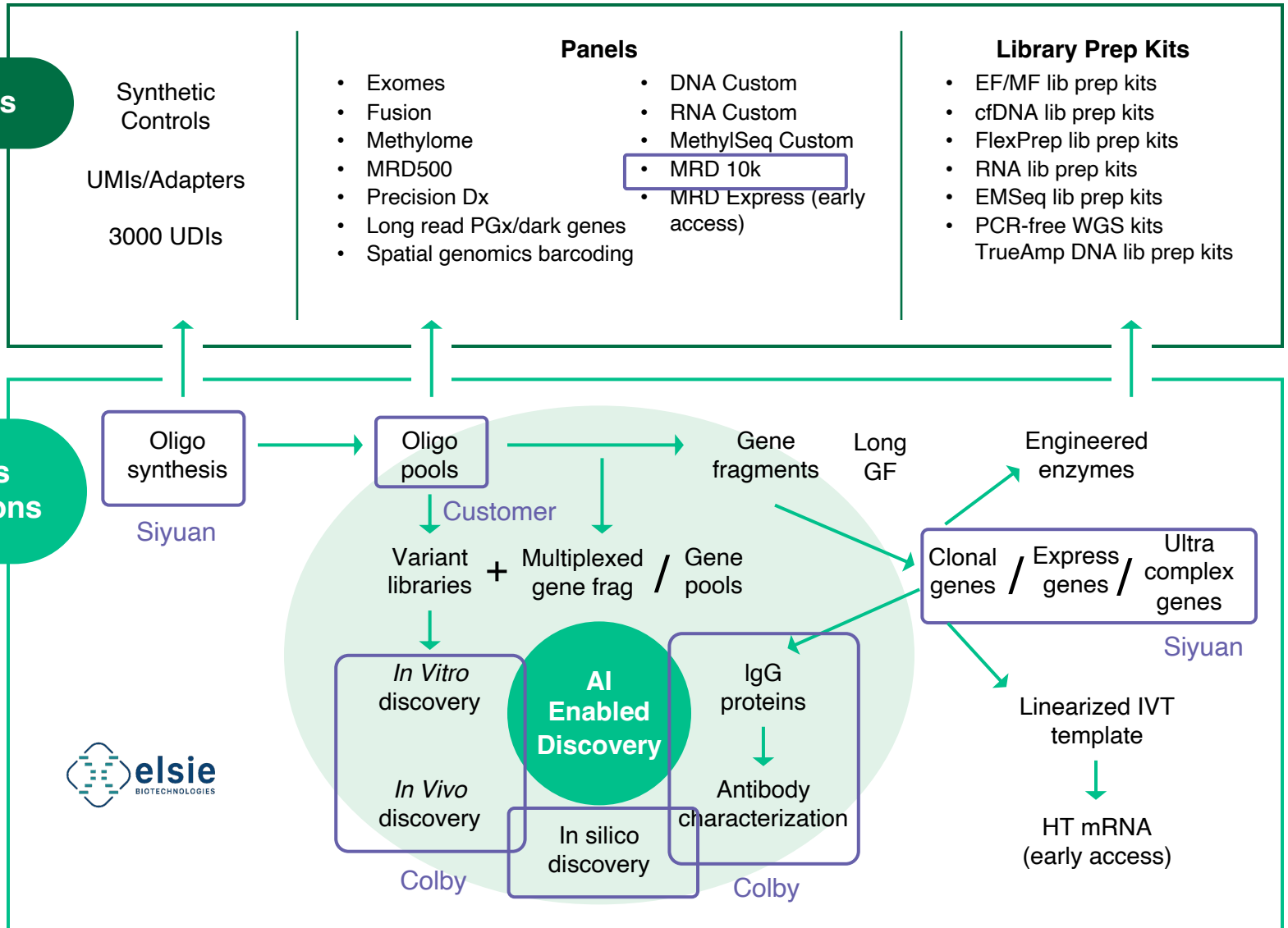
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2026



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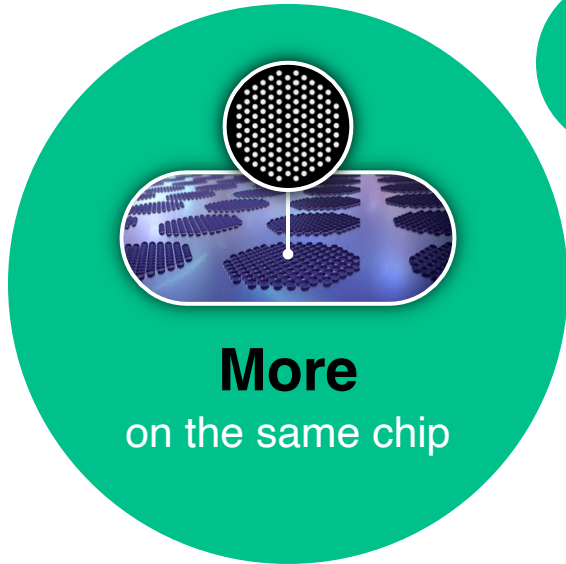
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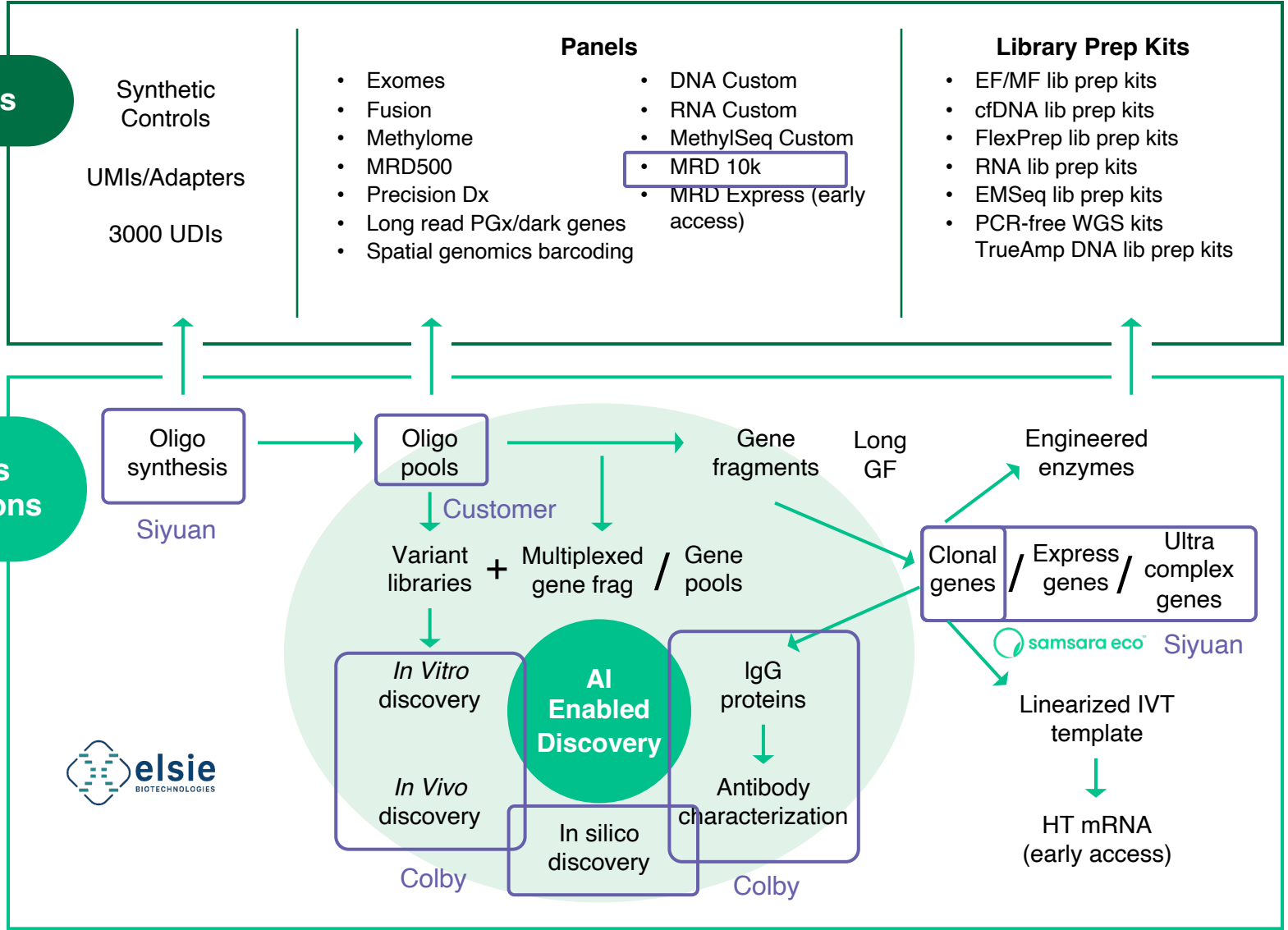
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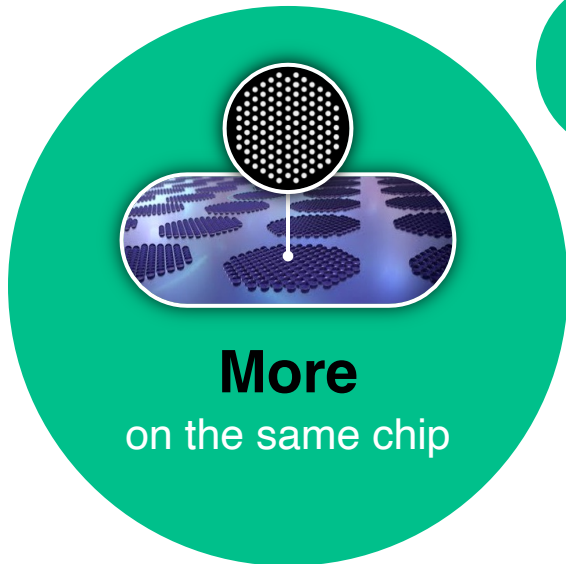
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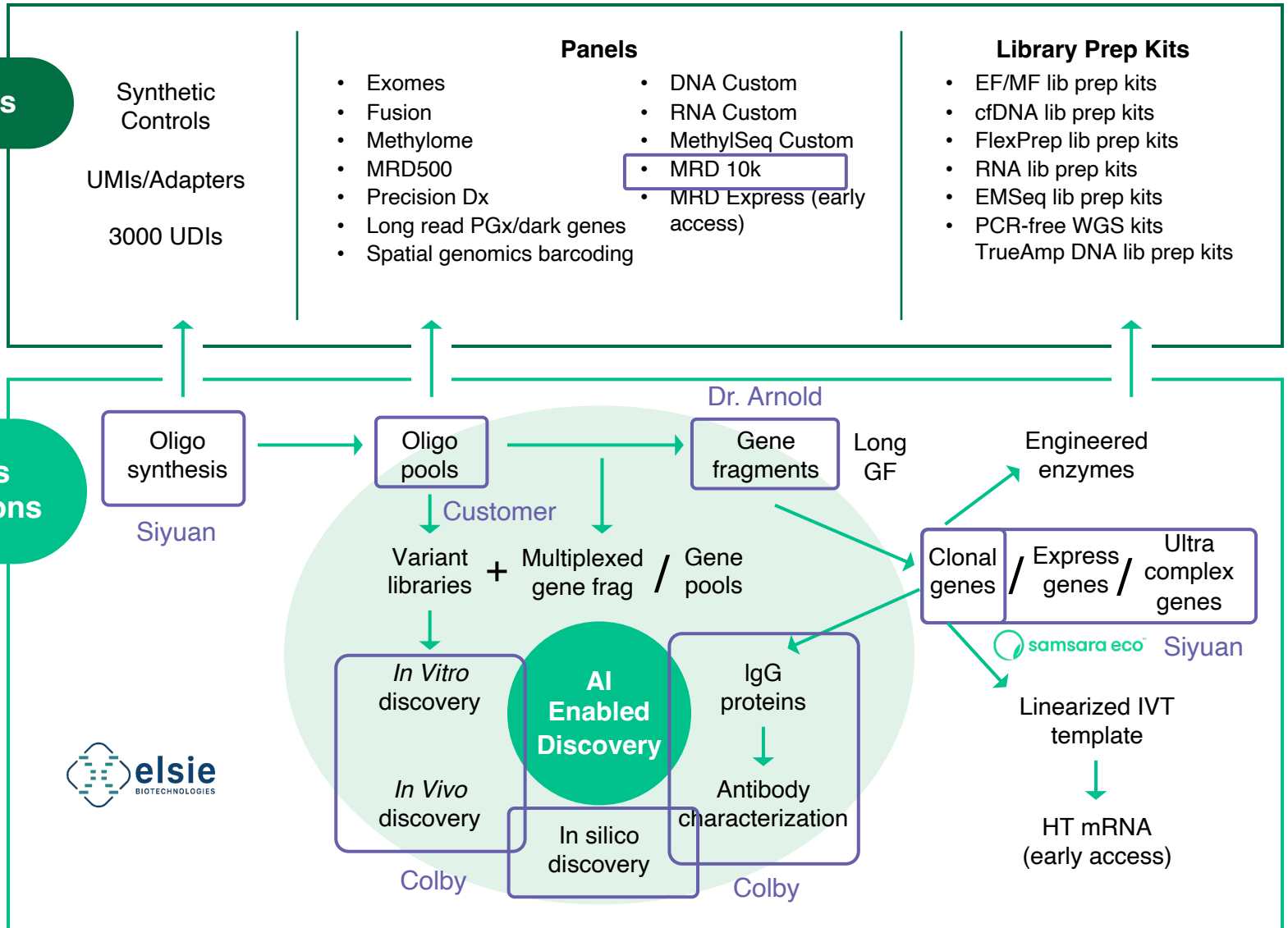
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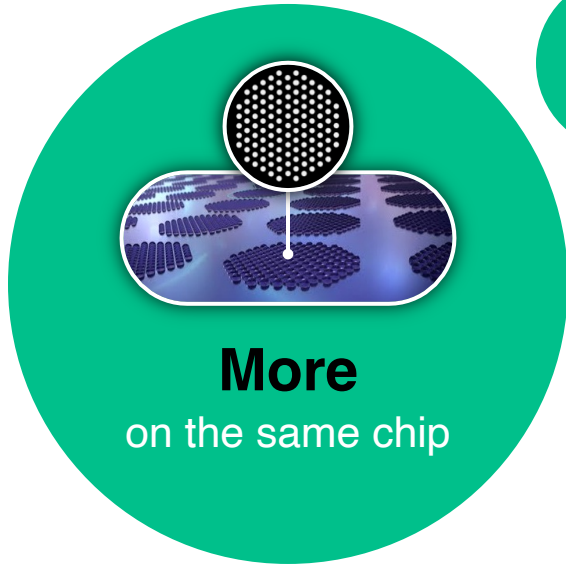
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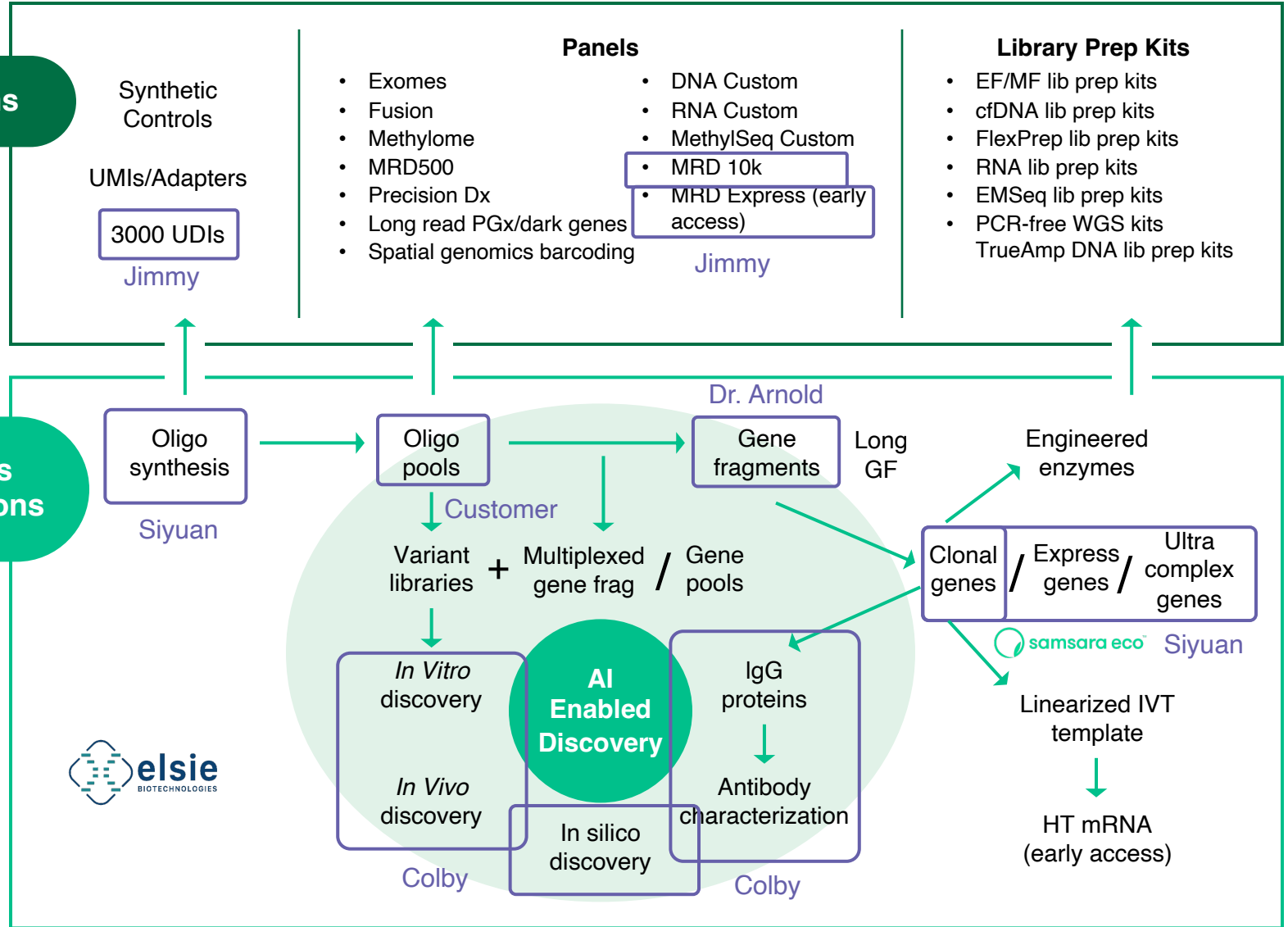
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2026



## NGS applications

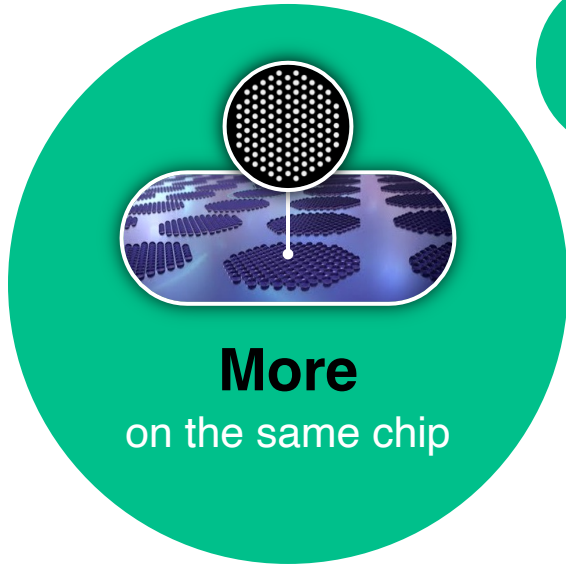
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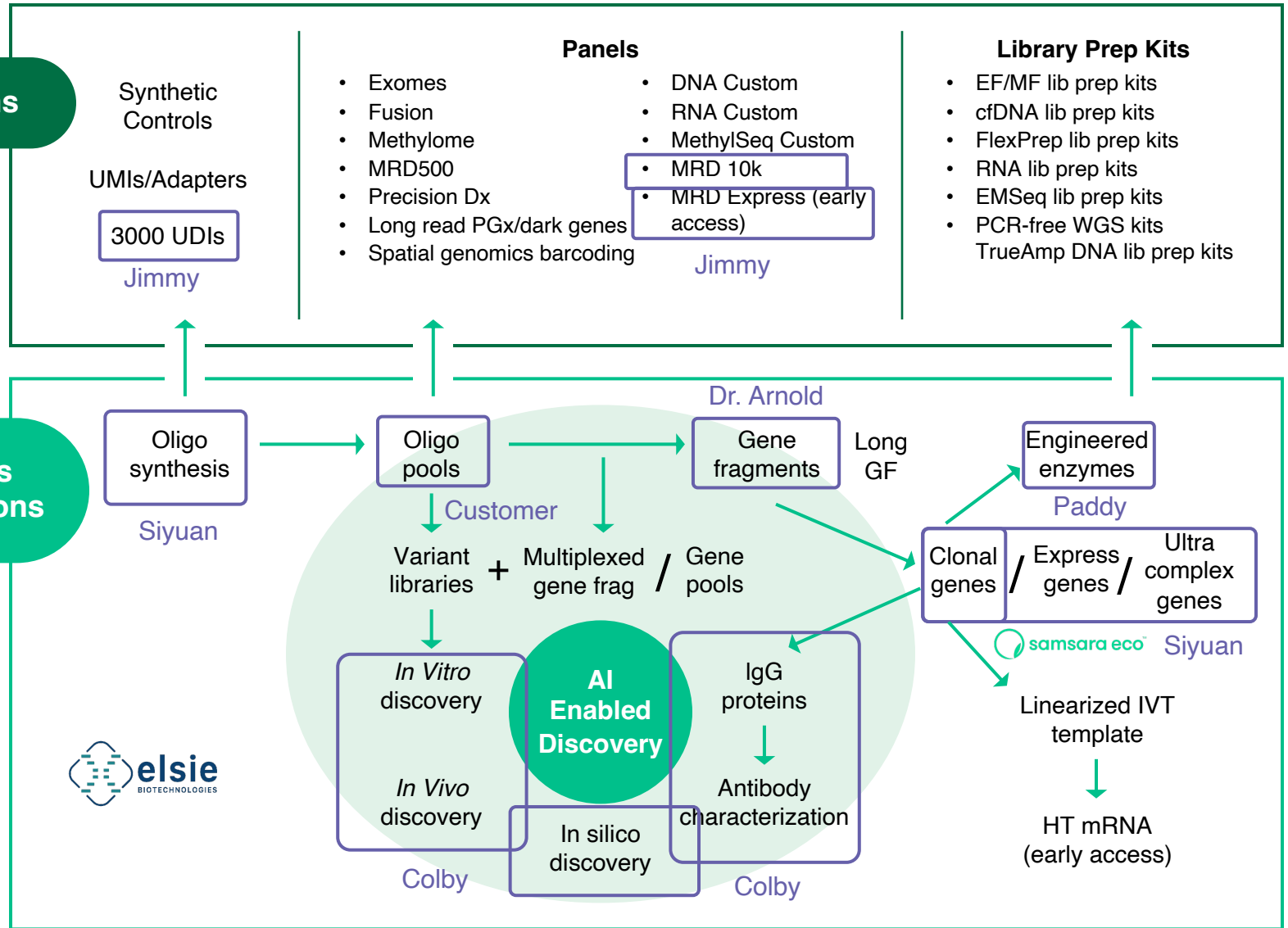
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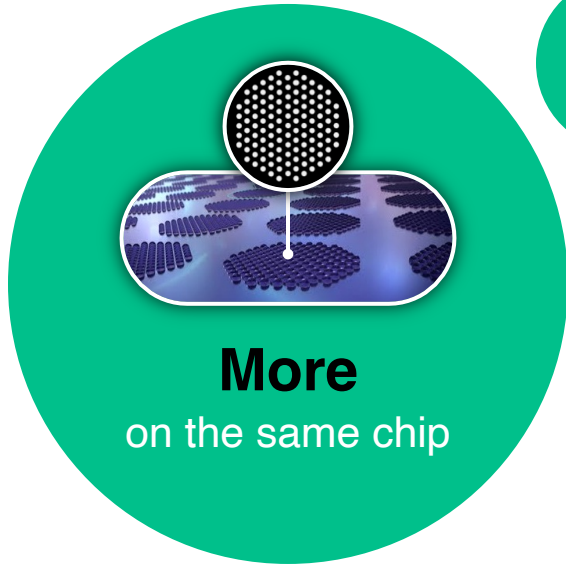
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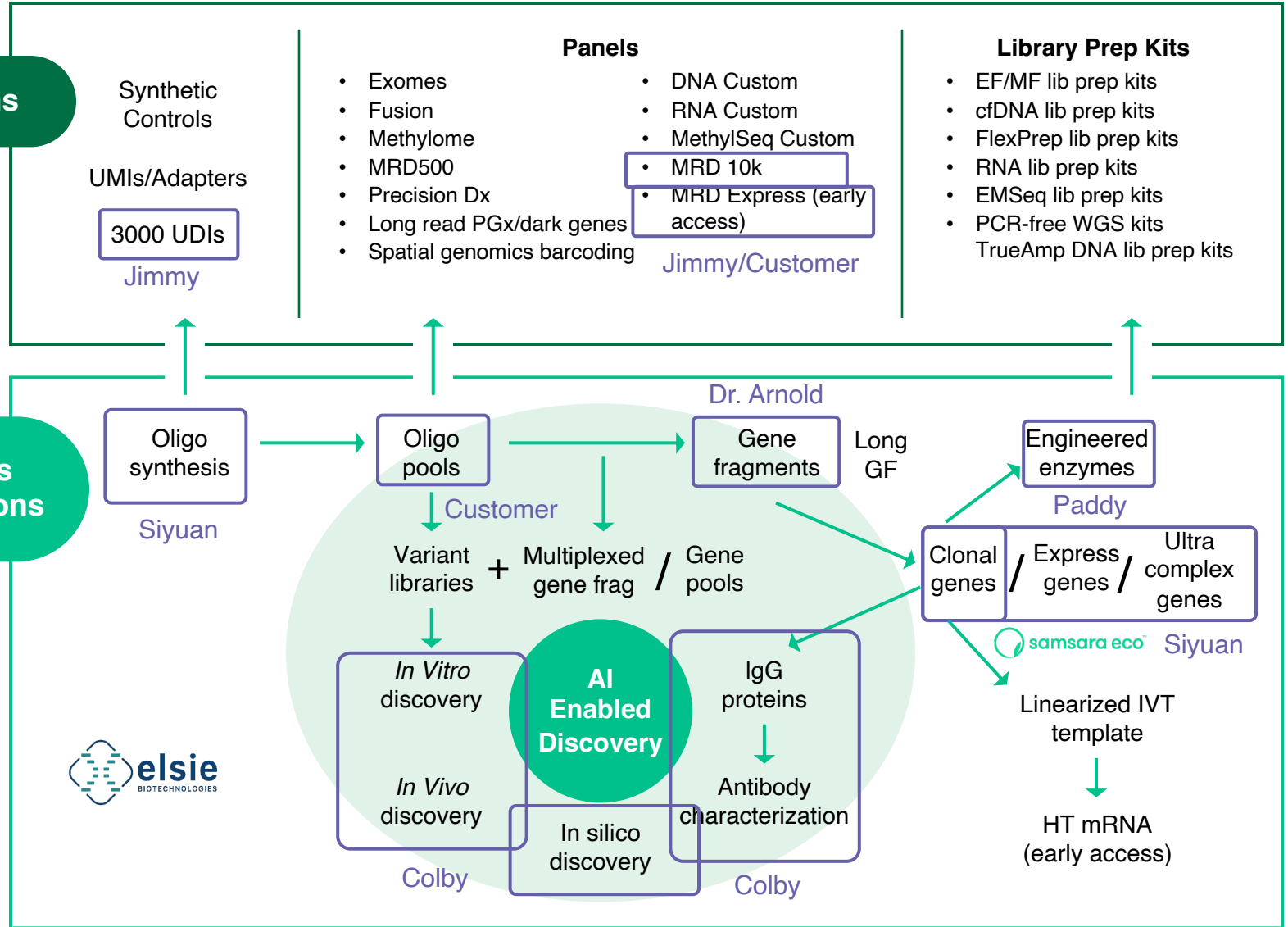
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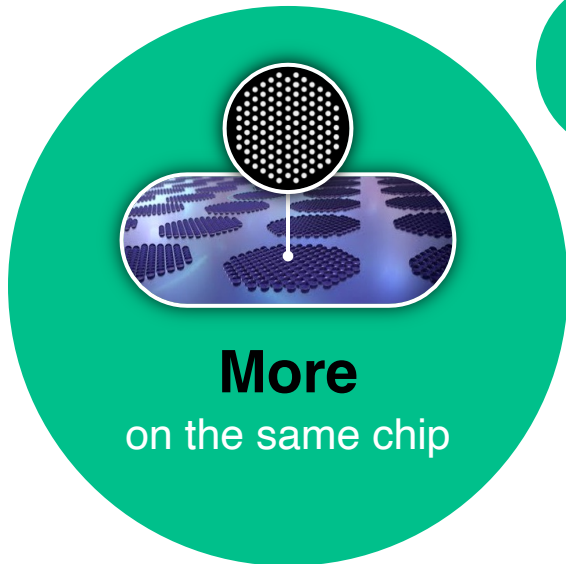
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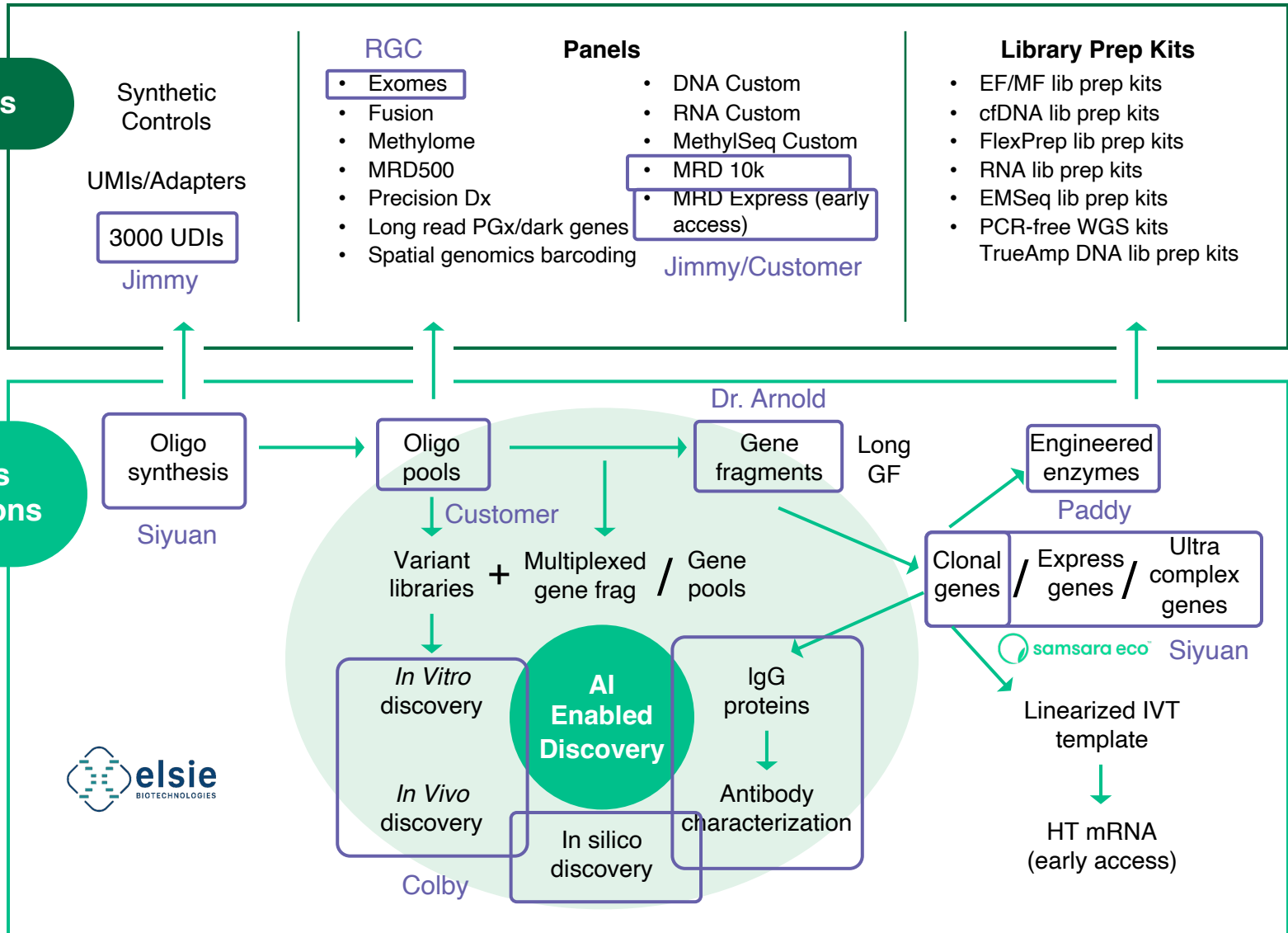
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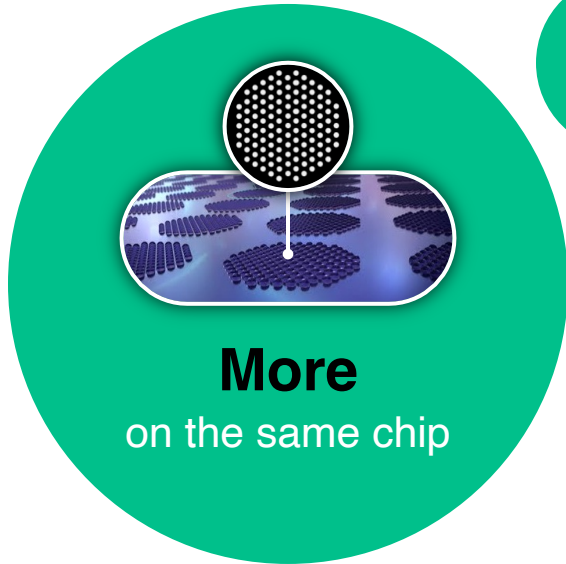
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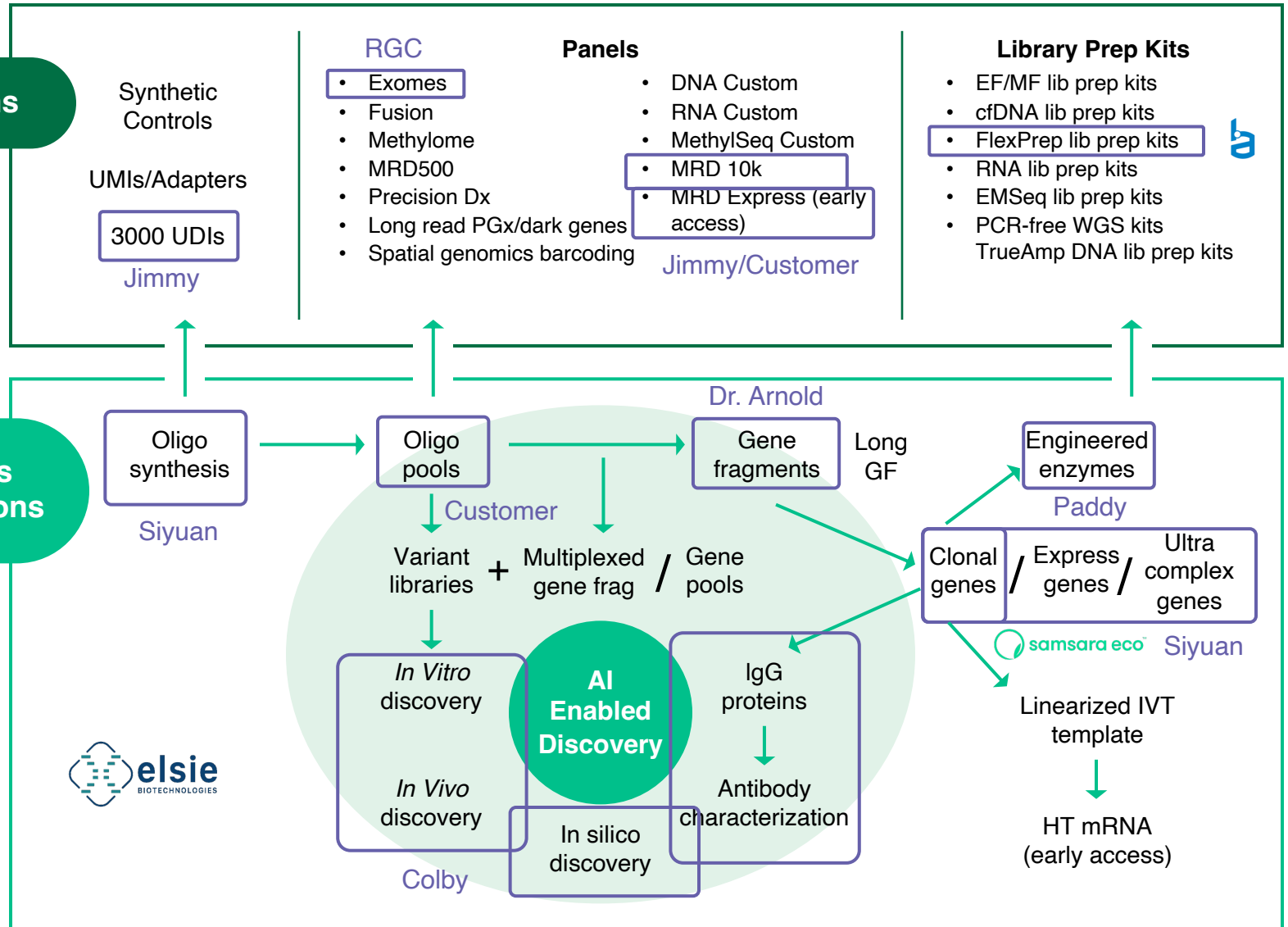
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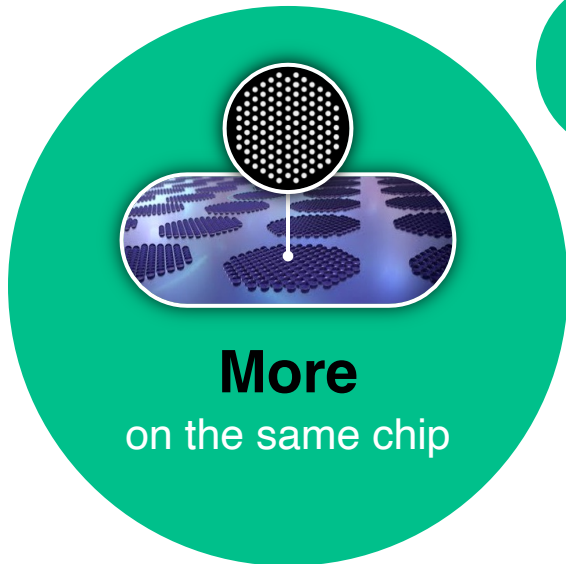
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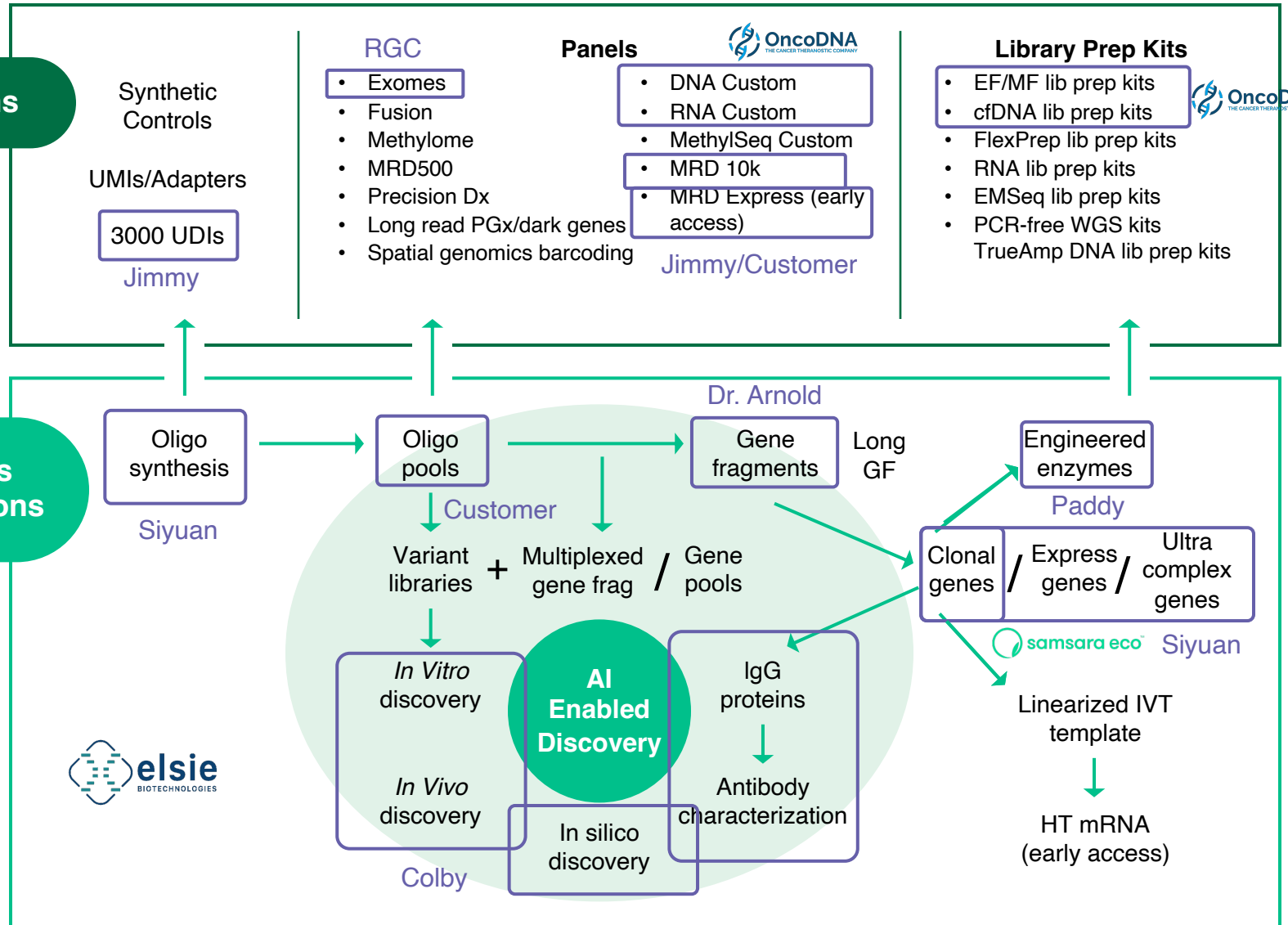
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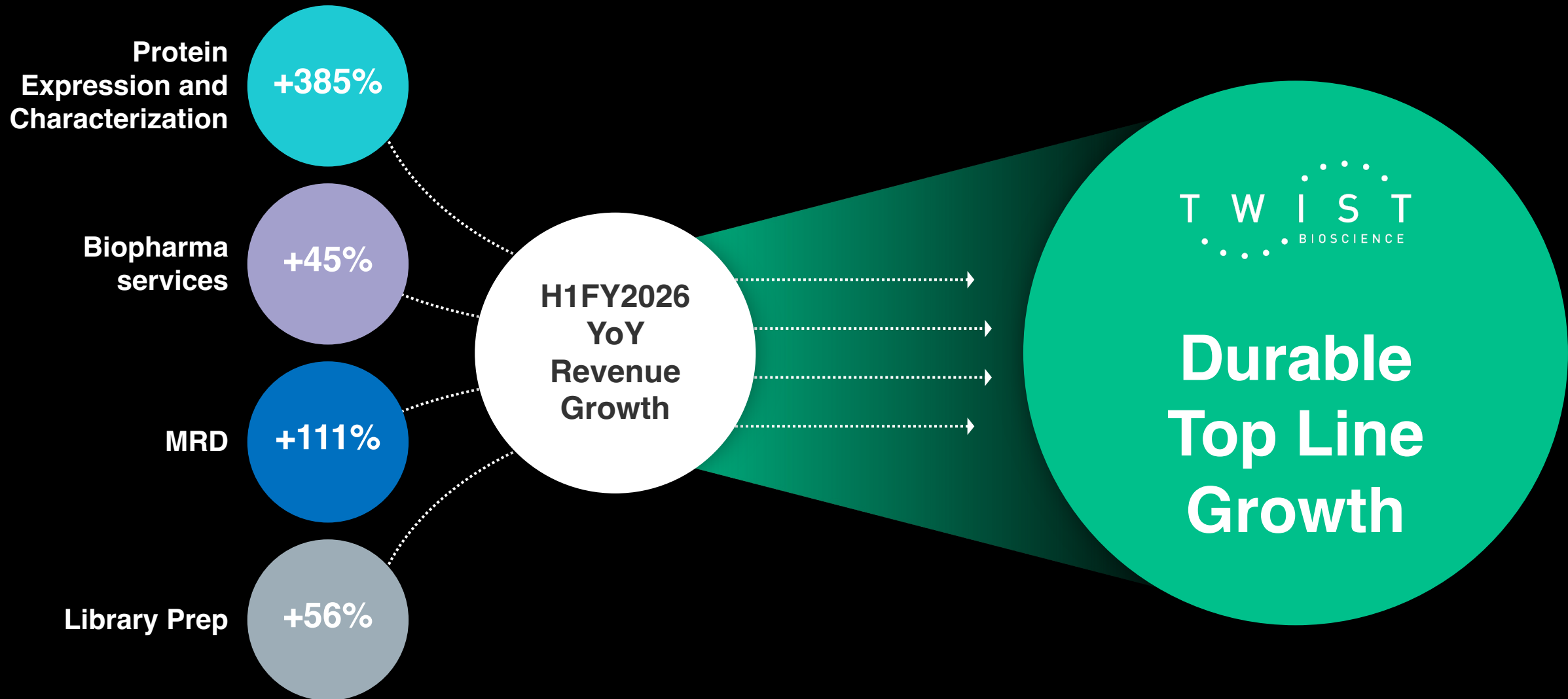
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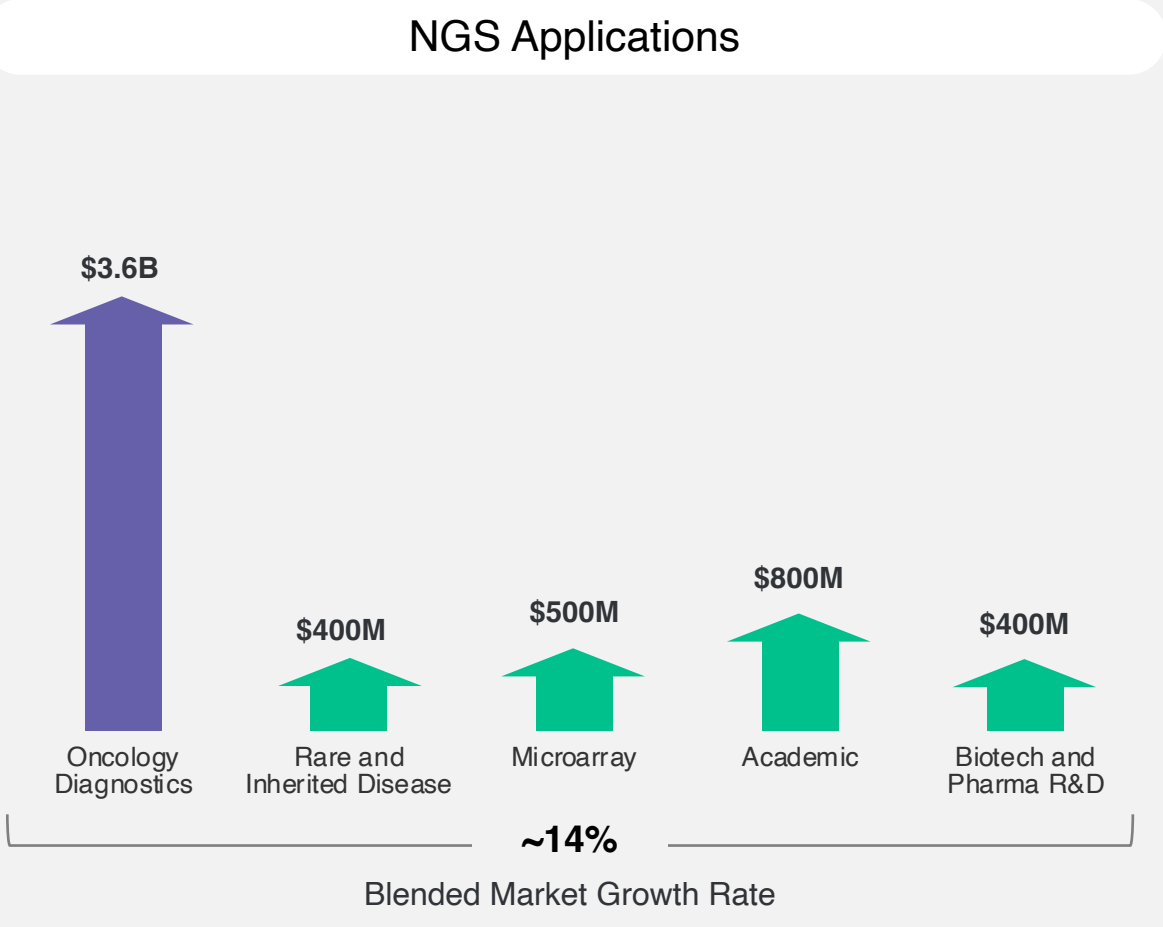
# Multiple Growth Levers – H1FY2026 to H1FY2025



# 2030: Continuing to Expand SAMs Driven by NPIs

**\$6B SAM\* and >\$90B TAM**

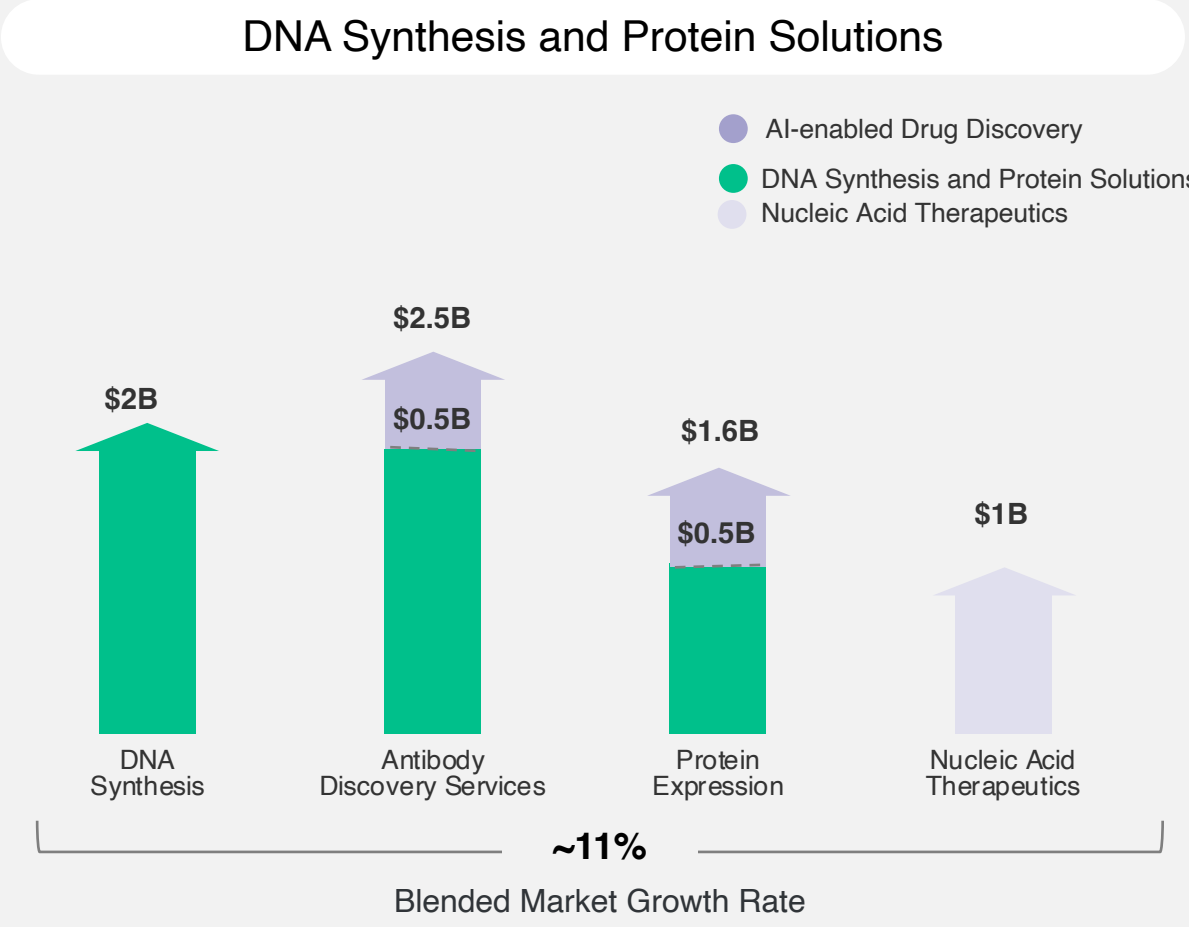
NGS Applications



\*Liquid biopsy (therapy selection, multicancer screening, minimal residual disease), comprehensive genomic profiling tissue  
 \*\*BCC reports, DeciBio, Twist internal estimates

**\$7B+ SAM\* and \$18B TAM**

DNA Synthesis and Protein Solutions



\*BCC reports, DeciBio, Grand View, Antibodies – recombinant protein market stat; Twist internal estimates

# Scaled Infrastructure with Expanding Operating Leverage

## **Industrialized**

DNA and protein  
synthesis platform

## **Manufacturing**

process paired with  
automation excellence

## **Automation & Software**

support scalable  
customization

## **Monetization**

many layers  
through portfolio  
expansion

## **Diversified**

customer base within  
multiple markets

## **Profitable Growth**

inflection point FY27-  
FY31

## **Durable**

growth ahead

## **Performance**

culture



# Thank you

# Adjusted EBITDA Reconciliation

| (In Thousands)  | FY 2020             | FY 2021            | FY 2022            | FY 2023            | FY 2024            | FY2025            |
|---|---------------------|--------------------|--------------------|--------------------|--------------------|-------------------|
| <b>GAAP Net Income (Loss)</b>                                   | <b>(\$ 139,931)</b> | <b>(\$152,098)</b> | <b>(\$217,863)</b> | <b>(\$204,619)</b> | <b>\$(208,726)</b> | <b>\$(77,670)</b> |
| <b>Add (Deduct) Adjustments:</b>                                |                     |                    |                    |                    |                    |                   |
| Interest income   | ( 1,499)            | (435)              | (3,062)            | (14,365)           | (15,344)           | (11,364)          |
| Interest expense  | 787                 | 367                | 80                 | —                  | —                  | —                 |
| Income tax expense (benefit)                                    | 382                 | (1,930)            | (10,411)           | 1,153              | 560                | 719               |
| Depreciation and amortization                                   | 6,677               | 9,750              | 16,514             | 29,310             | 31,432             | 24,853            |
| <b>EBITDA</b>   | <b>(\$ 133,584)</b> | <b>(\$144,346)</b> | <b>(\$217,742)</b> | <b>(\$188,521)</b> | <b>\$(192,079)</b> | <b>\$(63,462)</b> |
| <b>Add (Deduct) Adjustments:</b>                                |                     |                    |                    |                    |                    |                   |
| Other income/expense, net                                       | 182                 | 1,370              | 1,087              | 672                | 2,679              | 903               |
| Stock-based compensation expense                                | 17,096              | 36,998             | 79,664             | 30,278             | 50,925             | 64,459            |
| Gain on sale of business  | —                   | —                  | —                  | —                  | —                  | (48,847)          |
| Gain on deconsolidation of business                             | —                   | —                  | (4,607)            | —                  | —                  | —                 |
| Litigation settlement   | 22,500              | —                  | —                  | —                  | —                  | —                 |
| Change in fair value of contingent considerations and holdbacks | —                   | (534)              | (14,245)           | (5,912)            | —                  | —                 |
| Restructuring costs   | —                   | —                  | —                  | 9,384              | —                  | —                 |
| Impairment of long-lived assets                                 | —                   | —                  | —                  | 6,785              | 44,930             | —                 |
| <b>Adjusted EBITDA</b>  | <b>(\$ 93,806)</b>  | <b>(\$106,512)</b> | <b>(\$152,843)</b> | <b>(\$147,314)</b> | <b>\$(93,545)</b>  | <b>221</b>        |

# Adjusted R&D and SG&A Expenses Reconciliation

| (In Millions)                               | FY 2020        | FY 2021        | FY 2022        | FY 2023        | FY 2024        | FY 2025        |
|---|----------------|----------------|----------------|----------------|----------------|----------------|
| <b>R&amp;D Expenses — GAAP</b>              | <b>\$43.0</b>  | <b>\$69.1</b>  | <b>\$120.3</b> | <b>\$106.9</b> | <b>\$90.9</b>  | <b>\$80.3</b>  |
| <b>Adjusted to exclude:</b>                 |                |                |                |                |                |                |
| Depreciation and Amortization               | 3.0            | 3.2            | 3.5            | 4.0            | 3.0            | 1.3            |
| Stock-based Compensation Expense            | 3.3            | 10.2           | 19.5           | 13.9           | 11.2           | 9.0            |
| <b>Adjusted R&amp;D Expenses</b>            | <b>\$36.7</b>  | <b>\$55.7</b>  | <b>\$97.3</b>  | <b>\$88.9</b>  | <b>\$76.6</b>  | <b>\$70.0</b>  |
| <b>SG&amp;A Expenses — GAAP</b>             | <b>\$103.3</b> | <b>\$135.9</b> | <b>\$212.9</b> | <b>\$189.7</b> | <b>\$218.4</b> | <b>\$247.0</b> |
| <b>Adjusted to exclude:</b>                 |                |                |                |                |                |                |
| Depreciation and Amortization               | 1.8            | 3.6            | 6.5            | 6.9            | 6.8            | 6.5            |
| Stock-based Compensation Expense            | 12.5           | 24.2           | 55.5           | 11.8           | 35.7           | 48.5           |
| <b>Adjusted SG&amp;A Expenses</b>           | <b>\$89.0</b>  | <b>\$108.2</b> | <b>150.9</b>   | <b>\$171.1</b> | <b>\$175.9</b> | <b>\$192.0</b> |
| <b>Adjusted R&amp;D + SG&amp;A Expenses</b> | <b>\$125.7</b> | <b>\$163.9</b> | <b>248.2</b>   | <b>\$260.0</b> | <b>\$252.5</b> | <b>\$262.0</b> |