

Our journey to empower science



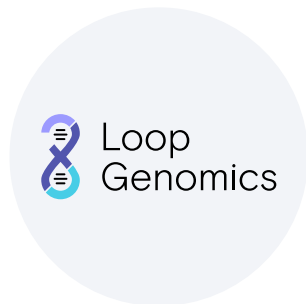
Element is founded by Molly He, Michael Previte and Matt Kellinger, three scientists seeking to disrupt genomics by reinventing every “element” of sequencing

JULY 2017



Company announces Series A financing led by Foresite Capital and Venrock

JUNE 2019



Element closes acquisition of Loop Genomics, enabling both short and long-read sequencing on the same desktop machine

FEBRUARY 2022



Element opens new headquarters of Alexandria Tech Center in San Diego

MAY 2022

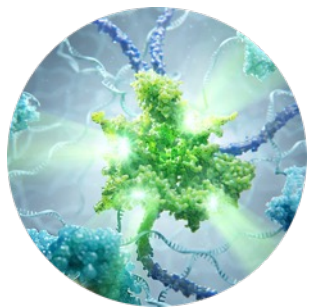


Element announces first set of global distributors, showing strong demand for AVITI around the world

APRIL 2023

MAY 2019

Element invents Avidity Sequencing, enabling high accuracy with low reagent consumption



JUNE 2021

Element closes \$276M Series C financing to deliver on the promise of disruptive sequencing



MARCH 2022

Element launches AVITI, making affordable, high-quality sequencing a reality for labs of all sizes



JANUARY 2023

Element announces the \$200 genome on AVITI, delivering the highest quality sequencing at an unprecedented low cost

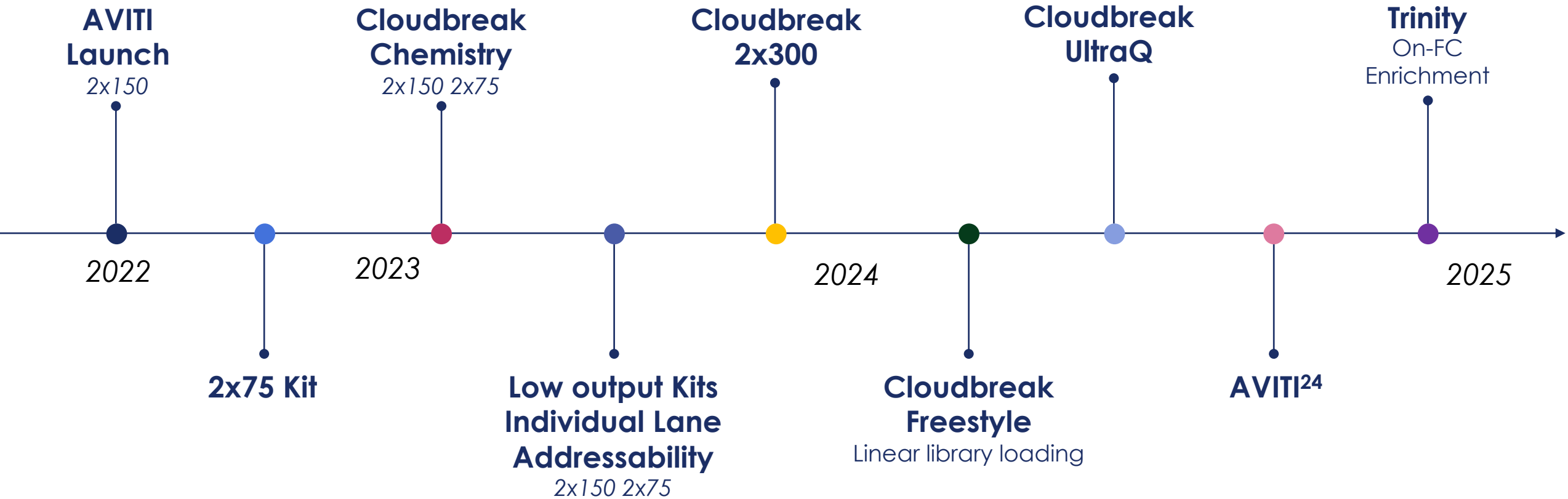


JUNE 2023

Element launches new Cloudbreak chemistry, advancing Avidity with even faster runtimes



AVITI past, present, future



Innovations in Next Generation Sequencing at the NUSeq Core

Solomon Hailu, PhD, MSc
Applications Technical Specialist



Outline

- Introduction
- Avidity Base Chemistry (ABC)
- Performance and Applications
- Upcoming Innovations



Element's AVITI™ - Empowering researchers with flexible genomic solutions

Features

- Dual independent flow cells
- Two addressable lanes per flow cells
- Q30 >90%, no PCR error propagations
- Negligible index hopping
- Low AT/GC bias and duplicate rates,
- Low-diversity samples (<5% PhiX)
- Simultaneous Single Cell Multiomics + Morphology*
- Long insert and flexible Library Preparation

Applications

- Single cell and bulk RNA sequencing
- WGS / Trios / lpWGS / liquid biopsy
- Exomes and panels
- Epigenetics: Hi-C, ATAC-Seq, ChIP-Seq (CUT&RUN / CUT&Tag)
- Low diversity and targeted sequencing
- Metagenomics, HLA typing and immune profiling
- Long-read sequencing - 6 Kb with LoopSeq



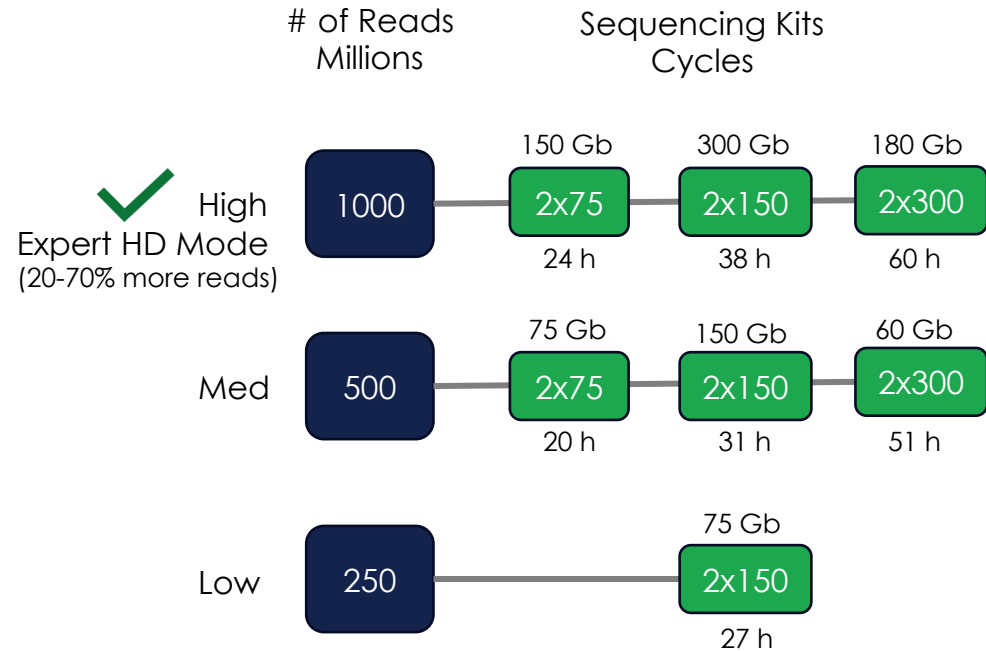
100M to 1B reads per side



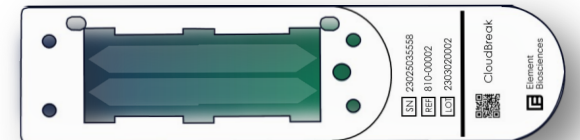
100M to 500M reads per side



*AVITI + Cellular Profiling
* Coming H2



AVITI LT - Med and Low flow cells
High 600 cycle (300M reads)
Med 600 cycle (100M reads)



Element's AVITI™ - Empowering researchers with flexible genomic solutions

Advanced Run Settings (Beta) ⓘ

Upload Intensities ⓘ

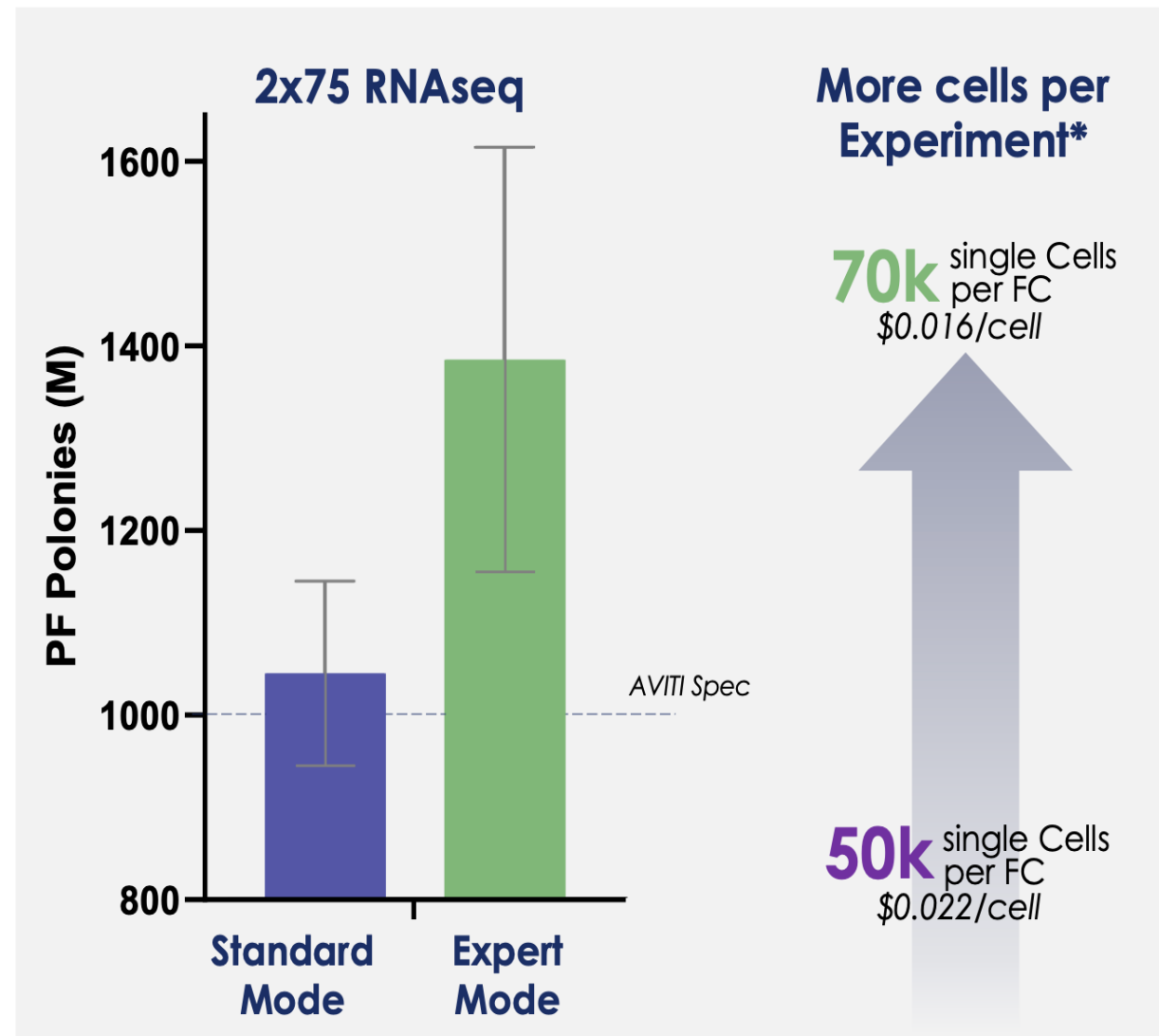
Polony Density ⓘ

Filter Mask ⓘ

Custom Recipe ⓘ

Advanced settings allow additional customization options for expert users

High Density Mode
Custom Recipes for Unique Applications



*Assuming 20k reads/cell using 2x75 HO kit, actual results may differ based on lab-specific factors.

Our partnerships make end-to-end application workflows accessible

Prepare



Sequence

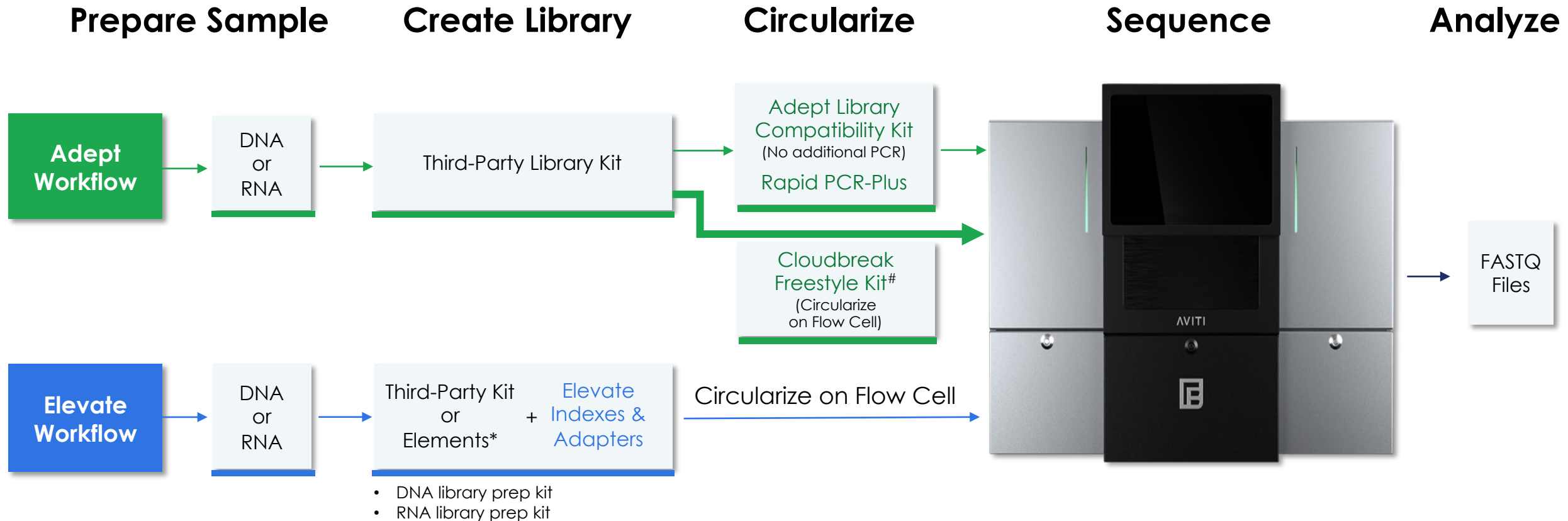


Epigenetics,
WGS Trios, lpWGS, WES,
RNA sequencing,
Single cell genomics

Analyze



Elevate library prep simplifies your workflow with onboard circularization

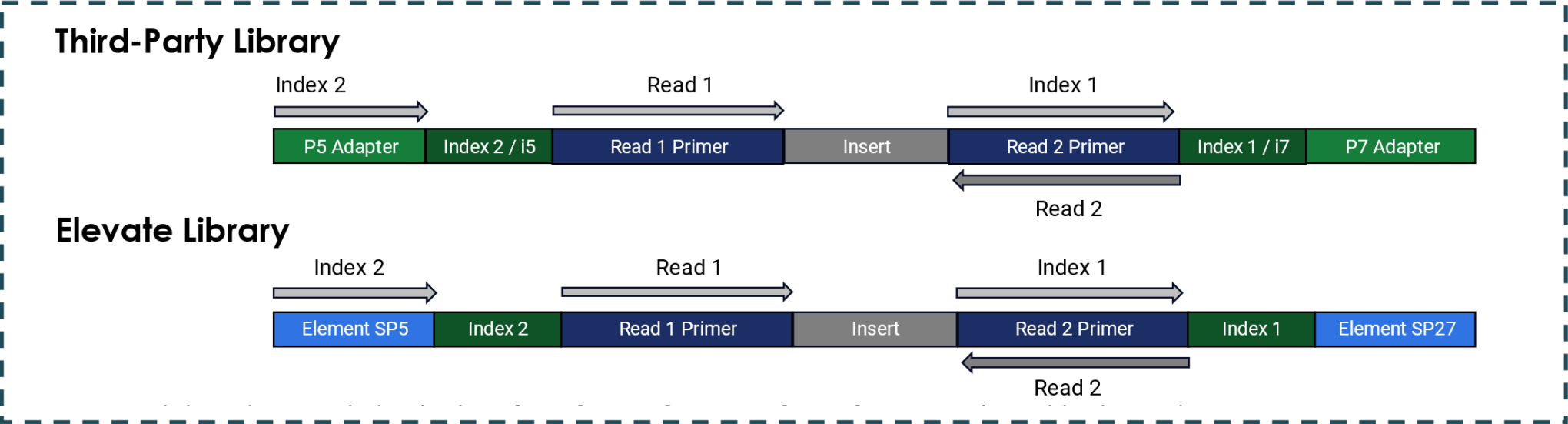


The Adept workflow enables adaption of existing libraries without any changes to the library prep

Visit <https://www.elementbiosciences.com/resources/compatible-kits-adept-library> for an up-to-date list of compatible third-party kits

Library structure

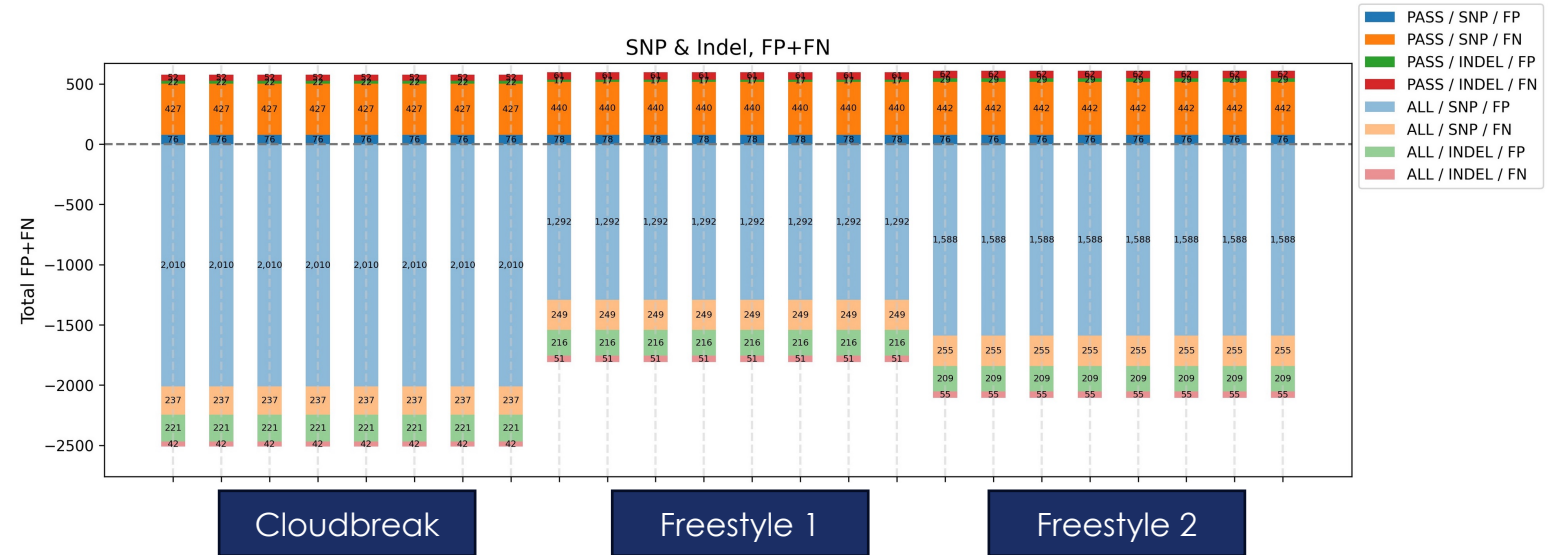
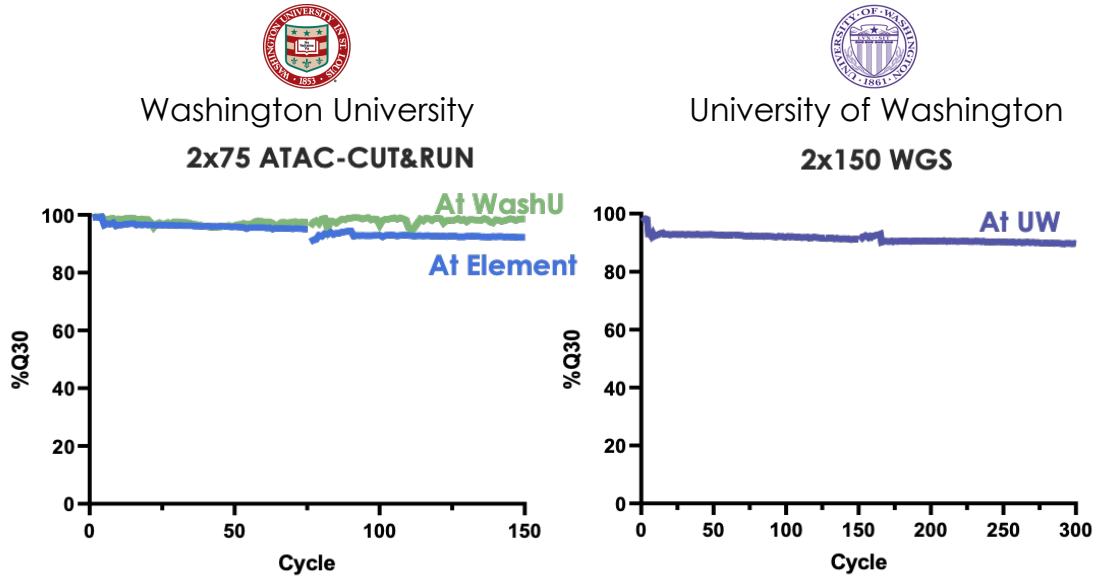
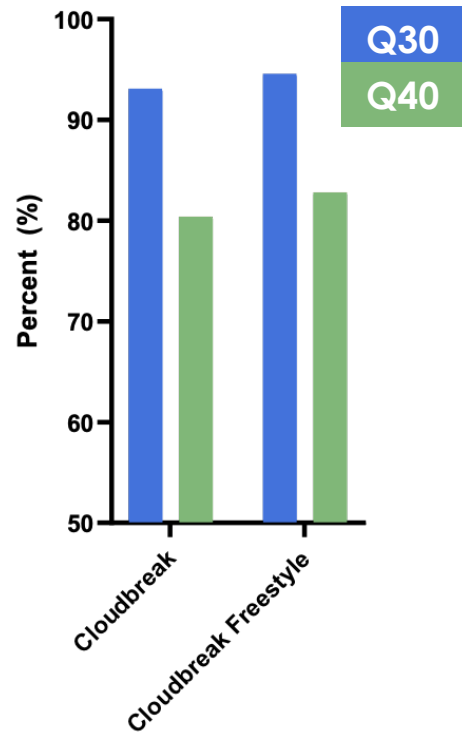
Cloudbreak **Freestyle** Chemistry



Adept Library



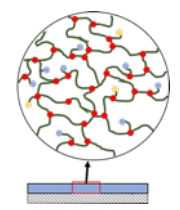
Cloudbreak freestyle delivers same high data quality with easier workflow



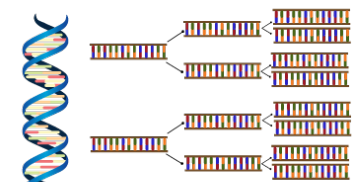
Every aspect of the DNA sequencing process redesigned to fit customer needs



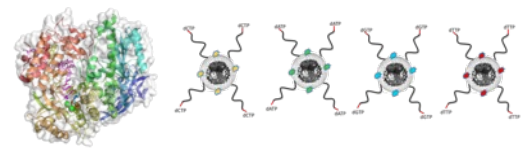
Accelerating
Science
Through
Innovation



Flow Cell / Surface
Reagent Cost, Accuracy



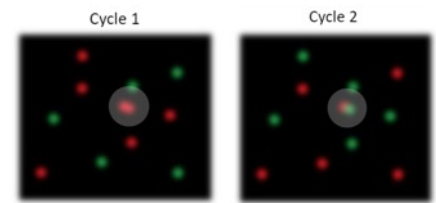
DNA Amplification
Ease of Use, Reagent
Cost, Accuracy



Avidity Base Chemistry
Reagent Cost, Accuracy,
Turnaround



Instrumentation
Throughput, COGS
Reduction



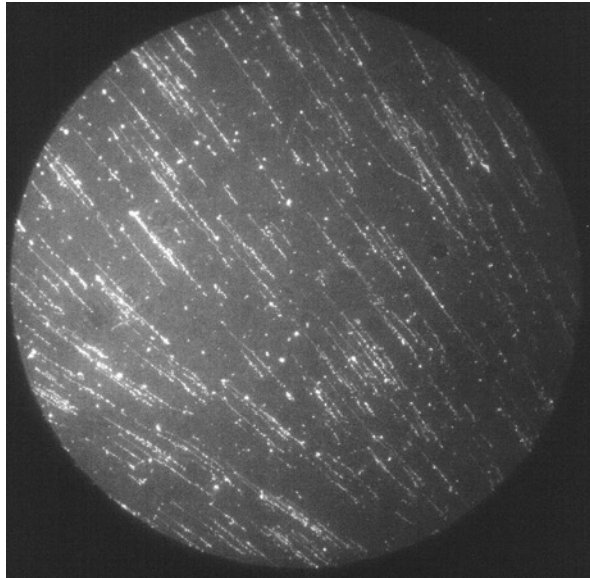
Base Calling
Accuracy, Throughput



Workflow
Ease of Use, Paired End,
Low Sample Input

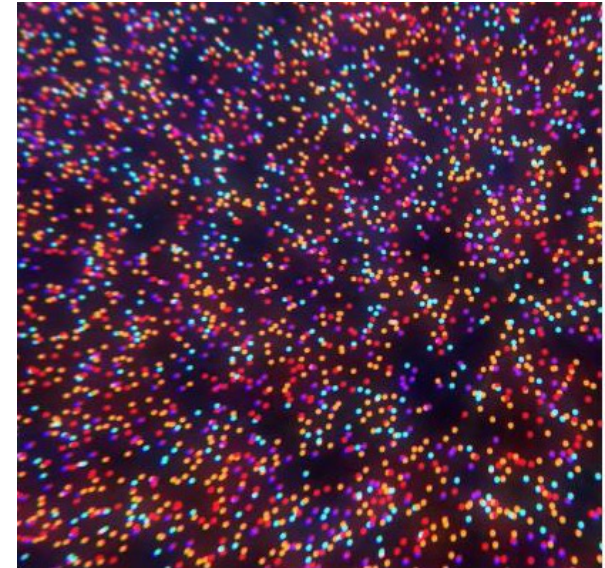
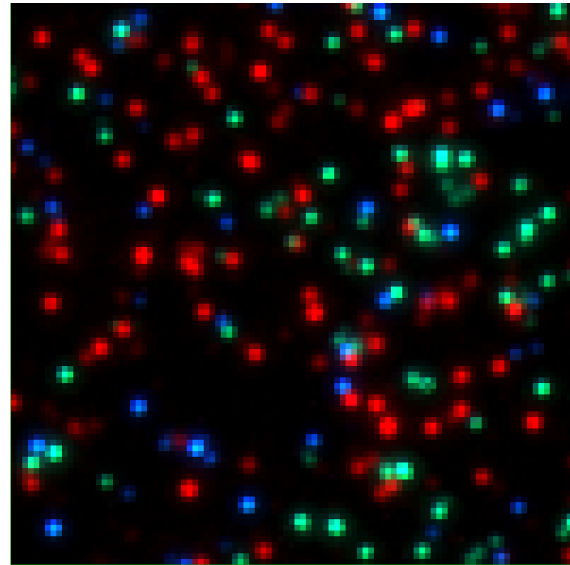
Low-binding surface chemistry: high signal to noise ratio even at higher density

“Stretched”



Limited throughput,
limited carrier to noise

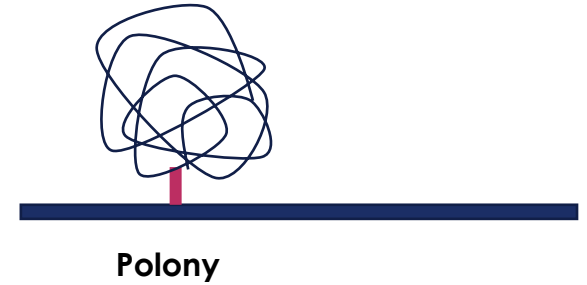
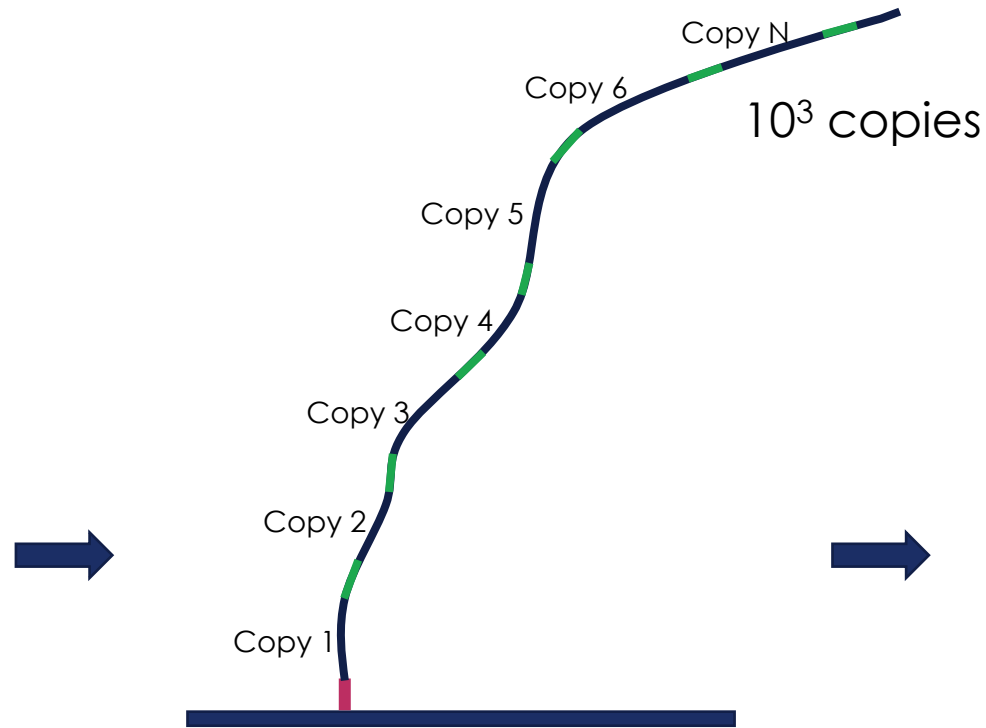
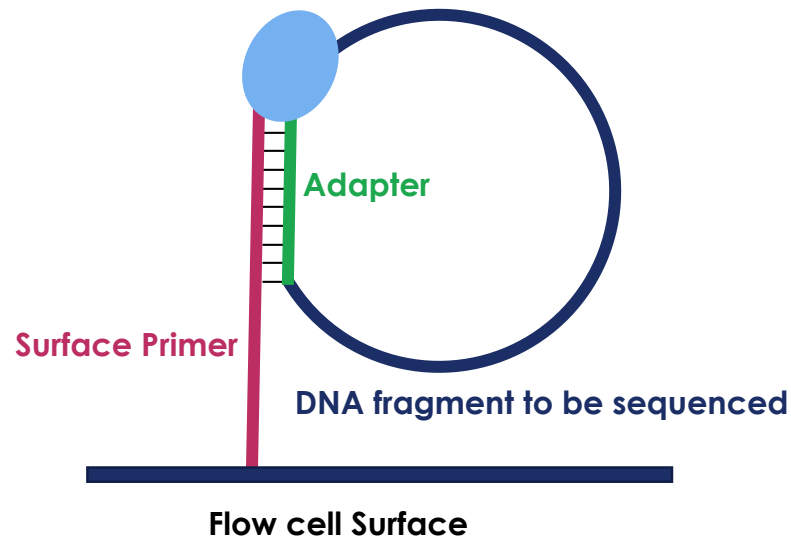
Element Colonies



Low binding surface makes signals pop, like bright stars against the night sky

Element's ABC workflow – Rolling circle amplification brings accuracy benefits

Rolling Circle Amplification (RCA)
Reduces PCR errors by copying the original



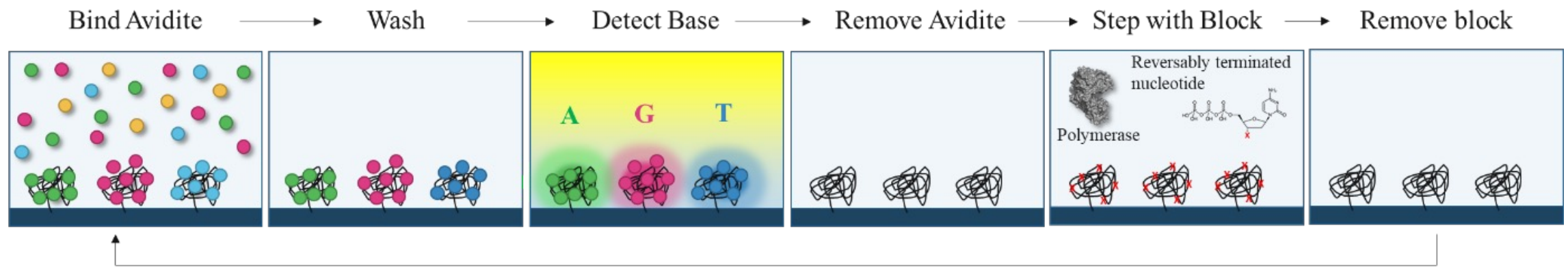
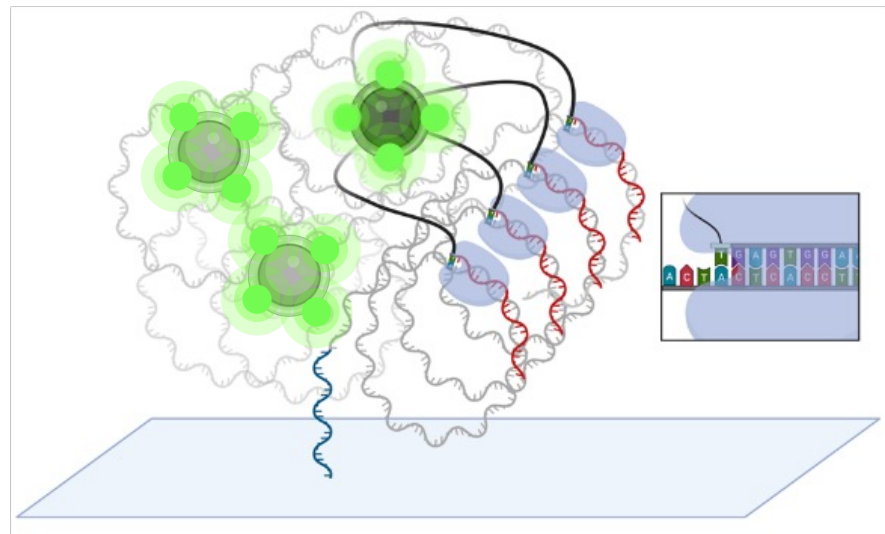
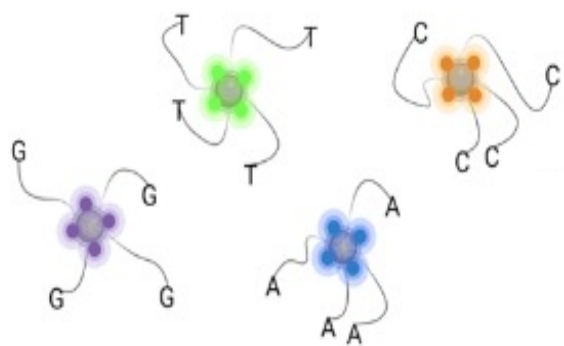
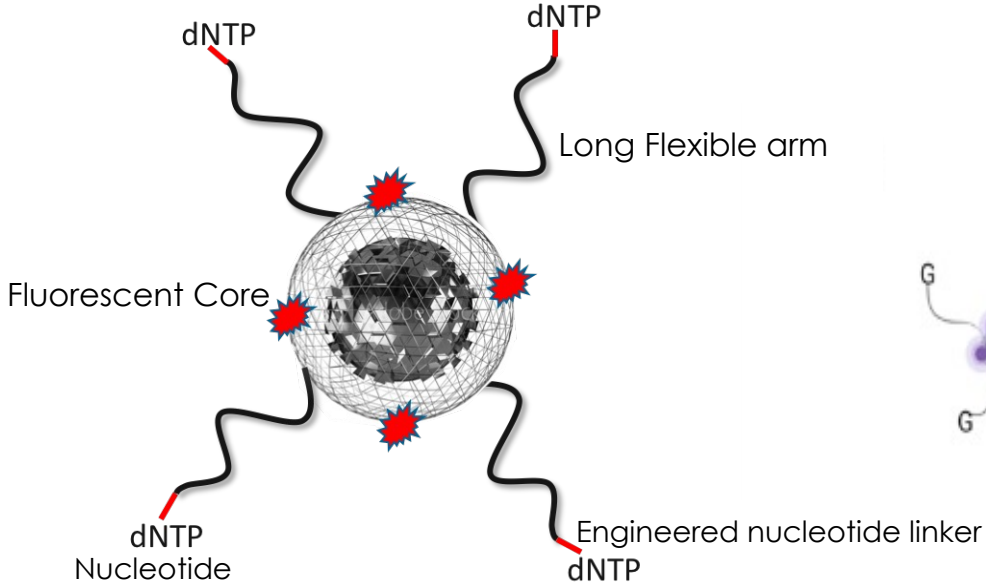
Primary sources of error removed

- ✓ No on-instrument PCR = less errors
- ✓ Reduced optical duplicates
- ✓ Index hopping undetectable

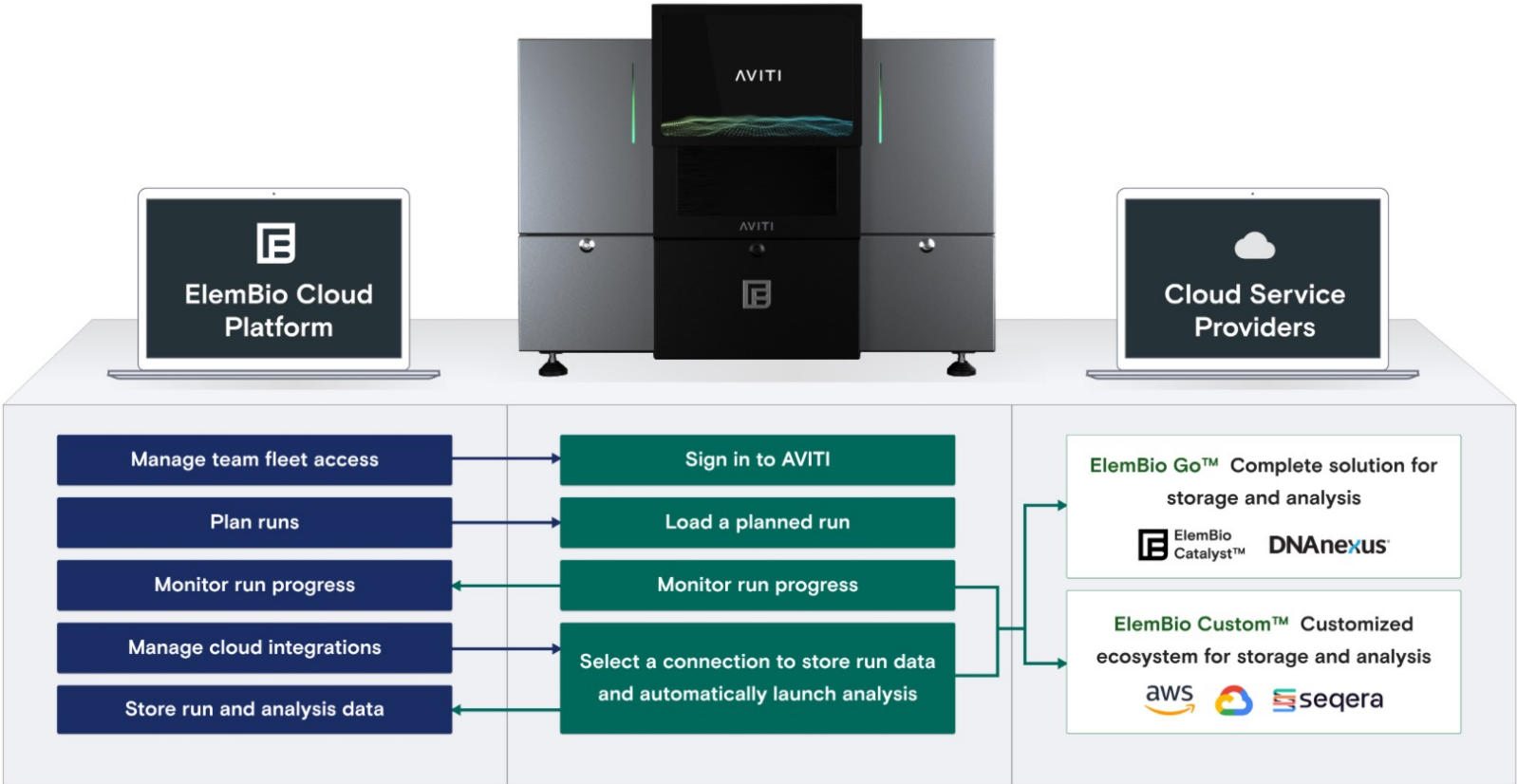


Link to Nature
Biotechnology Paper

ABC leverages multivalent binding increasing data quality and reducing cost



ElemBio Cloud: a transparent solution that enables end-to-end NGS workflow



Integrated solution for:
Remote Run Setup
Run Monitoring Visualizations
Connection to your cloud storage
Workflows for data analysis

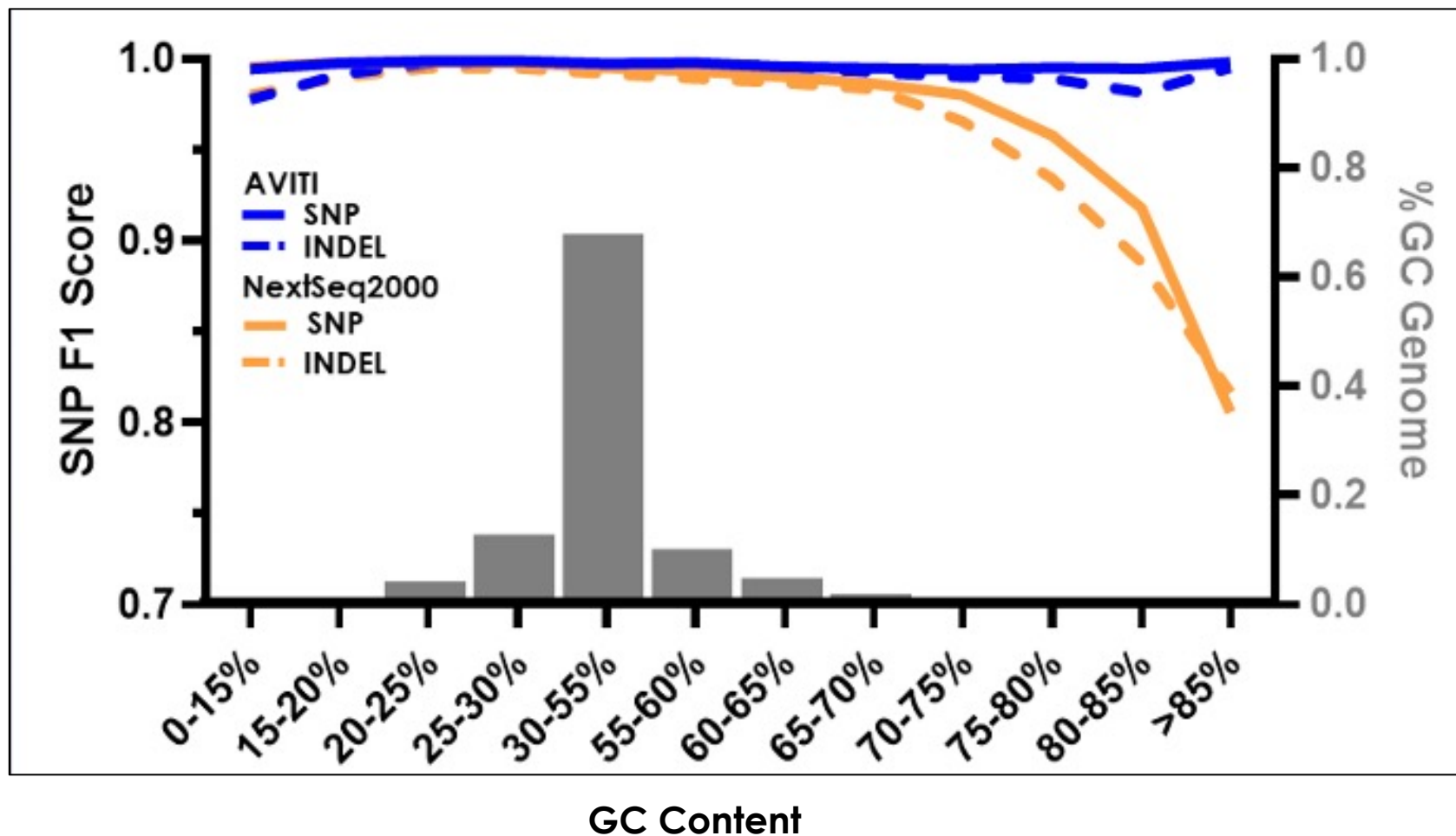


AVITI Performance



No on-instrument PCR limits AT/GC bias, providing more even coverage

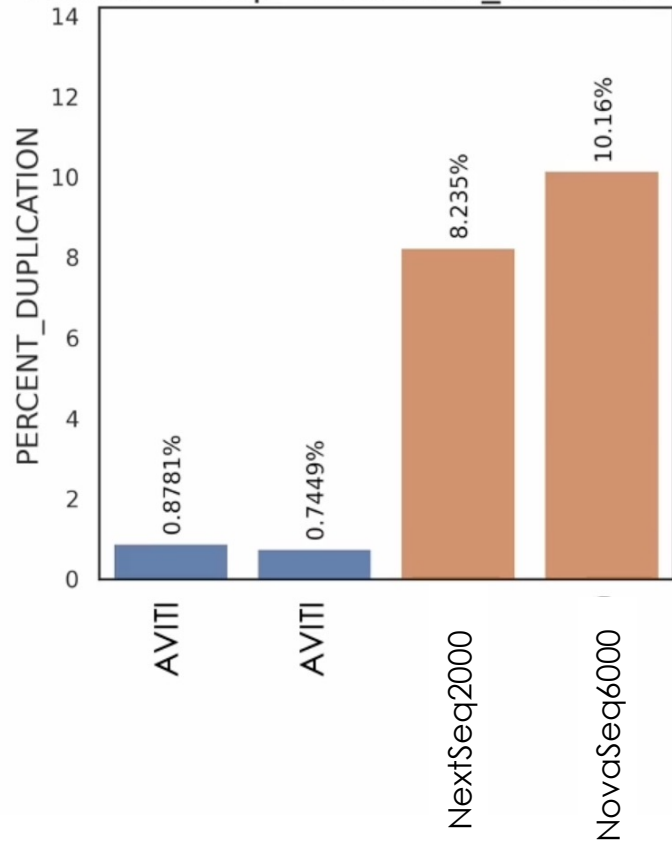
AVITI 2 x 300 variant-calling accuracy vs GC content



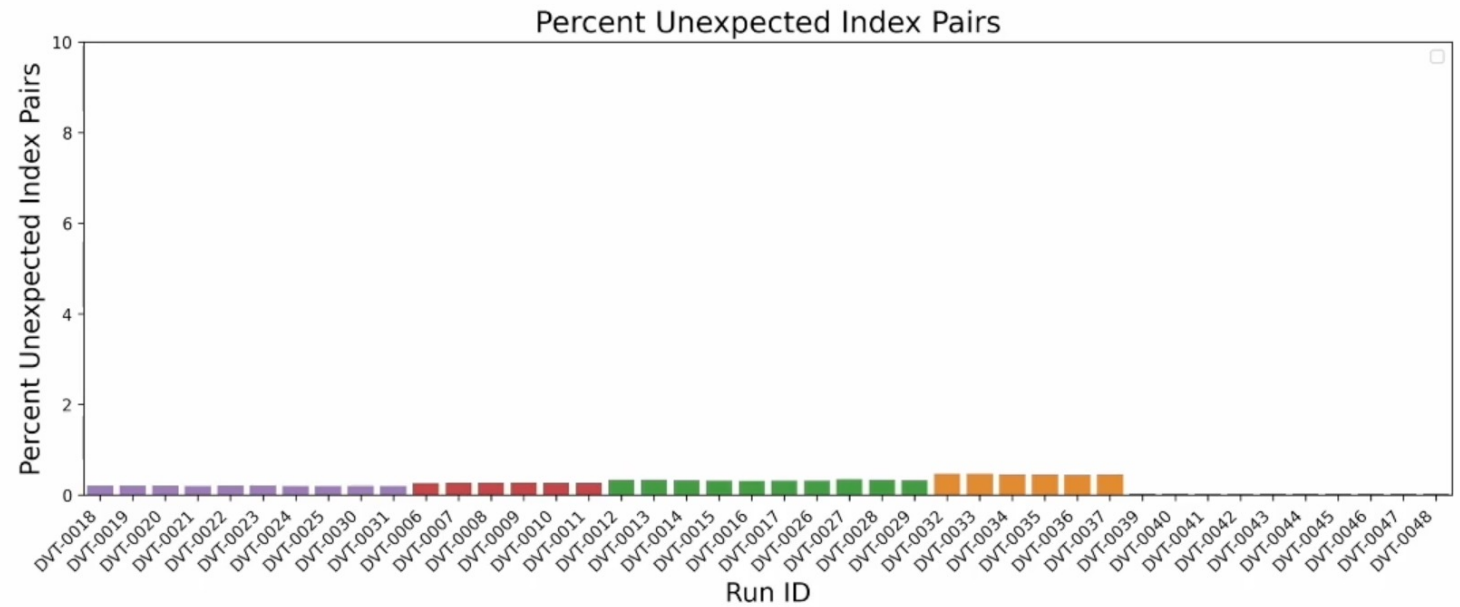
Negligible index hopping and duplication rate with ABC Sequencing

Ultra-low Duplicates

Picard DeDup - PERCENT_DUPLICATION

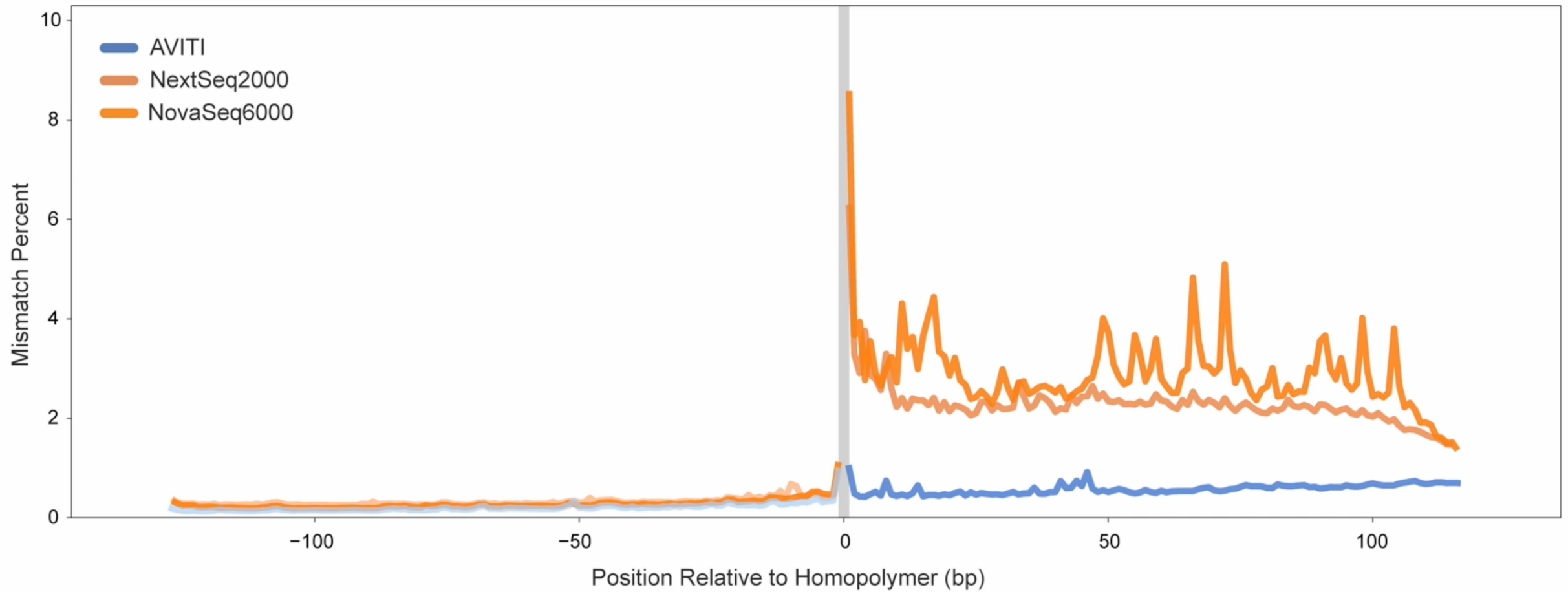


Negligible Index Hopping

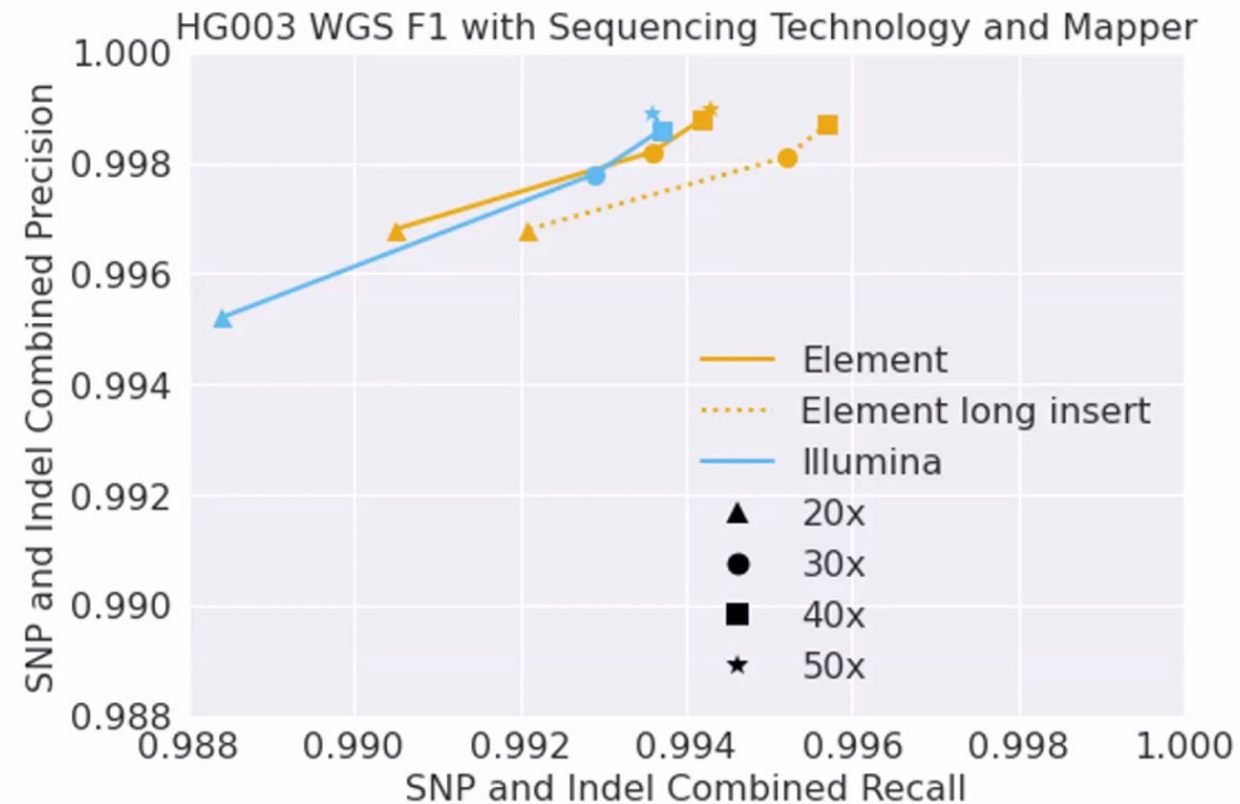
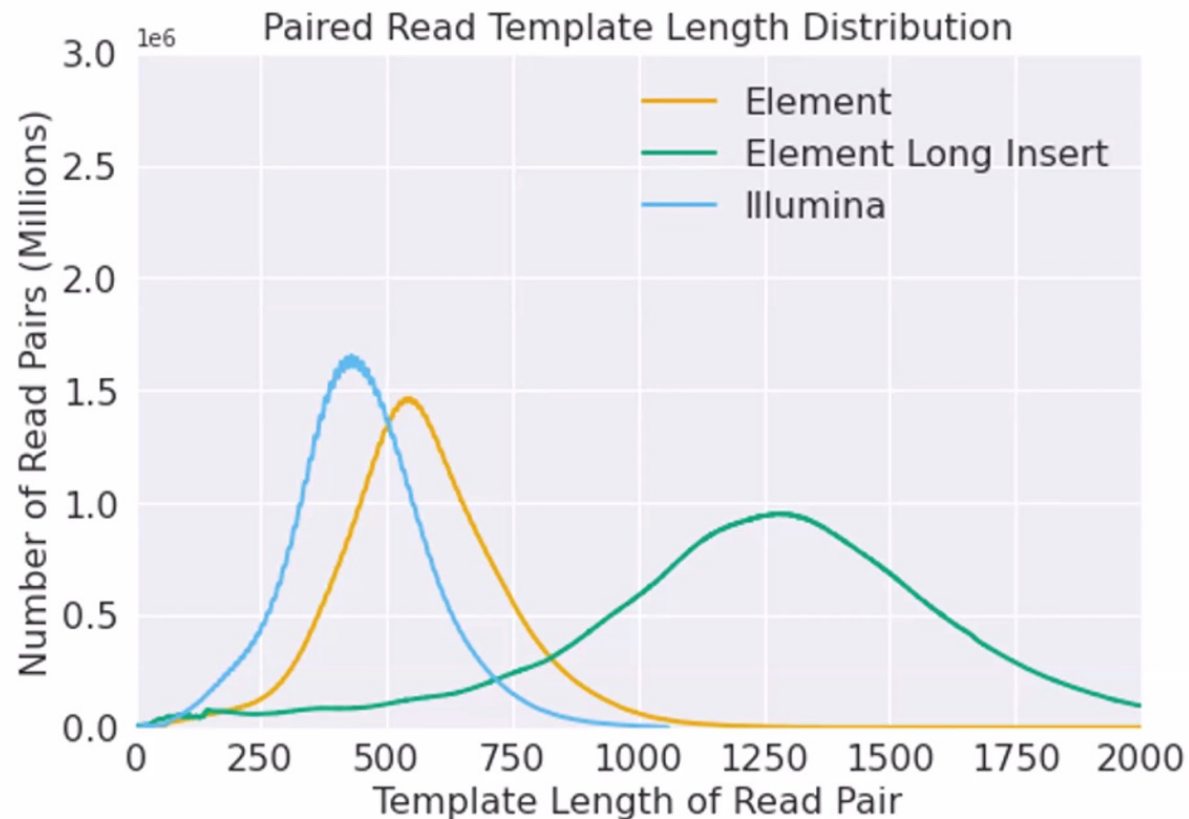


Exceptional performance across homopolymer regions

Avg mismatch percent after homopolymers of length > 11 (~700k genome wide)



Advantages of insert size on mapping and variant calling accuracy



[Accurate human genome analysis with Element Avidity sequencing](#)

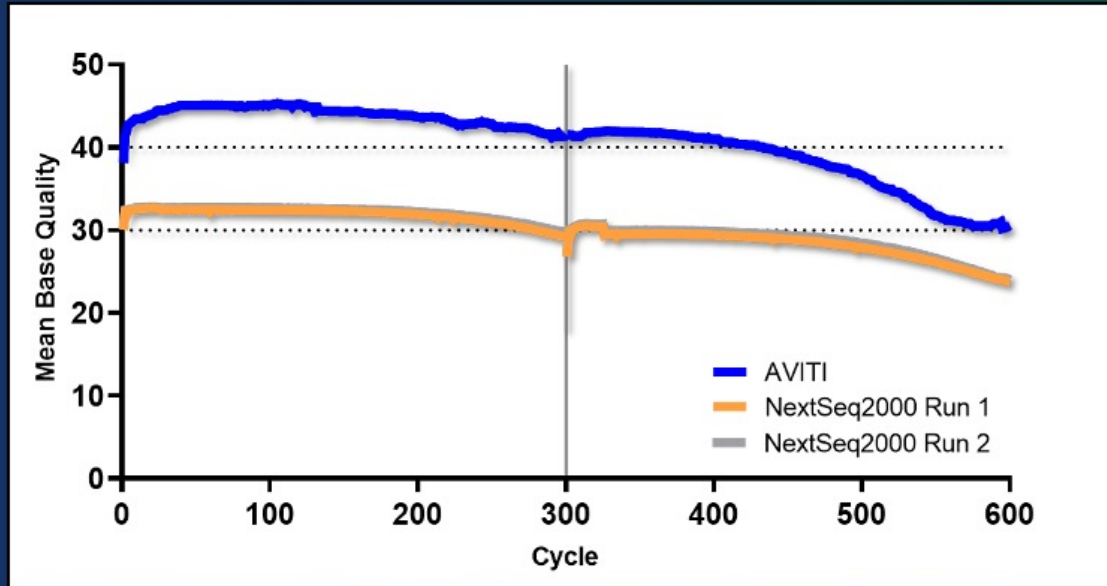
Andrew Carroll¹, Alexey Kolesnikov¹, Daniel E. Cook¹, Lucas Brambrink¹, Kelly N. Wiseman², Sophie M. Billings², Semyon Kruglyak², Bryan R. Lajoie², June Zhao², Shawn E. Levy², Cory Y. McLean¹, Kishwar Shafin¹, Maria Nattestad¹, Pi-Chuan Chang¹

1. Google LLC, Mountain View CA, USA

2. Element Biosciences, San Diego, CA, USA

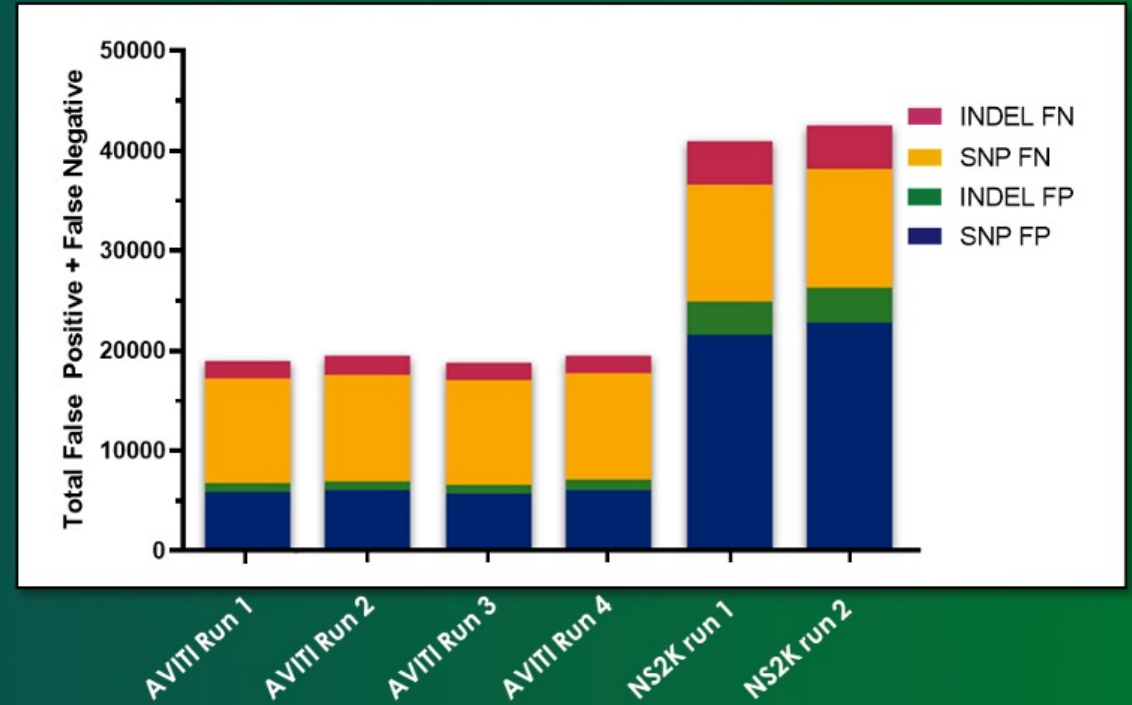
AVITI 2 x 300 Kit provides leading data quality

End-to-end Read Quality



Superior Q-values throughout the length of reads with an average ~10x increase in base call accuracy

Variant-calling Accuracy



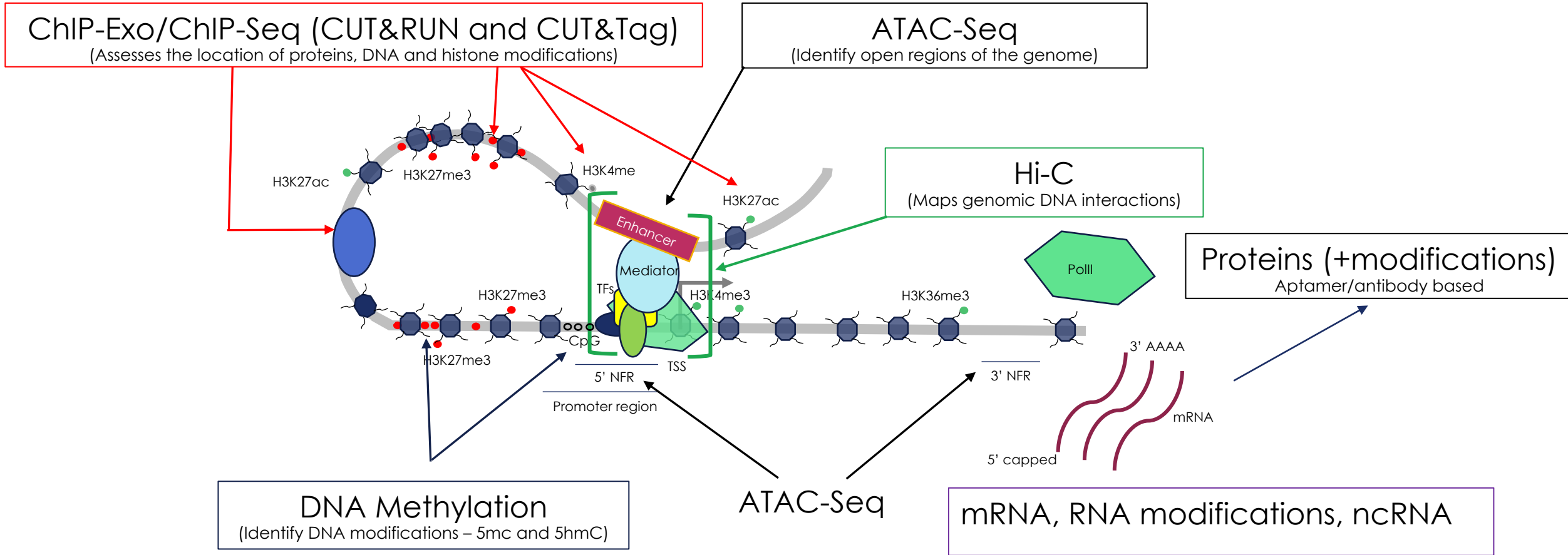
Greater than 50% reduction FP/FN rate with significantly higher SNP accuracy

PCR-free Elevate and Illumina fragment libraries for HG001 human control DNA generated using standard protocols. Elevate library sequenced on four separate runs at Element Biosciences; Illumina library sequenced twice via service provider. QC metrics from Illumina runs passed or exceeded specifications. Q values processed using GATK BaseRecalibrator and mean value across replicates plotted across paired reads for both platforms. Data from both platforms aligned and variant-calling performed using Google DeepVariant pipeline. Total errors plotted and binned by error type.

Applications



Approaches to investigate mechanisms of gene regulation

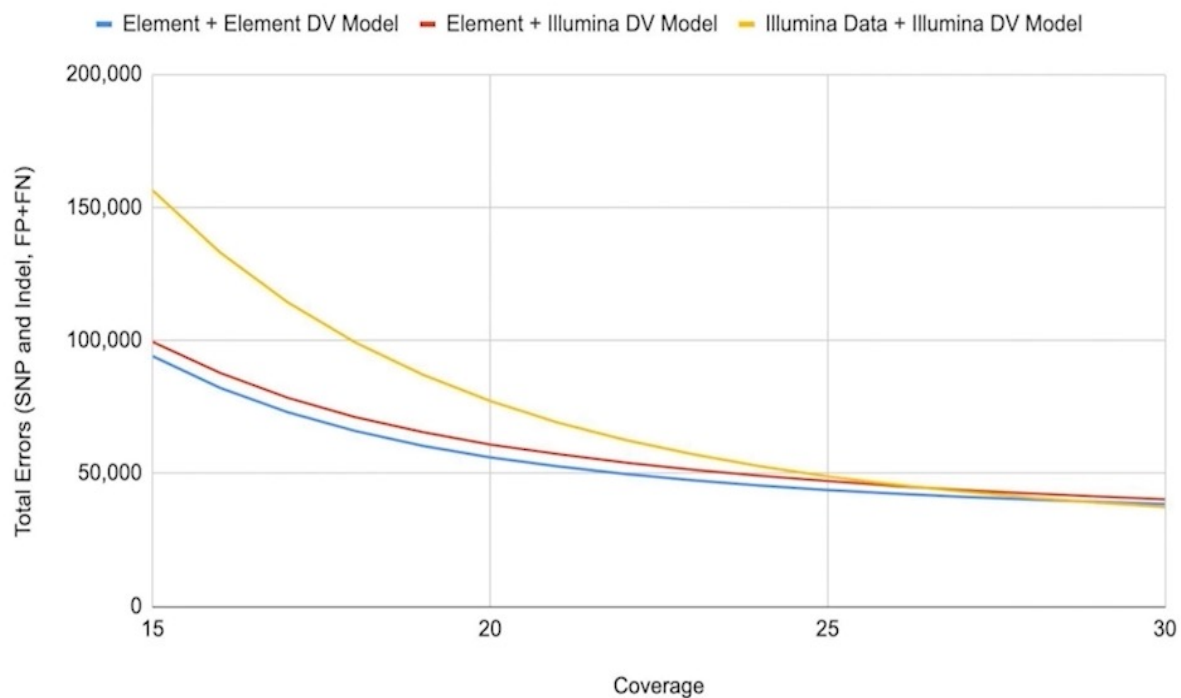


Combined with WGS and Immune profiling, can lead to better understanding of disease mechanisms

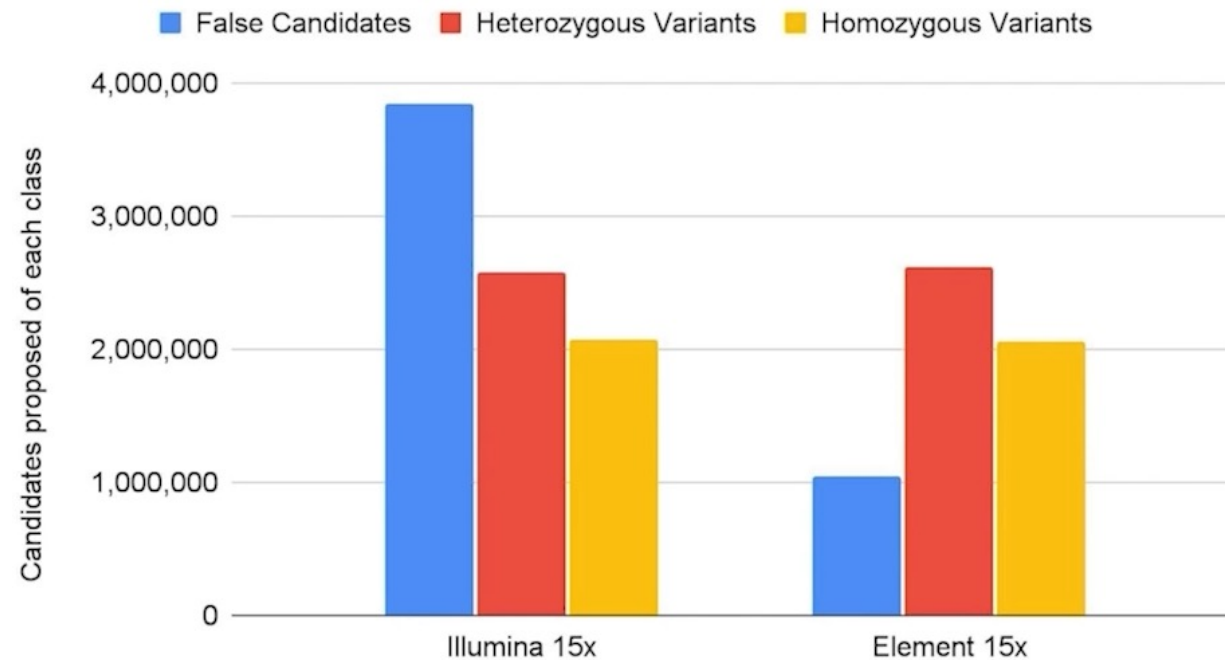
Benchmarking HG005 across coverage

AVITI produces better candidates

Total errors (SNP + Indel) as a function of coverage (HG005 full genome)



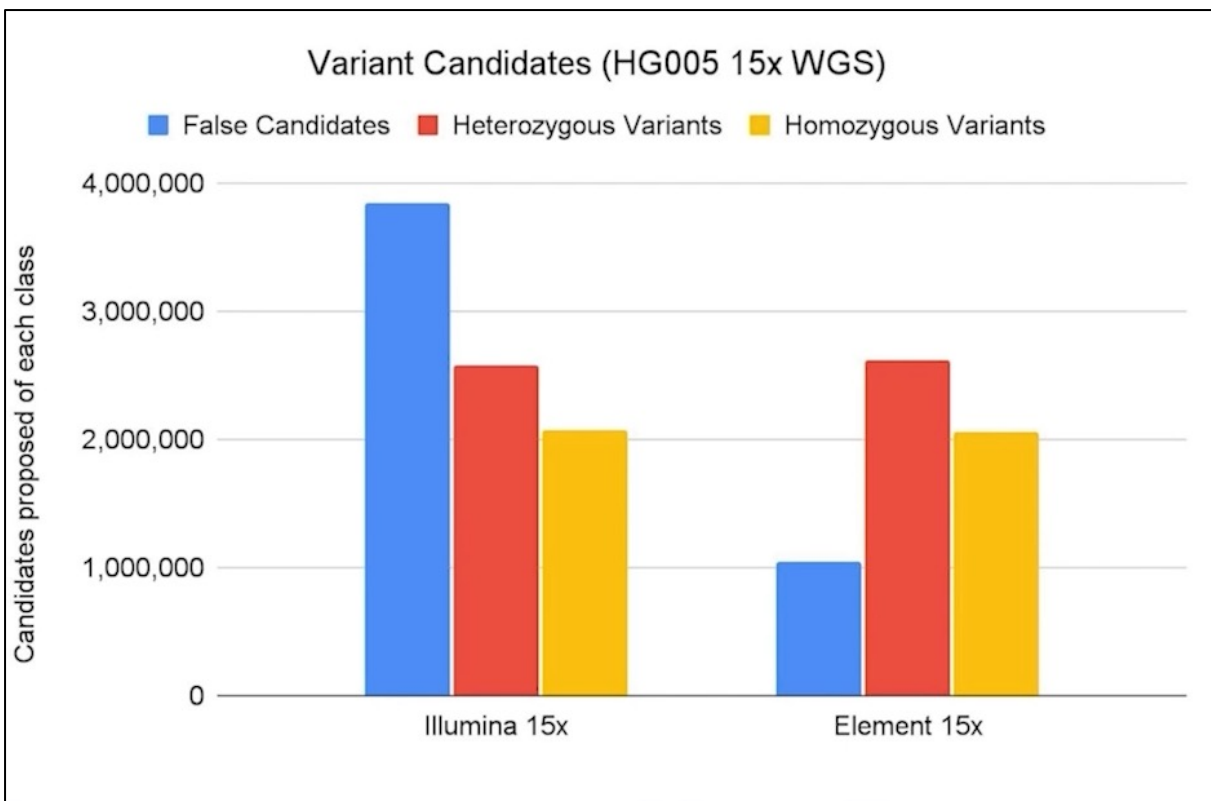
Variant Candidates (HG005 15x WGS)



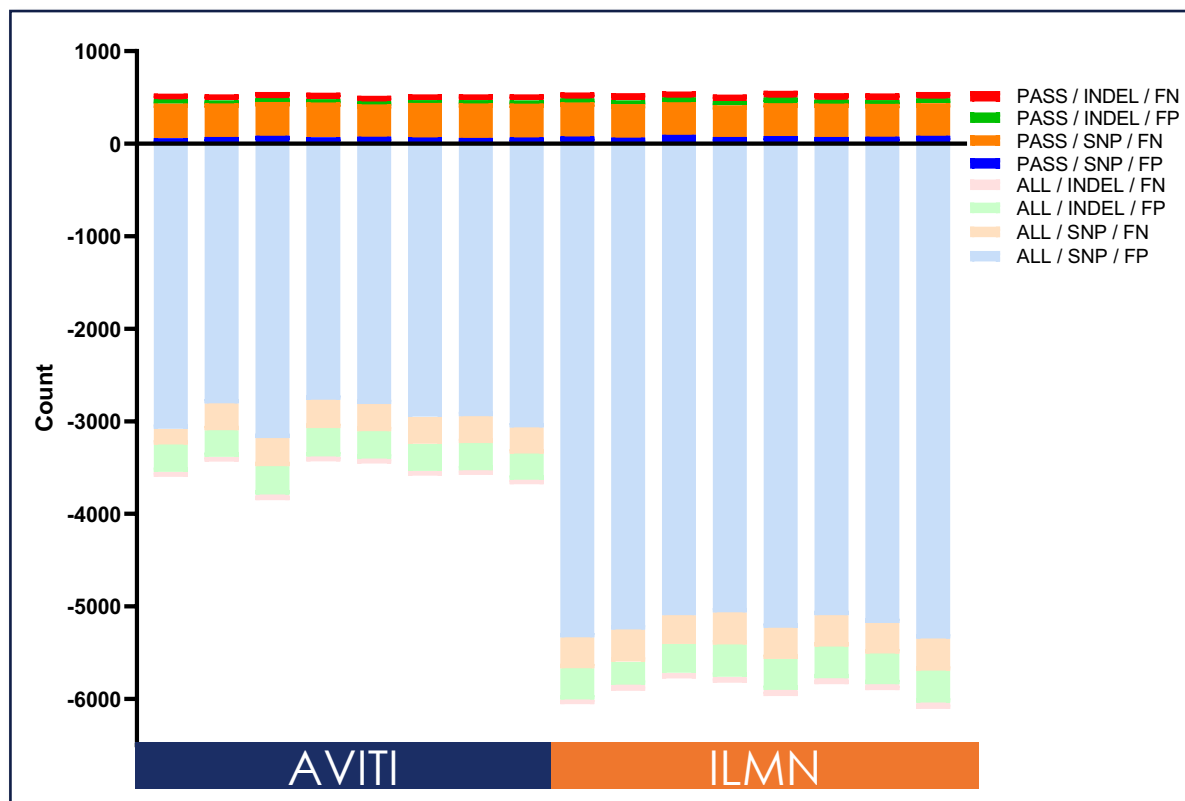
Benchmarking HG005 across coverage

AVITI produces better candidates

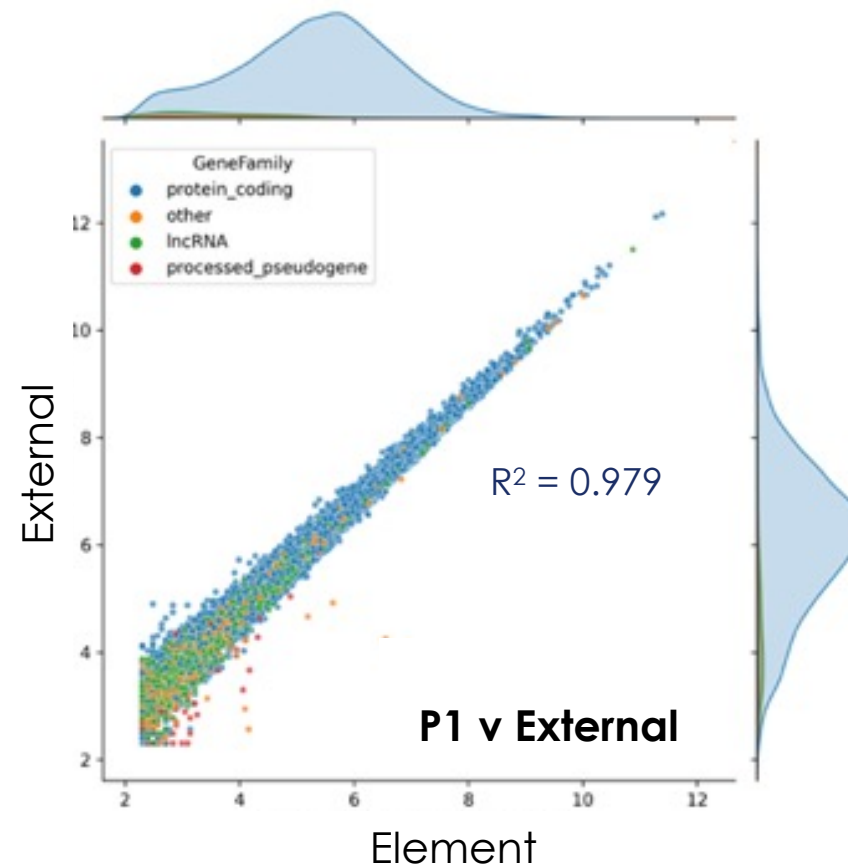
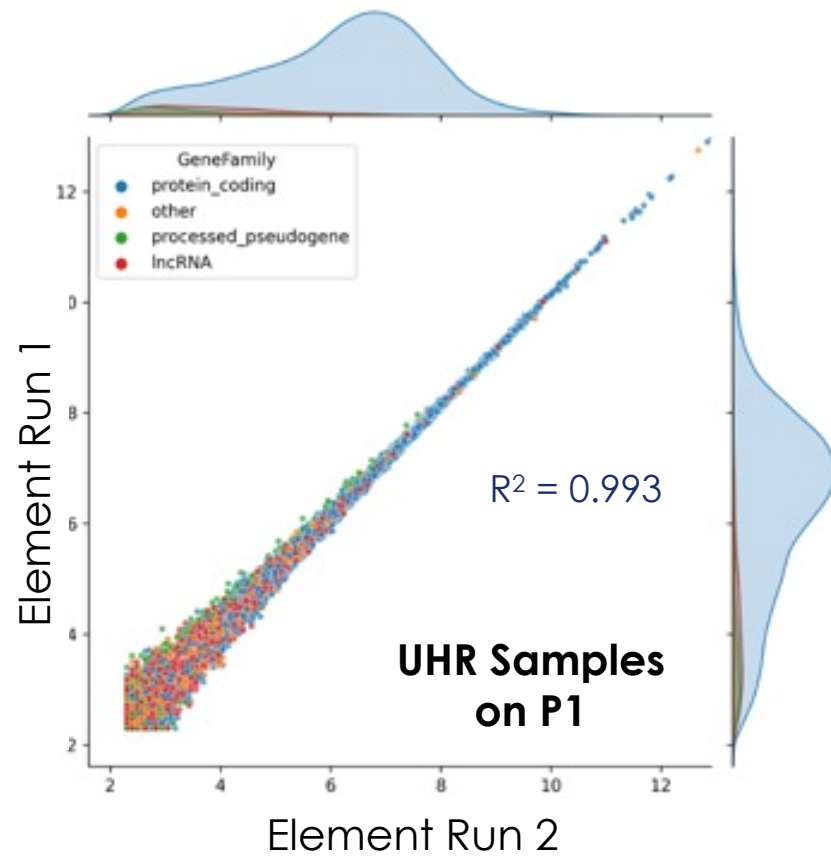
Variant Candidates (HG005 15x WGS)



Twist exome panel PASS vs ALL Candidate SNP & INDEL



Element bulk RNA sequencing produces data that is replicable and consistent



Sample-to-sample:
target $R^2 > 98\%$
actual $R^2 > 99.3\%$,

Platform-to-platform:
target $R^2 > 95\%$
actual $R^2 > 97.9\%$

Element bulk RNA sequencing produces better data

VIB Nucleomics Core – Leuven, Belgium

Experimental design

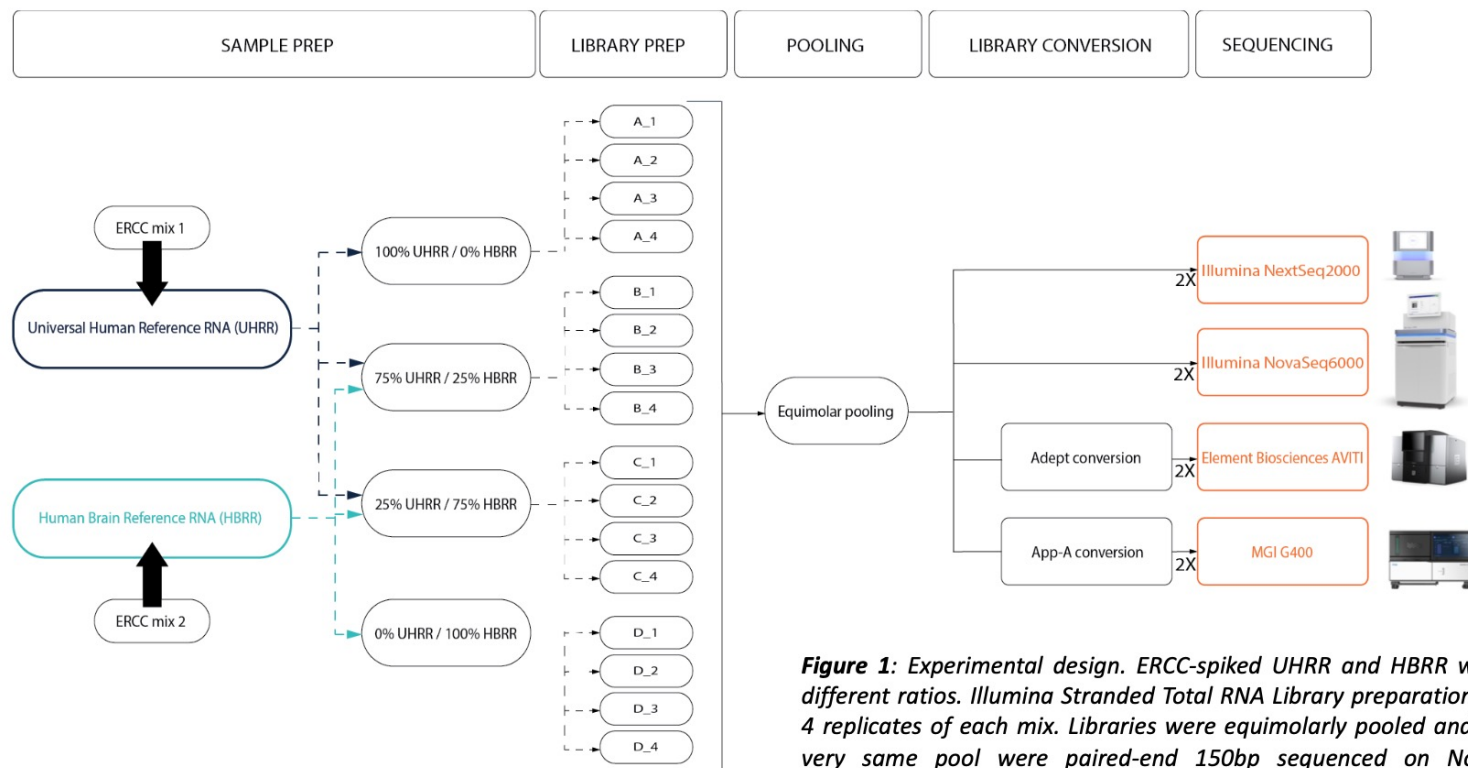


Figure 1: Experimental design. ERCC-spiked UHRR and HBRR were mixed at 4 different ratios. Illumina Stranded Total RNA Library preparation was applied to 4 replicates of each mix. Libraries were equimolarly pooled and aliquots of the very same pool were paired-end 150bp sequenced on NovaSeq6000 SP, NextSeq2000 P3, AVITI, and G400 FCL. Conversion steps were introduced following instructions by the providers to make the pool compatible with AVITI and G400 sequencing.

Quality scores

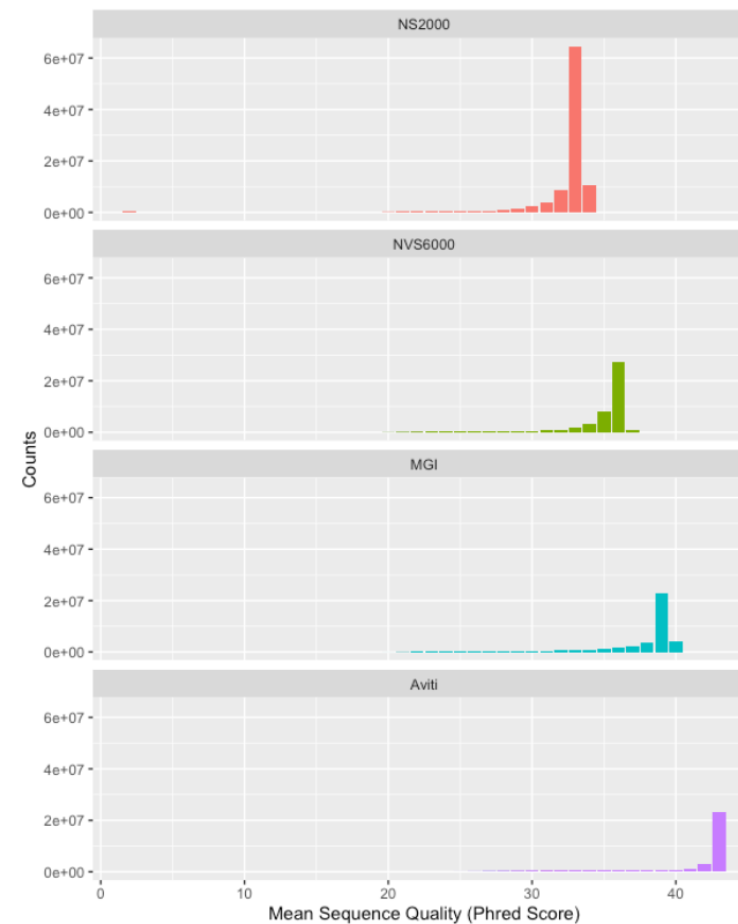
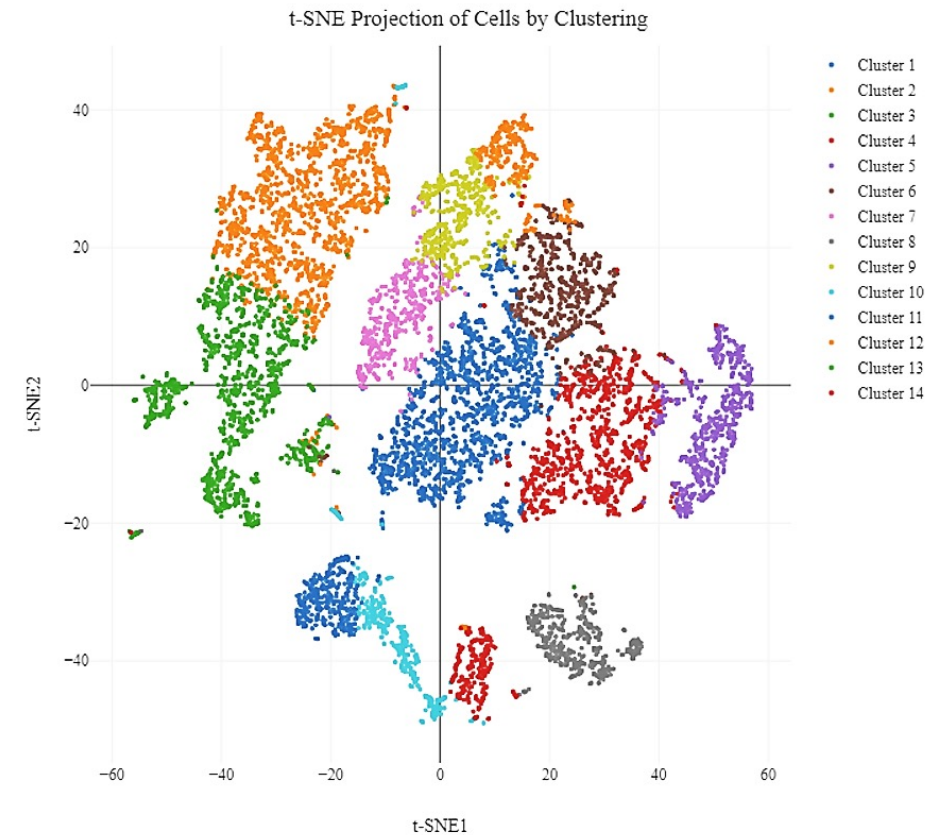


Figure 4: Read count versus mean Q-score of platforms

Element is a certified 10X genomics compatible partner

10K and 1K Human PBMC Reference from 10x Genomics

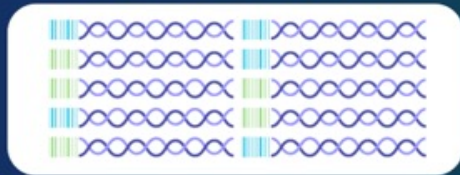
10X Cellranger Count Metrics (v7.0)	CPP Expectation	AVITI 10k cells	AVITI 1k cells
Valid Barcodes	>90%	97.5%	97.5%
Reads mapped confidently to Exonic Regions	>50%	53.0%	53.8%
Reads mapped confidently to Transcriptome	>40%	74.7%	77.8%
Fraction Reads in cells	>80%	95.5%	92.6%
Q30 bases in barcode	>85%	99.5%	99.5%
Q30 bases in RNA read	>75%	98.6%	98.8%
Mean Reads per cell	>50,000	61,326	68,766
Median Genes per cell	>1700	2,910	2,951
Estimated number of cells	+/- 20%	8,513	922



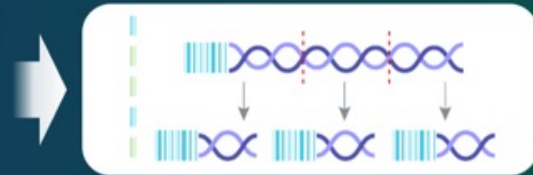
Sequencing data available for download on our website: www.elementbiosciences.com

LoopSeq™: On-demand access to long reads with AVITI

Leveraging a unique library prep chemistry, LoopSeq™ enables creation of assembled reads greater than 5Kb in length



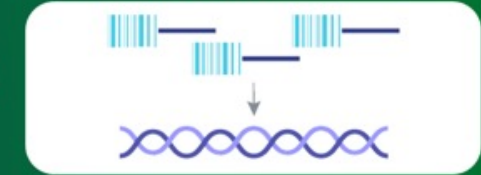
Barcode and Amplify



Distribute and Prep



Sequence



Reassemble

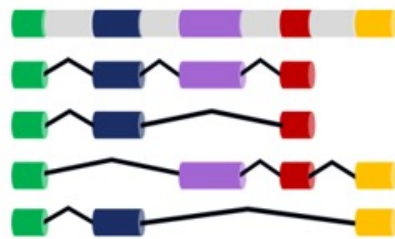
Key Applications

16S/18S Full-length Sequencing



Gain species-level resolution from complex communities

Isoform Sequencing



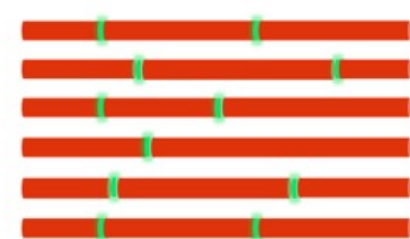
Uncover gene expression at the isoform level

Immune Repertoire Sequencing



Explore full-length VDJ sequences with isotype information

Long Amplicon Phasing



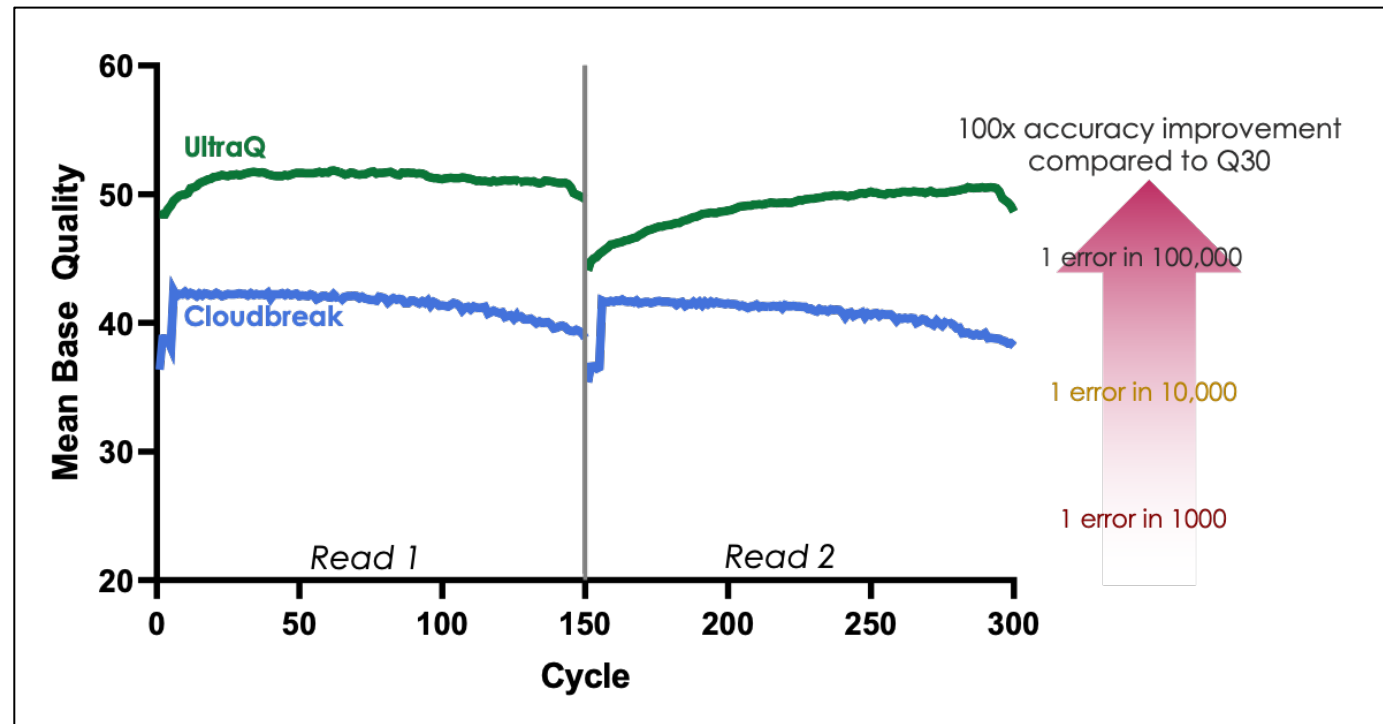
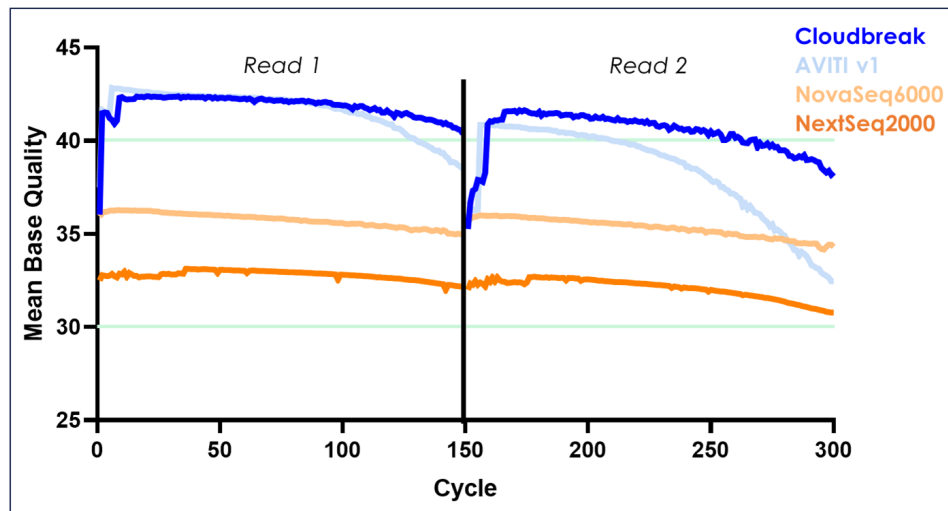
Phase variants in rapidly evolving populations and study true haplotypes

Targeted Sequencing for ACMG/PGx/CMRG genes, off-target assessment of CRISPR, RNA isoform discovery

Upcoming Innovations



Improved accuracy increases confidence in variant calling



UltraQ: High-Quality Kit
>70% Q50; coming H1 '2024

- Reduced coverage sequencing
- Identification of low frequency alleles
- Improvements to the reference genome
 - HG002 "Q100" project



bioRxiv

THE PREPRINT SERVER FOR BIOLOGY

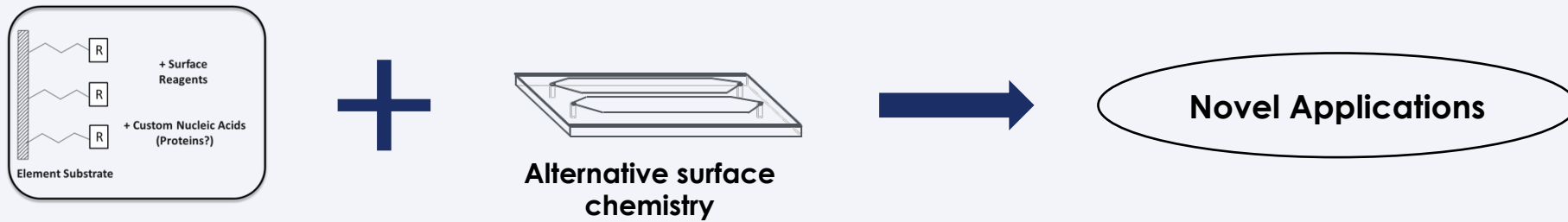
Characterizing and addressing error modes to improve sequencing accuracy

Semyon Kruglyak¹, Andrew Altomare¹, Mark Ambroso¹, Vivian Dien¹, Bryan Lajoie¹, Kelly N. Wiseman¹, Shawn Levy¹, and Matthew Kellinger¹

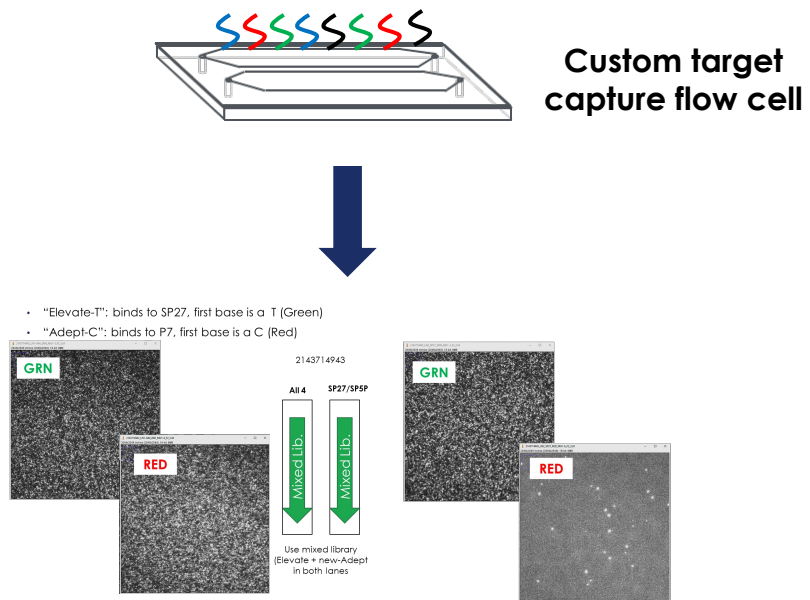
¹Element Biosciences, San Diego, CA

[Access here](#)

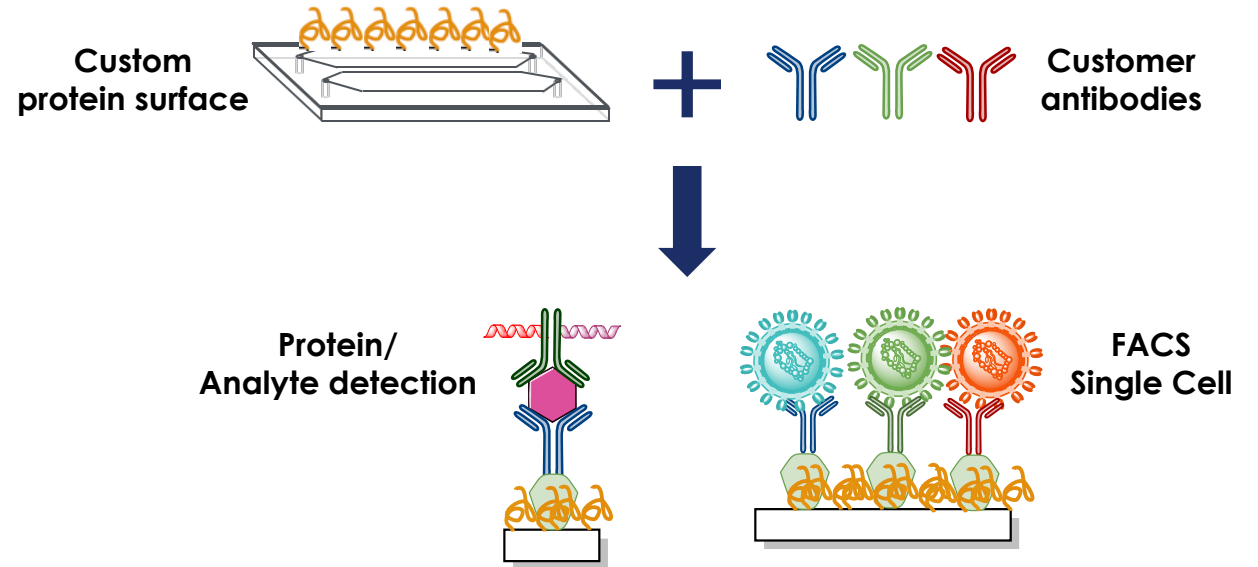
AVITI surface chemistry can be adapted to create application-specific flow cells



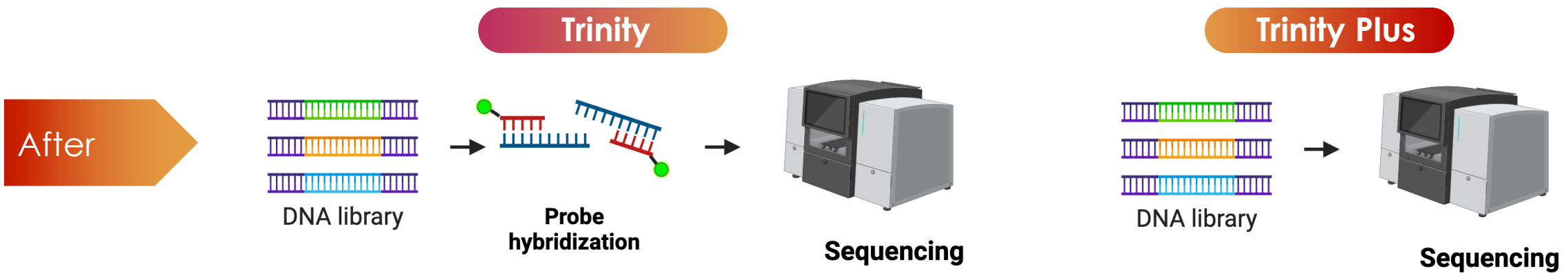
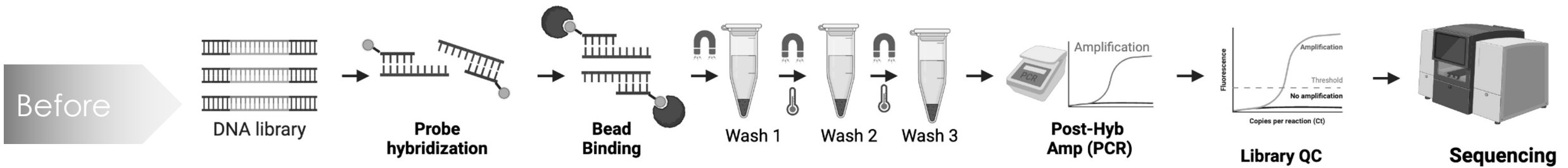
Target Enrichment Sequencing



Protein or Cell Capture



Trinity: On-flow cell targeted sequencing

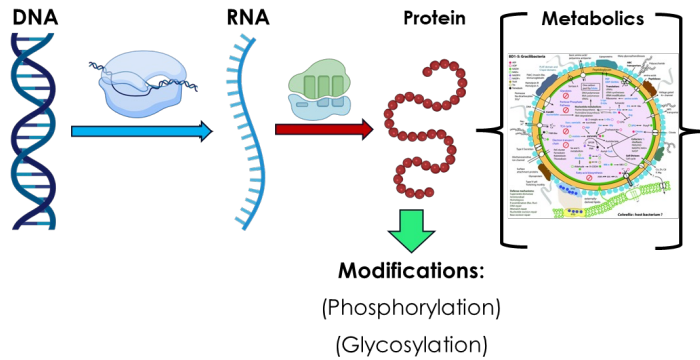


- Lower sample input
- Lower bait requirements and improved performance
- Minimal hand-on time (No bead handling and post-hybridization PCR)
- Coming Q3 '2024

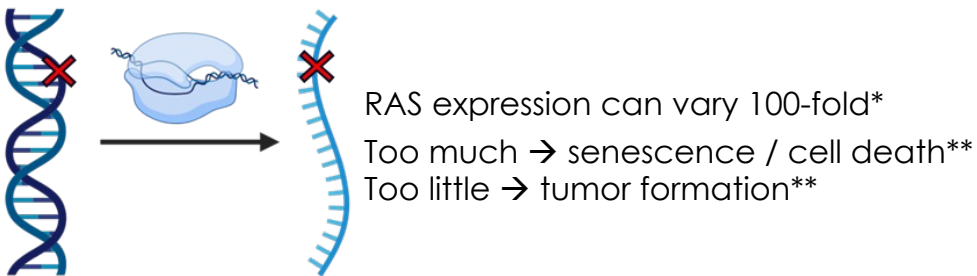
Critical Need: understand the rules that govern biology's circuits

Systems Biology assays must identify, quantify, and map multiple biological pieces at any given time

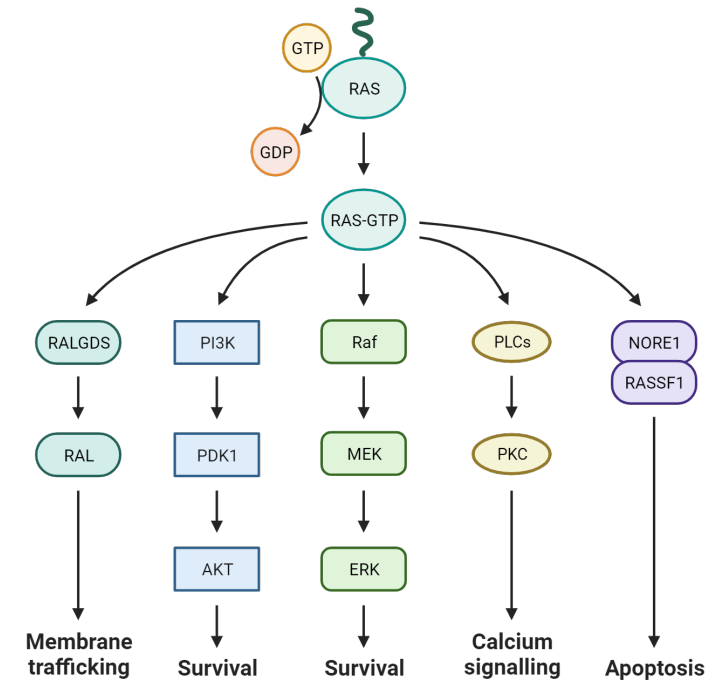
A single cell has
30B + functional molecules



19% of cancers have a
RAS mutation*



Biology's complex circuits



*Prior, IA, et al., *Cancer Res* (2020) 80 (14): 2969–2974.

**Sarkisian, CJ et al, *Nat. Cell. Biol.*, (2007) 9(50), 493.

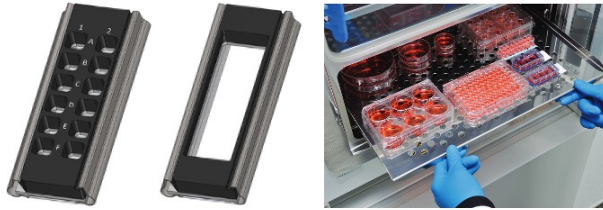
Teton™: library prep-free, system's biology multiomic assay

Coming H2 '2024

30-minute hands on time

24-hour experiment turnaround time

Step 1: Culture/Treat



Step 2: Wash/Fix/Perm

Step 3: Assemble

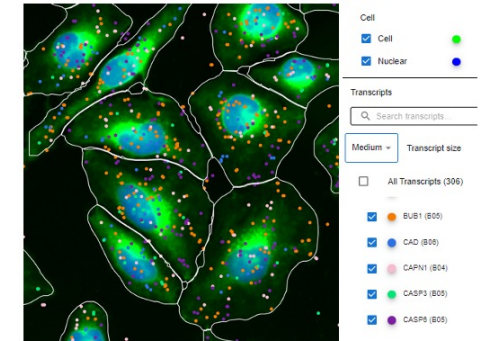


AVITI²⁴ (Load FC and Cartridge)



Analysis

Element Biosciences CytoDB



Teton Flow Cell

- Step 1: Cell Culture/Capture
- Step 2: Wash/Fix/Perm
- Step 3: Assemble

Teton Reagent Cartridge

- Cell point, RNA, Protein
- Phosphorylation detection
- In Vitro ABC 3D Sequencing

ElemBio Cloud

- AVITI²⁴ performs analysis and quant.
- Open data format

Contact us:

Scott Langwith (Account Manager)
scott.langwith@elembio.com

Bill Broach, PhD (FAS)
bill.broach@elembio.com

Solomon Hailu, PhD, MSc (ATS)
solomon.hailu@elembio.com

