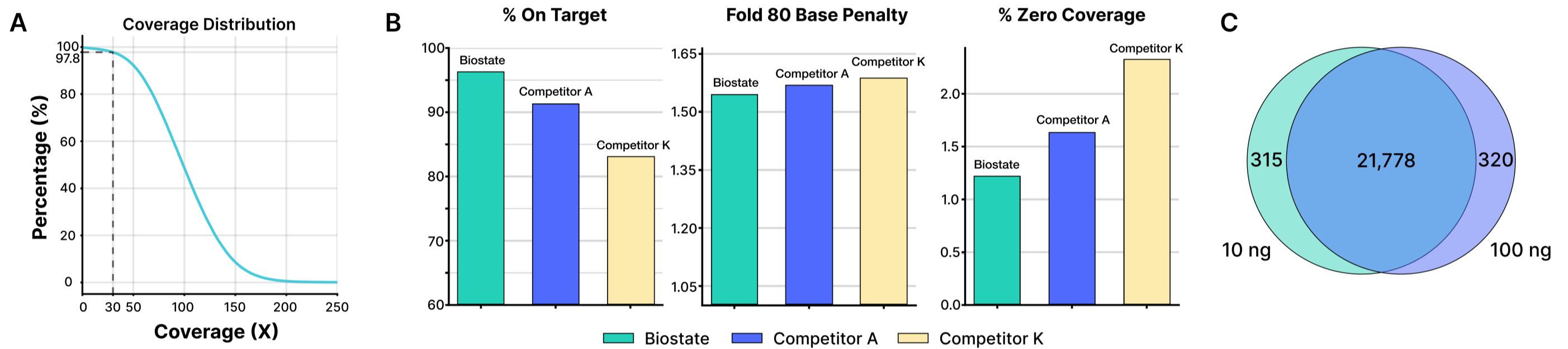


Affordable High-Performance Whole Exome Sequencing

Whole exome sequencing (WES) is the dominant method for identifying human gene mutations that are causative and correlative for disease. Current WES analyses services are expensive and incomplete, with some gene exons covered at essentially zero depth. Biostate's **patented BIRT and MARE technologies** dramatically improve both the affordability and the quality of WES. Furthermore, Biostate's proprietary **K-Dense AI** allows deep analysis of WES data using a conversational interface.

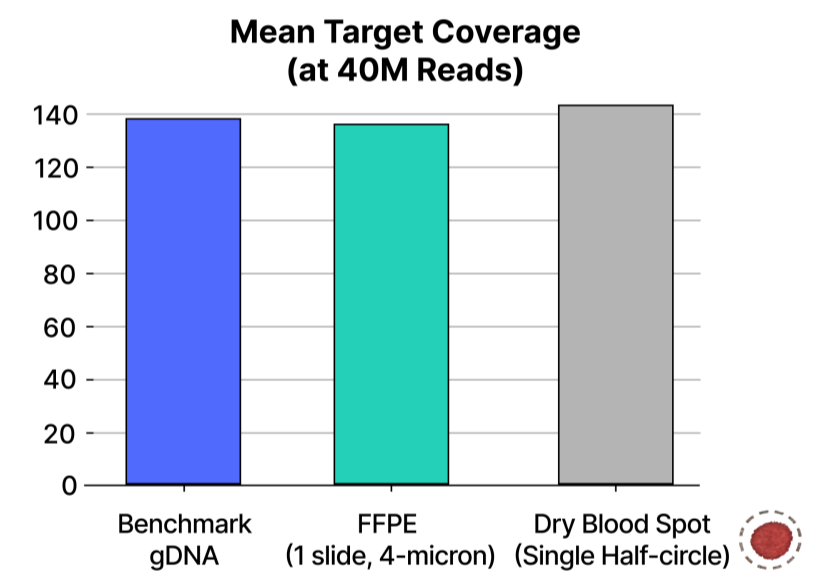
Optimized Chemistry Delivers Superior Performance

While most WES providers guarantee raw sequencing output, true value depends on data quality. Poor coverage uniformity and high duplication rates can undermine variant detection at critical loci. Biostate's optimized workflow demonstrates exceptional performance across key metrics (Figure 1). Our platform achieves rapid coverage convergence with >95% of bases covered with > 30X range (mean = 100X), maintains a superior on-target rate of ~96%, and minimizes zero-coverage regions to just 1.2%, significantly outperforming leading competitors. The Fold 80 Base Penalty of 1.52 indicates exceptional uniformity, translating to 15-20% reduction in sequencing costs while maintaining diagnostic quality. With this high-quality library performance, our WES platform demonstrates robust variant reproducibility using genomic DNA inputs as low as 10 ng, achieving 99% concordance with variant calls obtained from the standard 100 ng input, thereby enabling efficient sequencing of precious biological samples.



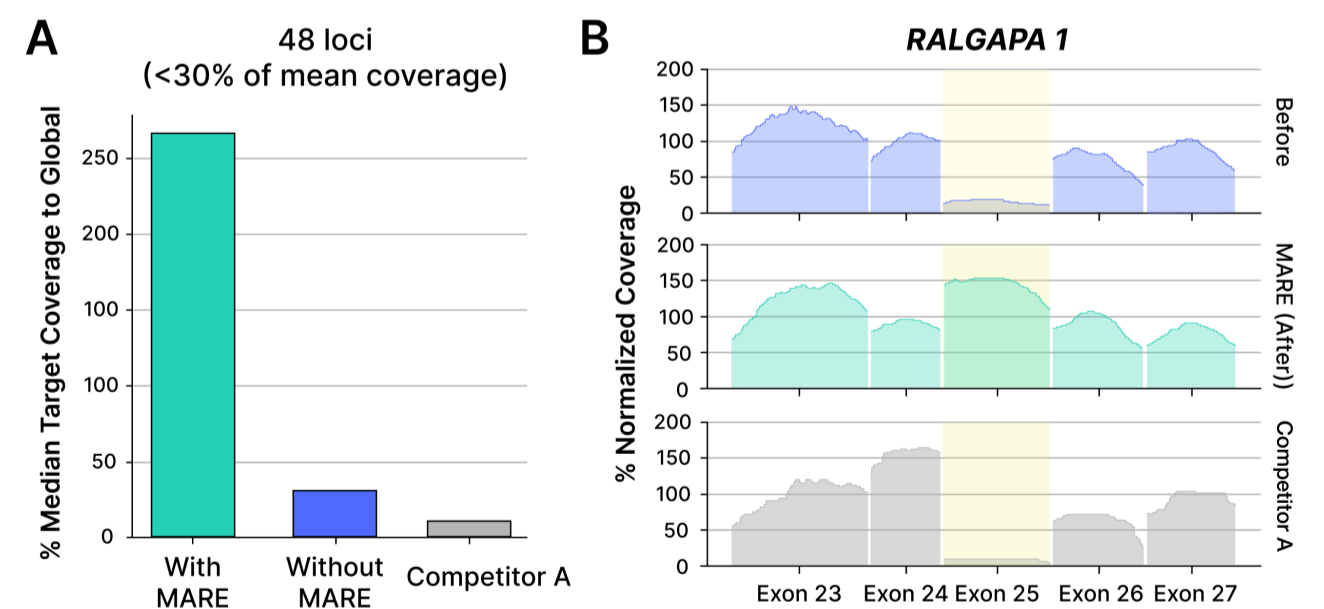
Consistent Performance Across Challenging Sample Types

Clinical samples come with diverse challenges. FFPE samples suffer from degradation, while dried blood spots offer limited quantities. The good news is that Biostate's platform delivers remarkably consistent mean target coverage of approximately 140X at 40 million reads across a single 4-micron FFPE slide, a single half-circle dried blood spot, or benchmark genomic DNA. (Figure 2). This consistency enables confident variant detection regardless of sample source and supports reliable somatic variant detection at allele frequencies as low as 5%, meeting clinical diagnostic requirements even from severely degraded materials.



MARE Technology Rescues Difficult Regions

Even with advances in probe design, exonic regions with extreme GC content remain systematically underrepresented in standard WES workflows. Our **Multiplexed Amplification to Rescue Enrichment (MARE)** technology dramatically improves coverage of these challenging regions. MARE achieves approximately 260% of median target coverage compared to just 30% for Competitor A and less than 10% for Competitor B (Figure 3A). This enhancement holds true across specific challenging exons such as *RALGAPA1* exon 25, where MARE maintains normalized coverage above 150% while competitors fail to exceed 15% (Figure 3B). The MARE target panel can be customized for specific genes of interest, ensuring comprehensive coverage for critical diagnostic regions.



Industry-Leading Pricing

Our proprietary BIRT technology streamlines library preparation and multiplexing, enabling whole exome sequencing starting at **\$125 per sample**. This breakthrough pricing, combined with our enhanced performance, makes large-scale genomics programs accessible where competitors typically charge \$250 to \$500 for standard WES.

Bioinformatic analysis of 10Gb+ FASTQ data files can be complex and error-prone. Biostate's unique, state-of-the-art **K-Dense AI** allows you to "talk to your WES data" conversationally. By leveraging and integrating over 16,000 software and bioinformatics tools, **K-Dense outperforms GPT-5** and other large language models by **over 50%**, based on public scientific and bioinformatic benchmarks.