



Download Day 2024





Download Day 2024



Agenda

Breakfast & Arrival at Recursion (Upper Level)

8:30 am – 9:30 am

Morning Session

9:30 am – 12:30 pm

Welcome

State of Recursion

Chris Gibson PhD – Co-Founder & CEO

Recursion OS

Lina Nilsson PhD – Senior VP of Inception Labs

Preclinical

Laura Schaevitz PhD – Senior VP and Head of Research

Fireside Chat with Deepak Nijhawan, MD, PhD

David Mauro MD PhD – Chief Medical Officer

Deepak Nijhawan MD PhD – UT Southwestern, Distinguished Chair in Biomedical Science

Tours & Demos

Senior Management

Lunch & Break (Upper Level, High Throughput Feeding)

12:30 – 1:30 pm

Afternoon Session

1:30 pm – 4:30 pm

Afternoon Convocation

Najat Khan PhD – Chief R&D Officer & Chief Commercial Officer

Partnerships

Matt Kinn – Senior VP of Business Development & Corporate Initiatives

John Marioni PhD – Genentech, Senior VP and Head of Computational Sciences

Clinical Programs

David Mauro MD PhD – Chief Medical Officer

Company & Milestones

Michael Secora PhD – Chief Financial Officer

Break

Fireside Chat with Jensen Huang

Chris Gibson PhD – Co-Founder & CEO

Jensen Huang – NVIDIA, Founder & CEO

Closing Remarks

Chris Gibson PhD – Co-Founder & CEO

Dinner — Mar Muntanya (Hyatt Regency)

5:00 – 7:00 pm

Welcome

State of the Company

Disclaimers

This presentation and any accompanying discussion and documents contain information that includes or is based upon "forward-looking statements" within the meaning of the Securities Litigation Reform Act of 1995. These forward-looking statements are based on our current expectations, estimates and projections about our industry and our company, management's beliefs and certain assumptions we have made. The words "plan," "anticipate," "believe," "continue," "estimate," "expect," "intend," "may," "will" and similar expressions are intended to identify forward-looking statements. Forward-looking statements made in this presentation include outcomes and benefits expected from the Tempus partnership, including our ability to leverage the datasets acquired through the license agreement into increased machine learning capabilities and accelerate clinical trial enrollment; outcomes and benefits expected from the Enamine partnership, including the generating and co-branding of new chemical libraries; outcomes and expected benefits from the Helix partnership, including the development of causal AI models and biomarker and patient stratification strategies; expected BioHive supercomputer capabilities; outcomes and benefits from licenses, partnerships and collaborations, including option exercises by partners, additional partnerships, and the ability to house tools on the BioNeMo Marketplace; the potential for additional partnerships and making data and tools available to third parties; advancements of our Recursion OS, including augmentation of our dataset; outcomes and benefits expected from the Large Language Model-Orchestrated Workflow Engine (LOWE); the occurrence or realization of any near- or medium-term potential milestones; the initiation, timing, progress, results, and cost of our research and development programs and our current and future preclinical and clinical studies, including timelines for enrollment in studies, data readouts, and progression toward IND-enabling studies; the potential size of the market opportunity for our drug candidates; our ability to identify viable new drug candidates for clinical development and the accelerating rate at which we expect to identify such candidates; our expectation that the assets that will drive the most value for us are those that we will identify in the future using our datasets and tools, and many others. Forward-looking statements made in this presentation are neither historical facts nor assurances of future performance, are subject to significant risks and uncertainties, and may not occur as actual results could differ materially and adversely from those anticipated or implied in the forward-looking statements. For a discussion of factors that could affect our business, please refer to the "Risk Factors" sections in our filings with the U.S. Securities and Exchange Commission, including our Annual Report for the Fiscal Year ended December 31, 2023, on Form 10-K and our most recent Quarterly Report on Form 10-Q. This presentation does not purport to contain all the information that may be required to make a full analysis of the subject matter. We undertake no obligation to correct or update any forward-looking statements, whether as a result of new information, future events or otherwise.

Certain information contained in this presentation relates to or is based on studies, publications, surveys and other data obtained from third-party sources and the company's own internal estimates and research. While the company believes these third-party sources to be reliable as of the date of this presentation, it has not independently verified, and makes no representation as to the adequacy, fairness, accuracy or completeness of, any information obtained from third-party sources. In addition, all of the market data included in this presentation involves a number of assumptions and limitations, and there can be no guarantee as to the accuracy or reliability of such assumptions. Finally, while the company believes its own internal research is reliable, such research has not been verified by any independent source.

Cross-trial or cross-candidate comparisons against other clinical trials and other drug candidates are not based on head-to-head studies and are presented for informational purposes; comparisons are based on publicly available information for other clinical trials and other drug candidates.

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Our Hopes for Today

Share details and updates on our:

- Pipeline – with 7 clinical trial readouts expected in the next ~18 months
- Partnerships - with potential near term options on both maps and programs
- Platform - with industry-leading data generation and compute

Help define what we view as a tipping point moment as BioTech transitions to TechBio and understand why Recursion is uniquely positioned to take advantage of this

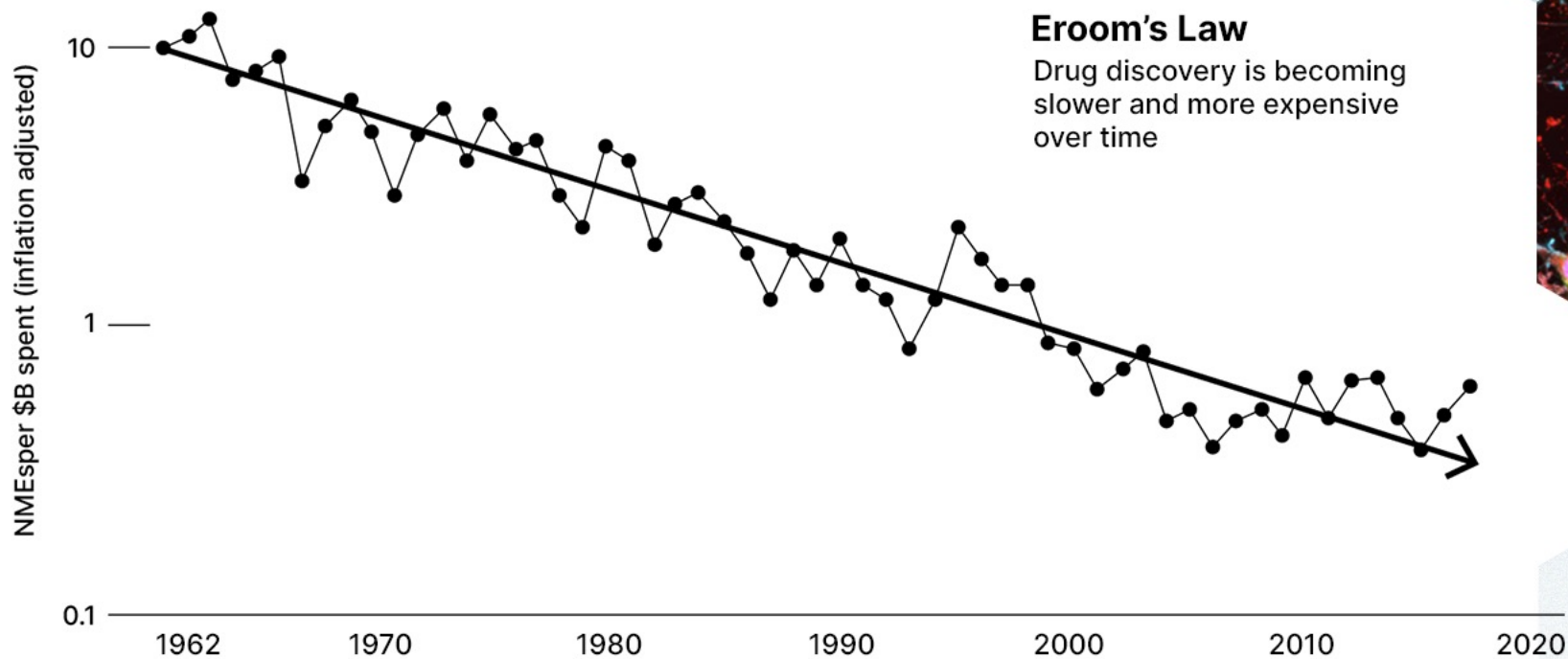
Let you get a feel for Recursion and hear from expert partners from outside Recursion about the current and potential future impact of our work



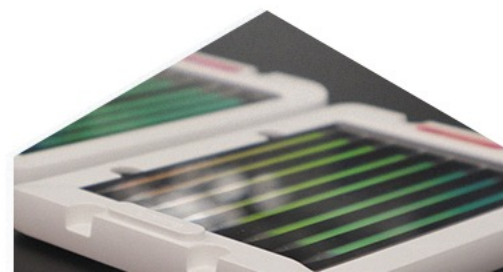
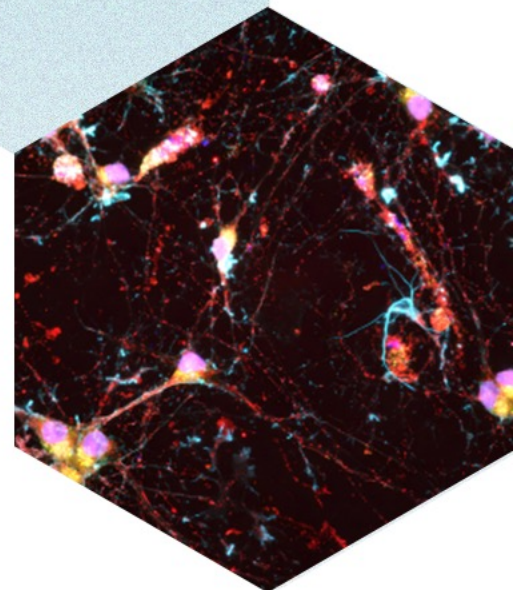
The Moment: A Tale of Two Cities



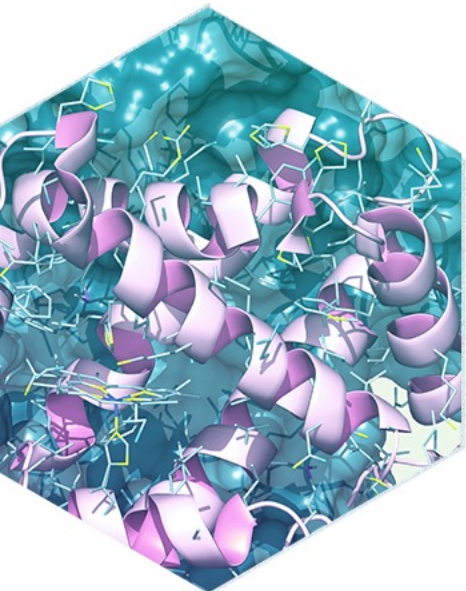
A Tale of Two Cities: BioPharma



Scannell et al., *Nature Reviews Drug Discovery* 11:191, 2012



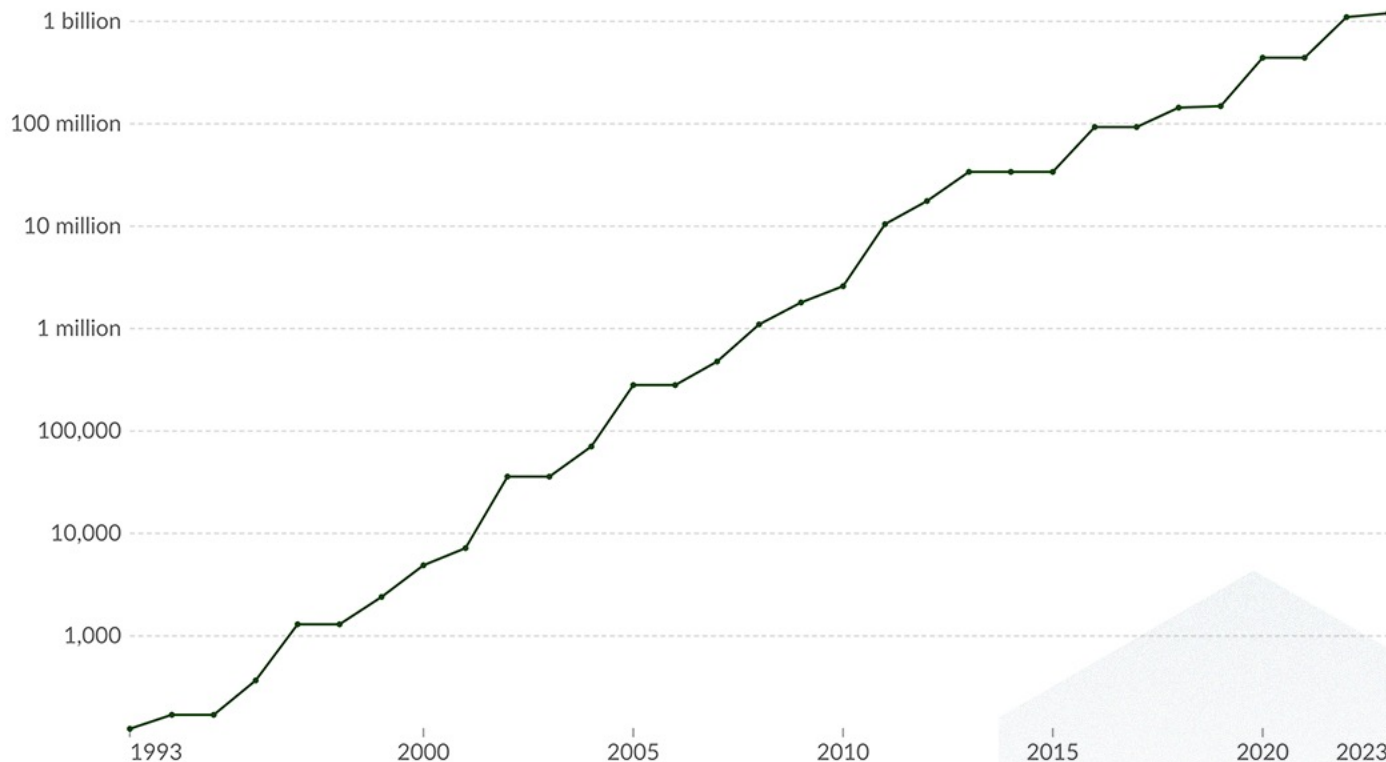
A Tale of Two Cities: Tech



Computational capacity of the fastest supercomputers

The number of floating-point operations¹ carried out per second by the fastest supercomputer in any given year. This is expressed in gigaFLOPS, equivalent to 10^9 floating-point operations per second.

Our World
in Data



Data source: Dongarra et al. (2023)

OurWorldInData.org/technological-change | CC BY

1. **Floating-point operation:** A floating-point operation (FLOP) is a type of computer operation. One FLOP represents a single arithmetic operation involving floating-point numbers, such as addition, subtraction, multiplication, or division.

The Evolution of BioTech into TechBio

We believe the transformation of BioPharma through AI is inevitable, just as we are seeing in so many industries — we believe it is a matter of **who**, **how** and **when**

New types of companies have emerged that are truly “**bilingual**” in **tech** and **science**

Data, **compute**, and **automation** are shifting the speed, cost, and quality of novel insights today, and we are nearing the stage where we can harvest the earliest of this jump forward

TechBio Origins: Point Solutions

Most BioTech companies have built a point solution - they've developed a tool, process, model or analysis to accomplish an important step in drug discovery.

This is how we started too.

But discovering and developing medicines requires hundreds of steps...

Cell Painting, a high-content image-based assay for morphological profiling using multiplexed fluorescent dyes

Mark-Anthony Bray¹, Shantanu Singh¹, Han Han², Chadwick T Davis², Blake Borgeson², Cathy Hartland³, Maria Kost-Alimova³, Sigrun M Gustafsdottir³, Christopher C Gibson² & Anne E Carpenter¹

¹Imaging Platform, Broad Institute of Harvard and MIT, Cambridge, Massachusetts, USA. ²Recursion Pharmaceuticals, Salt Lake City, Utah, USA. ³Center for the Science of Therapeutics, Broad Institute of Harvard and MIT, Cambridge, Massachusetts, USA. Correspondence should be addressed to C.C.G. (chris.gibson@recursionpharma.com) or A.E.C. (anne@broadinstitute.org).

Published online 25 August 2016; doi:10.1038/nprot.2016.105

In morphological profiling, quantitative data are extracted from microscopy images of cells to identify biologically relevant similarities and differences among samples based on these profiles. This protocol describes the design and execution of experiments using Cell Painting, which is a morphological profiling assay that multiplexes six fluorescent dyes, imaged in five channels, to reveal eight broadly relevant cellular components or organelles. Cells are plated in multiwell plates, perturbed with the treatments to be tested, stained, fixed, and imaged on a high-throughput microscope. Next, an automated image analysis software identifies individual cells and measures ~1,500 morphological features (various measures of size, shape, texture, intensity, and so on) to produce a rich profile that is suitable for the detection of subtle phenotypes. Profiles of cell populations treated with different experimental perturbations can be compared to suit many goals, such as identifying the phenotypic impact of chemical or genetic perturbations, grouping compounds and/or genes into functional pathways, and identifying signatures of disease. Cell culture and image acquisition takes 2 weeks; feature extraction and data analysis take an additional 1–2 weeks.

INTRODUCTION

Phenotypic screening has been tremendously powerful for identifying novel small molecules as probes and potential therapeutics, and for identifying genetic regulators of many biological processes^{1–4}. High-throughput microscopy has been a particularly fruitful type of phenotypic screening; it is often called high-content analysis because of the high information content that can be observed in images⁵. However, most large-scale imaging experiments extract only one or two features of cells⁶, and/or aim to identify just a few 'hits' in a screen, meaning that vast quantities of quantitative data about cellular state remain untapped.

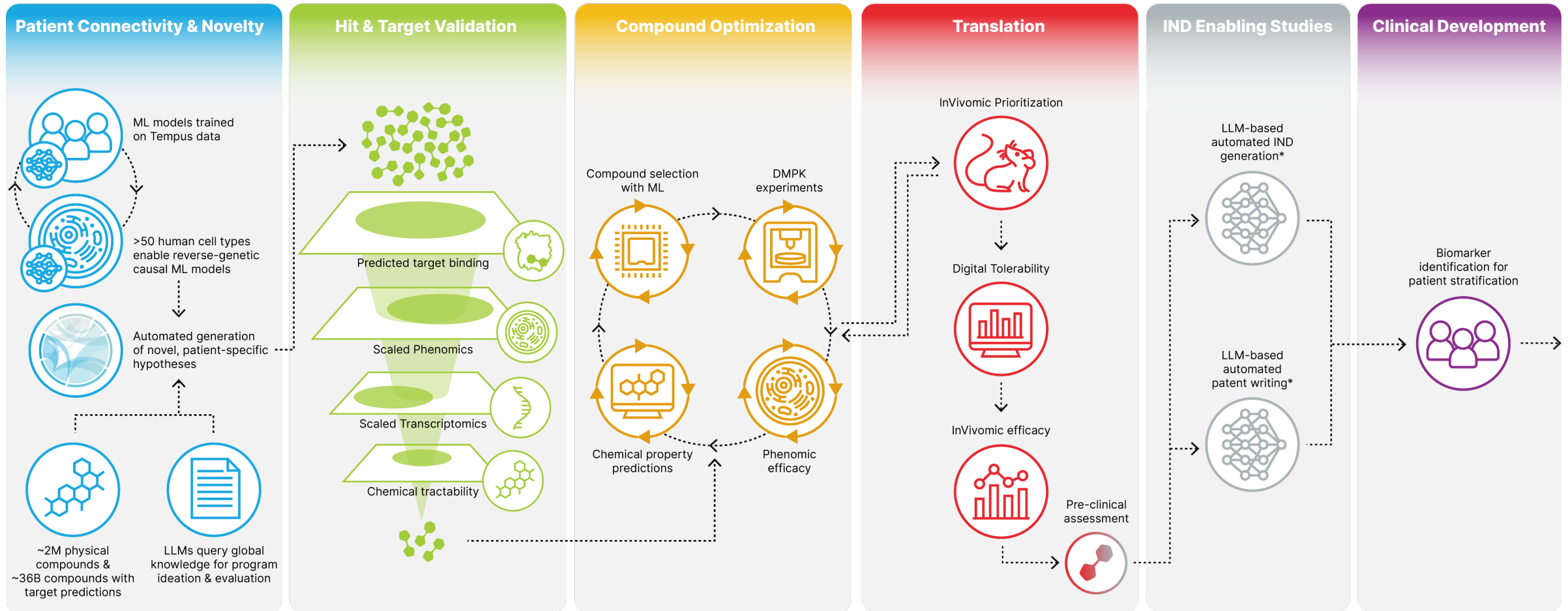
In this article, we detail a protocol for the Cell Painting assay, which is a generalizable and broadly applicable method for accessing the valuable biological information about cellular state that is contained in morphology. Cellular morphology is a potentially rich data source for interrogating biological perturbations, especially at a large scale^{5,7–10}. The techniques and technology that are necessary to generate these data have advanced rapidly, and they are now becoming accessible to nonspecialized laboratories¹¹. In this protocol, we discuss morphological profiling (also known as image-based profiling), contrast it with conventional image-

anticancer drug sensitivity reflect mechanisms of action¹²—and gene expression—in which signatures related to small molecules, genes, and diseases were identified¹³.

It is important to note that profiling differs from conventional screening assays in that the latter are focused on quantifying a relatively small number of features selected specifically because of a known association with the biology of interest. Profiling, on the other hand, casts a much wider net, and avoids the intensive customization that is usually necessary for problem-specific assay development in favor of a more generalizable method. Therefore, taking an unbiased approach via morphological profiling offers the opportunity for discovery unconstrained by what we know (or think we know). It also holds the potential to be more efficient, as a single experiment can be mined for many different biological processes or diseases of interest.

In morphological profiling, measured features include staining intensities, textural patterns, size, and shape of the labeled cellular structures, as well as correlations between stains across channels, and adjacency relationships between cells and among intracellular structures. The technique enables single-cell resolu-

To truly industrialize drug discovery, point solutions must be integrated as modules across many diverse steps

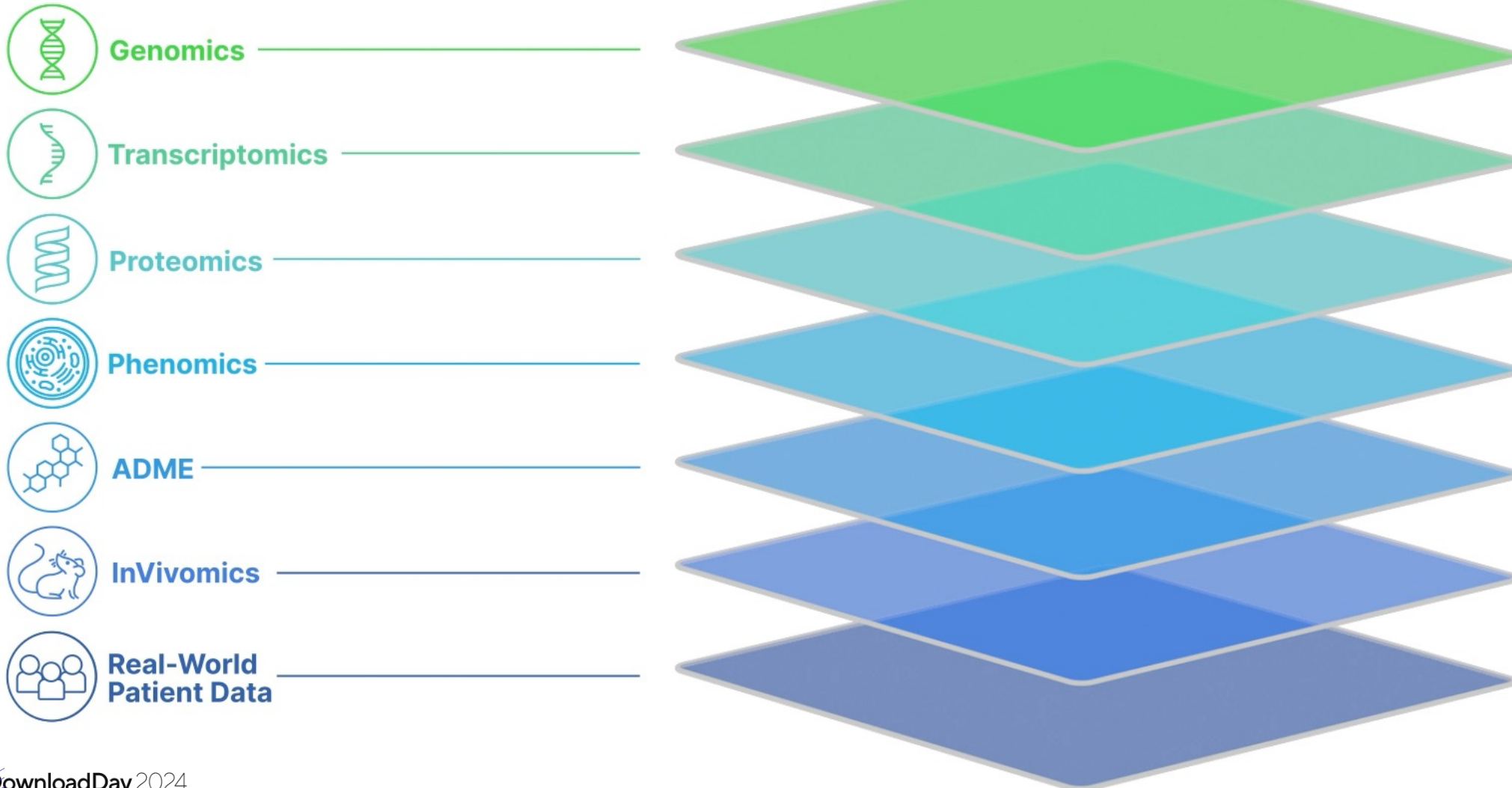


*Currently being explored

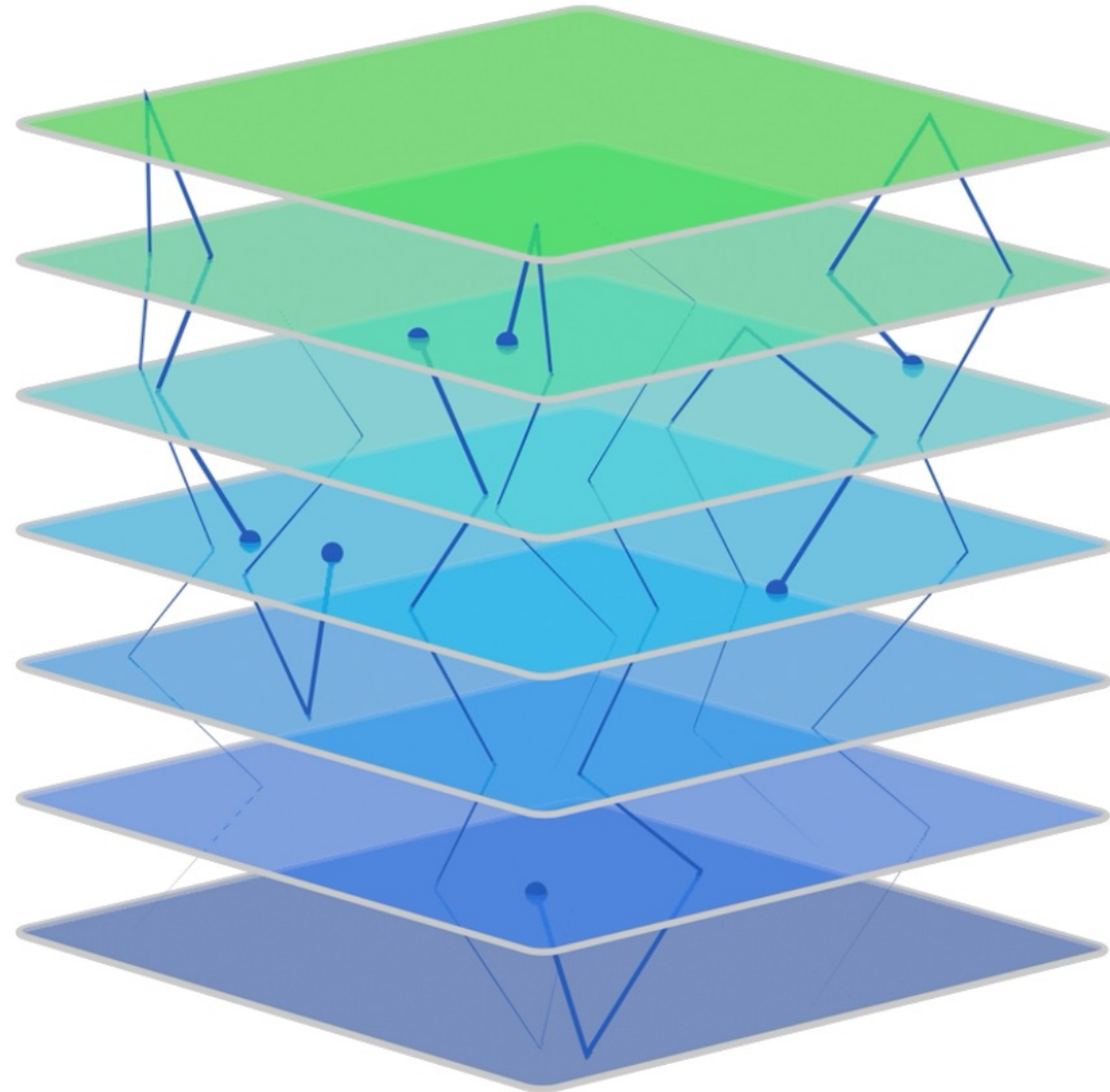
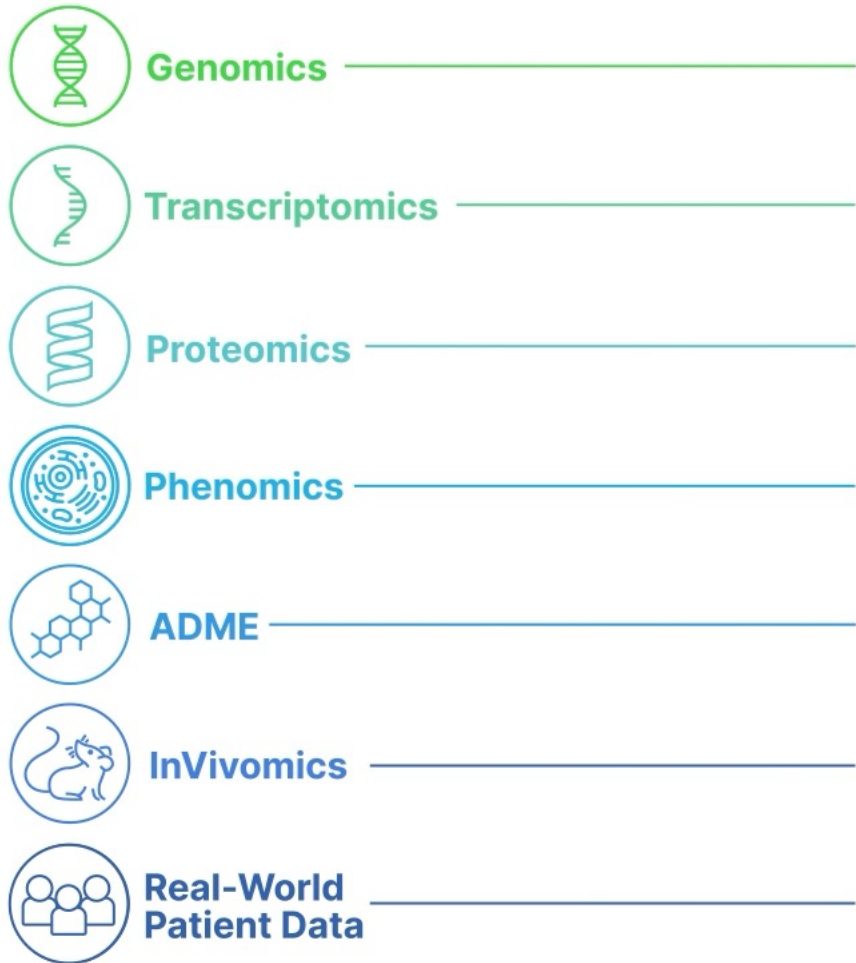


LOWE

Connecting data layers to build digital maps of biology



Connecting data layers to build digital maps of biology



Connecting data layers to build digital maps of biology



Genomics



Transcriptomics



Proteomics



Phenomics



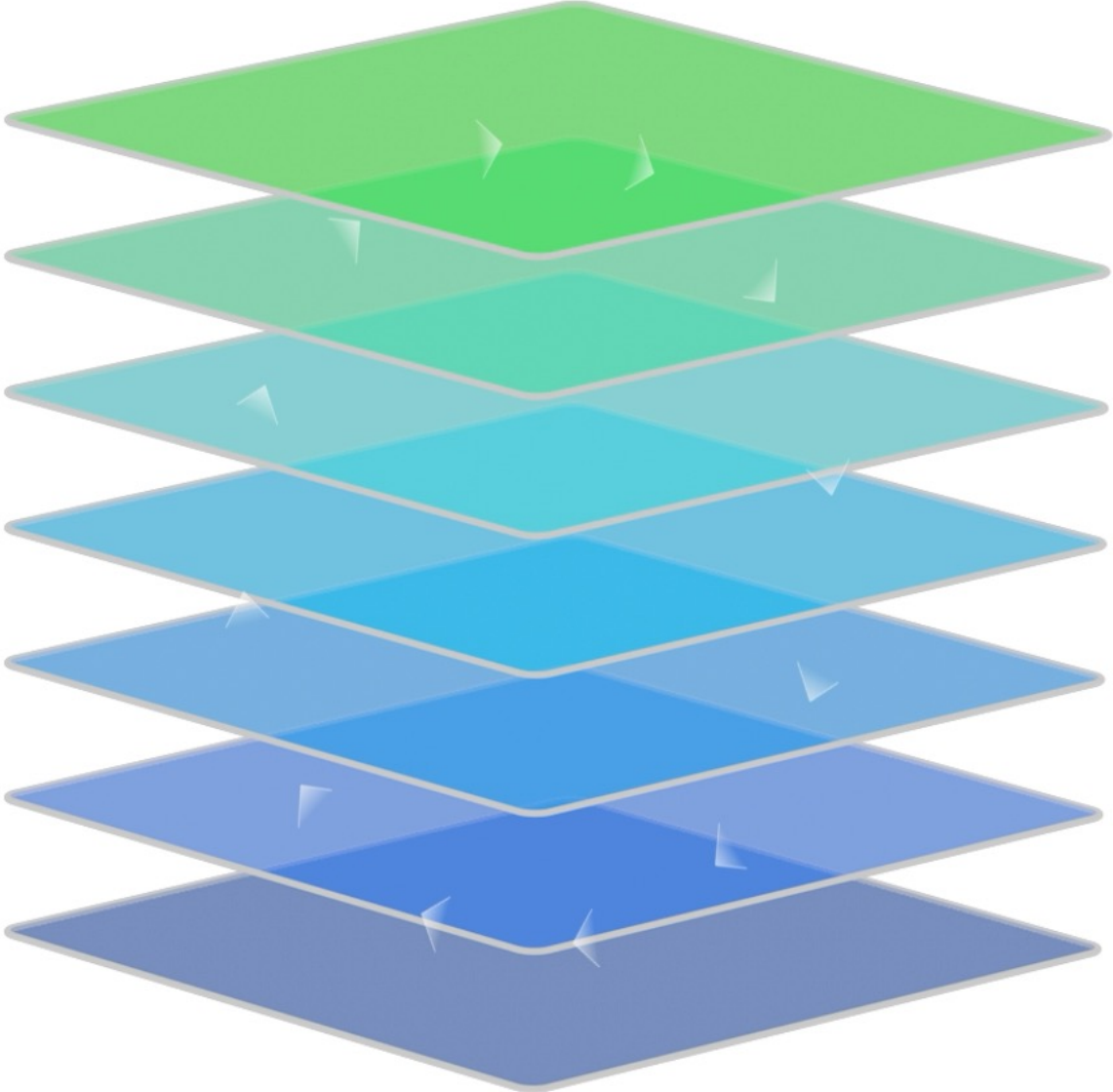
ADME



InVivomics



**Real-World
Patient Data**



Connecting data layers to build digital maps of biology



Genomics



Transcriptomics



Proteomics



Phenomics



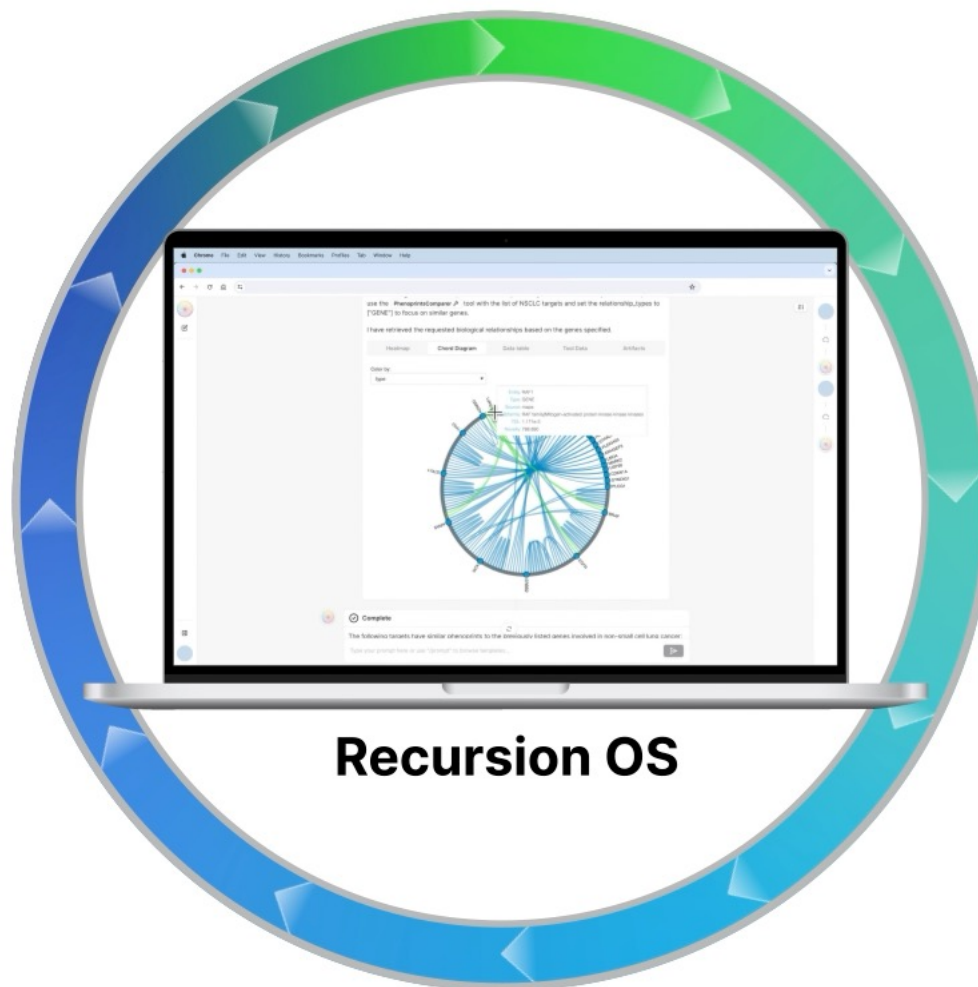
ADME



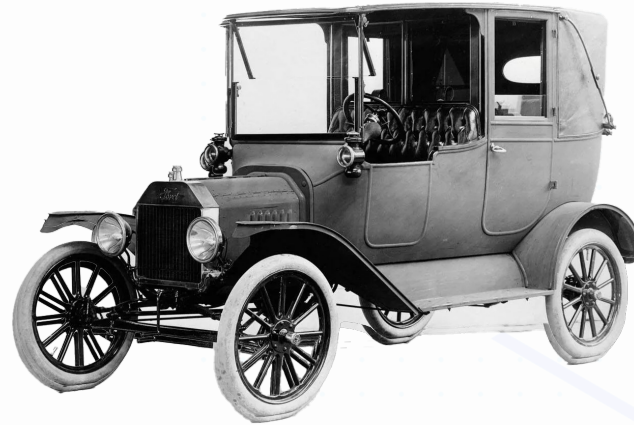
InVivomics



**Real-World
Patient Data**



Where are we right now?



What have we learned?

Fit for Purpose **Data** is Critical and the primary bottleneck

More **Compute** is needed and few are investing at our scale

More data and compute enables more generalizable **Models**

Industrializing stages of our drug discovery efforts leads to massive efficiency improvements



2022

Pre-Industrialization



2023

Post-Industrialization



Half of 2024

Continued Improvement

Team of **40** people



Team of **7** people



~1 FTE equivalent

30 program hypotheses explored



115 program hypotheses explored



201 program hypotheses *initiated*

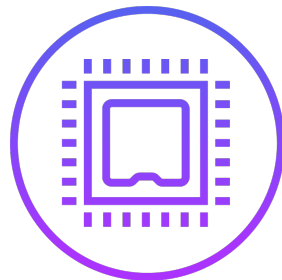
Four ingredients needed to continue leading TechBio at the tipping point



People



Data



Compute



Capital

Four ingredients needed to continue leading TechBio in an industry at the tipping point



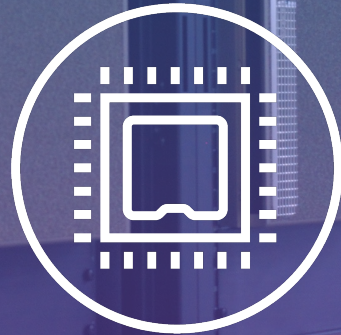
People

Four ingredients needed to continue leading TechBio in an industry at the tipping point



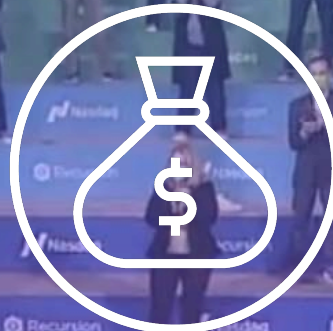
Data

Four ingredients needed to continue leading TechBio in an industry at the tipping point



Compute

Four ingredients needed to continue leading TechBio in an industry at the tipping point



Capital

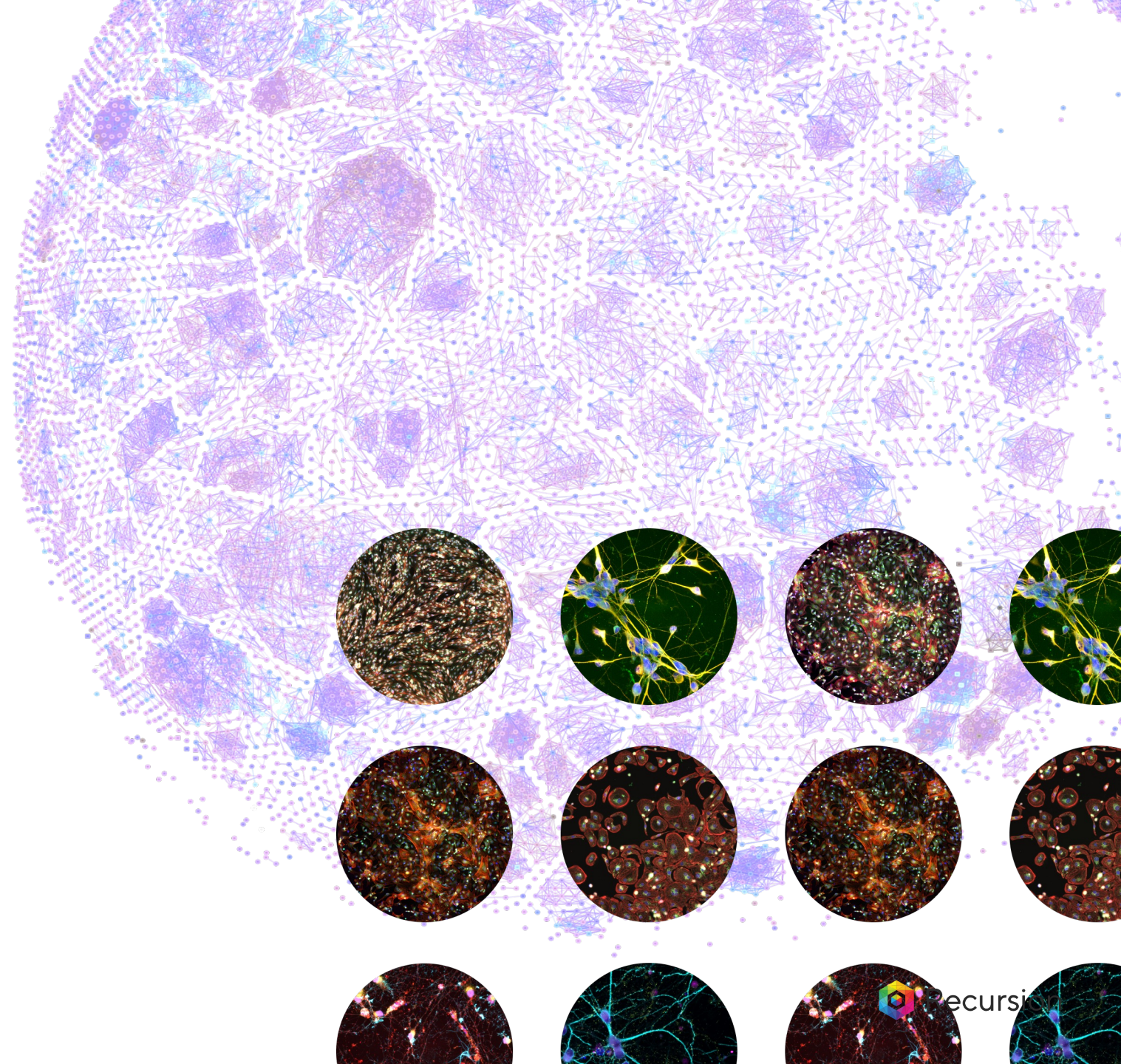


Our Purpose

We exist to run an experiment...

...An experiment to determine if there might be a better way to discover and develop drugs...

...We need this sort of ambition in BioTech if we hope to have a chance of transforming our ability to impact patients and drive down the cost of medicines.



What to Expect from Recursion in the Near Term

Pipeline

- 7 clinical trial readouts expect over the next ~18 months with new programs embracing our tools to drive novel chemistry against novel targets advancing quickly

Partnership

- Roche & Genentech: program optioned in oncology continues to progress with potential additional near-term program & very near-term map options
- Bayer: On track to complete 25 unique multi-modal data packages in Q3 2024 with first joint Project now advancing rapidly towards Lead Series nomination

Platform

- Internal programs now initiated by LLM with multiple hit nominations for LLM-generated programs with more on the way
- Moving towards large-scale multi-omics and generalizable foundation models with first genome-scale transcriptomics map and patient data
- Data and tools available to biopharma and commercial users: Bayer will be 1st beta-user of LOWE for drug discovery and development

The Recursion Operating System

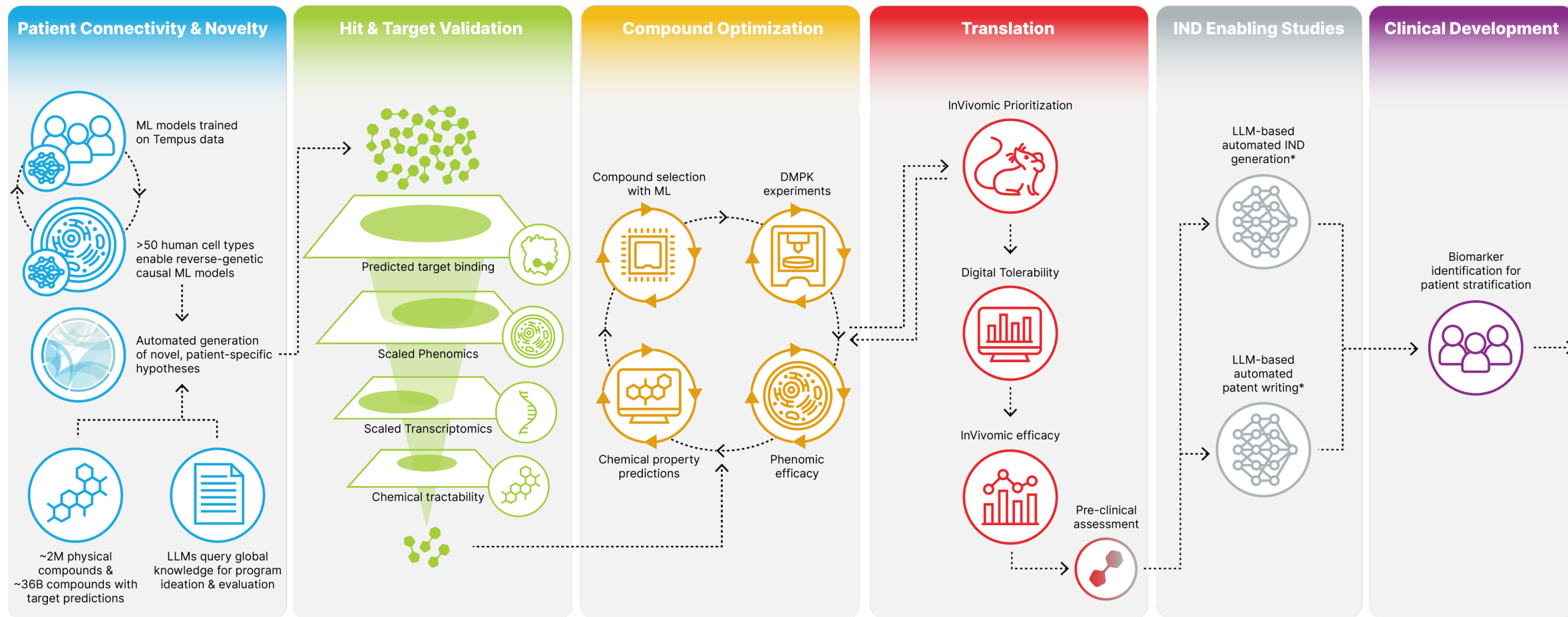


Wet Lab

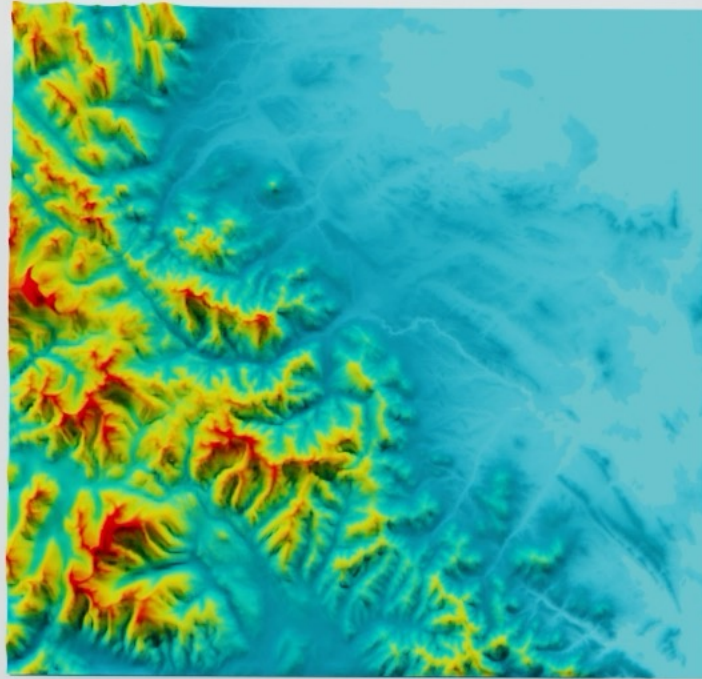


Dry Lab

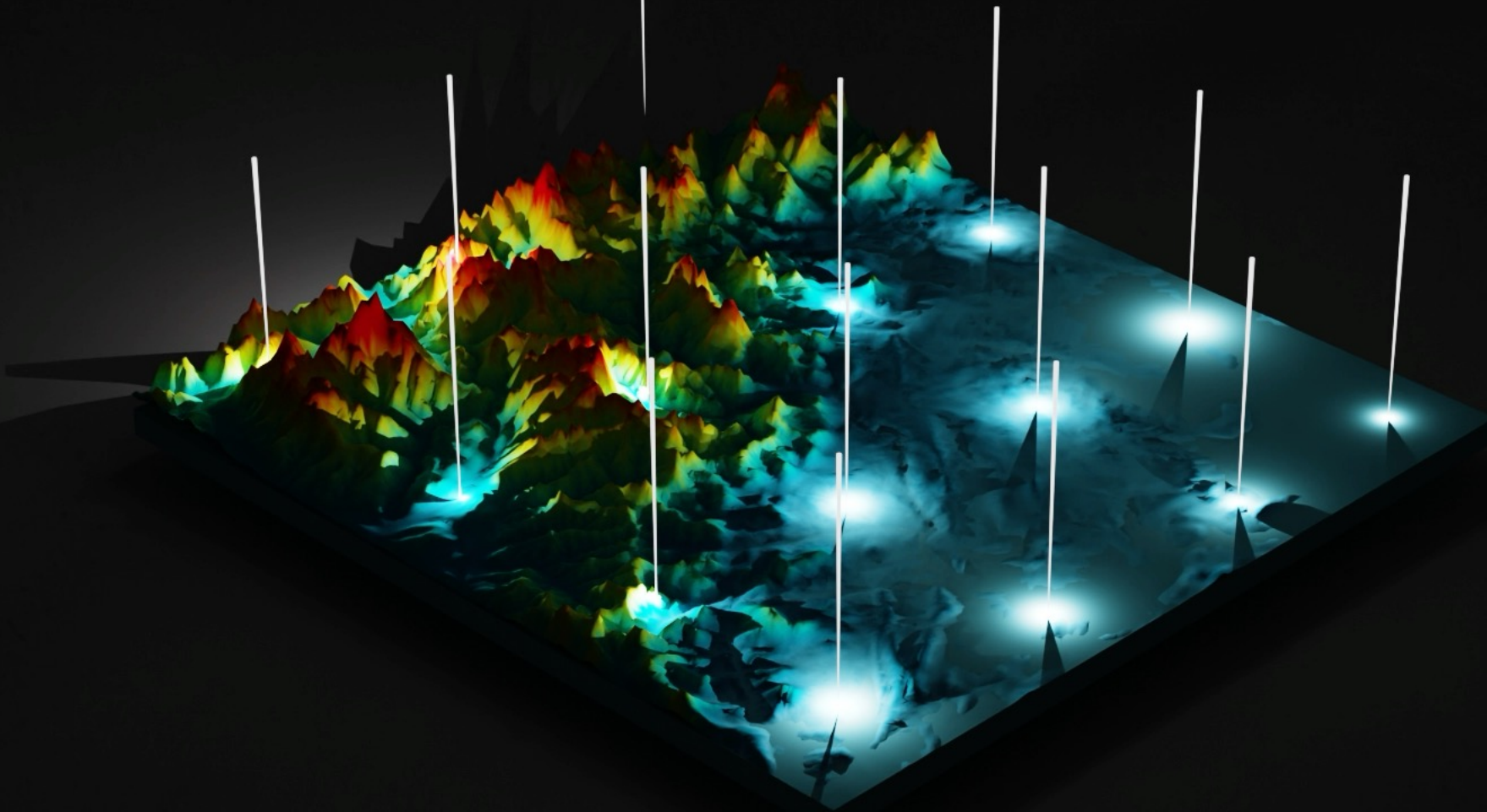
Virtuous Cycles Connect Systems for Efficient End-to-End Drug Discovery



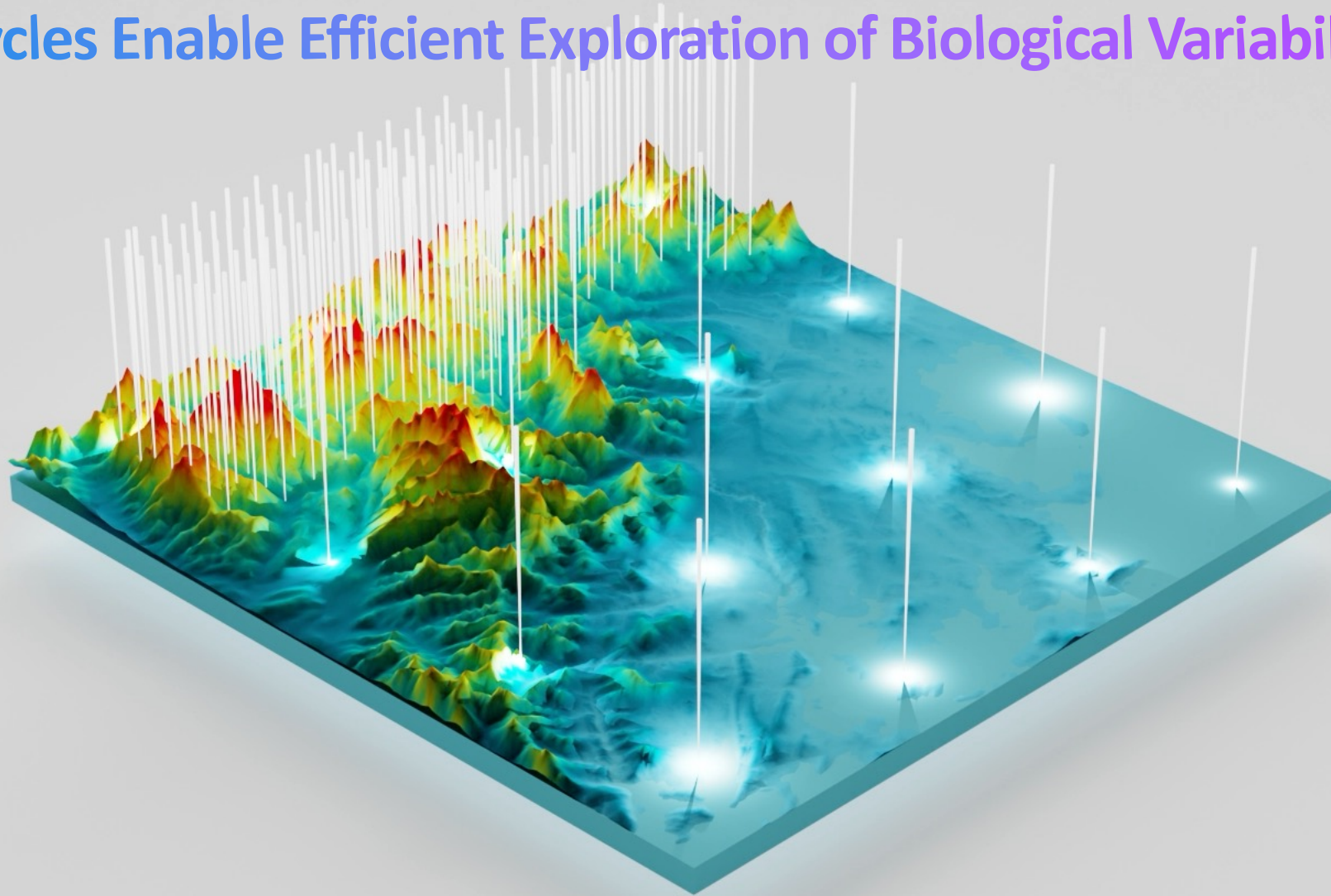
Virtuous Cycles Enable Efficient Exploration of Biological Variability



Virtuous Cycles Enable Efficient Exploration of Biological Variability

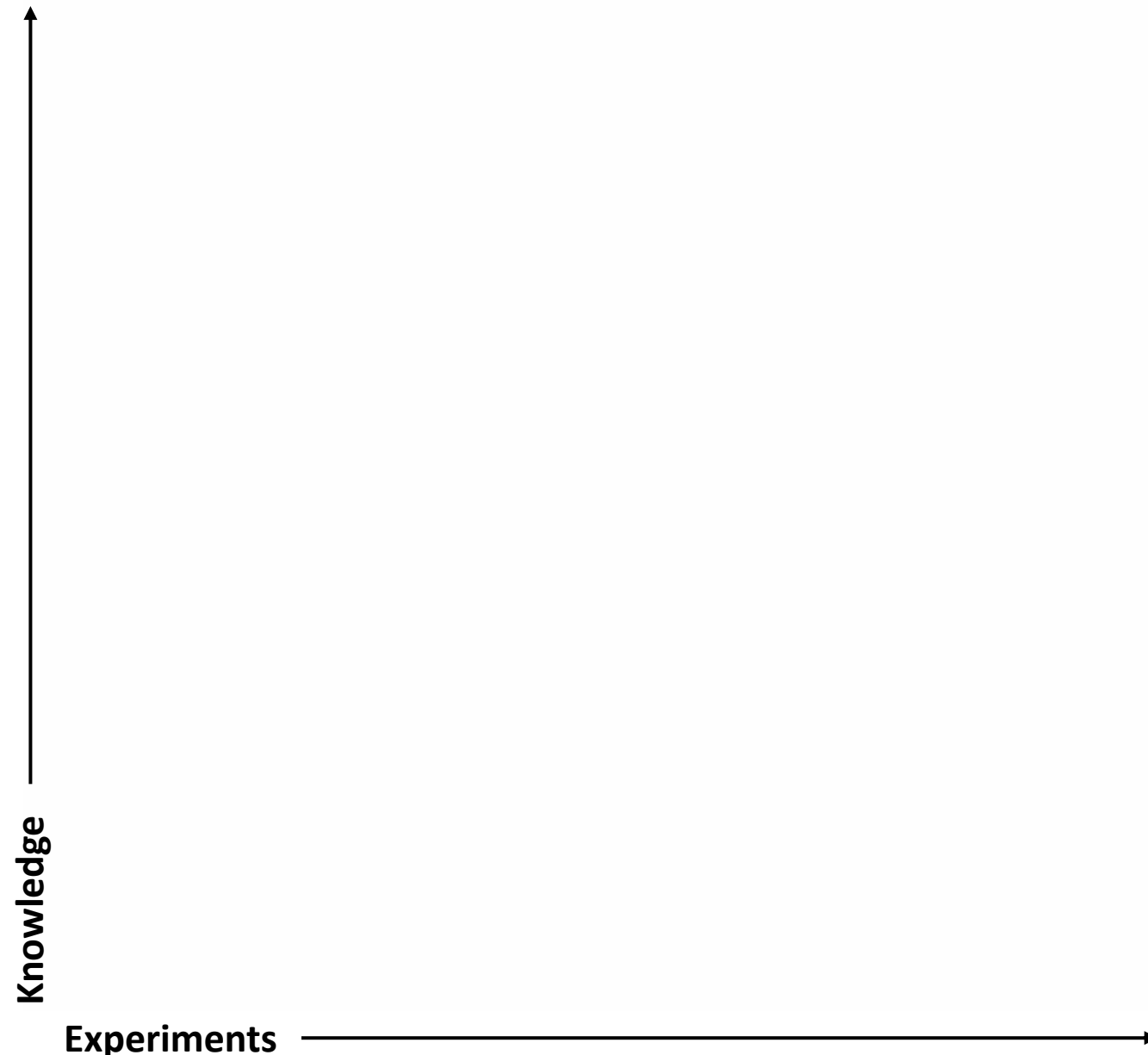


Virtuous Cycles Enable Efficient Exploration of Biological Variability

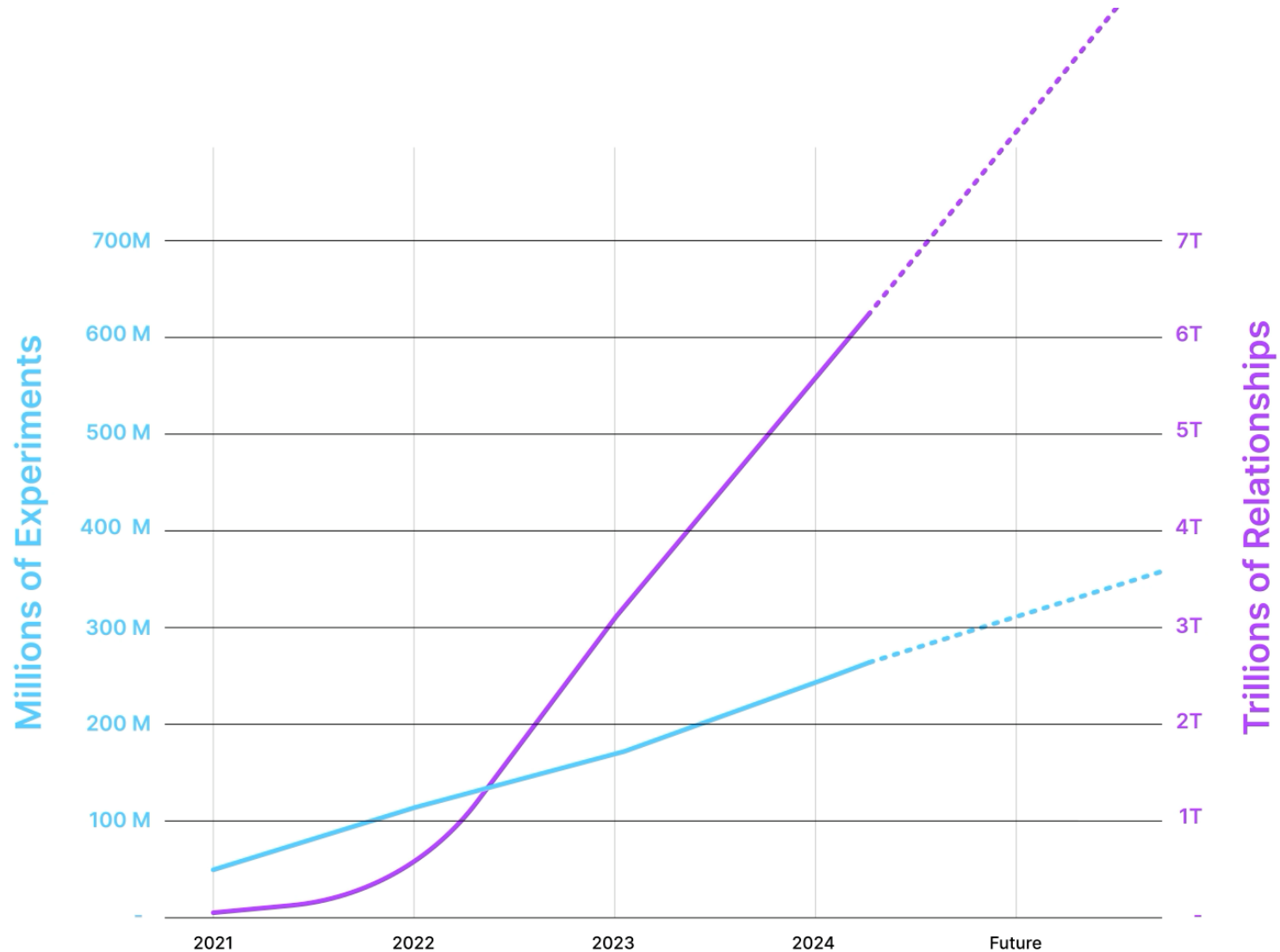


AI Strategy Experiments

Randomized Experiments



Virtuous Cycles Drive Superlinear Knowledge Creation





Data generation

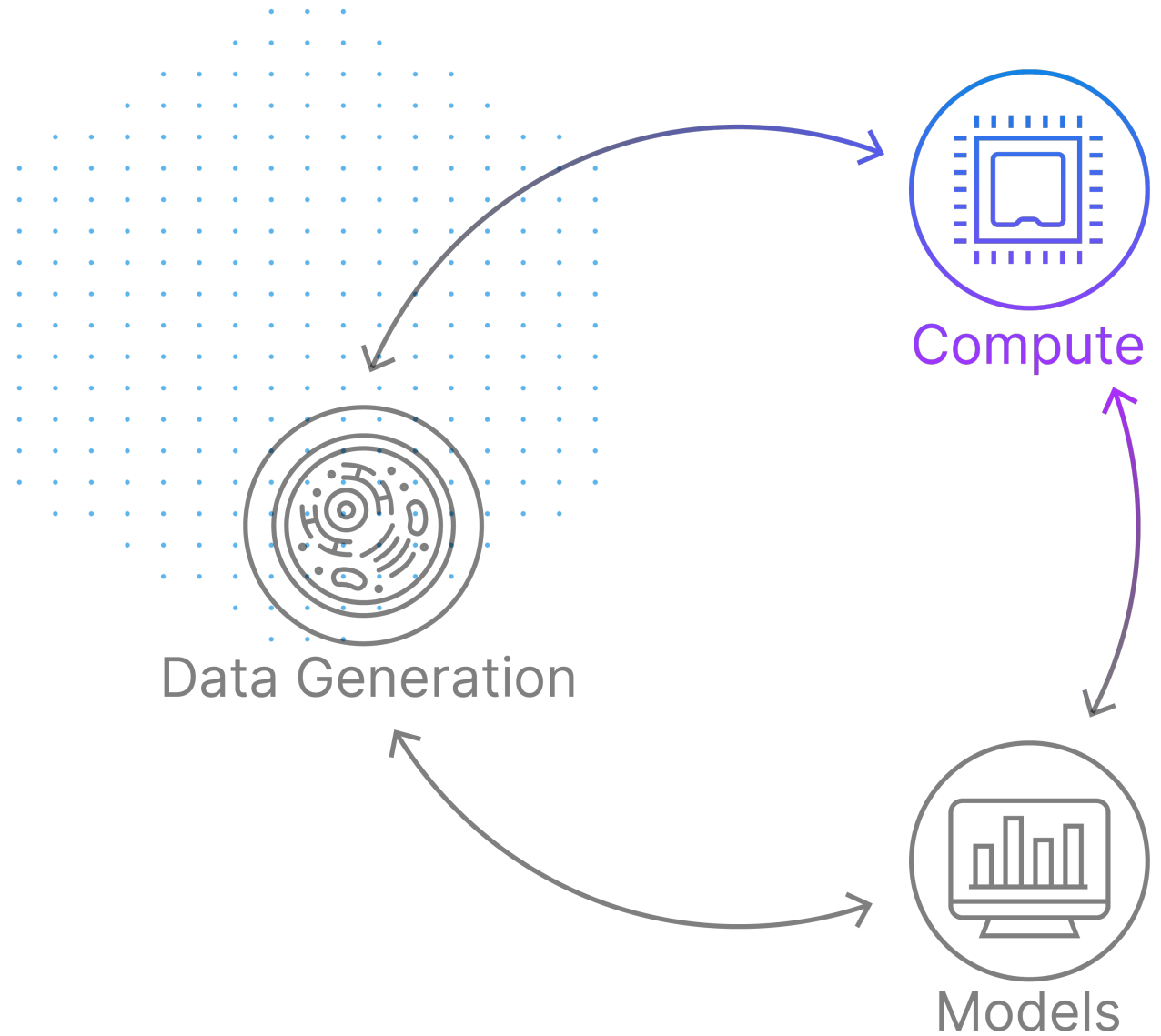


Compute



Models

Compute



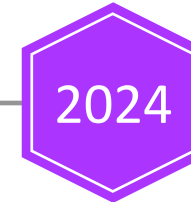
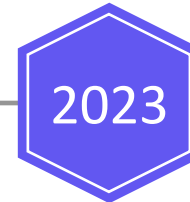
Ahead of the curve: our supercomputer journey

2020
Initial discussions began



BioHive-1:

- 320 NVIDIA A100's
- #84 on TOP500 list when built



BioHive-2:

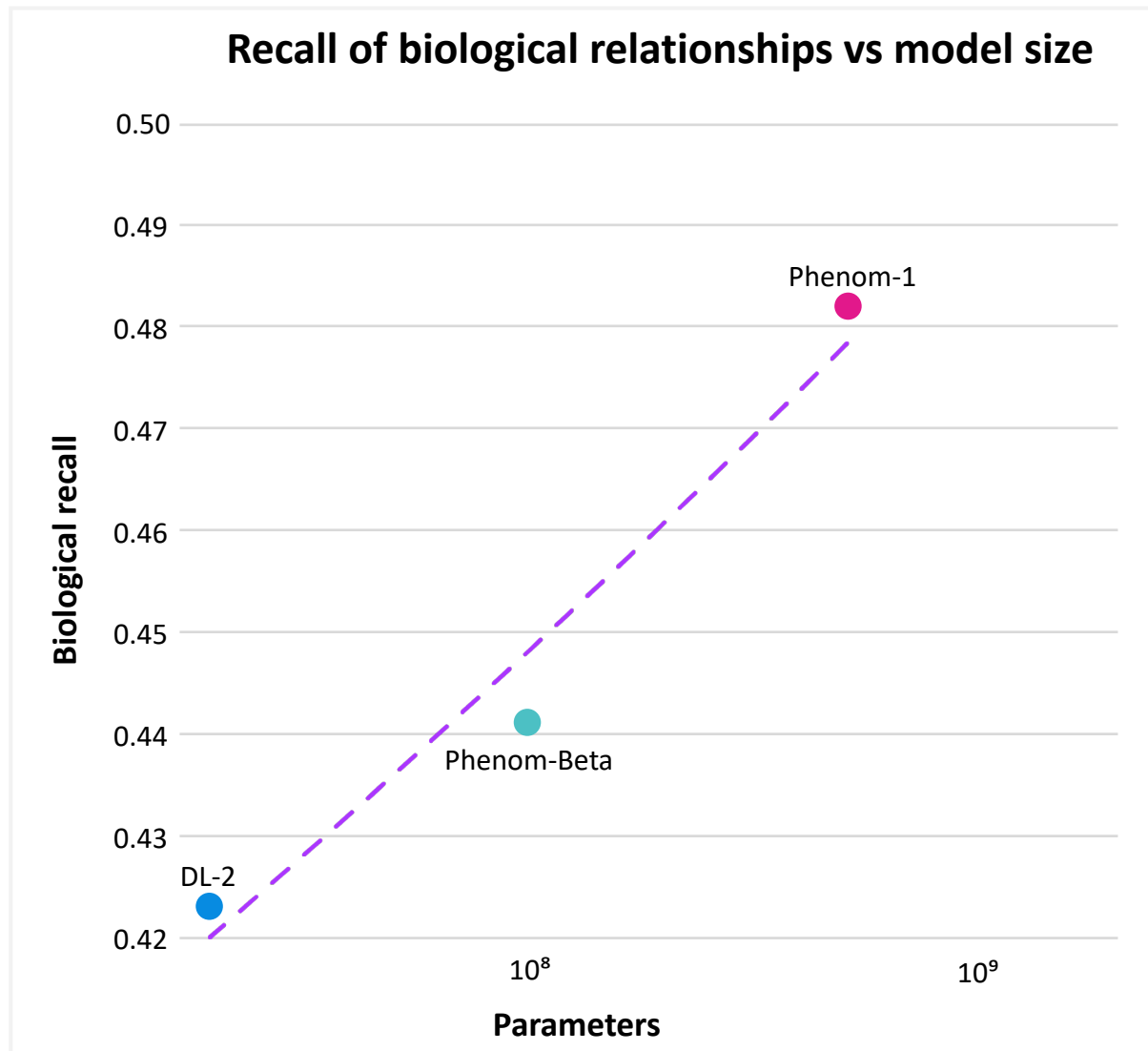
- 504 NVIDIA H100's, 4X BioHive-1
- Top ranked supercomputer in pharma
- #35 on TOP500 list



Nvidia invests \$50 million in biotech company Recursion for A.I. drug discovery



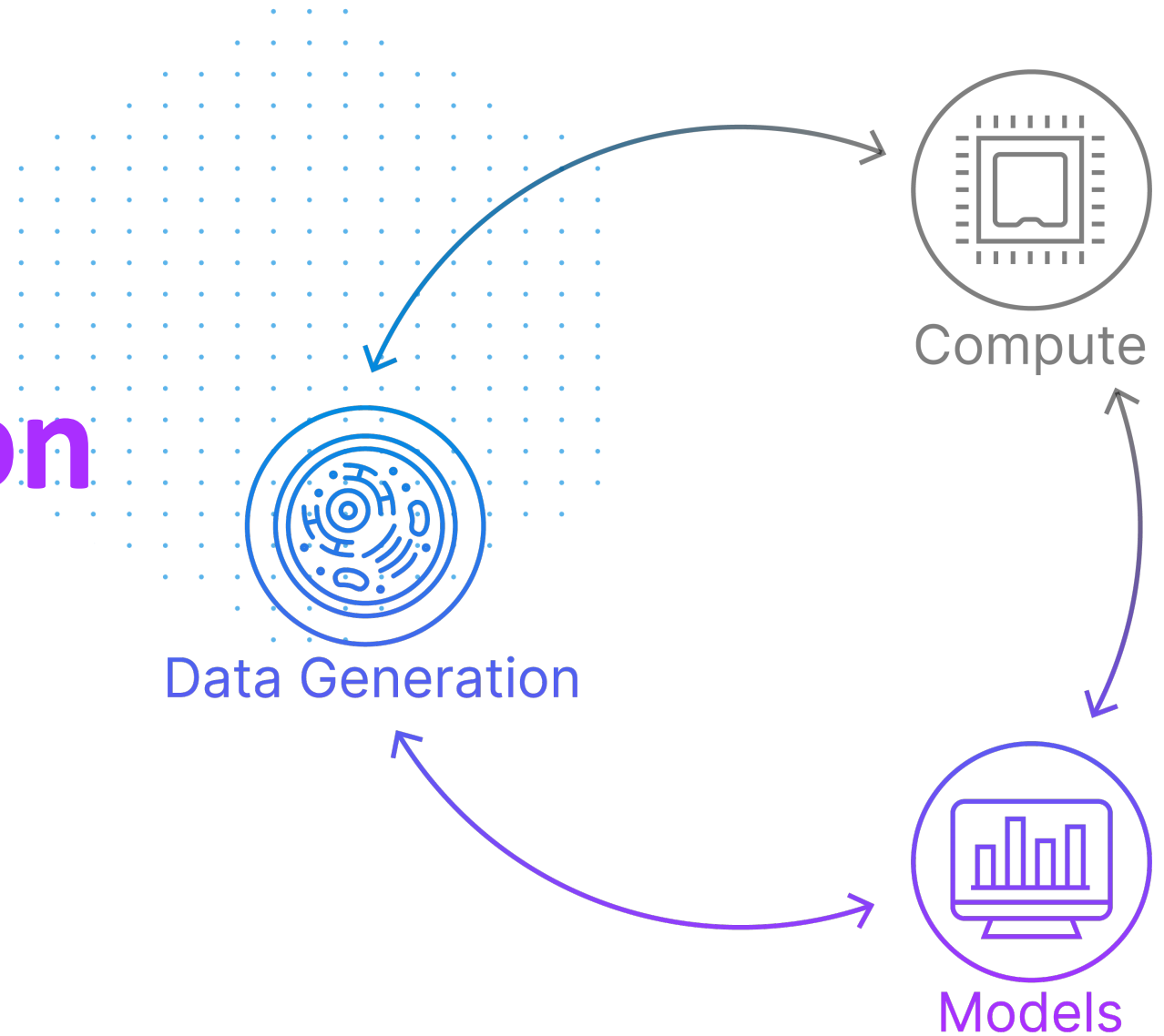
Larger datasets and Increased Computation Yield Superior Models



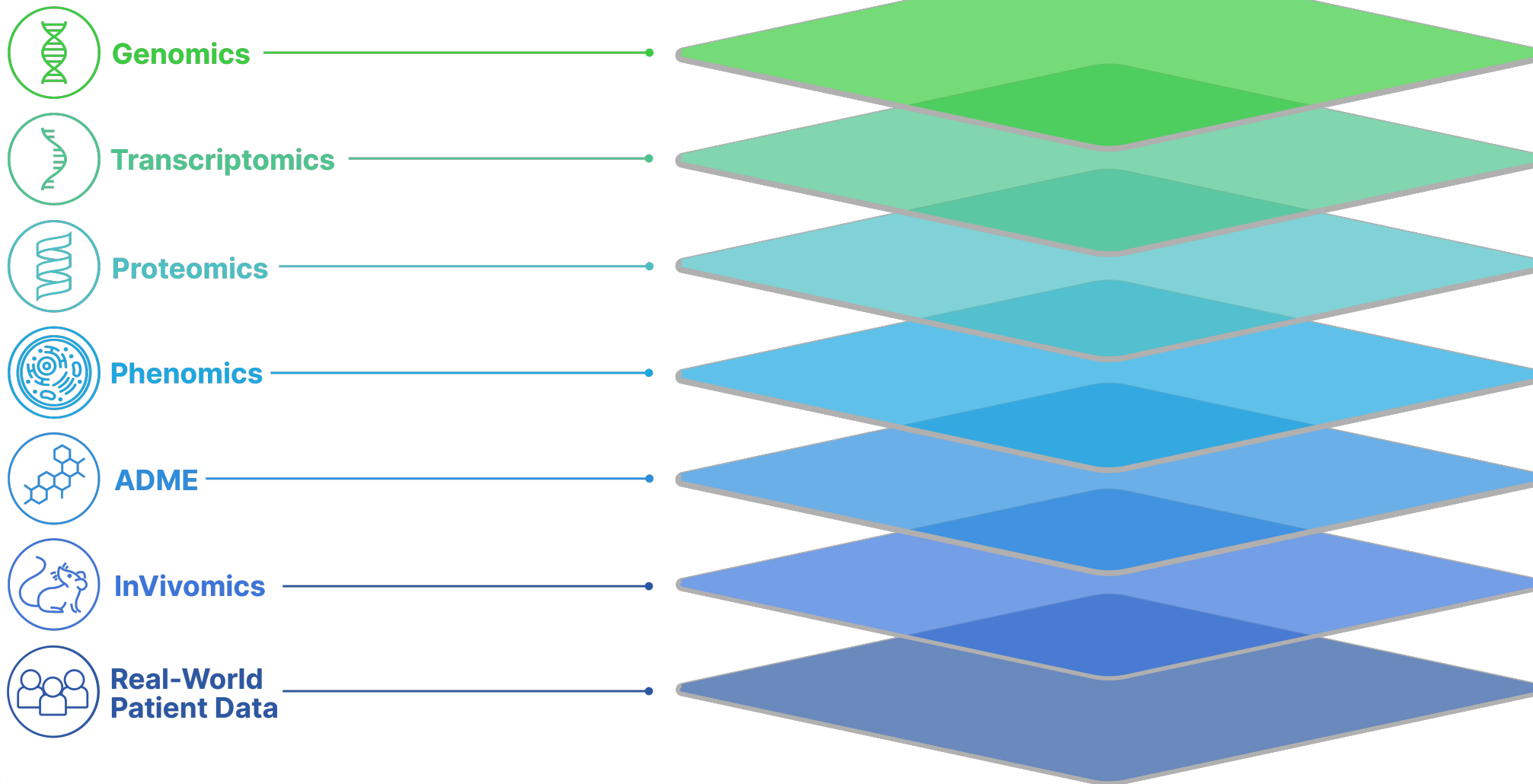
35th fastest supercomputer in the world!



Data Generation and Models



Standardizing and automating experiments to capture multiple layers of biology and chemistry





Phenomics: Foundation models improve at detecting biology

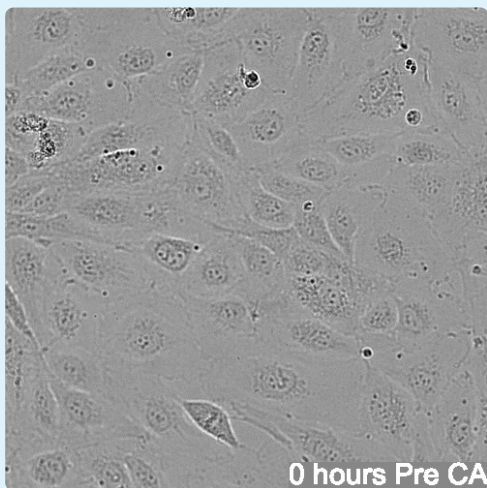
DATA GENERATION

>250 million experiments

>50 human cell types

>1 trillion neurons generated

Brightfield to capture dynamics



0 hours Pre CA

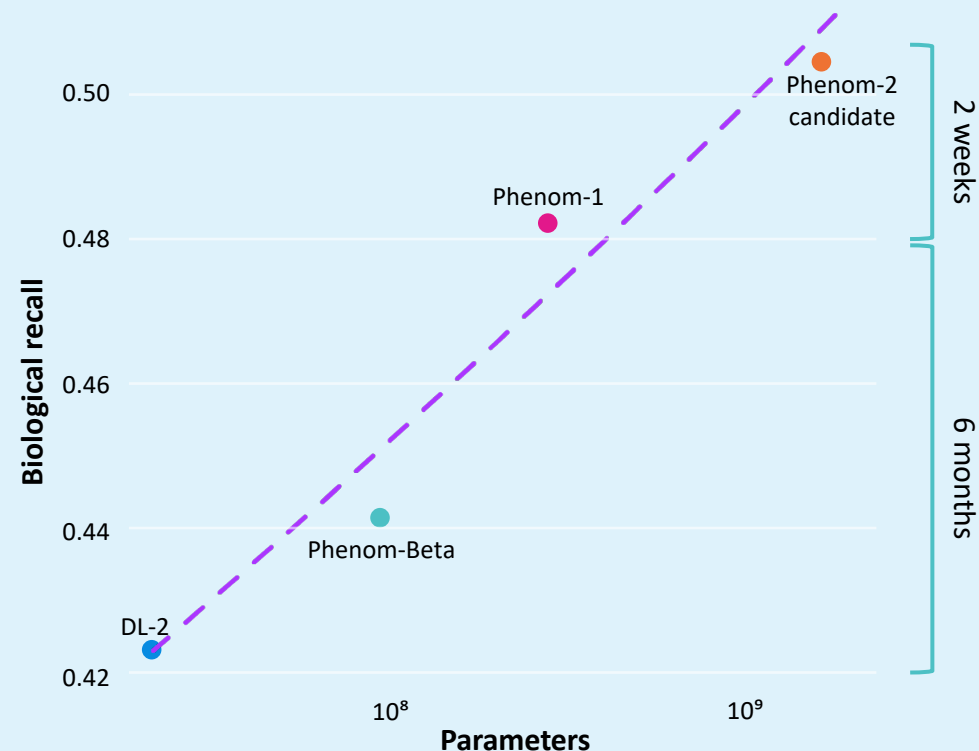
2 weeks of rapid iteration on Biohive-2 enabled

25.7%

increase in expressed gene knock-outs detected

MODELS

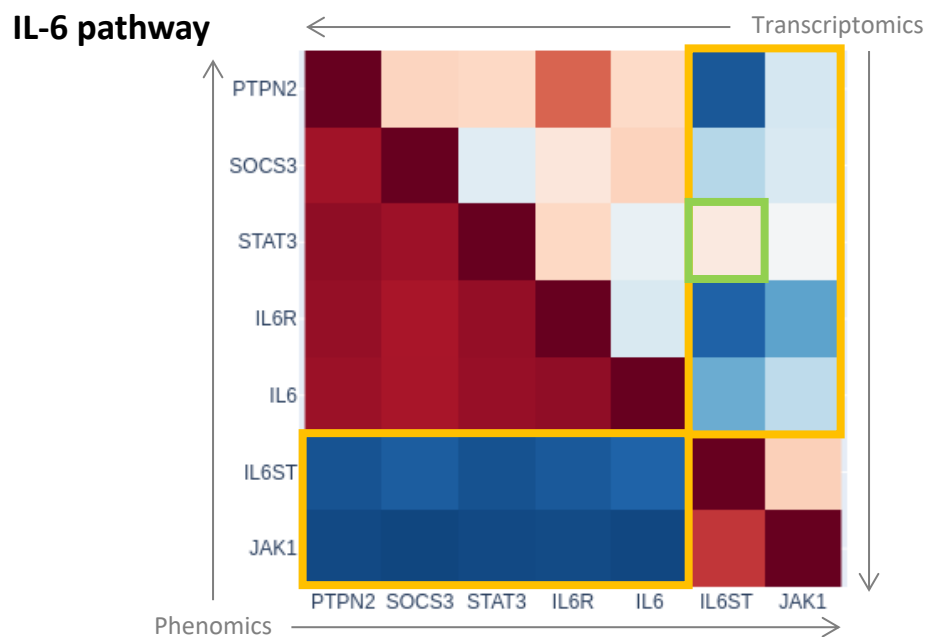
Recall of biological relationships vs model size



Transcriptomics: Multimodal data scales validation and mapping

DATA GENERATION

>1M samples sequenced
First genome-scale transcriptomic map



MODELS

Replaced time-consuming, disease-specific validation assays with portfolio-wide **multimodal model** workflow

90%

Ability to predict compounds that *failed* later disease-relevant assays in internal tests

60%

Ability to predict compounds that *passed* later disease-relevant assays in internal tests



ADME: Data and scale lead to State of the Art models

DATA GENERATION

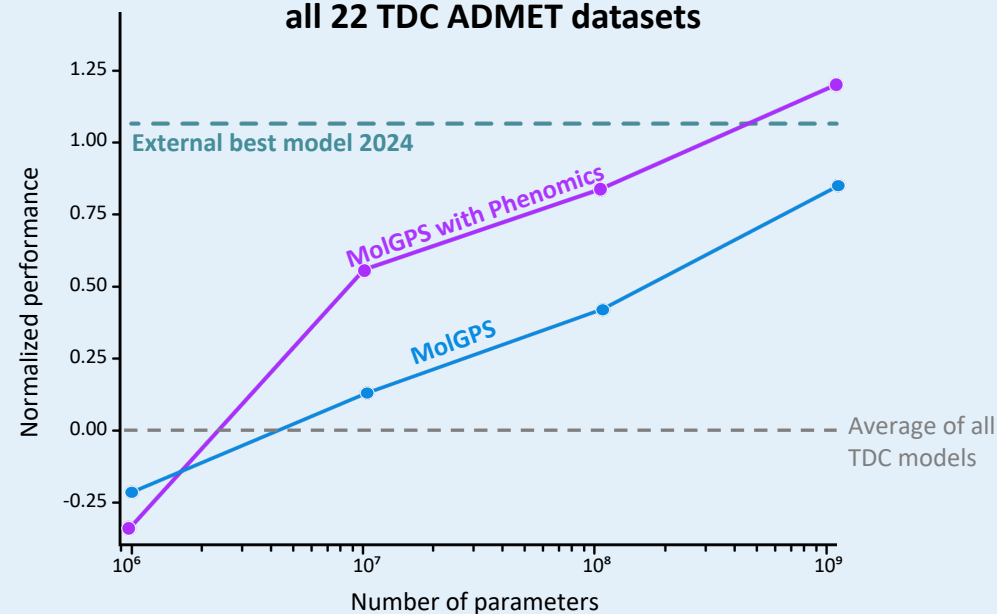
Estimated **90x** throughput over manual approach
>750 compounds per week



MODELS

Our single generalizable model improves with multimodal data and model size

Generalized performance over all 22 TDC ADMET datasets





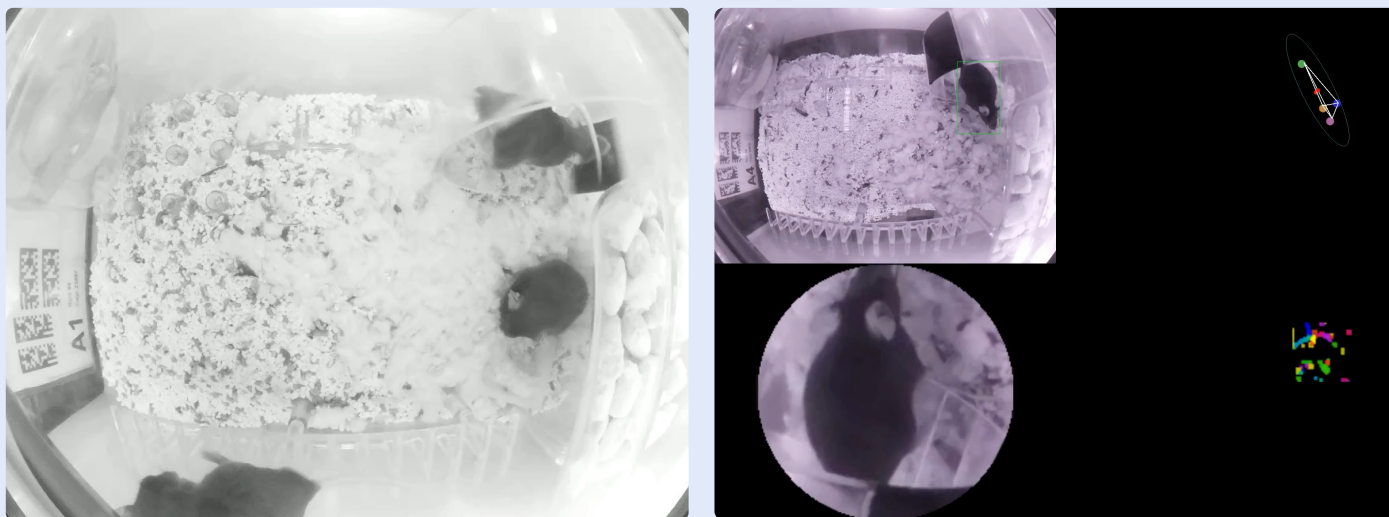
InVivomics accelerates decision-making in late discovery

DATA GENERATION

>1,000 digital mouse cages

150 digital rat cages in 2024

Social housing increases relevance



MODELS

- Machine learning enables scale by extracting signals from video and temperature sensors
- Applied across breadth of Recursion portfolio
- Designed to select the right molecule at the right dose before entering studies

Patient Data: Path to uncover novel disease drivers with Maps

DATA GENERATION

"TEMPUS

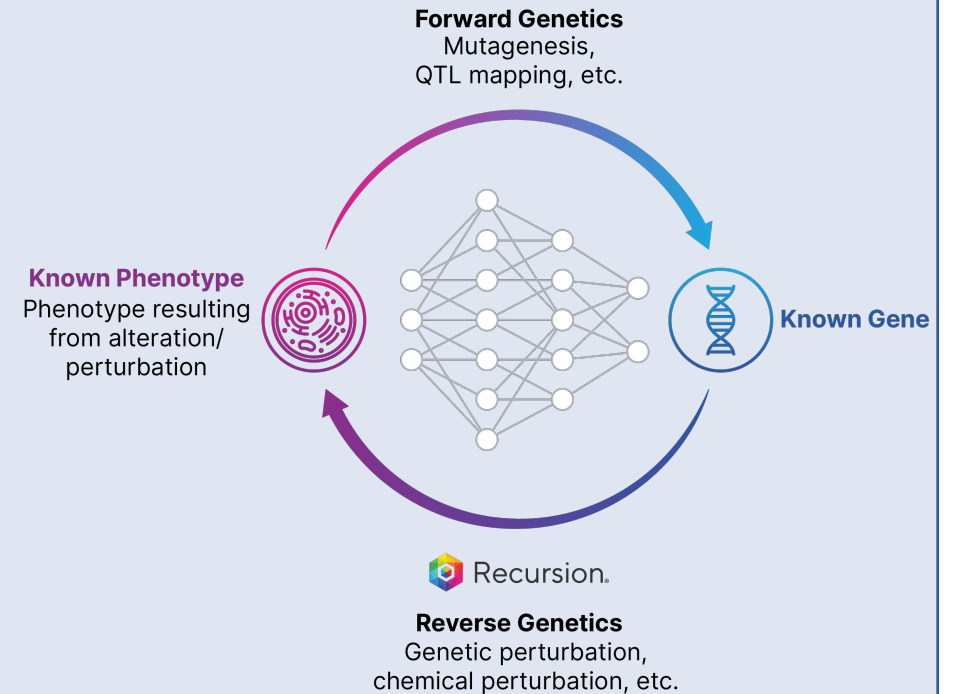
>20 PB of real-world multi-modal oncology data

Hundreds of thousands of unique de-identified patient records across diverse therapeutic areas

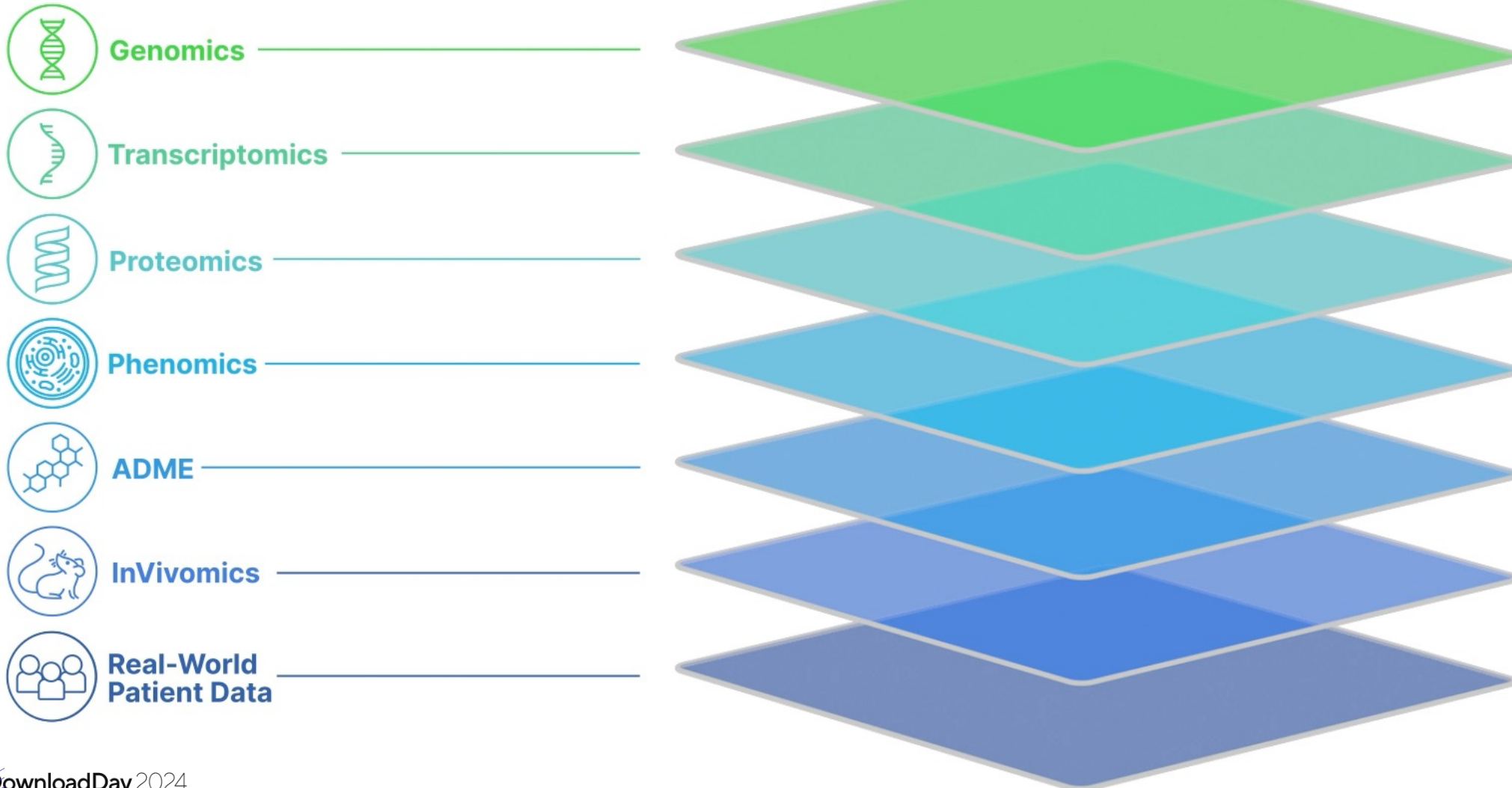


MODELS

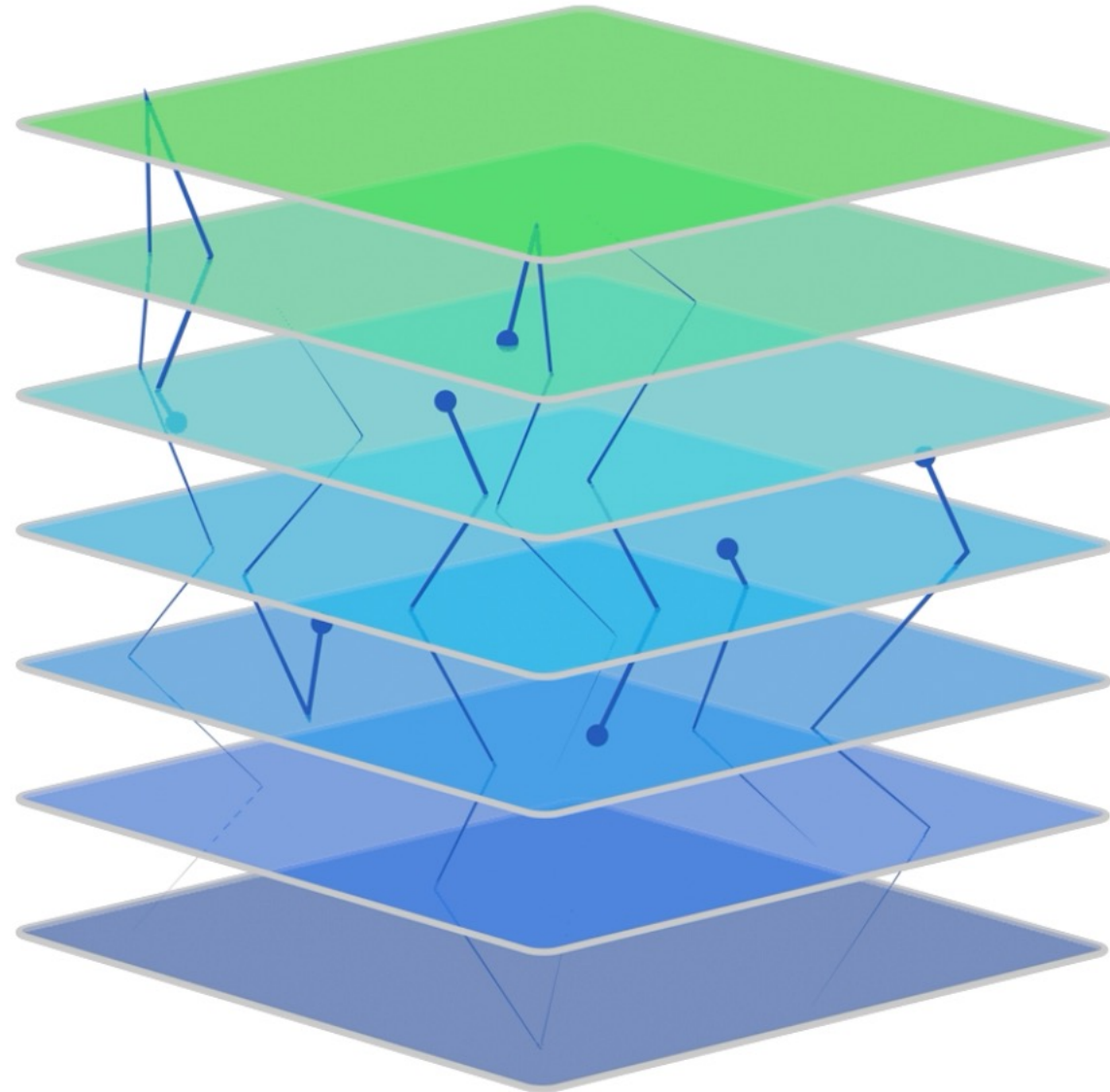
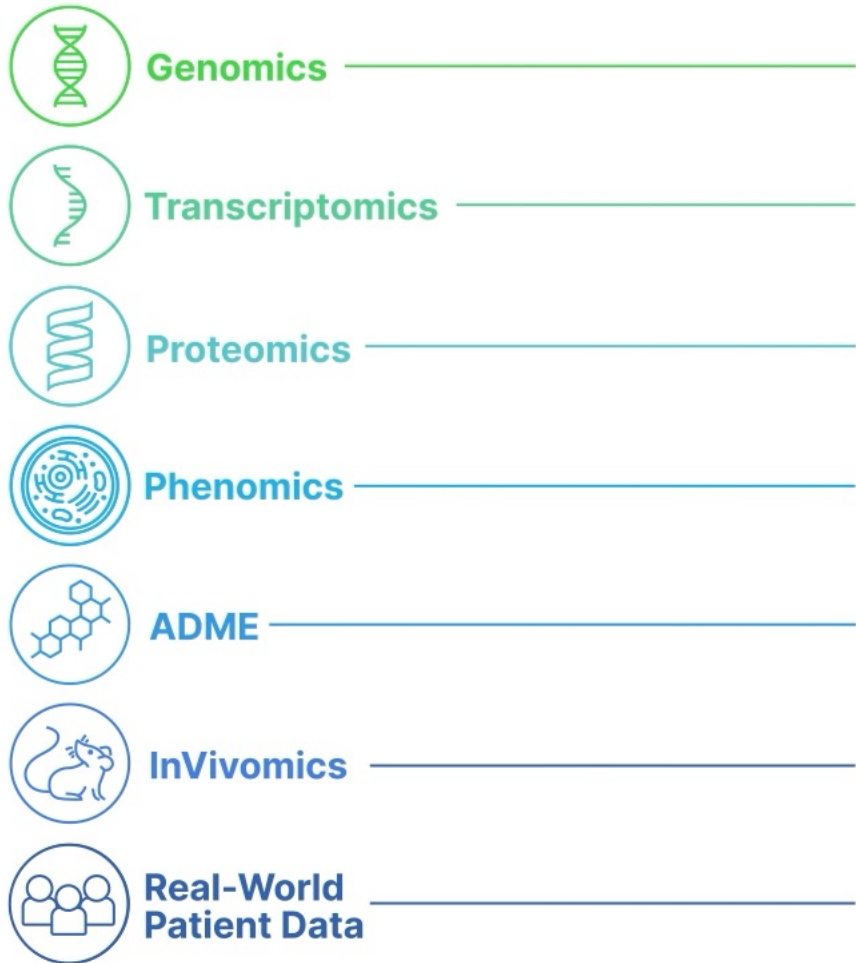
Combining Recursion maps of biology with patient clinical data unlocks causal modeling to find novel targets










Connecting data layers to build digital maps of biology

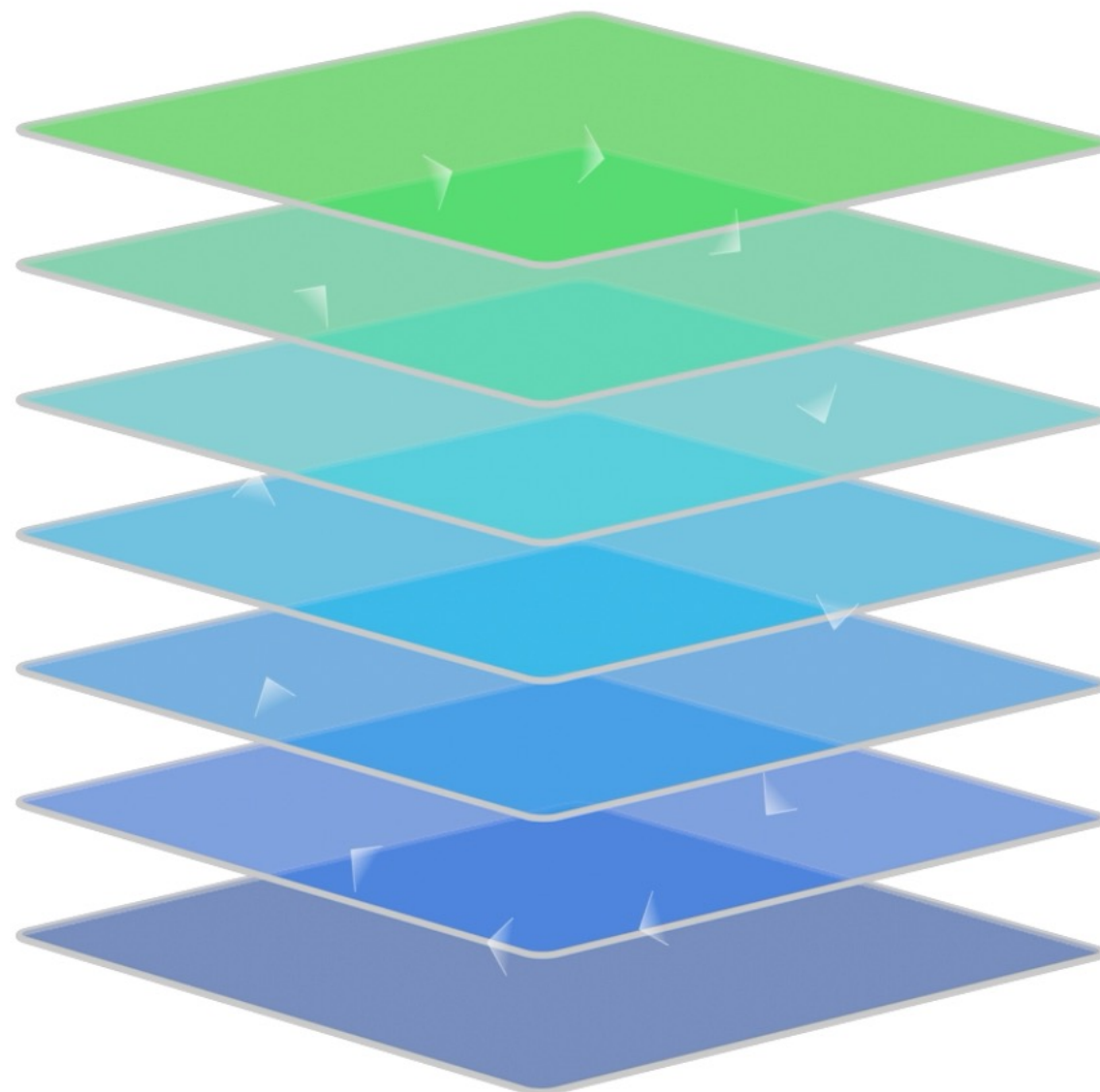


Connecting data layers to build digital maps of biology



Connecting data layers to build digital maps of biology

-  **Genomics**
-  **Transcriptomics**
-  **Proteomics**
-  **Phenomics**
-  **ADME**
-  **InVivomics**
-  **Real-World Patient Data**



Connecting data layers to build digital maps of biology



Genomics



Transcriptomics



Proteomics



Phenomics



ADME



InVivomics

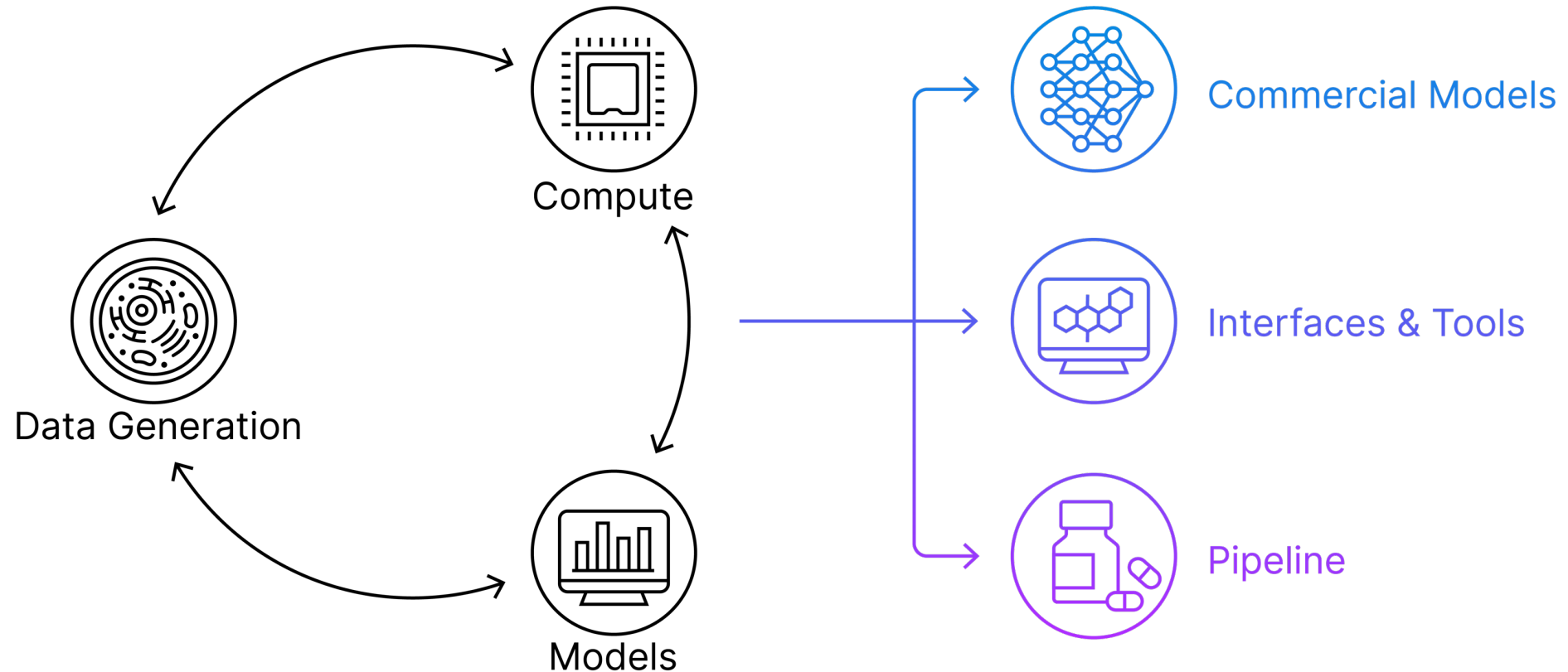


**Real-World
Patient Data**



Utility of the OS

The Recursion OS: Utility across multiple potential product verticals





Commercial Models: Capitalizing on our data and foundation models

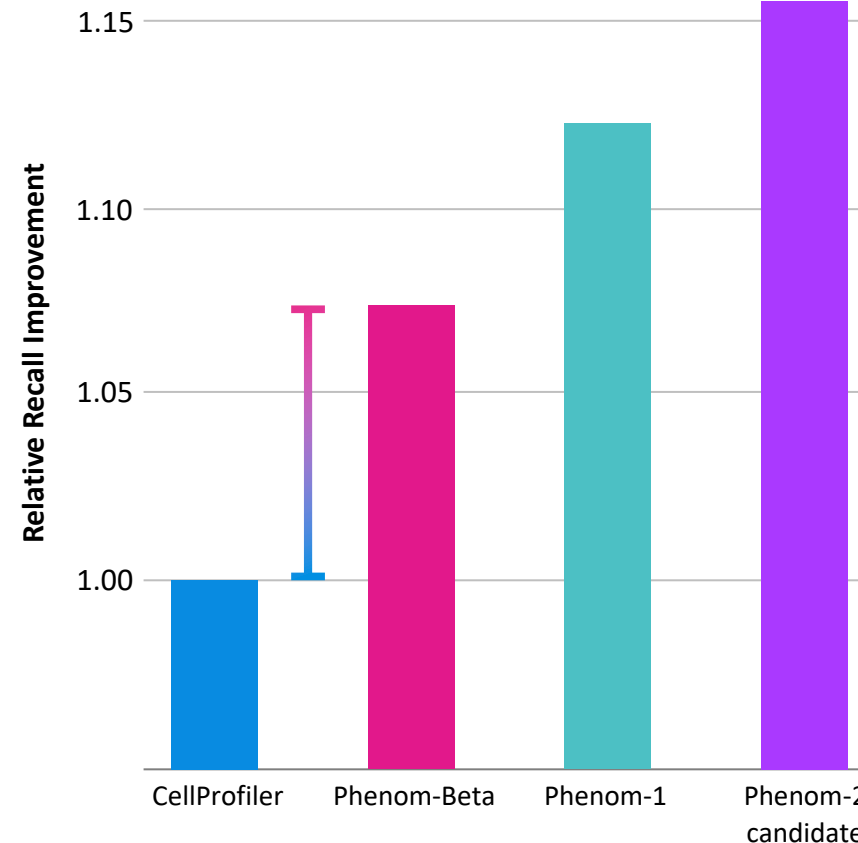
Phenomenal AI for Pharma: Recursion Brings Phenom-Beta Model to BioNeMo

Recursion is the first hosting partner offering an AI model through BioNeMo cloud APIs: Phenom-Beta, a vision transformer model that extracts biologically meaningful features from cellular microscopy images.

This capability can provide researchers with insights about cell function and help them learn how cells respond to drug candidates or genetic engineering.

Phenom-Beta performed well on image reconstruction tasks, a training metric to evaluate model performance. Read the [NeurIPS workshop paper](#) to learn more.

Phenom-Beta, available on NVIDIA BioNeMo, outperforms open-source "gold standard" CellProfiler





Interfaces and Tools: bringing together modules spanning the drug discovery process



Phenomics



Compound selection with ML



Patient-specific hypotheses



Phenom-1



Chemical tractability



InVivomic prioritization



LLMs & literature search



InVivomic efficacy



Chemical property predictions



Predicted target binding



Tempus data ML models



Phenomic efficacy



Patient stratification



Transcriptomics



MatchMaker



Digital tolerability



DMPK



Compound ordering



LOWE



The Future of TechBio

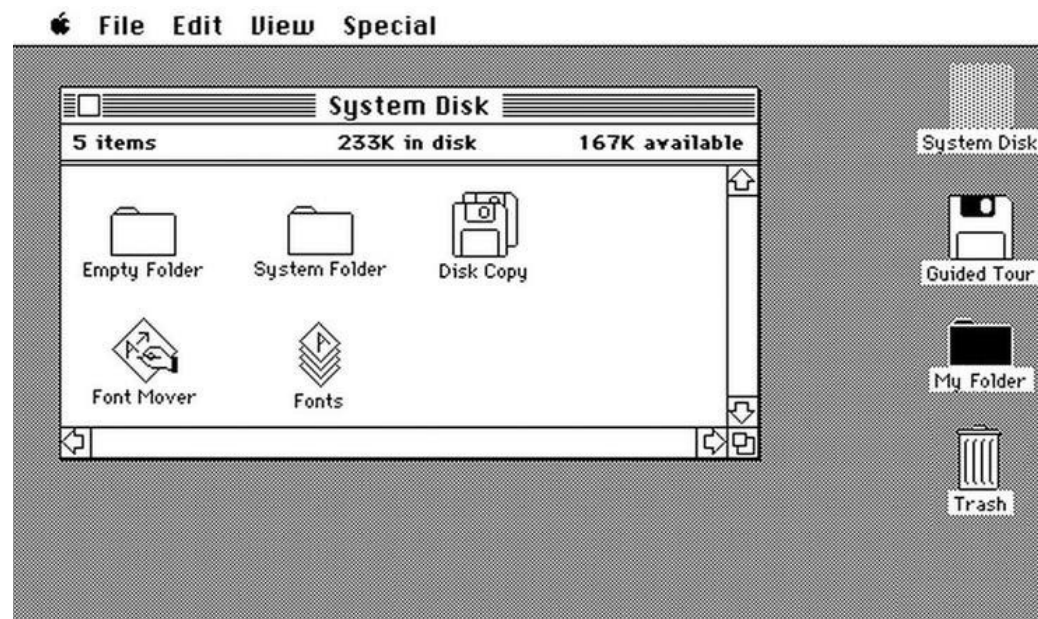
Turning drug discovery into a search problem





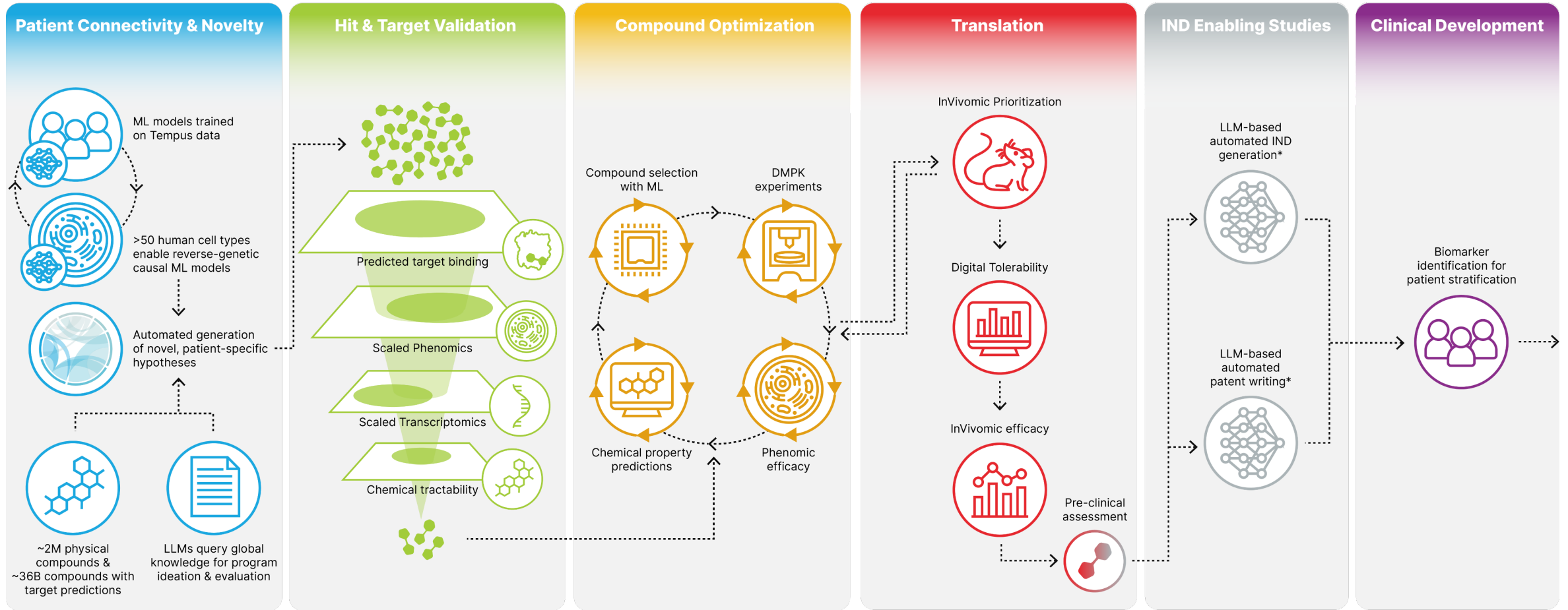
The Future of TechBio

Turning drug discovery into a search problem



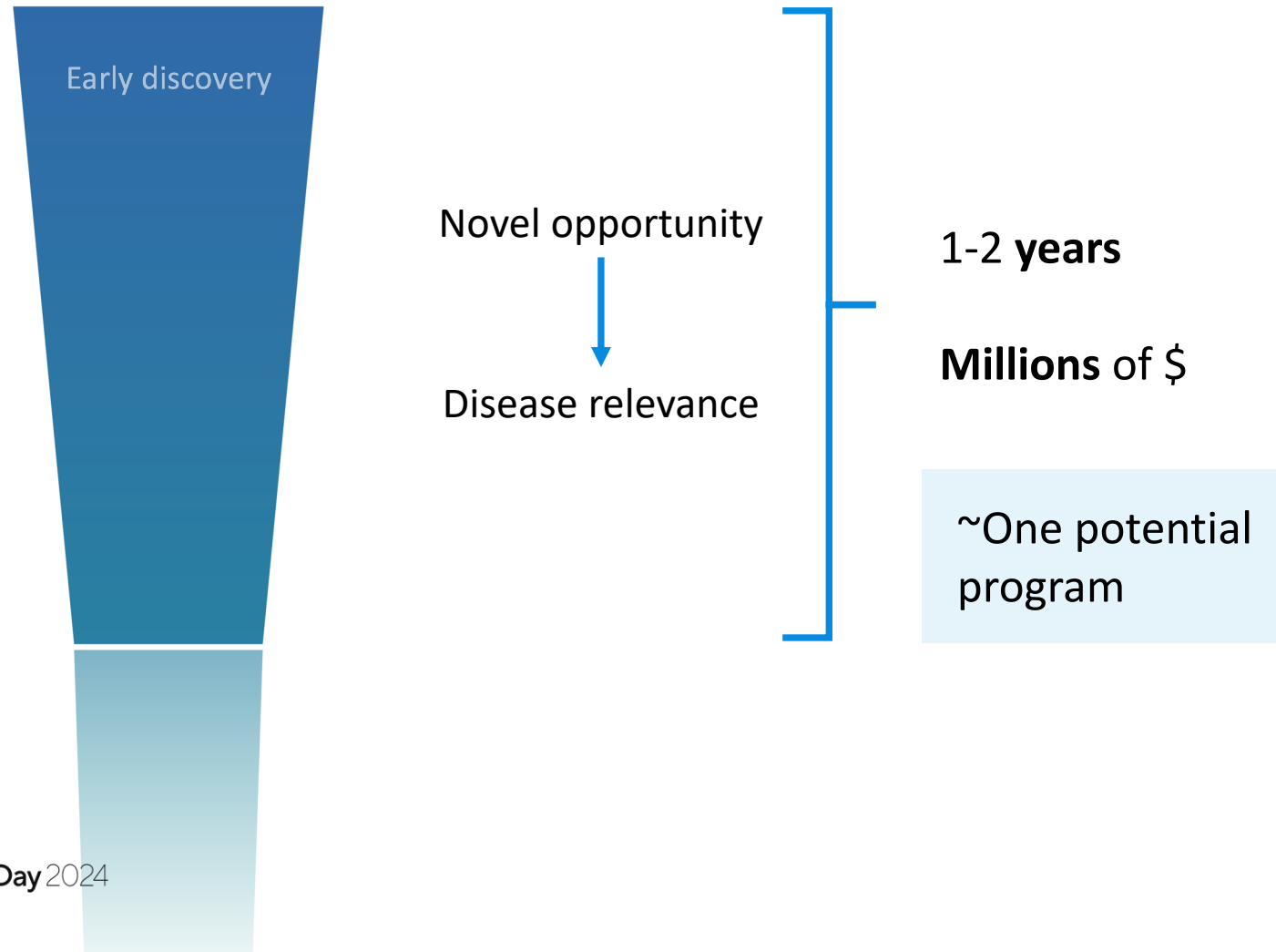


Pipeline: connecting systems into Industrialized Workflows

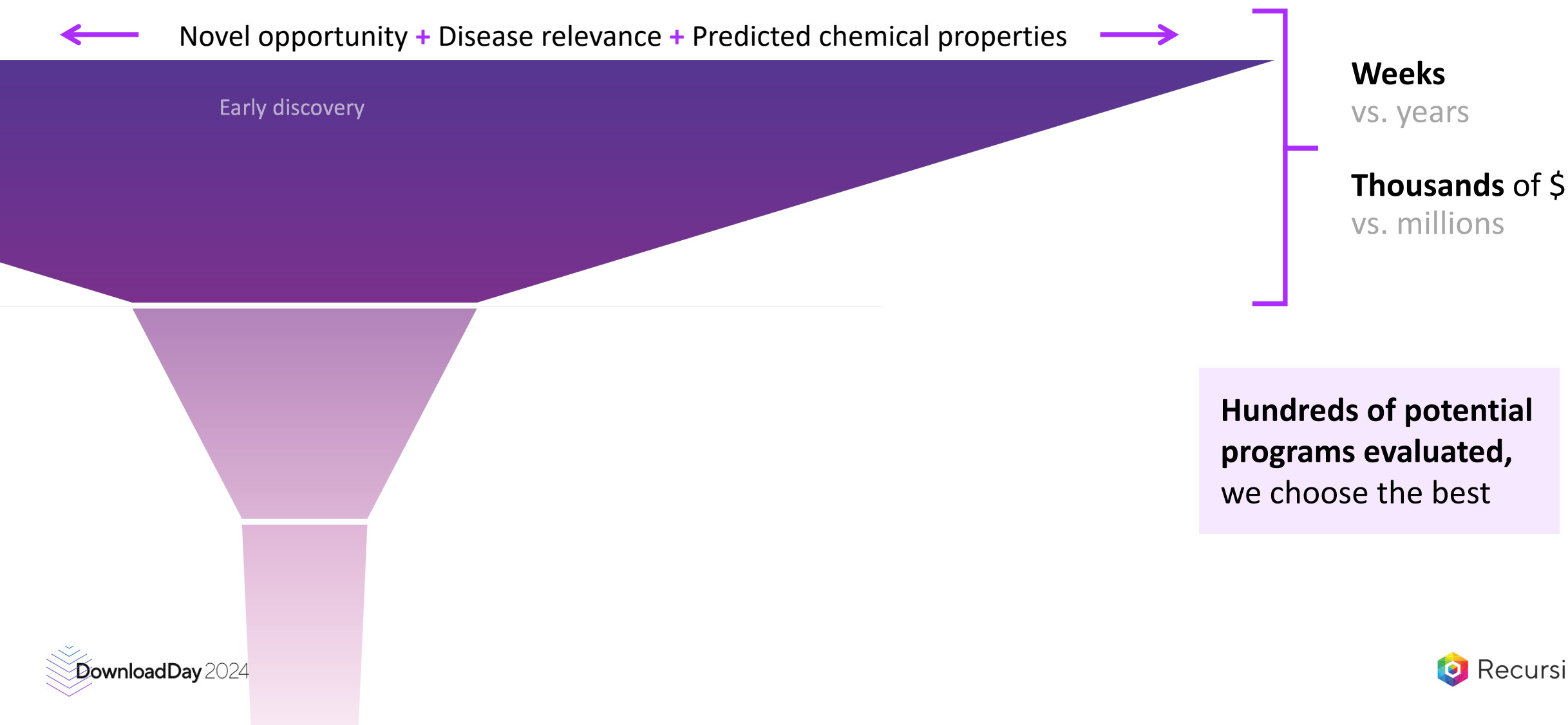


Preclinical: The Power of Prediction

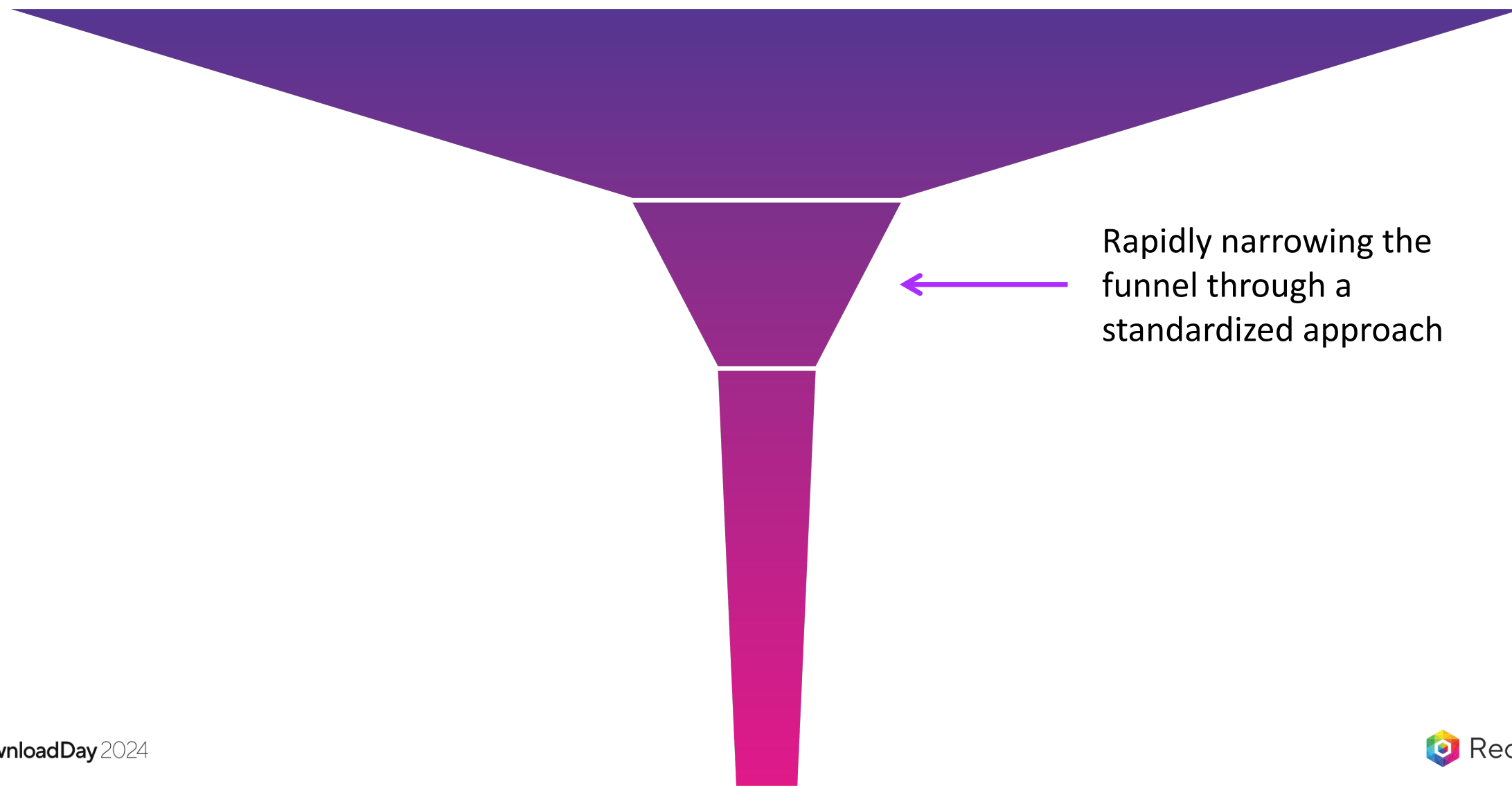
Traditional approach to initiating a new drug discovery program



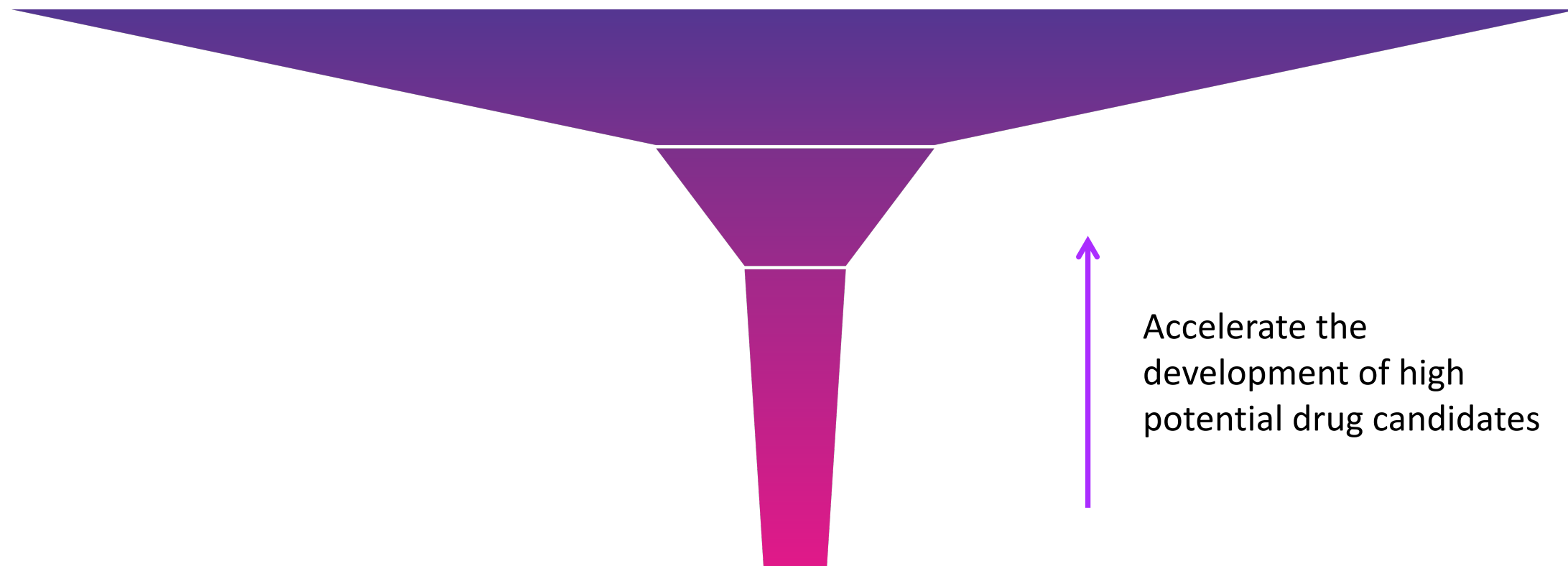
We are turning this into a search problem, evaluating new programs in bulk



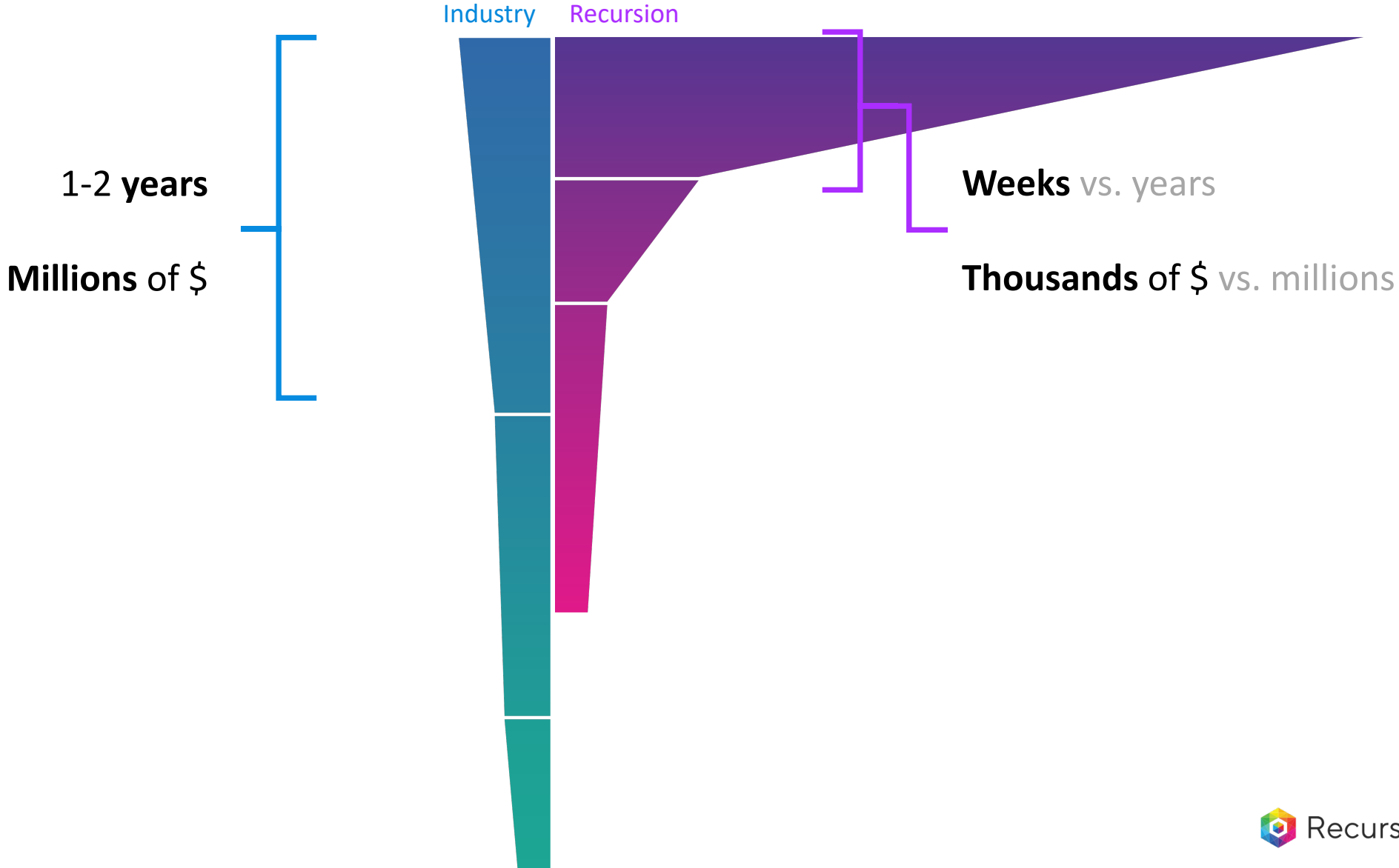
Recursion is designed to impact drug discovery productivity...



Recursion is designed to impact drug discovery productivity...



Reshaping the timelines and shape of drug discovery research

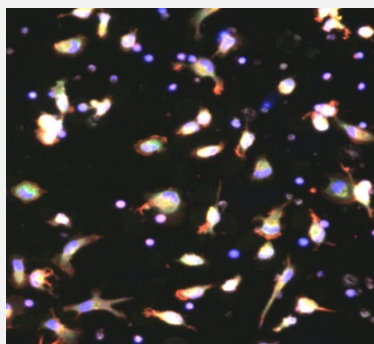


Case Study: Target Epsilon

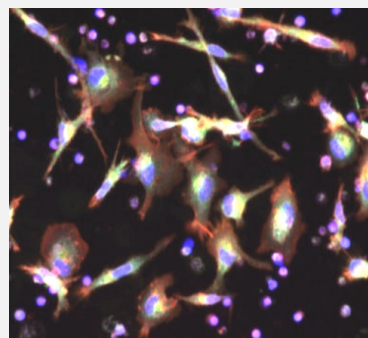
Identifying novel targets and optimizing novel chemistry

Power of Phenomics: Identify complex phenotypic rescue at scale

PBMC-derived fibrocyte assay



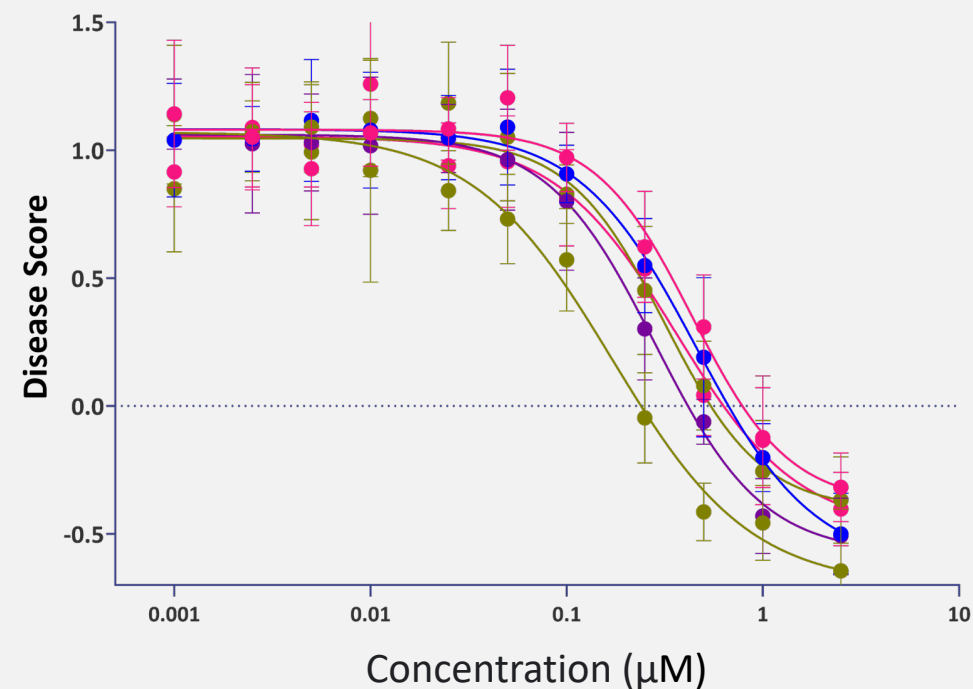
Control State:
10 $\mu\text{g}/\text{mL}$ control peptide



Disease State:
Undisclosed treatment

- Human-PBMCs are differentiated to fibrocytes
- Treatment with a control peptide gives desired impact on fibrocytes (**control state**)

Promising hits from phenotypic screen

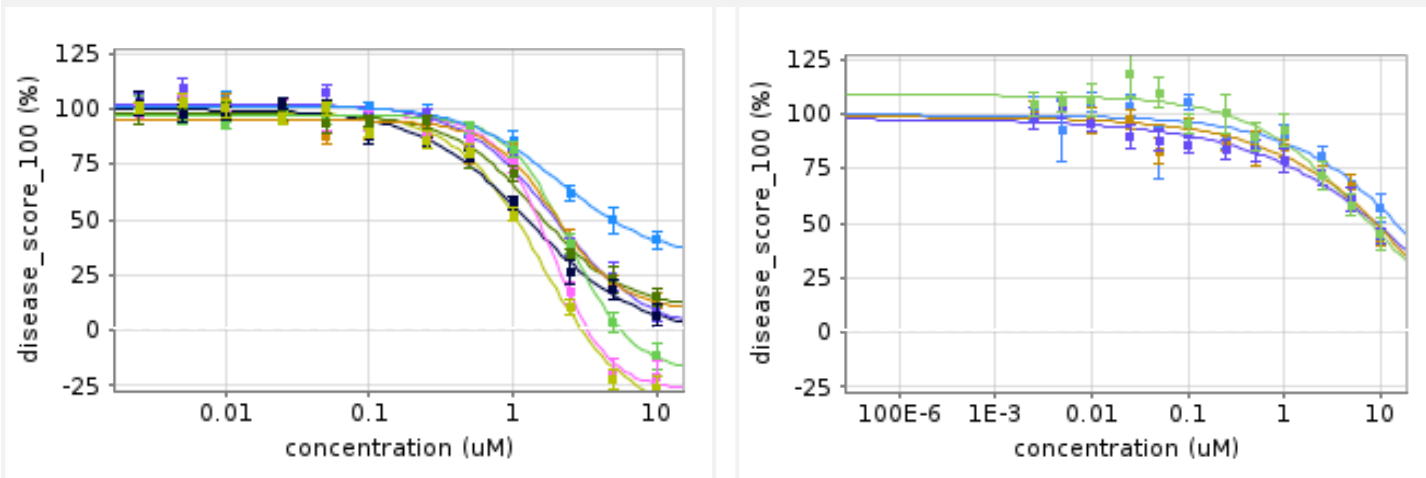


~100x potency gains driven entirely on phenomics assay

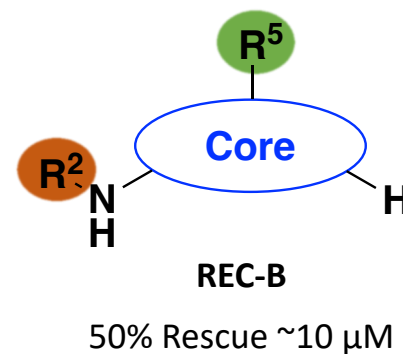
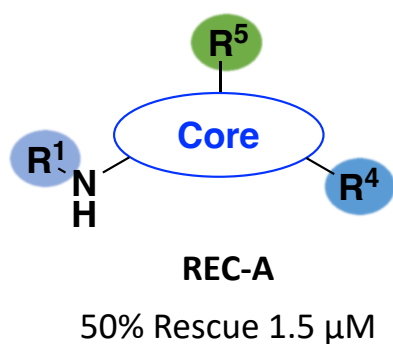
Disease State

Healthy Control State

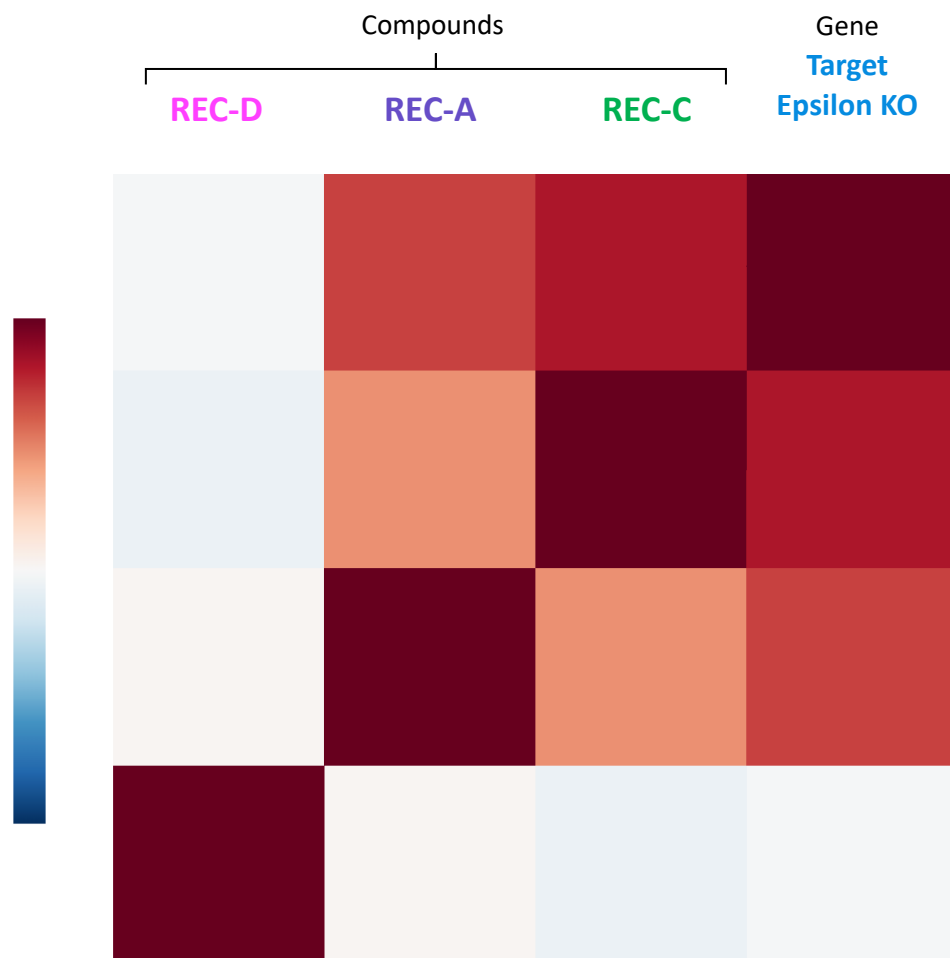
Representative concentration response curves (CRC) from the phenotypic assay



Significant reduction of disease modifying activity



Phenomics identified mechanism of action as a novel approach for treating fibrosis

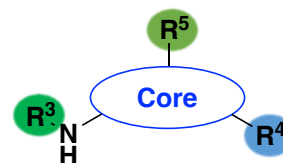


Target Epsilon KO

Epsilon
biochemical confirmation

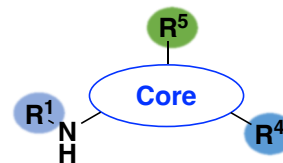
n/a

REC-C
2.5 μ M



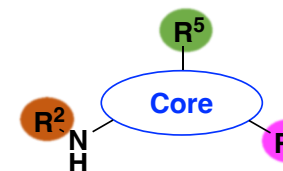
Target Epsilon IC₅₀
= 31.5 nM

REC-A
2.5 μ M



Target Epsilon IC₅₀
= 106 nM

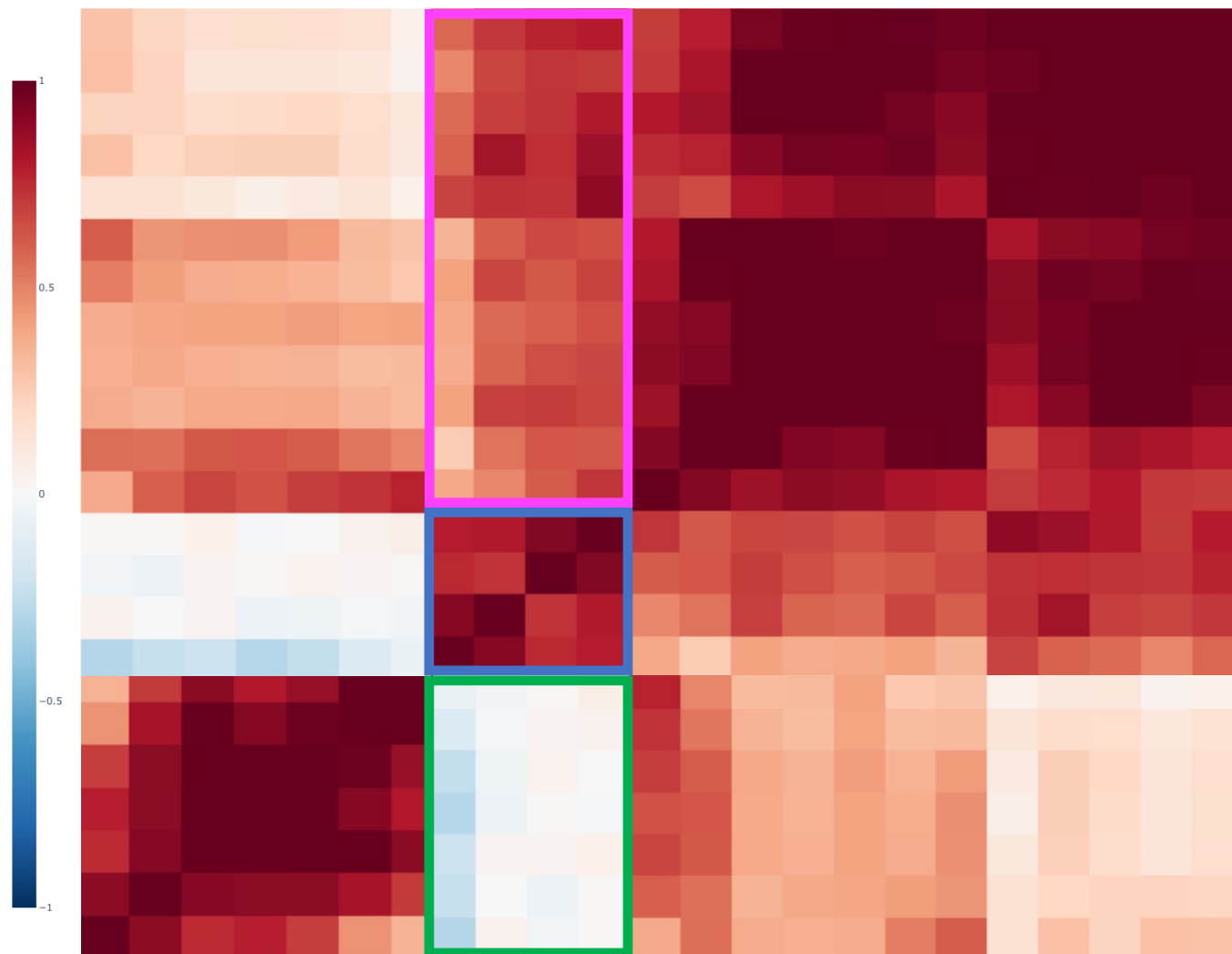
REC-D
2.5 μ M



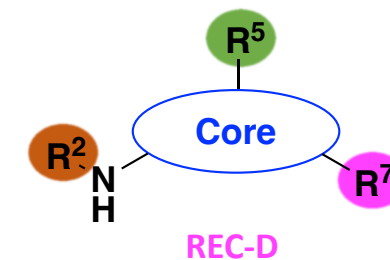
Target Epsilon IC₅₀
= 3600 nM

Power of Phenomics: Track and minimize off-target liabilities

Tubulin Related Genes



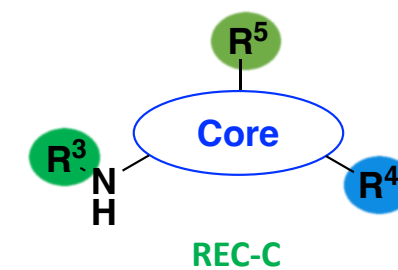
Compounds with
<math><10 \mu\text{M}</math> tubulin IC_{50}



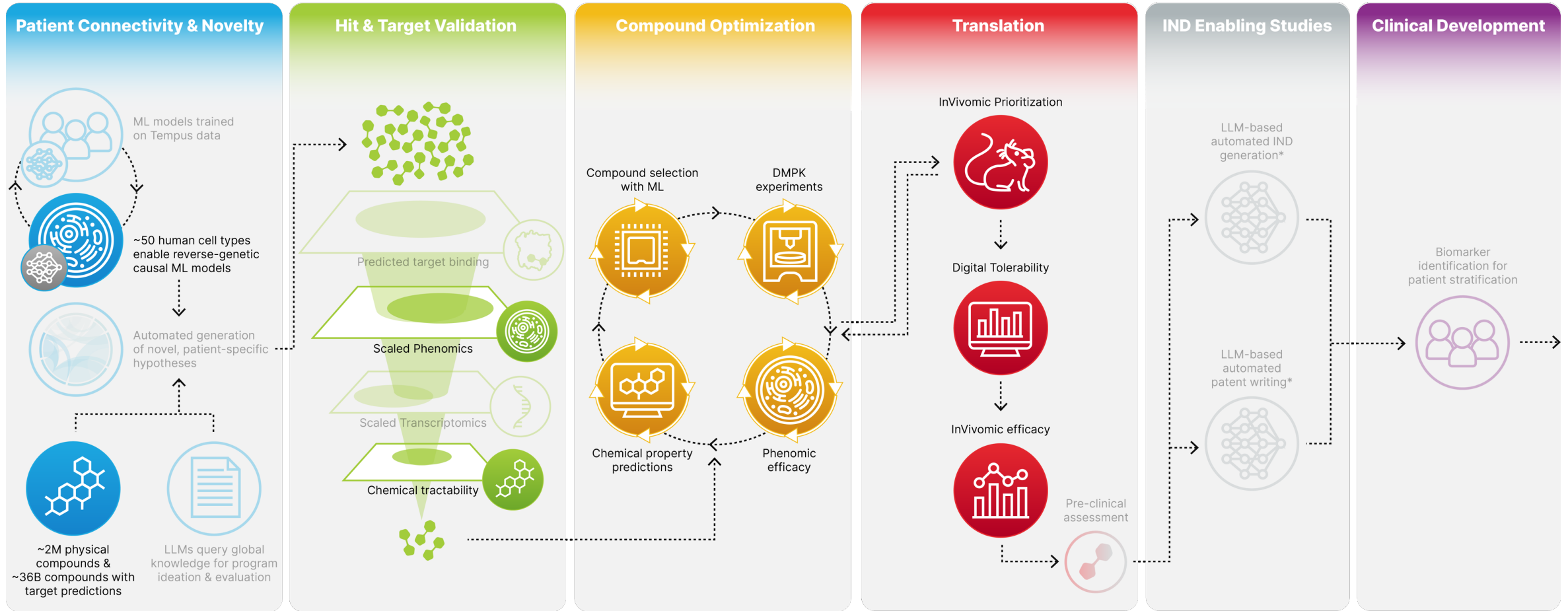
Phenomap correlates
with tubulin
polymerization
inhibition assay

Tubulin Related Genes

Compounds with
>math>30 \mu\text{M}</math> tubulin IC_{50}



Industrialized Drug Discovery: Optimizing novel chemical matter

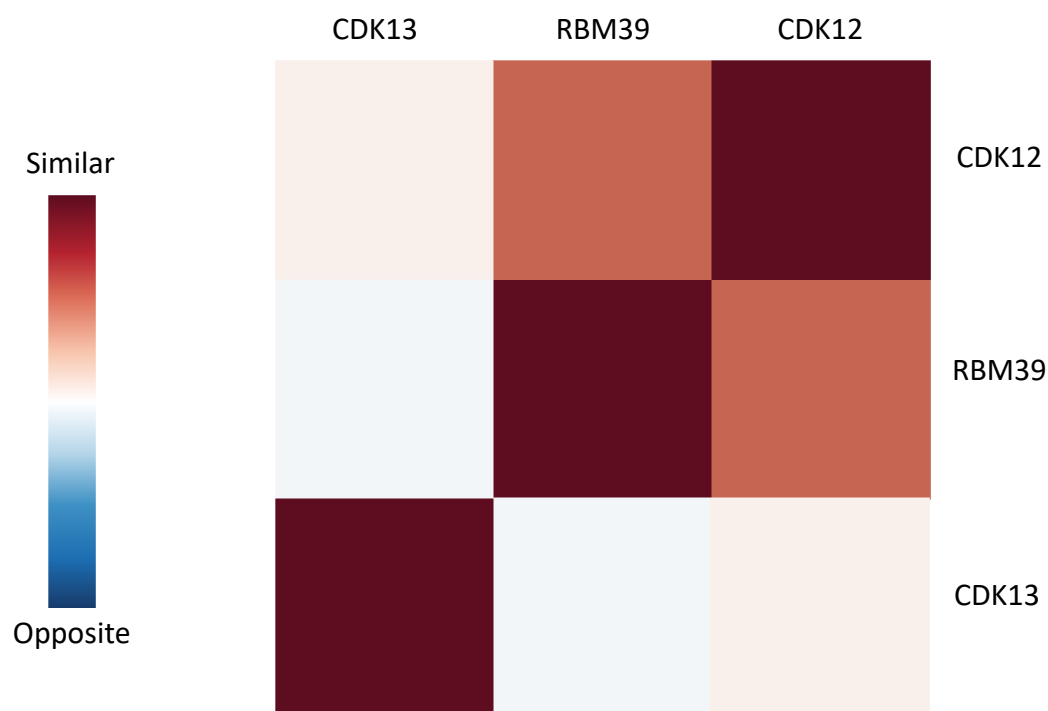


Case Study: RBM39

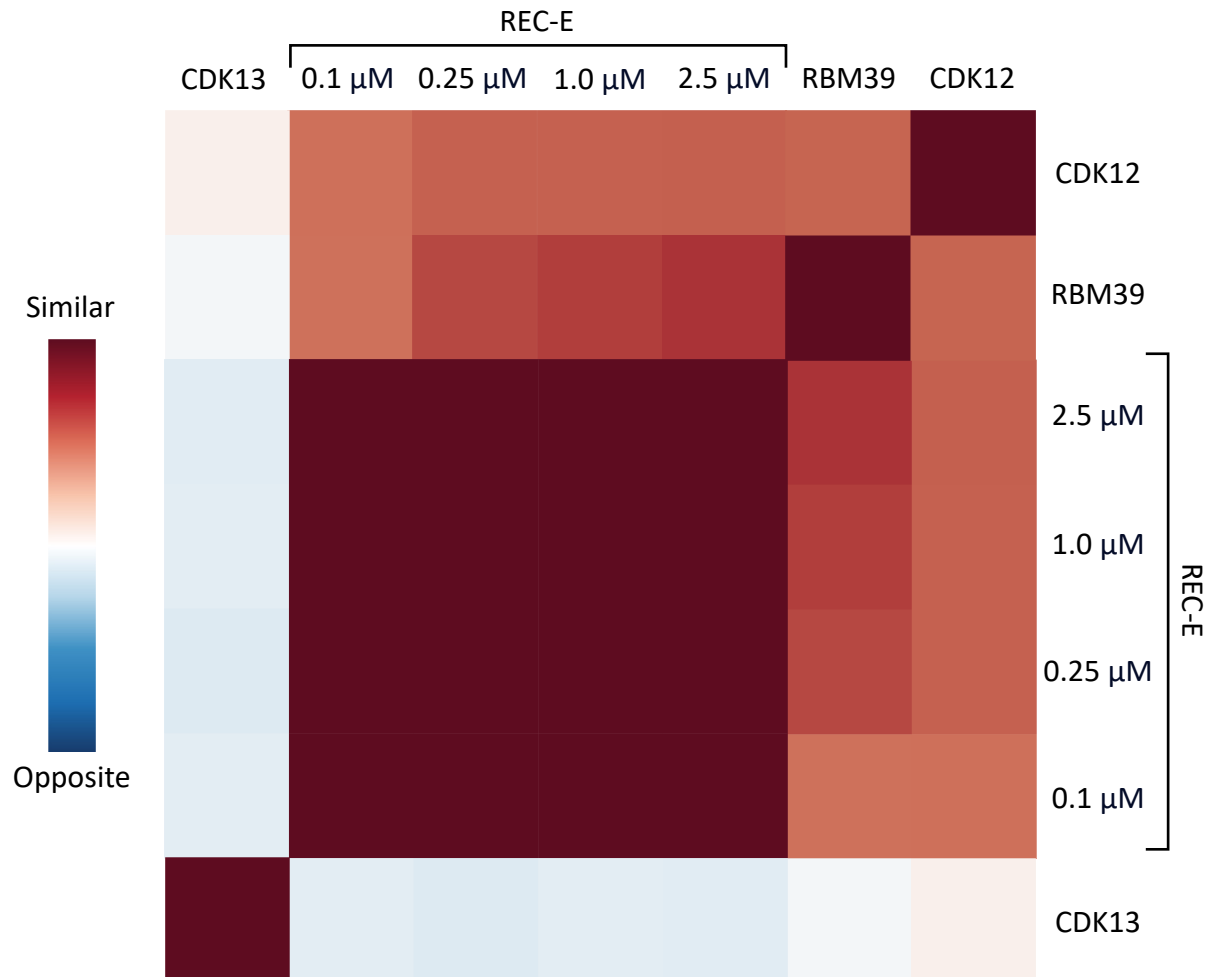
Accelerating to IND enabling studies
through in silico novel target prediction



Inference search reveals novel CDK12 adjacent target RBM39 and selective small molecule hits

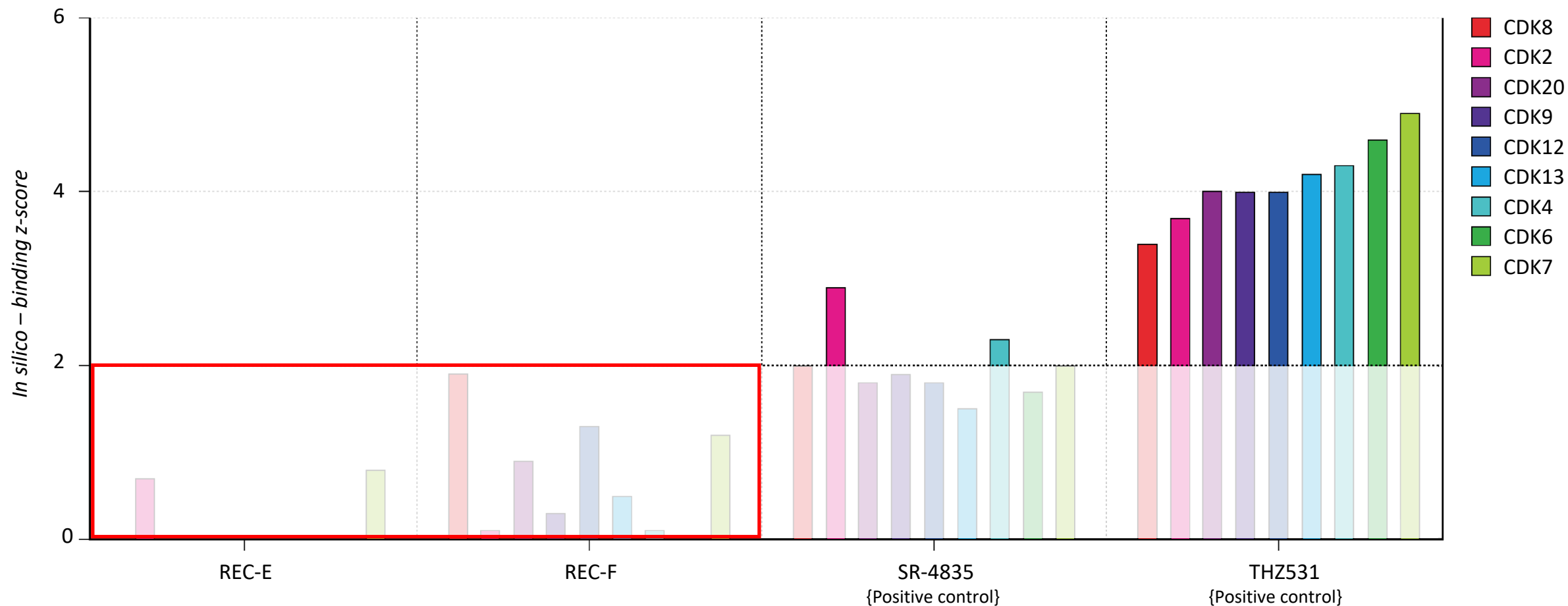


Inference search reveals novel CDK12 adjacent target RBM39 and selective small molecule hits

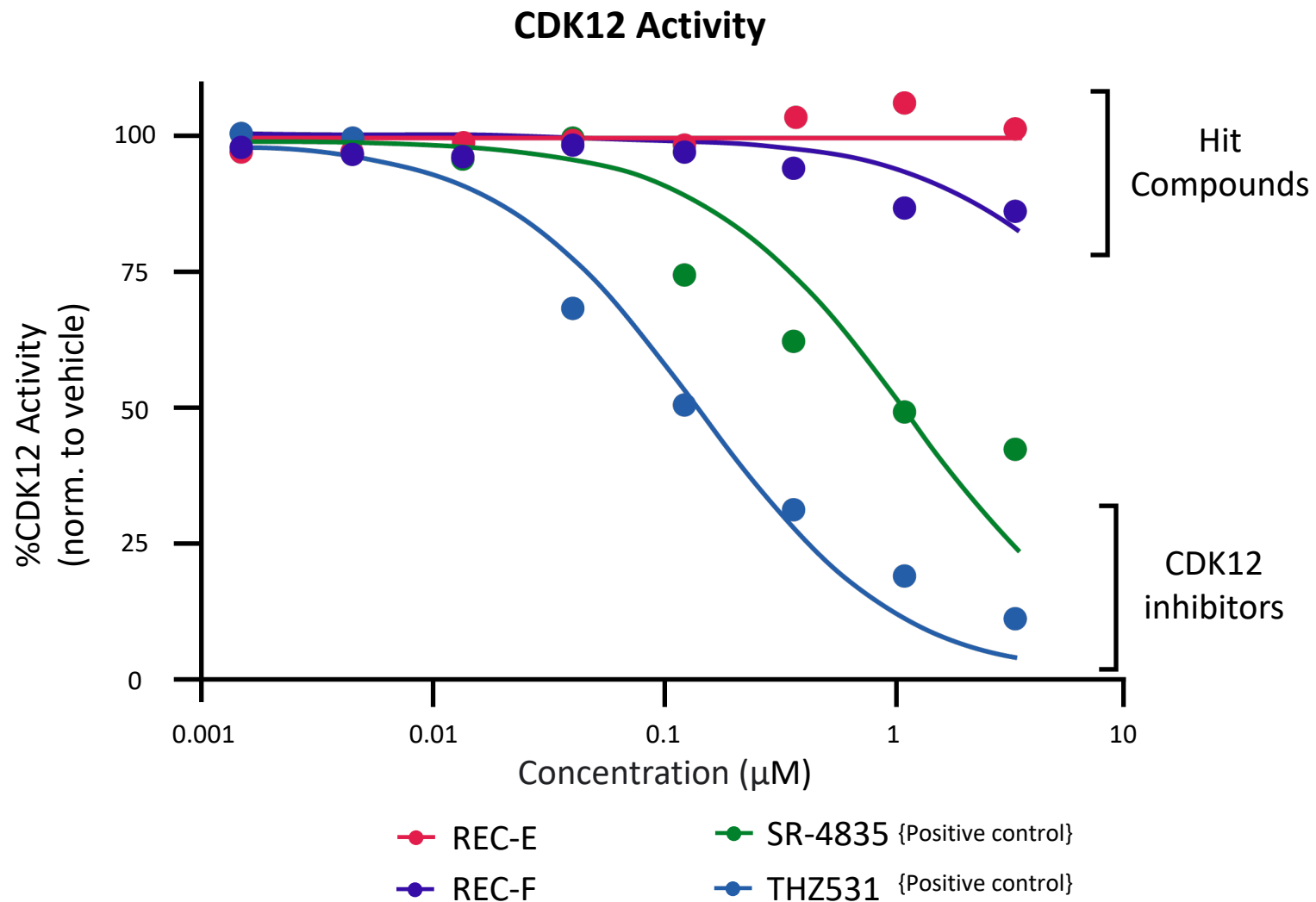


In silico MatchMaker predicts hit compounds are NOT CDK inhibitors

Probability of CDK Binding as predicted by **MatchMaker**



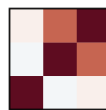
Physical data confirms digital hypothesis



Predictions and minimal standard experiments enabled rapid and efficient identification of development candidate

Number of Molecules

Profiled
~1,000,000



↓ Synthesized compounds

In Silico
2,700

Phenomics
Profiled
955

DMPK Profile
155

Efficacy
6

Candidate Quality
3

Initial Synthesis (or Design) to Advanced Candidate (9 months)

~1 day

- Design
- In silico assessment

6-8 weeks

- Phenomics profile

2-4 weeks

- Acceptable PK/ADME

10-12 weeks

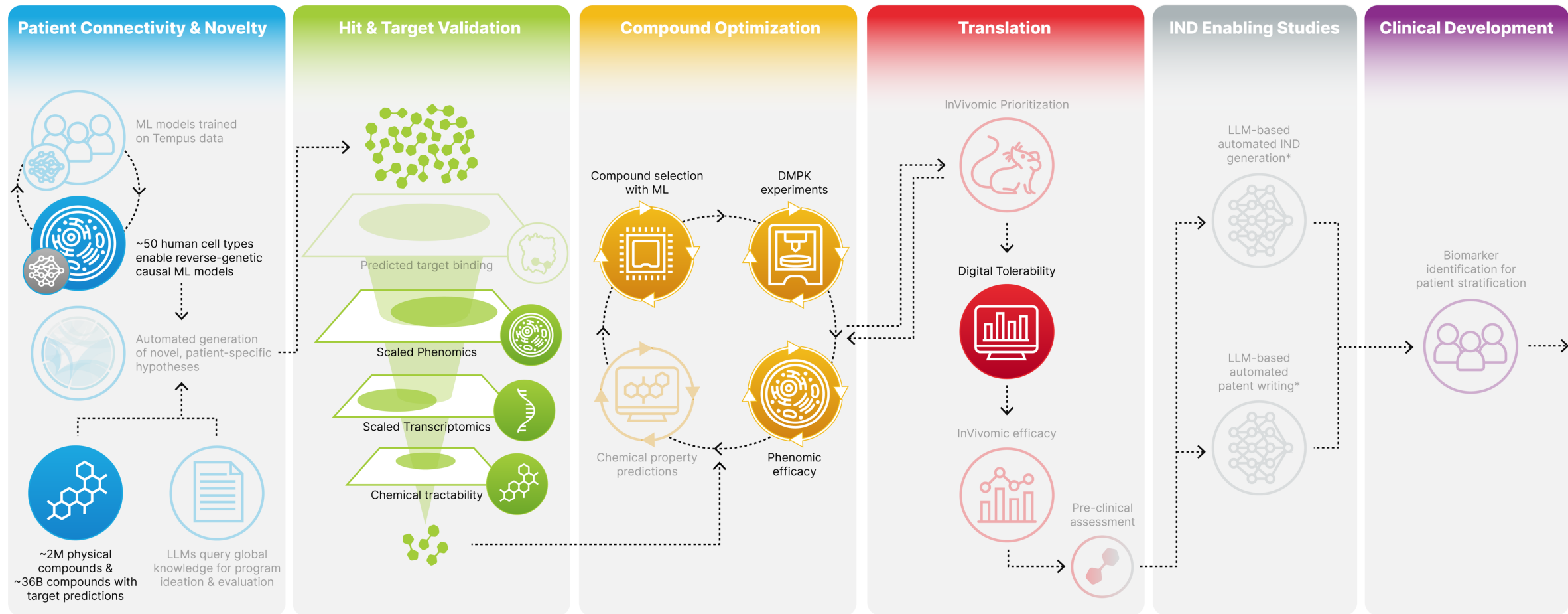
- Efficacy Readout

8-10 weeks

~3-4 days

- Initial Toxicology Readout
- Appropriate Therapeutic Index

Rapid in silico novel target identification



*Currently being explored

Time from target ID to IND enabling study

 Recursion



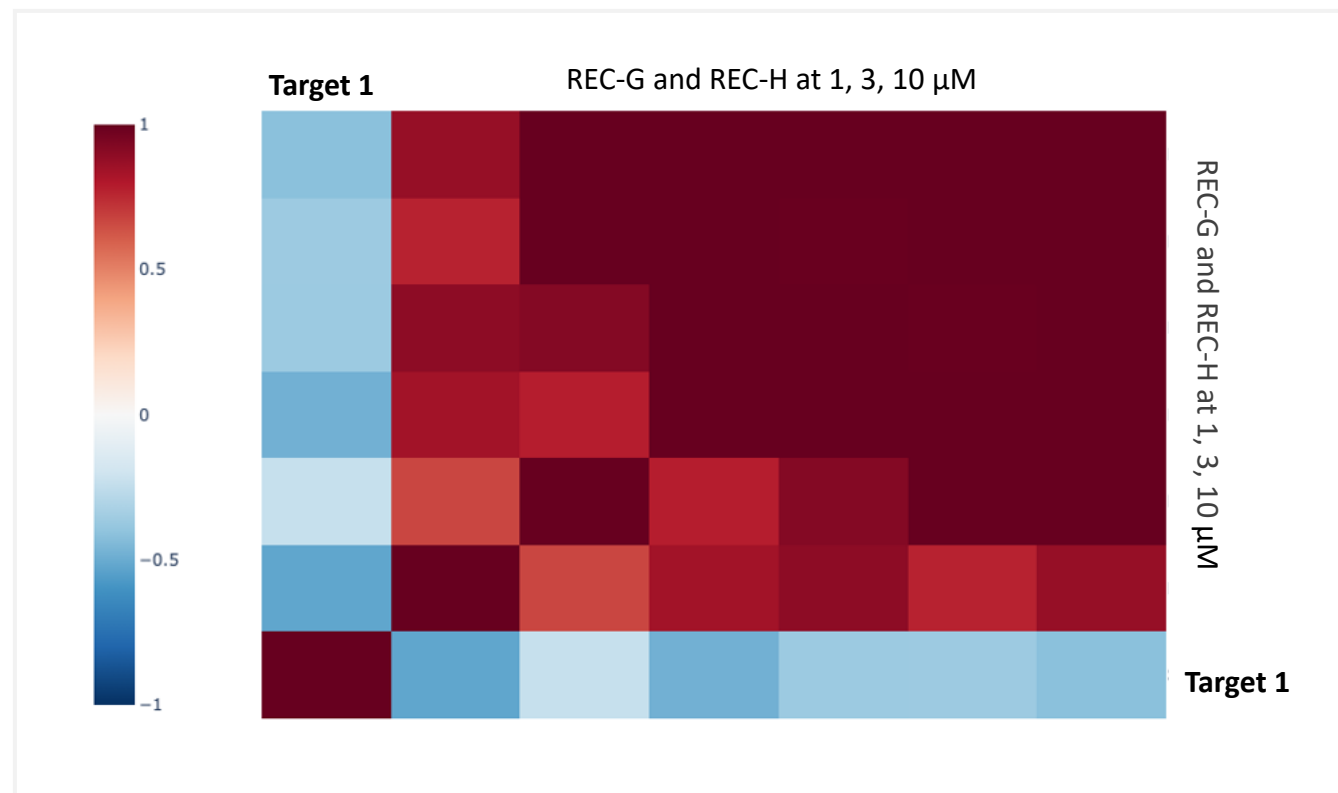
Industry



Case Study: Undisclosed Oncology Target 1

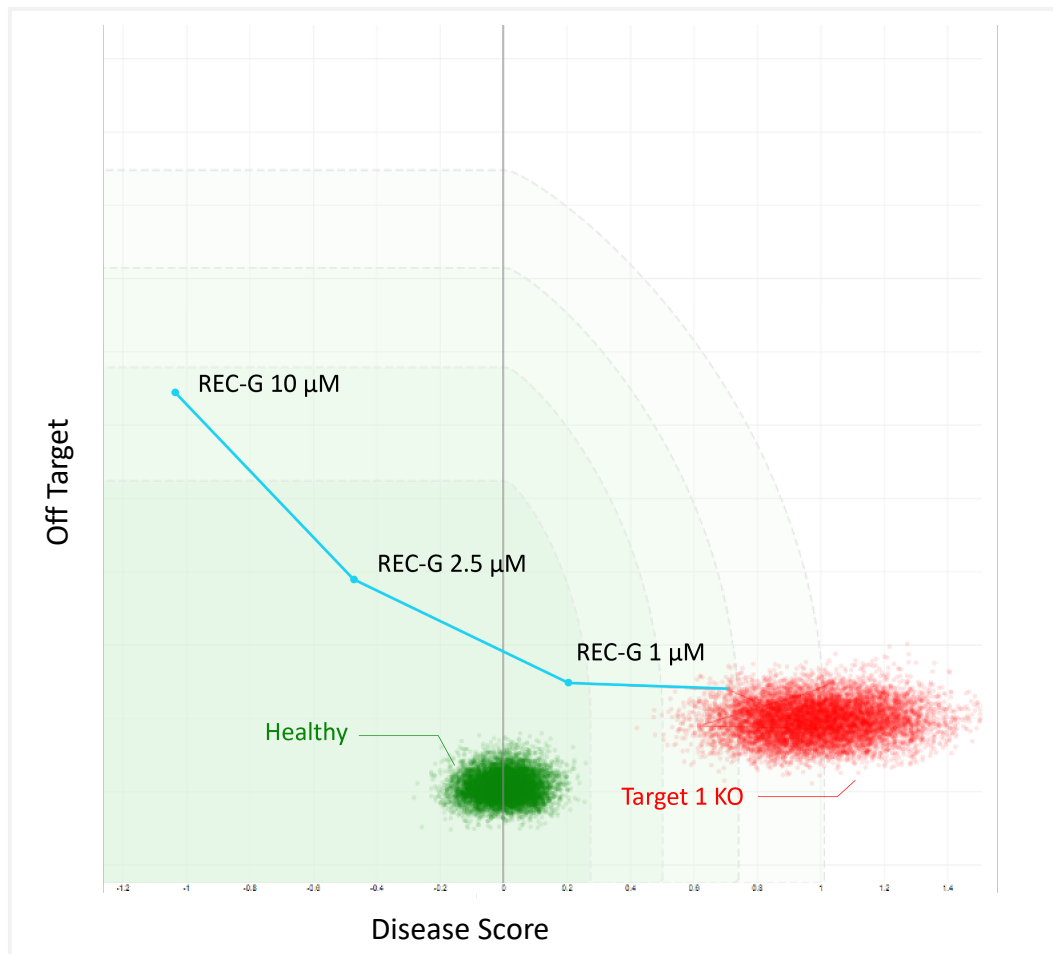
Connecting data layers end-to-end
improves quality and speed of insights

Identifying novel Target 1 and opposing molecules through automated, in silico analysis

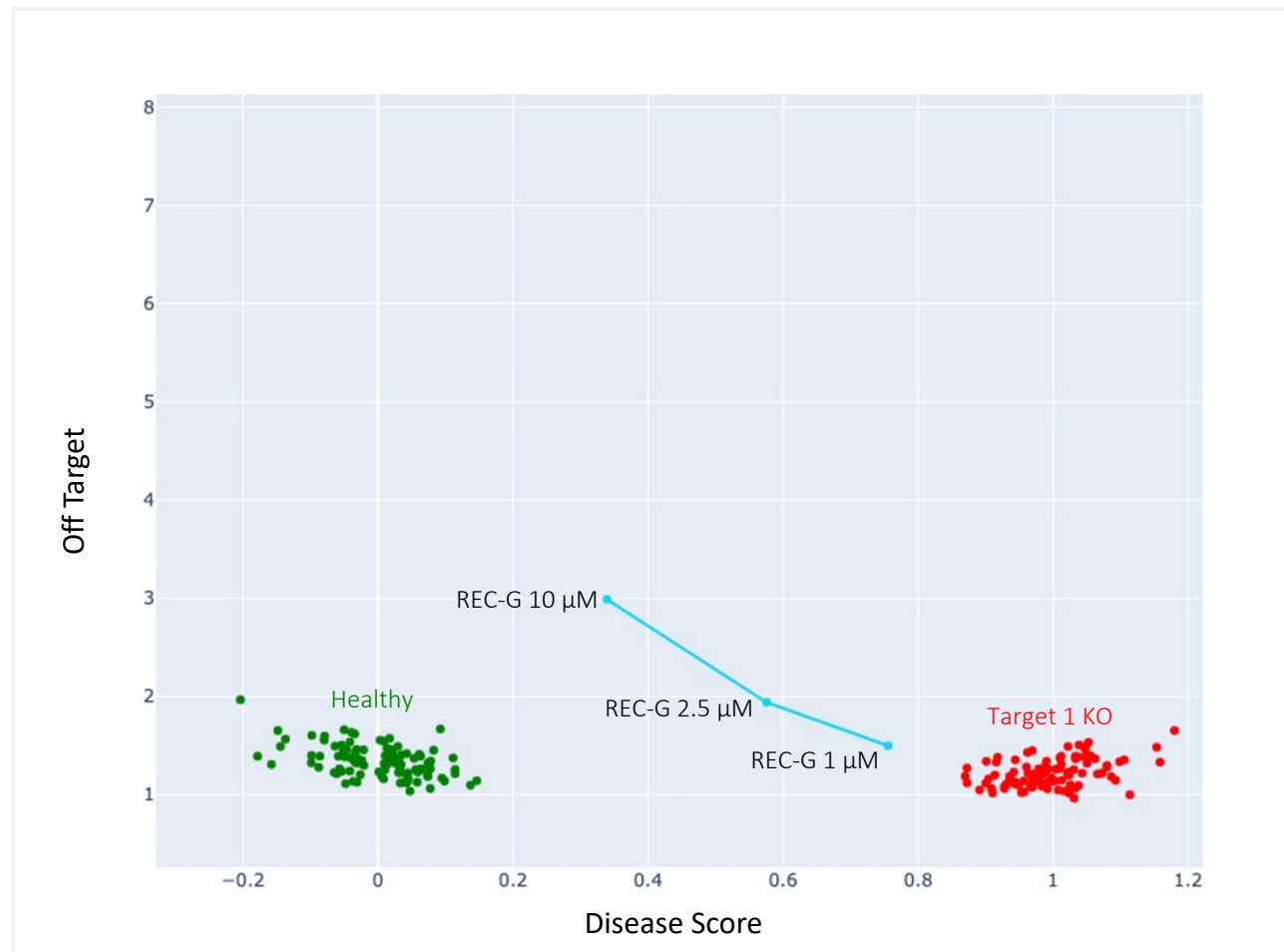


Physical data confirms digital hypothesis

Phenomics Confirmation Screen

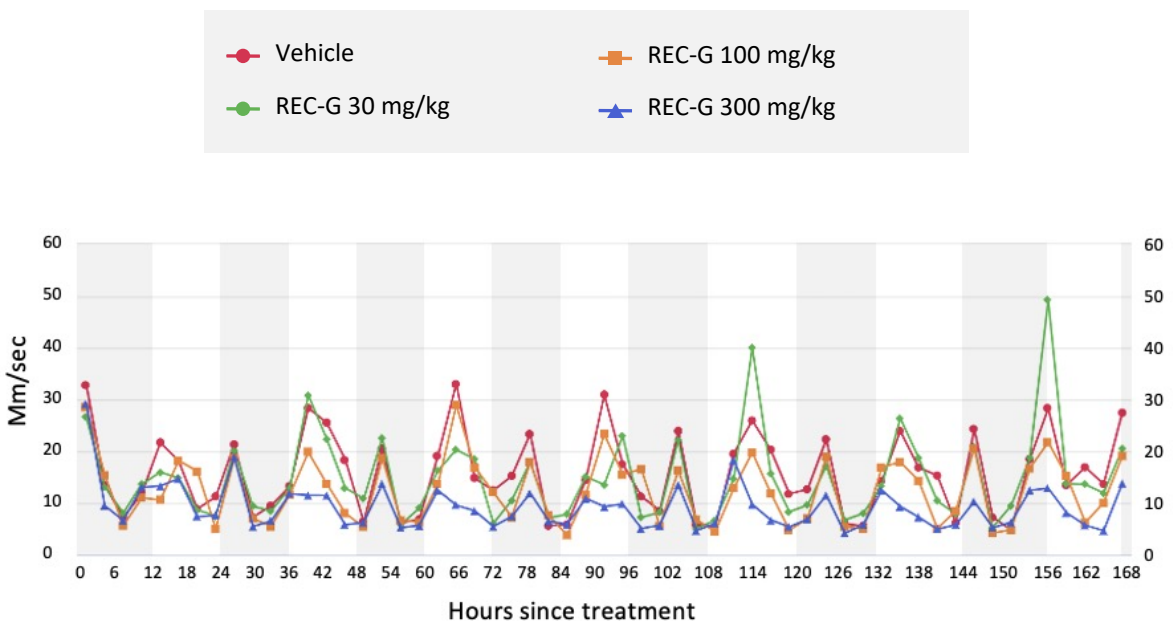


Transcriptomics Confirmation Screen

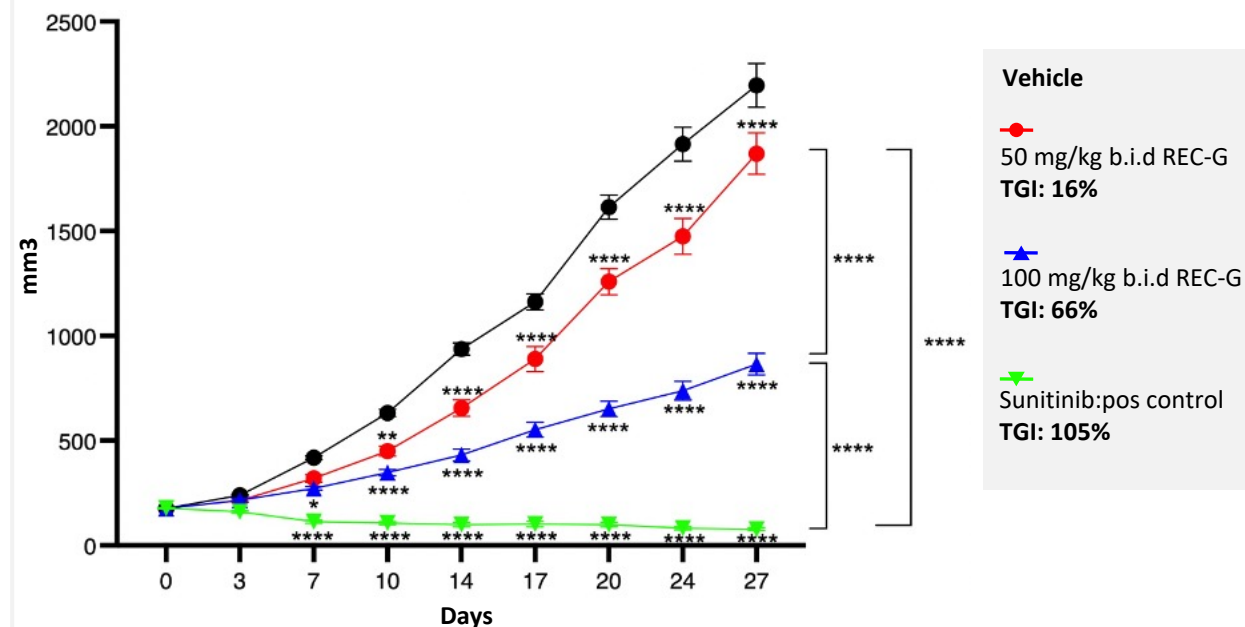


InVivomics enables identification of tolerable dose for rapid positive proof of concept readouts for unoptimized molecules

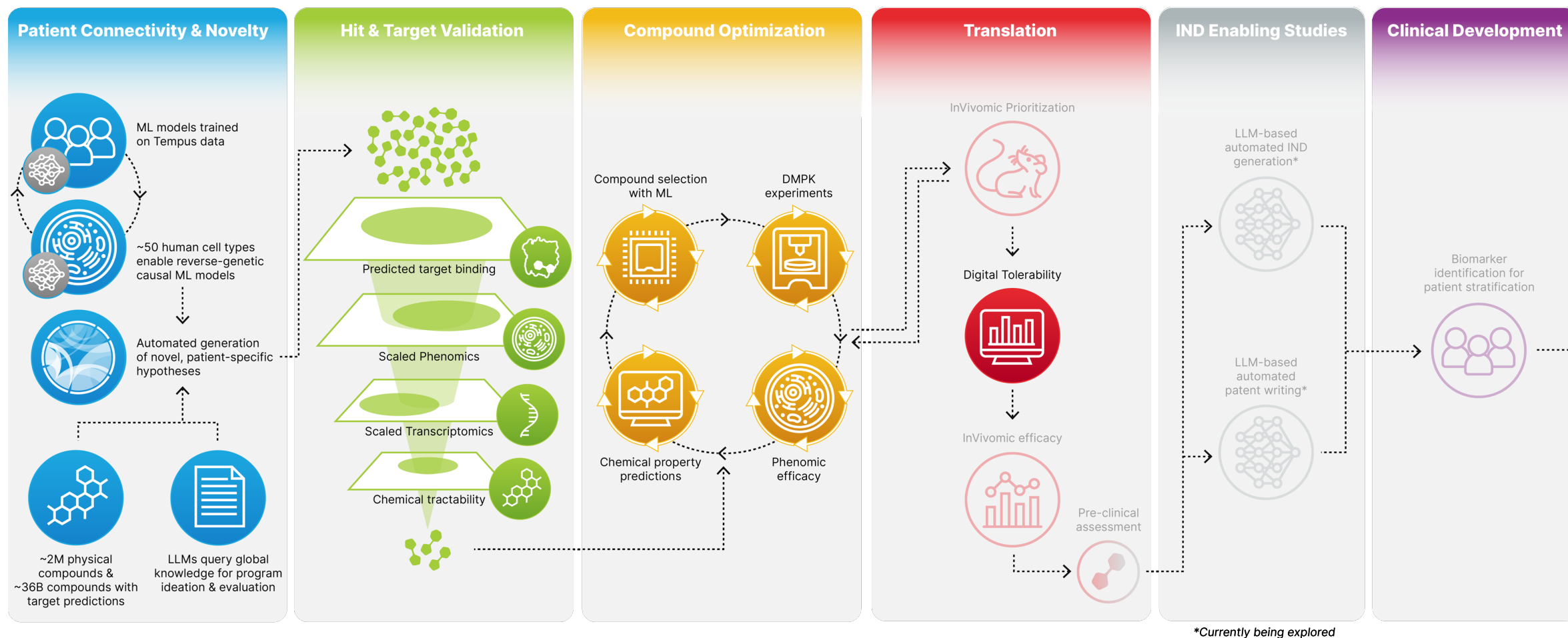
Daily Motion



Tumor Volume



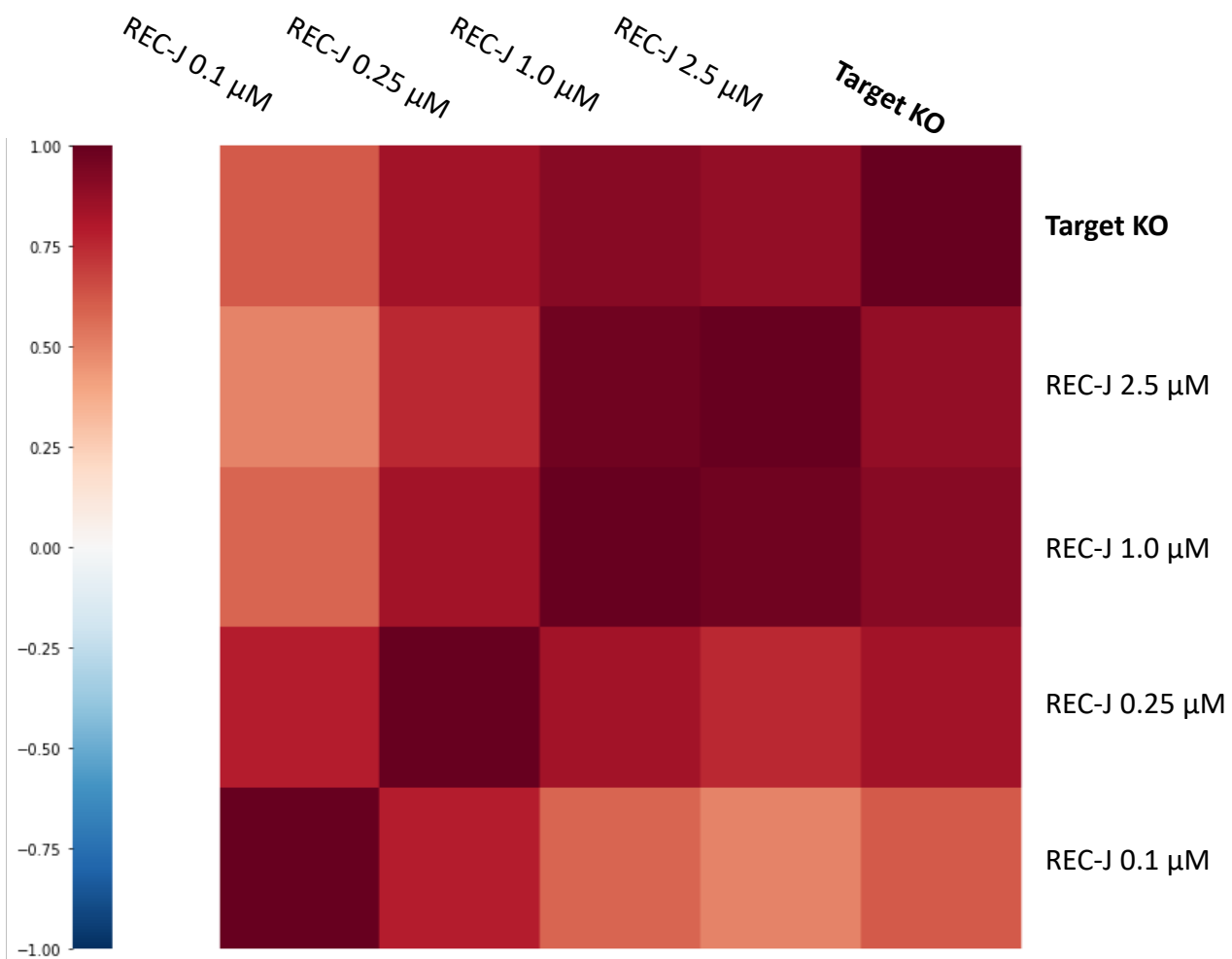
End-to-end automation drives significant efficiency gains to deliver lead in 10 months



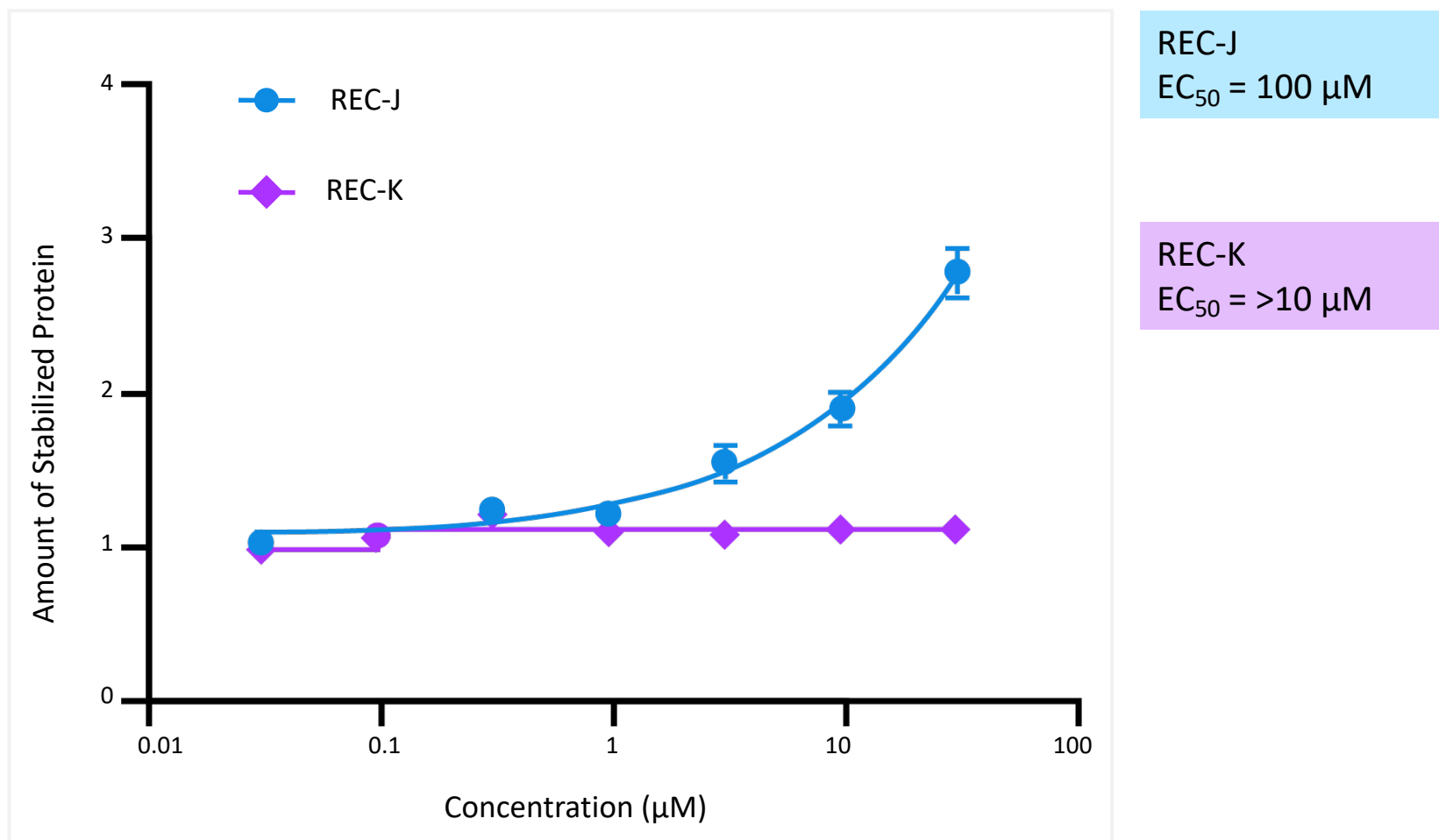
Case Study: Undisclosed Oncology Target 2

Identifying novel molecules for a previously undruggable target

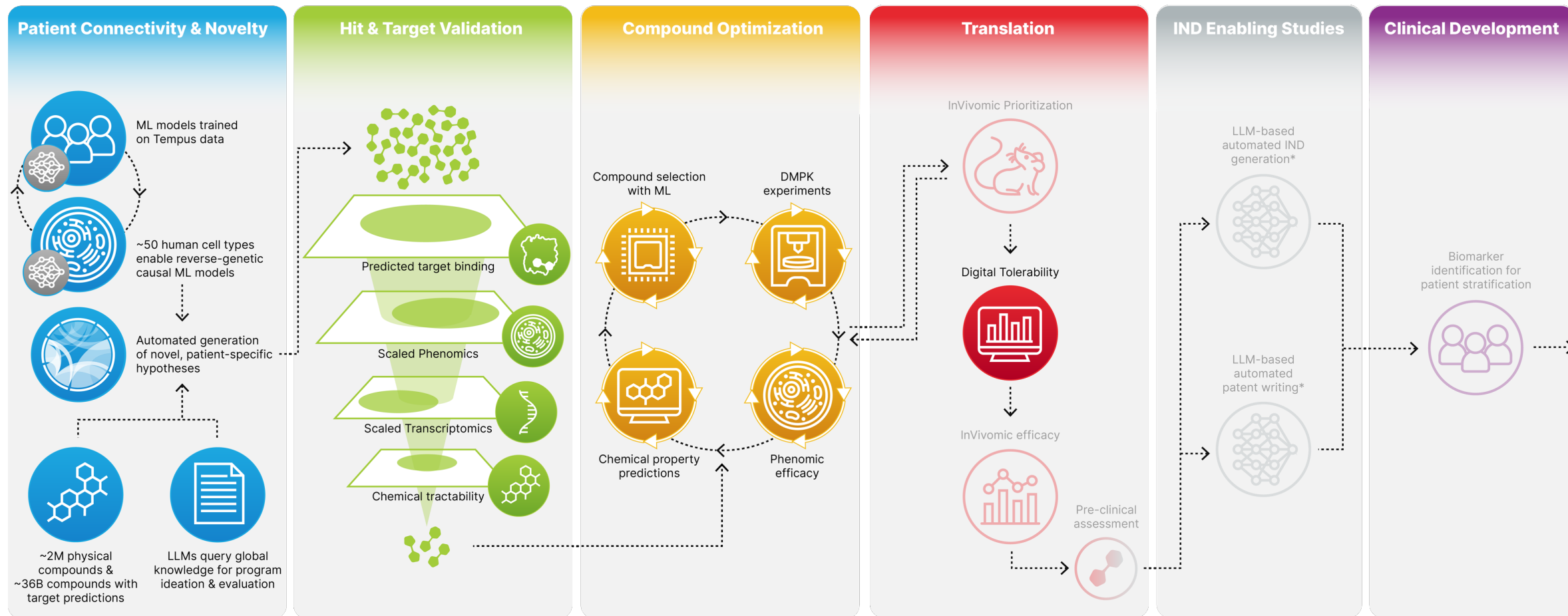
In silico analysis reveals compound highly phenosimilar to Target KO



Compound with high predicted phenosimilarity bind to Target 2

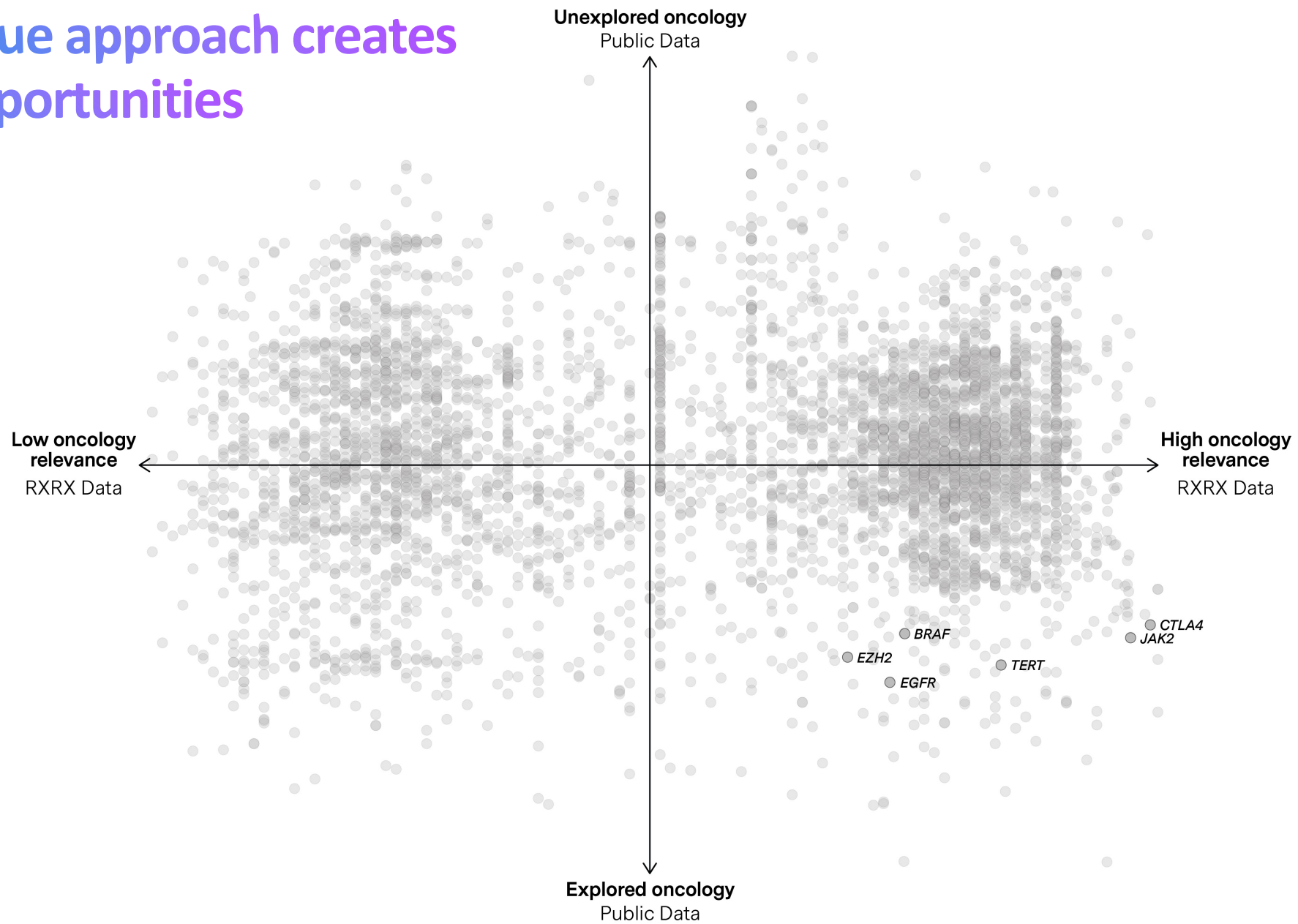


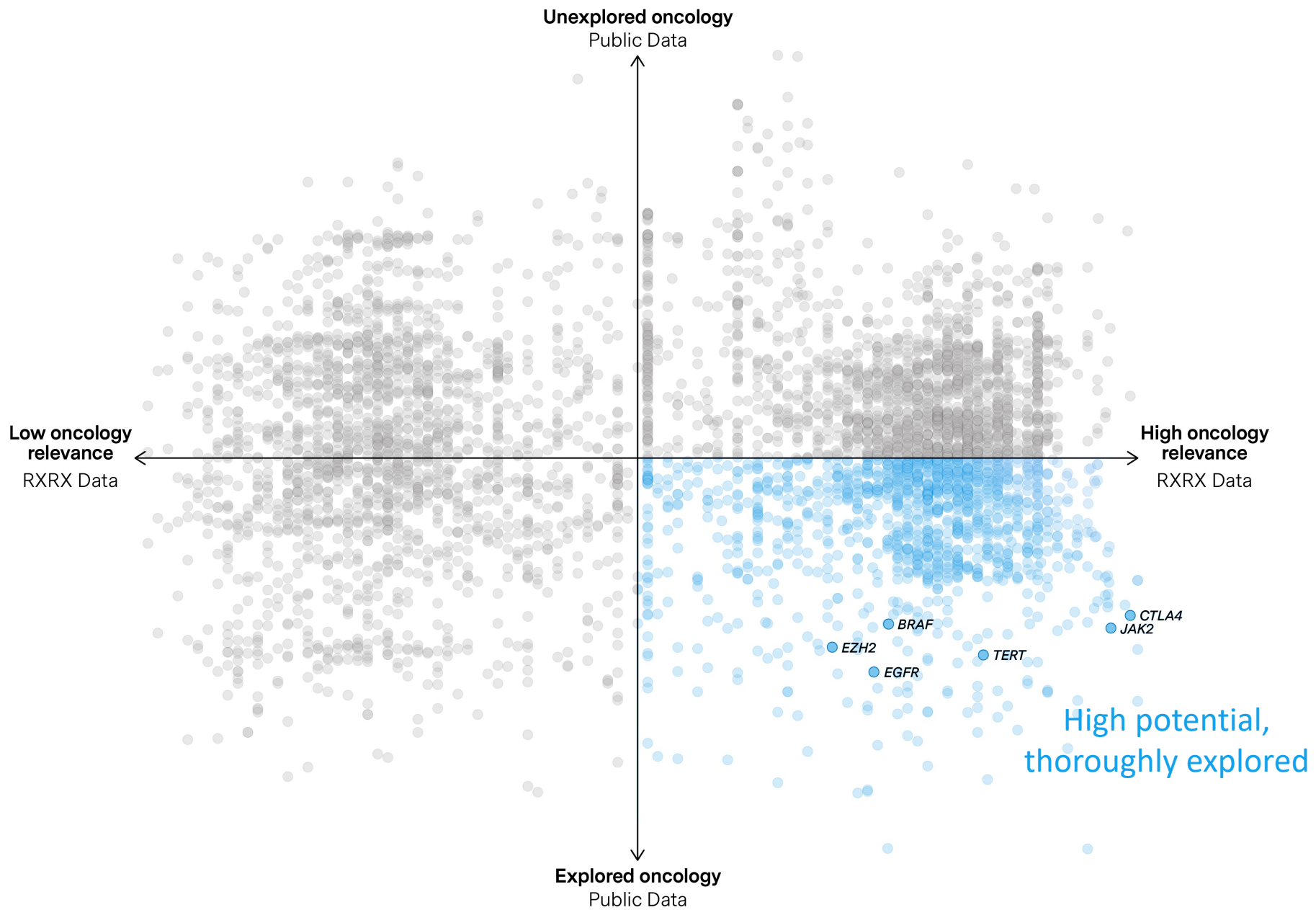
Overcoming the hurdles of drug discovery: undruggable targets

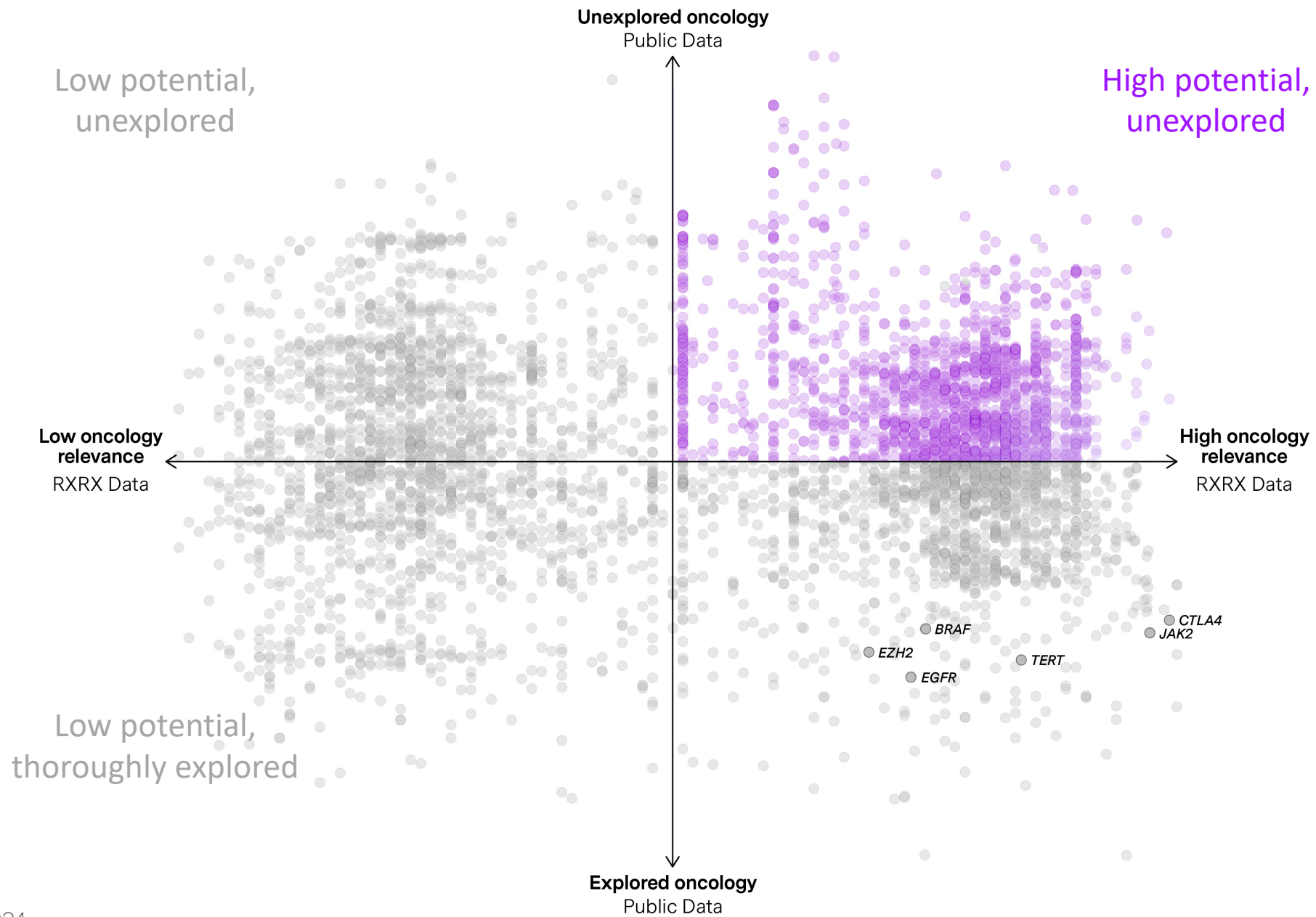


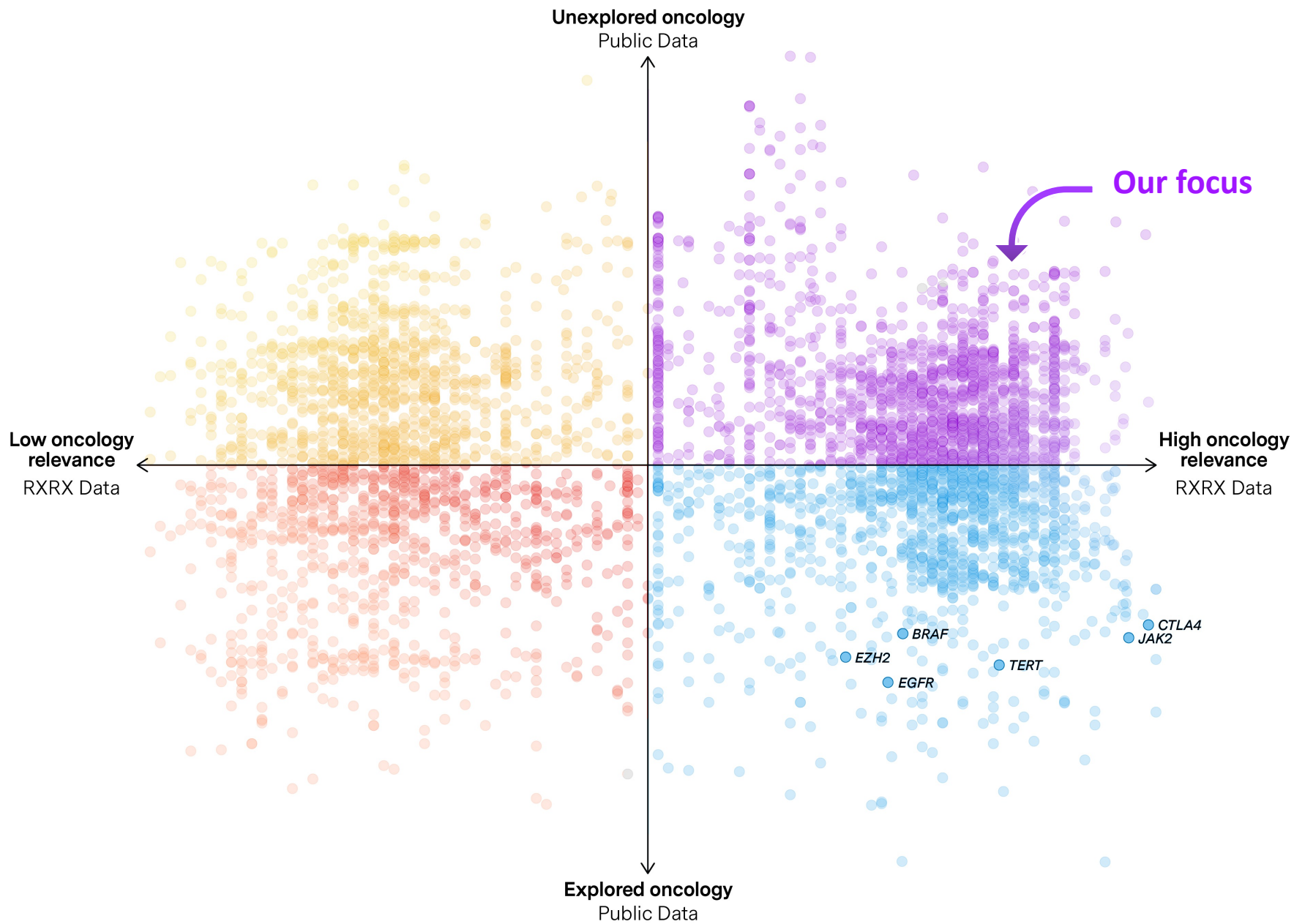
*Currently being explored

Our unique approach creates novel opportunities





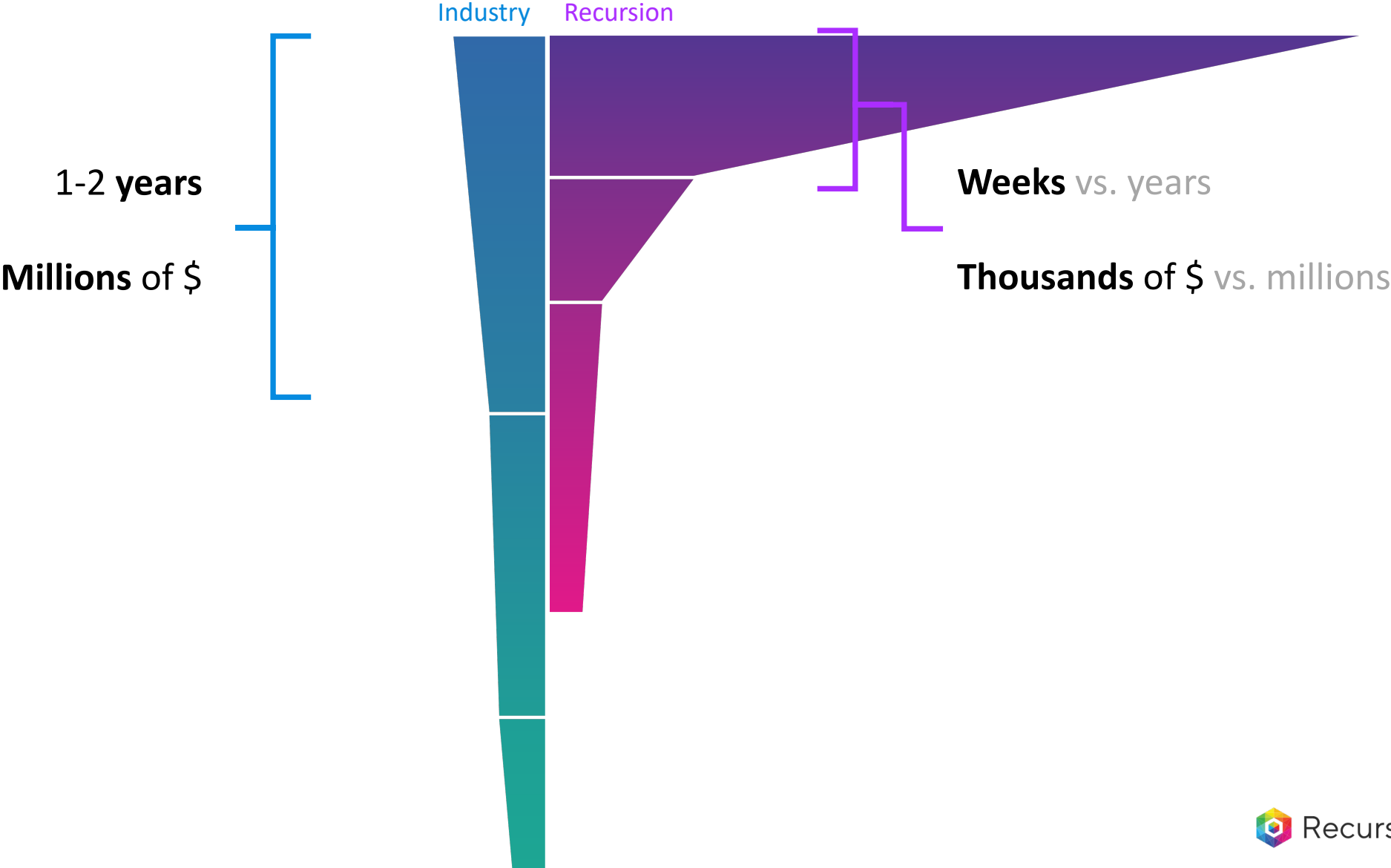




**We are turning this into a search problem,
evaluating new programs in bulk**



Reshaping the timelines and shape of drug discovery research



Fireside Chat:

Dr Deepak Nijhawan



Associate Professor in the Departments of Internal
Medicine and Biochemistry at UT Southwestern Medical Center

Afternoon Convocation

A collage of diverse people's faces, including children, adults, and elderly individuals, arranged in a grid of hexagonal frames. The overall color palette is purple and pink.

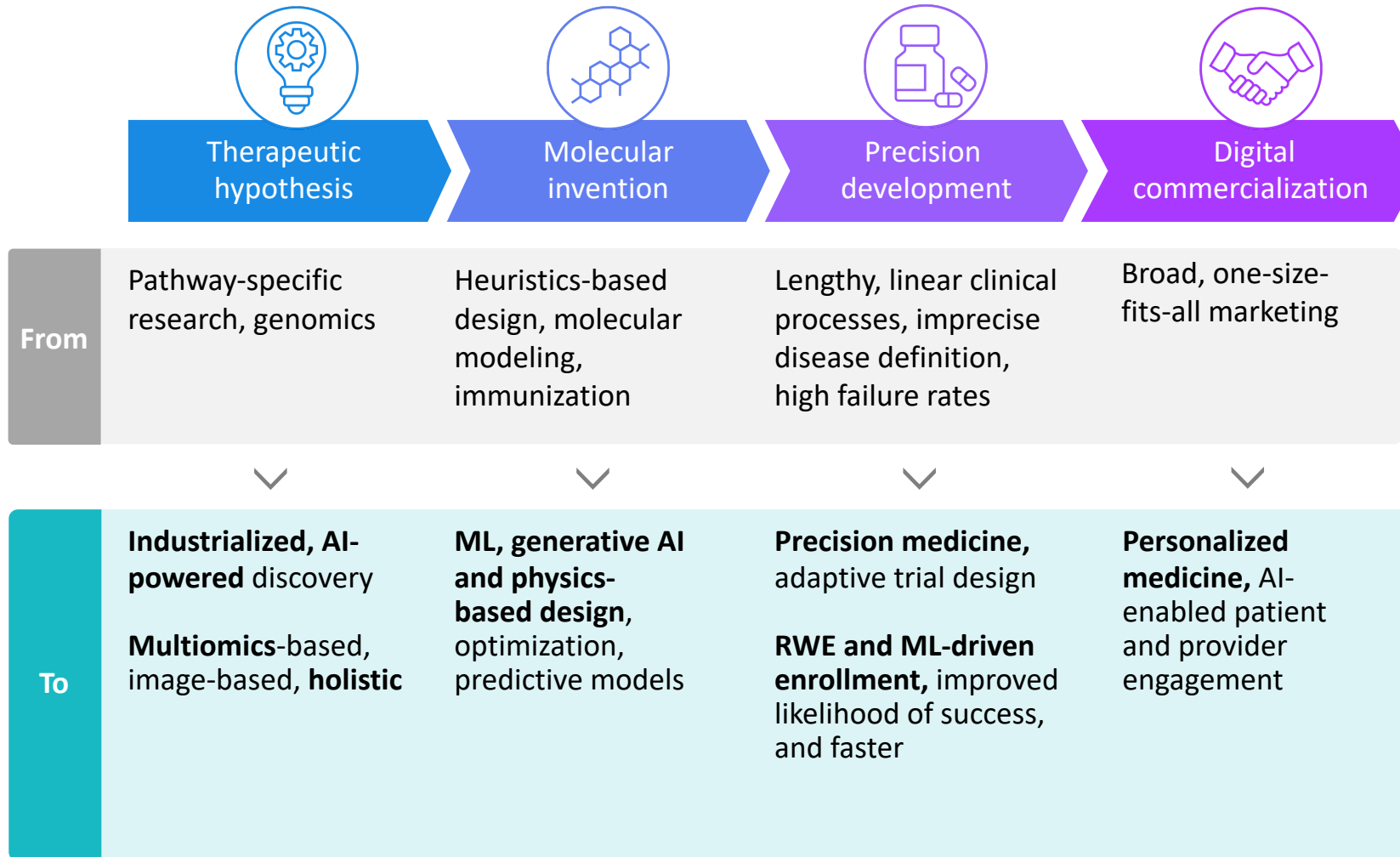
AI impact in healthcare

Patients are waiting

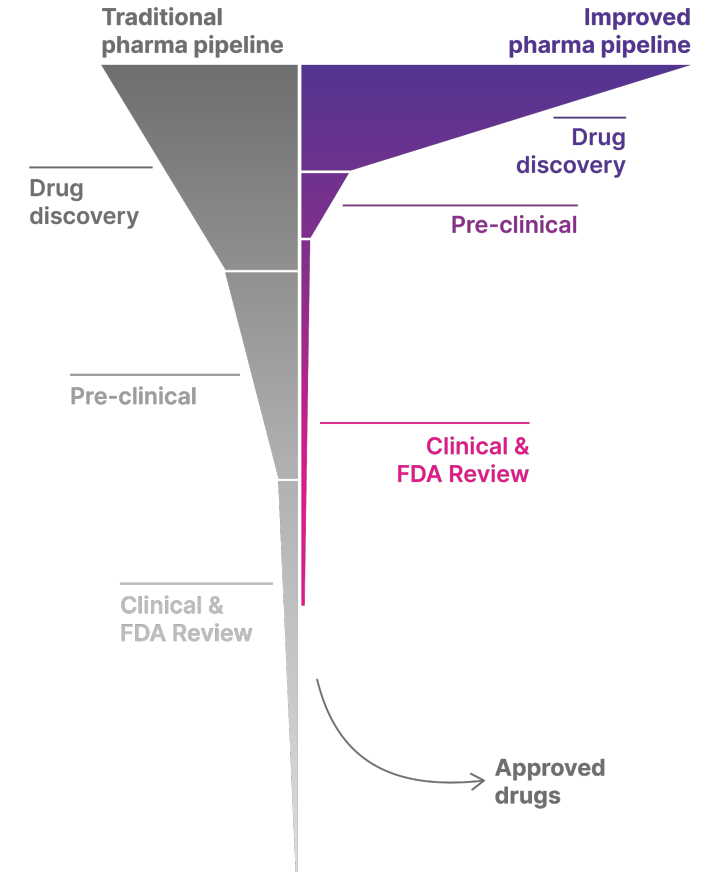
Why: Impact of AI & healthcare for patients



Why: Current state and the opportunity ahead



Improve success rates, faster execution



What: Industry's current state

The New York Times

Google Unveils A.I. for Predicting Behavior of Human Molecules

The system, AlphaFold3, could accelerate efforts to understand the human body and fight disease.

Listen to this article · 3:20 min

Share full article

bioRxiv

THE PREPRINT SERVER FOR BIOLOGY

Identification of potential treatments for COVID-19 through artificial intelligence-enabled phenomic analysis of human cells infected with SARS-CoV-2

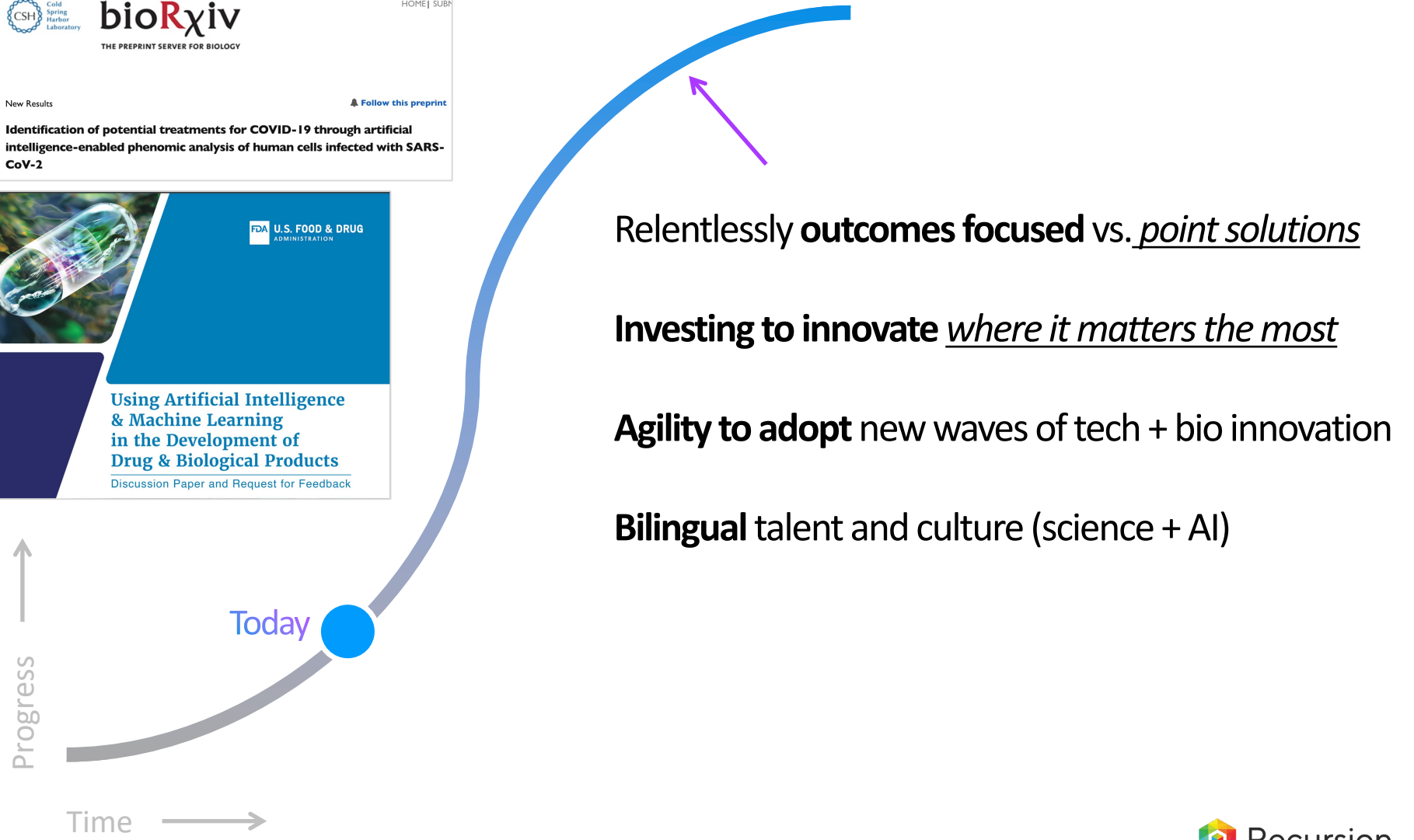
FDA U.S. FOOD & DRUG ADMINISTRATION

Using Artificial Intelligence & Machine Learning in the Development of Drug & Biological Products

Discussion Paper and Request for Feedback

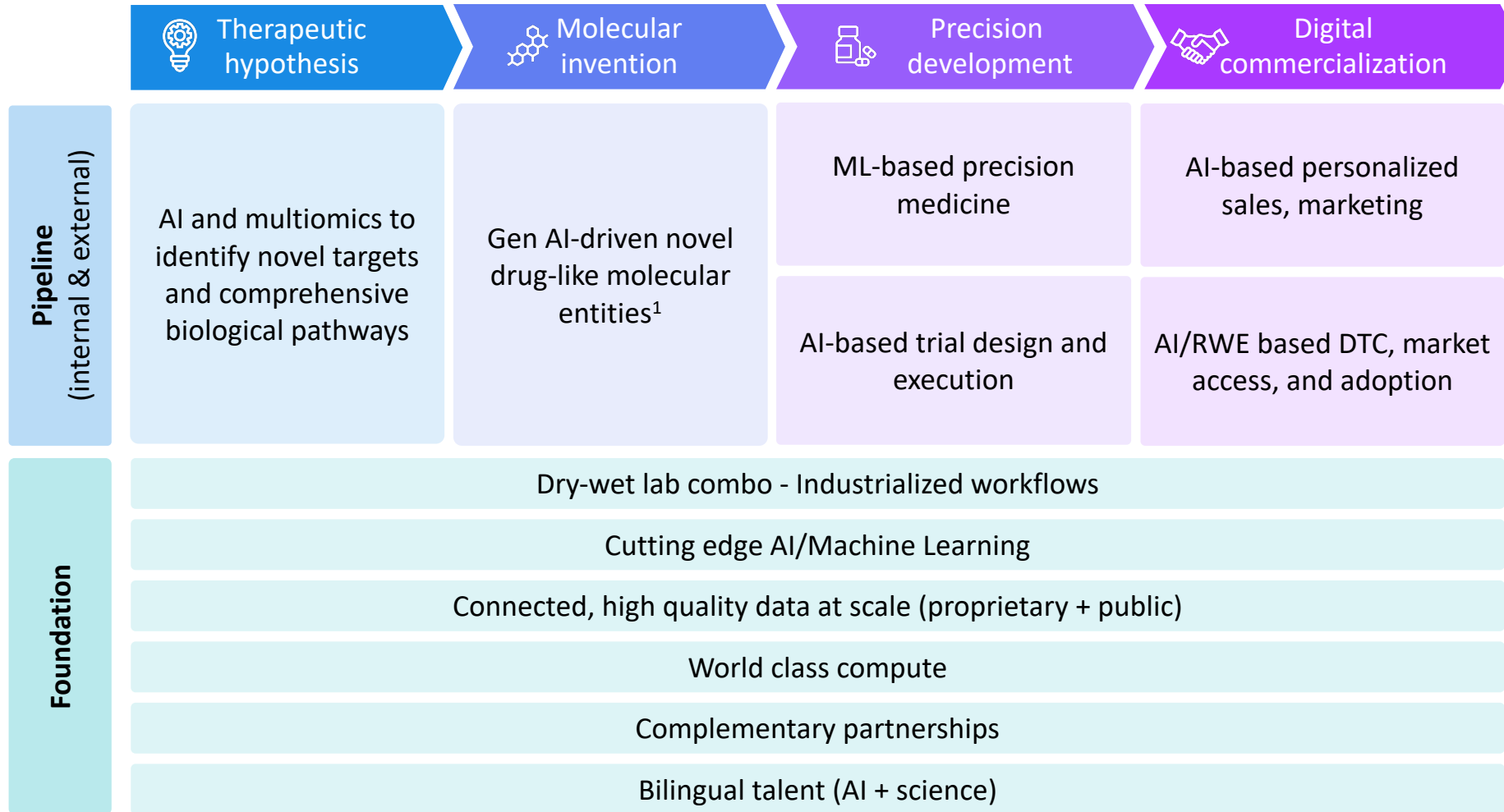
naturemedicine

Reimagining patient-centric cancer clinical trials: a multi-stakeholder international coalition



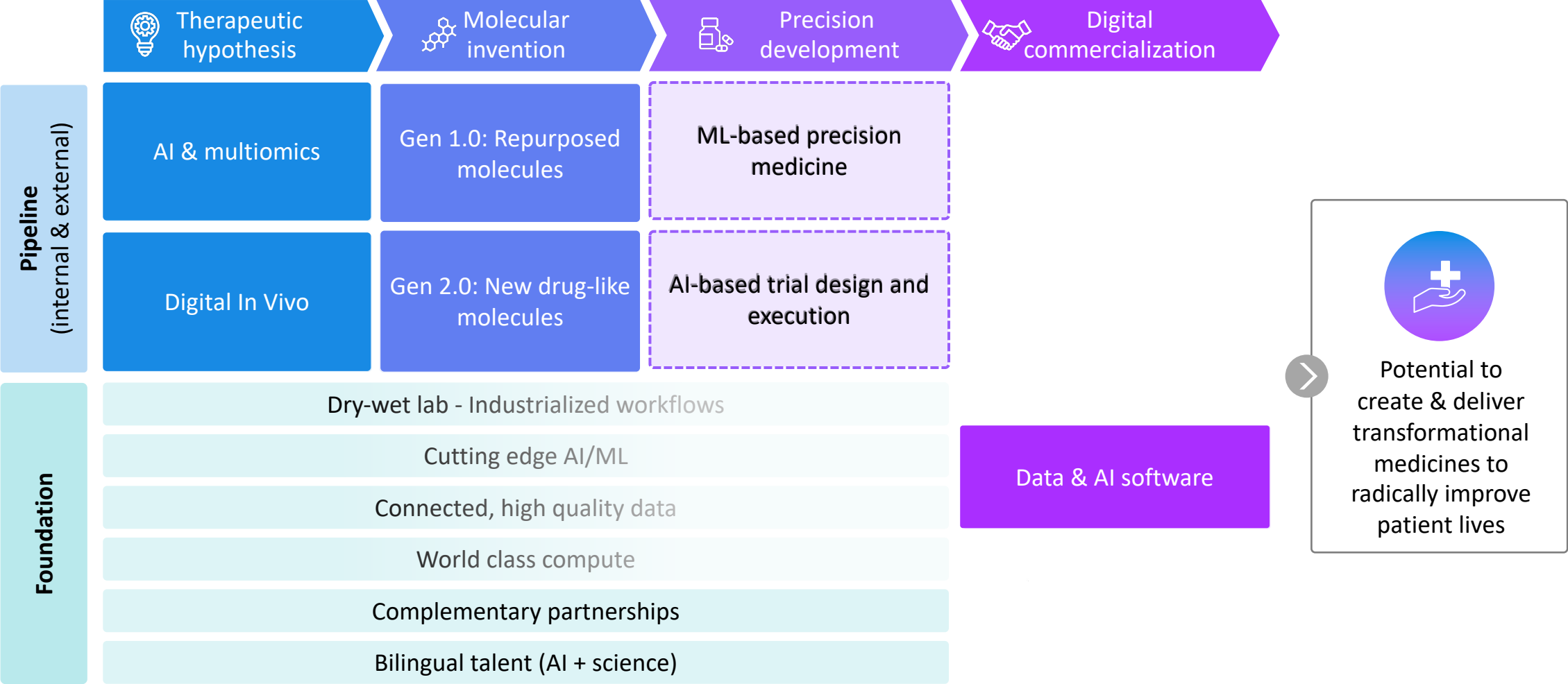
What: The pharma of tomorrow

Breadth and depth in AI and pharma excellence

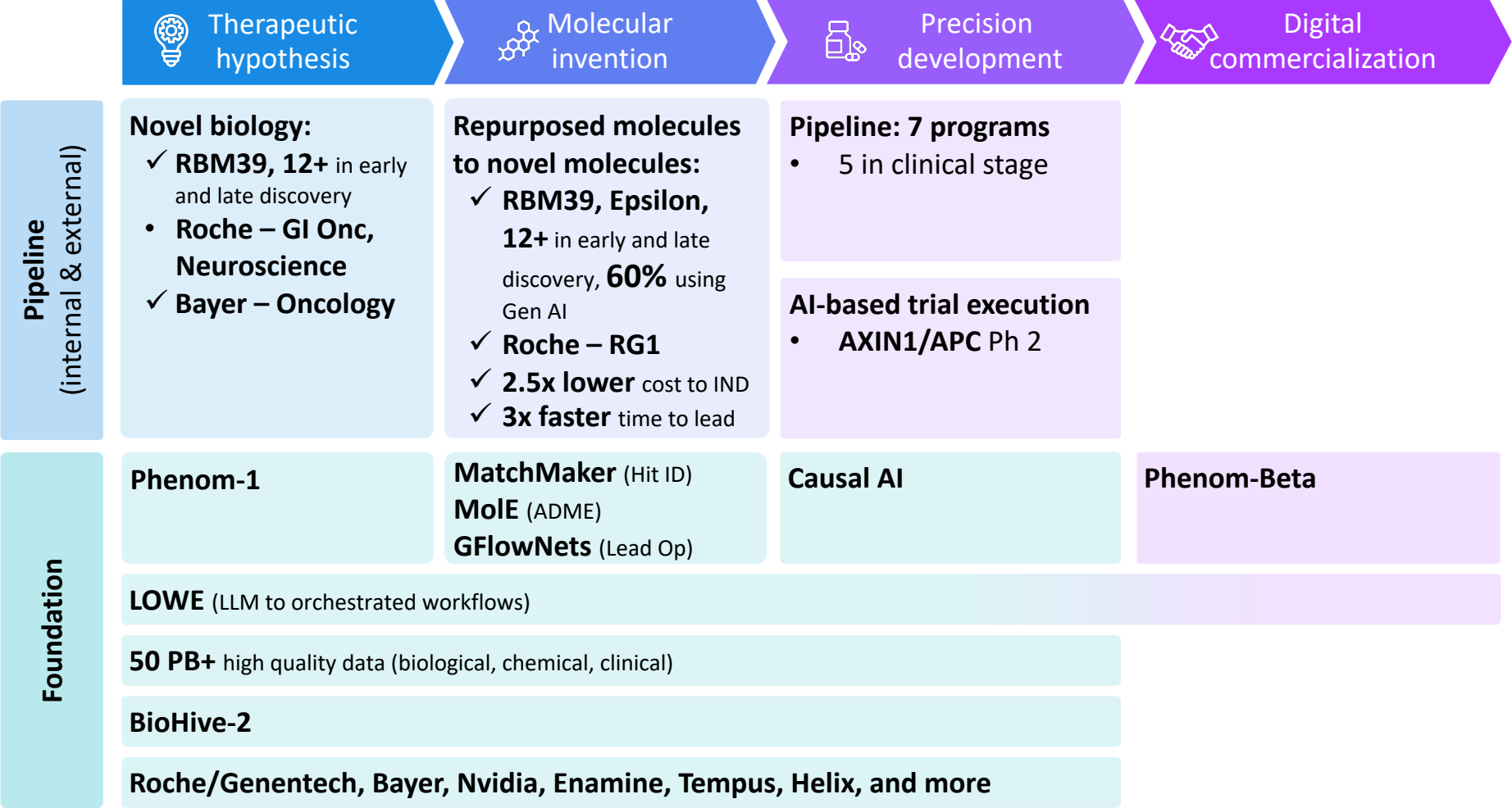



Potential to create & deliver transformational medicines to radically improve patient lives

RXRX Gen 1.0: The Rise of a TechBio



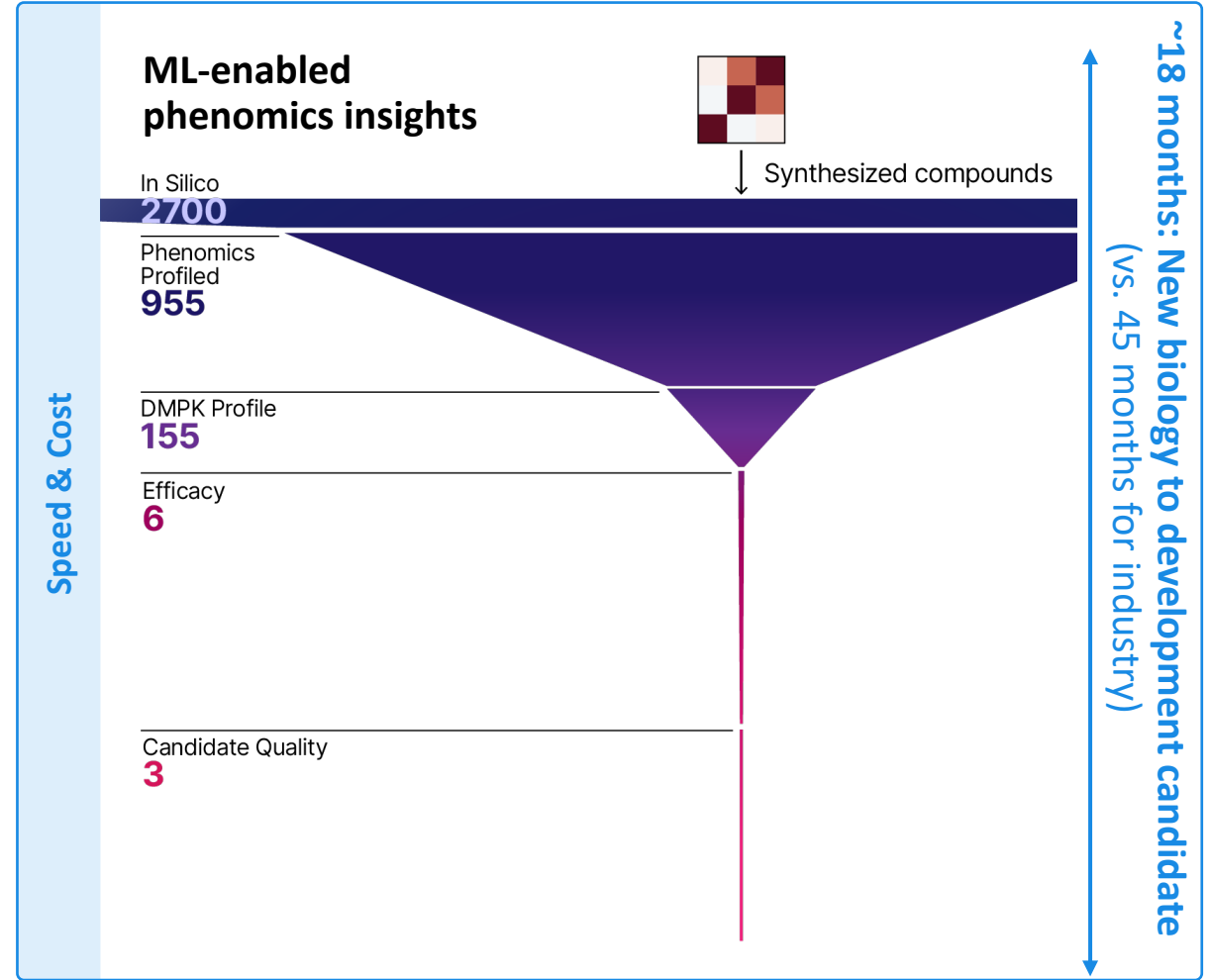
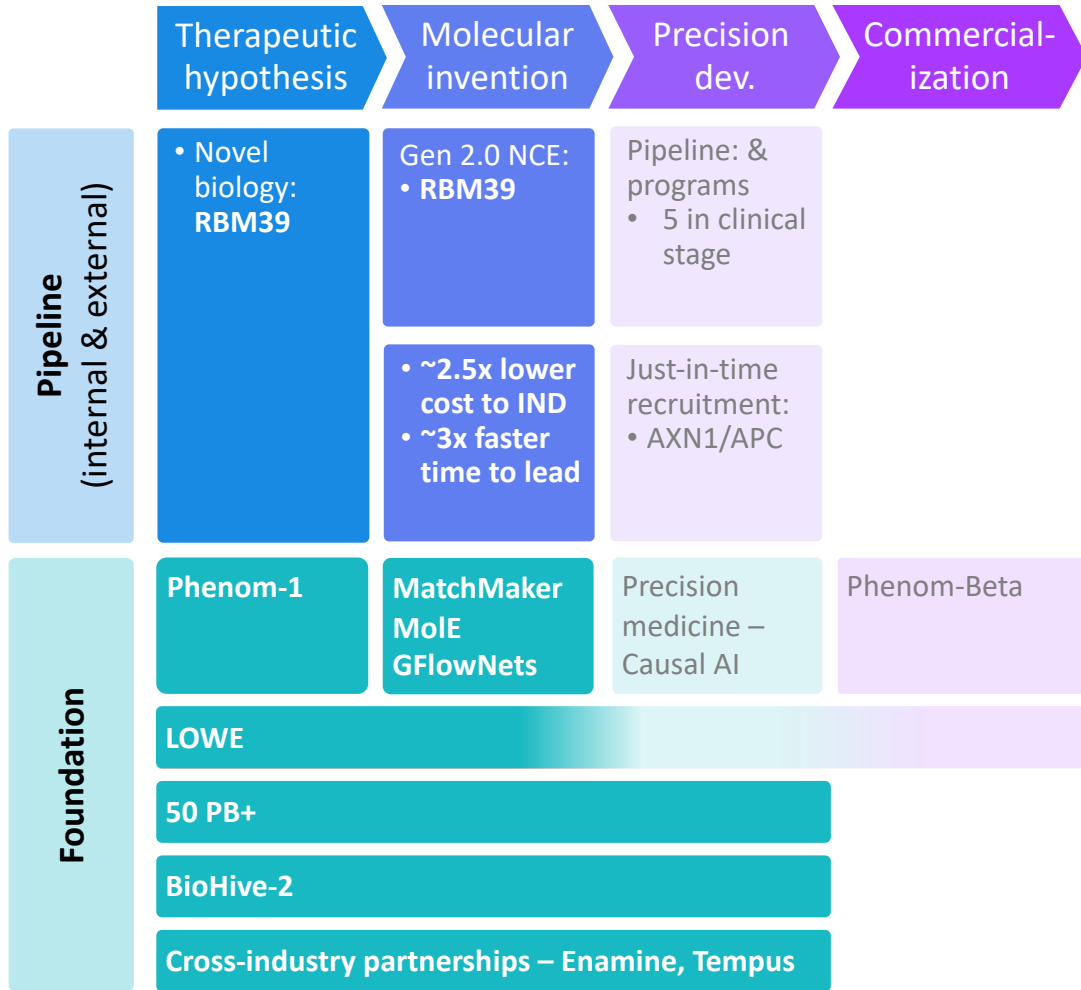
RXRX Gen 1.0: Emerging proof points



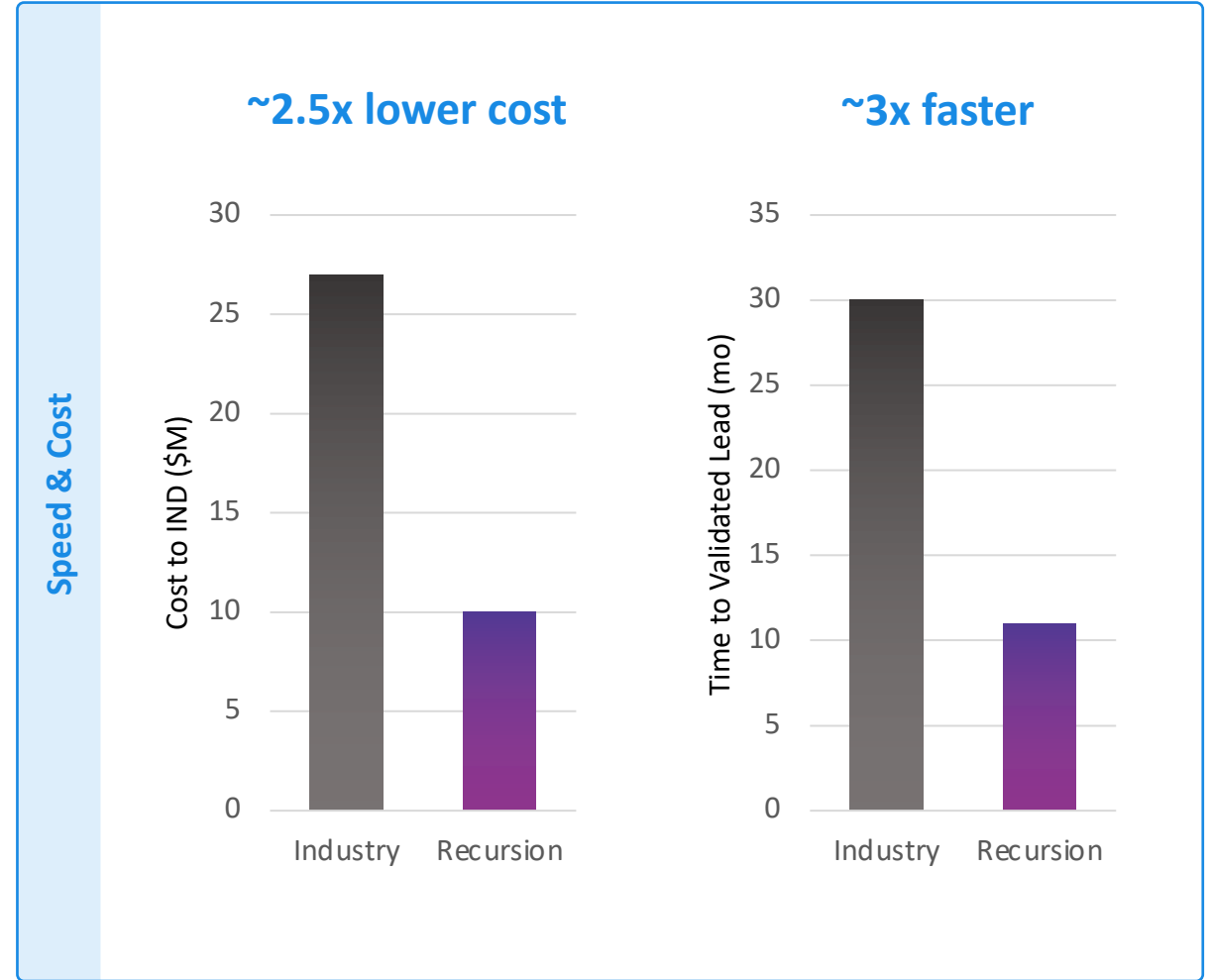
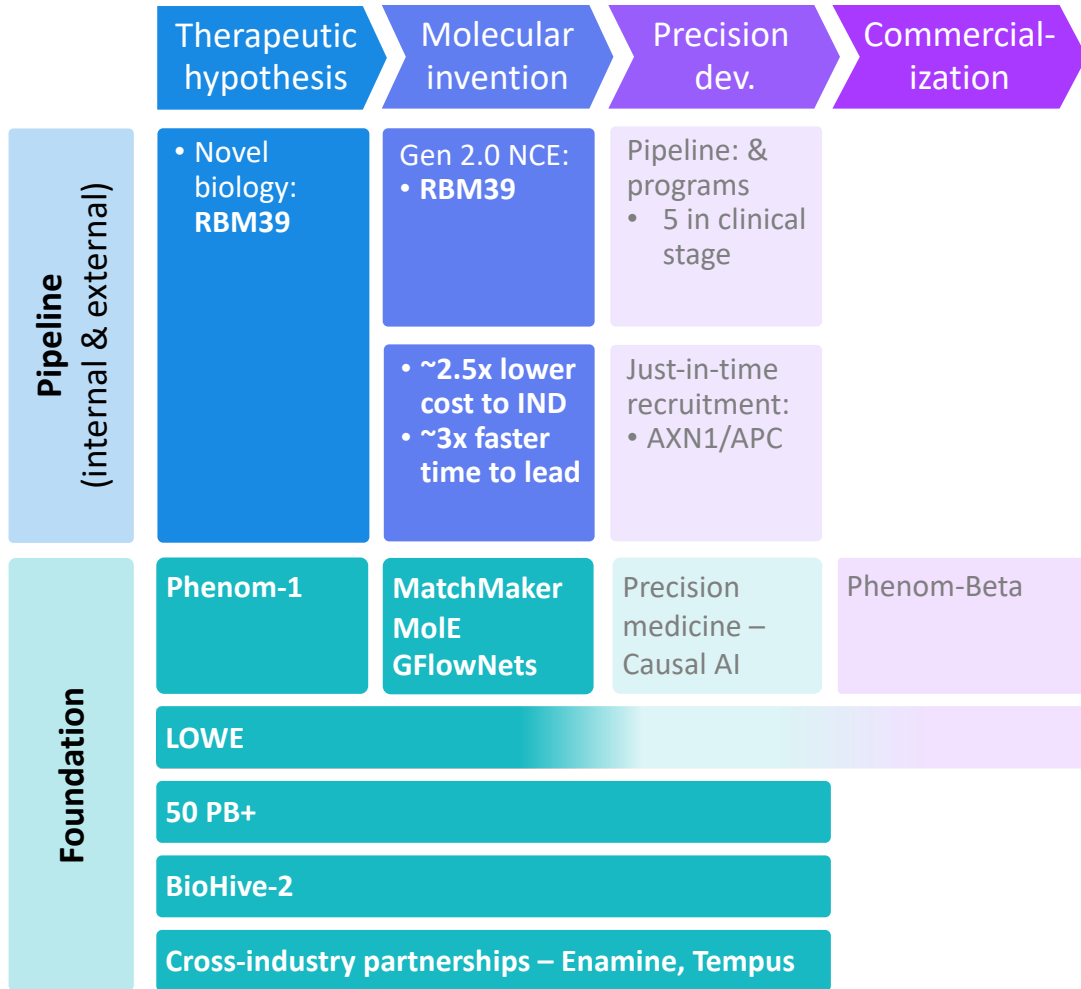


 Potential to create & deliver transformational medicines to radically improve patient lives

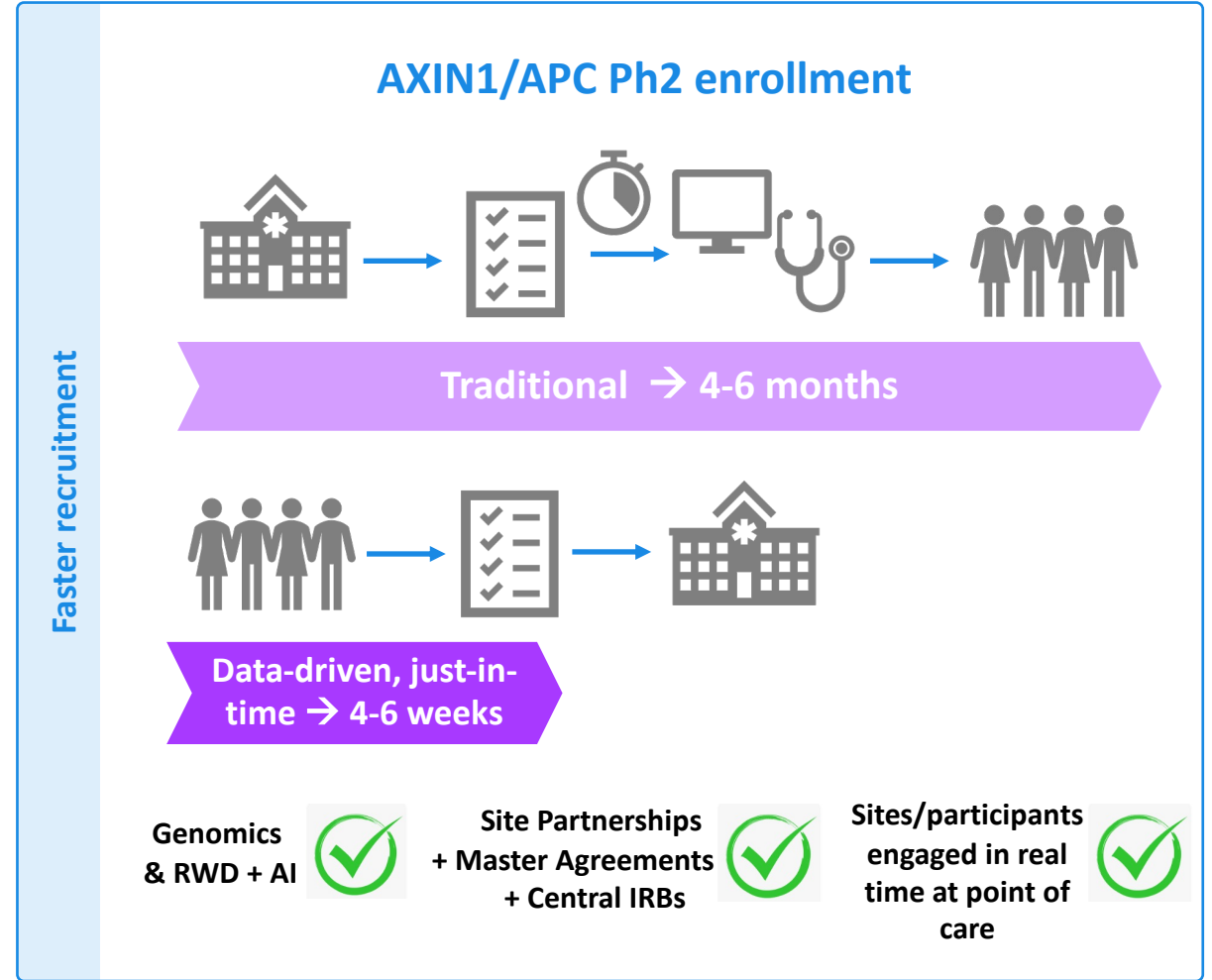
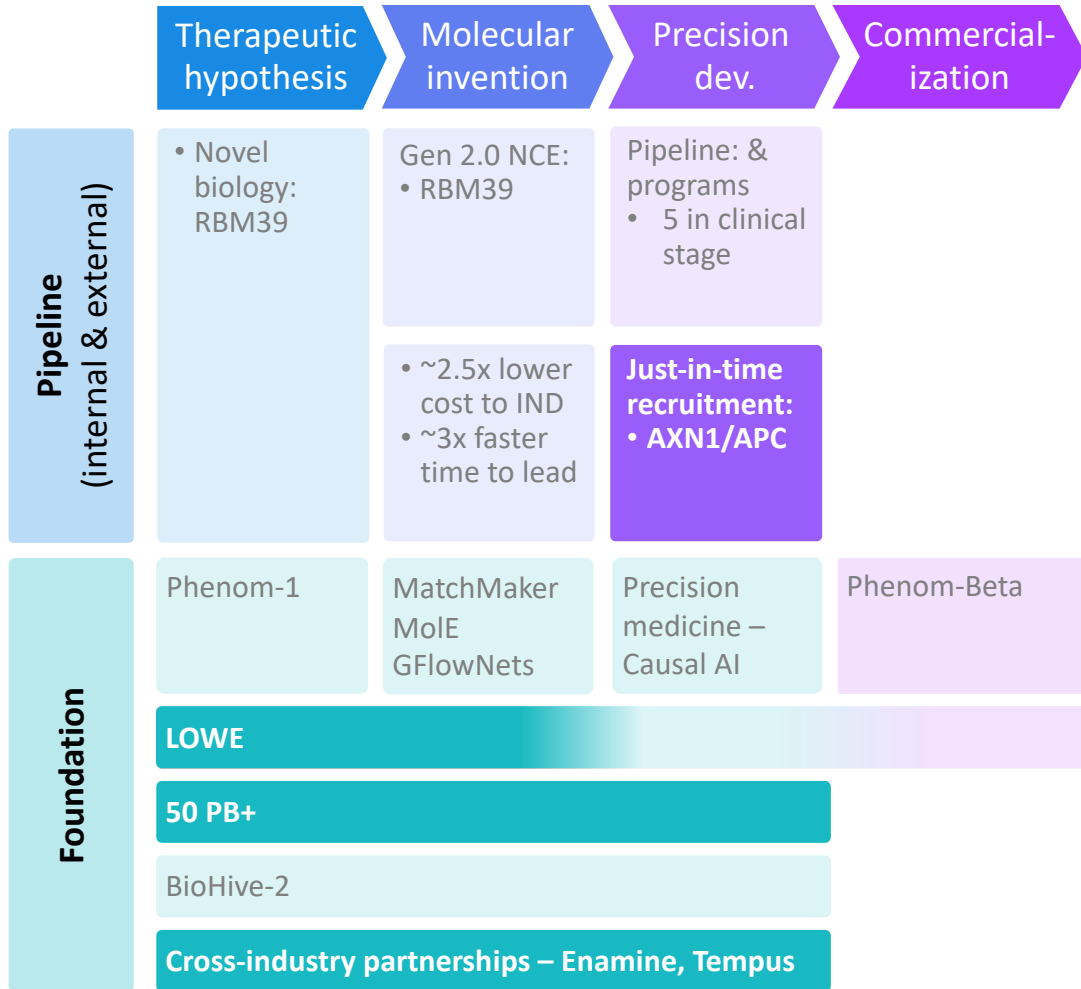
Use case 1: RBM39 – new biology and chemistry



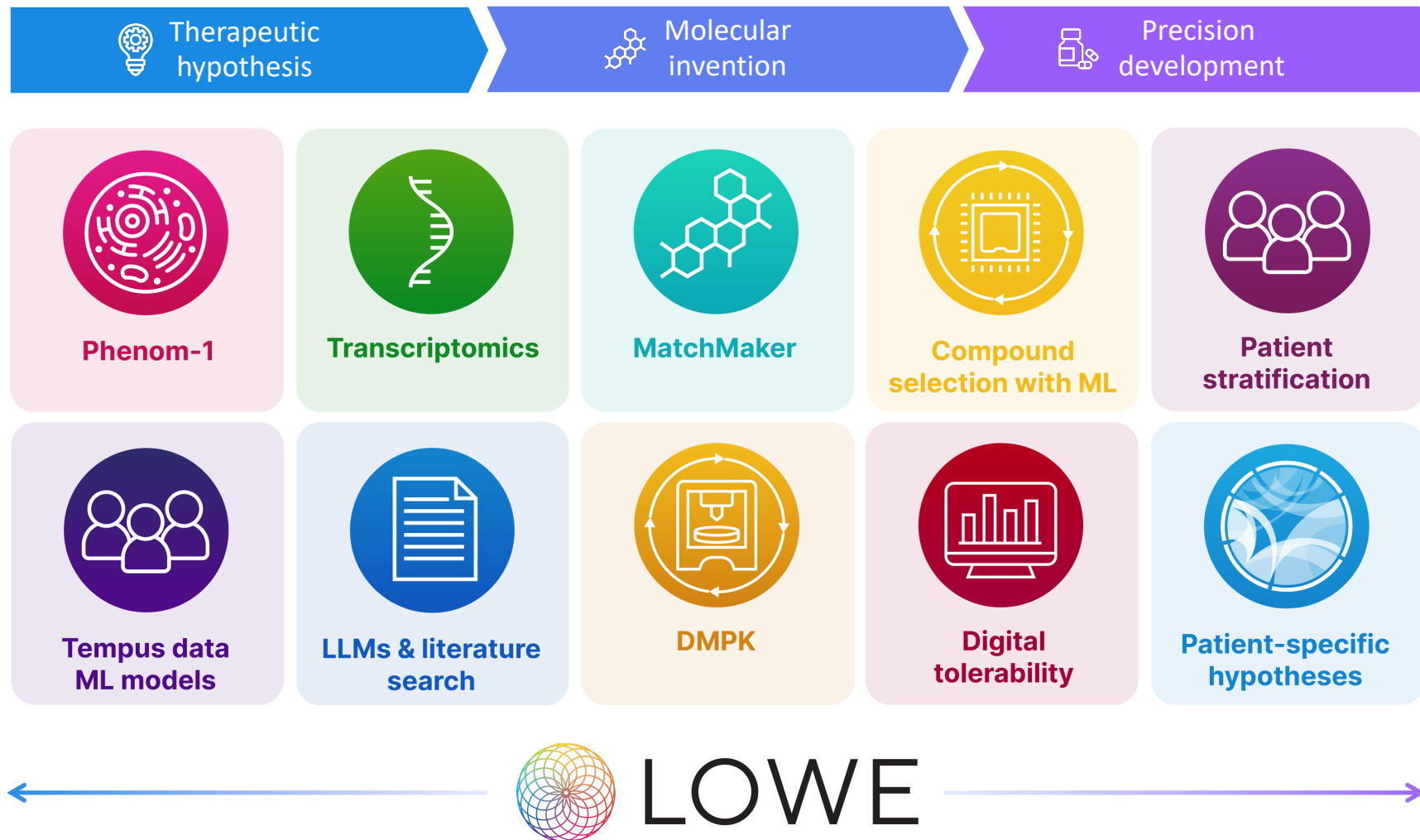
Use case 2: Faster execution, lower cost for preclinical programs



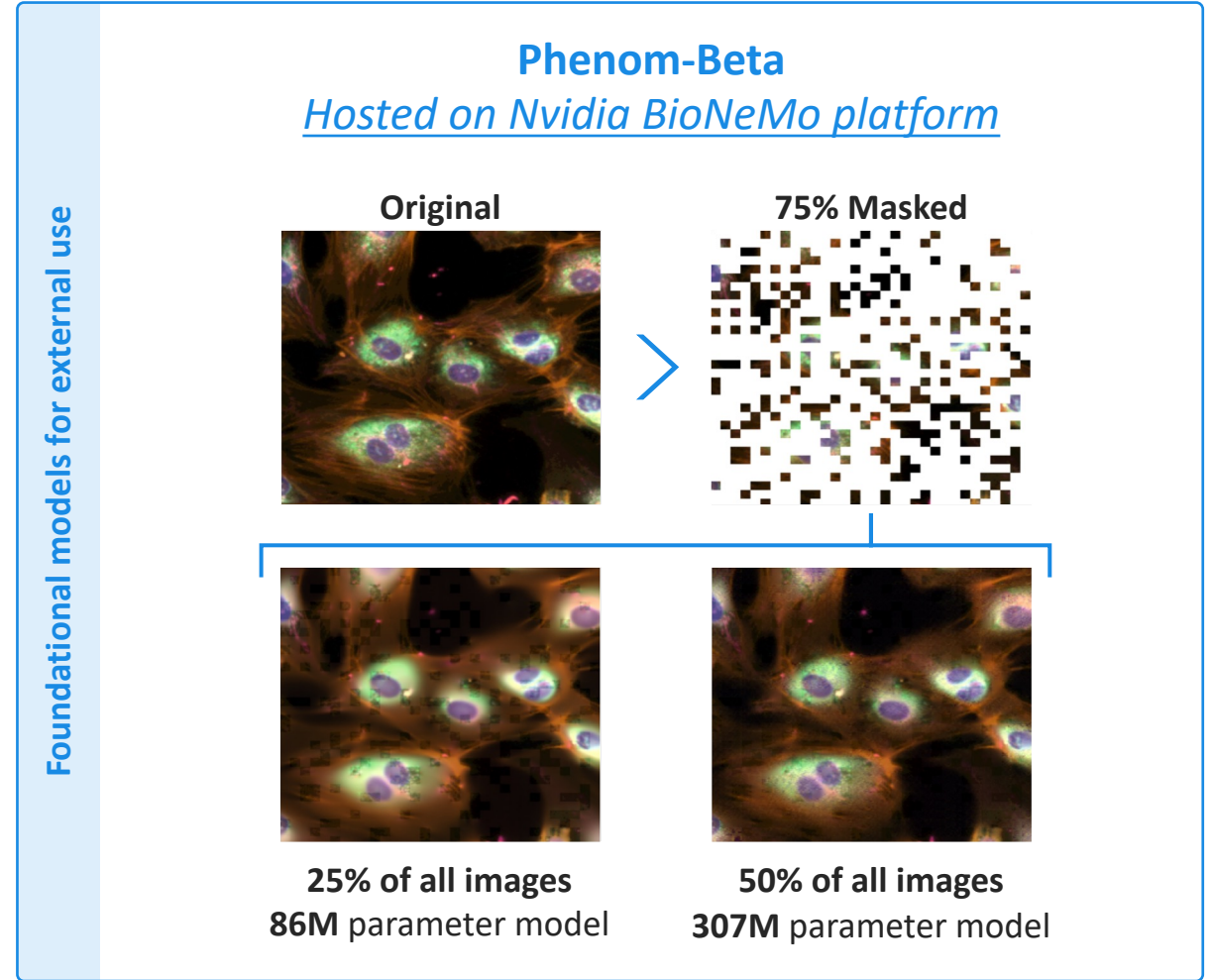
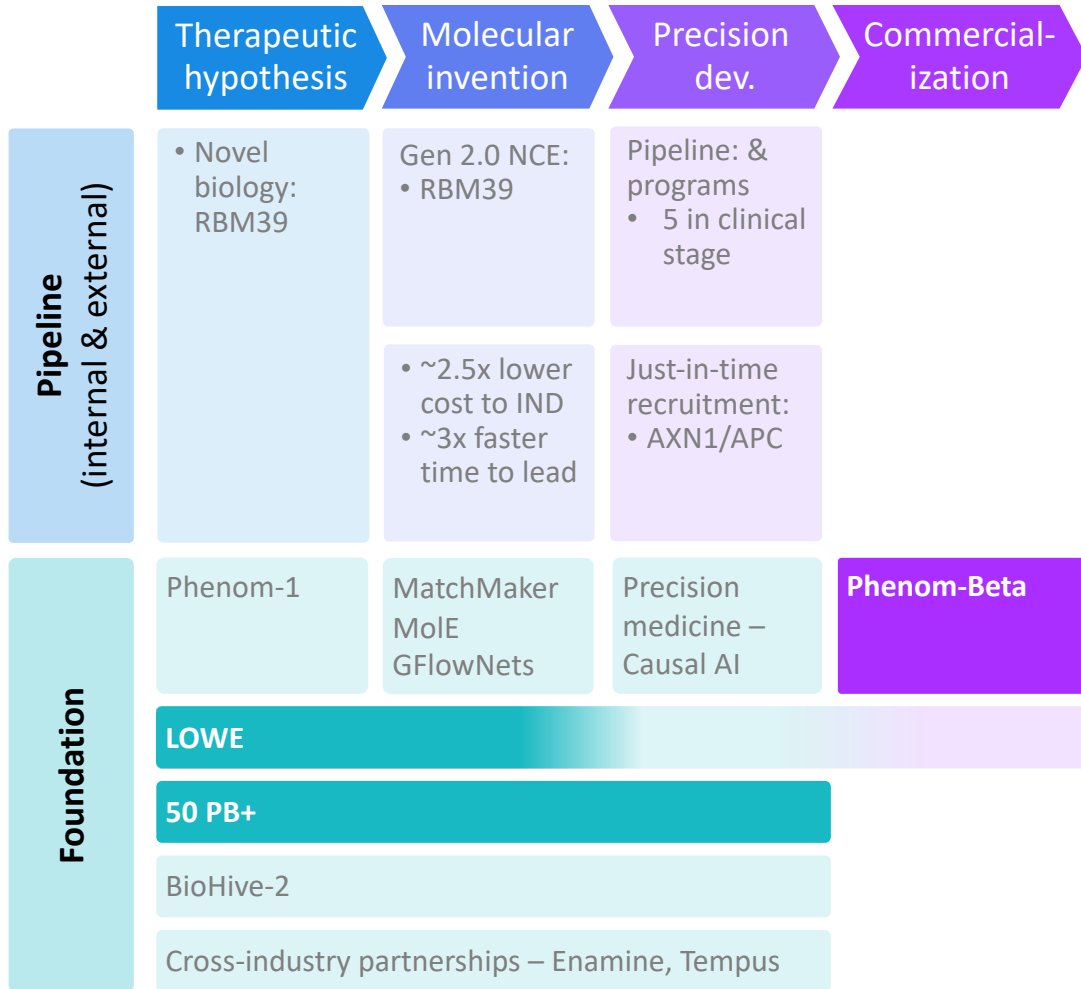
Use case 3: Advancing clinical execution using AI



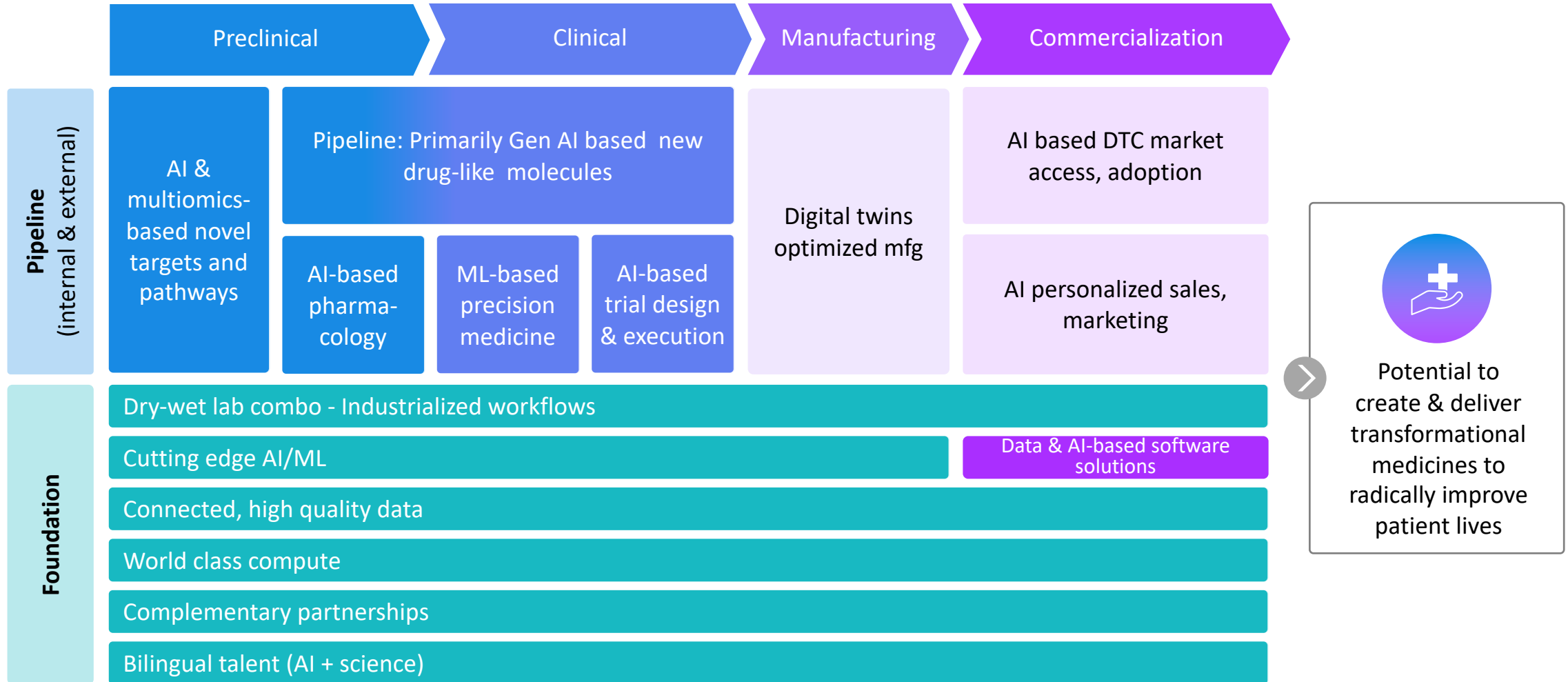
Use case 4: Suite of AI-first models



Use case 5: Foundational models for external use



What's next?



Path forward objectives – next 12 months



Advance Preclinical and Clinical Stage Programs



Enhance AI-Driven Chemistry



Innovate with AI across Clinical Development



Continue Investment in Scalable Infrastructure – wet and dry lab



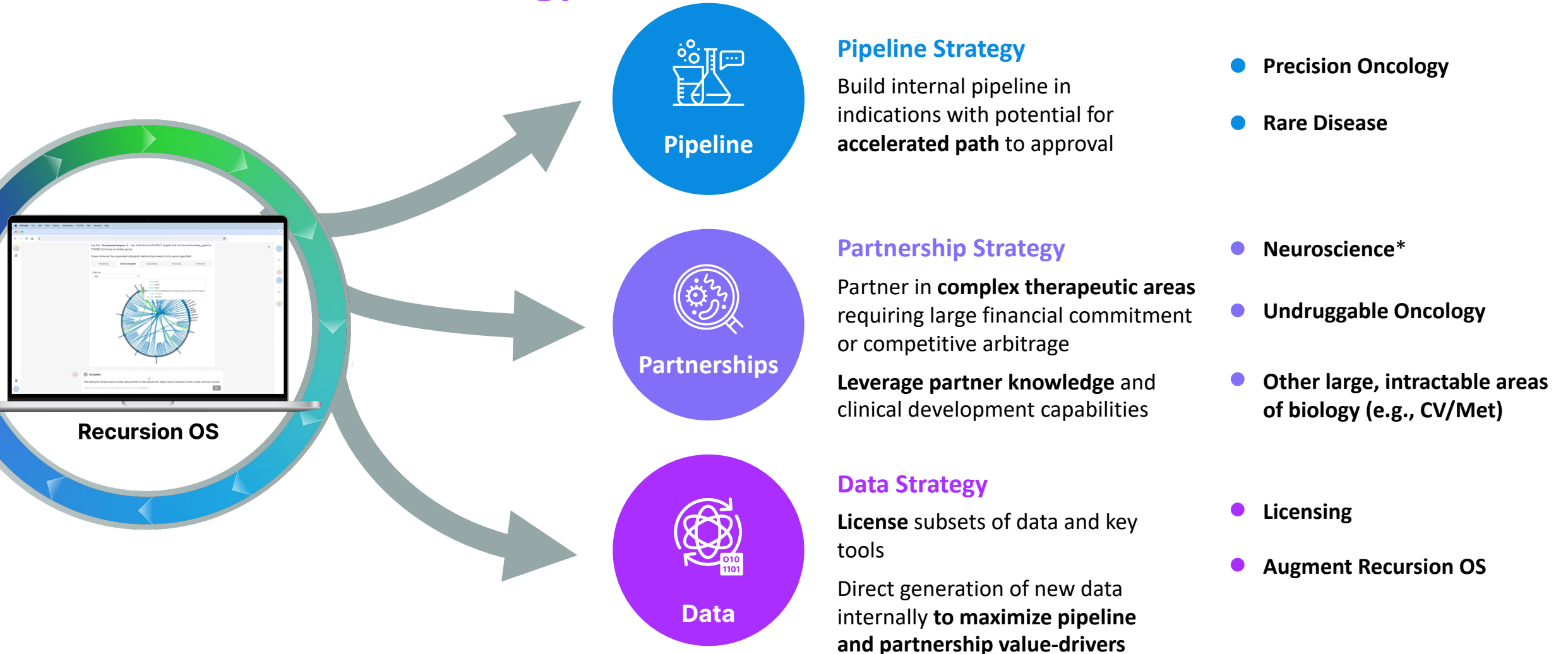
Deliver on Strategic Partnerships



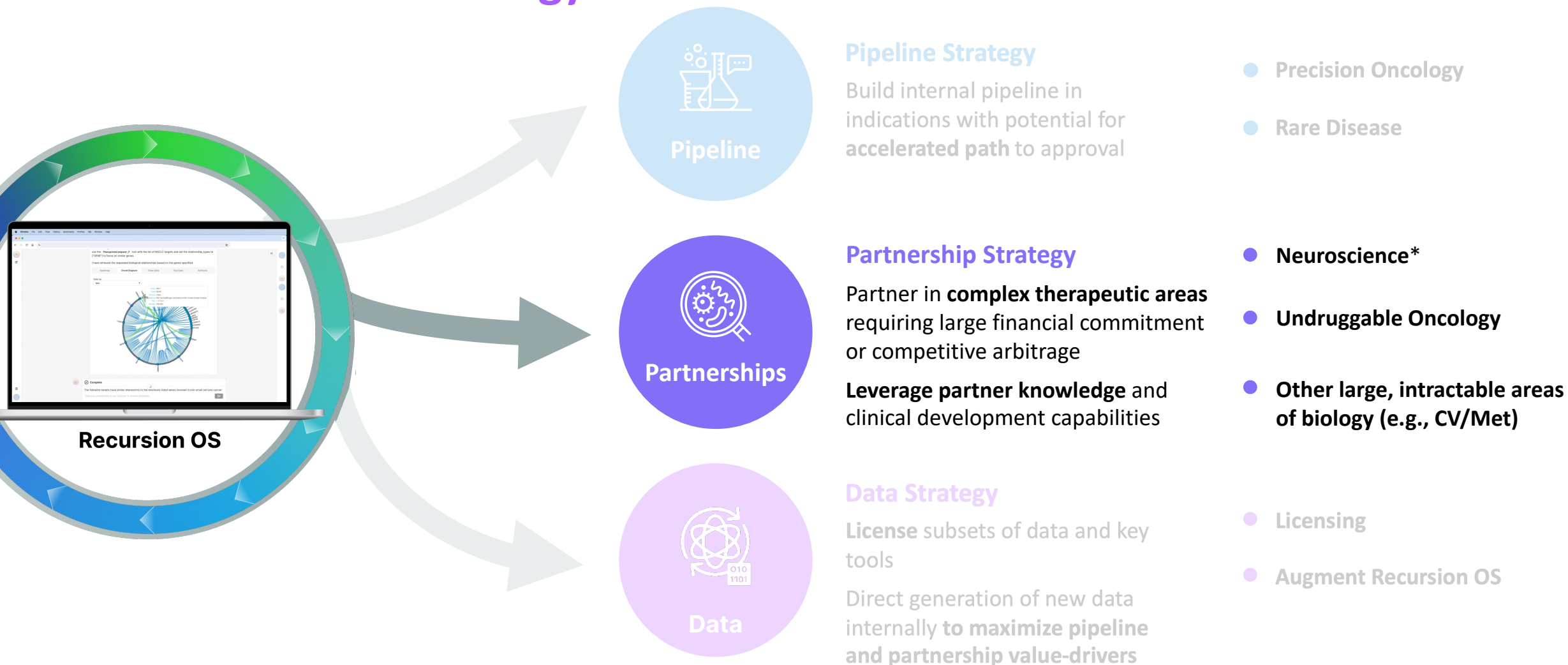
Create additional SaaS opportunities to advance the creation of medicines

Partnerships

We harness value from the Recursion OS with a multi-pronged capital-efficient business strategy



We harness value from the Recursion OS with a multi-pronged capital-efficient business strategy



Roche Genentech Partnership

Neuroscience
(and single oncology
indication)
Announced Dec 2021



**Undruggable oncology
targets**
Announced Sept 2020
Amended Nov 2023

Computational Sciences in Drug Development

John Marioni, PhD FMedSci

Senior Vice President & Head of Computational Sciences, gRED

Genentech

Fig: 1.

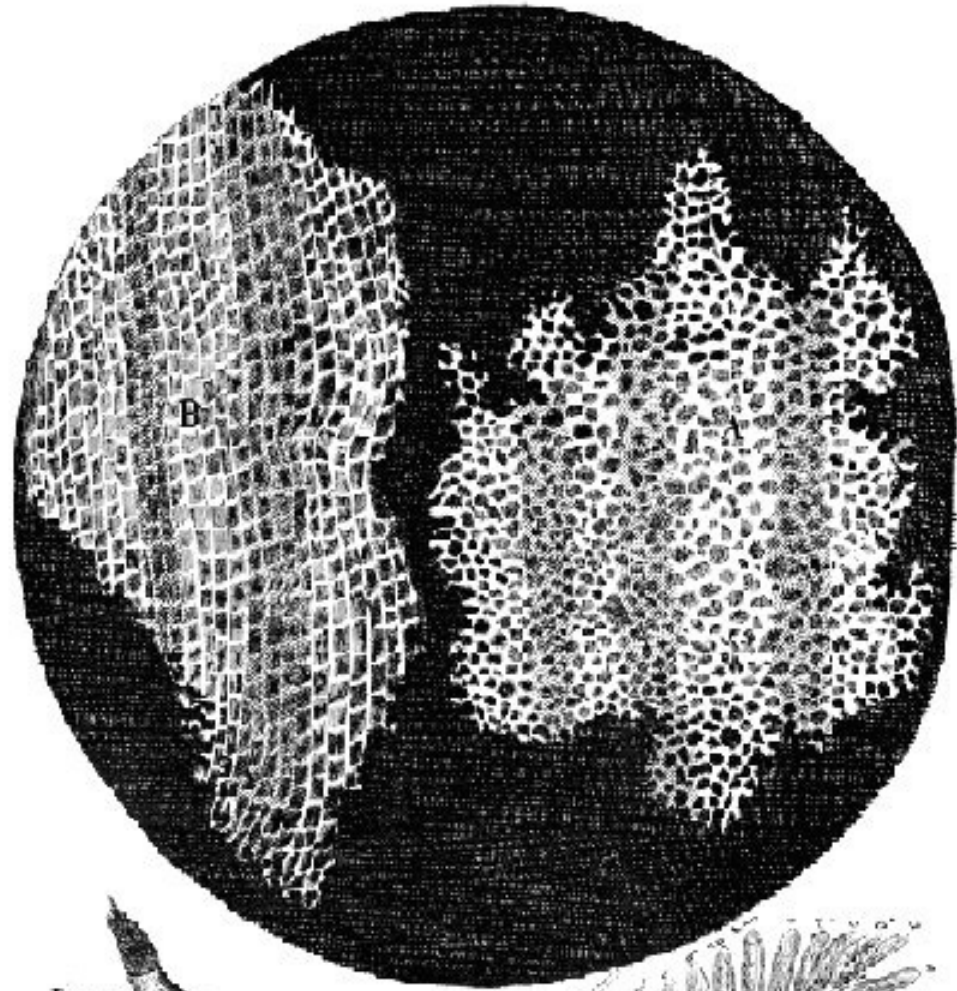
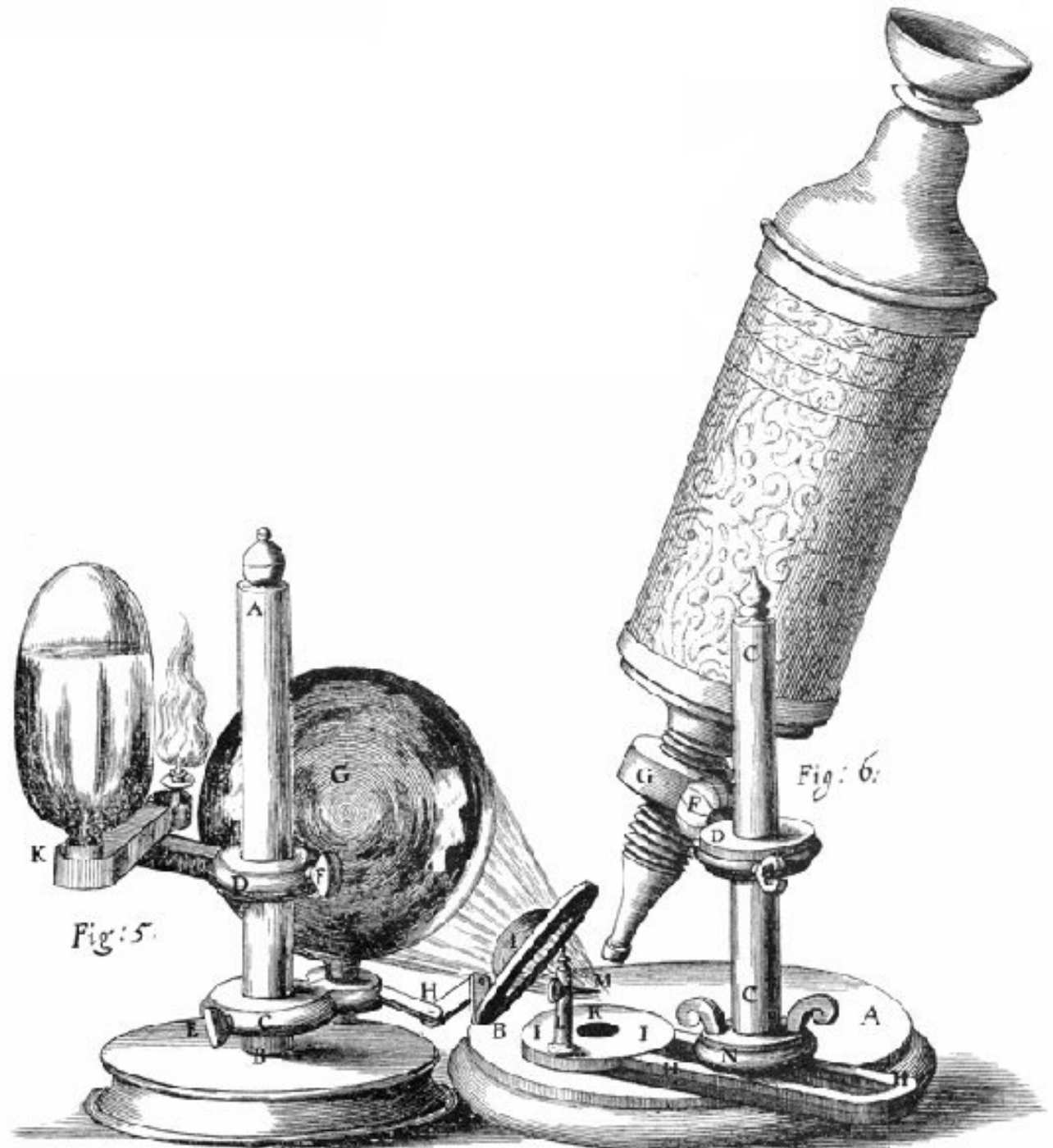
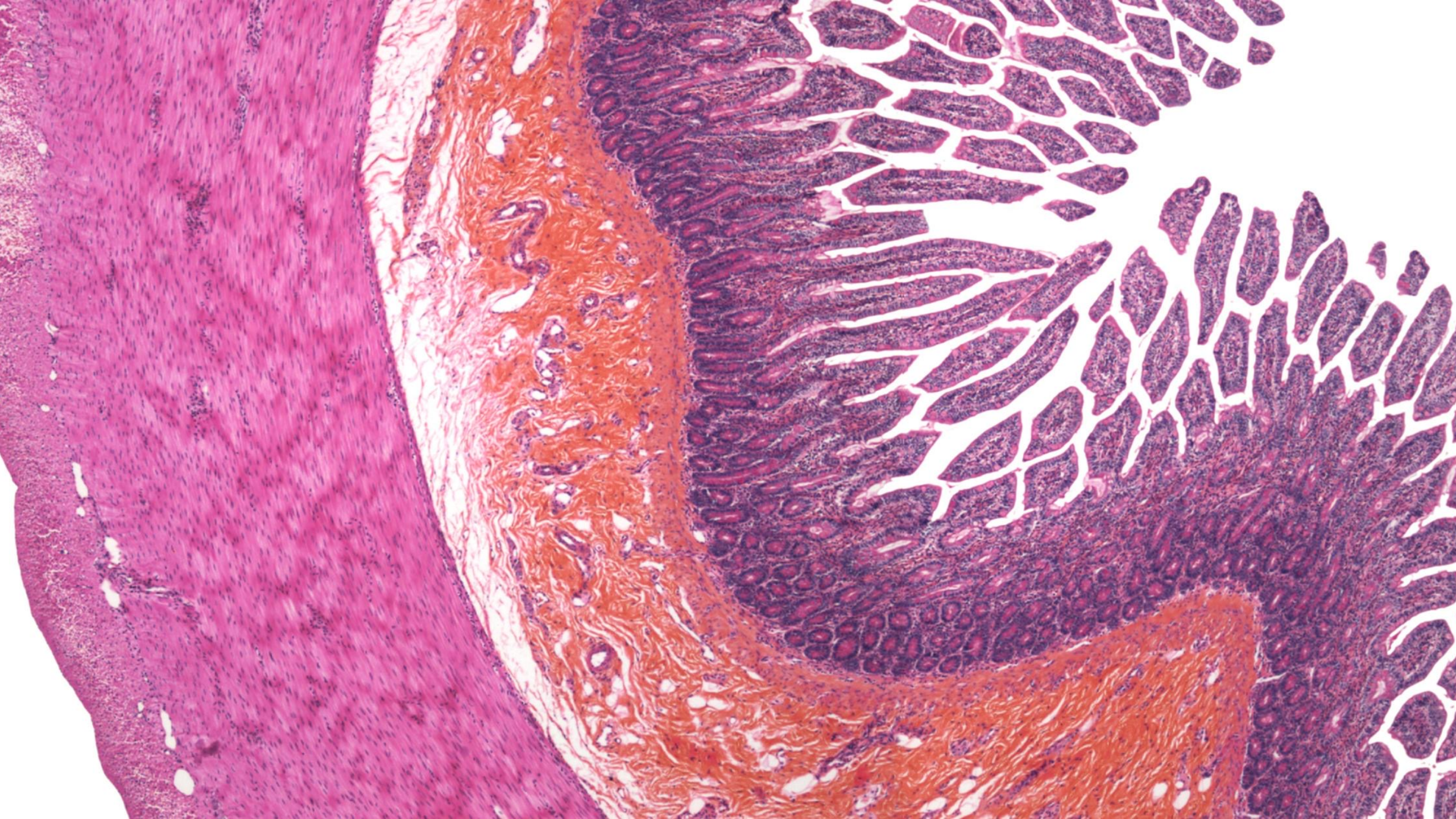
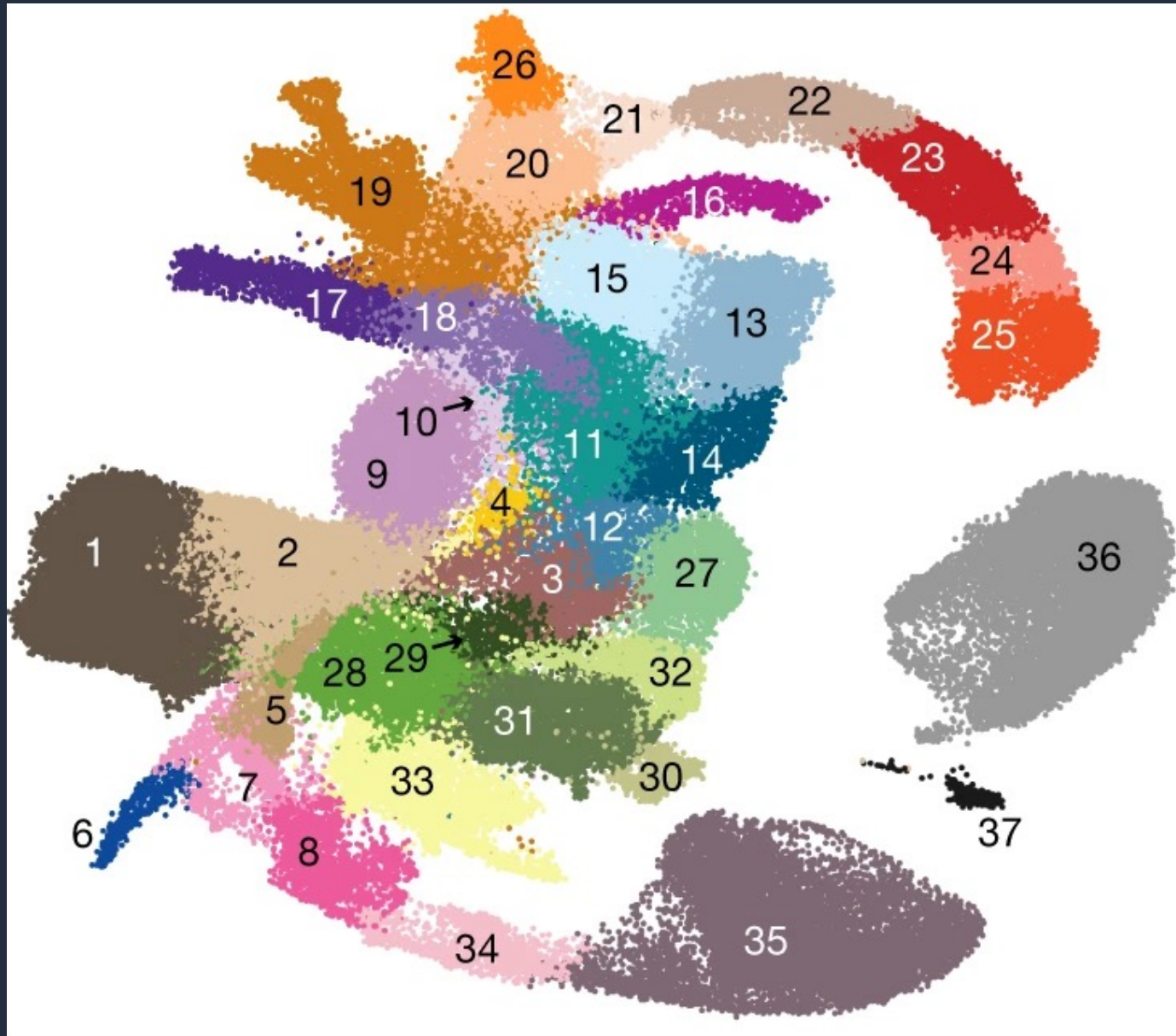


Fig: 2.







We can generate **huge amounts of data**—from both **healthy** and **perturbed** conditions... but how will we make sense of these data and make predictions about perturbations we have not seen?

10^4

CELL TYPES
AND STATES

2×10^4

GENES

4.24×10^8

VARIANT
COMBINATIONS

10^{13}

GENE
COMBINATIONS

This is one example where computational models, especially **foundation models** and **generative AI** can **transform** how we discover and develop **medicines**

This is one example where computational models, especially **foundation models** and **generative AI** can **transform** how we discover and develop **medicines**

gRED Computational Sciences (gCS) seeks to make this vision a reality

HOW?

DATA



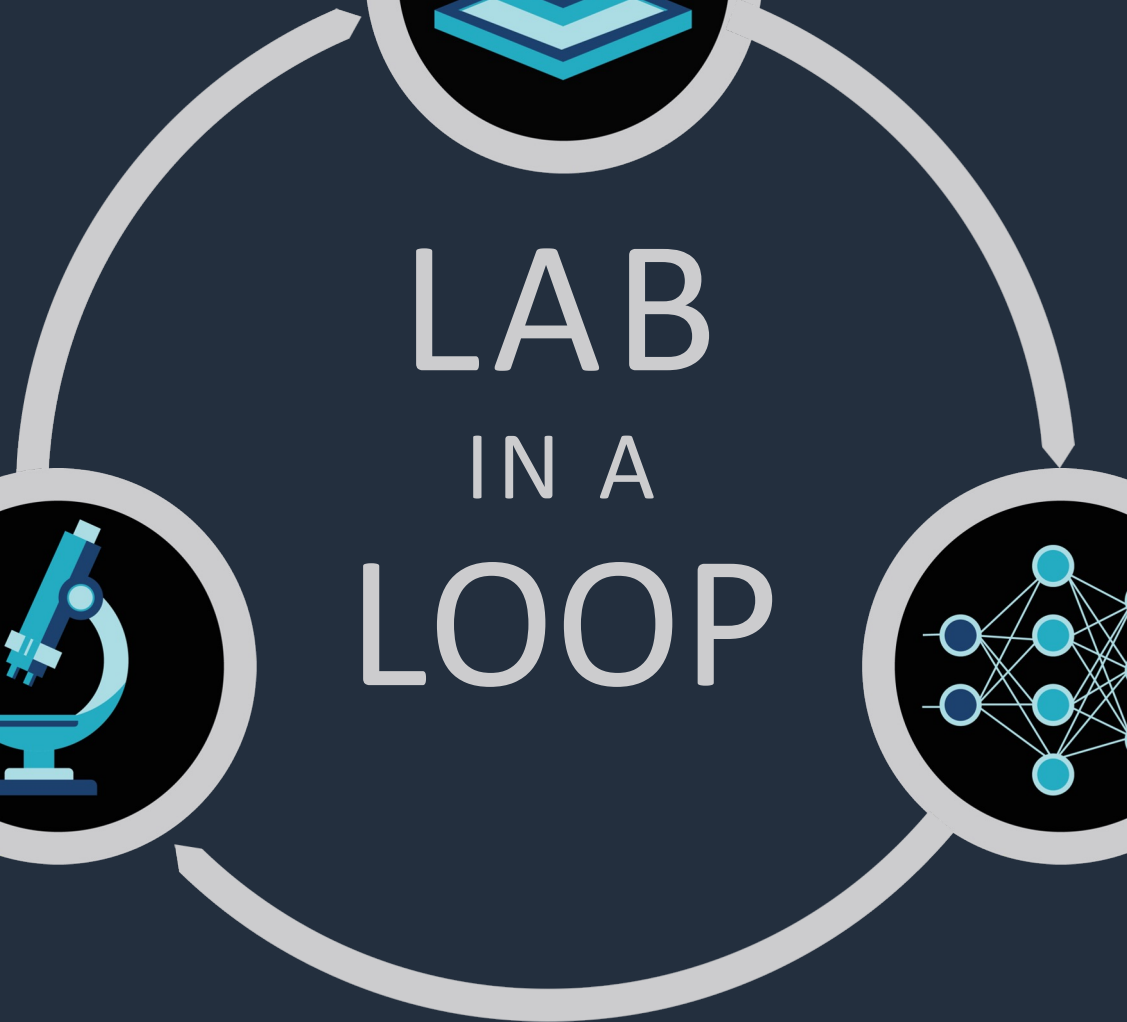
LAB
IN A
LOOP



AI/ML

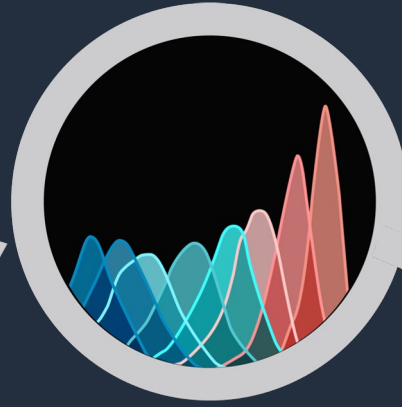


EXPERIMENT



TGCGAGGCACCCAGCTCTTIGAGGACAACACTATGCCCTGGCCGTGCTAGACAATGGAGACCCGCTGAACAATACCACC
AGGGGCCTCCCCAGGAGGCCTGCGGGAGCTGCAGCTTCGAAGCCTCACAGAGATCTTGAAAGGAGGGGGTCTTGATCC
CCCAGCTCTGCTACCAGGACACGATTTTGTGGAAGGACATCTTCCACAAGAACAACCAGCTGGCTCTCACACTGATAG
CTCTCGGGCCTGCCACCCCTGTTCTCCGATGTGTAAGGGCTCCCGCTGCTGGGGAGAGAGTCTGAGGATTGTCAGAG
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GACACCTAGCGGAGCGATGCCCAACCAGGCGCAGATGCGGATCCTGAAAGAGACGGAGCTGAGGAAGGTGAAGGTGC
CGCTTTTGGCACAGTCTACAAGGGCATCTGGATCCCTGATGGGGAGAATGTGAAAATTCCAGTGGCCATCAAAGTGTT
CATCCCCAAAGCCAACAAAGAAATCTTAGACGAAACGATCTCAA ACTTATTCTCAA ACTTCGCCCCGAGAGGGCCCT
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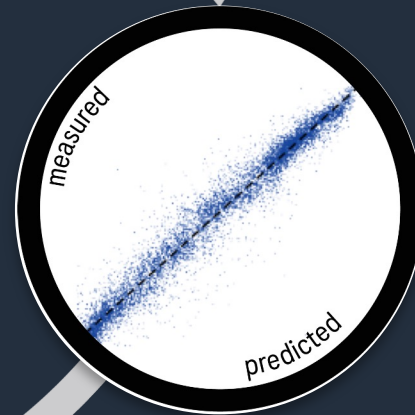
DATA



TRANSFORMER
BASED ORACLE

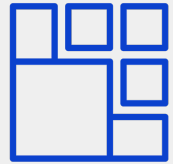
4^{80}
possibilities

EXPERIMENT

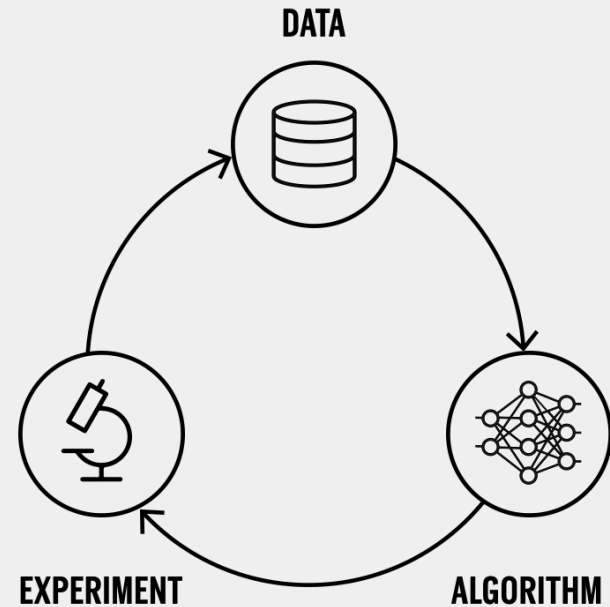


AI/ML

Our AI strategy for R&D



Lab in a Loop,
integrated

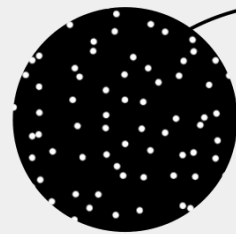


Full stack, across all aspects of R&D; up to “self drive”

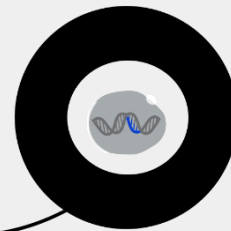


Scale & resolution

QUANTITY



QUALITY



Maximize benefit of large size: proprietary legacy data and data generation capacity



Strategic
partnerships

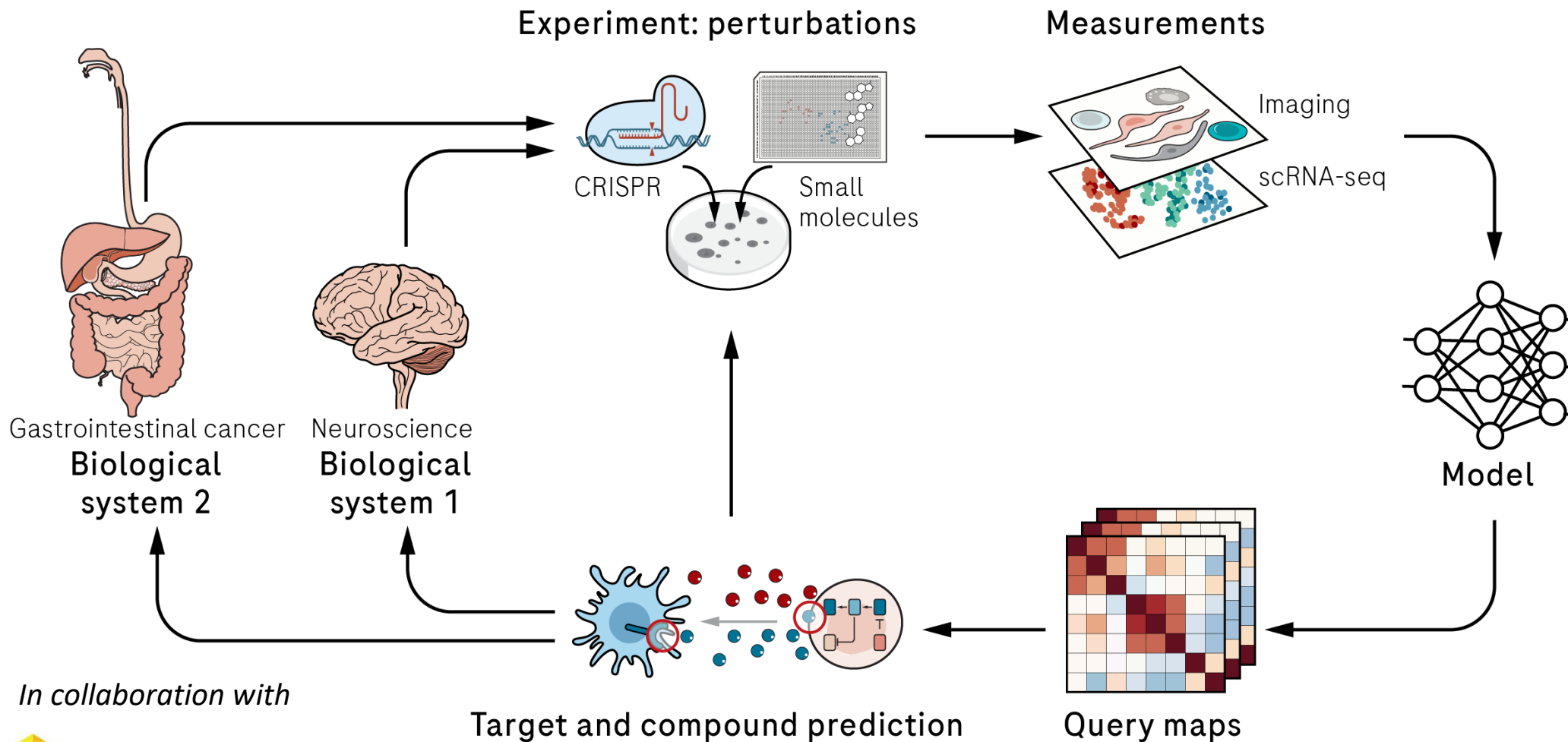
Key partnerships:



Partnership around unique data generation, AI/ML model development and hardware



RIGHT
TARGET OR
CHEMICAL
MATTER
FOR THE
DISEASE



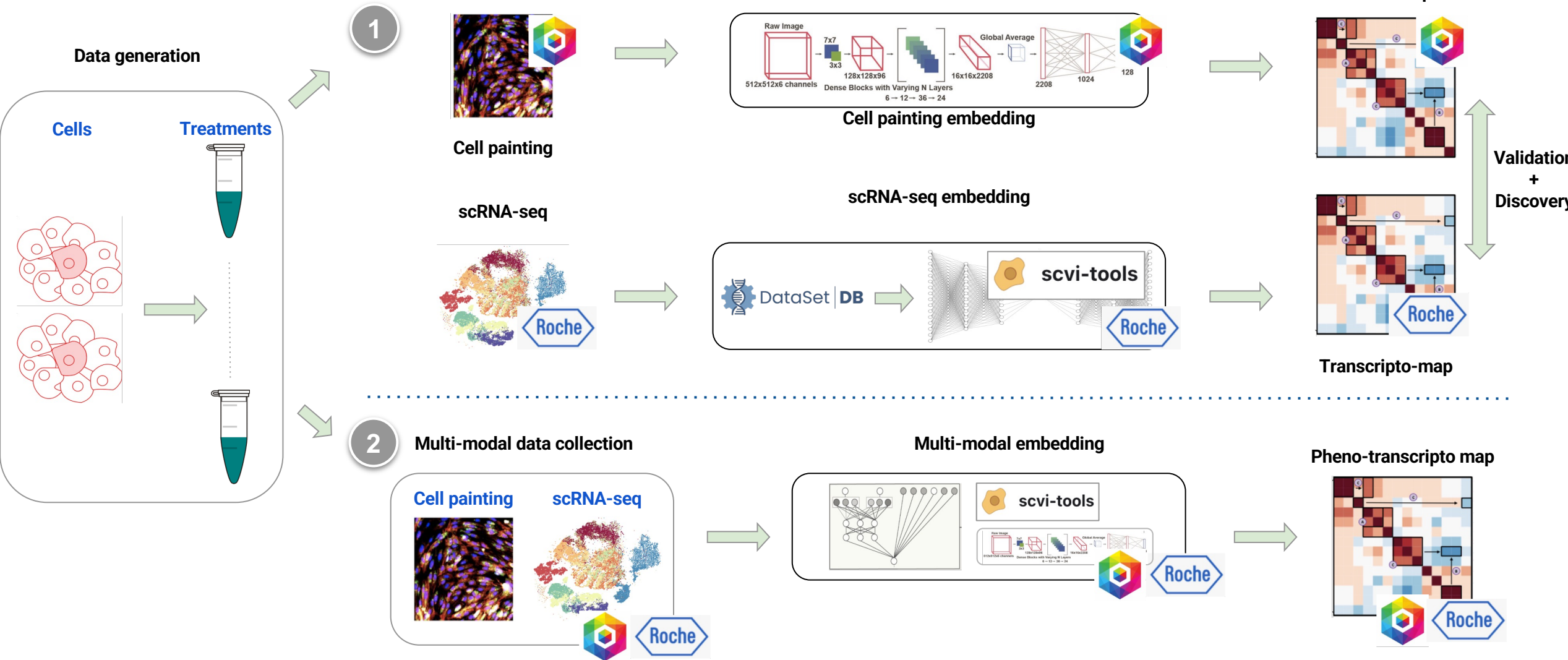
In collaboration with





RIGHT
MOLECULE

Multi-Modal Model Development



**MODELS ARE ONLY
AS GOOD AS
THE DATA**

Challenges

Data management, metadata and access

Integrating expertise from multiple disciplines

Access to scalable scientific computing for fitting/fine-tuning models

Democratizing access and ensuring use of data and models

Challenges... But already driving to solutions

Data management, metadata and access: modernizing our data stack and exploiting the cloud and associated tools

Integrating expertise from multiple disciplines: internal organizational structure and external partners

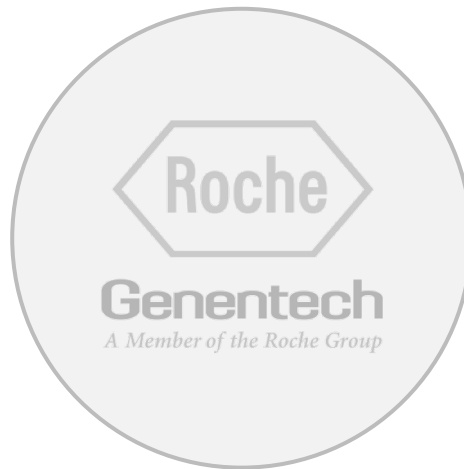
Access to scalable scientific computing for fitting/fine-tuning models: partnering with outstanding companies in the industry

Democratizing access and ensuring use of data and models: Autonomous agents as the next-generation scientific assistant

THANK YOU!

Bayer Partnership

Neuroscience
(and single oncology
indication)
Announced Dec 2021



**Undruggable oncology
targets**

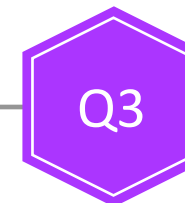
Collaboration announced Sept 2020
Amended Nov 2023

Scientific Collaborations: Undruggable Oncology Targets



Nov 2023
pivot to Oncology

Work initiated



On track to complete
25 unique multi-modal
data packages in Q3

Initiated 1st joint Project which
will now be advancing rapidly
towards Lead Series nomination

**Bayer expected to be the first
beta-user of our LOWE LLM-
orchestrated workflow software**

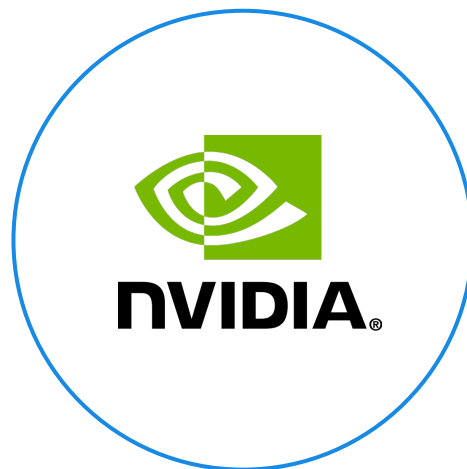
Scientific Collaborations: Undruggable Oncology Targets



Scientific Collaborations: Platform, Tech, and Data

Computation and
ML/AI

Announced July 2023

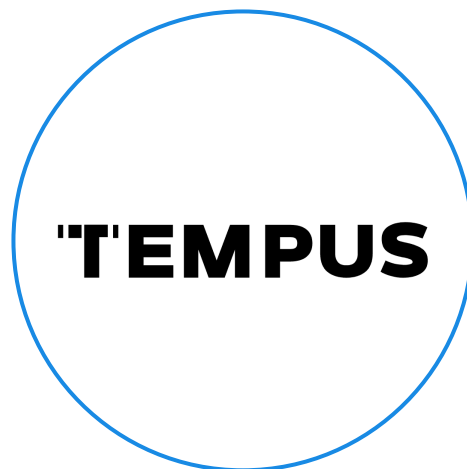


Cheminformatics and
chemical synthesis

Announced Dec 2023

Real-world data access
(oncology)

Announced Nov 2023



Real-world data access
(non-oncology)

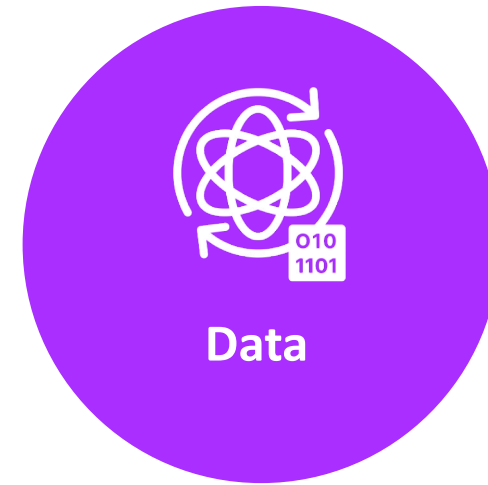
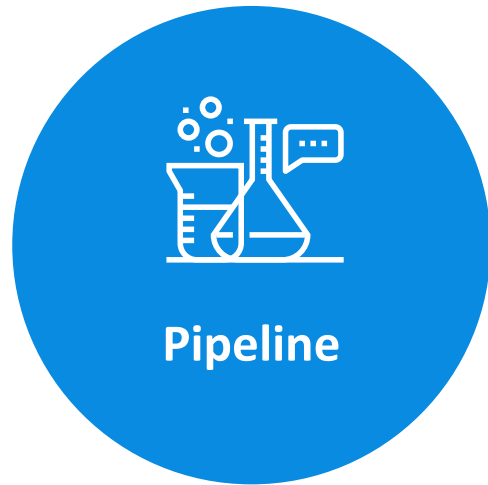
Announced May 2024

Scientific Collaborations: Real world (de-identified) data



- Multi-site network protocol continuously aggregating in **various therapeutic areas**
- **Geographically and demographically diverse** population consented for re-contact
- **Whole exome sequencing** paired with rich, **longitudinal clinical data** for all consenting patients
- Access to **hundreds of thousands of unique records** each year

We harness value from the Recursion OS with a multi-pronged capital-efficient business strategy



Clinical

Our pipeline reflects the scale and breadth of our approach

	Program	Indication	Target	Patient Population	Preclinical	Phase 1	Phase 2	Phase 3	Anticipated Near-Term Milestones
Rare & Other	REC-994	Cerebral Cavernous Malformation	Superoxide	~ 360K ¹	SYCAMORE				Topline readout in September 2024
	REC-2282	Neurofibromatosis Type 2	HDAC	~ 33K ²	POPLAR				Preliminary data readout in Q4 2024
	REC-4881	Familial Adenomatous Polyposis	MEK	~ 50K ³	TUPELO				Preliminary data readout in H1 2025
	REC-3964	<i>Clostridioides difficile</i> Infection	TcdB	~730K	ALDER				Ph2 initiation in Q4 2024
	Epsilon	Fibrotic Diseases	Undisclosed	~ 50K ^{4,5,6}					IND submission in early 2025
Oncology	REC-4881	Advanced AXIN1/APC-mutant Cancers	MEK	~ 104K ⁷	LILAC				Preliminary data readout in H1 2025
	RBM39	Advanced HR-Proficient Cancers	RBM39	~ 220K ⁸					IND submission in Q3 2024, Ph 1/2 initiation in Q4 2024

More than a dozen discovery and research programs in oncology or with our partners – first program optioned by Roche-Genentech in GI-oncology

All populations defined above are US and EU5 incidence unless otherwise noted. EU5 is defined as France, Germany, Italy, Spain, and UK. (1) Prevalence for hereditary and sporadic symptomatic population. (2) Annual US and EU5 incidence for all *NF2*-driven meningiomas. (3) Prevalence for adult and pediatric population. (4) Our program has the potential to address several indications. (5) We have not finalized a target product profile for a specific indication. (6) Incidence for US only. (7) 2L+ drug-treatable population. (8) 2L+ drug-treatable population comprising ovarian, prostate, breast, and pancreatic cancers.

REC-994 for the Treatment of Symptomatic Cerebral Cavernous Malformations (CCM)

Target / MOA	Superoxide Scavenger
Molecule Type	Small Molecule
Lead Indication(s)	Cerebral Cavernous Malformations
Status	Phase 2
Designation(s)	US & EU Orphan Drug
Source of Insight	Recursion OS



Clinical: CCM

SYCAMORE Clinical Trial: REC-994 for CCM Phase 2 Fully Enrolled

PREVALENCE & STANDARD OF CARE

~360,000

Symptomatic US + EU5,
>1 million patients worldwide
live with these lesions today

>5x larger US patient population than other rare diseases like Cystic Fibrosis (>31k patients)

No approved therapy

- Most patients receive no treatment or only symptomatic therapy
- Surgical resection or stereotactic radiosurgery not always feasible because of location and is not curative

CAUSE

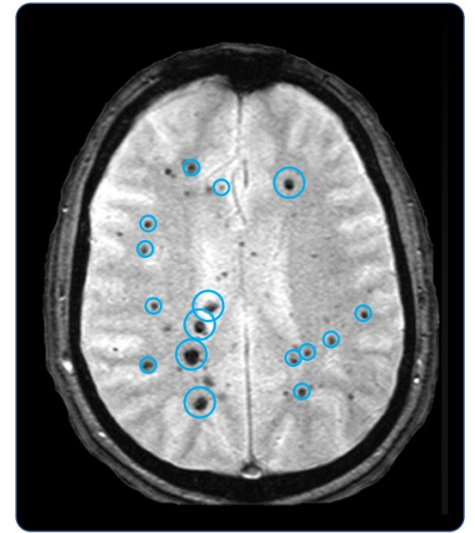
LOF mutations in genes *CCM1*, *CCM2* & *CCM3*, key for maintaining the structural integrity of the vasculature due to unknown mechanisms

PATHOPHYSIOLOGY & REASON TO BELIEVE

Vascular malformations of the CNS leading to focal neurological deficits, hemorrhage and other symptoms



Efficacy signal in Recursion OS as well as functional validation via scavenging of massive superoxide accumulation in cellular models; reduction in lesion number with chronic administration in mice



Vascular malformations (cavernomas)



Julia – living with CCM

KEY ELEMENTS

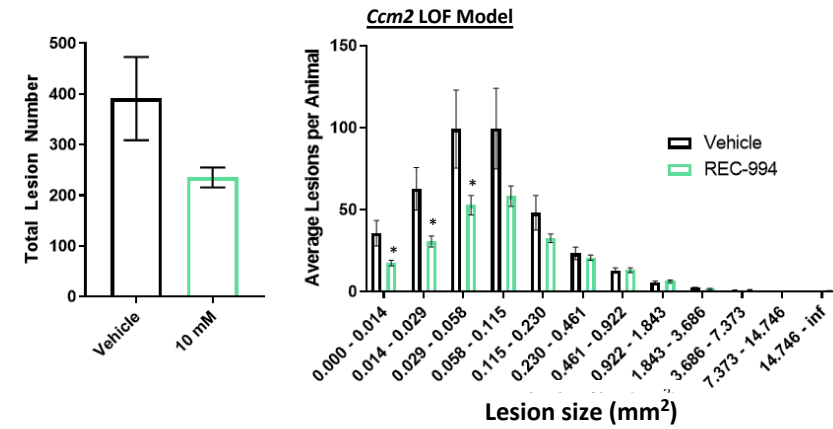
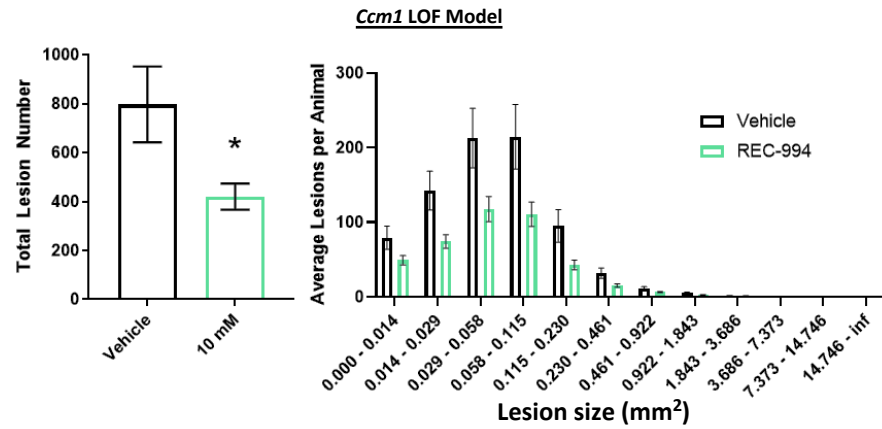
- Targeting **sporadic and familial symptomatic CCM** patients with *CCM1*, *CCM2*, and *CCM3* mutations
- Superoxide scavenger, small molecule
- Phase 2 readout **expected September 2024**
- US & EU **Orphan Drug Designation**



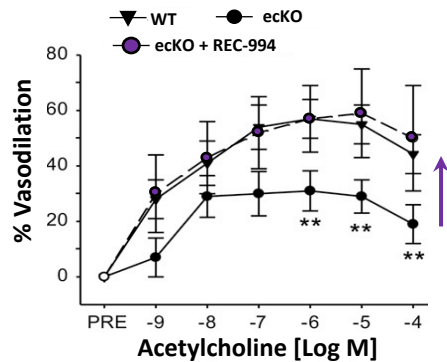
Preclinical Studies Confirm Insight

Preclinical Studies: REC-994 reduces lesion burden and ameliorates vascular defects in genetic mouse models of CCM

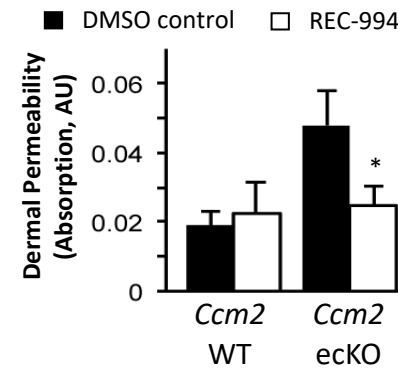
1 Reduces lesion number & size in *Ccm1* and *Ccm2* LOF mouse models



2 Rescues acetylcholine-induced vasodilation defect



3 Rescues dermal permeability defect in CCM2 mice



- REC-994 stabilizes the integrity of vasculature against challenges to permeability
- Altered vascular permeability is a clinically relevant feature of CCM lesions



Clinical: CCM

SYCAMORE Clinical Trial : REC-994 for CCM Phase 2 Fully Enrolled

Topline Data Expected September 2024

Enrollment Criteria

- MRI-confirmed CCM lesion(s)
- Familial or sporadic
- Symptoms directly related to CCM

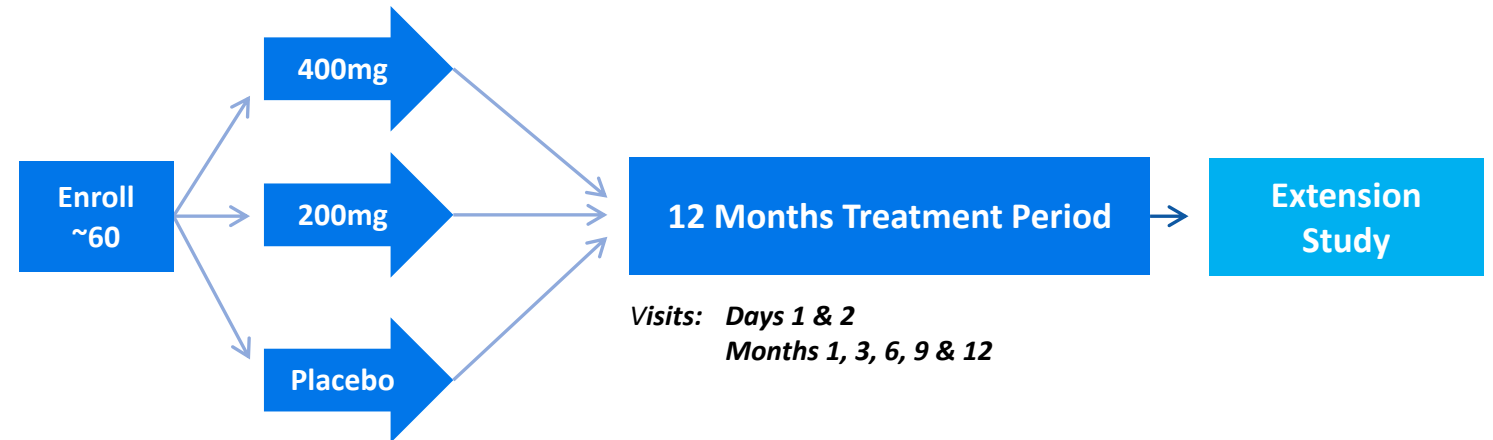
Outcome Measures

- Primary: Safety and tolerability
- Secondary: Efficacy
- Exploratory: Biomarkers

Screening & Randomization 1:1:1

Treatment

Follow-up





REC-994 for CCM: Expectations

Outcome Measures

- **Primary: Safety and Tolerability**
 - **Adverse events & symptoms**
- **Secondary & Exploratory:**
 - **Efficacy**
 - **Clinician-measured outcomes** (CGI, PGI)
 - **MRI Imaging**
 - **Impact of acute stroke** (mRS, NIHSS)
 - **Patient and Investigator reported outcomes** (SMSS, PROMIS-29, CCM-HI, symptom questionnaires)

Trial Update

- **Enrollment is complete**
- **Vast majority of participants** who completed 12 months of treatment continue to enter **long-term extension**
- **Analysis**
 - Identification of **trends across multiple endpoints**
 - **Changes in vascular permeability**
 - E.g., hemosiderin deposition
 - **Change in lesion burden**
 - **Subgroup**

REC-2282 for the Treatment of Progressive Neurofibromatosis Type 2 (NF2) Mutated Meningiomas

Target / MOA	HDAC Inhibitor
Molecule Type	Small Molecule
Lead Indication(s)	NF2 Mutated Meningiomas
Status	Phase 2/3
Designation(s)	Fast Track; US and EU Orphan Drug
Source of Insight	Recursion OS



Clinical: NF2

POPLAR Clinical Trial: REC-2282 for NF2 Part A Underway

PREVALENCE & STANDARD OF CARE

~33,000 Treatable US + EU

No approved therapy

- Surgery/RT is standard of care (when feasible)
- Location may make complete resection untenable, leading to hearing loss, facial paralysis, poor balance and visual difficulty
- **Stasis or shrinkage of tumor could improve prognosis**

CAUSE

LOF mutations in *NF2* tumor suppressor gene, leading to deficiencies in the tumor suppressor protein merlin

PATHOPHYSIOLOGY & REASON TO BELIEVE

Inherited rare **CNS tumor syndrome** leading to loss of hearing and mobility, other focal neurologic deficits

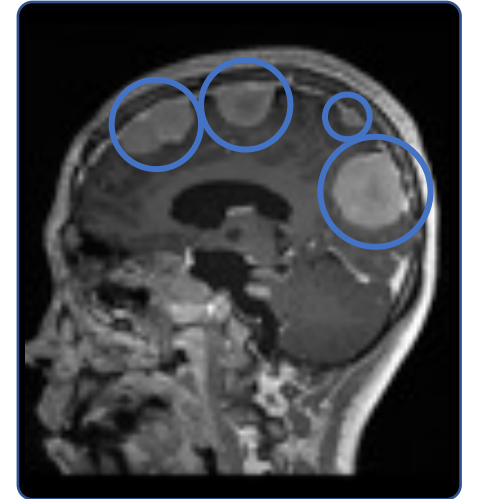


Efficacy signal in Recursion OS, cellular, and animal models; suppression of aberrant ERK, AKT, and S6 pathway activation in a Phase 1 PD Study in NF2 patient tumors



KEY ELEMENTS

- Targeting **familial & sporadic NF2 meningioma** patients
- HDAC inhibitor, small molecule
- Oral dosing
- Preliminary readout **expected Q4 2024**
- **Fast-Track** and US & EU **Orphan Drug Designation**



Intracranial meningiomas

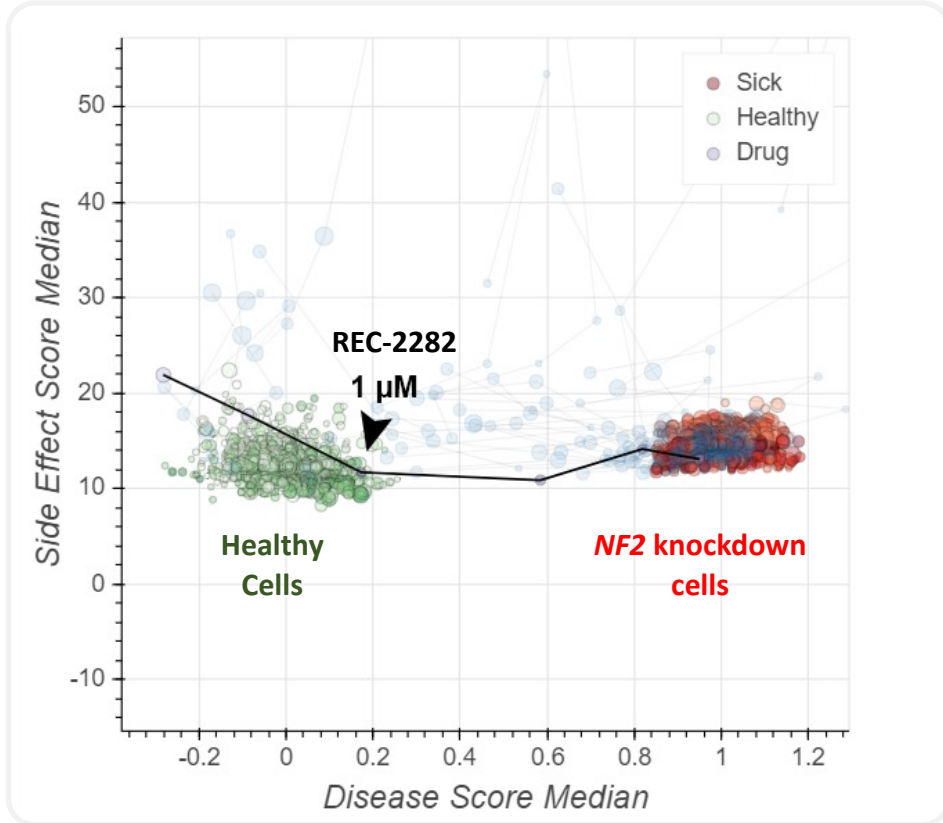


Ricki – living with NF2

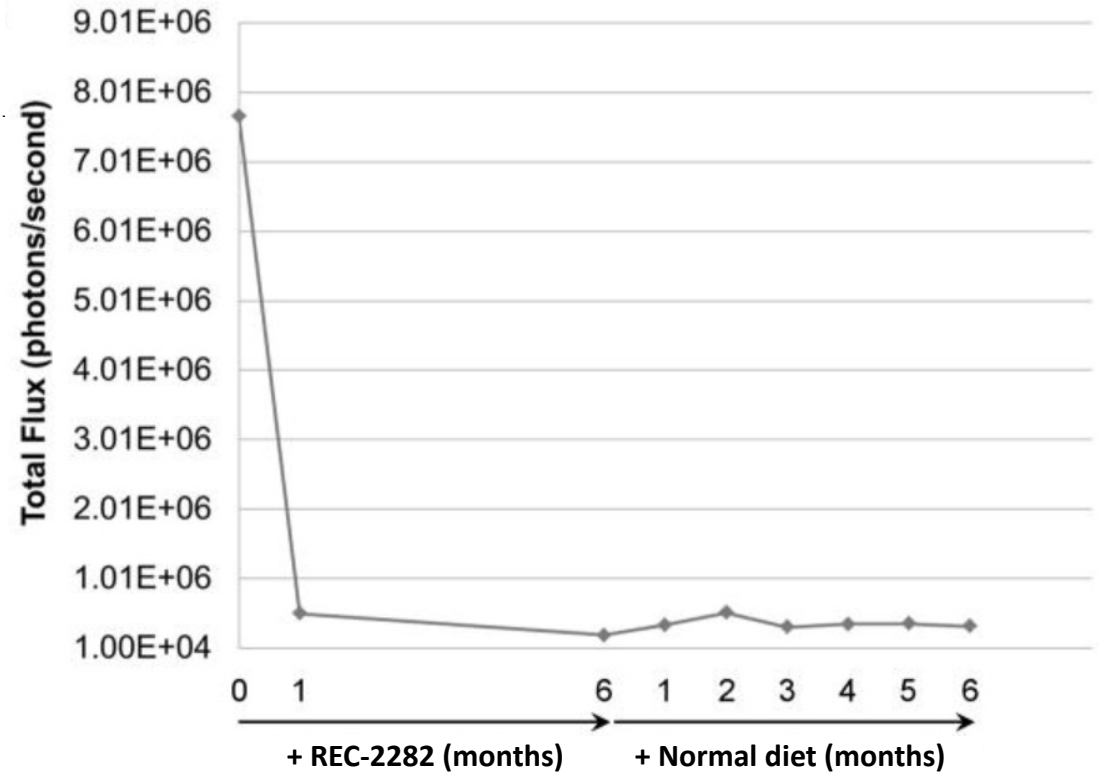


Clinical: NF2

Insight from OS : REC-2282 Rescued Loss of NF2



Prevents growth & regrowth of NF2-deficient meningioma model in mice





Clinical: NF2

POPLAR Trial: REC-2282 for NF2 Part A Underway

Key Enrollment Criteria

- MRI-confirmed progressive meningioma
- Sporadic meningioma with confirmed NF2 mutation
- Familial NF2 meningioma
- Have documented progression with past 24 months

Outcome Measures

- Primary: PFS6 defined as proportion of patients who are alive or progression free after
- Secondary: ORR, Safety, PK/PD

Phase 2/3 trial initiated in Q2 2022

Phase 2 portion

40 mg TIW
~6 Sporadic
~6 Familial

60 mg TIW
~6 Sporadic
~6 Familial

6-month PFS
(Futility Analysis)

FDA
Mtg

- **Go/No-go to Ph3**
- **Safety/Tolerability**
- **PK**
- **PFS**

Preliminary Phase 2 readout
(safety & preliminary efficacy)
expected in **Q4 2024**

REC-4881 for the Treatment of Familial Adenomatous Polyposis (FAP)

Target / MOA	MEK Inhibitor
Molecule Type	Small Molecule
Lead Indication(s)	Familial Adenomatous Polyposis
Status	Phase 2
Designation(s)	Fast Track; US and EU Orphan Drug
Source of Insight	Recursion OS



Clinical: FAP

TUPELO Clinical Trial : REC-4881 for FAP Phase 2 Underway

PREVALENCE & STANDARD OF CARE

~50,000 Diagnosed US + EU

No approved therapy

- Colectomy during adolescence (with or without removal of rectum) is standard of care
- Post-colectomy, patients still at significant risk of polyps progressing to GI cancer
- Significant decrease in quality-of-life post-colectomy (continued endoscopies, surgical intervention)

CAUSE

Inactivating mutations in the tumor suppressor gene *APC*

PATHOPHYSIOLOGY & REASON TO BELIEVE

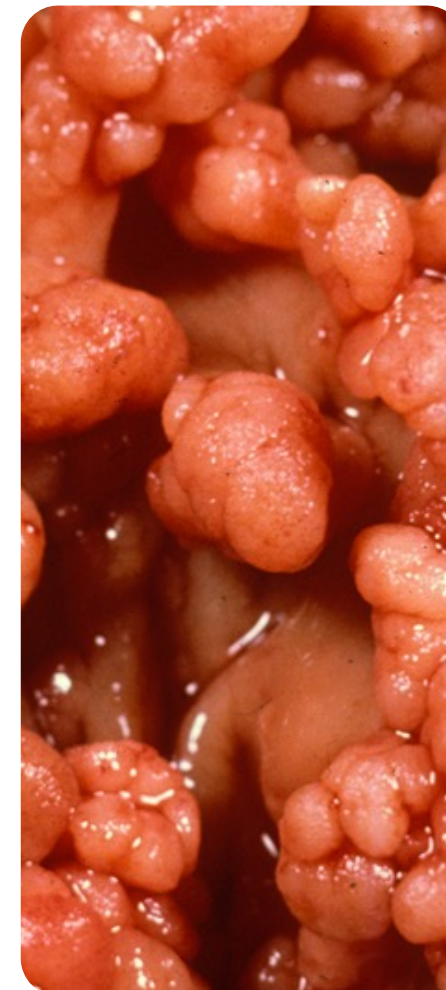
Polyps throughout the GI tract with extremely high risk of malignant transformation



Efficacy signal in the Recursion OS showed specific MEK 1/2 inhibitors had an effect in context of *APC* LOF. Subsequent *APC*^{min} mouse model showed potent reduction in polyps and dysplastic adenomas

KEY ELEMENTS

- Targeting **classical FAP patients (with *APC* mutation)**
- MEK inhibitor, small molecule
- Oral dosing
- Preliminary readout **expected H1 2025**
- **Fast-Track** and US & EU **Orphan Drug Designation**



Polyps Found in Colon and Upper GI Tract



Clinical: FAP

TUPELO Clinical Trial : REC-4881 for FAP Phase 2 Underway

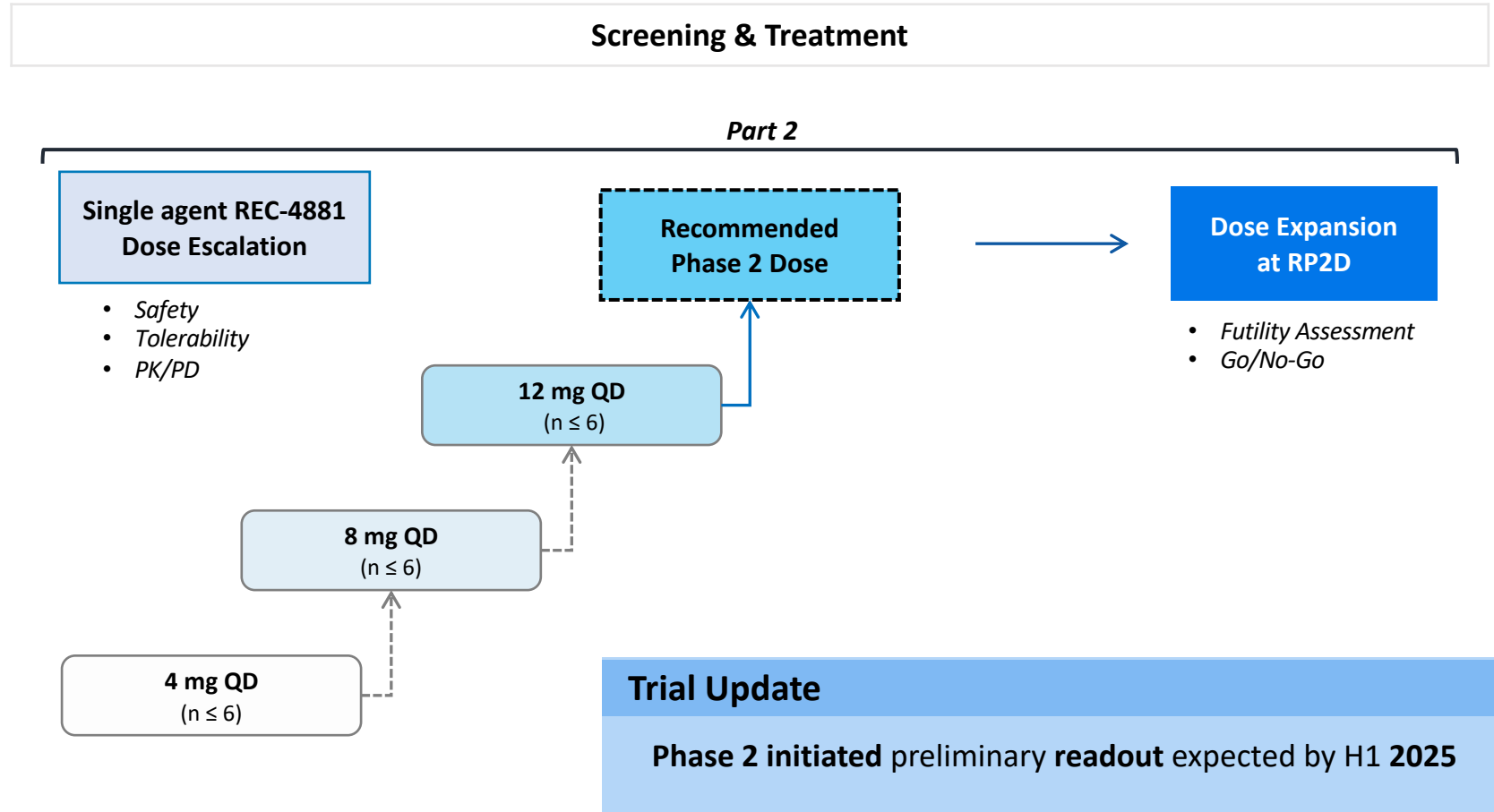
Part 2 Enrollment Commenced

Key Enrollment Criteria

- Confirmed *APC* mutation
- ≥ 55 years old
- Post-colectomy/proctocolectomy
- No cancer present
- Polyps in either duodenum (including ampulla of vater) or rectum/pouch

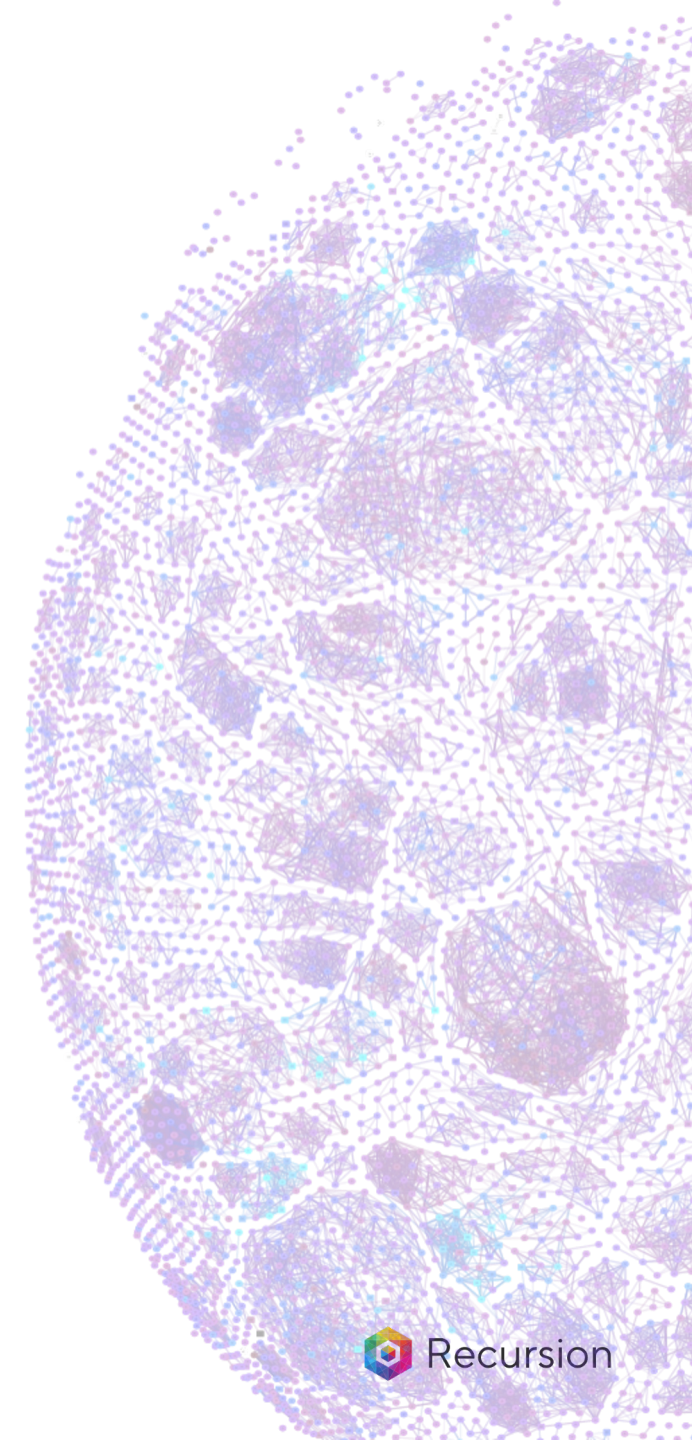
Outcome Measures

- Primary:
 - Safety & Tolerability
 - Change from baseline in polyp burden at 12 weeks
 - RP2D
- Secondary:
 - PK/PD



REC-4881 for the Treatment of Solid Tumors with AXIN1 or APC Mutations

Target / MOA	MEK Inhibitor
Molecule Type	Small Molecule
Lead Indication(s)	Solid Tumors with AXIN1 or APC Mutations
Status	Phase 2
Source of Insight	Recursion OS





Clinical: AXIN1 or APC

LILAC Clinical Trial: REC-4881 for AXIN1 or APC mutant cancers

~104,000 Treatable US + EU5

Substantial need for developing therapeutics for patients harboring mutations in *AXIN1* or *APC*, as these mutations are considered **undruggable**

To our knowledge, REC-4881 is the **only industry sponsored small molecule therapeutic** designed to enroll solid tumor patients harboring mutations in *AXIN1* or *APC*

CAUSE

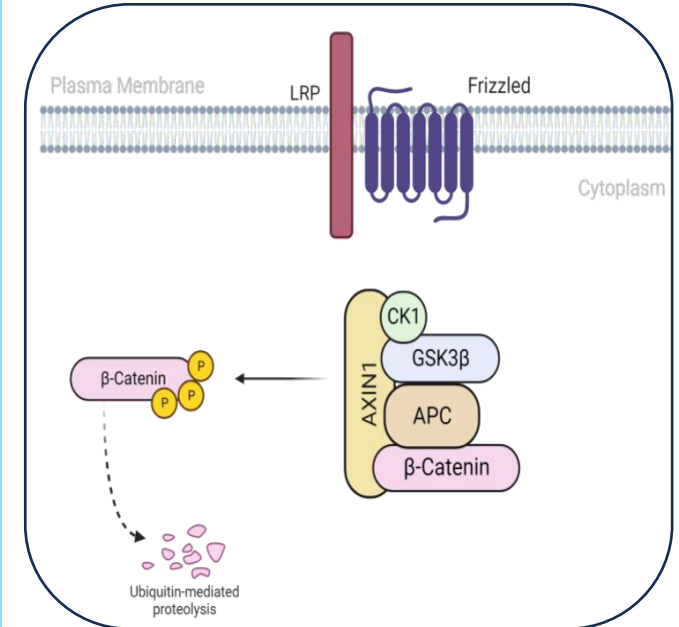
LOF mutations in *AXIN1* or *APC* tumor suppressor genes

PATHOPHYSIOLOGY & REASON TO BELIEVE

Alterations in the **WNT pathway** are found in a **wide variety of tumors** and confer poor prognosis and resistance to standard of care



Efficacy signal in the Recursion OS and favorable results in PDX models harboring *AXIN1* or *APC* mutations vs wild-type leading to a significant PFS benefit only in mutant models



AXIN1/APC regulate WNT pathway

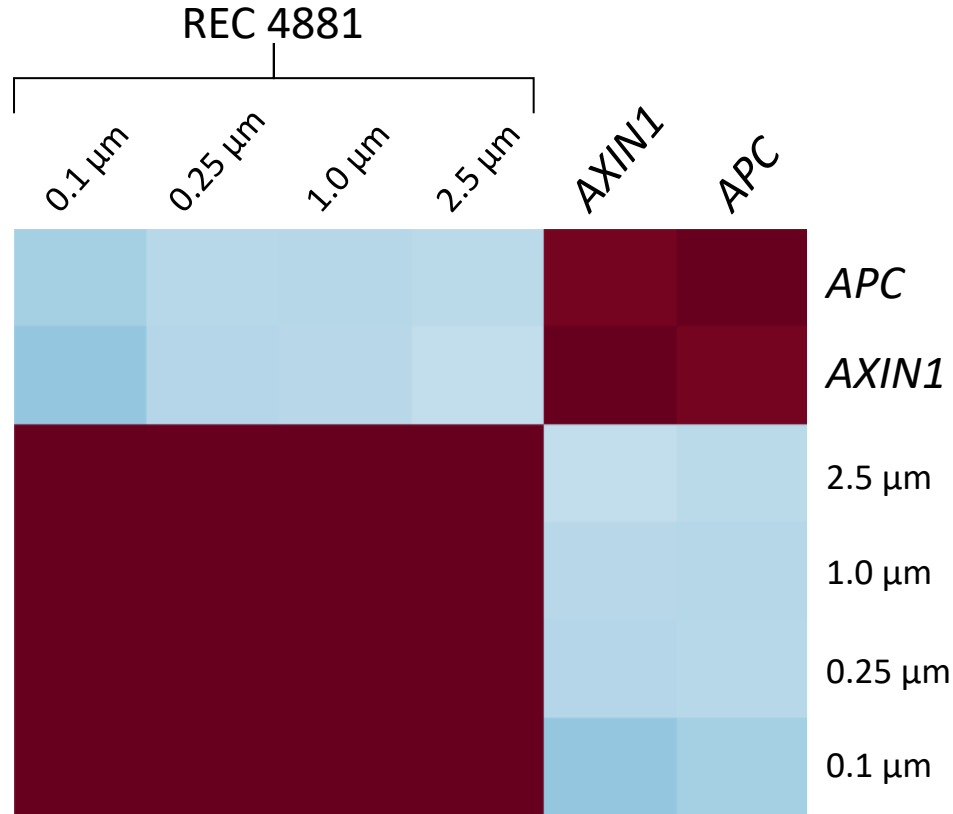
KEY ELEMENTS

- Targeting ***AXIN1* or *APC* mutant cancers**
- MEK inhibitor, small molecule
- Oral dosing
- **Enrollment ongoing**
- Phase 2 initial readout **expected H1 2025**



Clinical: AXIN1 or APC

Recursion OS Identified Novel Insight of AXIN1 & APC biology



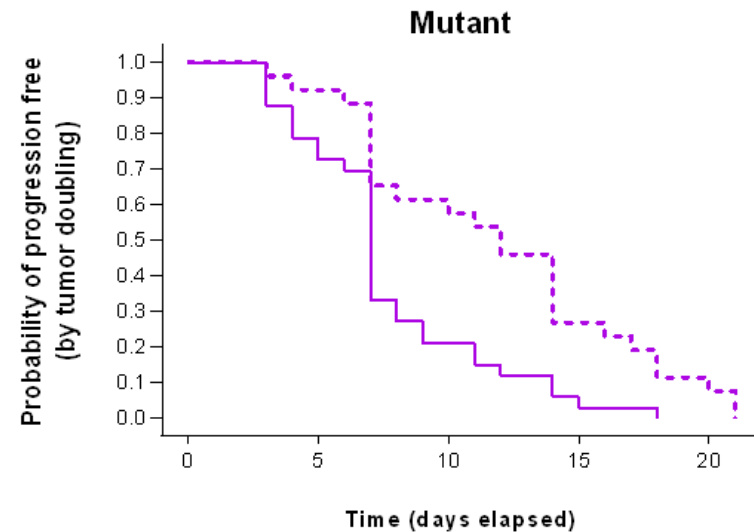
REC-4881 is phenotypically opposite to the genetic KO of **APC** and **AXIN1** providing a novel mechanism that may restore the disease state modeled by the loss of these genes

Significantly greater antitumor activity in mutant models led to significant PFS benefit

	Median PFS (days)	95% CI
REC-4881 (n = 33)	12.0	(7.18 - 20.01)
Vehicle (n = 33)	7.0	(4.19 - 11.70)

Log-rank p value < 0.001

HR = 0.49 (95% CI 0.29 - 0.83)





Clinical: AXIN1 or APC

LILAC Clinical Trial: REC-4881 for AXIN1 or APC mutant cancers

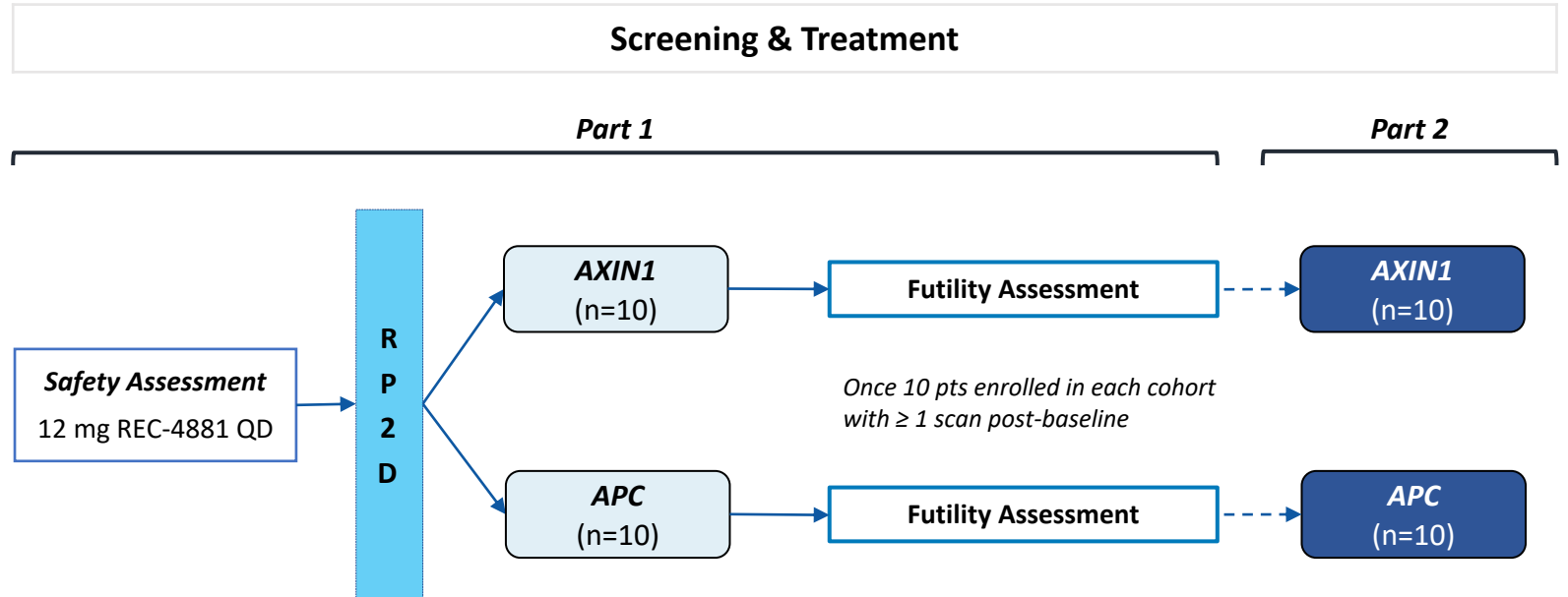
FPI achieved Q1 2024

Enrollment Criteria

- Unresectable, locally advanced, or metastatic cancers
- ≥ 55 years old
- *AXIN1* or *APC* mutation confirmed by NGS (tissue or blood)
- CRC patients must be *RAS* / *RAF* wildtype
- No MEK inhibitor treatment within 2 months of initial dose
- ≥ 1 prior line of therapy
- ECOG PS 0-1

Outcome Measures

- Primary
 - Safety/tolerability
 - ORR (RECIST 1.1)
- Secondary
 - PK
 - Additional efficacy parameters



Trial Update

- Utilizing genomics & RWD data for patient/site matching
- **Phase 2 initial readout expected H1 2025**

REC-3964 for the Prevention of *C. difficile* Infection (CDI)

Target / MOA	Selective <i>C. difficile</i> Toxin Inhibitor
Molecule Type	Small Molecule
Lead Indication(s)	Prevention of CDI
Status	Phase 2
Source of Insight	Recursion OS



Clinical: *C. difficile*

ALDER Clinical Trial: REC-3964 for *C. Difficile*

PREVALENCE & STANDARD OF CARE

~730,000 Diagnosed US
+ EU5 patients

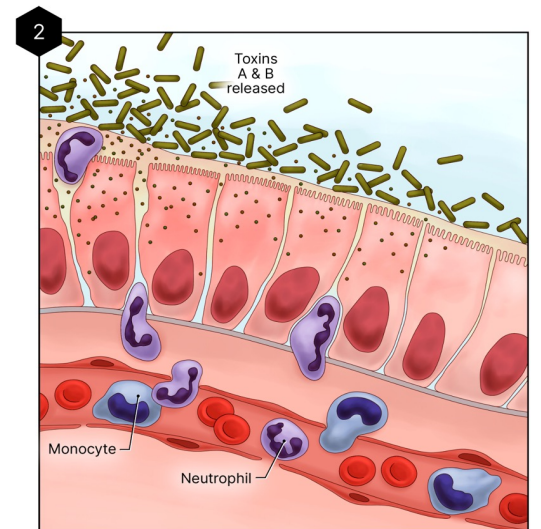
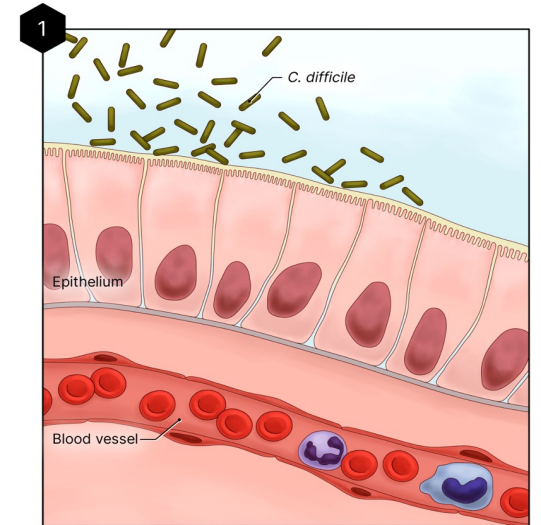
- **Severity of infection varies and can range from mild to severe, requiring colectomy**
 - **>29,000 patients** die in the US each year from CDI
- **Cost burden of up to \$4.8bn annually**

TREATMENT PARADIGM

- Standard of care for 1st occurrence: Antibiotics alone
- Recurrence (20-30% of patients) treated with antibiotics ± adjunct therapy (bezlotoxumab IV or fecal transplant)
- REC3964 inhibits the *C. difficile* toxins and is a non-antibiotic therapy

PATHOPHYSIOLOGY & REASON TO BELIEVE

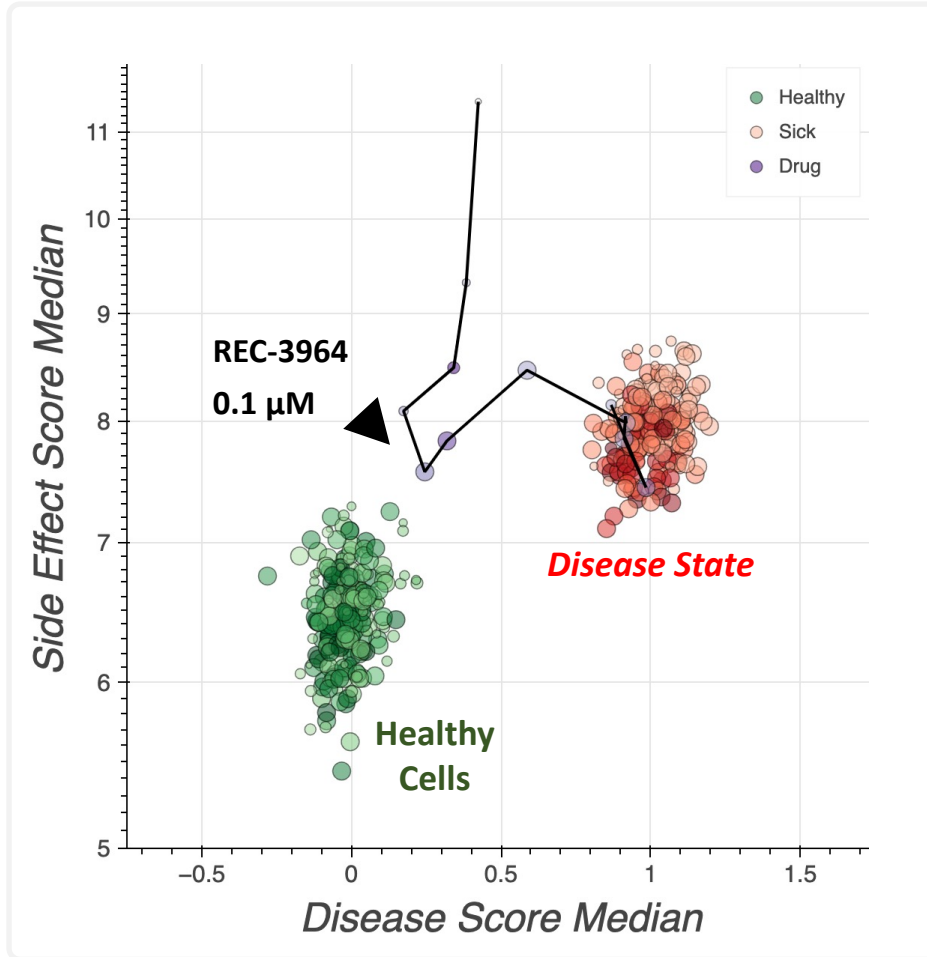
- Selective Inhibitor of *C. difficile* Toxins
- Recursion's 1st Small Molecule NCE to Reach the Clinic
- Binds and blocks catalytic activity of the toxin's innate glucosyltransferase, but not the host's



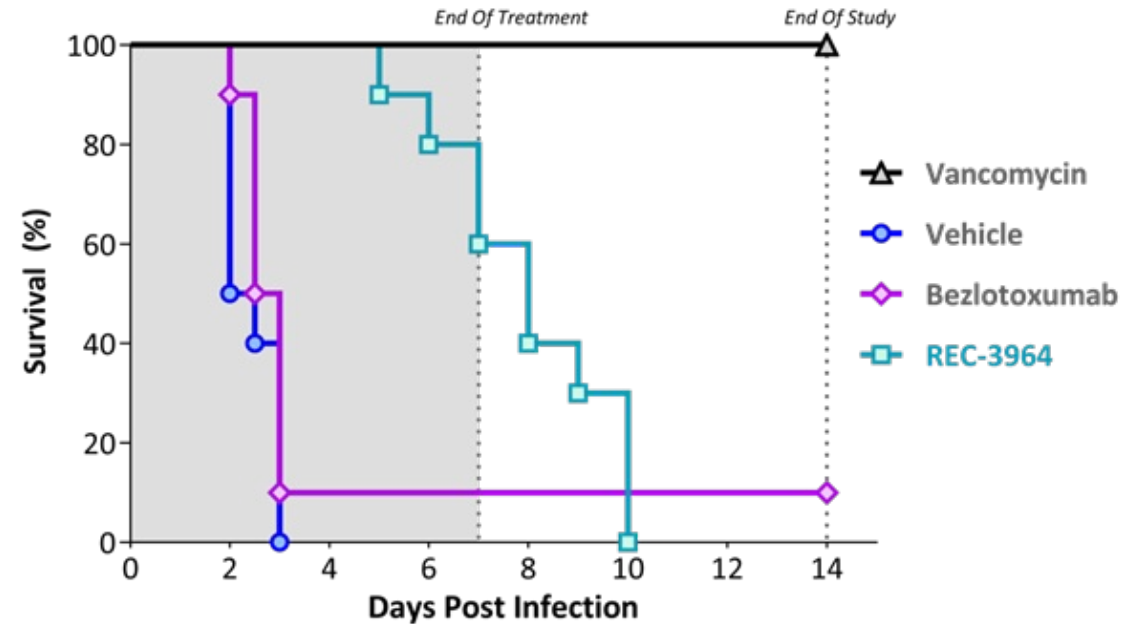


Clinical: *C. difficile*

Insight from OS: REC-3964 Rescued Cells Treated with *C. diff* Toxins



REC-3964 significantly extended survival over SOC



- REC-3964 potently inhibits toxin B with residual activity against toxin A, while bezlotoxumab is specific to toxin B.
- Significant difference in probability of survival vs bezlotoxumab alone at the end of treatment ($p < 0.001$, log-rank test)



Clinical: *C. difficile*

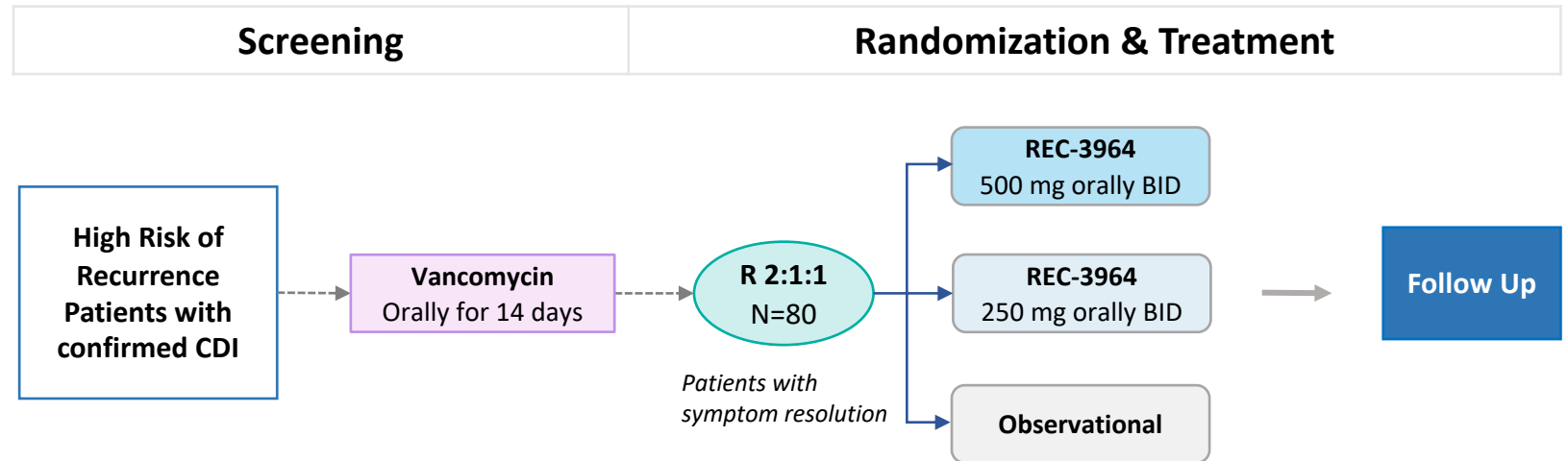
ALDER Clinical Trial: POC Phase 2 REC-3964 in Patients at High Risk of *C. Diff* Recurrence

Enrollment Criteria

- Patients at high risk of recurrence
- ≥ 3 bowel movements in 24 hours
- Confirm CDI using EIA (toxin)
- No fulminant CDI
- No history of chronic diarrheal illness due to other causes

Outcome Measures

- Primary
 - Rate of recurrence
- Secondary
 - Additional efficacy measures
 - Safety / tolerability
 - PK



Trial Updates

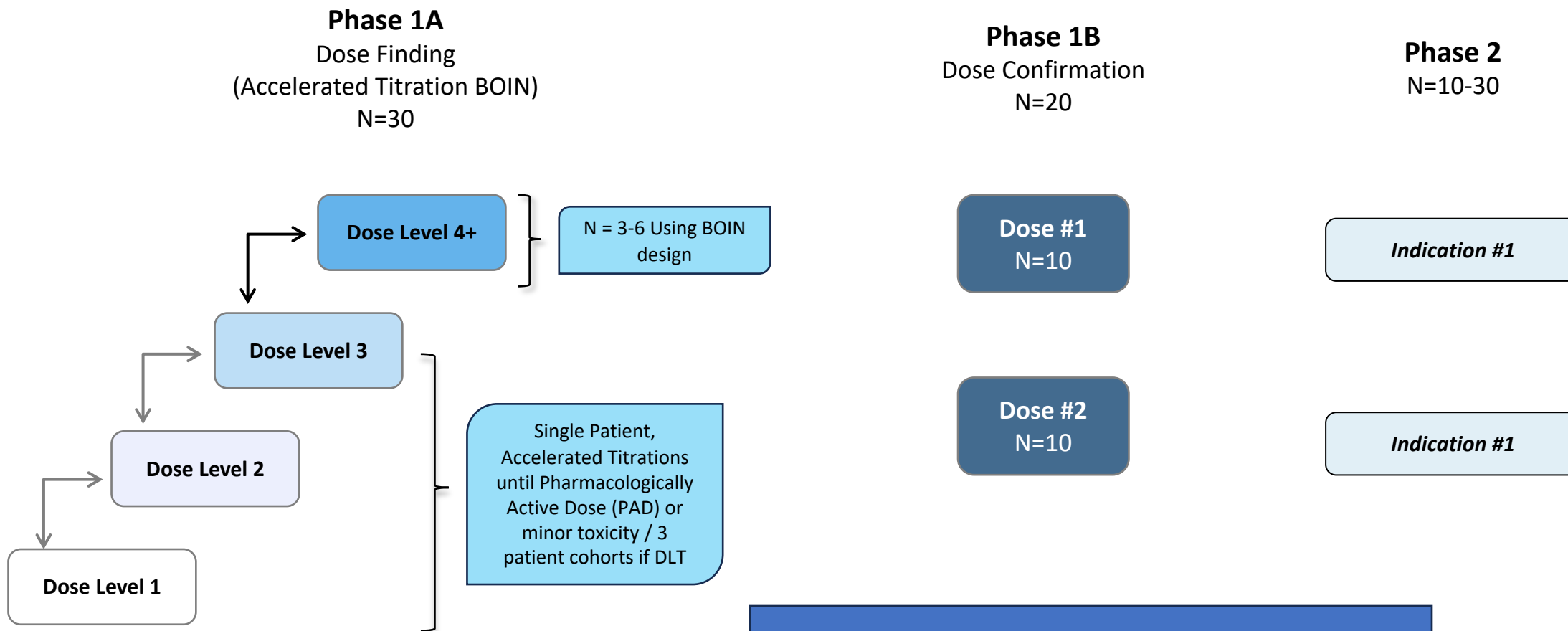
- Phase 1 and DDI studies completed
- **Phase 2 initiation** expected in **Q4 2024**, preliminary **readout** expected by end of **2025**

Novel Insights into RBM39 Degradation for the Treatment of Select HR-Proficient Solid Tumors

Target / MOA	RBM39 Molecular Glue Degradator
Molecule Type	Small Molecule
Lead Indication(s)	TBD
Status	IND submission in Q3 2024, Phase 1/2 initiation in Q4 2024
Source of Insight	Recursion OS

Anticipated RBM39 Trial Design

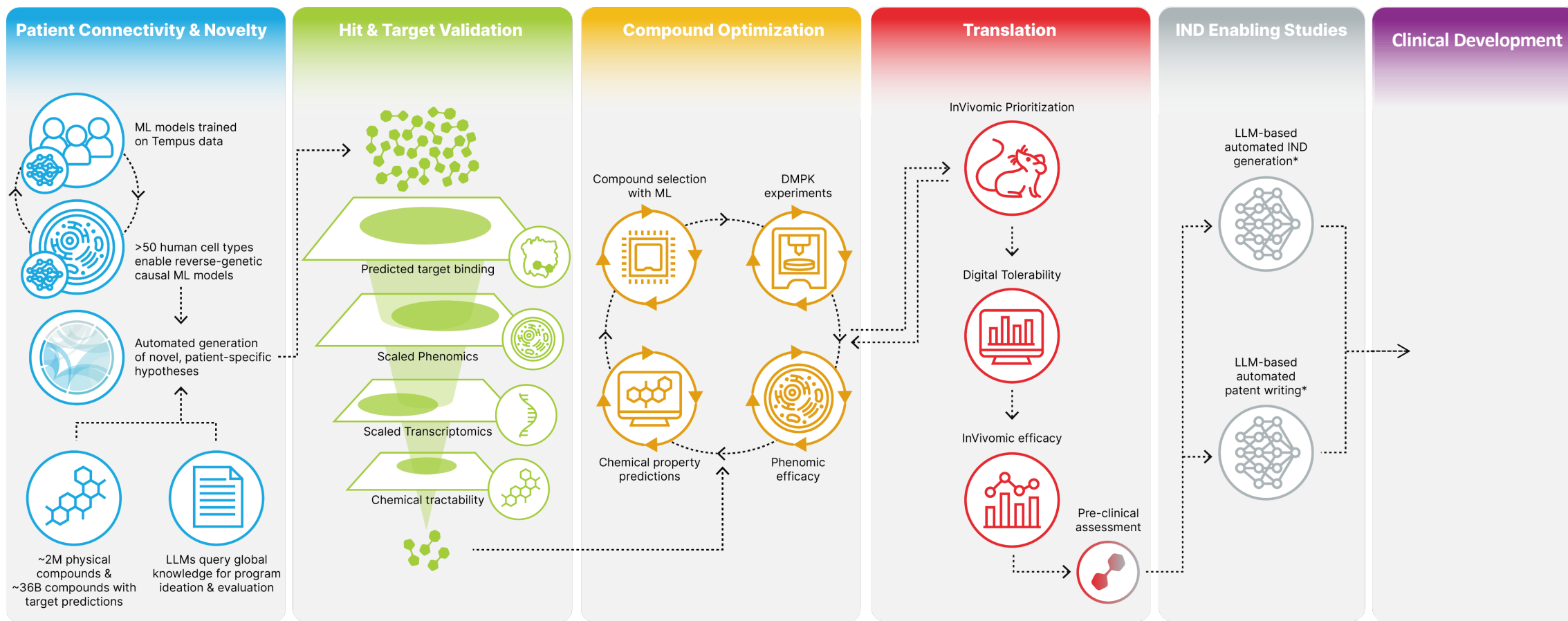
Planned Phase 1/2 study of RBM39 degrader in Biomarker Selected Relapsed Refractory HR-Proficient Solid Tumors



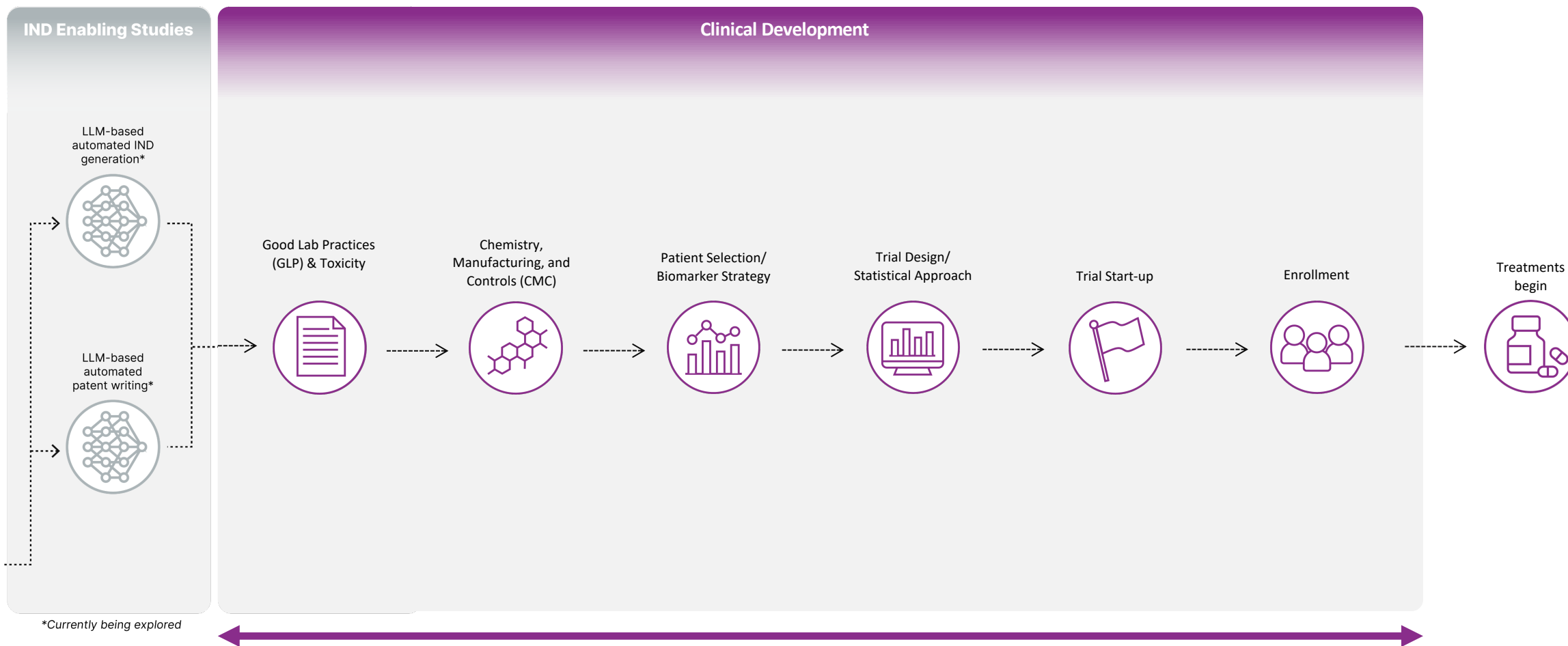
- IND submission expected in Q3 2024
- Phase 1/2 initiation expected in Q4 2024
- Phase 1 dose-escalation readout by end of 2025

Machine Learning:

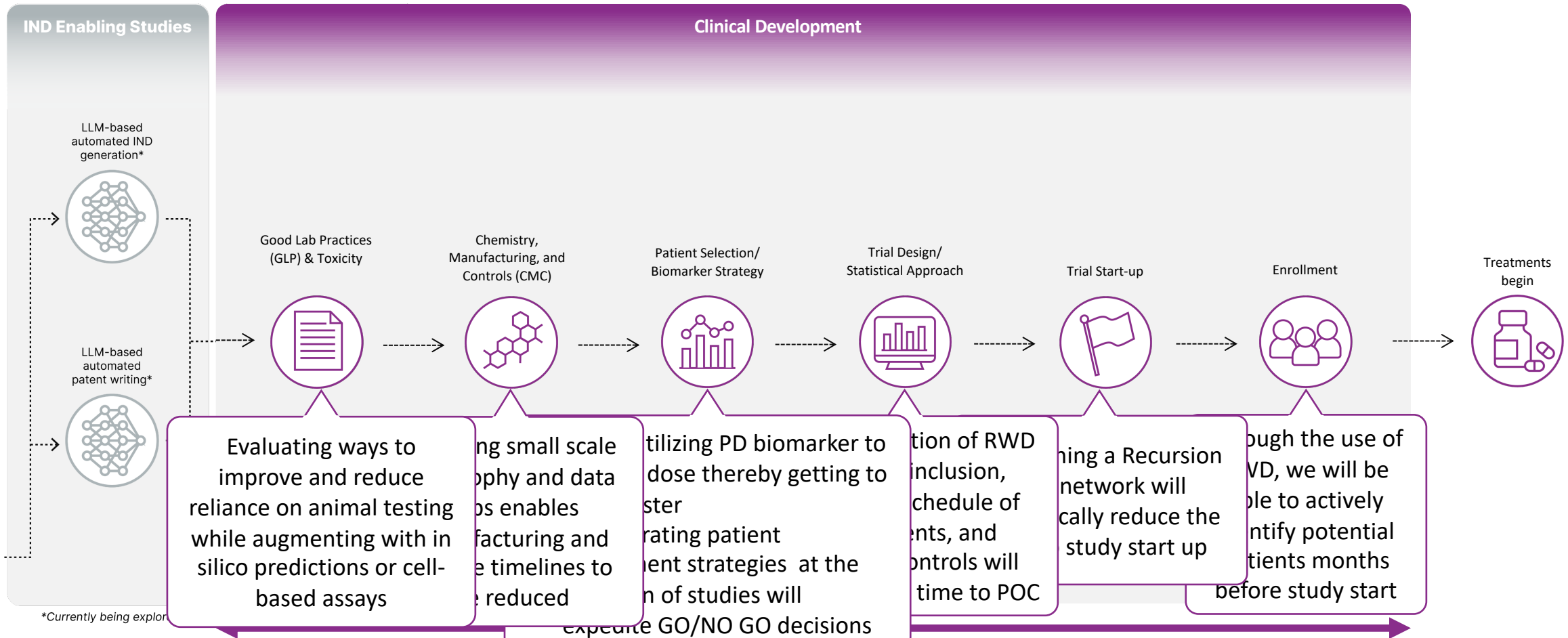
to truly industrialize drug discovery, data and AI solutions must be integrated as modules across many steps
Exciting scientific collaborations span biopharma, tech & data



Industrializing the clinical process, through data and operational efficiency



Industrializing the clinical process, through data and operational efficiency



Evaluating ways to improve and reduce reliance on animal testing while augmenting with in silico predictions or cell-based assays

Using small scale assays and data science enables faster manufacturing and testing timelines to be reduced

Utilizing PD biomarker to optimize dose thereby getting to the best patient strategies at the start of studies will expedite GO/NO GO decisions

Optimization of RWD inclusion, patient schedule of events, and controls will reduce time to POC

Using a Recursion network will significantly reduce the study start up

Through the use of RWD, we will be able to actively identify potential patients months before study start

Company & Milestones

Our Culture and People are Key to Driving Value

MISSION

Decoding Biology
to Radically Improve Lives

PRINCIPLES

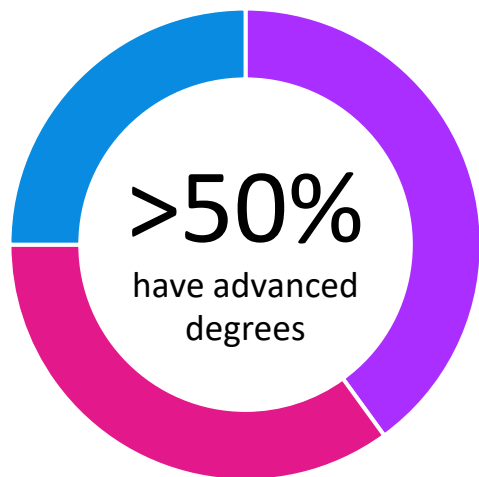
Explore the Uncharted
Create Virtuous Cycles
Build Connected Data
Industrialize to Scale
Optimize for the Portfolio
Challenge Assumptions

VALUES

We Care
We Deliver
We Learn
Act Boldly with Integrity
We are One Recursion

Our People

Functional Breakdown



>500 employees

- Technology – data science, software engineering, automation, etc.
- Life Sciences – biology, chemistry, development, etc.
- Strategic Operations

~43%
Female

~55%
Male

~1%
Non-Binary

Data shown reflective of Q1 2024, gender statistics include participating individuals

Parity Pledge Signer
gender parity and people of color parity

Locations

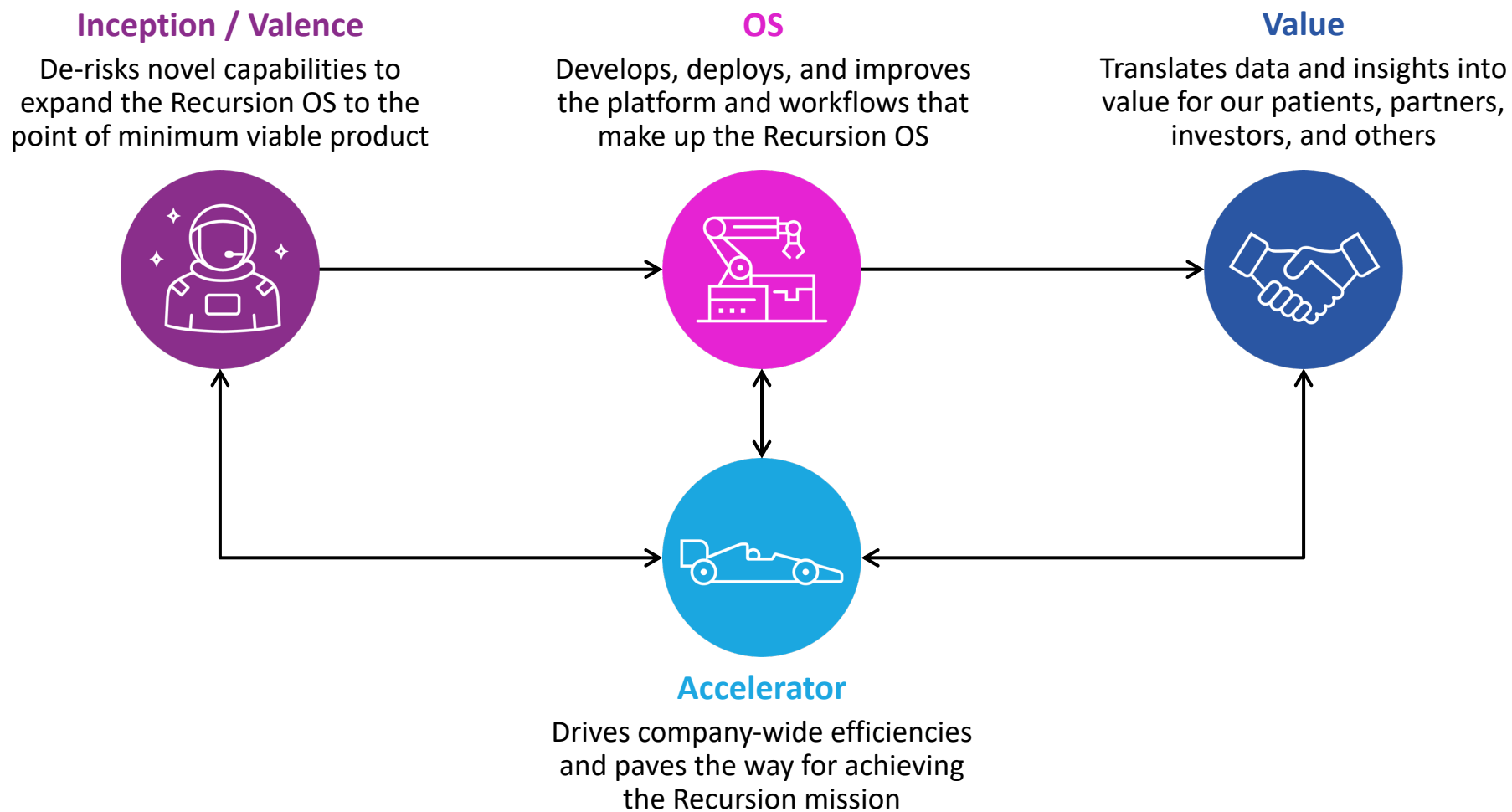


Headquarters in **Salt Lake City, Utah**
with additional locations in:

- San Francisco, California
- Toronto, Ontario
- Montréal, Québec
- London, England



Our Operating Model – Organizing Ourselves in line with Our Drug Discovery Process



Milestones: Pipeline – 7 Clinical Trial Readouts Expected in ~18 Months

Pipeline

- **CCM: Ph2** readout expected in **September 2024**
- **NF2: Ph2** safety & preliminary efficacy expected in **Q4 2024**
- **FAP: Ph2** safety & preliminary efficacy expected in **H1 2025**
- **AXIN1 or APC Mutant Cancers: Ph2 FPI** achieved in **Q1 2024** with safety & preliminary efficacy expected in **H1 2025**
- ***C. difficile* Infection: Ph2 initiation** expected in **Q4 2024** with preliminary **readout** expected by end of **2025**

- **Target RBM39 / HR-Proficient Cancers: IND** submission expected in **Q3 2024** and **Ph1/2 initiation** expected in **Q4 2024** with **Ph1 dose-escalation readout** by end of **2025**
- **Target Epsilon** (novel target in fibrotic diseases): **IND** submission expected in **early 2025** with **Ph1 healthy volunteer readout** by end of **2025**

- **Dozens of internal & partner programs** in early stages with first **LLM & causal model driven programs entering pipeline**



SYCAMORE



POPLAR



TUPELO



LILAC



ALDER

Milestones: Partnerships & Platform

Partnerships

- **Roche & Genentech:** validation **program option exercised** for 1st validated hit series in oncology, potential **program & map options** on the near or very near-term
- **Bayer:** delivered **multiple oncology data packages**, on track to complete **25 unique data packages** in **Q3 2024**, initiated and advancing **1st joint project** towards lead series nomination, potential near-term **program options**, agreed to be **1st beta-user of LOWE** for drug discovery and development
- **Tempus & Helix:** building large-scale **causal AI models** to generate **target hypotheses** across cancer and other disease areas, exploring **novel NSCLC targets**
- Potential for **additional partnership(s)** in large, intractable areas of biology

Platform

- Built our 1st genome-scale **transcriptomics KO map**, moving towards **multiomics foundation models**
- **Active learning** and exploration of **proteomics, organoids, spheroids, & automated synthesis**
- Potential to **make some data and tools available** to biopharma and commercial users
- OS moving towards **autonomous discovery**

Strong Financial Position

~\$296M in cash Q1 2024

Cash refers to cash and cash equivalents at the end of Q1 2024

Fireside Chat with Jensen Huang

Closing Remarks

Our Hopes for Today

Let you get a feel for Recursion and hear from expert partners from outside Recursion about the current and potential future impact of our work

Help define what we view as a tipping point moment as BioTech transitions to TechBio and understand why Recursion is uniquely positioned to take advantage of this

Share details and updates on our:

- Pipeline – with 7 clinical trial readouts expected in the next ~18 months
- Partnerships - with potential near term options on both maps and programs
- Platform - with industry-leading data generation and compute

