

# Accelerate your breeding program by accessing the full promise of the **NGS revolution**

Reap the benefits of genome-wide, higher resolution genomic selection data with low cost per sample, scalable genotyping by sequencing.

**With low run costs, the Element AVITI™ system can help even moderate throughput labs make the leap to genotyping by low-pass sequencing.**

- Combine trait selection and variant discovery in one easily operationalized, scalable assay.
- Simplify lab operations by consolidating assays onto one platform.
- Start multiple runs daily with two fully independent 300 Gb/1 billion read flow cells.
- Leverage low run costs of \$2–5 per Gb or \$0.6–1 per million reads without compromising turnaround time.
- Access the full suite of genomics applications.



## LOW PASS SEQUENCING

Leverage markers across the entire genome for simultaneous trait selection and variant discovery.



## SINGLE CELL/ RNA SEQUENCING

Understand the impact of genomics changes by quantifying changes in gene expression.



## METAGENOMICS

Understand the impact of microbial communities living in, on or around your species of interest.



## TARGETED SEQUENCING

Focus sequencing on critical genes or supplement low-pass genotyping data with key genetic markers.

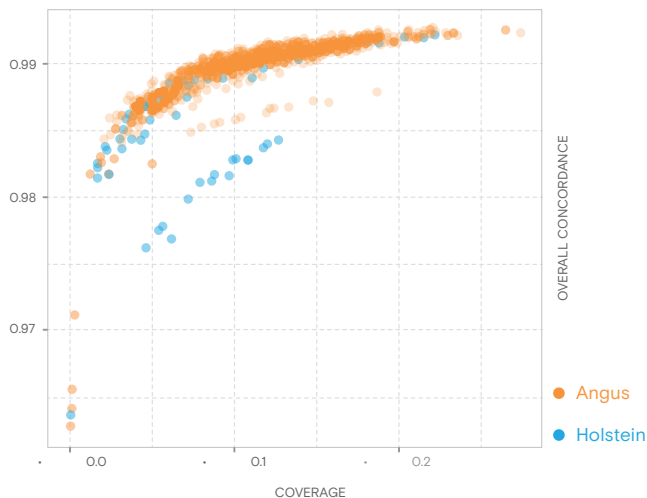


“AVITI has enabled a rapid evolution in our approach to assay development and service work. We are no longer constrained by the cost of coverage, giving us the freedom to consider methods that may require higher read depth per sample and facilitating faster turnaround time on projects without sacrificing quality and cost to our customers.”

– Adam Majot, PhD, Principal Scientist, Research & Development, AgriPlex Genomics.

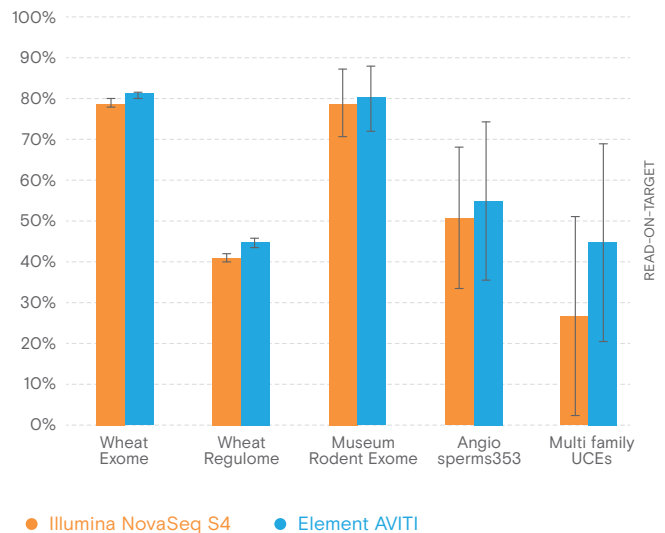
## High accuracy enables ultra-low pass

- 1,536 uniquely indexed samples were sequenced to a depth of ~0.1x coverage for ~\$2.20 / sample in sequencing costs.<sup>1</sup>
- 70 million sites imputed with Gencove pipeline.
- Overall concordance between calls at 0.1x coverage and a 0.5x coverage reference data set was nearly 99%.



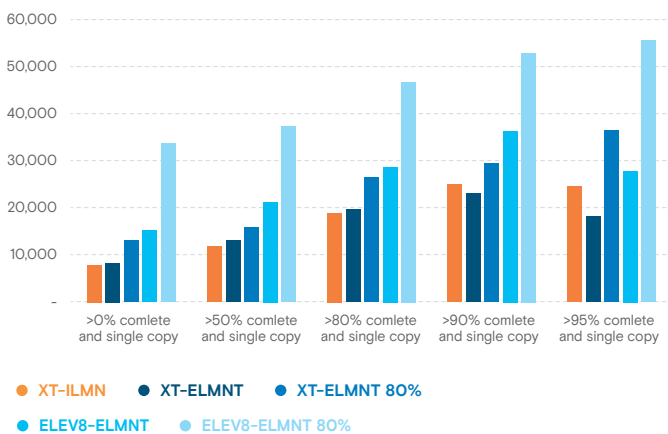
## Target capture with validated partners

- Target capture sequencing with Daicel Arbor myBaits achieves high on-target rates.<sup>2</sup>
- Determine insertion sites or flank sequence variable regions.
- Explore gene family and isoform diversity.



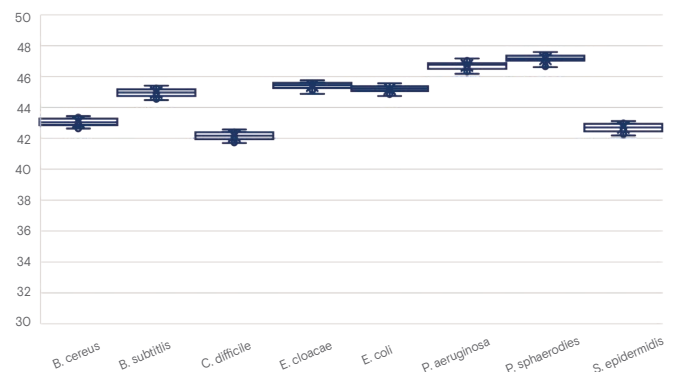
## High performance metagenome sequencing

- Generate 4x more MAGs at 95% or greater completeness.<sup>3</sup>
- Increase N50 by 1.8x compared to legacy sequencing.<sup>3</sup>
- Industry leading 2x300 accuracy for 16S sequencing



## Affordable microbial WGS, at any scale

- 384 multiplexed samples were aligned against the ATCC reference for each sample.<sup>4</sup>
- All replicates had a mean quality score >40.
- Low cost / Gb and range of kit sizes enables microbial WGS for ~\$37 – \$5 / per isolate in sequencing costs, from 24- 384-plex.



### REFERENCES

- Hoff, J., et al. 2023. Imputation accuracy of cattle in ultra-low pass whole genome sequencing. Poster presentation, AGBT Ag, San Antonio, TX.
- Devault, A., et al. 2023. A universal targeted sequencing system for any high-throughput sequencing platform. Poster presentation, PAG30, San Diego, CA.
- Levy, S. 2023. "Avidity-based sequencing improves sensitivity and detection in metagenomic analysis." Oral presentation, AGBT, Hollywood, FL.
- Hanek, A., et al. 2022. Scalable Transposase-based Multiplexed Library Prep on the Element AVITI™ System with plexWell™. Accuracy plot generated with the same data as the application note.

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