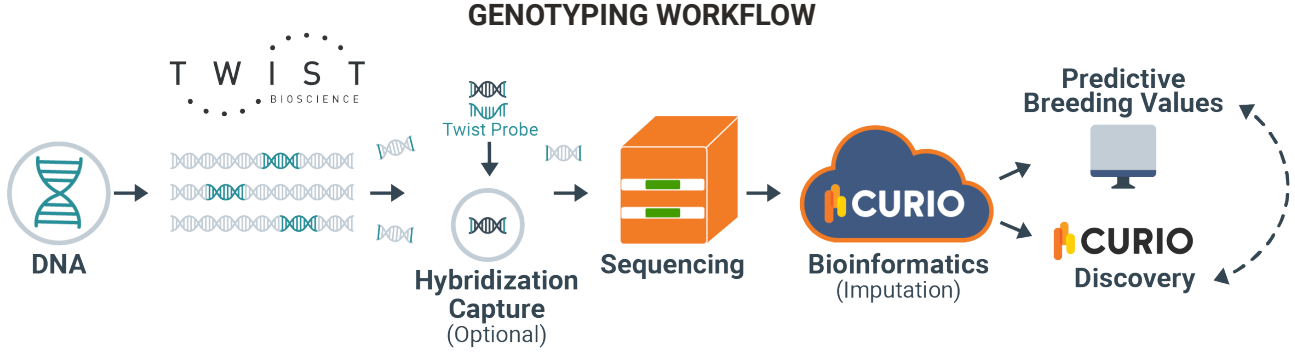
Complete and Cost-effective Agrigenomics Genotyping Across Large Breeding Populations

Twist Bioscience and Curio Genomics have partnered to deliver a powerful agrigenomics sequencing solution that combines high-quality data generation with cutting-edge bioinformatics for rapid and precise analysis of large and complex genomic datasets.

Scale your agrigenomics research with Twist's FlexPrep™ UHT Library Preparation Kit for low pass sequencing and Curio Genomics for streamlined analysis. Twist's flexible library prep integrates seamlessly with CURIO™, which offers high-throughput processing and efficient imputation, enabling cost-effective genotyping across large populations.

Twist's high-throughput library preparation solution integrates sample normalization with robust sample conversion to generate vast amounts of high-quality data. Interpreting this data into actionable insights requires an advanced bioinformatics solution for fast and accurate interpretation. CURIO™ meets this need by providing real-time data processing, variant calling, and imputation.

GENOTYPING WORKFLOW



The integrated Twist and Curio workflow provides seamless sequencing and analysis, optimizing efficiency for large-scale agrigenomics projects.

TWIST AND CURIO SOLUTION BENEFITS

- **Accelerates data processing and collaboration** – Intuitive, integrated workflow streamlines sequencing data analysis and visualization.
- **Delivers real-time insights** – High-speed data transfer enables immediate variant calling, imputation, and QC.
- **Unifies microarray and NGS data** – Seamlessly integrates legacy datasets with Twist-supported NGS data for harmonized analysis.
- **Provides a validated migration path** – A proven framework ensures a cost-effective transition from microarrays to NGS.
- **Enhances low-pass sequencing accuracy** – Leverages advanced statistical models to maximize imputation precision.
- **Scales effortlessly for large projects** – Designed to handle multi-petabyte datasets from highly multiplexed library prep workflows, making it ideal for breeding programs and research consortia.

TWIST AND CURIO WORKFLOW OPTIONS

Whether you're processing whole genome sequencing, targeted NGS genotyping, or imputation, Curio Genomics and Twist provide comprehensive support. We also assist with building and iterating reference panels for imputation, when needed.

PROVEN PERFORMANCE: Twist Capture Panel vs 70K Bovine Microarray

Curio Genomics' analysis demonstrates a 1:1 comparison of genotyping accuracy between Twist's NGS-based method and microarrays, confirming comparable performance across three different samples.

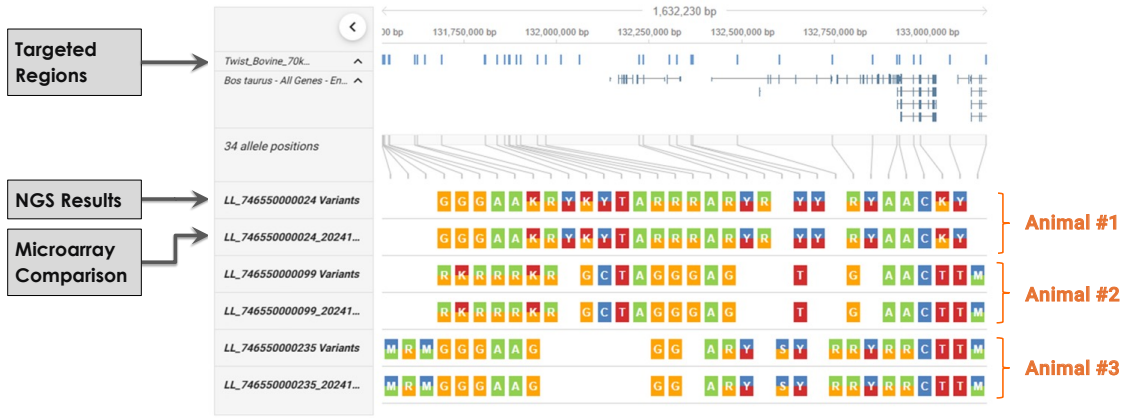


Figure 1. Microarray genotype data simultaneously visualized alongside the NGS-based genotype results within the CURIO platform for three different animals.

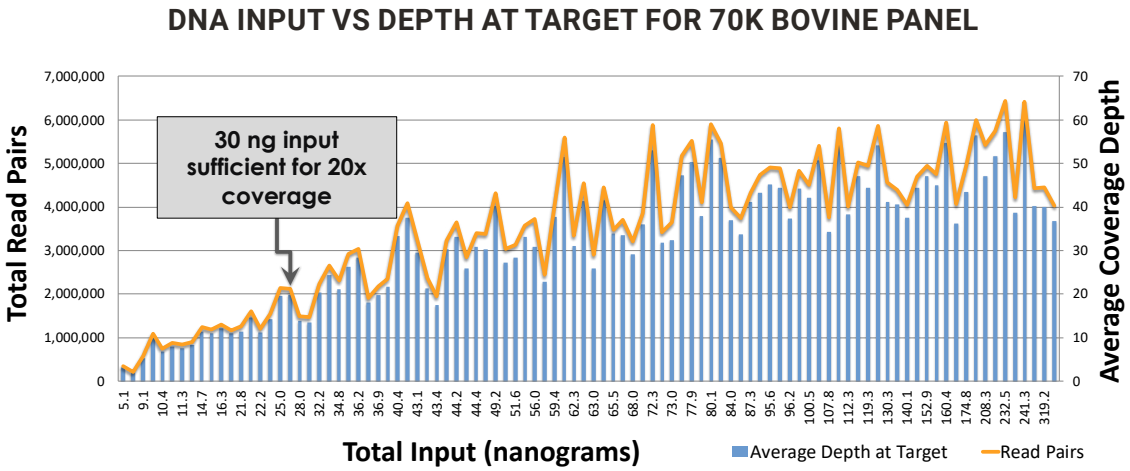


Figure 2. 96 bovine samples were prepared using different amounts of DNA input, and then the average coverage depth of the targeted regions (i.e. of the 70K bovine panel) was measured. A minimum of 30 nanograms consistently provided for 20x+ coverage at the targeted regions.

With the decreasing costs of sequencing and the ability to quickly process data at scale, the industry is shifting toward sequencing-based solutions for high-throughput genotyping. Twist's FlexPrep™ UHT Library Preparation Kit offers a cost-effective and scalable option for incorporating NGS into trait mapping or breeding programs.

By combining Twist Bioscience's advanced library prep technology with Curio Genomics' powerful analysis platform, researchers can achieve unmatched efficiency, accuracy, and scalability in agrigenomics research.

Twist and Curio Genomics products are for research use only. Not for use in diagnostic procedures.