Investor Overview

June 2021

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We have based these forward-looking statements largely on our current expectations and projections about future events and trends that we believe may affect our financial condition, results of operations, business strategy and financial needs. These forward-looking statements are subject to a number of risks, uncertainties and assumptions, including, among other things: our ability to successfully execute the development and commercialization of our Proteograph; our ability to implement our strategic plans for our business and our Proteograph; our ability to expand life sciences markets through the use of our technology; the demand for our Proteograph from our target customers and in general; the scope of protection we are able to successfully establish and maintain for intellectual property rights, including our Proteograph and nanoparticles; developments from our competitors, including competing technologies to our Proteograph; and our expectations regarding our gross margins, operating income and expenses. These risks are not exhaustive. New risk factors emerge from time to time and it is not possible for our management to predict all risk factors, nor can we assess the impact of all factors on our business or the extent to which any factor, or combination of factors, may cause actual results to differ materially from those contained in, or implied by, any forward-looking statements. You should not rely upon forward-looking statements as predictions of future events. Although we believe that the expectations reflected in the forward-looking statements are reasonable, we cannot guarantee future results, levels of activity, performance or achievements. Except as required by law, we undertake no obligation to update publicly any forward-looking statements for any reason after the date of this presentation.

This presentation also contains estimates and other statistical data made by independent parties and by us relating to market size and growth and other data about our industry. This data involves a number of assumptions and limitations, and you are cautioned not to give undue weight to such estimates. In addition, projections, assumptions, and estimates of our future performance and the future performance of the markets in which we operate are necessarily subject to a high degree of uncertainty and risk.

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Empowering Scientists Through Transformative Products for Proteomics

- Enabling unbiased, deep and rapid proteomics at scale
- Broadly accessible and durably differentiated technology
- Large potential market opportunity across proteomics and complementary markets
- Management team uniquely positioned to capitalize on proteomics

Making Strong Progress Across Multiple Fronts

Strong Progress With Our Measured Approach

MARKET

- Strong interest from wide range of customer types
- Broad geographical representation of interested customers
- High interest from genomic customers, especially commercial entities with translational and clinical focus

CUSTOMER

- Signed several Limited Release customers with the goal of high single-digit LR customers this year
- All four Collaboration Phase customers making strong progress
- Early data from customers reinforcing differentiated value of our technology

PRODUCT & TECHNOLOGY

- Strong flow of pilot studies and presentations
- Product robustness and experience proving out in the hands of customers
- Promising roadmap and potential

ECOSYSTEM

- Commercial partner progress – joint presentations, customer interest, co-marketing
- High value co-development opportunities underway with each partner
- Positive impact on conversations with new-to-proteomics customers

PEOPLE & CAPABILITIES

- Continuing to strengthen team at all levels with exceptional hires
- Build out of commercial capabilities and reach
- More to come in upcoming weeks and months…

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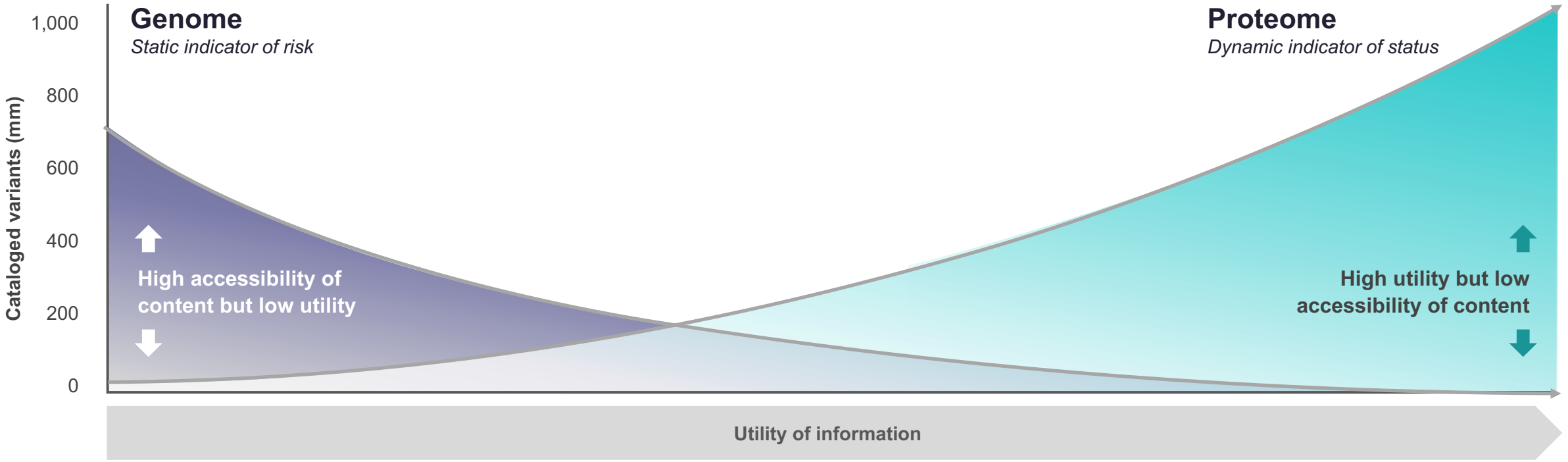
Full Characterization of the Proteome is Essential to Filling in the Missing Pieces of Biology



10M+ human exomes and 1M+ genomes and counting

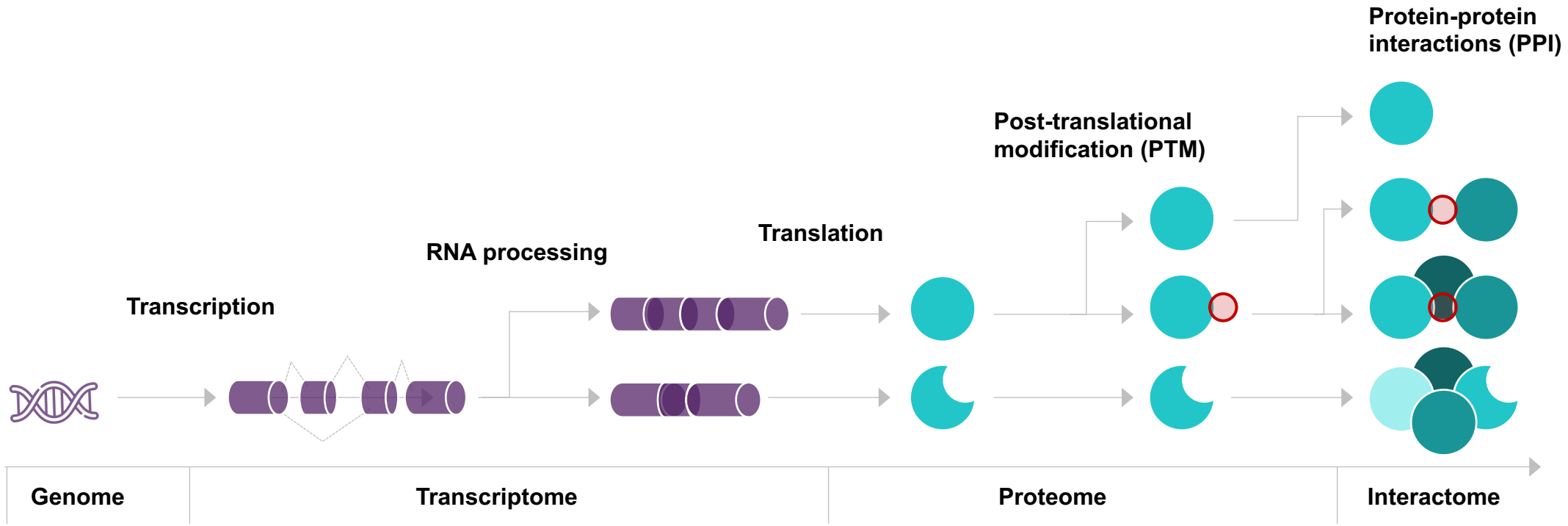
~695M genetic variants catalogued

< 0.2% of genetic variants fully characterized

Source: UniProt, PNAS, PLOS

Proteomes Are Dynamic and Far More Diverse Than Genomes

Unbiased deep proteomics at scale has the potential to reveal biological insight



STATIC

~20K Genes

~200K Transcripts

~1M Proteoforms

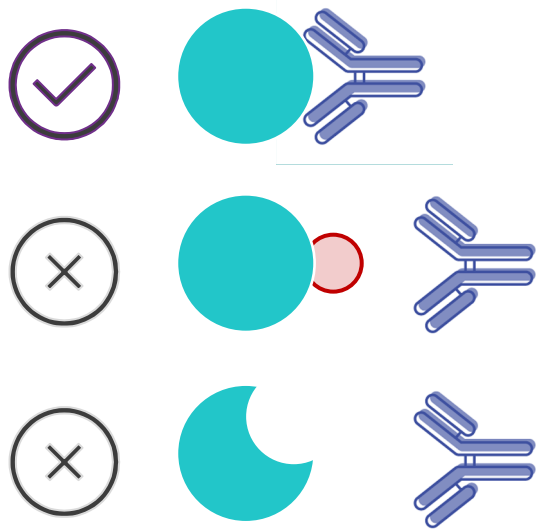
DYNAMIC

Source: Isabell Bludau et al. Proteomic and interactomic insights into the molecular basis of cell functional diversity. Nature Reviews Molecular Cell Biology (2020).

Targeted Approaches Are Limited for Discovery

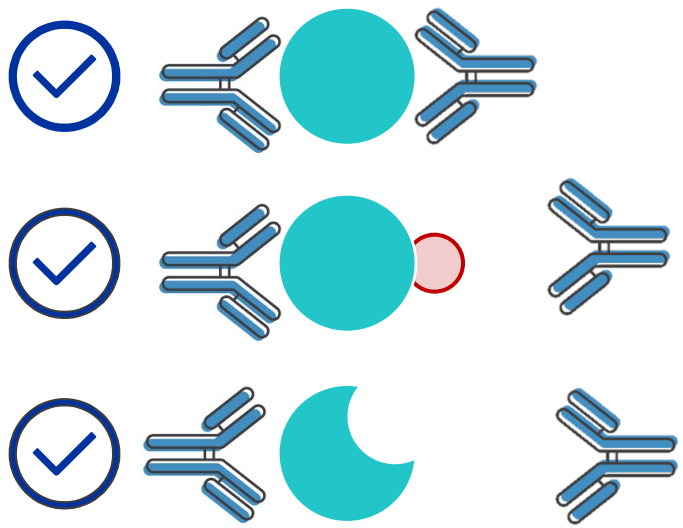
Discovery of novel protein variants will be essential to cataloguing variation and understanding the proteome

MONOCLONAL TARGETED APPROACHES



**Can design for a specific variant,
suited for single-low-plex targeted clinical applications**

POLYCLONAL TARGETED APPROACHES



**Cannot design to differentiate specific variants,
fundamentally limited in clinical applications**

Targeted approaches:

- Do not allow for novel variant and content discovery
- Are SPECIFIC by definition: they bind to a known protein or protein group
- Detect only a small part of a protein: average epitope is 5-8 aa, average protein is 472 aa
- Do not reach the depth, breadth or complexity needed to connect genotype to phenotype

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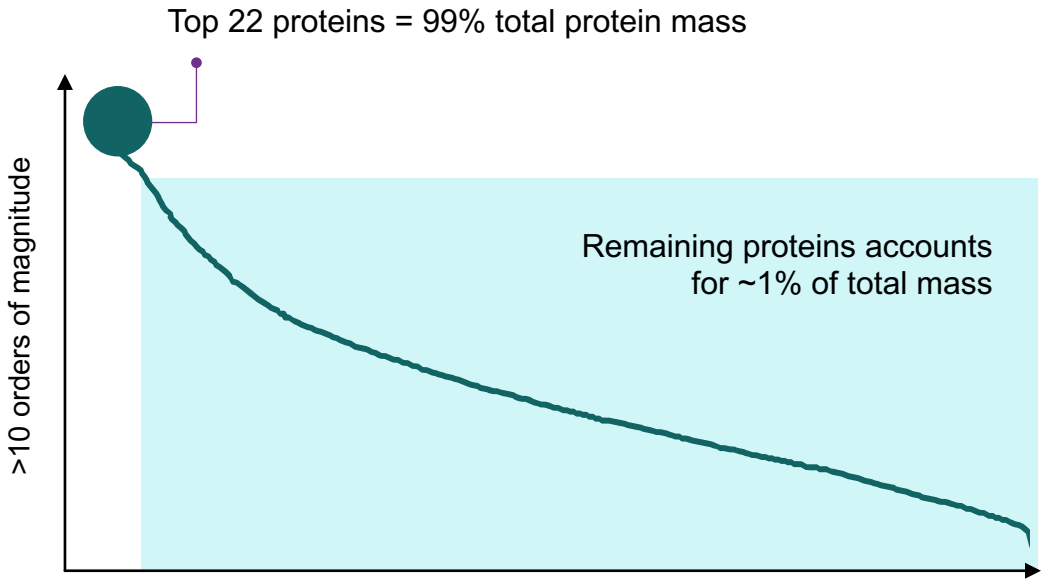
Existing Unbiased Approaches Do Not Scale

Complex sample-handling and lengthy processes limit sample throughput



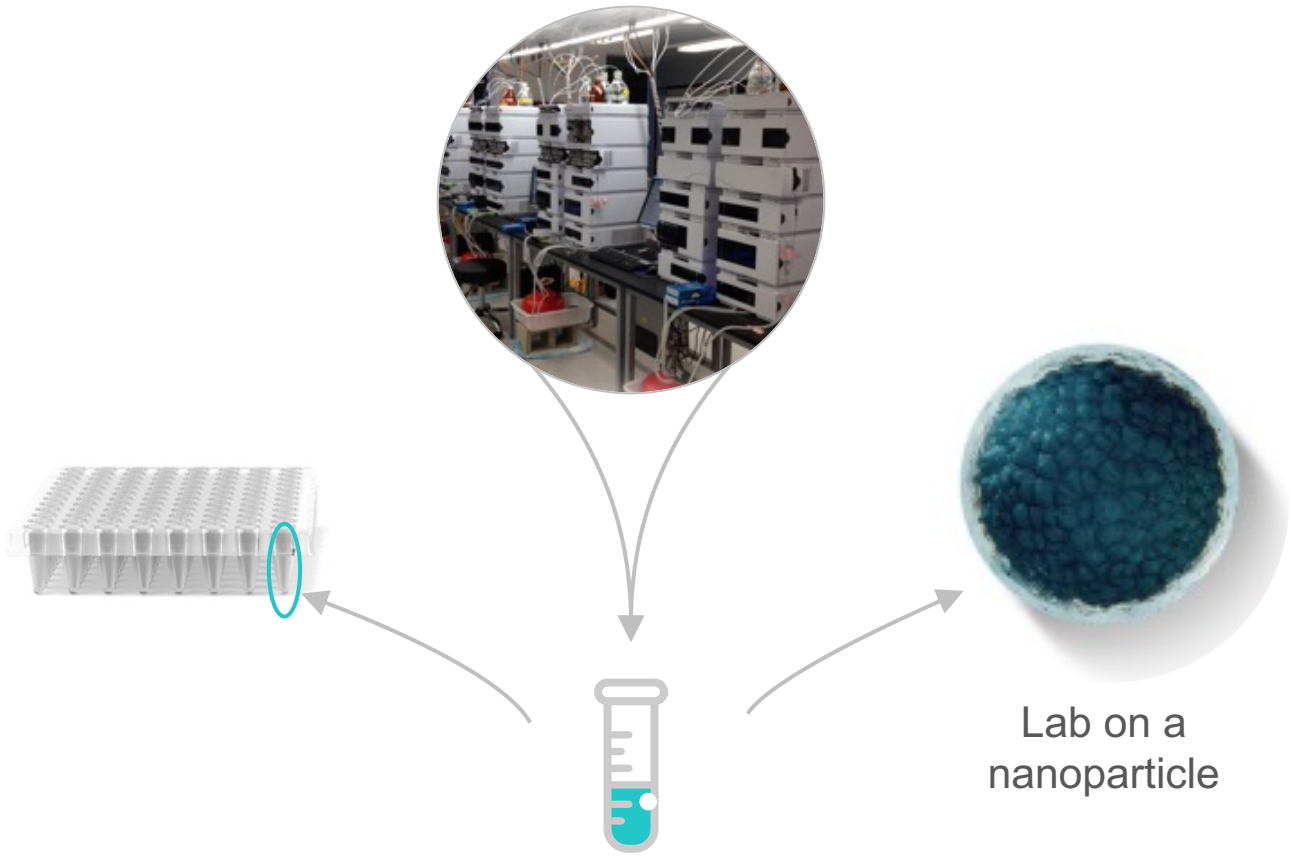
>10x dynamic range in protein expression requires lengthy and complex fractionation and depletion steps

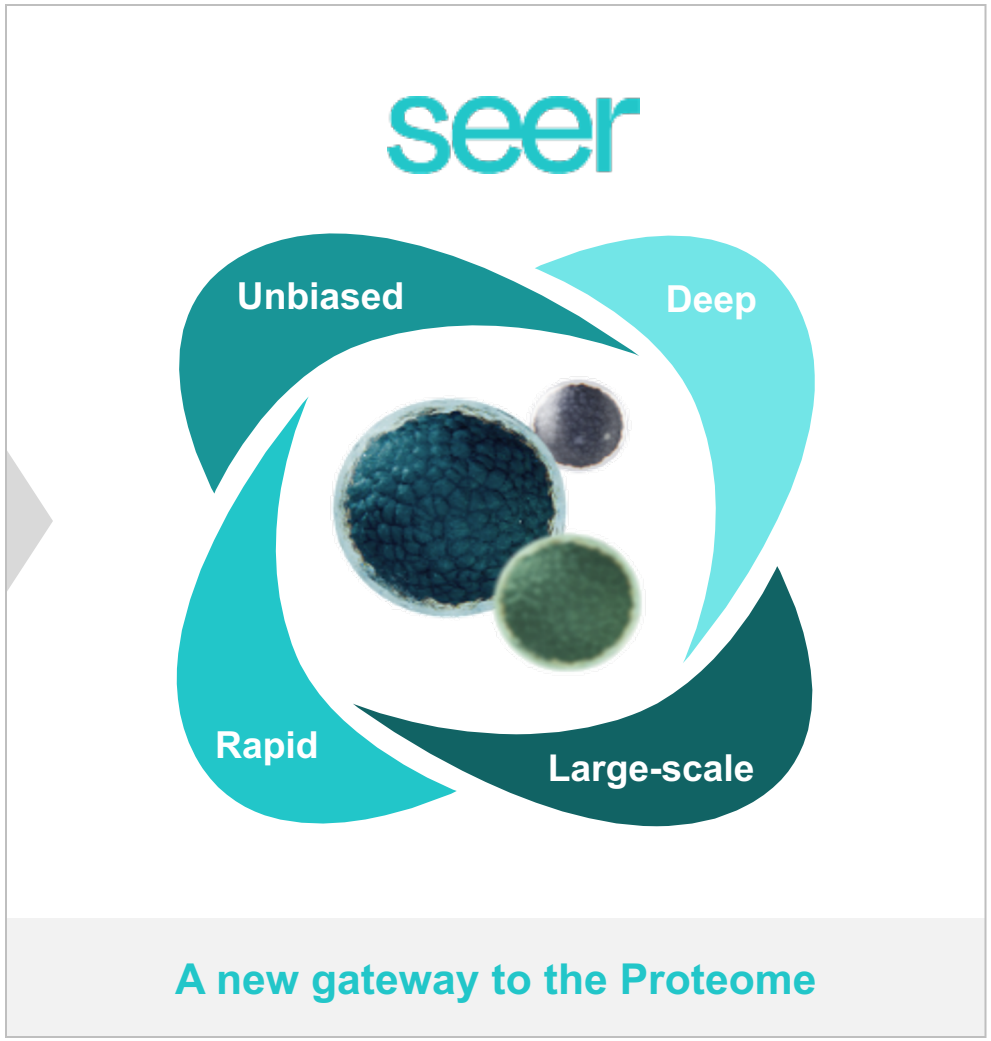
Drives complex and lengthy process with high infrastructure requirement

Combination typically limits scalability of current untargeted, deep methods to only 10s of samples*

Source: Isabell Bludau et al. Proteomic and interactomic insights into the molecular basis of cell functional diversity. Nature Reviews Molecular Cell Biology (2020).
* Applies to studies in plasma of >600 proteins

Seer Enables Unbiased, Deep and Rapid Proteomic Analysis At Scale





Seer's Nanoparticles Improve on Nature's Evolutionary Approach

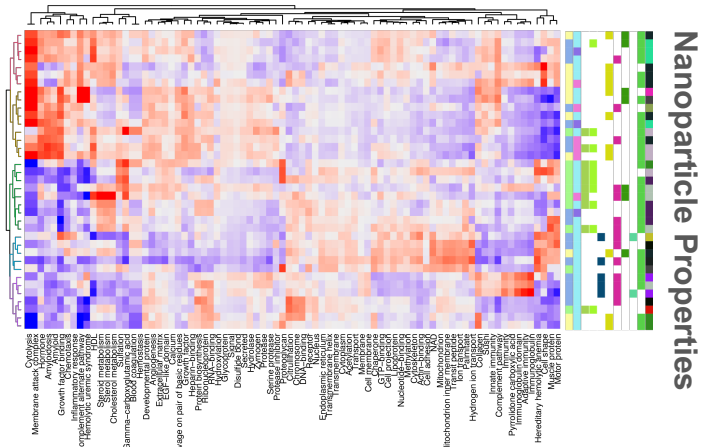
Machine-learning-based models of NP-protein interaction facilitate design of nanoparticles

Proteograph leverages the innate biology of proteins

Proteograph Product Suite

Specific Interactions
Evolution - millions of years

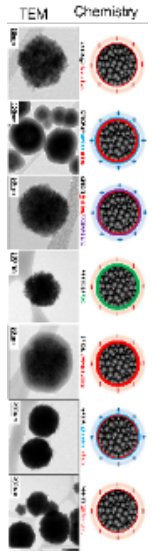
Physicochemical properties are the basis of nanoparticle-protein interaction



Protein Structures and Functions

Designed Interactions
Developed by machine learning - months

Almost an infinite possibility of nanoparticle physicochemical properties



Library of 275+ Nanoparticles

Designed Interactions
Deployed on different nanoparticles

Proteograph Enables Proteogenomics

Unmet need to characterize genomic variation and establish functional characterization

Oncology | Complex Disease | Rare Disease | Reproductive Health

Diagnostics | Infectious Disease | Therapeutics

PROTEOMICS

TODAY

UNMET NEED
Untargeted, deep, rapid, large-scale access to the proteome

TOMORROW

Practical, scalable untargeted proteomics

GENOMICS

UNMET NEED
Functional characterization of the genome

Accelerated functional characterization of genomic variants

PROTEOGENOMICS
Bridge the gap between genomics & proteomics to accelerate our understanding of biology

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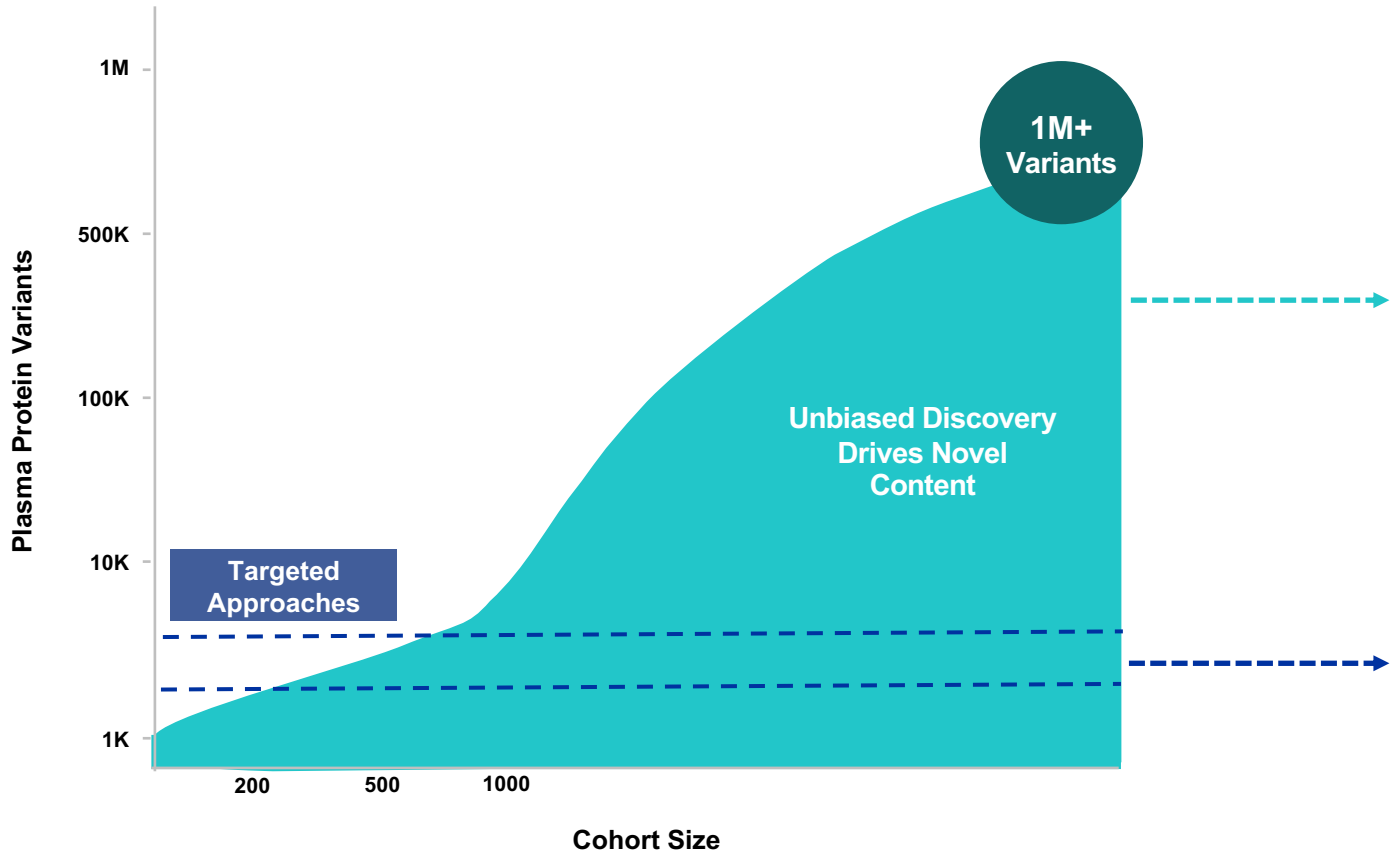
The Path to Whole Proteome Discovery

Deep, plasma proteomics-based discovery requires a scalable, unbiased approach



Untargeted Approaches

Promise to provide UNLIMITED potential to drive discovery of novel content, novel biology and all that targeted gives you - across the continuum from discovery to diagnostics

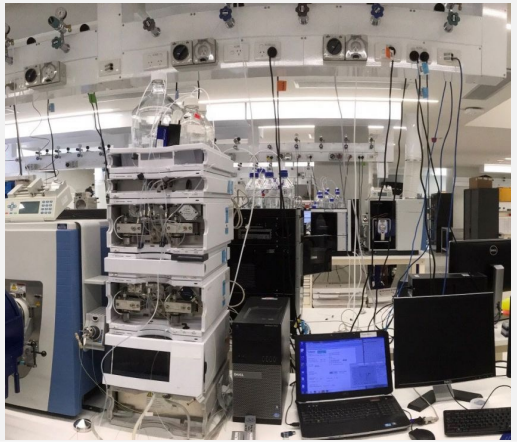
Targeted Approaches

Are limited to discovery of protein expression differences of known targets across cohorts - valuable but LIMITED

Seer Uniquely Addresses Unmet Need to Harness Power of Proteome

Accessing the depth and breadth of the proteome requires an unbiased, scalable approach

Scalability

	Targeted	Deep Unbiased
	Several solutions	seer
	Many solutions	

Deep, unbiased plasma proteomics at scale

- Catalog protein variants without *a priori* knowledge
- Observe rare & 'private' variants in any individual
- Perform population scale protein studies

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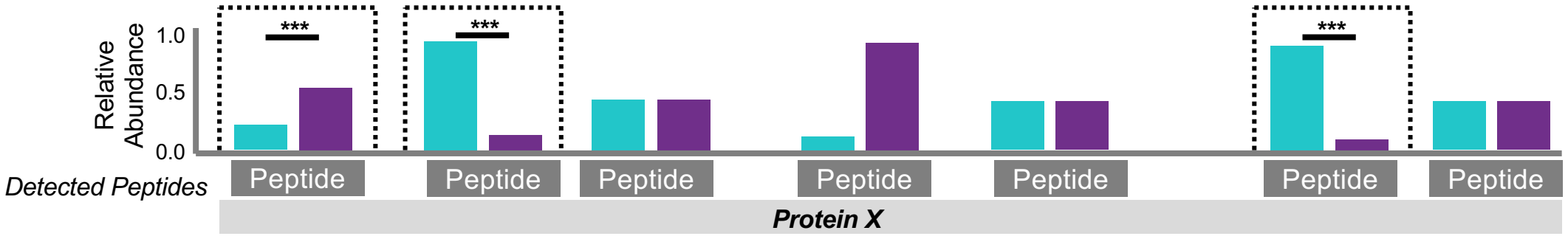
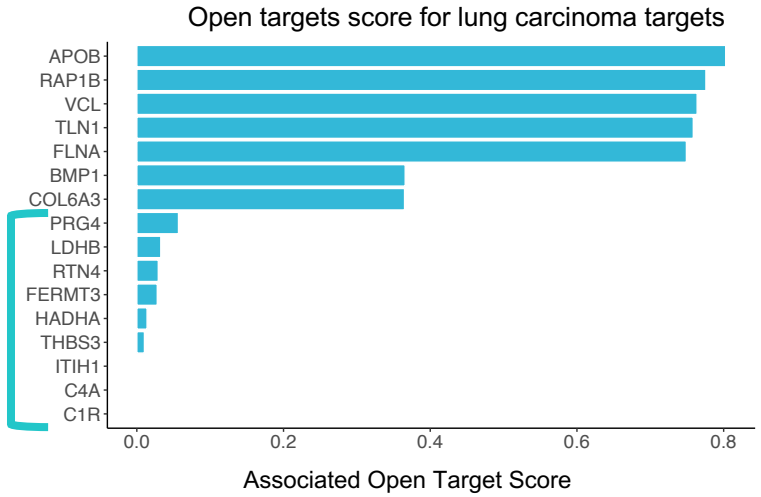
Putative Protein Isoforms Identified Using Peptide Abundance

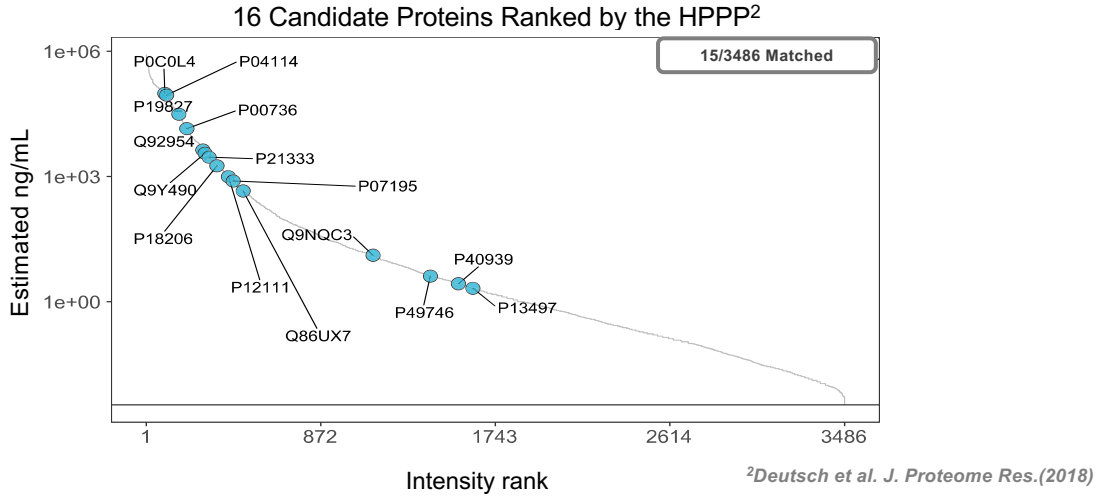
16 putative isoforms show known and novel associations with lung carcinoma targets, spanning the dynamic range

Protein isoform identification strategy



16 candidate protein isoforms



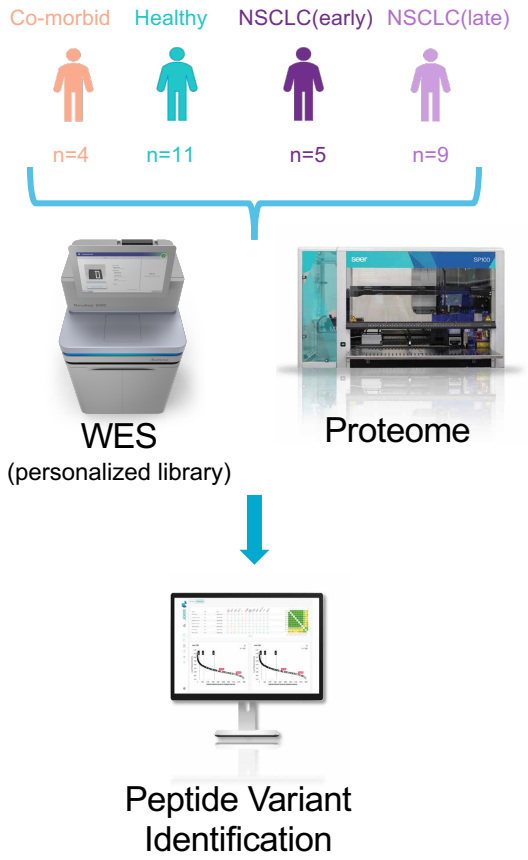


[2]*Deutsch et al. J. Proteome Res.(2018)*

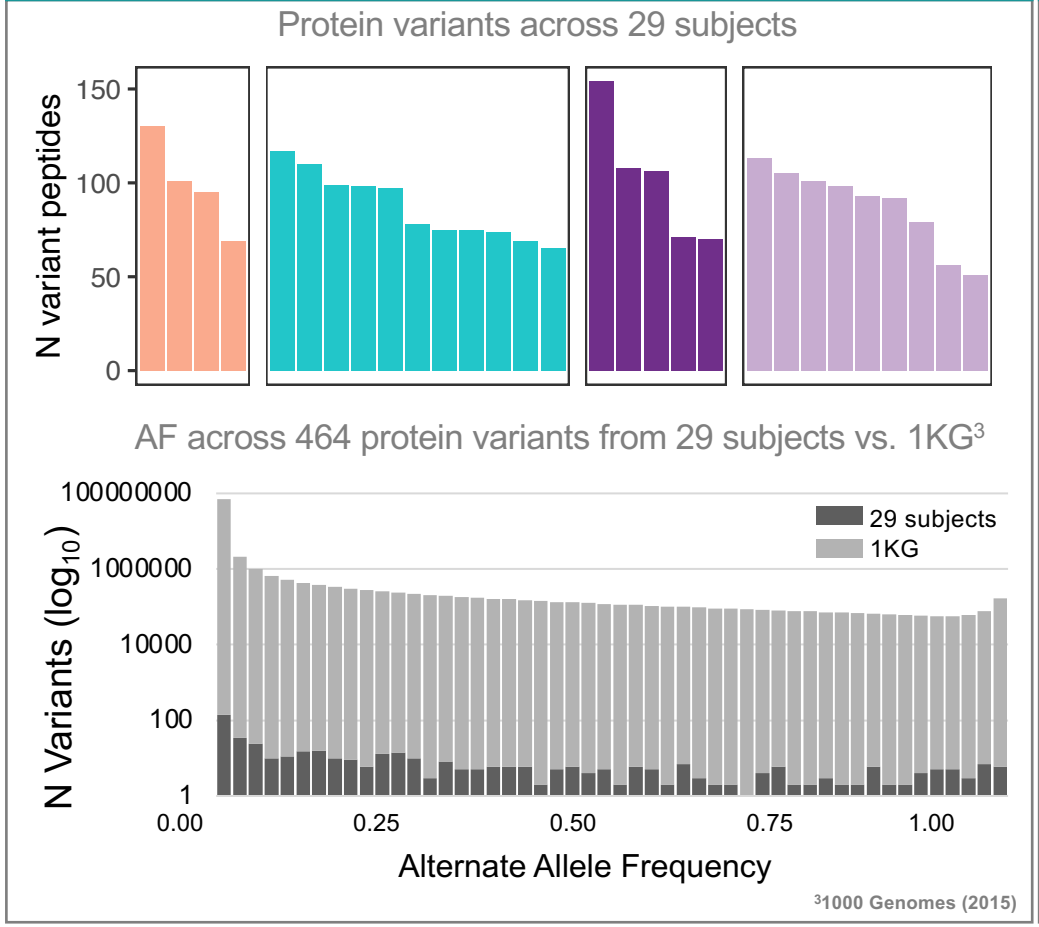
Proteogenomic Studies at Scale with an Unbiased, Deep and Rapid Method

Peptide variant identification using personalized libraries

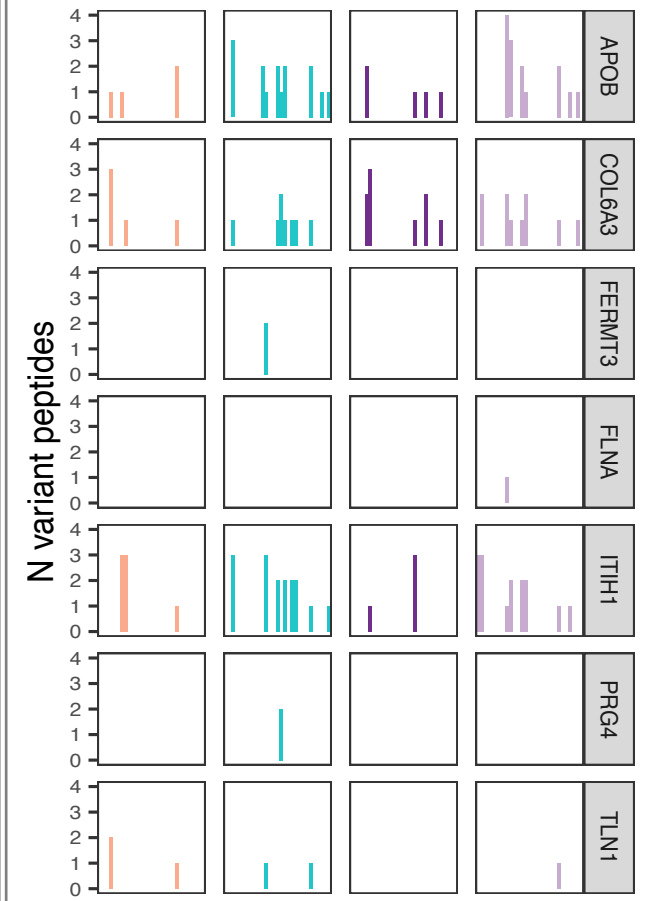
Study Design



464 protein variants from 29 subjects

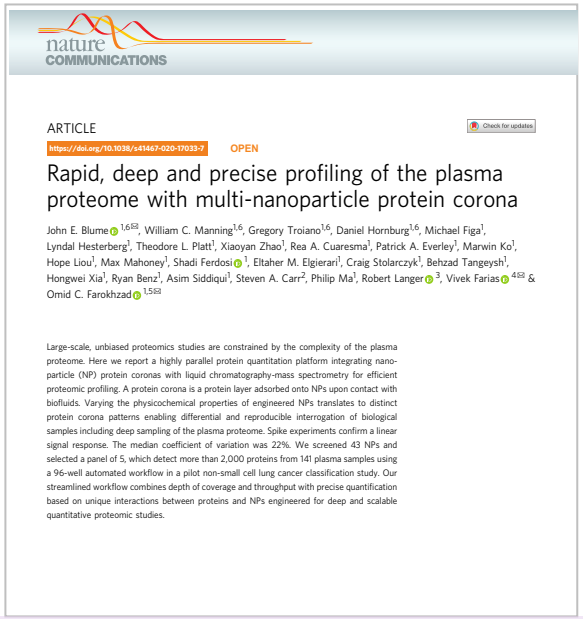


Detection of peptide variants in NSCLC-associated proteins



Deep, Unbiased, Scalable Proteomics Is Driving Powerful Insights

Publications


nature COMMUNICATIONS

ARTICLE

https://doi.org/10.1038/s41467-020-17033-7 OPEN

Rapid, deep and precise profiling of the plasma proteome with multi-nanoparticle protein corona

John E. Blume[1,6✉], William C. Manning[1,6], Gregory Troiano[1,6], Daniel Hornburg[1,6], Michael Figa[1], Lyndal Hesterberg[1], Theodore L. Platt[1], Xiaoyan Zhao[1], Rea A. Cuaresma[1], Patrick A. Everley[1], Marwin Ko[1], Hope Liou[1], Max Mahoney[1], Shadi Ferdosi[1], Eltaher M. Elgierari[1], Craig Stolarczyk[1], Behzad Tangeysh[1], Hongwei Xia[1], Ryan Benz[1], Asim Siddiqui[1], Steven A. Carr[2], Philip Ma[1], Robert Langer[3], Vivek Farias[4✉] & Omid C. Farokhzad[1,5✉]

Large-scale, unbiased proteomics studies are constrained by the complexity of the plasma proteome. Here we report a highly parallel protein quantitation platform integrating nanoparticle (NP) protein coronas with liquid chromatography-mass spectrometry for efficient proteomic profiling. A protein corona is a protein layer adsorbed onto NPs upon contact with biofluids. Varying the physicochemical properties of engineered NPs translates to distinct protein corona patterns enabling differential and reproducible interrogation of biological samples including deep sampling of the plasma proteome. Spike experiments confirm a linear signal response. The median coefficient of variation was 22%. We screened 43 NPs and selected a panel of 5, which detect more than 2,000 proteins from 141 plasma samples using a 96-well automated workflow in a pilot non-small cell lung cancer classification study. Our streamlined workflow combines depth of coverage and throughput with precise quantification based on unique interactions between proteins and NPs engineered for deep and scalable quantitative proteomic studies.

Additional publications coming in 2021

Scientific Conferences

>10 presentations and posters at scientific conferences in 2021

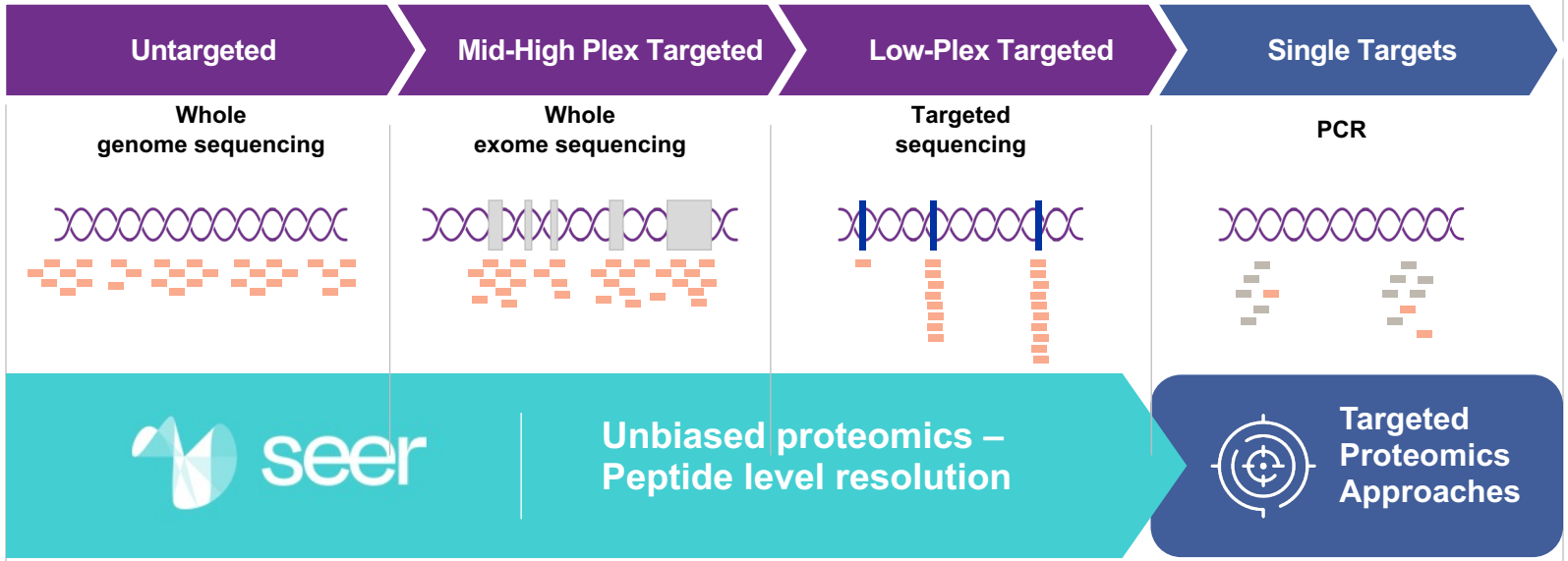
Collaboration Momentum

Sharing results and response from customers and partners

Unbiased Approaches are Needed to Create Substantial Value

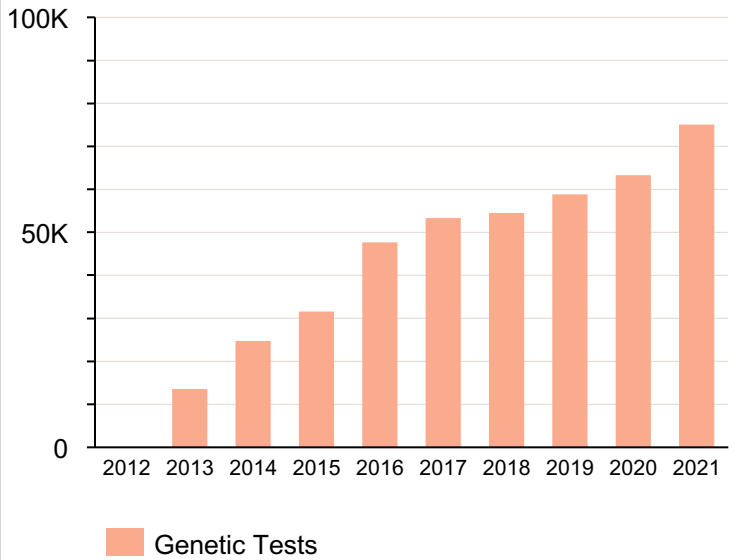
Peptide level resolution will enable the acceleration of variant discoveries and their clinical application

Single Base Resolution Was Necessary in Genomics to Enable Discovery



Peptide-level resolution will drive novel content, applications and tests in proteomics

Driving 10,000s of Genetic Tests

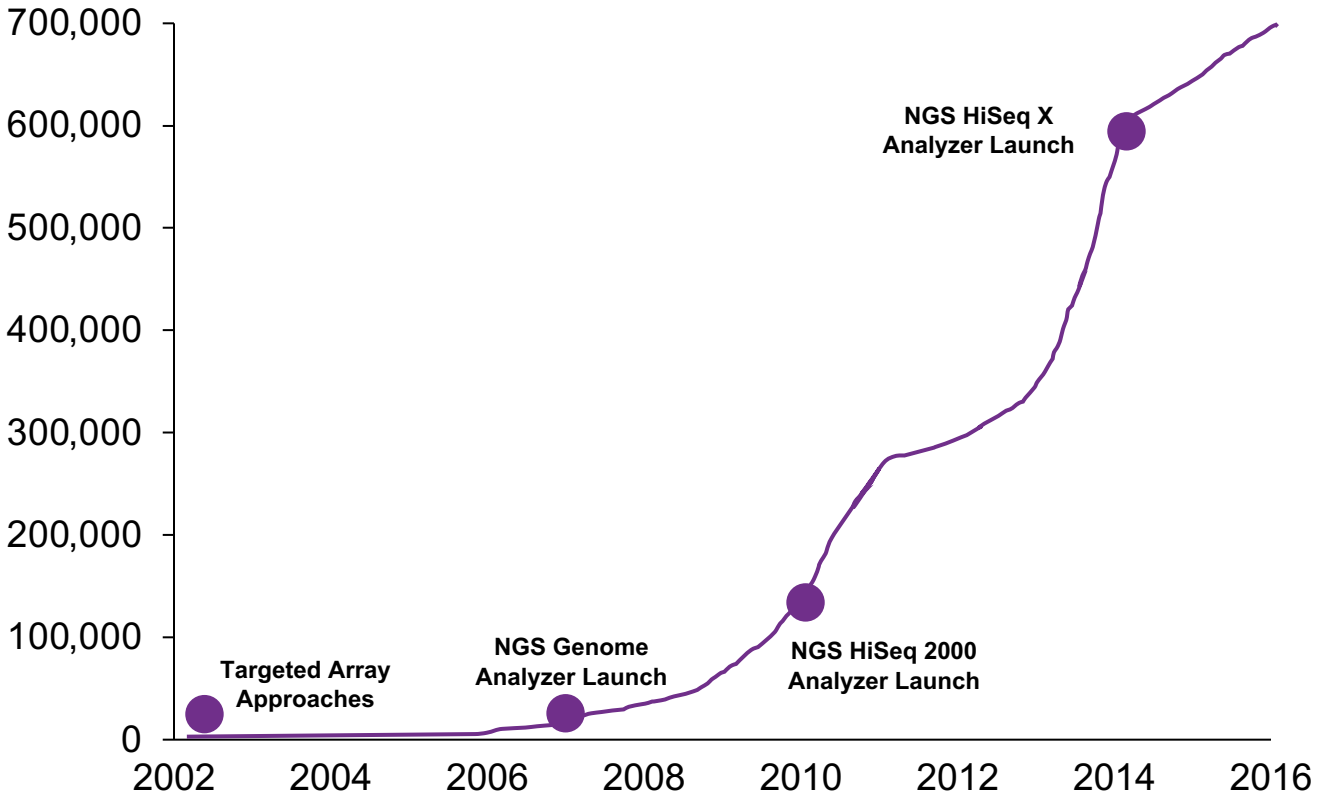


Unbiased tests

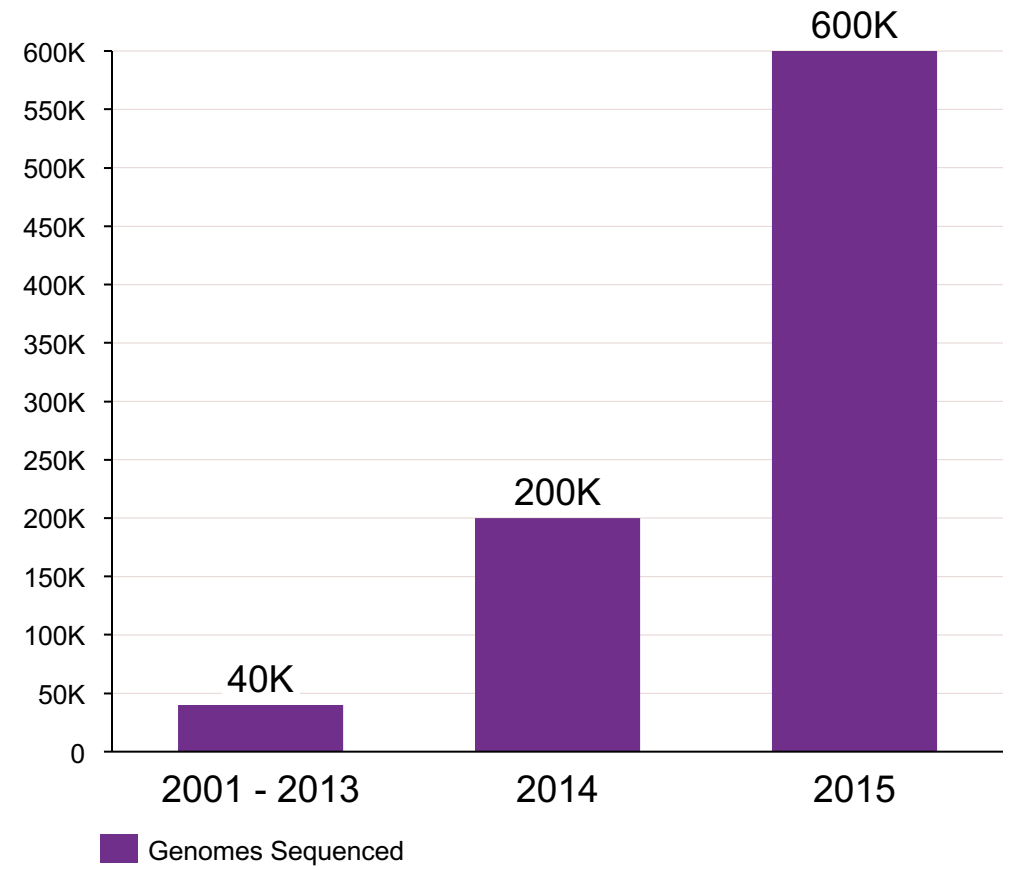
Novel Content and Methods Drive Value Creation

NGS, untargeted scalable genomics, drove genomic discovery and creation of novel content and insights

Increase in Genetic Variant Discovery 2002 to 2015



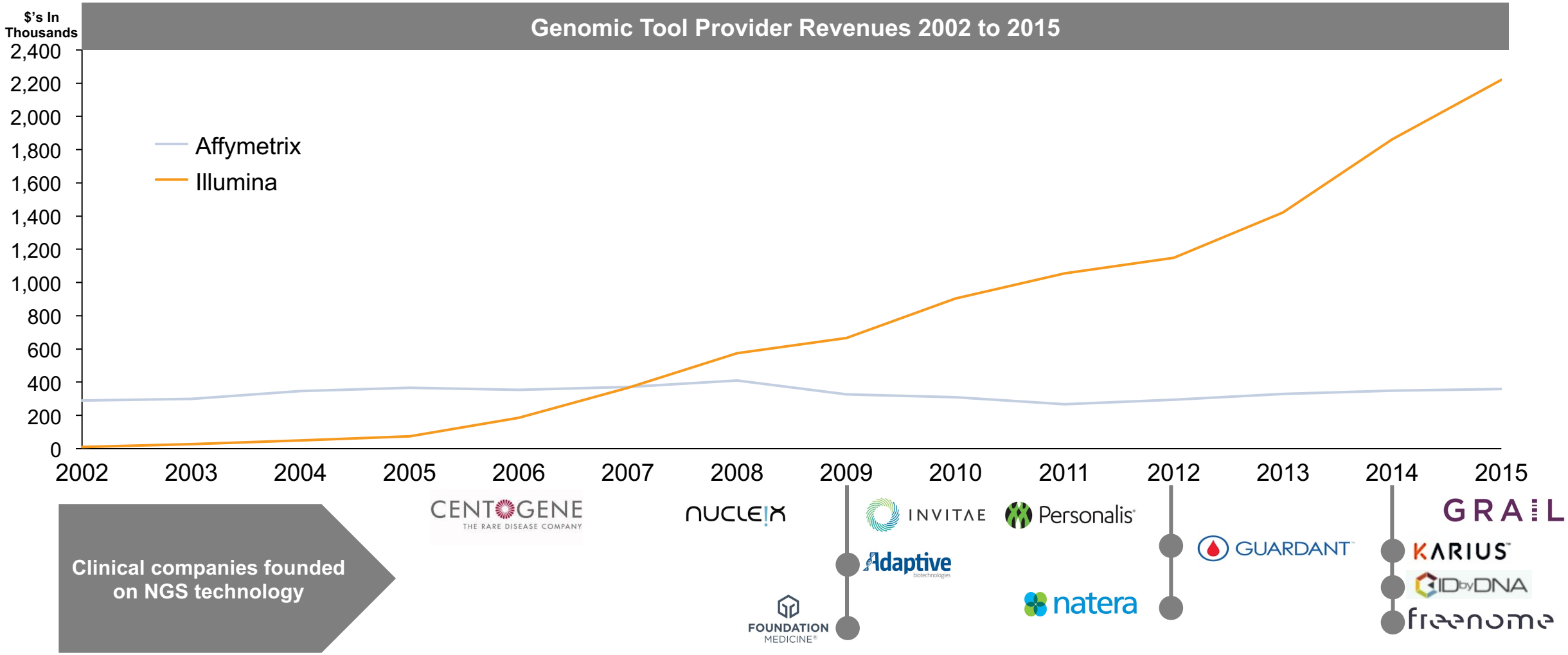
# of Genomes Sequenced



Sources: Database of Genomic Variants Increase in published structural variation data that have been added to the database since its start in 2004; the numbers reflect the year of publication; National Human Genome Research (NHGRI), Ark Investment Management

Novel Content and Methods Drive Value Creation

Untargeted scalable genomics drove market value indirect revenue and in the clinical ecosystem



Source: Public company information, SEC filings

Seer Is Uniquely Positioned Across the Continuum

1. # of outcomes gated by pace of discovery
2. Value creation highly affected by novel discoveries that lead to novel tests or therapeutics
3. Seer uniquely positioned to accelerate pace of discovery and value creation
4. NP technology can and will play across the entire continuum

Clinical Value Continues to Be Driven By Untargeted NGS

Clinical applications and clinical genomic value has shifted to untargeted and deeper genomic interrogation

Clinical Genomic Applications		Key Genomic Methods	Addressable Market
Non-Invasive Prenatal Testing	harmony® PRENATAL TEST, progenity®, illumina®, INVITAE, natera	• NGS	PCR / NGS: $2Billion (0 / 2)
Rare & Complex Genetic Disease	INVITAE, CENTOGENE THE RARE DISEASE COMPANY, illumina®	• NGS – Whole Exome & Genome	PCR / NGS: $86 Billion (0 / 86)
Infectious Disease	IDbyDNA, KARIUS, ThermoFisher SCIENTIFIC, COSMOSID®, QIAGEN	• PCR • NGS - Shotgun Metagenomics, Whole Genome	PCR / NGS: $1.5 Billion (1.30 / 0.20)
Early Cancer Detection	GUARDANT, GRAIL, NUCLEIX, freenome	• PCR • NGS - Whole Exome, Genome, and Methylation	PCR / NGS: $75Billion (2 / 74)
Cancer Therapy Selection & Monitoring	INVITAE, GUARDANT, FOUNDATION MEDICINE®, Adaptive biotechnologies	• NGS – Whole Exome & Genome	

Sources: Addressable Markets are estimated based on public company statements on market size including: Natera, Inc 2021 J.P. Morgan Healthcare Conference Presentation, Bio-Rad 2020 Earnings, Thermo 2020 Earning, Qiagen 2020 Earnings, Invitae JP Morgan 2021 presentation, Illumina Sept 21 Press Release

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Seer Is Uniquely Positioned Across the Continuum

REQUIREMENTS

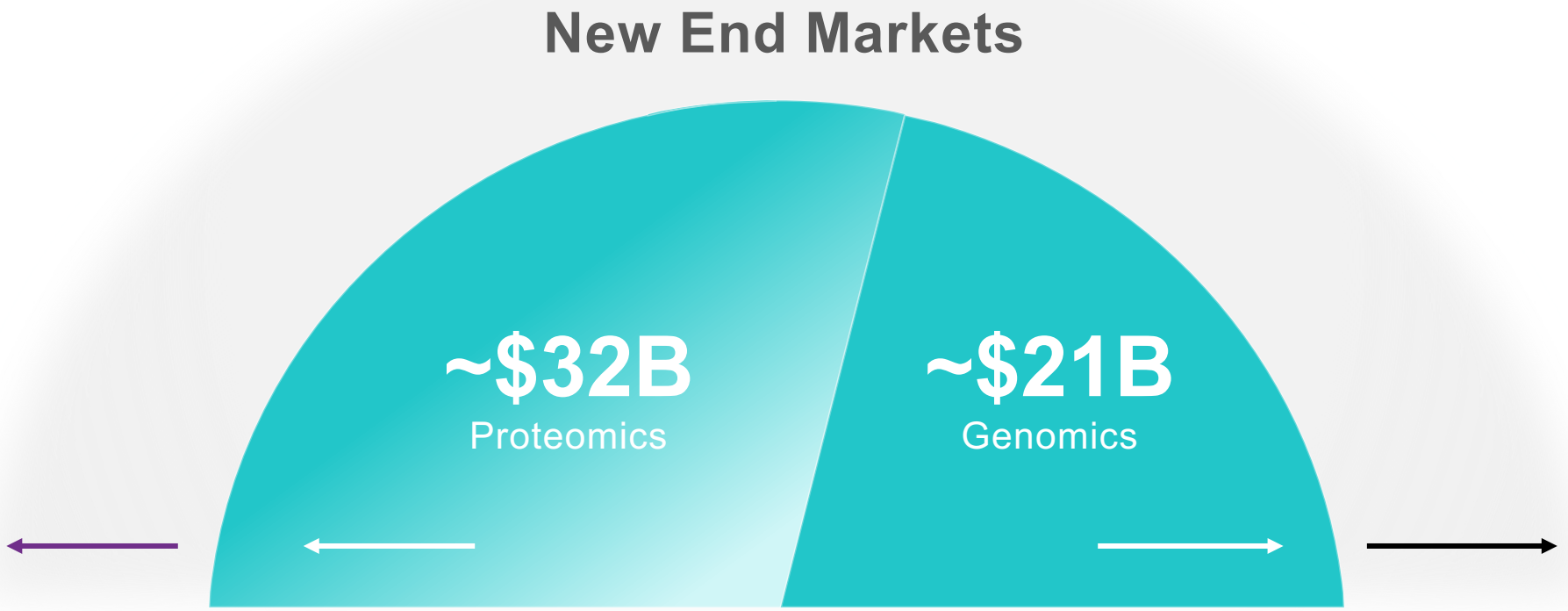
- Untargeted
- Scalable
- Resolve peptide level differences
- Clinical grade capability
- Same technology can be deployed

Peptide-level variation	Novel content	Novel biology
Protein isoforms	Lung cancer	smORFs

Inaccessible to targeted approaches

Opening a New Frontier

Expanding proteomics and genomics markets via unbiased, deep, and rapid proteomics at scale



Unmet need for deep, unbiased proteomics at scale

Basic research and discovery applications	Translational research applications	Diagnostic applications	Applied applications

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Driving Market Development Strategies to Expand Opportunity

Building an ecosystem around unbiased, deep proteomics

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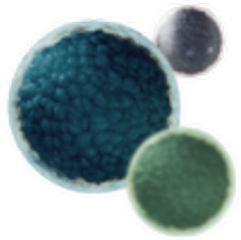
Establish Seer as premier provider in proteomics



02

Enable customers to build on our technology

DISCOVERY LIFE SCIENCES

BROAD INSTITUTE

KNIGHT CANCER Institute OHSU

salk Where cures begin.

03

Catalyze novel applications and business models

prognomiQ

04

Form strategic relationships to deliver end to end solutions

BRUKER

ThermoFisher SCIENTIFIC

SCIEX

Technologies that enable rapid, deep and unbiased analysis of the proteome, while retaining the ability to detect and quantify modifications like phosphorylation, are essential now and in the future of biology and clinical medicine." — *Steve Carr, Senior Director of Proteomics, Broad Institute*

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Advances & Limitations of Genomics Has Crystalized the Need for Novel Proteomics Discovery at Scale

Broad Range of Customer Types

- Academic
- Pharma
- Applied
- Translational
- CRO & Services
- Diagnostics

Hundreds using –omics at scale

Broad Range of Applications

- Cataloging protein diversity
- Proteogenomics
- Biomarker discovery
- Target identification and exploration
- Multi-omics for cancer
- Multi-omics for complex disease areas

With clear need for novel proteomics insights

Unmet Need:
Unbiased deep proteomics at scale to power discovery of novel insights
Seer is uniquely positioned to address this need across range of customers, applications and geographies

Early Customer Data Supports Unique Value of Proteograph

Consistently detecting far more proteins per sample across wide range of samples and workflow comparisons

Academic Medical Center (Translational Cancer Research)	Research Institute	Large-scale Service Provider
• Novel potential protein variants for prostate cancer found in pilot • Several large-scale follow on studies planned, including one with 500-1000 samples • Growing interest in deep, unbiased proteomics at institution	• Interested in model organisms, human complex disease, mechanisms of regulation and translation • Promising early data on *Arabadopsis* pilot • Early indications of difficult to get small proteins being detected	• Deeper coverage ~4x more proteins compared to their existing deep proteomics method • Increased number of low abundance proteins reported (including cytokines) • Proteograph scalability of great value for service business

- Promising early data increasing customer excitement, motivation to get access to product
- Planning on a regular cadence of customers sharing their experience (started with Mark Flory in May)
- Customer success and data will corroborate differentiated value, accelerate adoption and scaling

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Four Dimensions of Improvements

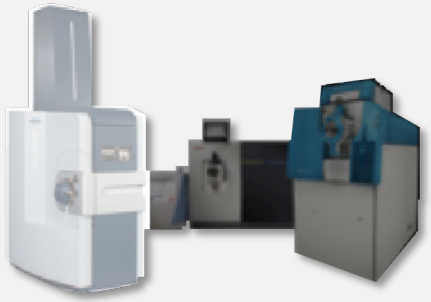
Improvements are multiplicative across the dimensions; the following slides give examples of each

Nanoparticles

Improving nanoparticle design through directed engineering

Assay

Improving Assay conditions to maximize detected proteins and peptides



Mass spectrometry

Developing new workflows for data acquisition

Data analysis

Creating new algorithms to maximize coverage and throughput

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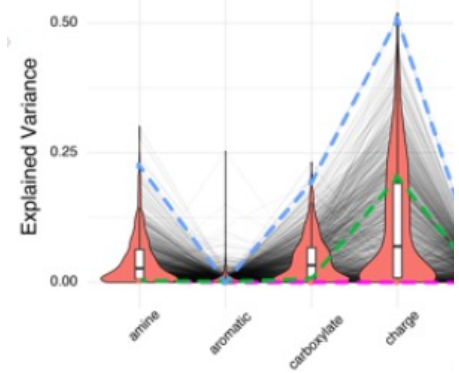
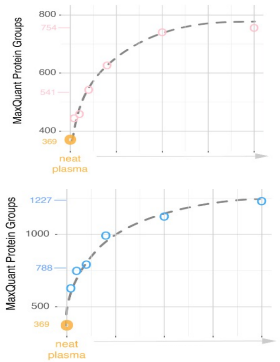
Four Dimensions of Improvements

Improvements are multiplicative across the dimensions; the following slides give examples of each



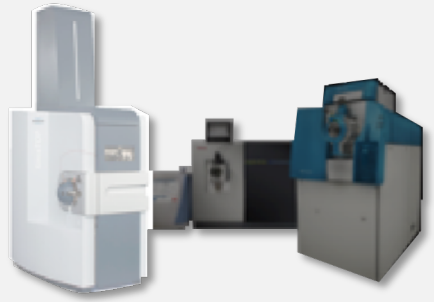
Maximize NP performance with AI

- Explore new NP properties
- Improve protein group numbers and efficiency of sampling of the whole panel.



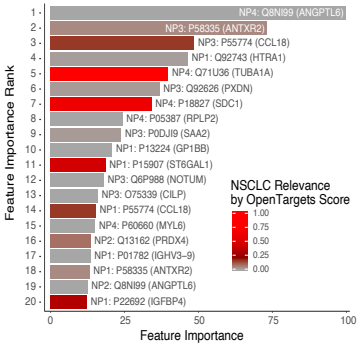
Optimize assay to increase protein numbers

- Modify assay conditions to increase protein groups
- Tune distinct binding of NPs
- Maximize overall protein counts obtained across assay conditions



Improve mass spec integration & data acquisition

- Develop methods to maximize protein and peptide ID & reproducibility
- Collaborate with customers & partners to streamline overall workflow & parameters
- Optimize MS configuration to generate a much larger number of proteins

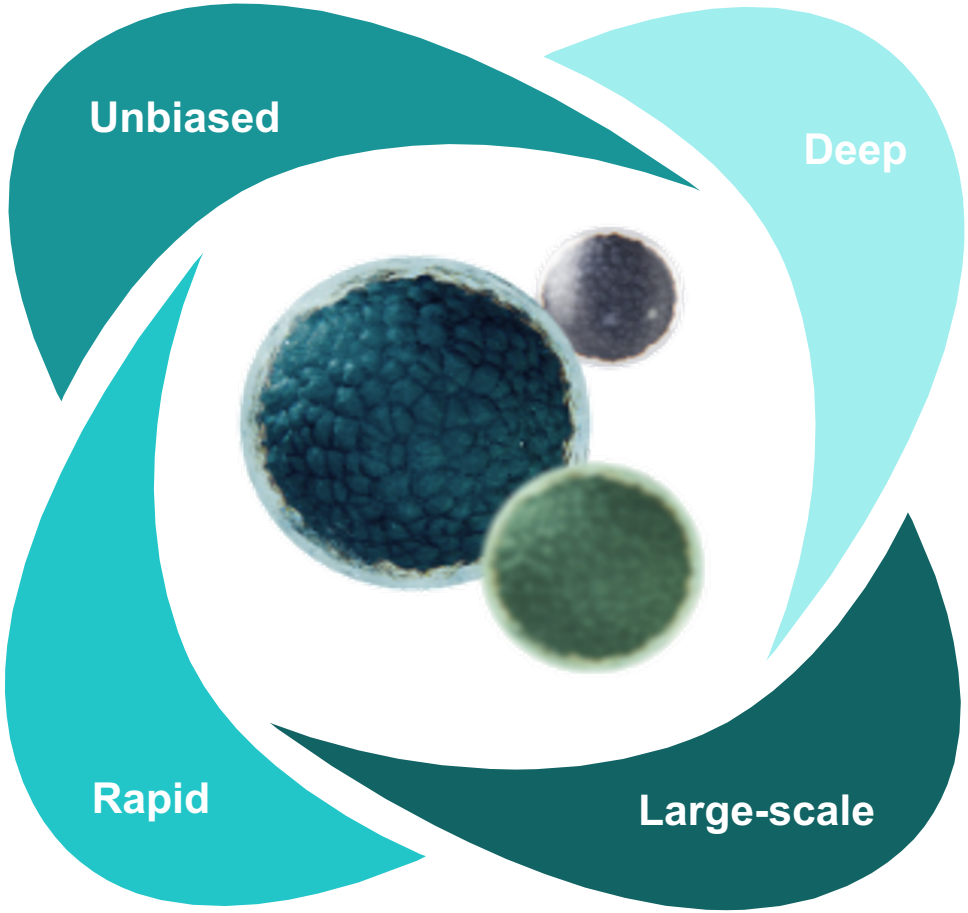


Expand data analysis tools

- Identify more proteins while maintaining a constant FDR.
- Augment search to include glycosylated peptides.

Seer: A New Gateway to the Proteome

Making strong progress since the IPO



Strong commercial progress

- Shipped to a second Phase 1 site
- Added third Phase 1 site

Positioned for market expansion

- Partnered with Thermo Fisher and Bruker

Extended technology & team

- Strengthened the management team
- Further evidenced key applications