Enabling core laboratories to expand access to genomics

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Staff Product Marketing Manager – Benchtop Systems, Americas

12th October 2023

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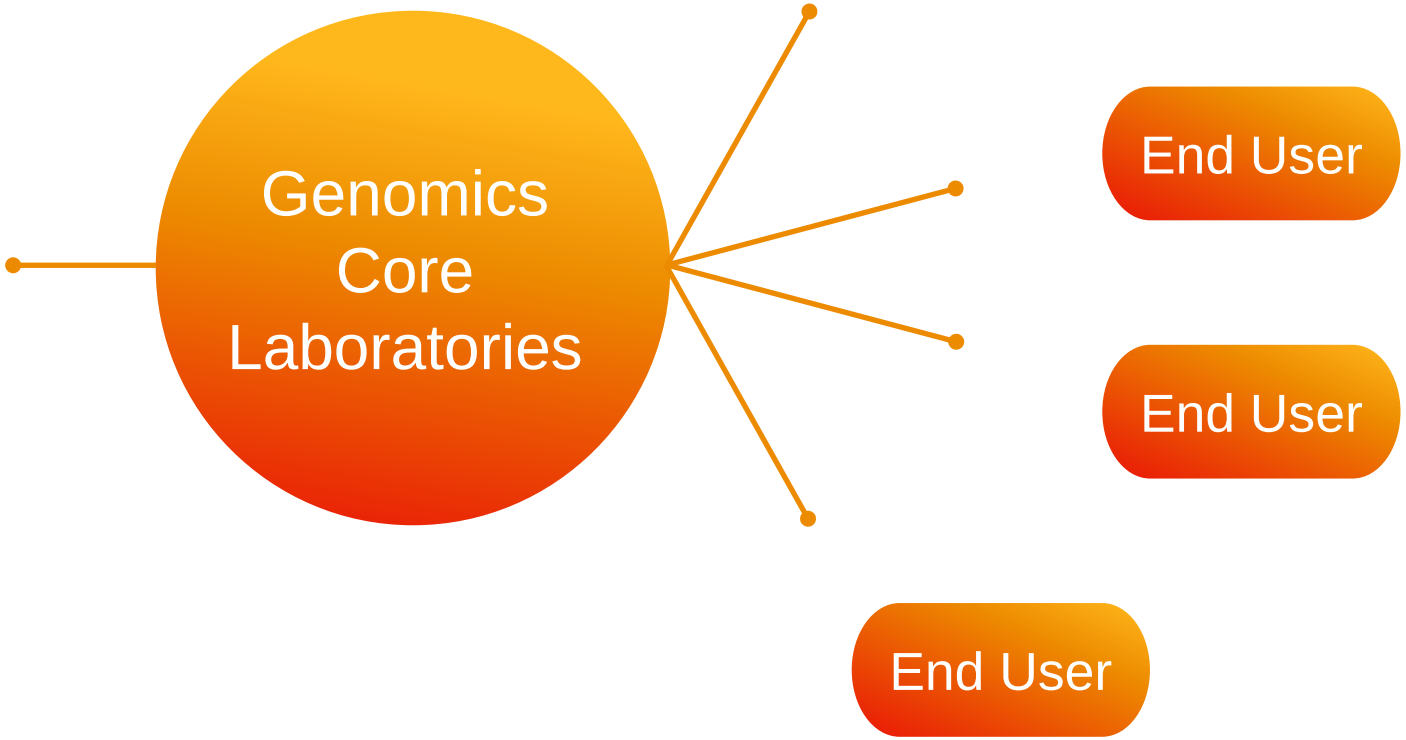
Core laboratories are an integral partner to vendors within the broader genomics ecosystem



Core labs democratize sequencing by helping researchers access equipment and expertise that would be otherwise inaccessible

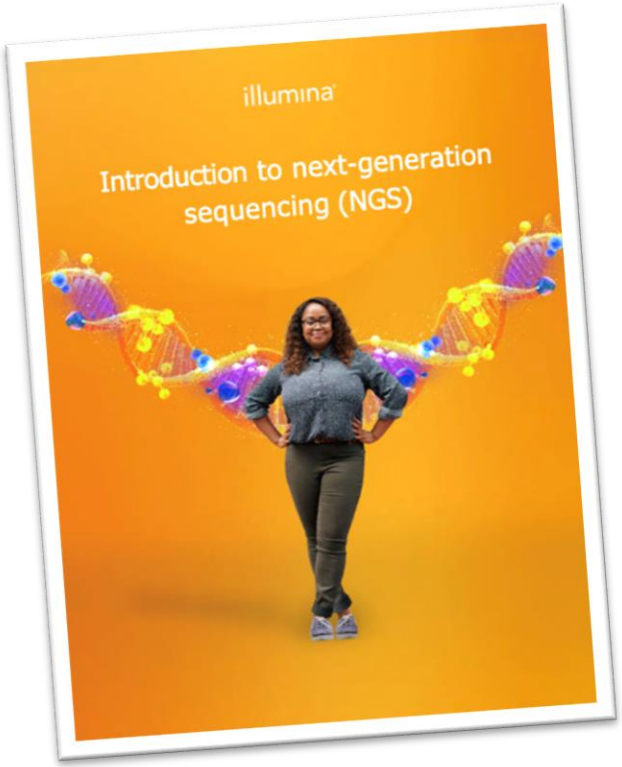
Cost and lack of bioinformatics experience are major barriers to entry

There's an "intimidation barrier" to NGS due to its relative complexity vs traditional methods

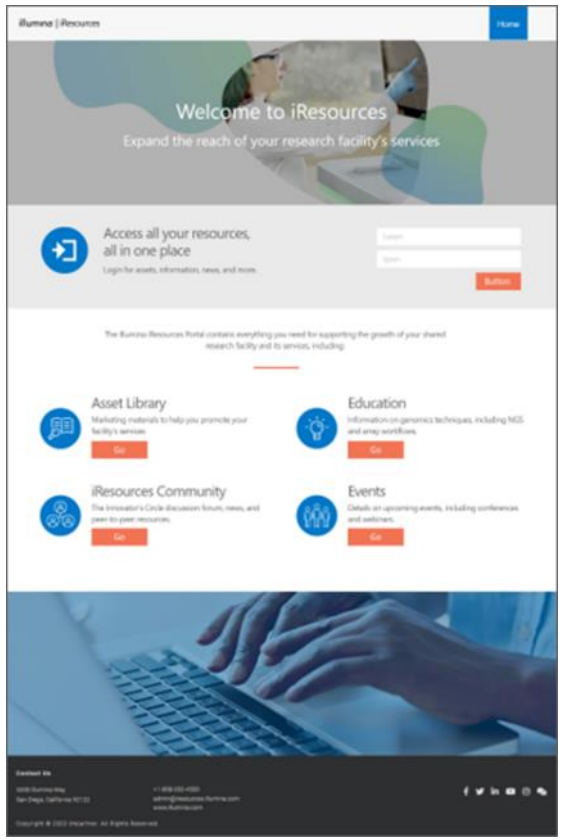
Core labs play a major role in educating the campus community about genomics fundamentals

Illumina is looking to partner with core labs to broaden the reach of genomics to more researchers

Content for researchers that are new to sequencing



Resources for core labs to promote facility services



Technology advancements to improve the core experience

XLEAP SBS™

New to Next Generation Sequencing (NGS)

Showing customers the value of collaborating with core labs and driving new research

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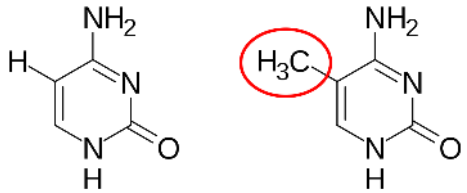
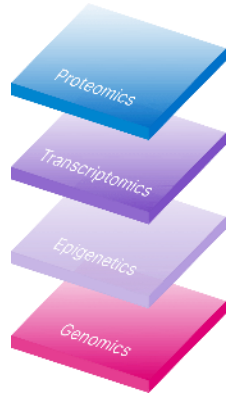
For most research customers, using NGS is a journey that starts small, but grows as they build expertise and confidence





New to NGS

New to NGS refers to the majority of researchers in biology that **do not currently use NGS** for research.

Recent NGS Adopters

Researchers who start using NGS almost invariably do so via **outsourcing** (usually at a local core lab).

Experienced NGS Users

Experienced researchers do not fear complexity and are ready to **reduce inference** from data by **combining omics** or using higher depth approaches.

New to NGS is a set of educational resources that helps researchers learn about NGS and promotes new customer relationships at core labs.

New to NGS focuses on affordable, well-established methods, not products

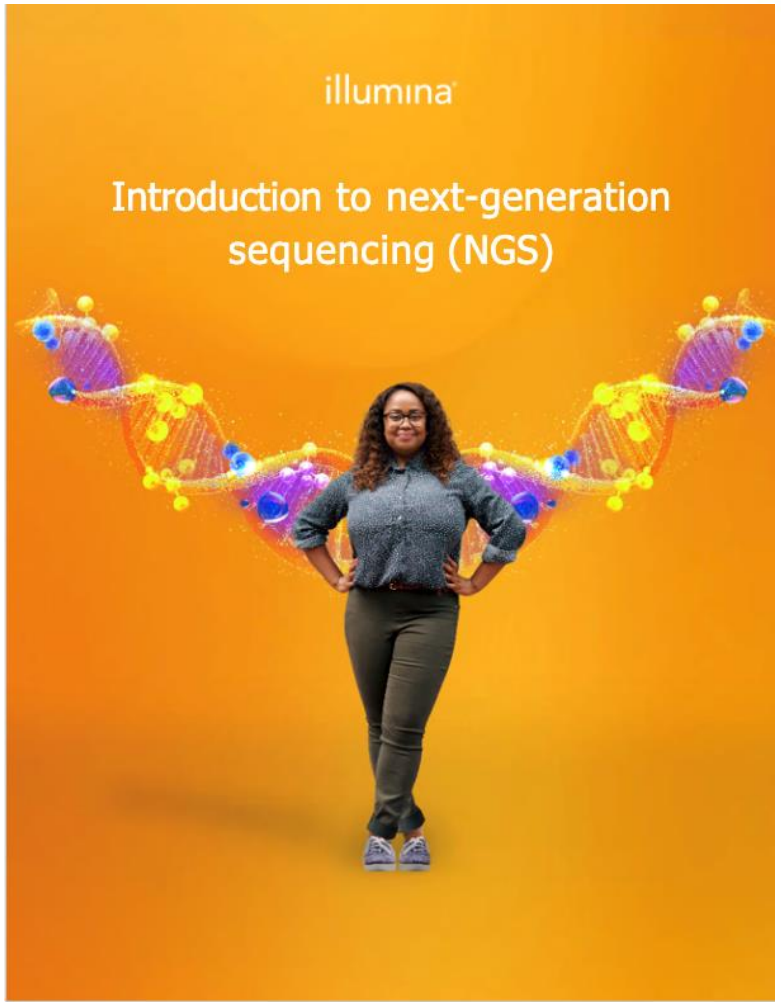
Key Themes:

- You don’t need to be an expert to get started, collaborate with your local core lab.
- Sequencing is more accessible and cost-effective than ever before, especially with counting methods
- A modern look at why and when it makes sense to cast a wider net vs targeted approaches.

Key methods for getting started with NGS:

- Bulk RNA Sequencing
- Single Cell RNA Sequencing

New to NGS eBook



An accessible introduction to illumina sequencing intended to overcome common intimidation barriers and promote collaboration with core labs

Infographics focus on grad students and postdocs who got started with genomics via core lab collaborations

RNA-Seq: A good place to start

NGS-based RNA sequencing (RNA-Seq) is a versatile NGS method that examines the expression of thousands of genes in a single assay, making it possible to characterize complex pathways.[8,9]

"For us, sequencing changed everything. If we wouldn't have been able to use bulk RNA sequencing, we wouldn't have been able to see what's going on at the chromosomal level in our mutants."
Mercedes Carro, PhD, Postdoctoral Associate Cohen Lab, Cornell University

"Working with the core lab gave me confidence. I was less worried about my experiment or quality control issues."
Connor Kean, Graduate Student, Grimson Lab, Cornell University

Get started with the help of NGS professionals

You don't need to be an expert to get started: collaborating with core labs and service providers is the best way to get assistance at each step of the NGS workflow, from designing your experiment to running your samples.

No bioinformatics expertise required

NGS produces large data sets that can be intimidating for new users. Core labs and the latest applications can help you analyze and understand your data, even without bioinformatics experience.

"I think this collaboration really gave me the confidence to know that I can do this type of analysis."
Amanda Touey, Graduate Student, Cohen Lab, Cornell University

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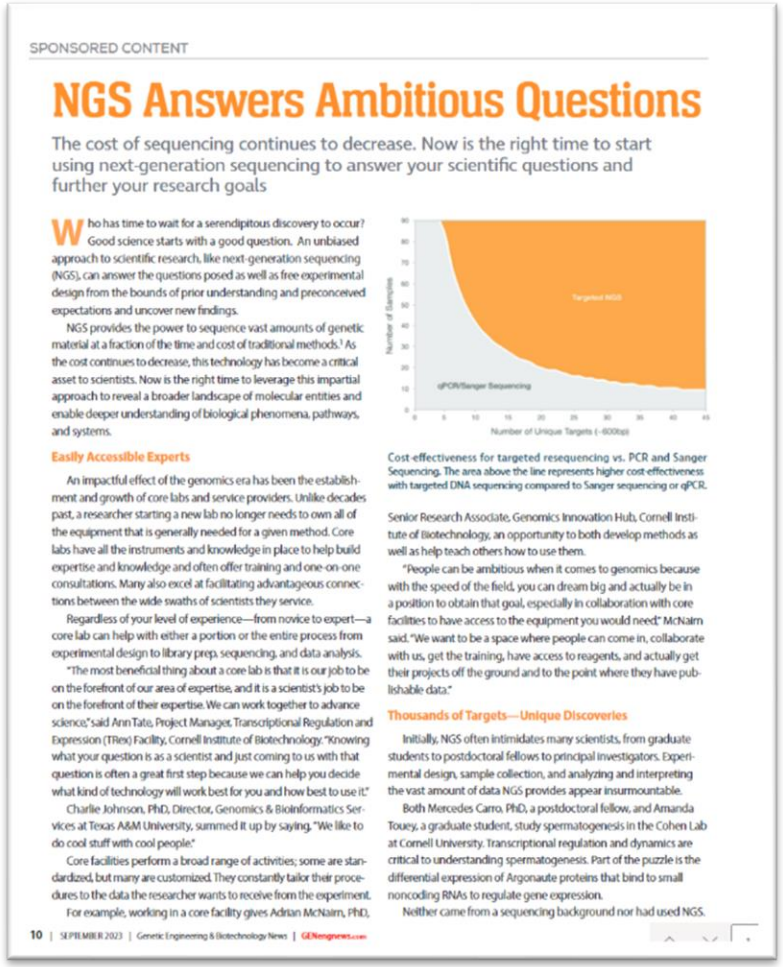
New to NGS articles in GEN and The Scientist focus on introduction to common sequencing methods and experiences of real users



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NGS Answers Ambitious Questions

The cost of sequencing continues to decrease. Now is the right time to start using next-generation sequencing to answer your scientific questions and further your research goals

Who has time to wait for a serendipitous discovery to occur? Good science starts with a good question. An unbiased approach to scientific research, like next-generation sequencing (NGS), can answer the questions posed as well as free experimental design from the bounds of prior understanding and preconceived expectations and uncover new findings.

NGS provides the power to sequence vast amounts of genetic material at a fraction of the time and cost of traditional methods.[1] As the cost continues to decrease, this technology has become a critical asset to scientists. Now is the right time to leverage this impartial approach to reveal a broader landscape of molecular entities and enable deeper understanding of biological phenomena, pathways, and systems.

Easily Accessible Experts

An impactful effect of the genomics era has been the establishment and growth of core labs and service providers. Unlike decades past, a researcher starting a new lab no longer needs to own all of the equipment that is generally needed for a given method. Core labs have all the instruments and knowledge in place to help build expertise and knowledge and often offer training and one-on-one consultations. Many also excel at facilitating advantageous connections between the wide swaths of scientists they service.

Regardless of your level of experience—from novice to expert—a core lab can help with either a portion or the entire process from experimental design to library prep, sequencing, and data analysis.

"The most beneficial thing about a core lab is that it is our job to be on the forefront of our area of expertise, and it is a scientist's job to be on the forefront of their expertise. We can work together to advance science," said Ann Tate, Project Manager, Transcriptional Regulation and Expression (TREx) Facility, Cornell Institute of Biotechnology. "Knowing what your question is as a scientist and just coming to us with that question is often a great first step because we can help you decide what kind of technology will work best for you and how best to use it."

Charlie Johnson, PhD, Director, Genomics & Bioinformatics Services at Texas A&M University, summed it up by saying, "We like to do cool stuff with cool people."

Core facilities perform a broad range of activities; some are standardized, but many are customized. They constantly tailor their procedures to the data the researcher wants to receive from the experiment.

For example, working in a core facility gives Adrian McNairn, PhD, Senior Research Associate, Genomics Innovation Hub, Cornell Institute of Biotechnology, an opportunity to both develop methods as well as help teach others how to use them.

Cost-effectiveness for targeted resequencing vs. PCR and Sanger Sequencing. The area above the line represents higher cost-effectiveness with targeted DNA sequencing compared to Sanger sequencing or qPCR.

"People can be ambitious when it comes to genomics because with the speed of the field, you can dream big and actually be in a position to obtain that goal, especially in collaboration with core facilities to have access to the equipment you would need," McNairn said. "We want to be a space where people can come in, collaborate with us, get the training, have access to reagents, and actually get their projects off the ground and to the point where they have publishable data."

Thousands of Targets—Unique Discoveries

Initially, NGS often intimidates many scientists, from graduate students to postdoctoral fellows to principal investigators. Experimental design, sample collection, and analyzing and interpreting the vast amount of data NGS provides appear insurmountable.

Both Mercedes Carro, PhD, a postdoctoral fellow, and Amanda Touey, a graduate student, study spermatogenesis in the Cohen Lab at Cornell University. Transcriptional regulation and dynamics are critical to understanding spermatogenesis. Part of the puzzle is the differential expression of Argonaute proteins that bind to small noncoding RNAs to regulate gene expression.

Neither came from a sequencing background nor had used NGS.

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Next-Generation Sequencing: A World without Limits

Centralized core facilities and commercial service providers specializing in NGS provide expertise and training for researchers new to the method.

From bulk and single cell methods to spatial and multiomic methods, advancements in sequencing and -omics research are accelerating at an exciting pace. Next-generation sequencing (NGS) provides researchers from various scientific fields the ability to cast a wide net and explore complex pathways and biological processes. With NGS, scientists can take an untargeted approach, generating data from many genetic loci at once.

Such open-ended discovery allows researchers to see details that may be overlooked in targeted approaches that assay one gene at a time. Despite this benefit, the technical aspects of library preparation and data analysis can be daunting for researchers new to NGS. Previously, high sequencing costs, lack of expertise, and enormous data volumes were seen as barriers to entry.[1] Over time, these barriers have diminished thanks to decreased costs and optimized workflows and bioinformatics pipelines.[1-3] In addition, numerous academic NGS core facilities and commercial service providers have been implemented globally to support researchers on their NGS journeys. Such access to centralized equipment and expertise makes NGS more approachable to researchers new to the method.

Support for Scientists Diving into NGS

Instead of entering the NGS world alone, scientists can take their experiments to a core facility and receive expert guidance. "Our core motto is reducing barriers to genomic technologies. That means that whatever point you are in your knowledge of genomics, we want to be there to help you," said Ann Tate, project manager for the Transcriptional Regulation and Gene Expression Facility (TREx) in the Biotechnology Resource Center (BRC) at Cornell University.

According to Tate, prior sequencing experience is not important when initiating an NGS project with a core facility. Some researchers may simply hand off their samples and wait for results, while others choose to take a hands-on approach, collaborating with core members from the onset of their project.

"We want to be a makerspace where people can come in, collaborate with us, get the training, have access to reagents, and actually get their projects off the ground and to the point where they have publishable data," said Adrian McNairn, the lead biologist for the Genomics Innovation Hub in the BRC. From new graduate students lacking wet bench experience to tenured professors trying bioinformatics for the first time, researchers can work side-by-side with NGS core members who use their expertise to tailor technologies to specific research questions, train scientists in sequencing best practices, and make data analysis more accessible.

Core facilities and commercial service providers democratize NGS so that all scientists can access this powerful technology. Working with a core that has equipment such as sequencers, incubators, and fragment analyzers provides access in a way that is no longer cost prohibitive. "An example of a cool project that I did with someone who now has access... is iridescent butterfly wings," said Tate. "We were sequencing butterfly wing cells. Five years ago, that would have been cost prohibitive to them." Additionally, samples from lesser-studied species may require changes to existing reagents, workflows, or data analyses, which core members help customize thanks to their deep-seeded NGS knowledge. "We have seen everything from shark eyeballs, to pond scum, to broccoli and cauliflower," Tate stated.

A hands-on, expert approach is also key when processing samples, building libraries, and analyzing data. As McNairn works with researchers, he evaluates the quality of their samples every step of the way. "Since we've worked with them through the whole process, we can go back and troubleshoot the areas that we know maybe went wrong," said McNairn. In addition to support at the facility, core members facilitate connections between researchers

- Explore stories of NGS becoming a crucial tool for early career researchers
- How a network of genomics core labs with Illumina technology can help researchers gain expertise and confidence in NGS approaches
- Focus heavily on actual user interviews so that the case for NGS is made from their real world perspective

New to NGS Poster in The Scientist

iResources, a new online portal exclusive to core lab facilities

iResources is an online destination that allows core lab members access to Illumina-provided content in one place

Explore & Engage

Laboratory management can be complex. Finding support doesn't have to be. Access all the resources you need for promoting your shared research facility's services, all in one place.

Asset Library

Marketing materials to help you promote your facility's services.

GO

Education

Information on genomics techniques, including NGS and array workflows.

GO

iResources Community

The Innovator's Circle discussion forum, news, and peer-to-peer resources.

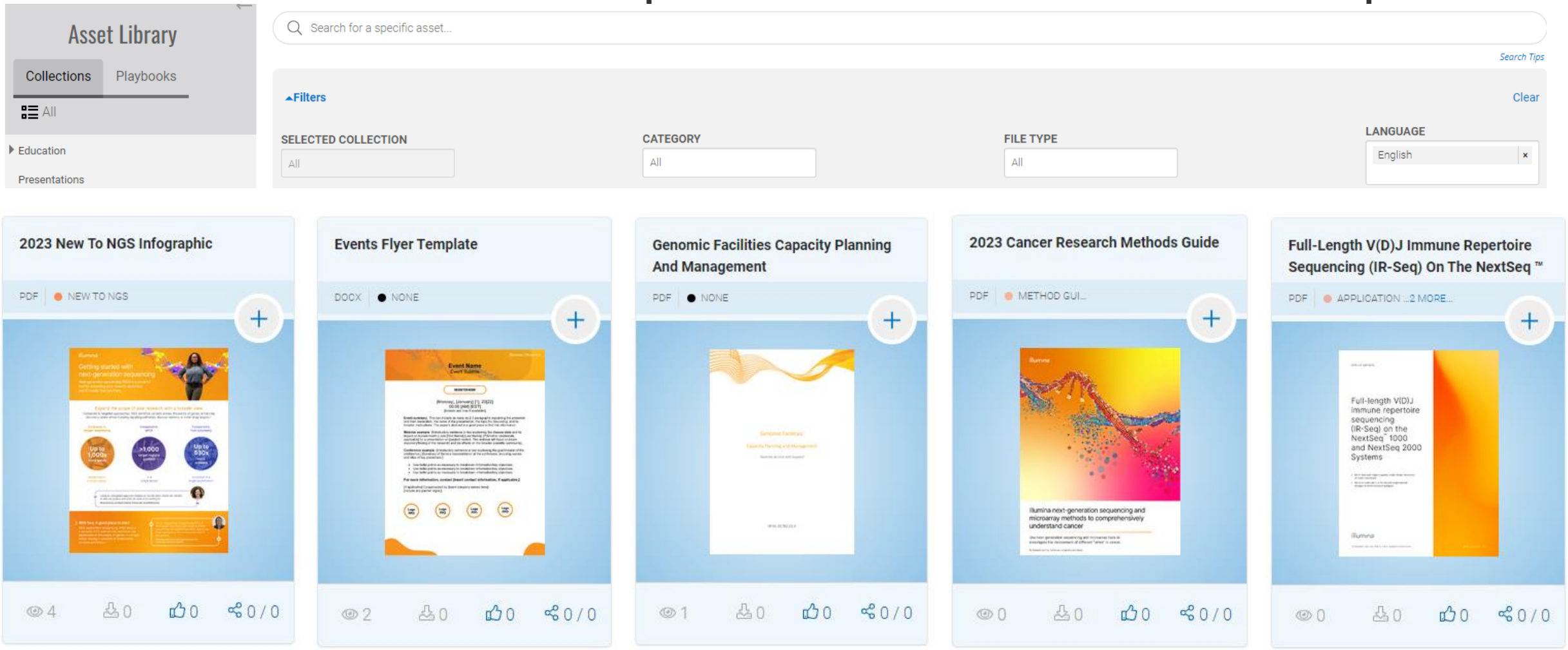
GO

Events

Details on upcoming events, including conferences and webinars.

GO

Asset Library provides educational content and marketing materials for core labs to promote their services and expertise



Education section specifically for new core lab team members

Learn how Illumina technology works and what it can do for you

From library prep to data analysis, Illumina offers tools and support throughout the entire NGS and array workflows. Learn more about each part of the process.

Methods

Learn about key methods like WTS, Single-cell RNA-Seq, WES, and more.

Learn More

Arrays

Resources about Illumina's bead-based array technology.

Learn More

Library Prep

Discover ways to optimize workflow with fast and simple library prep.

Learn More

Sequencing

Information about the diverse types of sequencing.

Learn More

QC & Troubleshooting

Discover methods for QC and troubleshooting to ensure confidence and accuracy in your sequencing.

Learn More

Analysis

Learn about the myriad of options for analyzing your samples with the latest software and informatics tools.

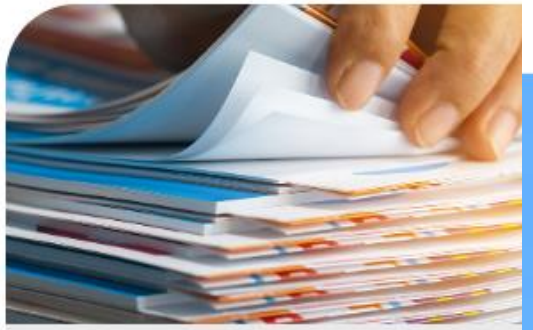
Learn More

iResources Community has the latest news in genomics and sequencing and links to the ABRF Community Site

Sequencing News

Read the latest news related to genomics, including NGS, arrays, and more.

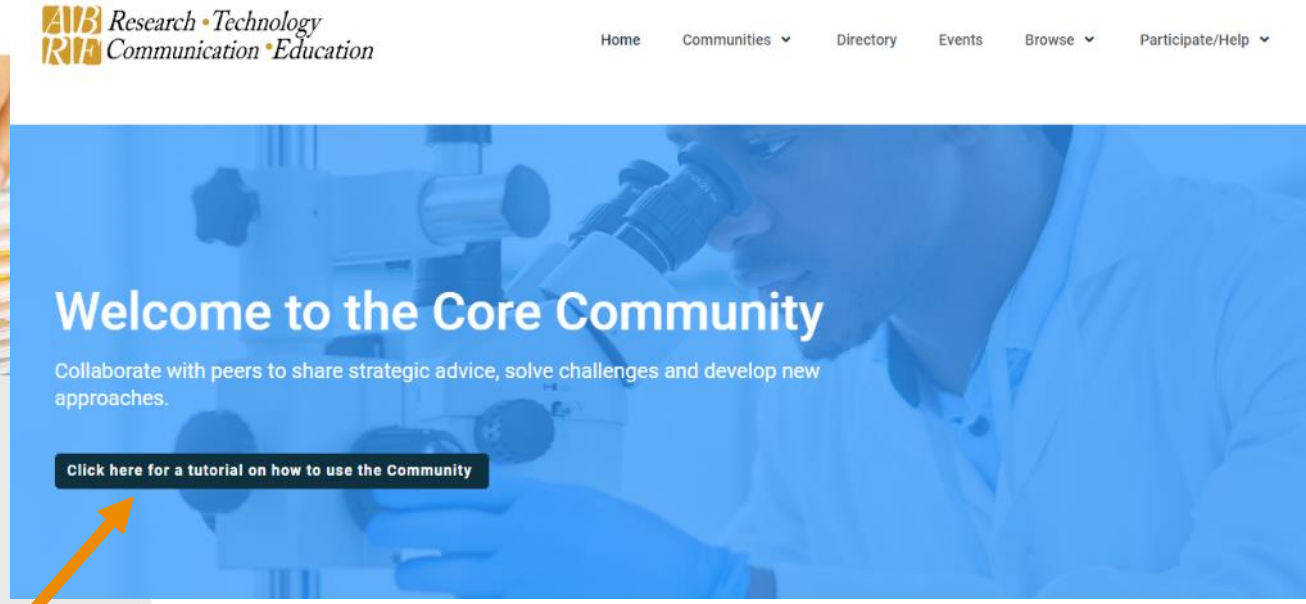
GO



Peer-to-Peer Resources

Share methods and learn how others are using NGS and array technologies in their shared research facilities.

GO



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Links both for Illumina events and webinars and ABRF conferences (like WACD!)

Core Community

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Missing Community messages? Click here to update your notification settings

ABRF 2024 Annual Meeting

Save the Dates....

Click Here for More Information!

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New Issue of *Journal of Biomolecular Techniques* now available

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See upcoming conferences hosted

Register Now

Webinars

Attend an online educational webinar.

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We’re just getting started together!

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iresources@illumina.com

Technology updates and innovation roadmap

The NovaSeq™ X Series provides more power to unlock the genome

Powerful

XLEAP-SBS™ Chemistry

2x speed improvement
2.5x throughput improvement[1]

>20,000 Genomes per year

Sustainable

Only high-throughput instrument with ambient ship reagents

61% Reduction of climate change impact[2]

90% Reduction in waste

Cost-Effective

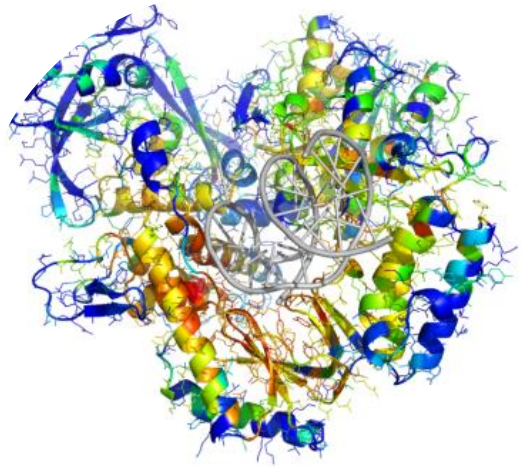
Only high-throughput instrument with integrated analysis

$200 Genome with analysis[3]

The NovaSeq X Series has **>40** new patents pending, and took **5** years and **1,500** scientists, engineers, developers, and designers to create

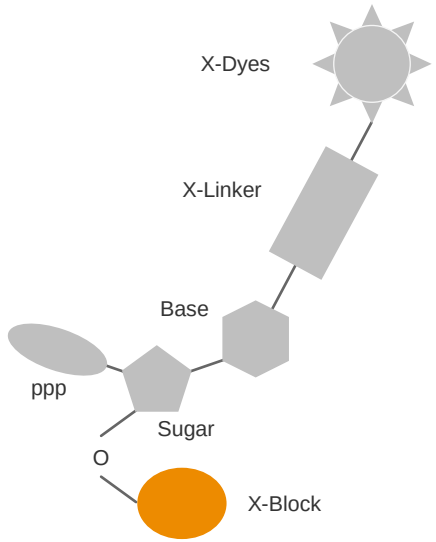
[1] Compared to NovaSeq 6000.
[2] Preliminary results of streamlined LCA conducted by external party regarding climate impact per Gb of genetic code of NovaSeq X 10B. 300 cycle kit compared to NovaSeq 6000 S4 300 cycle kit per Gb of genetic code.
[3] High-quality whole genome sequencing at scale with alignment, variant calling and lossless compression. $200 genome will be enabled by the 25B flow cell on NovaSeq X Series in Q4 of 2023.

Higher performance with XLEAP-SBS chemistry on NovaSeq X series and NextSeq™ 1000/2000



Novel Polymerase

Faster incorporation, higher fidelity



X-Block, X-Linker, X-Dyes

Most resistance to heat,~50x more stable in solution, ~500x more stable lyophilized, faster block cleave

Enables ambient shipment*

- Faster cycle times
- Greater accuracy
- More sustainable**

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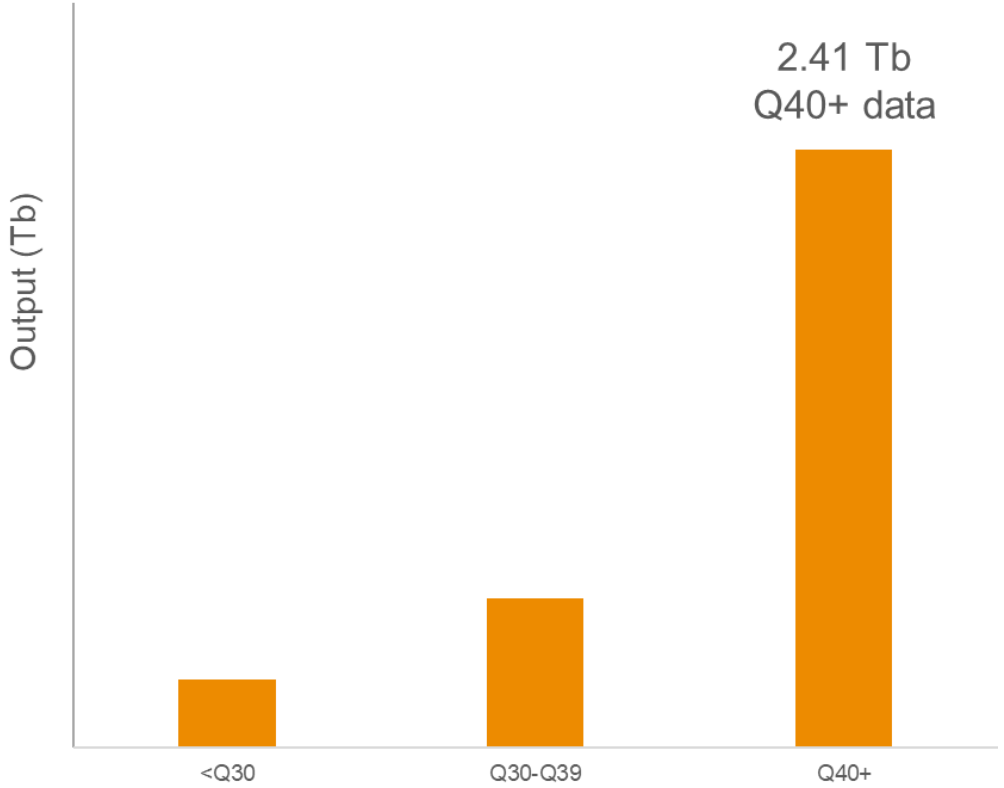
*Ambient shipment currently on NovaSeq X series only

**as compared to NovaSeq 6000

Illumina continues to demonstrate industry-leading performance – NovaSeq X data exceeds specifications

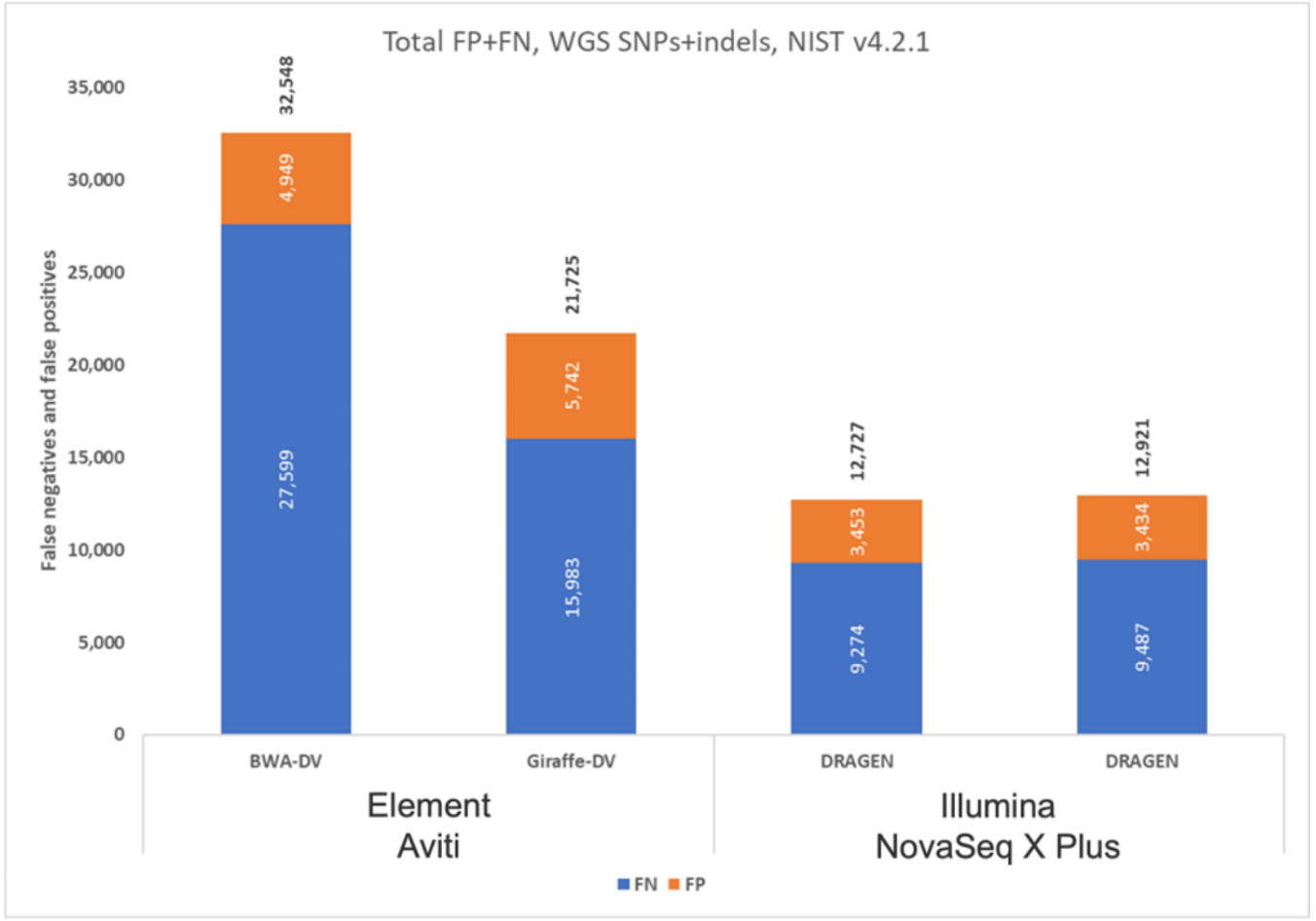
- NovaSeq X 10B specifications:
  - Data by Q-score: **85% ≥Q30**
  - Yield: **3 Tb**
- Unbinned Q-scoring shows most bases ≥ Q40*
  - **2.41 Tb** of called bases measured ≥Q40
  - Human PCR-free WGS 2x150 bp run



*Data generated with NovaSeq X 10B flow cell while measuring un-binned Q-scores via R&D configuration of RTA basecalling software

NovaSeq X + DRAGEN™ – more accurate variant calling

- Reported quality claims must align with assay accuracy to hold value
- Market participants claim higher %>Q40 output yet final accuracy results do not reflect an advantage
- Example: >30x human whole genome PCR-free (HG002 / NA24385)



https://go.elementbiosciences.com/access-seq-datasets-060622

Shrinking the Environmental Impact of High-Throughput Sequencing

61% Reduction of climate change impact[1]

90% Reduction in waste

90% Reduction in weight

The NovaSeq X Series is **the only** high-throughput instrument with ambient ship reagents

[1] Preliminary results of streamlined Life Cycle Assessment (LCA) conducted by external party regarding climate impact (per Gb of genetic code of NovaSeq X 10B 300 cycle kit compared to NovaSeq 6000 S4 300 cycle kit for the US market, and 41% reduction for UK market (savings are reduced for UK due to replacement of some air freight with truck transport)

More multiomics than ever before with 25B and better batching with 1.5B on the NovaSeq X series in Q4 2023

1.5B Flow Cell

≥1.6B clusters

~165-500 Gb

100c, 200c, 300c

≥85-90% Q30

~13-21 hrs

25B Flow Cell

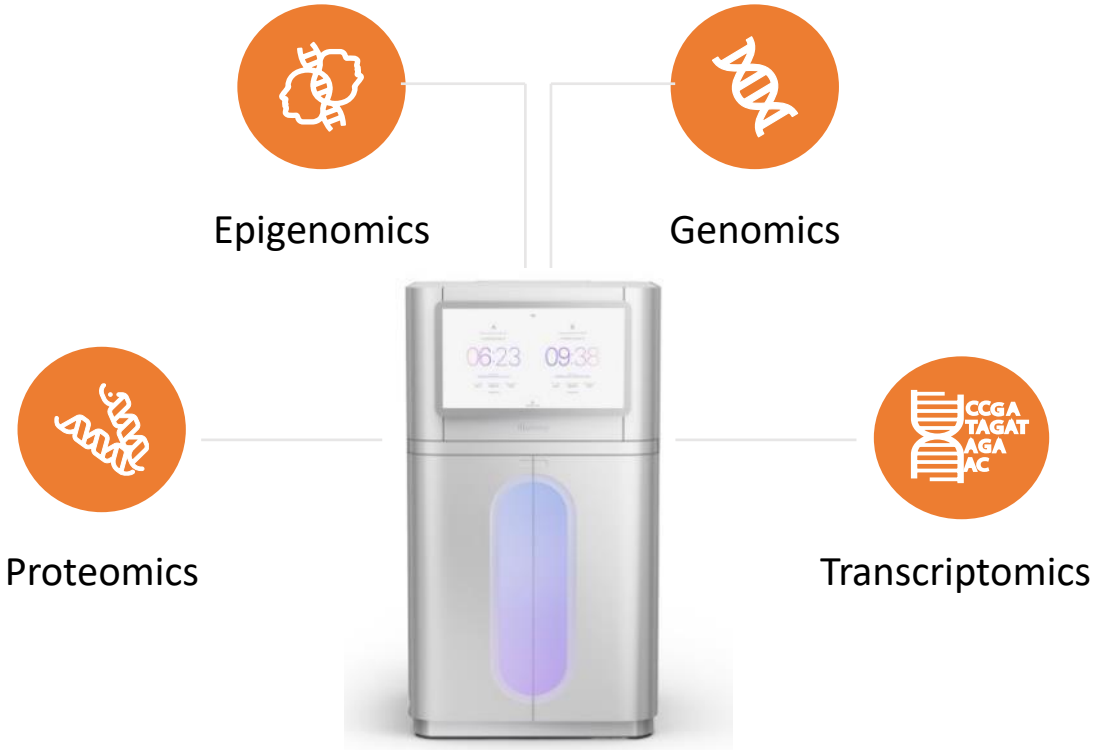
≥26B clusters

~8 Tb

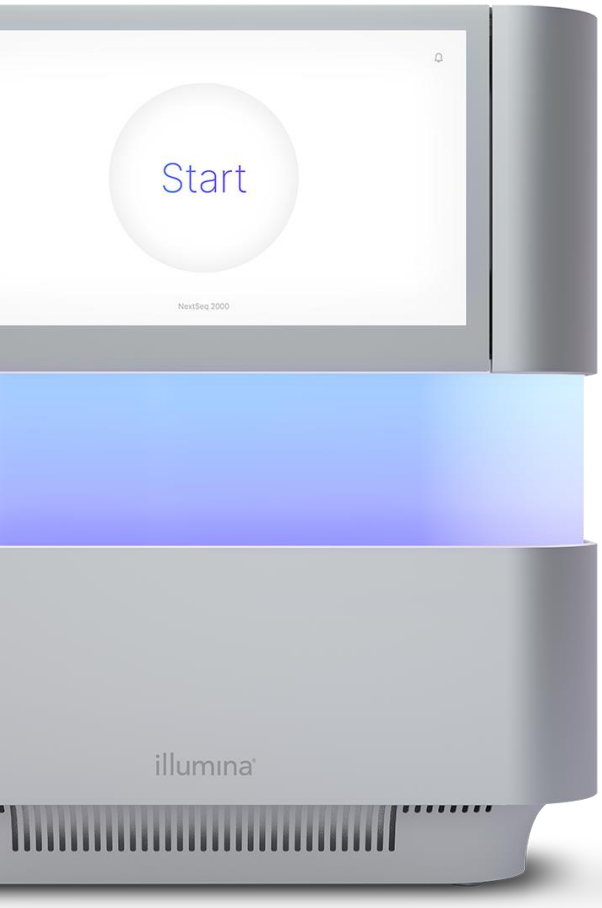
300c

≥85% Q30

~48 hrs



The NextSeq 1000/2000 has revolutionized benchtop sequencing



Flexible and Scalable

11 kit configurations with read lengths from **<50bp to 2x300 bp**; supports wide range of applications, from microbes and panels to large genomes

Streamlined Workflow

On-board denature & dilute, cluster generation simplifies run set up, **onboard DRAGEN** delivers simple, accurate and integrated analysis, no wash maintenance needed

Illumina Quality

A field-tested solution for providing reliable and consistent results, with thousands of publications and **1800+ system placements**

Continuous Innovation

Coming in H1 2024, **XLEAP-SBS Chemistry** will unlock the next level of scale, cost efficiencies, and capabilities

Longer reads capabilities on NextSeq 1000/2000 enables customers to expand applications and scale more efficiently

P1 & P2 600c kits

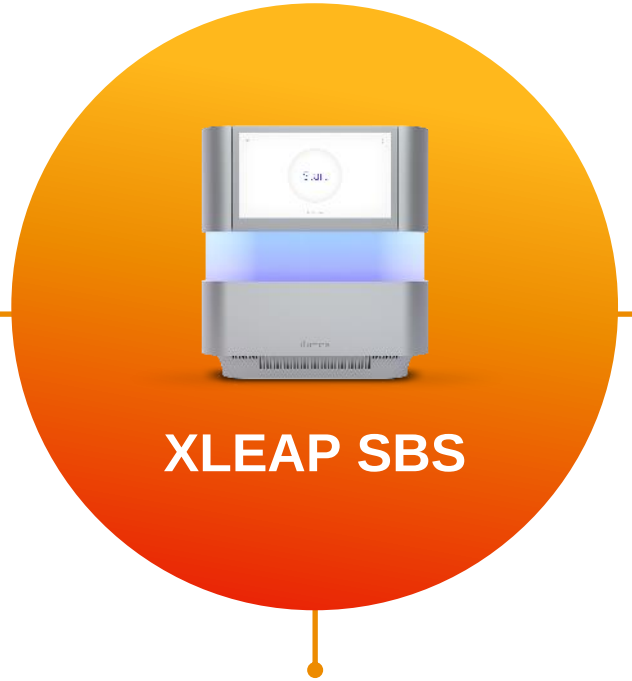
READ NUMBER	100M & 300M
OUTPUT	60Gb & 180Gb
RUN TIME	34 hr & 44 hr
QUALITY	≥ 80% of bases higher than Q30
APPLICATIONS	Metagenomics, immune repertoire, sWGS

NextSeq 1000/2000 with XLEAP-SBS™ Chemistry will unlock the next level of scale, cost efficiency and capabilities

Coming Q1 2024

New P4 Flow Cell*

*500Gb, 1.7B Reads***



Coming Q2 2024

Existing P1/P2/P3 Kits

Improved run time and performance

Pricing improvements for all new XLEAP-SBS kits

XLEAP-SBS compatibility will be available with a FREE software upgrade upon release

**Available only on the NextSeq 2000. **Preliminary spec target only. 500Gb for P4 300c kit.*

P4 reagents powered by XLEAP-SBS chemistry on NextSeq 2000

A variety of read lengths for application flexibility at scale

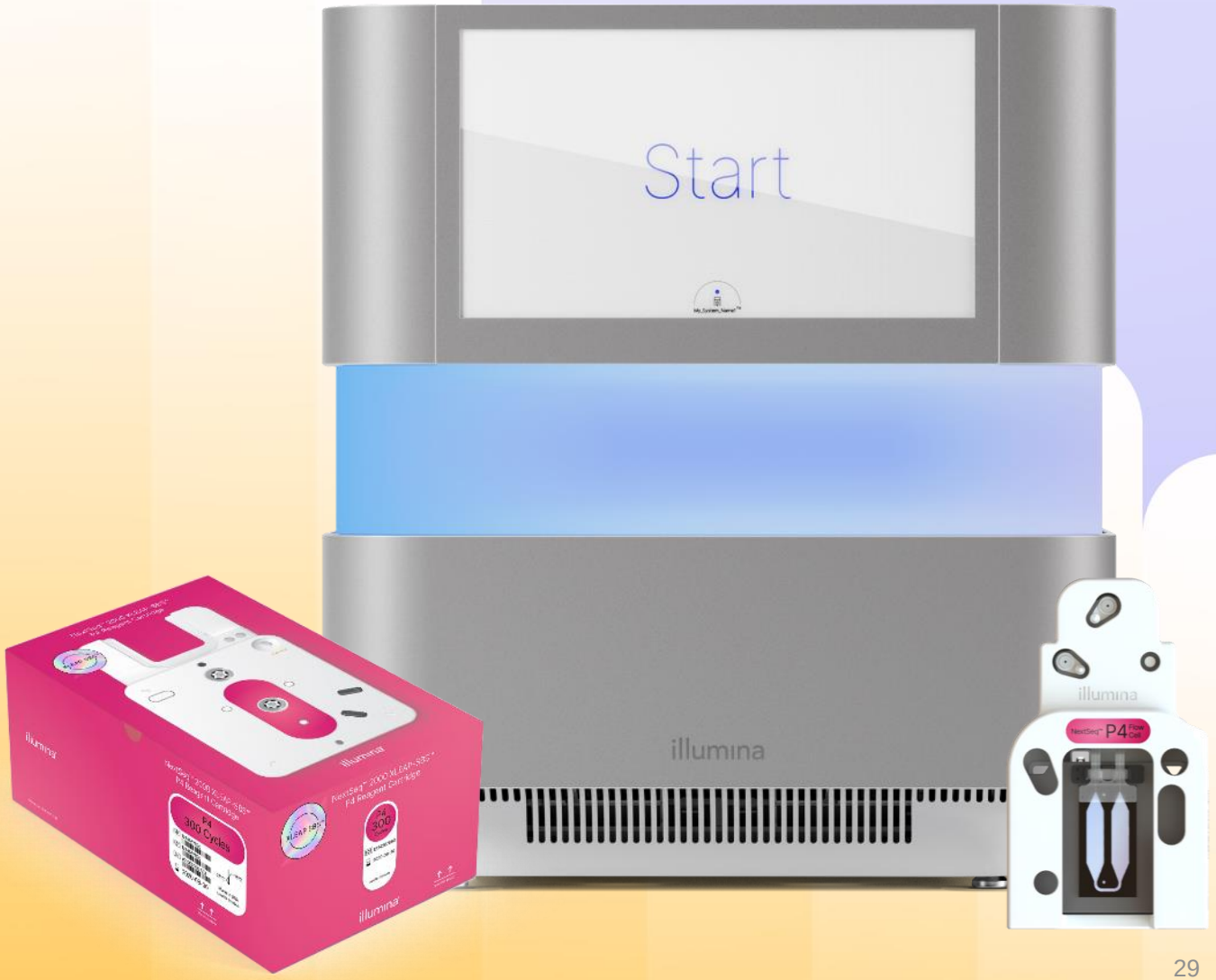
P4 available to order Q1 2024
~1.7B Clusters

50 cycles
~83 Gb
12-13 hrs

100 cycles
~167 Gb
19-20 hrs

200 cycles
~333 Gb
31-32 hrs

300 cycles
~500 Gb
43-44 hrs



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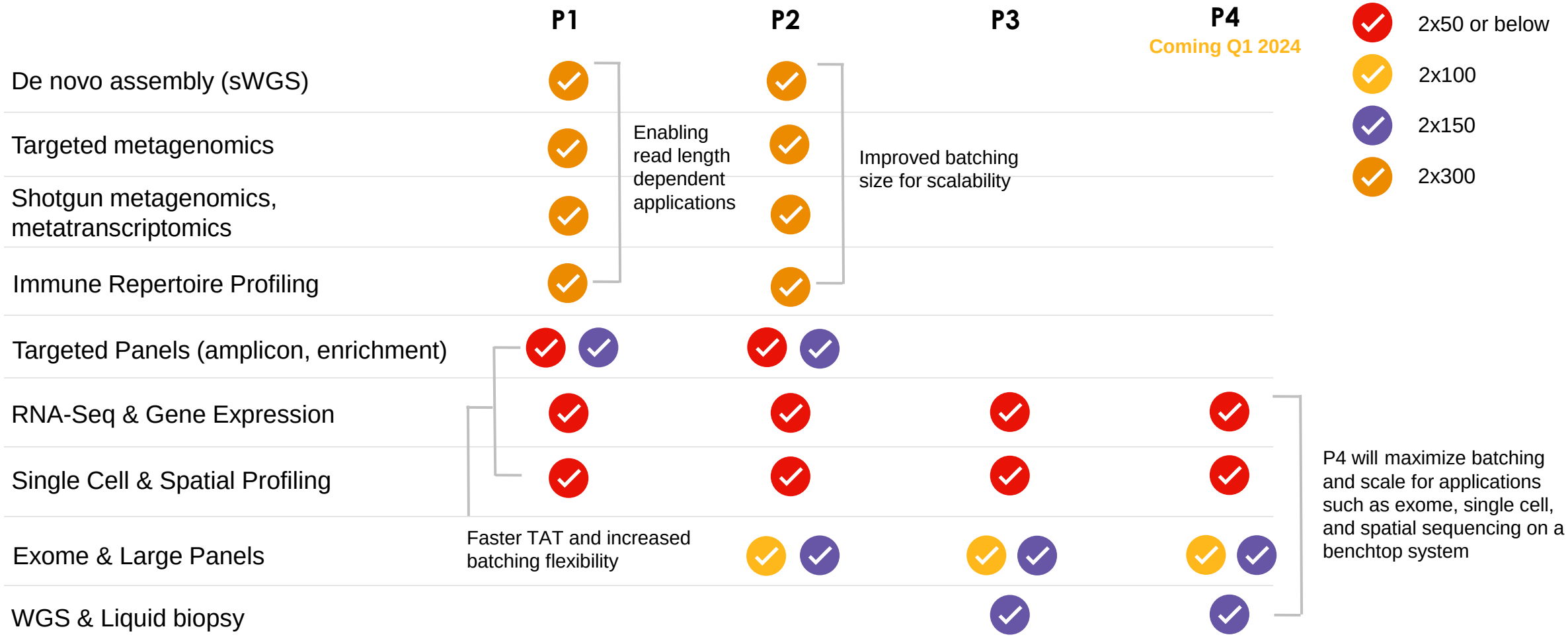
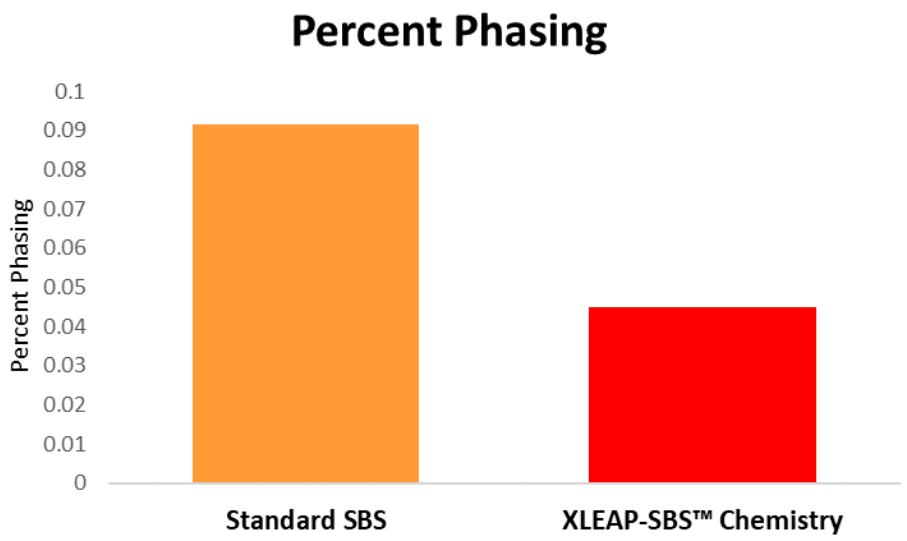
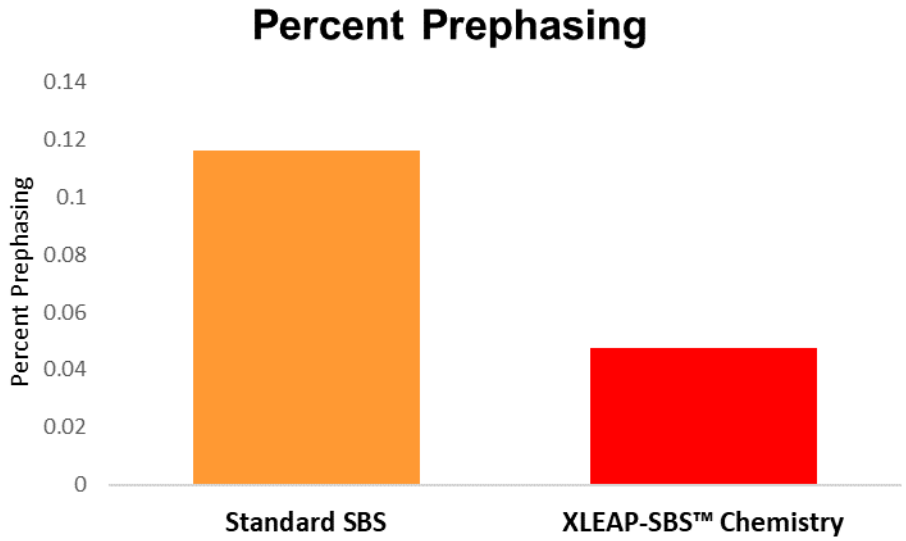
NextSeq 1000/2000's flexibility enables customers to expand applications and scale efficiently



XLEAP-SBS drives improved quality and performance on NextSeq 1000/2000



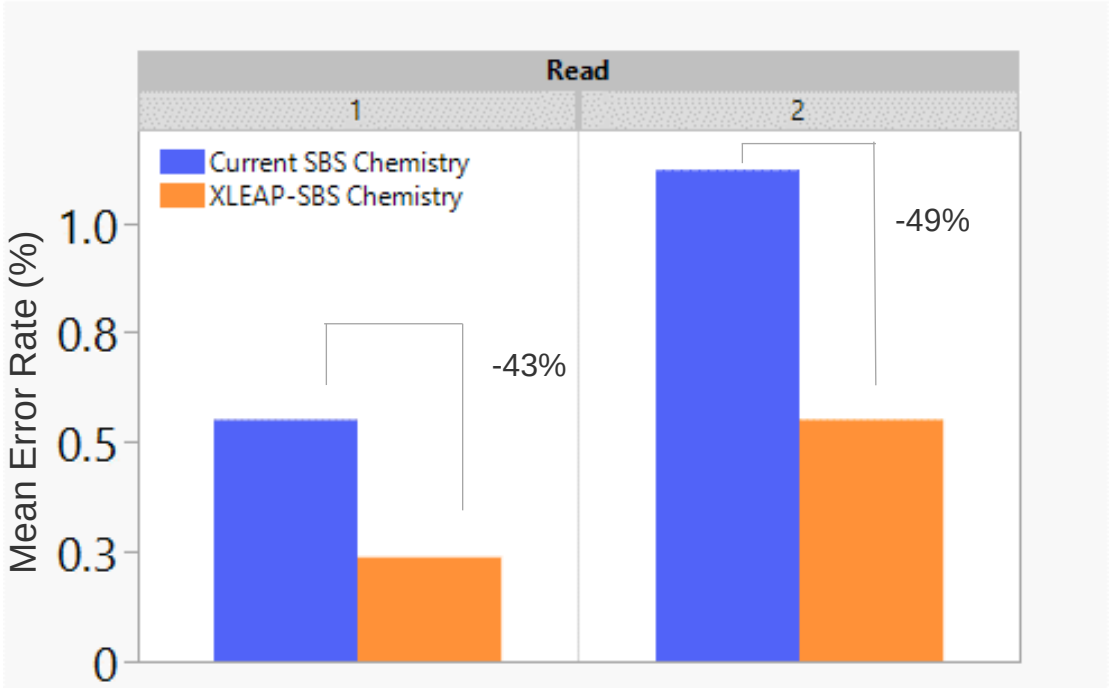


Greater than **50% reduction in phasing** and **prephasing** relative to standard Illumina SBS chemistry on NextSeq 1000/2000

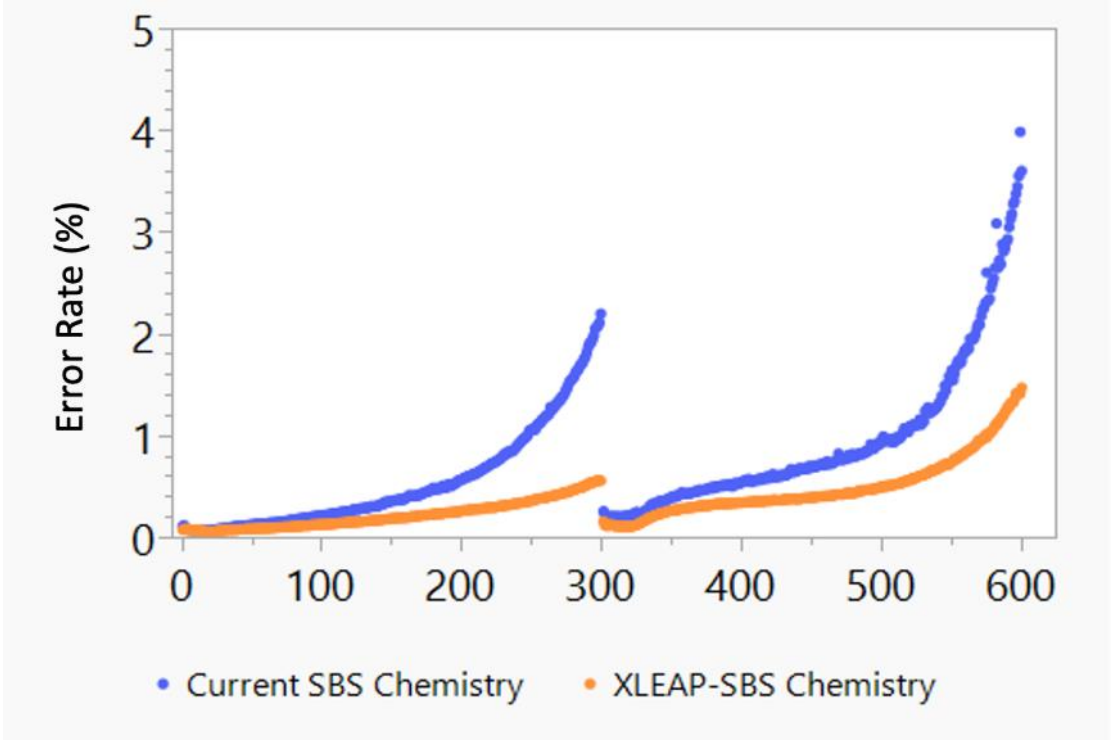
Data collected on R&D NextSeq 1000 / 2000 system.

XLEAP-SBS 600 cycle kits improves data quality on NextSeq 1000/2000

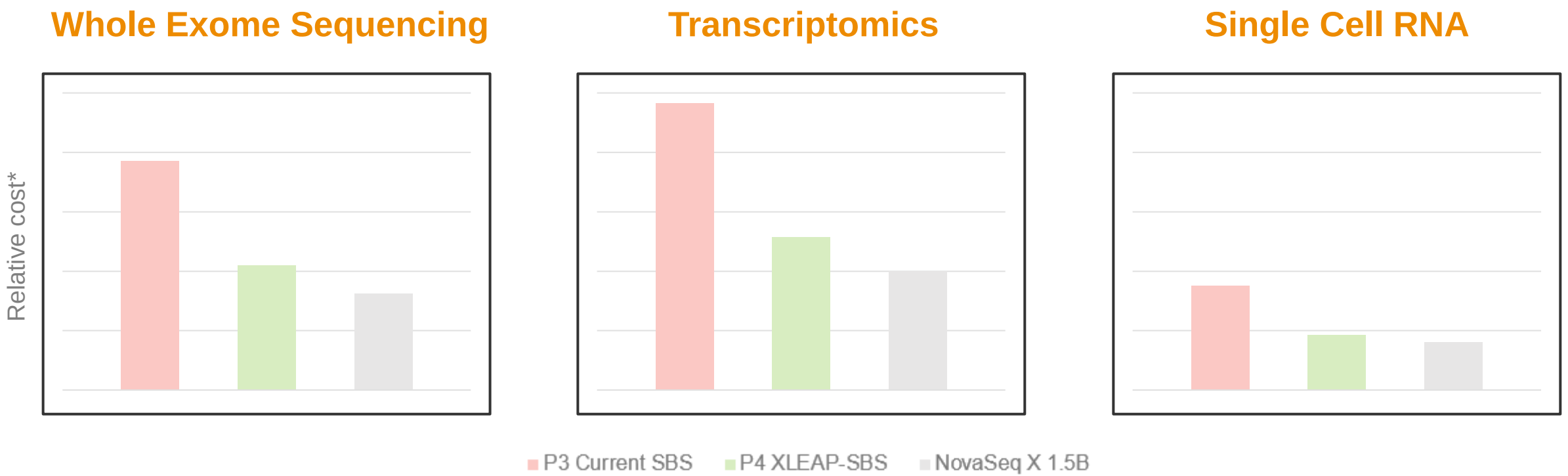
XLEAP-SBS error rates are significantly lower than current SBS Chemistry error rates



Testing demonstrates high quality data, especially at the end of the read length



XLEAP-SBS enables improved sequencing costs for data intensive methods with the P4 flow cell

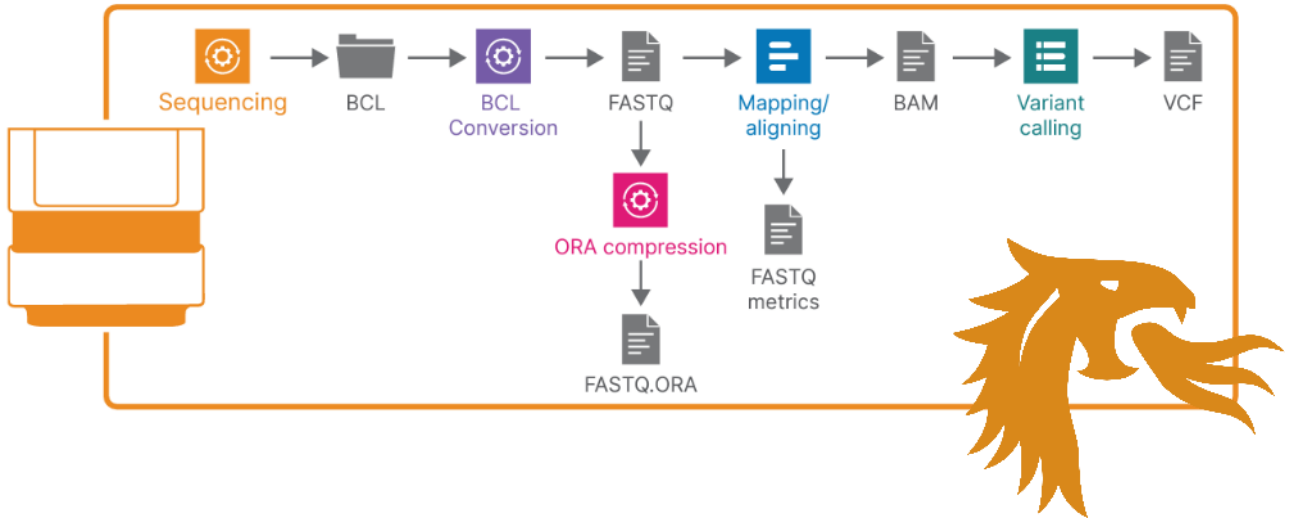


*Preliminary P4 pricing estimate

NextSeq 1000/2000 is the only benchtop sequencer with integrated, onboard analysis—at no extra cost

- Provides secondary analysis up to **16x faster** than open-source methods
- **Saves up to 80% on storage costs** with DRAGEN ORA file storage
- Achieves ~**4x lossless compression** of FASTQ files
- Enables push button analysis, integrated with the instrument, at **no additional cost**

Save >$100K over 5 years*



*Assuming data is analyzed with DRAGEN onboard and stored with Illumina cloud platforms (ICA or BaseSpace). Savings will vary.

DRAGEN v4.2 coming to NextSeq 1000/2000 in Q1 2024 – more accurate and comprehensive than ever before

Accuracy

- Enhanced Multigenome (graph) reference and Machine Learning (ML) improve small variant calling accuracy
- Improved CNV and Structural Variant calling accuracy
- New targeted callers for higher genotyping accuracy - HBA, LPA and RH, CYP21A2
- Accurate genotyping for 5 more pharmacogenes: BCHE, ABCG2, NAT2, F5, UGT2B17

Comprehensiveness

- Support for Telomere-to-Telomere CHM13 v2.0 reference
- DRAGEN Amplicon with CNV and SV support
- DRAGEN Germline with high sensitivity mode
- Sex chromosome low allele frequency variant support
- Imputation for haploid species and sex chromosomes
- Integrated RPIP/UPIP secondary analysis pipelines (Beta)

Efficiency

- Increase ORA compression speed up to 30% when mapping/align step is enabled
- Runtime improvements for joint genotyping pipelines compared to previous release

Connected Software enables both discovery and development

Illumina Connected Software

Clarity LIMS™	BaseSpace™	DRAGEN™	Connected Analytics
Lab Informatics	Run & Sequence	Secondary Analysis	Bioinformatics Platform

Discovery	Multiomics Discovery	DRAGEN & ICA Notebooks
Discovery	Literature Mining	Correlation Engine
PopGen	Populations	ICA Cohorts
Clinical Research	Infectious Disease	Explify™
Clinical Research	Genetic Disease	Emedgene™
Clinical Research	Oncology	Connected Insights*
Clinical Research	Reproductive Health	VeriSeq™ NIPT Solution v2**

* Not available in all countries. Illumina Connected Insights supports user-defined tertiary analysis through API calls to third-party knowledge sources.
** For In Vitro Diagnostic Use – Not available in all countries

Thank you

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